Table S1 Statistics of the assembled scaffolds only by short-read sequences

Number of scaffolds (>100 bp)	992,801
Total length (bp)	473,904,309
Average size (bp)	477
Maximum size (bp)	343,168
N50 (bp)	13,462

Table S2　Summary of BAC clones

BAC clones (Number of ends)	20,736 (41,476)
Number of sequenced ends	34,417
Number of nuclear sequences	27,904
Number of chloroplast	6,396
Number of mitochondria	36
Number of bacteria	80
Number of vecotor	1

Table S3 Linkages of both ends of scaffolds

ID of scaffold	Size of scaffold (bp)	Name of marker	Type of DNA marker		Primer sequence		Restriction enzyme	Probe seq.	Hybridization condition		Probe seq.	Hybridization condition		Linkage
					Forward	Reverse		Saya	temperature(°C)	SSC (x)	Aokubi	temperature(°C)	SSC (x)	
Rsa1.0_00002.1	601,661	Rsa00002_5’	dCAPS	co-dominant	ATCTCATTCAGAATTATAAGACCCG	TGTATTGTGTGTGGCATCTC	Hap II	–	–	–	–	–	–	LK
		Rsa00002_3’	CAPS	dominant	GGTGACTGCATTGCTTTCG	TCCATCCTGACGTTCTCCTC	Taq I	–	–	–	–	–	–	
Rsa1.0_00004.1	253,996	Rsa00004_5’	dCAPS	dominant	ATTTGTTTTTTTATGTTAAATTTCG	GGAAAGAGTTAAGGGCACTTGT	Taq I	–	–	–	–	–	–	LK
		Rsa00004_3’	dot-blot	dominant	CGCCATAGCTGTTCTCATCA	AGCTCGACCCAGAACATGAC	–	ACTCGGATGTATCTCTC	40	0.5	ACTCGGATATATCTCTC	40	0.5	
Rsa1.0_00019.1	301,669	Rsa00019_5’	dot-blot	co-dominant	GCTCTCCTTGTTTGCTCGTC	TCCAAGCAGATCGCCTTATC	–	ACCATCATTTTATATTA	40	0.5	ACCATCATCTTATATTA	40	0.5	LK
		Rsa00019_3’	dot-blot	dominant	TGCTTACGGTTCATCTTTGG	CCCTCATTTTCTACGAACTCTC	–	ATGTAATATAAAGAGAA	35	1	ATGTAATACAAAGAGAA	40	1	
Rsa1.0_00022.1	200,461	Rsa00022_5’	CAPS	co-dominant	GAGCTGGTCCTCCAGAGAAA	GTGGTCGTTGATGTCGTGAA	Alu I	–	–	–	–	–	–	LK
		Rsa00022_3’	dot-blot	co-dominant	ACTTCTGCCGTTGTGCTTTG	CATCTGCATGGGACAAAATG	–	CCAGTCAAGGATTTCTGG	40	0.5	CCAGTCAATAATTTCTGG	40	0.5	
Rsa1.0_00023.1	194,764	Rsa00023_5’	CAPS	dominant	GCTGCCTGCAGTTAAAGGAG	TGGGCGCTAAGGAATTGTAG	Kpn I	–	–	–	–	–	–	LK
		Rsa00023_3’	dot-blot	co-dominant	GATTTTCTCCCCAAAACCTC	GCGAAGTAGCGAGAATGATG	–	GTCTAACATGTTCAGGG	40	0.5	GTCTAACACGTTCAGGG	40	0.2	
Rsa1.0_00025.1	277,312	Rsa00025_5’	CAPS	dominant	TGGTGGGAGGTTCTTTAG	TCACAGTTCATCACTCTAGG	Mun I	–	–	–	–	–	–	LK
		Rsa00025_3’	CAPS	co-dominant	ATGGGGATTTTTGATCATGG	TGGTGAATTTGGAAGGGAAG	Ssp I	–	–	–	–	–	–	
Rsa1.0_00027.1	283,362	Rsa00027_5’	dot-blot	co-dominant	GTGAATGCTAGCAGTTGTCCA	ATACAAGTCTCCGGCACCAC	–	CATTGGAAGTTTAGACA	40	0.5	CATTGGAATTTTAGACA	40	1	LK
		Rsa00027_3’	dot-blot	co-dominant	GGAAGCGGTGATGGAGATAA	TGGAAGGGTAACGGATCTTG	–	TTTATTATGTTATTACA	35	1	TTTATTATATTATTACA	35	1	
Rsa1.0_00036.1	176,186	Rsa00036_5’	CAPS	dominant	TCGAACTTACCGTCGAAACC	AAAGATCCCACATTGCAAGC	Hae III	–	–	–	–	–	–	LK
		Rsa00036_3’	dot-blot	co-dominant	CGGTGTGAAGTTGTTTGTGG	AGTGGCACTGGGAAGACAAG	–	TTAGCTTTGACTTTGAG	50	0.5	TTAGCTTTAACTTTGAG	40	0.5	
Rsa1.0_00042.1	171,507	Rsa00042_5’	dCAPS	dominant	AGAGAATGAGAGCGAAGATG	CTATAGATAAAGTTTGACCAAACTCG	Taq I	–	–	–	–	–	–	LK
		Rsa00042_3’	CAPS	dominant	CTTGGCAGAAAAATAACCTC	TGAGAGAGTTTGCGGATGTG	Xba I	–	–	–	–	–	–	
Rsa1.0_00043.1	264,937	Rsa00043_5’	dCAPS	co-dominant	GTATTTGGATCCGTTCTCG	GTTATTACCTGACAAAAGAGTGATC	Taq I	–	–	–	–	–	–	LK
		Rsa00043_3’	CAPS	dominant	GCTCATCGTGTAGCTGCTGA	AAGCCGTTCTCATGGACTTG	Xsp I	–	–	–	–	–	–	
Rsa1.0_00048.1	167,185	Rsa00048_5’	dot-blot	co-dominant	TTGGGCTTGGGATTTGATAG	ACGAAACACAACACGACCAA	–	TAACACATTAAGAAATG	40	1	TAACACATGAAGAAATG	40	1	LK
		Rsa00048_3’	dot-blot	co-dominant	ACGTGGGCTTAAACTGAACG	TCCACAACATGCCGTATCTC	–	GCCGTCATCATTGCAGT	50	1	GCCGTCATGATTGCAGT	50	1	
Rsa1.0_00065.1	454,616	Rsa00065_5’	dot-blot	co-dominant	CGCCTTTAAAAGAGCTGGTA	TTTAGACGGCTGGGATGAAG	–	ATCAATAGGTCATATTC	35	1	ATCAATAGATCATATTC	40	0.5	LK
		Rsa00065_3’	CAPS	co-dominant	GACACATGGTTCAGTGACGTG	GCCTAAGTTGGCACGTTTAAG	Alu I	–	–	–	–	–	–	
Rsa1.0_00100.1	249,232	Rsa00100_5’	SCAR	co-dominant	AGTCACGGACAACGAAATCC	TGACACCGAGAACAGCAAAG	–	–	–	–	–	–	–	LK
		Rsa00100_3’	dot-blot	co-dominant	AATGGATAGCCAACCAAACG	ACACGCATTATCGCCTTCC	–	TTACCATAGATCATTGC	35	1	TTACCATAAATCATTGC	35	1	
Rsa1.0_00123.1	325,650	Rsa00123_5’	dot-blot	dominant	CCCTCCAAATAACGAAAGAGC	AGAGAAGATCGGTCCGAAGAG	–	GCCCTAATTCACTCGCC	50	1	GCCCTAATCCACTCGCC	50	1	LK
		Rsa00123_3’	dot-blot	co-dominant	AGAGTGCCAACATTTTATTGATACC	GAGCGCGACACATAGGAAAC	–	ATGACATGGCTTATAGT	35	1	ATGACATGACTTATAGT	35	1	
Rsa1.0_00125.1	253,043	Rsa00125_5’	dot-blot	co-dominant	AGTCTTGCCTTTTTGCTCCA	AAACTCTCAGCCGTTTGGAA	–	CAATCTTCTGACCGATT	45	0.5	CAATCTTCCGACCGATT	45	0.5	LK
		Rsa00125_3’	dot-blot	co-dominant	TTCGTCAACACCAAGCATTC	TTTTGGAGCCAAGTTTCTCA	–	AGAGAACCTTTCTCTATT	40	1	AGAGAAACTTTATCTATT	50	1	
Rsa1.0_00134.1	390,219	Rsa00134_5’	CAPS	co-dominant	GTCAAAATTCCAGGAGTTCCAC	AAGGTCACCATCTCCACCAG	Mun I	–	–	–	–	–	–	LK
		Rsa00134_3’	CAPS	co-dominant	GGCGCCAATTTGATGTTAG	TCCAATTCACTGATTGCAC	Dde I	–	–	–	–	–	–	
Rsa1.0_00152.1	257,730	Rsa00152_5’	dot-blot	co-dominant	AAACCCCTCAACCGTGAAG	CGTGCACTACAAGAAAACATCG	–	CGAGGAAACCCTATTGT	50	1	CGAGGAAATCCTATTGT	40	0.5	LK
		Rsa00152_3’	dot-blot	co-dominant	GCTCGCTGCTCAGTAAGAAAA	ACGCAGGCATAGACATCAAAC	–	AGTCACAACTCGTAAGT	50	1	AGTCACAAATCGTAAGT	40	0.5	
Rsa1.0_00173.1	288,743	Rsa00173_5’	dot-blot	co-dominant	GAATCAATGGGGAATCGAAG	TTTATCGGTTCGGTTCTGGA	–	ATCGAAGACGGGTTATT	50	1	ATCGAAGATGGGTTATT	50	1	LK
		Rsa00173_3’	dCAPS	co-dominant	AGTGTTTAGTATCGTCTCTCGAGAT	TAGAGCCTCTTGGGATTTTGAG	Mbo I	–	–	–	–	–	–	
Rsa1.0_00179.1	393,324	Rsa00179_5’	dCAPS	co-dominant	GAGACACAACATACGACAAC	CTTATGGAGTTCATGCTTTGAT	Mbo I	–	–	–	–	–	–	LK
		Rsa00179_3’	dot-blot	co-dominant	AGTAACAAACGAACGCCACA	CAACGATGTGGTGAAGAACG	–	TTAGTTAATTAGTGATC	35	1	TTAGTTAAGTAGTGATC	40	1	
Rsa1.0_00215.1	201,775	Rsa00215_5’	dot-blot	co-dominant	TCCTTCTTCCAAACCACCAC	CCTTGTGGAAAACCTCCTGA	–	GCATGCCTAGAGTAGGA	50	1	GCATGCCTCGAGTAGGA	50	0.5	LK
		Rsa00215_3’	dot-blot	co-dominant	ACTGAAATGCAACTGCGATG	TGACCTTGGGAAAGATGGAG	–	GTATTGAATACACTTTCA	40	0.5	TGTATTGAACACTTTCAA	40	0.5	
Rsa1.0_00224.1	327,530	Rsa00224_5’	dot-blot	dominant	CTGGGCTTTGTGCATTTTG	GCCACATTTGTGGTTCTCCT	–	AATATGTGAGAAACCTGT	40	0.2	AATATGTGTAAAACCTGT	40	1	LK
		Rsa00224_3’	dCAPS	dominant	GCACTCTGCAGCAGCCTGG	TCCCTAAGCAGCCGGTCAAG	Taq I	–	–	–	–	–	–	
Rsa1.0_00234.1	197,060	Rsa00234_5’	CAPS	dominant	GGCAACATCACGACTCTTCA	CTTCCGAAACAGAGCGATTC	Sac I	–	–	–	–	–	–	LK
		Rsa00234_3’	CAPS	co-dominant	CATCAACGCTCTGCTCTTTG	AGAAACAAAGCACGGTGTCC	Sph I	–	–	–	–	–	–	
Rsa1.0_00238.1	193,193	Rsa00238_5’	dCAPS	co-dominant	TTCCTTGGGGGTTTTAAGTG	GATGGTCGACTTGAATGGTAG	Bgl II	–	–	–	–	–	–	LK
		Rsa00238_3’	CAPS	co-dominant	ATGTGACGGAGGTTCCTTTG	ACCGCCATATTCTCATCGTC	Hae III	–	–	–	–	–	–	
Rsa1.0_00255.1	204,967	Rsa00255_5’	dot-blot	co-dominant	AGGTGCTGAATGGTGGTCTC	CTGCAAGTAGCACGACGAAG	–	TCTTGCAAGTTTATTGA	40	0.2	TCTTGCAAATTTATTGA	40	0.5	LK
		Rsa00255_3’	CAPS	dominant	ACACGTGTCCAAAGGAAACC	CGTGGAAGCATGAATCAAGA	Alu I	–	–	–	–	–	–	
Rsa1.0_00273.1	326,186	Rsa00273_5’	dCAPS	dominant	TTCCTAAACTTTCACTTGTCCTATC	GGACTTGAGCGGTGTTTTATAG	Taq I	–	–	–	–	–	–	LK
		Rsa00273_3’	dot-blot	dominant	TTCACCTACCAGGGAAGCAG	ACCTCCTCAAAACACGTTGG	–	AGAAGACTAACTTTAGC	40	1	AGAAGACTGACTTTAGC	40	1	
Rsa1.0_00307.1	199,003	Rsa00307_5’	CAPS	co-dominant	GTATGGGAGTTGCCCAAAA	CGGAGAATCTATTTGTGTTGAG	Dra I	–	–	–	–	–	–	LK
		Rsa00307_3’	dCAPS	co-dominant	AAAGCATTTGTTTTGATGTAC	ATATTCAAACAGCAAACCTGTA	Bsp1407 I	–	–	–	–	–	–	
Rsa1.0_00344.1	191,774	Rsa00344_5’	dCAPS	co-dominant	GAATTCAACTGCTTGGACAG	CTTACCACTACAAGTTTGCTTCG	Taq I	–	–	–	–	–	–	LK

		Rsa00344_3’	CAPS	co–dominant	GCCGCTAGAGCAAACTATGG	ACCCTAACCGTGTGAGCAAG	Xsp I	–	–	–	–	–	–	
Rsa1.0_00351.1	413,096	Rsa00351_5’	CAPS	co–dominant	GAATCCTAGGGCGATCATACTG	GGGTGTGAGTGTGATTGTATGG	EcoR V	–	–	–	–	–	–	LK
		Rsa00351_3’	dot–blot	dominant	GGACACAAATGAAACCGAGAC	CAAAGTCGGATTTGGATTGC	–	AATAATCTGCATTTTTG	40	1	AATAATCTTCATTTTTG	40	1	
Rsa1.0_00387.1	495,407	Rsa00387_5’	dot–blot	co–dominant	TGCATTGTATAGGAGGCATGA	ACAGAAGCCGTTCTTTGTGG	–	GAGAACTTCAAATAGTA	40	1	GAGAACTTTAAATAGTA	40	1	LK
		Rsa00387_3’	CAPS	dominant	GCGACAAAACGAGTTCTTCC	GCAACTCACTCGCAACTCAA	Xsp I	–	–	–	–	–	–	
Rsa1.0_00427.1	189,678	Rsa00427_5’	dot–blot	co–dominant	CTTGATGCCATTGATGTTGC	AAGTGGCATGCAAGGTTAGG	–	GAATGACTGTCGTGTTT	50	1	GAATGACTTTCGTGTTT	50	1	LK
		Rsa00427_3’	CAPS	co–dominant	GAGAGTCGGCAGAAAATCCA	CGGAGCTGTTCATTCGGTA	Taq I	–	–	–	–	–	–	
Rsa1.0_00490.1	186,713	Rsa00490_5’	CAPS	co–dominant	CCAGTCTCCATTGCAGAACA	GCGAGAATCTGACCAAGAGG	Alu I	–	–	–	–	–	–	LK
		Rsa00490_3’	dot–blot	co–dominant	ATCAAACACATGGCTTGCTG	TCCACGTCCGAGTTACATTG	–	TTAAAAGAGATCTTCAG	40	1	TTAAAAGAAATCTTCAG	40	1	
Rsa1.0_00576.1	178,949	Rsa00576_5’	dot–blot	dominant	TTGCAGTTTGCACGAAAAAG	ATCGTCGACCGTGTTCTCTC	–	TTATAGGATTGCAAACA	40	0.5	TTATAGGACTGCAAACA	40	0.5	LK
		Rsa00576_3’	dot–blot	dominant	GATCTTTGCGGGTTCATTTC	TAAGAGCCAAAACCGAATCC	–	AAAAGTAACATATCAAA	35	1	AAAAGTAAAATATCAAA	35	1	
Rsa1.0_00577.1	174,827	Rsa00577_5’	dot–blot	co–dominant	CAAATCCTCACGCCACACTA	GAGAGAGCATCGGAGACACC	–	CCGATTCTATTATATTC	40	0.5	CCGATTCTGTTATATTC	40	1	LK
		Rsa00577_3’	dot–blot	co–dominant	CTTGGGGAGACAGCAAAATC	AACGCTTCGACTCTTCCTTG	–	ACTCCTCATATTGCTTG	40	1	ACTCCTCACATTGCTTG	40	0.5	
Rsa1.0_00645.1	189,716	Rsa00645_5’	dCAPS	co–dominant	CCATGTTGTGGTGTTTGGAC	CAAACCCATTCTTAGCATTCCG	Hap II	–	–	–	–	–	–	LK
		Rsa00645_3’	CAPS	co–dominant	TTTCCATGTTTGCATCTTGC	CTCGCTTGTTGGTGTTGTTG	Hinf I	–	–	–	–	–	–	
Rsa1.0_00662.1	192,183	Rsa00662_5’	CAPS	co–dominant	CCCATGGACACACCTTCTG	GGAAGCTTTCTTTGAAGATTGG	AluI	–	–	–	–	–	–	LK
		Rsa00662_3’	CAPS	co–dominant	CGACCATTGCACAGAGAGAA	TGCTCCTGCGATTGTAGTTG	Dde I	–	–	–	–	–	–	
Rsa1.0_00743.1	177,459	Rsa00743_5’	dCAPS	dominant	CATACACATGAAAACGTATCATTA	TCTTCAGCATCACCATCACC	Vsp I	–	–	–	–	–	–	LK
		Rsa00743_3’	dot–blot	co–dominant	TTGATCTGCTTGTTCTGCAAG	GAGTACCTCCTCCGGGAAAC	–	CTTAAACAACTATAACT	35	0.5	TGCTTAAACTATAACTAT	35	1	
Rsa1.0_00750.1	190,548	Rsa00750_5’	dot–blot	dominant	CAGACCCGTGCATATACACATAA	TTGCTGCATAGCTGCATACG	–	AGAATCTACACAAATAT	40	1	AGAATCTATACAAATAT	35	1	LK
		Rsa00750_3’	dot–blot	co–dominant	CCCAGCTCTACCTGTATAATTTGA	ACCCATGGACGCTCTTAGTG	–	TATCAACCAGAATAGCA	50	1	TATCAACCATAATAGCA	50	1	
Rsa1.0_00816.1	403,350	Rsa00816_5’	dot–blot	dominant	GTCTATCGCGAGCAAGGAAC	TCTCCACCTCCGTTTCAATC	–	CGGATGAGAATGGAAAG	50	0.5	CGGATGAGGATGGAAAG	50	0.5	LK
		Rsa00816_3’	CAPS	co–dominant	GGACTAAAAGCAGCGTTCCA	CCGTGCAGTTTTGTGGTAAA	Hae III	–	–	–	–	–	–	
Rsa1.0_00835.1	278,058	Rsa00835_5’	dot–blot	co–dominant	TCATATGTAACATGGTCACG	GGGATTCAAAGTTGTAGAAGC	–	ACCTAACTATCATTACT	35	1	ACCTAACTGTCATTACT	35	1	LK
		Rsa00835_3’	CAPS	co–dominant	ATGTGTTGGAAGTTGCTTCG	CATGTGAATCGACATTGACC	Hind III	–	–	–	–	–	–	
Rsa1.0_00878.1	330,303	Rsa00878_5’	dCAPS	co–dominant	ACTATTTTAGCACAAGACCGGAGC	AGGATATGACCTGCGCCTTG	Alu I	–	–	–	–	–	–	LK
		Rsa00878_3’	dot–blot	co–dominant	CAATCACCATCCGACCTTTC	AACGTGGATTGATGACATGC	–	ACCCATCCTTCCACTAC	40	0.5	ACCCATTCTTTCACTAC	40	0.5	
Rsa1.0_00894.1	269,700	Rsa00894_3’	CAPS	co–dominant	TGACCATGCTACAGGAGAACA	CATTCTCGTGGTAGGTCTCG	Hinc II	–	–	–	–	–	–	LK
		Rsa00894_5’	CAPS	co–dominant	CAGCGGAAACTGCAACTTAAC	GGTGAAACTTATGGTGCCAGAC	Alu I	–	–	–	–	–	–	
Rsa1.0_00904.1	180,594	Rsa00904_5’	dot–blot	co–dominant	AAAACCGATCCGAAAATCAG	AGACCTGGACGTTTGTGTAT	–	CCGAATGAGTACACAAA	35	1	CCGAATGAATACACAAA	35	1	LK
		Rsa00904_3’	CAPS	co–dominant	CAAAACCATCCTCCATCTCC	TCCCAATGAGGTTCTTGAGG	Afl II	–	–	–	–	–	–	
Rsa1.0_00920.1	601,703	Rsa00920_5’	dot–blot	dominant	GCAATCAGCAAGTTGTTCCA	TCTGCTCGGTTGCATTACAG	–	GCCAGCAATTTCAGGTC	50	0.5	GCCAGCAACTTCAGGTC	50	1	LK
		Rsa00920_3’	dCAPS	dominant	AGAACATGAAGCCATTGTCTA	AAACTCCCCCTGATGAATGC	Xsp I	–	–	–	–	–	–	
Rsa1.0_00926.1	195,072	Rsa00926_5’	CAPS	co–dominant	CAGAATATCAAATCGGCGTTAC	TGTTACACTCTAGGGCCAACG	Afa I	–	–	–	–	–	–	LK
		Rsa00926_3’	CAPS	dominant	CTACTTCGCCCTACGTCTCG	GTTCCGGCCAAAAGAAGAAG	Alu I	–	–	–	–	–	–	
Rsa1.0_00934.1	193,516	Rsa00934_5’	dot–blot	dominant	ACTTCGGATACCCCCGAATA	TTTGGGTCTGTTTGGGTTTC	–	TATATAATGAATTTTAA	35	1	TATATAATAAATTTTAA	35	1	LK
		Rsa00934_3’	dot–blot	dominant	ATGTTGGCGCAGAAAAAGAG	CGACAGCTCCTCCTTGAGAC	–	TCCTTTTGAGATATCGA	40	0.5	TCCTTTCGAGCTATCGA	50	1	
Rsa1.0_00938.1	193,891	Rsa00938_5’	dot–blot	co–dominant	AAATCGTCGACCCCTCTCTC	CAGGGGCAGATCCAAGATAA	–	GGGATAAAAATGCTCTA	40	0.5	GGGATAAAGATGCTCTA	40	0.5	LK
		Rsa00938_3’	dot–blot	dominant	TGAAAGAAGCGAAGCAGAGAG	TTACCAAATCACACCGAAACC	–	ATAGCTCAAAGCTGAAA	50	0.5	ATAGCTCAGAGCTGAAA	50	0.5	
Rsa1.0_00977.1	198,001	Rsa00977_5’	dot–blot	dominant	TGGAGCAAAAAGGGATCTTG	ATACGCTCTACCACCGTTGC	–	TAGTCTCTGTTCTTGCAG	50	0.5	TAGTCTCTATTCTTGCAG	50	1	LK
		Rsa00977_3’	dCAPS	dominant	GATGAGAGATCCAGATTACTGCG	ATCACTCCTATTGCGGTTCC	Hha I	–	–	–	–	–	–	
Rsa1.0_01029.1	256,254	Rsa01029_5’	CAPS	co–dominant	GGAGCAAAAGGTGGTAACGA	TTTCGGTAAGACGCAGGTTC	Stu I	–	–	–	–	–	–	LK
		Rsa01029_3’	CAPS	dominant	TTGAGGTGGTGATTGTGGAG	TTTCCCACCCATATCCAAGA	Nde I	–	–	–	–	–	–	
Rsa1.0_01112.1	310,601	Rsa01112_5’	dot–blot	dominant	CTATTAGTGATATTGCAAATTAATGC	GCAAGGTCAATTGGTTATAG	–	AATAATAACATACATGT	30	1	AATAATAATATACATGT	30	1	LK
		Rsa01112_3’	CAPS	dominant	TCCATGGAGTTCAGTTCACC	AATACGCCCAAAGACCAATG	Sac I	–	–	–	–	–	–	
Rsa1.0_01504.1	189,978	Rsa01504_5’	dot–blot	dominant	GAATAGCCGTTTTCCGTCAA	TCGTCTGATGAGTTGCAAGG	–	TTTTAGCACAAGACCGG	50	1	TTTTAGCATAAGACCGG	40	0.5	LK
		Rsa01504_3’	dot–blot	dominant	TTTTGCAACTCGGAATCATC	ATGCACCAGGGAGTAAATGC	–	TAGAGTTAGTCAAAGTG	40	0.5	TAGAGTTATTCAAAGTG	40	1	
Rsa1.0_01544.1	185,602	Rsa01544_5’	CAPS	dominant	CCAAAGACAAAACCAACTCTC	CCGGGTTAGAGTTTCTTCAAA	Alu I	–	–	–	–	–	–	LK
		Rsa01544_3’	CAPS	dominant	TAAAGCCTTTGACCCATTCG	TGGAAAACGTGAACGTACCA	EcoR V	–	–	–	–	–	–	
Rsa1.0_01608.1	170,540	Rsa01608_5’	dot–blot	dominant	GTGGACTTCACGAGGAAACC	TCGTTTATCGTCCGTCGTAAC	–	GGAACTTACGACGAAAT	40	0.5	GGAACTTATGACGAAAT	40	0.5	LK
		Rsa01608_3’	dot–blot	dominant	CTCAACTCCATGTTCCCTCTG	TGGAAGCGCTTTAAAATTGG	–	TGAATCAAGATTTTGAA	40	0.5	TGAATCAAAATTTTGAA	40	0.5	
Rsa1.0_01674.1	168,300	Rsa01674_5’	dot–blot	co–dominant	TGTTGGAGCAGGCAATGTAG	CCACAAAAGGGTCTTTTCCA	–	GATGTCTTCTCCCTTAG	40	0.5	TGATGTCTCCCTTAGA	40	0.5	LK
		Rsa01674_3’	CAPS	co–dominant	TATCCCAACTTTCCCGTCTG	GCGGAGCCAGAAAACATTTA	Spe I	–	–	–	–	–	–	
Rsa1.0_02020.1	173,211	Rsa02020_5’	CAPS	dominant	TTAACGCCGACGAAAACAAC	TGATGCGTATGCAGGAAGAG	TaqI	–	–	–	–	–	–	LK
		Rsa02020_3’	dot–blot	dominant	TCAATTAAGGGGCTGACTGG	TTTGGGTTCGGTCTGAGTTC		TAAAAATTCAAAACCAA	35	0.5	TAAAAATTTAAAACCAA	35	1	
Rsa1.0_02270.1	249,821	Rsa02270_5’	CAPS	dominant	GATCACCCAAGGTCAATTCC	AGCTCTTTTCGGATCCATGA	Nco I	–	–	–	–	–	–	LK
		Rsa02270_3’	CAPS	dominant	ACATGACCGAGATGGGAGAC	GGGGAATAAGGTGCAGTCAA	Hind III	–	–	–	–	–	–	

Rsa1.0_02589.1	300,828	Rsa02589_5'	dot-blot	co-dominant	CCCATGAGTTCTCCTTTCCA	AACCACCTACATCCGCAAAC	–	ATAGCTTAAAAGTATCA	40	1	ATAGCTTACAAGTATCA	40	0.5	LK
		Rsa02589_3'	dot-blot	co-dominant	AAGTTTGGTTCGGGTTCGTA	AACCAAACCTGATCCGACTG	–	TTAACTATCTTTATATT	35	1	TTAACTATTTTTATATT	35	1	
Rsa1.0_00021.1	263,655	Rsa00021_5'	CAPS	dominant	TGGAGTCTCTCTTGGGGATG	TCTTGGAGTTGGCCTTGTTC	Taq I	–	–	–	–	–	–	NL
		Rsa00021_3'	CAPS	dominant	CGCACCTTCACAAAATACGA	TCATTTTGATCCGTGCAAAG	Afl II	–	–	–	–	–	–	
Rsa1.0_00915.1	194,446	Rsa00915_5'	dCAPS	co-dominant	GTGATATGGATATGCCACACAGGC	GCACGAACACCTCCAACAAC	Hae III	–	–	–	–	–	–	NL
		Rsa00915_3'	dot-blot	co-dominant	GGGTAAGCAGCAGAACTTCG	GCCCTTGCCATTTTAACAAA	–	CTGCTTCTTTCAACGTC	50	1	CTGCTTCTGTCAACGTC	50	1	
Rsa1.0_00917.1	182,012	Rsa00917_5'	CAPS	co-dominant	CAGAAATTAGTAGCCGTGACA	GCCAATGCAGATTTACAAG	Dde I	–	–	–	–	–	–	NL
		Rsa00917_3'	dot-blot	dominant	CTCACCCAAAGCCCAAATAA	TTCGGAGTGCTATGTCCAAG	–	AGGTATGGGATGCTAAA	40	0.5	AGGTATGGATGCTAAA	40	0.5	

LK, Both ends of scaffolds are linked.

NL, Both ends of scaffolds are not linked

Table S4 Genes of 80,521 predicted by Augustus.

	vs NR (Non Redundant Database: http://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins)										vs TAIR10 of A. thaliana						
Query	NR	Length (query)	Length (subject)	E-value	Length%	Identity%	Positive%	Product	Genbank	Species	Subject	Query	Subject	E-value	Length%	Identity%	Positve%
Rsa1.0_00001.1.g1.t1	ref|XP_002867679.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297313515|gb|EFH43938.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	498	498	0	100.0	88.6	93.4	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT4G24140.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:12530032-12533664 REVERSE LENGTH=498	498	498	0	100.0	88.0	93.4
Rsa1.0_00001.1.g2.t1	gb|AAB63610.1| hypothetical protein [Arabidopsis thaliana]	384	430	1.00E-128	112.0	71.1	78.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G24150.1 | Symbols: AtGRF8, GRF8 | growth-regulating factor 8 | chr4:12535972-12539387 FORWARD LENGTH=493	384	493	1.00E-126	128.4	64.1	70.8
Rsa1.0_00001.1.g3.t1	ref|XP_002869734.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297315570|gb|EFH45993.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	407	417	0	102.5	90.4	95.8	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT4G24160.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:12539871-12542210 FORWARD LENGTH=418	407	418	0	102.7	88.7	94.8
Rsa1.0_00001.1.g4.t1	emb|CAB51660.1| putative protein [Arabidopsis thaliana] gi|7269267|emb|CAB79327.1| putative protein [Arabidopsis thaliana]	1134	1263	0	111.4	45.5	50.8	putative protein	gbpln	Arabidopsis thaliana	AT4G24170.1 | Symbols: | ATP binding microtubule motor family protein | chr4:12543206-12546805 FORWARD LENGTH=1004	1134	1004	0	88.5	45.5	50.8
Rsa1.0_00001.1.g5.t1	ref|XP_002869733.1| hypothetical protein ARALYDRAFT_492444 [Arabidopsis lyrata subsp. lyrata] gi|297315569|gb|EFH45992.1| hypothetical protein ARALYDRAFT_492444 [Arabidopsis lyrata subsp. lyrata]	315	305	1.00E-131	96.8	77.1	87.0	hypothetical protein ARALYDRAFT_492444	gbpln	Arabidopsis lyrata	AT4G24175.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0307 (InterPro:IPR006839); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12547018-12548810 FORWARD LENGTH=306	315	306	1.00E-116	97.1	76.8	85.7
Rsa1.0_00001.1.g6.t1	gb|EOA17059.1| hypothetical protein CARUB_v10005297mg [Capsella rubella]	255	312	1.00E-132	122.4	89.4	94.9	hypothetical protein CARUB_v10005297mg	gbpln	Capsella rubella	AT4G24180.1 | Symbols: TLP1, ATTLP1 | THAUMATIN-LIKE PROTEIN 1 | chr4:12550356-12551221 REVERSE LENGTH=260	255	260	1.00E-130	102.0	88.6	93.3
Rsa1.0_00001.1.g7.t4	ref|XP_002867675.1| hypothetical protein ARALYDRAFT_329238 [Arabidopsis lyrata subsp. lyrata] gi|297313511|gb|EFH43934.1| hypothetical protein ARALYDRAFT_329238 [Arabidopsis lyrata subsp. lyrata]	162	157	2.00E-61	96.9	73.5	82.1	hypothetical protein ARALYDRAFT_329238	gbpln	Arabidopsis lyrata	AT4G24204.2 | Symbols: | RING/U-box superfamily protein | chr4:12562069-12562646 REVERSE LENGTH=157	162	157	2.00E-61	96.9	71.0	80.9
Rsa1.0_00001.1.g8.t1	gb|ACV88719.1| SLY1 F-box protein [Brassica napus]	147	146	3.00E-69	99.3	93.2	95.2	SLY1 F-box protein	gbpln	Brassica napus	AT4G24210.1 | Symbols: SLY1 | F-box family protein | chr4:12563658-12564113 FORWARD LENGTH=151	147	151	6.00E-62	102.7	78.2	86.4
Rsa1.0_00001.1.g9.t1	gb|EOA16797.1| hypothetical protein CARUB_v10005016mg [Capsella rubella]	390	388	0	99.5	85.9	93.1	hypothetical protein CARUB_v10005016mg	gbpln	Capsella rubella	AT4G24220.1 | Symbols: VEP1, AWI31 | NAD(P)-binding Rossmann-fold superfamily protein | chr4:12565219-12566474 FORWARD LENGTH=388	390	388	0	99.5	83.6	92.3
Rsa1.0_00001.1.g10.t1	gb|AAS21130.1| At4g24230 [Arabidopsis thaliana] gi|45773894|gb|AAS76751.1| At4g24230 [Arabidopsis thaliana]	392	362	6.00E-82	92.3	56.9	66.3	At4g24230	gbpln	Arabidopsis thaliana	AT4G24230.5 | Symbols: ACBP3 | acyl-CoA-binding domain 3 | chr4:12567240-12568754 REVERSE LENGTH=362	392	362	3.00E-84	92.3	56.9	66.3
Rsa1.0_00001.1.g11.t1	gb|ACQ99198.1| WRKY7 [Brassica rapa subsp. pekinensis]	341	307	1.00E-155	90.0	81.5	84.8	WRKY7	gbpln	Brassica rapa	AT4G24240.1 | Symbols: WRKY7, ATWRKY7 | WRKY DNA-binding protein 7 | chr4:12571930-12573446 FORWARD LENGTH=353	341	353	1.00E-134	103.5	77.1	84.5
Rsa1.0_00001.1.g12.t2	ref|XP_002867673.1| hypothetical protein ARALYDRAFT_914165 [Arabidopsis lyrata subsp. lyrata] gi|297313509|gb|EFH43932.1| hypothetical protein ARALYDRAFT_914165 [Arabidopsis lyrata subsp. lyrata]	498	482	0	96.8	84.7	90.0	hypothetical protein ARALYDRAFT_914165	gbpln	Arabidopsis lyrata	AT4G24250.1 | Symbols: MLO13, ATMLO13 | Seven transmembrane MLO family protein | chr4:12575008-12577517 REVERSE LENGTH=478	498	478	0	96.0	83.7	89.2
Rsa1.0_00001.1.g13.t1	ref|NP_194157.1| endoglucanase 21 [Arabidopsis thaliana] gi|75266338|sp|Q9STW8.1|GUN21_ARATH RecName: Full=Endoglucanase 21; AltName: Full=Endo-1,4-beta glucanase 21 gi|5051768|emb|CAB45061.1| endo-1, 4-beta-glucanase like protein [Arabidopsis thaliana] gi|7269276|emb|CAB79336.1| endo-1, 4-beta-glucanase like protein [Arabidopsis thaliana] gi|332659479|gb|AEE84879.1| endoglucanase 21 [Arabidopsis thaliana]	764	620	0	81.2	58.9	67.7	endoglucanase 21	gbpln	Arabidopsis thaliana	AT4G24260.1 | Symbols: ATGH9A3, KOR3, GH9A3 | glycosyl hydrolase 9A3 | chr4:12577871-12580133 REVERSE LENGTH=620	764	620	0	81.2	58.9	67.7

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<tr><td>Rsa1.0_00001.1.g14.t1</td><td>ref|XP_002867670.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297313506|gb|EFH43929.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>835</td><td>820</td><td>0</td><td>98.2</td><td>82.2</td><td>88.6</td><td>RNA recognition motif-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G24270.1 | Symbols: EMB140 | EMBRYO DEFECTIVE 140 | chr4:12581765-12587293 REVERSE LENGTH=816</td><td>835</td><td>816</td><td>0</td><td>97.7</td><td>82.0</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00001.1.g15.t1</td><td>gb|EOA15374.1| hypothetical protein CARUB_v10006044mg [Capsella rubella]</td><td>109</td><td>121</td><td>2.00E-25</td><td>111.0</td><td>67.9</td><td>77.1</td><td>hypothetical protein CARUB_v10006044mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G24275.1 | Symbols: | Identified as a screen for stress-responsive genes. | chr4:12588579-12588959 FORWARD LENGTH=126</td><td>109</td><td>126</td><td>3.00E-22</td><td>115.6</td><td>63.3</td><td>74.3</td></tr>
<tr><td>Rsa1.0_00001.1.g16.t1</td><td>gb|AAD25622.1|AC005287_24 Hypothetical protein [Arabidopsis thaliana]</td><td>161</td><td>224</td><td>3.00E-24</td><td>139.1</td><td>45.3</td><td>61.5</td><td>Hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384</td><td>161</td><td>384</td><td>1.00E-26</td><td>238.5</td><td>41.6</td><td>57.1</td></tr>
<tr><td>Rsa1.0_00001.1.g17.t1</td><td>ref|XP_002869727.1| cphsc70-1 [Arabidopsis lyrata subsp. lyrata] gi|297315563|gb|EFH45986.1| cphsc70-1 [Arabidopsis lyrata subsp. lyrata]</td><td>715</td><td>718</td><td>0</td><td>100.4</td><td>92.9</td><td>95.7</td><td>cphsc70-1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49910.1 | Symbols: CPHSC70-2EAT SHOCK PROTEIN 70-2, HSC70-7, cpHsc70-2 | chloroplast heat shock protein 70-2 | chr5:20303470-20306295 FORWARD LENGTH=718</td><td>715</td><td>718</td><td>0</td><td>100.4</td><td>91.5</td><td>95.2</td></tr>
<tr><td>Rsa1.0_00001.1.g18.t1</td><td>ref|NP_194159.1| chloroplast heat shock protein 70-1 [Arabidopsis thaliana] gi|75313889|sp|Q9STW6.1|HSP7F_ARATH RecName: Full=Heat shock 70 kDa protein 6, chloroplastic; AltName: Full=Chloroplast heat shock protein 70-1; Short=cpHsc70-1; AltName: Full=Heat shock protein 70-6; Short=AtHsp70-6; Flags: Precursor gi|5051770|emb|CAB45063.1| hsp 70-like protein [Arabidopsis thaliana] gi|7269278|emb|CAB79338.1| hsp 70-like protein [Arabidopsis thaliana] gi|18175969|gb|AAL59960.1| putative hsp 70 protein [Arabidopsis thaliana] gi|25054945|gb|AAN71949.1| putative hsp 70 protein [Arabidopsis thaliana] gi|332659484|gb|AEE84884.1| chloroplast heat shock protein 70-1 [Arabidopsis thaliana]</td><td>240</td><td>718</td><td>1.00E-66</td><td>299.2</td><td>55.4</td><td>62.9</td><td>chloroplast heat shock protein 70-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G24280.1 | Symbols: cpHsc70-1 | chloroplast heat shock protein 70-1 | chr4:12590094-12593437 FORWARD LENGTH=718</td><td>240</td><td>718</td><td>4.00E-69</td><td>299.2</td><td>55.4</td><td>62.9</td></tr>
<tr><td>Rsa1.0_00001.1.g19.t1</td><td>ref|XP_002869727.1| cphsc70-1 [Arabidopsis lyrata subsp. lyrata] gi|297315563|gb|EFH45986.1| cphsc70-1 [Arabidopsis lyrata subsp. lyrata]</td><td>935</td><td>718</td><td>0</td><td>76.8</td><td>53.8</td><td>58.8</td><td>cphsc70-1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G24280.1 | Symbols: cpHsc70-1 | chloroplast heat shock protein 70-1 | chr4:12590094-12593437 FORWARD LENGTH=718</td><td>935</td><td>718</td><td>0</td><td>76.8</td><td>53.4</td><td>58.6</td></tr>
<tr><td>Rsa1.0_00001.1.g20.t1</td><td>gb|EOA16263.1| hypothetical protein CARUB_v10004407mg [Capsella rubella]</td><td>606</td><td>606</td><td>0</td><td>100.0</td><td>88.9</td><td>92.7</td><td>hypothetical protein CARUB_v10004407mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G24290.2 | Symbols: | MAC/Perforin domain-containing protein | chr4:12594856-12597815 FORWARD LENGTH=606</td><td>606</td><td>606</td><td>0</td><td>100.0</td><td>87.5</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00001.1.g21.t1</td><td>ref|XP_002869724.1| hypothetical protein ARALYDRAFT_492419 [Arabidopsis lyrata subsp. lyrata] gi|297315560|gb|EFH45983.1| hypothetical protein ARALYDRAFT_492419 [Arabidopsis lyrata subsp. lyrata]</td><td>220</td><td>213</td><td>1.00E-103</td><td>96.8</td><td>87.7</td><td>90.5</td><td>hypothetical protein ARALYDRAFT_492419</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G24310.1 | Symbols: | Protein of unknown function (DUF679) | chr4:12600900-12601541 FORWARD LENGTH=213</td><td>220</td><td>213</td><td>1.00E-98</td><td>96.8</td><td>86.4</td><td>90.0</td></tr>
<tr><td>Rsa1.0_00001.1.g22.t1</td><td>ref|NP_194163.1| ubiquitin carboxyl-terminal hydrolase-like protein [Arabidopsis thaliana] gi|5051774|emb|CAB45067.1| putative protein [Arabidopsis thaliana] gi|7269282|emb|CAB79342.1| putative protein [Arabidopsis thaliana] gi|91805609|gb|ABE65533.1| hypothetical protein At4g24320 [Arabidopsis thaliana] gi|332659489|gb|AEE84889.1| ubiquitin carboxyl-terminal hydrolase-like protein [Arabidopsis thaliana]</td><td>379</td><td>395</td><td>1.00E-170</td><td>104.2</td><td>80.5</td><td>88.7</td><td>ubiquitin carboxyl-terminal hydrolase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G24320.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr4:12602298-12603485 REVERSE LENGTH=395</td><td>379</td><td>395</td><td>1.00E-172</td><td>104.2</td><td>80.5</td><td>88.7</td></tr>
<tr><td>Rsa1.0_00001.1.g23.t1</td><td>ref|NP_194164.1| uncharacterized protein [Arabidopsis thaliana] gi|5051775|emb|CAB45068.1| putative protein [Arabidopsis thaliana] gi|7269283|emb|CAB79343.1| putative protein [Arabidopsis thaliana] gi|58652054|gb|AAW80852.1| At4g24330 [Arabidopsis thaliana] gi|332659490|gb|AEE84890.1| uncharacterized protein AT4G24330 [Arabidopsis thaliana]</td><td>520</td><td>478</td><td>0</td><td>91.9</td><td>76.2</td><td>81.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G24330.1 | Symbols: | Protein of unknown function (DUF1682) | chr4:12603848-12606229 REVERSE LENGTH=478</td><td>520</td><td>478</td><td>0</td><td>91.9</td><td>76.2</td><td>81.9</td></tr>
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Rsa1.0_00001.1.g24.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1513	1499	0	99.1	64.8	79.0	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1513	158	7.00E-31	10.4	4.4	5.5
Rsa1.0_00001.1.g25.t1	ref|NP_567699.1| phosphorylase family protein [Arabidopsis thaliana] gi|26453148|dbj|BAC43650.1| unknown protein [Arabidopsis thaliana] gi|28950909|gb|AAO63378.1| At4g24340 [Arabidopsis thaliana] gi|332659491|gb|AEE84891.1| phosphorylase family protein [Arabidopsis thaliana]	343	338	1.00E-161	98.5	84.0	88.9	phosphorylase family protein	gbpln	Arabidopsis thaliana	AT4G24340.1 | Symbols: | Phosphorylase superfamily protein | chr4:12607475-12609148 FORWARD LENGTH=338	343	338	1.00E-164	98.5	84.0	88.9
Rsa1.0_00001.1.g26.t1	gb|AAM65580.1| unknown [Arabidopsis thaliana]	350	336	1.00E-159	96.0	78.3	85.4	unknown	gbpln	Arabidopsis thaliana	AT4G24350.1 | Symbols: | Phosphorylase superfamily protein | chr4:12609637-12611328 FORWARD LENGTH=336	350	336	1.00E-160	96.0	77.7	84.9
Rsa1.0_00001.1.g27.t1	ref|NP_567700.1| uncharacterized protein [Arabidopsis thaliana] gi|5051779|emb|CAB45072.1| hypothetical protein [Arabidopsis thaliana] gi|7269287|emb|CAB79347.1| hypothetical protein [Arabidopsis thaliana] gi|17381050|gb|AAL36337.1| unknown protein [Arabidopsis thaliana] gi|21436263|gb|AAM51270.1| unknown protein [Arabidopsis thaliana] gi|21555804|gb|AAM63937.1| unknown [Arabidopsis thaliana] gi|332659494|gb|AEE84894.1| uncharacterized protein AT4G24370 [Arabidopsis thaliana]	176	164	2.00E-41	93.2	65.3	77.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G24370.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12611608-12612102 REVERSE LENGTH=164	176	164	7.00E-44	93.2	65.3	77.3
Rsa1.0_00001.1.g28.t1	ref|NP_567701.1| uncharacterized protein [Arabidopsis thaliana] gi|26451917|dbj|BAC43051.1| unknown protein [Arabidopsis thaliana] gi|88196765|gb|ABD43025.1| At4g24380 [Arabidopsis thaliana] gi|332659495|gb|AEE84895.1| uncharacterized protein AT4G24380 [Arabidopsis thaliana]	234	234	1.00E-114	100.0	84.6	92.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G24380.1 | Symbols: | INVOLVED IN: 10-formyltetrahydrofolate biosynthetic process, folic acid and derivative biosynthetic process; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Serine hydrolase (InterPro:IPR005645); BEST Arabidopsis thaliana protein match is: alpha/beta-Hydrolases superfamily protein (TAIR:AT5G65400.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12612554-12613586 FORWARD LENGTH=234	234	234	1.00E-117	100.0	84.6	92.3
Rsa1.0_00001.1.g29.t1	gb|EOA18169.1| hypothetical protein CARUB_v10006645mg [Capsella rubella]	615	622	0	101.1	85.0	90.9	hypothetical protein CARUB_v10006645mg	gbpln	Capsella rubella	AT4G24390.1 | Symbols: | RNI-like superfamily protein | chr4:12613909-12615966 REVERSE LENGTH=623	615	623	0	101.3	84.2	90.7
Rsa1.0_00001.1.g30.t1	ref|NP_194171.1| CBL-interacting serine/threonine-protein kinase 8 [Arabidopsis thaliana] gi|75337651|sp|Q9STV4.1|CIPK8_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 8; AltName: Full=SNF1-related kinase 3.13; AltName: Full=SOS2-like protein kinase PKS11 gi|19343483|gb|AAK16683.2|AF290193_1 CBL-interacting protein kinase 8 [Arabidopsis thaliana] gi|5051782|emb|CAB45075.1| serine/threonine kinase-like protein [Arabidopsis thaliana] gi|7269290|emb|CAB79350.1| serine/threonine kinase-like protein [Arabidopsis thaliana] gi|24030396|gb|AAN41358.1| putative serine/threonine kinase [Arabidopsis thaliana] gi|332659499|gb|AEE84899.1| CBL-interacting serine/threonine-protein kinase 8 [Arabidopsis thaliana]	454	445	0	98.0	93.0	95.8	CBL-interacting serine/threonine-protein kinase 8	gbpln	Arabidopsis thaliana	AT4G24400.1 | Symbols: CIPK8, SnRK3.13, PKS11, ATCIPK8 | CBL-interacting protein kinase 8 | chr4:12617379-12620481 FORWARD LENGTH=445	454	445	0	98.0	93.0	95.8

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<tr><td>Rsa1.0_00001.1.g31.t1</td><td>ref|NP_567703.4| Rhamnogalacturonate lyase family protein [Arabidopsis thaliana] gi|5051785|emb|CAB45078.1| LG27/30-like gene [Arabidopsis thaliana] gi|7269293|emb|CAB79353.1| LG27/30-like gene [Arabidopsis thaliana] gi|332659503|gb|AEE84903.1| Rhamnogalacturonate lyase family protein [Arabidopsis thaliana]</td><td>645</td><td>646</td><td>0</td><td>100.2</td><td>88.2</td><td>94.0</td><td>Rhamnogalacturonate lyase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G24430.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr4:12630018-12632975 FORWARD LENGTH=646</td><td>645</td><td>646</td><td>0</td><td>100.2</td><td>88.2</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00001.1.g32.t1</td><td>ref|NP_194175.1| transcription initiation factor IIA subunit 2 [Arabidopsis thaliana] gi|30686529|ref|NP_849434.1| transcription initiation factor IIA subunit 2 [Arabidopsis thaliana] gi|297803670|ref|XP_002869719.1| transcription initiation factor IIA gamma chain [Arabidopsis lyrata subsp. lyrata] gi|20141796|sp|Q39236.2|T2AG_ARATH RecName: Full=Transcription initiation factor IIA subunit 2; AltName: Full=General transcription factor IIA subunit 2; AltName: Full=Transcription initiation factor IIA gamma chain; Short=TFIIA-gamma gi|2826882|emb|CAA11524.1| transcription factor IIA small subunit [Arabidopsis thaliana] gi|5051786|emb|CAB45079.1| transcription factor IIA small subunit [Arabidopsis thaliana] gi|7269294|emb|CAB79354.1| transcription factor IIA small subunit [Arabidopsis thaliana] gi|18176271|gb|AAL60014.1| putative transcription factor IIA small subunit [Arabidopsis thaliana] gi|20465319|gb|AAM20063.1| putative transcription factor IIA small subunit [Arabidopsis thaliana] gi|21553865|gb|AAM62958.1| transcription factor IIA small subunit [Arabidopsis thaliana] gi|39545876|gb|AAR28001.1| TFIIA-S</td><td>106</td><td>106</td><td>2.00E-55</td><td>100.0</td><td>99.1</td><td>100.0</td><td>transcription initiation factor IIA subunit 2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G24440.2 | Symbols: | transcription initiation factor IIA gamma chain / TFIIA-gamma (TFIIA-S) | chr4:12633460-12634553 FORWARD LENGTH=106</td><td>106</td><td>106</td><td>3.00E-58</td><td>100.0</td><td>99.1</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00001.1.g33.t6</td><td>ref|NP_194177.2| CRT (chloroquine-resistance transporter)-like transporter 2 [Arabidopsis thaliana] gi|334186873|ref|NP_001190820.1| CRT (chloroquine-resistance transporter)-like transporter 2 [Arabidopsis thaliana] gi|119935896|gb|ABM06027.1| At4g24460 [Arabidopsis thaliana] gi|332659507|gb|AEE84907.1| CRT (chloroquine-resistance transporter)-like transporter 2 [Arabidopsis thaliana] gi|332659508|gb|AEE84908.1| CRT (chloroquine-resistance transporter)-like transporter 2 [Arabidopsis thaliana]</td><td>432</td><td>431</td><td>0</td><td>99.8</td><td>82.2</td><td>89.4</td><td>CRT (chloroquine-resistance transporter)-like transporter 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G24460.2 | Symbols: CLT2 | CRT (chloroquine-resistance transporter)-like transporter 2 | chr4:12642888-12645310 FORWARD LENGTH=431</td><td>432</td><td>431</td><td>0</td><td>99.8</td><td>82.2</td><td>89.4</td></tr>
<tr><td>Rsa1.0_00001.1.g34.t1</td><td>gb|EOA17945.1| hypothetical protein CARUB_v10006355mg [Capsella rubella]</td><td>307</td><td>312</td><td>1.00E-137</td><td>101.6</td><td>82.4</td><td>87.3</td><td>hypothetical protein CARUB_v10006355mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G24470.2 | Symbols: ZIM, GATA25 | GATA-type zinc finger protein with TIFY domain | chr4:12645785-12647734 FORWARD LENGTH=309</td><td>307</td><td>309</td><td>1.00E-138</td><td>100.7</td><td>81.4</td><td>88.3</td></tr>
<tr><td>Rsa1.0_00001.1.g35.t1</td><td>ref|NP_194179.2| protein kinase family protein [Arabidopsis thaliana] gi|332659512|gb|AEE84912.1| protein kinase family protein [Arabidopsis thaliana]</td><td>958</td><td>956</td><td>0</td><td>99.8</td><td>81.8</td><td>88.1</td><td>protein kinase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G24480.1 | Symbols: | Protein kinase superfamily protein | chr4:12650410-12654755 FORWARD LENGTH=956</td><td>958</td><td>956</td><td>0</td><td>99.8</td><td>81.8</td><td>88.1</td></tr>
<tr><td>Rsa1.0_00001.1.g36.t1</td><td>ref|XP_002867663.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297313499|gb|EFH43922.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>671</td><td>677</td><td>0</td><td>100.9</td><td>82.0</td><td>90.2</td><td>protein binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G24490.2 | Symbols: | RAB geranylgeranyl transferase alpha subunit 1 | chr4:12655330-12658103 REVERSE LENGTH=678</td><td>671</td><td>678</td><td>0</td><td>101.0</td><td>82.0</td><td>90.3</td></tr>
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Rsa1.0_00001.1.g37.t1	ref|NP_567704.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|334186879|ref|NP_001190822.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|4220540|emb|CAA23013.1| hypothetical protein [Arabidopsis thaliana] gi|7269300|emb|CAB79360.1| hypothetical protein [Arabidopsis thaliana] gi|23296316|gb|AAN13039.1| unknown protein [Arabidopsis thaliana] gi|332659515|gb|AEE84915.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|332659517|gb|AEE84917.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	329	319	1.00E-114	97.0	72.3	80.2	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT4G24500.3 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:12658732-12660211 FORWARD LENGTH=319	329	319	1.00E-117	97.0	72.3	80.2
Rsa1.0_00001.1.g38.t1	ref|XP_002869713.1| hypothetical protein ARALYDRAFT_492392 [Arabidopsis lyrata subsp. lyrata] gi|297315549|gb|EFH45972.1| hypothetical protein ARALYDRAFT_492392 [Arabidopsis lyrata subsp. lyrata]	419	415	1.00E-180	99.0	74.9	85.2	hypothetical protein ARALYDRAFT_492392	gbpln	Arabidopsis lyrata	AT4G24510.1 | Symbols: CER2, VC2, VC-2 | HXXXD-type acyl-transferase family protein | chr4:12660929-12662537 FORWARD LENGTH=421	419	421	0	100.5	74.0	85.0
Rsa1.0_00001.1.g39.t1	ref|XP_002867662.1| hypothetical protein ARALYDRAFT_492391 [Arabidopsis lyrata subsp. lyrata] gi|297313498|gb|EFH43921.1| hypothetical protein ARALYDRAFT_492391 [Arabidopsis lyrata subsp. lyrata]	707	692	0	97.9	84.7	89.7	hypothetical protein ARALYDRAFT_492391	gbpln	Arabidopsis lyrata	AT4G24520.1 | Symbols: ATR1, AR1 | P450 reductase 1 | chr4:12663065-12667066 REVERSE LENGTH=692	707	692	0	97.9	83.9	89.1
Rsa1.0_00001.1.g40.t1	ref|XP_002867662.1| hypothetical protein ARALYDRAFT_492391 [Arabidopsis lyrata subsp. lyrata] gi|297313498|gb|EFH43921.1| hypothetical protein ARALYDRAFT_492391 [Arabidopsis lyrata subsp. lyrata]	694	692	0	99.7	90.3	95.0	hypothetical protein ARALYDRAFT_492391	gbpln	Arabidopsis lyrata	AT4G24520.1 | Symbols: ATR1, AR1 | P450 reductase 1 | chr4:12663065-12667066 REVERSE LENGTH=692	694	692	0	99.7	89.5	94.7
Rsa1.0_00001.1.g41.t1	gb|EOA18108.1| hypothetical protein CARUB_v10006569mg [Capsella rubella]	518	521	0	100.6	90.3	94.6	hypothetical protein CARUB_v10006569mg	gbpln	Capsella rubella	AT4G24530.1 | Symbols: | O-fucosyltransferase family protein | chr4:12667424-12669713 REVERSE LENGTH=519	518	519	0	100.2	88.8	94.0
Rsa1.0_00001.1.g42.t1	gb|AFM77900.1| MADS-box protein AGL24 [Brassica napus]	221	221	1.00E-122	100.0	98.2	99.1	MADS-box protein AGL24	gbpln	Brassica napus	AT4G24540.1 | Symbols: AGL24 | AGAMOUS-like 24 | chr4:12671160-12673645 REVERSE LENGTH=220	221	220	1.00E-106	99.5	86.9	92.8
Rsa1.0_00001.1.g43.t1	ref|XP_002869712.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297315548|gb|EFH45971.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata]	453	451	0	99.6	96.2	97.8	clathrin adaptor complexes medium subunit family protein	gbpln	Arabidopsis lyrata	AT4G24550.2 | Symbols: | Clathrin adaptor complexes medium subunit family protein | chr4:12675873-12678903 FORWARD LENGTH=451	453	451	0	99.6	95.8	98.0
Rsa1.0_00001.1.g44.t1	ref|XP_002867659.1| ubiquitin-specific protease 16 [Arabidopsis lyrata subsp. lyrata] gi|297313495|gb|EFH43918.1| ubiquitin-specific protease 16 [Arabidopsis lyrata subsp. lyrata]	1024	1007	0	98.3	76.2	84.1	ubiquitin-specific protease 16	gbpln	Arabidopsis lyrata	AT4G24560.1 | Symbols: UBP16 | ubiquitin-specific protease 16 | chr4:12679493-12684528 REVERSE LENGTH=1008	1024	1008	0	98.4	75.6	83.1
Rsa1.0_00001.1.g45.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00001.1.g46.t1	ref|XP_002869711.1| hypothetical protein ARALYDRAFT_914130 [Arabidopsis lyrata subsp. lyrata] gi|297315547|gb|EFH45970.1| hypothetical protein ARALYDRAFT_914130 [Arabidopsis lyrata subsp. lyrata]	317	314	1.00E-153	99.1	85.8	90.9	hypothetical protein ARALYDRAFT_914130	gbpln	Arabidopsis lyrata	AT4G24570.1 | Symbols: DIC2 | dicarboxylate carrier 2 | chr4:12686546-12687487 FORWARD LENGTH=313	317	313	1.00E-155	98.7	86.8	92.4
Rsa1.0_00001.1.g47.t2	ref|XP_002867658.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313494|gb|EFH43917.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	943	925	0	98.1	79.6	86.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G24580.1 | Symbols: REN1 | Rho GTPase activation protein (RhoGAP) with PH domain | chr4:12687879-12694248 REVERSE LENGTH=933	943	933	0	98.9	78.0	85.0
Rsa1.0_00001.1.g48.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00001.1.g49.t1	gb|EOA17092.1| hypothetical protein CARUB_v10005345mg, partial [Capsella rubella]	236	303	2.00E-96	128.4	79.7	88.6	hypothetical protein CARUB_v10005345mg, partial	gbpln	Capsella rubella	AT4G24590.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G49710.3); Has 105 Blast hits to 105 proteins in 26 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 3; Plants - 85; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr4:12696651-12698036 FORWARD LENGTH=241	236	241	4.00E-96	102.1	80.1	84.7
Rsa1.0_00001.1.g50.t1	gb|EOA15925.1| hypothetical protein CARUB_v10004019mg [Capsella rubella]	1147	1152	0	100.4	88.8	93.1	hypothetical protein CARUB_v10004019mg	gbpln	Capsella rubella	AT4G24610.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65440.1); Has 820 Blast hits to 264 proteins in 74 species: Archae - 0; Bacteria - 15; Metazoa - 77; Fungi - 83; Plants - 96; Viruses - 0; Other Eukaryotes - 549 (source: NCBI BLink). | chr4:12700837-12707899 REVERSE LENGTH=1150	1147	1150	0	100.3	88.2	92.5
Rsa1.0_00001.1.g51.t1	ref|XP_002869709.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315545|gb|EFH45968.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	420	408	0	97.1	81.0	89.8	zinc ion binding protein	gbpln	Arabidopsis lyrata	AT4G24630.1 | Symbols: | DHHC-type zinc finger family protein | chr4:12714919-12717111 FORWARD LENGTH=407	420	407	0	96.9	80.5	90.0
Rsa1.0_00001.1.g52.t1	gb|AAB48480.1| pollen-specific protein Bnm1 [Brassica napus]	187	182	5.00E-78	97.3	89.3	90.4	pollen-specific protein Bnm1	gbpln	Brassica napus	AT4G24640.1 | Symbols: APPB1 | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:12717851-12718804 FORWARD LENGTH=187	187	187	7.00E-72	100.0	79.1	86.6
Rsa1.0_00001.1.g53.t1	dbj|BAJ34347.1| unnamed protein product [Thellungiella halophila]	225	227	2.00E-99	100.9	89.8	93.3	unnamed protein product	----	----	AT4G24660.1 | Symbols: ATHB22, MEE68, HB22, ZHD2 | homeobox protein 22 | chr4:12724851-12725513 REVERSE LENGTH=220	225	220	3.00E-95	97.8	85.8	89.3
Rsa1.0_00001.1.g54.t1	gb|EOA15502.1| hypothetical protein CARUB_v10004822mg [Capsella rubella] gi|482551310|gb|EOA15503.1| hypothetical protein CARUB_v10004822mg [Capsella rubella]	445	441	0	99.1	79.1	86.3	hypothetical protein CARUB_v10004822mg	gbpln	Capsella rubella	AT4G24670.2 | Symbols: TAR2 | tryptophan aminotransferase related 2 | chr4:12727940-12730694 REVERSE LENGTH=440	445	440	0	98.9	78.7	86.1
Rsa1.0_00001.1.g55.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00001.1.g56.t1	ref|NP_194199.4| modifier of snc1 protein [Arabidopsis thaliana] gi|332659542|gb|AEE84942.1| modifier of snc1 protein [Arabidopsis thaliana]	1381	1427	0	103.3	74.7	82.2	modifier of snc1 protein	gbpln	Arabidopsis thaliana	AT4G24680.1 | Symbols: MOS1 | modifier of snc1 | chr4:12733425-12739737 FORWARD LENGTH=1427	1381	1427	0	103.3	74.7	82.2
Rsa1.0_00001.1.g57.t1	ref|XP_002869705.1| ubiquitin-associated /TS-N domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315541|gb|EFH45964.1| ubiquitin-associated /TS-N domain-containing protein [Arabidopsis lyrata subsp. lyrata]	700	709	0	101.3	80.7	88.0	ubiquitin-associated /TS-N domain-containing protein	gbpln	Arabidopsis lyrata	AT4G24690.1 | Symbols: | ubiquitin-associated (UBA)/TS-N domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein | chr4:12741191-12744202 FORWARD LENGTH=704	700	704	0	100.6	80.9	88.1
Rsa1.0_00001.1.g58.t1	ref|XP_002867652.1| hypothetical protein ARALYDRAFT_492372 [Arabidopsis lyrata subsp. lyrata] gi|297313488|gb|EFH43911.1| hypothetical protein ARALYDRAFT_492372 [Arabidopsis lyrata subsp. lyrata]	137	139	6.00E-43	101.5	77.4	84.7	hypothetical protein ARALYDRAFT_492372	gbpln	Arabidopsis lyrata	AT4G24700.1 | Symbols: | unknown protein; Has 20 Blast hits to 20 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:12744807-12745238 REVERSE LENGTH=143	137	143	1.00E-42	104.4	70.1	73.7
Rsa1.0_00001.1.g59.t1	ref|XP_002867651.1| hypothetical protein ARALYDRAFT_492371 [Arabidopsis lyrata subsp. lyrata] gi|297313487|gb|EFH43910.1| hypothetical protein ARALYDRAFT_492371 [Arabidopsis lyrata subsp. lyrata]	486	477	0	98.1	88.5	92.4	hypothetical protein ARALYDRAFT_492371	gbpln	Arabidopsis lyrata	AT4G24710.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:12745752-12748995 REVERSE LENGTH=475	486	475	0	97.7	87.9	92.2
Rsa1.0_00001.1.g60.t1	gb|EOA17431.1| hypothetical protein CARUB_v10005735mg [Capsella rubella]	208	208	1.00E-82	100.0	71.6	83.2	hypothetical protein CARUB_v10005735mg	gbpln	Capsella rubella	AT4G24730.4 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr4:12749879-12750872 REVERSE LENGTH=231	208	231	2.00E-79	111.1	69.2	79.3
Rsa1.0_00001.1.g61.t21	gb|EOA15516.1| hypothetical protein CARUB_v10004866mg [Capsella rubella]	742	428	0	57.7	53.1	54.9	hypothetical protein CARUB_v10004866mg	gbpln	Capsella rubella	AT4G24740.1 | Symbols: AFC2, AME1, FC2 | FUS3-complementing gene 2 | chr4:12754729-12757653 REVERSE LENGTH=427	742	427	0	57.5	53.0	54.7

Rsa1.0_00001.1.g62.t2	ref|XP_002867646.1| hypothetical protein ARALYDRAFT_492366 [Arabidopsis lyrata subsp. lyrata] gi|297313482|gb|EFH43905.1| hypothetical protein ARALYDRAFT_492366 [Arabidopsis lyrata subsp. lyrata]	366	365	0	99.7	93.7	97.3	hypothetical protein ARALYDRAFT_492366	gbpln	Arabidopsis lyrata	AT4G24760.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:12761482-12763564 REVERSE LENGTH=365	366	365	0	99.7	93.2	96.7
Rsa1.0_00001.1.g63.t1	ref|XP_002867645.1| RNA-binding protein cp31 [Arabidopsis lyrata subsp. lyrata] gi|297313481|gb|EFH43904.1| RNA-binding protein cp31 [Arabidopsis lyrata subsp. lyrata]	303	305	1.00E-133	100.7	83.5	87.5	RNA-binding protein cp31	gbpln	Arabidopsis lyrata	AT4G24770.1 | Symbols: RBP31, ATRBP31, CP31, ATRBP33 | 31-kDa RNA binding protein | chr4:12766223-12767952 REVERSE LENGTH=329	303	329	1.00E-126	108.6	80.5	87.8
Rsa1.0_00001.1.g64.t1	ref|NP_567707.1| putative pectate lyase 18 [Arabidopsis thaliana] gi|334186896|ref|NP_001190827.1| putative pectate lyase 18 [Arabidopsis thaliana] gi|32129908|sp|Q9C5M8.2|PEL18_ARATH RecName: Full=Probable pectate lyase 18; AltName: Full=Pectate lyase A10; Flags: Precursor gi|57222166|gb|AAW38990.1| At4g24780 [Arabidopsis thaliana] gi|332659555|gb|AEE84955.1| putative pectate lyase 18 [Arabidopsis thaliana] gi|332659556|gb|AEE84956.1| putative pectate lyase 18 [Arabidopsis thaliana]	406	408	0	100.5	93.6	97.8	putative pectate lyase 18	gbpln	Arabidopsis thaliana	AT4G24780.2 | Symbols: | Pectin lyase-like superfamily protein | chr4:12770631-12772227 REVERSE LENGTH=408	406	408	0	100.5	93.6	97.8
Rsa1.0_00001.1.g65.t1	ref|XP_002869702.1| hypothetical protein ARALYDRAFT_329184 [Arabidopsis lyrata subsp. lyrata] gi|297315538|gb|EFH45961.1| hypothetical protein ARALYDRAFT_329184 [Arabidopsis lyrata subsp. lyrata]	706	942	0	133.4	85.7	90.5	hypothetical protein ARALYDRAFT_329184	gbpln	Arabidopsis lyrata	AT4G24800.3 | Symbols: | MA3 domain-containing protein | chr4:12782463-12784902 FORWARD LENGTH=702	706	702	0	99.4	86.4	92.1
Rsa1.0_00001.1.g66.t1	ref|XP_002869702.1| hypothetical protein ARALYDRAFT_329184 [Arabidopsis lyrata subsp. lyrata] gi|297315538|gb|EFH45961.1| hypothetical protein ARALYDRAFT_329184 [Arabidopsis lyrata subsp. lyrata]	243	942	1.00E-113	387.7	88.1	94.2	hypothetical protein ARALYDRAFT_329184	gbpln	Arabidopsis lyrata	AT4G24805.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:12785315-12786058 FORWARD LENGTH=247	243	247	1.00E-111	101.6	88.1	94.7
Rsa1.0_00001.1.g67.t1	ref|XP_002867642.1| hypothetical protein ARALYDRAFT_492356 [Arabidopsis lyrata subsp. lyrata] gi|297313478|gb|EFH43901.1| hypothetical protein ARALYDRAFT_492356 [Arabidopsis lyrata subsp. lyrata]	366	387	0	105.7	95.4	97.5	hypothetical protein ARALYDRAFT_492356	gbpln	Arabidopsis lyrata	AT4G24820.2 | Symbols: | 26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain | chr4:12790471-12792599 REVERSE LENGTH=387	366	387	0	105.7	93.7	96.7
Rsa1.0_00001.1.g68.t1	gb|EOA16502.1| hypothetical protein CARUB_v10004661mg [Capsella rubella]	516	494	0	95.7	86.2	88.6	hypothetical protein CARUB_v10004661mg	gbpln	Capsella rubella	AT4G24830.1 | Symbols: | arginosuccinate synthase family | chr4:12793085-12795857 REVERSE LENGTH=494	516	494	0	95.7	88.6	92.8
Rsa1.0_00001.1.g69.t1	gb|EOA16079.1| hypothetical protein CARUB_v10004211mg [Capsella rubella]	758	754	0	99.5	85.4	91.6	hypothetical protein CARUB_v10004211mg	gbpln	Capsella rubella	AT4G24840.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein transport, Golgi organization; LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: COG complex component, COG2 (InterPro:IPR009316); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12796525-12800926 REVERSE LENGTH=756	758	756	0	99.7	85.2	91.4
Rsa1.0_00001.1.g70.t1	gb|EOA16242.1| hypothetical protein CARUB_v10004389mg [Capsella rubella]	616	617	0	100.2	85.7	93.0	hypothetical protein CARUB_v10004389mg	gbpln	Capsella rubella	AT4G24890.1 | Symbols: ATPAP24, PAP24 | purple acid phosphatase 24 | chr4:12811510-12814440 REVERSE LENGTH=615	616	615	0	99.8	84.3	91.2
Rsa1.0_00001.1.g71.t1	ref|NP_194220.2| uncharacterized protein [Arabidopsis thaliana] gi|332659574|gb|AEE84974.1| uncharacterized protein AT4G24900 [Arabidopsis thaliana]	386	421	1.00E-139	109.1	69.9	79.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G24900.1 | Symbols: | unknown protein; Has 119 Blast hits to 96 proteins in 40 species: Archae - 0; Bacteria - 0; Metazoa - 81; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:12814867-12817388 FORWARD LENGTH=421	386	421	1.00E-142	109.1	69.9	79.8
Rsa1.0_00001.1.g72.t1	gb|EOA15789.1| hypothetical protein CARUB_v10007135mg [Capsella rubella]	309	317	1.00E-127	102.6	79.9	87.4	hypothetical protein CARUB_v10007135mg	gbpln	Capsella rubella	AT4G24910.1 | Symbols: | Protein of unknown function (DUF579) | chr4:12817954-12818901 REVERSE LENGTH=315	309	315	1.00E-128	101.9	78.3	86.4

Rsa1.0_00001.1.g73.t1	ref|NP_194222.1| protein transport protein sec61 subunit gamma-1 [Arabidopsis thaliana] gi|18423153|ref|NP_568728.1| protein transport protein sec61 subunit gamma-1 [Arabidopsis thaliana] gi|297795847|ref|XP_002865808.1| hypothetical protein ARALYDRAFT_495113 [Arabidopsis lyrata subsp. lyrata] gi|297799504|ref|XP_002867636.1| hypothetical protein ARALYDRAFT_492346 [Arabidopsis lyrata subsp. lyrata] gi|408407792|sp|P0DI74.1|S61G1_ARATH RecName: Full=Protein transport protein Sec61 subunit gamma-1 gi|408407793|sp|P0DI75.1|S61G2_ARATH RecName: Full=Protein transport protein Sec61 subunit gamma-2 gi|13877813|gb|AAK43984.1|AF370169_1 putative protein translocation complex Sec61 gamma chain [Arabidopsis thaliana] gi|4455235|emb|CAB36734.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana] gi|7269342|emb|CAB79401.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana] gi|9758755|dbj|BAB09131.1| protein translocation complex Sec61 gamma chain [Arabidopsis thaliana] gi|16323486|gb|AAL15237.1| putative	69	69	1.00E-30	100.0	100.0	100.0	protein transport protein sec61 subunit gamma-1	gbpln	Arabidopsis lyrata	AT5G50460.1 | Symbols: | secE/sec61-gamma protein transport protein | chr5:20552168-20552509 REVERSE LENGTH=69	69	69	2.00E-33	100.0	100.0	100.0
Rsa1.0_00001.1.g74.t1	ref|NP_194223.1| thylakoid lumenal protein [Arabidopsis thaliana] gi|17369630|sp|Q9SW33.1|TL1Y_ARATH RecName: Full=Thylakoid lumenal 17.9 kDa protein, chloroplastic; Flags: Precursor gi|4455236|emb|CAB36735.1| hypothetical protein [Arabidopsis thaliana] gi|7269343|emb|CAB79402.1| hypothetical protein [Arabidopsis thaliana] gi|20260598|gb|AAM13197.1| unknown protein [Arabidopsis thaliana] gi|30023698|gb|AAP13382.1| At4g24930 [Arabidopsis thaliana] gi|332659577|gb|AEE84977.1| thylakoid lumenal protein 17.9 [Arabidopsis thaliana]	243	225	5.00E-98	92.6	77.4	84.4	thylakoid lumenal protein	gbpln	Arabidopsis thaliana	AT4G24930.1 | Symbols: | thylakoid lumenal 17.9 kDa protein, chloroplast | chr4:12821496-12822389 REVERSE LENGTH=225	243	225	1.00E-100	92.6	77.4	84.4
Rsa1.0_00001.1.g75.t4	gb|EOA17016.1| hypothetical protein CARUB_v10005251mg [Capsella rubella]	738	322	1.00E-160	43.6	37.9	40.0	hypothetical protein CARUB_v10005251mg	gbpln	Capsella rubella	AT4G24940.1 | Symbols: SAE1A, AT-SAE1-1, ATSAE1A | SUMO-activating enzyme 1A | chr4:12823651-12825971 FORWARD LENGTH=322	738	322	1.00E-161	43.6	37.9	39.3
Rsa1.0_00001.1.g76.t1	dbj|BAJ34072.1| unnamed protein product [Thellungiella halophila]	121	181	1.00E-31	149.6	54.5	56.2	unnamed protein product	----	----	AT4G24960.1 | Symbols: ATHVA22D, HVA22D | HVA22 homologue D | chr4:12828060-12828982 FORWARD LENGTH=135	121	135	5.00E-33	111.6	52.1	56.2
Rsa1.0_00001.1.g77.t1	ref|XP_002869696.1| hypothetical protein ARALYDRAFT_492340 [Arabidopsis lyrata subsp. lyrata] gi|297315532|gb|EFH45955.1| hypothetical protein ARALYDRAFT_492340 [Arabidopsis lyrata subsp. lyrata]	697	709	0	101.7	81.2	89.1	hypothetical protein ARALYDRAFT_492340	gbpln	Arabidopsis lyrata	AT4G24970.1 | Symbols: | Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein | chr4:12831125-12835449 FORWARD LENGTH=707	697	707	0	101.4	79.1	86.5
Rsa1.0_00001.1.g78.t1	ref|NP_974612.1| tapetum determinant 1 [Arabidopsis thaliana] gi|38607340|gb|AAR25553.1| TPD1 [Arabidopsis thaliana] gi|332659584|gb|AEE84984.1| tapetum determinant 1 [Arabidopsis thaliana]	172	176	2.00E-75	102.3	80.8	90.1	tapetum determinant 1	gbpln	Arabidopsis thaliana	AT4G24972.1 | Symbols: TPD1 | tapetum determinant 1 | chr4:12838220-12839619 FORWARD LENGTH=176	172	176	7.00E-78	102.3	80.8	90.1
Rsa1.0_00001.1.g79.t1	ref|XP_002867632.1| hypothetical protein ARALYDRAFT_492339 [Arabidopsis lyrata subsp. lyrata] gi|297313468|gb|EFH43891.1| hypothetical protein ARALYDRAFT_492339 [Arabidopsis lyrata subsp. lyrata] gi|482553486|gb|EOA17679.1| hypothetical protein CARUB_v10006048mg [Capsella rubella]	119	118	7.00E-58	99.2	95.8	96.6	hypothetical protein ARALYDRAFT_492339	gbpln	Arabidopsis lyrata	AT4G24990.1 | Symbols: ATGP4 | Ubiquitin family protein | chr4:12849973-12851249 REVERSE LENGTH=118	119	118	8.00E-60	99.2	94.1	96.6

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<tr><td>Rsa1.0_00001.1.g80.t2</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1760</td><td>1529</td><td>0</td><td>86.9</td><td>40.4</td><td>53.2</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>1760</td><td>746</td><td>3.00E-75</td><td>42.4</td><td>8.2</td><td>11.4</td></tr>
<tr><td>Rsa1.0_00001.1.g81.t1</td><td>gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]</td><td>1180</td><td>1485</td><td>0</td><td>125.8</td><td>49.2</td><td>65.7</td><td>hypothetical protein PRUPE_ppa017790mg</td><td>gbpln</td><td>Prunus persica</td><td>ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158</td><td>1180</td><td>158</td><td>5.00E-27</td><td>13.4</td><td>4.7</td><td>7.1</td></tr>
<tr><td>Rsa1.0_00001.1.g82.t1</td><td>ref|XP_002867630.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297313466|gb|EFH43889.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>268</td><td>280</td><td>1.00E-127</td><td>104.5</td><td>86.2</td><td>92.9</td><td>nodulin MtN3 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G25010.1 | Symbols: SWEET14, AtSWEET14 | Nodulin MtN3 family protein | chr4:12854630-12856351 REVERSE LENGTH=281</td><td>268</td><td>281</td><td>1.00E-128</td><td>104.9</td><td>85.1</td><td>91.8</td></tr>
<tr><td>Rsa1.0_00001.1.g83.t1</td><td>gb|EOA14264.1| hypothetical protein CARUB_v10027424mg, partial [Capsella rubella]</td><td>79</td><td>103</td><td>3.00E-26</td><td>130.4</td><td>67.1</td><td>82.3</td><td>hypothetical protein CARUB_v10027424mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G50810.1 | Symbols: TIM8 | translocase inner membrane subunit 8 | chr5:20675875-20676505 REVERSE LENGTH=77</td><td>79</td><td>77</td><td>3.00E-24</td><td>97.5</td><td>67.1</td><td>82.3</td></tr>
<tr><td>Rsa1.0_00001.1.g84.t2</td><td>ref|NP_194233.1| uncharacterized protein [Arabidopsis thaliana] gi|42573033|ref|NP_974613.1| uncharacterized protein [Arabidopsis thaliana] gi|4455246|emb|CAB36745.1| putative protein [Arabidopsis thaliana] gi|7269353|emb|CAB79412.1| putative protein [Arabidopsis thaliana] gi|21553767|gb|AAM62860.1| unknown [Arabidopsis thaliana] gi|89000969|gb|ABD59074.1| At4g25030 [Arabidopsis thaliana] gi|110736875|dbj|BAF00395.1| hypothetical protein [Arabidopsis thaliana] gi|222424032|dbj|BAH19977.1| AT4G25030 [Arabidopsis thaliana] gi|332659593|gb|AEE84993.1| uncharacterized protein AT4G25030 [Arabidopsis thaliana] gi|332659594|gb|AEE84994.1| uncharacterized protein AT4G25030 [Arabidopsis thaliana]</td><td>361</td><td>344</td><td>3.00E-59</td><td>95.3</td><td>32.1</td><td>33.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25030.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G45410.3); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:12865336-12866638 FORWARD LENGTH=344</td><td>361</td><td>344</td><td>7.00E-62</td><td>95.3</td><td>32.1</td><td>33.5</td></tr>
<tr><td>Rsa1.0_00002.1.g85.t1</td><td>ref|NP_195981.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75181338|sp|Q9LZS7.1|GDL71_ARATH RecName: Full=GDSL esterase/lipase At5g03610; AltName: Full=Extracellular lipase At5g03610; Flags: Precursor gi|13430834|gb|AAK26039.1|AF360329_1 unknown protein [Arabidopsis thaliana] gi|7340646|emb|CAB82926.1| putative protein [Arabidopsis thaliana] gi|21537326|gb|AAM61667.1| putative lipase/acylhydrolase [Arabidopsis thaliana] gi|332003250|gb|AED90633.1| GDSL esterase/lipase [Arabidopsis thaliana]</td><td>341</td><td>359</td><td>2.00E-94</td><td>105.3</td><td>55.1</td><td>70.1</td><td>GDSL esterase/lipase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G03610.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:915650-918326 FORWARD LENGTH=359</td><td>341</td><td>359</td><td>6.00E-97</td><td>105.3</td><td>55.1</td><td>70.1</td></tr>
<tr><td>Rsa1.0_00002.1.g86.t1</td><td>gb|EOA34211.1| hypothetical protein CARUB_v10021720mg [Capsella rubella]</td><td>351</td><td>352</td><td>1.00E-96</td><td>100.3</td><td>56.7</td><td>70.9</td><td>hypothetical protein CARUB_v10021720mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G03610.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:915650-918326 FORWARD LENGTH=359</td><td>351</td><td>359</td><td>5.00E-98</td><td>102.3</td><td>53.3</td><td>68.9</td></tr>
<tr><td>Rsa1.0_00002.1.g87.t1</td><td>ref|XP_003578788.1| PREDICTED: AP-2 complex subunit sigma-like [Brachypodium distachyon] gi|326523623|dbj|BAJ92982.1| predicted protein [Hordeum vulgare subsp. vulgare] gi|326532016|dbj|BAK01384.1| predicted protein [Hordeum vulgare subsp. vulgare]</td><td>84</td><td>142</td><td>1.00E-27</td><td>169.0</td><td>95.2</td><td>97.6</td><td>PREDICTED: AP-2 complex subunit sigma-like</td><td>gbpln</td><td>Brachypodium distachyon</td><td>AT1G47830.1 | Symbols: | SNARE-like superfamily protein | chr1:17613346-17614784 REVERSE LENGTH=142</td><td>84</td><td>142</td><td>3.00E-30</td><td>169.0</td><td>95.2</td><td>96.4</td></tr>
<tr><td>Rsa1.0_00002.1.g88.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00002.1.g89.t1</td><td>gb|EOA34211.1| hypothetical protein CARUB_v10021720mg [Capsella rubella]</td><td>346</td><td>352</td><td>5.00E-92</td><td>101.7</td><td>56.4</td><td>69.9</td><td>hypothetical protein CARUB_v10021720mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G03610.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:915650-918326 FORWARD LENGTH=359</td><td>346</td><td>359</td><td>3.00E-90</td><td>103.8</td><td>51.4</td><td>67.9</td></tr>
<tr><td>Rsa1.0_00002.1.g90.t1</td><td>gb|EOA13504.1| hypothetical protein CARUB_v10026565mg [Capsella rubella]</td><td>391</td><td>391</td><td>0</td><td>100.0</td><td>95.7</td><td>98.0</td><td>hypothetical protein CARUB_v10026565mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G43170.8 | Symbols: RP1 | ribosomal protein 1 | chr1:16266992-16268631 FORWARD LENGTH=389</td><td>391</td><td>389</td><td>0</td><td>99.5</td><td>92.1</td><td>96.2</td></tr>
<tr><td>Rsa1.0_00002.1.g91.t1</td><td>gb|EOA12392.1| hypothetical protein CARUB_v10026693mg [Capsella rubella]</td><td>352</td><td>350</td><td>0</td><td>99.4</td><td>93.5</td><td>97.2</td><td>hypothetical protein CARUB_v10026693mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G42420.1 | Symbols: | Nucleotide-sugar transporter family protein | chr5:16968819-16970225 FORWARD LENGTH=350</td><td>352</td><td>350</td><td>0</td><td>99.4</td><td>92.3</td><td>95.2</td></tr>
<tr><td>Rsa1.0_00002.1.g92.t1</td><td>dbj|BAJ34553.1| unnamed protein product [Thellungiella halophila]</td><td>391</td><td>389</td><td>0</td><td>99.5</td><td>95.9</td><td>98.0</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G43170.8 | Symbols: RP1 | ribosomal protein 1 | chr1:16266992-16268631 FORWARD LENGTH=389</td><td>391</td><td>389</td><td>0</td><td>99.5</td><td>92.1</td><td>95.9</td></tr>
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Rsa1.0_00002.1.g93.t1	ref|NP_199056.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|9759477|dbj|BAB10482.1| unnamed protein product [Arabidopsis thaliana] gi|332007424|gb|AED94807.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	123	111	2.00E-42	90.2	68.3	74.8	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT5G42410.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:16964764-16965099 FORWARD LENGTH=111	123	111	4.00E-45	90.2	68.3	74.8
Rsa1.0_00002.1.g94.t8	gb|ABV68922.1| SDG25 [Arabidopsis thaliana]	1274	1388	0	108.9	70.1	79.6	SDG25	gbpln	Arabidopsis thaliana	AT5G42400.1 | Symbols: ATXR7, SDG25 | SET domain protein 25 | chr5:16954469-16960671 REVERSE LENGTH=1423	1274	1423	0	111.7	52.8	60.9
Rsa1.0_00002.1.g95.t4	ref|XP_002865532.1| metalloendopeptidase [Arabidopsis lyrata subsp. lyrata] gi|297311367|gb|EFH41791.1| metalloendopeptidase [Arabidopsis lyrata subsp. lyrata]	1279	1275	0	99.7	90.2	94.2	metalloendopeptidase	gbpln	Arabidopsis lyrata	AT5G42390.1 | Symbols: | Insulinase (Peptidase family M16) family protein | chr5:16945308-16952647 FORWARD LENGTH=1265	1279	1265	0	98.9	89.9	94.1
Rsa1.0_00002.1.g96.t1	ref|XP_002863793.1| hypothetical protein ARALYDRAFT_917538 [Arabidopsis lyrata subsp. lyrata] gi|297309628|gb|EFH40052.1| hypothetical protein ARALYDRAFT_917538 [Arabidopsis lyrata subsp. lyrata]	165	185	2.00E-66	112.1	81.8	88.5	hypothetical protein ARALYDRAFT_917538	gbpln	Arabidopsis lyrata	AT5G42380.1 | Symbols: CML39, CML37 | calmodulin like 37 | chr5:16942758-16943315 REVERSE LENGTH=185	165	185	2.00E-68	112.1	81.2	87.9
Rsa1.0_00002.1.g97.t1	ref|XP_002863794.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309629|gb|EFH40053.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	455	460	0	101.1	83.7	90.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G42370.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:16939329-16941463 REVERSE LENGTH=447	455	447	0	98.2	82.0	89.5
Rsa1.0_00002.1.g98.t1	ref|XP_002870812.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316648|gb|EFH47071.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	222	223	6.00E-99	100.5	80.6	89.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G14630.1 | Symbols: GLP9 | germin-like protein 9 | chr4:8392920-8393680 FORWARD LENGTH=222	222	222	4.00E-94	100.0	75.7	84.2
Rsa1.0_00002.1.g99.t2	ref|XP_002865539.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311374|gb|EFH41798.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	556	561	0	100.9	80.6	88.3	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT5G42350.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:16932106-16933797 FORWARD LENGTH=563	556	563	0	101.3	78.2	87.6
Rsa1.0_00002.1.g100.t1	ref|XP_002863798.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297309633|gb|EFH40057.1| binding protein [Arabidopsis lyrata subsp. lyrata]	642	660	0	102.8	87.1	93.9	binding protein	gbpln	Arabidopsis lyrata	AT5G42340.1 | Symbols: PUB15 | Plant U-Box 15 | chr5:16928086-16930367 REVERSE LENGTH=660	642	660	0	102.8	86.3	92.8
Rsa1.0_00002.1.g101.t1	gb|EOA13429.1| hypothetical protein CARUB_v10026470mg [Capsella rubella]	433	423	0	97.7	87.3	91.0	hypothetical protein CARUB_v10026470mg	gbpln	Capsella rubella	AT5G42320.1 | Symbols: | Zn-dependent exopeptidases superfamily protein | chr5:16918651-16920845 REVERSE LENGTH=379	433	379	0	87.5	79.0	82.9
Rsa1.0_00002.1.g102.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g103.t1	ref|NP_198387.2| S-locus lectin protein kinase-like protein [Arabidopsis thaliana] gi|313471768|sp|O65238.2|Y5537_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At5g35370; Flags: Precursor gi|332006576|gb|AED93959.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	878	872	0	99.3	83.0	89.3	S-locus lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT5G35370.1 | Symbols: | S-locus lectin protein kinase family protein | chr5:13588564-13591182 REVERSE LENGTH=872	878	872	0	99.3	83.0	89.3
Rsa1.0_00002.1.g104.t1	ref|NP_199037.2| ubiquitin family protein [Arabidopsis thaliana] gi|22654985|gb|AAM98085.1| AT5g42220/K5J14_2 [Arabidopsis thaliana] gi|30102508|gb|AAP21172.1| AT5g42220/K5J14_2 [Arabidopsis thaliana] gi|332007398|gb|AED94781.1| ubiquitin family protein [Arabidopsis thaliana]	811	879	0	108.4	75.8	83.4	ubiquitin family protein	gbpln	Arabidopsis thaliana	AT5G42220.1 | Symbols: | Ubiquitin-like superfamily protein | chr5:16872962-16877455 FORWARD LENGTH=879	811	879	0	108.4	75.8	83.4
Rsa1.0_00002.1.g105.t1	ref|XP_002894570.1| HNH endonuclease domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297340412|gb|EFH70829.1| HNH endonuclease domain-containing protein [Arabidopsis lyrata subsp. lyrata]	288	283	1.00E-124	98.3	79.9	84.4	HNH endonuclease domain-containing protein	gbpln	Arabidopsis lyrata	AT2G23840.1 | Symbols: | HNH endonuclease | chr2:10153982-10155600 REVERSE LENGTH=284	288	284	1.00E-126	98.6	80.2	85.4

Rsa1.0_00002.1.g106.t1	ref|NP_175851.1| 5'−3' exoribonuclease 4 [Arabidopsis thaliana] gi|75262833|sp|Q9FQ04.1|XRN4_ARATH RecName: Full=5'−3' exoribonuclease 4; AltName: Full=Protein ACC INSENSITIVE 1; AltName: Full=Protein ETHYLENE INSENSITIVE 5; AltName: Full=Protein EXORIBONUCLEASE 4 gi|11875626|gb|AAG40731.1|AF286718_1 XRN4 [Arabidopsis thaliana] gi|17381112|gb|AAL36368.1| putative exonuclease [Arabidopsis thaliana] gi|20259665|gb|AAM14350.1| putative exonuclease [Arabidopsis thaliana] gi|109627646|gb|ABG34298.1| At1g54490 [Arabidopsis thaliana] gi|332194988|gb|AEE33109.1| 5'−3' exoribonuclease 4 [Arabidopsis thaliana]	951	947	0	99.6	84.4	89.1	5'−3' exoribonuclease 4	gbpln	Arabidopsis thaliana	AT1G54490.1 | Symbols: AIN1, EIN5, XRN4, ATXRN4 | exoribonuclease 4 | chr1:20350300−20356650 FORWARD LENGTH=947	951	947	0	99.6	84.4	89.1
Rsa1.0_00002.1.g107.t1	gb|EOA34142.1| hypothetical protein CARUB_v10021644mg [Capsella rubella]	700	649	2.00E−68	92.7	26.9	36.3	hypothetical protein CARUB_v10021644mg	gbpln	Capsella rubella	AT5G22355.1 | Symbols: | Cysteine/Histidine−rich C1 domain family protein | chr5:7401762−7403756 FORWARD LENGTH=664	700	664	5.00E−64	94.9	19.3	23.9
Rsa1.0_00002.1.g108.t1	ref|XP_002894589.1| hypothetical protein ARALYDRAFT_892695 [Arabidopsis lyrata subsp. lyrata] gi|297340431|gb|EFH70848.1| hypothetical protein ARALYDRAFT_892695 [Arabidopsis lyrata subsp. lyrata]	257	239	4.00E−99	93.0	74.3	83.3	hypothetical protein ARALYDRAFT_892695	gbpln	Arabidopsis lyrata	AT1G54540.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline−rich glycoprotein family | chr1:20367702−20368421 REVERSE LENGTH=239	257	239	2.00E−92	93.0	73.9	84.4
Rsa1.0_00002.1.g109.t1	ref|NP_175858.1| Myosin family protein with Dil domain [Arabidopsis thaliana] gi|332194997|gb|AEE33118.1| Myosin family protein with Dil domain [Arabidopsis thaliana]	1517	1529	0	100.8	92.9	97.2	Myosin family protein with Dil domain	gbpln	Arabidopsis thaliana	AT1G54560.1 | Symbols: XIE, ATXIE | Myosin family protein with Dil domain | chr1:20371649−20379745 REVERSE LENGTH=1529	1517	1529	0	100.8	92.9	97.2
Rsa1.0_00002.1.g110.t1	ref|XP_002894592.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297340434|gb|EFH70851.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	699	703	0	100.6	83.8	91.4	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT1G54570.1 | Symbols: | Esterase/lipase/thioesterase family protein | chr1:20380649−20384953 REVERSE LENGTH=704	699	704	0	100.7	84.0	90.7
Rsa1.0_00002.1.g111.t1	ref|NP_175862.1| putative serine/threonine−protein kinase [Arabidopsis thaliana] gi|186490957|ref|NP_001117490.1| putative serine/threonine−protein kinase [Arabidopsis thaliana] gi|75339093|sp|Q9ZVM9.1|Y1461_ARATH RecName: Full=Probable serine/threonine−protein kinase At1g54610 gi|13877619|gb|AAK43887.1|AF370510_1 Unknown protein [Arabidopsis thaliana] gi|3776559|gb|AAC64876.1| Strong similarity to gene F14J9.26 gi|3482933 cdc2 protein kinase homolog from A. thaliana BAC gb|AC003970. ESTs gb|Z35332 and gb|F19907 come from this gene [Arabidopsis thaliana] gi|22136480|gb|AAM91318.1| unknown protein [Arabidopsis thaliana] gi|332195002|gb|AEE33123.1| putative serine/threonine−protein kinase [Arabidopsis thaliana] gi|332195004|gb|AEE33125.1| putative serine/threonine−protein kinase [Arabidopsis thaliana]	560	572	0	102.1	89.5	93.9	putative serine/threonine−protein kinase	gbpln	Arabidopsis thaliana	AT1G54610.3 | Symbols: | Protein kinase superfamily protein | chr1:20393962−20396902 REVERSE LENGTH=572	560	572	0	102.1	89.5	93.9

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<tr><td>Rsa1.0_00002.1.g112.t1</td><td>ref|NP_564663.1| acyl carrier protein 3 [Arabidopsis thaliana] gi|21542384|sp|P25702.2|ACP3_ARATH RecName: Full=Acyl carrier protein 3, chloroplastic; Short=ACP-3; Flags: Precursor gi|3776561|gb|AAC64878.1| Identical to DNA for acyl carrier protein (ACP) gene A2 gb|X57699 from A. thaliana. ESTs gb|W43252, gb|T42821, gb|N65229, gb|N97267, gb|F15491 and gb|AA040955 come from this gene [Arabidopsis thaliana] gi|15451048|gb|AAK96795.1| acyl carrier protein (ACP) gene [Arabidopsis thaliana] gi|18377552|gb|AAL66942.1| acyl carrier protein (ACP) A2 [Arabidopsis thaliana] gi|332195006|gb|AEE33127.1| acyl carrier protein 3 [Arabidopsis thaliana]</td><td>131</td><td>136</td><td>7.00E-51</td><td>103.8</td><td>81.7</td><td>90.1</td><td>acyl carrier protein 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G54630.1 | Symbols: ACP3 | acyl carrier protein 3 | chr1:20401642-20402919 REVERSE LENGTH=136</td><td>131</td><td>136</td><td>2.00E-53</td><td>103.8</td><td>81.7</td><td>90.1</td></tr>
<tr><td>Rsa1.0_00002.1.g113.t1</td><td>ref|NP_180850.2| DCD (Development and Cell Death) domain protein [Arabidopsis thaliana] gi|330253667|gb|AEC08761.1| DCD (Development and Cell Death) domain protein [Arabidopsis thaliana]</td><td>680</td><td>691</td><td>1.00E-152</td><td>101.6</td><td>56.3</td><td>69.4</td><td>DCD (Development and Cell Death) domain protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G32910.1 | Symbols: | DCD (Development and Cell Death) domain protein | chr2:13959685-13961989 FORWARD LENGTH=691</td><td>680</td><td>691</td><td>1.00E-154</td><td>101.6</td><td>56.3</td><td>69.4</td></tr>
<tr><td>Rsa1.0_00002.1.g114.t1</td><td>ref|XP_002892399.1| hypothetical protein ARALYDRAFT_470766 [Arabidopsis lyrata subsp. lyrata] gi|297338241|gb|EFH68658.1| hypothetical protein ARALYDRAFT_470766 [Arabidopsis lyrata subsp. lyrata]</td><td>265</td><td>266</td><td>1.00E-125</td><td>100.4</td><td>81.5</td><td>89.1</td><td>hypothetical protein ARALYDRAFT_470766</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G07440.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:2286436-2287665 REVERSE LENGTH=266</td><td>265</td><td>266</td><td>1.00E-126</td><td>100.4</td><td>80.8</td><td>88.3</td></tr>
<tr><td>Rsa1.0_00002.1.g115.t1</td><td>ref|XP_002894600.1| hypothetical protein ARALYDRAFT_474746 [Arabidopsis lyrata subsp. lyrata] gi|297340442|gb|EFH70859.1| hypothetical protein ARALYDRAFT_474746 [Arabidopsis lyrata subsp. lyrata]</td><td>852</td><td>931</td><td>0</td><td>109.3</td><td>83.0</td><td>89.2</td><td>hypothetical protein ARALYDRAFT_474746</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G54710.1 | Symbols: ATATG18H, ATG18H | homolog of yeast autophagy 18 (ATG18) H | chr1:20417019-20420733 REVERSE LENGTH=927</td><td>852</td><td>927</td><td>0</td><td>108.8</td><td>81.5</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00002.1.g116.t1</td><td>ref|NP_563830.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|79317421|ref|NP_001031006.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|117940144|sp|O04036.3|ERD6_ARATH RecName: Full=Sugar transporter ERD6; AltName: Full=Early-responsive to dehydration protein 6; AltName: Full=Sugar transporter-like protein 1 gi|3123712|dbj|BAA25989.1| ERD6 protein [Arabidopsis thaliana] gi|6686825|emb|CAB64732.1| putative sugar transporter [Arabidopsis thaliana] gi|30794056|gb|AAP40473.1| putative zinc finger protein ATZF1 [Arabidopsis thaliana] gi|332190249|gb|AEE28370.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|332190250|gb|AEE28371.1| sugar transporter ERD6 [Arabidopsis thaliana]</td><td>343</td><td>496</td><td>1.00E-149</td><td>144.6</td><td>74.3</td><td>85.7</td><td>sugar transporter ERD6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G08930.2 | Symbols: ERD6 | Major facilitator superfamily protein | chr1:2873604-2876979 FORWARD LENGTH=496</td><td>343</td><td>496</td><td>1.00E-151</td><td>144.6</td><td>74.3</td><td>85.7</td></tr>
<tr><td>Rsa1.0_00002.1.g117.t1</td><td>ref|XP_002894606.1| hypothetical protein ARALYDRAFT_892725 [Arabidopsis lyrata subsp. lyrata] gi|297340448|gb|EFH70865.1| hypothetical protein ARALYDRAFT_892725 [Arabidopsis lyrata subsp. lyrata]</td><td>302</td><td>320</td><td>1.00E-119</td><td>106.0</td><td>73.5</td><td>85.4</td><td>hypothetical protein ARALYDRAFT_892725</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G72210.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:27180066-27182268 FORWARD LENGTH=320</td><td>302</td><td>320</td><td>6.00E-53</td><td>106.0</td><td>35.4</td><td>47.0</td></tr>
<tr><td>Rsa1.0_00002.1.g118.t1</td><td>ref|NP_175886.1| Late embryogenesis abundant-related protein [Arabidopsis thaliana] gi|9857516|gb|AAG00871.1|AC064840_2 Unknown protein [Arabidopsis thaliana] gi|12322166|gb|AAG51122.1|AC069144_19 late embryogenesis protein, putative [Arabidopsis thaliana] gi|332195039|gb|AEE33160.1| Late embryogenesis abundant-related protein [Arabidopsis thaliana]</td><td>349</td><td>347</td><td>1.00E-179</td><td>99.4</td><td>85.1</td><td>92.8</td><td>Late embryogenesis abundant-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G54890.1 | Symbols: | Late embryogenesis abundant (LEA) protein-related | chr1:20463107-20464407 FORWARD LENGTH=347</td><td>349</td><td>347</td><td>0</td><td>99.4</td><td>85.1</td><td>92.8</td></tr>
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Rsa1.0_00002.1.g119.t1	ref|XP_002891917.1| hypothetical protein ARALYDRAFT_474768 [Arabidopsis lyrata subsp. lyrata] gi|297337759|gb|EFH68176.1| hypothetical protein ARALYDRAFT_474768 [Arabidopsis lyrata subsp. lyrata]	865	894	0	103.4	67.4	75.3	hypothetical protein ARALYDRAFT_474768	gbpln	Arabidopsis lyrata	AT1G54920.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages. | chr1:20470916-20474898 FORWARD LENGTH=901	865	901	0	104.2	66.7	74.7
Rsa1.0_00002.1.g120.t1	ref|NP_175890.1| GRF zinc finger / Zinc knuckle protein [Arabidopsis thaliana] gi|9857519|gb|AAG00874.1|AC064840_5 Hypothetical protein [Arabidopsis thaliana] gi|12322160|gb|AAG51116.1|AC069144_13 hypothetical protein [Arabidopsis thaliana] gi|332195043|gb|AEE33164.1| GRF zinc finger / Zinc knuckle protein [Arabidopsis thaliana]	368	353	6.00E-57	95.9	43.5	56.3	GRF zinc finger / Zinc knuckle protein	gbpln	Arabidopsis thaliana	AT1G54930.1 | Symbols: | GRF zinc finger / Zinc knuckle protein | chr1:20478267-20479671 REVERSE LENGTH=353	368	353	1.00E-59	95.9	43.5	56.3
Rsa1.0_00002.1.g121.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g122.t1	ref|NP_001058585.1| Os06g0715500 [Oryza sativa Japonica Group] gi|53791783|dbj|BAD53577.1| putative SSR alpha subunit [Oryza sativa Japonica Group] gi|113596625|dbj|BAF20499.1| Os06g0715500 [Oryza sativa Japonica Group] gi|125598503|gb|EAZ38283.1| hypothetical protein OsJ_22661 [Oryza sativa Japonica Group] gi|215704734|dbj|BAG94762.1| unnamed protein product [Oryza sativa Japonica Group] gi|215765401|dbj|BAG87098.1| unnamed protein product [Oryza sativa Japonica Group] gi|215765644|dbj|BAG87341.1| unnamed protein product [Oryza sativa Japonica Group]	168	257	3.00E-23	153.0	31.5	39.3	Os06g0715500	gbpln	Oryza sativa	AT2G21160.1 | Symbols: | Translocon-associated protein (TRAP), alpha subunit | chr2:9068428-9070207 FORWARD LENGTH=258	168	258	6.00E-19	153.6	39.9	43.5
Rsa1.0_00002.1.g123.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g124.t1	gb|EOA34295.1| hypothetical protein CARUB_v10021810mg [Capsella rubella]	542	559	0	103.1	80.4	89.5	hypothetical protein CARUB_v10021810mg	gbpln	Capsella rubella	AT1G54940.1 | Symbols: PGSIP4 | plant glycogenin-like starch initiation protein 4 | chr1:20481690-20484541 FORWARD LENGTH=557	542	557	0	102.8	78.4	89.3
Rsa1.0_00002.1.g125.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g126.t1	ref|XP_002891939.1| hypothetical protein ARALYDRAFT_474779 [Arabidopsis lyrata subsp. lyrata] gi|297337781|gb|EFH68198.1| hypothetical protein ARALYDRAFT_474779 [Arabidopsis lyrata subsp. lyrata]	873	845	0	96.8	75.8	82.0	hypothetical protein ARALYDRAFT_474779	gbpln	Arabidopsis lyrata	AT1G55040.1 | Symbols: | zinc finger (Ran-binding) family protein | chr1:20534895-20538901 FORWARD LENGTH=849	873	849	0	97.3	77.0	82.7
Rsa1.0_00002.1.g127.t2	gb|EOA34587.1| hypothetical protein CARUB_v10022144mg [Capsella rubella]	329	349	1.00E-169	106.1	84.2	94.5	hypothetical protein CARUB_v10022144mg	gbpln	Capsella rubella	AT1G58725.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:21771935-21773365 REVERSE LENGTH=349	329	349	1.00E-172	106.1	85.1	94.2
Rsa1.0_00002.1.g128.t1	ref|XP_002891941.1| hypothetical protein ARALYDRAFT_474781 [Arabidopsis lyrata subsp. lyrata] gi|297337783|gb|EFH68200.1| hypothetical protein ARALYDRAFT_474781 [Arabidopsis lyrata subsp. lyrata]	801	892	0	111.4	65.0	76.8	hypothetical protein ARALYDRAFT_474781	gbpln	Arabidopsis lyrata	AT1G55050.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G09040.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:20542779-20545612 FORWARD LENGTH=915	801	915	0	114.2	61.9	73.8
Rsa1.0_00002.1.g129.t1	ref|XP_002891941.1| hypothetical protein ARALYDRAFT_474781 [Arabidopsis lyrata subsp. lyrata] gi|297337783|gb|EFH68200.1| hypothetical protein ARALYDRAFT_474781 [Arabidopsis lyrata subsp. lyrata]	802	892	0	111.2	66.3	77.8	hypothetical protein ARALYDRAFT_474781	gbpln	Arabidopsis lyrata	AT1G55050.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G09040.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:20542779-20545612 FORWARD LENGTH=915	802	915	0	114.1	62.2	74.3

Rsa1.0_00002.1.g130.t1	ref|XP_002888210.1| hypothetical protein ARALYDRAFT_475383 [Arabidopsis lyrata subsp. lyrata] gi|297334051|gb|EFH64469.1| hypothetical protein ARALYDRAFT_475383 [Arabidopsis lyrata subsp. lyrata]	309	350	1.00E-150	113.3	84.5	92.9	hypothetical protein ARALYDRAFT_475383	gbpln	Arabidopsis lyrata	AT1G58725.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:21771935-21773365 REVERSE LENGTH=349	309	349	1.00E-151	112.9	84.1	92.2
Rsa1.0_00002.1.g131.t1	ref|XP_002894623.1| hypothetical protein ARALYDRAFT_474782 [Arabidopsis lyrata subsp. lyrata] gi|297340465|gb|EFH70882.1| hypothetical protein ARALYDRAFT_474782 [Arabidopsis lyrata subsp. lyrata]	355	355	7.00E-94	100.0	67.9	77.7	hypothetical protein ARALYDRAFT_474782	gbpln	Arabidopsis lyrata	AT1G56210.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:21035715-21037019 FORWARD LENGTH=364	355	364	2.00E-92	102.5	66.8	77.7
Rsa1.0_00002.1.g132.t1	ref|XP_002891949.1| hypothetical protein ARALYDRAFT_892793 [Arabidopsis lyrata subsp. lyrata] gi|297337791|gb|EFH68208.1| hypothetical protein ARALYDRAFT_892793 [Arabidopsis lyrata subsp. lyrata]	669	691	0	103.3	84.8	91.3	hypothetical protein ARALYDRAFT_892793	gbpln	Arabidopsis lyrata	AT1G56290.1 | Symbols: | CwfJ-like family protein | chr1:21075939-21078608 FORWARD LENGTH=692	669	692	0	103.4	84.6	91.6
Rsa1.0_00002.1.g133.t1	gb|EOA33719.1| hypothetical protein CARUB_v10019911mg [Capsella rubella]	581	668	0	115.0	79.2	86.4	hypothetical protein CARUB_v10019911mg	gbpln	Capsella rubella	AT1G56310.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr1:21082863-21085564 FORWARD LENGTH=589	581	589	0	101.4	78.1	87.6
Rsa1.0_00002.1.g134.t1	dbj|BAA78331.1| serine decarboxylase [Brassica napus]	479	490	0	102.3	93.9	96.2	serine decarboxylase	gbpln	Brassica napus	AT1G43710.1 | Symbols: emb1075 | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr1:16486534-16488298 REVERSE LENGTH=482	479	482	0	100.6	89.1	92.7
Rsa1.0_00002.1.g135.t1	sp|O04267.1|SAR1B_BRACM RecName: Full=GTP-binding protein SAR1B gi|2108347|gb|AAC49717.1| small GTP-binding protein Bsar1b [Brassica rapa subsp. oleifera]	195	195	1.00E-109	100.0	99.0	99.5	RecName: Full=GTP-binding protein SAR1B gi|2108347|gb|AAC49717.1| small GTP-binding protein Bsar1b	gbpln	Brassica rapa	AT1G56330.1 | Symbols: SAR1, ATSAR1, ATSARA1B, ATSAR1B, SAR1B | secretion-associated RAS 1B | chr1:21086845-21088478 REVERSE LENGTH=193	195	193	1.00E-108	99.0	97.4	98.5
Rsa1.0_00002.1.g136.t1	ref|XP_002894642.1| pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297340484|gb|EFH70901.1| pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	296	321	1.00E-125	108.4	80.1	87.2	pseudouridine synthase family protein	gbpln	Arabidopsis lyrata	AT1G56345.1 | Symbols: | Pseudouridine synthase family protein | chr1:21093409-21094454 REVERSE LENGTH=322	296	322	1.00E-120	108.8	78.4	87.2
Rsa1.0_00002.1.g137.t2	ref|XP_002891952.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337794|gb|EFH68211.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	434	418	0	96.3	78.6	84.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G56340.1 | Symbols: CRT1, CRT1a, AtCRT1a | calreticulin 1a | chr1:21090059-21092630 REVERSE LENGTH=425	434	425	1.00E-177	97.9	76.7	78.6
Rsa1.0_00002.1.g138.t1	ref|NP_001117508.1| uncharacterized protein [Arabidopsis thaliana] gi|332195272|gb|AEE33393.1| uncharacterized protein AT1G56423 [Arabidopsis thaliana]	270	270	1.00E-126	100.0	82.6	91.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G56423.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:21129075-21130558 FORWARD LENGTH=270	270	270	1.00E-128	100.0	82.6	91.9
Rsa1.0_00002.1.g139.t1	gb|EOA35645.1| hypothetical protein CARUB_v10020862mg [Capsella rubella]	305	245	1.00E-134	80.3	75.1	78.4	hypothetical protein CARUB_v10020862mg	gbpln	Capsella rubella	AT1G56450.1 | Symbols: PBG1 | 20S proteasome beta subunit G1 | chr1:21141970-21144186 FORWARD LENGTH=246	305	246	1.00E-135	80.7	73.8	77.4
Rsa1.0_00002.1.g140.t1	gb|AAZ67609.1| 80A08_24 [Brassica rapa subsp. pekinensis]	330	475	3.00E-11	143.9	13.0	14.8	80A08_24	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00002.1.g141.t1	emb|CAB41158.1| putative protein [Arabidopsis thaliana]	645	669	1.00E-177	103.7	54.9	66.4	putative protein	gbpln	Arabidopsis thaliana	AT5G22355.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:7401762-7403756 FORWARD LENGTH=664	645	664	1.00E-172	102.9	52.2	63.7
Rsa1.0_00002.1.g142.t1	ref|XP_002891968.1| hypothetical protein ARALYDRAFT_892829 [Arabidopsis lyrata subsp. lyrata] gi|297337810|gb|EFH68227.1| hypothetical protein ARALYDRAFT_892829 [Arabidopsis lyrata subsp. lyrata]	1062	1058	0	99.6	89.3	93.4	hypothetical protein ARALYDRAFT_892829	gbpln	Arabidopsis lyrata	AT1G56500.1 | Symbols: | haloacid dehalogenase-like hydrolase family protein | chr1:21159775-21167092 FORWARD LENGTH=1055	1062	1055	0	99.3	88.6	92.7

Rsa1.0_00002.1.g143.t1	ref|NP_176050.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75173051|sp|Q9FXA9.1|PPR83_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At1g56570 gi|9954755|gb|AAG09106.1|AC009323_17 Hypothetical protein [Arabidopsis thaliana] gi|332195289|gb|AEE33410.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	609	611	0	100.3	88.0	94.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G56570.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:21195804-21197721 FORWARD LENGTH=611	609	611	0	100.3	88.0	94.1
Rsa1.0_00002.1.g144.t1	ref|NP_564720.1| uncharacterized protein [Arabidopsis thaliana] gi|9954754|gb|AAG09105.1|AC009323_16 Unknown protein [Arabidopsis thaliana] gi|16648669|gb|AAL25527.1| At1g56580/F25P12_18 [Arabidopsis thaliana] gi|20856239|gb|AAM26655.1| At1g56580/F25P12_18 [Arabidopsis thaliana] gi|332195290|gb|AEE33411.1| uncharacterized protein AT1G56580 [Arabidopsis thaliana]	155	166	4.00E-75	107.1	90.3	92.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G56580.1 | Symbols: SVB | Protein of unknown function, DUF538 | chr1:21198402-21198902 REVERSE LENGTH=166	155	166	1.00E-77	107.1	90.3	92.3
Rsa1.0_00002.1.g145.t1	ref|NP_176052.3| clathrin adaptor complexes medium subunit-like protein [Arabidopsis thaliana] gi|332195291|gb|AEE33412.1| clathrin adaptor complexes medium subunit-like protein [Arabidopsis thaliana]	435	415	0	95.4	87.4	91.5	clathrin adaptor complexes medium subunit-like protein	gbpln	Arabidopsis thaliana	AT1G56590.1 | Symbols: ZIP4 | Clathrin adaptor complexes medium subunit family protein | chr1:21202250-21204697 REVERSE LENGTH=415	435	415	0	95.4	87.4	91.5
Rsa1.0_00002.1.g146.t1	gb|AAM19710.1|AF499723_1 galactinol synthase-like protein [Eutrema halophilum]	331	337	1.00E-169	101.8	87.9	93.4	galactinol synthase-like protein	gbpln	Eutrema halophilum	AT1G56600.1 | Symbols: AtGolS2, GolS2 | galactinol synthase 2 | chr1:21207620-21209291 FORWARD LENGTH=335	331	335	1.00E-165	101.2	84.9	92.1
Rsa1.0_00002.1.g147.t1	ref|XP_002872685.1| hypothetical protein ARALYDRAFT_490081 [Arabidopsis lyrata subsp. lyrata] gi|297318522|gb|EFH48944.1| hypothetical protein ARALYDRAFT_490081 [Arabidopsis lyrata subsp. lyrata]	449	812	1.00E-109	180.8	53.9	63.7	hypothetical protein ARALYDRAFT_490081	gbpln	Arabidopsis lyrata	AT4G04220.1 | Symbols: AtRLP46, RLP46 | receptor like protein 46 | chr4:2033427-2035946 FORWARD LENGTH=811	449	811	1.00E-103	180.6	53.9	64.6
Rsa1.0_00002.1.g148.t1	#	#	#	#	#	#	#	–	----	----	AT1G56660.1 | Symbols: | unknown protein; Has 665200 Blast hits to 205811 proteins in 4684 species: Archae - 3320; Bacteria - 107592; Metazoa - 249086; Fungi - 76753; Plants - 38542; Viruses - 3008; Other Eukaryotes - 186899 (source: NCBI BLink). | chr1:21238809-21240377 FORWARD LENGTH=522	490	522	2.00E-11	106.5	11.2	14.3
Rsa1.0_00002.1.g149.t1	ref|NP_176059.1| GDSL esterase/lipase LIP-4 [Arabidopsis thaliana] gi|75173058|sp|Q9FXB6.1|LIP4_ARATH RecName: Full=GDSL esterase/lipase LIP-4; AltName: Full=Extracellular lipase LIP-4; Flags: Precursor gi|9954747|gb|AAG09098.1|AC009323_9 Similar to nodulins [Arabidopsis thaliana] gi|332195300|gb|AEE33421.1| GDSL esterase/lipase LIP-4 [Arabidopsis thaliana]	92	373	1.00E-34	405.4	82.6	89.1	GDSL esterase/lipase LIP-4	gbpln	Arabidopsis thaliana	AT1G56670.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:21241688-21243965 FORWARD LENGTH=373	92	373	2.00E-37	405.4	82.6	89.1
Rsa1.0_00002.1.g150.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1260	1214	0	96.3	34.5	52.2	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1260	626	1.00E-76	49.7	12.5	19.9
Rsa1.0_00002.1.g151.t1	ref|XP_002894685.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340527|gb|EFH70944.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	62	62	3.00E-21	100.0	75.8	91.9	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00002.1.g152.t1	gb|EOA33210.1| hypothetical protein CARUB_v10019892mg [Capsella rubella]	328	692	1.00E-109	211.0	71.6	75.6	hypothetical protein CARUB_v10019892mg	gbpln	Capsella rubella	AT1G57700.1 | Symbols: | Protein kinase superfamily protein | chr1:21371051-21373860 FORWARD LENGTH=692	328	692	1.00E-111	211.0	71.0	75.9

Rsa1.0_00002.1.g153.t1	ref|NP_176081.1| uncharacterized protein [Arabidopsis thaliana] gi|42571907|ref|NP_974044.1| uncharacterized protein [Arabidopsis thaliana] gi|12321352|gb|AAG50748.1|AC079733_16 hypothetical protein [Arabidopsis thaliana] gi|18176030|gb|AAL59971.1| unknown protein [Arabidopsis thaliana] gi|22136846|gb|AAM91767.1| unknown protein [Arabidopsis thaliana] gi|332195330|gb|AEE33451.1| uncharacterized protein AT1G57680 [Arabidopsis thaliana] gi|332195331|gb|AEE33452.1| uncharacterized protein AT1G57680 [Arabidopsis thaliana]	361	362	1.00E−158	100.3	84.5	90.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G57680.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031277 (InterPro:IPR016971); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr1:21362749−21363837 REVERSE LENGTH=362	361	362	1.00E−160	100.3	84.5	90.6
Rsa1.0_00002.1.g154.t1	ref|XP_002894649.1| hypothetical protein ARALYDRAFT_892826 [Arabidopsis lyrata subsp. lyrata] gi|297340491|gb|EFH70908.1| hypothetical protein ARALYDRAFT_892826 [Arabidopsis lyrata subsp. lyrata]	345	352	1.00E−130	102.0	67.2	78.6	hypothetical protein ARALYDRAFT_892826	gbpln	Arabidopsis lyrata	AT2G19150.1 | Symbols: | Pectin lyase−like superfamily protein | chr2:8305100−8307444 FORWARD LENGTH=339	345	339	2.00E−66	98.3	39.7	51.0
Rsa1.0_00002.1.g155.t1	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	1969	1274	0	64.7	30.5	41.5	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1969	575	1.00E−59	29.2	8.3	13.2
Rsa1.0_00002.1.g156.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00002.1.g157.t1	ref|XP_002888226.1| helicase domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297334067|gb|EFH64485.1| helicase domain−containing protein [Arabidopsis lyrata subsp. lyrata]	1425	1458	0	102.3	87.4	93.3	helicase domain−containing protein	gbpln	Arabidopsis lyrata	AT1G58060.1 | Symbols: | RNA helicase family protein | chr1:21489480−21501775 REVERSE LENGTH=1459	1425	1459	0	102.4	87.4	93.1
Rsa1.0_00002.1.g158.t1	gb|ACP30602.1| disease resistance protein [Brassica rapa subsp. pekinensis]	291	938	4.00E−27	322.3	24.1	27.5	disease resistance protein	gbpln	Brassica rapa	AT5G18350.1 | Symbols: | Disease resistance protein (TIR−NBS−LRR class) family | chr5:6074069−6078569 REVERSE LENGTH=1245	291	1245	2.00E−13	427.8	17.5	21.0
Rsa1.0_00002.1.g159.t1	gb|EOA34251.1| hypothetical protein CARUB_v10021763mg [Capsella rubella]	236	268	6.00E−84	113.6	78.4	85.6	hypothetical protein CARUB_v10021763mg	gbpln	Capsella rubella	AT1G58070.1 | Symbols: | unknown protein; Has 286 Blast hits to 266 proteins in 81 species: Archae − 2; Bacteria − 25; Metazoa − 90; Fungi − 19; Plants − 78; Viruses − 4; Other Eukaryotes − 68 (source: NCBI BLink). | chr1:21502968−21503822 FORWARD LENGTH=284	236	284	2.00E−83	120.3	78.8	86.4
Rsa1.0_00002.1.g160.t1	gb|AAT74597.1| chloroplast ATP phosphoribosyl transferase [Alyssum montanum]	409	405	0	99.0	88.3	93.2	chloroplast ATP phosphoribosyl transferase	gbpln	Alyssum montanum	AT1G58080.1 | Symbols: ATATP−PRT1, HISN1A, ATP−PRT1 | ATP phosphoribosyl transferase 1 | chr1:21504562−21507429 REVERSE LENGTH=411	409	411	0	100.5	86.6	91.0
Rsa1.0_00002.1.g161.t1	ref|XP_002888231.1| hypothetical protein ARALYDRAFT_475419 [Arabidopsis lyrata subsp. lyrata] gi|297334072|gb|EFH64490.1| hypothetical protein ARALYDRAFT_475419 [Arabidopsis lyrata subsp. lyrata]	394	390	1.00E−126	99.0	74.1	78.9	hypothetical protein ARALYDRAFT_475419	gbpln	Arabidopsis lyrata	AT1G58100.1 | Symbols: | TCP family transcription factor | chr1:21512680−21513885 REVERSE LENGTH=401	394	401	1.00E−128	101.8	75.1	81.0
Rsa1.0_00002.1.g162.t1	dbj|BAJ34015.1| unnamed protein product [Thellungiella halophila]	369	372	1.00E−170	100.8	85.4	91.1	unnamed protein product	−−−−	−−−−	AT1G58110.2 | Symbols: | Basic−leucine zipper (bZIP) transcription factor family protein | chr1:21515919−21517374 REVERSE LENGTH=374	369	374	1.00E−151	101.4	78.3	87.3
Rsa1.0_00002.1.g163.t1	gb|AEM45875.1| hypothetical protein [Brassica rapa subsp. oleifera]	423	419	0	99.1	87.9	92.9	hypothetical protein	gbpln	Brassica rapa	AT1G58120.1 | Symbols: | BEST Arabidopsis thaliana protein match is: methyltransferases (TAIR:AT5G01710.1); Has 93 Blast hits to 93 proteins in 15 species: Archae − 0; Bacteria − 0; Metazoa − 1; Fungi − 0; Plants − 92; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:21520962−21522224 FORWARD LENGTH=420	423	420	0	99.3	80.1	87.9
Rsa1.0_00002.1.g164.t1	gb|AAG50957.1|AC073943_7 hypothetical protein [Arabidopsis thaliana]	910	1195	0	131.3	85.2	90.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G58210.1 | Symbols: EMB1674 | kinase interacting family protein | chr1:21553621−21558056 FORWARD LENGTH=1246	910	1246	0	136.9	84.7	90.3

Rsa1.0_00002.1.g165.t1	ref|NP_176118.2| myb family transcription factor [Arabidopsis thaliana] gi|26449358|dbj|BAC41806.1| putative MYB-family transcription factor [Arabidopsis thaliana] gi|29029054|gb|AAO64906.1| At1g58220 [Arabidopsis thaliana] gi|41619072|gb|AAS10017.1| MYB transcription factor [Arabidopsis thaliana] gi|332195394|gb|AEE33515.1| myb family transcription factor [Arabidopsis thaliana]	716	834	0	116.5	71.6	81.1	myb family transcription factor	gbpln	Arabidopsis thaliana	AT1G58220.1 | Symbols: | Homeodomain-like superfamily protein | chr1:21558388-21562669 REVERSE LENGTH=834	716	834	0	116.5	71.6	81.1
Rsa1.0_00002.1.g166.t2	ref|XP_002888245.1| hypothetical protein ARALYDRAFT_475439 [Arabidopsis lyrata subsp. lyrata] gi|297334086|gb|EFH64504.1| hypothetical protein ARALYDRAFT_475439 [Arabidopsis lyrata subsp. lyrata]	2608	2607	0	100.0	86.9	92.5	hypothetical protein ARALYDRAFT_475439	gbpln	Arabidopsis lyrata	AT1G58250.1 | Symbols: SAB | Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain | chr1:21587317-21601373 REVERSE LENGTH=2607	2608	2607	0	100.0	87.0	92.4
Rsa1.0_00002.1.g167.t1	gb|ACR10268.1| sulfotransferase 5b [Brassica rapa subsp. pekinensis]	345	339	1.00E-177	98.3	90.7	94.2	sulfotransferase 5b	gbpln	Brassica rapa	AT1G74090.1 | Symbols: SOT18, ATSOT18, ATST5B | desulfo-glucosinolate sulfotransferase 18 | chr1:27863003-27864055 FORWARD LENGTH=350	345	350	1.00E-158	101.4	77.4	88.1
Rsa1.0_00002.1.g168.t1	gb|ACR10269.1| sulfotransferase 5b [Brassica rapa subsp. pekinensis]	339	342	1.00E-169	100.9	84.4	92.3	sulfotransferase 5b	gbpln	Brassica rapa	AT1G74090.1 | Symbols: SOT18, ATSOT18, ATST5B | desulfo-glucosinolate sulfotransferase 18 | chr1:27863003-27864055 FORWARD LENGTH=350	339	350	1.00E-143	103.2	71.7	84.7
Rsa1.0_00002.1.g169.t3	ref|NP_176126.1| heme oxygenase 4 [Arabidopsis thaliana] gi|75180109|sp|Q9LQC0.1|HMOX4_ARATH RecName: Full=Heme oxygenase 4, chloroplastic; Flags: Precursor gi|8979943|gb|AAF82257.1|AC008051_8 Contains similarity to heme oxygenase 1 (HO1) from Arabidopsis thaliana gb|AF132475 [Arabidopsis thaliana] gi|91805985|gb|ABE65721.1| heme oxygenase [Arabidopsis thaliana] gi|332195412|gb|AEE33533.1| heme oxygenase 4 [Arabidopsis thaliana]	339	283	1.00E-100	83.5	57.5	67.6	heme oxygenase 4	gbpln	Arabidopsis thaliana	AT1G58300.1 | Symbols: HO4 | heme oxygenase 4 | chr1:21628015-21629996 REVERSE LENGTH=283	339	283	1.00E-102	83.5	57.5	67.6
Rsa1.0_00002.1.g170.t1	dbj|BAJ33912.1| unnamed protein product [Thellungiella halophila]	532	539	0	101.3	94.2	96.8	unnamed protein product	----	----	AT1G58290.1 | Symbols: HEMA1 | Glutamyl-tRNA reductase family protein | chr1:21624028-21626051 REVERSE LENGTH=543	532	543	0	102.1	90.6	95.1
Rsa1.0_00002.1.g171.t4	ref|XP_002880114.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297325953|gb|EFH56373.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata]	506	507	0	100.2	90.1	94.1	glycosyl hydrolase family 1 protein	gbpln	Arabidopsis lyrata	AT2G44450.1 | Symbols: BGLU15 | beta glucosidase 15 | chr2:18340966-18343744 FORWARD LENGTH=506	506	506	0	100.0	92.1	97.0
Rsa1.0_00002.1.g172.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g173.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g174.t1	ref|XP_002888219.1| hypothetical protein ARALYDRAFT_893660 [Arabidopsis lyrata subsp. lyrata] gi|297334060|gb|EFH64478.1| hypothetical protein ARALYDRAFT_893660 [Arabidopsis lyrata subsp. lyrata]	531	532	0	100.2	91.1	95.5	hypothetical protein ARALYDRAFT_893660	gbpln	Arabidopsis lyrata	AT1G58340.1 | Symbols: ZF14 | MATE efflux family protein | chr1:21653162-21655117 FORWARD LENGTH=532	531	532	0	100.2	91.1	95.3
Rsa1.0_00002.1.g175.t1	ref|NP_564732.1| Putative serine esterase family protein [Arabidopsis thaliana] gi|186491769|ref|NP_001117514.1| Putative serine esterase family protein [Arabidopsis thaliana] gi|8979939|gb|AAF82253.1|AC008051_4 Identical to gene ZW18 from Arabidopsis thaliana gb|AB028199 [Arabidopsis thaliana] gi|6520167|dbj|BAA87940.1| ZW18 [Arabidopsis thaliana] gi|110741889|dbj|BAE98886.1| hypothetical protein [Arabidopsis thaliana] gi|332195417|gb|AEE33538.1| Putative serine esterase family protein [Arabidopsis thaliana] gi|332195418|gb|AEE33539.1| Putative serine esterase family protein [Arabidopsis thaliana]	786	794	0	101.0	87.5	93.8	Putative serine esterase family protein	gbpln	Arabidopsis thaliana	AT1G58350.2 | Symbols: ZW18 | Putative serine esterase family protein | chr1:21663131-21666827 REVERSE LENGTH=794	786	794	0	101.0	87.5	93.8
Rsa1.0_00002.1.g176.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00002.1.g177.t1	emb|CAD92449.1| amino acid permease 1 [Brassica napus]	509	485	0	95.3	94.1	94.9	amino acid permease 1	gbpln	Brassica napus	AT1G58360.1 | Symbols: AAP1, NAT2 | amino acid permease 1 | chr1:21676623-21680313 FORWARD LENGTH=485	509	485	0	95.3	87.2	92.3
Rsa1.0_00002.1.g178.t1	gb|EOA33499.1| hypothetical protein CARUB_v10019737mg [Capsella rubella]	919	941	0	102.4	88.7	93.5	hypothetical protein CARUB_v10019737mg	gbpln	Capsella rubella	AT1G58370.1 | Symbols: RXF12, ATXYN1 | glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein | chr1:21684751-21688209 FORWARD LENGTH=917	919	917	0	99.8	89.4	93.5
Rsa1.0_00002.1.g179.t1	gb|ACP30587.1| disease resistance protein [Brassica rapa subsp. pekinensis]	913	929	0	101.8	72.5	82.6	disease resistance protein	gbpln	Brassica rapa	AT1G58390.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:21690962-21693891 REVERSE LENGTH=907	913	907	0	99.3	55.8	68.6
Rsa1.0_00002.1.g180.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g181.t1	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	442	578	7.00E-97	130.8	48.9	65.4	hypothetical protein 27.t00126	gbpln	Brassica oleracea	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	442	1399	2.00E-20	316.5	10.9	15.4
Rsa1.0_00002.1.g182.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g183.t1	ref|NP_564733.1| uncharacterized protein [Arabidopsis thaliana] gi|12321051|gb|AAG50647.1|AC082643_11 hypothetical protein [Arabidopsis thaliana] gi|89111882|gb|ABD60713.1| At1g58420 [Arabidopsis thaliana] gi|332195426|gb|AEE33547.1| uncharacterized protein AT1G58420 [Arabidopsis thaliana] gi|343455557|gb|AEM36343.1| At1g58420 [Arabidopsis thaliana]	172	179	7.00E-60	104.1	83.7	90.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G58420.1 | Symbols: | Uncharacterised conserved protein UCP031279 | chr1:21707407-21707946 FORWARD LENGTH=179	172	179	3.00E-62	104.1	83.7	90.7
Rsa1.0_00002.1.g184.t2	ref|XP_002886690.1| hypothetical protein ARALYDRAFT_475389 [Arabidopsis lyrata subsp. lyrata] gi|297332531|gb|EFH62949.1| hypothetical protein ARALYDRAFT_475389 [Arabidopsis lyrata subsp. lyrata]	566	530	0	93.6	85.7	89.6	hypothetical protein ARALYDRAFT_475389	gbpln	Arabidopsis lyrata	AT1G58440.1 | Symbols: XF1, SQE1 | FAD/NAD(P)-binding oxidoreductase family protein | chr1:21714094-21717246 REVERSE LENGTH=531	566	531	0	93.8	84.6	88.5
Rsa1.0_00002.1.g185.t1	ref|XP_002888212.1| hypothetical protein ARALYDRAFT_315379 [Arabidopsis lyrata subsp. lyrata] gi|297334053|gb|EFH64471.1| hypothetical protein ARALYDRAFT_315379 [Arabidopsis lyrata subsp. lyrata]	152	150	4.00E-50	98.7	74.3	78.9	hypothetical protein ARALYDRAFT_315379	gbpln	Arabidopsis lyrata	AT1G58460.1 | Symbols: | unknown protein; Has 35 Blast hits to 35 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:21721404-21722429 FORWARD LENGTH=177	152	177	3.00E-46	116.4	73.0	77.0
Rsa1.0_00002.1.g186.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00002.1.g187.t1	gb|EOA35303.1| hypothetical protein CARUB_v10020477mg, partial [Capsella rubella]	362	377	1.00E-129	104.1	68.0	79.3	hypothetical protein CARUB_v10020477mg, partial	gbpln	Capsella rubella	AT1G58470.1 | Symbols: ATRBP1, RBP1 | RNA-binding protein 1 | chr1:21727374-21728539 FORWARD LENGTH=360	362	360	1.00E-131	99.4	68.5	79.3
Rsa1.0_00002.1.g188.t1	ref|NP_176403.1| Mitochondrial transcription termination factor family protein [Arabidopsis thaliana] gi|50253494|gb|AAT71949.1| At1g62120 [Arabidopsis thaliana] gi|53850523|gb|AAU95438.1| At1g62120 [Arabidopsis thaliana] gi|332195804|gb|AEE33925.1| Mitochondrial transcription termination factor family protein [Arabidopsis thaliana]	430	437	1.00E-150	101.6	64.9	79.1	Mitochondrial transcription termination factor family protein	gbpln	Arabidopsis thaliana	AT1G62120.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:22960326-22961639 REVERSE LENGTH=437	430	437	1.00E-153	101.6	64.9	79.1
Rsa1.0_00002.1.g189.t1	gb|AEM36358.1| At1g59510 [Arabidopsis thaliana]	447	382	1.00E-151	85.5	62.6	70.9	At1g59510	gbpln	Arabidopsis thaliana	AT1G59510.1 | Symbols: CF9 | Carbohydrate-binding protein | chr1:21859768-21860913 FORWARD LENGTH=381	447	381	1.00E-151	85.2	61.3	70.2
Rsa1.0_00002.1.g190.t1	ref|NP_176162.1| basic leucine-zipper 4 [Arabidopsis thaliana] gi|8778737|gb|AAF79745.1|AC009317_4 T30E16.6 [Arabidopsis thaliana] gi|14475943|gb|AAK62790.1|AC027036_11 G-box binding factor, putative [Arabidopsis thaliana] gi|15278035|gb|AAK94023.1|AF400619_1 transcription factor-like protein bZIP4 [Arabidopsis thaliana] gi|91805987|gb|ABE65722.1| bZIP transcription factor family protein [Arabidopsis thaliana] gi|225898030|dbj|BAH30347.1| hypothetical protein [Arabidopsis thaliana] gi|332195463|gb|AEE33584.1| basic leucine-zipper 4 [Arabidopsis thaliana]	365	148	2.00E-51	40.5	30.1	35.3	basic leucine-zipper 4	gbpln	Arabidopsis thaliana	AT1G59530.1 | Symbols: ATBZIP4, bZIP4 | basic leucine-zipper 4 | chr1:21868262-21868708 FORWARD LENGTH=148	365	148	5.00E-54	40.5	30.1	35.3

Rsa1.0_00002.1.g191.t1	ref|XP_002888202.1| ZCF125 [Arabidopsis lyrata subsp. lyrata] gi|297334043|gb|EFH64461.1| ZCF125 [Arabidopsis lyrata subsp. lyrata]	827	827	0	100.0	87.3	92.1	ZCF125	gbpln	Arabidopsis lyrata	AT1G59540.1 | Symbols: ZCF125 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:21874083-21879382 FORWARD LENGTH=823	827	823	0	99.5	86.2	92.0
Rsa1.0_00002.1.g192.t1	ref|XP_002864007.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309842|gb|EFH40266.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1017	3616	0	355.6	89.9	95.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G55860.2 | Symbols: UPL1 | ubiquitin-protein ligase 1 | chr1:20879900-20892910 REVERSE LENGTH=3681	1017	3681	1.00E-156	361.9	35.6	51.4
Rsa1.0_00003.1.g193.t1	ref|XP_002870026.1| hypothetical protein ARALYDRAFT_914806 [Arabidopsis lyrata subsp. lyrata] gi|297315862|gb|EFH46285.1| hypothetical protein ARALYDRAFT_914806 [Arabidopsis lyrata subsp. lyrata]	375	380	0	101.3	98.9	99.5	hypothetical protein ARALYDRAFT_914806	gbpln	Arabidopsis lyrata	AT4G18710.1 | Symbols: BIN2, DWF12, UCU1, ATSK21, SK21 | Protein kinase superfamily protein | chr4:10296474-10298913 FORWARD LENGTH=380	375	380	0	101.3	98.7	99.5
Rsa1.0_00003.1.g194.t1	ref|NP_191429.1| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|18415161|ref|NP_567563.1| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|30694822|ref|NP_568649.2| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|27735235|sp|P42794.2|RL112_ARATH RecName: Full=60S ribosomal protein L11-2; AltName: Full=L16 gi|11908058|gb|AAG41458.1|AF326876_1 putative ribosomal protein L11 [Arabidopsis thaliana] gi|12642874|gb|AAK00379.1|AF339697_1 putative ribosomal protein L11 [Arabidopsis thaliana] gi|14326537|gb|AAK60313.1|AF385722_1 AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|7630065|emb|CAB88287.1| ribosomal protein L11-like [Arabidopsis thaliana] gi|9758681|dbj|BAB09220.1| ribosomal protein L11-like [Arabidopsis thaliana] gi|14517470|gb|AAK62625.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|18700224|gb|AAL77722.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|21553372|gb|AAM62465.1| ribosomal protein L11, cytosolic [Arabidopsis thaliana] gi|21592421|gb|AAM64372.1| ribosomal protein L11, cytosolic [Arabidopsis thaliana] gi|22136574|gb|AAM91073.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|332007914|gb|AED95297.1|	182	182	1.00E-102	100.0	99.5	100.0	60S ribosomal protein L11-2	gbpln	Arabidopsis thaliana	AT5G45775.2 | Symbols: | Ribosomal L5P family protein | chr5:18565281-18566496 REVERSE LENGTH=182	182	182	1.00E-104	100.0	99.5	100.0
Rsa1.0_00003.1.g195.t1	gb|EOA18242.1| hypothetical protein CARUB_v10006734mg [Capsella rubella]	385	432	1.00E-159	112.2	80.0	87.3	hypothetical protein CARUB_v10006734mg	gbpln	Capsella rubella	AT4G18770.1 | Symbols: MYB98, AtMYB98 | myb domain protein 98 | chr4:10311068-10312557 FORWARD LENGTH=427	385	427	1.00E-157	110.9	77.7	85.5
Rsa1.0_00003.1.g196.t1	gb|ACS68199.1| cellulose synthase 8.2 catalytic subunit [Brassica napus]	985	984	0	99.9	98.4	98.6	cellulose synthase 8.2 catalytic subunit	gbpln	Brassica napus	AT4G18780.1 | Symbols: CESA8, IRX1, ATCESA8, LEW2 | cellulose synthase family protein | chr4:10312846-10316719 REVERSE LENGTH=985	985	985	0	100.0	94.6	96.8
Rsa1.0_00003.1.g197.t2	ref|XP_002867976.1| natural resistance-associated macrophage protein 5 [Arabidopsis lyrata subsp. lyrata] gi|297313812|gb|EFH44235.1| natural resistance-associated macrophage protein 5 [Arabidopsis lyrata subsp. lyrata]	549	529	0	96.4	87.6	90.3	natural resistance-associated macrophage protein 5	gbpln	Arabidopsis lyrata	AT4G18790.1 | Symbols: NRAMP5, ATNRAMP5 | NRAMP metal ion transporter family protein | chr4:10317785-10319660 REVERSE LENGTH=530	549	530	0	96.5	87.4	90.3
Rsa1.0_00003.1.g198.t1	gb|EOA17416.1| hypothetical protein CARUB_v10005719mg [Capsella rubella]	215	214	1.00E-111	99.5	92.1	96.3	hypothetical protein CARUB_v10005719mg	gbpln	Capsella rubella	AT4G18800.1 | Symbols: ATHSGBP, ATRAB11B, ATRABA1D, RABA1d | RAB GTPase homolog A1D | chr4:10320156-10321339 REVERSE LENGTH=214	215	214	1.00E-113	99.5	92.6	96.7
Rsa1.0_00003.1.g199.t1	ref|XP_002887691.1| nucleotide-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297333532|gb|EFH63950.1| nucleotide-binding family protein [Arabidopsis lyrata subsp. lyrata]	686	355	1.00E-160	51.7	39.5	45.5	nucleotide-binding family protein	gbpln	Arabidopsis lyrata	AT5G50960.1 | Symbols: NBP35, ATNBP35 | nucleotide binding protein 35 | chr5:20734267-20735824 FORWARD LENGTH=350	686	350	1.00E-158	51.0	38.9	45.0
Rsa1.0_00003.1.g200.t1	ref|NP_191844.1| zinc finger protein-like protein [Arabidopsis thaliana] gi|7362765|emb|CAB83135.1| putative protein [Arabidopsis thaliana] gi|332646881|gb|AEE80402.1| zinc finger protein-like protein [Arabidopsis thaliana]	302	472	1.00E-55	156.3	38.4	46.7	zinc finger protein-like protein	gbpln	Arabidopsis thaliana	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	302	472	3.00E-58	156.3	38.4	46.7

Rsa1.0_00003.1.g201.t1	ref|XP_002883636.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329476|gb|EFH59895.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	132	720	1.00E-26	545.5	47.0	54.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G04350.2 | Symbols: LACS8 | AMP-dependent synthetase and ligase family protein | chr2:1516086-1519178 FORWARD LENGTH=720	132	720	5.00E-28	545.5	46.2	53.0
Rsa1.0_00003.1.g202.t1	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	124	1250	3.00E-25	1008.1	58.1	66.1	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00003.1.g203.t2	ref|XP_002863624.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297309459|gb|EFH39883.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	352	365	1.00E-171	103.7	85.5	91.2	pfkB-type carbohydrate kinase family protein	gbpln	Arabidopsis lyrata	AT5G43910.2 | Symbols: | pfkB-like carbohydrate kinase family protein | chr5:17667537-17670085 REVERSE LENGTH=365	352	365	1.00E-166	103.7	84.4	90.6
Rsa1.0_00003.1.g204.t1	gb|EOA12791.1| hypothetical protein CARUB_v10025740mg [Capsella rubella]	1507	1506	0	99.9	94.8	97.3	hypothetical protein CARUB_v10025740mg	gbpln	Capsella rubella	AT5G43900.1 | Symbols: MYA2, ATMYA2, XI-2, XI-6 | myosin 2 | chr5:17657241-17666653 REVERSE LENGTH=1505	1507	1505	0	99.9	94.2	96.9
Rsa1.0_00003.1.g205.t3	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1849	1213	0	65.6	23.7	34.5	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1849	746	2.00E-58	40.3	7.0	11.2
Rsa1.0_00003.1.g206.t2	gb|EOA18770.1| hypothetical protein CARUB_v10007367mg [Capsella rubella]	365	335	1.00E-35	91.8	30.1	42.5	hypothetical protein CARUB_v10007367mg	gbpln	Capsella rubella	AT4G19360.1 | Symbols: | SCD6 protein-related | chr4:10564159-10565406 FORWARD LENGTH=268	365	268	4.00E-34	73.4	30.4	41.6
Rsa1.0_00003.1.g207.t1	ref|XP_002867943.1| hypothetical protein ARALYDRAFT_914728 [Arabidopsis lyrata subsp. lyrata] gi|297313779|gb|EFH44202.1| hypothetical protein ARALYDRAFT_914728 [Arabidopsis lyrata subsp. lyrata]	757	725	0	95.8	82.2	88.2	hypothetical protein ARALYDRAFT_914728	gbpln	Arabidopsis lyrata	AT4G19380.1 | Symbols: | Long-chain fatty alcohol dehydrogenase family protein | chr4:10568427-10572288 REVERSE LENGTH=726	757	726	0	95.9	80.8	86.4
Rsa1.0_00003.1.g208.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	1428	1489	0	104.3	55.9	70.5	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1428	1262	1.00E-163	88.4	19.1	25.9
Rsa1.0_00003.1.g209.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	599	1197	6.00E-83	199.8	30.4	42.6	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	599	575	1.00E-38	96.0	21.5	33.4
Rsa1.0_00003.1.g210.t1	gb|AAM62450.1| unknown [Arabidopsis thaliana]	169	160	8.00E-60	94.7	69.8	78.1	unknown	gbpln	Arabidopsis thaliana	AT4G19430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10598606-10599088 REVERSE LENGTH=160	169	160	1.00E-60	94.7	68.6	76.9
Rsa1.0_00003.1.g211.t1	#	#	#	#	#	#	#	-	----	----	AT4G19440.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:10602006-10604483 REVERSE LENGTH=825	53	825	1.00E-11	1556.6	60.4	67.9
Rsa1.0_00003.1.g212.t1	gb|AAC02664.1| polyprotein [Arabidopsis thaliana]	1410	1451	0	102.9	60.3	74.5	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1410	1262	1.00E-113	89.5	14.2	21.6
Rsa1.0_00003.1.g213.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00003.1.g214.t1	gb|EOA16195.1| hypothetical protein CARUB_v10004335mg [Capsella rubella]	657	649	0	98.8	67.1	79.1	hypothetical protein CARUB_v10004335mg	gbpln	Capsella rubella	AT4G23180.1 | Symbols: CRK10, RLK4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 | chr4:12138171-12140780 FORWARD LENGTH=669	657	669	0	101.8	62.7	74.9
Rsa1.0_00003.1.g215.t1	gb|EOA16319.1| hypothetical protein CARUB_v10004470mg [Capsella rubella]	572	571	0	99.8	91.4	95.3	hypothetical protein CARUB_v10004470mg	gbpln	Capsella rubella	AT4G19450.1 | Symbols: | Major facilitator superfamily protein | chr4:10606538-10609218 FORWARD LENGTH=572	572	572	0	100.0	93.2	96.5
Rsa1.0_00003.1.g216.t1	gb|EOA16458.1| hypothetical protein CARUB_v10004612mg, partial [Capsella rubella]	492	510	0	103.7	86.6	92.9	hypothetical protein CARUB_v10004612mg, partial	gbpln	Capsella rubella	AT4G19460.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr4:10610422-10611972 REVERSE LENGTH=516	492	516	0	104.9	85.4	92.7
Rsa1.0_00003.1.g217.t1	gb|ACP30627.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1225	1226	0	100.1	94.4	97.1	disease resistance protein	gbpln	Brassica rapa	AT4G12010.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:7197325-7201393 REVERSE LENGTH=1219	1225	1219	0	99.5	51.6	69.9
Rsa1.0_00003.1.g218.t1	gb|ACP30626.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1366	1276	0	93.4	75.9	82.9	disease resistance protein	gbpln	Brassica rapa	AT4G19500.2 | Symbols: | nucleoside-triphosphatases;transmembrane receptors;nucleotide binding;ATP binding | chr4:10627364-10631532 FORWARD LENGTH=834	1366	834	0	61.1	30.7	38.3

Rsa1.0_00003.1.g219.t1	gb|ACP30626.1| disease resistance protein [Brassica rapa subsp. pekinensis]	130	1276	1.00E-37	981.5	60.8	63.8	disease resistance protein	gbpln	Brassica rapa	AT4G19500.2 | Symbols: | nucleoside-triphosphatases;transmembrane receptors;nucleotide binding;ATP binding | chr4:10627364-10631532 FORWARD LENGTH=834	130	834	8.00E-21	641.5	36.2	50.8
Rsa1.0_00003.1.g220.t1	gb|ACI14393.1| WRKY28-1 transcription factor [Brassica napus]	215	312	5.00E-91	145.1	79.1	87.0	WRKY28-1 transcription factor	gbpln	Brassica napus	AT4G18170.1 | Symbols: WRKY28, ATWRKY28 | WRKY DNA-binding protein 28 | chr4:10061508-10062691 FORWARD LENGTH=318	215	318	2.00E-77	147.9	71.6	81.4
Rsa1.0_00003.1.g221.t1	ref|XP_002869986.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315822|gb|EFH46245.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	1182	1044	0	88.3	41.2	44.8	protein binding protein	gbpln	Arabidopsis lyrata	AT4G19490.2 | Symbols: ATVPS54, VPS54 | VPS54 | chr4:10616017-10622934 FORWARD LENGTH=1034	1182	1034	0	87.5	41.5	44.9
Rsa1.0_00003.1.g222.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1911	1274	0	66.7	34.3	45.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1911	575	3.00E-76	30.1	9.8	14.4
Rsa1.0_00003.1.g223.t1	ref|XP_002867933.1| hypothetical protein ARALYDRAFT_914714 [Arabidopsis lyrata subsp. lyrata] gi|297313769|gb|EFH44192.1| hypothetical protein ARALYDRAFT_914714 [Arabidopsis lyrata subsp. lyrata]	70	71	3.00E-25	101.4	81.4	87.1	hypothetical protein ARALYDRAFT_914714	gbpln	Arabidopsis lyrata	AT4G19520.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class) family | chr4:10639488-10647070 REVERSE LENGTH=1744	70	1744	2.00E-21	2491.4	55.7	57.1
Rsa1.0_00003.1.g224.t1	ref|NP_193687.3| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332658794|gb|AEE84194.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1497	1744	0	116.5	62.0	73.3	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT4G19520.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class) family | chr4:10639488-10647070 REVERSE LENGTH=1744	1497	1744	0	116.5	62.0	73.3
Rsa1.0_00003.1.g225.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00003.1.g226.t1	ref|NP_193688.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|2853080|emb|CAA16930.1| TMV resistance protein N-like [Arabidopsis thaliana] gi|7268749|emb|CAB78955.1| TMV resistance protein N-like [Arabidopsis thaliana] gi|332658795|gb|AEE84195.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1202	1167	0	97.1	64.8	73.3	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT4G19530.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class) family | chr4:10651962-10657090 FORWARD LENGTH=1167	1202	1167	0	97.1	64.8	73.3
Rsa1.0_00003.1.g227.t1	ref|XP_002869958.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata] gi|297315794|gb|EFH46217.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata]	422	428	1.00E-121	101.4	57.3	69.9	hypothetical protein ARALYDRAFT_914664	gbpln	Arabidopsis lyrata	AT4G19930.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:10803558-10804853 FORWARD LENGTH=431	422	431	1.00E-117	102.1	55.7	68.7
Rsa1.0_00003.1.g228.t1	gb|AAF26782.1|AC016829_6 putative trypsin inhibitor [Arabidopsis thaliana]	210	244	5.00E-14	116.2	34.8	42.9	putative trypsin inhibitor	gbpln	Arabidopsis thaliana	AT3G04320.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr3:1143815-1144426 FORWARD LENGTH=203	210	203	2.00E-16	96.7	34.8	42.9
Rsa1.0_00003.1.g229.t3	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	943	1274	0	135.1	48.0	63.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	943	575	7.00E-76	61.0	17.8	28.8
Rsa1.0_00003.1.g230.t1	ref|XP_002869970.1| iron-responsive transporter 2 [Arabidopsis lyrata subsp. lyrata] gi|297315806|gb|EFH46229.1| iron-responsive transporter 2 [Arabidopsis lyrata subsp. lyrata]	357	349	0	97.8	88.2	93.0	iron-responsive transporter 2	gbpln	Arabidopsis lyrata	AT4G19680.2 | Symbols: IRT2 | iron regulated transporter 2 | chr4:10703385-10704621 FORWARD LENGTH=350	357	350	0	98.0	87.4	93.6
Rsa1.0_00003.1.g231.t1	gb|AAD17352.1| contains similarity to retrovirus-related polyproteins [Arabidopsis thaliana] gi|7267379|emb|CAB77940.1| putative polyprotein [Arabidopsis thaliana]	1443	1366	0	94.7	39.5	54.9	contains similarity to retrovirus-related polyproteins	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1443	1262	1.00E-170	87.5	20.4	27.9
Rsa1.0_00003.1.g232.t1	gb|AFJ05595.1| iron-regulated transporter 1 [Raphanus sativus]	345	345	0	100.0	98.8	99.1	iron-regulated transporter 1	gbpln	Raphanus sativus	AT4G19690.2 | Symbols: IRT1 | iron-regulated transporter 1 | chr4:10707487-10708723 FORWARD LENGTH=347	345	347	1.00E-172	100.6	88.1	93.9
Rsa1.0_00003.1.g233.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00003.1.g234.t1	gb|EOA18607.1| hypothetical protein CARUB_v10007180mg [Capsella rubella]	345	345	0	100.0	89.6	96.5	hypothetical protein CARUB_v10007180mg	gbpln	Capsella rubella	AT4G19690.2 | Symbols: IRT1 | iron-regulated transporter 1 | chr4:10707487-10708723 FORWARD LENGTH=347	345	347	1.00E-175	100.6	89.0	95.9
Rsa1.0_00003.1.g235.t1	gb|AAL32681.1| putative protein [Arabidopsis thaliana] gi|21387161|gb|AAM47984.1| putative protein [Arabidopsis thaliana]	271	303	1.00E-103	111.8	74.9	82.7	putative protein	gbpln	Arabidopsis thaliana	AT4G19700.1 | Symbols: RING | SBP (S-ribonuclease binding protein) family protein | chr4:10713633-10714635 REVERSE LENGTH=304	271	304	1.00E-106	112.2	74.9	82.7

Rsa1.0_00003.1.g236.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00003.1.g237.t1	ref|NP_193723.3| Intracellular chloride channel–like protein [Arabidopsis thaliana] gi|24030218|gb|AAN41287.1| unknown protein [Arabidopsis thaliana] gi|332658839|gb|AEE84239.1| Intracellular chloride channel–like protein [Arabidopsis thaliana]	361	356	0	98.6	91.4	95.6	Intracellular chloride channel–like protein	gbpln	Arabidopsis thaliana	AT4G19880.1 | Symbols: | Glutathione S–transferase family protein | chr4:10784691–10786376 REVERSE LENGTH=356	361	356	0	98.6	91.4	95.6
Rsa1.0_00003.1.g238.t5	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00003.1.g239.t1	ref|XP_002869958.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata] gi|297315794|gb|EFH46217.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata]	161	428	9.00E–30	265.8	45.3	64.6	hypothetical protein ARALYDRAFT_914664	gbpln	Arabidopsis lyrata	AT4G19930.1 | Symbols: | F–box and associated interaction domains–containing protein | chr4:10803558–10804853 FORWARD LENGTH=431	161	431	1.00E–25	267.7	44.1	59.0
Rsa1.0_00003.1.g240.t1	ref|NP_001190775.1| K+ uptake permease 9 [Arabidopsis thaliana] gi|38502848|sp|O49423.2|POT9_ARATH RecName: Full=Potassium transporter 9; Short=AtPOT9 gi|332658852|gb|AEE84252.1| K+ uptake permease 9 [Arabidopsis thaliana]	807	807	0	100.0	88.4	93.3	K+ uptake permease 9	gbpln	Arabidopsis thaliana	AT4G19960.2 | Symbols: KUP9 | K+ uptake permease 9 | chr4:10813807–10816997 FORWARD LENGTH=807	807	807	0	100.0	88.4	93.3
Rsa1.0_00003.1.g241.t1	ref|NP_001190775.1| K+ uptake permease 9 [Arabidopsis thaliana] gi|38502848|sp|O49423.2|POT9_ARATH RecName: Full=Potassium transporter 9; Short=AtPOT9 gi|332658852|gb|AEE84252.1| K+ uptake permease 9 [Arabidopsis thaliana]	801	807	0	100.7	85.4	92.0	K+ uptake permease 9	gbpln	Arabidopsis thaliana	AT4G19960.2 | Symbols: KUP9 | K+ uptake permease 9 | chr4:10813807–10816997 FORWARD LENGTH=807	801	807	0	100.7	85.4	92.0
Rsa1.0_00003.1.g242.t1	ref|NP_001190775.1| K+ uptake permease 9 [Arabidopsis thaliana] gi|38502848|sp|O49423.2|POT9_ARATH RecName: Full=Potassium transporter 9; Short=AtPOT9 gi|332658852|gb|AEE84252.1| K+ uptake permease 9 [Arabidopsis thaliana]	730	807	0	110.5	78.8	86.2	K+ uptake permease 9	gbpln	Arabidopsis thaliana	AT4G19960.2 | Symbols: KUP9 | K+ uptake permease 9 | chr4:10813807–10816997 FORWARD LENGTH=807	730	807	0	110.5	78.8	86.2
Rsa1.0_00003.1.g243.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00003.1.g244.t1	gb|EOA16117.1| hypothetical protein CARUB_v10004249mg [Capsella rubella]	346	715	1.00E–173	206.6	84.4	88.7	hypothetical protein CARUB_v10004249mg	gbpln	Capsella rubella	AT4G19970.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nucleotide–diphospho–sugar transferase, predicted (InterPro:IPR005069); BEST Arabidopsis thaliana protein match is: Nucleotide–diphospho–sugar transferase family protein (TAIR:AT5G44820.1); Has 801 Blast hits to 466 proteins in 35 species: Archae – 0; Bacteria – 0; Metazoa – 2; Fungi – 0; Plants – 750; Viruses – 0; Other Eukaryotes – 49 (source: NCBI BLink). | chr4:10818242–10825343 FORWARD LENGTH=715	346	715	1.00E–175	206.6	84.7	89.3
Rsa1.0_00003.1.g245.t1	ref|XP_002869958.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata] gi|297315794|gb|EFH46217.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata]	427	428	1.00E–126	100.2	61.1	73.5	hypothetical protein ARALYDRAFT_914664	gbpln	Arabidopsis lyrata	AT4G19930.1 | Symbols: | F–box and associated interaction domains–containing protein | chr4:10803558–10804853 FORWARD LENGTH=431	427	431	1.00E–121	100.9	58.8	70.5
Rsa1.0_00003.1.g246.t1	gb|EOA15545.1| hypothetical protein CARUB_v10004988mg, partial [Capsella rubella]	375	394	1.00E–157	105.1	77.9	84.0	hypothetical protein CARUB_v10004988mg, partial	gbpln	Capsella rubella	AT4G20010.1 | Symbols: PTAC9, OSB2 | plastid transcriptionally active 9 | chr4:10842128–10843989 FORWARD LENGTH=371	375	371	1.00E–157	98.9	76.8	83.5
Rsa1.0_00003.1.g247.t1	ref|NP_567595.1| Pectin lyase–like protein [Arabidopsis thaliana] gi|16226216|gb|AAL16105.1|AF428273_1 AT4g20040/F18F4_140 [Arabidopsis thaliana] gi|22137222|gb|AAM91456.1| AT4g20040/F18F4_140 [Arabidopsis thaliana] gi|332658865|gb|AEE84265.1| Pectin lyase–like protein [Arabidopsis thaliana]	813	483	0	59.4	47.2	51.9	Pectin lyase–like protein	gbpln	Arabidopsis thaliana	AT4G20040.1 | Symbols: | Pectin lyase–like superfamily protein | chr4:10847348–10848963 REVERSE LENGTH=483	813	483	0	59.4	47.2	51.9
Rsa1.0_00004.1.g248.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838–20266 [Arabidopsis thaliana]	206	1142	3.00E–25	554.4	25.2	33.0	reverse transcriptase, putative; 16838–20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H–like superfamily protein | chr4:14333528–14335255 FORWARD LENGTH=575	206	575	2.00E–17	279.1	23.3	37.4
Rsa1.0_00004.1.g249.t1	gb|EOA34452.1| hypothetical protein CARUB_v10021988mg [Capsella rubella]	310	332	1.00E–65	107.1	55.8	63.2	hypothetical protein CARUB_v10021988mg	gbpln	Capsella rubella	AT1G68550.2 | Symbols: | Integrase–type DNA–binding superfamily protein | chr1:25725810–25726784 REVERSE LENGTH=324	310	324	1.00E–67	104.5	53.9	66.1
Rsa1.0_00004.1.g250.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#

Rsa1.0_00004.1.g251.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	758	1529	0	201.7	46.2	62.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	758	746	4.00E-74	98.4	21.0	29.9
Rsa1.0_00004.1.g252.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00004.1.g253.t1	ref|NP_177020.1| 3-ketoacyl-CoA synthase 6 [Arabidopsis thaliana] gi|75315046|sp|Q9XF43.1|KCS6_ARATH RecName: Full=3-ketoacyl-CoA synthase 6; Short=KCS-6; AltName: Full=Cuticular protein 1; AltName: Full=Very long-chain fatty acid condensing enzyme 6; Short=VLCFA condensing enzyme 6 gi|5001734|gb|AAD37122.1|AF129511_1 very-long-chain fatty acid condensing enzyme CUT1 [Arabidopsis thaliana] gi|12324880|gb|AAG52390.1|AC011915_4 very-long-chain fatty acid condensing enzyme (CUT1); 56079-54227 [Arabidopsis thaliana] gi|332196683|gb|AEE34804.1| 3-ketoacyl-CoA synthase 6 [Arabidopsis thaliana]	497	497	0	100.0	93.4	96.8	3-ketoacyl-CoA synthase 6	gbpln	Arabidopsis thaliana	AT1G68530.1 | Symbols: CUT1, POP1, CER6, G2, KCS6 | 3-ketoacyl-CoA synthase 6 | chr1:25712881-25714733 REVERSE LENGTH=497	497	497	0	100.0	93.4	96.8
Rsa1.0_00004.1.g254.t1	gb|EOA35226.1| hypothetical protein CARUB_v10020384mg [Capsella rubella]	402	410	1.00E-170	102.0	78.9	88.3	hypothetical protein CARUB_v10020384mg	gbpln	Capsella rubella	AT1G68520.1 | Symbols: | B-box type zinc finger protein with CCT domain | chr1:25709331-25710749 REVERSE LENGTH=406	402	406	1.00E-170	101.0	76.6	86.8
Rsa1.0_00004.1.g255.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00004.1.g256.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00004.1.g257.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00004.1.g258.t1	gb|EOA35949.1| hypothetical protein CARUB_v10021210mg [Capsella rubella]	87	93	7.00E-20	106.9	69.0	81.6	hypothetical protein CARUB_v10021210mg	gbpln	Capsella rubella	AT1G68500.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G25422.1); Has 16 Blast hits to 16 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25702041-25702322 FORWARD LENGTH=93	87	93	3.00E-22	106.9	72.4	82.8
Rsa1.0_00004.1.g259.t1	ref|NP_564931.1| uncharacterized protein [Arabidopsis thaliana] gi|12324888|gb|AAG52398.1|AC011915_12 unknown protein; 35272-36292 [Arabidopsis thaliana] gi|21593205|gb|AAM65154.1| unknown [Arabidopsis thaliana] gi|29028824|gb|AAO64791.1| At1g68490 [Arabidopsis thaliana] gi|110736380|dbj|BAF00159.1| hypothetical protein [Arabidopsis thaliana] gi|332196678|gb|AEE34799.1| uncharacterized protein AT1G68490 [Arabidopsis thaliana]	172	183	8.00E-59	106.4	77.3	83.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G68490.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G13390.2); Has 125 Blast hits to 125 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 125; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25693926-25694946 FORWARD LENGTH=183	172	183	3.00E-61	106.4	77.3	83.7
Rsa1.0_00004.1.g260.t1	ref|XP_002878905.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324744|gb|EFH55164.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	120	480	8.00E-17	400.0	35.8	52.5	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00004.1.g261.t2	gb|AAD32759.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	490	1356	1.00E-133	276.7	50.6	59.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	490	1262	7.00E-38	257.6	22.9	34.7
Rsa1.0_00004.1.g262.t2	ref|XP_002888667.1| hypothetical protein ARALYDRAFT_475967 [Arabidopsis lyrata subsp. lyrata] gi|297334508|gb|EFH64926.1| hypothetical protein ARALYDRAFT_475967 [Arabidopsis lyrata subsp. lyrata]	266	253	1.00E-105	95.1	78.2	82.7	hypothetical protein ARALYDRAFT_475967	gbpln	Arabidopsis lyrata	AT1G68480.1 | Symbols: JAG | C2H2 and C2HC zinc fingers superfamily protein | chr1:25684543-25685932 REVERSE LENGTH=253	266	253	1.00E-105	95.1	76.3	81.6
Rsa1.0_00004.1.g263.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00004.1.g264.t1	ref|XP_002882231.1| S-adenosylmethionine decarboxylase [Arabidopsis lyrata subsp. lyrata] gi|297328071|gb|EFH58490.1| S-adenosylmethionine decarboxylase [Arabidopsis lyrata subsp. lyrata]	181	366	1.00E-18	202.2	32.0	39.8	S-adenosylmethionine decarboxylase	gbpln	Arabidopsis lyrata	AT3G02470.4 | Symbols: | S-adenosylmethionine decarboxylase | chr3:510223-511323 FORWARD LENGTH=366	181	366	6.00E-20	202.2	30.4	39.2
Rsa1.0_00004.1.g265.t1	dbj|BAE43826.1| isopentenyltransferase [Brassica rapa subsp. pekinensis]	297	348	1.00E-153	117.2	92.9	95.3	isopentenyltransferase	gbpln	Brassica rapa	AT1G68460.1 | Symbols: ATIPT1, IPT1 | isopentenyltransferase 1 | chr1:25668976-25670049 REVERSE LENGTH=357	297	357	1.00E-130	120.2	78.8	87.5

Rsa1.0_00004.1.g266.t1	gb|EOA34020.1| hypothetical protein CARUB_v10021516mg [Capsella rubella]	147	148	4.00E-49	100.7	70.1	79.6	hypothetical protein CARUB_v10021516mg	gbpln	Capsella rubella	AT1G68450.1 | Symbols: | VQ motif-containing protein | chr1:25661721-25662179 REVERSE LENGTH=152	147	152	3.00E-45	103.4	66.0	78.9
Rsa1.0_00004.1.g267.t1	ref|XP_002868681.1| hypothetical protein ARALYDRAFT_916271 [Arabidopsis lyrata subsp. lyrata] gi|297314517|gb|EFH44940.1| hypothetical protein ARALYDRAFT_916271 [Arabidopsis lyrata subsp. lyrata]	169	1168	4.00E-55	691.1	77.5	81.7	hypothetical protein ARALYDRAFT_916271	gbpln	Arabidopsis lyrata	AT4G10320.1 | Symbols: | tRNA synthetase class I (I, L, M and V) family protein | chr4:6397526-6404509 REVERSE LENGTH=1190	169	1190	3.00E-54	704.1	73.4	81.7
Rsa1.0_00004.1.g268.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00004.1.g269.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00004.1.g270.t1	ref|NP_564930.1| uncharacterized protein [Arabidopsis thaliana] gi|6714347|gb|AAF26038.1|AC015986_1 unknown protein; 9003-8083 [Arabidopsis thaliana] gi|16648773|gb|AAL25577.1| At1g68440/T2E12_1 [Arabidopsis thaliana] gi|21592921|gb|AAM64871.1| unknown [Arabidopsis thaliana] gi|21700823|gb|AAM70535.1| At1g68440/T2E12_1 [Arabidopsis thaliana] gi|332196673|gb|AEE34794.1| uncharacterized protein AT1G68440 [Arabidopsis thaliana]	312	306	1.00E-103	98.1	73.4	84.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G68440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G25400.2); Has 86 Blast hits to 86 proteins in 29 species: Archae - 0; Bacteria - 6; Metazoa - 27; Fungi - 11; Plants - 24; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr1:25658115-25659035 FORWARD LENGTH=306	312	306	1.00E-105	98.1	73.4	84.3
Rsa1.0_00004.1.g271.t1	ref|XP_002888663.1| hypothetical protein ARALYDRAFT_894609 [Arabidopsis lyrata subsp. lyrata] gi|297334504|gb|EFH64922.1| hypothetical protein ARALYDRAFT_894609 [Arabidopsis lyrata subsp. lyrata]	147	145	3.00E-45	98.6	78.2	83.7	hypothetical protein ARALYDRAFT_894609	gbpln	Arabidopsis lyrata	AT1G68430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G66890.1); Has 35 Blast hits to 35 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25654989-25655429 REVERSE LENGTH=146	147	146	2.00E-43	99.3	78.2	84.4
Rsa1.0_00004.1.g272.t2	gb|AAL06846.1| AT3g02470/F16B3_10 [Arabidopsis thaliana]	171	366	5.00E-11	214.0	21.1	23.4	AT3g02470/F16B3_10	gbpln	Arabidopsis thaliana	AT3G02470.4 | Symbols: | S-adenosylmethionine decarboxylase | chr3:510223-511323 FORWARD LENGTH=366	171	366	1.00E-12	214.0	20.5	22.8
Rsa1.0_00004.1.g273.t1	gb|EOA35168.1| hypothetical protein CARUB_v10020313mg [Capsella rubella]	434	437	0	100.7	91.9	95.4	hypothetical protein CARUB_v10020313mg	gbpln	Capsella rubella	AT1G68410.2 | Symbols: | Protein phosphatase 2C family protein | chr1:25650262-25652255 REVERSE LENGTH=436	434	436	0	100.5	91.9	95.2
Rsa1.0_00004.1.g274.t1	ref|XP_002892766.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338608|gb|EFH69025.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	179	212	4.00E-22	118.4	37.4	52.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G34280.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:14470335-14471510 REVERSE LENGTH=391	179	391	1.00E-20	218.4	34.6	48.0
Rsa1.0_00004.1.g275.t19	ref|XP_002865187.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311022|gb|EFH41446.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	95	1162	1.00E-27	1223.2	66.3	78.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G22690.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:7541369-7544888 FORWARD LENGTH=1008	95	1008	6.00E-29	1061.1	61.1	80.0
Rsa1.0_00004.1.g276.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00004.1.g277.t1	ref|XP_002888661.1| At1g68400/T2E12_5 [Arabidopsis lyrata subsp. lyrata] gi|297334502|gb|EFH64920.1| At1g68400/T2E12_5 [Arabidopsis lyrata subsp. lyrata]	668	669	0	100.1	80.7	85.8	At1g68400/T2E12_5	gbpln	Arabidopsis lyrata	AT1G68400.1 | Symbols: | leucine-rich repeat transmembrane protein kinase family protein | chr1:25646401-25648916 REVERSE LENGTH=670	668	670	0	100.3	81.0	87.0
Rsa1.0_00004.1.g278.t1	ref|XP_002887179.1| hypothetical protein ARALYDRAFT_475958 [Arabidopsis lyrata subsp. lyrata] gi|297333020|gb|EFH63438.1| hypothetical protein ARALYDRAFT_475958 [Arabidopsis lyrata subsp. lyrata]	418	405	1.00E-180	96.9	78.5	84.2	hypothetical protein ARALYDRAFT_475958	gbpln	Arabidopsis lyrata	AT1G68390.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:25642838-25645484 FORWARD LENGTH=408	418	408	1.00E-170	97.6	78.2	84.0
Rsa1.0_00004.1.g279.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	186	1161	3.00E-33	624.2	46.2	60.8	F14N23.4	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	186	332	2.00E-31	178.5	40.9	51.6

Rsa1.0_00004.1.g280.t1	ref|XP_002888659.1| hypothetical protein ARALYDRAFT_894602 [Arabidopsis lyrata subsp. lyrata] gi|297334500|gb|EFH64918.1| hypothetical protein ARALYDRAFT_894602 [Arabidopsis lyrata subsp. lyrata]		302	410	2.00E-94	135.8	57.6	59.9	hypothetical protein ARALYDRAFT_894602	gbpln	Arabidopsis lyrata	AT1G68370.1 | Symbols: ARG1 | Chaperone DnaJ-domain superfamily protein | chr1:25632046-25634527 REVERSE LENGTH=410	302	410	1.00E-95	135.8	56.6	59.9
Rsa1.0_00004.1.g281.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]		227	1142	1.00E-46	503.1	46.3	59.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	227	292	1.00E-16	128.6	23.8	42.3
Rsa1.0_00004.1.g282.t1	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#
Rsa1.0_00005.1.g283.t1	emb|CAN79339.1| hypothetical protein VITISV_044312 [Vitis vinifera]		129	354	9.00E-19	274.4	40.3	58.1	hypothetical protein VITISV_044312	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00005.1.g284.t1	gb|EOA32296.1| hypothetical protein CARUB_v10015558mg [Capsella rubella]		564	570	0	101.1	95.7	97.5	hypothetical protein CARUB_v10015558mg	gbpln	Capsella rubella	AT3G20840.1 | Symbols: PLT1 | Integrase-type DNA-binding superfamily protein | chr3:7300764-7303370 FORWARD LENGTH=574	564	574	0	101.8	94.3	95.9
Rsa1.0_00005.1.g285.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]		914	1274	0	139.4	45.0	63.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	914	575	3.00E-55	62.9	15.4	27.4
Rsa1.0_00005.1.g286.t1	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#
Rsa1.0_00005.1.g287.t1	ref|XP_002885407.1| hypothetical protein ARALYDRAFT_898522 [Arabidopsis lyrata subsp. lyrata] gi|297331247|gb|EFH61666.1| hypothetical protein ARALYDRAFT_898522 [Arabidopsis lyrata subsp. lyrata]		64	64	9.00E-14	100.0	64.1	71.9	hypothetical protein ARALYDRAFT_898522	gbpln	Arabidopsis lyrata	AT3G20865.1 | Symbols: AGP40 | arabinogalactan protein 40 | chr3:7308699-7308887 REVERSE LENGTH=62	64	62	2.00E-13	96.9	65.6	70.3
Rsa1.0_00005.1.g288.t1	ref|NP_188724.2| WIP domain protein 4 [Arabidopsis thaliana] gi|18376500|emb|CAC86168.1| WIP4 protein [Arabidopsis thaliana] gi|332642914|gb|AEE76435.1| WIP domain protein 4 [Arabidopsis thaliana]		360	412	1.00E-156	114.4	79.4	84.2	WIP domain protein 4	gbpln	Arabidopsis thaliana	AT3G20880.1 | Symbols: WIP4 | WIP domain protein 4 | chr3:7313759-7315792 REVERSE LENGTH=412	360	412	1.00E-159	114.4	79.4	84.2
Rsa1.0_00005.1.g289.t1	dbj|BAB01899.1| unnamed protein product [Arabidopsis thaliana]		136	135	3.00E-28	99.3	60.3	69.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G20898.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G51355.1); Has 66 Blast hits to 66 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 66; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7323796-7324203 FORWARD LENGTH=108	136	108	8.00E-31	79.4	56.6	63.2
Rsa1.0_00005.1.g290.t1	#	#	#	#	#	#	#		–	----	----	AT3G20910.1 | Symbols: NF-YA9 | nuclear factor Y, subunit A9 | chr3:7326495-7328369 FORWARD LENGTH=303	110	303	4.00E-12	275.5	50.9	59.1
Rsa1.0_00005.1.g291.t1	gb|EOA30911.1| hypothetical protein CARUB_v10014058mg [Capsella rubella]		337	356	1.00E-175	105.6	90.8	95.5	hypothetical protein CARUB_v10014058mg	gbpln	Capsella rubella	AT3G20920.1 | Symbols: | translocation protein-related | chr3:7328763-7330698 REVERSE LENGTH=365	337	365	1.00E-176	108.3	91.1	95.8
Rsa1.0_00005.1.g292.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]		366	1489	5.00E-92	406.8	49.5	64.2	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	366	237	5.00E-23	64.8	15.8	24.6
Rsa1.0_00005.1.g293.t1	ref|XP_002883469.1| hypothetical protein ARALYDRAFT_898931 [Arabidopsis lyrata subsp. lyrata] gi|297329309|gb|EFH59728.1| hypothetical protein ARALYDRAFT_898931 [Arabidopsis lyrata subsp. lyrata]		266	242	5.00E-67	91.0	54.1	66.2	hypothetical protein ARALYDRAFT_898931	gbpln	Arabidopsis lyrata	AT2G16600.1 | Symbols: ROC3 | rotamase CYP 3 | chr2:7200862-7201383 FORWARD LENGTH=173	266	173	2.00E-57	65.0	42.5	49.2
Rsa1.0_00005.1.g294.t1	dbj|BAB01909.1| unnamed protein product [Arabidopsis thaliana]		253	294	2.00E-51	116.2	45.1	62.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G20980.1 | Symbols: | Gag-Pol-related retrotransposon family protein | chr3:7355963-7357966 FORWARD LENGTH=405	253	405	1.00E-41	160.1	37.9	57.3
Rsa1.0_00005.1.g295.t1	dbj|BAF01392.1| hypothetical protein [Arabidopsis thaliana]		406	438	3.00E-78	107.9	44.8	64.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G21000.1 | Symbols: | Gag-Pol-related retrotransposon family protein | chr3:7363921-7365138 FORWARD LENGTH=405	406	405	1.00E-72	99.8	42.6	60.1

Rsa1.0_00005.1.g296.t1	dbj|BAF01392.1| hypothetical protein [Arabidopsis thaliana]	367	438	1.00E-101	119.3	58.9	73.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G21000.1 | Symbols: | Gag-Pol-related retrotransposon family protein | chr3:7363921-7365138 FORWARD LENGTH=405	367	405	3.00E-78	110.4	46.6	66.2
Rsa1.0_00005.1.g297.t1	dbj|BAB01447.1| gag-pol polyprotein-like [Arabidopsis thaliana]	418	420	3.00E-91	100.5	46.2	55.7	gag-pol polyprotein-like	gbpln	Arabidopsis thaliana	AT3G21000.1 | Symbols: | Gag-Pol-related retrotransposon family protein | chr3:7363921-7365138 FORWARD LENGTH=405	418	405	3.00E-50	96.9	31.1	43.1
Rsa1.0_00005.1.g298.t1	ref|XP_002883282.1| hypothetical protein ARALYDRAFT_318845 [Arabidopsis lyrata subsp. lyrata] gi|297329122|gb|EFH59541.1| hypothetical protein ARALYDRAFT_318845 [Arabidopsis lyrata subsp. lyrata]	549	560	0	102.0	89.4	92.9	hypothetical protein ARALYDRAFT_318845	gbpln	Arabidopsis lyrata	AT3G21060.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:7377822-7379942 FORWARD LENGTH=547	549	547	0	99.6	86.0	90.3
Rsa1.0_00005.1.g299.t1	ref|NP_974347.1| NAD(H) kinase 1 [Arabidopsis thaliana] gi|94717660|sp|Q56YN3.2|NADK1_ARATH RecName: Full=NAD(H) kinase 1; Short=AtNADK-1 gi|39843359|gb|AAR32133.1| NADK1 [Arabidopsis thaliana] gi|51970406|dbj|BAD43895.1| unnamed protein product [Arabidopsis thaliana] gi|332642935|gb|AEE76456.1| NAD(H) kinase 1 [Arabidopsis thaliana]	580	524	0	90.3	66.6	76.6	NAD(H) kinase 1	gbpln	Arabidopsis thaliana	AT3G21070.2 | Symbols: NADK1 | NAD kinase 1 | chr3:7380434-7383874 REVERSE LENGTH=524	580	524	0	90.3	66.6	76.6
Rsa1.0_00005.1.g300.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00005.1.g301.t1	ref|XP_002885419.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297331259|gb|EFH61678.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata]	83	691	1.00E-14	832.5	60.2	62.7	abc transporter family protein	gbpln	Arabidopsis lyrata	AT3G21090.1 | Symbols: | ABC-2 type transporter family protein | chr3:7391497-7394933 REVERSE LENGTH=691	83	691	2.00E-17	832.5	60.2	62.7
Rsa1.0_00005.1.g302.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00005.1.g303.t1	ref|XP_002883283.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329123|gb|EFH59542.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	545	607	0	111.4	80.0	87.5	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT3G21100.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:7399162-7401870 FORWARD LENGTH=602	545	602	0	110.5	79.6	87.0
Rsa1.0_00005.1.g304.t1	ref|NP_188748.1| phosphoribosylaminoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] gi|79313319|ref|NP_001030739.1| phosphoribosylaminoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] gi|26454658|sp|P38025.2|PUR7_ARATH RecName: Full=Phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic; AltName: Full=SAICAR synthetase; Flags: Precursor gi|11994271|dbj|BAB01454.1| 5'-phosphoribosyl-4-(N-succinocarboxamide)-5- ami noimidazole synthetase [Arabidopsis thaliana] gi|27754219|gb|AAO22563.1| putative phosphoribosyamidoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] gi|332642941|gb|AEE76462.1| phosphoribosylaminoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] gi|332642942|gb|AEE76463.1| phosphoribosylaminoimidazole-succinocarboxamide synthase [Arabidopsis thaliana]	408	411	0	100.7	93.6	95.8	phosphoribosylaminoimidazole-succinocarboxamide synthase	gbpln	Arabidopsis thaliana	AT3G21110.2 | Symbols: PUR7, PURC | purin 7 | chr3:7402696-7405273 REVERSE LENGTH=411	408	411	0	100.7	93.6	95.8
Rsa1.0_00005.1.g305.t1	gb|EOA30727.1| hypothetical protein CARUB_v10013865mg [Capsella rubella]	399	402	0	100.8	90.7	94.0	hypothetical protein CARUB_v10013865mg	gbpln	Capsella rubella	AT1G51540.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:19115702-19117381 FORWARD LENGTH=415	399	415	0	104.0	88.7	94.0
Rsa1.0_00005.1.g306.t1	ref|XP_002885421.1| FMN binding protein [Arabidopsis lyrata subsp. lyrata] gi|297331261|gb|EFH61680.1| FMN binding protein [Arabidopsis lyrata subsp. lyrata]	370	387	1.00E-170	104.6	84.3	87.6	FMN binding protein	gbpln	Arabidopsis lyrata	AT3G21140.1 | Symbols: | Pyridoxamine 5'-phosphate oxidase family protein | chr3:7409696-7412086 REVERSE LENGTH=387	370	387	1.00E-170	104.6	82.7	86.5

Rsa1.0_00005.1.g307.t23	ref|NP_850618.1| GATA transcription factor 24 [Arabidopsis thaliana] gi|14596059|gb|AAK68757.1| Unknown protein [Arabidopsis thaliana] gi|17978695|gb|AAL47341.1| unknown protein [Arabidopsis thaliana] gi|332642950|gb|AEE76471.1| GATA transcription factor 24 [Arabidopsis thaliana]	289	295	1.00E−126	102.1	81.0	87.5	GATA transcription factor 24	gbpln	Arabidopsis thaliana	AT3G21175.2 | Symbols: ZML1, GATA24 | ZIM−like 1 | chr3:7422832−7424598 FORWARD LENGTH=295	289	295	1.00E−129	102.1	81.0	87.5
Rsa1.0_00005.1.g308.t1	ref|XP_002885425.1| hypothetical protein ARALYDRAFT_479639 [Arabidopsis lyrata subsp. lyrata] gi|297331265|gb|EFH61684.1| hypothetical protein ARALYDRAFT_479639 [Arabidopsis lyrata subsp. lyrata]	422	422	0	100.0	91.5	96.4	hypothetical protein ARALYDRAFT_479639	gbpln	Arabidopsis lyrata	AT3G21190.1 | Symbols: | O−fucosyltransferase family protein | chr3:7432579−7434543 REVERSE LENGTH=422	422	422	0	100.0	91.0	96.2
Rsa1.0_00005.1.g309.t1	ref|NP_175576.1| ATP synthase subunit epsilon [Arabidopsis thaliana] gi|2493052|sp|Q96253.3|ATP5E_ARATH RecName: Full=ATP synthase subunit epsilon, mitochondrial; Short=ATPase subunit epsilon gi|12321688|gb|AAG50890.1|AC025294_28 epsilon subunit of mitochondrial F1−ATPase [Arabidopsis thaliana] gi|1655486|dbj|BAA13602.1| epsilon subunit of mitochondrial F1−ATPase [Arabidopsis thaliana] gi|18252167|gb|AAL61916.1| epsilon subunit of mitochondrial F1−ATPase [Arabidopsis thaliana] gi|21386911|gb|AAM47859.1| epsilon subunit of mitochondrial F1−ATPase [Arabidopsis thaliana] gi|332194574|gb|AEE32695.1| ATP synthase subunit epsilon [Arabidopsis thaliana]	70	70	3.00E−30	100.0	88.6	94.3	ATP synthase subunit epsilon	gbpln	Arabidopsis thaliana	AT1G51650.1 | Symbols: | ATP synthase epsilon chain, mitochondrial | chr1:19152680−19153641 FORWARD LENGTH=70	70	70	6.00E−33	100.0	88.6	94.3
Rsa1.0_00005.1.g310.t1	ref|NP_683582.2| RNA recognition motif−containing protein [Arabidopsis thaliana] gi|13605613|gb|AAK32800.1|AF361632_1 At3g21211 [Arabidopsis thaliana] gi|23505943|gb|AAN28831.1| At3g21211/At3g21211 [Arabidopsis thaliana] gi|26451397|dbj|BAC42798.1| unknown protein [Arabidopsis thaliana] gi|110740646|dbj|BAE98426.1| hypothetical protein [Arabidopsis thaliana] gi|222423570|dbj|BAH19754.1| AT3G21215 [Arabidopsis thaliana] gi|332642956|gb|AEE76477.1| RNA recognition motif−containing protein [Arabidopsis thaliana]	349	339	1.00E−142	97.1	88.8	92.0	RNA recognition motif−containing protein	gbpln	Arabidopsis thaliana	AT3G21215.1 | Symbols: | RNA−binding (RRM/RBD/RNP motifs) family protein | chr3:7442873−7445231 REVERSE LENGTH=339	349	339	1.00E−145	97.1	88.8	92.0
Rsa1.0_00005.1.g311.t1	gb|ABF55665.1| double MYC−tagged mitogen activated protein kinase kinase 5 [synthetic construct]	332	380	1.00E−156	114.5	87.0	93.4	double MYC−tagged mitogen activated protein kinase kinase 5	gbenv	synthetic construct	AT3G21220.1 | Symbols: ATMKK5, ATMAP2K_ALPHA, MAP2K_A, MKK5, ATMEK5, MEK5 | MAP kinase kinase 5 | chr3:7445917−7446963 FORWARD LENGTH=348	332	348	1.00E−158	104.8	87.0	93.4
Rsa1.0_00005.1.g312.t1	gb|EOA29726.1| hypothetical protein CARUB_v10012814mg [Capsella rubella] gi|482565538|gb|EOA29727.1| hypothetical protein CARUB_v10012814mg [Capsella rubella]	1494	1464	0	98.0	82.5	89.6	hypothetical protein CARUB_v10012814mg	gbpln	Capsella rubella	AT3G21250.2 | Symbols: MRP6, ABCC8 | multidrug resistance−associated protein 6 | chr3:7457668−7463261 REVERSE LENGTH=1464	1494	1464	0	98.0	81.9	89.0
Rsa1.0_00005.1.g313.t1	ref|XP_002885432.1| hypothetical protein ARALYDRAFT_342275 [Arabidopsis lyrata subsp. lyrata] gi|297331272|gb|EFH61691.1| hypothetical protein ARALYDRAFT_342275 [Arabidopsis lyrata subsp. lyrata]	234	233	1.00E−110	99.6	88.9	94.4	hypothetical protein ARALYDRAFT_342275	gbpln	Arabidopsis lyrata	AT3G21260.3 | Symbols: | Glycolipid transfer protein (GLTP) family protein | chr3:7464132−7465785 REVERSE LENGTH=233	234	233	1.00E−112	99.6	88.5	93.6
Rsa1.0_00005.1.g314.t1	ref|XP_002883294.1| 55 kDa B regulatory subunit of phosphatase 2A [Arabidopsis lyrata subsp. lyrata] gi|297329134|gb|EFH59553.1| 55 kDa B regulatory subunit of phosphatase 2A [Arabidopsis lyrata subsp. lyrata]	511	514	0	100.6	88.3	91.6	55 kDa B regulatory subunit of phosphatase 2A	gbpln	Arabidopsis lyrata	AT1G51690.1 | Symbols: ATB ALPHA, B ALPHA | protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform | chr1:19166218−19169974 FORWARD LENGTH=513	511	513	0	100.4	82.2	89.8

Rsa1.0_00005.1.g315.t1	ref|XP_002883295.1| hypothetical protein ARALYDRAFT_898570 [Arabidopsis lyrata subsp. lyrata] gi|297329135|gb|EFH59554.1| hypothetical protein ARALYDRAFT_898570 [Arabidopsis lyrata subsp. lyrata]	207	199	3.00E-73	96.1	78.7	83.1	hypothetical protein ARALYDRAFT_898570	gbpln	Arabidopsis lyrata	AT3G21270.1 | Symbols: ADOF2, DOF2 | DOF zinc finger protein 2 | chr3:7474934-7475548 FORWARD LENGTH=204	207	204	1.00E-68	98.6	78.7	84.5
Rsa1.0_00005.1.g316.t1	ref|XP_002883297.1| hypothetical protein ARALYDRAFT_479651 [Arabidopsis lyrata subsp. lyrata] gi|297329137|gb|EFH59556.1| hypothetical protein ARALYDRAFT_479651 [Arabidopsis lyrata subsp. lyrata]	99	383	5.00E-32	386.9	72.7	79.8	hypothetical protein ARALYDRAFT_479651	gbpln	Arabidopsis lyrata	AT3G21310.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr3:7497774-7499011 FORWARD LENGTH=383	99	383	1.00E-33	386.9	70.7	77.8
Rsa1.0_00005.1.g317.t1	gb|EOA30281.1| hypothetical protein CARUB_v10013409mg [Capsella rubella]	537	538	0	100.2	75.6	84.0	hypothetical protein CARUB_v10013409mg	gbpln	Capsella rubella	AT3G21320.1 | Symbols: | BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT2G25930.1); Has 63 Blast hits to 58 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:7499408-7501312 REVERSE LENGTH=540	537	540	0	100.6	72.3	81.8
Rsa1.0_00005.1.g318.t1	emb|CAA57913.1| beta-glucosidase [Brassica napus]	338	514	1.00E-172	152.1	88.8	90.5	beta-glucosidase	gbpln	Brassica napus	AT3G21370.1 | Symbols: BGLU19 | beta glucosidase 19 | chr3:7524286-7527579 REVERSE LENGTH=527	338	527	1.00E-170	155.9	86.1	92.6
Rsa1.0_00005.1.g319.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1267	1475	0	116.4	37.1	49.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1267	1262	1.00E-78	99.6	12.3	15.7
Rsa1.0_00005.1.g320.t1	ref|XP_002883303.1| hypothetical protein ARALYDRAFT_479659 [Arabidopsis lyrata subsp. lyrata] gi|297329143|gb|EFH59562.1| hypothetical protein ARALYDRAFT_479659 [Arabidopsis lyrata subsp. lyrata]	407	461	1.00E-177	113.3	81.8	88.9	hypothetical protein ARALYDRAFT_479659	gbpln	Arabidopsis lyrata	AT3G21380.1 | Symbols: | Mannose-binding lectin superfamily protein | chr3:7528478-7530457 FORWARD LENGTH=460	407	460	1.00E-175	113.0	82.3	89.4
Rsa1.0_00005.1.g321.t1	gb|EOA30874.1| hypothetical protein CARUB_v10014020mg [Capsella rubella]	428	364	0	85.0	73.6	76.2	hypothetical protein CARUB_v10014020mg	gbpln	Capsella rubella	AT3G21420.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:7541579-7543221 FORWARD LENGTH=364	428	364	1.00E-178	85.0	73.1	76.6
Rsa1.0_00005.1.g322.t2	gb|ABD65050.1| hypothetical protein 27.t00005 [Brassica oleracea]	129	236	7.00E-26	182.9	52.7	56.6	hypothetical protein 27.t00005	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00005.1.g323.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00005.1.g324.t1	ref|XP_002885441.1| electron carrier/ protein disulfide oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297331281|gb|EFH61700.1| electron carrier/ protein disulfide oxidoreductase [Arabidopsis lyrata subsp. lyrata]	102	102	4.00E-49	100.0	92.2	97.1	electron carrier/ protein disulfide oxidoreductase	gbpln	Arabidopsis lyrata	AT3G21460.1 | Symbols: | Glutaredoxin family protein | chr3:7557567-7557875 REVERSE LENGTH=102	102	102	1.00E-51	100.0	92.2	97.1
Rsa1.0_00005.1.g325.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00005.1.g326.t1	ref|XP_002880880.1| hypothetical protein ARALYDRAFT_481599 [Arabidopsis lyrata subsp. lyrata] gi|297326719|gb|EFH57139.1| hypothetical protein ARALYDRAFT_481599 [Arabidopsis lyrata subsp. lyrata]	201	720	2.00E-19	358.2	40.8	46.3	hypothetical protein ARALYDRAFT_481599	gbpln	Arabidopsis lyrata	AT2G27100.1 | Symbols: SE | C2H2 zinc-finger protein SERRATE (SE) | chr2:11572587-11576357 FORWARD LENGTH=720	201	720	3.00E-20	358.2	40.8	45.8
Rsa1.0_00005.1.g327.t10	ref|XP_002515199.1| hypothetical protein RCOM_1343910 [Ricinus communis] gi|223545679|gb|EEF47183.1| hypothetical protein RCOM_1343910 [Ricinus communis]	224	627	2.00E-23	279.9	30.8	43.3	hypothetical protein RCOM_1343910	gbpln	Ricinus communis	AT3G62200.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:23023437-23025671 REVERSE LENGTH=673	224	673	1.00E-23	300.4	29.5	44.6
Rsa1.0_00005.1.g328.t1	#	#	#	#	#	#	#	–	----	----	AT3G62210.1 | Symbols: EDA32 | Putative endonuclease or glycosyl hydrolase | chr3:23026910-23028113 REVERSE LENGTH=279	151	279	1.00E-11	184.8	32.5	45.0
Rsa1.0_00005.1.g329.t1	ref|XP_002883306.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329146|gb|EFH59565.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	137	387	5.00E-11	282.5	29.9	35.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G21465.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G15640.1); Has 38 Blast hits to 38 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7560750-7563202 FORWARD LENGTH=388	137	388	5.00E-12	283.2	28.5	35.0

Rsa1.0_00005.1.g330.t1	gb|EOA29492.1| hypothetical protein CARUB_v10012880mg [Capsella rubella]	999	1044	0	104.5	67.1	77.0	hypothetical protein CARUB_v10012880mg	gbpln	Capsella rubella	AT3G21480.1 | Symbols: | BRCT domain-containing DNA repair protein | chr3:7567730-7571990 FORWARD LENGTH=1041	999	1041	0	104.2	65.4	73.9
Rsa1.0_00005.1.g331.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00005.1.g332.t1	ref|XP_002885445.1| histidine-containing phosphotransmitter 3 [Arabidopsis lyrata subsp. lyrata] gi|297331285|gb|EFH61704.1| histidine-containing phosphotransmitter 3 [Arabidopsis lyrata subsp. lyrata]	154	154	2.00E-74	100.0	96.1	99.4	histidine-containing phosphotransmitter 3	gbpln	Arabidopsis lyrata	AT3G21510.1 | Symbols: AHP1 | histidine-containing phosphotransmitter 1 | chr3:7578432-7579537 REVERSE LENGTH=154	154	154	4.00E-76	100.0	95.5	98.7
Rsa1.0_00005.1.g333.t1	gb|EOA31454.1| hypothetical protein CARUB_v10014640mg [Capsella rubella]	202	208	5.00E-98	103.0	88.6	93.6	hypothetical protein CARUB_v10014640mg	gbpln	Capsella rubella	AT3G21520.1 | Symbols: DMP1, AtDMP1 | DUF679 domain membrane protein 1 | chr3:7582000-7582623 FORWARD LENGTH=207	202	207	2.00E-99	102.5	90.1	94.6
Rsa1.0_00005.1.g334.t1	ref|XP_002885448.1| hypothetical protein ARALYDRAFT_898603 [Arabidopsis lyrata subsp. lyrata] gi|297331288|gb|EFH61707.1| hypothetical protein ARALYDRAFT_898603 [Arabidopsis lyrata subsp. lyrata]	185	185	8.00E-94	100.0	90.3	96.8	hypothetical protein ARALYDRAFT_898603	gbpln	Arabidopsis lyrata	AT3G21550.1 | Symbols: DMP2, AtDMP2 | DUF679 domain membrane protein 2 | chr3:7591708-7592262 REVERSE LENGTH=184	185	184	9.00E-94	99.5	88.1	95.1
Rsa1.0_00005.1.g335.t1	dbj|BAA77394.1| SAE1-S9-protein [Brassica rapa]	327	255	3.00E-73	78.0	45.9	53.2	SAE1-S9-protein	gbpln	Brassica rapa	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	327	295	1.00E-70	90.2	43.4	56.6
Rsa1.0_00005.1.g336.t1	emb|CAS03349.1| sinapate 1-glucosyltransferase [Brassica napus var. napus] gi|226533678|emb|CAS03357.1| sinapate 1-glucosyltransferase [Brassica napus var. napus]	489	497	0	101.6	93.3	96.5	sinapate 1-glucosyltransferase	gbpln	Brassica napus	AT3G21560.1 | Symbols: UGT84A2 | UDP-Glycosyltransferase superfamily protein | chr3:7595884-7597374 FORWARD LENGTH=496	489	496	0	101.4	84.3	92.0
Rsa1.0_00005.1.g337.t1	emb|CAS03358.1| hypothetical protein [Brassica napus var. napus]	139	138	2.00E-57	99.3	90.6	93.5	hypothetical protein	gbpln	Brassica napus	AT3G21570.1 | Symbols: | unknown protein; Has 43 Blast hits to 43 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7600297-7600707 REVERSE LENGTH=136	139	136	1.00E-55	97.8	77.7	87.8
Rsa1.0_00005.1.g338.t1	ref|NP_001185096.1| phospholipid-translocating ATPase [Arabidopsis thaliana] gi|332192532|gb|AEE30653.1| putative phospholipid-transporting ATPase 12 [Arabidopsis thaliana]	1164	1185	0	101.8	88.0	94.0	phospholipid-translocating ATPase	gbpln	Arabidopsis thaliana	AT1G26130.2 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:9033600-9038246 FORWARD LENGTH=1185	1164	1185	0	101.8	88.0	94.0
Rsa1.0_00005.1.g339.t9	ref|XP_002885459.1| nitrate transporter [Arabidopsis lyrata subsp. lyrata] gi|297331299|gb|EFH61718.1| nitrate transporter [Arabidopsis lyrata subsp. lyrata]	567	590	1.00E-111	104.1	40.4	43.6	nitrate transporter	gbpln	Arabidopsis lyrata	AT3G21670.1 | Symbols: | Major facilitator superfamily protein | chr3:7626942-7628954 REVERSE LENGTH=590	567	590	1.00E-112	104.1	40.2	43.0
Rsa1.0_00005.1.g340.t1	gb|EOA32900.1| hypothetical protein CARUB_v10016225mg [Capsella rubella]	112	125	3.00E-29	111.6	68.8	80.4	hypothetical protein CARUB_v10016225mg	gbpln	Capsella rubella	AT3G21680.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: root, flower, stamen; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; Has 34 Blast hits to 34 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7633494-7633853 REVERSE LENGTH=119	112	119	1.00E-28	106.3	75.0	82.1
Rsa1.0_00005.1.g341.t1	dbj|BAJ34540.1| unnamed protein product [Thellungiella halophila]	318	505	1.00E-153	158.8	91.2	95.0	unnamed protein product	----	----	AT3G21690.1 | Symbols: | MATE efflux family protein | chr3:7638750-7641861 FORWARD LENGTH=506	318	506	1.00E-151	159.1	89.6	93.7
Rsa1.0_00005.1.g342.t1	ref|XP_002883313.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297329153|gb|EFH59572.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	156	506	1.00E-68	324.4	87.2	93.6	mate efflux family protein	gbpln	Arabidopsis lyrata	AT3G21690.1 | Symbols: | MATE efflux family protein | chr3:7638750-7641861 FORWARD LENGTH=506	156	506	1.00E-70	324.4	86.5	92.9
Rsa1.0_00005.1.g343.t1	ref|XP_002883313.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297329153|gb|EFH59572.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	548	506	0	92.3	86.1	88.9	mate efflux family protein	gbpln	Arabidopsis lyrata	AT3G21690.1 | Symbols: | MATE efflux family protein | chr3:7638750-7641861 FORWARD LENGTH=506	548	506	0	92.3	85.4	88.3

Rsa1.0_00005.1.g344.t1	ref|NP_850622.1| Ras-related small GTP-binding family protein [Arabidopsis thaliana] gi|11994637|dbj|BAB02832.1| unnamed protein product [Arabidopsis thaliana] gi|22316556|emb|CAD44270.1| monomeric G-protein [Arabidopsis thaliana] gi|332643018|gb|AEE76539.1| Ras-related small GTP-binding family protein [Arabidopsis thaliana]	278	292	1.00E-128	105.0	88.5	93.9	Ras-related small GTP-binding family protein	gbpln	Arabidopsis thaliana	AT3G21700.3 | Symbols: SGP2 | Ras-related small GTP-binding family protein | chr3:7644581-7646190 FORWARD LENGTH=292	278	292	1.00E-131	105.0	88.5	93.9
Rsa1.0_00005.1.g345.t1	gb|EOA31309.1| hypothetical protein CARUB_v10014480mg [Capsella rubella]	333	247	1.00E-52	74.2	37.8	41.7	hypothetical protein CARUB_v10014480mg	gbpln	Capsella rubella	AT3G21710.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:7648380-7649533 FORWARD LENGTH=211	333	211	2.00E-54	63.4	36.9	40.8
Rsa1.0_00006.1.g346.t1	gb|ABG29728.1| chloroplast chlorophyll a/b binding protein [Brassica napus]	267	267	1.00E-151	100.0	99.3	99.6	chloroplast chlorophyll a/b binding protein	gbpln	Brassica napus	AT1G29930.1 | Symbols: CAB1, AB140, CAB140, LHCB1.3 | chlorophyll A/B binding protein 1 | chr1:10478071-10478874 FORWARD LENGTH=267	267	267	1.00E-150	100.0	97.4	99.3
Rsa1.0_00006.1.g347.t1	ref|XP_002884603.1| hypothetical protein ARALYDRAFT_896807 [Arabidopsis lyrata subsp. lyrata] gi|297330443|gb|EFH60862.1| hypothetical protein ARALYDRAFT_896807 [Arabidopsis lyrata subsp. lyrata]	863	948	0	109.8	64.5	74.7	hypothetical protein ARALYDRAFT_896807	gbpln	Arabidopsis lyrata	AT4G32670.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr4:15759527-15762847 REVERSE LENGTH=860	863	860	1.00E-174	99.7	44.6	59.0
Rsa1.0_00006.1.g348.t3	ref|NP_174275.2| Magnesium transporter CorA-like family protein [Arabidopsis thaliana] gi|186479046|ref|NP_001117384.1| Magnesium transporter CorA-like family protein [Arabidopsis thaliana] gi|332193013|gb|AEE31134.1| Magnesium transporter CorA-like family protein [Arabidopsis thaliana] gi|332193014|gb|AEE31135.1| Magnesium transporter CorA-like family protein [Arabidopsis thaliana]	738	540	0	73.2	64.2	68.8	Magnesium transporter CorA-like family protein	gbpln	Arabidopsis thaliana	AT1G29820.2 | Symbols: | Magnesium transporter CorA-like family protein | chr1:10438219-10440625 FORWARD LENGTH=540	738	540	0	73.2	64.2	68.8
Rsa1.0_00006.1.g349.t1	gb|EOA37993.1| hypothetical protein CARUB_v10009462mg [Capsella rubella]	374	376	0	100.5	86.9	94.1	hypothetical protein CARUB_v10009462mg	gbpln	Capsella rubella	AT1G29790.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:10430025-10431161 FORWARD LENGTH=378	374	378	0	101.1	87.7	94.1
Rsa1.0_00006.1.g350.t1	gb|EOA36491.1| hypothetical protein CARUB_v10011144mg [Capsella rubella]	106	104	1.00E-29	98.1	65.1	67.9	hypothetical protein CARUB_v10011144mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00006.1.g351.t1	ref|XP_002890830.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297336672|gb|EFH67089.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	230	221	3.00E-98	96.1	79.1	86.5	NLI interacting factor family protein	gbpln	Arabidopsis lyrata	AT1G29780.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:10426950-10427615 FORWARD LENGTH=221	230	221	9.00E-97	96.1	76.1	84.3
Rsa1.0_00006.1.g352.t1	ref|XP_002890829.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297336671|gb|EFH67088.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	276	277	1.00E-120	100.4	80.4	87.7	NLI interacting factor family protein	gbpln	Arabidopsis lyrata	AT1G29770.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:10424806-10425642 FORWARD LENGTH=278	276	278	1.00E-120	100.7	78.6	86.6
Rsa1.0_00006.1.g353.t1	ref|XP_002890828.1| hypothetical protein ARALYDRAFT_890503 [Arabidopsis lyrata subsp. lyrata] gi|297336670|gb|EFH67087.1| hypothetical protein ARALYDRAFT_890503 [Arabidopsis lyrata subsp. lyrata]	560	527	1.00E-156	94.1	56.3	65.4	hypothetical protein ARALYDRAFT_890503	gbpln	Arabidopsis lyrata	AT1G29760.1 | Symbols: | Putative adipose-regulatory protein (Seipin) | chr1:10422381-10424116 FORWARD LENGTH=526	560	526	1.00E-148	93.9	47.1	54.8
Rsa1.0_00006.1.g354.t1	ref|XP_002893580.1| hypothetical protein ARALYDRAFT_473178 [Arabidopsis lyrata subsp. lyrata] gi|297339422|gb|EFH69839.1| hypothetical protein ARALYDRAFT_473178 [Arabidopsis lyrata subsp. lyrata]	1003	1023	0	102.0	79.9	88.5	hypothetical protein ARALYDRAFT_473178	gbpln	Arabidopsis lyrata	AT1G29750.2 | Symbols: RKF1 | receptor-like kinase in flowers 1 | chr1:10414071-10420469 REVERSE LENGTH=1021	1003	1021	0	101.8	80.4	88.6
Rsa1.0_00006.1.g355.t2	gb|EOA38810.1| hypothetical protein CARUB_v10011128mg [Capsella rubella]	109	1008	2.00E-22	924.8	55.0	69.7	hypothetical protein CARUB_v10011128mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	109	1019	1.00E-23	934.9	56.0	70.6

Rsa1.0_00006.1.g356.t2	ref|NP_564335.3| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|325511374|sp|Q9ASQ6.3|Y1972_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g29720; Flags: Precursor gi|332193000|gb|AEE31121.1| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana]	973	1019	0	104.7	66.6	74.2	Leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	973	1019	0	104.7	66.6	74.2
Rsa1.0_00006.1.g357.t12	gb|EOA39568.1| hypothetical protein CARUB_v10008187mg [Capsella rubella]	935	1015	0	108.6	70.9	80.0	hypothetical protein CARUB_v10008187mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	935	1019	0	109.0	71.2	80.4
Rsa1.0_00006.1.g358.t1	gb|EOA39560.1| hypothetical protein CARUB_v10008178mg [Capsella rubella]	1082	1022	0	94.5	65.3	74.3	hypothetical protein CARUB_v10008178mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	1082	1019	0	94.2	64.5	72.9
Rsa1.0_00006.1.g359.t5	gb|EOA39560.1| hypothetical protein CARUB_v10008178mg [Capsella rubella]	1945	1022	0	52.5	36.5	41.5	hypothetical protein CARUB_v10008178mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	1945	1019	0	52.4	35.9	41.2
Rsa1.0_00006.1.g360.t1	ref|XP_002893575.1| hypothetical protein ARALYDRAFT_473173 [Arabidopsis lyrata subsp. lyrata] gi|297339417|gb|EFH69834.1| hypothetical protein ARALYDRAFT_473173 [Arabidopsis lyrata subsp. lyrata]	351	350	1.00E-173	99.7	87.7	93.2	hypothetical protein ARALYDRAFT_473173	gbpln	Arabidopsis lyrata	AT1G29700.1 | Symbols: | Metallo-hydrolase/oxidoreductase superfamily protein | chr1:10385196-10386906 REVERSE LENGTH=350	351	350	1.00E-174	99.7	86.3	92.9
Rsa1.0_00006.1.g361.t1	gb|EOA40030.1| hypothetical protein CARUB_v10008721mg [Capsella rubella]	566	565	0	99.8	92.6	95.9	hypothetical protein CARUB_v10008721mg	gbpln	Capsella rubella	AT1G29690.1 | Symbols: CAD1 | MAC/Perforin domain-containing protein | chr1:10379310-10381861 REVERSE LENGTH=561	566	561	0	99.1	91.5	94.7
Rsa1.0_00006.1.g362.t1	gb|AGJ83937.1| GLIP [Brassica napus]	360	361	0	100.3	95.6	97.5	GLIP	gbpln	Brassica napus	AT1G29670.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:10375843-10377717 FORWARD LENGTH=363	360	363	0	100.8	86.4	91.7
Rsa1.0_00006.1.g363.t1	ref|NP_174259.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75169353|sp|Q9C7N5.1|GDL14_ARATH RecName: Full=GDSL esterase/lipase At1g29660; AltName: Full=Extracellular lipase At1g29660; Flags: Precursor gi|12323544|gb|AAG51756.1|AC068667_35 lipase/hydrolase, putative; 114382-116051 [Arabidopsis thaliana] gi|15215768|gb|AAK91429.1| At1g29660/F15D2_21 [Arabidopsis thaliana] gi|22137090|gb|AAM91390.1| At1g29660/F15D2_21 [Arabidopsis thaliana] gi|332192994|gb|AEE31115.1| GDSL esterase/lipase [Arabidopsis thaliana]	386	364	0	94.3	80.3	86.5	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT1G29660.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:10371955-10373624 FORWARD LENGTH=364	386	364	0	94.3	80.3	86.5
Rsa1.0_00006.1.g364.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00006.1.g365.t1	ref|NP_174257.1| uncharacterized protein [Arabidopsis thaliana] gi|12323541|gb|AAG51753.1|AC068667_32 hypothetical protein; 98808-98386 [Arabidopsis thaliana] gi|28466825|gb|AAO44021.1| At1g29640 [Arabidopsis thaliana] gi|110743019|dbj|BAE99402.1| hypothetical protein [Arabidopsis thaliana] gi|332192993|gb|AEE31114.1| uncharacterized protein AT1G29640 [Arabidopsis thaliana]	139	140	5.00E-55	100.7	79.9	89.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G29640.1 | Symbols: | Protein of unknown function, DUF584 | chr1:10355959-10356381 REVERSE LENGTH=140	139	140	1.00E-57	100.7	79.9	89.2
Rsa1.0_00006.1.g366.t1	gb|EOA38491.1| hypothetical protein CARUB_v10010257mg [Capsella rubella]	219	219	1.00E-106	100.0	85.4	91.8	hypothetical protein CARUB_v10010257mg	gbpln	Capsella rubella	AT1G17180.1 | Symbols: ATGSTU25, GSTU25 | glutathione S-transferase TAU 25 | chr1:5872208-5872958 FORWARD LENGTH=221	219	221	1.00E-108	100.9	84.0	91.3
Rsa1.0_00006.1.g367.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1600	1213	0	75.8	25.6	38.2	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1600	626	1.00E-69	39.1	9.2	13.7
Rsa1.0_00006.1.g368.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00006.1.g369.t1	ref|XP_002881330.1| hypothetical protein ARALYDRAFT_482373 [Arabidopsis lyrata subsp. lyrata] gi|297327169|gb|EFH57589.1| hypothetical protein ARALYDRAFT_482373 [Arabidopsis lyrata subsp. lyrata]	235	241	9.00E-17	102.6	42.1	52.8	hypothetical protein ARALYDRAFT_482373	gbpln	Arabidopsis lyrata	AT1G29530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34310.3); Has 84 Blast hits to 78 proteins in 24 species: Archae - 2; Bacteria - 4; Metazoa - 9; Fungi - 8; Plants - 55; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:10325553-10326651 REVERSE LENGTH=236	235	236	3.00E-18	100.4	40.0	47.7
Rsa1.0_00006.1.g370.t1	gb|EOA37440.1| hypothetical protein CARUB_v10011510mg [Capsella rubella]	159	158	2.00E-71	99.4	92.5	95.6	hypothetical protein CARUB_v10011510mg	gbpln	Capsella rubella	AT1G29520.1 | Symbols: | AWPM-19-like family protein | chr1:10323735-10324525 FORWARD LENGTH=158	159	158	1.00E-73	99.4	91.8	96.2
Rsa1.0_00006.1.g371.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00006.1.g372.t1	gb|ABV89641.1| auxin-induced protein [Brassica rapa]	89	137	1.00E-17	153.9	49.4	53.9	auxin-induced protein	gbpln	Brassica rapa	AT1G29500.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:10321290-10321697 FORWARD LENGTH=135	89	135	3.00E-18	151.7	44.9	52.8
Rsa1.0_00006.1.g373.t1	gb|ABV89665.1| auxin-responsive protein [Brassica rapa]	138	139	4.00E-65	100.7	93.5	96.4	auxin-responsive protein	gbpln	Brassica rapa	AT1G29450.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:10305981-10306406 REVERSE LENGTH=141	138	141	2.00E-56	102.2	77.5	86.2
Rsa1.0_00006.1.g374.t1	ref|XP_002868389.1| hypothetical protein ARALYDRAFT_493566 [Arabidopsis lyrata subsp. lyrata] gi|297314225|gb|EFH44648.1| hypothetical protein ARALYDRAFT_493566 [Arabidopsis lyrata subsp. lyrata]	271	264	1.00E-106	97.4	81.9	86.7	hypothetical protein ARALYDRAFT_493566	gbpln	Arabidopsis lyrata	AT5G32440.1 | Symbols: | Ubiquitin system component Cue protein | chr5:12077014-12078396 FORWARD LENGTH=264	271	264	2.00E-99	97.4	80.8	85.6
Rsa1.0_00006.1.g375.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00006.1.g376.t1	gb|EOA36053.1| hypothetical protein CARUB_v10008372mg [Capsella rubella] gi|482571867|gb|EOA36054.1| hypothetical protein CARUB_v10008372mg [Capsella rubella]	704	767	0	108.9	90.6	95.3	hypothetical protein CARUB_v10008372mg	gbpln	Capsella rubella	AT1G29470.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:10310424-10313369 REVERSE LENGTH=770	704	770	0	109.4	90.2	95.2
Rsa1.0_00006.1.g377.t1	ref|NP_174231.2| carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana] gi|49823474|gb|AAT68720.1| hypothetical protein At1g29380 [Arabidopsis thaliana] gi|55740509|gb|AAV63847.1| hypothetical protein At1g29380 [Arabidopsis thaliana] gi|62320282|dbj|BAD94579.1| beta-1,3 glucanase [Arabidopsis thaliana] gi|332192957|gb|AEE31078.1| carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana]	325	315	2.00E-83	96.9	75.4	79.4	carbohydrate-binding X8 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G29380.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr1:10284209-10285671 FORWARD LENGTH=315	325	315	6.00E-86	96.9	75.4	79.4
Rsa1.0_00006.1.g378.t1	ref|NP_174229.2| uncharacterized protein [Arabidopsis thaliana] gi|332192954|gb|AEE31075.1| uncharacterized protein AT1G29350 [Arabidopsis thaliana]	865	831	0	96.1	73.2	80.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G29350.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr1:10268761-10273613 REVERSE LENGTH=831	865	831	0	96.1	73.2	80.3
Rsa1.0_00006.1.g379.t1	dbj|BAJ34586.1| unnamed protein product [Thellungiella halophila]	678	724	0	106.8	85.7	92.9	unnamed protein product	----	----	AT1G29340.1 | Symbols: PUB17, ATPUB17 | plant U-box 17 | chr1:10264412-10266601 FORWARD LENGTH=729	678	729	0	107.5	84.7	92.2
Rsa1.0_00006.1.g380.t1	ref|XP_002893557.1| hypothetical protein ARALYDRAFT_473143 [Arabidopsis lyrata subsp. lyrata] gi|297339399|gb|EFH69816.1| hypothetical protein ARALYDRAFT_473143 [Arabidopsis lyrata subsp. lyrata]	215	215	1.00E-118	100.0	95.8	99.1	hypothetical protein ARALYDRAFT_473143	gbpln	Arabidopsis lyrata	AT1G29330.1 | Symbols: ATERD2, AERD2, ERD2 | ER lumen protein retaining receptor family protein | chr1:10258580-10260906 REVERSE LENGTH=215	215	215	1.00E-119	100.0	94.4	98.1
Rsa1.0_00006.1.g381.t1	ref|NP_174226.1| WD40 domain-containing protein [Arabidopsis thaliana] gi|111074196|gb|ABH04471.1| At1g29320 [Arabidopsis thaliana] gi|332192951|gb|AEE31072.1| WD40 domain-containing protein [Arabidopsis thaliana]	444	468	0	105.4	84.2	90.5	WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G29320.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:10255355-10258238 FORWARD LENGTH=468	444	468	0	105.4	84.2	90.5
Rsa1.0_00006.1.g382.t1	ref|XP_002893556.1| hypothetical protein ARALYDRAFT_473140 [Arabidopsis lyrata subsp. lyrata] gi|297339398|gb|EFH69815.1| hypothetical protein ARALYDRAFT_473140 [Arabidopsis lyrata subsp. lyrata]	470	459	0	97.7	81.7	89.1	hypothetical protein ARALYDRAFT_473140	gbpln	Arabidopsis lyrata	AT1G29300.1 | Symbols: UNE1 | Plant protein of unknown function (DUF641) | chr1:10248120-10249499 REVERSE LENGTH=459	470	459	0	97.7	81.3	88.1

Rsa1.0_00006.1.g383.t1	ref|XP_002890803.1| hypothetical protein ARALYDRAFT_473139 [Arabidopsis lyrata subsp. lyrata] gi|297336645|gb|EFH67062.1| hypothetical protein ARALYDRAFT_473139 [Arabidopsis lyrata subsp. lyrata]	106	107	1.00E-40	100.9	81.1	90.6	hypothetical protein ARALYDRAFT_473139	gbpln	Arabidopsis lyrata	AT1G29290.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10245055-10245378 FORWARD LENGTH=107	106	107	2.00E-43	100.9	82.1	90.6
Rsa1.0_00006.1.g384.t1	gb|ACI14404.1| WRKY65-1 transcription factor [Brassica napus]	259	261	1.00E-116	100.8	85.3	88.8	WRKY65-1 transcription factor	gbpln	Brassica napus	AT1G29280.1 | Symbols: WRKY65, ATWRKY65 | WRKY DNA-binding protein 65 | chr1:10236589-10237467 FORWARD LENGTH=259	259	259	1.00E-112	100.0	84.6	89.2
Rsa1.0_00006.1.g385.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00006.1.g386.t1	ref|NP_174217.1| CBL-interacting serine/threonine-protein kinase 18 [Arabidopsis thaliana] gi|75335276|sp|Q9LP51.1|CIPKI_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 18; AltName: Full=SNF1-related kinase 3.20; AltName: Full=SOS2-like protein kinase PKS22 gi|9502417|gb|AAF88116.1|AC021043_9 Putative protein kinase [Arabidopsis thaliana] gi|14334388|gb|AAK59695.1| CBL-interacting protein kinase 18 [Arabidopsis thaliana] gi|332192942|gb|AEE31063.1| CBL-interacting serine/threonine-protein kinase 18 [Arabidopsis thaliana]	523	520	0	99.4	88.7	93.7	CBL-interacting serine/threonine-protein kinase 18	gbpln	Arabidopsis thaliana	AT1G29230.1 | Symbols: CIPK18, SnRK3.20, ATWL1, WL1, ATCIPK18 | CBL-interacting protein kinase 18 | chr1:10214860-10216422 FORWARD LENGTH=520	523	520	0	99.4	88.7	93.7
Rsa1.0_00006.1.g387.t1	ref|XP_002890798.1| hypothetical protein ARALYDRAFT_890443 [Arabidopsis lyrata subsp. lyrata] gi|297336640|gb|EFH67057.1| hypothetical protein ARALYDRAFT_890443 [Arabidopsis lyrata subsp. lyrata]	500	574	1.00E-168	114.8	69.8	82.0	hypothetical protein ARALYDRAFT_890443	gbpln	Arabidopsis lyrata	AT1G29240.1 | Symbols: | Protein of unknown function (DUF688) | chr1:10217023-10218924 REVERSE LENGTH=577	500	577	1.00E-168	115.4	70.8	81.4
Rsa1.0_00006.1.g388.t1	ref|NP_565781.1| Alba DNA/RNA-binding protein [Arabidopsis thaliana] gi|73921087|sp|O22969.1|Y2416_ARATH RecName: Full=Uncharacterized protein At2g34160 gi|2342735|gb|AAB67633.1| expressed protein [Arabidopsis thaliana] gi|21536653|gb|AAM60985.1| unknown [Arabidopsis thaliana] gi|26450089|dbj|BAC42164.1| unknown protein [Arabidopsis thaliana] gi|111074476|gb|ABH04611.1| At2g34160 [Arabidopsis thaliana] gi|330253832|gb|AEC08926.1| Alba DNA/RNA-binding protein [Arabidopsis thaliana]	130	130	1.00E-59	100.0	89.2	93.1	Alba DNA/RNA-binding protein	gbpln	Arabidopsis thaliana	AT2G34160.1 | Symbols: | Alba DNA/RNA-binding protein | chr2:14426283-14427220 FORWARD LENGTH=130	130	130	2.00E-62	100.0	89.2	93.1
Rsa1.0_00006.1.g389.t1	gb|ABB92566.1| peroxisomal import receptor PTS2 [Brassica napus]	317	317	1.00E-178	100.0	93.7	97.8	peroxisomal import receptor PTS2	gbpln	Brassica napus	AT1G29260.1 | Symbols: PEX7, ATPEX7 | peroxin 7 | chr1:10224923-10225876 FORWARD LENGTH=317	317	317	1.00E-180	100.0	93.1	97.8
Rsa1.0_00006.1.g390.t1	gb|EOA37296.1| hypothetical protein CARUB_v10010917mg [Capsella rubella]	172	184	4.00E-68	107.0	82.0	86.0	hypothetical protein CARUB_v10010917mg	gbpln	Capsella rubella	AT1G29195.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, 4 leaf senescence stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30230.1); Has 180 Blast hits to 180 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 180; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10202673-10203254 REVERSE LENGTH=193	172	193	2.00E-69	112.2	82.6	89.0
Rsa1.0_00006.1.g391.t1	ref|NP_001184912.1| uncharacterized protein [Arabidopsis thaliana] gi|332189732|gb|AEE27853.1| uncharacterized protein AT1G05550 [Arabidopsis thaliana]	372	385	7.00E-88	103.5	45.7	58.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G05550.3 | Symbols: | Protein of unknown function (DUF295) | chr1:1641229-1643748 REVERSE LENGTH=385	372	385	2.00E-90	103.5	45.7	58.9

Rsa1.0_00006.1.g392.t1	ref|NP_174212.2| protein SCAR3 [Arabidopsis thaliana] gi|75175509|sp|Q9LP46.1|SCAR3_ARATH RecName: Full=Protein SCAR3; Short=AtSCAR3; AltName: Full=Protein WAVE2 gi|9502422|gb|AAF88121.1|AC021043_14 Hypothetical protein [Arabidopsis thaliana] gi|53801280|gb|AAU93850.1| SCAR3 [Arabidopsis thaliana] gi|332192931|gb|AEE31052.1| protein SCAR3 [Arabidopsis thaliana]	940	1020	0	108.5	72.4	80.7	protein SCAR3	gbpln	Arabidopsis thaliana	AT1G29170.1 | Symbols: WAVE2, ATSCAR3, SCAR3 | SCAR family protein | chr1:10190352-10194900 REVERSE LENGTH=1020	940	1020	0	108.5	72.4	80.7
Rsa1.0_00006.1.g393.t1	gb|EOA37128.1| hypothetical protein CARUB_v10010402mg [Capsella rubella]	179	182	3.00E-79	101.7	86.6	89.9	hypothetical protein CARUB_v10010402mg	gbpln	Capsella rubella	AT1G29160.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr1:10183797-10184324 REVERSE LENGTH=175	179	175	4.00E-79	97.8	87.2	90.5
Rsa1.0_00006.1.g394.t1	ref|XP_002890794.1| hypothetical protein ARALYDRAFT_336019 [Arabidopsis lyrata subsp. lyrata] gi|297336636|gb|EFH67053.1| hypothetical protein ARALYDRAFT_336019 [Arabidopsis lyrata subsp. lyrata]	419	621	0	148.2	96.2	96.9	hypothetical protein ARALYDRAFT_336019	gbpln	Arabidopsis lyrata	AT1G29150.1 | Symbols: ATS9, RPN6 | non-ATPase subunit 9 | chr1:10181240-10182499 FORWARD LENGTH=419	419	419	0	100.0	97.6	98.6
Rsa1.0_00006.1.g395.t1	gb|EOA37644.1| hypothetical protein CARUB_v10012122mg [Capsella rubella]	171	171	6.00E-85	100.0	88.9	92.4	hypothetical protein CARUB_v10012122mg	gbpln	Capsella rubella	AT1G29140.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr1:10179029-10179811 FORWARD LENGTH=171	171	171	2.00E-85	100.0	86.5	91.8
Rsa1.0_00006.1.g396.t1	gb|EOA40380.1| hypothetical protein CARUB_v10009109mg [Capsella rubella]	451	452	0	100.2	89.4	92.7	hypothetical protein CARUB_v10009109mg	gbpln	Capsella rubella	AT1G29120.2 | Symbols: | Hydrolase-like protein family | chr1:10174481-10178143 FORWARD LENGTH=455	451	455	0	100.9	86.9	91.8
Rsa1.0_00006.1.g397.t1	ref|XP_002890790.1| ribosomal protein L34 family protein [Arabidopsis lyrata subsp. lyrata] gi|297336632|gb|EFH67049.1| ribosomal protein L34 family protein [Arabidopsis lyrata subsp. lyrata]	162	159	2.00E-51	98.1	77.8	84.6	ribosomal protein L34 family protein	gbpln	Arabidopsis lyrata	AT1G29070.1 | Symbols: | Ribosomal protein L34 | chr1:10149884-10151155 FORWARD LENGTH=157	162	157	2.00E-53	96.9	80.2	87.0
Rsa1.0_00006.1.g398.t1	ref|NP_567434.1| protein transport protein SFT1 [Arabidopsis thaliana] gi|75248462|sp|Q8VXX9.1|BETL1_ARATH RecName: Full=Bet1-like protein At4g14600 gi|18389246|gb|AAL67066.1| unknown protein [Arabidopsis thaliana] gi|20259643|gb|AAM14339.1| unknown protein [Arabidopsis thaliana] gi|21554084|gb|AAM63165.1| unknown [Arabidopsis thaliana] gi|26452326|dbj|BAC43249.1| unknown protein [Arabidopsis thaliana] gi|332658064|gb|AEE83464.1| Bet1-like protein [Arabidopsis thaliana]	137	137	2.00E-70	100.0	92.7	97.1	protein transport protein SFT1	gbpln	Arabidopsis thaliana	AT4G14600.1 | Symbols: | Target SNARE coiled-coil domain protein | chr4:8376562-8378078 FORWARD LENGTH=137	137	137	6.00E-73	100.0	92.7	97.1
Rsa1.0_00006.1.g399.t1	ref|XP_002893542.1| F1K23.5 [Arabidopsis lyrata subsp. lyrata] gi|297339384|gb|EFH69801.1| F1K23.5 [Arabidopsis lyrata subsp. lyrata]	210	269	2.00E-79	128.1	79.5	85.7	F1K23.5	gbpln	Arabidopsis lyrata	AT1G28960.5 | Symbols: ATNUDT15, ATNUDX15, NUDX15 | nudix hydrolase homolog 15 | chr1:10110135-10111607 REVERSE LENGTH=293	210	293	2.00E-78	139.5	63.8	64.8
Rsa1.0_00006.1.g400.t1	ref|XP_002890784.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336626|gb|EFH67043.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	119	117	6.00E-42	98.3	71.4	82.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G28815.1 | Symbols: | unknown protein; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10095812-10096244 FORWARD LENGTH=115	119	115	8.00E-40	96.6	63.9	79.0
Rsa1.0_00006.1.g401.t1	ref|NP_174190.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|193806502|sp|Q1PFQ9.2|PPR62_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g28690, mitochondrial; Flags: Precursor gi|332192893|gb|AEE31014.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	504	520	0	103.2	81.3	90.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G28690.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:10080042-10081604 REVERSE LENGTH=520	504	520	0	103.2	81.3	90.5
Rsa1.0_00006.1.g402.t4	gb|AAX62802.1| lipase 2 [Brassica napus]	241	389	5.00E-98	161.4	72.2	80.9	lipase 2	gbpln	Brassica napus	AT1G28670.1 | Symbols: ARAB-1 | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:10074669-10076250 REVERSE LENGTH=384	241	384	6.00E-94	159.3	68.5	78.0
Rsa1.0_00006.1.g403.t1	gb|AAC34342.1| Hypothetical protein [Arabidopsis thaliana]	355	374	7.00E-36	105.4	26.2	38.0	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	355	303	2.00E-38	85.4	26.2	38.0
Rsa1.0_00006.1.g404.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00006.1.g405.t1</td><td>gb|ABD64987.1| hypothetical protein 26.t00003 [Brassica oleracea]</td><td>589</td><td>330</td><td>6.00E−15</td><td>56.0</td><td>9.8</td><td>11.4</td><td>hypothetical protein 26.t00003</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00006.1.g406.t2</td><td>gb|AAF16748.1|AC010155_1 F3M18.1 [Arabidopsis thaliana] gi|6691212|gb|AAF24550.1|AC007508_13 F1K23.20 [Arabidopsis thaliana]</td><td>690</td><td>482</td><td>1.00E−167</td><td>69.9</td><td>44.1</td><td>51.9</td><td>F3M18.1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G28560.1 | Symbols: SRD2 | snRNA activating complex family protein | chr1:10038197−10040382 REVERSE LENGTH=375</td><td>690</td><td>375</td><td>1.00E−140</td><td>54.3</td><td>36.5</td><td>42.9</td></tr>
<tr><td>Rsa1.0_00006.1.g407.t1</td><td>ref|XP_002890782.1| hypothetical protein ARALYDRAFT_473075 [Arabidopsis lyrata subsp. lyrata] gi|297336624|gb|EFH67041.1| hypothetical protein ARALYDRAFT_473075 [Arabidopsis lyrata subsp. lyrata]</td><td>115</td><td>104</td><td>1.00E−38</td><td>90.4</td><td>74.8</td><td>81.7</td><td>hypothetical protein ARALYDRAFT_473075</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G28540.1 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 10 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 25; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:10035696−10036007 FORWARD LENGTH=103</td><td>115</td><td>103</td><td>1.00E−40</td><td>89.6</td><td>74.8</td><td>83.5</td></tr>
<tr><td>Rsa1.0_00006.1.g408.t1</td><td>gb|EOA37571.1| hypothetical protein CARUB_v10011901mg [Capsella rubella]</td><td>609</td><td>609</td><td>0</td><td>100.0</td><td>85.1</td><td>92.8</td><td>hypothetical protein CARUB_v10011901mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G28530.2 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; Has 20 Blast hits to 20 proteins in 6 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 20; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:10032127−10035496 REVERSE LENGTH=613</td><td>609</td><td>613</td><td>0</td><td>100.7</td><td>84.1</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00006.1.g409.t2</td><td>gb|EOA36887.1| hypothetical protein CARUB_v10008982mg [Capsella rubella]</td><td>476</td><td>486</td><td>0</td><td>102.1</td><td>85.1</td><td>88.2</td><td>hypothetical protein CARUB_v10008982mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G28520.2 | Symbols: VOZ1 | vascular plant one zinc finger protein | chr1:10029713−10031479 FORWARD LENGTH=486</td><td>476</td><td>486</td><td>0</td><td>102.1</td><td>84.2</td><td>87.8</td></tr>
<tr><td>Rsa1.0_00006.1.g410.t6</td><td>ref|NP_564311.1| Optic atrophy 3 protein (OPA3) [Arabidopsis thaliana] gi|6560770|gb|AAF16770.1|AC010155_23 F3M18.5 [Arabidopsis thaliana] gi|15724222|gb|AAL06504.1|AF412051_1 At1g28510/F3M18_5 [Arabidopsis thaliana] gi|18252247|gb|AAL62004.1| At1g28510/F3M18_5 [Arabidopsis thaliana] gi|21553821|gb|AAM62914.1| unknown [Arabidopsis thaliana] gi|332192864|gb|AEE30985.1| Optic atrophy 3 protein (OPA3) [Arabidopsis thaliana]</td><td>183</td><td>171</td><td>6.00E−77</td><td>93.4</td><td>78.7</td><td>88.0</td><td>Optic atrophy 3 protein (OPA3)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G28510.1 | Symbols: | Optic atrophy 3 protein (OPA3) | chr1:10024036−10025939 FORWARD LENGTH=171</td><td>183</td><td>171</td><td>2.00E−79</td><td>93.4</td><td>78.7</td><td>88.0</td></tr>
<tr><td>Rsa1.0_00006.1.g411.t1</td><td>ref|XP_002890776.1| hypothetical protein ARALYDRAFT_473063 [Arabidopsis lyrata subsp. lyrata] gi|297336618|gb|EFH67035.1| hypothetical protein ARALYDRAFT_473063 [Arabidopsis lyrata subsp. lyrata]</td><td>994</td><td>996</td><td>0</td><td>100.2</td><td>83.6</td><td>91.3</td><td>hypothetical protein ARALYDRAFT_473063</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G28440.1 | Symbols: HSL1 | HAESA−like 1 | chr1:9996914−10000171 FORWARD LENGTH=996</td><td>994</td><td>996</td><td>0</td><td>100.2</td><td>83.0</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00006.1.g412.t1</td><td>ref|XP_002890775.1| HB−1 [Arabidopsis lyrata subsp. lyrata] gi|297336617|gb|EFH67034.1| HB−1 [Arabidopsis lyrata subsp. lyrata]</td><td>1572</td><td>1705</td><td>0</td><td>108.5</td><td>81.7</td><td>88.5</td><td>HB−1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G28420.1 | Symbols: HB−1 | homeobox−1 | chr1:9979936−9987460 FORWARD LENGTH=1705</td><td>1572</td><td>1705</td><td>0</td><td>108.5</td><td>80.7</td><td>87.3</td></tr>
<tr><td>Rsa1.0_00006.1.g413.t1</td><td>ref|XP_002893510.1| hypothetical protein ARALYDRAFT_890356 [Arabidopsis lyrata subsp. lyrata] gi|297339352|gb|EFH69769.1| hypothetical protein ARALYDRAFT_890356 [Arabidopsis lyrata subsp. lyrata]</td><td>130</td><td>260</td><td>3.00E−37</td><td>200.0</td><td>65.4</td><td>69.2</td><td>hypothetical protein ARALYDRAFT_890356</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G28200.1 | Symbols: FIP1 | FH interacting protein 1 | chr1:9850395−9852300 REVERSE LENGTH=259</td><td>130</td><td>259</td><td>6.00E−37</td><td>199.2</td><td>62.3</td><td>66.9</td></tr>
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Rsa1.0_00007.1.g414.t1	sp|Q43133.1|GGPPS_SINAL RecName: Full=Geranylgeranyl pyrophosphate synthase, chloroplastic/chromoplastic; Short=GGPP synthase; Short=GGPS; AltName: Full=(2E,6E)-farnesyl diphosphate synthase; AltName: Full=Dimethylallyltranstransferase; AltName: Full=Farnesyl diphosphate synthase; AltName: Full=Farnesyltranstransferase; AltName: Full=Geranyltranstransferase; Flags: Precursor gi|1419758|emb|CAA67330.1| geranylgeranyl pyrophosphate synthase [Sinapis alba]	361	366	1.00E-156	101.4	80.1	89.2	RecName: Full=Geranylgeranyl pyrophosphate synthase, chloroplastic/chromoplastic; Short=GGPP synthase; Short=GGPS; AltName: Full=(2E,6E)-farnesyl diphosphate synthase; AltName: Full=Dimethylallyltranstransferase; AltName: Full=Farnesyl diphosphate synthase; AltName: Full=Farnesyltranstransferase; AltName: Full=Geranyltranstransferase; Flags: Precursor gi|1419758|emb|CAA67330.1| geranylgeranyl pyrophosphate synthase	gbpln	Sinapis alba	AT4G36810.1 | Symbols: GGPS1 | geranylgeranyl pyrophosphate synthase 1 | chr4:17343513-17344628 FORWARD LENGTH=371	361	371	1.00E-156	102.8	79.2	86.7
Rsa1.0_00007.1.g415.t1	gb|ACI16426.1| RUB1-conjugation enzyme [Brassica juncea]	185	185	1.00E-104	100.0	97.3	98.9	RUB1-conjugation enzyme	gbpln	Brassica juncea	AT4G36800.2 | Symbols: RCE1 | RUB1 conjugating enzyme 1 | chr4:17341237-17342148 REVERSE LENGTH=184	185	184	1.00E-105	99.5	97.3	98.9
Rsa1.0_00007.1.g416.t1	dbj|BAJ34484.1| unnamed protein product [Thellungiella halophila]	640	645	0	100.8	94.5	97.5	unnamed protein product	----	----	AT4G36760.1 | Symbols: ATAPP1, APP1 | aminopeptidase P1 | chr4:17326688-17329979 FORWARD LENGTH=645	640	645	0	100.8	92.2	96.3
Rsa1.0_00007.1.g417.t1	ref|XP_002866994.1| homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata] gi|297312830|gb|EFH43253.1| homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata]	221	217	1.00E-91	98.2	78.7	87.8	homeobox-leucine zipper protein ATHB-40	gbpln	Arabidopsis lyrata	AT4G36740.1 | Symbols: HB-5, ATHB40, HB40 | homeobox protein 40 | chr4:17314649-17316314 REVERSE LENGTH=216	221	216	5.00E-94	97.7	77.8	86.9
Rsa1.0_00007.1.g418.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00007.1.g419.t4	emb|CAA58774.1| G-box binding factor 1A [Brassica napus]	319	313	1.00E-144	98.1	84.6	87.1	G-box binding factor 1A	gbpln	Brassica napus	AT4G36730.1 | Symbols: GBF1 | G-box binding factor 1 | chr4:17309850-17311752 REVERSE LENGTH=315	319	315	1.00E-141	98.7	83.1	88.1
Rsa1.0_00007.1.g420.t1	ref|XP_002869026.1| hypothetical protein ARALYDRAFT_912692 [Arabidopsis lyrata subsp. lyrata] gi|297314862|gb|EFH45285.1| hypothetical protein ARALYDRAFT_912692 [Arabidopsis lyrata subsp. lyrata]	207	205	7.00E-89	99.0	76.8	88.9	hypothetical protein ARALYDRAFT_912692	gbpln	Arabidopsis lyrata	AT4G36720.1 | Symbols: HVA22K | HVA22-like protein K | chr4:17307769-17309668 FORWARD LENGTH=200	207	200	1.00E-85	96.6	72.9	84.5
Rsa1.0_00007.1.g421.t1	ref|NP_195388.2| cupin family protein [Arabidopsis thaliana] gi|332661291|gb|AEE86691.1| cupin family protein [Arabidopsis thaliana]	579	522	0	90.2	60.4	68.0	cupin family protein	gbpln	Arabidopsis thaliana	AT4G36700.1 | Symbols: | RmlC-like cupins superfamily protein | chr4:17298443-17300337 REVERSE LENGTH=522	579	522	0	90.2	60.4	68.0
Rsa1.0_00007.1.g422.t4	ref|XP_002866997.1| hypothetical protein ARALYDRAFT_490965 [Arabidopsis lyrata subsp. lyrata] gi|297312833|gb|EFH43256.1| hypothetical protein ARALYDRAFT_490965 [Arabidopsis lyrata subsp. lyrata]	560	567	0	101.3	79.5	86.1	hypothetical protein ARALYDRAFT_490965	gbpln	Arabidopsis lyrata	AT4G36690.4 | Symbols: ATU2AF65A | U2 snRNP auxilliary factor, large subunit, splicing factor | chr4:17294139-17297609 REVERSE LENGTH=551	560	551	0	98.4	79.5	85.5
Rsa1.0_00007.1.g423.t1	ref|XP_002866998.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297312834|gb|EFH43257.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	407	411	0	101.0	76.9	89.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G36680.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:17292479-17293717 REVERSE LENGTH=412	407	412	0	101.2	75.7	88.9
Rsa1.0_00007.1.g424.t1	gb|EOA16170.1| hypothetical protein CARUB_v10004306mg [Capsella rubella]	665	668	0	100.5	82.4	90.5	hypothetical protein CARUB_v10004306mg	gbpln	Capsella rubella	AT4G38030.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr4:17863206-17866730 REVERSE LENGTH=667	665	667	0	100.3	81.7	89.5
Rsa1.0_00007.1.g425.t1	gb|EOA18172.1| hypothetical protein CARUB_v10006648mg [Capsella rubella]	508	493	0	97.0	87.8	93.1	hypothetical protein CARUB_v10006648mg	gbpln	Capsella rubella	AT4G36670.1 | Symbols: | Major facilitator superfamily protein | chr4:17287680-17289483 REVERSE LENGTH=493	508	493	0	97.0	86.6	92.5
Rsa1.0_00007.1.g426.t1	gb|EOA18681.1| hypothetical protein CARUB_v10007257mg [Capsella rubella]	293	293	1.00E-159	100.0	90.4	94.9	hypothetical protein CARUB_v10007257mg	gbpln	Capsella rubella	AT4G36640.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr4:17277187-17278447 REVERSE LENGTH=294	293	294	1.00E-153	100.3	85.3	93.2

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<tr><td>Rsa1.0_00007.1.g427.t2</td><td>ref|NP_195381.6| Vacuolar sorting protein 39 [Arabidopsis thaliana] gi|20466826|gb|AAM20730.1| unknown protein [Arabidopsis thaliana] gi|332661279|gb|AEE86679.1| Vacuolar sorting protein 39 [Arabidopsis thaliana]</td><td>565</td><td>1000</td><td>0</td><td>177.0</td><td>71.9</td><td>81.2</td><td>Vacuolar sorting protein 39</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G36630.1 | Symbols: EMB2754 | Vacuolar sorting protein 39 | chr4:17272088-17276524 REVERSE LENGTH=1000</td><td>565</td><td>1000</td><td>0</td><td>177.0</td><td>71.9</td><td>81.2</td></tr>
<tr><td>Rsa1.0_00007.1.g428.t1</td><td>gb|ADP95696.1| class III heme peroxidase [Brassica rapa]</td><td>323</td><td>296</td><td>1.00E-119</td><td>91.6</td><td>65.0</td><td>74.0</td><td>class III heme peroxidase</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G36430.1 | Symbols: | Peroxidase superfamily protein | chr4:17204648-17205917 REVERSE LENGTH=331</td><td>323</td><td>331</td><td>1.00E-116</td><td>102.5</td><td>63.2</td><td>74.3</td></tr>
<tr><td>Rsa1.0_00007.1.g429.t1</td><td>ref|XP_002886383.1| hypothetical protein ARALYDRAFT_474974 [Arabidopsis lyrata subsp. lyrata] gi|297332224|gb|EFH62642.1| hypothetical protein ARALYDRAFT_474974 [Arabidopsis lyrata subsp. lyrata]</td><td>1034</td><td>1049</td><td>0</td><td>101.5</td><td>87.3</td><td>92.6</td><td>hypothetical protein ARALYDRAFT_474974</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G63810.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nrap protein (InterPro:IPR005554); Has 396 Blast hits to 382 proteins in 182 species: Archae - 3; Bacteria - 2; Metazoa - 142; Fungi - 146; Plants - 43; Viruses - 0; Other Eukaryotes - 60 (source: NCBI BLink). | chr1:23669690-23675542 REVERSE LENGTH=1053</td><td>1034</td><td>1053</td><td>0</td><td>101.8</td><td>86.2</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00007.1.g430.t1</td><td>gb|EOA18974.1| hypothetical protein CARUB_v10007612mg [Capsella rubella]</td><td>216</td><td>212</td><td>4.00E-86</td><td>98.1</td><td>80.6</td><td>87.0</td><td>hypothetical protein CARUB_v10007612mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G36620.1 | Symbols: GATA19 | GATA transcription factor 19 | chr4:17268906-17269662 REVERSE LENGTH=211</td><td>216</td><td>211</td><td>1.00E-81</td><td>97.7</td><td>82.9</td><td>88.4</td></tr>
<tr><td>Rsa1.0_00007.1.g431.t1</td><td>gb|EOA32387.1| hypothetical protein CARUB_v10015657mg [Capsella rubella]</td><td>294</td><td>313</td><td>8.00E-99</td><td>106.5</td><td>59.5</td><td>79.9</td><td>hypothetical protein CARUB_v10015657mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G36610.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:17265545-17267274 REVERSE LENGTH=317</td><td>294</td><td>317</td><td>1.00E-100</td><td>107.8</td><td>60.2</td><td>79.3</td></tr>
<tr><td>Rsa1.0_00007.1.g432.t1</td><td>gb|EOA18452.1| hypothetical protein CARUB_v10006996mg [Capsella rubella]</td><td>456</td><td>465</td><td>1.00E-128</td><td>102.0</td><td>65.1</td><td>75.0</td><td>hypothetical protein CARUB_v10006996mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G36600.1 | Symbols: | Late embryogenesis abundant (LEA) protein | chr4:17263666-17264968 FORWARD LENGTH=353</td><td>456</td><td>353</td><td>2.00E-94</td><td>77.4</td><td>52.2</td><td>59.9</td></tr>
<tr><td>Rsa1.0_00007.1.g433.t1</td><td>gb|EOA15655.1| hypothetical protein CARUB_v10006084mg, partial [Capsella rubella]</td><td>79</td><td>105</td><td>3.00E-37</td><td>132.9</td><td>94.9</td><td>96.2</td><td>hypothetical protein CARUB_v10006084mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G75250.1 | Symbols: ATRL6, RSM3, RL6 | RAD-like 6 | chr1:28245073-28245453 REVERSE LENGTH=126</td><td>79</td><td>126</td><td>2.00E-27</td><td>159.5</td><td>62.0</td><td>82.3</td></tr>
<tr><td>Rsa1.0_00007.1.g434.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00007.1.g435.t1</td><td>ref|XP_002867008.1| U-box domain-containing protein 5 [Arabidopsis lyrata subsp. lyrata] gi|297312844|gb|EFH43267.1| U-box domain-containing protein 5 [Arabidopsis lyrata subsp. lyrata]</td><td>748</td><td>751</td><td>0</td><td>100.4</td><td>69.7</td><td>80.2</td><td>U-box domain-containing protein 5</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36550.1 | Symbols: | ARM repeat superfamily protein | chr4:17245400-17247926 REVERSE LENGTH=718</td><td>748</td><td>718</td><td>0</td><td>96.0</td><td>69.1</td><td>79.0</td></tr>
<tr><td>Rsa1.0_00007.1.g436.t4</td><td>gb|EOA17086.1| hypothetical protein CARUB_v10005334mg [Capsella rubella]</td><td>299</td><td>304</td><td>1.00E-138</td><td>101.7</td><td>82.3</td><td>89.6</td><td>hypothetical protein CARUB_v10005334mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G36540.1 | Symbols: BEE2 | BR enhanced expression 2 | chr4:17243699-17244965 FORWARD LENGTH=304</td><td>299</td><td>304</td><td>1.00E-139</td><td>101.7</td><td>81.6</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00007.1.g437.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00007.1.g438.t1</td><td>ref|NP_195368.1| uncharacterized protein [Arabidopsis thaliana] gi|2464932|emb|CAB16811.1| putative protein [Arabidopsis thaliana] gi|7270598|emb|CAB80316.1| putative protein [Arabidopsis thaliana] gi|28393196|gb|AAO42028.1| unknown protein [Arabidopsis thaliana] gi|28827518|gb|AAO50603.1| unknown protein [Arabidopsis thaliana] gi|332661263|gb|AEE86663.1| uncharacterized protein AT4G36500 [Arabidopsis thaliana]</td><td>428</td><td>122</td><td>7.00E-56</td><td>28.5</td><td>27.3</td><td>27.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G36500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G18210.1); Has 50 Blast hits to 50 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17226139-17226507 REVERSE LENGTH=122</td><td>428</td><td>122</td><td>2.00E-58</td><td>28.5</td><td>27.3</td><td>27.6</td></tr>
<tr><td>Rsa1.0_00007.1.g439.t1</td><td>ref|NP_195365.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|4006915|emb|CAB16845.1| hypothetical protein [Arabidopsis thaliana] gi|7270595|emb|CAB80313.1| hypothetical protein [Arabidopsis thaliana] gi|48427662|gb|AAT42380.1| At4g36470 [Arabidopsis thaliana] gi|110741629|dbj|BAE98762.1| hypothetical protein [Arabidopsis thaliana] gi|332661259|gb|AEE86659.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]</td><td>400</td><td>371</td><td>1.00E-167</td><td>92.8</td><td>72.0</td><td>79.8</td><td>S-adenosyl-L-methionine-dependent methyltransferase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G36470.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:17215128-17216475 REVERSE LENGTH=371</td><td>400</td><td>371</td><td>1.00E-170</td><td>92.8</td><td>72.0</td><td>79.8</td></tr>
</table>

Rsa1.0_00007.1.g440.t1	ref|NP_176033.1| purple acid phosphatase 6 [Arabidopsis thaliana] gi|75268138|sp|Q9C510.1|PPA6_ARATH RecName: Full=Purple acid phosphatase 6; Flags: Precursor gi|12321764|gb|AAG50924.1|AC069159_25 purple acid phosphatase, putative [Arabidopsis thaliana] gi|12323034|gb|AAG51511.1|AC058785_14 purple acid phosphatase, putative [Arabidopsis thaliana] gi|91805975|gb|ABE65716.1| calcineurin-like phosphoesterase family protein [Arabidopsis thaliana] gi|111074186|gb|ABH04466.1| At1g56360 [Arabidopsis thaliana] gi|332195262|gb|AEE33383.1| purple acid phosphatase 6 [Arabidopsis thaliana]	463	466	0	100.6	82.9	90.3	purple acid phosphatase 6	gbpln	Arabidopsis thaliana	AT1G56360.1 | Symbols: PAP6, ATPAP6 | purple acid phosphatase 6 | chr1:21098603-21100842 REVERSE LENGTH=466	463	466	0	100.6	82.9	90.3
Rsa1.0_00007.1.g441.t1	ref|XP_002869039.1| ALDH3F1 [Arabidopsis lyrata subsp. lyrata] gi|297314875|gb|EFH45298.1| ALDH3F1 [Arabidopsis lyrata subsp. lyrata]	488	484	0	99.2	86.5	94.7	ALDH3F1	gbpln	Arabidopsis lyrata	AT4G36250.1 | Symbols: ALDH3F1 | aldehyde dehydrogenase 3F1 | chr4:17151029-17153381 FORWARD LENGTH=484	488	484	0	99.2	85.9	94.3
Rsa1.0_00007.1.g442.t1	gb|ACP30631.1| disease resistance protein [Brassica rapa subsp. pekinensis]	2009	1241	0	61.8	38.6	45.6	disease resistance protein	gbpln	Brassica rapa	AT4G36150.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:17104776-17108711 FORWARD LENGTH=1179	2009	1179	0	58.7	38.9	45.2
Rsa1.0_00007.1.g443.t1	gb|ABD65084.1| hypothetical protein 27.t00096 [Brassica oleracea]	158	645	5.00E-28	408.2	38.6	45.6	hypothetical protein 27.t00096	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00007.1.g444.t2	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	1053	521	3.00E-49	49.5	14.4	22.7	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	1053	336	1.00E-14	31.9	5.0	7.8
Rsa1.0_00007.1.g445.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00007.1.g446.t1	gb|EOA15885.1| hypothetical protein CARUB_v10003971mg [Capsella rubella]	1622	1947	0	120.0	53.1	62.0	hypothetical protein CARUB_v10003971mg	gbpln	Capsella rubella	AT4G36140.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr4:17098956-17104479 REVERSE LENGTH=1607	1622	1607	0	99.1	47.4	54.8
Rsa1.0_00007.1.g447.t1	gb|ACP30632.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1027	1238	0	120.5	58.9	65.5	disease resistance protein	gbpln	Brassica rapa	AT4G36140.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr4:17098956-17104479 REVERSE LENGTH=1607	1027	1607	0	156.5	54.6	63.1
Rsa1.0_00007.1.g448.t1	gb|ACP30631.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1268	1241	0	97.9	64.9	74.1	disease resistance protein	gbpln	Brassica rapa	AT4G36150.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:17104776-17108711 FORWARD LENGTH=1179	1268	1179	0	93.0	61.0	71.4
Rsa1.0_00007.1.g449.t1	gb|EOA15885.1| hypothetical protein CARUB_v10003971mg [Capsella rubella]	598	1947	1.00E-148	325.6	51.8	65.9	hypothetical protein CARUB_v10003971mg	gbpln	Capsella rubella	AT3G44670.2 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr3:16217242-16221425 FORWARD LENGTH=1219	598	1219	1.00E-127	203.8	39.5	51.3
Rsa1.0_00007.1.g450.t1	gb|EOA15884.1| hypothetical protein CARUB_v10003971mg [Capsella rubella]	1377	1946	0	141.3	33.0	39.0	hypothetical protein CARUB_v10003971mg	gbpln	Capsella rubella	AT4G36140.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr4:17098956-17104479 REVERSE LENGTH=1607	1377	1607	0	116.7	33.0	39.1
Rsa1.0_00007.1.g451.t1	ref|XP_002869043.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata] gi|297314879|gb|EFH45302.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata]	258	258	1.00E-145	100.0	98.1	99.6	60S ribosomal protein L8	gbpln	Arabidopsis lyrata	AT4G36130.1 | Symbols: | Ribosomal protein L2 family | chr4:17097613-17098656 FORWARD LENGTH=258	258	258	1.00E-147	100.0	97.3	99.6
Rsa1.0_00007.1.g452.t1	gb|AAM65223.1| unknown [Arabidopsis thaliana]	349	342	1.00E-133	98.0	80.2	85.1	unknown	gbpln	Arabidopsis thaliana	AT4G24060.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr4:12503970-12505417 FORWARD LENGTH=342	349	342	1.00E-131	98.0	80.2	85.7
Rsa1.0_00007.1.g453.t2	ref|XP_002869754.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 2 [Arabidopsis lyrata subsp. lyrata] gi|297315590|gb|EFH46013.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 2 [Arabidopsis lyrata subsp. lyrata]	230	350	7.00E-57	152.2	56.1	63.5	UDP-D-glucose/UDP-D-galactose 4-epimerase 2	gbpln	Arabidopsis lyrata	AT4G23920.1 | Symbols: UGE2, ATUGE2 | UDP-D-glucose/UDP-D-galactose 4-epimerase 2 | chr4:12431416-12433666 FORWARD LENGTH=350	230	350	2.00E-59	152.2	55.7	63.9

Rsa1.0_00007.1.g454.t1	ref|XP_002867686.1| hypothetical protein ARALYDRAFT_492479 [Arabidopsis lyrata subsp. lyrata] gi|297313522|gb|EFH43945.1| hypothetical protein ARALYDRAFT_492479 [Arabidopsis lyrata subsp. lyrata]	194	196	6.00E-72	101.0	75.8	83.0	hypothetical protein ARALYDRAFT_492479	gbpln	Arabidopsis lyrata	AT4G23880.1 | Symbols: | unknown protein; Has 73 Blast hits to 69 proteins in 22 species: Archae - 0; Bacteria - 4; Metazoa - 9; Fungi - 2; Plants - 18; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink). | chr4:12415789-12416388 REVERSE LENGTH=199	194	199	2.00E-70	102.6	75.3	83.0
Rsa1.0_00007.1.g455.t1	#	#	#	#	#	#	#	-	----	----	AT4G23770.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G23780.1); Has 17 Blast hits to 17 proteins in 6 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:12383514-12384050 REVERSE LENGTH=138	132	138	2.00E-12	104.5	37.1	53.0
Rsa1.0_00007.1.g456.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00007.1.g457.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00008.1.g458.t1	gb|EOA30677.1| hypothetical protein CARUB_v10013815mg [Capsella rubella]	203	415	7.00E-78	204.4	73.9	83.7	hypothetical protein CARUB_v10013815mg	gbpln	Capsella rubella	AT3G02340.1 | Symbols: | RING/U-box superfamily protein | chr3:477032-478261 FORWARD LENGTH=409	203	409	1.00E-67	201.5	67.5	78.8
Rsa1.0_00008.1.g459.t1	gb|EOA30007.1| hypothetical protein CARUB_v10013111mg [Capsella rubella]	226	690	2.00E-16	305.3	21.7	23.5	hypothetical protein CARUB_v10013111mg	gbpln	Capsella rubella	AT3G18480.1 | Symbols: AtCASP, CASP | CCAAT-displacement protein alternatively spliced product | chr3:6336924-6341596 FORWARD LENGTH=689	226	689	1.00E-18	304.9	21.7	23.5
Rsa1.0_00008.1.g460.t1	ref|XP_002882224.1| hypothetical protein ARALYDRAFT_477468 [Arabidopsis lyrata subsp. lyrata] gi|297328064|gb|EFH58483.1| hypothetical protein ARALYDRAFT_477468 [Arabidopsis lyrata subsp. lyrata]	544	561	0	103.1	91.4	94.7	hypothetical protein ARALYDRAFT_477468	gbpln	Arabidopsis lyrata	AT3G02350.1 | Symbols: GAUT9 | galacturonosyltransferase 9 | chr3:479248-481178 FORWARD LENGTH=561	544	561	0	103.1	90.8	94.5
Rsa1.0_00008.1.g461.t1	ref|NP_187562.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|6682231|gb|AAF23283.1|AC016661_8 putative non-LTR reverse transcriptase [Arabidopsis thaliana] gi|332641254|gb|AEE74775.1| RNase H domain-containing protein [Arabidopsis thaliana]	343	484	4.00E-62	141.1	35.6	50.1	RNase H domain-containing protein	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	343	484	1.00E-64	141.1	35.6	50.1
Rsa1.0_00008.1.g462.t1	ref|XP_002863143.1| hypothetical protein ARALYDRAFT_332990 [Arabidopsis lyrata subsp. lyrata] gi|297308977|gb|EFH39402.1| hypothetical protein ARALYDRAFT_332990 [Arabidopsis lyrata subsp. lyrata]	416	428	0	102.9	78.8	89.4	hypothetical protein ARALYDRAFT_332990	gbpln	Arabidopsis lyrata	AT4G13330.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:7754248-7755837 REVERSE LENGTH=428	416	428	0	102.9	77.9	89.4
Rsa1.0_00008.1.g463.t1	gb|EOA32415.1| hypothetical protein CARUB_v10015687mg [Capsella rubella]	437	644	1.00E-100	147.4	53.8	67.0	hypothetical protein CARUB_v10015687mg	gbpln	Capsella rubella	AT4G14490.1 | Symbols: | SMAD/FHA domain-containing protein | chr4:8332414-8333574 REVERSE LENGTH=386	437	386	5.00E-67	88.3	41.4	56.3
Rsa1.0_00008.1.g464.t3	ref|XP_002884318.1| hypothetical protein ARALYDRAFT_896208 [Arabidopsis lyrata subsp. lyrata] gi|297330158|gb|EFH60577.1| hypothetical protein ARALYDRAFT_896208 [Arabidopsis lyrata subsp. lyrata]	496	344	1.00E-141	69.4	52.4	55.8	hypothetical protein ARALYDRAFT_896208	gbpln	Arabidopsis lyrata	AT3G02420.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0121 (InterPro:IPR005344); Has 72 Blast hits to 71 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 2; Plants - 60; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr3:496179-498772 REVERSE LENGTH=348	496	348	1.00E-141	70.2	52.6	56.0
Rsa1.0_00008.1.g465.t1	ref|NP_186892.1| uncharacterized protein [Arabidopsis thaliana] gi|6957706|gb|AAF32450.1| hypothetical protein [Arabidopsis thaliana] gi|49660133|gb|AAT68357.1| hypothetical protein At3g02430 [Arabidopsis thaliana] gi|50058917|gb|AAT69203.1| hypothetical protein At3g02430 [Arabidopsis thaliana] gi|332640286|gb|AEE73807.1| uncharacterized protein AT3G02430 [Arabidopsis thaliana]	194	219	3.00E-92	112.9	85.6	91.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G02430.1 | Symbols: | Protein of unknown function (DUF679) | chr3:499360-500019 FORWARD LENGTH=219	194	219	1.00E-94	112.9	85.6	91.2

Rsa1.0_00008.1.g466.t1	gb|EOA33068.1| hypothetical protein CARUB_v10016401mg [Capsella rubella]	612	452	0	73.9	58.2	64.1	hypothetical protein CARUB_v10016401mg	gbpln	Capsella rubella	AT3G02440.1 | Symbols: TBL20 | TRICHOME BIREFRINGENCE-LIKE 20 | chr3:500804-502229 REVERSE LENGTH=373	612	373	1.00E-150	60.9	46.1	51.5
Rsa1.0_00008.1.g467.t1	gb|AAS45435.1| S-adenosylmethionine decarboxylase [Brassica juncea]	365	366	0	100.3	97.0	98.1	S-adenosylmethionine decarboxylase	gbpln	Brassica juncea	AT3G02470.4 | Symbols: | S-adenosylmethionine decarboxylase | chr3:510223-511323 FORWARD LENGTH=366	365	366	0	100.3	94.8	97.5
Rsa1.0_00008.1.g468.t1	gb|ABD96872.1| hypothetical protein [Cleome spinosa]	68	69	1.00E-18	101.5	72.1	83.8	hypothetical protein	gbpln	Cleome spinosa	AT3G02480.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr3:512384-512857 FORWARD LENGTH=68	68	68	7.00E-19	100.0	80.9	91.2
Rsa1.0_00008.1.g469.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00008.1.g470.t1	gb|ABD96872.1| hypothetical protein [Cleome spinosa]	68	69	2.00E-18	101.5	70.6	85.3	hypothetical protein	gbpln	Cleome spinosa	AT3G02480.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr3:512384-512857 FORWARD LENGTH=68	68	68	8.00E-20	100.0	83.8	92.6
Rsa1.0_00008.1.g471.t1	ref|NP_186900.3| regulator of chromosome condensation domain-containing protein [Arabidopsis thaliana] gi|110735845|dbj|BAE99899.1| hypothetical protein [Arabidopsis thaliana] gi|332640299|gb|AEE73820.1| regulator of chromosome condensation domain-containing protein [Arabidopsis thaliana]	392	393	0	100.3	93.6	96.7	regulator of chromosome condensation domain-containing protein	gbpln	Arabidopsis thaliana	AT3G02510.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:522086-524536 REVERSE LENGTH=393	392	393	0	100.3	93.6	96.7
Rsa1.0_00008.1.g472.t2	gb|AAP37970.1| seed specific protein Bn15D17A [Brassica napus]	343	264	1.00E-119	77.0	69.1	70.3	seed specific protein Bn15D17A	gbpln	Brassica napus	AT3G02550.1 | Symbols: LBD41 | LOB domain-containing protein 41 | chr3:536747-537650 REVERSE LENGTH=263	343	263	1.00E-117	76.7	62.1	66.5
Rsa1.0_00008.1.g473.t1	gb|EOA31548.1| hypothetical protein CARUB_v10014739mg [Capsella rubella]	172	185	1.00E-52	107.6	69.8	77.9	hypothetical protein CARUB_v10014739mg	gbpln	Capsella rubella	AT3G02555.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G16110.1); Has 130 Blast hits to 130 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 130; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:540024-540955 REVERSE LENGTH=162	172	162	6.00E-47	94.2	66.9	74.4
Rsa1.0_00008.1.g474.t1	sp|Q9XH45.1|RS7_BRAOL RecName: Full=40S ribosomal protein S7 gi|5532505|gb|AAD44761.1|AF144752_1 40S ribosomal protein S7 homolog [Brassica oleracea]	191	191	1.00E-104	100.0	97.9	98.4	RecName: Full=40S ribosomal protein S7 gi|5532505|gb|AAD44761.1|AF144752_1 40S ribosomal protein S7 homolog	gbpln	Brassica oleracea	AT3G02560.2 | Symbols: | Ribosomal protein S7e family protein | chr3:542341-543168 FORWARD LENGTH=191	191	191	2.00E-98	100.0	90.1	94.8
Rsa1.0_00008.1.g475.t1	gb|EOA29607.1| hypothetical protein CARUB_v10013753mg [Capsella rubella]	430	432	0	100.5	90.7	95.6	hypothetical protein CARUB_v10013753mg	gbpln	Capsella rubella	AT3G02570.1 | Symbols: MEE31, PMI1 | Mannose-6-phosphate isomerase, type I | chr3:543463-545478 REVERSE LENGTH=432	430	432	0	100.5	89.1	95.1
Rsa1.0_00008.1.g476.t1	gb|AAF32472.1| hypothetical protein [Arabidopsis thaliana]	530	1077	0	203.2	77.5	84.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G02645.1 | Symbols: | Plant protein of unknown function (DUF247) | chr3:566271-567860 FORWARD LENGTH=529	530	529	0	99.8	81.3	88.7
Rsa1.0_00008.1.g477.t1	gb|EOA31892.1| hypothetical protein CARUB_v10015120mg, partial [Capsella rubella]	569	582	0	102.3	78.4	86.5	hypothetical protein CARUB_v10015120mg, partial	gbpln	Capsella rubella	AT3G02650.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:568135-569865 FORWARD LENGTH=576	569	576	0	101.2	78.2	86.8
Rsa1.0_00008.1.g478.t1	ref|XP_002884331.1| tRNA synthetase class I family protein [Arabidopsis lyrata subsp. lyrata] gi|297330171|gb|EFH60590.1| tRNA synthetase class I family protein [Arabidopsis lyrata subsp. lyrata]	509	511	0	100.4	89.8	95.3	tRNA synthetase class I family protein	gbpln	Arabidopsis lyrata	AT3G02660.1 | Symbols: emb2768 | Tyrosyl-tRNA synthetase, class Ib, bacterial/mitochondrial | chr3:570221-571756 REVERSE LENGTH=511	509	511	0	100.4	88.2	94.1
Rsa1.0_00008.1.g479.t1	ref|XP_002882247.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|297328087|gb|EFH58506.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata]	419	424	0	101.2	86.4	92.8	integral membrane family protein	gbpln	Arabidopsis lyrata	AT3G02690.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:579627-581448 FORWARD LENGTH=417	419	417	0	99.5	86.6	93.1
Rsa1.0_00008.1.g480.t1	gb|EOA31304.1| hypothetical protein CARUB_v10014477mg [Capsella rubella]	252	249	1.00E-125	98.8	89.3	94.8	hypothetical protein CARUB_v10014477mg	gbpln	Capsella rubella	AT3G02700.1 | Symbols: | NC domain-containing protein-related | chr3:581727-582813 REVERSE LENGTH=252	252	252	1.00E-127	100.0	87.7	94.8
Rsa1.0_00008.1.g481.t1	gb|EOA30303.1| hypothetical protein CARUB_v10013428mg [Capsella rubella]	504	534	0	106.0	91.5	96.8	hypothetical protein CARUB_v10013428mg	gbpln	Capsella rubella	AT3G02710.1 | Symbols: | ARM repeat superfamily protein | chr3:583184-585780 FORWARD LENGTH=529	504	529	0	105.0	91.9	96.2
Rsa1.0_00008.1.g482.t1	sp|O48897.1|TRXF_BRANA RecName: Full=Thioredoxin F-type, chloroplastic; Short=Trx-F; Flags: Precursor gi|2921094|gb|AAC04671.1| thioredoxin-f [Brassica napus]	182	182	2.00E-93	100.0	95.1	96.7	RecName: Full=Thioredoxin F-type, chloroplastic; Short=Trx-F; Flags: Precursor gi|2921094|gb|AAC04671.1| thioredoxin-f	gbpln	Brassica napus	AT3G02730.1 | Symbols: TRXF1, ATF1 | thioredoxin F-type 1 | chr3:588570-589591 REVERSE LENGTH=178	182	178	2.00E-91	97.8	89.0	94.5

Rsa1.0_00008.1.g483.t1	ref|NP_186923.1| aspartyl protease-like protein [Arabidopsis thaliana] gi|6728988|gb|AAF26986.1|AC018363_31 putative aspartyl protease [Arabidopsis thaliana] gi|21593593|gb|AAM65560.1| putative aspartyl protease [Arabidopsis thaliana] gi|332640332|gb|AEE73853.1| aspartyl protease-like protein [Arabidopsis thaliana]	377	488	1.00E-130	129.4	73.5	82.0	aspartyl protease-like protein	gbpln	Arabidopsis thaliana	AT3G02740.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:590561-593089 FORWARD LENGTH=488	377	488	1.00E-132	129.4	73.5	82.0
Rsa1.0_00008.1.g484.t1	ref|XP_002884336.1| phosphatase 2C family protein [Arabidopsis lyrata subsp. lyrata] gi|297330176|gb|EFH60595.1| phosphatase 2C family protein [Arabidopsis lyrata subsp. lyrata]	476	490	0	102.9	87.4	94.5	phosphatase 2C family protein	gbpln	Arabidopsis lyrata	AT3G02750.2 | Symbols: | Protein phosphatase 2C family protein | chr3:593601-595457 REVERSE LENGTH=492	476	492	0	103.4	85.7	93.7
Rsa1.0_00008.1.g485.t1	gb|EOA29853.1| hypothetical protein CARUB_v10012946mg [Capsella rubella]	859	886	0	103.1	77.9	86.7	hypothetical protein CARUB_v10012946mg	gbpln	Capsella rubella	AT3G02760.1 | Symbols: | Class II aaRS and biotin synthetases superfamily protein | chr3:597588-600650 REVERSE LENGTH=883	859	883	0	102.8	77.3	86.3
Rsa1.0_00008.1.g486.t1	ref|XP_002884338.1| dimethylmenaquinone methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330178|gb|EFH60597.1| dimethylmenaquinone methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	166	166	7.00E-88	100.0	97.0	98.8	dimethylmenaquinone methyltransferase family protein	gbpln	Arabidopsis lyrata	AT3G02770.1 | Symbols: | Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase | chr3:601017-601884 REVERSE LENGTH=166	166	166	2.00E-89	100.0	95.8	98.2
Rsa1.0_00008.1.g487.t1	gb|AAF36996.1|AF236092_1 isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase [Brassica oleracea var. botrytis]	261	281	1.00E-133	107.7	90.8	95.8	isopentenyl pyrophosphate:dimethyl allyl pyrophosphate isomerase	gbpln	Brassica oleracea	AT3G02780.1 | Symbols: IPP2, IPIAT1, IDI2 | isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase 2 | chr3:602578-604648 REVERSE LENGTH=284	261	284	1.00E-128	108.8	87.0	92.3
Rsa1.0_00008.1.g488.t1	gb|AAF26980.1|AC018363_25 unknown protein [Arabidopsis thaliana] gi|34365627|gb|AAQ65125.1| At3g02800 [Arabidopsis thaliana]	204	199	2.00E-99	97.5	83.8	88.2	unknown protein	gbpln	Arabidopsis thaliana	AT3G02800.1 | Symbols: | Tyrosine phosphatase family protein | chr3:606638-607704 REVERSE LENGTH=203	204	203	1.00E-102	99.5	83.8	88.2
Rsa1.0_00008.1.g489.t1	ref|NP_180565.1| mitogen-activated protein kinase kinase kinase 14 [Arabidopsis thaliana] gi|3420047|gb|AAC31848.1| putative protein kinase [Arabidopsis thaliana] gi|24030256|gb|AAN41303.1| putative protein kinase [Arabidopsis thaliana] gi|330253244|gb|AEC08338.1| mitogen-activated protein kinase kinase kinase 14 [Arabidopsis thaliana]	422	463	1.00E-155	109.7	70.6	79.4	mitogen-activated protein kinase kinase kinase 14	gbpln	Arabidopsis thaliana	AT2G30040.1 | Symbols: MAPKKK14 | mitogen-activated protein kinase kinase kinase 14 | chr2:12821747-12823138 FORWARD LENGTH=463	422	463	1.00E-157	109.7	70.6	79.4
Rsa1.0_00008.1.g490.t1	dbj|BAJ34022.1| unnamed protein product [Thellungiella halophila]	370	395	1.00E-164	106.8	84.1	89.5	unnamed protein product	----	----	AT2G30020.1 | Symbols: | Protein phosphatase 2C family protein | chr2:12814437-12815904 FORWARD LENGTH=396	370	396	1.00E-162	107.0	81.4	87.6
Rsa1.0_00008.1.g491.t1	gb|EMT31378.1| Zinc finger CCCH domain-containing protein 30 [Aegilops tauschii]	110	671	2.00E-59	610.0	91.8	93.6	Zinc finger CCCH domain-containing protein 30	gbpln	Aegilops tauschii	AT2G30000.1 | Symbols: | PHF5-like protein | chr2:12804042-12804374 REVERSE LENGTH=110	110	110	6.00E-59	100.0	98.2	99.1
Rsa1.0_00008.1.g492.t1	ref|NP_180560.1| NADH dehydrogenase [Arabidopsis thaliana] gi|75318710|sp|O80874.1|NDA2_ARATH RecName: Full=Alternative NAD(P)H dehydrogenase 2, mitochondrial; Flags: Precursor gi|3420052|gb|AAC31853.1| putative NADH dehydrogenase (ubiquinone oxidoreductase) [Arabidopsis thaliana] gi|330253238|gb|AEC08332.1| alternative NAD(P)H dehydrogenase 2 [Arabidopsis thaliana]	504	508	0	100.8	91.1	94.2	NADH dehydrogenase	gbpln	Arabidopsis thaliana	AT2G29990.1 | Symbols: NDA2 | alternative NAD(P)H dehydrogenase 2 | chr2:12793562-12795913 REVERSE LENGTH=508	504	508	0	100.8	91.1	94.2
Rsa1.0_00008.1.g493.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00008.1.g494.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00008.1.g495.t1	ref|NP_001190256.1| syntaxin-132 [Arabidopsis thaliana] gi|332003861|gb|AED91244.1| syntaxin-132 [Arabidopsis thaliana]	270	315	5.00E-35	116.7	35.9	38.9	syntaxin-132	gbpln	Arabidopsis thaliana	AT5G08080.3 | Symbols: SYP132 | syntaxin of plants 132 | chr5:2588532-2591106 FORWARD LENGTH=315	270	315	1.00E-37	116.7	35.9	38.9
Rsa1.0_00008.1.g496.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2561	1274	0	49.7	24.2	32.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT3G02990.1 | Symbols: ATHSFA1E, HSFA1E | heat shock transcription factor A1E | chr3:673614-675988 FORWARD LENGTH=468	2561	468	0	18.3	14.7	15.9
Rsa1.0_00008.1.g497.t1	ref|XP_002874698.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320535|gb|EFH50957.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	295	372	7.00E-49	126.1	42.0	58.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G11580.1 | Symbols: | RNI-like superfamily protein | chr4:7006648-7007738 REVERSE LENGTH=333	295	333	2.00E-45	112.9	40.0	55.3

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<tr><td>Rsa1.0_00008.1.g498.t1</td><td>gb|EOA31596.1| hypothetical protein CARUB_v10014793mg [Capsella rubella]</td><td>170</td><td>165</td><td>5.00E-78</td><td>97.1</td><td>88.8</td><td>94.7</td><td>hypothetical protein CARUB_v10014793mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G03000.1 | Symbols: | EF hand calcium-binding protein family | chr3:677388-677885 FORWARD LENGTH=165</td><td>170</td><td>165</td><td>3.00E-79</td><td>97.1</td><td>88.2</td><td>93.5</td></tr>
<tr><td>Rsa1.0_00008.1.g499.t1</td><td>gb|EOA32660.1| hypothetical protein CARUB_v10015958mg [Capsella rubella]</td><td>175</td><td>180</td><td>2.00E-74</td><td>102.9</td><td>85.7</td><td>90.9</td><td>hypothetical protein CARUB_v10015958mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G03010.2 | Symbols: | Peptidyl-tRNA hydrolase II (PTH2) family protein | chr3:678982-680137 REVERSE LENGTH=179</td><td>175</td><td>179</td><td>5.00E-75</td><td>102.3</td><td>82.3</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00008.1.g500.t1</td><td>ref|NP_186953.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75264861|sp|Q9M8U4.1|FBL41_ARATH RecName: Full=F-box/LRR-repeat protein At3g03030 gi|6728959|gb|AAF26957.1|AC018363_2 unknown protein [Arabidopsis thaliana] gi|30102686|gb|AAP21261.1| At3g03030 [Arabidopsis thaliana] gi|110735742|dbj|BAE99850.1| hypothetical protein [Arabidopsis thaliana] gi|332640373|gb|AEE73894.1| F-box/LRR-repeat protein [Arabidopsis thaliana]</td><td>457</td><td>474</td><td>1.00E-160</td><td>103.7</td><td>63.9</td><td>77.0</td><td>F-box/LRR-repeat protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G03030.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:682252-683850 FORWARD LENGTH=474</td><td>457</td><td>474</td><td>1.00E-163</td><td>103.7</td><td>63.9</td><td>77.0</td></tr>
<tr><td>Rsa1.0_00008.1.g501.t1</td><td>gb|EOA30484.1| hypothetical protein CARUB_v10013608mg [Capsella rubella]</td><td>413</td><td>474</td><td>1.00E-130</td><td>114.8</td><td>60.5</td><td>75.5</td><td>hypothetical protein CARUB_v10013608mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G03030.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:682252-683850 FORWARD LENGTH=474</td><td>413</td><td>474</td><td>1.00E-131</td><td>114.8</td><td>60.0</td><td>75.1</td></tr>
<tr><td>Rsa1.0_00008.1.g502.t1</td><td>gb|EOA29758.1| hypothetical protein CARUB_v10012847mg [Capsella rubella]</td><td>1160</td><td>1147</td><td>0</td><td>98.9</td><td>95.0</td><td>97.0</td><td>hypothetical protein CARUB_v10012847mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G03050.1 | Symbols: CSLD3, KJK, ATCSLD3 | cellulose synthase-like D3 | chr3:687873-691629 FORWARD LENGTH=1145</td><td>1160</td><td>1145</td><td>0</td><td>98.7</td><td>94.1</td><td>96.5</td></tr>
<tr><td>Rsa1.0_00008.1.g503.t1</td><td>ref|XP_002882270.1| hypothetical protein ARALYDRAFT_340454 [Arabidopsis lyrata subsp. lyrata] gi|297328110|gb|EFH58529.1| hypothetical protein ARALYDRAFT_340454 [Arabidopsis lyrata subsp. lyrata]</td><td>639</td><td>642</td><td>0</td><td>100.5</td><td>90.5</td><td>93.9</td><td>hypothetical protein ARALYDRAFT_340454</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G03060.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:692188-695424 FORWARD LENGTH=628</td><td>639</td><td>628</td><td>0</td><td>98.3</td><td>89.2</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00008.1.g504.t1</td><td>ref|XP_002884353.1| hypothetical protein ARALYDRAFT_896292 [Arabidopsis lyrata subsp. lyrata] gi|297330193|gb|EFH60612.1| hypothetical protein ARALYDRAFT_896292 [Arabidopsis lyrata subsp. lyrata]</td><td>111</td><td>110</td><td>1.00E-54</td><td>99.1</td><td>91.9</td><td>97.3</td><td>hypothetical protein ARALYDRAFT_896292</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G03070.1 | Symbols: | NADH-ubiquinone oxidoreductase-related | chr3:696593-698069 REVERSE LENGTH=110</td><td>111</td><td>110</td><td>2.00E-56</td><td>99.1</td><td>90.1</td><td>96.4</td></tr>
<tr><td>Rsa1.0_00008.1.g505.t17</td><td>ref|NP_566192.1| putative NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 [Arabidopsis thaliana] gi|12644540|sp|Q9M9M9.1|NDUAC_ARATH RecName: Full=Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 gi|6714426|gb|AAF26114.1|AC012328_17 unknown protein [Arabidopsis thaliana] gi|13878173|gb|AAK44164.1|AF370349_1 unknown protein [Arabidopsis thaliana] gi|17104529|gb|AAL34153.1| unknown protein [Arabidopsis thaliana] gi|21593289|gb|AAM65238.1| probable NADH-ubiquinone oxidoreductase subunit B17.2 (Complex I-B17.2) (CI-B17.2) [Arabidopsis thaliana] gi|332640380|gb|AEE73901.1| putative NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 [Arabidopsis thaliana]</td><td>159</td><td>159</td><td>8.00E-87</td><td>100.0</td><td>95.6</td><td>98.1</td><td>putative NADH dehydrogenase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G03100.1 | Symbols: | NADH:ubiquinone oxidoreductase, 17.2kDa subunit | chr3:705564-707578 REVERSE LENGTH=159</td><td>159</td><td>159</td><td>3.00E-89</td><td>100.0</td><td>95.6</td><td>98.1</td></tr>
<tr><td>Rsa1.0_00008.1.g506.t1</td><td>ref|XP_002882274.1| hypothetical protein ARALYDRAFT_896304 [Arabidopsis lyrata subsp. lyrata] gi|297328114|gb|EFH58533.1| hypothetical protein ARALYDRAFT_896304 [Arabidopsis lyrata subsp. lyrata]</td><td>1099</td><td>1076</td><td>0</td><td>97.9</td><td>85.5</td><td>91.3</td><td>hypothetical protein ARALYDRAFT_896304</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G03110.1 | Symbols: XPO1B, CRM1B | exportin 1B | chr3:708966-716879 FORWARD LENGTH=1076</td><td>1099</td><td>1076</td><td>0</td><td>97.9</td><td>85.4</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00008.1.g507.t1</td><td>dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]</td><td>174</td><td>329</td><td>3.00E-24</td><td>189.1</td><td>38.5</td><td>56.3</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G42965.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17236736-17237125 FORWARD LENGTH=129</td><td>174</td><td>129</td><td>5.00E-11</td><td>74.1</td><td>18.4</td><td>29.3</td></tr>
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Rsa1.0_00008.1.g508.t1	ref|XP_002884360.1| hypothetical protein ARALYDRAFT_477561 [Arabidopsis lyrata subsp. lyrata] gi|297330200|gb|EFH60619.1| hypothetical protein ARALYDRAFT_477561 [Arabidopsis lyrata subsp. lyrata]	517	521	1.00E-126	100.8	63.8	76.2	hypothetical protein ARALYDRAFT_477561	gbpln	Arabidopsis lyrata	AT3G03130.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G17160.1); Has 7130 Blast hits to 3690 proteins in 504 species: Archae - 22; Bacteria - 2666; Metazoa - 1654; Fungi - 721; Plants - 246; Viruses - 56; Other Eukaryotes - 1765 (source: NCBI BLink). | chr3:721439-723564 REVERSE LENGTH=520	517	520	1.00E-127	100.6	63.1	74.9
Rsa1.0_00008.1.g509.t1	gb|EOA32118.1| hypothetical protein CARUB_v10015369mg [Capsella rubella]	684	761	0	111.3	78.8	86.4	hypothetical protein CARUB_v10015369mg	gbpln	Capsella rubella	AT3G03140.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr3:724348-727093 FORWARD LENGTH=769	684	769	0	112.4	77.5	86.3
Rsa1.0_00008.1.g510.t1	ref|NP_566196.1| uncharacterized protein [Arabidopsis thaliana] gi|89001025|gb|ABD59102.1| At3g03170 [Arabidopsis thaliana] gi|332640388|gb|AEE73909.1| uncharacterized protein AT3G03170 [Arabidopsis thaliana]	154	156	2.00E-65	101.3	87.0	90.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G03170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24890.1); Has 184 Blast hits to 184 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 184; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:732066-732729 FORWARD LENGTH=156	154	156	7.00E-68	101.3	87.0	90.9
Rsa1.0_00008.1.g511.t1	ref|NP_186968.2| Got1/Sft2-like vescicle transport protein [Arabidopsis thaliana] gi|38603916|gb|AAR24703.1| At3g03180 [Arabidopsis thaliana] gi|44681404|gb|AAS47642.1| At3g03180 [Arabidopsis thaliana] gi|332640389|gb|AEE73910.1| Got1/Sft2-like vescicle transport protein [Arabidopsis thaliana]	140	140	5.00E-68	100.0	96.4	97.9	Got1/Sft2-like vescicle transport protein	gbpln	Arabidopsis thaliana	AT3G03180.1 | Symbols: | Got1/Sft2-like vescicle transport protein family | chr3:733531-734421 FORWARD LENGTH=140	140	140	1.00E-70	100.0	96.4	97.9
Rsa1.0_00008.1.g512.t1	ref|XP_002884362.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330202|gb|EFH60621.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	478	481	0	100.6	87.9	93.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G03200.1 | Symbols: anac045, NAC045 | NAC domain containing protein 45 | chr3:736141-738527 REVERSE LENGTH=479	478	479	0	100.2	88.1	93.1
Rsa1.0_00008.1.g513.t1	#	#	#	#	#	#	#	-	----	----	AT3G03210.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 59 Blast hits to 59 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:740987-742093 FORWARD LENGTH=368	77	368	2.00E-12	477.9	67.5	76.6
Rsa1.0_00008.1.g514.t1	ref|NP_566197.1| expansin A13 [Arabidopsis thaliana] gi|20138030|sp|Q9M9P0.2|EXP13_ARATH RecName: Full=Expansin-A13; Short=AtEXPA13; AltName: Full=Alpha-expansin-13; Short=At-EXP13; Short=AtEx13; AltName: Full=Ath-ExpAlpha-1.22; Flags: Precursor gi|16604575|gb|AAL24089.1| putative expansin precursor protein [Arabidopsis thaliana] gi|21281243|gb|AAM45038.1| putative expansin precursor protein [Arabidopsis thaliana] gi|332640393|gb|AEE73914.1| expansin A13 [Arabidopsis thaliana]	264	266	1.00E-131	100.8	89.0	93.6	expansin A13	gbpln	Arabidopsis thaliana	AT3G03220.1 | Symbols: ATEXPA13, EXP13, ATEXP13, ATHEXP ALPHA 1.22, EXPA13 | expansin A13 | chr3:742655-743975 REVERSE LENGTH=266	264	266	1.00E-134	100.8	89.0	93.6
Rsa1.0_00008.1.g515.t1	ref|XP_002884364.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330204|gb|EFH60623.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	583	332	1.00E-158	56.9	46.7	53.3	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G03230.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:744478-746009 REVERSE LENGTH=333	583	333	1.00E-161	57.1	46.3	53.5
Rsa1.0_00008.1.g516.t1	gb|EOA30501.1| hypothetical protein CARUB_v10013624mg [Capsella rubella]	485	469	0	96.7	91.3	93.2	hypothetical protein CARUB_v10013624mg	gbpln	Capsella rubella	AT3G03250.1 | Symbols: UGP, UGP1, AtUGP1 | UDP-GLUCOSE PYROPHOSPHORYLASE 1 | chr3:749761-754014 REVERSE LENGTH=469	485	469	0	96.7	90.7	92.6
Rsa1.0_00008.1.g517.t1	ref|NP_565646.2| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|106879155|gb|ABF82607.1| At2g27330 [Arabidopsis thaliana] gi|330252880|gb|AEC07974.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	181	116	1.00E-11	64.1	20.4	21.5	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT2G27330.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:11695350-11696563 REVERSE LENGTH=116	181	116	4.00E-14	64.1	20.4	21.5

Rsa1.0_00008.1.g518.t1	ref|NP_186976.2| homeobox-leucine zipper protein HDG8 [Arabidopsis thaliana] gi|187471152|sp|Q9M9P4.2|HDG8_ARATH RecName: Full=Homeobox-leucine zipper protein HDG8; AltName: Full=HD-ZIP protein HDG8; AltName: Full=Homeodomain GLABRA 2-like protein 8; AltName: Full=Homeodomain transcription factor HDG8; AltName: Full=Protein HOMEODOMAIN GLABROUS 8 gi|332640397|gb|AEE73918.1| homeobox-leucine zipper protein HDG8 [Arabidopsis thaliana]	657	699	0	106.4	64.2	76.0	homeobox-leucine zipper protein HDG8	gbpln	Arabidopsis thaliana	AT3G03260.1 | Symbols: HDG8 | homeodomain GLABROUS 8 | chr3:755356-759234 REVERSE LENGTH=699	657	699	0	106.4	64.2	76.0
Rsa1.0_00008.1.g519.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00008.1.g520.t1	ref|NP_001118559.1| uncharacterized protein [Arabidopsis thaliana] gi|297832980|ref|XP_002884372.1| hypothetical protein ARALYDRAFT_477584 [Arabidopsis lyrata subsp. lyrata] gi|98962219|gb|ABF59439.1| unknown protein [Arabidopsis thaliana] gi|297330212|gb|EFH60631.1| hypothetical protein ARALYDRAFT_477584 [Arabidopsis lyrata subsp. lyrata] gi|332640411|gb|AEE73932.1| uncharacterized protein AT3G03341 [Arabidopsis thaliana] gi|482567721|gb|EOA31910.1| hypothetical protein CARUB_v10015139mg [Capsella rubella]	72	72	5.00E-33	100.0	98.6	100.0	uncharacterized protein	gbpln	Arabidopsis lyrata	AT3G03341.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:790338-790556 REVERSE LENGTH=72	72	72	8.00E-36	100.0	98.6	100.0
Rsa1.0_00008.1.g521.t38	gb|EOA29773.1| hypothetical protein CARUB_v10012864mg [Capsella rubella]	1202	1097	0	91.3	83.0	86.1	hypothetical protein CARUB_v10012864mg	gbpln	Capsella rubella	AT3G03380.1 | Symbols: DegP7 | DegP protease 7 | chr3:799720-808319 FORWARD LENGTH=1097	1202	1097	0	91.3	82.7	85.8
Rsa1.0_00008.1.g522.t1	ref|XP_002884376.1| hypothetical protein ARALYDRAFT_896341 [Arabidopsis lyrata subsp. lyrata] gi|297330216|gb|EFH60635.1| hypothetical protein ARALYDRAFT_896341 [Arabidopsis lyrata subsp. lyrata]	131	148	8.00E-51	113.0	80.2	86.3	hypothetical protein ARALYDRAFT_896341	gbpln	Arabidopsis lyrata	AT3G03400.1 | Symbols: | EF hand calcium-binding protein family | chr3:808745-809158 REVERSE LENGTH=137	131	137	2.00E-46	104.6	69.5	79.4
Rsa1.0_00008.1.g523.t1	gb|EOA32409.1| hypothetical protein CARUB_v10015681mg [Capsella rubella]	131	131	4.00E-44	100.0	67.9	80.2	hypothetical protein CARUB_v10015681mg	gbpln	Capsella rubella	AT3G03410.1 | Symbols: | EF hand calcium-binding protein family | chr3:811324-811719 REVERSE LENGTH=131	131	131	7.00E-44	100.0	64.9	78.6
Rsa1.0_00008.1.g524.t1	gb|EOA31513.1| hypothetical protein CARUB_v10014702mg [Capsella rubella]	195	194	1.00E-107	99.5	94.9	97.4	hypothetical protein CARUB_v10014702mg	gbpln	Capsella rubella	AT3G03420.1 | Symbols: | Ku70-binding family protein | chr3:812527-813644 FORWARD LENGTH=194	195	194	1.00E-109	99.5	94.4	97.4
Rsa1.0_00008.1.g525.t1	pir||S65145 pollen allergen group Ⅱ (clone 44) - rape	83	83	8.00E-39	100.0	97.6	98.8	pollen allergen group Ⅱ (clone 44) - rape	----	----	AT3G03430.1 | Symbols: | Calcium-binding EF-hand family protein | chr3:814481-814732 FORWARD LENGTH=83	83	83	1.00E-38	100.0	90.4	95.2
Rsa1.0_00008.1.g526.t1	ref|NP_186994.2| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332640423|gb|AEE73944.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	404	408	1.00E-179	101.0	90.1	94.6	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G03440.1 | Symbols: | ARM repeat superfamily protein | chr3:815709-818568 FORWARD LENGTH=408	404	408	0	101.0	90.1	94.6
Rsa1.0_00008.1.g527.t1	gb|EOA20745.1| hypothetical protein CARUB_v10001071mg, partial [Capsella rubella]	340	414	2.00E-82	121.8	56.5	65.0	hypothetical protein CARUB_v10001071mg, partial	gbpln	Capsella rubella	AT3G03460.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G17510.1); Has 19732 Blast hits to 8747 proteins in 456 species: Archae - 0; Bacteria - 449; Metazoa - 7438; Fungi - 2099; Plants - 1550; Viruses - 53; Other Eukaryotes - 8143 (source: NCBI BLink). | chr3:823069-824485 REVERSE LENGTH=354	340	354	2.00E-83	104.1	56.2	65.9
Rsa1.0_00008.1.g528.t1	ref|NP_187000.1| TatD related DNase [Arabidopsis thaliana] gi|6017102|gb|AAF01585.1|AC009895_6 unknown protein [Arabidopsis thaliana] gi|332640430|gb|AEE73951.1| TatD related DNase [Arabidopsis thaliana]	257	272	1.00E-127	105.8	87.9	92.6	TatD related DNase	gbpln	Arabidopsis thaliana	AT3G03500.1 | Symbols: | TatD related DNase | chr3:832929-834350 FORWARD LENGTH=272	257	272	1.00E-130	105.8	87.9	92.6

Rsa1.0_00008.1.g529.t1	ref|XP_002884391.1| hypothetical protein ARALYDRAFT_317234 [Arabidopsis lyrata subsp. lyrata] gi|297330231|gb|EFH60650.1| hypothetical protein ARALYDRAFT_317234 [Arabidopsis lyrata subsp. lyrata]	539	538	0	99.8	88.5	94.8	hypothetical protein ARALYDRAFT_317234	gbpln	Arabidopsis lyrata	AT3G03530.1 | Symbols: NPC4 | non-specific phospholipase C4 | chr3:842686-844970 REVERSE LENGTH=538	539	538	0	99.8	87.8	93.9
Rsa1.0_00008.1.g530.t1	ref|XP_002881179.1| hypothetical protein ARALYDRAFT_902186 [Arabidopsis lyrata subsp. lyrata] gi|297327018|gb|EFH57438.1| hypothetical protein ARALYDRAFT_902186 [Arabidopsis lyrata subsp. lyrata]	167	561	9.00E-54	335.9	67.7	68.3	hypothetical protein ARALYDRAFT_902186	gbpln	Arabidopsis lyrata	AT2G31510.1 | Symbols: ARI7, ATARI7 | IBR domain-containing protein | chr2:13416991-13421170 REVERSE LENGTH=562	167	562	2.00E-55	336.5	67.1	67.7
Rsa1.0_00008.1.g531.t1	gb|EMJ11865.1| hypothetical protein PRUPE_ppa022462mg [Prunus persica]	206	606	3.00E-39	294.2	40.8	56.8	hypothetical protein PRUPE_ppa022462mg	gbpln	Prunus persica	#	#	#	#	#	#	#
Rsa1.0_00008.1.g532.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00008.1.g533.t1	ref|XP_002884394.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297330234|gb|EFH60653.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	350	355	1.00E-119	101.4	73.4	81.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G03550.1 | Symbols: | RING/U-box superfamily protein | chr3:850391-851461 REVERSE LENGTH=356	350	356	1.00E-110	101.7	69.7	77.7
Rsa1.0_00008.1.g534.t1	ref|XP_002882299.1| hypothetical protein ARALYDRAFT_477606 [Arabidopsis lyrata subsp. lyrata] gi|297328139|gb|EFH58558.1| hypothetical protein ARALYDRAFT_477606 [Arabidopsis lyrata subsp. lyrata]	322	322	1.00E-169	100.0	91.6	96.0	hypothetical protein ARALYDRAFT_477606	gbpln	Arabidopsis lyrata	AT3G03610.1 | Symbols: | ELMO/CED-12 family protein | chr3:869479-871687 FORWARD LENGTH=323	322	323	1.00E-171	100.3	91.3	95.7
Rsa1.0_00008.1.g535.t1	gb|EOA30404.1| hypothetical protein CARUB_v10013529mg [Capsella rubella]	529	496	0	93.8	77.7	85.1	hypothetical protein CARUB_v10013529mg	gbpln	Capsella rubella	AT3G03620.1 | Symbols: | MATE efflux family protein | chr3:873904-876252 REVERSE LENGTH=500	529	500	0	94.5	77.3	85.1
Rsa1.0_00008.1.g536.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00008.1.g537.t1	ref|XP_002884400.1| hypothetical protein ARALYDRAFT_896375 [Arabidopsis lyrata subsp. lyrata] gi|297330240|gb|EFH60659.1| hypothetical protein ARALYDRAFT_896375 [Arabidopsis lyrata subsp. lyrata]	394	405	1.00E-175	102.8	87.1	91.4	hypothetical protein ARALYDRAFT_896375	gbpln	Arabidopsis lyrata	AT3G03630.1 | Symbols: CS26 | cysteine synthase 26 | chr3:878388-880400 REVERSE LENGTH=404	394	404	1.00E-168	102.5	86.0	90.4
Rsa1.0_00008.1.g538.t1	dbj|BAJ33819.1| unnamed protein product [Thellungiella halophila]	667	528	0	79.2	69.1	73.3	unnamed protein product	----	----	AT3G03640.1 | Symbols: GLUC, BGLU25 | beta glucosidase 25 | chr3:881028-884028 FORWARD LENGTH=531	667	531	0	79.6	67.8	71.4
Rsa1.0_00008.1.g539.t1	ref|NP_001118563.1| WUSCHEL related homeobox 11 [Arabidopsis thaliana] gi|332640448|gb|AEE73969.1| WUSCHEL related homeobox 11 [Arabidopsis thaliana]	301	297	1.00E-121	98.7	84.1	90.7	WUSCHEL related homeobox 11	gbpln	Arabidopsis thaliana	AT3G03660.2 | Symbols: WOX11 | WUSCHEL related homeobox 11 | chr3:889515-892162 REVERSE LENGTH=297	301	297	1.00E-124	98.7	84.1	90.7
Rsa1.0_00008.1.g540.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1810	1213	0	67.0	35.9	46.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1810	626	5.00E-78	34.6	8.7	14.0
Rsa1.0_00009.1.g541.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00009.1.g542.t1	ref|NP_172114.2| uncharacterized protein [Arabidopsis thaliana] gi|24030288|gb|AAN41316.1| unknown protein [Arabidopsis thaliana] gi|332189846|gb|AEE27967.1| uncharacterized protein AT1G06240 [Arabidopsis thaliana]	388	383	0	98.7	84.0	90.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G06240.1 | Symbols: | Protein of unknown function DUF455 | chr1:1911166-1912875 FORWARD LENGTH=383	388	383	0	98.7	84.0	90.2
Rsa1.0_00009.1.g543.t1	gb|EOA39214.1| hypothetical protein CARUB_v10012192mg [Capsella rubella]	448	423	0	94.4	73.2	79.5	hypothetical protein CARUB_v10012192mg	gbpln	Capsella rubella	AT1G06250.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:1913339-1914850 REVERSE LENGTH=423	448	423	0	94.4	72.1	79.7
Rsa1.0_00009.1.g544.t1	ref|NP_563764.1| cysteine proteinase-like protein [Arabidopsis thaliana] gi|8844131|gb|AAF80223.1|AC025290_12 Contains similarity to a cysteine endopeptidase 1 from Phaseolus vulgaris gb|U52970 and is a member of the papain cysteine protease family PF|00112 [Arabidopsis thaliana] gi|332189848|gb|AEE27969.1| cysteine proteinase-like protein [Arabidopsis thaliana]	343	343	1.00E-171	100.0	82.5	89.8	cysteine proteinase-like protein	gbpln	Arabidopsis thaliana	AT1G06260.1 | Symbols: | Cysteine proteinases superfamily protein | chr1:1916449-1917585 FORWARD LENGTH=343	343	343	1.00E-174	100.0	82.5	89.8

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<tr><td>Rsa1.0_00009.1.g546.t1</td><td>ref|NP_172121.2| uncharacterized protein [Arabidopsis thaliana] gi|91805751|gb|ABE65604.1| hypothetical protein At1g06320 [Arabidopsis thaliana] gi|332189853|gb|AEE27974.1| uncharacterized protein AT1G06320 [Arabidopsis thaliana]</td><td>198</td><td>195</td><td>4.00E−12</td><td>98.5</td><td>18.2</td><td>23.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G06320.1 | Symbols: | unknown protein; Has 24 Blast hits to 24 proteins in 10 species: Archae − 0; Bacteria − 2; Metazoa − 0; Fungi − 0; Plants − 20; Viruses − 0; Other Eukaryotes − 2 (source: NCBI BLink). | chr1:1930602−1931449 FORWARD LENGTH=195</td><td>198</td><td>195</td><td>1.00E−14</td><td>98.5</td><td>18.2</td><td>23.7</td></tr>
<tr><td>Rsa1.0_00009.1.g547.t1</td><td>ref|XP_002892336.1| fatty acid desaturase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338178|gb|EFH68595.1| fatty acid desaturase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>301</td><td>299</td><td>1.00E−143</td><td>99.3</td><td>81.4</td><td>88.4</td><td>fatty acid desaturase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06350.1 | Symbols: | Fatty acid desaturase family protein | chr1:1935510−1936789 REVERSE LENGTH=300</td><td>301</td><td>300</td><td>1.00E−142</td><td>99.7</td><td>79.7</td><td>88.4</td></tr>
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<tr><td>Rsa1.0_00009.1.g549.t1</td><td>ref|XP_002892337.1| fatty acid desaturase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338179|gb|EFH68596.1| fatty acid desaturase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>299</td><td>299</td><td>1.00E−143</td><td>100.0</td><td>84.9</td><td>91.0</td><td>fatty acid desaturase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06360.1 | Symbols: | Fatty acid desaturase family protein | chr1:1939173−1940417 REVERSE LENGTH=299</td><td>299</td><td>299</td><td>1.00E−144</td><td>100.0</td><td>84.6</td><td>89.6</td></tr>
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<tr><td>Rsa1.0_00009.1.g551.t3</td><td>dbj|BAJ33891.1| unnamed protein product [Thellungiella halophila]</td><td>695</td><td>693</td><td>0</td><td>99.7</td><td>92.8</td><td>95.0</td><td>unnamed protein product</td><td>−−−−</td><td>−−−−</td><td>AT1G06430.1 | Symbols: FTSH8 | FTSH protease 8 | chr1:1960214−1962525 REVERSE LENGTH=685</td><td>695</td><td>685</td><td>0</td><td>98.6</td><td>89.8</td><td>92.7</td></tr>
<tr><td>Rsa1.0_00009.1.g552.t1</td><td>ref|XP_002889605.1| hypothetical protein ARALYDRAFT_887850 [Arabidopsis lyrata subsp. lyrata] gi|297335447|gb|EFH65864.1| hypothetical protein ARALYDRAFT_887850 [Arabidopsis lyrata subsp. lyrata]</td><td>425</td><td>414</td><td>0</td><td>97.4</td><td>88.2</td><td>91.3</td><td>hypothetical protein ARALYDRAFT_887850</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06470.2 | Symbols: | Nucleotide/sugar transporter family protein | chr1:1970726−1973540 FORWARD LENGTH=414</td><td>425</td><td>414</td><td>0</td><td>97.4</td><td>87.3</td><td>90.8</td></tr>
<tr><td>Rsa1.0_00009.1.g553.t1</td><td>gb|EOA37916.1| hypothetical protein CARUB_v10009384mg [Capsella rubella]</td><td>399</td><td>392</td><td>0</td><td>98.2</td><td>82.7</td><td>89.2</td><td>hypothetical protein CARUB_v10009384mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G06550.1 | Symbols: | ATP−dependent caseinolytic (Clp) protease/crotonase family protein | chr1:2003834−2006564 REVERSE LENGTH=387</td><td>399</td><td>387</td><td>0</td><td>97.0</td><td>83.0</td><td>88.7</td></tr>
<tr><td>Rsa1.0_00009.1.g554.t12</td><td>ref|XP_002889609.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335451|gb|EFH65868.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>678</td><td>599</td><td>0</td><td>88.3</td><td>77.0</td><td>81.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06560.1 | Symbols: | NOL1/NOP2/sun family protein | chr1:2007660−2011824 FORWARD LENGTH=599</td><td>678</td><td>599</td><td>0</td><td>88.3</td><td>76.4</td><td>81.0</td></tr>
<tr><td>Rsa1.0_00009.1.g555.t1</td><td>ref|XP_002892352.1| hypothetical protein ARALYDRAFT_887868 [Arabidopsis lyrata subsp. lyrata] gi|297338194|gb|EFH68611.1| hypothetical protein ARALYDRAFT_887868 [Arabidopsis lyrata subsp. lyrata]</td><td>487</td><td>486</td><td>0</td><td>99.8</td><td>80.5</td><td>87.1</td><td>hypothetical protein ARALYDRAFT_887868</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30820.2); Has 166 Blast hits to 144 proteins in 35 species: Archae − 0; Bacteria − 17; Metazoa − 13; Fungi − 20; Plants − 104; Viruses − 0; Other Eukaryotes − 12 (source: NCBI BLink). | chr1:2037461−2040148 REVERSE LENGTH=481</td><td>487</td><td>481</td><td>0</td><td>98.8</td><td>78.2</td><td>85.0</td></tr>
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Rsa1.0_00009.1.g556.t1	sp|P11594.2|PSBP_SINAL RecName: Full=Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; AltName: Full=23 kDa subunit of oxygen evolving system of photosystem II; AltName: Full=23 kDa thylakoid membrane protein; AltName: Full=OEC 23 kDa subunit; Flags: Precursor gi|21133|emb|CAA35081.1| oxygen-evolving complex of photosystem II [Sinapis alba]	262	260	1.00E-138	99.2	96.6	97.3	RecName: Full=Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; AltName: Full=23 kDa subunit of oxygen evolving system of photosystem II; AltName: Full=23 kDa thylakoid membrane protein; AltName: Full=OEC 23 kDa subunit; Flags: Precursor gi|21133|emb|CAA35081.1| oxygen-evolving complex of photosystem II	gbpln	Sinapis alba	AT1G06680.1 | Symbols: PSBP-1, OEE2, PSII-P, OE23 | photosystem II subunit P-1 | chr1:2047940-2049186 FORWARD LENGTH=263	262	263	1.00E-129	100.4	91.6	96.6
Rsa1.0_00009.1.g557.t1	ref|NP_563770.1| NAD(P)-linked oxidoreductase-like protein [Arabidopsis thaliana] gi|75249772|sp|Q94A68.1|Y1669_ARATH RecName: Full=Uncharacterized oxidoreductase At1g06690, chloroplastic; Flags: Precursor gi|15215594|gb|AAK91342.1| At1g06690/F4H5_17 [Arabidopsis thaliana] gi|24111265|gb|AAN46756.1| At1g06690/F4H5_17 [Arabidopsis thaliana] gi|332189903|gb|AEE28024.1| NAD(P)-linked oxidoreductase-like protein [Arabidopsis thaliana]	358	377	0	105.3	94.1	96.9	NAD(P)-linked oxidoreductase-like protein	gbpln	Arabidopsis thaliana	AT1G06690.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr1:2049742-2052039 REVERSE LENGTH=377	358	377	0	105.3	94.1	96.9
Rsa1.0_00009.1.g558.t1	ref|XP_002889618.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335460|gb|EFH65877.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	203	204	3.00E-84	100.5	76.4	87.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G06790.1 | Symbols: | RNA polymerase Rpb7 N-terminal domain-containing protein | chr1:2087645-2089287 FORWARD LENGTH=204	203	204	1.00E-85	100.5	74.9	86.2
Rsa1.0_00009.1.g559.t1	gb|EOA38195.1| hypothetical protein CARUB_v10009673mg [Capsella rubella] gi|482574009|gb|EOA38196.1| hypothetical protein CARUB_v10009673mg [Capsella rubella]	320	336	1.00E-116	105.0	83.1	85.9	hypothetical protein CARUB_v10009673mg	gbpln	Capsella rubella	AT1G06850.1 | Symbols: AtbZIP52, bZIP52 | basic leucine-zipper 52 | chr1:2105233-2106518 FORWARD LENGTH=337	320	337	1.00E-110	105.3	78.4	83.1
Rsa1.0_00009.1.g560.t3	gb|EOA38106.1| hypothetical protein CARUB_v10009574mg [Capsella rubella]	325	355	1.00E-170	109.2	97.2	99.4	hypothetical protein CARUB_v10009574mg	gbpln	Capsella rubella	AT1G06890.2 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:2111728-2114038 REVERSE LENGTH=357	325	357	1.00E-171	109.8	97.2	99.1
Rsa1.0_00009.1.g561.t2	ref|NP_172173.2| putative N-arginine dibasic convertase [Arabidopsis thaliana] gi|332189930|gb|AEE28051.1| putative N-arginine dibasic convertase [Arabidopsis thaliana]	997	1024	0	102.7	89.8	94.4	putative N-arginine dibasic convertase	gbpln	Arabidopsis thaliana	AT1G06900.1 | Symbols: | Insulinase (Peptidase family M16) family protein | chr1:2115155-2120635 REVERSE LENGTH=1024	997	1024	0	102.7	89.8	94.4
Rsa1.0_00009.1.g562.t3	ref|NP_172176.1| translocon at the inner envelope membrane of chloroplasts 110 [Arabidopsis thaliana] gi|75157412|sp|Q8LPR9.1|TI110_ARATH RecName: Full=Protein TIC110, chloroplastic; AltName: Full=Translocon at the inner envelope membrane of chloroplasts 110; Short=AtTIC110; Flags: Precursor gi|20453114|gb|AAM19799.1| At1g06940/F4H5_1 [Arabidopsis thaliana] gi|332189936|gb|AEE28057.1| translocon at the inner envelope membrane of chloroplasts 110 [Arabidopsis thaliana]	1029	1016	0	98.7	90.2	94.0	translocon at the inner envelope membrane of chloroplasts 110	gbpln	Arabidopsis thaliana	AT1G06950.1 | Symbols: ATTIC110, TIC110 | translocon at the inner envelope membrane of chloroplasts 110 | chr1:2130303-2135563 REVERSE LENGTH=1016	1029	1016	0	98.7	90.2	94.0
Rsa1.0_00009.1.g563.t1	gb|EOA38940.1| hypothetical protein CARUB_v10011344mg [Capsella rubella]	831	829	0	99.8	81.3	92.1	hypothetical protein CARUB_v10011344mg	gbpln	Capsella rubella	AT1G06970.1 | Symbols: CHX14, ATCHX14 | cation/hydrogen exchanger 14 | chr1:2138109-2140818 FORWARD LENGTH=829	831	829	0	99.8	82.4	91.6

Rsa1.0_00009.1.g564.t1	ref|XP_002892370.1| hypothetical protein ARALYDRAFT_470720 [Arabidopsis lyrata subsp. lyrata] gi|297338212|gb|EFH68629.1| hypothetical protein ARALYDRAFT_470720 [Arabidopsis lyrata subsp. lyrata]	166	168	1.00E-67	101.2	88.0	91.6	hypothetical protein ARALYDRAFT_470720	gbpln	Arabidopsis lyrata	AT1G06980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: sepal, male gametophyte, carpel; EXPRESSED DURING: 4 anthesis; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30230.1); Has 159 Blast hits to 159 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 159; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2143248-2143757 REVERSE LENGTH=169	166	169	4.00E-68	101.8	86.1	91.0
Rsa1.0_00009.1.g565.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	569	657	1.00E-152	115.5	45.5	58.7	T14P8.10	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	569	332	4.00E-85	58.3	24.6	35.1
Rsa1.0_00009.1.g566.t1	gb|AAF82217.1|AC067971_25 Strong similarity to a mitochondrial carrier protein from Ribes nigrum gb|AJ007580. It contains a mitochondrial carrier protein domain PF|00153. ESTs gb|T46775, gb|R90539, gb|AW029646 and gb|AA605443 come from this gene [Arabidopsis thaliana]	162	781	2.00E-52	482.1	70.4	80.2	Strong similarity to a mitochondrial carrier protein from Ribes nigrum gb|AJ007580. It contains a mitochondrial carrier protein domain PF|00153. ESTs gb|T46775, gb|R90539, gb|AW029646 and gb|AA605443 come from this gene	gbpln	Arabidopsis thaliana	AT1G07020.1 | Symbols: | unknown protein; Has 39 Blast hits to 39 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 3; Plants - 28; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:2155319-2155884 REVERSE LENGTH=147	162	147	1.00E-53	90.7	70.4	80.2
Rsa1.0_00009.1.g567.t1	ref|XP_002892377.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338219|gb|EFH68636.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	197	194	9.00E-66	98.5	67.0	78.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G07050.1 | Symbols: | CCT motif family protein | chr1:2164327-2165133 REVERSE LENGTH=195	197	195	1.00E-64	99.0	66.5	78.2
Rsa1.0_00009.1.g568.t1	ref|NP_563779.1| GILT domain-containing protein [Arabidopsis thaliana] gi|15146334|gb|AAK83650.1| At1g07080/F10K1_15 [Arabidopsis thaliana] gi|15809756|gb|AAL06806.1| At1g07080/F10K1_15 [Arabidopsis thaliana] gi|332189954|gb|AEE28075.1| GILT domain-containing protein [Arabidopsis thaliana]	275	265	1.00E-118	96.4	77.1	84.7	GILT domain-containing protein	gbpln	Arabidopsis thaliana	AT1G07080.1 | Symbols: | Thioredoxin superfamily protein | chr1:2170069-2171861 FORWARD LENGTH=265	275	265	1.00E-120	96.4	77.1	84.7
Rsa1.0_00009.1.g569.t4	ref|NP_172191.1| fructose-2,6-bisphosphatase [Arabidopsis thaliana] gi|75192772|sp|Q9MB58.1|F26_ARATH RecName: Full=6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase; Short=6PF-2-K/Fru-2,6-P2ase; Short=AtF2KP; Short=PFK/FBPase; Includes: RecName: Full=6-phosphofructo-2-kinase; Includes: RecName: Full=Fructose-2,6-bisphosphatase gi|8117172|dbj|BAA96353.1| fructose-6-phosphate,2-kinase/fructose-2, 6-bisphosphatase [Arabidopsis thaliana] gi|332189956|gb|AEE28077.1| fructose-2,6-bisphosphatase [Arabidopsis thaliana]	1150	744	0	64.7	58.5	61.4	fructose-2,6-bisphosphatase	gbpln	Arabidopsis thaliana	AT1G07110.1 | Symbols: F2KP, ATF2KP, FKFBP | fructose-2,6-bisphosphatase | chr1:2178363-2183980 REVERSE LENGTH=744	1150	744	0	64.7	58.5	61.4
Rsa1.0_00009.1.g570.t1	gb|EOA36273.1| hypothetical protein CARUB_v10010524mg [Capsella rubella]	146	158	8.00E-58	108.2	75.3	84.2	hypothetical protein CARUB_v10010524mg	gbpln	Capsella rubella	AT1G07130.1 | Symbols: STN1, ATSTN1 | Nucleic acid-binding, OB-fold-like protein | chr1:2187928-2188410 FORWARD LENGTH=160	146	160	4.00E-56	109.6	69.2	82.2
Rsa1.0_00009.1.g571.t1	ref|XP_002892382.1| hypothetical protein ARALYDRAFT_470734 [Arabidopsis lyrata subsp. lyrata] gi|297338224|gb|EFH68641.1| hypothetical protein ARALYDRAFT_470734 [Arabidopsis lyrata subsp. lyrata]	278	145	8.00E-14	52.2	23.7	26.6	hypothetical protein ARALYDRAFT_470734	gbpln	Arabidopsis lyrata	AT1G07135.1 | Symbols: | glycine-rich protein | chr1:2190157-2190624 REVERSE LENGTH=155	278	155	5.00E-15	55.8	16.5	17.6
Rsa1.0_00009.1.g572.t1	gb|ABB97039.1| unknown [Brassica rapa]	225	225	1.00E-106	100.0	91.1	93.8	unknown	gbpln	Brassica rapa	AT1G07140.1 | Symbols: SIRANBP | Pleckstrin homology (PH) domain superfamily protein | chr1:2192360-2193688 REVERSE LENGTH=228	225	228	2.00E-95	101.3	87.6	91.6

Rsa1.0_00009.1.g573.t1	ref|XP_002889635.1| hypothetical protein ARALYDRAFT_887930 [Arabidopsis lyrata subsp. lyrata] gi|297335477|gb|EFH65894.1| hypothetical protein ARALYDRAFT_887930 [Arabidopsis lyrata subsp. lyrata]	513	509	0	99.2	90.8	94.7	hypothetical protein ARALYDRAFT_887930	gbpln	Arabidopsis lyrata	AT1G07180.1 | Symbols: ATNDI1, NDA1 | alternative NAD(P)H dehydrogenase 1 | chr1:2204414-2206773 FORWARD LENGTH=510	513	510	0	99.4	90.1	94.3
Rsa1.0_00009.1.g574.t1	gb|AAF79564.1|AC022464_22 F22G5.33 [Arabidopsis thaliana]	785	753	0	95.9	60.9	71.1	F22G5.33	gbpln	Arabidopsis thaliana	AT1G07330.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29620.1); Has 597 Blast hits to 536 proteins in 121 species: Archae - 2; Bacteria - 47; Metazoa - 170; Fungi - 43; Plants - 98; Viruses - 0; Other Eukaryotes - 237 (source: NCBI BLink). | chr1:2251131-2253585 FORWARD LENGTH=685	785	685	0	87.3	53.6	62.8
Rsa1.0_00009.1.g575.t1	ref|XP_002889642.1| sugar transport protein 2 [Arabidopsis lyrata subsp. lyrata] gi|297335484|gb|EFH65901.1| sugar transport protein 2 [Arabidopsis lyrata subsp. lyrata]	498	498	0	100.0	84.3	91.0	sugar transport protein 2	gbpln	Arabidopsis lyrata	AT1G07340.1 | Symbols: ATSTP2, STP2 | sugar transporter 2 | chr1:2254873-2256712 FORWARD LENGTH=498	498	498	0	100.0	83.5	90.8
Rsa1.0_00009.1.g576.t1	ref|XP_002892397.1| ceramidase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338239|gb|EFH68656.1| ceramidase family protein [Arabidopsis lyrata subsp. lyrata]	1224	776	0	63.4	52.7	56.0	ceramidase family protein	gbpln	Arabidopsis lyrata	AT1G07380.1 | Symbols: | Neutral/alkaline non-lysosomal ceramidase | chr1:2264829-2268306 REVERSE LENGTH=779	1224	779	0	63.6	52.7	56.0
Rsa1.0_00009.1.g577.t1	gb|EOA37095.1| hypothetical protein CARUB_v10010276mg [Capsella rubella]	216	216	1.00E-119	100.0	96.8	98.6	hypothetical protein CARUB_v10010276mg	gbpln	Capsella rubella	AT1G07410.1 | Symbols: ATRABA2B, RAB-A2B, ATRAB-A2B, RABA2b | RAB GTPase homolog A2B | chr1:2276270-2277154 FORWARD LENGTH=214	216	214	1.00E-119	99.1	96.8	97.7
Rsa1.0_00009.1.g578.t1	ref|XP_002889647.1| sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata] gi|297335489|gb|EFH65906.1| sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata]	277	266	1.00E-145	96.0	89.2	91.7	sterol 4-alpha-methyl-oxidase 2	gbpln	Arabidopsis lyrata	AT1G07420.1 | Symbols: ATSMO2, SMO2-1 | sterol 4-alpha-methyl-oxidase 2-1 | chr1:2277910-2280033 FORWARD LENGTH=266	277	266	2.33E-156	96.0	88.8	91.3
Rsa1.0_00009.1.g579.t1	gb|AAF79572.1|AC022464_30 F22G5.19 [Arabidopsis thaliana]	321	322	1.00E-122	100.3	77.3	86.3	F22G5.19	gbpln	Arabidopsis thaliana	AT2G29220.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr2:12562781-12564664 REVERSE LENGTH=627	321	627	1.00E-103	195.3	56.7	69.8
Rsa1.0_00009.1.g580.t1	ref|NP_172225.1| tropine dehydrogenase [Arabidopsis thaliana] gi|20258796|gb|AAM13920.1| putative tropinone reductase-I [Arabidopsis thaliana] gi|332190006|gb|AEE28127.1| tropinone reductase-like protein [Arabidopsis thaliana]	253	260	1.00E-109	102.8	75.9	87.4	tropine dehydrogenase	gbpln	Arabidopsis thaliana	AT1G07450.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:2288038-2289256 REVERSE LENGTH=260	253	260	1.00E-112	102.8	75.9	87.4
Rsa1.0_00009.1.g581.t1	ref|NP_172225.1| tropine dehydrogenase [Arabidopsis thaliana] gi|20258796|gb|AAM13920.1| putative tropinone reductase-I [Arabidopsis thaliana] gi|332190006|gb|AEE28127.1| tropinone reductase-like protein [Arabidopsis thaliana]	238	260	4.00E-99	109.2	78.6	87.8	tropine dehydrogenase	gbpln	Arabidopsis thaliana	AT1G07450.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:2288038-2289256 REVERSE LENGTH=260	238	260	1.00E-101	109.2	78.6	87.8
Rsa1.0_00009.1.g582.t1	dbj|BAJ33917.1| unnamed protein product [Thellungiella halophila]	464	375	1.00E-169	80.8	70.7	74.8	unnamed protein product	----	----	AT1G07480.2 | Symbols: | Transcription factor IIA, alpha/beta subunit | chr1:2296706-2299215 REVERSE LENGTH=375	464	375	1.00E-160	80.8	69.4	73.5
Rsa1.0_00009.1.g583.t1	ref|NP_200759.2| protein rotundifolia like 5 [Arabidopsis thaliana] gi|21553697|gb|AAM62790.1| unknown [Arabidopsis thaliana] gi|42822069|tpg|DAA02289.1| TPA_exp: DVL18 [Arabidopsis thaliana] gi|88900382|gb|ABD57503.1| At5g59510 [Arabidopsis thaliana] gi|332009816|gb|AED97199.1| protein rotundifolia like 5 [Arabidopsis thaliana]	111	144	3.00E-16	129.7	46.8	58.6	protein rotundifolia like 5	gbpln	Arabidopsis thaliana	AT5G59510.1 | Symbols: RTFL5, DVL18 | ROTUNDIFOLIA like 5 | chr5:23990089-23990523 FORWARD LENGTH=144	111	144	4.00E-19	129.7	46.8	58.6
Rsa1.0_00009.1.g584.t1	gb|EOA39018.1| hypothetical protein CARUB_v10011564mg [Capsella rubella]	98	78	5.00E-18	79.6	54.1	64.3	hypothetical protein CARUB_v10011564mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00009.1.g585.t1	dbj|BAJ34044.1| unnamed protein product [Thellungiella halophila]	764	772	0	101.0	83.4	88.4	unnamed protein product	----	----	AT1G07530.1 | Symbols: SCL14, ATGRAS2, GRAS2 | SCARECROW-like 14 | chr1:2313828-2316137 REVERSE LENGTH=769	764	769	0	100.7	80.4	87.4

Rsa1.0_00009.1.g586.t1	ref|NP_172234.2| telomere repeat-binding protein 5 [Arabidopsis thaliana] gi|296439813|sp|Q6R0E3.2|TRP5_ARATH RecName: Full=Telomere repeat-binding protein 5; AltName: Full=Protein TRF-LIKE 2 gi|332190019|gb|AEE28140.1| telomere repeat-binding protein 5 [Arabidopsis thaliana]	603	630	0	104.5	80.3	87.9	telomere repeat-binding protein 5	gbpln	Arabidopsis thaliana	AT1G07540.1 | Symbols: TRFL2 | TRF-like 2 | chr1:2318433-2321048 REVERSE LENGTH=630	603	630	0	104.5	80.3	87.9
Rsa1.0_00009.1.g587.t1	gb|EOA21150.1| hypothetical protein CARUB_v10001497mg [Capsella rubella]	282	315	9.00E-77	111.7	56.4	68.1	hypothetical protein CARUB_v10001497mg	gbpln	Capsella rubella	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	282	302	2.00E-76	107.1	56.4	68.1
Rsa1.0_00009.1.g588.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00009.1.g589.t1	gb|EOA24245.1| hypothetical protein CARUB_v10017480mg [Capsella rubella]	336	366	3.00E-81	108.9	47.0	62.8	hypothetical protein CARUB_v10017480mg	gbpln	Capsella rubella	AT5G52930.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21470370-21471449 FORWARD LENGTH=359	336	359	5.00E-80	106.8	43.5	56.8
Rsa1.0_00009.1.g590.t1	gb|EOA24245.1| hypothetical protein CARUB_v10017480mg [Capsella rubella]	420	366	4.00E-88	87.1	44.0	55.5	hypothetical protein CARUB_v10017480mg	gbpln	Capsella rubella	AT5G52930.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21470370-21471449 FORWARD LENGTH=359	420	359	1.00E-80	85.5	39.0	52.1
Rsa1.0_00009.1.g591.t1	gb|EOA38953.1| hypothetical protein CARUB_v10011370mg [Capsella rubella]	871	822	0	94.4	60.7	69.3	hypothetical protein CARUB_v10011370mg	gbpln	Capsella rubella	AT1G51890.2 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19274802-19278528 REVERSE LENGTH=828	871	828	0	95.1	44.2	58.9
Rsa1.0_00009.1.g592.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00009.1.g593.t1	gb|AAF75096.1|AC007583_32 It is a member of GTP1/OBG family PF|01018 [Arabidopsis thaliana]	489	1029	0	210.4	80.4	89.4	It is a member of GTP1/OBG family PF|01018	gbpln	Arabidopsis thaliana	AT1G07615.1 | Symbols: | GTP-binding protein Obg/CgtA | chr1:2342277-2344200 REVERSE LENGTH=493	489	493	0	100.8	80.2	89.2
Rsa1.0_00009.1.g594.t2	ref|NP_172241.2| GTP-binding protein Obg/CgtA [Arabidopsis thaliana] gi|332190029|gb|AEE28150.1| GTP-binding protein Obg/CgtA [Arabidopsis thaliana]	558	552	0	98.9	71.9	78.3	GTP-binding protein Obg/CgtA	gbpln	Arabidopsis thaliana	AT1G07620.1 | Symbols: ATOBGM | GTP-binding protein Obg/CgtA | chr1:2344556-2346374 REVERSE LENGTH=552	558	552	0	98.9	71.9	78.3
Rsa1.0_00009.1.g595.t1	gb|EOA39848.1| hypothetical protein CARUB_v10008517mg [Capsella rubella]	460	666	0	144.8	84.1	90.9	hypothetical protein CARUB_v10008517mg	gbpln	Capsella rubella	AT1G07630.1 | Symbols: PLL5 | pol-like 5 | chr1:2349189-2351437 FORWARD LENGTH=662	460	662	0	143.9	83.0	90.7
Rsa1.0_00009.1.g596.t1	gb|EOA38961.1| hypothetical protein CARUB_v10011378mg [Capsella rubella]	334	337	1.00E-132	100.9	79.3	85.0	hypothetical protein CARUB_v10011378mg	gbpln	Capsella rubella	AT1G07640.3 | Symbols: OBP2 | Dof-type zinc finger DNA-binding family protein | chr1:2354707-2356012 REVERSE LENGTH=339	334	339	1.00E-128	101.5	76.9	85.0
Rsa1.0_00009.1.g597.t1	ref|NP_172246.3| Ca2+-transporting ATPase [Arabidopsis thaliana] gi|12643934|sp|Q9XES1.2|ECA4_ARATH RecName: Full=Calcium-transporting ATPase 4, endoplasmic reticulum-type gi|8439902|gb|AAF75088.1|AC007583_24 Strong similarity to ER-type calcium pump protein from Arabidopsis thaliana gb|U93845. It is a member of Na+/K+ ATPase C-terminus PF|00690 and a member of E1-E2 ATPase PF|00122 [Arabidopsis thaliana] gi|332190039|gb|AEE28160.1| calcium-transporting ATPase 4 [Arabidopsis thaliana]	1059	1061	0	100.2	94.7	96.6	Ca2+-transporting ATPase	gbpln	Arabidopsis thaliana	AT1G07670.1 | Symbols: ATECA4, ECA4 | endomembrane-type CA-ATPase 4 | chr1:2370305-2374196 REVERSE LENGTH=1061	1059	1061	0	100.2	94.7	96.6
Rsa1.0_00009.1.g598.t1	sp|Q00332.3|RS15A_BRANA RecName: Full=40S ribosomal protein S15a; AltName: Full=PPCB8 gi|17863|emb|CAA42599.1| r-protein BnS15a [Brassica napus] gi|119720818|gb|ABL97979.1| 40S ribosomal protein S15a [Brassica rapa]	130	130	2.00E-69	100.0	100.0	100.0	RecName: Full=40S ribosomal protein S15a; AltName: Full=PPCB8 gi|17863|emb|CAA42599.1| r-protein BnS15a	gbpln	Brassica napus	AT5G59850.1 | Symbols: | Ribosomal protein S8 family protein | chr5:24112499-24113084 REVERSE LENGTH=130	130	130	7.00E-72	100.0	99.2	100.0
Rsa1.0_00009.1.g599.t1	gb|EOA38095.1| hypothetical protein CARUB_v10009562mg [Capsella rubella]	79	356	5.00E-29	450.6	73.4	81.0	hypothetical protein CARUB_v10009562mg	gbpln	Capsella rubella	AT1G07750.1 | Symbols: | RmlC-like cupins superfamily protein | chr1:2404300-2405863 REVERSE LENGTH=356	79	356	3.00E-31	450.6	74.7	79.7
Rsa1.0_00009.1.g600.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1361	1307	0	96.0	58.6	73.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1361	1262	1.00E-100	92.7	13.8	22.1
Rsa1.0_00009.1.g601.t1	gb|EOA38095.1| hypothetical protein CARUB_v10009562mg [Capsella rubella]	257	356	1.00E-132	138.5	90.7	93.8	hypothetical protein CARUB_v10009562mg	gbpln	Capsella rubella	AT1G07750.1 | Symbols: | RmlC-like cupins superfamily protein | chr1:2404300-2405863 REVERSE LENGTH=356	257	356	1.00E-132	138.5	88.3	92.6

Rsa1.0_00009.1.g602.t1	ref|NP_172254.2| DNA repair protein RAD51-like 4 [Arabidopsis thaliana] gi|83305360|sp|Q9LQQ2.2|RA51D_ARATH RecName: Full=DNA repair protein RAD51 homolog 4; Short=AtRAD51D gi|57283103|emb|CAD70703.1| putative DNA recombination protein [Arabidopsis thaliana] gi|58430742|dbj|BAD89165.1| AtRAD51D [Arabidopsis thaliana] gi|90969171|gb|ABE02570.1| RAD51D splice variant a [Arabidopsis thaliana] gi|90969179|gb|ABE02658.1| RAD51D splice variant a [Arabidopsis thaliana] gi|332190052|gb|AEE28173.1| DNA repair protein RAD51-like 4 [Arabidopsis thaliana]	67	322	1.00E-14	480.6	56.7	67.2	DNA repair protein RAD51-like 4	gbpln	Arabidopsis thaliana	AT1G07745.1 | Symbols: ATRAD51D, RAD51D, SSN1 | homolog of RAD51 D | chr1:2400797-2402842 REVERSE LENGTH=322	67	322	2.00E-17	480.6	56.7	67.2
Rsa1.0_00009.1.g603.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	442	441	1.00E-117	99.8	47.3	66.5	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	442	746	5.00E-92	168.8	38.2	52.7
Rsa1.0_00009.1.g604.t2	gb|EOA38341.1| hypothetical protein CARUB_v10009852mg, partial [Capsella rubella]	265	304	1.00E-119	114.7	82.3	90.2	hypothetical protein CARUB_v10009852mg, partial	gbpln	Capsella rubella	AT1G07745.2 | Symbols: ATRAD51D, RAD51D, SSN1 | homolog of RAD51 D | chr1:2400797-2402492 REVERSE LENGTH=304	265	304	1.00E-115	114.7	78.9	88.3
Rsa1.0_00010.1.g605.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00010.1.g606.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00010.1.g607.t1	ref|XP_004245047.1| PREDICTED: uncharacterized protein LOC101267914 [Solanum lycopersicum]	210	175	6.00E-22	83.3	26.7	35.2	PREDICTED: uncharacterized protein LOC101267914	gbpln	Solanum lycopersicum	AT5G21910.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7240789-7241127 FORWARD LENGTH=112	210	112	3.00E-17	53.3	41.0	42.4
Rsa1.0_00010.1.g608.t1	ref|NP_001142613.1| uncharacterized protein LOC100274882 [Zea mays] gi|195607320|gb|ACG25490.1| hypothetical protein [Zea mays]	253	248	1.00E-126	98.0	90.5	93.7	uncharacterized protein LOC100274882	gbenv/gbpln	Zea mays	AT5G21920.1 | Symbols: YLMG2, ATYLMG2 | YGGT family protein | chr5:7241350-7242765 REVERSE LENGTH=251	253	251	1.00E-115	99.2	81.8	89.7
Rsa1.0_00010.1.g609.t1	ref|XP_002871979.1| hypothetical protein ARALYDRAFT_910174 [Arabidopsis lyrata subsp. lyrata] gi|297317816|gb|EFH48238.1| hypothetical protein ARALYDRAFT_910174 [Arabidopsis lyrata subsp. lyrata]	887	887	0	100.0	91.2	94.9	hypothetical protein ARALYDRAFT_910174	gbpln	Arabidopsis lyrata	AT5G21930.2 | Symbols: PAA2, HMA8 | P-type ATPase of Arabidopsis 2 | chr5:7243129-7248721 FORWARD LENGTH=883	887	883	0	99.5	91.0	95.2
Rsa1.0_00010.1.g610.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00010.1.g611.t1	ref|XP_002874038.1| hypothetical protein ARALYDRAFT_910177 [Arabidopsis lyrata subsp. lyrata] gi|297319875|gb|EFH50297.1| hypothetical protein ARALYDRAFT_910177 [Arabidopsis lyrata subsp. lyrata]	229	213	1.00E-80	93.0	72.9	78.2	hypothetical protein ARALYDRAFT_910177	gbpln	Arabidopsis lyrata	AT5G21960.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:7258560-7259210 REVERSE LENGTH=216	229	216	4.00E-82	94.3	72.1	78.2
Rsa1.0_00010.1.g612.t1	ref|NP_680185.1| ubiquitin carboxyl-terminal hydrolase-like protein [Arabidopsis thaliana] gi|13374856|emb|CAC34490.1| putative protein [Arabidopsis thaliana] gi|22531217|gb|AAM97112.1| unknown protein [Arabidopsis thaliana] gi|29294056|gb|AAO73893.1| expressed protein [Arabidopsis thaliana] gi|110742391|dbj|BAE99118.1| hypothetical protein [Arabidopsis thaliana] gi|332005579|gb|AED92962.1| ubiquitin carboxyl-terminal hydrolase-like protein [Arabidopsis thaliana]	446	449	0	100.7	81.4	87.9	ubiquitin carboxyl-terminal hydrolase-like protein	gbpln	Arabidopsis thaliana	AT5G21970.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr5:7262071-7263420 FORWARD LENGTH=449	446	449	0	100.7	81.4	87.9
Rsa1.0_00010.1.g613.t1	ref|NP_680186.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|13374857|emb|CAC34491.1| putative protein [Arabidopsis thaliana] gi|29294058|gb|AAO73895.1| proline-rich protein family [Arabidopsis thaliana] gi|38454174|gb|AAR20781.1| At5g21280 [Arabidopsis thaliana] gi|38604048|gb|AAR24767.1| At5g21280 [Arabidopsis thaliana] gi|332005580|gb|AED92963.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	263	302	1.00E-83	114.8	77.2	83.7	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT5G21280.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:7264094-7265514 REVERSE LENGTH=302	263	302	4.00E-86	114.8	77.2	83.7

Rsa1.0_00010.1.g614.t1	ref|NP_680187.2| tetratricopeptide repeat domain–containing protein [Arabidopsis thaliana] gi|357580467|sp|B7ZWR6.1|OEP61_ARATH RecName: Full=Outer envelope protein 61, chloroplastic; AltName: Full=Tetratricopeptide repeat domain–containing protein 7 gi|219291100|gb|ACL13985.1| At5g21990 [Arabidopsis thaliana] gi|332005581|gb|AED92964.1| tetratricopeptide repeat domain–containing protein OEP61 [Arabidopsis thaliana]	613	554	0	90.4	77.0	82.2	tetratricopeptide repeat domain–containing protein	gbpln	Arabidopsis thaliana	AT5G21990.1 | Symbols: TPR7 | Tetratricopeptide repeat (TPR)–like superfamily protein | chr5:7273395–7276318 FORWARD LENGTH=554	613	554	0	90.4	77.0	82.2
Rsa1.0_00010.1.g615.t1	ref|NP_568410.1| E3 ubiquitin–protein ligase RHF2A [Arabidopsis thaliana] gi|30688246|ref|NP_851050.1| E3 ubiquitin–protein ligase RHF2A [Arabidopsis thaliana] gi|75315838|sp|Q9ZT42.1|RHF2A_ARATH RecName: Full=E3 ubiquitin–protein ligase RHF2A; AltName: Full=RING–H2 zinc finger protein RHF2a gi|11762136|gb|AAG40346.1|AF324994_1 CIC7E11 [Arabidopsis thaliana] gi|3790587|gb|AAC69856.1| RING–H2 finger protein RHF2a [Arabidopsis thaliana] gi|13374859|emb|CAC34493.1| RING–H2 finger protein RHF2a [Arabidopsis thaliana] gi|26983856|gb|AAN86180.1| unknown protein [Arabidopsis thaliana] gi|332005583|gb|AED92966.1| E3 ubiquitin–protein ligase RHF2A [Arabidopsis thaliana] gi|332005584|gb|AED92967.1| E3 ubiquitin–protein ligase RHF2A [Arabidopsis thaliana]	387	375	1.00E–167	96.9	83.2	86.8	E3 ubiquitin–protein ligase RHF2A	gbpln	Arabidopsis thaliana	AT5G22000.3 | Symbols: RHF2A | RING–H2 group F2A | chr5:7277436–7279553 FORWARD LENGTH=375	387	375	1.00E–170	96.9	83.2	86.8
Rsa1.0_00010.1.g616.t1	gb|EOA19946.1| hypothetical protein CARUB_v10000196mg [Capsella rubella]	1307	868	0	66.4	59.2	62.4	hypothetical protein CARUB_v10000196mg	gbpln	Capsella rubella	AT5G22030.1 | Symbols: UBP8 | ubiquitin–specific protease 8 | chr5:7290155–7296344 REVERSE LENGTH=913	1307	913	0	69.9	59.4	62.4
Rsa1.0_00010.1.g617.t1	ref|NP_568412.1| chaperone protein dnaJ 2 [Arabidopsis thaliana] gi|21431768|sp|P42825.2|DNAJ2_ARATH RecName: Full=Chaperone protein dnaJ 2; Short=AtDjA2; Flags: Precursor gi|13374865|emb|CAC34499.1| DNAJ PROTEIN HOMOLOG ATJ [Arabidopsis thaliana] gi|26451807|dbj|BAC42997.1| putative DnaJ protein homolog ATJ [Arabidopsis thaliana] gi|111074426|gb|ABH04586.1| At5g22060 [Arabidopsis thaliana] gi|332005594|gb|AED92977.1| chaperone protein dnaJ 2 [Arabidopsis thaliana]	421	419	0	99.5	91.9	96.2	chaperone protein dnaJ 2	gbpln	Arabidopsis thaliana	AT5G22060.1 | Symbols: ATJ2, J2 | DNAJ homologue 2 | chr5:7303798–7305668 REVERSE LENGTH=419	421	419	0	99.5	91.9	96.2
Rsa1.0_00010.1.g618.t1	gb|EOA21400.1| hypothetical protein CARUB_v10001767mg [Capsella rubella]	246	246	1.00E–132	100.0	95.1	97.6	hypothetical protein CARUB_v10001767mg	gbpln	Capsella rubella	AT5G22080.1 | Symbols: | Chaperone DnaJ–domain superfamily protein | chr5:7310600–7313540 REVERSE LENGTH=246	246	246	1.00E–123	100.0	96.3	97.2
Rsa1.0_00010.1.g619.t1	gb|AAM08751.1|AC025098_18 Putative copia–type polyprotein [Oryza sativa Japonica Group]	1367	1803	0	131.9	45.1	61.8	Putative copia–type polyprotein	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine–rich RLK (RECEPTOR–like protein kinase) 8 | chr4:12129485–12134086 FORWARD LENGTH=1262	1367	1262	1.00E–112	92.3	14.6	22.5
Rsa1.0_00010.1.g620.t1	ref|NP_680195.2| uncharacterized protein [Arabidopsis thaliana] gi|334187828|ref|NP_001190360.1| uncharacterized protein [Arabidopsis thaliana] gi|122175037|sp|Q0V865.1|FAFL_ARATH RecName: Full=Protein FAF–like, chloroplastic; Flags: Precursor gi|111074178|gb|ABH04462.1| At5g22090 [Arabidopsis thaliana] gi|332005598|gb|AED92981.1| uncharacterized protein AT5G22090 [Arabidopsis thaliana] gi|332005599|gb|AED92982.1| uncharacterized protein AT5G22090 [Arabidopsis thaliana]	457	463	1.00E–156	101.3	76.6	82.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G22090.2 | Symbols: | Protein of unknown function (DUF3049) | chr5:7315003–7316394 REVERSE LENGTH=463	457	463	1.00E–158	101.3	76.6	82.7
Rsa1.0_00010.1.g621.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00010.1.g622.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#

Rsa1.0_00010.1.g623.t1	ref|XP_002874051.1| pyridine nucleotide-disulfide oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319888|gb|EFH50310.1| pyridine nucleotide-disulfide oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	370	365	0	98.6	86.8	92.4	pyridine nucleotide-disulfide oxidoreductase family protein	gbpln	Arabidopsis lyrata	AT5G22140.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr5:7340284-7341657 REVERSE LENGTH=365	370	365	0	98.6	86.2	92.4
Rsa1.0_00010.1.g624.t1	ref|NP_680202.1| uncharacterized protein [Arabidopsis thaliana] gi|13374875|emb|CAC34509.1| putative protein [Arabidopsis thaliana] gi|332005608|gb|AED92991.1| uncharacterized protein AT5G22160 [Arabidopsis thaliana]	178	353	9.00E-39	198.3	50.0	61.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G22160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22150.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7346944-7349255 FORWARD LENGTH=353	178	353	4.00E-41	198.3	50.0	61.8
Rsa1.0_00010.1.g625.t1	ref|XP_002871991.1| hypothetical protein ARALYDRAFT_910206 [Arabidopsis lyrata subsp. lyrata] gi|297317828|gb|EFH48250.1| hypothetical protein ARALYDRAFT_910206 [Arabidopsis lyrata subsp. lyrata]	225	238	1.00E-38	105.8	44.0	60.9	hypothetical protein ARALYDRAFT_910206	gbpln	Arabidopsis lyrata	AT5G22150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22160.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7342567-7345956 FORWARD LENGTH=330	225	330	3.00E-36	146.7	36.9	48.9
Rsa1.0_00010.1.g626.t1	gb|EOA22413.1| hypothetical protein CARUB_v10003052mg [Capsella rubella]	208	363	5.00E-23	174.5	34.1	45.7	hypothetical protein CARUB_v10003052mg	gbpln	Capsella rubella	AT5G22160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22150.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7346944-7349255 FORWARD LENGTH=353	208	353	3.00E-23	169.7	37.0	48.6
Rsa1.0_00010.1.g627.t1	ref|XP_002871991.1| hypothetical protein ARALYDRAFT_910206 [Arabidopsis lyrata subsp. lyrata] gi|297317828|gb|EFH48250.1| hypothetical protein ARALYDRAFT_910206 [Arabidopsis lyrata subsp. lyrata]	234	238	2.00E-65	101.7	57.3	72.2	hypothetical protein ARALYDRAFT_910206	gbpln	Arabidopsis lyrata	AT5G22190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22160.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7354164-7354688 FORWARD LENGTH=117	234	117	3.00E-22	50.0	24.8	28.2
Rsa1.0_00010.1.g628.t1	gb|EOA21564.1| hypothetical protein CARUB_v10001972mg [Capsella rubella]	207	207	8.00E-84	100.0	73.9	84.5	hypothetical protein CARUB_v10001972mg	gbpln	Capsella rubella	AT3G44220.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:15928216-15929645 FORWARD LENGTH=206	207	206	4.00E-85	99.5	70.0	81.6
Rsa1.0_00010.1.g629.t1	emb|CBI28268.3| unnamed protein product [Vitis vinifera]	80	181	1.00E-26	226.3	72.5	83.8	unnamed protein product	gbpln	Vitis vinifera	AT5G22210.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:7359549-7359791 FORWARD LENGTH=80	80	80	2.00E-27	100.0	87.5	92.5
Rsa1.0_00010.1.g630.t1	ref|NP_001031921.3| E2F transcription factor 1 [Arabidopsis thaliana] gi|332005616|gb|AED92999.1| E2F transcription factor 1 [Arabidopsis thaliana]	410	466	0	113.7	82.7	88.3	E2F transcription factor 1	gbpln	Arabidopsis thaliana	AT5G22220.3 | Symbols: E2F1, E2FB, ATE2FB | E2F transcription factor 1 | chr5:7360749-7364120 FORWARD LENGTH=466	410	466	0	113.7	82.7	88.3
Rsa1.0_00010.1.g631.t1	ref|XP_002867007.1| hypothetical protein ARALYDRAFT_328110 [Arabidopsis lyrata subsp. lyrata] gi|297312843|gb|EFH43266.1| hypothetical protein ARALYDRAFT_328110 [Arabidopsis lyrata subsp. lyrata]	130	223	5.00E-14	171.5	35.4	52.3	hypothetical protein ARALYDRAFT_328110	gbpln	Arabidopsis lyrata	AT4G36590.1 | Symbols: | MADS-box transcription factor family protein | chr4:17261146-17262189 REVERSE LENGTH=248	130	248	2.00E-15	190.8	35.4	52.3
Rsa1.0_00010.1.g632.t1	gb|EOA21692.1| hypothetical protein CARUB_v10002117mg [Capsella rubella]	149	169	4.00E-35	113.4	49.7	57.0	hypothetical protein CARUB_v10002117mg	gbpln	Capsella rubella	AT5G22240.1 | Symbols: ATOFP10, OFP10 | Ovate family protein | chr5:7364689-7365279 FORWARD LENGTH=196	149	196	1.00E-35	131.5	46.3	52.3
Rsa1.0_00010.1.g633.t1	ref|XP_002874054.1| hypothetical protein ARALYDRAFT_489075 [Arabidopsis lyrata subsp. lyrata] gi|297319891|gb|EFH50313.1| hypothetical protein ARALYDRAFT_489075 [Arabidopsis lyrata subsp. lyrata]	286	274	1.00E-127	95.8	81.5	86.4	hypothetical protein ARALYDRAFT_489075	gbpln	Arabidopsis lyrata	AT5G22250.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:7365605-7366441 REVERSE LENGTH=278	286	278	1.00E-127	97.2	79.7	86.7

Rsa1.0_00010.1.g634.t1	ref|NP_197618.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana] gi|75262726|sp|Q9FMS5.1|MS1_ARATH RecName: Full=PHD finger protein MALE STERILITY 1 gi|9757806|dbj|BAB08324.1| unnamed protein product [Arabidopsis thaliana] gi|332005619|gb|AED93002.1| PHD finger protein MALE STERILITY 1 [Arabidopsis thaliana]	667	672	0	100.7	88.8	94.5	RING/FYVE/PHD zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT5G22260.1 | Symbols: MS1 | RING/FYVE/PHD zinc finger superfamily protein | chr5:7367707-7370192 REVERSE LENGTH=672	667	672	0	100.7	88.8	94.5
Rsa1.0_00010.1.g635.t1	ref|NP_568414.1| NAC domain containing protein 89 [Arabidopsis thaliana] gi|75165521|sp|Q94F58.1|NAC89_ARATH RecName: Full=NAC domain-containing protein 89; Short=ANAC089; AltName: Full=Protein FRUCTOSE-SENSING QUANTITATIVE TRAIT LOCUS 6 gi|14326465|gb|AAK60278.1|AF385685_1 AT5g22290/MWD9_7 [Arabidopsis thaliana] gi|18700194|gb|AAL77707.1| AT5g22290/MWD9_7 [Arabidopsis thaliana] gi|332005624|gb|AED93007.1| NAC domain containing protein 89 [Arabidopsis thaliana]	446	340	1.00E-147	76.2	56.5	65.5	NAC domain containing protein 89	gbpln	Arabidopsis thaliana	AT5G22290.1 | Symbols: anac089, NAC089 | NAC domain containing protein 89 | chr5:7376044-7377498 REVERSE LENGTH=340	446	340	1.00E-150	76.2	56.5	65.5
Rsa1.0_00010.1.g636.t1	ref|XP_002874061.1| hypothetical protein ARALYDRAFT_489082 [Arabidopsis lyrata subsp. lyrata] gi|297319898|gb|EFH50320.1| hypothetical protein ARALYDRAFT_489082 [Arabidopsis lyrata subsp. lyrata]	490	492	0	100.4	76.1	84.1	hypothetical protein ARALYDRAFT_489082	gbpln	Arabidopsis lyrata	AT5G22310.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11590.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7383742-7385345 REVERSE LENGTH=481	490	481	1.00E-180	98.2	75.7	83.3
Rsa1.0_00010.1.g637.t1	ref|NP_568416.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|9757812|dbj|BAB08330.1| unnamed protein product [Arabidopsis thaliana] gi|15912299|gb|AAL08283.1| AT5g22320/MWD9_11 [Arabidopsis thaliana] gi|19699236|gb|AAL90984.1| AT5g22320/MWD9_11 [Arabidopsis thaliana] gi|332005627|gb|AED93010.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	458	452	1.00E-178	98.7	81.2	90.6	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G22320.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:7388175-7390426 REVERSE LENGTH=452	458	452	0	98.7	81.2	90.6
Rsa1.0_00010.1.g638.t1	ref|XP_002874064.1| ATTIP49A/RIN1 [Arabidopsis lyrata subsp. lyrata] gi|297319901|gb|EFH50323.1| ATTIP49A/RIN1 [Arabidopsis lyrata subsp. lyrata]	458	458	0	100.0	98.7	99.6	ATTIP49A/RIN1	gbpln	Arabidopsis lyrata	AT5G22330.1 | Symbols: ATTIP49A, RIN1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:7391026-7394071 REVERSE LENGTH=458	458	458	0	100.0	98.3	99.6
Rsa1.0_00010.1.g639.t1	ref|XP_002874065.1| hypothetical protein ARALYDRAFT_910225 [Arabidopsis lyrata subsp. lyrata] gi|297319902|gb|EFH50324.1| hypothetical protein ARALYDRAFT_910225 [Arabidopsis lyrata subsp. lyrata]	421	427	0	101.4	92.4	97.1	hypothetical protein ARALYDRAFT_910225	gbpln	Arabidopsis lyrata	AT5G22350.1 | Symbols: ELM1 | Protein of unknown function (DUF1022) | chr5:7397762-7400746 REVERSE LENGTH=427	421	427	0	101.4	91.4	96.4
Rsa1.0_00010.1.g640.t1	ref|XP_002874066.1| vesicle-associated membrane protein 714 [Arabidopsis lyrata subsp. lyrata] gi|297319903|gb|EFH50325.1| vesicle-associated membrane protein 714 [Arabidopsis lyrata subsp. lyrata]	222	221	1.00E-120	99.5	95.0	97.7	vesicle-associated membrane protein 714	gbpln	Arabidopsis lyrata	AT5G22360.1 | Symbols: ATVAMP714, VAMP714 | vesicle-associated membrane protein 714 | chr5:7404379-7405654 REVERSE LENGTH=221	222	221	1.00E-121	99.5	92.8	97.7
Rsa1.0_00010.1.g641.t1	ref|XP_002874067.1| ANAC090 [Arabidopsis lyrata subsp. lyrata] gi|297319904|gb|EFH50326.1| ANAC090 [Arabidopsis lyrata subsp. lyrata]	235	235	1.00E-115	100.0	85.1	91.1	ANAC090	gbpln	Arabidopsis lyrata	AT5G22380.1 | Symbols: anac090, NAC090 | NAC domain containing protein 90 | chr5:7408924-7410038 REVERSE LENGTH=235	235	235	1.00E-115	100.0	83.0	89.4
Rsa1.0_00010.1.g642.t1	ref|XP_002874068.1| hypothetical protein ARALYDRAFT_489095 [Arabidopsis lyrata subsp. lyrata] gi|297319905|gb|EFH50327.1| hypothetical protein ARALYDRAFT_489095 [Arabidopsis lyrata subsp. lyrata]	186	194	4.00E-65	104.3	74.2	83.3	hypothetical protein ARALYDRAFT_489095	gbpln	Arabidopsis lyrata	AT5G22390.1 | Symbols: | Protein of unknown function (DUF3049) | chr5:7418383-7418991 REVERSE LENGTH=202	186	202	9.00E-64	108.6	68.8	80.1
Rsa1.0_00010.1.g643.t1	gb|EOA12263.1| hypothetical protein CARUB_v10007993mg [Capsella rubella]	173	493	6.00E-63	285.0	66.5	79.2	hypothetical protein CARUB_v10007993mg	gbpln	Capsella rubella	AT3G44550.1 | Symbols: FAR5 | fatty acid reductase 5 | chr3:16138060-16141409 FORWARD LENGTH=496	173	496	3.00E-62	286.7	66.5	78.6

Rsa1.0_00010.1.g644.t3	ref|NP_197634.1| putative fatty acyl-CoA reductase 7 [Arabidopsis thaliana] gi|75171715|sp|Q9FMQ9.1|FACR7_ARATH RecName: Full=Putative fatty acyl-CoA reductase 7 gi|9757823|dbj|BAB08341.1| acyl CoA reductase-like protein [Arabidopsis thaliana] gi|332005641|gb|AED93024.1| putative fatty acyl-CoA reductase 7 [Arabidopsis thaliana]	266	409	1.00E-103	153.8	67.3	81.6	putative fatty acyl-CoA reductase 7	gbpln	Arabidopsis thaliana	AT5G22420.1 | Symbols: FAR7 | fatty acid reductase 7 | chr5:7429903-7432586 FORWARD LENGTH=409	266	409	1.00E-106	153.8	67.3	81.6
Rsa1.0_00010.1.g645.t1	gb|EOA21532.1| hypothetical protein CARUB_v10001937mg [Capsella rubella]	212	217	1.00E-103	102.4	97.2	99.1	hypothetical protein CARUB_v10001937mg	gbpln	Capsella rubella	AT5G22440.2 | Symbols: | Ribosomal protein L1p/L10e family | chr5:7435328-7436486 REVERSE LENGTH=217	212	217	1.00E-106	102.4	97.6	98.1
Rsa1.0_00010.1.g646.t1	dbj|BAB08344.1| unnamed protein product [Arabidopsis thaliana]	1207	1180	0	97.8	82.5	87.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G22450.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G19390.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7437145-7442856 REVERSE LENGTH=1154	1207	1154	0	95.6	81.9	87.3
Rsa1.0_00010.1.g647.t1	ref|XP_002874071.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319908|gb|EFH50330.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	341	340	1.00E-167	99.7	81.5	90.6	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT5G22460.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:7443659-7445269 REVERSE LENGTH=340	341	340	1.00E-167	99.7	79.8	90.0
Rsa1.0_00010.1.g648.t1	dbj|BAB09119.1| seed maturation protein PM38 protein [Arabidopsis thaliana]	811	815	0	100.5	92.8	96.8	seed maturation protein PM38 protein	gbpln	Arabidopsis thaliana	AT5G22470.1 | Symbols: | NAD+ ADP-ribosyltransferases;NAD+ ADP-ribosyltransferases | chr5:7447045-7450743 FORWARD LENGTH=814	811	814	0	100.4	92.7	96.7
Rsa1.0_00010.1.g649.t1	ref|XP_002884569.1| hypothetical protein ARALYDRAFT_896743 [Arabidopsis lyrata subsp. lyrata] gi|297330409|gb|EFH60828.1| hypothetical protein ARALYDRAFT_896743 [Arabidopsis lyrata subsp. lyrata]	236	280	1.00E-27	118.6	29.7	48.7	hypothetical protein ARALYDRAFT_896743	gbpln	Arabidopsis lyrata	AT5G17080.1 | Symbols: | Cysteine proteinases superfamily protein | chr5:5619594-5620949 FORWARD LENGTH=298	236	298	2.00E-21	126.3	25.8	40.3
Rsa1.0_00010.1.g650.t1	ref|XP_002889471.1| hypothetical protein ARALYDRAFT_470343 [Arabidopsis lyrata subsp. lyrata] gi|297335313|gb|EFH65730.1| hypothetical protein ARALYDRAFT_470343 [Arabidopsis lyrata subsp. lyrata]	229	219	1.00E-25	95.6	38.4	52.0	hypothetical protein ARALYDRAFT_470343	gbpln	Arabidopsis lyrata	AT1G03710.2 | Symbols: | Cystatin/monellin superfamily protein | chr1:923492-924287 FORWARD LENGTH=202	229	202	2.00E-23	88.2	37.6	50.7
Rsa1.0_00010.1.g651.t3	ref|XP_002874072.1| zinc finger (ZPR1-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297319909|gb|EFH50331.1| zinc finger (ZPR1-type) family protein [Arabidopsis lyrata subsp. lyrata]	487	493	0	101.2	86.2	89.7	zinc finger (ZPR1-type) family protein	gbpln	Arabidopsis lyrata	AT5G37340.3 | Symbols: | ZPR1 zinc-finger domain protein | chr5:14787488-14792373 REVERSE LENGTH=493	487	493	0	101.2	85.2	88.7
Rsa1.0_00010.1.g652.t1	ref|XP_002872004.1| hypothetical protein ARALYDRAFT_910242 [Arabidopsis lyrata subsp. lyrata] gi|297317841|gb|EFH48263.1| hypothetical protein ARALYDRAFT_910242 [Arabidopsis lyrata subsp. lyrata]	493	491	0	99.6	86.6	94.1	hypothetical protein ARALYDRAFT_910242	gbpln	Arabidopsis lyrata	AT5G22500.1 | Symbols: FAR1 | fatty acid reductase 1 | chr5:7470541-7473916 FORWARD LENGTH=491	493	491	0	99.6	86.0	94.5
Rsa1.0_00011.1.g653.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00011.1.g654.t1	gb|EOA17296.1| hypothetical protein CARUB_v10005568mg [Capsella rubella]	263	253	1.00E-116	96.2	79.8	86.7	hypothetical protein CARUB_v10005568mg	gbpln	Capsella rubella	AT4G29260.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr4:14422310-14423409 REVERSE LENGTH=255	263	255	1.00E-117	97.0	78.3	85.2
Rsa1.0_00011.1.g655.t1	gb|EOA16729.1| hypothetical protein CARUB_v10004932mg [Capsella rubella]	406	413	1.00E-175	101.7	84.0	90.1	hypothetical protein CARUB_v10004932mg	gbpln	Capsella rubella	AT4G29240.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:14418826-14420073 FORWARD LENGTH=415	406	415	1.00E-173	102.2	72.2	78.1
Rsa1.0_00011.1.g656.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1166	1213	0	104.0	37.3	55.4	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1166	626	2.00E-66	53.7	13.0	21.5

Rsa1.0_00011.1.g657.t1	ref|NP_194652.1| NAC domain containing protein 75 [Arabidopsis thaliana] gi|7269821|emb|CAB79681.1| putative protein [Arabidopsis thaliana] gi|332660205|gb|AEE85605.1| NAC domain containing protein 75 [Arabidopsis thaliana]	523	498	0	95.2	86.4	89.1	NAC domain containing protein 75	gbpln	Arabidopsis thaliana	AT4G29230.1 | Symbols: anac075, NAC075 | NAC domain containing protein 75 | chr4:14410338-14414956 FORWARD LENGTH=498	523	498	0	95.2	86.4	89.1
Rsa1.0_00011.1.g658.t4	gb|AAM91591.1| pyrophosphate-dependent phosphofructo-1-kinase-like protein [Arabidopsis thaliana]	88	473	2.00E-13	537.5	44.3	48.9	pyrophosphate-dependent phosphofructo-1-kinase-like protein	gbpln	Arabidopsis thaliana	AT4G29220.1 | Symbols: PFK1 | phosphofructokinase 1 | chr4:14403621-14406071 REVERSE LENGTH=473	88	473	4.00E-16	537.5	44.3	48.9
Rsa1.0_00011.1.g659.t1	dbj|BAD22536.1| gamma-glutamyl transferase [Raphanus sativus]	639	635	0	99.4	79.3	88.4	gamma-glutamyl transferase	gbpln	Raphanus sativus	AT4G29210.1 | Symbols: GGT3, GGT4 | gamma-glutamyl transpeptidase 4 | chr4:14400990-14403319 FORWARD LENGTH=637	639	637	0	99.7	78.7	87.5
Rsa1.0_00011.1.g660.t1	ref|XP_002330525.1| predicted protein [Populus trichocarpa] gi|222872459|gb|EEF09590.1| predicted protein [Populus trichocarpa]	640	605	1.00E-168	94.5	48.3	63.4	predicted protein	gbpln	Populus trichocarpa	AT4G29210.1 | Symbols: GGT3, GGT4 | gamma-glutamyl transpeptidase 4 | chr4:14400990-14403319 FORWARD LENGTH=637	640	637	1.00E-164	99.5	47.7	61.1
Rsa1.0_00011.1.g661.t1	dbj|BAJ33902.1| unnamed protein product [Thellungiella halophila]	344	365	1.00E-168	106.1	86.6	92.2	unnamed protein product	----	----	AT4G29190.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr4:14392233-14393303 REVERSE LENGTH=356	344	356	1.00E-160	103.5	83.4	88.4
Rsa1.0_00011.1.g662.t1	ref|NP_001190865.1| protein root hair specific 16 [Arabidopsis thaliana] gi|264664523|sp|C0LGR6.2|Y4291_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g29180; Flags: Precursor gi|332660199|gb|AEE85599.1| probable LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	908	913	0	100.6	85.9	92.4	protein root hair specific 16	gbpln	Arabidopsis thaliana	AT4G29180.2 | Symbols: RHS16 | root hair specific 16 | chr4:14385631-14389524 FORWARD LENGTH=913	908	913	0	100.6	85.9	92.4
Rsa1.0_00011.1.g663.t1	ref|NP_194646.2| meiotic nuclear division protein 1-like protein [Arabidopsis thaliana] gi|75151407|sp|Q8GYD2.1|MND1_ARATH RecName: Full=Meiotic nuclear division protein 1 homolog; Short=AtMND1; AltName: Full=Meiotic nuclear division 1-like protein gi|26450501|dbj|BAC42364.1| unknown protein [Arabidopsis thaliana] gi|28973061|gb|AAO63855.1| unknown protein [Arabidopsis thaliana] gi|82408770|gb|ABB73190.1| meiotic nuclear division 1-like protein [Arabidopsis thaliana] gi|82775232|emb|CAJ44238.1| AtMnd1 protein [Arabidopsis thaliana] gi|332660196|gb|AEE85596.1| meiotic nuclear division protein 1-like protein [Arabidopsis thaliana]	256	230	1.00E-100	89.8	75.0	78.5	meiotic nuclear division protein 1-like protein	gbpln	Arabidopsis thaliana	AT4G29170.1 | Symbols: ATMND1 | Mnd1 family protein | chr4:14382985-14385128 FORWARD LENGTH=230	256	230	1.00E-102	89.8	75.0	78.5
Rsa1.0_00011.1.g664.t1	gb|EOA17400.1| hypothetical protein CARUB_v10005703mg [Capsella rubella] gi|482553208|gb|EOA17401.1| hypothetical protein CARUB_v10005703mg [Capsella rubella]	215	218	6.00E-96	101.4	96.3	98.1	hypothetical protein CARUB_v10005703mg	gbpln	Capsella rubella	AT4G29160.3 | Symbols: SNF7.1 | SNF7 family protein | chr4:14381019-14382342 FORWARD LENGTH=219	215	219	2.00E-92	101.9	92.6	94.4
Rsa1.0_00011.1.g665.t1	ref|XP_002869449.1| hypothetical protein ARALYDRAFT_491843 [Arabidopsis lyrata subsp. lyrata] gi|297315285|gb|EFH45708.1| hypothetical protein ARALYDRAFT_491843 [Arabidopsis lyrata subsp. lyrata]	388	385	1.00E-176	99.2	85.8	91.0	hypothetical protein ARALYDRAFT_491843	gbpln	Arabidopsis lyrata	AT4G29150.1 | Symbols: IQD25 | IQ-domain 25 | chr4:14378770-14380340 FORWARD LENGTH=399	388	399	1.00E-174	102.8	85.1	90.2
Rsa1.0_00011.1.g666.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00011.1.g667.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1032	1197	1.00E-110	116.0	18.9	25.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	1032	361	8.00E-19	35.0	5.4	7.4
Rsa1.0_00011.1.g668.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	779	1274	0	163.5	49.4	65.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	779	575	1.00E-74	73.8	23.4	35.7
Rsa1.0_00011.1.g669.t1	ref|XP_002869450.1| hypothetical protein ARALYDRAFT_913597 [Arabidopsis lyrata subsp. lyrata] gi|297315286|gb|EFH45709.1| hypothetical protein ARALYDRAFT_913597 [Arabidopsis lyrata subsp. lyrata]	538	533	0	99.1	88.1	93.5	hypothetical protein ARALYDRAFT_913597	gbpln	Arabidopsis lyrata	AT4G29140.1 | Symbols: | MATE efflux family protein | chr4:14369148-14370746 FORWARD LENGTH=532	538	532	0	98.9	85.7	91.6

Rsa1.0_00011.1.g670.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00011.1.g671.t1	ref|NP_194640.1| uncharacterized protein [Arabidopsis thaliana] gi|4972057|emb|CAB43925.1| putative protein [Arabidopsis thaliana] gi|7269809|emb|CAB79669.1| putative protein [Arabidopsis thaliana] gi|60547867|gb|AAX23897.1| hypothetical protein At4g29110 [Arabidopsis thaliana] gi|71905525|gb|AAZ52740.1| hypothetical protein At4g29110 [Arabidopsis thaliana] gi|149944337|gb|ABR46211.1| At4g29110 [Arabidopsis thaliana] gi|332660188|gb|AEE85588.1| uncharacterized protein AT4G29110 [Arabidopsis thaliana]	193	200	3.00E-82	103.6	81.9	87.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G29110.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to chitin; LOCATED IN: vacuole; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52140.1); Has 109 Blast hits to 109 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 109; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14348866-14349468 FORWARD LENGTH=200	193	200	9.00E-85	103.6	81.9	87.6
Rsa1.0_00011.1.g672.t1	emb|CAC14433.1| putative protein [Brassica napus]	385	389	0	101.0	93.0	95.8	putative protein	gbpln	Brassica napus	AT4G29100.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:14341140-14344575 FORWARD LENGTH=407	385	407	1.00E-171	105.7	88.1	92.5
Rsa1.0_00011.1.g673.t1	ref|NP_850981.1| aspartyl protease-like protein [Arabidopsis thaliana] gi|17065172|gb|AAL32740.1| nucellin-like protein [Arabidopsis thaliana] gi|24899795|gb|AAN65112.1| nucellin-like protein [Arabidopsis thaliana] gi|332197863|gb|AEE35984.1| aspartyl protease-like protein [Arabidopsis thaliana]	114	466	2.00E-37	408.8	72.8	78.9	aspartyl protease-like protein	gbpln	Arabidopsis thaliana	AT1G77480.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:29114705-29117150 REVERSE LENGTH=466	114	466	2.00E-40	408.8	72.8	78.9
Rsa1.0_00011.1.g674.t1	ref|XP_002892897.1| hypothetical protein ARALYDRAFT_471818 [Arabidopsis lyrata subsp. lyrata] gi|297338739|gb|EFH69156.1| hypothetical protein ARALYDRAFT_471818 [Arabidopsis lyrata subsp. lyrata]	70	233	8.00E-26	332.9	77.1	85.7	hypothetical protein ARALYDRAFT_471818	gbpln	Arabidopsis lyrata	AT1G16210.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1014 (InterPro:IPR010422); Has 16107 Blast hits to 8386 proteins in 1107 species: Archae - 26; Bacteria - 3370; Metazoa - 4013; Fungi - 1516; Plants - 526; Viruses - 120; Other Eukaryotes - 6536 (source: NCBI BLink). | chr1:5546352-5547447 REVERSE LENGTH=234	70	234	2.00E-27	334.3	74.3	82.9
Rsa1.0_00011.1.g675.t3	emb|CAC14431.1| hypothetical protein [Brassica napus]	203	151	2.00E-50	74.4	51.7	52.7	hypothetical protein	gbpln	Brassica napus	AT4G16295.1 | Symbols: SPH1 | S-protein homologue 1 | chr4:9215680-9216135 REVERSE LENGTH=151	203	151	2.00E-36	74.4	40.4	42.9
Rsa1.0_00011.1.g676.t1	dbj|BAC42653.1| putative glycine-rich protein [Arabidopsis thaliana] gi|28416867|gb|AAO42964.1| At4g29030 [Arabidopsis thaliana]	112	115	6.00E-13	102.7	35.7	39.3	putative glycine-rich protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00011.1.g677.t1	#	#	#	#	#	#	#	–	----	----	AT4G29020.2 | Symbols: | glycine-rich protein | chr4:14305032-14305508 FORWARD LENGTH=113	152	113	5.00E-13	74.3	22.4	23.0
Rsa1.0_00011.1.g678.t1	ref|NP_194630.1| enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase [Arabidopsis thaliana] gi|75315624|sp|Q9ZPI6.1|AIM1_ARATH RecName: Full=Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1; AltName: Full=Protein ABNORMAL INFLORESCENCE MERISTEM 1; Short=AtAIM1; Includes: RecName: Full=Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase; Includes: RecName: Full=3-hydroxyacyl-CoA dehydrogenase gi|4337025|gb|AAD18041.1| AIM1 protein [Arabidopsis thaliana] gi|4972047|emb|CAB43915.1| AIM1 protein [Arabidopsis thaliana] gi|7269799|emb|CAB79659.1| AIM1 protein [Arabidopsis thaliana] gi|16648891|gb|AAL24297.1| AIM1 protein [Arabidopsis thaliana] gi|18175606|gb|AAL59895.1| putative AIM1 protein [Arabidopsis thaliana] gi|20465649|gb|AAM20293.1| putative AIM1 protein [Arabidopsis thaliana] gi|332660172|gb|AEE85572.1| fatty acid beta-oxidation multifunctional protein AIM1 [Arabidopsis thaliana]	581	721	1.00E-167	124.1	52.2	56.8	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	gbpln	Arabidopsis thaliana	AT4G29010.1 | Symbols: AIM1 | Enoyl-CoA hydratase/isomerase family | chr4:14297312-14302016 REVERSE LENGTH=721	581	721	1.00E-170	124.1	52.2	56.8

<table>
<tr><td>Rsa1.0_00011.1.g679.t1</td><td>ref|XP_002869459.1| hypothetical protein ARALYDRAFT_491858 [Arabidopsis lyrata subsp. lyrata] gi|297315295|gb|EFH45718.1| hypothetical protein ARALYDRAFT_491858 [Arabidopsis lyrata subsp. lyrata]</td><td>525</td><td>601</td><td>0</td><td>114.5</td><td>77.5</td><td>84.6</td><td>hypothetical protein ARALYDRAFT_491858</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G29000.1 | Symbols: | Tesmin/TSO1-like CXC domain-containing protein | chr4:14293957-14296602 FORWARD LENGTH=603</td><td>525</td><td>603</td><td>0</td><td>114.9</td><td>75.6</td><td>82.7</td></tr>
<tr><td>Rsa1.0_00011.1.g680.t1</td><td>ref|NP_194628.1| RNA-binding-related protein [Arabidopsis thaliana] gi|4972045|emb|CAB43913.1| putative protein [Arabidopsis thaliana] gi|7269797|emb|CAB79657.1| putative protein [Arabidopsis thaliana] gi|115646852|gb|ABJ17140.1| At4g28990 [Arabidopsis thaliana] gi|332660169|gb|AEE85569.1| RNA-binding-related protein [Arabidopsis thaliana]</td><td>337</td><td>347</td><td>1.00E-80</td><td>103.0</td><td>63.5</td><td>70.9</td><td>RNA-binding-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G28990.1 | Symbols: | RNA-binding protein-related | chr4:14291205-14293018 FORWARD LENGTH=347</td><td>337</td><td>347</td><td>3.00E-83</td><td>103.0</td><td>63.5</td><td>70.9</td></tr>
<tr><td>Rsa1.0_00011.1.g681.t1</td><td>ref|XP_002517802.1| DNA topoisomerase II, putative [Ricinus communis] gi|223543074|gb|EEF44609.1| DNA topoisomerase II, putative [Ricinus communis]</td><td>170</td><td>1212</td><td>2.00E-16</td><td>712.9</td><td>35.9</td><td>46.5</td><td>DNA topoisomerase II, putative</td><td>gbpln</td><td>Ricinus communis</td><td>AT3G23890.2 | Symbols: TOPII, ATTOPII | topoisomerase II | chr3:8624931-8631106 FORWARD LENGTH=1438</td><td>170</td><td>1438</td><td>2.00E-12</td><td>845.9</td><td>24.7</td><td>28.8</td></tr>
<tr><td>Rsa1.0_00011.1.g682.t1</td><td>ref|XP_002869463.1| hypothetical protein ARALYDRAFT_491863 [Arabidopsis lyrata subsp. lyrata] gi|297315299|gb|EFH45722.1| hypothetical protein ARALYDRAFT_491863 [Arabidopsis lyrata subsp. lyrata]</td><td>350</td><td>348</td><td>1.00E-167</td><td>99.4</td><td>82.9</td><td>91.1</td><td>hypothetical protein ARALYDRAFT_491863</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G28940.1 | Symbols: | Phosphorylase superfamily protein | chr4:14274414-14276920 FORWARD LENGTH=348</td><td>350</td><td>348</td><td>1.00E-169</td><td>99.4</td><td>82.6</td><td>90.6</td></tr>
<tr><td>Rsa1.0_00011.1.g683.t1</td><td>ref|XP_002867431.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313267|gb|EFH43690.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>330</td><td>329</td><td>1.00E-121</td><td>99.7</td><td>67.6</td><td>80.3</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G28920.1 | Symbols: | Protein of unknown function (DUF626) | chr4:14268415-14269885 REVERSE LENGTH=292</td><td>330</td><td>292</td><td>2.00E-65</td><td>88.5</td><td>44.2</td><td>56.1</td></tr>
<tr><td>Rsa1.0_00011.1.g684.t1</td><td>ref|XP_002867431.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313267|gb|EFH43690.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>336</td><td>329</td><td>1.00E-123</td><td>97.9</td><td>67.6</td><td>81.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G28920.1 | Symbols: | Protein of unknown function (DUF626) | chr4:14268415-14269885 REVERSE LENGTH=292</td><td>336</td><td>292</td><td>6.00E-62</td><td>86.9</td><td>43.2</td><td>53.9</td></tr>
<tr><td>Rsa1.0_00011.1.g685.t1</td><td>ref|XP_002869465.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315301|gb|EFH45724.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>301</td><td>280</td><td>2.00E-84</td><td>93.0</td><td>55.8</td><td>64.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G19515.2 | Symbols: | CONTAINS InterPro DOMAIN/s: Apoptosis inhibitory 5 (InterPro:IPR008383); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23935.1); Has 546 Blast hits to 394 proteins in 84 species: Archae - 0; Bacteria - 3; Metazoa - 210; Fungi - 15; Plants - 143; Viruses - 0; Other Eukaryotes - 175 (source: NCBI BLink). | chr3:6766872-6771078 REVERSE LENGTH=805</td><td>301</td><td>805</td><td>2.00E-28</td><td>267.4</td><td>23.9</td><td>39.5</td></tr>
<tr><td>Rsa1.0_00011.1.g686.t1</td><td>gb|EOA16694.1| hypothetical protein CARUB_v10004886mg [Capsella rubella]</td><td>403</td><td>424</td><td>1.00E-157</td><td>105.2</td><td>78.4</td><td>84.9</td><td>hypothetical protein CARUB_v10004886mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G28910.3 | Symbols: NINJA | novel interactor of JAZ | chr4:14264330-14265680 REVERSE LENGTH=425</td><td>403</td><td>425</td><td>1.00E-155</td><td>105.5</td><td>75.4</td><td>82.6</td></tr>
<tr><td>Rsa1.0_00011.1.g687.t1</td><td>ref|XP_002867435.1| ring-H2 finger protein ATL4J precursor [Arabidopsis lyrata subsp. lyrata] gi|297313271|gb|EFH43694.1| ring-H2 finger protein ATL4J precursor [Arabidopsis lyrata subsp. lyrata]</td><td>596</td><td>435</td><td>1.00E-162</td><td>73.0</td><td>52.0</td><td>56.9</td><td>ring-H2 finger protein ATL4J precursor</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G28890.1 | Symbols: | RING/U-box superfamily protein | chr4:14256437-14257735 REVERSE LENGTH=432</td><td>596</td><td>432</td><td>1.00E-163</td><td>72.5</td><td>52.3</td><td>56.5</td></tr>
<tr><td>Rsa1.0_00011.1.g688.t1</td><td>gb|EOA16720.1| hypothetical protein CARUB_v10004924mg [Capsella rubella]</td><td>421</td><td>415</td><td>0</td><td>98.6</td><td>91.4</td><td>94.8</td><td>hypothetical protein CARUB_v10004924mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G28880.1 | Symbols: ckl3 | casein kinase I-like 3 | chr4:14251351-14254048 FORWARD LENGTH=415</td><td>421</td><td>415</td><td>0</td><td>98.6</td><td>91.7</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00011.1.g689.t1</td><td>gb|EOA18729.1| hypothetical protein CARUB_v10007311mg [Capsella rubella]</td><td>150</td><td>198</td><td>2.00E-55</td><td>132.0</td><td>73.3</td><td>79.3</td><td>hypothetical protein CARUB_v10007311mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G28840.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G20080.1); Has 71 Blast hits to 69 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:14240867-14242513 FORWARD LENGTH=193</td><td>150</td><td>193</td><td>7.00E-54</td><td>128.7</td><td>70.7</td><td>76.0</td></tr>
<tr><td>Rsa1.0_00011.1.g690.t1</td><td>gb|EOA17434.1| hypothetical protein CARUB_v10005737mg [Capsella rubella]</td><td>208</td><td>208</td><td>1.00E-107</td><td>100.0</td><td>94.7</td><td>98.6</td><td>hypothetical protein CARUB_v10005737mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G28830.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:14232490-14233917 FORWARD LENGTH=208</td><td>208</td><td>208</td><td>1.00E-109</td><td>100.0</td><td>94.7</td><td>98.1</td></tr>
</table>

Rsa1.0_00011.1.g691.t1	ref|NP_194611.2| HIT-type zinc finger protein [Arabidopsis thaliana] gi|92856590|gb|ABE77404.1| At4g28820 [Arabidopsis thaliana] gi|332660149|gb|AEE85549.1| HIT-type zinc finger protein [Arabidopsis thaliana]	198	173	9.00E-30	87.4	43.4	50.0	HIT-type zinc finger protein	gbpln	Arabidopsis thaliana	AT4G28820.1 | Symbols: | HIT-type Zinc finger family protein | chr4:14230815-14232287 REVERSE LENGTH=173	198	173	3.00E-32	87.4	43.4	50.0
Rsa1.0_00011.1.g692.t1	ref|XP_002869474.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297315310|gb|EFH45733.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	119	139	1.00E-35	116.8	61.3	78.2	expressed protein	gbpln	Arabidopsis lyrata	AT4G28775.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:14214817-14215233 FORWARD LENGTH=138	119	138	3.00E-37	116.0	61.3	76.5
Rsa1.0_00011.1.g693.t1	gb|EOA30311.1| hypothetical protein CARUB_v10013437mg [Capsella rubella]	544	532	0	97.8	80.9	86.2	hypothetical protein CARUB_v10013437mg	gbpln	Capsella rubella	AT3G24430.1 | Symbols: HCF101 | ATP binding | chr3:8868731-8872154 REVERSE LENGTH=532	544	532	0	97.8	78.9	82.0
Rsa1.0_00011.1.g694.t1	ref|XP_002869474.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297315310|gb|EFH45733.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	138	139	8.00E-46	100.7	68.1	82.6	expressed protein	gbpln	Arabidopsis lyrata	AT4G28775.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:14214817-14215233 FORWARD LENGTH=138	138	138	8.00E-45	100.0	60.9	72.5
Rsa1.0_00011.1.g695.t1	ref|XP_002869476.1| hypothetical protein ARALYDRAFT_913640 [Arabidopsis lyrata subsp. lyrata] gi|297315312|gb|EFH45735.1| hypothetical protein ARALYDRAFT_913640 [Arabidopsis lyrata subsp. lyrata]	338	328	1.00E-164	97.0	86.1	89.6	hypothetical protein ARALYDRAFT_913640	gbpln	Arabidopsis lyrata	AT4G28740.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3493 (InterPro:IPR021883); BEST Arabidopsis thaliana protein match is: tetratricopeptide repeat (TPR)-containing protein (TAIR:AT1G02910.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:14201051-14202542 FORWARD LENGTH=347	338	347	1.00E-166	102.7	84.3	89.3
Rsa1.0_00011.1.g696.t1	ref|NP_194602.2| glutaredoxin-C5 [Arabidopsis thaliana] gi|75151040|sp|Q8GWS0.1|GRXC5_ARATH RecName: Full=Glutaredoxin-C5, chloroplastic; Short=AtGrxC5; Flags: Precursor gi|26452363|dbj|BAC43267.1| unknown protein [Arabidopsis thaliana] gi|28372898|gb|AAO39931.1| At4g28730 [Arabidopsis thaliana] gi|332660135|gb|AEE85535.1| glutaredoxin-C5 [Arabidopsis thaliana]	184	174	7.00E-67	94.6	79.3	84.8	glutaredoxin-C5	gbpln	Arabidopsis thaliana	AT4G28730.1 | Symbols: | Glutaredoxin family protein | chr4:14199174-14200712 FORWARD LENGTH=174	184	174	2.00E-69	94.6	79.3	84.8
Rsa1.0_00011.1.g697.t1	ref|XP_002869437.1| hypothetical protein ARALYDRAFT_913571 [Arabidopsis lyrata subsp. lyrata] gi|297315273|gb|EFH45696.1| hypothetical protein ARALYDRAFT_913571 [Arabidopsis lyrata subsp. lyrata]	402	394	5.00E-94	98.0	48.3	61.9	hypothetical protein ARALYDRAFT_913571	gbpln	Arabidopsis lyrata	AT5G39560.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:15841885-15843096 REVERSE LENGTH=403	402	403	1.00E-70	100.2	47.5	61.4
Rsa1.0_00011.1.g698.t1	gb|EOA18879.1| hypothetical protein CARUB_v10007502mg [Capsella rubella]	511	506	0	99.0	89.0	95.3	hypothetical protein CARUB_v10007502mg	gbpln	Capsella rubella	AT4G28700.1 | Symbols: AMT1;4 | ammonium transporter 1;4 | chr4:14161681-14163195 FORWARD LENGTH=504	511	504	0	98.6	87.9	95.3

Rsa1.0_00011.1.g699.t1	ref|NP_567814.1| photosystem II reaction center PSB28 protein [Arabidopsis thaliana] gi|75161816|sp|Q8W0Y8.1|PSB28_ARATH RecName: Full=Photosystem II reaction center PSB28 protein, chloroplastic; AltName: Full=Photosystem II protein W-like; Flags: Precursor gi|18087645|gb|AAL58951.1|AF462867_1 AT4g28660/T5F17_110 [Arabidopsis thaliana] gi|21360421|gb|AAM47326.1| AT4g28660/T5F17_110 [Arabidopsis thaliana] gi|21592461|gb|AAM64412.1| photosystem II protein W-like [Arabidopsis thaliana] gi|332660119|gb|AEE85519.1| photosystem II reaction center PSB28 protein [Arabidopsis thaliana]	152	183	7.00E-72	120.4	88.8	92.1	photosystem II reaction center PSB28 protein	gbpln	Arabidopsis thaliana	AT4G28660.1 | Symbols: PSB28 | photosystem II reaction center PSB28 protein | chr4:14150008-14150933 FORWARD LENGTH=183	152	183	2.00E-74	120.4	88.8	92.1
Rsa1.0_00011.1.g700.t2	dbj|BAJ34152.1| unnamed protein product [Thellungiella halophila]	184	246	3.00E-35	133.7	52.2	56.0	unnamed protein product	----	----	AT4G28640.2 | Symbols: IAA11 | indole-3-acetic acid inducible 11 | chr4:14142288-14143928 FORWARD LENGTH=302	184	302	3.00E-33	164.1	48.9	51.1
Rsa1.0_00011.1.g701.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00011.1.g702.t1	ref|XP_002869492.1| hypothetical protein ARALYDRAFT_491906 [Arabidopsis lyrata subsp. lyrata] gi|297315328|gb|EFH45751.1| hypothetical protein ARALYDRAFT_491906 [Arabidopsis lyrata subsp. lyrata]	748	748	0	100.0	82.4	89.8	hypothetical protein ARALYDRAFT_491906	gbpln	Arabidopsis lyrata	AT4G28570.1 | Symbols: | Long-chain fatty alcohol dehydrogenase family protein | chr4:14119548-14121923 FORWARD LENGTH=748	748	748	0	100.0	82.1	88.9
Rsa1.0_00012.1.g703.t1	gb|AAP74222.1| RST1 [Arabidopsis thaliana]	291	1841	4.00E-44	632.6	34.4	38.1	RST1	gbpln	Arabidopsis thaliana	AT3G27670.1 | Symbols: RST1 | ARM repeat superfamily protein | chr3:10245338-10253158 FORWARD LENGTH=1841	291	1841	1.00E-46	632.6	34.4	38.1
Rsa1.0_00012.1.g704.t1	gb|EOA35360.1| hypothetical protein CARUB_v10020554mg [Capsella rubella]	304	353	1.00E-118	116.1	73.0	83.6	hypothetical protein CARUB_v10020554mg	gbpln	Capsella rubella	AT1G69523.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:26129827-26131157 FORWARD LENGTH=300	304	300	1.00E-109	98.7	65.5	79.6
Rsa1.0_00012.1.g705.t1	gb|EOA35360.1| hypothetical protein CARUB_v10020554mg [Capsella rubella]	289	353	1.00E-91	122.1	67.8	80.3	hypothetical protein CARUB_v10020554mg	gbpln	Capsella rubella	AT1G69523.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:26129827-26131157 FORWARD LENGTH=300	289	300	4.00E-85	103.8	59.2	74.0
Rsa1.0_00012.1.g706.t9	ref|XP_002871663.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317500|gb|EFH47922.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	568	593	0	104.4	73.1	83.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G15380.1 | Symbols: DRM1 | domains rearranged methylase 1 | chr5:4991347-4994826 FORWARD LENGTH=624	568	624	0	109.9	71.3	82.2
Rsa1.0_00012.1.g707.t1	gb|AFI56994.1| NAC2, partial [Brassica napus]	269	244	1.00E-134	90.7	86.2	87.4	NAC2, partial	gbpln	Brassica napus	AT1G69490.1 | Symbols: NAP, ANAC029, ATNAP | NAC-like, activated by AP3/PI | chr1:26122233-26123222 FORWARD LENGTH=268	269	268	1.00E-131	99.6	84.0	89.6
Rsa1.0_00012.1.g708.t1	ref|XP_002887236.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333077|gb|EFH63495.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	342	348	1.00E-156	101.8	81.3	86.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G69430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26650.1); Has 216 Blast hits to 215 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 216; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26098025-26099077 FORWARD LENGTH=350	342	350	1.00E-152	102.3	81.6	86.3
Rsa1.0_00012.1.g709.t1	ref|NP_177107.2| phosphate transporter PHO1-10 [Arabidopsis thaliana] gi|75127834|sp|Q6R8G0.1|PHO1A_ARATH RecName: Full=Phosphate transporter PHO1 homolog 10; AltName: Full=Protein PHO1 homolog 10; Short=AtPHO1;H10 gi|41079301|gb|AAR99492.1| PHO1-like protein [Arabidopsis thaliana] gi|332196809|gb|AEE34930.1| phosphate transporter PHO1-10 [Arabidopsis thaliana]	756	777	0	102.8	85.4	91.3	phosphate transporter PHO1-10	gbpln	Arabidopsis thaliana	AT1G69480.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr1:26114187-26117479 REVERSE LENGTH=777	756	777	0	102.8	85.4	91.3

Rsa1.0_00012.1.g710.t1	ref|NP_177105.2| emp24/gp25L/p24 family/GOLD domain-containing protein [Arabidopsis thaliana] gi|75304433|sp|Q8VY92.1|P24DA_ARATH RecName: Full=Transmembrane emp24 domain-containing protein p24delta10; AltName: Full=p24 family protein delta10; Short=p24delta10; AltName: Full=p24 family protein delta2d; Short=p24delta2d; Flags: Precursor gi|18252235|gb|AAL61950.1| unknown protein [Arabidopsis thaliana] gi|21387027|gb|AAM47917.1| unknown protein [Arabidopsis thaliana] gi|332196807|gb|AEE34928.1| emp24/gp25L/p24 family/GOLD domain-containing protein [Arabidopsis thaliana]	216	214	1.00E-105	99.1	83.3	94.0	emp24/gp25L/p24 family/GOLD domain-containing protein	gbpln	Arabidopsis thaliana	AT1G69460.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:26112054-26113160 REVERSE LENGTH=214	216	214	1.00E-108	99.1	83.3	94.0
Rsa1.0_00012.1.g711.t1	gb|EOA33694.1| hypothetical protein CARUB_v10019875mg [Capsella rubella]	720	709	0	98.5	87.4	92.8	hypothetical protein CARUB_v10019875mg	gbpln	Capsella rubella	AT1G69450.2 | Symbols: | Early-responsive to dehydration stress protein (ERD4) | chr1:26107120-26110006 REVERSE LENGTH=711	720	711	0	98.8	86.3	91.9
Rsa1.0_00012.1.g712.t1	ref|NP_177101.2| putative S-acyltransferase [Arabidopsis thaliana] gi|42572047|ref|NP_974114.1| putative S-acyltransferase [Arabidopsis thaliana] gi|223635846|sp|Q9C533.2|ZDHC1_ARATH RecName: Full=Probable S-acyltransferase At1g69420; AltName: Full=Probable palmitoyltransferase At1g69420; AltName: Full=Zinc finger DHHC domain-containing protein At1g69420 gi|332196801|gb|AEE34922.1| putative S-acyltransferase [Arabidopsis thaliana] gi|332196802|gb|AEE34923.1| putative S-acyltransferase [Arabidopsis thaliana]	597	596	0	99.8	89.6	94.5	putative S-acyltransferase	gbpln	Arabidopsis thaliana	AT1G69420.1 | Symbols: | DHHC-type zinc finger family protein | chr1:26093690-26096736 FORWARD LENGTH=596	597	596	0	99.8	89.6	94.5
Rsa1.0_00012.1.g713.t3	ref|NP_177100.1| translation initiation factor eIF-5A [Arabidopsis thaliana] gi|20138712|sp|Q9C505.1|IF5A3_ARATH RecName: Full=Eukaryotic translation initiation factor 5A-3; Short=eIF-5A-3 gi|12325087|gb|AAG52496.1|AC018364_14 putative eukaryotic initiation factor 5A (eIF-5A); 7607-6714 [Arabidopsis thaliana] gi|12597798|gb|AAG60110.1|AC073178_21 Eukaryotic initiation factor 5A , putative [Arabidopsis thaliana] gi|21592652|gb|AAM64601.1| initiation factor 5A-3 (eIF-5A 3) [Arabidopsis thaliana] gi|332196800|gb|AEE34921.1| translation initiation factor eIF-5A [Arabidopsis thaliana]	161	158	2.00E-83	98.1	95.0	96.3	translation initiation factor eIF-5A	gbpln	Arabidopsis thaliana	AT1G69410.1 | Symbols: ATELF5A-3, ELF5A-3 | eukaryotic elongation factor 5A-3 | chr1:26089301-26090194 FORWARD LENGTH=158	161	158	8.00E-86	98.1	95.0	96.3
Rsa1.0_00012.1.g714.t1	gb|AAZ23773.1| plastid division regulator MinE [Brassica napus]	210	224	4.00E-93	106.7	88.1	91.9	plastid division regulator MinE	gbpln	Brassica napus	AT1G69390.1 | Symbols: ATMINE1, MINE1, ARC12 | homologue of bacterial MinE 1 | chr1:26084721-26086284 FORWARD LENGTH=229	210	229	2.00E-86	109.0	81.9	89.5
Rsa1.0_00012.1.g715.t1	ref|XP_002888717.1| hypothetical protein ARALYDRAFT_476065 [Arabidopsis lyrata subsp. lyrata] gi|297334558|gb|EFH64976.1| hypothetical protein ARALYDRAFT_476065 [Arabidopsis lyrata subsp. lyrata]	368	373	1.00E-176	101.4	84.5	90.8	hypothetical protein ARALYDRAFT_476065	gbpln	Arabidopsis lyrata	AT1G69380.1 | Symbols: | Protein of unknown function (DUF155) | chr1:26081729-26083431 REVERSE LENGTH=373	368	373	1.00E-177	101.4	83.2	90.8
Rsa1.0_00012.1.g716.t1	gb|EOA35466.1| hypothetical protein CARUB_v10020675mg [Capsella rubella]	311	317	1.00E-155	101.9	88.4	92.6	hypothetical protein CARUB_v10020675mg	gbpln	Capsella rubella	AT1G69370.1 | Symbols: CM3, cm-3 | chorismate mutase 3 | chr1:26080098-26081559 FORWARD LENGTH=316	311	316	1.00E-152	101.6	86.5	91.0
Rsa1.0_00012.1.g717.t1	ref|XP_002888716.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334557|gb|EFH64975.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	851	905	0	106.3	70.0	79.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G69360.1 | Symbols: | Plant protein of unknown function (DUF863) | chr1:26072520-26075420 REVERSE LENGTH=896	851	896	0	105.3	69.2	78.3
Rsa1.0_00012.1.g718.t1	ref|XP_002887230.1| hypothetical protein ARALYDRAFT_476061 [Arabidopsis lyrata subsp. lyrata] gi|297333071|gb|EFH63489.1| hypothetical protein ARALYDRAFT_476061 [Arabidopsis lyrata subsp. lyrata]	788	1347	0	170.9	81.6	90.4	hypothetical protein ARALYDRAFT_476061	gbpln	Arabidopsis lyrata	AT1G69350.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:26069882-26072245 FORWARD LENGTH=787	788	787	0	99.9	80.7	89.5

Rsa1.0_00012.1.g719.t1	ref|XP_002887229.1| appr-1-p processing enzyme family protein [Arabidopsis lyrata subsp. lyrata] gi|297333070|gb|EFH63488.1| appr-1-p processing enzyme family protein [Arabidopsis lyrata subsp. lyrata]	570	562	0	98.6	89.1	91.9	appr-1-p processing enzyme family protein	gbpln	Arabidopsis lyrata	AT1G69340.1 | Symbols: | appr-1-p processing enzyme family protein | chr1:26066298-26069644 FORWARD LENGTH=562	570	562	0	98.6	88.6	91.6
Rsa1.0_00012.1.g720.t1	ref|XP_002888715.1| hypothetical protein ARALYDRAFT_476060 [Arabidopsis lyrata subsp. lyrata] gi|297334556|gb|EFH64974.1| hypothetical protein ARALYDRAFT_476060 [Arabidopsis lyrata subsp. lyrata]	266	264	1.00E-91	99.2	68.8	76.7	hypothetical protein ARALYDRAFT_476060	gbpln	Arabidopsis lyrata	AT1G69330.1 | Symbols: | RING/U-box superfamily protein | chr1:26064138-26064950 REVERSE LENGTH=270	266	270	1.00E-91	101.5	67.7	76.7
Rsa1.0_00012.1.g721.t1	gb|EOA35903.1| hypothetical protein CARUB_v10021160mg, partial [Capsella rubella]	143	121	3.00E-34	84.6	54.5	65.7	hypothetical protein CARUB_v10021160mg, partial	gbpln	Capsella rubella	AT1G69325.1 | Symbols: | Remorin family protein | chr1:26063205-26063736 FORWARD LENGTH=120	143	120	2.00E-30	83.9	51.0	59.4
Rsa1.0_00012.1.g722.t1	ref|NP_564958.2| protein CLAVATA3/ESR-related 10 [Arabidopsis thaliana] gi|75339321|sp|Q4PSX1.1|CLE10_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 10; Contains: RecName: Full=CLE10p; Flags: Precursor gi|67633494|gb|AAY78671.1| putative CLE10 [Arabidopsis thaliana] gi|332196789|gb|AEE34910.1| protein CLAVATA3/ESR-related 10 [Arabidopsis thaliana]	107	107	9.00E-37	100.0	76.6	86.9	protein CLAVATA3/ESR-related 10	gbpln	Arabidopsis thaliana	AT1G69320.1 | Symbols: CLE10 | CLAVATA3/ESR-RELATED 10 | chr1:26061925-26062248 FORWARD LENGTH=107	107	107	1.00E-39	100.0	76.6	86.9
Rsa1.0_00012.1.g723.t1	ref|XP_002888714.1| hypothetical protein ARALYDRAFT_476056 [Arabidopsis lyrata subsp. lyrata] gi|297334555|gb|EFH64973.1| hypothetical protein ARALYDRAFT_476056 [Arabidopsis lyrata subsp. lyrata]	296	285	1.00E-105	96.3	75.0	83.1	hypothetical protein ARALYDRAFT_476056	gbpln	Arabidopsis lyrata	AT1G69310.2 | Symbols: WRKY57, ATWRKY57 | WRKY DNA-binding protein 57 | chr1:26056118-26057909 REVERSE LENGTH=287	296	287	1.00E-105	97.0	76.7	83.1
Rsa1.0_00012.1.g724.t1	gb|EOA33837.1| hypothetical protein CARUB_v10021318mg, partial [Capsella rubella]	280	290	3.00E-32	103.6	25.7	38.6	hypothetical protein CARUB_v10021318mg, partial	gbpln	Capsella rubella	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	280	332	2.00E-28	118.6	21.4	32.9
Rsa1.0_00012.1.g725.t1	gb|EOA35673.1| hypothetical protein CARUB_v10020897mg [Capsella rubella]	281	228	1.00E-62	81.1	62.6	70.8	hypothetical protein CARUB_v10020897mg	gbpln	Capsella rubella	AT1G69295.1 | Symbols: PDCB4 | plasmodesmata callose-binding protein 4 | chr1:26050492-26051843 REVERSE LENGTH=222	281	222	2.00E-47	79.0	30.6	33.8
Rsa1.0_00012.1.g726.t3	ref|XP_002888712.1| hypothetical protein ARALYDRAFT_339164 [Arabidopsis lyrata subsp. lyrata] gi|297334553|gb|EFH64971.1| hypothetical protein ARALYDRAFT_339164 [Arabidopsis lyrata subsp. lyrata]	490	1042	4.00E-75	212.7	35.7	40.8	hypothetical protein ARALYDRAFT_339164	gbpln	Arabidopsis lyrata	AT1G69280.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03630.1); Has 885 Blast hits to 474 proteins in 40 species: Archae - 0; Bacteria - 4; Metazoa - 731; Fungi - 9; Plants - 68; Viruses - 0; Other Eukaryotes - 73 (source: NCBI BLink). | chr1:26045290-26046670 REVERSE LENGTH=400	490	400	2.00E-75	81.6	35.1	40.6
Rsa1.0_00012.1.g727.t1	ref|NP_564956.1| Ninja-family protein AFP1 [Arabidopsis thaliana] gi|75180099|sp|Q9LQ98.1|AFP1_ARATH RecName: Full=Ninja-family protein AFP1; AltName: Full=ABI five-binding protein 1; Short=ABI5-binding protein 1 gi|6730641|gb|AAF27062.1|AC008262_11 F4N2.22 [Arabidopsis thaliana] gi|22531038|gb|AAM97023.1| expressed protein [Arabidopsis thaliana] gi|23197982|gb|AAN15518.1| expressed protein [Arabidopsis thaliana] gi|332196782|gb|AEE34903.1| Ninja-family protein AFP1 [Arabidopsis thaliana]	336	345	1.00E-108	102.7	70.5	78.0	Ninja-family protein AFP1	gbpln	Arabidopsis thaliana	AT1G69260.1 | Symbols: AFP1 | ABI five binding protein | chr1:26039314-26040570 FORWARD LENGTH=345	336	345	1.00E-110	102.7	70.5	78.0
Rsa1.0_00012.1.g728.t1	ref|XP_002887226.1| hypothetical protein ARALYDRAFT_894705 [Arabidopsis lyrata subsp. lyrata] gi|297333067|gb|EFH63485.1| hypothetical protein ARALYDRAFT_894705 [Arabidopsis lyrata subsp. lyrata]	442	446	1.00E-104	100.9	52.5	67.4	hypothetical protein ARALYDRAFT_894705	gbpln	Arabidopsis lyrata	AT1G69250.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr1:26033163-26035301 FORWARD LENGTH=427	442	427	8.00E-99	96.6	48.0	63.8
Rsa1.0_00012.1.g729.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00012.1.g730.t1	gb|EOA18595.1| hypothetical protein CARUB_v10007167mg [Capsella rubella]	62	763	1.00E-13	1230.6	58.1	62.9	hypothetical protein CARUB_v10007167mg	gbpln	Capsella rubella	AT4G15430.2 | Symbols: | ERD (early-responsive to dehydration stress) family protein | chr4:8828214-8831354 FORWARD LENGTH=760	62	760	2.00E-16	1225.8	58.1	62.9

Rsa1.0_00012.1.g731.t1	ref|XP_002511619.1| conserved hypothetical protein [Ricinus communis] gi|223548799|gb|EEF50288.1| conserved hypothetical protein [Ricinus communis]	127	276	2.00E-15	217.3	38.6	50.4	conserved hypothetical protein	gbpln	Ricinus communis	#	#	#	#	#	#	#
Rsa1.0_00012.1.g732.t2	ref|XP_002887225.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333066|gb|EFH63484.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	604	612	0	101.3	82.8	88.1	pfkB-type carbohydrate kinase family protein	gbpln	Arabidopsis lyrata	AT1G69200.1 | Symbols: FLN2 | fructokinase-like 2 | chr1:26016018-26018365 FORWARD LENGTH=616	604	616	0	102.0	81.6	88.4
Rsa1.0_00012.1.g733.t3	gb|AAZ23116.1| transcription factor CRC [Brassica juncea] gi|482569951|gb|EOA34139.1| hypothetical protein CARUB_v10021641mg [Capsella rubella]	171	179	2.00E-87	104.7	95.9	97.7	transcription factor CRC	gbpln	Brassica juncea	AT1G69180.1 | Symbols: CRC | Plant-specific transcription factor YABBY family protein | chr1:26007734-26008940 REVERSE LENGTH=181	171	181	4.00E-82	105.8	95.9	97.7
Rsa1.0_00012.1.g734.t1	gb|ACG60678.1| unknown protein [Brassica oleracea var. alboglabra]	325	327	1.00E-101	100.6	70.8	77.5	unknown protein	gbpln	Brassica oleracea	AT1G69170.1 | Symbols: | Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein | chr1:26005626-26007041 FORWARD LENGTH=405	325	405	1.00E-102	124.6	70.8	81.5
Rsa1.0_00012.1.g735.t1	gb|ACG60677.1| hypothetical protein BoB028L01.120 [Brassica oleracea var. alboglabra]	324	322	1.00E-152	99.4	93.8	96.3	hypothetical protein BoB028L01.120	gbpln	Brassica oleracea	AT1G69160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13980.1); Has 173 Blast hits to 172 proteins in 54 species: Archae - 0; Bacteria - 0; Metazoa - 25; Fungi - 33; Plants - 84; Viruses - 2; Other Eukaryotes - 29 (source: NCBI BLink). | chr1:26000315-26001280 FORWARD LENGTH=321	324	321	1.00E-111	99.1	77.2	83.6
Rsa1.0_00012.1.g736.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00012.1.g737.t1	sp|P0DI14.1|AP1_BRARP RecName: Full=Floral homeotic protein APETALA 1; Short=BcpAP1; AltName: Full=Agamous-like MADS-box protein AP1	255	256	1.00E-139	100.4	97.3	99.6	RecName: Full=Floral homeotic protein APETALA 1; Short=BcpAP1; AltName: Full=Agamous-like MADS-box protein AP1	----	----	AT1G69120.1 | Symbols: AP1, AGL7 | K-box region and MADS-box transcription factor family protein | chr1:25982576-25986102 REVERSE LENGTH=256	255	256	1.00E-126	100.4	93.3	98.0
Rsa1.0_00013.1.g738.t1	ref|XP_002879065.1| aldehyde oxidase [Arabidopsis lyrata subsp. lyrata] gi|297324904|gb|EFH55324.1| aldehyde oxidase [Arabidopsis lyrata subsp. lyrata]	1328	1320	0	99.4	81.9	88.9	aldehyde oxidase	gbpln	Arabidopsis lyrata	AT2G27150.2 | Symbols: AAO3, At-AO3, AOdelta, AtAAO3 | abscisic aldehyde oxidase 3 | chr2:11601952-11607014 FORWARD LENGTH=1332	1328	1332	0	100.3	82.0	89.1
Rsa1.0_00013.1.g739.t1	ref|NP_190471.1| FBD-associated F-box protein [Arabidopsis thaliana] gi|75337428|sp|Q9SMT9.1|FBD9_ARATH RecName: Full=FBD-associated F-box protein At3g49020 gi|6522564|emb|CAB62008.1| putative protein [Arabidopsis thaliana] gi|67633680|gb|AAY78764.1| F-box family protein [Arabidopsis thaliana] gi|111074508|gb|ABH04627.1| At3g49020 [Arabidopsis thaliana] gi|332644966|gb|AEE78487.1| FBD-associated F-box protein [Arabidopsis thaliana]	386	447	1.00E-118	115.8	63.5	74.4	FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT3G49020.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr3:18169079-18170660 FORWARD LENGTH=447	386	447	1.00E-120	115.8	63.5	74.4
Rsa1.0_00013.1.g740.t1	ref|XP_002875956.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297321794|gb|EFH52215.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	611	448	1.00E-137	73.3	45.2	52.0	F-box family protein	gbpln	Arabidopsis lyrata	AT3G49020.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr3:18169079-18170660 FORWARD LENGTH=447	611	447	1.00E-135	73.2	44.5	53.4
Rsa1.0_00013.1.g741.t1	gb|EOA27572.1| hypothetical protein CARUB_v10023709mg, partial [Capsella rubella]	249	304	1.00E-142	122.1	98.8	99.6	hypothetical protein CARUB_v10023709mg, partial	gbpln	Capsella rubella	AT2G27020.1 | Symbols: PAG1 | 20S proteasome alpha subunit G1 | chr2:11528515-11530858 REVERSE LENGTH=249	249	249	1.00E-145	100.0	99.2	99.6
Rsa1.0_00013.1.g742.t1	ref|NP_850095.2| CBL-interacting serine/threonine-protein kinase 3 [Arabidopsis thaliana] gi|330252823|gb|AEC07917.1| CBL-interacting serine/threonine-protein kinase 3 [Arabidopsis thaliana]	440	451	0	102.5	95.9	97.7	CBL-interacting serine/threonine-protein kinase 3	gbpln	Arabidopsis thaliana	AT2G26980.4 | Symbols: CIPK3 | CBL-interacting protein kinase 3 | chr2:11515234-11518426 REVERSE LENGTH=451	440	451	0	102.5	95.9	97.7

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<tr><td>Rsa1.0_00013.1.g743.t1</td><td>ref|NP_180259.1| ABC transporter G family member 32 [Arabidopsis thaliana] gi|75318727|sp|O81016.1|AB32G_ARATH RecName: Full=ABC transporter G family member 32; Short=ABC transporter ABCG.32; Short=AtABCG32; AltName: Full=Probable pleiotropic drug resistance protein 4 gi|3426037|gb|AAC32236.1| putative ABC transporter [Arabidopsis thaliana] gi|28144347|tpg|DAA00872.1| TPA_exp: PDR4 ABC transporter [Arabidopsis thaliana] gi|330252812|gb|AEC07906.1| ABC transporter G family member 32 [Arabidopsis thaliana]</td><td>1420</td><td>1420</td><td>0</td><td>100.0</td><td>93.0</td><td>97.3</td><td>ABC transporter G family member 32</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G26910.1 | Symbols: PDR4, ATPDR4 | pleiotropic drug resistance 4 | chr2:11481623–11487874 FORWARD LENGTH=1420</td><td>1420</td><td>1420</td><td>0</td><td>100.0</td><td>93.0</td><td>97.3</td></tr>
<tr><td>Rsa1.0_00013.1.g744.t1</td><td>ref|XP_002880842.1| phosphoesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297326681|gb|EFH57101.1| phosphoesterase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>519</td><td>514</td><td>0</td><td>99.0</td><td>87.5</td><td>92.9</td><td>phosphoesterase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G26870.1 | Symbols: NPC2 | non–specific phospholipase C2 | chr2:11457117–11459355 REVERSE LENGTH=514</td><td>519</td><td>514</td><td>0</td><td>99.0</td><td>87.1</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00013.1.g745.t1</td><td>ref|NP_180238.2| protein pinoid2 [Arabidopsis thaliana] gi|75253187|sp|Q64FQ2.1|PID2_ARATH RecName: Full=Protein kinase PINOID 2; AltName: Full=Protein kinase AGC1–10 gi|51944867|gb|AAU14162.1| AGC1–10 [Arabidopsis thaliana] gi|51944869|gb|AAU14163.1| AGC1–10 [Arabidopsis thaliana] gi|330252783|gb|AEC07877.1| protein kinase PINOID 2 [Arabidopsis thaliana]</td><td>525</td><td>525</td><td>0</td><td>100.0</td><td>89.5</td><td>94.1</td><td>protein pinoid2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G26700.1 | Symbols: PID2 | AGC (cAMP–dependent, cGMP–dependent and protein kinase C) kinase family protein | chr2:11368613–11370951 FORWARD LENGTH=525</td><td>525</td><td>525</td><td>0</td><td>100.0</td><td>89.5</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00013.1.g746.t1</td><td>ref|XP_002892763.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338605|gb|EFH69022.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>150</td><td>804</td><td>3.00E–21</td><td>536.0</td><td>46.0</td><td>52.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G13630.2 | Symbols: | Tetratricopeptide repeat (TPR)–like superfamily protein | chr1:4670178–4672826 REVERSE LENGTH=798</td><td>150</td><td>798</td><td>3.00E–20</td><td>532.0</td><td>29.3</td><td>34.0</td></tr>
<tr><td>Rsa1.0_00013.1.g747.t1</td><td>ref|NP_180241.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|75219509|sp|O48788.1|Y2267_ARATH RecName: Full=Probable inactive receptor kinase At2g26730; Flags: Precursor gi|2760839|gb|AAB95307.1| putative receptor–like protein kinase [Arabidopsis thaliana] gi|60543329|gb|AAX22262.1| At2g26730 [Arabidopsis thaliana] gi|224589527|gb|ACN59297.1| leucine–rich repeat receptor–like protein kinase [Arabidopsis thaliana] gi|330252786|gb|AEC07880.1| putative inactive receptor kinase [Arabidopsis thaliana]</td><td>818</td><td>658</td><td>0</td><td>80.4</td><td>69.8</td><td>73.5</td><td>putative inactive receptor kinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G26730.1 | Symbols: | Leucine–rich repeat protein kinase family protein | chr2:11388621–11391286 FORWARD LENGTH=658</td><td>818</td><td>658</td><td>0</td><td>80.4</td><td>69.8</td><td>73.5</td></tr>
<tr><td>Rsa1.0_00013.1.g748.t1</td><td>ref|NP_180217.1| WD40 domain–containing protein [Arabidopsis thaliana] gi|2739374|gb|AAC14498.1| En/Spm–like transposon protein [Arabidopsis thaliana] gi|50253512|gb|AAT71958.1| At2g26490 [Arabidopsis thaliana] gi|53850519|gb|AAU95436.1| At2g26490 [Arabidopsis thaliana] gi|330252750|gb|AEC07844.1| WD40 domain–containing protein [Arabidopsis thaliana]</td><td>453</td><td>465</td><td>0</td><td>102.6</td><td>90.3</td><td>94.7</td><td>WD40 domain–containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G26490.1 | Symbols: | Transducin/WD40 repeat–like superfamily protein | chr2:11268035–11269432 FORWARD LENGTH=465</td><td>453</td><td>465</td><td>0</td><td>102.6</td><td>90.3</td><td>94.7</td></tr>
<tr><td>Rsa1.0_00013.1.g749.t1</td><td>emb|CAD30841.1| soluble epoxide hydrolase [Brassica napus]</td><td>318</td><td>318</td><td>1.00E–176</td><td>100.0</td><td>92.8</td><td>97.2</td><td>soluble epoxide hydrolase</td><td>gbpln</td><td>Brassica napus</td><td>AT2G26740.1 | Symbols: ATSEH, SEH | soluble epoxide hydrolase | chr2:11393148–11394257 REVERSE LENGTH=321</td><td>318</td><td>321</td><td>1.00E–154</td><td>100.9</td><td>83.6</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00013.1.g750.t1</td><td>ref|XP_002878977.1| hypothetical protein ARALYDRAFT_481517 [Arabidopsis lyrata subsp. lyrata] gi|297324816|gb|EFH55236.1| hypothetical protein ARALYDRAFT_481517 [Arabidopsis lyrata subsp. lyrata]</td><td>695</td><td>794</td><td>0</td><td>114.2</td><td>75.5</td><td>81.3</td><td>hypothetical protein ARALYDRAFT_481517</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G26570.1 | Symbols: WEB1 | Plant protein of unknown function (DUF827) | chr2:11299565–11302076 FORWARD LENGTH=807</td><td>695</td><td>807</td><td>0</td><td>116.1</td><td>75.1</td><td>82.4</td></tr>
<tr><td>Rsa1.0_00013.1.g751.t1</td><td>gb|ABV89757.1| purple acid phosphatase 12 protein family isoform 7 [Brassica napus] gi|157849936|gb|ABV89759.1| purple acid phosphatase 12 protein family isoform 7 [Brassica napus]</td><td>471</td><td>469</td><td>0</td><td>99.6</td><td>93.0</td><td>97.0</td><td>purple acid phosphatase 12 protein family isoform 7</td><td>gbpln</td><td>Brassica napus</td><td>AT2G27190.1 | Symbols: PAP1, ATPAP1, PAP12, ATPAP12 | purple acid phosphatase 12 | chr2:11621400–11623438 REVERSE LENGTH=469</td><td>471</td><td>469</td><td>0</td><td>99.6</td><td>87.3</td><td>91.3</td></tr>
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<tr><td>Rsa1.0_00013.1.g752.t1</td><td>gb|EOA27281.1| hypothetical protein CARUB_v10023399mg [Capsella rubella]</td><td>382</td><td>388</td><td>1.00E-162</td><td>101.6</td><td>78.5</td><td>85.3</td><td>hypothetical protein CARUB_v10023399mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G26360.1 | Symbols: | Mitochondrial substrate carrier family protein | chr2:11221603-11223160 REVERSE LENGTH=387</td><td>382</td><td>387</td><td>1.00E-157</td><td>101.3</td><td>75.9</td><td>83.0</td></tr>
<tr><td>Rsa1.0_00013.1.g753.t1</td><td>ref|NP_180199.3| chalcone-flavanone isomerase-like protein [Arabidopsis thaliana]
gi|487524115|sp|Q84RK2.2|FAP2_ARATH RecName: Full=Fatty-acid-binding protein 2; Short=AtFAP2; AltName: Full=Chalcone-flavanone isomerase family protein 2
gi|61742610|gb|AAX55126.1| hypothetical protein At2g26310 [Arabidopsis thaliana]
gi|330252727|gb|AEC07821.1| chalcone-flavanone isomerase-like protein [Arabidopsis thaliana]</td><td>381</td><td>398</td><td>1.00E-154</td><td>104.5</td><td>74.8</td><td>83.5</td><td>chalcone-flavanone isomerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G26310.1 | Symbols: | Chalcone-flavanone isomerase family protein | chr2:11201770-11203919 FORWARD LENGTH=398</td><td>381</td><td>398</td><td>1.00E-156</td><td>104.5</td><td>74.8</td><td>83.5</td></tr>
<tr><td>Rsa1.0_00013.1.g754.t1</td><td>ref|NP_180197.1| root-specific kinase 1 [Arabidopsis thaliana]
gi|3075390|gb|AAC14522.1| putative protein kinase [Arabidopsis thaliana]
gi|330252725|gb|AEC07819.1| root-specific kinase 1 [Arabidopsis thaliana]</td><td>424</td><td>424</td><td>0</td><td>100.0</td><td>87.5</td><td>94.3</td><td>root-specific kinase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G26290.1 | Symbols: ARSK1 | root-specific kinase 1 | chr2:11192237-11194259 REVERSE LENGTH=424</td><td>424</td><td>424</td><td>0</td><td>100.0</td><td>87.5</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00013.1.g755.t1</td><td>ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana]
gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR
gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana]
gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]</td><td>406</td><td>387</td><td>3.00E-90</td><td>95.3</td><td>47.8</td><td>61.1</td><td>F-box protein DOR</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387</td><td>406</td><td>387</td><td>8.00E-93</td><td>95.3</td><td>47.8</td><td>61.1</td></tr>
<tr><td>Rsa1.0_00013.1.g756.t1</td><td>gb|EOA26805.1| hypothetical protein CARUB_v10022901mg [Capsella rubella]
gi|482562617|gb|EOA26807.1| hypothetical protein CARUB_v10022901mg [Capsella rubella]
gi|482562618|gb|EOA26808.1| hypothetical protein CARUB_v10022901mg [Capsella rubella]</td><td>447</td><td>574</td><td>1.00E-167</td><td>128.4</td><td>78.1</td><td>85.5</td><td>hypothetical protein CARUB_v10022901mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G26280.1 | Symbols: CID7 | CTC-interacting domain 7 | chr2:11188143-11190579 REVERSE LENGTH=567</td><td>447</td><td>567</td><td>1.00E-149</td><td>126.8</td><td>63.1</td><td>69.6</td></tr>
<tr><td>Rsa1.0_00013.1.g757.t1</td><td>gb|EOA26905.1| hypothetical protein CARUB_v10022994mg [Capsella rubella]</td><td>519</td><td>525</td><td>0</td><td>101.2</td><td>82.1</td><td>87.5</td><td>hypothetical protein CARUB_v10022994mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G26270.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: BRCT domain-containing DNA repair protein (TAIR:AT3G43930.1); Has 29 Blast hits to 29 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:11184739-11187659 FORWARD LENGTH=470</td><td>519</td><td>470</td><td>0</td><td>90.6</td><td>68.4</td><td>74.4</td></tr>
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Rsa1.0_00013.1.g758.t1	ref|NP_180193.1| 3-ketoacyl-CoA synthase 10 [Arabidopsis thaliana] gi|114149941|sp|Q570B4.2|KCS10_ARATH RecName: Full=3-ketoacyl-CoA synthase 10; Short=KCS-10; AltName: Full=Protein FIDDLEHEAD; AltName: Full=Very long-chain fatty acid condensing enzyme 10; Short=VLCFA condensing enzyme 10 gi|8177699|gb|AAF73973.1|AF214490_1 fiddlehead protein [Arabidopsis thaliana] gi|12597467|gb|AAG60062.1|AF337910_1 putative beta-ketoacyl-CoA synthase FIDDLEHEAD [Arabidopsis thaliana] gi|3075394|gb|AAC14526.1| beta-ketoacyl-CoA synthase (FIDDLEHEAD) [Arabidopsis thaliana] gi|3559809|emb|CAA09311.1| fiddlehead protein [Arabidopsis thaliana] gi|14517456|gb|AAK62618.1| At2g26250/T1D16.11 [Arabidopsis thaliana] gi|23506207|gb|AAN31115.1| At2g26250/T1D16.11 [Arabidopsis thaliana] gi|26983882|gb|AAN86193.1| putative beta-ketoacyl-CoA synthase FIDDLEHEAD [Arabidopsis thaliana] gi|330252719|gb|AEC07813.1| 3-ketoacyl-CoA synthase 10 [Arabidopsis thaliana]	550	550	0	100.0	95.3	97.3	3-ketoacyl-CoA synthase 10	gbpln	Arabidopsis thaliana	AT2G26250.1 | Symbols: FDH, KCS10 | 3-ketoacyl-CoA synthase 10 | chr2:11170799-11173059 REVERSE LENGTH=550	550	550	0	100.0	95.3	97.3
Rsa1.0_00013.1.g759.t1	ref|NP_850076.1| Ankyrin repeat family protein [Arabidopsis thaliana] gi|17644149|gb|AAL38772.1| unknown protein [Arabidopsis thaliana] gi|20465459|gb|AAM20189.1| unknown protein [Arabidopsis thaliana] gi|330252714|gb|AEC07808.1| Ankyrin repeat family protein [Arabidopsis thaliana]	161	190	3.00E-65	118.0	79.5	88.8	Ankyrin repeat family protein	gbpln	Arabidopsis thaliana	AT2G26210.1 | Symbols: | Ankyrin repeat family protein | chr2:11157654-11159016 FORWARD LENGTH=190	161	190	1.00E-67	118.0	79.5	88.8
Rsa1.0_00013.1.g760.t1	ref|NP_850075.2| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|20197178|gb|AAC14529.2| hypothetical protein [Arabidopsis thaliana] gi|330252713|gb|AEC07807.1| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana]	532	565	0	106.2	87.2	91.9	S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G26200.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:11152875-11156330 FORWARD LENGTH=565	532	565	0	106.2	87.2	91.9
Rsa1.0_00013.1.g761.t1	ref|NP_565618.1| calmodulin-binding-like protein [Arabidopsis thaliana] gi|16930469|gb|AAL31920.1|AF419588_1 At2g26190/T1D16.17 [Arabidopsis thaliana] gi|3075398|gb|AAC14530.1| expressed protein [Arabidopsis thaliana] gi|20453237|gb|AAM19857.1| At2g26190/T1D16.17 [Arabidopsis thaliana] gi|22135809|gb|AAM91091.1| At2g26190/T1D16.17 [Arabidopsis thaliana] gi|330252712|gb|AEC07806.1| calmodulin-binding-like protein [Arabidopsis thaliana]	531	532	0	100.2	83.6	89.6	calmodulin-binding-like protein	gbpln	Arabidopsis thaliana	AT2G26190.1 | Symbols: | calmodulin-binding family protein | chr2:11147901-11150082 REVERSE LENGTH=532	531	532	0	100.2	83.6	89.6
Rsa1.0_00013.1.g762.t1	ref|NP_001078039.1| uncharacterized protein [Arabidopsis thaliana] gi|330254959|gb|AEC10053.1| uncharacterized protein AT2G41945 [Arabidopsis thaliana]	123	166	2.00E-23	135.0	61.8	69.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G41945.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G04040.1); Has 57 Blast hits to 57 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17509933-17512898 REVERSE LENGTH=166	123	166	3.00E-26	135.0	61.8	69.1
Rsa1.0_00013.1.g763.t1	ref|XP_002880762.1| IQ-domain 6 [Arabidopsis lyrata subsp. lyrata] gi|297326601|gb|EFH57021.1| IQ-domain 6 [Arabidopsis lyrata subsp. lyrata]	396	417	1.00E-158	105.3	85.4	90.9	IQ-domain 6	gbpln	Arabidopsis lyrata	AT2G26180.1 | Symbols: IQD6 | IQ-domain 6 | chr2:11143433-11144982 REVERSE LENGTH=416	396	416	1.00E-157	105.1	83.8	88.6
Rsa1.0_00013.1.g764.t1	dbj|BAJ33733.1| unnamed protein product [Thellungiella halophila]	720	717	0	99.6	93.1	96.3	unnamed protein product	----	----	AT2G26140.1 | Symbols: ftsh4 | FTSH protease 4 | chr2:11131939-11135126 REVERSE LENGTH=717	720	717	0	99.6	88.9	93.5

Rsa1.0_00013.1.g765.t2	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1511	1501	0	99.3	32.0	40.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1511	1262	1.00E-142	83.5	16.5	23.8
Rsa1.0_00013.1.g766.t1	ref|XP_002324769.1| predicted protein [Populus trichocarpa] gi|118482835|gb|ABK93333.1| unknown [Populus trichocarpa] gi|118486784|gb|ABK95227.1| unknown [Populus trichocarpa] gi|222866203|gb|EEF03334.1| predicted protein [Populus trichocarpa]	289	276	3.00E-60	95.5	48.4	65.7	predicted protein	gbpln	Populus trichocarpa	AT5G11890.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (TAIR:AT1G17620.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3831770-3832633 FORWARD LENGTH=287	289	287	3.00E-50	99.3	43.9	58.5
Rsa1.0_00013.1.g767.t1	gb|AAF79479.1|AC022492_23 F1L3.27 [Arabidopsis thaliana]	300	201	5.00E-71	67.0	49.3	55.0	F1L3.27	gbpln	Arabidopsis thaliana	AT1G17560.1 | Symbols: HLL | Ribosomal protein L14p/L23e family protein | chr1:6037635-6038574 REVERSE LENGTH=196	300	196	6.00E-73	65.3	49.0	54.7
Rsa1.0_00013.1.g768.t1	ref|XP_002880742.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297326581|gb|EFH57001.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	366	367	1.00E-175	100.3	87.7	94.0	galactosyltransferase family protein	gbpln	Arabidopsis lyrata	AT2G26100.1 | Symbols: | Galactosyltransferase family protein | chr2:11116212-11118129 REVERSE LENGTH=371	366	371	1.00E-172	101.4	86.3	93.2
Rsa1.0_00013.1.g769.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00013.1.g770.t1	ref|XP_002880729.1| hypothetical protein ARALYDRAFT_481452 [Arabidopsis lyrata subsp. lyrata] gi|297326568|gb|EFH56988.1| hypothetical protein ARALYDRAFT_481452 [Arabidopsis lyrata subsp. lyrata]	711	634	1.00E-126	89.2	35.7	37.4	hypothetical protein ARALYDRAFT_481452	gbpln	Arabidopsis lyrata	AT2G25970.1 | Symbols: | KH domain-containing protein | chr2:11071844-11075604 REVERSE LENGTH=632	711	632	1.00E-125	88.9	35.7	37.7
Rsa1.0_00013.1.g771.t1	ref|NP_565614.1| uncharacterized protein [Arabidopsis thaliana] gi|20197269|gb|AAC31240.2| expressed protein [Arabidopsis thaliana] gi|20197367|gb|AAM15044.1| expressed protein [Arabidopsis thaliana] gi|21593506|gb|AAM65473.1| unknown [Arabidopsis thaliana] gi|29028814|gb|AAO64786.1| At2g25950 [Arabidopsis thaliana] gi|110742984|dbj|BAE99386.1| hypothetical protein [Arabidopsis thaliana] gi|330252682|gb|AEC07776.1| uncharacterized protein AT2G25950 [Arabidopsis thaliana]	224	204	1.00E-99	91.1	82.1	84.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G25950.1 | Symbols: | Protein of unknown function (DUF1000) | chr2:11068735-11070524 FORWARD LENGTH=204	224	204	1.00E-102	91.1	82.1	84.8
Rsa1.0_00013.1.g772.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1956	1142	0	58.4	28.3	37.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1956	575	1.00E-91	29.4	9.7	15.3
Rsa1.0_00013.1.g773.t1	gb|EOA34405.1| hypothetical protein CARUB_v10021933mg [Capsella rubella]	657	566	0	86.1	51.8	60.3	hypothetical protein CARUB_v10021933mg	gbpln	Capsella rubella	AT1G65630.1 | Symbols: DegP3 | DegP protease 3 | chr1:24406542-24409068 REVERSE LENGTH=559	657	559	0	85.1	51.0	60.9
Rsa1.0_00013.1.g774.t1	ref|XP_002878908.1| hypothetical protein ARALYDRAFT_481449 [Arabidopsis lyrata subsp. lyrata] gi|297324747|gb|EFH55167.1| hypothetical protein ARALYDRAFT_481449 [Arabidopsis lyrata subsp. lyrata]	605	686	1.00E-160	113.4	65.5	74.7	hypothetical protein ARALYDRAFT_481449	gbpln	Arabidopsis lyrata	AT2G25930.1 | Symbols: ELF3, PYK20 | hydroxyproline-rich glycoprotein family protein | chr2:11059459-11063178 FORWARD LENGTH=695	605	695	1.00E-154	114.9	64.8	74.4
Rsa1.0_00013.1.g775.t1	ref|NP_127504.1| ORF I polyprotein [Petunia vein clearing virus] gi|82061579|sp|Q91DM0.1|POLG_PVCV1 RecName: Full=Genome polyprotein; Contains: RecName: Full=Movement protein; Short=MP; Contains: RecName: Full=Capsid protein; Short=CP; Contains: RecName: Full=Aspartic protease; Short=PR; Contains: RecName: Full=Reverse transcriptase; Short=RT gi|14574598|gb|AAK68664.1| ORF I polyprotein [petunia vein clearing virus]	1445	2179	1.00E-137	150.8	16.4	21.9	ORF I polyprotein	gbvrl	Petunia vein	#	#	#	#	#	#	#

Rsa1.0_00013.1.g776.t1	ref|XP_002880724.1| hypothetical protein ARALYDRAFT_481448 [Arabidopsis lyrata subsp. lyrata] gi|297326563|gb|EFH56983.1| hypothetical protein ARALYDRAFT_481448 [Arabidopsis lyrata subsp. lyrata]	333	342	1.00E-178	102.7	91.6	94.9	hypothetical protein ARALYDRAFT_481448	gbpln	Arabidopsis lyrata	AT2G25910.1 | Symbols: | 3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein | chr2:11049379-11051997 REVERSE LENGTH=341	333	341	1.00E-180	102.4	90.1	94.3
Rsa1.0_00013.1.g777.t1	ref|XP_002886495.1| hypothetical protein ARALYDRAFT_315184 [Arabidopsis lyrata subsp. lyrata] gi|297332336|gb|EFH62754.1| hypothetical protein ARALYDRAFT_315184 [Arabidopsis lyrata subsp. lyrata]	644	648	0	100.6	67.7	80.0	hypothetical protein ARALYDRAFT_315184	gbpln	Arabidopsis lyrata	AT2G46450.1 | Symbols: ATCNGC12, CNGC12 | cyclic nucleotide-gated channel 12 | chr2:19065845-19068364 FORWARD LENGTH=649	644	649	0	100.8	67.5	79.2
Rsa1.0_00013.1.g778.t1	ref|XP_002878899.1| hypothetical protein ARALYDRAFT_901265 [Arabidopsis lyrata subsp. lyrata] gi|297324738|gb|EFH55158.1| hypothetical protein ARALYDRAFT_901265 [Arabidopsis lyrata subsp. lyrata]	145	143	6.00E-50	98.6	78.6	85.5	hypothetical protein ARALYDRAFT_901265	gbpln	Arabidopsis lyrata	AT2G25890.1 | Symbols: | Oleosin family protein | chr2:11037435-11037884 FORWARD LENGTH=149	145	149	9.00E-49	102.8	73.8	80.7
Rsa1.0_00013.1.g779.t1	ref|XP_002878897.1| hypothetical protein ARALYDRAFT_901259 [Arabidopsis lyrata subsp. lyrata] gi|297324736|gb|EFH55156.1| hypothetical protein ARALYDRAFT_901259 [Arabidopsis lyrata subsp. lyrata]	608	584	0	96.1	85.7	90.1	hypothetical protein ARALYDRAFT_901259	gbpln	Arabidopsis lyrata	AT2G25870.1 | Symbols: | haloacid dehalogenase-like hydrolase family protein | chr2:11031159-11034302 FORWARD LENGTH=584	608	584	0	96.1	84.2	89.8
Rsa1.0_00013.1.g780.t1	ref|NP_187216.1| receptor like protein 32 [Arabidopsis thaliana] gi|6714445|gb|AAF26132.1|AC011620_8 putative disease resistance protein [Arabidopsis thaliana] gi|332640751|gb|AEE74272.1| receptor like protein 32 [Arabidopsis thaliana]	883	868	0	98.3	72.5	80.3	receptor like protein 32	gbpln	Arabidopsis thaliana	AT3G05650.1 | Symbols: AtRLP32, RLP32 | receptor like protein 32 | chr3:1645884-1648490 REVERSE LENGTH=868	883	868	0	98.3	72.5	80.3
Rsa1.0_00013.1.g781.t1	ref|XP_002878896.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324735|gb|EFH55155.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	180	411	1.00E-50	228.3	51.1	56.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G25840.1 | Symbols: OVA4 | Nucleotidylyl transferase superfamily protein | chr2:11021924-11025158 FORWARD LENGTH=408	180	408	1.00E-50	226.7	48.3	55.6
Rsa1.0_00013.1.g782.t1	ref|NP_175150.1| F-box protein [Arabidopsis thaliana] gi|75268184|sp|Q9C627.1|FB36_ARATH RecName: Full=Putative F-box protein At1g46984 gi|12321006|gb|AAG50624.1|AC083835_9 hypothetical protein [Arabidopsis thaliana] gi|332194012|gb|AEE32133.1| F-box protein [Arabidopsis thaliana]	378	370	5.00E-84	97.9	45.2	61.9	F-box protein	gbpln	Arabidopsis thaliana	AT1G46984.1 | Symbols: | F-box family protein | chr1:17274722-17275834 FORWARD LENGTH=370	378	370	1.00E-86	97.9	45.2	61.9
Rsa1.0_00013.1.g783.t1	ref|XP_002883380.1| hypothetical protein ARALYDRAFT_479795 [Arabidopsis lyrata subsp. lyrata] gi|297329220|gb|EFH59639.1| hypothetical protein ARALYDRAFT_479795 [Arabidopsis lyrata subsp. lyrata]	74	214	2.00E-23	289.2	73.0	79.7	hypothetical protein ARALYDRAFT_479795	gbpln	Arabidopsis lyrata	AT3G22845.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr3:8087373-8088550 FORWARD LENGTH=214	74	214	4.00E-26	289.2	73.0	79.7
Rsa1.0_00013.1.g784.t4	ref|NP_565611.1| poly(A) polymerase 2 [Arabidopsis thaliana] gi|31747891|gb|AAF66438.2|AF255297_1 nuclear poly(A) polymerase [Arabidopsis thaliana] gi|14532700|gb|AAK64151.1| putative poly(A) polymerase [Arabidopsis thaliana] gi|18491197|gb|AAL69501.1| putative poly(A) polymerase [Arabidopsis thaliana] gi|20197361|gb|AAC42245.2| putative poly(A) polymerase [Arabidopsis thaliana] gi|330252667|gb|AEC07761.1| poly(A) polymerase 2 [Arabidopsis thaliana]	801	800	0	99.9	77.4	84.3	poly(A) polymerase 2	gbpln	Arabidopsis thaliana	AT2G25850.2 | Symbols: PAPS2 | poly(A) polymerase 2 | chr2:11026123-11030440 REVERSE LENGTH=800	801	800	0	99.9	77.4	84.3
Rsa1.0_00013.1.g785.t1	ref|NP_565610.1| YebC-related protein [Arabidopsis thaliana] gi|22096384|sp|O82314.2|U082_ARATH RecName: Full=Probable transcriptional regulatory protein At2g25830 gi|20197365|gb|AAC42247.2| expressed protein [Arabidopsis thaliana] gi|330252663|gb|AEC07757.1| probable transcriptional regulatory protein [Arabidopsis thaliana]	330	331	1.00E-147	100.3	86.4	92.7	YebC-related protein	gbpln	Arabidopsis thaliana	AT2G25830.1 | Symbols: | YebC-related | chr2:11019091-11021665 REVERSE LENGTH=331	330	331	1.00E-150	100.3	86.4	92.7

Rsa1.0_00013.1.g786.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00013.1.g787.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00014.1.g788.t1	gb|EOA35551.1| hypothetical protein CARUB_v10020757mg [Capsella rubella]	271	280	2.00E-54	103.3	52.8	62.7	hypothetical protein CARUB_v10020757mg	gbpln	Capsella rubella	AT1G75360.1 | Symbols: | unknown protein; Has 74 Blast hits to 71 proteins in 15 species: Archae - 0; Bacteria - 4; Metazoa - 4; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr1:28275084-28275956 FORWARD LENGTH=290	271	290	3.00E-45	107.0	49.1	58.7
Rsa1.0_00014.1.g789.t1	ref|XP_002887591.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297333432|gb|EFH63850.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	416	173	4.00E-27	41.6	18.3	21.6	bZIP transcription factor family protein	gbpln	Arabidopsis lyrata	AT1G75390.1 | Symbols: AtbZIP44, bZIP44 | basic leucine-zipper 44 | chr1:28292224-28292745 FORWARD LENGTH=173	416	173	3.00E-29	41.6	17.8	21.2
Rsa1.0_00014.1.g790.t1	gb|EOA33370.1| hypothetical protein CARUB_v10020274mg [Capsella rubella] gi|482569183|gb|EOA33371.1| hypothetical protein CARUB_v10020274mg [Capsella rubella]	479	456	1.00E-180	95.2	77.9	82.7	hypothetical protein CARUB_v10020274mg	gbpln	Capsella rubella	AT1G75400.1 | Symbols: | RING/U-box superfamily protein | chr1:28297609-28299464 FORWARD LENGTH=455	479	455	0	95.0	78.7	82.7
Rsa1.0_00014.1.g791.t1	ref|NP_973745.1| beta glucosidase 11 [Arabidopsis thaliana] gi|332189360|gb|AEE27481.1| beta glucosidase 11 [Arabidopsis thaliana]	149	473	2.00E-25	317.4	41.6	49.0	beta glucosidase 11	gbpln	Arabidopsis thaliana	AT1G02850.3 | Symbols: BGLU11 | beta glucosidase 11 | chr1:630569-633085 FORWARD LENGTH=473	149	473	5.00E-28	317.4	41.6	49.0
Rsa1.0_00014.1.g792.t1	ref|NP_173217.1| PEP1 receptor 2 [Arabidopsis thaliana] gi|75334548|sp|Q9FZ59.1|PEPR2_ARATH RecName: Full=Leucine-rich repeat receptor-like protein kinase PEPR2; AltName: Full=Elicitor peptide 1 receptor 2; Short=PEP1 receptor 2; Flags: Precursor gi|9802748|gb|AAF99817.1|AC034257_9 Unknown protein [Arabidopsis thaliana] gi|224589394|gb|ACN59231.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332191511|gb|AEE29632.1| PEP1 receptor 2 [Arabidopsis thaliana]	92	1088	2.00E-24	1182.6	67.4	78.3	PEP1 receptor 2	gbpln	Arabidopsis thaliana	AT1G17750.1 | Symbols: PEPR2, AtPEPR2 | PEP1 receptor 2 | chr1:6106656-6110008 FORWARD LENGTH=1088	92	1088	3.00E-27	1182.6	67.4	78.3
Rsa1.0_00014.1.g793.t1	ref|NP_177674.1| BEL1-like homeodomain 3 [Arabidopsis thaliana] gi|145327251|ref|NP_001077827.1| BEL1-like homeodomain 3 [Arabidopsis thaliana] gi|75263117|sp|Q9FWS9.1|BLH3_ARATH RecName: Full=BEL1-like homeodomain protein 3; Short=BEL1-like protein 3 gi|10120440|gb|AAG13065.1|AC023754_3 Similar to homeodomain proteins [Arabidopsis thaliana] gi|13877515|gb|AAK43835.1|AF353093_1 BEL1-like homeodomain 3 [Arabidopsis thaliana] gi|21553417|gb|AAM62510.1| homeodomain protein BELL1, putative [Arabidopsis thaliana] gi|47059794|gb|AAT09418.1| BEL1-like homeodomain 3 protein [Arabidopsis thaliana] gi|332197595|gb|AEE35716.1| BEL1-like homeodomain 3 [Arabidopsis thaliana] gi|332197596|gb|AEE35717.1| BEL1-like homeodomain 3 [Arabidopsis thaliana]	505	524	0	103.8	80.8	86.9	BEL1-like homeodomain 3	gbpln	Arabidopsis thaliana	AT1G75410.2 | Symbols: BLH3 | BEL1-like homeodomain 3 | chr1:28300095-28301890 REVERSE LENGTH=524	505	524	0	103.8	80.8	86.9
Rsa1.0_00014.1.g794.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	101	1311	9.00E-13	1298.0	41.6	53.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	101	170	6.00E-12	168.3	35.6	49.5
Rsa1.0_00014.1.g795.t1	gb|ADA60976.1| short internode related sequence 5 [Brassica rapa subsp. pekinensis]	336	345	1.00E-159	102.7	93.2	96.1	short internode related sequence 5	gbpln	Brassica rapa	AT1G75520.1 | Symbols: SRS5 | SHI-related sequence 5 | chr1:28351779-28353179 REVERSE LENGTH=346	336	346	1.00E-156	103.0	86.0	89.9
Rsa1.0_00014.1.g796.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	927	1274	0	137.4	49.3	65.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	927	575	7.00E-59	62.0	17.8	27.3

Rsa1.0_00014.1.g797.t1	ref|NP_177685.1| Forkhead-associated (FHA) domain-containing protein [Arabidopsis thaliana] gi|332197609|gb|AEE35730.1| Forkhead-associated (FHA) domain-containing protein [Arabidopsis thaliana]	548	555	2.33E-156	101.3	58.0	69.7	Forkhead-associated (FHA) domain-containing protein	gbpln	Arabidopsis thaliana	AT1G75530.1 | Symbols: | Forkhead-associated (FHA) domain-containing protein | chr1:28359309-28361815 FORWARD LENGTH=555	548	555	1.00E-149	101.3	58.0	69.7
Rsa1.0_00014.1.g798.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	1748	1333	0	76.3	35.4	46.2	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1748	575	3.00E-97	32.9	11.0	17.0
Rsa1.0_00014.1.g799.t1	ref|NP_177686.1| putative salt tolerance-like protein [Arabidopsis thaliana] gi|17433066|sp|Q9LQZ7.1|STHX_ARATH RecName: Full=Probable salt tolerance-like protein At1g75540 gi|9369377|gb|AAF87126.1|AC006434_22 F10A5.24 [Arabidopsis thaliana] gi|225898084|dbj|BAH30374.1| hypothetical protein [Arabidopsis thaliana] gi|332197610|gb|AEE35731.1| putative salt tolerance-like protein [Arabidopsis thaliana]	319	331	1.00E-134	103.8	82.8	89.3	putative salt tolerance-like protein	gbpln	Arabidopsis thaliana	AT1G75540.1 | Symbols: STH2 | salt tolerance homolog2 | chr1:28366059-28367398 FORWARD LENGTH=331	319	331	1.00E-137	103.8	82.8	89.3
Rsa1.0_00014.1.g800.t1	ref|NP_177687.1| glycine-rich protein [Arabidopsis thaliana] gi|9369369|gb|AAF87118.1|AC006434_14 F10A5.23 [Arabidopsis thaliana] gi|332197611|gb|AEE35732.1| glycine-rich protein [Arabidopsis thaliana]	165	167	4.00E-44	101.2	85.5	90.9	glycine-rich protein	gbpln	Arabidopsis thaliana	AT1G75550.1 | Symbols: | glycine-rich protein | chr1:28369437-28369940 REVERSE LENGTH=167	165	167	1.00E-46	101.2	85.5	90.9
Rsa1.0_00014.1.g801.t1	gb|EOA35562.1| hypothetical protein CARUB_v10020768mg, partial [Capsella rubella]	271	278	1.00E-108	102.6	77.5	80.4	hypothetical protein CARUB_v10020768mg, partial	gbpln	Capsella rubella	AT1G75560.2 | Symbols: | zinc knuckle (CCHC-type) family protein | chr1:28371420-28372717 REVERSE LENGTH=257	271	257	1.00E-103	94.8	76.0	78.6
Rsa1.0_00014.1.g802.t1	ref|XP_002887604.1| hypothetical protein ARALYDRAFT_476705 [Arabidopsis lyrata subsp. lyrata] gi|297333445|gb|EFH63863.1| hypothetical protein ARALYDRAFT_476705 [Arabidopsis lyrata subsp. lyrata]	108	108	2.00E-54	100.0	95.4	96.3	hypothetical protein ARALYDRAFT_476705	gbpln	Arabidopsis lyrata	AT1G75580.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:28377530-28377856 FORWARD LENGTH=108	108	108	2.00E-56	100.0	94.4	95.4
Rsa1.0_00014.1.g803.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00014.1.g804.t1	dbj|BAJ34271.1| unnamed protein product [Thellungiella halophila]	147	152	3.00E-61	103.4	86.4	91.2	unnamed protein product	----	----	AT1G75590.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:28383250-28383714 REVERSE LENGTH=154	147	154	5.00E-62	104.8	86.4	92.5
Rsa1.0_00014.1.g805.t1	gb|EOA33194.1| hypothetical protein CARUB_v10021300mg [Capsella rubella]	552	547	0	99.1	78.3	86.8	hypothetical protein CARUB_v10021300mg	gbpln	Capsella rubella	AT1G75620.1 | Symbols: | glyoxal oxidase-related protein | chr1:28394951-28396594 REVERSE LENGTH=547	552	547	0	99.1	77.9	87.1
Rsa1.0_00014.1.g806.t1	ref|XP_002889035.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334876|gb|EFH65294.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	1144	1141	0	99.7	86.1	92.4	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G75640.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr1:28403600-28407022 REVERSE LENGTH=1140	1144	1140	0	99.7	85.2	91.6
Rsa1.0_00014.1.g807.t2	gb|EOA33199.1| hypothetical protein CARUB_v10019710mg [Capsella rubella]	996	1024	0	102.8	83.5	88.5	hypothetical protein CARUB_v10019710mg	gbpln	Capsella rubella	AT1G75660.1 | Symbols: XRN3, AtXRN3 | 5'-3' exoribonuclease 3 | chr1:28408289-28414825 FORWARD LENGTH=1020	996	1020	0	102.4	84.8	89.8
Rsa1.0_00014.1.g808.t1	gb|AAM63477.1| endo-beta-1,4-glucanase, putative [Arabidopsis thaliana]	527	525	0	99.6	84.6	91.1	endo-beta-1,4-glucanase, putative	gbpln	Arabidopsis thaliana	AT1G75680.1 | Symbols: AtGH9B7, GH9B7 | glycosyl hydrolase 9B7 | chr1:28417215-28419231 REVERSE LENGTH=525	527	525	0	99.6	84.6	91.3
Rsa1.0_00014.1.g809.t1	gb|EOA35847.1| hypothetical protein CARUB_v10021088mg [Capsella rubella]	159	155	5.00E-75	97.5	88.1	93.7	hypothetical protein CARUB_v10021088mg	gbpln	Capsella rubella	AT1G75690.1 | Symbols: | DnaJ/Hsp40 cysteine-rich domain superfamily protein | chr1:28422273-28423170 REVERSE LENGTH=154	159	154	2.00E-76	96.9	89.9	93.1
Rsa1.0_00014.1.g810.t1	ref|NP_177699.4| HVA22-like protein G [Arabidopsis thaliana] gi|334302815|sp|Q9LR09.2|HA22G_ARATH RecName: Full=Putative HVA22-like protein g; Short=AtHVA22g gi|332197626|gb|AEE35747.1| HVA22-like protein G [Arabidopsis thaliana]	187	177	1.00E-81	94.7	75.9	84.5	HVA22-like protein G	gbpln	Arabidopsis thaliana	AT1G75700.1 | Symbols: HVA22G | HVA22-like protein G | chr1:28423956-28424931 FORWARD LENGTH=177	187	177	4.00E-84	94.7	75.9	84.5
Rsa1.0_00014.1.g811.t1	ref|XP_002887608.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297333449|gb|EFH63867.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	456	461	0	101.1	87.3	90.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G75710.1 | Symbols: | C2H2-like zinc finger protein | chr1:28428806-28431128 FORWARD LENGTH=462	456	462	0	101.3	85.3	88.4

<table>
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<tr><td>Rsa1.0_00014.1.g813.t1</td><td>ref|XP_002889039.1| hypothetical protein ARALYDRAFT_316499 [Arabidopsis lyrata subsp. lyrata] gi|297334880|gb|EFH65298.1| hypothetical protein ARALYDRAFT_316499 [Arabidopsis lyrata subsp. lyrata]</td><td>227</td><td>202</td><td>6.00E-65</td><td>89.0</td><td>63.9</td><td>70.5</td><td>hypothetical protein ARALYDRAFT_316499</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G75720.2 | Symbols: | Plant protein of unknown function (DUF827) | chr1:28434648-28435321 REVERSE LENGTH=193</td><td>227</td><td>193</td><td>5.00E-66</td><td>85.0</td><td>65.6</td><td>71.4</td></tr>
<tr><td>Rsa1.0_00014.1.g814.t1</td><td>dbj|BAD42907.1| hypothetical protein [Arabidopsis thaliana]</td><td>507</td><td>589</td><td>2.33E-156</td><td>116.2</td><td>69.0</td><td>78.3</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G75730.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages. | chr1:28435991-28438983 REVERSE LENGTH=589</td><td>507</td><td>589</td><td>1.00E-148</td><td>116.2</td><td>69.0</td><td>78.3</td></tr>
<tr><td>Rsa1.0_00014.1.g815.t1</td><td>ref|NP_565116.1| gibberellin-regulated protein 1 [Arabidopsis thaliana] gi|21431770|sp|P46689.2|GASA1_ARATH RecName: Full=Gibberellin-regulated protein 1; AltName: Full=GAST1 protein homolog 1; Flags: Precursor gi|18087524|gb|AAL58896.1|AF462801_1 At1g75750/F10A5_16 [Arabidopsis thaliana] gi|332197633|gb|AEE35754.1| gibberellin-regulated protein 1 [Arabidopsis thaliana]</td><td>98</td><td>98</td><td>6.00E-34</td><td>100.0</td><td>88.8</td><td>91.8</td><td>gibberellin-regulated protein 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G75750.1 | Symbols: GASA1 | GAST1 protein homolog 1 | chr1:28441813-28442284 REVERSE LENGTH=98</td><td>98</td><td>98</td><td>1.00E-36</td><td>100.0</td><td>88.8</td><td>91.8</td></tr>
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<tr><td>Rsa1.0_00014.1.g818.t1</td><td>ref|XP_002873500.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319337|gb|EFH49759.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>887</td><td>959</td><td>0</td><td>108.1</td><td>69.9</td><td>77.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G11210.1 | Symbols: ATGLR2.5, GLR2.5 | glutamate receptor 2.5 | chr5:3571214-3574537 REVERSE LENGTH=829</td><td>887</td><td>829</td><td>0</td><td>93.5</td><td>67.0</td><td>75.6</td></tr>
<tr><td>Rsa1.0_00014.1.g819.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00014.1.g820.t1</td><td>ref|XP_002887610.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333451|gb|EFH63869.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>239</td><td>236</td><td>2.00E-55</td><td>98.7</td><td>58.2</td><td>69.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G75770.1 | Symbols: | unknown protein; Has 6 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:28450022-28450971 FORWARD LENGTH=230</td><td>239</td><td>230</td><td>5.00E-54</td><td>96.2</td><td>56.9</td><td>67.8</td></tr>
<tr><td>Rsa1.0_00014.1.g821.t1</td><td>dbj|BAJ33829.1| unnamed protein product [Thellungiella halophila]</td><td>447</td><td>447</td><td>0</td><td>100.0</td><td>99.6</td><td>99.8</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G75780.1 | Symbols: TUB1 | tubulin beta-1 chain | chr1:28451378-28453602 REVERSE LENGTH=447</td><td>447</td><td>447</td><td>0</td><td>100.0</td><td>98.4</td><td>99.6</td></tr>
<tr><td>Rsa1.0_00014.1.g822.t1</td><td>gb|ABV89616.1| pathogenesis-related thaumatin family protein [Brassica rapa] gi|157849670|gb|ABV89618.1| pathogenesis-related thaumatin family protein [Brassica rapa]</td><td>325</td><td>321</td><td>1.00E-155</td><td>98.8</td><td>84.3</td><td>87.4</td><td>pathogenesis-related thaumatin family protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G75800.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:28458889-28460447 FORWARD LENGTH=330</td><td>325</td><td>330</td><td>1.00E-153</td><td>101.5</td><td>86.2</td><td>89.8</td></tr>
<tr><td>Rsa1.0_00014.1.g823.t1</td><td>gb|ADD64789.1| CLAVATA1 [Brassica napus]</td><td>980</td><td>987</td><td>0</td><td>100.7</td><td>94.9</td><td>97.2</td><td>CLAVATA1</td><td>gbpln</td><td>Brassica napus</td><td>AT1G75820.1 | Symbols: CLV1, FAS3, FLO5, ATCLV1 | Leucine-rich receptor-like protein kinase family protein | chr1:28463631-28466652 REVERSE LENGTH=980</td><td>980</td><td>980</td><td>0</td><td>100.0</td><td>87.2</td><td>93.1</td></tr>
<tr><td>Rsa1.0_00014.1.g824.t1</td><td>sp|O24331.1|DEF4_RAPSA RecName: Full=Defensin-like protein 4; AltName: Full=Cysteine-rich antifungal protein 4; Short=AFP4; Flags: Precursor gi|1655683|emb|CAA65983.1| antifungal protein 4 [Raphanus sativus]</td><td>80</td><td>80</td><td>7.00E-40</td><td>100.0</td><td>100.0</td><td>100.0</td><td>RecName: Full=Defensin-like protein 4; AltName: Full=Cysteine-rich antifungal protein 4; Short=AFP4; Flags: Precursor gi|1655683|emb|CAA65983.1| antifungal protein 4</td><td>gbpln</td><td>Raphanus sativus</td><td>AT5G44420.1 | Symbols: PDF1.2, PDF1.2A, LCR77 | plant defensin 1.2 | chr5:17907216-17907550 REVERSE LENGTH=80</td><td>80</td><td>80</td><td>7.00E-37</td><td>100.0</td><td>83.8</td><td>92.5</td></tr>
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Rsa1.0_00014.1.g825.t1	emb|CAN68319.1| hypothetical protein VITISV_032191 [Vitis vinifera]	178	312	4.00E-13	175.3	19.1	21.3	hypothetical protein VITISV_032191	gbpln	Vitis vinifera	AT2G18510.1 | Symbols: emb2444 | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:8031554-8033517 REVERSE LENGTH=363	178	363	2.00E-14	203.9	18.5	20.2
Rsa1.0_00014.1.g826.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00014.1.g827.t1	sp|O24332.1|DEF3_RAPSA RecName: Full=Defensin-like protein 3; AltName: Full=Cysteine-rich antifungal protein 3; Short=AFP3; Flags: Precursor gi|1655685|emb|CAA65984.1| antifungal protein 3 [Raphanus sativus]	79	79	2.00E-38	100.0	100.0	100.0	RecName: Full=Defensin-like protein 3; AltName: Full=Cysteine-rich antifungal protein 3; Short=AFP3; Flags: Precursor gi|1655685|emb|CAA65984.1| antifungal protein 3	gbpln	Raphanus sativus	AT5G44420.1 | Symbols: PDF1.2, PDF1.2A, LCR77 | plant defensin 1.2 | chr5:17907216-17907550 REVERSE LENGTH=80	79	80	5.00E-34	101.3	83.5	93.7
Rsa1.0_00014.1.g828.t1	sp|P69241.1|DEF1_RAPSA RecName: Full=Defensin-like protein 1; AltName: Full=Cysteine-rich antifungal protein 1; Short=AFP1; Flags: Precursor gi|609322|gb|AAA69541.1| antifungal protein 1 preprotein [Raphanus sativus] gi|115529964|gb|ABJ09663.1| antifungal rafp1 [Raphanus sativus]	80	80	7.00E-38	100.0	95.0	97.5	RecName: Full=Defensin-like protein 1; AltName: Full=Cysteine-rich antifungal protein 1; Short=AFP1; Flags: Precursor gi|609322|gb|AAA69541.1| antifungal protein 1 preprotein	gbpln	Raphanus sativus	AT5G44420.1 | Symbols: PDF1.2, PDF1.2A, LCR77 | plant defensin 1.2 | chr5:17907216-17907550 REVERSE LENGTH=80	80	80	5.00E-38	100.0	87.5	96.3
Rsa1.0_00014.1.g829.t1	sp|P69241.1|DEF1_RAPSA RecName: Full=Defensin-like protein 1; AltName: Full=Cysteine-rich antifungal protein 1; Short=AFP1; Flags: Precursor gi|609322|gb|AAA69541.1| antifungal protein 1 preprotein [Raphanus sativus] gi|115529964|gb|ABJ09663.1| antifungal rafp1 [Raphanus sativus]	83	80	5.00E-28	96.4	75.9	81.9	RecName: Full=Defensin-like protein 1; AltName: Full=Cysteine-rich antifungal protein 1; Short=AFP1; Flags: Precursor gi|609322|gb|AAA69541.1| antifungal protein 1 preprotein	gbpln	Raphanus sativus	AT5G44420.1 | Symbols: PDF1.2, PDF1.2A, LCR77 | plant defensin 1.2 | chr5:17907216-17907550 REVERSE LENGTH=80	83	80	4.00E-27	96.4	66.3	77.1
Rsa1.0_00014.1.g830.t1	pdb|2NTY|C Chain C, Rop4-Gdp-Prone8 gi|126031217|pdb|2NTY|D Chain D, Rop4-Gdp-Prone8	196	180	1.00E-101	91.8	90.3	91.8	Chain C, Rop4-Gdp-Prone8 gi|126031217|pdb|2NTY|D Chain D, Rop4-Gdp-Prone8	----	----	AT1G75840.1 | Symbols: ARAC5, ATGP3, ROP4, ATROP4 | RAC-like GTP binding protein 5 | chr1:28475964-28477377 FORWARD LENGTH=196	196	196	1.00E-102	100.0	95.9	98.0
Rsa1.0_00014.1.g831.t1	ref|XP_002889047.1| hypothetical protein ARALYDRAFT_895460 [Arabidopsis lyrata subsp. lyrata] gi|297334888|gb|EFH65306.1| hypothetical protein ARALYDRAFT_895460 [Arabidopsis lyrata subsp. lyrata]	1106	791	0	71.5	68.1	69.9	hypothetical protein ARALYDRAFT_895460	gbpln	Arabidopsis lyrata	AT1G75850.1 | Symbols: VPS35B | VPS35 homolog B | chr1:28478053-28483874 REVERSE LENGTH=790	1106	790	0	71.4	68.0	69.8
Rsa1.0_00014.1.g832.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00014.1.g833.t1	ref|NP_974149.1| GDSL esterase/lipase EXL1 [Arabidopsis thaliana] gi|28393626|gb|AAO42232.1| putative family II extracellular lipase 1 (EXL1) [Arabidopsis thaliana] gi|28827430|gb|AAO50559.1| putative family II extracellular lipase 1 (EXL1) [Arabidopsis thaliana] gi|332197648|gb|AEE35769.1| GDSL esterase/lipase EXL1 [Arabidopsis thaliana]	340	374	1.00E-173	110.0	84.7	93.5	GDSL esterase/lipase EXL1	gbpln	Arabidopsis thaliana	AT1G75880.2 | Symbols: | SGNH hydrolase-type esterase superfamily protein | chr1:28490564-28492298 FORWARD LENGTH=374	340	374	1.00E-175	110.0	84.7	93.5
Rsa1.0_00014.1.g834.t1	ref|XP_002887618.1| T4O12.12 [Arabidopsis lyrata subsp. lyrata] gi|297333459|gb|EFH63877.1| T4O12.12 [Arabidopsis lyrata subsp. lyrata]	346	673	1.00E-173	194.5	84.4	89.9	T4O12.12	gbpln	Arabidopsis lyrata	AT1G75890.2 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:28493051-28495047 FORWARD LENGTH=366	346	366	1.00E-174	105.8	82.9	91.0
Rsa1.0_00015.1.g835.t1	gb|ABV89658.1| UVB-resistance protein UVR8 [Brassica rapa]	151	537	5.00E-31	355.6	71.5	76.8	UVB-resistance protein UVR8	gbpln	Brassica rapa	AT1G19880.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr1:6900648-6903818 REVERSE LENGTH=538	151	538	2.00E-29	356.3	62.9	72.8
Rsa1.0_00015.1.g836.t1	ref|XP_002893079.1| hypothetical protein ARALYDRAFT_472215 [Arabidopsis lyrata subsp. lyrata] gi|297338921|gb|EFH69338.1| hypothetical protein ARALYDRAFT_472215 [Arabidopsis lyrata subsp. lyrata]	548	549	0	100.2	83.2	90.7	hypothetical protein ARALYDRAFT_472215	gbpln	Arabidopsis lyrata	AT1G19900.1 | Symbols: | glyoxal oxidase-related protein | chr1:6907038-6908684 REVERSE LENGTH=548	548	548	0	100.0	81.0	89.8
Rsa1.0_00015.1.g837.t1	gb|ABV89658.1| UVB-resistance protein UVR8 [Brassica rapa]	535	537	0	100.4	87.9	93.1	UVB-resistance protein UVR8	gbpln	Brassica rapa	AT1G19880.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr1:6900648-6903818 REVERSE LENGTH=538	535	538	0	100.6	84.7	91.6

Rsa1.0_00015.1.g838.t1	ref|XP_002893077.1| protein IQ-DOMAIN 32 [Arabidopsis lyrata subsp. lyrata] gi|297338919|gb|EFH69336.1| protein IQ-DOMAIN 32 [Arabidopsis lyrata subsp. lyrata]	766	792	0	103.4	73.8	81.9	protein IQ-DOMAIN 32	gbpln	Arabidopsis lyrata	AT1G19870.1 | Symbols: iqd32 | IQ-domain 32 | chr1:6895400-6898539 REVERSE LENGTH=794	766	794	0	103.7	72.8	81.2
Rsa1.0_00015.1.g839.t2	ref|XP_002893076.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297338918|gb|EFH69335.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	448	411	1.00E-164	91.7	71.7	79.5	zinc finger (CCCH-type) family protein	gbpln	Arabidopsis lyrata	AT1G19860.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:6891654-6894400 REVERSE LENGTH=413	448	413	1.00E-164	92.2	71.0	79.9
Rsa1.0_00015.1.g840.t1	dbj|BAJ34343.1| unnamed protein product [Thellungiella halophila]	819	901	0	110.0	89.3	93.8	unnamed protein product	----	----	AT1G19850.1 | Symbols: MP, ARF5, IAA24 | Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related | chr1:6887353-6891182 FORWARD LENGTH=902	819	902	0	110.1	87.3	92.8
Rsa1.0_00015.1.g841.t1	gb|EOA18064.1| hypothetical protein CARUB_v10006510mg, partial [Capsella rubella]	92	555	5.00E-16	603.3	48.9	69.6	hypothetical protein CARUB_v10006510mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	92	566	1.00E-11	615.2	34.8	63.0
Rsa1.0_00015.1.g842.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	217	478	1.00E-47	220.3	44.7	65.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	217	746	3.00E-29	343.8	33.2	47.5
Rsa1.0_00015.1.g843.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	997	1274	0	127.8	56.0	71.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	997	575	3.00E-61	57.7	15.4	25.8
Rsa1.0_00015.1.g844.t1	sp|Q9SBK6.1|JMT_BRARP RecName: Full=Jasmonate O-methyltransferase; AltName: Full=Floral nectary-specific protein 1; AltName: Full=S-adenosyl-L-methionine;jasmonic acid carboxyl methyltransferase gi|6651395|gb|AAF22289.1|AF179222_1 floral nectary-specific protein [Brassica rapa subsp. pekinensis]	230	392	1.00E-113	170.4	85.7	91.7	RecName: Full=Jasmonate O-methyltransferase; AltName: Full=Floral nectary-specific protein 1; AltName: Full=S-adenosyl-L-methionine;jasmonic acid carboxyl methyltransferase gi|6651395|gb|AAF22289.1|AF179222_1 floral nectary-specific protein	gbpln	Brassica rapa	AT1G19640.1 | Symbols: JMT | jasmonic acid carboxyl methyltransferase | chr1:6789166-6791708 REVERSE LENGTH=389	230	389	1.00E-105	169.1	80.0	88.3
Rsa1.0_00015.1.g845.t1	gb|EOA38300.1| hypothetical protein CARUB_v10009793mg [Capsella rubella]	312	315	1.00E-40	101.0	42.6	57.1	hypothetical protein CARUB_v10009793mg	gbpln	Capsella rubella	AT1G19620.1 | Symbols: | unknown protein; Has 44 Blast hits to 24 proteins in 12 species: Archae - 0; Bacteria - 8; Metazoa - 22; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr1:6784020-6785075 FORWARD LENGTH=317	312	317	7.00E-28	101.6	34.9	44.9
Rsa1.0_00015.1.g846.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	768	1231	0	160.3	46.9	64.2	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	768	575	5.00E-98	74.9	24.9	38.7
Rsa1.0_00015.1.g847.t1	dbj|BAJ33664.1| unnamed protein product [Thellungiella halophila]	358	355	0	99.2	89.9	94.4	unnamed protein product	----	----	AT1G19600.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr1:6779085-6780898 FORWARD LENGTH=355	358	355	0	99.2	89.4	93.3
Rsa1.0_00015.1.g848.t1	ref|XP_002890347.1| F18O14.34 [Arabidopsis lyrata subsp. lyrata] gi|297336189|gb|EFH66606.1| F18O14.34 [Arabidopsis lyrata subsp. lyrata]	138	299	9.00E-24	216.7	46.4	55.8	F18O14.34	gbpln	Arabidopsis lyrata	AT1G19580.1 | Symbols: GAMMA CA1 | gamma carbonic anhydrase 1 | chr1:6774937-6777092 FORWARD LENGTH=275	138	275	1.00E-24	199.3	44.9	54.3
Rsa1.0_00015.1.g849.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00015.1.g850.t1	ref|XP_002893054.1| hypothetical protein ARALYDRAFT_472181 [Arabidopsis lyrata subsp. lyrata] gi|297338896|gb|EFH69313.1| hypothetical protein ARALYDRAFT_472181 [Arabidopsis lyrata subsp. lyrata]	213	213	1.00E-99	100.0	85.0	90.6	hypothetical protein ARALYDRAFT_472181	gbpln	Arabidopsis lyrata	AT1G19570.1 | Symbols: DHAR1, ATDHAR1, DHAR5 | dehydroascorbate reductase | chr1:6773462-6774413 REVERSE LENGTH=213	213	213	1.00E-101	100.0	84.5	90.1
Rsa1.0_00015.1.g851.t7	ref|XP_002890346.1| hypothetical protein ARALYDRAFT_472180 [Arabidopsis lyrata subsp. lyrata] gi|297336188|gb|EFH66605.1| hypothetical protein ARALYDRAFT_472180 [Arabidopsis lyrata subsp. lyrata]	597	308	1.00E-142	51.6	41.5	46.4	hypothetical protein ARALYDRAFT_472180	gbpln	Arabidopsis lyrata	AT1G19540.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr1:6765713-6767247 FORWARD LENGTH=310	597	310	1.00E-142	51.9	41.0	46.6

Rsa1.0_00015.1.g852.t1	gb|EOA38689.1| hypothetical protein CARUB_v10010689mg [Capsella rubella]	110	116	4.00E-49	105.5	88.2	92.7	hypothetical protein CARUB_v10010689mg	gbpln	Capsella rubella	AT1G19530.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation, anaerobic respiration; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf apex, inflorescence meristem, hypocotyl, root, flower; EXPRESSED DURING: petal differentiation and expansion stage; Has 47 Blast hits to 47 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6763976-6764686 FORWARD LENGTH=117	110	117	6.00E-42	106.4	80.9	89.1
Rsa1.0_00015.1.g853.t1	ref|NP_564088.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|8778424|gb|AAF79432.1|AC025808_14 F18O14.27 [Arabidopsis thaliana] gi|332191742|gb|AEE29863.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	717	725	0	101.1	78.7	87.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G19520.1 | Symbols: NFD5 | pentatricopeptide (PPR) repeat-containing protein | chr1:6760032-6762581 FORWARD LENGTH=725	717	725	0	101.1	78.7	87.6
Rsa1.0_00015.1.g854.t1	ref|NP_564087.2| RAD-like 5 protein [Arabidopsis thaliana] gi|75328898|sp|Q8GW75.1|RADL5_ARATH RecName: Full=Protein RADIALIS-like 5; Short=AtRL5; Short=Protein RAD-like 5; AltName: Full=Protein RADIALIS-LIKE SANT/MYB 4; Short=Protein RSM4 gi|26453068|dbj|BAC43610.1| putative myb-related protein [Arabidopsis thaliana] gi|28973505|gb|AAO64077.1| putative myb family transcription factor [Arabidopsis thaliana] gi|41618974|gb|AAS09994.1| MYB transcription factor [Arabidopsis thaliana] gi|87133605|gb|ABD24443.1| RAD-like protein 5 [Arabidopsis thaliana] gi|332191741|gb|AEE29862.1| protein RADIALIS-like 5 [Arabidopsis thaliana]	90	100	2.00E-36	111.1	81.1	85.6	RAD-like 5 protein	gbpln	Arabidopsis thaliana	AT1G19510.1 | Symbols: ATRL5, RSM4, RL5 | RAD-like 5 | chr1:6756483-6757290 REVERSE LENGTH=100	90	100	4.00E-39	111.1	81.1	85.6
Rsa1.0_00015.1.g855.t1	gb|EOA36128.1| hypothetical protein CARUB_v10012246mg, partial [Capsella rubella]	90	88	1.00E-23	97.8	64.4	74.4	hypothetical protein CARUB_v10012246mg, partial	gbpln	Capsella rubella	AT1G19500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35765.1); Has 9 Blast hits to 9 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 9; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6754952-6755536 REVERSE LENGTH=80	90	80	1.00E-24	88.9	63.3	72.2
Rsa1.0_00015.1.g856.t1	ref|XP_002893053.1| hypothetical protein ARALYDRAFT_312884 [Arabidopsis lyrata subsp. lyrata] gi|297338895|gb|EFH69312.1| hypothetical protein ARALYDRAFT_312884 [Arabidopsis lyrata subsp. lyrata]	466	647	1.00E-169	138.8	78.3	84.8	hypothetical protein ARALYDRAFT_312884	gbpln	Arabidopsis lyrata	AT1G19490.1 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr1:6751953-6753959 REVERSE LENGTH=471	466	471	1.00E-171	101.1	79.4	85.8
Rsa1.0_00015.1.g857.t1	ref|XP_002890343.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336185|gb|EFH66602.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	811	1262	0	155.6	78.3	86.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G19485.2 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:6747167-6751443 FORWARD LENGTH=815	811	815	0	100.5	76.9	85.2
Rsa1.0_00015.1.g858.t1	gb|AAF79431.1|AC025808_13 F18O14.25 [Arabidopsis thaliana]	362	1314	1.00E-150	363.0	78.7	87.0	F18O14.25	gbpln	Arabidopsis thaliana	AT1G19480.2 | Symbols: | DNA glycosylase superfamily protein | chr1:6744520-6745653 FORWARD LENGTH=377	362	377	1.00E-152	104.1	78.7	87.0

Rsa1.0_00015.1.g859.t1	ref|NP_173377.1| sugar transporter ERD6-like 4 [Arabidopsis thaliana] gi|75331761|sp|Q93YP9.1|ERDL4_ARATH RecName: Full=Sugar transporter ERD6-like 4 gi|16648957|gb|AAL24330.1| similar to integral membrane protein [Arabidopsis thaliana] gi|20259852|gb|AAM13273.1| similar to integral membrane protein [Arabidopsis thaliana] gi|332191732|gb|AEE29853.1| sugar transporter ERD6-like 4 [Arabidopsis thaliana]	487	488	0	100.2	95.7	98.4	sugar transporter ERD6-like 4	gbpln	Arabidopsis thaliana	AT1G19450.1 | Symbols: | Major facilitator superfamily protein | chr1:6731671-6734633 REVERSE LENGTH=488	487	488	0	100.2	95.7	98.4
Rsa1.0_00015.1.g860.t1	gb|EOA37579.1| hypothetical protein CARUB_v10011929mg [Capsella rubella]	515	512	0	99.4	91.8	96.5	hypothetical protein CARUB_v10011929mg	gbpln	Capsella rubella	AT1G19440.1 | Symbols: KCS4 | 3-ketoacyl-CoA synthase 4 | chr1:6729119-6730669 FORWARD LENGTH=516	515	516	0	100.2	91.5	95.7
Rsa1.0_00015.1.g861.t1	ref|NP_564084.1| putative methyltransferase PMT28 [Arabidopsis thaliana] gi|75174900|sp|Q9LN50.1|PMTS_ARATH RecName: Full=Probable methyltransferase PMT28 gi|8778438|gb|AAF79446.1|AC025808_28 F18O14.20 [Arabidopsis thaliana] gi|15810125|gb|AAL07206.1| unknown protein [Arabidopsis thaliana] gi|25054951|gb|AAN71952.1| unknown protein [Arabidopsis thaliana] gi|332191730|gb|AEE29851.1| putative methyltransferase PMT28 [Arabidopsis thaliana]	694	724	0	104.3	90.5	95.0	putative methyltransferase PMT28	gbpln	Arabidopsis thaliana	AT1G19430.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:6724669-6727533 REVERSE LENGTH=724	694	724	0	104.3	90.5	95.0
Rsa1.0_00015.1.g862.t1	ref|NP_173373.2| Erythronate-4-phosphate dehydrogenase family protein [Arabidopsis thaliana] gi|30686353|ref|NP_850946.1| Erythronate-4-phosphate dehydrogenase family protein [Arabidopsis thaliana] gi|18176223|gb|AAL60006.1| unknown protein [Arabidopsis thaliana] gi|20465771|gb|AAM20374.1| unknown protein [Arabidopsis thaliana] gi|110740824|dbj|BAE98509.1| hypothetical protein [Arabidopsis thaliana] gi|332191727|gb|AEE29848.1| Erythronate-4-phosphate dehydrogenase family protein [Arabidopsis thaliana] gi|332191728|gb|AEE29849.1| Erythronate-4-phosphate dehydrogenase family protein [Arabidopsis thaliana]	299	303	1.00E-147	101.3	87.6	91.3	Erythronate-4-phosphate dehydrogenase family protein	gbpln	Arabidopsis thaliana	AT1G19400.2 | Symbols: | Erythronate-4-phosphate dehydrogenase family protein | chr1:6712222-6713676 REVERSE LENGTH=303	299	303	1.00E-150	101.3	87.6	91.3
Rsa1.0_00015.1.g863.t1	ref|XP_002893045.1| hypothetical protein ARALYDRAFT_889371 [Arabidopsis lyrata subsp. lyrata] gi|297338887|gb|EFH69304.1| hypothetical protein ARALYDRAFT_889371 [Arabidopsis lyrata subsp. lyrata]	789	791	0	100.3	75.3	86.2	hypothetical protein ARALYDRAFT_889371	gbpln	Arabidopsis lyrata	AT1G19390.1 | Symbols: | Wall-associated kinase family protein | chr1:6700772-6703368 REVERSE LENGTH=788	789	788	0	99.9	74.5	84.5
Rsa1.0_00015.1.g864.t1	ref|XP_002890050.1| hypothetical protein ARALYDRAFT_312432 [Arabidopsis lyrata subsp. lyrata] gi|297335892|gb|EFH66309.1| hypothetical protein ARALYDRAFT_312432 [Arabidopsis lyrata subsp. lyrata]	96	431	1.00E-24	449.0	56.3	60.4	hypothetical protein ARALYDRAFT_312432	gbpln	Arabidopsis lyrata	AT1G14340.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:4897709-4898776 FORWARD LENGTH=244	96	244	7.00E-27	254.2	59.4	63.5
Rsa1.0_00015.1.g865.t2	ref|XP_002893045.1| hypothetical protein ARALYDRAFT_889371 [Arabidopsis lyrata subsp. lyrata] gi|297338887|gb|EFH69304.1| hypothetical protein ARALYDRAFT_889371 [Arabidopsis lyrata subsp. lyrata]	719	791	0	110.0	75.5	84.6	hypothetical protein ARALYDRAFT_889371	gbpln	Arabidopsis lyrata	AT1G19390.1 | Symbols: | Wall-associated kinase family protein | chr1:6700772-6703368 REVERSE LENGTH=788	719	788	0	109.6	75.1	85.0

Rsa1.0_00015.1.g866.t1	gb|EOA39384.1| hypothetical protein CARUB_v10012465mg [Capsella rubella]	599	609	0	101.7	84.8	92.0	hypothetical protein CARUB_v10012465mg	gbpln	Capsella rubella	AT1G19370.1 | Symbols: | unknown protein; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G75140.1); Has 45 Blast hits to 43 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:6692904-6694721 REVERSE LENGTH=605	599	605	0	101.0	85.1	91.8
Rsa1.0_00015.1.g867.t1	ref|XP_002893043.1| hypothetical protein ARALYDRAFT_472163 [Arabidopsis lyrata subsp. lyrata] gi|297338885|gb|EFH69302.1| hypothetical protein ARALYDRAFT_472163 [Arabidopsis lyrata subsp. lyrata]	423	428	0	101.2	91.3	95.5	hypothetical protein ARALYDRAFT_472163	gbpln	Arabidopsis lyrata	AT1G19360.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr1:6690672-6692211 REVERSE LENGTH=428	423	428	0	101.2	91.0	95.0
Rsa1.0_00015.1.g868.t1	dbj|BAJ33837.1| unnamed protein product [Thellungiella halophila]	336	329	1.00E-145	97.9	89.9	92.0	unnamed protein product	----	----	AT1G19350.3 | Symbols: BES1, BZR2 | Brassinosteroid signalling positive regulator (BZR1) family protein | chr1:6688680-6690165 FORWARD LENGTH=357	336	357	1.00E-140	106.3	87.2	91.4
Rsa1.0_00015.1.g869.t1	ref|XP_002890329.1| hypothetical protein ARALYDRAFT_472157 [Arabidopsis lyrata subsp. lyrata] gi|297336171|gb|EFH66588.1| hypothetical protein ARALYDRAFT_472157 [Arabidopsis lyrata subsp. lyrata]	416	410	0	98.6	80.5	87.5	hypothetical protein ARALYDRAFT_472157	gbpln	Arabidopsis lyrata	AT1G19340.1 | Symbols: | Methyltransferase MT-A70 family protein | chr1:6684798-6686798 FORWARD LENGTH=414	416	414	0	99.5	78.8	86.3
Rsa1.0_00015.1.g870.t1	ref|XP_002893042.1| hypothetical protein ARALYDRAFT_472155 [Arabidopsis lyrata subsp. lyrata] gi|297338884|gb|EFH69301.1| hypothetical protein ARALYDRAFT_472155 [Arabidopsis lyrata subsp. lyrata]	244	248	1.00E-117	101.6	88.9	93.0	hypothetical protein ARALYDRAFT_472155	gbpln	Arabidopsis lyrata	AT1G19330.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G75060.1); Has 145 Blast hits to 145 proteins in 43 species: Archae - 0; Bacteria - 0; Metazoa - 40; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:6680824-6683290 REVERSE LENGTH=242	244	242	1.00E-117	99.2	89.8	94.3
Rsa1.0_00015.1.g871.t2	ref|XP_002878802.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324641|gb|EFH55061.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	117	263	2.00E-37	224.8	67.5	76.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G19320.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:6679327-6680178 FORWARD LENGTH=247	117	247	2.00E-37	211.1	67.5	73.5
Rsa1.0_00015.1.g872.t2	gb|EOA36204.1| hypothetical protein CARUB_v10010116mg [Capsella rubella]	66	246	1.00E-25	372.7	89.4	93.9	hypothetical protein CARUB_v10010116mg	gbpln	Capsella rubella	AT1G19330.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G75060.1); Has 145 Blast hits to 145 proteins in 43 species: Archae - 0; Bacteria - 0; Metazoa - 40; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:6680824-6683290 REVERSE LENGTH=242	66	242	3.00E-27	366.7	84.8	92.4
Rsa1.0_00015.1.g873.t1	ref|XP_002890328.1| hypothetical protein ARALYDRAFT_472154 [Arabidopsis lyrata subsp. lyrata] gi|297336170|gb|EFH66587.1| hypothetical protein ARALYDRAFT_472154 [Arabidopsis lyrata subsp. lyrata]	246	244	6.00E-94	99.2	69.9	78.0	hypothetical protein ARALYDRAFT_472154	gbpln	Arabidopsis lyrata	AT1G19320.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:6679327-6680178 FORWARD LENGTH=247	246	247	4.00E-96	100.4	69.9	78.0
Rsa1.0_00015.1.g874.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1399	1715	0	122.6	42.5	60.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G25270.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:9203934-9204965 REVERSE LENGTH=343	1399	343	1.00E-76	24.5	10.0	15.0
Rsa1.0_00015.1.g875.t1	ref|XP_002893041.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297338883|gb|EFH69300.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	229	226	2.00E-96	98.7	82.5	86.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G19310.1 | Symbols: | RING/U-box superfamily protein | chr1:6676424-6677104 REVERSE LENGTH=226	229	226	5.00E-93	98.7	81.7	86.9

Rsa1.0_00015.1.g876.t1	ref|XP_002893040.1| hypothetical protein ARALYDRAFT_472152 [Arabidopsis lyrata subsp. lyrata] gi|297338882|gb|EFH69299.1| hypothetical protein ARALYDRAFT_472152 [Arabidopsis lyrata subsp. lyrata]	349	350	1.00E-167	100.3	91.4	95.1	hypothetical protein ARALYDRAFT_472152	gbpln	Arabidopsis lyrata	AT1G19300.1 | Symbols: GATL1, PARVUS, GLZ1, ATGATL1 | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:6671451-6672506 REVERSE LENGTH=351	349	351	1.00E-166	100.6	87.7	91.1
Rsa1.0_00015.1.g877.t1	ref|NP_173361.1| protein DA1 [Arabidopsis thaliana] gi|193806611|sp|P0C7Q8.1|DA1_ARATH RecName: Full=Protein DA1; AltName: Full=Protein SUPPRESSOR OF LARGE SEED AND ORGAN PHENOTYPES OF DA1-1 1 gi|332191704|gb|AEE29825.1| protein DA1 [Arabidopsis thaliana]	545	532	0	97.6	86.8	91.6	protein DA1	gbpln	Arabidopsis thaliana	AT1G19270.1 | Symbols: DA1 | DA1 | chr1:6663327-6665845 FORWARD LENGTH=532	545	532	0	97.6	86.8	91.6
Rsa1.0_00015.1.g878.t1	gb|AAF91318.1|AF242848_1 beta-ketoacyl-acyl carrier protein synthase [Brassica napus]	514	543	0	105.6	94.4	96.1	beta-ketoacyl-acyl carrier protein synthase	gbpln	Brassica napus	AT1G74960.3 | Symbols: FAB1 | fatty acid biosynthesis 1 | chr1:28152564-28155948 REVERSE LENGTH=541	514	541	0	105.3	81.5	88.1
Rsa1.0_00015.1.g879.t1	gb|EOA40127.1| hypothetical protein CARUB_v10008834mg [Capsella rubella]	525	528	0	100.6	91.0	95.6	hypothetical protein CARUB_v10008834mg	gbpln	Capsella rubella	AT1G19250.1 | Symbols: FMO1 | flavin-dependent monooxygenase 1 | chr1:6650656-6653053 REVERSE LENGTH=530	525	530	0	101.0	89.5	95.0
Rsa1.0_00015.1.g880.t1	gb|AAM61590.1| unknown [Arabidopsis thaliana]	103	104	3.00E-36	101.0	82.5	93.2	unknown	gbpln	Arabidopsis thaliana	AT1G19240.1 | Symbols: | unknown protein; Has 24 Blast hits to 24 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6649562-6650384 REVERSE LENGTH=104	103	104	2.00E-38	101.0	81.6	92.2
Rsa1.0_00015.1.g881.t1	ref|XP_002890325.1| hypothetical protein ARALYDRAFT_312861 [Arabidopsis lyrata subsp. lyrata] gi|297336167|gb|EFH66584.1| hypothetical protein ARALYDRAFT_312861 [Arabidopsis lyrata subsp. lyrata]	1009	946	0	93.8	81.9	86.1	hypothetical protein ARALYDRAFT_312861	gbpln	Arabidopsis lyrata	AT1G19230.2 | Symbols: | Riboflavin synthase-like superfamily protein | chr1:6644189-6649149 FORWARD LENGTH=934	1009	934	0	92.6	78.7	83.2
Rsa1.0_00015.1.g882.t1	gb|AFD01318.1| auxin response factor 19-2 [Brassica rapa subsp. pekinensis]	1074	1049	0	97.7	91.9	93.0	auxin response factor 19-2	gbpln	Brassica rapa	AT1G19220.1 | Symbols: ARF19, IAA22, ARF11 | auxin response factor 19 | chr1:6628395-6632779 REVERSE LENGTH=1086	1074	1086	0	101.1	87.9	90.4
Rsa1.0_00015.1.g883.t1	ref|XP_002893033.1| hypothetical protein ARALYDRAFT_472144 [Arabidopsis lyrata subsp. lyrata] gi|297338875|gb|EFH69292.1| hypothetical protein ARALYDRAFT_472144 [Arabidopsis lyrata subsp. lyrata]	161	186	4.00E-53	115.5	70.8	83.9	hypothetical protein ARALYDRAFT_472144	gbpln	Arabidopsis lyrata	AT1G19210.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:6626973-6627530 REVERSE LENGTH=185	161	185	5.00E-55	114.9	71.4	82.0
Rsa1.0_00015.1.g884.t1	ref|NP_567546.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|15451060|gb|AAK96801.1| putative protein [Arabidopsis thaliana] gi|20148333|gb|AAM10057.1| putative protein [Arabidopsis thaliana] gi|119657370|tpd|FAA00284.1| TPA: AT-hook motif nuclear localized protein 13 [Arabidopsis thaliana] gi|332658571|gb|AEE83971.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	294	439	6.00E-41	149.3	42.2	53.7	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT4G17950.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:9967295-9969007 REVERSE LENGTH=439	294	439	2.00E-43	149.3	42.2	53.7
Rsa1.0_00015.1.g885.t1	ref|NP_567546.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|15451060|gb|AAK96801.1| putative protein [Arabidopsis thaliana] gi|20148333|gb|AAM10057.1| putative protein [Arabidopsis thaliana] gi|119657370|tpd|FAA00284.1| TPA: AT-hook motif nuclear localized protein 13 [Arabidopsis thaliana] gi|332658571|gb|AEE83971.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	306	439	3.00E-44	143.5	53.3	66.7	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT4G17950.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:9967295-9969007 REVERSE LENGTH=439	306	439	7.00E-47	143.5	53.3	66.7
Rsa1.0_00015.1.g886.t1	gb|AAF82231.1|AC069143_7 Contains similarity to a hypothetical protein F9E10.21 gi|6646770 from Arabidopsis thaliana BAC F9E10 gb|AC013258 [Arabidopsis thaliana]	225	222	1.00E-54	98.7	56.0	71.1	Contains similarity to a hypothetical protein F9E10.21 gi|6646770 from Arabidopsis thaliana BAC F9E10 gb|AC013258	gbpln	Arabidopsis thaliana	AT1G19200.1 | Symbols: | Protein of unknown function (DUF581) | chr1:6625104-6625856 REVERSE LENGTH=215	225	215	5.00E-57	95.6	56.0	71.1

Rsa1.0_00015.1.g887.t1	ref|NP_173353.1| alpha/beta-hydrolase-like protein [Arabidopsis thaliana] gi|75335190|sp|Q9LMA7.1|CXE1_ARATH RecName: Full=Probable carboxylesterase 1; AltName: Full=AtCXE1 gi|8954057|gb|AAF82230.1|AC069143_6 Contains similarity to a PrMC3 from Pinus radiata gb|AF110333 [Arabidopsis thaliana] gi|119360077|gb|ABL66767.1| At1g19190 [Arabidopsis thaliana] gi|332191695|gb|AEE29816.1| probable carboxylesterase 1 [Arabidopsis thaliana]	320	318	1.00E-125	99.4	69.1	83.1	alpha/beta-hydrolase-like protein	gbpln	Arabidopsis thaliana	AT1G19190.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:6623876-6624832 FORWARD LENGTH=318	320	318	1.00E-127	99.4	69.1	83.1
Rsa1.0_00015.1.g888.t1	gb|EOA38428.1| hypothetical protein CARUB_v10010018mg [Capsella rubella]	254	268	6.00E-93	105.5	74.8	84.3	hypothetical protein CARUB_v10010018mg	gbpln	Capsella rubella	AT1G19180.1 | Symbols: JAZ1, TIFY10A | jasmonate-zim-domain protein 1 | chr1:6622312-6623271 FORWARD LENGTH=253	254	253	1.00E-93	99.6	76.0	81.5
Rsa1.0_00015.1.g889.t1	ref|NP_564074.1| uncharacterized protein [Arabidopsis thaliana] gi|8954052|gb|AAF82225.1|AC069143_1 Contains similarity to a HSPC326 mRNA from Homo sapiens gb|AF161444. EST gb|AI997162 comes from this gene [Arabidopsis thaliana] gi|332191689|gb|AEE29810.1| uncharacterized protein AT1G19140 [Arabidopsis thaliana]	312	311	1.00E-151	99.7	86.2	91.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G19140.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ubiquinone biosynthetic process; LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: COQ9 (InterPro:IPR013718), Ubiquinone biosynthesis protein COQ9 (InterPro:IPR012762); Has 748 Blast hits to 748 proteins in 260 species: Archae - 0; Bacteria - 218; Metazoa - 126; Fungi - 101; Plants - 39; Viruses - 0; Other Eukaryotes - 264 (source: NCBI BLink). | chr1:6611026-6612414 REVERSE LENGTH=311	312	311	1.00E-154	99.7	86.2	91.7
Rsa1.0_00015.1.g890.t1	ref|NP_173345.2| inter-alpha-trypsin inhibitor heavy chain-like protein [Arabidopsis thaliana] gi|22531102|gb|AAM97055.1| unknown protein [Arabidopsis thaliana] gi|23197960|gb|AAN15507.1| unknown protein [Arabidopsis thaliana] gi|332191682|gb|AEE29803.1| inter-alpha-trypsin inhibitor heavy chain-like protein [Arabidopsis thaliana]	756	754	0	99.7	88.2	94.2	inter-alpha-trypsin inhibitor heavy chain-like protein	gbpln	Arabidopsis thaliana	AT1G19110.1 | Symbols: | inter-alpha-trypsin inhibitor heavy chain-related | chr1:6602270-6605766 FORWARD LENGTH=754	756	754	0	99.7	88.2	94.2
Rsa1.0_00015.1.g891.t1	ref|NP_173344.2| Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein [Arabidopsis thaliana] gi|62320246|dbj|BAD94510.1| hypothetical protein [Arabidopsis thaliana] gi|332191681|gb|AEE29802.1| Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein [Arabidopsis thaliana]	696	663	0	95.3	79.3	84.5	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	gbpln	Arabidopsis thaliana	AT1G19100.1 | Symbols: | Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein | chr1:6595560-6601159 FORWARD LENGTH=663	696	663	0	95.3	79.3	84.5
Rsa1.0_00015.1.g892.t1	gb|EOA39914.1| hypothetical protein CARUB_v10008603mg [Capsella rubella]	617	616	0	99.8	80.6	88.2	hypothetical protein CARUB_v10008603mg	gbpln	Capsella rubella	AT1G19090.1 | Symbols: RKF2, CRK1 | receptor-like serine/threonine kinase 2 | chr1:6590350-6592615 FORWARD LENGTH=600	617	600	0	97.2	76.3	84.4
Rsa1.0_00015.1.g893.t1	ref|XP_002893028.1| hypothetical protein ARALYDRAFT_889335 [Arabidopsis lyrata subsp. lyrata] gi|297338870|gb|EFH69287.1| hypothetical protein ARALYDRAFT_889335 [Arabidopsis lyrata subsp. lyrata]	215	209	1.00E-89	97.2	84.7	91.2	hypothetical protein ARALYDRAFT_889335	gbpln	Arabidopsis lyrata	AT1G19050.1 | Symbols: ARR7 | response regulator 7 | chr1:6577919-6579078 REVERSE LENGTH=206	215	206	1.00E-87	95.8	78.6	87.0
Rsa1.0_00015.1.g894.t1	gb|EOA36368.1| hypothetical protein CARUB_v10010768mg [Capsella rubella]	86	87	3.00E-30	101.2	82.6	87.2	hypothetical protein CARUB_v10010768mg	gbpln	Capsella rubella	AT1G19020.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48180.1); Has 88 Blast hits to 88 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 88; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6568142-6568402 FORWARD LENGTH=86	86	86	3.00E-31	100.0	83.7	88.4
Rsa1.0_00015.1.g895.t1	ref|NP_173333.1| uncharacterized protein [Arabidopsis thaliana] gi|8778293|gb|AAF79302.1|AC068602_25 F14D16.14 [Arabidopsis thaliana] gi|27754600|gb|AAO22746.1| unknown protein [Arabidopsis thaliana] gi|332191666|gb|AEE29787.1| uncharacterized protein AT1G18990 [Arabidopsis thaliana]	510	524	0	102.7	84.9	92.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G18990.1 | Symbols: | Protein of unknown function, DUF593 | chr1:6558778-6560432 REVERSE LENGTH=524	510	524	0	102.7	84.9	92.4

Rsa1.0_00015.1.g896.t1	ref|NP_173332.1| germin-like protein subfamily T member 2 [Arabidopsis thaliana] gi|18203242|sp|Q9LMC9.1|GLT2_ARATH RecName: Full=Germin-like protein subfamily T member 2; Flags: Precursor gi|8778294|gb|AAF79303.1|AC068602_26 F14D16.13 [Arabidopsis thaliana] gi|21537092|gb|AAM61433.1| germin, putative [Arabidopsis thaliana] gi|89111904|gb|ABD60724.1| At1g18980 [Arabidopsis thaliana] gi|332191665|gb|AEE29786.1| germin-like protein subfamily T member 2 [Arabidopsis thaliana]	214	220	1.00E-103	102.8	89.3	92.5	germin-like protein subfamily T member 2	gbpln	Arabidopsis thaliana	AT1G18980.1 | Symbols: | RmlC-like cupins superfamily protein | chr1:6557364-6558026 REVERSE LENGTH=220	214	220	1.00E-106	102.8	89.3	92.5
Rsa1.0_00015.1.g897.t1	gb|AAF97281.1|AC010164_3 Hypothetical protein [Arabidopsis thaliana] gi|12324507|gb|AAG52212.1|AC022288_11 putative gag-pol polyprotein; 76173-77576 [Arabidopsis thaliana]	221	467	1.00E-73	211.3	62.4	79.2	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00015.1.g898.t3	ref|NP_173329.2| DDT domain-containing protein [Arabidopsis thaliana] gi|332191662|gb|AEE29783.1| DDT domain-containing protein [Arabidopsis thaliana]	815	750	0	92.0	75.6	81.0	DDT domain-containing protein	gbpln	Arabidopsis thaliana	AT1G18950.1 | Symbols: | DDT domain superfamily | chr1:6546539-6551549 FORWARD LENGTH=750	815	750	0	92.0	75.6	81.0
Rsa1.0_00015.1.g899.t1	gb|EOA40010.1| hypothetical protein CARUB_v10008700mg [Capsella rubella]	526	575	0	109.3	86.5	92.8	hypothetical protein CARUB_v10008700mg	gbpln	Capsella rubella	AT1G18940.1 | Symbols: | Nodulin-like / Major Facilitator Superfamily protein | chr1:6543852-6545592 FORWARD LENGTH=526	526	526	0	100.0	86.3	94.1
Rsa1.0_00015.1.g900.t1	ref|XP_002893023.1| F14D16.3 [Arabidopsis lyrata subsp. lyrata] gi|297338865|gb|EFH69282.1| F14D16.3 [Arabidopsis lyrata subsp. lyrata]	1189	1260	0	106.0	81.6	87.7	F14D16.3	gbpln	Arabidopsis lyrata	AT1G18910.1 | Symbols: | zinc ion binding;zinc ion binding | chr1:6532706-6537993 REVERSE LENGTH=1254	1189	1254	0	105.5	80.7	87.6
Rsa1.0_00015.1.g901.t1	ref|NP_173324.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|42571539|ref|NP_973860.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75151479|sp|Q8GYP6.1|PPR49_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g18900 gi|26450017|dbj|BAC42129.1| unknown protein [Arabidopsis thaliana] gi|28827402|gb|AAO50545.1| unknown protein [Arabidopsis thaliana] gi|332191657|gb|AEE29778.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332191658|gb|AEE29779.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	857	860	0	100.4	83.1	89.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G18900.2 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:6529778-6532360 FORWARD LENGTH=860	857	860	0	100.4	83.1	89.0
Rsa1.0_00015.1.g902.t1	dbj|BAJ34189.1| unnamed protein product [Thellungiella halophila]	548	545	0	99.5	90.3	94.3	unnamed protein product	----	----	AT1G18890.1 | Symbols: ATCDPK1, CPK10, CDPK1, AtCPK10 | calcium-dependent protein kinase 1 | chr1:6523468-6525736 REVERSE LENGTH=545	548	545	0	99.5	88.9	94.0
Rsa1.0_00015.1.g903.t1	ref|XP_002890304.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297336146|gb|EFH66563.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	613	587	0	95.8	84.2	87.8	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G18880.1 | Symbols: | Major facilitator superfamily protein | chr1:6520800-6523241 FORWARD LENGTH=587	613	587	0	95.8	83.2	86.9
Rsa1.0_00015.1.g904.t1	gb|EOA40359.1| hypothetical protein CARUB_v10009088mg, partial [Capsella rubella]	417	457	1.00E-179	109.6	75.5	85.9	hypothetical protein CARUB_v10009088mg, partial	gbpln	Capsella rubella	AT1G18850.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 40 Blast hits to 40 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6504928-6506127 REVERSE LENGTH=399	417	399	1.00E-173	95.7	73.6	83.0
Rsa1.0_00015.1.g905.t2	dbj|BAJ33816.1| unnamed protein product [Thellungiella halophila]	635	571	0	89.9	73.4	79.8	unnamed protein product	----	----	AT1G18840.2 | Symbols: IQD30 | IQ-domain 30 | chr1:6501068-6503435 REVERSE LENGTH=572	635	572	0	90.1	69.8	77.3

Rsa1.0_00015.1.g906.t1	ref|XP_002893019.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338861|gb|EFH69278.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	94	104	7.00E-27	110.6	80.9	86.2	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00015.1.g907.t1	ref|XP_002893018.1| hypothetical protein ARALYDRAFT_472107 [Arabidopsis lyrata subsp. lyrata] gi|297338860|gb|EFH69277.1| hypothetical protein ARALYDRAFT_472107 [Arabidopsis lyrata subsp. lyrata]	88	88	9.00E-39	100.0	89.8	92.0	hypothetical protein ARALYDRAFT_472107	gbpln	Arabidopsis lyrata	AT1G18835.1 | Symbols: MIF3 | mini zinc finger | chr1:6496106-6496372 REVERSE LENGTH=88	88	88	6.00E-37	100.0	90.9	93.2
Rsa1.0_00015.1.g908.t1	dbj|BAC42657.1| unknown protein [Arabidopsis thaliana] gi|28950777|gb|AAO63312.1| At1g18800 [Arabidopsis thaliana]	258	228	1.00E-112	88.4	79.1	83.3	unknown protein	gbpln	Arabidopsis thaliana	AT1G18800.1 | Symbols: NRP2 | NAP1-related protein 2 | chr1:6481466-6483463 REVERSE LENGTH=256	258	256	1.00E-112	99.2	77.5	81.0
Rsa1.0_00015.1.g909.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00015.1.g910.t1	gb|EOA36433.1| hypothetical protein CARUB_v10010970mg [Capsella rubella]	166	210	3.00E-23	126.5	42.8	57.8	hypothetical protein CARUB_v10010970mg	gbpln	Capsella rubella	AT1G18760.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr1:6471150-6471824 REVERSE LENGTH=224	166	224	2.00E-17	134.9	39.2	58.4
Rsa1.0_00015.1.g911.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	237	1555	7.00E-36	656.1	38.4	48.1	disease resistance protein	gbpln	Brassica rapa	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	237	170	2.00E-18	71.7	21.1	32.5
Rsa1.0_00015.1.g912.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00015.1.g913.t1	ref|XP_002882812.1| hypothetical protein ARALYDRAFT_341444 [Arabidopsis lyrata subsp. lyrata] gi|297328652|gb|EFH59071.1| hypothetical protein ARALYDRAFT_341444 [Arabidopsis lyrata subsp. lyrata]	147	315	1.00E-19	214.3	43.5	56.5	hypothetical protein ARALYDRAFT_341444	gbpln	Arabidopsis lyrata	AT3G13228.1 | Symbols: | RING/U-box superfamily protein | chr3:4267075-4268052 FORWARD LENGTH=325	147	325	2.00E-15	221.1	40.1	55.8
Rsa1.0_00015.1.g914.t1	ref|XP_002882812.1| hypothetical protein ARALYDRAFT_341444 [Arabidopsis lyrata subsp. lyrata] gi|297328652|gb|EFH59071.1| hypothetical protein ARALYDRAFT_341444 [Arabidopsis lyrata subsp. lyrata]	221	315	1.00E-50	142.5	51.6	65.2	hypothetical protein ARALYDRAFT_341444	gbpln	Arabidopsis lyrata	AT3G13228.1 | Symbols: | RING/U-box superfamily protein | chr3:4267075-4268052 FORWARD LENGTH=325	221	325	2.00E-45	147.1	47.1	61.5
Rsa1.0_00015.1.g915.t1	ref|XP_002890300.1| AGL102 [Arabidopsis lyrata subsp. lyrata] gi|297336142|gb|EFH66559.1| AGL102 [Arabidopsis lyrata subsp. lyrata]	153	383	3.00E-37	250.3	52.9	57.5	AGL102	gbpln	Arabidopsis lyrata	AT1G18750.1 | Symbols: AGL65 | AGAMOUS-like 65 | chr1:6467266-6469640 FORWARD LENGTH=389	153	389	2.00E-39	254.2	52.9	57.5
Rsa1.0_00015.1.g916.t1	ref|XP_002890299.1| hypothetical protein ARALYDRAFT_472100 [Arabidopsis lyrata subsp. lyrata] gi|297336141|gb|EFH66558.1| hypothetical protein ARALYDRAFT_472100 [Arabidopsis lyrata subsp. lyrata]	363	382	1.00E-170	105.2	85.1	91.2	hypothetical protein ARALYDRAFT_472100	gbpln	Arabidopsis lyrata	AT1G18740.1 | Symbols: | Protein of unknown function (DUF793) | chr1:6464125-6465273 FORWARD LENGTH=382	363	382	1.00E-170	105.2	84.8	91.2
Rsa1.0_00015.1.g917.t1	ref|NP_173308.2| NDH dependent flow 6 protein [Arabidopsis thaliana] gi|19310578|gb|AAL85020.1| unknown protein [Arabidopsis thaliana] gi|21436079|gb|AAM51240.1| unknown protein [Arabidopsis thaliana] gi|110741088|dbj|BAE98638.1| hypothetical protein [Arabidopsis thaliana] gi|332191632|gb|AEE29753.1| NDH dependent flow 6 protein [Arabidopsis thaliana]	176	175	2.00E-92	99.4	93.2	95.5	NDH dependent flow 6 protein	gbpln	Arabidopsis thaliana	AT1G18730.1 | Symbols: NDF6 | NDH dependent flow 6 | chr1:6460625-6462107 FORWARD LENGTH=175	176	175	9.00E-95	99.4	93.2	95.5
Rsa1.0_00015.1.g918.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	447	478	2.00E-83	106.9	33.1	45.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	447	746	5.00E-70	166.9	27.7	38.7
Rsa1.0_00015.1.g919.t1	ref|XP_002890296.1| hypothetical protein ARALYDRAFT_335127 [Arabidopsis lyrata subsp. lyrata] gi|297336138|gb|EFH66555.1| hypothetical protein ARALYDRAFT_335127 [Arabidopsis lyrata subsp. lyrata]	266	258	1.00E-97	97.0	69.5	79.3	hypothetical protein ARALYDRAFT_335127	gbpln	Arabidopsis lyrata	AT1G18710.1 | Symbols: AtMYB47, MYB47 | myb domain protein 47 | chr1:6450781-6452986 FORWARD LENGTH=267	266	267	2.00E-70	100.4	54.1	68.8
Rsa1.0_00015.1.g920.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00015.1.g921.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00015.1.g922.t1	gb|AAC02664.1| polyprotein [Arabidopsis thaliana]	1370	1451	0	105.9	66.6	78.4	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1370	1262	1.00E-110	92.1	14.5	20.8

Rsa1.0_00015.1.g923.t1	ref|NP_173304.2| putative glycosyltransferase 4 [Arabidopsis thaliana] gi|46576343|sp|Q9M9U0.1|GT4_ARATH RecName: Full=Putative glycosyltransferase 4; Short=AtGT4 gi|6730715|gb|AAF27110.1|AC011809_19 Similar to galactosyltransferase [Arabidopsis thaliana] gi|332191625|gb|AEE29746.1| putative glycosyltransferase 4 [Arabidopsis thaliana]	508	513	0	101.0	78.5	83.9	putative glycosyltransferase 4	gbpln	Arabidopsis thaliana	AT1G18690.1 | Symbols: | Galactosyl transferase GMA12/MNN10 family protein | chr1:6435153-6436694 FORWARD LENGTH=513	508	513	0	101.0	78.5	83.9
Rsa1.0_00015.1.g924.t4	ref|XP_002890292.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297336134|gb|EFH66551.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	555	476	0	85.8	78.9	81.3	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G18660.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:6421433-6425565 FORWARD LENGTH=486	555	486	0	87.6	78.2	80.9
Rsa1.0_00015.1.g925.t17	ref|NP_973858.1| phosphoserine phosphatase [Arabidopsis thaliana] gi|62900892|sp|O82796.2|SERB_ARATH RecName: Full=Phosphoserine phosphatase, chloroplastic; Short=PSP; Short=PSPase; AltName: Full=O-phosphoserine phosphohydrolase; Flags: Precursor gi|9795592|gb|AAF98410.1|AC026238_2 3-phosphoserine phosphatase [Arabidopsis thaliana] gi|17529132|gb|AAL38792.1| putative 3-phosphoserine phosphatase [Arabidopsis thaliana] gi|20465705|gb|AAM20321.1| putative 3-phosphoserine phosphatase [Arabidopsis thaliana] gi|21592986|gb|AAM64935.1| 3-phosphoserine phosphatase [Arabidopsis thaliana] gi|332191617|gb|AEE29738.1| phosphoserine phosphatase [Arabidopsis thaliana]	547	295	1.00E-149	53.9	49.7	51.4	phosphoserine phosphatase	gbpln	Arabidopsis thaliana	AT1G18640.2 | Symbols: PSP | 3-phosphoserine phosphatase | chr1:6416524-6418245 REVERSE LENGTH=295	547	295	1.00E-151	53.9	49.7	51.4
Rsa1.0_00015.1.g926.t1	ref|NP_173298.1| glycine-rich RNA-binding protein 6 [Arabidopsis thaliana] gi|75334552|sp|Q9FZ84.1|RBG6_ARATH RecName: Full=Glycine-rich RNA-binding protein 6, mitochondrial; Short=AtGR-RBP6; AltName: Full=AtRBG6; Flags: Precursor gi|9795594|gb|AAF98412.1|AC026238_4 Similar to glycine-rich RNA-binding proteins [Arabidopsis thaliana] gi|29029110|gb|AAO64934.1| At1g18630 [Arabidopsis thaliana] gi|110743184|dbj|BAE99483.1| hypothetical protein [Arabidopsis thaliana] gi|332191616|gb|AEE29737.1| glycine-rich RNA-binding protein 6 [Arabidopsis thaliana]	149	155	2.00E-47	104.0	61.1	71.1	glycine-rich RNA-binding protein 6	gbpln	Arabidopsis thaliana	AT1G18630.1 | Symbols: GR-RBP6 | glycine-rich RNA-binding protein 6 | chr1:6415226-6416283 FORWARD LENGTH=155	149	155	5.00E-50	104.0	61.1	71.1
Rsa1.0_00015.1.g927.t3	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	945	966	0	102.2	63.9	78.1	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	945	965	0	102.1	62.4	77.7
Rsa1.0_00015.1.g928.t2	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	932	966	0	103.6	63.1	76.5	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	932	965	0	103.5	61.6	76.6
Rsa1.0_00015.1.g929.t1	ref|NP_173296.3| galactose oxidase/kelch repeat domain-containing protein [Arabidopsis thaliana] gi|9795595|gb|AAF98413.1|AC026238_5 Hypothetical protein [Arabidopsis thaliana] gi|332191613|gb|AEE29734.1| galactose oxidase/kelch repeat domain-containing protein [Arabidopsis thaliana]	509	556	0	109.2	84.7	91.6	galactose oxidase/kelch repeat domain-containing protein	gbpln	Arabidopsis thaliana	AT1G18610.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:6405779-6408831 FORWARD LENGTH=556	509	556	0	109.2	84.7	91.6

Rsa1.0_00015.1.g930.t1	ref|NP_564058.1| RHOMBOID-like protein 12 [Arabidopsis thaliana] gi|9795596|gb|AAF98414.1|AC026238_6 Hypothetical protein [Arabidopsis thaliana] gi|13877607|gb|AAK43881.1|AF370504_1 Unknown protein [Arabidopsis thaliana] gi|20148713|gb|AAM10247.1| unknown protein [Arabidopsis thaliana] gi|21592397|gb|AAM64348.1| unknown [Arabidopsis thaliana] gi|332191612|gb|AEE29733.1| RHOMBOID-like protein 12 [Arabidopsis thaliana]	347	336	1.00E-144	96.8	82.1	88.5	RHOMBOID-like protein 12	gbpln	Arabidopsis thaliana	AT1G18600.1 | Symbols: ATRBL12, RBL12 | RHOMBOID-like protein 12 | chr1:6400647-6402587 FORWARD LENGTH=336	347	336	1.00E-147	96.8	82.1	88.5
Rsa1.0_00015.1.g931.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00015.1.g932.t1	ref|XP_002862798.1| hypothetical protein ARALYDRAFT_497292 [Arabidopsis lyrata subsp. lyrata] gi|297308526|gb|EFH39056.1| hypothetical protein ARALYDRAFT_497292 [Arabidopsis lyrata subsp. lyrata]	723	842	1.00E-179	116.5	55.5	67.6	hypothetical protein ARALYDRAFT_497292	gbpln	Arabidopsis lyrata	AT1G71400.1 | Symbols: AtRLP12, RLP12 | receptor like protein 12 | chr1:26909905-26912448 FORWARD LENGTH=847	723	847	1.00E-180	117.2	54.8	67.5
Rsa1.0_00015.1.g933.t1	ref|NP_188953.1| receptor like protein 38 [Arabidopsis thaliana] gi|9294202|dbj|BAB02104.1| disease resistance protein [Arabidopsis thaliana] gi|332643199|gb|AEE76720.1| receptor like protein 38 [Arabidopsis thaliana]	744	784	0	105.4	56.0	69.5	receptor like protein 38	gbpln	Arabidopsis thaliana	AT3G23120.1 | Symbols: AtRLP38, RLP38 | receptor like protein 38 | chr3:8227222-8229576 REVERSE LENGTH=784	744	784	0	105.4	56.0	69.5
Rsa1.0_00016.1.g934.t1	ref|NP_196791.1| transcription factor MYB46 [Arabidopsis thaliana] gi|75335627|sp|Q9LXV2.1|MYB46_ARATH RecName: Full=Transcription factor MYB46; AltName: Full=Myb-related protein 46; Short=AtMYB46 gi|7630043|emb|CAB88251.1| putative transcription factor (MYB46) [Arabidopsis thaliana] gi|23306410|gb|AAN17432.1| putative transcription factor (MYB46) [Arabidopsis thaliana] gi|27311887|gb|AAO00909.1| putative transcription factor (MYB46) [Arabidopsis thaliana] gi|41619388|gb|AAS10091.1| MYB transcription factor [Arabidopsis thaliana] gi|332004441|gb|AED91824.1| transcription factor MYB46 [Arabidopsis thaliana]	279	280	1.00E-126	100.4	84.9	90.7	transcription factor MYB46	gbpln	Arabidopsis thaliana	AT5G12870.1 | Symbols: ATMYB46, MYB46 | myb domain protein 46 | chr5:4062939-4064939 REVERSE LENGTH=280	279	280	1.00E-128	100.4	84.9	90.7
Rsa1.0_00016.1.g935.t1	ref|NP_568283.2| dicarboxylate transporter 1 [Arabidopsis thaliana] gi|75180949|sp|Q9LXV3.1|DIT1_ARATH RecName: Full=Dicarboxylate transporter 1, chloroplastic; AltName: Full=2-oxoglutarate/malate translocator 1; Short=AtpOMT1; Flags: Precursor gi|7630042|emb|CAB88250.1| 2-oxoglutarate/malate translocator precursor-like protein [Arabidopsis thaliana] gi|332004439|gb|AED91822.1| dicarboxylate transporter 1 [Arabidopsis thaliana]	596	557	0	93.5	86.9	89.1	dicarboxylate transporter 1	gbpln	Arabidopsis thaliana	AT5G12860.1 | Symbols: DiT1 | dicarboxylate transporter 1 | chr5:4059927-4061919 REVERSE LENGTH=557	596	557	0	93.5	86.9	89.1

<table>
<tr><td>Rsa1.0_00016.1.g936.t1</td><td>ref|NP_568282.1| nuclear transcription factor Y subunit A-1 [Arabidopsis thaliana] gi|42573353|ref|NP_974773.1| nuclear transcription factor Y subunit A-1 [Arabidopsis thaliana] gi|75180950|sp|Q9LXV5.1|NFYA1_ARATH RecName: Full=Nuclear transcription factor Y subunit A-1; Short=AtNF-YA-1; AltName: Full=Protein EMBRYO DEFECTIVE 2220; AltName: Full=Transcriptional activator HAP2A gi|7630040|emb|CAB88248.1| CCAAT box binding factor/ transcription factor Hap2a [Arabidopsis thaliana] gi|107738403|gb|ABF83691.1| At5g12840 [Arabidopsis thaliana] gi|332004434|gb|AED91817.1| nuclear transcription factor Y subunit A-1 [Arabidopsis thaliana] gi|332004437|gb|AED91820.1| nuclear transcription factor Y subunit A-1 [Arabidopsis thaliana]</td><td>290</td><td>272</td><td>1.00E-116</td><td>93.8</td><td>76.6</td><td>82.1</td><td>nuclear transcription factor Y subunit A-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G12840.3 | Symbols: HAP2A, ATHAP2A, NF-YA1 | nuclear factor Y, subunit A1 | chr5:4051147-4052961 REVERSE LENGTH=272</td><td>290</td><td>272</td><td>1.00E-118</td><td>93.8</td><td>76.6</td><td>82.1</td></tr>
<tr><td>Rsa1.0_00016.1.g937.t1</td><td>ref|XP_002873580.1| calmodulin-domain protein kinase 7 [Arabidopsis lyrata subsp. lyrata] gi|297319417|gb|EFH49839.1| calmodulin-domain protein kinase 7 [Arabidopsis lyrata subsp. lyrata]</td><td>531</td><td>535</td><td>0</td><td>100.8</td><td>94.4</td><td>97.0</td><td>calmodulin-domain protein kinase 7</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G12480.1 | Symbols: CPK7 | calmodulin-domain protein kinase 7 | chr5:4047817-4050035 REVERSE LENGTH=535</td><td>531</td><td>535</td><td>0</td><td>100.8</td><td>94.0</td><td>96.8</td></tr>
<tr><td>Rsa1.0_00016.1.g938.t1</td><td>ref|XP_002873579.1| hypothetical protein ARALYDRAFT_909228 [Arabidopsis lyrata subsp. lyrata] gi|297319416|gb|EFH49838.1| hypothetical protein ARALYDRAFT_909228 [Arabidopsis lyrata subsp. lyrata]</td><td>380</td><td>385</td><td>1.00E-175</td><td>101.3</td><td>86.1</td><td>92.1</td><td>hypothetical protein ARALYDRAFT_909228</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G12470.1 | Symbols: | Protein of unknown function (DUF3411) | chr5:4044950-4047290 REVERSE LENGTH=386</td><td>380</td><td>386</td><td>1.00E-175</td><td>101.6</td><td>84.2</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00016.1.g939.t1</td><td>gb|EOA19606.1| hypothetical protein CARUB_v10002857mg [Capsella rubella]</td><td>868</td><td>442</td><td>0</td><td>50.9</td><td>39.9</td><td>43.1</td><td>hypothetical protein CARUB_v10002857mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G12460.1 | Symbols: | Protein of unknown function (DUF604) | chr5:4043057-4044583 FORWARD LENGTH=441</td><td>868</td><td>441</td><td>0</td><td>50.8</td><td>38.4</td><td>41.9</td></tr>
<tr><td>Rsa1.0_00016.1.g940.t5</td><td>ref|XP_002314081.1| predicted protein [Populus trichocarpa] gi|222850489|gb|EEE88036.1| predicted protein [Populus trichocarpa]</td><td>926</td><td>418</td><td>1.00E-134</td><td>45.1</td><td>24.2</td><td>32.0</td><td>predicted protein</td><td>gbpln</td><td>Populus trichocarpa</td><td>AT5G12460.1 | Symbols: | Protein of unknown function (DUF604) | chr5:4043057-4044583 FORWARD LENGTH=441</td><td>926</td><td>441</td><td>1.00E-116</td><td>47.6</td><td>21.9</td><td>30.3</td></tr>
<tr><td>Rsa1.0_00016.1.g941.t1</td><td>ref|XP_002314081.1| predicted protein [Populus trichocarpa] gi|222850489|gb|EEE88036.1| predicted protein [Populus trichocarpa]</td><td>467</td><td>418</td><td>1.00E-138</td><td>89.5</td><td>49.5</td><td>65.3</td><td>predicted protein</td><td>gbpln</td><td>Populus trichocarpa</td><td>AT5G12460.1 | Symbols: | Protein of unknown function (DUF604) | chr5:4043057-4044583 FORWARD LENGTH=441</td><td>467</td><td>441</td><td>1.00E-119</td><td>94.4</td><td>43.3</td><td>60.8</td></tr>
<tr><td>Rsa1.0_00016.1.g942.t1</td><td>gb|EOA21902.1| hypothetical protein CARUB_v10002383mg [Capsella rubella]</td><td>74</td><td>74</td><td>1.00E-21</td><td>100.0</td><td>81.1</td><td>89.2</td><td>hypothetical protein CARUB_v10002383mg</td><td>gbpln</td><td>Capsella rubella</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00016.1.g943.t1</td><td>gb|EOA20141.1| hypothetical protein CARUB_v10000430mg [Capsella rubella]</td><td>639</td><td>645</td><td>0</td><td>100.9</td><td>72.0</td><td>80.3</td><td>hypothetical protein CARUB_v10000430mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G12440.3 | Symbols: | CCCH-type zinc fingerfamily protein with RNA-binding domain | chr5:4035891-4038604 REVERSE LENGTH=650</td><td>639</td><td>650</td><td>0</td><td>101.7</td><td>70.0</td><td>78.7</td></tr>
<tr><td>Rsa1.0_00016.1.g944.t1</td><td>ref|XP_002873572.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319409|gb|EFH49831.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>1157</td><td>1163</td><td>0</td><td>100.5</td><td>76.0</td><td>84.4</td><td>DNAJ heat shock N-terminal domain-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G12430.1 | Symbols: TPR16 | Heat shock protein DnaJ with tetratricopeptide repeat | chr5:4028475-4034086 REVERSE LENGTH=1165</td><td>1157</td><td>1165</td><td>0</td><td>100.7</td><td>75.0</td><td>83.7</td></tr>
<tr><td>Rsa1.0_00016.1.g945.t1</td><td>gb|EOA19414.1| hypothetical protein CARUB_v10001152mg, partial [Capsella rubella]</td><td>363</td><td>387</td><td>1.00E-163</td><td>106.6</td><td>84.6</td><td>90.4</td><td>hypothetical protein CARUB_v10001152mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G12410.1 | Symbols: | THUMP domain-containing protein | chr5:4021974-4023950 REVERSE LENGTH=376</td><td>363</td><td>376</td><td>1.00E-160</td><td>103.6</td><td>82.9</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00016.1.g946.t12</td><td>ref|NP_568273.2| PHD-finger and DNA binding domain-containing protein [Arabidopsis thaliana] gi|332004422|gb|AED91805.1| PHD-finger and DNA binding domain-containing protein [Arabidopsis thaliana]</td><td>1191</td><td>1602</td><td>0</td><td>134.5</td><td>65.8</td><td>76.7</td><td>PHD-finger and DNA binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G12400.1 | Symbols: | DNA binding;zinc ion binding;DNA binding | chr5:4013813-4021018 FORWARD LENGTH=1602</td><td>1191</td><td>1602</td><td>0</td><td>134.5</td><td>65.8</td><td>76.7</td></tr>
<tr><td>Rsa1.0_00016.1.g947.t1</td><td>gb|AFO66516.1| putative 17.9 kDa class II heat shock protein [Brassica napus]</td><td>154</td><td>154</td><td>2.00E-71</td><td>100.0</td><td>94.2</td><td>98.7</td><td>putative 17.9 kDa class II heat shock protein</td><td>gbpln</td><td>Brassica napus</td><td>AT5G12020.1 | Symbols: HSP17.6II | 17.6 kDa class II heat shock protein | chr5:3882409-3882876 REVERSE LENGTH=155</td><td>154</td><td>155</td><td>3.00E-69</td><td>100.6</td><td>90.3</td><td>95.5</td></tr>
</table>

Rsa1.0_00016.1.g948.t1	gb|AFO66517.1| putative kinase [Brassica napus]	503	1266	0	251.7	89.5	92.4	putative kinase	gbpln	Brassica napus	AT5G12010.1 | Symbols: | unknown protein; INVOLVED IN: response to salt stress; LOCATED IN: chloroplast, plasma membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G29780.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3877975-3879483 REVERSE LENGTH=502	503	502	0	99.8	83.7	89.5
Rsa1.0_00016.1.g949.t1	gb|AFO66517.1| putative kinase [Brassica napus]	698	1266	0	181.4	93.6	96.3	putative kinase	gbpln	Brassica napus	AT5G12000.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr5:3874151-3876780 REVERSE LENGTH=701	698	701	0	100.4	83.8	90.4
Rsa1.0_00016.1.g950.t1	ref|NP_196760.1| proline-rich family protein [Arabidopsis thaliana] gi|7573366|emb|CAB87672.1| putative protein [Arabidopsis thaliana] gi|332004365|gb|AED91748.1| proline-rich family protein [Arabidopsis thaliana]	249	181	2.00E-26	72.7	52.2	57.4	proline-rich family protein	gbpln	Arabidopsis thaliana	AT5G11990.1 | Symbols: | proline-rich family protein | chr5:3872651-3873196 REVERSE LENGTH=181	249	181	5.00E-29	72.7	52.2	57.4
Rsa1.0_00016.1.g951.t1	gb|AFO66519.1| putative ABC superfamily ATP binding cassette transporter [Brassica napus]	103	356	8.00E-41	345.6	83.5	88.3	putative ABC superfamily ATP binding cassette transporter	gbpln	Brassica napus	AT5G11970.1 | Symbols: | Protein of unknown function (DUF3511) | chr5:3863289-3863606 REVERSE LENGTH=105	103	105	1.00E-41	101.9	86.4	90.3
Rsa1.0_00016.1.g952.t1	gb|EOA20897.1| hypothetical protein CARUB_v10001232mg, partial [Capsella rubella]	384	364	1.00E-141	94.8	67.4	68.2	hypothetical protein CARUB_v10001232mg, partial	gbpln	Capsella rubella	AT5G11960.1 | Symbols: | Protein of unknown function (DUF803) | chr5:3858852-3861462 REVERSE LENGTH=344	384	344	1.00E-141	89.6	66.1	67.2
Rsa1.0_00016.1.g953.t1	gb|AFO66505.1| putative homodimerization protein [Brassica napus]	218	216	1.00E-119	99.1	95.4	97.2	putative homodimerization protein	gbpln	Brassica napus	AT5G11950.2 | Symbols: | Putative lysine decarboxylase family protein | chr5:3855072-3856815 FORWARD LENGTH=216	218	216	1.00E-117	99.1	92.2	96.3
Rsa1.0_00016.1.g954.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00016.1.g955.t1	gb|EOA22071.1| hypothetical protein CARUB_v10002611mg [Capsella rubella]	137	147	2.00E-46	107.3	82.5	89.8	hypothetical protein CARUB_v10002611mg	gbpln	Capsella rubella	AT5G11930.1 | Symbols: | Thioredoxin superfamily protein | chr5:3845165-3845611 REVERSE LENGTH=148	137	148	3.00E-48	108.0	81.0	87.6
Rsa1.0_00016.1.g956.t1	gb|AFO66503.1| putative fructan 1-exohydrolase [Brassica napus]	515	524	0	101.7	93.2	95.9	putative fructan 1-exohydrolase	gbpln	Brassica napus	AT5G11920.1 | Symbols: AtcwINV6, cwINV6 | 6-&1-fructan exohydrolase | chr5:3839490-3842206 FORWARD LENGTH=550	515	550	0	106.8	77.5	88.2
Rsa1.0_00016.1.g957.t1	ref|XP_002873537.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319374|gb|EFH49796.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	297	297	1.00E-150	100.0	87.9	92.9	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT5G11910.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:3836560-3838182 REVERSE LENGTH=297	297	297	2.33E-156	100.0	84.2	91.2
Rsa1.0_00016.1.g958.t1	gb|AFO66502.1| putative eukaryotic translation initiation factor SUI1 family protein [Brassica napus]	200	198	1.00E-105	99.0	97.0	98.0	putative eukaryotic translation initiation factor SUI1 family protein	gbpln	Brassica napus	AT5G11900.1 | Symbols: | Translation initiation factor SUI1 family protein | chr5:3834154-3836023 FORWARD LENGTH=198	200	198	1.00E-106	99.0	95.0	97.5
Rsa1.0_00016.1.g959.t1	gb|AFO66501.1| putative harpin-induced 1 [Brassica napus]	290	284	1.00E-121	97.9	89.0	92.4	putative harpin-induced 1	gbpln	Brassica napus	AT5G11890.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (TAIR:AT1G17620.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3831770-3832633 FORWARD LENGTH=287	290	287	1.00E-111	99.0	79.7	87.6
Rsa1.0_00016.1.g960.t2	gb|AFO66500.1| putative cf-9 protein precursor [Brassica napus]	1114	919	0	82.5	46.7	49.4	putative cf-9 protein precursor	gbpln	Brassica napus	AT3G05650.1 | Symbols: AtRLP32, RLP32 | receptor like protein 32 | chr3:1645884-1648490 REVERSE LENGTH=868	1114	868	0	77.9	38.1	44.0
Rsa1.0_00016.1.g961.t1	gb|AFO66534.1| putative diaminopimelate decarboxylase [Brassica napus]	485	485	0	100.0	96.3	98.1	putative diaminopimelate decarboxylase	gbpln	Brassica napus	AT5G11880.1 | Symbols: | Pyridoxal-dependent decarboxylase family protein | chr5:3827806-3829942 REVERSE LENGTH=489	485	489	0	100.8	92.2	95.9
Rsa1.0_00016.1.g962.t2	gb|AFO66499.1| putative membrane protein [Brassica napus]	192	202	6.00E-88	105.2	85.4	89.1	putative membrane protein	gbpln	Brassica napus	AT5G11870.1 | Symbols: | Alkaline phytoceramidase (aPHC) | chr5:3825720-3827241 FORWARD LENGTH=262	192	262	6.00E-83	136.5	78.1	85.4

Rsa1.0_00016.1.g963.t2	gb|AFO66533.1| putative NLI interacting factor family protein [Brassica napus]	326	477	1.00E-144	146.3	85.0	89.3	putative NLI interacting factor family protein	gbpln	Brassica napus	AT5G11860.4 | Symbols: | SCP1-like small phosphatase 5 | chr5:3822024-3823395 REVERSE LENGTH=305	326	305	1.00E-144	93.6	83.4	88.3
Rsa1.0_00016.1.g964.t1	gb|AFO66525.1| putative Myo28B1 [Brassica napus]	305	303	1.00E-156	99.3	89.8	95.7	putative Myo28B1	gbpln	Brassica napus	AT5G11810.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3808739-3810440 FORWARD LENGTH=306	305	306	1.00E-144	100.3	82.6	91.5
Rsa1.0_00016.1.g965.t1	gb|AFO66532.1| putative potassium ion transmembrane transporter [Brassica napus]	840	580	0	69.0	66.1	66.3	putative potassium ion transmembrane transporter	gbpln	Brassica napus	AT5G11800.1 | Symbols: KEA6, ATKEA6 | K+ efflux antiporter 6 | chr5:3803635-3808069 REVERSE LENGTH=597	840	597	0	71.1	62.4	64.9
Rsa1.0_00016.1.g966.t1	gb|AFO66497.1| putative SNF2 domain-containing protein [Brassica napus]	523	490	0	93.7	79.5	83.6	putative SNF2 domain-containing protein	gbpln	Brassica napus	AT5G11780.1 | Symbols: | unknown protein; Has 37 Blast hits to 37 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 3; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:3793928-3795983 FORWARD LENGTH=504	523	504	0	96.4	67.9	77.4
Rsa1.0_00016.1.g967.t1	sp|P42027.1|NDUS7_BRAOL RecName: Full=NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial; Flags: Precursor gi|562282|emb|CAA57725.1| PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]	217	215	1.00E-121	99.1	97.7	98.6	RecName: Full=NADH dehydrogenase	gbpln	Brassica oleracea	AT5G11770.1 | Symbols: | NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial | chr5:3791148-3792929 REVERSE LENGTH=218	217	218	1.00E-112	100.5	94.9	96.8
Rsa1.0_00016.1.g968.t1	gb|AFO66495.1| hypothetical protein [Brassica napus]	64	59	2.00E-19	92.2	92.2	92.2	hypothetical protein	gbpln	Brassica napus	AT5G11740.1 | Symbols: AGP15, ATAGP15 | arabinogalactan protein 15 | chr5:3784318-3784503 FORWARD LENGTH=61	64	61	1.00E-10	95.3	79.7	85.9
Rsa1.0_00016.1.g969.t1	gb|AFO66494.1| hypothetical protein [Brassica napus]	451	386	0	85.6	80.7	84.0	hypothetical protein	gbpln	Brassica napus	AT5G11730.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:3780963-3782473 FORWARD LENGTH=386	451	386	0	85.6	76.1	81.8
Rsa1.0_00016.1.g970.t1	ref|NP_001154709.2| uncharacterized protein [Arabidopsis thaliana] gi|332004329|gb|AED91712.1| uncharacterized protein AT5G11700 [Arabidopsis thaliana]	1429	1476	0	103.3	93.0	95.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G11700.2 | Symbols: | BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT4G32920.3); Has 8203 Blast hits to 3102 proteins in 389 species: Archae - 3; Bacteria - 5624; Metazoa - 852; Fungi - 139; Plants - 704; Viruses - 77; Other Eukaryotes - 804 (source: NCBI BLink). | chr5:3762961-3771123 REVERSE LENGTH=1476	1429	1476	0	103.3	93.0	95.9
Rsa1.0_00016.1.g971.t1	gb|EOA19413.1| hypothetical protein CARUB_v10001131mg [Capsella rubella]	394	396	0	100.5	90.4	93.1	hypothetical protein CARUB_v10001131mg	gbpln	Capsella rubella	AT5G11650.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:3745069-3746816 FORWARD LENGTH=390	394	390	0	99.0	88.6	92.1
Rsa1.0_00016.1.g972.t1	ref|NP_196724.3| uncharacterized protein [Arabidopsis thaliana] gi|7573377|emb|CAB87681.1| putative protein [Arabidopsis thaliana] gi|332004320|gb|AED91703.1| uncharacterized protein AT5G11630 [Arabidopsis thaliana]	93	93	7.00E-39	100.0	89.2	95.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G11630.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17310.1); Has 90 Blast hits to 90 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:3740545-3740909 FORWARD LENGTH=93	93	93	1.00E-41	100.0	89.2	95.7
Rsa1.0_00016.1.g973.t1	ref|XP_002873525.1| hypothetical protein ARALYDRAFT_350357 [Arabidopsis lyrata subsp. lyrata] gi|297319362|gb|EFH49784.1| hypothetical protein ARALYDRAFT_350357 [Arabidopsis lyrata subsp. lyrata]	277	272	1.00E-112	98.2	76.2	84.5	hypothetical protein ARALYDRAFT_350357	gbpln	Arabidopsis lyrata	AT5G11620.1 | Symbols: | SWIM zinc finger family protein / mitogen-activated protein kinase kinase kinase (MAPKKK)-related | chr5:3739076-3740127 REVERSE LENGTH=273	277	273	1.00E-112	98.6	75.5	84.1
Rsa1.0_00016.1.g974.t1	ref|XP_002873524.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297319361|gb|EFH49783.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	523	546	0	104.4	82.0	90.8	exostosin family protein	gbpln	Arabidopsis lyrata	AT5G11610.1 | Symbols: | Exostosin family protein | chr5:3735569-3737952 REVERSE LENGTH=546	523	546	0	104.4	80.5	88.9
Rsa1.0_00016.1.g975.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00016.1.g976.t1	ref|XP_002873522.1| hypothetical protein ARALYDRAFT_487996 [Arabidopsis lyrata subsp. lyrata] gi|297319359|gb|EFH49781.1| hypothetical protein ARALYDRAFT_487996 [Arabidopsis lyrata subsp. lyrata]	234	236	5.00E-96	100.9	79.9	88.5	hypothetical protein ARALYDRAFT_487996	gbpln	Arabidopsis lyrata	AT5G11590.1 | Symbols: TINY2 | Integrase-type DNA-binding superfamily protein | chr5:3727789-3728499 REVERSE LENGTH=236	234	236	1.00E-94	100.9	79.5	88.5
Rsa1.0_00016.1.g977.t1	ref|NP_196717.3| PQQ_DH domain-containing protein [Arabidopsis thaliana] gi|332004312|gb|AED91695.1| PQQ_DH domain-containing protein [Arabidopsis thaliana]	1549	982	0	63.4	57.4	60.4	PQQ_DH domain-containing protein	gbpln	Arabidopsis thaliana	AT5G11560.1 | Symbols: | catalytics | chr5:3709734-3713994 REVERSE LENGTH=982	1549	982	0	63.4	57.4	60.4
Rsa1.0_00016.1.g978.t1	ref|XP_002873518.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319355|gb|EFH49777.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	541	584	0	107.9	84.7	91.9	FAD-binding domain-containing protein	gbpln	Arabidopsis lyrata	AT5G11540.1 | Symbols: | D-arabinono-1,4-lactone oxidase family protein | chr5:3703002-3704981 REVERSE LENGTH=585	541	585	0	108.1	83.5	91.9
Rsa1.0_00016.1.g979.t1	gb|EOA19844.1| hypothetical protein CARUB_v10000092mg [Capsella rubella]	1052	1094	2.00E-34	104.0	12.5	16.1	hypothetical protein CARUB_v10000092mg	gbpln	Capsella rubella	AT5G11530.1 | Symbols: EMF1 | embryonic flower 1 (EMF1) | chr5:3697140-3700930 FORWARD LENGTH=1096	1052	1096	3.00E-33	104.2	12.5	16.7
Rsa1.0_00016.1.g980.t1	ref|XP_002871478.1| hypothetical protein ARALYDRAFT_487987 [Arabidopsis lyrata subsp. lyrata] gi|297317315|gb|EFH47737.1| hypothetical protein ARALYDRAFT_487987 [Arabidopsis lyrata subsp. lyrata]	1127	960	0	85.2	63.9	71.1	hypothetical protein ARALYDRAFT_487987	gbpln	Arabidopsis lyrata	AT5G11510.1 | Symbols: MYB3R-4, AtMYB3R4 | myb domain protein 3r-4 | chr5:3680452-3684684 FORWARD LENGTH=961	1127	961	0	85.3	63.0	70.0
Rsa1.0_00016.1.g981.t1	gb|EOA21135.1| hypothetical protein CARUB_v10001479mg [Capsella rubella]	310	318	1.00E-148	102.6	90.3	94.5	hypothetical protein CARUB_v10001479mg	gbpln	Capsella rubella	AT5G11480.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:3669350-3671471 REVERSE LENGTH=318	310	318	1.00E-144	102.6	87.1	92.3
Rsa1.0_00016.1.g982.t1	ref|XP_002873515.1| hypothetical protein ARALYDRAFT_487983 [Arabidopsis lyrata subsp. lyrata] gi|297319352|gb|EFH49774.1| hypothetical protein ARALYDRAFT_487983 [Arabidopsis lyrata subsp. lyrata]	655	695	0	106.1	63.2	75.0	hypothetical protein ARALYDRAFT_487983	gbpln	Arabidopsis lyrata	AT5G11470.1 | Symbols: | bromo-adjacent homology (BAH) domain-containing protein | chr5:3662757-3667041 REVERSE LENGTH=757	655	757	0	115.6	64.4	77.1
Rsa1.0_00016.1.g983.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00016.1.g984.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00016.1.g985.t1	gb|EOA21007.1| hypothetical protein CARUB_v10001342mg [Capsella rubella]	275	343	2.00E-82	124.7	65.1	77.8	hypothetical protein CARUB_v10001342mg	gbpln	Capsella rubella	AT5G11460.1 | Symbols: | Protein of unknown function (DUF581) | chr5:3657064-3658388 REVERSE LENGTH=344	275	344	2.00E-70	125.1	65.8	76.4
Rsa1.0_00016.1.g986.t2	ref|XP_002871475.1| hypothetical protein ARALYDRAFT_487981 [Arabidopsis lyrata subsp. lyrata] gi|297317312|gb|EFH47734.1| hypothetical protein ARALYDRAFT_487981 [Arabidopsis lyrata subsp. lyrata]	306	297	1.00E-122	97.1	78.8	84.3	hypothetical protein ARALYDRAFT_487981	gbpln	Arabidopsis lyrata	AT5G11450.1 | Symbols: | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | chr5:3654475-3656357 FORWARD LENGTH=297	306	297	1.00E-124	97.1	78.8	84.0
Rsa1.0_00016.1.g987.t1	ref|XP_002873513.1| CID5/IPD1 [Arabidopsis lyrata subsp. lyrata] gi|297319350|gb|EFH49772.1| CID5/IPD1 [Arabidopsis lyrata subsp. lyrata]	164	165	2.00E-53	100.6	73.2	82.3	CID5/IPD1	gbpln	Arabidopsis lyrata	AT5G11440.1 | Symbols: CID5, IPD1 | CTC-interacting domain 5 | chr5:3653060-3653607 REVERSE LENGTH=155	164	155	1.00E-54	94.5	72.6	81.7
Rsa1.0_00016.1.g988.t1	gb|EOA19945.1| hypothetical protein CARUB_v10000195mg [Capsella rubella]	901	869	0	96.4	74.6	82.6	hypothetical protein CARUB_v10000195mg	gbpln	Capsella rubella	AT5G11430.1 | Symbols: | SPOC domain / Transcription elongation factor S-II protein | chr5:3648469-3652256 FORWARD LENGTH=873	901	873	0	96.9	73.6	83.1
Rsa1.0_00016.1.g989.t1	ref|XP_002871473.1| hypothetical protein ARALYDRAFT_487977 [Arabidopsis lyrata subsp. lyrata] gi|297317310|gb|EFH47732.1| hypothetical protein ARALYDRAFT_487977 [Arabidopsis lyrata subsp. lyrata]	340	366	0	107.6	92.1	98.2	hypothetical protein ARALYDRAFT_487977	gbpln	Arabidopsis lyrata	AT5G11420.1 | Symbols: | Protein of unknown function, DUF642 | chr5:3644655-3646991 FORWARD LENGTH=366	340	366	0	107.6	91.5	97.9
Rsa1.0_00016.1.g990.t1	ref|NP_196702.1| protein kinase family protein [Arabidopsis thaliana] gi|8953403|emb|CAB96676.1| putative protein [Arabidopsis thaliana] gi|332004291|gb|AED91674.1| protein kinase family protein [Arabidopsis thaliana]	609	336	2.00E-81	55.2	28.4	35.5	protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G11410.1 | Symbols: | Protein kinase superfamily protein | chr5:3638431-3639883 REVERSE LENGTH=336	609	336	6.00E-84	55.2	28.4	35.5
Rsa1.0_00016.1.g991.t1	gb|EOA20067.1| hypothetical protein CARUB_v10000340mg [Capsella rubella]	694	709	0	102.2	80.3	89.0	hypothetical protein CARUB_v10000340mg	gbpln	Capsella rubella	AT5G11390.1 | Symbols: WIT1 | WPP domain-interacting protein 1 | chr5:3633971-3636418 FORWARD LENGTH=703	694	703	0	101.3	80.0	88.6

Rsa1.0_00016.1.g992.t2	ref|NP_196699.1| 1-deoxy-D-xylulose 5-phosphate synthase 3 [Arabidopsis thaliana] gi|8953400|emb|CAB96673.1| 1-D-deoxyxylulose 5-phosphate synthase-like protein [Arabidopsis thaliana] gi|332004286|gb|AED91669.1| 1-deoxy-D-xylulose 5-phosphate synthase 3 [Arabidopsis thaliana]	1465	700	0	47.8	42.4	44.6	1-deoxy-D-xylulose 5-phosphate synthase 3	gbpln	Arabidopsis thaliana	AT5G11380.1 | Symbols: DXPS3 | 1-deoxy-D-xylulose 5-phosphate synthase 3 | chr5:3630172-3633250 FORWARD LENGTH=700	1465	700	0	47.8	42.4	44.6
Rsa1.0_00016.1.g993.t1	ref|XP_002871470.1| hypothetical protein ARALYDRAFT_909096 [Arabidopsis lyrata subsp. lyrata] gi|297317307|gb|EFH47729.1| hypothetical protein ARALYDRAFT_909096 [Arabidopsis lyrata subsp. lyrata]	164	164	6.00E-89	100.0	95.7	99.4	hypothetical protein ARALYDRAFT_909096	gbpln	Arabidopsis lyrata	AT5G11340.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr5:3619226-3621068 FORWARD LENGTH=164	164	164	4.00E-88	100.0	92.1	97.6
Rsa1.0_00016.1.g994.t1	gb|EOA20763.1| hypothetical protein CARUB_v10001092mg [Capsella rubella]	406	408	0	100.5	84.7	91.4	hypothetical protein CARUB_v10001092mg	gbpln	Capsella rubella	AT5G11330.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr5:3617342-3618861 REVERSE LENGTH=408	406	408	0	100.5	85.0	91.1
Rsa1.0_00016.1.g995.t1	gb|EOA19559.1| hypothetical protein CARUB_v10002580mg [Capsella rubella]	412	412	0	100.0	84.5	88.8	hypothetical protein CARUB_v10002580mg	gbpln	Capsella rubella	AT5G11320.1 | Symbols: YUC4 | Flavin-binding monooxygenase family protein | chr5:3611429-3613361 REVERSE LENGTH=411	412	411	0	99.8	83.3	88.6
Rsa1.0_00016.1.g996.t1	gb|EOA19373.1| hypothetical protein CARUB_v10000508mg [Capsella rubella]	593	605	0	102.0	80.9	88.7	hypothetical protein CARUB_v10000508mg	gbpln	Capsella rubella	AT5G11310.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:3606490-3608409 FORWARD LENGTH=602	593	602	0	101.5	79.3	86.3
Rsa1.0_00016.1.g997.t1	ref|XP_002873505.1| hypothetical protein ARALYDRAFT_350326 [Arabidopsis lyrata subsp. lyrata] gi|297319342|gb|EFH49764.1| hypothetical protein ARALYDRAFT_350326 [Arabidopsis lyrata subsp. lyrata]	435	436	0	100.2	84.1	91.5	hypothetical protein ARALYDRAFT_350326	gbpln	Arabidopsis lyrata	AT5G11300.1 | Symbols: CYC3B, CYC2BAT, CYCA2;2 | mitotic-like cyclin 3B from Arabidopsis | chr5:3601811-3604466 REVERSE LENGTH=436	435	436	0	100.2	83.7	90.8
Rsa1.0_00016.1.g998.t1	gb|EOA21558.1| hypothetical protein CARUB_v10001967mg [Capsella rubella]	210	209	1.00E-102	99.5	87.6	95.2	hypothetical protein CARUB_v10001967mg	gbpln	Capsella rubella	AT5G11280.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80200.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:3597321-3598347 FORWARD LENGTH=209	210	209	1.00E-103	99.5	86.7	94.3
Rsa1.0_00016.1.g999.t1	ref|XP_002873503.1| hypothetical protein ARALYDRAFT_487959 [Arabidopsis lyrata subsp. lyrata] gi|297319340|gb|EFH49762.1| hypothetical protein ARALYDRAFT_487959 [Arabidopsis lyrata subsp. lyrata]	349	352	1.00E-130	100.9	82.2	88.8	hypothetical protein ARALYDRAFT_487959	gbpln	Arabidopsis lyrata	AT5G11270.1 | Symbols: OCP3 | overexpressor of cationic peroxidase 3 | chr5:3595557-3597076 REVERSE LENGTH=354	349	354	1.00E-116	101.4	75.1	82.8
Rsa1.0_00016.1.g1000.t1	ref|XP_002873502.1| hypothetical protein ARALYDRAFT_909087 [Arabidopsis lyrata subsp. lyrata] gi|297319339|gb|EFH49761.1| hypothetical protein ARALYDRAFT_909087 [Arabidopsis lyrata subsp. lyrata]	169	167	1.00E-66	98.8	88.8	91.7	hypothetical protein ARALYDRAFT_909087	gbpln	Arabidopsis lyrata	AT5G11260.1 | Symbols: HY5, TED 5 | Basic-leucine zipper (bZIP) transcription factor family protein | chr5:3593583-3594800 REVERSE LENGTH=168	169	168	8.00E-66	99.4	89.9	92.3
Rsa1.0_00016.1.g1001.t2	gb|ACP30577.1| disease resistance protein [Brassica rapa subsp. pekinensis]	485	1235	8.00E-91	254.6	48.9	63.3	disease resistance protein	gbpln	Brassica rapa	AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189	485	1189	5.00E-88	245.2	37.3	43.9
Rsa1.0_00016.1.g1002.t1	gb|EOA20202.1| hypothetical protein CARUB_v10000497mg [Capsella rubella]	606	612	0	101.0	86.3	92.4	hypothetical protein CARUB_v10000497mg	gbpln	Capsella rubella	AT5G11240.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:3582949-3586782 FORWARD LENGTH=615	606	615	0	101.5	86.0	91.4
Rsa1.0_00016.1.g1003.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00016.1.g1004.t1	gb|EOA22882.1| hypothetical protein CARUB_v10003614mg [Capsella rubella]	353	349	0	98.9	92.9	96.0	hypothetical protein CARUB_v10003614mg	gbpln	Capsella rubella	AT5G25400.1 | Symbols: | Nucleotide-sugar transporter family protein | chr5:8823283-8824332 FORWARD LENGTH=349	353	349	0	98.9	89.5	94.1
Rsa1.0_00016.1.g1005.t1	ref|XP_002886774.1| hypothetical protein ARALYDRAFT_893811 [Arabidopsis lyrata subsp. lyrata] gi|297332615|gb|EFH63033.1| hypothetical protein ARALYDRAFT_893811 [Arabidopsis lyrata subsp. lyrata]	310	303	1.00E-102	97.7	60.6	73.2	hypothetical protein ARALYDRAFT_893811	gbpln	Arabidopsis lyrata	AT1G64870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G45200.1); Has 99 Blast hits to 91 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 99; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:24102917-24103831 FORWARD LENGTH=304	310	304	1.00E-102	98.1	60.6	71.6

<table>
<tr><td>Rsa1.0_00016.1.g1006.t1</td><td>ref|NP_196670.1| serine-rich protein-like protein [Arabidopsis thaliana] gi|9795161|emb|CAC03457.1| putative protein [Arabidopsis thaliana] gi|21592828|gb|AAM64778.1| serine-rich protein [Arabidopsis thaliana] gi|28466931|gb|AAO44074.1| At5g11090 [Arabidopsis thaliana] gi|110743766|dbj|BAE99719.1| hypothetical protein [Arabidopsis thaliana] gi|332004251|gb|AED91634.1| serine-rich protein-like protein [Arabidopsis thaliana]</td><td>271</td><td>217</td><td>5.00E-76</td><td>80.1</td><td>62.0</td><td>66.4</td><td>serine-rich protein-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G11090.1 | Symbols: | serine-rich protein-related | chr5:3524796-3525449 FORWARD LENGTH=217</td><td>271</td><td>217</td><td>1.00E-78</td><td>80.1</td><td>62.0</td><td>66.4</td></tr>
<tr><td>Rsa1.0_00016.1.g1007.t1</td><td>ref|NP_175758.2| peptidase-S24/S26 domain-containing protein [Arabidopsis thaliana] gi|44681348|gb|AAS47614.1| At1g53530 [Arabidopsis thaliana] gi|45773848|gb|AAS76728.1| At1g53530 [Arabidopsis thaliana] gi|110738199|dbj|BAF01030.1| hypothetical protein [Arabidopsis thaliana] gi|332194831|gb|AEE32952.1| peptidase-S24/S26 domain-containing protein [Arabidopsis thaliana]</td><td>182</td><td>168</td><td>6.00E-79</td><td>92.3</td><td>81.3</td><td>86.3</td><td>peptidase-S24/S26 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G53530.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr1:19978249-19979778 FORWARD LENGTH=168</td><td>182</td><td>168</td><td>2.00E-81</td><td>92.3</td><td>81.3</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00016.1.g1008.t1</td><td>ref|NP_196668.1| uncharacterized protein [Arabidopsis thaliana] gi|9795159|emb|CAC03455.1| putative protein [Arabidopsis thaliana] gi|21593765|gb|AAM65732.1| unknown [Arabidopsis thaliana] gi|110740693|dbj|BAE98448.1| hypothetical protein [Arabidopsis thaliana] gi|332004248|gb|AED91631.1| uncharacterized protein AT5G11070 [Arabidopsis thaliana]</td><td>132</td><td>152</td><td>8.00E-53</td><td>115.2</td><td>79.5</td><td>87.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G11070.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3516440-3516898 REVERSE LENGTH=152</td><td>132</td><td>152</td><td>2.00E-55</td><td>115.2</td><td>79.5</td><td>87.1</td></tr>
<tr><td>Rsa1.0_00016.1.g1009.t1</td><td>ref|XP_002871450.1| hypothetical protein ARALYDRAFT_487936 [Arabidopsis lyrata subsp. lyrata] gi|297317287|gb|EFH47709.1| hypothetical protein ARALYDRAFT_487936 [Arabidopsis lyrata subsp. lyrata]</td><td>1183</td><td>1186</td><td>0</td><td>100.3</td><td>95.7</td><td>97.4</td><td>hypothetical protein ARALYDRAFT_487936</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G11040.1 | Symbols: TRS120, AtTRS120 | TRS120 | chr5:3495332-3500610 FORWARD LENGTH=1186</td><td>1183</td><td>1186</td><td>0</td><td>100.3</td><td>95.3</td><td>97.0</td></tr>
<tr><td>Rsa1.0_00016.1.g1010.t1</td><td>ref|XP_002873494.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319331|gb|EFH49753.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>588</td><td>592</td><td>0</td><td>100.7</td><td>69.0</td><td>78.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G11030.2 | Symbols: ALF4 | aberrant lateral root formation 4 | chr5:3490993-3495078 REVERSE LENGTH=602</td><td>588</td><td>602</td><td>0</td><td>102.4</td><td>66.0</td><td>76.2</td></tr>
<tr><td>Rsa1.0_00016.1.g1011.t1</td><td>gb|EOA20670.1| hypothetical protein CARUB_v10000982mg [Capsella rubella]</td><td>438</td><td>438</td><td>0</td><td>100.0</td><td>83.3</td><td>89.0</td><td>hypothetical protein CARUB_v10000982mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G11020.1 | Symbols: | Protein kinase superfamily protein | chr5:3486439-3488983 REVERSE LENGTH=433</td><td>438</td><td>433</td><td>0</td><td>98.9</td><td>81.1</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00016.1.g1012.t1</td><td>ref|NP_850805.1| Pre-mRNA cleavage complex II protein family [Arabidopsis thaliana] gi|42573337|ref|NP_974765.1| Pre-mRNA cleavage complex II protein family [Arabidopsis thaliana] gi|75161516|sp|Q8VYP6.1|NOL9_ARATH RecName: Full=Polynucleotide 5'-hydroxyl-kinase NOL9; AltName: Full=Nucleolar protein 9 homolog gi|17979299|gb|AAL49875.1| unknown protein [Arabidopsis thaliana] gi|20465981|gb|AAM20212.1| unknown protein [Arabidopsis thaliana] gi|332004238|gb|AED91621.1| Pre-mRNA cleavage complex II protein family [Arabidopsis thaliana] gi|332004239|gb|AED91622.1| Pre-mRNA cleavage complex II protein family [Arabidopsis thaliana]</td><td>370</td><td>368</td><td>1.00E-170</td><td>99.5</td><td>80.5</td><td>87.8</td><td>Pre-mRNA cleavage complex II protein family</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G11010.3 | Symbols: | Pre-mRNA cleavage complex II protein family | chr5:3484176-3486067 FORWARD LENGTH=368</td><td>370</td><td>368</td><td>1.00E-172</td><td>99.5</td><td>80.5</td><td>87.8</td></tr>
<tr><td>Rsa1.0_00016.1.g1013.t1</td><td>gb|EOA21927.1| hypothetical protein CARUB_v10002414mg [Capsella rubella]</td><td>222</td><td>390</td><td>1.00E-52</td><td>175.7</td><td>62.6</td><td>67.6</td><td>hypothetical protein CARUB_v10002414mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G11000.1 | Symbols: | Plant protein of unknown function (DUF868) | chr5:3479166-3480335 REVERSE LENGTH=389</td><td>222</td><td>389</td><td>1.00E-46</td><td>175.2</td><td>63.1</td><td>69.4</td></tr>
<tr><td>Rsa1.0_00016.1.g1014.t1</td><td>gb|EOA19498.1| hypothetical protein CARUB_v10002201mg [Capsella rubella]</td><td>148</td><td>149</td><td>8.00E-71</td><td>100.7</td><td>89.2</td><td>92.6</td><td>hypothetical protein CARUB_v10002201mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G10990.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:3476884-3477330 FORWARD LENGTH=148</td><td>148</td><td>148</td><td>2.00E-72</td><td>100.0</td><td>87.2</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00016.1.g1015.t1</td><td>gb|EOA22648.1| hypothetical protein CARUB_v10003340mg [Capsella rubella]</td><td>251</td><td>272</td><td>1.00E-101</td><td>108.4</td><td>76.9</td><td>84.5</td><td>hypothetical protein CARUB_v10003340mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G10970.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:3469268-3470086 FORWARD LENGTH=272</td><td>251</td><td>272</td><td>1.00E-100</td><td>108.4</td><td>72.9</td><td>82.9</td></tr>
</table>

Rsa1.0_00016.1.g1016.t1	ref|XP_002871445.1| hypothetical protein ARALYDRAFT_487926 [Arabidopsis lyrata subsp. lyrata] gi|297317282|gb|EFH47704.1| hypothetical protein ARALYDRAFT_487926 [Arabidopsis lyrata subsp. lyrata]	275	276	1.00E-142	100.4	88.4	96.0	hypothetical protein ARALYDRAFT_487926	gbpln	Arabidopsis lyrata	AT5G10960.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:3464581-3465414 FORWARD LENGTH=277	275	277	1.00E-143	100.7	88.0	95.3
Rsa1.0_00016.1.g1017.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1987	1274	0	64.1	30.5	41.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1987	575	1.00E-76	28.9	8.9	13.9
Rsa1.0_00016.1.g1018.t1	emb|CAN83015.1| hypothetical protein VITISV_041694 [Vitis vinifera]	243	1099	2.00E-88	452.3	63.4	76.1	hypothetical protein VITISV_041694	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	243	1262	5.00E-43	519.3	33.3	52.3
Rsa1.0_00016.1.g1019.t1	ref|XP_002873486.1| hypothetical protein ARALYDRAFT_487925 [Arabidopsis lyrata subsp. lyrata] gi|297319323|gb|EFH49745.1| hypothetical protein ARALYDRAFT_487925 [Arabidopsis lyrata subsp. lyrata]	754	755	0	100.1	89.0	94.3	hypothetical protein ARALYDRAFT_487925	gbpln	Arabidopsis lyrata	AT5G10940.2 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:3448890-3454127 REVERSE LENGTH=754	754	754	0	100.0	88.9	94.0
Rsa1.0_00016.1.g1020.t1	ref|NP_568241.2| CBL-interacting serine/threonine-protein kinase 5 [Arabidopsis thaliana] gi|75334907|sp|Q9LEU7.1|CIPK5_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 5; AltName: Full=SNF1-related kinase 3.24; AltName: Full=SOS2-like protein kinase PKS19 gi|19424694|gb|AAF86504.2|AF285105_1 CBL-interacting protein kinase 5 [Arabidopsis thaliana] gi|8979727|emb|CAB96848.1| serine/threonine protein kinase-like protein [Arabidopsis thaliana] gi|17065378|gb|AAL32843.1| serine/threonine protein kinase-like protein [Arabidopsis thaliana] gi|332004227|gb|AED91610.1| CBL-interacting serine/threonine-protein kinase 5 [Arabidopsis thaliana]	440	445	0	101.1	85.0	90.9	CBL-interacting serine/threonine-protein kinase 5	gbpln	Arabidopsis thaliana	AT5G10930.1 | Symbols: CIPK5, SnRK3.24 | CBL-interacting protein kinase 5 | chr5:3445569-3446906 REVERSE LENGTH=445	440	445	0	101.1	85.0	90.9
Rsa1.0_00016.1.g1021.t3	gb|EOA20415.1| hypothetical protein CARUB_v10000724mg [Capsella rubella]	519	518	0	99.8	91.9	95.2	hypothetical protein CARUB_v10000724mg	gbpln	Capsella rubella	AT5G10920.1 | Symbols: | L-Aspartase-like family protein | chr5:3441805-3443892 FORWARD LENGTH=517	519	517	0	99.6	92.5	96.0
Rsa1.0_00016.1.g1022.t1	ref|XP_002873483.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319320|gb|EFH49742.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	317	303	6.00E-89	95.6	60.6	73.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G10890.1 | Symbols: | myosin heavy chain-related | chr5:3434030-3435067 REVERSE LENGTH=295	317	295	4.00E-88	93.1	58.4	71.6
Rsa1.0_00016.1.g1023.t1	gb|EOA21983.1| hypothetical protein CARUB_v10002490mg [Capsella rubella]	207	206	1.00E-108	99.5	93.7	96.1	hypothetical protein CARUB_v10002490mg	gbpln	Capsella rubella	AT5G10860.1 | Symbols: | Cystathionine beta-synthase (CBS) family protein | chr5:3429173-3430142 REVERSE LENGTH=206	207	206	1.00E-109	99.5	92.8	95.2
Rsa1.0_00016.1.g1024.t1	#	#	#	#	#	#	#	-	----	----	AT5G10790.1 | Symbols: UBP22 | ubiquitin-specific protease 22 | chr5:3410638-3412559 FORWARD LENGTH=557	134	557	3.00E-12	415.7	22.4	23.9
Rsa1.0_00016.1.g1025.t1	gb|AAF79677.1|AC022314_18 F9C16.26 [Arabidopsis thaliana]	566	1902	3.00E-47	336.0	17.8	25.1	F9C16.26	gbpln	Arabidopsis thaliana	AT5G32613.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr5:12263255-12265041 FORWARD LENGTH=457	566	457	1.00E-15	80.7	8.0	11.8
Rsa1.0_00016.1.g1026.t1	gb|EOA20535.1| hypothetical protein CARUB_v10000848mg [Capsella rubella]	140	481	4.00E-17	343.6	42.1	53.6	hypothetical protein CARUB_v10000848mg	gbpln	Capsella rubella	AT5G10760.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:3400671-3402165 REVERSE LENGTH=464	140	464	7.00E-18	331.4	44.3	62.9
Rsa1.0_00016.1.g1027.t1	ref|XP_002873476.1| hypothetical protein ARALYDRAFT_325615 [Arabidopsis lyrata subsp. lyrata] gi|297319313|gb|EFH49735.1| hypothetical protein ARALYDRAFT_325615 [Arabidopsis lyrata subsp. lyrata]	479	475	1.00E-178	99.2	70.1	81.6	hypothetical protein ARALYDRAFT_325615	gbpln	Arabidopsis lyrata	AT5G10770.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:3403331-3405331 REVERSE LENGTH=474	479	474	1.00E-172	99.0	68.3	77.9
Rsa1.0_00016.1.g1028.t1	ref|XP_002873473.1| hypothetical protein ARALYDRAFT_487908 [Arabidopsis lyrata subsp. lyrata] gi|297319310|gb|EFH49732.1| hypothetical protein ARALYDRAFT_487908 [Arabidopsis lyrata subsp. lyrata]	328	373	1.00E-157	113.7	86.0	92.1	hypothetical protein ARALYDRAFT_487908	gbpln	Arabidopsis lyrata	AT5G10740.1 | Symbols: | Protein phosphatase 2C family protein | chr5:3393797-3395848 REVERSE LENGTH=354	328	354	1.00E-158	107.9	86.6	92.4

Rsa1.0_00016.1.g1029.t1	gb|EOA25676.1| hypothetical protein CARUB_v10019028mg [Capsella rubella]	479	476	0	99.4	76.2	87.5	hypothetical protein CARUB_v10019028mg	gbpln	Capsella rubella	AT3G28600.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:10722437-10723870 FORWARD LENGTH=477	479	477	0	99.6	76.0	86.2
Rsa1.0_00016.1.g1030.t1	ref|XP_002873472.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319309|gb|EFH49731.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata]	289	287	1.00E-151	99.3	95.2	97.6	catalytic/ coenzyme binding protein	gbpln	Arabidopsis lyrata	AT5G10730.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:3390822-3392947 REVERSE LENGTH=287	289	287	1.00E-150	99.3	95.2	97.6
Rsa1.0_00016.1.g1031.t1	ref|XP_002871436.1| hypothetical protein ARALYDRAFT_909030 [Arabidopsis lyrata subsp. lyrata] gi|297317273|gb|EFH47695.1| hypothetical protein ARALYDRAFT_909030 [Arabidopsis lyrata subsp. lyrata]	911	923	0	101.3	87.9	93.3	hypothetical protein ARALYDRAFT_909030	gbpln	Arabidopsis lyrata	AT5G10720.1 | Symbols: AHK5, CKI2, HK5 | histidine kinase 5 | chr5:3386835-3390541 FORWARD LENGTH=922	911	922	0	101.2	87.7	92.9
Rsa1.0_00016.1.g1032.t1	ref|NP_568234.1| uncharacterized protein [Arabidopsis thaliana] gi|19347741|gb|AAL86296.1| unknown protein [Arabidopsis thaliana] gi|24030282|gb|AAN41313.1| unknown protein [Arabidopsis thaliana] gi|332004199|gb|AED91582.1| uncharacterized protein AT5G10695 [Arabidopsis thaliana]	67	67	4.00E-27	100.0	86.6	89.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G10695.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G57123.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:3377817-3378020 FORWARD LENGTH=67	67	67	7.00E-30	100.0	86.6	89.6
Rsa1.0_00016.1.g1033.t1	ref|NP_196627.1| calmodulin-binding protein-like protein [Arabidopsis thaliana] gi|10129644|emb|CAC08240.1| vacuolar calcium binding protein-like [Arabidopsis thaliana] gi|53828561|gb|AAU94390.1| At5g10660 [Arabidopsis thaliana] gi|55733763|gb|AAV59278.1| At5g10660 [Arabidopsis thaliana] gi|332004195|gb|AED91578.1| calmodulin-binding protein-like protein [Arabidopsis thaliana]	355	407	3.00E-94	114.6	69.0	79.4	calmodulin-binding protein-like protein	gbpln	Arabidopsis thaliana	AT5G10660.1 | Symbols: | calmodulin-binding protein-related | chr5:3370553-3371776 FORWARD LENGTH=407	355	407	7.00E-97	114.6	69.0	79.4
Rsa1.0_00016.1.g1034.t1	ref|NP_196626.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|79327651|ref|NP_001031869.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|53850555|gb|AAU95454.1| At5g10650 [Arabidopsis thaliana] gi|58652060|gb|AAW80855.1| At5g10650 [Arabidopsis thaliana] gi|332004193|gb|AED91576.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332004194|gb|AED91577.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	521	525	0	100.8	74.7	83.7	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G10650.2 | Symbols: | RING/U-box superfamily protein | chr5:3365237-3367263 REVERSE LENGTH=525	521	525	0	100.8	74.7	83.7
Rsa1.0_00016.1.g1035.t1	#	#	#	#	#	#	#	–	----	----	AT5G10630.2 | Symbols: | Translation elongation factor EF1A/initiation factor IF2gamma family protein | chr5:3360561-3364414 FORWARD LENGTH=668	97	668	2.00E-11	688.7	32.0	35.1
Rsa1.0_00016.1.g1036.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00016.1.g1037.t1	emb|CAB89379.1| putative protein [Arabidopsis thaliana]	109	804	5.00E-52	737.6	88.1	91.7	putative protein	gbpln	Arabidopsis thaliana	AT5G10625.1 | Symbols: | BEST Arabidopsis thaliana protein match is: flowering promoting factor 1 (TAIR:AT5G24860.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:3358934-3359272 FORWARD LENGTH=112	109	112	2.00E-53	102.8	91.7	96.3
Rsa1.0_00016.1.g1038.t1	ref|NP_196624.1| putative RNA methyltransferase [Arabidopsis thaliana] gi|32171918|sp|Q9LXB4.1|Y5620_ARATH RecName: Full=Putative RNA methyltransferase At5g10620 gi|7671441|emb|CAB89381.1| putative protein [Arabidopsis thaliana] gi|332004189|gb|AED91572.1| putative RNA methyltransferase [Arabidopsis thaliana]	195	193	6.00E-99	99.0	87.7	91.3	putative RNA methyltransferase	gbpln	Arabidopsis thaliana	AT5G10620.1 | Symbols: | methyltransferases | chr5:3355466-3356615 REVERSE LENGTH=193	195	193	1.00E-101	99.0	87.7	91.3

Rsa1.0_00016.1.g1039.t1	ref|XP_002871428.1| CYP81K1 [Arabidopsis lyrata subsp. lyrata] gi|297317265|gb|EFH47687.1| CYP81K1 [Arabidopsis lyrata subsp. lyrata]	498	500	0	100.4	86.1	92.4	CYP81K1	gbpln	Arabidopsis lyrata	AT5G10610.1 | Symbols: CYP81K1 | cytochrome P450, family 81, subfamily K, polypeptide 1 | chr5:3353518-3355020 FORWARD LENGTH=500	498	500	0	100.4	85.5	92.0
Rsa1.0_00016.1.g1040.t1	ref|XP_002871428.1| CYP81K1 [Arabidopsis lyrata subsp. lyrata] gi|297317265|gb|EFH47687.1| CYP81K1 [Arabidopsis lyrata subsp. lyrata]	499	500	0	100.2	80.6	89.2	CYP81K1	gbpln	Arabidopsis lyrata	AT5G10610.1 | Symbols: CYP81K1 | cytochrome P450, family 81, subfamily K, polypeptide 1 | chr5:3353518-3355020 FORWARD LENGTH=500	499	500	0	100.2	80.0	88.2
Rsa1.0_00016.1.g1041.t1	gb|EOA21978.1| hypothetical protein CARUB_v10002483mg [Capsella rubella]	169	247	3.00E-79	146.2	86.4	93.5	hypothetical protein CARUB_v10002483mg	gbpln	Capsella rubella	AT5G10580.1 | Symbols: | Protein of unknown function, DUF599 | chr5:3347511-3348657 FORWARD LENGTH=246	169	246	2.00E-81	145.6	86.4	92.9
Rsa1.0_00016.1.g1042.t1	gb|EOA21164.1| hypothetical protein CARUB_v10001512mg [Capsella rubella]	302	313	1.00E-110	103.6	68.5	77.2	hypothetical protein CARUB_v10001512mg	gbpln	Capsella rubella	AT5G10440.1 | Symbols: CYCD4;2 | cyclin d4;2 | chr5:3280611-3282342 REVERSE LENGTH=298	302	298	1.00E-109	98.7	69.5	77.2
Rsa1.0_00016.1.g1043.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00016.1.g1044.t1	gb|AAZ66942.1| 117M18_23 [Brassica rapa]	483	518	0	107.2	78.3	89.0	117M18_23	gbpln	Brassica rapa	AT5G44050.1 | Symbols: | MATE efflux family protein | chr5:17722484-17726209 FORWARD LENGTH=491	483	491	0	101.7	76.6	86.3
Rsa1.0_00016.1.g1045.t3	gb|AAZ66942.1| 117M18_23 [Brassica rapa]	469	518	0	110.4	86.4	94.2	117M18_23	gbpln	Brassica rapa	AT5G44050.1 | Symbols: | MATE efflux family protein | chr5:17722484-17726209 FORWARD LENGTH=491	469	491	0	104.7	80.4	91.0
Rsa1.0_00016.1.g1046.t1	ref|NP_199218.1| mate efflux domain-containing protein [Arabidopsis thaliana] gi|9758564|dbj|BAB09065.1| unnamed protein product [Arabidopsis thaliana] gi|332007669|gb|AED95052.1| mate efflux domain-containing protein [Arabidopsis thaliana]	453	491	0	108.4	76.4	86.8	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT5G44050.1 | Symbols: | MATE efflux family protein | chr5:17722484-17726209 FORWARD LENGTH=491	453	491	0	108.4	76.4	86.8
Rsa1.0_00016.1.g1047.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00016.1.g1048.t1	ref|NP_199218.1| mate efflux domain-containing protein [Arabidopsis thaliana] gi|9758564|dbj|BAB09065.1| unnamed protein product [Arabidopsis thaliana] gi|332007669|gb|AED95052.1| mate efflux domain-containing protein [Arabidopsis thaliana]	506	491	0	97.0	80.0	87.5	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT5G44050.1 | Symbols: | MATE efflux family protein | chr5:17722484-17726209 FORWARD LENGTH=491	506	491	0	97.0	80.0	87.5
Rsa1.0_00016.1.g1049.t1	gb|EOA20878.1| hypothetical protein CARUB_v10001215mg [Capsella rubella]	352	369	1.00E-143	104.8	74.1	84.7	hypothetical protein CARUB_v10001215mg	gbpln	Capsella rubella	AT5G10410.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr5:3271952-3273082 FORWARD LENGTH=338	352	338	1.00E-139	96.0	69.0	79.8
Rsa1.0_00016.1.g1050.t1	tpg|DAA55311.1| TPA: histone H3.2 [Zea mays]	136	245	1.00E-72	180.1	100.0	100.0	TPA: histone H3.2	gbenv/gbpln	Zea mays	AT5G65360.1 | Symbols: | Histone superfamily protein | chr5:26120099-26120509 REVERSE LENGTH=136	136	136	5.00E-74	100.0	100.0	100.0
Rsa1.0_00016.1.g1051.t1	gb|AAG51247.1|AC055769_6 copia-type polyprotein, putative; 28768-32772 [Arabidopsis thaliana]	1341	1334	0	99.5	67.3	80.2	copia-type polyprotein, putative; 28768-32772	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1341	1262	4.00E-97	94.1	13.3	21.4
Rsa1.0_00016.1.g1052.t1	ref|XP_002871419.1| hypothetical protein ARALYDRAFT_350245 [Arabidopsis lyrata subsp. lyrata] gi|297317256|gb|EFH47678.1| hypothetical protein ARALYDRAFT_350245 [Arabidopsis lyrata subsp. lyrata]	386	306	3.00E-67	79.3	46.4	54.9	hypothetical protein ARALYDRAFT_350245	gbpln	Arabidopsis lyrata	AT5G10380.1 | Symbols: RING1, ATRING1 | RING/U-box superfamily protein | chr5:3267819-3268724 FORWARD LENGTH=301	386	301	7.00E-65	78.0	45.6	55.2
Rsa1.0_00016.1.g1053.t1	gb|AAZ66938.1| 117M18_19 [Brassica rapa]	1775	1755	0	98.9	82.4	89.7	117M18_19	gbpln	Brassica rapa	AT5G10370.1 | Symbols: | helicase domain-containing protein / IBR domain-containing protein / zinc finger protein-related | chr5:3261245-3267188 FORWARD LENGTH=1775	1775	1775	0	100.0	77.4	87.2
Rsa1.0_00016.1.g1054.t2	gb|AAZ67614.1| 80A08_29 [Brassica rapa subsp. pekinensis]	191	402	3.00E-32	210.5	44.5	51.3	80A08_29	gbpln	Brassica rapa	AT5G10320.1 | Symbols: | unknown protein; Has 54 Blast hits to 53 proteins in 19 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:3244180-3246603 REVERSE LENGTH=403	191	403	2.00E-25	211.0	37.2	47.6
Rsa1.0_00016.1.g1055.t1	gb|AAZ66937.1| 117M18_18 [Brassica rapa]	249	249	1.00E-138	100.0	98.4	99.6	117M18_18	gbpln	Brassica rapa	AT5G10360.1 | Symbols: EMB3010, RPS6B | Ribosomal protein S6e | chr5:3258734-3260142 REVERSE LENGTH=249	249	249	1.00E-136	100.0	95.6	97.6
Rsa1.0_00016.1.g1056.t1	gb|AAZ67615.1| 80A08_30 [Brassica rapa subsp. pekinensis]	225	223	1.00E-123	99.1	97.3	97.8	80A08_30	gbpln	Brassica rapa	AT5G65270.1 | Symbols: AtRABA4a, RABA4a | RAB GTPase homolog A4A | chr5:26083437-26084550 FORWARD LENGTH=226	225	226	1.00E-114	100.4	86.7	91.1

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<tr><td>Rsa1.0_00016.1.g1057.t1</td><td>gb|AAZ67614.1| 80A08_29 [Brassica rapa subsp. pekinensis]</td><td>397</td><td>402</td><td>0</td><td>101.3</td><td>90.9</td><td>94.2</td><td>80A08_29</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G10320.1 | Symbols: | unknown protein; Has 54 Blast hits to 53 proteins in 19 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:3244180-3246603 REVERSE LENGTH=403</td><td>397</td><td>403</td><td>1.00E-180</td><td>101.5</td><td>80.4</td><td>90.2</td></tr>
<tr><td>Rsa1.0_00016.1.g1058.t1</td><td>gb|AAZ67613.1| 80A08_28 [Brassica rapa subsp. pekinensis]</td><td>121</td><td>120</td><td>9.00E-58</td><td>99.2</td><td>92.6</td><td>95.0</td><td>80A08_28</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G10310.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13898.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3241666-3242127 REVERSE LENGTH=122</td><td>121</td><td>122</td><td>2.00E-50</td><td>100.8</td><td>74.4</td><td>78.5</td></tr>
<tr><td>Rsa1.0_00016.1.g1059.t1</td><td>ref|NP_196592.1| methyl esterase 5 [Arabidopsis thaliana] gi|75334959|sp|Q9LFT6.1|HNL_ARATH RecName: Full=Alpha-hydroxynitrile lyase; Short=AtHNL; AltName: Full=(R)-hydroxynitrile lyase; AltName: Full=(R)-oxynitrilase; AltName: Full=Methylesterase 5; Short=AtMES5 gi|254220946|pdb|3DQZ|A Chain A, Structure Of The Hydroxynitrile Lyase From Arabidopsis Thaliana gi|254220947|pdb|3DQZ|B Chain B, Structure Of The Hydroxynitrile Lyase From Arabidopsis Thaliana gi|254220948|pdb|3DQZ|C Chain C, Structure Of The Hydroxynitrile Lyase From Arabidopsis Thaliana gi|254220949|pdb|3DQZ|D Chain D, Structure Of The Hydroxynitrile Lyase From Arabidopsis Thaliana gi|8953411|emb|CAB96686.1| alpha-hydroxynitrile lyase-like protein [Arabidopsis thaliana] gi|20147249|gb|AAM10338.1| AT5g10300/F18D22_70 [Arabidopsis thaliana] gi|23296322|gb|AAN13041.1| putative alpha-hydroxynitrile lyase [Arabidopsis thaliana] gi|110740625|dbj|BAE98416.1| alpha-hydroxynitrile lyase-like protein [Arabidopsis thaliana] gi|332004135|gb|AED91518.1| methyl esterase 5 [Arabidopsis thaliana]</td><td>258</td><td>258</td><td>1.00E-133</td><td>100.0</td><td>87.2</td><td>93.0</td><td>methyl esterase 5</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G10300.1 | Symbols: ATMES5, MES5, HNL | methyl esterase 5 | chr5:3239684-3240724 FORWARD LENGTH=258</td><td>258</td><td>258</td><td>1.00E-135</td><td>100.0</td><td>87.2</td><td>93.0</td></tr>
<tr><td>Rsa1.0_00016.1.g1060.t1</td><td>ref|NP_196590.1| myb domain protein 92 [Arabidopsis thaliana] gi|3941524|gb|AAC83638.1| putative transcription factor [Arabidopsis thaliana] gi|8953409|emb|CAB96684.1| putative transcription factor MYB92 [Arabidopsis thaliana] gi|27754493|gb|AAO22694.1| putative myb family transcription factor [Arabidopsis thaliana] gi|28393977|gb|AAO42396.1| putative myb family transcription factor [Arabidopsis thaliana] gi|41619378|gb|AAS10089.1| MYB transcription factor [Arabidopsis thaliana] gi|332004133|gb|AED91516.1| myb domain protein 92 [Arabidopsis thaliana]</td><td>337</td><td>334</td><td>1.00E-151</td><td>99.1</td><td>80.4</td><td>87.8</td><td>myb domain protein 92</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G10280.1 | Symbols: MYB92, ATMYB92, ATMYB64 | myb domain protein 92 | chr5:3232776-3233956 FORWARD LENGTH=334</td><td>337</td><td>334</td><td>1.00E-154</td><td>99.1</td><td>80.4</td><td>87.8</td></tr>
<tr><td>Rsa1.0_00016.1.g1061.t1</td><td>gb|AAZ67608.1| 80A08_23 [Brassica rapa subsp. pekinensis]</td><td>510</td><td>543</td><td>0</td><td>106.5</td><td>95.5</td><td>96.7</td><td>80A08_23</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G10270.1 | Symbols: CDKC;1 | cyclin-dependent kinase C;1 | chr5:3221715-3224674 REVERSE LENGTH=505</td><td>510</td><td>505</td><td>0</td><td>99.0</td><td>86.9</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00016.1.g1062.t1</td><td>gb|AAZ67607.1| 80A08_22 [Brassica rapa subsp. pekinensis]</td><td>205</td><td>206</td><td>1.00E-110</td><td>100.5</td><td>97.1</td><td>97.6</td><td>80A08_22</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G10260.1 | Symbols: AtRABH1e, RABH1e | RAB GTPase homolog H1E | chr5:3219991-3221301 FORWARD LENGTH=207</td><td>205</td><td>207</td><td>1.00E-107</td><td>101.0</td><td>91.7</td><td>97.6</td></tr>
<tr><td>Rsa1.0_00016.1.g1063.t1</td><td>gb|AAZ67606.1| 80A08_21 [Brassica rapa subsp. pekinensis]</td><td>656</td><td>630</td><td>0</td><td>96.0</td><td>88.1</td><td>91.9</td><td>80A08_21</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G10250.1 | Symbols: DOT3 | Phototropic-responsive NPH3 family protein | chr5:3217028-3219368 REVERSE LENGTH=607</td><td>656</td><td>607</td><td>0</td><td>92.5</td><td>73.6</td><td>81.7</td></tr>
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Rsa1.0_00016.1.g1064.t1	gb|AAZ67605.1| 80A08_20 [Brassica rapa subsp. pekinensis]	316	316	0	100.0	97.5	98.7	80A08_20	gbpln	Brassica rapa	AT5G10230.1 | Symbols: ANNAT7, ANN7 | annexin 7 | chr5:3209738-3211396 REVERSE LENGTH=316	316	316	1.00E-170	100.0	89.2	94.6
Rsa1.0_00016.1.g1065.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2157	1274	0	59.1	28.2	38.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT5G10220.1 | Symbols: ANN6, ANNAT6 | annexin 6 | chr5:3206980-3208784 REVERSE LENGTH=318	2157	318	1.00E-151	14.7	11.9	12.9
Rsa1.0_00016.1.g1066.t1	ref|NP_196583.1| uncharacterized protein [Arabidopsis thaliana] gi|7960740|emb|CAB92062.1| putative protein [Arabidopsis thaliana] gi|38564316|gb|AAR23737.1| At5g10210 [Arabidopsis thaliana] gi|38604056|gb|AAR24771.1| At5g10210 [Arabidopsis thaliana] gi|332004125|gb|AED91508.1| uncharacterized protein AT5G10210 [Arabidopsis thaliana]	190	197	8.00E-82	103.7	80.5	91.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G10210.1 | Symbols: | CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3206236-3206829 FORWARD LENGTH=197	190	197	3.00E-84	103.7	80.5	91.1
Rsa1.0_00016.1.g1067.t1	gb|AAZ67602.1| 80A08_17 [Brassica rapa subsp. pekinensis]	633	631	0	99.7	95.6	98.1	80A08_17	gbpln	Brassica rapa	AT5G10200.1 | Symbols: | ARM-repeat/Tetratricopeptide repeat (TPR)-like protein | chr5:3202378-3204367 FORWARD LENGTH=631	633	631	0	99.7	94.6	97.9
Rsa1.0_00017.1.g1068.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1069.t1	ref|XP_002869338.1| hypothetical protein ARALYDRAFT_491614 [Arabidopsis lyrata subsp. lyrata] gi|297315174|gb|EFH45597.1| hypothetical protein ARALYDRAFT_491614 [Arabidopsis lyrata subsp. lyrata]	261	227	1.00E-122	87.0	82.8	85.1	hypothetical protein ARALYDRAFT_491614	gbpln	Arabidopsis lyrata	AT4G31290.1 | Symbols: | ChaC-like family protein | chr4:15186851-15188278 FORWARD LENGTH=227	261	227	1.00E-124	87.0	82.8	84.7
Rsa1.0_00017.1.g1070.t1	ref|XP_002869337.1| hypothetical protein ARALYDRAFT_328593 [Arabidopsis lyrata subsp. lyrata] gi|297315173|gb|EFH45596.1| hypothetical protein ARALYDRAFT_328593 [Arabidopsis lyrata subsp. lyrata]	247	234	1.00E-131	94.7	93.9	94.3	hypothetical protein ARALYDRAFT_328593	gbpln	Arabidopsis lyrata	AT4G31300.2 | Symbols: PBA1 | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr4:15188927-15190935 FORWARD LENGTH=234	247	234	1.00E-132	94.7	93.1	93.9
Rsa1.0_00017.1.g1071.t1	gb|EOA18510.1| hypothetical protein CARUB_v10007062mg [Capsella rubella]	188	191	7.00E-84	101.6	81.9	87.2	hypothetical protein CARUB_v10007062mg	gbpln	Capsella rubella	AT4G31320.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:15193993-15194562 REVERSE LENGTH=189	188	189	2.00E-83	100.5	79.8	86.2
Rsa1.0_00017.1.g1072.t2	ref|NP_567872.1| uncharacterized protein [Arabidopsis thaliana] gi|13507569|gb|AAK28647.1|AF360350_1 unknown protein [Arabidopsis thaliana] gi|15293233|gb|AAK93727.1| unknown protein [Arabidopsis thaliana] gi|332660492|gb|AEE85892.1| uncharacterized protein AT4G31330 [Arabidopsis thaliana]	382	239	1.00E-125	62.6	56.5	61.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G31330.1 | Symbols: | Protein of unknown function, DUF599 | chr4:15202354-15203151 FORWARD LENGTH=239	382	239	1.00E-127	62.6	56.5	61.0
Rsa1.0_00017.1.g1073.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1074.t2	ref|NP_567873.1| myosin heavy chain-related protein [Arabidopsis thaliana] gi|26983878|gb|AAN86191.1| unknown protein [Arabidopsis thaliana] gi|222423518|dbj|BAH19729.1| AT4G31340 [Arabidopsis thaliana] gi|332660493|gb|AEE85893.1| myosin heavy chain-related protein [Arabidopsis thaliana]	412	437	0	106.1	80.6	88.1	myosin heavy chain-related protein	gbpln	Arabidopsis thaliana	AT4G31340.1 | Symbols: | myosin heavy chain-related | chr4:15205662-15208950 FORWARD LENGTH=437	412	437	0	106.1	80.6	88.1
Rsa1.0_00017.1.g1075.t1	emb|CAA16538.1| predicted protein [Arabidopsis thaliana] gi|7270037|emb|CAB79853.1| predicted protein [Arabidopsis thaliana]	344	711	2.00E-20	206.7	20.3	29.1	predicted protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1076.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_00017.1.g1078.t1</td><td>ref|XP_002869331.1| hypothetical protein ARALYDRAFT_913334 [Arabidopsis lyrata subsp. lyrata] gi|297315167|gb|EFH45590.1| hypothetical protein ARALYDRAFT_913334 [Arabidopsis lyrata subsp. lyrata]</td><td>187</td><td>179</td><td>2.00E−58</td><td>95.7</td><td>73.8</td><td>77.5</td><td>hypothetical protein ARALYDRAFT_913334</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G31360.1 | Symbols: | selenium binding | chr4:15221945−15223310 FORWARD LENGTH=186</td><td>187</td><td>186</td><td>1.00E−60</td><td>99.5</td><td>73.3</td><td>77.5</td></tr>
<tr><td>Rsa1.0_00017.1.g1079.t1</td><td>ref|NP_194866.2| protein kinase family protein [Arabidopsis thaliana] gi|55978825|gb|AAV68874.1| hypothetical protein AT4G31380 [Arabidopsis thaliana] gi|60547875|gb|AAX23901.1| hypothetical protein At4g31380 [Arabidopsis thaliana] gi|332660502|gb|AEE85902.1| protein kinase family protein [Arabidopsis thaliana]</td><td>124</td><td>181</td><td>3.00E−55</td><td>146.0</td><td>94.4</td><td>97.6</td><td>protein kinase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G31380.1 | Symbols: FLP1 | FPF1−like protein 1 | chr4:15229837−15230382 FORWARD LENGTH=181</td><td>124</td><td>181</td><td>5.00E−58</td><td>146.0</td><td>94.4</td><td>97.6</td></tr>
<tr><td>Rsa1.0_00017.1.g1080.t1</td><td>ref|XP_002869329.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297315165|gb|EFH45588.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>674</td><td>682</td><td>0</td><td>101.2</td><td>92.1</td><td>95.3</td><td>ABC1 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G31390.1 | Symbols: | Protein kinase superfamily protein | chr4:15233126−15236764 FORWARD LENGTH=682</td><td>674</td><td>682</td><td>0</td><td>101.2</td><td>92.1</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00017.1.g1081.t1</td><td>gb|EOA17077.1| hypothetical protein CARUB_v10005326mg [Capsella rubella]</td><td>326</td><td>306</td><td>1.00E−120</td><td>93.9</td><td>74.5</td><td>79.4</td><td>hypothetical protein CARUB_v10005326mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G31410.2 | Symbols: | Protein of unknown function (DUF1644) | chr4:15244259−15245474 FORWARD LENGTH=308</td><td>326</td><td>308</td><td>1.00E−122</td><td>94.5</td><td>74.2</td><td>79.8</td></tr>
<tr><td>Rsa1.0_00017.1.g1082.t1</td><td>dbj|BAJ34316.1| unnamed protein product [Thellungiella halophila]</td><td>396</td><td>402</td><td>0</td><td>101.5</td><td>87.4</td><td>93.7</td><td>unnamed protein product</td><td>−−−−</td><td>−−−−</td><td>AT4G31420.1 | Symbols: | Zinc finger protein 622 | chr4:15245987−15247763 REVERSE LENGTH=404</td><td>396</td><td>404</td><td>0</td><td>102.0</td><td>83.1</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00017.1.g1083.t1</td><td>ref|XP_002869326.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315162|gb|EFH45585.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>529</td><td>571</td><td>1.00E−151</td><td>107.9</td><td>70.7</td><td>77.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G31430.2 | Symbols: | unknown protein; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr4:15248510−15252204 FORWARD LENGTH=574</td><td>529</td><td>574</td><td>1.00E−145</td><td>108.5</td><td>66.5</td><td>75.8</td></tr>
<tr><td>Rsa1.0_00017.1.g1084.t1</td><td>ref|XP_002869325.1| hypothetical protein ARALYDRAFT_491593 [Arabidopsis lyrata subsp. lyrata] gi|297315161|gb|EFH45584.1| hypothetical protein ARALYDRAFT_491593 [Arabidopsis lyrata subsp. lyrata]</td><td>382</td><td>394</td><td>1.00E−148</td><td>103.1</td><td>74.6</td><td>82.5</td><td>hypothetical protein ARALYDRAFT_491593</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G31440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24530.1); Has 210 Blast hits to 209 proteins in 55 species: Archae − 0; Bacteria − 72; Metazoa − 2; Fungi − 6; Plants − 128; Viruses − 0; Other Eukaryotes − 2 (source: NCBI BLink). | chr4:15253731−15254870 FORWARD LENGTH=379</td><td>382</td><td>379</td><td>1.00E−138</td><td>99.2</td><td>70.2</td><td>77.5</td></tr>
<tr><td>Rsa1.0_00017.1.g1085.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>−</td><td>−−−−</td><td>−−−−</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00017.1.g1086.t1</td><td>gb|EOA22078.1| hypothetical protein CARUB_v10002618mg [Capsella rubella]</td><td>164</td><td>892</td><td>3.00E−17</td><td>543.9</td><td>31.1</td><td>43.9</td><td>hypothetical protein CARUB_v10002618mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G32670.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr4:15759527−15762847 REVERSE LENGTH=860</td><td>164</td><td>860</td><td>1.00E−19</td><td>524.4</td><td>31.7</td><td>44.5</td></tr>
</table>

Rsa1.0_00017.1.g1087.t2	ref|XP_002867301.1| ribosomal protein L28 family protein [Arabidopsis lyrata subsp. lyrata] gi|297313137|gb|EFH43560.1| ribosomal protein L28 family protein [Arabidopsis lyrata subsp. lyrata]	217	212	2.00E-92	97.7	81.1	85.7	ribosomal protein L28 family protein	gbpln	Arabidopsis lyrata	AT4G31460.1 | Symbols: | Ribosomal L28 family | chr4:15259773-15260847 REVERSE LENGTH=212	217	212	9.00E-95	97.7	81.1	86.6
Rsa1.0_00017.1.g1088.t1	ref|NP_194876.2| coatomer subunit beta-1 [Arabidopsis thaliana] gi|334187063|ref|NP_001190880.1| coatomer subunit beta-1 [Arabidopsis thaliana] gi|146286090|sp|Q9SV21.2|COPB1_ARATH RecName: Full=Coatomer subunit beta-1; AltName: Full=Beta-coat protein 1; Short=Beta-COP 1 gi|332660518|gb|AEE85918.1| coatomer subunit beta-1 [Arabidopsis thaliana] gi|332660519|gb|AEE85919.1| coatomer subunit beta-1 [Arabidopsis thaliana]	948	948	0	100.0	97.2	98.5	coatomer subunit beta-1	gbpln	Arabidopsis thaliana	AT4G31480.2 | Symbols: | Coatomer, beta subunit | chr4:15264145-15267384 FORWARD LENGTH=948	948	948	0	100.0	97.2	98.5
Rsa1.0_00017.1.g1089.t1	ref|XP_002889985.1| CYP71B2 [Arabidopsis lyrata subsp. lyrata] gi|297335827|gb|EFH66244.1| CYP71B2 [Arabidopsis lyrata subsp. lyrata]	513	502	0	97.9	72.7	83.6	CYP71B2	gbpln	Arabidopsis lyrata	AT1G13080.1 | Symbols: CYP71B2 | cytochrome P450, family 71, subfamily B, polypeptide 2 | chr1:4459212-4460807 FORWARD LENGTH=502	513	502	0	97.9	72.1	82.5
Rsa1.0_00017.1.g1090.t1	ref|XP_002889985.1| CYP71B2 [Arabidopsis lyrata subsp. lyrata] gi|297335827|gb|EFH66244.1| CYP71B2 [Arabidopsis lyrata subsp. lyrata]	510	502	0	98.4	73.7	85.5	CYP71B2	gbpln	Arabidopsis lyrata	AT1G13080.1 | Symbols: CYP71B2 | cytochrome P450, family 71, subfamily B, polypeptide 2 | chr1:4459212-4460807 FORWARD LENGTH=502	510	502	0	98.4	72.4	82.9
Rsa1.0_00017.1.g1091.t1	ref|NP_194882.2| exocyst complex component 7 [Arabidopsis thaliana] gi|32347268|gb|AAP31853.1| EXO70-G1 protein [Arabidopsis thaliana] gi|332660526|gb|AEE85926.1| exocyst subunit exo70 family protein G1 [Arabidopsis thaliana]	673	687	0	102.1	90.6	95.2	exocyst complex component 7	gbpln	Arabidopsis thaliana	AT4G31540.1 | Symbols: ATEXO70G1, EXO70G1 | exocyst subunit exo70 family protein G1 | chr4:15284739-15286802 REVERSE LENGTH=687	673	687	0	102.1	90.6	95.2
Rsa1.0_00017.1.g1092.t1	gb|ACQ76798.1| WRKY transcription factor 11 [Brassica napus]	325	327	1.00E-164	100.6	89.8	94.5	WRKY transcription factor 11	gbpln	Brassica napus	AT4G31550.2 | Symbols: WRKY11, ATWRKY11 | WRKY DNA-binding protein 11 | chr4:15290065-15291458 REVERSE LENGTH=324	325	324	1.00E-149	99.7	79.7	88.0
Rsa1.0_00017.1.g1093.t1	gb|ABD65000.1| hypothetical protein 26.t00020 [Brassica oleracea]	447	302	2.00E-81	67.6	34.9	42.5	hypothetical protein 26.t00020	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	447	302	6.00E-58	67.6	27.5	38.0
Rsa1.0_00017.1.g1094.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	439	442	0	100.7	76.5	86.1	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	439	343	4.00E-33	78.1	13.7	17.8
Rsa1.0_00017.1.g1095.t1	ref|XP_002862560.1| hypothetical protein ARALYDRAFT_497397 [Arabidopsis lyrata subsp. lyrata] gi|297308158|gb|EFH38818.1| hypothetical protein ARALYDRAFT_497397 [Arabidopsis lyrata subsp. lyrata]	134	137	1.00E-53	102.2	80.6	85.8	hypothetical protein ARALYDRAFT_497397	gbpln	Arabidopsis lyrata	AT4G31560.1 | Symbols: HCF153 | high chlorophyll fluorescence 153 | chr4:15295219-15296028 FORWARD LENGTH=137	134	137	6.00E-56	102.2	79.9	85.8
Rsa1.0_00017.1.g1096.t2	ref|NP_194885.2| uncharacterized protein [Arabidopsis thaliana] gi|332660530|gb|AEE85930.1| uncharacterized protein AT4G31570 [Arabidopsis thaliana]	2708	2730	0	100.8	78.6	86.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G31570.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24460.1); Has 194354 Blast hits to 66887 proteins in 3244 species: Archae - 3688; Bacteria - 38556; Metazoa - 84828; Fungi - 17265; Plants - 10589; Viruses - 805; Other Eukaryotes - 38623 (source: NCBI BLink). | chr4:15297061-15306036 FORWARD LENGTH=2730	2708	2730	0	100.8	78.6	86.9

Rsa1.0_00017.1.g1097.t1	ref|NP_194887.1| putative xyloglucan glycosyltransferase 5 [Arabidopsis thaliana] gi|75201904|sp|Q9SB75.1|CSLC5_ARATH RecName: Full=Probable xyloglucan glycosyltransferase 5; AltName: Full=Cellulose synthase-like protein C5; Short=AtCslC5 gi|3281868|emb|CAA19764.1| putative protein [Arabidopsis thaliana] gi|7270062|emb|CAB79877.1| putative protein [Arabidopsis thaliana] gi|28058784|gb|AAO29953.1| putative protein [Arabidopsis thaliana] gi|30725520|gb|AAP37782.1| At4g31590 [Arabidopsis thaliana] gi|332660533|gb|AEE85933.1| putative xyloglucan glycosyltransferase 5 [Arabidopsis thaliana]	690	692	0	100.3	95.8	97.8	putative xyloglucan glycosyltransferase 5	gbpln	Arabidopsis thaliana	AT4G31590.1 | Symbols: ATCSLC05, CSLC05, ATCSLC5, CSLC5 | Cellulose-synthase-like C5 | chr4:15309889-15312336 REVERSE LENGTH=692	690	692	0	100.3	95.8	97.8
Rsa1.0_00017.1.g1098.t1	sp|O65098.1|REM1_BRAOB RecName: Full=B3 domain-containing protein REM1; AltName: Full=Protein REPRODUCTIVE MERISTEM 1; Short=BoREM1 gi|3170424|gb|AAC18082.1| reproductive meristem gene 1 [Brassica oleracea var. botrytis]	492	497	1.00E-176	101.0	72.0	80.5	RecName: Full=B3 domain-containing protein REM1; AltName: Full=Protein REPRODUCTIVE MERISTEM 1; Short=BoREM1 gi|3170424|gb|AAC18082.1| reproductive meristem gene 1	gbpln	Brassica oleracea	AT4G31610.1 | Symbols: REM1, ATREM1 | Transcriptional factor B3 family protein | chr4:15317700-15319776 FORWARD LENGTH=517	492	517	1.00E-122	105.1	54.1	68.1
Rsa1.0_00017.1.g1099.t1	sp|O65098.1|REM1_BRAOB RecName: Full=B3 domain-containing protein REM1; AltName: Full=Protein REPRODUCTIVE MERISTEM 1; Short=BoREM1 gi|3170424|gb|AAC18082.1| reproductive meristem gene 1 [Brassica oleracea var. botrytis]	488	497	0	101.8	72.3	81.1	RecName: Full=B3 domain-containing protein REM1; AltName: Full=Protein REPRODUCTIVE MERISTEM 1; Short=BoREM1 gi|3170424|gb|AAC18082.1| reproductive meristem gene 1	gbpln	Brassica oleracea	AT4G31610.1 | Symbols: REM1, ATREM1 | Transcriptional factor B3 family protein | chr4:15317700-15319776 FORWARD LENGTH=517	488	517	1.00E-133	105.9	58.8	72.1
Rsa1.0_00017.1.g1100.t1	gb|EOA16495.1| hypothetical protein CARUB_v10004653mg [Capsella rubella]	530	496	1.00E-165	93.6	59.1	71.3	hypothetical protein CARUB_v10004653mg	gbpln	Capsella rubella	AT4G31630.1 | Symbols: | Transcriptional factor B3 family protein | chr4:15325343-15327220 REVERSE LENGTH=512	530	512	1.00E-157	96.6	57.7	71.1
Rsa1.0_00017.1.g1101.t1	ref|XP_002867286.1| hypothetical protein ARALYDRAFT_913300 [Arabidopsis lyrata subsp. lyrata] gi|297313122|gb|EFH43545.1| hypothetical protein ARALYDRAFT_913300 [Arabidopsis lyrata subsp. lyrata]	507	632	1.00E-115	124.7	44.2	50.9	hypothetical protein ARALYDRAFT_913300	gbpln	Arabidopsis lyrata	AT4G31680.1 | Symbols: | Transcriptional factor B3 family protein | chr4:15340289-15342080 REVERSE LENGTH=462	507	462	1.00E-115	91.1	40.8	50.3
Rsa1.0_00017.1.g1102.t1	dbj|BAD44466.1| unknown protein [Arabidopsis thaliana]	615	631	0	102.6	80.5	87.0	unknown protein	gbpln	Arabidopsis thaliana	AT4G31670.1 | Symbols: UBP18 | ubiquitin-specific protease 18 | chr4:15336007-15339506 REVERSE LENGTH=631	615	631	0	102.6	80.7	87.2
Rsa1.0_00017.1.g1103.t1	ref|XP_002867286.1| hypothetical protein ARALYDRAFT_913300 [Arabidopsis lyrata subsp. lyrata] gi|297313122|gb|EFH43545.1| hypothetical protein ARALYDRAFT_913300 [Arabidopsis lyrata subsp. lyrata]	473	632	1.00E-152	133.6	61.5	73.6	hypothetical protein ARALYDRAFT_913300	gbpln	Arabidopsis lyrata	AT4G31680.1 | Symbols: | Transcriptional factor B3 family protein | chr4:15340289-15342080 REVERSE LENGTH=462	473	462	1.00E-140	97.7	58.4	70.6
Rsa1.0_00017.1.g1104.t1	gb|AAZ66937.1| 117M18_18 [Brassica rapa]	250	249	1.00E-137	99.6	97.2	98.4	117M18_18	gbpln	Brassica rapa	AT5G10360.1 | Symbols: EMB3010, RPS6B | Ribosomal protein S6e | chr5:3258734-3260142 REVERSE LENGTH=249	250	249	1.00E-134	99.6	94.4	96.4

Rsa1.0_00017.1.g1105.t1	ref|NP_194900.1| TBP-associated factor II 15 [Arabidopsis thaliana] gi|30689137|ref|NP_849481.1| TBP-associated factor II 15 [Arabidopsis thaliana] gi|13492648|gb|AAK28290.1|AF344879_1 putative TBP-associated 15 kDa subunit protein [Arabidopsis thaliana] gi|13549156|gb|AAK29671.1|AF352813_1 putative TBP associated factor 15kDa subunit [Arabidopsis thaliana] gi|2072626|emb|CAA73389.1| hypothetical protein [Arabidopsis thaliana] gi|3281856|emb|CAA19751.1| Transcription factor II homolog [Arabidopsis thaliana] gi|7270075|emb|CAB79890.1| Transcription factor II homolog [Arabidopsis thaliana] gi|21554584|gb|AAM63623.1| Transcription factor II homolog [Arabidopsis thaliana] gi|39545934|gb|AAR28030.1| TAF10 [Arabidopsis thaliana] gi|222424014|dbj|BAH19968.1| AT4G31720 [Arabidopsis thaliana] gi|332660549|gb|AEE85949.1| TBP-associated factor II 15 [Arabidopsis thaliana] gi|332660550|gb|AEE85950.1| TBP-associated factor II 15 [Arabidopsis thaliana]	134	134	3.00E-72	100.0	99.3	99.3	TBP-associated factor II 15	gbpln	Arabidopsis thaliana	AT4G31720.1 | Symbols: TAFII15, TAF10, STG1 | TBP-associated factor II 15 | chr4:15354223-15355704 REVERSE LENGTH=134	134	134	7.00E-75	100.0	99.3	99.3
Rsa1.0_00017.1.g1106.t1	gb|EOA15643.1| hypothetical protein CARUB_v10005898mg [Capsella rubella]	166	168	6.00E-60	101.2	69.9	79.5	hypothetical protein CARUB_v10005898mg	gbpln	Capsella rubella	AT4G31730.1 | Symbols: GDU1 | glutamine dumper 1 | chr4:15361207-15361683 FORWARD LENGTH=158	166	158	7.00E-58	95.2	68.7	77.7
Rsa1.0_00017.1.g1107.t1	ref|XP_002869315.1| ADP-ribosylation factor 3 [Arabidopsis lyrata subsp. lyrata] gi|297315151|gb|EFH45574.1| ADP-ribosylation factor 3 [Arabidopsis lyrata subsp. lyrata]	204	182	1.00E-102	89.2	88.7	89.2	ADP-ribosylation factor 3	gbpln	Arabidopsis lyrata	AT2G24765.1 | Symbols: ARF3, ARL1, ATARL1 | ADP-ribosylation factor 3 | chr2:10562822-10564961 FORWARD LENGTH=182	204	182	1.00E-103	89.2	86.3	89.2
Rsa1.0_00017.1.g1108.t1	ref|XP_002867281.1| hypothetical protein ARALYDRAFT_491566 [Arabidopsis lyrata subsp. lyrata] gi|297313117|gb|EFH43540.1| hypothetical protein ARALYDRAFT_491566 [Arabidopsis lyrata subsp. lyrata]	307	311	1.00E-167	101.3	96.1	97.7	hypothetical protein ARALYDRAFT_491566	gbpln	Arabidopsis lyrata	AT4G31750.1 | Symbols: WIN2 | HOPW1-1-interacting 2 | chr4:15364657-15367207 REVERSE LENGTH=311	307	311	1.00E-169	101.3	95.4	97.7
Rsa1.0_00017.1.g1109.t1	ref|NP_194906.1| Monogalactosyldiacylglycerol synthase 1 [Arabidopsis thaliana] gi|75100403|sp|O81770.1|MGDG1_ARATH RecName: Full=Monogalactosyldiacylglycerol synthase 1, chloroplastic; Short=AtMGD1; AltName: Full=MGDG synthase type A; Flags: Precursor gi|3281850|emb|CAA19745.1| monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana] gi|7270081|emb|CAB79896.1| monogalactosyldiacylglycerol synthase-like protein [Arabidopsis thaliana] gi|7621497|gb|AAF65066.1| monogalactosyldiacylglycerol synthase [Arabidopsis thaliana] gi|9927297|dbj|BAB12042.1| MGDG synthase type A [Arabidopsis thaliana] gi|20260132|gb|AAM12964.1| strong similarity to monogalactosyldiacylglycerol synthase, Cucumis sativus, PID:g1805254 [Arabidopsis thaliana] gi|31711946|gb|AAP68329.1| At4g31780 [Arabidopsis thaliana] gi|332660556|gb|AEE85956.1| Monogalactosyldiacylglycerol synthase 1 [Arabidopsis thaliana]	526	533	0	101.3	88.4	93.7	Monogalactosyldiacylglycerol synthase 1	gbpln	Arabidopsis thaliana	AT4G31780.2 | Symbols: MGD1, MGDA | monogalactosyl diacylglycerol synthase 1 | chr4:15374222-15376961 FORWARD LENGTH=533	526	533	0	101.3	88.4	93.7
Rsa1.0_00017.1.g1110.t1	gb|EOA17067.1| hypothetical protein CARUB_v10005307mg, partial [Capsella rubella]	277	310	1.00E-152	111.9	93.5	96.8	hypothetical protein CARUB_v10005307mg, partial	gbpln	Capsella rubella	AT4G31790.2 | Symbols: | Tetrapyrrole (Corrin/Porphyrin) Methylases | chr4:15377479-15378530 FORWARD LENGTH=277	277	277	1.00E-152	100.0	92.1	97.1

Rsa1.0_00017.1.g1111.t1	gb|AAS13378.1| WRKY1 [Brassica rapa subsp. chinensis]	313	308	1.00E-134	98.4	78.3	84.7	WRKY1	gbpln	Brassica rapa	AT4G31800.1 | Symbols: WRKY18, ATWRKY18 | WRKY DNA-binding protein 18 | chr4:15383296-15384812 FORWARD LENGTH=310	313	310	1.00E-132	99.0	78.0	85.3
Rsa1.0_00017.1.g1112.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1113.t1	gb|EOA16845.1| hypothetical protein CARUB_v10005068mg [Capsella rubella]	349	372	7.00E-25	106.6	29.8	47.6	hypothetical protein CARUB_v10005068mg	gbpln	Capsella rubella	AT4G14905.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:8526879-8527997 REVERSE LENGTH=372	349	372	1.00E-23	106.6	26.9	47.0
Rsa1.0_00017.1.g1114.t1	ref|NP_189957.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75182779|sp|Q9M2B5.1|FBK72_ARATH RecName: Full=Putative F-box/kelch-repeat protein At3g43710 gi|7362796|emb|CAB83072.1| putative protein [Arabidopsis thaliana] gi|332644299|gb|AEE77820.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	370	378	1.00E-115	102.2	58.4	70.5	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G43710.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:15605608-15606744 FORWARD LENGTH=378	370	378	1.00E-118	102.2	58.4	70.5
Rsa1.0_00017.1.g1115.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1116.t1	dbj|BAJ34065.1| unnamed protein product [Thellungiella halophila]	573	579	0	101.0	85.7	89.0	unnamed protein product	----	----	AT4G31820.1 | Symbols: ENP, NPY1, MAB4 | Phototropic-responsive NPH3 family protein | chr4:15390788-15393627 REVERSE LENGTH=571	573	571	0	99.7	83.9	88.3
Rsa1.0_00017.1.g1117.t1	ref|XP_002867277.1| hypothetical protein ARALYDRAFT_913282 [Arabidopsis lyrata subsp. lyrata] gi|297313113|gb|EFH43536.1| hypothetical protein ARALYDRAFT_913282 [Arabidopsis lyrata subsp. lyrata]	100	100	1.00E-48	100.0	96.0	99.0	hypothetical protein ARALYDRAFT_913282	gbpln	Arabidopsis lyrata	AT4G31830.1 | Symbols: | unknown protein; Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15400803-15401105 REVERSE LENGTH=100	100	100	3.00E-51	100.0	96.0	98.0
Rsa1.0_00017.1.g1118.t1	ref|XP_002869310.1| hypothetical protein ARALYDRAFT_491553 [Arabidopsis lyrata subsp. lyrata] gi|297315146|gb|EFH45569.1| hypothetical protein ARALYDRAFT_491553 [Arabidopsis lyrata subsp. lyrata]	174	177	8.00E-83	101.7	90.2	97.1	hypothetical protein ARALYDRAFT_491553	gbpln	Arabidopsis lyrata	AT4G31840.1 | Symbols: ENODL15, AtENODL15 | early nodulin-like protein 15 | chr4:15401798-15402426 FORWARD LENGTH=177	174	177	6.00E-83	101.7	88.5	94.8
Rsa1.0_00017.1.g1119.t1	ref|NP_194913.1| proton gradient regulation 3 [Arabidopsis thaliana] gi|75213543|sp|Q9SZ52.1|PP344_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g31850, chloroplastic; AltName: Full=Protein PROTON GRADIENT REGULATION 3; Flags: Precursor gi|4584524|emb|CAB40755.1| putative protein [Arabidopsis thaliana] gi|7270088|emb|CAB79903.1| putative protein [Arabidopsis thaliana] gi|332660567|gb|AEE85967.1| proton gradient regulation 3 [Arabidopsis thaliana]	1122	1112	0	99.1	83.7	91.3	proton gradient regulation 3	gbpln	Arabidopsis thaliana	AT4G31850.1 | Symbols: PGR3 | proton gradient regulation 3 | chr4:15403020-15406358 FORWARD LENGTH=1112	1122	1112	0	99.1	83.7	91.3
Rsa1.0_00017.1.g1120.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1121.t2	ref|NP_194916.2| uncharacterized protein [Arabidopsis thaliana] gi|26983792|gb|AAN86148.1| unknown protein [Arabidopsis thaliana] gi|332660572|gb|AEE85972.1| uncharacterized protein AT4G31880 [Arabidopsis thaliana]	869	873	0	100.5	63.4	71.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G31880.1 | Symbols: | LOCATED IN: cytosol, chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: Tudor/PWWP/MBT superfamily protein (TAIR:AT1G15940.1); Has 137162 Blast hits to 70781 proteins in 2973 species: Archae - 289; Bacteria - 24182; Metazoa - 56725; Fungi - 20130; Plants - 6559; Viruses - 758; Other Eukaryotes - 28519 (source: NCBI BLink). | chr4:15419435-15423939 REVERSE LENGTH=873	869	873	0	100.5	63.4	71.3

Rsa1.0_00017.1.g1122.t1	ref|NP_194917.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|334187073|ref|NP_001190883.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|4584528|emb|CAB40759.1| putative protein [Arabidopsis thaliana] gi|7270092|emb|CAB79907.1| putative protein [Arabidopsis thaliana] gi|110736926|dbj|BAF00420.1| hypothetical protein [Arabidopsis thaliana] gi|190341119|gb|ACE74718.1| At4g31890 [Arabidopsis thaliana] gi|332660574|gb|AEE85974.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332660575|gb|AEE85975.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	509	518	0	101.8	89.0	93.1	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G31890.2 | Symbols: | ARM repeat superfamily protein | chr4:15427290-15429049 REVERSE LENGTH=518	509	518	0	101.8	89.0	93.1
Rsa1.0_00017.1.g1123.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1913	1274	0	66.6	32.3	44.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1913	575	1.00E-67	30.1	9.2	14.3
Rsa1.0_00017.1.g1124.t1	ref|XP_002879859.1| hypothetical protein ARALYDRAFT_903307 [Arabidopsis lyrata subsp. lyrata] gi|297325698|gb|EFH56118.1| hypothetical protein ARALYDRAFT_903307 [Arabidopsis lyrata subsp. lyrata]	316	304	1.00E-78	96.2	52.5	64.6	hypothetical protein ARALYDRAFT_903307	gbpln	Arabidopsis lyrata	AT2G20620.1 | Symbols: | Protein of unknown function (DUF626) | chr2:8891929-8893244 REVERSE LENGTH=286	316	286	1.00E-52	90.5	32.9	47.5
Rsa1.0_00017.1.g1125.t4	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	346	1274	3.00E-77	368.2	46.0	62.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	346	303	7.00E-55	87.6	35.5	49.4
Rsa1.0_00017.1.g1126.t1	dbj|BAJ34619.1| unnamed protein product [Thellungiella halophila]	92	539	2.00E-19	585.9	57.6	58.7	unnamed protein product	----	----	AT4G31920.1 | Symbols: ARR10, RR10 | response regulator 10 | chr4:15444290-15446766 REVERSE LENGTH=552	92	552	3.00E-15	600.0	43.5	52.2
Rsa1.0_00017.1.g1127.t1	gb|EOA18383.1| hypothetical protein CARUB_v10006919mg [Capsella rubella]	232	660	4.00E-91	284.5	75.0	83.6	hypothetical protein CARUB_v10006919mg	gbpln	Capsella rubella	AT4G31980.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF247, plant (InterPro:IPR004158), Protein of unknown function DUF862, eukaryotic (InterPro:IPR008580); BEST Arabidopsis thaliana protein match is: Plant protein of unknown function (DUF247) (TAIR:AT5G11290.1); Has 1967 Blast hits to 1844 proteins in 183 species: Archae - 0; Bacteria - 6; Metazoa - 223; Fungi - 83; Plants - 1477; Viruses - 0; Other Eukaryotes - 178 (source: NCBI BLink). | chr4:15464905-15469204 FORWARD LENGTH=680	232	680	2.00E-92	293.1	75.0	84.5
Rsa1.0_00017.1.g1128.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1129.t3	gb|EOA16711.1| hypothetical protein CARUB_v10004912mg [Capsella rubella]	410	418	0	102.0	87.3	92.9	hypothetical protein CARUB_v10004912mg	gbpln	Capsella rubella	AT4G32000.1 | Symbols: | Protein kinase superfamily protein | chr4:15474083-15476655 REVERSE LENGTH=418	410	418	0	102.0	85.1	90.0
Rsa1.0_00017.1.g1130.t1	gb|EOA16061.1| hypothetical protein CARUB_v10004194mg [Capsella rubella]	131	775	3.00E-51	591.6	74.8	83.2	hypothetical protein CARUB_v10004194mg	gbpln	Capsella rubella	AT4G32010.1 | Symbols: HSL1, HSI2-L1, VAL2 | HSI2-like 1 | chr4:15481231-15484897 FORWARD LENGTH=780	131	780	4.00E-51	595.4	76.3	83.2
Rsa1.0_00017.1.g1131.t1	gb|EOA15616.1| hypothetical protein CARUB_v10005750mg [Capsella rubella]	190	205	2.00E-60	107.9	77.9	85.8	hypothetical protein CARUB_v10005750mg	gbpln	Capsella rubella	AT4G32020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25250.1); Has 65 Blast hits to 65 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 8; Plants - 54; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15488076-15488621 FORWARD LENGTH=181	190	181	6.00E-49	95.3	64.7	70.5

Rsa1.0_00017.1.g1132.t1	ref|XP_002867262.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313098|gb|EFH43521.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	82	107	3.00E−16	130.5	54.9	64.6	predicted protein	gbpln	Arabidopsis lyrata	AT4G32100.1 | Symbols: | Beta−1,3−N−Acetylglucosaminyltransferase family protein | chr4:15511757−15512218 REVERSE LENGTH=122	82	122	2.00E−17	148.8	51.2	63.4
Rsa1.0_00017.1.g1133.t1	ref|XP_002867258.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313094|gb|EFH43517.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	385	345	0	89.6	81.8	85.7	galactosyltransferase family protein	gbpln	Arabidopsis lyrata	AT4G32120.1 | Symbols: | Galactosyltransferase family protein | chr4:15517230−15519687 REVERSE LENGTH=345	385	345	0	89.6	81.0	84.4
Rsa1.0_00017.1.g1134.t5	ref|XP_002867255.1| vesicle−associated membrane protein 7C [Arabidopsis lyrata subsp. lyrata] gi|297313091|gb|EFH43514.1| vesicle−associated membrane protein 7C [Arabidopsis lyrata subsp. lyrata]	540	219	1.00E−103	40.6	33.9	34.6	vesicle−associated membrane protein 7C	gbpln	Arabidopsis lyrata	AT4G32150.1 | Symbols: VAMP711, ATVAMP711 | vesicle−associated membrane protein 711 | chr4:15526407−15527651 REVERSE LENGTH=219	540	219	1.00E−105	40.6	33.5	34.4
Rsa1.0_00017.1.g1135.t6	ref|NP_567888.2| Phox (PX) domain−containing protein [Arabidopsis thaliana] gi|332660612|gb|AEE86012.1| Phox (PX) domain−containing protein [Arabidopsis thaliana]	764	723	0	94.6	82.5	88.7	Phox (PX) domain−containing protein	gbpln	Arabidopsis thaliana	AT4G32160.1 | Symbols: | Phox (PX) domain−containing protein | chr4:15529056−15532892 FORWARD LENGTH=723	764	723	0	94.6	82.5	88.7
Rsa1.0_00017.1.g1136.t1	ref|XP_002867254.1| ATPANK2 [Arabidopsis lyrata subsp. lyrata] gi|297313090|gb|EFH43513.1| ATPANK2 [Arabidopsis lyrata subsp. lyrata]	915	902	0	98.6	94.9	96.7	ATPANK2	gbpln	Arabidopsis lyrata	AT4G32180.1 | Symbols: ATPANK2, PANK2 | pantothenate kinase 2 | chr4:15537724−15543715 REVERSE LENGTH=901	915	901	0	98.5	94.2	96.6
Rsa1.0_00017.1.g1137.t1	gb|EOA16055.1| hypothetical protein CARUB_v10004187mg [Capsella rubella]	758	780	0	102.9	77.4	89.1	hypothetical protein CARUB_v10004187mg	gbpln	Capsella rubella	AT4G32190.1 | Symbols: | Myosin heavy chain−related protein | chr4:15545052−15547689 FORWARD LENGTH=783	758	783	0	103.3	78.4	88.5
Rsa1.0_00017.1.g1138.t1	ref|NP_194953.1| F−type H+−transporting ATPase subunit b [Arabidopsis thaliana] gi|2864617|emb|CAA16964.1| H+−transporting ATP synthase chain9 − like protein [Arabidopsis thaliana] gi|5730141|emb|CAB52473.1| ATP synthase beta chain precursor (subunit II) [Arabidopsis thaliana] gi|7270130|emb|CAB79944.1| H+−transporting ATP synthase chain 9−like protein [Arabidopsis thaliana] gi|16604406|gb|AAL24209.1| AT4g32260/F10M6_100 [Arabidopsis thaliana] gi|21554175|gb|AAM63254.1| H+−transporting ATP synthase chain 9−like protein [Arabidopsis thaliana] gi|332660627|gb|AEE86027.1| F−type H+−transporting ATPase subunit b [Arabidopsis thaliana]	287	219	2.00E−85	76.3	64.1	68.3	F−type H+−transporting ATPase subunit b	gbpln	Arabidopsis thaliana	AT4G32260.1 | Symbols: | ATPase, F0 complex, subunit B/B', bacterial/chloroplast | chr4:15573859−15574586 REVERSE LENGTH=219	287	219	4.00E−88	76.3	64.1	68.3
Rsa1.0_00017.1.g1139.t1	gb|EOA16255.1| hypothetical protein CARUB_v10004401mg [Capsella rubella] gi|482552063|gb|EOA16256.1| hypothetical protein CARUB_v10004401mg [Capsella rubella]	613	611	0	99.7	89.7	94.3	hypothetical protein CARUB_v10004401mg	gbpln	Capsella rubella	AT4G32250.3 | Symbols: | Protein kinase superfamily protein | chr4:15570285−15572528 REVERSE LENGTH=611	613	611	0	99.7	89.2	94.1
Rsa1.0_00017.1.g1140.t2	ref|XP_002867250.1| hypothetical protein ARALYDRAFT_491506 [Arabidopsis lyrata subsp. lyrata] gi|297313086|gb|EFH43509.1| hypothetical protein ARALYDRAFT_491506 [Arabidopsis lyrata subsp. lyrata]	248	237	1.00E−106	95.6	77.8	84.7	hypothetical protein ARALYDRAFT_491506	gbpln	Arabidopsis lyrata	AT4G32270.1 | Symbols: | Ubiquitin−like superfamily protein | chr4:15575015−15576360 REVERSE LENGTH=239	248	239	1.00E−103	96.4	75.4	82.7
Rsa1.0_00017.1.g1141.t1	gb|EOA19749.1| hypothetical protein CARUB_v10003892mg [Capsella rubella]	450	457	6.00E−82	101.6	46.4	61.6	hypothetical protein CARUB_v10003892mg	gbpln	Capsella rubella	AT5G22730.1 | Symbols: | F−box/RNI−like/FBD−like domains−containing protein | chr5:7551632−7553219 REVERSE LENGTH=466	450	466	4.00E−76	103.6	45.3	57.8
Rsa1.0_00017.1.g1142.t1	ref|XP_002869286.1| hypothetical protein ARALYDRAFT_328503 [Arabidopsis lyrata subsp. lyrata] gi|297315122|gb|EFH45545.1| hypothetical protein ARALYDRAFT_328503 [Arabidopsis lyrata subsp. lyrata]	171	845	7.00E−56	494.2	73.1	83.6	hypothetical protein ARALYDRAFT_328503	gbpln	Arabidopsis lyrata	AT4G32280.1 | Symbols: IAA29 | indole−3−acetic acid inducible 29 | chr4:15583479−15584628 FORWARD LENGTH=251	171	251	8.00E−52	146.8	70.8	80.7
Rsa1.0_00017.1.g1143.t1	gb|EOA16210.1| hypothetical protein CARUB_v10004350mg [Capsella rubella]	633	637	0	100.6	90.7	94.2	hypothetical protein CARUB_v10004350mg	gbpln	Capsella rubella	AT4G32285.2 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr4:15586003−15587910 FORWARD LENGTH=635	633	635	0	100.3	89.6	93.7

Rsa1.0_00017.1.g1144.t1	ref|XP_002867248.1| hypothetical protein ARALYDRAFT_491501 [Arabidopsis lyrata subsp. lyrata] gi|297313084|gb|EFH43507.1| hypothetical protein ARALYDRAFT_491501 [Arabidopsis lyrata subsp. lyrata]	384	385	1.00E-177	100.3	81.3	88.0	hypothetical protein ARALYDRAFT_491501	gbpln	Arabidopsis lyrata	AT4G32290.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:15589839-15590993 REVERSE LENGTH=384	384	384	1.00E-171	100.0	79.2	88.0
Rsa1.0_00017.1.g1145.t1	ref|NP_680756.1| uncharacterized protein [Arabidopsis thaliana] gi|28392894|gb|AAO41883.1| unknown protein [Arabidopsis thaliana] gi|28827750|gb|AAO50719.1| unknown protein [Arabidopsis thaliana] gi|332660636|gb|AEE86036.1| uncharacterized protein AT4G32295 [Arabidopsis thaliana]	265	238	1.00E-106	89.8	79.6	82.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32295.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G24150.1); Has 39 Blast hits to 39 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15592960-15594080 FORWARD LENGTH=238	265	238	1.00E-109	89.8	79.6	82.6
Rsa1.0_00017.1.g1146.t1	ref|XP_002869284.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315120|gb|EFH45543.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	828	825	0	99.6	84.5	91.1	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT4G32300.1 | Symbols: SD2-5 | S-domain-2 5 | chr4:15599970-15602435 FORWARD LENGTH=821	828	821	0	99.2	84.4	91.1
Rsa1.0_00017.1.g1147.t1	ref|XP_002869284.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315120|gb|EFH45543.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	247	825	1.00E-60	334.0	55.1	64.4	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT4G32300.1 | Symbols: SD2-5 | S-domain-2 5 | chr4:15599970-15602435 FORWARD LENGTH=821	247	821	2.00E-61	332.4	54.3	63.6
Rsa1.0_00017.1.g1148.t1	ref|NP_567893.1| TPX2 (targeting protein for Xklp2) protein family [Arabidopsis thaliana] gi|186515493|ref|NP_001119094.1| TPX2 (targeting protein for Xklp2) protein family [Arabidopsis thaliana] gi|14334556|gb|AAK59686.1| unknown protein [Arabidopsis thaliana] gi|21280971|gb|AAM44942.1| unknown protein [Arabidopsis thaliana] gi|332660640|gb|AEE86040.1| TPX2 (targeting protein for Xklp2) protein family [Arabidopsis thaliana] gi|332660642|gb|AEE86042.1| TPX2 (targeting protein for Xklp2) protein family [Arabidopsis thaliana]	432	437	1.00E-168	101.2	76.4	85.0	TPX2 (targeting protein for Xklp2) protein family	gbpln	Arabidopsis thaliana	AT4G32330.3 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr4:15609801-15611867 FORWARD LENGTH=437	432	437	1.00E-170	101.2	76.4	85.0
Rsa1.0_00017.1.g1149.t1	ref|NP_194960.1| tetratricopeptide repeat domain-containing protein-like protein [Arabidopsis thaliana] gi|2864610|emb|CAA16957.1| putative protein [Arabidopsis thaliana] gi|4049336|emb|CAA22561.1| putative protein [Arabidopsis thaliana] gi|7270138|emb|CAB79951.1| putative protein [Arabidopsis thaliana] gi|21592985|gb|AAM64934.1| unknown [Arabidopsis thaliana] gi|23297278|gb|AAN12931.1| unknown protein [Arabidopsis thaliana] gi|332660643|gb|AEE86043.1| tetratricopeptide repeat domain-containing protein-like protein [Arabidopsis thaliana]	244	238	7.00E-77	97.5	72.1	79.9	tetratricopeptide repeat domain-containing protein-like protein	gbpln	Arabidopsis thaliana	AT4G32340.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:15612741-15614219 REVERSE LENGTH=238	244	238	2.00E-79	97.5	72.1	79.9
Rsa1.0_00017.1.g1150.t1	gb|EOA16104.1| hypothetical protein CARUB_v10004237mg [Capsella rubella]	643	724	0	112.6	73.6	83.0	hypothetical protein CARUB_v10004237mg	gbpln	Capsella rubella	AT4G32350.1 | Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr4:15617634-15620642 FORWARD LENGTH=732	643	732	0	113.8	72.0	81.6
Rsa1.0_00017.1.g1151.t1	ref|NP_194965.1| Nucleotide-sugar transporter family protein [Arabidopsis thaliana] gi|75209423|sp|Q9SUV2.1|PT432_ARATH RecName: Full=Probable sugar phosphate/phosphate translocator At4g32390 gi|4049341|emb|CAA22566.1| putative protein [Arabidopsis thaliana] gi|7270143|emb|CAB79956.1| putative protein [Arabidopsis thaliana] gi|332660651|gb|AEE86051.1| Nucleotide-sugar transporter family protein [Arabidopsis thaliana]	350	350	0	100.0	95.4	98.0	Nucleotide-sugar transporter family protein	gbpln	Arabidopsis thaliana	AT4G32390.1 | Symbols: | Nucleotide-sugar transporter family protein | chr4:15636550-15637602 FORWARD LENGTH=350	350	350	0	100.0	95.4	98.0

Rsa1.0_00017.1.g1152.t1	ref|XP_002869275.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297315111|gb|EFH45534.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	396	391	1.00E-180	98.7	85.6	89.9	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT4G32400.1 | Symbols: EMB104, SHS1, EMB42, ATBT1 | Mitochondrial substrate carrier family protein | chr4:15638686-15640238 FORWARD LENGTH=392	396	392	0	99.0	84.3	88.4
Rsa1.0_00017.1.g1153.t1	gb|ACS68190.1| cellulose synthase 1.2 catalytic subunit [Brassica napus]	1079	1083	0	100.4	97.3	99.1	cellulose synthase 1.2 catalytic subunit	gbpln	Brassica napus	AT4G32410.1 | Symbols: CESA1, RSW1, AtCESA1 | cellulose synthase 1 | chr4:15641009-15646388 REVERSE LENGTH=1081	1079	1081	0	100.2	94.5	97.6
Rsa1.0_00017.1.g1154.t10	ref|XP_002867244.1| hypothetical protein ARALYDRAFT_491484 [Arabidopsis lyrata subsp. lyrata] gi|297313080|gb|EFH43503.1| hypothetical protein ARALYDRAFT_491484 [Arabidopsis lyrata subsp. lyrata]	860	845	1.00E-160	98.3	55.8	62.2	hypothetical protein ARALYDRAFT_491484	gbpln	Arabidopsis lyrata	AT4G32420.3 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr4:15647550-15652103 REVERSE LENGTH=837	860	837	1.00E-128	97.3	38.1	43.7
Rsa1.0_00017.1.g1155.t1	ref|NP_194969.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75147159|sp|Q84MA3.1|PP345_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g32430, mitochondrial; Flags: Precursor gi|30102674|gb|AAP21255.1| At4g32430 [Arabidopsis thaliana] gi|110742925|dbj|BAE99358.1| hypothetical protein [Arabidopsis thaliana] gi|332660658|gb|AEE86058.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	769	763	0	99.2	79.7	88.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G32430.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:15652982-15655273 FORWARD LENGTH=763	769	763	0	99.2	79.7	88.6
Rsa1.0_00017.1.g1156.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1157.t1	gb|EOA17836.1| hypothetical protein CARUB_v10006237mg [Capsella rubella]	430	390	1.00E-151	90.7	65.1	68.6	hypothetical protein CARUB_v10006237mg	gbpln	Capsella rubella	AT4G32440.2 | Symbols: | Plant Tudor-like RNA-binding protein | chr4:15657295-15659354 FORWARD LENGTH=393	430	393	1.00E-152	91.4	66.5	72.3
Rsa1.0_00017.1.g1158.t1	dbj|BAD43544.1| putative protein [Arabidopsis thaliana]	557	537	0	96.4	68.9	79.5	putative protein	gbpln	Arabidopsis thaliana	AT4G32450.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:15661092-15662705 FORWARD LENGTH=537	557	537	0	96.4	68.9	79.5
Rsa1.0_00017.1.g1159.t1	ref|NP_567894.1| uncharacterized protein [Arabidopsis thaliana] gi|42573129|ref|NP_974661.1| uncharacterized protein [Arabidopsis thaliana] gi|21593257|gb|AAM65206.1| unknown [Arabidopsis thaliana] gi|94442427|gb|ABF19001.1| At4g32460 [Arabidopsis thaliana] gi|332660663|gb|AEE86063.1| uncharacterized protein AT4G32460 [Arabidopsis thaliana] gi|332660664|gb|AEE86064.1| uncharacterized protein AT4G32460 [Arabidopsis thaliana]	365	365	0	100.0	92.6	96.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32460.2 | Symbols: | Protein of unknown function, DUF642 | chr4:15663036-15664859 REVERSE LENGTH=365	365	365	0	100.0	92.6	96.7
Rsa1.0_00017.1.g1160.t1	gb|EOA17665.1| hypothetical protein CARUB_v10006035mg [Capsella rubella]	122	122	1.00E-57	100.0	89.3	95.9	hypothetical protein CARUB_v10006035mg	gbpln	Capsella rubella	AT4G32470.1 | Symbols: | Cytochrome bd ubiquinol oxidase, 14kDa subunit | chr4:15669641-15671095 REVERSE LENGTH=122	122	122	2.00E-59	100.0	87.7	95.9
Rsa1.0_00017.1.g1161.t1	gb|EOA18796.1| hypothetical protein CARUB_v10007410mg [Capsella rubella]	872	880	0	100.9	88.4	93.1	hypothetical protein CARUB_v10007410mg	gbpln	Capsella rubella	AT4G32500.1 | Symbols: AKT5, KT5 | K+ transporter 5 | chr4:15681122-15685214 FORWARD LENGTH=880	872	880	0	100.9	88.5	92.9
Rsa1.0_00017.1.g1162.t1	gb|EOA16174.1| hypothetical protein CARUB_v10004311mg, partial [Capsella rubella]	674	666	0	98.8	90.2	93.3	hypothetical protein CARUB_v10004311mg, partial	gbpln	Capsella rubella	AT4G32510.1 | Symbols: | HCO3- transporter family | chr4:15685903-15688811 REVERSE LENGTH=673	674	673	0	99.9	90.2	93.9
Rsa1.0_00017.1.g1163.t1	gb|EOA16417.1| hypothetical protein CARUB_v10004571mg [Capsella rubella]	525	529	0	100.8	90.1	94.9	hypothetical protein CARUB_v10004571mg	gbpln	Capsella rubella	AT4G32520.2 | Symbols: SHM3 | serine hydroxymethyltransferase 3 | chr4:15689642-15692334 REVERSE LENGTH=529	525	529	0	100.8	88.6	93.3
Rsa1.0_00017.1.g1164.t1	ref|XP_002880688.1| H+-transporting two-sector ATPase [Arabidopsis lyrata subsp. lyrata] gi|297326527|gb|EFH56947.1| H+-transporting two-sector ATPase [Arabidopsis lyrata subsp. lyrata]	177	179	8.00E-89	101.1	98.9	99.4	H+-transporting two-sector ATPase	gbpln	Arabidopsis lyrata	AT2G25610.1 | Symbols: | ATPase, F0/V0 complex, subunit C protein | chr2:10901585-10902494 REVERSE LENGTH=178	177	178	3.00E-91	100.6	98.3	99.4
Rsa1.0_00017.1.g1165.t1	ref|NP_567826.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|332660207|gb|AEE85607.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	458	460	0	100.4	82.3	88.6	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT4G29250.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr4:14420713-14422177 FORWARD LENGTH=460	458	460	0	100.4	82.3	88.6

<table>
<tr><td>Rsa1.0_00017.1.g1166.t1</td><td>ref|NP_189279.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|9294307|dbj|BAB02209.1| unnamed protein product [Arabidopsis thaliana] gi|332643644|gb|AEE77165.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]</td><td>760</td><td>764</td><td>0</td><td>100.5</td><td>70.7</td><td>81.3</td><td>transducin/WD40 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G26480.1 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr3:9687273-9690827 REVERSE LENGTH=764</td><td>760</td><td>764</td><td>0</td><td>100.5</td><td>70.7</td><td>81.3</td></tr>
<tr><td>Rsa1.0_00017.1.g1167.t1</td><td>gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]</td><td>221</td><td>1164</td><td>4.00E-43</td><td>526.7</td><td>42.1</td><td>57.9</td><td>similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G25720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:9380234-9381405 FORWARD LENGTH=282</td><td>221</td><td>282</td><td>4.00E-31</td><td>127.6</td><td>32.1</td><td>38.0</td></tr>
<tr><td>Rsa1.0_00017.1.g1168.t1</td><td>ref|XP_002869265.1| hypothetical protein ARALYDRAFT_353573 [Arabidopsis lyrata subsp. lyrata] gi|297315101|gb|EFH45524.1| hypothetical protein ARALYDRAFT_353573 [Arabidopsis lyrata subsp. lyrata]</td><td>424</td><td>414</td><td>0</td><td>97.6</td><td>84.9</td><td>89.9</td><td>hypothetical protein ARALYDRAFT_353573</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G32540.1 | Symbols: YUC, YUC1 | Flavin-binding monooxygenase family protein | chr4:15700904-15702870 FORWARD LENGTH=414</td><td>424</td><td>414</td><td>0</td><td>97.6</td><td>83.5</td><td>89.4</td></tr>
<tr><td>Rsa1.0_00017.1.g1169.t1</td><td>gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]</td><td>1855</td><td>1213</td><td>0</td><td>65.4</td><td>23.9</td><td>34.4</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1855</td><td>626</td><td>5.00E-70</td><td>33.7</td><td>7.8</td><td>12.0</td></tr>
<tr><td>Rsa1.0_00017.1.g1170.t1</td><td>ref|XP_002869264.1| hypothetical protein ARALYDRAFT_491464 [Arabidopsis lyrata subsp. lyrata] gi|297315100|gb|EFH45523.1| hypothetical protein ARALYDRAFT_491464 [Arabidopsis lyrata subsp. lyrata]</td><td>941</td><td>920</td><td>0</td><td>97.8</td><td>69.5</td><td>73.5</td><td>hypothetical protein ARALYDRAFT_491464</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G32551.1 | Symbols: LUG, RON2 | LisH dimerisation motif;WD40/YVTN repeat-like-containing domain | chr4:15707863-15713359 FORWARD LENGTH=931</td><td>941</td><td>931</td><td>0</td><td>98.9</td><td>69.1</td><td>73.5</td></tr>
<tr><td>Rsa1.0_00017.1.g1171.t20</td><td>ref|NP_001031771.1| paramyosin-related protein [Arabidopsis thaliana] gi|227202856|dbj|BAH56901.1| AT4G32560 [Arabidopsis thaliana] gi|332660680|gb|AEE86080.1| paramyosin-related protein [Arabidopsis thaliana]</td><td>539</td><td>304</td><td>1.00E-103</td><td>56.4</td><td>40.8</td><td>43.4</td><td>paramyosin-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G32560.3 | Symbols: | paramyosin-related | chr4:15713866-15716035 FORWARD LENGTH=304</td><td>539</td><td>304</td><td>1.00E-106</td><td>56.4</td><td>40.8</td><td>43.4</td></tr>
<tr><td>Rsa1.0_00017.1.g1172.t1</td><td>ref|NP_567898.1| protein TIFY 8 [Arabidopsis thaliana] gi|75147164|sp|Q84MB2.1|TIF8_ARATH RecName: Full=Protein TIFY 8 gi|30102642|gb|AAP21239.1| At4g32570 [Arabidopsis thaliana] gi|332660681|gb|AEE86081.1| protein TIFY 8 [Arabidopsis thaliana]</td><td>360</td><td>361</td><td>1.00E-129</td><td>100.3</td><td>75.3</td><td>81.7</td><td>protein TIFY 8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G32570.1 | Symbols: TIFY8 | TIFY domain protein 8 | chr4:15716433-15718702 REVERSE LENGTH=361</td><td>360</td><td>361</td><td>1.00E-132</td><td>100.3</td><td>75.3</td><td>81.7</td></tr>
<tr><td>Rsa1.0_00017.1.g1173.t1</td><td>gb|AAG50751.1|AC079733_19 polyprotein, putative [Arabidopsis thaliana]</td><td>1447</td><td>1468</td><td>0</td><td>101.5</td><td>50.9</td><td>67.6</td><td>polyprotein, putative</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1447</td><td>1262</td><td>1.00E-139</td><td>87.2</td><td>17.6</td><td>25.2</td></tr>
<tr><td>Rsa1.0_00017.1.g1174.t1</td><td>ref|XP_002869262.1| hypothetical protein ARALYDRAFT_913185 [Arabidopsis lyrata subsp. lyrata] gi|297315098|gb|EFH45521.1| hypothetical protein ARALYDRAFT_913185 [Arabidopsis lyrata subsp. lyrata]</td><td>155</td><td>175</td><td>3.00E-59</td><td>112.9</td><td>84.5</td><td>91.0</td><td>hypothetical protein ARALYDRAFT_913185</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G32590.1 | Symbols: | 2Fe-2S ferredoxin-like superfamily protein | chr4:15721417-15722776 FORWARD LENGTH=173</td><td>155</td><td>173</td><td>4.00E-60</td><td>111.6</td><td>82.6</td><td>89.7</td></tr>
<tr><td>Rsa1.0_00017.1.g1175.t2</td><td>ref|XP_002869261.1| hypothetical protein ARALYDRAFT_328473 [Arabidopsis lyrata subsp. lyrata] gi|297315097|gb|EFH45520.1| hypothetical protein ARALYDRAFT_328473 [Arabidopsis lyrata subsp. lyrata]</td><td>464</td><td>489</td><td>0</td><td>105.4</td><td>82.8</td><td>88.6</td><td>hypothetical protein ARALYDRAFT_328473</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G32600.1 | Symbols: | RING/U-box superfamily protein | chr4:15724010-15725737 FORWARD LENGTH=453</td><td>464</td><td>453</td><td>0</td><td>97.6</td><td>81.5</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00017.1.g1176.t1</td><td>emb|CAA18600.1| putative protein [Arabidopsis thaliana] gi|7270165|emb|CAB79978.1| putative protein [Arabidopsis thaliana]</td><td>167</td><td>557</td><td>2.00E-71</td><td>333.5</td><td>88.0</td><td>94.0</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G32605.1 | Symbols: | Mitochondrial glycoprotein family protein | chr4:15726429-15727864 REVERSE LENGTH=227</td><td>167</td><td>227</td><td>3.00E-73</td><td>135.9</td><td>88.0</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00017.1.g1177.t1</td><td>dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]</td><td>156</td><td>329</td><td>1.00E-17</td><td>210.9</td><td>37.2</td><td>52.6</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00017.1.g1178.t1</td><td>ref|NP_194987.2| copper ion binding protein [Arabidopsis thaliana] gi|110743171|dbj|BAE99477.1| hypothetical protein [Arabidopsis thaliana] gi|332660689|gb|AEE86089.1| copper ion binding protein [Arabidopsis thaliana]</td><td>318</td><td>315</td><td>1.00E-65</td><td>99.1</td><td>74.5</td><td>82.4</td><td>copper ion binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G32610.1 | Symbols: | copper ion binding | chr4:15728376-15729897 REVERSE LENGTH=315</td><td>318</td><td>315</td><td>3.00E-68</td><td>99.1</td><td>74.5</td><td>82.4</td></tr>
<tr><td>Rsa1.0_00017.1.g1179.t1</td><td>ref|XP_002869260.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315096|gb|EFH45519.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>1409</td><td>1550</td><td>0</td><td>110.0</td><td>42.2</td><td>46.4</td><td>nucleic acid binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G32620.2 | Symbols: | Enhancer of polycomb-like transcription factor protein | chr4:15731968-15737222 FORWARD LENGTH=1540</td><td>1409</td><td>1540</td><td>0</td><td>109.3</td><td>41.4</td><td>45.7</td></tr>
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Rsa1.0_00017.1.g1180.t1	ref|XP_002869259.1| hypothetical protein ARALYDRAFT_491451 [Arabidopsis lyrata subsp. lyrata] gi|297315095|gb|EFH45518.1| hypothetical protein ARALYDRAFT_491451 [Arabidopsis lyrata subsp. lyrata]	630	631	0	100.2	70.0	78.3	hypothetical protein ARALYDRAFT_491451	gbpln	Arabidopsis lyrata	AT4G32630.2 | Symbols: | ArfGap/RecO-like zinc finger domain-containing protein | chr4:15738315-15741412 FORWARD LENGTH=628	630	628	0	99.7	67.8	77.3
Rsa1.0_00017.1.g1181.t1	dbj|BAM76809.1| Sec24-like transport protein [Arabidopsis thaliana]	1083	1092	0	100.8	89.2	93.3	Sec24-like transport protein	gbpln	Arabidopsis thaliana	AT4G32640.2 | Symbols: | Sec23/Sec24 protein transport family protein | chr4:15742661-15750424 FORWARD LENGTH=1080	1083	1080	0	99.7	88.1	92.1
Rsa1.0_00017.1.g1182.t1	ref|NP_194991.1| Potassium channel KAT3 [Arabidopsis thaliana] gi|44888078|sp|P92960.1|KAT3_ARATH RecName: Full=Potassium channel KAT3; AltName: Full=AKT4; AltName: Full=AtKC1; AltName: Full=Potassium channel TKC gi|1708777|emb|CAB05669.1| potassium channel [Arabidopsis thaliana] gi|3063705|emb|CAA18596.1| potassium channel protein [Arabidopsis thaliana] gi|4090537|gb|AAC98810.1| K+ inward rectifying channel protein [Arabidopsis thaliana] gi|4098949|gb|AAD00503.1| K+ inward rectifying channel [Arabidopsis thaliana] gi|7270169|emb|CAB79982.1| potassium channel protein AtKC [Arabidopsis thaliana] gi|15529218|gb|AAK97703.1| AT4g32650/F4D11_150 [Arabidopsis thaliana] gi|27777708|gb|AAO23890.1| At4g32650/F4D11_150 [Arabidopsis thaliana] gi|332660697|gb|AEE86097.1| Potassium channel KAT3 [Arabidopsis thaliana]	723	662	0	91.6	74.7	82.2	Potassium channel KAT3	gbpln	Arabidopsis thaliana	AT4G32650.1 | Symbols: ATKC1, KAT3, KC1, AtLKT1 | potassium channel in Arabidopsis thaliana 3 | chr4:15751482-15754797 REVERSE LENGTH=662	723	662	0	91.6	74.7	82.2
Rsa1.0_00017.1.g1183.t1	ref|NP_194992.1| serine/threonine-protein kinase AFC3 [Arabidopsis thaliana] gi|5915680|sp|P51568.2|AFC3_ARATH RecName: Full=Serine/threonine-protein kinase AFC3 gi|642134|dbj|BAA08216.1| protein kinase [Arabidopsis thaliana] gi|3063704|emb|CAA18595.1| protein kinase AME3 [Arabidopsis thaliana] gi|7270170|emb|CAB79983.1| protein kinase AME3 [Arabidopsis thaliana] gi|119935963|gb|ABM06046.1| At4g32660 [Arabidopsis thaliana] gi|332660700|gb|AEE86100.1| serine/threonine-protein kinase AFC3 [Arabidopsis thaliana]	398	400	0	100.5	91.5	96.0	serine/threonine-protein kinase AFC3	gbpln	Arabidopsis thaliana	AT4G32660.1 | Symbols: AME3 | Protein kinase superfamily protein | chr4:15756396-15759107 FORWARD LENGTH=400	398	400	0	100.5	91.5	96.0
Rsa1.0_00017.1.g1184.t1	ref|XP_002867231.1| hypothetical protein ARALYDRAFT_491441 [Arabidopsis lyrata subsp. lyrata] gi|297313067|gb|EFH43490.1| hypothetical protein ARALYDRAFT_491441 [Arabidopsis lyrata subsp. lyrata]	741	861	1.00E-152	116.2	36.8	44.5	hypothetical protein ARALYDRAFT_491441	gbpln	Arabidopsis lyrata	AT4G32670.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr4:15759527-15762847 REVERSE LENGTH=860	741	860	1.00E-152	116.1	36.6	44.5
Rsa1.0_00017.1.g1185.t1	ref|NP_567900.1| uncharacterized protein [Arabidopsis thaliana] gi|332660703|gb|AEE86103.1| uncharacterized protein AT4G32680 [Arabidopsis thaliana]	280	282	1.00E-103	100.7	75.4	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32680.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52343.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15763462-15765039 REVERSE LENGTH=282	280	282	1.00E-105	100.7	75.4	83.9
Rsa1.0_00017.1.g1186.t1	ref|XP_002869254.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315090|gb|EFH45513.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	2151	2147	0	99.8	86.5	90.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G32700.2 | Symbols: | helicases;ATP-dependent helicases;nucleic acid binding;ATP binding;DNA-directed DNA polymerases;DNA binding | chr4:15767440-15779185 FORWARD LENGTH=2154	2151	2154	0	100.1	85.7	90.6

Rsa1.0_00017.1.g1187.t1	sp|O65530.1|PEK14_ARATH RecName: Full=Proline-rich receptor-like protein kinase PERK14; AltName: Full=Proline-rich extensin-like receptor kinase 14; Short=AtPERK14 gi|3063699|emb|CAA18590.1| putative protein [Arabidopsis thaliana] gi|7270175|emb|CAB79988.1| putative protein kinase [Arabidopsis thaliana]	705	731	0	103.7	72.5	77.7	RecName: Full=Proline-rich receptor-like protein kinase PERK14; AltName: Full=Proline-rich extensin-like receptor kinase 14; Short=AtPERK14 gi|3063699|emb|CAA18590.1| putative protein	gbpln	Arabidopsis thaliana	AT4G32710.1 | Symbols: | Protein kinase superfamily protein | chr4:15781362-15783242 FORWARD LENGTH=388	705	388	0	55.0	45.7	49.1
Rsa1.0_00017.1.g1188.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1189.t1	ref|XP_002869250.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315086|gb|EFH45509.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	435	433	0	99.5	87.1	92.4	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT4G32720.1 | Symbols: AtLa1, La1 | La protein 1 | chr4:15787313-15789683 FORWARD LENGTH=433	435	433	0	99.5	86.7	91.7
Rsa1.0_00017.1.g1190.t1	ref|NP_974718.1| myb-related protein 3R-1 [Arabidopsis thaliana] gi|332660712|gb|AEE86112.1| myb-related protein 3R-1 [Arabidopsis thaliana]	874	995	0	113.8	79.5	85.7	myb-related protein 3R-1	gbpln	Arabidopsis thaliana	AT4G32730.2 | Symbols: PC-MYB1, MYB3R-1, ATMYB3R-1, ATMYB3R1 | Homeodomain-like protein | chr4:15791039-15795643 FORWARD LENGTH=995	874	995	0	113.8	79.5	85.7
Rsa1.0_00017.1.g1191.t1	gb|EOA17128.1| hypothetical protein CARUB_v10005389mg [Capsella rubella]	284	292	1.00E-132	102.8	83.5	90.1	hypothetical protein CARUB_v10005389mg	gbpln	Capsella rubella	AT4G32750.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15796415-15798091 REVERSE LENGTH=293	284	293	1.00E-133	103.2	83.5	91.2
Rsa1.0_00017.1.g1192.t1	ref|NP_001190892.1| ENTH/VHS/GAT family protein [Arabidopsis thaliana] gi|332660715|gb|AEE86115.1| ENTH/VHS/GAT family protein [Arabidopsis thaliana]	659	676	0	102.6	86.0	90.1	ENTH/VHS/GAT family protein	gbpln	Arabidopsis thaliana	AT4G32760.2 | Symbols: | ENTH/VHS/GAT family protein | chr4:15799376-15803832 FORWARD LENGTH=676	659	676	0	102.6	86.0	90.1
Rsa1.0_00017.1.g1193.t1	gb|EOA16698.1| hypothetical protein CARUB_v10004890mg [Capsella rubella]	550	424	0	77.1	66.2	70.7	hypothetical protein CARUB_v10004890mg	gbpln	Capsella rubella	AT4G32780.1 | Symbols: | phosphoinositide binding | chr4:15808926-15810907 FORWARD LENGTH=270	550	270	1.00E-101	49.1	39.8	42.5
Rsa1.0_00017.1.g1194.t1	ref|NP_195006.1| ethylene-responsive transcription factor ERF043 [Arabidopsis thaliana] gi|75264505|sp|Q9M080.1|ERF43_ARATH RecName: Full=Ethylene-responsive transcription factor ERF043 gi|7270227|emb|CAB79997.1| transcription factor TINY homolog [Arabidopsis thaliana] gi|21618174|gb|AAM67224.1| transcription factor TINY homolog [Arabidopsis thaliana] gi|27754586|gb|AAO22740.1| putative transcription factor TINY [Arabidopsis thaliana] gi|28393859|gb|AAO42337.1| putative transcription factor TINY [Arabidopsis thaliana] gi|332660720|gb|AEE86120.1| ethylene-responsive transcription factor ERF043 [Arabidopsis thaliana]	231	221	9.00E-73	95.7	70.6	79.7	ethylene-responsive transcription factor ERF043	gbpln	Arabidopsis thaliana	AT4G32800.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:15819812-15820477 FORWARD LENGTH=221	231	221	3.00E-75	95.7	70.6	79.7
Rsa1.0_00017.1.g1195.t1	ref|NP_195032.2| peptidyl-prolyl cis-trans isomerase SDCCAG10 [Arabidopsis thaliana] gi|45680878|gb|AAS75308.1| multidomain cyclophilin type peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|95147300|gb|ABF57285.1| At4g33060 [Arabidopsis thaliana] gi|332660768|gb|AEE86168.1| peptidyl-prolyl cis-trans isomerase CYP57 [Arabidopsis thaliana]	124	504	7.00E-31	406.5	75.8	83.9	peptidyl-prolyl cis-trans isomerase SDCCAG10	gbpln	Arabidopsis thaliana	AT4G33060.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr4:15948535-15951954 FORWARD LENGTH=504	124	504	1.00E-33	406.5	75.8	83.9
Rsa1.0_00017.1.g1196.t1	ref|XP_002869241.1| hypothetical protein ARALYDRAFT_353547 [Arabidopsis lyrata subsp. lyrata] gi|297315077|gb|EFH45500.1| hypothetical protein ARALYDRAFT_353547 [Arabidopsis lyrata subsp. lyrata]	557	570	0	102.3	89.8	94.3	hypothetical protein ARALYDRAFT_353547	gbpln	Arabidopsis lyrata	AT4G32810.1 | Symbols: CCD8, MAX4, ATCCD8 | carotenoid cleavage dioxygenase 8 | chr4:15828348-15831299 FORWARD LENGTH=570	557	570	0	102.3	88.5	93.9

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<tr><td>Rsa1.0_00017.1.g1197.t1</td><td>ref|NP_195008.6| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana] gi|332660722|gb|AEE86122.1| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana]</td><td>1868</td><td>1863</td><td>0</td><td>99.7</td><td>86.3</td><td>91.5</td><td>tetratricopeptide repeat domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G32820.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:15831679-15841454 REVERSE LENGTH=1863</td><td>1868</td><td>1863</td><td>0</td><td>99.7</td><td>86.3</td><td>91.5</td></tr>
<tr><td>Rsa1.0_00017.1.g1198.t1</td><td>ref|XP_002869240.1| hypothetical protein ARALYDRAFT_913154 [Arabidopsis lyrata subsp. lyrata] gi|297315076|gb|EFH45499.1| hypothetical protein ARALYDRAFT_913154 [Arabidopsis lyrata subsp. lyrata]</td><td>295</td><td>290</td><td>1.00E-161</td><td>98.3</td><td>94.6</td><td>96.3</td><td>hypothetical protein ARALYDRAFT_913154</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G32830.1 | Symbols: AtAUR1, AUR1 | ataurora1 | chr4:15842557-15844354 FORWARD LENGTH=294</td><td>295</td><td>294</td><td>1.00E-161</td><td>99.7</td><td>93.6</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00017.1.g1199.t1</td><td>ref|NP_195010.1| 6-phosphofructokinase 6 [Arabidopsis thaliana] gi|75181422|sp|Q9M076.1|K6PF6_ARATH RecName: Full=6-phosphofructokinase 6; AltName: Full=Phosphofructokinase 6; AltName: Full=Phosphohexokinase 6 gi|7270231|emb|CAB80001.1| putative pyrophosphate--fructose-6-phosphate 1-phosphotransferase [Arabidopsis thaliana] gi|29029114|gb|AAO64936.1| At4g32840 [Arabidopsis thaliana] gi|110743163|dbj|BAE99473.1| putative pyrophosphate--fructose-6-phosphate 1-phosphotransferase [Arabidopsis thaliana] gi|332660725|gb|AEE86125.1| 6-phosphofructokinase 6 [Arabidopsis thaliana]</td><td>464</td><td>462</td><td>0</td><td>99.6</td><td>92.9</td><td>96.1</td><td>6-phosphofructokinase 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G32840.1 | Symbols: PFK6 | phosphofructokinase 6 | chr4:15845010-15848305 REVERSE LENGTH=462</td><td>464</td><td>462</td><td>0</td><td>99.6</td><td>92.9</td><td>96.1</td></tr>
<tr><td>Rsa1.0_00017.1.g1200.t1</td><td>gb|EOA16057.1| hypothetical protein CARUB_v10004188mg [Capsella rubella]</td><td>779</td><td>780</td><td>0</td><td>100.1</td><td>85.1</td><td>89.3</td><td>hypothetical protein CARUB_v10004188mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G32850.8 | Symbols: nPAP | nuclear poly(a) polymerase | chr4:15850134-15854443 FORWARD LENGTH=765</td><td>779</td><td>765</td><td>0</td><td>98.2</td><td>84.6</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00017.1.g1201.t1</td><td>emb|CAB80003.1| putative protein [Arabidopsis thaliana]</td><td>188</td><td>193</td><td>1.00E-84</td><td>102.7</td><td>84.0</td><td>90.4</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G32860.1 | Symbols: | unknown protein; Has 46 Blast hits to 46 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15856710-15857309 REVERSE LENGTH=199</td><td>188</td><td>199</td><td>6.00E-87</td><td>105.9</td><td>84.0</td><td>90.4</td></tr>
<tr><td>Rsa1.0_00017.1.g1202.t1</td><td>ref|XP_002869238.1| hypothetical protein ARALYDRAFT_491409 [Arabidopsis lyrata subsp. lyrata] gi|297315074|gb|EFH45497.1| hypothetical protein ARALYDRAFT_491409 [Arabidopsis lyrata subsp. lyrata]</td><td>164</td><td>157</td><td>3.00E-67</td><td>95.7</td><td>75.6</td><td>86.0</td><td>hypothetical protein ARALYDRAFT_491409</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G32870.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:15862168-15862641 FORWARD LENGTH=157</td><td>164</td><td>157</td><td>6.00E-67</td><td>95.7</td><td>72.6</td><td>84.8</td></tr>
<tr><td>Rsa1.0_00017.1.g1203.t1</td><td>ref|NP_195014.1| homeobox-leucine zipper protein ATHB-8 [Arabidopsis thaliana] gi|75220729|sp|Q39123.1|ATHB8_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-8; AltName: Full=HD-ZIP protein ATHB-8; AltName: Full=Homeodomain transcription factor ATHB-8 gi|1149569|emb|CAA90703.1| HD-zip [Arabidopsis thaliana] gi|7270235|emb|CAB80005.1| HD-zip transcription factor (athb-8) [Arabidopsis thaliana] gi|20152536|emb|CAD29660.1| homeodomain-leucine zipper protein 8 [Arabidopsis thaliana] gi|20466330|gb|AAM20482.1| HD-zip transcription factor (athb-8) [Arabidopsis thaliana] gi|31711762|gb|AAP68237.1| At4g32880 [Arabidopsis thaliana] gi|332660738|gb|AEE86138.1| homeobox-leucine zipper protein ATHB-8 [Arabidopsis thaliana]</td><td>833</td><td>833</td><td>0</td><td>100.0</td><td>97.0</td><td>99.2</td><td>homeobox-leucine zipper protein ATHB-8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G32880.1 | Symbols: ATHB-8, ATHB8, HB-8 | homeobox gene 8 | chr4:15863587-15867822 REVERSE LENGTH=833</td><td>833</td><td>833</td><td>0</td><td>100.0</td><td>97.0</td><td>99.2</td></tr>
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Rsa1.0_00017.1.g1204.t1	ref|NP_195015.1| GATA transcription factor 9 [Arabidopsis thaliana] gi|71159362|sp|O82632.1|GATA9_ARATH RecName: Full=GATA transcription factor 9 gi|3688170|emb|CAA21198.1| putative protein [Arabidopsis thaliana] gi|7270236|emb|CAB80006.1| putative protein [Arabidopsis thaliana] gi|26449440|dbj|BAC41847.1| unknown protein [Arabidopsis thaliana] gi|30725358|gb|AAP37701.1| At4g32890 [Arabidopsis thaliana] gi|332660739|gb|AEE86139.1| GATA transcription factor 9 [Arabidopsis thaliana]	320	308	1.00E-128	96.3	75.0	84.7	GATA transcription factor 9	gbpln	Arabidopsis thaliana	AT4G32890.1 | Symbols: GATA9 | GATA transcription factor 9 | chr4:15875598-15876615 FORWARD LENGTH=308	320	308	1.00E-131	96.3	75.0	84.7
Rsa1.0_00017.1.g1205.t1	gb|EOA17472.1| hypothetical protein CARUB_v10005799mg [Capsella rubella]	193	193	1.00E-91	100.0	85.0	92.7	hypothetical protein CARUB_v10005799mg	gbpln	Capsella rubella	AT4G32900.2 | Symbols: | Peptidyl-tRNA hydrolase II (PTH2) family protein | chr4:15878944-15880979 REVERSE LENGTH=193	193	193	3.00E-92	100.0	84.5	91.2
Rsa1.0_00017.1.g1206.t1	ref|NP_567908.1| uncharacterized protein [Arabidopsis thaliana] gi|75158853|sp|Q8RXH2.1|NUP85_ARATH RecName: Full=Nuclear pore complex protein Nup85; AltName: Full=Nucleoporin Nup85 gi|19698819|gb|AAL91145.1| putative protein [Arabidopsis thaliana] gi|332660742|gb|AEE86142.1| uncharacterized protein AT4G32910 [Arabidopsis thaliana]	814	716	0	88.0	79.1	83.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32910.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nuclear pore complex protein, Nucleoporin Nup85-like (InterPro:IPR011502); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15881364-15885210 FORWARD LENGTH=716	814	716	0	88.0	79.1	83.8
Rsa1.0_00017.1.g1207.t1	ref|XP_002867220.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata] gi|297313056|gb|EFH43479.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	1435	1424	0	99.2	86.8	92.9	glycine-rich protein	gbpln	Arabidopsis lyrata	AT4G32920.3 | Symbols: | glycine-rich protein | chr4:15888153-15896006 REVERSE LENGTH=1432	1435	1432	0	99.8	86.8	92.8
Rsa1.0_00017.1.g1208.t2	emb|CAA21202.1| putative protein [Arabidopsis thaliana] gi|7270240|emb|CAB80010.1| putative protein [Arabidopsis thaliana]	195	181	8.00E-87	92.8	82.6	86.2	putative protein	gbpln	Arabidopsis thaliana	AT4G32930.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF866, eukaryotic (InterPro:IPR008584); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15898878-15900185 FORWARD LENGTH=167	195	167	2.00E-87	85.6	82.1	84.1
Rsa1.0_00017.1.g1209.t1	dbj|BAJ33795.1| unnamed protein product [Thellungiella halophila]	489	478	0	97.8	86.1	91.2	unnamed protein product	----	----	AT4G32940.1 | Symbols: GAMMA-VPE, GAMMAVPE | gamma vacuolar processing enzyme | chr4:15900557-15903161 REVERSE LENGTH=494	489	494	0	101.0	85.5	89.0
Rsa1.0_00017.1.g1210.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1211.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1212.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1213.t1	ref|XP_002867215.1| hypothetical protein ARALYDRAFT_491396 [Arabidopsis lyrata subsp. lyrata] gi|297313051|gb|EFH43474.1| hypothetical protein ARALYDRAFT_491396 [Arabidopsis lyrata subsp. lyrata]	455	472	0	103.7	80.0	86.2	hypothetical protein ARALYDRAFT_491396	gbpln	Arabidopsis lyrata	AT4G32980.1 | Symbols: ATH1 | homeobox gene 1 | chr4:15914865-15916873 REVERSE LENGTH=473	455	473	0	104.0	78.2	85.7
Rsa1.0_00017.1.g1214.t1	gb|EOA17824.1| hypothetical protein CARUB_v10006225mg, partial [Capsella rubella]	195	241	2.00E-95	123.6	88.2	91.8	hypothetical protein CARUB_v10006225mg, partial	gbpln	Capsella rubella	AT4G33000.2 | Symbols: CBL10, SCABP8, ATCBL10 | calcineurin B-like protein 10 | chr4:15924821-15926398 FORWARD LENGTH=246	195	246	7.00E-95	126.2	84.6	90.8
Rsa1.0_00017.1.g1215.t1	ref|XP_002867212.1| hypothetical protein ARALYDRAFT_491390 [Arabidopsis lyrata subsp. lyrata] gi|297313048|gb|EFH43471.1| hypothetical protein ARALYDRAFT_491390 [Arabidopsis lyrata subsp. lyrata]	1043	1037	0	99.4	90.4	94.9	hypothetical protein ARALYDRAFT_491390	gbpln	Arabidopsis lyrata	AT4G33010.1 | Symbols: AtGLDP1, GLDP1 | glycine decarboxylase P-protein 1 | chr4:15926852-15931150 REVERSE LENGTH=1037	1043	1037	0	99.4	90.3	94.5
Rsa1.0_00017.1.g1216.t1	gb|EOA16962.1| hypothetical protein CARUB_v10005191mg [Capsella rubella]	390	340	1.00E-163	87.2	78.7	81.5	hypothetical protein CARUB_v10005191mg	gbpln	Capsella rubella	AT4G33020.1 | Symbols: ZIP9, ATZIP9 | ZIP metal ion transporter family | chr4:15932603-15934267 REVERSE LENGTH=344	390	344	1.00E-163	88.2	77.4	81.3

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<tr><td>Rsa1.0_00017.1.g1217.t1</td><td>ref|XP_002869229.1| hypothetical protein ARALYDRAFT_491388 [Arabidopsis lyrata subsp. lyrata] gi|297315065|gb|EFH45488.1| hypothetical protein ARALYDRAFT_491388 [Arabidopsis lyrata subsp. lyrata]</td><td>482</td><td>475</td><td>0</td><td>98.5</td><td>92.9</td><td>95.0</td><td>hypothetical protein ARALYDRAFT_491388</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G33030.1 | Symbols: SQD1 | sulfoquinovosyldiacylglycerol 1 | chr4:15936051-15937566 FORWARD LENGTH=477</td><td>482</td><td>477</td><td>0</td><td>99.0</td><td>91.9</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00017.1.g1218.t1</td><td>ref|NP_195030.1| glutaredoxin-C6 [Arabidopsis thaliana] gi|119370639|sp|Q8L9S3.2|GRXC6_ARATH RecName: Full=Glutaredoxin-C6; Short=AtGrxC6; AltName: Full=Protein ROXY 21 gi|3688185|emb|CAA21213.1| putative protein [Arabidopsis thaliana] gi|7270251|emb|CAB80021.1| putative protein [Arabidopsis thaliana] gi|18377674|gb|AAL66987.1| unknown protein [Arabidopsis thaliana] gi|20258937|gb|AAM14184.1| unknown protein [Arabidopsis thaliana] gi|226348218|gb|ACO50425.1| glutaredoxin [Arabidopsis thaliana] gi|332660763|gb|AEE86163.1| glutaredoxin-C6 [Arabidopsis thaliana]</td><td>144</td><td>144</td><td>2.00E-67</td><td>100.0</td><td>91.0</td><td>94.4</td><td>glutaredoxin-C6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G33040.1 | Symbols: | Thioredoxin superfamily protein | chr4:15940779-15941213 REVERSE LENGTH=144</td><td>144</td><td>144</td><td>5.00E-70</td><td>100.0</td><td>91.0</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00017.1.g1219.t1</td><td>gb|EOA16526.1| hypothetical protein CARUB_v10004685mg [Capsella rubella]</td><td>465</td><td>487</td><td>0</td><td>104.7</td><td>90.5</td><td>94.2</td><td>hypothetical protein CARUB_v10004685mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G33050.3 | Symbols: EDA39 | calmodulin-binding family protein | chr4:15944604-15946736 REVERSE LENGTH=488</td><td>465</td><td>488</td><td>0</td><td>104.9</td><td>90.8</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00017.1.g1220.t1</td><td>ref|NP_195032.2| peptidyl-prolyl cis-trans isomerase SDCCAG10 [Arabidopsis thaliana] gi|45680878|gb|AAS75308.1| multidomain cyclophilin type peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|95147300|gb|ABF57285.1| At4g33060 [Arabidopsis thaliana] gi|332660768|gb|AEE86168.1| peptidyl-prolyl cis-trans isomerase CYP57 [Arabidopsis thaliana]</td><td>492</td><td>504</td><td>0</td><td>102.4</td><td>87.2</td><td>93.5</td><td>peptidyl-prolyl cis-trans isomerase SDCCAG10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G33060.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr4:15948535-15951954 FORWARD LENGTH=504</td><td>492</td><td>504</td><td>0</td><td>102.4</td><td>87.2</td><td>93.5</td></tr>
<tr><td>Rsa1.0_00017.1.g1221.t1</td><td>dbj|BAC76896.1| protein kinase [Raphanus sativus]</td><td>518</td><td>518</td><td>0</td><td>100.0</td><td>99.6</td><td>99.6</td><td>protein kinase</td><td>gbpln</td><td>Raphanus sativus</td><td>AT4G33080.1 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr4:15960146-15964296 FORWARD LENGTH=519</td><td>518</td><td>519</td><td>0</td><td>100.2</td><td>95.4</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00017.1.g1222.t1</td><td>ref|NP_195035.2| aminopeptidase M1 [Arabidopsis thaliana] gi|17473511|gb|AAL38379.1| AT4g33090/F4I10_20 [Arabidopsis thaliana] gi|24209879|gb|AAN41401.1| aminopeptidase M [Arabidopsis thaliana] gi|29028734|gb|AAO64746.1| At4g33090/F4I10_20 [Arabidopsis thaliana] gi|110742477|dbj|BAE99157.1| aminopeptidase like protein [Arabidopsis thaliana] gi|332660772|gb|AEE86172.1| aminopeptidase M1 [Arabidopsis thaliana]</td><td>871</td><td>879</td><td>0</td><td>100.9</td><td>93.2</td><td>96.7</td><td>aminopeptidase M1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G33090.1 | Symbols: APM1, ATAPM1 | aminopeptidase M1 | chr4:15965915-15970418 REVERSE LENGTH=879</td><td>871</td><td>879</td><td>0</td><td>100.9</td><td>93.2</td><td>96.7</td></tr>
<tr><td>Rsa1.0_00017.1.g1223.t1</td><td>ref|NP_195036.1| uncharacterized protein [Arabidopsis thaliana] gi|9910632|sp|Q9SMZ9.1|Y4331_ARATH RecName: Full=Uncharacterized protein At4g33100 gi|4455324|emb|CAB36784.1| putative protein [Arabidopsis thaliana] gi|7270257|emb|CAB80027.1| putative protein [Arabidopsis thaliana] gi|37202052|gb|AAQ89641.1| At4g33100 [Arabidopsis thaliana] gi|51968658|dbj|BAD43021.1| putative protein [Arabidopsis thaliana] gi|51969898|dbj|BAD43641.1| putative protein [Arabidopsis thaliana] gi|332660773|gb|AEE86173.1| uncharacterized protein AT4G33100 [Arabidopsis thaliana]</td><td>84</td><td>92</td><td>2.00E-35</td><td>109.5</td><td>86.9</td><td>90.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G33100.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Mitochondrial distribution/morphology family 35/apoptosis (InterPro:IPR007918); Has 214 Blast hits to 214 proteins in 102 species: Archae - 0; Bacteria - 0; Metazoa - 110; Fungi - 69; Plants - 29; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr4:15971701-15972342 FORWARD LENGTH=92</td><td>84</td><td>92</td><td>4.00E-38</td><td>109.5</td><td>86.9</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00017.1.g1224.t1</td><td>ref|XP_002867201.1| coclaurine N-methyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297313037|gb|EFH43460.1| coclaurine N-methyltransferase [Arabidopsis lyrata subsp. lyrata]</td><td>322</td><td>355</td><td>1.00E-166</td><td>110.2</td><td>89.1</td><td>95.3</td><td>coclaurine N-methyltransferase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G33110.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:15972497-15974531 REVERSE LENGTH=355</td><td>322</td><td>355</td><td>1.00E-165</td><td>110.2</td><td>86.6</td><td>94.4</td></tr>
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Rsa1.0_00017.1.g1225.t1	gb|AAC02672.1| polyprotein [Arabidopsis arenosa]	168	1390	1.00E−48	827.4	57.1	70.2	polyprotein	gbpln	Arabidopsis arenosa	#	#	#	#	#	#	#
Rsa1.0_00017.1.g1226.t1	dbj|BAB10876.1| polyprotein [Arabidopsis thaliana]	1546	1429	0	92.4	44.6	54.5	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1546	1262	1.00E−115	81.6	13.3	19.7
Rsa1.0_00017.1.g1227.t1	ref|NP_200901.2| kinesin family member 4/7/21/27 [Arabidopsis thaliana] gi|332010015|gb|AED97398.1| kinesin family member 4/7/21/27 [Arabidopsis thaliana]	719	1294	1.00E−144	180.0	45.3	57.2	kinesin family member 4/7/21/27	gbpln	Arabidopsis thaliana	AT5G60930.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:24515398-24522511 REVERSE LENGTH=1294	719	1294	1.00E−147	180.0	45.3	57.2
Rsa1.0_00017.1.g1228.t4	ref|NP_195039.6| uncharacterized protein [Arabidopsis thaliana] gi|332660777|gb|AEE86177.1| uncharacterized protein AT4G33130 [Arabidopsis thaliana]	225	222	1.00E−101	98.7	82.7	93.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G33130.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF547 (TAIR:AT1G16750.1); Has 192 Blast hits to 192 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 189; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:15979437-15980655 REVERSE LENGTH=222	225	222	1.00E−104	98.7	82.7	93.8
Rsa1.0_00017.1.g1229.t1	gb|EOA16925.1| hypothetical protein CARUB_v10005149mg [Capsella rubella]	343	351	1.00E−143	102.3	80.5	86.0	hypothetical protein CARUB_v10005149mg	gbpln	Capsella rubella	AT4G33140.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr4:15981648-15984135 FORWARD LENGTH=353	343	353	1.00E−140	102.9	77.8	82.8
Rsa1.0_00017.1.g1230.t1	gb|AAB96826.1| lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]	1072	1064	0	99.3	90.9	95.4	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme	gbpln	Arabidopsis thaliana	AT4G33150.2 | Symbols: | lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme | chr4:15985479-15991069 REVERSE LENGTH=1064	1072	1064	0	99.3	90.8	95.3
Rsa1.0_00018.1.g1231.t1	gb|EOA38120.1| hypothetical protein CARUB_v10009590mg [Capsella rubella]	287	351	2.00E−75	122.3	55.7	69.3	hypothetical protein CARUB_v10009590mg	gbpln	Capsella rubella	AT2G03810.4 | Symbols: | 18S pre-ribosomal assembly protein gar2-related | chr2:1162703-1164286 FORWARD LENGTH=439	287	439	9.00E−42	153.0	48.8	63.8
Rsa1.0_00018.1.g1232.t1	ref|NP_563930.1| phosphatidylinositol 3- and 4-kinase-like protein [Arabidopsis thaliana] gi|16974596|gb|AAL31202.1| At1g13640/F21F23_7 [Arabidopsis thaliana] gi|23506173|gb|AAN31098.1| At1g13640/F21F23_7 [Arabidopsis thaliana] gi|332190932|gb|AEE29053.1| phosphatidylinositol 3- and 4-kinase-like protein [Arabidopsis thaliana]	617	622	0	100.8	85.7	92.4	phosphatidylinositol 3- and 4-kinase-like protein	gbpln	Arabidopsis thaliana	AT1G13640.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase family protein | chr1:4677276-4679144 REVERSE LENGTH=622	617	622	0	100.8	85.7	92.4
Rsa1.0_00018.1.g1233.t1	gb|EOA36932.1| hypothetical protein CARUB_v10009802mg [Capsella rubella]	302	314	1.00E−148	104.0	91.7	95.0	hypothetical protein CARUB_v10009802mg	gbpln	Capsella rubella	AT1G13635.2 | Symbols: | DNA glycosylase superfamily protein | chr1:4674248-4675784 FORWARD LENGTH=311	302	311	1.00E−144	103.0	89.4	93.0
Rsa1.0_00018.1.g1234.t2	gb|EOA39669.1| hypothetical protein CARUB_v10008310mg [Capsella rubella] gi|482575483|gb|EOA39670.1| hypothetical protein CARUB_v10008310mg [Capsella rubella]	873	835	0	95.6	71.6	81.3	hypothetical protein CARUB_v10008310mg	gbpln	Capsella rubella	AT1G13630.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4669784-4672826 REVERSE LENGTH=806	873	806	0	92.3	64.7	73.7
Rsa1.0_00018.1.g1235.t1	gb|EOA36406.1| hypothetical protein CARUB_v10010856mg [Capsella rubella]	104	110	7.00E−26	105.8	60.6	69.2	hypothetical protein CARUB_v10010856mg	gbpln	Capsella rubella	AT1G13620.1 | Symbols: RGF2 | Encodes a root meristem growth factor (RGF). Belongs to a family of functionally redundant homologous peptides that are secreted, tyrosine-sulfated, and expressed mainly in the stem cell area and the innermost layer of central columella cells. RGFs are required for maintenance of the root stem cell niche and transit amplifying cell proliferation. Members of this family include: At5g60810 (RGF1), At1g13620 (RGF2), At2g04025 (RGF3), At3g30350 (RGF4), At5g51451 (RGF5), At4g16515 (RGF6), At3g02240 (RGF7), At2g03830 (RGF8) and At5g64770 (RGF9). | chr1:4668494-4669225 FORWARD LENGTH=109	104	109	9.00E−22	104.8	63.5	70.2
Rsa1.0_00018.1.g1236.t1	ref|XP_002892762.1| hypothetical protein ARALYDRAFT_471522 [Arabidopsis lyrata subsp. lyrata] gi|297338604|gb|EFH69021.1| hypothetical protein ARALYDRAFT_471522 [Arabidopsis lyrata subsp. lyrata]	538	360	1.00E−165	66.9	52.6	57.6	hypothetical protein ARALYDRAFT_471522	gbpln	Arabidopsis lyrata	AT1G13610.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:4664008-4665975 REVERSE LENGTH=358	538	358	1.00E−161	66.5	51.3	56.3

Rsa1.0_00018.1.g1237.t1	gb|EOA29050.1| hypothetical protein CARUB_v10025304mg [Capsella rubella]	83	105	9.00E-14	126.5	51.8	63.9	hypothetical protein CARUB_v10025304mg	gbpln	Capsella rubella	AT2G25185.1 | Symbols: | Defensin-like (DEFL) family protein | chr2:10731622-10732024 FORWARD LENGTH=102	83	102	2.00E-15	122.9	48.2	60.2
Rsa1.0_00018.1.g1238.t1	gb|EOA29050.1| hypothetical protein CARUB_v10025304mg [Capsella rubella]	83	105	7.00E-13	126.5	49.4	63.9	hypothetical protein CARUB_v10025304mg	gbpln	Capsella rubella	AT2G25185.1 | Symbols: | Defensin-like (DEFL) family protein | chr2:10731622-10732024 FORWARD LENGTH=102	83	102	3.00E-15	122.9	48.2	60.2
Rsa1.0_00018.1.g1239.t1	gb|EOA14018.1| hypothetical protein CARUB_v10027151mg [Capsella rubella]	134	204	9.00E-28	152.2	44.8	47.8	hypothetical protein CARUB_v10027151mg	gbpln	Capsella rubella	AT5G54500.2 | Symbols: FQR1 | flavodoxin-like quinone reductase 1 | chr5:22124674-22126435 FORWARD LENGTH=244	134	244	5.00E-29	182.1	41.8	44.8
Rsa1.0_00018.1.g1240.t1	ref|NP_172817.2| basic leucine-zipper 58 [Arabidopsis thaliana] gi|8920564|gb|AAF81286.1|AC027656_3 Contains similarity to bZIP DNA-binding protein HBF-1 - soybean from Glycine max gb|Y10685. It contains a bZIP transcription factor PF|00170. EST gb|N37717 comes from this gene [Arabidopsis thaliana] gi|9802757|gb|AAF99826.1|AC027134_8 Hypothetical protein [Arabidopsis thaliana] gi|12083268|gb|AAG48793.1|AF332430_1 putative bZIP transcription factor [Arabidopsis thaliana] gi|225897922|dbj|BAH30293.1| hypothetical protein [Arabidopsis thaliana] gi|332190919|gb|AEE29040.1| basic leucine-zipper 58 [Arabidopsis thaliana]	196	196	4.00E-84	100.0	84.2	93.4	basic leucine-zipper 58	gbpln	Arabidopsis thaliana	AT1G13600.1 | Symbols: AtbZIP58, bZIP58 | basic leucine-zipper 58 | chr1:4650787-4651377 REVERSE LENGTH=196	196	196	1.00E-86	100.0	84.2	93.4
Rsa1.0_00018.1.g1241.t1	ref|NP_172816.2| phytosulfokine-beta [Arabidopsis thaliana] gi|41019236|sp|Q9LMY9.3|PSK1_ARATH RecName: Full=Phytosulfokines 1; Short=AtPSK1; Contains: RecName: Full=Phytosulfokine-alpha; Short=PSK-alpha; Short=Phytosulfokine-a; Contains: RecName: Full=Phytosulfokine-beta; Short=PSK-beta; Short=Phytosulfokine-b; Flags: Precursor gi|23466369|tpg|DAA00275.1| TPA_exp: putative phytosulfokine peptide precursor [Arabidopsis thaliana] gi|27529964|dbj|BAB72176.2| phytosulfokine precursor 1 [Arabidopsis thaliana] gi|51970324|dbj|BAD43854.1| hypothetical protein [Arabidopsis thaliana] gi|332190918|gb|AEE29039.1| phytosulfokine-beta [Arabidopsis thaliana]	91	87	6.00E-26	95.6	70.3	80.2	phytosulfokine-beta	gbpln	Arabidopsis thaliana	AT1G13590.1 | Symbols: ATPSK1, PSK1 | phytosulfokine 1 precursor | chr1:4647979-4648612 FORWARD LENGTH=87	91	87	9.00E-29	95.6	70.3	80.2
Rsa1.0_00018.1.g1242.t1	ref|XP_002892759.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297338601|gb|EFH69018.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	416	416	0	100.0	92.1	96.9	F-box family protein	gbpln	Arabidopsis lyrata	AT1G13570.1 | Symbols: | F-box/RNI-like superfamily protein | chr1:4642528-4643930 REVERSE LENGTH=416	416	416	0	100.0	90.9	95.7
Rsa1.0_00018.1.g1243.t1	ref|XP_002892758.1| hypothetical protein ARALYDRAFT_471515 [Arabidopsis lyrata subsp. lyrata] gi|297338600|gb|EFH69017.1| hypothetical protein ARALYDRAFT_471515 [Arabidopsis lyrata subsp. lyrata]	389	389	0	100.0	98.5	99.2	hypothetical protein ARALYDRAFT_471515	gbpln	Arabidopsis lyrata	AT1G13560.1 | Symbols: AAPT1, ATAAPT1 | aminoalcoholphosphotransferase 1 | chr1:4638834-4641691 REVERSE LENGTH=389	389	389	0	100.0	97.9	99.2
Rsa1.0_00018.1.g1244.t1	gb|EOA36528.1| hypothetical protein CARUB_v10011549mg [Capsella rubella]	387	385	0	99.5	85.8	90.4	hypothetical protein CARUB_v10011549mg	gbpln	Capsella rubella	AT1G13530.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4633740-4635129 REVERSE LENGTH=385	387	385	0	99.5	82.4	89.9
Rsa1.0_00018.1.g1245.t1	gb|EOA40223.1| hypothetical protein CARUB_v10008945mg [Capsella rubella]	497	495	0	99.6	83.7	89.7	hypothetical protein CARUB_v10008945mg	gbpln	Capsella rubella	AT1G13460.2 | Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr1:4616504-4618180 FORWARD LENGTH=492	497	492	0	99.0	84.9	90.7
Rsa1.0_00018.1.g1246.t1	gb|ABV89646.1| DNA binding protein GT-1 [Brassica rapa]	395	399	0	101.0	92.9	94.7	DNA binding protein GT-1	gbpln	Brassica rapa	AT1G13450.1 | Symbols: GT-1 | Homeodomain-like superfamily protein | chr1:4612999-4615115 REVERSE LENGTH=406	395	406	0	102.8	84.3	89.9
Rsa1.0_00018.1.g1247.t3	sp|P04796.2|G3PC_SINAL RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product [Sinapis alba]	579	338	0	58.4	54.9	55.1	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product	gbpln	Sinapis alba	AT3G04120.1 | Symbols: GAPC, GAPC-1, GAPC1 | glyceraldehyde-3-phosphate dehydrogenase C subunit 1 | chr3:1081077-1083131 FORWARD LENGTH=338	579	338	0	58.4	53.5	54.6

Rsa1.0_00018.1.g1248.t1	ref|XP_002892660.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338502|gb|EFH68919.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	348	367	1.00E-141	105.5	74.7	84.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G11900.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4013166-4014630 REVERSE LENGTH=367	348	367	1.00E-143	105.5	73.9	83.3
Rsa1.0_00018.1.g1249.t1	ref|XP_002869525.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315361|gb|EFH45784.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	686	707	0	103.1	75.2	86.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G28010.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:13930379-13932493 FORWARD LENGTH=704	686	704	0	102.6	75.1	86.9
Rsa1.0_00018.1.g1250.t1	ref|XP_002880840.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297326679|gb|EFH57099.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	371	371	1.00E-177	100.0	80.3	89.2	F-box family protein	gbpln	Arabidopsis lyrata	AT2G32560.1 | Symbols: | F-box family protein | chr2:13824820-13826761 FORWARD LENGTH=371	371	371	1.00E-177	100.0	81.9	89.8
Rsa1.0_00018.1.g1251.t1	ref|NP_564794.1| octicosapeptide/Phox/Be.1 domain-containing protein [Arabidopsis thaliana] gi|7940289|gb|AAF70848.1|AC003113_15 F2401.12 [Arabidopsis thaliana] gi|19423968|gb|AAL87265.1| unknown protein [Arabidopsis thaliana] gi|21281131|gb|AAM45044.1| unknown protein [Arabidopsis thaliana] gi|332195840|gb|AEE33961.1| octicosapeptide/Phox/Be.1 domain-containing protein [Arabidopsis thaliana]	740	751	0	101.5	75.9	84.2	octicosapeptide/Phox/Be.1 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G62390.1 | Symbols: Phox2 | Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein | chr1:23084632-23086887 REVERSE LENGTH=751	740	751	0	101.5	75.9	84.2
Rsa1.0_00018.1.g1252.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00018.1.g1253.t1	ref|XP_002889903.1| hypothetical protein ARALYDRAFT_471341 [Arabidopsis lyrata subsp. lyrata] gi|297335745|gb|EFH66162.1| hypothetical protein ARALYDRAFT_471341 [Arabidopsis lyrata subsp. lyrata]	234	329	1.00E-112	140.6	91.5	96.2	hypothetical protein ARALYDRAFT_471341	gbpln	Arabidopsis lyrata	AT1G11915.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G17350.1); Has 261 Blast hits to 261 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 261; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4021830-4023084 FORWARD LENGTH=329	234	329	1.00E-113	140.6	89.7	95.7
Rsa1.0_00018.1.g1254.t1	gb|EOA36500.1| hypothetical protein CARUB_v10011187mg [Capsella rubella]	372	385	1.00E-168	103.5	78.2	85.2	hypothetical protein CARUB_v10011187mg	gbpln	Capsella rubella	AT1G11920.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:4023667-4025097 REVERSE LENGTH=384	372	384	1.00E-170	103.2	78.2	85.5
Rsa1.0_00018.1.g1255.t1	gb|EOA36500.1| hypothetical protein CARUB_v10011187mg [Capsella rubella]	384	385	0	100.3	91.9	95.6	hypothetical protein CARUB_v10011187mg	gbpln	Capsella rubella	AT1G11920.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:4023667-4025097 REVERSE LENGTH=384	384	384	0	100.0	91.7	96.1
Rsa1.0_00018.1.g1256.t1	gb|EOA38666.1| hypothetical protein CARUB_v10010604mg [Capsella rubella]	140	140	1.00E-51	100.0	72.1	83.6	hypothetical protein CARUB_v10010604mg	gbpln	Capsella rubella	AT1G11925.1 | Symbols: | Stigma-specific Stig1 family protein | chr1:4026195-4026617 REVERSE LENGTH=140	140	140	4.00E-52	100.0	70.7	82.1
Rsa1.0_00018.1.g1257.t1	ref|NP_172660.5| putative ERD4 protein [Arabidopsis thaliana] gi|204324149|gb|ACI01072.1| putative membrane protein [Arabidopsis thaliana] gi|332190700|gb|AEE28821.1| putative ERD4 protein [Arabidopsis thaliana]	768	771	0	100.4	90.2	96.0	putative ERD4 protein	gbpln	Arabidopsis thaliana	AT1G11960.1 | Symbols: | ERD (early-responsive to dehydration stress) family protein | chr1:4039871-4043143 REVERSE LENGTH=771	768	771	0	100.4	90.2	96.0
Rsa1.0_00018.1.g1258.t1	ref|NP_172662.1| NEDD8-like protein RUB3 [Arabidopsis thaliana] gi|38258406|sp|O65381.1|RUB3_ARATH RecName: Full=NEDD8-like protein RUB3; AltName: Full=Ubiquitin-related protein 3; Short=AtRUB3; Flags: Precursor gi|3157940|gb|AAC17623.1| Contains similarity to Ubiquitin-like protein NEDD8 gb|D10918 from Mus musculus [Arabidopsis thaliana] gi|332190702|gb|AEE28823.1| NEDD8-like protein RUB3 [Arabidopsis thaliana]	90	78	2.00E-26	86.7	67.8	74.4	NEDD8-like protein RUB3	gbpln	Arabidopsis thaliana	AT1G11980.1 | Symbols: RUB3 | ubiquitin-related protein 3 | chr1:4045619-4045855 FORWARD LENGTH=78	90	78	4.00E-29	86.7	67.8	74.4
Rsa1.0_00018.1.g1259.t1	gb|AAC17628.1| Contains similarity to axi 1 gene gb|X80301 from Nicotiana tabacum [Arabidopsis thaliana]	622	627	0	100.8	78.3	86.3	Contains similarity to axi 1 gene gb|X80301 from Nicotiana tabacum	gbpln	Arabidopsis thaliana	AT1G11990.1 | Symbols: | O-fucosyltransferase family protein | chr1:4046246-4049060 REVERSE LENGTH=590	622	590	0	94.9	74.3	81.2

Rsa1.0_00018.1.g1260.t1	gb|EOA40028.1| hypothetical protein CARUB_v10008719mg [Capsella rubella]	567	567	0	100.0	95.6	97.9	hypothetical protein CARUB_v10008719mg	gbpln	Capsella rubella	AT1G12000.1 | Symbols: | Phosphofructokinase family protein | chr1:4050159-4053727 REVERSE LENGTH=566	567	566	0	99.8	95.6	97.5
Rsa1.0_00018.1.g1261.t7	dbj|BAJ33770.1| unnamed protein product [Thellungiella halophila]	278	416	1.00E-53	149.6	43.2	46.0	unnamed protein product	----	----	AT5G57630.1 | Symbols: CIPK21, SnRK3.4 | CBL-interacting protein kinase 21 | chr5:23341092-23343143 REVERSE LENGTH=416	278	416	2.00E-53	149.6	41.0	46.4
Rsa1.0_00018.1.g1262.t1	emb|CAA57285.1| ACC oxidase [Brassica oleracea]	320	321	1.00E-179	100.3	95.0	97.5	ACC oxidase	gbpln	Brassica oleracea	AT1G12010.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:4056274-4057670 FORWARD LENGTH=320	320	320	1.00E-175	100.0	90.9	94.7
Rsa1.0_00018.1.g1263.t1	gb|EOA37066.1| hypothetical protein CARUB_v10010193mg [Capsella rubella]	231	231	5.00E-80	100.0	73.6	82.3	hypothetical protein CARUB_v10010193mg	gbpln	Capsella rubella	AT1G12020.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G62422.1); Has 89 Blast hits to 88 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 87; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:4062625-4063305 REVERSE LENGTH=226	231	226	1.00E-78	97.8	71.4	78.8
Rsa1.0_00018.1.g1264.t1	gb|EOA38371.1| hypothetical protein CARUB_v10009904mg [Capsella rubella]	292	291	1.00E-116	99.7	78.1	83.9	hypothetical protein CARUB_v10009904mg	gbpln	Capsella rubella	AT1G12030.1 | Symbols: | Protein of unknown function (DUF506) | chr1:4064751-4066319 REVERSE LENGTH=295	292	295	1.00E-110	101.0	75.0	83.9
Rsa1.0_00018.1.g1265.t2	ref|XP_002889911.1| hypothetical protein ARALYDRAFT_471353 [Arabidopsis lyrata subsp. lyrata] gi|297335753|gb|EFH66170.1| hypothetical protein ARALYDRAFT_471353 [Arabidopsis lyrata subsp. lyrata]	450	421	0	93.6	84.0	86.2	hypothetical protein ARALYDRAFT_471353	gbpln	Arabidopsis lyrata	AT1G12050.1 | Symbols: | fumarylacetoacetase, putative | chr1:4072904-4075856 FORWARD LENGTH=421	450	421	0	93.6	82.2	86.0
Rsa1.0_00018.1.g1266.t1	gb|EOA37704.1| hypothetical protein CARUB_v10012423mg [Capsella rubella]	311	223	1.00E-106	71.7	64.3	67.8	hypothetical protein CARUB_v10012423mg	gbpln	Capsella rubella	AT1G12070.1 | Symbols: | Immunoglobulin E-set superfamily protein | chr1:4078913-4080106 REVERSE LENGTH=223	311	223	1.00E-107	71.7	63.7	67.8
Rsa1.0_00018.1.g1267.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00018.1.g1268.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00018.1.g1269.t1	gb|AAK30571.1|AF346659_1 extensin-like protein [Brassica napus]	137	137	3.00E-46	100.0	94.2	97.1	extensin-like protein	gbpln	Brassica napus	AT1G12090.1 | Symbols: ELP | extensin-like protein | chr1:4090176-4090589 REVERSE LENGTH=137	137	137	2.00E-45	100.0	95.6	97.8
Rsa1.0_00018.1.g1270.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00018.1.g1271.t1	gb|AEA35415.1| nitrate transporter [Brassica rapa subsp. chinensis]	590	589	0	99.8	93.4	97.3	nitrate transporter	gbpln	Brassica rapa	AT1G12110.1 | Symbols: NRT1.1, CHL1-1, NRT1, B-1, ATNRT1, CHL1 | nitrate transporter 1.1 | chr1:4105341-4109290 FORWARD LENGTH=590	590	590	0	100.0	92.2	95.9
Rsa1.0_00018.1.g1272.t1	gb|EOA40154.1| hypothetical protein CARUB_v10008871mg, partial [Capsella rubella]	410	516	1.00E-123	125.9	69.3	77.6	hypothetical protein CARUB_v10008871mg, partial	gbpln	Capsella rubella	AT1G12120.1 | Symbols: | Plant protein of unknown function (DUF863) | chr1:4114933-4116469 REVERSE LENGTH=483	410	483	1.00E-119	117.8	68.3	75.1
Rsa1.0_00018.1.g1273.t1	ref|NP_172679.1| uncharacterized protein [Arabidopsis thaliana] gi|75172923|sp|Q9FWW5.1|Y1215_ARATH RecName: Full=WEB family protein At1g12150 gi|10086518|gb|AAG12578.1|AC022522_11 Hypothetical protein [Arabidopsis thaliana] gi|332190722|gb|AEE28843.1| uncharacterized protein AT1G12150 [Arabidopsis thaliana]	63	548	2.00E-12	869.8	58.7	61.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G12150.1 | Symbols: | Plant protein of unknown function (DUF827) | chr1:4123530-4125328 REVERSE LENGTH=548	63	548	3.00E-15	869.8	58.7	61.9
Rsa1.0_00018.1.g1274.t1	ref|NP_172684.1| dimethylaniline monooxygenase (N-oxide forming) [Arabidopsis thaliana] gi|75172924|sp|Q9FWW9.1|GSXL2_ARATH RecName: Full=Flavin-containing monooxygenase FMO GS-OX-like 2; AltName: Full=Flavin-monooxygenase glucosinolate S-oxygenase-like 2 gi|10086514|gb|AAG12574.1|AC022522_7 Unknown protein [Arabidopsis thaliana] gi|20258836|gb|AAM13900.1| unknown protein [Arabidopsis thaliana] gi|22136992|gb|AAM91725.1| unknown protein [Arabidopsis thaliana] gi|332190727|gb|AEE28848.1| flavin-containing monooxygenase FMO GS-OX-like 2 [Arabidopsis thaliana]	463	465	0	100.4	90.9	95.2	dimethylaniline monooxygenase (N-oxide forming)	gbpln	Arabidopsis thaliana	AT1G12200.1 | Symbols: | Flavin-binding monooxygenase family protein | chr1:4137627-4139835 FORWARD LENGTH=465	463	465	0	100.4	90.9	95.2

Rsa1.0_00018.1.g1275.t1	ref|NP_563900.1| transaldolase [Arabidopsis thaliana] gi|10086511|gb|AAG12571.1|AC022522_4 Similar to transaldolase [Arabidopsis thaliana] gi|25083140|gb|AAN72047.1| expressed protein [Arabidopsis thaliana] gi|30725648|gb|AAP37846.1| At1g12230 [Arabidopsis thaliana] gi|332190732|gb|AEE28853.1| transaldolase [Arabidopsis thaliana]	409	405	0	99.0	91.0	96.6	transaldolase	gbpln	Arabidopsis thaliana	AT1G12230.1 | Symbols: | Aldolase superfamily protein | chr1:4148050-4150708 FORWARD LENGTH=405	409	405	0	99.0	91.0	96.6
Rsa1.0_00018.1.g1276.t2	gb|AAG36943.1|AF274299_1 acid invertase [Brassica oleracea]	665	662	0	99.5	95.6	97.0	acid invertase	gbpln	Brassica oleracea	AT1G12240.1 | Symbols: ATBETAFRUCT4, VAC-INV | Glycosyl hydrolases family 32 protein | chr1:4153699-4157457 FORWARD LENGTH=664	665	664	0	99.8	88.6	93.7
Rsa1.0_00018.1.g1277.t1	ref|XP_002892680.1| hypothetical protein ARALYDRAFT_471376 [Arabidopsis lyrata subsp. lyrata] gi|297338522|gb|EFH68939.1| hypothetical protein ARALYDRAFT_471376 [Arabidopsis lyrata subsp. lyrata]	396	395	0	99.7	88.1	91.2	hypothetical protein ARALYDRAFT_471376	gbpln	Arabidopsis lyrata	AT1G12260.1 | Symbols: VND4, EMB2749, ANAC007, NAC007 | NAC 007 | chr1:4163058-4164486 REVERSE LENGTH=395	396	395	0	99.7	88.1	91.2
Rsa1.0_00018.1.g1278.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00018.1.g1279.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00018.1.g1280.t1	ref|NP_172686.1| disease resistance protein RPS5 [Arabidopsis thaliana] gi|334182494|ref|NP_001184970.1| disease resistance protein RPS5 [Arabidopsis thaliana] gi|46396675|sp|O64973.2|RPS5_ARATH RecName: Full=Disease resistance protein RPS5; AltName: Full=Resistance to Pseudomonas syringae protein 5; AltName: Full=pNd3/pNd10 gi|10086512|gb|AAG12572.1|AC022522_5 resistance to Pseudomonas syringae protein 5 [Arabidopsis thaliana] gi|3309620|gb|AAC26126.1| resistance to Pseudomonas syringae protein 5 [Arabidopsis thaliana] gi|34849895|gb|AAQ82844.1| At1g12220 [Arabidopsis thaliana] gi|62319935|dbj|BAD94018.1| NBS/LRR disease resistance protein [Arabidopsis thaliana] gi|77632414|gb|ABB00204.1| disease resistance protein [Arabidopsis thaliana] gi|332190730|gb|AEE28851.1| disease resistance protein RPS5 [Arabidopsis thaliana] gi|332190731|gb|AEE28852.1| disease resistance protein RPS5 [Arabidopsis thaliana]	327	889	3.00E-67	271.9	41.6	52.6	disease resistance protein RPS5	gbpln	Arabidopsis thaliana	AT1G12220.2 | Symbols: RPS5 | Disease resistance protein (CC-NBS-LRR class) family | chr1:4145011-4147680 FORWARD LENGTH=889	327	889	9.00E-70	271.9	41.6	52.6
Rsa1.0_00018.1.g1281.t1	ref|XP_002879162.1| hypothetical protein ARALYDRAFT_320641 [Arabidopsis lyrata subsp. lyrata] gi|297325001|gb|EFH55421.1| hypothetical protein ARALYDRAFT_320641 [Arabidopsis lyrata subsp. lyrata]	279	709	3.00E-47	254.1	35.8	52.7	hypothetical protein ARALYDRAFT_320641	gbpln	Arabidopsis lyrata	AT1G12220.2 | Symbols: RPS5 | Disease resistance protein (CC-NBS-LRR class) family | chr1:4145011-4147680 FORWARD LENGTH=889	279	889	1.00E-47	318.6	39.1	50.5
Rsa1.0_00018.1.g1282.t1	gb|ACP30557.1| disease resistance protein [Brassica rapa subsp. pekinensis]	885	886	0	100.1	67.3	78.8	disease resistance protein	gbpln	Brassica rapa	AT1G12210.1 | Symbols: RFL1 | RPS5-like 1 | chr1:4140948-4143605 FORWARD LENGTH=885	885	885	0	100.0	66.1	78.0
Rsa1.0_00018.1.g1283.t1	gb|AAF79658.1|AC025416_32 F5O11.4 [Arabidopsis thaliana]	148	975	1.00E-78	658.8	96.6	98.6	F5O11.4	gbpln	Arabidopsis thaliana	AT1G12310.1 | Symbols: | Calcium-binding EF-hand family protein | chr1:4187500-4187946 REVERSE LENGTH=148	148	148	2.00E-80	100.0	97.3	99.3
Rsa1.0_00018.1.g1284.t1	ref|XP_002889928.1| hypothetical protein ARALYDRAFT_471382 [Arabidopsis lyrata subsp. lyrata] gi|297335770|gb|EFH66187.1| hypothetical protein ARALYDRAFT_471382 [Arabidopsis lyrata subsp. lyrata]	506	504	0	99.6	86.6	91.1	hypothetical protein ARALYDRAFT_471382	gbpln	Arabidopsis lyrata	AT1G12330.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12900.1); Has 249 Blast hits to 249 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 14; Plants - 217; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr1:4194673-4196627 FORWARD LENGTH=505	506	505	0	99.8	86.6	90.7
Rsa1.0_00018.1.g1285.t6	gb|EOA38925.1| hypothetical protein CARUB_v10011323mg [Capsella rubella]	699	666	0	95.3	87.3	90.4	hypothetical protein CARUB_v10011323mg	gbpln	Capsella rubella	AT1G12360.1 | Symbols: KEU | Sec1/munc18-like (SM) proteins superfamily | chr1:4201172-4206144 FORWARD LENGTH=666	699	666	0	95.3	86.4	90.0

Rsa1.0_00018.1.g1286.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00018.1.g1287.t1	ref|XP_002892685.1| hypothetical protein ARALYDRAFT_888561 [Arabidopsis lyrata subsp. lyrata] gi|297338527|gb|EFH68944.1| hypothetical protein ARALYDRAFT_888561 [Arabidopsis lyrata subsp. lyrata]	769	792	0	103.0	86.0	90.8	hypothetical protein ARALYDRAFT_888561	gbpln	Arabidopsis lyrata	AT1G12380.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G62870.1); Has 173 Blast hits to 170 proteins in 34 species: Archae - 0; Bacteria - 4; Metazoa - 25; Fungi - 8; Plants - 123; Viruses - 7; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:4214499-4216880 REVERSE LENGTH=793	769	793	0	103.1	86.0	91.5
Rsa1.0_00018.1.g1288.t2	ref|XP_002889932.1| cornichon family protein [Arabidopsis lyrata subsp. lyrata] gi|297335774|gb|EFH66191.1| cornichon family protein [Arabidopsis lyrata subsp. lyrata]	137	137	9.00E-69	100.0	93.4	96.4	cornichon family protein	gbpln	Arabidopsis lyrata	AT1G12390.1 | Symbols: | Cornichon family protein | chr1:4220347-4221481 FORWARD LENGTH=137	137	137	5.00E-71	100.0	92.7	95.6
Rsa1.0_00018.1.g1289.t1	gb|EOA38397.1| hypothetical protein CARUB_v10009963mg [Capsella rubella]	279	279	1.00E-156	100.0	95.0	97.8	hypothetical protein CARUB_v10009963mg	gbpln	Capsella rubella	AT1G12410.1 | Symbols: CLPR2, NCLPP2, CLP2 | CLP protease proteolytic subunit 2 | chr1:4223099-4224954 FORWARD LENGTH=279	279	279	1.00E-158	100.0	94.6	97.8
Rsa1.0_00018.1.g1290.t1	gb|EOA40435.1| hypothetical protein CARUB_v10009162mg [Capsella rubella]	441	441	0	100.0	93.7	95.9	hypothetical protein CARUB_v10009162mg	gbpln	Capsella rubella	AT1G12420.1 | Symbols: ACR8 | ACT domain repeat 8 | chr1:4226673-4228917 REVERSE LENGTH=441	441	441	0	100.0	93.7	95.9
Rsa1.0_00018.1.g1291.t1	ref|XP_002887985.1| hypothetical protein ARALYDRAFT_893174 [Arabidopsis lyrata subsp. lyrata] gi|297333826|gb|EFH64244.1| hypothetical protein ARALYDRAFT_893174 [Arabidopsis lyrata subsp. lyrata]	267	300	1.00E-128	112.4	85.0	92.9	hypothetical protein ARALYDRAFT_893174	gbpln	Arabidopsis lyrata	AT1G63000.1 | Symbols: NRS/ER, UER1 | nucleotide-rhamnose synthase/epimerase-reductase | chr1:23342510-23343859 FORWARD LENGTH=301	267	301	1.00E-127	112.7	85.0	92.9
Rsa1.0_00018.1.g1292.t1	gb|AAF88098.1|AC025417_26 T12C24.11 [Arabidopsis thaliana]	535	549	0	102.6	92.7	96.6	T12C24.11	gbpln	Arabidopsis thaliana	AT1G12570.1 | Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr1:4278192-4280753 REVERSE LENGTH=572	535	572	0	106.9	92.7	96.6
Rsa1.0_00018.1.g1293.t1	ref|NP_172721.1| dehydration-responsive element-binding protein 1F [Arabidopsis thaliana] gi|47605747|sp|Q9LN86.1|DRE1F_ARATH RecName: Full=Dehydration-responsive element-binding protein 1F; Short=Protein DREB1F gi|9502389|gb|AAF88096.1|AC025417_24 T12C24.14 [Arabidopsis thaliana] gi|48479384|gb|AAT44959.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|110736358|dbj|BAF00148.1| hypothetical protein [Arabidopsis thaliana] gi|332190780|gb|AEE28901.1| dehydration-responsive element-binding protein 1F [Arabidopsis thaliana]	231	209	4.00E-83	90.5	73.6	77.9	dehydration-responsive element-binding protein 1F	gbpln	Arabidopsis thaliana	AT1G12610.1 | Symbols: DDF1 | Integrase-type DNA-binding superfamily protein | chr1:4290205-4290834 REVERSE LENGTH=209	231	209	1.00E-85	90.5	73.6	77.9
Rsa1.0_00018.1.g1294.t1	ref|NP_172724.2| MBOAT (membrane bound O-acyl transferase)-like protein [Arabidopsis thaliana] gi|332190783|gb|AEE28904.1| MBOAT (membrane bound O-acyl transferase)-like protein [Arabidopsis thaliana]	465	462	0	99.4	92.3	95.9	MBOAT (membrane bound O-acyl transferase)-like protein	gbpln	Arabidopsis thaliana	AT1G12640.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr1:4303586-4305666 REVERSE LENGTH=462	465	462	0	99.4	92.3	95.9
Rsa1.0_00018.1.g1295.t1	gb|EOA37663.1| hypothetical protein CARUB_v10012242mg, partial [Capsella rubella]	133	137	6.00E-18	103.0	33.8	46.6	hypothetical protein CARUB_v10012242mg, partial	gbpln	Capsella rubella	AT1G12660.1 | Symbols: | Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant thionin (PR-13) family with the following members: At1g66100, At5g36910, At1g72260, At2g15010, At1g12663, At1g12660. | chr1:4308943-4309583 FORWARD LENGTH=137	133	137	2.00E-12	103.0	28.6	38.3
Rsa1.0_00018.1.g1296.t1	gb|EOA40316.1| hypothetical protein CARUB_v10009041mg [Capsella rubella]	451	470	0	104.2	86.9	91.6	hypothetical protein CARUB_v10009041mg	gbpln	Capsella rubella	AT1G12680.1 | Symbols: PEPKR2 | phosphoenolpyruvate carboxylase-related kinase 2 | chr1:4320123-4322269 REVERSE LENGTH=470	451	470	0	104.2	85.8	90.5
Rsa1.0_00018.1.g1297.t1	gb|EOA36152.1| hypothetical protein CARUB_v10009895mg [Capsella rubella]	284	294	1.00E-135	103.5	83.5	88.7	hypothetical protein CARUB_v10009895mg	gbpln	Capsella rubella	AT1G12710.1 | Symbols: AtPP2-A12, PP2-A12 | phloem protein 2-A12 | chr1:4326980-4328324 REVERSE LENGTH=291	284	291	1.00E-136	102.5	83.8	88.4
Rsa1.0_00018.1.g1298.t1	ref|XP_002889964.1| T12C24.27 [Arabidopsis lyrata subsp. lyrata] gi|297335806|gb|EFH66223.1| T12C24.27 [Arabidopsis lyrata subsp. lyrata]	478	478	0	100.0	92.3	95.2	T12C24.27	gbpln	Arabidopsis lyrata	AT1G12740.1 | Symbols: CYP87A2 | cytochrome P450, family 87, subfamily A, polypeptide 2 | chr1:4342462-4344569 FORWARD LENGTH=472	478	472	0	98.7	91.6	94.6
Rsa1.0_00018.1.g1299.t1	gb|EOA37577.1| hypothetical protein CARUB_v10011917mg [Capsella rubella]	304	304	1.00E-138	100.0	78.3	89.1	hypothetical protein CARUB_v10011917mg	gbpln	Capsella rubella	AT1G12750.3 | Symbols: RBL6 | RHOMBOID-like protein 6 | chr1:4345100-4346688 REVERSE LENGTH=307	304	307	1.00E-133	101.0	73.0	86.2

Rsa1.0_00018.1.g1300.t1	gb|EOA37885.1| hypothetical protein CARUB_v10009353mg [Capsella rubella]	407	397	1.00E−163	97.5	80.1	84.8	hypothetical protein CARUB_v10009353mg	gbpln	Capsella rubella	AT1G12760.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr1:4348728−4350512 FORWARD LENGTH=408	407	408	1.00E−161	100.2	77.4	81.1
Rsa1.0_00018.1.g1301.t1	gb|EOA38122.1| hypothetical protein CARUB_v10009592mg [Capsella rubella]	351	351	0	100.0	96.0	98.3	hypothetical protein CARUB_v10009592mg	gbpln	Capsella rubella	AT1G12780.1 | Symbols: UGE1, ATUGE1 | UDP−D−glucose/UDP−D−galactose 4−epimerase 1 | chr1:4356124−4358120 REVERSE LENGTH=351	351	351	0	100.0	95.4	97.4
Rsa1.0_00018.1.g1302.t1	gb|AAM65961.1| DNA ligase−like protein [Arabidopsis thaliana]	219	250	3.00E−97	114.2	84.9	92.2	DNA ligase−like protein	gbpln	Arabidopsis thaliana	AT1G12790.1 | Symbols: | CONTAINS InterPro DOMAIN/s: RuvA domain 2−like (InterPro:IPR010994); Has 29 Blast hits to 29 proteins in 9 species: Archae − 0; Bacteria − 2; Metazoa − 0; Fungi − 0; Plants − 27; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:4359597−4361222 REVERSE LENGTH=250	219	250	2.00E−98	114.2	84.5	91.3
Rsa1.0_00019.1.g1303.t2	ref|NP_195532.1| cellulose synthase−like protein D4 [Arabidopsis thaliana] gi|75213628|sp|Q9SZL9.1|CSLD4_ARATH RecName: Full=Cellulose synthase−like protein D4; Short=AtCslD4 gi|4467125|emb|CAB37559.1| putative protein [Arabidopsis thaliana] gi|7270803|emb|CAB80484.1| putative protein [Arabidopsis thaliana] gi|332661491|gb|AEE86891.1| cellulose synthase−like protein D4 [Arabidopsis thaliana]	1232	1111	0	90.2	87.7	88.7	cellulose synthase−like protein D4	gbpln	Arabidopsis thaliana	AT4G38190.1 | Symbols: ATCSLD4, CSLD4 | cellulose synthase like D4 | chr4:17910096−17913641 REVERSE LENGTH=1111	1232	1111	0	90.2	87.7	88.7
Rsa1.0_00019.1.g1304.t1	gb|EOA15893.1| hypothetical protein CARUB_v10003980mg [Capsella rubella]	1749	1688	0	96.5	86.8	91.7	hypothetical protein CARUB_v10003980mg	gbpln	Capsella rubella	AT4G38200.1 | Symbols: | SEC7−like guanine nucleotide exchange family protein | chr4:17915293−17922502 FORWARD LENGTH=1687	1749	1687	0	96.5	86.8	91.1
Rsa1.0_00019.1.g1305.t1	ref|XP_002868837.1| ATEXPA20 [Arabidopsis lyrata subsp. lyrata] gi|297314673|gb|EFH45096.1| ATEXPA20 [Arabidopsis lyrata subsp. lyrata]	256	256	1.00E−135	100.0	93.0	95.7	ATEXPA20	gbpln	Arabidopsis lyrata	AT4G38210.1 | Symbols: ATEXPA20, EXP20, ATEXP20, ATHEXP ALPHA 1.23, EXPA20 | expansin A20 | chr4:17922975−17923821 REVERSE LENGTH=256	256	256	1.00E−137	100.0	92.6	95.3
Rsa1.0_00019.1.g1306.t2	ref|NP_568036.2| Peptidase M20/M25/M40 family protein [Arabidopsis thaliana] gi|18650600|gb|AAL75900.1| AT4g38220/F20D10_340 [Arabidopsis thaliana] gi|332661494|gb|AEE86894.1| Peptidase M20/M25/M40 family protein [Arabidopsis thaliana]	559	430	0	76.9	63.1	66.7	Peptidase M20/M25/M40 family protein	gbpln	Arabidopsis thaliana	AT4G38220.1 | Symbols: | Peptidase M20/M25/M40 family protein | chr4:17925251−17926919 FORWARD LENGTH=430	559	430	0	76.9	63.1	66.7
Rsa1.0_00019.1.g1307.t1	gb|EOA18945.1| hypothetical protein CARUB_v10007579mg [Capsella rubella]	467	483	0	103.4	87.8	91.9	hypothetical protein CARUB_v10007579mg	gbpln	Capsella rubella	AT4G38360.2 | Symbols: LAZ1 | Protein of unknown function (DUF300) | chr4:17967389−17969798 FORWARD LENGTH=485	467	485	0	103.9	87.8	91.2
Rsa1.0_00019.1.g1308.t1	gb|EOA17245.1| hypothetical protein CARUB_v10005519mg [Capsella rubella]	269	263	1.00E−123	97.8	80.7	88.5	hypothetical protein CARUB_v10005519mg	gbpln	Capsella rubella	AT3G45970.1 | Symbols: ATEXLA1, EXPL1, ATEXPL1, ATHEXP BETA 2.1, EXLA1 | expansin−like A1 | chr3:16896238−16897189 FORWARD LENGTH=265	269	265	1.00E−121	98.5	82.9	89.2

Rsa1.0_00019.1.g1309.t1	ref|NP_195558.1| geranylgeranyl diphosphate synthase, type II [Arabidopsis thaliana] gi|85680919|sp|Q39108.2|GGR_ARATH RecName: Full=Heterodimeric geranylgeranyl pyrophosphate synthase small subunit, chloroplastic; Flags: Precursor gi|11908118|gb|AAG41488.1|AF326906_1 putative geranylgeranyl pyrophosphate synthase-related protein [Arabidopsis thaliana] gi|12642930|gb|AAK00407.1|AF339725_1 putative geranylgeranyl pyrophosphate synthase-related protein [Arabidopsis thaliana] gi|13926334|gb|AAK49631.1|AF372915_1 AT4g38460/F20M13_20 [Arabidopsis thaliana] gi|4467133|emb|CAB37502.1| geranylgeranyl pyrophosphate synthase-related protein [Arabidopsis thaliana] gi|7270829|emb|CAB80510.1| geranylgeranyl pyrophosphate synthase-related protein [Arabidopsis thaliana] gi|16323260|gb|AAL15364.1| AT4g38460/F20M13_20 [Arabidopsis thaliana] gi|21555524|gb|AAM63877.1| geranylgeranyl pyrophosphate synthase-related protein [Arabidopsis thaliana] gi|332661530|gb|AEE86930.1| geranylgeranyl reductase [Arabidopsis thaliana]	329	326	1.00E-126	99.1	76.3	84.5	geranylgeranyl diphosphate synthase, type II	gbpln	Arabidopsis thaliana	AT4G38460.1 | Symbols: GGR | geranylgeranyl reductase | chr4:17994849-17995974 FORWARD LENGTH=326	329	326	1.00E-129	99.1	76.3	84.5
Rsa1.0_00019.1.g1310.t1	ref|NP_568041.1| ACT-like protein tyrosine kinase family protein [Arabidopsis thaliana] gi|332661531|gb|AEE86931.1| ACT-like protein tyrosine kinase family protein [Arabidopsis thaliana]	564	575	0	102.0	85.5	91.1	ACT-like protein tyrosine kinase family protein	gbpln	Arabidopsis thaliana	AT4G38470.1 | Symbols: | ACT-like protein tyrosine kinase family protein | chr4:17999432-18003551 FORWARD LENGTH=575	564	575	0	102.0	85.5	91.1
Rsa1.0_00019.1.g1311.t1	gb|EOA18127.1| hypothetical protein CARUB_v10006588mg [Capsella rubella]	117	123	9.00E-47	105.1	79.5	87.2	hypothetical protein CARUB_v10006588mg	gbpln	Capsella rubella	AT4G38495.1 | Symbols: | CONTAINS InterPro DOMAIN/s: YL1 nuclear, C-terminal (InterPro:IPR013272); Has 279 Blast hits to 279 proteins in 147 species: Archae - 0; Bacteria - 0; Metazoa - 94; Fungi - 133; Plants - 35; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr4:18007466-18008025 REVERSE LENGTH=124	117	124	1.00E-47	106.0	76.9	86.3
Rsa1.0_00019.1.g1312.t2	gb|EOA17176.1| hypothetical protein CARUB_v10005442mg [Capsella rubella]	273	281	1.00E-139	102.9	90.8	93.4	hypothetical protein CARUB_v10005442mg	gbpln	Capsella rubella	AT4G38670.3 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr4:18069856-18071227 REVERSE LENGTH=281	273	281	1.00E-140	102.9	89.4	92.7
Rsa1.0_00019.1.g1313.t1	gb|EOA18006.1| hypothetical protein CARUB_v10006441mg [Capsella rubella]	98	98	3.00E-40	100.0	88.8	94.9	hypothetical protein CARUB_v10006441mg	gbpln	Capsella rubella	AT4G38840.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:18125174-18125473 REVERSE LENGTH=99	98	99	7.00E-39	101.0	83.7	93.9
Rsa1.0_00019.1.g1314.t1	gb|EOA15659.1| hypothetical protein CARUB_v10006088mg [Capsella rubella]	105	105	4.00E-53	100.0	96.2	100.0	hypothetical protein CARUB_v10006088mg	gbpln	Capsella rubella	AT4G38860.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:18130357-18130674 FORWARD LENGTH=105	105	105	4.00E-55	100.0	95.2	99.0
Rsa1.0_00019.1.g1315.t1	ref|NP_195599.1| amidophosphoribosyltransferase [Arabidopsis thaliana] gi|75213783|sp|Q9T0J5.1|ASE3_ARATH RecName: Full=Amidophosphoribosyltransferase 3, chloroplastic; Short=AtATase3; Short=PRPP3; AltName: Full=Glutamine phosphoribosylpyrophosphate amidotransferase 3; Short=AtGPRAT3; Flags: Precursor gi|4490340|emb|CAB38622.1| amidophosphoribosyltransferase-like protein [Arabidopsis thaliana] gi|7270871|emb|CAB80551.1| amidophosphoribosyltransferase-like protein [Arabidopsis thaliana] gi|332661586|gb|AEE86986.1| amidophosphoribosyltransferase 3 [Arabidopsis thaliana]	531	532	0	100.2	84.9	91.1	amidophosphoribosyltransferase	gbpln	Arabidopsis thaliana	AT4G38880.1 | Symbols: ATASE3, ASE3 | GLN phosphoribosyl pyrophosphate amidotransferase 3 | chr4:18134116-18135714 FORWARD LENGTH=532	531	532	0	100.2	84.9	91.1
Rsa1.0_00019.1.g1316.t1	ref|XP_002868869.1| dihydrouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314705|gb|EFH45128.1| dihydrouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	692	691	0	99.9	83.2	88.2	dihydrouridine synthase family protein	gbpln	Arabidopsis lyrata	AT4G38890.1 | Symbols: | FMN-linked oxidoreductases superfamily protein | chr4:18135909-18139100 REVERSE LENGTH=691	692	691	0	99.9	82.9	88.2

<table>
<tr><td>Rsa1.0_00019.1.g1317.t1</td><td>gb|ABU63288.1| GAGA-motif binding transcriptional activator, partial [Cardamine pratensis]</td><td>265</td><td>275</td><td>1.00E-123</td><td>103.8</td><td>80.8</td><td>90.9</td><td>GAGA-motif binding transcriptional activator, partial</td><td>gbpln</td><td>Cardamine pratensis</td><td>AT4G38910.2 | Symbols: BPC5 | basic pentacysteine 5 | chr4:18145478-18146429 REVERSE LENGTH=283</td><td>265</td><td>283</td><td>1.00E-116</td><td>106.8</td><td>76.6</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00019.1.g1318.t1</td><td>ref|NP_195606.2| ATP binding microtubule motor family protein [Arabidopsis thaliana]
gi|186517568|ref|NP_001119143.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]
gi|332661597|gb|AEE86997.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]
gi|332661598|gb|AEE86998.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]</td><td>800</td><td>836</td><td>0</td><td>104.5</td><td>85.8</td><td>91.3</td><td>ATP binding microtubule motor family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G38950.2 | Symbols: | ATP binding microtubule motor family protein | chr4:18154606-18158461 REVERSE LENGTH=836</td><td>800</td><td>836</td><td>0</td><td>104.5</td><td>85.8</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00019.1.g1319.t1</td><td>ref|XP_002868874.1| hypothetical protein ARALYDRAFT_490667 [Arabidopsis lyrata subsp. lyrata]
gi|297314710|gb|EFH45133.1| hypothetical protein ARALYDRAFT_490667 [Arabidopsis lyrata subsp. lyrata]</td><td>237</td><td>393</td><td>5.00E-72</td><td>165.8</td><td>54.4</td><td>56.1</td><td>hypothetical protein ARALYDRAFT_490667</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38970.1 | Symbols: FBA2 | fructose-bisphosphate aldolase 2 | chr4:18163714-18165659 REVERSE LENGTH=398</td><td>237</td><td>398</td><td>1.00E-73</td><td>167.9</td><td>55.3</td><td>56.5</td></tr>
<tr><td>Rsa1.0_00019.1.g1320.t1</td><td>gb|EOA18196.1| hypothetical protein CARUB_v10006679mg [Capsella rubella]</td><td>443</td><td>493</td><td>0</td><td>111.3</td><td>81.0</td><td>87.1</td><td>hypothetical protein CARUB_v10006679mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G39000.1 | Symbols: AtGH9B17, GH9B17 | glycosyl hydrolase 9B17 | chr4:18171722-18173797 REVERSE LENGTH=493</td><td>443</td><td>493</td><td>0</td><td>111.3</td><td>76.5</td><td>86.7</td></tr>
<tr><td>Rsa1.0_00019.1.g1321.t1</td><td>gb|EOA16494.1| hypothetical protein CARUB_v10004652mg [Capsella rubella]</td><td>472</td><td>496</td><td>0</td><td>105.1</td><td>92.2</td><td>95.8</td><td>hypothetical protein CARUB_v10004652mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G39010.1 | Symbols: AtGH9B18, GH9B18 | glycosyl hydrolase 9B18 | chr4:18176162-18179102 REVERSE LENGTH=497</td><td>472</td><td>497</td><td>0</td><td>105.3</td><td>92.6</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00019.1.g1322.t1</td><td>ref|XP_002866828.1| hypothetical protein ARALYDRAFT_490671 [Arabidopsis lyrata subsp. lyrata]
gi|297312664|gb|EFH43087.1| hypothetical protein ARALYDRAFT_490671 [Arabidopsis lyrata subsp. lyrata]</td><td>514</td><td>541</td><td>0</td><td>105.3</td><td>86.4</td><td>92.6</td><td>hypothetical protein ARALYDRAFT_490671</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G39030.1 | Symbols: EDS5, SID1 | MATE efflux family protein | chr4:18185740-18188898 FORWARD LENGTH=543</td><td>514</td><td>543</td><td>0</td><td>105.6</td><td>86.4</td><td>91.4</td></tr>
<tr><td>Rsa1.0_00019.1.g1323.t1</td><td>ref|XP_002868882.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]
gi|297314718|gb|EFH45141.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]</td><td>234</td><td>238</td><td>2.00E-97</td><td>101.7</td><td>83.3</td><td>88.0</td><td>zinc finger (B-box type) family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G39070.1 | Symbols: | B-box zinc finger family protein | chr4:18205061-18206421 REVERSE LENGTH=242</td><td>234</td><td>242</td><td>1.00E-100</td><td>103.4</td><td>82.9</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00019.1.g1324.t1</td><td>gb|EOA19105.1| hypothetical protein CARUB_v10007773mg [Capsella rubella]</td><td>794</td><td>819</td><td>0</td><td>103.1</td><td>92.7</td><td>96.9</td><td>hypothetical protein CARUB_v10007773mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G39080.1 | Symbols: VHA-A3 | vacuolar proton ATPase A3 | chr4:18209513-18214752 FORWARD LENGTH=821</td><td>794</td><td>821</td><td>0</td><td>103.4</td><td>90.7</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00019.1.g1325.t1</td><td>ref|XP_002868883.1| hypothetical protein ARALYDRAFT_490677 [Arabidopsis lyrata subsp. lyrata]
gi|297314719|gb|EFH45142.1| hypothetical protein ARALYDRAFT_490677 [Arabidopsis lyrata subsp. lyrata]</td><td>371</td><td>368</td><td>0</td><td>99.2</td><td>87.9</td><td>92.2</td><td>hypothetical protein ARALYDRAFT_490677</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G39090.1 | Symbols: RD19, RD19A | Papain family cysteine protease | chr4:18215826-18217326 REVERSE LENGTH=368</td><td>371</td><td>368</td><td>0</td><td>99.2</td><td>85.4</td><td>90.8</td></tr>
<tr><td>Rsa1.0_00019.1.g1326.t1</td><td>gb|EOA18823.1| hypothetical protein CARUB_v10007437mg [Capsella rubella]</td><td>110</td><td>110</td><td>2.00E-38</td><td>100.0</td><td>83.6</td><td>90.9</td><td>hypothetical protein CARUB_v10007437mg</td><td>gbpln</td><td>Capsella rubella</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00019.1.g1327.t1</td><td>gb|EOA18763.1| hypothetical protein CARUB_v10007359mg [Capsella rubella]</td><td>877</td><td>882</td><td>0</td><td>100.6</td><td>92.4</td><td>95.9</td><td>hypothetical protein CARUB_v10007359mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G39110.1 | Symbols: | Malectin/receptor-like protein kinase family protein | chr4:18222483-18225119 REVERSE LENGTH=878</td><td>877</td><td>878</td><td>0</td><td>100.1</td><td>91.6</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00019.1.g1328.t1</td><td>ref|NP_195624.1| Dehydrin family protein [Arabidopsis thaliana]
gi|4914425|emb|CAB43628.1| putative protein [Arabidopsis thaliana]
gi|7270896|emb|CAB80576.1| putative protein [Arabidopsis thaliana]
gi|21592637|gb|AAM64586.1| unknown [Arabidopsis thaliana]
gi|332661621|gb|AEE87021.1| Dehydrin family protein [Arabidopsis thaliana]</td><td>277</td><td>151</td><td>2.00E-44</td><td>54.5</td><td>34.3</td><td>40.8</td><td>Dehydrin family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G39130.1 | Symbols: | Dehydrin family protein | chr4:18228183-18228844 REVERSE LENGTH=151</td><td>277</td><td>151</td><td>7.00E-47</td><td>54.5</td><td>34.3</td><td>40.8</td></tr>
<tr><td>Rsa1.0_00019.1.g1329.t1</td><td>gb|EOA15554.1| hypothetical protein CARUB_v10005169mg [Capsella rubella]
gi|482551362|gb|EOA15555.1| hypothetical protein CARUB_v10005169mg [Capsella rubella]</td><td>344</td><td>344</td><td>0</td><td>100.0</td><td>88.4</td><td>95.6</td><td>hypothetical protein CARUB_v10005169mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G39150.2 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr4:18233651-18235740 REVERSE LENGTH=345</td><td>344</td><td>345</td><td>1.00E-180</td><td>100.3</td><td>87.5</td><td>95.3</td></tr>
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Rsa1.0_00019.1.g1330.t1	ref|NP_195631.1| 40S ribosomal protein S25-4 [Arabidopsis thaliana] gi|30580493|sp|Q9T029.1|RS254_ARATH RecName: Full=40S ribosomal protein S25-4 gi|4914432|emb|CAB43635.1| ribosomal protein S25 [Arabidopsis thaliana] gi|7270903|emb|CAB80583.1| ribosomal protein S25 [Arabidopsis thaliana] gi|14335026|gb|AAK59777.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gi|16323232|gb|AAL15350.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gi|21553704|gb|AAM62797.1| ribosomal protein S25 [Arabidopsis thaliana] gi|332661636|gb|AEE87036.1| 40S ribosomal protein S25-4 [Arabidopsis thaliana] gi|482553510|gb|EOA17703.1| hypothetical protein CARUB_v10006075mg [Capsella rubella]	108	108	3.00E-55	100.0	99.1	99.1	40S ribosomal protein S25-4	gbpln	Arabidopsis thaliana	AT4G39200.1 | Symbols: | Ribosomal protein S25 family protein | chr4:18257464-18258464 FORWARD LENGTH=108	108	108	5.00E-58	100.0	99.1	99.1
Rsa1.0_00019.1.g1331.t1	gb|EOA17728.1| hypothetical protein CARUB_v10006110mg [Capsella rubella]	82	100	2.00E-30	122.0	89.0	95.1	hypothetical protein CARUB_v10006110mg	gbpln	Capsella rubella	AT4G39250.1 | Symbols: ATRL1, RSM2, RL1 | RAD-like 1 | chr4:18271457-18271857 REVERSE LENGTH=100	82	100	1.00E-32	122.0	86.6	91.5
Rsa1.0_00019.1.g1332.t1	sp|Q05966.1|GRP10_BRANA RecName: Full=Glycine-rich RNA-binding protein 10 gi|17819|emb|CAA78513.1| glycine-rich RNA binding protein [Brassica napus]	163	169	5.00E-40	103.7	48.5	50.3	RecName: Full=Glycine-rich RNA-binding protein 10 gi|17819|emb|CAA78513.1| glycine-rich RNA binding protein	gbpln	Brassica napus	AT4G39260.3 | Symbols: CCR1, ATGRP8, GR-RBP8, GRP8 | cold, circadian rhythm, and RNA binding 1 | chr4:18274166-18274958 REVERSE LENGTH=92	163	92	2.00E-43	56.4	49.7	54.0
Rsa1.0_00019.1.g1333.t1	ref|XP_002866840.1| hypothetical protein ARALYDRAFT_912391 [Arabidopsis lyrata subsp. lyrata] gi|297312676|gb|EFH43099.1| hypothetical protein ARALYDRAFT_912391 [Arabidopsis lyrata subsp. lyrata]	152	173	1.00E-39	113.8	65.1	78.3	hypothetical protein ARALYDRAFT_912391	gbpln	Arabidopsis lyrata	AT4G39320.1 | Symbols: | microtubule-associated protein-related | chr4:18289102-18289702 FORWARD LENGTH=166	152	166	4.00E-36	109.2	59.9	73.7
Rsa1.0_00019.1.g1334.t1	ref|NP_195644.1| uncharacterized protein [Arabidopsis thaliana] gi|75213705|sp|Q9T039.1|EC14_ARATH RecName: Full=Egg cell-secreted protein 1.4; Flags: Precursor gi|4914446|emb|CAB43649.1| hypothetical protein [Arabidopsis thaliana] gi|7270918|emb|CAB80597.1| hypothetical protein [Arabidopsis thaliana] gi|91805627|gb|ABE65542.1| hypothetical protein At4g39340 [Arabidopsis thaliana] gi|332661658|gb|AEE87058.1| uncharacterized protein AT4G39340 [Arabidopsis thaliana]	129	127	6.00E-53	98.4	79.8	86.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G39340.1 | Symbols: | Protein of unknown function (DUF1278) | chr4:18293129-18293512 REVERSE LENGTH=127	129	127	1.00E-55	98.4	79.8	86.8
Rsa1.0_00019.1.g1335.t1	gb|EOA18118.1| hypothetical protein CARUB_v10006579mg [Capsella rubella]	115	136	4.00E-29	118.3	62.6	75.7	hypothetical protein CARUB_v10006579mg	gbpln	Capsella rubella	AT4G39360.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G21780.1); Has 13 Blast hits to 13 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:18303031-18303435 FORWARD LENGTH=134	115	134	1.00E-26	116.5	62.6	73.9
Rsa1.0_00019.1.g1336.t1	ref|NP_568059.1| nucleotide sugar transporter-KT 1 [Arabidopsis thaliana] gi|30692341|ref|NP_849527.1| nucleotide sugar transporter-KT 1 [Arabidopsis thaliana] gi|20259516|gb|AAM13878.1| unknown protein [Arabidopsis thaliana] gi|23296523|gb|AAN13117.1| unknown protein [Arabidopsis thaliana] gi|332661666|gb|AEE87066.1| nucleotide sugar transporter-KT 1 [Arabidopsis thaliana] gi|332661667|gb|AEE87067.1| nucleotide sugar transporter-KT 1 [Arabidopsis thaliana]	339	337	1.00E-171	99.4	92.3	95.0	nucleotide sugar transporter-KT 1	gbpln	Arabidopsis thaliana	AT4G39390.2 | Symbols: ATNST-KT1, NST-K1 | nucleotide sugar transporter-KT 1 | chr4:18316278-18317854 FORWARD LENGTH=337	339	337	1.00E-174	99.4	92.3	95.0
Rsa1.0_00019.1.g1337.t1	ref|XP_002866847.1| hypothetical protein ARALYDRAFT_912402 [Arabidopsis lyrata subsp. lyrata] gi|297312683|gb|EFH43106.1| hypothetical protein ARALYDRAFT_912402 [Arabidopsis lyrata subsp. lyrata]	1193	1195	0	100.2	89.3	93.6	hypothetical protein ARALYDRAFT_912402	gbpln	Arabidopsis lyrata	AT4G39400.1 | Symbols: BRI1, CBB2, DWF2, BIN1, ATBRI1 | Leucine-rich receptor-like protein kinase family protein | chr4:18324826-18328416 FORWARD LENGTH=1196	1193	1196	0	100.3	88.5	93.1

Rsa1.0_00019.1.g1338.t1	ref|NP_195651.1| putative WRKY transcription factor 13 [Arabidopsis thaliana] gi|29839686|sp|Q9SVB7.1|WRK13_ARATH RecName: Full=Probable WRKY transcription factor 13; AltName: Full=WRKY DNA-binding protein 13 gi|15991730|gb|AAL13042.1|AF421153_1 WRKY transcription factor 13 [Arabidopsis thaliana] gi|5042157|emb|CAB44676.1| putative WRKY DNA-binding protein [Arabidopsis thaliana] gi|7270925|emb|CAB80604.1| putative WRKY DNA-binding protein [Arabidopsis thaliana] gi|225898873|dbj|BAH30567.1| hypothetical protein [Arabidopsis thaliana] gi|332661671|gb|AEE87071.1| putative WRKY transcription factor 13 [Arabidopsis thaliana]	295	304	1.00E-102	103.1	73.9	82.7	putative WRKY transcription factor 13	gbpln	Arabidopsis thaliana	AT4G39410.1 | Symbols: WRKY13, ATWRKY13 | WRKY DNA-binding protein 13 | chr4:18332937-18334789 REVERSE LENGTH=304	295	304	1.00E-105	103.1	73.9	82.7
Rsa1.0_00019.1.g1339.t8	ref|NP_001154293.2| uncharacterized protein [Arabidopsis thaliana] gi|332661673|gb|AEE87073.1| uncharacterized protein AT4G39420 [Arabidopsis thaliana]	3143	3184	0	101.3	87.0	92.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G39420.2 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf; EXPRESSED DURING: LP.04 four leaves visible, LP.02 two leaves visible; Has 20 Blast hits to 19 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:18339731-18354701 FORWARD LENGTH=3184	3143	3184	0	101.3	87.0	92.2
Rsa1.0_00019.1.g1340.t1	gb|EOA12720.1| hypothetical protein CARUB_v10028124mg [Capsella rubella]	507	514	0	101.4	69.6	84.6	hypothetical protein CARUB_v10028124mg	gbpln	Capsella rubella	AT4G32170.1 | Symbols: CYP96A2 | cytochrome P450, family 96, subfamily A, polypeptide 2 | chr4:15533772-15535292 FORWARD LENGTH=506	507	506	0	99.8	65.9	79.7
Rsa1.0_00019.1.g1341.t1	ref|NP_195661.1| cytochrome P450, family 96, subfamily A, polypeptide 12 [Arabidopsis thaliana] gi|5042167|emb|CAB44686.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|7270935|emb|CAB80614.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|16604438|gb|AAL24225.1| AT4g39510/F23K16_140 [Arabidopsis thaliana] gi|27764938|gb|AAO23590.1| At4g39510/F23K16_140 [Arabidopsis thaliana] gi|332661680|gb|AEE87080.1| cytochrome P450, family 96, subfamily A, polypeptide 12 [Arabidopsis thaliana]	500	508	0	101.6	76.8	88.2	cytochrome P450, family 96, subfamily A, polypeptide 12	gbpln	Arabidopsis thaliana	AT4G39510.1 | Symbols: CYP96A12 | cytochrome P450, family 96, subfamily A, polypeptide 12 | chr4:18368945-18370471 REVERSE LENGTH=508	500	508	0	101.6	76.8	88.2
Rsa1.0_00019.1.g1342.t1	ref|NP_195662.1| GTP-binding protein-relatedlike protein [Arabidopsis thaliana] gi|5042168|emb|CAB44687.1| GTP-binding-like protein [Arabidopsis thaliana] gi|7270936|emb|CAB80615.1| GTP-binding-like protein [Arabidopsis thaliana] gi|14334722|gb|AAK59539.1| putative GTP-binding protein [Arabidopsis thaliana] gi|332661681|gb|AEE87081.1| GTP-binding protein-relatedlike protein [Arabidopsis thaliana]	369	369	0	100.0	97.0	98.4	GTP-binding protein-relatedlike protein	gbpln	Arabidopsis thaliana	AT4G39520.1 | Symbols: | GTP-binding protein-related | chr4:18371329-18374000 REVERSE LENGTH=369	369	369	0	100.0	97.0	98.4
Rsa1.0_00019.1.g1343.t1	ref|NP_195664.2| shikimate kinase 2 [Arabidopsis thaliana] gi|42573237|ref|NP_974715.1| shikimate kinase 2 [Arabidopsis thaliana] gi|75151384|sp|Q8GY88.1|SK2_ARATH RecName: Full=Shikimate kinase 2, chloroplastic; Short=AtSK2; Flags: Precursor gi|26450651|dbj|BAC42436.1| putative shikimate kinase [Arabidopsis thaliana] gi|28950863|gb|AAO63355.1| At4g39540 [Arabidopsis thaliana] gi|332661683|gb|AEE87083.1| shikimate kinase 2 [Arabidopsis thaliana] gi|332661684|gb|AEE87084.1| shikimate kinase 2 [Arabidopsis thaliana]	256	300	1.00E-111	117.2	84.4	89.8	shikimate kinase 2	gbpln	Arabidopsis thaliana	AT4G39540.2 | Symbols: SK2, ATSK2 | shikimate kinase 2 | chr4:18378561-18380253 FORWARD LENGTH=300	256	300	1.00E-113	117.2	84.4	89.8

Rsa1.0_00019.1.g1344.t1	ref|XP_002868913.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297314749|gb|EFH45172.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	400	389	1.00E-119	97.3	56.8	69.5	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G39550.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18380681-18381859 REVERSE LENGTH=392	400	392	1.00E-121	98.0	60.5	72.8
Rsa1.0_00019.1.g1345.t1	ref|XP_002868918.1| hypothetical protein ARALYDRAFT_490739 [Arabidopsis lyrata subsp. lyrata] gi|297314754|gb|EFH45177.1| hypothetical protein ARALYDRAFT_490739 [Arabidopsis lyrata subsp. lyrata]	391	400	7.00E-93	102.3	53.2	66.0	hypothetical protein ARALYDRAFT_490739	gbpln	Arabidopsis lyrata	AT4G39590.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18387515-18388723 REVERSE LENGTH=402	391	402	4.00E-90	102.8	52.2	63.4
Rsa1.0_00019.1.g1346.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00019.1.g1347.t1	gb|EOA39864.1| hypothetical protein CARUB_v10008540mg [Capsella rubella] gi|482575678|gb|EOA39865.1| hypothetical protein CARUB_v10008540mg [Capsella rubella] gi|482575679|gb|EOA39866.1| hypothetical protein CARUB_v10008540mg [Capsella rubella]	111	654	6.00E-11	589.2	39.6	46.8	hypothetical protein CARUB_v10008540mg	gbpln	Capsella rubella	AT1G14380.3 | Symbols: IQD28 | IQ-domain 28 | chr1:4918279-4920761 REVERSE LENGTH=664	111	664	3.00E-13	598.2	39.6	45.9
Rsa1.0_00019.1.g1348.t1	gb|EOA34391.1| hypothetical protein CARUB_v10021918mg [Capsella rubella]	407	403	7.00E-96	99.0	52.8	65.6	hypothetical protein CARUB_v10021918mg	gbpln	Capsella rubella	AT1G61540.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:22702498-22703706 FORWARD LENGTH=402	407	402	2.00E-96	98.8	53.1	63.9
Rsa1.0_00019.1.g1349.t1	ref|NP_195665.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75210850|sp|Q9SVA3.1|FBK98_ARATH RecName: Full=F-box/kelch-repeat protein At4g39550 gi|5042171|emb|CAB44690.1| putative protein [Arabidopsis thaliana] gi|7270939|emb|CAB80618.1| putative protein [Arabidopsis thaliana] gi|27808596|gb|AAO24578.1| At4g39550 [Arabidopsis thaliana] gi|110736223|dbj|BAF00082.1| hypothetical protein [Arabidopsis thaliana] gi|332661686|gb|AEE87086.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	392	392	1.00E-138	100.0	69.4	80.1	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT4G39550.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18380681-18381859 REVERSE LENGTH=392	392	392	1.00E-140	100.0	69.4	80.1
Rsa1.0_00019.1.g1350.t1	ref|XP_002868918.1| hypothetical protein ARALYDRAFT_490739 [Arabidopsis lyrata subsp. lyrata] gi|297314754|gb|EFH45177.1| hypothetical protein ARALYDRAFT_490739 [Arabidopsis lyrata subsp. lyrata]	385	400	1.00E-93	103.9	49.4	65.5	hypothetical protein ARALYDRAFT_490739	gbpln	Arabidopsis lyrata	AT4G39590.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18387515-18388723 REVERSE LENGTH=402	385	402	3.00E-94	104.4	51.4	66.5
Rsa1.0_00019.1.g1351.t1	gb|EOA34391.1| hypothetical protein CARUB_v10021918mg [Capsella rubella]	412	403	5.00E-93	97.8	50.2	63.8	hypothetical protein CARUB_v10021918mg	gbpln	Capsella rubella	AT1G61540.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:22702498-22703706 FORWARD LENGTH=402	412	402	2.00E-93	97.6	50.0	64.3
Rsa1.0_00019.1.g1352.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00019.1.g1353.t1	ref|NP_179734.1| coatomer subunit alpha-2 [Arabidopsis thaliana] gi|75337326|sp|Q9SJT9.1|COPA2_ARATH RecName: Full=Coatomer subunit alpha-2; AltName: Full=Alpha-coat protein 2; Short=Alpha-COP 2 gi|4567286|gb|AAD23699.1| coatomer alpha subunit [Arabidopsis thaliana] gi|110737300|dbj|BAF00596.1| coatomer alpha subunit [Arabidopsis thaliana] gi|330252079|gb|AEC07173.1| coatomer subunit alpha-2 [Arabidopsis thaliana]	1136	1218	0	107.2	79.2	86.4	coatomer subunit alpha-2	gbpln	Arabidopsis thaliana	AT2G21390.1 | Symbols: | Coatomer, alpha subunit | chr2:9152428-9156577 FORWARD LENGTH=1218	1136	1218	0	107.2	79.2	86.4
Rsa1.0_00019.1.g1354.t1	gb|EOA16490.1| hypothetical protein CARUB_v10004648mg [Capsella rubella]	500	497	0	99.4	85.6	90.4	hypothetical protein CARUB_v10004648mg	gbpln	Capsella rubella	AT4G39620.1 | Symbols: EMB2453, ATPPR5 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:18395294-18397578 FORWARD LENGTH=563	500	563	0	112.6	83.8	88.8
Rsa1.0_00019.1.g1355.t1	gb|ACJ65004.1| myo-inositol 1-phosphate synthase type 2 [Brassica napus]	510	510	0	100.0	98.8	99.6	myo-inositol 1-phosphate synthase type 2	gbpln	Brassica napus	AT4G39800.1 | Symbols: MI-1-P SYNTHASE, MIPS1, ATMIPS1, ATIPS1 | myo-inositol-1-phosphate synthase 1 | chr4:18469659-18471893 REVERSE LENGTH=511	510	511	0	100.2	95.1	98.2
Rsa1.0_00019.1.g1356.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00019.1.g1357.t1	ref|XP_002866887.1| hypothetical protein ARALYDRAFT_490769 [Arabidopsis lyrata subsp. lyrata] gi|297312723|gb|EFH43146.1| hypothetical protein ARALYDRAFT_490769 [Arabidopsis lyrata subsp. lyrata]	446	449	1.00E-166	100.7	83.2	88.3	hypothetical protein ARALYDRAFT_490769	gbpln	Arabidopsis lyrata	AT4G39840.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 20719 Blast hits to 6096 proteins in 607 species: Archae - 22; Bacteria - 3243; Metazoa - 4364; Fungi - 2270; Plants - 237; Viruses - 128; Other Eukaryotes - 10455 (source: NCBI BLink). | chr4:18485268-18486623 FORWARD LENGTH=451	446	451	1.00E-156	101.1	83.4	89.2
Rsa1.0_00019.1.g1358.t1	ref|XP_002866889.1| hypothetical protein ARALYDRAFT_912474 [Arabidopsis lyrata subsp. lyrata] gi|297312725|gb|EFH43148.1| hypothetical protein ARALYDRAFT_912474 [Arabidopsis lyrata subsp. lyrata]	621	297	1.00E-152	47.8	43.6	45.4	hypothetical protein ARALYDRAFT_912474	gbpln	Arabidopsis lyrata	AT4G39860.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G22270.1); Has 152 Blast hits to 146 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 146; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:18499909-18501472 FORWARD LENGTH=299	621	299	1.00E-150	48.1	43.5	45.4
Rsa1.0_00019.1.g1359.t1	gb|AAM63197.1| unknown [Arabidopsis thaliana]	180	178	2.00E-81	98.9	87.2	92.8	unknown	gbpln	Arabidopsis thaliana	AT4G39880.1 | Symbols: | Ribosomal protein L23/L15e family protein | chr4:18504601-18505137 FORWARD LENGTH=178	180	178	2.00E-76	98.9	85.0	90.6
Rsa1.0_00019.1.g1360.t1	ref|XP_002868935.1| hypothetical protein ARALYDRAFT_912479 [Arabidopsis lyrata subsp. lyrata] gi|297314771|gb|EFH45194.1| hypothetical protein ARALYDRAFT_912479 [Arabidopsis lyrata subsp. lyrata]	231	244	2.00E-90	105.6	78.4	87.4	hypothetical protein ARALYDRAFT_912479	gbpln	Arabidopsis lyrata	AT4G39900.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:18508569-18510289 REVERSE LENGTH=245	231	245	9.00E-92	106.1	77.1	84.4
Rsa1.0_00019.1.g1361.t1	ref|NP_568074.1| ubiquitin carboxyl-terminal hydrolase 3 [Arabidopsis thaliana] gi|62901126|sp|O24454.1|UBP3_ARATH RecName: Full=Ubiquitin carboxyl-terminal hydrolase 3; AltName: Full=Deubiquitinating enzyme 3; Short=AtUBP3; AltName: Full=Ubiquitin thioesterase 3; AltName: Full=Ubiquitin-specific-processing protease 3 gi|2347098|gb|AAB67966.1| ubiquitin-specific protease [Arabidopsis thaliana] gi|4490742|emb|CAB38904.1| ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana] gi|7271046|emb|CAB80654.1| ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana] gi|16604539|gb|AAL24275.1| AT4g39910/T5J17_80 [Arabidopsis thaliana] gi|18958042|gb|AAL79594.1| AT4g39910/T5J17_80 [Arabidopsis thaliana] gi|332661736|gb|AEE87136.1| ubiquitin carboxyl-terminal hydrolase 3 [Arabidopsis thaliana]	370	371	0	100.3	95.7	97.8	ubiquitin carboxyl-terminal hydrolase 3	gbpln	Arabidopsis thaliana	AT4G39910.1 | Symbols: ATUBP3, UBP3 | ubiquitin-specific protease 3 | chr4:18511858-18514139 REVERSE LENGTH=371	370	371	0	100.3	95.7	97.8
Rsa1.0_00019.1.g1362.t1	ref|XP_002866895.1| aps-kinase 2 [Arabidopsis lyrata subsp. lyrata] gi|297312731|gb|EFH43154.1| aps-kinase 2 [Arabidopsis lyrata subsp. lyrata]	293	292	1.00E-147	99.7	87.0	92.2	aps-kinase 2	gbpln	Arabidopsis lyrata	AT4G39940.1 | Symbols: AKN2, APK2 | APS-kinase 2 | chr4:18519787-18521276 FORWARD LENGTH=293	293	293	1.00E-148	100.0	87.7	92.8
Rsa1.0_00019.1.g1363.t1	gb|AAN76810.1|AF453287_1 cytochrome P450 [Brassica napus]	540	540	0	100.0	98.0	98.7	cytochrome P450	gbpln	Brassica napus	AT4G39950.1 | Symbols: CYP79B2 | cytochrome P450, family 79, subfamily B, polypeptide 2 | chr4:18525311-18527284 FORWARD LENGTH=541	540	541	0	100.2	93.5	97.4
Rsa1.0_00019.1.g1364.t1	ref|NP_680777.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|223635624|sp|Q3E9N1.2|PP359_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g39952, mitochondrial; Flags: Precursor gi|332661744|gb|AEE87144.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	781	775	0	99.2	82.1	89.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G39952.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:18527680-18530007 FORWARD LENGTH=775	781	775	0	99.2	82.1	89.4
Rsa1.0_00019.1.g1365.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1459	2301	0	157.7	82.5	89.1	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1459	1262	1.00E-108	86.5	13.9	21.2

Rsa1.0_00019.1.g1366.t1	ref|XP_002866900.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata] gi|297312736|gb|EFH43159.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata]	450	447	0	99.3	93.1	95.3	DNAJ heat shock family protein	gbpln	Arabidopsis lyrata	AT4G39960.1 | Symbols: | Molecular chaperone Hsp40/DnaJ family protein | chr4:18534194-18536320 FORWARD LENGTH=447	450	447	0	99.3	92.9	95.3
Rsa1.0_00019.1.g1367.t1	ref|XP_002866901.1| 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 [Arabidopsis lyrata subsp. lyrata] gi|297312737|gb|EFH43160.1| 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 [Arabidopsis lyrata subsp. lyrata]	528	528	0	100.0	93.9	95.8	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1	gbpln	Arabidopsis lyrata	AT4G39980.1 | Symbols: DHS1 | 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 | chr4:18539654-18541832 FORWARD LENGTH=525	528	525	0	99.4	93.6	95.3
Rsa1.0_00019.1.g1368.t1	gb|EOA17314.1| hypothetical protein CARUB_v10005586mg, partial [Capsella rubella]	224	250	1.00E-114	111.6	88.4	93.8	hypothetical protein CARUB_v10005586mg, partial	gbpln	Capsella rubella	AT4G39990.1 | Symbols: ATRABA4B, ATRAB11G, ATGB3, RABA4B | RAB GTPase homolog A4B | chr4:18542722-18543779 FORWARD LENGTH=224	224	224	1.00E-116	100.0	86.6	93.3
Rsa1.0_00019.1.g1369.t1	ref|XP_002865966.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata] gi|297311801|gb|EFH42225.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata]	429	455	1.00E-74	106.1	44.1	55.0	hypothetical protein ARALYDRAFT_357572	gbpln	Arabidopsis lyrata	AT1G30790.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:10932713-10933912 FORWARD LENGTH=399	429	399	6.00E-62	93.0	34.5	45.0
Rsa1.0_00019.1.g1370.t1	ref|XP_002866878.1| hypothetical protein ARALYDRAFT_490751 [Arabidopsis lyrata subsp. lyrata] gi|297312714|gb|EFH43137.1| hypothetical protein ARALYDRAFT_490751 [Arabidopsis lyrata subsp. lyrata]	133	657	1.00E-12	494.0	45.9	64.7	hypothetical protein ARALYDRAFT_490751	gbpln	Arabidopsis lyrata	AT4G39690.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 26 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Mitochondrial inner membrane protein Mitofilin (InterPro:IPR019133); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:18417755-18421633 FORWARD LENGTH=650	133	650	3.00E-14	488.7	45.9	63.2
Rsa1.0_00019.1.g1371.t1	gb|EOA37553.1| hypothetical protein CARUB_v10011820mg, partial [Capsella rubella]	380	374	1.00E-70	98.4	40.8	51.8	hypothetical protein CARUB_v10011820mg, partial	gbpln	Capsella rubella	AT1G30790.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:10932713-10933912 FORWARD LENGTH=399	380	399	2.00E-64	105.0	39.2	51.6
Rsa1.0_00019.1.g1372.t1	ref|NP_195710.3| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|332661751|gb|AEE87151.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	747	783	0	104.8	81.4	88.9	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT4G40000.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:18543989-18547443 REVERSE LENGTH=783	747	783	0	104.8	81.4	88.9
Rsa1.0_00019.1.g1373.t1	ref|XP_002868939.1| hypothetical protein ARALYDRAFT_353011 [Arabidopsis lyrata subsp. lyrata] gi|297314775|gb|EFH45198.1| hypothetical protein ARALYDRAFT_353011 [Arabidopsis lyrata subsp. lyrata]	350	350	1.00E-168	100.0	87.1	92.0	hypothetical protein ARALYDRAFT_353011	gbpln	Arabidopsis lyrata	AT4G40010.1 | Symbols: SNRK2-7, SNRK2.7, SRK2F | SNF1-related protein kinase 2.7 | chr4:18548704-18551056 REVERSE LENGTH=350	350	350	1.00E-165	100.0	88.0	91.4
Rsa1.0_00019.1.g1374.t1	ref|XP_002868940.1| hypothetical protein ARALYDRAFT_912494 [Arabidopsis lyrata subsp. lyrata] gi|297314776|gb|EFH45199.1| hypothetical protein ARALYDRAFT_912494 [Arabidopsis lyrata subsp. lyrata]	591	618	0	104.6	73.3	85.8	hypothetical protein ARALYDRAFT_912494	gbpln	Arabidopsis lyrata	AT4G40020.1 | Symbols: | Myosin heavy chain-related protein | chr4:18553453-18555300 REVERSE LENGTH=615	591	615	0	104.1	71.9	84.9
Rsa1.0_00019.1.g1375.t1	gb|AFW86017.1| histone H3 [Zea mays]	149	227	7.00E-73	152.3	91.3	91.9	histone H3	gbenv/gbpln	Zea mays	AT4G40030.2 | Symbols: | Histone superfamily protein | chr4:18555840-18556827 REVERSE LENGTH=164	149	164	5.00E-75	110.1	91.3	92.6
Rsa1.0_00019.1.g1376.t1	gb|EOA17741.1| hypothetical protein CARUB_v10006125mg [Capsella rubella]	91	92	6.00E-37	101.1	81.3	85.7	hypothetical protein CARUB_v10006125mg	gbpln	Capsella rubella	AT4G40042.1 | Symbols: | Microsomal signal peptidase 12 kDa subunit (SPC12) | chr4:18559289-18559570 FORWARD LENGTH=93	91	93	3.00E-37	102.2	76.9	82.4

Rsa1.0_00019.1.g1377.t1	ref|NP_568078.1| uncharacterized protein [Arabidopsis thaliana] gi|15450922|gb|AAK96732.1| Unknown protein [Arabidopsis thaliana] gi|17978747|gb|AAL47367.1| unknown protein [Arabidopsis thaliana] gi|21592335|gb|AAM64286.1| unknown [Arabidopsis thaliana] gi|110742774|dbj|BAE99292.1| hypothetical protein [Arabidopsis thaliana] gi|332661761|gb|AEE87161.1| uncharacterized protein AT4G40045 [Arabidopsis thaliana]	141	140	2.00E-52	99.3	80.1	87.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G40045.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:18559926-18560348 REVERSE LENGTH=140	141	140	4.00E-55	99.3	80.1	87.2
Rsa1.0_00019.1.g1378.t1	ref|XP_002866906.1| hypothetical protein ARALYDRAFT_490794 [Arabidopsis lyrata subsp. lyrata] gi|297312742|gb|EFH43165.1| hypothetical protein ARALYDRAFT_490794 [Arabidopsis lyrata subsp. lyrata]	595	603	0	101.3	90.4	95.0	hypothetical protein ARALYDRAFT_490794	gbpln	Arabidopsis lyrata	AT4G40050.1 | Symbols: | Protein of unknown function (DUF3550/UPF0682) | chr4:18561206-18563727 REVERSE LENGTH=599	595	599	0	100.7	88.4	94.3
Rsa1.0_00020.1.g1379.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00020.1.g1380.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00020.1.g1381.t1	ref|NP_172777.1| actin-related protein 3 [Arabidopsis thaliana] gi|75313139|sp|Q9SAF1.1|ARP3_ARATH RecName: Full=Actin-related protein 3; AltName: Full=Protein DISTORTED TRICHOMES 1 gi|4850401|gb|AAD31071.1|AC007357_20 Strong similarity to gb|U29610 Actin-like protein (Arp3) from Acanthamoeba castellanii and is a member of the PF|00022 Actin family [Arabidopsis thaliana] gi|21427461|gb|AAM53243.1|AF507911_1 actin-related protein 3 [Arabidopsis thaliana] gi|20260500|gb|AAM13148.1| similar to actin-like protein [Arabidopsis thaliana] gi|21489929|tpg|DAA00033.1| TPA_exp: actin-related protein 3; AtARP3 [Arabidopsis thaliana] gi|30387525|gb|AAP31928.1| At1g13180 [Arabidopsis thaliana] gi|332190859|gb|AEE28980.1| actin-related protein 3 [Arabidopsis thaliana]	427	427	0	100.0	95.1	97.2	actin-related protein 3	gbpln	Arabidopsis thaliana	AT1G13180.1 | Symbols: DIS1, ARP3, ATARP3 | Actin-like ATPase superfamily protein | chr1:4495394-4498204 FORWARD LENGTH=427	427	427	0	100.0	95.1	97.2
Rsa1.0_00020.1.g1382.t1	gb|AAK31592.1| cytochrome P450 [Brassica rapa subsp. pekinensis]	526	525	0	99.8	91.1	95.1	cytochrome P450	gbpln	Brassica rapa	AT1G13150.1 | Symbols: CYP86C4 | cytochrome P450, family 86, subfamily C, polypeptide 4 | chr1:4481995-4483584 REVERSE LENGTH=529	526	529	0	100.6	86.1	92.8
Rsa1.0_00020.1.g1383.t1	ref|NP_172767.1| cytochrome P450 71B2 [Arabidopsis thaliana] gi|38503391|sp|O65788.2|C71B2_ARATH RecName: Full=Cytochrome P450 71B2 gi|4850391|gb|AAD31061.1|AC007357_10 Identical to gb|D78605 cytochrome P450 monooxygenase from Arabidopsis thaliana and is a member of the PF|00067 Cytochrome P450 family. ESTs gb|Z18072, gb|Z35218 and gb|T43466 come from this gene [Arabidopsis thaliana] gi|28392854|gb|AAO41864.1| putative cytochrome P450 monooxygenase [Arabidopsis thaliana] gi|332190846|gb|AEE28967.1| cytochrome P450 71B2 [Arabidopsis thaliana]	502	502	0	100.0	81.7	92.0	cytochrome P450 71B2	gbpln	Arabidopsis thaliana	AT1G13080.1 | Symbols: CYP71B2 | cytochrome P450, family 71, subfamily B, polypeptide 2 | chr1:4459212-4460807 FORWARD LENGTH=502	502	502	0	100.0	81.7	92.0
Rsa1.0_00020.1.g1384.t1	gb|EOA40203.1| hypothetical protein CARUB_v10008923mg [Capsella rubella]	462	502	0	108.7	76.2	86.4	hypothetical protein CARUB_v10008923mg	gbpln	Capsella rubella	AT1G13080.1 | Symbols: CYP71B2 | cytochrome P450, family 71, subfamily B, polypeptide 2 | chr1:4459212-4460807 FORWARD LENGTH=502	462	502	0	108.7	75.5	86.1

Rsa1.0_00020.1.g1385.t1	ref|NP_172767.1| cytochrome P450 71B2 [Arabidopsis thaliana] gi|38503391|sp|O65788.2|C71B2_ARATH RecName: Full=Cytochrome P450 71B2 gi|4850391|gb|AAD31061.1|AC007357_10 Identical to gb|D78605 cytochrome P450 monooxygenase from Arabidopsis thaliana and is a member of the PF|00067 Cytochrome P450 family. ESTs gb|Z18072, gb|Z35218 and gb|T43466 come from this gene [Arabidopsis thaliana] gi|28392854|gb|AAO41864.1| putative cytochrome P450 monooxygenase [Arabidopsis thaliana] gi|332190846|gb|AEE28967.1| cytochrome P450 71B2 [Arabidopsis thaliana]	476	502	0	105.5	77.5	88.7	cytochrome P450 71B2	gbpln	Arabidopsis thaliana	AT1G13080.1 | Symbols: CYP71B2 | cytochrome P450, family 71, subfamily B, polypeptide 2 | chr1:4459212-4460807 FORWARD LENGTH=502	476	502	0	105.5	77.5	88.7
Rsa1.0_00020.1.g1386.t1	ref|NP_189265.1| proteasome subunit beta type-5-B [Arabidopsis thaliana] gi|75273433|sp|Q9LIP2.1|PSB5B_ARATH RecName: Full=Proteasome subunit beta type-5-B; AltName: Full=20S proteasome beta subunit E-2; AltName: Full=Proteasome epsilon-2 chain; Flags: Precursor gi|16612308|gb|AAL27514.1|AF439846_1 AT3g26340/F20C19_6 [Arabidopsis thaliana] gi|9294292|dbj|BAB02194.1| proteasome epsilon chain precursor [Arabidopsis thaliana] gi|21553804|gb|AAM62897.1| 26S proteasome beta subunit, putative [Arabidopsis thaliana] gi|21928101|gb|AAM78079.1| AT3g26340/F20C19_6 [Arabidopsis thaliana] gi|332643626|gb|AEE77147.1| proteasome subunit beta type-5-B [Arabidopsis thaliana]	274	273	1.00E-149	99.6	93.8	96.0	proteasome subunit beta type-5-B	gbpln	Arabidopsis thaliana	AT3G26340.1 | Symbols: | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:9650600-9652572 REVERSE LENGTH=273	274	273	1.00E-152	99.6	93.8	96.0
Rsa1.0_00020.1.g1387.t1	gb|EOA36472.1| hypothetical protein CARUB_v10011087mg [Capsella rubella]	320	317	1.00E-137	99.1	81.3	87.5	hypothetical protein CARUB_v10011087mg	gbpln	Capsella rubella	AT1G13050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G26350.1); Has 538 Blast hits to 510 proteins in 88 species: Archae - 0; Bacteria - 23; Metazoa - 81; Fungi - 36; Plants - 361; Viruses - 8; Other Eukaryotes - 29 (source: NCBI BLink). | chr1:4450568-4451521 FORWARD LENGTH=317	320	317	1.00E-134	99.1	82.2	88.1
Rsa1.0_00020.1.g1388.t1	ref|XP_002889980.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335822|gb|EFH66239.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	520	517	0	99.4	88.3	94.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G13040.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:4447647-4449200 FORWARD LENGTH=517	520	517	0	99.4	87.7	94.2
Rsa1.0_00020.1.g1389.t1	gb|EOA39000.1| hypothetical protein CARUB_v10011529mg [Capsella rubella]	519	519	0	100.0	91.1	96.0	hypothetical protein CARUB_v10011529mg	gbpln	Capsella rubella	AT1G12950.1 | Symbols: RSH2 | root hair specific 2 | chr1:4419849-4422462 FORWARD LENGTH=522	519	522	0	100.6	88.8	94.6
Rsa1.0_00020.1.g1390.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00020.1.g1391.t1	gb|EOA40211.1| hypothetical protein CARUB_v10008932mg [Capsella rubella]	503	500	0	99.4	92.2	96.2	hypothetical protein CARUB_v10008932mg	gbpln	Capsella rubella	AT1G12940.1 | Symbols: ATNRT2.5, NRT2.5 | nitrate transporter2.5 | chr1:4416405-4418337 FORWARD LENGTH=502	503	502	0	99.8	90.5	95.8
Rsa1.0_00020.1.g1392.t1	gb|ACZ71034.1| eukaryotic release factor 1-2 [Brassica oleracea var. botrytis]	435	435	0	100.0	99.8	100.0	eukaryotic release factor 1-2	gbpln	Brassica oleracea	AT1G12920.1 | Symbols: ERF1-2 | eukaryotic release factor 1-2 | chr1:4396555-4397859 REVERSE LENGTH=434	435	434	0	99.8	97.0	98.6
Rsa1.0_00020.1.g1393.t1	gb|EOA40353.1| hypothetical protein CARUB_v10009081mg [Capsella rubella]	446	461	1.00E-175	103.4	78.9	85.0	hypothetical protein CARUB_v10009081mg	gbpln	Capsella rubella	AT1G12860.1 | Symbols: SCRM2, ICE2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:4384758-4386392 FORWARD LENGTH=450	446	450	1.00E-168	100.9	78.3	84.5
Rsa1.0_00020.1.g1394.t1	ref|NP_563918.1| phosphoglycerate mutase-like protein [Arabidopsis thaliana] gi|14517376|gb|AAK62579.1| At1g12850/F13K23_8 [Arabidopsis thaliana] gi|21360535|gb|AAM47383.1| At1g12850/F13K23_8 [Arabidopsis thaliana] gi|332190817|gb|AEE28938.1| phosphoglycerate mutase-like protein [Arabidopsis thaliana]	403	405	1.00E-173	100.5	85.6	89.3	phosphoglycerate mutase-like protein	gbpln	Arabidopsis thaliana	AT1G12850.1 | Symbols: | Phosphoglycerate mutase family protein | chr1:4380022-4381577 REVERSE LENGTH=405	403	405	1.00E-175	100.5	85.6	89.3

Rsa1.0_00020.1.g1395.t1	ref|XP_002892717.1| hypothetical protein ARALYDRAFT_334590 [Arabidopsis lyrata subsp. lyrata] gi|297338559|gb|EFH68976.1| hypothetical protein ARALYDRAFT_334590 [Arabidopsis lyrata subsp. lyrata]	108	563	4.00E-35	521.3	74.1	79.6	hypothetical protein ARALYDRAFT_334590	gbpln	Arabidopsis lyrata	AT1G12845.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 8 Blast hits to 8 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4379023-4379382 REVERSE LENGTH=119	108	119	1.00E-35	110.2	72.2	77.8
Rsa1.0_00020.1.g1396.t1	ref|NP_563916.1| V-type proton ATPase subunit C [Arabidopsis thaliana] gi|12585488|sp|Q9SDS7.1|VATC_ARATH RecName: Full=V-type proton ATPase subunit C; Short=V-ATPase subunit C; AltName: Full=Vacuolar H(+)-ATPase subunit C; AltName: Full=Vacuolar proton pump subunit C gi|6636332|gb|AAF20146.1|AF208261_1 vacuolar ATP synthase subunit C [Arabidopsis thaliana] gi|8698731|gb|AAF78489.1|AC012187_9 Identical to vacuolar ATP sythase subunit C (DET3) from Arabidopsis thaliana gb|AF208261. ESTs gb|AA067533, gb|Z37481, gb|AA721838, gb|Z37180, gb|T21206 come from this gene [Arabidopsis thaliana] gi|12248023|gb|AAG50103.1|AF334725_1 putative vacuolar ATP synthase subunit C [Arabidopsis thaliana] gi|16649005|gb|AAL24354.1| Identical to vacuolar ATP sythase subunit C (DET3) [Arabidopsis thaliana] gi|20259972|gb|AAM13333.1| vacuolar ATP sythase subunit C [Arabidopsis thaliana] gi|225897918|dbj|BAH30291.1| hypothetical protein [Arabidopsis thaliana] gi|332190815|gb|AEE28936.1| V-type proton ATPase subunit C [Arabidopsis thaliana]	376	375	0	99.7	94.9	97.6	V-type proton ATPase subunit C	gbpln	Arabidopsis thaliana	AT1G12840.1 | Symbols: DET3, ATVHA-C | vacuolar ATP synthase subunit C (VATC) / V-ATPase C subunit / vacuolar proton pump C subunit (DET3) | chr1:4375584-4378220 FORWARD LENGTH=375	376	375	0	99.7	94.9	97.6
Rsa1.0_00020.1.g1397.t1	ref|XP_002892716.1| hypothetical protein ARALYDRAFT_471437 [Arabidopsis lyrata subsp. lyrata] gi|297338558|gb|EFH68975.1| hypothetical protein ARALYDRAFT_471437 [Arabidopsis lyrata subsp. lyrata]	192	212	2.00E-38	110.4	64.1	77.6	hypothetical protein ARALYDRAFT_471437	gbpln	Arabidopsis lyrata	AT1G12830.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 39778 Blast hits to 22088 proteins in 1060 species: Archae - 152; Bacteria - 6161; Metazoa - 14109; Fungi - 6144; Plants - 2156; Viruses - 601; Other Eukaryotes - 10455 (source: NCBI BLink). | chr1:4374412-4375053 REVERSE LENGTH=213	192	213	5.00E-39	110.9	64.6	73.4
Rsa1.0_00020.1.g1398.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1594	1223	0	76.7	34.3	47.0	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1594	746	1.00E-84	46.8	10.6	14.8
Rsa1.0_00020.1.g1399.t1	gb|ABQ50554.1| hypothetical protein [Brassica rapa]	595	590	0	99.2	93.4	95.5	hypothetical protein	gbpln	Brassica rapa	AT1G12820.1 | Symbols: AFB3 | auxin signaling F-box 3 | chr1:4368879-4370780 REVERSE LENGTH=577	595	577	0	97.0	86.1	91.9
Rsa1.0_00020.1.g1400.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00020.1.g1401.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00020.1.g1402.t1	dbj|BAH20409.1| AT1G12800 [Arabidopsis thaliana]	80	525	3.00E-25	656.3	76.3	80.0	AT1G12800	gbpln	Arabidopsis thaliana	AT1G12800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:4361778-4365189 REVERSE LENGTH=767	80	767	6.00E-28	958.8	76.3	80.0
Rsa1.0_00020.1.g1403.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00020.1.g1404.t1	gb|ABQ50560.1| hypothetical protein [Brassica rapa]	73	74	5.00E-30	101.4	86.3	94.5	hypothetical protein	gbpln	Brassica rapa	AT1G12805.1 | Symbols: | nucleotide binding | chr1:4366728-4366955 FORWARD LENGTH=75	73	75	1.00E-23	102.7	68.5	83.6
Rsa1.0_00020.1.g1405.t1	ref|XP_002892712.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata] gi|297338554|gb|EFH68971.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata]	351	351	0	100.0	94.9	96.9	UDP-D-glucose/UDP-D-galactose 4-epimerase 1	gbpln	Arabidopsis lyrata	AT1G12780.1 | Symbols: UGE1, ATUGE1 | UDP-D-glucose/UDP-D-galactose 4-epimerase 1 | chr1:4356124-4358120 REVERSE LENGTH=351	351	351	0	100.0	94.3	96.3

Rsa1.0_00020.1.g1406.t1	gb|ABQ50546.1| hypothetical protein [Brassica rapa]	1163	650	0	55.9	37.2	45.8	hypothetical protein	gbpln	Brassica rapa	AT1G12770.1 | Symbols: ISE1, EMB1586 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:4351888-4353543 FORWARD LENGTH=551	1163	551	0	47.4	39.1	40.8
Rsa1.0_00020.1.g1407.t1	gb|EOA36065.1| hypothetical protein CARUB_v10008555mg [Capsella rubella]	634	641	0	101.1	71.6	83.6	hypothetical protein CARUB_v10008555mg	gbpln	Capsella rubella	AT1G12300.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4184163-4186076 REVERSE LENGTH=637	634	637	0	100.5	69.6	82.0
Rsa1.0_00020.1.g1408.t1	ref|NP_172694.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|122242333|sp|Q0WKV3.1|PPR36_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g12300, mitochondrial; Flags: Precursor gi|110741411|dbj|BAF02254.1| hypothetical protein [Arabidopsis thaliana] gi|332190743|gb|AEE28864.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	566	637	0	112.5	67.3	82.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G12300.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4184163-4186076 REVERSE LENGTH=637	566	637	0	112.5	67.3	82.5
Rsa1.0_00020.1.g1409.t1	gb|EOA37885.1| hypothetical protein CARUB_v10009353mg [Capsella rubella]	402	397	1.00E-162	98.8	83.3	87.1	hypothetical protein CARUB_v10009353mg	gbpln	Capsella rubella	AT1G12760.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr1:4348728-4350512 FORWARD LENGTH=408	402	408	1.00E-160	101.5	77.9	81.3
Rsa1.0_00020.1.g1410.t1	gb|EOA40316.1| hypothetical protein CARUB_v10009041mg [Capsella rubella]	467	470	0	100.6	89.9	94.6	hypothetical protein CARUB_v10009041mg	gbpln	Capsella rubella	AT1G12680.1 | Symbols: PEPKR2 | phosphoenolpyruvate carboxylase-related kinase 2 | chr1:4320123-4322269 REVERSE LENGTH=470	467	470	0	100.6	87.8	92.9
Rsa1.0_00020.1.g1411.t1	ref|XP_002889943.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297335785|gb|EFH66202.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	191	192	2.00E-67	100.5	77.5	86.4	DNA binding protein	gbpln	Arabidopsis lyrata	AT1G12630.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:4298897-4299475 FORWARD LENGTH=192	191	192	8.00E-62	100.5	74.9	83.8
Rsa1.0_00020.1.g1412.t1	ref|XP_002885504.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297331344|gb|EFH61763.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	603	618	0	102.5	67.7	82.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G12300.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4184163-4186076 REVERSE LENGTH=637	603	637	0	105.6	68.7	83.7
Rsa1.0_00020.1.g1413.t1	ref|NP_563911.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75167758|sp|Q9ASZ8.1|PPR37_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g12620 gi|13605505|gb|AAK32746.1|AF361578_1 At1g12620/T12C24_25 [Arabidopsis thaliana] gi|24111307|gb|AAN46777.1| At1g12620/T12C24_25 [Arabidopsis thaliana] gi|332190781|gb|AEE28902.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	580	621	0	107.1	67.9	82.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G12620.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:4294883-4296748 REVERSE LENGTH=621	580	621	0	107.1	67.9	82.6
Rsa1.0_00020.1.g1414.t1	ref|NP_172721.1| dehydration-responsive element-binding protein 1F [Arabidopsis thaliana] gi|47605747|sp|Q9LN86.1|DRE1F_ARATH RecName: Full=Dehydration-responsive element-binding protein 1F; Short=Protein DREB1F gi|9502389|gb|AAF88096.1|AC025417_24 T12C24.14 [Arabidopsis thaliana] gi|48479384|gb|AAT44959.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|110736358|dbj|BAF00148.1| hypothetical protein [Arabidopsis thaliana] gi|332190780|gb|AEE28901.1| dehydration-responsive element-binding protein 1F [Arabidopsis thaliana]	202	209	4.00E-84	103.5	82.2	87.6	dehydration-responsive element-binding protein 1F	gbpln	Arabidopsis thaliana	AT1G12610.1 | Symbols: DDF1 | Integrase-type DNA-binding superfamily protein | chr1:4290205-4290834 REVERSE LENGTH=209	202	209	1.00E-86	103.5	82.2	87.6

Rsa1.0_00020.1.g1415.t3	ref|NP_172720.1| UDP-N-acetylglucosamine transporter-like protein [Arabidopsis thaliana] gi|75173863|sp|Q9LDX3.1|UTR4_ARATH RecName: Full=UDP-galactose/UDP-glucose transporter 4; Short=AtUTr4 gi|8778639|gb|AAF79647.1|AC025416_21 F5O11.33 [Arabidopsis thaliana] gi|9502390|gb|AAF88097.1|AC025417_25 T12C24.13 [Arabidopsis thaliana] gi|55978703|gb|AAV68813.1| hypothetical protein AT1G12600 [Arabidopsis thaliana] gi|60547555|gb|AAX23741.1| hypothetical protein At1g12600 [Arabidopsis thaliana] gi|332190779|gb|AEE28900.1| UDP-galactose/UDP-glucose transporter 4 [Arabidopsis thaliana]	536	349	1.00E-177	65.1	59.5	61.0	UDP-N-acetylglucosamine transporter-like protein	gbpln	Arabidopsis thaliana	AT1G12600.1 | Symbols: | UDP-N-acetylglucosamine (UAA) transporter family | chr1:4286414-4288859 REVERSE LENGTH=349	536	349	1.00E-179	65.1	59.5	61.0
Rsa1.0_00020.1.g1416.t1	ref|XP_002889942.1| hypothetical protein ARALYDRAFT_471407 [Arabidopsis lyrata subsp. lyrata] gi|297335784|gb|EFH66201.1| hypothetical protein ARALYDRAFT_471407 [Arabidopsis lyrata subsp. lyrata]	533	522	0	97.9	86.7	91.6	hypothetical protein ARALYDRAFT_471407	gbpln	Arabidopsis lyrata	AT1G12580.1 | Symbols: PEPKR1 | phosphoenolpyruvate carboxylase-related kinase 1 | chr1:4283635-4285675 FORWARD LENGTH=522	533	522	0	97.9	86.1	91.7
Rsa1.0_00020.1.g1417.t1	gb|AAF79648.1|AC025416_22 F5O11.31 [Arabidopsis thaliana]	537	539	0	100.4	93.1	96.6	F5O11.31	gbpln	Arabidopsis thaliana	AT1G12570.1 | Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr1:4278192-4280753 REVERSE LENGTH=572	537	572	0	106.5	93.1	96.6
Rsa1.0_00020.1.g1418.t1	gb|EOA36118.1| hypothetical protein CARUB_v10011828mg [Capsella rubella]	263	263	1.00E-144	100.0	92.8	97.7	hypothetical protein CARUB_v10011828mg	gbpln	Capsella rubella	AT1G12560.1 | Symbols: ATEXPA7, EXP7, ATEXP7, ATHEXP ALPHA 1.26, EXPA7 | expansin A7 | chr1:4276557-4277693 FORWARD LENGTH=262	263	262	1.00E-140	99.6	90.5	94.7
Rsa1.0_00020.1.g1419.t1	ref|XP_002892693.1| Cu/Zn-superoxide dismutase copper chaperone precursor [Arabidopsis lyrata subsp. lyrata] gi|297338535|gb|EFH68952.1| Cu/Zn-superoxide dismutase copper chaperone precursor [Arabidopsis lyrata subsp. lyrata]	316	318	1.00E-148	100.6	80.7	84.5	Cu/Zn-superoxide dismutase copper chaperone precursor	gbpln	Arabidopsis lyrata	AT1G12520.1 | Symbols: ATCCS, CCS | copper chaperone for SOD1 | chr1:4267277-4268900 REVERSE LENGTH=320	316	320	1.00E-145	101.3	87.7	91.8
Rsa1.0_00020.1.g1420.t1	ref|NP_172712.1| Nucleotide-sugar transporter family protein [Arabidopsis thaliana] gi|75173828|sp|Q9LDH3.1|PT112_ARATH RecName: Full=Probable sugar phosphate/phosphate translocator At1g12500 gi|8778643|gb|AAF79651.1|AC025416_25 F5O11.25 [Arabidopsis thaliana] gi|9502394|gb|AAF88101.1|AC025417_29 T12C24.5 [Arabidopsis thaliana] gi|26449593|dbj|BAC41922.1| unknown protein [Arabidopsis thaliana] gi|332190769|gb|AEE28890.1| Nucleotide-sugar transporter family protein [Arabidopsis thaliana]	361	361	0	100.0	96.7	98.9	Nucleotide-sugar transporter family protein	gbpln	Arabidopsis thaliana	AT1G12500.1 | Symbols: | Nucleotide-sugar transporter family protein | chr1:4263542-4264957 REVERSE LENGTH=361	361	361	0	100.0	96.7	98.9
Rsa1.0_00020.1.g1421.t1	gb|EOA39582.1| hypothetical protein CARUB_v10008200mg [Capsella rubella]	1148	988	0	86.1	80.1	83.2	hypothetical protein CARUB_v10008200mg	gbpln	Capsella rubella	AT1G12470.1 | Symbols: | zinc ion binding | chr1:4251359-4257201 FORWARD LENGTH=988	1148	988	0	86.1	79.2	82.8
Rsa1.0_00020.1.g1422.t1	ref|NP_172707.1| SNARE associated Golgi protein family [Arabidopsis thaliana] gi|34222066|gb|AAQ62869.1| At1g12450 [Arabidopsis thaliana] gi|62320872|dbj|BAD93843.1| hypothetical protein [Arabidopsis thaliana] gi|332190763|gb|AEE28884.1| SNARE associated Golgi protein family [Arabidopsis thaliana]	290	303	2.33E-156	104.5	90.0	95.5	SNARE associated Golgi protein family	gbpln	Arabidopsis thaliana	AT1G12450.1 | Symbols: | SNARE associated Golgi protein family | chr1:4244496-4245808 FORWARD LENGTH=303	290	303	1.00E-148	104.5	90.0	95.5
Rsa1.0_00020.1.g1423.t1	ref|NP_172704.1| ACT domain repeat 8 protein [Arabidopsis thaliana] gi|8778647|gb|AAF79655.1|AC025416_29 F5O11.14 [Arabidopsis thaliana] gi|22138106|gb|AAM93433.1| ACR8 [Arabidopsis thaliana] gi|110737291|dbj|BAF00592.1| hypothetical protein [Arabidopsis thaliana] gi|111074504|gb|ABH04625.1| At1g12420 [Arabidopsis thaliana] gi|332190757|gb|AEE28878.1| ACT domain repeat 8 protein [Arabidopsis thaliana]	441	441	0	100.0	89.8	95.2	ACT domain repeat 8 protein	gbpln	Arabidopsis thaliana	AT1G12420.1 | Symbols: ACR8 | ACT domain repeat 8 | chr1:4226673-4228917 REVERSE LENGTH=441	441	441	0	100.0	89.8	95.2

Rsa1.0_00020.1.g1424.t1	ref|NP_172701.2| protein cornichon-4 [Arabidopsis thaliana] gi|75148636|sp|Q84W04.1|CNIH4_ARATH RecName: Full=Protein cornichon homolog 4 gi|28416577|gb|AAO42819.1| At1g12390 [Arabidopsis thaliana] gi|110743211|dbj|BAE99496.1| hypothetical protein [Arabidopsis thaliana] gi|332190753|gb|AEE28874.1| protein cornichon-4 [Arabidopsis thaliana]	219	137	5.00E-63	62.6	55.3	58.0	protein cornichon-4	gbpln	Arabidopsis thaliana	AT1G12390.1 | Symbols: | Cornichon family protein | chr1:4220347-4221481 FORWARD LENGTH=137	219	137	2.00E-65	62.6	55.3	58.0
Rsa1.0_00020.1.g1425.t1	ref|XP_002892685.1| hypothetical protein ARALYDRAFT_888561 [Arabidopsis lyrata subsp. lyrata] gi|297338527|gb|EFH68944.1| hypothetical protein ARALYDRAFT_888561 [Arabidopsis lyrata subsp. lyrata]	765	792	0	103.5	86.1	90.3	hypothetical protein ARALYDRAFT_888561	gbpln	Arabidopsis lyrata	AT1G12380.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G62870.1); Has 173 Blast hits to 170 proteins in 34 species: Archae - 0; Bacteria - 4; Metazoa - 25; Fungi - 8; Plants - 123; Viruses - 7; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:4214499-4216880 REVERSE LENGTH=793	765	793	0	103.7	87.3	92.2
Rsa1.0_00020.1.g1426.t2	ref|XP_002892684.1| hypothetical protein ARALYDRAFT_471385 [Arabidopsis lyrata subsp. lyrata] gi|297338526|gb|EFH68943.1| hypothetical protein ARALYDRAFT_471385 [Arabidopsis lyrata subsp. lyrata]	493	496	0	100.6	89.5	93.9	hypothetical protein ARALYDRAFT_471385	gbpln	Arabidopsis lyrata	AT1G12370.2 | Symbols: PHR1, UVR2 | photolyase 1 | chr1:4206500-4208842 REVERSE LENGTH=496	493	496	0	100.6	88.4	93.5
Rsa1.0_00020.1.g1427.t1	ref|XP_002876578.1| hypothetical protein ARALYDRAFT_486544 [Arabidopsis lyrata subsp. lyrata] gi|297322416|gb|EFH52837.1| hypothetical protein ARALYDRAFT_486544 [Arabidopsis lyrata subsp. lyrata]	252	287	1.00E-112	113.9	80.6	82.5	hypothetical protein ARALYDRAFT_486544	gbpln	Arabidopsis lyrata	AT3G60720.1 | Symbols: PDLP8 | plasmodesmata-located protein 8 | chr3:22442035-22443608 FORWARD LENGTH=279	252	279	1.00E-113	110.7	81.0	82.9
Rsa1.0_00020.1.g1428.t1	ref|XP_002889928.1| hypothetical protein ARALYDRAFT_471382 [Arabidopsis lyrata subsp. lyrata] gi|297335770|gb|EFH66187.1| hypothetical protein ARALYDRAFT_471382 [Arabidopsis lyrata subsp. lyrata]	514	504	0	98.1	79.4	86.6	hypothetical protein ARALYDRAFT_471382	gbpln	Arabidopsis lyrata	AT1G12330.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12900.1); Has 249 Blast hits to 249 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 14; Plants - 217; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr1:4194673-4196627 FORWARD LENGTH=505	514	505	0	98.2	79.4	86.2
Rsa1.0_00020.1.g1429.t1	ref|XP_002889927.1| hypothetical protein ARALYDRAFT_471381 [Arabidopsis lyrata subsp. lyrata] gi|297335769|gb|EFH66186.1| hypothetical protein ARALYDRAFT_471381 [Arabidopsis lyrata subsp. lyrata]	218	213	4.00E-95	97.7	84.4	90.4	hypothetical protein ARALYDRAFT_471381	gbpln	Arabidopsis lyrata	AT1G12320.1 | Symbols: | Protein of unknown function (DUF1442) | chr1:4189424-4190209 FORWARD LENGTH=212	218	212	6.00E-93	97.2	83.0	89.4
Rsa1.0_00020.1.g1430.t1	gb|AAF79658.1|AC025416_32 F5O11.4 [Arabidopsis thaliana]	148	975	5.00E-78	658.8	95.9	98.6	F5O11.4	gbpln	Arabidopsis thaliana	AT1G12310.1 | Symbols: | Calcium-binding EF-hand family protein | chr1:4187500-4187946 REVERSE LENGTH=148	148	148	1.00E-79	100.0	96.6	99.3
Rsa1.0_00020.1.g1431.t1	ref|NP_172690.1| NAC domain-containing protein 7 [Arabidopsis thaliana] gi|238065075|sp|Q9FWX2.2|NAC7_ARATH RecName: Full=NAC domain-containing protein 7; Short=ANAC007; AltName: Full=Protein EMBRYO DEFECTIVE 2749; AltName: Full=Protein VASCULAR RELATED NAC-DOMAIN 4 gi|119935909|gb|ABM06031.1| At1g12260 [Arabidopsis thaliana] gi|332190738|gb|AEE28859.1| NAC domain-containing protein 7 [Arabidopsis thaliana]	391	395	0	101.0	89.3	92.6	NAC domain-containing protein 7	gbpln	Arabidopsis thaliana	AT1G12260.1 | Symbols: VND4, EMB2749, ANAC007, NAC007 | NAC 007 | chr1:4163058-4164486 REVERSE LENGTH=395	391	395	0	101.0	89.3	92.6
Rsa1.0_00020.1.g1432.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00020.1.g1433.t1	gb|AAK30571.1|AF346659_1 extensin-like protein [Brassica napus]	137	137	7.00E-47	100.0	96.4	98.5	extensin-like protein	gbpln	Brassica napus	AT1G12090.1 | Symbols: ELP | extensin-like protein | chr1:4090176-4090589 REVERSE LENGTH=137	137	137	4.00E-45	100.0	95.6	98.5

Rsa1.0_00021.1.g1434.t1	ref|NP_564293.1| transcription factor bHLH54 [Arabidopsis thaliana] gi|75301354|sp|Q8LEG1.1|BH054_ARATH RecName: Full=Transcription factor bHLH54; AltName: Full=Basic helix-loop-helix protein 54; Short=AtbHLH54; Short=bHLH 54; AltName: Full=Transcription factor EN 114; AltName: Full=bHLH transcription factor bHLH054 gi|21553570|gb|AAM62663.1| unknown [Arabidopsis thaliana] gi|225897974|dbj|BAH30319.1| hypothetical protein [Arabidopsis thaliana] gi|332192750|gb|AEE30871.1| transcription factor bHLH54 [Arabidopsis thaliana]	255	258	1.00E-120	101.2	88.6	92.9	transcription factor bHLH54	gbpln	Arabidopsis thaliana	AT1G27740.1 | Symbols: RSL4 | root hair defective 6-like 4 | chr1:9654753-9655806 FORWARD LENGTH=258	255	258	1.00E-122	101.2	88.6	92.9
Rsa1.0_00021.1.g1435.t2	gb|AAF24949.1|AC012375_12 T22C5.20 [Arabidopsis thaliana]	1115	1840	0	165.0	73.1	78.5	T22C5.20	gbpln	Arabidopsis thaliana	AT1G27750.1 | Symbols: | nucleic acid binding | chr1:9657425-9661750 FORWARD LENGTH=1075	1115	1075	0	96.4	65.5	69.5
Rsa1.0_00021.1.g1436.t1	ref|XP_002890749.1| hypothetical protein ARALYDRAFT_472983 [Arabidopsis lyrata subsp. lyrata] gi|297336591|gb|EFH67008.1| hypothetical protein ARALYDRAFT_472983 [Arabidopsis lyrata subsp. lyrata]	443	442	0	99.8	87.6	93.0	hypothetical protein ARALYDRAFT_472983	gbpln	Arabidopsis lyrata	AT1G27760.3 | Symbols: SAT32, ATSAT32 | interferon-related developmental regulator family protein / IFRD protein family | chr1:9668895-9671322 FORWARD LENGTH=441	443	441	0	99.5	87.1	92.3
Rsa1.0_00021.1.g1437.t1	ref|XP_002893491.1| ATCSA-1 [Arabidopsis lyrata subsp. lyrata] gi|297339333|gb|EFH69750.1| ATCSA-1 [Arabidopsis lyrata subsp. lyrata]	460	450	0	97.8	85.7	91.7	ATCSA-1	gbpln	Arabidopsis lyrata	AT1G27840.1 | Symbols: ATCSA-1 | Transducin/WD40 repeat-like superfamily protein | chr1:9693332-9696257 REVERSE LENGTH=450	460	450	0	97.8	84.6	90.9
Rsa1.0_00021.1.g1438.t1	gb|EOA36789.1| hypothetical protein CARUB_v10008135mg [Capsella rubella]	1038	1149	0	110.7	50.8	53.9	hypothetical protein CARUB_v10008135mg	gbpln	Capsella rubella	AT1G27850.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G40070.1); Has 9215 Blast hits to 5316 proteins in 473 species: Archae - 6; Bacteria - 773; Metazoa - 3392; Fungi - 1710; Plants - 539; Viruses - 143; Other Eukaryotes - 2652 (source: NCBI BLink). | chr1:9699265-9703701 FORWARD LENGTH=1148	1038	1148	0	110.6	50.6	53.3
Rsa1.0_00021.1.g1439.t1	gb|EOA39726.1| hypothetical protein CARUB_v10008370mg [Capsella rubella]	770	768	0	99.7	90.5	94.7	hypothetical protein CARUB_v10008370mg	gbpln	Capsella rubella	AT1G27910.1 | Symbols: PUB45, ATPUB45 | plant U-box 45 | chr1:9720962-9723975 REVERSE LENGTH=768	770	768	0	99.7	89.9	94.9
Rsa1.0_00021.1.g1440.t2	gb|AAG51477.1|AC069471_8 hypothetical protein [Arabidopsis thaliana]	584	592	0	101.4	81.2	86.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G27920.1 | Symbols: MAP65-8 | microtubule-associated protein 65-8 | chr1:9727106-9729848 FORWARD LENGTH=562	584	562	0	96.2	79.1	84.1
Rsa1.0_00021.1.g1441.t1	gb|AAM61740.1| unknown [Arabidopsis thaliana]	289	289	1.00E-150	100.0	91.0	95.5	unknown	gbpln	Arabidopsis thaliana	AT1G27930.1 | Symbols: | Protein of unknown function (DUF579) | chr1:9731510-9732379 REVERSE LENGTH=289	289	289	1.00E-153	100.0	91.0	95.2
Rsa1.0_00021.1.g1442.t1	ref|XP_002893495.1| P-glycoprotein 13 [Arabidopsis lyrata subsp. lyrata] gi|297339337|gb|EFH69754.1| P-glycoprotein 13 [Arabidopsis lyrata subsp. lyrata]	1167	1246	0	106.8	89.4	94.0	P-glycoprotein 13	gbpln	Arabidopsis lyrata	AT1G27940.1 | Symbols: PGP13 | P-glycoprotein 13 | chr1:9733597-9738129 REVERSE LENGTH=1245	1167	1245	0	106.7	88.9	93.6
Rsa1.0_00021.1.g1443.t1	ref|XP_002890752.1| hypothetical protein ARALYDRAFT_890328 [Arabidopsis lyrata subsp. lyrata] gi|297336594|gb|EFH67011.1| hypothetical protein ARALYDRAFT_890328 [Arabidopsis lyrata subsp. lyrata]	194	197	5.00E-78	101.5	82.0	89.2	hypothetical protein ARALYDRAFT_890328	gbpln	Arabidopsis lyrata	AT1G27950.1 | Symbols: LTPG1 | glycosylphosphatidylinositol-anchored lipid protein transfer 1 | chr1:9740740-9741991 FORWARD LENGTH=193	194	193	6.00E-76	99.5	77.3	86.6
Rsa1.0_00021.1.g1444.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00021.1.g1445.t1	ref|NP_174118.1| nuclear transport factor 2B [Arabidopsis thaliana] gi|15214148|sp|Q9C7F5.1|NTF2_ARATH RecName: Full=Nuclear transport factor 2; Short=NTF-2 gi|12323001|gb|AAG51491.1|AC069471_22 nuclear transport factor 2, putative [Arabidopsis thaliana] gi|98961065|gb|ABF59016.1| At1g27970 [Arabidopsis thaliana] gi|332192775|gb|AEE30896.1| nuclear transport factor 2B [Arabidopsis thaliana]	128	126	8.00E-66	98.4	93.8	96.1	nuclear transport factor 2B	gbpln	Arabidopsis thaliana	AT1G27970.1 | Symbols: NTF2B | nuclear transport factor 2B | chr1:9746921-9747787 FORWARD LENGTH=126	128	126	2.00E-68	98.4	93.8	96.1

Rsa1.0_00021.1.g1446.t1	gb|EOA37762.1| hypothetical protein CARUB_v10012601mg [Capsella rubella]	187	544	4.00E-34	290.9	55.1	62.0	hypothetical protein CARUB_v10012601mg	gbpln	Capsella rubella	AT1G27980.1 | Symbols: DPL1, ATDPL1 | dihydrosphingosine phosphate lyase | chr1:9748812-9752618 FORWARD LENGTH=544	187	544	6.00E-36	290.9	54.5	61.5
Rsa1.0_00021.1.g1447.t1	gb|EOA37464.1| hypothetical protein CARUB_v10011574mg [Capsella rubella]	271	270	1.00E-134	99.6	89.7	94.5	hypothetical protein CARUB_v10011574mg	gbpln	Capsella rubella	AT1G27990.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G52420.1); Has 86 Blast hits to 86 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 84; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:9752799-9753919 REVERSE LENGTH=271	271	271	1.00E-132	100.0	89.3	94.8
Rsa1.0_00021.1.g1448.t1	gb|EOA17180.1| hypothetical protein CARUB_v10005451mg [Capsella rubella]	289	278	9.00E-76	96.2	51.6	67.5	hypothetical protein CARUB_v10005451mg	gbpln	Capsella rubella	AT4G17700.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17990.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9854322-9855227 FORWARD LENGTH=164	289	164	7.00E-43	56.7	28.7	38.4
Rsa1.0_00021.1.g1449.t1	sp|Q9C7F1.2|PPR61_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At1g28020	564	566	1.00E-169	100.4	57.8	69.5	RecName: Full=Putative pentatricopeptide repeat-containing protein At1g28020	----	----	AT1G28020.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:9768395-9771157 REVERSE LENGTH=612	564	612	1.00E-163	108.5	55.1	66.7
Rsa1.0_00021.1.g1450.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	141	1142	1.00E-25	809.9	44.0	49.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00021.1.g1451.t1	gb|EOA39175.1| hypothetical protein CARUB_v10012135mg [Capsella rubella]	423	410	1.00E-120	96.9	56.0	67.1	hypothetical protein CARUB_v10012135mg	gbpln	Capsella rubella	AT1G28000.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:9756674-9757947 REVERSE LENGTH=388	423	388	1.00E-118	91.7	51.3	61.9
Rsa1.0_00021.1.g1452.t1	gb|EOA39175.1| hypothetical protein CARUB_v10012135mg [Capsella rubella]	304	410	1.00E-84	134.9	53.0	62.8	hypothetical protein CARUB_v10012135mg	gbpln	Capsella rubella	AT1G28000.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:9756674-9757947 REVERSE LENGTH=388	304	388	7.00E-84	127.6	53.9	62.8
Rsa1.0_00021.1.g1453.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	515	536	9.00E-68	104.1	23.9	31.3	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT5G28823.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: Zinc knuckle (CCHC-type) family protein (TAIR:AT2G07760.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:10837849-10839826 REVERSE LENGTH=568	515	568	8.00E-47	110.3	26.8	38.1
Rsa1.0_00021.1.g1454.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00021.1.g1455.t1	ref|XP_002890755.1| P-glycoprotein 14 [Arabidopsis lyrata subsp. lyrata] gi|297336597|gb|EFH67014.1| P-glycoprotein 14 [Arabidopsis lyrata subsp. lyrata]	1243	1248	0	100.4	88.2	94.0	P-glycoprotein 14	gbpln	Arabidopsis lyrata	AT1G28010.1 | Symbols: PGP14, ATABCB14, ABCB14 | P-glycoprotein 14 | chr1:9763436-9767917 FORWARD LENGTH=1247	1243	1247	0	100.3	87.4	93.7
Rsa1.0_00021.1.g1456.t1	ref|XP_002868101.1| hypothetical protein ARALYDRAFT_915040 [Arabidopsis lyrata subsp. lyrata] gi|297313937|gb|EFH44360.1| hypothetical protein ARALYDRAFT_915040 [Arabidopsis lyrata subsp. lyrata]	277	495	4.00E-70	178.7	52.7	69.7	hypothetical protein ARALYDRAFT_915040	gbpln	Arabidopsis lyrata	AT1G28020.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:9768395-9771157 REVERSE LENGTH=612	277	612	4.00E-49	220.9	39.0	47.7
Rsa1.0_00021.1.g1457.t1	gb|ABD64987.1| hypothetical protein 26.t00003 [Brassica oleracea]	468	330	2.00E-15	70.5	11.8	13.0	hypothetical protein 26.t00003	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00021.1.g1458.t1	ref|XP_002893501.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339343|gb|EFH69760.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	395	667	1.00E-112	168.9	61.0	72.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G28020.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:9768395-9771157 REVERSE LENGTH=612	395	612	1.00E-110	154.9	58.7	69.4
Rsa1.0_00021.1.g1459.t1	gb|EOA39175.1| hypothetical protein CARUB_v10012135mg [Capsella rubella]	375	410	1.00E-108	109.3	56.8	68.8	hypothetical protein CARUB_v10012135mg	gbpln	Capsella rubella	AT1G28000.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:9756674-9757947 REVERSE LENGTH=388	375	388	1.00E-105	103.5	50.1	60.5
Rsa1.0_00021.1.g1460.t1	gb|AAG50751.1|AC079733_19 polyprotein, putative [Arabidopsis thaliana]	1407	1468	0	104.3	55.4	70.5	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1407	1262	1.00E-140	89.7	17.2	25.3

Rsa1.0_00021.1.g1461.t1	gb|EOA39702.1| hypothetical protein CARUB_v10008347mg [Capsella rubella]	773	787	0	101.8	74.9	82.7	hypothetical protein CARUB_v10008347mg	gbpln	Capsella rubella	AT1G28060.1 | Symbols: | Pre-mRNA-splicing factor 3 | chr1:9779167-9782486 FORWARD LENGTH=786	773	786	0	101.7	74.3	82.3
Rsa1.0_00021.1.g1462.t1	ref|NP_174128.1| uncharacterized protein [Arabidopsis thaliana] gi|12323005|gb|AAG51495.1|AC069471_26 hypothetical protein [Arabidopsis thaliana] gi|44681470|gb|AAS47675.1| At1g28070 [Arabidopsis thaliana] gi|62318580|dbj|BAD94977.1| hypothetical protein [Arabidopsis thaliana] gi|332192787|gb|AEE30908.1| uncharacterized protein AT1G28070 [Arabidopsis thaliana]	149	176	4.00E-38	118.1	63.1	77.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G28070.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G33510.1); Has 85 Blast hits to 77 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 85; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:9783082-9783864 FORWARD LENGTH=176	149	176	1.00E-40	118.1	63.1	77.2
Rsa1.0_00021.1.g1463.t1	emb|CAN60947.1| hypothetical protein VITISV_015758 [Vitis vinifera]	336	1306	1.00E-102	388.7	61.9	69.3	hypothetical protein VITISV_015758	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00021.1.g1464.t1	ref|XP_002890758.1| hypothetical protein ARALYDRAFT_313512 [Arabidopsis lyrata subsp. lyrata] gi|297336600|gb|EFH67017.1| hypothetical protein ARALYDRAFT_313512 [Arabidopsis lyrata subsp. lyrata]	258	296	3.00E-91	114.7	71.7	81.4	hypothetical protein ARALYDRAFT_313512	gbpln	Arabidopsis lyrata	AT1G28080.1 | Symbols: | RING finger protein | chr1:9789826-9790918 FORWARD LENGTH=291	258	291	7.00E-86	112.8	65.9	76.0
Rsa1.0_00021.1.g1465.t1	gb|EOA40088.1| hypothetical protein CARUB_v10008782mg [Capsella rubella]	540	543	0	100.6	86.3	94.1	hypothetical protein CARUB_v10008782mg	gbpln	Capsella rubella	AT1G28090.1 | Symbols: | Polynucleotide adenylyltransferase family protein | chr1:9795826-9798891 FORWARD LENGTH=541	540	541	0	100.2	85.0	93.7
Rsa1.0_00021.1.g1466.t1	gb|EOA36155.1| hypothetical protein CARUB_v10009948mg [Capsella rubella]	337	282	1.00E-119	83.7	66.2	71.5	hypothetical protein CARUB_v10009948mg	gbpln	Capsella rubella	AT1G28100.2 | Symbols: | unknown protein; Has 64 Blast hits to 64 proteins in 27 species: Archae - 0; Bacteria - 14; Metazoa - 0; Fungi - 6; Plants - 42; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:9802120-9803981 FORWARD LENGTH=282	337	282	1.00E-121	83.7	66.2	71.8
Rsa1.0_00021.1.g1467.t1	gb|EOA37308.1| hypothetical protein CARUB_v10010972mg [Capsella rubella]	428	459	0	107.2	94.6	97.0	hypothetical protein CARUB_v10010972mg	gbpln	Capsella rubella	AT1G28110.2 | Symbols: SCPL45 | serine carboxypeptidase-like 45 | chr1:9804153-9806832 REVERSE LENGTH=461	428	461	0	107.7	93.7	96.5
Rsa1.0_00021.1.g1468.t1	#	#	#	#	#	#	#	-	----	----	AT1G30890.2 | Symbols: | Integral membrane HRF1 family protein | chr1:10994890-10995999 FORWARD LENGTH=269	231	269	1.00E-12	116.5	13.4	13.9
Rsa1.0_00021.1.g1469.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00021.1.g1470.t1	gb|EOA36105.1| hypothetical protein CARUB_v10011293mg [Capsella rubella]	595	608	0	102.2	94.3	98.2	hypothetical protein CARUB_v10011293mg	gbpln	Capsella rubella	AT1G28130.1 | Symbols: GH3.17 | Auxin-responsive GH3 family protein | chr1:9825431-9827883 FORWARD LENGTH=609	595	609	0	102.4	94.1	98.7
Rsa1.0_00021.1.g1471.t3	gb|AAG51484.1|AC069471_15 unknown protein [Arabidopsis thaliana]	292	295	1.00E-122	101.0	80.1	87.0	unknown protein	gbpln	Arabidopsis thaliana	AT1G28140.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2301, transmembrane (InterPro:IPR019275); Has 140 Blast hits to 140 proteins in 72 species: Archae - 0; Bacteria - 86; Metazoa - 10; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr1:9833029-9834390 REVERSE LENGTH=280	292	280	1.00E-124	95.9	80.1	87.0
Rsa1.0_00021.1.g1472.t1	ref|NP_174138.1| ethylene-responsive transcription factor ERF087 [Arabidopsis thaliana] gi|75263257|sp|Q9FZ90.1|ERF87_ARATH RecName: Full=Ethylene-responsive transcription factor ERF087 gi|9795622|gb|AAF98440.1|AC021044_19 Hypothetical protein [Arabidopsis thaliana] gi|12323000|gb|AAG51490.1|AC069471_21 AP2 domain transcription factor, putative [Arabidopsis thaliana] gi|91805861|gb|ABE65659.1| ethylene-responsive element-binding family protein [Arabidopsis thaliana] gi|332192805|gb|AEE30926.1| ethylene-responsive transcription factor ERF087 [Arabidopsis thaliana]	242	245	1.00E-97	101.2	82.2	88.4	ethylene-responsive transcription factor ERF087	gbpln	Arabidopsis thaliana	AT1G28160.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:9839387-9840124 FORWARD LENGTH=245	242	245	1.00E-100	101.2	82.2	88.4

Rsa1.0_00021.1.g1473.t1	ref|XP_002893509.1| hypothetical protein ARALYDRAFT_890355 [Arabidopsis lyrata subsp. lyrata] gi|297339351|gb|EFH69768.1| hypothetical protein ARALYDRAFT_890355 [Arabidopsis lyrata subsp. lyrata]	315	263	1.00E−88	83.5	59.7	66.3	hypothetical protein ARALYDRAFT_890355	gbpln	Arabidopsis lyrata	AT1G28190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12340.1); Has 166 Blast hits to 162 proteins in 36 species: Archae − 0; Bacteria − 2; Metazoa − 15; Fungi − 5; Plants − 124; Viruses − 0; Other Eukaryotes − 20 (source: NCBI BLink). | chr1:9847015−9847815 REVERSE LENGTH=266	315	266	8.00E−89	84.4	54.6	60.3
Rsa1.0_00021.1.g1474.t1	ref|XP_002873866.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata] gi|297319703|gb|EFH50125.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata]	369	384	1.00E−79	104.1	51.2	64.8	hypothetical protein ARALYDRAFT_909803	gbpln	Arabidopsis lyrata	AT5G18160.1 | Symbols: | F−box and associated interaction domains−containing protein | chr5:6002770−6003909 FORWARD LENGTH=379	369	379	4.00E−56	102.7	38.2	54.2
Rsa1.0_00021.1.g1475.t1	ref|XP_002873866.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata] gi|297319703|gb|EFH50125.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata]	376	384	6.00E−53	102.1	39.4	52.7	hypothetical protein ARALYDRAFT_909803	gbpln	Arabidopsis lyrata	AT1G50870.1 | Symbols: | F−box and associated interaction domains−containing protein | chr1:18855147−18856337 FORWARD LENGTH=396	376	396	3.00E−37	105.3	31.1	44.4
Rsa1.0_00022.1.g1476.t1	dbj|BAJ33863.1| unnamed protein product [Thellungiella halophila]	101	196	9.00E−32	194.1	69.3	77.2	unnamed protein product	----	----	AT5G65060.1 | Symbols: MAF3, FCL3, AGL70 | K−box region and MADS−box transcription factor family protein | chr5:25987527−25991065 FORWARD LENGTH=196	101	196	1.00E−30	194.1	64.4	73.3
Rsa1.0_00022.1.g1477.t1	dbj|BAJ33863.1| unnamed protein product [Thellungiella halophila]	62	196	8.00E−24	316.1	88.7	95.2	unnamed protein product	----	----	AT5G65050.2 | Symbols: AGL31, MAF2 | AGAMOUS−like 31 | chr5:25982415−25985743 FORWARD LENGTH=178	62	178	7.00E−25	287.1	85.5	91.9
Rsa1.0_00022.1.g1478.t1	gb|EOA14245.1| hypothetical protein CARUB_v10027399mg [Capsella rubella]	115	114	3.00E−44	99.1	76.5	85.2	hypothetical protein CARUB_v10027399mg	gbpln	Capsella rubella	AT5G65040.1 | Symbols: | Protein of unknown function (DUF581) | chr5:25977864−25978350 REVERSE LENGTH=113	115	113	2.00E−45	98.3	75.7	84.3
Rsa1.0_00022.1.g1479.t1	#	#	#	#	#	#	#	−	----	----	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:6485617−6487009 REVERSE LENGTH=365	154	365	7.00E−12	237.0	28.6	39.0
Rsa1.0_00022.1.g1480.t1	gb|ABD47519.1| annexin 2 [Brassica juncea] gi|124001973|gb|ABM87935.1| annexin 2 [Brassica juncea]	316	316	1.00E−173	100.0	93.4	97.2	annexin 2	gbpln	Brassica juncea	AT5G65020.1 | Symbols: ANNAT2 | annexin 2 | chr5:25973915−25975554 FORWARD LENGTH=317	316	317	1.00E−170	100.3	89.9	96.2
Rsa1.0_00022.1.g1481.t1	gb|EOA15086.1| hypothetical protein CARUB_v10028454mg [Capsella rubella]	414	427	0	103.1	84.5	91.5	hypothetical protein CARUB_v10028454mg	gbpln	Capsella rubella	AT5G64970.1 | Symbols: | Mitochondrial substrate carrier family protein | chr5:25958806−25960443 REVERSE LENGTH=428	414	428	0	103.4	82.4	89.4
Rsa1.0_00022.1.g1482.t1	ref|NP_201301.1| cyclin−dependent kinase C−2 [Arabidopsis thaliana] gi|152013386|sp|Q8W4P1.2|CDKC2_ARATH RecName: Full=Cyclin−dependent kinase C−2; Short=CDKC;2 gi|13430444|gb|AAK25844.1|AF360134_1 putative cdc2 protein kinase [Arabidopsis thaliana] gi|8843760|dbj|BAA97308.1| cdc2−like protein kinase [Arabidopsis thaliana] gi|14532732|gb|AAK64067.1| putative cdc2 protein kinase [Arabidopsis thaliana] gi|332010592|gb|AED97975.1| cyclin−dependent kinase C−2 [Arabidopsis thaliana]	574	513	0	89.4	82.8	84.5	cyclin−dependent kinase C−2	gbpln	Arabidopsis thaliana	AT5G64960.1 | Symbols: CDKC2, CDKC;2 | cyclin dependent kinase group C2 | chr5:25955497−25958427 FORWARD LENGTH=513	574	513	0	89.4	82.8	84.5
Rsa1.0_00022.1.g1483.t1	ref|NP_569001.1| elicitor peptide 1 [Arabidopsis thaliana] gi|75180610|sp|Q9LV87.1|PEP1_ARATH RecName: Full=Elicitor peptide 1; Flags: Precursor gi|8843754|dbj|BAA97302.1| unnamed protein product [Arabidopsis thaliana] gi|17065508|gb|AAL32908.1| Unknown protein [Arabidopsis thaliana] gi|20148667|gb|AAM10224.1| unknown protein [Arabidopsis thaliana] gi|332010583|gb|AED97966.1| elicitor peptide 1 [Arabidopsis thaliana]	109	92	8.00E−20	84.4	53.2	67.9	elicitor peptide 1	gbpln	Arabidopsis thaliana	AT5G64900.1 | Symbols: PROPEP1, ATPEP1, PEP1 | precursor of peptide 1 | chr5:25937253−25937939 FORWARD LENGTH=92	109	92	1.00E−22	84.4	53.2	67.9

Rsa1.0_00022.1.g1484.t1	ref|XP_002866640.1| hypothetical protein ARALYDRAFT_496707 [Arabidopsis lyrata subsp. lyrata] gi|297312475|gb|EFH42899.1| hypothetical protein ARALYDRAFT_496707 [Arabidopsis lyrata subsp. lyrata]	471	479	0	101.7	89.6	95.5	hypothetical protein ARALYDRAFT_496707	gbpln	Arabidopsis lyrata	AT5G64870.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr5:25929776-25931308 REVERSE LENGTH=479	471	479	0	101.7	91.3	96.6
Rsa1.0_00022.1.g1485.t1	ref|NP_201291.1| 4-alpha-glucanotransferase-like protein [Arabidopsis thaliana] gi|75180614|sp|Q9LV91.1|DPE1_ARATH RecName: Full=4-alpha-glucanotransferase DPE1, chloroplastic/amyloplastic; AltName: Full=Amylomaltase; AltName: Full=Disproportionating enzyme; Short=D-enzyme; AltName: Full=Protein DISPROPORTIONATING ENZYME 1; Flags: Precursor gi|8843750|dbj|BAA97298.1| 4-alpha-glucanotransferase [Arabidopsis thaliana] gi|14335104|gb|AAK59831.1| AT5g64860/MXK3_9 [Arabidopsis thaliana] gi|19548067|gb|AAL87397.1| AT5g64860/MXK3_9 [Arabidopsis thaliana] gi|332010579|gb|AED97962.1| 4-alpha-glucanotransferase DPE1 [Arabidopsis thaliana]	94	576	2.00E-27	612.8	64.9	69.1	4-alpha-glucanotransferase-like protein	gbpln	Arabidopsis thaliana	AT5G64860.1 | Symbols: DPE1 | disproportionating enzyme | chr5:25925373-25928788 REVERSE LENGTH=576	94	576	4.00E-30	612.8	64.9	69.1
Rsa1.0_00022.1.g1486.t1	ref|XP_002864926.1| hypothetical protein ARALYDRAFT_496705 [Arabidopsis lyrata subsp. lyrata] gi|297310761|gb|EFH41185.1| hypothetical protein ARALYDRAFT_496705 [Arabidopsis lyrata subsp. lyrata]	119	114	4.00E-31	95.8	63.9	70.6	hypothetical protein ARALYDRAFT_496705	gbpln	Arabidopsis lyrata	AT5G64850.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: RPM1-interacting protein 4, defence response (InterPro:IPR008700); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G09960.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:25921585-25923038 FORWARD LENGTH=114	119	114	6.00E-33	95.8	58.0	63.9
Rsa1.0_00022.1.g1487.t1	ref|XP_002866638.1| ATGCN5 [Arabidopsis lyrata subsp. lyrata] gi|297312473|gb|EFH42897.1| ATGCN5 [Arabidopsis lyrata subsp. lyrata]	690	694	0	100.6	93.2	97.4	ATGCN5	gbpln	Arabidopsis lyrata	AT5G64840.1 | Symbols: GCN5, ATGCN5 | general control non-repressible 5 | chr5:25916956-25919693 REVERSE LENGTH=692	690	692	0	100.3	92.2	97.0
Rsa1.0_00022.1.g1488.t1	ref|XP_002866636.1| hypothetical protein ARALYDRAFT_332703 [Arabidopsis lyrata subsp. lyrata] gi|297312471|gb|EFH42895.1| hypothetical protein ARALYDRAFT_332703 [Arabidopsis lyrata subsp. lyrata]	143	149	7.00E-61	104.2	86.7	90.9	hypothetical protein ARALYDRAFT_332703	gbpln	Arabidopsis lyrata	AT5G64820.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16850.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:25913999-25914523 REVERSE LENGTH=145	143	145	1.00E-59	101.4	82.5	89.5
Rsa1.0_00022.1.g1489.t1	ref|XP_002864921.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297310756|gb|EFH41180.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	671	485	0	72.3	60.8	65.9	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT5G64790.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:25902713-25904559 FORWARD LENGTH=485	671	485	0	72.3	60.8	65.9
Rsa1.0_00022.1.g1490.t1	ref|NP_201282.1| uncharacterized protein [Arabidopsis thaliana] gi|75170417|sp|Q9FGF6.1|RGF9_ARATH RecName: Full=Root meristem growth factor 9; Short=AtRGF9; Flags: Precursor gi|10177208|dbj|BAB10310.1| unnamed protein product [Arabidopsis thaliana] gi|27311821|gb|AAO00876.1| unknown protein [Arabidopsis thaliana] gi|30102780|gb|AAP21308.1| At5g64770 [Arabidopsis thaliana] gi|332010566|gb|AED97949.1| uncharacterized protein AT5G64770 [Arabidopsis thaliana]	79	79	5.00E-25	100.0	72.2	83.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G64770.1 | Symbols: RGF9 | Encodes a root meristem growth factor (RGF). Belongs to a family of functionally redundant homologous peptides that are secreted, tyrosine-sulfated, and expressed mainly in the stem cell area and the innermost layer of central columella cells. RGFs are required for maintenance of the root stem cell niche and transit amplifying cell proliferation. Members of this family include: At5g60810 (RGF1), At1g13620 (RGF2), At2g04025 (RGF3), At3g30350 (RGF4), At5g51451 (RGF5), At4g16515 (RGF6), At3g02240 (RGF7), At2g03830 (RGF8) and At5g64770 (RGF9). | chr5:25897681-25898085 REVERSE LENGTH=79	79	79	8.00E-28	100.0	72.2	83.5

Rsa1.0_00022.1.g1491.t1	ref|XP_002864920.1| hypothetical protein ARALYDRAFT_496690 [Arabidopsis lyrata subsp. lyrata] gi|297310755|gb|EFH41179.1| hypothetical protein ARALYDRAFT_496690 [Arabidopsis lyrata subsp. lyrata]	380	392	1.00E-122	103.2	78.4	83.4	hypothetical protein ARALYDRAFT_496690	gbpln	Arabidopsis lyrata	AT5G64750.1 | Symbols: ABR1 | Integrase-type DNA-binding superfamily protein | chr5:25891679-25893656 FORWARD LENGTH=391	380	391	1.00E-118	102.9	77.1	81.6
Rsa1.0_00022.1.g1492.t1	ref|NP_201279.1| cellulose synthase A catalytic subunit 6 [UDP-forming] [Arabidopsis thaliana] gi|73917714|sp|Q94JQ6.2|CESA6_ARATH RecName: Full=Cellulose synthase A catalytic subunit 6 [UDP-forming]; Short=AtCesA6; AltName: Full=AraxCelA; AltName: Full=Isoxaben-resistant protein 2; AltName: Full=Protein PROCUSTE 1; AltName: Full=Protein QUILL gi|10177205|dbj|BAB10307.1| cellulose synthase catalytic subunit [Arabidopsis thaliana] gi|332010562|gb|AED97945.1| cellulose synthase A catalytic subunit 6 [UDP-forming] [Arabidopsis thaliana]	1079	1084	0	100.5	96.4	98.6	cellulose synthase A catalytic subunit 6	gbpln	Arabidopsis thaliana	AT5G64740.1 | Symbols: CESA6, IXR2, E112, PRC1 | cellulose synthase 6 | chr5:25881555-25886333 FORWARD LENGTH=1084	1079	1084	0	100.5	96.4	98.6
Rsa1.0_00022.1.g1493.t1	ref|XP_002864917.1| hypothetical protein ARALYDRAFT_919795 [Arabidopsis lyrata subsp. lyrata] gi|297310752|gb|EFH41176.1| hypothetical protein ARALYDRAFT_919795 [Arabidopsis lyrata subsp. lyrata]	721	860	0	119.3	64.9	80.0	hypothetical protein ARALYDRAFT_919795	gbpln	Arabidopsis lyrata	AT5G64710.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr5:25869368-25872092 FORWARD LENGTH=841	721	841	0	116.6	64.4	77.8
Rsa1.0_00022.1.g1494.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00022.1.g1495.t1	gb|EOA12539.1| hypothetical protein CARUB_v10026529mg [Capsella rubella]	440	400	4.00E-82	90.9	54.8	64.5	hypothetical protein CARUB_v10026529mg	gbpln	Capsella rubella	AT5G64690.1 | Symbols: | neurofilament triplet H protein-related | chr5:25862969-25864521 FORWARD LENGTH=344	440	344	3.00E-64	78.2	40.5	49.1
Rsa1.0_00022.1.g1496.t1	ref|NP_201273.1| uncharacterized protein [Arabidopsis thaliana] gi|30698059|ref|NP_851270.1| uncharacterized protein [Arabidopsis thaliana] gi|10178071|dbj|BAB11435.1| unnamed protein product [Arabidopsis thaliana] gi|26452974|dbj|BAC43563.1| unknown protein [Arabidopsis thaliana] gi|28973531|gb|AAO64090.1| unknown protein [Arabidopsis thaliana] gi|332010553|gb|AED97936.1| uncharacterized protein AT5G64680 [Arabidopsis thaliana] gi|332010554|gb|AED97937.1| uncharacterized protein AT5G64680 [Arabidopsis thaliana]	200	203	2.00E-43	101.5	50.0	63.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G64680.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:25854433-25855331 FORWARD LENGTH=203	200	203	9.00E-46	101.5	50.0	63.5
Rsa1.0_00022.1.g1497.t1	dbj|BAE44362.1| alpha-L-arabinofuranosidase [Raphanus sativus]	778	780	0	100.3	91.0	94.5	alpha-L-arabinofuranosidase	gbpln	Raphanus sativus	AT5G64570.1 | Symbols: XYL4, ATBXL4 | beta-D-xylosidase 4 | chr5:25810227-25813309 REVERSE LENGTH=784	778	784	0	100.8	89.5	94.2
Rsa1.0_00022.1.g1498.t2	ref|XP_002866621.1| hypothetical protein ARALYDRAFT_496668 [Arabidopsis lyrata subsp. lyrata] gi|297312456|gb|EFH42880.1| hypothetical protein ARALYDRAFT_496668 [Arabidopsis lyrata subsp. lyrata]	660	395	1.00E-155	59.8	45.0	49.4	hypothetical protein ARALYDRAFT_496668	gbpln	Arabidopsis lyrata	AT5G64560.1 | Symbols: MGT9, MRS2-2, ATMGT9 | magnesium transporter 9 | chr5:25807025-25809395 REVERSE LENGTH=394	660	394	1.00E-152	59.7	44.8	49.2
Rsa1.0_00022.1.g1499.t1	ref|XP_002866619.1| hypothetical protein ARALYDRAFT_358659 [Arabidopsis lyrata subsp. lyrata] gi|297312454|gb|EFH42878.1| hypothetical protein ARALYDRAFT_358659 [Arabidopsis lyrata subsp. lyrata]	574	1082	0	188.5	89.9	93.4	hypothetical protein ARALYDRAFT_358659	gbpln	Arabidopsis lyrata	AT5G64550.1 | Symbols: | loricrin-related | chr5:25801794-25803698 REVERSE LENGTH=634	574	634	0	110.5	89.2	93.7
Rsa1.0_00022.1.g1500.t1	ref|NP_201258.2| xylem NAC domain 1 [Arabidopsis thaliana] gi|26452583|dbj|BAC43376.1| unknown protein [Arabidopsis thaliana] gi|107738104|gb|ABF83636.1| At5g64530 [Arabidopsis thaliana] gi|332010530|gb|AED97913.1| xylem NAC domain 1 [Arabidopsis thaliana]	185	187	1.00E-88	101.1	89.7	94.6	xylem NAC domain 1	gbpln	Arabidopsis thaliana	AT5G64530.1 | Symbols: ANAC104, XND1 | xylem NAC domain 1 | chr5:25795360-25796699 FORWARD LENGTH=187	185	187	5.00E-91	101.1	89.7	94.6

Rsa1.0_00022.1.g1501.t1	ref|XP_002864749.1| hypothetical protein ARALYDRAFT_496339 [Arabidopsis lyrata subsp. lyrata] gi|297310584|gb|EFH41008.1| hypothetical protein ARALYDRAFT_496339 [Arabidopsis lyrata subsp. lyrata]	390	390	6.00E-90	100.0	48.7	62.6	hypothetical protein ARALYDRAFT_496339	gbpln	Arabidopsis lyrata	AT5G61720.1 | Symbols: | Protein of unknown function (DUF1216) | chr5:24801621-24803006 FORWARD LENGTH=390	390	390	5.00E-91	100.0	47.7	63.1
Rsa1.0_00022.1.g1502.t2	ref|XP_002864902.1| N-acylethanolamine amidohydrolase [Arabidopsis lyrata subsp. lyrata] gi|297310737|gb|EFH41161.1| N-acylethanolamine amidohydrolase [Arabidopsis lyrata subsp. lyrata]	632	607	0	96.0	81.2	88.9	N-acylethanolamine amidohydrolase	gbpln	Arabidopsis lyrata	AT5G64440.1 | Symbols: AtFAAH, FAAH | fatty acid amide hydrolase | chr5:25766229-25770260 FORWARD LENGTH=607	632	607	0	96.0	80.9	88.0
Rsa1.0_00022.1.g1503.t1	gb|EOA12745.1| hypothetical protein CARUB_v10028367mg [Capsella rubella]	486	503	0	103.5	77.2	84.0	hypothetical protein CARUB_v10028367mg	gbpln	Capsella rubella	AT5G64430.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr5:25762540-25764081 REVERSE LENGTH=513	486	513	1.00E-174	105.6	79.2	85.6
Rsa1.0_00022.1.g1504.t1	gb|EOA12796.1| hypothetical protein CARUB_v10025747mg [Capsella rubella]	178	1306	2.00E-37	733.7	41.6	47.8	hypothetical protein CARUB_v10025747mg	gbpln	Capsella rubella	AT5G64420.1 | Symbols: | DNA polymerase V family | chr5:25756416-25761122 FORWARD LENGTH=1306	178	1306	1.00E-39	733.7	40.4	47.2
Rsa1.0_00022.1.g1505.t1	gb|AAM64614.1| Isp4-like protein [Arabidopsis thaliana]	729	729	0	100.0	94.1	97.4	Isp4-like protein	gbpln	Arabidopsis thaliana	AT5G64410.1 | Symbols: ATOPT4, OPT4 | oligopeptide transporter 4 | chr5:25750921-25754974 REVERSE LENGTH=729	729	729	0	100.0	94.1	97.1
Rsa1.0_00022.1.g1506.t1	gb|EOA12386.1| hypothetical protein CARUB_v10026348mg [Capsella rubella] gi|482548193|gb|EOA12387.1| hypothetical protein CARUB_v10026348mg [Capsella rubella]	381	469	1.00E-138	123.1	74.3	82.7	hypothetical protein CARUB_v10026348mg	gbpln	Capsella rubella	AT5G64360.4 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:25737208-25738602 REVERSE LENGTH=464	381	464	1.00E-132	121.8	73.2	80.8
Rsa1.0_00022.1.g1507.t1	dbj|BAB11643.1| unnamed protein product [Arabidopsis thaliana]	675	711	0	105.3	54.5	67.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G37210.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:14729225-14731508 REVERSE LENGTH=677	675	677	0	100.3	54.5	66.8
Rsa1.0_00022.1.g1508.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00022.1.g1509.t1	ref|XP_002866611.1| FK506-binding protein 12 kD [Arabidopsis lyrata subsp. lyrata] gi|297312446|gb|EFH42870.1| FK506-binding protein 12 kD [Arabidopsis lyrata subsp. lyrata]	126	112	3.00E-42	88.9	65.9	68.3	FK506-binding protein 12 kD	gbpln	Arabidopsis lyrata	AT5G64350.1 | Symbols: FKBP12, ATFKBP12 | FK506-binding protein 12 | chr5:25734810-25735990 REVERSE LENGTH=112	126	112	4.00E-43	88.9	64.3	65.9
Rsa1.0_00022.1.g1510.t1	dbj|BAJ34099.1| unnamed protein product [Thellungiella halophila]	270	329	6.00E-88	121.9	73.0	84.8	unnamed protein product	----	----	AT5G64340.1 | Symbols: SAC51 | sequence-specific DNA binding transcription factors;transcription regulators | chr5:25730890-25731936 REVERSE LENGTH=348	270	348	1.00E-87	128.9	74.8	85.6
Rsa1.0_00022.1.g1511.t1	gb|EOA12443.1| hypothetical protein CARUB_v10028516mg [Capsella rubella]	818	728	0	89.0	69.8	77.5	hypothetical protein CARUB_v10028516mg	gbpln	Capsella rubella	AT5G64320.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:25723247-25725439 REVERSE LENGTH=730	818	730	0	89.2	69.3	76.8
Rsa1.0_00022.1.g1512.t1	ref|NP_201233.1| dicarboxylate transporter 2.2 [Arabidopsis thaliana] gi|75171657|sp|Q9FMF8.1|DIT22_ARATH RecName: Full=Dicarboxylate transporter 2.2, chloroplastic; AltName: Full=AtpDCT2; Flags: Precursor gi|9759404|dbj|BAB09859.1| 2-oxoglutarate/malate translocator [Arabidopsis thaliana] gi|15028073|gb|AAK76567.1| putative 2-oxoglutarate/malate translocator protein [Arabidopsis thaliana] gi|22136830|gb|AAM91759.1| putative 2-oxoglutarate/malate translocator protein [Arabidopsis thaliana] gi|332010482|gb|AED97865.1| dicarboxylate transporter 2.2 [Arabidopsis thaliana]	558	549	0	98.4	85.8	91.9	dicarboxylate transporter 2.2	gbpln	Arabidopsis thaliana	AT5G64280.1 | Symbols: DiT2.2 | dicarboxylate transporter 2.2 | chr5:25711330-25713411 REVERSE LENGTH=549	558	549	0	98.4	85.8	91.9
Rsa1.0_00022.1.g1513.t1	gb|ABD65112.1| hypothetical protein 31.t00014 [Brassica oleracea]	102	122	8.00E-18	119.6	49.0	66.7	hypothetical protein 31.t00014	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00022.1.g1514.t1	dbj|BAJ33879.1| unnamed protein product [Thellungiella halophila]	301	304	2.33E-156	101.0	86.0	91.0	unnamed protein product	----	----	AT5G64260.1 | Symbols: EXL2 | EXORDIUM like 2 | chr5:25703980-25704897 FORWARD LENGTH=305	301	305	2.33E-156	101.3	84.1	90.0
Rsa1.0_00022.1.g1515.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	348	442	1.00E-136	127.0	69.0	77.9	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	348	343	1.00E-32	98.6	17.5	22.7

Rsa1.0_00022.1.g1516.t1	ref|NP_201229.1| metacaspase 3 [Arabidopsis thaliana] gi|75262715|sp|Q9FMG1.1|MCA3_ARATH RecName: Full=Metacaspase-3; Short=AtMC3; AltName: Full=Metacaspase 1a; Short=AtMCP1a gi|9759400|dbj|BAB09855.1| unnamed protein product [Arabidopsis thaliana] gi|21592565|gb|AAM64514.1| latex-abundant protein, putative [Arabidopsis thaliana] gi|27311579|gb|AAO00755.1| putative protein [Arabidopsis thaliana] gi|32482816|gb|AAP84708.1| metacaspase 3 [Arabidopsis thaliana] gi|34098865|gb|AAQ56815.1| At5g64240 [Arabidopsis thaliana] gi|332010477|gb|AED97860.1| metacaspase 3 [Arabidopsis thaliana]	386	362	1.00E-158	93.8	72.3	79.0	metacaspase 3	gbpln	Arabidopsis thaliana	AT5G64240.2 | Symbols: AtMC3, MC3 | metacaspase 3 | chr5:25695836-25697249 FORWARD LENGTH=362	386	362	1.00E-160	93.8	72.3	79.0
Rsa1.0_00022.1.g1517.t1	ref|XP_002870617.1| hypothetical protein ARALYDRAFT_916024 [Arabidopsis lyrata subsp. lyrata] gi|297316453|gb|EFH46876.1| hypothetical protein ARALYDRAFT_916024 [Arabidopsis lyrata subsp. lyrata]	679	704	0	103.7	76.4	86.7	hypothetical protein ARALYDRAFT_916024	gbpln	Arabidopsis lyrata	AT5G41770.1 | Symbols: | crooked neck protein, putative / cell cycle protein, putative | chr5:16718021-16720936 FORWARD LENGTH=705	679	705	0	103.8	76.7	86.9
Rsa1.0_00022.1.g1518.t1	ref|NP_568987.2| uncharacterized protein [Arabidopsis thaliana] gi|332010475|gb|AED97858.1| uncharacterized protein AT5G64230 [Arabidopsis thaliana]	371	379	1.00E-150	102.2	77.6	86.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G64230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G19920.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:25692572-25693909 FORWARD LENGTH=379	371	379	1.00E-153	102.2	77.6	86.0
Rsa1.0_00022.1.g1519.t1	ref|XP_002866597.1| hypothetical protein ARALYDRAFT_496610 [Arabidopsis lyrata subsp. lyrata] gi|297312432|gb|EFH42856.1| hypothetical protein ARALYDRAFT_496610 [Arabidopsis lyrata subsp. lyrata]	113	118	2.00E-47	104.4	88.5	91.2	hypothetical protein ARALYDRAFT_496610	gbpln	Arabidopsis lyrata	AT5G64130.1 | Symbols: | cAMP-regulated phosphoprotein 19-related protein | chr5:25664547-25665339 REVERSE LENGTH=115	113	115	5.00E-50	101.8	87.6	90.3
Rsa1.0_00022.1.g1520.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00022.1.g1521.t1	gb|EOA13703.1| hypothetical protein CARUB_v10026774mg [Capsella rubella]	328	328	1.00E-163	100.0	86.3	91.8	hypothetical protein CARUB_v10026774mg	gbpln	Capsella rubella	AT5G64120.1 | Symbols: | Peroxidase superfamily protein | chr5:25659551-25660946 REVERSE LENGTH=328	328	328	1.00E-163	100.0	84.8	91.5
Rsa1.0_00023.1.g1522.t2	ref|NP_564728.3| WD40 and Beach domain-containing protein [Arabidopsis thaliana] gi|332195397|gb|AEE33518.1| WD40 and Beach domain-containing protein [Arabidopsis thaliana]	2615	2604	0	99.6	90.6	94.7	WD40 and Beach domain-containing protein	gbpln	Arabidopsis thaliana	AT1G58230.1 | Symbols: | binding | chr1:21566331-21578865 FORWARD LENGTH=2604	2615	2604	0	99.6	90.6	94.7
Rsa1.0_00023.1.g1523.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1524.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1525.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	553	704	1.00E-104	127.3	32.7	34.4	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1526.t1	gb|ABD65073.1| hypothetical protein 27.t00059 [Brassica oleracea]	334	341	7.00E-21	102.1	14.4	17.4	hypothetical protein 27.t00059	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1527.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	508	1274	1.00E-131	250.8	51.0	63.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	508	575	1.00E-61	113.2	32.1	49.0
Rsa1.0_00023.1.g1528.t1	gb|AAG50957.1|AC073943_7 hypothetical protein [Arabidopsis thaliana]	940	1195	0	127.1	80.4	87.1	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G58210.1 | Symbols: EMB1674 | kinase interacting family protein | chr1:21553621-21558056 FORWARD LENGTH=1246	940	1246	0	132.6	79.9	86.7
Rsa1.0_00023.1.g1529.t1	ref|XP_002886709.1| EMB1674 [Arabidopsis lyrata subsp. lyrata] gi|297332550|gb|EFH62968.1| EMB1674 [Arabidopsis lyrata subsp. lyrata]	271	1287	2.00E-63	474.9	52.8	64.2	EMB1674	gbpln	Arabidopsis lyrata	AT1G58210.1 | Symbols: EMB1674 | kinase interacting family protein | chr1:21553621-21558056 FORWARD LENGTH=1246	271	1246	2.00E-62	459.8	53.9	67.5

Rsa1.0_00023.1.g1530.t2	ref|XP_002888236.1| hypothetical protein ARALYDRAFT_475431 [Arabidopsis lyrata subsp. lyrata] gi|297334077|gb|EFH64495.1| hypothetical protein ARALYDRAFT_475431 [Arabidopsis lyrata subsp. lyrata]	618	671	0	108.6	84.1	89.8	hypothetical protein ARALYDRAFT_475431	gbpln	Arabidopsis lyrata	AT1G58200.2 | Symbols: MSL3 | MSCS-like 3 | chr1:21548370-21552488 REVERSE LENGTH=678	618	678	0	109.7	82.4	89.0
Rsa1.0_00023.1.g1531.t1	gb|AAG50756.1|AC079131_1 hypothetical protein [Arabidopsis thaliana]	831	1784	0	214.7	73.3	82.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G58190.1 | Symbols: AtRLP9, RLP9 | receptor like protein 9 | chr1:21540720-21544330 FORWARD LENGTH=932	831	932	0	112.2	73.3	82.4
Rsa1.0_00023.1.g1532.t1	gb|AAD15321.1| putative reverse transcriptase [Arabidopsis thaliana] gi|7270688|emb|CAB77850.1| putative reverse transcriptase [Arabidopsis thaliana]	358	839	2.00E-27	234.4	19.8	30.4	putative reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1533.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1534.t1	gb|EOA35530.1| hypothetical protein CARUB_v10020737mg [Capsella rubella]	290	290	1.00E-151	100.0	87.6	94.5	hypothetical protein CARUB_v10020737mg	gbpln	Capsella rubella	AT1G58180.4 | Symbols: BCA6 | beta carbonic anhydrase 6 | chr1:21538010-21539711 REVERSE LENGTH=290	290	290	1.00E-151	100.0	86.6	92.4
Rsa1.0_00023.1.g1535.t1	gb|EOA34327.1| hypothetical protein CARUB_v10021847mg [Capsella rubella]	420	422	0	100.5	86.4	91.4	hypothetical protein CARUB_v10021847mg	gbpln	Capsella rubella	AT1G58120.1 | Symbols: | BEST Arabidopsis thaliana protein match is: methyltransferases (TAIR:AT5G01710.1); Has 93 Blast hits to 93 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 92; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:21520962-21522224 FORWARD LENGTH=420	420	420	0	100.0	86.9	92.4
Rsa1.0_00023.1.g1536.t2	ref|XP_002888232.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334073|gb|EFH64491.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	359	372	1.00E-131	103.6	75.8	82.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G58110.2 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr1:21515919-21517374 REVERSE LENGTH=374	359	374	1.00E-133	104.2	76.0	82.7
Rsa1.0_00023.1.g1537.t2	ref|NP_191684.1| myb domain protein 17 [Arabidopsis thaliana] gi|6850892|emb|CAB71055.1| putative transcription factor (MYB17) [Arabidopsis thaliana] gi|41619302|gb|AAS10071.1| MYB transcription factor [Arabidopsis thaliana] gi|193885153|gb|ACF28390.1| At3g61250 [Arabidopsis thaliana] gi|332646658|gb|AEE80179.1| myb domain protein 17 [Arabidopsis thaliana]	436	299	3.00E-65	68.6	35.3	43.1	myb domain protein 17	gbpln	Arabidopsis thaliana	AT3G61250.1 | Symbols: AtMYB17, MYB17 | myb domain protein 17 | chr3:22671306-22672551 FORWARD LENGTH=299	436	299	8.00E-68	68.6	35.3	43.1
Rsa1.0_00023.1.g1538.t1	gb|EOA34940.1| hypothetical protein CARUB_v10020024mg [Capsella rubella]	576	592	0	102.8	68.8	77.3	hypothetical protein CARUB_v10020024mg	gbpln	Capsella rubella	AT1G58025.1 | Symbols: | DNA-binding bromodomain-containing protein | chr1:21458219-21461757 REVERSE LENGTH=572	576	572	0	99.3	67.7	76.2
Rsa1.0_00023.1.g1539.t1	ref|XP_002879419.1| hypothetical protein ARALYDRAFT_902347 [Arabidopsis lyrata subsp. lyrata] gi|297325258|gb|EFH55678.1| hypothetical protein ARALYDRAFT_902347 [Arabidopsis lyrata subsp. lyrata]	173	336	2.00E-33	194.2	56.1	65.9	hypothetical protein ARALYDRAFT_902347	gbpln	Arabidopsis lyrata	AT2G32820.1 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr2:13926037-13926786 FORWARD LENGTH=249	173	249	3.00E-35	143.9	56.1	71.7
Rsa1.0_00023.1.g1540.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1541.t1	ref|NP_176081.1| uncharacterized protein [Arabidopsis thaliana] gi|42571907|ref|NP_974044.1| uncharacterized protein [Arabidopsis thaliana] gi|12321352|gb|AAG50748.1|AC079733_16 hypothetical protein [Arabidopsis thaliana] gi|18176030|gb|AAL59971.1| unknown protein [Arabidopsis thaliana] gi|22136846|gb|AAM91767.1| unknown protein [Arabidopsis thaliana] gi|332195330|gb|AEE33451.1| uncharacterized protein AT1G57680 [Arabidopsis thaliana] gi|332195331|gb|AEE33452.1| uncharacterized protein AT1G57680 [Arabidopsis thaliana]	354	362	1.00E-159	102.3	87.6	93.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G57680.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031277 (InterPro:IPR016971); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:21362749-21363837 REVERSE LENGTH=362	354	362	1.00E-161	102.3	87.6	93.8
Rsa1.0_00023.1.g1542.t1	ref|NP_176083.2| protein kinase-like protein [Arabidopsis thaliana] gi|332195333|gb|AEE33454.1| protein kinase-like protein [Arabidopsis thaliana]	683	692	0	101.3	84.6	91.1	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G57700.1 | Symbols: | Protein kinase superfamily protein | chr1:21371051-21373860 FORWARD LENGTH=692	683	692	0	101.3	84.6	91.1

Rsa1.0_00023.1.g1543.t1	ref|NP_176084.1| elongation factor EF-1 gamma subunit [Arabidopsis thaliana] gi|79320145|ref|NP_001031202.1| elongation factor EF-1 gamma subunit [Arabidopsis thaliana] gi|13626393|sp|Q9FVT2.1|EF1G2_ARATH RecName: Full=Probable elongation factor 1-gamma 2; Short=EF-1-gamma 2; AltName: Full=eEF-1B gamma 2 gi|12321359|gb|AAG50755.1|AC079733_23 elongation factor 1B gamma, putative [Arabidopsis thaliana] gi|13877603|gb|AAK43879.1|AF370502_1 Unknown protein [Arabidopsis thaliana] gi|15983511|gb|AAL11623.1|AF424630_1 At1g57720/T8L23_18 [Arabidopsis thaliana] gi|16226841|gb|AAL16277.1|AF428347_1 At1g57720/T8L23_18 [Arabidopsis thaliana] gi|17978699|gb|AAL47343.1| unknown protein [Arabidopsis thaliana] gi|21360471|gb|AAM47351.1| At1g57720/T8L23_18 [Arabidopsis thaliana] gi|21553395|gb|AAM62488.1| elongation factor 1B gamma, putative [Arabidopsis thaliana] gi|24030437|gb|AAN41373.1| putative elongation factor 1B gamma [Arabidopsis thaliana] gi|332195334|gb|AEE33455.1| elongation factor EF-1 gamma subunit [Arabidopsis thaliana] gi|332195335|gb|AEE33456.1| elongation factor EF-1 gamma subunit	413	413	0	100.0	93.0	96.6	elongation factor EF-1 gamma subunit	gbpln	Arabidopsis thaliana	AT1G57720.2 | Symbols: | Translation elongation factor EF1B, gamma chain | chr1:21377873-21380114 FORWARD LENGTH=413	413	413	0	100.0	93.0	96.6
Rsa1.0_00023.1.g1544.t1	gb|AAC97237.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	107	889	3.00E-30	830.8	55.1	71.0	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1545.t1	ref|NP_187098.2| endoribonuclease [Arabidopsis thaliana] gi|332640566|gb|AEE74087.1| endoribonuclease [Arabidopsis thaliana]	379	718	1.00E-101	189.4	49.3	51.5	endoribonuclease	gbpln	Arabidopsis thaliana	AT3G04480.1 | Symbols: | endoribonucleases | chr3:1193988-1197320 REVERSE LENGTH=718	379	718	1.00E-104	189.4	49.3	51.5
Rsa1.0_00023.1.g1546.t1	ref|XP_002884447.1| hypothetical protein ARALYDRAFT_896485 [Arabidopsis lyrata subsp. lyrata] gi|297330287|gb|EFH60706.1| hypothetical protein ARALYDRAFT_896485 [Arabidopsis lyrata subsp. lyrata]	227	371	6.00E-28	163.4	31.7	39.2	hypothetical protein ARALYDRAFT_896485	gbpln	Arabidopsis lyrata	AT5G19170.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:6445245-6447305 FORWARD LENGTH=391	227	391	1.00E-24	172.2	25.6	35.2
Rsa1.0_00023.1.g1547.t1	ref|NP_564725.1| F-box protein [Arabidopsis thaliana] gi|75172668|sp|Q9FVS1.1|FBK23_ARATH RecName: Full=F-box/kelch-repeat protein At1g57790 gi|11079521|gb|AAG29231.1|AC079732_2 hypothetical protein [Arabidopsis thaliana] gi|20466201|gb|AAM20418.1| unknown protein [Arabidopsis thaliana] gi|30984578|gb|AAP42752.1| At1g57790 [Arabidopsis thaliana] gi|332195346|gb|AEE33467.1| F-box protein [Arabidopsis thaliana]	331	352	1.00E-134	106.3	68.6	82.5	F-box protein	gbpln	Arabidopsis thaliana	AT1G57790.1 | Symbols: | F-box family protein | chr1:21404578-21405636 REVERSE LENGTH=352	331	352	1.00E-136	106.3	68.6	82.5
Rsa1.0_00023.1.g1548.t1	gb|EOA25688.1| hypothetical protein CARUB_v10019041mg [Capsella rubella]	236	203	8.00E-67	86.0	52.5	59.3	hypothetical protein CARUB_v10019041mg	gbpln	Capsella rubella	AT2G03300.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr2:1003468-1004222 REVERSE LENGTH=203	236	203	8.00E-69	86.0	55.5	61.9
Rsa1.0_00023.1.g1549.t3	gb|AAF67380.1| Hypothetical protein T15F17.l [Arabidopsis thaliana]	998	1141	1.00E-158	114.3	27.4	32.3	Hypothetical protein T15F17.l	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	998	1262	1.00E-14	126.5	5.8	9.9
Rsa1.0_00023.1.g1550.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00023.1.g1551.t1	gb|EOA35713.1| hypothetical protein CARUB_v10020940mg [Capsella rubella]	215	215	1.00E-101	100.0	80.9	87.9	hypothetical protein CARUB_v10020940mg	gbpln	Capsella rubella	AT1G57620.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:21342863-21344581 FORWARD LENGTH=212	215	212	1.00E-102	98.6	82.3	90.2

Rsa1.0_00023.1.g1552.t1	ref|NP_176074.2| uncharacterized protein [Arabidopsis thaliana] gi|42571905|ref|NP_974043.1| uncharacterized protein [Arabidopsis thaliana] gi|17979163|gb|AAL49777.1| unknown protein [Arabidopsis thaliana] gi|332195320|gb|AEE33441.1| uncharacterized protein AT1G57610 [Arabidopsis thaliana] gi|332195321|gb|AEE33442.1| uncharacterized protein AT1G57610 [Arabidopsis thaliana]	292	293	1.00E-125	100.3	79.8	87.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G57610.2 | Symbols: | Protein of unknown function (DUF607) | chr1:21337449-21338412 REVERSE LENGTH=293	292	293	1.00E-128	100.3	79.8	87.3
Rsa1.0_00023.1.g1553.t1	gb|EOA35193.1| hypothetical protein CARUB_v10020343mg [Capsella rubella]	391	425	1.00E-167	108.7	73.1	80.8	hypothetical protein CARUB_v10020343mg	gbpln	Capsella rubella	AT1G57590.1 | Symbols: | Pectinacetylesterase family protein | chr1:21327458-21329707 REVERSE LENGTH=444	391	444	1.00E-164	113.6	71.1	79.8
Rsa1.0_00024.1.g1554.t1	gb|EOA13735.1| hypothetical protein CARUB_v10026813mg [Capsella rubella]	312	312	1.00E-162	100.0	89.4	94.2	hypothetical protein CARUB_v10026813mg	gbpln	Capsella rubella	AT5G57330.1 | Symbols: | Galactose mutarotase-like superfamily protein | chr5:23218392-23220664 FORWARD LENGTH=312	312	312	1.00E-163	100.0	88.1	93.6
Rsa1.0_00024.1.g1555.t1	gb|EOA15125.1| hypothetical protein CARUB_v10028500mg [Capsella rubella]	965	982	0	101.8	86.8	93.0	hypothetical protein CARUB_v10028500mg	gbpln	Capsella rubella	AT5G57320.1 | Symbols: VLN5 | villin, putative | chr5:23212690-23217549 FORWARD LENGTH=962	965	962	0	99.7	86.4	92.2
Rsa1.0_00024.1.g1556.t1	ref|XP_002866199.1| hypothetical protein ARALYDRAFT_918901 [Arabidopsis lyrata subsp. lyrata] gi|297312034|gb|EFH42458.1| hypothetical protein ARALYDRAFT_918901 [Arabidopsis lyrata subsp. lyrata]	120	120	2.00E-30	100.0	94.2	95.8	hypothetical protein ARALYDRAFT_918901	gbpln	Arabidopsis lyrata	AT5G57290.1 | Symbols: | 60S acidic ribosomal protein family | chr5:23207049-23207835 REVERSE LENGTH=120	120	120	2.00E-31	100.0	93.3	95.0
Rsa1.0_00024.1.g1557.t1	gb|EOA13062.1| hypothetical protein CARUB_v10026062mg [Capsella rubella]	269	646	8.00E-59	240.1	40.5	54.3	hypothetical protein CARUB_v10026062mg	gbpln	Capsella rubella	AT5G60250.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24252226-24254710 FORWARD LENGTH=655	269	655	2.00E-60	243.5	40.9	53.2
Rsa1.0_00024.1.g1558.t1	gb|EOA22836.1| hypothetical protein CARUB_v10003560mg [Capsella rubella]	162	406	2.00E-26	250.6	50.6	64.8	hypothetical protein CARUB_v10003560mg	gbpln	Capsella rubella	AT4G11000.1 | Symbols: | Ankyrin repeat family protein | chr4:6731020-6732464 FORWARD LENGTH=406	162	406	3.00E-28	250.6	48.8	64.2
Rsa1.0_00024.1.g1559.t1	emb|CAR63886.1| cytochrome P450 monooxygenase [Arabidopsis thaliana]	493	491	0	99.6	87.0	93.3	cytochrome P450 monooxygenase	gbpln	Arabidopsis thaliana	AT5G57220.1 | Symbols: CYP81F2 | cytochrome P450, family 81, subfamily F, polypeptide 2 | chr5:23187911-23189681 FORWARD LENGTH=491	493	491	0	99.6	86.6	93.1
Rsa1.0_00024.1.g1560.t1	gb|AAC33958.1| contains similarity to Zea mays embryogenesis transmembrane protein (GB:X97570) [Arabidopsis thaliana]	475	417	1.00E-142	87.8	56.6	68.0	contains similarity to Zea mays embryogenesis transmembrane protein (GB:X97570)	gbpln	Arabidopsis thaliana	AT4G11000.1 | Symbols: | Ankyrin repeat family protein | chr4:6731020-6732464 FORWARD LENGTH=406	475	406	1.00E-106	85.5	46.3	58.5
Rsa1.0_00024.1.g1561.t4	gb|EOA14132.1| hypothetical protein CARUB_v10027277mg [Capsella rubella]	259	160	6.00E-33	61.8	26.3	28.2	hypothetical protein CARUB_v10027277mg	gbpln	Capsella rubella	AT5G57230.1 | Symbols: | Thioredoxin superfamily protein | chr5:23190572-23191485 FORWARD LENGTH=160	259	160	2.00E-35	61.8	26.3	27.8
Rsa1.0_00024.1.g1562.t1	ref|XP_002864506.1| CYP81F2 [Arabidopsis lyrata subsp. lyrata] gi|297310341|gb|EFH40765.1| CYP81F2 [Arabidopsis lyrata subsp. lyrata]	493	497	0	100.8	89.9	94.5	CYP81F2	gbpln	Arabidopsis lyrata	AT5G57220.1 | Symbols: CYP81F2 | cytochrome P450, family 81, subfamily F, polypeptide 2 | chr5:23187911-23189681 FORWARD LENGTH=491	493	491	0	99.6	88.2	93.7
Rsa1.0_00024.1.g1563.t1	ref|XP_002864505.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310340|gb|EFH40764.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	594	590	0	99.3	91.2	95.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G57200.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr5:23177696-23180601 FORWARD LENGTH=591	594	591	0	99.5	89.9	93.8
Rsa1.0_00024.1.g1564.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00024.1.g1565.t1	ref|XP_002864503.1| hypothetical protein ARALYDRAFT_495815 [Arabidopsis lyrata subsp. lyrata] gi|297310338|gb|EFH40762.1| hypothetical protein ARALYDRAFT_495815 [Arabidopsis lyrata subsp. lyrata]	373	426	7.00E-94	114.2	63.5	77.2	hypothetical protein ARALYDRAFT_495815	gbpln	Arabidopsis lyrata	AT5G57180.2 | Symbols: CIA2 | chloroplast import apparatus 2 | chr5:23168393-23170763 FORWARD LENGTH=435	373	435	2.00E-95	116.6	63.3	77.5
Rsa1.0_00024.1.g1566.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00024.1.g1567.t1	ref|XP_002864502.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297310337|gb|EFH40761.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	244	247	1.00E-125	101.2	92.6	96.7	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT5G57150.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:23152361-23154872 FORWARD LENGTH=247	244	247	1.00E-127	101.2	92.6	96.7
Rsa1.0_00024.1.g1568.t1	ref|XP_002864501.1| ATPAP28/PAP28 [Arabidopsis lyrata subsp. lyrata] gi|297310336|gb|EFH40760.1| ATPAP28/PAP28 [Arabidopsis lyrata subsp. lyrata]	426	400	1.00E-172	93.9	69.2	76.5	ATPAP28/PAP28	gbpln	Arabidopsis lyrata	AT5G57140.1 | Symbols: ATPAP28, PAP28 | purple acid phosphatase 28 | chr5:23149926-23151370 FORWARD LENGTH=397	426	397	1.00E-171	93.2	68.5	75.6

Rsa1.0_00024.1.g1569.t1	gb|EOA13758.1| hypothetical protein CARUB_v10026851mg [Capsella rubella]	364	304	3.00E−79	83.5	54.9	65.7	hypothetical protein CARUB_v10026851mg	gbpln	Capsella rubella	AT5G57120.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: LisH dimerisation motif (InterPro:IPR006594), SRP40, C-terminal (InterPro:IPR007718); Has 101969 Blast hits to 55488 proteins in 2506 species: Archae − 424; Bacteria − 13843; Metazoa − 37674; Fungi − 9726; Plants − 4941; Viruses − 569; Other Eukaryotes − 34792 (source: NCBI BLink). | chr5:23122767−23124400 REVERSE LENGTH=330	364	330	4.00E−73	90.7	59.6	71.7
Rsa1.0_00024.1.g1570.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00024.1.g1571.t4	dbj|BAJ34212.1| unnamed protein product [Thellungiella halophila]	1131	1073	0	94.9	89.4	92.0	unnamed protein product	----	----	AT5G57110.2 | Symbols: ACA8, AT-ACA8 | autoinhibited Ca2+ −ATPase, isoform 8 | chr5:23109729−23116857 REVERSE LENGTH=1074	1131	1074	0	95.0	87.9	91.1
Rsa1.0_00024.1.g1572.t1	gb|EOA13053.1| hypothetical protein CARUB_v10026053mg [Capsella rubella]	636	655	0	103.0	95.0	97.5	hypothetical protein CARUB_v10026053mg	gbpln	Capsella rubella	AT5G57090.1 | Symbols: EIR1, WAV6, ATPIN2, PIN2, AGR, AGR1 | Auxin efflux carrier family protein | chr5:23100765−23104456 FORWARD LENGTH=647	636	647	0	101.7	91.5	95.1
Rsa1.0_00024.1.g1573.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00024.1.g1574.t1	ref|NP_200517.2| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|332009460|gb|AED96843.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	83	575	2.00E−27	692.8	72.3	80.7	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT5G57070.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:23096221−23097948 FORWARD LENGTH=575	83	575	3.00E−30	692.8	72.3	80.7
Rsa1.0_00024.1.g1575.t1	ref|NP_180929.1| DEAD-box ATP-dependent RNA helicase 21 [Arabidopsis thaliana] gi|75319077|sp|P93008.1|RH21_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 21 gi|1707017|gb|AAC69128.1| putative U5 small nuclear ribonucleoprotein, an RNA helicase [Arabidopsis thaliana] gi|17473908|gb|AAL38370.1| putative U5 small nuclear ribonucleoprotein, an RNA helicase [Arabidopsis thaliana] gi|20259792|gb|AAM13243.1| putative U5 small nuclear ribonucleoprotein, an RNA helicase [Arabidopsis thaliana] gi|330253781|gb|AEC08875.1| DEAD-box ATP-dependent RNA helicase 21 [Arabidopsis thaliana]	1187	733	7.00E−69	61.8	12.0	13.6	DEAD-box ATP-dependent RNA helicase 21	gbpln	Arabidopsis thaliana	AT2G33730.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:14265679−14267880 REVERSE LENGTH=733	1187	733	2.00E−71	61.8	12.0	13.6
Rsa1.0_00024.1.g1576.t1	dbj|BAA97357.1| unnamed protein product [Arabidopsis thaliana]	372	607	1.00E−101	163.2	72.6	81.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G57070.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:23096221−23097948 FORWARD LENGTH=575	372	575	1.00E−103	154.6	72.6	81.2
Rsa1.0_00024.1.g1577.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00024.1.g1578.t1	gb|EOA15144.1| hypothetical protein CARUB_v10028520mg [Capsella rubella]	420	435	0	103.6	91.0	94.8	hypothetical protein CARUB_v10028520mg	gbpln	Capsella rubella	AT5G57015.1 | Symbols: ckl12 | casein kinase I-like 12 | chr5:23071508−23074577 FORWARD LENGTH=435	420	435	0	103.6	90.5	94.5
Rsa1.0_00024.1.g1579.t1	gb|EOA13247.1| hypothetical protein CARUB_v10026276mg [Capsella rubella]	511	499	0	97.7	83.6	90.2	hypothetical protein CARUB_v10026276mg	gbpln	Capsella rubella	AT5G57010.1 | Symbols: | calmodulin-binding family protein | chr5:23068207−23070203 FORWARD LENGTH=495	511	495	0	96.9	83.8	89.6
Rsa1.0_00024.1.g1580.t1	gb|EOA14040.1| hypothetical protein CARUB_v10027175mg [Capsella rubella]	192	195	8.00E−64	101.6	72.9	81.8	hypothetical protein CARUB_v10027175mg	gbpln	Capsella rubella	AT5G57000.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G72690.1); Has 153 Blast hits to 116 proteins in 29 species: Archae − 0; Bacteria − 6; Metazoa − 33; Fungi − 7; Plants − 82; Viruses − 0; Other Eukaryotes − 25 (source: NCBI BLink). | chr5:23063870−23065203 REVERSE LENGTH=187	192	187	2.00E−56	97.4	68.8	77.6

Rsa1.0_00024.1.g1581.t1	ref|XP_002866176.1| AT5g56980/MHM17_10 [Arabidopsis lyrata subsp. lyrata] gi|297312011|gb|EFH42435.1| AT5g56980/MHM17_10 [Arabidopsis lyrata subsp. lyrata]	371	375	1.00E−150	101.1	82.5	88.9	AT5g56980/MHM17_10	gbpln	Arabidopsis lyrata	AT5G56980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G26130.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:23056574−23057713 REVERSE LENGTH=379	371	379	1.00E−149	102.2	83.6	88.7
Rsa1.0_00024.1.g1582.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	362	1486	3.00E−60	410.5	35.9	51.7	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae − 0; Bacteria − 0; Metazoa − 4; Fungi − 0; Plants − 703; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:7447690−7448403 REVERSE LENGTH=237	362	237	3.00E−22	65.5	14.6	25.1
Rsa1.0_00025.1.g1583.t1	ref|NP_565516.1| uncharacterized protein [Arabidopsis thaliana] gi|20198097|gb|AAM15398.1| Expressed protein [Arabidopsis thaliana] gi|88900416|gb|ABD57520.1| At2g21655 [Arabidopsis thaliana] gi|91806234|gb|ABE65845.1| unknown [Arabidopsis thaliana] gi|330252114|gb|AEC07208.1| uncharacterized protein AT2G21655 [Arabidopsis thaliana]	161	156	2.00E−28	96.9	37.3	58.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G21655.1 | Symbols: | Protein of unknown function (DUF784) | chr2:9263584−9264054 FORWARD LENGTH=156	161	156	8.00E−31	96.9	37.3	58.4
Rsa1.0_00025.1.g1584.t25	gb|AAG51069.1|AC069472_9 unknown protein; 47773−46410 [Arabidopsis thaliana] gi|15795151|dbj|BAB03139.1| unnamed protein product [Arabidopsis thaliana]	154	238	6.00E−50	154.5	66.9	70.8	unknown protein; 47773−46410	gbpln	Arabidopsis thaliana	AT3G12300.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF667 (InterPro:IPR007714); Has 373 Blast hits to 371 proteins in 116 species: Archae − 0; Bacteria − 0; Metazoa − 213; Fungi − 4; Plants − 71; Viruses − 0; Other Eukaryotes − 85 (source: NCBI BLink). | chr3:3921787−3923092 REVERSE LENGTH=190	154	190	9.00E−52	123.4	66.2	70.1
Rsa1.0_00025.1.g1585.t1	ref|XP_002868305.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314141|gb|EFH44564.1| binding protein [Arabidopsis lyrata subsp. lyrata]	494	502	0	101.6	71.1	81.6	binding protein	gbpln	Arabidopsis lyrata	AT4G14190.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:8183594−8185180 REVERSE LENGTH=501	494	501	0	101.4	72.5	81.6
Rsa1.0_00025.1.g1586.t1	ref|XP_002884895.1| complex 1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297330735|gb|EFH61154.1| complex 1 family protein [Arabidopsis lyrata subsp. lyrata]	133	133	2.00E−71	100.0	95.5	100.0	complex 1 family protein	gbpln	Arabidopsis lyrata	AT3G12260.1 | Symbols: | LYR family of Fe/S cluster biogenesis protein | chr3:3909252−3910337 REVERSE LENGTH=133	133	133	2.00E−73	100.0	94.7	99.2
Rsa1.0_00025.1.g1587.t2	ref|NP_566415.3| transcription factor TGA6 [Arabidopsis thaliana] gi|42572393|ref|NP_974292.1| transcription factor TGA6 [Arabidopsis thaliana] gi|44888355|sp|Q39140.2|TGA6_ARATH RecName: Full=Transcription factor TGA6; AltName: Full=bZIP transcription factor 45; Short=AtbZIP45 gi|12322056|gb|AAG51079.1|AC069472_19 transcription factor HBP−1B−like; 31032−33264 [Arabidopsis thaliana] gi|14571607|emb|CAC42807.1| transcription factor TGA6 [Arabidopsis thaliana] gi|119360085|gb|ABL66771.1| At3g12250 [Arabidopsis thaliana] gi|225898635|dbj|BAH30448.1| hypothetical protein [Arabidopsis thaliana] gi|332641651|gb|AEE75172.1| transcription factor TGA6 [Arabidopsis thaliana] gi|332641652|gb|AEE75173.1| transcription factor TGA6 [Arabidopsis thaliana]	321	330	1.00E−165	102.8	95.6	96.9	transcription factor TGA6	gbpln	Arabidopsis thaliana	AT3G12250.2 | Symbols: TGA6, BZIP45 | TGACG motif−binding factor 6 | chr3:3906351−3908583 FORWARD LENGTH=330	321	330	1.00E−167	102.8	95.6	96.9

Rsa1.0_00025.1.g1588.t1	ref|XP_002884894.1| hypothetical protein ARALYDRAFT_897434 [Arabidopsis lyrata subsp. lyrata] gi|297330734|gb|EFH61153.1| hypothetical protein ARALYDRAFT_897434 [Arabidopsis lyrata subsp. lyrata]	711	435	1.00E-132	61.2	34.9	40.2	hypothetical protein ARALYDRAFT_897434	gbpln	Arabidopsis lyrata	AT3G12240.1 | Symbols: SCPL15 | serine carboxypeptidase-like 15 | chr3:3902436-3904918 REVERSE LENGTH=436	711	436	1.00E-134	61.3	35.0	39.2
Rsa1.0_00025.1.g1589.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00025.1.g1590.t6	ref|XP_002884894.1| hypothetical protein ARALYDRAFT_897434 [Arabidopsis lyrata subsp. lyrata] gi|297330734|gb|EFH61153.1| hypothetical protein ARALYDRAFT_897434 [Arabidopsis lyrata subsp. lyrata]	983	435	1.00E-177	44.3	31.4	36.1	hypothetical protein ARALYDRAFT_897434	gbpln	Arabidopsis lyrata	AT3G12240.1 | Symbols: SCPL15 | serine carboxypeptidase-like 15 | chr3:3902436-3904918 REVERSE LENGTH=436	983	436	1.00E-177	44.4	31.0	36.1
Rsa1.0_00025.1.g1591.t2	ref|XP_002884892.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330732|gb|EFH61151.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	530	570	0	107.5	81.1	87.4	kinase family protein	gbpln	Arabidopsis lyrata	AT3G12200.1 | Symbols: AtNek7, Nek7 | NIMA-related kinase 7 | chr3:3887173-3890550 REVERSE LENGTH=571	530	571	0	107.7	81.3	87.4
Rsa1.0_00025.1.g1592.t1	ref|XP_002882768.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297328608|gb|EFH59027.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	396	262	1.00E-123	66.2	56.1	60.4	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT3G12170.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr3:3881021-3882655 FORWARD LENGTH=262	396	262	1.00E-125	66.2	55.6	60.4
Rsa1.0_00025.1.g1593.t1	ref|NP_187823.1| RAB GTPase-like protein A4D [Arabidopsis thaliana] gi|297834018|ref|XP_002884891.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|75334990|sp|Q9LH50.1|RAA4D_ARATH RecName: Full=Ras-related protein RABA4d; Short=AtRABA4d gi|12322042|gb|AAG51065.1|AC069472_5 ras-related GTP-binding protein; 5118-4176 [Arabidopsis thaliana] gi|9294115|dbj|BAB01966.1| GTP-binding protein-like [Arabidopsis thaliana] gi|67633628|gb|AAY78738.1| Ras-related GTP-binding family protein [Arabidopsis thaliana] gi|297330731|gb|EFH61150.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|332641639|gb|AEE75160.1| RAB GTPase-like protein A4D [Arabidopsis thaliana] gi|482567210|gb|EOA31399.1| hypothetical protein CARUB_v10014578mg [Capsella rubella]	222	222	1.00E-125	100.0	97.7	99.5	RAB GTPase-like protein A4D	gbpln	Arabidopsis lyrata	AT3G12160.1 | Symbols: ATRABA4D, RABA4D | RAB GTPase homolog A4D | chr3:3879495-3880437 REVERSE LENGTH=222	222	222	1.00E-128	100.0	97.7	99.5
Rsa1.0_00025.1.g1594.t1	gb|ACX42230.1| polygalacturonase inhibitory protein [Brassica rapa subsp. oleifera]	325	325	1.00E-169	100.0	93.2	97.5	polygalacturonase inhibitory protein	gbpln	Brassica rapa	AT3G12145.1 | Symbols: FLR1, FLOR1 | Leucine-rich repeat (LRR) family protein | chr3:3874764-3876075 REVERSE LENGTH=325	325	325	1.00E-152	100.0	80.3	89.2
Rsa1.0_00025.1.g1595.t1	gb|AAF63175.1|AC010657_11 T5E21.11 [Arabidopsis thaliana]	141	1115	2.00E-36	790.8	58.2	66.7	T5E21.11	gbpln	Arabidopsis thaliana	AT1G14610.1 | Symbols: TWN2, VALRS | valyl-tRNA synthetase / valine--tRNA ligase (VALRS) | chr1:5008502-5014486 REVERSE LENGTH=1108	141	1108	2.00E-38	785.8	56.7	65.2
Rsa1.0_00025.1.g1596.t1	gb|EOA31025.1| hypothetical protein CARUB_v10014171mg [Capsella rubella]	328	327	1.00E-149	99.7	86.3	91.2	hypothetical protein CARUB_v10014171mg	gbpln	Capsella rubella	AT3G12140.2 | Symbols: | Emsy N Terminus (ENT)/ plant Tudor-like domains-containing protein | chr3:3868947-3870964 REVERSE LENGTH=327	328	327	1.00E-151	99.7	86.0	90.9
Rsa1.0_00025.1.g1597.t1	dbj|BAJ34617.1| unnamed protein product [Thellungiella halophila]	258	244	1.00E-115	94.6	89.9	92.2	unnamed protein product	----	----	AT3G12130.1 | Symbols: | KH domain-containing protein / zinc finger (CCCH type) family protein | chr3:3864486-3866406 REVERSE LENGTH=248	258	248	1.00E-112	96.1	85.7	91.9
Rsa1.0_00025.1.g1598.t1	gb|AFC41106.1| FAD2-1 [Brassica oleracea]	386	384	0	99.5	90.2	95.9	FAD2-1	gbpln	Brassica oleracea	AT3G12120.2 | Symbols: FAD2 | fatty acid desaturase 2 | chr3:3860592-3861743 REVERSE LENGTH=383	386	383	0	99.2	85.0	92.5
Rsa1.0_00025.1.g1599.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	841	657	0	78.1	43.0	53.3	T14P8.10	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	841	626	4.00E-83	74.4	17.8	25.9
Rsa1.0_00025.1.g1600.t1	dbj|BAB01957.1| senescence-associated protein-like [Arabidopsis thaliana]	282	270	1.00E-141	95.7	88.7	93.6	senescence-associated protein-like	gbpln	Arabidopsis thaliana	AT3G12090.1 | Symbols: TET6 | tetraspanin6 | chr3:3852326-3853714 REVERSE LENGTH=282	282	282	1.00E-143	100.0	92.9	97.9

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<tr><td>Rsa1.0_00025.1.g1601.t1</td><td>ref|XP_002882764.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328604|gb|EFH59023.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>524</td><td>559</td><td>0</td><td>106.7</td><td>75.8</td><td>85.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G12060.1 | Symbols: TBL1 | Plant protein of unknown function (DUF828) | chr3:3843142-3845150 FORWARD LENGTH=556</td><td>524</td><td>556</td><td>0</td><td>106.1</td><td>74.8</td><td>84.9</td></tr>
<tr><td>Rsa1.0_00025.1.g1602.t1</td><td>ref|XP_002871226.1| hypothetical protein ARALYDRAFT_908596 [Arabidopsis lyrata subsp. lyrata] gi|297317063|gb|EFH47485.1| hypothetical protein ARALYDRAFT_908596 [Arabidopsis lyrata subsp. lyrata]</td><td>196</td><td>196</td><td>8.00E-96</td><td>100.0</td><td>93.9</td><td>98.0</td><td>hypothetical protein ARALYDRAFT_908596</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G06660.1 | Symbols: | Protein of unknown function DUF106, transmembrane | chr5:2046863-2047453 FORWARD LENGTH=196</td><td>196</td><td>196</td><td>7.00E-98</td><td>100.0</td><td>93.9</td><td>98.0</td></tr>
<tr><td>Rsa1.0_00025.1.g1603.t1</td><td>gb|ABO14927.1| male sterility 2 [Brassica rapa subsp. chinensis]</td><td>610</td><td>616</td><td>0</td><td>101.0</td><td>95.9</td><td>97.7</td><td>male sterility 2</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G11980.1 | Symbols: MS2, FAR2 | Jojoba acyl CoA reductase-related male sterility protein | chr3:3814484-3816927 FORWARD LENGTH=616</td><td>610</td><td>616</td><td>0</td><td>101.0</td><td>90.5</td><td>95.4</td></tr>
<tr><td>Rsa1.0_00025.1.g1604.t1</td><td>ref|NP_187803.4| RNA binding protein [Arabidopsis thaliana] gi|332641610|gb|AEE75131.1| RNA binding protein [Arabidopsis thaliana]</td><td>1913</td><td>1896</td><td>0</td><td>99.1</td><td>84.9</td><td>91.2</td><td>RNA binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G11964.1 | Symbols: | RNA binding;RNA binding | chr3:3793957-3806626 REVERSE LENGTH=1896</td><td>1913</td><td>1896</td><td>0</td><td>99.1</td><td>84.9</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00025.1.g1605.t1</td><td>gb|EOA31455.1| hypothetical protein CARUB_v10014641mg [Capsella rubella]</td><td>207</td><td>207</td><td>1.00E-114</td><td>100.0</td><td>97.1</td><td>98.6</td><td>hypothetical protein CARUB_v10014641mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G37270.2 | Symbols: ATRPS5B, RPS5B | ribosomal protein 5B | chr2:15647883-15649042 REVERSE LENGTH=207</td><td>207</td><td>207</td><td>1.00E-116</td><td>100.0</td><td>96.1</td><td>99.0</td></tr>
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<tr><td>Rsa1.0_00025.1.g1608.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00025.1.g1609.t2</td><td>ref|XP_002882755.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328595|gb|EFH59014.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>612</td><td>629</td><td>0</td><td>102.8</td><td>73.0</td><td>80.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11920.1 | Symbols: | glutaredoxin-related | chr3:3772311-3774887 FORWARD LENGTH=630</td><td>612</td><td>630</td><td>0</td><td>102.9</td><td>72.5</td><td>79.7</td></tr>
<tr><td>Rsa1.0_00025.1.g1610.t1</td><td>ref|NP_187791.1| uncharacterized protein [Arabidopsis thaliana] gi|42572387|ref|NP_974289.1| uncharacterized protein [Arabidopsis thaliana] gi|6671941|gb|AAF23201.1|AC016795_14 hypothetical protein [Arabidopsis thaliana] gi|20466598|gb|AAM20616.1| unknown protein [Arabidopsis thaliana] gi|22136430|gb|AAM91293.1| unknown protein [Arabidopsis thaliana] gi|332641587|gb|AEE75108.1| uncharacterized protein AT3G11850 [Arabidopsis thaliana] gi|332641588|gb|AEE75109.1| uncharacterized protein AT3G11850 [Arabidopsis thaliana]</td><td>410</td><td>504</td><td>1.00E-106</td><td>122.9</td><td>58.3</td><td>71.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G11850.2 | Symbols: | Protein of unknown function, DUF593 | chr3:3739222-3741101 REVERSE LENGTH=504</td><td>410</td><td>504</td><td>1.00E-109</td><td>122.9</td><td>58.3</td><td>71.7</td></tr>
<tr><td>Rsa1.0_00025.1.g1611.t1</td><td>ref|NP_566402.1| plant U-box 24 protein [Arabidopsis thaliana] gi|332641586|gb|AEE75107.1| E3 ubiquitin-protein ligase PUB24 [Arabidopsis thaliana]</td><td>447</td><td>470</td><td>0</td><td>105.1</td><td>76.5</td><td>88.6</td><td>plant U-box 24 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G11840.1 | Symbols: PUB24 | plant U-box 24 | chr3:3736578-3738250 REVERSE LENGTH=470</td><td>447</td><td>470</td><td>0</td><td>105.1</td><td>76.5</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00025.1.g1612.t1</td><td>ref|NP_187789.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana] gi|6671939|gb|AAF23199.1|AC016795_12 putative T-complex protein 1, ETA subunit [Arabidopsis thaliana] gi|17979243|gb|AAL49938.1| AT3g11830/F26K24_12 [Arabidopsis thaliana] gi|20857172|gb|AAM26704.1| AT3g11830/F26K24_12 [Arabidopsis thaliana] gi|332641584|gb|AEE75105.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]</td><td>548</td><td>557</td><td>0</td><td>101.6</td><td>94.7</td><td>95.4</td><td>TCP-1/cpn60 chaperonin family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G11830.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:3732734-3736156 FORWARD LENGTH=557</td><td>548</td><td>557</td><td>0</td><td>101.6</td><td>94.7</td><td>95.4</td></tr>
<tr><td>Rsa1.0_00025.1.g1613.t1</td><td>ref|XP_002884864.1| hypothetical protein ARALYDRAFT_897381 [Arabidopsis lyrata subsp. lyrata] gi|297330704|gb|EFH61123.1| hypothetical protein ARALYDRAFT_897381 [Arabidopsis lyrata subsp. lyrata]</td><td>235</td><td>200</td><td>7.00E-97</td><td>85.1</td><td>74.0</td><td>78.3</td><td>hypothetical protein ARALYDRAFT_897381</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11770.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr3:3721490-3722092 REVERSE LENGTH=200</td><td>235</td><td>200</td><td>3.00E-98</td><td>85.1</td><td>72.8</td><td>77.4</td></tr>
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<tr><td>Rsa1.0_00025.1.g1615.t1</td><td>ref|XP_002884863.1| hypothetical protein ARALYDRAFT_478521 [Arabidopsis lyrata subsp. lyrata] gi|297330703|gb|EFH61122.1| hypothetical protein ARALYDRAFT_478521 [Arabidopsis lyrata subsp. lyrata]</td><td>153</td><td>146</td><td>2.00E-60</td><td>95.4</td><td>77.8</td><td>86.3</td><td>hypothetical protein ARALYDRAFT_478521</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11750.1 | Symbols: FOLB1 | Dihydroneopterin aldolase | chr3:3715071-3715904 REVERSE LENGTH=146</td><td>153</td><td>146</td><td>1.00E-61</td><td>95.4</td><td>76.5</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00025.1.g1616.t1</td><td>ref|XP_002882745.1| hypothetical protein ARALYDRAFT_478520 [Arabidopsis lyrata subsp. lyrata] gi|297328585|gb|EFH59004.1| hypothetical protein ARALYDRAFT_478520 [Arabidopsis lyrata subsp. lyrata]</td><td>194</td><td>193</td><td>5.00E-99</td><td>99.5</td><td>88.7</td><td>95.4</td><td>hypothetical protein ARALYDRAFT_478520</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11740.1 | Symbols: | Protein of unknown function (DUF567) | chr3:3712427-3713389 FORWARD LENGTH=194</td><td>194</td><td>194</td><td>1.00E-100</td><td>100.0</td><td>87.6</td><td>95.4</td></tr>
<tr><td>Rsa1.0_00025.1.g1617.t1</td><td>ref|NP_187779.1| Ras-related protein RABD1 [Arabidopsis thaliana] gi|75338904|sp|Q9ZRE2.1|RABD1_ARATH RecName: Full=Ras-related protein RABD1; Short=AtRABD1; AltName: Full=Ras-related protein ATFP8 gi|6671929|gb|AAF23189.1|AC016795_2 putative GTP-binding protein (ATFP8) [Arabidopsis thaliana] gi|4097557|gb|AAD00111.1| ATFP8 [Arabidopsis thaliana] gi|26451349|dbj|BAC42775.1| putative GTP-binding protein ATFP8 [Arabidopsis thaliana] gi|28973343|gb|AAO63996.1| putative GTP-binding protein (ATFP8) [Arabidopsis thaliana] gi|332641569|gb|AEE75090.1| Ras-related protein RABD1 [Arabidopsis thaliana]</td><td>206</td><td>205</td><td>1.00E-109</td><td>99.5</td><td>93.2</td><td>95.6</td><td>Ras-related protein RABD1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G11730.1 | Symbols: ATFP8, ATRABD1, RABD1 | Ras-related small GTP-binding family protein | chr3:3709490-3711397 REVERSE LENGTH=205</td><td>206</td><td>205</td><td>1.00E-112</td><td>99.5</td><td>93.2</td><td>95.6</td></tr>
<tr><td>Rsa1.0_00025.1.g1618.t1</td><td>ref|XP_002884859.1| hypothetical protein ARALYDRAFT_478516 [Arabidopsis lyrata subsp. lyrata] gi|297330699|gb|EFH61118.1| hypothetical protein ARALYDRAFT_478516 [Arabidopsis lyrata subsp. lyrata]</td><td>605</td><td>625</td><td>0</td><td>103.3</td><td>90.9</td><td>95.0</td><td>hypothetical protein ARALYDRAFT_478516</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11710.1 | Symbols: ATKRS-1 | lysyl-tRNA synthetase 1 | chr3:3702359-3705613 REVERSE LENGTH=626</td><td>605</td><td>626</td><td>0</td><td>103.5</td><td>87.9</td><td>93.9</td></tr>
<tr><td>Rsa1.0_00025.1.g1619.t1</td><td>gb|EOA30537.1| hypothetical protein CARUB_v10013670mg [Capsella rubella]</td><td>443</td><td>457</td><td>0</td><td>103.2</td><td>91.6</td><td>94.4</td><td>hypothetical protein CARUB_v10013670mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G11700.1 | Symbols: FLA18 | FASCICLIN-like arabinogalactan protein 18 precursor | chr3:3698992-3700971 FORWARD LENGTH=462</td><td>443</td><td>462</td><td>0</td><td>104.3</td><td>92.3</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00025.1.g1620.t1</td><td>ref|XP_002882743.1| hypothetical protein ARALYDRAFT_478514 [Arabidopsis lyrata subsp. lyrata] gi|297328583|gb|EFH59002.1| hypothetical protein ARALYDRAFT_478514 [Arabidopsis lyrata subsp. lyrata]</td><td>259</td><td>251</td><td>3.00E-80</td><td>96.9</td><td>74.9</td><td>83.4</td><td>hypothetical protein ARALYDRAFT_478514</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11690.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G06380.1); Has 84 Blast hits to 84 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 84; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3695484-3696242 FORWARD LENGTH=252</td><td>259</td><td>252</td><td>2.00E-77</td><td>97.3</td><td>69.5</td><td>76.4</td></tr>
<tr><td>Rsa1.0_00025.1.g1621.t1</td><td>gb|EOA32513.1| hypothetical protein CARUB_v10015793mg [Capsella rubella]</td><td>500</td><td>487</td><td>0</td><td>97.4</td><td>78.8</td><td>85.8</td><td>hypothetical protein CARUB_v10015793mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G11680.1 | Symbols: | Aluminium activated malate transporter family protein | chr3:3686995-3689329 REVERSE LENGTH=488</td><td>500</td><td>488</td><td>0</td><td>97.6</td><td>77.6</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00025.1.g1622.t1</td><td>gb|EOA33837.1| hypothetical protein CARUB_v10021318mg, partial [Capsella rubella]</td><td>261</td><td>290</td><td>2.00E-49</td><td>111.1</td><td>42.5</td><td>60.9</td><td>hypothetical protein CARUB_v10021318mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332</td><td>261</td><td>332</td><td>9.00E-49</td><td>127.2</td><td>35.6</td><td>54.8</td></tr>
</table>

Rsa1.0_00025.1.g1623.t1	ref|NP_566396.1| NDR1/HIN1-Like protein 1 [Arabidopsis thaliana] gi|6041819|gb|AAF02134.1|AC009918_6 unknown protein [Arabidopsis thaliana] gi|9502172|gb|AAF88021.1|AF264697_1 NDR1/HIN1-Like protein 1 [Arabidopsis thaliana] gi|21595601|gb|AAM66116.1| harpin-induced protein-like [Arabidopsis thaliana] gi|56381911|gb|AAV85674.1| At3g11660 [Arabidopsis thaliana] gi|58331799|gb|AAW70397.1| At3g11660 [Arabidopsis thaliana] gi|332641559|gb|AEE75080.1| NDR1/HIN1-Like protein 1 [Arabidopsis thaliana]	211	209	1.00E-102	99.1	85.3	91.0	NDR1/HIN1-Like protein 1	gbpln	Arabidopsis thaliana	AT3G11660.1 | Symbols: NHL1 | NDR1/HIN1-like 1 | chr3:3679031-3679660 REVERSE LENGTH=209	211	209	1.00E-104	99.1	85.3	91.0
Rsa1.0_00025.1.g1624.t1	gb|EOA32680.1| hypothetical protein CARUB_v10015978mg [Capsella rubella]	490	442	0	90.2	74.9	80.4	hypothetical protein CARUB_v10015978mg	gbpln	Capsella rubella	AT3G11490.1 | Symbols: | rac GTPase activating protein | chr3:3617523-3619567 REVERSE LENGTH=435	490	435	0	88.8	75.9	80.4
Rsa1.0_00025.1.g1625.t1	ref|XP_002882732.1| hypothetical protein ARALYDRAFT_478481 [Arabidopsis lyrata subsp. lyrata] gi|297328572|gb|EFH58991.1| hypothetical protein ARALYDRAFT_478481 [Arabidopsis lyrata subsp. lyrata]	500	551	0	110.2	74.8	80.6	hypothetical protein ARALYDRAFT_478481	gbpln	Arabidopsis lyrata	AT3G11440.1 | Symbols: ATMYB65, MYB65 | myb domain protein 65 | chr3:3603056-3604929 FORWARD LENGTH=553	500	553	0	110.6	73.0	80.0
Rsa1.0_00025.1.g1626.t1	ref|XP_002882731.1| glycerol-3-phosphate acyltransferase 5 [Arabidopsis lyrata subsp. lyrata] gi|297328571|gb|EFH58990.1| glycerol-3-phosphate acyltransferase 5 [Arabidopsis lyrata subsp. lyrata]	500	502	0	100.4	87.8	94.4	glycerol-3-phosphate acyltransferase 5	gbpln	Arabidopsis lyrata	AT3G11430.1 | Symbols: ATGPAT5, GPAT5 | glycerol-3-phosphate acyltransferase 5 | chr3:3595911-3597678 FORWARD LENGTH=502	500	502	0	100.4	87.2	93.8
Rsa1.0_00025.1.g1627.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1306	1274	0	97.5	43.3	58.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1306	575	7.00E-74	44.0	13.7	21.8
Rsa1.0_00025.1.g1628.t1	ref|XP_002882730.1| hypothetical protein ARALYDRAFT_478479 [Arabidopsis lyrata subsp. lyrata] gi|297328570|gb|EFH58989.1| hypothetical protein ARALYDRAFT_478479 [Arabidopsis lyrata subsp. lyrata]	508	505	0	99.4	84.4	90.7	hypothetical protein ARALYDRAFT_478479	gbpln	Arabidopsis lyrata	AT3G11420.1 | Symbols: | Protein of unknown function (DUF604) | chr3:3591834-3594323 FORWARD LENGTH=505	508	505	0	99.4	83.7	91.1
Rsa1.0_00025.1.g1629.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00025.1.g1630.t1	ref|XP_002884844.1| AHG3/ATPP2CA [Arabidopsis lyrata subsp. lyrata] gi|297330684|gb|EFH61103.1| AHG3/ATPP2CA [Arabidopsis lyrata subsp. lyrata]	388	396	1.00E-160	102.1	80.7	88.9	AHG3/ATPP2CA	gbpln	Arabidopsis lyrata	AT3G11410.1 | Symbols: ATPP2CA, AHG3, PP2CA | protein phosphatase 2CA | chr3:3584181-3585649 REVERSE LENGTH=399	388	399	1.00E-160	102.8	80.2	88.1
Rsa1.0_00025.1.g1631.t1	ref|NP_187747.1| translation initiation factor eIF-3 subunit 4 [Arabidopsis thaliana] gi|12322907|gb|AAG51445.1|AC008153_18 putative eukaryotic translation initiation factor 3 subunit; 21071-22901 [Arabidopsis thaliana] gi|16226341|gb|AAL16140.1|AF428308_1 AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|9755847|emb|CAC01929.1| translation initiation factor 3, subunit g (eIF3g) [Arabidopsis thaliana] gi|18377870|gb|AAL67121.1| AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|22137220|gb|AAM91455.1| AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|332641520|gb|AEE75041.1| translation initiation factor eIF-3 subunit 4 [Arabidopsis thaliana]	296	294	1.00E-157	99.3	91.2	94.9	translation initiation factor eIF-3 subunit 4	gbpln	Arabidopsis thaliana	AT3G11400.1 | Symbols: EIF3G1, ATEIF3G1 | eukaryotic translation initiation factor 3G1 | chr3:3578536-3580366 FORWARD LENGTH=294	296	294	1.00E-159	99.3	91.2	94.9
Rsa1.0_00025.1.g1632.t2	gb|EOA32620.1| hypothetical protein CARUB_v10015914mg [Capsella rubella]	385	293	3.00E-59	76.1	29.9	33.0	hypothetical protein CARUB_v10015914mg	gbpln	Capsella rubella	AT2G15710.1 | Symbols: | TRAF-like family protein | chr2:6842648-6845103 FORWARD LENGTH=365	385	365	2.00E-50	94.8	26.2	31.2
Rsa1.0_00025.1.g1633.t1	ref|NP_566390.1| uncharacterized protein [Arabidopsis thaliana] gi|110736642|dbj|BAF00285.1| hypothetical protein [Arabidopsis thaliana] gi|332641505|gb|AEE75026.1| uncharacterized protein AT3G11290 [Arabidopsis thaliana]	499	460	1.00E-176	92.2	64.1	76.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G11290.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11310.1); Has 720 Blast hits to 435 proteins in 28 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 32; Plants - 682; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr3:3535766-3537295 REVERSE LENGTH=460	499	460	1.00E-179	92.2	64.1	76.8

Rsa1.0_00025.1.g1634.t1	ref|NP_187737.1| duplicated SANT DNA-binding domain-containing protein [Arabidopsis thaliana] gi|30681667|ref|NP_850558.1| duplicated SANT DNA-binding domain-containing protein [Arabidopsis thaliana] gi|12321867|gb|AAG50963.1|AC073395_5 MYB-family transcription factor, putative; alternative splicing isoform 1 of 2;71559-70643 [Arabidopsis thaliana] gi|12321868|gb|AAG50964.1|AC073395_6 MYB-family transcription factor, putative; alternative splicing isoform 2 of 2;71559-70643 [Arabidopsis thaliana] gi|15810283|gb|AAL07029.1| putative MYB-family transcription factor [Arabidopsis thaliana] gi|20258977|gb|AAM14204.1| putative MYB-family transcription factor [Arabidopsis thaliana] gi|45357120|gb|AAS58519.1| MYB transcription factor [Arabidopsis thaliana] gi|332641503|gb|AEE75024.1| duplicated SANT DNA-binding domain-containing protein [Arabidopsis thaliana] gi|332641504|gb|AEE75025.1| duplicated SANT DNA-binding domain-containing protein [Arabidopsis thaliana]	259	263	1.00E-120	101.5	81.9	87.3	duplicated SANT DNA-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT3G11280.2 | Symbols: | Duplicated homeodomain-like superfamily protein | chr3:3533477-3534393 REVERSE LENGTH=263	259	263	1.00E-123	101.5	81.9	87.3
Rsa1.0_00025.1.g1635.t1	ref|NP_567015.1| splicing factor 3B subunit 3 [Arabidopsis thaliana] gi|18410226|ref|NP_567016.1| putative splicing factor [Arabidopsis thaliana] gi|7019653|emb|CAB75754.1| spliceosomal-like protein [Arabidopsis thaliana] gi|7019655|emb|CAB75756.1| spliceosomal-like protein [Arabidopsis thaliana] gi|332645831|gb|AEE79352.1| spliceosomal associated protein 130A [Arabidopsis thaliana] gi|332645833|gb|AEE79354.1| spliceosome-associated protein 130B [Arabidopsis thaliana]	1214	1214	0	100.0	95.4	98.4	splicing factor 3B subunit 3	gbpln	Arabidopsis thaliana	AT3G55200.1 | Symbols: | Cleavage and polyadenylation specificity factor (CPSF) A subunit protein | chr3:20460533-20464361 FORWARD LENGTH=1214	1214	1214	0	100.0	95.4	98.4
Rsa1.0_00025.1.g1636.t1	ref|NP_001078135.1| yippee-like protein [Arabidopsis thaliana] gi|332641497|gb|AEE75018.1| yippee-like protein [Arabidopsis thaliana]	129	162	4.00E-61	125.6	87.6	93.8	yippee-like protein	gbpln	Arabidopsis thaliana	AT3G11230.2 | Symbols: | Yippee family putative zinc-binding protein | chr3:3516683-3518193 FORWARD LENGTH=162	129	162	9.00E-64	125.6	87.6	93.8
Rsa1.0_00026.1.g1637.t1	dbj|BAJ33984.1| unnamed protein product [Thellungiella halophila]	696	699	0	100.4	96.7	99.1	unnamed protein product	----	----	AT5G56000.1 | Symbols: Hsp81.4, AtHsp90.4 | HEAT SHOCK PROTEIN 81.4 | chr5:22677602-22680067 REVERSE LENGTH=699	696	699	0	100.4	94.5	98.9
Rsa1.0_00026.1.g1638.t1	gb|EOA12588.1| hypothetical protein CARUB_v10027067mg [Capsella rubella]	226	226	1.00E-124	100.0	96.5	98.7	hypothetical protein CARUB_v10027067mg	gbpln	Capsella rubella	AT5G55990.1 | Symbols: CBL2, ATCBL2 | calcineurin B-like protein 2 | chr5:22672189-22673579 FORWARD LENGTH=226	226	226	1.00E-126	100.0	96.0	98.2
Rsa1.0_00026.1.g1639.t1	gb|EOA12638.1| hypothetical protein CARUB_v10027572mg [Capsella rubella]	753	758	0	100.7	92.8	97.5	hypothetical protein CARUB_v10027572mg	gbpln	Capsella rubella	AT5G55930.1 | Symbols: ATOPT1, OPT1 | oligopeptide transporter 1 | chr5:22652988-22655827 FORWARD LENGTH=755	753	755	0	100.3	92.4	96.7
Rsa1.0_00026.1.g1640.t1	ref|NP_850927.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|9758212|dbj|BAB08657.1| nucleolar protein-like [Arabidopsis thaliana] gi|332009316|gb|AED96699.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	663	682	0	102.9	75.9	87.0	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G55920.1 | Symbols: OLI2 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:22645742-22649383 REVERSE LENGTH=682	663	682	0	102.9	75.9	87.0
Rsa1.0_00026.1.g1641.t1	dbj|BAJ33984.1| unnamed protein product [Thellungiella halophila]	696	699	0	100.4	96.4	99.0	unnamed protein product	----	----	AT5G56000.1 | Symbols: Hsp81.4, AtHsp90.4 | HEAT SHOCK PROTEIN 81.4 | chr5:22677602-22680067 REVERSE LENGTH=699	696	699	0	100.4	94.4	98.9
Rsa1.0_00026.1.g1642.t1	ref|XP_002864413.1| hypothetical protein ARALYDRAFT_495666 [Arabidopsis lyrata subsp. lyrata] gi|297310248|gb|EFH40672.1| hypothetical protein ARALYDRAFT_495666 [Arabidopsis lyrata subsp. lyrata]	71	102	3.00E-28	143.7	87.3	91.5	hypothetical protein ARALYDRAFT_495666	gbpln	Arabidopsis lyrata	AT5G55850.1 | Symbols: NOI | RPM1-interacting protein 4 (RIN4) family protein | chr5:22603617-22604951 FORWARD LENGTH=114	71	114	8.00E-31	160.6	85.9	90.1
Rsa1.0_00026.1.g1643.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00026.1.g1644.t2	gb|EOA13370.1| hypothetical protein CARUB_v10026407mg, partial [Capsella rubella]	407	443	1.00E-167	108.8	81.6	90.7	hypothetical protein CARUB_v10026407mg, partial	gbpln	Capsella rubella	AT5G55730.2 | Symbols: FLA1 | FASCICLIN-like arabinogalactan 1 | chr5:22558375-22560392 REVERSE LENGTH=424	407	424	1.00E-163	104.2	79.4	86.0
Rsa1.0_00026.1.g1645.t1	ref|XP_002864408.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310243|gb|EFH40667.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata]	385	391	0	101.6	87.8	93.8	pectate lyase family protein	gbpln	Arabidopsis lyrata	AT5G55720.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:22556047-22557496 FORWARD LENGTH=392	385	392	0	101.8	85.5	92.7
Rsa1.0_00026.1.g1646.t1	gb|EOA14333.1| hypothetical protein CARUB_v10027511mg [Capsella rubella]	211	209	4.00E-97	99.1	88.2	91.5	hypothetical protein CARUB_v10027511mg	gbpln	Capsella rubella	AT5G55710.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: Uncharacterised conserved protein ycf60 (TAIR:AT2G47840.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:22554995-22555624 REVERSE LENGTH=209	211	209	2.00E-97	99.1	87.2	90.5
Rsa1.0_00026.1.g1647.t1	ref|NP_568829.2| inactive beta-amylase 4 [Arabidopsis thaliana] gi|75334054|sp|Q9FM68.1|BAM4_ARATH RecName: Full=Inactive beta-amylase 4, chloroplastic; AltName: Full=Inactive beta-amylase 6; Flags: Precursor gi|9758604|dbj|BAB09237.1| beta-amylase [Arabidopsis thaliana] gi|332009286|gb|AED96669.1| inactive beta-amylase 4 [Arabidopsis thaliana]	534	531	0	99.4	90.1	94.2	inactive beta-amylase 4	gbpln	Arabidopsis thaliana	AT5G55700.1 | Symbols: BMY6, BAM4 | beta-amylase 4 | chr5:22551873-22554702 FORWARD LENGTH=531	534	531	0	99.4	90.1	94.2
Rsa1.0_00026.1.g1648.t5	gb|EOA12471.1| hypothetical protein CARUB_v10025902mg [Capsella rubella]	1233	804	0	65.2	40.2	46.9	hypothetical protein CARUB_v10025902mg	gbpln	Capsella rubella	AT5G55660.1 | Symbols: | DEK domain-containing chromatin associated protein | chr5:22539375-22543142 FORWARD LENGTH=778	1233	778	1.00E-174	63.1	38.9	44.5
Rsa1.0_00026.1.g1649.t1	ref|NP_200370.1| pectinesterase QRT1 [Arabidopsis thaliana] gi|75171621|sp|Q9FM79.1|PME62_ARATH RecName: Full=Pectinesterase QRT1; Short=AtQRT1; Short=PE QRT1; AltName: Full=Pectin methylesterase 62; Short=AtPME62; AltName: Full=Pectin methylesterase QRT1; AltName: Full=Protein QUARTET 1; Flags: Precursor gi|9758593|dbj|BAB09226.1| unnamed protein product [Arabidopsis thaliana] gi|115490609|gb|ABI97858.1| quartet1 [Arabidopsis thaliana] gi|332009270|gb|AED96653.1| pectinesterase QRT1 [Arabidopsis thaliana]	392	380	1.00E-137	96.9	64.5	77.6	pectinesterase QRT1	gbpln	Arabidopsis thaliana	AT5G55590.1 | Symbols: QRT1 | Pectin lyase-like superfamily protein | chr5:22519911-22521699 FORWARD LENGTH=380	392	380	1.00E-140	96.9	64.5	77.6
Rsa1.0_00026.1.g1650.t1	gb|AAC33963.1| contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]	1916	1633	0	85.2	51.0	59.0	contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19)	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1916	1262	1.00E-179	65.9	15.3	20.0
Rsa1.0_00026.1.g1651.t1	ref|NP_201434.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|10177427|dbj|BAB10712.1| unnamed protein product [Arabidopsis thaliana] gi|17529198|gb|AAL38825.1| unknown protein [Arabidopsis thaliana] gi|21436283|gb|AAM51280.1| unknown protein [Arabidopsis thaliana] gi|332010817|gb|AED98200.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	360	418	1.00E-134	116.1	69.7	76.9	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G66330.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:26500531-26501787 REVERSE LENGTH=418	360	418	1.00E-137	116.1	69.7	76.9
Rsa1.0_00026.1.g1652.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00026.1.g1653.t1	gb|EOA12552.1| hypothetical protein CARUB_v10026802mg [Capsella rubella]	308	316	1.00E-149	102.6	83.4	88.3	hypothetical protein CARUB_v10026802mg	gbpln	Capsella rubella	AT5G55560.1 | Symbols: | Protein kinase superfamily protein | chr5:22506477-22507757 REVERSE LENGTH=314	308	314	1.00E-149	101.9	82.1	87.3

Rsa1.0_00026.1.g1654.t1	ref|XP_002866100.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311935|gb|EFH42359.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	788	790	0	100.3	77.8	84.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G55520.2 | Symbols: | CONTAINS InterPro DOMAIN/s: Kinesin-related protein (InterPro:IPR010544); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G26660.1); Has 31032 Blast hits to 19733 proteins in 1535 species: Archae - 330; Bacteria - 3150; Metazoa - 16413; Fungi - 2511; Plants - 1475; Viruses - 48; Other Eukaryotes - 7105 (source: NCBI BLink). | chr5:22488205-22491187 REVERSE LENGTH=801	788	801	0	101.6	77.8	85.3
Rsa1.0_00026.1.g1655.t1	ref|NP_174635.1| terpene cyclase, C1 domain-containing protein [Arabidopsis thaliana] gi|317412196|sp|Q9LQ27.2|TPS22_ARATH RecName: Full=Terpenoid synthase 22; Short=AtTPS22 gi|332193499|gb|AEE31620.1| terpenoid synthase 22 [Arabidopsis thaliana]	655	603	0	92.1	67.0	77.4	terpene cyclase, C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G33750.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr1:12233769-12236348 FORWARD LENGTH=603	655	603	0	92.1	67.0	77.4
Rsa1.0_00026.1.g1656.t1	gb|AAZ66923.1| 117M18_4 [Brassica rapa]	380	424	1.00E-129	111.6	65.5	78.4	117M18_4	gbpln	Brassica rapa	AT5G10010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64910.1); Has 33260 Blast hits to 16857 proteins in 1270 species: Archae - 88; Bacteria - 3040; Metazoa - 11915; Fungi - 3137; Plants - 1371; Viruses - 424; Other Eukaryotes - 13285 (source: NCBI BLink). | chr5:3128098-3131452 FORWARD LENGTH=434	380	434	1.00E-121	114.2	57.1	67.9
Rsa1.0_00026.1.g1657.t1	gb|EOA14260.1| hypothetical protein CARUB_v10027418mg [Capsella rubella]	118	106	6.00E-25	89.8	50.0	68.6	hypothetical protein CARUB_v10027418mg	gbpln	Capsella rubella	AT5G55450.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:22467560-22467874 FORWARD LENGTH=104	118	104	2.00E-25	88.1	54.2	67.8
Rsa1.0_00026.1.g1658.t1	ref|XP_002864390.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297310225|gb|EFH40649.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	107	107	3.00E-40	100.0	75.7	83.2	protease inhibitor/seed storage/lipid transfer protein family protein	gbpln	Arabidopsis lyrata	AT5G55410.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:22460677-22461081 FORWARD LENGTH=107	107	107	7.00E-42	100.0	72.9	81.3
Rsa1.0_00026.1.g1659.t1	gb|EOA12364.1| hypothetical protein CARUB_v10025745mg, partial [Capsella rubella]	1325	1349	0	101.8	74.7	84.6	hypothetical protein CARUB_v10025745mg, partial	gbpln	Capsella rubella	AT5G55390.2 | Symbols: EDM2 | ENHANCED DOWNY MILDEW 2 | chr5:22448152-22454414 REVERSE LENGTH=1297	1325	1297	0	97.9	74.5	83.6
Rsa1.0_00026.1.g1660.t1	ref|XP_002866093.1| hypothetical protein ARALYDRAFT_495621 [Arabidopsis lyrata subsp. lyrata] gi|297311928|gb|EFH42352.1| hypothetical protein ARALYDRAFT_495621 [Arabidopsis lyrata subsp. lyrata]	347	346	1.00E-152	99.7	76.7	84.1	hypothetical protein ARALYDRAFT_495621	gbpln	Arabidopsis lyrata	AT5G55380.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr5:22446846-22447871 REVERSE LENGTH=341	347	341	1.00E-148	98.3	75.5	83.3
Rsa1.0_00026.1.g1661.t1	ref|NP_200348.1| putative long-chain-alcohol O-fatty-acyltransferase 2 [Arabidopsis thaliana] gi|75170973|sp|Q9FJ73.1|WAXS2_ARATH RecName: Full=Probable long-chain-alcohol O-fatty-acyltransferase 2; AltName: Full=Wax synthase 2 gi|9758169|dbj|BAB08554.1| wax synthase-like protein [Arabidopsis thaliana] gi|332009238|gb|AED96621.1| putative long-chain-alcohol O-fatty-acyltransferase 2 [Arabidopsis thaliana]	489	343	1.00E-138	70.1	50.1	57.7	putative long-chain-alcohol O-fatty-acyltransferase 2	gbpln	Arabidopsis thaliana	AT5G55370.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr5:22445085-22446116 REVERSE LENGTH=343	489	343	1.00E-140	70.1	50.1	57.7
Rsa1.0_00026.1.g1662.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00026.1.g1663.t1	gb|EOA25182.1| hypothetical protein CARUB_v10018494mg [Capsella rubella]	181	282	7.00E-25	155.8	41.4	53.0	hypothetical protein CARUB_v10018494mg	gbpln	Capsella rubella	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	181	170	1.00E-19	93.9	29.3	40.9
Rsa1.0_00026.1.g1664.t1	ref|XP_002882965.1| hypothetical protein ARALYDRAFT_897881 [Arabidopsis lyrata subsp. lyrata] gi|297328805|gb|EFH59224.1| hypothetical protein ARALYDRAFT_897881 [Arabidopsis lyrata subsp. lyrata]	235	301	4.00E-95	128.1	71.5	83.4	hypothetical protein ARALYDRAFT_897881	gbpln	Arabidopsis lyrata	AT3G15820.1 | Symbols: ROD1 | phosphatidic acid phosphatase-related / PAP2-related | chr3:5351217-5353573 FORWARD LENGTH=301	235	301	2.00E-96	128.1	70.6	82.1

Rsa1.0_00026.1.g1665.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	812	1274	4.00E-90	156.9	25.4	36.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT5G55340.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr5:22439985-22440986 REVERSE LENGTH=333	812	333	4.00E-57	41.0	13.7	17.9
Rsa1.0_00026.1.g1666.t1	ref|XP_002866092.1| hypothetical protein ARALYDRAFT_495620 [Arabidopsis lyrata subsp. lyrata] gi|297311927|gb|EFH42351.1| hypothetical protein ARALYDRAFT_495620 [Arabidopsis lyrata subsp. lyrata]	339	345	1.00E-121	101.8	63.7	75.8	hypothetical protein ARALYDRAFT_495620	gbpln	Arabidopsis lyrata	AT5G55350.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr5:22442356-22443393 REVERSE LENGTH=345	339	345	1.00E-122	101.8	62.8	76.1
Rsa1.0_00026.1.g1667.t6	gb|EOA12470.1| hypothetical protein CARUB_v10025842mg [Capsella rubella]	1720	923	0	53.7	39.5	44.6	hypothetical protein CARUB_v10025842mg	gbpln	Capsella rubella	AT5G55300.2 | Symbols: TOP1ALPHA | DNA topoisomerase I alpha | chr5:22424701-22429045 REVERSE LENGTH=933	1720	933	0	54.2	39.5	44.5
Rsa1.0_00026.1.g1668.t1	gb|ACG70179.1| chloroplast FtsZ1-1 [Brassica oleracea var. botrytis]	425	425	0	100.0	92.5	94.8	chloroplast FtsZ1-1	gbpln	Brassica oleracea	AT5G55280.1 | Symbols: FTSZ1-1, ATFTSZ1-1, CPFTSZ | homolog of bacterial cytokinesis Z-ring protein FTSZ 1-1 | chr5:22420740-22422527 REVERSE LENGTH=433	425	433	0	101.9	90.1	94.4
Rsa1.0_00026.1.g1669.t1	ref|XP_002864385.1| atmap65-1 [Arabidopsis lyrata subsp. lyrata] gi|297310220|gb|EFH40644.1| atmap65-1 [Arabidopsis lyrata subsp. lyrata]	584	587	0	100.5	91.6	94.2	atmap65-1	gbpln	Arabidopsis lyrata	AT5G55230.1 | Symbols: ATMAP65-1, MAP65-1 | microtubule-associated proteins 65-1 | chr5:22402716-22405182 FORWARD LENGTH=587	584	587	0	100.5	90.8	94.0
Rsa1.0_00026.1.g1670.t1	ref|XP_002864384.1| trigger factor type chaperone family protein [Arabidopsis lyrata subsp. lyrata] gi|297310219|gb|EFH40643.1| trigger factor type chaperone family protein [Arabidopsis lyrata subsp. lyrata]	548	551	0	100.5	85.6	92.0	trigger factor type chaperone family protein	gbpln	Arabidopsis lyrata	AT5G55220.1 | Symbols: | trigger factor type chaperone family protein | chr5:22397677-22400678 FORWARD LENGTH=547	548	547	0	99.8	85.6	92.2
Rsa1.0_00026.1.g1671.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00026.1.g1672.t1	gb|EMJ23759.1| hypothetical protein PRUPE_ppa008371mg [Prunus persica]	221	335	1.00E-130	151.6	99.1	99.5	hypothetical protein PRUPE_ppa008371mg	gbpln	Prunus persica	AT5G55190.1 | Symbols: RAN3, ATRAN3 | RAN GTPase 3 | chr5:22392285-22393957 FORWARD LENGTH=221	221	221	1.00E-130	100.0	99.1	99.5
Rsa1.0_00026.1.g1673.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	544	530	1.00E-40	97.4	18.9	25.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	544	530	7.00E-17	97.4	7.7	13.2
Rsa1.0_00026.1.g1674.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1177	1213	0	103.1	38.2	56.2	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1177	626	4.00E-69	53.2	13.3	20.2
Rsa1.0_00026.1.g1675.t1	ref|XP_002864380.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297310215|gb|EFH40639.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	475	461	0	97.1	81.7	87.4	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT5G55180.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:22388834-22390550 FORWARD LENGTH=460	475	460	0	96.8	83.8	90.5
Rsa1.0_00026.1.g1676.t3	ref|XP_002866078.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311913|gb|EFH42337.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	381	375	1.00E-140	98.4	68.8	78.0	F-box family protein	gbpln	Arabidopsis lyrata	AT5G55150.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22382275-22383392 REVERSE LENGTH=360	381	360	1.00E-132	94.5	65.4	74.8
Rsa1.0_00026.1.g1677.t2	ref|NP_680438.1| uncharacterized protein [Arabidopsis thaliana] gi|91807044|gb|ABE66249.1| hypothetical protein At5g55135 [Arabidopsis thaliana] gi|332009207|gb|AED96590.1| uncharacterized protein AT5G55135 [Arabidopsis thaliana]	112	112	2.00E-33	100.0	68.8	81.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G55135.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:22379959-22380386 FORWARD LENGTH=112	112	112	3.00E-36	100.0	68.8	81.3
Rsa1.0_00026.1.g1678.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00026.1.g1679.t1	gb|EOA14782.1| hypothetical protein CARUB_v10028082mg [Capsella rubella]	57	76	1.00E-13	133.3	64.9	66.7	hypothetical protein CARUB_v10028082mg	gbpln	Capsella rubella	AT5G55125.2 | Symbols: | Ribosomal protein L31 | chr5:22372737-22372967 FORWARD LENGTH=76	57	76	2.00E-15	133.3	63.2	64.9
Rsa1.0_00026.1.g1680.t1	emb|CAN62821.1| hypothetical protein VITISV_013041 [Vitis vinifera]	1091	1357	1.00E-145	124.4	35.2	54.6	hypothetical protein VITISV_013041	gbpln	Vitis vinifera	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1091	158	2.00E-28	14.5	5.6	7.0
Rsa1.0_00026.1.g1681.t1	ref|NP_192687.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|7267644|emb|CAB78072.1| putative proteins [Arabidopsis thaliana] gi|332657356|gb|AEE82756.1| RNase H domain-containing protein [Arabidopsis thaliana]	90	170	8.00E-12	188.9	45.6	56.7	RNase H domain-containing protein	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	90	170	1.00E-14	188.9	45.6	56.7
Rsa1.0_00026.1.g1682.t1	gb|EOA14764.1| hypothetical protein CARUB_v10028061mg [Capsella rubella]	345	164	3.00E-59	47.5	34.8	36.5	hypothetical protein CARUB_v10028061mg	gbpln	Capsella rubella	AT5G55110.1 | Symbols: | Stigma-specific Stig1 family protein | chr5:22367870-22368361 FORWARD LENGTH=163	345	163	6.00E-59	47.2	32.5	34.5

Rsa1.0_00026.1.g1683.t1	ref|XP_002866076.1| swap (Suppressor-of-White-APricot)/surp domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311911|gb|EFH42335.1| swap (Suppressor-of-White-APricot)/surp domain-containing protein [Arabidopsis lyrata subsp. lyrata]	868	852	0	98.2	76.3	83.6	swap (Suppressor-of-White-APricot)/surp domain-containing protein	gbpln	Arabidopsis lyrata	AT5G55100.2 | Symbols: | SWAP (Suppressor-of-White-APricot)/surp domain-containing protein | chr5:22361401-22364664 REVERSE LENGTH=844	868	844	0	97.2	74.8	82.7
Rsa1.0_00026.1.g1684.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00026.1.g1685.t1	ref|NP_200320.1| mitogen-activated protein kinase kinase kinase 15 [Arabidopsis thaliana] gi|9758106|dbj|BAB08578.1| unnamed protein product [Arabidopsis thaliana] gi|332009196|gb|AED96579.1| mitogen-activated protein kinase kinase kinase 15 [Arabidopsis thaliana]	448	448	1.00E-176	100.0	73.2	81.3	mitogen-activated protein kinase kinase kinase 15	gbpln	Arabidopsis thaliana	AT5G55090.1 | Symbols: MAPKKK15 | mitogen-activated protein kinase kinase kinase 15 | chr5:22356852-22358198 REVERSE LENGTH=448	448	448	1.00E-179	100.0	73.2	81.3
Rsa1.0_00026.1.g1686.t3	gb|EOA13330.1| hypothetical protein CARUB_v10026364mg [Capsella rubella]	531	462	0	87.0	79.3	82.1	hypothetical protein CARUB_v10026364mg	gbpln	Capsella rubella	AT5G55070.1 | Symbols: | Dihydrolipoamide succinyltransferase | chr5:22347637-22350409 FORWARD LENGTH=464	531	464	0	87.4	76.8	79.5
Rsa1.0_00026.1.g1687.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00026.1.g1688.t1	ref|XP_002864371.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310206|gb|EFH40630.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	136	376	3.00E-50	276.5	67.6	77.9	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT5G55050.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:22337745-22339741 FORWARD LENGTH=376	136	376	2.00E-50	276.5	64.0	77.2
Rsa1.0_00026.1.g1689.t1	gb|EOA13535.1| hypothetical protein CARUB_v10026598mg [Capsella rubella]	377	378	1.00E-171	100.3	79.0	89.7	hypothetical protein CARUB_v10026598mg	gbpln	Capsella rubella	AT5G55050.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:22337745-22339741 FORWARD LENGTH=376	377	376	1.00E-168	99.7	78.8	90.7
Rsa1.0_00026.1.g1690.t1	ref|NP_200310.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|9758279|dbj|BAB08778.1| unnamed protein product [Arabidopsis thaliana] gi|332009183|gb|AED96566.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	282	226	1.00E-47	80.1	43.6	52.5	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G54990.1 | Symbols: | RING/U-box superfamily protein | chr5:22317505-22318185 FORWARD LENGTH=226	282	226	4.00E-50	80.1	43.6	52.5
Rsa1.0_00026.1.g1691.t1	ref|NP_200310.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|9758279|dbj|BAB08778.1| unnamed protein product [Arabidopsis thaliana] gi|332009183|gb|AED96566.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	249	226	7.00E-24	90.8	34.9	47.0	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G54990.1 | Symbols: | RING/U-box superfamily protein | chr5:22317505-22318185 FORWARD LENGTH=226	249	226	2.00E-26	90.8	34.9	47.0
Rsa1.0_00026.1.g1692.t1	dbj|BAJ33777.1| unnamed protein product [Thellungiella halophila]	569	552	0	97.0	85.4	88.9	unnamed protein product	----	----	AT3G02020.1 | Symbols: AK3 | aspartate kinase 3 | chr3:340739-343410 REVERSE LENGTH=559	569	559	0	98.2	82.8	88.9
Rsa1.0_00026.1.g1693.t2	ref|NP_568814.2| DTW domain-containing protein [Arabidopsis thaliana] gi|9758268|dbj|BAB08767.1| unnamed protein product [Arabidopsis thaliana] gi|15450589|gb|AAK96566.1| AT5g54880/MBG8_15 [Arabidopsis thaliana] gi|24797048|gb|AAN64536.1| At5g54880/MBG8_15 [Arabidopsis thaliana] gi|332009169|gb|AED96552.1| DTW domain-containing protein [Arabidopsis thaliana]	313	394	1.00E-124	125.9	77.6	86.9	DTW domain-containing protein	gbpln	Arabidopsis thaliana	AT5G54880.1 | Symbols: | DTW domain-containing protein | chr5:22291920-22293104 FORWARD LENGTH=394	313	394	1.00E-126	125.9	77.6	86.9
Rsa1.0_00026.1.g1694.t1	gb|EOA13149.1| hypothetical protein CARUB_v10026167mg, partial [Capsella rubella]	530	563	0	106.2	89.4	93.2	hypothetical protein CARUB_v10026167mg, partial	gbpln	Capsella rubella	AT5G54870.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27020.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:22289149-22291604 FORWARD LENGTH=531	530	531	0	100.2	87.4	91.1
Rsa1.0_00026.1.g1695.t1	gb|AAC63844.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1769	1231	0	69.6	36.8	45.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337-69884 REVERSE LENGTH=515	1769	515	1.00E-124	29.1	13.6	18.1
Rsa1.0_00026.1.g1696.t1	gb|AAD21699.1| Contains reverse transcriptase domain (rvt) PF|00078 [Arabidopsis thaliana]	226	1253	3.00E-28	554.4	24.3	35.4	Contains reverse transcriptase domain (rvt) PF|00078	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	226	289	2.00E-27	127.9	24.3	33.6

<table>
<tr><td>Rsa1.0_00026.1.g1697.t2</td><td>emb|CAB81573.1| putative protein [Arabidopsis thaliana]</td><td>321</td><td>510</td><td>7.00E-22</td><td>158.9</td><td>17.4</td><td>25.2</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530</td><td>321</td><td>530</td><td>1.00E-12</td><td>165.1</td><td>13.1</td><td>21.5</td></tr>
<tr><td>Rsa1.0_00026.1.g1698.t2</td><td>gb|AAG51873.1|AC079678_3 disease resistance protein, putative; 11609-15699 [Arabidopsis thaliana]</td><td>1057</td><td>1068</td><td>0</td><td>101.0</td><td>63.6</td><td>73.4</td><td>disease resistance protein, putative; 11609-15699</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G74170.1 | Symbols: AtRLP13, RLP13 | receptor like protein 13 | chr1:27891555-27895441 REVERSE LENGTH=1000</td><td>1057</td><td>1000</td><td>0</td><td>94.6</td><td>59.6</td><td>68.6</td></tr>
<tr><td>Rsa1.0_00027.1.g1699.t1</td><td>gb|EOA36095.1| hypothetical protein CARUB_v10010848mg, partial [Capsella rubella]</td><td>134</td><td>134</td><td>9.00E-14</td><td>100.0</td><td>32.1</td><td>50.0</td><td>hypothetical protein CARUB_v10010848mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170</td><td>134</td><td>170</td><td>1.00E-11</td><td>126.9</td><td>25.4</td><td>40.3</td></tr>
<tr><td>Rsa1.0_00027.1.g1700.t1</td><td>gb|EOA18568.1| hypothetical protein CARUB_v10007127mg [Capsella rubella]</td><td>973</td><td>969</td><td>0</td><td>99.6</td><td>93.7</td><td>96.9</td><td>hypothetical protein CARUB_v10007127mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G30160.1 | Symbols: VLN4, ATVLN4 | villin 4 | chr4:14754528-14759511 FORWARD LENGTH=974</td><td>973</td><td>974</td><td>0</td><td>100.1</td><td>92.3</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00027.1.g1701.t1</td><td>gb|EOA17560.1| hypothetical protein CARUB_v10005921mg [Capsella rubella]</td><td>159</td><td>159</td><td>2.00E-43</td><td>100.0</td><td>69.2</td><td>78.0</td><td>hypothetical protein CARUB_v10005921mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G18969.1 | Symbols: | BEST Arabidopsis thaliana protein match is: sequence-specific DNA binding transcription factors;transcription regulators (TAIR:AT4G30180.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:8229047-8229574 REVERSE LENGTH=175</td><td>159</td><td>175</td><td>3.00E-42</td><td>110.1</td><td>60.4</td><td>73.6</td></tr>
<tr><td>Rsa1.0_00027.1.g1702.t1</td><td>ref|NP_194748.1| H(+)-ATPase 2 [Arabidopsis thaliana] gi|114335|sp|P19456.2|PMA2_ARATH RecName: Full=ATPase 2, plasma membrane-type; AltName: Full=Proton pump 2 gi|166629|gb|AAA32751.1| H+-ATPase [Arabidopsis thaliana] gi|5730129|emb|CAB52463.1| H+-transporting ATPase type 2, plasma membrane [Arabidopsis thaliana] gi|7269919|emb|CAB81012.1| H+-transporting ATPase type 2, plasma membrane [Arabidopsis thaliana] gi|14334804|gb|AAK59580.1| putative H+-transporting ATPase [Arabidopsis thaliana] gi|23397277|gb|AAN31920.1| putative H+-transporting ATPase type 2 [Arabidopsis thaliana] gi|25055009|gb|AAN71968.1| putative H+-transporting ATPase [Arabidopsis thaliana] gi|332660331|gb|AEE85731.1| H(+)-ATPase 2 [Arabidopsis thaliana]</td><td>947</td><td>948</td><td>0</td><td>100.1</td><td>97.5</td><td>99.0</td><td>H(+)-ATPase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G30190.1 | Symbols: AHA2, PMA2, HA2 | H(+)-ATPase 2 | chr4:14770820-14775920 REVERSE LENGTH=948</td><td>947</td><td>948</td><td>0</td><td>100.1</td><td>97.5</td><td>99.0</td></tr>
<tr><td>Rsa1.0_00027.1.g1703.t1</td><td>ref|NP_194749.1| vernalization5/VIN3-like protein [Arabidopsis thaliana] gi|5730130|emb|CAB52464.1| putative protein [Arabidopsis thaliana] gi|7269920|emb|CAB81013.1| putative protein [Arabidopsis thaliana] gi|11177137|dbj|BAB17836.1| nuclear coiled-coil protein AT4g30200 [Arabidopsis thaliana] gi|118566356|gb|ABL01539.1| VIN3-like 2 protein [Arabidopsis thaliana] gi|332660335|gb|AEE85735.1| vernalization5/VIN3-like protein [Arabidopsis thaliana]</td><td>670</td><td>714</td><td>0</td><td>106.6</td><td>80.3</td><td>88.5</td><td>vernalization5/VIN3-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G30200.2 | Symbols: VEL1, VIL2 | vernalization5/VIN3-like | chr4:14786852-14790070 REVERSE LENGTH=714</td><td>670</td><td>714</td><td>0</td><td>106.6</td><td>80.3</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00027.1.g1704.t1</td><td>gb|AAB88009.1| heat shock cognate protein HSC70 [Brassica napus]</td><td>647</td><td>645</td><td>0</td><td>99.7</td><td>96.3</td><td>98.6</td><td>heat shock cognate protein HSC70</td><td>gbpln</td><td>Brassica napus</td><td>AT5G02500.1 | Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 | heat shock cognate protein 70-1 | chr5:554055-556334 REVERSE LENGTH=651</td><td>647</td><td>651</td><td>0</td><td>100.6</td><td>96.1</td><td>98.6</td></tr>
<tr><td>Rsa1.0_00027.1.g1705.t2</td><td>dbj|BAJ33878.1| unnamed protein product [Thellungiella halophila]</td><td>244</td><td>711</td><td>2.00E-73</td><td>291.4</td><td>65.2</td><td>73.4</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G30210.2 | Symbols: ATR2, AR2 | P450 reductase 2 | chr4:14796900-14800578 FORWARD LENGTH=711</td><td>244</td><td>711</td><td>3.00E-71</td><td>291.4</td><td>59.0</td><td>69.3</td></tr>
</table>

Rsa1.0_00027.1.g1706.t1	ref|NP_194751.1| small nuclear ribonucleoprotein F [Arabidopsis thaliana] gi|297798954|ref|XP_002867361.1| hypothetical protein ARALYDRAFT_913456 [Arabidopsis lyrata subsp. lyrata] gi|297836060|ref|XP_002885912.1| hypothetical protein ARALYDRAFT_899645 [Arabidopsis lyrata subsp. lyrata] gi|10720264|sp|Q9SUM2.1|RUXF_ARATH RecName: Full=Probable small nuclear ribonucleoprotein F; Short=snRNP-F; AltName: Full=Sm protein F; Short=Sm-F; Short=SmF gi|5730132|emb|CAB52466.1| snRNP Sm protein F-like [Arabidopsis thaliana] gi|7269922|emb|CAB81015.1| snRNP Sm protein F-like [Arabidopsis thaliana] gi|21593208|gb|AAM65157.1| snRNP Sm protein F-like [Arabidopsis thaliana] gi|30102544|gb|AAP21190.1| At4g30220 [Arabidopsis thaliana] gi|110743810|dbj|BAE99740.1| snRNP Sm protein F - like [Arabidopsis thaliana] gi|297313197|gb|EFH43620.1| hypothetical protein ARALYDRAFT_913456 [Arabidopsis lyrata subsp. lyrata] gi|297331752|gb|EFH62171.1| hypothetical protein ARALYDRAFT_899645 [Arabidopsis lyrata subsp. lyrata]	88	88	8.00E-43	100.0	97.7	98.9	small nuclear ribonucleoprotein F	gbpln	Arabidopsis lyrata	AT4G30220.1 | Symbols: RUXF | small nuclear ribonucleoprotein F | chr4:14803100-14804259 REVERSE LENGTH=88	88	88	1.00E-45	100.0	97.7	98.9
Rsa1.0_00027.1.g1707.t1	ref|NP_567842.1| Syntaxin/t-SNARE family protein [Arabidopsis thaliana] gi|16226657|gb|AAL16225.1|AF428456_1 AT4g30240/F9N11_90 [Arabidopsis thaliana] gi|22137126|gb|AAM91408.1| At4g30240/F9N11_90 [Arabidopsis thaliana] gi|332660342|gb|AEE85742.1| Syntaxin/t-SNARE family protein [Arabidopsis thaliana]	278	300	1.00E-108	107.9	73.7	83.8	Syntaxin/t-SNARE family protein	gbpln	Arabidopsis thaliana	AT4G30240.1 | Symbols: | Syntaxin/t-SNARE family protein | chr4:14808359-14809745 REVERSE LENGTH=300	278	300	1.00E-110	107.9	73.7	83.8
Rsa1.0_00027.1.g1708.t1	gb|EOA15588.1| hypothetical protein CARUB_v10005446mg [Capsella rubella]	284	280	1.00E-117	98.6	91.2	94.0	hypothetical protein CARUB_v10005446mg	gbpln	Capsella rubella	AT2G18840.1 | Symbols: | Integral membrane Yip1 family protein | chr2:8158288-8159848 FORWARD LENGTH=281	284	281	1.00E-115	98.9	86.3	90.1
Rsa1.0_00027.1.g1709.t1	gb|AEX07595.1| xyloglucosyl transferase 2, partial [Brassica juncea]	282	265	1.00E-144	94.0	85.8	89.4	xyloglucosyl transferase 2, partial	gbpln	Brassica juncea	AT4G30270.1 | Symbols: MERI5B, MERI-5, XTH24, SEN4 | xyloglucan endotransglucosylase/hydrolase 24 | chr4:14819445-14820448 REVERSE LENGTH=269	282	269	1.00E-142	95.4	84.8	89.4
Rsa1.0_00027.1.g1710.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	345	1274	2.00E-51	369.3	35.1	51.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	345	575	9.00E-30	166.7	26.4	47.2
Rsa1.0_00027.1.g1711.t1	ref|NP_176710.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|38605119|sp|O80803.1|XTH17_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 17; Short=At-XTH17; Short=XTH-17; Flags: Precursor gi|13877725|gb|AAK43940.1|AF370621_1 xylglucan endo-transglycolsylase-like protein [Arabidopsis thaliana] gi|3335340|gb|AAC27142.1| Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb|U27609, first exon contains strong similarity to meri 5 gene gb|Z17989 from A. thaliana. EST gb|N37583 comes from this gene [Arabidopsis thaliana] gi|124300988|gb|ABN04746.1| At1g65310 [Arabidopsis thaliana] gi|332196236|gb|AEE34357.1| probable xyloglucan endotransglucosylase/hydrolase protein 17 [Arabidopsis thaliana]	97	282	2.00E-44	290.7	86.6	91.8	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT1G65310.1 | Symbols: ATXTH17, XTH17 | xyloglucan endotransglucosylase/hydrolase 17 | chr1:24257262-24258319 FORWARD LENGTH=282	97	282	3.00E-47	290.7	86.6	91.8

Rsa1.0_00027.1.g1712.t1	ref|NP_199618.1| xyloglucan endotransglucosylase/hydrolase protein 20 [Arabidopsis thaliana] gi|38605469|sp|Q9FI31.1|XTH20_ARATH RecName: Full=Xyloglucan endotransglucosylase/hydrolase protein 20; Short=At-XTH20; Short=XTH-20; Flags: Precursor gi|10177758|dbj|BAB11071.1| xyloglucan endo-1,4-beta-D-glucanase [Arabidopsis thaliana] gi|45825157|gb|AAS77486.1| At5g48070 [Arabidopsis thaliana] gi|62320256|dbj|BAD94531.1| xyloglucan endo-1,4-beta-D-glucanase [Arabidopsis thaliana] gi|332008233|gb|AED95616.1| xyloglucan endotransglucosylase/hydrolase protein 20 [Arabidopsis thaliana]		280	282	1.00E-133	100.7	81.8	87.5	xyloglucan endotransglucosylase/hydrolase protein 20	gbpln	Arabidopsis thaliana	AT5G48070.1 | Symbols: ATXTH20, XTH20 | xyloglucan endotransglucosylase/hydrolase 20 | chr5:19482158-19483231 FORWARD LENGTH=282	280	282	1.00E-136	100.7	81.8	87.5
Rsa1.0_00027.1.g1713.t1	ref|XP_002867352.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297313188|gb|EFH43611.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]		153	169	2.00E-37	110.5	64.7	74.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G30370.1 | Symbols: | RING/U-box superfamily protein | chr4:14858743-14859273 REVERSE LENGTH=176	153	176	3.00E-39	115.0	64.1	75.8
Rsa1.0_00027.1.g1714.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00027.1.g1715.t1	gb|EOA17519.1| hypothetical protein CARUB_v10005852mg [Capsella rubella]		180	180	1.00E-81	100.0	87.2	95.0	hypothetical protein CARUB_v10005852mg	gbpln	Capsella rubella	AT4G30410.1 | Symbols: | sequence-specific DNA binding transcription factors | chr4:14871309-14871851 REVERSE LENGTH=180	180	180	2.00E-81	100.0	88.9	94.4
Rsa1.0_00027.1.g1716.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00027.1.g1717.t3	ref|NP_194771.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75181441|sp|Q9M0B8.1|WTR37_ARATH RecName: Full=WAT1-related protein At4g30420 gi|7269943|emb|CAB79760.1| nodulin-like protein [Arabidopsis thaliana] gi|332660363|gb|AEE85763.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]		390	373	1.00E-179	95.6	80.5	85.9	nodulin MtN21 /EamA-like transporter family protein	gbpln	Arabidopsis thaliana	AT4G30420.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:14877069-14878914 FORWARD LENGTH=373	390	373	0	95.6	80.5	85.9
Rsa1.0_00027.1.g1718.t1	gb|AAD22330.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		213	631	1.00E-30	296.2	34.7	53.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	213	746	9.00E-29	350.2	32.9	43.7
Rsa1.0_00027.1.g1719.t1	ref|NP_194782.1| class I glutamine amidotransferase domain-containing protein [Arabidopsis thaliana] gi|15294152|gb|AAK95253.1|AF410267_1 AT4g30530/F17I23_130 [Arabidopsis thaliana] gi|7269954|emb|CAB79771.1| putative protein [Arabidopsis thaliana] gi|20147269|gb|AAM10348.1| AT4g30530/F17I23_130 [Arabidopsis thaliana] gi|332660377|gb|AEE85777.1| class I glutamine amidotransferase domain-containing protein [Arabidopsis thaliana]		250	250	1.00E-129	100.0	88.8	93.6	class I glutamine amidotransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT4G30530.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr4:14920605-14922286 FORWARD LENGTH=250	250	250	1.00E-132	100.0	88.8	93.6
Rsa1.0_00027.1.g1720.t1	gb|EOA17311.1| hypothetical protein CARUB_v10005590mg [Capsella rubella]		253	249	1.00E-124	98.4	83.4	91.3	hypothetical protein CARUB_v10005590mg	gbpln	Capsella rubella	AT4G30550.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr4:14925618-14926713 FORWARD LENGTH=249	253	249	1.00E-125	98.4	85.4	91.7
Rsa1.0_00027.1.g1721.t1	gb|EOA18329.1| hypothetical protein CARUB_v10006848mg [Capsella rubella]		191	187	6.00E-68	97.9	71.7	78.5	hypothetical protein CARUB_v10006848mg	gbpln	Capsella rubella	AT4G30590.1 | Symbols: ENODL12, AtENODL12 | early nodulin-like protein 12 | chr4:14935760-14936469 REVERSE LENGTH=190	191	190	1.00E-64	99.5	73.3	80.6
Rsa1.0_00027.1.g1722.t1	ref|XP_002867336.1| hypothetical protein ARALYDRAFT_913413 [Arabidopsis lyrata subsp. lyrata] gi|297313172|gb|EFH43595.1| hypothetical protein ARALYDRAFT_913413 [Arabidopsis lyrata subsp. lyrata]		182	181	2.00E-85	99.5	91.8	94.5	hypothetical protein ARALYDRAFT_913413	gbpln	Arabidopsis lyrata	AT4G30620.1 | Symbols: | Uncharacterised BCR, YbaB family COG0718 | chr4:14948724-14950035 REVERSE LENGTH=180	182	180	5.00E-87	98.9	90.1	92.9
Rsa1.0_00027.1.g1723.t1	gb|EOA18905.1| hypothetical protein CARUB_v10007535mg [Capsella rubella]		301	301	1.00E-133	100.0	74.8	84.7	hypothetical protein CARUB_v10007535mg	gbpln	Capsella rubella	AT4G30640.1 | Symbols: | RNI-like superfamily protein | chr4:14952670-14953682 FORWARD LENGTH=301	301	301	1.00E-127	100.0	70.8	83.1
Rsa1.0_00027.1.g1724.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00027.1.g1725.t1	ref|XP_002869411.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315247|gb|EFH45670.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	272	280	2.00E-72	102.9	51.8	69.5	predicted protein	gbpln	Arabidopsis lyrata	AT4G29760.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G29770.2); Has 63 Blast hits to 63 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14574114-14575148 FORWARD LENGTH=280	272	280	1.00E-71	102.9	50.7	68.0
Rsa1.0_00027.1.g1726.t1	ref|XP_002869411.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315247|gb|EFH45670.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	270	280	2.00E-81	103.7	57.8	72.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G29760.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G29770.2); Has 63 Blast hits to 63 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14574114-14575148 FORWARD LENGTH=280	270	280	1.00E-79	103.7	56.7	71.5
Rsa1.0_00027.1.g1727.t6	ref|XP_002867329.1| hypothetical protein ARALYDRAFT_913400 [Arabidopsis lyrata subsp. lyrata] gi|297313165|gb|EFH43588.1| hypothetical protein ARALYDRAFT_913400 [Arabidopsis lyrata subsp. lyrata]	149	157	9.00E-67	105.4	87.9	91.9	hypothetical protein ARALYDRAFT_913400	gbpln	Arabidopsis lyrata	AT4G30770.1 | Symbols: | Putative membrane lipoprotein | chr4:14986140-14986613 REVERSE LENGTH=157	149	157	2.00E-61	105.4	86.6	90.6
Rsa1.0_00027.1.g1728.t1	gb|EOA16289.1| hypothetical protein CARUB_v10004435mg [Capsella rubella]	543	586	0	107.9	82.3	89.7	hypothetical protein CARUB_v10004435mg	gbpln	Capsella rubella	AT4G30780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24100.1); Has 109 Blast hits to 109 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 95; Viruses - 0; Other Eukaryotes - 13 (source: NCBI BLink). | chr4:14990523-14992855 FORWARD LENGTH=589	543	589	0	108.5	81.6	89.9
Rsa1.0_00027.1.g1729.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00027.1.g1730.t2	gb|EOA15927.1| hypothetical protein CARUB_v10004021mg [Capsella rubella]	267	1147	9.00E-34	429.6	31.8	41.6	hypothetical protein CARUB_v10004021mg	gbpln	Capsella rubella	AT4G30790.1 | Symbols: | INVOLVED IN: autophagy; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Autophagy-related protein 17 (InterPro:IPR007240), Autophagy-related protein 11 (InterPro:IPR019460); Has 8793 Blast hits to 6268 proteins in 570 species: Archae - 89; Bacteria - 657; Metazoa - 4844; Fungi - 808; Plants - 441; Viruses - 15; Other Eukaryotes - 1939 (source: NCBI BLink). | chr4:14993383-14997785 REVERSE LENGTH=1148	267	1148	2.00E-31	430.0	33.0	41.9
Rsa1.0_00027.1.g1731.t1	ref|NP_567854.1| carboxypeptidase D [Arabidopsis thaliana] gi|75332010|sp|Q949Q7.1|SCP29_ARATH RecName: Full=Serine carboxypeptidase-like 29; Flags: Precursor gi|15293049|gb|AAK93635.1| putative serine carboxypeptidase II [Arabidopsis thaliana] gi|22136958|gb|AAM91708.1| putative serine carboxypeptidase II [Arabidopsis thaliana] gi|332660411|gb|AEE85811.1| serine carboxypeptidase-like 29 [Arabidopsis thaliana]	472	479	0	101.5	85.6	92.2	carboxypeptidase D	gbpln	Arabidopsis thaliana	AT4G30810.1 | Symbols: scpl29 | serine carboxypeptidase-like 29 | chr4:15003474-15006017 FORWARD LENGTH=479	472	479	0	101.5	85.6	92.2
Rsa1.0_00027.1.g1732.t1	gb|EOA23552.1| hypothetical protein CARUB_v10016746mg [Capsella rubella]	502	722	2.00E-98	143.8	49.0	61.2	hypothetical protein CARUB_v10016746mg	gbpln	Capsella rubella	AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189	502	1189	1.00E-97	236.9	46.2	60.6
Rsa1.0_00027.1.g1733.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1382	1307	0	94.6	58.1	72.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1382	1262	1.00E-103	91.3	14.5	22.5
Rsa1.0_00027.1.g1734.t1	ref|XP_002870849.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316685|gb|EFH47108.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	394	1225	1.00E-143	310.9	61.9	74.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189	394	1189	1.00E-140	301.8	57.9	72.1
Rsa1.0_00027.1.g1735.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00027.1.g1736.t1	ref|XP_002869360.1| hypothetical protein ARALYDRAFT_491672 [Arabidopsis lyrata subsp. lyrata] gi|297315196|gb|EFH45619.1| hypothetical protein ARALYDRAFT_491672 [Arabidopsis lyrata subsp. lyrata]	183	182	3.00E-73	99.5	74.9	80.9	hypothetical protein ARALYDRAFT_491672	gbpln	Arabidopsis lyrata	AT4G30820.3 | Symbols: | cyclin-dependent kinase-activating kinase assembly factor-related / CDK-activating kinase assembly factor-related | chr4:15007144-15008378 FORWARD LENGTH=178	183	178	6.00E-67	97.3	71.6	79.2
Rsa1.0_00027.1.g1737.t1	ref|XP_002869358.1| SET domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315194|gb|EFH45617.1| SET domain-containing protein [Arabidopsis lyrata subsp. lyrata]	503	497	0	98.8	84.5	89.7	SET domain-containing protein	gbpln	Arabidopsis lyrata	AT4G30860.1 | Symbols: ASHR3, SDG4 | SET domain group 4 | chr4:15024546-15027427 FORWARD LENGTH=497	503	497	0	98.8	82.9	88.7
Rsa1.0_00027.1.g1738.t1	gb|EOA17813.1| hypothetical protein CARUB_v10006211mg [Capsella rubella]	110	109	8.00E-46	99.1	82.7	90.9	hypothetical protein CARUB_v10006211mg	gbpln	Capsella rubella	AT4G30880.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:15035229-15035750 FORWARD LENGTH=109	110	109	3.00E-47	99.1	82.7	87.3
Rsa1.0_00027.1.g1739.t3	gb|EOA16186.1| hypothetical protein CARUB_v10004326mg [Capsella rubella]	569	551	0	96.8	79.1	84.5	hypothetical protein CARUB_v10004326mg	gbpln	Capsella rubella	AT4G30890.3 | Symbols: UBP24 | ubiquitin-specific protease 24 | chr4:15036383-15038825 REVERSE LENGTH=551	569	551	0	96.8	76.4	82.2
Rsa1.0_00027.1.g1740.t1	ref|XP_002867320.1| hypothetical protein ARALYDRAFT_328625 [Arabidopsis lyrata subsp. lyrata] gi|297313156|gb|EFH43579.1| hypothetical protein ARALYDRAFT_328625 [Arabidopsis lyrata subsp. lyrata]	732	770	0	105.2	70.4	76.6	hypothetical protein ARALYDRAFT_328625	gbpln	Arabidopsis lyrata	AT4G30935.1 | Symbols: WRKY32, ATWRKY32 | WRKY DNA-binding protein 32 | chr4:15051916-15053908 REVERSE LENGTH=466	732	466	1.00E-159	63.7	42.8	46.9
Rsa1.0_00027.1.g1741.t1	ref|NP_178356.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|3184287|gb|AAC18934.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana] gi|330250497|gb|AEC05591.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	195	211	1.00E-41	108.2	40.0	57.9	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT2G02520.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr2:676771-678145 REVERSE LENGTH=211	195	211	4.00E-44	108.2	40.0	57.9
Rsa1.0_00027.1.g1742.t1	sp|P48627.1|FAD6C_BRANA RecName: Full=Omega-6 fatty acid desaturase, chloroplastic; Flags: Precursor gi|457631|gb|AAA50157.1| omega-6 desaturase [Brassica napus]	446	443	0	99.3	95.7	97.8	RecName: Full=Omega-6 fatty acid desaturase, chloroplastic; Flags: Precursor gi|457631|gb|AAA50157.1| omega-6 desaturase	gbpln	Brassica napus	AT4G30950.1 | Symbols: FAD6, FADC, SFD4 | fatty acid desaturase 6 | chr4:15057278-15059673 REVERSE LENGTH=448	446	448	0	100.4	91.7	96.4
Rsa1.0_00027.1.g1743.t1	ref|XP_002864803.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310638|gb|EFH41062.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	158	607	2.00E-12	384.2	31.6	35.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G62580.1 | Symbols: | ARM repeat superfamily protein | chr5:25120010-25122259 FORWARD LENGTH=615	158	615	7.00E-15	389.2	29.7	32.3
Rsa1.0_00027.1.g1744.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00027.1.g1745.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00027.1.g1746.t1	gb|AAG52094.1|AC012680_5 putative Mutator-like transposase; 12516-14947 [Arabidopsis thaliana]	771	761	0	98.7	49.8	63.6	putative Mutator-like transposase; 12516-14947	gbpln	Arabidopsis thaliana	AT3G30370.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Transposase, MuDR, plant (InterPro:IPR004332); BEST Arabidopsis thaliana protein match is: SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein (TAIR:AT1G18050.1); Has 35 Blast hits to 35 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:11965180-11965719 REVERSE LENGTH=179	771	179	5.00E-20	23.2	7.1	10.0
Rsa1.0_00027.1.g1747.t1	gb|EOA18341.1| hypothetical protein CARUB_v10006862mg [Capsella rubella]	424	448	0	105.7	92.0	96.2	hypothetical protein CARUB_v10006862mg	gbpln	Capsella rubella	AT4G30960.1 | Symbols: CIPK6, SIP3, SNRK3.14, ATCIPK6 | SOS3-interacting protein 3 | chr4:15067400-15068725 FORWARD LENGTH=441	424	441	0	104.0	92.0	96.2
Rsa1.0_00027.1.g1748.t2	ref|XP_002884524.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330364|gb|EFH60783.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	573	442	1.00E-170	77.1	56.4	60.4	protein binding protein	gbpln	Arabidopsis lyrata	AT3G05675.1 | Symbols: | BTB/POZ domain-containing protein | chr3:1658425-1659859 REVERSE LENGTH=441	573	441	1.00E-169	77.0	54.3	59.3
Rsa1.0_00027.1.g1749.t2	gb|ACP30603.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1111	1056	0	95.0	68.0	75.4	disease resistance protein	gbpln	Brassica rapa	AT5G18370.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6085036-6088926 REVERSE LENGTH=1210	1111	1210	0	108.9	48.7	61.7
Rsa1.0_00027.1.g1750.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00027.1.g1751.t3	gb|ACP30603.1| disease resistance protein [Brassica rapa subsp. pekinensis]	938	1056	0	112.6	66.2	74.3	disease resistance protein	gbpln	Brassica rapa	AT5G44510.1 | Symbols: TAO1 | target of AVRB operation1 | chr5:17929673-17934188 REVERSE LENGTH=1187	938	1187	1.00E-132	126.5	36.6	49.5
Rsa1.0_00027.1.g1752.t1	ref|XP_002882430.1| hypothetical protein ARALYDRAFT_477858 [Arabidopsis lyrata subsp. lyrata] gi|297328270|gb|EFH58689.1| hypothetical protein ARALYDRAFT_477858 [Arabidopsis lyrata subsp. lyrata]	860	869	0	101.0	77.4	84.2	hypothetical protein ARALYDRAFT_477858	gbpln	Arabidopsis lyrata	AT3G05670.1 | Symbols: | RING/U-box protein | chr3:1653888-1657022 FORWARD LENGTH=883	860	883	0	102.7	77.8	85.2
Rsa1.0_00027.1.g1753.t1	ref|NP_683531.2| tetratricopeptide repeat-containing protein [Arabidopsis thaliana] gi|27311659|gb|AAO00795.1| Unknown protein [Arabidopsis thaliana] gi|30023732|gb|AAP13399.1| At3g05625 [Arabidopsis thaliana] gi|332640747|gb|AEE74268.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	259	257	1.00E-135	99.2	88.4	94.6	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G05625.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:1632408-1633912 FORWARD LENGTH=257	259	257	1.00E-137	99.2	88.4	94.6
Rsa1.0_00027.1.g1754.t1	gb|EOA32651.1| hypothetical protein CARUB_v10015948mg [Capsella rubella]	772	702	0	90.9	71.0	78.0	hypothetical protein CARUB_v10015948mg	gbpln	Capsella rubella	AT3G05610.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:1625876-1627976 REVERSE LENGTH=669	772	669	0	86.7	68.8	76.2
Rsa1.0_00027.1.g1755.t1	ref|XP_002882427.1| hypothetical protein ARALYDRAFT_477850 [Arabidopsis lyrata subsp. lyrata] gi|297328267|gb|EFH58686.1| hypothetical protein ARALYDRAFT_477850 [Arabidopsis lyrata subsp. lyrata]	187	187	1.00E-100	100.0	97.3	98.9	hypothetical protein ARALYDRAFT_477850	gbpln	Arabidopsis lyrata	AT3G05590.1 | Symbols: RPL18 | ribosomal protein L18 | chr3:1621511-1622775 FORWARD LENGTH=187	187	187	1.00E-102	100.0	97.3	98.4
Rsa1.0_00027.1.g1756.t1	gb|EOA31060.1| hypothetical protein CARUB_v10014212mg [Capsella rubella]	203	318	1.00E-109	156.7	94.1	98.5	hypothetical protein CARUB_v10014212mg	gbpln	Capsella rubella	AT3G05580.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr3:1618216-1619850 REVERSE LENGTH=318	203	318	1.00E-112	156.7	93.6	98.5
Rsa1.0_00028.1.g1757.t1	gb|EOA12688.1| hypothetical protein CARUB_v10027918mg [Capsella rubella]	267	515	2.00E-97	192.9	71.9	79.0	hypothetical protein CARUB_v10027918mg	gbpln	Capsella rubella	AT5G48830.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19800269-19802625 REVERSE LENGTH=511	267	511	4.00E-78	191.4	66.3	76.4
Rsa1.0_00028.1.g1758.t1	gb|EOA12563.1| hypothetical protein CARUB_v10026830mg [Capsella rubella]	117	308	1.00E-24	263.2	47.0	52.1	hypothetical protein CARUB_v10026830mg	gbpln	Capsella rubella	AT5G48850.1 | Symbols: ATSDI1 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:19805576-19807699 REVERSE LENGTH=306	117	306	3.00E-21	261.5	37.6	41.9
Rsa1.0_00028.1.g1759.t1	gb|EOA12563.1| hypothetical protein CARUB_v10026830mg [Capsella rubella]	382	308	1.00E-145	80.6	64.1	68.1	hypothetical protein CARUB_v10026830mg	gbpln	Capsella rubella	AT5G48850.1 | Symbols: ATSDI1 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:19805576-19807699 REVERSE LENGTH=306	382	306	2.33E-156	80.1	66.8	69.6
Rsa1.0_00028.1.g1760.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00028.1.g1761.t1	ref|NP_199698.1| U6 snRNA-associated Sm-like protein LSm5 [Arabidopsis thaliana] gi|9758886|dbj|BAB09440.1| U6 snRNA-associated Sm-like protein-like [Arabidopsis thaliana] gi|16554971|gb|AAK61592.1| Sm-like protein [Arabidopsis thaliana] gi|106879147|gb|ABF82603.1| At5g48870 [Arabidopsis thaliana] gi|332008352|gb|AED95735.1| U6 snRNA-associated Sm-like protein LSm5 [Arabidopsis thaliana] gi|386305005|gb|AFJ05005.1| hypothetical protein [Arabidopsis thaliana]	141	88	1.00E-31	62.4	56.7	58.9	U6 snRNA-associated Sm-like protein LSm5	gbpln	Arabidopsis thaliana	AT5G48870.1 | Symbols: SAD1 | Small nuclear ribonucleoprotein family protein | chr5:19813407-19814362 FORWARD LENGTH=88	141	88	4.00E-34	62.4	56.7	58.9
Rsa1.0_00028.1.g1762.t1	ref|XP_002865685.1| KAT5/PKT1/PKT2 peroxisomal 3-keto-acyl-CoA thiolase [Arabidopsis lyrata subsp. lyrata] gi|297311520|gb|EFH41944.1| KAT5/PKT1/PKT2 peroxisomal 3-keto-acyl-CoA thiolase [Arabidopsis lyrata subsp. lyrata]	461	457	0	99.1	89.2	94.1	KAT5/PKT1/PKT2 peroxisomal 3-keto-acyl-CoA thiolase	gbpln	Arabidopsis lyrata	AT5G48880.3 | Symbols: | peroxisomal 3-keto-acyl-CoA thiolase 2 | chr5:19814576-19817021 REVERSE LENGTH=457	461	457	0	99.1	89.2	93.9

Rsa1.0_00028.1.g1763.t1	ref|NP_199700.1| C2H2-like zinc finger protein [Arabidopsis thaliana] gi|9758888|dbj|BAB09442.1| unnamed protein product [Arabidopsis thaliana] gi|332008356|gb|AED95739.1| C2H2-like zinc finger protein [Arabidopsis thaliana]	167	173	1.00E-54	103.6	72.5	79.6	C2H2-like zinc finger protein	gbpln	Arabidopsis thaliana	AT5G48890.1 | Symbols: | C2H2-like zinc finger protein | chr5:19820353-19820874 FORWARD LENGTH=173	167	173	6.00E-57	103.6	72.5	79.6
Rsa1.0_00028.1.g1764.t1	gb|EOA13438.1| hypothetical protein CARUB_v10026482mg [Capsella rubella]	417	417	0	100.0	93.5	95.4	hypothetical protein CARUB_v10026482mg	gbpln	Capsella rubella	AT5G48900.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:19825240-19828909 FORWARD LENGTH=417	417	417	0	100.0	94.7	97.4
Rsa1.0_00028.1.g1765.t1	ref|XP_002876919.1| hypothetical protein ARALYDRAFT_904719 [Arabidopsis lyrata subsp. lyrata] gi|297322757|gb|EFH53178.1| hypothetical protein ARALYDRAFT_904719 [Arabidopsis lyrata subsp. lyrata]	328	330	2.00E-63	100.6	44.2	55.5	hypothetical protein ARALYDRAFT_904719	gbpln	Arabidopsis lyrata	AT3G19520.2 | Symbols: | Protein of unknown function (DUF626) | chr3:6772773-6774209 FORWARD LENGTH=312	328	312	3.00E-50	95.1	35.7	51.8
Rsa1.0_00028.1.g1766.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00028.1.g1767.t3	emb|CAA54075.1| phytochrome E [Arabidopsis thaliana] gi|5816999|emb|CAB53654.1| phytochrome E [Arabidopsis thaliana] gi|7268606|emb|CAB78815.1| phytochrome E [Arabidopsis thaliana]	262	1112	6.00E-33	424.4	32.4	34.4	phytochrome E	gbpln	Arabidopsis thaliana	AT4G18130.1 | Symbols: PHYE | phytochrome E | chr4:10042312-10045948 REVERSE LENGTH=1112	262	1112	2.00E-35	424.4	32.4	34.4
Rsa1.0_00028.1.g1768.t1	gb|AAL32602.1| Unknown protein [Arabidopsis thaliana]	607	642	0	105.8	94.2	96.5	Unknown protein	gbpln	Arabidopsis thaliana	AT5G48960.1 | Symbols: | HAD-superfamily hydrolase, subfamily IG, 5'-nucleotidase | chr5:19849645-19853382 FORWARD LENGTH=642	607	642	0	105.8	94.2	96.5
Rsa1.0_00028.1.g1769.t1	ref|XP_002865696.1| hypothetical protein ARALYDRAFT_917838 [Arabidopsis lyrata subsp. lyrata] gi|297311531|gb|EFH41955.1| hypothetical protein ARALYDRAFT_917838 [Arabidopsis lyrata subsp. lyrata]	107	107	9.00E-50	100.0	86.0	95.3	hypothetical protein ARALYDRAFT_917838	gbpln	Arabidopsis lyrata	AT5G24860.1 | Symbols: FPF1, ATFPF1 | flowering promoting factor 1 | chr5:8541822-8542154 FORWARD LENGTH=110	107	110	1.00E-31	102.8	58.9	77.6
Rsa1.0_00028.1.g1770.t1	ref|NP_199713.2| histone-arginine methyltransferase CARM1 [Arabidopsis thaliana] gi|152013379|sp|A3KPF2.1|ANM14_ARATH RecName: Full=Probable histone-arginine methyltransferase 1.4; Short=AtPRMT14; AltName: Full=Coactivator-associated methyltransferase 1B; AltName: Full=Protein arginine N-methyltransferase 4A; Short=AtPRMT4A gi|126352276|gb|ABO09883.1| At5g49020 [Arabidopsis thaliana] gi|126352282|gb|ABO09886.1| At5g49020 [Arabidopsis thaliana] gi|332008378|gb|AED95761.1| protein arginine methyltransferase 4A [Arabidopsis thaliana]	526	528	0	100.4	89.0	92.0	histone-arginine methyltransferase CARM1	gbpln	Arabidopsis thaliana	AT5G49020.1 | Symbols: ATPRMT4A, PRMT4A | protein arginine methyltransferase 4A | chr5:19871341-19874683 FORWARD LENGTH=528	526	528	0	100.4	89.0	92.0
Rsa1.0_00028.1.g1771.t1	ref|NP_001190497.1| isoleucyl-tRNA synthetase [Arabidopsis thaliana] gi|332008381|gb|AED95764.1| isoleucyl-tRNA synthetase [Arabidopsis thaliana]	1048	1279	0	122.0	93.4	97.2	isoleucyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT5G49030.3 | Symbols: OVA2 | tRNA synthetase class I (I, L, M and V) family protein | chr5:19875091-19883251 REVERSE LENGTH=1279	1048	1279	0	122.0	93.4	97.2
Rsa1.0_00028.1.g1772.t1	ref|XP_002863949.1| hypothetical protein ARALYDRAFT_917855 [Arabidopsis lyrata subsp. lyrata] gi|297309784|gb|EFH40208.1| hypothetical protein ARALYDRAFT_917855 [Arabidopsis lyrata subsp. lyrata]	167	167	3.00E-79	100.0	85.6	92.8	hypothetical protein ARALYDRAFT_917855	gbpln	Arabidopsis lyrata	AT5G49050.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to stress; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: UspA (InterPro:IPR006016), Rossmann-like alpha/beta/alpha sandwich fold (InterPro:IPR014729); BEST Arabidopsis thaliana protein match is: Adenine nucleotide alpha hydrolases-like superfamily protein (TAIR:AT2G47710.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19883929-19884381 FORWARD LENGTH=150	167	150	1.00E-54	89.8	58.7	65.9
Rsa1.0_00028.1.g1773.t1	gb|EOA14459.1| hypothetical protein CARUB_v10027668mg [Capsella rubella]	404	465	0	115.1	84.9	93.3	hypothetical protein CARUB_v10027668mg	gbpln	Capsella rubella	AT5G49070.1 | Symbols: KCS21 | 3-ketoacyl-CoA synthase 21 | chr5:19888751-19890145 REVERSE LENGTH=464	404	464	0	114.9	83.9	93.3

Rsa1.0_00028.1.g1774.t1	ref|XP_002865709.1| hypothetical protein ARALYDRAFT_917876 [Arabidopsis lyrata subsp. lyrata] gi|297311544|gb|EFH41968.1| hypothetical protein ARALYDRAFT_917876 [Arabidopsis lyrata subsp. lyrata]	372	384	1.00E-109	103.2	71.0	78.2	hypothetical protein ARALYDRAFT_917876	gbpln	Arabidopsis lyrata	AT5G49100.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06868.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19897700-19898890 REVERSE LENGTH=396	372	396	1.00E-107	106.5	72.6	81.2
Rsa1.0_00028.1.g1775.t2	ref|XP_002863960.1| hypothetical protein ARALYDRAFT_917877 [Arabidopsis lyrata subsp. lyrata] gi|297309795|gb|EFH40219.1| hypothetical protein ARALYDRAFT_917877 [Arabidopsis lyrata subsp. lyrata]	1444	1450	0	100.4	83.2	90.1	hypothetical protein ARALYDRAFT_917877	gbpln	Arabidopsis lyrata	AT5G49110.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19900203-19905925 FORWARD LENGTH=1469	1444	1469	0	101.7	82.7	90.1
Rsa1.0_00028.1.g1776.t1	ref|XP_002863963.1| hypothetical protein ARALYDRAFT_917882 [Arabidopsis lyrata subsp. lyrata] gi|297309798|gb|EFH40222.1| hypothetical protein ARALYDRAFT_917882 [Arabidopsis lyrata subsp. lyrata]	1086	921	0	84.8	70.2	76.2	hypothetical protein ARALYDRAFT_917882	gbpln	Arabidopsis lyrata	AT5G49150.1 | Symbols: ATGEX2, GEX2 | gamete expressed 2 | chr5:19924760-19928527 FORWARD LENGTH=914	1086	914	0	84.2	69.0	75.2
Rsa1.0_00028.1.g1777.t1	ref|NP_199728.1| uncharacterized protein [Arabidopsis thaliana] gi|110737324|dbj|BAF00608.1| hypothetical protein [Arabidopsis thaliana] gi|332008395|gb|AED95778.1| uncharacterized protein AT5G49170 [Arabidopsis thaliana]	175	185	1.00E-53	105.7	69.1	75.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G49170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06840.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19938839-19939482 REVERSE LENGTH=185	175	185	6.00E-56	105.7	69.1	75.4
Rsa1.0_00028.1.g1778.t1	gb|ABB97028.1| unknown [Brassica rapa]	198	193	5.00E-89	97.5	82.8	91.4	unknown	gbpln	Brassica rapa	AT5G49210.2 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19950093-19951464 FORWARD LENGTH=195	198	195	1.00E-76	98.5	72.2	85.9
Rsa1.0_00028.1.g1779.t1	ref|NP_680409.1| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana] gi|20258821|gb|AAM14020.1| unknown protein [Arabidopsis thaliana] gi|22136814|gb|AAM91751.1| unknown protein [Arabidopsis thaliana] gi|332008401|gb|AED95784.1| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	444	449	0	101.1	83.1	89.2	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	gbpln	Arabidopsis thaliana	AT5G49215.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:19953670-19955874 FORWARD LENGTH=449	444	449	0	101.1	83.1	89.2
Rsa1.0_00028.1.g1780.t1	ref|XP_002863975.1| hypothetical protein ARALYDRAFT_494985 [Arabidopsis lyrata subsp. lyrata] gi|297309810|gb|EFH40234.1| hypothetical protein ARALYDRAFT_494985 [Arabidopsis lyrata subsp. lyrata]	409	418	2.33E-156	102.2	75.1	81.4	hypothetical protein ARALYDRAFT_494985	gbpln	Arabidopsis lyrata	AT5G49220.1 | Symbols: | Protein of unknown function (DUF789) | chr5:19956627-19958453 FORWARD LENGTH=409	409	409	1.00E-144	100.0	72.1	79.0
Rsa1.0_00028.1.g1781.t1	ref|XP_002863976.1| hypothetical protein ARALYDRAFT_357174 [Arabidopsis lyrata subsp. lyrata] gi|297309811|gb|EFH40235.1| hypothetical protein ARALYDRAFT_357174 [Arabidopsis lyrata subsp. lyrata]	496	280	4.00E-78	56.5	31.9	40.1	hypothetical protein ARALYDRAFT_357174	gbpln	Arabidopsis lyrata	AT5G49240.1 | Symbols: APRR4, PRR4 | pseudo-response regulator 4 | chr5:19962934-19964351 FORWARD LENGTH=292	496	292	2.00E-77	58.9	30.0	38.7
Rsa1.0_00028.1.g1782.t1	ref|XP_002865724.1| hypothetical protein ARALYDRAFT_494989 [Arabidopsis lyrata subsp. lyrata] gi|297311559|gb|EFH41983.1| hypothetical protein ARALYDRAFT_494989 [Arabidopsis lyrata subsp. lyrata]	167	161	2.00E-24	96.4	72.5	76.0	hypothetical protein ARALYDRAFT_494989	gbpln	Arabidopsis lyrata	AT5G49280.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:19976842-19977330 REVERSE LENGTH=162	167	162	1.00E-12	97.0	18.6	19.8
Rsa1.0_00028.1.g1783.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00028.1.g1784.t1	ref|NP_199741.1| GATA transcription factor 16 [Arabidopsis thaliana] gi|71660826|sp|Q9FJ10.1|GAT16_ARATH RecName: Full=GATA transcription factor 16 gi|10177159|dbj|BAB10348.1| unnamed protein product [Arabidopsis thaliana] gi|117168139|gb|ABK32152.1| At5g49300 [Arabidopsis thaliana] gi|225879100|dbj|BAH30620.1| hypothetical protein [Arabidopsis thaliana] gi|332008411|gb|AED95794.1| GATA transcription factor 16 [Arabidopsis thaliana]	136	139	2.00E-46	102.2	77.9	83.8	GATA transcription factor 16	gbpln	Arabidopsis thaliana	AT5G49300.1 | Symbols: GATA16 | GATA transcription factor 16 | chr5:19984849-19985475 REVERSE LENGTH=139	136	139	4.00E-49	102.2	77.9	83.8
Rsa1.0_00028.1.g1785.t1	ref|XP_002882488.1| AT-IMP [Arabidopsis lyrata subsp. lyrata] gi|297328328|gb|EFH58747.1| AT-IMP [Arabidopsis lyrata subsp. lyrata]	533	532	0	99.8	70.0	80.9	AT-IMP	gbpln	Arabidopsis lyrata	AT3G06720.2 | Symbols: AT-IMP, ATKAP ALPHA, AIMP ALPHA | importin alpha isoform 1 | chr3:2120559-2123555 FORWARD LENGTH=532	533	532	0	99.8	69.4	80.9
Rsa1.0_00028.1.g1786.t1	ref|XP_002865728.1| hypothetical protein ARALYDRAFT_917912 [Arabidopsis lyrata subsp. lyrata] gi|297311563|gb|EFH41987.1| hypothetical protein ARALYDRAFT_917912 [Arabidopsis lyrata subsp. lyrata]	257	257	1.00E-136	100.0	93.0	96.1	hypothetical protein ARALYDRAFT_917912	gbpln	Arabidopsis lyrata	AT5G49320.1 | Symbols: | Protein of unknown function (DUF1218) | chr5:19995083-19996214 REVERSE LENGTH=257	257	257	1.00E-137	100.0	92.6	95.3
Rsa1.0_00028.1.g1787.t1	ref|XP_002865730.1| hypothetical protein ARALYDRAFT_331346 [Arabidopsis lyrata subsp. lyrata] gi|297311565|gb|EFH41989.1| hypothetical protein ARALYDRAFT_331346 [Arabidopsis lyrata subsp. lyrata]	444	459	0	103.4	85.8	91.0	hypothetical protein ARALYDRAFT_331346	gbpln	Arabidopsis lyrata	AT5G49340.1 | Symbols: TBL4 | TRICHOME BIREFRINGENCE-LIKE 4 | chr5:20007348-20009038 REVERSE LENGTH=457	444	457	0	102.9	84.5	91.7
Rsa1.0_00028.1.g1788.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00028.1.g1789.t1	ref|NP_199747.1| beta-xylosidase 1 [Arabidopsis thaliana] gi|75262458|sp|Q9FGY1.1|BXL1_ARATH RecName: Full=Beta-D-xylosidase 1; Short=AtBXL1; AltName: Full=Alpha-L-arabinofuranosidase; Flags: Precursor gi|9759419|dbj|BAB09906.1| xylosidase [Arabidopsis thaliana] gi|21539545|gb|AAM53325.1| xylosidase [Arabidopsis thaliana] gi|332008419|gb|AED95802.1| beta-xylosidase 1 [Arabidopsis thaliana]	772	774	0	100.3	92.7	96.9	beta-xylosidase 1	gbpln	Arabidopsis thaliana	AT5G49360.1 | Symbols: BXL1, ATBXL1 | beta-xylosidase 1 | chr5:20012179-20016659 REVERSE LENGTH=774	772	774	0	100.3	92.7	96.9
Rsa1.0_00028.1.g1790.t1	ref|XP_002884605.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330445|gb|EFH60864.1| binding protein [Arabidopsis lyrata subsp. lyrata]	750	864	0	115.2	67.6	79.7	binding protein	gbpln	Arabidopsis lyrata	AT3G06670.1 | Symbols: | binding | chr3:2105908-2113136 REVERSE LENGTH=865	750	865	0	115.3	68.1	79.9
Rsa1.0_00028.1.g1791.t1	ref|XP_002314930.1| predicted protein [Populus trichocarpa] gi|222863970|gb|EEF01101.1| predicted protein [Populus trichocarpa]	277	258	9.00E-60	93.1	49.8	56.0	predicted protein	gbpln	Populus trichocarpa	AT5G49400.1 | Symbols: | zinc knuckle (CCHC-type) family protein | chr5:20031154-20031981 FORWARD LENGTH=275	277	275	1.00E-54	99.3	42.6	45.8
Rsa1.0_00028.1.g1792.t1	ref|XP_002863981.1| hypothetical protein ARALYDRAFT_357185 [Arabidopsis lyrata subsp. lyrata] gi|297309816|gb|EFH40240.1| hypothetical protein ARALYDRAFT_357185 [Arabidopsis lyrata subsp. lyrata]	142	143	2.00E-65	100.7	88.0	91.5	hypothetical protein ARALYDRAFT_357185	gbpln	Arabidopsis lyrata	AT5G49410.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73940.1); Has 58 Blast hits to 58 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:20032901-20033751 FORWARD LENGTH=145	142	145	2.00E-65	102.1	88.0	92.3
Rsa1.0_00028.1.g1793.t1	gb|EOA39471.1| hypothetical protein CARUB_v10008066mg [Capsella rubella]	81	2170	1.00E-31	2679.0	85.2	88.9	hypothetical protein CARUB_v10008066mg	gbpln	Capsella rubella	AT1G20960.2 | Symbols: emb1507 | U5 small nuclear ribonucleoprotein helicase, putative | chr1:7302591-7309914 REVERSE LENGTH=2171	81	2171	3.00E-33	2680.2	82.7	86.4
Rsa1.0_00028.1.g1794.t1	ref|XP_002865733.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297311568|gb|EFH41992.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	460	1662	1.00E-45	361.3	24.8	27.4	transducin family protein	gbpln	Arabidopsis lyrata	AT5G49430.1 | Symbols: | WD40/YVTN repeat-like-containing domain;Bromodomain | chr5:20037338-20045454 REVERSE LENGTH=1677	460	1677	8.00E-48	364.6	25.2	27.4
Rsa1.0_00028.1.g1795.t1	gb|EOA12770.1| hypothetical protein CARUB_v10028626mg [Capsella rubella]	504	608	0	120.6	86.5	90.1	hypothetical protein CARUB_v10028626mg	gbpln	Capsella rubella	AT5G49460.1 | Symbols: ACLB-2 | ATP citrate lyase subunit B 2 | chr5:20055048-20058195 FORWARD LENGTH=608	504	608	0	120.6	86.7	89.9
Rsa1.0_00028.1.g1796.t1	#	#	#	#	#	#	#	–	----	----	AT1G06900.1 | Symbols: | Insulinase (Peptidase family M16) family protein | chr1:2115155-2120635 REVERSE LENGTH=1024	236	1024	3.00E-12	433.9	27.1	45.8
Rsa1.0_00028.1.g1797.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00028.1.g1798.t1	#	#	#	#	#	#	#	–	----	----	AT1G10430.1 | Symbols: PP2A-2 | protein phosphatase 2A-2 | chr1:3428705-3430437 REVERSE LENGTH=306	141	306	8.00E-11	217.0	35.5	44.0
Rsa1.0_00028.1.g1799.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00028.1.g1800.t1	ref|NP_199763.1| putative WRKY transcription factor 48 [Arabidopsis thaliana] gi|20978785|sp|Q9FGZ4.1|WRK48_ARATH RecName: Full=Probable WRKY transcription factor 48; AltName: Full=WRKY DNA-binding protein 48 gi|17064166|gb|AAL35290.1|AF442397_1 WRKY transcription factor 48 [Arabidopsis thaliana] gi|10177618|dbj|BAB10765.1| unnamed protein product [Arabidopsis thaliana] gi|17380792|gb|AAL36226.1| unknown protein [Arabidopsis thaliana] gi|20259613|gb|AAM14163.1| unknown protein [Arabidopsis thaliana] gi|332008441|gb|AED95824.1| putative WRKY transcription factor 48 [Arabidopsis thaliana]	390	399	1.00E-125	102.3	77.4	85.9	putative WRKY transcription factor 48	gbpln	Arabidopsis thaliana	AT5G49520.1 | Symbols: WRKY48, ATWRKY48 | WRKY DNA-binding protein 48 | chr5:20090890-20092867 FORWARD LENGTH=399	390	399	1.00E-128	102.3	77.4	85.9
Rsa1.0_00028.1.g1801.t2	gb|EOA12473.1| hypothetical protein CARUB_v10025904mg [Capsella rubella]	613	800	5.00E-92	130.5	32.0	37.7	hypothetical protein CARUB_v10025904mg	gbpln	Capsella rubella	AT5G59560.2 | Symbols: SRR1 | sensitivity to red light reduced protein (SRR1) | chr5:24000747-24001574 REVERSE LENGTH=275	613	275	6.00E-94	44.9	28.1	33.3
Rsa1.0_00028.1.g1802.t1	ref|XP_002864001.1| hypothetical protein ARALYDRAFT_917948 [Arabidopsis lyrata subsp. lyrata] gi|297309836|gb|EFH40260.1| hypothetical protein ARALYDRAFT_917948 [Arabidopsis lyrata subsp. lyrata]	172	172	1.00E-72	100.0	82.0	89.5	hypothetical protein ARALYDRAFT_917948	gbpln	Arabidopsis lyrata	AT5G49600.1 | Symbols: | Protein of unknown function, DUF538 | chr5:20130780-20131295 FORWARD LENGTH=171	172	171	4.00E-72	99.4	76.7	81.4
Rsa1.0_00028.1.g1803.t1	gb|AAM60856.1| unknown [Arabidopsis thaliana]	359	359	1.00E-172	100.0	83.3	89.1	unknown	gbpln	Arabidopsis thaliana	AT5G49610.1 | Symbols: | F-box family protein | chr5:20131448-20132527 REVERSE LENGTH=359	359	359	1.00E-174	100.0	83.3	89.1
Rsa1.0_00028.1.g1804.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00028.1.g1805.t1	ref|XP_002865745.1| AtMYB78 [Arabidopsis lyrata subsp. lyrata] gi|297311580|gb|EFH42004.1| AtMYB78 [Arabidopsis lyrata subsp. lyrata]	318	306	1.00E-119	96.2	74.2	84.9	AtMYB78	gbpln	Arabidopsis lyrata	AT5G49620.1 | Symbols: AtMYB78, MYB78 | myb domain protein 78 | chr5:20137491-20139384 REVERSE LENGTH=307	318	307	1.00E-118	96.5	71.1	83.0
Rsa1.0_00028.1.g1806.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00028.1.g1807.t1	ref|XP_002872333.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318170|gb|EFH48592.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	238	238	1.00E-129	100.0	91.2	96.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G29560.1 | Symbols: | caleosin-related family protein | chr5:11190543-11191963 REVERSE LENGTH=220	238	220	1.00E-111	92.4	80.3	87.8
Rsa1.0_00028.1.g1808.t1	ref|NP_568512.3| myb family transcription factor [Arabidopsis thaliana] gi|75328846|sp|Q8GUN5.1|PHL1_ARATH RecName: Full=Protein PHR1-LIKE 1; AltName: Full=Myb-like transcription factor 1 gi|26983850|gb|AAN86177.1| unknown protein [Arabidopsis thaliana] gi|332006474|gb|AED93857.1| myb family transcription factor [Arabidopsis thaliana]	410	413	1.00E-159	100.7	77.1	84.1	myb family transcription factor	gbpln	Arabidopsis thaliana	AT5G29000.2 | Symbols: PHL1 | Homeodomain-like superfamily protein | chr5:11022336-11024229 REVERSE LENGTH=413	410	413	1.00E-161	100.7	77.1	84.1
Rsa1.0_00028.1.g1809.t1	ref|NP_568509.1| protein phosphatase 2 (formerly 2A), regulatory subunit B'' [Arabidopsis thaliana] gi|42740922|gb|AAS44557.1| protein phosphatase 2A beta [Arabidopsis thaliana] gi|332006463|gb|AED93846.1| protein phosphatase 2A B' beta [Arabidopsis thaliana]	458	536	0	117.0	77.5	86.5	protein phosphatase 2 (formerly 2A), regulatory subunit B''	gbpln	Arabidopsis thaliana	AT5G28850.2 | Symbols: | Calcium-binding EF-hand family protein | chr5:10877360-10881278 REVERSE LENGTH=536	458	536	0	117.0	77.5	86.5
Rsa1.0_00028.1.g1810.t7	ref|XP_002872330.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297318167|gb|EFH48589.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	625	536	0	85.8	70.9	75.2	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT5G28900.1 | Symbols: | Calcium-binding EF-hand family protein | chr5:10925852-10929892 FORWARD LENGTH=536	625	536	0	85.8	70.6	75.0
Rsa1.0_00028.1.g1811.t1	gb|AET14213.1| GDP-D-mannose-3,5-epimerase [Brassica rapa subsp. chinensis]	379	379	0	100.0	96.6	98.4	GDP-D-mannose-3,5-epimerase	gbpln	Brassica rapa	AT5G28840.2 | Symbols: GME | GDP-D-mannose 3',5'-epimerase | chr5:10862472-10864024 REVERSE LENGTH=377	379	377	0	99.5	96.3	97.6
Rsa1.0_00028.1.g1812.t1	dbj|BAJ34351.1| unnamed protein product [Thellungiella halophila]	354	319	1.00E-136	90.1	75.1	79.1	unnamed protein product	----	----	AT5G28770.2 | Symbols: BZO2H3 | bZIP transcription factor family protein | chr5:10796648-10798147 REVERSE LENGTH=314	354	314	1.00E-125	88.7	71.5	74.0

Rsa1.0_00028.1.g1813.t1	gb|EOA19859.1| hypothetical protein CARUB_v10000110mg, partial [Capsella rubella]	844	1050	0	124.4	71.4	74.4	hypothetical protein CARUB_v10000110mg, partial	gbpln	Capsella rubella	AT5G28740.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:10780774-10783772 FORWARD LENGTH=917	844	917	0	108.6	71.4	74.6
Rsa1.0_00028.1.g1814.t1	gb|EOA22561.1| hypothetical protein CARUB_v10003221mg [Capsella rubella]	854	859	0	100.6	88.5	94.6	hypothetical protein CARUB_v10003221mg	gbpln	Capsella rubella	AT5G28680.1 | Symbols: ANX2 | Malectin/receptor-like protein kinase family protein | chr5:10719437-10722013 REVERSE LENGTH=858	854	858	0	100.5	87.2	94.1
Rsa1.0_00029.1.g1815.t2	ref|XP_002881778.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327617|gb|EFH58037.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	428	326	1.00E-166	76.2	65.4	69.6	predicted protein	gbpln	Arabidopsis lyrata	AT2G41480.1 | Symbols: | Peroxidase superfamily protein | chr2:17296986-17298729 REVERSE LENGTH=341	428	341	1.00E-167	79.7	65.4	69.4
Rsa1.0_00029.1.g1816.t1	ref|XP_002879932.1| apurinic endonuclease-redox protein [Arabidopsis lyrata subsp. lyrata] gi|297325771|gb|EFH56191.1| apurinic endonuclease-redox protein [Arabidopsis lyrata subsp. lyrata]	522	550	0	105.4	81.8	89.3	apurinic endonuclease-redox protein	gbpln	Arabidopsis lyrata	AT2G41460.1 | Symbols: ARP | apurinic endonuclease-redox protein | chr2:17285731-17288769 FORWARD LENGTH=536	522	536	0	102.7	80.1	87.9
Rsa1.0_00029.1.g1817.t1	gb|ADP37978.1| ERD15 protein [Brassica napus]	143	157	2.00E-61	109.8	87.4	94.4	ERD15 protein	gbpln	Brassica napus	AT2G41430.5 | Symbols: ERD15 | dehydration-induced protein (ERD15) | chr2:17269736-17270314 FORWARD LENGTH=163	143	163	1.00E-52	114.0	83.2	88.8
Rsa1.0_00029.1.g1818.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00029.1.g1819.t1	ref|XP_002492787.1| Protein involved in positive regulation of both 1,3-beta-glucan synthesis and the Pkc1p-MAPK pathway [Komagataella pastoris GS115] gi|238032585|emb|CAY70608.1| Protein involved in positive regulation of both 1,3-beta-glucan synthesis and the Pkc1p-MAPK pathway [Komagataella pastoris GS115]	77	1338	5.00E-11	1737.7	48.1	48.1	Protein involved in positive regulation of both 1,3-beta-glucan synthesis and the Pkc1p-MAPK pathway	gbpln	Komagataella pastoris	#	#	#	#	#	#	#
Rsa1.0_00029.1.g1820.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00029.1.g1821.t1	gb|EOA29383.1| hypothetical protein CARUB_v10025670mg [Capsella rubella]	295	298	1.00E-155	101.0	91.5	96.6	hypothetical protein CARUB_v10025670mg	gbpln	Capsella rubella	AT2G41350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G21980.1); Has 188 Blast hits to 188 proteins in 66 species: Archae - 0; Bacteria - 12; Metazoa - 90; Fungi - 15; Plants - 54; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr2:17231565-17233458 FORWARD LENGTH=298	295	298	1.00E-156	101.0	90.8	96.3
Rsa1.0_00029.1.g1822.t1	gb|ABK28027.1| unknown [Arabidopsis thaliana]	82	83	5.00E-26	101.2	76.8	81.7	unknown	gbpln	Arabidopsis thaliana	AT2G41342.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:17230650-17230898 REVERSE LENGTH=82	82	82	4.00E-28	100.0	75.6	80.5
Rsa1.0_00029.1.g1823.t1	ref|XP_002879920.1| hypothetical protein ARALYDRAFT_903442 [Arabidopsis lyrata subsp. lyrata] gi|297325759|gb|EFH56179.1| hypothetical protein ARALYDRAFT_903442 [Arabidopsis lyrata subsp. lyrata]	49	67	4.00E-13	136.7	75.5	77.6	hypothetical protein ARALYDRAFT_903442	gbpln	Arabidopsis lyrata	AT3G57062.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system. | chr3:21121443-21121589 FORWARD LENGTH=48	49	48	1.00E-12	98.0	61.2	73.5
Rsa1.0_00029.1.g1824.t1	ref|XP_002881767.1| hypothetical protein ARALYDRAFT_321816 [Arabidopsis lyrata subsp. lyrata] gi|297327606|gb|EFH58026.1| hypothetical protein ARALYDRAFT_321816 [Arabidopsis lyrata subsp. lyrata]	369	370	0	100.3	88.3	94.9	hypothetical protein ARALYDRAFT_321816	gbpln	Arabidopsis lyrata	AT2G41300.1 | Symbols: SSL1 | strictosidine synthase-like 1 | chr2:17214312-17216292 REVERSE LENGTH=394	369	394	1.00E-171	106.8	77.0	81.8
Rsa1.0_00029.1.g1825.t1	ref|XP_002881766.1| hypothetical protein ARALYDRAFT_483200 [Arabidopsis lyrata subsp. lyrata] gi|297327605|gb|EFH58025.1| hypothetical protein ARALYDRAFT_483200 [Arabidopsis lyrata subsp. lyrata]	375	376	0	100.3	84.0	92.0	hypothetical protein ARALYDRAFT_483200	gbpln	Arabidopsis lyrata	AT2G41290.1 | Symbols: SSL2 | strictosidine synthase-like 2 | chr2:17210599-17212904 REVERSE LENGTH=376	375	376	0	100.3	83.2	90.1

Rsa1.0_00029.1_g1826.t1	ref|XP_002879918.1| hypothetical protein ARALYDRAFT_345920 [Arabidopsis lyrata subsp. lyrata] gi|297325757|gb|EFH56177.1| hypothetical protein ARALYDRAFT_345920 [Arabidopsis lyrata subsp. lyrata]	207	156	5.00E-18	75.4	37.7	43.5	hypothetical protein ARALYDRAFT_345920	gbpln	Arabidopsis lyrata	AT2G41280.1 | Symbols: M10, ATM10 | late embryogenesis abundant protein (M10) / LEA protein M10 | chr2:17209763-17210211 FORWARD LENGTH=107	207	107	1.00E-10	51.7	31.4	36.2
Rsa1.0_00029.1_g1827.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00029.1_g1828.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1632	1270	0	77.8	34.5	47.1	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1632	575	6.00E-81	35.2	10.5	16.8
Rsa1.0_00029.1_g1829.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00029.1_g1830.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00029.1_g1831.t1	gb|EOA30627.1| hypothetical protein CARUB_v10013762mg [Capsella rubella]	284	428	5.00E-42	150.7	31.7	34.9	hypothetical protein CARUB_v10013762mg	gbpln	Capsella rubella	AT3G03950.3 | Symbols: ECT1 | evolutionarily conserved C-terminal region 1 | chr3:1021502-1023767 FORWARD LENGTH=428	284	428	4.00E-44	150.7	31.7	33.8
Rsa1.0_00029.1_g1832.t1	ref|XP_002879915.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325754|gb|EFH56174.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata]	773	772	0	99.9	93.0	97.4	phosphatidylinositol-4-phosphate 5-kinase family protein	gbpln	Arabidopsis lyrata	AT2G41210.1 | Symbols: PIP5K5 | phosphatidylinositol- 4-phosphate 5-kinase 5 | chr2:17173627-17176575 FORWARD LENGTH=772	773	772	0	99.9	93.3	97.7
Rsa1.0_00029.1_g1833.t1	ref|XP_002879914.1| hypothetical protein ARALYDRAFT_483189 [Arabidopsis lyrata subsp. lyrata] gi|297325753|gb|EFH56173.1| hypothetical protein ARALYDRAFT_483189 [Arabidopsis lyrata subsp. lyrata]	140	161	3.00E-68	115.0	89.3	95.7	hypothetical protein ARALYDRAFT_483189	gbpln	Arabidopsis lyrata	AT2G41200.1 | Symbols: | unknown protein; Has 26 Blast hits to 26 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17171657-17172929 FORWARD LENGTH=161	140	161	2.00E-63	115.0	88.6	95.7
Rsa1.0_00029.1_g1834.t1	#	#	#	#	#	#	#	-	----	----	AT3G18000.1 | Symbols: NMT1, XPL1, PEAMT | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:6154578-6157331 FORWARD LENGTH=491	136	491	2.00E-11	361.0	23.5	27.9
Rsa1.0_00029.1_g1835.t1	ref|NP_030664.1| transmembrane amino acid transporter-like protein [Arabidopsis thaliana] gi|14532708|gb|AAK64155.1| unknown protein [Arabidopsis thaliana] gi|19310729|gb|AAL85095.1| unknown protein [Arabidopsis thaliana] gi|20197120|gb|AAD11993.2| expressed protein [Arabidopsis thaliana] gi|330254848|gb|AEC09942.1| transmembrane amino acid transporter-like protein [Arabidopsis thaliana]	544	536	0	98.5	78.5	83.1	transmembrane amino acid transporter-like protein	gbpln	Arabidopsis thaliana	AT2G41190.1 | Symbols: | Transmembrane amino acid transporter family protein | chr2:17167561-17170145 REVERSE LENGTH=536	544	536	0	98.5	78.5	83.1
Rsa1.0_00029.1_g1836.t1	ref|XP_002879913.1| hypothetical protein ARALYDRAFT_483187 [Arabidopsis lyrata subsp. lyrata] gi|297325752|gb|EFH56172.1| hypothetical protein ARALYDRAFT_483187 [Arabidopsis lyrata subsp. lyrata]	138	140	3.00E-52	101.4	80.4	87.0	hypothetical protein ARALYDRAFT_483187	gbpln	Arabidopsis lyrata	AT2G41180.1 | Symbols: | VQ motif-containing protein | chr2:17165242-17165667 FORWARD LENGTH=141	138	141	7.00E-52	102.2	77.5	84.1
Rsa1.0_00029.1_g1837.t2	gb|ABO36622.1| copia LTR rider [Solanum lycopersicum] gi|133711819|gb|ABO36636.1| copia LTR rider [Solanum lycopersicum]	957	1307	0	136.6	59.6	69.4	copia LTR rider	gbpln	Solanum lycopersicum	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	957	1262	2.00E-52	131.9	12.4	18.8
Rsa1.0_00029.1_g1838.t1	ref|NP_181647.1| CDPK-related kinase 1 [Arabidopsis thaliana] gi|75318680|sp|O80673.1|CAMK1_ARATH RecName: Full=CDPK-related kinase 1; Short=AtCRK1; AltName: Full=Calcium/calmodulin-dependent protein kinase 3; AltName: Full=Calmodulin-binding protein kinase 3; Short=AtCBK3; Short=CaM-binding protein kinase 3 gi|5020366|gb|AAD38058.1|AF153351_1 CDPK-related kinase 1 [Arabidopsis thaliana] gi|16904218|gb|AAL30816.1|AF435448_1 calcium/calmodulin-dependent protein kinase CaMK3 [Arabidopsis thaliana] gi|3402722|gb|AAD12016.1| CPDK-related protein kinase [Arabidopsis thaliana] gi|330254842|gb|AEC09936.1| CDPK-related kinase 1 [Arabidopsis thaliana]	520	576	0	110.8	94.8	96.7	CDPK-related kinase 1	gbpln	Arabidopsis thaliana	AT2G41140.1 | Symbols: CRK1, ATCRK1, ATCBK3 | CDPK-related kinase 1 | chr2:17150492-17153378 FORWARD LENGTH=576	520	576	0	110.8	94.8	96.7

Rsa1.0_00029.1.g1839.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1534	1342	0	87.5	43.5	60.6	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1534	1262	2.00E-87	82.3	12.3	17.4
Rsa1.0_00029.1.g1840.t1	ref|XP_002879910.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297325749|gb|EFH56169.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	263	253	1.00E-110	96.2	85.2	90.9	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT2G41130.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:17143360-17144686 FORWARD LENGTH=253	263	253	1.00E-111	96.2	84.0	90.9
Rsa1.0_00029.1.g1841.t1	gb|EOA26366.1| hypothetical protein CARUB_v10023283mg [Capsella rubella]	383	422	1.00E-144	110.2	67.9	79.4	hypothetical protein CARUB_v10023283mg	gbpln	Capsella rubella	AT2G40910.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17069938-17071554 REVERSE LENGTH=449	383	449	1.00E-138	117.2	62.9	78.9
Rsa1.0_00029.1.g1842.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00029.1.g1843.t2	gb|EOA26366.1| hypothetical protein CARUB_v10023283mg [Capsella rubella]	179	422	4.00E-28	235.8	41.3	53.6	hypothetical protein CARUB_v10023283mg	gbpln	Capsella rubella	AT2G40910.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17069938-17071554 REVERSE LENGTH=449	179	449	1.00E-29	250.8	35.8	45.3
Rsa1.0_00029.1.g1844.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00029.1.g1845.t1	ref|XP_002881746.1| hypothetical protein ARALYDRAFT_321778 [Arabidopsis lyrata subsp. lyrata] gi|297327585|gb|EFH58005.1| hypothetical protein ARALYDRAFT_321778 [Arabidopsis lyrata subsp. lyrata]	385	449	1.00E-134	116.6	62.6	77.4	hypothetical protein ARALYDRAFT_321778	gbpln	Arabidopsis lyrata	AT2G40910.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17069938-17071554 REVERSE LENGTH=449	385	449	1.00E-132	116.6	61.0	77.7
Rsa1.0_00029.1.g1846.t1	ref|NP_181623.2| F-box protein [Arabidopsis thaliana] gi|122215015|sp|Q3EBI7.1|FB130_ARATH RecName: Full=F-box protein At2g40910 gi|330254802|gb|AEC09896.1| F-box protein [Arabidopsis thaliana]	391	449	1.00E-82	114.8	43.0	54.5	F-box protein	gbpln	Arabidopsis thaliana	AT2G40910.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17069938-17071554 REVERSE LENGTH=449	391	449	3.00E-85	114.8	43.0	54.5
Rsa1.0_00029.1.g1847.t1	dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	361	1098	2.00E-58	304.2	30.5	35.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	361	237	8.00E-23	65.7	16.3	24.7
Rsa1.0_00029.1.g1848.t1	gb|EOA26681.1| hypothetical protein CARUB_v10022762mg [Capsella rubella]	780	696	0	89.2	76.9	81.8	hypothetical protein CARUB_v10022762mg	gbpln	Capsella rubella	AT2G40980.1 | Symbols: | Protein kinase superfamily protein | chr2:17102090-17104443 FORWARD LENGTH=617	780	617	0	79.1	57.1	60.0
Rsa1.0_00029.1.g1849.t1	ref|NP_850337.1| cytochrome P450 98A3 [Arabidopsis thaliana] gi|5915859|sp|O22203.1|C98A3_ARATH RecName: Full=Cytochrome P450 98A3; AltName: Full=Protein REDUCED EPIDERMAL FLUORESCENCE 8; AltName: Full=p-coumaroylshikimate/quinate 3'-hydrolxylase; Short=C3'H gi|330254799|gb|AEC09893.1| cytochrome P450 98A3 [Arabidopsis thaliana]	508	508	0	100.0	95.1	97.2	cytochrome P450 98A3	gbpln	Arabidopsis thaliana	AT2G40890.1 | Symbols: CYP98A3 | cytochrome P450, family 98, subfamily A, polypeptide 3 | chr2:17058291-17060532 REVERSE LENGTH=508	508	508	0	100.0	95.1	97.2
Rsa1.0_00029.1.g1850.t1	gb|AAL86314.1| putative cysteine proteinase inhibitor cystatin B [Arabidopsis thaliana]	116	116	5.00E-19	100.0	42.2	44.0	putative cysteine proteinase inhibitor cystatin B	gbpln	Arabidopsis thaliana	AT2G40880.1 | Symbols: FL3-27, ATCYSA, CYSA | cystatin A | chr2:17057463-17057930 FORWARD LENGTH=125	116	125	1.00E-21	107.8	42.2	44.0
Rsa1.0_00029.1.g1851.t2	dbj|BAJ33673.1| unnamed protein product [Thellungiella halophila]	684	654	0	95.6	84.8	89.2	unnamed protein product	----	----	AT2G40860.1 | Symbols: | protein kinase family protein / protein phosphatase 2C (PP2C) family protein | chr2:17053747-17057108 REVERSE LENGTH=658	684	658	0	96.2	83.6	89.5
Rsa1.0_00029.1.g1852.t1	ref|NP_181617.1| phosphoinositide 4-kinase gamma 1 [Arabidopsis thaliana] gi|2623299|gb|AAB86445.1| hypothetical protein [Arabidopsis thaliana] gi|330254796|gb|AEC09890.1| phosphoinositide 4-kinase gamma 1 [Arabidopsis thaliana]	541	561	0	103.7	86.5	91.9	phosphoinositide 4-kinase gamma 1	gbpln	Arabidopsis thaliana	AT2G40850.1 | Symbols: ATPI4K GAMMA 1, PI4K GAMMA 1 | phosphoinositide 4-kinase gamma 1 | chr2:17051575-17053260 FORWARD LENGTH=561	541	561	0	103.7	86.5	91.9
Rsa1.0_00029.1.g1853.t1	ref|XP_002879893.1| ring-H2 finger C1A [Arabidopsis lyrata subsp. lyrata] gi|297325732|gb|EFH56152.1| ring-H2 finger C1A [Arabidopsis lyrata subsp. lyrata]	310	329	1.00E-132	106.1	85.2	90.3	ring-H2 finger C1A	gbpln	Arabidopsis lyrata	AT2G40830.3 | Symbols: RHC1A | RING-H2 finger C1A | chr2:17043642-17044628 FORWARD LENGTH=328	310	328	1.00E-133	105.8	82.9	88.7

Rsa1.0_00029.1.g1854.t1	gb|AAB86442.1| hypothetical protein [Arabidopsis thaliana]	392	945	2.00E-97	241.1	63.0	71.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G40815.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:17034736-17036110 REVERSE LENGTH=367	392	367	3.00E-68	93.6	30.9	34.2
Rsa1.0_00029.1.g1855.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00029.1.g1856.t1	gb|EOA28930.1| hypothetical protein CARUB_v10025177mg [Capsella rubella]	331	322	2.00E-70	97.3	41.4	48.0	hypothetical protein CARUB_v10025177mg	gbpln	Capsella rubella	AT2G40815.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:17034736-17036110 REVERSE LENGTH=367	331	367	3.00E-68	110.9	44.4	51.1
Rsa1.0_00029.1.g1857.t2	ref|XP_002879696.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325535|gb|EFH55955.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	194	389	8.00E-12	200.5	21.1	22.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G56440.1 | Symbols: ATATG18D, ATG18D | homolog of yeast autophagy 18 (ATG18) D | chr3:20926874-20928797 FORWARD LENGTH=391	194	391	2.00E-12	201.5	19.6	21.1
Rsa1.0_00030.1.g1858.t1	ref|XP_002882450.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297328290|gb|EFH58709.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	206	202	1.00E-100	98.1	88.8	93.7	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT3G06120.1 | Symbols: MUTE | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:1846531-1848016 FORWARD LENGTH=202	206	202	1.00E-101	98.1	89.3	94.2
Rsa1.0_00030.1.g1859.t1	gb|EOA30708.1| hypothetical protein CARUB_v10013845mg [Capsella rubella]	394	407	0	103.3	89.1	95.2	hypothetical protein CARUB_v10013845mg	gbpln	Capsella rubella	AT3G06190.1 | Symbols: ATBPM2, BPM2 | BTB-POZ and MATH domain 2 | chr3:1874577-1876575 REVERSE LENGTH=406	394	406	0	103.0	88.6	94.4
Rsa1.0_00030.1.g1860.t1	ref|NP_187269.1| ribosomal protein L34e-like protein [Arabidopsis thaliana] gi|6862922|gb|AAF30311.1|AC018907_11 unknown protein [Arabidopsis thaliana] gi|62867643|gb|AAY17425.1| At3g06180 [Arabidopsis thaliana] gi|90962960|gb|ABE02404.1| At3g06180 [Arabidopsis thaliana] gi|332640836|gb|AEE74357.1| ribosomal protein L34e-like protein [Arabidopsis thaliana]	203	241	4.00E-73	118.7	87.2	93.1	ribosomal protein L34e-like protein	gbpln	Arabidopsis thaliana	AT3G06180.1 | Symbols: | Ribosomal protein L34e superfamily protein | chr3:1871705-1873554 FORWARD LENGTH=241	203	241	1.00E-75	118.7	87.2	93.1
Rsa1.0_00030.1.g1861.t1	gb|EOA29649.1| hypothetical protein CARUB_v10015151mg [Capsella rubella]	351	351	0	100.0	92.9	96.3	hypothetical protein CARUB_v10015151mg	gbpln	Capsella rubella	AT3G06260.1 | Symbols: GATL4 | galacturonosyltransferase-like 4 | chr3:1893804-1894859 REVERSE LENGTH=351	351	351	0	100.0	93.2	96.3
Rsa1.0_00030.1.g1862.t1	ref|XP_002882459.1| hypothetical protein ARALYDRAFT_477927 [Arabidopsis lyrata subsp. lyrata] gi|297328299|gb|EFH58718.1| hypothetical protein ARALYDRAFT_477927 [Arabidopsis lyrata subsp. lyrata]	351	348	1.00E-180	99.1	89.5	92.6	hypothetical protein ARALYDRAFT_477927	gbpln	Arabidopsis lyrata	AT3G06270.1 | Symbols: | Protein phosphatase 2C family protein | chr3:1896763-1897887 FORWARD LENGTH=348	351	348	0	99.1	88.6	92.0
Rsa1.0_00030.1.g1863.t1	ref|XP_002882462.1| hypothetical protein ARALYDRAFT_896744 [Arabidopsis lyrata subsp. lyrata] gi|297328302|gb|EFH58721.1| hypothetical protein ARALYDRAFT_896744 [Arabidopsis lyrata subsp. lyrata]	410	425	1.00E-132	103.7	61.5	76.3	hypothetical protein ARALYDRAFT_896744	gbpln	Arabidopsis lyrata	AT1G03710.2 | Symbols: | Cystatin/monellin superfamily protein | chr1:923492-924287 FORWARD LENGTH=202	410	202	3.00E-28	49.3	17.6	25.6
Rsa1.0_00030.1.g1864.t1	gb|EOA30590.1| hypothetical protein CARUB_v10013722mg [Capsella rubella]	436	440	1.00E-169	100.9	77.8	83.3	hypothetical protein CARUB_v10013722mg	gbpln	Capsella rubella	AT3G06330.1 | Symbols: | RING/U-box superfamily protein | chr3:1917334-1919709 FORWARD LENGTH=426	436	426	1.00E-169	97.7	75.5	82.1
Rsa1.0_00030.1.g1865.t1	ref|XP_002884573.1| EMB3004/MEE32 [Arabidopsis lyrata subsp. lyrata] gi|297330413|gb|EFH60832.1| EMB3004/MEE32 [Arabidopsis lyrata subsp. lyrata]	604	603	0	99.8	85.6	91.2	EMB3004/MEE32	gbpln	Arabidopsis lyrata	AT3G06350.1 | Symbols: EMB3004, MEE32 | dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative | chr3:1924536-1927701 REVERSE LENGTH=603	604	603	0	99.8	86.3	90.6
Rsa1.0_00030.1.g1866.t1	gb|EOA31716.1| hypothetical protein CARUB_v10014924mg [Capsella rubella]	126	126	4.00E-26	100.0	60.3	65.9	hypothetical protein CARUB_v10014924mg	gbpln	Capsella rubella	AT3G06360.1 | Symbols: AGP27, ATAGP27 | arabinogalactan protein 27 | chr3:1928976-1929353 FORWARD LENGTH=125	126	125	8.00E-28	99.2	73.8	83.3
Rsa1.0_00030.1.g1867.t1	dbj|BAF01676.1| hypothetical protein [Arabidopsis thaliana]	223	450	3.00E-46	201.8	47.1	65.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G26540.1 | Symbols: | Agenet domain-containing protein | chr1:9167783-9170795 REVERSE LENGTH=695	223	695	1.00E-48	311.7	47.1	65.0
Rsa1.0_00030.1.g1868.t1	ref|NP_182245.1| uncharacterized protein [Arabidopsis thaliana] gi|2275201|gb|AAB63823.1| unknown protein [Arabidopsis thaliana] gi|330255722|gb|AEC10816.1| uncharacterized protein AT2G47230 [Arabidopsis thaliana]	417	701	3.00E-91	168.1	50.8	61.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G47230.1 | Symbols: DUF6, ATDUF6 | DOMAIN OF UNKNOWN FUNCTION 724 6 | chr2:19387126-19390011 FORWARD LENGTH=701	417	701	8.00E-94	168.1	50.8	61.4
Rsa1.0_00030.1.g1869.t5	gb|EOA32811.1| hypothetical protein CARUB_v10016122mg [Capsella rubella]	616	1058	0	171.8	83.4	85.9	hypothetical protein CARUB_v10016122mg	gbpln	Capsella rubella	AT3G06400.1 | Symbols: CHR11 | chromatin-remodeling protein 11 | chr3:1941066-1946700 FORWARD LENGTH=1055	616	1055	0	171.3	83.9	86.2

<table>
<tr><td>Rsa1.0_00030.1.g1870.t1</td><td>gb|ADK63414.1| CCCH type zinc finger protein [Brassica rapa]</td><td>467</td><td>455</td><td>0</td><td>97.4</td><td>80.9</td><td>87.6</td><td>CCCH type zinc finger protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G06410.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr3:1947471-1949528 REVERSE LENGTH=462</td><td>467</td><td>462</td><td>1.00E-175</td><td>98.9</td><td>81.8</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00030.1.g1871.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>511</td><td>1274</td><td>2.00E-92</td><td>249.3</td><td>38.2</td><td>55.6</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>511</td><td>575</td><td>8.00E-62</td><td>112.5</td><td>30.5</td><td>47.7</td></tr>
<tr><td>Rsa1.0_00030.1.g1872.t1</td><td>ref|XP_002882368.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata] gi|297328208|gb|EFH58627.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata]</td><td>181</td><td>392</td><td>2.00E-32</td><td>216.6</td><td>45.9</td><td>58.6</td><td>hypothetical protein ARALYDRAFT_896506</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G29970.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:14662765-14663917 REVERSE LENGTH=283</td><td>181</td><td>283</td><td>1.00E-24</td><td>156.4</td><td>34.8</td><td>48.6</td></tr>
<tr><td>Rsa1.0_00030.1.g1873.t1</td><td>gb|EOA31508.1| hypothetical protein CARUB_v10014696mg [Capsella rubella]</td><td>183</td><td>196</td><td>7.00E-35</td><td>107.1</td><td>45.4</td><td>60.1</td><td>hypothetical protein CARUB_v10014696mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G06435.1 | Symbols: | Expressed protein | chr3:1970102-1970704 REVERSE LENGTH=200</td><td>183</td><td>200</td><td>3.00E-37</td><td>109.3</td><td>45.9</td><td>59.6</td></tr>
<tr><td>Rsa1.0_00030.1.g1874.t14</td><td>ref|NP_566284.1| putative beta-1,3-galactosyltransferase 16 [Arabidopsis thaliana] gi|75167739|sp|Q9ASW1.1|B3GTG_ARATH RecName: Full=Probable beta-1,3-galactosyltransferase 16 gi|13605629|gb|AAK32808.1|AF361640_1 AT3g06440/F24P17_7 [Arabidopsis thaliana] gi|25090104|gb|AAN72229.1| At3g06440/F24P17_7 [Arabidopsis thaliana] gi|332640872|gb|AEE74393.1| putative beta-1,3-galactosyltransferase 16 [Arabidopsis thaliana]</td><td>959</td><td>619</td><td>0</td><td>64.5</td><td>47.5</td><td>51.9</td><td>putative beta-1,3-galactosyltransferase 16</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G06440.1 | Symbols: | Galactosyltransferase family protein | chr3:1972913-1975272 REVERSE LENGTH=619</td><td>959</td><td>619</td><td>0</td><td>64.5</td><td>47.5</td><td>51.9</td></tr>
<tr><td>Rsa1.0_00030.1.g1875.t1</td><td>ref|NP_187298.1| GNS1/SUR4 membrane-like protein [Arabidopsis thaliana] gi|6437542|gb|AAF08569.1|AC011623_2 unknown protein [Arabidopsis thaliana] gi|332640878|gb|AEE74399.1| GNS1/SUR4 membrane-like protein [Arabidopsis thaliana]</td><td>273</td><td>278</td><td>1.00E-130</td><td>101.8</td><td>88.6</td><td>93.0</td><td>GNS1/SUR4 membrane-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G06470.1 | Symbols: | GNS1/SUR4 membrane protein family | chr3:1984206-1985042 FORWARD LENGTH=278</td><td>273</td><td>278</td><td>1.00E-132</td><td>101.8</td><td>88.6</td><td>93.0</td></tr>
<tr><td>Rsa1.0_00030.1.g1876.t1</td><td>ref|XP_002882473.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|297328313|gb|EFH58732.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata]</td><td>294</td><td>278</td><td>1.00E-115</td><td>94.6</td><td>72.1</td><td>79.3</td><td>GNS1/SUR4 membrane family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G06470.1 | Symbols: | GNS1/SUR4 membrane protein family | chr3:1984206-1985042 FORWARD LENGTH=278</td><td>294</td><td>278</td><td>1.00E-116</td><td>94.6</td><td>72.1</td><td>79.6</td></tr>
<tr><td>Rsa1.0_00030.1.g1877.t1</td><td>ref|NP_187298.1| GNS1/SUR4 membrane-like protein [Arabidopsis thaliana] gi|6437542|gb|AAF08569.1|AC011623_2 unknown protein [Arabidopsis thaliana] gi|332640878|gb|AEE74399.1| GNS1/SUR4 membrane-like protein [Arabidopsis thaliana]</td><td>236</td><td>278</td><td>8.00E-91</td><td>117.8</td><td>76.3</td><td>86.0</td><td>GNS1/SUR4 membrane-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G06470.1 | Symbols: | GNS1/SUR4 membrane protein family | chr3:1984206-1985042 FORWARD LENGTH=278</td><td>236</td><td>278</td><td>2.00E-93</td><td>117.8</td><td>76.3</td><td>86.0</td></tr>
<tr><td>Rsa1.0_00030.1.g1878.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00030.1.g1879.t1</td><td>ref|XP_002882474.1| botrytis-susceptible1, myb domain protein 108 [Arabidopsis lyrata subsp. lyrata] gi|297328314|gb|EFH58733.1| botrytis-susceptible1, myb domain protein 108 [Arabidopsis lyrata subsp. lyrata]</td><td>311</td><td>322</td><td>1.00E-150</td><td>103.5</td><td>89.4</td><td>94.5</td><td>botrytis-susceptible1, myb domain protein 108</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G06490.1 | Symbols: MYB108, AtMYB108, BOS1 | myb domain protein 108 | chr3:2004298-2006358 FORWARD LENGTH=323</td><td>311</td><td>323</td><td>1.00E-144</td><td>103.9</td><td>88.7</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00030.1.g1880.t1</td><td>ref|NP_566285.1| beta-glucosidase-like SFR2 [Arabidopsis thaliana] gi|75305863|sp|Q93Y07.1|SFR2_ARATH RecName: Full=Beta-glucosidase-like SFR2, chloroplastic; AltName: Full=Protein SENSITIVE TO FREEZING 2; Short=AtSFR2 gi|16649039|gb|AAL24371.1| beta-glucosidase, putative [Arabidopsis thaliana] gi|22077112|emb|CAD36512.1| putative beta-glycosidase [Arabidopsis thaliana] gi|25083735|gb|AAN72111.1| beta-glucosidase, putative [Arabidopsis thaliana] gi|332640883|gb|AEE74404.1| beta-glucosidase-like SFR2 [Arabidopsis thaliana]</td><td>570</td><td>622</td><td>0</td><td>109.1</td><td>84.4</td><td>91.6</td><td>beta-glucosidase-like SFR2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G06510.1 | Symbols: SFR2, ATSFR2 | Glycosyl hydrolase superfamily protein | chr3:2016450-2019533 FORWARD LENGTH=622</td><td>570</td><td>622</td><td>0</td><td>109.1</td><td>84.4</td><td>91.6</td></tr>
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Rsa1.0_00030.1.g1881.t1	ref|XP_002884591.1| hypothetical protein ARALYDRAFT_477961 [Arabidopsis lyrata subsp. lyrata] gi|297330431|gb|EFH60850.1| hypothetical protein ARALYDRAFT_477961 [Arabidopsis lyrata subsp. lyrata]	559	545	0	97.5	89.3	92.5	hypothetical protein ARALYDRAFT_477961	gbpln	Arabidopsis lyrata	AT3G06550.2 | Symbols: | O-acetyltransferase family protein | chr3:2039408-2042664 REVERSE LENGTH=568	559	568	0	101.6	88.7	92.7
Rsa1.0_00030.1.g1882.t1	ref|XP_002884593.1| hypothetical protein ARALYDRAFT_896791 [Arabidopsis lyrata subsp. lyrata] gi|297330433|gb|EFH60852.1| hypothetical protein ARALYDRAFT_896791 [Arabidopsis lyrata subsp. lyrata]	496	496	0	100.0	91.5	95.6	hypothetical protein ARALYDRAFT_896791	gbpln	Arabidopsis lyrata	AT3G06580.1 | Symbols: GAL1, GALK | Mevalonate/galactokinase family protein | chr3:2049141-2051867 REVERSE LENGTH=496	496	496	0	100.0	91.1	95.2
Rsa1.0_00030.1.g1883.t1	ref|XP_002884594.1| hypothetical protein ARALYDRAFT_477966 [Arabidopsis lyrata subsp. lyrata] gi|297330434|gb|EFH60853.1| hypothetical protein ARALYDRAFT_477966 [Arabidopsis lyrata subsp. lyrata]	229	217	8.00E-68	94.8	69.4	80.3	hypothetical protein ARALYDRAFT_477966	gbpln	Arabidopsis lyrata	AT3G06590.2 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:2054647-2055312 REVERSE LENGTH=221	229	221	2.00E-64	96.5	69.4	79.9
Rsa1.0_00030.1.g1884.t1	ref|NP_187312.1| uncharacterized protein [Arabidopsis thaliana] gi|186509849|ref|NP_001118593.1| uncharacterized protein [Arabidopsis thaliana] gi|12322684|gb|AAG51336.1|AC020580_16 hypothetical protein; 25909-26809 [Arabidopsis thaliana] gi|49660141|gb|AAT68361.1| hypothetical protein At3g06600 [Arabidopsis thaliana] gi|50058941|gb|AAT69215.1| hypothetical protein At3g06600 [Arabidopsis thaliana] gi|332640899|gb|AEE74420.1| uncharacterized protein AT3G06600 [Arabidopsis thaliana] gi|332640900|gb|AEE74421.1| uncharacterized protein AT3G06600 [Arabidopsis thaliana]	193	193	4.00E-64	100.0	73.1	82.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G06600.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:2059558-2060458 REVERSE LENGTH=193	193	193	1.00E-66	100.0	73.1	82.9
Rsa1.0_00030.1.g1885.t1	gb|EOA31742.1| hypothetical protein CARUB_v10014957mg [Capsella rubella]	115	115	2.00E-52	100.0	93.0	95.7	hypothetical protein CARUB_v10014957mg	gbpln	Capsella rubella	AT3G06610.1 | Symbols: | DNA-binding enhancer protein-related | chr3:2060837-2061845 FORWARD LENGTH=115	115	115	6.00E-55	100.0	91.3	93.9
Rsa1.0_00030.1.g1886.t2	ref|NP_187314.1| PAS domain-containing tyrosine kinase-like protein [Arabidopsis thaliana] gi|12322680|gb|AAG51332.1|AC020580_12 protein kinase, putative; 19229-23534 [Arabidopsis thaliana] gi|20258844|gb|AAM13904.1| putative protein kinase [Arabidopsis thaliana] gi|21689823|gb|AAM67555.1| putative protein kinase [Arabidopsis thaliana] gi|110741529|dbj|BAE98714.1| putative protein kinase [Arabidopsis thaliana] gi|332640902|gb|AEE74423.1| PAS domain-containing tyrosine kinase-like protein [Arabidopsis thaliana]	766	773	0	100.9	87.3	93.5	PAS domain-containing tyrosine kinase-like protein	gbpln	Arabidopsis thaliana	AT3G06620.1 | Symbols: | PAS domain-containing protein tyrosine kinase family protein | chr3:2062833-2067138 REVERSE LENGTH=773	766	773	0	100.9	87.3	93.5
Rsa1.0_00030.1.g1887.t2	ref|NP_187314.1| PAS domain-containing tyrosine kinase-like protein [Arabidopsis thaliana] gi|12322680|gb|AAG51332.1|AC020580_12 protein kinase, putative; 19229-23534 [Arabidopsis thaliana] gi|20258844|gb|AAM13904.1| putative protein kinase [Arabidopsis thaliana] gi|21689823|gb|AAM67555.1| putative protein kinase [Arabidopsis thaliana] gi|110741529|dbj|BAE98714.1| putative protein kinase [Arabidopsis thaliana] gi|332640902|gb|AEE74423.1| PAS domain-containing tyrosine kinase-like protein [Arabidopsis thaliana]	170	773	5.00E-53	454.7	61.8	70.0	PAS domain-containing tyrosine kinase-like protein	gbpln	Arabidopsis thaliana	AT3G06620.1 | Symbols: | PAS domain-containing protein tyrosine kinase family protein | chr3:2062833-2067138 REVERSE LENGTH=773	170	773	2.00E-55	454.7	61.8	70.0
Rsa1.0_00030.1.g1888.t1	ref|NP_683536.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|332640914|gb|AEE74435.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	329	264	4.00E-69	80.2	53.5	59.9	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT3G36659.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:2100189-2100983 FORWARD LENGTH=264	329	264	1.00E-71	80.2	53.5	59.9

Rsa1.0_00030.1.g1889.t1	ref|NP_566289.1| PAPA−1−like and zinc finger−HIT domain−containing protein [Arabidopsis thaliana] gi|14334462|gb|AAK59429.1| unknown protein [Arabidopsis thaliana] gi|21436325|gb|AAM51332.1| unknown protein [Arabidopsis thaliana] gi|332640915|gb|AEE74436.1| PAPA−1−like and zinc finger−HIT domain−containing protein [Arabidopsis thaliana]	391	427	1.00E−125	109.2	72.1	79.5	PAPA−1−like and zinc finger−HIT domain−containing protein	gbpln	Arabidopsis thaliana	AT3G06660.1 | Symbols: | PAPA−1−like family protein / zinc finger (HIT type) family protein | chr3:2103060−2104776 FORWARD LENGTH=427	391	427	1.00E−127	109.2	72.1	79.5
Rsa1.0_00030.1.g1890.t1	ref|XP_002884605.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330445|gb|EFH60864.1| binding protein [Arabidopsis lyrata subsp. lyrata]	868	864	0	99.5	91.5	95.6	binding protein	gbpln	Arabidopsis lyrata	AT3G06670.1 | Symbols: | binding | chr3:2105908−2113136 REVERSE LENGTH=865	868	865	0	99.7	91.2	95.5
Rsa1.0_00030.1.g1891.t1	ref|XP_002880967.1| 60S ribosomal protein L29 [Arabidopsis lyrata subsp. lyrata] gi|297326806|gb|EFH57226.1| 60S ribosomal protein L29 [Arabidopsis lyrata subsp. lyrata]	61	61	1.00E−25	100.0	95.1	100.0	60S ribosomal protein L29	gbpln	Arabidopsis lyrata	AT3G06700.3 | Symbols: | Ribosomal L29e protein family | chr3:2117519−2117800 REVERSE LENGTH=61	61	61	4.00E−28	100.0	95.1	98.4
Rsa1.0_00030.1.g1892.t1	ref|XP_002882489.1| hypothetical protein ARALYDRAFT_477988 [Arabidopsis lyrata subsp. lyrata] gi|297328329|gb|EFH58748.1| hypothetical protein ARALYDRAFT_477988 [Arabidopsis lyrata subsp. lyrata]	186	183	4.00E−84	98.4	84.4	90.9	hypothetical protein ARALYDRAFT_477988	gbpln	Arabidopsis lyrata	AT3G06730.1 | Symbols: TRX P, TRX z | Thioredoxin z | chr3:2124276−2125845 FORWARD LENGTH=183	186	183	1.00E−85	98.4	82.8	90.3
Rsa1.0_00030.1.g1893.t1	ref|NP_566290.1| GATA transcription factor 15 [Arabidopsis thaliana] gi|71660789|sp|Q8LG10.2|GAT15_ARATH RecName: Full=GATA transcription factor 15 gi|17380940|gb|AAL36282.1| unknown protein [Arabidopsis thaliana] gi|20258947|gb|AAM14189.1| unknown protein [Arabidopsis thaliana] gi|332640929|gb|AEE74450.1| GATA transcription factor 15 [Arabidopsis thaliana]	142	149	8.00E−50	104.9	78.2	85.9	GATA transcription factor 15	gbpln	Arabidopsis thaliana	AT3G06740.1 | Symbols: GATA15 | GATA transcription factor 15 | chr3:2126658−2127265 FORWARD LENGTH=149	142	149	2.00E−52	104.9	78.2	85.9
Rsa1.0_00030.1.g1894.t1	gb|EOA31388.1| hypothetical protein CARUB_v10014564mg [Capsella rubella]	187	226	1.00E−57	120.9	77.0	83.4	hypothetical protein CARUB_v10014564mg	gbpln	Capsella rubella	AT3G06760.1 | Symbols: | Drought−responsive family protein | chr3:2132971−2134355 FORWARD LENGTH=224	187	224	2.00E−56	119.8	74.3	81.3
Rsa1.0_00030.1.g1895.t1	ref|XP_002884609.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330449|gb|EFH60868.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	226	228	1.00E−106	100.9	83.6	90.3	heat shock protein binding protein	gbpln	Arabidopsis lyrata	AT3G06778.1 | Symbols: | Chaperone DnaJ−domain superfamily protein | chr3:2140249−2141437 REVERSE LENGTH=229	226	229	1.00E−107	101.3	82.7	88.9
Rsa1.0_00030.1.g1896.t1	ref|XP_002882368.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata] gi|297328208|gb|EFH58627.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata]	371	392	1.00E−114	105.7	61.5	74.4	hypothetical protein ARALYDRAFT_896506	gbpln	Arabidopsis lyrata	AT3G04660.1 | Symbols: | F−box and associated interaction domains−containing protein | chr3:1264794−1265966 FORWARD LENGTH=390	371	390	2.00E−78	105.1	47.7	62.0
Rsa1.0_00030.1.g1897.t1	gb|EOA31285.1| hypothetical protein CARUB_v10014458mg, partial [Capsella rubella]	216	253	9.00E−76	117.1	69.4	73.1	hypothetical protein CARUB_v10014458mg, partial	gbpln	Capsella rubella	AT3G06790.2 | Symbols: | plastid developmental protein DAG, putative | chr3:2144564−2145743 REVERSE LENGTH=244	216	244	1.00E−73	113.0	65.7	69.4
Rsa1.0_00030.1.g1898.t1	ref|XP_002882496.1| hypothetical protein ARALYDRAFT_478003 [Arabidopsis lyrata subsp. lyrata] gi|297328336|gb|EFH58755.1| hypothetical protein ARALYDRAFT_478003 [Arabidopsis lyrata subsp. lyrata]	187	187	2.00E−70	100.0	78.6	88.2	hypothetical protein ARALYDRAFT_478003	gbpln	Arabidopsis lyrata	AT3G06840.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G49170.1); Has 33 Blast hits to 33 proteins in 9 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 33; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:2156930−2157624 FORWARD LENGTH=187	187	187	3.00E−72	100.0	80.2	88.8
Rsa1.0_00030.1.g1899.t3	ref|XP_002884612.1| DIN3/LTA1 [Arabidopsis lyrata subsp. lyrata] gi|297330452|gb|EFH60871.1| DIN3/LTA1 [Arabidopsis lyrata subsp. lyrata]	229	484	1.00E−65	211.4	68.1	73.4	DIN3/LTA1	gbpln	Arabidopsis lyrata	AT3G06850.2 | Symbols: BCE2, LTA1, DIN3 | 2−oxoacid dehydrogenases acyltransferase family protein | chr3:2158212−2160465 REVERSE LENGTH=483	229	483	2.00E−64	210.9	65.5	72.1

Rsa1.0_00030.1.g1900.t1	sp|O49809.2|MFPA_BRANA RecName: Full=Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a; Includes: RecName: Full=Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase; Includes: RecName: Full=3-hydroxyacyl-CoA dehydrogenase gi|2832898|emb|CAA04386.1| Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]	726	725	0	99.9	90.9	95.9	RecName: Full=Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a; Includes: RecName: Full=Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase; Includes: RecName: Full=3-hydroxyacyl-CoA dehydrogenase gi|2832898|emb|CAA04386.1| Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation	gbpln	Brassica napus	AT3G06860.1 | Symbols: MFP2, ATMFP2 | multifunctional protein 2 | chr3:2161926-2166009 FORWARD LENGTH=725	726	725	0	99.9	89.0	93.9
Rsa1.0_00030.1.g1901.t1	ref|XP_002882498.1| hypothetical protein ARALYDRAFT_478007 [Arabidopsis lyrata subsp. lyrata] gi|297328338|gb|EFH58757.1| hypothetical protein ARALYDRAFT_478007 [Arabidopsis lyrata subsp. lyrata]	352	372	1.00E-136	105.7	82.7	88.6	hypothetical protein ARALYDRAFT_478007	gbpln	Arabidopsis lyrata	AT3G06868.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G49100.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:2167872-2168981 FORWARD LENGTH=369	352	369	1.00E-137	104.8	84.7	91.2
Rsa1.0_00030.1.g1902.t1	gb|EOA30495.1| hypothetical protein CARUB_v10013619mg [Capsella rubella]	439	471	1.00E-154	107.3	67.7	78.1	hypothetical protein CARUB_v10013619mg	gbpln	Capsella rubella	AT3G06910.1 | Symbols: ULP1A, ELS1, AtULP1a | UB-like protease 1A | chr3:2178905-2181188 REVERSE LENGTH=502	439	502	1.00E-153	114.4	66.7	77.7
Rsa1.0_00030.1.g1903.t1	ref|NP_566296.1| protein pigment defective 320 [Arabidopsis thaliana] gi|6729003|gb|AAF27000.1|AC016827_11 hypothetical protein [Arabidopsis thaliana] gi|14194139|gb|AAK56264.1|AF367275_1 AT3g06960/F17A9_11 [Arabidopsis thaliana] gi|16323342|gb|AAL15384.1| AT3g06960/F17A9_11 [Arabidopsis thaliana] gi|332640959|gb|AEE74480.1| protein pigment defective 320 [Arabidopsis thaliana]	464	479	0	103.2	84.5	90.3	protein pigment defective 320	gbpln	Arabidopsis thaliana	AT3G06960.1 | Symbols: PDE320, TGD4 | pigment defective 320 | chr3:2194379-2196504 REVERSE LENGTH=479	464	479	0	103.2	84.5	90.3
Rsa1.0_00030.1.g1904.t1	ref|XP_002882502.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|98961639|gb|ABF59149.1| unknown protein [Arabidopsis thaliana] gi|297328342|gb|EFH58761.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	69	69	4.00E-23	100.0	87.0	91.3	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00030.1.g1905.t2	gb|EOA30082.1| hypothetical protein CARUB_v10013187mg [Capsella rubella]	631	642	0	101.7	86.4	92.6	hypothetical protein CARUB_v10013187mg	gbpln	Capsella rubella	AT3G07020.2 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:2218120-2221590 REVERSE LENGTH=637	631	637	0	101.0	85.6	90.0
Rsa1.0_00030.1.g1906.t1	gb|AAC99466.1| disease resistance gene homolog 9N [Brassica napus]	903	926	0	102.5	89.5	94.7	disease resistance gene homolog 9N	gbpln	Brassica napus	AT3G07040.1 | Symbols: RPM1, RPS3 | NB-ARC domain-containing disease resistance protein | chr3:2226244-2229024 REVERSE LENGTH=926	903	926	0	102.5	82.5	89.8
Rsa1.0_00030.1.g1907.t1	ref|XP_002884623.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297330463|gb|EFH60882.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]	588	582	0	99.0	79.1	84.2	GTP-binding family protein	gbpln	Arabidopsis lyrata	AT3G07050.1 | Symbols: | GTP-binding family protein | chr3:2229602-2232279 REVERSE LENGTH=582	588	582	0	99.0	81.1	85.5
Rsa1.0_00030.1.g1908.t1	ref|NP_566298.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|75337179|sp|Q9SFT7.1|Y3707_ARATH RecName: Full=Serine/threonine-protein kinase At3g07070 gi|6642658|gb|AAF20239.1|AC012395_26 putative protein kinase [Arabidopsis thaliana] gi|332640974|gb|AEE74495.1| serine/threonine-protein kinase [Arabidopsis thaliana]	443	414	0	93.5	83.7	88.7	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G07070.1 | Symbols: | Protein kinase superfamily protein | chr3:2238455-2240074 FORWARD LENGTH=414	443	414	0	93.5	83.7	88.7

Rsa1.0_00030.1.g1909.t1	ref|XP_002884625.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330465|gb|EFH60884.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	253	265	1.00E-116	104.7	81.8	88.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G07090.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr3:2243153-2244476 REVERSE LENGTH=265	253	265	1.00E-118	104.7	81.4	90.5
Rsa1.0_00030.1.g1910.t1	ref|NP_187366.2| sec24-like transport protein [Arabidopsis thaliana] gi|78099801|sp|Q9SFU0.2|SC24A_ARATH RecName: Full=Protein transport protein Sec24-like At3g07100 gi|22531076|gb|AAM97042.1| putative Sec24-like COPII protein [Arabidopsis thaliana] gi|23197930|gb|AAN15492.1| putative Sec24-like COPII protein [Arabidopsis thaliana] gi|332640977|gb|AEE74498.1| sec24-like transport protein [Arabidopsis thaliana]	1002	1038	0	103.6	87.1	91.7	sec24-like transport protein	gbpln	Arabidopsis thaliana	AT3G07100.1 | Symbols: ERMO2, SEC24A | Sec23/Sec24 protein transport family protein | chr3:2245689-2250077 REVERSE LENGTH=1038	1002	1038	0	103.6	87.1	91.7
Rsa1.0_00030.1.g1911.t1	ref|NP_187368.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|6642653|gb|AAF20234.1|AC012395_21 putative RING zinc finger protein [Arabidopsis thaliana] gi|56381891|gb|AAV85664.1| At3g07120 [Arabidopsis thaliana] gi|58531344|gb|AAW78594.1| At3g07120 [Arabidopsis thaliana] gi|332640980|gb|AEE74501.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	348	360	1.00E-107	103.4	72.7	82.5	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G07120.1 | Symbols: | RING/U-box superfamily protein | chr3:2254560-2255642 FORWARD LENGTH=360	348	360	1.00E-109	103.4	72.7	82.5
Rsa1.0_00030.1.g1912.t1	gb|EOA30308.1| hypothetical protein CARUB_v10013434mg [Capsella rubella]	541	532	0	98.3	76.9	86.0	hypothetical protein CARUB_v10013434mg	gbpln	Capsella rubella	AT3G07130.1 | Symbols: ATPAP15, PAP15 | purple acid phosphatase 15 | chr3:2255763-2257981 REVERSE LENGTH=532	541	532	0	98.3	76.9	86.0
Rsa1.0_00030.1.g1913.t1	ref|NP_187372.5| callose synthase [Arabidopsis thaliana] gi|378405154|sp|Q9SFU6.2|CALS9_ARATH RecName: Full=Callose synthase 9; AltName: Full=1,3-beta-glucan synthase; AltName: Full=Protein GLUCAN SYNTHASE-LIKE 10 gi|332640985|gb|AEE74506.1| callose synthase 10 [Arabidopsis thaliana]	1864	1890	0	101.4	80.5	88.1	callose synthase	gbpln	Arabidopsis thaliana	AT3G07160.1 | Symbols: ATGSL10, gsl10, CALS9 | glucan synthase-like 10 | chr3:2265142-2279383 REVERSE LENGTH=1890	1864	1890	0	101.4	80.5	88.1
Rsa1.0_00030.1.g1914.t1	gb|EOA31542.1| hypothetical protein CARUB_v10014744mg [Capsella rubella]	154	183	8.00E-38	118.8	54.5	62.3	hypothetical protein CARUB_v10014744mg	gbpln	Capsella rubella	AT3G07200.2 | Symbols: | RING/U-box superfamily protein | chr3:2291343-2292223 FORWARD LENGTH=182	154	182	2.00E-38	118.2	53.2	62.3
Rsa1.0_00030.1.g1915.t1	ref|XP_002884637.1| hypothetical protein ARALYDRAFT_340917 [Arabidopsis lyrata subsp. lyrata] gi|297330477|gb|EFH60896.1| hypothetical protein ARALYDRAFT_340917 [Arabidopsis lyrata subsp. lyrata]	421	286	3.00E-77	67.9	41.3	47.7	hypothetical protein ARALYDRAFT_340917	gbpln	Arabidopsis lyrata	AT3G07250.1 | Symbols: | nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein | chr3:2300579-2308305 REVERSE LENGTH=1294	421	1294	2.00E-71	307.4	38.5	45.6
Rsa1.0_00031.1.g1916.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00031.1.g1917.t1	ref|XP_002878467.1| hypothetical protein ARALYDRAFT_907836 [Arabidopsis lyrata subsp. lyrata] gi|297324305|gb|EFH54726.1| hypothetical protein ARALYDRAFT_907836 [Arabidopsis lyrata subsp. lyrata]	285	380	3.00E-91	133.3	76.5	84.2	hypothetical protein ARALYDRAFT_907836	gbpln	Arabidopsis lyrata	AT3G62630.1 | Symbols: | Protein of unknown function (DUF1645) | chr3:23163937-23165079 REVERSE LENGTH=380	285	380	3.00E-92	133.3	75.4	82.8
Rsa1.0_00031.1.g1918.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1366	1307	0	95.7	59.7	73.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1366	1262	1.00E-100	92.4	14.2	22.5
Rsa1.0_00031.1.g1919.t1	ref|NP_191824.1| uncharacterized protein [Arabidopsis thaliana] gi|42572765|ref|NP_974478.1| uncharacterized protein [Arabidopsis thaliana] gi|7362745|emb|CAB83115.1| putative protein [Arabidopsis thaliana] gi|15450964|gb|AAK96753.1| putative protein [Arabidopsis thaliana] gi|17978723|gb|AAL47355.1| putative protein [Arabidopsis thaliana] gi|332646854|gb|AEE80375.1| uncharacterized protein AT3G62650 [Arabidopsis thaliana] gi|332646855|gb|AEE80376.1| uncharacterized protein AT3G62650 [Arabidopsis thaliana]	147	152	5.00E-48	103.4	75.5	83.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G62650.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G47485.1); Has 57 Blast hits to 57 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:23168531-23168989 FORWARD LENGTH=152	147	152	1.00E-50	103.4	75.5	83.7

Rsa1.0_00031.1.g1920.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00031.1.g1921.t1	ref|XP_002891930.1| hypothetical protein ARALYDRAFT_474772 [Arabidopsis lyrata subsp. lyrata] gi|297337772|gb|EFH68189.1| hypothetical protein ARALYDRAFT_474772 [Arabidopsis lyrata subsp. lyrata]	300	334	1.00E-88	111.3	76.7	81.3	hypothetical protein ARALYDRAFT_474772	gbpln	Arabidopsis lyrata	AT1G54970.1 | Symbols: ATPRP1, RHS7, PRP1 | proline-rich protein 1 | chr1:20505000-20506238 FORWARD LENGTH=335	300	335	2.00E-90	111.7	74.3	80.7
Rsa1.0_00031.1.g1922.t1	gb|AAF64548.1|AF110985_1 proline-rich protein 1 [Arabidopsis thaliana]	322	335	2.00E-25	104.0	39.8	43.2	proline-rich protein 1	gbpln	Arabidopsis thaliana	AT1G54970.1 | Symbols: ATPRP1, RHS7, PRP1 | proline-rich protein 1 | chr1:20505000-20506238 FORWARD LENGTH=335	322	335	3.00E-27	104.0	37.3	41.0
Rsa1.0_00031.1.g1923.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00031.1.g1924.t1	ref|NP_191830.1| glycosyl hydrolase-like protein [Arabidopsis thaliana] gi|7362751|emb|CAB83121.1| beta-D-glucan exohydrolase-like protein [Arabidopsis thaliana] gi|17065160|gb|AAL32734.1| beta-D-glucan exohydrolase-like protein [Arabidopsis thaliana] gi|20259922|gb|AAM13308.1| beta-D-glucan exohydrolase-like protein [Arabidopsis thaliana] gi|332646861|gb|AEE80382.1| glycosyl hydrolase-like protein [Arabidopsis thaliana]	642	650	0	101.2	82.1	89.1	glycosyl hydrolase-like protein	gbpln	Arabidopsis thaliana	AT3G62710.1 | Symbols: | Glycosyl hydrolase family protein | chr3:23197739-23200559 REVERSE LENGTH=650	642	650	0	101.2	82.1	89.1
Rsa1.0_00031.1.g1925.t1	ref|NP_191831.1| xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] gi|79316129|ref|NP_001030917.1| xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] gi|46577293|sp|Q9LZJ3.1|XT1_ARATH RecName: Full=Xyloglucan 6-xylosyltransferase; Short=AtXT1 gi|15983426|gb|AAL11581.1|AF424587_1 AT3g62720/F26K9_150 [Arabidopsis thaliana] gi|7362752|emb|CAB83122.1| alpha galactosyltransferase-like protein [Arabidopsis thaliana] gi|25141201|gb|AAN73295.1| At3g62720/F26K9_150 [Arabidopsis thaliana] gi|222424476|dbj|BAH20193.1| AT3G62720 [Arabidopsis thaliana] gi|332646862|gb|AEE80383.1| xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] gi|332646863|gb|AEE80384.1| xyloglucan 6-xylosyltransferase [Arabidopsis thaliana]	463	460	0	99.4	89.4	93.1	xyloglucan 6-xylosyltransferase	gbpln	Arabidopsis thaliana	AT3G62720.2 | Symbols: ATXT1, XT1, XXT1 | xylosyltransferase 1 | chr3:23201326-23202708 FORWARD LENGTH=460	463	460	0	99.4	89.4	93.1
Rsa1.0_00031.1.g1926.t1	dbj|BAJ34035.1| unnamed protein product [Thellungiella halophila]	498	506	0	101.6	77.9	86.7	unnamed protein product	----	----	AT4G27830.1 | Symbols: BGLU10 | beta glucosidase 10 | chr4:13861794-13864489 REVERSE LENGTH=508	498	508	0	102.0	76.7	88.2
Rsa1.0_00031.1.g1927.t1	dbj|BAJ34035.1| unnamed protein product [Thellungiella halophila]	501	506	0	101.0	76.0	84.0	unnamed protein product	----	----	AT4G27830.1 | Symbols: BGLU10 | beta glucosidase 10 | chr4:13861794-13864489 REVERSE LENGTH=508	501	508	0	101.4	73.1	84.8
Rsa1.0_00031.1.g1928.t1	ref|NP_191835.1| Glutathione S-transferase-like protein [Arabidopsis thaliana] gi|75335711|sp|Q9LZI9.1|GSTFD_ARATH RecName: Full=Glutathione S-transferase F13; Short=AtGSTF13; AltName: Full=GST class-phi member 13 gi|7362756|emb|CAB83126.1| Glutathione transferase III-like protein [Arabidopsis thaliana] gi|332646867|gb|AEE80388.1| glutathione S-transferase F13 [Arabidopsis thaliana]	219	219	1.00E-115	100.0	90.0	95.9	Glutathione S-transferase-like protein	gbpln	Arabidopsis thaliana	AT3G62760.1 | Symbols: ATGSTF13 | Glutathione S-transferase family protein | chr3:23217425-23218246 REVERSE LENGTH=219	219	219	1.00E-118	100.0	90.0	95.9
Rsa1.0_00031.1.g1929.t1	gb|EOA24065.1| hypothetical protein CARUB_v10017285mg [Capsella rubella]	421	435	0	103.3	88.8	93.6	hypothetical protein CARUB_v10017285mg	gbpln	Capsella rubella	AT3G62770.1 | Symbols: AtATG18a | Transducin/WD40 repeat-like superfamily protein | chr3:23218858-23221110 REVERSE LENGTH=425	421	425	0	101.0	85.7	90.7

<table>
<tr><td>Rsa1.0_00031.1.g1930.t1</td><td>ref|NP_191837.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana] gi|7362758|emb|CAB83128.1| shock protein SRC2-like [Arabidopsis thaliana] gi|42600565|gb|AAS21129.1| At3g62780 [Arabidopsis thaliana] gi|45773884|gb|AAS76746.1| At3g62780 [Arabidopsis thaliana] gi|332646870|gb|AEE80391.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana]</td><td>273</td><td>298</td><td>3.00E-99</td><td>109.2</td><td>75.8</td><td>80.2</td><td>calcium-dependent lipid-binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G62780.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:23222029-23222925 REVERSE LENGTH=298</td><td>273</td><td>298</td><td>1.00E-102</td><td>109.2</td><td>75.8</td><td>80.2</td></tr>
<tr><td>Rsa1.0_00031.1.g1931.t1</td><td>gb|EOA24988.1| hypothetical protein CARUB_v10018285mg [Capsella rubella] gi|482560798|gb|EOA24989.1| hypothetical protein CARUB_v10018285mg [Capsella rubella]</td><td>106</td><td>106</td><td>2.00E-48</td><td>100.0</td><td>91.5</td><td>96.2</td><td>hypothetical protein CARUB_v10018285mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G62810.1 | Symbols: | complex 1 family protein / LVR family protein | chr3:23227763-23228180 FORWARD LENGTH=106</td><td>106</td><td>106</td><td>4.00E-50</td><td>100.0</td><td>90.6</td><td>96.2</td></tr>
<tr><td>Rsa1.0_00031.1.g1932.t1</td><td>ref|NP_191842.1| UDP-glucuronic acid decarboxylase [Arabidopsis thaliana] gi|186511349|ref|NP_001118893.1| UDP-glucuronic acid decarboxylase [Arabidopsis thaliana] gi|75335709|sp|Q9LZI2.1|UXS2_ARATH RecName: Full=UDP-glucuronic acid decarboxylase 2; AltName: Full=UDP-XYL synthase 2; AltName: Full=UDP-glucuronate decarboxylase 2; Short=UGD; Short=UXS-2; AltName: Full=dTDP-glucose 4-6-dehydratase homolog D18 gi|7362763|emb|CAB83133.1| dTDP-glucose 4-6-dehydratase homolog D18 [Arabidopsis thaliana] gi|23505953|gb|AAN28836.1| At3g62830/F26K9_260 [Arabidopsis thaliana] gi|332646877|gb|AEE80398.1| UDP-glucuronic acid decarboxylase [Arabidopsis thaliana] gi|332646878|gb|AEE80399.1| UDP-glucuronic acid decarboxylase [Arabidopsis thaliana]</td><td>423</td><td>445</td><td>0</td><td>105.2</td><td>89.6</td><td>94.1</td><td>UDP-glucuronic acid decarboxylase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G62830.2 | Symbols: UXS2, ATUXS2 | NAD(P)-binding Rossmann-fold superfamily protein | chr3:23232539-23235353 FORWARD LENGTH=445</td><td>423</td><td>445</td><td>0</td><td>105.2</td><td>89.6</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00031.1.g1933.t4</td><td>ref|NP_850477.1| small nuclear ribonucleoprotein D2 [Arabidopsis thaliana] gi|42571273|ref|NP_973710.1| small nuclear ribonucleoprotein D2 [Arabidopsis thaliana] gi|145332931|ref|NP_001078331.1| small nuclear ribonucleoprotein D2 [Arabidopsis thaliana] gi|7362764|emb|CAB83134.1| small nuclear ribonucleoprotein-like protein [Arabidopsis thaliana] gi|28466881|gb|AAO44049.1| At2g47640 [Arabidopsis thaliana] gi|110743879|dbj|BAE99774.1| putative small nuclear ribonucleoprotein D2 [Arabidopsis thaliana] gi|330255774|gb|AEC10868.1| small nuclear ribonucleoprotein D2 [Arabidopsis thaliana] gi|330255775|gb|AEC10869.1| small nuclear ribonucleoprotein D2 [Arabidopsis thaliana] gi|332646880|gb|AEE80401.1| small nuclear ribonucleoprotein D2 [Arabidopsis thaliana] gi|482563987|gb|EOA28177.1| hypothetical protein CARUB_v10024367mg [Capsella rubella]</td><td>104</td><td>108</td><td>3.00E-53</td><td>103.8</td><td>100.0</td><td>100.0</td><td>small nuclear ribonucleoprotein D2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G62840.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr3:23235727-23236615 REVERSE LENGTH=108</td><td>104</td><td>108</td><td>5.00E-56</td><td>103.8</td><td>100.0</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00031.1.g1934.t1</td><td>gb|EOA27436.1| hypothetical protein CARUB_v10023573mg [Capsella rubella]</td><td>256</td><td>338</td><td>1.00E-141</td><td>132.0</td><td>96.9</td><td>97.7</td><td>hypothetical protein CARUB_v10023573mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G62870.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr3:23242862-23244273 REVERSE LENGTH=256</td><td>256</td><td>256</td><td>1.00E-140</td><td>100.0</td><td>94.1</td><td>97.3</td></tr>
<tr><td>Rsa1.0_00031.1.g1935.t1</td><td>gb|EOA26198.1| hypothetical protein CARUB_v10019636mg [Capsella rubella]</td><td>142</td><td>134</td><td>5.00E-50</td><td>94.4</td><td>78.2</td><td>85.9</td><td>hypothetical protein CARUB_v10019636mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G62880.2 | Symbols: ATOEP16-4 | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr3:23245103-23246002 REVERSE LENGTH=136</td><td>142</td><td>136</td><td>2.00E-49</td><td>95.8</td><td>74.6</td><td>82.4</td></tr>
</table>

Rsa1.0_00031.1.g1936.t1	gb|EOA24179.1| hypothetical protein CARUB_v10017414mg [Capsella rubella]	392	391	1.00E-172	99.7	78.8	86.0	hypothetical protein CARUB_v10017414mg	gbpln	Capsella rubella	AT1G21150.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:7406406-7407578 REVERSE LENGTH=390	392	390	1.00E-124	99.5	60.2	74.7
Rsa1.0_00031.1.g1937.t1	gb|EOA24095.1| hypothetical protein CARUB_v10017325mg [Capsella rubella]	411	422	0	102.7	92.0	95.9	hypothetical protein CARUB_v10017325mg	gbpln	Capsella rubella	AT3G62910.1 | Symbols: APG3 | Peptide chain release factor 1 | chr3:23257661-23260386 REVERSE LENGTH=422	411	422	0	102.7	91.5	95.9
Rsa1.0_00031.1.g1938.t1	gb|EOA23343.1| hypothetical protein CARUB_v10019414mg [Capsella rubella]	102	102	2.00E-49	100.0	93.1	98.0	hypothetical protein CARUB_v10019414mg	gbpln	Capsella rubella	AT3G62930.1 | Symbols: | Thioredoxin superfamily protein | chr3:23261538-23261846 REVERSE LENGTH=102	102	102	1.00E-50	100.0	89.2	95.1
Rsa1.0_00031.1.g1939.t1	ref|XP_002878488.1| hypothetical protein ARALYDRAFT_486799 [Arabidopsis lyrata subsp. lyrata] gi|297324326|gb|EFH54747.1| hypothetical protein ARALYDRAFT_486799 [Arabidopsis lyrata subsp. lyrata]	314	326	1.00E-138	103.8	84.1	91.1	hypothetical protein ARALYDRAFT_486799	gbpln	Arabidopsis lyrata	AT3G62940.3 | Symbols: | Cysteine proteinases superfamily protein | chr3:23263106-23264245 REVERSE LENGTH=332	314	332	1.00E-138	105.7	86.9	93.0
Rsa1.0_00031.1.g1940.t1	ref|NP_191854.1| glutaredoxin-C11 [Arabidopsis thaliana] gi|297817626|ref|XP_002876696.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|75264377|sp|Q9LYC6.1|GRC11_ARATH RecName: Full=Glutaredoxin-C11; Short=AtGrxC11; AltName: Full=Protein ROXY 4 gi|7573424|emb|CAB87740.1| glutaredoxin-like protein [Arabidopsis thaliana] gi|50253460|gb|AAT71932.1| At3g62950 [Arabidopsis thaliana] gi|51972084|gb|AAU15146.1| At3g62950 [Arabidopsis thaliana] gi|226348186|gb|ACO50409.1| glutaredoxin [Arabidopsis thaliana] gi|297322534|gb|EFH52955.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|332646895|gb|AEE80416.1| glutaredoxin-C11 [Arabidopsis thaliana]	103	103	4.00E-53	100.0	99.0	100.0	glutaredoxin-C11	gbpln	Arabidopsis lyrata	AT3G62950.1 | Symbols: | Thioredoxin superfamily protein | chr3:23266303-23266614 FORWARD LENGTH=103	103	103	6.00E-56	100.0	99.0	100.0
Rsa1.0_00031.1.g1941.t1	ref|NP_191855.1| glutaredoxin-C14 [Arabidopsis thaliana] gi|75181054|sp|Q9LYC5.1|GRC14_ARATH RecName: Full=Glutaredoxin-C14; Short=AtGrxC14; AltName: Full=Protein ROXY 8 gi|7573425|emb|CAB87741.1| glutaredoxin-like protein [Arabidopsis thaliana] gi|88900350|gb|ABD57487.1| At3g62960 [Arabidopsis thaliana] gi|226348194|gb|ACO50413.1| glutaredoxin [Arabidopsis thaliana] gi|332646896|gb|AEE80417.1| glutaredoxin-C14 [Arabidopsis thaliana] gi|482560809|gb|EOA25000.1| hypothetical protein CARUB_v10018297mg [Capsella rubella]	102	102	1.00E-51	100.0	97.1	98.0	glutaredoxin-C14	gbpln	Arabidopsis thaliana	AT3G62960.1 | Symbols: | Thioredoxin superfamily protein | chr3:23268780-23269088 FORWARD LENGTH=102	102	102	2.00E-54	100.0	97.1	98.0
Rsa1.0_00031.1.g1942.t1	ref|NP_001190481.1| phosphatidylinositol glycan, class X [Arabidopsis thaliana] gi|332008052|gb|AED95435.1| uncharacterized protein AT5G46850 [Arabidopsis thaliana]	132	325	5.00E-28	246.2	53.0	65.9	phosphatidylinositol glycan, class X	gbpln	Arabidopsis thaliana	AT5G46850.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: GPI anchor biosynthetic process; LOCATED IN: endoplasmic reticulum membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: PIG-X/PBN1 (InterPro:IPR013233). | chr5:19010714-19012010 FORWARD LENGTH=325	132	325	1.00E-30	246.2	53.0	65.9
Rsa1.0_00031.1.g1943.t1	gb|EOA23690.1| hypothetical protein CARUB_v10016894mg [Capsella rubella]	597	594	0	99.5	93.6	96.5	hypothetical protein CARUB_v10016894mg	gbpln	Capsella rubella	AT3G62980.1 | Symbols: TIR1 | F-box/RNI-like superfamily protein | chr3:23273479-23276181 REVERSE LENGTH=594	597	594	0	99.5	92.6	96.5
Rsa1.0_00031.1.g1944.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00031.1.g1945.t1	gb|EOA24114.1| hypothetical protein CARUB_v10017347mg [Capsella rubella]	414	413	0	99.8	90.1	96.9	hypothetical protein CARUB_v10017347mg	gbpln	Capsella rubella	AT3G63000.1 | Symbols: NPL41 | NPL4-like protein 1 | chr3:23283836-23285357 FORWARD LENGTH=413	414	413	0	99.8	90.3	96.9
Rsa1.0_00031.1.g1946.t1	gb|ADT78692.1| gibberellin receptor 1B [Brassica napus]	364	358	0	98.4	91.8	95.6	gibberellin receptor 1B	gbpln	Brassica napus	AT3G63010.1 | Symbols: ATGID1B, GID1B | alpha/beta-Hydrolases superfamily protein | chr3:23289717-23290998 FORWARD LENGTH=358	364	358	0	98.4	87.6	93.1

Rsa1.0_00031.1.g1947.t1	ref|XP_002876703.1| methyl-CpG-binding domain 4 [Arabidopsis lyrata subsp. lyrata] gi|297322541|gb|EFH52962.1| methyl-CpG-binding domain 4 [Arabidopsis lyrata subsp. lyrata]	327	182	7.00E-71	55.7	37.9	42.8	methyl-CpG-binding domain 4	gbpln	Arabidopsis lyrata	AT3G63030.1 | Symbols: MBD4 | methyl-CPG-binding domain 4 | chr3:23295394-23296425 FORWARD LENGTH=186	327	186	1.00E-71	56.9	36.4	41.6
Rsa1.0_00031.1.g1948.t1	gb|EOA25199.1| hypothetical protein CARUB_v10018512mg [Capsella rubella]	117	179	1.00E-12	153.0	41.0	52.1	hypothetical protein CARUB_v10018512mg	gbpln	Capsella rubella	AT3G63040.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:23296646-23297209 REVERSE LENGTH=187	117	187	4.00E-14	159.8	40.2	49.6
Rsa1.0_00031.1.g1949.t1	ref|XP_002878491.1| hypothetical protein ARALYDRAFT_486808 [Arabidopsis lyrata subsp. lyrata] gi|297324329|gb|EFH54750.1| hypothetical protein ARALYDRAFT_486808 [Arabidopsis lyrata subsp. lyrata]	131	135	2.00E-23	103.1	55.7	70.2	hypothetical protein ARALYDRAFT_486808	gbpln	Arabidopsis lyrata	AT3G63050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G48075.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:23297950-23298372 REVERSE LENGTH=140	131	140	9.00E-26	106.9	56.5	70.2
Rsa1.0_00031.1.g1950.t1	gb|AAF79749.1|AC009317_8 T30E16.12 [Arabidopsis thaliana]	351	341	1.00E-100	97.2	54.7	68.4	T30E16.12	gbpln	Arabidopsis thaliana	AT1G59560.1 | Symbols: ZCF61, DAL2 | E3 Ubiquitin ligase family protein | chr1:21881741-21883632 FORWARD LENGTH=338	351	338	1.00E-101	96.3	54.7	68.4
Rsa1.0_00031.1.g1951.t1	gb|EOA25934.1| hypothetical protein CARUB_v10019315mg [Capsella rubella]	1583	1353	0	85.5	60.7	68.3	hypothetical protein CARUB_v10019315mg	gbpln	Capsella rubella	AT2G48160.1 | Symbols: | Tudor/PWWP/MBT domain-containing protein | chr2:19689784-19696584 REVERSE LENGTH=1366	1583	1366	0	86.3	51.0	60.5
Rsa1.0_00031.1.g1952.t1	ref|NP_001078333.1| tetratricopeptide repeat-containing protein-like protein [Arabidopsis thaliana] gi|332646914|gb|AEE80435.1| tetratricopeptide repeat-containing protein-like protein [Arabidopsis thaliana]	258	250	6.00E-16	96.9	15.9	17.8	tetratricopeptide repeat-containing protein-like protein	gbpln	Arabidopsis thaliana	AT3G63095.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:23315506-23316258 FORWARD LENGTH=250	258	250	2.00E-18	96.9	15.9	17.8
Rsa1.0_00031.1.g1953.t1	ref|XP_002878496.1| ATIPT3 [Arabidopsis lyrata subsp. lyrata] gi|297324334|gb|EFH54755.1| ATIPT3 [Arabidopsis lyrata subsp. lyrata]	334	336	1.00E-167	100.6	86.8	92.8	ATIPT3	gbpln	Arabidopsis lyrata	AT3G63110.1 | Symbols: ATIPT3, IPT3 | isopentenyltransferase 3 | chr3:23318437-23319447 REVERSE LENGTH=336	334	336	1.00E-168	100.6	85.0	93.1
Rsa1.0_00031.1.g1954.t1	gb|EOA25999.1| hypothetical protein CARUB_v10019395mg [Capsella rubella]	528	535	0	101.3	80.3	89.0	hypothetical protein CARUB_v10019395mg	gbpln	Capsella rubella	AT3G63130.2 | Symbols: RANGAP1 | RAN GTPase activating protein 1 | chr3:23325108-23326715 FORWARD LENGTH=535	528	535	0	101.3	79.5	88.1
Rsa1.0_00031.1.g1955.t1	gb|EOA24136.1| hypothetical protein CARUB_v10017370mg [Capsella rubella]	449	404	0	90.0	78.4	81.3	hypothetical protein CARUB_v10017370mg	gbpln	Capsella rubella	AT3G63140.1 | Symbols: CSP41A | chloroplast stem-loop binding protein of 41 kDa | chr3:23327006-23328620 REVERSE LENGTH=406	449	406	0	90.4	78.8	82.0
Rsa1.0_00031.1.g1956.t1	ref|NP_567139.1| MIRO-related GTP-ase 2 [Arabidopsis thaliana] gi|332646920|gb|AEE80441.1| MIRO-related GTP-ase 2 [Arabidopsis thaliana]	646	643	0	99.5	90.4	94.9	MIRO-related GTP-ase 2	gbpln	Arabidopsis thaliana	AT3G63150.1 | Symbols: MIRO2, ATCBG | MIRO-related GTP-ase 2 | chr3:23329200-23332692 REVERSE LENGTH=643	646	643	0	99.5	90.4	94.9
Rsa1.0_00031.1.g1957.t1	ref|XP_002876711.1| hypothetical protein ARALYDRAFT_486819 [Arabidopsis lyrata subsp. lyrata] gi|297322549|gb|EFH52970.1| hypothetical protein ARALYDRAFT_486819 [Arabidopsis lyrata subsp. lyrata]	283	279	1.00E-132	98.6	83.0	90.5	hypothetical protein ARALYDRAFT_486819	gbpln	Arabidopsis lyrata	AT3G63170.1 | Symbols: | Chalcone-flavanone isomerase family protein | chr3:23334675-23335993 FORWARD LENGTH=279	283	279	1.00E-128	98.6	83.7	90.8
Rsa1.0_00032.1.g1958.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00032.1.g1959.t2	ref|XP_002882851.1| hypothetical protein ARALYDRAFT_478784 [Arabidopsis lyrata subsp. lyrata] gi|297328691|gb|EFH59110.1| hypothetical protein ARALYDRAFT_478784 [Arabidopsis lyrata subsp. lyrata]	498	507	0	101.8	81.7	89.2	hypothetical protein ARALYDRAFT_478784	gbpln	Arabidopsis lyrata	AT3G13810.1 | Symbols: AtIDD11, IDD11 | indeterminate(ID)-domain 11 | chr3:4544941-4547300 FORWARD LENGTH=513	498	513	0	103.0	80.7	87.3
Rsa1.0_00032.1.g1960.t1	gb|EOA31706.1| hypothetical protein CARUB_v10014912mg [Capsella rubella]	70	130	2.00E-13	185.7	88.6	90.0	hypothetical protein CARUB_v10014912mg	gbpln	Capsella rubella	#	#	#	#	#	#	#

Rsa1.0_00032.1.g1961.t1	ref|NP_188001.1| LOB domain-containing protein 22 [Arabidopsis thaliana] gi|29428016|sp|Q9LRW1.1|LBD22_ARATH RecName: Full=LOB domain-containing protein 22; AltName: Full=ASYMMETRIC LEAVES 2-like protein 30; Short=AS2-like protein 30 gi|9294609|dbj|BAB02910.1| unnamed protein product [Arabidopsis thaliana] gi|219807136|dbj|BAH10574.1| ASYMMETRIC LEAVES2-like 30 protein [Arabidopsis thaliana] gi|332641904|gb|AEE75425.1| LOB domain-containing protein 22 [Arabidopsis thaliana]	259	268	1.00E-112	103.5	80.3	90.3	LOB domain-containing protein 22	gbpln	Arabidopsis thaliana	AT3G13850.1 | Symbols: LBD22 | LOB domain-containing protein 22 | chr3:4559910-4560716 FORWARD LENGTH=268	259	268	1.00E-115	103.5	80.3	90.3
Rsa1.0_00032.1.g1962.t2	ref|NP_188003.1| Root hair defective 3 GTP-binding protein RHD3 [Arabidopsis thaliana] gi|75279781|sp|P93042.1|RHD3_ARATH RecName: Full=Protein ROOT HAIR DEFECTIVE 3; AltName: Full=Protein FRAGILE FIBER 4; AltName: Full=Protein SEY1 homolog 1 gi|1839188|gb|AAB58375.1| root hair defective 3 [Arabidopsis thaliana] gi|20260178|gb|AAM12987.1| unknown protein [Arabidopsis thaliana] gi|22136246|gb|AAM91201.1| unknown protein [Arabidopsis thaliana] gi|332641908|gb|AEE75429.1| Root hair defective 3 GTP-binding protein RHD3 [Arabidopsis thaliana]	851	802	0	94.2	86.0	90.4	Root hair defective 3 GTP-binding protein RHD3	gbpln	Arabidopsis thaliana	AT3G13870.1 | Symbols: RHD3 | Root hair defective 3 GTP-binding protein (RHD3) | chr3:4565762-4571109 REVERSE LENGTH=802	851	802	0	94.2	86.0	90.4
Rsa1.0_00032.1.g1963.t1	ref|XP_002882857.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] gi|297328697|gb|EFH59116.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	147	147	8.00E-65	100.0	89.1	92.5	structural constituent of ribosome	gbpln	Arabidopsis lyrata	AT3G13882.1 | Symbols: | Ribosomal protein L34 | chr3:4574600-4575852 FORWARD LENGTH=147	147	147	4.00E-66	100.0	87.1	91.8
Rsa1.0_00032.1.g1964.t2	gb|EOA32487.1| hypothetical protein CARUB_v10015767mg [Capsella rubella]	346	357	1.00E-128	103.2	77.7	84.4	hypothetical protein CARUB_v10015767mg	gbpln	Capsella rubella	AT3G13890.2 | Symbols: MYB26 | myb domain protein 26 | chr3:4576744-4578027 REVERSE LENGTH=358	346	358	1.00E-128	103.5	75.4	82.1
Rsa1.0_00032.1.g1965.t7	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1663	1352	1.00E-180	81.3	23.6	34.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1663	746	5.00E-50	44.9	7.6	10.6
Rsa1.0_00032.1.g1966.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00032.1.g1967.t1	ref|XP_002893400.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339242|gb|EFH69659.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	222	196	1.00E-52	88.3	48.2	52.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G46230.1 | Symbols: | PIN domain-like family protein | chr2:18984459-18985850 REVERSE LENGTH=196	222	196	2.00E-52	88.3	45.9	50.9
Rsa1.0_00032.1.g1968.t4	ref|XP_002882859.1| hypothetical protein ARALYDRAFT_341522 [Arabidopsis lyrata subsp. lyrata] gi|297328699|gb|EFH59118.1| hypothetical protein ARALYDRAFT_341522 [Arabidopsis lyrata subsp. lyrata]	1253	1243	0	99.2	92.6	95.7	hypothetical protein ARALYDRAFT_341522	gbpln	Arabidopsis lyrata	AT3G13900.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr3:4586151-4590681 FORWARD LENGTH=1243	1253	1243	0	99.2	92.2	95.7
Rsa1.0_00032.1.g1969.t1	gb|EOA31757.1| hypothetical protein CARUB_v10014974mg [Capsella rubella]	92	106	1.00E-33	115.2	84.8	91.3	hypothetical protein CARUB_v10014974mg	gbpln	Capsella rubella	AT3G13910.1 | Symbols: | Protein of unknown function (DUF3511) | chr3:4591124-4591432 REVERSE LENGTH=102	92	102	5.00E-32	110.9	69.6	72.8
Rsa1.0_00032.1.g1970.t1	gb|EOA30691.1| hypothetical protein CARUB_v10013828mg [Capsella rubella]	422	412	0	97.6	96.0	97.2	hypothetical protein CARUB_v10013828mg	gbpln	Capsella rubella	AT3G13920.1 | Symbols: EIF4A1, RH4, TIF4A1 | eukaryotic translation initiation factor 4A1 | chr3:4592635-4594128 REVERSE LENGTH=412	422	412	0	97.6	95.0	97.2

Rsa1.0_00032.1.g1971.t15	ref|NP_566470.1| dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex [Arabidopsis thaliana] gi|118573090|sp|Q8RWN9.2|OPD22_ARATH RecName: Full=Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex, mitochondrial; AltName: Full=Dihydrolipoamide S-acetyltransferase component 2 of pyruvate dehydrogenase complex; AltName: Full=Pyruvate dehydrogenase complex component E2 2; Short=PDC-E2 2; Short=PDCE2 2; Flags: Precursor gi|13605807|gb|AAK32889.1|AF367302_1 AT3g13930/MDC16_5 [Arabidopsis thaliana] gi|20147147|gb|AAM10290.1| AT3g13930/MDC16_5 [Arabidopsis thaliana] gi|23306388|gb|AAN17421.1| putative acetyltransferase [Arabidopsis thaliana] gi|23397124|gb|AAN31846.1| putative acetyltransferase [Arabidopsis thaliana] gi|24899791|gb|AAN65110.1| putative acetyltransferase [Arabidopsis thaliana] gi|332641921|gb|AEE75442.1| dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex [Arabidopsis thaliana]	868	539	0	62.1	49.1	52.4	dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex	gbpln	Arabidopsis thaliana	AT3G13930.1 | Symbols: | Dihydrolipoamide acetyltransferase, long form protein | chr3:4596240-4600143 FORWARD LENGTH=539	868	539	0	62.1	49.1	52.4
Rsa1.0_00032.1.g1972.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00032.1.g1973.t1	ref|XP_002862273.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307605|gb|EFH38531.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	203	219	3.00E-68	107.9	64.0	68.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G13950.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G13266.1); Has 339 Blast hits to 265 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 339; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4604149-4605195 FORWARD LENGTH=207	203	207	4.00E-69	102.0	62.6	69.0
Rsa1.0_00032.1.g1974.t1	gb|EOA30723.1| hypothetical protein CARUB_v10013860mg [Capsella rubella]	405	403	1.00E-175	99.5	81.5	88.9	hypothetical protein CARUB_v10013860mg	gbpln	Capsella rubella	AT3G13960.1 | Symbols: AtGRF5, GRF5 | growth-regulating factor 5 | chr3:4608526-4610160 FORWARD LENGTH=397	405	397	1.00E-154	98.0	80.2	88.1
Rsa1.0_00032.1.g1975.t1	ref|XP_002884999.1| hypothetical protein ARALYDRAFT_318183 [Arabidopsis lyrata subsp. lyrata] gi|297330839|gb|EFH61258.1| hypothetical protein ARALYDRAFT_318183 [Arabidopsis lyrata subsp. lyrata]	177	180	7.00E-22	101.7	58.2	63.3	hypothetical protein ARALYDRAFT_318183	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00032.1.g1976.t1	gb|EOA37234.1| hypothetical protein CARUB_v10010750mg [Capsella rubella]	94	94	8.00E-45	100.0	93.6	95.7	hypothetical protein CARUB_v10010750mg	gbpln	Capsella rubella	AT3G13970.1 | Symbols: APG12, APG12B | Ubiquitin-like superfamily protein | chr3:4613696-4614794 REVERSE LENGTH=94	94	94	3.00E-46	100.0	90.4	95.7
Rsa1.0_00032.1.g1977.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00032.1.g1978.t1	ref|NP_188014.1| uncharacterized protein [Arabidopsis thaliana] gi|11994369|dbj|BAB02328.1| unnamed protein product [Arabidopsis thaliana] gi|332641926|gb|AEE75447.1| uncharacterized protein AT3G13980 [Arabidopsis thaliana]	371	357	1.00E-108	96.2	73.9	81.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G13980.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G54200.1); Has 1485 Blast hits to 418 proteins in 98 species: Archae - 0; Bacteria - 6; Metazoa - 246; Fungi - 61; Plants - 107; Viruses - 6; Other Eukaryotes - 1059 (source: NCBI BLink). | chr3:4619189-4620262 REVERSE LENGTH=357	371	357	1.00E-110	96.2	73.9	81.4
Rsa1.0_00032.1.g1979.t17	ref|NP_001078149.1| uncharacterized protein [Arabidopsis thaliana] gi|110742569|dbj|BAE99198.1| hypothetical protein [Arabidopsis thaliana] gi|332641928|gb|AEE75449.1| uncharacterized protein AT3G13990 [Arabidopsis thaliana]	934	847	0	90.7	70.6	77.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G13990.2 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr3:4625708-4630383 REVERSE LENGTH=847	934	847	0	90.7	70.6	77.3

Rsa1.0_00032.1.g1980.t1	ref|NP_188016.2| protein Brevis radix-like 2 [Arabidopsis thaliana] gi|42572427|ref|NP_974309.1| protein Brevis radix-like 2 [Arabidopsis thaliana] gi|75151461|sp|Q8GYL9.1|BRXL2_ARATH RecName: Full=Protein Brevis radix-like 2; Short=AtBRXL2 gi|26450131|dbj|BAC42185.1| unknown protein [Arabidopsis thaliana] gi|115311461|gb|ABI93911.1| At3g14000 [Arabidopsis thaliana] gi|332641929|gb|AEE75450.1| protein Brevis radix-like 2 [Arabidopsis thaliana] gi|332641930|gb|AEE75451.1| protein Brevis radix-like 2 [Arabidopsis thaliana]	377	374	1.00E-160	99.2	81.2	89.1	protein Brevis radix-like 2	gbpln	Arabidopsis thaliana	AT3G14000.2 | Symbols: ATBRXL2, BRX-LIKE2 | DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein | chr3:4631170-4633353 REVERSE LENGTH=374	377	374	1.00E-162	99.2	81.2	89.1
Rsa1.0_00032.1.g1981.t19	dbj|BAB02332.1| unnamed protein product [Arabidopsis thaliana]	1337	596	1.00E-114	44.6	16.8	19.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G14010.3 | Symbols: CID4 | CTC-interacting domain 4 | chr3:4637164-4640691 FORWARD LENGTH=595	1337	595	1.00E-114	44.5	16.8	19.7
Rsa1.0_00032.1.g1982.t1	gb|AFP97582.1| nodulation signaling pathway 1-like protein [Brassica ruvo]	513	509	0	99.2	92.4	95.9	nodulation signaling pathway 1-like protein	gbpln	Brassica ruvo	AT3G13840.1 | Symbols: | GRAS family transcription factor | chr3:4555305-4556837 REVERSE LENGTH=510	513	510	0	99.4	77.0	86.0
Rsa1.0_00032.1.g1983.t1	ref|XP_002885006.1| hypothetical protein ARALYDRAFT_897663 [Arabidopsis lyrata subsp. lyrata] gi|297330846|gb|EFH61265.1| hypothetical protein ARALYDRAFT_897663 [Arabidopsis lyrata subsp. lyrata]	678	714	0	105.3	88.2	92.9	hypothetical protein ARALYDRAFT_897663	gbpln	Arabidopsis lyrata	AT3G14050.1 | Symbols: RSH2, AT-RSH2, ATRSH2 | RELA/SPOT homolog 2 | chr3:4650902-4653514 REVERSE LENGTH=709	678	709	0	104.6	87.5	91.6
Rsa1.0_00032.1.g1984.t1	ref|XP_002885009.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330849|gb|EFH61268.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]	778	777	0	99.9	92.5	95.2	subtilase family protein	gbpln	Arabidopsis lyrata	AT3G14067.1 | Symbols: | Subtilase family protein | chr3:4658421-4660754 REVERSE LENGTH=777	778	777	0	99.9	92.2	95.2
Rsa1.0_00032.1.g1985.t1	gb|EOA32738.1| hypothetical protein CARUB_v10016043mg [Capsella rubella]	638	643	0	100.8	85.6	93.7	hypothetical protein CARUB_v10016043mg	gbpln	Capsella rubella	AT3G14070.1 | Symbols: CAX9, CCX3, ATCCX3 | cation exchanger 9 | chr3:4661143-4663074 REVERSE LENGTH=643	638	643	0	100.8	84.5	93.3
Rsa1.0_00032.1.g1986.t1	ref|XP_002882867.1| hypothetical protein ARALYDRAFT_478821 [Arabidopsis lyrata subsp. lyrata] gi|297328707|gb|EFH59126.1| hypothetical protein ARALYDRAFT_478821 [Arabidopsis lyrata subsp. lyrata] gi|482567523|gb|EOA31712.1| hypothetical protein CARUB_v10014920mg [Capsella rubella]	129	128	1.00E-65	99.2	96.1	97.7	hypothetical protein ARALYDRAFT_478821	gbpln	Arabidopsis lyrata	AT3G14080.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr3:4667717-4668989 FORWARD LENGTH=128	129	128	2.00E-67	99.2	94.6	97.7
Rsa1.0_00032.1.g1987.t1	ref|NP_001147016.1| protein binding protein [Zea mays] gi|195606494|gb|ACG25077.1| protein binding protein [Zea mays]	617	618	0	100.2	87.5	91.2	protein binding protein	gbenv/gbpln	Zea mays	AT3G14090.1 | Symbols: ATEXO70D3, EXO70D3 | exocyst subunit exo70 family protein D3 | chr3:4669508-4671379 REVERSE LENGTH=623	617	623	0	101.0	81.7	88.0
Rsa1.0_00032.1.g1988.t1	ref|NP_566478.1| flourescent in blue light protein [Arabidopsis thaliana] gi|75331838|sp|Q940U6.1|FLU_ARATH RecName: Full=Protein FLUORESCENT IN BLUE LIGHT, chloroplastic; Flags: Precursor gi|17386154|gb|AAL38623.1|AF446890_1 AT3g14110/MAG2_6 [Arabidopsis thaliana] gi|15450619|gb|AAK96581.1| AT3g14110/MAG2_6 [Arabidopsis thaliana] gi|21593122|gb|AAM65071.1| unknown [Arabidopsis thaliana] gi|332641949|gb|AEE75470.1| flourescent in blue light protein [Arabidopsis thaliana]	312	316	1.00E-127	101.3	76.3	86.5	flourescent in blue light protein	gbpln	Arabidopsis thaliana	AT3G14110.1 | Symbols: FLU | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:4676222-4677602 REVERSE LENGTH=316	312	316	1.00E-129	101.3	76.3	86.5
Rsa1.0_00032.1.g1989.t1	gb|EOA32951.1| hypothetical protein CARUB_v10016280mg [Capsella rubella]	1072	1077	0	100.5	90.8	95.0	hypothetical protein CARUB_v10016280mg	gbpln	Capsella rubella	AT3G14120.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: transport; LOCATED IN: nuclear pore; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nuclear pore protein 84/107 (InterPro:IPR007252); Has 5399 Blast hits to 5001 proteins in 612 species: Archae - 19; Bacteria - 730; Metazoa - 2186; Fungi - 823; Plants - 382; Viruses - 37; Other Eukaryotes - 1222 (source: NCBI BLink). | chr3:4677993-4685455 FORWARD LENGTH=1101	1072	1101	0	102.7	90.4	94.8

<table>
<tr><td>Rsa1.0_00032.1.g1990.t1</td><td>ref|NP_566479.5| 2−oxoglutarate−dependent dioxygenase family protein [Arabidopsis thaliana] gi|9294641|dbj|BAB02980.1| unnamed protein product [Arabidopsis thaliana] gi|332641958|gb|AEE75479.1| 2−oxoglutarate−dependent dioxygenase family protein [Arabidopsis thaliana]</td><td>457</td><td>455</td><td>1.00E−148</td><td>99.6</td><td>65.0</td><td>74.6</td><td>2−oxoglutarate−dependent dioxygenase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G14160.1 | Symbols: | 2−oxoglutarate−dependent dioxygenase family protein | chr3:4693495−4695198 FORWARD LENGTH=455</td><td>457</td><td>455</td><td>1.00E−151</td><td>99.6</td><td>65.0</td><td>74.6</td></tr>
<tr><td>Rsa1.0_00032.1.g1991.t1</td><td>ref|XP_002885015.1| hypothetical protein ARALYDRAFT_478830 [Arabidopsis lyrata subsp. lyrata] gi|297330855|gb|EFH61274.1| hypothetical protein ARALYDRAFT_478830 [Arabidopsis lyrata subsp. lyrata]</td><td>543</td><td>506</td><td>0</td><td>93.2</td><td>74.4</td><td>82.3</td><td>hypothetical protein ARALYDRAFT_478830</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G14170.1 | Symbols: | Plant protein of unknown function (DUF936) | chr3:4696115−4697989 REVERSE LENGTH=505</td><td>543</td><td>505</td><td>0</td><td>93.0</td><td>72.6</td><td>81.2</td></tr>
<tr><td>Rsa1.0_00032.1.g1992.t1</td><td>ref|XP_002885016.1| hypothetical protein ARALYDRAFT_478831 [Arabidopsis lyrata subsp. lyrata] gi|297330856|gb|EFH61275.1| hypothetical protein ARALYDRAFT_478831 [Arabidopsis lyrata subsp. lyrata]</td><td>1161</td><td>1256</td><td>0</td><td>108.2</td><td>79.3</td><td>86.3</td><td>hypothetical protein ARALYDRAFT_478831</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G14172.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: COP1−interacting protein−related (TAIR:AT1G72410.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr3:4698860−4704773 REVERSE LENGTH=1270</td><td>1161</td><td>1270</td><td>0</td><td>109.4</td><td>78.5</td><td>85.3</td></tr>
<tr><td>Rsa1.0_00033.1.g1993.t1</td><td>gb|EOA17573.1| hypothetical protein CARUB_v10005934mg, partial [Capsella rubella]</td><td>138</td><td>154</td><td>7.00E−44</td><td>111.6</td><td>67.4</td><td>77.5</td><td>hypothetical protein CARUB_v10005934mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G15990.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G16024.1); Has 14 Blast hits to 14 proteins in 2 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 14; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr4:9061269−9061676 REVERSE LENGTH=135</td><td>138</td><td>135</td><td>3.00E−46</td><td>97.8</td><td>65.9</td><td>78.3</td></tr>
<tr><td>Rsa1.0_00033.1.g1994.t1</td><td>gb|EOA18428.1| hypothetical protein CARUB_v10006972mg [Capsella rubella]</td><td>522</td><td>641</td><td>0</td><td>122.8</td><td>63.8</td><td>76.8</td><td>hypothetical protein CARUB_v10006972mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G13992.1 | Symbols: | Cysteine/Histidine−rich C1 domain family protein | chr4:8087340−8089268 FORWARD LENGTH=642</td><td>522</td><td>642</td><td>0</td><td>123.0</td><td>62.5</td><td>76.1</td></tr>
<tr><td>Rsa1.0_00033.1.g1995.t1</td><td>ref|NP_193008.1| nudix hydrolase 7 [Arabidopsis thaliana] gi|30682217|ref|NP_849367.1| nudix hydrolase 7 [Arabidopsis thaliana] gi|30682219|ref|NP_849368.1| nudix hydrolase 7 [Arabidopsis thaliana] gi|68565949|sp|Q9SU14.1|NUDT7_ARATH RecName: Full=Nudix hydrolase 7; Short=AtNUDT7; AltName: Full=ADP−ribose pyrophosphatase; AltName: Full=NADH pyrophosphatase; AltName: Full=Protein GROWTH FACTOR GENE 1 gi|13272467|gb|AAK17172.1|AF325104_1 growth factor like protein [Arabidopsis thaliana] gi|13877893|gb|AAK44024.1|AF370209_1 putative growth factor [Arabidopsis thaliana] gi|4586248|emb|CAB40989.1| growth factor like protein [Arabidopsis thaliana] gi|7267973|emb|CAB78314.1| growth factor like protein [Arabidopsis thaliana] gi|15810611|gb|AAL07193.1| putative growth factor [Arabidopsis thaliana] gi|332657767|gb|AEE83167.1| nudix hydrolase 7 [Arabidopsis thaliana] gi|332657768|gb|AEE83168.1| nudix hydrolase 7 [Arabidopsis thaliana] gi|332657769|gb|AEE83169.1| nudix hydrolase 7 [Arabidopsis thaliana]</td><td>278</td><td>282</td><td>1.00E−128</td><td>101.4</td><td>75.2</td><td>87.8</td><td>nudix hydrolase 7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G12720.3 | Symbols: AtNUDT7, GFG1, ATNUDX7 | MutT/nudix family protein | chr4:7487716−7489557 FORWARD LENGTH=282</td><td>278</td><td>282</td><td>1.00E−131</td><td>101.4</td><td>75.2</td><td>87.8</td></tr>
<tr><td>Rsa1.0_00033.1.g1996.t1</td><td>dbj|BAJ34567.1| unnamed protein product [Thellungiella halophila]</td><td>99</td><td>97</td><td>2.00E−39</td><td>98.0</td><td>82.8</td><td>87.9</td><td>unnamed protein product</td><td>−−−−</td><td>−−−−</td><td>AT4G15910.1 | Symbols: ATDI21, DI21 | drought−induced 21 | chr4:9028657−9029269 FORWARD LENGTH=104</td><td>99</td><td>104</td><td>7.00E−40</td><td>105.1</td><td>83.8</td><td>85.9</td></tr>
<tr><td>Rsa1.0_00033.1.g1997.t1</td><td>gb|EOA32197.1| hypothetical protein CARUB_v10015453mg [Capsella rubella]</td><td>102</td><td>552</td><td>9.00E−20</td><td>541.2</td><td>42.2</td><td>66.7</td><td>hypothetical protein CARUB_v10015453mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G52950.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:19725483−19728007 FORWARD LENGTH=566</td><td>102</td><td>566</td><td>5.00E−14</td><td>554.9</td><td>33.3</td><td>52.0</td></tr>
</table>

Rsa1.0_00033.1.g1998.t2	ref|XP_002870205.1| hypothetical protein ARALYDRAFT_493299 [Arabidopsis lyrata subsp. lyrata] gi|297316041|gb|EFH46464.1| hypothetical protein ARALYDRAFT_493299 [Arabidopsis lyrata subsp. lyrata]	519	522	0	100.6	79.4	87.5	hypothetical protein ARALYDRAFT_493299	gbpln	Arabidopsis lyrata	AT4G15850.1 | Symbols: ATRH1, RH1 | RNA helicase 1 | chr4:9001426-9004534 FORWARD LENGTH=522	519	522	0	100.6	79.0	87.3
Rsa1.0_00033.1.g1999.t1	ref|NP_568712.1| FAD/NAD(P)-binding oxidoreductase family protein [Arabidopsis thaliana] gi|332008446|gb|AED95829.1| FAD/NAD(P)-binding oxidoreductase family protein [Arabidopsis thaliana]	566	556	0	98.2	89.6	93.5	FAD/NAD(P)-binding oxidoreductase family protein	gbpln	Arabidopsis thaliana	AT5G49555.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr5:20107411-20110602 REVERSE LENGTH=556	566	556	0	98.2	89.6	93.5
Rsa1.0_00033.1.g2000.t1	ref|NP_199767.1| Putative methyltransferase family protein [Arabidopsis thaliana] gi|10177622|dbj|BAB10769.1| unnamed protein product [Arabidopsis thaliana] gi|332008447|gb|AED95830.1| Putative methyltransferase family protein [Arabidopsis thaliana]	284	274	1.00E-114	96.5	75.0	83.8	Putative methyltransferase family protein	gbpln	Arabidopsis thaliana	AT5G49560.1 | Symbols: | Putative methyltransferase family protein | chr5:20110961-20111785 REVERSE LENGTH=274	284	274	1.00E-117	96.5	75.0	83.8
Rsa1.0_00033.1.g2001.t3	ref|XP_002868178.1| hypothetical protein ARALYDRAFT_355185 [Arabidopsis lyrata subsp. lyrata] gi|297314014|gb|EFH44437.1| hypothetical protein ARALYDRAFT_355185 [Arabidopsis lyrata subsp. lyrata]	1197	1153	0	96.3	57.0	68.3	hypothetical protein ARALYDRAFT_355185	gbpln	Arabidopsis lyrata	AT4G15810.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:8989162-8992591 REVERSE LENGTH=918	1197	918	1.00E-164	76.7	32.3	40.2
Rsa1.0_00033.1.g2002.t1	ref|NP_567475.5| uncharacterized protein [Arabidopsis thaliana] gi|18175846|gb|AAL59938.1| unknown protein [Arabidopsis thaliana] gi|21689873|gb|AAM67497.1| unknown protein [Arabidopsis thaliana] gi|332658252|gb|AEE83652.1| uncharacterized protein AT4G15790 [Arabidopsis thaliana]	146	147	7.00E-56	100.7	82.2	89.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G15790.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 411 Blast hits to 380 proteins in 121 species: Archae - 4; Bacteria - 107; Metazoa - 85; Fungi - 29; Plants - 59; Viruses - 0; Other Eukaryotes - 127 (source: NCBI BLink). | chr4:8982390-8984069 FORWARD LENGTH=147	146	147	2.00E-58	100.7	82.2	89.7
Rsa1.0_00033.1.g2003.t1	ref|NP_197566.1| vacuolar protein / peptidase dimerization domain-containing protein [Arabidopsis thaliana] gi|110741500|dbj|BAE98701.1| 24 kDa vacuolar protein - like [Arabidopsis thaliana] gi|332005489|gb|AED92872.1| vacuolar protein / peptidase dimerization domain-containing protein [Arabidopsis thaliana]	911	910	0	99.9	82.7	92.3	vacuolar protein / peptidase dimerization domain-containing protein	gbpln	Arabidopsis thaliana	AT5G20660.1 | Symbols: | Zn-dependent exopeptidases superfamily protein | chr5:6986402-6990947 FORWARD LENGTH=910	911	910	0	99.9	82.7	92.3
Rsa1.0_00033.1.g2004.t1	ref|XP_002868180.1| hypothetical protein ARALYDRAFT_915207 [Arabidopsis lyrata subsp. lyrata] gi|297314016|gb|EFH44439.1| hypothetical protein ARALYDRAFT_915207 [Arabidopsis lyrata subsp. lyrata]	222	222	1.00E-124	100.0	96.4	98.2	hypothetical protein ARALYDRAFT_915207	gbpln	Arabidopsis lyrata	AT4G15780.1 | Symbols: ATVAMP724, VAMP724 | vesicle-associated membrane protein 724 | chr4:8980081-8981697 REVERSE LENGTH=222	222	222	1.00E-118	100.0	96.8	98.6
Rsa1.0_00033.1.g2005.t1	gb|EOA15832.1| hypothetical protein CARUB_v10007453mg [Capsella rubella]	187	187	1.00E-99	100.0	93.6	96.8	hypothetical protein CARUB_v10007453mg	gbpln	Capsella rubella	AT4G15770.1 | Symbols: | RNA binding | chr4:8978060-8978623 FORWARD LENGTH=187	187	187	1.00E-100	100.0	92.0	95.7
Rsa1.0_00033.1.g2006.t1	gb|EOA19124.1| hypothetical protein CARUB_v10007793mg [Capsella rubella]	344	511	1.00E-151	148.5	75.0	86.0	hypothetical protein CARUB_v10007793mg	gbpln	Capsella rubella	AT5G24950.1 | Symbols: CYP71A15 | cytochrome P450, family 71, subfamily A, polypeptide 15 | chr5:8595209-8597761 REVERSE LENGTH=496	344	496	1.00E-119	144.2	62.5	75.6
Rsa1.0_00033.1.g2007.t1	gb|EOA19124.1| hypothetical protein CARUB_v10007793mg [Capsella rubella]	145	511	5.00E-43	352.4	57.2	62.1	hypothetical protein CARUB_v10007793mg	gbpln	Capsella rubella	AT4G13310.2 | Symbols: CYP71A20 | cytochrome P450, family 71, subfamily A, polypeptide 20 | chr4:7750453-7751856 FORWARD LENGTH=390	145	390	5.00E-45	269.0	58.6	62.8
Rsa1.0_00033.1.g2008.t1	gb|EOA19124.1| hypothetical protein CARUB_v10007793mg [Capsella rubella]	489	511	0	104.5	75.3	84.0	hypothetical protein CARUB_v10007793mg	gbpln	Capsella rubella	AT5G24950.1 | Symbols: CYP71A15 | cytochrome P450, family 71, subfamily A, polypeptide 15 | chr5:8595209-8597761 REVERSE LENGTH=496	489	496	0	101.4	63.4	76.3
Rsa1.0_00033.1.g2009.t1	gb|EOA18110.1| hypothetical protein CARUB_v10006571mg [Capsella rubella]	440	457	1.00E-163	103.9	68.4	78.9	hypothetical protein CARUB_v10006571mg	gbpln	Capsella rubella	AT4G15740.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:8964912-8966318 REVERSE LENGTH=468	440	468	1.00E-163	106.4	66.1	76.1

Rsa1.0_00033.1.g2010.t1	ref|XP_002870231.1| hypothetical protein ARALYDRAFT_915246 [Arabidopsis lyrata subsp. lyrata] gi|297316067|gb|EFH46490.1| hypothetical protein ARALYDRAFT_915246 [Arabidopsis lyrata subsp. lyrata]	334	335	1.00E−163	100.3	85.0	91.9	hypothetical protein ARALYDRAFT_915246	gbpln	Arabidopsis lyrata	AT4G15545.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16520.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:8875932−8877567 FORWARD LENGTH=337	334	337	1.00E−164	100.9	85.0	91.6
Rsa1.0_00033.1.g2011.t1	dbj|BAJ34577.1| unnamed protein product [Thellungiella halophila]	325	325	1.00E−169	100.0	88.0	95.7	unnamed protein product	----	----	AT3G59380.1 | Symbols: FTA, PLP, ATFTA, PFT/PGGT−IALPHA | farnesyltransferase A | chr3:21944209−21945781 FORWARD LENGTH=326	325	326	1.00E−165	100.3	87.7	94.5
Rsa1.0_00033.1.g2012.t1	ref|NP_849391.2| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana] gi|145333150|ref|NP_001078395.1| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana] gi|222423813|dbj|BAH19872.1| AT4G15530 [Arabidopsis thaliana] gi|332658217|gb|AEE83617.1| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana] gi|332658219|gb|AEE83619.1| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana]	92	956	8.00E−26	1039.1	62.0	73.9	pyruvate, phosphate dikinase 1	gbpln	Arabidopsis thaliana	AT4G15530.4 | Symbols: PPDK | pyruvate orthophosphate dikinase | chr4:8864828−8870727 REVERSE LENGTH=956	92	956	1.00E−28	1039.1	62.0	73.9
Rsa1.0_00033.1.g2013.t1	ref|NP_193288.2| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana] gi|222424574|dbj|BAH20242.1| AT4G15530 [Arabidopsis thaliana] gi|332658216|gb|AEE83616.1| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana]	875	875	0	100.0	94.9	98.5	pyruvate, phosphate dikinase 1	gbpln	Arabidopsis thaliana	AT4G15530.2 | Symbols: PPDK | pyruvate orthophosphate dikinase | chr4:8864828−8869183 REVERSE LENGTH=875	875	875	0	100.0	94.9	98.5
Rsa1.0_00033.1.g2014.t2	ref|NP_567468.1| PsbP domain−containing protein 1 [Arabidopsis thaliana] gi|13959580|sp|O23403.1|PPD1_ARATH RecName: Full=PsbP domain−containing protein 1, chloroplastic; AltName: Full=OEC23−like protein 3; AltName: Full=PsbP−related thylakoid lumenal protein 1; Flags: Precursor gi|2244908|emb|CAB10329.1| hypothetical protein [Arabidopsis thaliana] gi|7268298|emb|CAB78593.1| hypothetical protein [Arabidopsis thaliana] gi|332658213|gb|AEE83613.1| PsbP domain−containing protein 1 [Arabidopsis thaliana]	270	287	1.00E−115	106.3	80.7	85.9	PsbP domain−containing protein 1	gbpln	Arabidopsis thaliana	AT4G15510.1 | Symbols: | Photosystem II reaction center PsbP family protein | chr4:8860701−8862529 FORWARD LENGTH=287	270	287	1.00E−118	106.3	80.7	85.9
Rsa1.0_00033.1.g2015.t1	ref|XP_002885447.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297331287|gb|EFH61706.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	955	954	0	99.9	83.1	91.5	transducin family protein	gbpln	Arabidopsis lyrata	AT3G21540.1 | Symbols: | transducin family protein / WD−40 repeat family protein | chr3:7586100−7590856 REVERSE LENGTH=955	955	955	0	100.0	82.3	91.1
Rsa1.0_00033.1.g2016.t1	ref|XP_002870258.1| hypothetical protein ARALYDRAFT_493374 [Arabidopsis lyrata subsp. lyrata] gi|297316094|gb|EFH46517.1| hypothetical protein ARALYDRAFT_493374 [Arabidopsis lyrata subsp. lyrata]	330	451	2.00E−43	136.7	26.1	26.7	hypothetical protein ARALYDRAFT_493374	gbpln	Arabidopsis lyrata	AT4G15160.2 | Symbols: | Bifunctional inhibitor/lipid−transfer protein/seed storage 2S albumin superfamily protein | chr4:8646192−8647019 FORWARD LENGTH=193	330	193	2.00E−42	58.5	25.8	26.7
Rsa1.0_00033.1.g2017.t1	ref|NP_567450.1| SNARE associated Golgi protein [Arabidopsis thaliana] gi|53749170|gb|AAU90070.1| At4g14950 [Arabidopsis thaliana] gi|332658128|gb|AEE83528.1| SNARE associated Golgi protein [Arabidopsis thaliana]	441	416	0	94.3	82.8	85.9	SNARE associated Golgi protein	gbpln	Arabidopsis thaliana	AT4G14950.1 | Symbols: | SNARE associated Golgi protein family | chr4:8545517−8547722 FORWARD LENGTH=416	441	416	0	94.3	82.8	85.9
Rsa1.0_00033.1.g2018.t1	gb|AAL47166.1|AF449459_1 diamine oxidase [Brassica juncea]	649	649	0	100.0	96.6	98.6	diamine oxidase	gbpln	Brassica juncea	AT4G14940.1 | Symbols: ATAO1, AO1 | amine oxidase 1 | chr4:8541879−8544304 FORWARD LENGTH=650	649	650	0	100.2	90.1	95.4
Rsa1.0_00033.1.g2019.t1	ref|NP_567449.1| 5'−nucleotidase [Arabidopsis thaliana] gi|21593317|gb|AAM65266.1| unknown [Arabidopsis thaliana] gi|27311791|gb|AAO00861.1| expressed protein [Arabidopsis thaliana] gi|30984528|gb|AAP42727.1| At4g14930 [Arabidopsis thaliana] gi|332658124|gb|AEE83524.1| survival protein SurE−like phosphatase/nucleotidase [Arabidopsis thaliana]	296	315	1.00E−138	106.4	81.1	89.9	5'−nucleotidase	gbpln	Arabidopsis thaliana	AT4G14930.1 | Symbols: | Survival protein SurE−like phosphatase/nucleotidase | chr4:8538831−8541205 FORWARD LENGTH=315	296	315	1.00E−140	106.4	81.1	89.9

Rsa1.0_00033.1_g2020.t1	ref|NP_194638.1| Ribonuclease H-like protein [Arabidopsis thaliana] gi|4972055|emb|CAB43923.1| putative protein [Arabidopsis thaliana] gi|7269807|emb|CAB79667.1| putative protein [Arabidopsis thaliana] gi|67633766|gb|AAY78807.1| putative reverse transcriptase/RNA-dependent DNA polymerase [Arabidopsis thaliana] gi|332660185|gb|AEE85585.1| Ribonuclease H-like protein [Arabidopsis thaliana]	108	575	4.00E-16	532.4	35.2	43.5	Ribonuclease H-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	108	575	6.00E-19	532.4	35.2	43.5
Rsa1.0_00033.1_g2021.t1	ref|XP_002876895.1| hypothetical protein ARALYDRAFT_484284 [Arabidopsis lyrata subsp. lyrata] gi|297322733|gb|EFH53154.1| hypothetical protein ARALYDRAFT_484284 [Arabidopsis lyrata subsp. lyrata]	335	333	1.00E-166	99.4	84.5	91.3	hypothetical protein ARALYDRAFT_484284	gbpln	Arabidopsis lyrata	AT2G03750.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:1147968-1149023 REVERSE LENGTH=351	335	351	1.00E-161	104.8	82.1	90.1
Rsa1.0_00033.1_g2022.t1	emb|CAB10271.1| hypothetical protein [Arabidopsis thaliana] gi|7268238|emb|CAB78534.1| hypothetical protein [Arabidopsis thaliana]	420	1040	1.00E-106	247.6	64.0	75.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G14920.1 | Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein | chr4:8531157-8535842 REVERSE LENGTH=1138	420	1138	1.00E-108	271.0	64.0	75.0
Rsa1.0_00033.1_g2023.t1	ref|NP_001147025.1| ferredoxin [Zea mays] gi|195606586|gb|ACG25123.1| ferredoxin [Zea mays]	151	151	1.00E-75	100.0	92.7	96.0	ferredoxin	gbenv/gbpln	Zea mays	AT4G14890.1 | Symbols: FdC2 | 2Fe-2S ferredoxin-like superfamily protein | chr4:8520887-8521351 FORWARD LENGTH=154	151	154	3.00E-72	102.0	88.7	94.0
Rsa1.0_00033.1_g2024.t1	gb|ACX70136.1| O-acetylserine(thiol)lyase isoform A6 [Brassica rapa subsp. chinensis]	322	322	1.00E-180	100.0	98.1	98.8	O-acetylserine(thiol)lyase isoform A6	gbpln	Brassica rapa	AT4G14880.4 | Symbols: OASA1 | O-acetylserine (thiol) lyase (OAS-TL) isoform A1 | chr4:8518209-8520050 REVERSE LENGTH=322	322	322	1.00E-167	100.0	96.3	97.8
Rsa1.0_00033.1_g2025.t1	gb|EOA18180.1| hypothetical protein CARUB_v10006658mg [Capsella rubella]	371	177	3.00E-70	47.7	38.5	41.2	hypothetical protein CARUB_v10006658mg	gbpln	Capsella rubella	AT4G14870.1 | Symbols: SECE1 | secE/sec61-gamma protein transport protein | chr4:8517248-8517781 FORWARD LENGTH=177	371	177	1.00E-69	47.7	37.7	39.4
Rsa1.0_00033.1_g2026.t1	ref|NP_193218.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75274931|sp|O23337.1|PP311_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g14820 gi|2244839|emb|CAB10261.1| hypothetical protein [Arabidopsis thaliana] gi|7268228|emb|CAB78524.1| hypothetical protein [Arabidopsis thaliana] gi|332658106|gb|AEE83506.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	628	722	0	115.0	78.5	88.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G14820.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:8507794-8510038 REVERSE LENGTH=722	628	722	0	115.0	78.5	88.5
Rsa1.0_00033.1_g2027.t1	gb|EOA18115.1| hypothetical protein CARUB_v10006576mg [Capsella rubella]	106	106	2.00E-45	100.0	84.9	87.7	hypothetical protein CARUB_v10006576mg	gbpln	Capsella rubella	AT4G14819.1 | Symbols: | Protein of unknown function (DUF1677) | chr4:8507365-8507679 FORWARD LENGTH=104	106	104	1.00E-46	98.1	83.0	87.7
Rsa1.0_00033.1_g2028.t1	ref|XP_002870280.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316116|gb|EFH46539.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	165	155	1.00E-53	93.9	67.3	75.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G14815.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:8505122-8505760 FORWARD LENGTH=156	165	156	1.00E-52	94.5	64.2	73.9
Rsa1.0_00033.1_g2029.t1	ref|XP_002885514.1| hypothetical protein ARALYDRAFT_898737 [Arabidopsis lyrata subsp. lyrata] gi|297331354|gb|EFH61773.1| hypothetical protein ARALYDRAFT_898737 [Arabidopsis lyrata subsp. lyrata]	204	204	1.00E-111	100.0	94.1	99.5	hypothetical protein ARALYDRAFT_898737	gbpln	Arabidopsis lyrata	AT3G22630.1 | Symbols: PBD1, PRCGB | 20S proteasome beta subunit D1 | chr3:8009709-8010774 REVERSE LENGTH=204	204	204	1.00E-113	100.0	93.6	99.0
Rsa1.0_00033.1_g2030.t1	ref|NP_193215.2| ATP-dependent RNA helicase, mitochondrial (SUV3) [Arabidopsis thaliana] gi|5823579|emb|CAB53782.1| mitochondrial RNA helicase [Arabidopsis thaliana] gi|22655093|gb|AAM98137.1| RNA helicase like protein [Arabidopsis thaliana] gi|31711986|gb|AAP68349.1| At4g14790 [Arabidopsis thaliana] gi|332658099|gb|AEE83499.1| ATP-dependent RNA helicase, mitochondrial (SUV3) [Arabidopsis thaliana]	599	571	0	95.3	80.6	86.5	ATP-dependent RNA helicase, mitochondrial (SUV3)	gbpln	Arabidopsis thaliana	AT4G14790.1 | Symbols: ATSUV3, EDA15 | ATP-dependent RNA helicase, mitochondrial (SUV3) | chr4:8496351-8499829 REVERSE LENGTH=571	599	571	0	95.3	80.6	86.5

Rsa1.0_00033.1.g2031.t1	ref|NP_201386.1| F-box protein [Arabidopsis thaliana] gi|75170652|sp|Q9FHP3.1|FB300_ARATH RecName: Full=F-box protein At5g65850 gi|9759569|dbj|BAB11132.1| unnamed protein product [Arabidopsis thaliana] gi|50253490|gb|AAT71947.1| At5g65850 [Arabidopsis thaliana] gi|51972136|gb|AAU15172.1| At5g65850 [Arabidopsis thaliana] gi|332010731|gb|AED98114.1| F-box protein [Arabidopsis thaliana]	388	392	1.00E-81	101.0	46.6	63.4	F-box protein	gbpln	Arabidopsis thaliana	AT5G65850.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:26346317-26347495 FORWARD LENGTH=392	388	392	2.00E-84	101.0	46.6	63.4
Rsa1.0_00033.1.g2032.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	427	387	8.00E-77	90.6	43.1	56.7	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	427	387	2.00E-79	90.6	43.1	56.7
Rsa1.0_00033.1.g2033.t3	gb|AAC63844.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1332	1231	0	92.4	58.0	70.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17201414-17202323 REVERSE LENGTH=258	1332	258	6.00E-81	19.4	10.8	13.2
Rsa1.0_00033.1.g2034.t1	gb|EOA15412.1| hypothetical protein CARUB_v10007448mg [Capsella rubella]	647	675	0	104.3	75.0	83.3	hypothetical protein CARUB_v10007448mg	gbpln	Capsella rubella	AT4G14770.1 | Symbols: TCX2, ATTCX2 | TESMIN/TSO1-like CXC 2 | chr4:8481522-8484825 REVERSE LENGTH=674	647	674	0	104.2	75.4	83.6
Rsa1.0_00033.1.g2035.t1	gb|EOA15328.1| hypothetical protein CARUB_v10003978mg [Capsella rubella]	1606	1717	0	106.9	77.1	87.9	hypothetical protein CARUB_v10003978mg	gbpln	Capsella rubella	AT4G14760.1 | Symbols: | kinase interacting (KIP1-like) family protein | chr4:8475718-8481094 FORWARD LENGTH=1710	1606	1710	0	106.5	77.0	87.4
Rsa1.0_00033.1.g2036.t1	gb|AAL86322.1| unknown protein [Arabidopsis thaliana]	373	409	1.00E-150	109.7	78.8	86.3	unknown protein	gbpln	Arabidopsis thaliana	AT4G14750.1 | Symbols: IQD19 | IQ-domain 19 | chr4:8470449-8471903 FORWARD LENGTH=387	373	387	1.00E-152	103.8	78.8	86.3
Rsa1.0_00033.1.g2037.t1	ref|XP_002868255.1| hypothetical protein ARALYDRAFT_493423 [Arabidopsis lyrata subsp. lyrata] gi|297314091|gb|EFH44514.1| hypothetical protein ARALYDRAFT_493423 [Arabidopsis lyrata subsp. lyrata]	201	214	1.00E-77	106.5	73.1	83.6	hypothetical protein ARALYDRAFT_493423	gbpln	Arabidopsis lyrata	AT4G14746.1 | Symbols: | CONTAINS InterPro DOMAIN/s: EGF-like (InterPro:IPR006210); Has 259 Blast hits to 234 proteins in 55 species: Archae - 0; Bacteria - 0; Metazoa - 184; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr4:8462720-8464326 REVERSE LENGTH=212	201	212	2.00E-64	105.5	71.1	82.6
Rsa1.0_00033.1.g2038.t1	ref|NP_193210.2| uncharacterized protein [Arabidopsis thaliana] gi|42572905|ref|NP_974549.1| uncharacterized protein [Arabidopsis thaliana] gi|18377642|gb|AAL66971.1| unknown protein [Arabidopsis thaliana] gi|23297568|gb|AAN12896.1| unknown protein [Arabidopsis thaliana] gi|332658090|gb|AEE83490.1| uncharacterized protein AT4G14740 [Arabidopsis thaliana] gi|332658091|gb|AEE83491.1| uncharacterized protein AT4G14740 [Arabidopsis thaliana]	472	475	0	100.6	91.7	94.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G14740.2 | Symbols: | Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region | chr4:8450567-8453946 REVERSE LENGTH=475	472	475	0	100.6	91.7	94.9
Rsa1.0_00033.1.g2039.t1	gb|ACJ68113.1| hypothetical protein [Brassica napus]	239	239	1.00E-104	100.0	88.7	95.4	hypothetical protein	gbpln	Brassica napus	AT4G14730.1 | Symbols: | Bax inhibitor-1 family protein | chr4:8448607-8450001 FORWARD LENGTH=235	239	235	4.00E-89	98.3	71.1	84.1
Rsa1.0_00033.1.g2040.t1	ref|NP_001031641.1| epidermal patterning factor-like protein 4 [Arabidopsis thaliana] gi|122209356|sp|Q2V3I3.1|EPFL4_ARATH RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 4; Short=EPF-like protein 4; Flags: Precursor gi|98961833|gb|ABF59246.1| unknown protein [Arabidopsis thaliana] gi|332658088|gb|AEE83488.1| epidermal patterning factor-like protein 4 [Arabidopsis thaliana]	117	109	1.00E-32	93.2	62.4	67.5	epidermal patterning factor-like protein 4	gbpln	Arabidopsis thaliana	AT4G14723.1 | Symbols: | BEST Arabidopsis thaliana protein match is: allergen-related (TAIR:AT3G22820.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:8440167-8440693 FORWARD LENGTH=109	117	109	2.00E-35	93.2	62.4	67.5
Rsa1.0_00033.1.g2041.t1	gb|AAR03591.1| ARD-like protein [Brassica juncea]	204	195	1.00E-102	95.6	87.7	89.7	ARD-like protein	gbpln	Brassica juncea	AT4G14710.2 | Symbols: ATARD2 | RmlC-like cupins superfamily protein | chr4:8424897-8426360 REVERSE LENGTH=199	204	199	1.00E-99	97.5	83.3	86.8

Rsa1.0_00033.1.g2042.t1	ref|NP_567438.1| early light-inducible protein 2 [Arabidopsis thaliana] gi|13878007|gb|AAK44081.1|AF370266_1 unknown protein [Arabidopsis thaliana] gi|17104737|gb|AAL34257.1| unknown protein [Arabidopsis thaliana] gi|332658075|gb|AEE83475.1| early light-inducible protein 2 [Arabidopsis thaliana]	127	193	6.00E-55	152.0	84.3	88.2	early light-inducible protein 2	gbpln	Arabidopsis thaliana	AT4G14690.1 | Symbols: ELIP2 | Chlorophyll A-B binding family protein | chr4:8418373-8419129 FORWARD LENGTH=193	127	193	1.00E-57	152.0	84.3	88.2
Rsa1.0_00033.1.g2043.t1	gb|AAR03591.1| ARD-like protein [Brassica juncea]	195	195	1.00E-110	100.0	97.9	99.0	ARD-like protein	gbpln	Brassica juncea	AT4G14710.2 | Symbols: ATARD2 | RmlC-like cupins superfamily protein | chr4:8424897-8426360 REVERSE LENGTH=199	195	199	1.00E-106	102.1	93.3	96.9
Rsa1.0_00033.1.g2044.t1	gb|EOA18123.1| hypothetical protein CARUB_v10006584mg [Capsella rubella]	191	191	2.00E-80	100.0	85.3	90.1	hypothetical protein CARUB_v10006584mg	gbpln	Capsella rubella	AT4G14690.1 | Symbols: ELIP2 | Chlorophyll A-B binding family protein | chr4:8418373-8419129 FORWARD LENGTH=193	191	193	2.00E-79	101.0	85.3	90.6
Rsa1.0_00033.1.g2045.t1	gb|ACV04807.1| ATP sulfurylase 3 [Brassica napus]	862	465	0	53.9	50.5	51.5	ATP sulfurylase 3	gbpln	Brassica napus	AT4G14680.1 | Symbols: APS3 | Pseudouridine synthase/archaeosine transglycosylase-like family protein | chr4:8413443-8415311 REVERSE LENGTH=465	862	465	0	53.9	47.8	50.7
Rsa1.0_00033.1.g2046.t1	ref|NP_193202.2| DNA-directed RNA polymerase II subunit G [Arabidopsis thaliana] gi|149944323|gb|ABR46204.1| At4g14660 [Arabidopsis thaliana] gi|332658072|gb|AEE83472.1| DNA-directed RNA polymerase NRPE7 [Arabidopsis thaliana]	178	178	1.00E-78	100.0	77.0	91.0	DNA-directed RNA polymerase II subunit G	gbpln	Arabidopsis thaliana	AT4G14660.1 | Symbols: NRPE7 | RNA polymerase Rpb7-like, N-terminal domain | chr4:8406500-8407036 REVERSE LENGTH=178	178	178	4.00E-81	100.0	77.0	91.0
Rsa1.0_00033.1.g2047.t1	ref|XP_002868271.1| hypothetical protein ARALYDRAFT_493441 [Arabidopsis lyrata subsp. lyrata] gi|297314107|gb|EFH44530.1| hypothetical protein ARALYDRAFT_493441 [Arabidopsis lyrata subsp. lyrata]	299	604	5.00E-26	202.0	28.1	33.8	hypothetical protein ARALYDRAFT_493441	gbpln	Arabidopsis lyrata	AT4G14650.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: petal differentiation and expansion stage; Has 2407 Blast hits to 1833 proteins in 310 species: Archae - 19; Bacteria - 223; Metazoa - 708; Fungi - 285; Plants - 140; Viruses - 42; Other Eukaryotes - 990 (source: NCBI BLink). | chr4:8400760-8402817 REVERSE LENGTH=632	299	632	1.00E-25	211.4	26.1	33.1
Rsa1.0_00033.1.g2048.t1	ref|NP_188935.1| ADP-ribosylation factor C1 [Arabidopsis thaliana] gi|334185556|ref|NP_001189951.1| ADP-ribosylation factor C1 [Arabidopsis thaliana] gi|297788976|ref|XP_002862508.1| ADP-ribosylation factor C1 [Arabidopsis lyrata subsp. lyrata] gi|11994726|dbj|BAB03042.1| unnamed protein product [Arabidopsis thaliana] gi|17381004|gb|AAL36314.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gi|20465873|gb|AAM20041.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gi|21592454|gb|AAM64405.1| ADP-ribosylation factor, putative [Arabidopsis thaliana] gi|297308070|gb|EFH38766.1| ADP-ribosylation factor C1 [Arabidopsis lyrata subsp. lyrata] gi|332643174|gb|AEE76695.1| ADP-ribosylation factor C1 [Arabidopsis thaliana] gi|332643175|gb|AEE76696.1| ADP-ribosylation factor C1 [Arabidopsis thaliana]	183	183	1.00E-98	100.0	95.1	97.3	ADP-ribosylation factor C1	gbpln	Arabidopsis lyrata	AT3G22950.2 | Symbols: ARFC1 | ADP-ribosylation factor C1 | chr3:8136364-8137513 REVERSE LENGTH=183	183	183	1.00E-101	100.0	95.1	97.3
Rsa1.0_00033.1.g2049.t1	ref|NP_193198.2| uncharacterized protein [Arabidopsis thaliana] gi|22136618|gb|AAM91628.1| unknown protein [Arabidopsis thaliana] gi|332658067|gb|AEE83467.1| uncharacterized protein AT4G14620 [Arabidopsis thaliana]	362	341	1.00E-125	94.2	68.2	77.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G14620.1 | Symbols: | Protein of unknown function (DUF506) | chr4:8389246-8390448 REVERSE LENGTH=341	362	341	1.00E-127	94.2	68.2	77.9
Rsa1.0_00033.1.g2050.t1	gb|EOA18498.1| hypothetical protein CARUB_v10007049mg [Capsella rubella]	489	488	0	99.8	85.1	90.4	hypothetical protein CARUB_v10007049mg	gbpln	Capsella rubella	AT4G14605.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr4:8378815-8380564 FORWARD LENGTH=493	489	493	0	100.8	84.9	90.4
Rsa1.0_00033.1.g2051.t2	emb|CAB10171.1| disease resistance Cf-2 like protein [Arabidopsis thaliana] gi|7268096|emb|CAB78434.1| disease resistance Cf-2 like protein [Arabidopsis thaliana]	243	869	1.00E-45	357.6	44.9	52.7	disease resistance Cf-2 like protein	gbpln	Arabidopsis thaliana	AT4G13920.1 | Symbols: AtRLP50, RLP50 | receptor like protein 50 | chr4:8043861-8046536 FORWARD LENGTH=891	243	891	4.00E-48	366.7	44.9	52.7

Rsa1.0_00033.1.g2052.t1	gb|EOA15994.1| hypothetical protein CARUB_v10004113mg [Capsella rubella]	844	866	0	102.6	63.6	77.4	hypothetical protein CARUB_v10004113mg	gbpln	Capsella rubella	AT4G13810.1 | Symbols: AtRLP47, RLP47 | receptor like protein 47 | chr4:8005062-8007287 REVERSE LENGTH=741	844	741	0	87.8	55.8	67.8
Rsa1.0_00034.1.g2053.t1	gb|EOA38545.1| hypothetical protein CARUB_v10010350mg [Capsella rubella]	133	196	6.00E-72	147.4	99.2	100.0	hypothetical protein CARUB_v10010350mg	gbpln	Capsella rubella	AT1G20090.1 | Symbols: ARAC4, ROP2, ATROP2, ATRAC4 | RHO-related protein from plants 2 | chr1:6967223-6968603 FORWARD LENGTH=195	133	195	2.00E-74	146.6	99.2	100.0
Rsa1.0_00034.1.g2054.t1	ref|XP_002893089.1| hypothetical protein ARALYDRAFT_472236 [Arabidopsis lyrata subsp. lyrata] gi|297338931|gb|EFH69348.1| hypothetical protein ARALYDRAFT_472236 [Arabidopsis lyrata subsp. lyrata]	269	285	2.00E-69	105.9	67.3	77.7	hypothetical protein ARALYDRAFT_472236	gbpln	Arabidopsis lyrata	AT1G20100.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G75860.1); Has 471 Blast hits to 438 proteins in 92 species: Archae - 0; Bacteria - 14; Metazoa - 217; Fungi - 43; Plants - 91; Viruses - 1; Other Eukaryotes - 105 (source: NCBI BLink). | chr1:6969314-6970699 REVERSE LENGTH=285	269	285	2.00E-62	105.9	64.3	73.2
Rsa1.0_00034.1.g2055.t1	ref|NP_564103.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana] gi|13605833|gb|AAK32902.1|AF367315_1 At1g20110/T20H2_10 [Arabidopsis thaliana] gi|16226228|gb|AAL16109.1|AF428277_1 At1g20110/T20H2_10 [Arabidopsis thaliana] gi|23506043|gb|AAN28881.1| At1g20110/T20H2_10 [Arabidopsis thaliana] gi|332191816|gb|AEE29937.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana]	584	601	0	102.9	77.9	82.4	RING/FYVE/PHD zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT1G20110.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:6971554-6974578 FORWARD LENGTH=601	584	601	0	102.9	77.9	82.4
Rsa1.0_00034.1.g2056.t1	gb|EOA37331.1| hypothetical protein CARUB_v10011033mg [Capsella rubella]	321	389	1.00E-101	121.2	53.6	66.4	hypothetical protein CARUB_v10011033mg	gbpln	Capsella rubella	AT1G20132.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:6981358-6983495 FORWARD LENGTH=383	321	383	1.00E-101	119.3	52.6	64.8
Rsa1.0_00034.1.g2057.t1	ref|NP_173445.2| uncharacterized protein [Arabidopsis thaliana] gi|158706505|sp|Q6DYE5.2|U496K_ARATH RecName: Full=UPF0496 protein At1g20180 gi|8778981|gb|AAF79896.1|AC022472_5 Contains similarity to At14a protein from Arabidopsis thaliana gi|4589123 [Arabidopsis thaliana] gi|91805813|gb|ABE65635.1| hypothetical protein At1g20180 [Arabidopsis thaliana] gi|332191826|gb|AEE29947.1| uncharacterized protein AT1G20180 [Arabidopsis thaliana]	390	390	1.00E-150	100.0	77.7	85.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G20180.1 | Symbols: | Protein of unknown function (DUF677) | chr1:6996354-6997779 FORWARD LENGTH=390	390	390	1.00E-153	100.0	77.7	85.4
Rsa1.0_00034.1.g2058.t1	ref|XP_002893092.1| Alpha-expansin 11 precursor [Arabidopsis lyrata subsp. lyrata] gi|297338934|gb|EFH69351.1| Alpha-expansin 11 precursor [Arabidopsis lyrata subsp. lyrata]	213	252	1.00E-101	118.3	90.6	95.3	Alpha-expansin 11 precursor	gbpln	Arabidopsis lyrata	AT1G20190.1 | Symbols: ATEXPA11, EXP11, ATEXP11, ATHEXP ALPHA 1.14, EXPA11 | expansin 11 | chr1:6998762-6999710 REVERSE LENGTH=252	213	252	7.00E-99	118.3	91.1	95.3
Rsa1.0_00034.1.g2059.t1	ref|NP_173447.1| 26S proteasome regulatory subunit N3 [Arabidopsis thaliana] gi|30316389|sp|Q9LNU4.3|PSD31_ARATH RecName: Full=Probable 26S proteasome non-ATPase regulatory subunit 3a; Short=26S proteasome subunit S3-a; AltName: Full=26S proteasome regulatory subunit RPN3a; AltName: Full=Protein EMBRYO DEFECTIVE 2719 gi|32700016|gb|AAP86658.1| 26S proteasome subunit RPN3a [Arabidopsis thaliana] gi|332191829|gb|AEE29950.1| probable 26S proteasome non-ATPase regulatory subunit 3a [Arabidopsis thaliana]	463	488	0	105.4	95.0	97.6	26S proteasome regulatory subunit N3	gbpln	Arabidopsis thaliana	AT1G20200.1 | Symbols: EMB2719, HAP15 | PAM domain (PCI/PINT associated module) protein | chr1:7001409-7004154 REVERSE LENGTH=488	463	488	0	105.4	95.0	97.6
Rsa1.0_00034.1.g2060.t1	ref|XP_002893094.1| hypothetical protein ARALYDRAFT_312946 [Arabidopsis lyrata subsp. lyrata] gi|297338936|gb|EFH69353.1| hypothetical protein ARALYDRAFT_312946 [Arabidopsis lyrata subsp. lyrata]	369	529	1.00E-72	143.4	52.8	57.7	hypothetical protein ARALYDRAFT_312946	gbpln	Arabidopsis lyrata	AT1G76010.1 | Symbols: | Alba DNA/RNA-binding protein | chr1:28528505-28530488 REVERSE LENGTH=350	369	350	5.00E-73	94.9	53.4	60.2

Rsa1.0_00034.1.g2061.t2	ref|XP_002890376.1| hypothetical protein ARALYDRAFT_472256 [Arabidopsis lyrata subsp. lyrata] gi|297336218|gb|EFH66635.1| hypothetical protein ARALYDRAFT_472256 [Arabidopsis lyrata subsp. lyrata]	486	487	0	100.2	98.1	98.8	hypothetical protein ARALYDRAFT_472256	gbpln	Arabidopsis lyrata	AT1G20260.1 | Symbols: | ATPase, V1 complex, subunit B protein | chr1:7016971-7020290 FORWARD LENGTH=487	486	487	0	100.2	97.9	98.6
Rsa1.0_00034.1.g2062.t1	gb|EOA38379.1| hypothetical protein CARUB_v10009921mg [Capsella rubella]	289	287	1.00E-155	99.3	91.3	96.5	hypothetical protein CARUB_v10009921mg	gbpln	Capsella rubella	AT1G20270.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:7021383-7022923 REVERSE LENGTH=287	289	287	1.00E-157	99.3	91.0	96.2
Rsa1.0_00034.1.g2063.t1	dbj|BAJ33832.1| unnamed protein product [Thellungiella halophila]	165	167	5.00E-75	101.2	92.1	96.4	unnamed protein product	----	----	AT1G20340.1 | Symbols: DRT112, PETE2 | Cupredoxin superfamily protein | chr1:7042770-7043273 REVERSE LENGTH=167	165	167	6.00E-71	101.2	85.5	92.7
Rsa1.0_00034.1.g2064.t1	gb|EOA37077.1| hypothetical protein CARUB_v10010213mg, partial [Capsella rubella]	219	229	1.00E-74	104.6	68.9	78.1	hypothetical protein CARUB_v10010213mg, partial	gbpln	Capsella rubella	AT1G20350.1 | Symbols: ATTIM17-1, TIM17-1 | translocase inner membrane subunit 17-1 | chr1:7043737-7044393 FORWARD LENGTH=218	219	218	2.00E-69	99.5	63.5	76.7
Rsa1.0_00034.1.g2065.t1	gb|EOA37077.1| hypothetical protein CARUB_v10010213mg, partial [Capsella rubella]	220	229	2.00E-60	104.1	58.6	70.9	hypothetical protein CARUB_v10010213mg, partial	gbpln	Capsella rubella	AT1G20350.1 | Symbols: ATTIM17-1, TIM17-1 | translocase inner membrane subunit 17-1 | chr1:7043737-7044393 FORWARD LENGTH=218	220	218	4.00E-54	99.1	53.6	66.8
Rsa1.0_00034.1.g2066.t1	ref|NP_173472.1| 4-coumarate--CoA ligase-like 2 [Arabidopsis thaliana] gi|158564049|sp|Q84P25.2|4CLL2_ARATH RecName: Full=4-coumarate--CoA ligase-like 2 gi|332191856|gb|AEE29977.1| 4-coumarate--CoA ligase-like 2 [Arabidopsis thaliana]	556	565	0	101.6	80.6	89.0	4-coumarate--CoA ligase-like 2	gbpln	Arabidopsis thaliana	AT1G20480.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr1:7094978-7097073 REVERSE LENGTH=565	556	565	0	101.6	80.6	89.0
Rsa1.0_00034.1.g2067.t1	gb|AAP03015.1| 4-coumarate-CoA ligase-like protein [Arabidopsis thaliana]	534	550	0	103.0	76.2	86.9	4-coumarate-CoA ligase-like protein	gbpln	Arabidopsis thaliana	AT5G38120.1 | Symbols: 4CL8 | AMP-dependent synthetase and ligase family protein | chr5:15213773-15216137 FORWARD LENGTH=550	534	550	0	103.0	76.0	86.7
Rsa1.0_00034.1.g2068.t1	ref|XP_002893114.1| opc-8:0 CoA ligase1 [Arabidopsis lyrata subsp. lyrata] gi|297338956|gb|EFH69373.1| opc-8:0 CoA ligase1 [Arabidopsis lyrata subsp. lyrata]	548	546	0	99.6	92.2	96.4	opc-8:0 CoA ligase1	gbpln	Arabidopsis lyrata	AT1G20510.1 | Symbols: OPCL1 | OPC-8:0 CoA ligase1 | chr1:7103645-7105856 REVERSE LENGTH=546	548	546	0	99.6	91.2	95.8
Rsa1.0_00034.1.g2069.t1	gb|EOA36143.1| hypothetical protein CARUB_v10012650mg [Capsella rubella]	230	233	1.00E-100	101.3	80.0	91.3	hypothetical protein CARUB_v10012650mg	gbpln	Capsella rubella	AT1G20520.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr1:7106922-7107617 REVERSE LENGTH=231	230	231	1.00E-102	100.4	82.6	91.7
Rsa1.0_00034.1.g2070.t1	ref|XP_004291296.1| PREDICTED: small nuclear ribonucleoprotein Sm D3-like [Fragaria vesca subsp. vesca]	130	131	1.00E-61	100.8	90.8	94.6	PREDICTED: small nuclear ribonucleoprotein Sm D3-like	gbpln	Fragaria vesca	AT1G20580.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:7128979-7130371 FORWARD LENGTH=131	130	131	7.00E-60	100.8	95.4	96.2
Rsa1.0_00034.1.g2071.t1	ref|NP_173485.1| cyclin-B2-3 [Arabidopsis thaliana] gi|147743080|sp|Q9LDM4.2|CCB23_ARATH RecName: Full=Cyclin-B2-3; AltName: Full=G2/mitotic-specific cyclin-B2-3; Short=CycB2;3 gi|119935845|gb|ABM06010.1| At1g20610 [Arabidopsis thaliana] gi|332191872|gb|AEE29993.1| cyclin-B2-3 [Arabidopsis thaliana]	421	429	0	101.9	83.4	91.2	cyclin-B2-3	gbpln	Arabidopsis thaliana	AT1G20610.1 | Symbols: CYCB2;3 | Cyclin B2;3 | chr1:7135073-7137273 REVERSE LENGTH=429	421	429	0	101.9	83.4	91.2
Rsa1.0_00034.1.g2072.t1	gb|AAD30291.2|AF139538_1 catalase 2 [Raphanus sativus]	492	492	0	100.0	99.8	99.8	catalase 2	gbpln	Raphanus sativus	AT1G20620.1 | Symbols: CAT3, SEN2, ATCAT3 | catalase 3 | chr1:7143142-7146193 FORWARD LENGTH=492	492	492	0	100.0	98.6	99.4
Rsa1.0_00034.1.g2073.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00034.1.g2074.t1	gb|EOA39657.1| hypothetical protein CARUB_v10008300mg [Capsella rubella]	780	844	0	108.2	85.8	91.3	hypothetical protein CARUB_v10008300mg	gbpln	Capsella rubella	AT1G20640.2 | Symbols: | Plant regulator RWP-RK family protein | chr1:7155201-7157986 FORWARD LENGTH=844	780	844	0	108.2	86.0	91.0
Rsa1.0_00034.1.g2075.t1	ref|NP_173489.2| protein kinase-like protein [Arabidopsis thaliana] gi|8778594|gb|AAF79602.1|AC027665_3 F5M15.3 [Arabidopsis thaliana] gi|8886951|gb|AAF80637.1|AC069251_30 F2D10.13 [Arabidopsis thaliana] gi|51971194|dbj|BAD44289.1| unknown protein [Arabidopsis thaliana] gi|332191880|gb|AEE30001.1| protein kinase-like protein [Arabidopsis thaliana]	377	381	0	101.1	92.6	95.0	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G20650.1 | Symbols: | Protein kinase superfamily protein | chr1:7158422-7160022 REVERSE LENGTH=381	377	381	0	101.1	92.6	95.0

Rsa1.0_00034.1.g2076.t2	gb|EOA39820.1| hypothetical protein CARUB_v10008487mg, partial [Capsella rubella]	667	685	0	102.7	80.5	85.9	hypothetical protein CARUB_v10008487mg, partial	gbpln	Capsella rubella	AT1G20670.1 | Symbols: | DNA-binding bromodomain-containing protein | chr1:7164537-7167933 REVERSE LENGTH=652	667	652	0	97.8	77.4	83.1
Rsa1.0_00034.1.g2077.t2	ref|NP_173499.1| calcium-binding EF hand-containing protein [Arabidopsis thaliana] gi|8886934|gb|AAF80620.1|AC069251_13 F2D10.25 [Arabidopsis thaliana] gi|110742187|dbj|BAE99021.1| hypothetical protein [Arabidopsis thaliana] gi|332191898|gb|AEE30019.1| calcium-binding EF hand-containing protein [Arabidopsis thaliana]	1035	1019	0	98.5	84.5	88.2	calcium-binding EF hand-containing protein	gbpln	Arabidopsis thaliana	AT1G20760.1 | Symbols: | Calcium-binding EF hand family protein | chr1:7209515-7214773 FORWARD LENGTH=1019	1035	1019	0	98.5	84.5	88.2
Rsa1.0_00034.1.g2078.t1	ref|NP_173500.1| uncharacterized protein [Arabidopsis thaliana] gi|8886946|gb|AAF80632.1|AC069251_25 F2D10.26 [Arabidopsis thaliana] gi|38454150|gb|AAR20769.1| At1g20770 [Arabidopsis thaliana] gi|41349930|gb|AAS00350.1| At1g20770 [Arabidopsis thaliana] gi|332191899|gb|AEE30020.1| uncharacterized protein AT1G20770 [Arabidopsis thaliana]	223	215	9.00E-88	96.4	78.9	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G20770.1 | Symbols: | unknown protein; Has 59 Blast hits to 59 proteins in 24 species: Archae - 0; Bacteria - 0; Metazoa - 26; Fungi - 4; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7215345-7216648 REVERSE LENGTH=215	223	215	3.00E-90	96.4	78.9	83.9
Rsa1.0_00034.1.g2079.t1	gb|EOA39693.1| hypothetical protein CARUB_v10008332mg [Capsella rubella]	870	801	0	92.1	76.2	84.4	hypothetical protein CARUB_v10008332mg	gbpln	Capsella rubella	AT1G20780.1 | Symbols: PUB44, ATPUB44, SAUL1 | senescence-associated E3 ubiquitin ligase 1 | chr1:7217812-7220609 FORWARD LENGTH=801	870	801	0	92.1	76.7	83.6
Rsa1.0_00034.1.g2080.t1	ref|NP_173502.2| F-box protein [Arabidopsis thaliana] gi|75264017|sp|Q9LM75.1|FBK6_ARATH RecName: Full=Putative F-box/kelch-repeat protein At1g20790 gi|8886945|gb|AAF80631.1|AC069251_24 F2D10.28 [Arabidopsis thaliana] gi|332191901|gb|AEE30022.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	274	435	5.00E-64	158.8	50.4	64.2	F-box protein	gbpln	Arabidopsis thaliana	AT1G20790.1 | Symbols: | F-box family protein | chr1:7220961-7222268 REVERSE LENGTH=435	274	435	1.00E-66	158.8	50.4	64.2
Rsa1.0_00034.1.g2081.t1	ref|NP_173503.1| F-box family protein [Arabidopsis thaliana] gi|332191903|gb|AEE30024.1| F-box family protein [Arabidopsis thaliana]	150	492	4.00E-22	328.0	51.3	64.0	F-box family protein	gbpln	Arabidopsis thaliana	AT1G20800.1 | Symbols: | F-box family protein | chr1:7228718-7231600 REVERSE LENGTH=492	150	492	1.00E-24	328.0	51.3	64.0
Rsa1.0_00034.1.g2082.t1	gb|EOA36226.1| hypothetical protein CARUB_v10010177mg [Capsella rubella]	194	234	1.00E-81	120.6	85.1	92.3	hypothetical protein CARUB_v10010177mg	gbpln	Capsella rubella	AT1G20823.1 | Symbols: | RING/U-box superfamily protein | chr1:7238880-7239473 FORWARD LENGTH=197	194	197	4.00E-82	101.5	87.1	91.8
Rsa1.0_00034.1.g2083.t1	ref|NP_173507.1| multiple chloroplast division site 1 [Arabidopsis thaliana] gi|26452945|dbj|BAC43549.1| unknown protein [Arabidopsis thaliana] gi|29824121|gb|AAP04021.1| unknown protein [Arabidopsis thaliana] gi|332191908|gb|AEE30029.1| multiple chloroplast division site 1 [Arabidopsis thaliana]	347	349	1.00E-163	100.6	82.1	88.8	multiple chloroplast division site 1	gbpln	Arabidopsis thaliana	AT1G20830.1 | Symbols: MCD1 | multiple chloroplast division site 1 | chr1:7242933-7244736 FORWARD LENGTH=349	347	349	1.00E-166	100.6	82.1	88.8
Rsa1.0_00034.1.g2084.t1	dbj|BAJ33724.1| unnamed protein product [Thellungiella halophila]	730	733	0	100.4	92.7	95.8	unnamed protein product	----	----	AT1G20840.1 | Symbols: TMT1 | tonoplast monosaccharide transporter1 | chr1:7245107-7247674 REVERSE LENGTH=734	730	734	0	100.5	91.5	95.6
Rsa1.0_00034.1.g2085.t1	ref|XP_002890413.1| hypothetical protein ARALYDRAFT_472321 [Arabidopsis lyrata subsp. lyrata] gi|297336255|gb|EFH66672.1| hypothetical protein ARALYDRAFT_472321 [Arabidopsis lyrata subsp. lyrata]	356	357	0	100.3	92.4	94.7	hypothetical protein ARALYDRAFT_472321	gbpln	Arabidopsis lyrata	AT1G20850.1 | Symbols: XCP2 | xylem cysteine peptidase 2 | chr1:7252208-7253537 FORWARD LENGTH=356	356	356	0	100.0	92.4	95.5
Rsa1.0_00034.1.g2086.t1	ref|XP_002893134.1| phosphate transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297338976|gb|EFH69393.1| phosphate transporter family protein [Arabidopsis lyrata subsp. lyrata]	540	536	0	99.3	88.7	93.3	phosphate transporter family protein	gbpln	Arabidopsis lyrata	AT1G20860.1 | Symbols: PHT1;8 | phosphate transporter 1;8 | chr1:7254007-7258677 REVERSE LENGTH=534	540	534	0	98.9	86.7	90.7
Rsa1.0_00034.1.g2087.t1	gb|EOA35544.1| hypothetical protein CARUB_v10020749mg [Capsella rubella]	262	285	1.00E-113	108.8	79.0	88.9	hypothetical protein CARUB_v10020749mg	gbpln	Capsella rubella	AT1G76460.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:28686932-28688506 REVERSE LENGTH=285	262	285	1.00E-113	108.8	77.9	87.4
Rsa1.0_00034.1.g2088.t1	gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]	173	214	6.00E-29	123.7	48.0	61.3	trypsin inhibitor propeptide	gbpln	Brassica oleracea	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410-27548057 REVERSE LENGTH=215	173	215	5.00E-19	124.3	38.7	56.1
Rsa1.0_00034.1.g2089.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00034.1.g2090.t1</td><td>ref|NP_173514.1| putative DNA-binding protein ESCAROLA [Arabidopsis thaliana] gi|20532086|sp|Q9S7C9.1|ESCA_ARATH RecName: Full=Putative DNA-binding protein ESCAROLA gi|4836899|gb|AAD30602.1|AC007369_12 Unknown protein [Arabidopsis thaliana] gi|6319180|gb|AAF07197.1|AF194974_1 ESCAROLA [Arabidopsis thaliana] gi|30102700|gb|AAP21268.1| At1g20900 [Arabidopsis thaliana] gi|110736548|dbj|BAF00240.1| putative DNA-binding protein [Arabidopsis thaliana] gi|119657398|tpd|FAA00298.1| TPA: AT-hook motif nuclear localized protein 27 [Arabidopsis thaliana] gi|225897950|dbj|BAH30307.1| hypothetical protein [Arabidopsis thaliana] gi|332191917|gb|AEE30038.1| putative DNA-binding protein ESCAROLA [Arabidopsis thaliana]</td><td>314</td><td>311</td><td>1.00E-120</td><td>99.0</td><td>94.3</td><td>94.9</td><td>putative DNA-binding protein ESCAROLA</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G20900.1 | Symbols: ESC, ORE7, AHL27 | Predicted AT-hook DNA-binding family protein | chr1:7273024-7273959 FORWARD LENGTH=311</td><td>314</td><td>311</td><td>1.00E-123</td><td>99.0</td><td>94.3</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00034.1.g2091.t1</td><td>gb|EOA40571.1| hypothetical protein CARUB_v10009301mg [Capsella rubella]</td><td>374</td><td>410</td><td>1.00E-142</td><td>109.6</td><td>73.0</td><td>80.7</td><td>hypothetical protein CARUB_v10009301mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G20910.1 | Symbols: | ARID/BRIGHT DNA-binding domain-containing protein | chr1:7277209-7280635 REVERSE LENGTH=398</td><td>374</td><td>398</td><td>1.00E-140</td><td>106.4</td><td>71.7</td><td>79.9</td></tr>
<tr><td>Rsa1.0_00034.1.g2092.t1</td><td>gb|EOA39882.1| hypothetical protein CARUB_v10008559mg, partial [Capsella rubella]</td><td>619</td><td>639</td><td>0</td><td>103.2</td><td>94.0</td><td>97.1</td><td>hypothetical protein CARUB_v10008559mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G20950.1 | Symbols: | Phosphofructokinase family protein | chr1:7297467-7301336 REVERSE LENGTH=614</td><td>619</td><td>614</td><td>0</td><td>99.2</td><td>94.0</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00034.1.g2093.t1</td><td>ref|XP_002890421.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297336263|gb|EFH66680.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata]</td><td>243</td><td>246</td><td>1.00E-132</td><td>101.2</td><td>91.4</td><td>97.1</td><td>zinc-binding family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21000.2 | Symbols: | PLATZ transcription factor family protein | chr1:7338013-7339088 FORWARD LENGTH=243</td><td>243</td><td>243</td><td>1.00E-132</td><td>100.0</td><td>90.1</td><td>95.9</td></tr>
<tr><td>Rsa1.0_00034.1.g2094.t1</td><td>gb|EOA36953.1| hypothetical protein CARUB_v10009886mg [Capsella rubella]</td><td>209</td><td>296</td><td>4.00E-81</td><td>141.6</td><td>79.9</td><td>89.0</td><td>hypothetical protein CARUB_v10009886mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G21010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76600.1); Has 206 Blast hits to 206 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 206; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7346239-7346871 FORWARD LENGTH=210</td><td>209</td><td>210</td><td>3.00E-80</td><td>100.5</td><td>78.0</td><td>87.1</td></tr>
<tr><td>Rsa1.0_00034.1.g2095.t1</td><td>dbj|BAJ33623.1| unnamed protein product [Thellungiella halophila]</td><td>471</td><td>471</td><td>0</td><td>100.0</td><td>89.2</td><td>94.3</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G21400.1 | Symbols: | Thiamin diphosphate-binding fold (THDP-binding) superfamily protein | chr1:7493492-7496240 FORWARD LENGTH=472</td><td>471</td><td>472</td><td>0</td><td>100.2</td><td>88.1</td><td>93.8</td></tr>
<tr><td>Rsa1.0_00034.1.g2096.t1</td><td>ref|NP_564139.1| F-box protein SKP2A [Arabidopsis thaliana] gi|75177240|sp|Q9LPL4.1|SKP2A_ARATH RecName: Full=F-box protein SKP2A; AltName: Full=FBL5-like protein; Short=AtFBL5; AltName: Full=SKP2-like protein 1; Short=AtSKP2;1 gi|9454572|gb|AAF87895.1|AC015447_5 Unknown protein [Arabidopsis thaliana] gi|16604366|gb|AAL24189.1| At1g21410/F24J8_17 [Arabidopsis thaliana] gi|19699206|gb|AAL90969.1| At1g21410/F24J8_17 [Arabidopsis thaliana] gi|332191979|gb|AEE30100.1| F-box protein SKP2A [Arabidopsis thaliana]</td><td>284</td><td>360</td><td>1.00E-145</td><td>126.8</td><td>91.2</td><td>93.3</td><td>F-box protein SKP2A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21410.1 | Symbols: SKP2A | F-box/RNI-like superfamily protein | chr1:7497479-7499386 FORWARD LENGTH=360</td><td>284</td><td>360</td><td>1.00E-148</td><td>126.8</td><td>91.2</td><td>93.3</td></tr>
</table>

Rsa1.0_00034.1.g2097.t1	ref|NP_564140.1| Nodulin MtN3-like protein [Arabidopsis thaliana] gi|75154590|sp|Q8L9J7.1|SWET1_ARATH RecName: Full=Bidirectional sugar transporter SWEET1; Short=AtSWEET1 gi|21594011|gb|AAM65929.1| unknown [Arabidopsis thaliana] gi|28393568|gb|AAO42204.1| unknown protein [Arabidopsis thaliana] gi|28973143|gb|AAO63896.1| unknown protein [Arabidopsis thaliana] gi|332191983|gb|AEE30104.1| bidirectional sugar transporter SWEET1 [Arabidopsis thaliana]	250	247	1.00E-128	98.8	92.0	95.6	Nodulin MtN3-like protein	gbpln	Arabidopsis thaliana	AT1G21460.1 | Symbols: SWEET1, AtSWEET1 | Nodulin MtN3 family protein | chr1:7512030-7513281 REVERSE LENGTH=247	250	247	1.00E-130	98.8	92.0	95.6
Rsa1.0_00034.1.g2098.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00034.1.g2099.t1	ref|NP_564141.1| exostosin-like protein [Arabidopsis thaliana] gi|332191985|gb|AEE30106.1| exostosin-like protein [Arabidopsis thaliana]	466	462	0	99.1	92.7	95.5	exostosin-like protein	gbpln	Arabidopsis thaliana	AT1G21480.1 | Symbols: | Exostosin family protein | chr1:7519116-7521426 REVERSE LENGTH=462	466	462	0	99.1	92.7	95.5
Rsa1.0_00034.1.g2100.t1	gb|EMJ00939.1| hypothetical protein PRUPE_ppa002697mg [Prunus persica]	642	644	0	100.3	73.7	85.4	hypothetical protein PRUPE_ppa002697mg	gbpln	Prunus persica	AT1G77130.1 | Symbols: PGSIP2, GUX3 | plant glycogenin-like starch initiation protein 2 | chr1:28979066-28981228 REVERSE LENGTH=618	642	618	0	96.3	73.4	82.7
Rsa1.0_00034.1.g2101.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00034.1.g2102.t1	ref|XP_002893172.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata] gi|297339014|gb|EFH69431.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata]	73	71	2.00E-13	97.3	60.3	72.6	hypothetical protein ARALYDRAFT_472389	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00035.1.g2103.t2	ref|NP_176277.1| AP-1 complex subunit mu [Arabidopsis thaliana] gi|2462748|gb|AAB71967.1| putative Clathrin Coat Assembly protein [Arabidopsis thaliana] gi|20466372|gb|AAM20503.1| clathrin adaptor medium chain protein MU1B, putative [Arabidopsis thaliana] gi|25084014|gb|AAN72155.1| clathrin adaptor medium chain protein MU1B, putative [Arabidopsis thaliana] gi|332195610|gb|AEE33731.1| protein HAPLESS 13 [Arabidopsis thaliana]	888	428	0	48.2	45.9	46.7	AP-1 complex subunit mu	gbpln	Arabidopsis thaliana	AT1G60780.1 | Symbols: HAP13 | Clathrin adaptor complexes medium subunit family protein | chr1:22369289-22371885 REVERSE LENGTH=428	888	428	0	48.2	45.9	46.7
Rsa1.0_00035.1.g2104.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00035.1.g2105.t1	gb|AFO67891.1| leucine-rich repeat receptor-like kinase (mitochondrion) [Brassica rapa subsp. oleifera]	635	635	0	100.0	96.4	98.6	leucine-rich repeat receptor-like kinase (mitochondrion)	gbpln	Brassica rapa	AT1G60800.1 | Symbols: NIK3 | NSP-interacting kinase 3 | chr1:22383601-22386931 REVERSE LENGTH=632	635	632	0	99.5	91.8	96.2
Rsa1.0_00035.1.g2106.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	260	1142	5.00E-55	439.2	40.0	55.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	260	575	3.00E-25	221.2	29.2	42.7
Rsa1.0_00035.1.g2107.t1	ref|XP_002884699.1| D-alanine--D-alanine ligase family [Arabidopsis lyrata subsp. lyrata] gi|297330539|gb|EFH60958.1| D-alanine--D-alanine ligase family [Arabidopsis lyrata subsp. lyrata]	950	943	0	99.3	79.9	87.8	D-alanine--D-alanine ligase family	gbpln	Arabidopsis lyrata	AT3G08840.2 | Symbols: | D-alanine--D-alanine ligase family | chr3:2679648-2686157 REVERSE LENGTH=937	950	937	0	98.6	79.7	88.3
Rsa1.0_00035.1.g2108.t1	gb|EOA34924.1| hypothetical protein CARUB_v10020009mg [Capsella rubella]	612	603	0	98.5	60.8	63.1	hypothetical protein CARUB_v10020009mg	gbpln	Capsella rubella	AT1G60900.1 | Symbols: | U2 snRNP auxilliary factor, large subunit, splicing factor | chr1:22424008-22427806 FORWARD LENGTH=589	612	589	0	96.2	60.0	62.6
Rsa1.0_00035.1.g2109.t1	gb|AAM67112.1| putative serine/threonine-protein kinase [Arabidopsis thaliana]	352	361	1.00E-176	102.6	89.8	93.8	putative serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G60940.2 | Symbols: SNRK2-10, SNRK2.10, SRK2B | SNF1-related protein kinase 2.10 | chr1:22439398-22441896 REVERSE LENGTH=361	352	361	1.00E-178	102.6	89.5	93.5
Rsa1.0_00035.1.g2110.t1	gb|EOA37821.1| hypothetical protein CARUB_v10011995mg [Capsella rubella]	598	589	0	98.5	88.1	91.5	hypothetical protein CARUB_v10011995mg	gbpln	Capsella rubella	AT1G10950.1 | Symbols: TMN1, AtTMN1 | transmembrane nine 1 | chr1:3659322-3663622 FORWARD LENGTH=589	598	589	0	98.5	87.3	91.3
Rsa1.0_00035.1.g2111.t1	dbj|BAJ33728.1| unnamed protein product [Thellungiella halophila]	148	148	3.00E-75	100.0	92.6	97.3	unnamed protein product	----	----	AT1G60950.1 | Symbols: FED A, ATFD2 | 2Fe-2S ferredoxin-like superfamily protein | chr1:22444565-22445011 FORWARD LENGTH=148	148	148	7.00E-77	100.0	92.6	96.6
Rsa1.0_00035.1.g2112.t1	gb|AAK69430.1|AF275752_1 ZIP-like zinc transporter [Noccaea caerulescens]	416	422	0	101.4	86.5	90.4	ZIP-like zinc transporter	gbpln	Noccaea caerulescens	AT1G60960.1 | Symbols: IRT3, ATIRT3 | iron regulated transporter 3 | chr1:22445410-22447060 REVERSE LENGTH=425	416	425	0	102.2	85.3	90.6

Rsa1.0_00035.1.g2113.t1	ref|NP_568221.1| Protein kinase family protein [Arabidopsis thaliana] gi|14334482|gb|AAK59439.1| putative protein kinase [Arabidopsis thaliana] gi|15147869|dbj|BAB62845.1| Ndr kinase [Arabidopsis thaliana] gi|16323450|gb|AAL15219.1| putative protein kinase [Arabidopsis thaliana] gi|332004078|gb|AED91461.1| Protein kinase family protein [Arabidopsis thaliana]	525	515	0	98.1	90.1	93.5	Protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G09890.1 | Symbols: | Protein kinase family protein | chr5:3085810-3088842 REVERSE LENGTH=515	525	515	0	98.1	90.1	93.5
Rsa1.0_00035.1.g2114.t1	ref|NP_176294.1| gibberellin 20-oxidase 4 [Arabidopsis thaliana] gi|12323345|gb|AAG51653.1|AC018908_19 putative gibberellin 20-oxidase; 47658-49225 [Arabidopsis thaliana] gi|67633472|gb|AAY78660.1| putative gibberellin 20-oxidase [Arabidopsis thaliana] gi|332195634|gb|AEE33755.1| gibberellin 20-oxidase 4 [Arabidopsis thaliana]	369	376	1.00E-126	101.9	61.5	69.1	gibberellin 20-oxidase 4	gbpln	Arabidopsis thaliana	AT1G60980.1 | Symbols: ATGA20OX4, GA20OX4 | gibberellin 20-oxidase 4 | chr1:22452573-22454140 FORWARD LENGTH=376	369	376	1.00E-129	101.9	61.5	69.1
Rsa1.0_00035.1.g2115.t2	gb|ACY30421.1| C.BANa [Brassica napus]	135	338	2.00E-29	250.4	60.7	69.6	C.BANa	gbpln	Brassica napus	AT1G61720.1 | Symbols: BAN | NAD(P)-binding Rossmann-fold superfamily protein | chr1:22791326-22792757 REVERSE LENGTH=340	135	340	2.00E-29	251.9	57.0	67.4
Rsa1.0_00035.1.g2116.t1	gb|EOA34094.1| hypothetical protein CARUB_v10021594mg [Capsella rubella]	439	441	1.00E-175	100.5	76.3	83.8	hypothetical protein CARUB_v10021594mg	gbpln	Capsella rubella	AT1G61050.1 | Symbols: | alpha 1,4-glycosyltransferase family protein | chr1:22486736-22488043 FORWARD LENGTH=435	439	435	1.00E-171	99.1	76.8	84.1
Rsa1.0_00035.1.g2117.t1	ref|XP_002888111.1| At1g61040/T7P1_17 [Arabidopsis lyrata subsp. lyrata] gi|297333952|gb|EFH64370.1| At1g61040/T7P1_17 [Arabidopsis lyrata subsp. lyrata]	643	643	0	100.0	86.0	89.6	At1g61040/T7P1_17	gbpln	Arabidopsis lyrata	AT1G61040.1 | Symbols: VIP5 | plus-3 domain-containing protein | chr1:22483817-22485748 FORWARD LENGTH=643	643	643	0	100.0	85.7	89.9
Rsa1.0_00035.1.g2118.t1	gb|EOA33209.1| hypothetical protein CARUB_v10019868mg [Capsella rubella]	693	725	0	104.6	94.5	97.1	hypothetical protein CARUB_v10019868mg	gbpln	Capsella rubella	AT1G61010.3 | Symbols: CPSF73-I | cleavage and polyadenylation specificity factor 73-I | chr1:22474954-22477660 REVERSE LENGTH=693	693	693	0	100.0	93.7	96.5
Rsa1.0_00035.1.g2119.t1	ref|XP_002886570.1| hypothetical protein ARALYDRAFT_475227 [Arabidopsis lyrata subsp. lyrata] gi|297332411|gb|EFH62829.1| hypothetical protein ARALYDRAFT_475227 [Arabidopsis lyrata subsp. lyrata]	618	623	0	100.8	88.0	91.9	hypothetical protein ARALYDRAFT_475227	gbpln	Arabidopsis lyrata	AT1G60995.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: Membralin (InterPro:IPR019144); Has 172 Blast hits to 170 proteins in 70 species: Archae - 0; Bacteria - 0; Metazoa - 110; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 24 (source: NCBI BLink). | chr1:22465768-22470575 REVERSE LENGTH=623	618	623	0	100.8	87.9	91.6
Rsa1.0_00035.1.g2120.t3	ref|NP_176295.3| aminomethyltransferase [Arabidopsis thaliana] gi|145326078|ref|NP_001077748.1| aminomethyltransferase [Arabidopsis thaliana] gi|186492130|ref|NP_001117522.1| aminomethyltransferase [Arabidopsis thaliana] gi|51969110|dbj|BAD43247.1| unnamed protein product [Arabidopsis thaliana] gi|332195639|gb|AEE33760.1| aminomethyltransferase [Arabidopsis thaliana] gi|332195640|gb|AEE33761.1| aminomethyltransferase [Arabidopsis thaliana] gi|332195641|gb|AEE33762.1| aminomethyltransferase [Arabidopsis thaliana]	418	432	0	103.3	87.3	91.1	aminomethyltransferase	gbpln	Arabidopsis thaliana	AT1G60990.3 | Symbols: | Glycine cleavage T-protein family | chr1:22462771-22465416 REVERSE LENGTH=432	418	432	0	103.3	87.3	91.1
Rsa1.0_00035.1.g2121.t1	gb|EOA39455.1| hypothetical protein CARUB_v10012652mg [Capsella rubella]	340	320	1.00E-140	94.1	72.1	82.4	hypothetical protein CARUB_v10012652mg	gbpln	Capsella rubella	AT1G05250.1 | Symbols: | Peroxidase superfamily protein | chr1:1525924-1527169 REVERSE LENGTH=325	340	325	1.00E-132	95.6	65.0	77.4

Rsa1.0_00035.1.g2122.t1	ref|NP_001031213.1| defensin-like protein 245 [Arabidopsis thaliana] gi|55584174|sp|P82623.2|DF245_ARATH RecName: Full=Defensin-like protein 245; AltName: Full=S locus cysteine-rich-like protein 4; Short=Protein SCRL4; Short=SCR-like protein 4; Flags: Precursor gi|113204420|gb|ABI34004.1| unknown [Arabidopsis thaliana] gi|332195637|gb|AEE33758.1| defensin-like protein 245 [Arabidopsis thaliana]	96	97	9.00E-30	101.0	68.8	79.2	defensin-like protein 245	gbpln	Arabidopsis thaliana	AT1G60986.1 | Symbols: SCRL4 | SCR-like 4 | chr1:22459072-22459468 FORWARD LENGTH=97	96	97	2.00E-32	101.0	68.8	79.2
Rsa1.0_00035.1.g2123.t1	ref|XP_002886566.1| protease inhibitor II [Arabidopsis lyrata subsp. lyrata] gi|297332407|gb|EFH62825.1| protease inhibitor II [Arabidopsis lyrata subsp. lyrata]	77	76	2.00E-25	98.7	74.0	87.0	protease inhibitor II	gbpln	Arabidopsis lyrata	AT2G02130.1 | Symbols: PDF2.3, LCR68 | low-molecular-weight cysteine-rich 68 | chr2:540071-540407 FORWARD LENGTH=77	77	77	1.00E-25	100.0	64.9	74.0
Rsa1.0_00035.1.g2124.t1	ref|XP_002886565.1| hypothetical protein ARALYDRAFT_475218 [Arabidopsis lyrata subsp. lyrata] gi|297332406|gb|EFH62824.1| hypothetical protein ARALYDRAFT_475218 [Arabidopsis lyrata subsp. lyrata]	858	879	1.00E-127	102.4	33.2	34.6	hypothetical protein ARALYDRAFT_475218	gbpln	Arabidopsis lyrata	AT1G61080.1 | Symbols: | Hydroxyproline-rich glycoprotein family protein | chr1:22493194-22497019 REVERSE LENGTH=907	858	907	1.00E-129	105.7	32.3	33.8
Rsa1.0_00035.1.g2125.t1	dbj|BAJ34413.1| unnamed protein product [Thellungiella halophila]	770	809	0	105.1	80.1	87.0	unnamed protein product	----	----	AT1G61100.2 | Symbols: | disease resistance protein (TIR class), putative | chr1:22508831-22512122 REVERSE LENGTH=807	770	807	0	104.8	77.8	85.6
Rsa1.0_00035.1.g2126.t1	ref|NP_974060.1| Toll-Interleukin-Resistance (TIR) domain-containing protein [Arabidopsis thaliana] gi|332195661|gb|AEE33782.1| Toll-Interleukin-Resistance (TIR) domain-containing protein [Arabidopsis thaliana]	216	188	4.00E-81	87.0	67.1	74.5	Toll-Interleukin-Resistance (TIR) domain-containing protein	gbpln	Arabidopsis thaliana	AT1G61105.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr1:22513616-22514492 REVERSE LENGTH=188	216	188	1.00E-83	87.0	67.1	74.5
Rsa1.0_00035.1.g2127.t2	gb|EOA34398.1| hypothetical protein CARUB_v10021926mg [Capsella rubella]	448	462	0	103.1	80.6	87.9	hypothetical protein CARUB_v10021926mg	gbpln	Capsella rubella	AT1G61130.1 | Symbols: SCPL32 | serine carboxypeptidase-like 32 | chr1:22529024-22531784 REVERSE LENGTH=463	448	463	0	103.3	73.7	83.5
Rsa1.0_00035.1.g2128.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	116	149	4.00E-24	128.4	42.2	63.8	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	116	292	3.00E-12	251.7	30.2	51.7
Rsa1.0_00035.1.g2129.t1	ref|NP_176309.2| SNF2, helicase and zinc finger domain-containing protein [Arabidopsis thaliana] gi|332195665|gb|AEE33786.1| SNF2, helicase and zinc finger domain-containing protein [Arabidopsis thaliana]	1173	1280	0	109.1	74.9	83.8	SNF2, helicase and zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT1G61140.1 | Symbols: EDA16 | SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related | chr1:22535038-22540610 REVERSE LENGTH=1280	1173	1280	0	109.1	74.9	83.8
Rsa1.0_00035.1.g2130.t1	gb|EOA33443.1| hypothetical protein CARUB_v10020867mg [Capsella rubella]	226	226	1.00E-124	100.0	96.9	100.0	hypothetical protein CARUB_v10020867mg	gbpln	Capsella rubella	AT1G61150.6 | Symbols: | LisH and RanBPM domains containing protein | chr1:22542979-22544355 FORWARD LENGTH=226	226	226	1.00E-125	100.0	95.1	99.1
Rsa1.0_00035.1.g2131.t2	ref|NP_001154324.1| uncharacterized protein [Arabidopsis thaliana] gi|332190567|gb|AEE28688.1| uncharacterized protein AT1G11120 [Arabidopsis thaliana]	109	161	7.00E-26	147.7	63.3	78.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11120.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G28170.1); Has 94 Blast hits to 94 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 94; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:3715229-3717320 FORWARD LENGTH=161	109	161	1.00E-28	147.7	63.3	78.0
Rsa1.0_00035.1.g2132.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00035.1.g2133.t1	ref|NP_564773.1| uncharacterized protein [Arabidopsis thaliana] gi|2443885|gb|AAB71478.1| Unknown protein [Arabidopsis thaliana] gi|30017227|gb|AAP12847.1| At1g61170 [Arabidopsis thaliana] gi|110735914|dbj|BAE99932.1| hypothetical protein [Arabidopsis thaliana] gi|332195677|gb|AEE33798.1| uncharacterized protein AT1G61170 [Arabidopsis thaliana]	245	251	2.00E-82	102.4	78.4	84.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G61170.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G11125.1); Has 54 Blast hits to 54 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 17; Fungi - 0; Plants - 34; Viruses - 1; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:22549718-22550473 FORWARD LENGTH=251	245	251	6.00E-85	102.4	78.4	84.1
Rsa1.0_00035.1.g2134.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00036.1.g2135.t1	ref|XP_002887662.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297333503|gb|EFH63921.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	366	374	0	102.2	90.4	94.0	F-box family protein	gbpln	Arabidopsis lyrata	AT1G76920.1 | Symbols: | F-box family protein | chr1:28892295-28893419 FORWARD LENGTH=374	366	374	0	102.2	89.6	94.0
Rsa1.0_00036.1.g2136.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	600	536	1.00E-86	89.3	32.0	41.0	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	600	530	9.00E-50	88.3	16.5	20.3
Rsa1.0_00036.1.g2137.t1	ref|NP_177835.2| peroxidase 13 [Arabidopsis thaliana] gi|2829914|gb|AAC00622.1| putative peroxidase [Arabidopsis thaliana] gi|332197814|gb|AEE35935.1| peroxidase 13 [Arabidopsis thaliana]	319	336	1.00E-152	105.3	81.8	89.0	peroxidase 13	gbpln	Arabidopsis thaliana	AT1G77100.1 | Symbols: | Peroxidase superfamily protein | chr1:28965772-28967066 REVERSE LENGTH=336	319	336	1.00E-154	105.3	81.8	89.0
Rsa1.0_00036.1.g2138.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	242	1274	1.00E-29	526.4	40.1	53.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	242	303	2.00E-18	125.2	31.0	48.3
Rsa1.0_00036.1.g2139.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00036.1.g2140.t1	ref|XP_002887671.1| hypothetical protein ARALYDRAFT_476877 [Arabidopsis lyrata subsp. lyrata] gi|297333512|gb|EFH63930.1| hypothetical protein ARALYDRAFT_476877 [Arabidopsis lyrata subsp. lyrata]	569	569	0	100.0	96.7	98.1	hypothetical protein ARALYDRAFT_476877	gbpln	Arabidopsis lyrata	AT1G77140.1 | Symbols: VPS45, ATVPS45 | vacuolar protein sorting 45 | chr1:28984163-28987681 FORWARD LENGTH=569	569	569	0	100.0	95.8	97.9
Rsa1.0_00036.1.g2141.t1	ref|XP_002889128.1| hypothetical protein ARALYDRAFT_476882 [Arabidopsis lyrata subsp. lyrata] gi|297334969|gb|EFH65387.1| hypothetical protein ARALYDRAFT_476882 [Arabidopsis lyrata subsp. lyrata]	496	610	0	123.0	78.0	86.3	hypothetical protein ARALYDRAFT_476882	gbpln	Arabidopsis lyrata	AT1G77180.2 | Symbols: SKIP | chromatin protein family | chr1:28999791-29001632 REVERSE LENGTH=613	496	613	0	123.6	74.8	84.9
Rsa1.0_00036.1.g2142.t1	ref|XP_002889129.1| hypothetical protein ARALYDRAFT_476884 [Arabidopsis lyrata subsp. lyrata] gi|297334970|gb|EFH65388.1| hypothetical protein ARALYDRAFT_476884 [Arabidopsis lyrata subsp. lyrata]	224	247	6.00E-82	110.3	83.5	86.6	hypothetical protein ARALYDRAFT_476884	gbpln	Arabidopsis lyrata	AT1G77200.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:29004357-29005091 REVERSE LENGTH=244	224	244	9.00E-81	108.9	79.5	83.0
Rsa1.0_00036.1.g2143.t1	ref|XP_002890504.1| hypothetical protein ARALYDRAFT_889727 [Arabidopsis lyrata subsp. lyrata] gi|297336346|gb|EFH66763.1| hypothetical protein ARALYDRAFT_889727 [Arabidopsis lyrata subsp. lyrata]	419	426	1.00E-100	101.7	53.5	69.7	hypothetical protein ARALYDRAFT_889727	gbpln	Arabidopsis lyrata	AT1G25150.1 | Symbols: | F-box family protein | chr1:8821027-8822328 FORWARD LENGTH=433	419	433	1.00E-102	103.3	53.2	68.0
Rsa1.0_00036.1.g2144.t1	ref|XP_002893432.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339274|gb|EFH69691.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	412	414	5.00E-88	100.5	50.0	64.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G25150.1 | Symbols: | F-box family protein | chr1:8821027-8822328 FORWARD LENGTH=433	412	433	1.00E-89	105.1	50.0	63.6

Rsa1.0_00036.1.g2145.t1	ref|NP_001117347.1| F-box protein [Arabidopsis thaliana] gi|186478848|ref|NP_001117348.1| F-box protein [Arabidopsis thaliana] gi|186478854|ref|NP_001117350.1| F-box protein [Arabidopsis thaliana] gi|186478863|ref|NP_001117352.1| F-box protein [Arabidopsis thaliana] gi|334182847|ref|NP_001185091.1| F-box family protein [Arabidopsis thaliana] gi|380876887|sp|P0DI02.1|FBK10_ARATH RecName: Full=F-box/kelch-repeat protein At1g24800 gi|380876888|sp|P0DI03.1|FBK11_ARATH RecName: Full=F-box/kelch-repeat protein At1g24881 gi|380876889|sp|P0DI04.1|FBK12_ARATH RecName: Full=F-box/kelch-repeat protein At1g25055 gi|380876890|sp|P0DI05.1|FBK13_ARATH RecName: Full=F-box/kelch-repeat protein At1g25150 gi|380876891|sp|P0DI06.1|FBK14_ARATH RecName: Full=F-box/kelch-repeat protein At1g25211 gi|23297235|gb|AAN12922.1| unknown protein [Arabidopsis thaliana] gi|26452089|dbj|BAC43134.1| unknown protein [Arabidopsis thaliana] gi|33942045|gb|AAQ55275.1| At1g24880 [Arabidopsis thaliana] gi|62320789|dbj|BAD93716.1| hypothetical protein [Arabidopsis thaliana] gi|110735803|dbj|BAE99878.1|	422	433	1.00E-105	102.6	55.7	70.4	F-box protein	gbpln	Arabidopsis thaliana	AT1G25150.1 | Symbols: | F-box family protein | chr1:8821027-8822328 FORWARD LENGTH=433	422	433	1.00E-107	102.6	55.7	70.4
Rsa1.0_00036.1.g2146.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	317	1213	9.00E-35	382.6	27.8	42.3	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	317	626	1.00E-29	197.5	21.8	38.2
Rsa1.0_00036.1.g2147.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	186	390	8.00E-31	209.7	38.2	54.8	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	186	332	1.00E-26	178.5	32.3	52.7
Rsa1.0_00036.1.g2148.t1	ref|XP_002887672.1| hypothetical protein ARALYDRAFT_895607 [Arabidopsis lyrata subsp. lyrata] gi|297333513|gb|EFH63931.1| hypothetical protein ARALYDRAFT_895607 [Arabidopsis lyrata subsp. lyrata]	487	484	0	99.4	89.1	94.7	hypothetical protein ARALYDRAFT_895607	gbpln	Arabidopsis lyrata	AT1G77220.1 | Symbols: | Protein of unknown function (DUF300) | chr1:29013232-29015530 FORWARD LENGTH=484	487	484	0	99.4	88.5	94.3
Rsa1.0_00036.1.g2149.t1	emb|CAA64328.1| amp-binding protein [Brassica napus]	553	552	0	99.8	94.9	96.7	amp-binding protein	gbpln	Brassica napus	AT1G77240.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr1:29017958-29019595 REVERSE LENGTH=545	553	545	0	98.6	85.2	91.3
Rsa1.0_00036.1.g2150.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00036.1.g2151.t1	gb|EOA33584.1| hypothetical protein CARUB_v10019729mg [Capsella rubella]	547	969	1.00E-90	177.1	44.4	61.2	hypothetical protein CARUB_v10019729mg	gbpln	Capsella rubella	AT1G77270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G07730.1); Has 428 Blast hits to 388 proteins in 92 species: Archae - 0; Bacteria - 31; Metazoa - 189; Fungi - 10; Plants - 97; Viruses - 0; Other Eukaryotes - 101 (source: NCBI BLink). | chr1:29028342-29031068 FORWARD LENGTH=682	547	682	5.00E-86	124.7	42.2	58.0
Rsa1.0_00036.1.g2152.t1	ref|NP_177852.2| adenine nucleotide alpha hydrolases-domain containing protein kinase [Arabidopsis thaliana] gi|332197836|gb|AEE35957.1| adenine nucleotide alpha hydrolases-domain containing protein kinase [Arabidopsis thaliana]	723	794	0	109.8	80.5	88.1	adenine nucleotide alpha hydrolases-domain containing protein kinase	gbpln	Arabidopsis thaliana	AT1G77280.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:29031468-29035882 REVERSE LENGTH=794	723	794	0	109.8	80.5	88.1
Rsa1.0_00036.1.g2153.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00036.1.g2154.t1	gb|EOA33259.1| hypothetical protein CARUB_v10022136mg [Capsella rubella]	136	266	5.00E-25	195.6	56.6	64.0	hypothetical protein CARUB_v10022136mg	gbpln	Capsella rubella	AT1G77290.2 | Symbols: | Glutathione S-transferase family protein | chr1:29038917-29039815 FORWARD LENGTH=266	136	266	6.00E-27	195.6	56.6	64.0

Rsa1.0_00036.1.g2155.t1	ref|NP_177854.6| histone-lysine N-methyltransferase SETD2 [Arabidopsis thaliana] gi|157734196|gb|ABV68921.1| SDG8 [Arabidopsis thaliana] gi|332197839|gb|AEE35960.1| histone-lysine N-methyltransferase SETD2 [Arabidopsis thaliana]	1527	1805	0	118.2	72.1	79.2	histone-lysine N-methyltransferase SETD2	gbpln	Arabidopsis thaliana	AT1G77300.1 | Symbols: EFS, SDG8, CCR1, ASHH2, LAZ2 | histone methyltransferases(H3-K4 specific);histone methyltransferases(H3-K36 specific) | chr1:29040160-29048810 REVERSE LENGTH=1805	1527	1805	0	118.2	72.1	79.2
Rsa1.0_00036.1.g2156.t1	gb|EOA15566.1| hypothetical protein CARUB_v10005224mg [Capsella rubella]	187	329	1.00E-41	175.9	62.0	72.2	hypothetical protein CARUB_v10005224mg	gbpln	Capsella rubella	AT4G28430.1 | Symbols: | Reticulon family protein | chr4:14057846-14059772 FORWARD LENGTH=457	187	457	9.00E-39	244.4	56.7	66.3
Rsa1.0_00036.1.g2157.t1	gb|EJP69747.1| hypothetical protein BBA_01712 [Beauveria bassiana ARSEF 2860]	251	318	2.00E-67	126.7	48.6	68.9	hypothetical protein BBA_01712	gbenv/gbpln	Beauveria bassiana	#	#	#	#	#	#	#
Rsa1.0_00036.1.g2158.t2	gb|AAC34358.1| Hypothetical protein [Arabidopsis thaliana]	98	1767	3.00E-19	1803.1	53.1	55.1	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G77300.1 | Symbols: EFS, SDG8, CCR1, ASHH2, LAZ2 | histone methyltransferases(H3-K4 specific);histone methyltransferases(H3-K36 specific) | chr1:29040160-29048810 REVERSE LENGTH=1805	98	1805	4.00E-22	1841.8	53.1	55.1
Rsa1.0_00036.1.g2159.t2	ref|NP_177855.4| uncharacterized protein [Arabidopsis thaliana] gi|332197841|gb|AEE35962.1| uncharacterized protein AT1G77310 [Arabidopsis thaliana]	670	717	0	107.0	65.8	76.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G77310.1 | Symbols: | BEST Arabidopsis thaliana protein match is: wound-responsive family protein (TAIR:AT1G21610.1); Has 493 Blast hits to 482 proteins in 163 species: Archae - 0; Bacteria - 100; Metazoa - 172; Fungi - 66; Plants - 65; Viruses - 7; Other Eukaryotes - 83 (source: NCBI BLink). | chr1:29051671-29056179 FORWARD LENGTH=717	670	717	0	107.0	65.8	76.0
Rsa1.0_00036.1.g2160.t1	ref|NP_565154.1| aminocyclopropanecarboxylate oxidase [Arabidopsis thaliana] gi|122246564|sp|Q0WPW4.1|ACCO5_ARATH RecName: Full=1-aminocyclopropane-1-carboxylate oxidase 5; Short=ACC oxidase 5; Short=AtACO5 gi|110737793|dbj|BAF00835.1| hypothetical protein [Arabidopsis thaliana] gi|111074356|gb|ABH04551.1| At1g77330 [Arabidopsis thaliana] gi|332197844|gb|AEE35965.1| 1-aminocyclopropane-1-carboxylate oxidase 5 [Arabidopsis thaliana]	314	307	1.00E-170	97.8	93.3	96.2	aminocyclopropanecarboxylate oxidase	gbpln	Arabidopsis thaliana	AT1G77330.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:29063215-29064447 REVERSE LENGTH=307	314	307	1.00E-173	97.8	93.3	96.2
Rsa1.0_00036.1.g2161.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00036.1.g2162.t1	gb|EJP69747.1| hypothetical protein BBA_01712 [Beauveria bassiana ARSEF 2860]	248	318	5.00E-66	128.2	48.4	67.7	hypothetical protein BBA_01712	gbenv/gbpln	Beauveria bassiana	#	#	#	#	#	#	#
Rsa1.0_00036.1.g2163.t1	ref|NP_194638.1| Ribonuclease H-like protein [Arabidopsis thaliana] gi|4972055|emb|CAB43923.1| putative protein [Arabidopsis thaliana] gi|7269807|emb|CAB79667.1| putative protein [Arabidopsis thaliana] gi|67633766|gb|AAY78807.1| putative reverse transcriptase/RNA-dependent DNA polymerase [Arabidopsis thaliana] gi|332660185|gb|AEE85585.1| Ribonuclease H-like protein [Arabidopsis thaliana]	300	575	5.00E-30	191.7	33.0	51.0	Ribonuclease H-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	300	575	1.00E-32	191.7	33.0	51.0
Rsa1.0_00036.1.g2164.t1	gb|AAG29201.1|AC078898_11 hypothetical protein [Arabidopsis thaliana]	476	481	0	101.1	86.3	93.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G77360.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:29071983-29073536 REVERSE LENGTH=517	476	517	0	108.6	86.3	93.5
Rsa1.0_00036.1.g2165.t1	ref|NP_177864.1| uncharacterized protein [Arabidopsis thaliana] gi|11079486|gb|AAG29198.1|AC078898_8 hypothetical protein [Arabidopsis thaliana] gi|28466875|gb|AAO44046.1| At1g77400 [Arabidopsis thaliana] gi|51971947|dbj|BAD44638.1| At1g77400 [Arabidopsis thaliana] gi|110736099|dbj|BAF00022.1| hypothetical protein [Arabidopsis thaliana] gi|332197852|gb|AEE35973.1| uncharacterized protein AT1G77400 [Arabidopsis thaliana]	190	232	6.00E-50	122.1	83.2	85.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G77400.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF688 (InterPro:IPR007789); BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT1G21695.1); Has 328 Blast hits to 314 proteins in 61 species: Archae - 0; Bacteria - 12; Metazoa - 130; Fungi - 28; Plants - 92; Viruses - 10; Other Eukaryotes - 56 (source: NCBI BLink). | chr1:29085881-29086579 FORWARD LENGTH=232	190	232	2.00E-52	122.1	83.2	85.3
Rsa1.0_00036.1.g2166.t1	ref|XP_002887681.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297333522|gb|EFH63940.1| binding protein [Arabidopsis lyrata subsp. lyrata]	447	459	0	102.7	86.6	91.5	binding protein	gbpln	Arabidopsis lyrata	AT1G77405.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:29087145-29088521 FORWARD LENGTH=458	447	458	0	102.5	85.2	90.2

Rsa1.0_00036.1.g2167.t1	ref|XP_002889142.1| hypothetical protein ARALYDRAFT_476906 [Arabidopsis lyrata subsp. lyrata] gi|297334983|gb|EFH65401.1| hypothetical protein ARALYDRAFT_476906 [Arabidopsis lyrata subsp. lyrata]	818	818	0	100.0	84.5	91.1	hypothetical protein ARALYDRAFT_476906	gbpln	Arabidopsis lyrata	AT1G77410.1 | Symbols: BGAL16 | beta-galactosidase 16 | chr1:29088771-29093148 REVERSE LENGTH=815	818	815	0	99.6	83.6	90.6
Rsa1.0_00036.1.g2168.t1	gb|EOA35294.1| hypothetical protein CARUB_v10020464mg [Capsella rubella]	394	382	0	97.0	80.2	87.6	hypothetical protein CARUB_v10020464mg	gbpln	Capsella rubella	AT1G77420.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:29093641-29095442 FORWARD LENGTH=382	394	382	0	97.0	79.9	86.8
Rsa1.0_00036.1.g2169.t1	gb|AAP35055.1| NAC-domain protein 14 [Brassica napus]	261	260	1.00E-142	99.6	93.9	96.6	NAC-domain protein 14	gbpln	Brassica napus	AT1G77450.1 | Symbols: anac032, NAC032 | NAC domain containing protein 32 | chr1:29100029-29100981 FORWARD LENGTH=253	261	253	1.00E-119	96.9	83.9	87.0
Rsa1.0_00036.1.g2170.t1	gb|EOA30101.1| hypothetical protein CARUB_v10013211mg, partial [Capsella rubella]	92	628	5.00E-33	682.6	75.0	87.0	hypothetical protein CARUB_v10013211mg, partial	gbpln	Capsella rubella	AT3G10050.1 | Symbols: OMR1 | L-O-methylthreonine resistant 1 | chr3:3099164-3101741 REVERSE LENGTH=592	92	592	9.00E-36	643.5	73.9	87.0
Rsa1.0_00036.1.g2171.t1	ref|XP_002889143.1| hypothetical protein ARALYDRAFT_476911 [Arabidopsis lyrata subsp. lyrata] gi|297334984|gb|EFH65402.1| hypothetical protein ARALYDRAFT_476911 [Arabidopsis lyrata subsp. lyrata]	368	369	0	100.3	91.8	94.3	hypothetical protein ARALYDRAFT_476911	gbpln	Arabidopsis lyrata	AT1G77470.1 | Symbols: RFC3, RFC5 | replication factor C subunit 3 | chr1:29112194-29114323 REVERSE LENGTH=369	368	369	0	100.3	89.1	93.5
Rsa1.0_00036.1.g2172.t1	gb|EJP69747.1| hypothetical protein BBA_01712 [Beauveria bassiana ARSEF 2860]	251	318	2.00E-62	126.7	48.2	64.9	hypothetical protein BBA_01712	gbenv/gbpln	Beauveria bassiana	#	#	#	#	#	#	#
Rsa1.0_00036.1.g2173.t1	gb|ABB17025.1| protein disulfide isomerase [Brassica carinata]	511	509	0	99.6	84.9	91.6	protein disulfide isomerase	gbpln	Brassica carinata	AT1G77510.1 | Symbols: ATPDIL1-2, PDI6, ATPDI6, PDIL1-2 | PDI-like 1-2 | chr1:29126742-29129433 FORWARD LENGTH=508	511	508	0	99.4	82.0	89.2
Rsa1.0_00036.1.g2174.t1	ref|NP_177876.1| O-methyltransferase family protein [Arabidopsis thaliana] gi|12323395|gb|AAG51676.1|AC010704_20 putative caffeic acid 3-O-methyltransferase; 41078-42528 [Arabidopsis thaliana] gi|332197867|gb|AEE35988.1| O-methyltransferase family protein [Arabidopsis thaliana]	339	381	1.00E-152	112.4	80.2	87.0	O-methyltransferase family protein	gbpln	Arabidopsis thaliana	AT1G77520.1 | Symbols: | O-methyltransferase family protein | chr1:29130557-29132007 FORWARD LENGTH=381	339	381	1.00E-155	112.4	80.2	87.0
Rsa1.0_00037.1.g2175.t1	ref|XP_002867032.1| hypothetical protein ARALYDRAFT_491017 [Arabidopsis lyrata subsp. lyrata] gi|297312868|gb|EFH43291.1| hypothetical protein ARALYDRAFT_491017 [Arabidopsis lyrata subsp. lyrata]	377	376	0	99.7	85.9	92.3	hypothetical protein ARALYDRAFT_491017	gbpln	Arabidopsis lyrata	AT4G36160.1 | Symbols: ANAC076, VND2, NAC076 | NAC domain containing protein 76 | chr4:17110877-17112891 REVERSE LENGTH=377	377	377	0	100.0	85.9	91.0
Rsa1.0_00037.1.g2176.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00037.1.g2177.t1	ref|XP_002867031.1| hypothetical protein ARALYDRAFT_491015 [Arabidopsis lyrata subsp. lyrata] gi|297312867|gb|EFH43290.1| hypothetical protein ARALYDRAFT_491015 [Arabidopsis lyrata subsp. lyrata]	1120	1132	0	101.1	88.5	93.8	hypothetical protein ARALYDRAFT_491015	gbpln	Arabidopsis lyrata	AT4G36180.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr4:17120209-17123698 REVERSE LENGTH=1136	1120	1136	0	101.4	87.5	93.8
Rsa1.0_00037.1.g2178.t1	gb|EOA16518.1| hypothetical protein CARUB_v10004677mg [Capsella rubella]	473	489	0	103.4	88.2	93.0	hypothetical protein CARUB_v10004677mg	gbpln	Capsella rubella	AT4G36195.3 | Symbols: | Serine carboxypeptidase S28 family protein | chr4:17127202-17129787 FORWARD LENGTH=488	473	488	0	103.2	87.3	94.7
Rsa1.0_00037.1.g2179.t1	ref|NP_001078500.2| uncharacterized protein [Arabidopsis thaliana] gi|332661235|gb|AEE86635.1| uncharacterized protein AT4G36210 [Arabidopsis thaliana]	676	672	0	99.4	90.1	95.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G36210.3 | Symbols: | Protein of unknown function (DUF726) | chr4:17130354-17134302 FORWARD LENGTH=672	676	672	0	99.4	90.1	95.4
Rsa1.0_00037.1.g2180.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	106	1555	5.00E-17	1467.0	49.1	61.3	disease resistance protein	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00037.1.g2181.t1	gb|AAG14961.1|AF214007_1 cytochrome p450-dependent monooxygenase [Brassica napus]	520	520	0	100.0	97.3	98.7	cytochrome p450-dependent monooxygenase	gbpln	Brassica napus	AT4G36220.1 | Symbols: FAH1, CYP84A1 | ferulic acid 5-hydroxylase 1 | chr4:17137584-17139619 REVERSE LENGTH=520	520	520	0	100.0	92.9	96.7

Rsa1.0_00037.1.g2182.t1	ref|NP_195346.1| uncharacterized protein [Arabidopsis thaliana] gi|2961382|emb|CAA18129.1| putative glycine-rich cell wall protein [Arabidopsis thaliana] gi|7270576|emb|CAB80294.1| putative glycine-rich cell wall protein [Arabidopsis thaliana] gi|332661237|gb|AEE86637.1| uncharacterized protein AT4G36230 [Arabidopsis thaliana]	220	221	3.00E-11	100.5	20.0	25.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G36230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf apex, hypocotyl, flower; EXPRESSED DURING: petal differentiation and expansion stage; Has 250444 Blast hits to 52918 proteins in 2611 species: Archae - 614; Bacteria - 68464; Metazoa - 90603; Fungi - 16312; Plants - 24752; Viruses - 3701; Other Eukaryotes - 45998 (source: NCBI BLink). | chr4:17145586-17146251 FORWARD LENGTH=221	220	221	9.00E-14	100.5	20.0	25.0
Rsa1.0_00037.1.g2183.t1	ref|NP_195347.1| GATA transcription factor 7 [Arabidopsis thaliana] gi|71660767|sp|O65515.1|GATA7_ARATH RecName: Full=GATA transcription factor 7 gi|2961383|emb|CAA18130.1| putative protein [Arabidopsis thaliana] gi|7270577|emb|CAB80295.1| putative protein [Arabidopsis thaliana] gi|18252999|gb|AAL62426.1| putative protein [Arabidopsis thaliana] gi|21389681|gb|AAM48039.1| putative protein [Arabidopsis thaliana] gi|332661238|gb|AEE86638.1| GATA transcription factor 7 [Arabidopsis thaliana]	236	238	2.00E-91	100.8	74.2	80.1	GATA transcription factor 7	gbpln	Arabidopsis thaliana	AT4G36240.1 | Symbols: GATA7 | GATA transcription factor 7 | chr4:17147376-17148211 REVERSE LENGTH=238	236	238	7.00E-94	100.8	74.2	80.1
Rsa1.0_00037.1.g2184.t1	gb|EOA16534.1| hypothetical protein CARUB_v10004694mg [Capsella rubella]	481	485	0	100.8	87.1	95.8	hypothetical protein CARUB_v10004694mg	gbpln	Capsella rubella	AT4G36250.1 | Symbols: ALDH3F1 | aldehyde dehydrogenase 3F1 | chr4:17151029-17153381 FORWARD LENGTH=484	481	484	0	100.6	85.7	94.6
Rsa1.0_00037.1.g2185.t1	gb|ADA60974.1| stylish 2b [Brassica rapa subsp. pekinensis]	312	321	1.00E-125	102.9	88.5	92.6	stylish 2b	gbpln	Brassica rapa	AT4G36260.1 | Symbols: STY2, SRS2 | Lateral root primordium (LRP) protein-related | chr4:17155705-17157006 REVERSE LENGTH=322	312	322	1.00E-119	103.2	86.9	91.0
Rsa1.0_00037.1.g2186.t2	ref|XP_002867022.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312858|gb|EFH43281.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1325	631	0	47.6	38.4	42.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G36290.1 | Symbols: CRT1 | compromised recognition of TCV 1 | chr4:17169669-17173187 REVERSE LENGTH=635	1325	635	0	47.9	37.1	41.5
Rsa1.0_00037.1.g2187.t1	dbj|BAJ34544.1| unnamed protein product [Thellungiella halophila]	846	856	0	101.2	92.6	96.0	unnamed protein product	----	----	AT4G36360.1 | Symbols: BGAL3 | beta-galactosidase 3 | chr4:17176840-17181143 REVERSE LENGTH=856	846	856	0	101.2	91.6	95.6
Rsa1.0_00037.1.g2188.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00037.1.g2189.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00037.1.g2190.t1	ref|XP_002867019.1| cytochrome P450 [Arabidopsis lyrata subsp. lyrata] gi|297312855|gb|EFH43278.1| cytochrome P450 [Arabidopsis lyrata subsp. lyrata]	527	525	0	99.6	86.3	92.4	cytochrome P450	gbpln	Arabidopsis lyrata	AT4G36380.1 | Symbols: ROT3 | Cytochrome P450 superfamily protein | chr4:17187973-17192202 REVERSE LENGTH=524	527	524	0	99.4	85.6	91.3
Rsa1.0_00037.1.g2191.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00037.1.g2192.t1	emb|CAA18234.1| putative protein [Arabidopsis thaliana] gi|7269488|emb|CAB79491.1| putative protein [Arabidopsis thaliana]	368	1141	1.00E-58	310.1	34.5	52.7	putative protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	368	626	1.00E-37	170.1	25.8	38.9
Rsa1.0_00037.1.g2193.t1	ref|NP_001190937.1| Splicing factor U2af large subunit A [Arabidopsis thaliana] gi|332661290|gb|AEE86690.1| Splicing factor U2af large subunit A [Arabidopsis thaliana]	525	551	0	105.0	83.4	88.8	Splicing factor U2af large subunit A	gbpln	Arabidopsis thaliana	AT4G36690.4 | Symbols: ATU2AF65A | U2 snRNP auxilliary factor, large subunit, splicing factor | chr4:17294139-17297609 REVERSE LENGTH=551	525	551	0	105.0	83.4	88.8
Rsa1.0_00037.1.g2194.t4	gb|EOA16541.1| hypothetical protein CARUB_v10004700mg [Capsella rubella]	685	483	0	70.5	63.4	66.3	hypothetical protein CARUB_v10004700mg	gbpln	Capsella rubella	AT4G36710.1 | Symbols: | GRAS family transcription factor | chr4:17306060-17307520 FORWARD LENGTH=486	685	486	0	70.9	62.5	65.7
Rsa1.0_00037.1.g2195.t1	emb|CAA58774.1| G-box binding factor 1A [Brassica napus]	311	313	1.00E-155	100.6	92.6	95.2	G-box binding factor 1A	gbpln	Brassica napus	AT4G36730.1 | Symbols: GBF1 | G-box binding factor 1 | chr4:17309850-17311752 REVERSE LENGTH=315	311	315	1.00E-147	101.3	86.8	92.6
Rsa1.0_00037.1.g2196.t1	ref|XP_002866994.1| homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata] gi|297312830|gb|EFH43253.1| homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata]	217	217	1.00E-106	100.0	90.8	95.4	homeobox-leucine zipper protein ATHB-40	gbpln	Arabidopsis lyrata	AT4G36740.1 | Symbols: HB-5, ATHB40, HB40 | homeobox protein 40 | chr4:17314649-17316314 REVERSE LENGTH=216	217	216	1.00E-103	99.5	88.0	94.5
Rsa1.0_00037.1.g2197.t1	gb|EOA33837.1| hypothetical protein CARUB_v10021318mg, partial [Capsella rubella]	194	290	1.00E-48	149.5	52.1	67.0	hypothetical protein CARUB_v10021318mg, partial	gbpln	Capsella rubella	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	194	332	3.00E-41	171.1	41.8	53.1

Rsa1.0_00037.1.g2198.t1	gb|EOA18652.1| hypothetical protein CARUB_v10007228mg [Capsella rubella]	257	273	1.00E-123	106.2	88.7	92.2	hypothetical protein CARUB_v10007228mg	gbpln	Capsella rubella	AT4G36750.1 | Symbols: | Quinone reductase family protein | chr4:17324642-17326215 FORWARD LENGTH=273	257	273	1.00E-119	106.2	85.6	89.1
Rsa1.0_00037.1.g2199.t1	dbj|BAJ34484.1| unnamed protein product [Thellungiella halophila]	583	645	0	110.6	89.2	93.7	unnamed protein product	----	----	AT4G36760.1 | Symbols: ATAPP1, APP1 | aminopeptidase P1 | chr4:17326688-17329979 FORWARD LENGTH=645	583	645	0	110.6	87.5	92.5
Rsa1.0_00037.1.g2200.t1	ref|XP_002866993.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297312829|gb|EFH43252.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	462	457	0	98.9	83.8	91.1	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT4G36770.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr4:17330217-17331590 REVERSE LENGTH=457	462	457	0	98.9	83.5	90.0
Rsa1.0_00037.1.g2201.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00037.1.g2202.t1	gb|EOA17023.1| hypothetical protein CARUB_v10005257mg [Capsella rubella]	312	322	1.00E-135	103.2	89.4	92.3	hypothetical protein CARUB_v10005257mg	gbpln	Capsella rubella	AT4G36780.1 | Symbols: BEH2 | BES1/BZR1 homolog 2 | chr4:17332989-17334212 REVERSE LENGTH=265	312	265	5.00E-78	84.9	59.6	60.9
Rsa1.0_00037.1.g2203.t1	ref|XP_002869023.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314859|gb|EFH45282.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	433	489	0	112.9	93.3	96.5	predicted protein	gbpln	Arabidopsis lyrata	AT4G36790.1 | Symbols: | Major facilitator superfamily protein | chr4:17336360-17338304 FORWARD LENGTH=489	433	489	0	112.9	92.6	95.8
Rsa1.0_00037.1.g2204.t1	gb|ACI16426.1| RUB1-conjugation enzyme [Brassica juncea]	185	185	1.00E-103	100.0	96.8	98.9	RUB1-conjugation enzyme	gbpln	Brassica juncea	AT4G36800.2 | Symbols: RCE1 | RUB1 conjugating enzyme 1 | chr4:17341237-17342148 REVERSE LENGTH=184	185	184	1.00E-105	99.5	97.8	98.9
Rsa1.0_00037.1.g2205.t1	sp|Q43133.1|GGPPS_SINAL RecName: Full=Geranylgeranyl pyrophosphate synthase, chloroplastic/chromoplastic; Short=GGPP synthase; Short=GGPS; AltName: Full=(2E,6E)-farnesyl diphosphate synthase; AltName: Full=Dimethylallyltranstransferase; AltName: Full=Farnesyl diphosphate synthase; AltName: Full=Farnesyltranstransferase; AltName: Full=Geranyltranstransferase; Flags: Precursor gi|1419758|emb|CAA67330.1| geranylgeranyl pyrophosphate synthase [Sinapis alba]	368	366	0	99.5	92.7	97.3	RecName: Full=Geranylgeranyl pyrophosphate synthase, chloroplastic/chromoplastic; Short=GGPP synthase; Short=GGPS; AltName: Full=(2E,6E)-farnesyl diphosphate synthase; AltName: Full=Dimethylallyltransferase; AltName: Full=Farnesyl diphosphate synthase; AltName: Full=Farnesyltranstransferase; AltName: Full=Geranyltranstransferase; Flags: Precursor gi|1419758|emb|CAA67330.1| geranylgeranyl pyrophosphate synthase	gbpln	Sinapis alba	AT4G36810.1 | Symbols: GGPS1 | geranylgeranyl pyrophosphate synthase 1 | chr4:17343513-17344628 FORWARD LENGTH=371	368	371	1.00E-173	100.8	86.1	91.6
Rsa1.0_00037.1.g2206.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00037.1.g2207.t2	gb|EOA16793.1| hypothetical protein CARUB_v10005013mg, partial [Capsella rubella]	313	388	1.00E-139	124.0	79.6	87.5	hypothetical protein CARUB_v10005013mg, partial	gbpln	Capsella rubella	AT4G36820.1 | Symbols: | Protein of unknown function (DUF607) | chr4:17346889-17347994 FORWARD LENGTH=338	313	338	1.00E-131	108.0	74.1	85.3
Rsa1.0_00037.1.g2208.t1	ref|NP_568009.5| PQ-loop repeat family protein / transmembrane family protein [Arabidopsis thaliana] gi|15028159|gb|AAK76703.1| unknown protein [Arabidopsis thaliana] gi|332661309|gb|AEE86709.1| PQ-loop repeat family protein / transmembrane family protein [Arabidopsis thaliana]	384	392	0	102.1	88.3	92.2	PQ-loop repeat family protein / transmembrane family protein	gbpln	Arabidopsis thaliana	AT4G36850.1 | Symbols: | PQ-loop repeat family protein / transmembrane family protein | chr4:17353415-17355822 REVERSE LENGTH=392	384	392	0	102.1	88.3	92.2
Rsa1.0_00037.1.g2209.t3	ref|XP_002866988.1| hypothetical protein ARALYDRAFT_328082 [Arabidopsis lyrata subsp. lyrata] gi|297312824|gb|EFH43247.1| hypothetical protein ARALYDRAFT_328082 [Arabidopsis lyrata subsp. lyrata]	584	558	0	95.5	87.8	92.5	hypothetical protein ARALYDRAFT_328082	gbpln	Arabidopsis lyrata	AT4G36860.1 | Symbols: | LIM domain-containing protein | chr4:17358580-17361189 REVERSE LENGTH=553	584	553	0	94.7	86.5	91.1
Rsa1.0_00037.1.g2210.t2	gb|AAD51349.1| bel1-like homeodomain 2 [Arabidopsis thaliana] gi|15215857|gb|AAK91472.1| AT4g36870/C7A10_490 [Arabidopsis thaliana]	636	739	0	116.2	84.0	87.6	bel1-like homeodomain 2	gbpln	Arabidopsis thaliana	AT4G36870.2 | Symbols: BLH2, SAW1 | BEL1-like homeodomain 2 | chr4:17369423-17373723 FORWARD LENGTH=739	636	739	0	116.2	83.8	87.4

Rsa1.0_00037.1_g2211.t1	ref|XP_002867047.1| hypothetical protein ARALYDRAFT_328161 [Arabidopsis lyrata subsp. lyrata] gi|297312883|gb|EFH43306.1| hypothetical protein ARALYDRAFT_328161 [Arabidopsis lyrata subsp. lyrata]	457	459	0	100.4	85.3	91.9	hypothetical protein ARALYDRAFT_328161	gbpln	Arabidopsis lyrata	AT4G35910.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr4:17008817-17011014 REVERSE LENGTH=458	457	458	0	100.2	84.0	91.2
Rsa1.0_00037.1_g2212.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00037.1_g2213.t1	gb|EOA15637.1| hypothetical protein CARUB_v10005881mg [Capsella rubella]	171	173	2.00E-67	101.2	82.5	87.7	hypothetical protein CARUB_v10005881mg	gbpln	Capsella rubella	AT4G37240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G23690.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17524546-17525052 FORWARD LENGTH=168	171	168	9.00E-63	98.2	79.5	87.1
Rsa1.0_00037.1_g2214.t1	gb|AAM08751.1|AC025098_18 Putative copia-type polyprotein [Oryza sativa Japonica Group]	1074	1803	0	167.9	45.7	60.2	Putative copia-type polyprotein	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1074	1262	2.00E-85	117.5	15.7	23.1
Rsa1.0_00037.1_g2215.t1	ref|XP_002866981.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297312817|gb|EFH43240.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	450	498	1.00E-161	110.7	76.4	85.3	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G37210.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:17512376-17514421 FORWARD LENGTH=492	450	492	1.00E-153	109.3	73.8	82.2
Rsa1.0_00037.1_g2216.t3	gb|EOA17278.1| hypothetical protein CARUB_v10005573mg [Capsella rubella]	294	252	1.00E-107	85.7	68.7	73.5	hypothetical protein CARUB_v10005573mg	gbpln	Capsella rubella	AT4G37200.1 | Symbols: HCF164 | Thioredoxin superfamily protein | chr4:17509836-17511230 REVERSE LENGTH=261	294	261	1.00E-106	88.8	68.0	73.1
Rsa1.0_00037.1_g2217.t1	ref|NP_568018.1| myb family transcription factor [Arabidopsis thaliana] gi|115311427|gb|ABI93894.1| At4g37180 [Arabidopsis thaliana] gi|332661363|gb|AEE86763.1| myb family transcription factor [Arabidopsis thaliana]	342	356	1.00E-127	104.1	76.9	86.0	myb family transcription factor	gbpln	Arabidopsis thaliana	AT4G37180.1 | Symbols: | Homeodomain-like superfamily protein | chr4:17504648-17506107 FORWARD LENGTH=356	342	356	1.00E-130	104.1	76.9	86.0
Rsa1.0_00037.1_g2218.t1	ref|XP_002869013.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297314849|gb|EFH45272.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	1202	693	0	57.7	48.0	52.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G37170.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:17498580-17500655 REVERSE LENGTH=691	1202	691	0	57.5	47.8	52.0
Rsa1.0_00037.1_g2219.t1	ref|XP_002869010.1| hypothetical protein ARALYDRAFT_912657 [Arabidopsis lyrata subsp. lyrata] gi|297314846|gb|EFH45269.1| hypothetical protein ARALYDRAFT_912657 [Arabidopsis lyrata subsp. lyrata]	257	261	1.00E-124	101.6	82.1	90.3	hypothetical protein ARALYDRAFT_912657	gbpln	Arabidopsis lyrata	AT4G37150.1 | Symbols: ATMES9, MES9 | methyl esterase 9 | chr4:17492985-17494057 REVERSE LENGTH=256	257	256	1.00E-116	99.6	75.5	85.2
Rsa1.0_00037.1_g2220.t1	ref|NP_195430.2| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|20260346|gb|AAM13071.1| unknown protein [Arabidopsis thaliana] gi|31711924|gb|AAP68318.1| At4g37130 [Arabidopsis thaliana] gi|332661357|gb|AEE86757.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	510	513	0	100.6	75.9	79.8	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT4G37130.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:17489567-17491773 FORWARD LENGTH=513	510	513	0	100.6	75.9	79.8
Rsa1.0_00037.1_g2221.t1	gb|EOA16987.1| hypothetical protein CARUB_v10005219mg [Capsella rubella]	323	332	1.00E-140	102.8	75.9	87.0	hypothetical protein CARUB_v10005219mg	gbpln	Capsella rubella	AT4G25900.1 | Symbols: | Galactose mutarotase-like superfamily protein | chr4:13161487-13163397 FORWARD LENGTH=318	323	318	1.00E-135	98.5	73.4	83.3
Rsa1.0_00037.1_g2222.t1	ref|XP_002869009.1| hypothetical protein ARALYDRAFT_490927 [Arabidopsis lyrata subsp. lyrata] gi|297314845|gb|EFH45268.1| hypothetical protein ARALYDRAFT_490927 [Arabidopsis lyrata subsp. lyrata]	410	430	1.00E-150	104.9	72.4	82.4	hypothetical protein ARALYDRAFT_490927	gbpln	Arabidopsis lyrata	AT4G37110.1 | Symbols: | Zinc-finger domain of monoamine-oxidase A repressor R1 | chr4:17484343-17486197 REVERSE LENGTH=417	410	417	1.00E-138	101.7	67.3	79.0

Rsa1.0_00037.1.g2223.t1	ref|NP_195427.1| catalytic/ pyridoxal phosphate binding protein [Arabidopsis thaliana] gi|4006867|emb|CAB16785.1| putative protein [Arabidopsis thaliana] gi|7270659|emb|CAB80376.1| putative protein [Arabidopsis thaliana] gi|332661354|gb|AEE86754.1| catalytic/ pyridoxal phosphate binding protein [Arabidopsis thaliana]	882	896	0	101.6	84.8	90.8	catalytic/ pyridoxal phosphate binding protein	gbpln	Arabidopsis thaliana	AT4G37100.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr4:17479173-17481863 REVERSE LENGTH=896	882	896	0	101.6	84.8	90.8
Rsa1.0_00037.1.g2224.t2	gb|EOA16265.1| hypothetical protein CARUB_v10004409mg [Capsella rubella]	590	605	0	102.5	87.8	91.9	hypothetical protein CARUB_v10004409mg	gbpln	Capsella rubella	AT4G37080.3 | Symbols: | Protein of unknown function, DUF547 | chr4:17473719-17476716 FORWARD LENGTH=610	590	610	0	103.4	88.1	91.5
Rsa1.0_00037.1.g2225.t1	gb|EOA18418.1| hypothetical protein CARUB_v10006962mg [Capsella rubella]	408	414	0	101.5	83.6	93.9	hypothetical protein CARUB_v10006962mg	gbpln	Capsella rubella	AT4G37070.2 | Symbols: PLP1, PLA IVA, AtPLAIVA | Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein | chr4:17464916-17467058 REVERSE LENGTH=414	408	414	0	101.5	82.6	93.1
Rsa1.0_00037.1.g2226.t1	gb|EOA18418.1| hypothetical protein CARUB_v10006962mg [Capsella rubella]	336	414	1.00E-105	123.2	56.0	64.3	hypothetical protein CARUB_v10006962mg	gbpln	Capsella rubella	AT4G37070.2 | Symbols: PLP1, PLA IVA, AtPLAIVA | Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein | chr4:17464916-17467058 REVERSE LENGTH=414	336	414	1.00E-106	123.2	55.4	65.2
Rsa1.0_00037.1.g2227.t1	ref|XP_002869006.1| hypothetical protein ARALYDRAFT_490916 [Arabidopsis lyrata subsp. lyrata] gi|297314842|gb|EFH45265.1| hypothetical protein ARALYDRAFT_490916 [Arabidopsis lyrata subsp. lyrata]	412	412	0	100.0	77.4	87.9	hypothetical protein ARALYDRAFT_490916	gbpln	Arabidopsis lyrata	AT4G37050.1 | Symbols: PLP4, PLA V, AtPLAIVC | PATATIN-like protein 4 | chr4:17457261-17459642 REVERSE LENGTH=428	412	428	0	103.9	76.7	86.7
Rsa1.0_00037.1.g2228.t1	ref|XP_002866973.1| hypothetical protein ARALYDRAFT_912645 [Arabidopsis lyrata subsp. lyrata] gi|297312809|gb|EFH43232.1| hypothetical protein ARALYDRAFT_912645 [Arabidopsis lyrata subsp. lyrata]	351	350	0	99.7	91.2	95.4	hypothetical protein ARALYDRAFT_912645	gbpln	Arabidopsis lyrata	AT4G37040.1 | Symbols: MAP1D | methionine aminopeptidase 1D | chr4:17455175-17457085 FORWARD LENGTH=350	351	350	0	99.7	90.3	94.9
Rsa1.0_00037.1.g2229.t1	gb|ABV89640.1| heat shock factor 4 [Brassica rapa]	277	285	1.00E-138	102.9	93.1	94.9	heat shock factor 4	gbpln	Brassica rapa	AT4G36990.1 | Symbols: HSF4, HSFB1, AT-HSFB1, ATHSF4 | heat shock factor 4 | chr4:17440660-17441706 FORWARD LENGTH=284	277	284	1.00E-117	102.5	80.9	88.1
Rsa1.0_00037.1.g2230.t3	ref|XP_002869003.1| hypothetical protein ARALYDRAFT_490906 [Arabidopsis lyrata subsp. lyrata] gi|297314839|gb|EFH45262.1| hypothetical protein ARALYDRAFT_490906 [Arabidopsis lyrata subsp. lyrata]	547	505	0	92.3	75.5	80.6	hypothetical protein ARALYDRAFT_490906	gbpln	Arabidopsis lyrata	AT4G36980.4 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Splicing factor, suppressor of white apricot (InterPro:IPR019147). | chr4:17433861-17437012 REVERSE LENGTH=556	547	556	0	101.6	75.1	80.6
Rsa1.0_00038.1.g2231.t1	ref|XP_002891171.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337013|gb|EFH67430.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	133	151	2.00E-45	113.5	67.7	75.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G35260.1 | Symbols: MLP165 | MLP-like protein 165 | chr1:12937059-12937689 REVERSE LENGTH=152	133	152	2.00E-45	114.3	65.4	77.4
Rsa1.0_00038.1.g2232.t1	ref|XP_002875142.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320980|gb|EFH51401.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata]	459	455	0	99.1	81.0	88.9	pectate lyase family protein	gbpln	Arabidopsis lyrata	AT2G02720.1 | Symbols: | Pectate lyase family protein | chr2:763173-764834 FORWARD LENGTH=455	459	455	0	99.1	81.3	88.5
Rsa1.0_00038.1.g2233.t14	ref|NP_178378.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546778|sp|Q1PFA6.2|PP144_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g02750 gi|2947066|gb|AAC05347.1| hypothetical protein [Arabidopsis thaliana] gi|330250526|gb|AEC05620.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	638	613	0	96.1	76.3	84.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G02750.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:771641-773482 REVERSE LENGTH=613	638	613	0	96.1	76.3	84.2

Rsa1.0_00038.1.g2234.t1	ref|NP_565289.1| ubiquitin-conjugating enzyme E2 A [Arabidopsis thaliana] gi|297814522|ref|XP_002875144.1| ubiquiting-conjugating enzyme 2 [Arabidopsis lyrata subsp. lyrata] gi|1174844|sp|P42745.1|UBC2_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 2; AltName: Full=Ubiquitin carrier protein 2; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 2; AltName: Full=Ubiquitin-protein ligase 2 gi|13899127|gb|AAK48985.1|AF370558_1 putative ubiquitin-conjugating enzyme E2 [Arabidopsis thaliana] gi|431264|gb|AAA32899.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|2689243|emb|CAA73476.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|2947065|gb|AAC05346.1| E2, ubiquitin-conjugating enzyme 2 (UBC2) [Arabidopsis thaliana] gi|18377456|gb|AAL66894.1| putative ubiquitin-conjugating enzyme E2 [Arabidopsis thaliana] gi|66354400|gb|AAY44843.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|118197458|gb|ABK78692.1| ubiquitin conjugating enzyme [Brassica rapa] gi|297320982|gb|EFH51403.1| ubiquiting-conjugating enzyme 2 [Arabidopsis lyrata subsp. lyrata]	126	152	9.00E-64	120.6	100.0	100.0	ubiquitin-conjugating enzyme E2 A	gbpln	Arabidopsis lyrata	AT2G02760.1 | Symbols: ATUBC2, UBC2 | ubiquiting-conjugating enzyme 2 | chr2:774271-775149 FORWARD LENGTH=152	126	152	2.00E-66	120.6	100.0	100.0
Rsa1.0_00038.1.g2235.t1	ref|NP_178382.2| protein IQ-domain 29 [Arabidopsis thaliana] gi|330250530|gb|AEC05624.1| protein IQ-domain 29 [Arabidopsis thaliana]	595	636	0	106.9	71.6	81.8	protein IQ-domain 29	gbpln	Arabidopsis thaliana	AT2G02790.1 | Symbols: IQD29 | IQ-domain 29 | chr2:788708-790946 FORWARD LENGTH=636	595	636	0	106.9	71.6	81.8
Rsa1.0_00038.1.g2236.t1	gb|EOA23949.1| hypothetical protein CARUB_v10017166mg [Capsella rubella]	418	472	0	112.9	87.8	93.1	hypothetical protein CARUB_v10017166mg	gbpln	Capsella rubella	AT2G02870.3 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:838378-839781 FORWARD LENGTH=467	418	467	0	111.7	87.6	93.5
Rsa1.0_00038.1.g2237.t1	gb|AAD38033.1|AF149053_1 phytochrome kinase substrate 1 [Arabidopsis thaliana]	401	439	1.00E-138	109.5	73.1	81.5	phytochrome kinase substrate 1	gbpln	Arabidopsis thaliana	AT2G02950.1 | Symbols: PKS1 | phytochrome kinase substrate 1 | chr2:855149-856468 REVERSE LENGTH=439	401	439	1.00E-140	109.5	72.8	81.5
Rsa1.0_00038.1.g2238.t1	ref|XP_002875185.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321023|gb|EFH51444.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	416	376	1.00E-159	90.4	71.6	76.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G03060.2 | Symbols: AGL30 | AGAMOUS-like 30 | chr2:901614-903569 FORWARD LENGTH=386	416	386	1.00E-154	92.8	71.4	76.9
Rsa1.0_00038.1.g2239.t1	gb|EOA24327.1| hypothetical protein CARUB_v10017566mg [Capsella rubella]	339	344	1.00E-171	101.5	91.4	95.0	hypothetical protein CARUB_v10017566mg	gbpln	Capsella rubella	AT2G03120.1 | Symbols: ATSPP, SPP | signal peptide peptidase | chr2:937554-940083 FORWARD LENGTH=344	339	344	1.00E-173	101.5	91.2	94.1
Rsa1.0_00038.1.g2240.t1	ref|XP_002875191.1| EMB1579 [Arabidopsis lyrata subsp. lyrata] gi|297321029|gb|EFH51450.1| EMB1579 [Arabidopsis lyrata subsp. lyrata]	1285	1333	0	103.7	53.3	58.3	EMB1579	gbpln	Arabidopsis lyrata	AT2G03150.1 | Symbols: emb1579 | ATP/GTP-binding protein family | chr2:952313-959004 FORWARD LENGTH=1340	1285	1340	0	104.3	53.0	58.8
Rsa1.0_00038.1.g2241.t1	gb|AAF82795.1|AF274864_1 SKP1gamma1 protein [Brassica napus]	156	159	3.00E-59	101.9	73.1	82.7	SKP1gamma1 protein	gbpln	Brassica napus	AT2G03170.1 | Symbols: ASK14, SK14 | SKP1-like 14 | chr2:961322-961771 FORWARD LENGTH=149	156	149	4.00E-45	95.5	59.0	73.7
Rsa1.0_00038.1.g2242.t2	ref|XP_002875234.1| hypothetical protein ARALYDRAFT_484298 [Arabidopsis lyrata subsp. lyrata] gi|297321072|gb|EFH51493.1| hypothetical protein ARALYDRAFT_484298 [Arabidopsis lyrata subsp. lyrata]	181	99	3.00E-43	54.7	49.7	50.3	hypothetical protein ARALYDRAFT_484298	gbpln	Arabidopsis lyrata	AT2G03870.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr2:1180306-1181256 FORWARD LENGTH=99	181	99	3.00E-45	54.7	49.2	49.2
Rsa1.0_00038.1.g2243.t1	ref|XP_002875236.1| phosphatidylinositol 3- and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321074|gb|EFH51495.1| phosphatidylinositol 3- and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	627	650	0	103.7	86.6	92.3	phosphatidylinositol 3- and 4-kinase family protein	gbpln	Arabidopsis lyrata	AT2G03890.1 | Symbols: ATPI4K GAMMA 7, UBDK GAMMA 7, PI4K GAMMA 7 | phosphoinositide 4-kinase gamma 7 | chr2:1186199-1188151 FORWARD LENGTH=650	627	650	0	103.7	86.3	92.3
Rsa1.0_00038.1.g2244.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00038.1.g2245.t1	ref|XP_002875239.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321077|gb|EFH51498.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	365	366	1.00E-159	100.3	74.5	81.6	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT2G03980.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr2:1260907-1262408 FORWARD LENGTH=367	365	367	1.00E-157	100.5	70.7	81.9
Rsa1.0_00038.1.g2246.t1	ref|XP_002875239.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321077|gb|EFH51498.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	365	366	1.00E-159	100.3	74.0	82.7	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT2G03980.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr2:1260907-1262408 FORWARD LENGTH=367	365	367	1.00E-155	100.5	69.9	81.4
Rsa1.0_00038.1.g2247.t1	gb|EOA25349.1| hypothetical protein CARUB_v10018672mg [Capsella rubella]	779	781	0	100.3	92.8	95.3	hypothetical protein CARUB_v10018672mg	gbpln	Capsella rubella	AT2G04030.1 | Symbols: CR88, EMB1956, HSP90.5, Hsp88.1, AtHsp90.5 | Chaperone protein htpG family protein | chr2:1281983-1285909 FORWARD LENGTH=780	779	780	0	100.1	91.8	94.4
Rsa1.0_00038.1.g2248.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00038.1.g2249.t1	ref|NP_178489.1| basic leucine-zipper 48 [Arabidopsis thaliana] gi|20198170|gb|AAM15441.1| bZIP protein (AtbZIP48) [Arabidopsis thaliana] gi|225898102|dbj|BAH30383.1| hypothetical protein [Arabidopsis thaliana] gi|330250693|gb|AEC05787.1| basic leucine-zipper 48 [Arabidopsis thaliana]	185	166	1.00E-54	89.7	77.8	82.7	basic leucine-zipper 48	gbpln	Arabidopsis thaliana	AT2G04038.1 | Symbols: AtbZIP48, bZIP48 | basic leucine-zipper 48 | chr2:1331919-1332419 FORWARD LENGTH=166	185	166	4.00E-57	89.7	77.8	82.7
Rsa1.0_00038.1.g2250.t1	gb|EOA24583.1| hypothetical protein CARUB_v10017846mg [Capsella rubella]	174	265	6.00E-47	152.3	60.9	70.1	hypothetical protein CARUB_v10017846mg	gbpln	Capsella rubella	AT3G25545.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 38 Blast hits to 38 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9277637-9278440 FORWARD LENGTH=267	174	267	1.00E-48	153.4	63.2	68.4
Rsa1.0_00038.1.g2251.t1	gb|ADK13078.1| phytocystatin 5-3 [Brassica rapa subsp. pekinensis]	120	120	9.00E-52	100.0	80.8	93.3	phytocystatin 5-3	gbpln	Brassica rapa	AT5G47550.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:19286596-19286964 REVERSE LENGTH=122	120	122	4.00E-31	101.7	50.8	67.5
Rsa1.0_00038.1.g2252.t1	ref|XP_002875263.1| hypothetical protein ARALYDRAFT_904723 [Arabidopsis lyrata subsp. lyrata] gi|297321101|gb|EFH51522.1| hypothetical protein ARALYDRAFT_904723 [Arabidopsis lyrata subsp. lyrata]	330	423	1.00E-117	128.2	78.8	85.2	hypothetical protein ARALYDRAFT_904723	gbpln	Arabidopsis lyrata	AT3G25590.1 | Symbols: | unknown protein; Has 149 Blast hits to 140 proteins in 44 species: Archae - 0; Bacteria - 6; Metazoa - 40; Fungi - 6; Plants - 39; Viruses - 0; Other Eukaryotes - 58 (source: NCBI BLink). | chr3:9302271-9303542 FORWARD LENGTH=423	330	423	1.00E-115	128.2	76.1	82.1
Rsa1.0_00038.1.g2253.t1	ref|NP_189188.4| putative calcium-binding protein CML16 [Arabidopsis thaliana] gi|332278174|sp|Q9LI84.2|CML16_ARATH RecName: Full=Probable calcium-binding protein CML16; AltName: Full=Calmodulin-like protein 16 gi|28393082|gb|AAO41975.1| putative calmodulin [Arabidopsis thaliana] gi|48310609|gb|AAT41852.1| At3g25600 [Arabidopsis thaliana] gi|332643520|gb|AEE77041.1| putative calcium-binding protein CML16 [Arabidopsis thaliana]	161	161	7.00E-83	100.0	93.8	96.9	putative calcium-binding protein CML16	gbpln	Arabidopsis thaliana	AT3G25600.1 | Symbols: | Calcium-binding EF-hand family protein | chr3:9307367-9307852 FORWARD LENGTH=161	161	161	3.00E-85	100.0	93.8	96.9
Rsa1.0_00038.1.g2254.t1	ref|NP_189194.1| Amidase family protein [Arabidopsis thaliana] gi|75273321|sp|Q9LI77.1|GATA_ARATH RecName: Full=Glutamyl-tRNA(Gln) amidotransferase subunit A, chloroplastic/mitochondrial; Short=Glu-AdT subunit A; Flags: Precursor gi|11994757|dbj|BAB03086.1| glutamyl tRNA amidotransferase, subunit A [Arabidopsis thaliana] gi|15010726|gb|AAK74022.1| AT3g25660/T5M7_8 [Arabidopsis thaliana] gi|23308481|gb|AAN18210.1| At3g25660/T5M7_8 [Arabidopsis thaliana] gi|110741094|dbj|BAE98641.1| putative glutamyl-tRNA amidotransferase subunit A [Arabidopsis thaliana] gi|332643527|gb|AEE77048.1| Amidase family protein [Arabidopsis thaliana]	542	537	0	99.1	91.0	95.8	Amidase family protein	gbpln	Arabidopsis thaliana	AT3G25660.1 | Symbols: | Amidase family protein | chr3:9339640-9342044 REVERSE LENGTH=537	542	537	0	99.1	91.0	95.8

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<tr><td>Rsa1.0_00038.1.g2255.t1</td><td>ref|XP_002875269.1| hypothetical protein ARALYDRAFT_904734 [Arabidopsis lyrata subsp. lyrata] gi|297321107|gb|EFH51528.1| hypothetical protein ARALYDRAFT_904734 [Arabidopsis lyrata subsp. lyrata]</td><td>552</td><td>558</td><td>0</td><td>101.1</td><td>78.1</td><td>88.4</td><td>hypothetical protein ARALYDRAFT_904734</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G25680.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: S-layer homology domain (InterPro:IPR001119); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23890.1); Has 2454 Blast hits to 2065 proteins in 355 species: Archae - 39; Bacteria - 284; Metazoa - 1081; Fungi - 166; Plants - 264; Viruses - 45; Other Eukaryotes - 575 (source: NCBI BLink). | chr3:9349693-9352258 FORWARD LENGTH=558</td><td>552</td><td>558</td><td>0</td><td>101.1</td><td>76.4</td><td>87.0</td></tr>
<tr><td>Rsa1.0_00038.1.g2256.t1</td><td>ref|NP_850631.2| protein rotundifolia like 16 [Arabidopsis thaliana] gi|42822045|tpg|DAA02277.1| TPA_exp: DVL6 [Arabidopsis thaliana] gi|332643537|gb|AEE77058.1| protein rotundifolia like 16 [Arabidopsis thaliana]</td><td>40</td><td>40</td><td>4.00E-13</td><td>100.0</td><td>97.5</td><td>100.0</td><td>protein rotundifolia like 16</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G25717.1 | Symbols: RTFL16, DVL6 | ROTUNDIFOLIA like 16 | chr3:9375472-9375594 REVERSE LENGTH=40</td><td>40</td><td>40</td><td>7.00E-16</td><td>100.0</td><td>97.5</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00038.1.g2257.t1</td><td>gb|EOA24619.1| hypothetical protein CARUB_v10017888mg [Capsella rubella]</td><td>253</td><td>254</td><td>1.00E-121</td><td>100.4</td><td>86.2</td><td>92.9</td><td>hypothetical protein CARUB_v10017888mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G25770.1 | Symbols: AOC2 | allene oxide cyclase 2 | chr3:9406975-9407839 FORWARD LENGTH=253</td><td>253</td><td>253</td><td>1.00E-121</td><td>100.0</td><td>85.0</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00038.1.g2258.t1</td><td>gb|ACY74379.1| allene oxidase cyclase [Brassica napus]</td><td>253</td><td>253</td><td>1.00E-139</td><td>100.0</td><td>95.7</td><td>97.2</td><td>allene oxidase cyclase</td><td>gbpln</td><td>Brassica napus</td><td>AT3G25780.1 | Symbols: AOC3 | allene oxide cyclase 3 | chr3:9409362-9410409 FORWARD LENGTH=258</td><td>253</td><td>258</td><td>1.00E-121</td><td>102.0</td><td>89.3</td><td>93.3</td></tr>
<tr><td>Rsa1.0_00038.1.g2259.t1</td><td>ref|XP_002875280.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297321118|gb|EFH51539.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]</td><td>366</td><td>354</td><td>1.00E-132</td><td>96.7</td><td>68.9</td><td>80.1</td><td>myb family transcription factor</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G25790.1 | Symbols: | myb-like transcription factor family protein | chr3:9413196-9414951 FORWARD LENGTH=357</td><td>366</td><td>357</td><td>1.00E-130</td><td>97.5</td><td>68.3</td><td>79.0</td></tr>
<tr><td>Rsa1.0_00038.1.g2260.t3</td><td>gb|EMJ15110.1| hypothetical protein PRUPE_ppa005492mg [Prunus persica]</td><td>268</td><td>458</td><td>3.00E-26</td><td>170.9</td><td>20.9</td><td>21.6</td><td>hypothetical protein PRUPE_ppa005492mg</td><td>gbpln</td><td>Prunus persica</td><td>AT1G30270.1 | Symbols: CIPK23, SnRK3.23, ATCIPK23, LKS1 | CBL-interacting protein kinase 23 | chr1:10655270-10658524 FORWARD LENGTH=482</td><td>268</td><td>482</td><td>9.00E-29</td><td>179.9</td><td>20.9</td><td>21.3</td></tr>
<tr><td>Rsa1.0_00038.1.g2261.t1</td><td>ref|XP_002876929.1| hypothetical protein ARALYDRAFT_904748 [Arabidopsis lyrata subsp. lyrata] gi|297322767|gb|EFH53188.1| hypothetical protein ARALYDRAFT_904748 [Arabidopsis lyrata subsp. lyrata]</td><td>586</td><td>587</td><td>0</td><td>100.2</td><td>96.1</td><td>99.0</td><td>hypothetical protein ARALYDRAFT_904748</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G25800.1 | Symbols: PDF1, PR 65, PP2AA2 | protein phosphatase 2A subunit A2 | chr3:9422822-9425783 REVERSE LENGTH=587</td><td>586</td><td>587</td><td>0</td><td>100.2</td><td>95.6</td><td>98.8</td></tr>
<tr><td>Rsa1.0_00038.1.g2262.t1</td><td>ref|NP_566779.1| uncharacterized protein [Arabidopsis thaliana] gi|13877955|gb|AAK44055.1|AF370240_1 unknown protein [Arabidopsis thaliana] gi|17065628|gb|AAL33808.1| unknown protein [Arabidopsis thaliana] gi|332643550|gb|AEE77071.1| uncharacterized protein AT3G25805 [Arabidopsis thaliana]</td><td>338</td><td>335</td><td>1.00E-156</td><td>99.1</td><td>80.5</td><td>87.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G25805.1 | Symbols: | unknown protein; Has 98 Blast hits to 98 proteins in 45 species: Archae - 0; Bacteria - 51; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr3:9426354-9428169 REVERSE LENGTH=335</td><td>338</td><td>335</td><td>1.00E-158</td><td>99.1</td><td>80.5</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00038.1.g2263.t2</td><td>gb|EOA23468.1| hypothetical protein CARUB_v10016659mg [Capsella rubella]</td><td>929</td><td>916</td><td>0</td><td>98.6</td><td>74.8</td><td>81.5</td><td>hypothetical protein CARUB_v10016659mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G25840.1 | Symbols: | Protein kinase superfamily protein | chr3:9452993-9457446 REVERSE LENGTH=935</td><td>929</td><td>935</td><td>0</td><td>100.6</td><td>75.1</td><td>81.9</td></tr>
<tr><td>Rsa1.0_00038.1.g2264.t1</td><td>ref|NP_189215.1| 2-oxoacid dehydrogenases acyltransferase family protein [Arabidopsis thaliana] gi|5881963|gb|AAD55139.1|AF066079_1 dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana] gi|14335166|gb|AAK59863.1| AT3g25860/MPE11_1 [Arabidopsis thaliana] gi|26983848|gb|AAN86176.1| putative dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana] gi|332643559|gb|AEE77080.1| pyruvate decarboxylase E2 subunit [Arabidopsis thaliana]</td><td>479</td><td>480</td><td>0</td><td>100.2</td><td>85.2</td><td>89.4</td><td>2-oxoacid dehydrogenases acyltransferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G25860.1 | Symbols: LTA2, PLE2 | 2-oxoacid dehydrogenases acyltransferase family protein | chr3:9460632-9462585 FORWARD LENGTH=480</td><td>479</td><td>480</td><td>0</td><td>100.2</td><td>85.2</td><td>89.4</td></tr>
<tr><td>Rsa1.0_00038.1.g2265.t1</td><td>ref|XP_002893783.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339625|gb|EFH70042.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>296</td><td>276</td><td>2.00E-31</td><td>93.2</td><td>30.1</td><td>38.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G25882.1 | Symbols: NIMIN-2 | NIM1-interacting 2 | chr3:9470521-9470889 REVERSE LENGTH=122</td><td>296</td><td>122</td><td>1.00E-28</td><td>41.2</td><td>24.3</td><td>28.4</td></tr>
<tr><td>Rsa1.0_00038.1.g2266.t1</td><td>gb|EOA24563.1| hypothetical protein CARUB_v10017825mg [Capsella rubella]</td><td>272</td><td>273</td><td>1.00E-125</td><td>100.4</td><td>86.4</td><td>91.5</td><td>hypothetical protein CARUB_v10017825mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G25920.1 | Symbols: RPL15 | ribosomal protein L15 | chr3:9491268-9492558 REVERSE LENGTH=277</td><td>272</td><td>277</td><td>1.00E-121</td><td>101.8</td><td>81.3</td><td>87.5</td></tr>
</table>

Rsa1.0_00038.1.g2267.t1	ref|NP_189227.1| mitotic spindle checkpoint protein MAD2 [Arabidopsis thaliana] gi|12230292|sp|Q9LU93.1|MAD2_ARATH RecName: Full=Mitotic spindle checkpoint protein MAD2 gi|9279603|dbj|BAB01061.1| cell cycle checkpoint protein MAD2-like [Arabidopsis thaliana] gi|37202030|gb|AAQ89630.1| At3g25980 [Arabidopsis thaliana] gi|51968734|dbj|BAD43059.1| putative mitotic checkpoint protein [Arabidopsis thaliana] gi|51970868|dbj|BAD44126.1| putative mitotic checkpoint protein [Arabidopsis thaliana] gi|332643576|gb|AEE77097.1| mitotic spindle checkpoint protein MAD2 [Arabidopsis thaliana]	209	209	1.00E-115	100.0	95.7	99.0	mitotic spindle checkpoint protein MAD2	gbpln	Arabidopsis thaliana	AT3G25980.1 | Symbols: MAD2 | DNA-binding HORMA family protein | chr3:9503232-9504402 FORWARD LENGTH=209	209	209	1.00E-118	100.0	95.7	99.0
Rsa1.0_00038.1.g2268.t1	gb|EOA24007.1| hypothetical protein CARUB_v10017220mg [Capsella rubella] gi|482559817|gb|EOA24008.1| hypothetical protein CARUB_v10017220mg [Capsella rubella]	418	455	1.00E-167	108.9	78.2	85.9	hypothetical protein CARUB_v10017220mg	gbpln	Capsella rubella	AT3G26000.1 | Symbols: | Ribonuclease inhibitor | chr3:9507042-9508542 REVERSE LENGTH=453	418	453	1.00E-155	108.4	72.0	81.8
Rsa1.0_00038.1.g2269.t1	dbj|BAB01067.1| acetyltranferase-like protein [Arabidopsis thaliana]	458	455	0	99.3	82.3	90.6	acetyltranferase-like protein	gbpln	Arabidopsis thaliana	AT3G26040.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:9519741-9521069 FORWARD LENGTH=442	458	442	0	96.5	79.9	88.0
Rsa1.0_00038.1.g2270.t1	ref|NP_189238.2| regulator of G-protein signaling 1 [Arabidopsis thaliana] gi|75299756|sp|Q8H1F2.1|RGS1_ARATH RecName: Full=Regulator of G-protein signaling 1; Short=AtRGS1; AltName: Full=Putative uncharacterized protein At3g26090 gi|23297446|gb|AAN12971.1| unknown protein [Arabidopsis thaliana] gi|332643595|gb|AEE77116.1| regulator of G-protein signaling 1 [Arabidopsis thaliana]	470	459	0	97.7	79.8	86.4	regulator of G-protein signaling 1	gbpln	Arabidopsis thaliana	AT3G26090.1 | Symbols: RGS1, ATRGS1 | G-protein coupled receptors;GTPase activators | chr3:9532883-9535410 FORWARD LENGTH=459	470	459	0	97.7	79.8	86.4
Rsa1.0_00038.1.g2271.t1	ref|XP_002875307.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] gi|297321145|gb|EFH51566.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	541	533	0	98.5	88.0	93.7	regulator of chromosome condensation family protein	gbpln	Arabidopsis lyrata	AT3G26100.2 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:9538063-9540149 FORWARD LENGTH=532	541	532	0	98.3	86.7	93.0
Rsa1.0_00038.1.g2272.t1	ref|XP_002875308.1| hypothetical protein ARALYDRAFT_484375 [Arabidopsis lyrata subsp. lyrata] gi|297321146|gb|EFH51567.1| hypothetical protein ARALYDRAFT_484375 [Arabidopsis lyrata subsp. lyrata]	121	128	2.00E-17	105.8	60.3	66.9	hypothetical protein ARALYDRAFT_484375	gbpln	Arabidopsis lyrata	AT3G26110.1 | Symbols: | Anther-specific protein agp1-like | chr3:9541573-9541959 FORWARD LENGTH=128	121	128	6.00E-17	105.8	61.2	67.8
Rsa1.0_00038.1.g2273.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	139	442	3.00E-35	318.0	56.8	71.9	hypothetical protein 24.t00017	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00038.1.g2274.t3	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	365	258	4.00E-46	70.7	27.9	34.2	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT5G41220.1 | Symbols: ATGSTT3, GST10C, GSTT3 | glutathione S-transferase THETA 3 | chr5:16494560-16496969 REVERSE LENGTH=590	365	590	2.00E-41	161.6	24.7	29.6
Rsa1.0_00038.1.g2275.t1	ref|NP_189243.1| cytochrome P450, family 86, subfamily C, polypeptide 2 [Arabidopsis thaliana] gi|11994429|dbj|BAB02431.1| cytochrome P-450-like protein [Arabidopsis thaliana] gi|332643602|gb|AEE77123.1| cytochrome P450, family 86, subfamily C, polypeptide 2 [Arabidopsis thaliana]	533	541	0	101.5	89.1	94.4	cytochrome P450, family 86, subfamily C, polypeptide 2	gbpln	Arabidopsis thaliana	AT3G26125.1 | Symbols: CYP86C2 | cytochrome P450, family 86, subfamily C, polypeptide 2 | chr3:9551812-9553437 FORWARD LENGTH=541	533	541	0	101.5	89.1	94.4
Rsa1.0_00038.1.g2276.t1	ref|XP_002876956.1| CYP71B4 [Arabidopsis lyrata subsp. lyrata] gi|297322794|gb|EFH53215.1| CYP71B4 [Arabidopsis lyrata subsp. lyrata]	499	502	0	100.6	69.5	81.2	CYP71B4	gbpln	Arabidopsis lyrata	AT3G26280.1 | Symbols: CYP71B4 | cytochrome P450, family 71, subfamily B, polypeptide 4 | chr3:9630358-9631970 REVERSE LENGTH=504	499	504	0	101.0	69.9	82.2
Rsa1.0_00038.1.g2277.t1	ref|XP_002876956.1| CYP71B4 [Arabidopsis lyrata subsp. lyrata] gi|297322794|gb|EFH53215.1| CYP71B4 [Arabidopsis lyrata subsp. lyrata]	499	502	0	100.6	71.3	82.8	CYP71B4	gbpln	Arabidopsis lyrata	AT3G26280.1 | Symbols: CYP71B4 | cytochrome P450, family 71, subfamily B, polypeptide 4 | chr3:9630358-9631970 REVERSE LENGTH=504	499	504	0	101.0	70.1	83.0
Rsa1.0_00038.1.g2278.t1	gb|EOA26964.1| hypothetical protein CARUB_v10023060mg [Capsella rubella]	247	502	1.00E-71	203.2	55.9	66.8	hypothetical protein CARUB_v10023060mg	gbpln	Capsella rubella	AT2G38110.1 | Symbols: ATGPAT6, GPAT6 | glycerol-3-phosphate acyltransferase 6 | chr2:15952816-15955364 REVERSE LENGTH=501	247	501	5.00E-73	202.8	57.1	68.8

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<tr><td>Rsa1.0_00038.1.g2280.t1</td><td>gb|ABD64987.1| hypothetical protein 26.t00003 [Brassica oleracea]</td><td>234</td><td>330</td><td>1.00E-20</td><td>141.0</td><td>23.1</td><td>25.2</td><td>hypothetical protein 26.t00003</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>234</td><td>303</td><td>7.00E-17</td><td>129.5</td><td>22.6</td><td>31.2</td></tr>
<tr><td>Rsa1.0_00038.1.g2281.t1</td><td>gb|EOA25173.1| hypothetical protein CARUB_v10018485mg [Capsella rubella]</td><td>235</td><td>499</td><td>5.00E-71</td><td>212.3</td><td>57.0</td><td>61.7</td><td>hypothetical protein CARUB_v10018485mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G26330.1 | Symbols: CYP71B37 | cytochrome P450, family 71, subfamily B, polypeptide 37 | chr3:9646873-9648536 REVERSE LENGTH=500</td><td>235</td><td>500</td><td>8.00E-68</td><td>212.8</td><td>53.2</td><td>58.7</td></tr>
<tr><td>Rsa1.0_00038.1.g2282.t4</td><td>ref|NP_177511.1| mate efflux-like protein [Arabidopsis thaliana] gi|12324218|gb|AAG52084.1|AC012679_22 putative integral membrane protein; 47574-45498 [Arabidopsis thaliana] gi|332197378|gb|AEE35499.1| mate efflux-like protein [Arabidopsis thaliana]</td><td>462</td><td>476</td><td>1.00E-128</td><td>103.0</td><td>55.2</td><td>57.4</td><td>mate efflux-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G73700.1 | Symbols: | MATE efflux family protein | chr1:27717554-27719630 REVERSE LENGTH=476</td><td>462</td><td>476</td><td>1.00E-131</td><td>103.0</td><td>55.2</td><td>57.4</td></tr>
<tr><td>Rsa1.0_00039.1.g2283.t1</td><td>gb|EOA14133.1| hypothetical protein CARUB_v10027278mg [Capsella rubella]</td><td>161</td><td>160</td><td>3.00E-78</td><td>99.4</td><td>87.6</td><td>93.2</td><td>hypothetical protein CARUB_v10027278mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G63070.1 | Symbols: | Ribosomal protein S19 family protein | chr5:25299178-25299660 REVERSE LENGTH=160</td><td>161</td><td>160</td><td>5.00E-78</td><td>99.4</td><td>85.7</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00039.1.g2284.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00039.1.g2285.t1</td><td>ref|XP_002864835.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310670|gb|EFH41094.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>80</td><td>82</td><td>2.00E-18</td><td>102.5</td><td>68.8</td><td>80.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63085.1 | Symbols: | Plant thionin family protein | chr5:25302862-25303230 FORWARD LENGTH=81</td><td>80</td><td>81</td><td>3.00E-14</td><td>101.3</td><td>61.3</td><td>70.0</td></tr>
<tr><td>Rsa1.0_00039.1.g2286.t1</td><td>gb|EOA13869.1| hypothetical protein CARUB_v10026971mg [Capsella rubella]</td><td>247</td><td>263</td><td>1.00E-125</td><td>106.5</td><td>90.7</td><td>96.0</td><td>hypothetical protein CARUB_v10026971mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G63060.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr5:25295082-25296714 REVERSE LENGTH=263</td><td>247</td><td>263</td><td>1.00E-125</td><td>106.5</td><td>89.1</td><td>96.4</td></tr>
<tr><td>Rsa1.0_00039.1.g2287.t1</td><td>gb|EOA13639.1| hypothetical protein CARUB_v10026710mg [Capsella rubella]</td><td>346</td><td>345</td><td>1.00E-173</td><td>99.7</td><td>81.5</td><td>91.3</td><td>hypothetical protein CARUB_v10026710mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G63050.1 | Symbols: EMB2759 | embryo defective 2759 | chr5:25293109-25294799 FORWARD LENGTH=345</td><td>346</td><td>345</td><td>1.00E-170</td><td>99.7</td><td>79.8</td><td>89.6</td></tr>
<tr><td>Rsa1.0_00039.1.g2288.t1</td><td>ref|XP_002884098.1| hypothetical protein ARALYDRAFT_343424 [Arabidopsis lyrata subsp. lyrata] gi|297329938|gb|EFH60357.1| hypothetical protein ARALYDRAFT_343424 [Arabidopsis lyrata subsp. lyrata]</td><td>355</td><td>407</td><td>1.00E-144</td><td>114.6</td><td>75.8</td><td>81.1</td><td>hypothetical protein ARALYDRAFT_343424</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63040.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G48460.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:25288504-25290326 FORWARD LENGTH=366</td><td>355</td><td>366</td><td>1.00E-143</td><td>103.1</td><td>76.9</td><td>82.3</td></tr>
<tr><td>Rsa1.0_00039.1.g2289.t1</td><td>ref|XP_002866529.1| hypothetical protein ARALYDRAFT_919585 [Arabidopsis lyrata subsp. lyrata] gi|297312364|gb|EFH42788.1| hypothetical protein ARALYDRAFT_919585 [Arabidopsis lyrata subsp. lyrata]</td><td>125</td><td>125</td><td>2.00E-65</td><td>100.0</td><td>96.8</td><td>98.4</td><td>hypothetical protein ARALYDRAFT_919585</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63030.1 | Symbols: | Thioredoxin superfamily protein | chr5:25286352-25287517 FORWARD LENGTH=125</td><td>125</td><td>125</td><td>6.00E-66</td><td>100.0</td><td>92.8</td><td>98.4</td></tr>
<tr><td>Rsa1.0_00039.1.g2290.t1</td><td>ref|XP_002864830.1| EMB1692 [Arabidopsis lyrata subsp. lyrata] gi|297310665|gb|EFH41089.1| EMB1692 [Arabidopsis lyrata subsp. lyrata]</td><td>488</td><td>492</td><td>0</td><td>100.8</td><td>82.8</td><td>90.4</td><td>EMB1692</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G62990.1 | Symbols: emb1692 | Ubiquitin carboxyl-terminal hydrolase family protein | chr5:25277828-25279312 FORWARD LENGTH=494</td><td>488</td><td>494</td><td>0</td><td>101.2</td><td>78.5</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00039.1.g2291.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00039.1.g2292.t1</td><td>ref|XP_002866526.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312361|gb|EFH42785.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>100</td><td>177</td><td>9.00E-23</td><td>177.0</td><td>57.0</td><td>66.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00039.1.g2293.t1	dbj|BAB08839.1| unnamed protein product [Arabidopsis thaliana]	334	317	1.00E−133	94.9	77.2	80.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G62960.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10660.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr5:25269444-25271533 FORWARD LENGTH=347	334	347	1.00E−127	103.9	66.2	69.2
Rsa1.0_00039.1.g2294.t1	ref|NP_201100.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana] gi|334188590|ref|NP_001190602.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana] gi|32815911|gb|AAP88340.1| At5g62950 [Arabidopsis thaliana] gi|110743157|dbj|BAE99470.1| hypothetical protein [Arabidopsis thaliana] gi|332010294|gb|AED97677.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana] gi|332010296|gb|AED97679.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana]	160	139	2.00E−32	86.9	53.1	61.3	RNA polymerase II, Rpb4, core protein	gbpln	Arabidopsis thaliana	AT5G62950.3 | Symbols: | RNA polymerase II, Rpb4, core protein | chr5:25262355-25263033 REVERSE LENGTH=139	160	139	9.00E−35	86.9	53.1	61.3
Rsa1.0_00039.1.g2295.t1	ref|XP_002866523.1| hypothetical protein ARALYDRAFT_919576 [Arabidopsis lyrata subsp. lyrata] gi|297312358|gb|EFH42782.1| hypothetical protein ARALYDRAFT_919576 [Arabidopsis lyrata subsp. lyrata]	394	375	1.00E−120	95.2	62.7	68.5	hypothetical protein ARALYDRAFT_919576	gbpln	Arabidopsis lyrata	AT5G62940.1 | Symbols: HCA2, DOF5.6 | Dof-type zinc finger DNA-binding family protein | chr5:25257183-25258504 REVERSE LENGTH=372	394	372	1.00E−117	94.4	63.2	68.5
Rsa1.0_00039.1.g2296.t3	ref|NP_201094.1| nucleobase-ascorbate transporter 6 [Arabidopsis thaliana] gi|79600443|ref|NP_851251.2| nucleobase-ascorbate transporter 6 [Arabidopsis thaliana] gi|145323680|ref|NP_001032127.2| nucleobase-ascorbate transporter 6 [Arabidopsis thaliana] gi|122064607|sp|Q27GI3.2|NAT6_ARATH RecName: Full=Nucleobase-ascorbate transporter 6; Short=AtNAT6 gi|21326025|gb|AAM47573.1|AF466198_1 putative permease 1 [Arabidopsis thaliana] gi|10177467|dbj|BAB10858.1| permease 1 [Arabidopsis thaliana] gi|332010285|gb|AED97668.1| nucleobase-ascorbate transporter 6 [Arabidopsis thaliana] gi|332010286|gb|AED97669.1| nucleobase-ascorbate transporter 6 [Arabidopsis thaliana] gi|332010287|gb|AED97670.1| nucleobase-ascorbate transporter 6 [Arabidopsis thaliana]	563	532	0	94.5	89.3	90.6	nucleobase-ascorbate transporter 6	gbpln	Arabidopsis thaliana	AT5G62890.3 | Symbols: | Xanthine/uracil permease family protein | chr5:25243723-25247075 FORWARD LENGTH=532	563	532	0	94.5	89.3	90.6
Rsa1.0_00039.1.g2297.t1	ref|XP_002866520.1| hypothetical protein ARALYDRAFT_919569 [Arabidopsis lyrata subsp. lyrata] gi|297312355|gb|EFH42779.1| hypothetical protein ARALYDRAFT_919569 [Arabidopsis lyrata subsp. lyrata]	1500	1597	0	106.5	78.7	86.0	hypothetical protein ARALYDRAFT_919569	gbpln	Arabidopsis lyrata	AT3G48050.2 | Symbols: | BAH domain ;TFIIS helical bundle-like domain | chr3:17734270-17739412 REVERSE LENGTH=1613	1500	1613	0	107.5	26.9	32.7
Rsa1.0_00039.1.g2298.t1	ref|XP_002866520.1| hypothetical protein ARALYDRAFT_919569 [Arabidopsis lyrata subsp. lyrata] gi|297312355|gb|EFH42779.1| hypothetical protein ARALYDRAFT_919569 [Arabidopsis lyrata subsp. lyrata]	1398	1597	0	114.2	47.7	52.8	hypothetical protein ARALYDRAFT_919569	gbpln	Arabidopsis lyrata	AT3G48050.2 | Symbols: | BAH domain ;TFIIS helical bundle-like domain | chr3:17734270-17739412 REVERSE LENGTH=1613	1398	1613	0	115.4	26.0	28.5

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<tr><td>Rsa1.0_00039.1.g2299.t1</td><td>ref|NP_201093.1| Rac-like GTP-binding protein ARAC10 [Arabidopsis thaliana] gi|297793877|ref|XP_002864823.1| hypothetical protein ARALYDRAFT_496470 [Arabidopsis lyrata subsp. lyrata] gi|51701730|sp|O82481.1|RAC10_ARATH RecName: Full=Rac-like GTP-binding protein ARAC10; AltName: Full=GTPase protein ROP11 gi|7211193|gb|AAF40238.1|AF115467_1 Arac10 [Arabidopsis thaliana] gi|3702964|gb|AAC63014.1| rac GTP binding protein Arac10 [Arabidopsis thaliana] gi|10177466|dbj|BAB10857.1| rac GTP binding protein Arac10 [Arabidopsis thaliana] gi|27754724|gb|AAO22805.1| putative GTP binding protein Arac10 [Arabidopsis thaliana] gi|28394091|gb|AAO42453.1| putative GTP binding protein Arac10 [Arabidopsis thaliana] gi|51971983|dbj|BAD44656.1| Arac10 [Arabidopsis thaliana] gi|297310658|gb|EFH41082.1| hypothetical protein ARALYDRAFT_496470 [Arabidopsis lyrata subsp. lyrata] gi|332010284|gb|AED97667.1| Rac-like GTP-binding protein ARAC10 [Arabidopsis thaliana]</td><td>216</td><td>215</td><td>1.00E-113</td><td>99.5</td><td>97.7</td><td>99.5</td><td>Rac-like GTP-binding protein ARAC10</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G62880.1 | Symbols: ARAC10, ATRAC10, ATROP11, RAC10 | RAC-like 10 | chr5:25237236-25238939 FORWARD LENGTH=215</td><td>216</td><td>215</td><td>1.00E-116</td><td>99.5</td><td>97.7</td><td>99.5</td></tr>
<tr><td>Rsa1.0_00039.1.g2300.t1</td><td>ref|NP_201091.2| nodulin MtN3-like protein [Arabidopsis thaliana] gi|322967651|sp|Q9FM10.2|SWET5_ARATH RecName: Full=Bidirectional sugar transporter SWEET5; Short=AtSWEET5; AltName: Full=Protein VEGETATIVE CELL EXPRESSED 1; Short=AtVEX1 gi|332010281|gb|AED97664.1| bidirectional sugar transporter SWEET5 [Arabidopsis thaliana]</td><td>240</td><td>240</td><td>1.00E-123</td><td>100.0</td><td>87.9</td><td>95.8</td><td>nodulin MtN3-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G62850.1 | Symbols: AtVEX1, SWEET5, AtSWEET5 | Nodulin MtN3 family protein | chr5:25230204-25231527 REVERSE LENGTH=240</td><td>240</td><td>240</td><td>1.00E-126</td><td>100.0</td><td>87.9</td><td>95.8</td></tr>
<tr><td>Rsa1.0_00039.1.g2301.t1</td><td>ref|XP_002864820.1| hypothetical protein ARALYDRAFT_496464 [Arabidopsis lyrata subsp. lyrata] gi|297310655|gb|EFH41079.1| hypothetical protein ARALYDRAFT_496464 [Arabidopsis lyrata subsp. lyrata]</td><td>493</td><td>515</td><td>0</td><td>104.5</td><td>79.5</td><td>86.8</td><td>hypothetical protein ARALYDRAFT_496464</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G62810.1 | Symbols: PEX14, ATPEX14, PED2 | peroxin 14 | chr5:25220323-25223571 FORWARD LENGTH=507</td><td>493</td><td>507</td><td>0</td><td>102.8</td><td>79.5</td><td>85.8</td></tr>
<tr><td>Rsa1.0_00039.1.g2302.t2</td><td>ref|XP_002866510.1| 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Arabidopsis lyrata subsp. lyrata] gi|297312345|gb|EFH42769.1| 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Arabidopsis lyrata subsp. lyrata]</td><td>472</td><td>476</td><td>0</td><td>100.8</td><td>96.0</td><td>98.1</td><td>1-deoxy-D-xylulose-5-phosphate reductoisomerase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G62790.1 | Symbols: DXR, PDE129 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase | chr5:25214358-25217292 REVERSE LENGTH=477</td><td>472</td><td>477</td><td>0</td><td>101.1</td><td>96.4</td><td>98.3</td></tr>
<tr><td>Rsa1.0_00039.1.g2303.t1</td><td>dbj|BAE99884.1| hypothetical protein [Arabidopsis thaliana]</td><td>223</td><td>268</td><td>4.00E-71</td><td>120.2</td><td>72.6</td><td>80.7</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G62770.1 | Symbols: | Protein of unknown function (DUF1645) | chr5:25210564-25211370 FORWARD LENGTH=268</td><td>223</td><td>268</td><td>5.00E-65</td><td>120.2</td><td>72.6</td><td>81.2</td></tr>
<tr><td>Rsa1.0_00039.1.g2304.t1</td><td>gb|EOA13897.1| hypothetical protein CARUB_v10027013mg [Capsella rubella]</td><td>255</td><td>243</td><td>8.00E-98</td><td>95.3</td><td>77.6</td><td>84.7</td><td>hypothetical protein CARUB_v10027013mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G62720.1 | Symbols: | Integral membrane HPP family protein | chr5:25191969-25194845 FORWARD LENGTH=243</td><td>255</td><td>243</td><td>1.00E-99</td><td>95.3</td><td>76.1</td><td>83.9</td></tr>
<tr><td>Rsa1.0_00039.1.g2305.t2</td><td>ref|NP_201077.2| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|26451750|dbj|BAC42970.1| putative receptor like protein kinase [Arabidopsis thaliana] gi|224589741|gb|ACN59402.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332010262|gb|AED97645.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]</td><td>193</td><td>604</td><td>5.00E-32</td><td>313.0</td><td>37.3</td><td>38.9</td><td>leucine-rich repeat protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G62710.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:25187438-25190325 FORWARD LENGTH=604</td><td>193</td><td>604</td><td>2.00E-34</td><td>313.0</td><td>37.3</td><td>38.9</td></tr>
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Rsa1.0_00039.1.g2306.t1	ref|NP_201074.1| putative peptide/nitrate transporter [Arabidopsis thaliana] gi|75180586|sp|Q9LV10.1|PTR53_ARATH RecName: Full=Probable peptide/nitrate transporter At5g62680 gi|8809664|dbj|BAA97215.1| peptide transporter [Arabidopsis thaliana] gi|222423295|dbj|BAH19623.1| AT5G62680 [Arabidopsis thaliana] gi|332010259|gb|AED97642.1| probable peptide/nitrate transporter [Arabidopsis thaliana]	600	616	0	102.7	86.8	93.2	putative peptide/nitrate transporter	gbpln	Arabidopsis thaliana	AT5G62680.1 | Symbols: | Major facilitator superfamily protein | chr5:25165430-25167822 REVERSE LENGTH=616	600	616	0	102.7	86.8	93.2
Rsa1.0_00039.1.g2307.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00039.1.g2308.t1	gb|EOA13406.1| hypothetical protein CARUB_v10026444mg, partial [Capsella rubella]	416	430	1.00E-114	103.4	55.8	68.0	hypothetical protein CARUB_v10026444mg, partial	gbpln	Capsella rubella	AT5G62660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:25156326-25157465 REVERSE LENGTH=379	416	379	1.00E-112	91.1	50.7	62.7
Rsa1.0_00039.1.g2309.t1	ref|XP_002866500.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297312335|gb|EFH42759.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	118	282	3.00E-28	239.0	54.2	59.3	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT5G62610.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:25133117-25134600 REVERSE LENGTH=281	118	281	4.00E-30	238.1	53.4	58.5
Rsa1.0_00039.1.g2310.t1	ref|XP_002886534.1| hypothetical protein ARALYDRAFT_315221 [Arabidopsis lyrata subsp. lyrata] gi|297332375|gb|EFH62793.1| hypothetical protein ARALYDRAFT_315221 [Arabidopsis lyrata subsp. lyrata]	586	586	0	100.0	84.8	91.3	hypothetical protein ARALYDRAFT_315221	gbpln	Arabidopsis lyrata	AT1G61560.1 | Symbols: MLO6, ATMLO6 | Seven transmembrane MLO family protein | chr1:22708875-22712032 REVERSE LENGTH=583	586	583	0	99.5	84.6	91.3
Rsa1.0_00039.1.g2311.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00039.1.g2312.t1	ref|XP_002886531.1| hypothetical protein ARALYDRAFT_893358 [Arabidopsis lyrata subsp. lyrata] gi|297332372|gb|EFH62790.1| hypothetical protein ARALYDRAFT_893358 [Arabidopsis lyrata subsp. lyrata]	75	80	3.00E-18	106.7	62.7	73.3	hypothetical protein ARALYDRAFT_893358	gbpln	Arabidopsis lyrata	AT1G61566.1 | Symbols: RALFL9 | ralf-like 9 | chr1:22717265-22717492 REVERSE LENGTH=75	75	75	1.00E-20	100.0	64.0	70.7
Rsa1.0_00039.1.g2313.t1	gb|EOA35572.1| hypothetical protein CARUB_v10020781mg [Capsella rubella]	271	273	1.00E-140	100.7	95.9	98.2	hypothetical protein CARUB_v10020781mg	gbpln	Capsella rubella	AT1G61520.3 | Symbols: LHCA3 | photosystem I light harvesting complex gene 3 | chr1:22700152-22701149 FORWARD LENGTH=273	271	273	1.00E-141	100.7	94.5	98.2
Rsa1.0_00039.1.g2314.t1	ref|NP_176343.2| S-locus lectin protein kinase-like protein [Arabidopsis thaliana] gi|313471784|sp|O64771.2|Y1148_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At1g61480; Flags: Precursor gi|332195722|gb|AEE33843.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	806	809	0	100.4	77.9	86.6	S-locus lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G61480.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:22681420-22684404 REVERSE LENGTH=809	806	809	0	100.4	77.9	86.6
Rsa1.0_00039.1.g2315.t1	ref|XP_004295385.1| PREDICTED: uncharacterized protein LOC101312912 [Fragaria vesca subsp. vesca]	1628	1583	0	97.2	47.5	62.0	PREDICTED: uncharacterized protein LOC101312912	gbpln	Fragaria vesca	AT1G61490.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:22685154-22688267 REVERSE LENGTH=804	1628	804	0	49.4	37.6	41.6
Rsa1.0_00039.1.g2316.t1	ref|NP_176334.1| putative S-locus protein kinase [Arabidopsis thaliana] gi|75099193|sp|O64781.1|Y1639_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At1g61390; Flags: Precursor gi|3056591|gb|AAC13902.1|AAC13902 T1F9.12 [Arabidopsis thaliana] gi|332195709|gb|AEE33830.1| putative S-locus protein kinase [Arabidopsis thaliana]	783	831	0	106.1	83.1	90.5	putative S-locus protein kinase	gbpln	Arabidopsis thaliana	AT1G61390.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:22650338-22653639 REVERSE LENGTH=831	783	831	0	106.1	83.1	90.5

Rsa1.0_00039.1.g2317.t1	ref|NP_564775.1| protein S-domain-1 29 [Arabidopsis thaliana] gi|75099194|sp|O64782.1|SD129_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase SD1-29; AltName: Full=S-domain-1 (SD1) receptor kinase 29; Short=SD1-29; Flags: Precursor gi|3056592|gb|AAC13903.1|AAC13903 T1F9.13 [Arabidopsis thaliana] gi|19699075|gb|AAL90905.1| At1g61380/T1F9_13 [Arabidopsis thaliana] gi|23308469|gb|AAN18204.1| At1g61380/T1F9_13 [Arabidopsis thaliana] gi|332195708|gb|AEE33829.1| G-type lectin S-receptor-like serine/threonine-protein kinase SD1-29 [Arabidopsis thaliana]	813	805	0	99.0	78.8	86.3	protein S-domain-1 29	gbpln	Arabidopsis thaliana	AT1G61380.1 | Symbols: SD1-29 | S-domain-1 29 | chr1:22646277-22649401 REVERSE LENGTH=805	813	805	0	99.0	78.8	86.3
Rsa1.0_00039.1.g2318.t1	ref|XP_002888089.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297333930|gb|EFH64348.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	650	572	0	88.0	73.5	81.1	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT1G61350.1 | Symbols: | ARM repeat superfamily protein | chr1:22634099-22635820 FORWARD LENGTH=573	650	573	0	88.2	73.4	80.5
Rsa1.0_00039.1.g2319.t1	ref|XP_002886553.1| hypothetical protein ARALYDRAFT_893390 [Arabidopsis lyrata subsp. lyrata] gi|297332394|gb|EFH62812.1| hypothetical protein ARALYDRAFT_893390 [Arabidopsis lyrata subsp. lyrata]	127	352	4.00E-52	277.2	81.9	86.6	hypothetical protein ARALYDRAFT_893390	gbpln	Arabidopsis lyrata	AT1G61260.1 | Symbols: | Protein of unknown function (DUF761) | chr1:22593756-22594986 REVERSE LENGTH=344	127	344	1.00E-54	270.9	81.9	87.4
Rsa1.0_00039.1.g2320.t1	gb|EOA35839.1| hypothetical protein CARUB_v10021081mg [Capsella rubella]	113	158	3.00E-22	139.8	76.1	80.5	hypothetical protein CARUB_v10021081mg	gbpln	Capsella rubella	AT1G61255.1 | Symbols: | BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT4G21620.2); Has 58 Blast hits to 58 proteins in 12 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:22589260-22589691 REVERSE LENGTH=143	113	143	3.00E-19	126.5	56.6	61.1
Rsa1.0_00039.1.g2321.t1	ref|NP_176320.1| secretory carrier-associated membrane protein 3 [Arabidopsis thaliana] gi|75185088|sp|Q9M5P2.1|SCAM3_ARATH RecName: Full=Secretory carrier-associated membrane protein 3; Short=AtSC3; Short=Secretory carrier membrane protein 3 gi|7109228|gb|AAF36686.1|AF225920_1 secretory carrier membrane protein [Arabidopsis thaliana] gi|15027863|gb|AAK76462.1| putative secretory carrier membrane protein [Arabidopsis thaliana] gi|19310673|gb|AAL85067.1| putative secretory carrier membrane protein [Arabidopsis thaliana] gi|21555163|gb|AAM63793.1| secretory carrier membrane protein [Arabidopsis thaliana] gi|332195690|gb|AEE33811.1| secretory carrier-associated membrane protein 3 [Arabidopsis thaliana]	292	289	1.00E-154	99.0	91.1	95.2	secretory carrier-associated membrane protein 3	gbpln	Arabidopsis thaliana	AT1G61250.1 | Symbols: SC3 | secretory carrier 3 | chr1:22586035-22588664 FORWARD LENGTH=289	292	289	1.00E-156	99.0	91.1	95.2
Rsa1.0_00039.1.g2322.t1	ref|XP_002888099.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333940|gb|EFH64358.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	365	588	1.00E-160	161.1	75.3	85.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G57570.1 | Symbols: | Mannose-binding lectin superfamily protein | chr1:21321717-21324284 FORWARD LENGTH=614	365	614	1.00E-148	168.2	69.6	82.7
Rsa1.0_00039.1.g2323.t1	gb|EOA33627.1| hypothetical protein CARUB_v10019789mg [Capsella rubella]	861	846	0	98.3	61.8	73.4	hypothetical protein CARUB_v10019789mg	gbpln	Capsella rubella	AT1G61190.1 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr1:22557602-22560687 FORWARD LENGTH=967	861	967	0	112.3	63.4	74.2
Rsa1.0_00039.1.g2324.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00039.1.g2325.t3	gb|AAD24652.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	994	977	4.00E-75	98.3	20.4	29.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G41550.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16617232-16620785 REVERSE LENGTH=1085	994	1085	2.00E-64	109.2	11.6	14.1
Rsa1.0_00039.1.g2326.t16	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00039.1.g2327.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	104	1213	7.00E-15	1166.3	45.2	68.3	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	104	289	6.00E-16	277.9	40.4	64.4

Rsa1.0_00039.1.g2328.t1	ref|XP_002888109.1| ANAC025 [Arabidopsis lyrata subsp. lyrata] gi|297333950|gb|EFH64368.1| ANAC025 [Arabidopsis lyrata subsp. lyrata]	319	326	1.00E-161	102.2	93.7	97.2	ANAC025	gbpln	Arabidopsis lyrata	AT1G61110.1 | Symbols: anac025, NAC025 | NAC domain containing protein 25 | chr1:22516730-22518055 FORWARD LENGTH=323	319	323	1.00E-163	101.3	94.7	97.8
Rsa1.0_00039.1.g2329.t1	#	#	#	#	#	#	#	-	----	----	AT3G61860.1 | Symbols: ATRSP31, RSP31, At-RS31, RS31 | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:22900311-22902159 REVERSE LENGTH=264	191	264	4.00E-11	138.2	16.8	19.4
Rsa1.0_00039.1.g2330.t1	ref|NP_974060.1| Toll-Interleukin-Resistance (TIR) domain-containing protein [Arabidopsis thaliana] gi|332195661|gb|AEE33782.1| Toll-Interleukin-Resistance (TIR) domain-containing protein [Arabidopsis thaliana]	198	188	3.00E-83	94.9	76.3	83.3	Toll-Interleukin-Resistance (TIR) domain-containing protein	gbpln	Arabidopsis thaliana	AT1G61105.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr1:22513616-22514492 REVERSE LENGTH=188	198	188	9.00E-86	94.9	76.3	83.3
Rsa1.0_00039.1.g2331.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00039.1.g2332.t1	ref|XP_002317226.1| predicted protein [Populus trichocarpa] gi|222860291|gb|EEE97838.1| predicted protein [Populus trichocarpa]	911	792	1.00E-170	86.9	45.0	58.2	predicted protein	gbpln	Populus trichocarpa	AT1G61080.1 | Symbols: | Hydroxyproline-rich glycoprotein family protein | chr1:22493194-22497019 REVERSE LENGTH=907	911	907	1.00E-142	99.6	33.2	34.5
Rsa1.0_00039.1.g2333.t1	gb|EOA34094.1| hypothetical protein CARUB_v10021594mg [Capsella rubella]	440	441	1.00E-178	100.2	78.6	86.6	hypothetical protein CARUB_v10021594mg	gbpln	Capsella rubella	AT1G61050.1 | Symbols: | alpha 1,4-glycosyltransferase family protein | chr1:22486736-22488043 FORWARD LENGTH=435	440	435	1.00E-176	98.9	78.4	86.6
Rsa1.0_00039.1.g2334.t1	ref|NP_564767.1| coatomer subunit zeta-1 [Arabidopsis thaliana] gi|75163941|sp|Q940S5.1|COPZ1_ARATH RecName: Full=Coatomer subunit zeta-1; AltName: Full=Zeta-1-coat protein; AltName: Full=Zeta-COP 1 gi|15450727|gb|AAK96635.1| At1g60970/T7P1_11 [Arabidopsis thaliana] gi|22137000|gb|AAM91345.1| At1g60970/T7P1_11 [Arabidopsis thaliana] gi|332195633|gb|AEE33754.1| coatomer subunit zeta-1 [Arabidopsis thaliana]	177	177	8.00E-89	100.0	90.4	95.5	coatomer subunit zeta-1	gbpln	Arabidopsis thaliana	AT1G60970.1 | Symbols: | SNARE-like superfamily protein | chr1:22448008-22449387 REVERSE LENGTH=177	177	177	3.00E-91	100.0	90.4	95.5
Rsa1.0_00039.1.g2335.t1	ref|XP_002886573.1| hypothetical protein ARALYDRAFT_315258 [Arabidopsis lyrata subsp. lyrata] gi|297332414|gb|EFH62832.1| hypothetical protein ARALYDRAFT_315258 [Arabidopsis lyrata subsp. lyrata]	372	429	1.00E-177	115.3	90.6	95.7	hypothetical protein ARALYDRAFT_315258	gbpln	Arabidopsis lyrata	AT1G60960.1 | Symbols: IRT3, ATIRT3 | iron regulated transporter 3 | chr1:22445410-22447060 REVERSE LENGTH=425	372	425	1.00E-176	114.2	88.7	93.8
Rsa1.0_00039.1.g2336.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00039.1.g2337.t1	dbj|BAJ33728.1| unnamed protein product [Thellungiella halophila]	148	148	2.00E-74	100.0	91.9	96.6	unnamed protein product	----	----	AT1G60950.1 | Symbols: FED A, ATFD2 | 2Fe-2S ferredoxin-like superfamily protein | chr1:22444565-22445011 FORWARD LENGTH=148	148	148	4.00E-76	100.0	91.9	95.9
Rsa1.0_00039.1.g2338.t1	gb|EOA37821.1| hypothetical protein CARUB_v10011995mg [Capsella rubella]	668	589	0	88.2	78.3	81.7	hypothetical protein CARUB_v10011995mg	gbpln	Capsella rubella	AT1G10950.1 | Symbols: TMN1, AtTMN1 | transmembrane nine 1 | chr1:3659322-3663622 FORWARD LENGTH=589	668	589	0	88.2	77.5	81.6
Rsa1.0_00040.1.g2339.t1	ref|XP_002873716.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319553|gb|EFH49975.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	219	685	7.00E-76	312.8	68.9	77.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G15250.1 | Symbols: FTSH6, ATFTSH6 | FTSH protease 6 | chr5:4950411-4952777 REVERSE LENGTH=688	219	688	2.00E-77	314.2	67.6	76.7
Rsa1.0_00040.1.g2340.t1	ref|XP_002873717.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] gi|297319554|gb|EFH49976.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	215	235	1.00E-86	109.3	79.1	86.5	structural constituent of ribosome	gbpln	Arabidopsis lyrata	AT5G15260.1 | Symbols: | Ribosomal protein L34e superfamily protein | chr5:4953646-4954350 REVERSE LENGTH=234	215	234	2.00E-87	108.8	78.1	87.0
Rsa1.0_00040.1.g2341.t4	ref|NP_001078588.1| uncharacterized protein [Arabidopsis thaliana] gi|62319943|dbj|BAD94032.1| hypothetical protein [Arabidopsis thaliana] gi|332004757|gb|AED92140.1| uncharacterized protein AT5G15265 [Arabidopsis thaliana]	59	83	4.00E-16	140.7	67.8	81.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G15265.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 5 Blast hits to 5 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:4956505-4957351 FORWARD LENGTH=83	59	83	7.00E-19	140.7	67.8	81.4

Rsa1.0_00040.1.g2342.t1	ref|XP_002873718.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319555|gb|EFH49977.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	537	548	0	102.0	85.8	93.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G15300.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:4968384-4970030 REVERSE LENGTH=548	537	548	0	102.0	85.8	93.3
Rsa1.0_00040.1.g2343.t1	dbj|BAJ34432.1| unnamed protein product [Thellungiella halophila]	314	326	1.00E-147	103.8	87.3	91.7	unnamed protein product	----	----	AT5G15310.1 | Symbols: ATMYB16, ATMIXTA, MYB16 | myb domain protein 16 | chr5:4974894-4976106 FORWARD LENGTH=326	314	326	1.00E-142	103.8	84.4	90.1
Rsa1.0_00040.1.g2344.t1	ref|NP_197036.2| uncharacterized protein [Arabidopsis thaliana] gi|26451598|dbj|BAC42896.1| GPI-anchored protein [Arabidopsis thaliana] gi|88010805|gb|ABD38855.1| At5g15320 [Arabidopsis thaliana] gi|332004765|gb|AED92148.1| uncharacterized protein AT5G15320 [Arabidopsis thaliana]	51	53	6.00E-12	103.9	78.4	86.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G15320.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01130.1); Has 64 Blast hits to 64 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:4977647-4978658 FORWARD LENGTH=53	51	53	1.00E-14	103.9	78.4	86.3
Rsa1.0_00040.1.g2345.t1	ref|XP_002882199.1| hypothetical protein ARALYDRAFT_477417 [Arabidopsis lyrata subsp. lyrata] gi|297328039|gb|EFH58458.1| hypothetical protein ARALYDRAFT_477417 [Arabidopsis lyrata subsp. lyrata]	417	564	1.00E-176	135.3	72.2	81.8	hypothetical protein ARALYDRAFT_477417	gbpln	Arabidopsis lyrata	AT3G01120.1 | Symbols: MTO1, CGS, ATCYS1, CGS1 | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr3:39234-41865 REVERSE LENGTH=563	417	563	1.00E-179	135.0	71.9	82.0
Rsa1.0_00040.1.g2346.t1	gb|EOA21138.1| hypothetical protein CARUB_v10001482mg [Capsella rubella]	320	318	1.00E-154	99.4	87.5	92.2	hypothetical protein CARUB_v10001482mg	gbpln	Capsella rubella	AT5G15330.1 | Symbols: ATSPX4, SPX4 | SPX domain gene 4 | chr5:4980595-4982043 FORWARD LENGTH=318	320	318	1.00E-153	99.4	87.2	92.5
Rsa1.0_00040.1.g2347.t1	ref|NP_197038.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75180838|sp|Q9LXE8.1|PP386_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g15340, mitochondrial; Flags: Precursor gi|7671503|emb|CAB89344.1| putative protein [Arabidopsis thaliana] gi|332004768|gb|AED92151.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	774	623	0	80.5	68.0	72.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G15340.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:4982273-4984144 REVERSE LENGTH=623	774	623	0	80.5	68.0	72.9
Rsa1.0_00040.1.g2348.t1	ref|NP_197043.1| tRNA/rRNA methyltransferase (SpoU) family protein [Arabidopsis thaliana] gi|7671508|emb|CAB89349.1| rRNA methylase-like protein [Arabidopsis thaliana] gi|110737570|dbj|BAF00727.1| rRNA methylase - like protein [Arabidopsis thaliana] gi|332004772|gb|AED92155.1| tRNA/rRNA methyltransferase (SpoU) family protein [Arabidopsis thaliana]	364	350	1.00E-145	96.2	76.1	81.0	tRNA/rRNA methyltransferase (SpoU) family protein	gbpln	Arabidopsis thaliana	AT5G15390.1 | Symbols: | tRNA/rRNA methyltransferase (SpoU) family protein | chr5:4995333-4997255 FORWARD LENGTH=350	364	350	1.00E-147	96.2	76.1	81.0
Rsa1.0_00040.1.g2349.t1	gb|ABG89128.1| UFD2 [synthetic construct]	1077	1037	0	96.3	87.3	91.6	UFD2	gbenv	synthetic construct	AT5G15400.1 | Symbols: | U-box domain-containing protein | chr5:4997764-5002907 REVERSE LENGTH=1038	1077	1038	0	96.4	87.3	91.6
Rsa1.0_00040.1.g2350.t1	dbj|BAJ33868.1| unnamed protein product [Thellungiella halophila]	733	722	0	98.5	92.1	94.8	unnamed protein product	----	----	AT5G15410.1 | Symbols: DND1, ATCNGC2, CNGC2 | Cyclic nucleotide-regulated ion channel family protein | chr5:5003460-5006763 REVERSE LENGTH=726	733	726	0	99.0	91.5	95.1
Rsa1.0_00040.1.g2351.t1	ref|NP_197051.2| alpha-1,4-galacturonosyltransferase [Arabidopsis thaliana] gi|75151049|sp|Q8GWT1.1|GAUTE_ARATH RecName: Full=Probable galacturonosyltransferase 14 gi|26452322|dbj|BAC43247.1| unknown protein [Arabidopsis thaliana] gi|29028910|gb|AAO64834.1| At5g15470 [Arabidopsis thaliana] gi|332004782|gb|AED92165.1| probable galacturonosyltransferase 14 [Arabidopsis thaliana]	562	532	0	94.7	85.1	89.3	alpha-1,4-galacturonosyltransferase	gbpln	Arabidopsis thaliana	AT5G15470.1 | Symbols: GAUT14 | galacturonosyltransferase 14 | chr5:5021433-5024168 REVERSE LENGTH=532	562	532	0	94.7	85.1	89.3

Rsa1.0_00040.1.g2352.t1	gb|EOA20540.1| hypothetical protein CARUB_v10000855mg [Capsella rubella] gi|482556349|gb|EOA20541.1| hypothetical protein CARUB_v10000855mg [Capsella rubella] gi|482556350|gb|EOA20542.1| hypothetical protein CARUB_v10000855mg [Capsella rubella]	480	480	0	100.0	98.5	99.4	hypothetical protein CARUB_v10000855mg	gbpln	Capsella rubella	AT5G15490.1 | Symbols: | UDP-glucose 6-dehydrogenase family protein | chr5:5027872-5029314 REVERSE LENGTH=480	480	480	0	100.0	97.3	99.2
Rsa1.0_00040.1.g2353.t1	gb|AEI16468.1| acetyl-CoA carboxylase biotin-containing subunit [Brassica rapa]	248	257	1.00E-117	103.6	90.7	94.8	acetyl-CoA carboxylase biotin-containing subunit	gbpln	Brassica rapa	AT5G15530.1 | Symbols: BCCP2, CAC1-B | biotin carboxyl carrier protein 2 | chr5:5038955-5040437 FORWARD LENGTH=255	248	255	3.00E-94	102.8	78.2	84.7
Rsa1.0_00040.1.g2354.t1	ref|XP_002873731.1| sister chromatid cohesion 2 [Arabidopsis lyrata subsp. lyrata] gi|297319568|gb|EFH49990.1| sister chromatid cohesion 2 [Arabidopsis lyrata subsp. lyrata]	1842	1847	0	100.3	86.5	91.5	sister chromatid cohesion 2	gbpln	Arabidopsis lyrata	AT5G15540.1 | Symbols: EMB2773, ATSCC2, SCC2 | PHD finger family protein | chr5:5047887-5057411 REVERSE LENGTH=1846	1842	1846	0	100.2	85.5	90.8
Rsa1.0_00040.1.g2355.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00040.1.g2356.t1	gb|EMJ16100.1| hypothetical protein PRUPE_ppa000160mg [Prunus persica]	846	1582	4.00E-56	187.0	20.9	27.8	hypothetical protein PRUPE_ppa000160mg	gbpln	Prunus persica	AT5G07980.1 | Symbols: | dentin sialophosphoprotein-related | chr5:2549432-2554669 REVERSE LENGTH=1501	846	1501	9.00E-44	177.4	12.5	18.4
Rsa1.0_00040.1.g2357.t1	ref|NP_197059.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|9755810|emb|CAC01754.1| putative protein [Arabidopsis thaliana] gi|17381110|gb|AAL36367.1| unknown protein [Arabidopsis thaliana] gi|20258961|gb|AAM14196.1| unknown protein [Arabidopsis thaliana] gi|332004793|gb|AED92176.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	414	433	0	104.6	82.9	90.8	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G15550.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:5059051-5062003 REVERSE LENGTH=433	414	433	0	104.6	82.9	90.8
Rsa1.0_00040.1.g2358.t1	ref|XP_002871671.1| hypothetical protein ARALYDRAFT_909531 [Arabidopsis lyrata subsp. lyrata] gi|297317508|gb|EFH47930.1| hypothetical protein ARALYDRAFT_909531 [Arabidopsis lyrata subsp. lyrata]	362	380	1.00E-147	105.0	75.4	83.4	hypothetical protein ARALYDRAFT_909531	gbpln	Arabidopsis lyrata	AT5G15570.1 | Symbols: | Bromodomain transcription factor | chr5:5066851-5067996 FORWARD LENGTH=381	362	381	1.00E-148	105.2	74.9	83.1
Rsa1.0_00040.1.g2359.t1	gb|EOA19910.1| hypothetical protein CARUB_v10000160mg [Capsella rubella]	913	931	0	102.0	83.7	90.5	hypothetical protein CARUB_v10000160mg	gbpln	Capsella rubella	AT5G15580.1 | Symbols: LNG1 | longifolia1 | chr5:5068495-5071930 REVERSE LENGTH=927	913	927	0	101.5	81.9	89.3
Rsa1.0_00040.1.g2360.t1	ref|NP_198644.1| PR5-like receptor kinase [Arabidopsis thaliana] gi|10177803|dbj|BAB11294.1| receptor serine/threonine kinase [Arabidopsis thaliana] gi|332006906|gb|AED94289.1| PR5-like receptor kinase [Arabidopsis thaliana]	948	665	0	70.1	37.3	44.7	PR5-like receptor kinase	gbpln	Arabidopsis thaliana	AT5G38280.1 | Symbols: PR5K | PR5-like receptor kinase | chr5:15293325-15295838 REVERSE LENGTH=665	948	665	0	70.1	37.3	44.7
Rsa1.0_00040.1.g2361.t1	gb|EOA21793.1| hypothetical protein CARUB_v10002258mg [Capsella rubella] gi|482557602|gb|EOA21794.1| hypothetical protein CARUB_v10002258mg [Capsella rubella]	130	127	3.00E-40	97.7	78.5	86.9	hypothetical protein CARUB_v10002258mg	gbpln	Capsella rubella	AT5G15600.1 | Symbols: SP1L4 | SPIRAL1-like4 | chr5:5078405-5078863 FORWARD LENGTH=127	130	127	1.00E-42	97.7	80.8	86.2
Rsa1.0_00040.1.g2362.t1	ref|NP_197069.1| reversibly glycosylated polypeptide 2 [Arabidopsis thaliana] gi|75174193|sp|Q9LFW1.1|RGP2_ARATH RecName: Full=UDP-arabinopyranose mutase 2; AltName: Full=Reversibly glycosylated polypeptide 2; Short=AtRGP2; AltName: Full=UDP-L-arabinose mutase 2 gi|9755610|emb|CAC01764.1| reversibly glycosylated polypeptide-2 (AtRGB) [Arabidopsis thaliana] gi|14532444|gb|AAK63950.1| AT5g15650/F14F8_30 [Arabidopsis thaliana] gi|21464559|gb|AAM52234.1| AT5g15650/F14F8_30 [Arabidopsis thaliana] gi|332004805|gb|AED92188.1| reversibly glycosylated polypeptide 2 [Arabidopsis thaliana]	357	360	0	100.8	96.6	98.6	reversibly glycosylated polypeptide 2	gbpln	Arabidopsis thaliana	AT5G15650.1 | Symbols: RGP2, ATRGP2 | reversibly glycosylated polypeptide 2 | chr5:5092203-5094093 FORWARD LENGTH=360	357	360	0	100.8	96.6	98.6
Rsa1.0_00040.1.g2363.t1	ref|XP_002890654.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297336496|gb|EFH66913.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	398	665	2.00E-80	167.1	44.0	58.8	F-box family protein	gbpln	Arabidopsis lyrata	AT5G15660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:5095652-5097041 FORWARD LENGTH=438	398	438	9.00E-82	110.1	46.5	61.6

Rsa1.0_00040.1.g2364.t1	ref|NP_197070.1| putative F-box protein [Arabidopsis thaliana] gi|75174192|sp|Q9LFW0.1|FB257_ARATH RecName: Full=Putative F-box protein At5g15660 gi|9755611|emb|CAC01765.1| putative protein [Arabidopsis thaliana] gi|332004806|gb|AED92189.1| putative F-box protein [Arabidopsis thaliana]	386	438	1.00E-90	113.5	49.7	66.6	putative F-box protein	gbpln	Arabidopsis thaliana	AT5G15660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:5095652-5097041 FORWARD LENGTH=438	386	438	2.00E-93	113.5	49.7	66.6
Rsa1.0_00040.1.g2365.t1	ref|XP_002871678.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297317515|gb|EFH47937.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	440	430	8.00E-77	97.7	39.8	52.3	F-box family protein	gbpln	Arabidopsis lyrata	AT5G15660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:5095652-5097041 FORWARD LENGTH=438	440	438	3.00E-79	99.5	39.8	54.5
Rsa1.0_00040.1.g2366.t1	ref|XP_002877486.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323324|gb|EFH53745.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	461	362	1.00E-108	78.5	45.8	53.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G09650.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3125978-3127126 FORWARD LENGTH=382	461	382	1.00E-102	82.9	48.4	58.1
Rsa1.0_00040.1.g2367.t1	gb|EOA20674.1| hypothetical protein CARUB_v10000986mg [Capsella rubella]	452	437	0	96.7	87.4	92.3	hypothetical protein CARUB_v10000986mg	gbpln	Capsella rubella	AT5G15730.2 | Symbols: CRLK2, AtCRLK2 | Protein kinase superfamily protein | chr5:5131284-5133046 FORWARD LENGTH=436	452	436	0	96.5	86.5	89.4
Rsa1.0_00040.1.g2368.t1	ref|NP_197078.2| O-fucosyltransferase family protein [Arabidopsis thaliana] gi|66792694|gb|AAY56449.1| At5g15740 [Arabidopsis thaliana] gi|110743719|dbj|BAE99696.1| hypothetical protein [Arabidopsis thaliana] gi|332004817|gb|AED92200.1| O-fucosyltransferase family protein [Arabidopsis thaliana]	509	508	0	99.8	91.4	96.3	O-fucosyltransferase family protein	gbpln	Arabidopsis thaliana	AT5G15740.1 | Symbols: | O-fucosyltransferase family protein | chr5:5134788-5136956 REVERSE LENGTH=508	509	508	0	99.8	91.4	96.3
Rsa1.0_00040.1.g2369.t1	ref|XP_002871683.1| hypothetical protein ARALYDRAFT_488420 [Arabidopsis lyrata subsp. lyrata] gi|297317520|gb|EFH47942.1| hypothetical protein ARALYDRAFT_488420 [Arabidopsis lyrata subsp. lyrata]	174	183	3.00E-67	105.2	81.6	87.9	hypothetical protein ARALYDRAFT_488420	gbpln	Arabidopsis lyrata	AT5G15760.1 | Symbols: | Ribosomal protein PSRP-3/Ycf65 | chr5:5143100-5143905 FORWARD LENGTH=183	174	183	4.00E-68	105.2	79.3	86.8
Rsa1.0_00040.1.g2370.t1	ref|XP_002873740.1| hypothetical protein ARALYDRAFT_909552 [Arabidopsis lyrata subsp. lyrata] gi|297319577|gb|EFH49999.1| hypothetical protein ARALYDRAFT_909552 [Arabidopsis lyrata subsp. lyrata]	159	149	6.00E-66	93.7	76.1	84.9	hypothetical protein ARALYDRAFT_909552	gbpln	Arabidopsis lyrata	AT5G15770.1 | Symbols: AtGNA1, GNA1 | glucose-6-phosphate acetyltransferase 1 | chr5:5144093-5144542 REVERSE LENGTH=149	159	149	8.00E-67	93.7	74.8	83.6
Rsa1.0_00040.1.g2371.t1	ref|XP_002873740.1| hypothetical protein ARALYDRAFT_909552 [Arabidopsis lyrata subsp. lyrata] gi|297319577|gb|EFH49999.1| hypothetical protein ARALYDRAFT_909552 [Arabidopsis lyrata subsp. lyrata]	160	149	1.00E-65	93.1	74.4	84.4	hypothetical protein ARALYDRAFT_909552	gbpln	Arabidopsis lyrata	AT5G15770.1 | Symbols: AtGNA1, GNA1 | glucose-6-phosphate acetyltransferase 1 | chr5:5144093-5144542 REVERSE LENGTH=149	160	149	4.00E-67	93.1	73.8	83.8
Rsa1.0_00040.1.g2372.t1	ref|XP_002873741.1| hypothetical protein ARALYDRAFT_488422 [Arabidopsis lyrata subsp. lyrata] gi|297319578|gb|EFH50000.1| hypothetical protein ARALYDRAFT_488422 [Arabidopsis lyrata subsp. lyrata]	361	363	2.00E-92	100.6	55.1	61.5	hypothetical protein ARALYDRAFT_488422	gbpln	Arabidopsis lyrata	AT5G15780.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:5144898-5146297 REVERSE LENGTH=401	361	401	2.00E-87	111.1	44.0	47.9
Rsa1.0_00040.1.g2373.t1	ref|NP_197083.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|42573377|ref|NP_974785.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|9755624|emb|CAC01778.1| putative protein [Arabidopsis thaliana] gi|22655214|gb|AAM98197.1| unknown protein [Arabidopsis thaliana] gi|30023690|gb|AAP13378.1| At5g15790 [Arabidopsis thaliana] gi|110738178|dbj|BAF01020.1| hypothetical protein [Arabidopsis thaliana] gi|332004822|gb|AED92205.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332004823|gb|AED92206.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	231	232	4.00E-98	100.4	79.7	90.9	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G15790.2 | Symbols: | RING/U-box superfamily protein | chr5:5149800-5150964 FORWARD LENGTH=232	231	232	1.00E-100	100.4	79.7	90.9

Rsa1.0_00040.1.g2374.t1	gb|AAA32732.1| transcription factor [Arabidopsis thaliana] gi|52547968|gb|AAU81987.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547972|gb|AAU81989.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547974|gb|AAU81990.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547976|gb|AAU81991.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547978|gb|AAU81992.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547980|gb|AAU81993.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547982|gb|AAU81994.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547984|gb|AAU81995.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547986|gb|AAU81996.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547988|gb|AAU81997.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547990|gb|AAU81998.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547992|gb|AAU81999.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547994|gb|AAU82000.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547996|gb|AAU82001.1| SEPALLATA1 [Arabidopsis thaliana] gi|52547998|gb|AAU82002.1| SEPALLATA1 [Arabidopsis thaliana] gi|52548002|gb|AAU82004.1| SEPALLATA1 [Arabidopsis thaliana]	105	248	3.00E-49	236.2	90.5	94.3	transcription factor	gbpln	Arabidopsis thaliana	AT5G15800.1 | Symbols: SEP1, AGL2 | K-box region and MADS-box transcription factor family protein | chr5:5151594-5153767 REVERSE LENGTH=251	105	251	4.00E-42	239.0	92.4	96.2
Rsa1.0_00040.1.g2375.t1	gb|ADR83588.1| Sepallata 1-like protein [Platanus x acerifolia]	62	244	1.00E-27	393.5	98.4	98.4	Sepallata 1-like protein	gbpln	Platanus x	AT2G03710.3 | Symbols: SEP4, AGL3 | K-box region and MADS-box transcription factor family protein | chr2:1129622-1131242 FORWARD LENGTH=187	62	187	5.00E-29	301.6	91.9	96.8
Rsa1.0_00040.1.g2376.t1	ref|NP_850827.1| uncharacterized protein [Arabidopsis thaliana] gi|297811719|ref|XP_002873743.1| hypothetical protein ARALYDRAFT_326030 [Arabidopsis lyrata subsp. lyrata] gi|26450077|dbj|BAC42158.1| unknown protein [Arabidopsis thaliana] gi|28827744|gb|AAO50716.1| unknown protein [Arabidopsis thaliana] gi|297319580|gb|EFH50002.1| hypothetical protein ARALYDRAFT_326030 [Arabidopsis lyrata subsp. lyrata] gi|332004826|gb|AED92209.1| uncharacterized protein AT5G15802 [Arabidopsis thaliana]	101	99	1.00E-41	98.0	86.1	90.1	uncharacterized protein	gbpln	Arabidopsis lyrata	AT5G15802.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 35 Blast hits to 35 proteins in 15 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:5156578-5157520 REVERSE LENGTH=99	101	99	2.00E-44	98.0	86.1	90.1
Rsa1.0_00040.1.g2377.t1	gb|EOA20072.1| hypothetical protein CARUB_v10000341mg [Capsella rubella]	589	709	0	120.4	89.8	93.7	hypothetical protein CARUB_v10000341mg	gbpln	Capsella rubella	AT5G15810.1 | Symbols: | N2,N2-dimethylguanosine tRNA methyltransferase | chr5:5157798-5161121 FORWARD LENGTH=691	589	691	0	117.3	90.0	94.4
Rsa1.0_00040.1.g2378.t1	gb|EOA21044.1| hypothetical protein CARUB_v10001383mg [Capsella rubella]	334	336	2.00E-44	100.6	43.7	57.8	hypothetical protein CARUB_v10001383mg	gbpln	Capsella rubella	AT5G15820.1 | Symbols: | RING/U-box superfamily protein | chr5:5161787-5162833 FORWARD LENGTH=348	334	348	5.00E-36	104.2	39.5	52.7
Rsa1.0_00040.1.g2379.t1	dbj|BAJ33807.1| unnamed protein product [Thellungiella halophila]	189	190	7.00E-77	100.5	81.0	90.5	unnamed protein product	----	----	AT5G15830.1 | Symbols: AtbZIP3, bZIP3 | basic leucine-zipper 3 | chr5:5168591-5169151 FORWARD LENGTH=186	189	186	4.00E-69	98.4	78.8	88.9
Rsa1.0_00040.1.g2380.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00040.1.g2381.t1	gb|AAG27546.1| constans-like protein [Brassica nigra]	375	380	0	101.3	92.5	96.3	constans-like protein	gbpln	Brassica nigra	AT5G15840.1 | Symbols: CO, FG | B-box type zinc finger protein with CCT domain | chr5:5171343-5172697 REVERSE LENGTH=373	375	373	1.00E-151	99.5	75.2	84.0
Rsa1.0_00040.1.g2382.t1	gb|AAN09808.1| COL1 protein [Brassica nigra] gi|22854912|gb|AAN09811.1| COL1 protein [Brassica nigra] gi|22854914|gb|AAN09812.1| COL1 protein [Brassica nigra] gi|22854918|gb|AAN09814.1| COL1 protein [Brassica nigra]	354	348	1.00E-175	98.3	89.5	93.2	COL1 protein	gbpln	Brassica nigra	AT5G15850.1 | Symbols: COL1, ATCOL1 | CONSTANS-like 1 | chr5:5176297-5177473 REVERSE LENGTH=355	354	355	1.00E-131	100.3	74.3	81.9
Rsa1.0_00040.1.g2383.t1	gb|AAP42646.1| putative beta-glucan elicitor receptor [Brassica napus]	759	752	0	99.1	93.1	95.7	putative beta-glucan elicitor receptor	gbpln	Brassica napus	AT5G15870.1 | Symbols: | glycosyl hydrolase family 81 protein | chr5:5182641-5184878 REVERSE LENGTH=745	759	745	0	98.2	83.1	89.5

Rsa1.0_00040.1.g2384.t1	ref|NP_197092.1| uncharacterized protein [Arabidopsis thaliana] gi|9755634|emb|CAC01787.1| putative protein [Arabidopsis thaliana] gi|20466278|gb|AAM20456.1| putative protein [Arabidopsis thaliana] gi|31711832|gb|AAP68272.1| At5g15880 [Arabidopsis thaliana] gi|332004837|gb|AED92220.1| uncharacterized protein AT5G15880 [Arabidopsis thaliana]	216	348	5.00E-48	161.1	61.6	67.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G15880.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5185788-5187461 FORWARD LENGTH=348	216	348	2.00E-50	161.1	61.6	67.1
Rsa1.0_00040.1.g2385.t1	gb|EOA22444.1| hypothetical protein CARUB_v10003090mg [Capsella rubella]	460	517	0	112.4	79.8	88.7	hypothetical protein CARUB_v10003090mg	gbpln	Capsella rubella	AT5G15890.1 | Symbols: TBL21 | TRICHOME BIREFRINGENCE-LIKE 21 | chr5:5187687-5189348 REVERSE LENGTH=526	460	526	0	114.3	78.3	88.0
Rsa1.0_00040.1.g2386.t1	ref|XP_002873749.1| hypothetical protein ARALYDRAFT_488438 [Arabidopsis lyrata subsp. lyrata] gi|297319586|gb|EFH50008.1| hypothetical protein ARALYDRAFT_488438 [Arabidopsis lyrata subsp. lyrata]	425	426	0	100.2	83.1	92.0	hypothetical protein ARALYDRAFT_488438	gbpln	Arabidopsis lyrata	AT5G15900.1 | Symbols: TBL19 | TRICHOME BIREFRINGENCE-LIKE 19 | chr5:5189524-5192070 REVERSE LENGTH=426	425	426	0	100.2	81.2	90.4
Rsa1.0_00040.1.g2387.t2	gb|AAR15894.1| S-adenosyl-L-methionine decarboxylase [Brassica juncea]	617	369	0	59.8	54.1	56.2	S-adenosyl-L-methionine decarboxylase	gbpln	Brassica juncea	AT5G15950.2 | Symbols: | Adenosylmethionine decarboxylase family protein | chr5:5206706-5207794 FORWARD LENGTH=362	617	362	0	58.7	52.4	55.4
Rsa1.0_00040.1.g2388.t1	gb|AAG13408.1|AF297472_1 BN28b [Brassica napus]	65	65	4.00E-25	100.0	92.3	98.5	BN28b	gbpln	Brassica napus	#	#	#	#	#	#	#
Rsa1.0_00040.1.g2389.t1	gb|EOA20115.1| hypothetical protein CARUB_v10000394mg [Capsella rubella]	662	670	0	101.2	73.0	84.0	hypothetical protein CARUB_v10000394mg	gbpln	Capsella rubella	AT5G15980.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:5213290-5215296 FORWARD LENGTH=668	662	668	0	100.9	71.8	82.6
Rsa1.0_00040.1.g2390.t1	ref|XP_002871697.1| nsp-interacting kinase 1 [Arabidopsis lyrata subsp. lyrata] gi|297317534|gb|EFH47956.1| nsp-interacting kinase 1 [Arabidopsis lyrata subsp. lyrata]	645	638	0	98.9	91.3	94.3	nsp-interacting kinase 1	gbpln	Arabidopsis lyrata	AT5G16000.1 | Symbols: NIK1 | NSP-interacting kinase 1 | chr5:5224264-5227003 FORWARD LENGTH=638	645	638	0	98.9	91.3	93.6
Rsa1.0_00040.1.g2391.t1	gb|EOA34948.1| hypothetical protein CARUB_v10020033mg [Capsella rubella]	604	591	0	97.8	81.1	89.4	hypothetical protein CARUB_v10020033mg	gbpln	Capsella rubella	AT1G72550.1 | Symbols: | tRNA synthetase beta subunit family protein | chr1:27319947-27323908 REVERSE LENGTH=598	604	598	0	99.0	78.8	88.9
Rsa1.0_00040.1.g2392.t1	ref|XP_002871699.1| hypothetical protein ARALYDRAFT_488440 [Arabidopsis lyrata subsp. lyrata] gi|297317536|gb|EFH47958.1| hypothetical protein ARALYDRAFT_488440 [Arabidopsis lyrata subsp. lyrata]	938	640	0	68.2	56.6	60.7	hypothetical protein ARALYDRAFT_488440	gbpln	Arabidopsis lyrata	AT5G16020.1 | Symbols: GEX3 | gamete-expressed 3 | chr5:5229692-5232241 FORWARD LENGTH=641	938	641	0	68.3	54.7	59.1
Rsa1.0_00040.1.g2393.t1	ref|XP_002871700.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317537|gb|EFH47959.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	350	338	1.00E-135	96.6	74.9	86.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G16030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02500.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5238242-5240578 FORWARD LENGTH=339	350	339	1.00E-136	96.9	76.0	86.0
Rsa1.0_00040.1.g2394.t1	gb|EOA19527.1| hypothetical protein CARUB_v10002448mg [Capsella rubella]	413	396	0	95.9	89.6	92.0	hypothetical protein CARUB_v10002448mg	gbpln	Capsella rubella	AT5G16040.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr5:5240860-5243308 REVERSE LENGTH=396	413	396	0	95.9	89.6	91.8
Rsa1.0_00040.1.g2395.t1	ref|XP_002871701.1| hypothetical protein ARALYDRAFT_488456 [Arabidopsis lyrata subsp. lyrata] gi|297317538|gb|EFH47960.1| hypothetical protein ARALYDRAFT_488456 [Arabidopsis lyrata subsp. lyrata]	96	95	3.00E-44	99.0	90.6	93.8	hypothetical protein ARALYDRAFT_488456	gbpln	Arabidopsis lyrata	AT5G16060.1 | Symbols: | Cytochrome c oxidase biogenesis protein Cmc1-like | chr5:5246161-5247209 FORWARD LENGTH=95	96	95	2.00E-46	99.0	89.6	92.7
Rsa1.0_00040.1.g2396.t1	ref|XP_002884325.1| hypothetical protein ARALYDRAFT_477487 [Arabidopsis lyrata subsp. lyrata] gi|297330165|gb|EFH60584.1| hypothetical protein ARALYDRAFT_477487 [Arabidopsis lyrata subsp. lyrata]	536	535	0	99.8	97.2	99.1	hypothetical protein ARALYDRAFT_477487	gbpln	Arabidopsis lyrata	AT5G16070.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr5:5247549-5251050 REVERSE LENGTH=535	536	535	0	99.8	97.9	98.7

Rsa1.0_00040.1.g2397.t1	ref|XP_002873755.1| hypothetical protein ARALYDRAFT_488458 [Arabidopsis lyrata subsp. lyrata] gi|297319592|gb|EFH50014.1| hypothetical protein ARALYDRAFT_488458 [Arabidopsis lyrata subsp. lyrata]	338	343	1.00E-170	101.5	87.6	93.2	hypothetical protein ARALYDRAFT_488458	gbpln	Arabidopsis lyrata	AT5G16080.1 | Symbols: AtCXE17, CXE17 | carboxyesterase 17 | chr5:5252533-5253567 REVERSE LENGTH=344	338	344	1.00E-170	101.8	85.8	92.6
Rsa1.0_00040.1.g2398.t1	gb|ABY66298.1| RAD23-like protein [Brassica napus]	70	357	3.00E-15	510.0	52.9	57.1	RAD23-like protein	gbpln	Brassica napus	#	#	#	#	#	#	#
Rsa1.0_00040.1.g2399.t1	gb|ABY66298.1| RAD23-like protein [Brassica napus]	310	357	9.00E-98	115.2	66.1	76.5	RAD23-like protein	gbpln	Brassica napus	AT5G38470.2 | Symbols: RAD23D | Rad23 UV excision repair protein family | chr5:15404720-15407251 FORWARD LENGTH=332	310	332	1.00E-38	107.1	36.1	51.0
Rsa1.0_00040.1.g2400.t3	gb|ABY66298.1| RAD23-like protein [Brassica napus]	420	357	1.00E-114	85.0	58.8	69.8	RAD23-like protein	gbpln	Brassica napus	AT5G38470.1 | Symbols: RAD23D | Rad23 UV excision repair protein family | chr5:15404720-15407500 FORWARD LENGTH=378	420	378	6.00E-37	90.0	32.9	46.9
Rsa1.0_00040.1.g2401.t5	gb|ABY66299.1| DNA repair protein RAD23 [Brassica napus]	236	327	3.00E-53	138.6	64.4	75.0	DNA repair protein RAD23	gbpln	Brassica napus	AT5G38470.2 | Symbols: RAD23D | Rad23 UV excision repair protein family | chr5:15404720-15407251 FORWARD LENGTH=332	236	332	8.00E-20	140.7	23.7	29.2
Rsa1.0_00040.1.g2402.t1	gb|EOA12107.1| hypothetical protein CARUB_v10000012mg, partial [Capsella rubella]	189	238	3.00E-66	125.9	82.0	86.2	hypothetical protein CARUB_v10000012mg, partial	gbpln	Capsella rubella	AT5G16110.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02555.1); Has 133 Blast hits to 133 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 133; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:5261171-5262668 REVERSE LENGTH=244	189	244	9.00E-68	129.1	81.0	86.2
Rsa1.0_00040.1.g2403.t3	ref|NP_197117.1| 40S ribosomal protein S7-3 [Arabidopsis thaliana] gi|115311860|sp|Q8LD03.2|RS73_ARATH RecName: Full=40S ribosomal protein S7-3 gi|9755823|emb|CAC01854.1| 40S ribosomal protein S7-like [Arabidopsis thaliana] gi|90568000|gb|ABD94070.1| At5g16130 [Arabidopsis thaliana] gi|110742740|dbj|BAE99279.1| 40S ribosomal protein S7-like [Arabidopsis thaliana] gi|332004867|gb|AED92250.1| 40S ribosomal protein S7-3 [Arabidopsis thaliana]	190	190	1.00E-100	100.0	93.7	96.8	40S ribosomal protein S7-3	gbpln	Arabidopsis thaliana	AT5G16130.1 | Symbols: | Ribosomal protein S7e family protein | chr5:5268984-5269912 FORWARD LENGTH=190	190	190	1.00E-103	100.0	93.7	96.8
Rsa1.0_00040.1.g2404.t1	gb|EOA21457.1| hypothetical protein CARUB_v10001847mg [Capsella rubella]	241	239	1.00E-125	99.2	90.0	95.0	hypothetical protein CARUB_v10001847mg	gbpln	Capsella rubella	AT5G16140.2 | Symbols: | Peptidyl-tRNA hydrolase family protein | chr5:5270308-5271517 REVERSE LENGTH=240	241	240	1.00E-123	99.6	88.8	92.9
Rsa1.0_00040.1.g2405.t1	ref|XP_002871705.1| GLT1 [Arabidopsis lyrata subsp. lyrata] gi|297317542|gb|EFH47964.1| GLT1 [Arabidopsis lyrata subsp. lyrata]	530	545	0	102.8	93.0	95.3	GLT1	gbpln	Arabidopsis lyrata	AT5G16150.3 | Symbols: GLT1, PGLCT | plastidic GLC translocator | chr5:5272904-5275678 FORWARD LENGTH=546	530	546	0	103.0	92.8	95.7
Rsa1.0_00040.1.g2406.t1	gb|EOA20743.1| hypothetical protein CARUB_v10001069mg [Capsella rubella]	312	414	1.00E-155	132.7	86.5	92.9	hypothetical protein CARUB_v10001069mg	gbpln	Capsella rubella	AT5G16170.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:5277926-5279751 FORWARD LENGTH=411	312	411	1.00E-154	131.7	83.7	91.3
Rsa1.0_00040.1.g2407.t4	gb|EOA20451.1| hypothetical protein CARUB_v10000762mg [Capsella rubella]	505	507	0	100.4	88.1	94.5	hypothetical protein CARUB_v10000762mg	gbpln	Capsella rubella	AT4G13410.1 | Symbols: ATCSLA15, CSLA15 | Nucleotide-diphospho-sugar transferases superfamily protein | chr4:7792219-7795824 REVERSE LENGTH=537	505	537	0	106.3	82.6	90.5
Rsa1.0_00041.1.g2408.t1	gb|EOA31480.1| hypothetical protein CARUB_v10014673mg [Capsella rubella]	203	200	4.00E-78	98.5	79.8	84.2	hypothetical protein CARUB_v10014673mg	gbpln	Capsella rubella	AT3G04510.1 | Symbols: LSH2 | Protein of unknown function (DUF640) | chr3:1215812-1216417 REVERSE LENGTH=201	203	201	9.00E-76	99.0	79.3	83.7
Rsa1.0_00041.1.g2409.t1	gb|EOA31608.1| hypothetical protein CARUB_v10014805mg, partial [Capsella rubella]	103	161	1.00E-33	156.3	74.8	77.7	hypothetical protein CARUB_v10014805mg, partial	gbpln	Capsella rubella	AT3G04400.1 | Symbols: emb2171 | Ribosomal protein L14p/L23e family protein | chr3:1167339-1168308 FORWARD LENGTH=140	103	140	4.00E-36	135.9	74.8	77.7
Rsa1.0_00041.1.g2410.t1	gb|EOA31608.1| hypothetical protein CARUB_v10014805mg, partial [Capsella rubella]	140	161	1.00E-74	115.0	99.3	100.0	hypothetical protein CARUB_v10014805mg, partial	gbpln	Capsella rubella	AT3G04400.1 | Symbols: emb2171 | Ribosomal protein L14p/L23e family protein | chr3:1167339-1168308 FORWARD LENGTH=140	140	140	1.00E-76	100.0	99.3	100.0
Rsa1.0_00041.1.g2411.t1	gb|EOA31980.1| hypothetical protein CARUB_v10015223mg [Capsella rubella]	564	567	0	100.5	84.8	91.8	hypothetical protein CARUB_v10015223mg	gbpln	Capsella rubella	AT3G04350.1 | Symbols: | Plant protein of unknown function (DUF946) | chr3:1153972-1156469 REVERSE LENGTH=567	564	567	0	100.5	86.5	93.8

Rsa1.0_00041.1.g2412.t1	gb|EOA30270.1| hypothetical protein CARUB_v10013391mg [Capsella rubella]	552	548	0	99.3	88.9	94.0	hypothetical protein CARUB_v10013391mg	gbpln	Capsella rubella	AT5G18480.1 | Symbols: PGSIP6 | plant glycogenin-like starch initiation protein 6 | chr5:6131307-6133787 REVERSE LENGTH=537	552	537	0	97.3	80.6	88.2
Rsa1.0_00041.1.g2413.t1	ref|NP_187076.2| plastid transcriptionally active 3 [Arabidopsis thaliana] gi|332640537|gb|AEE74058.1| plastid transcriptionally active 3 [Arabidopsis thaliana]	908	910	0	100.2	91.3	95.0	plastid transcriptionally active 3	gbpln	Arabidopsis thaliana	AT3G04260.1 | Symbols: PTAC3 | plastid transcriptionally active 3 | chr3:1123231-1127515 REVERSE LENGTH=910	908	910	0	100.2	91.3	95.0
Rsa1.0_00041.1.g2414.t1	gb|AAN08437.1| hypothetical protein [Arabidopsis thaliana]	620	538	1.00E-133	86.8	43.2	53.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G43220.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:17964340-17965956 FORWARD LENGTH=538	620	538	1.00E-135	86.8	42.6	52.6
Rsa1.0_00041.1.g2415.t1	ref|NP_187074.1| putative UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC [Arabidopsis thaliana] gi|75336082|sp|Q9M8Y0.1|SEC_ARATH RecName: Full=Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC; AltName: Full=Protein SECRET AGENT gi|6721161|gb|AAF26789.1|AC016829_13 putative O-linked GlcNAc transferase [Arabidopsis thaliana] gi|18139887|gb|AAL60196.1|AF441079_1 O-linked N-acetyl glucosamine transferase [Arabidopsis thaliana] gi|20259324|gb|AAM13988.1| putative O-linked GlcNAc transferase [Arabidopsis thaliana] gi|21436429|gb|AAM51415.1| putative O-linked GlcNAc transferase [Arabidopsis thaliana] gi|110742062|dbj|BAE98963.1| O-linked GlcNAc transferase like protein [Arabidopsis thaliana] gi|332640535|gb|AEE74056.1| putative UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC [Arabidopsis thaliana]	980	977	0	99.7	93.5	96.0	putative UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC	gbpln	Arabidopsis thaliana	AT3G04240.1 | Symbols: SEC | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:1114187-1120722 REVERSE LENGTH=977	980	977	0	99.7	93.5	96.0
Rsa1.0_00041.1.g2416.t1	gb|EOA17608.1| hypothetical protein CARUB_v10005968mg [Capsella rubella] gi|482557559|gb|EOA21751.1| hypothetical protein CARUB_v10002207mg [Capsella rubella]	146	146	5.00E-74	100.0	93.2	95.2	hypothetical protein CARUB_v10005968mg	gbpln	Capsella rubella	AT5G18380.1 | Symbols: | Ribosomal protein S5 domain 2-like superfamily protein | chr5:6090253-6090693 REVERSE LENGTH=146	146	146	6.00E-76	100.0	92.5	95.2
Rsa1.0_00041.1.g2417.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00041.1.g2418.t1	dbj|BAJ33926.1| unnamed protein product [Thellungiella halophila]	338	338	0	100.0	96.7	98.5	unnamed protein product	----	----	AT3G04120.1 | Symbols: GAPC, GAPC-1, GAPC1 | glyceraldehyde-3-phosphate dehydrogenase C subunit 1 | chr3:1081077-1083131 FORWARD LENGTH=338	338	338	0	100.0	95.6	98.2
Rsa1.0_00041.1.g2419.t2	ref|NP_187061.1| glutamate receptor 1.1 [Arabidopsis thaliana] gi|41017234|sp|Q9M8W7.1|GLR11_ARATH RecName: Full=Glutamate receptor 1.1; Short=AtGLR1; AltName: Full=Ligand-gated ion channel 1.1; Flags: Precursor gi|6721174|gb|AAF26802.1|AC016829_26 putative glutamate receptor (GLR1) [Arabidopsis thaliana] gi|26450250|dbj|BAC42242.1| putative glutamate receptor GLR1 [Arabidopsis thaliana] gi|332640517|gb|AEE74038.1| glutamate receptor 1.1 [Arabidopsis thaliana]	796	808	0	101.5	70.1	80.9	glutamate receptor 1.1	gbpln	Arabidopsis thaliana	AT3G04110.1 | Symbols: GLR1, ATGLR1.1, GLR1.1 | glutamate receptor 1.1 | chr3:1077361-1080236 FORWARD LENGTH=808	796	808	0	101.5	70.1	80.9
Rsa1.0_00041.1.g2420.t1	ref|XP_002882329.1| MADS-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297328169|gb|EFH58588.1| MADS-box family protein [Arabidopsis lyrata subsp. lyrata]	187	205	2.00E-45	109.6	56.7	70.6	MADS-box family protein	gbpln	Arabidopsis lyrata	AT3G04100.1 | Symbols: AGL57 | AGAMOUS-like 57 | chr3:1075299-1075922 FORWARD LENGTH=207	187	207	1.00E-43	110.7	51.9	67.9
Rsa1.0_00041.1.g2421.t1	ref|NP_197329.4| nucleoside-triphosphatase [Arabidopsis thaliana] gi|332005149|gb|AED92532.1| nucleoside-triphosphatase [Arabidopsis thaliana]	749	578	0	77.2	56.2	61.8	nucleoside-triphosphatase	gbpln	Arabidopsis thaliana	AT5G18280.1 | Symbols: ATAPY2, APY2 | apyrase 2 | chr5:6050799-6054875 REVERSE LENGTH=578	749	578	0	77.2	56.2	61.8

<table>
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<tr><td>Rsa1.0_00041.1.g2423.t1</td><td>ref|XP_002884425.1| ANAC046 [Arabidopsis lyrata subsp. lyrata] gi|297330265|gb|EFH60684.1| ANAC046 [Arabidopsis lyrata subsp. lyrata]</td><td>342</td><td>342</td><td>1.00E-164</td><td>100.0</td><td>82.5</td><td>88.6</td><td>ANAC046</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04060.1 | Symbols: anac046, NAC046 | NAC domain containing protein 46 | chr3:1053625-1054952 REVERSE LENGTH=338</td><td>342</td><td>338</td><td>1.00E-164</td><td>98.8</td><td>82.5</td><td>87.1</td></tr>
<tr><td>Rsa1.0_00041.1.g2424.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00041.1.g2425.t1</td><td>ref|XP_002882328.1| hypothetical protein ARALYDRAFT_340564 [Arabidopsis lyrata subsp. lyrata] gi|297328168|gb|EFH58587.1| hypothetical protein ARALYDRAFT_340564 [Arabidopsis lyrata subsp. lyrata]</td><td>487</td><td>510</td><td>0</td><td>104.7</td><td>80.3</td><td>88.7</td><td>hypothetical protein ARALYDRAFT_340564</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04050.1 | Symbols: | Pyruvate kinase family protein | chr3:1049795-1051522 FORWARD LENGTH=510</td><td>487</td><td>510</td><td>0</td><td>104.7</td><td>79.9</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00041.1.g2426.t7</td><td>ref|XP_002863119.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308943|gb|EFH39378.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>1394</td><td>1121</td><td>0</td><td>80.4</td><td>43.7</td><td>51.9</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189</td><td>1394</td><td>1189</td><td>0</td><td>85.3</td><td>42.0</td><td>51.6</td></tr>
<tr><td>Rsa1.0_00041.1.g2427.t1</td><td>ref|XP_002863119.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308943|gb|EFH39378.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>1100</td><td>1121</td><td>0</td><td>101.9</td><td>56.9</td><td>70.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189</td><td>1100</td><td>1189</td><td>0</td><td>108.1</td><td>56.4</td><td>69.7</td></tr>
<tr><td>Rsa1.0_00041.1.g2428.t1</td><td>ref|NP_187048.1| 3-oxoacyl-[acyl-carrier protein] reductase [Arabidopsis thaliana] gi|6223643|gb|AAF05857.1|AC011698_8 putative short-chain type dehydrogenase/reductase [Arabidopsis thaliana] gi|332640501|gb|AEE74022.1| NAD(P)-binding Rossmann-fold domain-containing protein [Arabidopsis thaliana]</td><td>263</td><td>270</td><td>1.00E-126</td><td>102.7</td><td>86.3</td><td>93.5</td><td>3-oxoacyl-</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G03980.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:1031786-1033081 FORWARD LENGTH=270</td><td>263</td><td>270</td><td>1.00E-129</td><td>102.7</td><td>86.3</td><td>93.5</td></tr>
<tr><td>Rsa1.0_00041.1.g2429.t1</td><td>gb|ACP30572.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>1266</td><td>1184</td><td>0</td><td>93.5</td><td>44.6</td><td>56.8</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189</td><td>1266</td><td>1189</td><td>0</td><td>93.9</td><td>46.1</td><td>57.7</td></tr>
<tr><td>Rsa1.0_00041.1.g2430.t1</td><td>ref|NP_196686.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|8953387|emb|CAB96660.1| RPP1 disease resistance protein-like [Arabidopsis thaliana] gi|332004269|gb|AED91652.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]</td><td>1644</td><td>1189</td><td>0</td><td>72.3</td><td>41.0</td><td>50.5</td><td>TIR-NBS-LRR class disease resistance protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189</td><td>1644</td><td>1189</td><td>0</td><td>72.3</td><td>41.0</td><td>50.5</td></tr>
<tr><td>Rsa1.0_00041.1.g2431.t1</td><td>gb|EOA32860.1| hypothetical protein CARUB_v10016174mg [Capsella rubella]</td><td>567</td><td>549</td><td>0</td><td>96.8</td><td>93.3</td><td>94.9</td><td>hypothetical protein CARUB_v10016174mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G03960.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:1024432-1027604 FORWARD LENGTH=549</td><td>567</td><td>549</td><td>0</td><td>96.8</td><td>92.9</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00041.1.g2432.t1</td><td>ref|XP_002882321.1| hypothetical protein ARALYDRAFT_477648 [Arabidopsis lyrata subsp. lyrata] gi|297328161|gb|EFH58580.1| hypothetical protein ARALYDRAFT_477648 [Arabidopsis lyrata subsp. lyrata]</td><td>415</td><td>428</td><td>0</td><td>103.1</td><td>84.8</td><td>90.8</td><td>hypothetical protein ARALYDRAFT_477648</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G03950.3 | Symbols: ECT1 | evolutionarily conserved C-terminal region 1 | chr3:1021502-1023767 FORWARD LENGTH=428</td><td>415</td><td>428</td><td>0</td><td>103.1</td><td>83.1</td><td>89.4</td></tr>
<tr><td>Rsa1.0_00041.1.g2433.t1</td><td>ref|NP_196686.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|8953387|emb|CAB96660.1| RPP1 disease resistance protein-like [Arabidopsis thaliana] gi|332004269|gb|AED91652.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]</td><td>1078</td><td>1189</td><td>0</td><td>110.3</td><td>57.4</td><td>71.5</td><td>TIR-NBS-LRR class disease resistance protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189</td><td>1078</td><td>1189</td><td>0</td><td>110.3</td><td>57.4</td><td>71.5</td></tr>
<tr><td>Rsa1.0_00041.1.g2434.t1</td><td>ref|NP_187044.1| protein kinase-like protein [Arabidopsis thaliana] gi|6223639|gb|AAF05853.1|AC011698_4 putative casein kinase [Arabidopsis thaliana] gi|332640493|gb|AEE74014.1| protein kinase-like protein [Arabidopsis thaliana]</td><td>704</td><td>701</td><td>0</td><td>99.6</td><td>92.6</td><td>96.3</td><td>protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G03940.1 | Symbols: | Protein kinase family protein | chr3:1014412-1018244 REVERSE LENGTH=701</td><td>704</td><td>701</td><td>0</td><td>99.6</td><td>92.6</td><td>96.3</td></tr>
</table>

Rsa1.0_00041.1.g2435.t1	ref|NP_566217.1| H/ACA ribonucleoprotein complex subunit 1 [Arabidopsis thaliana] gi|68565918|sp|Q8VZT0.1|NLAL1_ARATH RecName: Full=Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1 gi|17380836|gb|AAL36230.1| putative GAR1 protein [Arabidopsis thaliana] gi|20259633|gb|AAM14173.1| putative GAR1 protein [Arabidopsis thaliana] gi|332640491|gb|AEE74012.1| H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein [Arabidopsis thaliana]	208	202	4.00E-51	97.1	58.2	59.6	H/ACA ribonucleoprotein complex subunit 1	gbpln	Arabidopsis thaliana	AT3G03920.1 | Symbols: | H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein | chr3:1009123-1010379 REVERSE LENGTH=202	208	202	1.00E-53	97.1	58.2	59.6
Rsa1.0_00041.1.g2436.t1	#	#	#	#	#	#	#	–	----	----	AT3G03910.1 | Symbols: GDH3 | glutamate dehydrogenase 3 | chr3:1006913-1008846 FORWARD LENGTH=411	37	411	5.00E-13	1110.8	81.1	83.8
Rsa1.0_00041.1.g2437.t1	gb|EOA32962.1| hypothetical protein CARUB_v10016292mg [Capsella rubella]	411	411	0	100.0	94.6	98.3	hypothetical protein CARUB_v10016292mg	gbpln	Capsella rubella	AT3G03910.1 | Symbols: GDH3 | glutamate dehydrogenase 3 | chr3:1006913-1008846 FORWARD LENGTH=411	411	411	0	100.0	93.9	98.1
Rsa1.0_00041.1.g2438.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00041.1.g2439.t1	gb|EOA31260.1| hypothetical protein CARUB_v10014432mg [Capsella rubella]	286	260	5.00E-92	90.9	64.3	72.7	hypothetical protein CARUB_v10014432mg	gbpln	Capsella rubella	AT3G03870.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18130.1); Has 47 Blast hits to 47 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:995520-997180 FORWARD LENGTH=266	286	266	2.00E-91	93.0	65.7	72.7
Rsa1.0_00041.1.g2440.t1	ref|XP_002882315.1| hypothetical protein ARALYDRAFT_477638 [Arabidopsis lyrata subsp. lyrata] gi|297328155|gb|EFH58574.1| hypothetical protein ARALYDRAFT_477638 [Arabidopsis lyrata subsp. lyrata]	302	300	1.00E-137	99.3	80.5	89.4	hypothetical protein ARALYDRAFT_477638	gbpln	Arabidopsis lyrata	AT3G03860.1 | Symbols: ATAPRL5, APRL5 | APR-like 5 | chr3:992465-994315 FORWARD LENGTH=300	302	300	1.00E-140	99.3	80.5	89.4
Rsa1.0_00041.1.g2441.t1	ref|XP_002884412.1| hypothetical protein ARALYDRAFT_477634 [Arabidopsis lyrata subsp. lyrata] gi|297330252|gb|EFH60671.1| hypothetical protein ARALYDRAFT_477634 [Arabidopsis lyrata subsp. lyrata]	656	656	0	100.0	91.8	95.9	hypothetical protein ARALYDRAFT_477634	gbpln	Arabidopsis lyrata	AT3G03810.1 | Symbols: EDA30 | O-fucosyltransferase family protein | chr3:972190-975901 REVERSE LENGTH=656	656	656	0	100.0	91.2	95.4
Rsa1.0_00041.1.g2442.t1	ref|NP_187030.1| syntaxin 1B/2/3 [Arabidopsis thaliana] gi|28380139|sp|Q9SRV7.1|SY131_ARATH RecName: Full=Putative syntaxin-131; Short=AtSYP131 gi|6006872|gb|AAF00648.1|AC009540_25s-syntaxin-like protein [Arabidopsis thaliana] gi|332640474|gb|AEE73995.1| putative syntaxin-131 [Arabidopsis thaliana]	278	306	1.00E-135	110.1	91.7	95.7	syntaxin 1B/2/3	gbpln	Arabidopsis thaliana	AT3G03800.1 | Symbols: SYP131, ATSYP131 | syntaxin of plants 131 | chr3:969314-971460 FORWARD LENGTH=306	278	306	1.00E-137	110.1	91.7	95.7
Rsa1.0_00041.1.g2443.t1	gb|ACP30600.1| disease resistance protein [Brassica rapa subsp. pekinensis]	645	909	1.00E-167	140.9	49.9	66.7	disease resistance protein	gbpln	Brassica rapa	AT5G18360.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6080049-6083027 REVERSE LENGTH=900	645	900	1.00E-169	139.5	50.1	66.8
Rsa1.0_00041.1.g2444.t1	ref|NP_683525.2| HSP20-like chaperon-like protein [Arabidopsis thaliana] gi|73921112|sp|Q6ID70.1|Y3377_ARATH RecName: Full=Uncharacterized protein At3g03773 gi|48310264|gb|AAT41786.1| At3g03773 [Arabidopsis thaliana] gi|49823520|gb|AAT68743.1| hypothetical protein At3g03773 [Arabidopsis thaliana] gi|50198936|gb|AAT70471.1| At3g03773 [Arabidopsis thaliana] gi|61742697|gb|AAX55169.1| hypothetical protein At3g03773 [Arabidopsis thaliana] gi|332640465|gb|AEE73986.1| HSP20-like chaperon-like protein [Arabidopsis thaliana]	150	150	8.00E-75	100.0	90.7	96.0	HSP20-like chaperon-like protein	gbpln	Arabidopsis thaliana	AT3G03773.1 | Symbols: | HSP20-like chaperones superfamily protein | chr3:951885-953490 FORWARD LENGTH=150	150	150	3.00E-77	100.0	90.7	96.0
Rsa1.0_00041.1.g2445.t1	ref|XP_002877469.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323307|gb|EFH53728.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	336	328	1.00E-43	97.6	27.1	37.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	336	289	1.00E-31	86.0	22.3	28.6

Rsa1.0_00041.1.g2446.t1	ref|XP_002882305.1| LOB domain protein 20 [Arabidopsis lyrata subsp. lyrata] gi|297328145|gb|EFH58564.1| LOB domain protein 20 [Arabidopsis lyrata subsp. lyrata]	273	281	1.00E-117	102.9	83.9	87.5	LOB domain protein 20	gbpln	Arabidopsis lyrata	AT3G03760.1 | Symbols: LBD20 | LOB domain-containing protein 20 | chr3:943632-944673 FORWARD LENGTH=273	273	273	1.00E-116	100.0	86.4	89.4
Rsa1.0_00042.1.g2447.t1	gb|AAD10829.1| putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]	646	646	0	100.0	86.8	90.7	putative inositol polyphosphate 5-phosphatase At5P2	gbpln	Arabidopsis thaliana	AT4G18010.1 | Symbols: IP5PII, AT5PTASE2, 5PTASE2 | myo-inositol polyphosphate 5-phosphatase 2 | chr4:9991194-9994099 REVERSE LENGTH=646	646	646	0	100.0	86.8	90.7
Rsa1.0_00042.1.g2448.t1	gb|EMJ12169.1| hypothetical protein PRUPE_ppa022548mg [Prunus persica]	792	495	1.00E-167	62.5	38.4	45.1	hypothetical protein PRUPE_ppa022548mg	gbpln	Prunus persica	AT5G46570.1 | Symbols: BSK2 | BR-signaling kinase 2 | chr5:18894687-18897198 FORWARD LENGTH=489	792	489	1.00E-169	61.7	38.6	46.1
Rsa1.0_00042.1.g2449.t1	ref|XP_002868027.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313863|gb|EFH44286.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	286	261	1.00E-126	91.3	78.0	81.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G17980.1 | Symbols: anac071, NAC071 | NAC domain containing protein 71 | chr4:9978850-9980038 REVERSE LENGTH=262	286	262	1.00E-120	91.6	75.2	79.0
Rsa1.0_00042.1.g2450.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00042.1.g2451.t1	ref|NP_193531.1| aluminum-activated, malate transporter 12 [Arabidopsis thaliana] gi|75219677|sp|O49696.1|ALMTC_ARATH RecName: Full=Aluminum-activated malate transporter 12; Short=AtALMT12; AltName: Full=Quick anion channel 1 gi|2894606|emb|CAA17140.1| putative protein [Arabidopsis thaliana] gi|7268549|emb|CAB78799.1| putative protein [Arabidopsis thaliana] gi|332658573|gb|AEE83973.1| aluminum-activated, malate transporter 12 [Arabidopsis thaliana]	536	560	0	104.5	90.5	94.2	aluminum-activated, malate transporter 12	gbpln	Arabidopsis thaliana	AT4G17970.1 | Symbols: ALMT12, ATALMT12 | aluminum-activated, malate transporter 12 | chr4:9975482-9977722 FORWARD LENGTH=560	536	560	0	104.5	90.5	94.2
Rsa1.0_00042.1.g2452.t1	ref|NP_567546.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|15451060|gb|AAK96801.1| putative protein [Arabidopsis thaliana] gi|20148333|gb|AAM10057.1| putative protein [Arabidopsis thaliana] gi|119657370|tpd|FAA00284.1| TPA: AT-hook motif nuclear localized protein 13 [Arabidopsis thaliana] gi|332658571|gb|AEE83971.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	346	439	5.00E-57	126.9	48.0	58.7	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT4G17950.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:9967295-9969007 REVERSE LENGTH=439	346	439	1.00E-59	126.9	48.0	58.7
Rsa1.0_00042.1.g2453.t1	ref|XP_002885669.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata] gi|297331509|gb|EFH61928.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata]	485	467	1.00E-132	96.3	52.2	63.5	hypothetical protein ARALYDRAFT_319176	gbpln	Arabidopsis lyrata	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	485	472	1.00E-132	97.3	49.7	61.6
Rsa1.0_00042.1.g2454.t1	ref|NP_567546.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|15451060|gb|AAK96801.1| putative protein [Arabidopsis thaliana] gi|20148333|gb|AAM10057.1| putative protein [Arabidopsis thaliana] gi|119657370|tpd|FAA00284.1| TPA: AT-hook motif nuclear localized protein 13 [Arabidopsis thaliana] gi|332658571|gb|AEE83971.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	306	439	4.00E-57	143.5	54.2	67.6	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT4G17950.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:9967295-9969007 REVERSE LENGTH=439	306	439	1.00E-59	143.5	54.2	67.6

Rsa1.0_00042.1.g2455.t2	ref|NP_195449.1| cytochrome P450, family 81, subfamily D, polypeptide 5 [Arabidopsis thaliana] gi|4376088|emb|CAB16770.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|7270715|emb|CAB80398.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|27754487|gb|AAO22691.1| putative cytochrome p450 family protein [Arabidopsis thaliana] gi|28394071|gb|AAO42443.1| putative cytochrome p450 family protein [Arabidopsis thaliana] gi|332661381|gb|AEE86781.1| cytochrome P450, family 81, subfamily D, polypeptide 5 [Arabidopsis thaliana]	474	495	0	104.4	79.3	87.6	cytochrome P450, family 81, subfamily D, polypeptide 5	gbpln	Arabidopsis thaliana	AT4G37320.1 | Symbols: CYP81D5 | cytochrome P450, family 81, subfamily D, polypeptide 5 | chr4:17559742-17561690 REVERSE LENGTH=495	474	495	0	104.4	79.3	87.6
Rsa1.0_00042.1.g2456.t1	ref|XP_002868029.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297313865|gb|EFH44288.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	298	294	1.00E-118	98.7	73.5	78.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G17920.1 | Symbols: | RING/U-box superfamily protein | chr4:9963221-9964090 REVERSE LENGTH=289	298	289	1.00E-116	97.0	74.8	81.2
Rsa1.0_00042.1.g2457.t1	sp|P0C043.1|PP318_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At4g17915	464	463	0	99.8	88.8	95.3	RecName: Full=Putative pentatricopeptide repeat-containing protein At4g17915	----	----	AT5G46680.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr5:18941118-18942524 FORWARD LENGTH=468	464	468	0	100.9	68.5	84.1
Rsa1.0_00042.1.g2458.t1	gb|EOA17250.1| hypothetical protein CARUB_v10005524mg, partial [Capsella rubella]	350	262	1.00E-118	74.9	58.3	60.0	hypothetical protein CARUB_v10005524mg, partial	gbpln	Capsella rubella	AT4G17900.1 | Symbols: | PLATZ transcription factor family protein | chr4:9946046-9947697 FORWARD LENGTH=227	350	227	1.00E-120	64.9	58.3	59.4
Rsa1.0_00042.1.g2459.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00042.1.g2460.t1	ref|XP_002870079.1| hypothetical protein ARALYDRAFT_329738 [Arabidopsis lyrata subsp. lyrata] gi|297315915|gb|EFH46338.1| hypothetical protein ARALYDRAFT_329738 [Arabidopsis lyrata subsp. lyrata]	685	1082	0	158.0	58.7	68.2	hypothetical protein ARALYDRAFT_329738	gbpln	Arabidopsis lyrata	AT4G17895.1 | Symbols: UBP20 | ubiquitin-specific protease 20 | chr4:9939914-9942698 FORWARD LENGTH=695	685	695	1.00E-175	101.5	57.5	68.3
Rsa1.0_00042.1.g2461.t1	ref|NP_567543.1| putative ADP-ribosylation factor GTPase-activating protein AGD8 [Arabidopsis thaliana] gi|75244593|sp|Q8H100.1|AGD8_ARATH RecName: Full=Probable ADP-ribosylation factor GTPase-activating protein AGD8; Short=ARF GAP AGD8; AltName: Full=Protein ARF-GAP DOMAIN 8; Short=AtAGD8 gi|24030421|gb|AAN41368.1| unknown protein [Arabidopsis thaliana] gi|51970716|dbj|BAD44050.1| unknown protein [Arabidopsis thaliana] gi|51971433|dbj|BAD44381.1| unknown protein [Arabidopsis thaliana] gi|62319827|dbj|BAD93852.1| hypothetical protein [Arabidopsis thaliana] gi|62320091|dbj|BAD94263.1| hypothetical protein [Arabidopsis thaliana] gi|110739292|dbj|BAF01559.1| hypothetical protein [Arabidopsis thaliana] gi|332658561|gb|AEE83961.1| putative ADP-ribosylation factor GTPase-activating protein AGD8 [Arabidopsis thaliana]	409	413	0	101.0	86.6	92.2	putative ADP-ribosylation factor GTPase-activating protein AGD8	gbpln	Arabidopsis thaliana	AT4G17890.1 | Symbols: AGD8 | ARF-GAP domain 8 | chr4:9937121-9939146 FORWARD LENGTH=413	409	413	0	101.0	86.6	92.2
Rsa1.0_00042.1.g2462.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00042.1.g2463.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00042.1.g2464.t1	gb|ABD65174.1| hypothetical protein 40.t00061 [Brassica oleracea]	404	407	0	100.7	90.6	92.8	hypothetical protein 40.t00061	gbpln	Brassica oleracea	AT4G17840.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Abortive infection protein (InterPro:IPR003675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35260.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9918222-9920190 REVERSE LENGTH=422	404	422	0	104.5	87.9	91.6
Rsa1.0_00042.1.g2465.t1	gb|ABD65175.1| Streptomyces cyclase/dehydrase family protein [Brassica oleracea]	191	191	1.00E-105	100.0	96.3	98.4	Streptomyces cyclase/dehydrase family protein	gbpln	Brassica oleracea	AT4G17870.1 | Symbols: PYR1, RCAR11 | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:9928792-9929367 FORWARD LENGTH=191	191	191	1.00E-101	100.0	90.1	94.8
Rsa1.0_00042.1.g2466.t1	gb|ABD65173.1| acetylornithine deacetylase, putative [Brassica oleracea]	438	437	0	99.8	98.6	99.1	acetylornithine deacetylase, putative	gbpln	Brassica oleracea	AT4G17830.1 | Symbols: | Peptidase M20/M25/M40 family protein | chr4:9915916-9918049 FORWARD LENGTH=440	438	440	0	100.5	90.4	95.7
Rsa1.0_00042.1.g2467.t1	gb|EOA38195.1| hypothetical protein CARUB_v10009673mg [Capsella rubella] gi|482574009|gb|EOA38196.1| hypothetical protein CARUB_v10009673mg [Capsella rubella]	87	336	2.00E-15	386.2	66.7	71.3	hypothetical protein CARUB_v10009673mg	gbpln	Capsella rubella	AT1G06850.1 | Symbols: AtbZIP52, bZIP52 | basic leucine-zipper 52 | chr1:2105233-2106518 FORWARD LENGTH=337	87	337	4.00E-16	387.4	62.1	67.8
Rsa1.0_00042.1.g2468.t1	gb|ABD65171.1| zinc finger (C2H2 type) containing protein [Brassica oleracea]	206	200	1.00E-107	97.1	90.3	92.7	zinc finger (C2H2 type) containing protein	gbpln	Brassica oleracea	AT4G17810.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr4:9906918-9907532 FORWARD LENGTH=204	206	204	1.00E-93	99.0	81.6	87.4
Rsa1.0_00042.1.g2469.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00042.1.g2470.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00042.1.g2471.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	469	390	2.00E-80	83.2	37.1	49.0	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	469	746	4.00E-63	159.1	28.4	37.5
Rsa1.0_00042.1.g2472.t1	gb|ABD65169.1| hypothetical protein 40.t00056 [Brassica oleracea]	270	293	1.00E-139	108.5	95.2	95.6	hypothetical protein 40.t00056	gbpln	Brassica oleracea	AT4G17800.1 | Symbols: | Predicted AT-hook DNA-binding family protein | chr4:9895549-9896427 REVERSE LENGTH=292	270	292	1.00E-101	108.1	90.0	91.5
Rsa1.0_00042.1.g2473.t1	gb|ABD65614.1| hypothetical protein 23.t00026 [Brassica oleracea]	264	257	1.00E-125	97.3	88.3	91.3	hypothetical protein 23.t00026	gbpln	Brassica oleracea	AT4G17790.1 | Symbols: | SNARE associated Golgi protein family | chr4:9891425-9892675 FORWARD LENGTH=264	264	264	1.00E-125	100.0	85.2	89.0
Rsa1.0_00042.1.g2474.t1	gb|ABD65167.1| myb family transcription factor [Brassica oleracea]	341	337	1.00E-168	98.8	85.0	90.0	myb family transcription factor	gbpln	Brassica oleracea	AT4G17785.1 | Symbols: MYB39 | myb domain protein 39 | chr4:9881867-9883368 REVERSE LENGTH=360	341	360	1.00E-150	105.6	78.6	85.9
Rsa1.0_00042.1.g2475.t1	gb|ABD65165.1| trehalose-6-phosphate synthase, putative [Brassica oleracea]	861	857	0	99.5	95.0	96.9	trehalose-6-phosphate synthase, putative	gbpln	Brassica oleracea	AT4G17770.1 | Symbols: ATTPS5, TPS5 | trehalose phosphatase/synthase 5 | chr4:9877055-9880084 FORWARD LENGTH=862	861	862	0	100.1	92.5	96.1
Rsa1.0_00042.1.g2476.t1	gb|ABD65164.1| hypothetical protein 40.t00049 [Brassica oleracea]	297	297	1.00E-169	100.0	97.0	97.6	hypothetical protein 40.t00049	gbpln	Brassica oleracea	AT4G17760.1 | Symbols: | damaged DNA binding;exodeoxyribonuclease IIIs | chr4:9871820-9873257 FORWARD LENGTH=300	297	300	1.00E-167	101.0	93.9	95.3
Rsa1.0_00042.1.g2477.t1	ref|XP_002868041.1| hypothetical protein ARALYDRAFT_329753 [Arabidopsis lyrata subsp. lyrata] gi|297313877|gb|EFH44300.1| hypothetical protein ARALYDRAFT_329753 [Arabidopsis lyrata subsp. lyrata]	510	515	0	101.0	91.0	95.1	hypothetical protein ARALYDRAFT_329753	gbpln	Arabidopsis lyrata	AT4G17740.1 | Symbols: | Peptidase S41 family protein | chr4:9867088-9869719 REVERSE LENGTH=515	510	515	0	101.0	90.6	94.3
Rsa1.0_00042.1.g2478.t1	gb|ABD65159.1| syntaxin, putative [Brassica oleracea]	281	303	1.00E-130	107.8	90.0	93.6	syntaxin, putative	gbpln	Brassica oleracea	AT4G17730.2 | Symbols: SYP23, ATSYP23 | syntaxin of plants 23 | chr4:9865351-9866717 FORWARD LENGTH=262	281	262	1.00E-114	93.2	78.3	85.1
Rsa1.0_00042.1.g2479.t2	gb|ABD65158.1| RNA recognition motif (RRM)-containing protein [Brassica oleracea]	312	300	1.00E-151	96.2	87.8	88.5	RNA recognition motif (RRM)-containing protein	gbpln	Brassica oleracea	AT4G17720.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:9862660-9864498 REVERSE LENGTH=313	312	313	1.00E-152	100.3	87.5	90.4

Rsa1.0_00042.1.g2480.t1	gb|ABD65155.1| hypothetical protein 40.t00037 [Brassica oleracea] gi|89257700|gb|ABD65187.1| hypothetical protein 40.t00083 [Brassica oleracea]	99	101	2.00E−28	102.0	67.7	73.7	hypothetical protein 40.t00037	gbpln	Brassica oleracea	AT4G17718.1 | Symbols: | Defensin-like (DEFL) family protein | chr4:9861596-9861995 REVERSE LENGTH=101	99	101	1.00E−28	102.0	59.6	73.7
Rsa1.0_00042.1.g2481.t1	gb|ABD65154.1| hypothetical protein 40.t00036 [Brassica oleracea] gi|89257699|gb|ABD65186.1| hypothetical protein 40.t00081 [Brassica oleracea]	95	161	1.00E−30	169.5	71.6	75.8	hypothetical protein 40.t00036	gbpln	Brassica oleracea	AT4G17718.1 | Symbols: | Defensin-like (DEFL) family protein | chr4:9861596-9861995 REVERSE LENGTH=101	95	101	9.00E−29	106.3	66.3	74.7
Rsa1.0_00042.1.g2482.t1	gb|ABD65151.1| peroxidase, putative [Brassica oleracea]	329	329	0	100.0	96.0	98.5	peroxidase, putative	gbpln	Brassica oleracea	AT4G17690.1 | Symbols: | Peroxidase superfamily protein | chr4:9846127-9847107 FORWARD LENGTH=326	329	326	1.00E−160	99.1	82.4	92.1
Rsa1.0_00043.1.g2483.t1	gb|ABE65512.1| hypothetical protein At4g04650 [Arabidopsis thaliana]	225	296	2.00E−52	131.6	47.6	68.0	hypothetical protein At4g04650	gbpln	Arabidopsis thaliana	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	225	320	2.00E−54	142.2	46.2	65.3
Rsa1.0_00043.1.g2484.t1	gb|EOA38594.1| hypothetical protein CARUB_v10010427mg [Capsella rubella]	176	178	1.00E−68	101.1	75.6	83.5	hypothetical protein CARUB_v10010427mg	gbpln	Capsella rubella	AT1G32583.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: tapetum determinant 1 (TAIR:AT4G24972.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:11787351-11788103 FORWARD LENGTH=179	176	179	3.00E−65	101.7	71.0	81.8
Rsa1.0_00043.1.g2485.t1	ref|XP_004288454.1| PREDICTED: MATH domain-containing protein At5g43560-like [Fragaria vesca subsp. vesca]	410	1138	1.00E−121	277.6	54.4	66.8	PREDICTED: MATH domain-containing protein At5g43560-like	gbpln	Fragaria vesca	AT1G04300.1 | Symbols: | TRAF-like superfamily protein | chr1:1148818-1153895 REVERSE LENGTH=1074	410	1074	1.00E−118	262.0	55.4	64.9
Rsa1.0_00043.1.g2486.t1	ref|NP_174539.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|79319084|ref|NP_001031129.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|6714285|gb|AAF25981.1|AC017118_18 F6N18.2 [Arabidopsis thaliana] gi|34146860|gb|AAQ62438.1| At1g32610 [Arabidopsis thaliana] gi|51969172|dbj|BAD43278.1| unknown protein [Arabidopsis thaliana] gi|51971371|dbj|BAD44350.1| unknown protein [Arabidopsis thaliana] gi|332193389|gb|AEE31510.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|332193390|gb|AEE31511.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana]	199	291	5.00E−15	146.2	49.2	57.3	hydroxyproline-rich glycoprotein-like protein	gbpln	Arabidopsis thaliana	AT1G32610.2 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:11795892-11796767 REVERSE LENGTH=291	199	291	2.00E−17	146.2	49.2	57.3
Rsa1.0_00043.1.g2487.t1	gb|EOA37193.1| hypothetical protein CARUB_v10010595mg [Capsella rubella]	155	141	1.00E−27	91.0	63.2	73.5	hypothetical protein CARUB_v10010595mg	gbpln	Capsella rubella	AT1G32630.1 | Symbols: | unknown protein; Has 18 Blast hits to 18 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 2; Plants - 12; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:11797942-11798343 FORWARD LENGTH=133	155	133	7.00E−26	85.8	56.1	66.5
Rsa1.0_00043.1.g2488.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2489.t1	gb|ABS11038.1| MYC [Brassica oleracea var. gemmifera]	614	610	0	99.3	93.5	95.8	MYC	gbpln	Brassica oleracea	AT1G32640.1 | Symbols: ATMYC2, RD22BP1, JAI1, JIN1, MYC2, ZBF1 | Basic helix-loop-helix (bHLH) DNA-binding family protein | chr1:11799042-11800913 REVERSE LENGTH=623	614	623	0	101.5	88.1	93.3
Rsa1.0_00043.1.g2490.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2491.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1930	1274	0	66.0	30.8	43.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1930	575	1.00E−69	29.8	9.3	14.5
Rsa1.0_00043.1.g2492.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2493.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00043.1.g2494.t1	gb|AAF82236.1|AC069143_12 Contains similarity to a transposable element Tip100 protein for transposase from Ipomoea purpurea gb|4063769 and is a member of the transmembrane 4 family PF|00335 [Arabidopsis thaliana]	621	811	0	130.6	69.2	82.8	Contains similarity to a transposable element Tip100 protein for transposase from Ipomoea purpurea gb|4063769 and is a member of the transmembrane 4 family PF|00335	gbpln	Arabidopsis thaliana	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	621	769	0	123.8	69.2	82.8
Rsa1.0_00043.1.g2495.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2496.t1	ref|NP_174546.1| uncharacterized protein [Arabidopsis thaliana] gi|38566628|gb|AAR24204.1| At1g32690 [Arabidopsis thaliana] gi|40824115|gb|AAR92349.1| At1g32690 [Arabidopsis thaliana] gi|332193396|gb|AEE31517.1| uncharacterized protein AT1G32690 [Arabidopsis thaliana]	197	200	3.00E-69	101.5	80.2	87.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G32690.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35200.1); Has 45 Blast hits to 45 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:11821079-11821681 REVERSE LENGTH=200	197	200	1.00E-71	101.5	80.2	87.8
Rsa1.0_00043.1.g2497.t1	ref|NP_199370.1| Ulp1 protease family protein [Arabidopsis thaliana] gi|10177930|dbj|BAB11195.1| unnamed protein product [Arabidopsis thaliana] gi|332007886|gb|AED95269.1| Ulp1 protease family protein [Arabidopsis thaliana]	126	921	6.00E-17	731.0	27.8	46.8	Ulp1 protease family protein	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	126	921	1.00E-19	731.0	27.8	46.8
Rsa1.0_00043.1.g2498.t1	ref|NP_564407.1| uncharacterized protein [Arabidopsis thaliana] gi|6714274|gb|AAF25970.1|AC017118_7 F6N18.11 [Arabidopsis thaliana] gi|21536980|gb|AAM61321.1| unknown [Arabidopsis thaliana] gi|225897996|dbj|BAH30330.1| hypothetical protein [Arabidopsis thaliana] gi|332193401|gb|AEE31522.1| uncharacterized protein AT1G32730 [Arabidopsis thaliana]	260	327	2.00E-93	125.8	72.7	83.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G32730.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF702 (InterPro:IPR007818); Has 120 Blast hits to 118 proteins in 39 species: Archae - 0; Bacteria - 8; Metazoa - 63; Fungi - 4; Plants - 33; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr1:11841077-11842956 FORWARD LENGTH=327	260	327	6.00E-96	125.8	72.7	83.8
Rsa1.0_00043.1.g2499.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2500.t1	gb|EOA37570.1| hypothetical protein CARUB_v10011900mg [Capsella rubella]	360	368	1.00E-174	102.2	87.5	91.9	hypothetical protein CARUB_v10011900mg	gbpln	Capsella rubella	AT1G32770.1 | Symbols: ANAC012, SND1, NST3, NAC012 | NAC domain containing protein 12 | chr1:11865343-11866950 REVERSE LENGTH=358	360	358	1.00E-173	99.4	85.3	89.2
Rsa1.0_00043.1.g2501.t1	gb|EOA37905.1| hypothetical protein CARUB_v10009372mg [Capsella rubella]	394	394	0	100.0	90.9	95.7	hypothetical protein CARUB_v10009372mg	gbpln	Capsella rubella	AT1G32780.1 | Symbols: | GroES-like zinc-binding dehydrogenase family protein | chr1:11869977-11872595 REVERSE LENGTH=394	394	394	0	100.0	90.9	94.4
Rsa1.0_00043.1.g2502.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2503.t2	ref|XP_002891012.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336854|gb|EFH67271.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	833	894	0	107.3	72.3	82.5	ubiquitin carboxyl-terminal hydrolase family protein	gbpln	Arabidopsis lyrata	AT1G32850.1 | Symbols: UBP11 | ubiquitin-specific protease 11 | chr1:11902629-11906900 FORWARD LENGTH=892	833	892	0	107.1	69.7	81.0
Rsa1.0_00043.1.g2504.t1	ref|NP_174566.1| granule-bound starch synthase [Arabidopsis thaliana] gi|29337142|sp|Q9MAQ0.1|SSG1_ARATH RecName: Full=Probable granule-bound starch synthase 1, chloroplastic/amyloplastic; AltName: Full=Granule-bound starch synthase I; Short=GBSS-I; Flags: Precursor gi|6910568|gb|AAF31273.1|AC006424_2 granule-bound starch synthase [Arabidopsis thaliana] gi|20453077|gb|AAM19783.1| At1g32900/F9L11_8 [Arabidopsis thaliana] gi|21595154|gb|AAM66076.1| starch synthase, putative [Arabidopsis thaliana] gi|21703108|gb|AAM74496.1| At1g32900/F9L11_8 [Arabidopsis thaliana] gi|23506181|gb|AAN31102.1| At1g32900/F9L11_8 [Arabidopsis thaliana] gi|332193416|gb|AEE31537.1| granule-bound starch synthase [Arabidopsis thaliana]	608	610	0	100.3	90.0	93.9	granule-bound starch synthase	gbpln	Arabidopsis thaliana	AT1G32900.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:11920582-11923506 REVERSE LENGTH=610	608	610	0	100.3	90.0	93.9

Rsa1.0_00043.1.g2505.t1	ref|NP_199780.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75264223|sp|Q9LTA3.1|U91C1_ARATH RecName: Full=UDP-glycosyltransferase 91C1 gi|8978266|dbj|BAA98157.1| anthocyanidin-3-glucoside rhamnosyltransferase-like [Arabidopsis thaliana] gi|26449402|dbj|BAC41828.1| putative anthocyanidin-3-glucoside rhamnosyltransferase [Arabidopsis thaliana] gi|28951061|gb|AAO63454.1| At5g49690 [Arabidopsis thaliana] gi|332008462|gb|AED95845.1| UDP-glycosyltransferase 91C1 [Arabidopsis thaliana]	453	460	0	101.5	75.1	83.7	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G49690.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:20189968-20191350 REVERSE LENGTH=460	453	460	0	101.5	75.1	83.7
Rsa1.0_00043.1.g2506.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1466	1485	0	101.3	41.3	54.4	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1466	158	7.00E-28	10.8	3.8	5.5
Rsa1.0_00043.1.g2507.t1	ref|XP_002893492.1| hypothetical protein ARALYDRAFT_890322 [Arabidopsis lyrata subsp. lyrata] gi|297339334|gb|EFH69751.1| hypothetical protein ARALYDRAFT_890322 [Arabidopsis lyrata subsp. lyrata]	334	322	1.00E-81	96.4	49.1	68.3	hypothetical protein ARALYDRAFT_890322	gbpln	Arabidopsis lyrata	AT1G61470.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr1:22678185-22679021 FORWARD LENGTH=278	334	278	4.00E-78	83.2	41.6	55.7
Rsa1.0_00043.1.g2508.t1	ref|XP_002891017.1| hypothetical protein ARALYDRAFT_473474 [Arabidopsis lyrata subsp. lyrata] gi|297336859|gb|EFH67276.1| hypothetical protein ARALYDRAFT_473474 [Arabidopsis lyrata subsp. lyrata]	78	82	7.00E-20	105.1	73.1	80.8	hypothetical protein ARALYDRAFT_473474	gbpln	Arabidopsis lyrata	AT1G32928.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G32920.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:11931332-11931586 FORWARD LENGTH=84	78	84	2.00E-22	107.7	75.6	82.1
Rsa1.0_00043.1.g2509.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2510.t1	gb|EOA37890.1| hypothetical protein CARUB_v10009358mg [Capsella rubella]	79	397	5.00E-18	502.5	63.3	74.7	hypothetical protein CARUB_v10009358mg	gbpln	Capsella rubella	AT1G32930.1 | Symbols: | Galactosyltransferase family protein | chr1:11931980-11934399 REVERSE LENGTH=399	79	399	6.00E-20	505.1	63.3	73.4
Rsa1.0_00043.1.g2511.t1	ref|XP_002872503.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318340|gb|EFH48762.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	86	89	1.00E-30	103.5	76.7	86.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G10270.1 | Symbols: | Wound-responsive family protein | chr4:6374805-6375077 FORWARD LENGTH=90	86	90	1.00E-29	104.7	74.4	82.6
Rsa1.0_00043.1.g2512.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2513.t1	gb|EOA35150.1| hypothetical protein CARUB_v10020289mg, partial [Capsella rubella]	556	449	1.00E-139	80.8	45.5	52.0	hypothetical protein CARUB_v10020289mg, partial	gbpln	Capsella rubella	AT1G73810.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:27752506-27755208 REVERSE LENGTH=418	556	418	1.00E-138	75.2	45.3	50.5
Rsa1.0_00043.1.g2514.t1	ref|NP_174606.2| tetratricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332193468|gb|AEE31589.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	832	798	0	95.9	78.4	85.9	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G33400.1 | Symbols: TPR9 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:12104891-12109488 REVERSE LENGTH=798	832	798	0	95.9	78.4	85.9
Rsa1.0_00043.1.g2515.t1	ref|NP_001185129.1| suppressor of auxin resistance1 protein [Arabidopsis thaliana] gi|332193470|gb|AEE31591.1| suppressor of auxin resistance1 protein [Arabidopsis thaliana]	1468	1504	0	102.5	82.2	89.1	suppressor of auxin resistance1 protein	gbpln	Arabidopsis thaliana	AT1G33410.2 | Symbols: SAR1 | SUPPRESSOR OF AUXIN RESISTANCE1 | chr1:12109769-12118828 REVERSE LENGTH=1504	1468	1504	0	102.5	82.2	89.1
Rsa1.0_00043.1.g2516.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00043.1.g2517.t1	gb|EOA37671.1| hypothetical protein CARUB_v10012280mg [Capsella rubella]	720	704	0	97.8	76.8	84.4	hypothetical protein CARUB_v10012280mg	gbpln	Capsella rubella	AT1G33420.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:12121063-12123346 REVERSE LENGTH=697	720	697	0	96.8	77.1	83.5
Rsa1.0_00043.1.g2518.t1	ref|XP_002885337.1| hypothetical protein ARALYDRAFT_898378 [Arabidopsis lyrata subsp. lyrata] gi|297331177|gb|EFH61596.1| hypothetical protein ARALYDRAFT_898378 [Arabidopsis lyrata subsp. lyrata]	374	392	1.00E-104	104.8	55.6	73.0	hypothetical protein ARALYDRAFT_898378	gbpln	Arabidopsis lyrata	AT3G20030.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6990254-6991462 FORWARD LENGTH=402	374	402	3.00E-97	107.5	55.6	70.3
Rsa1.0_00043.1.g2519.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00043.1.g2520.t1	gb|EOA37666.1| hypothetical protein CARUB_v10012254mg [Capsella rubella]	389	401	0	103.1	94.9	97.2	hypothetical protein CARUB_v10012254mg	gbpln	Capsella rubella	AT1G33430.1 | Symbols: | Galactosyltransferase family protein | chr1:12124438-12126052 REVERSE LENGTH=395	389	395	0	101.5	93.8	96.9
Rsa1.0_00043.1.g2521.t1	dbj|BAE79546.1| carotenoid isomerase [Chrysanthemum x morifolium]	66	641	2.00E-30	971.2	92.4	98.5	carotenoid isomerase	gbpln	Chrysanthemum x	AT1G06820.1 | Symbols: CRTISO, CCR2 | carotenoid isomerase | chr1:2093145-2096220 REVERSE LENGTH=595	66	595	3.00E-25	901.5	72.7	75.8
Rsa1.0_00044.1.g2522.t1	gb|EOA20241.1| hypothetical protein CARUB_v10000542mg [Capsella rubella]	584	588	0	100.7	94.5	97.3	hypothetical protein CARUB_v10000542mg	gbpln	Capsella rubella	AT5G25880.1 | Symbols: ATNADP-ME3, NADP-ME3 | NADP-malic enzyme 3 | chr5:9024549-9028260 FORWARD LENGTH=588	584	588	0	100.7	93.5	96.6
Rsa1.0_00044.1.g2523.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00044.1.g2524.t1	ref|NP_568478.1| auxin-responsive protein IAA28 [Arabidopsis thaliana] gi|11131406|sp|Q9XFM0.1|IAA28_ARATH RecName: Full=Auxin-responsive protein IAA28; AltName: Full=Indoleacetic acid-induced protein 28 gi|4929493|gb|AAD34019.1|AF149816_1 IAA28 [Arabidopsis thaliana] gi|23306354|gb|AAN17404.1| putative protein [Arabidopsis thaliana] gi|25084149|gb|AAN72186.1| putative protein [Arabidopsis thaliana] gi|49616373|gb|AAT67083.1| IAA28 [Arabidopsis thaliana] gi|110736579|dbj|BAF00255.1| IAA28 [Arabidopsis thaliana] gi|284794587|gb|ADB93666.1| indole-3-acetic acid inducible 28 [Arabidopsis thaliana] gi|284794589|gb|ADB93667.1| indole-3-acetic acid inducible 28 [Arabidopsis thaliana] gi|284794591|gb|ADB93668.1| indole-3-acetic acid inducible 28 [Arabidopsis thaliana] gi|304322548|gb|ADL70761.1| indole-3-acetic acid inducible 28 [Arabidopsis thaliana] gi|304322560|gb|ADL70767.1| indole-3-acetic acid inducible 28 [Arabidopsis thaliana] gi|304322566|gb|ADL70770.1| indole-3-acetic acid inducible 28 [Arabidopsis thaliana] gi|304322570|gb|ADL70772.1| indole-3-acetic acid inducible 28 [Arabidopsis	174	175	2.00E-77	100.6	89.7	93.1	auxin-responsive protein IAA28	gbpln	Arabidopsis thaliana	AT5G25890.1 | Symbols: IAA28, IAR2 | indole-3-acetic acid inducible 28 | chr5:9033480-9034554 FORWARD LENGTH=175	174	175	6.00E-80	100.6	89.7	93.1
Rsa1.0_00044.1.g2525.t1	dbj|BAJ33740.1| unnamed protein product [Thellungiella halophila]	506	506	0	100.0	91.3	95.3	unnamed protein product	----	----	AT5G25900.1 | Symbols: GA3, CYP701A3, ATKO1 | GA requiring 3 | chr5:9036073-9038278 FORWARD LENGTH=509	506	509	0	100.6	89.7	95.3
Rsa1.0_00044.1.g2526.t1	ref|XP_002872190.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297318027|gb|EFH48449.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	1005	1005	0	100.0	81.7	87.7	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT5G25930.1 | Symbols: | Protein kinase family protein with leucine-rich repeat domain | chr5:9050880-9053978 FORWARD LENGTH=1005	1005	1005	0	100.0	81.1	87.3
Rsa1.0_00044.1.g2527.t1	ref|NP_197965.1| Protein kinase family protein with leucine-rich repeat domain [Arabidopsis thaliana] gi|5107831|gb|AAD40144.1|AF149413_25 contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana] gi|28393326|gb|AAO42089.1| putative receptor protein kinase [Arabidopsis thaliana] gi|224589685|gb|ACN59374.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332006119|gb|AED93502.1| Protein kinase family protein with leucine-rich repeat domain [Arabidopsis thaliana]	371	1005	2.00E-56	270.9	29.4	35.3	Protein kinase family protein with leucine-rich repeat domain	gbpln	Arabidopsis thaliana	AT5G25930.1 | Symbols: | Protein kinase family protein with leucine-rich repeat domain | chr5:9050880-9053978 FORWARD LENGTH=1005	371	1005	5.00E-59	270.9	29.4	35.3
Rsa1.0_00044.1.g2528.t1	ref|XP_002874288.1| hypothetical protein ARALYDRAFT_351609 [Arabidopsis lyrata subsp. lyrata] gi|297320125|gb|EFH50547.1| hypothetical protein ARALYDRAFT_351609 [Arabidopsis lyrata subsp. lyrata]	412	413	0	100.2	79.4	87.6	hypothetical protein ARALYDRAFT_351609	gbpln	Arabidopsis lyrata	AT5G25950.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:9057929-9059860 REVERSE LENGTH=432	412	432	0	104.9	75.5	86.4
Rsa1.0_00044.1.g2529.t1	gb|EOA19883.1| hypothetical protein CARUB_v10000132mg [Capsella rubella]	160	1006	1.00E-55	628.8	66.3	78.1	hypothetical protein CARUB_v10000132mg	gbpln	Capsella rubella	AT5G25930.1 | Symbols: | Protein kinase family protein with leucine-rich repeat domain | chr5:9050880-9053978 FORWARD LENGTH=1005	160	1005	1.00E-57	628.1	65.0	78.1

<table>
<tr><td>Rsa1.0_00044.1.g2530.t1</td><td>ref|XP_002874288.1| hypothetical protein ARALYDRAFT_351609 [Arabidopsis lyrata subsp. lyrata] gi|297320125|gb|EFH50547.1| hypothetical protein ARALYDRAFT_351609 [Arabidopsis lyrata subsp. lyrata]</td><td>412</td><td>413</td><td>0</td><td>100.2</td><td>79.6</td><td>89.3</td><td>hypothetical protein ARALYDRAFT_351609</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G25950.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:9057929-9059860 REVERSE LENGTH=432</td><td>412</td><td>432</td><td>0</td><td>104.9</td><td>74.0</td><td>86.2</td></tr>
<tr><td>Rsa1.0_00044.1.g2531.t1</td><td>ref|XP_002872192.1| hypothetical protein ARALYDRAFT_910666 [Arabidopsis lyrata subsp. lyrata] gi|297318029|gb|EFH48451.1| hypothetical protein ARALYDRAFT_910666 [Arabidopsis lyrata subsp. lyrata]</td><td>448</td><td>386</td><td>0</td><td>86.2</td><td>73.7</td><td>79.0</td><td>hypothetical protein ARALYDRAFT_910666</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G25970.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:9066697-9067974 FORWARD LENGTH=387</td><td>448</td><td>387</td><td>0</td><td>86.4</td><td>72.5</td><td>78.1</td></tr>
<tr><td>Rsa1.0_00044.1.g2532.t1</td><td>gb|EOA23016.1| hypothetical protein CARUB_v10003772mg [Capsella rubella]</td><td>338</td><td>331</td><td>1.00E-157</td><td>97.9</td><td>82.0</td><td>89.1</td><td>hypothetical protein CARUB_v10003772mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G26010.1 | Symbols: | Protein phosphatase 2C family protein | chr5:9085512-9087372 REVERSE LENGTH=331</td><td>338</td><td>331</td><td>1.00E-158</td><td>97.9</td><td>83.7</td><td>89.6</td></tr>
<tr><td>Rsa1.0_00044.1.g2533.t1</td><td>ref|XP_002872194.1| ferrochelatase I [Arabidopsis lyrata subsp. lyrata] gi|297318031|gb|EFH48453.1| ferrochelatase I [Arabidopsis lyrata subsp. lyrata]</td><td>466</td><td>466</td><td>0</td><td>100.0</td><td>86.9</td><td>91.4</td><td>ferrochelatase I</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G26030.2 | Symbols: FC1, FC-I, ATFC-I | ferrochelatase 1 | chr5:9096675-9098752 FORWARD LENGTH=466</td><td>466</td><td>466</td><td>0</td><td>100.0</td><td>85.4</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00044.1.g2534.t1</td><td>ref|NP_568480.2| histone deacetylase 2 [Arabidopsis thaliana] gi|145558941|sp|Q944K3.2|HDA2_ARATH RecName: Full=Histone deacetylase 2 gi|332006134|gb|AED93517.1| histone deacetylase 2 [Arabidopsis thaliana]</td><td>349</td><td>387</td><td>0</td><td>110.9</td><td>88.8</td><td>93.4</td><td>histone deacetylase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G26040.2 | Symbols: HDA2 | histone deacetylase 2 | chr5:9099321-9101598 REVERSE LENGTH=387</td><td>349</td><td>387</td><td>0</td><td>110.9</td><td>88.8</td><td>93.4</td></tr>
<tr><td>Rsa1.0_00044.1.g2535.t1</td><td>gb|AAD40130.1|AF149413_11 T1N24.10 gene product [Arabidopsis thaliana]</td><td>157</td><td>375</td><td>5.00E-69</td><td>238.9</td><td>80.3</td><td>90.4</td><td>T1N24.10 gene product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G26050.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:9103395-9103877 REVERSE LENGTH=160</td><td>157</td><td>160</td><td>3.00E-70</td><td>101.9</td><td>80.3</td><td>90.4</td></tr>
<tr><td>Rsa1.0_00044.1.g2536.t1</td><td>ref|NP_568481.1| self-incompatibility S1 family protein [Arabidopsis thaliana] gi|51969422|dbj|BAD43403.1| unknown protein [Arabidopsis thaliana] gi|51969814|dbj|BAD43599.1| unknown protein [Arabidopsis thaliana] gi|91806910|gb|ABE66182.1| S1 self-incompatibility protein-like protein [Arabidopsis thaliana] gi|332006136|gb|AED93519.1| self-incompatibility S1 family protein [Arabidopsis thaliana]</td><td>155</td><td>154</td><td>2.00E-70</td><td>99.4</td><td>79.4</td><td>92.3</td><td>self-incompatibility S1 family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G26060.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:9105013-9105477 REVERSE LENGTH=154</td><td>155</td><td>154</td><td>5.00E-73</td><td>99.4</td><td>79.4</td><td>92.3</td></tr>
<tr><td>Rsa1.0_00044.1.g2537.t1</td><td>ref|NP_197979.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|67633826|gb|AAY78837.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|332006137|gb|AED93520.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]</td><td>166</td><td>102</td><td>6.00E-13</td><td>61.4</td><td>47.0</td><td>49.4</td><td>hydroxyproline-rich glycoprotein family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G26070.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:9106341-9106649 FORWARD LENGTH=102</td><td>166</td><td>102</td><td>2.00E-15</td><td>61.4</td><td>47.0</td><td>49.4</td></tr>
<tr><td>Rsa1.0_00044.1.g2538.t1</td><td>gb|EOA19542.1| hypothetical protein CARUB_v10002514mg [Capsella rubella]</td><td>194</td><td>398</td><td>1.00E-68</td><td>205.2</td><td>64.4</td><td>71.6</td><td>hypothetical protein CARUB_v10002514mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G26090.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:9109026-9113235 REVERSE LENGTH=401</td><td>194</td><td>401</td><td>3.00E-68</td><td>206.7</td><td>59.8</td><td>68.6</td></tr>
<tr><td>Rsa1.0_00044.1.g2539.t1</td><td>ref|XP_002886410.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297332251|gb|EFH62669.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>386</td><td>226</td><td>1.00E-110</td><td>58.5</td><td>51.0</td><td>53.4</td><td>ATP binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G26110.1 | Symbols: | Protein kinase superfamily protein | chr5:9118239-9119352 REVERSE LENGTH=226</td><td>386</td><td>226</td><td>1.00E-112</td><td>58.5</td><td>51.0</td><td>52.8</td></tr>
<tr><td>Rsa1.0_00044.1.g2540.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>111</td><td>1274</td><td>3.00E-24</td><td>1147.7</td><td>49.5</td><td>63.1</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00044.1.g2541.t1</td><td>ref|NP_197988.3| uncharacterized protein [Arabidopsis thaliana] gi|30793967|gb|AAP40435.1| unknown protein [Arabidopsis thaliana] gi|110736920|dbj|BAF00417.1| hypothetical protein [Arabidopsis thaliana] gi|332006148|gb|AED93531.1| uncharacterized protein AT5G26160 [Arabidopsis thaliana]</td><td>926</td><td>976</td><td>0</td><td>105.4</td><td>74.4</td><td>83.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G26160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G20610.1); Has 197 Blast hits to 158 proteins in 44 species: Archae - 0; Bacteria - 14; Metazoa - 28; Fungi - 15; Plants - 117; Viruses - 2; Other Eukaryotes - 21 (source: NCBI BLink). | chr5:9143269-9146312 FORWARD LENGTH=976</td><td>926</td><td>976</td><td>0</td><td>105.4</td><td>74.4</td><td>83.2</td></tr>
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Rsa1.0_00044.1.g2542.t1	ref|NP_197989.2| putative WRKY transcription factor 50 [Arabidopsis thaliana] gi|29839580|sp|Q8VWQ5.1|WRK50_ARATH RecName: Full=Probable WRKY transcription factor 50; AltName: Full=WRKY DNA-binding protein 50 gi|18252117|gb|AAL61857.1| WRKY transcription factor 50 [Arabidopsis thaliana] gi|225898933|dbj|BAH30597.1| hypothetical protein [Arabidopsis thaliana] gi|332006149|gb|AED93532.1| putative WRKY transcription factor 50 [Arabidopsis thaliana]	177	173	3.00E-67	97.7	78.0	85.3	putative WRKY transcription factor 50	gbpln	Arabidopsis thaliana	AT5G26170.1 | Symbols: WRKY50, ATWRKY50 | WRKY DNA-binding protein 50 | chr5:9147176-9148128 REVERSE LENGTH=173	177	173	1.00E-69	97.7	78.0	85.3
Rsa1.0_00044.1.g2543.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00044.1.g2544.t1	gb|EOA22853.1| hypothetical protein CARUB_v10003583mg [Capsella rubella]	340	344	1.00E-174	101.2	87.9	94.7	hypothetical protein CARUB_v10003583mg	gbpln	Capsella rubella	AT5G26200.1 | Symbols: | Mitochondrial substrate carrier family protein | chr5:9157268-9158296 FORWARD LENGTH=342	340	342	1.00E-174	100.6	86.5	94.7
Rsa1.0_00044.1.g2545.t1	ref|XP_002516111.1| DNA binding protein, putative [Ricinus communis] gi|223544597|gb|EEF46113.1| DNA binding protein, putative [Ricinus communis]	260	251	1.00E-107	96.5	79.6	88.5	DNA binding protein, putative	gbpln	Ricinus communis	AT5G26210.1 | Symbols: AL4 | alfin-like 4 | chr5:9158566-9160221 REVERSE LENGTH=255	260	255	5.00E-97	98.1	88.8	93.5
Rsa1.0_00044.1.g2546.t1	ref|NP_198719.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|75333904|sp|Q9FID5.1|Y5393_ARATH RecName: Full=Probable receptor-like protein kinase At5g39030; Flags: Precursor gi|10177548|dbj|BAB10827.1| receptor protein kinase-like protein [Arabidopsis thaliana] gi|332007006|gb|AED94389.1| putative receptor-like protein kinase [Arabidopsis thaliana]	780	806	0	103.3	64.5	76.4	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G39030.1 | Symbols: | Protein kinase superfamily protein | chr5:15620066-15622486 FORWARD LENGTH=806	780	806	0	103.3	64.5	76.4
Rsa1.0_00044.1.g2547.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00044.1.g2548.t1	ref|NP_197995.1| uncharacterized protein [Arabidopsis thaliana] gi|122214260|sp|Q3E936.1|MAKR1_ARATH RecName: Full=Probable membrane-associated kinase regulator 1 gi|332006156|gb|AED93539.1| uncharacterized protein AT5G26230 [Arabidopsis thaliana]	331	341	1.00E-105	103.0	78.5	85.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G26230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9173517-9174542 REVERSE LENGTH=341	331	341	1.00E-108	103.0	78.5	85.8
Rsa1.0_00044.1.g2549.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00044.1.g2550.t1	ref|NP_197996.1| chloride channel protein CLC-d [Arabidopsis thaliana] gi|41688458|sp|P92943.2|CLCD_ARATH RecName: Full=Chloride channel protein CLC-d; Short=AtCLC-d; AltName: Full=CBS domain-containing protein CBSCLC2 gi|332006157|gb|AED93540.1| chloride channel protein CLC-d [Arabidopsis thaliana]	793	792	0	99.9	96.3	97.9	chloride channel protein CLC-d	gbpln	Arabidopsis thaliana	AT5G26240.1 | Symbols: CLC-D, ATCLC-D | chloride channel D | chr5:9189622-9194347 FORWARD LENGTH=792	793	792	0	99.9	96.3	97.9
Rsa1.0_00044.1.g2551.t1	gb|EOA22969.1| hypothetical protein CARUB_v10003709mg [Capsella rubella]	499	507	0	101.6	83.6	92.0	hypothetical protein CARUB_v10003709mg	gbpln	Capsella rubella	AT5G26250.1 | Symbols: | Major facilitator superfamily protein | chr5:9196758-9198681 FORWARD LENGTH=507	499	507	0	101.6	83.6	92.0
Rsa1.0_00044.1.g2552.t1	ref|XP_002872211.1| hypothetical protein ARALYDRAFT_489472 [Arabidopsis lyrata subsp. lyrata] gi|297318048|gb|EFH48470.1| hypothetical protein ARALYDRAFT_489472 [Arabidopsis lyrata subsp. lyrata]	350	350	1.00E-174	100.0	86.0	89.7	hypothetical protein ARALYDRAFT_489472	gbpln	Arabidopsis lyrata	AT5G26280.1 | Symbols: | TRAF-like family protein | chr5:9208724-9210403 FORWARD LENGTH=350	350	350	1.00E-176	100.0	85.4	90.0
Rsa1.0_00044.1.g2553.t3	ref|XP_002872211.1| hypothetical protein ARALYDRAFT_489472 [Arabidopsis lyrata subsp. lyrata] gi|297318048|gb|EFH48470.1| hypothetical protein ARALYDRAFT_489472 [Arabidopsis lyrata subsp. lyrata]	357	350	1.00E-158	98.0	79.0	85.2	hypothetical protein ARALYDRAFT_489472	gbpln	Arabidopsis lyrata	AT5G26280.1 | Symbols: | TRAF-like family protein | chr5:9208724-9210403 FORWARD LENGTH=350	357	350	1.00E-157	98.0	76.8	84.6

Rsa1.0_00044.1.g2554.t1	ref|NP_198006.1| sugar transport protein 13 [Arabidopsis thaliana] gi|85701281|sp|Q94AZ2.2|STP13_ARATH RecName: Full=Sugar transport protein 13; AltName: Full=Hexose transporter 13; AltName: Full=Multicopy suppressor of snf4 deficiency protein 1 gi|9965739|gb|AAG10146.1|AF250340_1 putative hexose transporter MSS1 [Arabidopsis thaliana] gi|3319354|gb|AAC26243.1| contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana] gi|15450649|gb|AAK96596.1| AT5g26340/F9D12_17 [Arabidopsis thaliana] gi|15487258|emb|CAC69074.1| STP13 protein [Arabidopsis thaliana] gi|332006170|gb|AED93553.1| sugar transport protein 13 [Arabidopsis thaliana]	349	526	1.00E−153	150.7	76.5	81.4	sugar transport protein 13	gbpln	Arabidopsis thaliana	AT5G26340.1 | Symbols: MSS1, STP13, ATSTP13 | Major facilitator superfamily protein | chr5:9243851−9246994 REVERSE LENGTH=526	349	526	1.00E−155	150.7	76.5	81.4
Rsa1.0_00044.1.g2555.t1	gb|EOA20395.1| hypothetical protein CARUB_v10000707mg [Capsella rubella]	196	525	6.00E−92	267.9	88.8	92.9	hypothetical protein CARUB_v10000707mg	gbpln	Capsella rubella	AT5G26340.1 | Symbols: MSS1, STP13, ATSTP13 | Major facilitator superfamily protein | chr5:9243851−9246994 REVERSE LENGTH=526	196	526	3.00E−92	268.4	85.7	90.3
Rsa1.0_00044.1.g2556.t8	gb|AAD21778.1| putative non−LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1831	1715	0	93.7	32.4	46.5	putative non−LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G26667.3 | Symbols: PYR6 | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:9276659−9278091 FORWARD LENGTH=202	1831	202	1.00E−105	11.0	10.3	10.6
Rsa1.0_00044.1.g2557.t1	emb|CAA09196.1| RNA helicase [Arabidopsis thaliana]	813	748	0	92.0	83.8	87.2	RNA helicase	gbpln	Arabidopsis thaliana	AT5G26742.2 | Symbols: emb1138 | DEAD box RNA helicase (RH3) | chr5:9285540−9288871 REVERSE LENGTH=748	813	748	0	92.0	83.8	87.2
Rsa1.0_00044.1.g2558.t1	gb|EOA20719.1| hypothetical protein CARUB_v10001039mg [Capsella rubella]	420	422	0	100.5	92.6	94.5	hypothetical protein CARUB_v10001039mg	gbpln	Capsella rubella	AT5G26740.3 | Symbols: | Protein of unknown function (DUF300) | chr5:9292436−9294407 FORWARD LENGTH=422	420	422	0	100.5	91.7	94.0
Rsa1.0_00044.1.g2559.t1	gb|AAM64547.1| unknown [Arabidopsis thaliana]	101	99	6.00E−22	98.0	60.4	64.4	unknown	gbpln	Arabidopsis thaliana	AT5G26731.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:9295676−9295975 FORWARD LENGTH=99	101	99	1.00E−24	98.0	60.4	64.4
Rsa1.0_00044.1.g2560.t1	gb|EOA19490.1| hypothetical protein CARUB_v10002163mg, partial [Capsella rubella]	100	158	3.00E−37	158.0	80.0	93.0	hypothetical protein CARUB_v10002163mg, partial	gbpln	Capsella rubella	AT3G05936.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr3:1774062−1774403 REVERSE LENGTH=113	100	113	1.00E−28	113.0	61.0	75.0
Rsa1.0_00044.1.g2561.t1	ref|NP_850872.1| Fasciclin−like arabinogalactan family protein [Arabidopsis thaliana] gi|332006188|gb|AED93571.1| Fasciclin−like arabinogalactan family protein [Arabidopsis thaliana]	105	268	3.00E−40	255.2	89.5	95.2	Fasciclin−like arabinogalactan family protein	gbpln	Arabidopsis thaliana	AT5G26730.1 | Symbols: | Fasciclin−like arabinogalactan family protein | chr5:9300422−9301990 FORWARD LENGTH=268	105	268	4.00E−43	255.2	89.5	95.2
Rsa1.0_00044.1.g2562.t1	ref|XP_002872222.1| hypothetical protein ARALYDRAFT_351658 [Arabidopsis lyrata subsp. lyrata] gi|297318059|gb|EFH48481.1| hypothetical protein ARALYDRAFT_351658 [Arabidopsis lyrata subsp. lyrata]	147	285	1.00E−52	193.9	66.7	85.0	hypothetical protein ARALYDRAFT_351658	gbpln	Arabidopsis lyrata	AT5G26730.1 | Symbols: | Fasciclin−like arabinogalactan family protein | chr5:9300422−9301990 FORWARD LENGTH=268	147	268	7.00E−55	182.3	66.7	85.0
Rsa1.0_00044.1.g2563.t2	ref|NP_850873.1| uncharacterized protein [Arabidopsis thaliana] gi|26451568|dbj|BAC42881.1| unknown protein [Arabidopsis thaliana] gi|28827232|gb|AAO50460.1| unknown protein [Arabidopsis thaliana] gi|332006189|gb|AED93572.1| uncharacterized protein AT5G26720 [Arabidopsis thaliana]	376	134	3.00E−25	35.6	23.4	28.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G26720.1 | Symbols: | unknown protein; Has 15 Blast hits to 15 proteins in 5 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 15; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr5:9304105−9304509 FORWARD LENGTH=134	376	134	7.00E−28	35.6	23.4	28.5
Rsa1.0_00044.1.g2564.t1	gb|AAM61454.1| unknown [Arabidopsis thaliana]	126	126	1.00E−28	100.0	56.3	73.0	unknown	gbpln	Arabidopsis thaliana	AT3G05920.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1768991−1769522 REVERSE LENGTH=126	126	126	3.00E−31	100.0	56.3	73.0

<table>
<tr><td>Rsa1.0_00044.1.g2565.t1</td><td>ref|XP_002874315.1| hypothetical protein ARALYDRAFT_489493 [Arabidopsis lyrata subsp. lyrata] gi|297320152|gb|EFH50574.1| hypothetical protein ARALYDRAFT_489493 [Arabidopsis lyrata subsp. lyrata]</td><td>417</td><td>448</td><td>0</td><td>107.4</td><td>90.9</td><td>95.2</td><td>hypothetical protein ARALYDRAFT_489493</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G26680.2 | Symbols: | 5'-3' exonuclease family protein | chr5:9311882-9315458 REVERSE LENGTH=383</td><td>417</td><td>383</td><td>0</td><td>91.8</td><td>82.5</td><td>85.4</td></tr>
<tr><td>Rsa1.0_00044.1.g2566.t1</td><td>ref|NP_850878.2| Pectinacetylesterase family protein [Arabidopsis thaliana] gi|51536518|gb|AAU05497.1| At5g26670 [Arabidopsis thaliana] gi|332006195|gb|AED93578.1| Pectinacetylesterase family protein [Arabidopsis thaliana]</td><td>416</td><td>416</td><td>0</td><td>100.0</td><td>92.8</td><td>96.6</td><td>Pectinacetylesterase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G26670.1 | Symbols: | Pectinacetylesterase family protein | chr5:9318456-9320816 FORWARD LENGTH=416</td><td>416</td><td>416</td><td>0</td><td>100.0</td><td>92.8</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00044.1.g2567.t1</td><td>gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]</td><td>1755</td><td>1213</td><td>0</td><td>69.1</td><td>25.2</td><td>37.9</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1755</td><td>626</td><td>2.00E-62</td><td>35.7</td><td>9.2</td><td>15.2</td></tr>
<tr><td>Rsa1.0_00044.1.g2568.t1</td><td>ref|NP_850879.1| transcription factor MYB86 [Arabidopsis thaliana] gi|56749347|sp|Q8LPH6.1|MYB86_ARATH RecName: Full=Transcription factor MYB86; AltName: Full=Myb homolog 4; Short=AtMyb4; AltName: Full=Myb-related protein 86; Short=AtMYB86 gi|20466622|gb|AAM20628.1| transcription factor ATMYB4 [Arabidopsis thaliana] gi|30984580|gb|AAP42753.1| At5g26655 [Arabidopsis thaliana] gi|41619424|gb|AAS10099.1| MYB transcription factor [Arabidopsis thaliana] gi|332006197|gb|AED93580.1| transcription factor MYB86 [Arabidopsis thaliana]</td><td>355</td><td>352</td><td>1.00E-159</td><td>99.2</td><td>85.9</td><td>90.4</td><td>transcription factor MYB86</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G26660.1 | Symbols: ATMYB86, MYB86 | myb domain protein 86 | chr5:9331775-9333044 REVERSE LENGTH=352</td><td>355</td><td>352</td><td>1.00E-162</td><td>99.2</td><td>85.9</td><td>90.4</td></tr>
<tr><td>Rsa1.0_00044.1.g2569.t2</td><td>gb|AAD21687.1| Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078 [Arabidopsis thaliana]</td><td>1188</td><td>1415</td><td>0</td><td>119.1</td><td>37.4</td><td>44.9</td><td>Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1188</td><td>1262</td><td>9.00E-86</td><td>106.2</td><td>14.3</td><td>21.9</td></tr>
<tr><td>Rsa1.0_00044.1.g2570.t1</td><td>ref|NP_174444.1| agamous-like MADS-box protein AGL86 [Arabidopsis thaliana] gi|75333444|sp|Q9C6V3.1|AGL86_ARATH RecName: Full=Agamous-like MADS-box protein AGL86 gi|12597831|gb|AAG60141.1|AC074360_6 MADS-box protein, putative [Arabidopsis thaliana] gi|67633410|gb|AAY78630.1| MADS-box family protein [Arabidopsis thaliana] gi|332193257|gb|AEE31378.1| agamous-like MADS-box protein AGL86 [Arabidopsis thaliana]</td><td>364</td><td>339</td><td>7.00E-45</td><td>93.1</td><td>35.7</td><td>49.2</td><td>agamous-like MADS-box protein AGL86</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31630.1 | Symbols: AGL86 | AGAMOUS-like 86 | chr1:11318528-11319547 REVERSE LENGTH=339</td><td>364</td><td>339</td><td>2.00E-47</td><td>93.1</td><td>35.7</td><td>49.2</td></tr>
<tr><td>Rsa1.0_00044.1.g2571.t1</td><td>gb|EAY96485.1| hypothetical protein OsI_18385 [Oryza sativa Indica Group] gi|222630128|gb|EEE62260.1| hypothetical protein OsJ_17047 [Oryza sativa Japonica Group]</td><td>62</td><td>92</td><td>3.00E-19</td><td>148.4</td><td>77.4</td><td>83.9</td><td>hypothetical protein OsI_18385</td><td>gbpln</td><td>Oryza sativa</td><td>AT3G05880.1 | Symbols: RCI2A | Low temperature and salt responsive protein family | chr3:1756195-1756494 REVERSE LENGTH=54</td><td>62</td><td>54</td><td>2.00E-18</td><td>87.1</td><td>67.7</td><td>75.8</td></tr>
<tr><td>Rsa1.0_00044.1.g2572.t1</td><td>ref|XP_004287934.1| PREDICTED: anaphase-promoting complex subunit 11-like isoform 2 [Fragaria vesca subsp. vesca]</td><td>95</td><td>92</td><td>9.00E-42</td><td>96.8</td><td>87.4</td><td>92.6</td><td>PREDICTED: anaphase-promoting complex subunit 11-like isoform 2</td><td>gbpln</td><td>Fragaria vesca</td><td>AT3G05870.2 | Symbols: APC11 | anaphase-promoting complex/cyclosome 11 | chr3:1753961-1754802 FORWARD LENGTH=87</td><td>95</td><td>87</td><td>7.00E-44</td><td>91.6</td><td>88.4</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00044.1.g2573.t1</td><td>gb|EOA19465.1| hypothetical protein CARUB_v10001920mg [Capsella rubella]</td><td>218</td><td>220</td><td>1.00E-48</td><td>100.9</td><td>51.8</td><td>68.3</td><td>hypothetical protein CARUB_v10001920mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G26630.1 | Symbols: | MADS-box transcription factor family protein | chr5:9350815-9351471 FORWARD LENGTH=218</td><td>218</td><td>218</td><td>2.00E-47</td><td>100.0</td><td>48.6</td><td>66.5</td></tr>
<tr><td>Rsa1.0_00044.1.g2574.t1</td><td>ref|XP_002883989.1| hypothetical protein ARALYDRAFT_899939 [Arabidopsis lyrata subsp. lyrata] gi|297329829|gb|EFH60248.1| hypothetical protein ARALYDRAFT_899939 [Arabidopsis lyrata subsp. lyrata]</td><td>240</td><td>352</td><td>3.00E-33</td><td>146.7</td><td>32.5</td><td>44.6</td><td>hypothetical protein ARALYDRAFT_899939</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G19515.2 | Symbols: | CONTAINS InterPro DOMAIN/s: Apoptosis inhibitory 5 (InterPro:IPR008383); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23935.1); Has 546 Blast hits to 394 proteins in 84 species: Archae - 0; Bacteria - 3; Metazoa - 210; Fungi - 15; Plants - 143; Viruses - 0; Other Eukaryotes - 175 (source: NCBI BLink). | chr3:6766872-6771078 REVERSE LENGTH=805</td><td>240</td><td>805</td><td>2.00E-11</td><td>335.4</td><td>22.9</td><td>38.3</td></tr>
<tr><td>Rsa1.0_00044.1.g2575.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00044.1.g2576.t1	gb|ABE65560.1| hypothetical protein At5g26620 [Arabidopsis thaliana]	86	88	2.00E-35	102.3	90.7	94.2	hypothetical protein At5g26620	gbpln	Arabidopsis thaliana	AT3G05858.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26620.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:1749464-1749736 FORWARD LENGTH=90	86	90	6.00E-30	104.7	80.2	86.0
Rsa1.0_00044.1.g2577.t1	ref|XP_002886053.1| hypothetical protein ARALYDRAFT_899963 [Arabidopsis lyrata subsp. lyrata] gi|297331893|gb|EFH62312.1| hypothetical protein ARALYDRAFT_899963 [Arabidopsis lyrata subsp. lyrata]	320	288	9.00E-49	90.0	36.9	50.0	hypothetical protein ARALYDRAFT_899963	gbpln	Arabidopsis lyrata	AT1G22090.1 | Symbols: emb2204 | Protein of unknown function (DUF626) | chr1:7795721-7797252 FORWARD LENGTH=329	320	329	3.00E-32	102.8	29.7	43.4
Rsa1.0_00044.1.g2578.t1	gb|EOA20562.1| hypothetical protein CARUB_v10000875mg [Capsella rubella]	475	473	0	99.6	83.8	90.5	hypothetical protein CARUB_v10000875mg	gbpln	Capsella rubella	AT5G26600.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr5:9377455-9378882 FORWARD LENGTH=475	475	475	0	100.0	82.7	90.3
Rsa1.0_00044.1.g2579.t1	gb|EOA22823.1| hypothetical protein CARUB_v10003541mg [Capsella rubella]	406	409	0	100.7	96.6	97.3	hypothetical protein CARUB_v10003541mg	gbpln	Capsella rubella	AT5G26751.1 | Symbols: ATSK11, SK 11 | shaggy-related kinase 11 | chr5:9399582-9401839 REVERSE LENGTH=405	406	405	0	99.8	96.3	97.3
Rsa1.0_00044.1.g2580.t1	ref|NP_974839.1| uncharacterized protein [Arabidopsis thaliana] gi|380877125|sp|F4K1B1.1|RPAP2_ARATH RecName: Full=Putative RNA polymerase II subunit B1 CTD phosphatase RPAP2 homolog; AltName: Full=RNA polymerase II-associated protein 2 homolog gi|332006215|gb|AED93598.1| uncharacterized protein AT5G26760 [Arabidopsis thaliana]	82	735	1.00E-22	896.3	63.4	75.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G26760.2 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF408 (InterPro:IPR007308); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:9403869-9407170 REVERSE LENGTH=735	82	735	2.00E-25	896.3	63.4	75.6
Rsa1.0_00044.1.g2581.t1	ref|NP_568487.1| uncharacterized protein [Arabidopsis thaliana] gi|42573487|ref|NP_974840.1| uncharacterized protein [Arabidopsis thaliana] gi|332006216|gb|AED93599.1| uncharacterized protein AT5G26770 [Arabidopsis thaliana] gi|332006217|gb|AED93600.1| uncharacterized protein AT5G26770 [Arabidopsis thaliana]	331	335	1.00E-158	101.2	84.9	92.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G26770.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G05830.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:9407981-9409735 REVERSE LENGTH=335	331	335	1.00E-160	101.2	84.9	92.7
Rsa1.0_00045.1.g2582.t1	ref|XP_002874373.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297320210|gb|EFH50632.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	358	370	1.00E-141	103.4	72.9	79.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G27420.1 | Symbols: CNI1, ATL31 | carbon/nitrogen insensitive 1 | chr5:9684119-9685225 FORWARD LENGTH=368	358	368	1.00E-138	102.8	70.7	77.7
Rsa1.0_00045.1.g2583.t1	ref|NP_001190410.1| branched-chain-amino-acid aminotransferase-like protein 2 [Arabidopsis thaliana] gi|332006301|gb|AED93684.1| branched-chain-amino-acid aminotransferase-like protein 2 [Arabidopsis thaliana]	528	936	0	177.3	83.3	90.9	branched-chain-amino-acid aminotransferase-like protein 2	gbpln	Arabidopsis thaliana	AT5G27410.2 | Symbols: | D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein | chr5:9676362-9682468 FORWARD LENGTH=936	528	936	0	177.3	83.3	90.9
Rsa1.0_00045.1.g2584.t1	tpg|DAA63922.1| TPA: hypothetical protein ZEAMMB73_644873 [Zea mays]	92	194	1.00E-11	210.9	41.3	57.6	TPA: hypothetical protein ZEAMMB73_644873	gbenv/gbpln	Zea mays	AT5G27395.2 | Symbols: | Mitochondrial inner membrane translocase complex, subunit Tim44-related protein | chr5:9671845-9674085 REVERSE LENGTH=296	92	296	6.00E-14	321.7	40.2	41.3
Rsa1.0_00045.1.g2585.t1	sp|O23732.1|GSHB_BRAJU RecName: Full=Glutathione synthetase, chloroplastic; Short=GSH synthetase; Short=GSH-S; Short=Glutathione synthase; Flags: Precursor gi|2243118|emb|CAA71878.1| glutathione synthetase [Brassica juncea]	530	530	0	100.0	94.0	95.8	RecName: Full=Glutathione synthetase, chloroplastic; Short=GSH synthetase; Short=GSH-S; Short=Glutathione synthase; Flags: Precursor gi|2243118|emb|CAA71878.1| glutathione synthetase	gbpln	Brassica juncea	AT5G27380.1 | Symbols: GSH2, GSHB | glutathione synthetase 2 | chr5:9668211-9670912 REVERSE LENGTH=539	530	539	0	101.7	77.2	84.9

Rsa1.0_00045.1.g2586.t3	ref|NP_187148.2| DHHC−type zinc finger−containing protein [Arabidopsis thaliana] gi|122214962|sp|Q3EBC2.1|ZDHC5_ARATH RecName: Full=Probable S−acyltransferase At3g04970; AltName: Full=Probable palmitoyltransferase At3g04970; AltName: Full=Zinc finger DHHC domain−containing protein At3g04970 gi|332640648|gb|AEE74169.1| DHHC−type zinc finger−containing protein [Arabidopsis thaliana]	381	397	1.00E−167	104.2	77.2	86.1	DHHC−type zinc finger−containing protein	gbpln	Arabidopsis thaliana	AT3G04970.1 | Symbols: | DHHC−type zinc finger family protein | chr3:1376240−1378339 FORWARD LENGTH=397	381	397	1.00E−169	104.2	77.2	86.1
Rsa1.0_00045.1.g2587.t1	ref|NP_198076.1| DNAJ heat shock N−terminal domain−containing protein [Arabidopsis thaliana] gi|332006279|gb|AED93662.1| DNAJ heat shock N−terminal domain−containing protein [Arabidopsis thaliana]	1063	1104	0	103.9	63.1	75.2	DNAJ heat shock N−terminal domain−containing protein	gbpln	Arabidopsis thaliana	AT5G27240.1 | Symbols: | DNAJ heat shock N−terminal domain−containing protein | chr5:9597552−9600866 FORWARD LENGTH=1104	1063	1104	0	103.9	63.1	75.2
Rsa1.0_00045.1.g2588.t1	gb|EOA19886.1| hypothetical protein CARUB_v10000134mg [Capsella rubella]	866	1000	0	115.5	63.0	77.4	hypothetical protein CARUB_v10000134mg	gbpln	Capsella rubella	AT5G27230.1 | Symbols: | Frigida−like protein | chr5:9584255−9587838 FORWARD LENGTH=948	866	948	0	109.5	62.4	77.4
Rsa1.0_00045.1.g2589.t1	ref|XP_002874392.1| hypothetical protein ARALYDRAFT_910868 [Arabidopsis lyrata subsp. lyrata] gi|297320229|gb|EFH50651.1| hypothetical protein ARALYDRAFT_910868 [Arabidopsis lyrata subsp. lyrata]	855	994	0	116.3	65.7	79.3	hypothetical protein ARALYDRAFT_910868	gbpln	Arabidopsis lyrata	AT5G27230.1 | Symbols: | Frigida−like protein | chr5:9584255−9587838 FORWARD LENGTH=948	855	948	0	110.9	65.3	78.0
Rsa1.0_00045.1.g2590.t1	ref|XP_002874393.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320230|gb|EFH50652.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1192	1191	0	99.9	56.9	72.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G27220.1 | Symbols: | Frigida−like protein | chr5:9578757−9582752 FORWARD LENGTH=1181	1192	1181	0	99.1	54.6	69.6
Rsa1.0_00045.1.g2591.t2	gb|AAC33961.1| contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]	1154	1662	0	144.0	37.2	55.4	contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57)	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1154	575	3.00E−37	49.8	6.4	10.7
Rsa1.0_00045.1.g2592.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00045.1.g2593.t2	ref|XP_002874393.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320230|gb|EFH50652.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	561	1191	8.00E−40	212.3	19.1	22.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G27220.1 | Symbols: | Frigida−like protein | chr5:9578757−9582752 FORWARD LENGTH=1181	561	1181	3.00E−42	210.5	18.7	23.0
Rsa1.0_00045.1.g2594.t1	ref|XP_002866462.1| hypothetical protein ARALYDRAFT_496364 [Arabidopsis lyrata subsp. lyrata] gi|297312297|gb|EFH42721.1| hypothetical protein ARALYDRAFT_496364 [Arabidopsis lyrata subsp. lyrata]	146	400	1.00E−25	274.0	37.7	43.8	hypothetical protein ARALYDRAFT_496364	gbpln	Arabidopsis lyrata	AT5G61930.2 | Symbols: APO3 | Arabidopsis thaliana protein of unknown function (DUF794) | chr5:24866230−24867665 REVERSE LENGTH=402	146	402	1.00E−27	275.3	37.0	43.2
Rsa1.0_00045.1.g2595.t6	gb|EOA13406.1| hypothetical protein CARUB_v10026444mg, partial [Capsella rubella]	929	430	1.00E−107	46.3	24.4	29.9	hypothetical protein CARUB_v10026444mg, partial	gbpln	Capsella rubella	AT5G62660.1 | Symbols: | F−box and associated interaction domains−containing protein | chr5:25156326−25157465 REVERSE LENGTH=379	929	379	1.00E−101	40.8	21.6	26.6
Rsa1.0_00045.1.g2596.t25	ref|XP_002874217.1| hypothetical protein ARALYDRAFT_489332 [Arabidopsis lyrata subsp. lyrata] gi|297320054|gb|EFH50476.1| hypothetical protein ARALYDRAFT_489332 [Arabidopsis lyrata subsp. lyrata]	1281	1376	0	107.4	84.9	89.0	hypothetical protein ARALYDRAFT_489332	gbpln	Arabidopsis lyrata	AT5G24710.1 | Symbols: | Transducin/WD40 repeat−like superfamily protein | chr5:8459148−8467920 REVERSE LENGTH=1377	1281	1377	0	107.5	84.9	89.1
Rsa1.0_00045.1.g2597.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00045.1.g2598.t1	ref|NP_198074.1| Frigida−like protein [Arabidopsis thaliana] gi|2191186|gb|AAB61071.1| contains similarity to tropomyosin and kinesin [Arabidopsis thaliana] gi|332006276|gb|AED93659.1| Frigida−like protein [Arabidopsis thaliana]	1421	1181	1.00E−177	83.1	35.4	48.9	Frigida−like protein	gbpln	Arabidopsis thaliana	AT5G27220.1 | Symbols: | Frigida−like protein | chr5:9578757−9582752 FORWARD LENGTH=1181	1421	1181	1.00E−180	83.1	35.4	48.9
Rsa1.0_00045.1.g2599.t1	ref|XP_002874393.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320230|gb|EFH50652.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	869	1191	0	137.1	51.9	69.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G27220.1 | Symbols: | Frigida−like protein | chr5:9578757−9582752 FORWARD LENGTH=1181	869	1181	0	135.9	50.7	67.9

Rsa1.0_00045.1.g2600.t1	ref|NP_198073.1| uncharacterized protein [Arabidopsis thaliana] gi|332006275|gb|AED93658.1| uncharacterized protein AT5G27210 [Arabidopsis thaliana]	331	297	1.00E-140	89.7	77.9	82.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G27210.1 | Symbols: | Protein of unknown function, transmembrane-40 | chr5:9572333-9574075 REVERSE LENGTH=297	331	297	1.00E-143	89.7	77.9	82.5
Rsa1.0_00045.1.g2601.t1	gb|ACZ92142.1| Na+/H+ antiporter [Brassica napus]	546	542	0	99.3	96.3	97.8	Na+/H+ antiporter	gbpln	Brassica napus	AT5G27150.1 | Symbols: NHX1, ATNHX, AT-NHX1, ATNHX1 | Na+/H+ exchanger 1 | chr5:9554251-9557266 FORWARD LENGTH=538	546	538	0	98.5	90.7	95.1
Rsa1.0_00045.1.g2602.t1	ref|NP_198064.1| putative nucleolar protein 5-1 [Arabidopsis thaliana] gi|147744575|sp|O04658.2|NOP5A_ARATH RecName: Full=Probable nucleolar protein 5-1; AltName: Full=MAR-binding NOP56/58 homolog 1; AltName: Full=NOP58-like protein F108; AltName: Full=Nucleolar protein 58-1 gi|11878185|gb|AAG40836.1|AF302490_1 NOP58-like protein F108 [Arabidopsis thaliana] gi|18377656|gb|AAL66978.1| putative SAR DNA-binding protein [Arabidopsis thaliana] gi|20465699|gb|AAM20318.1| putative SAR DNA-binding protein [Arabidopsis thaliana] gi|332006269|gb|AED93652.1| putative nucleolar protein 5-1 [Arabidopsis thaliana]	532	533	0	100.2	75.6	79.9	putative nucleolar protein 5-1	gbpln	Arabidopsis thaliana	AT5G27120.1 | Symbols: | NOP56-like pre RNA processing ribonucleoprotein | chr5:9541287-9543684 FORWARD LENGTH=533	532	533	0	100.2	75.6	79.9
Rsa1.0_00045.1.g2603.t1	ref|XP_002874409.1| seed maturation family protein [Arabidopsis lyrata subsp. lyrata] gi|297320246|gb|EFH50668.1| seed maturation family protein [Arabidopsis lyrata subsp. lyrata]	185	192	1.00E-73	103.8	87.0	90.8	seed maturation family protein	gbpln	Arabidopsis lyrata	AT5G27980.1 | Symbols: | Seed maturation protein | chr5:10015883-10016676 REVERSE LENGTH=192	185	192	9.00E-76	103.8	87.0	90.8
Rsa1.0_00045.1.g2604.t1	gb|EOA21519.1| hypothetical protein CARUB_v10001923mg, partial [Capsella rubella]	194	220	8.00E-58	113.4	63.4	76.3	hypothetical protein CARUB_v10001923mg, partial	gbpln	Capsella rubella	AT5G27990.1 | Symbols: | Pre-rRNA-processing protein TSR2, conserved region | chr5:10017358-10018265 FORWARD LENGTH=184	194	184	2.00E-56	94.8	59.8	70.6
Rsa1.0_00045.1.g2605.t1	emb|CAA71799.1| O-acetylserine(thiol) lyase [Brassica juncea]	323	345	1.00E-163	106.8	94.4	97.8	O-acetylserine(thiol) lyase	gbpln	Brassica juncea	AT5G28020.6 | Symbols: CYSD2, ATCYSD2 | cysteine synthase D2 | chr5:10026395-10028166 REVERSE LENGTH=323	323	323	1.00E-156	100.0	88.2	94.7
Rsa1.0_00045.1.g2606.t1	dbj|BAJ34422.1| unnamed protein product [Thellungiella halophila]	323	323	1.00E-161	100.0	93.5	98.5	unnamed protein product	----	----	AT5G28030.1 | Symbols: DES1 | L-cysteine desulfhydrase 1 | chr5:10030493-10032285 REVERSE LENGTH=323	323	323	1.00E-154	100.0	89.5	95.4
Rsa1.0_00045.1.g2607.t1	dbj|BAC42632.1| unknown protein [Arabidopsis thaliana] gi|28950993|gb|AAO63420.1| At5g28040 [Arabidopsis thaliana]	387	427	1.00E-132	110.3	72.9	81.7	unknown protein	gbpln	Arabidopsis thaliana	AT5G28040.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr5:10037654-10038937 REVERSE LENGTH=427	387	427	1.00E-135	110.3	72.9	82.2
Rsa1.0_00045.1.g2608.t1	ref|XP_002882383.1| 40S ribosomal protein S24 [Arabidopsis lyrata subsp. lyrata] gi|297328223|gb|EFH58642.1| 40S ribosomal protein S24 [Arabidopsis lyrata subsp. lyrata]	133	133	8.00E-69	100.0	99.2	99.2	40S ribosomal protein S24	gbpln	Arabidopsis lyrata	AT3G04920.1 | Symbols: | Ribosomal protein S24e family protein | chr3:1360989-1362065 FORWARD LENGTH=133	133	133	1.00E-70	100.0	98.5	98.5
Rsa1.0_00045.1.g2609.t1	gb|EOA20484.1| hypothetical protein CARUB_v10000796mg [Capsella rubella]	446	498	1.00E-150	111.7	67.7	78.9	hypothetical protein CARUB_v10000796mg	gbpln	Capsella rubella	AT3G04910.1 | Symbols: WNK1, ZIK4, ATWNK1 | with no lysine (K) kinase 1 | chr3:1355084-1358057 FORWARD LENGTH=700	446	700	1.00E-121	157.0	45.3	50.9
Rsa1.0_00045.1.g2610.t1	gb|EOA12246.1| hypothetical protein CARUB_v10012686mg [Capsella rubella]	417	417	0	100.0	95.7	97.4	hypothetical protein CARUB_v10012686mg	gbpln	Capsella rubella	AT5G30510.1 | Symbols: RPS1, ARRPS1 | ribosomal protein S1 | chr5:11619262-11621223 REVERSE LENGTH=416	417	416	0	99.8	96.2	98.6
Rsa1.0_00045.1.g2611.t1	gb|EOA12248.1| hypothetical protein CARUB_v10012688mg [Capsella rubella]	241	237	3.00E-71	98.3	78.0	83.0	hypothetical protein CARUB_v10012688mg	gbpln	Capsella rubella	AT5G30490.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Craniofacial development protein 1/Bucentaur (InterPro:IPR011421); Has 333 Blast hits to 324 proteins in 149 species: Archae - 0; Bacteria - 18; Metazoa - 117; Fungi - 96; Plants - 49; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink). | chr5:11612199-11614271 FORWARD LENGTH=236	241	236	1.00E-73	97.9	77.2	82.6
Rsa1.0_00045.1.g2612.t1	ref|XP_002872334.1| hypothetical protein ARALYDRAFT_489677 [Arabidopsis lyrata subsp. lyrata] gi|297318171|gb|EFH48593.1| hypothetical protein ARALYDRAFT_489677 [Arabidopsis lyrata subsp. lyrata]	198	196	4.00E-84	99.0	77.3	87.9	hypothetical protein ARALYDRAFT_489677	gbpln	Arabidopsis lyrata	AT5G30495.1 | Symbols: | Fcf2 pre-rRNA processing protein | chr5:11380190-11381391 FORWARD LENGTH=196	198	196	3.00E-85	99.0	75.8	87.4

Rsa1.0_00045.1.g2613.t1	ref|NP_568512.3| myb family transcription factor [Arabidopsis thaliana] gi|75328846|sp|Q8GUN5.1|PHL1_ARATH RecName: Full=Protein PHR1-LIKE 1; AltName: Full=Myb-like transcription factor 1 gi|26983850|gb|AAN86177.1| unknown protein [Arabidopsis thaliana] gi|332006474|gb|AED93857.1| myb family transcription factor [Arabidopsis thaliana]	429	413	1.00E-174	96.3	75.1	81.4	myb family transcription factor	gbpln	Arabidopsis thaliana	AT5G29000.2 | Symbols: PHL1 | Homeodomain-like superfamily protein | chr5:11022336-11024229 REVERSE LENGTH=413	429	413	1.00E-177	96.3	75.1	81.4
Rsa1.0_00045.1.g2614.t1	ref|XP_002874460.1| hypothetical protein ARALYDRAFT_489671 [Arabidopsis lyrata subsp. lyrata] gi|297320297|gb|EFH50719.1| hypothetical protein ARALYDRAFT_489671 [Arabidopsis lyrata subsp. lyrata]	531	533	0	100.4	83.8	91.7	hypothetical protein ARALYDRAFT_489671	gbpln	Arabidopsis lyrata	AT5G28910.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28960.1); Has 82 Blast hits to 80 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr5:10930633-10932575 REVERSE LENGTH=535	531	535	0	100.8	83.6	90.8
Rsa1.0_00045.1.g2615.t1	ref|XP_002884444.1| hypothetical protein ARALYDRAFT_896477 [Arabidopsis lyrata subsp. lyrata] gi|297330284|gb|EFH60703.1| hypothetical protein ARALYDRAFT_896477 [Arabidopsis lyrata subsp. lyrata]	634	640	0	100.9	78.5	86.3	hypothetical protein ARALYDRAFT_896477	gbpln	Arabidopsis lyrata	AT3G04470.1 | Symbols: | Ankyrin repeat family protein | chr3:1189841-1191853 REVERSE LENGTH=640	634	640	0	100.9	75.7	82.6
Rsa1.0_00045.1.g2616.t1	ref|XP_002872330.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297318167|gb|EFH48589.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	509	536	0	105.3	88.6	95.3	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT5G28900.1 | Symbols: | Calcium-binding EF-hand family protein | chr5:10925852-10929892 FORWARD LENGTH=536	509	536	0	105.3	87.4	94.9
Rsa1.0_00045.1.g2617.t1	gb|EOA21064.1| hypothetical protein CARUB_v10001403mg [Capsella rubella]	330	331	1.00E-141	100.3	76.4	87.6	hypothetical protein CARUB_v10001403mg	gbpln	Capsella rubella	AT5G28830.1 | Symbols: | calcium-binding EF hand family protein | chr5:10856801-10858394 FORWARD LENGTH=324	330	324	1.00E-140	98.2	77.0	87.3
Rsa1.0_00045.1.g2618.t1	gb|EOA21752.1| hypothetical protein CARUB_v10002208mg [Capsella rubella]	142	146	8.00E-50	102.8	90.1	91.5	hypothetical protein CARUB_v10002208mg	gbpln	Capsella rubella	AT5G28750.1 | Symbols: | Bacterial sec-independent translocation protein mttA/Hcf106 | chr5:10784142-10785677 REVERSE LENGTH=147	142	147	1.00E-45	103.5	71.1	73.9
Rsa1.0_00045.1.g2619.t1	ref|NP_187113.1| Alba DNA/RNA-binding protein [Arabidopsis thaliana] gi|6175166|gb|AAF04892.1|AC011437_7 unknown protein [Arabidopsis thaliana] gi|38454036|gb|AAR20712.1| At3g04620 [Arabidopsis thaliana] gi|38604012|gb|AAR24749.1| At3g04620 [Arabidopsis thaliana] gi|332640586|gb|AEE74107.1| Alba DNA/RNA-binding protein [Arabidopsis thaliana]	159	164	6.00E-45	103.1	61.6	67.9	Alba DNA/RNA-binding protein	gbpln	Arabidopsis thaliana	AT3G04620.1 | Symbols: | Alba DNA/RNA-binding protein | chr3:1255660-1256739 REVERSE LENGTH=164	159	164	2.00E-47	103.1	61.6	67.9
Rsa1.0_00045.1.g2620.t1	gb|AAF88010.1| Hypothetical protein T10I18.2 [Arabidopsis thaliana]	143	131	3.00E-25	91.6	67.8	78.3	Hypothetical protein T10I18.2	gbpln	Arabidopsis thaliana	AT5G28610.1 | Symbols: | BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT5G28630.1); Has 1536 Blast hits to 1202 proteins in 136 species: Archae - 0; Bacteria - 8; Metazoa - 888; Fungi - 120; Plants - 71; Viruses - 39; Other Eukaryotes - 410 (source: NCBI BLink). | chr5:10610976-10611347 FORWARD LENGTH=123	143	123	6.00E-24	86.0	63.6	73.4
Rsa1.0_00045.1.g2621.t1	ref|XP_002874429.1| hypothetical protein ARALYDRAFT_489653 [Arabidopsis lyrata subsp. lyrata] gi|297320266|gb|EFH50688.1| hypothetical protein ARALYDRAFT_489653 [Arabidopsis lyrata subsp. lyrata]	159	217	3.00E-25	136.5	41.5	46.5	hypothetical protein ARALYDRAFT_489653	gbpln	Arabidopsis lyrata	AT5G28590.1 | Symbols: | DNA-binding family protein | chr5:10579446-10581559 REVERSE LENGTH=216	159	216	2.00E-25	135.8	41.5	45.3
Rsa1.0_00045.1.g2622.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00045.1.g2623.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	473	1142	1.00E-38	241.4	20.3	29.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	473	256	2.00E-17	54.1	11.4	15.6
Rsa1.0_00045.1.g2624.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00045.1.g2625.t2</td><td>gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]</td><td>358</td><td>1231</td><td>7.00E-72</td><td>343.9</td><td>44.7</td><td>62.8</td><td>Very similar to retrotransposon reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>358</td><td>575</td><td>3.00E-42</td><td>160.6</td><td>27.1</td><td>45.5</td></tr>
<tr><td>Rsa1.0_00045.1.g2626.t1</td><td>ref|XP_002874426.1| light-dependent short hypocotyls 1 [Arabidopsis lyrata subsp. lyrata] gi|297320263|gb|EFH50685.1| light-dependent short hypocotyls 1 [Arabidopsis lyrata subsp. lyrata]</td><td>192</td><td>192</td><td>6.00E-81</td><td>100.0</td><td>88.5</td><td>92.7</td><td>light-dependent short hypocotyls 1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G28490.1 | Symbols: LSH1 | Protein of unknown function (DUF640) | chr5:10454541-10455113 REVERSE LENGTH=190</td><td>192</td><td>190</td><td>3.00E-82</td><td>99.0</td><td>89.6</td><td>93.8</td></tr>
<tr><td>Rsa1.0_00045.1.g2627.t1</td><td>emb|CAB75932.1| putative protein [Arabidopsis thaliana]</td><td>1175</td><td>1339</td><td>0</td><td>114.0</td><td>72.3</td><td>79.2</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1175</td><td>1262</td><td>7.00E-58</td><td>107.4</td><td>10.2</td><td>15.7</td></tr>
<tr><td>Rsa1.0_00045.1.g2628.t1</td><td>ref|NP_568711.1| uncharacterized protein [Arabidopsis thaliana] gi|363579829|sp|F4K657.1|BL1S2_ARATH RecName: Full=Biogenesis of lysosome-related organelles complex 1 subunit 2; Short=BLOC-1 subunit 2 gi|332008445|gb|AED95828.1| uncharacterized protein AT5G49550 [Arabidopsis thaliana]</td><td>126</td><td>127</td><td>3.00E-55</td><td>100.8</td><td>88.9</td><td>93.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G49550.1 | Symbols: BLOS2 | Putative homolog of mammalian BLOC-1 Subunit 2. Protein - protein interaction with BLOS1. | chr5:20106702-20107156 REVERSE LENGTH=127</td><td>126</td><td>127</td><td>6.00E-58</td><td>100.8</td><td>88.9</td><td>93.7</td></tr>
<tr><td>Rsa1.0_00045.1.g2629.t1</td><td>gb|EOA31472.1| hypothetical protein CARUB_v10014658mg [Capsella rubella]</td><td>194</td><td>204</td><td>4.00E-60</td><td>105.2</td><td>62.4</td><td>75.8</td><td>hypothetical protein CARUB_v10014658mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04320.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr3:1143815-1144426 FORWARD LENGTH=203</td><td>194</td><td>203</td><td>5.00E-58</td><td>104.6</td><td>57.2</td><td>72.7</td></tr>
<tr><td>Rsa1.0_00045.1.g2630.t2</td><td>ref|NP_187083.1| Kunitz family trypsin and protease inhibitor protein [Arabidopsis thaliana] gi|6721153|gb|AAF26781.1|AC016829_5 putative trypsin inhibitor [Arabidopsis thaliana] gi|332640546|gb|AEE74067.1| Kunitz family trypsin and protease inhibitor protein [Arabidopsis thaliana]</td><td>295</td><td>202</td><td>3.00E-43</td><td>68.5</td><td>33.9</td><td>42.0</td><td>Kunitz family trypsin and protease inhibitor protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G04330.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr3:1145757-1146365 FORWARD LENGTH=202</td><td>295</td><td>202</td><td>7.00E-46</td><td>68.5</td><td>33.9</td><td>42.0</td></tr>
<tr><td>Rsa1.0_00045.1.g2631.t1</td><td>gb|EOA14246.1| hypothetical protein CARUB_v10027400mg [Capsella rubella]</td><td>124</td><td>114</td><td>2.00E-51</td><td>91.9</td><td>83.1</td><td>85.5</td><td>hypothetical protein CARUB_v10027400mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G49540.1 | Symbols: | Rab5-interacting family protein | chr5:20104804-20105609 REVERSE LENGTH=114</td><td>124</td><td>114</td><td>7.00E-53</td><td>91.9</td><td>80.6</td><td>83.9</td></tr>
<tr><td>Rsa1.0_00045.1.g2632.t1</td><td>ref|XP_002863991.1| hypothetical protein ARALYDRAFT_917932 [Arabidopsis lyrata subsp. lyrata] gi|297309826|gb|EFH40250.1| hypothetical protein ARALYDRAFT_917932 [Arabidopsis lyrata subsp. lyrata]</td><td>382</td><td>396</td><td>1.00E-118</td><td>103.7</td><td>78.5</td><td>85.9</td><td>hypothetical protein ARALYDRAFT_917932</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49520.1 | Symbols: WRKY48, ATWRKY48 | WRKY DNA-binding protein 48 | chr5:20090890-20092867 FORWARD LENGTH=399</td><td>382</td><td>399</td><td>1.00E-118</td><td>104.5</td><td>73.3</td><td>79.1</td></tr>
<tr><td>Rsa1.0_00045.1.g2633.t3</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00045.1.g2634.t1</td><td>ref|XP_002863987.1| hypothetical protein ARALYDRAFT_495005 [Arabidopsis lyrata subsp. lyrata] gi|297309822|gb|EFH40246.1| hypothetical protein ARALYDRAFT_495005 [Arabidopsis lyrata subsp. lyrata]</td><td>161</td><td>161</td><td>8.00E-61</td><td>100.0</td><td>82.0</td><td>85.1</td><td>hypothetical protein ARALYDRAFT_495005</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49480.1 | Symbols: ATCP1, CP1 | Ca2+-binding protein 1 | chr5:20070812-20071294 FORWARD LENGTH=160</td><td>161</td><td>160</td><td>5.00E-63</td><td>99.4</td><td>80.7</td><td>83.9</td></tr>
<tr><td>Rsa1.0_00045.1.g2635.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00045.1.g2636.t1</td><td>ref|NP_001190501.1| PAS domain-containing protein tyrosine kinase [Arabidopsis thaliana] gi|332008435|gb|AED95818.1| PAS domain-containing protein tyrosine kinase [Arabidopsis thaliana]</td><td>624</td><td>770</td><td>0</td><td>123.4</td><td>89.1</td><td>95.0</td><td>PAS domain-containing protein tyrosine kinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G49470.3 | Symbols: | PAS domain-containing protein tyrosine kinase family protein | chr5:20063616-20068311 FORWARD LENGTH=770</td><td>624</td><td>770</td><td>0</td><td>123.4</td><td>89.1</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00045.1.g2637.t1</td><td>ref|XP_002863985.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297309820|gb|EFH40244.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>130</td><td>856</td><td>3.00E-41</td><td>658.5</td><td>76.9</td><td>81.5</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49470.2 | Symbols: | PAS domain-containing protein tyrosine kinase family protein | chr5:20063616-20068311 FORWARD LENGTH=831</td><td>130</td><td>831</td><td>6.00E-44</td><td>639.2</td><td>75.4</td><td>80.8</td></tr>
<tr><td>Rsa1.0_00045.1.g2638.t1</td><td>ref|XP_002863984.1| ATP-citrate lyase B-2 [Arabidopsis lyrata subsp. lyrata] gi|297309819|gb|EFH40243.1| ATP-citrate lyase B-2 [Arabidopsis lyrata subsp. lyrata]</td><td>608</td><td>608</td><td>0</td><td>100.0</td><td>99.2</td><td>99.8</td><td>ATP-citrate lyase B-2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49460.1 | Symbols: ACLB-2 | ATP citrate lyase subunit B 2 | chr5:20055048-20058195 FORWARD LENGTH=608</td><td>608</td><td>608</td><td>0</td><td>100.0</td><td>98.5</td><td>99.5</td></tr>
<tr><td>Rsa1.0_00045.1.g2639.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00045.1.g2640.t1</td><td>dbj|BAJ33845.1| unnamed protein product [Thellungiella halophila]</td><td>140</td><td>141</td><td>4.00E-59</td><td>100.7</td><td>85.7</td><td>92.9</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G49450.1 | Symbols: AtbZIP1, bZIP1 | basic leucine-zipper 1 | chr5:20052145-20052582 FORWARD LENGTH=145</td><td>140</td><td>145</td><td>1.00E-58</td><td>103.6</td><td>83.6</td><td>90.7</td></tr>
<tr><td>Rsa1.0_00045.1.g2641.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00045.1.g2642.t1	ref|NP_199747.1| beta-xylosidase 1 [Arabidopsis thaliana] gi|75262458|sp|Q9FGY1.1|BXL1_ARATH RecName: Full=Beta-D-xylosidase 1; Short=AtBXL1; AltName: Full=Alpha-L-arabinofuranosidase; Flags: Precursor gi|9759419|dbj|BAB09906.1| xylosidase [Arabidopsis thaliana] gi|21539545|gb|AAM53325.1| xylosidase [Arabidopsis thaliana] gi|332008419|gb|AED95802.1| beta-xylosidase 1 [Arabidopsis thaliana]	562	774	0	137.7	90.9	94.5	beta-xylosidase 1	gbpln	Arabidopsis thaliana	AT5G49360.1 | Symbols: BXL1, ATBXL1 | beta-xylosidase 1 | chr5:20012179-20016659 REVERSE LENGTH=774	562	774	0	137.7	90.9	94.5
Rsa1.0_00045.1.g2643.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	261	258	5.00E-57	98.9	51.7	67.8	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	261	302	2.00E-47	115.7	43.7	64.0
Rsa1.0_00045.1.g2644.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	611	442	1.00E-157	72.3	43.5	51.2	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT5G49360.1 | Symbols: BXL1, ATBXL1 | beta-xylosidase 1 | chr5:20012179-20016659 REVERSE LENGTH=774	611	774	1.00E-111	126.7	31.8	34.0
Rsa1.0_00045.1.g2645.t1	ref|XP_002865730.1| hypothetical protein ARALYDRAFT_331346 [Arabidopsis lyrata subsp. lyrata] gi|297311565|gb|EFH41989.1| hypothetical protein ARALYDRAFT_331346 [Arabidopsis lyrata subsp. lyrata]	279	459	4.00E-63	164.5	44.8	50.5	hypothetical protein ARALYDRAFT_331346	gbpln	Arabidopsis lyrata	AT5G49340.1 | Symbols: TBL4 | TRICHOME BIREFRINGENCE-LIKE 4 | chr5:20007348-20009038 REVERSE LENGTH=457	279	457	8.00E-64	163.8	43.0	50.5
Rsa1.0_00045.1.g2646.t1	gb|ADZ98865.1| MYB domain protein 111 [Brassica rapa subsp. rapa]	341	343	1.00E-149	100.6	79.2	86.2	MYB domain protein 111	gbpln	Brassica rapa	AT5G49330.1 | Symbols: MYB111, ATMYB111, PFG3 | myb domain protein 111 | chr5:19999147-20001293 REVERSE LENGTH=342	341	342	1.00E-143	100.3	77.1	83.9
Rsa1.0_00045.1.g2647.t1	gb|EOA14118.1| hypothetical protein CARUB_v10027260mg [Capsella rubella]	164	166	2.00E-25	101.2	69.5	76.8	hypothetical protein CARUB_v10027260mg	gbpln	Capsella rubella	AT5G49280.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:19976842-19977330 REVERSE LENGTH=162	164	162	1.00E-12	98.8	18.3	20.7
Rsa1.0_00045.1.g2648.t1	ref|XP_002865723.1| hypothetical protein ARALYDRAFT_494988 [Arabidopsis lyrata subsp. lyrata] gi|297311558|gb|EFH41982.1| hypothetical protein ARALYDRAFT_494988 [Arabidopsis lyrata subsp. lyrata]	663	661	0	99.7	85.4	91.6	hypothetical protein ARALYDRAFT_494988	gbpln	Arabidopsis lyrata	AT5G49270.1 | Symbols: SHV2, DER9, MRH4, COBL9 | COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family | chr5:19972021-19974398 REVERSE LENGTH=663	663	663	0	100.0	85.8	92.2
Rsa1.0_00045.1.g2649.t1	ref|NP_196810.5| ARMADILLO BTB protein 1 [Arabidopsis thaliana] gi|325529879|sp|B7U179.1|ABAP1_ARATH RecName: Full=ARMADILLO BTB ARABIDOPSIS PROTEIN 1; Short=ABAP1 gi|213391123|gb|ACJ46331.1| ABAP1 [Arabidopsis thaliana] gi|332004463|gb|AED91846.1| ARMADILLO BTB protein 1 [Arabidopsis thaliana]	717	737	0	102.8	84.4	90.9	ARMADILLO BTB protein 1	gbpln	Arabidopsis thaliana	AT5G13060.1 | Symbols: ABAP1 | ARMADILLO BTB protein 1 | chr5:4142958-4146952 FORWARD LENGTH=737	717	737	0	102.8	84.4	90.9
Rsa1.0_00045.1.g2650.t1	gb|AEK67480.1| ZZ [Arabidopsis thaliana]	154	206	2.00E-46	133.8	73.4	82.5	ZZ	gbpln	Arabidopsis thaliana	AT5G49230.1 | Symbols: HRB1 | Drought-responsive family protein | chr5:19959048-19960422 REVERSE LENGTH=211	154	211	2.00E-48	137.0	73.4	82.5
Rsa1.0_00045.1.g2651.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00045.1.g2652.t1	ref|XP_002863962.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309797|gb|EFH40221.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	414	501	1.00E-139	121.0	60.9	63.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G49130.1 | Symbols: | MATE efflux family protein | chr5:19915904-19917525 FORWARD LENGTH=502	414	502	1.00E-138	121.3	59.2	62.6
Rsa1.0_00045.1.g2653.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	386	1213	3.00E-92	314.2	48.7	65.3	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	386	289	1.00E-51	74.9	28.5	41.5
Rsa1.0_00046.1.g2654.t1	gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]	209	214	8.00E-62	102.4	64.1	73.2	trypsin inhibitor propeptide	gbpln	Brassica oleracea	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410-27548057 REVERSE LENGTH=215	209	215	3.00E-54	102.9	58.4	67.9
Rsa1.0_00046.1.g2655.t1	gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]	211	214	3.00E-66	101.4	66.4	73.9	trypsin inhibitor propeptide	gbpln	Brassica oleracea	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410-27548057 REVERSE LENGTH=215	211	215	9.00E-56	101.9	55.5	70.1
Rsa1.0_00046.1.g2656.t1	ref|NP_565061.1| kunitz trypsin inhibitor 1 [Arabidopsis thaliana] gi|19698953|gb|AAL91212.1| putative trypsin inhibitor [Arabidopsis thaliana] gi|27311885|gb|AAO00908.1| putative trypsin inhibitor [Arabidopsis thaliana] gi|110740417|dbj|BAF02103.1| putative trypsin inhibitor [Arabidopsis thaliana] gi|332197314|gb|AEE35435.1| kunitz trypsin inhibitor 1 [Arabidopsis thaliana]	202	215	2.00E-89	106.4	78.7	88.6	kunitz trypsin inhibitor 1	gbpln	Arabidopsis thaliana	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410-27548057 REVERSE LENGTH=215	202	215	7.00E-92	106.4	78.7	88.6

Rsa1.0_00046.1.g2657.t1	ref|XP_002888917.1| GDP-4-keto-6-deoxymannose-3,5-epimerase-4-reductase 1 [Arabidopsis lyrata subsp. lyrata] gi|297334758|gb|EFH65176.1| GDP-4-keto-6-deoxymannose-3,5-epimerase-4-reductase 1 [Arabidopsis lyrata subsp. lyrata]	313	323	1.00E-171	103.2	91.4	95.8	GDP-4-keto-6-deoxymannose-3,5-epimerase-4-reductase 1	gbpln	Arabidopsis lyrata	AT1G73250.1 | Symbols: ATFX, GER1 | GDP-4-keto-6-deoxymannose-3,5-epimerase-4-reductase 1 | chr1:27545213-27546360 REVERSE LENGTH=323	313	323	1.00E-174	103.2	91.4	95.8
Rsa1.0_00046.1.g2658.t1	ref|XP_002888916.1| hypothetical protein ARALYDRAFT_476456 [Arabidopsis lyrata subsp. lyrata] gi|297334757|gb|EFH65175.1| hypothetical protein ARALYDRAFT_476456 [Arabidopsis lyrata subsp. lyrata]	507	519	0	102.4	86.4	93.5	hypothetical protein ARALYDRAFT_476456	gbpln	Arabidopsis lyrata	AT1G73240.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nucleoporin protein Ndc1-Nup (InterPro:IPR019049); Has 36 Blast hits to 36 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27542397-27544668 REVERSE LENGTH=519	507	519	0	102.4	86.2	93.1
Rsa1.0_00046.1.g2659.t1	ref|NP_177466.1| nascent polypeptide-associated complex subunit beta [Arabidopsis thaliana] gi|297842067|ref|XP_002888915.1| nascent polypeptide-associated complex domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|12324314|gb|AAG52123.1|AC010556_5 putative transcription factor BTF3 (RNA polymerase B transcription factor 3); 26343-27201 [Arabidopsis thaliana] gi|13877981|gb|AAK44068.1|AF370253_1 putative RNA polymerase B transcription factor BTF3 [Arabidopsis thaliana] gi|17104709|gb|AAL34243.1| putative RNA polymerase B transcription factor 3 [Arabidopsis thaliana] gi|297334756|gb|EFH65174.1| nascent polypeptide-associated complex domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|332197311|gb|AEE35432.1| nascent polypeptide-associated complex subunit beta [Arabidopsis thaliana]	167	165	1.00E-73	98.8	91.6	94.0	nascent polypeptide-associated complex subunit beta	gbpln	Arabidopsis lyrata	AT1G73230.1 | Symbols: | Nascent polypeptide-associated complex NAC | chr1:27540506-27541364 REVERSE LENGTH=165	167	165	5.00E-76	98.8	91.6	94.0
Rsa1.0_00046.1.g2660.t1	ref|NP_565059.2| organic cation/carnitine transporter1 [Arabidopsis thaliana] gi|75262291|sp|Q9CAT6.1|OCT1_ARATH RecName: Full=Organic cation/carnitine transporter 1; Short=AtOCT1 gi|12324316|gb|AAG52125.1|AC010556_7 putative transporter; 29320-27598 [Arabidopsis thaliana] gi|27311699|gb|AAO00815.1| putative transporter [Arabidopsis thaliana] gi|31711954|gb|AAP68333.1| At1g73220 [Arabidopsis thaliana] gi|332197310|gb|AEE35431.1| organic cation/carnitine transporter1 [Arabidopsis thaliana]	556	539	0	96.9	83.6	89.6	organic cation/carnitine transporter1	gbpln	Arabidopsis thaliana	AT1G73220.1 | Symbols: AtOCT1, 1-Oct | organic cation/carnitine transporter1 | chr1:27538387-27540109 FORWARD LENGTH=539	556	539	0	96.9	83.6	89.6
Rsa1.0_00046.1.g2661.t1	ref|NP_177464.1| uncharacterized protein [Arabidopsis thaliana] gi|12324319|gb|AAG52128.1|AC010556_10 hypothetical protein; 37254-39279 [Arabidopsis thaliana] gi|53828629|gb|AAU94424.1| At1g73210 [Arabidopsis thaliana] gi|332197308|gb|AEE35429.1| uncharacterized protein AT1G73210 [Arabidopsis thaliana]	312	314	1.00E-157	100.6	86.9	92.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G73210.1 | Symbols: | Protein of unknown function (DUF789) | chr1:27528428-27530453 REVERSE LENGTH=314	312	314	1.00E-159	100.6	86.9	92.9
Rsa1.0_00046.1.g2662.t1	ref|XP_002888912.1| hypothetical protein ARALYDRAFT_895179 [Arabidopsis lyrata subsp. lyrata] gi|297334753|gb|EFH65171.1| hypothetical protein ARALYDRAFT_895179 [Arabidopsis lyrata subsp. lyrata]	763	779	0	102.1	79.4	87.8	hypothetical protein ARALYDRAFT_895179	gbpln	Arabidopsis lyrata	AT1G73200.1 | Symbols: | Putative integral membrane protein conserved region (DUF2404) | chr1:27523454-27526573 REVERSE LENGTH=779	763	779	0	102.1	78.5	87.3
Rsa1.0_00046.1.g2663.t1	gb|EOA34775.1| hypothetical protein CARUB_v10022350mg [Capsella rubella]	267	265	1.00E-130	99.3	93.3	97.0	hypothetical protein CARUB_v10022350mg	gbpln	Capsella rubella	AT1G73190.1 | Symbols: ALPHA-TIP, TIP3;1 | Aquaporin-like superfamily protein | chr1:27522155-27523171 FORWARD LENGTH=268	267	268	1.00E-129	100.4	91.4	95.9

Rsa1.0_00046.1.g2664.t1	ref|NP_177455.1| uncharacterized protein [Arabidopsis thaliana] gi|12324324|gb|AAG52133.1|AC010556_15 hypothetical protein; 69822-70342 [Arabidopsis thaliana] gi|26449662|dbj|BAC41955.1| unknown protein [Arabidopsis thaliana] gi|28416835|gb|AAO42948.1| At1g73120 [Arabidopsis thaliana] gi|332197295|gb|AEE35416.1| uncharacterized protein AT1G73120 [Arabidopsis thaliana]	110	109	7.00E-46	99.1	81.8	90.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G73120.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; EXPRESSED IN: root, cultured cell; Has 36 Blast hits to 36 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27497365-27497885 REVERSE LENGTH=109	110	109	1.00E-48	99.1	81.8	90.0
Rsa1.0_00046.1.g2665.t2	ref|NP_177454.1| putative Rubisco activase 2 [Arabidopsis thaliana] gi|13605706|gb|AAK32846.1|AF361834_1 At1g73110/F3N23_39 [Arabidopsis thaliana] gi|18700270|gb|AAL77745.1| At1g73110/F3N23_39 [Arabidopsis thaliana] gi|26452888|dbj|BAC43522.1| unknown protein [Arabidopsis thaliana] gi|332197294|gb|AEE35415.1| putative Rubisco activase 2 [Arabidopsis thaliana]	435	432	0	99.3	90.6	94.0	putative Rubisco activase 2	gbpln	Arabidopsis thaliana	AT1G73110.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:27494344-27496844 REVERSE LENGTH=432	435	432	0	99.3	90.6	94.0
Rsa1.0_00046.1.g2666.t1	ref|XP_002887472.1| hypothetical protein ARALYDRAFT_895166 [Arabidopsis lyrata subsp. lyrata] gi|297333313|gb|EFH63731.1| hypothetical protein ARALYDRAFT_895166 [Arabidopsis lyrata subsp. lyrata]	672	669	0	99.6	81.7	88.1	hypothetical protein ARALYDRAFT_895166	gbpln	Arabidopsis lyrata	AT1G73100.1 | Symbols: SUVH3, SDG19 | SU(VAR)3-9 homolog 3 | chr1:27491970-27493979 FORWARD LENGTH=669	672	669	0	99.6	79.9	86.9
Rsa1.0_00046.1.g2667.t1	ref|NP_001117591.1| Leucine-rich repeat family protein [Arabidopsis thaliana] gi|5903096|gb|AAD55654.1|AC008017_27 Highly similar to receptor-like protein kinase [Arabidopsis thaliana] gi|26449861|dbj|BAC42053.1| unknown protein [Arabidopsis thaliana] gi|332197289|gb|AEE35410.1| Leucine-rich repeat family protein [Arabidopsis thaliana]	951	598	0	62.9	49.8	54.4	Leucine-rich repeat family protein	gbpln	Arabidopsis thaliana	AT1G73066.1 | Symbols: | Leucine-rich repeat family protein | chr1:27481785-27483581 FORWARD LENGTH=598	951	598	0	62.9	49.8	54.4
Rsa1.0_00046.1.g2668.t1	gb|EOA33724.1| hypothetical protein CARUB_v10019915mg [Capsella rubella]	660	664	0	100.6	91.5	95.9	hypothetical protein CARUB_v10019915mg	gbpln	Capsella rubella	AT1G73020.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF590 (InterPro:IPR007632). | chr1:27469714-27473181 REVERSE LENGTH=665	660	665	0	100.8	90.5	95.2
Rsa1.0_00046.1.g2669.t1	ref|XP_002888902.1| hypothetical protein ARALYDRAFT_476431 [Arabidopsis lyrata subsp. lyrata] gi|297334743|gb|EFH65161.1| hypothetical protein ARALYDRAFT_476431 [Arabidopsis lyrata subsp. lyrata]	292	294	1.00E-139	100.7	86.0	91.8	hypothetical protein ARALYDRAFT_476431	gbpln	Arabidopsis lyrata	AT1G73010.1 | Symbols: ATPS2, PS2 | phosphate starvation-induced gene 2 | chr1:27464780-27466180 REVERSE LENGTH=295	292	295	1.00E-139	101.0	84.2	90.8
Rsa1.0_00046.1.g2670.t1	gb|EOA20703.1| hypothetical protein CARUB_v10001020mg [Capsella rubella]	145	427	7.00E-32	294.5	52.4	55.2	hypothetical protein CARUB_v10001020mg	gbpln	Capsella rubella	AT5G25220.1 | Symbols: KNAT3 | KNOTTED1-like homeobox gene 3 | chr5:8736208-8738115 FORWARD LENGTH=431	145	431	2.00E-34	297.2	52.4	55.2
Rsa1.0_00046.1.g2671.t1	gb|EOA33560.1| hypothetical protein CARUB_v10019685mg [Capsella rubella]	1159	1170	0	100.9	84.8	92.1	hypothetical protein CARUB_v10019685mg	gbpln	Capsella rubella	AT1G72960.1 | Symbols: | Root hair defective 3 GTP-binding protein (RHD3) | chr1:27446263-27450862 FORWARD LENGTH=795	1159	795	0	68.6	61.8	65.3
Rsa1.0_00046.1.g2672.t5	gb|EOA31387.1| hypothetical protein CARUB_v10014563mg [Capsella rubella]	129	226	2.00E-16	175.2	51.9	61.2	hypothetical protein CARUB_v10014563mg	gbpln	Capsella rubella	AT3G16770.1 | Symbols: RAP2.3, ATEBP, ERF72, EBP | ethylene-responsive element binding protein | chr3:5705784-5706768 FORWARD LENGTH=248	129	248	7.00E-13	192.2	26.4	27.9
Rsa1.0_00046.1.g2673.t1	gb|ACP30576.1| disease resistance protein [Brassica rapa subsp. pekinensis]	437	426	0	97.5	81.7	87.6	disease resistance protein	gbpln	Brassica rapa	AT1G72890.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27429947-27431717 FORWARD LENGTH=438	437	438	1.00E-173	100.2	71.2	83.1
Rsa1.0_00046.1.g2674.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00046.1.g2675.t1	gb|EOA35268.1| hypothetical protein CARUB_v10020451mg [Capsella rubella]	381	385	0	101.0	86.4	92.9	hypothetical protein CARUB_v10020451mg	gbpln	Capsella rubella	AT1G72880.1 | Symbols: | Survival protein SurE-like phosphatase/nucleotidase | chr1:27423678-27425928 REVERSE LENGTH=385	381	385	0	101.0	86.1	91.6

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<tr><td>Rsa1.0_00046.1.g2677.t1</td><td>ref|XP_002888896.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334737|gb|EFH65155.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>154</td><td>1169</td><td>1.00E-66</td><td>759.1</td><td>81.8</td><td>89.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G72860.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:27417096-27420778 REVERSE LENGTH=1163</td><td>154</td><td>1163</td><td>1.00E-48</td><td>755.2</td><td>55.8</td><td>71.4</td></tr>
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<tr><td>Rsa1.0_00046.1.g2680.t1</td><td>ref|NP_177427.2| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|110737528|dbj|BAF00706.1| hypothetical protein [Arabidopsis thaliana] gi|332197259|gb|AEE35380.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]</td><td>1017</td><td>1042</td><td>0</td><td>102.5</td><td>53.2</td><td>65.0</td><td>TIR-NBS-LRR class disease resistance protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G72840.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr1:27410020-27413485 REVERSE LENGTH=1042</td><td>1017</td><td>1042</td><td>0</td><td>102.5</td><td>53.2</td><td>65.0</td></tr>
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<tr><td>Rsa1.0_00046.1.g2682.t1</td><td>ref|NP_565049.1| nuclear transcription factor Y subunit A-3 [Arabidopsis thaliana] gi|81174954|sp|Q93ZH2.2|NFYA3_ARATH RecName: Full=Nuclear transcription factor Y subunit A-3; Short=AtNF-YA-3; AltName: Full=Transcriptional activator HAP2C gi|5903072|gb|AAD55630.1|AC008017_3 Transcription Factor [Arabidopsis thaliana] gi|22655158|gb|AAM98169.1| CCAAT-binding factor B subunit-like protein, putative [Arabidopsis thaliana] gi|31711816|gb|AAP68264.1| At1g72830 [Arabidopsis thaliana] gi|332197257|gb|AEE35378.1| nuclear transcription factor Y subunit A-3 [Arabidopsis thaliana]</td><td>116</td><td>340</td><td>4.00E-37</td><td>293.1</td><td>75.9</td><td>83.6</td><td>nuclear transcription factor Y subunit A-3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G72830.1 | Symbols: HAP2C, ATHAP2C, NF-YA3 | nuclear factor Y, subunit A3 | chr1:27405699-27407088 REVERSE LENGTH=340</td><td>116</td><td>340</td><td>6.00E-40</td><td>293.1</td><td>75.9</td><td>83.6</td></tr>
<tr><td>Rsa1.0_00046.1.g2683.t1</td><td>gb|EOA35384.1| hypothetical protein CARUB_v10020581mg [Capsella rubella] gi|482571197|gb|EOA35385.1| hypothetical protein CARUB_v10020581mg [Capsella rubella]</td><td>350</td><td>346</td><td>0</td><td>98.9</td><td>91.1</td><td>94.3</td><td>hypothetical protein CARUB_v10020581mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G72820.1 | Symbols: | Mitochondrial substrate carrier family protein | chr1:27403457-27404506 FORWARD LENGTH=349</td><td>350</td><td>349</td><td>1.00E-179</td><td>99.7</td><td>91.1</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00046.1.g2684.t1</td><td>gb|EOA35815.1| hypothetical protein CARUB_v10021053mg [Capsella rubella] gi|482571628|gb|EOA35816.1| hypothetical protein CARUB_v10021053mg [Capsella rubella]</td><td>156</td><td>166</td><td>2.00E-68</td><td>106.4</td><td>84.6</td><td>89.7</td><td>hypothetical protein CARUB_v10021053mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G72510.2 | Symbols: | Protein of unknown function (DUF1677) | chr1:27303906-27304403 FORWARD LENGTH=165</td><td>156</td><td>165</td><td>1.00E-70</td><td>105.8</td><td>84.0</td><td>91.0</td></tr>
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<tr><td>Rsa1.0_00047.1.g2685.t1</td><td>ref|NP_568344.2| myb family transcription factor [Arabidopsis thaliana] gi|332005027|gb|AED92410.1| myb family transcription factor [Arabidopsis thaliana]</td><td>372</td><td>387</td><td>1.00E-132</td><td>104.0</td><td>75.5</td><td>82.3</td><td>myb family transcription factor</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G17300.1 | Symbols: RVE1 | Homeodomain-like superfamily protein | chr5:5690435-5692435 REVERSE LENGTH=387</td><td>372</td><td>387</td><td>1.00E-135</td><td>104.0</td><td>75.5</td><td>82.3</td></tr>
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<tr><td>Rsa1.0_00047.1.g2687.t5</td><td>gb|EOA22499.1| hypothetical protein CARUB_v10003154mg [Capsella rubella]</td><td>134</td><td>143</td><td>2.00E-25</td><td>106.7</td><td>63.4</td><td>68.7</td><td>hypothetical protein CARUB_v10003154mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G17280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Oxidoreductase-like, N-terminal (InterPro:IPR019180); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5686355-5686762 FORWARD LENGTH=135</td><td>134</td><td>135</td><td>2.00E-26</td><td>100.7</td><td>58.2</td><td>65.7</td></tr>
<tr><td>Rsa1.0_00047.1.g2688.t1</td><td>gb|EOA23087.1| hypothetical protein CARUB_v10003869mg [Capsella rubella]</td><td>498</td><td>489</td><td>0</td><td>98.2</td><td>78.9</td><td>85.1</td><td>hypothetical protein CARUB_v10003869mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G17260.1 | Symbols: anac086, NAC086 | NAC domain containing protein 86 | chr5:5675323-5677912 REVERSE LENGTH=476</td><td>498</td><td>476</td><td>0</td><td>95.6</td><td>76.7</td><td>83.5</td></tr>
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<tr><td>Rsa1.0_00047.1.g2690.t1</td><td>gb|AEX31286.1| phytoene synthase [Brassica oleracea] gi|371486488|gb|AEX31289.1| phytoene synthase [Brassica napus]</td><td>423</td><td>424</td><td>0</td><td>100.2</td><td>95.3</td><td>97.6</td><td>phytoene synthase</td><td>gbpln</td><td>Brassica napus</td><td>AT5G17230.2 | Symbols: PSY | PHYTOENE SYNTHASE | chr5:5659839-5662087 REVERSE LENGTH=422</td><td>423</td><td>422</td><td>0</td><td>99.8</td><td>89.4</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00047.1.g2691.t1</td><td>dbj|BAJ34302.1| unnamed protein product [Thellungiella halophila]</td><td>213</td><td>214</td><td>1.00E-108</td><td>100.5</td><td>87.8</td><td>93.9</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G17220.1 | Symbols: ATGSTF12, GST26, TT19, GSTF12 | glutathione S-transferase phi 12 | chr5:5658528-5659322 FORWARD LENGTH=214</td><td>213</td><td>214</td><td>1.00E-104</td><td>100.5</td><td>83.1</td><td>92.0</td></tr>
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<tr><td>Rsa1.0_00047.1.g2693.t1</td><td>ref|NP_197222.1| polygalacturonase [Arabidopsis thaliana] gi|10177065|dbj|BAB10507.1| polygalacturonase-like protein [Arabidopsis thaliana] gi|332005012|gb|AED92395.1| pectin lyase-like superfamily protein [Arabidopsis thaliana]</td><td>428</td><td>421</td><td>1.00E-161</td><td>98.4</td><td>68.0</td><td>78.7</td><td>polygalacturonase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G17200.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:5653524-5655336 REVERSE LENGTH=421</td><td>428</td><td>421</td><td>1.00E-164</td><td>98.4</td><td>68.0</td><td>78.7</td></tr>
<tr><td>Rsa1.0_00047.1.g2694.t1</td><td>ref|NP_197220.1| uncharacterized protein [Arabidopsis thaliana] gi|10177063|dbj|BAB10505.1| unnamed protein product [Arabidopsis thaliana] gi|117168077|gb|ABK32121.1| At5g17180 [Arabidopsis thaliana] gi|332005010|gb|AED92393.1| uncharacterized protein AT5G17180 [Arabidopsis thaliana]</td><td>124</td><td>123</td><td>8.00E-14</td><td>99.2</td><td>37.9</td><td>48.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G17180.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5651436-5651807 FORWARD LENGTH=123</td><td>124</td><td>123</td><td>2.00E-16</td><td>99.2</td><td>37.9</td><td>48.4</td></tr>
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Rsa1.0_00047.1.g2696.t1	ref|XP_002873814.1| hypothetical protein ARALYDRAFT_488576 [Arabidopsis lyrata subsp. lyrata] gi|297319651|gb|EFH50073.1| hypothetical protein ARALYDRAFT_488576 [Arabidopsis lyrata subsp. lyrata]	767	568	1.00E−111	74.1	34.2	40.3	hypothetical protein ARALYDRAFT_488576	gbpln	Arabidopsis lyrata	AT5G17160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03130.1); Has 14330 Blast hits to 10381 proteins in 896 species: Archae − 94; Bacteria − 2881; Metazoa − 4019; Fungi − 1576; Plants − 515; Viruses − 110; Other Eukaryotes − 5135 (source: NCBI BLink). | chr5:5639843−5642427 REVERSE LENGTH=569	767	569	1.00E−113	74.2	33.4	40.4
Rsa1.0_00047.1.g2697.t1	gb|AAM19705.1|AF499718_1 protein phosphatase 2c−like protein [Eutrema halophilum]	233	378	8.00E−16	162.2	22.3	26.6	protein phosphatase 2c−like protein	gbpln	Eutrema halophilum	AT3G51370.2 | Symbols: | Protein phosphatase 2C family protein | chr3:19070387−19071975 FORWARD LENGTH=294	233	294	1.00E−15	126.2	20.6	25.3
Rsa1.0_00047.1.g2698.t3	ref|XP_002871747.1| hypothetical protein ARALYDRAFT_488569 [Arabidopsis lyrata subsp. lyrata] gi|297317584|gb|EFH48006.1| hypothetical protein ARALYDRAFT_488569 [Arabidopsis lyrata subsp. lyrata] gi|482557425|gb|EOA21617.1| hypothetical protein CARUB_v10002030mg [Capsella rubella]	211	192	1.00E−105	91.0	90.0	91.0	hypothetical protein ARALYDRAFT_488569	gbpln	Arabidopsis lyrata	AT5G17060.1 | Symbols: ATARFB1B, ARFB1B | ADP−ribosylation factor B1B | chr5:5611056−5612639 FORWARD LENGTH=192	211	192	1.00E−106	91.0	89.6	90.5
Rsa1.0_00047.1.g2699.t6	ref|XP_002871746.1| hypothetical protein ARALYDRAFT_909689 [Arabidopsis lyrata subsp. lyrata] gi|297317583|gb|EFH48005.1| hypothetical protein ARALYDRAFT_909689 [Arabidopsis lyrata subsp. lyrata]	1072	1076	0	100.4	94.5	96.5	hypothetical protein ARALYDRAFT_909689	gbpln	Arabidopsis lyrata	AT5G17020.1 | Symbols: XPO1A, ATCRM1, ATXPO1, XPO1, HIT2 | exportin 1A | chr5:5594904−5602467 FORWARD LENGTH=1075	1072	1075	0	100.3	94.2	96.4
Rsa1.0_00047.1.g2700.t1	dbj|BAJ33830.1| unnamed protein product [Thellungiella halophila]	352	351	0	99.7	90.3	96.0	unnamed protein product	−−−−	−−−−	AT5G16970.1 | Symbols: AT−AER, AER | alkenal reductase | chr5:5576291−5578001 REVERSE LENGTH=345	352	345	1.00E−178	98.0	84.4	90.9
Rsa1.0_00047.1.g2701.t1	ref|NP_197195.2| AAA−type ATPase family protein [Arabidopsis thaliana] gi|19424059|gb|AAL87351.1| unknown protein [Arabidopsis thaliana] gi|22136966|gb|AAM91712.1| unknown protein [Arabidopsis thaliana] gi|332004976|gb|AED92359.1| AAA−type ATPase family protein [Arabidopsis thaliana]	663	644	0	97.1	87.6	92.0	AAA−type ATPase family protein	gbpln	Arabidopsis thaliana	AT5G16930.1 | Symbols: | AAA−type ATPase family protein | chr5:5568578−5571565 FORWARD LENGTH=644	663	644	0	97.1	87.6	92.0
Rsa1.0_00047.1.g2702.t1	ref|XP_002871742.1| hypothetical protein ARALYDRAFT_488554 [Arabidopsis lyrata subsp. lyrata] gi|297317579|gb|EFH48001.1| hypothetical protein ARALYDRAFT_488554 [Arabidopsis lyrata subsp. lyrata]	1135	1143	0	100.7	89.1	93.5	hypothetical protein ARALYDRAFT_488554	gbpln	Arabidopsis lyrata	AT5G16910.1 | Symbols: ATCSLD2, CSLD2 | cellulose−synthase like D2 | chr5:5561679−5565290 FORWARD LENGTH=1145	1135	1145	0	100.9	87.8	92.4
Rsa1.0_00047.1.g2703.t1	gb|EOA22278.1| hypothetical protein CARUB_v10002876mg [Capsella rubella]	505	513	0	101.6	86.7	91.7	hypothetical protein CARUB_v10002876mg	gbpln	Capsella rubella	AT5G16890.1 | Symbols: | Exostosin family protein | chr5:5551664−5554741 FORWARD LENGTH=511	505	511	0	101.2	84.8	89.3
Rsa1.0_00047.1.g2704.t1	ref|XP_002870649.1| hypothetical protein ARALYDRAFT_355852 [Arabidopsis lyrata subsp. lyrata] gi|297316485|gb|EFH46908.1| hypothetical protein ARALYDRAFT_355852 [Arabidopsis lyrata subsp. lyrata]	756	634	1.00E−121	83.9	37.0	45.4	hypothetical protein ARALYDRAFT_355852	gbpln	Arabidopsis lyrata	AT5G41690.1 | Symbols: | RNA−binding (RRM/RBD/RNP motifs) family protein | chr5:16670126−16674189 REVERSE LENGTH=567	756	567	1.00E−106	75.0	32.8	41.4

Rsa1.0_00047.1.g2705.t1	ref|NP_197190.1| Target of Myb protein 1 [Arabidopsis thaliana] gi|30686076|ref|NP_850833.1| Target of Myb protein 1 [Arabidopsis thaliana] gi|9755689|emb|CAC01701.1| TOM (target of myb1)-like protein [Arabidopsis thaliana] gi|15983761|gb|AAL10477.1| AT5g16880/F2K13_30 [Arabidopsis thaliana] gi|17065128|gb|AAL32718.1| TOM (target of myb1)-like protein [Arabidopsis thaliana] gi|21537352|gb|AAM61693.1| TOM (target of myb1)-like protein [Arabidopsis thaliana] gi|27311895|gb|AAO00913.1| TOM (target of myb1)-like protein [Arabidopsis thaliana] gi|332004970|gb|AED92353.1| Target of Myb protein 1 [Arabidopsis thaliana] gi|332004971|gb|AED92354.1| Target of Myb protein 1 [Arabidopsis thaliana]	408	407	0	99.8	89.7	93.9	Target of Myb protein 1	gbpln	Arabidopsis thaliana	AT5G16880.2 | Symbols: | Target of Myb protein 1 | chr5:5549658-5551274 FORWARD LENGTH=407	408	407	0	99.8	89.7	93.9
Rsa1.0_00047.1.g2706.t2	ref|NP_568340.1| Peptidyl-tRNA hydrolase II (PTH2) family protein [Arabidopsis thaliana] gi|98960911|gb|ABF58939.1| At5g16870 [Arabidopsis thaliana] gi|332004968|gb|AED92351.1| Peptidyl-tRNA hydrolase II (PTH2) family protein [Arabidopsis thaliana]	175	169	7.00E-79	96.6	89.7	90.9	Peptidyl-tRNA hydrolase II (PTH2) family protein	gbpln	Arabidopsis thaliana	AT5G16870.1 | Symbols: | Peptidyl-tRNA hydrolase II (PTH2) family protein | chr5:5546975-5548542 REVERSE LENGTH=169	175	169	3.00E-81	96.6	89.7	90.9
Rsa1.0_00047.1.g2707.t1	ref|XP_002871739.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317576|gb|EFH47998.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	837	850	0	101.6	85.7	92.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G16860.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:5543834-5546386 FORWARD LENGTH=850	837	850	0	101.6	84.9	91.8
Rsa1.0_00047.1.g2708.t2	gb|AAD54276.1|AF172097_1 telomerase reverse transcriptase catalytic subunit [Arabidopsis thaliana]	1066	1123	0	105.3	74.2	81.9	telomerase reverse transcriptase catalytic subunit	gbpln	Arabidopsis thaliana	AT5G16850.1 | Symbols: ATTERT, TERT | telomerase reverse transcriptase | chr5:5538323-5543444 REVERSE LENGTH=1123	1066	1123	0	105.3	74.2	81.9
Rsa1.0_00047.1.g2709.t1	gb|EOA19437.1| hypothetical protein CARUB_v10001749mg [Capsella rubella]	262	260	1.00E-118	99.2	84.7	90.5	hypothetical protein CARUB_v10001749mg	gbpln	Capsella rubella	AT5G16840.1 | Symbols: BPA1 | binding partner of acd11 1 | chr5:5536042-5538026 FORWARD LENGTH=259	262	259	1.00E-119	98.9	85.9	92.4
Rsa1.0_00047.1.g2710.t1	ref|XP_002887653.1| 12-oxophytodienoate reductase 1 [Arabidopsis lyrata subsp. lyrata] gi|297333494|gb|EFH63912.1| 12-oxophytodienoate reductase 1 [Arabidopsis lyrata subsp. lyrata]	369	372	0	100.8	89.7	93.8	12-oxophytodienoate reductase 1	gbpln	Arabidopsis lyrata	AT1G76680.1 | Symbols: OPR1, ATOPR1 | 12-oxophytodienoate reductase 1 | chr1:28776982-28778271 FORWARD LENGTH=372	369	372	0	100.8	88.6	93.0
Rsa1.0_00047.1.g2711.t1	gb|ABB83612.1| syntaxin-like protein [Brassica oleracea]	281	276	1.00E-141	98.2	89.3	92.9	syntaxin-like protein	gbpln	Brassica oleracea	AT5G16830.1 | Symbols: SYP21, ATSYP21, PEP12, ATPEP12, PEP12P | syntaxin of plants 21 | chr5:5533076-5535152 REVERSE LENGTH=279	281	279	1.00E-130	99.3	81.1	89.0
Rsa1.0_00047.1.g2712.t1	gb|EOA22596.1| hypothetical protein CARUB_v10003259mg [Capsella rubella]	468	478	0	102.1	73.5	82.5	hypothetical protein CARUB_v10003259mg	gbpln	Capsella rubella	AT5G16820.2 | Symbols: HSF3, HSFA1B, ATHSFA1B | heat shock factor 3 | chr5:5530446-5532497 FORWARD LENGTH=481	468	481	1.00E-179	102.8	72.0	80.1
Rsa1.0_00047.1.g2713.t2	ref|NP_974793.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] gi|44681356|gb|AAS47618.1| At5g16800 [Arabidopsis thaliana] gi|45773876|gb|AAS76742.1| At5g16800 [Arabidopsis thaliana] gi|332004956|gb|AED92339.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana]	257	270	1.00E-132	105.1	88.3	93.8	GCN5-related N-acetyltransferase (GNAT) family protein	gbpln	Arabidopsis thaliana	AT5G16800.2 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr5:5524509-5526295 REVERSE LENGTH=270	257	270	1.00E-134	105.1	88.3	93.8
Rsa1.0_00047.1.g2714.t1	ref|XP_002873791.1| hypothetical protein ARALYDRAFT_488536 [Arabidopsis lyrata subsp. lyrata] gi|297319628|gb|EFH50050.1| hypothetical protein ARALYDRAFT_488536 [Arabidopsis lyrata subsp. lyrata]	812	812	0	100.0	82.8	89.5	hypothetical protein ARALYDRAFT_488536	gbpln	Arabidopsis lyrata	AT5G16780.1 | Symbols: DOT2, MDF | SART-1 family | chr5:5517784-5521566 REVERSE LENGTH=820	812	820	0	101.0	82.4	89.2
Rsa1.0_00047.1.g2715.t1	emb|CAC01841.1| putative transcription factor (MYB9) [Arabidopsis thaliana]	328	325	1.00E-156	99.1	83.8	89.6	putative transcription factor (MYB9)	gbpln	Arabidopsis thaliana	AT5G16770.2 | Symbols: AtMYB9, MYB9 | myb domain protein 9 | chr5:5515209-5516734 FORWARD LENGTH=336	328	336	1.00E-158	102.4	83.8	89.6

Rsa1.0_00047.1.g2716.t1	ref|NP_197178.1| inositol-tetrakisphosphate 1-kinase 1 [Arabidopsis thaliana] gi|75202063|sp|Q9SBA5.1|ITPK1_ARATH RecName: Full=Inositol-tetrakisphosphate 1-kinase 1; AltName: Full=Inositol 1,3,4-trisphosphate 5/6-kinase 1; Short=AtItpk-1; Short=Inositol-triphosphate 5/6-kinase 1; Short=Ins(1,3,4)P(3) 5/6-kinase 1 gi|3660465|emb|CAA04976.1| Inositol 1,3,4-Trisphosphate 5/6 kinase [Arabidopsis thaliana] gi|9755728|emb|CAC01840.1| Inositol 1, 3, 4-Trisphosphate 5/6 kinase [Arabidopsis thaliana] gi|18176069|gb|AAL59978.1| putative Inositol 1,3,4-Trisphosphate 5/6 kinase [Arabidopsis thaliana] gi|20465297|gb|AAM20052.1| putative inositol 1,3,4-trisphosphate 5/6 kinase [Arabidopsis thaliana] gi|21592636|gb|AAM64585.1| inositol 1,3,4-Trisphosphate 5/6 kinase [Arabidopsis thaliana] gi|332004951|gb|AED92334.1| inositol-tetrakisphosphate 1-kinase 1 [Arabidopsis thaliana	326	319	1.00E-158	97.9	86.5	92.3	inositol-tetrakisphosphate 1-kinase 1	gbpln	Arabidopsis thaliana	AT5G16760.1 | Symbols: | Inositol 1,3,4-trisphosphate 5/6-kinase family protein | chr5:5509890-5510849 FORWARD LENGTH=319	326	319	1.00E-161	97.9	86.5	92.3
Rsa1.0_00047.1.g2717.t1	gb|EOA19941.1| hypothetical protein CARUB_v10000193mg [Capsella rubella]	872	876	0	100.5	92.3	96.3	hypothetical protein CARUB_v10000193mg	gbpln	Capsella rubella	AT5G16750.1 | Symbols: TOZ | Transducin family protein / WD-40 repeat family protein | chr5:5504541-5509266 REVERSE LENGTH=876	872	876	0	100.5	91.2	95.6
Rsa1.0_00047.1.g2718.t1	ref|NP_178413.2| alpha/beta-hydrolases-like protein [Arabidopsis thaliana] gi|330250573|gb|AEC05667.1| alpha/beta-hydrolases-like protein [Arabidopsis thaliana]	1754	1797	0	102.5	73.2	83.1	alpha/beta-hydrolases-like protein	gbpln	Arabidopsis thaliana	AT2G03140.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:942000-949337 FORWARD LENGTH=1797	1754	1797	0	102.5	73.2	83.1
Rsa1.0_00047.1.g2719.t1	gb|EOA19951.1| hypothetical protein CARUB_v10000202mg [Capsella rubella]	816	857	0	105.0	78.2	89.7	hypothetical protein CARUB_v10000202mg	gbpln	Capsella rubella	AT5G16730.1 | Symbols: | Plant protein of unknown function (DUF827) | chr5:5497890-5500775 FORWARD LENGTH=853	816	853	0	104.5	76.7	87.5
Rsa1.0_00047.1.g2720.t1	ref|XP_002871733.1| hypothetical protein ARALYDRAFT_909657 [Arabidopsis lyrata subsp. lyrata] gi|297317570|gb|EFH47992.1| hypothetical protein ARALYDRAFT_909657 [Arabidopsis lyrata subsp. lyrata]	684	688	0	100.6	74.9	83.5	hypothetical protein ARALYDRAFT_909657	gbpln	Arabidopsis lyrata	AT5G16720.1 | Symbols: | Protein of unknown function, DUF593 | chr5:5494309-5496562 FORWARD LENGTH=675	684	675	0	98.7	74.4	83.6
Rsa1.0_00047.1.g2721.t1	gb|EOA19901.1| hypothetical protein CARUB_v10000149mg [Capsella rubella]	1284	975	0	75.9	71.7	73.5	hypothetical protein CARUB_v10000149mg	gbpln	Capsella rubella	AT5G16715.1 | Symbols: EMB2247 | ATP binding;valine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases | chr5:5485353-5493229 FORWARD LENGTH=974	1284	974	0	75.9	71.4	73.4
Rsa1.0_00047.1.g2722.t1	ref|NP_197172.1| glycosyl hydrolase family 5 protein [Arabidopsis thaliana] gi|9755722|emb|CAC01834.1| putative protein [Arabidopsis thaliana] gi|332004944|gb|AED92327.1| glycosyl hydrolase family 5 protein [Arabidopsis thaliana]	291	488	1.00E-113	167.7	72.2	78.7	glycosyl hydrolase family 5 protein	gbpln	Arabidopsis thaliana	AT5G16700.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr5:5480763-5483045 FORWARD LENGTH=488	291	488	1.00E-116	167.7	72.2	78.7
Rsa1.0_00048.1.g2723.t1	ref|XP_002869161.1| hypothetical protein ARALYDRAFT_912968 [Arabidopsis lyrata subsp. lyrata] gi|297314997|gb|EFH45420.1| hypothetical protein ARALYDRAFT_912968 [Arabidopsis lyrata subsp. lyrata]	723	844	0	116.7	89.6	95.6	hypothetical protein ARALYDRAFT_912968	gbpln	Arabidopsis lyrata	AT4G34260.1 | Symbols: FUC95A | 1,2-alpha-L-fucosidases | chr4:16398130-16401591 FORWARD LENGTH=843	723	843	0	116.6	90.0	95.4
Rsa1.0_00048.1.g2724.t1	ref|XP_002869160.1| hypothetical protein ARALYDRAFT_491242 [Arabidopsis lyrata subsp. lyrata] gi|297314996|gb|EFH45419.1| hypothetical protein ARALYDRAFT_491242 [Arabidopsis lyrata subsp. lyrata]	101	94	8.00E-34	93.1	77.2	82.2	hypothetical protein ARALYDRAFT_491242	gbpln	Arabidopsis lyrata	AT2G15000.5 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G34265.2); Has 80 Blast hits to 80 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 80; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:6481839-6482316 REVERSE LENGTH=101	101	101	1.00E-35	100.0	75.2	87.1

Rsa1.0_00048.1.g2725.t1	ref|XP_002867124.1| hypothetical protein ARALYDRAFT_491240 [Arabidopsis lyrata subsp. lyrata] gi|297312960|gb|EFH43383.1| hypothetical protein ARALYDRAFT_491240 [Arabidopsis lyrata subsp. lyrata]	290	290	1.00E-150	100.0	89.3	94.5	hypothetical protein ARALYDRAFT_491240	gbpln	Arabidopsis lyrata	AT4G34270.1 | Symbols: | TIP41-like family protein | chr4:16404138-16406153 REVERSE LENGTH=290	290	290	1.00E-150	100.0	87.6	94.1
Rsa1.0_00048.1.g2726.t1	gb|EOA24746.1| hypothetical protein CARUB_v10018023mg [Capsella rubella]	210	210	1.00E-109	100.0	91.0	96.2	hypothetical protein CARUB_v10018023mg	gbpln	Capsella rubella	AT3G25580.1 | Symbols: | Thioredoxin superfamily protein | chr3:9292557-9294148 FORWARD LENGTH=210	210	210	1.00E-108	100.0	89.0	95.2
Rsa1.0_00048.1.g2727.t1	ref|XP_002869159.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297314995|gb|EFH45418.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	739	785	0	106.2	79.8	88.4	transducin family protein	gbpln	Arabidopsis lyrata	AT4G34280.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr4:16407084-16410644 FORWARD LENGTH=783	739	783	0	106.0	78.9	87.4
Rsa1.0_00048.1.g2728.t1	gb|EOA19159.1| hypothetical protein CARUB_v10007836mg [Capsella rubella]	139	150	4.00E-56	107.9	84.2	91.4	hypothetical protein CARUB_v10007836mg	gbpln	Capsella rubella	AT4G34290.1 | Symbols: | SWIB/MDM2 domain superfamily protein | chr4:16410883-16412122 FORWARD LENGTH=144	139	144	8.00E-56	103.6	81.3	87.8
Rsa1.0_00048.1.g2729.t1	ref|XP_002869156.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314992|gb|EFH45415.1| binding protein [Arabidopsis lyrata subsp. lyrata]	1221	1228	0	100.6	91.0	94.1	binding protein	gbpln	Arabidopsis lyrata	AT4G34310.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:16414113-16419542 FORWARD LENGTH=1228	1221	1228	0	100.6	90.2	93.9
Rsa1.0_00048.1.g2730.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1327	1374	0	103.5	54.6	72.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1327	575	1.00E-180	43.3	21.9	31.3
Rsa1.0_00048.1.g2731.t1	ref|XP_002867123.1| hypothetical protein ARALYDRAFT_491232 [Arabidopsis lyrata subsp. lyrata] gi|297312959|gb|EFH43382.1| hypothetical protein ARALYDRAFT_491232 [Arabidopsis lyrata subsp. lyrata]	355	355	1.00E-125	100.0	73.5	83.1	hypothetical protein ARALYDRAFT_491232	gbpln	Arabidopsis lyrata	AT4G34340.1 | Symbols: TAF8 | TBP-associated factor 8 | chr4:16426771-16427832 REVERSE LENGTH=353	355	353	1.00E-126	99.4	72.4	82.8
Rsa1.0_00048.1.g2732.t1	ref|XP_002885880.1| hypothetical protein ARALYDRAFT_899583 [Arabidopsis lyrata subsp. lyrata] gi|297331720|gb|EFH62139.1| hypothetical protein ARALYDRAFT_899583 [Arabidopsis lyrata subsp. lyrata]	166	183	1.00E-11	110.2	30.1	41.0	hypothetical protein ARALYDRAFT_899583	gbpln	Arabidopsis lyrata	AT5G33330.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:12591754-12592896 REVERSE LENGTH=183	166	183	2.00E-11	110.2	21.1	31.3
Rsa1.0_00048.1.g2733.t1	gb|EOA16580.1| hypothetical protein CARUB_v10004745mg [Capsella rubella]	466	467	0	100.2	93.6	97.4	hypothetical protein CARUB_v10004745mg	gbpln	Capsella rubella	AT4G34350.1 | Symbols: CLB6, ISPH, HDR | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | chr4:16428681-16431038 REVERSE LENGTH=466	466	466	0	100.0	92.5	96.4
Rsa1.0_00048.1.g2734.t1	gb|EOA17276.1| hypothetical protein CARUB_v10005548mg [Capsella rubella]	257	256	1.00E-129	99.6	87.9	93.4	hypothetical protein CARUB_v10005548mg	gbpln	Capsella rubella	AT4G34360.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:16432011-16433752 FORWARD LENGTH=248	257	248	1.00E-127	96.5	85.6	89.5
Rsa1.0_00048.1.g2735.t1	ref|XP_002869152.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297314988|gb|EFH45411.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata]	592	597	0	100.8	83.6	91.7	IBR domain-containing protein	gbpln	Arabidopsis lyrata	AT4G34370.1 | Symbols: ATARI1, ARI1 | RING/U-box superfamily protein | chr4:16434547-16437037 FORWARD LENGTH=597	592	597	0	100.8	82.4	91.7
Rsa1.0_00048.1.g2736.t1	gb|EOA18995.1| hypothetical protein CARUB_v10007640mg [Capsella rubella]	527	492	0	93.4	75.9	83.5	hypothetical protein CARUB_v10007640mg	gbpln	Capsella rubella	AT4G34380.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:16438835-16440322 FORWARD LENGTH=495	527	495	0	93.9	74.6	82.5
Rsa1.0_00048.1.g2737.t1	ref|XP_002869151.1| extra-large GTP-binding protein 2 [Arabidopsis lyrata subsp. lyrata] gi|297314987|gb|EFH45410.1| extra-large GTP-binding protein 2 [Arabidopsis lyrata subsp. lyrata]	842	859	0	102.0	76.7	85.6	extra-large GTP-binding protein 2	gbpln	Arabidopsis lyrata	AT4G34390.1 | Symbols: XLG2 | extra-large GTP-binding protein 2 | chr4:16441579-16444840 FORWARD LENGTH=861	842	861	0	102.3	77.3	85.3
Rsa1.0_00048.1.g2738.t1	gb|EOA15869.1| hypothetical protein CARUB_v10007825mg [Capsella rubella]	276	272	1.00E-100	98.6	80.4	87.7	hypothetical protein CARUB_v10007825mg	gbpln	Capsella rubella	AT4G34410.1 | Symbols: RRTF1 | redox responsive transcription factor 1 | chr4:16451992-16452798 FORWARD LENGTH=268	276	268	1.00E-92	97.1	79.0	85.5
Rsa1.0_00048.1.g2739.t1	gb|EOA17538.1| hypothetical protein CARUB_v10005889mg [Capsella rubella]	98	172	3.00E-38	175.5	78.6	89.8	hypothetical protein CARUB_v10005889mg	gbpln	Capsella rubella	AT4G34412.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Kinase binding protein CGI-121 (InterPro:IPR013926); Has 275 Blast hits to 275 proteins in 139 species: Archae - 0; Bacteria - 5; Metazoa - 98; Fungi - 109; Plants - 42; Viruses - 0; Other Eukaryotes - 21 (source: NCBI BLink). | chr4:16453099-16454515 REVERSE LENGTH=172	98	172	5.00E-40	175.5	78.6	88.8

Rsa1.0_00048.1.g2740.t1	ref|NP_001190912.1| uncharacterized protein [Arabidopsis thaliana] gi|51970964|dbj|BAD44174.1| hypothetical protein [Arabidopsis thaliana] gi|332660971|gb|AEE86371.1| uncharacterized protein AT4G34419 [Arabidopsis thaliana]	129	129	5.00E-61	100.0	87.6	93.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G34419.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G19200.1). | chr4:16456597-16456986 FORWARD LENGTH=129	129	129	1.00E-63	100.0	87.6	93.0
Rsa1.0_00048.1.g2741.t1	gb|EOA15557.1| hypothetical protein CARUB_v10005172mg [Capsella rubella]	343	344	0	100.3	88.6	94.2	hypothetical protein CARUB_v10005172mg	gbpln	Capsella rubella	AT4G34420.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:16458430-16460526 FORWARD LENGTH=342	343	342	0	99.7	87.8	93.6
Rsa1.0_00048.1.g2742.t1	ref|XP_002869145.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314981|gb|EFH45404.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	677	669	0	98.8	83.0	89.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G34440.1 | Symbols: | Protein kinase superfamily protein | chr4:16466008-16468748 FORWARD LENGTH=670	677	670	0	99.0	80.9	87.7
Rsa1.0_00048.1.g2743.t1	ref|NP_195171.2| coatomer subunit gamma [Arabidopsis thaliana] gi|146286094|sp|Q0WW26.2|COPG_ARATH RecName: Full=Coatomer subunit gamma; AltName: Full=Gamma-coat protein; Short=Gamma-COP gi|222424705|dbj|BAH20306.1| AT4G34450 [Arabidopsis thaliana] gi|332660978|gb|AEE86378.1| coatomer subunit gamma [Arabidopsis thaliana]	886	886	0	100.0	96.5	98.8	coatomer subunit gamma	gbpln	Arabidopsis thaliana	AT4G34450.1 | Symbols: | coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative | chr4:16471956-16476795 FORWARD LENGTH=886	886	886	0	100.0	96.5	98.8
Rsa1.0_00048.1.g2744.t1	dbj|BAJ34135.1| unnamed protein product [Thellungiella halophila]	411	377	0	91.7	88.3	90.3	unnamed protein product	----	----	AT4G34460.1 | Symbols: AGB1, ELK4, ATAGB1 | GTP binding protein beta 1 | chr4:16477393-16479266 REVERSE LENGTH=377	411	377	0	91.7	86.1	89.1
Rsa1.0_00048.1.g2745.t1	ref|NP_195174.6| glucan endo-1,3-beta-glucosidase 7 [Arabidopsis thaliana] gi|259016223|sp|Q9M069.2|E137_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 7; AltName: Full=(1-3)-beta-glucan endohydrolase 7; Short=(1-3)-beta-glucanase 7; AltName: Full=Beta-1,3-endoglucanase 7; Short=Beta-1,3-glucanase 7; Flags: Precursor gi|332660984|gb|AEE86384.1| glucan endo-1,3-beta-glucosidase 7 [Arabidopsis thaliana]	509	504	0	99.0	81.7	87.6	glucan endo-1,3-beta-glucosidase 7	gbpln	Arabidopsis thaliana	AT4G34480.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr4:16481147-16483988 REVERSE LENGTH=504	509	504	0	99.0	81.7	87.6
Rsa1.0_00048.1.g2746.t1	ref|NP_195175.1| cyclase associated protein 1 [Arabidopsis thaliana] gi|3096918|emb|CAA18828.1| putative cyclase associated protein CAP [Arabidopsis thaliana] gi|3169136|dbj|BAA28621.1| Atcap1 [Arabidopsis thaliana] gi|7270399|emb|CAB80166.1| putative cyclase associated protein CAP [Arabidopsis thaliana] gi|115646727|gb|ABJ17096.1| At4g34490 [Arabidopsis thaliana] gi|332660985|gb|AEE86385.1| cyclase associated protein 1 [Arabidopsis thaliana]	479	476	0	99.4	93.3	97.3	cyclase associated protein 1	gbpln	Arabidopsis thaliana	AT4G34490.1 | Symbols: ATCAP1, CAP 1, CAP1 | cyclase associated protein 1 | chr4:16484896-16487355 REVERSE LENGTH=476	479	476	0	99.4	93.3	97.3
Rsa1.0_00048.1.g2747.t1	gb|EOA16482.1| hypothetical protein CARUB_v10004641mg, partial [Capsella rubella]	442	499	0	112.9	85.7	90.3	hypothetical protein CARUB_v10004641mg, partial	gbpln	Capsella rubella	AT4G34500.1 | Symbols: | Protein kinase superfamily protein | chr4:16488005-16490792 REVERSE LENGTH=437	442	437	0	98.9	87.3	91.6
Rsa1.0_00048.1.g2748.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	691	723	0	104.6	57.0	73.8	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	691	696	7.00E-45	100.7	19.7	37.6
Rsa1.0_00048.1.g2749.t1	ref|NP_195180.1| NmrA-like negative transcriptional regulator family protein [Arabidopsis thaliana] gi|3641839|emb|CAA18833.1| isoflavone reductase-like protein [Arabidopsis thaliana] gi|7270404|emb|CAB80171.1| isoflavone reductase-like protein [Arabidopsis thaliana] gi|332660990|gb|AEE86390.1| NmrA-like negative transcriptional regulator family protein [Arabidopsis thaliana]	672	306	2.33E-156	45.5	38.1	41.5	NmrA-like negative transcriptional regulator family protein	gbpln	Arabidopsis thaliana	AT4G34540.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr4:16500506-16501932 FORWARD LENGTH=306	672	306	1.00E-149	45.5	38.1	41.5

Rsa1.0_00048.1.g2750.t1	gb|EOA17396.1| hypothetical protein CARUB_v10005690mg [Capsella rubella]	216	221	3.00E-75	102.3	75.5	85.2	hypothetical protein CARUB_v10005690mg	gbpln	Capsella rubella	AT4G34560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66440.1); Has 67 Blast hits to 66 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:16507923-16508588 FORWARD LENGTH=221	216	221	2.00E-69	102.3	73.1	81.9
Rsa1.0_00048.1.g2751.t1	ref|NP_195183.2| thymidylate synthase [Arabidopsis thaliana] gi|150421542|sp|Q05763.2|DRTS2_ARATH RecName: Full=Bifunctional dihydrofolate reductase-thymidylate synthase 2; Short=DHFR-TS 2; Includes: RecName: Full=Dihydrofolate reductase; Includes: RecName: Full=Thymidylate synthase gi|110743754|dbj|BAE99713.1| dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana] gi|332660994|gb|AEE86394.1| thymidylate synthase [Arabidopsis thaliana]	559	565	0	101.1	87.8	93.0	thymidylate synthase	gbpln	Arabidopsis thaliana	AT4G34570.1 | Symbols: THY-2 | thymidylate synthase 2 | chr4:16511129-16514110 REVERSE LENGTH=565	559	565	0	101.1	87.8	93.0
Rsa1.0_00048.1.g2752.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00048.1.g2753.t1	ref|XP_002883443.1| hypothetical protein ARALYDRAFT_342502 [Arabidopsis lyrata subsp. lyrata] gi|297329283|gb|EFH59702.1| hypothetical protein ARALYDRAFT_342502 [Arabidopsis lyrata subsp. lyrata]	326	454	2.00E-19	139.3	21.8	35.0	hypothetical protein ARALYDRAFT_342502	gbpln	Arabidopsis lyrata	AT1G01355.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr1:138513-139568 FORWARD LENGTH=228	326	228	4.00E-12	69.9	19.0	27.6
Rsa1.0_00048.1.g2754.t2	ref|NP_195184.2| Sec14p-like phosphatidylinositol transfer family protein [Arabidopsis thaliana] gi|332660995|gb|AEE86395.1| Sec14p-like phosphatidylinositol transfer family protein [Arabidopsis thaliana]	551	554	0	100.5	91.1	95.3	Sec14p-like phosphatidylinositol transfer family protein	gbpln	Arabidopsis thaliana	AT4G34580.1 | Symbols: COW1, SRH1 | Sec14p-like phosphatidylinositol transfer family protein | chr4:16515422-16518527 FORWARD LENGTH=554	551	554	0	100.5	91.1	95.3
Rsa1.0_00048.1.g2755.t1	gb|EOA17614.1| hypothetical protein CARUB_v10005978mg [Capsella rubella]	154	143	1.00E-59	92.9	77.3	81.2	hypothetical protein CARUB_v10005978mg	gbpln	Capsella rubella	AT4G34590.1 | Symbols: ATB2, GBF6, AtbZIP11, BZIP11 | G-box binding factor 6 | chr4:16522449-16522928 FORWARD LENGTH=159	154	159	1.00E-59	103.2	74.7	81.2
Rsa1.0_00048.1.g2756.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00048.1.g2757.t1	ref|NP_195186.1| uncharacterized protein [Arabidopsis thaliana] gi|3096929|emb|CAA18839.1| putative protein [Arabidopsis thaliana] gi|7270410|emb|CAB80177.1| putative protein [Arabidopsis thaliana] gi|38566572|gb|AAR24176.1| At4g34600 [Arabidopsis thaliana] gi|47550671|gb|AAT35234.1| At4g34600 [Arabidopsis thaliana] gi|332660998|gb|AEE86398.1| uncharacterized protein AT4G34600 [Arabidopsis thaliana]	80	83	2.00E-28	103.8	83.8	92.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G34600.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: pollen tube growth; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: M germinated pollen stage, LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G16385.1); Has 17 Blast hits to 17 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:16529280-16529958 FORWARD LENGTH=83	80	83	3.00E-31	103.8	83.8	92.5
Rsa1.0_00048.1.g2758.t1	gb|EOA39417.1| hypothetical protein CARUB_v10012524mg [Capsella rubella]	169	535	7.00E-25	316.6	33.7	40.8	hypothetical protein CARUB_v10012524mg	gbpln	Capsella rubella	AT1G48920.1 | Symbols: ATNUC-L1, PARL1, NUC-L1 | nucleolin like 1 | chr1:18098186-18101422 FORWARD LENGTH=557	169	557	2.00E-26	329.6	34.3	41.4
Rsa1.0_00048.1.g2759.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00048.1.g2760.t1	ref|XP_002867110.1| hypothetical protein ARALYDRAFT_912923 [Arabidopsis lyrata subsp. lyrata] gi|297312946|gb|EFH43369.1| hypothetical protein ARALYDRAFT_912923 [Arabidopsis lyrata subsp. lyrata]	113	113	7.00E-58	100.0	94.7	99.1	hypothetical protein ARALYDRAFT_912923	gbpln	Arabidopsis lyrata	AT4G34620.1 | Symbols: SSR16 | small subunit ribosomal protein 16 | chr4:16535084-16536092 REVERSE LENGTH=113	113	113	2.00E-57	100.0	89.4	96.5
Rsa1.0_00048.1.g2761.t1	ref|XP_002867109.1| hypothetical protein ARALYDRAFT_491192 [Arabidopsis lyrata subsp. lyrata] gi|297312945|gb|EFH43368.1| hypothetical protein ARALYDRAFT_491192 [Arabidopsis lyrata subsp. lyrata]	221	210	4.00E-67	95.0	67.9	76.0	hypothetical protein ARALYDRAFT_491192	gbpln	Arabidopsis lyrata	AT4G34630.1 | Symbols: | unknown protein; Has 30 Blast hits to 30 proteins in 10 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:16537093-16537692 REVERSE LENGTH=199	221	199	2.00E-56	90.0	61.5	70.6

Rsa1.0_00048.1.g2762.t1	ref|XP_002869133.1| hypothetical protein ARALYDRAFT_912921 [Arabidopsis lyrata subsp. lyrata] gi|297314969|gb|EFH45392.1| hypothetical protein ARALYDRAFT_912921 [Arabidopsis lyrata subsp. lyrata]	396	412	0	104.0	81.3	84.8	hypothetical protein ARALYDRAFT_912921	gbpln	Arabidopsis lyrata	AT4G34640.1 | Symbols: SQS1, ERG9 | squalene synthase 1 | chr4:16538489-16541655 FORWARD LENGTH=410	396	410	0	103.5	79.8	84.1
Rsa1.0_00048.1.g2763.t1	ref|NP_195191.2| squalene synthase 2 [Arabidopsis thaliana] gi|5678626|emb|CAA18844.2| putative squalene synthase [Arabidopsis thaliana] gi|7270415|emb|CAB80182.1| putative squalene synthase [Arabidopsis thaliana] gi|332661004|gb|AEE86404.1| squalene synthase 2 [Arabidopsis thaliana]	416	413	0	99.3	84.1	91.3	squalene synthase 2	gbpln	Arabidopsis thaliana	AT4G34650.1 | Symbols: SQS2 | squalene synthase 2 | chr4:16542377-16544915 FORWARD LENGTH=413	416	413	0	99.3	84.1	91.3
Rsa1.0_00048.1.g2764.t1	gb|EOA16836.1| hypothetical protein CARUB_v10005057mg [Capsella rubella]	375	377	0	100.5	94.4	98.1	hypothetical protein CARUB_v10005057mg	gbpln	Capsella rubella	AT4G34660.1 | Symbols: | SH3 domain-containing protein | chr4:16545595-16548294 REVERSE LENGTH=368	375	368	0	98.1	92.3	96.0
Rsa1.0_00048.1.g2765.t1	gb|EOA17249.1| hypothetical protein CARUB_v10005523mg [Capsella rubella]	262	262	1.00E-138	100.0	93.9	98.5	hypothetical protein CARUB_v10005523mg	gbpln	Capsella rubella	AT4G34670.1 | Symbols: | Ribosomal protein S3Ae | chr4:16548724-16550222 FORWARD LENGTH=262	262	262	1.00E-139	100.0	93.9	96.9
Rsa1.0_00048.1.g2766.t2	gb|EOA17609.1| hypothetical protein CARUB_v10005980mg, partial [Capsella rubella]	143	140	4.00E-56	97.9	75.5	77.6	hypothetical protein CARUB_v10005980mg, partial	gbpln	Capsella rubella	AT4G34700.1 | Symbols: CIB22, AtCIB22 | LYR family of Fe/S cluster biogenesis protein | chr4:16556874-16558362 FORWARD LENGTH=117	143	117	4.00E-58	81.8	73.4	74.1
Rsa1.0_00048.1.g2767.t1	gb|AAR08423.1| arginine decarboxylase 2 [Pringlea antiscorbutica]	275	711	1.00E-120	258.5	81.5	88.7	arginine decarboxylase 2	gbpln	Pringlea antiscorbutica	AT4G34710.2 | Symbols: ADC2, SPE2, ATADC2 | arginine decarboxylase 2 | chr4:16560315-16562450 REVERSE LENGTH=711	275	711	1.00E-114	258.5	78.9	86.5
Rsa1.0_00049.1.g2768.t1	dbj|BAJ33888.1| unnamed protein product [Thellungiella halophila]	243	245	1.00E-81	100.8	90.1	93.0	unnamed protein product	----	----	AT4G20260.3 | Symbols: ATPCAP1, PCAP1 | plasma-membrane associated cation-binding protein 1 | chr4:10941593-10943227 FORWARD LENGTH=225	243	225	1.00E-76	92.6	79.0	83.1
Rsa1.0_00049.1.g2769.t1	gb|EOA19016.1| hypothetical protein CARUB_v10007667mg [Capsella rubella]	595	557	0	93.6	66.6	73.6	hypothetical protein CARUB_v10007667mg	gbpln	Capsella rubella	AT4G20200.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr4:10908672-10911151 REVERSE LENGTH=604	595	604	0	101.5	50.6	64.5
Rsa1.0_00049.1.g2770.t2	ref|XP_002867888.1| hypothetical protein ARALYDRAFT_492849 [Arabidopsis lyrata subsp. lyrata] gi|297313724|gb|EFH44147.1| hypothetical protein ARALYDRAFT_492849 [Arabidopsis lyrata subsp. lyrata]	393	394	1.00E-174	100.3	84.5	91.1	hypothetical protein ARALYDRAFT_492849	gbpln	Arabidopsis lyrata	AT4G20190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G44660.1); Has 271 Blast hits to 209 proteins in 52 species: Archae - 0; Bacteria - 15; Metazoa - 63; Fungi - 14; Plants - 48; Viruses - 3; Other Eukaryotes - 128 (source: NCBI BLink). | chr4:10906508-10907677 REVERSE LENGTH=389	393	389	1.00E-174	99.0	83.2	89.3
Rsa1.0_00049.1.g2771.t1	ref|NP_193750.1| uncharacterized protein [Arabidopsis thaliana] gi|2982434|emb|CAA18242.1| putative protein [Arabidopsis thaliana] gi|7268812|emb|CAB79017.1| putative protein [Arabidopsis thaliana] gi|332658882|gb|AEE84282.1| uncharacterized protein AT4G20170 [Arabidopsis thaliana]	504	504	0	100.0	84.9	90.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G20170.1 | Symbols: | Domain of unknown function (DUF23) | chr4:10896810-10898794 FORWARD LENGTH=504	504	504	0	100.0	84.9	90.9
Rsa1.0_00049.1.g2772.t1	ref|NP_193749.1| uncharacterized protein [Arabidopsis thaliana] gi|2982433|emb|CAA18241.1| Glu-rich protein [Arabidopsis thaliana] gi|7268811|emb|CAB79016.1| Glu-rich protein [Arabidopsis thaliana] gi|332658881|gb|AEE84281.1| uncharacterized protein AT4G20160 [Arabidopsis thaliana]	1223	1188	0	97.1	57.4	67.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G20160.1 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: RING/U-box superfamily protein (TAIR:AT1G30860.1); Has 64917 Blast hits to 39974 proteins in 1949 species: Archae - 279; Bacteria - 7425; Metazoa - 26604; Fungi - 5788; Plants - 3193; Viruses - 275; Other Eukaryotes - 21353 (source: NCBI BLink). | chr4:10890983-10894971 FORWARD LENGTH=1188	1223	1188	0	97.1	57.4	67.9
Rsa1.0_00049.1.g2773.t2	ref|XP_002869946.1| hypothetical protein ARALYDRAFT_354732 [Arabidopsis lyrata subsp. lyrata] gi|297315782|gb|EFH46205.1| hypothetical protein ARALYDRAFT_354732 [Arabidopsis lyrata subsp. lyrata]	1144	1252	0	109.4	41.6	44.0	hypothetical protein ARALYDRAFT_354732	gbpln	Arabidopsis lyrata	AT4G20140.1 | Symbols: GSO1 | Leucine-rich repeat transmembrane protein kinase | chr4:10884220-10888045 FORWARD LENGTH=1249	1144	1249	0	109.2	40.9	43.9

Rsa1.0_00049.1.g2774.t1	ref|XP_002869946.1| hypothetical protein ARALYDRAFT_354732 [Arabidopsis lyrata subsp. lyrata] gi|297315782|gb|EFH46205.1| hypothetical protein ARALYDRAFT_354732 [Arabidopsis lyrata subsp. lyrata]	1255	1252	0	99.8	87.6	92.6	hypothetical protein ARALYDRAFT_354732	gbpln	Arabidopsis lyrata	AT4G20140.1 | Symbols: GSO1 | Leucine-rich repeat transmembrane protein kinase | chr4:10884220-10888045 FORWARD LENGTH=1249	1255	1249	0	99.5	85.9	91.4
Rsa1.0_00049.1.g2775.t1	ref|XP_002869948.1| hypothetical protein ARALYDRAFT_492857 [Arabidopsis lyrata subsp. lyrata] gi|297315784|gb|EFH46207.1| hypothetical protein ARALYDRAFT_492857 [Arabidopsis lyrata subsp. lyrata]	631	625	0	99.0	89.2	95.4	hypothetical protein ARALYDRAFT_492857	gbpln	Arabidopsis lyrata	AT4G20110.1 | Symbols: VSR7, VSR3;1, BP80-3;1 | VACUOLAR SORTING RECEPTOR 7 | chr4:10875567-10878545 FORWARD LENGTH=625	631	625	0	99.0	88.7	95.1
Rsa1.0_00049.1.g2776.t1	ref|XP_002867892.1| EMB1025 [Arabidopsis lyrata subsp. lyrata] gi|297313728|gb|EFH44151.1| EMB1025 [Arabidopsis lyrata subsp. lyrata]	612	658	0	107.5	81.5	89.4	EMB1025	gbpln	Arabidopsis lyrata	AT4G20090.1 | Symbols: EMB1025 | Pentatricopeptide repeat (PPR) superfamily protein | chr4:10868400-10870382 REVERSE LENGTH=660	612	660	0	107.8	80.6	88.9
Rsa1.0_00049.1.g2777.t1	ref|XP_002867893.1| EMB1895 [Arabidopsis lyrata subsp. lyrata] gi|297313729|gb|EFH44152.1| EMB1895 [Arabidopsis lyrata subsp. lyrata]	1131	1134	0	100.3	79.0	87.5	EMB1895	gbpln	Arabidopsis lyrata	AT4G20060.1 | Symbols: EMB1895 | ARM repeat superfamily protein | chr4:10854790-10859330 REVERSE LENGTH=1134	1131	1134	0	100.3	78.7	87.5
Rsa1.0_00049.1.g2778.t1	gb|AFL69960.1| polygalacturonase [Brassica napus]	475	475	0	100.0	93.5	95.6	polygalacturonase	gbpln	Brassica napus	AT4G20050.2 | Symbols: QRT3 | Pectin lyase-like superfamily protein | chr4:10849911-10852090 REVERSE LENGTH=481	475	481	0	101.3	87.4	94.9
Rsa1.0_00049.1.g2779.t2	gb|EOA18460.1| hypothetical protein CARUB_v10007004mg [Capsella rubella]	466	485	0	104.1	81.8	90.1	hypothetical protein CARUB_v10007004mg	gbpln	Capsella rubella	AT4G20040.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:10847348-10848963 REVERSE LENGTH=483	466	483	0	103.6	79.8	87.6
Rsa1.0_00049.1.g2780.t1	gb|EOA17585.1| hypothetical protein CARUB_v10005947mg [Capsella rubella]	154	152	6.00E-68	98.7	83.8	90.9	hypothetical protein CARUB_v10005947mg	gbpln	Capsella rubella	AT4G20030.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:10846362-10847246 FORWARD LENGTH=152	154	152	3.00E-69	98.7	82.5	89.6
Rsa1.0_00049.1.g2781.t1	ref|NP_193735.1| uncharacterized protein [Arabidopsis thaliana] gi|2827656|emb|CAA16610.1| DAG-like protein [Arabidopsis thaliana] gi|7268797|emb|CAB79002.1| DAG-like protein [Arabidopsis thaliana] gi|27754272|gb|AAO22589.1| putative DAG protein [Arabidopsis thaliana] gi|332658862|gb|AEE84262.1| uncharacterized protein AT4G20020 [Arabidopsis thaliana]	381	419	1.00E-154	110.0	78.5	85.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G20020.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G44780.1); Has 28928 Blast hits to 16023 proteins in 1033 species: Archae - 4; Bacteria - 4155; Metazoa - 15463; Fungi - 2938; Plants - 3091; Viruses - 205; Other Eukaryotes - 3072 (source: NCBI BLink). | chr4:10844433-10846085 REVERSE LENGTH=419	381	419	1.00E-157	110.0	78.5	85.3
Rsa1.0_00049.1.g2782.t1	ref|XP_002867898.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297313734|gb|EFH44157.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	211	209	9.00E-73	99.1	72.5	82.0	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT4G20000.1 | Symbols: | VQ motif-containing protein | chr4:10838367-10838993 FORWARD LENGTH=208	211	208	4.00E-67	98.6	67.8	78.2
Rsa1.0_00049.1.g2783.t1	dbj|BAJ33925.1| unnamed protein product [Thellungiella halophila]	858	752	0	87.6	69.2	74.9	unnamed protein product	----	----	AT4G19990.2 | Symbols: FRS1 | FAR1-related sequence 1 | chr4:10832848-10835559 FORWARD LENGTH=774	858	774	0	90.2	66.0	71.7
Rsa1.0_00049.1.g2784.t1	ref|XP_002867900.1| hypothetical protein ARALYDRAFT_492876 [Arabidopsis lyrata subsp. lyrata] gi|297313736|gb|EFH44159.1| hypothetical protein ARALYDRAFT_492876 [Arabidopsis lyrata subsp. lyrata]	240	236	9.00E-99	98.3	79.2	82.5	hypothetical protein ARALYDRAFT_492876	gbpln	Arabidopsis lyrata	AT4G19985.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr4:10830542-10831711 REVERSE LENGTH=237	240	237	4.00E-95	98.8	75.8	80.0
Rsa1.0_00049.1.g2785.t1	gb|EOA17660.1| hypothetical protein CARUB_v10006027mg [Capsella rubella]	127	125	3.00E-46	98.4	79.5	81.1	hypothetical protein CARUB_v10006027mg	gbpln	Capsella rubella	AT4G19980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: root, pedicel; EXPRESSED DURING: 4 anthesis; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10828153-10828536 REVERSE LENGTH=127	127	127	2.00E-43	100.0	74.0	81.1

Rsa1.0_00049.1.g2786.t1	dbj|BAJ34335.1| unnamed protein product [Thellungiella halophila]	374	374	0	100.0	89.8	94.7	unnamed protein product	----	----	AT4G19970.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nucleotide-diphospho-sugar transferase, predicted (InterPro:IPR005069); BEST Arabidopsis thaliana protein match is: Nucleotide-diphospho-sugar transferase family protein (TAIR:AT5G44820.1); Has 801 Blast hits to 466 proteins in 35 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 750; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink). | chr4:10818242-10825343 FORWARD LENGTH=715	374	715	0	191.2	86.1	90.9
Rsa1.0_00049.1.g2787.t2	gb|EOA16028.1| hypothetical protein CARUB_v10004157mg [Capsella rubella]	812	812	0	100.0	87.9	92.7	hypothetical protein CARUB_v10004157mg	gbpln	Capsella rubella	AT4G19960.2 | Symbols: KUP9 | K+ uptake permease 9 | chr4:10813807-10816997 FORWARD LENGTH=807	812	807	0	99.4	87.9	92.1
Rsa1.0_00049.1.g2788.t1	ref|NP_193728.2| uncharacterized protein [Arabidopsis thaliana] gi|50253430|gb|AAT71917.1| At4g19950 [Arabidopsis thaliana] gi|51972070|gb|AAU15139.1| At4g19950 [Arabidopsis thaliana] gi|332658850|gb|AEE84250.1| uncharacterized protein AT4G19950 [Arabidopsis thaliana]	318	321	1.00E-147	100.9	85.5	93.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G19950.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G44860.1); Has 338 Blast hits to 330 proteins in 72 species: Archae - 2; Bacteria - 94; Metazoa - 7; Fungi - 0; Plants - 232; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr4:10809977-10810942 FORWARD LENGTH=321	318	321	1.00E-150	100.9	85.5	93.1
Rsa1.0_00049.1.g2789.t1	ref|NP_001190774.1| Pentatricopeptide repeat domain-containing protein [Arabidopsis thaliana] gi|223635614|sp|P0C8Q3.1|PP326_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g19890 gi|332658842|gb|AEE84242.1| Pentatricopeptide repeat domain-containing protein [Arabidopsis thaliana]	700	701	0	100.1	89.4	94.1	Pentatricopeptide repeat domain-containing protein	gbpln	Arabidopsis thaliana	AT4G19890.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr4:10786948-10789053 REVERSE LENGTH=701	700	701	0	100.1	89.4	94.1
Rsa1.0_00049.1.g2790.t2	gb|EOA33274.1| hypothetical protein CARUB_v10019647mg [Capsella rubella]	2355	2361	0	100.3	97.9	98.9	hypothetical protein CARUB_v10019647mg	gbpln	Capsella rubella	AT1G80070.1 | Symbols: SUS2, EMB33, EMB177, EMB14 | Pre-mRNA-processing-splicing factor | chr1:30118052-30127574 FORWARD LENGTH=2359	2355	2359	0	100.2	97.6	98.6
Rsa1.0_00049.1.g2791.t1	ref|XP_002867917.1| lecithin:cholesterol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313753|gb|EFH44176.1| lecithin:cholesterol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	533	535	0	100.4	90.6	95.1	lecithin:cholesterol acyltransferase family protein	gbpln	Arabidopsis lyrata	AT4G19860.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:10777655-10780260 REVERSE LENGTH=535	533	535	0	100.4	90.2	95.1
Rsa1.0_00049.1.g2792.t1	ref|NP_001154254.2| protein PHLOEM protein 2-LIKE A2 [Arabidopsis thaliana] gi|332658834|gb|AEE84234.1| protein PHLOEM protein 2-LIKE A2 [Arabidopsis thaliana]	221	220	3.00E-66	99.5	62.0	68.3	protein PHLOEM protein 2-LIKE A2	gbpln	Arabidopsis thaliana	AT4G19850.2 | Symbols: | lectin-related | chr4:10776657-10777588 FORWARD LENGTH=220	221	220	1.00E-68	99.5	62.0	68.3
Rsa1.0_00049.1.g2793.t1	ref|NP_193719.1| protein PHLOEM protein 2-LIKE A1 [Arabidopsis thaliana] gi|75100453|sp|O81865.1|P2A01_ARATH RecName: Full=Protein PHLOEM PROTEIN 2-LIKE A1; Short=AtPP2-A1 gi|3250693|emb|CAA19701.1| lectin like protein [Arabidopsis thaliana] gi|7268780|emb|CAB78986.1| lectin like protein [Arabidopsis thaliana] gi|19699298|gb|AAL91260.1| AT4g19840/T16H5_200 [Arabidopsis thaliana] gi|21689635|gb|AAM67439.1| AT4g19840/T16H5_200 [Arabidopsis thaliana] gi|332658832|gb|AEE84232.1| protein PHLOEM protein 2-LIKE A1 [Arabidopsis thaliana]	217	246	2.00E-73	113.4	71.4	80.6	protein PHLOEM protein 2-LIKE A1	gbpln	Arabidopsis thaliana	AT4G19840.1 | Symbols: ATPP2-A1, ATPP2A-1, PP2-A1 | phloem protein 2-A1 | chr4:10774336-10775701 FORWARD LENGTH=246	217	246	7.00E-76	113.4	71.4	80.6
Rsa1.0_00049.1.g2794.t1	gb|EOA16822.1| hypothetical protein CARUB_v10005044mg [Capsella rubella]	380	380	0	100.0	90.0	94.5	hypothetical protein CARUB_v10005044mg	gbpln	Capsella rubella	AT4G19810.1 | Symbols: | Glycosyl hydrolase family protein with chitinase insertion domain | chr4:10764151-10765753 REVERSE LENGTH=379	380	379	0	99.7	89.5	93.7
Rsa1.0_00049.1.g2795.t1	gb|EOA15450.1| hypothetical protein CARUB_v10004092mg [Capsella rubella]	923	920	0	99.7	94.1	96.5	hypothetical protein CARUB_v10004092mg	gbpln	Capsella rubella	AT4G19710.2 | Symbols: AK-HSDH II, AK-HSDH | aspartate kinase-homoserine dehydrogenase ii | chr4:10725229-10729536 FORWARD LENGTH=916	923	916	0	99.2	93.4	96.3
Rsa1.0_00049.1.g2796.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00050.1.g2797.t1	ref|XP_002893450.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297339292|gb|EFH69709.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	253	251	1.00E-133	99.2	91.3	95.3	protein binding protein	gbpln	Arabidopsis lyrata	AT1G24440.1 | Symbols: | RING/U-box superfamily protein | chr1:8662340-8663777 FORWARD LENGTH=251	253	251	1.00E-135	99.2	90.9	94.9

Rsa1.0_00050.1.g2798.t1	ref|XP_002893449.1| hypothetical protein ARALYDRAFT_472903 [Arabidopsis lyrata subsp. lyrata] gi|297339291|gb|EFH69708.1| hypothetical protein ARALYDRAFT_472903 [Arabidopsis lyrata subsp. lyrata]	190	190	3.00E-73	100.0	74.7	85.3	hypothetical protein ARALYDRAFT_472903	gbpln	Arabidopsis lyrata	AT1G24450.1 | Symbols: NFD2 | Ribonuclease III family protein | chr1:8664201-8665077 FORWARD LENGTH=191	190	191	2.00E-74	100.5	74.7	85.3
Rsa1.0_00050.1.g2799.t2	gb|EOA37586.1| hypothetical protein CARUB_v10011938mg [Capsella rubella]	1792	1772	0	98.9	76.0	85.8	hypothetical protein CARUB_v10011938mg	gbpln	Capsella rubella	AT1G24460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G31570.1); Has 181008 Blast hits to 85359 proteins in 3551 species: Archae - 3290; Bacteria - 48304; Metazoa - 70793; Fungi - 13943; Plants - 10118; Viruses - 785; Other Eukaryotes - 33775 (source: NCBI BLink). | chr1:8666072-8672338 FORWARD LENGTH=1807	1792	1807	0	100.8	75.3	84.8
Rsa1.0_00050.1.g2800.t1	gb|EOA38309.1| hypothetical protein CARUB_v10009809mg [Capsella rubella]	318	313	1.00E-151	98.4	84.3	88.1	hypothetical protein CARUB_v10009809mg	gbpln	Capsella rubella	AT1G24470.1 | Symbols: KCR2, ATKCR2 | beta-ketoacyl reductase 2 | chr1:8674056-8676277 FORWARD LENGTH=312	318	312	1.00E-152	98.1	84.3	88.1
Rsa1.0_00050.1.g2801.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00050.1.g2802.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1389	1501	0	108.1	57.0	71.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1389	1262	1.00E-130	90.9	16.4	24.7
Rsa1.0_00050.1.g2803.t1	ref|XP_002880790.1| ania-6a type cyclin [Arabidopsis lyrata subsp. lyrata] gi|297326629|gb|EFH57049.1| ania-6a type cyclin [Arabidopsis lyrata subsp. lyrata]	413	415	0	100.5	86.9	91.8	ania-6a type cyclin	gbpln	Arabidopsis lyrata	AT2G26430.1 | Symbols: RCY1, ATRCY1 | arginine-rich cyclin 1 | chr2:11243433-11245504 REVERSE LENGTH=416	413	416	0	100.7	82.3	89.1
Rsa1.0_00050.1.g2804.t1	ref|NP_173858.5| ALBINO3-like protein 1 [Arabidopsis thaliana] gi|223590242|sp|Q9FYL3.3|ALB31_ARATH RecName: Full=ALBINO3-like protein 1, chloroplastic; AltName: Full=Arabidopsis thaliana envelope membrane integrase; AltName: Full=Protein ALBINA 4; Short=Ath4; AltName: Full=Protein ARTEMIS; Flags: Precursor gi|91680591|emb|CAJ45566.1| Alb protein [Arabidopsis thaliana] gi|332192418|gb|AEE30539.1| ALBINO3-like protein 1 [Arabidopsis thaliana]	485	499	0	102.9	86.0	92.2	ALBINO3-like protein 1	gbpln	Arabidopsis thaliana	AT1G24490.1 | Symbols: ALB4, ARTEMIS | OxaA/YidC-like membrane insertion protein | chr1:8682364-8684966 FORWARD LENGTH=499	485	499	0	102.9	86.0	92.2
Rsa1.0_00050.1.g2805.t1	ref|NP_173859.1| T-complex protein 1 subunit epsilon [Arabidopsis thaliana] gi|3024697|sp|O04450.1|TCPE_ARATH RecName: Full=T-complex protein 1 subunit epsilon; Short=TCP-1-epsilon; AltName: Full=CCT-epsilon gi|9743353|gb|AAF97977.1|AC000103_27 F21J9.17 [Arabidopsis thaliana] gi|19715605|gb|AAL91625.1| At1g24510/F21J9_150 [Arabidopsis thaliana] gi|23463047|gb|AAN33193.1| At1g24510/F21J9_150 [Arabidopsis thaliana] gi|332192420|gb|AEE30541.1| T-complex protein 1 subunit epsilon [Arabidopsis thaliana]	535	535	0	100.0	97.6	99.4	T-complex protein 1 subunit epsilon	gbpln	Arabidopsis thaliana	AT1G24510.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr1:8685504-8688101 REVERSE LENGTH=535	535	535	0	100.0	97.6	99.4
Rsa1.0_00050.1.g2806.t1	emb|CAA48292.1| bgp1 [Brassica rapa] gi|448272|prf||1916399A Bgp1 gene	108	119	3.00E-12	110.2	62.0	70.4	bgp1	gbpln	Brassica rapa	AT1G24520.1 | Symbols: BCP1 | homolog of Brassica campestris pollen protein 1 | chr1:8688699-8689058 FORWARD LENGTH=119	108	119	7.00E-13	110.2	51.9	62.0
Rsa1.0_00050.1.g2807.t1	ref|XP_002893441.1| hypothetical protein ARALYDRAFT_472892 [Arabidopsis lyrata subsp. lyrata] gi|297339283|gb|EFH69700.1| hypothetical protein ARALYDRAFT_472892 [Arabidopsis lyrata subsp. lyrata]	700	679	0	97.0	82.0	88.9	hypothetical protein ARALYDRAFT_472892	gbpln	Arabidopsis lyrata	AT1G24560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G49055.1); Has 71940 Blast hits to 38124 proteins in 2481 species: Archae - 1358; Bacteria - 12126; Metazoa - 32861; Fungi - 6786; Plants - 4024; Viruses - 195; Other Eukaryotes - 14590 (source: NCBI BLink). | chr1:8702644-8705640 FORWARD LENGTH=678	700	678	0	96.9	82.0	88.3

Rsa1.0_00050.1.g2808.t5	ref|XP_002893440.1| hypothetical protein ARALYDRAFT_313424 [Arabidopsis lyrata subsp. lyrata] gi|297339282|gb|EFH69699.1| hypothetical protein ARALYDRAFT_313424 [Arabidopsis lyrata subsp. lyrata]	396	363	0	91.7	77.8	84.1	hypothetical protein ARALYDRAFT_313424	gbpln	Arabidopsis lyrata	AT1G24570.1 | Symbols: | Protein of unknown function (DUF707) | chr1:8707197-8709491 FORWARD LENGTH=381	396	381	0	96.2	79.3	86.6
Rsa1.0_00050.1.g2809.t1	ref|NP_564220.1| uncharacterized protein [Arabidopsis thaliana] gi|21593326|gb|AAM65275.1| unknown [Arabidopsis thaliana] gi|56236092|gb|AAV84502.1| At1g24575 [Arabidopsis thaliana] gi|57222124|gb|AAW38969.1| At1g24575 [Arabidopsis thaliana] gi|88900286|gb|ABD57455.1| At1g24575 [Arabidopsis thaliana] gi|332192428|gb|AEE30549.1| uncharacterized protein AT1G24575 [Arabidopsis thaliana]	78	88	1.00E-11	112.8	48.7	62.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G24575.1 | Symbols: | unknown protein; Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:8711211-8711477 REVERSE LENGTH=88	78	88	2.00E-14	112.8	48.7	62.8
Rsa1.0_00050.1.g2810.t1	ref|XP_002893438.1| hypothetical protein ARALYDRAFT_890209 [Arabidopsis lyrata subsp. lyrata] gi|297339280|gb|EFH69697.1| hypothetical protein ARALYDRAFT_890209 [Arabidopsis lyrata subsp. lyrata]	70	72	3.00E-14	102.9	65.7	77.1	hypothetical protein ARALYDRAFT_890209	gbpln	Arabidopsis lyrata	AT1G24600.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67920.1); Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:8720375-8720593 FORWARD LENGTH=72	70	72	9.00E-15	102.9	61.4	74.3
Rsa1.0_00050.1.g2811.t1	gb|EOA40117.1| hypothetical protein CARUB_v10008819mg, partial [Capsella rubella] gi|482575931|gb|EOA40118.1| hypothetical protein CARUB_v10008819mg, partial [Capsella rubella]	475	532	0	112.0	86.1	93.3	hypothetical protein CARUB_v10008819mg, partial	gbpln	Capsella rubella	AT1G24610.1 | Symbols: | Rubisco methyltransferase family protein | chr1:8720906-8722711 REVERSE LENGTH=476	475	476	0	100.2	87.6	94.3
Rsa1.0_00050.1.g2812.t1	ref|NP_173866.1| putative calcium-binding protein CML25 [Arabidopsis thaliana] gi|75334522|sp|Q9FYK2.1|CML25_ARATH RecName: Full=Probable calcium-binding protein CML25; AltName: Full=Calmodulin-like protein 25 gi|9743349|gb|AAF97973.1|AC000103_23 F21J9.28 [Arabidopsis thaliana] gi|91805849|gb|ABE65653.1| polcalcin [Arabidopsis thaliana] gi|332192433|gb|AEE30554.1| putative calcium-binding protein CML25 [Arabidopsis thaliana]	187	186	6.00E-87	99.5	89.3	90.9	putative calcium-binding protein CML25	gbpln	Arabidopsis thaliana	AT1G24620.1 | Symbols: | EF hand calcium-binding protein family | chr1:8723893-8724453 REVERSE LENGTH=186	187	186	2.00E-89	99.5	89.3	90.9
Rsa1.0_00050.1.g2813.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00050.1.g2814.t1	ref|XP_002890697.1| At1g68060/T23K23_9 [Arabidopsis lyrata subsp. lyrata] gi|297336539|gb|EFH66956.1| At1g68060/T23K23_9 [Arabidopsis lyrata subsp. lyrata]	632	634	0	100.3	91.3	94.9	At1g68060/T23K23_9	gbpln	Arabidopsis lyrata	AT1G24764.1 | Symbols: ATMAP70-2, MAP70-2 | microtubule-associated proteins 70-2 | chr1:8760001-8763256 REVERSE LENGTH=634	632	634	0	100.3	90.3	94.6
Rsa1.0_00050.1.g2815.t1	ref|NP_173893.1| anthranilate synthase beta subunit 1 [Arabidopsis thaliana] gi|11067285|gb|AAG28813.1|AC079374_16 anthranilate synthase beta subunit [Arabidopsis thaliana] gi|403434|gb|AAA32742.1| anthranilate synthase beta subunit [Arabidopsis thaliana] gi|20466736|gb|AAM20685.1| anthranilate synthase beta subunit [Arabidopsis thaliana] gi|30023756|gb|AAP13411.1| At1g25220 [Arabidopsis thaliana] gi|110741096|dbj|BAE98642.1| hypothetical protein [Arabidopsis thaliana] gi|332192468|gb|AEE30589.1| anthranilate synthase beta subunit 1 [Arabidopsis thaliana]	262	276	1.00E-122	105.3	87.0	92.0	anthranilate synthase beta subunit 1	gbpln	Arabidopsis thaliana	AT1G25220.1 | Symbols: ASB1, TRP4, WEI7 | anthranilate synthase beta subunit 1 | chr1:8837430-8839478 REVERSE LENGTH=276	262	276	1.00E-125	105.3	87.0	92.0
Rsa1.0_00050.1.g2816.t1	ref|XP_002893431.1| hypothetical protein ARALYDRAFT_890187 [Arabidopsis lyrata subsp. lyrata] gi|297339273|gb|EFH69690.1| hypothetical protein ARALYDRAFT_890187 [Arabidopsis lyrata subsp. lyrata]	475	376	0	79.2	68.6	73.9	hypothetical protein ARALYDRAFT_890187	gbpln	Arabidopsis lyrata	AT1G25240.1 | Symbols: | ENTH/VHS/GAT family protein | chr1:8845231-8846361 FORWARD LENGTH=376	475	376	0	79.2	67.8	73.7

Rsa1.0_00050.1.g2817.t1	ref|XP_002893430.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339272|gb|EFH69689.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	382	385	1.00E-170	100.8	81.4	88.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G25250.1 | Symbols: AtIDD16, IDD16 | indeterminate(ID)-domain 16 | chr1:8849549-8851520 FORWARD LENGTH=362	382	362	1.00E-156	94.8	73.6	79.8
Rsa1.0_00050.1.g2818.t8	gb|AAD21687.1| Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078 [Arabidopsis thaliana]	241	1415	4.00E-65	587.1	53.5	68.0	Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00050.1.g2819.t1	ref|NP_564226.1| Ribosomal protein L10 family protein [Arabidopsis thaliana] gi|15028333|gb|AAK76643.1| unknown protein [Arabidopsis thaliana] gi|19310645|gb|AAL85053.1| unknown protein [Arabidopsis thaliana] gi|21593993|gb|AAM65913.1| unknown [Arabidopsis thaliana] gi|332192473|gb|AEE30594.1| Ribosomal protein L10 family protein [Arabidopsis thaliana]	287	235	1.00E-106	81.9	67.2	71.4	Ribosomal protein L10 family protein	gbpln	Arabidopsis thaliana	AT1G25260.1 | Symbols: | Ribosomal protein L10 family protein | chr1:8854163-8855766 REVERSE LENGTH=235	287	235	1.00E-109	81.9	67.2	71.4
Rsa1.0_00050.1.g2820.t1	ref|NP_173898.2| putative MtN21 nodulin protein [Arabidopsis thaliana] gi|75339341|sp|Q4PT23.1|WTR6_ARATH RecName: Full=WAT1-related protein At1g25270 gi|67633390|gb|AAY78620.1| nodulin MtN21 family protein [Arabidopsis thaliana] gi|332192474|gb|AEE30595.1| WAT1-related protein [Arabidopsis thaliana]	364	355	1.00E-160	97.5	76.1	87.9	putative MtN21 nodulin protein	gbpln	Arabidopsis thaliana	AT1G25270.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:8857726-8859909 FORWARD LENGTH=355	364	355	1.00E-163	97.5	76.1	87.9
Rsa1.0_00050.1.g2821.t1	gb|EOA40428.1| hypothetical protein CARUB_v10009152mg [Capsella rubella]	442	442	0	100.0	88.7	92.8	hypothetical protein CARUB_v10009152mg	gbpln	Capsella rubella	AT1G25280.1 | Symbols: AtTLP10, TLP10 | tubby like protein 10 | chr1:8864961-8866608 FORWARD LENGTH=445	442	445	0	100.7	87.3	92.3
Rsa1.0_00050.1.g2822.t1	gb|EOA40428.1| hypothetical protein CARUB_v10009152mg [Capsella rubella]	209	442	1.00E-24	211.5	28.2	28.7	hypothetical protein CARUB_v10009152mg	gbpln	Capsella rubella	AT1G25280.3 | Symbols: AtTLP10, TLP10 | tubby like protein 10 | chr1:8865676-8866608 FORWARD LENGTH=267	209	267	2.00E-23	127.8	27.3	27.8
Rsa1.0_00050.1.g2823.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1167	1213	0	103.9	37.0	56.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1167	626	1.00E-60	53.6	11.5	20.4
Rsa1.0_00050.1.g2824.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	647	530	3.00E-39	81.9	12.2	17.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	647	530	2.00E-12	81.9	5.7	11.3
Rsa1.0_00050.1.g2825.t1	gb|EOA39802.1| hypothetical protein CARUB_v10008465mg [Capsella rubella]	700	700	0	100.0	84.7	92.4	hypothetical protein CARUB_v10008465mg	gbpln	Capsella rubella	AT1G25320.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:8877988-8880180 FORWARD LENGTH=702	700	702	0	100.3	85.7	92.3
Rsa1.0_00050.1.g2826.t1	ref|NP_564230.1| myb domain protein 116 [Arabidopsis thaliana] gi|15375295|gb|AAK25748.2|AF334815_1 putative transcription factor MYB116 [Arabidopsis thaliana] gi|41619120|gb|AAS10028.1| MYB transcription factor [Arabidopsis thaliana] gi|91805853|gb|ABE65655.1| myb family transcription factor [Arabidopsis thaliana] gi|332192487|gb|AEE30608.1| myb domain protein 116 [Arabidopsis thaliana]	287	283	1.00E-120	98.6	75.3	84.0	myb domain protein 116	gbpln	Arabidopsis thaliana	AT1G25340.1 | Symbols: MYB116, AtMYB116 | myb domain protein 116 | chr1:8885210-8886271 FORWARD LENGTH=283	287	283	1.00E-122	98.6	75.3	84.0
Rsa1.0_00050.1.g2827.t1	ref|NP_173906.2| putative tRNA-glutamine synthetase [Arabidopsis thaliana] gi|17065036|gb|AAL32672.1| Unknown protein [Arabidopsis thaliana] gi|21387137|gb|AAM47972.1| unknown protein [Arabidopsis thaliana] gi|332192489|gb|AEE30610.1| putative tRNA-glutamine synthetase [Arabidopsis thaliana]	818	795	0	97.2	86.6	91.2	putative tRNA-glutamine synthetase	gbpln	Arabidopsis thaliana	AT1G25350.1 | Symbols: OVA9 | glutamine-tRNA ligase, putative / glutaminyl-tRNA synthetase, putative / GlnRS, putative | chr1:8889280-8894205 REVERSE LENGTH=795	818	795	0	97.2	86.6	91.2
Rsa1.0_00050.1.g2828.t1	pir||F86383 hypothetical protein F4F7.22 - Arabidopsis thaliana	277	767	8.00E-62	276.9	57.8	65.3	hypothetical protein F4F7.22 - Arabidopsis thaliana	----	----	AT1G25370.1 | Symbols: | Protein of unknown function (DUF1639) | chr1:8898046-8898934 REVERSE LENGTH=263	277	263	1.00E-63	94.9	57.8	65.3

Rsa1.0_00050.1.g2829.t1	ref|NP_564232.1| Metallo-beta-lactamase domain-containing protein [Arabidopsis thaliana] gi|51968784|dbj|BAD43084.1| unknown protein [Arabidopsis thaliana] gi|332192493|gb|AEE30614.1| Metallo-beta-lactamase domain-containing protein [Arabidopsis thaliana]	589	524	0	89.0	70.5	76.7	Metallo-beta-lactamase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G25375.1 | Symbols: | Metallo-hydrolase/oxidoreductase superfamily protein | chr1:8900279-8903220 REVERSE LENGTH=524	589	524	0	89.0	70.5	76.7
Rsa1.0_00050.1.g2830.t1	ref|XP_002893428.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297339270|gb|EFH69687.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	360	364	1.00E-171	101.1	87.5	95.3	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT1G25380.1 | Symbols: ATNDT2, NDT2 | NAD+ transporter 2 | chr1:8903726-8905818 FORWARD LENGTH=363	360	363	1.00E-171	100.8	86.1	94.4
Rsa1.0_00050.1.g2831.t1	ref|NP_173910.1| protein kinase-like protein [Arabidopsis thaliana] gi|12321510|gb|AAG50813.1|AC079281_15 wall-associated kinase, putative [Arabidopsis thaliana] gi|332192495|gb|AEE30616.1| protein kinase-like protein [Arabidopsis thaliana]	609	629	0	103.3	77.8	85.4	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G25390.1 | Symbols: | Protein kinase superfamily protein | chr1:8906640-8908800 REVERSE LENGTH=629	609	629	0	103.3	77.8	85.4
Rsa1.0_00050.1.g2832.t1	ref|XP_002887289.1| hypothetical protein ARALYDRAFT_476148 [Arabidopsis lyrata subsp. lyrata] gi|297333130|gb|EFH63548.1| hypothetical protein ARALYDRAFT_476148 [Arabidopsis lyrata subsp. lyrata]	687	801	1.00E-120	116.6	33.2	38.0	hypothetical protein ARALYDRAFT_476148	gbpln	Arabidopsis lyrata	AT1G25390.1 | Symbols: | Protein kinase superfamily protein | chr1:8906640-8908800 REVERSE LENGTH=629	687	629	1.00E-118	91.6	35.7	47.6
Rsa1.0_00050.1.g2833.t1	gb|ABK28015.1| unknown [Arabidopsis thaliana]	84	108	3.00E-21	128.6	60.7	67.9	unknown	gbpln	Arabidopsis thaliana	AT1G25422.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G68500.1); Has 16 Blast hits to 16 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:8919087-8919410 FORWARD LENGTH=107	84	107	5.00E-24	127.4	60.7	67.9
Rsa1.0_00050.1.g2834.t1	gb|ABK28016.1| unknown [Arabidopsis thaliana]	96	97	3.00E-31	101.0	77.1	88.5	unknown	gbpln	Arabidopsis thaliana	AT1G25425.1 | Symbols: CLE43 | CLAVATA3/ESR-RELATED 43 | chr1:8922832-8923122 FORWARD LENGTH=96	96	96	6.00E-34	100.0	77.1	88.5
Rsa1.0_00050.1.g2835.t1	ref|NP_173915.2| zinc finger protein CONSTANS-LIKE 16 [Arabidopsis thaliana] gi|52782786|sp|Q8RWD0.2|COL16_ARATH RecName: Full=Zinc finger protein CONSTANS-LIKE 16 gi|53749166|gb|AAU90068.1| At1g25440 [Arabidopsis thaliana] gi|110740969|dbj|BAE98579.1| hypothetical protein [Arabidopsis thaliana] gi|332192504|gb|AEE30625.1| zinc finger protein CONSTANS-LIKE 16 [Arabidopsis thaliana]	414	417	1.00E-179	100.7	82.4	89.1	zinc finger protein CONSTANS-LIKE 16	gbpln	Arabidopsis thaliana	AT1G25440.1 | Symbols: | B-box type zinc finger protein with CCT domain | chr1:8933939-8935284 REVERSE LENGTH=417	414	417	0	100.7	82.4	89.1
Rsa1.0_00051.1.g2836.t1	ref|NP_197839.1| large subunit ribosomal protein LP1 [Arabidopsis thaliana] gi|10177851|dbj|BAB11203.1| 60s acidic ribosomal protein P1 [Arabidopsis thaliana] gi|67633816|gb|AAY78832.1| putative 60S acidic ribosomal protein P1 [Arabidopsis thaliana] gi|332005935|gb|AED93318.1| 60S acidic ribosomal protein family [Arabidopsis thaliana]	111	111	5.00E-38	100.0	72.1	82.0	large subunit ribosomal protein LP1	gbpln	Arabidopsis thaliana	AT5G24510.1 | Symbols: | 60S acidic ribosomal protein family | chr5:8369295-8369866 REVERSE LENGTH=111	111	111	8.00E-41	100.0	72.1	82.0
Rsa1.0_00051.1.g2837.t1	ref|NP_001154738.1| DNA-binding protein BIN4 [Arabidopsis thaliana] gi|332005958|gb|AED93341.1| DNA-binding protein BIN4 [Arabidopsis thaliana]	419	446	1.00E-107	106.4	62.3	71.8	DNA-binding protein BIN4	gbpln	Arabidopsis thaliana	AT5G24630.5 | Symbols: BIN4 | double-stranded DNA binding | chr5:8432523-8435682 REVERSE LENGTH=446	419	446	1.00E-109	106.4	62.3	71.8

Rsa1.0_00051.1.g2838.t1	ref|NP_193753.1| terpene cyclase, C1 domain-containing protein [Arabidopsis thaliana] gi|317412200|sp|O65434.2|TPS07_ARATH RecName: Full=Putative terpenoid synthase 7; Short=AtTPS07 gi|332658884|gb|AEE84284.1| putative terpenoid synthase 7 [Arabidopsis thaliana]	559	604	1.00E-179	108.1	57.2	72.3	terpene cyclase, C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G20200.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr4:10908672-10911151 REVERSE LENGTH=604	559	604	0	108.1	57.2	72.3
Rsa1.0_00051.1.g2839.t1	ref|XP_002874216.1| hypothetical protein ARALYDRAFT_910514 [Arabidopsis lyrata subsp. lyrata] gi|297320053|gb|EFH50475.1| hypothetical protein ARALYDRAFT_910514 [Arabidopsis lyrata subsp. lyrata]	535	520	0	97.2	83.0	89.2	hypothetical protein ARALYDRAFT_910514	gbpln	Arabidopsis lyrata	AT5G24690.1 | Symbols: | Protein of unknown function (DUF3411) | chr5:8455783-8458513 REVERSE LENGTH=521	535	521	0	97.4	82.8	88.8
Rsa1.0_00051.1.g2840.t3	ref|XP_002874217.1| hypothetical protein ARALYDRAFT_489332 [Arabidopsis lyrata subsp. lyrata] gi|297320054|gb|EFH50476.1| hypothetical protein ARALYDRAFT_489332 [Arabidopsis lyrata subsp. lyrata]	1419	1376	0	97.0	84.9	88.9	hypothetical protein ARALYDRAFT_489332	gbpln	Arabidopsis lyrata	AT5G24710.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:8459148-8467920 REVERSE LENGTH=1377	1419	1377	0	97.0	84.6	88.7
Rsa1.0_00051.1.g2841.t2	sp|Q84KJ5.2|CRYD_ARATH RecName: Full=Cryptochrome DASH, chloroplastic/mitochondrial; AltName: Full=Cryptochrome-3; Flags: Precursor	128	569	2.00E-47	444.5	75.0	78.9	RecName: Full=Cryptochrome DASH, chloroplastic/mitochondrial; AltName: Full=Cryptochrome-3; Flags: Precursor	----	----	AT5G24850.1 | Symbols: CRY3 | cryptochrome 3 | chr5:8535399-8538016 REVERSE LENGTH=526	128	526	4.00E-50	410.9	75.0	78.9
Rsa1.0_00051.1.g2842.t1	gb|EOA23031.1| hypothetical protein CARUB_v10003797mg [Capsella rubella]	108	108	7.00E-51	100.0	90.7	95.4	hypothetical protein CARUB_v10003797mg	gbpln	Capsella rubella	AT5G24860.1 | Symbols: FPF1, ATFPF1 | flowering promoting factor 1 | chr5:8541822-8542154 FORWARD LENGTH=110	108	110	1.00E-51	101.9	89.8	94.4
Rsa1.0_00051.1.g2843.t1	gb|EOA21407.1| hypothetical protein CARUB_v10001780mg [Capsella rubella]	206	255	2.00E-65	123.8	77.7	85.4	hypothetical protein CARUB_v10001780mg	gbpln	Capsella rubella	AT5G24890.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24550.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8558357-8559172 REVERSE LENGTH=240	206	240	7.00E-67	116.5	76.2	84.0
Rsa1.0_00051.1.g2844.t1	ref|XP_002872134.1| hypothetical protein ARALYDRAFT_489353 [Arabidopsis lyrata subsp. lyrata] gi|297317971|gb|EFH48393.1| hypothetical protein ARALYDRAFT_489353 [Arabidopsis lyrata subsp. lyrata]	348	360	1.00E-165	103.4	89.7	94.3	hypothetical protein ARALYDRAFT_489353	gbpln	Arabidopsis lyrata	AT5G24930.1 | Symbols: ATCOL4, COL4 | CONSTANS-like 4 | chr5:8589325-8590949 FORWARD LENGTH=406	348	406	1.00E-165	116.7	89.7	94.5
Rsa1.0_00051.1.g2845.t1	ref|XP_002874237.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297320074|gb|EFH50496.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	947	948	0	100.1	87.8	93.9	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT5G25060.1 | Symbols: | RNA recognition motif (RRM)-containing protein | chr5:8634219-8639984 REVERSE LENGTH=946	947	946	0	99.9	87.9	93.8
Rsa1.0_00051.1.g2846.t1	ref|NP_197890.1| Sas10/Utp3/C1D family protein [Arabidopsis thaliana] gi|14190385|gb|AAK55673.1|AF378870_1 AT5g25080/T11H3_90 [Arabidopsis thaliana] gi|15215877|gb|AAK91482.1| AT5g25080/T11H3_90 [Arabidopsis thaliana] gi|21593008|gb|AAM64957.1| unknown [Arabidopsis thaliana] gi|332006014|gb|AED93397.1| Sas10/Utp3/C1D family protein [Arabidopsis thaliana]	181	217	5.00E-72	119.9	71.8	83.4	Sas10/Utp3/C1D family protein	gbpln	Arabidopsis thaliana	AT5G25080.1 | Symbols: | Sas10/Utp3/C1D family | chr5:8643782-8646306 FORWARD LENGTH=217	181	217	2.00E-74	119.9	71.8	83.4
Rsa1.0_00051.1.g2847.t1	gb|EOA21643.1| hypothetical protein CARUB_v10002061mg [Capsella rubella]	187	184	3.00E-68	98.4	76.5	81.8	hypothetical protein CARUB_v10002061mg	gbpln	Capsella rubella	AT5G25090.1 | Symbols: ENODL13, AtENODL13 | early nodulin-like protein 13 | chr5:8647117-8647755 REVERSE LENGTH=186	187	186	1.00E-62	99.5	74.3	82.9
Rsa1.0_00051.1.g2848.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00051.1.g2849.t1	ref|XP_002872140.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata] gi|297317977|gb|EFH48399.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata]	468	496	0	106.0	77.4	87.8	CYP71B11	gbpln	Arabidopsis lyrata	AT5G25140.1 | Symbols: CYP71B13 | cytochrome P450, family 71, subfamily B, polypeptide 13 | chr5:8672989-8674557 FORWARD LENGTH=496	468	496	0	106.0	77.8	87.6

Rsa1.0_00051.1.g2850.t1	gb|EOA19571.1| hypothetical protein CARUB_v10002639mg [Capsella rubella]	674	668	0	99.1	92.0	95.3	hypothetical protein CARUB_v10002639mg	gbpln	Capsella rubella	AT5G25150.1 | Symbols: TAF5 | TBP–associated factor 5 | chr5:8677117–8682058 FORWARD LENGTH=669	674	669	0	99.3	91.4	95.0
Rsa1.0_00051.1.g2851.t1	ref|XP_002872142.1| hypothetical protein ARALYDRAFT_910560 [Arabidopsis lyrata subsp. lyrata] gi|297317979|gb|EFH48401.1| hypothetical protein ARALYDRAFT_910560 [Arabidopsis lyrata subsp. lyrata]	247	232	6.00E–91	93.9	69.6	78.9	hypothetical protein ARALYDRAFT_910560	gbpln	Arabidopsis lyrata	AT5G25160.1 | Symbols: ZFP3 | zinc finger protein 3 | chr5:8687524–8688231 FORWARD LENGTH=235	247	235	7.00E–88	95.1	69.2	78.9
Rsa1.0_00051.1.g2852.t1	ref|XP_002874244.1| hypothetical protein ARALYDRAFT_489371 [Arabidopsis lyrata subsp. lyrata] gi|297320081|gb|EFH50503.1| hypothetical protein ARALYDRAFT_489371 [Arabidopsis lyrata subsp. lyrata]	180	183	2.00E–70	101.7	81.7	87.2	hypothetical protein ARALYDRAFT_489371	gbpln	Arabidopsis lyrata	AT5G25190.1 | Symbols: | Integrase–type DNA–binding superfamily protein | chr5:8707007–8707655 REVERSE LENGTH=181	180	181	2.00E–71	100.6	77.2	82.8
Rsa1.0_00051.1.g2853.t1	ref|NP_197906.1| uncharacterized protein [Arabidopsis thaliana] gi|26450052|dbj|BAC42146.1| unknown protein [Arabidopsis thaliana] gi|28827680|gb|AAO50684.1| unknown protein [Arabidopsis thaliana] gi|332006033|gb|AED93416.1| uncharacterized protein AT5G25240 [Arabidopsis thaliana]	124	131	3.00E–44	105.6	77.4	87.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G25240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae – 0; Bacteria – 0; Metazoa – 736; Fungi – 347; Plants – 385; Viruses – 0; Other Eukaryotes – 339 (source: NCBI BLink). | chr5:8746779–8747174 REVERSE LENGTH=131	124	131	5.00E–47	105.6	77.4	87.1
Rsa1.0_00051.1.g2854.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00051.1.g2855.t1	ref|XP_002874247.1| hypothetical protein ARALYDRAFT_910571 [Arabidopsis lyrata subsp. lyrata] gi|297320084|gb|EFH50506.1| hypothetical protein ARALYDRAFT_910571 [Arabidopsis lyrata subsp. lyrata]	357	367	0	102.8	89.4	95.0	hypothetical protein ARALYDRAFT_910571	gbpln	Arabidopsis lyrata	AT5G25265.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, membrane; EXPRESSED IN: cultured cell, leaf; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25260.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae – 12; Bacteria – 1396; Metazoa – 17338; Fungi – 3422; Plants – 5037; Viruses – 0; Other Eukaryotes – 2996 (source: NCBI BLink). | chr5:8754794–8756855 REVERSE LENGTH=366	357	366	0	102.5	89.4	94.4
Rsa1.0_00051.1.g2856.t1	ref|NP_566112.1| uncharacterized protein [Arabidopsis thaliana] gi|75100577|sp|O82251.1|TI202_ARATH RecName: Full=Protein TIC 20–II, chloroplastic; AltName: Full=Translocon at the inner envelope membrane of chloroplasts 20–II; Short=AtTIC20–II; Flags: Precursor gi|3738296|gb|AAC63638.1| expressed protein [Arabidopsis thaliana] gi|330255801|gb|AEC10895.1| protein TIC 20–II [Arabidopsis thaliana]	206	208	3.00E–96	101.0	89.3	93.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G47840.1 | Symbols: | Uncharacterised conserved protein ycf60 | chr2:19594331–19594957 REVERSE LENGTH=208	206	208	1.00E–98	101.0	89.3	93.2
Rsa1.0_00051.1.g2857.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00051.1.g2858.t1	gb|ABL97972.1| serine–rich protein [Brassica rapa]	200	193	1.00E–78	96.5	85.0	88.5	serine–rich protein	gbpln	Brassica rapa	AT5G25280.2 | Symbols: | serine–rich protein–related | chr5:8773882–8774544 FORWARD LENGTH=220	200	220	1.00E–69	110.0	66.0	70.5
Rsa1.0_00051.1.g2859.t2	ref|NP_197917.1| EIN3–binding F–box protein 2 [Arabidopsis thaliana] gi|75325708|sp|Q708Y0.1|EBF2_ARATH RecName: Full=EIN3–binding F–box protein 2 gi|38705081|gb|AAR27072.1| EIN3–binding F–box protein 2 [Arabidopsis thaliana] gi|40641627|emb|CAE75865.1| F–box protein [Arabidopsis thaliana] gi|110735710|dbj|BAE99835.1| leucine–rich repeats containing protein [Arabidopsis thaliana] gi|332006046|gb|AED93429.1| EIN3–binding F–box protein 2 [Arabidopsis thaliana]	600	623	0	103.8	86.8	93.5	EIN3–binding F–box protein 2	gbpln	Arabidopsis thaliana	AT5G25350.1 | Symbols: EBF2 | EIN3–binding F box protein 2 | chr5:8794842–8796882 REVERSE LENGTH=623	600	623	0	103.8	86.8	93.5

Rsa1.0_00051.1.g2860.t1	ref|XP_002874256.1| hypothetical protein ARALYDRAFT_326806 [Arabidopsis lyrata subsp. lyrata] gi|297320093|gb|EFH50515.1| hypothetical protein ARALYDRAFT_326806 [Arabidopsis lyrata subsp. lyrata]	185	189	1.00E-82	102.2	83.8	88.6	hypothetical protein ARALYDRAFT_326806	gbpln	Arabidopsis lyrata	AT5G25390.2 | Symbols: SHN2 | Integrase-type DNA-binding superfamily protein | chr5:8820637-8821741 FORWARD LENGTH=189	185	189	1.00E-84	102.2	82.7	88.6
Rsa1.0_00051.1.g2861.t1	ref|XP_002869301.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315137|gb|EFH45560.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	418	677	1.00E-154	162.0	67.9	79.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G31980.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF247, plant (InterPro:IPR004158), Protein of unknown function DUF862, eukaryotic (InterPro:IPR008580); BEST Arabidopsis thaliana protein match is: Plant protein of unknown function (DUF247) (TAIR:AT5G11290.1); Has 1967 Blast hits to 1844 proteins in 183 species: Archae - 0; Bacteria - 6; Metazoa - 223; Fungi - 83; Plants - 1477; Viruses - 0; Other Eukaryotes - 178 (source: NCBI BLink). | chr4:15464905-15469204 FORWARD LENGTH=680	418	680	1.00E-153	162.7	67.5	78.0
Rsa1.0_00051.1.g2862.t1	ref|XP_002869301.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315137|gb|EFH45560.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	421	677	1.00E-161	160.8	67.9	80.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G31980.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF247, plant (InterPro:IPR004158), Protein of unknown function DUF862, eukaryotic (InterPro:IPR008580); BEST Arabidopsis thaliana protein match is: Plant protein of unknown function (DUF247) (TAIR:AT5G11290.1); Has 1967 Blast hits to 1844 proteins in 183 species: Archae - 0; Bacteria - 6; Metazoa - 223; Fungi - 83; Plants - 1477; Viruses - 0; Other Eukaryotes - 178 (source: NCBI BLink). | chr4:15464905-15469204 FORWARD LENGTH=680	421	680	1.00E-157	161.5	66.3	79.6
Rsa1.0_00051.1.g2863.t1	ref|XP_002874258.1| CYCA2_1 [Arabidopsis lyrata subsp. lyrata] gi|297320095|gb|EFH50517.1| CYCA2_1 [Arabidopsis lyrata subsp. lyrata]	104	433	4.00E-16	416.3	55.8	65.4	CYCA2_1	gbpln	Arabidopsis lyrata	AT5G25380.1 | Symbols: CYCA2;1 | cyclin a2;1 | chr5:8815230-8817566 FORWARD LENGTH=437	104	437	8.00E-18	420.2	53.8	64.4
Rsa1.0_00051.1.g2864.t1	gb|EOA18383.1| hypothetical protein CARUB_v10006919mg [Capsella rubella]	437	660	1.00E-141	151.0	57.7	67.0	hypothetical protein CARUB_v10006919mg	gbpln	Capsella rubella	AT4G31980.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF247, plant (InterPro:IPR004158), Protein of unknown function DUF862, eukaryotic (InterPro:IPR008580); BEST Arabidopsis thaliana protein match is: Plant protein of unknown function (DUF247) (TAIR:AT5G11290.1); Has 1967 Blast hits to 1844 proteins in 183 species: Archae - 0; Bacteria - 6; Metazoa - 223; Fungi - 83; Plants - 1477; Viruses - 0; Other Eukaryotes - 178 (source: NCBI BLink). | chr4:15464905-15469204 FORWARD LENGTH=680	437	680	1.00E-138	155.6	56.1	65.4
Rsa1.0_00051.1.g2865.t10	ref|XP_002874259.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320096|gb|EFH50518.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1459	547	0	37.5	32.1	34.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G65550.1 | Symbols: | Xanthine/uracil permease family protein | chr1:24367694-24370800 REVERSE LENGTH=541	1459	541	0	37.1	31.3	33.2
Rsa1.0_00051.1.g2866.t1	gb|EOA13406.1| hypothetical protein CARUB_v10026444mg, partial [Capsella rubella]	411	430	1.00E-108	104.6	58.2	68.6	hypothetical protein CARUB_v10026444mg, partial	gbpln	Capsella rubella	AT5G62510.1 | Symbols: | F-box family protein | chr5:25095373-25096635 REVERSE LENGTH=420	411	420	1.00E-100	102.2	53.8	64.5
Rsa1.0_00051.1.g2867.t1	ref|XP_002874263.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320100|gb|EFH50522.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	258	280	9.00E-70	108.5	59.3	71.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G25475.4 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:8867920-8869492 REVERSE LENGTH=324	258	324	6.00E-71	125.6	58.1	74.0
Rsa1.0_00051.1.g2868.t1	ref|XP_002874266.1| hypothetical protein ARALYDRAFT_489409 [Arabidopsis lyrata subsp. lyrata] gi|297320103|gb|EFH50525.1| hypothetical protein ARALYDRAFT_489409 [Arabidopsis lyrata subsp. lyrata]	492	499	0	101.4	85.4	92.7	hypothetical protein ARALYDRAFT_489409	gbpln	Arabidopsis lyrata	AT5G25510.1 | Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr5:8882728-8884325 REVERSE LENGTH=500	492	500	0	101.6	86.6	93.9
Rsa1.0_00051.1.g2869.t1	gb|EOA20666.1| hypothetical protein CARUB_v10000978mg, partial [Capsella rubella]	439	439	0	100.0	83.6	88.4	hypothetical protein CARUB_v10000978mg, partial	gbpln	Capsella rubella	AT5G25620.2 | Symbols: YUC6 | Flavin-binding monooxygenase family protein | chr5:8935312-8938200 REVERSE LENGTH=426	439	426	0	97.0	83.4	86.6

Rsa1.0_00051.1.g2870.t1	gb|EOA19383.1| hypothetical protein CARUB_v10000581mg [Capsella rubella]	571	571	0	100.0	87.2	92.5	hypothetical protein CARUB_v10000581mg	gbpln	Capsella rubella	AT5G25630.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:8947426-8949424 FORWARD LENGTH=574	571	574	0	100.5	85.8	92.1
Rsa1.0_00051.1.g2871.t1	ref|XP_002874282.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320119|gb|EFH50541.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	925	402	0	43.5	33.3	36.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G25770.3 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:8969308-8971806 REVERSE LENGTH=421	925	421	0	45.5	32.5	36.3
Rsa1.0_00052.1.g2872.t13	gb|EOA30455.1| hypothetical protein CARUB_v10013580mg [Capsella rubella]	770	481	0	62.5	50.8	53.8	hypothetical protein CARUB_v10013580mg	gbpln	Capsella rubella	AT3G22810.1 | Symbols: | Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region | chr3:8068595-8071559 FORWARD LENGTH=472	770	472	0	61.3	49.1	52.5
Rsa1.0_00052.1.g2873.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00052.1.g2874.t1	ref|XP_002885525.1| hypothetical protein ARALYDRAFT_479793 [Arabidopsis lyrata subsp. lyrata] gi|297331365|gb|EFH61784.1| hypothetical protein ARALYDRAFT_479793 [Arabidopsis lyrata subsp. lyrata]	117	108	2.00E-32	92.3	60.7	70.1	hypothetical protein ARALYDRAFT_479793	gbpln	Arabidopsis lyrata	AT3G22820.1 | Symbols: | allergen-related | chr3:8073451-8074061 REVERSE LENGTH=107	117	107	3.00E-32	91.5	63.2	71.8
Rsa1.0_00052.1.g2875.t1	gb|AAF97279.1|AC010164_1 Hypothetical protein [Arabidopsis thaliana]	117	352	7.00E-13	300.9	34.2	52.1	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00052.1.g2876.t4	gb|AAF06087.1|AC007918_11 Similar to gi|4325351 T25H8.2 TNP2 protein homolog from Arabidopsis thaliana BAC gb|AF128394 [Arabidopsis thaliana]	307	1121	3.00E-45	365.1	42.0	58.0	Similar to gi|4325351 T25H8.2 TNP2 protein homolog from Arabidopsis thaliana BAC gb|AF128394	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00052.1.g2877.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	412	414	1.00E-104	100.5	58.0	64.3	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00052.1.g2878.t1	gb|EOA30671.1| hypothetical protein CARUB_v10013808mg [Capsella rubella]	398	417	1.00E-163	104.8	76.6	86.7	hypothetical protein CARUB_v10013808mg	gbpln	Capsella rubella	AT3G22830.1 | Symbols: AT-HSFA6B, HSFA6B | heat shock transcription factor A6B | chr3:8078981-8080895 FORWARD LENGTH=406	398	406	1.00E-164	102.0	78.1	86.4
Rsa1.0_00052.1.g2879.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00052.1.g2880.t1	gb|AAR11456.1| ELIP [Brassica rapa subsp. pekinensis]	196	194	3.00E-94	99.0	96.4	96.9	ELIP	gbpln	Brassica rapa	AT3G22840.1 | Symbols: ELIP1, ELIP | Chlorophyll A-B binding family protein | chr3:8084628-8085445 REVERSE LENGTH=195	196	195	5.00E-84	99.5	88.3	90.8
Rsa1.0_00052.1.g2881.t1	gb|EOA26720.1| hypothetical protein CARUB_v10022808mg [Capsella rubella]	71	645	9.00E-15	908.5	64.8	73.2	hypothetical protein CARUB_v10022808mg	gbpln	Capsella rubella	AT2G35610.1 | Symbols: XEG113 | xyloglucanase 113 | chr2:14947617-14951106 REVERSE LENGTH=644	71	644	4.00E-16	907.0	66.2	73.2
Rsa1.0_00052.1.g2882.t1	ref|NP_188924.3| emp24/gp25L/p24 family/GOLD domain-containing protein [Arabidopsis thaliana] gi|75273406|sp|Q9LIL4.1|P24B3_ARATH RecName: Full=Transmembrane emp24 domain-containing protein p24beta3; AltName: Full=p24 family protein beta2; Short=p24beta2; AltName: Full=p24 family protein beta3; Short=p24beta3; Flags: Precursor gi|11994713|dbj|BAB03029.1| coated vesicle membrane protein-like [Arabidopsis thaliana] gi|17979492|gb|AAL50082.1| AT3g22845/MWI23_22 [Arabidopsis thaliana] gi|20147305|gb|AAM10366.1| AT3g22845/MWI23_22 [Arabidopsis thaliana] gi|332643162|gb|AEE76683.1| emp24/gp25L/p24 family/GOLD domain-containing protein [Arabidopsis thaliana]	218	214	1.00E-114	98.2	91.3	95.9	emp24/gp25L/p24 family/GOLD domain-containing protein	gbpln	Arabidopsis thaliana	AT3G22845.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr3:8087373-8088550 FORWARD LENGTH=214	218	214	1.00E-116	98.2	91.3	95.9
Rsa1.0_00052.1.g2883.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00052.1.g2884.t1	gb|EOA32024.1| hypothetical protein CARUB_v10015267mg [Capsella rubella]	402	729	6.00E-62	181.3	41.3	55.0	hypothetical protein CARUB_v10015267mg	gbpln	Capsella rubella	AT3G14950.1 | Symbols: TTL2 | tetratricopetide-repeat thioredoxin-like 2 | chr3:5030216-5032892 REVERSE LENGTH=721	402	721	1.00E-63	179.4	39.8	53.0
Rsa1.0_00052.1.g2885.t1	ref|XP_002883384.1| RNA polymerase Rpb7 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329224|gb|EFH59643.1| RNA polymerase Rpb7 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	175	174	8.00E-65	99.4	68.6	82.9	RNA polymerase Rpb7 N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT3G22900.1 | Symbols: NRPD7 | RNA polymerase Rpb7-like, N-terminal domain | chr3:8115645-8116169 FORWARD LENGTH=174	175	174	9.00E-67	99.4	68.6	82.9

Rsa1.0_00052.1.g2886.t1	ref|XP_002885529.1| hypothetical protein ARALYDRAFT_898774 [Arabidopsis lyrata subsp. lyrata] gi|297331369|gb|EFH61788.1| hypothetical protein ARALYDRAFT_898774 [Arabidopsis lyrata subsp. lyrata]	1021	1022	0	100.1	91.7	95.6	hypothetical protein ARALYDRAFT_898774	gbpln	Arabidopsis lyrata	AT3G22910.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr3:8116335-8119388 REVERSE LENGTH=1017	1021	1017	0	99.6	90.7	94.5
Rsa1.0_00052.1.g2887.t1	ref|NP_188933.1| calmodulin-like protein 11 [Arabidopsis thaliana] gi|75335042|sp|Q9LIK5.1|CML11_ARATH RecName: Full=Calmodulin-like protein 11 gi|16226344|gb|AAL16141.1|AF428309_1 AT3g22930/F5N5_10 [Arabidopsis thaliana] gi|11994722|dbj|BAB03038.1| unnamed protein product [Arabidopsis thaliana] gi|21436047|gb|AAM51601.1| AT3g22930/F5N5_10 [Arabidopsis thaliana] gi|332643171|gb|AEE76692.1| calmodulin-like protein 11 [Arabidopsis thaliana]	205	173	4.00E-75	84.4	68.3	70.2	calmodulin-like protein 11	gbpln	Arabidopsis thaliana	AT3G22930.1 | Symbols: CML11 | calmodulin-like 11 | chr3:8124286-8125835 REVERSE LENGTH=173	205	173	1.00E-77	84.4	68.3	70.2
Rsa1.0_00052.1.g2888.t1	ref|NP_191135.1| uncharacterized protein [Arabidopsis thaliana] gi|30694316|ref|NP_850708.1| uncharacterized protein [Arabidopsis thaliana] gi|334186001|ref|NP_001190098.1| uncharacterized protein [Arabidopsis thaliana] gi|58652076|gb|AAW80863.1| At3g55760 [Arabidopsis thaliana] gi|332645910|gb|AEE79431.1| uncharacterized protein AT3G55760 [Arabidopsis thaliana] gi|332645911|gb|AEE79432.1| uncharacterized protein AT3G55760 [Arabidopsis thaliana] gi|332645912|gb|AEE79433.1| uncharacterized protein AT3G55760 [Arabidopsis thaliana]	566	578	0	102.1	82.9	89.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G55760.3 | Symbols: | unknown protein; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G42430.2). | chr3:20700648-20702886 FORWARD LENGTH=578	566	578	0	102.1	82.9	89.6
Rsa1.0_00052.1.g2889.t1	ref|NP_850746.1| G-protein gamma subunit 2 [Arabidopsis thaliana] gi|75163105|sp|Q93V47.1|GG2_ARATH RecName: Full=Guanine nucleotide-binding protein subunit gamma 2; AltName: Full=Ggamma-subunit 2; AltName: Full=Heterotrimeric G protein gamma-subunit 2; Short=AtAGG2; Flags: Precursor gi|14625852|gb|AAK71536.1|AF347077_1 heterotrimeric G-protein gamma subunit 2 [Arabidopsis thaliana] gi|14625854|gb|AAK71537.1|AF347078_1 heterotrimeric G-protein gamma subunit 2 [Arabidopsis thaliana] gi|88900340|gb|ABD57482.1| At3g22942 [Arabidopsis thaliana] gi|110736567|dbj|BAF00249.1| hypothetical protein [Arabidopsis thaliana] gi|332643173|gb|AEE76694.1| G-protein gamma subunit 2 [Arabidopsis thaliana]	143	100	6.00E-35	69.9	59.4	61.5	G-protein gamma subunit 2	gbpln	Arabidopsis thaliana	AT3G22942.1 | Symbols: AGG2 | G-protein gamma subunit 2 | chr3:8134475-8135667 FORWARD LENGTH=100	143	100	2.00E-37	69.9	59.4	61.5
Rsa1.0_00052.1.g2890.t1	ref|NP_566720.1| Pyruvate kinase family protein [Arabidopsis thaliana] gi|75311203|sp|Q9LIK0.1|PKP1_ARATH RecName: Full=Plastidial pyruvate kinase 1, chloroplastic; Short=PK1; Short=PKp1; AltName: Full=Pyruvate kinase II; AltName: Full=Pyruvate kinase isozyme A; Short=PKP-ALPHA; Flags: Precursor gi|11994727|dbj|BAB03043.1| pyruvate kinase [Arabidopsis thaliana] gi|15983775|gb|AAL10484.1| AT3g22960/F5N5_15 [Arabidopsis thaliana] gi|16604372|gb|AAL24192.1| AT3g22960/F5N5_15 [Arabidopsis thaliana] gi|26983820|gb|AAN86162.1| putative pyruvate kinase [Arabidopsis thaliana] gi|332643176|gb|AEE76697.1| Pyruvate kinase family protein [Arabidopsis thaliana]	606	596	0	98.3	85.1	89.3	Pyruvate kinase family protein	gbpln	Arabidopsis thaliana	AT3G22960.1 | Symbols: PKP1, PKP-ALPHA | Pyruvate kinase family protein | chr3:8139369-8141771 FORWARD LENGTH=596	606	596	0	98.3	85.1	89.3

Rsa1.0_00052.1.g2891.t1	gb|EOA20393.1| hypothetical protein CARUB_v10000704mg [Capsella rubella]	517	525	0	101.5	74.3	84.7	hypothetical protein CARUB_v10000704mg	gbpln	Capsella rubella	AT5G22110.1 | Symbols: ATDPB2, CYL2, DPB2 | DNA polymerase epsilon subunit B2 | chr5:7331071-7334178 REVERSE LENGTH=526	517	526	0	101.7	73.3	83.2
Rsa1.0_00052.1.g2892.t1	ref|NP_001118679.1| uncharacterized protein [Arabidopsis thaliana] gi|11994728|dbj|BAB03044.1| unnamed protein product [Arabidopsis thaliana] gi|332643177|gb|AEE76698.1| uncharacterized protein AT3G22961 [Arabidopsis thaliana]	285	223	8.00E-28	78.2	31.9	44.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G22961.1 | Symbols: | Paired amphipathic helix (PAH2) superfamily protein | chr3:8142138-8142809 FORWARD LENGTH=223	285	223	2.00E-30	78.2	31.9	44.9
Rsa1.0_00052.1.g2893.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00052.1.g2894.t1	ref|NP_188940.1| CBL-interacting serine/threonine-protein kinase 7 [Arabidopsis thaliana] gi|75338665|sp|Q9XIW0.1|CIPK7_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 7; AltName: Full=SNF1-related kinase 3.10; AltName: Full=SOS2-like protein kinase PKS7; AltName: Full=Serine/threonine-protein kinase SR2; Short=AtSR2; Short=AtSRPK1 gi|13249113|gb|AAK16682.1|AF290192_1 CBL-interacting protein kinase 7 [Arabidopsis thaliana] gi|13448039|gb|AAK26846.1|AF339148_1 SOS2-like protein kinase PKS7 [Arabidopsis thaliana] gi|5478791|dbj|BAA77716.2| SNF1 related protein kinase [Arabidopsis thaliana] gi|9294189|dbj|BAB02091.1| SNF1 related protein kinase [Arabidopsis thaliana] gi|57222172|gb|AAW38993.1| At3g23000 [Arabidopsis thaliana] gi|114213519|gb|ABI54342.1| At3g23000 [Arabidopsis thaliana] gi|332643183|gb|AEE76704.1| CBL-interacting serine/threonine-protein kinase 7 [Arabidopsis thaliana]	413	429	0	103.9	82.6	90.3	CBL-interacting serine/threonine-protein kinase 7	gbpln	Arabidopsis thaliana	AT3G23000.1 | Symbols: CIPK7, SnRK3.10, PKS7, ATSRPK1, ATSR2 | CBL-interacting protein kinase 7 | chr3:8172654-8173943 FORWARD LENGTH=429	413	429	0	103.9	82.6	90.3
Rsa1.0_00052.1.g2895.t1	emb|CCD74510.1| unknown, partial [Arabidopsis halleri subsp. halleri]	172	300	3.00E-27	174.4	35.5	52.9	unknown, partial	gbpln	Arabidopsis halleri	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	172	575	6.00E-12	334.3	26.2	45.9
Rsa1.0_00052.1.g2896.t1	ref|XP_002885542.1| indoleacetic acid-induced protein 2 [Arabidopsis lyrata subsp. lyrata] gi|297331382|gb|EFH61801.1| indoleacetic acid-induced protein 2 [Arabidopsis lyrata subsp. lyrata]	172	174	2.00E-79	101.2	89.0	91.9	indoleacetic acid-induced protein 2	gbpln	Arabidopsis lyrata	AT3G23030.1 | Symbols: IAA2 | indole-3-acetic acid inducible 2 | chr3:8181069-8181685 REVERSE LENGTH=174	172	174	2.00E-81	101.2	87.2	91.9
Rsa1.0_00053.1.g2897.t1	ref|XP_002886390.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata] gi|297332231|gb|EFH62649.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata]	262	298	6.00E-90	113.7	61.8	79.0	hypothetical protein ARALYDRAFT_893070	gbpln	Arabidopsis lyrata	AT2G42470.1 | Symbols: | TRAF-like family protein | chr2:17679887-17685187 REVERSE LENGTH=898	262	898	2.00E-73	342.7	53.1	73.3
Rsa1.0_00053.1.g2898.t1	ref|NP_198882.1| ATP synthase mitochondrial F1 complex assembly factor 2 [Arabidopsis thaliana] gi|14517426|gb|AAK62603.1| AT5g40660/MNF13_180 [Arabidopsis thaliana] gi|22655442|gb|AAM98313.1| At5g40660/MNF13_180 [Arabidopsis thaliana] gi|332007196|gb|AED94579.1| ATP12 protein-related [Arabidopsis thaliana]	114	325	1.00E-35	285.1	71.1	75.4	ATP synthase mitochondrial F1 complex assembly factor 2	gbpln	Arabidopsis thaliana	AT5G40660.1 | Symbols: | ATP12 protein-related | chr5:16283650-16285161 REVERSE LENGTH=325	114	325	2.00E-38	285.1	71.1	75.4
Rsa1.0_00053.1.g2899.t1	gb|EOA35049.1| hypothetical protein CARUB_v10020154mg [Capsella rubella]	399	514	2.00E-38	128.8	20.1	24.8	hypothetical protein CARUB_v10020154mg	gbpln	Capsella rubella	AT1G80710.1 | Symbols: DRS1 | DROUGHT SENSITIVE 1 | chr1:30333499-30335796 REVERSE LENGTH=516	399	516	7.00E-41	129.3	20.3	24.6
Rsa1.0_00053.1.g2900.t1	ref|NP_564758.2| Pectin lyase-like protein [Arabidopsis thaliana] gi|2462753|gb|AAB71972.1| putative polygalacturonase [Arabidopsis thaliana] gi|332195579|gb|AEE33700.1| Pectin lyase-like protein [Arabidopsis thaliana]	538	540	0	100.4	83.6	88.8	Pectin lyase-like protein	gbpln	Arabidopsis thaliana	AT1G60590.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:22314426-22316867 REVERSE LENGTH=540	538	540	0	100.4	83.6	88.8

Rsa1.0_00053.1.g2901.t1	ref|XP_002886390.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata] gi|297332231|gb|EFH62649.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata]	318	298	3.00E−97	93.7	55.7	73.9	hypothetical protein ARALYDRAFT_893070	gbpln	Arabidopsis lyrata	AT2G42470.1 | Symbols: | TRAF−like family protein | chr2:17679887−17685187 REVERSE LENGTH=898	318	898	2.00E−80	282.4	49.7	67.6
Rsa1.0_00053.1.g2902.t1	ref|NP_176255.2| naphthoate synthase [Arabidopsis thaliana] gi|327488386|sp|Q8GYN9.2|MENB_ARATH RecName: Full=1,4−Dihydroxy−2−naphthoyl−CoA synthase, peroxisomal; Short=DHNS; AltName: Full=Enoyl−CoA hydratase/isomerase D; Short=ECHID; AltName: Full=Naphthoate synthase gi|192571726|gb|ACF04808.1| At1g60550 [Arabidopsis thaliana] gi|332195575|gb|AEE33696.1| 1,4−Dihydroxy−2−naphthoyl−CoA synthase [Arabidopsis thaliana]	338	337	1.00E−174	99.7	87.3	93.5	naphthoate synthase	gbpln	Arabidopsis thaliana	AT1G60550.1 | Symbols: ECHID, DHNS | enoyl−CoA hydratase/isomerase D | chr1:22305988−22308092 REVERSE LENGTH=337	338	337	1.00E−177	99.7	87.3	93.5
Rsa1.0_00053.1.g2903.t1	ref|XP_002888139.1| dynamin family protein [Arabidopsis lyrata subsp. lyrata] gi|297333980|gb|EFH64398.1| dynamin family protein [Arabidopsis lyrata subsp. lyrata]	659	659	0	100.0	86.0	91.0	dynamin family protein	gbpln	Arabidopsis lyrata	AT1G60500.1 | Symbols: DRP4C | Dynamin related protein 4C | chr1:22291582−22293822 FORWARD LENGTH=669	659	669	0	101.5	82.5	90.0
Rsa1.0_00053.1.g2904.t1	ref|XP_002888139.1| dynamin family protein [Arabidopsis lyrata subsp. lyrata] gi|297333980|gb|EFH64398.1| dynamin family protein [Arabidopsis lyrata subsp. lyrata]	677	659	0	97.3	85.5	90.3	dynamin family protein	gbpln	Arabidopsis lyrata	AT1G60500.1 | Symbols: DRP4C | Dynamin related protein 4C | chr1:22291582−22293822 FORWARD LENGTH=669	677	669	0	98.8	81.2	89.1
Rsa1.0_00053.1.g2905.t10	emb|CBI39638.3| unnamed protein product [Vitis vinifera]	181	591	1.00E−102	326.5	98.9	99.4	unnamed protein product	gbpln	Vitis vinifera	AT1G10630.1 | Symbols: ATARFA1F, ARFA1F | ADP−ribosylation factor A1F | chr1:3513189−3514230 REVERSE LENGTH=181	181	181	1.00E−104	100.0	98.9	100.0
Rsa1.0_00053.1.g2906.t1	gb|EOA35424.1| hypothetical protein CARUB_v10020626mg [Capsella rubella]	332	334	1.00E−177	100.6	90.4	95.2	hypothetical protein CARUB_v10020626mg	gbpln	Capsella rubella	AT1G60470.1 | Symbols: AtGolS4, GolS4 | galactinol synthase 4 | chr1:22279181−22280454 REVERSE LENGTH=334	332	334	1.00E−179	100.6	91.0	95.5
Rsa1.0_00053.1.g2907.t1	gb|AAC24075.1| Strong similarity to water stress−induced protein, WSI76 isolog T08I13.2 gb|2275196 from A. thaliana BAC gb|AC002337 [Arabidopsis thaliana]	49	345	6.00E−16	704.1	73.5	85.7	Strong similarity to water stress−induced protein, WSI76 isolog T08I13.2 gb|2275196 from A. thaliana BAC gb|AC002337	gbpln	Arabidopsis thaliana	AT1G60450.1 | Symbols: AtGolS7, GolS7 | galactinol synthase 7 | chr1:22271226−22273214 REVERSE LENGTH=332	49	332	1.00E−18	677.6	73.5	85.7
Rsa1.0_00053.1.g2908.t11	ref|XP_002886619.1| ATCOAA/ATPANK1 [Arabidopsis lyrata subsp. lyrata] gi|297332460|gb|EFH62878.1| ATCOAA/ATPANK1 [Arabidopsis lyrata subsp. lyrata]	607	384	0	63.3	55.4	57.7	ATCOAA/ATPANK1	gbpln	Arabidopsis lyrata	AT1G60440.1 | Symbols: ATCOAA, ATPANK1, PANK1 | pantothenate kinase 1 | chr1:22266653−22269070 REVERSE LENGTH=383	607	383	0	63.1	56.0	58.0
Rsa1.0_00053.1.g2909.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00053.1.g2910.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00053.1.g2911.t1	ref|XP_002889769.1| MYB transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297335611|gb|EFH66028.1| MYB transcription factor [Arabidopsis lyrata subsp. lyrata]	230	844	1.00E−102	367.0	84.3	90.4	MYB transcription factor	gbpln	Arabidopsis lyrata	AT1G09770.1 | Symbols: ATCDC5, CDC5, ATMYBCDC5 | cell division cycle 5 | chr1:3162002−3165122 FORWARD LENGTH=844	230	844	1.00E−104	367.0	84.3	90.4
Rsa1.0_00053.1.g2912.t1	emb|CCD74525.1| polygalacturonase 1 [Arabidopsis halleri subsp. halleri]	625	626	0	100.2	81.9	89.9	polygalacturonase 1	gbpln	Arabidopsis halleri	AT1G60390.1 | Symbols: PG1 | polygalacturonase 1 | chr1:22247611−22249556 REVERSE LENGTH=624	625	624	0	99.8	81.0	89.0
Rsa1.0_00053.1.g2913.t1	ref|XP_002886632.1| radical SAM domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297332473|gb|EFH62891.1| radical SAM domain−containing protein [Arabidopsis lyrata subsp. lyrata]	447	458	0	102.5	90.4	95.1	radical SAM domain−containing protein	gbpln	Arabidopsis lyrata	AT1G60230.1 | Symbols: | Radical SAM superfamily protein | chr1:22212223−22214346 REVERSE LENGTH=458	447	458	0	102.5	89.5	94.2
Rsa1.0_00053.1.g2914.t2	gb|EOA34334.1| hypothetical protein CARUB_v10021854mg [Capsella rubella]	593	593	0	100.0	64.8	77.1	hypothetical protein CARUB_v10021854mg	gbpln	Capsella rubella	AT1G60220.1 | Symbols: OTS1, ULP1D | UB−like protease 1D | chr1:22208332−22211910 FORWARD LENGTH=584	593	584	0	98.5	65.6	75.9
Rsa1.0_00053.1.g2915.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00053.1.g2916.t1	ref|XP_002886636.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332477|gb|EFH62895.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	301	302	1.00E−153	100.3	89.4	93.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G60080.1 | Symbols: | 3'−5'−exoribonuclease family protein | chr1:22152605−22154339 REVERSE LENGTH=302	301	302	1.00E−145	100.3	87.7	93.4
Rsa1.0_00053.1.g2917.t1	gb|AAC63844.1| putative non−LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1769	1231	0	69.6	40.4	50.2	putative non−LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337−69884 REVERSE LENGTH=515	1769	515	1.00E−117	29.1	13.7	18.4

<table>
<tr><td>Rsa1.0_00053.1.g2918.t1</td><td>ref|NP_564753.1| serine/threonine-protein kinase WNK (With No lysine)-related protein [Arabidopsis thaliana] gi|4249385|gb|AAD14482.1|AAD14482 T2K10.11 [Arabidopsis thaliana] gi|21537011|gb|AAM61352.1| unknown [Arabidopsis thaliana] gi|225898034|dbj|BAH30349.1| hypothetical protein [Arabidopsis thaliana] gi|332195533|gb|AEE33654.1| serine/threonine-protein kinase WNK (With No lysine)-related protein [Arabidopsis thaliana]</td><td>364</td><td>386</td><td>1.00E-159</td><td>106.0</td><td>79.7</td><td>82.4</td><td>serine/threonine-protein kinase WNK (With No lysine)-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G60060.1 | Symbols: | Serine/threonine-protein kinase WNK (With No Lysine)-related | chr1:22139282-22141585 FORWARD LENGTH=386</td><td>364</td><td>386</td><td>1.00E-161</td><td>106.0</td><td>79.7</td><td>82.4</td></tr>
<tr><td>Rsa1.0_00053.1.g2919.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00053.1.g2920.t1</td><td>ref|XP_002886638.1| hypothetical protein ARALYDRAFT_315326 [Arabidopsis lyrata subsp. lyrata] gi|297332479|gb|EFH62897.1| hypothetical protein ARALYDRAFT_315326 [Arabidopsis lyrata subsp. lyrata]</td><td>373</td><td>373</td><td>0</td><td>100.0</td><td>89.3</td><td>93.0</td><td>hypothetical protein ARALYDRAFT_315326</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G60050.1 | Symbols: | Nodulin MtN21 /EamA-like transporter family protein | chr1:22121550-22123702 REVERSE LENGTH=374</td><td>373</td><td>374</td><td>0</td><td>100.3</td><td>90.6</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00053.1.g2921.t1</td><td>ref|NP_564752.1| uncharacterized protein [Arabidopsis thaliana] gi|4249380|gb|AAD14477.1| ESTs gb|Z37637, gb|AA042498 and gb|AA042269 come from this gene [Arabidopsis thaliana] gi|26450481|dbj|BAC42354.1| unknown protein [Arabidopsis thaliana] gi|28827334|gb|AAO50511.1| unknown protein [Arabidopsis thaliana] gi|332195529|gb|AEE33650.1| uncharacterized protein AT1G60010 [Arabidopsis thaliana]</td><td>169</td><td>173</td><td>3.00E-74</td><td>102.4</td><td>82.2</td><td>92.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G60010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10530.1); Has 185 Blast hits to 185 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 3; Plants - 180; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:22095660-22096434 REVERSE LENGTH=173</td><td>169</td><td>173</td><td>1.00E-76</td><td>102.4</td><td>82.2</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00053.1.g2922.t1</td><td>gb|EOA35601.1| hypothetical protein CARUB_v10020814mg [Capsella rubella]</td><td>255</td><td>262</td><td>1.00E-116</td><td>102.7</td><td>84.3</td><td>90.2</td><td>hypothetical protein CARUB_v10020814mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G60000.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:22093678-22094540 REVERSE LENGTH=258</td><td>255</td><td>258</td><td>1.00E-118</td><td>101.2</td><td>82.7</td><td>89.0</td></tr>
<tr><td>Rsa1.0_00053.1.g2923.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00053.1.g2924.t1</td><td>ref|XP_002888160.1| hypothetical protein ARALYDRAFT_475312 [Arabidopsis lyrata subsp. lyrata] gi|297334001|gb|EFH64419.1| hypothetical protein ARALYDRAFT_475312 [Arabidopsis lyrata subsp. lyrata]</td><td>597</td><td>418</td><td>1.00E-177</td><td>70.0</td><td>53.8</td><td>56.1</td><td>hypothetical protein ARALYDRAFT_475312</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G59980.1 | Symbols: ATDJC39, ARL2 | ARG1-like 2 | chr1:22081069-22083491 FORWARD LENGTH=414</td><td>597</td><td>414</td><td>1.00E-175</td><td>69.3</td><td>52.8</td><td>55.4</td></tr>
<tr><td>Rsa1.0_00053.1.g2925.t1</td><td>ref|XP_002891550.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata] gi|297337392|gb|EFH67809.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata]</td><td>429</td><td>422</td><td>2.00E-96</td><td>98.4</td><td>49.7</td><td>65.7</td><td>hypothetical protein ARALYDRAFT_474131</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G49990.1 | Symbols: | F-box family protein | chr1:18513696-18514988 FORWARD LENGTH=430</td><td>429</td><td>430</td><td>2.00E-97</td><td>100.2</td><td>49.2</td><td>66.2</td></tr>
<tr><td>Rsa1.0_00053.1.g2926.t1</td><td>ref|XP_002888162.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334003|gb|EFH64421.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>359</td><td>351</td><td>1.00E-152</td><td>97.8</td><td>74.9</td><td>83.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G59970.1 | Symbols: | Matrixin family protein | chr1:22073601-22074683 FORWARD LENGTH=360</td><td>359</td><td>360</td><td>1.00E-154</td><td>100.3</td><td>73.8</td><td>84.1</td></tr>
<tr><td>Rsa1.0_00053.1.g2927.t1</td><td>ref|NP_176204.1| putative Aldo/keto reductase [Arabidopsis thaliana] gi|5080826|gb|AAD39335.1|AC007258_24 Putative Aldo/keto reductase [Arabidopsis thaliana] gi|15451098|gb|AAK96820.1| Putative Aldo/keto reductase [Arabidopsis thaliana] gi|18377508|gb|AAL66920.1| putative aldo/keto reductase [Arabidopsis thaliana] gi|332195523|gb|AEE33644.1| putative Aldo/keto reductase [Arabidopsis thaliana]</td><td>323</td><td>326</td><td>1.00E-162</td><td>100.9</td><td>85.8</td><td>92.9</td><td>putative Aldo/keto reductase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G59960.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr1:22071410-22073067 REVERSE LENGTH=326</td><td>323</td><td>326</td><td>1.00E-164</td><td>100.9</td><td>85.8</td><td>92.9</td></tr>
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Rsa1.0_00053.1.g2928.t2	ref|NP_683446.1| putative disease resistance protein RDL5/RF45 [Arabidopsis thaliana] gi|387942479|sp|F4IBE4.1|DRL10_ARATH RecName: Full=Probable disease resistance protein RF45 gi|387942481|sp|P0DI16.1|DRL44_ARATH RecName: Full=Probable disease resistance protein RDL5 gi|332195441|gb|AEE33562.1| putative disease resistance protein RDL5/RF45 [Arabidopsis thaliana]	1129	1017	0	90.1	50.5	64.0	putative disease resistance protein RDL5/RF45	gbpln	Arabidopsis thaliana	AT1G58807.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:21780574-21783793 FORWARD LENGTH=1017	1129	1017	0	90.1	50.5	64.0
Rsa1.0_00053.1.g2929.t1	ref|XP_002886657.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332498|gb|EFH62916.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	334	608	2.00E-72	182.0	49.4	60.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G35450.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr5:13667809-13670685 FORWARD LENGTH=901	334	901	5.00E-75	269.8	46.7	60.2
Rsa1.0_00053.1.g2930.t1	gb|EOA33570.1| hypothetical protein CARUB_v10019704mg [Capsella rubella]	379	1046	0	276.0	92.9	95.5	hypothetical protein CARUB_v10019704mg	gbpln	Capsella rubella	AT1G59760.1 | Symbols: | RNA helicase, ATP-dependent, SK12/DOB1 protein | chr1:21984571-21990110 REVERSE LENGTH=988	379	988	0	260.7	91.8	95.8
Rsa1.0_00053.1.g2931.t1	gb|EOA33570.1| hypothetical protein CARUB_v10019704mg [Capsella rubella]	564	1046	0	185.5	92.6	96.3	hypothetical protein CARUB_v10019704mg	gbpln	Capsella rubella	AT1G59760.1 | Symbols: | RNA helicase, ATP-dependent, SK12/DOB1 protein | chr1:21984571-21990110 REVERSE LENGTH=988	564	988	0	175.2	93.4	97.2
Rsa1.0_00053.1.g2932.t1	ref|XP_002888185.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297334026|gb|EFH64444.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	739	592	0	80.1	71.6	75.0	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G59740.1 | Symbols: | Major facilitator superfamily protein | chr1:21968227-21972312 FORWARD LENGTH=591	739	591	0	80.0	71.3	74.8
Rsa1.0_00053.1.g2933.t1	ref|XP_002886664.1| thioredoxin H-type 7 [Arabidopsis lyrata subsp. lyrata] gi|297332505|gb|EFH62923.1| thioredoxin H-type 7 [Arabidopsis lyrata subsp. lyrata]	128	128	3.00E-61	100.0	89.1	93.8	thioredoxin H-type 7	gbpln	Arabidopsis lyrata	AT1G59730.1 | Symbols: ATH7, TH7 | thioredoxin H-type 7 | chr1:21952759-21953392 REVERSE LENGTH=129	128	129	5.00E-61	100.8	87.5	91.4
Rsa1.0_00053.1.g2934.t1	ref|NP_172506.1| putative DNAJ heat-shock protein [Arabidopsis thaliana] gi|4914337|gb|AAD32885.1|AC005489_23 F14N23.23 [Arabidopsis thaliana] gi|13430680|gb|AAK25962.1|AF360252_1 putative heat-shock protein [Arabidopsis thaliana] gi|14532888|gb|AAK64126.1| putative heat-shock protein [Arabidopsis thaliana] gi|332190448|gb|AEE28569.1| putative DNAJ heat-shock protein [Arabidopsis thaliana]	424	349	1.00E-121	82.3	57.8	66.7	putative DNAJ heat-shock protein	gbpln	Arabidopsis thaliana	AT1G10350.1 | Symbols: | DNAJ heat shock family protein | chr1:3393595-3394860 REVERSE LENGTH=349	424	349	1.00E-123	82.3	57.8	66.7
Rsa1.0_00053.1.g2935.t1	gb|EOA35526.1| hypothetical protein CARUB_v10020734mg [Capsella rubella]	291	293	1.00E-154	100.7	91.1	95.5	hypothetical protein CARUB_v10020734mg	gbpln	Capsella rubella	AT1G59710.1 | Symbols: | Protein of unknown function (DUF569) | chr1:21938623-21939673 FORWARD LENGTH=300	291	300	1.00E-143	103.1	89.3	95.2
Rsa1.0_00053.1.g2936.t1	ref|NP_176178.1| glutathione S-transferase TAU 16 [Arabidopsis thaliana] gi|75338642|sp|Q9XIF8.1|GSTUG_ARATH RecName: Full=Glutathione S-transferase U16; Short=AtGSTU16; AltName: Full=GST class-tau member 16 gi|5080803|gb|AAD39312.1|AC007258_1 Similar to glutathione transferase [Arabidopsis thaliana] gi|8778752|gb|AAF79760.1|AC009317_19 T30E16.30 [Arabidopsis thaliana] gi|48310666|gb|AAT41863.1| At1g59700 [Arabidopsis thaliana] gi|332195484|gb|AEE33605.1| glutathione S-transferase TAU 16 [Arabidopsis thaliana]	267	234	1.00E-107	87.6	74.2	81.3	glutathione S-transferase TAU 16	gbpln	Arabidopsis thaliana	AT1G59700.1 | Symbols: ATGSTU16, GSTU16 | glutathione S-transferase TAU 16 | chr1:21936459-21937763 FORWARD LENGTH=234	267	234	1.00E-110	87.6	74.2	81.3
Rsa1.0_00053.1.g2937.t1	gb|EOA13425.1| hypothetical protein CARUB_v10026465mg [Capsella rubella] gi|482549232|gb|EOA13426.1| hypothetical protein CARUB_v10026465mg [Capsella rubella]	112	423	2.00E-12	377.7	33.0	48.2	hypothetical protein CARUB_v10026465mg	gbpln	Capsella rubella	AT5G56420.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22850863-22852334 REVERSE LENGTH=422	112	422	1.00E-13	376.8	32.1	47.3

Rsa1.0_00053.1.g2938.t1	ref|NP_189971.1| uncharacterized protein [Arabidopsis thaliana] gi|7362785|emb|CAB83157.1| putative protein [Arabidopsis thaliana] gi|332644314|gb|AEE77835.1| uncharacterized protein AT3G43850 [Arabidopsis thaliana]	134	270	4.00E-33	201.5	53.0	60.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G43850.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G21940.1); Has 215 Blast hits to 215 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 213; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:15702085-15704152 REVERSE LENGTH=270	134	270	1.00E-35	201.5	53.0	60.4
Rsa1.0_00053.1.g2939.t1	dbj|BAJ34445.1| unnamed protein product [Thellungiella halophila]	231	229	1.00E-101	99.1	77.5	87.9	unnamed protein product	----	----	AT1G59700.1 | Symbols: ATGSTU16, GSTU16 | glutathione S-transferase TAU 16 | chr1:21936459-21937763 FORWARD LENGTH=234	231	234	1.00E-102	101.3	75.3	84.8
Rsa1.0_00053.1.g2940.t1	gb|EOA34239.1| hypothetical protein CARUB_v10021751mg, partial [Capsella rubella]	970	978	0	100.8	61.9	70.7	hypothetical protein CARUB_v10021751mg, partial	gbpln	Capsella rubella	AT1G59660.1 | Symbols: | Nucleoporin autopeptidase | chr1:21924693-21929233 FORWARD LENGTH=997	970	997	0	102.8	60.5	68.9
Rsa1.0_00053.1.g2941.t1	gb|EOA35051.1| hypothetical protein CARUB_v10020162mg [Capsella rubella]	511	511	0	100.0	89.0	92.6	hypothetical protein CARUB_v10020162mg	gbpln	Capsella rubella	AT1G59650.1 | Symbols: CW14 | Protein of unknown function (DUF1336) | chr1:21920099-21922670 FORWARD LENGTH=492	511	492	0	96.3	86.5	89.8
Rsa1.0_00053.1.g2942.t6	gb|AEM36350.1| At1g58602 [Arabidopsis thaliana]	1190	1133	0	95.2	40.2	51.8	At1g58602	gbpln	Arabidopsis thaliana	AT1G58602.2 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr1:21760167-21763765 FORWARD LENGTH=1138	1190	1138	0	95.6	40.1	51.7
Rsa1.0_00054.1.g2943.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00054.1.g2944.t1	gb|EOA29338.1| hypothetical protein CARUB_v10025620mg [Capsella rubella]	208	198	3.00E-32	95.2	40.9	57.7	hypothetical protein CARUB_v10025620mg	gbpln	Capsella rubella	AT3G28620.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr3:10727826-10728461 FORWARD LENGTH=211	208	211	2.00E-30	101.4	39.9	55.3
Rsa1.0_00054.1.g2945.t1	ref|XP_002880588.1| ATRPA2/ROR1/RPA2 [Arabidopsis lyrata subsp. lyrata] gi|297326427|gb|EFH56847.1| ATRPA2/ROR1/RPA2 [Arabidopsis lyrata subsp. lyrata]	273	279	1.00E-132	102.2	85.0	92.7	ATRPA2/ROR1/RPA2	gbpln	Arabidopsis lyrata	AT2G24490.2 | Symbols: RPA2, ATRPA2, ROR1, ATRPA32A, RPA32A | replicon protein A2 | chr2:10398651-10400416 REVERSE LENGTH=279	273	279	1.00E-132	102.2	83.5	91.6
Rsa1.0_00054.1.g2946.t2	gb|ACP30611.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1069	1050	0	98.2	38.4	49.8	disease resistance protein	gbpln	Brassica rapa	AT5G22690.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:7541369-7544888 FORWARD LENGTH=1008	1069	1008	0	94.3	37.3	48.1
Rsa1.0_00054.1.g2947.t1	dbj|BAJ34463.1| unnamed protein product [Thellungiella halophila]	382	403	1.00E-172	105.5	85.3	90.6	unnamed protein product	----	----	AT2G24500.1 | Symbols: FZF | Zinc finger protein 622 | chr2:10401259-10402805 REVERSE LENGTH=395	382	395	1.00E-167	103.4	82.2	87.2
Rsa1.0_00054.1.g2948.t1	gb|ACG60669.1| copia-type polyprotein-like protein [Brassica oleracea var. alboglabra]	112	196	2.00E-40	175.0	71.4	83.0	copia-type polyprotein-like protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00054.1.g2949.t1	ref|XP_002878766.1| hypothetical protein ARALYDRAFT_900997 [Arabidopsis lyrata subsp. lyrata] gi|297324605|gb|EFH55025.1| hypothetical protein ARALYDRAFT_900997 [Arabidopsis lyrata subsp. lyrata]	328	409	1.00E-108	124.7	72.0	81.7	hypothetical protein ARALYDRAFT_900997	gbpln	Arabidopsis lyrata	AT2G24530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G31440.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:10422597-10423820 FORWARD LENGTH=407	328	407	1.00E-110	124.1	70.4	81.4
Rsa1.0_00054.1.g2950.t1	gb|EOA29338.1| hypothetical protein CARUB_v10025620mg [Capsella rubella]	210	198	4.00E-34	94.3	41.0	57.6	hypothetical protein CARUB_v10025620mg	gbpln	Capsella rubella	AT2G24480.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr2:10397588-10398184 FORWARD LENGTH=198	210	198	4.00E-34	94.3	39.5	58.6
Rsa1.0_00054.1.g2951.t1	ref|XP_002878766.1| hypothetical protein ARALYDRAFT_900997 [Arabidopsis lyrata subsp. lyrata] gi|297324605|gb|EFH55025.1| hypothetical protein ARALYDRAFT_900997 [Arabidopsis lyrata subsp. lyrata]	264	409	9.00E-54	154.9	46.6	53.0	hypothetical protein ARALYDRAFT_900997	gbpln	Arabidopsis lyrata	AT2G24530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G31440.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:10422597-10423820 FORWARD LENGTH=407	264	407	2.00E-55	154.2	45.8	52.7
Rsa1.0_00054.1.g2952.t1	gb|EOA29338.1| hypothetical protein CARUB_v10025620mg [Capsella rubella]	210	198	4.00E-34	94.3	41.4	58.1	hypothetical protein CARUB_v10025620mg	gbpln	Capsella rubella	AT2G24480.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr2:10397588-10398184 FORWARD LENGTH=198	210	198	6.00E-32	94.3	38.6	56.7

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<tr><td>Rsa1.0_00054.1.g2953.t1</td><td>ref|XP_002880584.1| hypothetical protein ARALYDRAFT_481301 [Arabidopsis lyrata subsp. lyrata] gi|297326423|gb|EFH56843.1| hypothetical protein ARALYDRAFT_481301 [Arabidopsis lyrata subsp. lyrata]</td><td>288</td><td>279</td><td>1.00E-118</td><td>96.9</td><td>81.6</td><td>89.9</td><td>hypothetical protein ARALYDRAFT_481301</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G24450.1 | Symbols: FLA3 | FASCICLIN-like arabinogalactan protein 3 precursor | chr2:10393019-10393861 REVERSE LENGTH=280</td><td>288</td><td>280</td><td>1.00E-114</td><td>97.2</td><td>80.6</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00054.1.g2954.t1</td><td>ref|NP_565570.1| selenium binding protein [Arabidopsis thaliana] gi|4337201|gb|AAD18115.1| expressed protein [Arabidopsis thaliana] gi|21553632|gb|AAM62725.1| unknown [Arabidopsis thaliana] gi|21805670|gb|AAM76749.1| hypothetical protein [Arabidopsis thaliana] gi|50058859|gb|AAT69174.1| hypothetical protein At2g24440 [Arabidopsis thaliana] gi|330252484|gb|AEC07578.1| selenium binding protein [Arabidopsis thaliana]</td><td>191</td><td>183</td><td>8.00E-32</td><td>95.8</td><td>37.2</td><td>44.0</td><td>selenium binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G24440.1 | Symbols: | selenium binding | chr2:10391124-10392492 FORWARD LENGTH=183</td><td>191</td><td>183</td><td>3.00E-34</td><td>95.8</td><td>37.2</td><td>44.0</td></tr>
<tr><td>Rsa1.0_00054.1.g2955.t1</td><td>gb|EOA12673.1| hypothetical protein CARUB_v10027827mg, partial [Capsella rubella]</td><td>497</td><td>438</td><td>1.00E-137</td><td>88.1</td><td>52.9</td><td>66.0</td><td>hypothetical protein CARUB_v10027827mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G49020.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr3:18169079-18170660 FORWARD LENGTH=447</td><td>497</td><td>447</td><td>1.00E-136</td><td>89.9</td><td>53.9</td><td>65.6</td></tr>
<tr><td>Rsa1.0_00054.1.g2956.t1</td><td>gb|EOA29236.1| hypothetical protein CARUB_v10025508mg [Capsella rubella]</td><td>317</td><td>318</td><td>1.00E-172</td><td>100.3</td><td>94.3</td><td>97.2</td><td>hypothetical protein CARUB_v10025508mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G24430.2 | Symbols: ANAC039 | NAC domain containing protein 38 | chr2:10383517-10386386 REVERSE LENGTH=316</td><td>317</td><td>316</td><td>1.00E-172</td><td>99.7</td><td>94.3</td><td>96.5</td></tr>
<tr><td>Rsa1.0_00054.1.g2957.t1</td><td>ref|NP_200800.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|17225050|gb|AAL37222.1|AF321919_1 ULI3 [Arabidopsis thaliana] gi|332009868|gb|AED97251.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]</td><td>716</td><td>710</td><td>0</td><td>99.2</td><td>50.8</td><td>62.2</td><td>cysteine/histidine-rich C1 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G59920.1 | Symbols: ULI3 | Cysteine/Histidine-rich C1 domain family protein | chr5:24128756-24130888 FORWARD LENGTH=710</td><td>716</td><td>710</td><td>0</td><td>99.2</td><td>50.8</td><td>62.2</td></tr>
<tr><td>Rsa1.0_00054.1.g2958.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT4G23630.1 | Symbols: BTI1, RTNLB1 | VIRB2-interacting protein 1 | chr4:12318070-12319574 FORWARD LENGTH=275</td><td>88</td><td>275</td><td>7.00E-12</td><td>312.5</td><td>35.2</td><td>43.2</td></tr>
<tr><td>Rsa1.0_00054.1.g2959.t1</td><td>dbj|BAB08360.1| Ta11-like non-LTR retroelement protein-like [Arabidopsis thaliana]</td><td>648</td><td>655</td><td>0</td><td>101.1</td><td>57.3</td><td>71.3</td><td>Ta11-like non-LTR retroelement protein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G59920.1 | Symbols: ULI3 | Cysteine/Histidine-rich C1 domain family protein | chr5:24128756-24130888 FORWARD LENGTH=710</td><td>648</td><td>710</td><td>0</td><td>109.6</td><td>55.7</td><td>69.6</td></tr>
<tr><td>Rsa1.0_00054.1.g2960.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00054.1.g2961.t1</td><td>ref|NP_180016.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|4337198|gb|AAD18112.1| putative auxin-regulated protein [Arabidopsis thaliana] gi|38566584|gb|AAR24182.1| At2g24400 [Arabidopsis thaliana] gi|40824022|gb|AAR92327.1| At2g24400 [Arabidopsis thaliana] gi|330252478|gb|AEC07572.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]</td><td>178</td><td>178</td><td>7.00E-80</td><td>100.0</td><td>86.0</td><td>91.6</td><td>SAUR-like auxin-responsive protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G24400.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:10377993-10378529 REVERSE LENGTH=178</td><td>178</td><td>178</td><td>3.00E-82</td><td>100.0</td><td>86.0</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00054.1.g2962.t1</td><td>ref|NP_850052.1| chaperone protein dnaJ-related protein [Arabidopsis thaliana] gi|44917527|gb|AAS49088.1| At2g24395 [Arabidopsis thaliana] gi|62321035|dbj|BAD94100.1| hypothetical protein [Arabidopsis thaliana] gi|330252477|gb|AEC07571.1| chaperone protein dnaJ-related protein [Arabidopsis thaliana]</td><td>132</td><td>132</td><td>5.00E-44</td><td>100.0</td><td>70.5</td><td>81.8</td><td>chaperone protein dnaJ-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G24395.1 | Symbols: | chaperone protein dnaJ-related | chr2:10375497-10376081 FORWARD LENGTH=132</td><td>132</td><td>132</td><td>1.00E-46</td><td>100.0</td><td>70.5</td><td>81.8</td></tr>
<tr><td>Rsa1.0_00054.1.g2963.t1</td><td>gb|EOA27992.1| hypothetical protein CARUB_v10024168mg [Capsella rubella]</td><td>153</td><td>175</td><td>2.00E-71</td><td>114.4</td><td>82.4</td><td>90.2</td><td>hypothetical protein CARUB_v10024168mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G24390.1 | Symbols: | AIG2-like (avirulence induced gene) family protein | chr2:10373796-10374654 FORWARD LENGTH=152</td><td>153</td><td>152</td><td>1.00E-70</td><td>99.3</td><td>79.1</td><td>89.5</td></tr>
<tr><td>Rsa1.0_00054.1.g2964.t1</td><td>gb|EOA29306.1| hypothetical protein CARUB_v10025585mg [Capsella rubella]</td><td>763</td><td>806</td><td>0</td><td>105.6</td><td>90.0</td><td>96.6</td><td>hypothetical protein CARUB_v10025585mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G24370.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr2:10369979-10373063 REVERSE LENGTH=788</td><td>763</td><td>788</td><td>0</td><td>103.3</td><td>88.2</td><td>94.6</td></tr>
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Rsa1.0_00054.1.g2966.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00054.1.g2967.t1	ref|XP_002893652.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297339494|gb|EFH69911.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	208	725	3.00E-62	348.6	53.8	57.2	protein binding protein	gbpln	Arabidopsis lyrata	AT1G30860.1 | Symbols: | RING/U-box superfamily protein | chr1:10986696-10989246 REVERSE LENGTH=730	208	730	3.00E-61	351.0	51.0	55.3
Rsa1.0_00054.1.g2968.t1	ref|XP_002866147.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311982|gb|EFH42406.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	462	423	4.00E-64	91.6	35.3	51.1	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56420.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22850863-22852334 REVERSE LENGTH=422	462	422	4.00E-65	91.3	35.3	51.3
Rsa1.0_00054.1.g2969.t1	gb|EOA40378.1| hypothetical protein CARUB_v10009105mg [Capsella rubella]	455	453	0	99.6	76.9	84.6	hypothetical protein CARUB_v10009105mg	gbpln	Capsella rubella	AT1G01430.1 | Symbols: TBL25 | TRICHOME BIREFRINGENCE-LIKE 25 | chr1:156953-158536 REVERSE LENGTH=456	455	456	0	100.2	76.0	84.6
Rsa1.0_00054.1.g2970.t1	ref|XP_002864982.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297310817|gb|EFH41241.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	242	392	2.00E-37	162.0	43.4	59.1	F-box family protein	gbpln	Arabidopsis lyrata	AT5G65850.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:26346317-26347495 FORWARD LENGTH=392	242	392	5.00E-39	162.0	43.8	59.5
Rsa1.0_00054.1.g2971.t1	gb|EOA27207.1| hypothetical protein CARUB_v10023317mg [Capsella rubella]	411	412	0	100.2	89.1	94.2	hypothetical protein CARUB_v10023317mg	gbpln	Capsella rubella	AT4G31170.3 | Symbols: | Protein kinase superfamily protein | chr4:15153499-15154846 REVERSE LENGTH=412	411	412	0	100.2	83.5	90.3
Rsa1.0_00054.1.g2972.t1	ref|XP_002878748.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324587|gb|EFH55007.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	580	534	1.00E-171	92.1	59.0	71.0	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT2G24350.1 | Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr2:10361239-10364223 FORWARD LENGTH=537	580	537	1.00E-168	92.6	57.4	69.8
Rsa1.0_00054.1.g2973.t1	ref|XP_002879925.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297325764|gb|EFH56184.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	379	371	3.00E-52	97.9	42.5	54.4	F-box family protein	gbpln	Arabidopsis lyrata	AT2G41360.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:17234374-17235956 FORWARD LENGTH=387	379	387	1.00E-45	102.1	36.7	46.4
Rsa1.0_00054.1.g2974.t1	ref|XP_002880573.1| hypothetical protein ARALYDRAFT_900957 [Arabidopsis lyrata subsp. lyrata] gi|297326412|gb|EFH56832.1| hypothetical protein ARALYDRAFT_900957 [Arabidopsis lyrata subsp. lyrata]	406	411	1.00E-178	101.2	76.8	85.5	hypothetical protein ARALYDRAFT_900957	gbpln	Arabidopsis lyrata	AT2G24330.1 | Symbols: | Protein of unknown function (DUF2296) | chr2:10347340-10349566 REVERSE LENGTH=408	406	408	1.00E-174	100.5	75.4	83.7
Rsa1.0_00054.1.g2975.t1	ref|XP_002880572.1| hypothetical protein ARALYDRAFT_320242 [Arabidopsis lyrata subsp. lyrata] gi|297326411|gb|EFH56831.1| hypothetical protein ARALYDRAFT_320242 [Arabidopsis lyrata subsp. lyrata]	295	301	1.00E-147	102.0	82.7	94.2	hypothetical protein ARALYDRAFT_320242	gbpln	Arabidopsis lyrata	AT2G24320.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:10345659-10346829 REVERSE LENGTH=286	295	286	1.00E-147	96.9	80.7	91.9
Rsa1.0_00054.1.g2976.t1	ref|XP_002878745.1| hypothetical protein ARALYDRAFT_481288 [Arabidopsis lyrata subsp. lyrata] gi|297324584|gb|EFH55004.1| hypothetical protein ARALYDRAFT_481288 [Arabidopsis lyrata subsp. lyrata]	287	345	2.00E-43	120.2	57.8	67.9	hypothetical protein ARALYDRAFT_481288	gbpln	Arabidopsis lyrata	AT2G24310.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G47170.1); Has 9168 Blast hits to 2316 proteins in 376 species: Archae - 2; Bacteria - 1905; Metazoa - 1700; Fungi - 1409; Plants - 76; Viruses - 48; Other Eukaryotes - 4028 (source: NCBI BLink). | chr2:10344361-10345329 FORWARD LENGTH=322	287	322	1.00E-38	112.2	51.9	64.5
Rsa1.0_00054.1.g2977.t1	ref|XP_002878744.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] gi|297324583|gb|EFH55003.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	601	599	0	99.7	89.5	94.3	calmodulin-binding protein	gbpln	Arabidopsis lyrata	AT2G24300.2 | Symbols: | Calmodulin-binding protein | chr2:10340913-10343457 FORWARD LENGTH=599	601	599	0	99.7	90.0	94.2
Rsa1.0_00054.1.g2978.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00054.1.g2979.t1	dbj|BAJ33970.1| unnamed protein product [Thellungiella halophila]	494	494	0	100.0	94.1	97.4	unnamed protein product	----	----	AT2G24280.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:10334622-10336927 FORWARD LENGTH=494	494	494	0	100.0	91.1	95.1
Rsa1.0_00054.1.g2980.t1	gb|ABD64940.1| hypothetical protein 24.t00018 [Brassica oleracea]	134	380	2.00E-27	283.6	50.0	61.2	hypothetical protein 24.t00018	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	134	302	2.00E-19	225.4	38.8	55.2
Rsa1.0_00054.1.g2981.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_00055.1.g2983.t1</td><td>gb|EOA30756.1| hypothetical protein CARUB_v10013898mg [Capsella rubella]</td><td>393</td><td>393</td><td>0</td><td>100.0</td><td>93.6</td><td>97.5</td><td>hypothetical protein CARUB_v10013898mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04460.1 | Symbols: PEX12, ATPEX12, APM4 | peroxin-12 | chr3:1186641-1189094 FORWARD LENGTH=393</td><td>393</td><td>393</td><td>0</td><td>100.0</td><td>92.9</td><td>96.7</td></tr>
<tr><td>Rsa1.0_00055.1.g2984.t1</td><td>gb|EOA29968.1| hypothetical protein CARUB_v10013071mg [Capsella rubella]</td><td>711</td><td>721</td><td>0</td><td>101.4</td><td>85.8</td><td>92.8</td><td>hypothetical protein CARUB_v10013071mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04480.1 | Symbols: | endoribonucleases | chr3:1193988-1197320 REVERSE LENGTH=718</td><td>711</td><td>718</td><td>0</td><td>101.0</td><td>85.7</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00055.1.g2985.t1</td><td>ref|XP_002878332.1| hypothetical protein ARALYDRAFT_907560 [Arabidopsis lyrata subsp. lyrata] gi|297324170|gb|EFH54591.1| hypothetical protein ARALYDRAFT_907560 [Arabidopsis lyrata subsp. lyrata]</td><td>388</td><td>741</td><td>1.00E-57</td><td>191.0</td><td>35.1</td><td>38.4</td><td>hypothetical protein ARALYDRAFT_907560</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G60380.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT4G16790.1); Has 6102 Blast hits to 3981 proteins in 424 species: Archae - 6; Bacteria - 372; Metazoa - 2603; Fungi - 655; Plants - 291; Viruses - 28; Other Eukaryotes - 2147 (source: NCBI BLink). | chr3:22316913-22319144 REVERSE LENGTH=743</td><td>388</td><td>743</td><td>2.00E-46</td><td>191.5</td><td>34.0</td><td>37.4</td></tr>
<tr><td>Rsa1.0_00055.1.g2986.t1</td><td>gb|EOA31480.1| hypothetical protein CARUB_v10014673mg [Capsella rubella]</td><td>191</td><td>200</td><td>2.00E-78</td><td>104.7</td><td>86.9</td><td>90.6</td><td>hypothetical protein CARUB_v10014673mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04510.1 | Symbols: LSH2 | Protein of unknown function (DUF640) | chr3:1215812-1216417 REVERSE LENGTH=201</td><td>191</td><td>201</td><td>1.00E-77</td><td>105.2</td><td>84.3</td><td>89.0</td></tr>
<tr><td>Rsa1.0_00055.1.g2987.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>818</td><td>1142</td><td>0</td><td>139.6</td><td>47.6</td><td>61.7</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292</td><td>818</td><td>292</td><td>8.00E-32</td><td>35.7</td><td>9.8</td><td>16.3</td></tr>
<tr><td>Rsa1.0_00055.1.g2988.t1</td><td>ref|XP_002882364.1| tRNA synthetase class I family protein [Arabidopsis lyrata subsp. lyrata] gi|297328204|gb|EFH58623.1| tRNA synthetase class I family protein [Arabidopsis lyrata subsp. lyrata]</td><td>155</td><td>402</td><td>5.00E-80</td><td>259.4</td><td>94.8</td><td>98.1</td><td>tRNA synthetase class I family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04600.3 | Symbols: | Nucleotidylyl transferase superfamily protein | chr3:1243152-1245958 FORWARD LENGTH=402</td><td>155</td><td>402</td><td>2.00E-81</td><td>259.4</td><td>93.5</td><td>98.1</td></tr>
<tr><td>Rsa1.0_00055.1.g2989.t1</td><td>dbj|BAB08360.1| Ta11-like non-LTR retroelement protein-like [Arabidopsis thaliana]</td><td>643</td><td>655</td><td>0</td><td>101.9</td><td>59.3</td><td>70.8</td><td>Ta11-like non-LTR retroelement protein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G59920.1 | Symbols: ULI3 | Cysteine/Histidine-rich C1 domain family protein | chr5:24128756-24130888 FORWARD LENGTH=710</td><td>643</td><td>710</td><td>0</td><td>110.4</td><td>57.2</td><td>68.4</td></tr>
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<tr><td>Rsa1.0_00055.1.g2991.t1</td><td>gb|EOA29585.1| hypothetical protein CARUB_v10013041mg [Capsella rubella]</td><td>746</td><td>750</td><td>0</td><td>100.5</td><td>91.4</td><td>95.7</td><td>hypothetical protein CARUB_v10013041mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719</td><td>746</td><td>719</td><td>9.00E-42</td><td>96.4</td><td>17.2</td><td>29.9</td></tr>
<tr><td>Rsa1.0_00055.1.g2992.t1</td><td>gb|EOA30196.1| hypothetical protein CARUB_v10013313mg [Capsella rubella]</td><td>577</td><td>582</td><td>0</td><td>100.9</td><td>74.2</td><td>83.7</td><td>hypothetical protein CARUB_v10013313mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G03670.1 | Symbols: | ankyrin repeat family protein | chr1:914222-916222 REVERSE LENGTH=616</td><td>577</td><td>616</td><td>3.00E-48</td><td>106.8</td><td>25.8</td><td>44.0</td></tr>
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<tr><td>Rsa1.0_00055.1.g2995.t1</td><td>dbj|BAH19881.1| AT3G04630 [Arabidopsis thaliana]</td><td>279</td><td>286</td><td>1.00E-109</td><td>102.5</td><td>79.6</td><td>87.5</td><td>AT3G04630</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G04630.3 | Symbols: WDL1 | WVD2-like 1 | chr3:1259231-1260652 FORWARD LENGTH=286</td><td>279</td><td>286</td><td>1.00E-111</td><td>102.5</td><td>79.2</td><td>87.1</td></tr>
<tr><td>Rsa1.0_00055.1.g2996.t1</td><td>gb|EOA30431.1| hypothetical protein CARUB_v10013555mg [Capsella rubella]</td><td>491</td><td>487</td><td>0</td><td>99.2</td><td>90.6</td><td>94.7</td><td>hypothetical protein CARUB_v10013555mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04650.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr3:1262017-1264343 FORWARD LENGTH=486</td><td>491</td><td>486</td><td>0</td><td>99.0</td><td>89.0</td><td>92.5</td></tr>
<tr><td>Rsa1.0_00055.1.g2997.t1</td><td>dbj|BAJ34400.1| unnamed protein product [Thellungiella halophila]</td><td>320</td><td>330</td><td>1.00E-150</td><td>103.1</td><td>85.6</td><td>90.9</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G04670.1 | Symbols: WRKY39, ATWRKY39 | WRKY DNA-binding protein 39 | chr3:1266530-1267691 REVERSE LENGTH=330</td><td>320</td><td>330</td><td>1.00E-151</td><td>103.1</td><td>85.0</td><td>91.3</td></tr>
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<tr><td>Rsa1.0_00055.1.g2999.t1</td><td>ref|XP_002882370.1| hypothetical protein ARALYDRAFT_477736 [Arabidopsis lyrata subsp. lyrata] gi|297328210|gb|EFH58629.1| hypothetical protein ARALYDRAFT_477736 [Arabidopsis lyrata subsp. lyrata]</td><td>192</td><td>191</td><td>1.00E−77</td><td>99.5</td><td>81.8</td><td>88.5</td><td>hypothetical protein ARALYDRAFT_477736</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04700.1 | Symbols: | Protein of unknown function (DUF1685) | chr3:1276948−1277607 FORWARD LENGTH=191</td><td>192</td><td>191</td><td>5.00E−79</td><td>99.5</td><td>80.2</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00055.1.g3000.t1</td><td>gb|EOA30549.1| hypothetical protein CARUB_v10013671mg [Capsella rubella]</td><td>251</td><td>456</td><td>1.00E−118</td><td>181.7</td><td>84.5</td><td>90.8</td><td>hypothetical protein CARUB_v10013671mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04710.3 | Symbols: TPR10 | ankyrin repeat family protein | chr3:1276948−1280942 FORWARD LENGTH=680</td><td>251</td><td>680</td><td>1.00E−119</td><td>270.9</td><td>83.3</td><td>90.0</td></tr>
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<tr><td>Rsa1.0_00055.1.g3002.t1</td><td>gb|EOA31668.1| hypothetical protein CARUB_v10014871mg [Capsella rubella]</td><td>141</td><td>141</td><td>1.00E−71</td><td>100.0</td><td>90.1</td><td>96.5</td><td>hypothetical protein CARUB_v10014871mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04720.1 | Symbols: PR4, HEL, PR−4 | pathogenesis−related 4 | chr3:1285691−1286531 REVERSE LENGTH=212</td><td>141</td><td>212</td><td>5.00E−47</td><td>150.4</td><td>58.9</td><td>68.8</td></tr>
<tr><td>Rsa1.0_00055.1.g3003.t1</td><td>gb|AAN23106.2| PR4−type protein [Brassica rapa subsp. pekinensis] gi|195536976|dbj|BAG68208.1| PR4 protein [Brassica rapa subsp. chinensis] gi|244539681|dbj|BAH82748.1| pathogenesis related protein 4 [Brassica rapa subsp. chinensis]</td><td>141</td><td>140</td><td>3.00E−72</td><td>99.3</td><td>95.0</td><td>96.5</td><td>PR4−type protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G04720.1 | Symbols: PR4, HEL, PR−4 | pathogenesis−related 4 | chr3:1285691−1286531 REVERSE LENGTH=212</td><td>141</td><td>212</td><td>5.00E−51</td><td>150.4</td><td>63.8</td><td>72.3</td></tr>
<tr><td>Rsa1.0_00055.1.g3004.t1</td><td>dbj|BAJ33708.1| unnamed protein product [Thellungiella halophila]</td><td>213</td><td>214</td><td>1.00E−104</td><td>100.5</td><td>85.9</td><td>90.6</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G04720.1 | Symbols: PR4, HEL, PR−4 | pathogenesis−related 4 | chr3:1285691−1286531 REVERSE LENGTH=212</td><td>213</td><td>212</td><td>1.00E−100</td><td>99.5</td><td>87.8</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00055.1.g3005.t1</td><td>ref|XP_002882372.1| hypothetical protein ARALYDRAFT_477743 [Arabidopsis lyrata subsp. lyrata] gi|297328212|gb|EFH58631.1| hypothetical protein ARALYDRAFT_477743 [Arabidopsis lyrata subsp. lyrata]</td><td>283</td><td>1702</td><td>1.00E−61</td><td>601.4</td><td>51.6</td><td>54.1</td><td>hypothetical protein ARALYDRAFT_477743</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04740.1 | Symbols: SWP, MED14, ATMED14 | RNA polymerase II transcription mediators | chr3:1294037−1300555 FORWARD LENGTH=1703</td><td>283</td><td>1703</td><td>2.00E−60</td><td>601.8</td><td>50.2</td><td>53.0</td></tr>
<tr><td>Rsa1.0_00055.1.g3006.t1</td><td>gb|EOA39027.1| hypothetical protein CARUB_v10011597mg [Capsella rubella]</td><td>173</td><td>186</td><td>2.00E−11</td><td>107.5</td><td>27.2</td><td>48.0</td><td>hypothetical protein CARUB_v10011597mg</td><td>gbpln</td><td>Capsella rubella</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00055.1.g3007.t1</td><td>gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]</td><td>250</td><td>484</td><td>1.00E−82</td><td>193.6</td><td>65.2</td><td>78.4</td><td>hypothetical protein 27.t00116</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G14800.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:5099572−5102558 FORWARD LENGTH=384</td><td>250</td><td>384</td><td>4.00E−11</td><td>153.6</td><td>13.6</td><td>26.4</td></tr>
<tr><td>Rsa1.0_00055.1.g3008.t1</td><td>ref|XP_002882372.1| hypothetical protein ARALYDRAFT_477743 [Arabidopsis lyrata subsp. lyrata] gi|297328212|gb|EFH58631.1| hypothetical protein ARALYDRAFT_477743 [Arabidopsis lyrata subsp. lyrata]</td><td>119</td><td>1702</td><td>1.00E−11</td><td>1430.3</td><td>34.5</td><td>39.5</td><td>hypothetical protein ARALYDRAFT_477743</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04740.1 | Symbols: SWP, MED14, ATMED14 | RNA polymerase II transcription mediators | chr3:1294037−1300555 FORWARD LENGTH=1703</td><td>119</td><td>1703</td><td>2.00E−14</td><td>1431.1</td><td>34.5</td><td>39.5</td></tr>
<tr><td>Rsa1.0_00055.1.g3009.t1</td><td>ref|NP_566238.1| uncharacterized protein [Arabidopsis thaliana] gi|85701293|sp|Q9SQZ9.2|PITH1_ARATH RecName: Full=PITH domain−containing protein At3g04780 gi|16648681|gb|AAL25533.1| AT3g04780/F7O18_27 [Arabidopsis thaliana] gi|20147247|gb|AAM10337.1| AT3g04780/F7O18_27 [Arabidopsis thaliana] gi|21593799|gb|AAM65766.1| unknown [Arabidopsis thaliana] gi|332640614|gb|AEE74135.1| uncharacterized protein AT3G04780 [Arabidopsis thaliana]</td><td>64</td><td>176</td><td>9.00E−18</td><td>275.0</td><td>75.0</td><td>76.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G04780.1 | Symbols: | Protein of unknown function (DUF1000) | chr3:1311447−1313013 REVERSE LENGTH=176</td><td>64</td><td>176</td><td>1.00E−20</td><td>275.0</td><td>75.0</td><td>76.6</td></tr>
</table>

Rsa1.0_00055.1.g3010.t1	ref|NP_187132.1| serine/threonine-protein kinase Nek2 [Arabidopsis thaliana] gi|79607883|ref|NP_974221.2| serine/threonine-protein kinase Nek2 [Arabidopsis thaliana] gi|75333670|sp|Q9CAU7.1|NEK2_ARATH RecName: Full=Serine/threonine-protein kinase Nek2; AltName: Full=NimA-related protein kinase 2; Short=AtNek2 gi|12322861|gb|AAG51423.1|AC009465_23 putative kinase; 86849-83844 [Arabidopsis thaliana] gi|24030188|gb|AAN41275.1| putative kinase [Arabidopsis thaliana] gi|332640617|gb|AEE74138.1| serine/threonine-protein kinase Nek2 [Arabidopsis thaliana] gi|332640618|gb|AEE74139.1| serine/threonine-protein kinase Nek2 [Arabidopsis thaliana]	572	606	0	105.9	92.0	94.8	serine/threonine-protein kinase Nek2	gbpln	Arabidopsis thaliana	AT3G04810.2 | Symbols: ATNEK2, NEK2 | NIMA-related kinase 2 | chr3:1318096-1321101 FORWARD LENGTH=606	572	606	0	105.9	92.0	94.8
Rsa1.0_00055.1.g3011.t1	ref|NP_187133.3| pseudouridine synthase [Arabidopsis thaliana] gi|52354299|gb|AAU44470.1| hypothetical protein AT3G04820 [Arabidopsis thaliana] gi|61742699|gb|AAX55170.1| hypothetical protein At3g04820 [Arabidopsis thaliana] gi|332640619|gb|AEE74140.1| pseudouridine synthase [Arabidopsis thaliana]	663	715	0	107.8	88.7	94.0	pseudouridine synthase	gbpln	Arabidopsis thaliana	AT3G04820.1 | Symbols: | Pseudouridine synthase family protein | chr3:1321453-1325949 REVERSE LENGTH=715	663	715	0	107.8	88.7	94.0
Rsa1.0_00055.1.g3012.t1	gb|EOA31103.1| hypothetical protein CARUB_v10014256mg [Capsella rubella]	302	304	1.00E-166	100.7	94.7	98.3	hypothetical protein CARUB_v10014256mg	gbpln	Capsella rubella	AT3G04830.1 | Symbols: | Protein prenylyltransferase superfamily protein | chr3:1326289-1329132 FORWARD LENGTH=303	302	303	1.00E-166	100.3	92.7	97.7
Rsa1.0_00055.1.g3013.t3	ref|XP_002882386.1| hypothetical protein ARALYDRAFT_477772 [Arabidopsis lyrata subsp. lyrata] gi|297328226|gb|EFH58645.1| hypothetical protein ARALYDRAFT_477772 [Arabidopsis lyrata subsp. lyrata]	250	230	1.00E-101	92.0	75.6	80.8	hypothetical protein ARALYDRAFT_477772	gbpln	Arabidopsis lyrata	AT3G04950.1 | Symbols: | CONTAINS InterPro DOMAIN/s: SEC-C motif (InterPro:IPR004027); Has 583 Blast hits to 583 proteins in 248 species: Archae - 0; Bacteria - 488; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 61 (source: NCBI BLink). | chr3:1371786-1373300 FORWARD LENGTH=231	250	231	1.00E-104	92.4	76.8	81.2
Rsa1.0_00055.1.g3014.t1	emb|CAA31519.1| ACP preprotein [Brassica napus]	133	134	1.00E-55	100.8	85.7	91.7	ACP preprotein	gbpln	Brassica napus	AT3G05020.1 | Symbols: ACP1, ACP | acyl carrier protein 1 | chr3:1391863-1392878 REVERSE LENGTH=137	133	137	2.00E-52	103.0	82.0	90.2
Rsa1.0_00055.1.g3015.t1	ref|XP_002882392.1| hypothetical protein ARALYDRAFT_477790 [Arabidopsis lyrata subsp. lyrata] gi|297328232|gb|EFH58651.1| hypothetical protein ARALYDRAFT_477790 [Arabidopsis lyrata subsp. lyrata]	140	144	5.00E-56	102.9	83.6	91.4	hypothetical protein ARALYDRAFT_477790	gbpln	Arabidopsis lyrata	AT3G05070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: mRNA splicing factor, Cwf18 (InterPro:IPR013169); Has 292 Blast hits to 292 proteins in 153 species: Archae - 0; Bacteria - 0; Metazoa - 118; Fungi - 83; Plants - 38; Viruses - 11; Other Eukaryotes - 42 (source: NCBI BLink). | chr3:1416480-1417533 FORWARD LENGTH=144	140	144	3.00E-57	102.9	82.1	91.4
Rsa1.0_00055.1.g3016.t2	gb|ACY38730.1| salt-induced WD protein 1 [Brassica napus]	757	754	0	99.6	94.6	97.5	salt-induced WD protein 1	gbpln	Brassica napus	AT3G05090.2 | Symbols: LRS1 | Transducin/WD40 repeat-like superfamily protein | chr3:1418573-1422723 REVERSE LENGTH=753	757	753	0	99.5	91.3	95.5
Rsa1.0_00055.1.g3017.t1	ref|XP_002882393.1| hypothetical protein ARALYDRAFT_317378 [Arabidopsis lyrata subsp. lyrata] gi|297328233|gb|EFH58652.1| hypothetical protein ARALYDRAFT_317378 [Arabidopsis lyrata subsp. lyrata]	369	341	1.00E-159	92.4	77.2	82.4	hypothetical protein ARALYDRAFT_317378	gbpln	Arabidopsis lyrata	AT3G05100.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:1424155-1425667 FORWARD LENGTH=336	369	336	1.00E-156	91.1	76.4	81.6
Rsa1.0_00055.1.g3018.t1	dbj|BAJ33907.1| unnamed protein product [Thellungiella halophila]	552	595	0	107.8	91.5	93.1	unnamed protein product	----	----	AT5G60790.1 | Symbols: ATGCN1, GCN1 | ABC transporter family protein | chr5:24453760-24455767 REVERSE LENGTH=595	552	595	0	107.8	89.9	92.2
Rsa1.0_00055.1.g3019.t9	ref|XP_002866393.1| hypothetical protein ARALYDRAFT_332324 [Arabidopsis lyrata subsp. lyrata] gi|297312228|gb|EFH42652.1| hypothetical protein ARALYDRAFT_332324 [Arabidopsis lyrata subsp. lyrata]	394	1109	1.00E-172	281.5	80.2	84.8	hypothetical protein ARALYDRAFT_332324	gbpln	Arabidopsis lyrata	AT5G60740.1 | Symbols: | ABC transporter family protein | chr5:24425824-24430269 REVERSE LENGTH=1109	394	1109	1.00E-174	281.5	79.9	84.5
Rsa1.0_00055.1.g3020.t1	gb|EOA20112.1| hypothetical protein CARUB_v10000391mg [Capsella rubella]	416	672	1.00E-139	161.5	64.4	75.5	hypothetical protein CARUB_v10000391mg	gbpln	Capsella rubella	AT3G62310.1 | Symbols: | RNA helicase family protein | chr3:23057516-23060561 REVERSE LENGTH=726	416	726	1.00E-137	174.5	63.2	76.9

Rsa1.0_00055.1.g3021.t1	gb|EOA32865.1| hypothetical protein CARUB_v10016180mg [Capsella rubella]	71	922	1.00E-13	1298.6	62.0	74.6	hypothetical protein CARUB_v10016180mg	gbpln	Capsella rubella	AT3G03710.1 | Symbols: RIF10, PNP | polyribonucleotide nucleotidyltransferase, putative | chr3:919542-924906 FORWARD LENGTH=922	71	922	1.00E-13	1298.6	63.4	70.4
Rsa1.0_00055.1.g3022.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00055.1.g3023.t1	ref|XP_002884492.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330332|gb|EFH60751.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	501	469	0	93.6	79.6	86.0	kinase family protein	gbpln	Arabidopsis lyrata	AT3G05140.1 | Symbols: RBK2 | ROP binding protein kinases 2 | chr3:1435817-1437800 REVERSE LENGTH=460	501	460	0	91.8	77.8	84.6
Rsa1.0_00055.1.g3024.t1	ref|NP_566249.1| E3 ubiquitin-protein ligase ATL6 [Arabidopsis thaliana] gi|68565231|sp|Q8RXX9.2|ATL6_ARATH RecName: Full=E3 ubiquitin-protein ligase ATL6; AltName: Full=RING-H2 finger protein ATL6; Flags: Precursor gi|70905101|gb|AAZ14076.1| At3g05200 [Arabidopsis thaliana] gi|332640683|gb|AEE74204.1| E3 ubiquitin-protein ligase ATL6 [Arabidopsis thaliana]	384	398	0	103.6	87.2	91.7	E3 ubiquitin-protein ligase ATL6	gbpln	Arabidopsis thaliana	AT3G05200.1 | Symbols: ATL6 | RING/U-box superfamily protein | chr3:1477377-1478573 FORWARD LENGTH=398	384	398	0	103.6	87.2	91.7
Rsa1.0_00055.1.g3025.t1	gb|EOA30233.1| hypothetical protein CARUB_v10013356mg [Capsella rubella]	501	565	1.00E-55	112.8	63.1	68.7	hypothetical protein CARUB_v10013356mg	gbpln	Capsella rubella	AT3G05220.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1488808-1491171 FORWARD LENGTH=577	501	577	8.00E-43	115.2	23.8	25.7
Rsa1.0_00055.1.g3026.t1	ref|XP_002882405.1| signal peptidase subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297328245|gb|EFH58664.1| signal peptidase subunit family protein [Arabidopsis lyrata subsp. lyrata]	167	167	8.00E-89	100.0	92.2	97.0	signal peptidase subunit family protein	gbpln	Arabidopsis lyrata	AT3G05230.1 | Symbols: | Signal peptidase subunit | chr3:1492304-1493452 FORWARD LENGTH=167	167	167	3.00E-90	100.0	91.0	97.0
Rsa1.0_00055.1.g3027.t1	ref|NP_566558.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75274278|sp|Q9LUQ9.1|FBK56_ARATH RecName: Full=F-box/kelch-repeat protein At3g16740 gi|11994629|dbj|BAB02766.1| unnamed protein product [Arabidopsis thaliana] gi|28466967|gb|AAO44092.1| At3g16740 [Arabidopsis thaliana] gi|110743773|dbj|BAE99722.1| hypothetical protein [Arabidopsis thaliana] gi|332642338|gb|AEE75859.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	396	391	1.00E-122	98.7	59.1	74.0	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G16740.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:5699476-5700651 FORWARD LENGTH=391	396	391	1.00E-124	98.7	59.1	74.0
Rsa1.0_00055.1.g3028.t1	ref|NP_187179.2| Integral membrane Yip1-like protein [Arabidopsis thaliana] gi|26452921|dbj|BAC43538.1| unknown protein [Arabidopsis thaliana] gi|28973139|gb|AAO63894.1| unknown protein [Arabidopsis thaliana] gi|332640694|gb|AEE74215.1| Integral membrane Yip1-like protein [Arabidopsis thaliana]	445	281	1.00E-149	63.1	60.2	62.2	Integral membrane Yip1-like protein	gbpln	Arabidopsis thaliana	AT3G05280.1 | Symbols: | Integral membrane Yip1 family protein | chr3:1503992-1505554 REVERSE LENGTH=281	445	281	1.00E-152	63.1	60.2	62.2
Rsa1.0_00055.1.g3029.t1	ref|XP_002884499.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297330339|gb|EFH60758.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	321	322	1.00E-156	100.3	87.9	93.1	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT3G05290.1 | Symbols: PNC1 | peroxisomal adenine nucleotide carrier 1 | chr3:1506129-1507614 REVERSE LENGTH=322	321	322	1.00E-158	100.3	87.2	93.1
Rsa1.0_00055.1.g3030.t3	ref|XP_002882407.1| hypothetical protein ARALYDRAFT_477819 [Arabidopsis lyrata subsp. lyrata] gi|297328247|gb|EFH58666.1| hypothetical protein ARALYDRAFT_477819 [Arabidopsis lyrata subsp. lyrata]	641	647	0	100.9	62.1	78.0	hypothetical protein ARALYDRAFT_477819	gbpln	Arabidopsis lyrata	AT3G05310.1 | Symbols: MIRO3 | MIRO-related GTP-ase 3 | chr3:1510160-1513301 FORWARD LENGTH=648	641	648	0	101.1	61.0	77.7
Rsa1.0_00055.1.g3031.t1	ref|XP_002882412.1| acyl-CoA binding protein 4, acyl-CoA-binding domain 4 [Arabidopsis lyrata subsp. lyrata] gi|297328252|gb|EFH58671.1| acyl-CoA binding protein 4, acyl-CoA-binding domain 4 [Arabidopsis lyrata subsp. lyrata]	267	669	1.00E-127	250.6	80.9	87.6	acyl-CoA binding protein 4, acyl-CoA-binding domain 4	gbpln	Arabidopsis lyrata	AT3G05420.1 | Symbols: ACBP4 | acyl-CoA binding protein 4 | chr3:1561880-1567047 FORWARD LENGTH=668	267	668	1.00E-128	250.2	80.1	88.0
Rsa1.0_00055.1.g3032.t3	gb|ACP30603.1| disease resistance protein [Brassica rapa subsp. pekinensis]	2468	1056	0	42.8	31.5	34.8	disease resistance protein	gbpln	Brassica rapa	AT5G18370.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6085036-6088926 REVERSE LENGTH=1210	2468	1210	0	49.0	22.6	29.1

Rsa1.0_00055.1.g3033.t22	ref|NP_187219.5| embryo defective 2016 protein [Arabidopsis thaliana] gi|332640756|gb|AEE74277.1| embryo defective 2016 protein [Arabidopsis thaliana]	2601	2138	0	82.2	71.4	75.3	embryo defective 2016 protein	gbpln	Arabidopsis thaliana	AT3G05680.1 | Symbols: EMB2016 | embryo defective 2016 | chr3:1660802-1672015 REVERSE LENGTH=2138	2601	2138	0	82.2	71.4	75.3
Rsa1.0_00055.1.g3034.t1	emb|CAA74049.1| Transcription factor [Arabidopsis thaliana]	286	295	1.00E-128	103.1	80.1	86.4	Transcription factor	gbpln	Arabidopsis thaliana	AT3G05690.1 | Symbols: UNE8, ATHAP2B, HAP2B, NF-YA2 | nuclear factor Y, subunit A2 | chr3:1676922-1678324 REVERSE LENGTH=295	286	295	1.00E-130	103.1	80.1	86.4
Rsa1.0_00055.1.g3035.t1	gb|EOA32343.1| hypothetical protein CARUB_v10015609mg [Capsella rubella]	454	444	3.00E-56	97.8	33.5	43.6	hypothetical protein CARUB_v10015609mg	gbpln	Capsella rubella	AT3G05770.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G54300.1); Has 105 Blast hits to 105 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 99; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr3:1710328-1712165 REVERSE LENGTH=410	454	410	3.00E-54	90.3	30.6	35.5
Rsa1.0_00055.1.g3036.t1	ref|NP_566260.1| transcription factor bHLH150 [Arabidopsis thaliana] gi|75191236|sp|Q9M9L6.1|BH150_ARATH RecName: Full=Transcription factor bHLH150; AltName: Full=ATBS1 interacting factor 1; AltName: Full=Basic helix-loop-helix protein 150; Short=AtbHLH150; Short=bHLH 150; AltName: Full=Transcription factor EN 145; AltName: Full=bHLH transcription factor bHLH150 gi|6714393|gb|AAF26082.1|AC012393_8 hypothetical protein [Arabidopsis thaliana] gi|21554259|gb|AAM63334.1| unknown [Arabidopsis thaliana] gi|51971903|dbj|BAD44616.1| unknown protein [Arabidopsis thaliana] gi|94442469|gb|ABF19022.1| At3g05800 [Arabidopsis thaliana] gi|225898621|dbj|BAH30441.1| hypothetical protein [Arabidopsis thaliana] gi|332640777|gb|AEE74298.1| transcription factor bHLH150 [Arabidopsis thaliana]	182	211	2.00E-61	115.9	78.0	84.1	transcription factor bHLH150	gbpln	Arabidopsis thaliana	AT3G05800.1 | Symbols: AIF1 | AtBS1(activation-tagged BRI1 suppressor 1)-interacting factor 1 | chr3:1727476-1728111 FORWARD LENGTH=211	182	211	8.00E-64	115.9	78.0	84.1
Rsa1.0_00055.1.g3037.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00055.1.g3038.t1	ref|XP_002882438.1| hypothetical protein ARALYDRAFT_477878 [Arabidopsis lyrata subsp. lyrata] gi|297328278|gb|EFH58697.1| hypothetical protein ARALYDRAFT_477878 [Arabidopsis lyrata subsp. lyrata]	476	409	0	85.9	80.3	82.6	hypothetical protein ARALYDRAFT_477878	gbpln	Arabidopsis lyrata	AT3G05840.1 | Symbols: ATSK12 | Protein kinase superfamily protein | chr3:1740793-1742927 FORWARD LENGTH=409	476	409	0	85.9	79.8	82.4
Rsa1.0_00055.1.g3039.t1	ref|XP_002882439.1| hypothetical protein ARALYDRAFT_896682 [Arabidopsis lyrata subsp. lyrata] gi|297328279|gb|EFH58698.1| hypothetical protein ARALYDRAFT_896682 [Arabidopsis lyrata subsp. lyrata]	90	90	1.00E-39	100.0	93.3	95.6	hypothetical protein ARALYDRAFT_896682	gbpln	Arabidopsis lyrata	AT3G05858.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26620.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:1749464-1749736 FORWARD LENGTH=90	90	90	1.00E-41	100.0	92.2	93.3
Rsa1.0_00055.1.g3040.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00055.1.g3041.t1	gb|AFC41201.1| PM-YC3.6-Lti6b [Binary expression vector PM-YC3.6-LTI6b]	83	726	5.00E-15	874.7	49.4	62.7	PM-YC3.6-Lti6b	----	----	AT3G05890.1 | Symbols: RCI2B | Low temperature and salt responsive protein family | chr3:1758179-1758452 REVERSE LENGTH=54	83	54	2.00E-14	65.1	43.4	50.6
Rsa1.0_00055.1.g3042.t1	gb|AFC41201.1| PM-YC3.6-Lti6b [Binary expression vector PM-YC3.6-LTI6b]	55	726	6.00E-22	1320.0	85.5	92.7	PM-YC3.6-Lti6b	----	----	AT3G05890.1 | Symbols: RCI2B | Low temperature and salt responsive protein family | chr3:1758179-1758452 REVERSE LENGTH=54	55	54	7.00E-21	98.2	85.5	92.7

Rsa1.0_00055.1.g3043.t1	ref|NP_566263.1| Pectin lyase-like protein [Arabidopsis thaliana] gi|6671966|gb|AAF23225.1|AC013454_12 putative pectinacetylesterase [Arabidopsis thaliana] gi|16226325|gb|AAL16135.1|AF428303_1 AT3g05910/F2O10_3 [Arabidopsis thaliana] gi|15292827|gb|AAK92782.1| putative pectinacetylesterase [Arabidopsis thaliana] gi|20465793|gb|AAM20385.1| putative pectinacetylesterase [Arabidopsis thaliana] gi|332640793|gb|AEE74314.1| Pectin lyase-like protein [Arabidopsis thaliana]	416	415	0	99.8	93.0	96.6	Pectin lyase-like protein	gbpln	Arabidopsis thaliana	AT3G05910.1 | Symbols: | Pectinacetylesterase family protein | chr3:1764509-1767240 REVERSE LENGTH=415	416	415	0	99.8	93.0	96.6
Rsa1.0_00055.1.g3044.t1	ref|XP_002882441.1| hypothetical protein ARALYDRAFT_896692 [Arabidopsis lyrata subsp. lyrata] gi|297328281|gb|EFH58700.1| hypothetical protein ARALYDRAFT_896692 [Arabidopsis lyrata subsp. lyrata]	218	219	9.00E-97	100.5	80.7	88.5	hypothetical protein ARALYDRAFT_896692	gbpln	Arabidopsis lyrata	AT3G05930.1 | Symbols: GLP8 | germin-like protein 8 | chr3:1770377-1771183 FORWARD LENGTH=219	218	219	2.00E-98	100.5	80.3	88.5
Rsa1.0_00055.1.g3045.t1	ref|XP_002884544.1| hypothetical protein ARALYDRAFT_896695 [Arabidopsis lyrata subsp. lyrata] gi|297330384|gb|EFH60803.1| hypothetical protein ARALYDRAFT_896695 [Arabidopsis lyrata subsp. lyrata]	103	101	2.00E-21	98.1	80.6	82.5	hypothetical protein ARALYDRAFT_896695	gbpln	Arabidopsis lyrata	AT5G26731.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:9295676-9295975 FORWARD LENGTH=99	103	99	4.00E-17	96.1	44.7	53.4
Rsa1.0_00055.1.g3046.t1	ref|NP_198008.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana] gi|27754225|gb|AAO22566.1| putative chaperonin gamma chain [Arabidopsis thaliana] gi|332006171|gb|AED93554.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]	559	555	0	99.3	94.1	97.5	TCP-1/cpn60 chaperonin family protein	gbpln	Arabidopsis thaliana	AT5G26360.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr5:9255561-9258891 REVERSE LENGTH=555	559	555	0	99.3	94.1	97.5
Rsa1.0_00055.1.g3047.t1	ref|NP_187247.1| sugar transport protein 6 [Arabidopsis thaliana] gi|75337175|sp|Q9SFG0.1|STP6_ARATH RecName: Full=Sugar transport protein 6; AltName: Full=Hexose transporter 6 gi|6671961|gb|AAF23220.1|AC013454_7 putative hexose transporter [Arabidopsis thaliana] gi|15487256|emb|CAC69073.1| STP6 protein [Arabidopsis thaliana] gi|332640802|gb|AEE74323.1| sugar transport protein 6 [Arabidopsis thaliana]	508	507	0	99.8	89.0	94.7	sugar transport protein 6	gbpln	Arabidopsis thaliana	AT3G05960.1 | Symbols: ATSTP6, STP6 | sugar transporter 6 | chr3:1783587-1785334 REVERSE LENGTH=507	508	507	0	99.8	89.0	94.7
Rsa1.0_00055.1.g3048.t1	emb|CAA96522.1| AMP-binding protein [Brassica napus]	686	677	0	98.7	95.0	96.8	AMP-binding protein	gbpln	Brassica napus	AT3G05970.1 | Symbols: LACS6, ATLACS6 | long-chain acyl-CoA synthetase 6 | chr3:1786510-1791746 REVERSE LENGTH=701	686	701	0	102.2	92.9	95.5
Rsa1.0_00055.1.g3049.t1	ref|XP_002882446.1| hypothetical protein ARALYDRAFT_896708 [Arabidopsis lyrata subsp. lyrata] gi|297328286|gb|EFH58705.1| hypothetical protein ARALYDRAFT_896708 [Arabidopsis lyrata subsp. lyrata]	246	299	5.00E-63	121.5	69.5	78.5	hypothetical protein ARALYDRAFT_896708	gbpln	Arabidopsis lyrata	AT3G06020.1 | Symbols: | Protein of unknown function (DUF3049) | chr3:1813267-1814169 FORWARD LENGTH=300	246	300	3.00E-64	122.0	72.0	81.7
Rsa1.0_00055.1.g3050.t1	ref|NP_566267.1| glycoprotein membrane precursor GPI-anchored protein [Arabidopsis thaliana] gi|34395875|sp|Q84MC0.1|UGPI4_ARATH RecName: Full=Uncharacterized GPI-anchored protein At3g06035; Flags: Precursor gi|30102608|gb|AAP21222.1| At3g06035 [Arabidopsis thaliana] gi|110735967|dbj|BAE99958.1| hypothetical protein [Arabidopsis thaliana] gi|332640812|gb|AEE74333.1| glycoprotein membrane precursor GPI-anchored protein [Arabidopsis thaliana]	342	200	2.00E-70	58.5	38.3	44.2	glycoprotein membrane precursor GPI-anchored protein	gbpln	Arabidopsis thaliana	AT3G06035.1 | Symbols: | Glycoprotein membrane precursor GPI-anchored | chr3:1823172-1824110 REVERSE LENGTH=200	342	200	6.00E-73	58.5	38.3	44.2

Rsa1.0_00055.1.g3051.t1	ref|XP_002884557.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330397|gb|EFH60816.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	148	152	9.00E-52	102.7	75.0	87.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G06070.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19190.1); Has 33 Blast hits to 33 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:1831305-1831846 REVERSE LENGTH=151	148	151	4.00E-52	102.0	74.3	85.8
Rsa1.0_00055.1.g3052.t1	gb|EOA30487.1| hypothetical protein CARUB_v10013611mg [Capsella rubella]	458	473	0	103.3	84.9	91.5	hypothetical protein CARUB_v10013611mg	gbpln	Capsella rubella	AT3G06080.2 | Symbols: | Plant protein of unknown function (DUF828) | chr3:1834959-1837524 REVERSE LENGTH=469	458	469	0	102.4	83.8	90.4
Rsa1.0_00055.1.g3053.t1	ref|NP_187263.1| transcription factor MUTE [Arabidopsis thaliana] gi|75312289|sp|Q9M8K6.1|MUTE_ARATH RecName: Full=Transcription factor MUTE; AltName: Full=Basic helix-loop-helix protein 45; Short=AtbHLH45; Short=bHLH 45; AltName: Full=Transcription factor EN 20; AltName: Full=bHLH transcription factor bHLH045 gi|6862916|gb|AAF30305.1|AC018907_5 putative helix-loop-helix DNA-binding protein [Arabidopsis thaliana] gi|91806385|gb|ABE65920.1| basic helix-loop-helix family protein [Arabidopsis thaliana] gi|113206517|gb|ABI34465.1| basic helix-loop-helix protein [Arabidopsis thaliana] gi|114446460|gb|ABI74926.1| helix-loop-helix protein [Arabidopsis thaliana] gi|332640826|gb|AEE74347.1| transcription factor MUTE [Arabidopsis thaliana]	205	202	1.00E-102	98.5	91.2	95.1	transcription factor MUTE	gbpln	Arabidopsis thaliana	AT3G06120.1 | Symbols: MUTE | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:1846531-1848016 FORWARD LENGTH=202	205	202	1.00E-104	98.5	91.2	95.1
Rsa1.0_00055.1.g3054.t1	ref|XP_002884560.1| hypothetical protein ARALYDRAFT_477915 [Arabidopsis lyrata subsp. lyrata] gi|297330400|gb|EFH60819.1| hypothetical protein ARALYDRAFT_477915 [Arabidopsis lyrata subsp. lyrata]	469	445	1.00E-68	94.9	38.0	41.6	hypothetical protein ARALYDRAFT_477915	gbpln	Arabidopsis lyrata	AT3G06130.2 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1853193-1854673 REVERSE LENGTH=349	469	349	5.00E-66	74.4	36.7	40.5
Rsa1.0_00055.1.g3055.t1	ref|NP_187266.1| uncharacterized protein [Arabidopsis thaliana] gi|6862919|gb|AAF30308.1|AC018907_8 unknown protein [Arabidopsis thaliana] gi|332640832|gb|AEE74353.1| uncharacterized protein AT3G06150 [Arabidopsis thaliana]	586	594	0	101.4	80.5	89.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G06150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19060.1); Has 61 Blast hits to 59 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:1861971-1863755 REVERSE LENGTH=594	586	594	0	101.4	80.5	89.8
Rsa1.0_00055.1.g3056.t1	gb|EOA30708.1| hypothetical protein CARUB_v10013845mg [Capsella rubella]	400	407	0	101.8	93.0	96.5	hypothetical protein CARUB_v10013845mg	gbpln	Capsella rubella	AT3G06190.1 | Symbols: ATBPM2, BPM2 | BTB-POZ and MATH domain 2 | chr3:1874577-1876575 REVERSE LENGTH=406	400	406	0	101.5	91.5	95.5
Rsa1.0_00055.1.g3057.t1	ref|NP_566277.2| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75151183|sp|Q8GXC7.1|FBK50_ARATH RecName: Full=F-box/kelch-repeat protein At3g06240 gi|26451648|dbj|BAC42921.1| unknown protein [Arabidopsis thaliana] gi|29824145|gb|AAP04033.1| putative F-box protein family [Arabidopsis thaliana] gi|332640843|gb|AEE74364.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	405	427	1.00E-127	105.4	61.7	74.6	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G06240.1 | Symbols: | F-box family protein | chr3:1887336-1888619 FORWARD LENGTH=427	405	427	1.00E-129	105.4	61.7	74.6
Rsa1.0_00055.1.g3058.t1	ref|NP_566277.2| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75151183|sp|Q8GXC7.1|FBK50_ARATH RecName: Full=F-box/kelch-repeat protein At3g06240 gi|26451648|dbj|BAC42921.1| unknown protein [Arabidopsis thaliana] gi|29824145|gb|AAP04033.1| putative F-box protein family [Arabidopsis thaliana] gi|332640843|gb|AEE74364.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	411	427	1.00E-144	103.9	67.9	78.8	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G06240.1 | Symbols: | F-box family protein | chr3:1887336-1888619 FORWARD LENGTH=427	411	427	2.33E-156	103.9	67.9	78.8

Rsa1.0_00055.1.g3059.t1	ref|XP_002869401.1| aspartyl protease family [Arabidopsis lyrata subsp. lyrata] gi|297315237|gb|EFH45660.1| aspartyl protease family [Arabidopsis lyrata subsp. lyrata]	399	438	1.00E-35	109.8	28.3	42.9	aspartyl protease family	gbpln	Arabidopsis lyrata	AT4G30030.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr4:14682210-14683484 REVERSE LENGTH=424	399	424	6.00E-31	106.3	25.6	41.9
Rsa1.0_00055.1.g3060.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	137	1197	2.00E-13	873.7	27.7	46.7	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00055.1.g3061.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	153	1311	1.00E-14	856.9	30.1	43.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	153	303	2.00E-11	198.0	27.5	44.4
Rsa1.0_00055.1.g3062.t1	ref|XP_002882653.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328493|gb|EFH58912.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	260	173	4.00E-20	66.5	26.9	36.2	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00055.1.g3063.t1	ref|NP_187318.2| fip1 motif-containing protein [Arabidopsis thaliana] gi|334185148|ref|NP_001189830.1| fip1 motif-containing protein [Arabidopsis thaliana] gi|332640906|gb|AEE74427.1| fip1 motif-containing protein [Arabidopsis thaliana] gi|332640907|gb|AEE74428.1| fip1 motif-containing protein [Arabidopsis thaliana]	991	997	0	100.6	58.1	68.5	fip1 motif-containing protein	gbpln	Arabidopsis thaliana	AT3G66652.2 | Symbols: | fip1 motif-containing protein | chr3:2084030-2087556 FORWARD LENGTH=997	991	997	0	100.6	58.1	68.5
Rsa1.0_00056.1.g3064.t1	dbj|BAH56865.1| AT5G61660 [Arabidopsis thaliana]	141	113	1.00E-25	80.1	62.4	64.5	AT5G61660	gbpln	Arabidopsis thaliana	AT5G61660.1 | Symbols: | glycine-rich protein | chr5:24779458-24779862 REVERSE LENGTH=134	141	134	1.00E-27	95.0	42.6	44.7
Rsa1.0_00056.1.g3065.t1	gb|ADF57182.1| AP2/ERF transcription factor [Brassica napus]	204	200	2.00E-87	98.0	83.8	89.2	AP2/ERF transcription factor	gbpln	Brassica napus	AT5G61590.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:24764653-24765258 REVERSE LENGTH=201	204	201	1.00E-84	98.5	83.3	87.7
Rsa1.0_00056.1.g3066.t1	gb|EOA14619.1| hypothetical protein CARUB_v10027877mg [Capsella rubella]	264	849	1.00E-142	321.6	92.0	95.1	hypothetical protein CARUB_v10027877mg	gbpln	Capsella rubella	AT5G61550.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:24748325-24751558 FORWARD LENGTH=845	264	845	1.00E-139	320.1	88.6	93.6
Rsa1.0_00056.1.g3067.t7	gb|EOA14619.1| hypothetical protein CARUB_v10027877mg [Capsella rubella]	794	849	0	106.9	81.4	87.8	hypothetical protein CARUB_v10027877mg	gbpln	Capsella rubella	AT5G61550.2 | Symbols: | U-box domain-containing protein kinase family protein | chr5:24748325-24751805 FORWARD LENGTH=860	794	860	0	108.3	78.2	86.9
Rsa1.0_00056.1.g3068.t1	ref|XP_002864736.1| small G protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297310571|gb|EFH40995.1| small G protein family protein [Arabidopsis lyrata subsp. lyrata]	376	376	0	100.0	93.4	96.8	small G protein family protein	gbpln	Arabidopsis lyrata	AT5G61530.1 | Symbols: | small G protein family protein / RhoGAP family protein | chr5:24742630-24744586 FORWARD LENGTH=376	376	376	0	100.0	91.5	96.0
Rsa1.0_00056.1.g3069.t2	gb|EOA15037.1| hypothetical protein CARUB_v10028392mg [Capsella rubella]	411	400	0	97.3	85.2	90.5	hypothetical protein CARUB_v10028392mg	gbpln	Capsella rubella	AT5G61510.1 | Symbols: | GroES-like zinc-binding alcohol dehydrogenase family protein | chr5:24737084-24738975 REVERSE LENGTH=406	411	406	0	98.8	86.6	90.8
Rsa1.0_00056.1.g3070.t2	gb|AAO85536.1| terpene synthase [Arabidopsis thaliana]	546	603	0	110.4	60.4	79.7	terpene synthase	gbpln	Arabidopsis thaliana	AT3G29410.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr3:11302574-11305060 REVERSE LENGTH=603	546	603	0	110.4	61.0	78.8
Rsa1.0_00056.1.g3071.t1	gb|ACR48179.1| MYB domain protein 28-2 [Brassica rapa subsp. pekinensis]	361	357	0	98.9	90.6	93.1	MYB domain protein 28-2	gbpln	Brassica rapa	AT5G61420.2 | Symbols: MYB28, HAG1 | myb domain protein 28 | chr5:24689475-24690795 REVERSE LENGTH=366	361	366	1.00E-166	101.4	80.9	88.6
Rsa1.0_00056.1.g3072.t1	#	#	#	#	#	#	#	-	----	----	AT5G61412.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G33145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:24686761-24686994 REVERSE LENGTH=77	76	77	3.00E-13	101.3	43.4	46.1
Rsa1.0_00056.1.g3073.t1	ref|XP_002864731.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310566|gb|EFH40990.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	645	732	0	113.5	76.4	86.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G61400.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:24681550-24683514 FORWARD LENGTH=654	645	654	0	101.4	76.0	85.4
Rsa1.0_00056.1.g3074.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00056.1.g3075.t1	ref|NP_200947.3| exonuclease-like protein [Arabidopsis thaliana] gi|111074224|gb|ABH04485.1| At5g61390 [Arabidopsis thaliana] gi|332010078|gb|AED97461.1| exonuclease-like protein [Arabidopsis thaliana]	335	487	1.00E-145	145.4	77.3	84.8	exonuclease-like protein	gbpln	Arabidopsis thaliana	AT5G61390.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:24678802-24680857 REVERSE LENGTH=487	335	487	1.00E-148	145.4	77.3	84.8
Rsa1.0_00056.1.g3076.t1	gb|ADA58344.1| pseudo-response regulator 1b [Brassica rapa]	549	509	0	92.7	83.6	86.2	pseudo-response regulator 1b	gbpln	Brassica rapa	AT5G61380.1 | Symbols: TOC1, APRR1, PRR1, AtTOC1 | CCT motif -containing response regulator protein | chr5:24675540-24678176 FORWARD LENGTH=618	549	618	0	112.6	84.3	89.8
Rsa1.0_00056.1.g3077.t1	gb|EOA14352.1| hypothetical protein CARUB_v10027533mg [Capsella rubella]	836	842	0	100.7	88.2	93.9	hypothetical protein CARUB_v10027533mg	gbpln	Capsella rubella	AT5G61350.1 | Symbols: | Protein kinase superfamily protein | chr5:24667973-24670501 FORWARD LENGTH=842	836	842	0	100.7	87.6	92.9
Rsa1.0_00056.1.g3078.t1	gb|EOA13720.1| hypothetical protein CARUB_v10026789mg [Capsella rubella]	319	322	1.00E-131	100.9	80.3	89.7	hypothetical protein CARUB_v10026789mg	gbpln	Capsella rubella	AT5G61340.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26650.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:24662064-24663044 REVERSE LENGTH=326	319	326	1.00E-132	102.2	82.4	89.7
Rsa1.0_00056.1.g3079.t1	gb|EOA15044.1| hypothetical protein CARUB_v10028402mg [Capsella rubella]	190	447	2.00E-19	235.3	23.7	24.7	hypothetical protein CARUB_v10028402mg	gbpln	Capsella rubella	AT5G61330.1 | Symbols: | rRNA processing protein-related | chr5:24657287-24660103 REVERSE LENGTH=436	190	436	3.00E-21	229.5	23.2	23.7
Rsa1.0_00056.1.g3080.t1	gb|EOA13427.1| hypothetical protein CARUB_v10026466mg [Capsella rubella]	390	423	1.00E-82	108.5	51.5	65.4	hypothetical protein CARUB_v10026466mg	gbpln	Capsella rubella	AT5G62510.1 | Symbols: | F-box family protein | chr5:25095373-25096635 REVERSE LENGTH=420	390	420	3.00E-80	107.7	49.2	62.6
Rsa1.0_00056.1.g3081.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00056.1.g3082.t1	gb|AGJ70091.1| LRR-like disease resistance protein [Brassica oleracea var. italica]	327	326	1.00E-178	99.7	93.3	95.4	LRR-like disease resistance protein	gbpln	Brassica oleracea	AT5G61240.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:24629485-24631958 FORWARD LENGTH=326	327	326	1.00E-179	99.7	92.0	95.1
Rsa1.0_00056.1.g3083.t1	gb|EOA14101.1| hypothetical protein CARUB_v10027241mg [Capsella rubella]	241	173	4.00E-81	71.8	60.2	63.1	hypothetical protein CARUB_v10027241mg	gbpln	Capsella rubella	AT5G61230.1 | Symbols: | Ankyrin repeat family protein | chr5:24628254-24628778 FORWARD LENGTH=174	241	174	5.00E-81	72.2	58.1	61.4
Rsa1.0_00056.1.g3084.t2	ref|XP_002864722.1| hypothetical protein ARALYDRAFT_496271 [Arabidopsis lyrata subsp. lyrata] gi|297310557|gb|EFH40981.1| hypothetical protein ARALYDRAFT_496271 [Arabidopsis lyrata subsp. lyrata]	707	955	1.00E-165	135.1	59.1	68.7	hypothetical protein ARALYDRAFT_496271	gbpln	Arabidopsis lyrata	AT5G61190.1 | Symbols: | putative endonuclease or glycosyl hydrolase with C2H2-type zinc finger domain | chr5:24615480-24619886 FORWARD LENGTH=995	707	995	1.00E-143	140.7	50.4	59.7
Rsa1.0_00056.1.g3085.t1	gb|EOA14082.1| hypothetical protein CARUB_v10027219mg, partial [Capsella rubella]	143	180	1.00E-75	125.9	95.8	96.5	hypothetical protein CARUB_v10027219mg, partial	gbpln	Capsella rubella	AT5G61170.1 | Symbols: | Ribosomal protein S19e family protein | chr5:24611158-24612202 FORWARD LENGTH=143	143	143	9.00E-78	100.0	96.5	96.5
Rsa1.0_00056.1.g3086.t2	gb|EOA13076.1| hypothetical protein CARUB_v10026081mg [Capsella rubella]	661	626	0	94.7	76.7	83.1	hypothetical protein CARUB_v10026081mg	gbpln	Capsella rubella	AT5G61150.2 | Symbols: VIP4 | leo1-like family protein | chr5:24603846-24607528 REVERSE LENGTH=623	661	623	0	94.3	75.6	82.6
Rsa1.0_00056.1.g3087.t1	gb|EOA14034.1| hypothetical protein CARUB_v10027167mg [Capsella rubella]	199	198	3.00E-78	99.5	76.4	84.4	hypothetical protein CARUB_v10027167mg	gbpln	Capsella rubella	AT5G61130.1 | Symbols: PDCB1 | plasmodesmata callose-binding protein 1 | chr5:24587438-24589369 REVERSE LENGTH=201	199	201	1.00E-67	101.0	74.4	80.4
Rsa1.0_00056.1.g3088.t1	ref|XP_002866412.1| hypothetical protein ARALYDRAFT_919345 [Arabidopsis lyrata subsp. lyrata] gi|297312247|gb|EFH42671.1| hypothetical protein ARALYDRAFT_919345 [Arabidopsis lyrata subsp. lyrata]	681	660	0	96.9	79.0	85.5	hypothetical protein ARALYDRAFT_919345	gbpln	Arabidopsis lyrata	AT5G61060.1 | Symbols: HDA05, HDA5, ATHDA5 | histone deacetylase 5 | chr5:24567137-24570917 REVERSE LENGTH=660	681	660	0	96.9	78.1	85.3
Rsa1.0_00056.1.g3089.t1	ref|XP_002866412.1| hypothetical protein ARALYDRAFT_919345 [Arabidopsis lyrata subsp. lyrata] gi|297312247|gb|EFH42671.1| hypothetical protein ARALYDRAFT_919345 [Arabidopsis lyrata subsp. lyrata]	223	660	8.00E-96	296.0	73.1	84.3	hypothetical protein ARALYDRAFT_919345	gbpln	Arabidopsis lyrata	AT5G61060.2 | Symbols: HDA05 | histone deacetylase 5 | chr5:24567137-24570917 REVERSE LENGTH=664	223	664	3.00E-98	297.8	74.0	84.3
Rsa1.0_00056.1.g3090.t1	gb|EOA13791.1| hypothetical protein CARUB_v10026886mg [Capsella rubella]	254	295	5.00E-55	116.1	41.3	44.9	hypothetical protein CARUB_v10026886mg	gbpln	Capsella rubella	AT5G61030.1 | Symbols: GR-RBP3 | glycine-rich RNA-binding protein 3 | chr5:24560870-24562152 FORWARD LENGTH=309	254	309	2.00E-55	121.7	41.3	45.7

Rsa1.0_00056.1.g3091.t1	ref|NP_200908.1| Replication factor-A protein 1-like protein [Arabidopsis thaliana] gi|10177323|dbj|BAB10649.1| replication protein A1 [Arabidopsis thaliana] gi|28393124|gb|AAO41995.1| putative RNA helicase [Arabidopsis thaliana] gi|332010026|gb|AED97409.1| Replication factor-A protein 1-like protein [Arabidopsis thaliana]	626	629	0	100.5	90.3	95.7	Replication factor-A protein 1-like protein	gbpln	Arabidopsis thaliana	AT5G61000.1 | Symbols: RPA70D, ATRPA70D | Replication factor-A protein 1-related | chr5:24549682-24552641 REVERSE LENGTH=629	626	629	0	100.5	90.3	95.7
Rsa1.0_00056.1.g3092.t1	ref|NP_200906.2| nuclear transport factor 2 and RNA recognition motif domain-containing protein [Arabidopsis thaliana] gi|10177321|dbj|BAB10647.1| unnamed protein product [Arabidopsis thaliana] gi|17063173|gb|AAL32982.1| AT5g60980/MSL3_100 [Arabidopsis thaliana] gi|27764908|gb|AAO23575.1| At5g60980/MSL3_100 [Arabidopsis thaliana] gi|332010024|gb|AED97407.1| nuclear transport factor 2 and RNA recognition motif domain-containing protein [Arabidopsis thaliana]	460	460	1.00E-171	100.0	77.8	84.3	nuclear transport factor 2 and RNA recognition motif domain-containing protein	gbpln	Arabidopsis thaliana	AT5G60980.2 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr5:24543988-24546027 FORWARD LENGTH=460	460	460	1.00E-173	100.0	77.8	84.3
Rsa1.0_00056.1.g3093.t1	gb|EOA13591.1| hypothetical protein CARUB_v10026656mg [Capsella rubella]	341	359	1.00E-145	105.3	83.0	88.3	hypothetical protein CARUB_v10026656mg	gbpln	Capsella rubella	AT5G60970.1 | Symbols: TCP5 | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 5 | chr5:24535570-24536652 REVERSE LENGTH=360	341	360	1.00E-138	105.6	80.6	86.8
Rsa1.0_00056.1.g3094.t1	gb|EOA14836.1| hypothetical protein CARUB_v10028146mg [Capsella rubella]	206	204	3.00E-89	99.0	75.7	82.5	hypothetical protein CARUB_v10028146mg	gbpln	Capsella rubella	AT5G60950.1 | Symbols: COBL5 | COBRA-like protein 5 precursor | chr5:24527157-24528005 REVERSE LENGTH=204	206	204	3.00E-89	99.0	74.8	84.0
Rsa1.0_00056.1.g3095.t1	gb|EOA13179.1| hypothetical protein CARUB_v10026206mg, partial [Capsella rubella]	456	537	0	117.8	92.8	96.3	hypothetical protein CARUB_v10026206mg, partial	gbpln	Capsella rubella	AT5G60920.1 | Symbols: COB | COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family | chr5:24511466-24513932 REVERSE LENGTH=456	456	456	0	100.0	90.8	94.1
Rsa1.0_00056.1.g3096.t3	ref|XP_002889590.1| hypothetical protein ARALYDRAFT_887817 [Arabidopsis lyrata subsp. lyrata] gi|297335432|gb|EFH65849.1| hypothetical protein ARALYDRAFT_887817 [Arabidopsis lyrata subsp. lyrata]	431	341	2.00E-53	79.1	32.5	37.6	hypothetical protein ARALYDRAFT_887817	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00056.1.g3097.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	522	1164	1.00E-105	223.0	37.4	54.6	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	522	746	2.00E-51	142.9	23.9	36.4
Rsa1.0_00056.1.g3098.t1	emb|CAD47852.1| MADS-box protein FUL-d [Brassica oleracea var. botrytis] gi|89279392|gb|ABD67165.1| Ful-like protein [Brassica napus]	162	242	4.00E-85	149.4	98.1	98.1	MADS-box protein FUL-d	gbpln	Brassica napus	AT5G60910.1 | Symbols: AGL8, FUL | AGAMOUS-like 8 | chr5:24502736-24506013 REVERSE LENGTH=242	162	242	2.00E-86	149.4	96.3	97.5
Rsa1.0_00056.1.g3099.t1	sp|Q39202.2|RLK1_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase RLK1; AltName: Full=Receptor-like protein kinase 1; Flags: Precursor	821	832	0	101.3	68.5	79.4	RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase RLK1; AltName: Full=Receptor-like protein kinase 1; Flags: Precursor	----	----	AT5G60900.1 | Symbols: RLK1 | receptor-like protein kinase 1 | chr5:24498467-24501494 REVERSE LENGTH=748	821	748	0	91.1	64.3	74.1
Rsa1.0_00056.1.g3100.t1	ref|XP_002866401.1| hypothetical protein ARALYDRAFT_496241 [Arabidopsis lyrata subsp. lyrata] gi|297312236|gb|EFH42660.1| hypothetical protein ARALYDRAFT_496241 [Arabidopsis lyrata subsp. lyrata]	467	758	1.00E-162	162.3	64.5	73.4	hypothetical protein ARALYDRAFT_496241	gbpln	Arabidopsis lyrata	AT5G60900.1 | Symbols: RLK1 | receptor-like protein kinase 1 | chr5:24498467-24501494 REVERSE LENGTH=748	467	748	1.00E-152	160.2	60.2	70.4
Rsa1.0_00056.1.g3101.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00056.1.g3102.t1	gb|ACR48184.1| MYB domain protein 34-1 [Brassica rapa subsp. pekinensis]	299	302	1.00E-143	101.0	87.0	91.6	MYB domain protein 34-1	gbpln	Brassica rapa	AT5G60890.1 | Symbols: ATMYB34, ATR1, MYB34 | myb domain protein 34 | chr5:24495029-24496220 FORWARD LENGTH=295	299	295	1.00E-117	98.7	75.3	82.6
Rsa1.0_00056.1.g3103.t1	ref|XP_002866400.1| hypothetical protein ARALYDRAFT_919327 [Arabidopsis lyrata subsp. lyrata] gi|297312235|gb|EFH42659.1| hypothetical protein ARALYDRAFT_919327 [Arabidopsis lyrata subsp. lyrata]	255	264	7.00E-91	103.5	80.0	85.9	hypothetical protein ARALYDRAFT_919327	gbpln	Arabidopsis lyrata	AT5G60880.1 | Symbols: BASL | breaking of asymmetry in the stomatal lineage | chr5:24488553-24489703 REVERSE LENGTH=262	255	262	4.00E-92	102.7	76.9	83.9

Rsa1.0_00056.1.g3104.t1	ref|NP_200893.1| Dof zinc finger protein DOF5.4 [Arabidopsis thaliana] gi|55584037|sp|Q8LDR0.2|DOF54_ARATH RecName: Full=Dof zinc finger protein DOF5.4; Short=AtDOF5.4; AltName: Full=OBF-binding protein 4 gi|10176912|dbj|BAB10105.1| zinc finger protein [Arabidopsis thaliana] gi|15912271|gb|AAL08269.1| AT5g60850/mae1_100 [Arabidopsis thaliana] gi|19547997|gb|AAL87362.1| AT5g60850/mae1_100 [Arabidopsis thaliana] gi|332010003|gb|AED97386.1| Dof zinc finger protein DOF5.4 [Arabidopsis thaliana]	252	307	2.00E-77	121.8	74.6	81.0	Dof zinc finger protein DOF5.4	gbpln	Arabidopsis thaliana	AT5G60850.1 | Symbols: OBP4 | OBF binding protein 4 | chr5:24480578-24481501 FORWARD LENGTH=307	252	307	5.00E-80	121.8	74.6	81.0
Rsa1.0_00056.1.g3105.t1	gb|EOA14747.1| hypothetical protein CARUB_v10028041mg [Capsella rubella]	183	204	1.00E-64	111.5	72.1	82.5	hypothetical protein CARUB_v10028041mg	gbpln	Capsella rubella	AT5G60830.1 | Symbols: AtbZIP70, bZIP70 | basic leucine-zipper 70 | chr5:24472639-24473319 FORWARD LENGTH=206	183	206	2.00E-65	112.6	72.1	82.0
Rsa1.0_00056.1.g3106.t1	ref|XP_002872033.1| hypothetical protein ARALYDRAFT_910314 [Arabidopsis lyrata subsp. lyrata] gi|297317870|gb|EFH48292.1| hypothetical protein ARALYDRAFT_910314 [Arabidopsis lyrata subsp. lyrata]	251	281	1.00E-101	112.0	74.5	83.3	hypothetical protein ARALYDRAFT_910314	gbpln	Arabidopsis lyrata	AT5G23070.1 | Symbols: | Thymidine kinase | chr5:7741979-7742827 FORWARD LENGTH=282	251	282	1.00E-101	112.4	75.3	83.7
Rsa1.0_00056.1.g3107.t1	ref|XP_002874111.1| hypothetical protein ARALYDRAFT_489162 [Arabidopsis lyrata subsp. lyrata] gi|297319948|gb|EFH50370.1| hypothetical protein ARALYDRAFT_489162 [Arabidopsis lyrata subsp. lyrata]	942	944	0	100.2	78.3	83.9	hypothetical protein ARALYDRAFT_489162	gbpln	Arabidopsis lyrata	AT5G23080.1 | Symbols: TGH | SWAP (Suppressor-of-White-APricot)/surp domain-containing protein | chr5:7743226-7748889 REVERSE LENGTH=930	942	930	0	98.7	80.4	86.7
Rsa1.0_00056.1.g3108.t1	ref|NP_001031927.1| protein Dr1-like protein [Arabidopsis thaliana] gi|332005738|gb|AED93121.1| protein Dr1-like protein [Arabidopsis thaliana]	163	158	9.00E-81	96.9	92.0	93.9	protein Dr1-like protein	gbpln	Arabidopsis thaliana	AT5G23090.4 | Symbols: NF-YB13 | nuclear factor Y, subunit B13 | chr5:7749391-7750203 FORWARD LENGTH=158	163	158	3.00E-83	96.9	92.0	93.9
Rsa1.0_00056.1.g3109.t1	ref|XP_002872035.1| hypothetical protein ARALYDRAFT_910318 [Arabidopsis lyrata subsp. lyrata] gi|297317872|gb|EFH48294.1| hypothetical protein ARALYDRAFT_910318 [Arabidopsis lyrata subsp. lyrata]	253	278	1.00E-113	109.9	87.4	92.9	hypothetical protein ARALYDRAFT_910318	gbpln	Arabidopsis lyrata	AT5G23100.1 | Symbols: | Protein of unknown function, DUF617 | chr5:7753557-7754390 FORWARD LENGTH=277	253	277	1.00E-111	109.5	86.6	90.1
Rsa1.0_00056.1.g3110.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00056.1.g3111.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00056.1.g3112.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	664	442	1.00E-153	66.6	39.8	47.4	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	664	343	2.00E-32	51.7	9.2	11.6
Rsa1.0_00056.1.g3113.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00056.1.g3114.t1	gb|AEF32147.1| MADS-box DNA-binding domain transcription factor [Brassica napus]	231	244	1.00E-105	105.6	86.6	91.8	MADS-box DNA-binding domain transcription factor	gbpln	Brassica napus	AT5G23260.3 | Symbols: TT16, ABS, AGL32 | K-box region and MADS-box transcription factor family protein | chr5:7836442-7838340 FORWARD LENGTH=238	231	238	1.00E-99	103.0	77.1	90.0
Rsa1.0_00056.1.g3115.t1	ref|NP_197719.1| transcription factor TCP7 [Arabidopsis thaliana] gi|75171749|sp|Q9FMX2.1|TCP7_ARATH RecName: Full=Transcription factor TCP7 gi|10177817|dbj|BAB11183.1| unnamed protein product [Arabidopsis thaliana] gi|332005764|gb|AED93147.1| transcription factor TCP7 [Arabidopsis thaliana]	209	250	9.00E-81	119.6	82.3	86.6	transcription factor TCP7	gbpln	Arabidopsis thaliana	AT5G23280.1 | Symbols: | TCP family transcription factor | chr5:7843017-7843769 FORWARD LENGTH=250	209	250	3.00E-83	119.6	82.3	86.6
Rsa1.0_00056.1.g3116.t1	gb|EOA21748.1| hypothetical protein CARUB_v10002195mg [Capsella rubella]	153	151	6.00E-72	98.7	89.5	94.8	hypothetical protein CARUB_v10002195mg	gbpln	Capsella rubella	AT5G23290.1 | Symbols: PFD5 | prefoldin 5 | chr5:7846144-7847428 FORWARD LENGTH=151	153	151	2.00E-74	98.7	89.5	94.8
Rsa1.0_00056.1.g3117.t1	gb|EOA20609.1| hypothetical protein CARUB_v10000920mg [Capsella rubella]	459	460	0	100.2	94.1	96.1	hypothetical protein CARUB_v10000920mg	gbpln	Capsella rubella	AT5G23300.1 | Symbols: PYRD | pyrimidine d | chr5:7847792-7850243 REVERSE LENGTH=460	459	460	0	100.2	93.2	96.1

Rsa1.0_00056.1.g3118.t1	ref|XP_002872050.1| hypothetical protein ARALYDRAFT_489192 [Arabidopsis lyrata subsp. lyrata] gi|297317887|gb|EFH48309.1| hypothetical protein ARALYDRAFT_489192 [Arabidopsis lyrata subsp. lyrata]	488	263	4.00E-33	53.9	21.1	23.6	hypothetical protein ARALYDRAFT_489192	gbpln	Arabidopsis lyrata	AT5G23310.1 | Symbols: FSD3 | Fe superoxide dismutase 3 | chr5:7850624-7852241 FORWARD LENGTH=263	488	263	2.00E-34	53.9	14.1	14.8
Rsa1.0_00056.1.g3119.t1	ref|XP_002874125.1| hypothetical protein ARALYDRAFT_910349 [Arabidopsis lyrata subsp. lyrata] gi|297319962|gb|EFH50384.1| hypothetical protein ARALYDRAFT_910349 [Arabidopsis lyrata subsp. lyrata]	213	219	1.00E-104	102.8	87.8	94.4	hypothetical protein ARALYDRAFT_910349	gbpln	Arabidopsis lyrata	AT5G23370.1 | Symbols: | GRAM domain-containing protein / ABA-responsive protein-related | chr5:7863542-7864201 REVERSE LENGTH=219	213	219	1.00E-103	102.8	85.0	92.0
Rsa1.0_00056.1.g3120.t1	ref|NP_197729.1| uncharacterized protein [Arabidopsis thaliana] gi|9758537|dbj|BAB08944.1| unnamed protein product [Arabidopsis thaliana] gi|332005774|gb|AED93157.1| uncharacterized protein AT5G23380 [Arabidopsis thaliana]	283	301	2.00E-76	106.4	56.2	73.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G23380.1 | Symbols: | Protein of unknown function (DUF789) | chr5:7866742-7870098 FORWARD LENGTH=301	283	301	6.00E-79	106.4	56.2	73.1
Rsa1.0_00056.1.g3121.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00056.1.g3122.t1	dbj|BAJ34388.1| unnamed protein product [Thellungiella halophila]	583	587	0	100.7	83.4	90.9	unnamed protein product	----	----	AT5G23400.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:7880603-7882372 FORWARD LENGTH=589	583	589	0	101.0	80.6	89.7
Rsa1.0_00056.1.g3123.t1	gb|EOA13406.1| hypothetical protein CARUB_v10026444mg, partial [Capsella rubella]	402	430	1.00E-105	107.0	56.7	69.2	hypothetical protein CARUB_v10026444mg, partial	gbpln	Capsella rubella	AT5G62660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:25156326-25157465 REVERSE LENGTH=379	402	379	1.00E-101	94.3	51.5	62.2
Rsa1.0_00056.1.g3124.t1	gb|EOA21466.1| hypothetical protein CARUB_v10001858mg [Capsella rubella]	350	236	1.00E-78	67.4	52.9	57.4	hypothetical protein CARUB_v10001858mg	gbpln	Capsella rubella	AT5G23420.1 | Symbols: HMGB6 | high-mobility group box 6 | chr5:7888712-7890111 REVERSE LENGTH=241	350	241	2.00E-65	68.9	46.9	51.4
Rsa1.0_00056.1.g3125.t1	ref|NP_200428.1| LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 [Arabidopsis thaliana] gi|9758637|dbj|BAB09299.1| unnamed protein product [Arabidopsis thaliana] gi|23306374|gb|AAN17414.1| putative protein [Arabidopsis thaliana] gi|24899659|gb|AAN65044.1| putative protein [Arabidopsis thaliana] gi|332009346|gb|AED96729.1| LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 [Arabidopsis thaliana]	127	168	1.00E-28	132.3	48.8	60.6	LORELEI-LIKE-GPI-ANCHORED PROTEIN 1	gbpln	Arabidopsis thaliana	AT5G56170.1 | Symbols: LLG1 | LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 | chr5:22736072-22737108 FORWARD LENGTH=168	127	168	2.00E-31	132.3	48.8	60.6
Rsa1.0_00056.1.g3126.t1	ref|NP_197740.2| uncharacterized protein [Arabidopsis thaliana] gi|332005792|gb|AED93175.1| uncharacterized protein AT5G23490 [Arabidopsis thaliana]	741	729	0	98.4	75.4	83.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G23490.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G08440.1); Has 202 Blast hits to 197 proteins in 48 species: Archae - 0; Bacteria - 13; Metazoa - 25; Fungi - 9; Plants - 109; Viruses - 0; Other Eukaryotes - 46 (source: NCBI BLink). | chr5:7919831-7926499 FORWARD LENGTH=729	741	729	0	98.4	75.4	83.8
Rsa1.0_00056.1.g3127.t1	ref|NP_197744.1| carboxyesterase 18 [Arabidopsis thaliana] gi|75335430|sp|Q9LT10.1|CXE18_ARATH RecName: Full=Probable carboxylesterase 18; AltName: Full=AtCXE18 gi|8809707|dbj|BAA97248.1| unnamed protein product [Arabidopsis thaliana] gi|110742010|dbj|BAE98944.1| hypothetical protein [Arabidopsis thaliana] gi|114050665|gb|ABI49482.1| At5g23530 [Arabidopsis thaliana] gi|332005796|gb|AED93179.1| carboxyesterase 18 [Arabidopsis thaliana]	332	335	1.00E-164	100.9	83.7	92.8	carboxyesterase 18	gbpln	Arabidopsis thaliana	AT5G23530.1 | Symbols: AtCXE18, CXE18 | carboxyesterase 18 | chr5:7933366-7934373 REVERSE LENGTH=335	332	335	1.00E-167	100.9	83.7	92.8

Rsa1.0_00056.1.g3128.t1	ref|NP_680212.1| 50S ribosomal protein L24-like protein [Arabidopsis thaliana] gi|297808355|ref|XP_002872061.1| KOW domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|8809706|dbj|BAA97247.1| 50S ribosomal protein L24 [Arabidopsis thaliana] gi|44681334|gb|AAS47607.1| At5g23535 [Arabidopsis thaliana] gi|45773844|gb|AAS76726.1| At5g23535 [Arabidopsis thaliana] gi|110735795|dbj|BAE99874.1| 50S ribosomal protein L24 [Arabidopsis thaliana] gi|297317898|gb|EFH48320.1| KOW domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|332005797|gb|AED93180.1| 50S ribosomal protein L24-like protein [Arabidopsis thaliana]	201	159	6.00E-86	79.1	78.6	78.6	50S ribosomal protein L24-like protein	gbpln	Arabidopsis lyrata	AT5G23535.1 | Symbols: | KOW domain-containing protein | chr5:7935871-7937127 FORWARD LENGTH=159	201	159	2.00E-88	79.1	78.6	78.6
Rsa1.0_00056.1.g3129.t1	ref|NP_197745.1| 26S proteasome non-ATPase regulatory subunit 14 [Arabidopsis thaliana] gi|51701846|sp|Q9LT08.1|PSDE_ARATH RecName: Full=26S proteasome non-ATPase regulatory subunit 14; AltName: Full=26S proteasome regulatory subunit rpn11 gi|8809705|dbj|BAA97246.1| 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gi|17979145|gb|AAL49768.1| putative 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gi|20259105|gb|AAM14268.1| putative 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gi|32700040|gb|AAP86670.1| 26S proteasome subunit RPN11A [Arabidopsis thaliana] gi|32700042|gb|AAP86671.1| 26S proteasome subunit RPN11a [Arabidopsis thaliana] gi|32700044|gb|AAP86672.1| 26S proteasome subunit RPN11 [Arabidopsis thaliana] gi|110737189|dbj|BAF00543.1| 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gi|332005798|gb|AED93181.1| 26S proteasome non-ATPase regulatory subunit 14 [Arabidopsis thaliana]	308	308	0	100.0	100.0	100.0	26S proteasome non-ATPase regulatory subunit 14	gbpln	Arabidopsis thaliana	AT5G23540.1 | Symbols: | Mov34/MPN/PAD-1 family protein | chr5:7937772-7939339 FORWARD LENGTH=308	308	308	0	100.0	100.0	100.0
Rsa1.0_00056.1.g3130.t4	gb|EOA19564.1| hypothetical protein CARUB_v10002585mg [Capsella rubella]	210	175	1.00E-75	83.3	73.3	77.6	hypothetical protein CARUB_v10002585mg	gbpln	Capsella rubella	AT5G23550.1 | Symbols: | Got1/Sft2-like vescicle transport protein family | chr5:7939914-7941479 REVERSE LENGTH=175	210	175	7.00E-76	83.3	71.4	77.1
Rsa1.0_00056.1.g3131.t1	gb|EOA20190.1| hypothetical protein CARUB_v10000486mg [Capsella rubella]	331	616	1.00E-33	186.1	34.4	47.7	hypothetical protein CARUB_v10000486mg	gbpln	Capsella rubella	AT5G23570.1 | Symbols: SGS3, ATSGS3 | XS domain-containing protein / XS zinc finger domain-containing protein-related | chr5:7943621-7945874 FORWARD LENGTH=625	331	625	1.00E-28	188.8	19.9	24.8
Rsa1.0_00056.1.g3132.t3	ref|NP_680213.1| transmembrane CLPTM1 family protein [Arabidopsis thaliana] gi|17381232|gb|AAL36035.1| AT5g08500/MAH20_6 [Arabidopsis thaliana] gi|23506007|gb|AAN28863.1| At5g08500/MAH20_6 [Arabidopsis thaliana] gi|332005802|gb|AED93185.1| transmembrane CLPTM1 family protein [Arabidopsis thaliana]	519	593	1.00E-179	114.3	70.5	78.4	transmembrane CLPTM1 family protein	gbpln	Arabidopsis thaliana	AT5G23575.1 | Symbols: | Transmembrane CLPTM1 family protein | chr5:7946563-7950041 FORWARD LENGTH=593	519	593	0	114.3	70.5	78.4
Rsa1.0_00056.1.g3133.t1	ref|XP_002874139.1| calcium-dependent protein kinase 9 [Arabidopsis lyrata subsp. lyrata] gi|297319976|gb|EFH50398.1| calcium-dependent protein kinase 9 [Arabidopsis lyrata subsp. lyrata]	96	489	1.00E-39	509.4	84.4	95.8	calcium-dependent protein kinase 9	gbpln	Arabidopsis lyrata	AT5G23580.1 | Symbols: CDPK9, ATCDPK9, CPK12, ATCPK12 | calmodulin-like domain protein kinase 9 | chr5:7950388-7952433 REVERSE LENGTH=490	96	490	2.00E-42	510.4	84.4	95.8
Rsa1.0_00056.1.g3134.t1	gb|AAD15471.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	230	1277	1.00E-24	555.2	24.3	26.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	230	746	4.00E-26	324.3	22.2	26.5
Rsa1.0_00057.1.g3135.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00057.1.g3136.t1	gb|EOA14510.1| hypothetical protein CARUB_v10027730mg [Capsella rubella]	417	237	7.00E-75	56.8	36.0	45.1	hypothetical protein CARUB_v10027730mg	gbpln	Capsella rubella	AT5G43650.1 | Symbols: BHLH92 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:17533310-17534758 REVERSE LENGTH=247	417	247	3.00E-77	59.2	37.9	45.8
Rsa1.0_00057.1.g3137.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3138.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3139.t1	gb|EOA12931.1| hypothetical protein CARUB_v10025910mg [Capsella rubella] gi|482548738|gb|EOA12932.1| hypothetical protein CARUB_v10025910mg [Capsella rubella]	754	791	0	104.9	88.1	93.8	hypothetical protein CARUB_v10025910mg	gbpln	Capsella rubella	AT5G43670.1 | Symbols: | Sec23/Sec24 protein transport family protein | chr5:17539025-17541733 REVERSE LENGTH=794	754	794	0	105.3	88.3	93.8
Rsa1.0_00057.1.g3140.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3141.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3142.t1	emb|CAN60947.1| hypothetical protein VITISV_015758 [Vitis vinifera]	275	1306	5.00E-61	474.9	48.0	64.7	hypothetical protein VITISV_015758	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3143.t1	gb|AAG10810.1|AC018460_4 Hypothetical protein [Arabidopsis thaliana] gi|12320956|gb|AAG50601.1|AC079605_6 hypothetical protein [Arabidopsis thaliana]	156	484	1.00E-55	310.3	63.5	71.8	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3144.t5	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1785	1274	0	71.4	30.5	42.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT5G43680.2 | Symbols: | unknown protein; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages. | chr5:17544074-17545354 FORWARD LENGTH=232	1785	232	2.00E-79	13.0	8.7	9.9
Rsa1.0_00057.1.g3145.t1	ref|XP_002865424.1| hypothetical protein ARALYDRAFT_494656 [Arabidopsis lyrata subsp. lyrata] gi|297311259|gb|EFH41683.1| hypothetical protein ARALYDRAFT_494656 [Arabidopsis lyrata subsp. lyrata]	174	379	4.00E-35	217.8	54.6	66.7	hypothetical protein ARALYDRAFT_494656	gbpln	Arabidopsis lyrata	AT5G43420.1 | Symbols: | RING/U-box superfamily protein | chr5:17451790-17452917 FORWARD LENGTH=375	174	375	2.00E-35	215.5	51.1	64.4
Rsa1.0_00057.1.g3146.t4	gb|AAF99785.1|AC012463_2 T2E6.4 [Arabidopsis thaliana]	569	740	7.00E-46	130.1	22.3	29.5	T2E6.4	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3147.t1	gb|EOA13697.1| hypothetical protein CARUB_v10026768mg, partial [Capsella rubella]	346	330	1.00E-130	95.4	73.7	78.9	hypothetical protein CARUB_v10026768mg, partial	gbpln	Capsella rubella	AT5G43720.1 | Symbols: | Protein of unknown function (DUF2361) | chr5:17557431-17559238 REVERSE LENGTH=329	346	329	1.00E-127	95.1	73.1	76.0
Rsa1.0_00057.1.g3148.t1	ref|XP_002882671.1| hypothetical protein ARALYDRAFT_897225 [Arabidopsis lyrata subsp. lyrata] gi|297328511|gb|EFH58930.1| hypothetical protein ARALYDRAFT_897225 [Arabidopsis lyrata subsp. lyrata]	262	136	4.00E-25	51.9	21.8	28.6	hypothetical protein ARALYDRAFT_897225	gbpln	Arabidopsis lyrata	AT1G09245.1 | Symbols: | Plant self-incompatibility protein S1 family | chr1:2986948-2987367 REVERSE LENGTH=139	262	139	2.00E-15	53.1	15.3	22.1
Rsa1.0_00057.1.g3149.t1	dbj|BAB09269.1| unnamed protein product [Arabidopsis thaliana]	554	422	1.00E-115	76.2	36.8	50.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	554	746	3.00E-27	134.7	13.4	24.4
Rsa1.0_00057.1.g3150.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	258	1838	2.00E-59	712.4	43.0	50.4	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3151.t1	ref|NP_199189.1| 3-ketoacyl-CoA synthase 19 [Arabidopsis thaliana] gi|75262422|sp|Q9FG87.1|KCS19_ARATH RecName: Full=3-ketoacyl-CoA synthase 19; Short=KCS-19; AltName: Full=Very long-chain fatty acid condensing enzyme 19; Short=VLCFA condensing enzyme 19 gi|15983491|gb|AAL11613.1|AF424620_1 AT5g43760/MQD19_11 [Arabidopsis thaliana] gi|10177945|dbj|BAB11304.1| beta-ketoacyl-CoA synthase [Arabidopsis thaliana] gi|23297625|gb|AAN12994.1| beta-ketoacyl-CoA synthase [Arabidopsis thaliana] gi|332007624|gb|AED95007.1| 3-ketoacyl-CoA synthase 19 [Arabidopsis thaliana]	704	529	0	75.1	69.9	71.9	3-ketoacyl-CoA synthase 19	gbpln	Arabidopsis thaliana	AT5G43760.1 | Symbols: KCS20 | 3-ketoacyl-CoA synthase 20 | chr5:17585903-17588486 FORWARD LENGTH=529	704	529	0	75.1	69.9	71.9
Rsa1.0_00057.1.g3152.t1	emb|CAA11416.1| ATP sulfurylase [Brassica juncea]	469	470	0	100.2	95.9	97.7	ATP sulfurylase	gbpln	Brassica juncea	AT5G43780.1 | Symbols: APS4 | Pseudouridine synthase/archaeosine transglycosylase-like family protein | chr5:17589631-17591480 REVERSE LENGTH=469	469	469	0	100.0	88.7	93.4

Rsa1.0_00057.1.g3153.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	377	1197	3.00E-37	317.5	27.6	39.5	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315	377	315	3.00E-29	83.6	21.0	26.5
Rsa1.0_00057.1.g3154.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3155.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	124	1024	6.00E-15	825.8	45.2	57.3	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3156.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00057.1.g3157.t2	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	536	1023	4.00E-65	190.9	26.5	35.6	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	536	575	4.00E-25	107.3	13.4	18.7
Rsa1.0_00057.1.g3158.t1	ref|XP_002865401.1| hypothetical protein ARALYDRAFT_917259 [Arabidopsis lyrata subsp. lyrata] gi|297311236|gb|EFH41660.1| hypothetical protein ARALYDRAFT_917259 [Arabidopsis lyrata subsp. lyrata]	984	983	0	99.9	94.1	96.3	hypothetical protein ARALYDRAFT_917259	gbpln	Arabidopsis lyrata	AT5G43810.2 | Symbols: ZLL | Stabilizer of iron transporter SufD / Polynucleotidyl transferase | chr5:17611939-17616562 FORWARD LENGTH=988	984	988	0	100.4	93.8	96.3
Rsa1.0_00057.1.g3159.t1	dbj|BAB11311.1| unnamed protein product [Arabidopsis thaliana]	731	680	0	93.0	73.5	82.1	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G43820.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:17618948-17620588 FORWARD LENGTH=546	731	546	0	74.7	58.5	65.0
Rsa1.0_00058.1.g3160.t1	ref|XP_002862428.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307936|gb|EFH38686.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	209	218	2.00E-76	104.3	77.0	83.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G08480.2 | Symbols: | VQ motif-containing protein | chr5:2744486-2745007 FORWARD LENGTH=173	209	173	4.00E-70	82.8	71.3	75.6
Rsa1.0_00058.1.g3161.t1	gb|AAG44817.1| peroxisome biogenesis protein PEX1 [Arabidopsis thaliana]	1125	1119	0	99.5	88.0	93.2	peroxisome biogenesis protein PEX1	gbpln	Arabidopsis thaliana	AT5G08470.1 | Symbols: PEX1 | peroxisome 1 | chr5:2735925-2742731 FORWARD LENGTH=1130	1125	1130	0	100.4	88.0	93.2
Rsa1.0_00058.1.g3162.t1	ref|XP_002871339.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317176|gb|EFH47598.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	373	383	0	102.7	86.1	91.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G08460.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:2733220-2735351 FORWARD LENGTH=385	373	385	0	103.2	85.3	91.4
Rsa1.0_00058.1.g3163.t1	ref|NP_196462.2| uncharacterized protein [Arabidopsis thaliana] gi|30682392|ref|NP_851033.1| uncharacterized protein [Arabidopsis thaliana] gi|79327334|ref|NP_001031857.1| uncharacterized protein [Arabidopsis thaliana] gi|20259547|gb|AAM13893.1| unknown protein [Arabidopsis thaliana] gi|21689693|gb|AAM67468.1| unknown protein [Arabidopsis thaliana] gi|332003920|gb|AED91303.1| uncharacterized protein AT5G08450 [Arabidopsis thaliana] gi|332003921|gb|AED91304.1| uncharacterized protein AT5G08450 [Arabidopsis thaliana] gi|332003922|gb|AED91305.1| uncharacterized protein AT5G08450 [Arabidopsis thaliana]	474	918	1.00E-180	193.7	66.7	69.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G08450.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Histone deacetylation protein Rxt3 (InterPro:IPR013951); Has 34444 Blast hits to 20801 proteins in 1175 species: Archae - 64; Bacteria - 2390; Metazoa - 15568; Fungi - 3729; Plants - 1886; Viruses - 208; Other Eukaryotes - 10599 (source: NCBI BLink). | chr5:2727970-2732572 REVERSE LENGTH=918	474	918	0	193.7	66.7	69.8
Rsa1.0_00058.1.g3164.t1	ref|XP_003534058.1| PREDICTED: uncharacterized protein LOC100811756 [Glycine max]	453	481	1.00E-133	106.2	57.0	73.3	PREDICTED: uncharacterized protein LOC100811756	gbenv/gbpln	Glycine max	AT5G41980.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43722.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:16793765-16794889 FORWARD LENGTH=374	453	374	1.00E-58	82.6	31.6	42.8
Rsa1.0_00058.1.g3165.t1	ref|XP_002871327.1| hypothetical protein ARALYDRAFT_325441 [Arabidopsis lyrata subsp. lyrata] gi|297317164|gb|EFH47586.1| hypothetical protein ARALYDRAFT_325441 [Arabidopsis lyrata subsp. lyrata]	720	724	0	100.6	83.6	89.2	hypothetical protein ARALYDRAFT_325441	gbpln	Arabidopsis lyrata	AT5G08440.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23490.1); Has 141 Blast hits to 139 proteins in 35 species: Archae - 0; Bacteria - 9; Metazoa - 21; Fungi - 6; Plants - 94; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr5:2721037-2726970 FORWARD LENGTH=726	720	726	0	100.8	84.0	90.0

Rsa1.0_00058.1.g3166.t1	ref|XP_002871325.1| hypothetical protein ARALYDRAFT_487679 [Arabidopsis lyrata subsp. lyrata] gi|297317162|gb|EFH47584.1| hypothetical protein ARALYDRAFT_487679 [Arabidopsis lyrata subsp. lyrata]	554	391	1.00E-153	70.6	53.6	60.8	hypothetical protein ARALYDRAFT_487679	gbpln	Arabidopsis lyrata	AT5G08420.1 | Symbols: | RNA-binding KH domain-containing protein | chr5:2713555-2716064 FORWARD LENGTH=391	554	391	1.00E-152	70.6	55.1	61.4
Rsa1.0_00058.1.g3167.t1	gb|EOA21459.1| hypothetical protein CARUB_v10001850mg [Capsella rubella]	230	238	8.00E-91	103.5	83.5	88.3	hypothetical protein CARUB_v10001850mg	gbpln	Capsella rubella	AT5G08330.1 | Symbols: | TCP family transcription factor | chr5:2680828-2681547 FORWARD LENGTH=239	230	239	1.00E-88	103.9	80.9	85.2
Rsa1.0_00058.1.g3168.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	145	1142	6.00E-26	787.6	49.7	62.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00058.1.g3169.t1	gb|EOA15137.1| hypothetical protein CARUB_v10028512mg [Capsella rubella]	80	81	3.00E-27	101.3	73.8	85.0	hypothetical protein CARUB_v10028512mg	gbpln	Capsella rubella	AT5G08315.1 | Symbols: | Defensin-like (DEFL) family protein | chr5:2676177-2676580 REVERSE LENGTH=82	80	82	5.00E-28	102.5	72.5	82.5
Rsa1.0_00058.1.g3170.t1	gb|EOA19347.1| hypothetical protein CARUB_v10000227mg [Capsella rubella]	892	830	0	93.0	74.0	82.4	hypothetical protein CARUB_v10000227mg	gbpln	Capsella rubella	AT5G08310.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:2672756-2675254 REVERSE LENGTH=832	892	832	0	93.3	74.7	82.3
Rsa1.0_00058.1.g3171.t1	ref|XP_002871316.1| hypothetical protein ARALYDRAFT_487662 [Arabidopsis lyrata subsp. lyrata] gi|297317153|gb|EFH47575.1| hypothetical protein ARALYDRAFT_487662 [Arabidopsis lyrata subsp. lyrata]	345	347	0	100.6	95.9	98.3	hypothetical protein ARALYDRAFT_487662	gbpln	Arabidopsis lyrata	AT5G08300.1 | Symbols: | Succinyl-CoA ligase, alpha subunit | chr5:2667579-2669672 FORWARD LENGTH=347	345	347	0	100.6	95.7	98.3
Rsa1.0_00058.1.g3172.t1	gb|EEC67208.1| hypothetical protein OsI_34094 [Oryza sativa Indica Group]	142	274	9.00E-79	193.0	96.5	100.0	hypothetical protein OsI_34094	gbpln	Oryza sativa	AT5G08290.1 | Symbols: YLS8 | mRNA splicing factor, thioredoxin-like U5 snRNP | chr5:2666043-2666936 FORWARD LENGTH=142	142	142	7.00E-81	100.0	97.9	100.0
Rsa1.0_00058.1.g3173.t2	ref|XP_002873350.1| hypothetical protein ARALYDRAFT_908776 [Arabidopsis lyrata subsp. lyrata] gi|297319187|gb|EFH49609.1| hypothetical protein ARALYDRAFT_908776 [Arabidopsis lyrata subsp. lyrata]	379	382	0	100.8	92.6	95.5	hypothetical protein ARALYDRAFT_908776	gbpln	Arabidopsis lyrata	AT5G08280.1 | Symbols: HEMC | hydroxymethylbilane synthase | chr5:2663763-2665596 REVERSE LENGTH=382	379	382	0	100.8	91.3	95.0
Rsa1.0_00058.1.g3174.t1	ref|XP_002871313.1| hypothetical protein ARALYDRAFT_908774 [Arabidopsis lyrata subsp. lyrata] gi|297317150|gb|EFH47572.1| hypothetical protein ARALYDRAFT_908774 [Arabidopsis lyrata subsp. lyrata]	825	479	0	58.1	46.5	50.4	hypothetical protein ARALYDRAFT_908774	gbpln	Arabidopsis lyrata	AT5G08260.1 | Symbols: scpl35 | serine carboxypeptidase-like 35 | chr5:2657236-2661272 FORWARD LENGTH=480	825	480	0	58.2	45.8	50.1
Rsa1.0_00058.1.g3175.t2	gb|EOA20528.1| hypothetical protein CARUB_v10000841mg [Capsella rubella]	560	483	1.00E-125	86.3	40.4	45.7	hypothetical protein CARUB_v10000841mg	gbpln	Capsella rubella	AT5G08260.1 | Symbols: scpl35 | serine carboxypeptidase-like 35 | chr5:2657236-2661272 FORWARD LENGTH=480	560	480	1.00E-126	85.7	39.8	45.2
Rsa1.0_00058.1.g3176.t1	ref|XP_002873348.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319185|gb|EFH49607.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	263	252	4.00E-96	95.8	70.7	81.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G08240.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23160.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 1; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:2651382-2652336 REVERSE LENGTH=258	263	258	2.00E-98	98.1	72.2	83.3
Rsa1.0_00058.1.g3177.t1	gb|EOA19452.1| hypothetical protein CARUB_v10001842mg [Capsella rubella]	238	240	1.00E-124	100.8	90.3	95.4	hypothetical protein CARUB_v10001842mg	gbpln	Capsella rubella	AT5G23140.1 | Symbols: CLPP2, NCLPP7 | nuclear-encoded CLP protease P7 | chr5:7783811-7784826 FORWARD LENGTH=241	238	241	1.00E-126	101.3	89.5	94.1
Rsa1.0_00058.1.g3178.t1	gb|EOA19796.1| hypothetical protein CARUB_v10000043mg [Capsella rubella] gi|482555605|gb|EOA19797.1| hypothetical protein CARUB_v10000043mg [Capsella rubella]	1399	1392	0	99.5	57.8	67.3	hypothetical protein CARUB_v10000043mg	gbpln	Capsella rubella	AT5G08230.1 | Symbols: | Tudor/PWWP/MBT domain-containing protein | chr5:2643846-2649788 REVERSE LENGTH=1445	1399	1445	0	103.3	49.0	55.2
Rsa1.0_00058.1.g3179.t1	ref|XP_002871312.1| hypothetical protein ARALYDRAFT_487656 [Arabidopsis lyrata subsp. lyrata] gi|297317149|gb|EFH47571.1| hypothetical protein ARALYDRAFT_487656 [Arabidopsis lyrata subsp. lyrata]	419	407	0	97.1	85.2	90.7	hypothetical protein ARALYDRAFT_487656	gbpln	Arabidopsis lyrata	AT5G08200.1 | Symbols: | peptidoglycan-binding LysM domain-containing protein | chr5:2638385-2640508 FORWARD LENGTH=409	419	409	0	97.6	84.7	90.0
Rsa1.0_00058.1.g3180.t1	gb|EOA21718.1| hypothetical protein CARUB_v10002155mg [Capsella rubella]	164	160	2.00E-79	97.6	86.0	92.1	hypothetical protein CARUB_v10002155mg	gbpln	Capsella rubella	AT5G23090.1 | Symbols: NF-YB13 | nuclear factor Y, subunit B13 | chr5:7749391-7750203 FORWARD LENGTH=159	164	159	1.00E-80	97.0	86.0	91.5

Rsa1.0_00058.1.g3181.t1	ref|XP_002873346.1| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis lyrata subsp. lyrata] gi|297319183|gb|EFH49605.1| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis lyrata subsp. lyrata]	156	156	3.00E-77	100.0	92.3	97.4	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	gbpln	Arabidopsis lyrata	AT5G08180.2 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr5:2631843-2633374 REVERSE LENGTH=156	156	156	3.00E-79	100.0	91.7	96.8
Rsa1.0_00058.1.g3182.t1	ref|NP_196433.1| serine/threonine protein kinase 3 [Arabidopsis thaliana] gi|11762274|gb|AAG40409.1|AF325057_1 AT5g08160 [Arabidopsis thaliana] gi|2109293|gb|AAB69123.1| serine/threonine protein kinase [Arabidopsis thaliana] gi|8346553|emb|CAB93717.1| serine/threonine protein kinase [Arabidopsis thaliana] gi|24417498|gb|AAN60359.1| unknown [Arabidopsis thaliana] gi|94442405|gb|ABF18990.1| At5g08160 [Arabidopsis thaliana] gi|332003876|gb|AED91259.1| serine/threonine protein kinase 3 [Arabidopsis thaliana]	340	347	0	102.1	93.2	95.9	serine/threonine protein kinase 3	gbpln	Arabidopsis thaliana	AT5G08160.1 | Symbols: ATPK3, PK3 | serine/threonine protein kinase 3 | chr5:2625903-2627942 REVERSE LENGTH=347	340	347	0	102.1	93.2	95.9
Rsa1.0_00058.1.g3183.t1	ref|XP_002873343.1| hypothetical protein ARALYDRAFT_908765 [Arabidopsis lyrata subsp. lyrata] gi|297319180|gb|EFH49602.1| hypothetical protein ARALYDRAFT_908765 [Arabidopsis lyrata subsp. lyrata]	134	140	4.00E-31	104.5	75.4	83.6	hypothetical protein ARALYDRAFT_908765	gbpln	Arabidopsis lyrata	AT5G08150.1 | Symbols: SOB5 | suppressor of phytochrome b 5 | chr5:2622164-2622598 REVERSE LENGTH=144	134	144	8.00E-26	107.5	71.6	80.6
Rsa1.0_00058.1.g3184.t1	emb|CAB93715.1| putative protein [Arabidopsis thaliana]	379	530	5.00E-93	139.8	59.9	71.8	putative protein	gbpln	Arabidopsis thaliana	AT5G08139.1 | Symbols: | RING/U-box superfamily protein | chr5:2616487-2617617 FORWARD LENGTH=376	379	376	2.00E-94	99.2	60.2	72.0
Rsa1.0_00058.1.g3185.t1	ref|XP_002873342.1| hypothetical protein ARALYDRAFT_908762 [Arabidopsis lyrata subsp. lyrata] gi|297319179|gb|EFH49601.1| hypothetical protein ARALYDRAFT_908762 [Arabidopsis lyrata subsp. lyrata]	551	540	0	98.0	82.4	86.8	hypothetical protein ARALYDRAFT_908762	gbpln	Arabidopsis lyrata	AT5G08130.4 | Symbols: BIM1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:2606655-2609571 REVERSE LENGTH=529	551	529	0	96.0	79.7	84.6
Rsa1.0_00058.1.g3186.t1	ref|NP_196429.1| movement protein binding protein 2C [Arabidopsis thaliana] gi|13877923|gb|AAK44039.1|AF370224_1 putative myosin heavy chain [Arabidopsis thaliana] gi|8346549|emb|CAB93713.1| myosin heavy chain-like protein [Arabidopsis thaliana] gi|21436331|gb|AAM51335.1| putative myosin heavy chain [Arabidopsis thaliana] gi|332003866|gb|AED91249.1| movement protein binding protein 2C [Arabidopsis thaliana]	329	326	1.00E-157	99.1	83.3	92.7	movement protein binding protein 2C	gbpln	Arabidopsis thaliana	AT5G08120.1 | Symbols: MPB2C | movement protein binding protein 2C | chr5:2600743-2602678 REVERSE LENGTH=326	329	326	1.00E-160	99.1	83.3	92.7
Rsa1.0_00058.1.g3187.t1	gb|EOA22920.1| hypothetical protein CARUB_v10003654mg [Capsella rubella]	1498	1153	0	77.0	56.9	64.3	hypothetical protein CARUB_v10003654mg	gbpln	Capsella rubella	AT5G08110.1 | Symbols: | nucleic acid binding;ATP-dependent helicases;ATP binding;helicases;ATP-dependent helicases | chr5:2594854-2600114 REVERSE LENGTH=1141	1498	1141	0	76.2	54.9	62.2
Rsa1.0_00058.1.g3188.t1	gb|EOA21213.1| hypothetical protein CARUB_v10001560mg [Capsella rubella]	465	304	1.00E-101	65.4	46.7	49.2	hypothetical protein CARUB_v10001560mg	gbpln	Capsella rubella	AT5G08080.1 | Symbols: SYP132, ATSYP132 | syntaxin of plants 132 | chr5:2588532-2591106 FORWARD LENGTH=304	465	304	1.00E-102	65.4	46.0	49.0
Rsa1.0_00058.1.g3189.t1	gb|AAM64394.1| unknown [Arabidopsis thaliana]	130	131	2.00E-60	100.8	83.1	93.1	unknown	gbpln	Arabidopsis thaliana	AT5G08060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 16 growth stages; Has 42 Blast hits to 42 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:2580588-2580983 FORWARD LENGTH=131	130	131	6.00E-63	100.8	83.1	93.1
Rsa1.0_00058.1.g3190.t1	dbj|BAF81519.1| glycerophosphodiester phosphodiesterase [Brassica rapa]	379	372	0	98.2	94.7	95.8	glycerophosphodiester phosphodiesterase	gbpln	Brassica rapa	AT5G08030.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr5:2575152-2576770 REVERSE LENGTH=372	379	372	0	98.2	84.4	89.7

Rsa1.0_00058.1.g3191.t1	gb|EOA20180.1| hypothetical protein CARUB_v10000503mg [Capsella rubella]	423	607	1.00E-180	143.5	73.3	78.5	hypothetical protein CARUB_v10000503mg	gbpln	Capsella rubella	AT5G08020.1 | Symbols: ATRPA70B, RPA70B | RPA70-kDa subunit B | chr5:2572107-2574879 FORWARD LENGTH=604	423	604	0	142.8	73.3	78.7
Rsa1.0_00058.1.g3192.t1	ref|XP_002871301.1| hypothetical protein ARALYDRAFT_487634 [Arabidopsis lyrata subsp. lyrata] gi|297317138|gb|EFH47560.1| hypothetical protein ARALYDRAFT_487634 [Arabidopsis lyrata subsp. lyrata]	573	571	1.00E-175	99.7	70.0	78.5	hypothetical protein ARALYDRAFT_487634	gbpln	Arabidopsis lyrata	AT5G08010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61040.1); Has 5732 Blast hits to 4319 proteins in 440 species: Archae - 66; Bacteria - 397; Metazoa - 2437; Fungi - 292; Plants - 238; Viruses - 35; Other Eukaryotes - 2267 (source: NCBI BLink). | chr5:2569606-2571613 FORWARD LENGTH=566	573	566	1.00E-169	98.8	68.8	76.6
Rsa1.0_00058.1.g3193.t2	ref|XP_002871299.1| hypothetical protein ARALYDRAFT_350051 [Arabidopsis lyrata subsp. lyrata] gi|297317136|gb|EFH47558.1| hypothetical protein ARALYDRAFT_350051 [Arabidopsis lyrata subsp. lyrata]	198	194	6.00E-75	98.0	81.8	87.9	hypothetical protein ARALYDRAFT_350051	gbpln	Arabidopsis lyrata	AT5G08000.1 | Symbols: E13L3, PDCB2 | glucan endo-1,3-beta-glucosidase-like protein 3 | chr5:2563684-2565282 FORWARD LENGTH=194	198	194	4.00E-73	98.0	76.3	82.8
Rsa1.0_00058.1.g3194.t1	gb|ABC58722.1| flavonoid 3'-hydroxylase [Brassica napus] gi|84380743|gb|ABC58723.1| flavonoid 3'-hydroxylase [Brassica napus]	511	511	0	100.0	97.7	98.8	flavonoid 3'-hydroxylase	gbpln	Brassica napus	AT5G07990.1 | Symbols: TT7, CYP75B1, D501 | Cytochrome P450 superfamily protein | chr5:2560437-2562859 FORWARD LENGTH=513	511	513	0	100.4	89.0	94.3
Rsa1.0_00059.1.g3195.t1	ref|NP_177241.3| MLP-like protein 31 [Arabidopsis thaliana] gi|148872485|sp|Q941R6.2|MLP31_ARATH RecName: Full=MLP-like protein 31 gi|19424013|gb|AAL87294.1| unknown protein [Arabidopsis thaliana] gi|21689799|gb|AAM67543.1| unknown protein [Arabidopsis thaliana] gi|110740998|dbj|BAE98593.1| hypothetical protein [Arabidopsis thaliana] gi|332197005|gb|AEE35126.1| MLP-like protein 31 [Arabidopsis thaliana]	182	171	2.00E-60	94.0	61.5	75.3	MLP-like protein 31	gbpln	Arabidopsis thaliana	AT1G70840.1 | Symbols: MLP31 | MLP-like protein 31 | chr1:26713170-26714014 REVERSE LENGTH=171	182	171	9.00E-63	94.0	61.5	75.3
Rsa1.0_00059.1.g3196.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00059.1.g3197.t1	gb|EOA39173.1| hypothetical protein CARUB_v10012133mg [Capsella rubella]	632	631	0	99.8	94.5	98.1	hypothetical protein CARUB_v10012133mg	gbpln	Capsella rubella	AT1G23090.1 | Symbols: AST91, SULTR3;3 | sulfate transporter 91 | chr1:8185238-8188954 REVERSE LENGTH=631	632	631	0	99.8	93.4	97.5
Rsa1.0_00059.1.g3198.t1	ref|XP_002890553.1| hypothetical protein ARALYDRAFT_472555 [Arabidopsis lyrata subsp. lyrata] gi|297336395|gb|EFH66812.1| hypothetical protein ARALYDRAFT_472555 [Arabidopsis lyrata subsp. lyrata]	136	158	7.00E-35	116.2	77.2	83.8	hypothetical protein ARALYDRAFT_472555	gbpln	Arabidopsis lyrata	AT1G23050.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:8168631-8169116 FORWARD LENGTH=161	136	161	1.00E-32	118.4	73.5	81.6
Rsa1.0_00059.1.g3199.t1	ref|NP_564187.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|2462823|gb|AAB72158.1| unknown [Arabidopsis thaliana] gi|2829907|gb|AAC00615.1| Unknown protein [Arabidopsis thaliana] gi|98960877|gb|ABF58922.1| At1g23040 [Arabidopsis thaliana] gi|110738822|dbj|BAF01334.1| predicted GPI-anchored protein [Arabidopsis thaliana] gi|332192205|gb|AEE30326.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	144	144	4.00E-41	100.0	80.6	86.8	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT1G23040.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:8165025-8165459 FORWARD LENGTH=144	144	144	1.00E-43	100.0	80.6	86.8
Rsa1.0_00059.1.g3200.t1	ref|XP_002890550.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297336392|gb|EFH66809.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	613	612	0	99.8	89.7	94.1	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT1G23030.1 | Symbols: | ARM repeat superfamily protein | chr1:8156745-8158842 FORWARD LENGTH=612	613	612	0	99.8	88.9	93.5
Rsa1.0_00059.1.g3201.t1	gb|ABG81320.1| low-phosphate root 1 [Arabidopsis thaliana]	566	581	0	102.7	88.7	93.1	low-phosphate root 1	gbpln	Arabidopsis thaliana	AT1G23010.1 | Symbols: LPR1 | Cupredoxin superfamily protein | chr1:8147353-8149580 FORWARD LENGTH=581	566	581	0	102.7	88.7	93.1
Rsa1.0_00059.1.g3202.t1	ref|NP_173713.1| heavy-metal-associated domain-containing protein [Arabidopsis thaliana] gi|124301010|gb|ABN04757.1| At1g23000 [Arabidopsis thaliana] gi|332192199|gb|AEE30320.1| heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	356	358	1.00E-103	100.6	72.8	81.5	heavy-metal-associated domain-containing protein	gbpln	Arabidopsis thaliana	AT1G23000.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:8143614-8144865 FORWARD LENGTH=358	356	358	1.00E-106	100.6	72.8	81.5

Rsa1.0_00059.1.g3203.t1	gb|AAN23108.2| putative farnesylated protein [Brassica rapa subsp. pekinensis]	152	152	1.00E-82	100.0	97.4	98.7	putative farnesylated protein	gbpln	Brassica rapa	AT1G22990.1 | Symbols: HIPP22 | Heavy metal transport/detoxification superfamily protein | chr1:8139221-8140045 FORWARD LENGTH=152	152	152	7.00E-83	100.0	93.4	98.0
Rsa1.0_00059.1.g3204.t1	ref|XP_002893254.1| hypothetical protein ARALYDRAFT_472548 [Arabidopsis lyrata subsp. lyrata] gi|297339096|gb|EFH69513.1| hypothetical protein ARALYDRAFT_472548 [Arabidopsis lyrata subsp. lyrata]	356	355	1.00E-161	99.7	83.4	90.7	hypothetical protein ARALYDRAFT_472548	gbpln	Arabidopsis lyrata	AT1G22970.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G71150.1); Has 134 Blast hits to 132 proteins in 48 species: Archae - 0; Bacteria - 0; Metazoa - 66; Fungi - 10; Plants - 48; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:8130840-8132199 REVERSE LENGTH=357	356	357	1.00E-159	100.3	82.9	90.7
Rsa1.0_00059.1.g3205.t1	gb|EOA36666.1| hypothetical protein CARUB_v10011979mg [Capsella rubella]	748	720	0	96.3	67.1	77.8	hypothetical protein CARUB_v10011979mg	gbpln	Capsella rubella	AT1G22960.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:8128086-8130242 REVERSE LENGTH=718	748	718	0	96.0	68.2	78.6
Rsa1.0_00059.1.g3206.t2	ref|NP_173708.3| uncharacterized PKHD-type hydroxylase [Arabidopsis thaliana] gi|193806639|sp|Q3ED68.2|Y1295_ARATH RecName: Full=Uncharacterized PKHD-type hydroxylase At1g22950 gi|332192193|gb|AEE30314.1| uncharacterized PKHD-type hydroxylase [Arabidopsis thaliana]	389	397	1.00E-176	102.1	77.9	87.7	uncharacterized PKHD-type hydroxylase	gbpln	Arabidopsis thaliana	AT1G22950.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:8125291-8127168 REVERSE LENGTH=397	389	397	1.00E-179	102.1	77.9	87.7
Rsa1.0_00059.1.g3207.t1	sp|O48881.1|TPS1_BRANA RecName: Full=Thiamine biosynthetic bifunctional enzyme BTH1, chloroplastic; Includes: RecName: Full=Thiamine-phosphate synthase; Short=TP synthase; Short=TPS; AltName: Full=Thiamine-phosphate pyrophosphorylase; Short=TMP pyrophosphorylase; Short=TMP-PPase; Includes: RecName: Full=Hydroxymethylpyrimidine kinase; Short=HMP kinase; Flags: Precursor gi|2746079|gb|AAC31298.1| BTH1 [Brassica napus]	526	523	0	99.4	94.1	97.0	RecName: Full=Thiamine biosynthetic bifunctional enzyme BTH1, chloroplastic; Includes: RecName: Full=Thiamine-phosphate synthase; Short=TP synthase; Short=TPS; AltName: Full=Thiamine-phosphate pyrophosphorylase; Short=TMP pyrophosphorylase; Short=TMP-PPase; Includes: RecName: Full=Hydroxymethylpyrimidine kinase; Short=HMP kinase; Flags: Precursor gi|2746079|gb|AAC31298.1| BTH1	gbpln	Brassica napus	AT1G22940.1 | Symbols: TH1, TH-1, THIE | thiamin biosynthesis protein, putative | chr1:8122384-8124908 FORWARD LENGTH=522	526	522	0	99.2	90.5	94.9
Rsa1.0_00059.1.g3208.t1	ref|XP_002890962.1| hypothetical protein ARALYDRAFT_890756 [Arabidopsis lyrata subsp. lyrata] gi|297336804|gb|EFH67221.1| hypothetical protein ARALYDRAFT_890756 [Arabidopsis lyrata subsp. lyrata]	160	159	2.00E-53	99.4	67.5	76.9	hypothetical protein ARALYDRAFT_890756	gbpln	Arabidopsis lyrata	AT1G56270.1 | Symbols: | unknown protein; Has 38 Blast hits to 38 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:21071148-21071636 REVERSE LENGTH=162	160	162	1.00E-22	101.3	40.0	57.5
Rsa1.0_00059.1.g3209.t1	ref|XP_002890545.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata] gi|297336387|gb|EFH66804.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata]	1203	1130	0	93.9	78.3	84.3	T-complex protein 11	gbpln	Arabidopsis lyrata	AT1G22930.1 | Symbols: | T-complex protein 11 | chr1:8117521-8121854 FORWARD LENGTH=1131	1203	1131	0	94.0	77.4	83.2
Rsa1.0_00059.1.g3210.t2	ref|XP_002893252.1| hypothetical protein ARALYDRAFT_472541 [Arabidopsis lyrata subsp. lyrata] gi|297339094|gb|EFH69511.1| hypothetical protein ARALYDRAFT_472541 [Arabidopsis lyrata subsp. lyrata]	384	357	0	93.0	85.4	88.5	hypothetical protein ARALYDRAFT_472541	gbpln	Arabidopsis lyrata	AT1G22920.1 | Symbols: CSN5A, JAB1, AJH1 | COP9 signalosome 5A | chr1:8109882-8111895 REVERSE LENGTH=357	384	357	1.00E-180	93.0	84.1	87.8
Rsa1.0_00059.1.g3211.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00059.1.g3212.t1	ref|XP_002890544.1| hypothetical protein ARALYDRAFT_889804 [Arabidopsis lyrata subsp. lyrata] gi|297336386|gb|EFH66803.1| hypothetical protein ARALYDRAFT_889804 [Arabidopsis lyrata subsp. lyrata]	244	252	1.00E-109	103.3	88.1	91.4	hypothetical protein ARALYDRAFT_889804	gbpln	Arabidopsis lyrata	AT1G22910.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:8105808-8107659 FORWARD LENGTH=249	244	249	1.00E-111	102.0	88.5	91.0
Rsa1.0_00059.1.g3213.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00059.1.g3214.t1	ref|XP_002863772.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297791781|ref|XP_002863775.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297309607|gb|EFH40031.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297309610|gb|EFH40034.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata]	185	185	8.00E-82	100.0	80.5	88.1	disease resistance-responsive family protein	gbpln	Arabidopsis lyrata	AT5G42500.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr5:16994359-16994916 REVERSE LENGTH=185	185	185	1.00E-79	100.0	80.5	89.2
Rsa1.0_00059.1.g3215.t1	ref|XP_002863772.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297791781|ref|XP_002863775.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297309607|gb|EFH40031.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297309610|gb|EFH40034.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata]	185	185	1.00E-74	100.0	76.8	83.8	disease resistance-responsive family protein	gbpln	Arabidopsis lyrata	AT5G42500.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr5:16994359-16994916 REVERSE LENGTH=185	185	185	1.00E-69	100.0	75.1	83.2
Rsa1.0_00059.1.g3216.t1	gb|EOA39826.1| hypothetical protein CARUB_v10008493mg [Capsella rubella]	680	681	0	100.1	74.1	81.5	hypothetical protein CARUB_v10008493mg	gbpln	Capsella rubella	AT1G22882.1 | Symbols: | Galactose-binding protein | chr1:8099150-8101220 FORWARD LENGTH=660	680	660	0	97.1	71.6	79.3
Rsa1.0_00059.1.g3217.t8	gb|EOA36793.1| hypothetical protein CARUB_v10008204mg [Capsella rubella]	1812	983	0	54.2	48.0	50.8	hypothetical protein CARUB_v10008204mg	gbpln	Capsella rubella	AT1G22860.1 | Symbols: | Vacuolar sorting protein 39 | chr1:8083400-8088867 FORWARD LENGTH=961	1812	961	0	53.0	46.1	49.1
Rsa1.0_00059.1.g3218.t1	gb|EOA38177.1| hypothetical protein CARUB_v10009653mg [Capsella rubella]	326	340	1.00E-124	104.3	81.0	85.0	hypothetical protein CARUB_v10009653mg	gbpln	Capsella rubella	AT1G22850.1 | Symbols: | SNARE associated Golgi protein family | chr1:8080671-8082816 REVERSE LENGTH=344	326	344	1.00E-126	105.5	82.2	86.5
Rsa1.0_00059.1.g3219.t1	gb|EOA38639.1| hypothetical protein CARUB_v10010544mg, partial [Capsella rubella]	112	154	7.00E-59	137.5	97.3	99.1	hypothetical protein CARUB_v10010544mg, partial	gbpln	Capsella rubella	AT1G22840.1 | Symbols: CYTC-1, ATCYTC-A | CYTOCHROME C-1 | chr1:8079384-8080286 FORWARD LENGTH=114	112	114	8.00E-60	101.8	94.6	98.2
Rsa1.0_00059.1.g3220.t1	gb|EOA37595.1| hypothetical protein CARUB_v10011955mg [Capsella rubella]	130	147	4.00E-58	113.1	88.5	96.2	hypothetical protein CARUB_v10011955mg	gbpln	Capsella rubella	AT1G22810.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:8074535-8074969 REVERSE LENGTH=144	130	144	2.00E-57	110.8	86.2	93.1
Rsa1.0_00059.1.g3221.t2	ref|XP_002890535.1| hypothetical protein ARALYDRAFT_889792 [Arabidopsis lyrata subsp. lyrata] gi|297336377|gb|EFH66794.1| hypothetical protein ARALYDRAFT_889792 [Arabidopsis lyrata subsp. lyrata]	357	355	1.00E-177	99.4	86.6	92.4	hypothetical protein ARALYDRAFT_889792	gbpln	Arabidopsis lyrata	AT1G22800.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:8072020-8074039 FORWARD LENGTH=355	357	355	1.00E-179	99.4	87.1	91.9
Rsa1.0_00059.1.g3222.t1	ref|XP_002890534.1| hypothetical protein ARALYDRAFT_889791 [Arabidopsis lyrata subsp. lyrata] gi|297336376|gb|EFH66793.1| hypothetical protein ARALYDRAFT_889791 [Arabidopsis lyrata subsp. lyrata]	214	214	5.00E-55	100.0	65.4	72.0	hypothetical protein ARALYDRAFT_889791	gbpln	Arabidopsis lyrata	AT1G22790.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G34010.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:8070271-8071292 FORWARD LENGTH=216	214	216	1.00E-53	100.9	64.0	70.1
Rsa1.0_00059.1.g3223.t1	gb|AEB33730.1| GIGANTEA [Brassica rapa]	1177	1183	0	100.5	95.7	97.0	GIGANTEA	gbpln	Brassica rapa	AT1G22770.1 | Symbols: GI, FB | gigantea protein (GI) | chr1:8062398-8067447 FORWARD LENGTH=1173	1177	1173	0	99.7	91.8	94.2
Rsa1.0_00059.1.g3224.t2	ref|XP_002890530.1| hypothetical protein ARALYDRAFT_472519 [Arabidopsis lyrata subsp. lyrata] gi|297336372|gb|EFH66789.1| hypothetical protein ARALYDRAFT_472519 [Arabidopsis lyrata subsp. lyrata]	451	256	1.00E-113	56.8	45.7	48.8	hypothetical protein ARALYDRAFT_472519	gbpln	Arabidopsis lyrata	AT1G22750.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1475 (InterPro:IPR009943); Has 185 Blast hits to 155 proteins in 21 species: Archae - 0; Bacteria - 8; Metazoa - 3; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 110 (source: NCBI BLink). | chr1:8050911-8052618 FORWARD LENGTH=244	451	244	1.00E-114	54.1	45.7	48.3

Rsa1.0_00059.1.g3225.t1	ref|NP_173687.1| MA3 domain-containing protein [Arabidopsis thaliana] gi|3287683|gb|AAC25511.1| Similar to apoptosis protein MA-3 gb|D50465 from Mus musculus [Arabidopsis thaliana] gi|14334598|gb|AAK59477.1| putative topoisomerase [Arabidopsis thaliana] gi|22136820|gb|AAM91754.1| putative topoisomerase [Arabidopsis thaliana] gi|332192157|gb|AEE30278.1| MA3 domain-containing protein [Arabidopsis thaliana]	687	693	0	100.9	82.5	88.9	MA3 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G22730.1 | Symbols: | MA3 domain-containing protein | chr1:8046511-8048769 FORWARD LENGTH=693	687	693	0	100.9	82.5	88.9
Rsa1.0_00059.1.g3226.t1	ref|XP_002893745.1| hypothetical protein ARALYDRAFT_336372 [Arabidopsis lyrata subsp. lyrata] gi|297339587|gb|EFH70004.1| hypothetical protein ARALYDRAFT_336372 [Arabidopsis lyrata subsp. lyrata]	176	180	4.00E-75	102.3	82.4	90.9	hypothetical protein ARALYDRAFT_336372	gbpln	Arabidopsis lyrata	AT3G03773.1 | Symbols: | HSP20-like chaperones superfamily protein | chr3:951885-953490 FORWARD LENGTH=150	176	150	3.00E-29	85.2	33.5	46.0
Rsa1.0_00060.1.g3227.t1	gb|EOA23115.1| hypothetical protein CARUB_v10003908mg [Capsella rubella]	531	1282	5.00E-73	241.4	31.6	52.0	hypothetical protein CARUB_v10003908mg	gbpln	Capsella rubella	AT4G09420.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr4:5962319-5963776 REVERSE LENGTH=457	531	457	1.00E-72	86.1	35.0	50.5
Rsa1.0_00060.1.g3228.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00060.1.g3229.t1	gb|AAD49099.1|AF177535_3 contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]	619	664	5.00E-60	107.3	26.8	41.7	contains similarity to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	619	785	7.00E-19	126.8	11.1	19.2
Rsa1.0_00060.1.g3230.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	350	1142	3.00E-88	326.3	48.3	63.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	350	575	3.00E-34	164.3	29.1	48.6
Rsa1.0_00060.1.g3231.t1	ref|XP_002888896.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334737|gb|EFH65155.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1140	1169	0	102.5	50.2	64.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G72840.2 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr1:27409504-27413485 REVERSE LENGTH=1183	1140	1183	0	103.8	48.1	62.8
Rsa1.0_00060.1.g3232.t1	ref|XP_002887455.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333296|gb|EFH63714.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	419	412	1.00E-145	98.3	65.9	77.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G72850.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27413971-27415335 FORWARD LENGTH=422	419	422	1.00E-130	100.7	59.9	73.7
Rsa1.0_00060.1.g3233.t1	ref|NP_001185386.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332197260|gb|AEE35381.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1087	1183	0	108.8	52.3	66.1	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT1G72840.2 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr1:27409504-27413485 REVERSE LENGTH=1183	1087	1183	0	108.8	52.3	66.1
Rsa1.0_00060.1.g3234.t1	emb|CAA74050.1| Transcription factor [Arabidopsis thaliana]	336	340	1.00E-134	101.2	76.5	83.0	Transcription factor	gbpln	Arabidopsis thaliana	AT1G72830.1 | Symbols: HAP2C, ATHAP2C, NF-YA3 | nuclear factor Y, subunit A3 | chr1:27405699-27407088 REVERSE LENGTH=340	336	340	1.00E-137	101.2	76.8	83.6
Rsa1.0_00060.1.g3235.t1	gb|EOA35384.1| hypothetical protein CARUB_v10020581mg [Capsella rubella] gi|482571197|gb|EOA35385.1| hypothetical protein CARUB_v10020581mg [Capsella rubella]	342	346	0	101.2	91.8	95.0	hypothetical protein CARUB_v10020581mg	gbpln	Capsella rubella	AT1G72820.1 | Symbols: | Mitochondrial substrate carrier family protein | chr1:27403457-27404506 FORWARD LENGTH=349	342	349	0	102.0	93.6	96.5
Rsa1.0_00060.1.g3236.t1	gb|EOA34998.1| hypothetical protein CARUB_v10020090mg [Capsella rubella]	532	550	1.00E-166	103.4	74.6	82.3	hypothetical protein CARUB_v10020090mg	gbpln	Capsella rubella	AT1G72790.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:27394848-27396533 FORWARD LENGTH=561	532	561	1.00E-166	105.5	73.9	81.4

Rsa1.0_00060.1.g3237.t1	ref|NP_177417.1| translation initiation factor 4A-3 [Arabidopsis thaliana] gi|75333652|sp|Q9CAI7.1|IF4A3_ARATH RecName: Full=Eukaryotic initiation factor 4A-3; Short=eIF-4A-3; AltName: Full=ATP-dependent RNA helicase eIF4A-3; AltName: Full=DEAD-box ATP-dependent RNA helicase 23 gi|12323781|gb|AAG51861.1|AC010926_24 putative Eukaryotic initiation factor 4A; 30924-32477 [Arabidopsis thaliana] gi|16974629|gb|AAL31217.1| At1g72730/F28P22_8 [Arabidopsis thaliana] gi|21593752|gb|AAM65719.1| putative Eukaryotic initiation factor 4A [Arabidopsis thaliana] gi|22655476|gb|AAM98330.1| At1g72730/F28P22_8 [Arabidopsis thaliana] gi|332197244|gb|AEE35365.1| translation initiation factor 4A-3 [Arabidopsis thaliana]	108	414	5.00E-17	383.3	35.2	40.7	translation initiation factor 4A-3	gbpln	Arabidopsis thaliana	AT1G72730.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr1:27378040-27379593 REVERSE LENGTH=414	108	414	8.00E-20	383.3	35.2	40.7
Rsa1.0_00060.1.g3238.t1	ref|NP_177411.1| IQ-domain 8 protein [Arabidopsis thaliana] gi|12323773|gb|AAG51853.1|AC010926_16 hypothetical protein; 51860-53619 [Arabidopsis thaliana] gi|38016019|gb|AAR07516.1| At1g72670 [Arabidopsis thaliana] gi|51969960|dbj|BAD43672.1| unknown protein [Arabidopsis thaliana] gi|332197238|gb|AEE35359.1| IQ-domain 8 protein [Arabidopsis thaliana]	165	414	2.00E-28	250.9	58.8	68.5	IQ-domain 8 protein	gbpln	Arabidopsis thaliana	AT1G72670.1 | Symbols: iqd8 | IQ-domain 8 | chr1:27356898-27358657 REVERSE LENGTH=414	165	414	6.00E-31	250.9	58.8	68.5
Rsa1.0_00060.1.g3239.t1	ref|XP_002887444.1| hypothetical protein ARALYDRAFT_476400 [Arabidopsis lyrata subsp. lyrata] gi|297333285|gb|EFH63703.1| hypothetical protein ARALYDRAFT_476400 [Arabidopsis lyrata subsp. lyrata]	576	627	0	108.9	70.7	78.5	hypothetical protein ARALYDRAFT_476400	gbpln	Arabidopsis lyrata	AT1G72650.2 | Symbols: TRFL6 | TRF-like 6 | chr1:27350253-27353483 FORWARD LENGTH=630	576	630	0	109.4	69.1	78.3
Rsa1.0_00060.1.g3240.t1	gb|EOA33816.1| hypothetical protein CARUB_v10021290mg [Capsella rubella]	337	338	1.00E-159	100.3	81.0	92.3	hypothetical protein CARUB_v10021290mg	gbpln	Capsella rubella	AT1G72620.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:27341079-27342401 FORWARD LENGTH=335	337	335	1.00E-159	99.4	80.7	91.7
Rsa1.0_00060.1.g3241.t1	ref|NP_177405.1| germin-like protein subfamily 3 member 1 [Arabidopsis thaliana] gi|18202460|sp|P94040.1|GL31_ARATH RecName: Full=Germin-like protein subfamily 3 member 1; Short=At-GERM1; Short=AtGER1; Short=AtGLP1; Flags: Precursor gi|12323768|gb|AAG51848.1|AC010926_11 germin-like protein; 70589-71215 [Arabidopsis thaliana] gi|1755156|gb|AAB51567.1| germin-like protein [Arabidopsis thaliana] gi|1755158|gb|AAB51568.1| germin-like protein [Arabidopsis thaliana] gi|1755170|gb|AAB51574.1| germin-like protein [Arabidopsis thaliana] gi|1755172|gb|AAB51575.1| germin-like protein [Arabidopsis thaliana] gi|1755180|gb|AAB51579.1| germin-like protein [Arabidopsis thaliana] gi|1755190|gb|AAB51584.1| germin-like protein [Arabidopsis thaliana] gi|1934728|gb|AAB51751.1| germin-like protein [Arabidopsis thaliana] gi|4154285|gb|AAD05223.1| germin-like protein 1 [Arabidopsis thaliana] gi|4666248|dbj|BAA77207.1| germin-like protein precursor [Arabidopsis thaliana] gi|21554080|gb|AAM63161.1| germin-like protein [Arabidopsis thaliana] gi|24417314|gb|AAN60267.1| unknown [Arabidopsis thaliana] gi|332197227|gb|AEE35348.1| germin-	208	208	5.00E-98	100.0	91.8	94.7	germin-like protein subfamily 3 member 1	gbpln	Arabidopsis thaliana	AT1G72610.1 | Symbols: GLP1, ATGER1, GER1 | germin-like protein 1 | chr1:27339302-27339928 REVERSE LENGTH=208	208	208	1.00E-100	100.0	91.8	94.7
Rsa1.0_00060.1.g3242.t1	gb|EOA34366.1| hypothetical protein CARUB_v10021890mg [Capsella rubella]	392	448	0	114.3	86.2	94.1	hypothetical protein CARUB_v10021890mg	gbpln	Capsella rubella	AT1G72540.1 | Symbols: | Protein kinase superfamily protein | chr1:27314932-27316669 REVERSE LENGTH=450	392	450	0	114.8	87.2	94.9

Rsa1.0_00060.1.g3243.t1	gb|EOA35762.1| hypothetical protein CARUB_v10020995mg [Capsella rubella]	295	188	7.00E-54	63.7	34.6	37.6	hypothetical protein CARUB_v10020995mg	gbpln	Capsella rubella	AT1G72530.1 | Symbols: | plastid developmental protein DAG, putative | chr1:27312999-27313937 FORWARD LENGTH=188	295	188	2.00E-55	63.7	33.2	38.0
Rsa1.0_00060.1.g3244.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1362	1307	0	96.0	60.4	74.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1362	1262	1.00E-102	92.7	14.3	22.5
Rsa1.0_00060.1.g3245.t1	gb|EOA35532.1| hypothetical protein CARUB_v10020740mg [Capsella rubella]	291	288	1.00E-135	99.0	85.6	90.7	hypothetical protein CARUB_v10020740mg	gbpln	Capsella rubella	AT1G72490.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17400.1); Has 75 Blast hits to 75 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 4; Plants - 58; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:27289435-27290732 REVERSE LENGTH=287	291	287	1.00E-134	98.6	83.5	89.7
Rsa1.0_00060.1.g3246.t1	ref|NP_177391.1| exocyst subunit exo70-D1 [Arabidopsis thaliana] gi|12325284|gb|AAG52591.1|AC016529_22 unknown protein; 29470-27569 [Arabidopsis thaliana] gi|332197207|gb|AEE35328.1| exocyst subunit exo70-D1 [Arabidopsis thaliana]	629	633	0	100.6	89.7	96.0	exocyst subunit exo70-D1	gbpln	Arabidopsis thaliana	AT1G72470.1 | Symbols: ATEXO70D1, EXO70D1 | exocyst subunit exo70 family protein D1 | chr1:27283759-27285660 FORWARD LENGTH=633	629	633	0	100.6	89.7	96.0
Rsa1.0_00060.1.g3247.t1	gb|EOA34527.1| hypothetical protein CARUB_v10022071mg [Capsella rubella]	649	644	0	99.2	75.7	86.1	hypothetical protein CARUB_v10022071mg	gbpln	Capsella rubella	AT1G72460.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:27279510-27281533 FORWARD LENGTH=644	649	644	0	99.2	74.7	85.7
Rsa1.0_00060.1.g3248.t1	gb|AFC38438.1| small auxin up RNA protein [Sinapis alba]	118	118	5.00E-62	100.0	98.3	99.2	small auxin up RNA protein	gbpln	Sinapis alba	AT1G72430.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:27265150-27265509 REVERSE LENGTH=119	118	119	3.00E-61	100.8	94.9	97.5
Rsa1.0_00060.1.g3249.t1	sp|Q9ZSR8.1|RSSA_BRANA RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor-like protein; AltName: Full=p40 gi|3769681|gb|AAC97937.1| laminin receptor-like protein [Brassica napus]	350	292	1.00E-160	83.4	78.9	79.7	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor-like protein; AltName: Full=p40 gi|3769681|gb|AAC97937.1| laminin receptor-like protein	gbpln	Brassica napus	AT1G72370.1 | Symbols: P40, AP40, RP40, RPSAA | 40s ribosomal protein SA | chr1:27243148-27244842 REVERSE LENGTH=298	350	298	1.00E-137	85.1	67.4	68.9
Rsa1.0_00060.1.g3250.t1	ref|NP_001117587.1| ethylene-responsive transcription factor ERF073 [Arabidopsis thaliana] gi|332197191|gb|AEE35312.1| ethylene-responsive transcription factor ERF073 [Arabidopsis thaliana]	262	260	4.00E-61	99.2	55.7	69.1	ethylene-responsive transcription factor ERF073	gbpln	Arabidopsis thaliana	AT1G72360.3 | Symbols: HRE1 | Integrase-type DNA-binding superfamily protein | chr1:27241904-27242777 FORWARD LENGTH=260	262	260	1.00E-63	99.2	55.7	69.1
Rsa1.0_00060.1.g3251.t1	gb|EOA34308.1| hypothetical protein CARUB_v10021825mg [Capsella rubella]	213	222	1.00E-71	104.2	65.3	75.6	hypothetical protein CARUB_v10021825mg	gbpln	Capsella rubella	AT1G72350.1 | Symbols: | MADS-box transcription factor family protein | chr1:27239273-27239947 REVERSE LENGTH=224	213	224	1.00E-70	105.2	67.1	77.0
Rsa1.0_00060.1.g3252.t1	gb|EOA33336.1| hypothetical protein CARUB_v10020102mg [Capsella rubella]	181	543	7.00E-22	300.0	31.5	33.7	hypothetical protein CARUB_v10020102mg	gbpln	Capsella rubella	AT1G72330.3 | Symbols: ALAAT2 | alanine aminotransferase 2 | chr1:27233637-27236571 FORWARD LENGTH=553	181	553	3.00E-24	305.5	31.5	33.1
Rsa1.0_00060.1.g3253.t1	ref|XP_002887428.1| hypothetical protein ARALYDRAFT_476359 [Arabidopsis lyrata subsp. lyrata] gi|297333269|gb|EFH63687.1| hypothetical protein ARALYDRAFT_476359 [Arabidopsis lyrata subsp. lyrata]	163	324	1.00E-26	198.8	46.0	54.0	hypothetical protein ARALYDRAFT_476359	gbpln	Arabidopsis lyrata	AT1G72310.1 | Symbols: ATL3 | RING/U-box superfamily protein | chr1:27226405-27227379 FORWARD LENGTH=324	163	324	7.00E-25	198.8	40.5	47.2
Rsa1.0_00060.1.g3254.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1357	1274	0	93.9	45.3	61.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1357	575	2.00E-64	42.4	12.3	19.5

Rsa1.0_00060.1.g3255.t1	ref|NP_177366.1| transcription factor bHLH96 [Arabidopsis thaliana] gi|75308860|sp|Q9C7T4.1|BH096_ARATH RecName: Full=Transcription factor bHLH96; AltName: Full=Basic helix-loop-helix protein 96; Short=AtbHLH96; Short=bHLH 96; AltName: Full=Transcription factor EN 15; AltName: Full=bHLH transcription factor bHLH096 gi|12323671|gb|AAG51804.1|AC067754_20 unknown protein; 44011-46213 [Arabidopsis thaliana] gi|20520637|emb|CAD30833.1| basic-helix-loop-helix transcription factor [Arabidopsis thaliana] gi|28392970|gb|AAO41920.1| putative bHLH protein [Arabidopsis thaliana] gi|29824221|gb|AAP04071.1| putative bHLH protein [Arabidopsis thaliana] gi|332197168|gb|AEE35289.1| transcription factor bHLH96 [Arabidopsis thaliana]	323	320	1.00E-142	99.1	81.4	89.2	transcription factor bHLH96	gbpln	Arabidopsis thaliana	AT1G72210.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:27180066-27182268 FORWARD LENGTH=320	323	320	1.00E-144	99.1	81.4	89.2
Rsa1.0_00060.1.g3256.t1	gb|EOA34977.1| hypothetical protein CARUB_v10020065mg [Capsella rubella]	525	567	0	108.0	81.1	86.5	hypothetical protein CARUB_v10020065mg	gbpln	Capsella rubella	AT1G72150.1 | Symbols: PATL1 | PATELLIN 1 | chr1:27148558-27150652 FORWARD LENGTH=573	525	573	0	109.1	77.0	83.6
Rsa1.0_00060.1.g3257.t1	gb|EOA34991.1| hypothetical protein CARUB_v10020083mg [Capsella rubella]	552	556	0	100.7	81.2	90.9	hypothetical protein CARUB_v10020083mg	gbpln	Capsella rubella	AT1G72140.1 | Symbols: | Major facilitator superfamily protein | chr1:27141877-27144346 FORWARD LENGTH=555	552	555	0	100.5	81.7	90.6
Rsa1.0_00060.1.g3258.t1	ref|XP_002887414.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata] gi|297333255|gb|EFH63673.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata]	527	535	0	101.5	76.7	87.5	hypothetical protein ARALYDRAFT_316182	gbpln	Arabidopsis lyrata	AT1G72130.1 | Symbols: | Major facilitator superfamily protein | chr1:27137201-27139223 FORWARD LENGTH=538	527	538	0	102.1	74.8	87.3
Rsa1.0_00060.1.g3259.t1	ref|XP_002887414.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata] gi|297333255|gb|EFH63673.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata]	529	535	0	101.1	73.5	84.5	hypothetical protein ARALYDRAFT_316182	gbpln	Arabidopsis lyrata	AT1G72130.1 | Symbols: | Major facilitator superfamily protein | chr1:27137201-27139223 FORWARD LENGTH=538	529	538	0	101.7	73.0	84.7
Rsa1.0_00060.1.g3260.t1	ref|XP_002887414.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata] gi|297333255|gb|EFH63673.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata]	547	535	0	97.8	75.7	82.6	hypothetical protein ARALYDRAFT_316182	gbpln	Arabidopsis lyrata	AT1G72130.1 | Symbols: | Major facilitator superfamily protein | chr1:27137201-27139223 FORWARD LENGTH=538	547	538	0	98.4	72.6	81.7
Rsa1.0_00060.1.g3261.t1	ref|NP_001117585.1| putative peptide/nitrate transporter [Arabidopsis thaliana] gi|310947338|sp|Q0WSZ6.2|PTR23_ARATH RecName: Full=Probable peptide/nitrate transporter At1g72125 gi|332197156|gb|AEE35277.1| probable peptide/nitrate transporter [Arabidopsis thaliana]	557	561	0	100.7	81.3	89.2	putative peptide/nitrate transporter	gbpln	Arabidopsis thaliana	AT1G72125.1 | Symbols: | Major facilitator superfamily protein | chr1:27134168-27136257 FORWARD LENGTH=561	557	561	0	100.7	81.3	89.2
Rsa1.0_00060.1.g3262.t1	dbj|BAJ33896.1| unnamed protein product [Thellungiella halophila]	479	467	0	97.5	81.0	88.7	unnamed protein product	----	----	AT1G72110.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr1:27129253-27131354 REVERSE LENGTH=479	479	479	0	100.0	78.9	89.4
Rsa1.0_00060.1.g3263.t2	gb|EOA34693.1| hypothetical protein CARUB_v10022259mg [Capsella rubella]	402	401	1.00E-176	99.8	78.4	85.1	hypothetical protein CARUB_v10022259mg	gbpln	Capsella rubella	AT1G72050.2 | Symbols: TFIIIA | transcription factor IIIA | chr1:27115082-27117228 FORWARD LENGTH=412	402	412	1.00E-178	102.5	77.6	84.1
Rsa1.0_00060.1.g3264.t1	ref|XP_002868530.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314366|gb|EFH44789.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	731	851	0	116.4	70.6	81.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G15890.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:5461406-5463961 FORWARD LENGTH=851	731	851	0	116.4	66.3	76.2
Rsa1.0_00060.1.g3265.t1	gb|AET08927.1| sucrose transporter [Brassica napus]	447	514	0	115.0	92.8	94.9	sucrose transporter	gbpln	Brassica napus	AT1G71880.1 | Symbols: SUC1, ATSUC1 | sucrose-proton symporter 1 | chr1:27054334-27056100 FORWARD LENGTH=513	447	513	0	114.8	84.3	90.6
Rsa1.0_00060.1.g3266.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	261	1274	5.00E-21	488.1	31.0	42.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_00060.1.g3267.t1</td><td>ref|NP_173802.1| AP-1 complex subunit gamma-1 [Arabidopsis thaliana] gi|30688616|ref|NP_849701.1| AP-1 complex subunit gamma-1 [Arabidopsis thaliana] gi|75146766|sp|Q84K16.1|AP1G1_ARATH RecName: Full=AP-1 complex subunit gamma-1; AltName: Full=Adapter-related protein complex 1 subunit gamma-1; AltName: Full=Adaptor protein complex AP-1 large subunit gamma-1; AltName: Full=Clathrin assembly protein complex 1 gamma-1 large chain; Short=At-g-Ad; Short=At-gamma-Ad; AltName: Full=Gamma-adaptin 1 gi|28393791|gb|AAO42305.1| putative gamma-adaptin [Arabidopsis thaliana] gi|28973305|gb|AAO63977.1| putative gamma-adaptin [Arabidopsis thaliana] gi|332192327|gb|AEE30448.1| AP-1 complex subunit gamma-1 [Arabidopsis thaliana] gi|332192328|gb|AEE30449.1| AP-1 complex subunit gamma-1 [Arabidopsis thaliana]</td><td>160</td><td>876</td><td>4.00E-28</td><td>547.5</td><td>40.6</td><td>42.5</td><td>AP-1 complex subunit gamma-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G23900.2 | Symbols: GAMMA-ADAPTIN 1 | gamma-adaptin 1 | chr1:8441379-8447152 FORWARD LENGTH=876</td><td>160</td><td>876</td><td>2.00E-30</td><td>547.5</td><td>40.6</td><td>42.5</td></tr>
<tr><td>Rsa1.0_00060.1.g3268.t1</td><td>ref|NP_849877.1| uncharacterized protein [Arabidopsis thaliana] gi|26453012|dbj|BAC43582.1| unknown protein [Arabidopsis thaliana] gi|28973253|gb|AAO63951.1| unknown protein [Arabidopsis thaliana] gi|332197123|gb|AEE35244.1| uncharacterized protein AT1G71865 [Arabidopsis thaliana]</td><td>101</td><td>99</td><td>2.00E-32</td><td>98.0</td><td>88.1</td><td>89.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G71865.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 33 Blast hits to 33 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27030117-27030416 FORWARD LENGTH=99</td><td>101</td><td>99</td><td>3.00E-35</td><td>98.0</td><td>88.1</td><td>89.1</td></tr>
<tr><td>Rsa1.0_00060.1.g3269.t1</td><td>gb|AAF43237.1|AC012654_21 Contains similarity to the vegetative incompatibility protein HET-E-1 from Podospora ansering gi|3023956; It contains 5 WD40 domains PF|00400 [Arabidopsis thaliana]</td><td>119</td><td>370</td><td>3.00E-32</td><td>310.9</td><td>58.0</td><td>61.3</td><td>Contains similarity to the vegetative incompatibility protein HET-E-1 from Podospora ansering gi|3023956; It contains 5 WD40 domains PF|00400</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G71840.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr1:27022424-27024380 FORWARD LENGTH=407</td><td>119</td><td>407</td><td>6.00E-35</td><td>342.0</td><td>58.0</td><td>61.3</td></tr>
<tr><td>Rsa1.0_00060.1.g3270.t1</td><td>ref|NP_850465.1| cytochrome P450, family 709, subfamily B, polypeptide 1 [Arabidopsis thaliana] gi|330255683|gb|AEC10777.1| cytochrome P450, family 709, subfamily B, polypeptide 1 [Arabidopsis thaliana]</td><td>200</td><td>403</td><td>5.00E-89</td><td>201.5</td><td>75.5</td><td>87.5</td><td>cytochrome P450, family 709, subfamily B, polypeptide 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46960.1 | Symbols: CYP709B1 | cytochrome P450, family 709, subfamily B, polypeptide 1 | chr2:19292295-19293765 REVERSE LENGTH=403</td><td>200</td><td>403</td><td>2.00E-91</td><td>201.5</td><td>75.5</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00060.1.g3271.t3</td><td>gb|AAF43237.1|AC012654_21 Contains similarity to the vegetative incompatibility protein HET-E-1 from Podospora ansering gi|3023956; It contains 5 WD40 domains PF|00400 [Arabidopsis thaliana]</td><td>379</td><td>370</td><td>0</td><td>97.6</td><td>86.0</td><td>92.9</td><td>Contains similarity to the vegetative incompatibility protein HET-E-1 from Podospora ansering gi|3023956; It contains 5 WD40 domains PF|00400</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G71840.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr1:27022424-27024380 FORWARD LENGTH=407</td><td>379</td><td>407</td><td>0</td><td>107.4</td><td>85.2</td><td>91.8</td></tr>
<tr><td>Rsa1.0_00060.1.g3272.t1</td><td>ref|XP_002887391.1| hypothetical protein ARALYDRAFT_476305 [Arabidopsis lyrata subsp. lyrata] gi|297333232|gb|EFH63650.1| hypothetical protein ARALYDRAFT_476305 [Arabidopsis lyrata subsp. lyrata]</td><td>851</td><td>785</td><td>0</td><td>92.2</td><td>85.1</td><td>87.7</td><td>hypothetical protein ARALYDRAFT_476305</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G71820.1 | Symbols: SEC6 | SEC6 | chr1:27010022-27016745 FORWARD LENGTH=752</td><td>851</td><td>752</td><td>0</td><td>88.4</td><td>84.3</td><td>86.1</td></tr>
<tr><td>Rsa1.0_00060.1.g3273.t1</td><td>gb|EOA34351.1| hypothetical protein CARUB_v10021875mg [Capsella rubella]</td><td>453</td><td>458</td><td>0</td><td>101.1</td><td>85.9</td><td>91.2</td><td>hypothetical protein CARUB_v10021875mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G71800.1 | Symbols: CSTF64 | cleavage stimulating factor 64 | chr1:26999606-27001850 FORWARD LENGTH=461</td><td>453</td><td>461</td><td>0</td><td>101.8</td><td>82.6</td><td>89.2</td></tr>
<tr><td>Rsa1.0_00060.1.g3274.t1</td><td>gb|EOA35753.1| hypothetical protein CARUB_v10020985mg [Capsella rubella]</td><td>233</td><td>194</td><td>1.00E-46</td><td>83.3</td><td>40.8</td><td>45.1</td><td>hypothetical protein CARUB_v10020985mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G71780.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; Has 34 Blast hits to 34 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26995406-26996638 REVERSE LENGTH=197</td><td>233</td><td>197</td><td>9.00E-47</td><td>84.5</td><td>39.9</td><td>45.1</td></tr>
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Rsa1.0_00060.1.g3275.t1	ref|XP_002888846.1| hypothetical protein ARALYDRAFT_339396 [Arabidopsis lyrata subsp. lyrata] gi|297334687|gb|EFH65105.1| hypothetical protein ARALYDRAFT_339396 [Arabidopsis lyrata subsp. lyrata]	662	685	0	103.5	83.1	89.6	hypothetical protein ARALYDRAFT_339396	gbpln	Arabidopsis lyrata	AT1G71770.2 | Symbols: PAB5 | poly(A)-binding protein 5 | chr1:26990777-26993489 REVERSE LENGTH=682	662	682	0	103.0	79.6	87.5
Rsa1.0_00060.1.g3276.t1	ref|NP_177295.1| receptor like protein 11 [Arabidopsis thaliana] gi|12323717|gb|AAG51813.1|AC016163_2 putative disease resistance protein; 69620-67266 [Arabidopsis thaliana] gi|332197075|gb|AEE35196.1| receptor like protein 11 [Arabidopsis thaliana]	740	784	0	105.9	68.9	79.5	receptor like protein 11	gbpln	Arabidopsis thaliana	AT1G71390.1 | Symbols: AtRLP11, RLP11 | receptor like protein 11 | chr1:26906453-26908807 FORWARD LENGTH=784	740	784	0	105.9	68.9	79.5
Rsa1.0_00060.1.g3277.t1	gb|EOA15757.1| hypothetical protein CARUB_v10006835mg [Capsella rubella]	441	438	0	99.3	93.0	96.1	hypothetical protein CARUB_v10006835mg	gbpln	Capsella rubella	AT5G42090.1 | Symbols: | Lung seven transmembrane receptor family protein | chr5:16826830-16828149 FORWARD LENGTH=439	441	439	0	99.5	91.4	95.5
Rsa1.0_00060.1.g3278.t1	ref|XP_002887372.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata] gi|297333213|gb|EFH63631.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata]	206	832	3.00E-76	403.9	71.8	81.1	hypothetical protein ARALYDRAFT_476271	gbpln	Arabidopsis lyrata	AT1G71390.1 | Symbols: AtRLP11, RLP11 | receptor like protein 11 | chr1:26906453-26908807 FORWARD LENGTH=784	206	784	4.00E-73	380.6	68.0	80.1
Rsa1.0_00060.1.g3279.t1	gb|EOA34941.1| hypothetical protein CARUB_v10020025mg [Capsella rubella]	569	592	0	104.0	75.4	83.1	hypothetical protein CARUB_v10020025mg	gbpln	Capsella rubella	AT1G71360.1 | Symbols: | Galactose-binding protein | chr1:26892214-26894166 REVERSE LENGTH=596	569	596	0	104.7	72.9	82.6
Rsa1.0_00060.1.g3280.t1	ref|NP_851080.1| serine hydroxymethyltransferase 2 [Arabidopsis thaliana] gi|227202628|dbj|BAH56787.1| AT5G26780 [Arabidopsis thaliana] gi|332006219|gb|AED93602.1| serine hydroxymethyltransferase 2 [Arabidopsis thaliana]	539	517	0	95.9	88.3	91.3	serine hydroxymethyltransferase 2	gbpln	Arabidopsis thaliana	AT5G26780.1 | Symbols: SHM2 | serine hydroxymethyltransferase 2 | chr5:9418299-9421725 FORWARD LENGTH=517	539	517	0	95.9	88.3	91.3
Rsa1.0_00060.1.g3281.t1	ref|XP_002887361.1| hydrolase/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297333202|gb|EFH63620.1| hydrolase/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	420	400	0	95.2	77.6	82.4	hydrolase/ zinc ion binding protein	gbpln	Arabidopsis lyrata	AT5G24670.1 | Symbols: | Cytidine/deoxycytidylate deaminase family protein | chr5:8448880-8451046 FORWARD LENGTH=400	420	400	0	95.2	75.2	81.2
Rsa1.0_00060.1.g3282.t1	ref|NP_177287.1| cobalt ion binding protein [Arabidopsis thaliana] gi|30698791|ref|NP_849876.1| cobalt ion binding protein [Arabidopsis thaliana] gi|12323832|gb|AAG51886.1|AC016162_7 hypothetical protein; 63020-64147 [Arabidopsis thaliana] gi|22135986|gb|AAM91575.1| unknown protein [Arabidopsis thaliana] gi|23198344|gb|AAN15699.1| unknown protein [Arabidopsis thaliana] gi|332197065|gb|AEE35186.1| cobalt ion binding protein [Arabidopsis thaliana] gi|332197066|gb|AEE35187.1| cobalt ion binding protein [Arabidopsis thaliana]	179	176	3.00E-79	98.3	81.0	87.7	cobalt ion binding protein	gbpln	Arabidopsis thaliana	AT1G71310.1 | Symbols: | cobalt ion binding | chr1:26878717-26879844 REVERSE LENGTH=176	179	176	1.00E-81	98.3	81.0	87.7
Rsa1.0_00060.1.g3283.t1	ref|XP_002887358.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333199|gb|EFH63617.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	347	374	1.00E-163	107.8	83.3	91.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G71250.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:26860125-26861582 FORWARD LENGTH=374	347	374	1.00E-165	107.8	81.8	91.1

Rsa1.0_00061.1.g3284.t1	ref|NP_192117.1| GTP-binding protein SAR1A [Arabidopsis thaliana] gi|3334323|sp|O04834.1|SAR1A_ARATH RecName: Full=GTP-binding protein SAR1A gi|1314860|gb|AAA99827.1| Sar1 homolog [Arabidopsis thaliana] gi|2104532|gb|AAC78700.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|2104550|gb|AAB57799.1| AGAA.4 [Arabidopsis thaliana] gi|7268592|emb|CAB80701.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|17529144|gb|AAL38798.1| putative SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|20465729|gb|AAM20333.1| putative SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|21618030|gb|AAM67080.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|332656722|gb|AEE82122.1| GTP-binding protein SAR1A [Arabidopsis thaliana]	458	193	1.00E-101	42.1	41.3	41.7	GTP-binding protein SAR1A	gbpln	Arabidopsis thaliana	AT4G02080.1 | Symbols: ASAR1, ATSARA1C, ATSAR2, SAR2 | secretion-associated RAS super family 2 | chr4:921554-922547 FORWARD LENGTH=193	458	193	1.00E-104	42.1	41.3	41.7
Rsa1.0_00061.1.g3285.t1	sp|P34794.1|RUB2_BRANA RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor gi|415925|emb|CAA81736.1| chaperonin-60 alpha subunit [Brassica napus]	183	583	5.00E-60	318.6	63.9	66.7	RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor gi|415925|emb|CAA81736.1| chaperonin-60 alpha subunit	gbpln	Brassica napus	AT2G28000.1 | Symbols: CPN60A, CH-CPN60A, SLP | chaperonin-60alpha | chr2:11926603-11929184 FORWARD LENGTH=586	183	586	4.00E-55	320.2	57.9	60.7
Rsa1.0_00061.1.g3286.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00061.1.g3287.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00061.1.g3288.t1	gb|EOA21485.1| hypothetical protein CARUB_v10001882mg [Capsella rubella]	214	230	1.00E-71	107.5	76.6	86.4	hypothetical protein CARUB_v10001882mg	gbpln	Capsella rubella	AT4G02075.1 | Symbols: PIT1 | RING/FYVE/PHD zinc finger superfamily protein | chr4:913555-916414 REVERSE LENGTH=218	214	218	4.00E-74	101.9	77.6	86.9
Rsa1.0_00061.1.g3289.t1	dbj|BAJ33893.1| unnamed protein product [Thellungiella halophila]	718	716	0	99.7	96.2	97.9	unnamed protein product	----	----	AT4G02060.2 | Symbols: PRL | Minichromosome maintenance (MCM2/3/5) family protein | chr4:901484-905297 FORWARD LENGTH=716	718	716	0	99.7	94.7	97.4
Rsa1.0_00061.1.g3290.t1	ref|XP_002872859.1| hypothetical protein ARALYDRAFT_327595 [Arabidopsis lyrata subsp. lyrata] gi|297318696|gb|EFH49118.1| hypothetical protein ARALYDRAFT_327595 [Arabidopsis lyrata subsp. lyrata]	511	515	0	100.8	92.4	96.5	hypothetical protein ARALYDRAFT_327595	gbpln	Arabidopsis lyrata	AT4G02050.1 | Symbols: STP7 | sugar transporter protein 7 | chr4:898387-900095 REVERSE LENGTH=513	511	513	0	100.4	92.0	95.9
Rsa1.0_00061.1.g3291.t1	ref|XP_002874944.1| hypothetical protein ARALYDRAFT_490376 [Arabidopsis lyrata subsp. lyrata] gi|297320781|gb|EFH51203.1| hypothetical protein ARALYDRAFT_490376 [Arabidopsis lyrata subsp. lyrata]	152	154	6.00E-35	101.3	59.9	71.7	hypothetical protein ARALYDRAFT_490376	gbpln	Arabidopsis lyrata	AT4G02040.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 30 Blast hits to 30 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:897563-898021 FORWARD LENGTH=152	152	152	3.00E-34	100.0	57.2	70.4
Rsa1.0_00061.1.g3292.t1	gb|EOA19997.1| hypothetical protein CARUB_v10000264mg [Capsella rubella]	759	786	0	103.6	91.0	94.5	hypothetical protein CARUB_v10000264mg	gbpln	Capsella rubella	AT4G02030.1 | Symbols: | Vps51/Vps67 family (components of vesicular transport) protein | chr4:892262-897175 FORWARD LENGTH=780	759	780	0	102.8	90.8	94.3
Rsa1.0_00061.1.g3293.t6	ref|XP_002874946.1| swinger [Arabidopsis lyrata subsp. lyrata] gi|297320783|gb|EFH51205.1| swinger [Arabidopsis lyrata subsp. lyrata]	908	846	0	93.2	69.6	75.3	swinger	gbpln	Arabidopsis lyrata	AT4G02020.1 | Symbols: EZA1, SWN, SDG10 | SET domain-containing protein | chr4:886693-891743 FORWARD LENGTH=856	908	856	0	94.3	69.2	76.1
Rsa1.0_00061.1.g3294.t1	gb|ADQ20113.1| stachyose synthase [Brassica napus]	874	873	0	99.9	92.6	97.0	stachyose synthase	gbpln	Brassica napus	AT4G01970.1 | Symbols: AtSTS, STS | stachyose synthase | chr4:854073-856953 REVERSE LENGTH=876	874	876	0	100.2	84.8	93.1

Rsa1.0_00061.1.g3295.t1	ref|NP_192105.1| uncharacterized protein [Arabidopsis thaliana] gi|4558565|gb|AAD22658.1|AC007138_22 predicted protein of unknown function [Arabidopsis thaliana] gi|7268580|emb|CAB80689.1| predicted protein of unknown function [Arabidopsis thaliana] gi|21537343|gb|AAM61684.1| unknown [Arabidopsis thaliana] gi|88196763|gb|ABD43024.1| At4g01960 [Arabidopsis thaliana] gi|110738203|dbj|BAF01032.1| hypothetical protein [Arabidopsis thaliana] gi|332656705|gb|AEE82105.1| uncharacterized protein AT4G01960 [Arabidopsis thaliana]	229	236	2.00E-81	103.1	80.8	89.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G01960.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02380.1); Has 67 Blast hits to 67 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:851387-852441 REVERSE LENGTH=236	229	236	7.00E-84	103.1	80.8	89.1
Rsa1.0_00061.1.g3296.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1454	1142	0	78.5	22.8	32.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1454	575	1.00E-40	39.5	5.8	9.1
Rsa1.0_00061.1.g3297.t1	dbj|BAJ34109.1| unnamed protein product [Thellungiella halophila]	521	521	0	100.0	88.1	93.7	unnamed protein product	----	----	AT4G01950.1 | Symbols: ATGPAT3, GPAT3 | glycerol-3-phosphate acyltransferase 3 | chr4:844597-846710 REVERSE LENGTH=520	521	520	0	99.8	87.1	93.5
Rsa1.0_00061.1.g3298.t1	gb|EOA22935.1| hypothetical protein CARUB_v10003671mg, partial [Capsella rubella]	517	145	5.00E-17	28.0	9.9	13.3	hypothetical protein CARUB_v10003671mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00061.1.g3299.t1	gb|EOA30146.1| hypothetical protein CARUB_v10013253mg [Capsella rubella]	104	609	4.00E-44	585.6	83.7	87.5	hypothetical protein CARUB_v10013253mg	gbpln	Capsella rubella	AT3G18060.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:6183880-6186788 FORWARD LENGTH=609	104	609	7.00E-47	585.6	83.7	86.5
Rsa1.0_00061.1.g3300.t1	gb|AAF98181.1|AC000107_4 F17F8.5 [Arabidopsis thaliana]	301	872	7.00E-70	289.7	49.2	67.4	F17F8.5	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	301	746	4.00E-46	247.8	38.5	54.2
Rsa1.0_00061.1.g3301.t1	ref|XP_002872902.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata] gi|297318739|gb|EFH49161.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata]	348	356	1.00E-144	102.3	74.7	81.9	hypothetical protein ARALYDRAFT_912111	gbpln	Arabidopsis lyrata	AT4G01220.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr4:513431-515648 REVERSE LENGTH=360	348	360	1.00E-144	103.4	70.4	77.3
Rsa1.0_00061.1.g3302.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00061.1.g3303.t1	ref|XP_002872902.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata] gi|297318739|gb|EFH49161.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata]	342	356	1.00E-145	104.1	72.8	78.9	hypothetical protein ARALYDRAFT_912111	gbpln	Arabidopsis lyrata	AT4G01220.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr4:513431-515648 REVERSE LENGTH=360	342	360	1.00E-145	105.3	71.9	78.7
Rsa1.0_00061.1.g3304.t2	ref|XP_002874954.1| hypothetical protein ARALYDRAFT_327611 [Arabidopsis lyrata subsp. lyrata] gi|297320791|gb|EFH51213.1| hypothetical protein ARALYDRAFT_327611 [Arabidopsis lyrata subsp. lyrata]	386	226	3.00E-93	58.5	47.4	49.5	hypothetical protein ARALYDRAFT_327611	gbpln	Arabidopsis lyrata	AT4G01883.1 | Symbols: | Polyketide cyclase / dehydrase and lipid transport protein | chr4:813162-814800 FORWARD LENGTH=224	386	224	1.00E-90	58.0	45.9	49.2
Rsa1.0_00061.1.g3305.t1	ref|NP_192095.2| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|30678983|ref|NP_849536.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|19699003|gb|AAL91237.1| unknown protein [Arabidopsis thaliana] gi|32306503|gb|AAP78935.1| At4g01860 [Arabidopsis thaliana] gi|332656686|gb|AEE82086.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|332656687|gb|AEE82087.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	1615	1308	0	81.0	67.2	72.3	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G01860.2 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr4:801713-808018 REVERSE LENGTH=1308	1615	1308	0	81.0	67.2	72.3

Rsa1.0_00061.1.g3306.t1	sp|Q5DNB1.1|METK_BRARP RecName: Full=S–adenosylmethionine synthase; Short=AdoMet synthase; AltName: Full=Methionine adenosyltransferase; Short=MAT gi|75306462|sp|Q94FA4.1|METK5_BRAJU RecName: Full=S–adenosylmethionine synthase 5; Short=AdoMet synthase 5; AltName: Full=Methionine adenosyltransferase 5; Short=MAT 5 gi|14600072|gb|AAK71235.1| S–adenosylmethionine synthetase [Brassica juncea] gi|56130947|gb|AAV80205.1| S–adenosyl–L–methionine synthetase [Brassica rapa subsp. pekinensis]	393	393	0	100.0	99.7	100.0	RecName: Full=S–adenosylmethionine synthase; Short=AdoMet synthase; AltName: Full=Methionine adenosyltransferase; Short=MAT gi|75306462|sp|Q94FA4.1|METK5_BRAJU RecName: Full=S–adenosylmethionine synthase 5; Short=AdoMet synthase 5; AltName: Full=Methionine adenosyltransferase 5; Short=MAT 5 gi|14600072|gb|AAK71235.1| S–adenosylmethionine svnthetase	gbpln	Brassica juncea	AT4G01850.2 | Symbols: SAM–2, MAT2, SAM2, AtSAM2 | S–adenosylmethionine synthetase 2 | chr4:796298–797479 REVERSE LENGTH=393	393	393	0	100.0	99.2	99.7
Rsa1.0_00061.1.g3307.t1	gb|EOA20795.1| hypothetical protein CARUB_v10001130mg [Capsella rubella]	401	396	0	98.8	84.0	89.0	hypothetical protein CARUB_v10001130mg	gbpln	Capsella rubella	AT4G01840.1 | Symbols: KCO5, ATTPK5, ATKCO5, TPK5 | Ca2+ activated outward rectifying K+ channel 5 | chr4:793403–794933 FORWARD LENGTH=408	401	408	1.00E–178	101.7	81.5	87.5
Rsa1.0_00061.1.g3308.t1	ref|XP_002872875.1| hypothetical protein ARALYDRAFT_490398 [Arabidopsis lyrata subsp. lyrata] gi|297318712|gb|EFH49134.1| hypothetical protein ARALYDRAFT_490398 [Arabidopsis lyrata subsp. lyrata]	651	882	0	135.5	67.7	69.3	hypothetical protein ARALYDRAFT_490398	gbpln	Arabidopsis lyrata	AT4G01810.1 | Symbols: | Sec23/Sec24 protein transport family protein | chr4:776734–779802 REVERSE LENGTH=880	651	880	0	135.2	67.6	69.3
Rsa1.0_00061.1.g3309.t1	gb|EOA22935.1| hypothetical protein CARUB_v10003671mg, partial [Capsella rubella]	600	145	7.00E–19	24.2	9.2	14.3	hypothetical protein CARUB_v10003671mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00061.1.g3310.t1	ref|NP_192081.1| putative WRKY transcription factor 47 [Arabidopsis thaliana] gi|20978798|sp|Q9ZSI7.2|WRK47_ARATH RecName: Full=Probable WRKY transcription factor 47; AltName: Full=WRKY DNA–binding protein 47 gi|19172392|gb|AAL85881.1|AF480165_1 WRKY transcription factor 47 [Arabidopsis thaliana] gi|7268215|emb|CAB77742.1| putative DNA–binding protein [Arabidopsis thaliana] gi|30794136|gb|AAP40510.1| putative WRKY family transcription factor [Arabidopsis thaliana] gi|110738911|dbj|BAF01377.1| putative DNA–binding protein [Arabidopsis thaliana] gi|115311505|gb|ABI93933.1| At4g01720 [Arabidopsis thaliana] gi|332656669|gb|AEE82069.1| putative WRKY transcription factor 47 [Arabidopsis thaliana]	488	489	0	100.2	79.9	87.5	putative WRKY transcription factor 47	gbpln	Arabidopsis thaliana	AT4G01720.1 | Symbols: WRKY47, AtWRKY47 | WRKY family transcription factor | chr4:744949–748219 FORWARD LENGTH=489	488	489	0	100.2	79.9	87.5
Rsa1.0_00062.1.g3311.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3312.t1	gb|AAF24531.1|AC007534_12 F7F22.17 [Arabidopsis thaliana]	629	1799	7.00E–92	286.0	29.1	39.7	F7F22.17	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3313.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3314.t1	gb|EOA28006.1| hypothetical protein CARUB_v10024183mg [Capsella rubella]	69	170	2.00E–19	246.4	69.6	72.5	hypothetical protein CARUB_v10024183mg	gbpln	Capsella rubella	AT5G37070.1 | Symbols: | Protein of unknown function, DUF538 | chr5:14651091–14652147 FORWARD LENGTH=170	69	170	8.00E–22	246.4	66.7	75.4
Rsa1.0_00062.1.g3315.t1	dbj|BAJ33618.1| unnamed protein product [Thellungiella halophila]	508	510	0	100.4	90.4	93.3	unnamed protein product	––––	––––	AT3G50660.1 | Symbols: DWF4, CYP90B1, CLM, SNP2, SAV1, PSC1 | Cytochrome P450 superfamily protein | chr3:18814262–18817168 REVERSE LENGTH=513	508	513	0	101.0	87.6	90.9
Rsa1.0_00062.1.g3316.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1878	1213	0	64.6	31.1	40.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I–like superfamily protein | chr1:16528880–16531065 REVERSE LENGTH=626	1878	626	5.00E–74	33.3	7.9	12.1
Rsa1.0_00062.1.g3317.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3318.t1	dbj|BAB01972.1| copia–like retrotransposable element [Arabidopsis thaliana]	169	1499	4.00E–25	887.0	35.5	50.3	copia–like retrotransposable element	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00062.1.g3319.t1	ref|XP_002877765.1| UDP-glucosyl transferase 72E1 [Arabidopsis lyrata subsp. lyrata] gi|297323603|gb|EFH54024.1| UDP-glucosyl transferase 72E1 [Arabidopsis lyrata subsp. lyrata]	488	487	0	99.8	76.6	86.9	UDP-glucosyl transferase 72E1	gbpln	Arabidopsis lyrata	AT3G50740.1 | Symbols: UGT72E1 | UDP-glucosyl transferase 72E1 | chr3:18855348-18856811 REVERSE LENGTH=487	488	487	0	99.8	75.4	86.9
Rsa1.0_00062.1.g3320.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3321.t1	ref|NP_566938.1| coniferyl-alcohol glucosyltransferase [Arabidopsis thaliana] gi|75306318|sp|Q94A84.1|U72E1_ARATH RecName: Full=UDP-glycosyltransferase 72E1 gi|15146272|gb|AAK83619.1| AT3g50740/T3A5_120 [Arabidopsis thaliana] gi|53749150|gb|AAU90060.1| At3g50740 [Arabidopsis thaliana] gi|332645182|gb|AEE78703.1| UDP-glucosyl transferase 72E1 [Arabidopsis thaliana]	482	487	0	101.0	80.1	90.0	coniferyl-alcohol glucosyltransferase	gbpln	Arabidopsis thaliana	AT3G50740.1 | Symbols: UGT72E1 | UDP-glucosyl transferase 72E1 | chr3:18855348-18856811 REVERSE LENGTH=487	482	487	0	101.0	80.1	90.0
Rsa1.0_00062.1.g3322.t1	#	#	#	#	#	#	#	-	----	----	AT2G23450.1 | Symbols: | Protein kinase superfamily protein | chr2:9988926-9991244 REVERSE LENGTH=708	62	708	2.00E-11	1141.9	54.8	67.7
Rsa1.0_00062.1.g3323.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3324.t1	ref|NP_001154670.1| PLATZ transcription factor family protein [Arabidopsis thaliana] gi|254801606|sp|P0CB19.1|Y3081_ARATH RecName: Full=Uncharacterized protein At3g50808 gi|332645191|gb|AEE78712.1| PLATZ transcription factor family protein [Arabidopsis thaliana]	226	110	5.00E-27	48.7	25.2	36.3	PLATZ transcription factor family protein	gbpln	Arabidopsis thaliana	AT3G50808.1 | Symbols: | PLATZ transcription factor family protein | chr3:18887614-18888047 REVERSE LENGTH=110	226	110	2.00E-29	48.7	25.2	36.3
Rsa1.0_00062.1.g3325.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3326.t1	ref|XP_002877774.1| photosystem II subunit O-2 [Arabidopsis lyrata subsp. lyrata] gi|297323612|gb|EFH54033.1| photosystem II subunit O-2 [Arabidopsis lyrata subsp. lyrata]	333	331	0	99.4	96.4	97.6	photosystem II subunit O-2	gbpln	Arabidopsis lyrata	AT3G50820.1 | Symbols: PSBO2, PSBO-2, OEC33 | photosystem II subunit O-2 | chr3:18891008-18892311 REVERSE LENGTH=331	333	331	0	99.4	95.5	97.0
Rsa1.0_00062.1.g3327.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	689	723	0	104.9	56.6	74.0	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	689	696	5.00E-46	101.0	21.2	37.7
Rsa1.0_00062.1.g3328.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3329.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3330.t1	ref|XP_002876050.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321888|gb|EFH52309.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	283	294	1.00E-113	103.9	80.9	87.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G50870.1 | Symbols: MNP, HAN, GATA18 | GATA type zinc finger transcription factor family protein | chr3:18911112-18912369 FORWARD LENGTH=295	283	295	1.00E-115	104.2	79.5	86.6
Rsa1.0_00062.1.g3331.t1	ref|XP_002876053.1| hypothetical protein ARALYDRAFT_906429 [Arabidopsis lyrata subsp. lyrata] gi|297321891|gb|EFH52312.1| hypothetical protein ARALYDRAFT_906429 [Arabidopsis lyrata subsp. lyrata]	108	114	7.00E-40	105.6	77.8	85.2	hypothetical protein ARALYDRAFT_906429	gbpln	Arabidopsis lyrata	AT3G50900.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66490.1); Has 45 Blast hits to 45 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:18918122-18918466 FORWARD LENGTH=114	108	114	2.00E-42	105.6	75.9	84.3
Rsa1.0_00062.1.g3332.t1	gb|EOA23929.1| hypothetical protein CARUB_v10017143mg [Capsella rubella]	199	444	6.00E-33	223.1	37.7	43.2	hypothetical protein CARUB_v10017143mg	gbpln	Capsella rubella	AT3G50910.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66480.1); Has 76 Blast hits to 75 proteins in 28 species: Archae - 0; Bacteria - 10; Metazoa - 7; Fungi - 2; Plants - 49; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr3:18920189-18921999 FORWARD LENGTH=447	199	447	1.00E-32	224.6	36.2	41.7
Rsa1.0_00062.1.g3333.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00062.1.g3334.t1	ref|XP_002876055.1| hypothetical protein ARALYDRAFT_906432 [Arabidopsis lyrata subsp. lyrata] gi|297321893|gb|EFH52314.1| hypothetical protein ARALYDRAFT_906432 [Arabidopsis lyrata subsp. lyrata]	222	268	2.00E-60	120.7	66.7	75.2	hypothetical protein ARALYDRAFT_906432	gbpln	Arabidopsis lyrata	AT5G66440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G34560.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:26530274-26531032 REVERSE LENGTH=252	222	252	2.00E-51	113.5	54.1	68.0
Rsa1.0_00062.1.g3335.t1	ref|NP_568344.2| myb family transcription factor [Arabidopsis thaliana] gi|332005027|gb|AED92410.1| myb family transcription factor [Arabidopsis thaliana]	378	387	1.00E-147	102.4	78.8	85.2	myb family transcription factor	gbpln	Arabidopsis thaliana	AT5G17300.1 | Symbols: RVE1 | Homeodomain-like superfamily protein | chr5:5690435-5692435 REVERSE LENGTH=387	378	387	1.00E-149	102.4	78.8	85.2
Rsa1.0_00062.1.g3336.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3337.t1	gb|EOA19553.1| hypothetical protein CARUB_v10002574mg [Capsella rubella]	1061	724	0	68.2	41.0	49.3	hypothetical protein CARUB_v10002574mg	gbpln	Capsella rubella	AT5G17320.1 | Symbols: HDG9 | homeodomain GLABROUS 9 | chr5:5703380-5707637 REVERSE LENGTH=718	1061	718	0	67.7	40.1	48.6
Rsa1.0_00062.1.g3338.t3	gb|ACB59199.1| copia-like protein [Brassica oleracea]	829	975	1.00E-121	117.6	31.7	40.4	copia-like protein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	829	1262	5.00E-37	152.2	11.8	18.3
Rsa1.0_00062.1.g3339.t1	gb|EOA20468.1| hypothetical protein CARUB_v10000781mg [Capsella rubella]	195	502	4.00E-58	257.4	64.1	70.3	hypothetical protein CARUB_v10000781mg	gbpln	Capsella rubella	AT5G17330.1 | Symbols: GAD, GAD1 | glutamate decarboxylase | chr5:5711141-5714839 FORWARD LENGTH=502	195	502	9.00E-60	257.4	62.6	70.8
Rsa1.0_00062.1.g3340.t2	gb|ABA70759.1| baby boom interacting protein 1B [Brassica napus]	116	711	6.00E-20	612.9	39.7	44.8	baby boom interacting protein 1B	gbpln	Brassica napus	AT1G73360.1 | Symbols: HDG11, EDT1, ATHDG11 | homeodomain GLABROUS 11 | chr1:27578893-27581820 REVERSE LENGTH=722	116	722	1.00E-21	622.4	37.9	44.8
Rsa1.0_00062.1.g3341.t1	ref|NP_197236.1| Putative membrane lipoprotein [Arabidopsis thaliana] gi|10177079|dbj|BAB10521.1| unnamed protein product [Arabidopsis thaliana] gi|62867603|gb|AAY17405.1| At5g17340 [Arabidopsis thaliana] gi|66841346|gb|AAY57310.1| At5g17340 [Arabidopsis thaliana] gi|332005032|gb|AED92415.1| Putative membrane lipoprotein [Arabidopsis thaliana]	164	160	6.00E-52	97.6	70.7	82.9	Putative membrane lipoprotein	gbpln	Arabidopsis thaliana	AT5G17340.1 | Symbols: | Putative membrane lipoprotein | chr5:5715736-5716218 REVERSE LENGTH=160	164	160	2.00E-54	97.6	70.7	82.9
Rsa1.0_00062.1.g3342.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00062.1.g3343.t1	ref|NP_197237.1| uncharacterized protein [Arabidopsis thaliana] gi|9755758|emb|CAC01730.1| putative protein [Arabidopsis thaliana] gi|21537084|gb|AAM61425.1| unknown [Arabidopsis thaliana] gi|110737524|dbj|BAF00704.1| hypothetical protein [Arabidopsis thaliana] gi|332005033|gb|AED92416.1| uncharacterized protein AT5G17350 [Arabidopsis thaliana]	186	183	5.00E-69	98.4	78.0	84.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G17350.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 8 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03280.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5718853-5719404 FORWARD LENGTH=183	186	183	2.00E-71	98.4	78.0	84.4
Rsa1.0_00062.1.g3344.t1	gb|EOA20498.1| hypothetical protein CARUB_v10000811mg [Capsella rubella]	536	492	0	91.8	69.8	78.7	hypothetical protein CARUB_v10000811mg	gbpln	Capsella rubella	AT5G17370.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:5721801-5724719 REVERSE LENGTH=529	536	529	0	98.7	69.6	77.8
Rsa1.0_00062.1.g3345.t5	gb|ACS68197.1| cellulose synthase 7.1 catalytic subunit [Brassica napus]	1016	1031	0	101.5	98.2	99.0	cellulose synthase 7.1 catalytic subunit	gbpln	Brassica napus	AT5G17420.1 | Symbols: IRX3, CESA7, ATCESA7, MUR10 | Cellulose synthase family protein | chr5:5736859-5741407 REVERSE LENGTH=1026	1016	1026	0	101.0	95.2	97.2
Rsa1.0_00062.1.g3346.t1	ref|XP_002873828.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319665|gb|EFH50087.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	579	587	0	101.4	80.1	86.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G17430.1 | Symbols: BBM | Integrase-type DNA-binding superfamily protein | chr5:5742542-5745568 REVERSE LENGTH=584	579	584	0	100.9	77.4	83.4
Rsa1.0_00062.1.g3347.t1	ref|NP_568347.1| LUC7 related protein [Arabidopsis thaliana] gi|15450599|gb|AAK96571.1| AT5g17440/K3M16_10 [Arabidopsis thaliana] gi|17380624|gb|AAL36075.1| AT5g17440/K3M16_10 [Arabidopsis thaliana] gi|332005043|gb|AED92426.1| LUC7 related protein [Arabidopsis thaliana]	406	404	1.00E-174	99.5	73.4	76.4	LUC7 related protein	gbpln	Arabidopsis thaliana	AT5G17440.1 | Symbols: | LUC7 related protein | chr5:5749849-5753415 FORWARD LENGTH=404	406	404	1.00E-177	99.5	73.4	76.4

Rsa1.0_00062.1.g3348.t2	gb|EOA37750.1| hypothetical protein CARUB_v10012565mg [Capsella rubella]	549	679	1.00E-114	123.7	45.9	66.1	hypothetical protein CARUB_v10012565mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	549	696	3.00E-21	126.8	14.4	23.7
Rsa1.0_00062.1.g3349.t2	ref|NP_197247.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|297807767|ref|XP_002871767.1| hypothetical protein ARALYDRAFT_488611 [Arabidopsis lyrata subsp. lyrata] gi|9755769|emb|CAC01889.1| farnesylated protein ATFP6-like protein [Arabidopsis thaliana] gi|117168109|gb|ABK32137.1| At5g17450 [Arabidopsis thaliana] gi|297317604|gb|EFH48026.1| hypothetical protein ARALYDRAFT_488611 [Arabidopsis lyrata subsp. lyrata] gi|332005044|gb|AED92427.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|482555303|gb|EOA19495.1| hypothetical protein CARUB_v10002198mg [Capsella rubella]	149	149	4.00E-73	100.0	94.6	96.0	heavy metal transport/detoxification domain-containing protein	gbpln	Arabidopsis lyrata	AT5G17450.1 | Symbols: HIPP21 | Heavy metal transport/detoxification superfamily protein | chr5:5755386-5756743 FORWARD LENGTH=149	149	149	1.00E-75	100.0	94.6	96.0
Rsa1.0_00062.1.g3350.t1	ref|XP_002873829.1| hypothetical protein ARALYDRAFT_909741 [Arabidopsis lyrata subsp. lyrata] gi|297319666|gb|EFH50088.1| hypothetical protein ARALYDRAFT_909741 [Arabidopsis lyrata subsp. lyrata]	305	309	1.00E-135	101.3	87.5	90.8	hypothetical protein ARALYDRAFT_909741	gbpln	Arabidopsis lyrata	AT5G17460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to salt stress; LOCATED IN: mitochondrion; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5757582-5758867 REVERSE LENGTH=309	305	309	1.00E-137	101.3	86.9	90.8
Rsa1.0_00062.1.g3351.t1	sp|P69196.1|POLC1_BRANA RecName: Full=Polcalcin Bra n 1; AltName: Full=Calcium-binding pollen allergen Bra n 1; AltName: Allergen=Bra n 1 gi|59800144|sp|P69197.1|POLC1_BRARA RecName: Full=Polcalcin Bra r 1; AltName: Full=Calcium-binding pollen allergen Bra r 1; AltName: Allergen=Bra r 1 gi|1255536|dbj|BAA09632.1| calcium-binding protein [Brassica napus] gi|1255540|dbj|BAA09634.1| calcium-binding protein [Brassica rapa] gi|7415719|dbj|BAA93509.1| pollen calcium-binding protein [Brassica rapa]	80	79	9.00E-34	98.8	91.3	93.8	RecName: Full=Polcalcin Bra n 1; AltName: Full=Calcium-binding pollen allergen Bra n 1; AltName: Allergen=Bra n 1 gi|59800144|sp|P69197.1|POLC1_BRARA RecName: Full=Polcalcin Bra r 1; AltName: Full=Calcium-binding pollen allergen Bra r 1; AltName: Allergen=Bra r 1 gi|1255536|dbj|BAA09632.1| calcium-binding protein	gbpln	Brassica napus	AT5G17480.1 | Symbols: APC1, PC1 | pollen calcium-binding protein 1 | chr5:5762689-5762940 FORWARD LENGTH=83	80	83	4.00E-33	103.8	83.8	90.0
Rsa1.0_00063.1.g3352.t1	ref|NP_172188.1| 60S ribosomal protein L35a-1 [Arabidopsis thaliana] gi|297843500|ref|XP_002889631.1| 60S ribosomal protein L35a [Arabidopsis lyrata subsp. lyrata] gi|75174783|sp|Q9LMK0.1|R35A1_ARATH RecName: Full=60S ribosomal protein L35a-1 gi|8954039|gb|AAF82213.1|AC067971_21 Strong similarity to a ribosomal protein from Arabidopsis thaliana gb|AL161667. It contains a ribosomal protein L35Ae domain PF|01247 [Arabidopsis thaliana] gi|21555376|gb|AAM63844.1| ribosomal protein, putative [Arabidopsis thaliana] gi|26453120|dbj|BAC43636.1| unknown protein [Arabidopsis thaliana] gi|28416859|gb|AAO42960.1| At1g07070 [Arabidopsis thaliana] gi|297335473|gb|EFH65890.1| 60S ribosomal protein L35a [Arabidopsis lyrata subsp. lyrata] gi|332189953|gb|AEE28074.1| 60S ribosomal protein L35a-1 [Arabidopsis thaliana]	242	112	4.00E-57	46.3	43.4	44.6	60S ribosomal protein L35a-1	gbpln	Arabidopsis lyrata	AT1G07070.1 | Symbols: | Ribosomal protein L35Ae family protein | chr1:2168652-2169703 FORWARD LENGTH=112	242	112	1.00E-59	46.3	43.4	44.6

Rsa1.0_00063.1.g3353.t1	gb|EOA33304.1| hypothetical protein CARUB_v10019953mg [Capsella rubella]	619	634	0	102.4	78.8	87.4	hypothetical protein CARUB_v10019953mg	gbpln	Capsella rubella	AT1G74250.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr1:27920328-27922414 FORWARD LENGTH=630	619	630	0	101.8	76.7	88.0
Rsa1.0_00063.1.g3354.t1	ref|XP_002887533.1| hypothetical protein ARALYDRAFT_339621 [Arabidopsis lyrata subsp. lyrata] gi|297333374|gb|EFH63792.1| hypothetical protein ARALYDRAFT_339621 [Arabidopsis lyrata subsp. lyrata]	333	364	1.00E-131	109.3	73.3	80.2	hypothetical protein ARALYDRAFT_339621	gbpln	Arabidopsis lyrata	AT1G74240.1 | Symbols: | Mitochondrial substrate carrier family protein | chr1:27917437-27919987 FORWARD LENGTH=364	333	364	1.00E-126	109.3	66.7	71.2
Rsa1.0_00063.1.g3355.t1	gb|ABB97027.1| unknown [Brassica rapa]	261	208	2.00E-56	79.7	41.0	41.8	unknown	gbpln	Brassica rapa	AT1G74230.1 | Symbols: GR-RBP5 | glycine-rich RNA-binding protein 5 | chr1:27915346-27916857 FORWARD LENGTH=289	261	289	1.00E-55	110.7	40.2	41.8
Rsa1.0_00063.1.g3356.t3	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	689	966	1.00E-134	140.2	46.3	56.9	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	689	965	1.00E-132	140.1	45.7	56.2
Rsa1.0_00063.1.g3357.t1	ref|NP_565084.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|264664459|sp|C0LGJ1.1|Y1743_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g74360; Flags: Precursor gi|224589485|gb|ACN59276.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332197461|gb|AEE35582.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	771	1106	0	143.5	70.7	78.1	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G74360.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:27954299-27957911 FORWARD LENGTH=1106	771	1106	0	143.5	70.7	78.1
Rsa1.0_00063.1.g3358.t2	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	932	966	0	103.6	77.3	87.4	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	932	965	0	103.5	76.1	85.7
Rsa1.0_00063.1.g3359.t1	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	136	966	2.00E-39	710.3	69.9	80.9	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G54470.1 | Symbols: RPP27 | RNI-like superfamily protein | chr1:20344738-20347339 FORWARD LENGTH=457	136	457	7.00E-38	336.0	58.1	71.3
Rsa1.0_00063.1.g3360.t1	ref|NP_177559.1| receptor like protein 15 [Arabidopsis thaliana] gi|12323812|gb|AAG51871.1|AC079678_1 disease resistance protein, putative; 1096-4664 [Arabidopsis thaliana] gi|332197443|gb|AEE35564.1| receptor like protein 15 [Arabidopsis thaliana]	594	965	1.00E-150	162.5	52.2	64.6	receptor like protein 15	gbpln	Arabidopsis thaliana	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	594	965	1.00E-153	162.5	52.2	64.6
Rsa1.0_00063.1.g3361.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00063.1.g3362.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00063.1.g3363.t1	gb|EOA33578.1| hypothetical protein CARUB_v10019719mg, partial [Capsella rubella]	212	984	9.00E-64	464.2	63.2	72.6	hypothetical protein CARUB_v10019719mg, partial	gbpln	Capsella rubella	AT2G25470.1 | Symbols: AtRLP21, RLP21 | receptor like protein 21 | chr2:10838420-10841881 FORWARD LENGTH=935	212	935	2.00E-54	441.0	52.8	65.1
Rsa1.0_00063.1.g3364.t1	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	788	966	0	122.6	56.6	67.1	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	788	965	0	122.5	56.7	66.1
Rsa1.0_00063.1.g3365.t1	ref|XP_002887529.1| hypothetical protein ARALYDRAFT_476557 [Arabidopsis lyrata subsp. lyrata] gi|297333370|gb|EFH63788.1| hypothetical protein ARALYDRAFT_476557 [Arabidopsis lyrata subsp. lyrata]	1007	1029	0	102.2	81.9	87.4	hypothetical protein ARALYDRAFT_476557	gbpln	Arabidopsis lyrata	AT1G74160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G18620.1); Has 3407 Blast hits to 2217 proteins in 314 species: Archae - 0; Bacteria - 264; Metazoa - 1296; Fungi - 318; Plants - 346; Viruses - 34; Other Eukaryotes - 1149 (source: NCBI BLink). | chr1:27887164-27891151 FORWARD LENGTH=1025	1007	1025	0	101.8	81.5	86.8
Rsa1.0_00063.1.g3366.t1	ref|XP_002887528.1| hypothetical protein ARALYDRAFT_316360 [Arabidopsis lyrata subsp. lyrata] gi|297333369|gb|EFH63787.1| hypothetical protein ARALYDRAFT_316360 [Arabidopsis lyrata subsp. lyrata]	486	567	0	116.7	70.4	77.8	hypothetical protein ARALYDRAFT_316360	gbpln	Arabidopsis lyrata	AT1G74150.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:27880528-27883626 FORWARD LENGTH=569	486	569	0	117.1	70.2	77.0
Rsa1.0_00063.1.g3367.t2	gb|EOA34985.1| hypothetical protein CARUB_v10020076mg [Capsella rubella]	429	561	1.00E-141	130.8	56.9	63.9	hypothetical protein CARUB_v10020076mg	gbpln	Capsella rubella	AT1G74150.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:27880528-27883626 FORWARD LENGTH=569	429	569	1.00E-143	132.6	57.3	64.1

Rsa1.0_00063.1.g3368.t1	gb|ADW54463.1| sulfotransferase [Brassica oleracea var. botrytis]	337	337	0	100.0	95.3	97.6	sulfotransferase	gbpln	Brassica oleracea	AT1G74100.1 | Symbols: SOT16, ATSOT16, CORI-7, ATST5A | sulfotransferase 16 | chr1:27864489-27865505 REVERSE LENGTH=338	337	338	0	100.3	94.1	96.1
Rsa1.0_00063.1.g3369.t1	gb|ADW54463.1| sulfotransferase [Brassica oleracea var. botrytis]	339	337	0	99.4	90.9	95.6	sulfotransferase	gbpln	Brassica oleracea	AT1G74100.1 | Symbols: SOT16, ATSOT16, CORI-7, ATST5A | sulfotransferase 16 | chr1:27864489-27865505 REVERSE LENGTH=338	339	338	0	99.7	89.7	95.0
Rsa1.0_00063.1.g3370.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00063.1.g3371.t1	ref|NP_177548.1| myb domain protein 122 [Arabidopsis thaliana] gi|12325142|gb|AAG52518.1|AC016662_12 putative transcription factor; 17206-15746 [Arabidopsis thaliana] gi|14161427|gb|AAK54746.1|AF371983_1 putative transcription factor MYB122 [Arabidopsis thaliana] gi|114050657|gb|ABI49478.1| At1g74080 [Arabidopsis thaliana] gi|225898078|dbj|BAH30371.1| hypothetical protein [Arabidopsis thaliana] gi|332197425|gb|AEE35546.1| myb domain protein 122 [Arabidopsis thaliana]	106	333	3.00E-25	314.2	56.6	64.2	myb domain protein 122	gbpln	Arabidopsis thaliana	AT1G74080.1 | Symbols: ATMYB122, MYB122 | myb domain protein 122 | chr1:27855972-27857432 FORWARD LENGTH=333	106	333	4.00E-28	314.2	56.6	64.2
Rsa1.0_00063.1.g3372.t2	gb|AAD15534.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	759	1664	1.00E-180	219.2	45.7	58.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	759	1262	4.00E-24	166.3	7.4	10.0
Rsa1.0_00063.1.g3373.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00063.1.g3374.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	921	1307	1.00E-166	141.9	33.3	42.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	921	1262	8.00E-71	137.0	17.5	28.2
Rsa1.0_00063.1.g3375.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	1272	1164	1.00E-180	91.5	28.4	39.4	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1272	626	5.00E-51	49.2	8.4	13.8
Rsa1.0_00063.1.g3376.t1	ref|NP_177548.1| myb domain protein 122 [Arabidopsis thaliana] gi|12325142|gb|AAG52518.1|AC016662_12 putative transcription factor; 17206-15746 [Arabidopsis thaliana] gi|14161427|gb|AAK54746.1|AF371983_1 putative transcription factor MYB122 [Arabidopsis thaliana] gi|114050657|gb|ABI49478.1| At1g74080 [Arabidopsis thaliana] gi|225898078|dbj|BAH30371.1| hypothetical protein [Arabidopsis thaliana] gi|332197425|gb|AEE35546.1| myb domain protein 122 [Arabidopsis thaliana]	334	333	1.00E-130	99.7	76.3	84.1	myb domain protein 122	gbpln	Arabidopsis thaliana	AT1G74080.1 | Symbols: ATMYB122, MYB122 | myb domain protein 122 | chr1:27855972-27857432 FORWARD LENGTH=333	334	333	1.00E-132	99.7	76.3	84.1
Rsa1.0_00063.1.g3377.t1	gb|EOA35264.1| hypothetical protein CARUB_v10020433mg [Capsella rubella]	322	362	1.00E-138	112.4	80.1	87.6	hypothetical protein CARUB_v10020433mg	gbpln	Capsella rubella	AT1G74070.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr1:27851749-27852861 REVERSE LENGTH=317	322	317	1.00E-139	98.4	82.0	89.1
Rsa1.0_00063.1.g3378.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00063.1.g3379.t1	gb|EOA33232.1| hypothetical protein CARUB_v10021263mg [Capsella rubella]	321	233	1.00E-109	72.6	66.0	69.2	hypothetical protein CARUB_v10021263mg	gbpln	Capsella rubella	AT1G74050.1 | Symbols: | Ribosomal protein L6 family protein | chr1:27847256-27848680 REVERSE LENGTH=233	321	233	1.00E-109	72.6	66.4	68.5
Rsa1.0_00063.1.g3380.t1	dbj|BAJ34366.1| unnamed protein product [Thellungiella halophila]	328	328	1.00E-169	100.0	93.6	97.3	unnamed protein product	----	----	AT1G74020.1 | Symbols: SS2 | strictosidine synthase 2 | chr1:27835289-27837277 REVERSE LENGTH=335	328	335	1.00E-169	102.1	88.7	91.5
Rsa1.0_00063.1.g3381.t1	ref|XP_002888957.1| strictosidine synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334798|gb|EFH65216.1| strictosidine synthase family protein [Arabidopsis lyrata subsp. lyrata]	327	326	1.00E-154	99.7	86.2	91.7	strictosidine synthase family protein	gbpln	Arabidopsis lyrata	AT1G74010.1 | Symbols: | Calcium-dependent phosphotriesterase superfamily protein | chr1:27832432-27834017 REVERSE LENGTH=325	327	325	1.00E-153	99.4	85.3	90.2
Rsa1.0_00063.1.g3382.t1	ref|XP_002888956.1| hypothetical protein ARALYDRAFT_476540 [Arabidopsis lyrata subsp. lyrata] gi|297334797|gb|EFH65215.1| hypothetical protein ARALYDRAFT_476540 [Arabidopsis lyrata subsp. lyrata]	325	327	1.00E-145	100.6	79.1	85.8	hypothetical protein ARALYDRAFT_476540	gbpln	Arabidopsis lyrata	AT1G74000.1 | Symbols: SS3 | strictosidine synthase 3 | chr1:27829266-27831401 REVERSE LENGTH=329	325	329	1.00E-144	101.2	76.9	85.2
Rsa1.0_00063.1.g3383.t1	gb|EOA23321.1| hypothetical protein CARUB_v10019219mg [Capsella rubella]	431	444	1.00E-112	103.0	50.1	63.8	hypothetical protein CARUB_v10019219mg	gbpln	Capsella rubella	AT2G40920.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17072586-17074012 REVERSE LENGTH=436	431	436	3.00E-72	101.2	37.4	53.4

Rsa1.0_00064.1.g3384.t1	ref|XP_002880263.1| hypothetical protein ARALYDRAFT_346489 [Arabidopsis lyrata subsp. lyrata] gi|297326102|gb|EFH56522.1| hypothetical protein ARALYDRAFT_346489 [Arabidopsis lyrata subsp. lyrata]	328	334	1.00E-112	101.8	76.2	80.8	hypothetical protein ARALYDRAFT_346489	gbpln	Arabidopsis lyrata	AT2G46780.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:19229516-19231043 FORWARD LENGTH=336	328	336	1.00E-115	102.4	83.8	87.2
Rsa1.0_00064.1.g3385.t1	dbj|BAJ34373.1| unnamed protein product [Thellungiella halophila]	431	486	0	112.8	81.2	87.7	unnamed protein product	----	----	AT2G46790.1 | Symbols: APRR9, PRR9, TL1 | pseudo-response regulator 9 | chr2:19232874-19234901 FORWARD LENGTH=468	431	468	1.00E-173	108.6	75.9	85.4
Rsa1.0_00064.1.g3386.t1	gb|AAO83658.1| cation-efflux transporter [Brassica juncea]	389	387	1.00E-180	99.5	88.4	90.7	cation-efflux transporter	gbpln	Brassica juncea	AT2G46800.2 | Symbols: ZAT, ATMTP1, MTP1, ZAT1, ATCDF1 | zinc transporter of Arabidopsis thaliana | chr2:19238128-19239324 FORWARD LENGTH=398	389	398	1.00E-172	102.3	84.3	87.9
Rsa1.0_00064.1.g3387.t1	#	#	#	#	#	#	#	–	----	----	AT2G47000.1 | Symbols: MDR4, PGP4, ABCB4, ATPGP4 | ATP binding cassette subfamily B4 | chr2:19310008-19314750 REVERSE LENGTH=1286	100	1286	9.00E-12	1286.0	34.0	41.0
Rsa1.0_00064.1.g3388.t3	ref|XP_002864330.1| hypothetical protein ARALYDRAFT_495521 [Arabidopsis lyrata subsp. lyrata] gi|297310165|gb|EFH40589.1| hypothetical protein ARALYDRAFT_495521 [Arabidopsis lyrata subsp. lyrata]	559	356	1.00E-115	63.7	38.5	46.3	hypothetical protein ARALYDRAFT_495521	gbpln	Arabidopsis lyrata	AT5G54330.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22064993-22066063 FORWARD LENGTH=356	559	356	1.00E-118	63.7	38.5	46.3
Rsa1.0_00064.1.g3389.t1	ref|NP_001189765.1| uncharacterized protein [Arabidopsis thaliana] gi|330255688|gb|AEC10782.1| uncharacterized protein AT2G46980 [Arabidopsis thaliana]	119	790	4.00E-23	663.9	52.1	54.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G46980.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown. | chr2:19299868-19303429 REVERSE LENGTH=790	119	790	7.00E-26	663.9	52.1	54.6
Rsa1.0_00064.1.g3390.t1	ref|NP_001189765.1| uncharacterized protein [Arabidopsis thaliana] gi|330255688|gb|AEC10782.1| uncharacterized protein AT2G46980 [Arabidopsis thaliana]	401	790	1.00E-45	197.0	34.4	39.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G46980.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown. | chr2:19299868-19303429 REVERSE LENGTH=790	401	790	3.00E-48	197.0	34.4	39.4
Rsa1.0_00064.1.g3391.t1	ref|NP_001031550.1| homeobox-leucine zipper protein ATHB-7 [Arabidopsis thaliana] gi|330255646|gb|AEC10740.1| homeobox-leucine zipper protein ATHB-7 [Arabidopsis thaliana]	71	256	1.00E-27	360.6	85.9	91.5	homeobox-leucine zipper protein ATHB-7	gbpln	Arabidopsis thaliana	AT2G46680.2 | Symbols: ATHB-7, ATHB7, HB-7 | homeobox 7 | chr2:19165777-19166773 REVERSE LENGTH=256	71	256	2.00E-30	360.6	85.9	91.5
Rsa1.0_00064.1.g3392.t1	ref|NP_200244.1| uncharacterized protein [Arabidopsis thaliana] gi|9759506|dbj|BAB10756.1| unnamed protein product [Arabidopsis thaliana] gi|93007389|gb|ABE97197.1| hypothetical protein At5g54330 [Arabidopsis thaliana] gi|332009102|gb|AED96485.1| uncharacterized protein AT5G54330 [Arabidopsis thaliana]	380	356	1.00E-113	93.7	56.8	68.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54330.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22064993-22066063 FORWARD LENGTH=356	380	356	1.00E-115	93.7	56.8	68.7
Rsa1.0_00064.1.g3393.t1	dbj|BAM14091.1| basic helix-loop-helix DNA-binding superfamily protein [Arabidopsis thaliana]	325	359	1.00E-110	110.5	75.1	86.2	basic helix-loop-helix DNA-binding superfamily protein	gbpln	Arabidopsis thaliana	AT2G46810.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:19239694-19242373 FORWARD LENGTH=371	325	371	1.00E-109	114.2	72.3	85.2
Rsa1.0_00064.1.g3394.t1	gb|EOA27989.1| hypothetical protein CARUB_v10024165mg [Capsella rubella]	181	175	4.00E-67	96.7	76.8	87.3	hypothetical protein CARUB_v10024165mg	gbpln	Capsella rubella	AT2G46820.2 | Symbols: PTAC8, TMP14, PSAP, PSI-P | photosystem I P subunit | chr2:19243729-19244870 FORWARD LENGTH=174	181	174	1.00E-54	96.1	71.8	83.4
Rsa1.0_00064.1.g3395.t2	ref|XP_002880270.1| hypothetical protein ARALYDRAFT_483853 [Arabidopsis lyrata subsp. lyrata] gi|297326109|gb|EFH56529.1| hypothetical protein ARALYDRAFT_483853 [Arabidopsis lyrata subsp. lyrata]	220	216	1.00E-118	98.2	93.6	95.9	hypothetical protein ARALYDRAFT_483853	gbpln	Arabidopsis lyrata	AT2G46860.1 | Symbols: AtPPa3, PPa3 | pyrophosphorylase 3 | chr2:19253843-19255060 FORWARD LENGTH=216	220	216	1.00E-119	98.2	92.3	95.0

Rsa1.0_00064.1.g3396.t1	ref|NP_566089.1| B3 domain-containing transcription factor NGA1 [Arabidopsis thaliana] gi|75100798|sp|O82799.1|NGA1_ARATH RecName: Full=B3 domain-containing transcription factor NGA1; AltName: Full=Protein NGATHA 1 gi|3522951|gb|AAC34233.1| putative RAV-like B3 domain DNA binding protein [Arabidopsis thaliana] gi|20197317|gb|AAM15018.1| putative RAV-like B3 domain DNA binding protein [Arabidopsis thaliana] gi|26451145|dbj|BAC42676.1| putative RAV-like B3 domain DNA binding protein [Arabidopsis thaliana] gi|30793817|gb|AAP40361.1| putative RAV B3 domain DNA binding protein [Arabidopsis thaliana] gi|330255671|gb|AEC10765.1| B3 domain-containing transcription factor NGA1 [Arabidopsis thaliana]	298	310	1.00E-118	104.0	78.9	85.2	B3 domain-containing transcription factor NGA1	gbpln	Arabidopsis thaliana	AT2G46870.1 | Symbols: NGA1 | AP2/B3-like transcriptional factor family protein | chr2:19261313-19262245 FORWARD LENGTH=310	298	310	1.00E-120	104.0	78.9	85.2
Rsa1.0_00064.1.g3397.t1	ref|NP_182211.2| purple acid phosphatase 14 [Arabidopsis thaliana] gi|75272080|sp|Q84LR6.1|PPA14_ARATH RecName: Full=Probable inactive purple acid phosphatase 14; Flags: Precursor gi|30267807|gb|AAP21684.1| hypothetical protein [Arabidopsis thaliana] gi|50058953|gb|AAT69221.1| hypothetical protein At2g46880 [Arabidopsis thaliana] gi|330255673|gb|AEC10767.1| purple acid phosphatase 14 [Arabidopsis thaliana]	394	401	1.00E-179	101.8	79.4	87.3	purple acid phosphatase 14	gbpln	Arabidopsis thaliana	AT2G46880.1 | Symbols: ATPAP14, PAP14 | purple acid phosphatase 14 | chr2:19264910-19266412 REVERSE LENGTH=401	394	401	0	101.8	79.4	87.3
Rsa1.0_00064.1.g3398.t1	ref|XP_002882091.1| hypothetical protein ARALYDRAFT_904159 [Arabidopsis lyrata subsp. lyrata] gi|297327930|gb|EFH58350.1| hypothetical protein ARALYDRAFT_904159 [Arabidopsis lyrata subsp. lyrata]	325	322	1.00E-165	99.1	90.2	95.1	hypothetical protein ARALYDRAFT_904159	gbpln	Arabidopsis lyrata	AT2G46890.1 | Symbols: | Protein of unknown function (DUF1295) | chr2:19266879-19268134 REVERSE LENGTH=322	325	322	1.00E-160	99.1	88.3	93.5
Rsa1.0_00064.1.g3399.t1	ref|NP_566090.1| uncharacterized protein [Arabidopsis thaliana] gi|3522948|gb|AAC34230.1| expressed protein [Arabidopsis thaliana] gi|14532608|gb|AAK64032.1| unknown protein [Arabidopsis thaliana] gi|23296678|gb|AAN13144.1| unknown protein [Arabidopsis thaliana] gi|330255675|gb|AEC10769.1| uncharacterized protein AT2G46900 [Arabidopsis thaliana]	108	627	2.00E-28	580.6	59.3	65.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G46900.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Basic helix-loop-helix, Nulp1-type (InterPro:IPR006994); Has 2929 Blast hits to 2464 proteins in 333 species: Archae - 2; Bacteria - 151; Metazoa - 913; Fungi - 372; Plants - 141; Viruses - 47; Other Eukaryotes - 1303 (source: NCBI BLink). | chr2:19269678-19271987 FORWARD LENGTH=627	108	627	3.00E-31	580.6	59.3	65.7
Rsa1.0_00064.1.g3400.t1	ref|XP_002885669.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata] gi|297331509|gb|EFH61928.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata]	448	467	1.00E-113	104.2	51.3	62.5	hypothetical protein ARALYDRAFT_319176	gbpln	Arabidopsis lyrata	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	448	472	1.00E-112	105.4	49.1	61.2
Rsa1.0_00064.1.g3401.t1	ref|XP_002880272.1| hypothetical protein ARALYDRAFT_483858 [Arabidopsis lyrata subsp. lyrata] gi|297326111|gb|EFH56531.1| hypothetical protein ARALYDRAFT_483858 [Arabidopsis lyrata subsp. lyrata]	577	634	0	109.9	74.4	84.6	hypothetical protein ARALYDRAFT_483858	gbpln	Arabidopsis lyrata	AT2G46900.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Basic helix-loop-helix, Nulp1-type (InterPro:IPR006994); Has 2929 Blast hits to 2464 proteins in 333 species: Archae - 2; Bacteria - 151; Metazoa - 913; Fungi - 372; Plants - 141; Viruses - 47; Other Eukaryotes - 1303 (source: NCBI BLink). | chr2:19269678-19271987 FORWARD LENGTH=627	577	627	0	108.7	72.1	82.8
Rsa1.0_00064.1.g3402.t1	ref|XP_002880273.1| plastid-lipid associated protein pap [Arabidopsis lyrata subsp. lyrata] gi|297326112|gb|EFH56532.1| plastid-lipid associated protein pap [Arabidopsis lyrata subsp. lyrata]	281	283	1.00E-143	100.7	88.6	94.3	plastid-lipid associated protein pap	gbpln	Arabidopsis lyrata	AT2G46910.1 | Symbols: | Plastid-lipid associated protein PAP / fibrillin family protein | chr2:19272427-19273856 FORWARD LENGTH=284	281	284	1.00E-141	101.1	87.2	93.6
Rsa1.0_00064.1.g3403.t2	gb|EOA26563.1| hypothetical protein CARUB_v10022621mg [Capsella rubella]	854	858	0	100.5	91.1	95.1	hypothetical protein CARUB_v10022621mg	gbpln	Capsella rubella	AT2G46920.2 | Symbols: POL | Protein phosphatase 2C family protein | chr2:19278106-19280921 REVERSE LENGTH=856	854	856	0	100.2	89.8	94.8

<table>
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<tr><td>Rsa1.0_00064.1.g3405.t1</td><td>ref|NP_182217.4| uncharacterized protein [Arabidopsis thaliana] gi|330255681|gb|AEC10775.1| uncharacterized protein AT2G46940 [Arabidopsis thaliana]</td><td>249</td><td>252</td><td>4.00E-81</td><td>101.2</td><td>74.7</td><td>80.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46940.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G62070.1); Has 143 Blast hits to 141 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 139; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19286658-19287505 REVERSE LENGTH=252</td><td>249</td><td>252</td><td>1.00E-83</td><td>101.2</td><td>74.7</td><td>80.7</td></tr>
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<tr><td>Rsa1.0_00064.1.g3408.t1</td><td>ref|XP_002889561.1| hypothetical protein ARALYDRAFT_470580 [Arabidopsis lyrata subsp. lyrata] gi|297335403|gb|EFH65820.1| hypothetical protein ARALYDRAFT_470580 [Arabidopsis lyrata subsp. lyrata]</td><td>132</td><td>149</td><td>3.00E-30</td><td>112.9</td><td>48.5</td><td>51.5</td><td>hypothetical protein ARALYDRAFT_470580</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G05730.1 | Symbols: | Eukaryotic protein of unknown function (DUF842) | chr1:1719107-1720159 FORWARD LENGTH=149</td><td>132</td><td>149</td><td>8.00E-33</td><td>112.9</td><td>48.5</td><td>51.5</td></tr>
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<tr><td>Rsa1.0_00064.1.g3410.t1</td><td>gb|EOA28335.1| hypothetical protein CARUB_v10024536mg [Capsella rubella]</td><td>437</td><td>441</td><td>2.00E-74</td><td>100.9</td><td>43.7</td><td>58.8</td><td>hypothetical protein CARUB_v10024536mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G60960.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:22535729-22536940 FORWARD LENGTH=403</td><td>437</td><td>403</td><td>9.00E-71</td><td>92.2</td><td>39.6</td><td>55.8</td></tr>
<tr><td>Rsa1.0_00064.1.g3411.t1</td><td>ref|XP_002882048.1| hypothetical protein ARALYDRAFT_904059 [Arabidopsis lyrata subsp. lyrata] gi|297327887|gb|EFH58307.1| hypothetical protein ARALYDRAFT_904059 [Arabidopsis lyrata subsp. lyrata]</td><td>436</td><td>448</td><td>9.00E-70</td><td>102.8</td><td>33.7</td><td>40.1</td><td>hypothetical protein ARALYDRAFT_904059</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10270.1 | Symbols: GRP23 | glutamine-rich protein 23 | chr1:3363535-3366276 FORWARD LENGTH=913</td><td>436</td><td>913</td><td>2.00E-21</td><td>209.4</td><td>15.1</td><td>22.0</td></tr>
<tr><td>Rsa1.0_00064.1.g3412.t7</td><td>ref|NP_850466.2| uncharacterized protein [Arabidopsis thaliana] gi|110736851|dbj|BAF00383.1| hypothetical protein [Arabidopsis thaliana] gi|330255687|gb|AEC10781.1| uncharacterized protein AT2G46980 [Arabidopsis thaliana]</td><td>872</td><td>793</td><td>0</td><td>90.9</td><td>67.9</td><td>75.0</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46980.2 | Symbols: | unknown protein; Has 3995 Blast hits to 3325 proteins in 374 species: Archae - 19; Bacteria - 205; Metazoa - 2201; Fungi - 364; Plants - 149; Viruses - 22; Other Eukaryotes - 1035 (source: NCBI BLink). | chr2:19299868-19303429 REVERSE LENGTH=793</td><td>872</td><td>793</td><td>0</td><td>90.9</td><td>67.9</td><td>75.0</td></tr>
<tr><td>Rsa1.0_00064.1.g3413.t1</td><td>ref|XP_002882100.1| P-glycoprotein 4, P-glycoprotein4 [Arabidopsis lyrata subsp. lyrata] gi|297327939|gb|EFH58359.1| P-glycoprotein 4, P-glycoprotein4 [Arabidopsis lyrata subsp. lyrata]</td><td>1262</td><td>1286</td><td>0</td><td>101.9</td><td>93.1</td><td>97.4</td><td>P-glycoprotein 4, P-glycoprotein4</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G47000.1 | Symbols: MDR4, PGP4, ABCB4, ATPGP4 | ATP binding cassette subfamily B4 | chr2:19310008-19314750 REVERSE LENGTH=1286</td><td>1262</td><td>1286</td><td>0</td><td>101.9</td><td>93.6</td><td>97.3</td></tr>
<tr><td>Rsa1.0_00064.1.g3414.t1</td><td>ref|XP_002880277.1| At2g47010/F14M4.16 [Arabidopsis lyrata subsp. lyrata] gi|297326116|gb|EFH56536.1| At2g47010/F14M4.16 [Arabidopsis lyrata subsp. lyrata]</td><td>478</td><td>493</td><td>0</td><td>103.1</td><td>88.3</td><td>93.3</td><td>At2g47010/F14M4.16</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G47010.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17030.1); Has 72 Blast hits to 72 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 71; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:19317505-19319252 FORWARD LENGTH=493</td><td>478</td><td>493</td><td>0</td><td>103.1</td><td>86.8</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00064.1.g3415.t1</td><td>gb|EOA27206.1| hypothetical protein CARUB_v10023316mg [Capsella rubella]</td><td>418</td><td>412</td><td>0</td><td>98.6</td><td>84.9</td><td>90.2</td><td>hypothetical protein CARUB_v10023316mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G47020.1 | Symbols: | Peptide chain release factor 1 | chr2:19320090-19322279 REVERSE LENGTH=413</td><td>418</td><td>413</td><td>0</td><td>98.8</td><td>84.9</td><td>89.7</td></tr>
</table>

Rsa1.0_00064.1.g3416.t1	gb|EOA28312.1| hypothetical protein CARUB_v10024512mg [Capsella rubella]	595	595	0	100.0	86.1	93.9	hypothetical protein CARUB_v10024512mg	gbpln	Capsella rubella	AT2G47040.1 | Symbols: VGD1 | Plant invertase/pectin methylesterase inhibitor superfamily | chr2:19328186-19330060 REVERSE LENGTH=595	595	595	0	100.0	86.1	93.6
Rsa1.0_00064.1.g3417.t1	gb|EOA28856.1| hypothetical protein CARUB_v10025101mg [Capsella rubella]	216	216	1.00E-106	100.0	84.3	92.6	hypothetical protein CARUB_v10025101mg	gbpln	Capsella rubella	AT2G47050.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr2:19331927-19332577 REVERSE LENGTH=216	216	216	1.00E-108	100.0	84.7	92.1
Rsa1.0_00064.1.g3418.t1	gb|EOA27227.1| hypothetical protein CARUB_v10023336mg, partial [Capsella rubella]	362	407	0	112.4	95.6	97.0	hypothetical protein CARUB_v10023336mg, partial	gbpln	Capsella rubella	AT2G47060.4 | Symbols: | Protein kinase superfamily protein | chr2:19333116-19334759 REVERSE LENGTH=397	362	397	0	109.7	93.1	95.6
Rsa1.0_00064.1.g3419.t1	ref|XP_002880278.1| hypothetical protein ARALYDRAFT_483883 [Arabidopsis lyrata subsp. lyrata] gi|297326117|gb|EFH56537.1| hypothetical protein ARALYDRAFT_483883 [Arabidopsis lyrata subsp. lyrata]	925	899	0	97.2	82.5	89.0	hypothetical protein ARALYDRAFT_483883	gbpln	Arabidopsis lyrata	AT2G47070.1 | Symbols: SPL1 | squamosa promoter binding protein-like 1 | chr2:19337144-19340552 FORWARD LENGTH=881	925	881	0	95.2	81.1	87.1
Rsa1.0_00064.1.g3420.t1	gb|EOA27267.1| hypothetical protein CARUB_v10023387mg [Capsella rubella]	391	391	0	100.0	98.7	99.5	hypothetical protein CARUB_v10023387mg	gbpln	Capsella rubella	AT1G02500.2 | Symbols: SAM1, SAM-1, MAT1, AtSAM1 | S-adenosylmethionine synthetase 1 | chr1:519037-520218 FORWARD LENGTH=393	391	393	0	100.5	93.1	96.4
Rsa1.0_00064.1.g3421.t1	ref|XP_002882106.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297327945|gb|EFH58365.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	681	735	0	107.9	72.4	80.8	nucleic acid binding protein	gbpln	Arabidopsis lyrata	AT2G47090.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:19341444-19344297 REVERSE LENGTH=766	681	766	0	112.5	73.3	82.1
Rsa1.0_00064.1.g3422.t1	ref|XP_002882109.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327948|gb|EFH58368.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	262	257	1.00E-130	98.1	87.8	93.9	predicted protein	gbpln	Arabidopsis lyrata	AT2G47140.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:19350970-19352059 REVERSE LENGTH=257	262	257	1.00E-131	98.1	86.6	92.7
Rsa1.0_00064.1.g3423.t1	ref|NP_850737.1| putative protein phosphatase 2C 49 [Arabidopsis thaliana] gi|122214683|sp|Q3EAF9.1|P2C49_ARATH RecName: Full=Probable protein phosphatase 2C 49; Short=AtPP2C49 gi|332646807|gb|AEE80328.1| putative protein phosphatase 2C 49 [Arabidopsis thaliana]	387	384	1.00E-143	99.2	67.7	80.4	putative protein phosphatase 2C 49	gbpln	Arabidopsis thaliana	AT3G62260.2 | Symbols: | Protein phosphatase 2C family protein | chr3:23038516-23040391 REVERSE LENGTH=384	387	384	1.00E-145	99.2	67.7	80.4
Rsa1.0_00064.1.g3424.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00064.1.g3425.t1	ref|NP_182241.1| myb domain protein 2 [Arabidopsis thaliana] gi|506189|dbj|BAA03534.1| ATMYB2 [Arabidopsis thaliana] gi|2275197|gb|AAB63819.1| MYB transcription factor (Atmyb2) [Arabidopsis thaliana] gi|14970986|dbj|BAB62128.1| MYB transcription factor Atmyb2 [Arabidopsis thaliana] gi|38603964|gb|AAR24727.1| At2g47190 [Arabidopsis thaliana] gi|41619210|gb|AAS10049.1| MYB transcription factor [Arabidopsis thaliana] gi|44681444|gb|AAS47662.1| At2g47190 [Arabidopsis thaliana] gi|110738166|dbj|BAF01014.1| MYB transcription factor [Arabidopsis thaliana] gi|330255718|gb|AEC10812.1| myb domain protein 2 [Arabidopsis thaliana]	275	273	1.00E-135	99.3	86.5	93.5	myb domain protein 2	gbpln	Arabidopsis thaliana	AT2G47190.1 | Symbols: ATMYB2, MYB2 | myb domain protein 2 | chr2:19376284-19377297 FORWARD LENGTH=273	275	273	1.00E-138	99.3	86.5	93.5
Rsa1.0_00064.1.g3426.t1	ref|XP_002882113.1| hypothetical protein ARALYDRAFT_322367 [Arabidopsis lyrata subsp. lyrata] gi|297327952|gb|EFH58372.1| hypothetical protein ARALYDRAFT_322367 [Arabidopsis lyrata subsp. lyrata]	86	89	2.00E-27	103.5	74.4	82.6	hypothetical protein ARALYDRAFT_322367	gbpln	Arabidopsis lyrata	AT2G47200.1 | Symbols: | unknown protein; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19377884-19378150 REVERSE LENGTH=88	86	88	1.00E-27	102.3	68.6	79.1
Rsa1.0_00064.1.g3427.t1	dbj|BAJ34105.1| unnamed protein product [Thellungiella halophila]	433	439	0	101.4	93.5	96.5	unnamed protein product	----	----	AT2G47210.1 | Symbols: | myb-like transcription factor family protein | chr2:19379039-19382204 FORWARD LENGTH=441	433	441	0	101.8	91.5	95.2
Rsa1.0_00064.1.g3428.t1	gb|EOA40254.1| hypothetical protein CARUB_v10008975mg [Capsella rubella]	482	487	1.00E-140	101.0	62.4	72.4	hypothetical protein CARUB_v10008975mg	gbpln	Capsella rubella	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	482	513	1.00E-138	106.4	61.4	72.6

Rsa1.0_00064.1.g3429.t1	gb|EOA37307.1| hypothetical protein CARUB_v10010977mg [Capsella rubella]	151	711	1.00E-28	470.9	51.7	72.2	hypothetical protein CARUB_v10010977mg	gbpln	Capsella rubella	AT1G26540.1 | Symbols: | Agenet domain-containing protein | chr1:9167783-9170795 REVERSE LENGTH=695	151	695	1.00E-29	460.3	49.7	70.9
Rsa1.0_00064.1.g3430.t3	gb|EOA36732.1| hypothetical protein CARUB_v10012522mg [Capsella rubella]	416	617	4.00E-48	148.3	21.9	26.2	hypothetical protein CARUB_v10012522mg	gbpln	Capsella rubella	AT1G26540.1 | Symbols: | Agenet domain-containing protein | chr1:9167783-9170795 REVERSE LENGTH=695	416	695	2.00E-50	167.1	21.2	26.2
Rsa1.0_00064.1.g3431.t2	ref|XP_002880290.1| long-chain-fatty-acid--CoA ligase family protein [Arabidopsis lyrata subsp. lyrata] gi|297326129|gb|EFH56549.1| long-chain-fatty-acid--CoA ligase family protein [Arabidopsis lyrata subsp. lyrata]	636	660	0	103.8	82.1	88.4	long-chain-fatty-acid--CoA ligase family protein	gbpln	Arabidopsis lyrata	AT2G47240.2 | Symbols: LACS1 | AMP-dependent synthetase and ligase family protein | chr2:19393835-19397616 FORWARD LENGTH=660	636	660	0	103.8	79.7	86.5
Rsa1.0_00064.1.g3432.t1	ref|XP_002882114.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327953|gb|EFH58373.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	317	337	1.00E-121	106.3	81.1	87.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G47260.1 | Symbols: WRKY23, ATWRKY23 | WRKY DNA-binding protein 23 | chr2:19405045-19406446 REVERSE LENGTH=337	317	337	1.00E-114	106.3	80.4	86.8
Rsa1.0_00064.1.g3433.t1	ref|NP_566098.1| transcription factor bHLH151 [Arabidopsis thaliana] gi|75097628|sp|O22901.1|BH151_ARATH RecName: Full=Transcription factor UPBEAT1; AltName: Full=Basic helix-loop-helix protein 151; Short=AtbHLH151; Short=bHLH 151; AltName: Full=Transcription factor EN 146; AltName: Full=Transcription factor bHLH151; AltName: Full=bHLH transcription factor bHLH151 gi|2275205|gb|AAB63827.1| expressed protein [Arabidopsis thaliana] gi|89111836|gb|ABD60690.1| At2g47270 [Arabidopsis thaliana] gi|225898607|dbj|BAH30434.1| hypothetical protein [Arabidopsis thaliana] gi|330255728|gb|AEC10822.1| transcription factor bHLH151 [Arabidopsis thaliana]	102	102	5.00E-47	100.0	90.2	98.0	transcription factor bHLH151	gbpln	Arabidopsis thaliana	AT2G47270.1 | Symbols: UPB1 | sequence-specific DNA binding transcription factors;transcription regulators | chr2:19411741-19412049 REVERSE LENGTH=102	102	102	9.00E-50	100.0	90.2	98.0
Rsa1.0_00064.1.g3434.t1	ref|NP_566099.1| DEAD-box ATP-dependent RNA helicase 24 [Arabidopsis thaliana] gi|75318047|sp|O22907.2|RH24_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 24 gi|16323192|gb|AAL15330.1| At2g47330/T8I13.17 [Arabidopsis thaliana] gi|20196880|gb|AAB63833.2| putative ATP-dependent RNA helicase [Arabidopsis thaliana] gi|21700913|gb|AAM70580.1| At2g47330/T8I13.17 [Arabidopsis thaliana] gi|330255734|gb|AEC10828.1| DEAD-box ATP-dependent RNA helicase 24 [Arabidopsis thaliana]	727	760	0	104.5	88.3	92.8	DEAD-box ATP-dependent RNA helicase 24	gbpln	Arabidopsis thaliana	AT2G47330.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:19429083-19431617 REVERSE LENGTH=760	727	760	0	104.5	88.3	92.8
Rsa1.0_00064.1.g3435.t1	ref|XP_002880296.1| hypothetical protein ARALYDRAFT_904210 [Arabidopsis lyrata subsp. lyrata] gi|297326135|gb|EFH56555.1| hypothetical protein ARALYDRAFT_904210 [Arabidopsis lyrata subsp. lyrata]	472	487	0	103.2	77.8	86.2	hypothetical protein ARALYDRAFT_904210	gbpln	Arabidopsis lyrata	AT2G47350.1 | Symbols: | HIT zinc finger ;PAPA-1-like conserved region | chr2:19434588-19437045 FORWARD LENGTH=486	472	486	0	103.0	76.9	84.7
Rsa1.0_00064.1.g3436.t1	ref|XP_002880297.1| hypothetical protein ARALYDRAFT_904211 [Arabidopsis lyrata subsp. lyrata] gi|297326136|gb|EFH56556.1| hypothetical protein ARALYDRAFT_904211 [Arabidopsis lyrata subsp. lyrata]	308	305	1.00E-124	99.0	83.4	89.9	hypothetical protein ARALYDRAFT_904211	gbpln	Arabidopsis lyrata	AT2G47360.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02570.1); Has 58 Blast hits to 55 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19437820-19438731 FORWARD LENGTH=303	308	303	1.00E-125	98.4	83.4	89.9

Rsa1.0_00064.1.g3437.t1	ref|NP_565392.1| calcium-dependent phosphotriesterase-like protein [Arabidopsis thaliana] gi|4581119|gb|AAD24609.1| expressed protein [Arabidopsis thaliana] gi|21537036|gb|AAM61377.1| unknown [Arabidopsis thaliana] gi|26451541|dbj|BAC42868.1| unknown protein [Arabidopsis thaliana] gi|28973387|gb|AAO64018.1| unknown protein [Arabidopsis thaliana] gi|330251441|gb|AEC06535.1| calcium-dependent phosphotriesterase-like protein [Arabidopsis thaliana]	334	327	1.00E-161	97.9	85.9	92.2	calcium-dependent phosphotriesterase-like protein	gbpln	Arabidopsis thaliana	AT2G16760.1 | Symbols: | Calcium-dependent phosphotriesterase superfamily protein | chr2:7275739-7277122 FORWARD LENGTH=327	334	327	1.00E-163	97.9	85.9	92.2
Rsa1.0_00064.1.g3438.t2	gb|EOA34962.1| hypothetical protein CARUB_v10020048mg [Capsella rubella] gi|482570775|gb|EOA34963.1| hypothetical protein CARUB_v10020048mg [Capsella rubella]	716	575	0	80.3	52.5	59.8	hypothetical protein CARUB_v10020048mg	gbpln	Capsella rubella	AT3G09360.1 | Symbols: | Cyclin/Brf1-like TBP-binding protein | chr3:2873796-2878432 FORWARD LENGTH=604	716	604	1.00E-164	84.4	43.4	53.2
Rsa1.0_00064.1.g3439.t1	ref|NP_182264.1| dimethyladenosine transferase [Arabidopsis thaliana] gi|2529685|gb|AAC62868.1| putative dimethyladenosine transferase [Arabidopsis thaliana] gi|14532650|gb|AAK64053.1| putative dimethyladenosine transferase [Arabidopsis thaliana] gi|21280901|gb|AAM44912.1| putative dimethyladenosine transferase [Arabidopsis thaliana] gi|330255745|gb|AEC10839.1| dimethyladenosine transferase [Arabidopsis thaliana]	347	353	1.00E-166	101.7	91.1	94.5	dimethyladenosine transferase	gbpln	Arabidopsis thaliana	AT2G47420.1 | Symbols: | Ribosomal RNA adenine dimethylase family protein | chr2:19457574-19458777 FORWARD LENGTH=353	347	353	1.00E-169	101.7	91.1	94.5
Rsa1.0_00064.1.g3440.t1	ref|NP_182265.1| histidine kinase CKI1 [Arabidopsis thaliana] gi|75097398|sp|O22267.1|CKI1_ARATH RecName: Full=Histidine kinase CKI1; AltName: Full=Protein CYTOKININ-INDEPENDENT 1 gi|1679803|dbj|BAA13416.1| histidine kinase homolog [Arabidopsis thaliana] gi|2529684|gb|AAC62867.1| putative histidine kinase [Arabidopsis thaliana] gi|330255746|gb|AEC10840.1| histidine kinase CKI1 [Arabidopsis thaliana]	1093	1122	0	102.7	72.0	80.6	histidine kinase CKI1	gbpln	Arabidopsis thaliana	AT2G47430.1 | Symbols: CKI1 | Signal transduction histidine kinase | chr2:19459167-19463122 REVERSE LENGTH=1122	1093	1122	0	102.7	72.0	80.6
Rsa1.0_00065.1.g3441.t1	ref|XP_002892917.1| hypothetical protein ARALYDRAFT_471862 [Arabidopsis lyrata subsp. lyrata] gi|297338759|gb|EFH69176.1| hypothetical protein ARALYDRAFT_471862 [Arabidopsis lyrata subsp. lyrata]	830	823	0	99.2	62.3	73.1	hypothetical protein ARALYDRAFT_471862	gbpln	Arabidopsis lyrata	AT1G16630.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G16270.1); Has 10587 Blast hits to 5736 proteins in 617 species: Archae - 88; Bacteria - 963; Metazoa - 3686; Fungi - 820; Plants - 541; Viruses - 438; Other Eukaryotes - 4051 (source: NCBI BLink). | chr1:5682212-5684749 REVERSE LENGTH=845	830	845	0	101.8	62.5	72.5
Rsa1.0_00065.1.g3442.t1	ref|XP_002890176.1| hypothetical protein ARALYDRAFT_889054 [Arabidopsis lyrata subsp. lyrata] gi|297336018|gb|EFH66435.1| hypothetical protein ARALYDRAFT_889054 [Arabidopsis lyrata subsp. lyrata]	813	770	0	94.7	77.4	82.5	hypothetical protein ARALYDRAFT_889054	gbpln	Arabidopsis lyrata	AT1G79090.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Topoisomerase II-associated protein PAT1 (InterPro:IPR019167); BEST Arabidopsis thaliana protein match is: Topoisomerase II-associated protein PAT1 (TAIR:AT3G22270.1); Has 1260 Blast hits to 1163 proteins in 186 species: Archae - 0; Bacteria - 32; Metazoa - 596; Fungi - 277; Plants - 212; Viruses - 0; Other Eukaryotes - 143 (source: NCBI BLink). | chr1:29749551-29752945 REVERSE LENGTH=793	813	793	0	97.5	65.6	75.5
Rsa1.0_00065.1.g3443.t2	gb|EOA40545.1| hypothetical protein CARUB_v10009275mg [Capsella rubella] gi|482576359|gb|EOA40546.1| hypothetical protein CARUB_v10009275mg [Capsella rubella]	459	416	2.00E-82	90.6	43.8	46.0	hypothetical protein CARUB_v10009275mg	gbpln	Capsella rubella	AT1G16610.3 | Symbols: SR45 | arginine/serine-rich 45 | chr1:5675925-5678686 REVERSE LENGTH=425	459	425	2.00E-72	92.6	37.3	39.4
Rsa1.0_00065.1.g3444.t1	gb|EOA39738.1| hypothetical protein CARUB_v10008384mg [Capsella rubella]	728	761	0	104.5	80.6	89.3	hypothetical protein CARUB_v10008384mg	gbpln	Capsella rubella	AT1G78960.1 | Symbols: ATLUP2, LUP2 | lupeol synthase 2 | chr1:29696722-29701024 FORWARD LENGTH=763	728	763	0	104.8	74.2	85.3

Rsa1.0_00065.1.g3445.t1	ref|XP_002892915.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338757|gb|EFH69174.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	457	465	0	101.8	93.7	96.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G16570.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:5670763-5673423 REVERSE LENGTH=465	457	465	0	101.8	92.8	95.6
Rsa1.0_00065.1.g3446.t2	gb|EOA38074.1| hypothetical protein CARUB_v10009543mg, partial [Capsella rubella]	344	358	1.00E-179	104.1	88.4	93.3	hypothetical protein CARUB_v10009543mg, partial	gbpln	Capsella rubella	AT1G16560.3 | Symbols: | Per1-like family protein | chr1:5668945-5670343 FORWARD LENGTH=342	344	342	1.00E-173	99.4	84.6	90.7
Rsa1.0_00065.1.g3447.t1	ref|NP_564001.1| Molybdenum cofactor sulfurase [Arabidopsis thaliana] gi|75169006|sp|Q9C5X8.1|MOCOS_ARATH RecName: Full=Molybdenum cofactor sulfurase; Short=MOS; Short=MoCo sulfurase; AltName: Full=Abscisic acid protein 3; AltName: Full=Low expression of osmotically expressive genes protein 5; AltName: Full=Molybdenum cofactor sulfurtransferase gi|13123673|gb|AAK12939.1|AF325457_1 molybdenum cofactor sulfurase [Arabidopsis thaliana] gi|15407262|gb|AAK58888.1| molybdenum cofactor sulfurase [Arabidopsis thaliana] gi|332191346|gb|AEE29467.1| Molybdenum cofactor sulfurase [Arabidopsis thaliana]	821	819	0	99.8	86.4	92.2	Molybdenum cofactor sulfurase	gbpln	Arabidopsis thaliana	AT1G16540.1 | Symbols: SIR3, LOS5, ABA3, ATABA3, ACI2 | molybdenum cofactor sulfurase (LOS5) (ABA3) | chr1:5659465-5665201 FORWARD LENGTH=819	821	819	0	99.8	86.4	92.2
Rsa1.0_00065.1.g3448.t1	ref|XP_002892914.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338756|gb|EFH69173.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	166	164	5.00E-77	98.8	83.1	89.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G16530.1 | Symbols: LBD3, ASL9 | ASYMMETRIC LEAVES 2-like 9 | chr1:5651470-5652839 REVERSE LENGTH=165	166	165	1.00E-74	99.4	78.9	87.3
Rsa1.0_00065.1.g3449.t1	ref|XP_002890170.1| hypothetical protein ARALYDRAFT_471850 [Arabidopsis lyrata subsp. lyrata] gi|297336012|gb|EFH66429.1| hypothetical protein ARALYDRAFT_471850 [Arabidopsis lyrata subsp. lyrata]	319	325	1.00E-152	101.9	86.8	90.9	hypothetical protein ARALYDRAFT_471850	gbpln	Arabidopsis lyrata	AT1G16520.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G56080.1); Has 243 Blast hits to 234 proteins in 69 species: Archae - 2; Bacteria - 2; Metazoa - 61; Fungi - 9; Plants - 125; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink). | chr1:5648904-5650998 FORWARD LENGTH=325	319	325	1.00E-152	101.9	88.4	92.5
Rsa1.0_00065.1.g3450.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00065.1.g3451.t1	gb|ADP37974.1| auxin-responsive family protein [Brassica napus]	145	145	6.00E-76	100.0	97.9	98.6	auxin-responsive family protein	gbpln	Brassica napus	AT1G16510.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:5644784-5645227 REVERSE LENGTH=147	145	147	2.00E-67	101.4	87.6	93.1
Rsa1.0_00065.1.g3452.t1	ref|XP_002863230.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297309064|gb|EFH39489.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	802	817	0	101.9	76.6	83.9	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT4G12640.1 | Symbols: | RNA recognition motif (RRM)-containing protein | chr4:7462697-7467630 FORWARD LENGTH=823	802	823	0	102.6	74.8	83.2
Rsa1.0_00065.1.g3453.t1	ref|XP_002889235.1| hypothetical protein ARALYDRAFT_316812 [Arabidopsis lyrata subsp. lyrata] gi|297335076|gb|EFH65494.1| hypothetical protein ARALYDRAFT_316812 [Arabidopsis lyrata subsp. lyrata]	249	238	7.00E-71	95.6	63.5	70.7	hypothetical protein ARALYDRAFT_316812	gbpln	Arabidopsis lyrata	AT1G16500.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G79160.1); Has 136 Blast hits to 134 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 131; Viruses - 1; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5639079-5639995 FORWARD LENGTH=259	249	259	2.00E-70	104.0	66.7	77.5
Rsa1.0_00065.1.g3454.t1	gb|AAM62687.1| putative myb-related transcription factor [Arabidopsis thaliana]	326	272	5.00E-98	83.4	53.4	59.2	putative myb-related transcription factor	gbpln	Arabidopsis thaliana	AT1G16490.1 | Symbols: ATMYB58, MYB58 | myb domain protein 58 | chr1:5629859-5630844 REVERSE LENGTH=274	326	274	1.00E-100	84.0	53.4	59.2
Rsa1.0_00065.1.g3455.t1	gb|ACB59214.1| cytoplasmic thiosulfate:cyanide sulfur transferase [Brassica oleracea]	378	379	0	100.3	93.9	98.4	cytoplasmic thiosulfate:cyanide sulfur transferase	gbpln	Brassica oleracea	AT1G79230.1 | Symbols: ST1, ATMST1, MST1, ATRDH1, STR1 | mercaptopyruvate sulfurtransferase 1 | chr1:29800824-29803679 FORWARD LENGTH=379	378	379	1.00E-178	100.3	78.6	87.8
Rsa1.0_00065.1.g3456.t1	ref|NP_173094.4| protein root hair specific 3 [Arabidopsis thaliana] gi|332191330|gb|AEE29451.1| protein root hair specific 3 [Arabidopsis thaliana]	646	499	0	77.2	62.5	67.3	protein root hair specific 3	gbpln	Arabidopsis thaliana	AT1G16440.1 | Symbols: RSH3 | root hair specific 3 | chr1:5615841-5617632 FORWARD LENGTH=499	646	499	0	77.2	62.5	67.3

Rsa1.0_00065.1.g3457.t1	gb|ACR10252.1| cytochrome P450 79f1 [Brassica rapa subsp. pekinensis]	540	537	0	99.4	95.9	98.0	cytochrome P450 79f1	gbpln	Brassica rapa	AT1G16410.1 | Symbols: CYP79F1, BUS1, SPS1 | cytochrome p450 79f1 | chr1:5608862-5611118 FORWARD LENGTH=538	540	538	0	99.6	83.1	90.2
Rsa1.0_00065.1.g3458.t1	gb|ACB59211.1| antiporter family protein [Brassica oleracea]	790	756	0	95.7	90.9	93.0	antiporter family protein	gbpln	Brassica oleracea	AT1G16380.1 | Symbols: ATCHX1, CHX1 | Cation/hydrogen exchanger family protein | chr1:5598453-5601367 REVERSE LENGTH=785	790	785	0	99.4	85.6	91.6
Rsa1.0_00065.1.g3459.t1	ref|NP_173087.1| organic cation/carnitine transporter 6 [Arabidopsis thaliana] gi|75265503|sp|Q9SA36.1|OCT6_ARATH RecName: Full=Organic cation/carnitine transporter 6; Short=AtOCT6 gi|4966358|gb|AAD34689.1|AC006341_17 Is a member of the PF|00083 sugar transporter family [Arabidopsis thaliana] gi|110738583|dbj|BAF01217.1| putative transport protein [Arabidopsis thaliana] gi|332191322|gb|AEE29443.1| organic cation/carnitine transporter 6 [Arabidopsis thaliana]	521	521	0	100.0	85.4	91.9	organic cation/carnitine transporter 6	gbpln	Arabidopsis thaliana	AT1G16370.1 | Symbols: ATOCT6, OCT6 | organic cation/carnitine transporter 6 | chr1:5596762-5598327 FORWARD LENGTH=521	521	521	0	100.0	85.4	91.9
Rsa1.0_00065.1.g3460.t1	dbj|BAJ33639.1| unnamed protein product [Thellungiella halophila]	119	176	2.00E-11	147.9	31.1	37.8	unnamed protein product	----	----	#	#	#	#	#	#	#
Rsa1.0_00065.1.g3461.t1	ref|NP_173087.1| organic cation/carnitine transporter 6 [Arabidopsis thaliana] gi|75265503|sp|Q9SA36.1|OCT6_ARATH RecName: Full=Organic cation/carnitine transporter 6; Short=AtOCT6 gi|4966358|gb|AAD34689.1|AC006341_17 Is a member of the PF|00083 sugar transporter family [Arabidopsis thaliana] gi|110738583|dbj|BAF01217.1| putative transport protein [Arabidopsis thaliana] gi|332191322|gb|AEE29443.1| organic cation/carnitine transporter 6 [Arabidopsis thaliana]	524	521	0	99.4	80.5	90.3	organic cation/carnitine transporter 6	gbpln	Arabidopsis thaliana	AT1G16370.1 | Symbols: ATOCT6, OCT6 | organic cation/carnitine transporter 6 | chr1:5596762-5598327 FORWARD LENGTH=521	524	521	0	99.4	80.5	90.3
Rsa1.0_00065.1.g3462.t1	ref|NP_173085.1| IMP dehydrogenase [Arabidopsis thaliana] gi|14194878|sp|Q9SA34.1|IMDH2_ARATH RecName: Full=Inosine-5'-monophosphate dehydrogenase 2; Short=IMP dehydrogenase 2; Short=IMPD 2; Short=IMPDH 2 gi|4966356|gb|AAD34687.1|AC006341_15 Strong similarity to gb|L34684 inosine monophosphate dehydrogenase (IMPDH) from Arabidopsis thaliana and is a member of the PF|00478 IMP dehydrogenase family [Arabidopsis thaliana] gi|332191320|gb|AEE29441.1| IMP dehydrogenase [Arabidopsis thaliana]	521	502	0	96.4	90.6	93.9	IMP dehydrogenase	gbpln	Arabidopsis thaliana	AT1G16350.1 | Symbols: | Aldolase-type TIM barrel family protein | chr1:5590951-5592872 FORWARD LENGTH=502	521	502	0	96.4	90.6	93.9
Rsa1.0_00065.1.g3463.t1	gb|EOA37727.1| hypothetical protein CARUB_v10012501mg [Capsella rubella]	608	646	0	106.3	76.8	84.7	hypothetical protein CARUB_v10012501mg	gbpln	Capsella rubella	AT1G16330.1 | Symbols: CYCB3;1 | cyclin b3;1 | chr1:5582387-5587391 REVERSE LENGTH=648	608	648	0	106.6	75.3	84.0
Rsa1.0_00065.1.g3464.t1	gb|EOA38416.1| hypothetical protein CARUB_v10009990mg [Capsella rubella]	275	274	1.00E-120	99.6	81.1	90.5	hypothetical protein CARUB_v10009990mg	gbpln	Capsella rubella	AT1G16320.1 | Symbols: | Uncharacterized conserved protein (DUF2358) | chr1:5580951-5581932 FORWARD LENGTH=273	275	273	1.00E-122	99.3	81.8	90.5
Rsa1.0_00065.1.g3465.t1	gb|AAD34683.1|AC006341_11 F3O9.11 [Arabidopsis thaliana] gi|17529248|gb|AAL38851.1| unknown protein [Arabidopsis thaliana]	398	398	0	100.0	95.0	97.5	F3O9.11	gbpln	Arabidopsis thaliana	AT1G16310.1 | Symbols: | Cation efflux family protein | chr1:5578435-5580585 FORWARD LENGTH=428	398	428	0	107.5	95.0	97.5
Rsa1.0_00065.1.g3466.t1	ref|XP_002890157.1| GAPCP-2 [Arabidopsis lyrata subsp. lyrata] gi|297335999|gb|EFH66416.1| GAPCP-2 [Arabidopsis lyrata subsp. lyrata]	420	420	0	100.0	93.6	96.7	GAPCP-2	gbpln	Arabidopsis lyrata	AT1G16300.1 | Symbols: GAPCP-2 | glyceraldehyde-3-phosphate dehydrogenase of plastid 2 | chr1:5574433-5577406 FORWARD LENGTH=420	420	420	0	100.0	94.0	96.9

Rsa1.0_00065.1.g3467.t1	ref|XP_002892901.1| hypothetical protein ARALYDRAFT_312606 [Arabidopsis lyrata subsp. lyrata] gi|297338743|gb|EFH69160.1| hypothetical protein ARALYDRAFT_312606 [Arabidopsis lyrata subsp. lyrata]	433	458	0	105.8	88.0	92.6	hypothetical protein ARALYDRAFT_312606	gbpln	Arabidopsis lyrata	AT1G16290.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, vacuole; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Lytic transglycosylase-like, catalytic (InterPro:IPR008258); Has 171 Blast hits to 155 proteins in 40 species: Archae - 0; Bacteria - 54; Metazoa - 0; Fungi - 0; Plants - 55; Viruses - 0; Other Eukaryotes - 62 (source: NCBI BLink). | chr1:5570938-5573538 REVERSE LENGTH=419	433	419	0	96.8	84.1	90.3
Rsa1.0_00065.1.g3468.t1	gb|EOA16203.1| hypothetical protein CARUB_v10004342mg [Capsella rubella]	294	637	8.00E-29	216.7	25.5	31.0	hypothetical protein CARUB_v10004342mg	gbpln	Capsella rubella	AT4G12670.1 | Symbols: | Homeodomain-like superfamily protein | chr4:7472530-7474519 FORWARD LENGTH=499	294	499	9.00E-29	169.7	22.1	25.5
Rsa1.0_00065.1.g3469.t1	gb|EOA36788.1| hypothetical protein CARUB_v10008134mg [Capsella rubella]	1130	1156	0	102.3	80.3	85.9	hypothetical protein CARUB_v10008134mg	gbpln	Capsella rubella	AT1G16270.2 | Symbols: | Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain | chr1:5563890-5568145 FORWARD LENGTH=1147	1130	1147	0	101.5	80.0	85.2
Rsa1.0_00065.1.g3470.t1	ref|NP_173075.3| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|122242689|sp|Q0WW40.1|FBK5_ARATH RecName: Full=F-box/kelch-repeat protein At1g16250 gi|110741130|dbj|BAE98658.1| hypothetical protein [Arabidopsis thaliana] gi|119360151|gb|ABL66804.1| At1g16250 [Arabidopsis thaliana] gi|332191305|gb|AEE29426.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	435	383	1.00E-156	88.0	66.2	73.3	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT1G16250.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:5557214-5558697 FORWARD LENGTH=383	435	383	1.00E-159	88.0	66.2	73.3
Rsa1.0_00065.1.g3471.t1	ref|NP_563994.1| syntaxin-51 [Arabidopsis thaliana] gi|79318036|ref|NP_001031054.1| syntaxin-51 [Arabidopsis thaliana] gi|28380164|sp|Q9SA23.1|SYP51_ARATH RecName: Full=Syntaxin-51; Short=AtSYP51 gi|4966344|gb|AAD34675.1|AC006341_3 ESTs gb|F15498, gb|H37515, gb|T41906, gb|T22448, gb|W43356 and gb|T20739 come from this gene [Arabidopsis thaliana] gi|13811644|gb|AAK40223.1|AF355755_1 syntaxin of plants 51 [Arabidopsis thaliana] gi|18650630|gb|AAL75885.1| At1g16240/F3O9_4 [Arabidopsis thaliana] gi|20453319|gb|AAM19898.1| At1g16240/F3O9_4 [Arabidopsis thaliana] gi|21553458|gb|AAM62551.1| unknown [Arabidopsis thaliana] gi|222424478|dbj|BAH20194.1| AT1G16240 [Arabidopsis thaliana] gi|332191302|gb|AEE29423.1| syntaxin-51 [Arabidopsis thaliana] gi|332191303|gb|AEE29424.1| syntaxin-51 [Arabidopsis thaliana]	233	232	1.00E-116	99.6	88.0	95.7	syntaxin-51	gbpln	Arabidopsis thaliana	AT1G16240.2 | Symbols: SYP51, ATSYP51 | syntaxin of plants 51 | chr1:5555183-5556340 REVERSE LENGTH=232	233	232	1.00E-118	99.6	88.0	95.7
Rsa1.0_00065.1.g3472.t1	ref|NP_173072.1| putative protein phosphatase 2C 6 [Arabidopsis thaliana] gi|75200039|sp|Q9SA22.1|P2C06_ARATH RecName: Full=Probable protein phosphatase 2C 6; Short=AtPP2C06 gi|4966343|gb|AAD34674.1|AC006341_2 Is a member of PF|00481 Protein phosphatase 2C family [Arabidopsis thaliana] gi|332191299|gb|AEE29420.1| putative protein phosphatase 2C 6 [Arabidopsis thaliana]	492	491	0	99.8	84.3	90.0	putative protein phosphatase 2C 6	gbpln	Arabidopsis thaliana	AT1G16220.1 | Symbols: | Protein phosphatase 2C family protein | chr1:5548653-5550553 FORWARD LENGTH=491	492	491	0	99.8	84.3	90.0
Rsa1.0_00065.1.g3473.t1	gb|EOA39107.1| hypothetical protein CARUB_v10011879mg [Capsella rubella]	366	368	1.00E-174	100.5	85.5	91.5	hypothetical protein CARUB_v10011879mg	gbpln	Capsella rubella	AT1G16190.1 | Symbols: RAD23A | Rad23 UV excision repair protein family | chr1:5543267-5545892 FORWARD LENGTH=368	366	368	1.00E-174	100.5	85.5	91.5
Rsa1.0_00065.1.g3474.t1	gb|EOA14759.1| hypothetical protein CARUB_v10028056mg [Capsella rubella]	258	270	9.00E-49	104.7	40.3	47.7	hypothetical protein CARUB_v10028056mg	gbpln	Capsella rubella	AT5G45220.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18298926-18301069 REVERSE LENGTH=546	258	546	1.00E-35	211.6	30.2	41.1

Rsa1.0_00065.1.g3475.t2	gb|EOA40567.1| hypothetical protein CARUB_v10009295mg [Capsella rubella]	185	412	7.00E-50	222.7	69.2	73.0	hypothetical protein CARUB_v10009295mg	gbpln	Capsella rubella	AT1G16180.2 | Symbols: | Serinc-domain containing serine and sphingolipid biosynthesis protein | chr1:5540905-5542670 FORWARD LENGTH=412	185	412	1.00E-50	222.7	69.2	73.5
Rsa1.0_00065.1.g3476.t1	gb|EOA33804.1| hypothetical protein CARUB_v10021275mg [Capsella rubella]	91	93	1.00E-30	102.2	76.9	90.1	hypothetical protein CARUB_v10021275mg	gbpln	Capsella rubella	AT1G79660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16170.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:29976294-29976575 FORWARD LENGTH=93	91	93	3.00E-33	102.2	76.9	87.9
Rsa1.0_00065.1.g3477.t1	gb|EOA33654.1| hypothetical protein CARUB_v10019823mg [Capsella rubella]	716	794	0	110.9	59.9	71.8	hypothetical protein CARUB_v10019823mg	gbpln	Capsella rubella	AT1G79670.1 | Symbols: RFO1, WAKL22 | Wall-associated kinase family protein | chr1:29976887-29979337 REVERSE LENGTH=751	716	751	0	104.9	57.5	71.8
Rsa1.0_00065.1.g3478.t1	gb|EOA38313.1| hypothetical protein CARUB_v10009813mg [Capsella rubella]	310	312	1.00E-155	100.6	88.4	94.5	hypothetical protein CARUB_v10009813mg	gbpln	Capsella rubella	AT1G16080.1 | Symbols: | unknown protein; LOCATED IN: apoplast, chloroplast stroma, chloroplast, chloroplast envelope; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; Has 81 Blast hits to 81 proteins in 28 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 62; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr1:5514394-5515761 FORWARD LENGTH=313	310	313	1.00E-151	101.0	87.1	92.6
Rsa1.0_00065.1.g3479.t1	ref|XP_002892894.1| hypothetical protein ARALYDRAFT_471808 [Arabidopsis lyrata subsp. lyrata] gi|297338736|gb|EFH69153.1| hypothetical protein ARALYDRAFT_471808 [Arabidopsis lyrata subsp. lyrata]	398	397	0	99.7	89.4	95.0	hypothetical protein ARALYDRAFT_471808	gbpln	Arabidopsis lyrata	AT1G16070.1 | Symbols: AtTLP8, TLP8 | tubby like protein 8 | chr1:5511899-5513779 REVERSE LENGTH=397	398	397	0	99.7	88.2	94.0
Rsa1.0_00065.1.g3480.t1	ref|XP_002890145.1| hypothetical protein ARALYDRAFT_471806 [Arabidopsis lyrata subsp. lyrata] gi|297335987|gb|EFH66404.1| hypothetical protein ARALYDRAFT_471806 [Arabidopsis lyrata subsp. lyrata]	338	332	2.33E-156	98.2	84.0	90.8	hypothetical protein ARALYDRAFT_471806	gbpln	Arabidopsis lyrata	AT1G16060.1 | Symbols: ADAP | ARIA-interacting double AP2 domain protein | chr1:5508563-5511609 FORWARD LENGTH=345	338	345	1.00E-149	102.1	84.3	92.0
Rsa1.0_00065.1.g3481.t1	ref|XP_002890143.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335985|gb|EFH66402.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	231	228	4.00E-93	98.7	74.9	84.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G16040.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: GPI anchor biosynthetic process; LOCATED IN: integral to membrane, endoplasmic reticulum membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: GPI biosynthesis protein Pig-F (InterPro:IPR009580); Has 280 Blast hits to 280 proteins in 133 species: Archae - 0; Bacteria - 0; Metazoa - 113; Fungi - 111; Plants - 44; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr1:5504747-5506456 FORWARD LENGTH=226	231	226	3.00E-81	97.8	68.8	81.8
Rsa1.0_00065.1.g3482.t1	dbj|BAJ34597.1| unnamed protein product [Thellungiella halophila]	649	647	0	99.7	94.9	97.7	unnamed protein product	----	----	AT1G16030.1 | Symbols: Hsp70b | heat shock protein 70B | chr1:5502386-5504326 REVERSE LENGTH=646	649	646	0	99.5	93.1	97.4
Rsa1.0_00065.1.g3483.t1	ref|NP_173051.1| cyclic nucleotide gated channel 7 [Arabidopsis thaliana] gi|332191272|gb|AEE29393.1| cyclic nucleotide gated channel 7 [Arabidopsis thaliana]	713	709	0	99.4	94.2	97.2	cyclic nucleotide gated channel 7	gbpln	Arabidopsis thaliana	AT1G15990.1 | Symbols: ATCNGC7, CNGC7 | cyclic nucleotide gated channel 7 | chr1:5491304-5493772 REVERSE LENGTH=709	713	709	0	99.4	94.2	97.2
Rsa1.0_00065.1.g3484.t1	ref|NP_563986.1| NDH-dependent cyclic electron flow 1 [Arabidopsis thaliana] gi|6587804|gb|AAF18495.1|AC010924_8 ESTs gb|T43280, gb|AA395195 come from this gene [Arabidopsis thaliana] gi|16323198|gb|AAL15333.1| At1g15980/T24D18_8 [Arabidopsis thaliana] gi|21537186|gb|AAM61527.1| unknown [Arabidopsis thaliana] gi|21700921|gb|AAM70584.1| At1g15980/T24D18_8 [Arabidopsis thaliana] gi|332191271|gb|AEE29392.1| NDH-dependent cyclic electron flow 1 [Arabidopsis thaliana]	461	461	0	100.0	89.4	94.1	NDH-dependent cyclic electron flow 1	gbpln	Arabidopsis thaliana	AT1G15980.1 | Symbols: NDF1, NDH48 | NDH-dependent cyclic electron flow 1 | chr1:5489314-5491199 FORWARD LENGTH=461	461	461	0	100.0	89.4	94.1
Rsa1.0_00065.1.g3485.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00065.1.g3486.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00065.1.g3487.t5	ref|NP_173048.3| metal transporter Nramp6 [Arabidopsis thaliana] gi|30173130|sp|Q9S9N8.2|NRAM6_ARATH RecName: Full=Metal transporter Nramp6; Short=AtNramp6 gi|12666983|emb|CAC28123.1| putative metal transporter [Arabidopsis thaliana] gi|332191269|gb|AEE29390.1| metal transporter Nramp6 [Arabidopsis thaliana]	475	527	0	110.9	92.2	94.9	metal transporter Nramp6	gbpln	Arabidopsis thaliana	AT1G15960.1 | Symbols: NRAMP6, ATNRAMP6 | NRAMP metal ion transporter 6 | chr1:5482202-5485066 REVERSE LENGTH=527	475	527	0	110.9	92.2	94.9
Rsa1.0_00065.1.g3488.t1	gb|ADC40029.1| cinnamoyl-CoA reductase [Isatis tinctoria]	344	341	0	99.1	94.2	96.5	cinnamoyl-CoA reductase	gbpln	Isatis tinctoria	AT1G15950.1 | Symbols: CCR1, IRX4, ATCCR1 | cinnamoyl coa reductase 1 | chr1:5478855-5481915 FORWARD LENGTH=344	344	344	0	100.0	95.3	96.8
Rsa1.0_00065.1.g3489.t1	ref|NP_173046.2| aspartyl beta-hydroxylase N-terminal region domain-containing protein [Arabidopsis thaliana] gi|6587800|gb|AAF18491.1|AC010924_4 T24D18.4 [Arabidopsis thaliana] gi|332191266|gb|AEE29387.1| aspartyl beta-hydroxylase N-terminal region domain-containing protein [Arabidopsis thaliana]	836	990	0	118.4	50.5	62.4	aspartyl beta-hydroxylase N-terminal region domain-containing protein	gbpln	Arabidopsis thaliana	AT1G15940.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr1:5473672-5478050 FORWARD LENGTH=990	836	990	0	118.4	50.5	62.4
Rsa1.0_00065.1.g3490.t1	gb|EOA36301.1| hypothetical protein CARUB_v10010589mg [Capsella rubella]	144	142	5.00E-71	98.6	95.8	97.9	hypothetical protein CARUB_v10010589mg	gbpln	Capsella rubella	AT2G32060.2 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr2:13639228-13640104 REVERSE LENGTH=144	144	144	6.00E-63	100.0	84.0	91.7
Rsa1.0_00065.1.g3491.t5	ref|XP_002890135.1| hypothetical protein ARALYDRAFT_312580 [Arabidopsis lyrata subsp. lyrata] gi|297335977|gb|EFH66394.1| hypothetical protein ARALYDRAFT_312580 [Arabidopsis lyrata subsp. lyrata]	119	113	4.00E-41	95.0	82.4	89.1	hypothetical protein ARALYDRAFT_312580	gbpln	Arabidopsis lyrata	AT1G15900.1 | Symbols: | unknown protein; Has 19 Blast hits to 19 proteins in 10 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 15; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:5464356-5464697 FORWARD LENGTH=113	119	113	1.00E-42	95.0	81.5	86.6
Rsa1.0_00065.1.g3492.t1	ref|NP_173041.1| CC-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|374095383|sp|Q9LMP6.2|DRL3_ARATH RecName: Full=Probable disease resistance protein At1g15890 gi|332191259|gb|AEE29380.1| CC-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	867	851	0	98.2	67.7	78.9	CC-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT1G15890.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:5461406-5463961 FORWARD LENGTH=851	867	851	0	98.2	67.7	78.9
Rsa1.0_00065.1.g3493.t1	gb|EOA36249.1| hypothetical protein CARUB_v10010239mg [Capsella rubella]	263	223	2.00E-95	84.8	67.3	69.2	hypothetical protein CARUB_v10010239mg	gbpln	Capsella rubella	AT1G15880.1 | Symbols: GOS11, atgos11 | golgi snare 11 | chr1:5458718-5460089 REVERSE LENGTH=223	263	223	1.00E-97	84.8	66.9	69.6
Rsa1.0_00065.1.g3494.t1	ref|NP_001154344.1| uncharacterized protein [Arabidopsis thaliana] gi|240254082|ref|NP_563983.4| uncharacterized protein [Arabidopsis thaliana] gi|32815875|gb|AAP88334.1| At1g15860 [Arabidopsis thaliana] gi|332191253|gb|AEE29374.1| uncharacterized protein AT1G15860 [Arabidopsis thaliana] gi|332191254|gb|AEE29375.1| uncharacterized protein AT1G15860 [Arabidopsis thaliana]	229	227	1.00E-110	99.1	82.5	87.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G15860.2 | Symbols: | Domain of unknown function (DUF298) | chr1:5455055-5456741 FORWARD LENGTH=227	229	227	1.00E-112	99.1	82.5	87.8
Rsa1.0_00065.1.g3495.t1	gb|EOA38586.1| hypothetical protein CARUB_v10010411mg [Capsella rubella]	197	181	6.00E-39	91.9	51.8	70.6	hypothetical protein CARUB_v10010411mg	gbpln	Capsella rubella	AT4G00420.2 | Symbols: | Double-stranded RNA-binding domain (DsRBD)-containing protein | chr4:181518-182629 REVERSE LENGTH=190	197	190	1.00E-39	96.4	49.2	62.4
Rsa1.0_00065.1.g3496.t1	gb|AAF82153.1|AC034256_17 Contains similarity to extensin (atExt1) from Arabidopsis thaliana gb|U43627 and is rich in proline and glycine. EST gb|Z37262 comes from this gene [Arabidopsis thaliana]	711	1006	4.00E-72	141.5	34.7	39.7	Contains similarity to extensin (atExt1) from Arabidopsis thaliana gb|U43627 and is rich in proline and glycine. EST gb|Z37262 comes from this gene	gbpln	Arabidopsis thaliana	AT1G15825.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:5448149-5448529 REVERSE LENGTH=126	711	126	2.00E-37	17.7	13.1	14.8
Rsa1.0_00065.1.g3497.t1	ref|XP_002892885.1| Lhcb6 protein [Arabidopsis lyrata subsp. lyrata] gi|297338727|gb|EFH69144.1| Lhcb6 protein [Arabidopsis lyrata subsp. lyrata]	256	256	1.00E-134	100.0	94.1	96.5	Lhcb6 protein	gbpln	Arabidopsis lyrata	AT1G15820.1 | Symbols: LHCB6, CP24 | light harvesting complex photosystem II subunit 6 | chr1:5446685-5447676 REVERSE LENGTH=258	256	258	1.00E-134	100.8	93.0	95.7

Rsa1.0_00065.1.g3498.t1	ref|NP_563982.1| S15/NS1, RNA-binding protein [Arabidopsis thaliana] gi|8927660|gb|AAF82151.1|AC034256_15 Contains similarity to an unknown protein T21F11.5 gi|6730725 from Arabidopsis thaliana BAC T21F11 gb|AC018849 and contains a Ribosomal Protein S15 PF|00312 domain [Arabidopsis thaliana] gi|13605577|gb|AAK32782.1|AF361614_1 At1g15810/F7H2_23 [Arabidopsis thaliana] gi|22137170|gb|AAM91430.1| At1g15810/F7H2_23 [Arabidopsis thaliana] gi|332191247|gb|AEE29368.1| S15/NS1, RNA-binding protein [Arabidopsis thaliana]	418	419	1.00E-124	100.2	64.6	73.9	S15/NS1, RNA-binding protein	gbpln	Arabidopsis thaliana	AT1G15810.1 | Symbols: | S15/NS1, RNA-binding protein | chr1:5444496-5446271 FORWARD LENGTH=419	418	419	1.00E-127	100.2	64.6	73.9
Rsa1.0_00065.1.g3499.t1	ref|XP_002892884.1| hypothetical protein ARALYDRAFT_312568 [Arabidopsis lyrata subsp. lyrata] gi|297338726|gb|EFH69143.1| hypothetical protein ARALYDRAFT_312568 [Arabidopsis lyrata subsp. lyrata]	143	308	6.00E-35	215.4	62.9	67.8	hypothetical protein ARALYDRAFT_312568	gbpln	Arabidopsis lyrata	AT1G15800.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80610.1); Has 56 Blast hits to 52 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5441425-5443584 REVERSE LENGTH=207	143	207	4.00E-33	144.8	59.4	62.9
Rsa1.0_00065.1.g3500.t1	dbj|BAM73280.1| gibberellin 3 oxidase 1 [Raphanus sativus]	359	359	0	100.0	99.2	99.4	gibberellin 3 oxidase 1	gbpln	Raphanus sativus	AT1G15550.1 | Symbols: GA4, ATGA3OX1, GA3OX1 | gibberellin 3-oxidase 1 | chr1:5344569-5346078 REVERSE LENGTH=358	359	358	0	99.7	88.0	92.8
Rsa1.0_00065.1.g3501.t1	ref|XP_002890109.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335951|gb|EFH66368.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	322	322	1.00E-166	100.0	84.2	92.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G15540.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:5342587-5343705 FORWARD LENGTH=320	322	320	1.00E-160	99.4	85.7	92.2
Rsa1.0_00065.1.g3502.t1	ref|NP_173005.1| ABC transporter G family member 40 [Arabidopsis thaliana] gi|75336094|sp|Q9M9E1.1|AB40G_ARATH RecName: Full=ABC transporter G family member 40; Short=ABC transporter ABCG.40; Short=AtABCG40; AltName: Full=Pleiotropic drug resistance protein 12 gi|8072390|gb|AAF71978.1|AC013453_3 Putative ABC transporter [Arabidopsis thaliana] gi|28144321|tpg|DAA00880.1| TPA_exp: PDR12 ABC transporter [Arabidopsis thaliana] gi|332191211|gb|AEE29332.1| ABC transporter G family member 40 [Arabidopsis thaliana]	1414	1423	0	100.6	94.2	97.8	ABC transporter G family member 40	gbpln	Arabidopsis thaliana	AT1G15520.1 | Symbols: PDR12, ATPDR12, ABCG40, ATABCG40 | pleiotropic drug resistance 12 | chr1:5331993-5338175 REVERSE LENGTH=1423	1414	1423	0	100.6	94.2	97.8
Rsa1.0_00065.1.g3503.t1	ref|NP_173004.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75191104|sp|Q9M9E2.1|PPR45_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g15510, chloroplastic; Flags: Precursor gi|8072389|gb|AAF71977.1|AC013453_2 Hypothetical protein [Arabidopsis thaliana] gi|300825685|gb|ADK35876.1| chloroplast vanilla cream 1 [Arabidopsis thaliana] gi|332191210|gb|AEE29331.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	865	866	0	100.1	89.2	95.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G15510.1 | Symbols: ATECB2, ECB2, VAC1 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:5329111-5331711 FORWARD LENGTH=866	865	866	0	100.1	89.2	95.1
Rsa1.0_00065.1.g3504.t1	gb|EOA39910.1| hypothetical protein CARUB_v10008598mg [Capsella rubella]	608	618	0	101.6	92.4	95.7	hypothetical protein CARUB_v10008598mg	gbpln	Capsella rubella	AT1G15500.1 | Symbols: ATNTT2 | TLC ATP/ADP transporter | chr1:5326426-5328688 FORWARD LENGTH=618	608	618	0	101.6	92.8	95.2
Rsa1.0_00065.1.g3505.t1	ref|NP_173002.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|5103847|gb|AAD39677.1|AC007591_42 Contains PF|00561 alpha/beta hydrolase fold [Arabidopsis thaliana] gi|17529298|gb|AAL38876.1| unknown protein [Arabidopsis thaliana] gi|26983890|gb|AAN86197.1| unknown protein [Arabidopsis thaliana] gi|332191208|gb|AEE29329.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana]	636	648	0	101.9	85.4	89.0	alpha/beta-hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G15490.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:5320859-5323422 REVERSE LENGTH=648	636	648	0	101.9	85.4	89.0

Rsa1.0_00065.1.g3506.t1	ref|NP_563978.1| serine–threonine kinase receptor–associated protein [Arabidopsis thaliana] gi|5103845|gb|AAD39675.1|AC007591_40 Strong similarity to gb|AF096285 serine–threonine kinase receptor–associated protein from Mus musculus and contains 5 PF|00400 WD40, G–beta repeat domains. EST gb|F14050 comes from this gene [Arabidopsis thaliana] gi|21536836|gb|AAM61168.1| Similar to unr–interacting protein and contains WD40 domains [Arabidopsis thaliana] gi|24030339|gb|AAN41335.1| unknown protein [Arabidopsis thaliana] gi|332191206|gb|AEE29327.1| transducin/WD40 repeat–like superfamily protein [Arabidopsis thaliana]	335	333	0	99.4	94.0	96.7	serine–threonine kinase receptor–associated protein	gbpln	Arabidopsis thaliana	AT1G15470.1 | Symbols: | Transducin/WD40 repeat–like superfamily protein | chr1:5315838–5317696 FORWARD LENGTH=333	335	333	0	99.4	94.0	96.7
Rsa1.0_00065.1.g3507.t1	ref|NP_172999.1| boron transporter 4 [Arabidopsis thaliana] gi|75215622|sp|Q9XI23.1|BOR4_ARATH RecName: Full=Boron transporter 4 gi|5103843|gb|AAD39673.1|AC007591_38 Is a member of the PF|00955 Anion exchanger family [Arabidopsis thaliana] gi|17978949|gb|AAL47440.1| At1g15460/T16N11_24 [Arabidopsis thaliana] gi|332191205|gb|AEE29326.1| boron transporter 4 [Arabidopsis thaliana]	678	683	0	100.7	91.4	95.4	boron transporter 4	gbpln	Arabidopsis thaliana	AT1G15460.1 | Symbols: ATBOR4, BOR4 | HCO3– transporter family | chr1:5310196–5313376 REVERSE LENGTH=683	678	683	0	100.7	91.4	95.4
Rsa1.0_00065.1.g3508.t1	gb|EOA39629.1| hypothetical protein CARUB_v10008260mg [Capsella rubella]	888	900	0	101.4	89.6	95.0	hypothetical protein CARUB_v10008260mg	gbpln	Capsella rubella	AT1G15440.1 | Symbols: PWP2, ATPWP2 | periodic tryptophan protein 2 | chr1:5306159–5309460 REVERSE LENGTH=900	888	900	0	101.4	88.3	95.3
Rsa1.0_00065.1.g3509.t1	gb|EOA36181.1| hypothetical protein CARUB_v10010051mg [Capsella rubella]	268	260	1.00E–100	97.0	71.3	81.3	hypothetical protein CARUB_v10010051mg	gbpln	Capsella rubella	AT1G15430.2 | Symbols: | Protein of unknown function (DUF1644) | chr1:5305011–5305790 FORWARD LENGTH=259	268	259	1.00E–98	96.6	68.3	79.9
Rsa1.0_00065.1.g3510.t1	ref|NP_172994.1| uncharacterized protein [Arabidopsis thaliana] gi|5103841|gb|AAD39671.1|AC007591_36 F9L1.37 [Arabidopsis thaliana] gi|332191199|gb|AEE29320.1| uncharacterized protein AT1G15415 [Arabidopsis thaliana]	101	96	6.00E–36	95.0	78.2	86.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G15415.1 | Symbols: | The protein encoded by this gene was identified as a part of pollen proteome by mass spec analysis. It has weak homology to LEA (late embryo abundant) proteins. Encodes protein phosphatase 2A (PP2A) B'gamma subunit. Targeted to nucleus and cytosol. | chr1:5300931–5301412 REVERSE LENGTH=96	101	96	1.00E–38	95.0	78.2	86.1
Rsa1.0_00065.1.g3511.t1	ref|NP_172993.1| aspartate–glutamate racemase–like protein [Arabidopsis thaliana] gi|5103839|gb|AAD39669.1|AC007591_34 Is a member of the PF|01177 Aspartate–glutamate racemase family. EST gb|T43554 comes from this gene [Arabidopsis thaliana] gi|26983862|gb|AAN86183.1| unknown protein [Arabidopsis thaliana] gi|332191198|gb|AEE29319.1| aspartate–glutamate racemase–like protein [Arabidopsis thaliana]	330	330	1.00E–158	100.0	83.9	89.7	aspartate–glutamate racemase–like protein	gbpln	Arabidopsis thaliana	AT1G15410.1 | Symbols: | aspartate–glutamate racemase family | chr1:5299577–5300681 FORWARD LENGTH=330	330	330	1.00E–160	100.0	83.9	89.7
Rsa1.0_00065.1.g3512.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00065.1.g3513.t1	gb|EOA37299.1| hypothetical protein CARUB_v10010935mg [Capsella rubella]	145	148	4.00E–50	102.1	74.5	85.5	hypothetical protein CARUB_v10010935mg	gbpln	Capsella rubella	AT1G15400.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80180.1); Has 84 Blast hits to 84 proteins in 17 species: Archae – 0; Bacteria – 6; Metazoa – 0; Fungi – 0; Plants – 75; Viruses – 0; Other Eukaryotes – 3 (source: NCBI BLink). | chr1:5296019–5296824 REVERSE LENGTH=148	145	148	2.00E–46	102.1	66.9	77.2

<table>
<tr><td>Rsa1.0_00065.1.g3514.t1</td><td>ref|XP_002890102.1| hypothetical protein ARALYDRAFT_334826 [Arabidopsis lyrata subsp. lyrata] gi|297335944|gb|EFH66361.1| hypothetical protein ARALYDRAFT_334826 [Arabidopsis lyrata subsp. lyrata]</td><td>265</td><td>270</td><td>1.00E-121</td><td>101.9</td><td>84.5</td><td>90.6</td><td>hypothetical protein ARALYDRAFT_334826</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G15390.1 | Symbols: PDF1A, ATDEF1 | peptide deformylase 1A | chr1:5294653-5295625 FORWARD LENGTH=269</td><td>265</td><td>269</td><td>1.00E-123</td><td>101.5</td><td>83.8</td><td>89.8</td></tr>
<tr><td>Rsa1.0_00065.1.g3515.t1</td><td>gb|ABD65019.1| Sulfite oxidase, putative [Brassica oleracea]</td><td>389</td><td>404</td><td>0</td><td>103.9</td><td>95.9</td><td>99.2</td><td>Sulfite oxidase, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G01910.1 | Symbols: SOX, AT-SO, AtSO | sulfite oxidase | chr3:314919-317274 REVERSE LENGTH=393</td><td>389</td><td>393</td><td>0</td><td>101.0</td><td>91.8</td><td>97.2</td></tr>
<tr><td>Rsa1.0_00065.1.g3516.t1</td><td>ref|XP_002892864.1| hypothetical protein ARALYDRAFT_888930 [Arabidopsis lyrata subsp. lyrata] gi|297338706|gb|EFH69123.1| hypothetical protein ARALYDRAFT_888930 [Arabidopsis lyrata subsp. lyrata]</td><td>74</td><td>76</td><td>9.00E-22</td><td>102.7</td><td>73.0</td><td>74.3</td><td>hypothetical protein ARALYDRAFT_888930</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G15385.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF761, plant (InterPro:IPR008480); Has 6 Blast hits to 6 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5292976-5293197 REVERSE LENGTH=73</td><td>74</td><td>73</td><td>4.00E-22</td><td>98.6</td><td>67.6</td><td>70.3</td></tr>
<tr><td>Rsa1.0_00065.1.g3517.t1</td><td>gb|EOA38607.1| hypothetical protein CARUB_v10010450mg [Capsella rubella]</td><td>174</td><td>174</td><td>1.00E-87</td><td>100.0</td><td>88.5</td><td>94.3</td><td>hypothetical protein CARUB_v10010450mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G15380.2 | Symbols: | Lactoylglutathione lyase / glyoxalase I family protein | chr1:5290955-5292287 FORWARD LENGTH=174</td><td>174</td><td>174</td><td>8.00E-87</td><td>100.0</td><td>86.2</td><td>93.1</td></tr>
<tr><td>Rsa1.0_00066.1.g3518.t1</td><td>ref|XP_002876205.1| hypothetical protein ARALYDRAFT_485718 [Arabidopsis lyrata subsp. lyrata] gi|297322043|gb|EFH52464.1| hypothetical protein ARALYDRAFT_485718 [Arabidopsis lyrata subsp. lyrata]</td><td>504</td><td>515</td><td>1.00E-133</td><td>102.2</td><td>61.5</td><td>71.2</td><td>hypothetical protein ARALYDRAFT_485718</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G53440.2 | Symbols: | Homeodomain-like superfamily protein | chr3:19810936-19812474 FORWARD LENGTH=512</td><td>504</td><td>512</td><td>1.00E-126</td><td>101.6</td><td>59.3</td><td>69.8</td></tr>
<tr><td>Rsa1.0_00066.1.g3519.t1</td><td>gb|EOA25801.1| hypothetical protein CARUB_v10019168mg [Capsella rubella]</td><td>216</td><td>215</td><td>1.00E-114</td><td>99.5</td><td>93.1</td><td>96.8</td><td>hypothetical protein CARUB_v10019168mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G53450.1 | Symbols: | Putative lysine decarboxylase family protein | chr3:19812977-19815430 REVERSE LENGTH=215</td><td>216</td><td>215</td><td>1.00E-117</td><td>99.5</td><td>93.5</td><td>96.3</td></tr>
<tr><td>Rsa1.0_00066.1.g3520.t1</td><td>dbj|BAA06519.1| RNA-binding protein cp29 [Arabidopsis thaliana]</td><td>330</td><td>326</td><td>1.00E-110</td><td>98.8</td><td>78.2</td><td>83.3</td><td>RNA-binding protein cp29</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G53460.3 | Symbols: CP29 | chloroplast RNA-binding protein 29 | chr3:19819738-19821423 REVERSE LENGTH=342</td><td>330</td><td>342</td><td>1.00E-110</td><td>103.6</td><td>75.8</td><td>80.6</td></tr>
<tr><td>Rsa1.0_00066.1.g3521.t1</td><td>ref|NP_190915.1| uncharacterized protein [Arabidopsis thaliana] gi|6729498|emb|CAB67654.1| putative protein [Arabidopsis thaliana] gi|26450564|dbj|BAC42394.1| unknown protein [Arabidopsis thaliana] gi|28416887|gb|AAO42974.1| At3g53470 [Arabidopsis thaliana] gi|332645573|gb|AEE79094.1| uncharacterized protein AT3G53470 [Arabidopsis thaliana]</td><td>134</td><td>135</td><td>6.00E-44</td><td>100.7</td><td>77.6</td><td>84.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G53470.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 35 Blast hits to 35 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:19822813-19823298 FORWARD LENGTH=135</td><td>134</td><td>135</td><td>1.00E-46</td><td>100.7</td><td>77.6</td><td>84.3</td></tr>
<tr><td>Rsa1.0_00066.1.g3522.t1</td><td>ref|NP_190918.3| RNA recognition motif and CCHC-type zinc finger domain-containing protein [Arabidopsis thaliana] gi|75334513|sp|Q9FYB7.1|RSZ32_ARATH RecName: Full=Serine/arginine-rich splicing factor RS2Z32; AltName: Full=RS-containing zinc finger protein 32; Short=At-RS2Z32; Short=At-RSZ32 gi|9795142|emb|CAB67657.2| splicing factor-like protein [Arabidopsis thaliana] gi|222422875|dbj|BAH19424.1| AT3G53500 [Arabidopsis thaliana] gi|332645577|gb|AEE79098.1| serine/arginine-rich splicing factor RS2Z32 [Arabidopsis thaliana]</td><td>316</td><td>284</td><td>1.00E-114</td><td>89.9</td><td>81.6</td><td>85.1</td><td>RNA recognition motif and CCHC-type zinc finger domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G53500.2 | Symbols: RSZ32, RS2Z32, At-RS2Z | RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain | chr3:19834557-19836507 REVERSE LENGTH=284</td><td>316</td><td>284</td><td>1.00E-116</td><td>89.9</td><td>81.6</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00066.1.g3523.t1</td><td>gb|EOA26043.1| hypothetical protein CARUB_v10019457mg, partial [Capsella rubella]</td><td>419</td><td>489</td><td>0</td><td>116.7</td><td>95.9</td><td>97.6</td><td>hypothetical protein CARUB_v10019457mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G53520.1 | Symbols: UXS1, ATUXS1 | UDP-glucuronic acid decarboxylase 1 | chr3:19841635-19844057 FORWARD LENGTH=435</td><td>419</td><td>435</td><td>0</td><td>103.8</td><td>95.0</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00066.1.g3524.t1</td><td>emb|CAB67660.1| putative protein [Arabidopsis thaliana]</td><td>256</td><td>250</td><td>1.00E-103</td><td>97.7</td><td>76.6</td><td>83.6</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G53530.1 | Symbols: NAKR3 | Chloroplast-targeted copper chaperone protein | chr3:19845199-19846583 FORWARD LENGTH=247</td><td>256</td><td>247</td><td>1.00E-103</td><td>96.5</td><td>75.4</td><td>82.4</td></tr>
</table>

Rsa1.0_00066.1.g3525.t1	ref|NP_190922.3| uncharacterized protein [Arabidopsis thaliana] gi|332645585|gb|AEE79106.1| uncharacterized protein AT3G53540 [Arabidopsis thaliana]	897	924	0	103.0	78.6	86.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G53540.1 | Symbols: | unknown protein; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3741 (InterPro:IPR022212); BEST Arabidopsis thaliana protein match is: Protein of unknown function (DUF3741) (TAIR:AT4G28760.2); Has 1710 Blast hits to 868 proteins in 206 species: Archae - 2; Bacteria - 409; Metazoa - 304; Fungi - 204; Plants - 304; Viruses - 2; Other Eukaryotes - 485 (source: NCBI BLink). | chr3:19846805-19850670 REVERSE LENGTH=924	897	924	0	103.0	78.6	86.6
Rsa1.0_00066.1.g3526.t1	gb|EOA22416.1| hypothetical protein CARUB_v10003055mg, partial [Capsella rubella]	512	466	1.00E-110	91.0	47.1	58.2	hypothetical protein CARUB_v10003055mg, partial	gbpln	Capsella rubella	AT1G22000.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr1:7744189-7747123 FORWARD LENGTH=717	512	717	1.00E-98	140.0	43.4	56.1
Rsa1.0_00066.1.g3527.t1	emb|CAB67663.1| putative protein [Arabidopsis thaliana]	324	388	4.00E-94	119.8	62.7	78.7	putative protein	gbpln	Arabidopsis thaliana	AT3G53560.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:19859954-19860976 REVERSE LENGTH=340	324	340	1.00E-96	104.9	62.7	78.7
Rsa1.0_00066.1.g3528.t15	ref|XP_002877927.1| fus3-complementing gene 1 [Arabidopsis lyrata subsp. lyrata] gi|297323765|gb|EFH54186.1| fus3-complementing gene 1 [Arabidopsis lyrata subsp. lyrata]	496	469	0	94.6	88.7	90.9	fus3-complementing gene 1	gbpln	Arabidopsis lyrata	AT3G53570.4 | Symbols: AFC1, AME2, FC1 | FUS3-complementing gene 1 | chr3:19861449-19864125 REVERSE LENGTH=467	496	467	0	94.2	89.3	91.1
Rsa1.0_00066.1.g3529.t1	ref|NP_190926.1| diaminopimelate epimerase [Arabidopsis thaliana] gi|75263858|sp|Q9LFG2.1|DAPF_ARATH RecName: Full=Diaminopimelate epimerase, chloroplastic; Short=DAP epimerase; Flags: Precursor gi|6729509|emb|CAB67665.1| diaminopimelate epimerase-like protein [Arabidopsis thaliana] gi|22022530|gb|AAM83223.1| AT3g53580/F4P12_280 [Arabidopsis thaliana] gi|23505901|gb|AAN28810.1| At3g53580/F4P12_280 [Arabidopsis thaliana] gi|332645592|gb|AEE79113.1| diaminopimelate epimerase [Arabidopsis thaliana]	366	362	0	98.9	87.7	92.3	diaminopimelate epimerase	gbpln	Arabidopsis thaliana	AT3G53580.1 | Symbols: | diaminopimelate epimerase family protein | chr3:19864784-19866907 FORWARD LENGTH=362	366	362	0	98.9	87.7	92.3
Rsa1.0_00066.1.g3530.t1	gb|EOA16369.1| hypothetical protein CARUB_v10004519mg [Capsella rubella]	541	550	0	101.7	81.3	89.8	hypothetical protein CARUB_v10004519mg	gbpln	Capsella rubella	AT4G31180.2 | Symbols: | Class II aminoacyl-tRNA and biotin synthetases superfamily protein | chr4:15156696-15159362 FORWARD LENGTH=558	541	558	0	103.1	79.5	88.4
Rsa1.0_00066.1.g3531.t6	emb|CAA90080.1| small GTP-binding protein [Pisum sativum]	216	216	1.00E-116	100.0	92.1	98.1	small GTP-binding protein	gbpln	Pisum sativum	AT3G53610.3 | Symbols: ATRAB8, RAB8 | RAB GTPase homolog 8 | chr3:19876531-19878264 REVERSE LENGTH=216	216	216	1.00E-115	100.0	91.7	94.0
Rsa1.0_00066.1.g3532.t1	ref|NP_190930.1| pyrophosphorylase 4 [Arabidopsis thaliana] gi|6729513|emb|CAB67669.1| inorganic pyrophosphatase-like protein [Arabidopsis thaliana] gi|110741493|dbj|BAE98700.1| inorganic pyrophosphatase -like protein [Arabidopsis thaliana] gi|332645599|gb|AEE79120.1| pyrophosphorylase 4 [Arabidopsis thaliana]	217	216	1.00E-116	99.5	93.5	96.8	pyrophosphorylase 4	gbpln	Arabidopsis thaliana	AT3G53620.1 | Symbols: AtPPa4, PPa4 | pyrophosphorylase 4 | chr3:19881491-19883308 FORWARD LENGTH=216	217	216	1.00E-119	99.5	93.5	96.8
Rsa1.0_00066.1.g3533.t1	ref|XP_002876217.1| hypothetical protein ARALYDRAFT_485749 [Arabidopsis lyrata subsp. lyrata] gi|297322055|gb|EFH52476.1| hypothetical protein ARALYDRAFT_485749 [Arabidopsis lyrata subsp. lyrata]	187	192	1.00E-66	102.7	81.3	87.2	hypothetical protein ARALYDRAFT_485749	gbpln	Arabidopsis lyrata	AT3G53630.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G18692.1); Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:19883986-19885568 FORWARD LENGTH=194	187	194	3.00E-68	103.7	80.7	86.6
Rsa1.0_00066.1.g3534.t1	ref|XP_002532621.1| histone h2b, putative [Ricinus communis] gi|223527641|gb|EEF29752.1| histone h2b, putative [Ricinus communis]	138	141	3.00E-62	102.2	93.5	98.6	histone h2b, putative	gbpln	Ricinus communis	AT2G37470.1 | Symbols: | Histone superfamily protein | chr2:15736832-15737248 FORWARD LENGTH=138	138	138	5.00E-64	100.0	95.7	97.8

Rsa1.0_00066.1.g3535.t1	ref|NP_190935.1| uncharacterized protein [Arabidopsis thaliana] gi|334185954|ref|NP_001190081.1| uncharacterized protein [Arabidopsis thaliana] gi|14423470|gb|AAK62417.1|AF386972_1 putative protein [Arabidopsis thaliana] gi|6729518|emb|CAB67674.1| putative protein [Arabidopsis thaliana] gi|18377574|gb|AAL66953.1| putative protein [Arabidopsis thaliana] gi|332645603|gb|AEE79124.1| uncharacterized protein AT3G53670 [Arabidopsis thaliana] gi|332645604|gb|AEE79125.1| uncharacterized protein AT3G53670 [Arabidopsis thaliana]	209	203	1.00E-56	97.1	67.0	76.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G53670.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G37480.1). | chr3:19891104-19892214 FORWARD LENGTH=203	209	203	3.00E-59	97.1	67.0	76.1
Rsa1.0_00066.1.g3536.t1	ref|NP_190936.2| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein [Arabidopsis thaliana] gi|225898713|dbj|BAH30487.1| hypothetical protein [Arabidopsis thaliana] gi|332645606|gb|AEE79127.1| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein [Arabidopsis thaliana]	858	841	0	98.0	68.2	74.6	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT3G53680.1 | Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain | chr3:19892863-19897412 REVERSE LENGTH=841	858	841	0	98.0	68.2	74.6
Rsa1.0_00066.1.g3537.t1	ref|NP_190940.1| cation/H(+) antiporter 20 [Arabidopsis thaliana] gi|75311818|sp|Q9M353.1|CHX20_ARATH RecName: Full=Cation/H(+) antiporter 20; AltName: Full=Protein CATION/H+ EXCHANGER 20; Short=AtCHX20 gi|7629992|emb|CAB88334.1| putative protein [Arabidopsis thaliana] gi|27311847|gb|AAO00889.1| putative protein [Arabidopsis thaliana] gi|38603806|gb|AAR24648.1| At3g53720 [Arabidopsis thaliana] gi|110742710|dbj|BAE99266.1| hypothetical protein [Arabidopsis thaliana] gi|332645611|gb|AEE79132.1| cation/H(+) antiporter 20 [Arabidopsis thaliana]	834	842	0	101.0	90.0	94.6	cation/H(+) antiporter 20	gbpln	Arabidopsis thaliana	AT3G53720.1 | Symbols: ATCHX20, CHX20 | cation/H+ exchanger 20 | chr3:19905826-19910027 REVERSE LENGTH=842	834	842	0	101.0	90.0	94.6
Rsa1.0_00066.1.g3538.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00066.1.g3539.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	583	1164	2.00E-84	199.7	26.9	40.8	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	583	746	3.00E-64	128.0	26.4	38.9
Rsa1.0_00066.1.g3540.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_00066.1.g3541.t1	ref|NP_850697.1| 60S ribosomal protein L36-2 [Arabidopsis thaliana] gi|79314916|ref|NP_001030855.1| 60S ribosomal protein L36-2 [Arabidopsis thaliana] gi|145332827|ref|NP_001078279.1| 60S ribosomal protein L36-2 [Arabidopsis thaliana] gi|17865567|sp|Q9M352.1|RL362_ARATH RecName: Full=60S ribosomal protein L36-2 gi|7629994|emb|CAB88336.1| 60S RIBOSOMAL PROTEIN L36 homolog [Arabidopsis thaliana] gi|17065430|gb|AAL32869.1| 60S RIBOSOMAL PROTEIN L36 homolog [Arabidopsis thaliana] gi|20148501|gb|AAM10141.1| 60S ribosomal protein L36-like protein [Arabidopsis thaliana] gi|332645614|gb|AEE79135.1| 60S ribosomal protein L36-2 [Arabidopsis thaliana] gi|332645615|gb|AEE79136.1| 60S ribosomal protein L36-2 [Arabidopsis thaliana] gi|332645616|gb|AEE79137.1| 60S ribosomal protein L36-2 [Arabidopsis thaliana]	112	112	7.00E-52	100.0	94.6	99.1	60S ribosomal protein L36-2	gbpln	Arabidopsis thaliana	AT3G53740.4 | Symbols: | Ribosomal protein L36e family protein | chr3:19913921-19914813 REVERSE LENGTH=112	112	112	1.00E-54	100.0	94.6	99.1

Rsa1.0_00066.1.g3542.t1	ref|NP_566988.1| actin 3 [Arabidopsis thaliana] gi|30687201|ref|NP_850284.1| actin 1 [Arabidopsis thaliana] gi|79324605|ref|NP_001031504.1| actin 1 [Arabidopsis thaliana] gi|460415910|ref|XP_004253296.1| PREDICTED: actin-1-like [Solanum lycopersicum] gi|317374840|sp|P0CJ46.1|ACT1_ARATH RecName: Full=Actin-1 gi|317374841|sp|P0CJ47.1|ACT3_ARATH RecName: Full=Actin-3 gi|1145695|gb|AAA98562.1| actin 3 [Arabidopsis thaliana] gi|15146304|gb|AAK83635.1| AT3g53750/F5K20_50 [Arabidopsis thaliana] gi|18650648|gb|AAL75893.1| At2g37620/F13M22.12 [Arabidopsis thaliana] gi|20147381|gb|AAM10400.1| At2g37620/F13M22.12 [Arabidopsis thaliana] gi|21554576|gb|AAM63620.1| actin (ACT3) [Arabidopsis thaliana] gi|25090278|gb|AAN72268.1| At3g53750/F5K20_50 [Arabidopsis thaliana] gi|330254332|gb|AEC09426.1| actin 1 [Arabidopsis thaliana] gi|330254333|gb|AEC09427.1| actin 1 [Arabidopsis thaliana] gi|332645617|gb|AEE79138.1| actin 3 [Arabidopsis thaliana]	377	377	0	100.0	99.5	99.7	actin 3	gbpln	Arabidopsis thaliana	AT3G53750.1 | Symbols: ACT3 | actin 3 | chr3:19915924-19917371 FORWARD LENGTH=377	377	377	0	100.0	99.5	99.7
Rsa1.0_00066.1.g3543.t1	gb|EOA23531.1| hypothetical protein CARUB_v10016729mg [Capsella rubella]	748	745	0	99.6	92.1	94.9	hypothetical protein CARUB_v10016729mg	gbpln	Capsella rubella	AT3G53760.1 | Symbols: GCP4, ATGCP4 | GAMMA-TUBULIN COMPLEX PROTEIN 4 | chr3:19918182-19922264 REVERSE LENGTH=745	748	745	0	99.6	91.6	94.8
Rsa1.0_00066.1.g3544.t1	gb|EOA24166.1| hypothetical protein CARUB_v10017398mg [Capsella rubella]	392	396	0	101.0	90.6	95.4	hypothetical protein CARUB_v10017398mg	gbpln	Capsella rubella	AT3G53780.2 | Symbols: ATRBL4, RBL4 | RHOMBOID-like protein 4 | chr3:19924729-19926648 REVERSE LENGTH=394	392	394	0	100.5	88.5	94.6
Rsa1.0_00066.1.g3545.t1	ref|NP_190948.1| hsp70-interacting protein [Arabidopsis thaliana] gi|7630000|emb|CAB88342.1| putative protein [Arabidopsis thaliana] gi|21593297|gb|AAM65246.1| unknown [Arabidopsis thaliana] gi|332645624|gb|AEE79145.1| hsp70-interacting protein FES1B-like protein [Arabidopsis thaliana]	363	363	0	100.0	88.7	93.7	hsp70-interacting protein	gbpln	Arabidopsis thaliana	AT3G53800.1 | Symbols: Fes1B | Fes1B | chr3:19930942-19932719 FORWARD LENGTH=363	363	363	0	100.0	88.7	93.7
Rsa1.0_00066.1.g3546.t1	gb|EOA25977.1| hypothetical protein CARUB_v10019366mg [Capsella rubella]	677	723	0	106.8	85.2	92.0	hypothetical protein CARUB_v10019366mg	gbpln	Capsella rubella	AT3G53810.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:19933153-19935186 REVERSE LENGTH=677	677	677	0	100.0	84.6	91.6
Rsa1.0_00066.1.g3547.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	553	1529	4.00E-99	276.5	38.5	55.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	553	746	3.00E-63	134.9	27.1	36.5
Rsa1.0_00066.1.g3548.t1	ref|XP_002876227.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297322065|gb|EFH52486.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	180	142	5.00E-53	78.9	57.8	67.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G53820.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr3:19938706-19939134 FORWARD LENGTH=142	180	142	2.00E-54	78.9	57.8	66.7
Rsa1.0_00066.1.g3549.t1	gb|EOA23633.1| hypothetical protein CARUB_v10016831mg [Capsella rubella]	644	638	0	99.1	82.9	89.1	hypothetical protein CARUB_v10016831mg	gbpln	Capsella rubella	AT3G53840.1 | Symbols: | Protein kinase superfamily protein | chr3:19945571-19947719 FORWARD LENGTH=639	644	639	0	99.2	81.5	87.7
Rsa1.0_00066.1.g3550.t1	ref|NP_566990.1| uncharacterized protein [Arabidopsis thaliana] gi|75164334|sp|Q945M8.1|CSPLI_ARATH RecName: Full=CASP-like protein At3g53850 gi|15724236|gb|AAL06511.1|AF412058_1 AT4g31460/F3L17_30 [Arabidopsis thaliana] gi|21464571|gb|AAM52240.1| AT4g31460/F3L17_30 [Arabidopsis thaliana] gi|332645629|gb|AEE79150.1| uncharacterized protein AT3G53850 [Arabidopsis thaliana]	167	154	5.00E-42	92.2	55.7	64.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G53850.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr3:19948262-19948994 REVERSE LENGTH=154	167	154	2.00E-44	92.2	55.7	64.7
Rsa1.0_00066.1.g3551.t1	gb|EOA24417.1| hypothetical protein CARUB_v10017668mg [Capsella rubella]	289	315	1.00E-150	109.0	93.4	96.2	hypothetical protein CARUB_v10017668mg	gbpln	Capsella rubella	AT3G53880.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr3:19953238-19955171 FORWARD LENGTH=315	289	315	1.00E-151	109.0	91.3	95.8
Rsa1.0_00066.1.g3552.t1	gb|EOA25028.1| hypothetical protein CARUB_v10018334mg [Capsella rubella]	82	82	1.00E-39	100.0	95.1	97.6	hypothetical protein CARUB_v10018334mg	gbpln	Capsella rubella	AT5G27700.1 | Symbols: | Ribosomal protein S21e | chr5:9807541-9808048 REVERSE LENGTH=82	82	82	1.00E-41	100.0	93.9	96.3

<table>
<tr><td>Rsa1.0_00066.1.g3553.t1</td><td>ref|XP_002877946.1| hypothetical protein ARALYDRAFT_323928 [Arabidopsis lyrata subsp. lyrata] gi|297323784|gb|EFH54205.1| hypothetical protein ARALYDRAFT_323928 [Arabidopsis lyrata subsp. lyrata]</td><td>328</td><td>295</td><td>1.00E-131</td><td>89.9</td><td>75.3</td><td>79.9</td><td>hypothetical protein ARALYDRAFT_323928</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G53900.2 | Symbols: UPP, PYRR | uracil phosphoribosyltransferase | chr3:19956914-19959006 REVERSE LENGTH=296</td><td>328</td><td>296</td><td>1.00E-133</td><td>90.2</td><td>75.0</td><td>80.2</td></tr>
<tr><td>Rsa1.0_00066.1.g3554.t1</td><td>gb|EOA23672.1| hypothetical protein CARUB_v10016879mg [Capsella rubella]</td><td>593</td><td>602</td><td>0</td><td>101.5</td><td>83.3</td><td>92.4</td><td>hypothetical protein CARUB_v10016879mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G53960.1 | Symbols: | Major facilitator superfamily protein | chr3:19978306-19980886 REVERSE LENGTH=602</td><td>593</td><td>602</td><td>0</td><td>101.5</td><td>82.3</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00067.1.g3555.t1</td><td>ref|NP_173609.1| ethylene-responsive transcription factor ERF012 [Arabidopsis thaliana] gi|75265793|sp|Q9SFE4.1|ERF12_ARATH RecName: Full=Ethylene-responsive transcription factor ERF012 gi|6552733|gb|AAF16532.1|AC013482_6 T26F17.14 [Arabidopsis thaliana] gi|51971555|dbj|BAD44442.1| TINY like protein [Arabidopsis thaliana] gi|88196743|gb|ABD43014.1| At1g21910 [Arabidopsis thaliana] gi|332192050|gb|AEE30171.1| ethylene-responsive transcription factor ERF012 [Arabidopsis thaliana]</td><td>227</td><td>230</td><td>2.00E-70</td><td>101.3</td><td>74.4</td><td>84.6</td><td>ethylene-responsive transcription factor ERF012</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21910.1 | Symbols: DREB26 | Integrase-type DNA-binding superfamily protein | chr1:7696655-7697347 FORWARD LENGTH=230</td><td>227</td><td>230</td><td>5.00E-73</td><td>101.3</td><td>74.4</td><td>84.6</td></tr>
<tr><td>Rsa1.0_00067.1.g3556.t1</td><td>gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]</td><td>142</td><td>1164</td><td>6.00E-11</td><td>819.7</td><td>26.1</td><td>39.4</td><td>similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00067.1.g3557.t1</td><td>ref|XP_002893188.1| emp24/gp25L/p24 family protein [Arabidopsis lyrata subsp. lyrata] gi|297339030|gb|EFH69447.1| emp24/gp25L/p24 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>224</td><td>216</td><td>1.00E-103</td><td>96.4</td><td>80.8</td><td>87.1</td><td>emp24/gp25L/p24 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21900.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:7691165-7692327 REVERSE LENGTH=216</td><td>224</td><td>216</td><td>1.00E-103</td><td>96.4</td><td>79.5</td><td>84.8</td></tr>
<tr><td>Rsa1.0_00067.1.g3558.t1</td><td>gb|EOA40579.1| hypothetical protein CARUB_v10009309mg, partial [Capsella rubella]</td><td>387</td><td>409</td><td>0</td><td>105.7</td><td>90.7</td><td>95.1</td><td>hypothetical protein CARUB_v10009309mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G21890.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:7682808-7685581 REVERSE LENGTH=389</td><td>387</td><td>389</td><td>0</td><td>100.5</td><td>89.4</td><td>93.3</td></tr>
<tr><td>Rsa1.0_00067.1.g3559.t1</td><td>ref|NP_564153.1| LysM domain-containing GPI-anchored protein 1 [Arabidopsis thaliana] gi|38258218|sp|Q93ZH0.1|LYM1_ARATH RecName: Full=LysM domain-containing GPI-anchored protein 1; Flags: Precursor gi|15982870|gb|AAL09782.1| At1g21880/T26F17_5 [Arabidopsis thaliana] gi|53749174|gb|AAU90072.1| At1g21880 [Arabidopsis thaliana] gi|332192047|gb|AEE30168.1| LysM domain-containing GPI-anchored protein 1 [Arabidopsis thaliana]</td><td>447</td><td>416</td><td>0</td><td>93.1</td><td>81.4</td><td>87.9</td><td>LysM domain-containing GPI-anchored protein 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21880.2 | Symbols: LYM1 | lysm domain GPI-anchored protein 1 precursor | chr1:7680689-7682526 FORWARD LENGTH=416</td><td>447</td><td>416</td><td>0</td><td>93.1</td><td>81.4</td><td>87.9</td></tr>
<tr><td>Rsa1.0_00067.1.g3560.t1</td><td>ref|XP_002893185.1| hypothetical protein ARALYDRAFT_313074 [Arabidopsis lyrata subsp. lyrata] gi|297339027|gb|EFH69444.1| hypothetical protein ARALYDRAFT_313074 [Arabidopsis lyrata subsp. lyrata]</td><td>273</td><td>205</td><td>9.00E-73</td><td>75.1</td><td>60.4</td><td>62.6</td><td>hypothetical protein ARALYDRAFT_313074</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21830.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF740 (InterPro:IPR008004); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G44608.1); Has 49 Blast hits to 49 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7661429-7662521 REVERSE LENGTH=206</td><td>273</td><td>206</td><td>6.00E-73</td><td>75.5</td><td>59.7</td><td>62.6</td></tr>
<tr><td>Rsa1.0_00067.1.g3561.t1</td><td>ref|XP_002890465.1| hypothetical protein ARALYDRAFT_472418 [Arabidopsis lyrata subsp. lyrata] gi|297336307|gb|EFH66724.1| hypothetical protein ARALYDRAFT_472418 [Arabidopsis lyrata subsp. lyrata]</td><td>280</td><td>288</td><td>1.00E-144</td><td>102.9</td><td>90.7</td><td>93.9</td><td>hypothetical protein ARALYDRAFT_472418</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21790.1 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr1:7654357-7655691 FORWARD LENGTH=288</td><td>280</td><td>288</td><td>1.00E-144</td><td>102.9</td><td>90.0</td><td>93.6</td></tr>
<tr><td>Rsa1.0_00067.1.g3562.t1</td><td>ref|XP_002890464.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297336306|gb|EFH66723.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>384</td><td>326</td><td>0</td><td>84.9</td><td>80.2</td><td>82.8</td><td>BTB/POZ domain-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21780.2 | Symbols: | BTB/POZ domain-containing protein | chr1:7652476-7653866 FORWARD LENGTH=326</td><td>384</td><td>326</td><td>0</td><td>84.9</td><td>79.9</td><td>82.6</td></tr>
<tr><td>Rsa1.0_00067.1.g3563.t1</td><td>gb|EOA38692.1| hypothetical protein CARUB_v10010702mg [Capsella rubella]</td><td>104</td><td>110</td><td>7.00E-42</td><td>105.8</td><td>82.7</td><td>91.3</td><td>hypothetical protein CARUB_v10010702mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G21770.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr1:7651843-7652249 REVERSE LENGTH=111</td><td>104</td><td>111</td><td>2.00E-43</td><td>106.7</td><td>81.7</td><td>88.5</td></tr>
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<tr><td>Rsa1.0_00067.1.g3564.t1</td><td>ref|XP_002890463.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297336305|gb|EFH66722.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>323</td><td>328</td><td>1.00E-179</td><td>101.5</td><td>94.7</td><td>96.9</td><td>F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21760.1 | Symbols: ATFBP7, FBP7 | F-box protein 7 | chr1:7649324-7651613 FORWARD LENGTH=328</td><td>323</td><td>328</td><td>1.00E-179</td><td>101.5</td><td>92.6</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00067.1.g3565.t1</td><td>tpg|DAA63284.1| TPA: hypothetical protein ZEAMMB73_434507 [Zea mays]</td><td>292</td><td>704</td><td>3.00E-25</td><td>241.1</td><td>30.1</td><td>54.8</td><td>TPA: hypothetical protein ZEAMMB73_434507</td><td>gbenv/gbpln</td><td>Zea mays</td><td>AT5G19820.1 | Symbols: emb2734 | ARM repeat superfamily protein | chr5:6695731-6701247 REVERSE LENGTH=1116</td><td>292</td><td>1116</td><td>2.00E-26</td><td>382.2</td><td>30.1</td><td>55.1</td></tr>
<tr><td>Rsa1.0_00067.1.g3566.t1</td><td>ref|XP_002890462.1| hypothetical protein ARALYDRAFT_889647 [Arabidopsis lyrata subsp. lyrata] gi|297336304|gb|EFH66721.1| hypothetical protein ARALYDRAFT_889647 [Arabidopsis lyrata subsp. lyrata]</td><td>495</td><td>501</td><td>0</td><td>101.2</td><td>80.6</td><td>88.3</td><td>hypothetical protein ARALYDRAFT_889647</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21750.1 | Symbols: ATPDIL1-1, ATPDI5, PDI5, PDIL1-1 | PDI-like 1-1 | chr1:7645767-7648514 FORWARD LENGTH=501</td><td>495</td><td>501</td><td>0</td><td>101.2</td><td>79.6</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00067.1.g3567.t1</td><td>ref|XP_002890461.1| hypothetical protein ARALYDRAFT_472413 [Arabidopsis lyrata subsp. lyrata] gi|297336303|gb|EFH66720.1| hypothetical protein ARALYDRAFT_472413 [Arabidopsis lyrata subsp. lyrata]</td><td>934</td><td>942</td><td>0</td><td>100.9</td><td>81.9</td><td>88.0</td><td>hypothetical protein ARALYDRAFT_472413</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21740.1 | Symbols: | Protein of unknown function (DUF630 and DUF632) | chr1:7641580-7645078 FORWARD LENGTH=953</td><td>934</td><td>953</td><td>0</td><td>102.0</td><td>82.0</td><td>88.3</td></tr>
<tr><td>Rsa1.0_00067.1.g3568.t1</td><td>ref|NP_173592.3| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|16902292|dbj|BAB71851.1| kinesin-related protein [Arabidopsis thaliana] gi|332192027|gb|AEE30148.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana]</td><td>925</td><td>890</td><td>0</td><td>96.2</td><td>83.4</td><td>87.8</td><td>P-loop containing nucleoside triphosphate hydrolase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21730.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:7630365-7636247 FORWARD LENGTH=890</td><td>925</td><td>890</td><td>0</td><td>96.2</td><td>83.4</td><td>87.8</td></tr>
<tr><td>Rsa1.0_00067.1.g3569.t1</td><td>gb|EOA36141.1| hypothetical protein CARUB_v10012612mg [Capsella rubella]</td><td>224</td><td>229</td><td>8.00E-86</td><td>102.2</td><td>77.7</td><td>87.5</td><td>hypothetical protein CARUB_v10012612mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G21722.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G78922.1); Has 47 Blast hits to 47 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 1; Plants - 42; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr1:7628456-7629252 FORWARD LENGTH=233</td><td>224</td><td>233</td><td>1.00E-86</td><td>104.0</td><td>77.7</td><td>86.6</td></tr>
<tr><td>Rsa1.0_00067.1.g3570.t1</td><td>ref|NP_564149.1| proteasome subunit beta type-3-A [Arabidopsis thaliana] gi|288558823|sp|Q9XI05.2|PSB3A_ARATH RecName: Full=Proteasome subunit beta type-3-A; AltName: Full=20S proteasome beta subunit C-1; AltName: Full=Proteasome component T gi|17473525|gb|AAL38246.1| proteasome subunit [Arabidopsis thaliana] gi|21387087|gb|AAM47947.1| proteasome subunit [Arabidopsis thaliana] gi|110740894|dbj|BAE98543.1| 20S proteasome beta subunit PBC2 like protein [Arabidopsis thaliana] gi|332192025|gb|AEE30146.1| proteasome subunit beta type-3-A [Arabidopsis thaliana]</td><td>204</td><td>204</td><td>1.00E-116</td><td>100.0</td><td>99.0</td><td>100.0</td><td>proteasome subunit beta type-3-A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21720.1 | Symbols: PBC1 | proteasome beta subunit C1 | chr1:7626394-7628070 FORWARD LENGTH=204</td><td>204</td><td>204</td><td>1.00E-118</td><td>100.0</td><td>99.0</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00067.1.g3571.t1</td><td>gb|EOA36733.1| hypothetical protein CARUB_v10012527mg, partial [Capsella rubella]</td><td>778</td><td>833</td><td>0</td><td>107.1</td><td>82.3</td><td>89.2</td><td>hypothetical protein CARUB_v10012527mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G21700.1 | Symbols: ATSWI3C, CHB4, SWI3C | SWITCH/sucrose nonfermenting 3C | chr1:7620156-7623978 REVERSE LENGTH=807</td><td>778</td><td>807</td><td>0</td><td>103.7</td><td>82.6</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00067.1.g3572.t1</td><td>ref|XP_002890454.1| hypothetical protein ARALYDRAFT_472409 [Arabidopsis lyrata subsp. lyrata] gi|297336296|gb|EFH66713.1| hypothetical protein ARALYDRAFT_472409 [Arabidopsis lyrata subsp. lyrata]</td><td>211</td><td>205</td><td>7.00E-36</td><td>97.2</td><td>55.0</td><td>64.0</td><td>hypothetical protein ARALYDRAFT_472409</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21695.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:7619132-7619785 FORWARD LENGTH=217</td><td>211</td><td>217</td><td>1.00E-29</td><td>102.8</td><td>53.6</td><td>63.0</td></tr>
<tr><td>Rsa1.0_00067.1.g3573.t1</td><td>ref|XP_002890453.1| EMB1968 [Arabidopsis lyrata subsp. lyrata] gi|297336295|gb|EFH66712.1| EMB1968 [Arabidopsis lyrata subsp. lyrata]</td><td>339</td><td>339</td><td>0</td><td>100.0</td><td>93.2</td><td>96.8</td><td>EMB1968</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G21690.1 | Symbols: EMB1968, RFC4 | ATPase family associated with various cellular activities (AAA) | chr1:7615675-7618362 FORWARD LENGTH=339</td><td>339</td><td>339</td><td>0</td><td>100.0</td><td>92.9</td><td>96.5</td></tr>
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Rsa1.0_00067.1.g3574.t1	ref|XP_002890452.1| hypothetical protein ARALYDRAFT_472406 [Arabidopsis lyrata subsp. lyrata] gi|297336294|gb|EFH66711.1| hypothetical protein ARALYDRAFT_472406 [Arabidopsis lyrata subsp. lyrata]	665	706	0	106.2	86.5	92.8	hypothetical protein ARALYDRAFT_472406	gbpln	Arabidopsis lyrata	AT1G21680.1 | Symbols: | DPP6 N-terminal domain-like protein | chr1:7613028-7615148 FORWARD LENGTH=706	665	706	0	106.2	85.6	91.3
Rsa1.0_00067.1.g3575.t1	dbj|BAF01687.1| hypothetical protein [Arabidopsis thaliana]	657	1072	1.00E-134	163.2	39.9	57.2	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	657	746	2.00E-60	113.5	21.3	31.5
Rsa1.0_00067.1.g3576.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00067.1.g3577.t2	gb|AAG51081.1|AC027032_1 hypothetical protein [Arabidopsis thaliana]	1327	1678	0	126.5	38.4	49.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1327	331	5.00E-57	24.9	8.4	11.5
Rsa1.0_00067.1.g3578.t1	ref|XP_002890451.1| hypothetical protein ARALYDRAFT_472405 [Arabidopsis lyrata subsp. lyrata] gi|297336293|gb|EFH66710.1| hypothetical protein ARALYDRAFT_472405 [Arabidopsis lyrata subsp. lyrata]	705	703	0	99.7	78.9	87.1	hypothetical protein ARALYDRAFT_472405	gbpln	Arabidopsis lyrata	AT1G21670.1 | Symbols: | LOCATED IN: cell wall, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: WD40-like Beta Propeller (InterPro:IPR011659), Six-bladed beta-propeller, TolB-like (InterPro:IPR011042); BEST Arabidopsis thaliana protein match is: DPP6 N-terminal domain-like protein (TAIR:AT1G21680.1); Has 8461 Blast hits to 5060 proteins in 1257 species: Archae - 79; Bacteria - 5567; Metazoa - 37; Fungi - 70; Plants - 117; Viruses - 0; Other Eukaryotes - 2591 (source: NCBI BLink). | chr1:7610409-7612520 FORWARD LENGTH=703	705	703	0	99.7	76.6	85.1
Rsa1.0_00067.1.g3579.t9	gb|EOA40087.1| hypothetical protein CARUB_v10008781mg [Capsella rubella]	539	544	1.00E-176	100.9	67.7	76.3	hypothetical protein CARUB_v10008781mg	gbpln	Capsella rubella	AT1G21660.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:7605924-7608835 FORWARD LENGTH=523	539	523	1.00E-170	97.0	65.9	74.0
Rsa1.0_00067.1.g3580.t1	gb|EOA35901.1| hypothetical protein CARUB_v10021156mg [Capsella rubella]	147	121	2.00E-49	82.3	71.4	78.9	hypothetical protein CARUB_v10021156mg	gbpln	Capsella rubella	AT1G77350.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function KRTCAP2 (InterPro:IPR018614); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:29070497-29071545 FORWARD LENGTH=122	147	122	2.00E-51	83.0	72.8	80.3
Rsa1.0_00067.1.g3581.t1	gb|EOA39091.1| hypothetical protein CARUB_v10011823mg [Capsella rubella]	806	1799	0	223.2	73.6	83.9	hypothetical protein CARUB_v10011823mg	gbpln	Capsella rubella	AT1G21650.3 | Symbols: SECA2 | Preprotein translocase SecA family protein | chr1:7592891-7604152 REVERSE LENGTH=1805	806	1805	0	223.9	73.4	84.9
Rsa1.0_00067.1.g3582.t1	ref|XP_002890449.1| hypothetical protein ARALYDRAFT_889629 [Arabidopsis lyrata subsp. lyrata] gi|297336291|gb|EFH66708.1| hypothetical protein ARALYDRAFT_889629 [Arabidopsis lyrata subsp. lyrata]	1009	983	0	97.4	85.5	90.4	hypothetical protein ARALYDRAFT_889629	gbpln	Arabidopsis lyrata	AT1G21640.1 | Symbols: NADK2, ATNADK2 | NAD kinase 2 | chr1:7588726-7592669 FORWARD LENGTH=985	1009	985	0	97.6	84.9	89.6
Rsa1.0_00067.1.g3583.t1	ref|NP_173582.2| calcium-binding EF-hand-containing protein [Arabidopsis thaliana] gi|332192007|gb|AEE30128.1| calcium-binding EF-hand-containing protein [Arabidopsis thaliana]	1228	1218	0	99.2	83.0	87.5	calcium-binding EF-hand-containing protein	gbpln	Arabidopsis thaliana	AT1G21630.1 | Symbols: | Calcium-binding EF hand family protein | chr1:7581457-7587796 FORWARD LENGTH=1218	1228	1218	0	99.2	83.0	87.5
Rsa1.0_00067.1.g3584.t2	ref|XP_002893178.1| hypothetical protein ARALYDRAFT_472396 [Arabidopsis lyrata subsp. lyrata] gi|297339020|gb|EFH69437.1| hypothetical protein ARALYDRAFT_472396 [Arabidopsis lyrata subsp. lyrata]	334	328	1.00E-162	98.2	90.1	92.2	hypothetical protein ARALYDRAFT_472396	gbpln	Arabidopsis lyrata	AT1G21600.2 | Symbols: PTAC6 | plastid transcriptionally active 6 | chr1:7571514-7573782 REVERSE LENGTH=328	334	328	1.00E-150	98.2	85.0	87.7
Rsa1.0_00067.1.g3585.t3	ref|NP_173577.2| zinc finger CCCH domain-containing protein [Arabidopsis thaliana] gi|332191999|gb|AEE30120.1| zinc finger CCCH domain-containing protein [Arabidopsis thaliana]	2016	2166	0	107.4	64.7	74.6	zinc finger CCCH domain-containing protein	gbpln	Arabidopsis thaliana	AT1G21580.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:7557822-7565655 REVERSE LENGTH=2166	2016	2166	0	107.4	64.7	74.6

Rsa1.0_00067.1.g3586.t1	ref|XP_002890445.1| hypothetical protein ARALYDRAFT_889619 [Arabidopsis lyrata subsp. lyrata] gi|297336287|gb|EFH66704.1| hypothetical protein ARALYDRAFT_889619 [Arabidopsis lyrata subsp. lyrata]	379	394	7.00E-86	104.0	53.3	64.4	hypothetical protein ARALYDRAFT_889619	gbpln	Arabidopsis lyrata	AT1G21560.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01170.1). | chr1:7555208-7556789 FORWARD LENGTH=399	379	399	5.00E-83	105.3	51.7	64.1
Rsa1.0_00067.1.g3587.t1	gb|EOA39012.1| hypothetical protein CARUB_v10011559mg [Capsella rubella]	142	159	1.00E-56	112.0	78.2	85.9	hypothetical protein CARUB_v10011559mg	gbpln	Capsella rubella	AT1G21550.1 | Symbols: | Calcium-binding EF-hand family protein | chr1:7553317-7553784 REVERSE LENGTH=155	142	155	2.00E-58	109.2	76.1	87.3
Rsa1.0_00067.1.g3588.t1	ref|XP_002893174.1| hypothetical protein ARALYDRAFT_889616 [Arabidopsis lyrata subsp. lyrata] gi|297339016|gb|EFH69433.1| hypothetical protein ARALYDRAFT_889616 [Arabidopsis lyrata subsp. lyrata]	550	550	0	100.0	94.4	97.6	hypothetical protein ARALYDRAFT_889616	gbpln	Arabidopsis lyrata	AT1G21540.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr1:7548758-7550521 REVERSE LENGTH=550	550	550	0	100.0	92.7	97.3
Rsa1.0_00067.1.g3589.t1	gb|EOA36652.1| hypothetical protein CARUB_v10011926mg [Capsella rubella]	69	72	1.00E-14	104.3	71.0	78.3	hypothetical protein CARUB_v10011926mg	gbpln	Capsella rubella	AT1G21528.1 | Symbols: | unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7542830-7543039 REVERSE LENGTH=69	69	69	7.00E-16	100.0	65.2	75.4
Rsa1.0_00067.1.g3590.t1	ref|XP_002893172.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata] gi|297339014|gb|EFH69431.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata]	70	71	3.00E-16	101.4	68.6	81.4	hypothetical protein ARALYDRAFT_472389	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00067.1.g3591.t1	ref|XP_002893172.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata] gi|297339014|gb|EFH69431.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata]	73	71	2.00E-19	97.3	72.6	79.5	hypothetical protein ARALYDRAFT_472389	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00067.1.g3592.t1	ref|XP_002893171.1| hypothetical protein ARALYDRAFT_889613 [Arabidopsis lyrata subsp. lyrata] gi|297339013|gb|EFH69430.1| hypothetical protein ARALYDRAFT_889613 [Arabidopsis lyrata subsp. lyrata]	59	66	5.00E-12	111.9	72.9	79.7	hypothetical protein ARALYDRAFT_889613	gbpln	Arabidopsis lyrata	AT1G21520.1 | Symbols: | unknown protein; Has 9 Blast hits to 9 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 9; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7534533-7534733 REVERSE LENGTH=66	59	66	2.00E-13	111.9	71.2	76.3
Rsa1.0_00067.1.g3593.t1	ref|XP_002893170.1| hypothetical protein ARALYDRAFT_472387 [Arabidopsis lyrata subsp. lyrata] gi|297339012|gb|EFH69429.1| hypothetical protein ARALYDRAFT_472387 [Arabidopsis lyrata subsp. lyrata]	325	326	1.00E-117	100.3	75.7	84.0	hypothetical protein ARALYDRAFT_472387	gbpln	Arabidopsis lyrata	AT1G21510.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: cotyledon; Has 380 Blast hits to 286 proteins in 63 species: Archae - 0; Bacteria - 6; Metazoa - 254; Fungi - 44; Plants - 13; Viruses - 5; Other Eukaryotes - 58 (source: NCBI BLink). | chr1:7531534-7532505 REVERSE LENGTH=323	325	323	1.00E-110	99.4	71.7	82.5
Rsa1.0_00067.1.g3594.t9	sp|Q9LNF6.3|FB48_ARATH RecName: Full=F-box protein At1g48060	256	365	2.00E-30	142.6	39.5	59.8	RecName: Full=F-box protein At1g48060	----	----	AT1G48060.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:17728295-17729448 FORWARD LENGTH=353	256	353	7.00E-33	137.9	39.5	59.8
Rsa1.0_00067.1.g3595.t1	gb|EOA39248.1| hypothetical protein CARUB_v10012244mg [Capsella rubella]	114	253	4.00E-12	221.9	43.0	51.8	hypothetical protein CARUB_v10012244mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00067.1.g3596.t1	ref|NP_564141.1| exostosin-like protein [Arabidopsis thaliana] gi|332191985|gb|AEE30106.1| exostosin-like protein [Arabidopsis thaliana]	445	462	0	103.8	92.6	96.2	exostosin-like protein	gbpln	Arabidopsis thaliana	AT1G21480.1 | Symbols: | Exostosin family protein | chr1:7519116-7521426 REVERSE LENGTH=462	445	462	0	103.8	92.6	96.2
Rsa1.0_00067.1.g3597.t1	ref|XP_002893163.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297339005|gb|EFH69422.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	247	247	1.00E-126	100.0	91.1	95.1	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT1G21460.1 | Symbols: SWEET1, AtSWEET1 | Nodulin MtN3 family protein | chr1:7512030-7513281 REVERSE LENGTH=247	247	247	1.00E-126	100.0	89.5	94.3
Rsa1.0_00067.1.g3598.t1	dbj|BAJ33657.1| unnamed protein product [Thellungiella halophila]	571	595	0	104.2	87.4	93.3	unnamed protein product	----	----	AT1G21450.1 | Symbols: SCL1 | SCARECROW-like 1 | chr1:7509721-7511502 FORWARD LENGTH=593	571	593	0	103.9	85.1	91.6

Rsa1.0_00067.1.g3599.t1	ref|NP_191713.1| peptidase family protein [Arabidopsis thaliana] gi|6850845|emb|CAB71084.1| prolyl aminopeptidase-like protein [Arabidopsis thaliana] gi|15450667|gb|AAK96605.1| AT3g61540/F2A19_140 [Arabidopsis thaliana] gi|17380608|gb|AAL36067.1| AT3g61540/F2A19_140 [Arabidopsis thaliana] gi|332646699|gb|AEE80220.1| peptidase family protein [Arabidopsis thaliana]	93	515	9.00E-36	553.8	78.5	82.8	peptidase family protein	gbpln	Arabidopsis thaliana	AT3G61540.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:22773399-22775699 FORWARD LENGTH=515	93	515	1.00E-38	553.8	78.5	82.8
Rsa1.0_00067.1.g3600.t1	gb|EOA38182.1| hypothetical protein CARUB_v10009659mg [Capsella rubella]	352	338	1.00E-159	96.0	81.0	84.9	hypothetical protein CARUB_v10009659mg	gbpln	Capsella rubella	AT1G21440.1 | Symbols: | Phosphoenolpyruvate carboxylase family protein | chr1:7502325-7504103 REVERSE LENGTH=336	352	336	1.00E-161	95.5	81.0	84.7
Rsa1.0_00067.1.g3601.t1	gb|EOA37849.1| hypothetical protein CARUB_v10011440mg [Capsella rubella]	382	390	0	102.1	82.2	89.8	hypothetical protein CARUB_v10011440mg	gbpln	Capsella rubella	AT1G21430.1 | Symbols: YUC11 | Flavin-binding monooxygenase family protein | chr1:7500845-7502186 FORWARD LENGTH=391	382	391	0	102.4	79.3	87.4
Rsa1.0_00067.1.g3602.t1	dbj|BAJ33623.1| unnamed protein product [Thellungiella halophila]	472	471	0	99.8	91.5	94.1	unnamed protein product	----	----	AT1G21400.1 | Symbols: | Thiamin diphosphate-binding fold (THDP-binding) superfamily protein | chr1:7493492-7496240 FORWARD LENGTH=472	472	472	0	100.0	91.1	94.7
Rsa1.0_00067.1.g3603.t3	gb|EOA38425.1| hypothetical protein CARUB_v10010005mg, partial [Capsella rubella]	215	271	3.00E-66	126.0	65.1	76.3	hypothetical protein CARUB_v10010005mg, partial	gbpln	Capsella rubella	AT1G21390.1 | Symbols: emb2170 | embryo defective 2170 | chr1:7489385-7490554 REVERSE LENGTH=248	215	248	3.00E-64	115.3	65.6	74.9
Rsa1.0_00067.1.g3604.t1	ref|XP_002890439.1| hypothetical protein ARALYDRAFT_472372 [Arabidopsis lyrata subsp. lyrata] gi|297336281|gb|EFH66698.1| hypothetical protein ARALYDRAFT_472372 [Arabidopsis lyrata subsp. lyrata]	334	341	1.00E-163	102.1	83.8	91.3	hypothetical protein ARALYDRAFT_472372	gbpln	Arabidopsis lyrata	AT1G21370.2 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF218 (InterPro:IPR003848); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:7484250-7485451 FORWARD LENGTH=342	334	342	1.00E-161	102.4	82.3	91.0
Rsa1.0_00067.1.g3605.t1	ref|XP_002890438.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336280|gb|EFH66697.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	222	222	1.00E-109	100.0	86.5	91.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G21360.1 | Symbols: GLTP2 | glycolipid transfer protein 2 | chr1:7481365-7483237 FORWARD LENGTH=223	222	223	1.00E-109	100.5	84.2	91.0
Rsa1.0_00067.1.g3606.t1	ref|XP_002893159.1| electron carrier/ oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297339001|gb|EFH69418.1| electron carrier/ oxidoreductase [Arabidopsis lyrata subsp. lyrata]	254	253	1.00E-121	99.6	84.3	89.4	electron carrier/ oxidoreductase	gbpln	Arabidopsis lyrata	AT1G21350.3 | Symbols: | Thioredoxin superfamily protein | chr1:7477376-7479012 REVERSE LENGTH=252	254	252	1.00E-119	99.2	81.5	89.0
Rsa1.0_00067.1.g3607.t1	gb|EOA38986.1| hypothetical protein CARUB_v10011507mg [Capsella rubella]	256	260	1.00E-116	101.6	84.0	90.6	hypothetical protein CARUB_v10011507mg	gbpln	Capsella rubella	AT1G21340.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr1:7476087-7476869 FORWARD LENGTH=260	256	260	1.00E-118	101.6	84.4	89.5
Rsa1.0_00067.1.g3608.t1	gb|EOA36400.1| hypothetical protein CARUB_v10010842mg [Capsella rubella]	204	237	1.00E-43	116.2	64.2	75.5	hypothetical protein CARUB_v10010842mg	gbpln	Capsella rubella	AT1G21326.1 | Symbols: | VQ motif-containing protein | chr1:7469002-7469721 REVERSE LENGTH=239	204	239	8.00E-37	117.2	57.8	70.1
Rsa1.0_00067.1.g3609.t1	ref|NP_001154354.1| nucleic acid/nucleotide binding protein [Arabidopsis thaliana] gi|332191964|gb|AEE30085.1| nucleic acid/nucleotide binding protein [Arabidopsis thaliana]	230	253	4.00E-80	110.0	73.5	82.2	nucleic acid/nucleotide binding protein	gbpln	Arabidopsis thaliana	AT1G21320.2 | Symbols: | nucleotide binding;nucleic acid binding | chr1:7462834-7466164 REVERSE LENGTH=253	230	253	1.00E-82	110.0	73.5	82.2
Rsa1.0_00067.1.g3610.t1	ref|NP_173553.1| extensin 3 [Arabidopsis thaliana] gi|334302912|sp|Q9FS16.3|EXTN3_ARATH RecName: Full=Extensin-3; Short=AtExt3; Short=AtExt5; Flags: Precursor gi|8920638|gb|AAF81360.1|AC036104_9 Contains similarity to Extensin (atExt1) from Arabidopsis thaliana gb|U43627 and contains 12 concatamers of 28 amino acids rich in proline. ESTs gb|AA597816, gb|AA712635, gb|N65860, gb|AA598180, gb|H77085, gb|AA394416, gb|AA394413, gb|AA650774, gb|AA650748, gb|Z25975, gb|AA597958, gb|AA597955 come from this gene [Arabidopsis thaliana] gi|332191962|gb|AEE30083.1| extensin 3 [Arabidopsis thaliana]	449	431	1.00E-98	96.0	94.4	94.9	extensin 3	gbpln	Arabidopsis thaliana	AT1G21310.1 | Symbols: ATEXT3, RSH, EXT3 | extensin 3 | chr1:7453693-7454988 REVERSE LENGTH=431	449	431	1.00E-101	96.0	94.4	94.9

Rsa1.0_00067.1.g3611.t1	ref|NP_173550.1| uncharacterized protein [Arabidopsis thaliana] gi|28393025|gb|AAO41947.1| unknown protein [Arabidopsis thaliana] gi|28827240|gb|AAO50464.1| unknown protein [Arabidopsis thaliana] gi|55740501|gb|AAV63843.1| hypothetical protein At1g21280 [Arabidopsis thaliana] gi|332191960|gb|AEE30081.1| uncharacterized protein AT1G21280 [Arabidopsis thaliana]	170	237	4.00E-32	139.4	50.6	64.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	170	237	2.00E-34	139.4	50.6	64.7
Rsa1.0_00067.1.g3612.t1	ref|NP_173546.1| wall-associated receptor kinase 5 [Arabidopsis thaliana] gi|75174802|sp|Q9LMN7.1|WAK5_ARATH RecName: Full=Wall-associated receptor kinase 5; Flags: Precursor gi|8920637|gb|AAF81359.1|AC036104_8 Strong similarity to wall-associated kinase 1 from Arabidopsis thaliana gb|AJ009696 and contains Eukaryotic protein kinase PF|00069 and EGF-like PF|00008 domains [Arabidopsis thaliana] gi|332191955|gb|AEE30076.1| wall-associated receptor kinase 5 [Arabidopsis thaliana]	737	733	0	99.5	70.7	81.3	wall-associated receptor kinase 5	gbpln	Arabidopsis thaliana	AT1G21230.1 | Symbols: WAK5 | wall associated kinase 5 | chr1:7429980-7432346 FORWARD LENGTH=733	737	733	0	99.5	70.7	81.3
Rsa1.0_00067.1.g3613.t1	gb|EOA39743.1| hypothetical protein CARUB_v10008400mg [Capsella rubella]	738	740	0	100.3	72.1	82.4	hypothetical protein CARUB_v10008400mg	gbpln	Capsella rubella	AT1G21270.1 | Symbols: WAK2 | wall-associated kinase 2 | chr1:7444997-7447345 FORWARD LENGTH=732	738	732	0	99.2	69.5	80.4
Rsa1.0_00067.1.g3614.t1	gb|EOA39743.1| hypothetical protein CARUB_v10008400mg [Capsella rubella]	690	740	0	107.2	73.6	83.3	hypothetical protein CARUB_v10008400mg	gbpln	Capsella rubella	AT1G21230.1 | Symbols: WAK5 | wall associated kinase 5 | chr1:7429980-7432346 FORWARD LENGTH=733	690	733	0	106.2	70.1	81.6
Rsa1.0_00067.1.g3615.t1	gb|EOA39743.1| hypothetical protein CARUB_v10008400mg [Capsella rubella]	737	740	0	100.4	72.5	82.8	hypothetical protein CARUB_v10008400mg	gbpln	Capsella rubella	AT1G21270.1 | Symbols: WAK2 | wall-associated kinase 2 | chr1:7444997-7447345 FORWARD LENGTH=732	737	732	0	99.3	70.1	80.7
Rsa1.0_00067.1.g3616.t2	gb|EOA39743.1| hypothetical protein CARUB_v10008400mg [Capsella rubella]	717	740	0	103.2	80.6	90.2	hypothetical protein CARUB_v10008400mg	gbpln	Capsella rubella	AT1G21270.1 | Symbols: WAK2 | wall-associated kinase 2 | chr1:7444997-7447345 FORWARD LENGTH=732	717	732	0	102.1	72.2	82.4
Rsa1.0_00067.1.g3617.t1	gb|EOA40426.1| hypothetical protein CARUB_v10009151mg [Capsella rubella] gi|482576240|gb|EOA40427.1| hypothetical protein CARUB_v10009151mg [Capsella rubella]	416	442	0	106.3	84.6	91.3	hypothetical protein CARUB_v10009151mg	gbpln	Capsella rubella	AT1G21200.1 | Symbols: | sequence-specific DNA binding transcription factors | chr1:7421483-7422814 FORWARD LENGTH=443	416	443	1.00E-180	106.5	82.9	90.4
Rsa1.0_00067.1.g3618.t1	ref|XP_002893156.1| hypothetical protein ARALYDRAFT_472357 [Arabidopsis lyrata subsp. lyrata] gi|297338998|gb|EFH69415.1| hypothetical protein ARALYDRAFT_472357 [Arabidopsis lyrata subsp. lyrata]	292	98	8.00E-32	33.6	24.3	24.3	hypothetical protein ARALYDRAFT_472357	gbpln	Arabidopsis lyrata	AT1G21190.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:7419989-7420856 REVERSE LENGTH=97	292	97	3.00E-34	33.2	24.0	24.3
Rsa1.0_00067.1.g3619.t1	ref|NP_189952.1| vacuolar iron transporter-like protein [Arabidopsis thaliana] gi|75182792|sp|Q9M2C0.1|VITH4_ARATH RecName: Full=Vacuolar iron transporter homolog 4; AltName: Full=Protein NODULIN-LIKE 4 gi|7362791|emb|CAB83067.1| nodulin-like protein [Arabidopsis thaliana] gi|34365643|gb|AAQ65133.1| At3g43660 [Arabidopsis thaliana] gi|51970300|dbj|BAD43842.1| nodulin -like protein [Arabidopsis thaliana] gi|332644295|gb|AEE77816.1| vacuolar iron transporter homolog 4 [Arabidopsis thaliana]	201	198	3.00E-92	98.5	83.1	91.0	vacuolar iron transporter-like protein	gbpln	Arabidopsis thaliana	AT3G43660.1 | Symbols: | Vacuolar iron transporter (VIT) family protein | chr3:15565332-15565928 FORWARD LENGTH=198	201	198	1.00E-94	98.5	83.1	91.0
Rsa1.0_00067.1.g3620.t1	gb|AAM67269.1| O-methyltransferase, putative [Arabidopsis thaliana]	345	373	1.00E-173	108.1	91.6	95.7	O-methyltransferase, putative	gbpln	Arabidopsis thaliana	AT1G21130.1 | Symbols: | O-methyltransferase family protein | chr1:7399170-7400470 REVERSE LENGTH=373	345	373	1.00E-175	108.1	91.3	95.1

Rsa1.0_00067.1.g3621.t1	ref|NP_173537.1| O-methyltransferase-like protein [Arabidopsis thaliana] gi|8886988|gb|AAF80648.1|AC012190_4 Contains similarity to caffeic acid 3-O-Methyltransferase from Saccharum officinarum gb|AJ231133. It is a member of O-methyltransferase family. ESTs gb|AI994592 and gb|T20793 come from this gene [Arabidopsis thaliana] gi|332191946|gb|AEE30067.1| O-methyltransferase-like protein [Arabidopsis thaliana]	373	373	0	100.0	93.6	96.5	O-methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT1G21130.1 | Symbols: | O-methyltransferase family protein | chr1:7399170-7400470 REVERSE LENGTH=373	373	373	0	100.0	93.6	96.5
Rsa1.0_00067.1.g3622.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00067.1.g3623.t1	ref|NP_173537.1| O-methyltransferase-like protein [Arabidopsis thaliana] gi|8886988|gb|AAF80648.1|AC012190_4 Contains similarity to caffeic acid 3-O-Methyltransferase from Saccharum officinarum gb|AJ231133. It is a member of O-methyltransferase family. ESTs gb|AI994592 and gb|T20793 come from this gene [Arabidopsis thaliana] gi|332191946|gb|AEE30067.1| O-methyltransferase-like protein [Arabidopsis thaliana]	369	373	0	101.1	91.9	95.9	O-methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT1G21130.1 | Symbols: | O-methyltransferase family protein | chr1:7399170-7400470 REVERSE LENGTH=373	369	373	0	101.1	91.9	95.9
Rsa1.0_00067.1.g3624.t1	ref|NP_173537.1| O-methyltransferase-like protein [Arabidopsis thaliana] gi|8886988|gb|AAF80648.1|AC012190_4 Contains similarity to caffeic acid 3-O-Methyltransferase from Saccharum officinarum gb|AJ231133. It is a member of O-methyltransferase family. ESTs gb|AI994592 and gb|T20793 come from this gene [Arabidopsis thaliana] gi|332191946|gb|AEE30067.1| O-methyltransferase-like protein [Arabidopsis thaliana]	372	373	0	100.3	91.9	94.6	O-methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT1G21130.1 | Symbols: | O-methyltransferase family protein | chr1:7399170-7400470 REVERSE LENGTH=373	372	373	0	100.3	91.9	94.6
Rsa1.0_00067.1.g3625.t1	ref|NP_564135.1| cupredoxin-like protein [Arabidopsis thaliana] gi|111074298|gb|ABH04522.1| At1g21090 [Arabidopsis thaliana] gi|332191942|gb|AEE30063.1| cupredoxin-like protein [Arabidopsis thaliana]	243	242	1.00E-109	99.6	85.2	88.9	cupredoxin-like protein	gbpln	Arabidopsis thaliana	AT1G21090.1 | Symbols: | Cupredoxin superfamily protein | chr1:7384854-7386199 FORWARD LENGTH=242	243	242	1.00E-111	99.6	85.2	88.9
Rsa1.0_00067.1.g3626.t1	gb|AAW50121.1| DnaJ-like protein [Brassica juncea]	368	390	1.00E-178	106.0	86.4	90.2	DnaJ-like protein	gbpln	Brassica juncea	AT1G21080.3 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr1:7378822-7382275 REVERSE LENGTH=400	368	400	1.00E-177	108.7	83.7	87.0
Rsa1.0_00067.1.g3627.t1	ref|XP_002890424.1| hypothetical protein ARALYDRAFT_472343 [Arabidopsis lyrata subsp. lyrata] gi|297336266|gb|EFH66683.1| hypothetical protein ARALYDRAFT_472343 [Arabidopsis lyrata subsp. lyrata]	726	505	0	69.6	51.8	57.3	hypothetical protein ARALYDRAFT_472343	gbpln	Arabidopsis lyrata	AT1G21060.1 | Symbols: | Protein of unknown function, DUF547 | chr1:7371799-7374085 FORWARD LENGTH=505	726	505	0	69.6	51.2	57.0
Rsa1.0_00067.1.g3628.t1	ref|XP_002890423.1| hypothetical protein ARALYDRAFT_889559 [Arabidopsis lyrata subsp. lyrata] gi|297336265|gb|EFH66682.1| hypothetical protein ARALYDRAFT_889559 [Arabidopsis lyrata subsp. lyrata]	249	244	1.00E-104	98.0	86.7	89.2	hypothetical protein ARALYDRAFT_889559	gbpln	Arabidopsis lyrata	AT1G21050.1 | Symbols: | Protein of unknown function, DUF617 | chr1:7366859-7367596 FORWARD LENGTH=245	249	245	1.00E-104	98.4	83.5	89.2
Rsa1.0_00067.1.g3629.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00068.1.g3630.t3	ref|NP_178398.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546779|sp|Q8LK93.2|PP145_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g02980 gi|3461822|gb|AAC32916.1| hypothetical protein [Arabidopsis thaliana] gi|330250557|gb|AEC05651.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	362	603	1.00E-108	166.6	51.1	55.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G02980.1 | Symbols: OTP85 | Pentatricopeptide repeat (PPR) superfamily protein | chr2:868468-870279 FORWARD LENGTH=603	362	603	1.00E-110	166.6	51.1	55.8
Rsa1.0_00068.1.g3631.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00068.1.g3632.t1	gb|EOA25480.1| hypothetical protein CARUB_v10018819mg [Capsella rubella]	101	191	2.00E-35	189.1	81.2	91.1	hypothetical protein CARUB_v10018819mg	gbpln	Capsella rubella	AT2G01580.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G07510.2); Has 129 Blast hits to 129 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 129; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:265181-265756 REVERSE LENGTH=191	101	191	5.00E-34	189.1	72.3	79.2
Rsa1.0_00068.1.g3633.t1	ref|NP_973517.1| serine carboxypeptidase-like 9 [Arabidopsis thaliana] gi|330252302|gb|AEC07396.1| serine carboxypeptidase-like 9 [Arabidopsis thaliana]	163	437	5.00E-67	268.1	75.5	87.1	serine carboxypeptidase-like 9	gbpln	Arabidopsis thaliana	AT2G23010.2 | Symbols: SCPL9 | serine carboxypeptidase-like 9 | chr2:9798843-9802485 FORWARD LENGTH=437	163	437	2.00E-69	268.1	75.5	87.1
Rsa1.0_00068.1.g3634.t5	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00068.1.g3635.t1	ref|NP_179884.1| serine carboxypeptidase-like 9 [Arabidopsis thaliana] gi|75099209|sp|O64811.1|SCP9_ARATH RecName: Full=Serine carboxypeptidase-like 9; AltName: Full=Sinapoylglucose--sinapoylglucose O-sinapoyltransferase; Short=SST; AltName: Full=Sinapoylglucose--sinapoylglucose acyltransferase; Flags: Precursor gi|3169175|gb|AAC17818.1| putative serine carboxypeptidase I [Arabidopsis thaliana] gi|330252303|gb|AEC07397.1| serine carboxypeptidase-like 9 [Arabidopsis thaliana]	158	437	5.00E-47	276.6	55.1	59.5	serine carboxypeptidase-like 9	gbpln	Arabidopsis thaliana	AT2G23010.1 | Symbols: SCPL9 | serine carboxypeptidase-like 9 | chr2:9798843-9802485 FORWARD LENGTH=437	158	437	2.00E-49	276.6	55.1	59.5
Rsa1.0_00068.1.g3636.t1	ref|XP_002875182.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297321020|gb|EFH51441.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	607	605	0	99.7	82.9	89.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT2G02980.1 | Symbols: OTP85 | Pentatricopeptide repeat (PPR) superfamily protein | chr2:868468-870279 FORWARD LENGTH=603	607	603	0	99.3	80.4	89.1
Rsa1.0_00068.1.g3637.t1	gb|AFI98882.1| phytochrome kinase substrate [Brassica juncea var. tumida]	434	376	1.00E-171	86.6	74.2	76.5	phytochrome kinase substrate	gbpln	Brassica juncea	AT2G02950.1 | Symbols: PKS1 | phytochrome kinase substrate 1 | chr2:855149-856468 REVERSE LENGTH=439	434	439	1.00E-150	101.2	70.7	80.6
Rsa1.0_00068.1.g3638.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1320	1307	0	99.0	60.2	75.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1320	1262	2.00E-91	95.6	13.0	19.9
Rsa1.0_00068.1.g3639.t1	ref|XP_002876849.1| hypothetical protein ARALYDRAFT_484201 [Arabidopsis lyrata subsp. lyrata] gi|297322687|gb|EFH53108.1| hypothetical protein ARALYDRAFT_484201 [Arabidopsis lyrata subsp. lyrata]	472	468	0	99.2	88.1	94.1	hypothetical protein ARALYDRAFT_484201	gbpln	Arabidopsis lyrata	AT2G02910.1 | Symbols: | Protein of unknown function (DUF616) | chr2:847335-849371 REVERSE LENGTH=460	472	460	0	97.5	85.8	91.3
Rsa1.0_00068.1.g3640.t1	gb|EOA24405.1| hypothetical protein CARUB_v10017655mg, partial [Capsella rubella]	344	321	1.00E-128	93.3	71.8	78.5	hypothetical protein CARUB_v10017655mg, partial	gbpln	Capsella rubella	AT2G02880.1 | Symbols: | mucin-related | chr2:841303-843151 FORWARD LENGTH=314	344	314	1.00E-126	91.3	71.8	77.3

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<tr><td>Rsa1.0_00068.1.g3642.t2</td><td>ref|NP_178389.1| sucrose transport protein SUC3 [Arabidopsis thaliana] gi|75223209|sp|O80605.1|SUC3_ARATH RecName: Full=Sucrose transport protein SUC3; AltName: Full=Sucrose permease 3; AltName: Full=Sucrose transporter 2; AltName: Full=Sucrose-proton symporter 3 gi|3461813|gb|AAC32907.1| putative sucrose/H+ symporter [Arabidopsis thaliana] gi|8052190|emb|CAB92307.1| sucrose transporter [Arabidopsis thaliana] gi|110742223|dbj|BAE99038.1| Sucrose transporter [Arabidopsis thaliana] gi|330250541|gb|AEC05635.1| sucrose transport protein SUC3 [Arabidopsis thaliana]</td><td>592</td><td>594</td><td>0</td><td>100.3</td><td>87.0</td><td>91.6</td><td>sucrose transport protein SUC3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G02860.1 | Symbols: SUT2, ATSUC3, SUC3, ATSUT2 | sucrose transporter 2 | chr2:828546-832296 REVERSE LENGTH=594</td><td>592</td><td>594</td><td>0</td><td>100.3</td><td>87.0</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00068.1.g3643.t1</td><td>ref|XP_002876842.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322680|gb|EFH53101.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>129</td><td>129</td><td>1.00E-58</td><td>100.0</td><td>82.9</td><td>91.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G02850.1 | Symbols: ARPN | plantacyanin | chr2:826630-827720 REVERSE LENGTH=129</td><td>129</td><td>129</td><td>5.00E-60</td><td>100.0</td><td>81.4</td><td>88.4</td></tr>
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<tr><td>Rsa1.0_00068.1.g3645.t1</td><td>gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]</td><td>312</td><td>657</td><td>3.00E-17</td><td>210.6</td><td>19.6</td><td>28.8</td><td>T14P8.10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>312</td><td>626</td><td>7.00E-13</td><td>200.6</td><td>13.1</td><td>20.8</td></tr>
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<tr><td>Rsa1.0_00068.1.g3647.t1</td><td>gb|EOA23904.1| hypothetical protein CARUB_v10017119mg [Capsella rubella]</td><td>465</td><td>483</td><td>0</td><td>103.9</td><td>77.8</td><td>86.2</td><td>hypothetical protein CARUB_v10017119mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G02820.2 | Symbols: MYB88 | myb domain protein 88 | chr2:804716-807139 REVERSE LENGTH=484</td><td>465</td><td>484</td><td>0</td><td>104.1</td><td>80.0</td><td>88.4</td></tr>
<tr><td>Rsa1.0_00068.1.g3648.t1</td><td>gb|EOA24258.1| hypothetical protein CARUB_v10017499mg [Capsella rubella]</td><td>332</td><td>363</td><td>1.00E-180</td><td>109.3</td><td>95.2</td><td>97.9</td><td>hypothetical protein CARUB_v10017499mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G02810.1 | Symbols: ATUTR1, UTR1 | UDP-galactose transporter 1 | chr2:801643-803289 FORWARD LENGTH=332</td><td>332</td><td>332</td><td>0</td><td>100.0</td><td>94.3</td><td>97.9</td></tr>
<tr><td>Rsa1.0_00068.1.g3649.t1</td><td>ref|XP_002876829.1| hypothetical protein ARALYDRAFT_484186 [Arabidopsis lyrata subsp. lyrata] gi|297322667|gb|EFH53088.1| hypothetical protein ARALYDRAFT_484186 [Arabidopsis lyrata subsp. lyrata]</td><td>472</td><td>426</td><td>0</td><td>90.3</td><td>86.0</td><td>88.1</td><td>hypothetical protein ARALYDRAFT_484186</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G02800.2 | Symbols: APK2B | protein kinase 2B | chr2:796889-799250 REVERSE LENGTH=426</td><td>472</td><td>426</td><td>0</td><td>90.3</td><td>85.4</td><td>88.1</td></tr>
<tr><td>Rsa1.0_00068.1.g3650.t1</td><td>gb|EOA23708.1| hypothetical protein CARUB_v10016916mg [Capsella rubella]</td><td>565</td><td>584</td><td>0</td><td>103.4</td><td>77.2</td><td>87.1</td><td>hypothetical protein CARUB_v10016916mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G02790.1 | Symbols: IQD29 | IQ-domain 29 | chr2:788708-790946 FORWARD LENGTH=636</td><td>565</td><td>636</td><td>0</td><td>112.6</td><td>76.5</td><td>86.0</td></tr>
<tr><td>Rsa1.0_00068.1.g3651.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00068.1.g3652.t1</td><td>ref|NP_196645.2| endomembrane family protein 70 [Arabidopsis thaliana] gi|332004219|gb|AED91602.1| endomembrane family protein 70 [Arabidopsis thaliana]</td><td>606</td><td>648</td><td>0</td><td>106.9</td><td>93.4</td><td>96.7</td><td>endomembrane family protein 70</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G10840.1 | Symbols: | Endomembrane protein 70 protein family | chr5:3424910-3427797 REVERSE LENGTH=648</td><td>606</td><td>648</td><td>0</td><td>106.9</td><td>93.4</td><td>96.7</td></tr>
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Rsa1.0_00068.1.g3653.t1	ref|NP_565289.1| ubiquitin-conjugating enzyme E2 A [Arabidopsis thaliana] gi|297814522|ref|XP_002875144.1| ubiquiting-conjugating enzyme 2 [Arabidopsis lyrata subsp. lyrata] gi|1174844|sp|P42745.1|UBC2_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 2; AltName: Full=Ubiquitin carrier protein 2; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 2; AltName: Full=Ubiquitin-protein ligase 2 gi|13899127|gb|AAK48985.1|AF370558_1 putative ubiquitin-conjugating enzyme E2 [Arabidopsis thaliana] gi|431264|gb|AAA32899.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|2689243|emb|CAA73476.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|2947065|gb|AAC05346.1| E2, ubiquitin-conjugating enzyme 2 (UBC2) [Arabidopsis thaliana] gi|18377456|gb|AAL66894.1| putative ubiquitin-conjugating enzyme E2 [Arabidopsis thaliana] gi|66354400|gb|AAY44843.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|118197458|gb|ABK78692.1| ubiquitin conjugating enzyme [Brassica rapa] gi|297320982|gb|EFH51403.1| ubiquiting-conjugating enzyme 2 [Arabidopsis lyrata subsp. lyrata] gi|312281529|dbj|BAJ33630.1| unnamed	152	152	3.00E-84	100.0	99.3	100.0	ubiquitin-conjugating enzyme E2 A	gbpln	Arabidopsis lyrata	AT2G02760.1 | Symbols: ATUBC2, UBC2 | ubiquiting-conjugating enzyme 2 | chr2:774271-775149 FORWARD LENGTH=152	152	152	1.00E-86	100.0	99.3	100.0
Rsa1.0_00068.1.g3654.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00068.1.g3655.t1	ref|NP_178375.1| putative pectate lyase 6 [Arabidopsis thaliana] gi|32129832|sp|O64510.1|PEL6_ARATH RecName: Full=Probable pectate lyase 6; Flags: Precursor gi|2947069|gb|AAC05350.1| putative pectate lyase [Arabidopsis thaliana] gi|28973690|gb|AAO64162.1| putative pectate lyase [Arabidopsis thaliana] gi|54606856|gb|AAV34776.1| At2g02720 [Arabidopsis thaliana] gi|330250521|gb|AEC05615.1| putative pectate lyase 6 [Arabidopsis thaliana]	457	455	0	99.6	83.8	90.6	putative pectate lyase 6	gbpln	Arabidopsis thaliana	AT2G02720.1 | Symbols: | Pectate lyase family protein | chr2:763173-764834 FORWARD LENGTH=455	457	455	0	99.6	83.8	90.6
Rsa1.0_00068.1.g3656.t1	ref|NP_564190.1| polyketide cyclase/dehydrase and lipid transport-like protein [Arabidopsis thaliana] gi|2829899|gb|AAC00607.1| similar to ripening-induced protein, gp|AJ001449|2465015 and major#latex protein, gp|X91961|1107495 [Arabidopsis thaliana] gi|14517378|gb|AAK62580.1| At1g23130/T26J12_10 [Arabidopsis thaliana] gi|15450533|gb|AAK96444.1| At1g23130/T26J12_10 [Arabidopsis thaliana] gi|332192222|gb|AEE30343.1| polyketide cyclase/dehydrase and lipid transport-like protein [Arabidopsis thaliana]	161	160	4.00E-58	99.4	67.1	83.2	polyketide cyclase/dehydrase and lipid transport-like protein	gbpln	Arabidopsis thaliana	AT1G23130.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:8200434-8200997 FORWARD LENGTH=160	161	160	1.00E-60	99.4	67.1	83.2
Rsa1.0_00069.1.g3657.t3	ref|NP_563620.1| L-fucokinase/GDP-L-fucose pyrophosphorylase [Arabidopsis thaliana] gi|332313388|sp|Q9LNJ9.2|FKGP_ARATH RecName: Full=Bifunctional fucokinase/fucose pyrophosphorylase; Short=AtFKGP; Includes: RecName: Full=L-fucokinase; Includes: RecName: Full=Fucose-1-phosphate guanylyltransferase; AltName: Full=GDP-fucose pyrophosphorylase gi|332189134|gb|AEE27255.1| L-fucokinase/GDP-L-fucose pyrophosphorylase [Arabidopsis thaliana]	1369	1055	0	77.1	70.5	73.3	L-fucokinase/GDP-L-fucose pyrophosphorylase	gbpln	Arabidopsis thaliana	AT1G01220.1 | Symbols: FKGP, AtFKGP | L-fucokinase/GDP-L-fucose pyrophosphorylase | chr1:91750-95552 FORWARD LENGTH=1055	1369	1055	0	77.1	70.5	73.3
Rsa1.0_00069.1.g3658.t1	ref|XP_002892079.1| ORMDL family protein [Arabidopsis lyrata subsp. lyrata] gi|297337921|gb|EFH68338.1| ORMDL family protein [Arabidopsis lyrata subsp. lyrata]	157	157	7.00E-80	100.0	88.5	94.9	ORMDL family protein	gbpln	Arabidopsis lyrata	AT1G01230.1 | Symbols: | ORMDL family protein | chr1:97620-99046 FORWARD LENGTH=157	157	157	5.00E-82	100.0	87.9	94.9

Rsa1.0_00069.1.g3659.t1	ref|XP_002892078.1| hypothetical protein ARALYDRAFT_470152 [Arabidopsis lyrata subsp. lyrata] gi|297337920|gb|EFH68337.1| hypothetical protein ARALYDRAFT_470152 [Arabidopsis lyrata subsp. lyrata]	345	334	1.00E-127	96.8	76.8	85.8	hypothetical protein ARALYDRAFT_470152	gbpln	Arabidopsis lyrata	AT1G01240.3 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G46550.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:100683-101678 FORWARD LENGTH=331	345	331	1.00E-129	95.9	77.7	85.8
Rsa1.0_00069.1.g3660.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00069.1.g3661.t1	ref|NP_188299.1| ethylene-responsive transcription factor RAP2-3 [Arabidopsis thaliana] gi|27735162|sp|P42736.2|RAP23_ARATH RecName: Full=Ethylene-responsive transcription factor RAP2-3; AltName: Full=Cadmium-induced protein AS30; AltName: Full=Ethylene response factor 72; Short=ERF72; AltName: Full=Ethylene-responsive element binding protein; Short=AtEBP; AltName: Full=Protein RELATED TO APETALA2 3; Short=Related to AP2 3 gi|2281631|gb|AAC49769.1| AP2 domain containing protein RAP2.3 [Arabidopsis thaliana] gi|11994632|dbj|BAB02769.1| AP2 domain transcription factor RAP2.3 [Arabidopsis thaliana] gi|14334854|gb|AAK59605.1| putative AP2 domain containing protein RAP2.3 [Arabidopsis thaliana] gi|16649095|gb|AAL24399.1| AP2 domain transcription factor RAP2.3 [Arabidopsis thaliana] gi|21593082|gb|AAM65031.1| AP2 domain containing protein RAP2.3 [Arabidopsis thaliana] gi|23296611|gb|AAN13131.1| putative AP2 domain containing protein RAP2.3 [Arabidopsis thaliana] gi|332642342|gb|AEE75863.1| ethylene-responsive transcription factor RAP2-3 [Arabidopsis thaliana]	155	248	7.00E-28	160.0	49.7	51.6	ethylene-responsive transcription factor RAP2-3	gbpln	Arabidopsis thaliana	AT3G16770.1 | Symbols: RAP2.3, ATEBP, ERF72, EBP | ethylene-responsive element binding protein | chr3:5705784-5706768 FORWARD LENGTH=248	155	248	2.00E-30	160.0	49.7	51.6
Rsa1.0_00069.1.g3662.t1	dbj|BAJ34192.1| unnamed protein product [Thellungiella halophila]	184	197	6.00E-81	107.1	89.1	94.6	unnamed protein product	----	----	AT1G01250.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:104731-105309 REVERSE LENGTH=192	184	192	6.00E-80	104.3	86.4	90.8
Rsa1.0_00069.1.g3663.t1	gb|EOA38419.1| hypothetical protein CARUB_v10009994mg, partial [Capsella rubella] gi|482574233|gb|EOA38420.1| hypothetical protein CARUB_v10009994mg, partial [Capsella rubella] gi|482574234|gb|EOA38421.1| hypothetical protein CARUB_v10009994mg, partial [Capsella rubella]	238	273	1.00E-109	114.7	86.1	93.7	hypothetical protein CARUB_v10009994mg, partial	gbpln	Capsella rubella	AT1G01290.2 | Symbols: CNX3 | cofactor of nitrate reductase and xanthine dehydrogenase 3 | chr1:114299-115296 FORWARD LENGTH=270	238	270	1.00E-108	113.4	84.5	90.8
Rsa1.0_00069.1.g3664.t1	ref|XP_002892072.1| hypothetical protein ARALYDRAFT_470143 [Arabidopsis lyrata subsp. lyrata] gi|297337914|gb|EFH68331.1| hypothetical protein ARALYDRAFT_470143 [Arabidopsis lyrata subsp. lyrata]	240	241	3.00E-93	100.4	74.2	80.8	hypothetical protein ARALYDRAFT_470143	gbpln	Arabidopsis lyrata	AT1G01310.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr1:120221-120946 FORWARD LENGTH=241	240	241	8.00E-91	100.4	72.9	79.6
Rsa1.0_00069.1.g3665.t1	gb|EOA38162.1| hypothetical protein CARUB_v10009639mg [Capsella rubella]	327	342	1.00E-166	104.6	89.3	94.8	hypothetical protein CARUB_v10009639mg	gbpln	Capsella rubella	AT1G01350.1 | Symbols: | Zinc finger (CCCH-type/C3HC4-type RING finger) family protein | chr1:136732-137970 FORWARD LENGTH=343	327	343	1.00E-159	104.9	88.1	93.3
Rsa1.0_00069.1.g3666.t1	dbj|BAF49733.1| centromeric histone H3-like protein_1 [Raphanus sativus]	178	178	7.00E-98	100.0	100.0	100.0	centromeric histone H3-like protein_1	gbpln	Raphanus sativus	AT1G01370.2 | Symbols: HTR12, CENH3 | Histone superfamily protein | chr1:143773-145400 FORWARD LENGTH=178	178	178	2.00E-65	100.0	70.2	83.7
Rsa1.0_00069.1.g3667.t1	gb|EOA38963.1| hypothetical protein CARUB_v10011382mg [Capsella rubella]	79	85	6.00E-30	107.6	79.7	86.1	hypothetical protein CARUB_v10011382mg	gbpln	Capsella rubella	AT4G01060.1 | Symbols: ETC3, CPL3 | CAPRICE-like MYB3 | chr4:460534-460967 FORWARD LENGTH=77	79	77	2.00E-26	97.5	72.2	84.8
Rsa1.0_00069.1.g3668.t1	ref|XP_002889366.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335208|gb|EFH65625.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	689	970	0	140.8	83.3	91.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G01450.1 | Symbols: | Protein kinase superfamily protein | chr1:164105-165517 REVERSE LENGTH=470	689	470	0	68.2	52.2	57.2

Rsa1.0_00069.1.g3669.t1	gb|AAF81309.1|AC061957_5 Contains a weak similarity to a farnesylated protein GMFP5 mRNA from Glycine max gb|U64916. ESTs gb|AI993148, gb|T44360 come from this gene [Arabidopsis thaliana]	162	203	2.00E−32	125.3	83.3	85.2	Contains a weak similarity to a farnesylated protein GMFP5 mRNA from Glycine max gb|U64916. ESTs gb|AI993148, gb|T44360 come from this gene	gbpln	Arabidopsis thaliana	AT1G01490.2 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:180401−182066 REVERSE LENGTH=177	162	177	3.00E−34	109.3	83.3	85.2
Rsa1.0_00069.1.g3670.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00069.1.g3671.t1	ref|XP_002892061.1| hypothetical protein ARALYDRAFT_311286 [Arabidopsis lyrata subsp. lyrata] gi|297337903|gb|EFH68320.1| hypothetical protein ARALYDRAFT_311286 [Arabidopsis lyrata subsp. lyrata]	315	1248	1.00E−136	396.2	79.4	83.8	hypothetical protein ARALYDRAFT_311286	gbpln	Arabidopsis lyrata	AT1G01500.1 | Symbols: | Erythronate−4−phosphate dehydrogenase family protein | chr1:185260−186573 FORWARD LENGTH=327	315	327	1.00E−134	103.8	78.1	83.2
Rsa1.0_00069.1.g3672.t1	ref|NP_563629.1| Rossmann−fold NAD(P)−binding domain−containing protein [Arabidopsis thaliana] gi|75274951|sp|O23702.1|CTBP_ARATH RecName: Full=C−terminal binding protein AN; Short=CtBP; AltName: Full=Protein ANGUSTIFOLIA gi|2505877|emb|CAA73306.1| dehydrogenase [Arabidopsis thaliana] gi|332189177|gb|AEE27298.1| C−terminal binding protein AN [Arabidopsis thaliana]	628	636	0	101.3	90.6	94.1	Rossmann−fold NAD(P)−binding domain−containing protein	gbpln	Arabidopsis thaliana	AT1G01510.1 | Symbols: AN | NAD(P)−binding Rossmann−fold superfamily protein | chr1:187235−189836 FORWARD LENGTH=636	628	636	0	101.3	90.6	94.1
Rsa1.0_00069.1.g3673.t1	ref|XP_002892058.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297337900|gb|EFH68317.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	397	472	0	118.9	93.7	95.7	kinase family protein	gbpln	Arabidopsis lyrata	AT1G01540.2 | Symbols: | Protein kinase superfamily protein | chr1:195980−198383 FORWARD LENGTH=472	397	472	0	118.9	93.5	95.5
Rsa1.0_00069.1.g3674.t1	gb|EOA38922.1| hypothetical protein CARUB_v10011320mg [Capsella rubella]	111	568	4.00E−37	511.7	73.9	79.3	hypothetical protein CARUB_v10011320mg	gbpln	Capsella rubella	AT1G04890.1 | Symbols: | Protein of unknown function, DUF593 | chr1:1381116−1382546 REVERSE LENGTH=411	111	411	2.00E−36	370.3	75.7	82.0
Rsa1.0_00069.1.g3675.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	682	657	0	96.3	49.9	64.1	T14P8.10	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr4:2353989−2355213 REVERSE LENGTH=332	682	332	1.00E−56	48.7	15.5	22.3
Rsa1.0_00069.1.g3676.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	813	1161	3.00E−99	142.8	22.1	30.9	F14N23.4	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I−like superfamily protein | chr1:16528880−16531065 REVERSE LENGTH=626	813	626	1.00E−74	77.0	19.2	28.3
Rsa1.0_00069.1.g3677.t1	ref|XP_002892053.1| hypothetical protein ARALYDRAFT_470119 [Arabidopsis lyrata subsp. lyrata] gi|297337895|gb|EFH68312.1| hypothetical protein ARALYDRAFT_470119 [Arabidopsis lyrata subsp. lyrata]	707	725	0	102.5	85.4	92.1	hypothetical protein ARALYDRAFT_470119	gbpln	Arabidopsis lyrata	AT1G01580.1 | Symbols: FRO2, FRD1, ATFRO2 | ferric reduction oxidase 2 | chr1:209395−212810 FORWARD LENGTH=725	707	725	0	102.5	84.3	91.1
Rsa1.0_00069.1.g3678.t2	gb|AFH02721.1| sn−glycerol−3−phosphate acyltransferase 4 isoform C1, partial [Brassica napus] gi|383289233|gb|AFH02724.1| sn−glycerol−3−phosphate acyltransferase 4 isoform C1, partial [Brassica napus]	298	505	1.00E−158	169.5	96.3	97.0	sn−glycerol−3−phosphate acyltransferase 4 isoform C1, partial	gbpln	Brassica napus	AT4G00400.1 | Symbols: GPAT8, AtGPAT8 | glycerol−3−phosphate acyltransferase 8 | chr4:174312−176734 REVERSE LENGTH=500	298	500	1.00E−157	167.8	89.6	92.3
Rsa1.0_00069.1.g3679.t1	dbj|BAJ34288.1| unnamed protein product [Thellungiella halophila]	286	286	1.00E−160	100.0	96.5	99.7	unnamed protein product	−−−−	−−−−	AT4G00430.1 | Symbols: TMP−C, PIP1;4, PIP1E | plasma membrane intrinsic protein 1;4 | chr4:186143−187531 REVERSE LENGTH=287	286	287	1.00E−160	100.3	96.2	99.3
Rsa1.0_00069.1.g3680.t1	ref|XP_002892050.1| hypothetical protein ARALYDRAFT_470113 [Arabidopsis lyrata subsp. lyrata] gi|297337892|gb|EFH68309.1| hypothetical protein ARALYDRAFT_470113 [Arabidopsis lyrata subsp. lyrata]	268	256	1.00E−123	95.5	76.5	84.7	hypothetical protein ARALYDRAFT_470113	gbpln	Arabidopsis lyrata	AT1G01630.1 | Symbols: | Sec14p−like phosphatidylinositol transfer family protein | chr1:229206−230675 FORWARD LENGTH=255	268	255	1.00E−125	95.1	76.1	84.3
Rsa1.0_00069.1.g3681.t1	ref|XP_002889358.1| peptidase [Arabidopsis lyrata subsp. lyrata] gi|297335200|gb|EFH65617.1| peptidase [Arabidopsis lyrata subsp. lyrata]	516	540	0	104.7	92.4	95.3	peptidase	gbpln	Arabidopsis lyrata	AT1G01650.1 | Symbols: SPPL4, ATSPPL4 | SIGNAL PEPTIDE PEPTIDASE−LIKE 4 | chr1:233188−237647 REVERSE LENGTH=540	516	540	0	104.7	91.9	94.8
Rsa1.0_00069.1.g3682.t1	ref|XP_002453623.1| hypothetical protein SORBIDRAFT_04g009135 [Sorghum bicolor] gi|241933454|gb|EES06599.1| hypothetical protein SORBIDRAFT_04g009135 [Sorghum bicolor]	147	801	3.00E−21	544.9	39.5	49.7	hypothetical protein SORBIDRAFT_04g009135	gbpln	Sorghum bicolor	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709−228431 REVERSE LENGTH=240	147	240	1.00E−13	163.3	23.8	33.3

Rsa1.0_00069.1.g3683.t1	ref|NP_001117211.1| Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein [Arabidopsis thaliana] gi|332189202|gb|AEE27323.1| Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein [Arabidopsis thaliana]	437	433	1.00E-90	99.1	50.8	64.8	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein	gbpln	Arabidopsis thaliana	AT1G01695.1 | Symbols: | Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-related | chr1:252947-254495 FORWARD LENGTH=433	437	433	3.00E-93	99.1	50.8	64.8
Rsa1.0_00069.1.g3684.t1	gb|EOA37536.1| hypothetical protein CARUB_v10011760mg [Capsella rubella]	368	140	3.00E-73	38.0	35.9	37.0	hypothetical protein CARUB_v10011760mg	gbpln	Capsella rubella	AT1G01750.1 | Symbols: ADF11 | actin depolymerizing factor 11 | chr1:275528-276126 FORWARD LENGTH=140	368	140	6.00E-75	38.0	35.3	37.0
Rsa1.0_00069.1.g3685.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00069.1.g3686.t1	ref|XP_002892044.1| hypothetical protein ARALYDRAFT_470098 [Arabidopsis lyrata subsp. lyrata] gi|297337886|gb|EFH68303.1| hypothetical protein ARALYDRAFT_470098 [Arabidopsis lyrata subsp. lyrata]	686	634	0	92.4	80.5	85.4	hypothetical protein ARALYDRAFT_470098	gbpln	Arabidopsis lyrata	AT1G01770.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1446 (InterPro:IPR010839); Has 1597 Blast hits to 1509 proteins in 306 species: Archae - 4; Bacteria - 843; Metazoa - 22; Fungi - 131; Plants - 31; Viruses - 0; Other Eukaryotes - 566 (source: NCBI BLink). | chr1:278759-282490 FORWARD LENGTH=632	686	632	0	92.1	80.0	84.8
Rsa1.0_00069.1.g3687.t1	gb|EOA37281.1| hypothetical protein CARUB_v10010886mg [Capsella rubella]	205	205	1.00E-111	100.0	93.7	96.6	hypothetical protein CARUB_v10010886mg	gbpln	Capsella rubella	AT1G01780.1 | Symbols: | GATA type zinc finger transcription factor family protein | chr1:282919-284082 FORWARD LENGTH=205	205	205	1.00E-112	100.0	92.7	96.1
Rsa1.0_00069.1.g3688.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00069.1.g3689.t1	ref|XP_002892042.1| hypothetical protein ARALYDRAFT_311263 [Arabidopsis lyrata subsp. lyrata] gi|297337884|gb|EFH68301.1| hypothetical protein ARALYDRAFT_311263 [Arabidopsis lyrata subsp. lyrata]	1167	1171	0	100.3	83.6	89.4	hypothetical protein ARALYDRAFT_311263	gbpln	Arabidopsis lyrata	AT1G01790.1 | Symbols: KEA1, ATKEA1 | K+ efflux antiporter 1 | chr1:284781-290869 FORWARD LENGTH=1193	1167	1193	0	102.2	83.3	89.3
Rsa1.0_00069.1.g3690.t1	ref|XP_002889352.1| peroxisomal biogenesis factor 11 family protein [Arabidopsis lyrata subsp. lyrata] gi|297335194|gb|EFH65611.1| peroxisomal biogenesis factor 11 family protein [Arabidopsis lyrata subsp. lyrata]	237	235	1.00E-128	99.2	94.1	97.0	peroxisomal biogenesis factor 11 family protein	gbpln	Arabidopsis lyrata	AT1G01820.1 | Symbols: PEX11C | peroxin 11c | chr1:296213-297723 REVERSE LENGTH=235	237	235	1.00E-129	99.2	92.8	96.6
Rsa1.0_00069.1.g3691.t1	ref|NP_171690.1| Ribosomal RNA adenine dimethylase family protein [Arabidopsis thaliana] gi|3005590|gb|AAC09322.1| dimethyladenosine transferase [Arabidopsis thaliana] gi|26449914|dbj|BAC42078.1| putative dimethyladenosine transferase [Arabidopsis thaliana] gi|28827572|gb|AAO50630.1| putative dimethyladenosine transferase [Arabidopsis thaliana] gi|332189223|gb|AEE27344.1| Ribosomal RNA adenine dimethylase family protein [Arabidopsis thaliana]	374	343	1.00E-149	91.7	72.7	76.7	Ribosomal RNA adenine dimethylase family protein	gbpln	Arabidopsis thaliana	AT1G01860.1 | Symbols: PFC1 | Ribosomal RNA adenine dimethylase family protein | chr1:304439-306275 REVERSE LENGTH=343	374	343	1.00E-151	91.7	72.7	76.7
Rsa1.0_00069.1.g3692.t1	gb|EOA36590.1| hypothetical protein CARUB_v10011785mg [Capsella rubella]	599	597	0	99.7	77.8	86.6	hypothetical protein CARUB_v10011785mg	gbpln	Capsella rubella	AT1G01880.1 | Symbols: | 5'-3' exonuclease family protein | chr1:306558-308991 REVERSE LENGTH=599	599	599	0	100.0	77.6	85.5
Rsa1.0_00069.1.g3693.t1	gb|EOA38113.1| hypothetical protein CARUB_v10009581mg [Capsella rubella]	358	353	1.00E-175	98.6	89.4	92.2	hypothetical protein CARUB_v10009581mg	gbpln	Capsella rubella	AT1G01910.4 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:313595-315831 REVERSE LENGTH=353	358	353	1.00E-177	98.6	88.5	92.2
Rsa1.0_00069.1.g3694.t1	ref|NP_171694.3| SET domain-containing protein [Arabidopsis thaliana] gi|332189232|gb|AEE27353.1| SET domain-containing protein [Arabidopsis thaliana]	547	572	0	104.6	80.8	88.5	SET domain-containing protein	gbpln	Arabidopsis thaliana	AT1G01920.1 | Symbols: | SET domain-containing protein | chr1:316204-319507 FORWARD LENGTH=572	547	572	0	104.6	80.8	88.5
Rsa1.0_00069.1.g3695.t1	ref|XP_002889345.1| hypothetical protein ARALYDRAFT_470081 [Arabidopsis lyrata subsp. lyrata] gi|297335187|gb|EFH65604.1| hypothetical protein ARALYDRAFT_470081 [Arabidopsis lyrata subsp. lyrata]	582	579	0	99.5	80.2	86.9	hypothetical protein ARALYDRAFT_470081	gbpln	Arabidopsis lyrata	AT1G01930.1 | Symbols: | zinc finger protein-related | chr1:320041-322809 REVERSE LENGTH=580	582	580	0	99.7	78.7	84.7

Rsa1.0_00069.1.g3696.t1	ref|XP_002892036.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata] gi|297337878|gb|EFH68295.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata]	160	160	5.00E-88	100.0	96.9	98.8	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	gbpln	Arabidopsis lyrata	AT1G01940.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr1:323082-324719 FORWARD LENGTH=160	160	160	3.00E-90	100.0	96.9	98.1
Rsa1.0_00069.1.g3697.t1	ref|NP_171697.3| armadillo repeat-containing kinesin-like protein 2 [Arabidopsis thaliana] gi|193806751|sp|Q9LPC6.2|ARK2_ARATH RecName: Full=Armadillo repeat-containing kinesin-like protein 2 gi|162958325|dbj|BAF95586.1| armadillo repeat kinesin2 [Arabidopsis thaliana] gi|332189236|gb|AEE27357.1| armadillo repeat-containing kinesin-like protein 2 [Arabidopsis thaliana]	898	894	0	99.6	94.9	96.9	armadillo repeat-containing kinesin-like protein 2	gbpln	Arabidopsis thaliana	AT1G01950.1 | Symbols: ARK2 | armadillo repeat kinesin 2 | chr1:325473-330403 FORWARD LENGTH=894	898	894	0	99.6	94.9	96.9
Rsa1.0_00069.1.g3698.t1	gb|EOA36031.1| hypothetical protein CARUB_v10008079mg [Capsella rubella]	1754	1780	0	101.5	94.0	97.0	hypothetical protein CARUB_v10008079mg	gbpln	Capsella rubella	AT1G01960.1 | Symbols: EDA10 | SEC7-like guanine nucleotide exchange family protein | chr1:330830-337582 REVERSE LENGTH=1750	1754	1750	0	99.8	93.4	96.3
Rsa1.0_00069.1.g3699.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1186	1342	0	113.2	49.6	67.1	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1186	1262	1.00E-57	106.4	11.4	16.9
Rsa1.0_00069.1.g3700.t2	dbj|BAJ34466.1| unnamed protein product [Thellungiella halophila]	689	675	0	98.0	90.9	93.8	unnamed protein product	----	----	AT1G02010.1 | Symbols: SEC1A | secretory 1A | chr1:348046-352197 FORWARD LENGTH=673	689	673	0	97.7	90.9	93.8
Rsa1.0_00069.1.g3701.t1	ref|XP_002889340.1| hypothetical protein ARALYDRAFT_333453 [Arabidopsis lyrata subsp. lyrata] gi|297335182|gb|EFH65599.1| hypothetical protein ARALYDRAFT_333453 [Arabidopsis lyrata subsp. lyrata]	258	264	6.00E-97	102.3	80.2	89.5	hypothetical protein ARALYDRAFT_333453	gbpln	Arabidopsis lyrata	AT1G02040.1 | Symbols: | C2H2-type zinc finger family protein | chr1:358104-359078 REVERSE LENGTH=324	258	324	2.00E-99	125.6	81.8	88.4
Rsa1.0_00069.1.g3702.t1	ref|XP_002892031.1| hypothetical protein ARALYDRAFT_470069 [Arabidopsis lyrata subsp. lyrata] gi|297337873|gb|EFH68290.1| hypothetical protein ARALYDRAFT_470069 [Arabidopsis lyrata subsp. lyrata]	337	323	1.00E-100	95.8	64.1	70.3	hypothetical protein ARALYDRAFT_470069	gbpln	Arabidopsis lyrata	AT1G02065.1 | Symbols: SPL8 | squamosa promoter binding protein-like 8 | chr1:365625-367149 FORWARD LENGTH=333	337	333	7.00E-95	98.8	62.3	70.9
Rsa1.0_00069.1.g3703.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00069.1.g3704.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	584	484	3.00E-91	82.9	28.3	34.8	hypothetical protein 27.t00116	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	584	566	2.00E-12	96.9	15.6	29.5
Rsa1.0_00069.1.g3705.t1	gb|EOA39027.1| hypothetical protein CARUB_v10011597mg [Capsella rubella]	186	186	2.00E-15	100.0	26.9	45.2	hypothetical protein CARUB_v10011597mg	gbpln	Capsella rubella	AT5G53910.1 | Symbols: | RING/U-box superfamily protein | chr5:21890643-21891335 FORWARD LENGTH=230	186	230	6.00E-11	123.7	14.5	18.8
Rsa1.0_00069.1.g3706.t1	ref|XP_003609124.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula] gi|355510179|gb|AES91321.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula]	1509	1558	0	103.2	44.1	60.8	ATP-dependent DNA helicase PIF1	gbpln	Medicago truncatula	AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907-10814173 REVERSE LENGTH=337	1509	337	5.00E-70	22.3	8.7	12.2
Rsa1.0_00069.1.g3707.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00069.1.g3708.t1	gb|AAG10809.1|AC018460_3 Similar to mutator transposase [Arabidopsis thaliana]	436	884	7.00E-17	202.8	19.0	30.5	Similar to mutator transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00069.1.g3709.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00069.1.g3710.t1	gb|ADK13090.1| annexin 1 [Brassica napus]	317	317	0	100.0	98.1	99.4	annexin 1	gbpln	Brassica napus	AT1G35720.1 | Symbols: ANNAT1, OXY5, ATOXY5 | annexin 1 | chr1:13225304-13226939 FORWARD LENGTH=317	317	317	1.00E-176	100.0	93.4	97.8
Rsa1.0_00069.1.g3711.t1	gb|EOA39555.1| hypothetical protein CARUB_v10008173mg [Capsella rubella]	1037	1027	0	99.0	74.4	85.3	hypothetical protein CARUB_v10008173mg	gbpln	Capsella rubella	AT4G08850.1 | Symbols: | Leucine-rich repeat receptor-like protein kinase family protein | chr4:5636693-5640496 REVERSE LENGTH=1045	1037	1045	0	100.8	70.6	83.7
Rsa1.0_00069.1.g3712.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00069.1.g3713.t1	ref|NP_174807.1| calcium-dependent protein kinase 2 [Arabidopsis thaliana] gi|332278169|sp|Q39016.2|CDPKB_ARATH RecName: Full=Calcium-dependent protein kinase 11; AltName: Full=Calcium-dependent protein kinase isoform CDPK2; Short=AtCDPK2 gi|15293095|gb|AAK93658.1| putative calcium-dependent protein kinase [Arabidopsis thaliana] gi|21281141|gb|AAM45034.1| putative calcium-dependent protein kinase [Arabidopsis thaliana] gi|332193701|gb|AEE31822.1| calcium-dependent protein kinase 2 [Arabidopsis thaliana]	497	495	0	99.6	97.4	98.2	calcium-dependent protein kinase 2	gbpln	Arabidopsis thaliana	AT1G35670.1 | Symbols: ATCDPK2, CPK11, ATCPK11, CDPK2 | calcium-dependent protein kinase 2 | chr1:13205456-13208058 FORWARD LENGTH=495	497	495	0	99.6	97.4	98.2
Rsa1.0_00069.1.g3714.t1	gb|EOA40451.1| hypothetical protein CARUB_v10009176mg [Capsella rubella]	468	438	0	93.6	78.6	84.6	hypothetical protein CARUB_v10009176mg	gbpln	Capsella rubella	AT1G35620.1 | Symbols: ATPDIL5-2, ATPDI8, PDI8, PDIL5-2 | PDI-like 5-2 | chr1:13156504-13158280 FORWARD LENGTH=440	468	440	0	94.0	78.0	84.0
Rsa1.0_00070.1.g3715.t1	#	#	#	#	#	#	#	–	----	----	AT4G24590.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G49710.3); Has 105 Blast hits to 105 proteins in 26 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 3; Plants - 85; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr4:12696651-12698036 FORWARD LENGTH=241	71	241	2.00E-11	339.4	47.9	52.1
Rsa1.0_00070.1.g3716.t1	gb|EOA15984.1| hypothetical protein CARUB_v10004098mg [Capsella rubella]	897	907	0	101.1	77.5	83.5	hypothetical protein CARUB_v10004098mg	gbpln	Capsella rubella	AT4G24580.1 | Symbols: REN1 | Rho GTPase activation protein (RhoGAP) with PH domain | chr4:12687879-12694248 REVERSE LENGTH=933	897	933	0	104.0	79.3	86.1
Rsa1.0_00070.1.g3717.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00070.1.g3718.t1	ref|XP_002867659.1| ubiquitin-specific protease 16 [Arabidopsis lyrata subsp. lyrata] gi|297313495|gb|EFH43918.1| ubiquitin-specific protease 16 [Arabidopsis lyrata subsp. lyrata]	1009	1007	0	99.8	77.6	85.7	ubiquitin-specific protease 16	gbpln	Arabidopsis lyrata	AT4G24560.1 | Symbols: UBP16 | ubiquitin-specific protease 16 | chr4:12679493-12684528 REVERSE LENGTH=1008	1009	1008	0	99.9	78.0	85.5
Rsa1.0_00070.1.g3719.t1	gb|AFM77897.1| MADS-box protein AGL24 [Brassica napus]	233	221	1.00E-119	94.8	91.4	94.0	MADS-box protein AGL24	gbpln	Brassica napus	AT4G24540.1 | Symbols: AGL24 | AGAMOUS-like 24 | chr4:12671160-12673645 REVERSE LENGTH=220	233	220	1.00E-102	94.4	80.3	88.0
Rsa1.0_00070.1.g3720.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00070.1.g3721.t1	gb|EOA23805.1| hypothetical protein CARUB_v10017019mg [Capsella rubella]	160	520	5.00E-13	325.0	25.6	29.4	hypothetical protein CARUB_v10017019mg	gbpln	Capsella rubella	AT4G24530.1 | Symbols: | O-fucosyltransferase family protein | chr4:12667424-12669713 REVERSE LENGTH=519	160	519	2.00E-14	324.4	21.3	21.3
Rsa1.0_00070.1.g3722.t1	ref|XP_002867662.1| hypothetical protein ARALYDRAFT_492391 [Arabidopsis lyrata subsp. lyrata] gi|297313498|gb|EFH43921.1| hypothetical protein ARALYDRAFT_492391 [Arabidopsis lyrata subsp. lyrata]	695	692	0	99.6	91.2	94.8	hypothetical protein ARALYDRAFT_492391	gbpln	Arabidopsis lyrata	AT4G24520.1 | Symbols: ATR1, AR1 | P450 reductase 1 | chr4:12663065-12667066 REVERSE LENGTH=692	695	692	0	99.6	89.8	94.2
Rsa1.0_00070.1.g3723.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00070.1.g3724.t6	gb|EOA37111.1| hypothetical protein CARUB_v10010324mg [Capsella rubella] gi|482572925|gb|EOA37112.1| hypothetical protein CARUB_v10010324mg [Capsella rubella]	211	203	4.00E-75	96.2	69.7	77.3	hypothetical protein CARUB_v10010324mg	gbpln	Capsella rubella	AT1G07700.1 | Symbols: | Thioredoxin superfamily protein | chr1:2380214-2381127 FORWARD LENGTH=204	211	204	3.00E-73	96.7	65.4	73.9
Rsa1.0_00070.1.g3725.t1	gb|EOA17945.1| hypothetical protein CARUB_v10006355mg [Capsella rubella]	131	312	1.00E-53	238.2	76.3	85.5	hypothetical protein CARUB_v10006355mg	gbpln	Capsella rubella	AT4G24470.2 | Symbols: ZIM, GATA25 | GATA-type zinc finger protein with TIFY domain | chr4:12645785-12647734 FORWARD LENGTH=309	131	309	2.00E-55	235.9	76.3	86.3
Rsa1.0_00070.1.g3726.t2	ref|XP_002869716.1| zinc-finger protein expressed in inflorescence meristem [Arabidopsis lyrata subsp. lyrata] gi|297315552|gb|EFH45975.1| zinc-finger protein expressed in inflorescence meristem [Arabidopsis lyrata subsp. lyrata]	183	311	5.00E-54	169.9	67.2	72.1	zinc-finger protein expressed in inflorescence meristem	gbpln	Arabidopsis lyrata	AT4G24470.2 | Symbols: ZIM, GATA25 | GATA-type zinc finger protein with TIFY domain | chr4:12645785-12647734 FORWARD LENGTH=309	183	309	9.00E-54	168.9	67.2	72.1
Rsa1.0_00070.1.g3727.t1	gb|EOA17710.1| hypothetical protein CARUB_v10006082mg [Capsella rubella]	106	106	6.00E-55	100.0	98.1	100.0	hypothetical protein CARUB_v10006082mg	gbpln	Capsella rubella	AT4G24440.2 | Symbols: | transcription initiation factor IIA gamma chain / TFIIA-gamma (TFIIA-S) | chr4:12633460-12634553 FORWARD LENGTH=106	106	106	3.00E-57	100.0	97.2	100.0
Rsa1.0_00070.1.g3728.t1	gb|EOA29907.1| hypothetical protein CARUB_v10013001mg [Capsella rubella]	1093	803	3.00E-75	73.5	18.4	23.6	hypothetical protein CARUB_v10013001mg	gbpln	Capsella rubella	AT3G02930.2 | Symbols: | Plant protein of unknown function (DUF827) | chr3:655158-658319 FORWARD LENGTH=804	1093	804	1.00E-70	73.6	17.6	22.6

Rsa1.0_00070.1.g3729.t3	ref|NP_194164.1| uncharacterized protein [Arabidopsis thaliana] gi|5051775|emb|CAB45068.1| putative protein [Arabidopsis thaliana] gi|7269283|emb|CAB79343.1| putative protein [Arabidopsis thaliana] gi|58652054|gb|AAW80852.1| At4g24330 [Arabidopsis thaliana] gi|332659490|gb|AEE84890.1| uncharacterized protein AT4G24330 [Arabidopsis thaliana]	477	478	0	100.2	81.1	87.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G24330.1 | Symbols: | Protein of unknown function (DUF1682) | chr4:12603848-12606229 REVERSE LENGTH=478	477	478	0	100.2	81.1	87.4
Rsa1.0_00070.1.g3730.t1	ref|XP_002869727.1| cphsc70-1 [Arabidopsis lyrata subsp. lyrata] gi|297315563|gb|EFH45986.1| cphsc70-1 [Arabidopsis lyrata subsp. lyrata]	713	718	0	100.7	93.8	96.4	cphsc70-1	gbpln	Arabidopsis lyrata	AT4G24280.1 | Symbols: cpHsc70-1 | chloroplast heat shock protein 70-1 | chr4:12590094-12593437 FORWARD LENGTH=718	713	718	0	100.7	88.9	91.4
Rsa1.0_00070.1.g3731.t1	gb|EOA15374.1| hypothetical protein CARUB_v10006044mg [Capsella rubella]	125	121	1.00E-27	96.8	65.6	75.2	hypothetical protein CARUB_v10006044mg	gbpln	Capsella rubella	AT4G24275.1 | Symbols: | Identified as a screen for stress-responsive genes. | chr4:12588579-12588959 FORWARD LENGTH=126	125	126	1.00E-26	100.8	71.2	80.8
Rsa1.0_00070.1.g3732.t1	gb|EOA15955.1| hypothetical protein CARUB_v10004057mg [Capsella rubella]	843	1002	0	118.9	64.1	70.9	hypothetical protein CARUB_v10004057mg	gbpln	Capsella rubella	AT4G24200.1 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr4:12556927-12559929 REVERSE LENGTH=1000	843	1000	0	118.6	63.9	70.6
Rsa1.0_00070.1.g3733.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00070.1.g3734.t1	ref|NP_194157.1| endoglucanase 21 [Arabidopsis thaliana] gi|75266338|sp|Q9STW8.1|GUN21_ARATH RecName: Full=Endoglucanase 21; AltName: Full=Endo-1,4-beta glucanase 21 gi|5051768|emb|CAB45061.1| endo-1, 4-beta-glucanase like protein [Arabidopsis thaliana] gi|7269276|emb|CAB79336.1| endo-1, 4-beta-glucanase like protein [Arabidopsis thaliana] gi|332659479|gb|AEE84879.1| endoglucanase 21 [Arabidopsis thaliana]	643	620	0	96.4	73.7	82.7	endoglucanase 21	gbpln	Arabidopsis thaliana	AT4G24260.1 | Symbols: ATGH9A3, KOR3, GH9A3 | glycosyl hydrolase 9A3 | chr4:12577871-12580133 REVERSE LENGTH=620	643	620	0	96.4	73.7	82.7
Rsa1.0_00070.1.g3735.t1	ref|XP_002867673.1| hypothetical protein ARALYDRAFT_914165 [Arabidopsis lyrata subsp. lyrata] gi|297313509|gb|EFH43932.1| hypothetical protein ARALYDRAFT_914165 [Arabidopsis lyrata subsp. lyrata]	449	482	0	107.3	87.1	92.0	hypothetical protein ARALYDRAFT_914165	gbpln	Arabidopsis lyrata	AT4G24250.1 | Symbols: MLO13, ATMLO13 | Seven transmembrane MLO family protein | chr4:12575008-12577517 REVERSE LENGTH=478	449	478	0	106.5	86.2	91.8
Rsa1.0_00070.1.g3736.t1	gb|ACQ76809.1| WRKY transcription factor 7 [Brassica napus]	352	348	1.00E-170	98.9	90.1	92.6	WRKY transcription factor 7	gbpln	Brassica napus	AT4G24240.1 | Symbols: WRKY7, ATWRKY7 | WRKY DNA-binding protein 7 | chr4:12571930-12573446 FORWARD LENGTH=353	352	353	1.00E-139	100.3	76.4	83.5
Rsa1.0_00070.1.g3737.t1	ref|NP_194154.1| acyl-CoA-binding domain 3 [Arabidopsis thaliana] gi|145333919|ref|NP_001078439.1| acyl-CoA-binding domain 3 [Arabidopsis thaliana] gi|145333930|ref|NP_001078440.1| acyl-CoA-binding domain 3 [Arabidopsis thaliana] gi|145333941|ref|NP_001078441.1| acyl-CoA-binding domain 3 [Arabidopsis thaliana] gi|75207746|sp|Q9STX1.1|ACBP3_ARATH RecName: Full=Acyl-CoA-binding domain-containing protein 3; Short=Acyl-CoA binding protein 3; Flags: Precursor gi|5051765|emb|CAB45058.1| putative protein [Arabidopsis thaliana] gi|7269273|emb|CAB79333.1| putative protein [Arabidopsis thaliana] gi|110742400|dbj|BAE99122.1| hypothetical protein [Arabidopsis thaliana] gi|332659471|gb|AEE84871.1| acyl-CoA-binding domain 3 [Arabidopsis thaliana] gi|332659472|gb|AEE84872.1| acyl-CoA-binding domain 3 [Arabidopsis thaliana] gi|332659473|gb|AEE84873.1| acyl-CoA-binding domain 3 [Arabidopsis thaliana] gi|332659474|gb|AEE84874.1| acyl-CoA-binding domain 3 [Arabidopsis thaliana]	368	362	2.00E-88	98.4	61.4	72.0	acyl-CoA-binding domain 3	gbpln	Arabidopsis thaliana	AT4G24230.5 | Symbols: ACBP3 | acyl-CoA-binding domain 3 | chr4:12567240-12568754 REVERSE LENGTH=362	368	362	5.00E-91	98.4	61.4	72.0

Rsa1.0_00070.1.g3738.t1	gb|AFD96485.1| putative enone 5-beta-reductase [Brassica oleracea var. gemmifera]	380	382	0	100.5	91.1	96.6	putative enone 5-beta-reductase	gbpln	Brassica oleracea	AT4G24220.1 | Symbols: VEP1, AWI31 | NAD(P)-binding Rossmann-fold superfamily protein | chr4:12565219-12566474 FORWARD LENGTH=388	380	388	1.00E-178	102.1	78.7	90.3
Rsa1.0_00070.1.g3739.t1	gb|AAD09508.1| ATFP4, partial [Arabidopsis thaliana]	159	179	6.00E-33	112.6	65.4	72.3	ATFP4, partial	gbpln	Arabidopsis thaliana	AT3G07600.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:2424300-2424954 REVERSE LENGTH=157	159	157	4.00E-35	98.7	65.4	72.3
Rsa1.0_00070.1.g3740.t2	ref|XP_002891519.1| hypothetical protein ARALYDRAFT_337099 [Arabidopsis lyrata subsp. lyrata] gi|297337361|gb|EFH67778.1| hypothetical protein ARALYDRAFT_337099 [Arabidopsis lyrata subsp. lyrata]	643	1163	4.00E-40	180.9	23.5	36.5	hypothetical protein ARALYDRAFT_337099	gbpln	Arabidopsis lyrata	AT1G67370.1 | Symbols: ASY1, ATASY1 | DNA-binding HORMA family protein | chr1:25239347-25243713 REVERSE LENGTH=596	643	596	4.00E-33	92.7	12.8	14.5
Rsa1.0_00070.1.g3741.t1	ref|XP_002862875.1| hypothetical protein ARALYDRAFT_920182 [Arabidopsis lyrata subsp. lyrata] gi|297308637|gb|EFH39134.1| hypothetical protein ARALYDRAFT_920182 [Arabidopsis lyrata subsp. lyrata]	310	315	3.00E-31	101.6	32.3	46.5	hypothetical protein ARALYDRAFT_920182	gbpln	Arabidopsis lyrata	AT1G02770.1 | Symbols: | Protein of unknown function (DUF626) | chr1:605071-606624 REVERSE LENGTH=316	310	316	7.00E-34	101.9	31.9	49.4
Rsa1.0_00070.1.g3742.t1	ref|XP_002867675.1| hypothetical protein ARALYDRAFT_329238 [Arabidopsis lyrata subsp. lyrata] gi|297313511|gb|EFH43934.1| hypothetical protein ARALYDRAFT_329238 [Arabidopsis lyrata subsp. lyrata]	121	157	3.00E-40	129.8	68.6	81.8	hypothetical protein ARALYDRAFT_329238	gbpln	Arabidopsis lyrata	AT4G24204.3 | Symbols: | RING/U-box superfamily protein | chr4:12562069-12562815 REVERSE LENGTH=178	121	178	1.00E-42	147.1	70.2	81.0
Rsa1.0_00070.1.g3743.t1	ref|XP_002867676.1| hypothetical protein ARALYDRAFT_492440 [Arabidopsis lyrata subsp. lyrata] gi|297313512|gb|EFH43935.1| hypothetical protein ARALYDRAFT_492440 [Arabidopsis lyrata subsp. lyrata]	986	1002	0	101.6	79.5	87.3	hypothetical protein ARALYDRAFT_492440	gbpln	Arabidopsis lyrata	AT4G24200.1 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr4:12556927-12559929 REVERSE LENGTH=1000	986	1000	0	101.4	77.9	86.0
Rsa1.0_00070.1.g3744.t1	ref|XP_002867677.1| hypothetical protein ARALYDRAFT_492441 [Arabidopsis lyrata subsp. lyrata] gi|297313513|gb|EFH43936.1| hypothetical protein ARALYDRAFT_492441 [Arabidopsis lyrata subsp. lyrata]	804	823	0	102.4	93.5	96.5	hypothetical protein ARALYDRAFT_492441	gbpln	Arabidopsis lyrata	AT4G24190.1 | Symbols: SHD, HSP90.7, AtHsp90.7, AtHsp90-7 | Chaperone protein htpG family protein | chr4:12551902-12555851 REVERSE LENGTH=823	804	823	0	102.4	92.2	95.9
Rsa1.0_00070.1.g3745.t1	emb|CAB45053.1| thaumatin-like protein [Arabidopsis thaliana] gi|7269268|emb|CAB79328.1| thaumatin-like protein [Arabidopsis thaliana]	256	255	1.00E-130	99.6	89.1	94.1	thaumatin-like protein	gbpln	Arabidopsis thaliana	AT4G24180.1 | Symbols: TLP1, ATTLP1 | THAUMATIN-LIKE PROTEIN 1 | chr4:12550356-12551221 REVERSE LENGTH=260	256	260	1.00E-131	101.6	89.1	94.1
Rsa1.0_00070.1.g3746.t1	ref|XP_002869734.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297315570|gb|EFH45993.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	407	417	0	102.5	88.2	94.1	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT4G24160.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:12539871-12542210 FORWARD LENGTH=418	407	418	0	102.7	88.7	94.1
Rsa1.0_00070.1.g3747.t1	ref|XP_002869735.1| hypothetical protein ARALYDRAFT_354358 [Arabidopsis lyrata subsp. lyrata] gi|297315571|gb|EFH45994.1| hypothetical protein ARALYDRAFT_354358 [Arabidopsis lyrata subsp. lyrata]	435	431	1.00E-139	99.1	68.0	76.3	hypothetical protein ARALYDRAFT_354358	gbpln	Arabidopsis lyrata	AT4G24150.1 | Symbols: AtGRF8, GRF8 | growth-regulating factor 8 | chr4:12535972-12539387 FORWARD LENGTH=493	435	493	1.00E-134	113.3	62.8	71.5
Rsa1.0_00070.1.g3748.t1	gb|EOA16234.1| hypothetical protein CARUB_v10004382mg [Capsella rubella]	591	622	0	105.2	74.6	82.7	hypothetical protein CARUB_v10004382mg	gbpln	Capsella rubella	AT4G24260.1 | Symbols: ATGH9A3, KOR3, GH9A3 | glycosyl hydrolase 9A3 | chr4:12577871-12580133 REVERSE LENGTH=620	591	620	0	104.9	75.0	83.9
Rsa1.0_00070.1.g3749.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00070.1.g3750.t1	gb|EOA17566.1| hypothetical protein CARUB_v10005927mg [Capsella rubella]	157	157	7.00E-73	100.0	83.4	91.7	hypothetical protein CARUB_v10005927mg	gbpln	Capsella rubella	AT4G24130.1 | Symbols: | Protein of unknown function, DUF538 | chr4:12527861-12528423 FORWARD LENGTH=157	157	157	1.00E-74	100.0	83.4	91.7
Rsa1.0_00070.1.g3751.t1	gb|EOA16163.1| hypothetical protein CARUB_v10004301mg [Capsella rubella]	403	672	0	166.7	91.6	96.8	hypothetical protein CARUB_v10004301mg	gbpln	Capsella rubella	AT4G24120.1 | Symbols: YSL1, ATYSL1 | YELLOW STRIPE like 1 | chr4:12524581-12527023 FORWARD LENGTH=673	403	673	0	167.0	90.6	96.0
Rsa1.0_00071.1.g3752.t1	gb|EOA14930.1| hypothetical protein CARUB_v10028273mg [Capsella rubella]	1265	1269	0	100.3	92.0	95.6	hypothetical protein CARUB_v10028273mg	gbpln	Capsella rubella	AT5G64270.1 | Symbols: | splicing factor, putative | chr5:25706909-25710718 FORWARD LENGTH=1269	1265	1269	0	100.3	90.8	94.9

Rsa1.0_00071.1.g3753.t1	ref|NP_201234.1| dicarboxylate transport 2.1 [Arabidopsis thaliana] gi|75171656|sp|Q9FMF7.1|DIT21_ARATH RecName: Full=Dicarboxylate transporter 2.1, chloroplastic; AltName: Full=AtpDCT1; AltName: Full=Glutamate/malate translocator; Flags: Precursor gi|9759405|dbj|BAB09860.1| 2-oxoglutarate/malate translocator [Arabidopsis thaliana] gi|15810581|gb|AAL07178.1| putative 2-oxoglutarate/malate translocator protein [Arabidopsis thaliana] gi|23397031|gb|AAN31801.1| putative 2-oxoglutarate/malate translocator [Arabidopsis thaliana] gi|53850569|gb|AAU95461.1| At5g64290 [Arabidopsis thaliana] gi|332010483|gb|AED97866.1| dicarboxylate transport 2.1 [Arabidopsis thaliana]	560	563	0	100.5	93.4	96.4	dicarboxylate transport 2.1	gbpln	Arabidopsis thaliana	AT5G64290.1 | Symbols: DCT, DIT2.1 | dicarboxylate transport 2.1 | chr5:25714495-25716642 REVERSE LENGTH=563	560	563	0	100.5	93.4	96.4
Rsa1.0_00071.1.g3754.t1	gb|EOA12507.1| hypothetical protein CARUB_v10026209mg [Capsella rubella]	520	534	0	102.7	86.5	90.2	hypothetical protein CARUB_v10026209mg	gbpln	Capsella rubella	AT5G64300.1 | Symbols: ATGCH, GCH, ATRIBA1, RFD1 | GTP cyclohydrolase II | chr5:25718459-25720790 FORWARD LENGTH=543	520	543	0	104.4	86.0	90.4
Rsa1.0_00071.1.g3755.t4	dbj|BAB09864.1| non-phototropic hypocotyl 3 [Arabidopsis thaliana]	1146	745	0	65.0	54.5	56.7	non-phototropic hypocotyl 3	gbpln	Arabidopsis thaliana	AT5G64330.1 | Symbols: NPH3, RPT3, JK218 | Phototropic-responsive NPH3 family protein | chr5:25727568-25730225 FORWARD LENGTH=746	1146	746	0	65.1	54.5	56.6
Rsa1.0_00071.1.g3756.t1	ref|XP_002269289.1| PREDICTED: uncharacterized protein C6C3.02c [Vitis vinifera] gi|296088792|emb|CBI38242.3| unnamed protein product [Vitis vinifera]	162	145	5.00E-38	89.5	59.9	69.8	PREDICTED: uncharacterized protein C6C3.02c	gbpln	Vitis vinifera	AT5G09570.1 | Symbols: | Cox19-like CHCH family protein | chr5:2970733-2971970 FORWARD LENGTH=139	162	139	3.00E-40	85.8	52.5	63.0
Rsa1.0_00071.1.g3757.t1	gb|EOA13529.1| hypothetical protein CARUB_v10026593mg [Capsella rubella] gi|482549336|gb|EOA13530.1| hypothetical protein CARUB_v10026593mg [Capsella rubella]	360	379	1.00E-157	105.3	76.7	83.6	hypothetical protein CARUB_v10026593mg	gbpln	Capsella rubella	AT5G64520.1 | Symbols: XRCC2, ATXRCC2 | homolog of X-ray repair cross complementing 2 (XRCC2) | chr5:25788069-25790204 FORWARD LENGTH=372	360	372	1.00E-152	103.3	76.7	84.7
Rsa1.0_00071.1.g3758.t1	ref|XP_002864908.1| ANAC104/XND1 [Arabidopsis lyrata subsp. lyrata] gi|297310743|gb|EFH41167.1| ANAC104/XND1 [Arabidopsis lyrata subsp. lyrata]	188	188	1.00E-89	100.0	92.6	96.8	ANAC104/XND1	gbpln	Arabidopsis lyrata	AT5G64530.1 | Symbols: ANAC104, XND1 | xylem NAC domain 1 | chr5:25795360-25796699 FORWARD LENGTH=187	188	187	7.00E-91	99.5	89.4	94.1
Rsa1.0_00071.1.g3759.t1	ref|XP_002866619.1| hypothetical protein ARALYDRAFT_358659 [Arabidopsis lyrata subsp. lyrata] gi|297312454|gb|EFH42878.1| hypothetical protein ARALYDRAFT_358659 [Arabidopsis lyrata subsp. lyrata]	513	1082	0	210.9	86.4	90.3	hypothetical protein ARALYDRAFT_358659	gbpln	Arabidopsis lyrata	AT5G64550.1 | Symbols: | loricrin-related | chr5:25801794-25803698 REVERSE LENGTH=634	513	634	0	123.6	86.0	89.7
Rsa1.0_00071.1.g3760.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	331	1447	5.00E-37	437.2	30.5	50.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	331	295	1.00E-32	89.1	26.9	45.0
Rsa1.0_00071.1.g3761.t1	gb|EOA12936.1| hypothetical protein CARUB_v10025915mg [Capsella rubella]	778	784	0	100.8	89.2	94.0	hypothetical protein CARUB_v10025915mg	gbpln	Capsella rubella	AT5G64570.1 | Symbols: XYL4, ATBXL4 | beta-D-xylosidase 4 | chr5:25810227-25813309 REVERSE LENGTH=784	778	784	0	100.8	87.4	93.2
Rsa1.0_00071.1.g3762.t1	ref|XP_002864909.1| hypothetical protein ARALYDRAFT_496672 [Arabidopsis lyrata subsp. lyrata] gi|297310744|gb|EFH41168.1| hypothetical protein ARALYDRAFT_496672 [Arabidopsis lyrata subsp. lyrata]	639	521	0	81.5	66.7	70.6	hypothetical protein ARALYDRAFT_496672	gbpln	Arabidopsis lyrata	AT5G64600.1 | Symbols: | O-fucosyltransferase family protein | chr5:25825178-25827931 FORWARD LENGTH=522	639	522	0	81.7	66.0	69.8
Rsa1.0_00071.1.g3763.t1	gb|EOA13365.1| hypothetical protein CARUB_v10026402mg [Capsella rubella]	438	445	0	101.6	92.7	95.4	hypothetical protein CARUB_v10026402mg	gbpln	Capsella rubella	AT5G64610.1 | Symbols: HAM1 | histone acetyltransferase of the MYST family 1 | chr5:25828333-25830503 REVERSE LENGTH=445	438	445	0	101.6	92.2	94.5
Rsa1.0_00071.1.g3764.t2	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	728	1164	1.00E-110	159.9	26.6	40.5	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT5G64620.1 | Symbols: C/VIF2, ATC/VIF2 | cell wall / vacuolar inhibitor of fructosidase 2 | chr5:25831875-25832417 FORWARD LENGTH=180	728	180	7.00E-61	24.7	15.9	17.2
Rsa1.0_00071.1.g3765.t1	ref|XP_002864912.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310747|gb|EFH41171.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	570	602	0	105.6	85.3	91.6	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT5G64640.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:25836820-25839053 FORWARD LENGTH=602	570	602	0	105.6	84.2	91.1

Rsa1.0_00071.1.g3766.t1	gb|EOA21717.1| hypothetical protein CARUB_v10002154mg [Capsella rubella]	161	160	9.00E-81	99.4	91.3	93.8	hypothetical protein CARUB_v10002154mg	gbpln	Capsella rubella	AT5G64650.1 | Symbols: | Ribosomal protein L17 family protein | chr5:25839542-25840775 REVERSE LENGTH=160	161	160	7.00E-82	99.4	90.1	93.2
Rsa1.0_00071.1.g3767.t1	ref|XP_002866628.1| ribosomal protein L15 family protein [Arabidopsis lyrata subsp. lyrata] gi|297312463|gb|EFH42887.1| ribosomal protein L15 family protein [Arabidopsis lyrata subsp. lyrata]	286	281	1.00E-145	98.3	91.3	93.7	ribosomal protein L15 family protein	gbpln	Arabidopsis lyrata	AT5G64670.1 | Symbols: | Ribosomal protein L18e/L15 superfamily protein | chr5:25852535-25853880 REVERSE LENGTH=281	286	281	2.33E-156	98.3	90.6	93.4
Rsa1.0_00071.1.g3768.t1	ref|NP_201273.1| uncharacterized protein [Arabidopsis thaliana] gi|30698059|ref|NP_851270.1| uncharacterized protein [Arabidopsis thaliana] gi|10178071|dbj|BAB11435.1| unnamed protein product [Arabidopsis thaliana] gi|26452974|dbj|BAC43563.1| unknown protein [Arabidopsis thaliana] gi|28973531|gb|AAO64090.1| unknown protein [Arabidopsis thaliana] gi|332010553|gb|AED97936.1| uncharacterized protein AT5G64680 [Arabidopsis thaliana] gi|332010554|gb|AED97937.1| uncharacterized protein AT5G64680 [Arabidopsis thaliana]	145	203	1.00E-21	140.0	49.0	62.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G64680.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:25854433-25855331 FORWARD LENGTH=203	145	203	3.00E-24	140.0	49.0	62.1
Rsa1.0_00071.1.g3769.t1	ref|XP_002866629.1| hypothetical protein ARALYDRAFT_332687 [Arabidopsis lyrata subsp. lyrata] gi|297312464|gb|EFH42888.1| hypothetical protein ARALYDRAFT_332687 [Arabidopsis lyrata subsp. lyrata]	109	95	8.00E-33	87.2	72.5	79.8	hypothetical protein ARALYDRAFT_332687	gbpln	Arabidopsis lyrata	AT5G09830.1 | Symbols: | BolA-like family protein | chr5:3057816-3058769 REVERSE LENGTH=93	109	93	3.00E-32	85.3	64.2	72.5
Rsa1.0_00071.1.g3770.t1	gb|EOA12539.1| hypothetical protein CARUB_v10026529mg [Capsella rubella]	399	400	6.00E-94	100.3	63.9	76.2	hypothetical protein CARUB_v10026529mg	gbpln	Capsella rubella	AT5G64690.1 | Symbols: | neurofilament triplet H protein-related | chr5:25862969-25864521 FORWARD LENGTH=344	399	344	3.00E-75	86.2	53.1	66.7
Rsa1.0_00071.1.g3771.t1	ref|NP_201275.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75170420|sp|Q9FGG3.1|WTR45_ARATH RecName: Full=WAT1-related protein At5g64700 gi|10177201|dbj|BAB10303.1| nodulin-like protein [Arabidopsis thaliana] gi|332010557|gb|AED97940.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]	354	359	1.00E-163	101.4	87.9	92.4	nodulin MtN21 /EamA-like transporter family protein	gbpln	Arabidopsis thaliana	AT5G64700.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:25865190-25866845 REVERSE LENGTH=359	354	359	1.00E-166	101.4	87.9	92.4
Rsa1.0_00071.1.g3772.t1	gb|EOA14833.1| hypothetical protein CARUB_v10028143mg [Capsella rubella]	157	158	2.00E-64	100.6	75.2	86.0	hypothetical protein CARUB_v10028143mg	gbpln	Capsella rubella	AT5G64720.1 | Symbols: | Protein of unknown function (DUF1278) | chr5:25872346-25872813 REVERSE LENGTH=155	157	155	3.00E-66	98.7	73.9	85.4
Rsa1.0_00071.1.g3773.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00071.1.g3774.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1770	1213	0	68.5	37.9	48.1	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	1770	289	2.00E-79	16.3	8.0	10.5
Rsa1.0_00071.1.g3775.t2	gb|ACS68196.1| cellulose synthase 6.1 catalytic subunit [Brassica napus]	1082	1084	0	100.2	99.1	99.4	cellulose synthase 6.1 catalytic subunit	gbpln	Brassica napus	AT5G64740.1 | Symbols: CESA6, IXR2, E112, PRC1 | cellulose synthase 6 | chr5:25881555-25886333 FORWARD LENGTH=1084	1082	1084	0	100.2	95.7	98.0
Rsa1.0_00071.1.g3776.t1	gb|AFI57747.1| ethylene-responsive transcription factor ABR1 [Brassica juncea]	318	381	1.00E-106	119.8	70.4	77.7	ethylene-responsive transcription factor ABR1	gbpln	Brassica juncea	AT5G64750.1 | Symbols: ABR1 | Integrase-type DNA-binding superfamily protein | chr5:25891679-25893656 FORWARD LENGTH=391	318	391	1.00E-104	123.0	78.6	83.0
Rsa1.0_00071.1.g3777.t3	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1164	910	0	78.2	28.0	37.5	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1164	626	2.00E-68	53.8	10.7	15.6
Rsa1.0_00071.1.g3778.t1	ref|XP_002864811.1| hypothetical protein ARALYDRAFT_358470 [Arabidopsis lyrata subsp. lyrata] gi|297310646|gb|EFH41070.1| hypothetical protein ARALYDRAFT_358470 [Arabidopsis lyrata subsp. lyrata]	348	556	2.00E-78	159.8	47.7	56.9	hypothetical protein ARALYDRAFT_358470	gbpln	Arabidopsis lyrata	AT5G62660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:25156326-25157465 REVERSE LENGTH=379	348	379	9.00E-74	108.9	45.7	54.6
Rsa1.0_00071.1.g3779.t1	ref|XP_002864921.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297310756|gb|EFH41180.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	485	485	0	100.0	87.0	92.0	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT5G64790.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:25902713-25904559 FORWARD LENGTH=485	485	485	0	100.0	85.8	92.4

Rsa1.0_00071.1.g3780.t1	ref|XP_002864923.1| WRKY DNA-binding protein 51 [Arabidopsis lyrata subsp. lyrata] gi|297310758|gb|EFH41182.1| WRKY DNA-binding protein 51 [Arabidopsis lyrata subsp. lyrata]	166	194	2.00E-68	116.9	81.3	84.9	WRKY DNA-binding protein 51	gbpln	Arabidopsis lyrata	AT5G64810.1 | Symbols: WRKY51, ATWRKY51 | WRKY DNA-binding protein 51 | chr5:25908415-25909687 FORWARD LENGTH=194	166	194	8.00E-70	116.9	79.5	84.9
Rsa1.0_00071.1.g3781.t1	ref|NP_568996.1| Ras-related small GTP-binding family protein [Arabidopsis thaliana] gi|29839609|sp|Q9C5J9.1|Y5483_ARATH RecName: Full=Uncharacterized GTP-binding protein At5g64813 gi|13430582|gb|AAK25913.1|AF360203_1 unknown protein [Arabidopsis thaliana] gi|14532852|gb|AAK64108.1| unknown protein [Arabidopsis thaliana] gi|332010571|gb|AED97954.1| Ras-related small GTP-binding family protein [Arabidopsis thaliana]	323	342	1.00E-165	105.9	92.9	96.3	Ras-related small GTP-binding family protein	gbpln	Arabidopsis thaliana	AT5G64813.1 | Symbols: LIP1 | Ras-related small GTP-binding family protein | chr5:25910836-25912625 FORWARD LENGTH=342	323	342	1.00E-168	105.9	92.9	96.3
Rsa1.0_00071.1.g3782.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00071.1.g3783.t1	ref|XP_002864926.1| hypothetical protein ARALYDRAFT_496705 [Arabidopsis lyrata subsp. lyrata] gi|297310761|gb|EFH41185.1| hypothetical protein ARALYDRAFT_496705 [Arabidopsis lyrata subsp. lyrata]	141	114	3.00E-40	80.9	63.1	65.2	hypothetical protein ARALYDRAFT_496705	gbpln	Arabidopsis lyrata	AT5G64850.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: RPM1-interacting protein 4, defence response (InterPro:IPR008700); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G09960.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:25921585-25923038 FORWARD LENGTH=114	141	114	1.00E-41	80.9	61.7	65.2
Rsa1.0_00071.1.g3784.t3	ref|NP_201291.1| 4-alpha-glucanotransferase-like protein [Arabidopsis thaliana] gi|75180614|sp|Q9LV91.1|DPE1_ARATH RecName: Full=4-alpha-glucanotransferase DPE1, chloroplastic/amyloplastic; AltName: Full=Amylomaltase; AltName: Full=Disproportionating enzyme; Short=D-enzyme; AltName: Full=Protein DISPROPORTIONATING ENZYME 1; Flags: Precursor gi|8843750|dbj|BAA97298.1| 4-alpha-glucanotransferase [Arabidopsis thaliana] gi|14335104|gb|AAK59831.1| AT5g64860/MXK3_9 [Arabidopsis thaliana] gi|19548067|gb|AAL87397.1| AT5g64860/MXK3_9 [Arabidopsis thaliana] gi|332010579|gb|AED97962.1| 4-alpha-glucanotransferase DPE1 [Arabidopsis thaliana]	579	576	0	99.5	85.3	89.8	4-alpha-glucanotransferase-like protein	gbpln	Arabidopsis thaliana	AT5G64860.1 | Symbols: DPE1 | disproportionating enzyme | chr5:25925373-25928788 REVERSE LENGTH=576	579	576	0	99.5	85.3	89.8
Rsa1.0_00071.1.g3785.t1	gb|EOA14807.1| hypothetical protein CARUB_v10028114mg [Capsella rubella]	297	335	1.00E-102	112.8	73.4	80.5	hypothetical protein CARUB_v10028114mg	gbpln	Capsella rubella	AT5G64920.1 | Symbols: CIP8 | COP1-interacting protein 8 | chr5:25944338-25945342 REVERSE LENGTH=334	297	334	2.00E-98	112.5	76.4	82.2
Rsa1.0_00071.1.g3786.t1	gb|EOA13275.1| hypothetical protein CARUB_v10026304mg [Capsella rubella]	483	486	0	100.6	88.0	94.0	hypothetical protein CARUB_v10026304mg	gbpln	Capsella rubella	AT5G65380.1 | Symbols: | MATE efflux family protein | chr5:26123241-26126352 REVERSE LENGTH=486	483	486	0	100.6	87.2	93.0
Rsa1.0_00071.1.g3787.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00071.1.g3788.t1	ref|XP_002866670.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312505|gb|EFH42929.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	288	305	1.00E-137	105.9	84.7	90.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G65420.1 | Symbols: CYCD4;1 | CYCLIN D4;1 | chr5:26141592-26143750 REVERSE LENGTH=308	288	308	1.00E-134	106.9	84.4	88.9
Rsa1.0_00071.1.g3789.t1	gb|EOA13890.1| hypothetical protein CARUB_v10026999mg [Capsella rubella]	248	248	1.00E-136	100.0	94.4	98.0	hypothetical protein CARUB_v10026999mg	gbpln	Capsella rubella	AT5G65430.1 | Symbols: GRF8, 14-3-3KAPPA, GF14 KAPPA | general regulatory factor 8 | chr5:26148546-26150255 REVERSE LENGTH=248	248	248	1.00E-138	100.0	94.4	98.0

Rsa1.0_00071.1.g3790.t1	gb|EOA12401.1| hypothetical protein CARUB_v10027313mg [Capsella rubella]	165	149	1.00E-30	90.3	53.3	60.0	hypothetical protein CARUB_v10027313mg	gbpln	Capsella rubella	AT5G65480.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G38060.2); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:26176827-26177434 FORWARD LENGTH=153	165	153	2.00E-31	92.7	49.1	53.3
Rsa1.0_00071.1.g3791.t1	gb|EOA12374.1| hypothetical protein CARUB_v10025893mg, partial [Capsella rubella]	788	825	0	104.7	84.0	91.9	hypothetical protein CARUB_v10025893mg, partial	gbpln	Capsella rubella	AT5G65500.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:26181093-26183997 REVERSE LENGTH=791	788	791	0	100.4	81.6	90.1
Rsa1.0_00071.1.g3792.t1	ref|NP_201355.1| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana] gi|8978280|dbj|BAA98171.1| unnamed protein product [Arabidopsis thaliana] gi|26453066|dbj|BAC43609.1| unknown protein [Arabidopsis thaliana] gi|28973455|gb|AAO64052.1| unknown protein [Arabidopsis thaliana] gi|332010683|gb|AED98066.1| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana]	181	206	9.00E-94	113.8	93.4	97.8	tetratricopeptide repeat domain-containing protein	gbpln	Arabidopsis thaliana	AT5G65520.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:26189876-26190496 REVERSE LENGTH=206	181	206	4.00E-96	113.8	93.4	97.8
Rsa1.0_00071.1.g3793.t1	dbj|BAJ34054.1| unnamed protein product [Thellungiella halophila]	153	650	1.00E-16	424.8	35.3	39.2	unnamed protein product	----	----	AT5G02500.1 | Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 | heat shock cognate protein 70-1 | chr5:554055-556334 REVERSE LENGTH=651	153	651	2.00E-18	425.5	33.3	37.3
Rsa1.0_00071.1.g3794.t2	ref|NP_201353.4| U-box domain-containing protein kinase family protein [Arabidopsis thaliana] gi|332010681|gb|AED98064.1| U-box domain-containing protein kinase family protein [Arabidopsis thaliana]	180	791	1.00E-12	439.4	20.0	23.3	U-box domain-containing protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G65500.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:26181093-26183997 REVERSE LENGTH=791	180	791	4.00E-15	439.4	20.0	23.3
Rsa1.0_00071.1.g3795.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00071.1.g3796.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00071.1.g3797.t1	ref|XP_002864981.1| hypothetical protein ARALYDRAFT_496816 [Arabidopsis lyrata subsp. lyrata] gi|297310816|gb|EFH41240.1| hypothetical protein ARALYDRAFT_496816 [Arabidopsis lyrata subsp. lyrata]	361	374	1.00E-169	103.6	86.4	89.2	hypothetical protein ARALYDRAFT_496816	gbpln	Arabidopsis lyrata	AT5G65790.1 | Symbols: ATMYB68, MYB68 | myb domain protein 68 | chr5:26323035-26324385 FORWARD LENGTH=374	361	374	1.00E-164	103.6	85.9	88.4
Rsa1.0_00071.1.g3798.t1	ref|XP_002866689.1| hypothetical protein ARALYDRAFT_332796 [Arabidopsis lyrata subsp. lyrata] gi|297312524|gb|EFH42948.1| hypothetical protein ARALYDRAFT_332796 [Arabidopsis lyrata subsp. lyrata]	470	470	0	100.0	96.2	98.3	hypothetical protein ARALYDRAFT_332796	gbpln	Arabidopsis lyrata	AT5G65800.1 | Symbols: ACS5, CIN5, ETO2, ATACS5 | ACC synthase 5 | chr5:26331096-26332698 REVERSE LENGTH=470	470	470	0	100.0	96.2	98.7
Rsa1.0_00071.1.g3799.t1	gb|AAM65141.1| unknown [Arabidopsis thaliana]	261	258	1.00E-135	98.9	88.5	96.2	unknown	gbpln	Arabidopsis thaliana	AT5G65810.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G49720.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26337833-26339144 REVERSE LENGTH=258	261	258	1.00E-137	98.9	88.1	95.8
Rsa1.0_00071.1.g3800.t1	gb|EOA24531.1| hypothetical protein CARUB_v10017786mg [Capsella rubella]	281	282	1.00E-107	100.4	73.3	81.1	hypothetical protein CARUB_v10017786mg	gbpln	Capsella rubella	AT5G65830.1 | Symbols: ATRLP57, RLP57 | receptor like protein 57 | chr5:26342396-26343235 REVERSE LENGTH=279	281	279	1.00E-106	99.3	75.1	84.3
Rsa1.0_00071.1.g3801.t1	ref|XP_002866692.1| hypothetical protein ARALYDRAFT_496819 [Arabidopsis lyrata subsp. lyrata] gi|297312527|gb|EFH42951.1| hypothetical protein ARALYDRAFT_496819 [Arabidopsis lyrata subsp. lyrata]	267	265	1.00E-115	99.3	77.2	85.0	hypothetical protein ARALYDRAFT_496819	gbpln	Arabidopsis lyrata	AT5G65840.1 | Symbols: | Thioredoxin superfamily protein | chr5:26344097-26346057 REVERSE LENGTH=275	267	275	1.00E-114	103.0	76.4	84.3

Rsa1.0_00071.1.g3802.t1	ref|NP_201393.1| U-box domain-containing protein 31 [Arabidopsis thaliana] gi|75170648|sp|Q9FHN9.1|PUB31_ARATH RecName: Full=U-box domain-containing protein 31; AltName: Full=Plant U-box protein 31 gi|9759576|dbj|BAB11139.1| unnamed protein product [Arabidopsis thaliana] gi|332010740|gb|AED98123.1| U-box domain-containing protein 31 [Arabidopsis thaliana]	442	444	0	100.5	84.2	90.0	U-box domain-containing protein 31	gbpln	Arabidopsis thaliana	AT5G65920.1 | Symbols: | ARM repeat superfamily protein | chr5:26364323-26365657 REVERSE LENGTH=444	442	444	0	100.5	84.2	90.0
Rsa1.0_00071.1.g3803.t1	ref|NP_201563.1| uncharacterized protein [Arabidopsis thaliana] gi|9757883|dbj|BAB08470.1| unnamed protein product [Arabidopsis thaliana] gi|32815941|gb|AAP88355.1| At5g67620 [Arabidopsis thaliana] gi|110736456|dbj|BAF00196.1| hypothetical protein [Arabidopsis thaliana] gi|332010985|gb|AED98368.1| uncharacterized protein AT5G67620 [Arabidopsis thaliana]	177	182	3.00E-73	102.8	83.6	90.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G67620.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: microtubule; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G62900.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:26964891-26965720 REVERSE LENGTH=182	177	182	1.00E-75	102.8	83.6	90.4
Rsa1.0_00071.1.g3804.t1	ref|XP_002866696.1| hypothetical protein ARALYDRAFT_358798 [Arabidopsis lyrata subsp. lyrata] gi|297312531|gb|EFH42955.1| hypothetical protein ARALYDRAFT_358798 [Arabidopsis lyrata subsp. lyrata]	156	154	2.00E-75	98.7	91.0	94.2	hypothetical protein ARALYDRAFT_358798	gbpln	Arabidopsis lyrata	AT5G67590.1 | Symbols: FRO1 | NADH-ubiquinone oxidoreductase-related | chr5:26958073-26959356 FORWARD LENGTH=154	156	154	2.00E-75	98.7	88.5	92.3
Rsa1.0_00071.1.g3805.t1	gb|EOA13780.1| hypothetical protein CARUB_v10026874mg [Capsella rubella]	115	299	1.00E-30	260.0	70.4	75.7	hypothetical protein CARUB_v10026874mg	gbpln	Capsella rubella	AT5G67580.2 | Symbols: TRB2, ATTRB2, TBP3, ATTBP3 | Homeodomain-like/winged-helix DNA-binding family protein | chr5:26955843-26957073 REVERSE LENGTH=299	115	299	4.00E-27	260.0	65.2	70.4
Rsa1.0_00071.1.g3806.t1	ref|NP_201556.2| uncharacterized protein [Arabidopsis thaliana] gi|91807108|gb|ABE66281.1| unknown [Arabidopsis thaliana] gi|332010976|gb|AED98359.1| uncharacterized protein AT5G67550 [Arabidopsis thaliana]	509	509	0	100.0	81.9	89.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G67550.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; EXPRESSED DURING: 4 anthesis; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G71110.1); Has 161 Blast hits to 154 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 161; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:26946908-26949112 REVERSE LENGTH=509	509	509	0	100.0	81.9	89.8
Rsa1.0_00071.1.g3807.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	136	390	7.00E-27	286.8	44.9	61.8	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	136	295	6.00E-12	216.9	32.4	50.7
Rsa1.0_00071.1.g3808.t1	gb|AAW22622.1| porin-like protein [Brassica napus]	276	276	1.00E-152	100.0	97.5	98.9	porin-like protein	gbpln	Brassica napus	AT5G67500.1 | Symbols: VDAC2, ATVDAC2 | voltage dependent anion channel 2 | chr5:26935223-26937123 FORWARD LENGTH=276	276	276	1.00E-144	100.0	89.9	95.7
Rsa1.0_00071.1.g3809.t1	gb|AAB53260.1| zinc-finger protein-1 [Brassica rapa subsp. oleifera]	236	235	5.00E-86	99.6	79.2	84.3	zinc-finger protein-1	gbpln	Brassica rapa	AT5G67450.1 | Symbols: AZF1, ZF1 | zinc-finger protein 1 | chr5:26919142-26919879 REVERSE LENGTH=245	236	245	1.00E-82	103.8	76.3	79.7

Rsa1.0_00072.1.g3810.t1	ref|NP_564548.1| uncharacterized protein [Arabidopsis thaliana] gi|5430751|gb|AAD43151.1|AC007504_6 Unknown protein [Arabidopsis thaliana] gi|13926179|gb|AAK49571.1|AF370563_1 Unknown protein [Arabidopsis thaliana] gi|17381288|gb|AAL36062.1| At1g49500/F13F21_6 [Arabidopsis thaliana] gi|20453373|gb|AAM19925.1| At1g49500/F13F21_6 [Arabidopsis thaliana] gi|20466376|gb|AAM20505.1| unknown protein [Arabidopsis thaliana] gi|21592836|gb|AAM64786.1| unknown [Arabidopsis thaliana] gi|22136326|gb|AAM91241.1| unknown protein [Arabidopsis thaliana] gi|25083427|gb|AAN72075.1| expressed protein [Arabidopsis thaliana] gi|332194315|gb|AEE32436.1| uncharacterized protein AT1G49500 [Arabidopsis thaliana]	63	63	2.00E-21	100.0	79.4	93.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G49500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G19030.1); Has 24 Blast hits to 24 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18321988-18322179 REVERSE LENGTH=63	63	63	4.00E-24	100.0	79.4	93.7
Rsa1.0_00072.1.g3811.t1	ref|XP_002893547.1| peptidase C1A papain family protein [Arabidopsis lyrata subsp. lyrata] gi|297339389|gb|EFH69806.1| peptidase C1A papain family protein [Arabidopsis lyrata subsp. lyrata]	106	345	1.00E-39	325.5	70.8	81.1	peptidase C1A papain family protein	gbpln	Arabidopsis lyrata	AT1G29080.1 | Symbols: | Papain family cysteine protease | chr1:10157494-10158674 REVERSE LENGTH=346	106	346	1.00E-40	326.4	67.9	80.2
Rsa1.0_00072.1.g3812.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3813.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3814.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3815.t1	#	#	#	#	#	#	#	-	----	----	AT5G08380.1 | Symbols: AtAGAL1, AGAL1 | alpha-galactosidase 1 | chr5:2694851-2697616 REVERSE LENGTH=410	40	410	1.00E-12	1025.0	75.0	82.5
Rsa1.0_00072.1.g3816.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3817.t1	gb|EOA32197.1| hypothetical protein CARUB_v10015453mg [Capsella rubella]	208	552	1.00E-24	265.4	25.0	39.9	hypothetical protein CARUB_v10015453mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	208	566	5.00E-18	272.1	22.1	34.6
Rsa1.0_00072.1.g3818.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	409	1333	2.00E-77	325.9	42.1	58.4	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254 .1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	409	626	2.00E-19	153.1	19.6	32.0
Rsa1.0_00072.1.g3819.t1	ref|XP_002893547.1| peptidase C1A papain family protein [Arabidopsis lyrata subsp. lyrata] gi|297339389|gb|EFH69806.1| peptidase C1A papain family protein [Arabidopsis lyrata subsp. lyrata]	300	345	1.00E-107	115.0	63.0	78.0	peptidase C1A papain family protein	gbpln	Arabidopsis lyrata	AT1G29080.1 | Symbols: | Papain family cysteine protease | chr1:10157494-10158674 REVERSE LENGTH=346	300	346	1.00E-108	115.3	62.7	78.7
Rsa1.0_00072.1.g3820.t1	gb|AAZ41812.1| 01P13-2 [Brassica rapa subsp. pekinensis]	340	558	1.00E-75	164.1	48.2	63.5	01P13-2	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3821.t1	gb|AAG10812.1|AC018460_6 Putative retroelement polyprotein [Arabidopsis thaliana]	664	1404	0	211.4	64.5	77.0	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	664	1262	2.00E-94	190.1	29.1	40.1
Rsa1.0_00072.1.g3822.t1	ref|XP_002894196.1| nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] gi|297340038|gb|EFH70455.1| nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	838	839	0	100.1	88.8	93.6	nucleotide binding protein	gbpln	Arabidopsis lyrata	AT1G49540.2 | Symbols: ELP2, AtELP2 | elongator protein 2 | chr1:18333767-18337382 REVERSE LENGTH=840	838	840	0	100.2	87.8	92.6
Rsa1.0_00072.1.g3823.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3824.t1	ref|XP_002891521.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337363|gb|EFH67780.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	628	350	1.00E-176	55.7	48.9	51.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G49570.1 | Symbols: | Peroxidase superfamily protein | chr1:18347077-18348712 FORWARD LENGTH=350	628	350	1.00E-178	55.7	48.9	51.8

Rsa1.0_00072.1.g3825.t1	ref|NP_175381.1| putative calcium-dependent protein kinase [Arabidopsis thaliana] gi|75334455|sp|Q9FX86.1|CAMK8_ARATH RecName: Full=CDPK-related kinase 8; Short=AtCRK8; AltName: Full=Calcium/calmodulin-dependent protein kinase CRK8 gi|10120419|gb|AAG13044.1|AC011807_3 Putative CDPK-related protein kinase [Arabidopsis thaliana] gi|37202008|gb|AAQ89619.1| At1g49580 [Arabidopsis thaliana] gi|110738705|dbj|BAF01277.1| putative CDPK-related protein kinase [Arabidopsis thaliana] gi|332194323|gb|AEE32444.1| CDPK-related kinase 8 [Arabidopsis thaliana]	594	606	0	102.0	89.9	93.8	putative calcium-dependent protein kinase	gbpln	Arabidopsis thaliana	AT1G49580.1 | Symbols: | Calcium-dependent protein kinase (CDPK) family protein | chr1:18351611-18354384 FORWARD LENGTH=606	594	606	0	102.0	89.9	93.8
Rsa1.0_00072.1.g3826.t1	dbj|BAB09912.1| MADS-box protein-like [Arabidopsis thaliana]	347	368	6.00E-47	106.1	32.0	43.5	MADS-box protein-like	gbpln	Arabidopsis thaliana	AT5G49420.1 | Symbols: | MADS-box transcription factor family protein | chr5:20035166-20036170 REVERSE LENGTH=334	347	334	2.00E-49	96.3	32.0	43.5
Rsa1.0_00072.1.g3827.t1	gb|AAG50652.1|AC073433_4 transposase, putative [Arabidopsis thaliana]	81	659	2.00E-23	813.6	66.7	82.7	transposase, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3828.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3829.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	215	414	1.00E-17	192.6	20.9	23.7	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3830.t1	gb|EOA14700.1| hypothetical protein CARUB_v10027975mg [Capsella rubella]	396	766	1.00E-124	193.4	59.8	75.5	hypothetical protein CARUB_v10027975mg	gbpln	Capsella rubella	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	396	769	1.00E-126	194.2	60.6	75.0
Rsa1.0_00072.1.g3831.t1	ref|XP_002894219.1| hypothetical protein ARALYDRAFT_474111 [Arabidopsis lyrata subsp. lyrata] gi|297340061|gb|EFH70478.1| hypothetical protein ARALYDRAFT_474111 [Arabidopsis lyrata subsp. lyrata]	112	102	4.00E-32	91.1	67.0	76.8	hypothetical protein ARALYDRAFT_474111	gbpln	Arabidopsis lyrata	AT1G49800.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: sepal, male gametophyte, stamen; EXPRESSED DURING: 4 anthesis; Has 12 Blast hits to 12 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18438550-18438876 REVERSE LENGTH=108	112	108	2.00E-29	96.4	65.2	80.4
Rsa1.0_00072.1.g3832.t1	gb|AAP53216.2| retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa Japonica Group]	440	1262	1.00E-64	286.8	35.0	43.6	retrotransposon protein, putative, Ty1-copia subclass	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	440	1262	2.00E-23	286.8	16.4	24.3
Rsa1.0_00072.1.g3833.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1667	1274	0	76.4	29.8	41.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1667	575	1.00E-48	34.5	6.5	10.4
Rsa1.0_00072.1.g3834.t1	ref|XP_002894216.1| U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297340058|gb|EFH70475.1| U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata]	424	421	0	99.3	88.9	95.0	U-box domain-containing protein	gbpln	Arabidopsis lyrata	AT1G49780.1 | Symbols: PUB26 | plant U-box 26 | chr1:18429024-18430289 REVERSE LENGTH=421	424	421	0	99.3	87.7	94.6
Rsa1.0_00072.1.g3835.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	318	1557	2.00E-15	489.6	17.6	30.5	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00072.1.g3836.t1	ref|NP_178819.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|3327395|gb|AAC26677.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana] gi|330251037|gb|AEC06131.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	338	530	4.00E-42	156.8	23.4	30.5	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	338	530	1.00E-44	156.8	23.4	30.5
Rsa1.0_00072.1.g3837.t1	ref|NP_188563.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|11994454|dbj|BAB02456.1| unnamed protein product [Arabidopsis thaliana] gi|332642702|gb|AEE76223.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	489	493	1.00E-165	100.8	68.7	77.1	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G19320.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:6696395-6698073 REVERSE LENGTH=493	489	493	1.00E-168	100.8	68.7	77.1

Rsa1.0_00073.1.g3838.t1	gb|AAC35532.1| contains similarity to proteases [Arabidopsis thaliana]	1351	1392	0	103.0	55.5	70.0	contains similarity to proteases	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1351	1262	1.00E-112	93.4	13.8	22.3
Rsa1.0_00073.1.g3839.t1	ref|NP_001190617.1| K-box region and MADS-box transcription factor family protein [Arabidopsis thaliana] gi|332010614|gb|AED97997.1| K-box region and MADS-box transcription factor family protein [Arabidopsis thaliana]	67	232	7.00E-22	346.3	74.6	89.6	K-box region and MADS-box transcription factor family protein	gbpln	Arabidopsis thaliana	AT5G65070.3 | Symbols: MAF4 | K-box region and MADS-box transcription factor family protein | chr5:25992310-25995930 FORWARD LENGTH=232	67	232	1.00E-24	346.3	74.6	89.6
Rsa1.0_00073.1.g3840.t1	gb|EOA35746.1| hypothetical protein CARUB_v10020979mg [Capsella rubella]	173	197	1.00E-30	113.9	48.0	59.5	hypothetical protein CARUB_v10020979mg	gbpln	Capsella rubella	AT5G65070.1 | Symbols: MAF4, FCL4, AGL69 | K-box region and MADS-box transcription factor family protein | chr5:25992310-25995930 FORWARD LENGTH=200	173	200	4.00E-32	115.6	48.6	58.4
Rsa1.0_00073.1.g3841.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00073.1.g3842.t5	gb|EOA12728.1| hypothetical protein CARUB_v10028173mg [Capsella rubella]	211	197	5.00E-72	93.4	69.2	80.1	hypothetical protein CARUB_v10028173mg	gbpln	Capsella rubella	AT5G65070.1 | Symbols: MAF4, FCL4, AGL69 | K-box region and MADS-box transcription factor family protein | chr5:25992310-25995930 FORWARD LENGTH=200	211	200	2.00E-73	94.8	68.2	79.1
Rsa1.0_00073.1.g3843.t2	ref|XP_002864939.1| hypothetical protein ARALYDRAFT_332725 [Arabidopsis lyrata subsp. lyrata] gi|297310774|gb|EFH41198.1| hypothetical protein ARALYDRAFT_332725 [Arabidopsis lyrata subsp. lyrata]	554	527	0	95.1	80.3	85.0	hypothetical protein ARALYDRAFT_332725	gbpln	Arabidopsis lyrata	AT5G65090.1 | Symbols: MRH3, BST1, DER4 | DNAse I-like superfamily protein | chr5:26004282-26006656 FORWARD LENGTH=529	554	529	0	95.5	79.2	84.1
Rsa1.0_00073.1.g3844.t1	ref|XP_002864941.1| hypothetical protein ARALYDRAFT_919839 [Arabidopsis lyrata subsp. lyrata] gi|297310776|gb|EFH41200.1| hypothetical protein ARALYDRAFT_919839 [Arabidopsis lyrata subsp. lyrata]	272	286	5.00E-98	105.1	69.1	80.5	hypothetical protein ARALYDRAFT_919839	gbpln	Arabidopsis lyrata	AT5G65130.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:26017403-26018236 FORWARD LENGTH=277	272	277	6.00E-98	101.8	71.3	80.9
Rsa1.0_00073.1.g3845.t1	gb|EOA13558.1| hypothetical protein CARUB_v10026620mg [Capsella rubella]	375	369	0	98.4	84.5	90.4	hypothetical protein CARUB_v10026620mg	gbpln	Capsella rubella	AT5G65140.1 | Symbols: TPPJ | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:26019878-26022077 REVERSE LENGTH=370	375	370	0	98.7	85.3	90.1
Rsa1.0_00073.1.g3846.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00073.1.g3847.t1	gb|EOA14828.1| hypothetical protein CARUB_v10028138mg [Capsella rubella]	174	175	1.00E-80	100.6	79.9	85.6	hypothetical protein CARUB_v10028138mg	gbpln	Capsella rubella	AT5G65158.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr5:26030390-26030704 FORWARD LENGTH=104	174	104	3.00E-56	59.8	56.9	58.6
Rsa1.0_00073.1.g3848.t1	ref|NP_680465.2| succinate dehydrogenase [ubiquinone] iron-sulfur subunit 3 [Arabidopsis thaliana] gi|75262571|sp|Q9FJP9.1|DHSB3_ARATH RecName: Full=Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 3, mitochondrial; AltName: Full=Iron-sulfur subunit of complex II; Short=Ip; Flags: Precursor gi|10178178|dbj|BAB11652.1| succinate dehydrogenase iron-sulfur protein-like [Arabidopsis thaliana] gi|12049602|emb|CAC19857.1| mitochondrial succinate dehydrogenase iron-sulphur subunit [Arabidopsis thaliana] gi|332010628|gb|AED98011.1| succinate dehydrogenase [ubiquinone] iron-sulfur subunit 3 [Arabidopsis thaliana]	306	309	1.00E-163	101.0	89.5	93.8	succinate dehydrogenase	gbpln	Arabidopsis thaliana	AT5G65165.1 | Symbols: SDH2-3 | succinate dehydrogenase 2-3 | chr5:26034515-26035922 REVERSE LENGTH=309	306	309	1.00E-165	101.0	89.5	93.8
Rsa1.0_00073.1.g3849.t1	ref|NP_201321.1| VQ motif-containing protein [Arabidopsis thaliana] gi|10178179|dbj|BAB11653.1| unnamed protein product [Arabidopsis thaliana] gi|44917435|gb|AAS49042.1| At5g65170 [Arabidopsis thaliana] gi|46931270|gb|AAT06439.1| At5g65170 [Arabidopsis thaliana] gi|332010630|gb|AED98013.1| VQ motif-containing protein [Arabidopsis thaliana]	335	362	1.00E-105	108.1	70.4	78.5	VQ motif-containing protein	gbpln	Arabidopsis thaliana	AT5G65170.1 | Symbols: | VQ motif-containing protein | chr5:26041218-26042306 FORWARD LENGTH=362	335	362	1.00E-107	108.1	70.4	78.5

Rsa1.0_00073.1.g3850.t1	ref|XP_002866656.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297312491|gb|EFH42915.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	544	547	0	100.6	83.3	89.7	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT5G65200.1 | Symbols: PUB38, ATPUB38 | plant U-box 38 | chr5:26048173-26049843 REVERSE LENGTH=556	544	556	0	102.2	83.5	90.8
Rsa1.0_00073.1.g3851.t1	ref|XP_002866657.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297312492|gb|EFH42916.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	285	285	1.00E-145	100.0	87.4	92.6	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT5G65205.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:26050926-26052017 REVERSE LENGTH=285	285	285	1.00E-144	100.0	85.6	91.6
Rsa1.0_00073.1.g3852.t1	ref|NP_680466.1| uncharacterized protein [Arabidopsis thaliana] gi|19347918|gb|AAL85980.1| unknown protein [Arabidopsis thaliana] gi|21689793|gb|AAM67540.1| unknown protein [Arabidopsis thaliana] gi|26453218|dbj|BAC43683.1| unknown protein [Arabidopsis thaliana] gi|332010635|gb|AED98018.1| uncharacterized protein AT5G65207 [Arabidopsis thaliana]	72	73	3.00E-21	101.4	72.2	84.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G65207.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G10040.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26052364-26052585 REVERSE LENGTH=73	72	73	4.00E-24	101.4	72.2	84.7
Rsa1.0_00073.1.g3853.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00073.1.g3854.t1	gb|ACU32463.1| TGA2 protein [Brassica rapa subsp. pekinensis]	370	367	0	99.2	89.7	93.8	TGA2 protein	gbpln	Brassica rapa	AT5G65210.5 | Symbols: TGA1 | bZIP transcription factor family protein | chr5:26059031-26060749 FORWARD LENGTH=368	370	368	0	99.5	87.6	94.3
Rsa1.0_00073.1.g3855.t1	ref|XP_004288191.1| PREDICTED: 50S ribosomal protein L29, chloroplastic-like [Fragaria vesca subsp. vesca]	94	174	2.00E-16	185.1	45.7	59.6	PREDICTED: 50S ribosomal protein L29, chloroplastic-like	gbpln	Fragaria vesca	AT5G65220.1 | Symbols: | Ribosomal L29 family protein | chr5:26061301-26062506 FORWARD LENGTH=173	94	173	2.00E-18	184.0	47.9	57.4
Rsa1.0_00073.1.g3856.t1	ref|XP_002866660.1| hypothetical protein ARALYDRAFT_496756 [Arabidopsis lyrata subsp. lyrata] gi|297312495|gb|EFH42919.1| hypothetical protein ARALYDRAFT_496756 [Arabidopsis lyrata subsp. lyrata]	279	299	1.00E-108	107.2	77.4	84.6	hypothetical protein ARALYDRAFT_496756	gbpln	Arabidopsis lyrata	AT5G65250.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26078699-26080051 REVERSE LENGTH=300	279	300	1.00E-110	107.5	77.1	85.3
Rsa1.0_00073.1.g3857.t1	gb|EOA12395.1| hypothetical protein CARUB_v10027046mg, partial [Capsella rubella]	211	233	1.00E-105	110.4	89.6	93.4	hypothetical protein CARUB_v10027046mg, partial	gbpln	Capsella rubella	AT5G65260.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:26080501-26082984 REVERSE LENGTH=220	211	220	1.00E-105	104.3	91.5	96.2
Rsa1.0_00073.1.g3858.t1	ref|XP_002864951.1| LMBR1 integral membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|297310786|gb|EFH41210.1| LMBR1 integral membrane family protein [Arabidopsis lyrata subsp. lyrata]	733	733	0	100.0	91.8	95.8	LMBR1 integral membrane family protein	gbpln	Arabidopsis lyrata	AT5G65290.1 | Symbols: | LMBR1-like membrane protein | chr5:26089814-26094337 FORWARD LENGTH=733	733	733	0	100.0	91.8	95.5
Rsa1.0_00073.1.g3859.t1	ref|XP_002866663.1| hypothetical protein ARALYDRAFT_496763 [Arabidopsis lyrata subsp. lyrata] gi|297312498|gb|EFH42922.1| hypothetical protein ARALYDRAFT_496763 [Arabidopsis lyrata subsp. lyrata]	149	150	4.00E-37	100.7	65.1	76.5	hypothetical protein ARALYDRAFT_496763	gbpln	Arabidopsis lyrata	AT5G65300.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26095266-26095718 REVERSE LENGTH=150	149	150	9.00E-30	100.7	61.7	73.8
Rsa1.0_00073.1.g3860.t1	gb|EOA13730.1| hypothetical protein CARUB_v10026808mg [Capsella rubella]	312	315	1.00E-133	101.0	83.3	88.5	hypothetical protein CARUB_v10026808mg	gbpln	Capsella rubella	AT5G65310.1 | Symbols: ATHB5, ATHB-5, HB5 | homeobox protein 5 | chr5:26102457-26104217 REVERSE LENGTH=312	312	312	1.00E-135	100.0	82.7	89.4
Rsa1.0_00073.1.g3861.t1	gb|EOA14656.1| hypothetical protein CARUB_v10027920mg [Capsella rubella]	257	293	3.00E-86	114.0	68.9	82.1	hypothetical protein CARUB_v10027920mg	gbpln	Capsella rubella	AT5G65320.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:26107368-26108640 REVERSE LENGTH=296	257	296	1.00E-82	115.2	69.3	80.9
Rsa1.0_00073.1.g3862.t1	ref|NP_201336.1| protein agamous-like 78 [Arabidopsis thaliana] gi|9759613|dbj|BAB11555.1| unnamed protein product [Arabidopsis thaliana] gi|32402412|gb|AAN52788.1| MADS-box protein AGL78 [Arabidopsis thaliana] gi|332010657|gb|AED98040.1| protein agamous-like 78 [Arabidopsis thaliana]	339	341	1.00E-71	100.6	50.7	63.4	protein agamous-like 78	gbpln	Arabidopsis thaliana	AT5G65330.1 | Symbols: AGL78 | AGAMOUS-like 78 | chr5:26110326-26111351 FORWARD LENGTH=341	339	341	3.00E-74	100.6	50.7	63.4
Rsa1.0_00073.1.g3863.t1	gb|AAD32950.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	258	773	3.00E-26	299.6	29.1	43.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	258	575	2.00E-15	222.9	29.8	45.7

Rsa1.0_00073.1.g3864.t1	ref|NP_201337.1| uncharacterized protein [Arabidopsis thaliana] gi|9759614|dbj|BAB11556.1| unnamed protein product [Arabidopsis thaliana] gi|34146816|gb|AAQ62416.1| At5g65340 [Arabidopsis thaliana] gi|51969418|dbj|BAD43401.1| putative protein [Arabidopsis thaliana] gi|332010658|gb|AED98041.1| uncharacterized protein AT5G65340 [Arabidopsis thaliana]	251	253	1.00E-118	100.8	86.1	94.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G65340.1 | Symbols: | Protein of unknown function, DUF617 | chr5:26113684-26114445 REVERSE LENGTH=253	251	253	1.00E-121	100.8	86.1	94.0
Rsa1.0_00073.1.g3865.t1	tpg|DAA55311.1| TPA: histone H3.2 [Zea mays]	136	245	1.00E-72	180.1	100.0	100.0	TPA: histone H3.2	gbenv/gbpln	Zea mays	AT5G65360.1 | Symbols: | Histone superfamily protein | chr5:26120099-26120509 REVERSE LENGTH=136	136	136	5.00E-74	100.0	100.0	100.0
Rsa1.0_00073.1.g3866.t1	ref|XP_002864953.1| hypothetical protein ARALYDRAFT_358736 [Arabidopsis lyrata subsp. lyrata] gi|297310788|gb|EFH41212.1| hypothetical protein ARALYDRAFT_358736 [Arabidopsis lyrata subsp. lyrata]	293	295	1.00E-122	100.7	73.0	84.0	hypothetical protein ARALYDRAFT_358736	gbpln	Arabidopsis lyrata	AT5G65370.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr5:26121708-26122749 FORWARD LENGTH=295	293	295	1.00E-118	100.7	70.6	80.9
Rsa1.0_00073.1.g3867.t1	gb|EOA13275.1| hypothetical protein CARUB_v10026304mg [Capsella rubella]	301	486	1.00E-139	161.5	84.1	92.0	hypothetical protein CARUB_v10026304mg	gbpln	Capsella rubella	AT5G65380.1 | Symbols: | MATE efflux family protein | chr5:26123241-26126352 REVERSE LENGTH=486	301	486	1.00E-141	161.5	84.1	92.0
Rsa1.0_00073.1.g3868.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00073.1.g3869.t1	gb|EOA13872.1| hypothetical protein CARUB_v10026973mg [Capsella rubella]	258	261	1.00E-110	101.2	77.9	86.4	hypothetical protein CARUB_v10026973mg	gbpln	Capsella rubella	AT5G65400.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:26131448-26133062 FORWARD LENGTH=252	258	252	1.00E-106	97.7	77.5	86.4
Rsa1.0_00073.1.g3870.t1	dbj|BAJ34581.1| unnamed protein product [Thellungiella halophila]	262	286	3.00E-98	109.2	82.4	88.2	unnamed protein product	----	----	AT5G65410.1 | Symbols: ATHB25, ZFHD2, HB25, ZHD1 | homeobox protein 25 | chr5:26136179-26137018 FORWARD LENGTH=279	262	279	8.00E-92	106.5	77.5	83.2
Rsa1.0_00073.1.g3871.t3	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	356	1311	1.00E-28	368.3	33.7	43.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	356	303	5.00E-26	85.1	21.1	34.3
Rsa1.0_00073.1.g3872.t1	ref|XP_002864958.1| hypothetical protein ARALYDRAFT_496780 [Arabidopsis lyrata subsp. lyrata] gi|297310793|gb|EFH41217.1| hypothetical protein ARALYDRAFT_496780 [Arabidopsis lyrata subsp. lyrata]	506	504	0	99.6	91.5	94.9	hypothetical protein ARALYDRAFT_496780	gbpln	Arabidopsis lyrata	AT5G65470.1 | Symbols: | O-fucosyltransferase family protein | chr5:26172432-26174904 FORWARD LENGTH=504	506	504	0	99.6	90.7	94.9
Rsa1.0_00073.1.g3873.t1	gb|AAL87313.1| unknown protein [Arabidopsis thaliana]	89	645	9.00E-24	724.7	60.7	64.0	unknown protein	gbpln	Arabidopsis thaliana	AT5G65490.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: SGT1 (InterPro:IPR010770); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:26178003-26180309 REVERSE LENGTH=643	89	643	1.00E-26	722.5	60.7	64.0
Rsa1.0_00073.1.g3874.t1	gb|EOA30867.1| hypothetical protein CARUB_v10014010mg [Capsella rubella]	403	366	1.00E-148	90.8	65.0	73.9	hypothetical protein CARUB_v10014010mg	gbpln	Capsella rubella	AT3G57640.1 | Symbols: | Protein kinase superfamily protein | chr3:21344921-21345991 REVERSE LENGTH=356	403	356	3.00E-86	88.3	45.9	57.6
Rsa1.0_00073.1.g3875.t1	ref|NP_201356.2| protein kinase family protein [Arabidopsis thaliana] gi|332010684|gb|AED98067.1| protein kinase family protein [Arabidopsis thaliana]	470	456	0	97.0	84.9	90.6	protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G65530.1 | Symbols: | Protein kinase superfamily protein | chr5:26190844-26192826 REVERSE LENGTH=456	470	456	0	97.0	84.9	90.6
Rsa1.0_00073.1.g3876.t1	ref|NP_201362.1| Dof zinc finger protein DOF5.7 [Arabidopsis thaliana] gi|55583993|sp|Q9LSL6.1|DOF57_ARATH RecName: Full=Dof zinc finger protein DOF5.7; Short=AtDOF5.7 gi|8978287|dbj|BAA98178.1| DOF zinc finger protein-like [Arabidopsis thaliana] gi|50198797|gb|AAT70432.1| At5g65590 [Arabidopsis thaliana] gi|52421291|gb|AAU45215.1| At4g35930 [Arabidopsis thaliana] gi|225879166|dbj|BAH30653.1| hypothetical protein [Arabidopsis thaliana] gi|332010691|gb|AED98074.1| Dof zinc finger protein DOF5.7 [Arabidopsis thaliana]	288	316	1.00E-119	109.7	80.6	87.2	Dof zinc finger protein DOF5.7	gbpln	Arabidopsis thaliana	AT5G65590.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr5:26212084-26213034 REVERSE LENGTH=316	288	316	1.00E-122	109.7	80.6	87.2

Rsa1.0_00073.1.g3877.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00074.1.g3878.t1	dbj|BAB11288.1| unnamed protein product [Arabidopsis thaliana]	955	978	0	102.4	66.0	76.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT1G66880.1 | Symbols: | Protein kinase superfamily protein | chr1:24946928-24955438 FORWARD LENGTH=1296	955	1296	0	135.7	53.5	67.1
Rsa1.0_00074.1.g3879.t1	gb|AAC26241.1| F9D12.15 gene product [Arabidopsis thaliana]	789	850	1.00E-111	107.7	34.5	49.3	F9D12.15 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00074.1.g3880.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00074.1.g3881.t1	ref|XP_002870862.1| hypothetical protein ARALYDRAFT_494160 [Arabidopsis lyrata subsp. lyrata] gi|297316698|gb|EFH47121.1| hypothetical protein ARALYDRAFT_494160 [Arabidopsis lyrata subsp. lyrata]	427	436	0	102.1	90.4	96.5	hypothetical protein ARALYDRAFT_494160	gbpln	Arabidopsis lyrata	AT5G38200.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr5:15256383-15258474 FORWARD LENGTH=436	427	436	0	102.1	89.9	96.3
Rsa1.0_00074.1.g3882.t1	ref|NP_198631.2| plastid movement impaired 15 protein [Arabidopsis thaliana] gi|334302885|sp|Q9FF41.3|PMI15_ARATH RecName: Full=Protein PLASTID MOVEMENT IMPAIRED 15 gi|332006890|gb|AED94273.1| plastid movement impaired 15 protein [Arabidopsis thaliana]	573	579	1.00E-157	101.0	60.9	75.9	plastid movement impaired 15 protein	gbpln	Arabidopsis thaliana	AT5G38150.1 | Symbols: PMI15 | Plant protein of unknown function (DUF827) | chr5:15223116-15224950 REVERSE LENGTH=579	573	579	1.00E-160	101.0	60.9	75.9
Rsa1.0_00074.1.g3883.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1225	1529	0	124.8	34.6	46.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1225	746	1.00E-86	60.9	13.8	19.0
Rsa1.0_00074.1.g3884.t1	ref|NP_198630.2| nuclear transcription factor Y subunit C-10 [Arabidopsis thaliana] gi|75221594|sp|Q58CM8.1|NFYCA_ARATH RecName: Full=Nuclear transcription factor Y subunit C-10; Short=AtNF-YC-10 gi|61656131|gb|AAX49368.1| At5g38140 [Arabidopsis thaliana] gi|107738227|gb|ABF83665.1| At5g38140 [Arabidopsis thaliana] gi|332006889|gb|AED94272.1| nuclear transcription factor Y subunit C-10 [Arabidopsis thaliana]	218	195	3.00E-56	89.4	54.1	64.7	nuclear transcription factor Y subunit C-10	gbpln	Arabidopsis thaliana	AT5G38140.1 | Symbols: NF-YC12 | nuclear factor Y, subunit C12 | chr5:15220377-15222025 REVERSE LENGTH=195	218	195	9.00E-59	89.4	54.1	64.7
Rsa1.0_00074.1.g3885.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00074.1.g3886.t1	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	436	703	8.00E-70	161.2	30.7	36.0	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00074.1.g3887.t1	gb|EOA26039.1| hypothetical protein CARUB_v10019447mg [Capsella rubella]	437	442	0	101.1	74.8	84.4	hypothetical protein CARUB_v10019447mg	gbpln	Capsella rubella	AT5G38130.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:15217956-15219344 REVERSE LENGTH=462	437	462	0	105.7	74.1	85.1
Rsa1.0_00074.1.g3888.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00074.1.g3889.t1	gb|ABV21212.1| Ty1_Copia-element protein [Arabidopsis thaliana]	473	438	1.00E-85	92.6	35.7	53.1	Ty1_Copia-element protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	473	746	1.00E-55	157.7	28.1	42.9
Rsa1.0_00074.1.g3890.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00074.1.g3891.t1	dbj|BAB02625.1| unnamed protein product [Arabidopsis thaliana]	395	420	2.00E-85	106.3	47.8	61.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G28223.1 | Symbols: | F-box family protein | chr3:10527669-10528921 REVERSE LENGTH=391	395	391	2.00E-76	99.0	42.0	58.2
Rsa1.0_00074.1.g3892.t1	dbj|BAC41800.2| putative disease resistance protein [Arabidopsis thaliana]	435	977	9.00E-91	224.6	46.9	62.8	putative disease resistance protein	gbpln	Arabidopsis thaliana	AT5G40910.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16395507-16399129 FORWARD LENGTH=1104	435	1104	2.00E-93	253.8	46.9	62.8
Rsa1.0_00074.1.g3893.t1	ref|XP_002868590.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314426|gb|EFH44849.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	786	624	0	79.4	57.8	66.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G41550.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16617232-16620785 REVERSE LENGTH=1085	786	1085	0	138.0	56.0	64.5
Rsa1.0_00074.1.g3894.t1	ref|XP_002870580.1| hypothetical protein ARALYDRAFT_915957 [Arabidopsis lyrata subsp. lyrata] gi|297316416|gb|EFH46839.1| hypothetical protein ARALYDRAFT_915957 [Arabidopsis lyrata subsp. lyrata]	329	286	4.00E-71	86.9	40.4	50.2	hypothetical protein ARALYDRAFT_915957	gbpln	Arabidopsis lyrata	AT5G37890.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr5:15090512-15091822 REVERSE LENGTH=286	329	286	9.00E-70	86.9	38.6	49.2
Rsa1.0_00074.1.g3895.t1	gb|AAC95173.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1231	1200	0	97.5	47.8	59.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1231	1262	9.00E-44	102.5	7.2	11.5

Rsa1.0_00074.1.g3896.t1	sp|O65780.1|GALE1_CYATE RecName: Full=UDP-glucose 4-epimerase GEPI42; AltName: Full=Galactowaldenase; AltName: Full=UDP-galactose 4-epimerase gi|3021355|emb|CAA06338.1| UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]	73	354	2.00E-21	484.9	64.4	69.9	RecName: Full=UDP-glucose 4-epimerase GEPI42; AltName: Full=Galactowaldenase; AltName: Full=UDP-galactose 4-epimerase gi|3021355|emb|CAA06338.1| UDP-galactose 4-epimerase	gbpln	Cyamopsis tetragonoloba	AT1G12780.1 | Symbols: UGE1, ATUGE1 | UDP-D-glucose/UDP-D-galactose 4-epimerase 1 | chr1:4356124-4358120 REVERSE LENGTH=351	73	351	6.00E-23	480.8	63.0	68.5
Rsa1.0_00074.1.g3897.t1	ref|XP_002870573.1| hypothetical protein ARALYDRAFT_355742 [Arabidopsis lyrata subsp. lyrata] gi|297316409|gb|EFH46832.1| hypothetical protein ARALYDRAFT_355742 [Arabidopsis lyrata subsp. lyrata]	242	267	2.00E-91	110.3	78.9	86.8	hypothetical protein ARALYDRAFT_355742	gbpln	Arabidopsis lyrata	AT5G37860.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:15069578-15070555 REVERSE LENGTH=262	242	262	1.00E-93	108.3	78.1	86.4
Rsa1.0_00074.1.g3898.t1	gb|ABE73472.1| putative pyridoxal kinase splice variant 1 [Brassica napus]	331	334	1.00E-171	100.9	91.2	92.7	putative pyridoxal kinase splice variant 1	gbpln	Brassica napus	AT5G37850.2 | Symbols: SOS4 | pfkB-like carbohydrate kinase family protein | chr5:15065621-15068783 FORWARD LENGTH=309	331	309	1.00E-168	93.4	88.5	91.8
Rsa1.0_00074.1.g3899.t2	dbj|BAB10363.1| unnamed protein product [Arabidopsis thaliana]	213	219	1.00E-65	102.8	64.8	72.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G37840.1 | Symbols: | BEST Arabidopsis thaliana protein match is: plastid movement impaired 2 (TAIR:AT1G66480.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:15062192-15063327 REVERSE LENGTH=214	213	214	4.00E-68	100.5	64.8	71.8
Rsa1.0_00075.1.g3900.t1	dbj|BAB59032.1| cytokinin synthase [Arabidopsis thaliana]	334	330	1.00E-172	98.8	87.7	94.9	cytokinin synthase	gbpln	Arabidopsis thaliana	AT5G19040.1 | Symbols: ATIPT5, IPT5 | isopentenyltransferase 5 | chr5:6362389-6363381 REVERSE LENGTH=330	334	330	1.00E-174	98.8	87.4	94.9
Rsa1.0_00075.1.g3901.t1	ref|XP_002880309.1| hypothetical protein ARALYDRAFT_483931 [Arabidopsis lyrata subsp. lyrata] gi|297326148|gb|EFH56568.1| hypothetical protein ARALYDRAFT_483931 [Arabidopsis lyrata subsp. lyrata]	74	492	4.00E-14	664.9	50.0	51.4	hypothetical protein ARALYDRAFT_483931	gbpln	Arabidopsis lyrata	AT2G47510.2 | Symbols: FUM1 | fumarase 1 | chr2:19498614-19502020 FORWARD LENGTH=492	74	492	7.00E-17	664.9	50.0	51.4
Rsa1.0_00075.1.g3902.t1	ref|NP_187269.1| ribosomal protein L34e-like protein [Arabidopsis thaliana] gi|6862922|gb|AAF30311.1|AC018907_11 unknown protein [Arabidopsis thaliana] gi|62867643|gb|AAY17425.1| At3g06180 [Arabidopsis thaliana] gi|90962960|gb|ABE02404.1| At3g06180 [Arabidopsis thaliana] gi|332640836|gb|AEE74357.1| ribosomal protein L34e-like protein [Arabidopsis thaliana]	221	241	1.00E-58	109.0	68.3	74.7	ribosomal protein L34e-like protein	gbpln	Arabidopsis thaliana	AT3G06180.1 | Symbols: | Ribosomal protein L34e superfamily protein | chr3:1871705-1873554 FORWARD LENGTH=241	221	241	3.00E-61	109.0	68.3	74.7
Rsa1.0_00075.1.g3903.t1	ref|NP_197403.2| mitochondrial editing factor 18 [Arabidopsis thaliana] gi|223635651|sp|P0C8Q8.1|PP394_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g19020, mitochondrial; Flags: Precursor gi|332005257|gb|AED92640.1| mitochondrial editing factor 18 [Arabidopsis thaliana]	696	685	0	98.4	82.8	90.7	mitochondrial editing factor 18	gbpln	Arabidopsis thaliana	AT5G19020.1 | Symbols: MEF18 | mitochondrial editing factor 18 | chr5:6352771-6354828 REVERSE LENGTH=685	696	685	0	98.4	82.8	90.7
Rsa1.0_00075.1.g3904.t1	ref|NP_197402.1| mitogen-activated protein kinase 16 [Arabidopsis thaliana] gi|114152844|sp|Q8W4J2.2|MPK16_ARATH RecName: Full=Mitogen-activated protein kinase 16; Short=AtMPK16; Short=MAP kinase 16 gi|332005256|gb|AED92639.1| mitogen-activated protein kinase 16 [Arabidopsis thaliana]	600	567	0	94.5	88.5	90.0	mitogen-activated protein kinase 16	gbpln	Arabidopsis thaliana	AT5G19010.1 | Symbols: MPK16 | mitogen-activated protein kinase 16 | chr5:6345096-6347676 REVERSE LENGTH=567	600	567	0	94.5	88.5	90.0

Rsa1.0_00075.1.g3905.t1	ref|NP_197401.2| BTB-POZ and math domain-containing protein [Arabidopsis thaliana] gi|75301130|sp|Q8L765.1|BPM1_ARATH RecName: Full=BTB/POZ and MATH domain-containing protein 1; AltName: Full=Protein BTB-POZ AND MATH DOMAIN 1; Short=AtBPM1 gi|22531225|gb|AAM97116.1| putative protein [Arabidopsis thaliana] gi|27311975|gb|AAO00953.1| putative protein [Arabidopsis thaliana] gi|332005254|gb|AED92637.1| BTB-POZ and math domain-containing protein [Arabidopsis thaliana]	425	407	0	95.8	76.0	81.6	BTB-POZ and math domain-containing protein	gbpln	Arabidopsis thaliana	AT5G19000.1 | Symbols: ATBPM1, BPM1 | BTB-POZ and MATH domain 1 | chr5:6342563-6344641 FORWARD LENGTH=407	425	407	0	95.8	76.0	81.6
Rsa1.0_00075.1.g3906.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00075.1.g3907.t1	gb|EOA19340.1| hypothetical protein CARUB_v10000220mg [Capsella rubella]	834	835	0	100.1	88.0	93.2	hypothetical protein CARUB_v10000220mg	gbpln	Capsella rubella	AT5G18980.1 | Symbols: | ARM repeat superfamily protein | chr5:6334944-6337943 REVERSE LENGTH=835	834	835	0	100.1	87.5	92.9
Rsa1.0_00075.1.g3908.t1	gb|EOA21686.1| hypothetical protein CARUB_v10002111mg [Capsella rubella]	170	170	9.00E-86	100.0	92.9	95.9	hypothetical protein CARUB_v10002111mg	gbpln	Capsella rubella	AT5G18970.1 | Symbols: | AWPM-19-like family protein | chr5:6333714-6334539 REVERSE LENGTH=171	170	171	6.00E-86	100.6	91.8	95.3
Rsa1.0_00075.1.g3909.t1	gb|EOA22563.1| hypothetical protein CARUB_v10003224mg [Capsella rubella]	507	486	0	95.9	70.4	81.7	hypothetical protein CARUB_v10003224mg	gbpln	Capsella rubella	AT5G18950.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:6328519-6329970 REVERSE LENGTH=483	507	483	0	95.3	68.4	80.1
Rsa1.0_00075.1.g3910.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00075.1.g3911.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00075.1.g3912.t1	gb|EOA22928.1| hypothetical protein CARUB_v10003664mg [Capsella rubella]	350	347	1.00E-170	99.1	86.0	93.1	hypothetical protein CARUB_v10003664mg	gbpln	Capsella rubella	AT5G18930.1 | Symbols: BUD2, SAMDC4 | Adenosylmethionine decarboxylase family protein | chr5:6312172-6313215 REVERSE LENGTH=347	350	347	1.00E-173	99.1	86.0	91.4
Rsa1.0_00075.1.g3913.t1	gb|EOA19930.1| hypothetical protein CARUB_v10000179mg [Capsella rubella]	1011	893	0	88.3	73.8	79.5	hypothetical protein CARUB_v10000179mg	gbpln	Capsella rubella	AT5G18860.1 | Symbols: | inosine-uridine preferring nucleoside hydrolase family protein | chr5:6291023-6295581 FORWARD LENGTH=890	1011	890	0	88.0	72.9	78.5
Rsa1.0_00075.1.g3914.t1	gb|EOA22613.1| hypothetical protein CARUB_v10003281mg [Capsella rubella]	62	96	2.00E-17	154.8	67.7	75.8	hypothetical protein CARUB_v10003281mg	gbpln	Capsella rubella	AT5G18850.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:6286896-6287272 FORWARD LENGTH=99	62	99	1.00E-18	159.7	69.4	74.2
Rsa1.0_00075.1.g3915.t1	ref|NP_568367.1| sugar transporter ERD6-like 16 [Arabidopsis thaliana] gi|118572295|sp|Q8LBI9.2|EDL16_ARATH RecName: Full=Sugar transporter ERD6-like 16 gi|17381265|gb|AAL36051.1| AT5g18840/F17K4_90 [Arabidopsis thaliana] gi|23309019|gb|AAN18269.1| At5g18840/F17K4_90 [Arabidopsis thaliana] gi|332005237|gb|AED92620.1| sugar transporter ERD6-like 16 [Arabidopsis thaliana]	488	482	0	98.8	88.7	92.0	sugar transporter ERD6-like 16	gbpln	Arabidopsis thaliana	AT5G18840.1 | Symbols: | Major facilitator superfamily protein | chr5:6282954-6286399 FORWARD LENGTH=482	488	482	0	98.8	88.7	92.0
Rsa1.0_00075.1.g3916.t1	dbj|BAJ34638.1| unnamed protein product [Thellungiella halophila]	784	803	0	102.4	87.0	93.0	unnamed protein product	----	----	AT5G18830.1 | Symbols: SPL7, ATSPL7 | squamosa promoter binding protein-like 7 | chr5:6276116-6280227 FORWARD LENGTH=801	784	801	0	102.2	83.9	90.4
Rsa1.0_00075.1.g3917.t1	#	#	#	#	#	#	#	–	----	----	AT5G16620.1 | Symbols: PDE120, TIC40, ATTIC40 | hydroxyproline-rich glycoprotein family protein | chr5:5450808-5454256 FORWARD LENGTH=447	53	447	2.00E-12	843.4	64.2	69.8

Rsa1.0_00075.1.g3918.t1	ref|NP_197381.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 8 [Arabidopsis thaliana] gi|30687007|ref|NP_850849.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 8 [Arabidopsis thaliana] gi|297807915|ref|XP_002871841.1| NADH-ubiquinone oxidoreductase 19 kDa subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|75156052|sp|Q8LGE7.1|NDA8B_ARATH RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B gi|21536569|gb|AAM60901.1| NADH:ubiquinone oxidoreductase-like protein [Arabidopsis thaliana] gi|28466879|gb|AAO44048.1| At5g18800 [Arabidopsis thaliana] gi|110735767|dbj|BAE99861.1| NADH:ubiquinone oxidoreductase like protein [Arabidopsis thaliana] gi|297317678|gb|EFH48100.1| NADH-ubiquinone oxidoreductase 19 kDa subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|332005230|gb|AED92613.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 8 [Arabidopsis thaliana] gi|332005231|gb|AED92614.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 8 [Arabidopsis thaliana] gi|482557653|gb|EOA21845.1| hypothetical protein	106	106	6.00E-56	100.0	99.1	100.0	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 8	gbpln	Arabidopsis lyrata	AT5G18800.2 | Symbols: | Cox19-like CHCH family protein | chr5:6267304-6268393 FORWARD LENGTH=106	106	106	1.00E-58	100.0	99.1	100.0
Rsa1.0_00075.1.g3919.t1	gb|EOA32347.1| hypothetical protein CARUB_v10015614mg [Capsella rubella]	119	97	3.00E-26	81.5	48.7	51.3	hypothetical protein CARUB_v10015614mg	gbpln	Capsella rubella	AT5G18790.1 | Symbols: | Ribosomal protein L33 family protein | chr5:6266324-6266500 REVERSE LENGTH=58	119	58	4.00E-28	48.7	47.9	48.7
Rsa1.0_00075.1.g3920.t1	gb|EOA19923.1| hypothetical protein CARUB_v10000173mg [Capsella rubella]	858	903	0	105.2	66.4	77.9	hypothetical protein CARUB_v10000173mg	gbpln	Capsella rubella	AT5G18750.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:6255177-6257831 FORWARD LENGTH=884	858	884	0	103.0	66.0	78.4
Rsa1.0_00075.1.g3921.t1	gb|EOA20118.1| hypothetical protein CARUB_v10000401mg [Capsella rubella]	560	666	0	118.9	61.6	72.7	hypothetical protein CARUB_v10000401mg	gbpln	Capsella rubella	AT5G18730.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Molecular chaperone, heat shock protein, Hsp40, DnaJ (InterPro:IPR015609); BEST Arabidopsis thaliana protein match is: Domain of unknown function (DUF3444) (TAIR:AT5G18740.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6247611-6249197 FORWARD LENGTH=528	560	528	0	94.3	62.1	72.0
Rsa1.0_00075.1.g3922.t1	gb|EOA20118.1| hypothetical protein CARUB_v10000401mg [Capsella rubella]	1010	666	1.00E-179	65.9	31.2	37.4	hypothetical protein CARUB_v10000401mg	gbpln	Capsella rubella	AT5G18730.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Molecular chaperone, heat shock protein, Hsp40, DnaJ (InterPro:IPR015609); BEST Arabidopsis thaliana protein match is: Domain of unknown function (DUF3444) (TAIR:AT5G18740.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6247611-6249197 FORWARD LENGTH=528	1010	528	1.00E-173	52.3	30.7	36.0
Rsa1.0_00075.1.g3923.t1	gb|EOA22541.1| hypothetical protein CARUB_v10003196mg [Capsella rubella]	532	554	0	104.1	67.3	78.2	hypothetical protein CARUB_v10003196mg	gbpln	Capsella rubella	AT5G18730.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Molecular chaperone, heat shock protein, Hsp40, DnaJ (InterPro:IPR015609); BEST Arabidopsis thaliana protein match is: Domain of unknown function (DUF3444) (TAIR:AT5G18740.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6247611-6249197 FORWARD LENGTH=528	532	528	1.00E-176	99.2	58.8	70.7

Rsa1.0_00075.1.g3924.t1	ref|XP_002871829.1| hypothetical protein ARALYDRAFT_488759 [Arabidopsis lyrata subsp. lyrata] gi|297317666|gb|EFH48088.1| hypothetical protein ARALYDRAFT_488759 [Arabidopsis lyrata subsp. lyrata]	587	566	0	96.4	65.1	74.1	hypothetical protein ARALYDRAFT_488759	gbpln	Arabidopsis lyrata	AT5G18730.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Molecular chaperone, heat shock protein, Hsp40, DnaJ (InterPro:IPR015609); BEST Arabidopsis thaliana protein match is: Domain of unknown function (DUF3444) (TAIR:AT5G18740.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6247611-6249197 FORWARD LENGTH=528	587	528	1.00E-122	89.9	41.4	55.5
Rsa1.0_00075.1.g3925.t1	ref|XP_002873912.1| EMB3013 [Arabidopsis lyrata subsp. lyrata] gi|297319749|gb|EFH50171.1| EMB3013 [Arabidopsis lyrata subsp. lyrata]	1362	1366	0	100.3	91.6	95.8	EMB3013	gbpln	Arabidopsis lyrata	AT5G18700.1 | Symbols: RUK, EMB3013 | Protein kinase family protein with ARM repeat domain | chr5:6235387-6240733 REVERSE LENGTH=1366	1362	1366	0	100.3	90.3	95.0
Rsa1.0_00075.1.g3926.t1	gb|EOA19299.1| hypothetical protein CARUB_v10002269mg [Capsella rubella]	133	122	2.00E-21	91.7	63.9	70.7	hypothetical protein CARUB_v10002269mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00075.1.g3927.t1	ref|NP_197369.2| Tubby-like F-box protein 11 [Arabidopsis thaliana] gi|75223283|sp|Q6NPQ1.1|TLP11_ARATH RecName: Full=Tubby-like F-box protein 11; Short=AtTLP11 gi|38564318|gb|AAR23738.1| At5g18680 [Arabidopsis thaliana] gi|58652098|gb|AAW80874.1| At5g18680 [Arabidopsis thaliana] gi|225898921|dbj|BAH30591.1| hypothetical protein [Arabidopsis thaliana] gi|332005215|gb|AED92598.1| Tubby-like F-box protein 11 [Arabidopsis thaliana]	393	389	0	99.0	87.5	92.1	Tubby-like F-box protein 11	gbpln	Arabidopsis thaliana	AT5G18680.1 | Symbols: AtTLP11, TLP11 | tubby like protein 11 | chr5:6228358-6230426 REVERSE LENGTH=389	393	389	0	99.0	87.5	92.1
Rsa1.0_00075.1.g3928.t1	ref|NP_197368.1| inactive beta-amylase 9 [Arabidopsis thaliana] gi|75331155|sp|Q8VYW2.1|BAM9_ARATH RecName: Full=Inactive beta-amylase 9; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Inactive beta-amylase 3 gi|17978935|gb|AAL47434.1| AT5g18670/T1A4_50 [Arabidopsis thaliana] gi|21592648|gb|AAM64597.1| beta-amylase-like proten [Arabidopsis thaliana] gi|22655358|gb|AAM98271.1| At5g18670/T1A4_50 [Arabidopsis thaliana] gi|332005214|gb|AED92597.1| inactive beta-amylase 9 [Arabidopsis thaliana]	536	536	0	100.0	85.4	90.3	inactive beta-amylase 9	gbpln	Arabidopsis thaliana	AT5G18670.1 | Symbols: BMY3, BAM9 | beta-amylase 3 | chr5:6226138-6227999 FORWARD LENGTH=536	536	536	0	100.0	85.4	90.3
Rsa1.0_00075.1.g3929.t5	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00075.1.g3930.t1	ref|XP_002873908.1| pale-green and chlorophyll B reduced 2 [Arabidopsis lyrata subsp. lyrata] gi|297319745|gb|EFH50167.1| pale-green and chlorophyll B reduced 2 [Arabidopsis lyrata subsp. lyrata]	419	417	0	99.5	83.5	90.2	pale-green and chlorophyll B reduced 2	gbpln	Arabidopsis lyrata	AT5G18660.1 | Symbols: PCB2 | NAD(P)-binding Rossmann-fold superfamily protein | chr5:6220872-6222125 REVERSE LENGTH=417	419	417	0	99.5	82.6	90.2
Rsa1.0_00075.1.g3931.t2	ref|XP_002871827.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297317664|gb|EFH48086.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	258	267	1.00E-137	103.5	91.1	96.1	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G18650.1 | Symbols: | CHY-type/CTCHY-type/RING-type Zinc finger protein | chr5:6218260-6220374 FORWARD LENGTH=267	258	267	1.00E-138	103.5	90.3	95.0
Rsa1.0_00076.1.g3932.t1	ref|XP_002880944.1| hypothetical protein ARALYDRAFT_481690 [Arabidopsis lyrata subsp. lyrata] gi|297326783|gb|EFH57203.1| hypothetical protein ARALYDRAFT_481690 [Arabidopsis lyrata subsp. lyrata]	284	276	1.00E-110	97.2	78.9	84.2	hypothetical protein ARALYDRAFT_481690	gbpln	Arabidopsis lyrata	AT2G28200.1 | Symbols: | C2H2-type zinc finger family protein | chr2:12024321-12025181 FORWARD LENGTH=286	284	286	1.00E-111	100.7	79.2	85.2
Rsa1.0_00076.1.g3933.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00076.1.g3934.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	703	1164	0	165.6	56.9	71.0	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	703	746	1.00E-63	106.1	19.3	27.3
Rsa1.0_00076.1.g3935.t1	gb|EOA27882.1| hypothetical protein CARUB_v10024052mg [Capsella rubella]	213	213	1.00E-115	100.0	95.3	98.6	hypothetical protein CARUB_v10024052mg	gbpln	Capsella rubella	AT2G28305.1 | Symbols: LOG1, ATLOG1 | Putative lysine decarboxylase family protein | chr2:12081186-12084307 FORWARD LENGTH=213	213	213	1.00E-116	100.0	94.4	98.1

Rsa1.0_00076.1.g3936.t3	ref|XP_002880936.1| hypothetical protein ARALYDRAFT_481676 [Arabidopsis lyrata subsp. lyrata] gi|297326775|gb|EFH57195.1| hypothetical protein ARALYDRAFT_481676 [Arabidopsis lyrata subsp. lyrata]	379	381	0	100.5	91.0	92.1	hypothetical protein ARALYDRAFT_481676	gbpln	Arabidopsis lyrata	AT2G28310.3 | Symbols: | Protein of unknown function (DUF707) | chr2:12085773-12087888 FORWARD LENGTH=374	379	374	0	98.7	90.2	92.3
Rsa1.0_00076.1.g3937.t1	ref|XP_002880935.1| hypothetical protein ARALYDRAFT_320561 [Arabidopsis lyrata subsp. lyrata] gi|297326774|gb|EFH57194.1| hypothetical protein ARALYDRAFT_320561 [Arabidopsis lyrata subsp. lyrata]	341	342	0	100.3	96.8	98.2	hypothetical protein ARALYDRAFT_320561	gbpln	Arabidopsis lyrata	AT2G28315.1 | Symbols: | Nucleotide/sugar transporter family protein | chr2:12088896-12090570 FORWARD LENGTH=342	341	342	0	100.3	96.5	98.2
Rsa1.0_00076.1.g3938.t1	ref|XP_002880933.1| hypothetical protein ARALYDRAFT_901675 [Arabidopsis lyrata subsp. lyrata] gi|297326772|gb|EFH57192.1| hypothetical protein ARALYDRAFT_901675 [Arabidopsis lyrata subsp. lyrata]	290	320	1.00E-77	110.3	57.9	72.1	hypothetical protein ARALYDRAFT_901675	gbpln	Arabidopsis lyrata	AT1G08010.2 | Symbols: GATA11 | GATA transcription factor 11 | chr1:2486202-2487402 REVERSE LENGTH=303	290	303	5.00E-71	104.5	53.8	67.2
Rsa1.0_00076.1.g3939.t2	ref|NP_180403.4| SIT4 phosphatase-associated-like protein [Arabidopsis thaliana] gi|330253018|gb|AEC08112.1| SIT4 phosphatase-associated-like protein [Arabidopsis thaliana]	798	788	0	98.7	82.2	88.0	SIT4 phosphatase-associated-like protein	gbpln	Arabidopsis thaliana	AT2G28360.1 | Symbols: | SIT4 phosphatase-associated family protein | chr2:12124604-12129879 REVERSE LENGTH=788	798	788	0	98.7	82.2	88.0
Rsa1.0_00076.1.g3940.t1	ref|NP_565671.1| uncharacterized protein [Arabidopsis thaliana] gi|75206504|sp|Q9SKN3.1|CSPL6_ARATH RecName: Full=CASP-like protein At2g28370 gi|14030701|gb|AAK53025.1|AF375441_1 At2g28370/T1B3.11 [Arabidopsis thaliana] gi|4432840|gb|AAD20689.1| expressed protein [Arabidopsis thaliana] gi|21553379|gb|AAM62472.1| unknown [Arabidopsis thaliana] gi|23506069|gb|AAN28894.1| At2g28370/T1B3.11 [Arabidopsis thaliana] gi|330253019|gb|AEC08113.1| uncharacterized protein AT2G28370 [Arabidopsis thaliana]	185	179	2.00E-82	96.8	89.7	93.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G28370.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr2:12132092-12133447 FORWARD LENGTH=179	185	179	6.00E-85	96.8	89.7	93.5
Rsa1.0_00076.1.g3941.t1	gb|EOA27124.1| hypothetical protein CARUB_v10023224mg [Capsella rubella]	436	443	0	101.6	78.7	85.1	hypothetical protein CARUB_v10023224mg	gbpln	Capsella rubella	AT2G28380.1 | Symbols: DRB2 | dsRNA-binding protein 2 | chr2:12134098-12135915 REVERSE LENGTH=434	436	434	1.00E-180	99.5	78.2	84.9
Rsa1.0_00076.1.g3942.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00076.1.g3943.t1	ref|XP_002879098.1| hypothetical protein ARALYDRAFT_481665 [Arabidopsis lyrata subsp. lyrata] gi|297324937|gb|EFH55357.1| hypothetical protein ARALYDRAFT_481665 [Arabidopsis lyrata subsp. lyrata]	162	164	4.00E-59	101.2	78.4	87.0	hypothetical protein ARALYDRAFT_481665	gbpln	Arabidopsis lyrata	AT2G28400.1 | Symbols: | Protein of unknown function, DUF584 | chr2:12148513-12149001 REVERSE LENGTH=162	162	162	2.00E-59	100.0	77.8	86.4
Rsa1.0_00076.1.g3944.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00076.1.g3945.t1	gb|EOA28155.1| hypothetical protein CARUB_v10024345mg [Capsella rubella]	116	118	2.00E-44	101.7	77.6	83.6	hypothetical protein CARUB_v10024345mg	gbpln	Capsella rubella	AT2G28410.1 | Symbols: | unknown protein; Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:12156202-12156549 FORWARD LENGTH=115	116	115	6.00E-43	99.1	70.7	81.0
Rsa1.0_00076.1.g3946.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00076.1.g3947.t1	ref|NP_180411.1| proline-rich protein [Arabidopsis thaliana] gi|4432833|gb|AAD20682.1| En/Spm-like transposon protein [Arabidopsis thaliana] gi|67633550|gb|AAY78699.1| proline-rich family protein [Arabidopsis thaliana] gi|330253029|gb|AEC08123.1| proline-rich protein [Arabidopsis thaliana]	168	268	3.00E-23	159.5	53.6	61.3	proline-rich protein	gbpln	Arabidopsis thaliana	AT2G28440.1 | Symbols: | proline-rich family protein | chr2:12161226-12162032 FORWARD LENGTH=268	168	268	1.00E-25	159.5	53.6	61.3
Rsa1.0_00076.1.g3948.t1	gb|AAC98462.1| putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana] gi|20197956|gb|AAM15330.1| putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]	429	389	1.00E-138	90.7	58.7	70.6	putative chloroplast nucleoid DNA binding protein	gbpln	Arabidopsis thaliana	AT2G28040.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:11936203-11937390 REVERSE LENGTH=395	429	395	1.00E-141	92.1	58.7	70.6
Rsa1.0_00076.1.g3949.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00076.1.g3950.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00076.1.g3951.t1	ref|NP_180417.2| LOB domain-containing protein 11 [Arabidopsis thaliana] gi|334302828|sp|Q9SK08.2|LBD11_ARATH RecName: Full=LOB domain-containing protein 11; AltName: Full=ASYMMETRIC LEAVES 2-like protein 7; Short=AS2-like protein 7 gi|330253037|gb|AEC08131.1| LOB domain-containing protein 11 [Arabidopsis thaliana]	236	232	1.00E-101	98.3	89.8	93.2	LOB domain-containing protein 11	gbpln	Arabidopsis thaliana	AT2G28500.1 | Symbols: LBD11 | LOB domain-containing protein 11 | chr2:12186603-12188110 REVERSE LENGTH=232	236	232	1.00E-103	98.3	89.8	93.2
Rsa1.0_00076.1.g3952.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00077.1.g3953.t1	ref|XP_002894568.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297340410|gb|EFH70827.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	180	433	5.00E-48	240.6	61.1	67.8	transferase family protein	gbpln	Arabidopsis lyrata	AT5G48930.1 | Symbols: HCT | hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase | chr5:19836654-19838092 REVERSE LENGTH=433	180	433	3.00E-49	240.6	58.3	65.6
Rsa1.0_00077.1.g3954.t1	ref|XP_002870182.1| hypothetical protein ARALYDRAFT_915160 [Arabidopsis lyrata subsp. lyrata] gi|297316018|gb|EFH46441.1| hypothetical protein ARALYDRAFT_915160 [Arabidopsis lyrata subsp. lyrata]	652	676	0	103.7	80.7	86.7	hypothetical protein ARALYDRAFT_915160	gbpln	Arabidopsis lyrata	AT4G16110.1 | Symbols: ARR2, RR2 | response regulator 2 | chr4:9112979-9115785 FORWARD LENGTH=664	652	664	0	101.8	77.8	84.0
Rsa1.0_00077.1.g3955.t1	ref|XP_002868161.1| ATSEB1 [Arabidopsis lyrata subsp. lyrata] gi|297313997|gb|EFH44420.1| ATSEB1 [Arabidopsis lyrata subsp. lyrata]	660	658	0	99.7	83.6	89.4	ATSEB1	gbpln	Arabidopsis lyrata	AT4G16120.1 | Symbols: ATSEB1, COBL7, SEB1 | COBRA-like protein-7 precursor | chr4:9116591-9119138 REVERSE LENGTH=661	660	661	0	100.2	84.5	91.8
Rsa1.0_00077.1.g3956.t13	ref|XP_002870181.1| hypothetical protein ARALYDRAFT_355153 [Arabidopsis lyrata subsp. lyrata] gi|297316017|gb|EFH46440.1| hypothetical protein ARALYDRAFT_355153 [Arabidopsis lyrata subsp. lyrata]	1027	989	0	96.3	90.2	93.6	hypothetical protein ARALYDRAFT_355153	gbpln	Arabidopsis lyrata	AT4G16130.1 | Symbols: ARA1, ISA1, ATISA1 | arabinose kinase | chr4:9120875-9127656 FORWARD LENGTH=1039	1027	1039	0	101.2	90.4	93.4
Rsa1.0_00077.1.g3957.t1	gb|EOA17545.1| hypothetical protein CARUB_v10005904mg [Capsella rubella]	177	166	3.00E-20	93.8	33.9	36.7	hypothetical protein CARUB_v10005904mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00077.1.g3958.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00077.1.g3959.t1	gb|EOA17527.1| hypothetical protein CARUB_v10005860mg [Capsella rubella]	184	178	4.00E-57	96.7	72.8	84.2	hypothetical protein CARUB_v10005860mg	gbpln	Capsella rubella	AT4G16141.1 | Symbols: | GATA type zinc finger transcription factor family protein | chr4:9131872-9132893 REVERSE LENGTH=197	184	197	2.00E-58	107.1	75.5	84.8
Rsa1.0_00077.1.g3960.t1	gb|EOA18223.1| hypothetical protein CARUB_v10006712mg [Capsella rubella]	528	533	0	100.9	92.8	95.5	hypothetical protein CARUB_v10006712mg	gbpln	Capsella rubella	AT4G16143.2 | Symbols: IMPA-2 | importin alpha isoform 2 | chr4:9134450-9137134 REVERSE LENGTH=535	528	535	0	101.3	92.6	95.8
Rsa1.0_00077.1.g3961.t1	gb|AAV85709.1| At4g16144 [Arabidopsis thaliana]	530	507	0	95.7	87.0	90.8	At4g16144	gbpln	Arabidopsis thaliana	AT4G16144.1 | Symbols: AMSH3 | associated molecule with the SH3 domain of STAM 3 | chr4:9138053-9141422 REVERSE LENGTH=507	530	507	0	95.7	87.0	90.6
Rsa1.0_00077.1.g3962.t1	gb|EOA17716.1| hypothetical protein CARUB_v10006097mg [Capsella rubella]	117	103	2.00E-27	88.0	59.0	65.8	hypothetical protein CARUB_v10006097mg	gbpln	Capsella rubella	AT4G16146.1 | Symbols: | cAMP-regulated phosphoprotein 19-related protein | chr4:9142663-9144356 REVERSE LENGTH=102	117	102	9.00E-29	87.2	55.6	63.2
Rsa1.0_00077.1.g3963.t2	ref|XP_002867797.1| hypothetical protein ARALYDRAFT_329412 [Arabidopsis lyrata subsp. lyrata] gi|297313633|gb|EFH44056.1| hypothetical protein ARALYDRAFT_329412 [Arabidopsis lyrata subsp. lyrata]	718	732	0	101.9	87.5	93.9	hypothetical protein ARALYDRAFT_329412	gbpln	Arabidopsis lyrata	AT4G04910.1 | Symbols: NSF | AAA-type ATPase family protein | chr4:2489696-2495666 REVERSE LENGTH=742	718	742	0	103.3	75.6	85.8
Rsa1.0_00077.1.g3964.t1	gb|EOA16331.1| hypothetical protein CARUB_v10004481mg [Capsella rubella]	563	564	0	100.2	94.0	96.6	hypothetical protein CARUB_v10004481mg	gbpln	Capsella rubella	AT4G16155.1 | Symbols: | dihydrolipoyl dehydrogenases | chr4:9153570-9157322 REVERSE LENGTH=630	563	630	0	111.9	94.8	96.4
Rsa1.0_00077.1.g3965.t3	gb|EOA15607.1| hypothetical protein CARUB_v10005679mg [Capsella rubella] gi|482551415|gb|EOA15608.1| hypothetical protein CARUB_v10005679mg [Capsella rubella]	229	224	1.00E-80	97.8	75.1	81.7	hypothetical protein CARUB_v10005679mg	gbpln	Capsella rubella	AT3G17100.2 | Symbols: | sequence-specific DNA binding transcription factors | chr3:5831552-5832244 FORWARD LENGTH=230	229	230	6.00E-58	100.4	62.0	74.7

Rsa1.0_00077.1.g3966.t1	ref|XP_002868153.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313989|gb|EFH44412.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	820	822	0	100.2	93.5	96.6	predicted protein	gbpln	Arabidopsis lyrata	AT4G16180.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G28720.1); Has 5 Blast hits to 5 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr4:9165365-9170323 REVERSE LENGTH=820	820	820	0	100.0	91.2	94.3
Rsa1.0_00077.1.g3967.t1	gb|EOA16872.1| hypothetical protein CARUB_v10005098mg [Capsella rubella]	368	365	0	99.2	86.1	91.0	hypothetical protein CARUB_v10005098mg	gbpln	Capsella rubella	AT4G16190.1 | Symbols: | Papain family cysteine protease | chr4:9171512-9172877 FORWARD LENGTH=373	368	373	0	101.4	86.7	91.6
Rsa1.0_00077.1.g3968.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00077.1.g3969.t1	gb|EOA17085.1| hypothetical protein CARUB_v10005333mg [Capsella rubella]	307	305	1.00E-147	99.3	83.7	89.3	hypothetical protein CARUB_v10005333mg	gbpln	Capsella rubella	AT3G17000.1 | Symbols: UBC32 | ubiquitin-conjugating enzyme 32 | chr3:5797296-5799467 FORWARD LENGTH=309	307	309	1.00E-119	100.7	70.0	81.4
Rsa1.0_00077.1.g3970.t1	ref|NP_567490.1| RNA polymerases M/15 Kd subunit [Arabidopsis thaliana] gi|297800522|ref|XP_002868145.1| hypothetical protein ARALYDRAFT_493259 [Arabidopsis lyrata subsp. lyrata] gi|21537166|gb|AAM61507.1| RNA Polymerase II subunit 14.5 kD, putative [Arabidopsis thaliana] gi|114050701|gb|ABI49500.1| At4g16265 [Arabidopsis thaliana] gi|297313981|gb|EFH44404.1| hypothetical protein ARALYDRAFT_493259 [Arabidopsis lyrata subsp. lyrata] gi|332658323|gb|AEE83723.1| RNA polymerases M/15 Kd subunit [Arabidopsis thaliana] gi|482553494|gb|EOA17687.1| hypothetical protein CARUB_v10006057mg [Capsella rubella]	114	114	1.00E-61	100.0	99.1	99.1	RNA polymerases M/15 Kd subunit	gbpln	Arabidopsis lyrata	AT4G16265.1 | Symbols: NRPB9B, NRPD9B, NRPE9B | RNA polymerases M/15 Kd subunit | chr4:9202529-9203975 REVERSE LENGTH=114	114	114	2.00E-64	100.0	99.1	99.1
Rsa1.0_00077.1.g3971.t1	ref|XP_002870166.1| peroxidase 40 [Arabidopsis lyrata subsp. lyrata] gi|297316002|gb|EFH46425.1| peroxidase 40 [Arabidopsis lyrata subsp. lyrata]	359	362	1.00E-179	100.8	87.2	90.5	peroxidase 40	gbpln	Arabidopsis lyrata	AT4G16270.1 | Symbols: | Peroxidase superfamily protein | chr4:9205038-9206483 FORWARD LENGTH=362	359	362	1.00E-173	100.8	82.7	86.4
Rsa1.0_00077.1.g3972.t1	gb|AAL61622.1|AF414188_1 FCA gamma [Brassica napus]	572	715	0	125.0	89.0	92.1	FCA gamma	gbpln	Brassica napus	AT4G16280.4 | Symbols: | RNA binding;abscisic acid binding | chr4:9207164-9214187 REVERSE LENGTH=672	572	672	0	117.5	76.7	81.6
Rsa1.0_00077.1.g3973.t1	emb|CAB41488.2| putative FCA orthologue [Brassica napus]	266	384	3.00E-47	144.4	39.5	42.1	putative FCA orthologue	gbpln	Brassica napus	AT4G16280.2 | Symbols: FCA | RNA binding;abscisic acid binding | chr4:9207164-9214412 REVERSE LENGTH=747	266	747	3.00E-26	280.8	28.9	33.8
Rsa1.0_00077.1.g3974.t1	ref|XP_002883592.1| hypothetical protein ARALYDRAFT_342698 [Arabidopsis lyrata subsp. lyrata] gi|297329432|gb|EFH59851.1| hypothetical protein ARALYDRAFT_342698 [Arabidopsis lyrata subsp. lyrata]	288	369	2.00E-85	128.1	61.1	75.3	hypothetical protein ARALYDRAFT_342698	gbpln	Arabidopsis lyrata	AT3G19470.2 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6749766-6750914 FORWARD LENGTH=382	288	382	1.00E-78	132.6	59.4	72.2
Rsa1.0_00077.1.g3975.t1	ref|XP_002868142.1| hypothetical protein ARALYDRAFT_355126 [Arabidopsis lyrata subsp. lyrata] gi|297313978|gb|EFH44401.1| hypothetical protein ARALYDRAFT_355126 [Arabidopsis lyrata subsp. lyrata]	342	338	1.00E-168	98.8	83.9	91.5	hypothetical protein ARALYDRAFT_355126	gbpln	Arabidopsis lyrata	AT4G16330.2 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:9226298-9227914 REVERSE LENGTH=364	342	364	1.00E-156	106.4	76.9	82.7
Rsa1.0_00077.1.g3976.t2	ref|XP_002868141.1| hypothetical protein ARALYDRAFT_493252 [Arabidopsis lyrata subsp. lyrata] gi|297313977|gb|EFH44400.1| hypothetical protein ARALYDRAFT_493252 [Arabidopsis lyrata subsp. lyrata]	1826	1830	0	100.2	96.4	98.0	hypothetical protein ARALYDRAFT_493252	gbpln	Arabidopsis lyrata	AT4G16340.1 | Symbols: SPK1 | guanyl-nucleotide exchange factors;GTPase binding;GTP binding | chr4:9228773-9241060 REVERSE LENGTH=1830	1826	1830	0	100.2	95.8	97.8
Rsa1.0_00077.1.g3977.t2	ref|XP_002868140.1| hypothetical protein ARALYDRAFT_493251 [Arabidopsis lyrata subsp. lyrata] gi|297313976|gb|EFH44399.1| hypothetical protein ARALYDRAFT_493251 [Arabidopsis lyrata subsp. lyrata]	263	226	1.00E-90	85.9	61.6	69.2	hypothetical protein ARALYDRAFT_493251	gbpln	Arabidopsis lyrata	AT4G16350.1 | Symbols: CBL6, SCABP2 | calcineurin B-like protein 6 | chr4:9242505-9243669 REVERSE LENGTH=226	263	226	9.00E-92	85.9	60.5	68.1

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<tr><td>Rsa1.0_00077.1.g3979.t1</td><td>emb|CAC01940.1| 67kD chloroplastic RNA-binding protein, P67.1 [Raphanus sativus]</td><td>701</td><td>700</td><td>0</td><td>99.9</td><td>98.4</td><td>99.1</td><td>67kD chloroplastic RNA-binding protein, P67.1</td><td>gbpln</td><td>Raphanus sativus</td><td>AT4G16390.1 | Symbols: SVR7 | pentatricopeptide (PPR) repeat-containing protein | chr4:9257985-9260093 FORWARD LENGTH=702</td><td>701</td><td>702</td><td>0</td><td>100.1</td><td>86.7</td><td>92.7</td></tr>
<tr><td>Rsa1.0_00077.1.g3980.t1</td><td>emb|CAB10417.1| hypothetical protein [Arabidopsis thaliana] gi|7268389|emb|CAB78682.1| hypothetical protein [Arabidopsis thaliana]</td><td>96</td><td>209</td><td>6.00E-18</td><td>217.7</td><td>52.1</td><td>66.7</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G16400.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13175.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9260564-9262102 FORWARD LENGTH=218</td><td>96</td><td>218</td><td>1.00E-20</td><td>227.1</td><td>52.1</td><td>66.7</td></tr>
<tr><td>Rsa1.0_00077.1.g3981.t1</td><td>ref|XP_002870160.1| hypothetical protein ARALYDRAFT_329873 [Arabidopsis lyrata subsp. lyrata] gi|297315996|gb|EFH46419.1| hypothetical protein ARALYDRAFT_329873 [Arabidopsis lyrata subsp. lyrata]</td><td>88</td><td>192</td><td>2.00E-39</td><td>218.2</td><td>85.2</td><td>98.9</td><td>hypothetical protein ARALYDRAFT_329873</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G16400.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13175.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9260564-9262102 FORWARD LENGTH=218</td><td>88</td><td>218</td><td>3.00E-41</td><td>247.7</td><td>83.0</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00077.1.g3982.t1</td><td>ref|NP_193376.1| transcription factor bHLH3 [Arabidopsis thaliana] gi|75318117|sp|O23487.1|BH003_ARATH RecName: Full=Transcription factor bHLH3; AltName: Full=Basic helix-loop-helix protein 3; Short=AtbHLH3; Short=bHLH 3; AltName: Full=Transcription factor EN 34; AltName: Full=bHLH transcription factor bHLH003 gi|16226919|gb|AAL16298.1|AF428368_1 AT4g16430/dl4240w [Arabidopsis thaliana] gi|18026954|gb|AAL55710.1|AF251688_1 putative transcription factor BHLH3 [Arabidopsis thaliana] gi|2244999|emb|CAB10419.1| transcription factor like protein [Arabidopsis thaliana] gi|7268393|emb|CAB78685.1| transcription factor like protein [Arabidopsis thaliana] gi|16323045|gb|AAL15257.1| AT4g16430/dl4240w [Arabidopsis thaliana] gi|25141207|gb|AAN73298.1| At4g16430/dl4240w [Arabidopsis thaliana] gi|332658347|gb|AEE83747.1| transcription factor bHLH3 [Arabidopsis thaliana]</td><td>465</td><td>467</td><td>0</td><td>100.4</td><td>86.0</td><td>91.2</td><td>transcription factor bHLH3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G16430.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:9267599-9269002 FORWARD LENGTH=467</td><td>465</td><td>467</td><td>0</td><td>100.4</td><td>86.0</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00077.1.g3983.t1</td><td>ref|XP_002868134.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313970|gb|EFH44393.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>468</td><td>474</td><td>0</td><td>101.3</td><td>88.9</td><td>96.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G16440.1 | Symbols: | ferredoxin hydrogenases | chr4:9269263-9271510 REVERSE LENGTH=474</td><td>468</td><td>474</td><td>0</td><td>101.3</td><td>89.1</td><td>96.2</td></tr>
<tr><td>Rsa1.0_00077.1.g3984.t1</td><td>ref|XP_002868133.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|341958538|sp|D7M9V1.1|CSPL7_ARALL RecName: Full=CASP-like protein ARALYDRAFT_915107 gi|297313969|gb|EFH44392.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata]</td><td>206</td><td>182</td><td>5.00E-72</td><td>88.3</td><td>63.1</td><td>76.7</td><td>integral membrane family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G16442.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:9272042-9272970 REVERSE LENGTH=182</td><td>206</td><td>182</td><td>5.00E-74</td><td>88.3</td><td>62.6</td><td>76.2</td></tr>
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<tr><td>Rsa1.0_00078.1.g3986.t1</td><td>gb|AAM63759.1| unknown [Arabidopsis thaliana]</td><td>187</td><td>187</td><td>2.00E-83</td><td>100.0</td><td>84.0</td><td>90.4</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G02910.1 | Symbols: | AIG2-like (avirulence induced gene) family protein | chr3:649986-650549 FORWARD LENGTH=187</td><td>187</td><td>187</td><td>3.00E-85</td><td>100.0</td><td>83.4</td><td>89.3</td></tr>
<tr><td>Rsa1.0_00078.1.g3987.t1</td><td>ref|NP_186943.1| uncharacterized protein [Arabidopsis thaliana] gi|75186537|sp|Q9M8T5.1|Y3293_ARATH RecName: Full=WEB family protein At3g02930, chloroplastic; Flags: Precursor gi|6728968|gb|AAF26966.1|AC018363_11 unknown protein [Arabidopsis thaliana] gi|332640360|gb|AEE73881.1| uncharacterized protein AT3G02930 [Arabidopsis thaliana]</td><td>740</td><td>806</td><td>0</td><td>108.9</td><td>70.0</td><td>84.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G02930.1 | Symbols: | Plant protein of unknown function (DUF827) | chr3:655306-658319 FORWARD LENGTH=806</td><td>740</td><td>806</td><td>0</td><td>108.9</td><td>70.0</td><td>84.1</td></tr>
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<tr><td>Rsa1.0_00078.1.g3989.t5</td><td>ref|NP_566189.1| Tho complex subunit 7/Mft1p [Arabidopsis thaliana] gi|6728966|gb|AAF26964.1|AC018363_9 unknown protein [Arabidopsis thaliana] gi|15983444|gb|AAL11590.1|AF424596_1 AT3g02950/F13E7_10 [Arabidopsis thaliana] gi|48310661|gb|AAT41862.1| At3g02950 [Arabidopsis thaliana] gi|332640363|gb|AEE73884.1| Tho complex subunit 7/Mft1p [Arabidopsis thaliana]</td><td>236</td><td>236</td><td>1.00E-109</td><td>100.0</td><td>88.1</td><td>94.5</td><td>Tho complex subunit 7/Mft1p</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G02950.1 | Symbols: THO7, AtTHO7 | Tho complex subunit 7/Mft1p | chr3:665631-666439 REVERSE LENGTH=236</td><td>236</td><td>236</td><td>1.00E-111</td><td>100.0</td><td>88.1</td><td>94.5</td></tr>
<tr><td>Rsa1.0_00078.1.g3990.t2</td><td>ref|NP_186947.1| protein exordium like 6 [Arabidopsis thaliana] gi|6728964|gb|AAF26962.1|AC018363_7 phi-1-like protein [Arabidopsis thaliana] gi|332640365|gb|AEE73886.1| protein exordium like 6 [Arabidopsis thaliana]</td><td>603</td><td>332</td><td>1.00E-144</td><td>55.1</td><td>42.0</td><td>45.6</td><td>protein exordium like 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G02970.1 | Symbols: EXL6 | EXORDIUM like 6 | chr3:669217-670495 REVERSE LENGTH=332</td><td>603</td><td>332</td><td>2.33E-156</td><td>55.1</td><td>42.0</td><td>45.6</td></tr>
<tr><td>Rsa1.0_00078.1.g3991.t1</td><td>gb|EOA30505.1| hypothetical protein CARUB_v10013628mg [Capsella rubella]</td><td>462</td><td>468</td><td>0</td><td>101.3</td><td>80.3</td><td>86.8</td><td>hypothetical protein CARUB_v10013628mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G02990.1 | Symbols: ATHSFA1E, HSFA1E | heat shock transcription factor A1E | chr3:673614-675988 FORWARD LENGTH=468</td><td>462</td><td>468</td><td>0</td><td>101.3</td><td>81.4</td><td>88.3</td></tr>
<tr><td>Rsa1.0_00078.1.g3992.t1</td><td>ref|NP_186924.1| putative protein phosphatase 2C 33 [Arabidopsis thaliana] gi|79295498|ref|NP_001030624.1| putative protein phosphatase 2C 33 [Arabidopsis thaliana] gi|75186497|sp|Q9M8R7.1|P2C33_ARATH RecName: Full=Probable protein phosphatase 2C 33; Short=AtPP2C33; AltName: Full=AtPPC6;1 gi|6728987|gb|AAF26985.1|AC018363_30 putative protein phosphatase-2C (PP2C) [Arabidopsis thaliana] gi|58652052|gb|AAW80851.1| At3g02750 [Arabidopsis thaliana] gi|115311509|gb|ABI93935.1| At3g02750 [Arabidopsis thaliana] gi|332640333|gb|AEE73854.1| putative protein phosphatase 2C 33 [Arabidopsis thaliana] gi|332640334|gb|AEE73855.1| putative protein phosphatase 2C 33 [Arabidopsis thaliana]</td><td>193</td><td>492</td><td>5.00E-40</td><td>254.9</td><td>54.4</td><td>58.0</td><td>putative protein phosphatase 2C 33</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G02750.2 | Symbols: | Protein phosphatase 2C family protein | chr3:593601-595457 REVERSE LENGTH=492</td><td>193</td><td>492</td><td>2.00E-42</td><td>254.9</td><td>54.4</td><td>58.0</td></tr>
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Rsa1.0_00078.1.g3993.t1	ref|NP_186923.1| aspartyl protease-like protein [Arabidopsis thaliana] gi|6728988|gb|AAF26986.1|AC018363_31 putative aspartyl protease [Arabidopsis thaliana] gi|21593593|gb|AAM65560.1| putative aspartyl protease [Arabidopsis thaliana] gi|332640332|gb|AEE73853.1| aspartyl protease-like protein [Arabidopsis thaliana]	490	488	0	99.6	83.9	90.6	aspartyl protease-like protein	gbpln	Arabidopsis thaliana	AT3G02740.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:590561-593089 FORWARD LENGTH=488	490	488	0	99.6	83.9	90.6
Rsa1.0_00078.1.g3994.t1	ref|XP_002884335.1| thioredoxin F-type 1 [Arabidopsis lyrata subsp. lyrata] gi|297330175|gb|EFH60594.1| thioredoxin F-type 1 [Arabidopsis lyrata subsp. lyrata]	182	178	4.00E-82	97.8	84.1	87.9	thioredoxin F-type 1	gbpln	Arabidopsis lyrata	AT3G02730.1 | Symbols: TRXF1, ATF1 | thioredoxin F-type 1 | chr3:588570-589591 REVERSE LENGTH=178	182	178	4.00E-83	97.8	82.4	87.9
Rsa1.0_00078.1.g3995.t2	gb|EOA14628.1| hypothetical protein CARUB_v10027900mg [Capsella rubella]	524	550	0	105.0	64.3	76.0	hypothetical protein CARUB_v10027900mg	gbpln	Capsella rubella	AT5G54050.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:21933663-21935970 REVERSE LENGTH=580	524	580	0	110.7	66.2	80.0
Rsa1.0_00078.1.g3996.t1	ref|XP_002882249.1| hypothetical protein ARALYDRAFT_896249 [Arabidopsis lyrata subsp. lyrata] gi|297328089|gb|EFH58508.1| hypothetical protein ARALYDRAFT_896249 [Arabidopsis lyrata subsp. lyrata]	388	388	0	100.0	92.0	95.4	hypothetical protein ARALYDRAFT_896249	gbpln	Arabidopsis lyrata	AT3G02720.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr3:586336-588088 FORWARD LENGTH=388	388	388	0	100.0	91.0	94.8
Rsa1.0_00078.1.g3997.t1	ref|NP_566174.1| 14-3-3-like protein GF14 nu [Arabidopsis thaliana] gi|3023217|sp|Q96300.1|14337_ARATH RecName: Full=14-3-3-like protein GF14 nu; AltName: Full=General regulatory factor 7 gi|5802792|gb|AAD51782.1|AF145299_1 14-3-3 protein GF14 nu [Arabidopsis thaliana] gi|1531631|gb|AAB49335.1| GF14 nu [Arabidopsis thaliana] gi|6957715|gb|AAF32459.1| putative 14-3-3 protein [Arabidopsis thaliana] gi|17529080|gb|AAL38750.1| putative 14-3-3 protein GF14nu (grf7) [Arabidopsis thaliana] gi|20465433|gb|AAM20176.1| putative 14-3-3 protein [Arabidopsis thaliana] gi|21593311|gb|AAM65260.1| 14-3-3 protein GF14nu (grf7) [Arabidopsis thaliana] gi|332640301|gb|AEE73822.1| 14-3-3-like protein GF14 nu [Arabidopsis thaliana]	261	265	1.00E-141	101.5	95.0	98.1	14-3-3-like protein GF14 nu	gbpln	Arabidopsis thaliana	AT3G02520.1 | Symbols: GRF7, GF14 NU | general regulatory factor 7 | chr3:526800-527915 REVERSE LENGTH=265	261	265	1.00E-144	101.5	95.0	98.1
Rsa1.0_00078.1.g3998.t1	ref|XP_002884325.1| hypothetical protein ARALYDRAFT_477487 [Arabidopsis lyrata subsp. lyrata] gi|297330165|gb|EFH60584.1| hypothetical protein ARALYDRAFT_477487 [Arabidopsis lyrata subsp. lyrata]	535	535	0	100.0	98.7	99.8	hypothetical protein ARALYDRAFT_477487	gbpln	Arabidopsis lyrata	AT3G02530.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:528806-532457 REVERSE LENGTH=535	535	535	0	100.0	98.1	99.6
Rsa1.0_00078.1.g3999.t1	sp|Q9XH45.1|RS7_BRAOL RecName: Full=40S ribosomal protein S7 gi|5532505|gb|AAD44761.1|AF144752_1 40S ribosomal protein S7 homolog [Brassica oleracea]	202	191	1.00E-100	94.6	87.6	91.6	RecName: Full=40S ribosomal protein S7 gi|5532505|gb|AAD44761.1|AF144752_1 40S ribosomal protein S7 homolog	gbpln	Brassica oleracea	AT3G02560.2 | Symbols: | Ribosomal protein S7e family protein | chr3:542341-543168 FORWARD LENGTH=191	202	191	1.00E-100	94.6	85.1	91.1
Rsa1.0_00078.1.g4000.t2	ref|NP_186906.1| mannose-6-phosphate isomerase [Arabidopsis thaliana] gi|75336067|sp|Q9M884.1|MPI1_ARATH RecName: Full=Mannose-6-phosphate isomerase 1; AltName: Full=Phosphohexomutase 1; AltName: Full=Phosphomannose isomerase 1; Short=PMI1; AltName: Full=Protein MATERNAL EFFECT EMBRYO ARREST 31 gi|6957720|gb|AAF32464.1| putative mannose-6-phosphate isomerase [Arabidopsis thaliana] gi|17979416|gb|AAL49850.1| putative mannose-6-phosphate isomerase [Arabidopsis thaliana] gi|20465985|gb|AAM20214.1| putative mannose-6-phosphate isomerase [Arabidopsis thaliana] gi|332640310|gb|AEE73831.1| mannose-6-phosphate isomerase [Arabidopsis thaliana]	427	432	0	101.2	92.0	95.6	mannose-6-phosphate isomerase	gbpln	Arabidopsis thaliana	AT3G02570.1 | Symbols: MEE31, PMI1 | Mannose-6-phosphate isomerase, type I | chr3:543463-545478 REVERSE LENGTH=432	427	432	0	101.2	92.0	95.6

Rsa1.0_00078.1.g4001.t1	ref|NP_186907.1| delta(7)-sterol-C5(6)-desaturase 1 [Arabidopsis thaliana] gi|33301592|sp|Q39208.2|SC5D1_ARATH RecName: Full=Delta(7)-sterol-C5(6)-desaturase 1; AltName: Full=Delta(7)-sterol-C5-desaturase 1; AltName: Full=Delta-7-C-5 sterol desaturase 1; AltName: Full=Protein DWARF 7; AltName: Full=Protein STEROL 1 gi|4234768|gb|AAD12944.1| sterol-C5-desaturase [Arabidopsis thaliana] gi|6957721|gb|AAF32465.1| sterol-C5-desaturase [Arabidopsis thaliana] gi|51971639|dbj|BAD44484.1| sterol-C5-desaturase [Arabidopsis thaliana] gi|105829795|gb|ABF74704.1| At3g02580 [Arabidopsis thaliana] gi|332640311|gb|AEE73832.1| delta(7)-sterol-C5(6)-desaturase 1 [Arabidopsis thaliana]	276	281	1.00E-144	101.8	89.1	94.2	delta(7)-sterol-C5(6)-desaturase 1	gbpln	Arabidopsis thaliana	AT3G02580.1 | Symbols: STE1, DWF7, BUL1 | sterol 1 | chr3:547048-548615 FORWARD LENGTH=281	276	281	1.00E-147	101.8	89.1	94.2
Rsa1.0_00078.1.g4002.t4	gb|EOA30892.1| hypothetical protein CARUB_v10014038mg [Capsella rubella]	374	360	0	96.3	84.0	86.6	hypothetical protein CARUB_v10014038mg	gbpln	Capsella rubella	AT3G02600.1 | Symbols: LPP3, ATLPP3 | lipid phosphate phosphatase 3 | chr3:551534-554411 FORWARD LENGTH=364	374	364	0	97.3	82.4	86.1
Rsa1.0_00078.1.g4003.t1	ref|NP_186910.2| acyl-[acyl-carrier-protein] desaturase [Arabidopsis thaliana] gi|332640318|gb|AEE73839.1| acyl-[acyl-carrier-protein] desaturase [Arabidopsis thaliana]	409	413	0	101.0	90.0	92.9	acyl-	gbpln	Arabidopsis thaliana	AT3G02610.1 | Symbols: | Plant stearoyl-acyl-carrier-protein desaturase family protein | chr3:555665-557458 FORWARD LENGTH=413	409	413	0	101.0	90.0	92.9
Rsa1.0_00078.1.g4004.t1	gb|AAM65632.1| PhD-finger protein, putative [Arabidopsis thaliana]	684	429	1.00E-104	62.7	34.4	42.8	PhD-finger protein, putative	gbpln	Arabidopsis thaliana	AT1G14770.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:5086867-5088437 REVERSE LENGTH=429	684	429	1.00E-106	62.7	34.4	42.8
Rsa1.0_00078.1.g4005.t1	gb|ADG57793.1| S-adenosyl-l-methionine decarboxylase 3-2 [Brassica napus]	364	368	0	101.1	96.2	98.6	S-adenosyl-l-methionine decarboxylase 3-2	gbpln	Brassica napus	AT3G02470.4 | Symbols: | S-adenosylmethionine decarboxylase | chr3:510223-511323 FORWARD LENGTH=366	364	366	0	100.5	93.4	97.5
Rsa1.0_00078.1.g4006.t2	gb|EOA30699.1| hypothetical protein CARUB_v10013836mg [Capsella rubella]	387	409	0	105.7	86.8	92.8	hypothetical protein CARUB_v10013836mg	gbpln	Capsella rubella	AT3G02410.1 | Symbols: ICME-LIKE2 | alpha/beta-Hydrolases superfamily protein | chr3:492118-494877 REVERSE LENGTH=422	387	422	0	109.0	85.8	92.0
Rsa1.0_00078.1.g4007.t1	gb|EOA30433.1| hypothetical protein CARUB_v10013557mg [Capsella rubella]	488	486	0	99.6	96.3	98.4	hypothetical protein CARUB_v10013557mg	gbpln	Capsella rubella	AT3G02360.1 | Symbols: | 6-phosphogluconate dehydrogenase family protein | chr3:482498-483958 FORWARD LENGTH=486	488	486	0	99.6	95.7	98.4
Rsa1.0_00078.1.g4008.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00078.1.g4009.t1	ref|XP_002884314.1| SEPALLATA2 [Arabidopsis lyrata subsp. lyrata] gi|297330154|gb|EFH60573.1| SEPALLATA2 [Arabidopsis lyrata subsp. lyrata]	294	250	1.00E-120	85.0	76.2	79.6	SEPALLATA2	gbpln	Arabidopsis lyrata	AT3G02310.1 | Symbols: SEP2, AGL4 | K-box region and MADS-box transcription factor family protein | chr3:464554-466687 REVERSE LENGTH=250	294	250	1.00E-122	85.0	75.9	79.6
Rsa1.0_00078.1.g4010.t1	ref|XP_002882220.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] gi|297328060|gb|EFH58479.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	472	471	0	99.8	96.4	97.5	regulator of chromosome condensation family protein	gbpln	Arabidopsis lyrata	AT3G02300.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:461551-463929 FORWARD LENGTH=471	472	471	0	99.8	94.5	96.2
Rsa1.0_00078.1.g4011.t1	emb|CAB86926.1| putative protein [Arabidopsis thaliana]	431	977	5.00E-93	226.7	48.7	65.9	putative protein	gbpln	Arabidopsis thaliana	AT3G58980.1 | Symbols: | F-box family protein | chr3:21794445-21797006 REVERSE LENGTH=594	431	594	3.00E-95	137.8	48.7	65.9
Rsa1.0_00078.1.g4012.t2	gb|EOA31362.1| hypothetical protein CARUB_v10014539mg [Capsella rubella]	221	231	1.00E-92	104.5	86.0	92.3	hypothetical protein CARUB_v10014539mg	gbpln	Capsella rubella	AT3G02290.1 | Symbols: | RING/U-box superfamily protein | chr3:459385-460688 FORWARD LENGTH=231	221	231	1.00E-94	104.5	86.9	92.3
Rsa1.0_00078.1.g4013.t1	ref|XP_002884312.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330152|gb|EFH60571.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	5062	5090	0	100.6	91.2	95.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G02260.1 | Symbols: BIG, DOC1, TIR3, UMB1, ASA1, LPR1, CRM1 | auxin transport protein (BIG) | chr3:431152-448489 REVERSE LENGTH=5098	5062	5098	0	100.7	91.0	95.3
Rsa1.0_00078.1.g4014.t2	ref|XP_002884311.1| hypothetical protein ARALYDRAFT_896190 [Arabidopsis lyrata subsp. lyrata] gi|297330151|gb|EFH60570.1| hypothetical protein ARALYDRAFT_896190 [Arabidopsis lyrata subsp. lyrata]	469	513	0	109.4	82.9	88.1	hypothetical protein ARALYDRAFT_896190	gbpln	Arabidopsis lyrata	AT3G02250.1 | Symbols: | O-fucosyltransferase family protein | chr3:424185-426376 REVERSE LENGTH=512	469	512	0	109.2	82.5	87.4

Rsa1.0_00078.1.g4015.t1	ref|XP_002882216.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328056|gb|EFH58475.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	104	106	1.00E-16	101.9	51.0	57.7	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00078.1.g4016.t1	ref|NP_186872.1| reversibly glycosylated polypeptide 1 [Arabidopsis thaliana] gi|297828664|ref|XP_002882214.1| hypothetical protein ARALYDRAFT_477458 [Arabidopsis lyrata subsp. lyrata] gi|75207399|sp|Q9SRT9.1|RGP1_ARATH RecName: Full=UDP-arabinopyranose mutase 1; AltName: Full=Reversibly glycosylated polypeptide 1; Short=AtRGP1; AltName: Full=UDP-L-arabinose mutase 1 gi|6041795|gb|AAF02115.1|AC009755_8 reversibly glycosylated polypeptide-1 [Arabidopsis thaliana] gi|27311607|gb|AAO00769.1| reversibly glycosylated polypeptide-1 [Arabidopsis thaliana] gi|31711848|gb|AAP68280.1| At3g02230 [Arabidopsis thaliana] gi|297328054|gb|EFH58473.1| hypothetical protein ARALYDRAFT_477458 [Arabidopsis lyrata subsp. lyrata] gi|332640260|gb|AEE73781.1| reversibly glycosylated polypeptide 1 [Arabidopsis thaliana]	357	357	0	100.0	97.5	99.2	reversibly glycosylated polypeptide 1	gbpln	Arabidopsis lyrata	AT3G02230.1 | Symbols: RGP1, ATRGP1 | reversibly glycosylated polypeptide 1 | chr3:415463-417304 FORWARD LENGTH=357	357	357	0	100.0	97.5	99.2
Rsa1.0_00078.1.g4017.t1	ref|XP_002884309.1| hypothetical protein ARALYDRAFT_477457 [Arabidopsis lyrata subsp. lyrata] gi|297330149|gb|EFH60568.1| hypothetical protein ARALYDRAFT_477457 [Arabidopsis lyrata subsp. lyrata]	227	227	1.00E-103	100.0	82.8	86.3	hypothetical protein ARALYDRAFT_477457	gbpln	Arabidopsis lyrata	AT3G02220.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2039 (InterPro:IPR019351); Has 215 Blast hits to 215 proteins in 94 species: Archae - 2; Bacteria - 2; Metazoa - 125; Fungi - 4; Plants - 38; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink). | chr3:412210-413536 REVERSE LENGTH=227	227	227	1.00E-102	100.0	81.9	87.2
Rsa1.0_00078.1.g4018.t1	ref|XP_002884308.1| phytochelatin synthetase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330148|gb|EFH60567.1| phytochelatin synthetase family protein [Arabidopsis lyrata subsp. lyrata]	475	451	0	94.9	87.4	90.9	phytochelatin synthetase family protein	gbpln	Arabidopsis lyrata	AT3G02210.1 | Symbols: COBL1 | COBRA-like protein 1 precursor | chr3:409352-411478 REVERSE LENGTH=452	475	452	0	95.2	86.9	90.5
Rsa1.0_00078.1.g4019.t1	gb|AAF02117.1|AC009755_10 unknown protein [Arabidopsis thaliana] gi|6513915|gb|AAF14819.1|AC011664_1 unknown protein [Arabidopsis thaliana]	397	400	0	100.8	87.2	95.2	unknown protein	gbpln	Arabidopsis thaliana	AT3G02200.2 | Symbols: | Proteasome component (PCI) domain protein | chr3:406692-408919 FORWARD LENGTH=417	397	417	0	105.0	84.6	93.5
Rsa1.0_00078.1.g4020.t1	gb|EOA31810.1| hypothetical protein CARUB_v10015033mg, partial [Capsella rubella]	51	74	4.00E-19	145.1	92.2	96.1	hypothetical protein CARUB_v10015033mg, partial	gbpln	Capsella rubella	AT3G02190.1 | Symbols: | Ribosomal protein L39 family protein | chr3:406005-406342 REVERSE LENGTH=51	51	51	1.00E-21	100.0	94.1	96.1
Rsa1.0_00078.1.g4021.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00079.1.g4022.t1	gb|AAM65279.1| unknown [Arabidopsis thaliana]	192	185	1.00E-61	96.4	78.6	84.4	unknown	gbpln	Arabidopsis thaliana	AT1G67740.1 | Symbols: PSBY, YCF32 | photosystem II BY | chr1:25394429-25394998 REVERSE LENGTH=189	192	189	2.00E-62	98.4	77.1	82.3
Rsa1.0_00079.1.g4023.t1	gb|AFQ32095.1| 3-ketoacyl-CoA reductase 1 [Eutrema halophilum]	319	318	1.00E-169	99.7	88.4	94.7	3-ketoacyl-CoA reductase 1	gbpln	Eutrema halophilum	AT1G67730.1 | Symbols: YBR159, KCR1, ATKCR1 | beta-ketoacyl reductase 1 | chr1:25391676-25393365 FORWARD LENGTH=318	319	318	1.00E-166	99.7	86.2	92.8
Rsa1.0_00079.1.g4024.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00079.1.g4025.t1	gb|EOA33252.1| hypothetical protein CARUB_v10021974mg [Capsella rubella]	932	929	0	99.7	89.6	94.7	hypothetical protein CARUB_v10021974mg	gbpln	Capsella rubella	AT1G67720.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:25386494-25390856 FORWARD LENGTH=929	932	929	0	99.7	89.9	95.1
Rsa1.0_00079.1.g4026.t1	gb|EOA39791.1| hypothetical protein CARUB_v10008446mg [Capsella rubella]	708	718	0	101.4	91.7	95.3	hypothetical protein CARUB_v10008446mg	gbpln	Capsella rubella	AT5G42270.1 | Symbols: VAR1, FTSH5 | FtsH extracellular protease family | chr5:16902659-16905102 FORWARD LENGTH=704	708	704	0	99.4	88.4	93.5
Rsa1.0_00079.1.g4027.t2	ref|XP_002891605.1| hypothetical protein ARALYDRAFT_892050 [Arabidopsis lyrata subsp. lyrata] gi|297337447|gb|EFH67864.1| hypothetical protein ARALYDRAFT_892050 [Arabidopsis lyrata subsp. lyrata]	481	507	0	105.4	80.2	87.9	hypothetical protein ARALYDRAFT_892050	gbpln	Arabidopsis lyrata	AT1G50990.1 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr1:18902930-18905204 FORWARD LENGTH=507	481	507	0	105.4	79.2	87.7

Rsa1.0_00079.1.g4028.t1	ref|XP_002888617.1| hypothetical protein ARALYDRAFT_894522 [Arabidopsis lyrata subsp. lyrata] gi|297334458|gb|EFH64876.1| hypothetical protein ARALYDRAFT_894522 [Arabidopsis lyrata subsp. lyrata]	521	529	0	101.5	81.8	87.1	hypothetical protein ARALYDRAFT_894522	gbpln	Arabidopsis lyrata	AT1G67710.1 | Symbols: ARR11 | response regulator 11 | chr1:25376994-25378905 REVERSE LENGTH=521	521	521	0	100.0	80.0	85.6
Rsa1.0_00079.1.g4029.t1	gb|EOA33518.1| hypothetical protein CARUB_v10019853mg [Capsella rubella]	701	759	0	108.3	88.6	93.4	hypothetical protein CARUB_v10019853mg	gbpln	Capsella rubella	AT1G67690.1 | Symbols: | Zincin-like metalloproteases family protein | chr1:25369086-25373730 FORWARD LENGTH=710	701	710	0	101.3	87.4	93.3
Rsa1.0_00079.1.g4030.t1	ref|NP_195616.2| Kinesin motor family protein [Arabidopsis thaliana] gi|16902294|dbj|BAB71852.1| kinesin-related protein [Arabidopsis thaliana] gi|23297817|gb|AAN13032.1| putative kinesin protein [Arabidopsis thaliana] gi|332661612|gb|AEE87012.1| Kinesin motor family protein [Arabidopsis thaliana]	239	1055	3.00E-32	441.4	27.6	29.7	Kinesin motor family protein	gbpln	Arabidopsis thaliana	AT4G39050.1 | Symbols: | Kinesin motor family protein | chr4:18193462-18200148 FORWARD LENGTH=1055	239	1055	1.00E-34	441.4	27.6	29.7
Rsa1.0_00079.1.g4031.t1	ref|NP_188326.1| AP2/B3 domain-containing protein [Arabidopsis thaliana] gi|75274019|sp|Q9LSP6.1|Y3701_ARATH RecName: Full=B3 domain-containing protein At3g17010 gi|7670025|dbj|BAA94979.1| unnamed protein product [Arabidopsis thaliana] gi|225898651|dbj|BAH30456.1| hypothetical protein [Arabidopsis thaliana] gi|332642373|gb|AEE75894.1| AP2/B3 domain-containing protein [Arabidopsis thaliana]	249	302	1.00E-19	121.3	18.9	23.3	AP2/B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G17010.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr3:5800460-5802303 FORWARD LENGTH=302	249	302	3.00E-22	121.3	18.9	23.3
Rsa1.0_00079.1.g4032.t1	ref|NP_176936.1| signal recognition particle subunit SRP72 [Arabidopsis thaliana] gi|11072013|gb|AAG28892.1|AC008113_8 F12A21.17 [Arabidopsis thaliana] gi|28392947|gb|AAO41909.1| unknown protein [Arabidopsis thaliana] gi|28827690|gb|AAO50689.1| unknown protein [Arabidopsis thaliana] gi|332196560|gb|AEE34681.1| signal recognition particle subunit SRP72 [Arabidopsis thaliana]	660	664	0	100.6	82.6	88.3	signal recognition particle subunit SRP72	gbpln	Arabidopsis thaliana	AT1G67680.1 | Symbols: | SRP72 RNA-binding domain | chr1:25365962-25368464 REVERSE LENGTH=664	660	664	0	100.6	82.6	88.3
Rsa1.0_00079.1.g4033.t1	dbj|BAJ34583.1| unnamed protein product [Thellungiella halophila]	321	352	3.00E-96	109.7	60.4	67.0	unnamed protein product	----	----	AT1G67660.3 | Symbols: | Restriction endonuclease, type II-like superfamily protein | chr1:25364065-25365069 FORWARD LENGTH=334	321	334	5.00E-90	104.0	55.8	64.8
Rsa1.0_00079.1.g4034.t2	ref|XP_002874699.1| hypothetical protein ARALYDRAFT_352228 [Arabidopsis lyrata subsp. lyrata] gi|297320536|gb|EFH50958.1| hypothetical protein ARALYDRAFT_352228 [Arabidopsis lyrata subsp. lyrata]	170	304	2.00E-25	178.8	46.5	62.4	hypothetical protein ARALYDRAFT_352228	gbpln	Arabidopsis lyrata	AT4G11580.1 | Symbols: | RNI-like superfamily protein | chr4:7006648-7007738 REVERSE LENGTH=333	170	333	5.00E-22	195.9	30.6	41.2
Rsa1.0_00079.1.g4035.t1	ref|XP_002887133.1| hypothetical protein ARALYDRAFT_894509 [Arabidopsis lyrata subsp. lyrata] gi|297332974|gb|EFH63392.1| hypothetical protein ARALYDRAFT_894509 [Arabidopsis lyrata subsp. lyrata]	292	248	4.00E-63	84.9	44.5	56.2	hypothetical protein ARALYDRAFT_894509	gbpln	Arabidopsis lyrata	AT1G67623.1 | Symbols: | F-box family protein | chr1:25342111-25343243 FORWARD LENGTH=296	292	296	3.00E-59	101.4	43.5	57.9
Rsa1.0_00079.1.g4036.t1	gb|EOA35764.1| hypothetical protein CARUB_v10020997mg [Capsella rubella]	190	188	4.00E-58	98.9	62.1	71.6	hypothetical protein CARUB_v10020997mg	gbpln	Capsella rubella	AT1G67620.1 | Symbols: | Lojap-related protein | chr1:25340585-25341770 FORWARD LENGTH=184	190	184	3.00E-56	96.8	59.5	68.4
Rsa1.0_00079.1.g4037.t1	ref|NP_176927.1| Acid phosphatase/vanadium-dependent haloperoxidase-related protein [Arabidopsis thaliana] gi|11072018|gb|AAG28897.1|AC008113_13 F12A21.27 [Arabidopsis thaliana] gi|21555489|gb|AAM63870.1| unknown [Arabidopsis thaliana] gi|89274151|gb|ABD65596.1| At1g67600 [Arabidopsis thaliana] gi|332196549|gb|AEE34670.1| Acid phosphatase/vanadium-dependent haloperoxidase-related protein [Arabidopsis thaliana]	177	163	3.00E-78	92.1	81.4	88.1	Acid phosphatase/vanadium-dependent haloperoxidase-related protein	gbpln	Arabidopsis thaliana	AT1G67600.1 | Symbols: | Acid phosphatase/vanadium-dependent haloperoxidase-related protein | chr1:25336701-25337455 REVERSE LENGTH=163	177	163	1.00E-80	92.1	81.4	88.1

<table>
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<tr><td>Rsa1.0_00079.1.g4039.t2</td><td>ref|XP_002888609.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334450|gb|EFH64868.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>818</td><td>756</td><td>0</td><td>92.4</td><td>77.0</td><td>81.7</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G67580.2 | Symbols: | Protein kinase superfamily protein | chr1:25327727-25330965 REVERSE LENGTH=752</td><td>818</td><td>752</td><td>0</td><td>91.9</td><td>76.0</td><td>80.6</td></tr>
<tr><td>Rsa1.0_00079.1.g4040.t2</td><td>ref|NP_564899.1| uncharacterized protein [Arabidopsis thaliana] gi|332196544|gb|AEE34665.1| uncharacterized protein AT1G67570 [Arabidopsis thaliana]</td><td>455</td><td>456</td><td>0</td><td>100.2</td><td>84.8</td><td>88.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G67570.1 | Symbols: | Protein of unknown function (DUF3537) | chr1:25325318-25326938 FORWARD LENGTH=456</td><td>455</td><td>456</td><td>0</td><td>100.2</td><td>84.8</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00079.1.g4041.t1</td><td>gb|EOA34286.1| hypothetical protein CARUB_v10021801mg [Capsella rubella]</td><td>254</td><td>255</td><td>3.00E-73</td><td>100.4</td><td>60.2</td><td>70.9</td><td>hypothetical protein CARUB_v10021801mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G67540.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: petal, leaf whorl, male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, petal differentiation and expansion stage; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:25311496-25312351 REVERSE LENGTH=255</td><td>254</td><td>255</td><td>5.00E-73</td><td>100.4</td><td>59.8</td><td>70.9</td></tr>
<tr><td>Rsa1.0_00079.1.g4042.t1</td><td>gb|EOA22397.1| hypothetical protein CARUB_v10003032mg [Capsella rubella]</td><td>504</td><td>595</td><td>1.00E-167</td><td>118.1</td><td>61.3</td><td>72.6</td><td>hypothetical protein CARUB_v10003032mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G01480.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:192990-194231 FORWARD LENGTH=413</td><td>504</td><td>413</td><td>1.00E-115</td><td>81.9</td><td>43.7</td><td>50.8</td></tr>
<tr><td>Rsa1.0_00079.1.g4043.t1</td><td>ref|NP_176683.1| WD40 domain-containing protein [Arabidopsis thaliana] gi|53828631|gb|AAU94425.1| At1g65030 [Arabidopsis thaliana] gi|332196196|gb|AEE34317.1| WD40 domain-containing protein [Arabidopsis thaliana]</td><td>344</td><td>345</td><td>0</td><td>100.3</td><td>90.4</td><td>95.9</td><td>WD40 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G65030.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:24156798-24158511 FORWARD LENGTH=345</td><td>344</td><td>345</td><td>0</td><td>100.3</td><td>90.4</td><td>95.9</td></tr>
<tr><td>Rsa1.0_00079.1.g4044.t1</td><td>gb|AAF06043.1|AC009360_8 EST gb|T44882 comes from this gene, partial [Arabidopsis thaliana]</td><td>107</td><td>135</td><td>3.00E-44</td><td>126.2</td><td>86.9</td><td>90.7</td><td>EST gb|T44882 comes from this gene, partial</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G65032.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:24158895-24159170 REVERSE LENGTH=91</td><td>107</td><td>91</td><td>2.00E-46</td><td>85.0</td><td>81.3</td><td>84.1</td></tr>
<tr><td>Rsa1.0_00079.1.g4045.t1</td><td>gb|EOA28341.1| hypothetical protein CARUB_v10024542mg [Capsella rubella]</td><td>267</td><td>247</td><td>2.00E-70</td><td>92.5</td><td>52.8</td><td>68.5</td><td>hypothetical protein CARUB_v10024542mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G42730.1 | Symbols: | F-box family protein | chr2:17787454-17791218 REVERSE LENGTH=737</td><td>267</td><td>737</td><td>4.00E-71</td><td>276.0</td><td>55.8</td><td>68.9</td></tr>
<tr><td>Rsa1.0_00079.1.g4046.t1</td><td>ref|XP_002888603.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334444|gb|EFH64862.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>713</td><td>718</td><td>0</td><td>100.7</td><td>88.8</td><td>93.3</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G67510.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:25297477-25300184 REVERSE LENGTH=719</td><td>713</td><td>719</td><td>0</td><td>100.8</td><td>86.1</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00079.1.g4047.t1</td><td>gb|EOA22975.1| hypothetical protein CARUB_v10003716mg [Capsella rubella]</td><td>284</td><td>281</td><td>1.00E-37</td><td>98.9</td><td>38.0</td><td>51.8</td><td>hypothetical protein CARUB_v10003716mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G27070.1 | Symbols: AGL53 | AGAMOUS-like 53 | chr5:9527741-9528604 FORWARD LENGTH=287</td><td>284</td><td>287</td><td>2.00E-34</td><td>101.1</td><td>42.6</td><td>54.9</td></tr>
<tr><td>Rsa1.0_00079.1.g4048.t1</td><td>ref|NP_181801.1| F-box protein [Arabidopsis thaliana] gi|4512680|gb|AAD21734.1| hypothetical protein [Arabidopsis thaliana] gi|330255067|gb|AEC10161.1| F-box protein [Arabidopsis thaliana]</td><td>260</td><td>737</td><td>2.00E-69</td><td>283.5</td><td>59.6</td><td>70.0</td><td>F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G42730.1 | Symbols: | F-box family protein | chr2:17787454-17791218 REVERSE LENGTH=737</td><td>260</td><td>737</td><td>5.00E-72</td><td>283.5</td><td>59.6</td><td>70.0</td></tr>
<tr><td>Rsa1.0_00079.1.g4049.t19</td><td>ref|NP_001185336.1| HEAT repeat-containing protein [Arabidopsis thaliana] gi|332196480|gb|AEE34601.1| HEAT repeat-containing protein [Arabidopsis thaliana]</td><td>2376</td><td>2223</td><td>0</td><td>93.6</td><td>77.9</td><td>82.3</td><td>HEAT repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G67140.3 | Symbols: SWEETIE | HEAT repeat-containing protein | chr1:25101016-25117372 REVERSE LENGTH=2223</td><td>2376</td><td>2223</td><td>0</td><td>93.6</td><td>77.9</td><td>82.3</td></tr>
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Rsa1.0_00079.1.g4050.t1	ref|XP_002887107.1| hypothetical protein ARALYDRAFT_475814 [Arabidopsis lyrata subsp. lyrata] gi|297332948|gb|EFH63366.1| hypothetical protein ARALYDRAFT_475814 [Arabidopsis lyrata subsp. lyrata]	328	364	1.00E-134	111.0	76.2	85.1	hypothetical protein ARALYDRAFT_475814	gbpln	Arabidopsis lyrata	AT1G67170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14750.1); Has 5478 Blast hits to 4354 proteins in 533 species: Archae - 87; Bacteria - 653; Metazoa - 2554; Fungi - 380; Plants - 418; Viruses - 16; Other Eukaryotes - 1370 (source: NCBI BLink). | chr1:25127727-25129145 FORWARD LENGTH=359	328	359	1.00E-132	109.5	74.1	83.2
Rsa1.0_00079.1.g4051.t1	gb|EOA35210.1| hypothetical protein CARUB_v10020360mg [Capsella rubella]	419	419	0	100.0	93.6	97.1	hypothetical protein CARUB_v10020360mg	gbpln	Capsella rubella	AT1G67190.2 | Symbols: | F-box/RNI-like superfamily protein | chr1:25133054-25134313 FORWARD LENGTH=419	419	419	0	100.0	92.8	96.9
Rsa1.0_00079.1.g4052.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00079.1.g4053.t1	ref|NP_176892.1| protein little nuclei1 [Arabidopsis thaliana] gi|332196494|gb|AEE34615.1| protein little nuclei1 [Arabidopsis thaliana]	1094	1132	0	103.5	80.3	89.9	protein little nuclei1	gbpln	Arabidopsis thaliana	AT1G67230.1 | Symbols: LINC1 | little nuclei1 | chr1:25151561-25156032 REVERSE LENGTH=1132	1094	1132	0	103.5	80.3	89.9
Rsa1.0_00079.1.g4054.t1	emb|CAN64046.1| hypothetical protein VITISV_040537 [Vitis vinifera]	428	1259	1.00E-74	294.2	31.8	39.5	hypothetical protein VITISV_040537	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00079.1.g4055.t1	gb|AAG00256.1|AC002130_21 F1N21.7 [Arabidopsis thaliana]	141	303	1.00E-69	214.9	87.9	95.0	F1N21.7	gbpln	Arabidopsis thaliana	AT1G67250.1 | Symbols: | Proteasome maturation factor UMP1 | chr1:25163808-25164967 REVERSE LENGTH=141	141	141	4.00E-71	100.0	88.7	95.0
Rsa1.0_00079.1.g4056.t1	ref|NP_174229.2| uncharacterized protein [Arabidopsis thaliana] gi|332192954|gb|AEE31075.1| uncharacterized protein AT1G29350 [Arabidopsis thaliana]	869	831	0	95.6	74.9	81.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G29350.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr1:10268761-10273613 REVERSE LENGTH=831	869	831	0	95.6	74.9	81.6
Rsa1.0_00079.1.g4057.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	376	411	4.00E-88	109.3	53.2	69.7	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT2G38590.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:16142897-16144171 FORWARD LENGTH=424	376	424	1.00E-89	112.8	54.0	69.7
Rsa1.0_00079.1.g4058.t1	emb|CBI30817.3| unnamed protein product [Vitis vinifera]	375	195	1.00E-34	52.0	23.7	29.1	unnamed protein product	gbpln	Vitis vinifera	AT2G30933.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr2:13164179-13166517 REVERSE LENGTH=227	375	227	2.00E-30	60.5	15.5	18.7
Rsa1.0_00079.1.g4059.t1	ref|NP_564327.1| cold regulated 314 thylakoid membrane 2 [Arabidopsis thaliana] gi|426019472|sp|F4I1G5.1|CRIM2_ARATH RecName: Full=Cold-regulated 413 inner membrane protein 2, chloroplastic; Short=AtCOR413-IM2; AltName: Full=Cold-regulated 413 thylakoid membrane 2; Short=AtCOR413-TM2; Flags: Precursor gi|332192959|gb|AEE31080.1| cold regulated 314 thylakoid membrane 2 [Arabidopsis thaliana]	223	226	1.00E-97	101.3	81.2	89.7	cold regulated 314 thylakoid membrane 2	gbpln	Arabidopsis thaliana	AT1G29390.1 | Symbols: COR314-TM2, COR413IM2 | cold regulated 314 thylakoid membrane 2 | chr1:10286409-10287878 REVERSE LENGTH=226	223	226	1.00E-100	101.3	81.2	89.7
Rsa1.0_00079.1.g4060.t1	gb|EOA39685.1| hypothetical protein CARUB_v10008326mg [Capsella rubella]	805	798	0	99.1	83.2	89.4	hypothetical protein CARUB_v10008326mg	gbpln	Capsella rubella	AT1G29400.2 | Symbols: AML5, ML5 | MEI2-like protein 5 | chr1:10290393-10293696 REVERSE LENGTH=800	805	800	0	99.4	83.4	89.1
Rsa1.0_00079.1.g4061.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00079.1.g4062.t1	gb|ABV89665.1| auxin-responsive protein [Brassica rapa]	137	139	1.00E-56	101.5	82.5	90.5	auxin-responsive protein	gbpln	Brassica rapa	AT1G29500.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:10321290-10321697 FORWARD LENGTH=135	137	135	9.00E-56	98.5	77.4	83.9
Rsa1.0_00079.1.g4063.t1	gb|AAM64520.1| auxin-induced protein, putative [Arabidopsis thaliana]	142	141	1.00E-57	99.3	83.8	90.1	auxin-induced protein, putative	gbpln	Arabidopsis thaliana	AT1G29450.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:10305981-10306406 REVERSE LENGTH=141	142	141	3.00E-59	99.3	83.1	89.4
Rsa1.0_00079.1.g4064.t1	#	#	#	#	#	#	#	-	----	----	AT2G24280.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:10334622-10336927 FORWARD LENGTH=494	106	494	4.00E-12	466.0	33.0	34.9
Rsa1.0_00079.1.g4065.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00079.1.g4066.t1	emb|CAA48292.1| bgp1 [Brassica rapa] gi|448272|prf||1916399A Bgp1 gene	57	119	9.00E-12	208.8	73.7	77.2	bgp1	gbpln	Brassica rapa	AT1G24520.1 | Symbols: BCP1 | homolog of Brassica campestris pollen protein 1 | chr1:8688699-8689058 FORWARD LENGTH=119	57	119	7.00E-14	208.8	73.7	77.2
Rsa1.0_00079.1.g4067.t1	ref|XP_002893444.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297339286|gb|EFH69703.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	536	418	0	78.0	67.4	70.7	transducin family protein	gbpln	Arabidopsis lyrata	AT1G24530.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:8693287-8694543 FORWARD LENGTH=418	536	418	0	78.0	66.8	70.3

Rsa1.0_00079.1.g4068.t12	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2006	1274	0	63.5	17.1	23.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2006	575	7.00E-52	28.7	6.1	10.2
Rsa1.0_00079.1.g4069.t1	ref|XP_002893443.1| CYP86C1 [Arabidopsis lyrata subsp. lyrata] gi|297339285|gb|EFH69702.1| CYP86C1 [Arabidopsis lyrata subsp. lyrata]	517	522	0	101.0	83.0	91.1	CYP86C1	gbpln	Arabidopsis lyrata	AT1G24540.1 | Symbols: CYP86C1 | cytochrome P450, family 86, subfamily C, polypeptide 1 | chr1:8699751-8701319 FORWARD LENGTH=522	517	522	0	101.0	82.0	90.3
Rsa1.0_00079.1.g4070.t1	ref|XP_002890706.1| hypothetical protein ARALYDRAFT_890218 [Arabidopsis lyrata subsp. lyrata] gi|297336548|gb|EFH66965.1| hypothetical protein ARALYDRAFT_890218 [Arabidopsis lyrata subsp. lyrata]	393	421	1.00E-173	107.1	77.6	85.2	hypothetical protein ARALYDRAFT_890218	gbpln	Arabidopsis lyrata	AT1G67800.4 | Symbols: | Copine (Calcium-dependent phospholipid-binding protein) family | chr1:25421029-25423237 REVERSE LENGTH=433	393	433	1.00E-166	110.2	72.5	81.7
Rsa1.0_00079.1.g4071.t1	gb|AAC23765.1| Mutator-like transposase [Arabidopsis thaliana]	481	784	2.00E-23	163.0	11.4	15.8	Mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00079.1.g4072.t1	ref|XP_002882271.1| hypothetical protein ARALYDRAFT_896293 [Arabidopsis lyrata subsp. lyrata] gi|297328111|gb|EFH58530.1| hypothetical protein ARALYDRAFT_896293 [Arabidopsis lyrata subsp. lyrata]	207	164	4.00E-16	79.2	21.7	28.5	hypothetical protein ARALYDRAFT_896293	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00079.1.g4073.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1716	1213	0	70.7	40.0	51.6	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1716	626	2.00E-74	36.5	8.9	14.8
Rsa1.0_00079.1.g4074.t2	gb|EOA39560.1| hypothetical protein CARUB_v10008178mg [Capsella rubella]	956	1022	0	106.9	77.2	85.7	hypothetical protein CARUB_v10008178mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	956	1019	0	106.6	73.0	82.1
Rsa1.0_00079.1.g4075.t1	ref|XP_002863747.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309582|gb|EFH40006.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	965	989	0	102.5	58.8	73.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G46470.1 | Symbols: RPS6 | disease resistance protein (TIR-NBS-LRR class) family | chr5:18842701-18846809 FORWARD LENGTH=1127	965	1127	0	116.8	56.1	63.6
Rsa1.0_00079.1.g4076.t3	ref|XP_002893580.1| hypothetical protein ARALYDRAFT_473178 [Arabidopsis lyrata subsp. lyrata] gi|297339422|gb|EFH69839.1| hypothetical protein ARALYDRAFT_473178 [Arabidopsis lyrata subsp. lyrata]	1017	1023	0	100.6	78.5	87.9	hypothetical protein ARALYDRAFT_473178	gbpln	Arabidopsis lyrata	AT1G29750.2 | Symbols: RKF1 | receptor-like kinase in flowers 1 | chr1:10414071-10420469 REVERSE LENGTH=1021	1017	1021	0	100.4	78.3	87.7
Rsa1.0_00080.1.g4077.t1	ref|XP_002882754.1| hypothetical protein ARALYDRAFT_897397 [Arabidopsis lyrata subsp. lyrata] gi|297328594|gb|EFH59013.1| hypothetical protein ARALYDRAFT_897397 [Arabidopsis lyrata subsp. lyrata]	433	432	0	99.8	87.8	94.0	hypothetical protein ARALYDRAFT_897397	gbpln	Arabidopsis lyrata	AT3G11900.1 | Symbols: ANT1 | aromatic and neutral transporter 1 | chr3:3758523-3760103 FORWARD LENGTH=432	433	432	0	99.8	88.0	94.5
Rsa1.0_00080.1.g4078.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00080.1.g4079.t6	ref|XP_002884872.1| hypothetical protein ARALYDRAFT_317971 [Arabidopsis lyrata subsp. lyrata] gi|297330712|gb|EFH61131.1| hypothetical protein ARALYDRAFT_317971 [Arabidopsis lyrata subsp. lyrata]	1175	1115	0	94.9	84.6	88.9	hypothetical protein ARALYDRAFT_317971	gbpln	Arabidopsis lyrata	AT3G11910.1 | Symbols: UBP13 | ubiquitin-specific protease 13 | chr3:3761758-3770290 REVERSE LENGTH=1115	1175	1115	0	94.9	84.0	88.6
Rsa1.0_00080.1.g4080.t1	ref|XP_002882756.1| universal stress protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297328596|gb|EFH59015.1| universal stress protein family protein [Arabidopsis lyrata subsp. lyrata]	200	200	3.00E-93	100.0	82.5	89.0	universal stress protein family protein	gbpln	Arabidopsis lyrata	AT3G11930.2 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:3776371-3777393 FORWARD LENGTH=200	200	200	2.00E-94	100.0	82.5	90.5
Rsa1.0_00080.1.g4081.t1	gb|EOA27796.1| hypothetical protein CARUB_v10023948mg, partial [Capsella rubella]	207	241	1.00E-114	116.4	96.6	98.6	hypothetical protein CARUB_v10023948mg, partial	gbpln	Capsella rubella	AT2G37270.2 | Symbols: ATRPS5B, RPS5B | ribosomal protein 5B | chr2:15647883-15649042 REVERSE LENGTH=207	207	207	1.00E-116	100.0	95.7	98.6
Rsa1.0_00080.1.g4082.t2	ref|XP_002884874.1| prenyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297330714|gb|EFH61133.1| prenyltransferase [Arabidopsis lyrata subsp. lyrata]	326	385	1.00E-176	118.1	92.9	95.7	prenyltransferase	gbpln	Arabidopsis lyrata	AT3G11945.1 | Symbols: PDS2, ATHST, HST | homogentisate prenyltransferase | chr3:3780041-3782880 REVERSE LENGTH=386	326	386	1.00E-175	118.4	92.9	95.1
Rsa1.0_00080.1.g4083.t1	ref|XP_002882731.1| glycerol-3-phosphate acyltransferase 5 [Arabidopsis lyrata subsp. lyrata] gi|297328571|gb|EFH58990.1| glycerol-3-phosphate acyltransferase 5 [Arabidopsis lyrata subsp. lyrata]	113	502	8.00E-39	444.2	72.6	81.4	glycerol-3-phosphate acyltransferase 5	gbpln	Arabidopsis lyrata	AT3G11430.1 | Symbols: ATGPAT5, GPAT5 | glycerol-3-phosphate acyltransferase 5 | chr3:3595911-3597678 FORWARD LENGTH=502	113	502	6.00E-40	444.2	70.8	80.5

Rsa1.0_00080.1.g4084.t3	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1498	1496	0	99.9	58.9	71.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1498	1262	1.00E-140	84.2	16.0	22.2
Rsa1.0_00080.1.g4085.t2	ref|NP_187803.4| RNA binding protein [Arabidopsis thaliana] gi|332641610|gb|AEE75131.1| RNA binding protein [Arabidopsis thaliana]	1929	1896	0	98.3	84.2	90.6	RNA binding protein	gbpln	Arabidopsis thaliana	AT3G11964.1 | Symbols: | RNA binding;RNA binding | chr3:3793957-3806626 REVERSE LENGTH=1896	1929	1896	0	98.3	84.2	90.6
Rsa1.0_00080.1.g4086.t1	gb|EOA31497.1| hypothetical protein CARUB_v10014683mg [Capsella rubella]	274	198	2.00E-53	72.3	43.1	43.4	hypothetical protein CARUB_v10014683mg	gbpln	Capsella rubella	AT1G55310.3 | Symbols: SR33, SCL33, At-SCL33 | SC35-like splicing factor 33 | chr1:20630676-20632695 FORWARD LENGTH=300	274	300	1.00E-41	109.5	33.6	39.1
Rsa1.0_00080.1.g4087.t1	ref|XP_002882759.1| hypothetical protein ARALYDRAFT_478549 [Arabidopsis lyrata subsp. lyrata] gi|297328599|gb|EFH59018.1| hypothetical protein ARALYDRAFT_478549 [Arabidopsis lyrata subsp. lyrata]	616	616	0	100.0	90.3	95.3	hypothetical protein ARALYDRAFT_478549	gbpln	Arabidopsis lyrata	AT3G11980.1 | Symbols: MS2, FAR2 | Jojoba acyl CoA reductase-related male sterility protein | chr3:3814484-3816927 FORWARD LENGTH=616	616	616	0	100.0	89.4	94.8
Rsa1.0_00080.1.g4088.t1	ref|NP_564494.1| protein downregulated in DIF1 18 [Arabidopsis thaliana] gi|7767668|gb|AAF69165.1|AC007915_17 F27F5.27 [Arabidopsis thaliana] gi|332193971|gb|AEE32092.1| protein downregulated in DIF1 18 [Arabidopsis thaliana]	169	172	2.00E-48	101.8	53.8	74.6	protein downregulated in DIF1 18	gbpln	Arabidopsis thaliana	AT1G45190.1 | Symbols: DD18 | downregulated in DIF1 18 | chr1:17104406-17104924 FORWARD LENGTH=172	169	172	7.00E-51	101.8	53.8	74.6
Rsa1.0_00080.1.g4089.t1	gb|EOA33095.1| hypothetical protein CARUB_v10016433mg [Capsella rubella]	128	685	2.00E-32	535.2	56.3	60.2	hypothetical protein CARUB_v10016433mg	gbpln	Capsella rubella	AT3G12010.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: sperm cell, cultured cell; CONTAINS InterPro DOMAIN/s: Colon cancer-associated Mic1-like (InterPro:IPR009755); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:3821337-3825537 FORWARD LENGTH=682	128	682	5.00E-35	532.8	55.5	60.2
Rsa1.0_00080.1.g4090.t2	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	708	1231	0	173.9	47.3	64.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	708	575	1.00E-100	81.2	28.4	44.5
Rsa1.0_00080.1.g4091.t1	ref|NP_187809.3| kinesin motor protein-like protein [Arabidopsis thaliana] gi|332641616|gb|AEE75137.1| kinesin motor protein-like protein [Arabidopsis thaliana]	955	965	0	101.0	88.6	93.2	kinesin motor protein-like protein	gbpln	Arabidopsis thaliana	AT3G12020.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:3827016-3834146 FORWARD LENGTH=965	955	965	0	101.0	88.6	93.2
Rsa1.0_00080.1.g4092.t1	ref|NP_187811.1| DNA-3-methyladenine glycosylase [Arabidopsis thaliana] gi|2833373|sp|Q39147.1|3MG_ARATH RecName: Full=DNA-3-methyladenine glycosylase; AltName: Full=3-methyladenine DNA glycosidase gi|12322001|gb|AAG51039.1|AC069473_1 DNA-3-methlyadenine glycosylase (MAG); 45351-46783 [Arabidopsis thaliana] gi|429157|emb|CAA53763.1| 3-methyladenine glycosylase [Arabidopsis thaliana] gi|10998145|dbj|BAB03116.1| DNA-3-methyladenine glycosylase (3-methyladenine DNA glycosidase) [Arabidopsis thaliana] gi|332641619|gb|AEE75140.1| DNA-3-methyladenine glycosylase [Arabidopsis thaliana]	253	254	1.00E-123	100.4	85.8	91.7	DNA-3-methyladenine glycosylase	gbpln	Arabidopsis thaliana	AT3G12040.1 | Symbols: | DNA-3-methyladenine glycosylase (MAG) | chr3:3835349-3836781 REVERSE LENGTH=254	253	254	1.00E-126	100.4	85.8	91.7
Rsa1.0_00080.1.g4093.t2	gb|EOA30887.1| hypothetical protein CARUB_v10014031mg [Capsella rubella]	427	362	1.00E-154	84.8	65.1	69.3	hypothetical protein CARUB_v10014031mg	gbpln	Capsella rubella	AT3G12050.1 | Symbols: | Aha1 domain-containing protein | chr3:3839289-3841303 FORWARD LENGTH=360	427	360	1.00E-153	84.3	65.1	69.8
Rsa1.0_00080.1.g4094.t1	ref|XP_002882764.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328604|gb|EFH59023.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	537	559	0	104.1	78.4	87.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G12060.1 | Symbols: TBL1 | Plant protein of unknown function (DUF828) | chr3:3843142-3845150 FORWARD LENGTH=556	537	556	0	103.5	76.9	86.0
Rsa1.0_00080.1.g4095.t1	gb|EOA30058.1| hypothetical protein CARUB_v10013165mg [Capsella rubella]	657	655	0	99.7	87.1	91.9	hypothetical protein CARUB_v10013165mg	gbpln	Capsella rubella	AT3G12080.1 | Symbols: emb2738 | GTP-binding family protein | chr3:3847851-3851980 FORWARD LENGTH=663	657	663	0	100.9	88.0	92.5

Rsa1.0_00080.1.g4096.t1	ref|XP_002884881.1| hypothetical protein ARALYDRAFT_478564 [Arabidopsis lyrata subsp. lyrata] gi|297330721|gb|EFH61140.1| hypothetical protein ARALYDRAFT_478564 [Arabidopsis lyrata subsp. lyrata]	282	282	1.00E-143	100.0	95.7	97.9	hypothetical protein ARALYDRAFT_478564	gbpln	Arabidopsis lyrata	AT3G12090.1 | Symbols: TET6 | tetraspanin6 | chr3:3852326-3853714 REVERSE LENGTH=282	282	282	1.00E-145	100.0	94.7	97.9
Rsa1.0_00080.1.g4097.t2	dbj|BAJ34578.1| unnamed protein product [Thellungiella halophila]	605	393	0	65.0	59.0	61.3	unnamed protein product	----	----	AT3G12100.1 | Symbols: | Cation efflux family protein | chr3:3854741-3857270 REVERSE LENGTH=393	605	393	0	65.0	58.5	60.5
Rsa1.0_00080.1.g4098.t1	ref|NP_187818.1| actin-11 [Arabidopsis thaliana] gi|1703129|sp|P53496.1|ACT11_ARATH RecName: Full=Actin-11 gi|12322007|gb|AAG51045.1|AC069473_7 actin 11 (ACT11); 24016-22523 [Arabidopsis thaliana] gi|1002533|gb|AAB39404.1| actin-11 [Arabidopsis thaliana] gi|9294108|dbj|BAB01959.1| actin 11 [Arabidopsis thaliana] gi|21593328|gb|AAM65277.1| actin 11 (ACT11) [Arabidopsis thaliana] gi|26451746|dbj|BAC42968.1| unknown protein [Arabidopsis thaliana] gi|28973377|gb|AAO64013.1| putative actin 11 (ACT11) [Arabidopsis thaliana] gi|332641630|gb|AEE75151.1| actin-11 [Arabidopsis thaliana]	186	377	1.00E-103	202.7	97.3	99.5	actin-11	gbpln	Arabidopsis thaliana	AT3G12110.1 | Symbols: ACT11 | actin-11 | chr3:3858116-3859609 FORWARD LENGTH=377	186	377	1.00E-105	202.7	97.3	99.5
Rsa1.0_00080.1.g4099.t1	gb|AFC41106.1| FAD2-1 [Brassica oleracea]	384	384	0	100.0	97.1	98.7	FAD2-1	gbpln	Brassica oleracea	AT3G12120.2 | Symbols: FAD2 | fatty acid desaturase 2 | chr3:3860592-3861743 REVERSE LENGTH=383	384	383	0	99.7	90.9	94.8
Rsa1.0_00080.1.g4100.t1	ref|XP_002884884.1| KH domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330724|gb|EFH61143.1| KH domain-containing protein [Arabidopsis lyrata subsp. lyrata]	245	245	1.00E-114	100.0	90.2	94.3	KH domain-containing protein	gbpln	Arabidopsis lyrata	AT3G12130.1 | Symbols: | KH domain-containing protein / zinc finger (CCCH type) family protein | chr3:3864486-3866406 REVERSE LENGTH=248	245	248	1.00E-110	101.2	86.9	93.5
Rsa1.0_00080.1.g4101.t1	ref|XP_002889521.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335363|gb|EFH65780.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	183	1043	1.00E-10	569.9	20.2	24.0	kinase family protein	gbpln	Arabidopsis lyrata	AT1G04700.1 | Symbols: | PB1 domain-containing protein tyrosine kinase | chr1:1316919-1320653 FORWARD LENGTH=1042	183	1042	2.00E-12	569.4	18.6	23.0
Rsa1.0_00080.1.g4102.t1	ref|XP_002871631.1| hypothetical protein ARALYDRAFT_488325 [Arabidopsis lyrata subsp. lyrata] gi|297317468|gb|EFH47890.1| hypothetical protein ARALYDRAFT_488325 [Arabidopsis lyrata subsp. lyrata]	384	384	0	100.0	91.7	96.6	hypothetical protein ARALYDRAFT_488325	gbpln	Arabidopsis lyrata	AT5G14780.1 | Symbols: FDH | formate dehydrogenase | chr5:4777043-4779190 FORWARD LENGTH=384	384	384	0	100.0	89.6	95.6
Rsa1.0_00080.1.g4103.t1	ref|XP_002884885.1| hypothetical protein ARALYDRAFT_341336 [Arabidopsis lyrata subsp. lyrata] gi|297330725|gb|EFH61144.1| hypothetical protein ARALYDRAFT_341336 [Arabidopsis lyrata subsp. lyrata]	476	431	1.00E-101	90.5	47.1	63.2	hypothetical protein ARALYDRAFT_341336	gbpln	Arabidopsis lyrata	AT1G50920.1 | Symbols: | Nucleolar GTP-binding protein | chr1:18870555-18872570 FORWARD LENGTH=671	476	671	1.00E-74	141.0	40.1	57.8
Rsa1.0_00080.1.g4104.t4	ref|XP_002884889.1| leucine-rich repeat protein FLR1 [Arabidopsis lyrata subsp. lyrata] gi|297330729|gb|EFH61148.1| leucine-rich repeat protein FLR1 [Arabidopsis lyrata subsp. lyrata]	484	325	1.00E-109	67.1	41.1	48.6	leucine-rich repeat protein FLR1	gbpln	Arabidopsis lyrata	AT3G12145.1 | Symbols: FLR1, FLOR1 | Leucine-rich repeat (LRR) family protein | chr3:3874764-3876075 REVERSE LENGTH=325	484	325	1.00E-111	67.1	41.3	48.1
Rsa1.0_00081.1.g4105.t2	ref|XP_002875887.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321725|gb|EFH52146.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	367	315	1.00E-130	85.8	62.9	73.6	predicted protein	gbpln	Arabidopsis lyrata	AT3G48210.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Kinetochore-Ndc80 complex, subunit Spc25 (InterPro:IPR013255); Has 194 Blast hits to 194 proteins in 72 species: Archae - 0; Bacteria - 4; Metazoa - 72; Fungi - 39; Plants - 62; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr3:17849435-17851396 FORWARD LENGTH=315	367	315	1.00E-131	85.8	62.9	72.2
Rsa1.0_00081.1.g4106.t1	ref|XP_002875882.1| hypothetical protein ARALYDRAFT_323420 [Arabidopsis lyrata subsp. lyrata] gi|297321720|gb|EFH52141.1| hypothetical protein ARALYDRAFT_323420 [Arabidopsis lyrata subsp. lyrata]	3068	3832	0	124.9	84.0	89.0	hypothetical protein ARALYDRAFT_323420	gbpln	Arabidopsis lyrata	AT3G48190.1 | Symbols: ATM, ATATM | ataxia-telangiectasia mutated | chr3:17797628-17828361 FORWARD LENGTH=3845	3068	3845	0	125.3	83.7	88.9
Rsa1.0_00081.1.g4107.t5	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00081.1.g4108.t5	ref|XP_002889872.1| At1g11500 [Arabidopsis lyrata subsp. lyrata] gi|297335714|gb|EFH66131.1| At1g11500 [Arabidopsis lyrata subsp. lyrata]	250	184	7.00E-56	73.6	44.8	50.0	At1g11500	gbpln	Arabidopsis lyrata	AT1G11500.1 | Symbols: | Protein of unknown function (DUF1218) | chr1:3870833-3871570 FORWARD LENGTH=184	250	184	8.00E-57	73.6	46.8	51.2
Rsa1.0_00081.1.g4109.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00081.1.g4110.t1	ref|XP_002889873.1| C-terminal cysteine residue is changed to A serine 1 [Arabidopsis lyrata subsp. lyrata] gi|297335715|gb|EFH66132.1| C-terminal cysteine residue is changed to A serine 1 [Arabidopsis lyrata subsp. lyrata]	126	118	5.00E-53	93.7	79.4	88.9	C-terminal cysteine residue is changed to A serine 1	gbpln	Arabidopsis lyrata	AT1G11530.1 | Symbols: ATCXXS1, CXXS1 | C-terminal cysteine residue is changed to a serine 1 | chr1:3874518-3875311 FORWARD LENGTH=118	126	118	4.00E-55	93.7	78.6	87.3
Rsa1.0_00081.1.g4111.t1	gb|AAF16642.1|AC011661_20 T23J18.21 [Arabidopsis thaliana]	175	304	3.00E-43	173.7	46.9	49.7	T23J18.21	gbpln	Arabidopsis thaliana	AT1G11545.1 | Symbols: XTH8 | xyloglucan endotransglucosylase/hydrolase 8 | chr1:3878689-3880286 REVERSE LENGTH=305	175	305	1.00E-45	174.3	46.9	49.7
Rsa1.0_00081.1.g4112.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00081.1.g4113.t1	ref|XP_002889875.1| hypothetical protein ARALYDRAFT_888463 [Arabidopsis lyrata subsp. lyrata] gi|297335717|gb|EFH66134.1| hypothetical protein ARALYDRAFT_888463 [Arabidopsis lyrata subsp. lyrata]	89	89	7.00E-38	100.0	88.8	93.3	hypothetical protein ARALYDRAFT_888463	gbpln	Arabidopsis lyrata	AT1G11572.1 | Symbols: | Plant thionin family protein | chr1:3884455-3884724 FORWARD LENGTH=89	89	89	5.00E-38	100.0	83.1	91.0
Rsa1.0_00081.1.g4114.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00081.1.g4115.t1	ref|XP_002889876.1| At1g11580/T23J18_33 [Arabidopsis lyrata subsp. lyrata] gi|297335718|gb|EFH66135.1| At1g11580/T23J18_33 [Arabidopsis lyrata subsp. lyrata]	554	556	0	100.4	87.0	94.0	At1g11580/T23J18_33	gbpln	Arabidopsis lyrata	AT1G11580.1 | Symbols: ATPMEPCRA, PMEPCRA | methylesterase PCR A | chr1:3888730-3890649 FORWARD LENGTH=557	554	557	0	100.5	87.0	93.7
Rsa1.0_00081.1.g4116.t1	gb|ABJ98060.1| glucose 6-Pi/Pi transporter [Eutrema halophilum]	442	388	0	87.8	79.4	82.4	glucose 6-Pi/Pi transporter	gbpln	Eutrema halophilum	AT1G61800.1 | Symbols: GPT2, ATGPT2 | glucose-6-phosphate/phosphate translocator 2 | chr1:22824527-22826459 FORWARD LENGTH=388	442	388	1.00E-175	87.8	69.5	76.7
Rsa1.0_00081.1.g4117.t1	ref|XP_002889880.1| CYP77B1 [Arabidopsis lyrata subsp. lyrata] gi|297335722|gb|EFH66139.1| CYP77B1 [Arabidopsis lyrata subsp. lyrata]	476	510	0	107.1	88.2	92.6	CYP77B1	gbpln	Arabidopsis lyrata	AT1G11600.1 | Symbols: CYP77B1 | cytochrome P450, family 77, subfamily B, polypeptide 1 | chr1:3902090-3903622 FORWARD LENGTH=510	476	510	0	107.1	88.0	92.4
Rsa1.0_00081.1.g4118.t4	gb|EOA40397.1| hypothetical protein CARUB_v10009124mg, partial [Capsella rubella]	495	448	1.00E-121	90.5	42.8	44.8	hypothetical protein CARUB_v10009124mg, partial	gbpln	Capsella rubella	AT1G11650.1 | Symbols: ATRBP45B, RBP45B | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:3914895-3917301 FORWARD LENGTH=306	495	306	1.00E-113	61.8	41.2	43.4
Rsa1.0_00081.1.g4119.t1	ref|XP_002889884.1| hypothetical protein ARALYDRAFT_471303 [Arabidopsis lyrata subsp. lyrata] gi|297335726|gb|EFH66143.1| hypothetical protein ARALYDRAFT_471303 [Arabidopsis lyrata subsp. lyrata]	115	113	2.00E-41	98.3	76.5	82.6	hypothetical protein ARALYDRAFT_471303	gbpln	Arabidopsis lyrata	AT1G11655.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G21902.1); Has 22 Blast hits to 22 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:3919338-3919679 FORWARD LENGTH=113	115	113	2.00E-43	98.3	73.9	82.6
Rsa1.0_00081.1.g4120.t1	ref|XP_002893783.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339625|gb|EFH70042.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	223	276	5.00E-13	123.8	28.3	42.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G03495.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:873804-875025 REVERSE LENGTH=226	223	226	1.00E-12	101.3	30.0	41.7
Rsa1.0_00081.1.g4121.t1	ref|NP_001184966.1| ATP-dependent Clp protease proteolytic subunit 6 [Arabidopsis thaliana] gi|332190658|gb|AEE28779.1| ATP-dependent Clp protease proteolytic subunit 6 [Arabidopsis thaliana]	193	289	5.00E-43	149.7	47.2	48.2	ATP-dependent Clp protease proteolytic subunit 6	gbpln	Arabidopsis thaliana	AT1G11750.2 | Symbols: CLPP6 | CLP protease proteolytic subunit 6 | chr1:3967609-3969535 FORWARD LENGTH=289	193	289	2.00E-45	149.7	47.2	48.2
Rsa1.0_00081.1.g4122.t1	ref|NP_849642.1| self-incompatibility protein S1 family [Arabidopsis thaliana] gi|4835779|gb|AAD30245.1|AC007296_6 F25C20.8 [Arabidopsis thaliana] gi|26452159|dbj|BAC43168.1| unknown protein [Arabidopsis thaliana] gi|28416883|gb|AAO42972.1| At1g11763 [Arabidopsis thaliana] gi|332190661|gb|AEE28782.1| self-incompatibility protein S1 family [Arabidopsis thaliana]	124	137	2.00E-32	110.5	56.5	74.2	self-incompatibility protein S1 family	gbpln	Arabidopsis thaliana	AT1G11765.1 | Symbols: | Plant self-incompatibility protein S1 family | chr1:3973908-3974321 FORWARD LENGTH=137	124	137	3.00E-35	110.5	56.5	74.2
Rsa1.0_00081.1.g4123.t1	gb|EOA37855.1| hypothetical protein CARUB_v10011450mg [Capsella rubella]	126	137	7.00E-31	108.7	54.0	66.7	hypothetical protein CARUB_v10011450mg	gbpln	Capsella rubella	AT1G11765.1 | Symbols: | Plant self-incompatibility protein S1 family | chr1:3973908-3974321 FORWARD LENGTH=137	126	137	3.00E-33	108.7	50.0	70.6

Rsa1.0_00081.1.g4124.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	466	255	5.00E-96	54.7	38.0	43.8	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	466	302	1.00E-40	64.8	20.4	28.3
Rsa1.0_00081.1.g4125.t1	ref|XP_002889895.1| hypothetical protein ARALYDRAFT_471318 [Arabidopsis lyrata subsp. lyrata] gi|297335737|gb|EFH66154.1| hypothetical protein ARALYDRAFT_471318 [Arabidopsis lyrata subsp. lyrata]	538	536	0	99.6	79.9	87.9	hypothetical protein ARALYDRAFT_471318	gbpln	Arabidopsis lyrata	AT1G11770.1 | Symbols: | FAD-binding Berberine family protein | chr1:3975679-3977289 FORWARD LENGTH=536	538	536	0	99.6	80.5	90.1
Rsa1.0_00081.1.g4126.t1	ref|XP_002892656.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297338498|gb|EFH68915.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	647	345	1.00E-179	53.3	47.1	49.8	oxidoreductase	gbpln	Arabidopsis lyrata	AT1G11780.1 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr1:3977614-3979177 REVERSE LENGTH=345	647	345	1.00E-180	53.3	46.8	49.5
Rsa1.0_00081.1.g4127.t1	ref|NP_563894.2| endonuclease/exonuclease/phosphatase-like protein [Arabidopsis thaliana] gi|4835775|gb|AAD30241.1|AC007296_2 EST gb|F14156 comes from this gene [Arabidopsis thaliana] gi|22135816|gb|AAM91094.1| At1g11800/F25C20_3 [Arabidopsis thaliana] gi|23308397|gb|AAN18168.1| At1g11800/F25C20_3 [Arabidopsis thaliana] gi|332190667|gb|AEE28788.1| endonuclease/exonuclease/phosphatase-like protein [Arabidopsis thaliana]	442	441	0	99.8	78.7	85.3	endonuclease/exonuclease/phosphatase-like protein	gbpln	Arabidopsis thaliana	AT1G11800.1 | Symbols: | endonuclease/exonuclease/phosphatase family protein | chr1:3985520-3987263 REVERSE LENGTH=441	442	441	0	99.8	78.7	85.3
Rsa1.0_00081.1.g4128.t1	ref|NP_001184967.1| O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana] gi|357529541|sp|O65399.3|E131_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 1; AltName: Full=(1-3)-beta-glucan endohydrolase 1; Short=(1-3)-beta-glucanase 1; AltName: Full=Beta-1,3-endoglucanase 1; Short=Beta-1,3-glucanase 1; Flags: Precursor gi|332190670|gb|AEE28791.1| O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana]	525	511	0	97.3	75.6	81.7	O-Glycosyl hydrolases family 17 protein	gbpln	Arabidopsis thaliana	AT1G11820.2 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr1:3991144-3993327 REVERSE LENGTH=511	525	511	0	97.3	75.6	81.7
Rsa1.0_00081.1.g4129.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00081.1.g4130.t1	gb|EOA37702.1| hypothetical protein CARUB_v10012421mg [Capsella rubella]	816	515	0	63.1	56.7	59.3	hypothetical protein CARUB_v10012421mg	gbpln	Capsella rubella	AT1G11870.2 | Symbols: ATSRS, SRS | Seryl-tRNA synthetase | chr1:4003895-4006556 FORWARD LENGTH=514	816	514	0	63.0	57.1	59.8
Rsa1.0_00081.1.g4131.t2	ref|XP_002892659.1| hypothetical protein ARALYDRAFT_471336 [Arabidopsis lyrata subsp. lyrata] gi|297338501|gb|EFH68918.1| hypothetical protein ARALYDRAFT_471336 [Arabidopsis lyrata subsp. lyrata]	513	494	0	96.3	78.6	86.2	hypothetical protein ARALYDRAFT_471336	gbpln	Arabidopsis lyrata	AT1G11880.1 | Symbols: | transferases, transferring hexosyl groups | chr1:4007909-4010327 REVERSE LENGTH=489	513	489	0	95.3	78.0	85.2
Rsa1.0_00081.1.g4132.t1	ref|NP_172653.1| vesicle transport protein SEC22 [Arabidopsis thaliana] gi|27805717|sp|Q94AU2.1|SEC22_ARATH RecName: Full=25.3 kDa vesicle transport protein; Short=AtSEC22 gi|15027877|gb|AAK76469.1| putative vesicle transport protein [Arabidopsis thaliana] gi|19310827|gb|AAL85144.1| putative vesicle transport protein [Arabidopsis thaliana] gi|21555190|gb|AAM63800.1| putative vesicle transport protein [Arabidopsis thaliana] gi|332190688|gb|AEE28809.1| vesicle transport protein SEC22 [Arabidopsis thaliana]	218	218	1.00E-124	100.0	98.2	99.1	vesicle transport protein SEC22	gbpln	Arabidopsis thaliana	AT1G11890.1 | Symbols: SEC22, ATSEC22 | Synaptobrevin family protein | chr1:4011509-4012835 FORWARD LENGTH=218	218	218	1.00E-126	100.0	98.2	99.1
Rsa1.0_00081.1.g4133.t1	ref|NP_849648.4| B-cell receptor-associated protein 31-like protein [Arabidopsis thaliana] gi|22655198|gb|AAM98189.1| unknown protein [Arabidopsis thaliana] gi|332190690|gb|AEE28811.1| B-cell receptor-associated protein 31-like protein [Arabidopsis thaliana]	245	221	2.00E-91	90.2	73.5	83.3	B-cell receptor-associated protein 31-like protein	gbpln	Arabidopsis thaliana	AT1G11905.1 | Symbols: | B-cell receptor-associated protein 31-like | chr1:4014958-4016222 FORWARD LENGTH=221	245	221	6.00E-94	90.2	73.5	83.3
Rsa1.0_00081.1.g4134.t1	gb|AAC32240.1| unknown protein [Arabidopsis thaliana]	310	346	1.00E-101	111.6	69.0	81.0	unknown protein	gbpln	Arabidopsis thaliana	AT2G32560.1 | Symbols: | F-box family protein | chr2:13824820-13826761 FORWARD LENGTH=371	310	371	1.00E-95	119.7	61.3	68.1
Rsa1.0_00081.1.g4135.t2	gb|AAB03108.1| aspartic protease [Brassica napus]	414	506	0	122.2	98.8	99.3	aspartic protease	gbpln	Brassica napus	AT1G11910.1 | Symbols: APA1, ATAPA1 | aspartic proteinase A1 | chr1:4017119-4019874 REVERSE LENGTH=506	414	506	0	122.2	95.4	97.8

Rsa1.0_00082.1.g4136.t2	ref|NP_196627.1| calmodulin-binding protein-like protein [Arabidopsis thaliana] gi|10129644|emb|CAC08240.1| vacuolar calcium binding protein-like [Arabidopsis thaliana] gi|53828561|gb|AAU94390.1| At5g10660 [Arabidopsis thaliana] gi|55733763|gb|AAV59278.1| At5g10660 [Arabidopsis thaliana] gi|332004195|gb|AED91578.1| calmodulin-binding protein-like protein [Arabidopsis thaliana]	452	407	5.00E-97	90.0	56.4	63.5	calmodulin-binding protein-like protein	gbpln	Arabidopsis thaliana	AT5G10660.1 | Symbols: | calmodulin-binding protein-related | chr5:3370553-3371776 FORWARD LENGTH=407	452	407	1.00E-99	90.0	56.4	63.5
Rsa1.0_00082.1.g4137.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00082.1.g4138.t1	ref|XP_002871436.1| hypothetical protein ARALYDRAFT_909030 [Arabidopsis lyrata subsp. lyrata] gi|297317273|gb|EFH47695.1| hypothetical protein ARALYDRAFT_909030 [Arabidopsis lyrata subsp. lyrata]	911	923	0	101.3	86.2	92.4	hypothetical protein ARALYDRAFT_909030	gbpln	Arabidopsis lyrata	AT5G10720.1 | Symbols: AHK5, CKI2, HK5 | histidine kinase 5 | chr5:3386835-3390541 FORWARD LENGTH=922	911	922	0	101.2	86.1	91.9
Rsa1.0_00082.1.g4139.t1	ref|XP_002873472.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319309|gb|EFH49731.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata]	287	287	2.33E-156	100.0	94.1	96.5	catalytic/ coenzyme binding protein	gbpln	Arabidopsis lyrata	AT5G10730.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:3390822-3392947 REVERSE LENGTH=287	287	287	1.00E-144	100.0	93.4	96.9
Rsa1.0_00082.1.g4140.t1	gb|EOA25676.1| hypothetical protein CARUB_v10019028mg [Capsella rubella]	484	476	0	98.3	74.2	85.3	hypothetical protein CARUB_v10019028mg	gbpln	Capsella rubella	AT3G28600.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:10722437-10723870 FORWARD LENGTH=477	484	477	0	98.6	73.8	83.5
Rsa1.0_00082.1.g4141.t1	ref|XP_002873473.1| hypothetical protein ARALYDRAFT_487908 [Arabidopsis lyrata subsp. lyrata] gi|297319310|gb|EFH49732.1| hypothetical protein ARALYDRAFT_487908 [Arabidopsis lyrata subsp. lyrata]	344	373	1.00E-164	108.4	87.5	93.6	hypothetical protein ARALYDRAFT_487908	gbpln	Arabidopsis lyrata	AT5G10740.1 | Symbols: | Protein phosphatase 2C family protein | chr5:3393797-3395848 REVERSE LENGTH=354	344	354	1.00E-163	102.9	82.6	88.4
Rsa1.0_00082.1.g4142.t6	ref|XP_002873476.1| hypothetical protein ARALYDRAFT_325615 [Arabidopsis lyrata subsp. lyrata] gi|297319313|gb|EFH49735.1| hypothetical protein ARALYDRAFT_325615 [Arabidopsis lyrata subsp. lyrata]	980	475	0	48.5	40.6	44.0	hypothetical protein ARALYDRAFT_325615	gbpln	Arabidopsis lyrata	AT5G10770.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:3403331-3405331 REVERSE LENGTH=474	980	474	0	48.4	39.4	42.2
Rsa1.0_00082.1.g4143.t8	ref|XP_002871441.1| ubiquitin-specific protease 22 [Arabidopsis lyrata subsp. lyrata] gi|297317278|gb|EFH47700.1| ubiquitin-specific protease 22 [Arabidopsis lyrata subsp. lyrata]	565	557	0	98.6	83.7	88.1	ubiquitin-specific protease 22	gbpln	Arabidopsis lyrata	AT5G10790.1 | Symbols: UBP22 | ubiquitin-specific protease 22 | chr5:3410638-3412559 FORWARD LENGTH=557	565	557	0	98.6	83.0	87.6
Rsa1.0_00082.1.g4144.t1	ref|NP_196643.1| major facilitator protein [Arabidopsis thaliana] gi|75173996|sp|Q9LEV7.1|FBT6_ARATH RecName: Full=Probable folate-biopterin transporter 6 gi|8979716|emb|CAB96837.1| putative protein [Arabidopsis thaliana] gi|332004217|gb|AED91600.1| probable folate-biopterin transporter 6 [Arabidopsis thaliana]	573	503	0	87.8	72.3	77.1	major facilitator protein	gbpln	Arabidopsis thaliana	AT5G10820.1 | Symbols: | Major facilitator superfamily protein | chr5:3420876-3423166 REVERSE LENGTH=503	573	503	0	87.8	72.3	77.1
Rsa1.0_00082.1.g4145.t1	ref|XP_002871442.1| hypothetical protein ARALYDRAFT_487916 [Arabidopsis lyrata subsp. lyrata] gi|297317279|gb|EFH47701.1| hypothetical protein ARALYDRAFT_487916 [Arabidopsis lyrata subsp. lyrata]	261	261	1.00E-137	100.0	87.7	95.8	hypothetical protein ARALYDRAFT_487916	gbpln	Arabidopsis lyrata	AT5G10830.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:3423731-3424649 FORWARD LENGTH=261	261	261	1.00E-138	100.0	87.0	95.4
Rsa1.0_00082.1.g4146.t1	ref|XP_002873480.1| hypothetical protein ARALYDRAFT_909044 [Arabidopsis lyrata subsp. lyrata] gi|297319317|gb|EFH49739.1| hypothetical protein ARALYDRAFT_909044 [Arabidopsis lyrata subsp. lyrata]	634	648	0	102.2	94.6	96.1	hypothetical protein ARALYDRAFT_909044	gbpln	Arabidopsis lyrata	AT5G10840.1 | Symbols: | Endomembrane protein 70 protein family | chr5:3424910-3427797 REVERSE LENGTH=648	634	648	0	102.2	95.1	96.7
Rsa1.0_00082.1.g4147.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00082.1.g4148.t1	ref|NP_181089.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|3608142|gb|AAC36175.1| similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana] gi|330254016|gb|AEC09110.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	206	238	4.00E-52	115.5	48.5	66.5	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT2G35460.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:14905788-14906504 FORWARD LENGTH=238	206	238	1.00E-54	115.5	48.5	66.5
Rsa1.0_00082.1.g4149.t1	ref|XP_002873481.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319318|gb|EFH49740.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	206	206	1.00E-108	100.0	92.2	95.6	CBS domain-containing protein	gbpln	Arabidopsis lyrata	AT5G10860.1 | Symbols: | Cystathionine beta-synthase (CBS) family protein | chr5:3429173-3430142 REVERSE LENGTH=206	206	206	1.00E-110	100.0	91.7	95.6
Rsa1.0_00082.1.g4150.t1	ref|XP_002873482.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319319|gb|EFH49741.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	259	265	1.00E-123	102.3	85.3	91.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G10870.1 | Symbols: ATCM2, CM2 | chorismate mutase 2 | chr5:3430691-3432272 REVERSE LENGTH=265	259	265	1.00E-122	102.3	86.1	90.7
Rsa1.0_00082.1.g4151.t1	ref|XP_002873483.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319320|gb|EFH49742.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	450	303	4.00E-96	67.3	46.4	55.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G10890.1 | Symbols: | myosin heavy chain-related | chr5:3434030-3435067 REVERSE LENGTH=295	450	295	1.00E-94	65.6	44.9	54.2
Rsa1.0_00082.1.g4152.t1	gb|EOA20114.1| hypothetical protein CARUB_v10000393mg, partial [Capsella rubella]	635	670	0	105.5	83.9	91.3	hypothetical protein CARUB_v10000393mg, partial	gbpln	Capsella rubella	AT5G10900.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:3436413-3439221 REVERSE LENGTH=600	635	600	0	94.5	79.5	86.6
Rsa1.0_00082.1.g4153.t1	gb|EOA20415.1| hypothetical protein CARUB_v10000724mg [Capsella rubella]	203	518	1.00E-79	255.2	75.4	77.8	hypothetical protein CARUB_v10000724mg	gbpln	Capsella rubella	AT5G10920.1 | Symbols: | L-Aspartase-like family protein | chr5:3441805-3443892 FORWARD LENGTH=517	203	517	7.00E-82	254.7	75.4	78.3
Rsa1.0_00082.1.g4154.t1	gb|AFW86017.1| histone H3 [Zea mays]	136	227	1.00E-72	166.9	100.0	100.0	histone H3	gbenv/gbpln	Zea mays	AT4G40030.2 | Symbols: | Histone superfamily protein | chr4:18555840-18556827 REVERSE LENGTH=164	136	164	9.00E-75	120.6	100.0	100.0
Rsa1.0_00082.1.g4155.t1	ref|NP_196660.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|8979733|emb|CAB96854.1| putative protein [Arabidopsis thaliana] gi|88900398|gb|ABD57511.1| At5g10990 [Arabidopsis thaliana] gi|332004235|gb|AED91618.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	147	148	9.00E-63	100.7	81.0	91.2	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT5G10990.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:3476884-3477330 FORWARD LENGTH=148	147	148	3.00E-65	100.7	81.0	91.2
Rsa1.0_00082.1.g4156.t1	gb|EOA21927.1| hypothetical protein CARUB_v10002414mg [Capsella rubella]	355	390	1.00E-134	109.9	77.7	87.0	hypothetical protein CARUB_v10002414mg	gbpln	Capsella rubella	AT5G11000.1 | Symbols: | Plant protein of unknown function (DUF868) | chr5:3479166-3480335 REVERSE LENGTH=389	355	389	1.00E-134	109.6	78.9	87.3
Rsa1.0_00082.1.g4157.t1	gb|EOA19826.1| hypothetical protein CARUB_v10000071mg [Capsella rubella]	103	1186	1.00E-11	1151.5	53.4	56.3	hypothetical protein CARUB_v10000071mg	gbpln	Capsella rubella	AT5G11040.1 | Symbols: TRS120, AtTRS120 | TRS120 | chr5:3495332-3500610 FORWARD LENGTH=1186	103	1186	2.00E-14	1151.5	53.4	56.3
Rsa1.0_00082.1.g4158.t1	gb|EOA20808.1| hypothetical protein CARUB_v10001144mg [Capsella rubella]	515	391	0	75.9	67.8	70.7	hypothetical protein CARUB_v10001144mg	gbpln	Capsella rubella	AT5G11060.1 | Symbols: KNAT4 | KNOTTED1-like homeobox gene 4 | chr5:3510408-3512967 FORWARD LENGTH=393	515	393	0	76.3	67.6	70.1
Rsa1.0_00082.1.g4159.t1	ref|NP_196668.1| uncharacterized protein [Arabidopsis thaliana] gi|9795159|emb|CAC03455.1| putative protein [Arabidopsis thaliana] gi|21593765|gb|AAM65732.1| unknown [Arabidopsis thaliana] gi|110740693|dbj|BAE98448.1| hypothetical protein [Arabidopsis thaliana] gi|332004248|gb|AED91631.1| uncharacterized protein AT5G11070 [Arabidopsis thaliana]	121	152	3.00E-53	125.6	84.3	92.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G11070.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3516440-3516898 REVERSE LENGTH=152	121	152	5.00E-56	125.6	84.3	92.6
Rsa1.0_00082.1.g4160.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00082.1.g4161.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00082.1.g4162.t1	ref|XP_002871454.1| hypothetical protein ARALYDRAFT_487941 [Arabidopsis lyrata subsp. lyrata] gi|297317291|gb|EFH47713.1| hypothetical protein ARALYDRAFT_487941 [Arabidopsis lyrata subsp. lyrata]	216	223	2.00E-72	103.2	73.6	81.9	hypothetical protein ARALYDRAFT_487941	gbpln	Arabidopsis lyrata	AT5G11090.1 | Symbols: | serine-rich protein-related | chr5:3524796-3525449 FORWARD LENGTH=217	216	217	6.00E-74	100.5	74.5	82.4

Rsa1.0_00082.1.g4163.t4	ref|XP_002871455.1| plant synaptotagmin [Arabidopsis lyrata subsp. lyrata] gi|297317292|gb|EFH47714.1| plant synaptotagmin [Arabidopsis lyrata subsp. lyrata]	555	569	0	102.5	92.3	96.9	plant synaptotagmin	gbpln	Arabidopsis lyrata	AT5G11100.1 | Symbols: SYTD, ATSYTD, NTMC2TYPE2.2, NTMC2T2.2, SYT4 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr5:3532402-3535221 FORWARD LENGTH=569	555	569	0	102.5	91.5	96.6
Rsa1.0_00082.1.g4164.t1	ref|NP_196674.2| putative glycosyltransferase [Arabidopsis thaliana] gi|292630779|sp|Q9LFP3.2|GLYT4_ARATH RecName: Full=Probable glycosyltransferase At5g11130 gi|332004254|gb|AED91637.1| putative glycosyltransferase [Arabidopsis thaliana]	605	480	0	79.3	58.2	63.8	putative glycosyltransferase	gbpln	Arabidopsis thaliana	AT5G11130.1 | Symbols: | Exostosin family protein | chr5:3542320-3544724 FORWARD LENGTH=480	605	480	0	79.3	58.2	63.8
Rsa1.0_00082.1.g4165.t1	ref|NP_196677.1| adenine phosphoribosyltransferase 5 [Arabidopsis thaliana] gi|297807153|ref|XP_002871460.1| hypothetical protein ARALYDRAFT_487948 [Arabidopsis lyrata subsp. lyrata] gi|8953378|emb|CAB96651.1| adenine phosphoribosyltransferase-like protein [Arabidopsis thaliana] gi|28393271|gb|AAO42064.1| putative adenine phosphoribosyltransferase [Arabidopsis thaliana] gi|28827532|gb|AAO50610.1| putative adenine phosphoribosyltransferase [Arabidopsis thaliana] gi|297317297|gb|EFH47719.1| hypothetical protein ARALYDRAFT_487948 [Arabidopsis lyrata subsp. lyrata] gi|332004257|gb|AED91640.1| adenine phosphoribosyltransferase 5 [Arabidopsis thaliana]	191	191	1.00E-101	100.0	96.3	98.4	adenine phosphoribosyltransferase 5	gbpln	Arabidopsis lyrata	AT5G11160.1 | Symbols: APT5 | adenine phosphoribosyltransferase 5 | chr5:3550774-3551986 FORWARD LENGTH=191	191	191	1.00E-104	100.0	96.3	98.4
Rsa1.0_00082.1.g4166.t1	ref|NP_850807.2| DEAD-box ATP-dependent RNA helicase 56 [Arabidopsis thaliana] gi|332004258|gb|AED91641.1| DEAD-box ATP-dependent RNA helicase 56 [Arabidopsis thaliana]	344	344	0	100.0	96.5	98.3	DEAD-box ATP-dependent RNA helicase 56	gbpln	Arabidopsis thaliana	AT5G11170.2 | Symbols: | DEAD/DEAH box RNA helicase family protein | chr5:3554272-3556646 FORWARD LENGTH=344	344	344	0	100.0	96.5	98.3
Rsa1.0_00082.1.g4167.t1	emb|CAB96655.1| DEAD BOX RNA helicase RH15 [Arabidopsis thaliana]	467	427	0	91.4	87.4	88.7	DEAD BOX RNA helicase RH15	gbpln	Arabidopsis thaliana	AT5G11170.1 | Symbols: | DEAD/DEAH box RNA helicase family protein | chr5:3553334-3556646 FORWARD LENGTH=427	467	427	0	91.4	86.9	88.2
Rsa1.0_00082.1.g4168.t1	sp|Q9LFN5.2|GLR25_ARATH RecName: Full=Glutamate receptor 2.5; AltName: Full=Ligand-gated ion channel 2.5; Flags: Precursor	859	918	0	106.9	79.9	88.9	RecName: Full=Glutamate receptor 2.5; AltName: Full=Ligand-gated ion channel 2.5; Flags: Precursor	----	----	AT5G11210.1 | Symbols: ATGLR2.5, GLR2.5 | glutamate receptor 2.5 | chr5:3571214-3574537 REVERSE LENGTH=829	859	829	0	96.5	73.8	82.7
Rsa1.0_00082.1.g4169.t1	gb|EOA21704.1| hypothetical protein CARUB_v10002138mg [Capsella rubella]	164	164	2.00E-86	100.0	93.9	96.3	hypothetical protein CARUB_v10002138mg	gbpln	Capsella rubella	AT5G11340.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr5:3619226-3621068 FORWARD LENGTH=164	164	164	3.00E-86	100.0	90.9	95.1
Rsa1.0_00082.1.g4170.t1	gb|EOA20066.1| hypothetical protein CARUB_v10000340mg [Capsella rubella]	188	695	5.00E-18	369.7	32.4	37.8	hypothetical protein CARUB_v10000340mg	gbpln	Capsella rubella	AT5G11390.1 | Symbols: WIT1 | WPP domain-interacting protein 1 | chr5:3633971-3636418 FORWARD LENGTH=703	188	703	5.00E-19	373.9	30.9	37.2
Rsa1.0_00082.1.g4171.t1	ref|XP_002873510.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319347|gb|EFH49769.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	320	334	1.00E-75	104.4	52.8	67.8	kinase family protein	gbpln	Arabidopsis lyrata	AT5G11410.1 | Symbols: | Protein kinase superfamily protein | chr5:3638431-3639883 REVERSE LENGTH=336	320	336	4.00E-78	105.0	52.8	65.6
Rsa1.0_00082.1.g4172.t1	ref|XP_002871473.1| hypothetical protein ARALYDRAFT_487977 [Arabidopsis lyrata subsp. lyrata] gi|297317310|gb|EFH47732.1| hypothetical protein ARALYDRAFT_487977 [Arabidopsis lyrata subsp. lyrata]	366	366	0	100.0	93.4	98.6	hypothetical protein ARALYDRAFT_487977	gbpln	Arabidopsis lyrata	AT5G11420.1 | Symbols: | Protein of unknown function, DUF642 | chr5:3644655-3646991 FORWARD LENGTH=366	366	366	0	100.0	92.9	98.4

Rsa1.0_00082.1.g4173.t1	ref|NP_196705.1| CTC-interacting domain 5 [Arabidopsis thaliana] gi|7573401|emb|CAB87704.1| putative protein [Arabidopsis thaliana] gi|52354449|gb|AAU44545.1| hypothetical protein AT5G11440 [Arabidopsis thaliana] gi|55740661|gb|AAV63923.1| hypothetical protein At5g11440 [Arabidopsis thaliana] gi|332004297|gb|AED91680.1| CTC-interacting domain 5 [Arabidopsis thaliana]	161	155	2.00E-55	96.3	75.2	81.4	CTC-interacting domain 5	gbpln	Arabidopsis thaliana	AT5G11440.1 | Symbols: CID5, IPD1 | CTC-interacting domain 5 | chr5:3653060-3653607 REVERSE LENGTH=155	161	155	6.00E-58	96.3	75.2	81.4
Rsa1.0_00082.1.g4174.t1	gb|ABX10747.1| unknown [Brassica juncea]	78	215	8.00E-23	275.6	69.2	70.5	unknown	gbpln	Brassica juncea	AT5G11500.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF814 (InterPro:IPR008532). | chr5:3676747-3678946 FORWARD LENGTH=214	78	214	3.00E-25	274.4	69.2	69.2
Rsa1.0_00082.1.g4175.t2	dbj|BAJ33906.1| unnamed protein product [Thellungiella halophila]	243	453	3.00E-64	186.4	55.1	61.3	unnamed protein product	----	----	AT5G11520.1 | Symbols: ASP3, YLS4 | aspartate aminotransferase 3 | chr5:3685257-3687721 REVERSE LENGTH=449	243	449	2.00E-64	184.8	53.5	60.9
Rsa1.0_00083.1.g4176.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	883	1274	0	144.3	45.9	61.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	883	626	5.00E-36	70.9	12.6	20.8
Rsa1.0_00083.1.g4177.t1	gb|EOA19987.1| hypothetical protein CARUB_v10000251mg [Capsella rubella]	807	806	0	99.9	87.4	92.8	hypothetical protein CARUB_v10000251mg	gbpln	Capsella rubella	AT5G13690.1 | Symbols: CYL1, NAGLU | alpha-N-acetylglucosaminidase family / NAGLU family | chr5:4415808-4420159 FORWARD LENGTH=806	807	806	0	99.9	86.5	91.4
Rsa1.0_00083.1.g4178.t1	ref|NP_196871.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75171811|sp|Q9FNA5.1|WTR39_ARATH RecName: Full=WAT1-related protein At5g13670 gi|9758033|dbj|BAB08694.1| unnamed protein product [Arabidopsis thaliana] gi|21536666|gb|AAM60998.1| nodulin-like protein [Arabidopsis thaliana] gi|332004543|gb|AED91926.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]	379	377	1.00E-180	99.5	81.5	89.2	nodulin MtN21 /EamA-like transporter family protein	gbpln	Arabidopsis thaliana	AT5G13670.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:4407205-4408955 REVERSE LENGTH=377	379	377	0	99.5	81.5	89.2
Rsa1.0_00083.1.g4179.t1	ref|XP_002871578.1| elongation factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297317415|gb|EFH47837.1| elongation factor family protein [Arabidopsis lyrata subsp. lyrata]	695	675	0	97.1	91.8	93.8	elongation factor family protein	gbpln	Arabidopsis lyrata	AT5G13650.1 | Symbols: | elongation factor family protein | chr5:4397821-4402364 FORWARD LENGTH=675	695	675	0	97.1	91.7	93.7
Rsa1.0_00083.1.g4180.t1	ref|NP_196868.1| phospholipid:diacylglycerol acyltransferase 1 [Arabidopsis thaliana] gi|75171814|sp|Q9FNA9.1|PDAT1_ARATH RecName: Full=Phospholipid:diacylglycerol acyltransferase 1; Short=AtPDAT gi|9758029|dbj|BAB08690.1| unnamed protein product [Arabidopsis thaliana] gi|15450695|gb|AAK96619.1| AT5g13640/MSH12_10 [Arabidopsis thaliana] gi|332004538|gb|AED91921.1| phospholipid:diacylglycerol acyltransferase 1 [Arabidopsis thaliana]	665	671	0	100.9	91.9	95.5	phospholipid:diacylglycerol acyltransferase 1	gbpln	Arabidopsis thaliana	AT5G13640.1 | Symbols: ATPDAT, PDAT, PDAT1 | phospholipid:diacylglycerol acyltransferase | chr5:4393529-4397213 FORWARD LENGTH=671	665	671	0	100.9	91.9	95.5
Rsa1.0_00083.1.g4181.t1	gb|EOA22855.1| hypothetical protein CARUB_v10003585mg [Capsella rubella]	285	318	2.00E-74	111.6	53.7	66.3	hypothetical protein CARUB_v10003585mg	gbpln	Capsella rubella	AT5G13620.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49290.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4385385-4386373 REVERSE LENGTH=301	285	301	1.00E-74	105.6	53.7	68.4

Rsa1.0_00083.1.g4182.t1	gb|EOA22855.1| hypothetical protein CARUB_v10003585mg [Capsella rubella]	296	318	2.00E−83	107.4	58.8	71.6	hypothetical protein CARUB_v10003585mg	gbpln	Capsella rubella	AT5G13620.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49290.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:4385385−4386373 REVERSE LENGTH=301	296	301	4.00E−81	101.7	58.1	70.6
Rsa1.0_00083.1.g4183.t3	ref|XP_002871575.1| phototropic−responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297317412|gb|EFH47834.1| phototropic−responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	407	591	1.00E−101	145.2	45.0	48.6	phototropic−responsive NPH3 family protein	gbpln	Arabidopsis lyrata	AT5G13600.1 | Symbols: | Phototropic−responsive NPH3 family protein | chr5:4380432−4382497 FORWARD LENGTH=591	407	591	1.00E−103	145.2	44.7	48.6
Rsa1.0_00083.1.g4184.t1	ref|NP_196824.1| GEM−like protein 5 [Arabidopsis thaliana] gi|75181135|sp|Q9LYV6.1|GEML5_ARATH RecName: Full=GEM−like protein 5 gi|7529275|emb|CAB86627.1| ABA−responsive protein−like [Arabidopsis thaliana] gi|38454154|gb|AAR20771.1| At5g13200 [Arabidopsis thaliana] gi|46402484|gb|AAS92344.1| At5g13200 [Arabidopsis thaliana] gi|110738428|dbj|BAF01140.1| ABA−responsive protein − like [Arabidopsis thaliana] gi|332004480|gb|AED91863.1| GEM−like protein 5 [Arabidopsis thaliana]	279	272	1.00E−135	97.5	84.6	90.3	GEM−like protein 5	gbpln	Arabidopsis thaliana	AT5G13200.1 | Symbols: | GRAM domain family protein | chr5:4207081−4208079 FORWARD LENGTH=272	279	272	1.00E−137	97.5	84.6	90.3
Rsa1.0_00083.1.g4185.t1	ref|NP_568286.1| uncharacterized protein [Arabidopsis thaliana] gi|14334510|gb|AAK59452.1| unknown protein [Arabidopsis thaliana] gi|17104547|gb|AAL34162.1| unknown protein [Arabidopsis thaliana] gi|21593874|gb|AAM65841.1| unknown [Arabidopsis thaliana] gi|332004479|gb|AED91862.1| uncharacterized protein AT5G13190 [Arabidopsis thaliana]	168	134	1.00E−70	79.8	76.8	77.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G13190.1 | Symbols: | CONTAINS InterPro DOMAIN/s: LPS−induced tumor necrosis factor alpha factor (InterPro:IPR006629); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:4204987−4206205 REVERSE LENGTH=134	168	134	6.00E−73	79.8	76.8	77.4
Rsa1.0_00083.1.g4186.t1	gb|AFI56995.1| NAC5 [Brassica napus]	248	249	1.00E−120	100.4	91.1	95.6	NAC5	gbpln	Brassica napus	AT5G13180.1 | Symbols: ANAC083, VNI2, NAC083 | NAC domain containing protein 83 | chr5:4196643−4197577 FORWARD LENGTH=252	248	252	1.00E−113	101.6	87.1	94.0
Rsa1.0_00083.1.g4187.t3	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00083.1.g4188.t1	gb|ABK28247.1| unknown [Arabidopsis thaliana]	550	372	8.00E−70	67.6	25.5	35.5	unknown	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691−14272776 FORWARD LENGTH=361	550	361	1.00E−23	65.6	11.3	19.3
Rsa1.0_00083.1.g4189.t1	ref|XP_002873602.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297319439|gb|EFH49861.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	307	295	1.00E−133	96.1	78.8	87.0	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT5G13170.1 | Symbols: SAG29, SWEET15, AtSWEET15 | senescence−associated gene 29 | chr5:4181331−4183171 REVERSE LENGTH=292	307	292	1.00E−131	95.1	77.5	84.0
Rsa1.0_00083.1.g4190.t1	gb|EOA20310.1| hypothetical protein CARUB_v10000618mg, partial [Capsella rubella]	447	554	0	123.9	95.3	97.3	hypothetical protein CARUB_v10000618mg, partial	gbpln	Capsella rubella	AT5G13160.1 | Symbols: PBS1 | Protein kinase superfamily protein | chr5:4176854−4179682 FORWARD LENGTH=456	447	456	0	102.0	94.4	97.5
Rsa1.0_00083.1.g4191.t2	dbj|BAB10837.1| retroelement pol polyprotein−like [Arabidopsis thaliana]	205	1462	8.00E−61	713.2	54.1	66.3	retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00083.1.g4192.t1	ref|XP_002873600.1| hypothetical protein ARALYDRAFT_488130 [Arabidopsis lyrata subsp. lyrata] gi|297319437|gb|EFH49859.1| hypothetical protein ARALYDRAFT_488130 [Arabidopsis lyrata subsp. lyrata]	270	267	1.00E−106	98.9	77.8	82.6	hypothetical protein ARALYDRAFT_488130	gbpln	Arabidopsis lyrata	AT5G13140.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:4170688−4171744 REVERSE LENGTH=267	270	267	1.00E−104	98.9	77.4	83.7
Rsa1.0_00083.1.g4193.t1	ref|XP_002871545.1| hypothetical protein ARALYDRAFT_488123 [Arabidopsis lyrata subsp. lyrata] gi|297317382|gb|EFH47804.1| hypothetical protein ARALYDRAFT_488123 [Arabidopsis lyrata subsp. lyrata]	671	183	2.00E−97	27.3	25.0	25.3	hypothetical protein ARALYDRAFT_488123	gbpln	Arabidopsis lyrata	AT5G13070.1 | Symbols: | MSF1−like family protein | chr5:4148216−4149062 FORWARD LENGTH=183	671	183	3.00E−99	27.3	24.7	25.2
Rsa1.0_00083.1.g4194.t1	gb|EOA16200.1| hypothetical protein CARUB_v10004340mg [Capsella rubella]	646	644	0	99.7	79.9	88.9	hypothetical protein CARUB_v10004340mg	gbpln	Capsella rubella	AT4G13460.2 | Symbols: SDG22, SUVH9, SET22 | SU(VAR)3−9 homolog 9 | chr4:7824653−7826605 REVERSE LENGTH=650	646	650	0	100.6	75.9	85.8

Rsa1.0_00083.1.g4195.t1	emb|CAB88266.1| putative protein [Arabidopsis thaliana]	409	414	0	101.2	85.6	92.4	putative protein	gbpln	Arabidopsis thaliana	AT5G13020.1 | Symbols: | Emsy N Terminus (ENT)/ plant Tudor-like domains-containing protein | chr5:4129691-4132089 REVERSE LENGTH=397	409	397	0	97.1	82.6	89.0
Rsa1.0_00083.1.g4196.t1	dbj|BAJ33947.1| unnamed protein product [Thellungiella halophila]	1230	1255	0	102.0	91.7	96.2	unnamed protein product	----	----	AT5G13010.1 | Symbols: EMB3011 | RNA helicase family protein | chr5:4122747-4128660 FORWARD LENGTH=1255	1230	1255	0	102.0	89.1	94.6
Rsa1.0_00083.1.g4197.t3	ref|NP_196804.6| callose synthase [Arabidopsis thaliana] gi|357529555|sp|Q9LXT9.3|CALS3_ARATH RecName: Full=Callose synthase 3; AltName: Full=1,3-beta-glucan synthase; AltName: Full=Protein GLUCAN SYNTHASE-LIKE 12 gi|332004456|gb|AED91839.1| callose synthase [Arabidopsis thaliana]	2009	1955	0	97.3	93.2	95.4	callose synthase	gbpln	Arabidopsis thaliana	AT5G13000.1 | Symbols: ATGSL12, gsl12 | glucan synthase-like 12 | chr5:4110445-4121202 REVERSE LENGTH=1955	2009	1955	0	97.3	93.2	95.4
Rsa1.0_00083.1.g4198.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00083.1.g4199.t1	ref|XP_002873592.1| hypothetical protein ARALYDRAFT_488115 [Arabidopsis lyrata subsp. lyrata] gi|297319429|gb|EFH49851.1| hypothetical protein ARALYDRAFT_488115 [Arabidopsis lyrata subsp. lyrata]	85	80	2.00E-14	94.1	54.1	63.5	hypothetical protein ARALYDRAFT_488115	gbpln	Arabidopsis lyrata	AT5G12990.1 | Symbols: CLE40 | CLAVATA3/ESR-RELATED 40 | chr5:4109234-4109768 REVERSE LENGTH=80	85	80	1.00E-11	94.1	49.4	58.8
Rsa1.0_00083.1.g4200.t1	gb|EOA19944.1| hypothetical protein CARUB_v10000198mg [Capsella rubella]	903	863	0	95.6	82.3	87.7	hypothetical protein CARUB_v10000198mg	gbpln	Capsella rubella	AT5G12950.1 | Symbols: | Putative glycosyl hydrolase of unknown function (DUF1680) | chr5:4093117-4096806 FORWARD LENGTH=861	903	861	0	95.3	81.5	86.7
Rsa1.0_00083.1.g4201.t1	gb|EOA22730.1| hypothetical protein CARUB_v10003437mg [Capsella rubella]	372	373	1.00E-165	100.3	75.3	84.4	hypothetical protein CARUB_v10003437mg	gbpln	Capsella rubella	AT5G12940.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:4087782-4088897 FORWARD LENGTH=371	372	371	1.00E-165	99.7	75.0	85.8
Rsa1.0_00083.1.g4202.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00083.1.g4203.t1	ref|XP_002873588.1| hypothetical protein ARALYDRAFT_909241 [Arabidopsis lyrata subsp. lyrata] gi|297319425|gb|EFH49847.1| hypothetical protein ARALYDRAFT_909241 [Arabidopsis lyrata subsp. lyrata]	458	442	1.00E-167	96.5	73.6	81.0	hypothetical protein ARALYDRAFT_909241	gbpln	Arabidopsis lyrata	AT5G12930.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4083155-4085222 REVERSE LENGTH=439	458	439	1.00E-168	95.9	72.3	79.9
Rsa1.0_00083.1.g4204.t1	ref|XP_002873586.1| hypothetical protein ARALYDRAFT_488108 [Arabidopsis lyrata subsp. lyrata] gi|297319423|gb|EFH49845.1| hypothetical protein ARALYDRAFT_488108 [Arabidopsis lyrata subsp. lyrata]	494	559	0	113.2	79.8	84.8	hypothetical protein ARALYDRAFT_488108	gbpln	Arabidopsis lyrata	AT5G12900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G12330.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4072151-4074445 REVERSE LENGTH=562	494	562	0	113.8	78.9	84.8
Rsa1.0_00083.1.g4205.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00083.1.g4206.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00083.1.g4207.t1	ref|NP_196791.1| transcription factor MYB46 [Arabidopsis thaliana] gi|75335627|sp|Q9LXV2.1|MYB46_ARATH RecName: Full=Transcription factor MYB46; AltName: Full=Myb-related protein 46; Short=AtMYB46 gi|7630043|emb|CAB88251.1| putative transcription factor (MYB46) [Arabidopsis thaliana] gi|23306410|gb|AAN17432.1| putative transcription factor (MYB46) [Arabidopsis thaliana] gi|27311887|gb|AAO00909.1| putative transcription factor (MYB46) [Arabidopsis thaliana] gi|41619388|gb|AAS10091.1| MYB transcription factor [Arabidopsis thaliana] gi|332004441|gb|AED91824.1| transcription factor MYB46 [Arabidopsis thaliana]	279	280	1.00E-122	100.4	83.2	90.7	transcription factor MYB46	gbpln	Arabidopsis thaliana	AT5G12870.1 | Symbols: ATMYB46, MYB46 | myb domain protein 46 | chr5:4062939-4064939 REVERSE LENGTH=280	279	280	1.00E-125	100.4	83.2	90.7
Rsa1.0_00083.1.g4208.t1	dbj|BAJ33608.1| unnamed protein product [Thellungiella halophila]	680	707	0	104.0	86.9	91.5	unnamed protein product	----	----	AT5G12850.1 | Symbols: | CCCH-type zinc finger protein with ARM repeat domain | chr5:4057068-4059188 FORWARD LENGTH=706	680	706	0	103.8	84.4	89.0

Rsa1.0_00083.1.g4209.t1	gb|EOA21339.1| hypothetical protein CARUB_v10001701mg [Capsella rubella]	430	272	3.00E-99	63.3	48.6	50.2	hypothetical protein CARUB_v10001701mg	gbpln	Capsella rubella	AT5G12840.3 | Symbols: HAP2A, ATHAP2A, NF-YA1 | nuclear factor Y, subunit A1 | chr5:4051147-4052961 REVERSE LENGTH=272	430	272	1.00E-98	63.3	48.1	50.2
Rsa1.0_00083.1.g4210.t1	ref|XP_002873570.1| hypothetical protein ARALYDRAFT_488089 [Arabidopsis lyrata subsp. lyrata] gi|297319407|gb|EFH49829.1| hypothetical protein ARALYDRAFT_488089 [Arabidopsis lyrata subsp. lyrata]	535	480	0	89.7	70.5	78.7	hypothetical protein ARALYDRAFT_488089	gbpln	Arabidopsis lyrata	AT5G12420.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:4024568-4026715 REVERSE LENGTH=480	535	480	0	89.7	70.1	78.3
Rsa1.0_00083.1.g4211.t1	ref|XP_002873570.1| hypothetical protein ARALYDRAFT_488089 [Arabidopsis lyrata subsp. lyrata] gi|297319407|gb|EFH49829.1| hypothetical protein ARALYDRAFT_488089 [Arabidopsis lyrata subsp. lyrata]	456	480	0	105.3	71.5	81.1	hypothetical protein ARALYDRAFT_488089	gbpln	Arabidopsis lyrata	AT5G12420.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:4024568-4026715 REVERSE LENGTH=480	456	480	0	105.3	71.7	81.4
Rsa1.0_00083.1.g4212.t1	ref|NP_568273.2| PHD-finger and DNA binding domain-containing protein [Arabidopsis thaliana] gi|332004422|gb|AED91805.1| PHD-finger and DNA binding domain-containing protein [Arabidopsis thaliana]	1539	1602	0	104.1	74.6	84.7	PHD-finger and DNA binding domain-containing protein	gbpln	Arabidopsis thaliana	AT5G12400.1 | Symbols: | DNA binding;zinc ion binding;DNA binding | chr5:4013813-4021018 FORWARD LENGTH=1602	1539	1602	0	104.1	74.6	84.7
Rsa1.0_00083.1.g4213.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00083.1.g4214.t1	ref|XP_002873568.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319405|gb|EFH49827.1| binding protein [Arabidopsis lyrata subsp. lyrata]	171	167	2.00E-73	97.7	81.3	87.1	binding protein	gbpln	Arabidopsis lyrata	AT5G12390.1 | Symbols: FIS1B | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:4010948-4011950 REVERSE LENGTH=167	171	167	2.00E-75	97.7	81.9	87.1
Rsa1.0_00083.1.g4215.t1	ref|XP_002871523.1| ran GTPase binding protein [Arabidopsis lyrata subsp. lyrata] gi|297317360|gb|EFH47782.1| ran GTPase binding protein [Arabidopsis lyrata subsp. lyrata]	1073	1075	0	100.2	94.3	97.5	ran GTPase binding protein	gbpln	Arabidopsis lyrata	AT5G12350.1 | Symbols: | Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain | chr5:3995789-4000545 FORWARD LENGTH=1075	1073	1075	0	100.2	94.1	97.2
Rsa1.0_00084.1.g4216.t1	gb|AAC28197.1| contains similarity to reverse transcriptases [Arabidopsis thaliana] gi|7267156|emb|CAB77868.1| putative reverse transcriptase [Arabidopsis thaliana]	409	1077	1.00E-64	263.3	29.6	37.2	contains similarity to reverse transcriptases	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	409	154	2.00E-18	37.7	11.5	15.6
Rsa1.0_00084.1.g4217.t1	ref|XP_002885986.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331826|gb|EFH62245.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	583	740	0	126.9	64.0	67.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G15880.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr2:6918039-6920319 REVERSE LENGTH=727	583	727	0	124.7	66.7	70.7
Rsa1.0_00084.1.g4218.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	339	1225	3.00E-22	361.4	17.4	26.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	339	256	4.00E-21	75.5	19.8	29.5
Rsa1.0_00084.1.g4219.t4	gb|EOA29790.1| hypothetical protein CARUB_v10012885mg [Capsella rubella]	1027	1012	0	98.5	81.0	88.9	hypothetical protein CARUB_v10012885mg	gbpln	Capsella rubella	AT2G15900.1 | Symbols: | Phox-associated domain;Phox-like;Sorting nexin, C-terminal | chr2:6927390-6932535 FORWARD LENGTH=994	1027	994	0	96.8	79.3	86.4
Rsa1.0_00084.1.g4220.t1	gb|EOA32338.1| hypothetical protein CARUB_v10015605mg, partial [Capsella rubella]	146	247	2.00E-17	169.2	40.4	47.3	hypothetical protein CARUB_v10015605mg, partial	gbpln	Capsella rubella	AT2G15910.1 | Symbols: | CSL zinc finger domain-containing protein | chr2:6932917-6935333 REVERSE LENGTH=367	146	367	7.00E-18	251.4	38.4	47.9
Rsa1.0_00084.1.g4221.t1	ref|NP_179191.1| CSL zinc finger domain-containing protein [Arabidopsis thaliana] gi|5306242|gb|AAD41975.1| unknown protein [Arabidopsis thaliana] gi|330251353|gb|AEC06447.1| CSL zinc finger domain-containing protein [Arabidopsis thaliana]	81	367	2.00E-38	453.1	92.6	93.8	CSL zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT2G15910.1 | Symbols: | CSL zinc finger domain-containing protein | chr2:6932917-6935333 REVERSE LENGTH=367	81	367	3.00E-41	453.1	92.6	93.8
Rsa1.0_00084.1.g4222.t1	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	194	326	6.00E-27	168.0	34.0	56.2	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00084.1.g4223.t1	gb|ABD65624.1| hypothetical protein 23.t00036 [Brassica oleracea]	912	842	1.00E-58	92.3	17.2	24.2	hypothetical protein 23.t00036	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	912	874	3.00E-26	95.8	8.9	14.7

Rsa1.0_00084.1.g4224.t1	ref|XP_002883931.1| hypothetical protein ARALYDRAFT_899833 [Arabidopsis lyrata subsp. lyrata] gi|297329771|gb|EFH60190.1| hypothetical protein ARALYDRAFT_899833 [Arabidopsis lyrata subsp. lyrata]	3634	3792	0	104.3	80.5	87.6	hypothetical protein ARALYDRAFT_899833	gbpln	Arabidopsis lyrata	AT1G50030.2 | Symbols: TOR | target of rapamycin | chr1:18522626-18539619 REVERSE LENGTH=2454	3634	2454	8.00E-64	67.5	5.1	8.0
Rsa1.0_00084.1.g4225.t1	ref|XP_002877500.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323338|gb|EFH53759.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	181	136	9.00E-21	75.1	30.9	39.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	181	332	4.00E-12	183.4	21.0	32.0
Rsa1.0_00084.1.g4226.t2	gb|EOA12473.1| hypothetical protein CARUB_v10025904mg [Capsella rubella]	116	800	7.00E-23	689.7	48.3	58.6	hypothetical protein CARUB_v10025904mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00084.1.g4227.t1	emb|CAN65769.1| hypothetical protein VITISV_002387 [Vitis vinifera]	964	806	6.00E-70	83.6	21.2	31.2	hypothetical protein VITISV_002387	gbpln	Vitis vinifera	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	964	295	2.00E-47	30.6	10.0	15.0
Rsa1.0_00084.1.g4228.t1	dbj|BAJ34053.1| unnamed protein product [Thellungiella halophila]	198	197	5.00E-97	99.5	88.4	95.5	unnamed protein product	----	----	AT2G15970.1 | Symbols: COR413-PM1, WCOR413, WCOR413-LIKE, ATCOR413-PM1, FL3-5A3, ATCYP19 | cold regulated 413 plasma membrane 1 | chr2:6950163-6951012 FORWARD LENGTH=197	198	197	7.00E-83	99.5	78.8	87.4
Rsa1.0_00084.1.g4229.t1	ref|NP_179197.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75267579|sp|Q9XIM8.1|PP155_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g15980 gi|5306237|gb|AAD41970.1| hypothetical protein [Arabidopsis thaliana] gi|330251359|gb|AEC06453.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	486	498	0	102.5	78.4	88.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G15980.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:6951349-6952845 REVERSE LENGTH=498	486	498	0	102.5	78.4	88.3
Rsa1.0_00084.1.g4230.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1199	1223	0	102.0	51.9	68.7	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1199	746	1.00E-101	62.2	15.6	20.6
Rsa1.0_00084.1.g4231.t1	ref|NP_179203.2| Cysteine/Histidine-rich C1 domain family protein [Arabidopsis thaliana] gi|330251368|gb|AEC06462.1| Cysteine/Histidine-rich C1 domain family protein [Arabidopsis thaliana]	242	243	1.00E-128	100.4	90.9	95.9	Cysteine/Histidine-rich C1 domain family protein	gbpln	Arabidopsis thaliana	AT2G16050.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:6980450-6981939 FORWARD LENGTH=243	242	243	1.00E-130	100.4	90.9	95.9
Rsa1.0_00084.1.g4232.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00084.1.g4233.t1	ref|XP_002875620.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321458|gb|EFH51879.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	173	78	5.00E-21	45.1	27.7	30.6	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00084.1.g4234.t2	gb|AAP37043.1| nonsymbiotic hemoglobin [Raphanus sativus]	417	160	7.00E-76	38.4	34.1	34.3	nonsymbiotic hemoglobin	gbpln	Raphanus sativus	AT2G16060.1 | Symbols: GLB1, AHB1, ARATH GLB1, NSHB1, ATGLB1, HB1 | hemoglobin 1 | chr2:6982782-6983522 REVERSE LENGTH=160	417	160	2.00E-74	38.4	32.1	33.3
Rsa1.0_00084.1.g4235.t1	ref|NP_028242.1| plastid division2 protein [Arabidopsis thaliana] gi|75215718|sp|Q9XII1.1|PDV2_ARATH RecName: Full=Plastid division protein PDV2; AltName: Full=Protein PLASTID DIVISION2 gi|4678204|gb|AAD26950.1| expressed protein [Arabidopsis thaliana] gi|19423944|gb|AAL87305.1| unknown protein [Arabidopsis thaliana] gi|21281205|gb|AAM45024.1| unknown protein [Arabidopsis thaliana] gi|21618067|gb|AAM67117.1| unknown [Arabidopsis thaliana] gi|117413982|dbj|BAF36495.1| plastid division protein PDV2 [Arabidopsis thaliana] gi|117413986|dbj|BAF36497.1| plastid division protein PDV2 [Arabidopsis thaliana] gi|330251371|gb|AEC06465.1| plastid division protein PDV2 [Arabidopsis thaliana]	287	307	1.00E-120	107.0	81.2	88.9	plastid division2 protein	gbpln	Arabidopsis thaliana	AT2G16070.2 | Symbols: PDV2 | plastid division2 | chr2:6984072-6985356 REVERSE LENGTH=307	287	307	1.00E-122	107.0	81.2	88.9

Rsa1.0_00084.1.g4236.t1	ref|XP_002886198.1| hypothetical protein ARALYDRAFT_480784 [Arabidopsis lyrata subsp. lyrata] gi|297332038|gb|EFH62457.1| hypothetical protein ARALYDRAFT_480784 [Arabidopsis lyrata subsp. lyrata]	559	598	0	107.0	84.6	91.6	hypothetical protein ARALYDRAFT_480784	gbpln	Arabidopsis lyrata	AT2G16090.1 | Symbols: ARI2, ATARI2 | RING/U−box superfamily protein | chr2:6987367−6989822 REVERSE LENGTH=593	559	593	0	106.1	81.9	89.4
Rsa1.0_00085.1.g4237.t1	ref|NP_172022.1| zinc transporter 5 [Arabidopsis thaliana] gi|37090146|sp|O23039.1|ZIP5_ARATH RecName: Full=Zinc transporter 5; AltName: Full=ZRT/IRT−like protein 5; Flags: Precursor gi|17385784|gb|AAL38432.1|AF369909_1 putative metal transporter ZIP5 [Arabidopsis thaliana] gi|2388566|gb|AAB71447.1| Similar to Arabidopsis Fe(II) transport protein (gb|U27590) [Arabidopsis thaliana] gi|48596981|gb|AAT46031.1| At1g05300 [Arabidopsis thaliana] gi|51971447|dbj|BAD44388.1| putative zinc transporter [Arabidopsis thaliana] gi|332189699|gb|AEE27820.1| zinc transporter 5 [Arabidopsis thaliana]	363	360	1.00E−171	99.2	88.2	92.6	zinc transporter 5	gbpln	Arabidopsis thaliana	AT1G05300.1 | Symbols: ZIP5 | zinc transporter 5 precursor | chr1:1545258−1547709 REVERSE LENGTH=360	363	360	1.00E−174	99.2	88.2	92.6
Rsa1.0_00085.1.g4238.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00085.1.g4239.t1	dbj|BAA09643.1| CTP:phosphocholine cytidylyltransferase [Brassica napus]	80	324	2.00E−20	405.0	71.3	83.8	CTP:phosphocholine cytidylyltransferase	gbpln	Brassica napus	AT2G32260.1 | Symbols: ATCCT1, CCT1 | phosphorylcholine cytidylyltransferase | chr2:13697645−13700241 FORWARD LENGTH=332	80	332	8.00E−20	415.0	56.3	71.3
Rsa1.0_00085.1.g4240.t1	gb|EOA37878.1| hypothetical protein CARUB_v10011474mg [Capsella rubella]	1017	864	0	85.0	52.4	64.1	hypothetical protein CARUB_v10011474mg	gbpln	Capsella rubella	AT1G05320.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: fruit, egg cell; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G32240.1); Has 267444 Blast hits to 119656 proteins in 3886 species: Archae − 3699; Bacteria − 62432; Metazoa − 106542; Fungi − 19875; Plants − 13918; Viruses − 1288; Other Eukaryotes − 59690 (source: NCBI BLink). | chr1:1554856−1557658 FORWARD LENGTH=790	1017	790	0	77.7	49.7	61.3
Rsa1.0_00085.1.g4241.t1	gb|EOA28176.1| hypothetical protein CARUB_v10024366mg [Capsella rubella]	73	109	2.00E−19	149.3	72.6	80.8	hypothetical protein CARUB_v10024366mg	gbpln	Capsella rubella	AT2G32210.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G32190.1); Has 214 Blast hits to 214 proteins in 21 species: Archae − 0; Bacteria − 0; Metazoa − 1; Fungi − 10; Plants − 203; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr2:13678077−13678554 FORWARD LENGTH=71	73	71	8.00E−21	97.3	68.5	76.7
Rsa1.0_00085.1.g4242.t1	ref|NP_172027.2| ubiquitin−like modifier−activating enzyme 5 [Arabidopsis thaliana] gi|290463407|sp|O23034.2|UBA5_ARATH RecName: Full=Ubiquitin−like modifier−activating enzyme 5; Short=Ubiquitin−activating enzyme 5 gi|332189707|gb|AEE27828.1| ubiquitin−like modifier−activating enzyme 5 [Arabidopsis thaliana]	429	431	0	100.5	93.7	96.0	ubiquitin−like modifier−activating enzyme 5	gbpln	Arabidopsis thaliana	AT1G05350.1 | Symbols: | NAD(P)−binding Rossmann−fold superfamily protein | chr1:1560891−1564005 REVERSE LENGTH=431	429	431	0	100.5	93.7	96.0
Rsa1.0_00085.1.g4243.t1	ref|NP_172029.2| Sec.4−like phosphatidylinositol transfer family protein [Arabidopsis thaliana] gi|332189709|gb|AEE27830.1| Sec.4−like phosphatidylinositol transfer family protein [Arabidopsis thaliana]	419	417	0	99.5	93.3	96.2	Sec.4−like phosphatidylinositol transfer family protein	gbpln	Arabidopsis thaliana	AT1G05370.1 | Symbols: | Sec14p−like phosphatidylinositol transfer family protein | chr1:1569418−1572280 REVERSE LENGTH=417	419	417	0	99.5	93.3	96.2
Rsa1.0_00085.1.g4244.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_00085.1.g4245.t1	ref|NP_563736.3| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein [Arabidopsis thaliana] gi|186478156|ref|NP_001117233.1| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein [Arabidopsis thaliana] gi|8778713|gb|AAF79721.1|AC005106_2 T25N20.3 [Arabidopsis thaliana] gi|332189710|gb|AEE27831.1| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein [Arabidopsis thaliana] gi|332189711|gb|AEE27832.1| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein [Arabidopsis thaliana]	1098	1138	0	103.6	71.4	81.0	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein	gbpln	Arabidopsis thaliana	AT1G05380.2 | Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein | chr1:1577231-1582190 FORWARD LENGTH=1138	1098	1138	0	103.6	71.4	81.0
Rsa1.0_00085.1.g4246.t1	ref|NP_563737.1| LOW PSII accumulation 19 protein [Arabidopsis thaliana] gi|8778732|gb|AAF79740.1|AC005106_21 T25N20.4 [Arabidopsis thaliana] gi|13877959|gb|AAK44057.1|AF370242_1 unknown protein [Arabidopsis thaliana] gi|23296694|gb|AAN13149.1| unknown protein [Arabidopsis thaliana] gi|332189712|gb|AEE27833.1| LOW PSII accumulation 19 protein [Arabidopsis thaliana]	195	199	1.00E-80	102.1	79.5	87.7	LOW PSII accumulation 19 protein	gbpln	Arabidopsis thaliana	AT1G05385.1 | Symbols: LPA19, Psb27-H1 | photosystem II 11 kDa protein-related | chr1:1582747-1583648 REVERSE LENGTH=199	195	199	3.00E-83	102.1	79.5	87.7
Rsa1.0_00085.1.g4247.t1	ref|XP_002892288.1| hypothetical protein ARALYDRAFT_887726 [Arabidopsis lyrata subsp. lyrata] gi|297338130|gb|EFH68547.1| hypothetical protein ARALYDRAFT_887726 [Arabidopsis lyrata subsp. lyrata]	234	230	4.00E-71	98.3	69.7	79.5	hypothetical protein ARALYDRAFT_887726	gbpln	Arabidopsis lyrata	AT1G05420.1 | Symbols: ATOFP12, OFP12 | ovate family protein 12 | chr1:1590073-1590753 FORWARD LENGTH=226	234	226	9.00E-72	96.6	69.7	78.2
Rsa1.0_00085.1.g4248.t1	gb|EOA40311.1| hypothetical protein CARUB_v10009042mg [Capsella rubella]	478	470	0	98.3	76.4	84.9	hypothetical protein CARUB_v10009042mg	gbpln	Capsella rubella	AT1G05410.1 | Symbols: | Protein of unknown function (DUF1423) | chr1:1585504-1587268 REVERSE LENGTH=471	478	471	0	98.5	76.6	85.4
Rsa1.0_00085.1.g4249.t1	ref|XP_002892289.1| hypothetical protein ARALYDRAFT_470544 [Arabidopsis lyrata subsp. lyrata] gi|297338131|gb|EFH68548.1| hypothetical protein ARALYDRAFT_470544 [Arabidopsis lyrata subsp. lyrata]	259	269	1.00E-90	103.9	68.7	79.2	hypothetical protein ARALYDRAFT_470544	gbpln	Arabidopsis lyrata	AT1G05430.1 | Symbols: | unknown protein; Has 31 Blast hits to 31 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1594227-1595731 REVERSE LENGTH=269	259	269	1.00E-91	103.9	68.0	79.2
Rsa1.0_00085.1.g4250.t1	gb|AAF79737.1|AC005106_18 T25N20.9 [Arabidopsis thaliana]	371	393	1.00E-129	105.9	67.1	75.5	T25N20.9	gbpln	Arabidopsis thaliana	AT1G05440.1 | Symbols: | C-8 sterol isomerases | chr1:1596374-1597843 REVERSE LENGTH=384	371	384	1.00E-132	103.5	67.1	75.5
Rsa1.0_00085.1.g4251.t1	ref|XP_002867509.1| hypothetical protein ARALYDRAFT_913808 [Arabidopsis lyrata subsp. lyrata] gi|297313345|gb|EFH43768.1| hypothetical protein ARALYDRAFT_913808 [Arabidopsis lyrata subsp. lyrata]	269	312	2.00E-33	116.0	33.8	43.5	hypothetical protein ARALYDRAFT_913808	gbpln	Arabidopsis lyrata	AT3G49610.1 | Symbols: | Domain of unknown function (DUF313) | chr3:18390413-18391417 REVERSE LENGTH=334	269	334	1.00E-34	124.2	27.1	34.2
Rsa1.0_00085.1.g4252.t1	gb|ABK28778.1| unknown [Arabidopsis thaliana]	201	206	1.00E-60	102.5	70.1	80.6	unknown	gbpln	Arabidopsis thaliana	AT1G05450.2 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:1600004-1601086 FORWARD LENGTH=205	201	205	5.00E-63	102.0	70.1	80.6
Rsa1.0_00085.1.g4253.t1	gb|AAK40099.1|AF339908_1 RNA helicase SDE3 [Arabidopsis thaliana]	1054	1002	0	95.1	79.7	84.9	RNA helicase SDE3	gbpln	Arabidopsis thaliana	AT1G05460.1 | Symbols: SDE3 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:1601357-1604658 REVERSE LENGTH=1002	1054	1002	0	95.1	79.6	84.7
Rsa1.0_00085.1.g4254.t1	ref|NP_172038.4| Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Arabidopsis thaliana] gi|259016256|sp|Q9LR47.2|IP5P3_ARATH RecName: Full=Type I inositol 1,4,5-trisphosphate 5-phosphatase CVP2; AltName: Full=Protein COTYLEDON VASCULAR PATTERN 2 gi|332189723|gb|AEE27844.1| Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Arabidopsis thaliana]	617	617	0	100.0	95.1	97.4	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2	gbpln	Arabidopsis thaliana	AT1G05470.1 | Symbols: CVP2 | DNAse I-like superfamily protein | chr1:1608558-1611291 REVERSE LENGTH=617	617	617	0	100.0	95.1	97.4

Rsa1.0_00085.1.g4255.t1	ref|XP_002892292.1| hypothetical protein ARALYDRAFT_470549 [Arabidopsis lyrata subsp. lyrata] gi|297338134|gb|EFH68551.1| hypothetical protein ARALYDRAFT_470549 [Arabidopsis lyrata subsp. lyrata]	1691	1406	0	83.1	45.5	51.0	hypothetical protein ARALYDRAFT_470549	gbpln	Arabidopsis lyrata	AT1G05490.1 | Symbols: chr31 | chromatin remodeling 31 | chr1:1618795-1623195 REVERSE LENGTH=1410	1691	1410	0	83.4	45.4	51.2
Rsa1.0_00085.1.g4256.t3	ref|NP_172041.2| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana] gi|75301121|sp|Q8L706.1|SYT5_ARATH RecName: Full=Synaptotagmin-5; AltName: Full=NTMC2T2.1; AltName: Full=Synaptotagmin E gi|22655178|gb|AAM98179.1| Ca2+-dependent lipid-binding protein, putative [Arabidopsis thaliana] gi|31711980|gb|AAP68346.1| At1g05500 [Arabidopsis thaliana] gi|110737090|dbj|BAF00497.1| putative Ca2+-dependent lipid-binding protein [Arabidopsis thaliana] gi|332189725|gb|AEE27846.1| synaptotagmin-5 [Arabidopsis thaliana]	594	560	0	94.3	87.7	91.4	calcium-dependent lipid-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G05500.1 | Symbols: SYTE, ATSYTE, NTMC2TYPE2.1, NTMC2T2.1, SYT5 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:1625098-1628940 FORWARD LENGTH=560	594	560	0	94.3	87.7	91.4
Rsa1.0_00085.1.g4257.t1	ref|NP_172042.1| uncharacterized protein [Arabidopsis thaliana] gi|8778719|gb|AAF79727.1|AC005106_8 T25N20.16 [Arabidopsis thaliana] gi|17979351|gb|AAL49901.1| unknown protein [Arabidopsis thaliana] gi|20466017|gb|AAM20230.1| unknown protein [Arabidopsis thaliana] gi|110741000|dbj|BAE98594.1| hypothetical protein [Arabidopsis thaliana] gi|332189726|gb|AEE27847.1| uncharacterized protein AT1G05510 [Arabidopsis thaliana]	241	241	1.00E-134	100.0	92.9	98.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G05510.1 | Symbols: | Protein of unknown function (DUF1264) | chr1:1629527-1630690 FORWARD LENGTH=241	241	241	1.00E-137	100.0	92.9	98.3
Rsa1.0_00085.1.g4258.t1	ref|NP_172045.1| uncharacterized protein [Arabidopsis thaliana] gi|8778720|gb|AAF79728.1|AC005106_9 T25N20.19 [Arabidopsis thaliana] gi|332189729|gb|AEE27850.1| uncharacterized protein AT1G05540 [Arabidopsis thaliana]	366	367	1.00E-154	100.3	72.4	85.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G05540.1 | Symbols: | Protein of unknown function (DUF295) | chr1:1639348-1640707 FORWARD LENGTH=367	366	367	1.00E-157	100.3	72.4	85.0
Rsa1.0_00085.1.g4259.t2	ref|NP_001184912.1| uncharacterized protein [Arabidopsis thaliana] gi|332189732|gb|AEE27853.1| uncharacterized protein AT1G05550 [Arabidopsis thaliana]	443	385	1.00E-117	86.9	48.5	57.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G05550.3 | Symbols: | Protein of unknown function (DUF295) | chr1:1641229-1643748 REVERSE LENGTH=385	443	385	1.00E-120	86.9	48.5	57.6
Rsa1.0_00085.1.g4260.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00085.1.g4261.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00085.1.g4262.t6	ref|NP_001184912.1| uncharacterized protein [Arabidopsis thaliana] gi|332189732|gb|AEE27853.1| uncharacterized protein AT1G05550 [Arabidopsis thaliana]	368	385	1.00E-139	104.6	65.2	75.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G05550.3 | Symbols: | Protein of unknown function (DUF295) | chr1:1641229-1643748 REVERSE LENGTH=385	368	385	1.00E-142	104.6	65.2	75.8
Rsa1.0_00085.1.g4263.t1	dbj|BAJ33712.1| unnamed protein product [Thellungiella halophila]	457	456	0	99.8	84.2	89.7	unnamed protein product	----	----	AT1G05560.1 | Symbols: UGT1, UGT75B1 | UDP-glucosyltransferase 75B1 | chr1:1645674-1647083 REVERSE LENGTH=469	457	469	0	102.6	80.3	88.8
Rsa1.0_00085.1.g4264.t1	gb|AAF79731.1|AC005106_12 T25N20.20 [Arabidopsis thaliana]	127	493	4.00E-23	388.2	46.5	52.8	T25N20.20	gbpln	Arabidopsis thaliana	AT1G05550.3 | Symbols: | Protein of unknown function (DUF295) | chr1:1641229-1643748 REVERSE LENGTH=385	127	385	1.00E-25	303.1	44.9	51.2
Rsa1.0_00085.1.g4265.t1	dbj|BAJ33712.1| unnamed protein product [Thellungiella halophila]	427	456	0	106.8	82.7	87.4	unnamed protein product	----	----	AT1G05560.1 | Symbols: UGT1, UGT75B1 | UDP-glucosyltransferase 75B1 | chr1:1645674-1647083 REVERSE LENGTH=469	427	469	0	109.8	79.9	87.4
Rsa1.0_00085.1.g4266.t1	gb|AAK37413.1|AF237733_1 callose synthase 1 catalytic subunit [Arabidopsis thaliana]	1939	1950	0	100.6	94.2	97.1	callose synthase 1 catalytic subunit	gbpln	Arabidopsis thaliana	AT1G05570.1 | Symbols: CALS1, GSL06, ATGSL6, ATGSL06, GSL6 | callose synthase 1 | chr1:1647880-1658677 REVERSE LENGTH=1950	1939	1950	0	100.6	94.5	97.2
Rsa1.0_00086.1.g4267.t2	ref|XP_002886385.1| hypothetical protein ARALYDRAFT_893060 [Arabidopsis lyrata subsp. lyrata] gi|297332226|gb|EFH62644.1| hypothetical protein ARALYDRAFT_893060 [Arabidopsis lyrata subsp. lyrata]	199	294	8.00E-81	147.7	76.9	82.9	hypothetical protein ARALYDRAFT_893060	gbpln	Arabidopsis lyrata	AT1G63780.1 | Symbols: IMP4 | Ribosomal RNA processing Brix domain protein | chr1:23665045-23667243 REVERSE LENGTH=294	199	294	8.00E-80	147.7	71.9	77.9

Rsa1.0_00086.1.g4268.t1	ref|XP_002886402.1| hypothetical protein ARALYDRAFT_475012 [Arabidopsis lyrata subsp. lyrata] gi|297332243|gb|EFH62661.1| hypothetical protein ARALYDRAFT_475012 [Arabidopsis lyrata subsp. lyrata]	156	154	2.00E-64	98.7	80.1	88.5	hypothetical protein ARALYDRAFT_475012	gbpln	Arabidopsis lyrata	AT1G63310.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G20362.1); Has 78 Blast hits to 77 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:23486580-23487044 REVERSE LENGTH=154	156	154	1.00E-66	98.7	79.5	88.5
Rsa1.0_00086.1.g4269.t1	gb|ABA18088.1| ABC transporter family protein [Olimarabidopsis pumila]	211	231	1.00E-114	109.5	95.3	99.5	ABC transporter family protein	gbpln	Olimarabidopsis pumila	AT1G63270.1 | Symbols: ATNAP10, NAP10 | non-intrinsic ABC protein 10 | chr1:23469664-23470353 REVERSE LENGTH=229	211	229	1.00E-116	108.5	94.3	99.5
Rsa1.0_00086.1.g4270.t1	ref|NP_176514.1| putative DEAD-box ATP-dependent RNA helicase 48 [Arabidopsis thaliana] gi|75333533|sp|Q9C8S9.1|RH48_ARATH RecName: Full=Probable DEAD-box ATP-dependent RNA helicase 48 gi|12324351|gb|AAG52143.1|AC022355_4 putative RNA helicase; 42376-45543 [Arabidopsis thaliana] gi|332195955|gb|AEE34076.1| putative DEAD-box ATP-dependent RNA helicase 48 [Arabidopsis thaliana]	786	798	0	101.5	86.3	91.2	putative DEAD-box ATP-dependent RNA helicase 48	gbpln	Arabidopsis thaliana	AT1G63250.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr1:23463284-23466451 REVERSE LENGTH=798	786	798	0	101.5	86.3	91.2
Rsa1.0_00086.1.g4271.t1	ref|XP_002886433.1| phloem protein 2-A11 [Arabidopsis lyrata subsp. lyrata] gi|297332274|gb|EFH62692.1| phloem protein 2-A11 [Arabidopsis lyrata subsp. lyrata]	144	287	4.00E-66	199.3	79.9	89.6	phloem protein 2-A11	gbpln	Arabidopsis lyrata	AT1G12710.1 | Symbols: AtPP2-A12, PP2-A12 | phloem protein 2-A12 | chr1:4326980-4328324 REVERSE LENGTH=291	144	291	1.00E-64	202.1	75.7	87.5
Rsa1.0_00086.1.g4272.t1	ref|NP_176493.1| membrane bound O-acyl transferase domain-containing protein [Arabidopsis thaliana] gi|12323260|gb|AAG51612.1|AC010795_16 unknown protein; 29405-27288 [Arabidopsis thaliana] gi|18175648|gb|AAL59903.1| unknown protein [Arabidopsis thaliana] gi|21689737|gb|AAM67512.1| unknown protein [Arabidopsis thaliana] gi|332195924|gb|AEE34045.1| membrane bound O-acyl transferase domain-containing protein [Arabidopsis thaliana]	466	465	0	99.8	92.1	96.6	membrane bound O-acyl transferase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G63050.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr1:23376061-23378178 REVERSE LENGTH=465	466	465	0	99.8	92.1	96.6
Rsa1.0_00086.1.g4273.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00086.1.g4274.t1	gb|EOA34651.1| hypothetical protein CARUB_v10022214mg [Capsella rubella]	245	257	3.00E-74	104.9	73.5	82.0	hypothetical protein CARUB_v10022214mg	gbpln	Capsella rubella	AT1G12630.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:4298897-4299475 FORWARD LENGTH=192	245	192	2.00E-43	78.4	46.5	51.8
Rsa1.0_00086.1.g4275.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00086.1.g4276.t1	ref|XP_002883360.1| time for coffee [Arabidopsis lyrata subsp. lyrata] gi|297329200|gb|EFH59619.1| time for coffee [Arabidopsis lyrata subsp. lyrata]	131	1550	3.00E-46	1183.2	83.2	89.3	time for coffee	gbpln	Arabidopsis lyrata	AT3G22380.2 | Symbols: TIC | time for coffee | chr3:7913181-7918967 FORWARD LENGTH=1555	131	1555	6.00E-45	1187.0	81.7	87.0
Rsa1.0_00086.1.g4277.t1	gb|EOA34129.1| hypothetical protein CARUB_v10021630mg [Capsella rubella]	696	699	0	100.4	93.1	96.8	hypothetical protein CARUB_v10021630mg	gbpln	Capsella rubella	AT1G63010.4 | Symbols: | Major Facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein | chr1:23347972-23351026 REVERSE LENGTH=699	696	699	0	100.4	92.8	96.4
Rsa1.0_00086.1.g4278.t1	ref|XP_002887985.1| hypothetical protein ARALYDRAFT_893174 [Arabidopsis lyrata subsp. lyrata] gi|297333826|gb|EFH64244.1| hypothetical protein ARALYDRAFT_893174 [Arabidopsis lyrata subsp. lyrata]	297	300	1.00E-166	101.0	95.3	98.7	hypothetical protein ARALYDRAFT_893174	gbpln	Arabidopsis lyrata	AT1G63000.1 | Symbols: NRS/ER, UER1 | nucleotide-rhamnose synthase/epimerase-reductase | chr1:23342510-23343859 FORWARD LENGTH=301	297	301	1.00E-167	101.3	94.6	98.7
Rsa1.0_00086.1.g4279.t1	gb|EOA35527.1| hypothetical protein CARUB_v10020735mg [Capsella rubella]	290	292	1.00E-154	100.7	92.8	94.1	hypothetical protein CARUB_v10020735mg	gbpln	Capsella rubella	AT1G62990.1 | Symbols: KNAT7, IXR11 | KNOTTED-like homeobox of Arabidopsis thaliana 7 | chr1:23337468-23340348 FORWARD LENGTH=291	290	291	1.00E-155	100.3	92.1	94.1
Rsa1.0_00086.1.g4280.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00086.1.g4281.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00086.1.g4282.t1	ref|XP_002887990.1| hypothetical protein ARALYDRAFT_475057 [Arabidopsis lyrata subsp. lyrata] gi|297333831|gb|EFH64249.1| hypothetical protein ARALYDRAFT_475057 [Arabidopsis lyrata subsp. lyrata]	804	772	0	96.0	61.6	68.5	hypothetical protein ARALYDRAFT_475057	gbpln	Arabidopsis lyrata	AT1G62970.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:23323358-23325751 FORWARD LENGTH=797	804	797	0	99.1	62.2	70.1

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<tr><td>Rsa1.0_00086.1.g4283.t1</td><td>ref|NP_564804.1| putative aminotransferase ACS10 [Arabidopsis thaliana] gi|50400664|sp|Q9LQ10.1|1A110_ARATH RecName: Full=Probable aminotransferase ACS10 gi|8493584|gb|AAF75807.1|AC011000_10 Strong similarity to ACS5 from Lupinus albus gb|AF119414, and contains an Aminotransferase-classI domain PF|00155 [Arabidopsis thaliana] gi|13194768|gb|AAK15546.1|AF348575_1 aminotransferase [Arabidopsis thaliana] gi|15451222|gb|AAK96882.1| Strong similarity to ACS5 from Lupinus albus gb|AF119414, and contains an Aminotransferase-classI domain PF|00155 [Arabidopsis thaliana] gi|31711978|gb|AAP68345.1| At1g62960 [Arabidopsis thaliana] gi|332195906|gb|AEE34027.1| putative aminotransferase ACS10 [Arabidopsis thaliana]</td><td>551</td><td>557</td><td>0</td><td>101.1</td><td>83.8</td><td>91.3</td><td>putative aminotransferase ACS10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G62960.1 | Symbols: ACS10 | ACC synthase 10 | chr1:23318271-23320229 REVERSE LENGTH=557</td><td>551</td><td>557</td><td>0</td><td>101.1</td><td>83.8</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00086.1.g4284.t1</td><td>ref|XP_002887991.1| hypothetical protein ARALYDRAFT_475059 [Arabidopsis lyrata subsp. lyrata] gi|297333832|gb|EFH64250.1| hypothetical protein ARALYDRAFT_475059 [Arabidopsis lyrata subsp. lyrata]</td><td>74</td><td>888</td><td>1.00E-21</td><td>1200.0</td><td>68.9</td><td>79.7</td><td>hypothetical protein ARALYDRAFT_475059</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G62950.1 | Symbols: | leucine-rich repeat transmembrane protein kinase family protein | chr1:23315294-23318061 FORWARD LENGTH=890</td><td>74</td><td>890</td><td>6.00E-24</td><td>1202.7</td><td>66.2</td><td>79.7</td></tr>
<tr><td>Rsa1.0_00086.1.g4285.t1</td><td>gb|ABE65414.1| hypothetical protein At1g62935 [Arabidopsis thaliana]</td><td>164</td><td>178</td><td>2.00E-43</td><td>108.5</td><td>65.2</td><td>73.8</td><td>hypothetical protein At1g62935</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G62935.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 45 Blast hits to 45 proteins in 13 species: Archae - 0; Bacteria - 2; Metazoa - 6; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 29 (source: NCBI BLink). | chr1:23308880-23309410 REVERSE LENGTH=176</td><td>164</td><td>176</td><td>7.00E-46</td><td>107.3</td><td>65.2</td><td>73.8</td></tr>
<tr><td>Rsa1.0_00086.1.g4286.t1</td><td>ref|XP_002888002.1| cornichon family protein [Arabidopsis lyrata subsp. lyrata] gi|297333843|gb|EFH64261.1| cornichon family protein [Arabidopsis lyrata subsp. lyrata]</td><td>137</td><td>137</td><td>2.00E-64</td><td>100.0</td><td>90.5</td><td>94.9</td><td>cornichon family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G12390.1 | Symbols: | Cornichon family protein | chr1:4220347-4221481 FORWARD LENGTH=137</td><td>137</td><td>137</td><td>6.00E-64</td><td>100.0</td><td>83.2</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00086.1.g4287.t1</td><td>gb|EOA28932.1| hypothetical protein CARUB_v10025180mg [Capsella rubella]</td><td>216</td><td>244</td><td>3.00E-76</td><td>113.0</td><td>63.0</td><td>78.2</td><td>hypothetical protein CARUB_v10025180mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G08080.1 | Symbols: ATACA7, ACA7 | alpha carbonic anhydrase 7 | chr1:2517022-2518546 REVERSE LENGTH=275</td><td>216</td><td>275</td><td>2.00E-75</td><td>127.3</td><td>68.1</td><td>82.9</td></tr>
<tr><td>Rsa1.0_00086.1.g4288.t1</td><td>ref|NP_190240.1| mitochondrial import inner membrane translocase subunit Tim9 [Arabidopsis thaliana] gi|12643936|sp|Q9XGX9.2|TIM9_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM9; AltName: Full=Protein EMBRYO DEFECTIVE 2474 gi|6523059|emb|CAB62326.1| small zinc finger-like protein TIM9 [Arabidopsis thaliana] gi|15028235|gb|AAK76614.1| putative small zinc finger protein TIM9 [Arabidopsis thaliana] gi|19310825|gb|AAL85143.1| putative small zinc finger protein TIM9 [Arabidopsis thaliana] gi|332644651|gb|AEE78172.1| mitochondrial import inner membrane translocase subunit Tim9 [Arabidopsis thaliana]</td><td>93</td><td>93</td><td>5.00E-43</td><td>100.0</td><td>91.4</td><td>94.6</td><td>mitochondrial import inner membrane translocase subunit Tim9</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G46560.1 | Symbols: TIM9, emb2474 | Tim10/DDP family zinc finger protein | chr3:17138632-17139301 FORWARD LENGTH=93</td><td>93</td><td>93</td><td>9.00E-46</td><td>100.0</td><td>91.4</td><td>94.6</td></tr>
<tr><td>Rsa1.0_00086.1.g4289.t1</td><td>pir||E84492 probable retroelement pol polyprotein [imported] - Arabidopsis thaliana</td><td>267</td><td>531</td><td>1.00E-48</td><td>198.9</td><td>40.4</td><td>53.6</td><td>probable retroelement pol polyprotein</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00086.1.g4290.t1</td><td>gb|EOA33664.1| hypothetical protein CARUB_v10019841mg [Capsella rubella]</td><td>758</td><td>772</td><td>0</td><td>101.8</td><td>84.0</td><td>90.5</td><td>hypothetical protein CARUB_v10019841mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G62870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G12380.1); Has 351 Blast hits to 343 proteins in 42 species: Archae - 2; Bacteria - 0; Metazoa - 27; Fungi - 5; Plants - 299; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr1:23284220-23286508 REVERSE LENGTH=762</td><td>758</td><td>762</td><td>0</td><td>100.5</td><td>83.1</td><td>90.1</td></tr>
</table>

Rsa1.0_00086.1.g4291.t1	gb|EOA35655.1| hypothetical protein CARUB_v10020879mg [Capsella rubella]	254	236	1.00E-111	92.9	79.9	85.4	hypothetical protein CARUB_v10020879mg	gbpln	Capsella rubella	AT1G62850.3 | Symbols: | Class I peptide chain release factor | chr1:23272608-23274211 REVERSE LENGTH=236	254	236	1.00E-113	92.9	80.3	85.4
Rsa1.0_00086.1.g4292.t1	ref|XP_002886450.1| amine oxidase family protein [Arabidopsis lyrata subsp. lyrata] gi|297332291|gb|EFH62709.1| amine oxidase family protein [Arabidopsis lyrata subsp. lyrata]	704	840	0	119.3	83.1	88.6	amine oxidase family protein	gbpln	Arabidopsis lyrata	AT1G62830.1 | Symbols: LDL1, SWP1, ATSWP1, ATLSD1, LSD1 | LSD1-like 1 | chr1:23264638-23267172 REVERSE LENGTH=844	704	844	0	119.9	82.7	88.1
Rsa1.0_00086.1.g4293.t1	ref|XP_002886453.1| hypothetical protein ARALYDRAFT_475071 [Arabidopsis lyrata subsp. lyrata] gi|297332294|gb|EFH62712.1| hypothetical protein ARALYDRAFT_475071 [Arabidopsis lyrata subsp. lyrata]	405	405	0	100.0	83.7	93.6	hypothetical protein ARALYDRAFT_475071	gbpln	Arabidopsis lyrata	AT1G62800.2 | Symbols: ASP4 | aspartate aminotransferase 4 | chr1:23253934-23257416 REVERSE LENGTH=405	405	405	0	100.0	82.5	93.8
Rsa1.0_00086.1.g4294.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00086.1.g4295.t1	ref|NP_176463.2| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|6630459|gb|AAF19547.1|AC007190_15 F23N19.12 [Arabidopsis thaliana] gi|332195880|gb|AEE34001.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	204	312	2.00E-74	152.9	67.6	74.5	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT1G62760.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:23237574-23238512 REVERSE LENGTH=312	204	312	5.00E-77	152.9	67.6	74.5
Rsa1.0_00086.1.g4296.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4297.t1	ref|XP_002882423.1| hypothetical protein ARALYDRAFT_477844 [Arabidopsis lyrata subsp. lyrata] gi|297328263|gb|EFH58682.1| hypothetical protein ARALYDRAFT_477844 [Arabidopsis lyrata subsp. lyrata]	411	428	1.00E-162	104.1	81.5	89.5	hypothetical protein ARALYDRAFT_477844	gbpln	Arabidopsis lyrata	AT3G05545.1 | Symbols: | RING/U-box superfamily protein | chr3:1609436-1612133 FORWARD LENGTH=425	411	425	1.00E-162	103.4	81.5	88.8
Rsa1.0_00087.1.g4298.t1	ref|XP_002886149.1| ATPAP11/PAP11 [Arabidopsis lyrata subsp. lyrata] gi|297331989|gb|EFH62408.1| ATPAP11/PAP11 [Arabidopsis lyrata subsp. lyrata]	133	461	2.00E-59	346.6	80.5	91.7	ATPAP11/PAP11	gbpln	Arabidopsis lyrata	AT1G52940.1 | Symbols: PAP5, ATPAP5 | purple acid phosphatase 5 | chr1:19716402-19723716 FORWARD LENGTH=396	133	396	5.00E-60	297.7	78.9	91.0
Rsa1.0_00087.1.g4299.t1	dbj|BAB21595.1| Tat binding protein like protein [Brassica rapa]	403	424	0	105.2	99.0	99.5	Tat binding protein like protein	gbpln	Brassica rapa	AT3G05530.1 | Symbols: RPT5A, ATS6A.2 | regulatory particle triple-A ATPase 5A | chr3:1603540-1605993 FORWARD LENGTH=424	403	424	0	105.2	98.8	99.3
Rsa1.0_00087.1.g4300.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4301.t1	ref|XP_002882419.1| rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297328259|gb|EFH58678.1| rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata]	245	246	1.00E-121	100.4	91.4	97.6	rubber elongation factor family protein	gbpln	Arabidopsis lyrata	AT3G05500.1 | Symbols: | Rubber elongation factor protein (REF) | chr3:1593540-1594802 FORWARD LENGTH=246	245	246	1.00E-123	100.4	91.0	97.6
Rsa1.0_00087.1.g4302.t1	ref|XP_002882418.1| hypothetical protein ARALYDRAFT_477838 [Arabidopsis lyrata subsp. lyrata] gi|297328258|gb|EFH58677.1| hypothetical protein ARALYDRAFT_477838 [Arabidopsis lyrata subsp. lyrata]	119	118	4.00E-45	99.2	88.2	93.3	hypothetical protein ARALYDRAFT_477838	gbpln	Arabidopsis lyrata	AT3G05490.1 | Symbols: RALFL22 | ralf-like 22 | chr3:1591381-1591740 FORWARD LENGTH=119	119	119	2.00E-46	100.0	85.7	91.6
Rsa1.0_00087.1.g4303.t1	ref|XP_002882417.1| cell cycle checkpoint control protein family [Arabidopsis lyrata subsp. lyrata] gi|297328257|gb|EFH58676.1| cell cycle checkpoint control protein family [Arabidopsis lyrata subsp. lyrata]	439	438	0	99.8	86.3	92.5	cell cycle checkpoint control protein family	gbpln	Arabidopsis lyrata	AT3G05480.1 | Symbols: ATRAD9, RAD9 | cell cycle checkpoint control protein family | chr3:1585383-1588238 FORWARD LENGTH=439	439	439	0	100.0	87.0	92.3
Rsa1.0_00087.1.g4304.t1	ref|XP_002884514.1| hypothetical protein ARALYDRAFT_317406 [Arabidopsis lyrata subsp. lyrata] gi|297330354|gb|EFH60773.1| hypothetical protein ARALYDRAFT_317406 [Arabidopsis lyrata subsp. lyrata]	840	896	0	106.7	86.7	90.8	hypothetical protein ARALYDRAFT_317406	gbpln	Arabidopsis lyrata	AT3G05470.1 | Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr3:1579667-1582547 REVERSE LENGTH=884	840	884	0	105.2	85.0	89.5
Rsa1.0_00087.1.g4305.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	417	1142	5.00E-94	273.9	47.2	63.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	417	575	2.00E-52	137.9	34.1	55.9

Rsa1.0_00087.1.g4306.t1	ref|XP_002884511.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330351|gb|EFH60770.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	222	473	6.00E-62	213.1	57.2	71.6	predicted protein	gbpln	Arabidopsis lyrata	AT3G05450.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Cystatin-related, plant (InterPro:IPR006525); BEST Arabidopsis thaliana protein match is: Cystatin/monellin superfamily protein (TAIR:AT3G05685.1); Has 2098 Blast hits to 1525 proteins in 202 species: Archae - 2; Bacteria - 561; Metazoa - 485; Fungi - 302; Plants - 191; Viruses - 20; Other Eukaryotes - 537 (source: NCBI BLink). | chr3:1573909-1576418 REVERSE LENGTH=440	222	440	9.00E-45	198.2	50.9	63.5
Rsa1.0_00087.1.g4307.t1	#	#	#	#	#	#	#	-	----	----	AT1G45130.1 | Symbols: BGAL5 | beta-galactosidase 5 | chr1:17065447-17069110 FORWARD LENGTH=732	60	732	5.00E-12	1220.0	50.0	51.7
Rsa1.0_00087.1.g4308.t1	ref|XP_002884511.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330351|gb|EFH60770.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	231	473	7.00E-64	204.8	59.3	71.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G05450.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Cystatin-related, plant (InterPro:IPR006525); BEST Arabidopsis thaliana protein match is: Cystatin/monellin superfamily protein (TAIR:AT3G05685.1); Has 2098 Blast hits to 1525 proteins in 202 species: Archae - 2; Bacteria - 561; Metazoa - 485; Fungi - 302; Plants - 191; Viruses - 20; Other Eukaryotes - 537 (source: NCBI BLink). | chr3:1573909-1576418 REVERSE LENGTH=440	231	440	1.00E-46	190.5	51.1	62.8
Rsa1.0_00087.1.g4309.t1	ref|XP_002884570.1| hypothetical protein ARALYDRAFT_340813 [Arabidopsis lyrata subsp. lyrata] gi|297330410|gb|EFH60829.1| hypothetical protein ARALYDRAFT_340813 [Arabidopsis lyrata subsp. lyrata]	263	265	2.00E-19	100.8	28.9	47.1	hypothetical protein ARALYDRAFT_340813	gbpln	Arabidopsis lyrata	AT1G03720.1 | Symbols: | Cysteine proteinases superfamily protein | chr1:924996-926373 REVERSE LENGTH=274	263	274	3.00E-18	104.2	23.6	37.6
Rsa1.0_00087.1.g4310.t4	ref|NP_187193.3| acyl-CoA binding protein 4 [Arabidopsis thaliana] gi|75264903|sp|Q9MA55.1|ACBP4_ARATH RecName: Full=Acyl-CoA-binding domain-containing protein 4; Short=Acyl-CoA binding protein 4 gi|7596769|gb|AAF64540.1| unknown protein [Arabidopsis thaliana] gi|30102696|gb|AAP21266.1| At3g05420 [Arabidopsis thaliana] gi|110736070|dbj|BAF00008.1| hypothetical protein [Arabidopsis thaliana] gi|332640716|gb|AEE74237.1| acyl-CoA binding protein 4 [Arabidopsis thaliana]	760	668	0	87.9	79.3	82.2	acyl-CoA binding protein 4	gbpln	Arabidopsis thaliana	AT3G05420.1 | Symbols: ACBP4 | acyl-CoA binding protein 4 | chr3:1561880-1567047 FORWARD LENGTH=668	760	668	0	87.9	79.3	82.2
Rsa1.0_00087.1.g4311.t1	gb|EOA31164.1| hypothetical protein CARUB_v10014330mg [Capsella rubella]	270	283	1.00E-125	104.8	85.9	92.2	hypothetical protein CARUB_v10014330mg	gbpln	Capsella rubella	AT3G05410.2 | Symbols: | Photosystem II reaction center PsbP family protein | chr3:1554783-1561456 FORWARD LENGTH=280	270	280	1.00E-127	103.7	85.2	89.6
Rsa1.0_00087.1.g4312.t1	ref|NP_187191.2| sugar transporter ERD6-like 12 [Arabidopsis thaliana] gi|75331208|sp|Q8VZT3.1|EDL12_ARATH RecName: Full=Sugar transporter ERD6-like 12; AltName: Full=Sugar transporter-like protein 5 gi|17380764|gb|AAL36212.1| putative sugar transporter protein [Arabidopsis thaliana] gi|20259597|gb|AAM14155.1| putative sugar transporter [Arabidopsis thaliana] gi|332640712|gb|AEE74233.1| sugar transporter ERD6-like 12 [Arabidopsis thaliana]	462	462	0	100.0	84.4	91.8	sugar transporter ERD6-like 12	gbpln	Arabidopsis thaliana	AT3G05400.1 | Symbols: | Major facilitator superfamily protein | chr3:1549702-1553942 FORWARD LENGTH=462	462	462	0	100.0	84.4	91.8
Rsa1.0_00087.1.g4313.t1	gb|EOA32093.1| hypothetical protein CARUB_v10015342mg [Capsella rubella]	465	463	0	99.6	91.6	96.3	hypothetical protein CARUB_v10015342mg	gbpln	Capsella rubella	AT3G05390.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF248, methyltransferase putative (InterPro:IPR004159); BEST Arabidopsis thaliana protein match is: S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (TAIR:AT4G01240.1); Has 507 Blast hits to 498 proteins in 33 species: Archae - 4; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 493; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:1546585-1547976 REVERSE LENGTH=463	465	463	0	99.6	90.8	95.7

Rsa1.0_00087.1.g4314.t3	ref|NP_001030643.1| protein ALWAYS EARLY 2 [Arabidopsis thaliana] gi|334185096|ref|NP_001189812.1| protein ALWAYS EARLY 2 [Arabidopsis thaliana] gi|334185098|ref|NP_001189813.1| protein ALWAYS EARLY 2 [Arabidopsis thaliana] gi|332640707|gb|AEE74228.1| protein ALWAYS EARLY 2 [Arabidopsis thaliana] gi|332640709|gb|AEE74230.1| protein ALWAYS EARLY 2 [Arabidopsis thaliana] gi|332640710|gb|AEE74231.1| protein ALWAYS EARLY 2 [Arabidopsis thaliana]	1058	1052	0	99.4	77.5	84.7	protein ALWAYS EARLY 2	gbpln	Arabidopsis thaliana	AT3G05380.4 | Symbols: ALY2 | DIRP ;Myb-like DNA-binding domain | chr3:1540562-1546139 FORWARD LENGTH=1052	1058	1052	0	99.4	77.5	84.7
Rsa1.0_00087.1.g4315.t1	ref|NP_187186.5| metallopeptidase M24-like protein [Arabidopsis thaliana] gi|19310478|gb|AAL84973.1| AT3g05350/T12H1_32 [Arabidopsis thaliana] gi|24111421|gb|AAN46861.1| At3g05350/T12H1_32 [Arabidopsis thaliana] gi|332640703|gb|AEE74224.1| metallopeptidase M24-like protein [Arabidopsis thaliana]	722	710	0	98.3	88.5	92.1	metallopeptidase M24-like protein	gbpln	Arabidopsis thaliana	AT3G05350.1 | Symbols: | Metallopeptidase M24 family protein | chr3:1527103-1533843 REVERSE LENGTH=710	722	710	0	98.3	88.5	92.1
Rsa1.0_00087.1.g4316.t1	gb|EOA32090.1| hypothetical protein CARUB_v10015337mg [Capsella rubella]	648	661	0	102.0	78.9	88.9	hypothetical protein CARUB_v10015337mg	gbpln	Capsella rubella	AT3G05340.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:1524071-1526047 REVERSE LENGTH=658	648	658	0	101.5	78.5	88.6
Rsa1.0_00087.1.g4317.t1	gb|EOA30452.1| hypothetical protein CARUB_v10013577mg [Capsella rubella]	458	482	0	105.2	82.5	89.3	hypothetical protein CARUB_v10013577mg	gbpln	Capsella rubella	AT3G05330.1 | Symbols: ATN, ATTAN | cyclin family | chr3:1519162-1521159 REVERSE LENGTH=444	458	444	0	96.9	76.0	82.8
Rsa1.0_00087.1.g4318.t1	ref|XP_002884502.1| hypothetical protein ARALYDRAFT_477821 [Arabidopsis lyrata subsp. lyrata] gi|297330342|gb|EFH60761.1| hypothetical protein ARALYDRAFT_477821 [Arabidopsis lyrata subsp. lyrata]	209	212	6.00E-98	101.4	81.3	91.4	hypothetical protein ARALYDRAFT_477821	gbpln	Arabidopsis lyrata	AT3G05327.1 | Symbols: | Cyclin family protein | chr3:1517581-1518399 REVERSE LENGTH=212	209	212	1.00E-100	101.4	82.3	90.9
Rsa1.0_00087.1.g4319.t1	ref|NP_187183.3| O-fucosyltransferase family protein [Arabidopsis thaliana] gi|6729042|gb|AAF27038.1|AC009177_28 unknown protein [Arabidopsis thaliana] gi|332640698|gb|AEE74219.1| O-fucosyltransferase family protein [Arabidopsis thaliana]	419	445	0	106.2	89.5	94.3	O-fucosyltransferase family protein	gbpln	Arabidopsis thaliana	AT3G05320.1 | Symbols: | O-fucosyltransferase family protein | chr3:1513558-1514895 REVERSE LENGTH=445	419	445	0	106.2	89.5	94.3
Rsa1.0_00087.1.g4320.t1	gb|EOA30122.1| hypothetical protein CARUB_v10013232mg [Capsella rubella]	651	621	0	95.4	77.3	85.1	hypothetical protein CARUB_v10013232mg	gbpln	Capsella rubella	AT3G05270.2 | Symbols: | Plant protein of unknown function (DUF869) | chr3:1500803-1502926 REVERSE LENGTH=615	651	615	0	94.5	76.8	84.5
Rsa1.0_00087.1.g4321.t1	gb|EOA31145.1| hypothetical protein CARUB_v10014308mg [Capsella rubella]	289	289	1.00E-153	100.0	90.7	94.5	hypothetical protein CARUB_v10014308mg	gbpln	Capsella rubella	AT3G05260.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:1497665-1498919 REVERSE LENGTH=289	289	289	1.00E-153	100.0	89.3	94.1
Rsa1.0_00087.1.g4322.t1	ref|NP_187176.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|26450611|dbj|BAC42417.1| unknown protein [Arabidopsis thaliana] gi|31711722|gb|AAP68217.1| At3g05250 [Arabidopsis thaliana] gi|70905075|gb|AAZ14063.1| At3g05250 [Arabidopsis thaliana] gi|332640690|gb|AEE74211.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	270	278	1.00E-113	103.0	75.6	84.8	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G05250.1 | Symbols: | RING/U-box superfamily protein | chr3:1495635-1497387 FORWARD LENGTH=278	270	278	1.00E-116	103.0	75.6	84.8
Rsa1.0_00087.1.g4323.t1	ref|NP_187175.2| mitochondrial editing factor 19 [Arabidopsis thaliana] gi|218546759|sp|Q9MA95.2|PP214_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At3g05240 gi|332640689|gb|AEE74210.1| mitochondrial editing factor 19 [Arabidopsis thaliana]	564	565	0	100.2	80.5	90.4	mitochondrial editing factor 19	gbpln	Arabidopsis thaliana	AT3G05240.1 | Symbols: MEF19 | mitochondrial editing factor 19 | chr3:1493684-1495381 REVERSE LENGTH=565	564	565	0	100.2	80.5	90.4
Rsa1.0_00087.1.g4324.t1	ref|XP_002882405.1| signal peptidase subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297328245|gb|EFH58664.1| signal peptidase subunit family protein [Arabidopsis lyrata subsp. lyrata]	783	167	3.00E-91	21.3	20.1	20.6	signal peptidase subunit family protein	gbpln	Arabidopsis lyrata	AT3G05230.1 | Symbols: | Signal peptidase subunit | chr3:1492304-1493452 FORWARD LENGTH=167	783	167	5.00E-93	21.3	19.8	20.6

Rsa1.0_00087.1.g4325.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1822	1274	0	69.9	33.0	45.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1822	575	9.00E-69	31.6	9.8	15.0
Rsa1.0_00087.1.g4326.t1	ref|NP_187172.1| DNA excision repair protein ERCC-1 [Arabidopsis thaliana] gi|55976606|sp|Q9MA98.1|ERCC1_ARATH RecName: Full=DNA excision repair protein ERCC-1; Short=AtERCC1; Short=AtRAD10; AltName: Full=Ultraviolet hypersensitive 7 gi|6729031|gb|AAF27027.1|AC009177_17 putative nucleotide repair protein [Arabidopsis thaliana] gi|9800490|gb|AAF99316.1|AF276082_1 ERCC1 [Arabidopsis thaliana] gi|15215614|gb|AAK91352.1| AT3g05210/T12H1_18 [Arabidopsis thaliana] gi|21435979|gb|AAM51569.1| AT3g05210/T12H1_18 [Arabidopsis thaliana] gi|21618171|gb|AAM67221.1| putative nucleotide repair protein [Arabidopsis thaliana] gi|332640684|gb|AEE74205.1| DNA excision repair protein ERCC-1 [Arabidopsis thaliana]	408	410	0	100.5	87.0	91.9	DNA excision repair protein ERCC-1	gbpln	Arabidopsis thaliana	AT3G05210.1 | Symbols: ERCC1, UVR7 | nucleotide repair protein, putative | chr3:1479591-1481823 FORWARD LENGTH=410	408	410	0	100.5	87.0	91.9
Rsa1.0_00087.1.g4327.t1	ref|XP_002884492.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330332|gb|EFH60751.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	501	469	0	93.6	80.4	85.0	kinase family protein	gbpln	Arabidopsis lyrata	AT3G05140.1 | Symbols: RBK2 | ROP binding protein kinases 2 | chr3:1435817-1437800 REVERSE LENGTH=460	501	460	0	91.8	77.8	83.0
Rsa1.0_00087.1.g4328.t1	ref|NP_187164.1| uncharacterized protein [Arabidopsis thaliana] gi|6729023|gb|AAF27019.1|AC009177_9 hypothetical protein [Arabidopsis thaliana] gi|332640668|gb|AEE74189.1| uncharacterized protein AT3G05130 [Arabidopsis thaliana]	580	634	1.00E-167	109.3	64.0	79.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G05130.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Prefoldin chaperone subunit family protein (TAIR:AT5G27330.1); Has 171032 Blast hits to 82560 proteins in 3364 species: Archae - 2835; Bacteria - 33550; Metazoa - 71995; Fungi - 13365; Plants - 9598; Viruses - 592; Other Eukaryotes - 39097 (source: NCBI BLink). | chr3:1433475-1435379 REVERSE LENGTH=634	580	634	1.00E-170	109.3	64.0	79.5
Rsa1.0_00087.1.g4329.t1	ref|NP_187163.1| putative gibberellin receptor GID1L1 [Arabidopsis thaliana] gi|75336145|sp|Q9MAA7.1|GID1A_ARATH RecName: Full=Gibberellin receptor GID1A; AltName: Full=AtCXE10; AltName: Full=Carboxylesterase 10; AltName: Full=GID1-like protein 1; AltName: Full=Protein GA INSENSITIVE DWARF 1A; Short=AtGID1A gi|6729022|gb|AAF27018.1|AC009177_8 unknown protein [Arabidopsis thaliana] gi|22530934|gb|AAM96971.1| unknown protein [Arabidopsis thaliana] gi|27311999|gb|AAO00965.1| unknown protein [Arabidopsis thaliana] gi|332640667|gb|AEE74188.1| putative gibberellin receptor GID1L1 [Arabidopsis thaliana]	353	345	1.00E-176	97.7	85.3	92.4	putative gibberellin receptor GID1L1	gbpln	Arabidopsis thaliana	AT3G05120.1 | Symbols: ATGID1A, GID1A | alpha/beta-Hydrolases superfamily protein | chr3:1430682-1432287 FORWARD LENGTH=345	353	345	1.00E-178	97.7	85.3	92.4
Rsa1.0_00087.1.g4330.t1	ref|XP_002884491.1| hypothetical protein ARALYDRAFT_340677 [Arabidopsis lyrata subsp. lyrata] gi|297330331|gb|EFH60750.1| hypothetical protein ARALYDRAFT_340677 [Arabidopsis lyrata subsp. lyrata]	545	633	1.00E-105	116.1	46.4	65.1	hypothetical protein ARALYDRAFT_340677	gbpln	Arabidopsis lyrata	AT3G04960.3 | Symbols: | Domain of unknown function (DUF3444) | chr3:1373819-1375769 FORWARD LENGTH=605	545	605	5.00E-91	111.0	41.7	60.9
Rsa1.0_00087.1.g4331.t1	gb|EOA29113.1| hypothetical protein CARUB_v10025380mg [Capsella rubella]	174	821	1.00E-11	471.8	17.8	20.1	hypothetical protein CARUB_v10025380mg	gbpln	Capsella rubella	AT2G39360.1 | Symbols: | Protein kinase superfamily protein | chr2:16437592-16440039 REVERSE LENGTH=815	174	815	2.00E-13	468.4	18.4	20.7
Rsa1.0_00087.1.g4332.t2	gb|EOA23889.1| hypothetical protein CARUB_v10017105mg [Capsella rubella]	523	488	0	93.3	84.1	88.3	hypothetical protein CARUB_v10017105mg	gbpln	Capsella rubella	AT3G42950.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:15015383-15017800 FORWARD LENGTH=484	523	484	0	92.5	81.8	87.8
Rsa1.0_00087.1.g4333.t1	ref|NP_179553.1| F-box protein [Arabidopsis thaliana] gi|75216815|sp|Q9ZUN0.1|FB113_ARATH RecName: Full=Putative F-box protein At2g19630 gi|4191792|gb|AAD10161.1| hypothetical protein [Arabidopsis thaliana] gi|330251810|gb|AEC06904.1| F-box protein [Arabidopsis thaliana]	292	297	2.00E-42	101.7	40.8	57.2	F-box protein	gbpln	Arabidopsis thaliana	AT2G19630.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:8490217-8491110 REVERSE LENGTH=297	292	297	4.00E-45	101.7	40.8	57.2

Rsa1.0_00087.1.g4334.t1	gb|ACY38730.1| salt-induced WD protein 1 [Brassica napus]	757	754	0	99.6	90.2	95.2	salt-induced WD protein 1	gbpln	Brassica napus	AT3G05090.2 | Symbols: LRS1 | Transducin/WD40 repeat-like superfamily protein | chr3:1418573-1422723 REVERSE LENGTH=753	757	753	0	99.5	90.0	94.5
Rsa1.0_00087.1.g4335.t1	ref|XP_002882392.1| hypothetical protein ARALYDRAFT_477790 [Arabidopsis lyrata subsp. lyrata] gi|297328232|gb|EFH58651.1| hypothetical protein ARALYDRAFT_477790 [Arabidopsis lyrata subsp. lyrata]	148	144	9.00E-63	97.3	85.1	90.5	hypothetical protein ARALYDRAFT_477790	gbpln	Arabidopsis lyrata	AT3G05070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: mRNA splicing factor, Cwf18 (InterPro:IPR013169); Has 292 Blast hits to 292 proteins in 153 species: Archae - 0; Bacteria - 0; Metazoa - 118; Fungi - 83; Plants - 38; Viruses - 11; Other Eukaryotes - 42 (source: NCBI BLink). | chr3:1416480-1417533 FORWARD LENGTH=144	148	144	2.00E-64	97.3	83.8	91.2
Rsa1.0_00087.1.g4336.t1	ref|NP_187156.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|6729015|gb|AAF27011.1|AC009177_1 putative cyclin-dependent protein kinase [Arabidopsis thaliana] gi|14532508|gb|AAK63982.1| AT3g05050/T12H1_1 [Arabidopsis thaliana] gi|23506083|gb|AAN28901.1| At3g05050/T12H1_1 [Arabidopsis thaliana] gi|332640659|gb|AEE74180.1| protein kinase domain-containing protein [Arabidopsis thaliana]	587	593	0	101.0	81.4	89.9	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G05050.1 | Symbols: | Protein kinase superfamily protein | chr3:1408789-1411194 REVERSE LENGTH=593	587	593	0	101.0	81.4	89.9
Rsa1.0_00087.1.g4337.t1	ref|XP_002884488.1| hypothetical protein ARALYDRAFT_477786 [Arabidopsis lyrata subsp. lyrata] gi|297330328|gb|EFH60747.1| hypothetical protein ARALYDRAFT_477786 [Arabidopsis lyrata subsp. lyrata]	1185	1202	0	101.4	81.9	88.5	hypothetical protein ARALYDRAFT_477786	gbpln	Arabidopsis lyrata	AT3G05040.1 | Symbols: HST, HST1 | ARM repeat superfamily protein | chr3:1401479-1408095 REVERSE LENGTH=1202	1185	1202	0	101.4	81.3	88.4
Rsa1.0_00087.1.g4338.t1	gb|ABD65028.1| hypothetical protein 26.t00082 [Brassica oleracea]	341	220	6.00E-81	64.5	44.0	53.4	hypothetical protein 26.t00082	gbpln	Brassica oleracea	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	341	384	8.00E-52	112.6	30.8	45.5
Rsa1.0_00087.1.g4339.t1	ref|XP_002884487.1| hypothetical protein ARALYDRAFT_477785 [Arabidopsis lyrata subsp. lyrata] gi|297330327|gb|EFH60746.1| hypothetical protein ARALYDRAFT_477785 [Arabidopsis lyrata subsp. lyrata]	552	543	0	98.4	92.6	95.7	hypothetical protein ARALYDRAFT_477785	gbpln	Arabidopsis lyrata	AT3G05030.1 | Symbols: NHX2, ATNHX2 | sodium hydrogen exchanger 2 | chr3:1393456-1396784 REVERSE LENGTH=546	552	546	0	98.9	91.8	95.8
Rsa1.0_00087.1.g4340.t1	ref|XP_002864564.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310399|gb|EFH40823.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	381	447	1.00E-108	117.3	64.0	76.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G58340.2 | Symbols: | myb-like HTH transcriptional regulator family protein | chr5:23582607-23584245 FORWARD LENGTH=448	381	448	1.00E-110	117.6	64.8	77.2
Rsa1.0_00087.1.g4341.t1	sp|P10352.2|ACP1_BRANA RecName: Full=Acyl carrier protein, chloroplastic; AltName: Full=ACP05; Short=ACP; AltName: Full=Clone 29C08; Flags: Precursor gi|295796|emb|CAA34247.1| acyl carrier protein [Brassica napus]	131	134	5.00E-55	102.3	89.3	93.1	RecName: Full=Acyl carrier protein, chloroplastic; AltName: Full=ACP05; Short=ACP; AltName: Full=Clone 29C08; Flags: Precursor gi|295796|emb|CAA34247.1| acyl carrier protein	gbpln	Brassica napus	AT3G05020.1 | Symbols: ACP1, ACP | acyl carrier protein 1 | chr3:1391863-1392878 REVERSE LENGTH=137	131	137	2.00E-48	104.6	80.2	89.3
Rsa1.0_00087.1.g4342.t2	ref|XP_002884485.1| hypothetical protein ARALYDRAFT_340666 [Arabidopsis lyrata subsp. lyrata] gi|297330325|gb|EFH60744.1| hypothetical protein ARALYDRAFT_340666 [Arabidopsis lyrata subsp. lyrata]	790	810	0	102.5	86.5	92.4	hypothetical protein ARALYDRAFT_340666	gbpln	Arabidopsis lyrata	AT4G08630.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48860.2); Has 1487 Blast hits to 747 proteins in 184 species: Archae - 0; Bacteria - 56; Metazoa - 305; Fungi - 197; Plants - 180; Viruses - 3; Other Eukaryotes - 746 (source: NCBI BLink). | chr4:5506998-5511959 REVERSE LENGTH=845	790	845	0	107.0	82.9	89.9
Rsa1.0_00087.1.g4343.t1	ref|NP_187151.1| Transport protein particle (TRAPP) component [Arabidopsis thaliana] gi|12322850|gb|AAG51412.1|AC009465_12 unknown protein; 16248-17501 [Arabidopsis thaliana] gi|27754554|gb|AAO22724.1| unknown protein [Arabidopsis thaliana] gi|28394073|gb|AAO42444.1| unknown protein [Arabidopsis thaliana] gi|332640653|gb|AEE74174.1| Transport protein particle (TRAPP) component [Arabidopsis thaliana]	240	173	1.00E-92	72.1	67.9	68.3	Transport protein particle (TRAPP) component	gbpln	Arabidopsis thaliana	AT3G05000.1 | Symbols: | Transport protein particle (TRAPP) component | chr3:1387444-1388697 REVERSE LENGTH=173	240	173	4.00E-95	72.1	67.9	68.3

Rsa1.0_00087.1.g4344.t2	ref|XP_002862604.1| hypothetical protein ARALYDRAFT_920493 [Arabidopsis lyrata subsp. lyrata] gi|297308231|gb|EFH38862.1| hypothetical protein ARALYDRAFT_920493 [Arabidopsis lyrata subsp. lyrata]	739	1235	4.00E-94	167.1	33.6	43.4	hypothetical protein ARALYDRAFT_920493	gbpln	Arabidopsis lyrata	AT3G04990.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Frigida-like protein (TAIR:AT5G27220.1); Has 30900 Blast hits to 17560 proteins in 1427 species: Archae - 757; Bacteria - 4112; Metazoa - 14311; Fungi - 2221; Plants - 1348; Viruses - 71; Other Eukaryotes - 8080 (source: NCBI BLink). | chr3:1383996-1384679 REVERSE LENGTH=227	739	227	1.00E-31	30.7	12.0	14.6
Rsa1.0_00087.1.g4345.t1	ref|XP_002862604.1| hypothetical protein ARALYDRAFT_920493 [Arabidopsis lyrata subsp. lyrata] gi|297308231|gb|EFH38862.1| hypothetical protein ARALYDRAFT_920493 [Arabidopsis lyrata subsp. lyrata]	631	1235	1.00E-104	195.7	39.8	51.2	hypothetical protein ARALYDRAFT_920493	gbpln	Arabidopsis lyrata	AT5G27220.1 | Symbols: | Frigida-like protein | chr5:9578757-9582752 FORWARD LENGTH=1181	631	1181	3.00E-29	187.2	14.6	22.7
Rsa1.0_00087.1.g4346.t1	ref|NP_187149.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] gi|12322856|gb|AAG51418.1|AC009465_18 hypothetical protein, contains DnaJ motif: prokaryotic heat shock protein motif; 22764-26261 [Arabidopsis thaliana] gi|332640650|gb|AEE74171.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	1092	1165	0	106.7	62.9	74.8	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT3G04980.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr3:1378684-1382181 REVERSE LENGTH=1165	1092	1165	0	106.7	62.9	74.8
Rsa1.0_00087.1.g4347.t1	ref|XP_002882388.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297328228|gb|EFH58647.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	371	398	1.00E-170	107.3	80.6	86.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G04970.1 | Symbols: | DHHC-type zinc finger family protein | chr3:1376240-1378339 FORWARD LENGTH=397	371	397	1.00E-170	107.0	79.5	86.3
Rsa1.0_00087.1.g4348.t1	ref|XP_002882387.1| hypothetical protein ARALYDRAFT_477773 [Arabidopsis lyrata subsp. lyrata] gi|297328227|gb|EFH58646.1| hypothetical protein ARALYDRAFT_477773 [Arabidopsis lyrata subsp. lyrata]	564	609	1.00E-112	108.0	45.6	63.3	hypothetical protein ARALYDRAFT_477773	gbpln	Arabidopsis lyrata	AT3G04960.4 | Symbols: | Domain of unknown function (DUF3444) | chr3:1373819-1375769 FORWARD LENGTH=553	564	553	1.00E-110	98.0	43.8	58.3
Rsa1.0_00087.1.g4349.t1	ref|XP_002882387.1| hypothetical protein ARALYDRAFT_477773 [Arabidopsis lyrata subsp. lyrata] gi|297328227|gb|EFH58646.1| hypothetical protein ARALYDRAFT_477773 [Arabidopsis lyrata subsp. lyrata]	847	609	1.00E-102	71.9	24.7	34.7	hypothetical protein ARALYDRAFT_477773	gbpln	Arabidopsis lyrata	AT3G04960.3 | Symbols: | Domain of unknown function (DUF3444) | chr3:1373819-1375769 FORWARD LENGTH=605	847	605	1.00E-104	71.4	28.8	42.3
Rsa1.0_00087.1.g4350.t1	gb|AAG03119.1|AC004133_13 F5A9.24 [Arabidopsis thaliana]	828	1254	0	151.4	49.0	65.3	F5A9.24	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	828	154	9.00E-44	18.6	9.4	13.4
Rsa1.0_00087.1.g4351.t1	ref|XP_002882385.1| hypothetical protein ARALYDRAFT_896550 [Arabidopsis lyrata subsp. lyrata] gi|297328225|gb|EFH58644.1| hypothetical protein ARALYDRAFT_896550 [Arabidopsis lyrata subsp. lyrata]	331	324	1.00E-142	97.9	80.1	88.5	hypothetical protein ARALYDRAFT_896550	gbpln	Arabidopsis lyrata	AT3G04940.1 | Symbols: ATCYSD1, CYSD1 | cysteine synthase D1 | chr3:1365681-1367508 FORWARD LENGTH=324	331	324	1.00E-144	97.9	79.2	88.5
Rsa1.0_00087.1.g4352.t1	gb|AAG51407.1|AC009465_7 putative cysteine synthase; 39489-37437 [Arabidopsis thaliana]	321	399	1.00E-145	124.3	82.6	92.2	putative cysteine synthase; 39489-37437	gbpln	Arabidopsis thaliana	AT3G04940.1 | Symbols: ATCYSD1, CYSD1 | cysteine synthase D1 | chr3:1365681-1367508 FORWARD LENGTH=324	321	324	2.33E-156	100.9	82.6	92.2
Rsa1.0_00087.1.g4353.t1	gb|EOA30558.1| hypothetical protein CARUB_v10013683mg [Capsella rubella]	436	453	1.00E-160	103.9	78.7	85.8	hypothetical protein CARUB_v10013683mg	gbpln	Capsella rubella	AT3G04930.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr3:1363029-1364399 FORWARD LENGTH=456	436	456	1.00E-154	104.6	78.0	84.6
Rsa1.0_00087.1.g4354.t1	ref|XP_002882383.1| 40S ribosomal protein S24 [Arabidopsis lyrata subsp. lyrata] gi|297328223|gb|EFH58642.1| 40S ribosomal protein S24 [Arabidopsis lyrata subsp. lyrata]	133	133	4.00E-68	100.0	98.5	98.5	40S ribosomal protein S24	gbpln	Arabidopsis lyrata	AT5G28060.1 | Symbols: | Ribosomal protein S24e family protein | chr5:10069791-10070792 REVERSE LENGTH=133	133	133	3.00E-68	100.0	94.7	96.2

Rsa1.0_00087.1.g4355.t1	ref|NP_187142.1| serine/threonine-protein kinase WNK1 [Arabidopsis thaliana] gi|75262294|sp|Q9CAV6.1|WNK1_ARATH RecName: Full=Serine/threonine-protein kinase WNK1; Short=AtWNK1; AltName: Full=Protein kinase with no lysine 1 gi|12322854|gb|AAG51416.1|AC009465_16 putative mitogen activated protein kinase kinase; 49861-46888 [Arabidopsis thaliana] gi|20302596|dbj|BAB91125.1| Ser/Thr kinase [Arabidopsis thaliana] gi|332640634|gb|AEE74155.1| serine/threonine-protein kinase WNK1 [Arabidopsis thaliana]	686	700	0	102.0	87.3	91.4	serine/threonine-protein kinase WNK1	gbpln	Arabidopsis thaliana	AT3G04910.1 | Symbols: WNK1, ZIK4, ATWNK1 | with no lysine (K) kinase 1 | chr3:1355084-1358057 FORWARD LENGTH=700	686	700	0	102.0	87.3	91.4
Rsa1.0_00087.1.g4356.t1	gb|EOA31421.1| hypothetical protein CARUB_v10014601mg [Capsella rubella]	263	217	7.00E-86	82.5	61.6	68.8	hypothetical protein CARUB_v10014601mg	gbpln	Capsella rubella	AT3G04890.1 | Symbols: | Uncharacterized conserved protein (DUF2358) | chr3:1347708-1349066 FORWARD LENGTH=216	263	216	5.00E-85	82.1	58.9	66.2
Rsa1.0_00087.1.g4357.t1	ref|NP_566241.1| DNA-damage-repair/toleration protein DRT102 [Arabidopsis thaliana] gi|148872800|sp|Q05212.2|DR102_ARATH RecName: Full=DNA-damage-repair/toleration protein DRT102 gi|15529165|gb|AAK97677.1| AT3g04880/T9J14_17 [Arabidopsis thaliana] gi|23505883|gb|AAN28801.1| At3g04880/T9J14_17 [Arabidopsis thaliana] gi|332640629|gb|AEE74150.1| DNA-damage-repair/toleration protein DRT102 [Arabidopsis thaliana]	284	310	1.00E-135	109.2	88.7	92.3	DNA-damage-repair/toleration protein DRT102	gbpln	Arabidopsis thaliana	AT3G04880.1 | Symbols: DRT102 | DNA-damage-repair/toleration protein (DRT102) | chr3:1346431-1347363 REVERSE LENGTH=310	284	310	1.00E-138	109.2	88.7	92.3
Rsa1.0_00087.1.g4358.t1	gb|ACM68701.1| zeta-carotene desaturase [Brassica rapa subsp. pekinensis]	584	561	0	96.1	93.8	94.3	zeta-carotene desaturase	gbpln	Brassica rapa	AT3G04870.2 | Symbols: ZDS, PDE181, SPC1 | zeta-carotene desaturase | chr3:1342842-1346189 FORWARD LENGTH=558	584	558	0	95.5	90.4	92.8
Rsa1.0_00087.1.g4359.t1	ref|XP_002884475.1| hypothetical protein ARALYDRAFT_477757 [Arabidopsis lyrata subsp. lyrata] gi|297330315|gb|EFH60734.1| hypothetical protein ARALYDRAFT_477757 [Arabidopsis lyrata subsp. lyrata]	291	289	1.00E-130	99.3	81.4	91.4	hypothetical protein ARALYDRAFT_477757	gbpln	Arabidopsis lyrata	AT3G04860.1 | Symbols: | Plant protein of unknown function (DUF868) | chr3:1339349-1340218 REVERSE LENGTH=289	291	289	1.00E-132	99.3	82.1	90.7
Rsa1.0_00087.1.g4360.t1	sp|P49396.2|RS3A_BRARA RecName: Full=40S ribosomal protein S3a; AltName: Full=S phase-specific protein BIS289 gi|387909|gb|AAA33013.1| S-phase-specific protein [Brassica rapa] gi|397401|emb|CAA81030.1| unnamed protein product [Brassica rapa]	262	262	1.00E-138	100.0	97.3	98.5	RecName: Full=40S ribosomal protein S3a; AltName: Full=S phase-specific protein BIS289 gi|387909|gb|AAA33013.1| S-phase-specific protein	gbpln	Brassica rapa	AT4G34670.1 | Symbols: | Ribosomal protein S3Ae | chr4:16548724-16550222 FORWARD LENGTH=262	262	262	1.00E-139	100.0	93.1	96.2
Rsa1.0_00087.1.g4361.t1	gb|EOA31103.1| hypothetical protein CARUB_v10014256mg [Capsella rubella]	303	304	1.00E-166	100.3	93.7	98.0	hypothetical protein CARUB_v10014256mg	gbpln	Capsella rubella	AT3G04830.1 | Symbols: | Protein prenylyltransferase superfamily protein | chr3:1326289-1329132 FORWARD LENGTH=303	303	303	1.00E-166	100.0	92.4	97.7
Rsa1.0_00087.1.g4362.t1	ref|NP_187132.1| serine/threonine-protein kinase Nek2 [Arabidopsis thaliana] gi|79607883|ref|NP_974221.2| serine/threonine-protein kinase Nek2 [Arabidopsis thaliana] gi|75333670|sp|Q9CAU7.1|NEK2_ARATH RecName: Full=Serine/threonine-protein kinase Nek2; AltName: Full=NimA-related protein kinase 2; Short=AtNek2 gi|12322861|gb|AAG51423.1|AC009465_23 putative kinase; 86849-83844 [Arabidopsis thaliana] gi|24030188|gb|AAN41275.1| putative kinase [Arabidopsis thaliana] gi|332640617|gb|AEE74138.1| serine/threonine-protein kinase Nek2 [Arabidopsis thaliana] gi|332640618|gb|AEE74139.1| serine/threonine-protein kinase Nek2 [Arabidopsis thaliana]	537	606	0	112.8	87.0	91.2	serine/threonine-protein kinase Nek2	gbpln	Arabidopsis thaliana	AT3G04810.2 | Symbols: ATNEK2, NEK2 | NIMA-related kinase 2 | chr3:1318096-1321101 FORWARD LENGTH=606	537	606	0	112.8	87.0	91.2
Rsa1.0_00087.1.g4363.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00087.1.g4364.t1	dbj|BAJ33930.1| unnamed protein product [Thellungiella halophila]	275	278	1.00E-139	101.1	92.7	96.0	unnamed protein product	----	----	AT3G04790.1 | Symbols: | Ribose 5-phosphate isomerase, type A protein | chr3:1313365-1314195 FORWARD LENGTH=276	275	276	1.00E-140	100.4	91.3	95.3
Rsa1.0_00087.1.g4365.t1	gb|EOA31567.1| hypothetical protein CARUB_v10014759mg [Capsella rubella]	176	176	2.00E-96	100.0	97.2	98.9	hypothetical protein CARUB_v10014759mg	gbpln	Capsella rubella	AT3G04780.1 | Symbols: | Protein of unknown function (DUF1000) | chr3:1311447-1313013 REVERSE LENGTH=176	176	176	4.00E-98	100.0	96.6	98.3
Rsa1.0_00087.1.g4366.t1	ref|XP_002893313.1| hypothetical protein ARALYDRAFT_472658 [Arabidopsis lyrata subsp. lyrata] gi|297339155|gb|EFH69572.1| hypothetical protein ARALYDRAFT_472658 [Arabidopsis lyrata subsp. lyrata]	321	378	6.00E-91	117.8	59.5	73.8	hypothetical protein ARALYDRAFT_472658	gbpln	Arabidopsis lyrata	AT1G23950.3 | Symbols: | Protein of unknown function (DUF626) | chr1:8469712-8471353 REVERSE LENGTH=368	321	368	1.00E-89	114.6	56.4	71.3
Rsa1.0_00087.1.g4367.t1	ref|XP_002884468.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330308|gb|EFH60727.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	589	598	0	101.5	89.6	95.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G04760.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr3:1303884-1305692 REVERSE LENGTH=602	589	602	0	102.2	87.4	94.4
Rsa1.0_00087.1.g4368.t1	gb|EOA32570.1| hypothetical protein CARUB_v10015860mg [Capsella rubella]	660	651	0	98.6	80.5	86.7	hypothetical protein CARUB_v10015860mg	gbpln	Capsella rubella	AT3G04750.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:1301391-1303376 REVERSE LENGTH=661	660	661	0	100.2	79.1	85.0
Rsa1.0_00087.1.g4369.t1	ref|XP_002882372.1| hypothetical protein ARALYDRAFT_477743 [Arabidopsis lyrata subsp. lyrata] gi|297328212|gb|EFH58631.1| hypothetical protein ARALYDRAFT_477743 [Arabidopsis lyrata subsp. lyrata]	1666	1702	0	102.2	89.7	93.8	hypothetical protein ARALYDRAFT_477743	gbpln	Arabidopsis lyrata	AT3G04740.1 | Symbols: SWP, MED14, ATMED14 | RNA polymerase II transcription mediators | chr3:1294037-1300555 FORWARD LENGTH=1703	1666	1703	0	102.2	89.7	93.8
Rsa1.0_00087.1.g4370.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4371.t1	ref|XP_002874695.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320532|gb|EFH50954.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	83	84	2.00E-11	101.2	49.4	55.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G11510.1 | Symbols: RALFL28 | ralf-like 28 | chr4:6984051-6984308 REVERSE LENGTH=85	83	85	3.00E-12	102.4	51.8	59.0
Rsa1.0_00087.1.g4372.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4373.t1	gb|ABV89663.1| indoleacetic acid-induced protein 16 [Brassica rapa]	236	231	1.00E-122	97.9	91.9	94.5	indoleacetic acid-induced protein 16	gbpln	Brassica rapa	AT3G04730.1 | Symbols: IAA16 | indoleacetic acid-induced protein 16 | chr3:1288993-1290415 REVERSE LENGTH=236	236	236	1.00E-119	100.0	92.4	95.3
Rsa1.0_00087.1.g4374.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4375.t1	ref|XP_002882370.1| hypothetical protein ARALYDRAFT_477736 [Arabidopsis lyrata subsp. lyrata] gi|297328210|gb|EFH58629.1| hypothetical protein ARALYDRAFT_477736 [Arabidopsis lyrata subsp. lyrata]	146	191	2.00E-56	130.8	87.0	93.2	hypothetical protein ARALYDRAFT_477736	gbpln	Arabidopsis lyrata	AT3G04700.1 | Symbols: | Protein of unknown function (DUF1685) | chr3:1276948-1277607 FORWARD LENGTH=191	146	191	2.00E-58	130.8	85.6	92.5
Rsa1.0_00087.1.g4376.t1	dbj|BAJ34400.1| unnamed protein product [Thellungiella halophila]	317	330	1.00E-149	104.1	87.4	91.2	unnamed protein product	----	----	AT3G04670.1 | Symbols: WRKY39, ATWRKY39 | WRKY DNA-binding protein 39 | chr3:1266530-1267691 REVERSE LENGTH=330	317	330	1.00E-145	104.1	85.2	89.3
Rsa1.0_00087.1.g4377.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4378.t1	dbj|BAH19881.1| AT3G04630 [Arabidopsis thaliana]	278	286	1.00E-107	102.9	79.9	87.4	AT3G04630	gbpln	Arabidopsis thaliana	AT3G04630.3 | Symbols: WDL1 | WVD2-like 1 | chr3:1259231-1260652 FORWARD LENGTH=286	278	286	1.00E-109	102.9	80.2	87.8
Rsa1.0_00087.1.g4379.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	693	1142	0	164.8	51.9	65.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	693	575	4.00E-77	83.0	25.4	38.4
Rsa1.0_00087.1.g4380.t2	emb|CAA22150.1| hypothetical protein [Arabidopsis thaliana] gi|7269091|emb|CAB79200.1| hypothetical protein [Arabidopsis thaliana]	108	457	5.00E-13	423.1	33.3	38.0	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4381.t1	ref|XP_002884451.1| hypothetical protein ARALYDRAFT_896493 [Arabidopsis lyrata subsp. lyrata] gi|297330291|gb|EFH60710.1| hypothetical protein ARALYDRAFT_896493 [Arabidopsis lyrata subsp. lyrata]	413	415	0	100.5	87.4	92.5	hypothetical protein ARALYDRAFT_896493	gbpln	Arabidopsis lyrata	AT3G04560.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 16 growth stages; Has 227 Blast hits to 225 proteins in 83 species: Archae - 0; Bacteria - 17; Metazoa - 98; Fungi - 29; Plants - 51; Viruses - 1; Other Eukaryotes - 31 (source: NCBI BLink). | chr3:1227506-1229338 REVERSE LENGTH=417	413	417	0	101.0	87.7	92.7

<table>
<tr><td>Rsa1.0_00087.1.g4382.t1</td><td>gb|EOA31191.1| hypothetical protein CARUB_v10014357mg [Capsella rubella]</td><td>313</td><td>278</td><td>1.00E-132</td><td>88.8</td><td>73.8</td><td>79.9</td><td>hypothetical protein CARUB_v10014357mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04530.1 | Symbols: PPCK2, PEPCK2, ATPPCK2 | phosphoenolpyruvate carboxylase kinase 2 | chr3:1221546-1222456 FORWARD LENGTH=278</td><td>313</td><td>278</td><td>1.00E-133</td><td>88.8</td><td>73.2</td><td>79.9</td></tr>
<tr><td>Rsa1.0_00087.1.g4383.t1</td><td>ref|NP_566228.1| threonine aldolase 2 [Arabidopsis thaliana] gi|11762214|gb|AAG40385.1|AF325033_1 AT3g04520 [Arabidopsis thaliana] gi|20268680|gb|AAM14044.1| putative L-allo-threonine aldolase [Arabidopsis thaliana] gi|21553589|gb|AAM62682.1| L-allo-threonine aldolase, putative [Arabidopsis thaliana] gi|21689845|gb|AAM67566.1| putative L-allo-threonine aldolase [Arabidopsis thaliana] gi|51968832|dbj|BAD43108.1| L-allo-threonine aldolase like protein [Arabidopsis thaliana] gi|332640570|gb|AEE74091.1| threonine aldolase 2 [Arabidopsis thaliana]</td><td>391</td><td>355</td><td>0</td><td>90.8</td><td>83.6</td><td>88.0</td><td>threonine aldolase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G04520.1 | Symbols: THA2 | threonine aldolase 2 | chr3:1217397-1219571 REVERSE LENGTH=355</td><td>391</td><td>355</td><td>0</td><td>90.8</td><td>83.6</td><td>88.0</td></tr>
<tr><td>Rsa1.0_00087.1.g4384.t1</td><td>gb|EOA31480.1| hypothetical protein CARUB_v10014673mg [Capsella rubella]</td><td>191</td><td>200</td><td>6.00E-77</td><td>104.7</td><td>87.4</td><td>90.6</td><td>hypothetical protein CARUB_v10014673mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04510.1 | Symbols: LSH2 | Protein of unknown function (DUF640) | chr3:1215812-1216417 REVERSE LENGTH=201</td><td>191</td><td>201</td><td>2.00E-75</td><td>105.2</td><td>87.4</td><td>89.5</td></tr>
<tr><td>Rsa1.0_00087.1.g4385.t1</td><td>ref|XP_002882350.1| transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297328190|gb|EFH58609.1| transcription factor [Arabidopsis lyrata subsp. lyrata]</td><td>412</td><td>440</td><td>2.33E-156</td><td>106.8</td><td>73.3</td><td>81.1</td><td>transcription factor</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04450.1 | Symbols: | Homeodomain-like superfamily protein | chr3:1184302-1186264 FORWARD LENGTH=442</td><td>412</td><td>442</td><td>1.00E-147</td><td>107.3</td><td>73.8</td><td>81.6</td></tr>
<tr><td>Rsa1.0_00087.1.g4386.t1</td><td>ref|NP_187088.2| histone-lysine N-methyltransferase SUVR4 [Arabidopsis thaliana] gi|94730582|sp|Q8W595.2|SUVR4_ARATH RecName: Full=Histone-lysine N-methyltransferase SUVR4; AltName: Full=Protein SET DOMAIN GROUP 31; AltName: Full=Suppressor of variegation 3-9-related protein 4; Short=Su(var)3-9-related protein 4 gi|332640552|gb|AEE74073.1| histone-lysine N-methyltransferase SUVR4 [Arabidopsis thaliana]</td><td>949</td><td>492</td><td>0</td><td>51.8</td><td>38.9</td><td>44.2</td><td>histone-lysine N-methyltransferase SUVR4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G04380.1 | Symbols: SUVR4, SDG31 | SET-domain containing protein lysine methyltransferase family protein | chr3:1161602-1164539 FORWARD LENGTH=492</td><td>949</td><td>492</td><td>0</td><td>51.8</td><td>38.9</td><td>44.2</td></tr>
<tr><td>Rsa1.0_00087.1.g4387.t1</td><td>gb|EOA35181.1| hypothetical protein CARUB_v10020326mg [Capsella rubella]</td><td>399</td><td>430</td><td>1.00E-155</td><td>107.8</td><td>72.7</td><td>84.5</td><td>hypothetical protein CARUB_v10020326mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G77840.1 | Symbols: | Translation initiation factor IF2/IF5 | chr1:29269087-29270400 FORWARD LENGTH=437</td><td>399</td><td>437</td><td>1.00E-154</td><td>109.5</td><td>72.4</td><td>83.7</td></tr>
<tr><td>Rsa1.0_00087.1.g4388.t1</td><td>ref|NP_566225.4| Calcium-dependent lipid-binding (CaLB domain) family protein [Arabidopsis thaliana] gi|332640549|gb|AEE74070.1| Calcium-dependent lipid-binding (CaLB domain) family protein [Arabidopsis thaliana]</td><td>361</td><td>391</td><td>1.00E-139</td><td>108.3</td><td>88.9</td><td>93.1</td><td>Calcium-dependent lipid-binding (CaLB domain) family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G04360.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:1157025-1158200 REVERSE LENGTH=391</td><td>361</td><td>391</td><td>1.00E-142</td><td>108.3</td><td>88.9</td><td>93.1</td></tr>
<tr><td>Rsa1.0_00087.1.g4389.t1</td><td>ref|NP_974091.1| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana] gi|332196212|gb|AEE34333.1| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana]</td><td>1106</td><td>1147</td><td>0</td><td>103.7</td><td>61.4</td><td>76.0</td><td>Ubiquitin carboxyl-terminal hydrolase-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G65120.2 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr1:24191457-24195907 REVERSE LENGTH=1147</td><td>1106</td><td>1147</td><td>0</td><td>103.7</td><td>61.4</td><td>76.0</td></tr>
<tr><td>Rsa1.0_00087.1.g4390.t1</td><td>ref|NP_974091.1| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana] gi|332196212|gb|AEE34333.1| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana]</td><td>1121</td><td>1147</td><td>0</td><td>102.3</td><td>60.2</td><td>74.8</td><td>Ubiquitin carboxyl-terminal hydrolase-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G65120.2 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr1:24191457-24195907 REVERSE LENGTH=1147</td><td>1121</td><td>1147</td><td>0</td><td>102.3</td><td>60.2</td><td>74.8</td></tr>
<tr><td>Rsa1.0_00087.1.g4391.t6</td><td>gb|EOA33079.1| hypothetical protein CARUB_v10016416mg [Capsella rubella]</td><td>1259</td><td>1317</td><td>0</td><td>104.6</td><td>84.6</td><td>91.3</td><td>hypothetical protein CARUB_v10016416mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04340.1 | Symbols: emb2458 | FtsH extracellular protease family | chr3:1146943-1153341 REVERSE LENGTH=1320</td><td>1259</td><td>1320</td><td>0</td><td>104.8</td><td>85.1</td><td>91.1</td></tr>
<tr><td>Rsa1.0_00087.1.g4392.t1</td><td>ref|NP_187080.1| cupin domain-containing protein [Arabidopsis thaliana] gi|6721156|gb|AAF26784.1|AC016829_8 hypothetical protein [Arabidopsis thaliana] gi|37202048|gb|AAQ89639.1| At3g04300 [Arabidopsis thaliana] gi|51968382|dbj|BAD42883.1| unknown protein [Arabidopsis thaliana] gi|332640543|gb|AEE74064.1| cupin domain-containing protein [Arabidopsis thaliana]</td><td>95</td><td>96</td><td>1.00E-43</td><td>101.1</td><td>91.6</td><td>97.9</td><td>cupin domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G04300.1 | Symbols: | RmlC-like cupins superfamily protein | chr3:1140318-1140723 FORWARD LENGTH=96</td><td>95</td><td>96</td><td>2.00E-46</td><td>101.1</td><td>91.6</td><td>97.9</td></tr>
</table>

Rsa1.0_00087.1.g4393.t1	ref|XP_002884438.1| Li-tolerant lipase 1 [Arabidopsis lyrata subsp. lyrata] gi|297330278|gb|EFH60697.1| Li-tolerant lipase 1 [Arabidopsis lyrata subsp. lyrata]	366	366	0	100.0	95.9	98.1	Li-tolerant lipase 1	gbpln	Arabidopsis lyrata	AT3G04290.1 | Symbols: ATLTL1, LTL1 | Li-tolerant lipase 1 | chr3:1133620-1136223 REVERSE LENGTH=366	366	366	0	100.0	95.1	97.5
Rsa1.0_00087.1.g4394.t1	gb|AAC62225.1| response regulator protein [Brassica napus]	136	136	4.00E-67	100.0	94.9	96.3	response regulator protein	gbpln	Brassica napus	AT3G04280.3 | Symbols: ARR22, RR22 | response regulator 22 | chr3:1130138-1130689 REVERSE LENGTH=142	136	142	2.00E-57	104.4	81.6	87.5
Rsa1.0_00087.1.g4395.t1	gb|EOA32751.1| hypothetical protein CARUB_v10016056mg [Capsella rubella]	124	130	1.00E-21	104.8	42.7	58.9	hypothetical protein CARUB_v10016056mg	gbpln	Capsella rubella	AT3G04280.3 | Symbols: ARR22, RR22 | response regulator 22 | chr3:1130138-1130689 REVERSE LENGTH=142	124	142	3.00E-19	114.5	48.4	59.7
Rsa1.0_00087.1.g4396.t1	gb|EOA17608.1| hypothetical protein CARUB_v10005968mg [Capsella rubella] gi|482557559|gb|EOA21751.1| hypothetical protein CARUB_v10002207mg [Capsella rubella]	146	146	2.00E-74	100.0	93.2	95.9	hypothetical protein CARUB_v10005968mg	gbpln	Capsella rubella	AT5G18380.1 | Symbols: | Ribosomal protein S5 domain 2-like superfamily protein | chr5:6090253-6090693 REVERSE LENGTH=146	146	146	2.00E-76	100.0	92.5	95.9
Rsa1.0_00087.1.g4397.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4398.t1	ref|XP_002863119.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308943|gb|EFH39378.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1197	1121	0	93.7	45.5	61.2	predicted protein	gbpln	Arabidopsis lyrata	AT2G14080.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr2:5925225-5929600 FORWARD LENGTH=1215	1197	1215	0	101.5	45.2	60.9
Rsa1.0_00087.1.g4399.t1	ref|XP_002863119.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308943|gb|EFH39378.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1173	1121	0	95.6	45.7	61.1	predicted protein	gbpln	Arabidopsis lyrata	AT2G14080.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr2:5925225-5929600 FORWARD LENGTH=1215	1173	1215	0	103.6	44.8	60.9
Rsa1.0_00087.1.g4400.t1	ref|XP_002884430.1| hypothetical protein ARALYDRAFT_477678 [Arabidopsis lyrata subsp. lyrata] gi|297330270|gb|EFH60689.1| hypothetical protein ARALYDRAFT_477678 [Arabidopsis lyrata subsp. lyrata]	193	704	2.00E-48	364.8	58.5	65.3	hypothetical protein ARALYDRAFT_477678	gbpln	Arabidopsis lyrata	AT3G04160.1 | Symbols: | unknown protein; Has 1711 Blast hits to 1353 proteins in 195 species: Archae - 0; Bacteria - 64; Metazoa - 693; Fungi - 201; Plants - 207; Viruses - 0; Other Eukaryotes - 546 (source: NCBI BLink). | chr3:1091647-1094296 REVERSE LENGTH=712	193	712	4.00E-50	368.9	57.0	63.7
Rsa1.0_00087.1.g4401.t1	ref|NP_179024.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|330251184|gb|AEC06278.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1153	1215	0	105.4	45.4	61.2	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT2G14080.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr2:5925225-5929600 FORWARD LENGTH=1215	1153	1215	0	105.4	45.4	61.2
Rsa1.0_00087.1.g4402.t1	gb|EOA29984.1| hypothetical protein CARUB_v10013089mg [Capsella rubella]	119	703	5.00E-42	590.8	71.4	79.0	hypothetical protein CARUB_v10013089mg	gbpln	Capsella rubella	AT3G04160.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 7 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage. | chr3:1091647-1094296 REVERSE LENGTH=714	119	714	3.00E-40	600.0	68.1	70.6
Rsa1.0_00087.1.g4403.t1	ref|NP_187064.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|6721171|gb|AAF26799.1|AC016829_23 unknown protein [Arabidopsis thaliana] gi|17065146|gb|AAL32727.1| Unknown protein [Arabidopsis thaliana] gi|20259844|gb|AAM13269.1| unknown protein [Arabidopsis thaliana] gi|332640521|gb|AEE74042.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	640	656	0	102.5	82.3	88.4	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G04140.1 | Symbols: | Ankyrin repeat family protein | chr3:1087063-1089106 FORWARD LENGTH=656	640	656	0	102.5	82.3	88.4
Rsa1.0_00087.1.g4404.t1	ref|NP_566222.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|79312733|ref|NP_001030630.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546763|sp|Q9M8W9.2|PP211_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g04130, mitochondrial; Flags: Precursor gi|332640519|gb|AEE74040.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332640520|gb|AEE74041.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	508	508	0	100.0	82.9	90.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G04130.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:1084136-1085662 FORWARD LENGTH=508	508	508	0	100.0	82.9	90.6
Rsa1.0_00087.1.g4405.t1	dbj|BAJ33926.1| unnamed protein product [Thellungiella halophila]	356	338	0	94.9	92.7	93.8	unnamed protein product	----	----	AT3G04120.1 | Symbols: GAPC, GAPC-1, GAPC1 | glyceraldehyde-3-phosphate dehydrogenase C subunit 1 | chr3:1081077-1083131 FORWARD LENGTH=338	356	338	0	94.9	91.6	93.5

Rsa1.0_00087.1.g4406.t1	ref|XP_002882329.1| MADS-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297328169|gb|EFH58588.1| MADS-box family protein [Arabidopsis lyrata subsp. lyrata]	171	205	4.00E-42	119.9	51.5	69.6	MADS-box family protein	gbpln	Arabidopsis lyrata	AT3G04100.1 | Symbols: AGL57 | AGAMOUS-like 57 | chr3:1075299-1075922 FORWARD LENGTH=207	171	207	1.00E-43	121.1	51.5	67.8
Rsa1.0_00087.1.g4407.t1	ref|XP_002884428.1| SIP1_1 [Arabidopsis lyrata subsp. lyrata] gi|297330268|gb|EFH60687.1| SIP1_1 [Arabidopsis lyrata subsp. lyrata]	239	240	1.00E-113	100.4	90.8	94.1	SIP1_1	gbpln	Arabidopsis lyrata	AT3G04090.1 | Symbols: SIP1;1, SIP1A | small and basic intrinsic protein 1A | chr3:1072340-1074031 REVERSE LENGTH=240	239	240	1.00E-106	100.4	84.1	88.3
Rsa1.0_00087.1.g4408.t1	gb|EOA30494.1| hypothetical protein CARUB_v10013618mg [Capsella rubella]	428	471	0	110.0	90.4	94.9	hypothetical protein CARUB_v10013618mg	gbpln	Capsella rubella	AT3G04080.1 | Symbols: ATAPY1, APY1 | apyrase 1 | chr3:1068068-1070917 REVERSE LENGTH=471	428	471	0	110.0	90.7	95.3
Rsa1.0_00087.1.g4409.t1	ref|NP_568371.1| uncharacterized protein [Arabidopsis thaliana] gi|91806882|gb|ABE66168.1| hypothetical protein At5g19270 [Arabidopsis thaliana] gi|332005295|gb|AED92678.1| uncharacterized protein AT5G19270 [Arabidopsis thaliana]	175	365	4.00E-27	208.6	36.6	49.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365	175	365	2.00E-29	208.6	36.6	49.7
Rsa1.0_00087.1.g4410.t1	ref|NP_187057.2| NAC domain containing protein 47 [Arabidopsis thaliana] gi|29029082|gb|AAO64920.1| At3g04070 [Arabidopsis thaliana] gi|110743057|dbj|BAE99421.1| NAM-like protein [Arabidopsis thaliana] gi|332640512|gb|AEE74033.1| NAC domain containing protein 47 [Arabidopsis thaliana]	357	359	1.00E-164	100.6	80.7	87.1	NAC domain containing protein 47	gbpln	Arabidopsis thaliana	AT3G04070.1 | Symbols: anac047, NAC047 | NAC domain containing protein 47 | chr3:1061573-1062976 REVERSE LENGTH=359	357	359	1.00E-167	100.6	80.7	87.1
Rsa1.0_00087.1.g4411.t1	ref|NP_187056.1| NAC domain containing protein 46 [Arabidopsis thaliana] gi|6223650|gb|AAF05864.1|AC011698_15 NAM-like protein (no apical meristem) [Arabidopsis thaliana] gi|13605595|gb|AAK32791.1|AF361623_1 AT3g04060/T11I18_17 [Arabidopsis thaliana] gi|19548079|gb|AAL87404.1| AT3g04060/T11I18_17 [Arabidopsis thaliana] gi|21537076|gb|AAM61417.1| NAM-like protein (no apical meristem) [Arabidopsis thaliana] gi|332640511|gb|AEE74032.1| NAC domain containing protein 46 [Arabidopsis thaliana]	326	338	1.00E-147	103.7	78.8	86.8	NAC domain containing protein 46	gbpln	Arabidopsis thaliana	AT3G04060.1 | Symbols: anac046, NAC046 | NAC domain containing protein 46 | chr3:1053625-1054952 REVERSE LENGTH=338	326	338	1.00E-150	103.7	78.8	86.8
Rsa1.0_00087.1.g4412.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00087.1.g4413.t1	ref|NP_187038.2| uncharacterized protein [Arabidopsis thaliana] gi|27754515|gb|AAO22705.1| unknown protein [Arabidopsis thaliana] gi|28393971|gb|AAO42393.1| unknown protein [Arabidopsis thaliana] gi|332640486|gb|AEE74007.1| uncharacterized protein AT3G03880 [Arabidopsis thaliana]	192	193	2.00E-73	100.5	76.0	85.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G03880.1 | Symbols: | Protein of unknown function (DUF1639) | chr3:998123-999029 FORWARD LENGTH=193	192	193	7.00E-76	100.5	76.0	85.9
Rsa1.0_00087.1.g4414.t1	gb|EOA31260.1| hypothetical protein CARUB_v10014432mg [Capsella rubella]	256	260	3.00E-86	101.6	70.3	78.9	hypothetical protein CARUB_v10014432mg	gbpln	Capsella rubella	AT3G03870.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18130.1); Has 47 Blast hits to 47 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:995520-997180 FORWARD LENGTH=266	256	266	3.00E-88	103.9	73.8	80.9
Rsa1.0_00087.1.g4415.t1	ref|NP_566214.1| protein alfin-like 5 [Arabidopsis thaliana] gi|75163676|sp|Q93YX4.1|APRL5_ARATH RecName: Full=5'-adenylylsulfate reductase-like 5; AltName: Full=Adenosine 5'-phosphosulfate reductase-like 5; Short=APR-like 5; Short=AtAPRL5; Flags: Precursor gi|16604553|gb|AAL24078.1| unknown protein [Arabidopsis thaliana] gi|20259149|gb|AAM14290.1| unknown protein [Arabidopsis thaliana] gi|332640483|gb|AEE74004.1| protein alfin-like 5 [Arabidopsis thaliana]	310	300	1.00E-133	96.8	79.4	87.1	protein alfin-like 5	gbpln	Arabidopsis thaliana	AT3G03860.1 | Symbols: ATAPRL5, APRL5 | APR-like 5 | chr3:992465-994315 FORWARD LENGTH=300	310	300	1.00E-136	96.8	79.4	87.1
Rsa1.0_00087.1.g4416.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00087.1.g4417.t2	ref|NP_187030.1| syntaxin 1B/2/3 [Arabidopsis thaliana] gi|28380139|sp|Q9SRV7.1|SY131_ARATH RecName: Full=Putative syntaxin-131; Short=AtSYP131 gi|6006872|gb|AAF00648.1|AC009540_25s-syntaxin-like protein [Arabidopsis thaliana] gi|332640474|gb|AEE73995.1| putative syntaxin-131 [Arabidopsis thaliana]	278	306	1.00E-138	110.1	93.9	97.1	syntaxin 1B/2/3	gbpln	Arabidopsis thaliana	AT3G03800.1 | Symbols: SYP131, ATSYP131 | syntaxin of plants 131 | chr3:969314-971460 FORWARD LENGTH=306	278	306	1.00E-140	110.1	93.9	97.1
Rsa1.0_00087.1.g4418.t2	gb|EOA29778.1| hypothetical protein CARUB_v10012869mg [Capsella rubella]	1083	1084	0	100.1	84.7	90.8	hypothetical protein CARUB_v10012869mg	gbpln	Capsella rubella	AT3G03790.2 | Symbols: | ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein | chr3:963195-967857 FORWARD LENGTH=1081	1083	1081	0	99.8	84.8	90.5
Rsa1.0_00087.1.g4419.t1	dbj|BAJ33898.1| unnamed protein product [Thellungiella halophila]	710	765	0	107.7	95.5	97.5	unnamed protein product	----	----	AT3G03780.3 | Symbols: ATMS2, MS2 | methionine synthase 2 | chr3:957602-960740 FORWARD LENGTH=765	710	765	0	107.7	94.2	96.6
Rsa1.0_00088.1.g4420.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00088.1.g4421.t1	ref|NP_196927.4| uncharacterized protein [Arabidopsis thaliana] gi|332004620|gb|AED92003.1| uncharacterized protein AT5G14230 [Arabidopsis thaliana]	779	751	0	96.4	83.6	89.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G14230.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ankyrin repeat-containing domain (InterPro:IPR020683), Ankyrin repeat (InterPro:IPR002110); BEST Arabidopsis thaliana protein match is: XB3 ortholog 2 in Arabidopsis thaliana (TAIR:AT5G57740.1); Has 66374 Blast hits to 25358 proteins in 1201 species: Archae - 121; Bacteria - 8133; Metazoa - 29530; Fungi - 5885; Plants - 3349; Viruses - 785; Other Eukaryotes - 18571 (source: NCBI BLink). | chr5:4591883-4595775 FORWARD LENGTH=751	779	751	0	96.4	83.6	89.7
Rsa1.0_00088.1.g4422.t1	ref|XP_002873657.1| hypothetical protein ARALYDRAFT_488258 [Arabidopsis lyrata subsp. lyrata] gi|297319494|gb|EFH49916.1| hypothetical protein ARALYDRAFT_488258 [Arabidopsis lyrata subsp. lyrata]	256	256	1.00E-126	100.0	91.8	95.7	hypothetical protein ARALYDRAFT_488258	gbpln	Arabidopsis lyrata	AT5G14240.1 | Symbols: | Thioredoxin superfamily protein | chr5:4596223-4597568 REVERSE LENGTH=256	256	256	1.00E-128	100.0	91.0	94.9
Rsa1.0_00088.1.g4423.t1	ref|XP_002871610.1| SET domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317447|gb|EFH47869.1| SET domain-containing protein [Arabidopsis lyrata subsp. lyrata]	985	516	0	52.4	46.3	48.9	SET domain-containing protein	gbpln	Arabidopsis lyrata	AT5G14260.2 | Symbols: | Rubisco methyltransferase family protein | chr5:4601139-4603873 FORWARD LENGTH=514	985	514	0	52.2	46.1	48.5
Rsa1.0_00088.1.g4424.t1	ref|NP_001147134.1| transcription regulator [Zea mays] gi|195607552|gb|ACG25606.1| transcription regulator [Zea mays]	256	255	1.00E-129	99.6	94.9	98.0	transcription regulator	gbenv/gbpln	Zea mays	AT5G14280.1 | Symbols: | DNA-binding storekeeper protein-related | chr5:4609123-4611444 FORWARD LENGTH=572	256	572	1.00E-128	223.4	85.5	91.0
Rsa1.0_00088.1.g4425.t1	gb|EOA20643.1| hypothetical protein CARUB_v10000956mg [Capsella rubella]	444	446	0	100.5	88.1	91.4	hypothetical protein CARUB_v10000956mg	gbpln	Capsella rubella	AT5G14310.1 | Symbols: AtCXE16, CXE16 | carboxyesterase 16 | chr5:4615592-4617422 FORWARD LENGTH=446	444	446	0	100.5	87.2	91.2
Rsa1.0_00088.1.g4426.t1	gb|EOA21688.1| hypothetical protein CARUB_v10002113mg [Capsella rubella]	132	169	6.00E-69	128.0	97.7	98.5	hypothetical protein CARUB_v10002113mg	gbpln	Capsella rubella	AT5G14320.1 | Symbols: | Ribosomal protein S13/S18 family | chr5:4617839-4618772 REVERSE LENGTH=169	132	169	3.00E-71	128.0	97.0	98.5
Rsa1.0_00088.1.g4427.t1	ref|NP_196937.1| uncharacterized protein [Arabidopsis thaliana] gi|7573458|emb|CAB87772.1| putative protein [Arabidopsis thaliana] gi|332004635|gb|AED92018.1| uncharacterized protein AT5G14330 [Arabidopsis thaliana]	74	128	4.00E-16	173.0	70.3	81.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G14330.1 | Symbols: | unknown protein; Has 8 Blast hits to 8 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:4619947-4620551 REVERSE LENGTH=128	74	128	7.00E-19	173.0	70.3	81.1
Rsa1.0_00088.1.g4428.t1	ref|NP_196938.1| myb domain protein 40 [Arabidopsis thaliana] gi|7573459|emb|CAB87773.1| MYB40-putative transcription factor [Arabidopsis thaliana] gi|41619392|gb|AAS10092.1| MYB transcription factor [Arabidopsis thaliana] gi|332004636|gb|AED92019.1| myb domain protein 40 [Arabidopsis thaliana]	267	263	1.00E-111	98.5	78.7	84.3	myb domain protein 40	gbpln	Arabidopsis thaliana	AT5G14340.1 | Symbols: AtMYB40, MYB40 | myb domain protein 40 | chr5:4623367-4624779 FORWARD LENGTH=263	267	263	1.00E-114	98.5	78.7	84.3
Rsa1.0_00088.1.g4429.t1	ref|NP_001078582.1| early nodulin-like protein 21 [Arabidopsis thaliana] gi|332004637|gb|AED92020.1| early nodulin-like protein 21 [Arabidopsis thaliana]	145	145	4.00E-60	100.0	75.9	84.1	early nodulin-like protein 21	gbpln	Arabidopsis thaliana	AT5G14345.1 | Symbols: ENODL21, AtENODL21 | early nodulin-like protein 21 | chr5:4626175-4626722 REVERSE LENGTH=145	145	145	1.00E-62	100.0	75.9	84.1
Rsa1.0_00088.1.g4430.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00088.1.g4431.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00088.1.g4432.t1	ref|NP_568300.1| CCT motif family protein [Arabidopsis thaliana] gi|15292917|gb|AAK92829.1| unknown protein [Arabidopsis thaliana] gi|20259039|gb|AAM14235.1| unknown protein [Arabidopsis thaliana] gi|332004640|gb|AED92023.1| CCT motif family protein [Arabidopsis thaliana]	554	339	1.00E-116	61.2	45.8	50.7	CCT motif family protein	gbpln	Arabidopsis thaliana	AT5G14370.1 | Symbols: | CCT motif family protein | chr5:4632147-4633651 REVERSE LENGTH=339	554	339	1.00E-118	61.2	45.8	50.7
Rsa1.0_00088.1.g4433.t1	emb|CAB42531.1| AGP6 protein [Arabidopsis thaliana]	153	150	3.00E-37	98.0	71.2	79.1	AGP6 protein	gbpln	Arabidopsis thaliana	AT5G14380.1 | Symbols: AGP6 | arabinogalactan protein 6 | chr5:4636088-4636540 REVERSE LENGTH=150	153	150	1.00E-39	98.0	70.6	78.4
Rsa1.0_00088.1.g4434.t1	ref|NP_196943.1| alpha/beta-hydrolasefamily protein [Arabidopsis thaliana] gi|7573464|emb|CAB87778.1| putative protein [Arabidopsis thaliana] gi|17529314|gb|AAL38884.1| unknown protein [Arabidopsis thaliana] gi|21436177|gb|AAM51376.1| unknown protein [Arabidopsis thaliana] gi|332004642|gb|AED92025.1| alpha/beta-hydrolasefamily protein [Arabidopsis thaliana]	373	369	0	98.9	91.2	95.4	alpha/beta-hydrolasefamily protein	gbpln	Arabidopsis thaliana	AT5G14390.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:4637551-4639575 REVERSE LENGTH=369	373	369	0	98.9	91.2	95.4
Rsa1.0_00088.1.g4435.t2	ref|XP_002871617.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317454|gb|EFH47876.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	529	381	0	72.0	64.1	68.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G14400.1 | Symbols: CYP724A1 | cytochrome P450, family 724, subfamily A, polypeptide 1 | chr5:4644128-4646382 FORWARD LENGTH=367	529	367	0	69.4	61.2	65.4
Rsa1.0_00088.1.g4436.t1	gb|EOA19501.1| hypothetical protein CARUB_v10002248mg [Capsella rubella]	134	132	2.00E-45	98.5	79.9	90.3	hypothetical protein CARUB_v10002248mg	gbpln	Capsella rubella	AT5G14410.1 | Symbols: | unknown protein; Has 23 Blast hits to 23 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:4646897-4647398 REVERSE LENGTH=133	134	133	3.00E-47	99.3	79.9	88.8
Rsa1.0_00088.1.g4437.t1	gb|EOA20582.1| hypothetical protein CARUB_v10000894mg [Capsella rubella]	465	466	0	100.2	87.7	92.9	hypothetical protein CARUB_v10000894mg	gbpln	Capsella rubella	AT5G14420.2 | Symbols: RGLG2 | RING domain ligase2 | chr5:4648355-4650563 REVERSE LENGTH=468	465	468	0	100.6	86.9	91.6
Rsa1.0_00088.1.g4438.t1	ref|XP_002871620.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317457|gb|EFH47879.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	391	386	0	98.7	91.6	94.6	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT5G14450.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:4658488-4660034 FORWARD LENGTH=389	391	389	0	99.5	91.3	94.4
Rsa1.0_00088.1.g4439.t1	gb|EOA22627.1| hypothetical protein CARUB_v10003297mg [Capsella rubella]	521	538	0	103.3	83.7	89.3	hypothetical protein CARUB_v10003297mg	gbpln	Capsella rubella	AT5G14460.1 | Symbols: | Pseudouridine synthase family protein | chr5:4660239-4662543 REVERSE LENGTH=540	521	540	0	103.6	82.7	88.1
Rsa1.0_00088.1.g4440.t1	ref|XP_002873669.1| hypothetical protein ARALYDRAFT_325917 [Arabidopsis lyrata subsp. lyrata] gi|297319506|gb|EFH49928.1| hypothetical protein ARALYDRAFT_325917 [Arabidopsis lyrata subsp. lyrata]	367	366	0	99.7	93.2	97.0	hypothetical protein ARALYDRAFT_325917	gbpln	Arabidopsis lyrata	AT5G14470.1 | Symbols: | GHMP kinase family protein | chr5:4663029-4664657 REVERSE LENGTH=366	367	366	0	99.7	90.7	95.9
Rsa1.0_00088.1.g4441.t1	gb|EOA20817.1| hypothetical protein CARUB_v10001154mg [Capsella rubella]	389	387	0	99.5	86.4	93.6	hypothetical protein CARUB_v10001154mg	gbpln	Capsella rubella	AT5G14480.1 | Symbols: | beta-1,4-N-acetylglucosaminyltransferase family protein | chr5:4667984-4669693 FORWARD LENGTH=387	389	387	0	99.5	85.3	92.3
Rsa1.0_00088.1.g4442.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00088.1.g4443.t5	ref|XP_002873676.1| hypothetical protein ARALYDRAFT_909422 [Arabidopsis lyrata subsp. lyrata] gi|297319513|gb|EFH49935.1| hypothetical protein ARALYDRAFT_909422 [Arabidopsis lyrata subsp. lyrata]	372	369	0	99.2	87.6	93.5	hypothetical protein ARALYDRAFT_909422	gbpln	Arabidopsis lyrata	AT5G14550.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:4691321-4693732 REVERSE LENGTH=377	372	377	0	101.3	86.0	93.3
Rsa1.0_00088.1.g4444.t2	ref|XP_002873678.1| hypothetical protein ARALYDRAFT_488299 [Arabidopsis lyrata subsp. lyrata] gi|297319515|gb|EFH49937.1| hypothetical protein ARALYDRAFT_488299 [Arabidopsis lyrata subsp. lyrata]	947	992	0	104.8	85.7	92.5	hypothetical protein ARALYDRAFT_488299	gbpln	Arabidopsis lyrata	AT5G14580.1 | Symbols: | polyribonucleotide nucleotidyltransferase, putative | chr5:4697612-4703013 REVERSE LENGTH=991	947	991	0	104.6	83.3	91.2

Rsa1.0_00088.1.g4445.t1	ref|NP_568302.1| tRNA (adenine-N1-)-methyltransferase [Arabidopsis thaliana] gi|28393527|gb|AAO42184.1| unknown protein [Arabidopsis thaliana] gi|28827644|gb|AAO50666.1| unknown protein [Arabidopsis thaliana] gi|332004669|gb|AED92052.1| tRNA (adenine-N1-)-methyltransferase-like protein [Arabidopsis thaliana]	322	318	1.00E-166	98.8	88.8	94.7	tRNA (adenine-N1-)-methyltransferase	gbpln	Arabidopsis thaliana	AT5G14600.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:4707518-4709022 FORWARD LENGTH=318	322	318	1.00E-169	98.8	88.8	94.7
Rsa1.0_00088.1.g4446.t1	ref|XP_002873681.1| hypothetical protein ARALYDRAFT_488304 [Arabidopsis lyrata subsp. lyrata] gi|297319518|gb|EFH49940.1| hypothetical protein ARALYDRAFT_488304 [Arabidopsis lyrata subsp. lyrata]	605	629	0	104.0	73.4	84.6	hypothetical protein ARALYDRAFT_488304	gbpln	Arabidopsis lyrata	AT5G14620.1 | Symbols: DRM2, DMT7 | domains rearranged methyltransferase 2 | chr5:4715429-4718578 REVERSE LENGTH=626	605	626	0	103.5	71.9	83.0
Rsa1.0_00088.1.g4447.t1	ref|NP_196969.1| polygalacturonase [Arabidopsis thaliana] gi|7573314|emb|CAB87632.1| polygalacturonase-like protein [Arabidopsis thaliana] gi|332004675|gb|AED92058.1| pectin lyase-like superfamily protein [Arabidopsis thaliana]	439	435	0	99.1	87.5	92.5	polygalacturonase	gbpln	Arabidopsis thaliana	AT5G14650.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:4724509-4726328 FORWARD LENGTH=435	439	435	0	99.1	87.5	92.5
Rsa1.0_00088.1.g4448.t1	ref|XP_002873683.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319520|gb|EFH49942.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	299	273	1.00E-127	91.3	75.6	79.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G14660.2 | Symbols: PDF1B, DEF2, ATDEF2 | peptide deformylase 1B | chr5:4727129-4728671 REVERSE LENGTH=273	299	273	1.00E-130	91.3	75.3	79.6
Rsa1.0_00088.1.g4449.t1	emb|CBI39638.3| unnamed protein product [Vitis vinifera]	191	591	1.00E-100	309.4	94.2	94.8	unnamed protein product	gbpln	Vitis vinifera	AT5G14670.1 | Symbols: ATARFA1B, ARFA1B | ADP-ribosylation factor A1B | chr5:4729319-4730495 FORWARD LENGTH=188	191	188	1.00E-101	98.4	93.7	93.7
Rsa1.0_00088.1.g4450.t1	gb|EOA21670.1| hypothetical protein CARUB_v10002093mg [Capsella rubella]	394	175	3.00E-59	44.4	27.7	28.9	hypothetical protein CARUB_v10002093mg	gbpln	Capsella rubella	AT5G14680.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr5:4731620-4733025 REVERSE LENGTH=175	394	175	2.00E-61	44.4	27.4	28.7
Rsa1.0_00088.1.g4451.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	443	1555	4.00E-77	351.0	34.5	44.5	disease resistance protein	gbpln	Brassica rapa	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	443	575	7.00E-44	129.8	26.0	38.6
Rsa1.0_00088.1.g4452.t1	ref|XP_002873686.1| hypothetical protein ARALYDRAFT_488312 [Arabidopsis lyrata subsp. lyrata] gi|297319523|gb|EFH49945.1| hypothetical protein ARALYDRAFT_488312 [Arabidopsis lyrata subsp. lyrata]	370	368	0	99.5	90.0	96.2	hypothetical protein ARALYDRAFT_488312	gbpln	Arabidopsis lyrata	AT5G14700.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:4740502-4743327 REVERSE LENGTH=368	370	368	0	99.5	89.5	94.6
Rsa1.0_00088.1.g4453.t1	gb|AAL38867.1| putative protein kinase [Arabidopsis thaliana]	711	674	0	94.8	81.6	85.8	putative protein kinase	gbpln	Arabidopsis thaliana	AT5G14720.1 | Symbols: | Protein kinase superfamily protein | chr5:4748212-4752642 REVERSE LENGTH=674	711	674	0	94.8	81.6	85.8
Rsa1.0_00088.1.g4454.t1	ref|NP_196977.1| uncharacterized protein [Arabidopsis thaliana] gi|9755741|emb|CAC01872.1| putative protein [Arabidopsis thaliana] gi|38454160|gb|AAR20774.1| At5g14730 [Arabidopsis thaliana] gi|45592916|gb|AAS68112.1| At5g14730 [Arabidopsis thaliana] gi|110737749|dbj|BAF00813.1| hypothetical protein [Arabidopsis thaliana] gi|332004684|gb|AED92067.1| uncharacterized protein AT5G14730 [Arabidopsis thaliana]	262	246	2.00E-61	93.9	56.5	68.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G14730.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1645 (InterPro:IPR012442); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01513.1); Has 85 Blast hits to 83 proteins in 14 species: Archae - 0; Bacteria - 9; Metazoa - 0; Fungi - 0; Plants - 76; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:4756282-4757022 FORWARD LENGTH=246	262	246	5.00E-64	93.9	56.5	68.3
Rsa1.0_00089.1.g4455.t1	gb|EOA35144.1| hypothetical protein CARUB_v10020279mg [Capsella rubella]	227	454	5.00E-82	200.0	67.0	72.2	hypothetical protein CARUB_v10020279mg	gbpln	Capsella rubella	AT1G67320.2 | Symbols: | DNA primase, large subunit family | chr1:25205520-25208966 REVERSE LENGTH=454	227	454	3.00E-84	200.0	66.5	72.2
Rsa1.0_00089.1.g4456.t1	gb|AAF99785.1|AC012463_2 T2E6.4 [Arabidopsis thaliana]	480	740	1.00E-166	154.2	59.8	74.0	T2E6.4	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	480	746	1.00E-83	155.4	33.5	42.3
Rsa1.0_00089.1.g4457.t1	gb|EOA35144.1| hypothetical protein CARUB_v10020279mg [Capsella rubella]	82	454	5.00E-22	553.7	68.3	73.2	hypothetical protein CARUB_v10020279mg	gbpln	Capsella rubella	AT1G67320.1 | Symbols: | DNA primase, large subunit family | chr1:25205520-25208966 REVERSE LENGTH=449	82	449	5.00E-24	547.6	67.1	72.0
Rsa1.0_00089.1.g4458.t2	gb|EOA35534.1| hypothetical protein CARUB_v10020741mg [Capsella rubella]	306	288	1.00E-133	94.1	82.7	87.3	hypothetical protein CARUB_v10020741mg	gbpln	Capsella rubella	AT1G67325.2 | Symbols: | Ran BP2/NZF zinc finger-like superfamily protein | chr1:25209825-25212412 REVERSE LENGTH=288	306	288	1.00E-135	94.1	83.0	86.9

Rsa1.0_00089.1.g4459.t1	ref|XP_002887113.1| hypothetical protein ARALYDRAFT_475830 [Arabidopsis lyrata subsp. lyrata] gi|297332954|gb|EFH63372.1| hypothetical protein ARALYDRAFT_475830 [Arabidopsis lyrata subsp. lyrata]	291	291	1.00E-149	100.0	85.6	91.1	hypothetical protein ARALYDRAFT_475830	gbpln	Arabidopsis lyrata	AT1G67330.1 | Symbols: | Protein of unknown function (DUF579) | chr1:25214118-25214993 FORWARD LENGTH=291	291	291	1.00E-148	100.0	83.5	90.4
Rsa1.0_00089.1.g4460.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1785	1270	0	71.1	35.5	48.1	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1785	575	3.00E-95	32.2	10.8	16.9
Rsa1.0_00089.1.g4461.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00089.1.g4462.t1	ref|XP_002887115.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297332956|gb|EFH63374.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	352	375	1.00E-164	106.5	84.9	89.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G67340.1 | Symbols: | HCP-like superfamily protein with MYND-type zinc finger | chr1:25230323-25231622 FORWARD LENGTH=379	352	379	1.00E-162	107.7	83.0	88.1
Rsa1.0_00089.1.g4463.t1	ref|XP_002888592.1| rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297334433|gb|EFH64851.1| rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata]	100	246	2.00E-15	246.0	50.0	59.0	rubber elongation factor family protein	gbpln	Arabidopsis lyrata	AT1G67360.1 | Symbols: | Rubber elongation factor protein (REF) | chr1:25237072-25237913 REVERSE LENGTH=240	100	240	6.00E-18	240.0	49.0	58.0
Rsa1.0_00089.1.g4464.t1	gb|EOA22363.1| hypothetical protein CARUB_v10002992mg [Capsella rubella]	282	401	3.00E-14	142.2	21.6	34.4	hypothetical protein CARUB_v10002992mg	gbpln	Capsella rubella	AT1G31000.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11053377-11054561 REVERSE LENGTH=363	282	363	8.00E-17	128.7	35.5	55.0
Rsa1.0_00089.1.g4465.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00089.1.g4466.t1	dbj|BAJ34244.1| unnamed protein product [Thellungiella halophila]	232	234	5.00E-99	100.9	78.4	85.8	unnamed protein product	----	----	AT1G67360.1 | Symbols: | Rubber elongation factor protein (REF) | chr1:25237072-25237913 REVERSE LENGTH=240	232	240	3.00E-98	103.4	76.3	86.6
Rsa1.0_00089.1.g4467.t2	ref|NP_176908.2| exostosin-like protein [Arabidopsis thaliana] gi|115311405|gb|ABI93883.1| At1g67410 [Arabidopsis thaliana] gi|332196520|gb|AEE34641.1| exostosin-like protein [Arabidopsis thaliana]	426	430	0	100.9	83.3	91.5	exostosin-like protein	gbpln	Arabidopsis thaliana	AT1G67410.1 | Symbols: | Exostosin family protein | chr1:25251606-25253568 REVERSE LENGTH=430	426	430	0	100.9	83.3	91.5
Rsa1.0_00089.1.g4468.t1	ref|XP_002887120.1| peptidase [Arabidopsis lyrata subsp. lyrata] gi|297332961|gb|EFH63379.1| peptidase [Arabidopsis lyrata subsp. lyrata]	873	873	0	100.0	84.4	91.6	peptidase	gbpln	Arabidopsis lyrata	AT1G67420.2 | Symbols: | Zn-dependent exopeptidases superfamily protein | chr1:25255264-25260358 FORWARD LENGTH=922	873	922	0	105.6	83.6	90.7
Rsa1.0_00089.1.g4469.t1	ref|NP_176910.1| 60S ribosomal protein L17-2 [Arabidopsis thaliana] gi|297838479|ref|XP_002887121.1| 60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata] gi|27735241|sp|P51413.2|RL172_ARATH RecName: Full=60S ribosomal protein L17-2 gi|3176668|gb|AAC18792.1| Similar to ribosomal protein L17 gb|X62724 from Hordeum vulgare. ESTs gb|Z34728, gb|F19974, gb|T75677 and gb|Z33937 come from this gene [Arabidopsis thaliana] gi|14596149|gb|AAK68802.1| ribosomal protein L17-like protein [Arabidopsis thaliana] gi|20148391|gb|AAM10086.1| unknown protein [Arabidopsis thaliana] gi|110736681|dbj|BAF00304.1| ribosomal protein L17-like protein [Arabidopsis thaliana] gi|297332962|gb|EFH63380.1| 60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata] gi|332196523|gb|AEE34644.1| 60S ribosomal protein L17-2 [Arabidopsis thaliana]	175	175	7.00E-98	100.0	98.3	99.4	60S ribosomal protein L17-2	gbpln	Arabidopsis lyrata	AT1G67430.1 | Symbols: | Ribosomal protein L22p/L17e family protein | chr1:25262209-25263627 FORWARD LENGTH=175	175	175	1.00E-100	100.0	98.3	99.4
Rsa1.0_00089.1.g4470.t1	ref|XP_002883830.1| hypothetical protein ARALYDRAFT_480339 [Arabidopsis lyrata subsp. lyrata] gi|297329670|gb|EFH60089.1| hypothetical protein ARALYDRAFT_480339 [Arabidopsis lyrata subsp. lyrata]	76	73	1.00E-22	96.1	76.3	82.9	hypothetical protein ARALYDRAFT_480339	gbpln	Arabidopsis lyrata	AT2G14247.1 | Symbols: | Expressed protein | chr2:6034472-6034708 FORWARD LENGTH=78	76	78	8.00E-20	102.6	69.7	81.6
Rsa1.0_00089.1.g4471.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	354	368	4.00E-65	104.0	44.9	59.6	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	354	370	3.00E-66	104.5	46.6	60.7

<table>
<thead><tr><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></tr></thead>
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<tr><td>Rsa1.0_00089.1.g4472.t1</td><td>gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]</td><td>291</td><td>368</td><td>2.00E-62</td><td>126.5</td><td>48.5</td><td>63.2</td><td>hypothetical protein CARUB_v10027748mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370</td><td>291</td><td>370</td><td>1.00E-54</td><td>127.1</td><td>47.1</td><td>61.9</td></tr>
<tr><td>Rsa1.0_00089.1.g4473.t1</td><td>ref|XP_002886270.1| hypothetical protein ARALYDRAFT_900378 [Arabidopsis lyrata subsp. lyrata] gi|297332110|gb|EFH62529.1| hypothetical protein ARALYDRAFT_900378 [Arabidopsis lyrata subsp. lyrata]</td><td>229</td><td>346</td><td>5.00E-20</td><td>151.1</td><td>22.3</td><td>27.1</td><td>hypothetical protein ARALYDRAFT_900378</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370</td><td>229</td><td>370</td><td>8.00E-18</td><td>161.6</td><td>24.9</td><td>33.6</td></tr>
<tr><td>Rsa1.0_00089.1.g4474.t25</td><td>gb|EOA22909.1| hypothetical protein CARUB_v10003642mg [Capsella rubella]</td><td>480</td><td>282</td><td>2.00E-29</td><td>58.8</td><td>21.3</td><td>27.5</td><td>hypothetical protein CARUB_v10003642mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G27070.1 | Symbols: AGL53 | AGAMOUS-like 53 | chr5:9527741-9528604 FORWARD LENGTH=287</td><td>480</td><td>287</td><td>3.00E-27</td><td>59.8</td><td>20.8</td><td>27.3</td></tr>
<tr><td>Rsa1.0_00089.1.g4475.t1</td><td>ref|NP_176917.2| DNA polymerase zeta subunit [Arabidopsis thaliana] gi|34330129|dbj|BAC82450.1| catalytic subunit of polymerase zeta [Arabidopsis thaliana] gi|332196534|gb|AEE34655.1| DNA polymerase zeta subunit [Arabidopsis thaliana]</td><td>1864</td><td>1890</td><td>0</td><td>101.4</td><td>85.2</td><td>91.3</td><td>DNA polymerase zeta subunit</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G67500.1 | Symbols: ATREV3, REV3 | recovery protein 3 | chr1:25287707-25296714 REVERSE LENGTH=1890</td><td>1864</td><td>1890</td><td>0</td><td>101.4</td><td>85.2</td><td>91.3</td></tr>
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<tr><td>Rsa1.0_00089.1.g4477.t1</td><td>ref|XP_002886270.1| hypothetical protein ARALYDRAFT_900378 [Arabidopsis lyrata subsp. lyrata] gi|297332110|gb|EFH62529.1| hypothetical protein ARALYDRAFT_900378 [Arabidopsis lyrata subsp. lyrata]</td><td>231</td><td>346</td><td>2.00E-19</td><td>149.8</td><td>22.5</td><td>26.4</td><td>hypothetical protein ARALYDRAFT_900378</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370</td><td>231</td><td>370</td><td>1.00E-19</td><td>160.2</td><td>25.5</td><td>34.2</td></tr>
<tr><td>Rsa1.0_00089.1.g4478.t1</td><td>ref|XP_002886268.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata] gi|297332108|gb|EFH62527.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata]</td><td>350</td><td>346</td><td>2.00E-74</td><td>98.9</td><td>46.9</td><td>60.6</td><td>hypothetical protein ARALYDRAFT_900376</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370</td><td>350</td><td>370</td><td>1.00E-70</td><td>105.7</td><td>46.0</td><td>62.9</td></tr>
<tr><td>Rsa1.0_00089.1.g4479.t1</td><td>ref|XP_002886735.1| hypothetical protein ARALYDRAFT_315436 [Arabidopsis lyrata subsp. lyrata] gi|297332576|gb|EFH62994.1| hypothetical protein ARALYDRAFT_315436 [Arabidopsis lyrata subsp. lyrata]</td><td>595</td><td>649</td><td>0</td><td>109.1</td><td>76.1</td><td>82.0</td><td>hypothetical protein ARALYDRAFT_315436</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G57820.1 | Symbols: VIM1, ORTH2 | Zinc finger (C3HC4-type RING finger) family protein | chr1:21414342-21417902 REVERSE LENGTH=645</td><td>595</td><td>645</td><td>0</td><td>108.4</td><td>72.6</td><td>79.3</td></tr>
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<tr><td>Rsa1.0_00089.1.g4481.t1</td><td>ref|XP_002887130.1| lipoxygenase family protein [Arabidopsis lyrata subsp. lyrata] gi|297332971|gb|EFH63389.1| lipoxygenase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>918</td><td>917</td><td>0</td><td>99.9</td><td>87.7</td><td>93.4</td><td>lipoxygenase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G67560.1 | Symbols: LOX6 | PLAT/LH2 domain-containing lipoxygenase family protein | chr1:25319926-25324117 FORWARD LENGTH=917</td><td>918</td><td>917</td><td>0</td><td>99.9</td><td>86.8</td><td>92.7</td></tr>
<tr><td>Rsa1.0_00089.1.g4482.t1</td><td>ref|NP_564899.1| uncharacterized protein [Arabidopsis thaliana] gi|332196544|gb|AEE34665.1| uncharacterized protein AT1G67570 [Arabidopsis thaliana]</td><td>460</td><td>456</td><td>0</td><td>99.1</td><td>80.9</td><td>87.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G67570.1 | Symbols: | Protein of unknown function (DUF3537) | chr1:25325318-25326938 FORWARD LENGTH=456</td><td>460</td><td>456</td><td>0</td><td>99.1</td><td>80.9</td><td>87.2</td></tr>
<tr><td>Rsa1.0_00089.1.g4483.t2</td><td>ref|NP_176936.1| signal recognition particle subunit SRP72 [Arabidopsis thaliana] gi|11072013|gb|AAG28892.1|AC008113_8 F12A21.17 [Arabidopsis thaliana] gi|28392947|gb|AAO41909.1| unknown protein [Arabidopsis thaliana] gi|28827690|gb|AAO50689.1| unknown protein [Arabidopsis thaliana] gi|332196560|gb|AEE34681.1| signal recognition particle subunit SRP72 [Arabidopsis thaliana]</td><td>654</td><td>664</td><td>0</td><td>101.5</td><td>80.9</td><td>87.6</td><td>signal recognition particle subunit SRP72</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G67680.1 | Symbols: | SRP72 RNA-binding domain | chr1:25365962-25368464 REVERSE LENGTH=664</td><td>654</td><td>664</td><td>0</td><td>101.5</td><td>80.9</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00089.1.g4484.t21</td><td>ref|NP_850972.1| uncharacterized protein [Arabidopsis thaliana] gi|15215606|gb|AAK91348.1| At1g67700/F12A21_30 [Arabidopsis thaliana] gi|21435985|gb|AAM51570.1| At1g67700/F12A21_30 [Arabidopsis thaliana] gi|332196562|gb|AEE34683.1| uncharacterized protein AT1G67700 [Arabidopsis thaliana]</td><td>263</td><td>230</td><td>1.00E-111</td><td>87.5</td><td>77.2</td><td>79.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G67700.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 49 Blast hits to 49 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr1:25374295-25375716 FORWARD LENGTH=230</td><td>263</td><td>230</td><td>1.00E-114</td><td>87.5</td><td>77.2</td><td>79.5</td></tr>
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Rsa1.0_00089.1.g4486.t1	ref|XP_002888618.1| hypothetical protein ARALYDRAFT_475878 [Arabidopsis lyrata subsp. lyrata] gi|297334459|gb|EFH64877.1| hypothetical protein ARALYDRAFT_475878 [Arabidopsis lyrata subsp. lyrata]	146	185	3.00E-37	126.7	71.9	79.5	hypothetical protein ARALYDRAFT_475878	gbpln	Arabidopsis lyrata	AT1G67740.1 | Symbols: PSBY, YCF32 | photosystem II BY | chr1:25394429-25394998 REVERSE LENGTH=189	146	189	3.00E-37	129.5	69.2	75.3
Rsa1.0_00089.1.g4487.t1	ref|XP_002887142.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332983|gb|EFH63401.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	562	542	0	96.4	76.3	82.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G26100.2 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:9538063-9540149 FORWARD LENGTH=532	562	532	0	94.7	60.1	69.8
Rsa1.0_00089.1.g4488.t1	ref|XP_002887143.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata] gi|297332984|gb|EFH63402.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata]	407	408	0	100.2	92.6	95.3	pectate lyase family protein	gbpln	Arabidopsis lyrata	AT1G67750.1 | Symbols: | Pectate lyase family protein | chr1:25401660-25403165 FORWARD LENGTH=408	407	408	0	100.2	92.6	95.1
Rsa1.0_00089.1.g4489.t1	ref|XP_002886268.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata] gi|297332108|gb|EFH62527.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata]	347	346	1.00E-63	99.7	45.8	62.0	hypothetical protein ARALYDRAFT_900376	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	347	370	1.00E-62	106.6	46.4	59.4
Rsa1.0_00089.1.g4490.t1	ref|NP_198119.1| histone H2A 7 [Arabidopsis thaliana] gi|75306451|sp|Q94F49.1|H2A5_ARATH RecName: Full=Probable histone H2A.5; AltName: Full=HTA7 gi|14326516|gb|AAK60303.1|AF385711_1 AT5g27670/F15A18_130 [Arabidopsis thaliana] gi|18700220|gb|AAL77720.1| AT5g27670/F15A18_130 [Arabidopsis thaliana] gi|332006330|gb|AED93713.1| histone H2A 7 [Arabidopsis thaliana]	89	150	1.00E-25	168.5	67.4	76.4	histone H2A 7	gbpln	Arabidopsis thaliana	AT5G27670.1 | Symbols: HTA7 | histone H2A 7 | chr5:9792807-9793365 REVERSE LENGTH=150	89	150	2.00E-28	168.5	67.4	76.4
Rsa1.0_00089.1.g4491.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00089.1.g4492.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00089.1.g4493.t1	ref|XP_002886268.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata] gi|297332108|gb|EFH62527.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata]	359	346	3.00E-71	96.4	46.5	61.6	hypothetical protein ARALYDRAFT_900376	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	359	370	3.00E-70	103.1	46.2	61.8
Rsa1.0_00089.1.g4494.t1	ref|NP_683481.1| uncharacterized protein [Arabidopsis thaliana] gi|297841483|ref|XP_002888623.1| hypothetical protein ARALYDRAFT_475883 [Arabidopsis lyrata subsp. lyrata] gi|17528968|gb|AAL38694.1| unknown protein [Arabidopsis thaliana] gi|20465479|gb|AAM20199.1| unknown protein [Arabidopsis thaliana] gi|21618233|gb|AAM67283.1| unknown [Arabidopsis thaliana] gi|26450708|dbj|BAC42463.1| unknown protein [Arabidopsis thaliana] gi|297334464|gb|EFH64882.1| hypothetical protein ARALYDRAFT_475883 [Arabidopsis lyrata subsp. lyrata] gi|332196574|gb|AEE34695.1| uncharacterized protein AT1G67785 [Arabidopsis thaliana]	63	63	3.00E-27	100.0	96.8	100.0	uncharacterized protein	gbpln	Arabidopsis lyrata	AT1G67785.1 | Symbols: | unknown protein; Has 30 Blast hits to 30 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25416100-25416984 REVERSE LENGTH=63	63	63	4.00E-30	100.0	96.8	100.0
Rsa1.0_00089.1.g4495.t1	ref|XP_002887371.1| hypothetical protein ARALYDRAFT_476270 [Arabidopsis lyrata subsp. lyrata] gi|297333212|gb|EFH63630.1| hypothetical protein ARALYDRAFT_476270 [Arabidopsis lyrata subsp. lyrata]	705	768	0	108.9	66.7	76.0	hypothetical protein ARALYDRAFT_476270	gbpln	Arabidopsis lyrata	AT1G71390.1 | Symbols: AtRLP11, RLP11 | receptor like protein 11 | chr1:26906453-26908807 FORWARD LENGTH=784	705	784	0	111.2	65.1	74.8

Rsa1.0_00089.1.g4496.t1	ref|NP_177295.1| receptor like protein 11 [Arabidopsis thaliana] gi|12323717|gb|AAG51813.1|AC016163_2 putative disease resistance protein; 69620-67266 [Arabidopsis thaliana] gi|332197075|gb|AEE35196.1| receptor like protein 11 [Arabidopsis thaliana]	741	784	0	105.8	67.3	77.3	receptor like protein 11	gbpln	Arabidopsis thaliana	AT1G71390.1 | Symbols: AtRLP11, RLP11 | receptor like protein 11 | chr1:26906453-26908807 FORWARD LENGTH=784	741	784	0	105.8	67.3	77.3
Rsa1.0_00089.1.g4497.t1	ref|NP_564908.1| chloroplast sensor kinase [Arabidopsis thaliana] gi|332196584|gb|AEE34705.1| chloroplast sensor kinase [Arabidopsis thaliana]	609	611	0	100.3	88.8	92.3	chloroplast sensor kinase	gbpln	Arabidopsis thaliana	AT1G67840.1 | Symbols: CSK | chloroplast sensor kinase | chr1:25434156-25436839 FORWARD LENGTH=611	609	611	0	100.3	88.8	92.3
Rsa1.0_00089.1.g4498.t2	ref|NP_564909.1| uncharacterized protein [Arabidopsis thaliana] gi|42572023|ref|NP_974102.1| uncharacterized protein [Arabidopsis thaliana] gi|14326582|gb|AAK60335.1|AF385745_1 At1g67850/F12A21_2 [Arabidopsis thaliana] gi|25090152|gb|AAN72241.1| At1g67850/F12A21_2 [Arabidopsis thaliana] gi|222423797|dbj|BAH19864.1| AT1G67850 [Arabidopsis thaliana] gi|222424761|dbj|BAH20333.1| AT1G67850 [Arabidopsis thaliana] gi|332196585|gb|AEE34706.1| uncharacterized protein AT1G67850 [Arabidopsis thaliana] gi|332196586|gb|AEE34707.1| uncharacterized protein AT1G67850 [Arabidopsis thaliana]	362	404	0	111.6	92.3	96.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G67850.2 | Symbols: | Protein of unknown function (DUF707) | chr1:25439204-25441904 FORWARD LENGTH=404	362	404	0	111.6	92.3	96.7
Rsa1.0_00089.1.g4499.t1	gb|EOA35521.1| hypothetical protein CARUB_v10020730mg [Capsella rubella]	264	295	3.00E-62	111.7	61.4	70.5	hypothetical protein CARUB_v10020730mg	gbpln	Capsella rubella	AT1G67870.1 | Symbols: | glycine-rich protein | chr1:25449593-25450943 REVERSE LENGTH=279	264	279	4.00E-18	105.7	26.5	31.8
Rsa1.0_00089.1.g4500.t1	ref|XP_002888633.1| glycosyl transferase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297334474|gb|EFH64892.1| glycosyl transferase family 17 protein [Arabidopsis lyrata subsp. lyrata]	392	390	0	99.5	91.6	96.9	glycosyl transferase family 17 protein	gbpln	Arabidopsis lyrata	AT1G67880.1 | Symbols: | beta-1,4-N-acetylglucosaminyltransferase family protein | chr1:25454081-25455453 REVERSE LENGTH=390	392	390	0	99.5	91.6	96.7
Rsa1.0_00089.1.g4501.t1	gb|EOA33765.1| hypothetical protein CARUB_v10019960mg [Capsella rubella]	583	630	0	108.1	93.0	96.7	hypothetical protein CARUB_v10019960mg	gbpln	Capsella rubella	AT1G67900.3 | Symbols: | Phototropic-responsive NPH3 family protein | chr1:25467737-25469888 FORWARD LENGTH=631	583	631	0	108.2	92.8	96.6
Rsa1.0_00089.1.g4502.t1	ref|XP_002888634.1| hypothetical protein ARALYDRAFT_894552 [Arabidopsis lyrata subsp. lyrata] gi|297334475|gb|EFH64893.1| hypothetical protein ARALYDRAFT_894552 [Arabidopsis lyrata subsp. lyrata]	91	102	7.00E-31	112.1	73.6	83.5	hypothetical protein ARALYDRAFT_894552	gbpln	Arabidopsis lyrata	AT1G67910.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24577.1). | chr1:25471534-25471809 REVERSE LENGTH=91	91	91	1.00E-30	100.0	69.2	80.2
Rsa1.0_00089.1.g4503.t1	dbj|BAJ34019.1| unnamed protein product [Thellungiella halophila]	67	66	4.00E-24	98.5	88.1	94.0	unnamed protein product	----	----	AT1G67920.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24600.1); Has 22 Blast hits to 22 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25473731-25473934 FORWARD LENGTH=67	67	67	3.00E-24	100.0	86.6	92.5
Rsa1.0_00089.1.g4504.t1	gb|AAO03559.1| lipoxygenase 2 [Brassica napus]	889	892	0	100.3	87.6	93.1	lipoxygenase 2	gbpln	Brassica napus	AT3G45140.1 | Symbols: LOX2, ATLOX2 | lipoxygenase 2 | chr3:16525437-16529233 FORWARD LENGTH=896	889	896	0	100.8	74.2	85.7
Rsa1.0_00089.1.g4505.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00089.1.g4506.t1	gb|AAO03559.1| lipoxygenase 2 [Brassica napus]	889	892	0	100.3	90.6	94.3	lipoxygenase 2	gbpln	Brassica napus	AT3G45140.1 | Symbols: LOX2, ATLOX2 | lipoxygenase 2 | chr3:16525437-16529233 FORWARD LENGTH=896	889	896	0	100.8	75.7	86.5
Rsa1.0_00089.1.g4507.t1	gb|AAO03559.1| lipoxygenase 2 [Brassica napus]	892	892	0	100.0	89.1	93.6	lipoxygenase 2	gbpln	Brassica napus	AT3G45140.1 | Symbols: LOX2, ATLOX2 | lipoxygenase 2 | chr3:16525437-16529233 FORWARD LENGTH=896	892	896	0	100.4	76.3	87.3
Rsa1.0_00089.1.g4508.t3	gb|AAM77369.1|AF521301_1 phosphatidylinositol synthase [Brassica napus]	245	227	1.00E-123	92.7	88.6	90.2	phosphatidylinositol synthase	gbpln	Brassica napus	AT1G68000.1 | Symbols: ATPIS1, ATPIS, PIS1 | phosphatidylinositol synthase 1 | chr1:25491346-25492930 FORWARD LENGTH=227	245	227	1.00E-124	92.7	86.5	89.8
Rsa1.0_00089.1.g4509.t1	gb|EOA34815.1| hypothetical protein CARUB_v10022393mg, partial [Capsella rubella]	386	379	0	98.2	96.4	97.4	hypothetical protein CARUB_v10022393mg, partial	gbpln	Capsella rubella	AT1G68010.1 | Symbols: HPR, ATHPR1 | hydroxypyruvate reductase | chr1:25493418-25495720 FORWARD LENGTH=386	386	386	0	100.0	97.4	98.4

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<tr><td>Rsa1.0_00089.1.g4510.t1</td><td>ref|XP_002888643.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334484|gb|EFH64902.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>860</td><td>857</td><td>0</td><td>99.7</td><td>93.8</td><td>96.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68020.2 | Symbols: ATTPS6, TPS6 | UDP-Glycosyltransferase / trehalose-phosphatase family protein | chr1:25497493-25500241 FORWARD LENGTH=860</td><td>860</td><td>860</td><td>0</td><td>100.0</td><td>92.9</td><td>96.2</td></tr>
<tr><td>Rsa1.0_00089.1.g4511.t1</td><td>ref|NP_176973.1| microtubule-associated proteins 70-1 [Arabidopsis thaliana] gi|75169797|sp|Q9C9X0.1|MP701_ARATH RecName: Full=Microtubule-associated protein 70-1; Short=AtMAP70-1; AltName: Full=70 kDa microtubule-associated protein 1 gi|12324091|gb|AAG52019.1|AC012563_29 unknown protein; 30164-32998 [Arabidopsis thaliana] gi|18377700|gb|AAL67000.1| unknown protein [Arabidopsis thaliana] gi|20465647|gb|AAM20292.1| unknown protein [Arabidopsis thaliana] gi|76058012|emb|CAJ31078.1| 70 kDa microtubule associated protein Type 1 [Arabidopsis thaliana] gi|332196621|gb|AEE34742.1| microtubule-associated proteins 70-1 [Arabidopsis thaliana]</td><td>614</td><td>622</td><td>0</td><td>101.3</td><td>91.4</td><td>95.3</td><td>microtubule-associated proteins 70-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68060.1 | Symbols: ATMAP70-1, MAP70-1 | microtubule-associated proteins 70-1 | chr1:25511392-25514226 REVERSE LENGTH=622</td><td>614</td><td>622</td><td>0</td><td>101.3</td><td>91.4</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00089.1.g4512.t1</td><td>ref|NP_176975.2| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase domain-containing protein [Arabidopsis thaliana] gi|56236062|gb|AAV84487.1| At1g68080 [Arabidopsis thaliana] gi|58531340|gb|AAW78592.1| At1g68080 [Arabidopsis thaliana] gi|60547659|gb|AAX23793.1| hypothetical protein At1g68080 [Arabidopsis thaliana] gi|71905461|gb|AAZ52708.1| expressed protein [Arabidopsis thaliana] gi|332196623|gb|AEE34744.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase domain-containing protein [Arabidopsis thaliana]</td><td>392</td><td>389</td><td>1.00E-173</td><td>99.2</td><td>77.3</td><td>88.5</td><td>2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68080.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:25517530-25519240 FORWARD LENGTH=389</td><td>392</td><td>389</td><td>1.00E-175</td><td>99.2</td><td>77.3</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00089.1.g4513.t1</td><td>gb|EOA35125.1| hypothetical protein CARUB_v10020247mg [Capsella rubella]</td><td>466</td><td>466</td><td>0</td><td>100.0</td><td>81.8</td><td>88.8</td><td>hypothetical protein CARUB_v10020247mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68100.1 | Symbols: IAR1 | ZIP metal ion transporter family | chr1:25521325-25524032 FORWARD LENGTH=469</td><td>466</td><td>469</td><td>0</td><td>100.6</td><td>82.2</td><td>88.0</td></tr>
<tr><td>Rsa1.0_00089.1.g4514.t1</td><td>ref|XP_002888637.1| atidd14-domain 14 [Arabidopsis lyrata subsp. lyrata] gi|297334478|gb|EFH64896.1| atidd14-domain 14 [Arabidopsis lyrata subsp. lyrata]</td><td>413</td><td>423</td><td>0</td><td>102.4</td><td>85.5</td><td>90.6</td><td>atidd14-domain 14</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68130.1 | Symbols: AtIDD14, IDD14 | indeterminate(ID)-domain 14 | chr1:25532484-25534317 FORWARD LENGTH=419</td><td>413</td><td>419</td><td>0</td><td>101.5</td><td>83.5</td><td>88.1</td></tr>
<tr><td>Rsa1.0_00089.1.g4515.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00089.1.g4516.t1</td><td>gb|EOA35581.1| hypothetical protein CARUB_v10020790mg [Capsella rubella]</td><td>258</td><td>270</td><td>2.00E-76</td><td>104.7</td><td>67.8</td><td>77.5</td><td>hypothetical protein CARUB_v10020790mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68160.1 | Symbols: | Protein of unknown function (DUF3755) | chr1:25546168-25548625 REVERSE LENGTH=273</td><td>258</td><td>273</td><td>3.00E-60</td><td>105.8</td><td>58.9</td><td>70.2</td></tr>
<tr><td>Rsa1.0_00089.1.g4517.t1</td><td>ref|XP_002891889.1| hypothetical protein ARALYDRAFT_474711 [Arabidopsis lyrata subsp. lyrata] gi|297337731|gb|EFH68148.1| hypothetical protein ARALYDRAFT_474711 [Arabidopsis lyrata subsp. lyrata]</td><td>102</td><td>551</td><td>6.00E-30</td><td>540.2</td><td>67.6</td><td>73.5</td><td>hypothetical protein ARALYDRAFT_474711</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G54380.1 | Symbols: | spliceosome protein-related | chr1:20298287-20300899 REVERSE LENGTH=515</td><td>102</td><td>515</td><td>2.00E-32</td><td>504.9</td><td>66.7</td><td>73.5</td></tr>
<tr><td>Rsa1.0_00089.1.g4518.t1</td><td>gb|EOA36691.1| hypothetical protein CARUB_v10012096mg [Capsella rubella]</td><td>293</td><td>327</td><td>1.00E-104</td><td>111.6</td><td>62.5</td><td>75.8</td><td>hypothetical protein CARUB_v10012096mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G43690.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273-17547268 FORWARD LENGTH=331</td><td>293</td><td>331</td><td>1.00E-106</td><td>113.0</td><td>62.5</td><td>75.8</td></tr>
<tr><td>Rsa1.0_00090.1.g4519.t1</td><td>ref|XP_002866178.1| hypothetical protein ARALYDRAFT_918860 [Arabidopsis lyrata subsp. lyrata] gi|297312013|gb|EFH42437.1| hypothetical protein ARALYDRAFT_918860 [Arabidopsis lyrata subsp. lyrata]</td><td>231</td><td>232</td><td>9.00E-81</td><td>100.4</td><td>63.2</td><td>76.2</td><td>hypothetical protein ARALYDRAFT_918860</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G56920.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:23025000-23025765 FORWARD LENGTH=227</td><td>231</td><td>227</td><td>5.00E-43</td><td>98.3</td><td>39.8</td><td>58.4</td></tr>
<tr><td>Rsa1.0_00090.1.g4520.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>1472</td><td>1274</td><td>0</td><td>86.5</td><td>38.2</td><td>52.7</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1472</td><td>575</td><td>2.00E-65</td><td>39.1</td><td>10.4</td><td>15.6</td></tr>
<tr><td>Rsa1.0_00090.1.g4521.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_00090.1.g4522.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1797	1213	0	67.5	24.9	37.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I−like superfamily protein | chr1:16528880−16531065 REVERSE LENGTH=626	1797	626	2.00E−71	34.8	8.1	14.3
Rsa1.0_00090.1.g4523.t1	ref|XP_002887971.1| hypothetical protein ARALYDRAFT_893147 [Arabidopsis lyrata subsp. lyrata] gi|297333812|gb|EFH64230.1| hypothetical protein ARALYDRAFT_893147 [Arabidopsis lyrata subsp. lyrata]	310	296	8.00E−35	95.5	32.9	46.1	hypothetical protein ARALYDRAFT_893147	gbpln	Arabidopsis lyrata	AT5G05050.1 | Symbols: | Cysteine proteinases superfamily protein | chr5:1491639−1493457 FORWARD LENGTH=299	310	299	5.00E−22	96.5	22.6	34.8
Rsa1.0_00090.1.g4524.t2	ref|XP_002863021.1| hypothetical protein ARALYDRAFT_359201 [Arabidopsis lyrata subsp. lyrata] gi|297793205|ref|XP_002864487.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308821|gb|EFH39280.1| hypothetical protein ARALYDRAFT_359201 [Arabidopsis lyrata subsp. lyrata] gi|297310322|gb|EFH40746.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	488	166	4.00E−28	34.0	15.4	18.6	hypothetical protein ARALYDRAFT_359201	gbpln	Arabidopsis lyrata	AT1G63200.1 | Symbols: | Cystatin/monellin superfamily protein | chr1:23433630−23434600 REVERSE LENGTH=216	488	216	5.00E−23	44.3	12.5	19.5
Rsa1.0_00090.1.g4525.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00090.1.g4526.t15	ref|NP_200501.1| proteinase inhibitor I25, cystatin, conserved region−containing protein [Arabidopsis thaliana] gi|8777431|dbj|BAA97021.1| unnamed protein product [Arabidopsis thaliana] gi|21595644|gb|AAM66120.1| unknown [Arabidopsis thaliana] gi|26452958|dbj|BAC43555.1| unknown protein [Arabidopsis thaliana] gi|28973159|gb|AAO63904.1| unknown protein [Arabidopsis thaliana] gi|332009439|gb|AED96822.1| proteinase inhibitor I25, cystatin, conserved region−containing protein [Arabidopsis thaliana]	461	224	7.00E−63	48.6	26.7	34.7	proteinase inhibitor I25, cystatin, conserved region−containing protein	gbpln	Arabidopsis thaliana	AT5G56910.1 | Symbols: | Proteinase inhibitor I25, cystatin, conserved region | chr5:23022996−23024008 FORWARD LENGTH=224	461	224	2.00E−65	48.6	26.7	34.7
Rsa1.0_00090.1.g4527.t1	gb|EOA12814.1| hypothetical protein CARUB_v10025774mg [Capsella rubella]	116	1110	2.00E−19	956.9	45.7	51.7	hypothetical protein CARUB_v10025774mg	gbpln	Capsella rubella	AT5G56890.1 | Symbols: | Protein kinase superfamily protein | chr5:23010801−23015559 REVERSE LENGTH=1113	116	1113	1.00E−20	959.5	42.2	50.0
Rsa1.0_00090.1.g4528.t1	ref|NP_200499.1| uncharacterized protein [Arabidopsis thaliana] gi|8809656|dbj|BAA97207.1| unnamed protein product [Arabidopsis thaliana] gi|208879512|gb|ACI31301.1| At5g56880 [Arabidopsis thaliana] gi|332009435|gb|AED96818.1| uncharacterized protein AT5G56880 [Arabidopsis thaliana]	162	159	9.00E−54	98.1	68.5	78.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G56880.1 | Symbols: | unknown protein; Has 9 Blast hits to 9 proteins in 5 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 9; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr5:23009140−23009619 REVERSE LENGTH=159	162	159	3.00E−56	98.1	68.5	78.4
Rsa1.0_00090.1.g4529.t1	ref|XP_002864484.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310319|gb|EFH40743.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	722	726	0	100.6	92.9	96.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G56870.1 | Symbols: BGAL4 | beta−galactosidase 4 | chr5:23004284−23008410 FORWARD LENGTH=724	722	724	0	100.3	92.0	95.3
Rsa1.0_00090.1.g4530.t1	gb|EOA13498.1| hypothetical protein CARUB_v10026556mg [Capsella rubella]	387	395	1.00E−139	102.1	82.2	88.6	hypothetical protein CARUB_v10026556mg	gbpln	Capsella rubella	AT5G56860.1 | Symbols: GNC, GATA21 | GATA type zinc finger transcription factor family protein | chr5:22989630−22991351 REVERSE LENGTH=398	387	398	1.00E−137	102.8	80.1	86.8
Rsa1.0_00090.1.g4531.t1	gb|EOA13221.1| hypothetical protein CARUB_v10026246mg [Capsella rubella]	469	511	1.00E−177	109.0	74.2	83.8	hypothetical protein CARUB_v10026246mg	gbpln	Capsella rubella	AT5G56850.1 | Symbols: | unknown protein; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr5:22985432−22987977 REVERSE LENGTH=551	469	551	1.00E−172	117.5	74.4	84.6
Rsa1.0_00090.1.g4532.t1	gb|EOA13846.1| hypothetical protein CARUB_v10026949mg [Capsella rubella]	233	272	5.00E−89	116.7	74.7	85.4	hypothetical protein CARUB_v10026949mg	gbpln	Capsella rubella	AT5G56840.1 | Symbols: | myb−like transcription factor family protein | chr5:22980789−22982152 FORWARD LENGTH=233	233	233	3.00E−86	100.0	76.4	86.7
Rsa1.0_00090.1.g4533.t1	dbj|BAB09901.1| unnamed protein product [Arabidopsis thaliana]	275	242	3.00E−46	88.0	36.4	45.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G21000.1 | Symbols: | Gag−Pol−related retrotransposon family protein | chr3:7363921−7365138 FORWARD LENGTH=405	275	405	1.00E−10	147.3	20.7	37.8
Rsa1.0_00090.1.g4534.t1	gb|EOA13381.1| hypothetical protein CARUB_v10026420mg [Capsella rubella]	111	438	2.00E−18	394.6	52.3	68.5	hypothetical protein CARUB_v10026420mg	gbpln	Capsella rubella	AT5G56810.1 | Symbols: | F−box/RNI−like/FBD−like domains−containing protein | chr5:22974520−22975992 FORWARD LENGTH=435	111	435	3.00E−20	391.9	48.6	61.3

Rsa1.0_00090.1.g4535.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00090.1.g4536.t1	ref|NP_200492.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262578|sp|Q9FJT2.1|FDL40_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g56810 gi|10176785|dbj|BAB09899.1| unnamed protein product [Arabidopsis thaliana] gi|332009427|gb|AED96810.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	347	435	1.00E-103	125.4	60.8	72.0	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G56810.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22974520-22975992 FORWARD LENGTH=435	347	435	1.00E-106	125.4	60.8	72.0
Rsa1.0_00090.1.g4537.t1	ref|XP_002864481.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297310316|gb|EFH40740.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	432	428	1.00E-117	99.1	56.5	70.1	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56810.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22974520-22975992 FORWARD LENGTH=435	432	435	1.00E-117	100.7	56.0	70.6
Rsa1.0_00090.1.g4538.t1	gb|AFK13856.1| Ty3/gypsy retrotransposon protein [Beta vulgaris subsp. vulgaris]	1644	1631	0	99.2	46.6	60.6	Ty3/gypsy retrotransposon protein	gbpln	Beta vulgaris	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1644	158	1.00E-38	9.6	4.6	5.8
Rsa1.0_00090.1.g4539.t1	ref|XP_002864437.1| hypothetical protein ARALYDRAFT_495701 [Arabidopsis lyrata subsp. lyrata] gi|297310272|gb|EFH40696.1| hypothetical protein ARALYDRAFT_495701 [Arabidopsis lyrata subsp. lyrata]	149	148	1.00E-78	99.3	93.3	97.3	hypothetical protein ARALYDRAFT_495701	gbpln	Arabidopsis lyrata	AT5G56150.2 | Symbols: UBC30 | ubiquitin-conjugating enzyme 30 | chr5:22729756-22730964 FORWARD LENGTH=148	149	148	3.00E-80	99.3	91.9	96.0
Rsa1.0_00090.1.g4540.t10	gb|EOA14478.1| hypothetical protein CARUB_v10027692mg [Capsella rubella]	402	580	1.00E-164	144.3	78.9	87.1	hypothetical protein CARUB_v10027692mg	gbpln	Capsella rubella	AT5G56160.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr5:22732444-22735380 FORWARD LENGTH=577	402	577	1.00E-160	143.5	75.1	84.1
Rsa1.0_00090.1.g4541.t1	ref|NP_200428.1| LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 [Arabidopsis thaliana] gi|9758637|dbj|BAB09299.1| unnamed protein product [Arabidopsis thaliana] gi|23306374|gb|AAN17414.1| putative protein [Arabidopsis thaliana] gi|24899659|gb|AAN65044.1| putative protein [Arabidopsis thaliana] gi|332009346|gb|AED96729.1| LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 [Arabidopsis thaliana]	148	168	9.00E-50	113.5	66.2	72.3	LORELEI-LIKE-GPI-ANCHORED PROTEIN 1	gbpln	Arabidopsis thaliana	AT5G56170.1 | Symbols: LLG1 | LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 | chr5:22736072-22737108 FORWARD LENGTH=168	148	168	3.00E-52	113.5	66.2	72.3
Rsa1.0_00090.1.g4542.t1	gb|EOA13271.1| hypothetical protein CARUB_v10026299mg [Capsella rubella]	382	489	1.00E-110	128.0	63.6	72.8	hypothetical protein CARUB_v10026299mg	gbpln	Capsella rubella	AT5G56200.1 | Symbols: | C2H2 type zinc finger transcription factor family | chr5:22747768-22749249 FORWARD LENGTH=493	382	493	1.00E-102	129.1	63.1	71.2
Rsa1.0_00090.1.g4543.t1	ref|NP_001190554.1| uncharacterized protein [Arabidopsis thaliana] gi|332009356|gb|AED96739.1| uncharacterized protein AT5G56240 [Arabidopsis thaliana]	995	987	0	99.2	61.6	70.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G56240.2 | Symbols: | INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hapless 8 (TAIR:AT5G56250.1). | chr5:22760088-22763539 REVERSE LENGTH=987	995	987	0	99.2	61.6	70.6
Rsa1.0_00090.1.g4544.t1	ref|NP_200436.1| protein hapless 8 [Arabidopsis thaliana] gi|42573690|ref|NP_974941.1| protein hapless 8 [Arabidopsis thaliana] gi|9758752|dbj|BAB09116.1| unnamed protein product [Arabidopsis thaliana] gi|18389250|gb|AAL67068.1| unknown protein [Arabidopsis thaliana] gi|20465799|gb|AAM20388.1| unknown protein [Arabidopsis thaliana] gi|332009357|gb|AED96740.1| protein hapless 8 [Arabidopsis thaliana] gi|332009358|gb|AED96741.1| protein hapless 8 [Arabidopsis thaliana]	760	811	0	106.7	69.6	76.8	protein hapless 8	gbpln	Arabidopsis thaliana	AT5G56250.1 | Symbols: HAP8 | hapless 8 | chr5:22768918-22771869 REVERSE LENGTH=811	760	811	0	106.7	69.6	76.8

Rsa1.0_00090.1.g4545.t1	ref|NP_200437.1| Regulator of ribonuclease-like protein 3 [Arabidopsis thaliana] gi|17368897|sp|Q9FH13.1|RRAA3_ARATH RecName: Full=Regulator of ribonuclease-like protein 3 gi|9758753|dbj|BAB09117.1| S-adenosylmethionine:2-demethylmenaquinone methyltransferase-like [Arabidopsis thaliana] gi|38603850|gb|AAR24670.1| At5g56260 [Arabidopsis thaliana] gi|38603934|gb|AAR24712.1| At5g56260 [Arabidopsis thaliana] gi|332009359|gb|AED96742.1| Regulator of ribonuclease-like protein 3 [Arabidopsis thaliana]	166	166	2.00E-86	100.0	95.2	97.0	Regulator of ribonuclease-like protein 3	gbpln	Arabidopsis thaliana	AT5G56260.1 | Symbols: | Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase | chr5:22775549-22776049 REVERSE LENGTH=166	166	166	9.00E-89	100.0	95.2	97.0
Rsa1.0_00090.1.g4546.t1	ref|NP_200438.1| putative WRKY transcription factor 2 [Arabidopsis thaliana] gi|29839620|sp|Q9FG77.1|WRKY2_ARATH RecName: Full=Probable WRKY transcription factor 2; AltName: Full=WRKY DNA-binding protein 2 gi|15991724|gb|AAL13039.1|AF418308_1 WRKY transcription factor 2 [Arabidopsis thaliana] gi|9758400|dbj|BAB08871.1| transcription factor NtWRKY4-like [Arabidopsis thaliana] gi|20465416|gb|AAM20132.1| putative transcription factor NtWRKY4 [Arabidopsis thaliana] gi|21689791|gb|AAM67539.1| putative transcription factor NtWRKY4 [Arabidopsis thaliana] gi|332009360|gb|AED96743.1| putative WRKY transcription factor 2 [Arabidopsis thaliana]	1016	687	0	67.6	49.6	53.4	putative WRKY transcription factor 2	gbpln	Arabidopsis thaliana	AT5G56270.1 | Symbols: WRKY2, ATWRKY2 | WRKY DNA-binding protein 2 | chr5:22780816-22783137 FORWARD LENGTH=687	1016	687	0	67.6	49.6	53.4
Rsa1.0_00090.1.g4547.t2	gb|ABB92565.1| peroxisomal import receptor PTS1 [Brassica napus]	724	731	0	101.0	95.2	97.0	peroxisomal import receptor PTS1	gbpln	Brassica napus	AT5G56290.1 | Symbols: PEX5, ATPEX5 | peroxin 5 | chr5:22786655-22791972 FORWARD LENGTH=728	724	728	0	100.6	89.9	94.1
Rsa1.0_00090.1.g4548.t1	gb|EOA27690.1| hypothetical protein CARUB_v10023843mg, partial [Capsella rubella]	275	271	2.00E-28	98.5	30.5	48.4	hypothetical protein CARUB_v10023843mg, partial	gbpln	Capsella rubella	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	275	303	3.00E-30	110.2	31.3	48.7
Rsa1.0_00090.1.g4549.t1	ref|XP_002864445.1| hypothetical protein ARALYDRAFT_918774 [Arabidopsis lyrata subsp. lyrata] gi|297310280|gb|EFH40704.1| hypothetical protein ARALYDRAFT_918774 [Arabidopsis lyrata subsp. lyrata]	384	388	0	101.0	88.0	93.8	hypothetical protein ARALYDRAFT_918774	gbpln	Arabidopsis lyrata	AT5G56300.1 | Symbols: GAMT2 | gibberellic acid methyltransferase 2 | chr5:22799571-22801484 FORWARD LENGTH=387	384	387	0	100.8	86.5	92.4
Rsa1.0_00090.1.g4550.t1	ref|XP_002864446.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310281|gb|EFH40705.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	541	531	0	98.2	79.5	88.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G56310.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:22802322-22803914 FORWARD LENGTH=530	541	530	0	98.0	78.7	88.0
Rsa1.0_00090.1.g4551.t3	ref|NP_564398.1| putative FBD-associated F-box protein [Arabidopsis thaliana] gi|302425238|sp|Q9LQM1.2|FBD39_ARATH RecName: Full=Probable FBD-associated F-box protein At1g32375 gi|332193353|gb|AEE31474.1| putative FBD-associated F-box protein [Arabidopsis thaliana]	428	422	1.00E-128	98.6	57.7	72.4	putative FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	428	422	1.00E-131	98.6	57.7	72.4
Rsa1.0_00090.1.g4552.t1	ref|NP_564398.1| putative FBD-associated F-box protein [Arabidopsis thaliana] gi|302425238|sp|Q9LQM1.2|FBD39_ARATH RecName: Full=Probable FBD-associated F-box protein At1g32375 gi|332193353|gb|AEE31474.1| putative FBD-associated F-box protein [Arabidopsis thaliana]	429	422	1.00E-128	98.4	58.3	73.9	putative FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	429	422	1.00E-131	98.4	58.3	73.9
Rsa1.0_00090.1.g4553.t1	ref|XP_002864451.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310286|gb|EFH40710.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	374	395	1.00E-141	105.6	80.5	88.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G56340.1 | Symbols: ATCRT1 | RING/U-box superfamily protein | chr5:22818254-22819444 FORWARD LENGTH=396	374	396	1.00E-137	105.9	74.3	80.5

Rsa1.0_00090.1.g4554.t1	ref|NP_200446.1| pyruvate kinase [Arabidopsis thaliana] gi|297796505|ref|XP_002866137.1| hypothetical protein ARALYDRAFT_495726 [Arabidopsis lyrata subsp. lyrata] gi|10177833|dbj|BAB11262.1| pyruvate kinase [Arabidopsis thaliana] gi|15450942|gb|AAK96742.1| pyruvate kinase [Arabidopsis thaliana] gi|17978781|gb|AAL47384.1| pyruvate kinase [Arabidopsis thaliana] gi|21592702|gb|AAM64651.1| pyruvate kinase [Arabidopsis thaliana] gi|297311972|gb|EFH42396.1| hypothetical protein ARALYDRAFT_495726 [Arabidopsis lyrata subsp. lyrata] gi|332009369|gb|AED96752.1| pyruvate kinase [Arabidopsis thaliana]	498	498	0	100.0	96.6	98.4	pyruvate kinase	gbpln	Arabidopsis lyrata	AT5G56350.1 | Symbols: | Pyruvate kinase family protein | chr5:22820254-22822529 REVERSE LENGTH=498	498	498	0	100.0	96.6	98.4
Rsa1.0_00090.1.g4555.t5	ref|XP_002866138.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] gi|297311973|gb|EFH42397.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	846	653	0	77.2	63.7	69.0	calmodulin-binding protein	gbpln	Arabidopsis lyrata	AT5G56360.1 | Symbols: PSL4 | calmodulin-binding protein | chr5:22823586-22827950 REVERSE LENGTH=647	846	647	0	76.5	61.2	66.7
Rsa1.0_00090.1.g4556.t1	gb|ABM55734.1| nitrilase 2 [Brassica rapa]	331	350	1.00E-130	105.7	73.7	81.6	nitrilase 2	gbpln	Brassica rapa	AT3G44300.1 | Symbols: NIT2, AtNIT2 | nitrilase 2 | chr3:15983351-15985172 FORWARD LENGTH=339	331	339	1.00E-131	102.4	72.5	81.0
Rsa1.0_00090.1.g4557.t1	ref|XP_002866141.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311976|gb|EFH42400.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	414	424	1.00E-160	102.4	70.5	83.1	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56370.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22836200-22837619 REVERSE LENGTH=421	414	421	1.00E-153	101.7	69.1	80.2
Rsa1.0_00090.1.g4558.t2	gb|EOA14711.1| hypothetical protein CARUB_v10027989mg [Capsella rubella]	424	420	1.00E-150	99.1	67.5	77.4	hypothetical protein CARUB_v10027989mg	gbpln	Capsella rubella	AT5G56380.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22838836-22840353 REVERSE LENGTH=439	424	439	1.00E-132	103.5	60.8	74.3
Rsa1.0_00090.1.g4559.t1	ref|NP_564398.1| putative FBD-associated F-box protein [Arabidopsis thaliana] gi|302425238|sp|Q9LQM1.2|FBD39_ARATH RecName: Full=Probable FBD-associated F-box protein At1g32375 gi|332193353|gb|AEE31474.1| putative FBD-associated F-box protein [Arabidopsis thaliana]	422	422	1.00E-128	100.0	60.4	73.9	putative FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	422	422	1.00E-130	100.0	60.4	73.9
Rsa1.0_00090.1.g4560.t1	ref|NP_564398.1| putative FBD-associated F-box protein [Arabidopsis thaliana] gi|302425238|sp|Q9LQM1.2|FBD39_ARATH RecName: Full=Probable FBD-associated F-box protein At1g32375 gi|332193353|gb|AEE31474.1| putative FBD-associated F-box protein [Arabidopsis thaliana]	419	422	1.00E-125	100.7	61.1	73.7	putative FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	419	422	1.00E-127	100.7	61.1	73.7
Rsa1.0_00090.1.g4561.t1	ref|NP_564398.1| putative FBD-associated F-box protein [Arabidopsis thaliana] gi|302425238|sp|Q9LQM1.2|FBD39_ARATH RecName: Full=Probable FBD-associated F-box protein At1g32375 gi|332193353|gb|AEE31474.1| putative FBD-associated F-box protein [Arabidopsis thaliana]	915	422	1.00E-120	46.1	27.2	33.7	putative FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	915	422	1.00E-122	46.1	27.2	33.7
Rsa1.0_00090.1.g4562.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	698	1274	0	182.5	52.6	69.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	698	575	9.00E-38	82.4	11.6	19.3
Rsa1.0_00091.1.g4563.t1	emb|CCD74546.1| F-box family protein [Arabidopsis halleri subsp. halleri]	463	530	8.00E-95	114.5	49.7	63.7	F-box family protein	gbpln	Arabidopsis halleri	AT2G26030.3 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr2:11091505-11093000 REVERSE LENGTH=442	463	442	3.00E-95	95.5	49.2	62.6

Rsa1.0_00091.1.g4564.t1	ref|NP_567204.3| cysteine-rich receptor-like protein kinase 41 [Arabidopsis thaliana] gi|152013451|sp|O23081.2|CRK41_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 41; Short=Cysteine-rich RLK41; Flags: Precursor gi|332656562|gb|AEE81962.1| cysteine-rich receptor-like protein kinase 41 [Arabidopsis thaliana]	611	665	0	108.8	72.8	84.5	cysteine-rich receptor-like protein kinase 41	gbpln	Arabidopsis thaliana	AT4G00970.1 | Symbols: CRK41 | cysteine-rich RLK (RECEPTOR-like protein kinase) 41 | chr4:418437-421694 FORWARD LENGTH=665	611	665	0	108.8	72.8	84.5
Rsa1.0_00091.1.g4565.t1	ref|XP_002879092.1| hypothetical protein ARALYDRAFT_481654 [Arabidopsis lyrata subsp. lyrata] gi|297324931|gb|EFH55351.1| hypothetical protein ARALYDRAFT_481654 [Arabidopsis lyrata subsp. lyrata]	297	330	2.00E-52	111.1	52.9	63.3	hypothetical protein ARALYDRAFT_481654	gbpln	Arabidopsis lyrata	AT2G27505.1 | Symbols: | FBD-like domain family protein | chr2:11756746-11757829 FORWARD LENGTH=298	297	298	1.00E-54	100.3	50.2	61.6
Rsa1.0_00091.1.g4566.t1	gb|EOA23440.1| hypothetical protein CARUB_v10016624mg [Capsella rubella]	1014	1017	0	100.3	96.0	98.2	hypothetical protein CARUB_v10016624mg	gbpln	Capsella rubella	AT3G55410.1 | Symbols: | 2-oxoglutarate dehydrogenase, E1 component | chr3:20541897-20545728 FORWARD LENGTH=1017	1014	1017	0	100.3	95.7	98.1
Rsa1.0_00091.1.g4567.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	189	478	6.00E-45	252.9	50.3	63.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	189	746	3.00E-38	394.7	38.1	49.7
Rsa1.0_00091.1.g4568.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00091.1.g4569.t1	ref|NP_199308.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262649|sp|Q9FLA2.1|FDL34_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g44950 gi|10177487|dbj|BAB10878.1| unnamed protein product [Arabidopsis thaliana] gi|332007796|gb|AED95179.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	446	438	1.00E-107	98.2	52.9	65.7	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G44950.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:18151665-18153164 FORWARD LENGTH=438	446	438	1.00E-109	98.2	52.9	65.7
Rsa1.0_00091.1.g4570.t1	ref|NP_199313.3| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|62320508|dbj|BAD95061.1| putative protein [Arabidopsis thaliana] gi|332007804|gb|AED95187.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	445	419	1.00E-164	94.2	64.9	74.4	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G45000.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18165427-18167005 FORWARD LENGTH=419	445	419	1.00E-166	94.2	64.9	74.4
Rsa1.0_00091.1.g4571.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00091.1.g4572.t1	ref|NP_851134.1| S-ribonuclease binding protein [Arabidopsis thaliana] gi|9758985|dbj|BAB09495.1| unnamed protein product [Arabidopsis thaliana] gi|16604442|gb|AAL24227.1| AT5g45100/K17O22_9 [Arabidopsis thaliana] gi|23505847|gb|AAN28783.1| At5g45100/K17O22_9 [Arabidopsis thaliana] gi|332007818|gb|AED95201.1| S-ribonuclease binding protein [Arabidopsis thaliana]	280	294	2.00E-94	105.0	70.4	78.9	S-ribonuclease binding protein	gbpln	Arabidopsis thaliana	AT5G45100.1 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr5:18218769-18219741 FORWARD LENGTH=294	280	294	6.00E-97	105.0	70.4	78.9
Rsa1.0_00091.1.g4573.t1	gb|EOA14460.1| hypothetical protein CARUB_v10027669mg [Capsella rubella]	257	299	6.00E-96	116.3	70.8	80.9	hypothetical protein CARUB_v10027669mg	gbpln	Capsella rubella	AT5G45105.2 | Symbols: ZIP8 | zinc transporter 8 precursor | chr5:18223453-18224946 REVERSE LENGTH=299	257	299	1.00E-96	116.3	70.4	80.2
Rsa1.0_00091.1.g4574.t1	gb|EOA14334.1| hypothetical protein CARUB_v10027512mg [Capsella rubella]	495	488	0	98.6	84.4	91.5	hypothetical protein CARUB_v10027512mg	gbpln	Capsella rubella	AT5G45120.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:18241003-18242478 FORWARD LENGTH=491	495	491	0	99.2	83.6	89.9
Rsa1.0_00091.1.g4575.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1380	1459	0	105.7	53.2	71.2	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1380	1262	1.00E-112	91.4	14.2	20.9
Rsa1.0_00091.1.g4576.t1	gb|EOA14027.1| hypothetical protein CARUB_v10027159mg [Capsella rubella]	200	200	1.00E-110	100.0	97.5	98.0	hypothetical protein CARUB_v10027159mg	gbpln	Capsella rubella	AT5G45130.1 | Symbols: ATRAB5A, ATRABF2A, RABF2A, RAB5A, RHA1, ATRAB-F2A, RAB-F2A | RAB homolog 1 | chr5:18244495-18246060 FORWARD LENGTH=200	200	200	1.00E-112	100.0	97.0	98.0
Rsa1.0_00091.1.g4577.t1	gb|EOA14759.1| hypothetical protein CARUB_v10028056mg [Capsella rubella]	296	270	3.00E-68	91.2	51.4	62.5	hypothetical protein CARUB_v10028056mg	gbpln	Capsella rubella	AT5G45220.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18298926-18301069 REVERSE LENGTH=546	296	546	5.00E-46	184.5	34.1	44.9

<table>
<tr><td>Rsa1.0_00091.1.g4578.t1</td><td>ref|XP_002862525.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308098|gb|EFH38783.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>180</td><td>497</td><td>9.00E-63</td><td>276.1</td><td>72.8</td><td>83.9</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G45210.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18295521-18298434 FORWARD LENGTH=697</td><td>180</td><td>697</td><td>2.00E-58</td><td>387.2</td><td>62.8</td><td>73.3</td></tr>
<tr><td>Rsa1.0_00091.1.g4579.t1</td><td>ref|XP_002863534.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309369|gb|EFH39793.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>2279</td><td>1360</td><td>0</td><td>59.7</td><td>35.1</td><td>40.3</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G45050.1 | Symbols: TTR1, ATWRKY16, WRKY16 | Disease resistance protein (TIR-NBS-LRR class) | chr5:18177016-18181805 REVERSE LENGTH=1372</td><td>2279</td><td>1372</td><td>0</td><td>60.2</td><td>34.3</td><td>39.5</td></tr>
<tr><td>Rsa1.0_00091.1.g4580.t1</td><td>dbj|BAH59426.1| putative disease resistance protein [Arabidopsis thaliana]</td><td>1207</td><td>1217</td><td>0</td><td>100.8</td><td>76.1</td><td>84.0</td><td>putative disease resistance protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G45250.1 | Symbols: RPS4 | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18321914-18326022 REVERSE LENGTH=1217</td><td>1207</td><td>1217</td><td>0</td><td>100.8</td><td>75.9</td><td>83.9</td></tr>
<tr><td>Rsa1.0_00091.1.g4581.t1</td><td>gb|AAD21699.1| Contains reverse transcriptase domain (rvt) PF|00078 [Arabidopsis thaliana]</td><td>1002</td><td>1253</td><td>1.00E-165</td><td>125.0</td><td>34.6</td><td>53.3</td><td>Contains reverse transcriptase domain (rvt) PF|00078</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1002</td><td>626</td><td>9.00E-57</td><td>62.5</td><td>13.1</td><td>21.2</td></tr>
<tr><td>Rsa1.0_00091.1.g4582.t1</td><td>gb|EOA13616.1| hypothetical protein CARUB_v10026683mg [Capsella rubella]</td><td>354</td><td>354</td><td>1.00E-165</td><td>100.0</td><td>80.5</td><td>90.4</td><td>hypothetical protein CARUB_v10026683mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G45310.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: stem, inflorescence meristem, root, leaf; EXPRESSED DURING: LP.04 four leaves visible; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:18359373-18360796 REVERSE LENGTH=352</td><td>354</td><td>352</td><td>1.00E-166</td><td>99.4</td><td>80.8</td><td>90.1</td></tr>
<tr><td>Rsa1.0_00091.1.g4583.t1</td><td>ref|XP_002868101.1| hypothetical protein ARALYDRAFT_915040 [Arabidopsis lyrata subsp. lyrata] gi|297313937|gb|EFH44360.1| hypothetical protein ARALYDRAFT_915040 [Arabidopsis lyrata subsp. lyrata]</td><td>322</td><td>495</td><td>1.00E-107</td><td>153.7</td><td>63.7</td><td>80.7</td><td>hypothetical protein ARALYDRAFT_915040</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G28020.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:9768395-9771157 REVERSE LENGTH=612</td><td>322</td><td>612</td><td>4.00E-42</td><td>190.1</td><td>33.5</td><td>50.0</td></tr>
<tr><td>Rsa1.0_00091.1.g4584.t1</td><td>ref|XP_002865271.1| hypothetical protein ARALYDRAFT_917000 [Arabidopsis lyrata subsp. lyrata] gi|297311106|gb|EFH41530.1| hypothetical protein ARALYDRAFT_917000 [Arabidopsis lyrata subsp. lyrata]</td><td>731</td><td>712</td><td>0</td><td>97.4</td><td>64.0</td><td>76.6</td><td>hypothetical protein ARALYDRAFT_917000</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36140.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr4:17098956-17104479 REVERSE LENGTH=1607</td><td>731</td><td>1607</td><td>1.00E-157</td><td>219.8</td><td>43.8</td><td>59.0</td></tr>
<tr><td>Rsa1.0_00091.1.g4585.t1</td><td>ref|XP_002863518.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309353|gb|EFH39777.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>1135</td><td>1150</td><td>0</td><td>101.3</td><td>70.8</td><td>82.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36150.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:17104776-17108711 FORWARD LENGTH=1179</td><td>1135</td><td>1179</td><td>0</td><td>103.9</td><td>49.3</td><td>65.5</td></tr>
<tr><td>Rsa1.0_00091.1.g4586.t1</td><td>ref|XP_002863489.1| hypothetical protein ARALYDRAFT_916947 [Arabidopsis lyrata subsp. lyrata] gi|297309324|gb|EFH39748.1| hypothetical protein ARALYDRAFT_916947 [Arabidopsis lyrata subsp. lyrata]</td><td>552</td><td>570</td><td>0</td><td>103.3</td><td>71.2</td><td>79.9</td><td>hypothetical protein ARALYDRAFT_916947</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G45330.1 | Symbols: DCP5-L | decapping 5-like | chr5:18363701-18366544 REVERSE LENGTH=571</td><td>552</td><td>571</td><td>0</td><td>103.4</td><td>65.9</td><td>73.0</td></tr>
<tr><td>Rsa1.0_00091.1.g4587.t1</td><td>gb|EOA13319.1| hypothetical protein CARUB_v10026354mg [Capsella rubella]</td><td>467</td><td>466</td><td>0</td><td>99.8</td><td>92.7</td><td>97.0</td><td>hypothetical protein CARUB_v10026354mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G45340.1 | Symbols: CYP707A3 | cytochrome P450, family 707, subfamily A, polypeptide 3 | chr5:18368977-18370909 REVERSE LENGTH=463</td><td>467</td><td>463</td><td>0</td><td>99.1</td><td>92.5</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00092.1.g4588.t1</td><td>dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]</td><td>804</td><td>1072</td><td>1.00E-179</td><td>133.3</td><td>40.4</td><td>58.1</td><td>non-LTR retroelement reverse transcriptase-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295</td><td>804</td><td>295</td><td>2.00E-74</td><td>36.7</td><td>17.8</td><td>24.0</td></tr>
<tr><td>Rsa1.0_00092.1.g4589.t2</td><td>gb|AAB96826.1| lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]</td><td>591</td><td>1064</td><td>0</td><td>180.0</td><td>83.4</td><td>88.8</td><td>lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G33150.2 | Symbols: | lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme | chr4:15985479-15991069 REVERSE LENGTH=1064</td><td>591</td><td>1064</td><td>0</td><td>180.0</td><td>83.4</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00092.1.g4590.t2</td><td>ref|NP_567913.1| 5' nucleotidase, deoxy (Pyrimidine), cytosolic type C protein domain containing protein-like protein [Arabidopsis thaliana] gi|15982925|gb|AAL09809.1| AT4g33140/F4I10_70 [Arabidopsis thaliana] gi|22137262|gb|AAM91476.1| AT4g33140/F4I10_70 [Arabidopsis thaliana] gi|332660780|gb|AEE86180.1| 5' nucleotidase, deoxy (Pyrimidine), cytosolic type C protein domain containing protein-like protein [Arabidopsis thaliana]</td><td>166</td><td>353</td><td>2.00E-77</td><td>212.7</td><td>79.5</td><td>86.1</td><td>5' nucleotidase, deoxy (Pyrimidine), cytosolic type C protein domain containing protein-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G33140.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr4:15981648-15984135 FORWARD LENGTH=353</td><td>166</td><td>353</td><td>9.00E-80</td><td>212.7</td><td>79.5</td><td>86.1</td></tr>
</table>

Rsa1.0_00092.1.g4591.t1	ref|XP_002867201.1| coclaurine N-methyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297313037|gb|EFH43460.1| coclaurine N-methyltransferase [Arabidopsis lyrata subsp. lyrata]	355	355	0	100.0	90.7	98.0	coclaurine N-methyltransferase	gbpln	Arabidopsis lyrata	AT4G33110.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:15972497-15974531 REVERSE LENGTH=355	355	355	0	100.0	87.6	96.9
Rsa1.0_00092.1.g4592.t1	ref|XP_002867210.1| hypothetical protein ARALYDRAFT_491387 [Arabidopsis lyrata subsp. lyrata] gi|297313046|gb|EFH43469.1| hypothetical protein ARALYDRAFT_491387 [Arabidopsis lyrata subsp. lyrata]	143	142	1.00E-62	99.3	86.7	89.5	hypothetical protein ARALYDRAFT_491387	gbpln	Arabidopsis lyrata	AT4G33040.1 | Symbols: | Thioredoxin superfamily protein | chr4:15940779-15941213 REVERSE LENGTH=144	143	144	9.00E-65	100.7	87.4	90.9
Rsa1.0_00092.1.g4593.t1	ref|XP_002869229.1| hypothetical protein ARALYDRAFT_491388 [Arabidopsis lyrata subsp. lyrata] gi|297315065|gb|EFH45488.1| hypothetical protein ARALYDRAFT_491388 [Arabidopsis lyrata subsp. lyrata]	479	475	0	99.2	94.2	96.7	hypothetical protein ARALYDRAFT_491388	gbpln	Arabidopsis lyrata	AT4G33030.1 | Symbols: SQD1 | sulfoquinovosyldiacylglycerol 1 | chr4:15936051-15937566 FORWARD LENGTH=477	479	477	0	99.6	94.2	97.1
Rsa1.0_00092.1.g4594.t1	gb|EOA17824.1| hypothetical protein CARUB_v10006225mg, partial [Capsella rubella]	250	241	1.00E-119	96.4	85.6	90.0	hypothetical protein CARUB_v10006225mg, partial	gbpln	Capsella rubella	AT4G33000.2 | Symbols: CBL10, SCABP8, ATCBL10 | calcineurin B-like protein 10 | chr4:15924821-15926398 FORWARD LENGTH=246	250	246	1.00E-121	98.4	85.2	90.0
Rsa1.0_00092.1.g4595.t1	ref|XP_002867215.1| hypothetical protein ARALYDRAFT_491396 [Arabidopsis lyrata subsp. lyrata] gi|297313051|gb|EFH43474.1| hypothetical protein ARALYDRAFT_491396 [Arabidopsis lyrata subsp. lyrata]	451	472	0	104.7	78.7	84.3	hypothetical protein ARALYDRAFT_491396	gbpln	Arabidopsis lyrata	AT4G32980.1 | Symbols: ATH1 | homeobox gene 1 | chr4:15914865-15916873 REVERSE LENGTH=473	451	473	0	104.9	76.7	83.4
Rsa1.0_00092.1.g4596.t1	ref|XP_002867217.1| hypothetical protein ARALYDRAFT_491398 [Arabidopsis lyrata subsp. lyrata] gi|297313053|gb|EFH43476.1| hypothetical protein ARALYDRAFT_491398 [Arabidopsis lyrata subsp. lyrata]	262	264	1.00E-129	100.8	84.0	89.3	hypothetical protein ARALYDRAFT_491398	gbpln	Arabidopsis lyrata	AT4G32960.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32970.1); Has 106 Blast hits to 106 proteins in 39 species: Archae - 0; Bacteria - 0; Metazoa - 62; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr4:15908785-15910141 REVERSE LENGTH=264	262	264	1.00E-131	100.8	83.6	88.5
Rsa1.0_00092.1.g4597.t1	ref|NP_195021.1| putative protein phosphatase 2C 61 [Arabidopsis thaliana] gi|75100739|sp|O82637.1|P2C61_ARATH RecName: Full=Probable protein phosphatase 2C 61; Short=AtPP2C61 gi|3688176|emb|CAA21204.1| putative protein [Arabidopsis thaliana] gi|7270242|emb|CAB80012.1| putative protein [Arabidopsis thaliana] gi|332660751|gb|AEE86151.1| putative protein phosphatase 2C 61 [Arabidopsis thaliana]	326	326	1.00E-164	100.0	84.4	91.1	putative protein phosphatase 2C 61	gbpln	Arabidopsis thaliana	AT4G32950.1 | Symbols: | Protein phosphatase 2C family protein | chr4:15904444-15906010 REVERSE LENGTH=326	326	326	1.00E-166	100.0	84.4	91.1
Rsa1.0_00092.1.g4598.t1	emb|CAA21202.1| putative protein [Arabidopsis thaliana] gi|7270240|emb|CAB80010.1| putative protein [Arabidopsis thaliana]	211	181	3.00E-86	85.8	76.3	78.2	putative protein	gbpln	Arabidopsis thaliana	AT4G32930.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF866, eukaryotic (InterPro:IPR008584); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15898878-15900185 FORWARD LENGTH=167	211	167	4.00E-87	79.1	75.4	76.8
Rsa1.0_00092.1.g4599.t1	ref|XP_002867220.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata] gi|297313056|gb|EFH43479.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	1405	1424	0	101.4	88.3	93.7	glycine-rich protein	gbpln	Arabidopsis lyrata	AT4G32920.3 | Symbols: | glycine-rich protein | chr4:15888153-15896006 REVERSE LENGTH=1432	1405	1432	0	101.9	88.5	94.0
Rsa1.0_00092.1.g4600.t1	gb|EOA17574.1| hypothetical protein CARUB_v10005935mg [Capsella rubella]	121	154	4.00E-33	127.3	61.2	66.9	hypothetical protein CARUB_v10005935mg	gbpln	Capsella rubella	AT4G32915.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: regulation of translational fidelity; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Glu-tRNAGln amidotransferase, C subunit (InterPro:IPR003837); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15885549-15886628 FORWARD LENGTH=155	121	155	1.00E-34	128.1	57.0	62.0

Rsa1.0_00092.1.g4601.t1	ref|XP_002869237.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297315073|gb|EFH45496.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	314	309	1.00E-126	98.4	75.5	82.2	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G32890.1 | Symbols: GATA9 | GATA transcription factor 9 | chr4:15875598-15876615 FORWARD LENGTH=308	314	308	1.00E-128	98.1	75.5	81.8
Rsa1.0_00092.1.g4602.t1	gb|ACS68190.1| cellulose synthase 1.2 catalytic subunit [Brassica napus]	1165	1083	0	93.0	91.9	92.2	cellulose synthase 1.2 catalytic subunit	gbpln	Brassica napus	AT4G32410.1 | Symbols: CESA1, RSW1, AtCESA1 | cellulose synthase 1 | chr4:15641009-15646388 REVERSE LENGTH=1081	1165	1081	0	92.8	87.7	90.0
Rsa1.0_00092.1.g4603.t2	gb|ACP30555.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1110	1074	0	96.8	77.5	85.0	disease resistance protein	gbpln	Brassica rapa	AT5G48770.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:19773277-19777242 REVERSE LENGTH=1190	1110	1190	0	107.2	44.0	57.4
Rsa1.0_00092.1.g4604.t1	gb|ACP30556.1| disease resistance protein [Brassica rapa subsp. pekinensis]	506	522	1.00E-171	103.2	65.8	75.3	disease resistance protein	gbpln	Brassica rapa	AT1G72870.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27421086-27422999 FORWARD LENGTH=512	506	512	3.00E-61	101.2	37.0	52.2
Rsa1.0_00092.1.g4605.t1	ref|XP_002869282.1| hypothetical protein ARALYDRAFT_491495 [Arabidopsis lyrata subsp. lyrata] gi|297315118|gb|EFH45541.1| hypothetical protein ARALYDRAFT_491495 [Arabidopsis lyrata subsp. lyrata]	424	437	1.00E-168	103.1	79.2	86.3	hypothetical protein ARALYDRAFT_491495	gbpln	Arabidopsis lyrata	AT4G32330.2 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr4:15609801-15611867 FORWARD LENGTH=436	424	436	1.00E-169	102.8	77.4	84.9
Rsa1.0_00092.1.g4606.t1	ref|XP_002869283.1| hypothetical protein ARALYDRAFT_913218 [Arabidopsis lyrata subsp. lyrata] gi|297315119|gb|EFH45542.1| hypothetical protein ARALYDRAFT_913218 [Arabidopsis lyrata subsp. lyrata]	303	329	1.00E-142	108.6	84.2	90.4	hypothetical protein ARALYDRAFT_913218	gbpln	Arabidopsis lyrata	AT4G32320.1 | Symbols: APX6 | ascorbate peroxidase 6 | chr4:15602777-15605234 FORWARD LENGTH=329	303	329	1.00E-144	108.6	83.5	90.4
Rsa1.0_00092.1.g4607.t1	ref|XP_002869284.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315120|gb|EFH45543.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	820	825	0	100.6	84.6	91.2	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT4G32300.1 | Symbols: SD2-5 | S-domain-2 5 | chr4:15599970-15602435 FORWARD LENGTH=821	820	821	0	100.1	83.3	90.2
Rsa1.0_00092.1.g4608.t1	ref|NP_680756.1| uncharacterized protein [Arabidopsis thaliana] gi|28392894|gb|AAO41883.1| unknown protein [Arabidopsis thaliana] gi|28827750|gb|AAO50719.1| unknown protein [Arabidopsis thaliana] gi|332660636|gb|AEE86036.1| uncharacterized protein AT4G32295 [Arabidopsis thaliana]	259	238	1.00E-108	91.9	78.8	83.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32295.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G24150.1); Has 39 Blast hits to 39 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15592960-15594080 FORWARD LENGTH=238	259	238	1.00E-110	91.9	78.8	83.4
Rsa1.0_00092.1.g4609.t1	ref|XP_002867248.1| hypothetical protein ARALYDRAFT_491501 [Arabidopsis lyrata subsp. lyrata] gi|297313084|gb|EFH43507.1| hypothetical protein ARALYDRAFT_491501 [Arabidopsis lyrata subsp. lyrata]	380	385	1.00E-176	101.3	81.3	89.5	hypothetical protein ARALYDRAFT_491501	gbpln	Arabidopsis lyrata	AT4G32290.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:15589839-15590993 REVERSE LENGTH=384	380	384	1.00E-172	101.1	80.3	89.7
Rsa1.0_00092.1.g4610.t2	ref|NP_567891.1| auxin-responsive protein IAA29 [Arabidopsis thaliana] gi|46395937|sp|Q93WC4.2|IAA29_ARATH RecName: Full=Auxin-responsive protein IAA29; AltName: Full=Indoleacetic acid-induced protein 29 gi|49616375|gb|AAT67084.1| IAA29 [Arabidopsis thaliana] gi|110739230|dbj|BAF01529.1| hypothetical protein [Arabidopsis thaliana] gi|225898845|dbj|BAH30553.1| hypothetical protein [Arabidopsis thaliana] gi|225898847|dbj|BAH30554.1| hypothetical protein [Arabidopsis thaliana] gi|332660632|gb|AEE86032.1| auxin-responsive protein IAA29 [Arabidopsis thaliana]	283	251	7.00E-89	88.7	63.6	71.4	auxin-responsive protein IAA29	gbpln	Arabidopsis thaliana	AT4G32280.1 | Symbols: IAA29 | indole-3-acetic acid inducible 29 | chr4:15583479-15584628 FORWARD LENGTH=251	283	251	2.00E-91	88.7	63.6	71.4
Rsa1.0_00092.1.g4611.t1	ref|XP_002867249.1| hypothetical protein ARALYDRAFT_491505 [Arabidopsis lyrata subsp. lyrata] gi|297313085|gb|EFH43508.1| hypothetical protein ARALYDRAFT_491505 [Arabidopsis lyrata subsp. lyrata]	337	342	1.00E-177	101.5	89.9	95.5	hypothetical protein ARALYDRAFT_491505	gbpln	Arabidopsis lyrata	AT4G32272.1 | Symbols: | Nucleotide/sugar transporter family protein | chr4:15577195-15579689 REVERSE LENGTH=344	337	344	1.00E-176	102.1	89.0	95.8

Rsa1.0_00092.1.g4612.t1	ref|NP_567888.2| Phox (PX) domain-containing protein [Arabidopsis thaliana] gi|332660612|gb|AEE86012.1| Phox (PX) domain-containing protein [Arabidopsis thaliana]	715	723	0	101.1	84.8	90.8	Phox (PX) domain-containing protein	gbpln	Arabidopsis thaliana	AT4G32160.1 | Symbols: | Phox (PX) domain-containing protein | chr4:15529056-15532892 FORWARD LENGTH=723	715	723	0	101.1	84.8	90.8
Rsa1.0_00092.1.g4613.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00092.1.g4614.t1	ref|XP_002867264.1| hypothetical protein ARALYDRAFT_353622 [Arabidopsis lyrata subsp. lyrata] gi|297313100|gb|EFH43523.1| hypothetical protein ARALYDRAFT_353622 [Arabidopsis lyrata subsp. lyrata]	120	127	6.00E-37	105.8	62.5	75.0	hypothetical protein ARALYDRAFT_353622	gbpln	Arabidopsis lyrata	AT4G32090.1 | Symbols: | Beta-1,3-N-Acetylglucosaminyltransferase family protein | chr4:15509990-15510820 REVERSE LENGTH=124	120	124	2.00E-38	103.3	62.5	74.2
Rsa1.0_00092.1.g4615.t1	gb|EOA16049.1| hypothetical protein CARUB_v10004180mg [Capsella rubella]	711	784	0	110.3	83.8	91.6	hypothetical protein CARUB_v10004180mg	gbpln	Capsella rubella	AT4G32070.1 | Symbols: Phox4 | Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein | chr4:15504662-15507097 REVERSE LENGTH=811	711	811	0	114.1	84.5	92.3
Rsa1.0_00092.1.g4616.t1	ref|NP_194932.1| homeobox protein knotted-1-like 5 [Arabidopsis thaliana] gi|12644283|sp|P48002.2|KNAT5_ARATH RecName: Full=Homeobox protein knotted-1-like 5; AltName: Full=Homeodomain-containing protein 1; AltName: Full=Protein KNAT5 gi|17224610|gb|AAL37042.1|AF306661_1 homeodomain transcription factor KNAT5 [Arabidopsis thaliana] gi|2506031|dbj|BAA22602.1| homeodomein containing protein 1 [Arabidopsis thaliana] gi|3858938|emb|CAA16585.1| homeodomain containing protein 1 [Arabidopsis thaliana] gi|7270108|emb|CAB79922.1| homeodomain containing protein 1 [Arabidopsis thaliana] gi|109946421|gb|ABG48389.1| At4g32040 [Arabidopsis thaliana] gi|332660597|gb|AEE85997.1| homeobox protein knotted-1-like 5 [Arabidopsis thaliana]	371	383	1.00E-171	103.2	85.7	91.4	homeobox protein knotted-1-like 5	gbpln	Arabidopsis thaliana	AT4G32040.1 | Symbols: KNAT5 | KNOTTED1-like homeobox gene 5 | chr4:15494127-15496009 FORWARD LENGTH=383	371	383	1.00E-174	103.2	85.7	91.4
Rsa1.0_00092.1.g4617.t1	ref|XP_002869297.1| hypothetical protein ARALYDRAFT_913253 [Arabidopsis lyrata subsp. lyrata] gi|297315133|gb|EFH45556.1| hypothetical protein ARALYDRAFT_913253 [Arabidopsis lyrata subsp. lyrata]	124	256	2.00E-41	206.5	73.4	82.3	hypothetical protein ARALYDRAFT_913253	gbpln	Arabidopsis lyrata	AT4G32030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80610.1); Has 63 Blast hits to 59 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 0; Plants - 53; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:15490903-15493007 FORWARD LENGTH=253	124	253	3.00E-43	204.0	75.0	83.9
Rsa1.0_00092.1.g4618.t1	gb|EOA15616.1| hypothetical protein CARUB_v10005750mg [Capsella rubella]	180	205	4.00E-61	113.9	76.7	82.8	hypothetical protein CARUB_v10005750mg	gbpln	Capsella rubella	AT4G32020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25250.1); Has 65 Blast hits to 65 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 8; Plants - 54; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15488076-15488621 FORWARD LENGTH=181	180	181	1.00E-52	100.6	70.6	75.0
Rsa1.0_00092.1.g4619.t1	gb|EOA16061.1| hypothetical protein CARUB_v10004194mg [Capsella rubella]	797	775	0	97.2	81.9	88.6	hypothetical protein CARUB_v10004194mg	gbpln	Capsella rubella	AT4G32010.1 | Symbols: HSL1, HSI2-L1, VAL2 | HSI2-like 1 | chr4:15481231-15484897 FORWARD LENGTH=780	797	780	0	97.9	81.9	88.1
Rsa1.0_00092.1.g4620.t1	ref|XP_002867266.1| hypothetical protein ARALYDRAFT_491537 [Arabidopsis lyrata subsp. lyrata] gi|297313102|gb|EFH43525.1| hypothetical protein ARALYDRAFT_491537 [Arabidopsis lyrata subsp. lyrata]	453	453	0	100.0	94.9	98.0	hypothetical protein ARALYDRAFT_491537	gbpln	Arabidopsis lyrata	AT4G31990.2 | Symbols: ASP5, AAT3, ATAAT1 | aspartate aminotransferase 5 | chr4:15471074-15473521 REVERSE LENGTH=453	453	453	0	100.0	94.3	97.6
Rsa1.0_00092.1.g4621.t1	emb|CBI21094.3| unnamed protein product [Vitis vinifera]	44	112	5.00E-16	254.5	93.2	97.7	unnamed protein product	gbpln	Vitis vinifera	AT4G31985.1 | Symbols: | Ribosomal protein L39 family protein | chr4:15469931-15470366 FORWARD LENGTH=51	44	51	4.00E-18	115.9	95.5	95.5

Rsa1.0_00092.1.g4622.t1	ref|XP_002867268.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297313104|gb|EFH43527.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	245	234	1.00E-107	95.5	77.6	85.3	mitochondrial glycoprotein family protein	gbpln	Arabidopsis lyrata	AT4G31930.1 | Symbols: | Mitochondrial glycoprotein family protein | chr4:15449710-15450804 REVERSE LENGTH=234	245	234	1.00E-107	95.5	75.9	83.7
Rsa1.0_00092.1.g4623.t1	dbj|BAJ34619.1| unnamed protein product [Thellungiella halophila]	516	539	0	104.5	81.2	87.2	unnamed protein product	----	----	AT4G31920.1 | Symbols: ARR10, RR10 | response regulator 10 | chr4:15444290-15446766 REVERSE LENGTH=552	516	552	0	107.0	75.6	83.5
Rsa1.0_00092.1.g4624.t1	ref|XP_002869305.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315141|gb|EFH45564.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	460	461	0	100.2	86.7	92.0	transferase family protein	gbpln	Arabidopsis lyrata	AT4G31910.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr4:15441125-15443696 FORWARD LENGTH=458	460	458	0	99.6	84.3	90.2
Rsa1.0_00092.1.g4625.t1	ref|XP_002878829.1| PKL/SSL2 [Arabidopsis lyrata subsp. lyrata] gi|297324668|gb|EFH55088.1| PKL/SSL2 [Arabidopsis lyrata subsp. lyrata]	666	1399	1.00E-132	210.1	34.8	41.3	PKL/SSL2	gbpln	Arabidopsis lyrata	AT2G25170.1 | Symbols: PKL, GYM, CHD3, CHR6, SSL2 | chromatin remodeling factor CHD3 (PICKLE) | chr2:10714411-10723763 FORWARD LENGTH=1384	666	1384	1.00E-135	207.8	34.7	41.4
Rsa1.0_00092.1.g4626.t1	ref|XP_002867272.1| hypothetical protein ARALYDRAFT_491547 [Arabidopsis lyrata subsp. lyrata] gi|297313108|gb|EFH43531.1| hypothetical protein ARALYDRAFT_491547 [Arabidopsis lyrata subsp. lyrata]	1040	864	0	83.1	33.0	37.4	hypothetical protein ARALYDRAFT_491547	gbpln	Arabidopsis lyrata	AT4G31880.2 | Symbols: | LOCATED IN: cytosol; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: Tudor/PWWP/MBT superfamily protein (TAIR:AT1G15940.1). | chr4:15419435-15423939 REVERSE LENGTH=872	1040	872	0	83.8	32.6	37.0
Rsa1.0_00092.1.g4627.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	678	536	2.00E-91	79.1	33.2	46.0	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	678	530	1.00E-47	78.2	12.4	15.3
Rsa1.0_00092.1.g4628.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00092.1.g4629.t1	gb|AAM12502.1|AF411209_1 glutathione peroxidase [Brassica napus]	223	232	1.00E-120	104.0	97.3	97.3	glutathione peroxidase	gbpln	Brassica napus	AT4G31870.1 | Symbols: ATGPX7, GPX7 | glutathione peroxidase 7 | chr4:15410205-15411617 FORWARD LENGTH=233	223	233	5.00E-91	104.5	76.2	83.0
Rsa1.0_00092.1.g4630.t1	gb|EOA16897.1| hypothetical protein CARUB_v10005121mg [Capsella rubella]	351	359	0	102.3	93.4	98.0	hypothetical protein CARUB_v10005121mg	gbpln	Capsella rubella	AT4G31860.1 | Symbols: | Protein phosphatase 2C family protein | chr4:15406685-15408589 REVERSE LENGTH=357	351	357	0	101.7	91.7	96.3
Rsa1.0_00092.1.g4631.t1	ref|NP_194913.1| proton gradient regulation 3 [Arabidopsis thaliana] gi|75213543|sp|Q9SZ52.1|PP344_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g31850, chloroplastic; AltName: Full=Protein PROTON GRADIENT REGULATION 3; Flags: Precursor gi|4584524|emb|CAB40755.1| putative protein [Arabidopsis thaliana] gi|7270088|emb|CAB79903.1| putative protein [Arabidopsis thaliana] gi|332660567|gb|AEE85967.1| proton gradient regulation 3 [Arabidopsis thaliana]	1107	1112	0	100.5	86.8	93.6	proton gradient regulation 3	gbpln	Arabidopsis thaliana	AT4G31850.1 | Symbols: PGR3 | proton gradient regulation 3 | chr4:15403020-15406358 FORWARD LENGTH=1112	1107	1112	0	100.5	86.8	93.6
Rsa1.0_00092.1.g4632.t1	ref|XP_002869310.1| hypothetical protein ARALYDRAFT_491553 [Arabidopsis lyrata subsp. lyrata] gi|297315146|gb|EFH45569.1| hypothetical protein ARALYDRAFT_491553 [Arabidopsis lyrata subsp. lyrata]	170	177	7.00E-69	104.1	82.9	87.1	hypothetical protein ARALYDRAFT_491553	gbpln	Arabidopsis lyrata	AT4G31840.1 | Symbols: ENODL15, AtENODL15 | early nodulin-like protein 15 | chr4:15401798-15402426 FORWARD LENGTH=177	170	177	2.00E-70	104.1	81.8	86.5
Rsa1.0_00092.1.g4633.t1	ref|XP_002867277.1| hypothetical protein ARALYDRAFT_913282 [Arabidopsis lyrata subsp. lyrata] gi|297313113|gb|EFH43536.1| hypothetical protein ARALYDRAFT_913282 [Arabidopsis lyrata subsp. lyrata]	85	100	2.00E-33	117.6	87.1	92.9	hypothetical protein ARALYDRAFT_913282	gbpln	Arabidopsis lyrata	AT4G31830.1 | Symbols: | unknown protein; Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15400803-15401105 REVERSE LENGTH=100	85	100	5.00E-36	117.6	87.1	91.8
Rsa1.0_00092.1.g4634.t1	ref|XP_002867283.1| hypothetical protein ARALYDRAFT_913296 [Arabidopsis lyrata subsp. lyrata] gi|297313119|gb|EFH43542.1| hypothetical protein ARALYDRAFT_913296 [Arabidopsis lyrata subsp. lyrata]	263	394	6.00E-55	149.8	43.3	52.9	hypothetical protein ARALYDRAFT_913296	gbpln	Arabidopsis lyrata	AT2G24645.1 | Symbols: | Transcriptional factor B3 family protein | chr2:10480728-10482650 REVERSE LENGTH=490	263	490	7.00E-31	186.3	37.6	55.1

Rsa1.0_00092.1.g4635.t13	ref|NP_198062.2| glutamate receptor 2.1 [Arabidopsis thaliana] gi|41017064|sp|O04660.2|GLR21_ARATH RecName: Full=Glutamate receptor 2.1; AltName: Full=Ligand-gated ion channel 2.1; Short=AtGLR3; Flags: Precursor gi|110735998|dbj|BAE99973.1| ion channel - like protein [Arabidopsis thaliana] gi|332006267|gb|AED93650.1| glutamate receptor 2.1 [Arabidopsis thaliana]	851	901	0	105.9	79.3	88.1	glutamate receptor 2.1	gbpln	Arabidopsis thaliana	AT5G27100.1 | Symbols: ATGLR2.1, GLR2.1 | glutamate receptor 2.1 | chr5:9535160-9538311 REVERSE LENGTH=901	851	901	0	105.9	79.3	88.1
Rsa1.0_00092.1.g4636.t1	gb|EOA16495.1| hypothetical protein CARUB_v10004653mg [Capsella rubella]	499	496	1.00E-156	99.4	60.9	69.7	hypothetical protein CARUB_v10004653mg	gbpln	Capsella rubella	AT4G31630.1 | Symbols: | Transcriptional factor B3 family protein | chr4:15325343-15327220 REVERSE LENGTH=512	499	512	1.00E-154	102.6	59.9	72.9
Rsa1.0_00092.1.g4637.t1	ref|NP_194887.1| putative xyloglucan glycosyltransferase 5 [Arabidopsis thaliana] gi|75201904|sp|Q9SB75.1|CSLC5_ARATH RecName: Full=Probable xyloglucan glycosyltransferase 5; AltName: Full=Cellulose synthase-like protein C5; Short=AtCslC5 gi|3281868|emb|CAA19764.1| putative protein [Arabidopsis thaliana] gi|7270062|emb|CAB79877.1| putative protein [Arabidopsis thaliana] gi|28058784|gb|AAO29953.1| putative protein [Arabidopsis thaliana] gi|30725520|gb|AAP37782.1| At4g31590 [Arabidopsis thaliana] gi|332660533|gb|AEE85933.1| putative xyloglucan glycosyltransferase 5 [Arabidopsis thaliana]	688	692	0	100.6	94.8	97.5	putative xyloglucan glycosyltransferase 5	gbpln	Arabidopsis thaliana	AT4G31590.1 | Symbols: ATCSLC05, CSLC05, ATCSLC5, CSLC5 | Cellulose-synthase-like C5 | chr4:15309889-15312336 REVERSE LENGTH=692	688	692	0	100.6	94.8	97.5
Rsa1.0_00092.1.g4638.t23	ref|NP_194885.2| uncharacterized protein [Arabidopsis thaliana] gi|332660530|gb|AEE85930.1| uncharacterized protein AT4G31570 [Arabidopsis thaliana]	2870	2730	0	95.1	72.3	79.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G31570.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24460.1); Has 194354 Blast hits to 66887 proteins in 3244 species: Archae - 3688; Bacteria - 38556; Metazoa - 84828; Fungi - 17265; Plants - 10589; Viruses - 805; Other Eukaryotes - 38623 (source: NCBI BLink). | chr4:15297061-15306036 FORWARD LENGTH=2730	2870	2730	0	95.1	72.3	79.3
Rsa1.0_00092.1.g4639.t1	ref|NP_194884.1| high chlorophyll fluorescence 153 protein [Arabidopsis thaliana] gi|11692862|gb|AAG40034.1|AF324683_1 AT4g31560 [Arabidopsis thaliana] gi|11908100|gb|AAG41479.1|AF326897_1 unknown protein [Arabidopsis thaliana] gi|12642912|gb|AAK00398.1|AF339716_1 unknown protein [Arabidopsis thaliana] gi|13926337|gb|AAK49632.1|AF372916_1 AT4g31560/F3L17_130 [Arabidopsis thaliana] gi|5262767|emb|CAB45915.1| putative protein [Arabidopsis thaliana] gi|7270059|emb|CAB79874.1| putative protein [Arabidopsis thaliana] gi|21592375|gb|AAM64326.1| unknown [Arabidopsis thaliana] gi|27363346|gb|AAO11592.1| At4g31560/F3L17_130 [Arabidopsis thaliana] gi|332660529|gb|AEE85929.1| high chlorophyll fluorescence 153 protein [Arabidopsis thaliana]	140	137	1.00E-50	97.9	75.7	81.4	high chlorophyll fluorescence 153 protein	gbpln	Arabidopsis thaliana	AT4G31560.1 | Symbols: HCF153 | high chlorophyll fluorescence 153 | chr4:15295219-15296028 FORWARD LENGTH=137	140	137	3.00E-53	97.9	75.7	81.4
Rsa1.0_00092.1.g4640.t1	emb|CAB43904.1| putative protein [Arabidopsis thaliana] gi|7269745|emb|CAB81478.1| putative protein [Arabidopsis thaliana]	1132	1415	0	125.0	55.9	71.5	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1132	1262	4.00E-35	111.5	6.3	9.0
Rsa1.0_00092.1.g4641.t1	gb|ACQ76798.1| WRKY transcription factor 11 [Brassica napus]	462	327	2.33E-156	70.8	56.7	62.1	WRKY transcription factor 11	gbpln	Brassica napus	AT4G31550.2 | Symbols: WRKY11, ATWRKY11 | WRKY DNA-binding protein 11 | chr4:15290065-15291458 REVERSE LENGTH=324	462	324	1.00E-142	70.1	55.0	61.5
Rsa1.0_00092.1.g4642.t1	ref|XP_002869322.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315158|gb|EFH45581.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata]	327	324	1.00E-142	99.1	84.4	89.9	catalytic/ coenzyme binding protein	gbpln	Arabidopsis lyrata	AT4G31530.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:15282281-15284064 FORWARD LENGTH=324	327	324	1.00E-144	99.1	85.0	89.9

Rsa1.0_00092.1.g4643.t1	ref|NP_172767.1| cytochrome P450 71B2 [Arabidopsis thaliana] gi|38503391|sp|O65788.2|C71B2_ARATH RecName: Full=Cytochrome P450 71B2 gi|4850391|gb|AAD31061.1|AC007357_10 Identical to gb|D78605 cytochrome P450 monooxygenase from Arabidopsis thaliana and is a member of the PF|00067 Cytochrome P450 family. ESTs gb|Z18072, gb|Z35218 and gb|T43466 come from this gene [Arabidopsis thaliana] gi|28392854|gb|AAO41864.1| putative cytochrome P450 monooxygenase [Arabidopsis thaliana] gi|332190846|gb|AEE28967.1| cytochrome P450 71B2 [Arabidopsis thaliana]	512	502	0	98.0	72.9	83.0	cytochrome P450 71B2	gbpln	Arabidopsis thaliana	AT1G13080.1 | Symbols: CYP71B2 | cytochrome P450, family 71, subfamily B, polypeptide 2 | chr1:4459212-4460807 FORWARD LENGTH=502	512	502	0	98.0	72.9	83.0
Rsa1.0_00092.1.g4644.t1	ref|XP_002867298.1| hypothetical protein ARALYDRAFT_491586 [Arabidopsis lyrata subsp. lyrata] gi|297313134|gb|EFH43557.1| hypothetical protein ARALYDRAFT_491586 [Arabidopsis lyrata subsp. lyrata]	222	202	3.00E-52	91.0	64.4	71.6	hypothetical protein ARALYDRAFT_491586	gbpln	Arabidopsis lyrata	AT4G31510.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24550.1); Has 205 Blast hits to 205 proteins in 31 species: Archae - 0; Bacteria - 0; Metazoa - 5; Fungi - 3; Plants - 187; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr4:15276328-15277219 REVERSE LENGTH=214	222	214	8.00E-53	96.4	64.4	73.9
Rsa1.0_00092.1.g4645.t1	gb|EOA15441.1| hypothetical protein CARUB_v10004083mg [Capsella rubella]	948	948	0	100.0	96.8	98.5	hypothetical protein CARUB_v10004083mg	gbpln	Capsella rubella	AT4G31480.2 | Symbols: | Coatomer, beta subunit | chr4:15264145-15267384 FORWARD LENGTH=948	948	948	0	100.0	96.6	98.2
Rsa1.0_00092.1.g4646.t1	gb|EOA17929.1| hypothetical protein CARUB_v10006338mg [Capsella rubella]	183	186	7.00E-85	101.6	84.2	90.7	hypothetical protein CARUB_v10006338mg	gbpln	Capsella rubella	AT4G31470.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:15261746-15262303 REVERSE LENGTH=185	183	185	1.00E-82	101.1	82.5	88.5
Rsa1.0_00092.1.g4647.t1	ref|XP_002867302.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297313138|gb|EFH43561.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	448	499	1.00E-174	111.4	81.0	86.6	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G31450.1 | Symbols: | RING/U-box superfamily protein | chr4:15255955-15257977 REVERSE LENGTH=497	448	497	1.00E-169	110.9	79.2	85.0
Rsa1.0_00092.1.g4648.t1	gb|EOA18912.1| hypothetical protein CARUB_v10007542mg [Capsella rubella]	351	404	1.00E-126	115.1	72.9	82.6	hypothetical protein CARUB_v10007542mg	gbpln	Capsella rubella	AT4G31440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24530.1); Has 210 Blast hits to 209 proteins in 55 species: Archae - 0; Bacteria - 72; Metazoa - 2; Fungi - 6; Plants - 128; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:15253731-15254870 FORWARD LENGTH=379	351	379	1.00E-115	108.0	68.4	76.4
Rsa1.0_00092.1.g4649.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00092.1.g4650.t1	gb|EOA16535.1| hypothetical protein CARUB_v10004695mg [Capsella rubella]	488	484	0	99.2	84.4	92.0	hypothetical protein CARUB_v10004695mg	gbpln	Capsella rubella	AT4G31140.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr4:15141581-15143188 FORWARD LENGTH=484	488	484	0	99.2	83.2	92.0
Rsa1.0_00092.1.g4651.t1	gb|EOA18616.1| hypothetical protein CARUB_v10007189mg [Capsella rubella]	638	642	0	100.6	93.3	96.4	hypothetical protein CARUB_v10007189mg	gbpln	Capsella rubella	AT4G31120.1 | Symbols: SKB1, ATPRMT5 | SHK1 binding protein 1 | chr4:15132185-15136568 REVERSE LENGTH=642	638	642	0	100.6	91.7	95.9
Rsa1.0_00092.1.g4652.t4	ref|NP_849478.1| uncharacterized protein [Arabidopsis thaliana] gi|19310420|gb|AAL84947.1| AT4g31110/F6E21_30 [Arabidopsis thaliana] gi|21436035|gb|AAM51595.1| AT4g31110/F6E21_30 [Arabidopsis thaliana] gi|332660458|gb|AEE85858.1| uncharacterized protein AT4G31115 [Arabidopsis thaliana]	275	250	4.00E-99	90.9	73.5	78.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G31115.1 | Symbols: | Protein of unknown function (DUF1997) | chr4:15130243-15131847 FORWARD LENGTH=250	275	250	1.00E-101	90.9	73.5	78.5
Rsa1.0_00092.1.g4653.t1	gb|EOA15750.1| hypothetical protein CARUB_v10006795mg [Capsella rubella]	764	806	0	105.5	69.5	78.8	hypothetical protein CARUB_v10006795mg	gbpln	Capsella rubella	AT4G31100.1 | Symbols: | wall-associated kinase, putative | chr4:15123862-15126426 FORWARD LENGTH=786	764	786	0	102.9	66.9	77.7
Rsa1.0_00092.1.g4654.t1	ref|XP_002867315.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297313151|gb|EFH43574.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	600	598	0	99.7	79.3	87.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G31070.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:15118696-15120537 REVERSE LENGTH=613	600	613	0	102.2	76.5	85.3

<table>
<tr><td>Rsa1.0_00092.1.g4655.t1</td><td>ref|XP_002867317.1| hypothetical protein ARALYDRAFT_328615 [Arabidopsis lyrata subsp. lyrata] gi|297313153|gb|EFH43576.1| hypothetical protein ARALYDRAFT_328615 [Arabidopsis lyrata subsp. lyrata]</td><td>294</td><td>294</td><td>1.00E-163</td><td>100.0</td><td>92.9</td><td>96.9</td><td>hypothetical protein ARALYDRAFT_328615</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G31020.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:15108832-15110079 REVERSE LENGTH=294</td><td>294</td><td>294</td><td>1.00E-165</td><td>100.0</td><td>92.5</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00092.1.g4656.t1</td><td>ref|XP_002869353.1| hypothetical protein ARALYDRAFT_353720 [Arabidopsis lyrata subsp. lyrata] gi|297315189|gb|EFH45612.1| hypothetical protein ARALYDRAFT_353720 [Arabidopsis lyrata subsp. lyrata]</td><td>2637</td><td>2855</td><td>0</td><td>108.3</td><td>72.8</td><td>83.5</td><td>hypothetical protein ARALYDRAFT_353720</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G30990.1 | Symbols: | ARM repeat superfamily protein | chr4:15084456-15097860 FORWARD LENGTH=2599</td><td>2637</td><td>2599</td><td>0</td><td>98.6</td><td>72.4</td><td>83.2</td></tr>
<tr><td>Rsa1.0_00092.1.g4657.t1</td><td>ref|NP_194825.1| CBL-interacting serine/threonine-protein kinase 6 [Arabidopsis thaliana] gi|75318580|sp|O65554.1|CIPK6_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 6; AltName: Full=SNF1-related kinase 3.14; AltName: Full=SOS2-like protein kinase PKS4; AltName: Full=SOS3-interacting protein 3 gi|9280634|gb|AAF86505.1|AF285106_1 CBL-interacting protein kinase 6 [Arabidopsis thaliana] gi|13448033|gb|AAK26843.1|AF339145_1 SOS2-like protein kinase PKS4 [Arabidopsis thaliana] gi|16930695|gb|AAL32013.1|AF436831_1 AT4g30960/F6I18_130 [Arabidopsis thaliana] gi|2980770|emb|CAA18197.1| putative protein kinase [Arabidopsis thaliana] gi|7269998|emb|CAB79814.1| putative protein kinase [Arabidopsis thaliana] gi|14334746|gb|AAK59551.1| putative protein kinase [Arabidopsis thaliana] gi|15293235|gb|AAK93728.1| putative protein kinase [Arabidopsis thaliana] gi|332660435|gb|AEE85835.1| CBL-interacting serine/threonine-protein kinase 6 [Arabidopsis thaliana]</td><td>432</td><td>441</td><td>0</td><td>102.1</td><td>90.0</td><td>96.1</td><td>CBL-interacting serine/threonine-protein kinase 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G30960.1 | Symbols: CIPK6, SIP3, SNRK3.14, ATCIPK6 | SOS3-interacting protein 3 | chr4:15067400-15068725 FORWARD LENGTH=441</td><td>432</td><td>441</td><td>0</td><td>102.1</td><td>90.0</td><td>96.1</td></tr>
<tr><td>Rsa1.0_00092.1.g4658.t1</td><td>ref|NP_001184904.1| uncharacterized protein [Arabidopsis thaliana] gi|332189512|gb|AEE27633.1| uncharacterized protein AT1G03910 [Arabidopsis thaliana]</td><td>454</td><td>716</td><td>1.00E-111</td><td>157.7</td><td>50.7</td><td>54.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G03910.2 | Symbols: | EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Cactin protein, cactus-binding domain, C-terminal (InterPro:IPR019134), Cactin, central region (InterPro:IPR018816); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G36815.2). | chr1:996432-1000231 FORWARD LENGTH=716</td><td>454</td><td>716</td><td>1.00E-114</td><td>157.7</td><td>50.7</td><td>54.2</td></tr>
<tr><td>Rsa1.0_00092.1.g4659.t1</td><td>ref|XP_002867320.1| hypothetical protein ARALYDRAFT_328625 [Arabidopsis lyrata subsp. lyrata] gi|297313156|gb|EFH43579.1| hypothetical protein ARALYDRAFT_328625 [Arabidopsis lyrata subsp. lyrata]</td><td>559</td><td>770</td><td>1.00E-138</td><td>137.7</td><td>47.8</td><td>52.4</td><td>hypothetical protein ARALYDRAFT_328625</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G30935.1 | Symbols: WRKY32, ATWRKY32 | WRKY DNA-binding protein 32 | chr4:15051916-15053908 REVERSE LENGTH=466</td><td>559</td><td>466</td><td>1.00E-140</td><td>83.4</td><td>47.4</td><td>51.9</td></tr>
<tr><td>Rsa1.0_00092.1.g4660.t2</td><td>ref|NP_567861.1| 50S ribosomal protein L21 [Arabidopsis thaliana] gi|29839556|sp|Q8L9A0.1|RM21_ARATH RecName: Full=50S ribosomal protein L21, mitochondrial; Flags: Precursor gi|12641613|emb|CAC27453.1| putative ribosomal protein L21 [Arabidopsis thaliana] gi|21595368|gb|AAM66095.1| unknown [Arabidopsis thaliana] gi|29028852|gb|AAO64805.1| At4g30930 [Arabidopsis thaliana] gi|110736393|dbj|BAF00165.1| hypothetical protein [Arabidopsis thaliana] gi|225898835|dbj|BAH30548.1| hypothetical protein [Arabidopsis thaliana] gi|332660431|gb|AEE85831.1| 50S ribosomal protein L21 [Arabidopsis thaliana]</td><td>263</td><td>270</td><td>1.00E-103</td><td>102.7</td><td>82.9</td><td>86.7</td><td>50S ribosomal protein L21</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G30930.1 | Symbols: NFD1 | Ribosomal protein L21 | chr4:15050170-15051630 REVERSE LENGTH=270</td><td>263</td><td>270</td><td>1.00E-105</td><td>102.7</td><td>82.9</td><td>86.7</td></tr>
</table>

Rsa1.0_00092.1.g4661.t1	ref|XP_002867326.1| hypothetical protein ARALYDRAFT_491666 [Arabidopsis lyrata subsp. lyrata] gi|297313162|gb|EFH43585.1| hypothetical protein ARALYDRAFT_491666 [Arabidopsis lyrata subsp. lyrata]	362	360	1.00E−180	99.4	84.0	91.4	hypothetical protein ARALYDRAFT_491666	gbpln	Arabidopsis lyrata	AT4G30850.2 | Symbols: HHP2 | heptahelical transmembrane protein2 | chr4:15020540−15022278 REVERSE LENGTH=358	362	358	1.00E−180	98.9	83.1	91.4
Rsa1.0_00092.1.g4662.t1	dbj|BAJ33617.1| unnamed protein product [Thellungiella halophila]	123	121	2.00E−47	98.4	79.7	87.8	unnamed protein product	−−−−	−−−−	AT4G30845.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 16 Blast hits to 16 proteins in 8 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 16; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr4:15019895−15020319 FORWARD LENGTH=114	123	114	3.00E−42	92.7	74.0	83.7
Rsa1.0_00092.1.g4663.t6	gb|EOA15356.1| hypothetical protein CARUB_v10005095mg [Capsella rubella]	412	366	1.00E−142	88.8	66.0	76.2	hypothetical protein CARUB_v10005095mg	gbpln	Capsella rubella	AT4G30830.1 | Symbols: | Protein of unknown function, DUF593 | chr4:15015506−15016683 REVERSE LENGTH=363	412	363	1.00E−143	88.1	64.8	76.2
Rsa1.0_00092.1.g4664.t1	ref|NP_567854.1| carboxypeptidase D [Arabidopsis thaliana] gi|75332010|sp|Q949Q7.1|SCP29_ARATH RecName: Full=Serine carboxypeptidase−like 29; Flags: Precursor gi|15293049|gb|AAK93635.1| putative serine carboxypeptidase II [Arabidopsis thaliana] gi|22136958|gb|AAM91708.1| putative serine carboxypeptidase II [Arabidopsis thaliana] gi|332660411|gb|AEE85811.1| serine carboxypeptidase−like 29 [Arabidopsis thaliana]	479	479	0	100.0	80.8	88.1	carboxypeptidase D	gbpln	Arabidopsis thaliana	AT4G30810.1 | Symbols: scpl29 | serine carboxypeptidase−like 29 | chr4:15003474−15006017 FORWARD LENGTH=479	479	479	0	100.0	80.8	88.1
Rsa1.0_00092.1.g4665.t1	gb|EOA29140.1| hypothetical protein CARUB_v10025409mg [Capsella rubella]	272	549	1.00E−17	201.8	22.4	41.2	hypothetical protein CARUB_v10025409mg	gbpln	Capsella rubella	AT3G11870.1 | Symbols: | Endoribonuclease/protein kinase IRE1−like | chr3:3746998−3749093 REVERSE LENGTH=554	272	554	1.00E−15	203.7	21.3	42.6
Rsa1.0_00092.1.g4666.t1	ref|NP_194808.1| uncharacterized protein [Arabidopsis thaliana] gi|5725443|emb|CAB52452.1| putative protein [Arabidopsis thaliana] gi|7269980|emb|CAB79797.1| putative protein [Arabidopsis thaliana] gi|332660409|gb|AEE85809.1| uncharacterized protein AT4G30790 [Arabidopsis thaliana]	1129	1148	0	101.7	85.1	91.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G30790.1 | Symbols: | INVOLVED IN: autophagy; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Autophagy−related protein 17 (InterPro:IPR007240), Autophagy−related protein 11 (InterPro:IPR019460); Has 8793 Blast hits to 6268 proteins in 570 species: Archae − 89; Bacteria − 657; Metazoa − 4844; Fungi − 808; Plants − 441; Viruses − 15; Other Eukaryotes − 1939 (source: NCBI BLink). | chr4:14993383−14997785 REVERSE LENGTH=1148	1129	1148	0	101.7	85.1	91.5
Rsa1.0_00092.1.g4667.t1	ref|XP_002869363.1| hypothetical protein ARALYDRAFT_491676 [Arabidopsis lyrata subsp. lyrata] gi|297315199|gb|EFH45622.1| hypothetical protein ARALYDRAFT_491676 [Arabidopsis lyrata subsp. lyrata]	562	587	0	104.4	83.8	89.9	hypothetical protein ARALYDRAFT_491676	gbpln	Arabidopsis lyrata	AT4G30780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24100.1); Has 109 Blast hits to 109 proteins in 18 species: Archae − 0; Bacteria − 0; Metazoa − 1; Fungi − 0; Plants − 95; Viruses − 0; Other Eukaryotes − 13 (source: NCBI BLink). | chr4:14990523−14992855 FORWARD LENGTH=589	562	589	0	104.8	83.3	89.7
Rsa1.0_00092.1.g4668.t1	ref|XP_002867329.1| hypothetical protein ARALYDRAFT_913400 [Arabidopsis lyrata subsp. lyrata] gi|297313165|gb|EFH43588.1| hypothetical protein ARALYDRAFT_913400 [Arabidopsis lyrata subsp. lyrata]	154	157	5.00E−72	101.9	86.4	94.2	hypothetical protein ARALYDRAFT_913400	gbpln	Arabidopsis lyrata	AT4G30770.1 | Symbols: | Putative membrane lipoprotein | chr4:14986140−14986613 REVERSE LENGTH=157	154	157	5.00E−68	101.9	85.7	93.5

Rsa1.0_00092.1.g4669.t1	ref|NP_194781.2| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|75331150|sp|Q8VYT3.1|Y4052_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g30520; Flags: Precursor gi|17979065|gb|AAL49800.1| putative receptor kinase homolog [Arabidopsis thaliana] gi|20465457|gb|AAM20188.1| putative receptor kinase-like protein [Arabidopsis thaliana] gi|224589641|gb|ACN59353.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332660376|gb|AEE85776.1| probable LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	653	648	0	99.2	90.5	94.3	leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT4G30520.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:14908193-14911040 REVERSE LENGTH=648	653	648	0	99.2	90.5	94.3
Rsa1.0_00092.1.g4670.t1	sp|Q8H1Q8.2|AT18B_ARATH RecName: Full=Autophagy-related protein 18b; Short=AtATG18b	361	366	0	101.4	91.7	95.8	RecName: Full=Autophagy-related protein 18b; Short=AtATG18b	----	----	AT4G30510.1 | Symbols: ATATG18B, ATG18B, G18B | homolog of yeast autophagy 18 (ATG18) B | chr4:14905299-14906915 REVERSE LENGTH=312	361	312	1.00E-169	86.4	79.8	83.4
Rsa1.0_00092.1.g4671.t1	gb|AAM61727.1| unknown [Arabidopsis thaliana]	187	173	4.00E-80	92.5	78.6	85.0	unknown	gbpln	Arabidopsis thaliana	AT2G23940.1 | Symbols: | Protein of unknown function (DUF788) | chr2:10184199-10185097 FORWARD LENGTH=173	187	173	3.00E-82	92.5	78.1	85.0
Rsa1.0_00092.1.g4672.t1	ref|XP_002867344.1| hypothetical protein ARALYDRAFT_491701 [Arabidopsis lyrata subsp. lyrata] gi|297313180|gb|EFH43603.1| hypothetical protein ARALYDRAFT_491701 [Arabidopsis lyrata subsp. lyrata]	500	497	0	99.4	89.2	95.6	hypothetical protein ARALYDRAFT_491701	gbpln	Arabidopsis lyrata	AT4G30490.1 | Symbols: | AFG1-like ATPase family protein | chr4:14899226-14901883 REVERSE LENGTH=497	500	497	0	99.4	88.0	94.6
Rsa1.0_00092.1.g4673.t1	ref|NP_194777.3| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana] gi|7269949|emb|CAB79766.1| putative protein [Arabidopsis thaliana] gi|222422923|dbj|BAH19448.1| AT4G30480 [Arabidopsis thaliana] gi|332660370|gb|AEE85770.1| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana]	282	277	1.00E-109	98.2	77.3	83.3	tetratricopeptide repeat domain-containing protein	gbpln	Arabidopsis thaliana	AT4G30480.2 | Symbols: TPR1, AtTPR1 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:14897500-14898937 FORWARD LENGTH=277	282	277	1.00E-111	98.2	77.3	83.3
Rsa1.0_00092.1.g4674.t1	dbj|BAJ34378.1| unnamed protein product [Thellungiella halophila]	303	303	1.00E-169	100.0	95.7	97.0	unnamed protein product	----	----	AT4G30470.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:14894263-14896506 FORWARD LENGTH=303	303	303	1.00E-167	100.0	96.0	97.4
Rsa1.0_00092.1.g4675.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00092.1.g4676.t1	ref|XP_002881484.1| RNA polymerase sigma-70 factor [Arabidopsis lyrata subsp. lyrata] gi|297327323|gb|EFH57743.1| RNA polymerase sigma-70 factor [Arabidopsis lyrata subsp. lyrata]	145	546	9.00E-33	376.6	48.3	51.7	RNA polymerase sigma-70 factor	gbpln	Arabidopsis lyrata	AT2G36990.1 | Symbols: SIGF, SIG6, ATSIG6, SOLDAT8 | RNApolymerase sigma-subunit F | chr2:15537502-15540016 REVERSE LENGTH=547	145	547	8.00E-35	377.2	47.6	51.7
Rsa1.0_00092.1.g4677.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00092.1.g4678.t1	ref|NP_194773.1| UDP-D-glucuronate 4-epimerase 1 [Arabidopsis thaliana] gi|297798928|ref|XP_002867348.1| UDP-D-glucuronate 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata] gi|75311748|sp|Q9M0B6.1|GAE1_ARATH RecName: Full=UDP-glucuronate 4-epimerase 1; AltName: Full=UDP-glucuronic acid epimerase 1; Short=AtUGlcAE3 gi|7269945|emb|CAB79762.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|15810529|gb|AAL07152.1| putative nucleotide sugar epimerase [Arabidopsis thaliana] gi|20466778|gb|AAM20706.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|21553636|gb|AAM62729.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|23198200|gb|AAN15627.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|50429331|gb|AAT77233.1| UDP-D-glucuronate 4-epimerase [Arabidopsis thaliana] gi|297313184|gb|EFH43607.1| UDP-D-glucuronate 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata] gi|332660365|gb|AEE85765.1| UDP-D-glucuronate 4-epimerase 1 [Arabidopsis thaliana] gi|385137886|gb|AFI41204.1| UDP-D-glucuronate 4-epimerase 1	429	429	0	100.0	97.9	98.6	UDP-D-glucuronate 4-epimerase 1	gbpln	Arabidopsis lyrata	AT4G30440.1 | Symbols: GAE1 | UDP-D-glucuronate 4-epimerase 1 | chr4:14881976-14883265 REVERSE LENGTH=429	429	429	0	100.0	97.9	98.6
Rsa1.0_00092.1.g4679.t1	ref|XP_002869378.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315214|gb|EFH45637.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	353	371	1.00E-163	105.1	78.5	89.5	predicted protein	gbpln	Arabidopsis lyrata	AT4G30420.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:14877069-14878914 FORWARD LENGTH=373	353	373	1.00E-163	105.7	77.3	88.1
Rsa1.0_00093.1.g4680.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00093.1.g4681.t1	gb|EOA38661.1| hypothetical protein CARUB_v10010598mg [Capsella rubella]	141	140	4.00E-68	99.3	92.2	93.6	hypothetical protein CARUB_v10010598mg	gbpln	Capsella rubella	AT1G10590.3 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:3502324-3503033 REVERSE LENGTH=153	141	153	4.00E-69	108.5	90.8	95.0
Rsa1.0_00093.1.g4682.t1	ref|NP_172531.2| transcription factor bHLH90 [Arabidopsis thaliana] gi|122229969|sp|Q0WNR2.1|BH090_ARATH RecName: Full=Transcription factor bHLH90; AltName: Full=Basic helix-loop-helix protein 90; Short=AtbHLH90; Short=bHLH 90; AltName: Full=Transcription factor EN 50; AltName: Full=bHLH transcription factor bHLH090 gi|110738624|dbj|BAF01237.1| putative bHLH transcription factor bHLH090 [Arabidopsis thaliana] gi|332190488|gb|AEE28609.1| transcription factor bHLH90 [Arabidopsis thaliana]	386	441	1.00E-153	114.2	74.9	84.2	transcription factor bHLH90	gbpln	Arabidopsis thaliana	AT1G10610.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:3506463-3508752 FORWARD LENGTH=441	386	441	1.00E-156	114.2	74.9	84.2
Rsa1.0_00093.1.g4683.t1	ref|NP_172532.1| protein kinase-like protein [Arabidopsis thaliana] gi|310947344|sp|Q9SGY7.2|PEK11_ARATH RecName: Full=Putative proline-rich receptor-like protein kinase PERK11; AltName: Full=Proline-rich extensin-like receptor kinase 11; Short=AtPERK11 gi|332190489|gb|AEE28610.1| putative proline-rich receptor-like protein kinase PERK11 [Arabidopsis thaliana]	627	718	0	114.5	75.9	82.6	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G10620.1 | Symbols: | Protein kinase superfamily protein | chr1:3509001-3511975 REVERSE LENGTH=718	627	718	0	114.5	75.9	82.6
Rsa1.0_00093.1.g4684.t1	gb|EOA40072.1| hypothetical protein CARUB_v10008765mg [Capsella rubella]	533	549	0	103.0	87.4	94.0	hypothetical protein CARUB_v10008765mg	gbpln	Capsella rubella	AT1G10640.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:3515478-3517807 REVERSE LENGTH=532	533	532	0	99.8	86.7	94.2
Rsa1.0_00093.1.g4685.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	628	627	3.00E-65	99.8	23.7	34.7	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00093.1.g4686.t1	gb|AAM61038.1| S-ribonuclease binding protein SBP1, putative [Arabidopsis thaliana]	348	337	1.00E-155	96.8	79.9	85.9	S-ribonuclease binding protein SBP1, putative	gbpln	Arabidopsis thaliana	AT1G10650.1 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr1:3524122-3525318 REVERSE LENGTH=339	348	339	1.00E-155	97.4	80.5	86.5

<table>
<tr><td>Rsa1.0_00093.1.g4687.t1</td><td>ref|XP_002889822.1| hypothetical protein ARALYDRAFT_471189 [Arabidopsis lyrata subsp. lyrata] gi|297335664|gb|EFH66081.1| hypothetical protein ARALYDRAFT_471189 [Arabidopsis lyrata subsp. lyrata]</td><td>102</td><td>101</td><td>8.00E-47</td><td>99.0</td><td>86.3</td><td>93.1</td><td>hypothetical protein ARALYDRAFT_471189</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10657.2 | Symbols: | Plant protein 1589 of unknown function | chr1:3530652-3531522 FORWARD LENGTH=101</td><td>102</td><td>101</td><td>1.00E-48</td><td>99.0</td><td>85.3</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00093.1.g4688.t1</td><td>ref|XP_002889823.1| hypothetical protein ARALYDRAFT_888344 [Arabidopsis lyrata subsp. lyrata] gi|297335665|gb|EFH66082.1| hypothetical protein ARALYDRAFT_888344 [Arabidopsis lyrata subsp. lyrata]</td><td>268</td><td>319</td><td>1.00E-112</td><td>119.0</td><td>75.4</td><td>79.1</td><td>hypothetical protein ARALYDRAFT_888344</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10660.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G62960.1); Has 155 Blast hits to 154 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 10; Fungi - 4; Plants - 139; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:3533009-3534781 FORWARD LENGTH=320</td><td>268</td><td>320</td><td>1.00E-108</td><td>119.4</td><td>74.6</td><td>79.5</td></tr>
<tr><td>Rsa1.0_00093.1.g4689.t1</td><td>ref|NP_172538.1| ABC transporter B family member 10 [Arabidopsis thaliana] gi|229470217|sp|Q9SGY1.2|AB10B_ARATH RecName: Full=ABC transporter B family member 10; Short=ABC transporter ABCB.10; Short=AtABCB10; AltName: Full=Multidrug resistance protein 10; AltName: Full=P-glycoprotein 10 gi|332190507|gb|AEE28628.1| ABC transporter B family member 10 [Arabidopsis thaliana]</td><td>497</td><td>1227</td><td>0</td><td>246.9</td><td>90.7</td><td>96.0</td><td>ABC transporter B family member 10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10680.1 | Symbols: PGP10 | P-glycoprotein 10 | chr1:3538470-3543782 REVERSE LENGTH=1227</td><td>497</td><td>1227</td><td>0</td><td>246.9</td><td>90.7</td><td>96.0</td></tr>
<tr><td>Rsa1.0_00093.1.g4690.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1366</td><td>1307</td><td>0</td><td>95.7</td><td>58.4</td><td>73.9</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1366</td><td>1262</td><td>1.00E-104</td><td>92.4</td><td>14.5</td><td>22.2</td></tr>
<tr><td>Rsa1.0_00093.1.g4691.t1</td><td>ref|XP_002892589.1| P-glycoprotein 10 [Arabidopsis lyrata subsp. lyrata] gi|297338431|gb|EFH68848.1| P-glycoprotein 10 [Arabidopsis lyrata subsp. lyrata]</td><td>718</td><td>1229</td><td>0</td><td>171.2</td><td>86.9</td><td>91.6</td><td>P-glycoprotein 10</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10680.1 | Symbols: PGP10 | P-glycoprotein 10 | chr1:3538470-3543782 REVERSE LENGTH=1227</td><td>718</td><td>1227</td><td>0</td><td>170.9</td><td>86.6</td><td>91.8</td></tr>
<tr><td>Rsa1.0_00093.1.g4692.t1</td><td>ref|NP_172539.1| uncharacterized protein [Arabidopsis thaliana] gi|4874279|gb|AAD31344.1|AC007354_17 ESTs gb|T75618 and gb|AA404816 come from this gene [Arabidopsis thaliana] gi|45825137|gb|AAS77476.1| At1g10690 [Arabidopsis thaliana] gi|46359777|gb|AAS88752.1| At1g10690 [Arabidopsis thaliana] gi|332190508|gb|AEE28629.1| uncharacterized protein AT1G10690 [Arabidopsis thaliana]</td><td>110</td><td>110</td><td>1.00E-40</td><td>100.0</td><td>79.1</td><td>86.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10690.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G60783.1); Has 59 Blast hits to 59 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 59; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:3550236-3550568 REVERSE LENGTH=110</td><td>110</td><td>110</td><td>2.00E-43</td><td>100.0</td><td>79.1</td><td>86.4</td></tr>
<tr><td>Rsa1.0_00093.1.g4693.t1</td><td>ref|NP_172540.1| ribose-phosphate pyrophosphokinase 3 [Arabidopsis thaliana] gi|62286943|sp|Q93Z66.1|KPRS3_ARATH RecName: Full=Ribose-phosphate pyrophosphokinase 3, chloroplastic; AltName: Full=Phosphoribosyl pyrophosphate synthase 3; Flags: Precursor gi|16604386|gb|AAL24199.1| At1g10700/F20B24.13 [Arabidopsis thaliana] gi|19699210|gb|AAL90971.1| At1g10700/F20B24.13 [Arabidopsis thaliana] gi|332190509|gb|AEE28630.1| ribose-phosphate pyrophosphokinase 3 [Arabidopsis thaliana]</td><td>409</td><td>411</td><td>0</td><td>100.5</td><td>94.4</td><td>97.6</td><td>ribose-phosphate pyrophosphokinase 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10700.1 | Symbols: PRS3 | phosphoribosyl pyrophosphate (PRPP) synthase 3 | chr1:3554157-3556274 FORWARD LENGTH=411</td><td>409</td><td>411</td><td>0</td><td>100.5</td><td>94.4</td><td>97.6</td></tr>
<tr><td>Rsa1.0_00093.1.g4694.t1</td><td>gb|AAF17660.1|AC009398_9 F20B24.15 [Arabidopsis thaliana]</td><td>412</td><td>452</td><td>2.33E-156</td><td>109.7</td><td>77.2</td><td>83.7</td><td>F20B24.15</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10720.1 | Symbols: | BSD domain-containing protein | chr1:3562964-3564446 FORWARD LENGTH=429</td><td>412</td><td>429</td><td>1.00E-145</td><td>104.1</td><td>77.2</td><td>83.7</td></tr>
<tr><td>Rsa1.0_00093.1.g4695.t1</td><td>gb|EOA40487.1| hypothetical protein CARUB_v10009212mg [Capsella rubella] gi|482576301|gb|EOA40488.1| hypothetical protein CARUB_v10009212mg [Capsella rubella]</td><td>428</td><td>428</td><td>0</td><td>100.0</td><td>97.9</td><td>99.3</td><td>hypothetical protein CARUB_v10009212mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G60780.1 | Symbols: HAP13 | Clathrin adaptor complexes medium subunit family protein | chr1:22369289-22371885 REVERSE LENGTH=428</td><td>428</td><td>428</td><td>0</td><td>100.0</td><td>96.3</td><td>99.3</td></tr>
<tr><td>Rsa1.0_00093.1.g4696.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00093.1.g4697.t1</td><td>gb|AAZ20131.1| pectin methylesterase inhibitor [Brassica oleracea var. botrytis]</td><td>168</td><td>168</td><td>7.00E-74</td><td>100.0</td><td>82.7</td><td>88.7</td><td>pectin methylesterase inhibitor</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G10770.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:3591859-3592362 REVERSE LENGTH=167</td><td>168</td><td>167</td><td>5.00E-69</td><td>99.4</td><td>77.4</td><td>88.1</td></tr>
</table>

Rsa1.0_00093.1.g4698.t1	ref|NP_172548.2| F-box/RNI-like protein [Arabidopsis thaliana] gi|75265517|sp|Q9SAC4.1|FB2_ARATH RecName: Full=F-box protein At1g10780 gi|4874270|gb|AAD31335.1|AC007354_8 T16B5.8 [Arabidopsis thaliana] gi|50253496|gb|AAT71950.1| At1g10780 [Arabidopsis thaliana] gi|53850513|gb|AAU95433.1| At1g10780 [Arabidopsis thaliana] gi|332190524|gb|AEE28645.1| F-box/RNI-like protein [Arabidopsis thaliana]	144	418	2.00E-49	290.3	69.4	75.0	F-box/RNI-like protein	gbpln	Arabidopsis thaliana	AT1G10780.1 | Symbols: | F-box/RNI-like superfamily protein | chr1:3592875-3594310 REVERSE LENGTH=418	144	418	5.00E-52	290.3	69.4	75.0
Rsa1.0_00093.1.g4699.t1	ref|XP_002889837.1| hypothetical protein ARALYDRAFT_312123 [Arabidopsis lyrata subsp. lyrata] gi|297335679|gb|EFH66096.1| hypothetical protein ARALYDRAFT_312123 [Arabidopsis lyrata subsp. lyrata]	335	330	2.00E-92	98.5	58.5	69.3	hypothetical protein ARALYDRAFT_312123	gbpln	Arabidopsis lyrata	AT1G10790.1 | Symbols: | BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT3G56590.2); Has 78 Blast hits to 78 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:3596360-3597847 FORWARD LENGTH=336	335	336	1.00E-90	100.3	55.5	66.6
Rsa1.0_00093.1.g4700.t1	gb|AAF17663.1|AC009398_12 F20B24.22 [Arabidopsis thaliana]	233	236	4.00E-96	101.3	80.7	89.3	F20B24.22	gbpln	Arabidopsis thaliana	AT1G10800.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: inflorescence meristem, hypocotyl, root, flower; EXPRESSED DURING: petal differentiation and expansion stage; Has 23 Blast hits to 23 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:3598158-3598514 REVERSE LENGTH=118	233	118	1.00E-49	50.6	40.3	44.2
Rsa1.0_00093.1.g4701.t17	ref|XP_002892601.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338443|gb|EFH68860.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	335	263	2.00E-96	78.5	54.3	60.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G10820.2 | Symbols: | Protein of unknown function (DUF3755) | chr1:3601437-3604650 REVERSE LENGTH=258	335	258	1.00E-91	77.0	52.8	58.2
Rsa1.0_00093.1.g4702.t1	gb|EOA38040.1| hypothetical protein CARUB_v10009509mg [Capsella rubella]	364	366	1.00E-179	100.5	89.6	94.5	hypothetical protein CARUB_v10009509mg	gbpln	Capsella rubella	AT1G10830.1 | Symbols: Z-ISO, Z-ISO1.1 | 15-cis-zeta-carotene isomerase | chr1:3605736-3607449 REVERSE LENGTH=367	364	367	1.00E-177	100.8	89.3	94.8
Rsa1.0_00093.1.g4703.t1	ref|NP_563880.1| translation initiation factor eIF-3 subunit 3 [Arabidopsis thaliana] gi|23396619|sp|Q9C5Z2.2|EIF3H_ARATH RecName: Full=Eukaryotic translation initiation factor 3 subunit H; Short=eIF3h; AltName: Full=Eukaryotic translation initiation factor 3 subunit 3; AltName: Full=eIF-3-gamma; AltName: Full=eIF3 p38 subunit gi|4874264|gb|AAD31329.1|AC007354_2 Similar to gb|U54559 eIF3-p40 subunit from Homo sapiens and is a member of the PF|01398 Mov34 family. ESTs gb|N96623 and gb|N07519 come from this gene [Arabidopsis thaliana] gi|15451122|gb|AAK96832.1| Unknown protein [Arabidopsis thaliana] gi|20148435|gb|AAM10108.1| unknown protein [Arabidopsis thaliana] gi|21592938|gb|AAM64888.1| putative translation initiation factor [Arabidopsis thaliana] gi|23397245|gb|AAN31904.1| putative translation initiation factor [Arabidopsis thaliana] gi|332190533|gb|AEE28654.1| translation initiation factor 3 subunit H1 [Arabidopsis thaliana]	337	337	0	100.0	97.6	98.2	translation initiation factor eIF-3 subunit 3	gbpln	Arabidopsis thaliana	AT1G10840.1 | Symbols: TIF3H1 | translation initiation factor 3 subunit H1 | chr1:3607885-3610299 REVERSE LENGTH=337	337	337	0	100.0	97.6	98.2
Rsa1.0_00093.1.g4704.t1	gb|EOA38849.1| hypothetical protein CARUB_v10011198mg [Capsella rubella]	666	662	0	99.4	86.6	91.3	hypothetical protein CARUB_v10011198mg	gbpln	Capsella rubella	AT1G10850.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:3612228-3614343 FORWARD LENGTH=663	666	663	0	99.5	85.6	90.5
Rsa1.0_00093.1.g4705.t1	ref|XP_002892606.1| ARF-GAP domain 4 [Arabidopsis lyrata subsp. lyrata] gi|297338448|gb|EFH68865.1| ARF-GAP domain 4 [Arabidopsis lyrata subsp. lyrata]	769	773	0	100.5	91.4	94.7	ARF-GAP domain 4	gbpln	Arabidopsis lyrata	AT1G10870.1 | Symbols: AGD4 | ARF-GAP domain 4 | chr1:3616905-3623612 REVERSE LENGTH=775	769	775	0	100.8	91.0	94.4

Rsa1.0_00093.1.g4706.t1	dbj|BAF00442.1| hypothetical protein [Arabidopsis thaliana]	379	386	0	101.8	85.0	91.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G10880.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:3624035-3627021 REVERSE LENGTH=651	379	651	1.00E-173	171.8	78.9	84.4
Rsa1.0_00093.1.g4707.t1	ref|NP_172558.4| arginine and glutamate-rich protein 1 [Arabidopsis thaliana] gi|332190539|gb|AEE28660.1| uncharacterized protein AT1G10890 [Arabidopsis thaliana]	288	288	2.00E-81	100.0	89.9	94.1	arginine and glutamate-rich protein 1	gbpln	Arabidopsis thaliana	AT1G10890.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: petal, flower, leaf; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13340.1); Has 11769 Blast hits to 8435 proteins in 698 species: Archae - 22; Bacteria - 971; Metazoa - 5937; Fungi - 1065; Plants - 592; Viruses - 101; Other Eukaryotes - 3081 (source: NCBI BLink). | chr1:3628081-3630545 FORWARD LENGTH=288	288	288	4.00E-84	100.0	89.9	94.1
Rsa1.0_00093.1.g4708.t1	gb|AAB65487.1| phosphatidylinositol-4-phosphate 5-kinase isolog; 89655-95590 [Arabidopsis thaliana]	758	859	0	113.3	86.3	92.5	phosphatidylinositol-4-phosphate 5-kinase isolog; 89655-95590	gbpln	Arabidopsis thaliana	AT1G10900.1 | Symbols: | Phosphatidylinositol-4-phosphate 5-kinase family protein | chr1:3632396-3636416 REVERSE LENGTH=754	758	754	0	99.5	86.3	92.5
Rsa1.0_00093.1.g4709.t1	ref|NP_172560.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|122242678|sp|Q0WVV0.1|PPR31_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g10910, chloroplastic; Flags: Precursor gi|110741600|dbj|BAE98748.1| membrane-associated salt-inducible protein isolog [Arabidopsis thaliana] gi|332190541|gb|AEE28662.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	671	664	0	99.0	84.6	90.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G10910.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:3639908-3643974 FORWARD LENGTH=664	671	664	0	99.0	84.6	90.8
Rsa1.0_00093.1.g4710.t1	gb|AAA33003.1| serine/threonine protein kinase [Brassica napus] gi|1097353|prf||2113401A protein kinase	357	359	0	100.6	95.5	97.2	serine/threonine protein kinase	gbpln	Brassica napus	AT1G10940.1 | Symbols: ASK1, SNRK2-4, SNRK2.4, SRK2A | Protein kinase superfamily protein | chr1:3656050-3658170 REVERSE LENGTH=363	357	363	0	101.7	94.1	96.9
Rsa1.0_00093.1.g4711.t1	gb|EOA37821.1| hypothetical protein CARUB_v10011995mg [Capsella rubella]	583	589	0	101.0	95.0	97.1	hypothetical protein CARUB_v10011995mg	gbpln	Capsella rubella	AT1G10950.1 | Symbols: TMN1, AtTMN1 | transmembrane nine 1 | chr1:3659322-3663622 FORWARD LENGTH=589	583	589	0	101.0	93.7	96.4
Rsa1.0_00093.1.g4712.t1	dbj|BAJ33728.1| unnamed protein product [Thellungiella halophila]	147	148	1.00E-60	100.7	78.2	87.8	unnamed protein product	----	----	AT1G60950.1 | Symbols: FED A, ATFD2 | 2Fe-2S ferredoxin-like superfamily protein | chr1:22444565-22445011 FORWARD LENGTH=148	147	148	5.00E-61	100.7	76.9	85.7
Rsa1.0_00093.1.g4713.t1	gb|AAB65494.1| hypothetical protein; 51018-49636 [Arabidopsis thaliana]	149	281	3.00E-27	188.6	48.3	66.4	hypothetical protein; 51018-49636	gbpln	Arabidopsis thaliana	AT1G11020.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:3676968-3678350 FORWARD LENGTH=321	149	321	2.00E-29	215.4	49.7	67.1
Rsa1.0_00093.1.g4714.t1	ref|XP_002888117.1| fed A [Arabidopsis lyrata subsp. lyrata] gi|297333958|gb|EFH64376.1| fed A [Arabidopsis lyrata subsp. lyrata]	153	148	9.00E-58	96.7	73.2	81.7	fed A	gbpln	Arabidopsis lyrata	AT1G60950.1 | Symbols: FED A, ATFD2 | 2Fe-2S ferredoxin-like superfamily protein | chr1:22444565-22445011 FORWARD LENGTH=148	153	148	1.00E-59	96.7	73.2	81.0
Rsa1.0_00093.1.g4715.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00093.1.g4716.t1	gb|EOA16130.1| hypothetical protein CARUB_v10004265mg [Capsella rubella]	720	701	0	97.4	52.6	67.6	hypothetical protein CARUB_v10004265mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	720	696	5.00E-63	96.7	25.0	44.3
Rsa1.0_00093.1.g4717.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00093.1.g4718.t1	ref|XP_002889844.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297335686|gb|EFH66103.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	350	323	2.00E-38	92.3	26.3	34.0	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G11020.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:3676968-3678350 FORWARD LENGTH=321	350	321	4.00E-40	91.7	25.4	33.1
Rsa1.0_00093.1.g4719.t1	ref|XP_002892615.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338457|gb|EFH68874.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	424	438	0	103.3	85.4	92.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G11040.1 | Symbols: | HSP40/DnaJ peptide-binding protein | chr1:3679225-3680924 REVERSE LENGTH=438	424	438	0	103.3	84.7	92.5
Rsa1.0_00093.1.g4720.t2	ref|XP_002889846.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335688|gb|EFH66105.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	868	873	0	100.6	84.9	90.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G11060.1 | Symbols: | WAPL (Wings apart-like protein regulation of heterochromatin) protein | chr1:3684568-3689537 FORWARD LENGTH=930	868	930	0	107.1	83.9	88.9

Rsa1.0_00093.1.g4721.t1	ref|NP_172574.5| uncharacterized protein [Arabidopsis thaliana] gi|332190558|gb|AEE28679.1| uncharacterized protein AT1G11070 [Arabidopsis thaliana]	855	763	0	89.2	56.7	64.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11070.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Hydroxyproline-rich glycoprotein family protein (TAIR:AT1G61080.1); Has 579 Blast hits to 567 proteins in 152 species: Archae - 0; Bacteria - 68; Metazoa - 159; Fungi - 113; Plants - 172; Viruses - 0; Other Eukaryotes - 67 (source: NCBI BLink). | chr1:3690406-3693648 REVERSE LENGTH=763	855	763	0	89.2	56.7	64.7
Rsa1.0_00093.1.g4722.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00093.1.g4723.t1	ref|NP_172575.2| carboxypeptidase C [Arabidopsis thaliana] gi|334302853|sp|O04084.2|SCP31_ARATH RecName: Full=Serine carboxypeptidase-like 31; Flags: Precursor gi|133778908|gb|ABO38794.1| At1g11080 [Arabidopsis thaliana] gi|332190559|gb|AEE28680.1| carboxypeptidase C [Arabidopsis thaliana]	491	492	0	100.2	89.4	92.9	carboxypeptidase C	gbpln	Arabidopsis thaliana	AT1G11080.1 | Symbols: scpl31 | serine carboxypeptidase-like 31 | chr1:3694917-3697759 REVERSE LENGTH=492	491	492	0	100.2	89.4	92.9
Rsa1.0_00093.1.g4724.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	469	1142	1.00E-127	243.5	51.8	66.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	469	575	6.00E-56	122.6	33.3	52.0
Rsa1.0_00093.1.g4725.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00093.1.g4726.t1	gb|EOA36604.1| hypothetical protein CARUB_v10011807mg [Capsella rubella]	46	322	5.00E-16	700.0	84.8	93.5	hypothetical protein CARUB_v10011807mg	gbpln	Capsella rubella	AT1G11090.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:3702655-3703629 FORWARD LENGTH=324	46	324	4.00E-17	704.3	82.6	91.3
Rsa1.0_00093.1.g4727.t1	ref|NP_001117267.1| uncharacterized protein [Arabidopsis thaliana] gi|98961969|gb|ABF59314.1| unknown protein [Arabidopsis thaliana] gi|332190565|gb|AEE28686.1| uncharacterized protein AT1G11112 [Arabidopsis thaliana]	77	78	2.00E-18	101.3	76.6	83.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11112.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:3713220-3713456 REVERSE LENGTH=78	77	78	4.00E-21	101.3	76.6	83.1
Rsa1.0_00093.1.g4728.t1	ref|NP_172579.2| uncharacterized protein [Arabidopsis thaliana] gi|332190566|gb|AEE28687.1| uncharacterized protein AT1G11120 [Arabidopsis thaliana]	183	187	3.00E-64	102.2	79.2	85.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11120.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G09812.1); Has 270 Blast hits to 255 proteins in 62 species: Archae - 0; Bacteria - 2; Metazoa - 93; Fungi - 14; Plants - 126; Viruses - 0; Other Eukaryotes - 35 (source: NCBI BLink). | chr1:3715229-3717320 FORWARD LENGTH=187	183	187	1.00E-66	102.2	79.2	85.8
Rsa1.0_00093.1.g4729.t1	ref|NP_001184959.1| uncharacterized protein [Arabidopsis thaliana] gi|332190568|gb|AEE28689.1| uncharacterized protein AT1G11125 [Arabidopsis thaliana]	273	265	7.00E-80	97.1	65.6	75.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11125.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G61170.1). | chr1:3718846-3719643 FORWARD LENGTH=265	273	265	2.00E-82	97.1	65.6	75.5
Rsa1.0_00094.1.g4730.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00094.1.g4731.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00094.1.g4732.t1	gb|AAG30607.1|AF314656_1 aquaporin [Brassica oleracea]	282	281	1.00E-156	99.6	97.2	98.2	aquaporin	gbpln	Brassica oleracea	AT4G35100.2 | Symbols: PIP3 | plasma membrane intrinsic protein 3 | chr4:16708672-16709958 FORWARD LENGTH=280	282	280	1.00E-155	99.3	95.0	97.5
Rsa1.0_00094.1.g4733.t1	ref|XP_002867091.1| hypothetical protein ARALYDRAFT_353319 [Arabidopsis lyrata subsp. lyrata] gi|297312927|gb|EFH43350.1| hypothetical protein ARALYDRAFT_353319 [Arabidopsis lyrata subsp. lyrata]	373	386	1.00E-154	103.5	77.5	87.9	hypothetical protein ARALYDRAFT_353319	gbpln	Arabidopsis lyrata	AT4G35110.2 | Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) family | chr4:16712660-16713987 REVERSE LENGTH=386	373	386	1.00E-149	103.5	74.8	85.3
Rsa1.0_00094.1.g4734.t1	ref|XP_002869106.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297314942|gb|EFH45365.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	353	399	3.00E-93	113.0	56.9	71.1	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G35120.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:16716806-16718017 FORWARD LENGTH=389	353	389	1.00E-84	110.2	53.5	65.7
Rsa1.0_00094.1.g4735.t1	ref|XP_002869107.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297314943|gb|EFH45366.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	381	413	1.00E-103	108.4	58.3	70.9	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G35120.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:16716806-16718017 FORWARD LENGTH=389	381	389	3.00E-92	102.1	54.3	66.9

Rsa1.0_00094.1.g4736.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00094.1.g4737.t1	ref|XP_002869106.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297314942|gb|EFH45365.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	380	399	1.00E-92	105.0	53.7	68.4	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G35120.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:16716806-16718017 FORWARD LENGTH=389	380	389	1.00E-80	102.4	49.5	64.5
Rsa1.0_00094.1.g4738.t1	ref|XP_002869106.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297314942|gb|EFH45365.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	385	399	9.00E-87	103.6	51.7	64.9	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G35120.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:16716806-16718017 FORWARD LENGTH=389	385	389	4.00E-81	101.0	50.6	64.9
Rsa1.0_00094.1.g4739.t1	ref|NP_195239.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75098809|sp|O49619.1|PP350_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g35130, chloroplastic; Flags: Precursor gi|2924523|emb|CAA17777.1| putative protein [Arabidopsis thaliana] gi|7270464|emb|CAB80230.1| putative protein [Arabidopsis thaliana] gi|332661071|gb|AEE86471.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	802	804	0	100.2	77.2	87.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G35130.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:16721084-16723498 REVERSE LENGTH=804	802	804	0	100.2	77.2	87.5
Rsa1.0_00094.1.g4740.t1	ref|XP_002867089.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297312925|gb|EFH43348.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	482	494	0	102.5	78.2	86.9	transducin family protein	gbpln	Arabidopsis lyrata	AT4G35140.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:16723873-16726477 REVERSE LENGTH=496	482	496	0	102.9	78.2	87.1
Rsa1.0_00094.1.g4741.t1	ref|XP_002867086.1| hypothetical protein ARALYDRAFT_491132 [Arabidopsis lyrata subsp. lyrata] gi|297312922|gb|EFH43345.1| hypothetical protein ARALYDRAFT_491132 [Arabidopsis lyrata subsp. lyrata]	479	478	0	99.8	76.0	85.2	hypothetical protein ARALYDRAFT_491132	gbpln	Arabidopsis lyrata	AT4G35180.1 | Symbols: LHT7 | LYS/HIS transporter 7 | chr4:16738517-16740385 REVERSE LENGTH=478	479	478	0	99.8	76.0	85.4
Rsa1.0_00094.1.g4742.t1	ref|XP_002869102.1| hypothetical protein ARALYDRAFT_912862 [Arabidopsis lyrata subsp. lyrata] gi|297314938|gb|EFH45361.1| hypothetical protein ARALYDRAFT_912862 [Arabidopsis lyrata subsp. lyrata]	235	225	1.00E-117	95.7	87.2	91.1	hypothetical protein ARALYDRAFT_912862	gbpln	Arabidopsis lyrata	AT4G35190.1 | Symbols: | Putative lysine decarboxylase family protein | chr4:16746724-16748090 FORWARD LENGTH=228	235	228	1.00E-113	97.0	86.0	90.2
Rsa1.0_00094.1.g4743.t1	gb|EOA17153.1| hypothetical protein CARUB_v10005421mg [Capsella rubella]	273	286	1.00E-135	104.8	87.5	93.4	hypothetical protein CARUB_v10005421mg	gbpln	Capsella rubella	AT4G35220.1 | Symbols: | Cyclase family protein | chr4:16752636-16753966 FORWARD LENGTH=272	273	272	1.00E-133	99.6	82.8	87.5
Rsa1.0_00094.1.g4744.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00094.1.g4745.t1	ref|NP_567980.1| BR-signaling kinase 1 [Arabidopsis thaliana] gi|75331881|sp|Q944A7.1|Y4523_ARATH RecName: Full=Probable serine/threonine-protein kinase At4g35230 gi|16612249|gb|AAL27496.1|AF439824_1 AT4g35230/F23E12_210 [Arabidopsis thaliana] gi|22655470|gb|AAM98327.1| At4g35230/F23E12_210 [Arabidopsis thaliana] gi|332661082|gb|AEE86482.1| BR-signaling kinase 1 [Arabidopsis thaliana]	518	512	0	98.8	92.7	94.6	BR-signaling kinase 1	gbpln	Arabidopsis thaliana	AT4G35230.1 | Symbols: BSK1 | BR-signaling kinase 1 | chr4:16755325-16758041 REVERSE LENGTH=512	518	512	0	98.8	92.7	94.6
Rsa1.0_00094.1.g4746.t1	ref|NP_195250.2| uncharacterized protein [Arabidopsis thaliana] gi|334187179|ref|NP_001190921.1| uncharacterized protein [Arabidopsis thaliana] gi|332661083|gb|AEE86483.1| uncharacterized protein AT4G35240 [Arabidopsis thaliana] gi|332661084|gb|AEE86484.1| uncharacterized protein AT4G35240 [Arabidopsis thaliana]	869	865	0	99.5	81.8	87.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G35240.2 | Symbols: | Protein of unknown function (DUF630 and DUF632) | chr4:16761334-16764324 REVERSE LENGTH=865	869	865	0	99.5	81.8	87.1
Rsa1.0_00094.1.g4747.t1	ref|XP_002864695.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310530|gb|EFH40954.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	376	376	0	100.0	94.7	97.3	phospholipid/glycerol acyltransferase family protein	gbpln	Arabidopsis lyrata	AT5G60620.1 | Symbols: GPAT9 | glycerol-3-phosphate acyltransferase 9 | chr5:24367266-24369647 FORWARD LENGTH=376	376	376	0	100.0	93.6	97.3

<table>
<tr><td>Rsa1.0_00094.1.g4748.t1</td><td>gb|AAO61647.1| NAD-dependent isocitrate dehydrogenase beta subunit [Brassica napus]</td><td>401</td><td>367</td><td>0</td><td>91.5</td><td>89.5</td><td>90.5</td><td>NAD-dependent isocitrate dehydrogenase beta subunit</td><td>gbpln</td><td>Brassica napus</td><td>AT4G35260.1 | Symbols: IDH1, IDH-I | isocitrate dehydrogenase 1 | chr4:16774494-16776233 REVERSE LENGTH=367</td><td>401</td><td>367</td><td>0</td><td>91.5</td><td>87.5</td><td>89.8</td></tr>
<tr><td>Rsa1.0_00094.1.g4749.t1</td><td>gb|EOA15973.1| hypothetical protein CARUB_v10004068mg [Capsella rubella] gi|482551781|gb|EOA15974.1| hypothetical protein CARUB_v10004068mg [Capsella rubella] gi|482551782|gb|EOA15975.1| hypothetical protein CARUB_v10004068mg [Capsella rubella]</td><td>965</td><td>972</td><td>0</td><td>100.7</td><td>84.6</td><td>89.6</td><td>hypothetical protein CARUB_v10004068mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G35270.1 | Symbols: | Plant regulator RWP-RK family protein | chr4:16777657-16780824 REVERSE LENGTH=963</td><td>965</td><td>963</td><td>0</td><td>99.8</td><td>83.7</td><td>89.3</td></tr>
<tr><td>Rsa1.0_00094.1.g4750.t1</td><td>ref|XP_002867079.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297312915|gb|EFH43338.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>269</td><td>283</td><td>4.00E-92</td><td>105.2</td><td>71.0</td><td>77.0</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G35280.1 | Symbols: | C2H2-like zinc finger protein | chr4:16787429-16788283 REVERSE LENGTH=284</td><td>269</td><td>284</td><td>1.00E-94</td><td>105.6</td><td>70.6</td><td>76.2</td></tr>
<tr><td>Rsa1.0_00094.1.g4751.t1</td><td>gb|EOA30237.1| hypothetical protein CARUB_v10013359mg [Capsella rubella]</td><td>548</td><td>563</td><td>1.00E-145</td><td>102.7</td><td>62.0</td><td>72.1</td><td>hypothetical protein CARUB_v10013359mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G17200.1 | Symbols: DSK2 | ubiquitin family protein | chr2:7482133-7485090 REVERSE LENGTH=551</td><td>548</td><td>551</td><td>2.33E-156</td><td>100.5</td><td>62.4</td><td>72.6</td></tr>
<tr><td>Rsa1.0_00094.1.g4752.t1</td><td>gb|AAQ02674.1| glutamate receptor [Raphanus sativus var. sativus]</td><td>913</td><td>915</td><td>0</td><td>100.2</td><td>98.2</td><td>98.8</td><td>glutamate receptor</td><td>gbpln</td><td>Raphanus sativus</td><td>AT4G35290.1 | Symbols: GLUR2, GLR3.2, ATGLR3.2, ATGLUR2 | glutamate receptor 2 | chr4:16790290-16793461 FORWARD LENGTH=912</td><td>913</td><td>912</td><td>0</td><td>99.9</td><td>85.1</td><td>92.8</td></tr>
<tr><td>Rsa1.0_00094.1.g4753.t1</td><td>gb|EOA16091.1| hypothetical protein CARUB_v10004225mg [Capsella rubella] gi|482551899|gb|EOA16092.1| hypothetical protein CARUB_v10004225mg [Capsella rubella]</td><td>741</td><td>740</td><td>0</td><td>99.9</td><td>93.8</td><td>97.6</td><td>hypothetical protein CARUB_v10004225mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G35300.4 | Symbols: TMT2 | tonoplast monosaccharide transporter2 | chr4:16796432-16799071 REVERSE LENGTH=739</td><td>741</td><td>739</td><td>0</td><td>99.7</td><td>93.7</td><td>97.7</td></tr>
<tr><td>Rsa1.0_00094.1.g4754.t1</td><td>gb|EOA16342.1| hypothetical protein CARUB_v10004491mg [Capsella rubella]</td><td>557</td><td>560</td><td>0</td><td>100.5</td><td>91.9</td><td>95.0</td><td>hypothetical protein CARUB_v10004491mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G35310.1 | Symbols: CPK5, ATCPK5 | calmodulin-domain protein kinase 5 | chr4:16802436-16804628 FORWARD LENGTH=556</td><td>557</td><td>556</td><td>0</td><td>99.8</td><td>90.7</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00094.1.g4755.t1</td><td>ref|NP_567982.1| uncharacterized protein [Arabidopsis thaliana] gi|13605511|gb|AAK32749.1|AF361581_1 AT4g35320/F23E12_120 [Arabidopsis thaliana] gi|16323284|gb|AAL15397.1| AT4g35320/F23E12_120 [Arabidopsis thaliana] gi|332661099|gb|AEE86499.1| uncharacterized protein AT4G35320 [Arabidopsis thaliana]</td><td>146</td><td>147</td><td>4.00E-55</td><td>100.7</td><td>81.5</td><td>91.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G35320.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G17300.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16806139-16806582 REVERSE LENGTH=147</td><td>146</td><td>147</td><td>1.00E-57</td><td>100.7</td><td>81.5</td><td>91.1</td></tr>
<tr><td>Rsa1.0_00094.1.g4756.t1</td><td>gb|EOA16913.1| hypothetical protein CARUB_v10005136mg [Capsella rubella]</td><td>357</td><td>354</td><td>0</td><td>99.2</td><td>92.2</td><td>96.9</td><td>hypothetical protein CARUB_v10005136mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G35350.1 | Symbols: XCP1 | xylem cysteine peptidase 1 | chr4:16810529-16811875 FORWARD LENGTH=355</td><td>357</td><td>355</td><td>0</td><td>99.4</td><td>91.6</td><td>96.1</td></tr>
<tr><td>Rsa1.0_00094.1.g4757.t1</td><td>ref|XP_002867075.1| hypothetical protein ARALYDRAFT_491111 [Arabidopsis lyrata subsp. lyrata] gi|297312911|gb|EFH43334.1| hypothetical protein ARALYDRAFT_491111 [Arabidopsis lyrata subsp. lyrata]</td><td>367</td><td>367</td><td>0</td><td>100.0</td><td>96.2</td><td>98.1</td><td>hypothetical protein ARALYDRAFT_491111</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G35360.1 | Symbols: | Uncharacterised conserved protein (UCP030210) | chr4:16812303-16814656 REVERSE LENGTH=367</td><td>367</td><td>367</td><td>0</td><td>100.0</td><td>95.6</td><td>97.0</td></tr>
<tr><td>Rsa1.0_00094.1.g4758.t1</td><td>ref|XP_002870014.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297315850|gb|EFH46273.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>476</td><td>493</td><td>1.00E-160</td><td>103.6</td><td>64.7</td><td>77.7</td><td>transducin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G18905.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:10360234-10362991 FORWARD LENGTH=494</td><td>476</td><td>494</td><td>1.00E-161</td><td>103.8</td><td>64.1</td><td>77.5</td></tr>
<tr><td>Rsa1.0_00094.1.g4759.t2</td><td>ref|XP_002869091.1| hypothetical protein ARALYDRAFT_491109 [Arabidopsis lyrata subsp. lyrata] gi|297314927|gb|EFH45350.1| hypothetical protein ARALYDRAFT_491109 [Arabidopsis lyrata subsp. lyrata]</td><td>1706</td><td>1704</td><td>0</td><td>99.9</td><td>90.5</td><td>95.1</td><td>hypothetical protein ARALYDRAFT_491109</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G35380.1 | Symbols: | SEC7-like guanine nucleotide exchange family protein | chr4:16819883-16825960 FORWARD LENGTH=1706</td><td>1706</td><td>1706</td><td>0</td><td>100.0</td><td>90.0</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00094.1.g4760.t1</td><td>ref|NP_195265.2| AT-hook protein of GA feedback 1 [Arabidopsis thaliana] gi|50198777|gb|AAT70422.1| At4g35390 [Arabidopsis thaliana] gi|53828597|gb|AAU94408.1| At4g35390 [Arabidopsis thaliana] gi|119657394|tpd|FAA00296.1| TPA: AT-hook motif nuclear localized protein 25 [Arabidopsis thaliana] gi|332661106|gb|AEE86506.1| AT-hook protein of GA feedback 1 [Arabidopsis thaliana]</td><td>284</td><td>299</td><td>1.00E-100</td><td>105.3</td><td>88.4</td><td>91.5</td><td>AT-hook protein of GA feedback 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G35390.1 | Symbols: AGF1 | AT-hook protein of GA feedback 1 | chr4:16829603-16830502 FORWARD LENGTH=299</td><td>284</td><td>299</td><td>1.00E-103</td><td>105.3</td><td>88.4</td><td>91.5</td></tr>
</table>

Rsa1.0_00094.1.g4761.t1	ref|XP_002884054.1| hypothetical protein ARALYDRAFT_480622 [Arabidopsis lyrata subsp. lyrata] gi|297329894|gb|EFH60313.1| hypothetical protein ARALYDRAFT_480622 [Arabidopsis lyrata subsp. lyrata] gi|482567420|gb|EOA31609.1| hypothetical protein CARUB_v10014806mg [Capsella rubella]	161	161	1.00E-86	100.0	96.9	98.1	hypothetical protein ARALYDRAFT_480622	gbpln	Arabidopsis lyrata	AT2G17380.1 | Symbols: AP19 | associated protein 19 | chr2:7553122-7554887 FORWARD LENGTH=161	161	161	1.00E-88	100.0	96.3	97.5
Rsa1.0_00094.1.g4762.t1	ref|XP_002880609.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata] gi|297326448|gb|EFH56868.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata]	445	464	1.00E-110	104.3	53.3	68.3	hypothetical protein ARALYDRAFT_901029	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	445	456	1.00E-111	102.5	51.9	67.0
Rsa1.0_00094.1.g4763.t1	ref|NP_567985.1| chloride channel protein CLC-e [Arabidopsis thaliana] gi|41688502|sp|Q8GX93.2|CLCE_ARATH RecName: Full=Chloride channel protein CLC-e; Short=AtCLC-e; AltName: Full=CBS domain-containing protein CBSCLC3 gi|332661110|gb|AEE86510.1| chloride channel protein CLC-e [Arabidopsis thaliana]	700	710	0	101.4	85.3	92.7	chloride channel protein CLC-e	gbpln	Arabidopsis thaliana	AT4G35440.1 | Symbols: CLC-E, ATCLC-E, CLCE | chloride channel E | chr4:16836384-16839345 REVERSE LENGTH=710	700	710	0	101.4	85.3	92.7
Rsa1.0_00094.1.g4764.t1	dbj|BAJ33771.1| unnamed protein product [Thellungiella halophila]	353	342	1.00E-166	96.9	87.3	90.9	unnamed protein product	----	----	AT4G35450.1 | Symbols: AKR2, AFT, AKR2A | ankyrin repeat-containing protein 2 | chr4:16839862-16841759 FORWARD LENGTH=342	353	342	1.00E-164	96.9	86.4	91.5
Rsa1.0_00095.1.g4765.t1	gb|EOA28951.1| hypothetical protein CARUB_v10025202mg, partial [Capsella rubella]	350	409	8.00E-61	116.9	42.6	53.1	hypothetical protein CARUB_v10025202mg, partial	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	350	735	8.00E-61	210.0	44.9	58.0
Rsa1.0_00095.1.g4766.t21	ref|NP_567423.1| phragmoplast-associated kinesin-related protein 1 [Arabidopsis thaliana] gi|75173840|sp|Q9LDN0.1|KN12A_ARATH RecName: Full=Kinesin-like protein KIN12A; AltName: Full=Phragmoplast-associated kinesin-related protein 1; Short=AtPAKRP1 gi|8745333|gb|AAF78893.1| phragmoplast-associated kinesin-related protein 1 [Arabidopsis thaliana] gi|8745335|gb|AAF78894.1| phragmoplast-associated kinesin-related protein 1 [Arabidopsis thaliana] gi|332657984|gb|AEE83384.1| phragmoplast-associated kinesin-related protein 1 [Arabidopsis thaliana]	1309	1292	0	98.7	80.4	87.2	phragmoplast-associated kinesin-related protein 1	gbpln	Arabidopsis thaliana	AT4G14150.1 | Symbols: PAKRP1, KINESIN-12A | phragmoplast-associated kinesin-related protein 1 | chr4:8158645-8165008 REVERSE LENGTH=1292	1309	1292	0	98.7	80.4	87.2
Rsa1.0_00095.1.g4767.t1	ref|XP_002870333.1| hypothetical protein ARALYDRAFT_493493 [Arabidopsis lyrata subsp. lyrata] gi|297316169|gb|EFH46592.1| hypothetical protein ARALYDRAFT_493493 [Arabidopsis lyrata subsp. lyrata]	775	763	0	98.5	91.5	95.5	hypothetical protein ARALYDRAFT_493493	gbpln	Arabidopsis lyrata	AT4G14160.2 | Symbols: | Sec23/Sec24 protein transport family protein | chr4:8167574-8173026 FORWARD LENGTH=772	775	772	0	99.6	87.6	92.4
Rsa1.0_00095.1.g4768.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00095.1.g4769.t1	ref|XP_003596591.1| Histone H3 [Medicago truncatula] gi|355485639|gb|AES66842.1| Histone H3 [Medicago truncatula]	142	146	2.00E-45	102.8	67.6	70.4	Histone H3	gbpln	Medicago truncatula	AT5G65360.1 | Symbols: | Histone superfamily protein | chr5:26120099-26120509 REVERSE LENGTH=136	142	136	5.00E-47	95.8	64.8	66.2
Rsa1.0_00095.1.g4770.t1	gb|EOA14799.1| hypothetical protein CARUB_v10028105mg [Capsella rubella]	316	329	2.00E-48	104.1	41.5	57.3	hypothetical protein CARUB_v10028105mg	gbpln	Capsella rubella	AT5G38620.1 | Symbols: | MADS-box transcription factor family protein | chr5:15463858-15464907 REVERSE LENGTH=349	316	349	3.00E-50	110.4	42.4	57.6
Rsa1.0_00095.1.g4771.t1	gb|AFK65668.1| chloroplast phytoene desaturase [Brassica rapa subsp. oleifera]	555	563	0	101.4	98.7	99.8	chloroplast phytoene desaturase	gbpln	Brassica rapa	AT4G14210.1 | Symbols: PDS3, PDS, PDE226 | phytoene desaturase 3 | chr4:8190426-8194769 REVERSE LENGTH=566	555	566	0	102.0	94.8	98.6
Rsa1.0_00095.1.g4772.t1	gb|EOA16503.1| hypothetical protein CARUB_v10004662mg [Capsella rubella]	533	493	0	92.5	83.7	87.2	hypothetical protein CARUB_v10004662mg	gbpln	Capsella rubella	AT4G14240.1 | Symbols: | CBS domain-containing protein with a domain of unknown function (DUF21) | chr4:8204712-8207273 REVERSE LENGTH=494	533	494	0	92.7	83.7	86.9
Rsa1.0_00095.1.g4773.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00095.1.g4774.t1	gb|EOA18833.1| hypothetical protein CARUB_v10007447mg, partial [Capsella rubella]	490	436	1.00E-101	89.0	45.7	61.6	hypothetical protein CARUB_v10007447mg, partial	gbpln	Capsella rubella	AT4G14250.2 | Symbols: | structural constituent of ribosome | chr4:8208985-8213237 REVERSE LENGTH=815	490	815	1.00E-103	166.3	42.4	55.3

Rsa1.0_00095.1.g4775.t1	gb|AGH62811.1| UBX1 [Brassica napus]	388	386	1.00E-159	99.5	74.5	82.5	UBX1	gbpln	Brassica napus	AT4G14250.1 | Symbols: | structural constituent of ribosome | chr4:8208985-8213237 REVERSE LENGTH=821	388	821	2.00E-92	211.6	47.9	59.8
Rsa1.0_00095.1.g4776.t1	emb|CAB10204.1| hypothetical protein [Arabidopsis thaliana] gi|7268130|emb|CAB78467.1| hypothetical protein [Arabidopsis thaliana]	424	724	1.00E-113	170.8	53.8	65.3	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G14250.1 | Symbols: | structural constituent of ribosome | chr4:8208985-8213237 REVERSE LENGTH=821	424	821	1.00E-115	193.6	53.5	64.9
Rsa1.0_00095.1.g4777.t1	gb|AGH62811.1| UBX1 [Brassica napus]	295	386	6.00E-61	130.8	40.3	51.5	UBX1	gbpln	Brassica napus	AT4G14250.1 | Symbols: | structural constituent of ribosome | chr4:8208985-8213237 REVERSE LENGTH=821	295	821	8.00E-58	278.3	50.8	62.0
Rsa1.0_00095.1.g4778.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00095.1.g4779.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00095.1.g4780.t1	ref|XP_002868166.1| hypothetical protein ARALYDRAFT_915171 [Arabidopsis lyrata subsp. lyrata] gi|297314002|gb|EFH44425.1| hypothetical protein ARALYDRAFT_915171 [Arabidopsis lyrata subsp. lyrata]	135	135	3.00E-52	100.0	74.1	83.0	hypothetical protein ARALYDRAFT_915171	gbpln	Arabidopsis lyrata	AT4G15990.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G16024.1); Has 14 Blast hits to 14 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:9061269-9061676 REVERSE LENGTH=135	135	135	2.00E-53	100.0	71.9	83.0
Rsa1.0_00095.1.g4781.t1	ref|XP_002870327.1| hypothetical protein ARALYDRAFT_493483 [Arabidopsis lyrata subsp. lyrata] gi|297316163|gb|EFH46586.1| hypothetical protein ARALYDRAFT_493483 [Arabidopsis lyrata subsp. lyrata]	154	144	1.00E-44	93.5	61.0	72.7	hypothetical protein ARALYDRAFT_493483	gbpln	Arabidopsis lyrata	AT4G14270.1 | Symbols: | Protein containing PAM2 motif which mediates interaction with the PABC domain of polyadenyl binding proteins. | chr4:8218517-8219037 FORWARD LENGTH=143	154	143	4.00E-45	92.9	60.4	69.5
Rsa1.0_00095.1.g4782.t1	ref|NP_189482.1| F-box domain-containing protein [Arabidopsis thaliana] gi|334302799|sp|Q9LSJ3.2|FBL48_ARATH RecName: Full=Putative F-box/LRR-repeat protein At3g28410 gi|332643920|gb|AEE77441.1| F-box domain-containing protein [Arabidopsis thaliana]	290	465	1.00E-59	160.3	52.4	66.9	F-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G28410.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:10640152-10642071 REVERSE LENGTH=465	290	465	3.00E-62	160.3	52.4	66.9
Rsa1.0_00095.1.g4783.t1	gb|EOA16349.1| hypothetical protein CARUB_v10004497mg [Capsella rubella]	536	556	0	103.7	89.6	93.8	hypothetical protein CARUB_v10004497mg	gbpln	Capsella rubella	AT4G14290.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:8225547-8230057 REVERSE LENGTH=558	536	558	0	104.1	89.4	93.8
Rsa1.0_00095.1.g4784.t1	gb|AAZ67609.1| 80A08_24 [Brassica rapa subsp. pekinensis]	377	475	8.00E-18	126.0	17.2	20.4	80A08_24	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00095.1.g4785.t1	ref|NP_001031637.1| Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein [Arabidopsis thaliana] gi|62321523|dbj|BAD95003.1| hypothetical protein [Arabidopsis thaliana] gi|98961831|gb|ABF59245.1| unknown protein [Arabidopsis thaliana] gi|332658013|gb|AEE83413.1| Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein [Arabidopsis thaliana]	185	185	1.00E-94	100.0	89.7	94.6	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	gbpln	Arabidopsis thaliana	AT4G14305.1 | Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr4:8235335-8236605 REVERSE LENGTH=185	185	185	4.00E-97	100.0	89.7	94.6
Rsa1.0_00095.1.g4786.t1	ref|NP_198678.1| MADS-box protein AGL73 [Arabidopsis thaliana] gi|10176830|dbj|BAB10152.1| MADS-box protein-like [Arabidopsis thaliana] gi|32402438|gb|AAN52801.1| MADS-box protein AGL73 [Arabidopsis thaliana] gi|332006959|gb|AED94342.1| MADS-box protein AGL73 [Arabidopsis thaliana]	311	349	2.00E-48	112.2	43.4	59.8	MADS-box protein AGL73	gbpln	Arabidopsis thaliana	AT5G38620.1 | Symbols: | MADS-box transcription factor family protein | chr5:15463858-15464907 REVERSE LENGTH=349	311	349	4.00E-51	112.2	43.4	59.8
Rsa1.0_00095.1.g4787.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1581	1501	0	94.9	51.1	64.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1581	1262	1.00E-130	79.8	13.9	19.9
Rsa1.0_00095.1.g4788.t1	emb|CAD22562.1| reverse transcriptase [Brassica rapa subsp. oleifera]	241	137	7.00E-57	56.8	42.3	51.0	reverse transcriptase	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00095.1.g4789.t1	gb|AAM82603.1|AF525305_1 putative DNA/RNA binding protein [Brassica napus]	129	306	8.00E-14	237.2	34.1	46.5	putative DNA/RNA binding protein	gbpln	Brassica napus	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	129	530	1.00E-10	410.9	27.1	45.0
Rsa1.0_00095.1.g4790.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00096.1.g4791.t1	gb|EOA33755.1| hypothetical protein CARUB_v10019950mg [Capsella rubella]	326	635	7.00E-58	194.8	38.7	47.5	hypothetical protein CARUB_v10019950mg	gbpln	Capsella rubella	AT1G80790.1 | Symbols: | XH/XS domain-containing protein | chr1:30360280-30362856 FORWARD LENGTH=634	326	634	3.00E-54	194.5	32.8	42.6

Rsa1.0_00096.1.g4792.t1	gb|EOA33755.1| hypothetical protein CARUB_v10019950mg [Capsella rubella]	295	635	5.00E-59	215.3	49.2	66.1	hypothetical protein CARUB_v10019950mg	gbpln	Capsella rubella	AT4G00380.1 | Symbols: | XH/XS domain-containing protein | chr4:167959-170448 FORWARD LENGTH=635	295	635	1.00E-57	215.3	42.0	61.0
Rsa1.0_00096.1.g4793.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00096.1.g4794.t1	gb|EOA33982.1| hypothetical protein CARUB_v10021476mg [Capsella rubella]	259	306	1.00E-133	118.1	92.3	95.8	hypothetical protein CARUB_v10021476mg	gbpln	Capsella rubella	AT1G80760.1 | Symbols: NIP6;1, NIP6, NLM7 | NOD26-like intrinsic protein 6;1 | chr1:30350640-30352015 REVERSE LENGTH=305	259	305	1.00E-133	117.8	91.1	93.8
Rsa1.0_00096.1.g4795.t1	gb|EOA35639.1| hypothetical protein CARUB_v10020853mg [Capsella rubella]	265	249	1.00E-124	94.0	83.0	89.8	hypothetical protein CARUB_v10020853mg	gbpln	Capsella rubella	AT1G80750.1 | Symbols: | Ribosomal protein L30/L7 family protein | chr1:30349052-30350434 FORWARD LENGTH=247	265	247	1.00E-119	93.2	81.1	87.5
Rsa1.0_00096.1.g4796.t1	ref|XP_002887812.1| zinc-finger protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297333653|gb|EFH64071.1| zinc-finger protein 1 [Arabidopsis lyrata subsp. lyrata]	207	220	9.00E-82	106.3	83.1	89.4	zinc-finger protein 1	gbpln	Arabidopsis lyrata	AT1G80730.1 | Symbols: ZFP1, ATZFP1 | zinc-finger protein 1 | chr1:30339493-30340179 REVERSE LENGTH=228	207	228	3.00E-81	110.1	81.2	88.4
Rsa1.0_00096.1.g4797.t3	gb|EOA35616.1| hypothetical protein CARUB_v10020831mg, partial [Capsella rubella]	240	255	1.00E-88	106.3	66.7	75.0	hypothetical protein CARUB_v10020831mg, partial	gbpln	Capsella rubella	AT1G15860.2 | Symbols: | Domain of unknown function (DUF298) | chr1:5455055-5456741 FORWARD LENGTH=227	240	227	8.00E-90	94.6	66.7	75.8
Rsa1.0_00096.1.g4798.t2	dbj|BAJ34529.1| unnamed protein product [Thellungiella halophila]	192	1042	4.00E-72	542.7	72.4	75.0	unnamed protein product	----	----	AT1G80680.1 | Symbols: SAR3, MOS3, PRE, NUP96 | SUPPRESSOR OF AUXIN RESISTANCE 3 | chr1:30324219-30328489 FORWARD LENGTH=1046	192	1046	1.00E-70	544.8	68.2	73.4
Rsa1.0_00096.1.g4799.t1	ref|NP_178182.1| Rae1-like protein [Arabidopsis thaliana] gi|83305440|sp|Q38942.2|RAE1L_ARATH RecName: Full=Rae1-like protein At1g80670 gi|6503279|gb|AAF14655.1|AC011713_3 F23A5.2(form2) [Arabidopsis thaliana] gi|21593271|gb|AAM65220.1| mRNA export protein, putative [Arabidopsis thaliana] gi|94442413|gb|ABF18994.1| At1g80670 [Arabidopsis thaliana] gi|332198314|gb|AEE36435.1| Rae1-like protein [Arabidopsis thaliana]	346	349	0	100.9	92.2	96.2	Rae1-like protein	gbpln	Arabidopsis thaliana	AT1G80670.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:30320809-30323543 REVERSE LENGTH=349	346	349	0	100.9	92.2	96.2
Rsa1.0_00096.1.g4800.t1	ref|NP_178180.1| RNAse THREE-like protein 1 [Arabidopsis thaliana] gi|75264856|sp|Q9M8N2.1|RTL1_ARATH RecName: Full=Ribonuclease 3-like protein 1; AltName: Full=Ribonuclease III-like protein 1; Short=RNase III-like protein 1; AltName: Full=Ribonuclease three-like protein 1 gi|6730736|gb|AAF27126.1|AC018849_14 hypothetical protein; 4021-3030 [Arabidopsis thaliana] gi|26449780|dbj|BAC42013.1| unknown protein [Arabidopsis thaliana] gi|28950719|gb|AAO63283.1| At1g80650 [Arabidopsis thaliana] gi|332198311|gb|AEE36432.1| RNAse THREE-like protein 1 [Arabidopsis thaliana]	208	198	6.00E-51	95.2	62.5	71.2	RNAse THREE-like protein 1	gbpln	Arabidopsis thaliana	AT1G80650.1 | Symbols: RTL1 | RNAse THREE-like protein 1 | chr1:30314609-30315600 FORWARD LENGTH=198	208	198	2.00E-53	95.2	62.5	71.2
Rsa1.0_00096.1.g4801.t1	gb|EOA35187.1| hypothetical protein CARUB_v10020332mg [Capsella rubella]	420	428	0	101.9	87.1	91.7	hypothetical protein CARUB_v10020332mg	gbpln	Capsella rubella	AT1G80640.1 | Symbols: | Protein kinase superfamily protein | chr1:30311979-30314238 FORWARD LENGTH=427	420	427	0	101.7	87.9	92.6
Rsa1.0_00096.1.g4802.t1	gb|EOA35169.1| hypothetical protein CARUB_v10020315mg [Capsella rubella]	392	435	1.00E-133	111.0	72.4	80.6	hypothetical protein CARUB_v10020315mg	gbpln	Capsella rubella	AT1G80620.1 | Symbols: | S15/NS1, RNA-binding protein | chr1:30305404-30307182 FORWARD LENGTH=414	392	414	1.00E-134	105.6	69.9	79.6
Rsa1.0_00096.1.g4803.t1	ref|XP_002892884.1| hypothetical protein ARALYDRAFT_312568 [Arabidopsis lyrata subsp. lyrata] gi|297338726|gb|EFH69143.1| hypothetical protein ARALYDRAFT_312568 [Arabidopsis lyrata subsp. lyrata]	316	308	4.00E-36	97.5	42.7	55.7	hypothetical protein ARALYDRAFT_312568	gbpln	Arabidopsis lyrata	AT1G80610.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15800.1); Has 73 Blast hits to 69 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 2; Plants - 55; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink). | chr1:30301204-30303960 REVERSE LENGTH=211	316	211	4.00E-32	66.8	25.3	27.5

Rsa1.0_00096.1.g4804.t1	ref|NP_178175.1| acetylornithine aminotransferase [Arabidopsis thaliana] gi|75312291|sp|Q9M8M7.1|ARGD_ARATH RecName: Full=Acetylornithine aminotransferase, chloroplastic/mitochondrial; Short=ACOAT; AltName: Full=Acetylornithine transaminase; Short=AOTA; AltName: Full=Protein HOPW1-1-INTERACTING 1; Flags: Precursor gi|6730727|gb|AAF27117.1|AC018849_5 putative acetylornithine transaminase; 18117-19955 [Arabidopsis thaliana] gi|15451028|gb|AAK96785.1| putative acetylornithine transaminase [Arabidopsis thaliana] gi|27311957|gb|AAO00944.1| putative acetylornithine transaminase [Arabidopsis thaliana] gi|158939876|gb|ABW84224.1| putative mitochondrial acetylornithine transaminase [Arabidopsis thaliana] gi|332198305|gb|AEE36426.1| acetylornithine aminotransferase [Arabidopsis thaliana]	451	457	0	101.3	91.8	95.6	acetylornithine aminotransferase	gbpln	Arabidopsis thaliana	AT1G80600.1 | Symbols: WIN1 | HOPW1-1-interacting 1 | chr1:30298675-30300513 REVERSE LENGTH=457	451	457	0	101.3	91.8	95.6
Rsa1.0_00096.1.g4805.t1	ref|NP_176829.1| putative WRKY transcription factor 64 [Arabidopsis thaliana] gi|29839608|sp|Q9C557.1|WRK64_ARATH RecName: Full=Probable WRKY transcription factor 64; AltName: Full=WRKY DNA-binding protein 64 gi|12322262|gb|AAG51157.1|AC074025_7 hypothetical protein [Arabidopsis thaliana] gi|12322288|gb|AAG51170.1|AC079285_3 hypothetical protein [Arabidopsis thaliana] gi|18252119|gb|AAL61860.1| WRKY transcription factor 64 [Arabidopsis thaliana] gi|332196406|gb|AEE34527.1| putative WRKY transcription factor 64 [Arabidopsis thaliana]	262	249	1.00E-64	95.0	52.7	65.6	putative WRKY transcription factor 64	gbpln	Arabidopsis thaliana	AT1G66560.1 | Symbols: WRKY64, ATWRKY64 | WRKY DNA-binding protein 64 | chr1:24833579-24834631 FORWARD LENGTH=249	262	249	3.00E-67	95.0	52.7	65.6
Rsa1.0_00096.1.g4806.t1	ref|NP_001117559.1| putative WRKY transcription factor 67 [Arabidopsis thaliana] gi|12322264|gb|AAG51159.1|AC074025_9 wrky-type DNA binding protein, putative [Arabidopsis thaliana] gi|225898054|dbj|BAH30359.1| hypothetical protein [Arabidopsis thaliana] gi|332196404|gb|AEE34525.1| putative WRKY transcription factor 67 [Arabidopsis thaliana]	258	249	2.00E-60	96.5	48.8	64.0	putative WRKY transcription factor 67	gbpln	Arabidopsis thaliana	AT1G66550.2 | Symbols: WRKY67, ATWRKY67 | WRKY DNA-binding protein 67 | chr1:24828537-24829589 FORWARD LENGTH=249	258	249	5.00E-63	96.5	48.8	64.0
Rsa1.0_00096.1.g4807.t1	ref|XP_002887821.1| ethylene-responsive element-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297333662|gb|EFH64080.1| ethylene-responsive element-binding family protein [Arabidopsis lyrata subsp. lyrata]	260	258	2.00E-72	99.2	67.3	71.2	ethylene-responsive element-binding family protein	gbpln	Arabidopsis lyrata	AT1G80580.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:30293558-30294328 FORWARD LENGTH=256	260	256	8.00E-64	98.5	65.0	72.3
Rsa1.0_00096.1.g4808.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1435	1529	0	106.6	40.8	58.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1435	746	5.00E-93	52.0	12.8	17.4
Rsa1.0_00096.1.g4809.t1	ref|NP_001077854.1| nucleotide-diphospho-sugar transferase [Arabidopsis thaliana] gi|332198263|gb|AEE36384.1| nucleotide-diphospho-sugar transferase [Arabidopsis thaliana]	344	337	1.00E-149	98.0	82.3	88.4	nucleotide-diphospho-sugar transferase	gbpln	Arabidopsis thaliana	AT1G80290.2 | Symbols: | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:30188420-30189574 FORWARD LENGTH=337	344	337	1.00E-152	98.0	82.3	88.4
Rsa1.0_00096.1.g4810.t1	ref|XP_002889297.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335138|gb|EFH65556.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	320	320	1.00E-171	100.0	87.8	93.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G80320.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:30196782-30197896 FORWARD LENGTH=320	320	320	1.00E-170	100.0	86.6	92.5
Rsa1.0_00096.1.g4811.t1	ref|XP_002887836.1| gibberellin 3-oxidase 4 [Arabidopsis lyrata subsp. lyrata] gi|297333677|gb|EFH64095.1| gibberellin 3-oxidase 4 [Arabidopsis lyrata subsp. lyrata]	348	355	1.00E-170	102.0	81.9	91.4	gibberellin 3-oxidase 4	gbpln	Arabidopsis lyrata	AT1G80330.1 | Symbols: ATGA3OX4, GA3OX4 | gibberellin 3-oxidase 4 | chr1:30198061-30199537 REVERSE LENGTH=355	348	355	1.00E-170	102.0	81.9	89.9

Rsa1.0_00096.1.g4812.t1	ref|XP_002887835.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333676|gb|EFH64094.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	359	355	0	98.9	86.4	92.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G80340.1 | Symbols: GA4H, ATGA3OX2, GA3OX2 | gibberellin 3-oxidase 2 | chr1:30200695-30202163 REVERSE LENGTH=347	359	347	1.00E-175	96.7	85.2	90.0
Rsa1.0_00096.1.g4813.t1	ref|XP_002887834.1| katanin [Arabidopsis lyrata subsp. lyrata] gi|297333675|gb|EFH64093.1| katanin [Arabidopsis lyrata subsp. lyrata]	529	522	0	98.7	91.5	95.3	katanin	gbpln	Arabidopsis lyrata	AT1G80350.1 | Symbols: ERH3, AAA1, FRA2, LUE1, ATKTN1, KTN1, FRC2, BOT1, FTR | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:30205499-30208050 REVERSE LENGTH=523	529	523	0	98.9	90.9	94.7
Rsa1.0_00096.1.g4814.t1	gb|EOA33402.1| hypothetical protein CARUB_v10020424mg [Capsella rubella]	383	394	0	102.9	88.8	94.3	hypothetical protein CARUB_v10020424mg	gbpln	Capsella rubella	AT1G80360.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr1:30208736-30210643 REVERSE LENGTH=394	383	394	0	102.9	86.4	93.0
Rsa1.0_00096.1.g4815.t1	gb|EOA35146.1| hypothetical protein CARUB_v10020281mg [Capsella rubella]	443	454	0	102.5	78.1	86.2	hypothetical protein CARUB_v10020281mg	gbpln	Capsella rubella	AT1G80380.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:30217332-30219784 FORWARD LENGTH=456	443	456	0	102.9	78.1	86.0
Rsa1.0_00096.1.g4816.t1	ref|XP_002889294.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297335135|gb|EFH65553.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	398	401	1.00E-172	100.8	79.1	85.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G80400.1 | Symbols: | RING/U-box superfamily protein | chr1:30225864-30227360 FORWARD LENGTH=407	398	407	1.00E-174	102.3	78.9	83.9
Rsa1.0_00096.1.g4817.t5	gb|AAM08130.1|AF324348_1 putative DNA repair protein XRCC1 [Arabidopsis thaliana] gi|11181954|emb|CAC16136.1| putative DNA repair protein XRCC1 [Arabidopsis thaliana]	355	353	1.00E-141	99.4	75.8	82.3	putative DNA repair protein XRCC1	gbpln	Arabidopsis thaliana	AT1G80420.3 | Symbols: ATXRCC1 | BRCT domain-containing DNA repair protein | chr1:30235444-30237163 REVERSE LENGTH=353	355	353	1.00E-143	99.4	75.5	82.0
Rsa1.0_00096.1.g4818.t1	ref|XP_002887829.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297333670|gb|EFH64088.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	170	180	1.00E-61	105.9	77.6	85.3	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT1G80450.1 | Symbols: | VQ motif-containing protein | chr1:30244155-30244688 REVERSE LENGTH=177	170	177	3.00E-63	104.1	74.7	81.2
Rsa1.0_00096.1.g4819.t2	gb|ABK32113.1| At1g80460 [Arabidopsis thaliana]	163	522	3.00E-29	320.2	37.4	40.5	At1g80460	gbpln	Arabidopsis thaliana	AT1G80460.1 | Symbols: NHO1, GLI1 | Actin-like ATPase superfamily protein | chr1:30246960-30249055 REVERSE LENGTH=522	163	522	6.00E-26	320.2	38.0	41.1
Rsa1.0_00096.1.g4820.t1	ref|NP_178163.1| plastid transcriptionally active 17 protein [Arabidopsis thaliana] gi|6730739|gb|AAF27129.1|AC018849_17 hypothetical protein; 58060-60358 [Arabidopsis thaliana] gi|48958493|gb|AAT47799.1| At1g80480 [Arabidopsis thaliana] gi|51536562|gb|AAU05519.1| At1g80480 [Arabidopsis thaliana] gi|332198289|gb|AEE36410.1| plastid transcriptionally active 17 protein [Arabidopsis thaliana]	812	444	0	54.7	46.4	49.1	plastid transcriptionally active 17 protein	gbpln	Arabidopsis thaliana	AT1G80480.1 | Symbols: PTAC17 | plastid transcriptionally active 17 | chr1:30258272-30260570 REVERSE LENGTH=444	812	444	0	54.7	46.4	49.1
Rsa1.0_00096.1.g4821.t1	ref|NP_178169.4| uncharacterized protein [Arabidopsis thaliana] gi|332198296|gb|AEE36417.1| uncharacterized protein AT1G80540 [Arabidopsis thaliana]	536	538	0	100.4	89.6	94.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G80540.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G12400.1); Has 175 Blast hits to 171 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 171; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:30281638-30284258 REVERSE LENGTH=538	536	538	0	100.4	89.6	94.0
Rsa1.0_00096.1.g4822.t1	ref|XP_002889287.1| hypothetical protein ARALYDRAFT_895936 [Arabidopsis lyrata subsp. lyrata] gi|297335128|gb|EFH65546.1| hypothetical protein ARALYDRAFT_895936 [Arabidopsis lyrata subsp. lyrata]	409	404	0	98.8	85.1	89.2	hypothetical protein ARALYDRAFT_895936	gbpln	Arabidopsis lyrata	AT1G80560.1 | Symbols: ATIMD2, IMD2 | isopropylmalate dehydrogenase 2 | chr1:30287833-30290126 FORWARD LENGTH=405	409	405	1.00E-148	99.0	61.9	77.5
Rsa1.0_00096.1.g4823.t1	ref|XP_002889287.1| hypothetical protein ARALYDRAFT_895936 [Arabidopsis lyrata subsp. lyrata] gi|297335128|gb|EFH65546.1| hypothetical protein ARALYDRAFT_895936 [Arabidopsis lyrata subsp. lyrata]	415	404	1.00E-137	97.3	57.3	73.0	hypothetical protein ARALYDRAFT_895936	gbpln	Arabidopsis lyrata	AT1G80560.1 | Symbols: ATIMD2, IMD2 | isopropylmalate dehydrogenase 2 | chr1:30287833-30290126 FORWARD LENGTH=405	415	405	1.00E-138	97.6	56.9	74.0
Rsa1.0_00096.1.g4824.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	411	1223	7.00E-11	297.6	9.2	13.1	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	411	746	1.00E-11	181.5	10.2	14.1

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<tr><td>Rsa1.0_00096.1.g4825.t1</td><td>sp|P29102.1|LEU3_BRANA RecName: Full=3-isopropylmalate dehydrogenase, chloroplastic; Short=3-IPM-DH; Short=IMDH; AltName: Full=Beta-IPM dehydrogenase; Flags: Precursor gi|17827|emb|CAA42596.1| 3-isopropylmalate dehydrogenase [Brassica napus]</td><td>402</td><td>406</td><td>0</td><td>101.0</td><td>98.3</td><td>99.3</td><td>RecName: Full=3-isopropylmalate dehydrogenase, chloroplastic; Short=3-IPM-DH; Short=IMDH; AltName: Full=Beta-IPM dehydrogenase; Flags: Precursor gi|17827|emb|CAA42596.1| 3-isopropylmalate dehydrogenase</td><td>gbpln</td><td>Brassica napus</td><td>AT1G80560.1 | Symbols: ATIMD2, IMD2 | isopropylmalate dehydrogenase 2 | chr1:30287833-30290126 FORWARD LENGTH=405</td><td>402</td><td>405</td><td>0</td><td>100.7</td><td>92.8</td><td>96.3</td></tr>
<tr><td>Rsa1.0_00096.1.g4826.t2</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>370</td><td>1142</td><td>5.00E-26</td><td>308.6</td><td>19.5</td><td>24.3</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256</td><td>370</td><td>256</td><td>1.00E-18</td><td>69.2</td><td>17.8</td><td>28.6</td></tr>
<tr><td>Rsa1.0_00097.1.g4827.t1</td><td>gb|EOA37184.1| hypothetical protein CARUB_v10010566mg [Capsella rubella]</td><td>172</td><td>148</td><td>2.00E-51</td><td>86.0</td><td>66.3</td><td>72.7</td><td>hypothetical protein CARUB_v10010566mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G04555.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G33380.1); Has 84 Blast hits to 83 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 9; Fungi - 0; Plants - 75; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1242743-1243949 FORWARD LENGTH=152</td><td>172</td><td>152</td><td>2.00E-53</td><td>88.4</td><td>65.1</td><td>72.1</td></tr>
<tr><td>Rsa1.0_00097.1.g4828.t9</td><td>gb|EOA40141.1| hypothetical protein CARUB_v10008852mg [Capsella rubella]</td><td>828</td><td>522</td><td>1.00E-123</td><td>63.0</td><td>25.4</td><td>26.6</td><td>hypothetical protein CARUB_v10008852mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G04510.1 | Symbols: MAC3A | MOS4-associated complex 3A | chr1:1226749-1230592 FORWARD LENGTH=523</td><td>828</td><td>523</td><td>1.00E-120</td><td>63.2</td><td>25.0</td><td>26.0</td></tr>
<tr><td>Rsa1.0_00097.1.g4829.t1</td><td>ref|NP_171944.2| CCT motif-containing protein [Arabidopsis thaliana] gi|91805737|gb|ABE65597.1| zinc finger CONSTANS-like protein [Arabidopsis thaliana] gi|225897874|dbj|BAH30269.1| hypothetical protein [Arabidopsis thaliana] gi|332189584|gb|AEE27705.1| CCT motif-containing protein [Arabidopsis thaliana]</td><td>360</td><td>386</td><td>1.00E-158</td><td>107.2</td><td>82.5</td><td>87.8</td><td>CCT motif-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G04500.1 | Symbols: | CCT motif family protein | chr1:1221757-1224235 REVERSE LENGTH=386</td><td>360</td><td>386</td><td>1.00E-161</td><td>107.2</td><td>82.5</td><td>87.8</td></tr>
<tr><td>Rsa1.0_00097.1.g4830.t1</td><td>gb|EOA31608.1| hypothetical protein CARUB_v10014805mg, partial [Capsella rubella]</td><td>140</td><td>161</td><td>8.00E-75</td><td>115.0</td><td>100.0</td><td>100.0</td><td>hypothetical protein CARUB_v10014805mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G04400.1 | Symbols: emb2171 | Ribosomal protein L14p/L23e family protein | chr3:1167339-1168308 FORWARD LENGTH=140</td><td>140</td><td>140</td><td>8.00E-77</td><td>100.0</td><td>100.0</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00097.1.g4831.t1</td><td>ref|XP_002889506.1| hypothetical protein ARALYDRAFT_470423 [Arabidopsis lyrata subsp. lyrata] gi|297335348|gb|EFH65765.1| hypothetical protein ARALYDRAFT_470423 [Arabidopsis lyrata subsp. lyrata]</td><td>168</td><td>154</td><td>3.00E-28</td><td>91.7</td><td>47.6</td><td>57.7</td><td>hypothetical protein ARALYDRAFT_470423</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G04445.1 | Symbols: | C2H2-like zinc finger protein | chr1:1207344-1207862 FORWARD LENGTH=172</td><td>168</td><td>172</td><td>5.00E-25</td><td>102.4</td><td>47.0</td><td>60.1</td></tr>
<tr><td>Rsa1.0_00097.1.g4832.t1</td><td>ref|NP_563706.1| putative methyltransferase PMT8 [Arabidopsis thaliana] gi|186478123|ref|NP_001117225.1| putative methyltransferase PMT8 [Arabidopsis thaliana] gi|75249499|sp|Q940J9.1|PMT8_ARATH RecName: Full=Probable methyltransferase PMT8 gi|15450900|gb|AAK96721.1| Unknown protein [Arabidopsis thaliana] gi|17978687|gb|AAL47337.1| unknown protein [Arabidopsis thaliana] gi|332189575|gb|AEE27696.1| putative methyltransferase PMT8 [Arabidopsis thaliana] gi|332189576|gb|AEE27697.1| putative methyltransferase PMT8 [Arabidopsis thaliana]</td><td>621</td><td>623</td><td>0</td><td>100.3</td><td>91.8</td><td>96.9</td><td>putative methyltransferase PMT8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G04430.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:1198860-1201301 FORWARD LENGTH=623</td><td>621</td><td>623</td><td>0</td><td>100.3</td><td>91.8</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00097.1.g4833.t1</td><td>dbj|BAJ34213.1| unnamed protein product [Thellungiella halophila]</td><td>332</td><td>332</td><td>0</td><td>100.0</td><td>98.2</td><td>99.7</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G04410.1 | Symbols: | Lactate/malate dehydrogenase family protein | chr1:1189418-1191267 REVERSE LENGTH=332</td><td>332</td><td>332</td><td>0</td><td>100.0</td><td>97.6</td><td>99.7</td></tr>
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Rsa1.0_00097.1.g4834.t7	ref|XP_002892212.1| hypothetical protein ARALYDRAFT_470414 [Arabidopsis lyrata subsp. lyrata] gi|297338054|gb|EFH68471.1| hypothetical protein ARALYDRAFT_470414 [Arabidopsis lyrata subsp. lyrata]	194	346	2.00E-76	178.4	74.2	83.5	hypothetical protein ARALYDRAFT_470414	gbpln	Arabidopsis lyrata	AT1G04380.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:1177142-1178384 REVERSE LENGTH=345	194	345	2.00E-76	177.8	72.7	82.5
Rsa1.0_00097.1.g4835.t1	ref|XP_002889500.1| hypothetical protein ARALYDRAFT_470412 [Arabidopsis lyrata subsp. lyrata] gi|297335342|gb|EFH65759.1| hypothetical protein ARALYDRAFT_470412 [Arabidopsis lyrata subsp. lyrata]	350	361	1.00E-166	103.1	82.6	89.1	hypothetical protein ARALYDRAFT_470412	gbpln	Arabidopsis lyrata	AT1G04350.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:1165296-1166538 FORWARD LENGTH=360	350	360	1.00E-164	102.9	80.0	87.7
Rsa1.0_00097.1.g4836.t1	gb|AAO11668.1| hypothetical protein [Arabidopsis thaliana]	95	221	6.00E-13	232.6	37.9	58.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G04420.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:1535561-1536226 FORWARD LENGTH=221	95	221	2.00E-15	232.6	37.9	58.9
Rsa1.0_00097.1.g4837.t1	ref|NP_171929.1| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana] gi|2341039|gb|AAB70443.1| Similar to Nicotiana lesion-inducing ORF (gb|U66269) [Arabidopsis thaliana] gi|17979509|gb|AAL50090.1| At1g04340/F19P19_23 [Arabidopsis thaliana] gi|20147297|gb|AAM10362.1| At1g04340/F19P19_23 [Arabidopsis thaliana] gi|332189565|gb|AEE27686.1| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana]	168	159	8.00E-61	94.6	70.8	81.0	HR-like lesion-inducing protein-like protein	gbpln	Arabidopsis thaliana	AT1G04340.1 | Symbols: | HR-like lesion-inducing protein-related | chr1:1163345-1164737 REVERSE LENGTH=159	168	159	3.00E-63	94.6	70.8	81.0
Rsa1.0_00097.1.g4838.t1	ref|NP_171927.1| ethylene response sensor 2 [Arabidopsis thaliana] gi|75101250|sp|P93825.2|ERS2_ARATH RecName: Full=Ethylene response sensor 2; Short=AtERS2; AltName: Full=Protein ERS2 gi|2341041|gb|AAB70445.1| Arabidopsis thaliana putative ethylene receptor (ERS2) gene (gb|AF047976). EST gb|W43451 comes from this gene [Arabidopsis thaliana] gi|3687656|gb|AAC62209.1| putative ethylene receptor [Arabidopsis thaliana] gi|332189563|gb|AEE27684.1| ethylene response sensor 2 [Arabidopsis thaliana]	626	645	0	103.0	79.2	86.3	ethylene response sensor 2	gbpln	Arabidopsis thaliana	AT1G04310.1 | Symbols: ERS2 | ethylene response sensor 2 | chr1:1155116-1157125 REVERSE LENGTH=645	626	645	0	103.0	79.2	86.3
Rsa1.0_00097.1.g4839.t1	ref|XP_002892207.1| hypothetical protein ARALYDRAFT_470409 [Arabidopsis lyrata subsp. lyrata] gi|297338049|gb|EFH68466.1| hypothetical protein ARALYDRAFT_470409 [Arabidopsis lyrata subsp. lyrata]	1056	1071	0	101.4	79.7	86.6	hypothetical protein ARALYDRAFT_470409	gbpln	Arabidopsis lyrata	AT1G04300.1 | Symbols: | TRAF-like superfamily protein | chr1:1148818-1153895 REVERSE LENGTH=1074	1056	1074	0	101.7	79.0	86.6
Rsa1.0_00097.1.g4840.t1	ref|XP_002892206.1| thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338048|gb|EFH68465.1| thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	160	155	2.00E-59	96.9	73.8	81.9	thioesterase family protein	gbpln	Arabidopsis lyrata	AT1G04290.1 | Symbols: | Thioesterase superfamily protein | chr1:1147721-1148352 REVERSE LENGTH=155	160	155	2.00E-61	96.9	73.1	81.3
Rsa1.0_00097.1.g4841.t1	gb|EOA39428.1| hypothetical protein CARUB_v10012550mg [Capsella rubella]	286	538	1.00E-111	188.1	69.9	76.6	hypothetical protein CARUB_v10012550mg	gbpln	Capsella rubella	AT1G04280.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:1143643-1146541 REVERSE LENGTH=534	286	534	1.00E-112	186.7	68.9	76.9
Rsa1.0_00097.1.g4842.t1	gb|EOA36082.1| hypothetical protein CARUB_v10010394mg, partial [Capsella rubella]	152	186	1.00E-81	122.4	98.7	100.0	hypothetical protein CARUB_v10010394mg, partial	gbpln	Capsella rubella	AT1G04270.1 | Symbols: RPS15 | cytosolic ribosomal protein S15 | chr1:1141852-1142960 REVERSE LENGTH=152	152	152	8.00E-84	100.0	99.3	99.3
Rsa1.0_00097.1.g4843.t1	gb|EOA36534.1| hypothetical protein CARUB_v10011583mg [Capsella rubella]	176	182	1.00E-80	103.4	86.9	93.8	hypothetical protein CARUB_v10011583mg	gbpln	Capsella rubella	AT1G04260.1 | Symbols: MPI7, MPIP7, PRA1.D | CAMV movement protein interacting protein 7 | chr1:1140749-1141297 REVERSE LENGTH=182	176	182	1.00E-82	103.4	85.2	94.3

Rsa1.0_00097.1.g4844.t1	ref|NP_171921.1| auxin-responsive protein IAA17 [Arabidopsis thaliana] gi|11131276|sp|P93830.2|IAA17_ARATH RecName: Full=Auxin-responsive protein IAA17; AltName: Full=Auxin response 3; AltName: Full=Indoleacetic acid-induced protein 17 gi|12484197|gb|AAG53997.1|AF336916_1 auxin-induced protein, IAA17/AXR3-1 [Arabidopsis thaliana] gi|2618723|gb|AAB84354.1| IAA17 [Arabidopsis thaliana] gi|2921756|gb|AAC39439.1| IAA17/AXR3 protein [Arabidopsis thaliana] gi|4389514|gb|AAB70451.2| Identical to Arabidopsis gb|AF040632 and gb|U49073 IAA17/AXR3 gene. ESTs gb|H36782 and gb|F14074 come from this gene [Arabidopsis thaliana] gi|17979185|gb|AAL49831.1| auxin-induced protein IAA17/AXR3-1 [Arabidopsis thaliana] gi|21436239|gb|AAM51258.1| auxin-induced protein IAA17/AXR3-1 [Arabidopsis thaliana] gi|332189553|gb|AEE27674.1| auxin-responsive protein IAA17 [Arabidopsis thaliana]	229	229	1.00E-118	100.0	90.0	93.4	auxin-responsive protein IAA17	gbpln	Arabidopsis thaliana	AT1G04250.1 | Symbols: AXR3, IAA17 | AUX/IAA transcriptional regulator family protein | chr1:1136382-1138340 FORWARD LENGTH=229	229	229	1.00E-120	100.0	90.0	93.4
Rsa1.0_00097.1.g4845.t1	ref|NP_171918.1| 3-ketoacyl-CoA synthase 17 [Arabidopsis thaliana] gi|114149942|sp|Q5XEP9.2|KCS17_ARATH RecName: Full=3-ketoacyl-CoA synthase 17; Short=KCS-17; AltName: Full=Very long-chain fatty acid condensing enzyme 17; Short=VLCFA condensing enzyme 17 gi|3142289|gb|AAC16740.1| Strong similarity to beta-keto-Coa synthase gb|U37088 from Simmondsia chinensis [Arabidopsis thaliana] gi|332189550|gb|AEE27671.1| 3-ketoacyl-CoA synthase 17 [Arabidopsis thaliana]	499	528	0	105.8	85.6	90.8	3-ketoacyl-CoA synthase 17	gbpln	Arabidopsis thaliana	AT1G04220.1 | Symbols: KCS2 | 3-ketoacyl-CoA synthase 2 | chr1:1119853-1122483 REVERSE LENGTH=528	499	528	0	105.8	85.6	90.8
Rsa1.0_00097.1.g4846.t1	ref|NP_171915.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana] gi|19423984|gb|AAL87273.1| unknown protein [Arabidopsis thaliana] gi|21281239|gb|AAM45091.1| unknown protein [Arabidopsis thaliana] gi|332189547|gb|AEE27668.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	325	328	1.00E-168	100.9	90.2	93.8	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G04190.1 | Symbols: TPR3 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1106617-1108557 REVERSE LENGTH=328	325	328	1.00E-171	100.9	90.2	93.8
Rsa1.0_00097.1.g4847.t1	gb|EOA40138.1| hypothetical protein CARUB_v10008849mg, partial [Capsella rubella]	465	523	0	112.5	95.9	98.3	hypothetical protein CARUB_v10008849mg, partial	gbpln	Capsella rubella	AT1G04170.1 | Symbols: EIF2 GAMMA | eukaryotic translation initiation factor 2 gamma subunit | chr1:1097423-1099702 FORWARD LENGTH=465	465	465	0	100.0	95.9	98.1
Rsa1.0_00097.1.g4848.t1	gb|EOA37524.1| hypothetical protein CARUB_v10011722mg [Capsella rubella]	826	790	0	95.6	82.3	86.9	hypothetical protein CARUB_v10011722mg	gbpln	Capsella rubella	AT1G04140.2 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr1:1075992-1080321 REVERSE LENGTH=793	826	793	0	96.0	79.9	85.6
Rsa1.0_00097.1.g4849.t1	ref|XP_002889490.1| hypothetical protein ARALYDRAFT_333729 [Arabidopsis lyrata subsp. lyrata] gi|297335332|gb|EFH65749.1| hypothetical protein ARALYDRAFT_333729 [Arabidopsis lyrata subsp. lyrata]	753	1328	0	176.4	79.8	86.6	hypothetical protein ARALYDRAFT_333729	gbpln	Arabidopsis lyrata	AT1G04080.1 | Symbols: PRP39 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1051803-1056550 FORWARD LENGTH=768	753	768	0	102.0	82.5	89.4
Rsa1.0_00097.1.g4850.t1	ref|NP_563698.1| HAD superfamily, subfamily IIIB acid phosphatase [Arabidopsis thaliana] gi|13926198|gb|AAK49578.1|AF370572_1 Similar to acid phosphatase [Arabidopsis thaliana] gi|16226693|gb|AAL16234.1|AF428465_1 At1g04040/F21M11_2 [Arabidopsis thaliana] gi|4204285|gb|AAD10666.1| Similar to acid phosphatase [Arabidopsis thaliana] gi|332189528|gb|AEE27649.1| HAD superfamily, subfamily IIIB acid phosphatase [Arabidopsis thaliana]	271	271	1.00E-138	100.0	84.1	93.4	HAD superfamily, subfamily IIIB acid phosphatase	gbpln	Arabidopsis thaliana	AT1G04040.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr1:1042564-1043819 REVERSE LENGTH=271	271	271	1.00E-140	100.0	84.1	93.4

Rsa1.0_00097.1.g4851.t1	ref|XP_002889488.1| ATBARD1/BARD1 [Arabidopsis lyrata subsp. lyrata] gi|297335330|gb|EFH65747.1| ATBARD1/BARD1 [Arabidopsis lyrata subsp. lyrata]	698	708	0	101.4	76.2	83.5	ATBARD1/BARD1	gbpln	Arabidopsis lyrata	AT1G04020.2 | Symbols: ATBARD1, BARD1 | breast cancer associated RING 1 | chr1:1036610-1040045 FORWARD LENGTH=713	698	713	0	102.1	75.1	83.8
Rsa1.0_00097.1.g4852.t1	ref|XP_002889485.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297335327|gb|EFH65744.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	534	539	0	100.9	85.0	91.2	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT1G03960.1 | Symbols: | Calcium-binding EF hand family protein | chr1:1014085-1017472 FORWARD LENGTH=529	534	529	0	99.1	83.3	89.5
Rsa1.0_00097.1.g4853.t1	ref|XP_002892189.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|297338031|gb|EFH68448.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	211	210	1.00E-108	99.5	93.4	97.2	SNF7 family protein	gbpln	Arabidopsis lyrata	AT1G03950.1 | Symbols: VPS2.3 | vacuolar protein sorting-associated protein 2.3 | chr1:1011388-1013212 REVERSE LENGTH=210	211	210	1.00E-110	99.5	93.4	96.2
Rsa1.0_00097.1.g4854.t1	ref|XP_002892187.1| transferase [Arabidopsis lyrata subsp. lyrata] gi|297338029|gb|EFH68446.1| transferase [Arabidopsis lyrata subsp. lyrata]	477	464	0	97.3	79.7	87.8	transferase	gbpln	Arabidopsis lyrata	AT1G03940.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:1009542-1010951 REVERSE LENGTH=469	477	469	0	98.3	79.0	87.6
Rsa1.0_00097.1.g4855.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00097.1.g4856.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00097.1.g4857.t1	gb|EOA38377.1| hypothetical protein CARUB_v10009912mg [Capsella rubella]	292	290	1.00E-150	99.3	90.4	94.2	hypothetical protein CARUB_v10009912mg	gbpln	Capsella rubella	AT1G03905.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:993478-995594 FORWARD LENGTH=290	292	290	1.00E-150	99.3	91.1	94.2
Rsa1.0_00097.1.g4858.t1	ref|NP_563693.1| non-intrinsic ABC protein 4 [Arabidopsis thaliana] gi|75116803|sp|Q681Q7.1|Y1390_ARATH RecName: Full=Uncharacterized protein At1g03900 gi|51968466|dbj|BAD42925.1| unknown protein [Arabidopsis thaliana] gi|51969262|dbj|BAD43323.1| unknown protein [Arabidopsis thaliana] gi|51970966|dbj|BAD44175.1| unknown protein [Arabidopsis thaliana] gi|332189509|gb|AEE27630.1| non-intrinsic ABC protein 4 [Arabidopsis thaliana]	261	272	3.00E-38	104.2	46.4	47.5	non-intrinsic ABC protein 4	gbpln	Arabidopsis thaliana	AT1G03900.1 | Symbols: ATNAP4, NAP4 | non-intrinsic ABC protein 4 | chr1:991252-992852 FORWARD LENGTH=272	261	272	8.00E-41	104.2	46.4	47.5
Rsa1.0_00097.1.g4859.t2	gb|EOA35015.1| hypothetical protein CARUB_v10020118mg [Capsella rubella]	563	535	0	95.0	87.0	92.0	hypothetical protein CARUB_v10020118mg	gbpln	Capsella rubella	AT1G65660.1 | Symbols: SMP1 | Pre-mRNA splicing Prp18-interacting factor | chr1:24418295-24421231 REVERSE LENGTH=535	563	535	0	95.0	86.7	91.7
Rsa1.0_00097.1.g4860.t2	gb|EOA38381.1| hypothetical protein CARUB_v10009925mg [Capsella rubella]	515	286	1.00E-160	55.5	54.2	55.0	hypothetical protein CARUB_v10009925mg	gbpln	Capsella rubella	AT1G03860.3 | Symbols: ATPHB2, PHB2 | prohibitin 2 | chr1:979611-981157 REVERSE LENGTH=286	515	286	1.00E-155	55.5	53.6	55.0
Rsa1.0_00097.1.g4861.t1	ref|NP_563691.1| monothiol glutaredoxin-S13 [Arabidopsis thaliana] gi|119370631|sp|Q84TF4.2|GRS13_ARATH RecName: Full=Monothiol glutaredoxin-S13; Short=AtGrxS13; AltName: Full=Protein ROXY 18 gi|14334678|gb|AAK59517.1| unknown protein [Arabidopsis thaliana] gi|17104675|gb|AAL34226.1| unknown protein [Arabidopsis thaliana] gi|21555130|gb|AAM63783.1| unknown [Arabidopsis thaliana] gi|110736837|dbj|BAF00376.1| hypothetical protein [Arabidopsis thaliana] gi|332189502|gb|AEE27623.1| monothiol glutaredoxin-S13 [Arabidopsis thaliana]	153	150	1.00E-50	98.0	69.9	81.0	monothiol glutaredoxin-S13	gbpln	Arabidopsis thaliana	AT1G03850.2 | Symbols: | Glutaredoxin family protein | chr1:977233-977685 REVERSE LENGTH=150	153	150	4.00E-53	98.0	69.9	81.0
Rsa1.0_00097.1.g4862.t4	ref|NP_001184903.1| guanylate-binding protein [Arabidopsis thaliana] gi|332189498|gb|AEE27619.1| guanylate-binding protein [Arabidopsis thaliana]	647	1013	1.00E-142	156.6	40.3	44.5	guanylate-binding protein	gbpln	Arabidopsis thaliana	AT1G03830.2 | Symbols: | guanylate-binding family protein | chr1:962128-966622 REVERSE LENGTH=1013	647	1013	1.00E-145	156.6	40.3	44.5
Rsa1.0_00097.1.g4863.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00097.1.g4864.t1	ref|XP_002879939.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325778|gb|EFH56198.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	197	236	5.00E−26	119.8	49.2	66.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G41470.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41440.1); Has 1066 Blast hits to 825 proteins in 144 species: Archae − 7; Bacteria − 46; Metazoa − 465; Fungi − 36; Plants − 67; Viruses − 4; Other Eukaryotes − 441 (source: NCBI BLink). | chr2:17289952−17293749 REVERSE LENGTH=414	197	414	4.00E−27	210.2	44.7	56.3
Rsa1.0_00097.1.g4865.t1	dbj|BAJ33922.1| unnamed protein product [Thellungiella halophila]	49	226	1.00E−12	461.2	81.6	85.7	unnamed protein product	----	----	AT1G04250.1 | Symbols: AXR3, IAA17 | AUX/IAA transcriptional regulator family protein | chr1:1136382−1138340 FORWARD LENGTH=229	49	229	3.00E−15	467.3	81.6	83.7
Rsa1.0_00098.1.g4866.t2	ref|XP_002864957.1| hypothetical protein ARALYDRAFT_332761 [Arabidopsis lyrata subsp. lyrata] gi|297310792|gb|EFH41216.1| hypothetical protein ARALYDRAFT_332761 [Arabidopsis lyrata subsp. lyrata]	666	731	0	109.8	56.5	64.1	hypothetical protein ARALYDRAFT_332761	gbpln	Arabidopsis lyrata	AT5G65450.1 | Symbols: UBP17 | ubiquitin−specific protease 17 | chr5:26157863−26161096 FORWARD LENGTH=731	666	731	0	109.8	56.6	63.2
Rsa1.0_00098.1.g4867.t1	ref|NP_201321.1| VQ motif−containing protein [Arabidopsis thaliana] gi|10178179|dbj|BAB11653.1| unnamed protein product [Arabidopsis thaliana] gi|44917435|gb|AAS49042.1| At5g65170 [Arabidopsis thaliana] gi|46931270|gb|AAT06439.1| At5g65170 [Arabidopsis thaliana] gi|332010630|gb|AED98013.1| VQ motif−containing protein [Arabidopsis thaliana]	357	362	1.00E−110	101.4	70.0	76.8	VQ motif−containing protein	gbpln	Arabidopsis thaliana	AT5G65170.1 | Symbols: | VQ motif−containing protein | chr5:26041218−26042306 FORWARD LENGTH=362	357	362	1.00E−113	101.4	70.0	76.8
Rsa1.0_00098.1.g4868.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00098.1.g4869.t1	gb|EOA12626.1| hypothetical protein CARUB_v10027509mg [Capsella rubella]	590	591	0	100.2	88.6	93.2	hypothetical protein CARUB_v10027509mg	gbpln	Capsella rubella	AT5G65160.1 | Symbols: TPR14 | tetratricopeptide repeat (TPR)−containing protein | chr5:26031457−26033668 REVERSE LENGTH=593	590	593	0	100.5	87.1	91.2
Rsa1.0_00098.1.g4870.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00098.1.g4871.t1	gb|EOA13558.1| hypothetical protein CARUB_v10026620mg [Capsella rubella]	377	369	0	97.9	82.8	89.1	hypothetical protein CARUB_v10026620mg	gbpln	Capsella rubella	AT5G65140.1 | Symbols: TPPJ | Haloacid dehalogenase−like hydrolase (HAD) superfamily protein | chr5:26019878−26022077 REVERSE LENGTH=370	377	370	1.00E−179	98.1	83.3	89.4
Rsa1.0_00098.1.g4872.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00098.1.g4873.t1	ref|NP_181032.1| embryo sac development arrest 3 protein [Arabidopsis thaliana] gi|145330358|ref|NP_001078004.1| embryo sac development arrest 3 protein [Arabidopsis thaliana] gi|3033382|gb|AAC12826.1| unknown protein [Arabidopsis thaliana] gi|20466396|gb|AAM20515.1| unknown protein [Arabidopsis thaliana] gi|22136346|gb|AAM91251.1| unknown protein [Arabidopsis thaliana] gi|330253937|gb|AEC09031.1| embryo sac development arrest 3 protein [Arabidopsis thaliana] gi|330253938|gb|AEC09032.1| embryo sac development arrest 3 protein [Arabidopsis thaliana]	340	186	6.00E−33	54.7	22.4	25.6	embryo sac development arrest 3 protein	gbpln	Arabidopsis thaliana	AT2G34860.2 | Symbols: EDA3 | DnaJ/Hsp40 cysteine−rich domain superfamily protein | chr2:14708380−14709804 FORWARD LENGTH=186	340	186	1.00E−35	54.7	22.4	25.6
Rsa1.0_00098.1.g4874.t1	ref|XP_002866642.1| hypothetical protein ARALYDRAFT_496712 [Arabidopsis lyrata subsp. lyrata] gi|297312477|gb|EFH42901.1| hypothetical protein ARALYDRAFT_496712 [Arabidopsis lyrata subsp. lyrata]	560	559	0	99.8	65.5	78.6	hypothetical protein ARALYDRAFT_496712	gbpln	Arabidopsis lyrata	AT5G64930.1 | Symbols: CPR5, HYS1 | CPR5 protein, putative | chr5:25945885−25948321 REVERSE LENGTH=564	560	564	0	100.7	62.1	77.0
Rsa1.0_00098.1.g4875.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00098.1.g4876.t1	gb|EOA14237.1| hypothetical protein CARUB_v10027392mg [Capsella rubella]	108	116	7.00E−21	107.4	51.9	68.5	hypothetical protein CARUB_v10027392mg	gbpln	Capsella rubella	AT5G64900.1 | Symbols: PROPEP1, ATPEP1, PEP1 | precursor of peptide 1 | chr5:25937253−25937939 FORWARD LENGTH=92	108	92	3.00E−21	85.2	47.2	63.0

Rsa1.0_00098.1.g4877.t1	ref|NP_568999.1| uncharacterized protein [Arabidopsis thaliana] gi|8843752|dbj|BAA97300.1| unnamed protein product [Arabidopsis thaliana] gi|110738041|dbj|BAF00955.1| hypothetical protein [Arabidopsis thaliana] gi|332010581|gb|AED97964.1| uncharacterized protein AT5G64880 [Arabidopsis thaliana]	156	171	1.00E-38	109.6	66.7	80.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G64880.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:25932353-25933874 FORWARD LENGTH=171	156	171	4.00E-41	109.6	66.7	80.1
Rsa1.0_00098.1.g4878.t1	ref|XP_002866640.1| hypothetical protein ARALYDRAFT_496707 [Arabidopsis lyrata subsp. lyrata] gi|297312475|gb|EFH42899.1| hypothetical protein ARALYDRAFT_496707 [Arabidopsis lyrata subsp. lyrata]	472	479	0	101.5	91.3	96.2	hypothetical protein ARALYDRAFT_496707	gbpln	Arabidopsis lyrata	AT5G64870.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr5:25929776-25931308 REVERSE LENGTH=479	472	479	0	101.5	92.8	97.0
Rsa1.0_00098.1.g4879.t1	ref|XP_002864926.1| hypothetical protein ARALYDRAFT_496705 [Arabidopsis lyrata subsp. lyrata] gi|297310761|gb|EFH41185.1| hypothetical protein ARALYDRAFT_496705 [Arabidopsis lyrata subsp. lyrata]	114	114	2.00E-38	100.0	76.3	80.7	hypothetical protein ARALYDRAFT_496705	gbpln	Arabidopsis lyrata	AT5G64850.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: RPM1-interacting protein 4, defence response (InterPro:IPR008700); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G09960.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:25921585-25923038 FORWARD LENGTH=114	114	114	2.00E-40	100.0	74.6	79.8
Rsa1.0_00098.1.g4880.t1	gb|EOA13510.1| hypothetical protein CARUB_v10026577mg, partial [Capsella rubella]	523	386	1.00E-157	73.8	55.1	60.6	hypothetical protein CARUB_v10026577mg, partial	gbpln	Capsella rubella	AT5G64830.1 | Symbols: | programmed cell death 2 C-terminal domain-containing protein | chr5:25914911-25916512 REVERSE LENGTH=380	523	380	1.00E-150	72.7	55.1	61.2
Rsa1.0_00098.1.g4881.t1	dbj|BAA97293.1| unnamed protein product [Arabidopsis thaliana]	129	651	1.00E-61	504.7	87.6	89.1	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G64816.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:25913487-25913879 FORWARD LENGTH=130	129	130	5.00E-62	100.8	87.6	89.1
Rsa1.0_00098.1.g4882.t1	ref|NP_568996.1| Ras-related small GTP-binding family protein [Arabidopsis thaliana] gi|29839609|sp|Q9C5J9.1|Y5483_ARATH RecName: Full=Uncharacterized GTP-binding protein At5g64813 gi|13430582|gb|AAK25913.1|AF360203_1 unknown protein [Arabidopsis thaliana] gi|14532852|gb|AAK64108.1| unknown protein [Arabidopsis thaliana] gi|332010571|gb|AED97954.1| Ras-related small GTP-binding family protein [Arabidopsis thaliana]	346	342	0	98.8	93.4	95.4	Ras-related small GTP-binding family protein	gbpln	Arabidopsis thaliana	AT5G64813.1 | Symbols: LIP1 | Ras-related small GTP-binding family protein | chr5:25910836-25912625 FORWARD LENGTH=342	346	342	0	98.8	93.4	95.4
Rsa1.0_00098.1.g4883.t1	ref|XP_002864923.1| WRKY DNA-binding protein 51 [Arabidopsis lyrata subsp. lyrata] gi|297310758|gb|EFH41182.1| WRKY DNA-binding protein 51 [Arabidopsis lyrata subsp. lyrata]	206	194	2.00E-85	94.2	79.1	87.4	WRKY DNA-binding protein 51	gbpln	Arabidopsis lyrata	AT5G64810.1 | Symbols: WRKY51, ATWRKY51 | WRKY DNA-binding protein 51 | chr5:25908415-25909687 FORWARD LENGTH=194	206	194	2.00E-87	94.2	78.6	87.9
Rsa1.0_00098.1.g4884.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00098.1.g4885.t1	ref|XP_002891409.1| hypothetical protein ARALYDRAFT_336931 [Arabidopsis lyrata subsp. lyrata] gi|297337251|gb|EFH67668.1| hypothetical protein ARALYDRAFT_336931 [Arabidopsis lyrata subsp. lyrata]	279	379	4.00E-25	135.8	39.4	55.9	hypothetical protein ARALYDRAFT_336931	gbpln	Arabidopsis lyrata	AT4G21240.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:11322411-11323664 FORWARD LENGTH=417	279	417	3.00E-24	149.5	41.6	57.7
Rsa1.0_00098.1.g4886.t1	gb|EOA13972.1| hypothetical protein CARUB_v10027097mg, partial [Capsella rubella]	171	219	3.00E-66	128.1	74.9	86.5	hypothetical protein CARUB_v10027097mg, partial	gbpln	Capsella rubella	AT5G64780.1 | Symbols: | Uncharacterised conserved protein UCP009193 | chr5:25900700-25901955 REVERSE LENGTH=175	171	175	1.00E-66	102.3	75.4	85.4

Rsa1.0_00098.1.g4887.t1	ref|NP_201282.1| uncharacterized protein [Arabidopsis thaliana] gi|75170417|sp|Q9FGF6.1|RGF9_ARATH RecName: Full=Root meristem growth factor 9; Short=AtRGF9; Flags: Precursor gi|10177208|dbj|BAB10310.1| unnamed protein product [Arabidopsis thaliana] gi|27311821|gb|AAO00876.1| unknown protein [Arabidopsis thaliana] gi|30102780|gb|AAP21308.1| At5g64770 [Arabidopsis thaliana] gi|332010566|gb|AED97949.1| uncharacterized protein AT5G64770 [Arabidopsis thaliana]	79	79	5.00E-24	100.0	72.2	78.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G64770.1 | Symbols: RGF9 | Encodes a root meristem growth factor (RGF). Belongs to a family of functionally redundant homologous peptides that are secreted, tyrosine-sulfated, and expressed mainly in the stem cell area and the innermost layer of central columella cells. RGFs are required for maintenance of the root stem cell niche and transit amplifying cell proliferation. Members of this family include: At5g60810 (RGF1), At1g13620 (RGF2), At2g04025 (RGF3), At3g30350 (RGF4), At5g51451 (RGF5), At4g16515 (RGF6), At3g02240 (RGF7), At2g03830 (RGF8) and At5g64770 (RGF9). | chr5:25897681-25898085 REVERSE LENGTH=79	79	79	8.00E-27	100.0	72.2	78.5
Rsa1.0_00098.1.g4888.t1	ref|XP_002864920.1| hypothetical protein ARALYDRAFT_496690 [Arabidopsis lyrata subsp. lyrata] gi|297310755|gb|EFH41179.1| hypothetical protein ARALYDRAFT_496690 [Arabidopsis lyrata subsp. lyrata]	390	392	1.00E-129	100.5	75.9	81.8	hypothetical protein ARALYDRAFT_496690	gbpln	Arabidopsis lyrata	AT5G64750.1 | Symbols: ABR1 | Integrase-type DNA-binding superfamily protein | chr5:25891679-25893656 FORWARD LENGTH=391	390	391	1.00E-130	100.3	76.4	81.8
Rsa1.0_00098.1.g4889.t1	ref|NP_201279.1| cellulose synthase A catalytic subunit 6 [UDP-forming] [Arabidopsis thaliana] gi|73917714|sp|Q94JQ6.2|CESA6_ARATH RecName: Full=Cellulose synthase A catalytic subunit 6 [UDP-forming]; Short=AtCesA6; AltName: Full=AraxCelA; AltName: Full=Isoxaben-resistant protein 2; AltName: Full=Protein PROCUSTE 1; AltName: Full=Protein QUILL gi|10177205|dbj|BAB10307.1| cellulose synthase catalytic subunit [Arabidopsis thaliana] gi|332010562|gb|AED97945.1| cellulose synthase A catalytic subunit 6 [UDP-forming] [Arabidopsis thaliana]	1079	1084	0	100.5	95.6	97.9	cellulose synthase A catalytic subunit 6	gbpln	Arabidopsis thaliana	AT5G64740.1 | Symbols: CESA6, IXR2, E112, PRC1 | cellulose synthase 6 | chr5:25881555-25886333 FORWARD LENGTH=1084	1079	1084	0	100.5	95.6	97.9
Rsa1.0_00098.1.g4890.t1	ref|XP_002864918.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297310753|gb|EFH41177.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	301	300	1.00E-168	99.7	96.3	99.0	transducin family protein	gbpln	Arabidopsis lyrata	AT5G64730.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:25873146-25875021 FORWARD LENGTH=299	301	299	1.00E-170	99.3	94.7	98.3
Rsa1.0_00098.1.g4891.t1	ref|XP_002866632.1| hypothetical protein ARALYDRAFT_919796 [Arabidopsis lyrata subsp. lyrata] gi|297312467|gb|EFH42891.1| hypothetical protein ARALYDRAFT_919796 [Arabidopsis lyrata subsp. lyrata]	147	154	1.00E-54	104.8	72.1	81.0	hypothetical protein ARALYDRAFT_919796	gbpln	Arabidopsis lyrata	AT5G64720.1 | Symbols: | Protein of unknown function (DUF1278) | chr5:25872346-25872813 REVERSE LENGTH=155	147	155	5.00E-56	105.4	71.4	80.3
Rsa1.0_00098.1.g4892.t1	gb|EOA12540.1| hypothetical protein CARUB_v10026557mg, partial [Capsella rubella]	354	395	1.00E-165	111.6	86.7	91.2	hypothetical protein CARUB_v10026557mg, partial	gbpln	Capsella rubella	AT5G64700.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:25865190-25866845 REVERSE LENGTH=359	354	359	1.00E-165	101.4	87.0	91.8
Rsa1.0_00098.1.g4893.t1	gb|EOA12539.1| hypothetical protein CARUB_v10026529mg [Capsella rubella]	312	400	9.00E-70	128.2	66.0	75.6	hypothetical protein CARUB_v10026529mg	gbpln	Capsella rubella	AT5G64690.1 | Symbols: | neurofilament triplet H protein-related | chr5:25862969-25864521 FORWARD LENGTH=344	312	344	5.00E-70	110.3	60.6	72.1
Rsa1.0_00098.1.g4894.t1	ref|XP_002866628.1| ribosomal protein L15 family protein [Arabidopsis lyrata subsp. lyrata] gi|297312463|gb|EFH42887.1| ribosomal protein L15 family protein [Arabidopsis lyrata subsp. lyrata]	283	281	1.00E-147	99.3	92.6	96.5	ribosomal protein L15 family protein	gbpln	Arabidopsis lyrata	AT5G64670.1 | Symbols: | Ribosomal protein L18e/L15 superfamily protein | chr5:25852535-25853880 REVERSE LENGTH=281	283	281	1.00E-147	99.3	90.8	95.4
Rsa1.0_00098.1.g4895.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00098.1.g4896.t1	gb|EOA14653.1| hypothetical protein CARUB_v10027914mg [Capsella rubella]	419	419	0	100.0	89.7	95.7	hypothetical protein CARUB_v10027914mg	gbpln	Capsella rubella	AT5G64660.1 | Symbols: ATCMPG2, CMPG2 | CYS, MET, PRO, and GLY protein 2 | chr5:25842119-25843381 REVERSE LENGTH=420	419	420	0	100.2	87.6	94.0
Rsa1.0_00098.1.g4897.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	102	1231	1.00E-21	1206.9	55.9	73.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00098.1.g4898.t1	ref|XP_002864912.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310747|gb|EFH41171.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	595	602	0	101.2	84.0	88.9	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT5G64640.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:25836820-25839053 FORWARD LENGTH=602	595	602	0	101.2	83.4	89.1

<table>
<tr><td>Rsa1.0_00098.1.g4899.t1</td><td>ref|NP_974991.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|75337830|sp|Q9SXY1.1|FAS2_ARATH RecName: Full=Chromatin assembly factor 1 subunit FAS2; Short=CAF-1 subunit FAS2; AltName: Full=CAF-1 p60 homolog; AltName: Full=Protein FASCIATA 2 gi|4884488|dbj|BAA77766.1| FAS2 [Arabidopsis thaliana] gi|10178066|dbj|BAB11430.1| FAS2 [Arabidopsis thaliana] gi|332010547|gb|AED97930.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]</td><td>479</td><td>487</td><td>0</td><td>101.7</td><td>88.5</td><td>93.3</td><td>transducin/WD40 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G64630.2 | Symbols: FAS2, NFB01, NFB1, MUB3.9 | Transducin/WD40 repeat-like superfamily protein | chr5:25833298-25836158 FORWARD LENGTH=487</td><td>479</td><td>487</td><td>0</td><td>101.7</td><td>88.5</td><td>93.3</td></tr>
<tr><td>Rsa1.0_00098.1.g4900.t1</td><td>ref|XP_002864910.1| C/VIF2 [Arabidopsis lyrata subsp. lyrata] gi|297310745|gb|EFH41169.1| C/VIF2 [Arabidopsis lyrata subsp. lyrata]</td><td>179</td><td>179</td><td>5.00E-77</td><td>100.0</td><td>78.8</td><td>86.6</td><td>C/VIF2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G64620.1 | Symbols: C/VIF2, ATC/VIF2 | cell wall / vacuolar inhibitor of fructosidase 2 | chr5:25831875-25832417 FORWARD LENGTH=180</td><td>179</td><td>180</td><td>7.00E-78</td><td>100.6</td><td>78.8</td><td>85.5</td></tr>
<tr><td>Rsa1.0_00098.1.g4901.t1</td><td>ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]</td><td>182</td><td>390</td><td>3.00E-32</td><td>214.3</td><td>40.1</td><td>55.5</td><td>hypothetical protein ARALYDRAFT_917455</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320</td><td>182</td><td>320</td><td>3.00E-22</td><td>175.8</td><td>32.4</td><td>50.5</td></tr>
<tr><td>Rsa1.0_00098.1.g4902.t1</td><td>ref|XP_002888154.1| hypothetical protein ARALYDRAFT_893536 [Arabidopsis lyrata subsp. lyrata] gi|297333995|gb|EFH64413.1| hypothetical protein ARALYDRAFT_893536 [Arabidopsis lyrata subsp. lyrata]</td><td>367</td><td>404</td><td>2.00E-44</td><td>110.1</td><td>39.2</td><td>55.6</td><td>hypothetical protein ARALYDRAFT_893536</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G21240.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:11322411-11323664 FORWARD LENGTH=417</td><td>367</td><td>417</td><td>4.00E-41</td><td>113.6</td><td>37.6</td><td>53.4</td></tr>
<tr><td>Rsa1.0_00098.1.g4903.t9</td><td>ref|NP_201263.2| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332010540|gb|AED97923.1| AAA-type ATPase family protein [Arabidopsis thaliana]</td><td>709</td><td>855</td><td>6.00E-65</td><td>120.6</td><td>18.1</td><td>18.8</td><td>AAA-type ATPase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G64580.1 | Symbols: | AAA-type ATPase family protein | chr5:25817391-25821465 REVERSE LENGTH=855</td><td>709</td><td>855</td><td>1.00E-67</td><td>120.6</td><td>18.1</td><td>18.8</td></tr>
<tr><td>Rsa1.0_00098.1.g4904.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00098.1.g4905.t1</td><td>ref|XP_002888154.1| hypothetical protein ARALYDRAFT_893536 [Arabidopsis lyrata subsp. lyrata] gi|297333995|gb|EFH64413.1| hypothetical protein ARALYDRAFT_893536 [Arabidopsis lyrata subsp. lyrata]</td><td>247</td><td>404</td><td>3.00E-37</td><td>163.6</td><td>45.3</td><td>61.5</td><td>hypothetical protein ARALYDRAFT_893536</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G21240.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:11322411-11323664 FORWARD LENGTH=417</td><td>247</td><td>417</td><td>2.00E-38</td><td>168.8</td><td>45.7</td><td>61.5</td></tr>
<tr><td>Rsa1.0_00099.1.g4906.t1</td><td>gb|EOA13133.1| hypothetical protein CARUB_v10026150mg [Capsella rubella]</td><td>570</td><td>577</td><td>0</td><td>101.2</td><td>93.9</td><td>95.8</td><td>hypothetical protein CARUB_v10026150mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G60020.1 | Symbols: LAC17, ATLAC17 | laccase 17 | chr5:24168072-24170223 FORWARD LENGTH=577</td><td>570</td><td>577</td><td>0</td><td>101.2</td><td>93.2</td><td>96.0</td></tr>
<tr><td>Rsa1.0_00099.1.g4907.t7</td><td>gb|ADA58340.1| pseudo-response regulator 3 [Brassica rapa]</td><td>469</td><td>492</td><td>0</td><td>104.9</td><td>85.7</td><td>90.0</td><td>pseudo-response regulator 3</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G60100.3 | Symbols: PRR3 | pseudo-response regulator 3 | chr5:24198215-24200502 REVERSE LENGTH=495</td><td>469</td><td>495</td><td>0</td><td>105.5</td><td>79.3</td><td>85.5</td></tr>
<tr><td>Rsa1.0_00099.1.g4908.t1</td><td>ref|XP_002864667.1| APUM18 [Arabidopsis lyrata subsp. lyrata] gi|297310502|gb|EFH40926.1| APUM18 [Arabidopsis lyrata subsp. lyrata]</td><td>332</td><td>328</td><td>1.00E-134</td><td>98.8</td><td>72.9</td><td>83.1</td><td>APUM18</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G60110.1 | Symbols: APUM18, PUM18 | pumilio 18 | chr5:24201954-24202937 FORWARD LENGTH=327</td><td>332</td><td>327</td><td>1.00E-124</td><td>98.5</td><td>71.7</td><td>81.6</td></tr>
<tr><td>Rsa1.0_00099.1.g4909.t1</td><td>ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>326</td><td>530</td><td>2.00E-27</td><td>162.6</td><td>22.1</td><td>30.4</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00099.1.g4910.t2</td><td>dbj|BAJ34032.1| unnamed protein product [Thellungiella halophila]</td><td>459</td><td>492</td><td>0</td><td>107.2</td><td>83.2</td><td>87.6</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G60120.1 | Symbols: TOE2 | target of early activation tagged (EAT) 2 | chr5:24208153-24211067 FORWARD LENGTH=485</td><td>459</td><td>485</td><td>0</td><td>105.7</td><td>78.4</td><td>84.3</td></tr>
<tr><td>Rsa1.0_00099.1.g4911.t1</td><td>gb|EOA14648.1| hypothetical protein CARUB_v10027909mg [Capsella rubella]</td><td>291</td><td>320</td><td>6.00E-79</td><td>110.0</td><td>55.7</td><td>72.5</td><td>hypothetical protein CARUB_v10027909mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G60130.2 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:24211871-24213112 REVERSE LENGTH=300</td><td>291</td><td>300</td><td>6.00E-79</td><td>103.1</td><td>56.0</td><td>75.3</td></tr>
<tr><td>Rsa1.0_00099.1.g4912.t1</td><td>ref|NP_001119463.2| AP2/B3-like transcriptional factor family protein [Arabidopsis thaliana] gi|357529134|sp|Q9LST3.3|Y5142_ARATH RecName: Full=B3 domain-containing protein At5g60142 gi|332009902|gb|AED97285.1| AP2/B3-like transcriptional factor family protein [Arabidopsis thaliana]</td><td>212</td><td>346</td><td>2.00E-49</td><td>163.2</td><td>42.9</td><td>49.1</td><td>AP2/B3-like transcriptional factor family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G60142.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:24216180-24217591 REVERSE LENGTH=346</td><td>212</td><td>346</td><td>5.00E-52</td><td>163.2</td><td>42.9</td><td>49.1</td></tr>
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Rsa1.0_00099.1.g4913.t1	ref|NP_200823.1| uncharacterized protein [Arabidopsis thaliana] gi|332009903|gb|AED97286.1| uncharacterized protein AT5G60150 [Arabidopsis thaliana]	1200	1195	0	99.6	51.1	60.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G60150.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:24218211-24223245 FORWARD LENGTH=1195	1200	1195	0	99.6	51.1	60.6
Rsa1.0_00099.1.g4914.t2	ref|XP_002864671.1| hypothetical protein ARALYDRAFT_358235 [Arabidopsis lyrata subsp. lyrata] gi|297310506|gb|EFH40930.1| hypothetical protein ARALYDRAFT_358235 [Arabidopsis lyrata subsp. lyrata]	1027	1001	0	97.5	76.0	83.5	hypothetical protein ARALYDRAFT_358235	gbpln	Arabidopsis lyrata	AT5G60170.2 | Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr5:24228178-24232394 FORWARD LENGTH=987	1027	987	0	96.1	74.7	81.9
Rsa1.0_00099.1.g4915.t1	ref|XP_002864667.1| APUM18 [Arabidopsis lyrata subsp. lyrata] gi|297310502|gb|EFH40926.1| APUM18 [Arabidopsis lyrata subsp. lyrata]	323	328	1.00E-104	101.5	62.8	73.7	APUM18	gbpln	Arabidopsis lyrata	AT5G60110.1 | Symbols: APUM18, PUM18 | pumilio 18 | chr5:24201954-24202937 FORWARD LENGTH=327	323	327	3.00E-95	101.2	61.0	72.8
Rsa1.0_00099.1.g4916.t1	ref|XP_002864666.1| hypothetical protein ARALYDRAFT_358227 [Arabidopsis lyrata subsp. lyrata] gi|297310501|gb|EFH40925.1| hypothetical protein ARALYDRAFT_358227 [Arabidopsis lyrata subsp. lyrata]	370	530	1.00E-65	143.2	42.7	53.0	hypothetical protein ARALYDRAFT_358227	gbpln	Arabidopsis lyrata	AT5G60250.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24252226-24254710 FORWARD LENGTH=655	370	655	1.00E-56	177.0	37.3	51.9
Rsa1.0_00099.1.g4917.t1	ref|XP_002864672.1| Ulp1 protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297310507|gb|EFH40931.1| Ulp1 protease family protein [Arabidopsis lyrata subsp. lyrata]	228	226	1.00E-103	99.1	77.6	89.5	Ulp1 protease family protein	gbpln	Arabidopsis lyrata	AT5G60190.1 | Symbols: | Cysteine proteinases superfamily protein | chr5:24235319-24235999 FORWARD LENGTH=226	228	226	1.00E-106	99.1	79.4	90.4
Rsa1.0_00099.1.g4918.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00099.1.g4919.t1	gb|EOA13642.1| hypothetical protein CARUB_v10026713mg [Capsella rubella]	259	344	1.00E-117	132.8	83.4	90.3	hypothetical protein CARUB_v10026713mg	gbpln	Capsella rubella	AT5G60200.1 | Symbols: TMO6 | TARGET OF MONOPTEROS 6 | chr5:24241078-24241951 FORWARD LENGTH=257	259	257	1.00E-115	99.2	81.1	87.3
Rsa1.0_00099.1.g4920.t1	ref|NP_200829.5| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|334188518|ref|NP_001190579.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|75180396|sp|Q9LSS5.1|ICR3_ARATH RecName: Full=Interactor of constitutive active ROPs 3 gi|8885572|dbj|BAA97502.1| myosin heavy chain-like [Arabidopsis thaliana] gi|332009910|gb|AED97293.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|332009911|gb|AED97294.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana]	515	564	0	109.5	74.8	83.1	interactor of constitutive active ROPs 3	gbpln	Arabidopsis thaliana	AT5G60210.2 | Symbols: RIP5 | ROP interactive partner 5 | chr5:24243529-24245889 REVERSE LENGTH=564	515	564	0	109.5	74.8	83.1
Rsa1.0_00099.1.g4921.t1	ref|NP_974966.1| tRNA-splicing endonuclease subunit Sen2-2 [Arabidopsis thaliana] gi|332009914|gb|AED97297.1| tRNA-splicing endonuclease subunit Sen2-2 [Arabidopsis thaliana]	417	255	1.00E-103	61.2	42.0	46.5	tRNA-splicing endonuclease subunit Sen2-2	gbpln	Arabidopsis thaliana	AT5G60230.2 | Symbols: SEN2, ATSEN2 | splicing endonuclease 2 | chr5:24250185-24250952 REVERSE LENGTH=255	417	255	1.00E-105	61.2	42.0	46.5
Rsa1.0_00099.1.g4922.t1	ref|NP_200833.1| C3H4 type zinc finger protein [Arabidopsis thaliana] gi|8885575|dbj|BAA97505.1| unnamed protein product [Arabidopsis thaliana] gi|332009916|gb|AED97299.1| C3H4 type zinc finger protein [Arabidopsis thaliana]	794	655	0	82.5	53.4	60.7	C3H4 type zinc finger protein	gbpln	Arabidopsis thaliana	AT5G60250.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24252226-24254710 FORWARD LENGTH=655	794	655	0	82.5	53.4	60.7
Rsa1.0_00099.1.g4923.t1	ref|NP_001118679.1| uncharacterized protein [Arabidopsis thaliana] gi|11994728|dbj|BAB03044.1| unnamed protein product [Arabidopsis thaliana] gi|332643177|gb|AEE76698.1| uncharacterized protein AT3G22961 [Arabidopsis thaliana]	278	223	7.00E-26	80.2	30.9	42.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G22961.1 | Symbols: | Paired amphipathic helix (PAH2) superfamily protein | chr3:8142138-8142809 FORWARD LENGTH=223	278	223	2.00E-28	80.2	30.9	42.1
Rsa1.0_00099.1.g4924.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00099.1.g4925.t1	ref|XP_002864676.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310511|gb|EFH40935.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	670	668	0	99.7	77.6	86.4	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT5G60270.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:24257761-24259767 FORWARD LENGTH=668	670	668	0	99.7	76.9	86.3

Rsa1.0_00099.1.g4926.t1	ref|XP_002864676.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310511|gb|EFH40935.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	665	668	0	100.5	77.6	87.4	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT5G60270.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:24257761-24259767 FORWARD LENGTH=668	665	668	0	100.5	77.3	87.2
Rsa1.0_00099.1.g4927.t1	gb|EOA36785.1| hypothetical protein CARUB_v10008113mg [Capsella rubella]	166	1222	6.00E-16	736.1	25.3	27.7	hypothetical protein CARUB_v10008113mg	gbpln	Capsella rubella	AT1G17500.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:6018757-6023201 FORWARD LENGTH=1216	166	1216	7.00E-18	732.5	24.7	27.1
Rsa1.0_00099.1.g4928.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	231	1231	1.00E-53	532.9	48.1	63.2	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	231	575	4.00E-31	248.9	30.7	50.6
Rsa1.0_00099.1.g4929.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	283	1142	8.00E-53	403.5	38.9	50.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	283	256	6.00E-22	90.5	19.8	25.8
Rsa1.0_00099.1.g4930.t1	ref|XP_002864676.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310511|gb|EFH40935.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	672	668	0	99.4	81.0	89.0	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT5G60270.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:24257761-24259767 FORWARD LENGTH=668	672	668	0	99.4	80.7	89.0
Rsa1.0_00099.1.g4931.t1	ref|NP_200836.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana] gi|75335417|sp|Q9LSR9.1|LRK18_ARATH RecName: Full=L-type lectin-domain containing receptor kinase I.8; Short=LecRK-I.8; Flags: Precursor gi|8885578|dbj|BAA97508.1| receptor-like protein kinase [Arabidopsis thaliana] gi|34365777|gb|AAQ65200.1| At5g60280 [Arabidopsis thaliana] gi|62320942|dbj|BAD93956.1| receptor like protein kinase [Arabidopsis thaliana] gi|332009919|gb|AED97302.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana]	672	657	0	97.8	78.3	87.9	concanavalin A-like lectin kinase-like protein	gbpln	Arabidopsis thaliana	AT5G60280.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:24260563-24262536 FORWARD LENGTH=657	672	657	0	97.8	78.3	87.9
Rsa1.0_00099.1.g4932.t1	ref|NP_200838.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana] gi|30697356|ref|NP_851230.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana] gi|8885579|dbj|BAA97509.1| receptor-like protein kinase [Arabidopsis thaliana] gi|21539487|gb|AAM53296.1| tRNA intron endonuclease-like protein [Arabidopsis thaliana] gi|22655060|gb|AAM98121.1| unknown protein [Arabidopsis thaliana] gi|23198282|gb|AAN15668.1| tRNA intron endonuclease-like protein [Arabidopsis thaliana] gi|332009921|gb|AED97304.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana] gi|332009922|gb|AED97305.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana]	691	718	0	103.9	82.1	91.2	concanavalin A-like lectin kinase-like protein	gbpln	Arabidopsis thaliana	AT5G60300.2 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:24264862-24267018 FORWARD LENGTH=718	691	718	0	103.9	82.1	91.2
Rsa1.0_00099.1.g4933.t7	gb|EOA14027.1| hypothetical protein CARUB_v10027159mg [Capsella rubella]	187	200	2.00E-33	107.0	46.0	53.5	hypothetical protein CARUB_v10027159mg	gbpln	Capsella rubella	AT5G45130.1 | Symbols: ATRAB5A, ATRABF2A, RABF2A, RAB5A, RHA1, ATRAB-F2A, RAB-F2A | RAB homolog 1 | chr5:18244495-18246060 FORWARD LENGTH=200	187	200	2.00E-35	107.0	45.5	53.5
Rsa1.0_00099.1.g4934.t1	gb|EOA34414.1| hypothetical protein CARUB_v10021942mg, partial [Capsella rubella]	328	361	1.00E-158	110.1	83.5	90.2	hypothetical protein CARUB_v10021942mg, partial	gbpln	Capsella rubella	AT1G74020.1 | Symbols: SS2 | strictosidine synthase 2 | chr1:27835289-27837277 REVERSE LENGTH=335	328	335	1.00E-100	102.1	54.9	68.9

Rsa1.0_00099.1.g4935.t1	gb|EOA15422.1| hypothetical protein CARUB_v10007751mg [Capsella rubella]	227	108	4.00E-29	47.6	29.5	35.2	hypothetical protein CARUB_v10007751mg	gbpln	Capsella rubella	AT4G02655.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G18486.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:1158876-1159241 FORWARD LENGTH=121	227	121	8.00E-26	53.3	27.3	34.4
Rsa1.0_00099.1.g4936.t1	dbj|BAJ34485.1| unnamed protein product [Thellungiella halophila]	706	682	0	96.6	89.4	92.9	unnamed protein product	----	----	AT1G73990.1 | Symbols: SPPA, SPPA1 | signal peptide peptidase | chr1:27824465-27828807 FORWARD LENGTH=677	706	677	0	95.9	85.8	90.8
Rsa1.0_00099.1.g4937.t1	ref|XP_002888955.1| phosphoribulokinase/uridine kinase [Arabidopsis lyrata subsp. lyrata] gi|297334796|gb|EFH65214.1| phosphoribulokinase/uridine kinase [Arabidopsis lyrata subsp. lyrata]	581	643	0	110.7	70.7	82.3	phosphoribulokinase/uridine kinase	gbpln	Arabidopsis lyrata	AT1G73980.1 | Symbols: | Phosphoribulokinase / Uridine kinase family | chr1:27820292-27823527 REVERSE LENGTH=643	581	643	0	110.7	70.7	82.1
Rsa1.0_00099.1.g4938.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00099.1.g4939.t1	dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	271	1098	6.00E-37	405.2	35.8	45.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G73980.1 | Symbols: | Phosphoribulokinase / Uridine kinase family | chr1:27820292-27823527 REVERSE LENGTH=643	271	643	1.00E-13	237.3	15.1	18.8
Rsa1.0_00099.1.g4940.t1	ref|XP_002887517.1| hypothetical protein ARALYDRAFT_476537 [Arabidopsis lyrata subsp. lyrata] gi|297333358|gb|EFH63776.1| hypothetical protein ARALYDRAFT_476537 [Arabidopsis lyrata subsp. lyrata]	802	803	0	100.1	83.7	89.9	hypothetical protein ARALYDRAFT_476537	gbpln	Arabidopsis lyrata	AT1G73970.1 | Symbols: | unknown protein; Has 34 Blast hits to 33 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:27817140-27819963 FORWARD LENGTH=803	802	803	0	100.1	83.8	90.0
Rsa1.0_00100.1.g4941.t1	gb|EOA24820.1| hypothetical protein CARUB_v10018107mg [Capsella rubella]	174	176	2.00E-82	101.1	84.5	92.0	hypothetical protein CARUB_v10018107mg	gbpln	Capsella rubella	AT3G56290.1 | Symbols: | unknown protein; Has 39 Blast hits to 39 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:20878743-20879541 REVERSE LENGTH=173	174	173	2.00E-79	99.4	86.8	92.5
Rsa1.0_00100.1.g4942.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	210	1142	4.00E-47	543.8	46.7	62.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	210	575	6.00E-22	273.8	30.5	48.1
Rsa1.0_00100.1.g4943.t1	ref|XP_002876361.1| hypothetical protein ARALYDRAFT_486071 [Arabidopsis lyrata subsp. lyrata] gi|297322199|gb|EFH52620.1| hypothetical protein ARALYDRAFT_486071 [Arabidopsis lyrata subsp. lyrata]	432	430	0	99.5	91.9	96.1	hypothetical protein ARALYDRAFT_486071	gbpln	Arabidopsis lyrata	AT3G56310.1 | Symbols: | Melibiase family protein | chr3:20882886-20885745 FORWARD LENGTH=437	432	437	0	101.2	91.9	95.8
Rsa1.0_00100.1.g4944.t1	ref|NP_191191.2| PAP/OAS1 substrate-binding domain-containing protein [Arabidopsis thaliana] gi|30725328|gb|AAP37686.1| At3g56320 [Arabidopsis thaliana] gi|110736147|dbj|BAF00045.1| hypothetical protein [Arabidopsis thaliana] gi|332645988|gb|AEE79509.1| PAP/OAS1 substrate-binding domain-containing protein [Arabidopsis thaliana]	567	603	0	106.3	81.5	90.5	PAP/OAS1 substrate-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT3G56320.1 | Symbols: | PAP/OAS1 substrate-binding domain superfamily | chr3:20886193-20888624 REVERSE LENGTH=603	567	603	0	106.3	81.5	90.5
Rsa1.0_00100.1.g4945.t1	ref|XP_002876362.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322200|gb|EFH52621.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	434	431	0	99.3	84.8	90.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G56330.1 | Symbols: | N2,N2-dimethylguanosine tRNA methyltransferase | chr3:20890250-20891933 FORWARD LENGTH=433	434	433	0	99.8	84.8	91.5
Rsa1.0_00100.1.g4946.t1	ref|XP_002878080.1| hypothetical protein ARALYDRAFT_324152 [Arabidopsis lyrata subsp. lyrata] gi|297323918|gb|EFH54339.1| hypothetical protein ARALYDRAFT_324152 [Arabidopsis lyrata subsp. lyrata]	355	241	1.00E-116	67.9	56.6	58.9	hypothetical protein ARALYDRAFT_324152	gbpln	Arabidopsis lyrata	AT3G56350.1 | Symbols: | Iron/manganese superoxide dismutase family protein | chr3:20894155-20895625 REVERSE LENGTH=241	355	241	1.00E-118	67.9	56.1	59.2

Rsa1.0_00100.1.g4947.t1	ref|XP_002876363.1| hypothetical protein ARALYDRAFT_907078 [Arabidopsis lyrata subsp. lyrata] gi|297322201|gb|EFH52622.1| hypothetical protein ARALYDRAFT_907078 [Arabidopsis lyrata subsp. lyrata]	228	233	2.00E-82	102.2	76.8	82.9	hypothetical protein ARALYDRAFT_907078	gbpln	Arabidopsis lyrata	AT3G56360.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G05250.1); Has 45 Blast hits to 45 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:20896641-20897342 FORWARD LENGTH=233	228	233	7.00E-81	102.2	75.0	80.7
Rsa1.0_00100.1.g4948.t1	ref|NP_191196.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|7594515|emb|CAB88040.1| putative protein [Arabidopsis thaliana] gi|19032341|dbj|BAB85646.1| inflorescence and root apices receptor-like kinase [Arabidopsis thaliana] gi|19032343|dbj|BAB85647.1| inflorescence and root apices receptor-like kinase [Arabidopsis thaliana] gi|224589604|gb|ACN59335.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332645993|gb|AEE79514.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]	959	964	0	100.5	89.2	94.8	leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT3G56370.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:20899403-20902390 REVERSE LENGTH=964	959	964	0	100.5	89.2	94.8
Rsa1.0_00100.1.g4949.t1	gb|EOA25718.1| hypothetical protein CARUB_v10019069mg, partial [Capsella rubella]	125	148	4.00E-55	118.4	89.6	94.4	hypothetical protein CARUB_v10019069mg, partial	gbpln	Capsella rubella	AT3G56380.1 | Symbols: ARR17, RR17 | response regulator 17 | chr3:20905480-20906368 FORWARD LENGTH=153	125	153	8.00E-58	122.4	92.0	94.4
Rsa1.0_00100.1.g4950.t1	gb|ACQ76810.1| WRKY transcription factor 70 [Brassica napus]	278	276	1.00E-134	99.3	89.2	93.2	WRKY transcription factor 70	gbpln	Brassica napus	AT3G56400.1 | Symbols: WRKY70, ATWRKY70 | WRKY DNA-binding protein 70 | chr3:20909082-20910409 REVERSE LENGTH=294	278	294	1.00E-101	105.8	66.2	76.6
Rsa1.0_00100.1.g4951.t1	ref|XP_002878083.1| hypothetical protein ARALYDRAFT_486082 [Arabidopsis lyrata subsp. lyrata] gi|297323921|gb|EFH54342.1| hypothetical protein ARALYDRAFT_486082 [Arabidopsis lyrata subsp. lyrata]	645	1485	6.00E-44	230.2	20.2	23.4	hypothetical protein ARALYDRAFT_486082	gbpln	Arabidopsis lyrata	AT3G56410.2 | Symbols: | Protein of unknown function (DUF3133) | chr3:20916320-20921134 REVERSE LENGTH=1535	645	1535	3.00E-44	238.0	18.6	21.4
Rsa1.0_00100.1.g4952.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00100.1.g4953.t1	gb|EOA24904.1| hypothetical protein CARUB_v10018194mg [Capsella rubella]	129	147	7.00E-68	114.0	96.9	99.2	hypothetical protein CARUB_v10018194mg	gbpln	Capsella rubella	AT3G56490.1 | Symbols: HIT3, HINT1 | HIS triad family protein 3 | chr3:20941532-20943129 FORWARD LENGTH=147	129	147	8.00E-70	114.0	96.1	98.4
Rsa1.0_00100.1.g4954.t1	ref|XP_002878090.1| hypothetical protein ARALYDRAFT_486092 [Arabidopsis lyrata subsp. lyrata] gi|297323928|gb|EFH54349.1| hypothetical protein ARALYDRAFT_486092 [Arabidopsis lyrata subsp. lyrata]	259	256	1.00E-122	98.8	87.3	94.2	hypothetical protein ARALYDRAFT_486092	gbpln	Arabidopsis lyrata	AT3G56510.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:20944348-20946235 REVERSE LENGTH=257	259	257	1.00E-122	99.2	86.1	94.2
Rsa1.0_00100.1.g4955.t1	ref|XP_002878093.1| hypothetical protein ARALYDRAFT_486095 [Arabidopsis lyrata subsp. lyrata] gi|297323931|gb|EFH54352.1| hypothetical protein ARALYDRAFT_486095 [Arabidopsis lyrata subsp. lyrata]	282	301	5.00E-51	106.7	47.5	63.5	hypothetical protein ARALYDRAFT_486095	gbpln	Arabidopsis lyrata	AT3G56530.1 | Symbols: anac064, NAC064 | NAC domain containing protein 64 | chr3:20948911-20950045 REVERSE LENGTH=319	282	319	2.00E-47	113.1	44.3	58.9
Rsa1.0_00100.1.g4956.t1	ref|NP_191214.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75180975|sp|Q9LXY5.1|PP284_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g56550 gi|7594533|emb|CAB88058.1| putative protein [Arabidopsis thaliana] gi|91806586|gb|ABE66020.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332646013|gb|AEE79534.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	578	581	0	100.5	82.9	91.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G56550.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:20952896-20954641 REVERSE LENGTH=581	578	581	0	100.5	82.9	91.0

Rsa1.0_00100.1.g4957.t1	ref|XP_002886390.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata] gi|297332231|gb|EFH62649.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata]	192	298	2.00E−42	155.2	49.5	65.6	hypothetical protein ARALYDRAFT_893070	gbpln	Arabidopsis lyrata	AT2G42470.1 | Symbols: | TRAF−like family protein | chr2:17679887−17685187 REVERSE LENGTH=898	192	898	7.00E−34	467.7	46.9	64.6
Rsa1.0_00100.1.g4958.t1	ref|XP_002876372.1| SET domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322210|gb|EFH52631.1| SET domain−containing protein [Arabidopsis lyrata subsp. lyrata]	484	518	0	107.0	77.5	87.8	SET domain−containing protein	gbpln	Arabidopsis lyrata	AT3G56570.1 | Symbols: | SET domain−containing protein | chr3:20958660−20961137 FORWARD LENGTH=531	484	531	0	109.7	77.7	88.0
Rsa1.0_00100.1.g4959.t1	ref|NP_567039.1| RING/U−box domain−containing protein [Arabidopsis thaliana] gi|42572705|ref|NP_974448.1| RING/U−box domain−containing protein [Arabidopsis thaliana] gi|79315364|ref|NP_001030874.1| RING/U−box domain−containing protein [Arabidopsis thaliana] gi|15028361|gb|AAK76657.1| unknown protein [Arabidopsis thaliana] gi|20465561|gb|AAM20263.1| unknown protein [Arabidopsis thaliana] gi|66865932|gb|AAY57600.1| RING finger family protein [Arabidopsis thaliana] gi|332646016|gb|AEE79537.1| RING/U−box domain−containing protein [Arabidopsis thaliana] gi|332646017|gb|AEE79538.1| RING/U−box domain−containing protein [Arabidopsis thaliana] gi|332646018|gb|AEE79539.1| RING/U−box domain−containing protein [Arabidopsis thaliana]	323	320	1.00E−116	99.1	73.7	82.7	RING/U−box domain−containing protein	gbpln	Arabidopsis thaliana	AT3G56580.3 | Symbols: | RING/U−box superfamily protein | chr3:20962563−20963525 FORWARD LENGTH=320	323	320	1.00E−119	99.1	73.7	82.7
Rsa1.0_00100.1.g4960.t1	ref|XP_002878091.1| hypothetical protein ARALYDRAFT_324164 [Arabidopsis lyrata subsp. lyrata] gi|297323929|gb|EFH54350.1| hypothetical protein ARALYDRAFT_324164 [Arabidopsis lyrata subsp. lyrata]	398	167	3.00E−38	42.0	22.6	26.9	hypothetical protein ARALYDRAFT_324164	gbpln	Arabidopsis lyrata	AT3G56520.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr3:20947107−20947731 REVERSE LENGTH=175	398	175	2.00E−40	44.0	21.9	26.4
Rsa1.0_00100.1.g4961.t1	ref|NP_191218.2| hydroxyproline−rich glycoprotein family protein [Arabidopsis thaliana] gi|110741964|dbj|BAE98922.1| hypothetical protein [Arabidopsis thaliana] gi|332646019|gb|AEE79540.1| hydroxyproline−rich glycoprotein family protein [Arabidopsis thaliana]	507	477	1.00E−175	94.1	72.8	79.1	hydroxyproline−rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT3G56590.1 | Symbols: | hydroxyproline−rich glycoprotein family protein | chr3:20965105−20967675 FORWARD LENGTH=477	507	477	1.00E−178	94.1	72.8	79.1
Rsa1.0_00100.1.g4962.t1	ref|XP_002876374.1| inositol or phosphatidylinositol kinase [Arabidopsis lyrata subsp. lyrata] gi|297322212|gb|EFH52633.1| inositol or phosphatidylinositol kinase [Arabidopsis lyrata subsp. lyrata]	534	535	0	100.2	81.1	87.5	inositol or phosphatidylinositol kinase	gbpln	Arabidopsis lyrata	AT3G56600.2 | Symbols: | Protein kinase superfamily protein | chr3:20969087−20970697 FORWARD LENGTH=536	534	536	0	100.4	81.3	87.8
Rsa1.0_00100.1.g4963.t1	ref|NP_191221.1| nodulin MtN21 /EamA−like transporter protein [Arabidopsis thaliana] gi|75180969|sp|Q9LXX8.1|WTR27_ARATH RecName: Full=WAT1−related protein At3g56620 gi|7594540|emb|CAB88065.1| nodulin−like protein [Arabidopsis thaliana] gi|332646024|gb|AEE79545.1| WAT1−related protein [Arabidopsis thaliana]	383	377	1.00E−176	98.4	83.3	87.7	nodulin MtN21 /EamA−like transporter protein	gbpln	Arabidopsis thaliana	AT3G56620.1 | Symbols: | nodulin MtN21 /EamA−like transporter family protein | chr3:20972696−20974495 REVERSE LENGTH=377	383	377	1.00E−179	98.4	83.3	87.7
Rsa1.0_00100.1.g4964.t1	gb|EOA25848.1| hypothetical protein CARUB_v10019225mg [Capsella rubella]	789	790	0	100.1	94.6	97.6	hypothetical protein CARUB_v10019225mg	gbpln	Capsella rubella	AT3G56640.1 | Symbols: SEC15A | exocyst complex component sec15A | chr3:20981964−20984336 FORWARD LENGTH=790	789	790	0	100.1	93.8	97.5
Rsa1.0_00100.1.g4965.t1	ref|XP_002878101.1| CIP111 [Arabidopsis lyrata subsp. lyrata] gi|297323939|gb|EFH54360.1| CIP111 [Arabidopsis lyrata subsp. lyrata]	1022	1025	0	100.3	84.4	89.5	CIP111	gbpln	Arabidopsis lyrata	AT3G56690.1 | Symbols: CIP111 | Cam interacting protein 111 | chr3:20993869−20998531 REVERSE LENGTH=1022	1022	1022	0	100.0	83.0	88.8
Rsa1.0_00100.1.g4966.t1	sp|B9TSP7.1|FACR6_ARATH RecName: Full=Fatty acyl−CoA reductase 6, chloroplastic; Flags: Precursor gi|167077488|gb|ABZ10953.1| fatty acyl CoA reductase long isoform [Arabidopsis thaliana]	463	548	0	118.4	73.4	83.2	RecName: Full=Fatty acyl−CoA reductase 6, chloroplastic; Flags: Precursor gi|167077488|gb|ABZ10953.1| fatty acyl CoA reductase long isoform	gbpln	Arabidopsis thaliana	AT3G56700.1 | Symbols: FAR6 | fatty acid reductase 6 | chr3:20999731−21002058 REVERSE LENGTH=527	463	527	1.00E−169	113.8	69.5	78.8

Rsa1.0_00100.1.g4967.t2	ref|XP_002878104.1| hypothetical protein ARALYDRAFT_486111 [Arabidopsis lyrata subsp. lyrata] gi|297323942|gb|EFH54363.1| hypothetical protein ARALYDRAFT_486111 [Arabidopsis lyrata subsp. lyrata]	283	155	7.00E-41	54.8	32.5	37.5	hypothetical protein ARALYDRAFT_486111	gbpln	Arabidopsis lyrata	AT3G56710.1 | Symbols: SIB1 | sigma factor binding protein 1 | chr3:21007053-21007508 REVERSE LENGTH=151	283	151	7.00E-40	53.4	31.8	37.1
Rsa1.0_00100.1.g4968.t1	ref|NP_191233.1| Ubiquitin-associated (UBA) protein [Arabidopsis thaliana] gi|9662993|emb|CAC00737.1| putative protein [Arabidopsis thaliana] gi|21553945|gb|AAM63026.1| unknown [Arabidopsis thaliana] gi|28950711|gb|AAO63279.1| At3g56740 [Arabidopsis thaliana] gi|110735889|dbj|BAE99920.1| hypothetical protein [Arabidopsis thaliana] gi|332646039|gb|AEE79560.1| Ubiquitin-associated (UBA) protein [Arabidopsis thaliana]	295	293	1.00E-149	99.3	94.2	96.9	Ubiquitin-associated (UBA) protein	gbpln	Arabidopsis thaliana	AT3G56740.1 | Symbols: | Ubiquitin-associated (UBA) protein | chr3:21015631-21017883 FORWARD LENGTH=293	295	293	1.00E-152	99.3	94.2	96.9
Rsa1.0_00100.1.g4969.t1	gb|EOA24144.1| hypothetical protein CARUB_v10017377mg [Capsella rubella]	403	403	0	100.0	92.1	96.0	hypothetical protein CARUB_v10017377mg	gbpln	Capsella rubella	AT3G56750.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41150.2); Has 128 Blast hits to 128 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 117; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr3:21018326-21020192 REVERSE LENGTH=403	403	403	0	100.0	90.1	95.0
Rsa1.0_00100.1.g4970.t1	gb|EOA27855.1| hypothetical protein CARUB_v10024013mg [Capsella rubella]	149	224	2.00E-80	150.3	100.0	100.0	hypothetical protein CARUB_v10024013mg	gbpln	Capsella rubella	AT2G27030.3 | Symbols: CAM5 | calmodulin 5 | chr2:11532069-11534176 FORWARD LENGTH=181	149	181	9.00E-83	121.5	100.0	100.0
Rsa1.0_00100.1.g4971.t1	gb|EOA24368.1| hypothetical protein CARUB_v10017605mg [Capsella rubella]	333	333	1.00E-126	100.0	75.7	83.5	hypothetical protein CARUB_v10017605mg	gbpln	Capsella rubella	AT3G56810.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 14 Blast hits to 14 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:21036927-21038927 REVERSE LENGTH=332	333	332	1.00E-128	99.7	75.1	84.7
Rsa1.0_00100.1.g4972.t1	ref|XP_002878111.1| hypothetical protein ARALYDRAFT_486120 [Arabidopsis lyrata subsp. lyrata] gi|297323949|gb|EFH54370.1| hypothetical protein ARALYDRAFT_486120 [Arabidopsis lyrata subsp. lyrata]	221	218	5.00E-95	98.6	80.5	88.7	hypothetical protein ARALYDRAFT_486120	gbpln	Arabidopsis lyrata	AT3G56820.1 | Symbols: | unknown protein; Has 34 Blast hits to 34 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr3:21040061-21041711 REVERSE LENGTH=220	221	220	5.00E-90	99.5	80.1	86.0
Rsa1.0_00100.1.g4973.t1	ref|NP_191242.2| uncharacterized protein [Arabidopsis thaliana] gi|332646049|gb|AEE79570.1| uncharacterized protein AT3G56830 [Arabidopsis thaliana]	214	230	5.00E-81	107.5	74.8	79.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G56830.1 | Symbols: | Protein of unknown function (DUF565) | chr3:21042755-21043840 REVERSE LENGTH=230	214	230	1.00E-83	107.5	74.8	79.4
Rsa1.0_00100.1.g4974.t1	ref|NP_191243.1| FAD-dependent oxidoreductase-like protein [Arabidopsis thaliana] gi|9663003|emb|CAC00747.1| putative protein [Arabidopsis thaliana] gi|332646052|gb|AEE79573.1| FAD-dependent oxidoreductase-like protein [Arabidopsis thaliana]	426	483	0	113.4	89.2	94.8	FAD-dependent oxidoreductase-like protein	gbpln	Arabidopsis thaliana	AT3G56840.1 | Symbols: | FAD-dependent oxidoreductase family protein | chr3:21044317-21046177 FORWARD LENGTH=483	426	483	0	113.4	89.2	94.8

Rsa1.0_00100.1.g4975.t1	ref|NP_191244.1| abscisic acid-insensitive 5-like protein 2 [Arabidopsis thaliana] gi|75334900|sp|Q9LES3.1|AI5L2_ARATH RecName: Full=ABSCISIC ACID-INSENSITIVE 5-like protein 2; AltName: Full=ABA-responsive element-binding protein 3; AltName: Full=Dc3 promoter-binding factor 3; Short=AtDPBF3; AltName: Full=bZIP transcription factor 66; Short=AtbZIP66 gi|9663004|emb|CAC00748.1| promoter-binding factor-like protein [Arabidopsis thaliana] gi|9967421|dbj|BAB12406.1| ABA-responsive element binding protein 3 (AREB3) [Arabidopsis thaliana] gi|17064744|gb|AAL32526.1| promoter-binding factor-like protein [Arabidopsis thaliana] gi|20148683|gb|AAM10232.1| promoter-binding factor-like protein [Arabidopsis thaliana] gi|332646053|gb|AEE79574.1| abscisic acid-insensitive 5-like protein 2 [Arabidopsis thaliana]	287	297	1.00E-137	103.5	87.8	92.7	abscisic acid-insensitive 5-like protein 2	gbpln	Arabidopsis thaliana	AT3G56850.1 | Symbols: AREB3, DPBF3 | ABA-responsive element binding protein 3 | chr3:21046554-21047894 REVERSE LENGTH=297	287	297	1.00E-140	103.5	87.8	92.7
Rsa1.0_00100.1.g4976.t1	dbj|BAJ33737.1| unnamed protein product [Thellungiella halophila]	464	479	0	103.2	73.7	78.2	unnamed protein product	----	----	AT3G56860.5 | Symbols: UBA2A | UBP1-associated protein 2A | chr3:21050708-21052144 REVERSE LENGTH=478	464	478	0	103.0	73.5	78.2
Rsa1.0_00100.1.g4977.t1	gb|EOA23551.1| hypothetical protein CARUB_v10016745mg [Capsella rubella]	811	722	0	89.0	47.8	56.6	hypothetical protein CARUB_v10016745mg	gbpln	Capsella rubella	AT3G56870.1 | Symbols: | unknown protein; Has 204 Blast hits to 201 proteins in 58 species: Archae - 0; Bacteria - 10; Metazoa - 72; Fungi - 8; Plants - 41; Viruses - 0; Other Eukaryotes - 73 (source: NCBI BLink). | chr3:21053077-21055518 FORWARD LENGTH=700	811	700	1.00E-180	86.3	46.5	54.7
Rsa1.0_00100.1.g4978.t1	ref|XP_002883443.1| hypothetical protein ARALYDRAFT_342502 [Arabidopsis lyrata subsp. lyrata] gi|297329283|gb|EFH59702.1| hypothetical protein ARALYDRAFT_342502 [Arabidopsis lyrata subsp. lyrata]	281	454	1.00E-19	161.6	23.1	35.9	hypothetical protein ARALYDRAFT_342502	gbpln	Arabidopsis lyrata	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	281	472	6.00E-17	168.0	22.1	35.2
Rsa1.0_00100.1.g4979.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	120	1274	3.00E-17	1061.7	43.3	58.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	120	170	2.00E-11	141.7	35.8	52.5
Rsa1.0_00100.1.g4980.t1	ref|XP_002876384.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322222|gb|EFH52643.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	231	242	1.00E-90	104.8	80.1	88.3	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT3G56880.1 | Symbols: | VQ motif-containing protein | chr3:21060044-21060781 FORWARD LENGTH=245	231	245	3.00E-92	106.1	77.9	85.7
Rsa1.0_00100.1.g4981.t1	ref|XP_002878117.1| hypothetical protein ARALYDRAFT_324196 [Arabidopsis lyrata subsp. lyrata] gi|297323955|gb|EFH54376.1| hypothetical protein ARALYDRAFT_324196 [Arabidopsis lyrata subsp. lyrata]	158	170	5.00E-68	107.6	81.0	90.5	hypothetical protein ARALYDRAFT_324196	gbpln	Arabidopsis lyrata	AT3G56891.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:21064199-21064922 REVERSE LENGTH=166	158	166	9.00E-67	105.1	79.1	88.6
Rsa1.0_00100.1.g4982.t1	ref|NP_191249.2| aladin-related / adracalin-related protein [Arabidopsis thaliana] gi|26452390|dbj|BAC43280.1| unknown protein [Arabidopsis thaliana] gi|28951013|gb|AAO63430.1| At3g56900 [Arabidopsis thaliana] gi|332646063|gb|AEE79584.1| aladin-related / adracalin-related protein [Arabidopsis thaliana]	444	447	0	100.7	87.4	93.2	aladin-related / adracalin-related protein	gbpln	Arabidopsis thaliana	AT3G56900.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:21066330-21069343 FORWARD LENGTH=447	444	447	0	100.7	87.4	93.2
Rsa1.0_00100.1.g4983.t1	gb|EOA24894.1| hypothetical protein CARUB_v10018185mg [Capsella rubella]	144	151	2.00E-32	104.9	84.0	90.3	hypothetical protein CARUB_v10018185mg	gbpln	Capsella rubella	AT3G56910.1 | Symbols: PSRP5 | plastid-specific 50S ribosomal protein 5 | chr3:21069558-21070257 REVERSE LENGTH=148	144	148	5.00E-34	102.8	84.0	88.2
Rsa1.0_00100.1.g4984.t6	emb|CAC00755.1| putative protein [Arabidopsis thaliana]	259	319	1.00E-113	123.2	76.1	86.5	putative protein	gbpln	Arabidopsis thaliana	AT3G56920.1 | Symbols: | DHHC-type zinc finger family protein | chr3:21070834-21072441 FORWARD LENGTH=338	259	338	1.00E-112	130.5	76.1	86.5
Rsa1.0_00100.1.g4985.t1	gb|EOA23934.1| hypothetical protein CARUB_v10017149mg [Capsella rubella] gi|482559744|gb|EOA23935.1| hypothetical protein CARUB_v10017149mg [Capsella rubella]	468	474	0	101.3	85.3	91.7	hypothetical protein CARUB_v10017149mg	gbpln	Capsella rubella	AT3G56930.1 | Symbols: | DHHC-type zinc finger family protein | chr3:21073805-21075873 FORWARD LENGTH=477	468	477	0	101.9	83.8	90.0

Rsa1.0_00100.1.g4986.t1	gb|EOA24121.1| hypothetical protein CARUB_v10017355mg [Capsella rubella]	409	409	0	100.0	94.4	96.3	hypothetical protein CARUB_v10017355mg	gbpln	Capsella rubella	AT3G56940.1 | Symbols: CRD1, CHL27, ACSF | dicarboxylate diiron protein, putative (Crd1) | chr3:21076594-21078269 FORWARD LENGTH=409	409	409	0	100.0	92.7	95.8
Rsa1.0_00100.1.g4987.t1	ref|NP_001190113.1| putative aquaporin SIP2-1 [Arabidopsis thaliana] gi|332646071|gb|AEE79592.1| putative aquaporin SIP2-1 [Arabidopsis thaliana]	237	260	1.00E-110	109.7	81.9	92.0	putative aquaporin SIP2-1	gbpln	Arabidopsis thaliana	AT3G56950.2 | Symbols: SIP2;1 | small and basic intrinsic protein 2;1 | chr3:21078411-21079644 REVERSE LENGTH=260	237	260	1.00E-113	109.7	81.9	92.0
Rsa1.0_00100.1.g4988.t1	ref|XP_002882328.1| hypothetical protein ARALYDRAFT_340564 [Arabidopsis lyrata subsp. lyrata] gi|297328168|gb|EFH58587.1| hypothetical protein ARALYDRAFT_340564 [Arabidopsis lyrata subsp. lyrata]	489	510	0	104.3	80.8	88.3	hypothetical protein ARALYDRAFT_340564	gbpln	Arabidopsis lyrata	AT3G04050.1 | Symbols: | Pyruvate kinase family protein | chr3:1049795-1051522 FORWARD LENGTH=510	489	510	0	104.3	80.4	88.3
Rsa1.0_00100.1.g4989.t1	ref|NP_191255.1| phosphatidylinositol-4-phosphate 5-kinase 4 [Arabidopsis thaliana] gi|75181907|sp|Q9M1K2.1|PI5K4_ARATH RecName: Full=Phosphatidylinositol 4-phosphate 5-kinase 4; Short=AtPIP5K4; AltName: Full=1-phosphatidylinositol 4-phosphate kinase 4; AltName: Full=Diphosphoinositide kinase 4; AltName: Full=PtdIns(4)P-5-kinase 4 gi|6911866|emb|CAB72166.1| phosphatidylinositol-4-phosphate 5-kinase-like protein [Arabidopsis thaliana] gi|332646072|gb|AEE79593.1| phosphatidylinositol-4-phosphate 5-kinase 4 [Arabidopsis thaliana]	781	779	0	99.7	93.3	96.9	phosphatidylinositol-4-phosphate 5-kinase 4	gbpln	Arabidopsis thaliana	AT3G56960.1 | Symbols: PIP5K4 | phosphatidyl inositol monophosphate 5 kinase 4 | chr3:21080957-21083885 FORWARD LENGTH=779	781	779	0	99.7	93.3	96.9
Rsa1.0_00101.1.g4990.t1	ref|NP_201050.2| uncharacterized protein [Arabidopsis thaliana] gi|20385491|gb|AAM21312.1|AF371327_1 EMB514 [Arabidopsis thaliana] gi|21593438|gb|AAM65405.1| unknown [Arabidopsis thaliana] gi|30793885|gb|AAP40395.1| unknown protein [Arabidopsis thaliana] gi|30794104|gb|AAP40494.1| unknown protein [Arabidopsis thaliana] gi|51968752|dbj|BAD43068.1| unnamed protein product [Arabidopsis thaliana] gi|110739286|dbj|BAF01556.1| hypothetical protein [Arabidopsis thaliana] gi|332010225|gb|AED97608.1| uncharacterized protein AT5G62440 [Arabidopsis thaliana]	164	202	1.00E-59	123.2	67.1	70.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G62440.1 | Symbols: | Protein of unknown function (DUF3223) | chr5:25072620-25073917 REVERSE LENGTH=202	164	202	4.00E-62	123.2	67.1	70.1
Rsa1.0_00101.1.g4991.t1	gb|EOA14154.1| hypothetical protein CARUB_v10027301mg, partial [Capsella rubella]	122	152	4.00E-62	124.6	96.7	96.7	hypothetical protein CARUB_v10027301mg, partial	gbpln	Capsella rubella	AT3G47370.3 | Symbols: | Ribosomal protein S10p/S20e family protein | chr3:17453671-17454437 REVERSE LENGTH=122	122	122	7.00E-64	100.0	95.9	95.9
Rsa1.0_00101.1.g4992.t1	ref|NP_201044.1| NAC-domain protein 101 [Arabidopsis thaliana] gi|8809651|dbj|BAA97202.1| NAM (no apical meristem)-like protein [Arabidopsis thaliana] gi|67633908|gb|AAY78878.1| no apical meristem family protein [Arabidopsis thaliana] gi|111074488|gb|ABH04617.1| At5g62380 [Arabidopsis thaliana] gi|332010219|gb|AED97602.1| NAC-domain protein 101 [Arabidopsis thaliana]	317	348	1.00E-153	109.8	83.9	90.5	NAC-domain protein 101	gbpln	Arabidopsis thaliana	AT5G62380.1 | Symbols: VND6, ANAC101, NAC101 | NAC-domain protein 101 | chr5:25050684-25051858 FORWARD LENGTH=348	317	348	1.00E-155	109.8	83.9	90.5
Rsa1.0_00101.1.g4993.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00101.1.g4994.t1	gb|EOA13946.1| hypothetical protein CARUB_v10027064mg [Capsella rubella]	202	228	3.00E-89	112.9	83.2	87.6	hypothetical protein CARUB_v10027064mg	gbpln	Capsella rubella	AT5G62360.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:25040699-25041310 FORWARD LENGTH=203	202	203	4.00E-86	100.5	82.2	88.1
Rsa1.0_00101.1.g4995.t1	ref|XP_002864781.1| hypothetical protein ARALYDRAFT_332462 [Arabidopsis lyrata subsp. lyrata] gi|297310616|gb|EFH41040.1| hypothetical protein ARALYDRAFT_332462 [Arabidopsis lyrata subsp. lyrata]	244	235	1.00E-111	96.3	85.7	90.6	hypothetical protein ARALYDRAFT_332462	gbpln	Arabidopsis lyrata	AT5G62280.1 | Symbols: | Protein of unknown function (DUF1442) | chr5:25017165-25017985 FORWARD LENGTH=236	244	236	1.00E-108	96.7	87.7	91.8
Rsa1.0_00101.1.g4996.t1	gb|ABD65101.1| hypothetical protein 31.t00082 [Brassica oleracea]	249	226	2.00E-46	90.8	41.0	59.0	hypothetical protein 31.t00082	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	249	566	4.00E-11	227.3	22.1	47.4

<table>
<tr><td>Rsa1.0_00101.1.g4997.t1</td><td>gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]</td><td>525</td><td>467</td><td>1.00E-144</td><td>89.0</td><td>49.0</td><td>60.0</td><td>hypothetical protein 31.t00031</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566</td><td>525</td><td>566</td><td>6.00E-80</td><td>107.8</td><td>33.3</td><td>54.3</td></tr>
<tr><td>Rsa1.0_00101.1.g4998.t1</td><td>gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]</td><td>522</td><td>467</td><td>1.00E-141</td><td>89.5</td><td>47.9</td><td>60.7</td><td>hypothetical protein 31.t00031</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566</td><td>522</td><td>566</td><td>2.00E-82</td><td>108.4</td><td>33.9</td><td>54.6</td></tr>
<tr><td>Rsa1.0_00101.1.g4999.t1</td><td>gb|EOA15396.1| hypothetical protein CARUB_v10006640mg [Capsella rubella]</td><td>170</td><td>171</td><td>6.00E-73</td><td>100.6</td><td>78.2</td><td>90.6</td><td>hypothetical protein CARUB_v10006640mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25040.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:12868320-12869319 FORWARD LENGTH=170</td><td>170</td><td>170</td><td>8.00E-75</td><td>100.0</td><td>82.4</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00101.1.g5000.t1</td><td>gb|EOA17627.1| hypothetical protein CARUB_v10005992mg [Capsella rubella]</td><td>135</td><td>136</td><td>7.00E-58</td><td>100.7</td><td>88.9</td><td>93.3</td><td>hypothetical protein CARUB_v10005992mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25050.1 | Symbols: ACP4 | acyl carrier protein 4 | chr4:12870178-12871024 FORWARD LENGTH=137</td><td>135</td><td>137</td><td>2.00E-56</td><td>101.5</td><td>85.9</td><td>91.1</td></tr>
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<tr><td>Rsa1.0_00101.1.g5002.t1</td><td>gb|ABO76902.1| high-affinity K+ transporter HAK5 [Eutrema halophilum]</td><td>780</td><td>790</td><td>0</td><td>101.3</td><td>89.1</td><td>93.6</td><td>high-affinity K+ transporter HAK5</td><td>gbpln</td><td>Eutrema halophilum</td><td>AT4G13420.1 | Symbols: HAK5, ATHAK5 | high affinity K+ transporter 5 | chr4:7797038-7802174 REVERSE LENGTH=785</td><td>780</td><td>785</td><td>0</td><td>100.6</td><td>86.5</td><td>92.2</td></tr>
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<tr><td>Rsa1.0_00101.1.g5004.t1</td><td>ref|XP_002867624.1| protein-methionine-s-oxide reductase [Arabidopsis lyrata subsp. lyrata] gi|297313460|gb|EFH43883.1| protein-methionine-s-oxide reductase [Arabidopsis lyrata subsp. lyrata]</td><td>253</td><td>257</td><td>1.00E-125</td><td>101.6</td><td>83.0</td><td>91.3</td><td>protein-methionine-s-oxide reductase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G25130.1 | Symbols: PMSR4 | peptide met sulfoxide reductase 4 | chr4:12898802-12899998 REVERSE LENGTH=258</td><td>253</td><td>258</td><td>1.00E-125</td><td>102.0</td><td>83.0</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00101.1.g5005.t1</td><td>sp|P29110.1|OLEO3_BRANA RecName: Full=Oleosin Bn-III; Short=BnIII gi|17839|emb|CAA43941.1| oleosin BN-III [Brassica napus] gi|196122088|gb|ACG69519.1| oleosin S3-7 [Brassica napus] gi|742387|prf||2009397A oleosin</td><td>196</td><td>195</td><td>3.00E-82</td><td>99.5</td><td>87.2</td><td>90.8</td><td>RecName: Full=Oleosin Bn-III; Short=BnIII gi|17839|emb|CAA43941.1| oleosin BN-III</td><td>gbpln</td><td>Brassica napus</td><td>AT4G25140.1 | Symbols: OLEO1, OLE1 | oleosin 1 | chr4:12900498-12901259 FORWARD LENGTH=173</td><td>196</td><td>173</td><td>1.00E-73</td><td>88.3</td><td>81.6</td><td>83.2</td></tr>
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<tr><td>Rsa1.0_00101.1.g5007.t1</td><td>ref|XP_002867620.1| hypothetical protein ARALYDRAFT_492315 [Arabidopsis lyrata subsp. lyrata] gi|297313456|gb|EFH43879.1| hypothetical protein ARALYDRAFT_492315 [Arabidopsis lyrata subsp. lyrata]</td><td>513</td><td>412</td><td>1.00E-154</td><td>80.3</td><td>60.0</td><td>67.6</td><td>hypothetical protein ARALYDRAFT_492315</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G25190.1 | Symbols: QWRF7 | Family of unknown function (DUF566) | chr4:12914400-12916001 REVERSE LENGTH=394</td><td>513</td><td>394</td><td>1.00E-155</td><td>76.8</td><td>58.9</td><td>67.3</td></tr>
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<tr><td>Rsa1.0_00101.1.g5009.t1</td><td>gb|EOA17732.1| hypothetical protein CARUB_v10006114mg [Capsella rubella]</td><td>56</td><td>98</td><td>1.00E-20</td><td>175.0</td><td>80.4</td><td>89.3</td><td>hypothetical protein CARUB_v10006114mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25225.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35736.2); Has 78 Blast hits to 78 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:12923086-12923256 REVERSE LENGTH=56</td><td>56</td><td>56</td><td>1.00E-21</td><td>100.0</td><td>78.6</td><td>85.7</td></tr>
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<tr><td>Rsa1.0_00101.1.g5011.t1</td><td>ref|NP_194255.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|4454013|emb|CAA23066.1| putative protein [Arabidopsis thaliana] gi|7269376|emb|CAB81336.1| putative protein [Arabidopsis thaliana] gi|28416607|gb|AAO42834.1| At4g25250 [Arabidopsis thaliana] gi|110743315|dbj|BAE99546.1| hypothetical protein [Arabidopsis thaliana] gi|332659631|gb|AEE85031.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]</td><td>261</td><td>199</td><td>2.00E-81</td><td>76.2</td><td>57.9</td><td>67.0</td><td>plant invertase/pectin methylesterase inhibitor domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25250.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:12934632-12935231 FORWARD LENGTH=199</td><td>261</td><td>199</td><td>4.00E-84</td><td>76.2</td><td>57.9</td><td>67.0</td></tr>
<tr><td>Rsa1.0_00101.1.g5012.t1</td><td>gb|EOA30196.1| hypothetical protein CARUB_v10013313mg [Capsella rubella]</td><td>577</td><td>582</td><td>0</td><td>100.9</td><td>75.0</td><td>84.6</td><td>hypothetical protein CARUB_v10013313mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G03460.1 | Symbols: | Ankyrin repeat family protein | chr4:1536404-1540111 REVERSE LENGTH=677</td><td>577</td><td>677</td><td>7.00E-50</td><td>117.3</td><td>28.1</td><td>42.5</td></tr>
<tr><td>Rsa1.0_00101.1.g5013.t1</td><td>gb|EOA17445.1| hypothetical protein CARUB_v10005764mg [Capsella rubella]</td><td>201</td><td>202</td><td>8.00E-91</td><td>100.5</td><td>82.1</td><td>90.0</td><td>hypothetical protein CARUB_v10005764mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25260.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:12936005-12936610 REVERSE LENGTH=201</td><td>201</td><td>201</td><td>4.00E-92</td><td>100.0</td><td>80.1</td><td>89.1</td></tr>
<tr><td>Rsa1.0_00101.1.g5014.t1</td><td>ref|NP_194259.4| DNA photolyase [Arabidopsis thaliana] gi|332659635|gb|AEE85035.1| DNA photolyase [Arabidopsis thaliana]</td><td>688</td><td>692</td><td>0</td><td>100.6</td><td>83.1</td><td>89.8</td><td>DNA photolyase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25290.1 | Symbols: | DNA photolyases;DNA photolyases | chr4:12941486-12944994 REVERSE LENGTH=692</td><td>688</td><td>692</td><td>0</td><td>100.6</td><td>83.1</td><td>89.8</td></tr>
<tr><td>Rsa1.0_00101.1.g5015.t1</td><td>ref|XP_002869680.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297315516|gb|EFH45939.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]</td><td>346</td><td>356</td><td>1.00E-152</td><td>102.9</td><td>76.0</td><td>86.1</td><td>oxidoreductase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G25300.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:12945263-12946642 FORWARD LENGTH=356</td><td>346</td><td>356</td><td>1.00E-154</td><td>102.9</td><td>75.4</td><td>86.7</td></tr>
<tr><td>Rsa1.0_00101.1.g5016.t2</td><td>ref|NP_001190835.1| uncharacterized protein [Arabidopsis thaliana] gi|332659640|gb|AEE85040.1| uncharacterized protein AT4G25315 [Arabidopsis thaliana]</td><td>108</td><td>108</td><td>5.00E-50</td><td>100.0</td><td>83.3</td><td>93.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25315.2 | Symbols: | Expressed protein | chr4:12951659-12952834 REVERSE LENGTH=108</td><td>108</td><td>108</td><td>8.00E-53</td><td>100.0</td><td>83.3</td><td>93.5</td></tr>
<tr><td>Rsa1.0_00101.1.g5017.t3</td><td>gb|EOA16732.1| hypothetical protein CARUB_v10004935mg [Capsella rubella]</td><td>367</td><td>411</td><td>1.00E-126</td><td>112.0</td><td>78.2</td><td>85.3</td><td>hypothetical protein CARUB_v10004935mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25320.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:12954488-12956342 FORWARD LENGTH=404</td><td>367</td><td>404</td><td>1.00E-127</td><td>110.1</td><td>78.5</td><td>83.9</td></tr>
<tr><td>Rsa1.0_00101.1.g5018.t1</td><td>gb|EOA19111.1| hypothetical protein CARUB_v10007779mg [Capsella rubella]</td><td>222</td><td>224</td><td>5.00E-80</td><td>100.9</td><td>66.2</td><td>82.4</td><td>hypothetical protein CARUB_v10007779mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25330.1 | Symbols: | unknown protein; Has 21 Blast hits to 21 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:12957834-12958683 FORWARD LENGTH=229</td><td>222</td><td>229</td><td>6.00E-76</td><td>103.2</td><td>59.9</td><td>77.5</td></tr>
<tr><td>Rsa1.0_00101.1.g5019.t2</td><td>ref|NP_567717.1| peptidylprolyl isomerase [Arabidopsis thaliana] gi|75163771|sp|Q93ZG9.1|FKB53_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP53; Short=PPIase FKBP53; AltName: Full=FK506-binding protein 53; Short=AtFKBP53; AltName: Full=Immunophilin FKBP53; AltName: Full=Rotamase gi|15982872|gb|AAL09783.1| AT4g25340/T30C3_20 [Arabidopsis thaliana] gi|23506115|gb|AAN28917.1| At4g25340/T30C3_20 [Arabidopsis thaliana] gi|332659643|gb|AEE85043.1| peptidylprolyl isomerase [Arabidopsis thaliana]</td><td>455</td><td>477</td><td>1.00E-137</td><td>104.8</td><td>67.9</td><td>80.4</td><td>peptidylprolyl isomerase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25340.1 | Symbols: FKBP53, ATFKBP53 | FK506 BINDING PROTEIN 53 | chr4:12959657-12962632 REVERSE LENGTH=477</td><td>455</td><td>477</td><td>1.00E-139</td><td>104.8</td><td>67.9</td><td>80.4</td></tr>
<tr><td>Rsa1.0_00101.1.g5020.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00101.1.g5021.t1	ref|NP_567718.1| Double Clp-N motif protein [Arabidopsis thaliana] gi|14334924|gb|AAK59640.1| unknown protein [Arabidopsis thaliana] gi|16323364|gb|AAL15176.1| unknown protein [Arabidopsis thaliana] gi|21555497|gb|AAM63872.1| unknown [Arabidopsis thaliana] gi|195604812|gb|ACG24236.1| ATP-dependent Clp protease ATP-binding subunit clpA [Zea mays] gi|332659648|gb|AEE85048.1| Double Clp-N motif protein [Arabidopsis thaliana]	235	238	1.00E-100	101.3	80.4	86.4	Double Clp-N motif protein	gbpln	Arabidopsis thaliana	AT4G25370.1 | Symbols: | Double Clp-N motif protein | chr4:12972747-12974580 FORWARD LENGTH=238	235	238	1.00E-103	101.3	80.4	86.4
Rsa1.0_00101.1.g5022.t1	ref|NP_194268.1| zinc finger A20 and AN1 domain-containing stress-associated protein 10 [Arabidopsis thaliana] gi|75266322|sp|Q9STJ9.1|SAP10_ARATH RecName: Full=Zinc finger A20 and AN1 domain-containing stress-associated protein 10; Short=AtSAP10 gi|5123927|emb|CAB45515.1| putative protein [Arabidopsis thaliana] gi|7269389|emb|CAB81349.1| putative protein [Arabidopsis thaliana] gi|117168073|gb|ABK32119.1| At4g25380 [Arabidopsis thaliana] gi|332659649|gb|AEE85049.1| zinc finger A20 and AN1 domain-containing stress-associated protein 10 [Arabidopsis thaliana]	136	130	6.00E-45	95.6	66.2	73.5	zinc finger A20 and AN1 domain-containing stress-associated protein 10	gbpln	Arabidopsis thaliana	AT4G25380.1 | Symbols: SAP10 | stress-associated protein 10 | chr4:12975936-12976328 REVERSE LENGTH=130	136	130	1.00E-47	95.6	66.2	73.5
Rsa1.0_00101.1.g5023.t1	ref|XP_002869674.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315510|gb|EFH45933.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	612	649	0	106.0	80.9	85.8	kinase family protein	gbpln	Arabidopsis lyrata	AT4G25390.1 | Symbols: | Protein kinase superfamily protein | chr4:12977491-12979446 FORWARD LENGTH=651	612	651	0	106.4	80.6	86.3
Rsa1.0_00101.1.g5024.t1	gb|EOA17859.1| hypothetical protein CARUB_v10006264mg [Capsella rubella]	185	197	2.00E-65	106.5	68.1	75.1	hypothetical protein CARUB_v10006264mg	gbpln	Capsella rubella	AT4G25400.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:12981295-12982335 FORWARD LENGTH=163	185	163	4.00E-66	88.1	64.9	75.7
Rsa1.0_00101.1.g5025.t1	ref|XP_002869672.1| basix helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297315508|gb|EFH45931.1| basix helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	188	222	2.00E-67	118.1	73.9	81.9	basix helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT4G25410.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:12985772-12987149 FORWARD LENGTH=230	188	230	1.00E-68	122.3	70.7	79.8
Rsa1.0_00101.1.g5026.t1	dbj|BAM73279.1| gibberellin 20 oxidase 1 [Raphanus sativus]	381	381	0	100.0	99.0	99.5	gibberellin 20 oxidase 1	gbpln	Raphanus sativus	AT4G25420.1 | Symbols: GA5, GA20OX1, AT2301, ATGA20OX1 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:12990982-12992409 REVERSE LENGTH=377	381	377	0	99.0	85.8	89.5
Rsa1.0_00101.1.g5027.t1	gb|EOA14349.1| hypothetical protein CARUB_v10027529mg [Capsella rubella]	165	222	3.00E-47	134.5	66.7	80.6	hypothetical protein CARUB_v10027529mg	gbpln	Capsella rubella	AT5G51870.1 | Symbols: AGL71 | AGAMOUS-like 71 | chr5:21085635-21087923 REVERSE LENGTH=207	165	207	2.00E-24	125.5	43.0	62.4
Rsa1.0_00101.1.g5028.t1	gb|AAD45623.1|AF084185_1 dehydration responsive element binding protein [Brassica napus]	214	214	1.00E-107	100.0	92.1	95.8	dehydration responsive element binding protein	gbpln	Brassica napus	AT4G25470.1 | Symbols: CBF2, DREB1C, FTQ4, ATCBF2 | C-repeat/DRE binding factor 2 | chr4:13015436-13016086 REVERSE LENGTH=216	214	216	9.00E-97	100.9	79.0	87.9
Rsa1.0_00101.1.g5029.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00101.1.g5030.t1	gb|EOA15349.1| hypothetical protein CARUB_v10004256mg [Capsella rubella]	340	708	1.00E-61	208.2	48.2	56.8	hypothetical protein CARUB_v10004256mg	gbpln	Capsella rubella	AT4G25520.1 | Symbols: SLK1 | SEUSS-like 1 | chr4:13032450-13035803 REVERSE LENGTH=748	340	748	5.00E-61	220.0	50.0	57.9
Rsa1.0_00101.1.g5031.t1	gb|EOA15349.1| hypothetical protein CARUB_v10004256mg [Capsella rubella]	559	708	1.00E-173	126.7	65.1	76.7	hypothetical protein CARUB_v10004256mg	gbpln	Capsella rubella	AT4G25515.1 | Symbols: SLK3 | SEUSS-like 3 | chr4:13028219-13031463 FORWARD LENGTH=685	559	685	1.00E-175	122.5	65.8	77.3
Rsa1.0_00101.1.g5032.t1	ref|XP_002869669.1| hypothetical protein ARALYDRAFT_354233 [Arabidopsis lyrata subsp. lyrata] gi|297315505|gb|EFH45928.1| hypothetical protein ARALYDRAFT_354233 [Arabidopsis lyrata subsp. lyrata]	655	663	1.00E-141	101.2	42.3	48.9	hypothetical protein ARALYDRAFT_354233	gbpln	Arabidopsis lyrata	AT4G25515.1 | Symbols: SLK3 | SEUSS-like 3 | chr4:13028219-13031463 FORWARD LENGTH=685	655	685	1.00E-137	104.6	41.5	48.9
Rsa1.0_00101.1.g5033.t4	gb|EOA17496.1| hypothetical protein CARUB_v10005830mg [Capsella rubella]	219	184	2.00E-56	84.0	57.5	62.1	hypothetical protein CARUB_v10005830mg	gbpln	Capsella rubella	AT5G52200.1 | Symbols: | phosphoprotein phosphatase inhibitors | chr5:21202818-21204719 REVERSE LENGTH=191	219	191	8.00E-45	87.2	50.2	58.0

Rsa1.0_00101.1.g5034.t1	ref|NP_194284.2| DNA mismatch repair protein Msh3 [Arabidopsis thaliana] gi|12644077|sp|O65607.2|MSH3_ARATH RecName: Full=DNA mismatch repair protein MSH3; Short=AtMSH3; AltName: Full=MutS protein homolog 3 gi|3319876|emb|CAA07684.1| Msh3 protein [Arabidopsis thaliana] gi|332659675|gb|AEE85075.1| DNA mismatch repair protein Msh3 [Arabidopsis thaliana]	1038	1081	0	104.1	85.2	90.2	DNA mismatch repair protein Msh3	gbpln	Arabidopsis thaliana	AT4G25540.1 | Symbols: MSH3, ATMSH3 | homolog of DNA mismatch repair protein MSH3 | chr4:13042700-13048115 REVERSE LENGTH=1081	1038	1081	0	104.1	85.2	90.2
Rsa1.0_00101.1.g5035.t1	ref|NP_173360.1| TTF-type zinc finger protein with HAT dimerization domain [Arabidopsis thaliana] gi|332191703|gb|AEE29824.1| TTF-type zinc finger protein with HAT dimerization domain [Arabidopsis thaliana]	574	769	4.00E-97	134.0	29.3	37.5	TTF-type zinc finger protein with HAT dimerization domain	gbpln	Arabidopsis thaliana	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	574	769	1.00E-100	134.0	29.3	37.5
Rsa1.0_00101.1.g5036.t1	ref|XP_002869667.1| AtMYB18 [Arabidopsis lyrata subsp. lyrata] gi|297315503|gb|EFH45926.1| AtMYB18 [Arabidopsis lyrata subsp. lyrata]	264	262	1.00E-101	99.2	73.9	79.9	AtMYB18	gbpln	Arabidopsis lyrata	AT4G25560.1 | Symbols: AtMYB18, MYB18 | myb domain protein 18 | chr4:13052555-13053573 FORWARD LENGTH=283	264	283	1.00E-102	107.2	73.1	80.7
Rsa1.0_00101.1.g5037.t1	gb|AAM62824.1| cytochrome b561 [Arabidopsis thaliana]	235	237	1.00E-110	100.9	88.9	94.0	cytochrome b561	gbpln	Arabidopsis thaliana	AT4G25570.1 | Symbols: ACYB-2 | Cytochrome b561/ferric reductase transmembrane protein family | chr4:13053887-13055518 REVERSE LENGTH=239	235	239	1.00E-110	101.7	88.5	93.6
Rsa1.0_00101.1.g5038.t1	gb|EOA18495.1| hypothetical protein CARUB_v10007046mg [Capsella rubella]	543	573	1.00E-153	105.5	69.8	78.5	hypothetical protein CARUB_v10007046mg	gbpln	Capsella rubella	AT4G25580.1 | Symbols: | CAP160 protein | chr4:13056320-13058657 FORWARD LENGTH=626	543	626	1.00E-150	115.3	70.3	81.4
Rsa1.0_00101.1.g5039.t1	gb|EOA18372.1| hypothetical protein CARUB_v10006893mg [Capsella rubella]	129	137	1.00E-63	106.2	92.2	95.3	hypothetical protein CARUB_v10006893mg	gbpln	Capsella rubella	AT4G25590.1 | Symbols: ADF7 | actin depolymerizing factor 7 | chr4:13059137-13060050 REVERSE LENGTH=137	129	137	3.00E-65	106.2	91.5	94.6
Rsa1.0_00101.1.g5040.t1	ref|XP_002894416.1| hypothetical protein ARALYDRAFT_892322 [Arabidopsis lyrata subsp. lyrata] gi|297340258|gb|EFH70675.1| hypothetical protein ARALYDRAFT_892322 [Arabidopsis lyrata subsp. lyrata]	155	137	2.00E-23	88.4	37.4	52.3	hypothetical protein ARALYDRAFT_892322	gbpln	Arabidopsis lyrata	AT3G15360.1 | Symbols: ATHM4, TRX-M4, ATM4 | thioredoxin M-type 4 | chr3:5188448-5189457 FORWARD LENGTH=193	155	193	1.00E-23	124.5	30.3	45.8
Rsa1.0_00101.1.g5041.t1	ref|NP_194291.2| C2H2-like zinc finger protein [Arabidopsis thaliana] gi|19698895|gb|AAL91183.1| unknown protein [Arabidopsis thaliana] gi|23198356|gb|AAN15705.1| unknown protein [Arabidopsis thaliana] gi|332659682|gb|AEE85082.1| C2H2-like zinc finger protein [Arabidopsis thaliana]	938	586	0	62.5	49.4	54.3	C2H2-like zinc finger protein	gbpln	Arabidopsis thaliana	AT4G25610.1 | Symbols: | C2H2-like zinc finger protein | chr4:13063801-13066860 FORWARD LENGTH=586	938	586	0	62.5	49.4	54.3
Rsa1.0_00101.1.g5042.t1	gb|EOA16635.1| hypothetical protein CARUB_v10004810mg [Capsella rubella]	446	444	1.00E-148	99.6	71.3	80.0	hypothetical protein CARUB_v10004810mg	gbpln	Capsella rubella	AT4G25620.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:13067447-13069296 REVERSE LENGTH=449	446	449	1.00E-149	100.7	72.6	80.3
Rsa1.0_00101.1.g5043.t1	ref|NP_567724.1| rRNA 2'-O-methyltransferase fibrillarin 2 [Arabidopsis thaliana] gi|67461067|sp|Q94AH9.2|MD36A_ARATH RecName: Full=Mediator of RNA polymerase II transcription subunit 36a; AltName: Full=Fibrillarin-like protein 2; AltName: Full=rRNA 2'-O-methyltransferase fibrillarin 2 gi|9965655|gb|AAG10104.1|AF233444_1 fibrillarin 2 [Arabidopsis thaliana] gi|4914455|emb|CAB43694.1| fibrillarin-like protein [Arabidopsis thaliana] gi|7269413|emb|CAB81373.1| fibrillarin-like protein [Arabidopsis thaliana] gi|9965796|gb|AAG10153.1| fibrillarin 2 [Arabidopsis thaliana] gi|21536840|gb|AAM61172.1| fibrillarin 2 (AtFib2) [Arabidopsis thaliana] gi|23297150|gb|AAN13105.1| fibrillarin 2 (AtFib2) [Arabidopsis thaliana] gi|332659685|gb|AEE85085.1| rRNA 2'-O-methyltransferase fibrillarin 2 [Arabidopsis thaliana]	305	320	1.00E-134	104.9	76.1	79.3	rRNA 2'-O-methyltransferase fibrillarin 2	gbpln	Arabidopsis thaliana	AT4G25630.1 | Symbols: FIB2, ATFIB2 | fibrillarin 2 | chr4:13074239-13076205 FORWARD LENGTH=320	305	320	1.00E-137	104.9	76.1	79.3
Rsa1.0_00101.1.g5044.t1	dbj|BAJ33972.1| unnamed protein product [Thellungiella halophila]	490	488	0	99.6	89.2	94.5	unnamed protein product	----	----	AT4G25640.1 | Symbols: ATDTX35, FFT, DTX35 | detoxifying efflux carrier 35 | chr4:13076953-13078965 REVERSE LENGTH=488	490	488	0	99.6	89.6	95.5

<table>
<tr><td>Rsa1.0_00101.1.g5045.t1</td><td>emb|CAB43698.1| hypothetical protein [Arabidopsis thaliana] gi|7269417|emb|CAB81377.1| hypothetical protein [Arabidopsis thaliana]</td><td>219</td><td>247</td><td>4.00E-85</td><td>112.8</td><td>78.1</td><td>84.0</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25670.2 | Symbols: | unknown protein; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25690.2). | chr4:13085431-13085997 REVERSE LENGTH=188</td><td>219</td><td>188</td><td>4.00E-69</td><td>85.8</td><td>61.6</td><td>66.2</td></tr>
<tr><td>Rsa1.0_00101.1.g5046.t1</td><td>gb|AAS55552.1| putative beta-carotene hydroxylase [Brassica rapa] gi|73697713|gb|AAZ81472.1| beta-carotene hydroxylase [Brassica rapa]</td><td>307</td><td>300</td><td>1.00E-161</td><td>97.7</td><td>93.2</td><td>94.8</td><td>putative beta-carotene hydroxylase</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G25700.1 | Symbols: BETA-OHASE 1, B1, chy1, BCH1 | beta-hydroxylase 1 | chr4:13094142-13095866 REVERSE LENGTH=310</td><td>307</td><td>310</td><td>1.00E-152</td><td>101.0</td><td>86.3</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00101.1.g5047.t1</td><td>gb|EOA15458.1| hypothetical protein CARUB_v10004151mg [Capsella rubella]</td><td>820</td><td>814</td><td>0</td><td>99.3</td><td>81.5</td><td>89.8</td><td>hypothetical protein CARUB_v10004151mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25730.1 | Symbols: | FtsJ-like methyltransferase family protein | chr4:13102906-13106718 REVERSE LENGTH=821</td><td>820</td><td>821</td><td>0</td><td>100.1</td><td>79.8</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00101.1.g5048.t1</td><td>gb|EOA13969.1| hypothetical protein CARUB_v10027094mg, partial [Capsella rubella]</td><td>181</td><td>220</td><td>4.00E-76</td><td>121.5</td><td>86.7</td><td>89.0</td><td>hypothetical protein CARUB_v10027094mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25740.1 | Symbols: | RNA binding Plectin/S10 domain-containing protein | chr4:13107488-13108751 REVERSE LENGTH=177</td><td>181</td><td>177</td><td>2.00E-73</td><td>97.8</td><td>90.6</td><td>92.8</td></tr>
<tr><td>Rsa1.0_00102.1.g5049.t2</td><td>ref|XP_002518263.1| cation-transporting atpase plant, putative [Ricinus communis] gi|223542610|gb|EEF44149.1| cation-transporting atpase plant, putative [Ricinus communis]</td><td>1067</td><td>1075</td><td>0</td><td>100.7</td><td>51.4</td><td>66.5</td><td>cation-transporting atpase plant, putative</td><td>gbpln</td><td>Ricinus communis</td><td>AT5G57110.2 | Symbols: ACA8, AT-ACA8 | autoinhibited Ca2+ -ATPase, isoform 8 | chr5:23109729-23116857 REVERSE LENGTH=1074</td><td>1067</td><td>1074</td><td>0</td><td>100.7</td><td>50.3</td><td>65.9</td></tr>
<tr><td>Rsa1.0_00102.1.g5050.t1</td><td>gb|EOA15699.1| hypothetical protein CARUB_v10006454mg [Capsella rubella]</td><td>580</td><td>312</td><td>1.00E-137</td><td>53.8</td><td>42.1</td><td>44.1</td><td>hypothetical protein CARUB_v10006454mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G26010.1 | Symbols: | Peroxidase superfamily protein | chr4:13200653-13201688 FORWARD LENGTH=310</td><td>580</td><td>310</td><td>1.00E-128</td><td>53.4</td><td>39.0</td><td>41.9</td></tr>
<tr><td>Rsa1.0_00102.1.g5051.t2</td><td>ref|NP_194335.2| plant intracellular ras group-related LRR 8 [Arabidopsis thaliana] gi|20260486|gb|AAM13141.1| putative leucine-rich-repeat protein [Arabidopsis thaliana] gi|30725612|gb|AAP37828.1| At4g26050 [Arabidopsis thaliana] gi|332659749|gb|AEE85149.1| plant intracellular ras group-related LRR 8 [Arabidopsis thaliana]</td><td>399</td><td>383</td><td>1.00E-175</td><td>96.0</td><td>84.0</td><td>88.0</td><td>plant intracellular ras group-related LRR 8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26050.1 | Symbols: PIRL8 | plant intracellular ras group-related LRR 8 | chr4:13210522-13213149 FORWARD LENGTH=383</td><td>399</td><td>383</td><td>1.00E-177</td><td>96.0</td><td>84.0</td><td>88.0</td></tr>
<tr><td>Rsa1.0_00102.1.g5052.t1</td><td>dbj|BAJ34574.1| unnamed protein product [Thellungiella halophila]</td><td>415</td><td>439</td><td>0</td><td>105.8</td><td>93.5</td><td>97.3</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G26080.1 | Symbols: ABI1, AtABI1 | Protein phosphatase 2C family protein | chr4:13220231-13221828 REVERSE LENGTH=434</td><td>415</td><td>434</td><td>0</td><td>104.6</td><td>89.4</td><td>93.5</td></tr>
<tr><td>Rsa1.0_00102.1.g5053.t1</td><td>ref|XP_002868748.1| DSBA oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314584|gb|EFH45007.1| DSBA oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>170</td><td>217</td><td>3.00E-13</td><td>127.6</td><td>26.5</td><td>31.8</td><td>DSBA oxidoreductase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G38900.1 | Symbols: | Thioredoxin superfamily protein | chr5:15573745-15574945 REVERSE LENGTH=217</td><td>170</td><td>217</td><td>2.00E-15</td><td>127.6</td><td>26.5</td><td>31.2</td></tr>
<tr><td>Rsa1.0_00102.1.g5054.t1</td><td>ref|NP_199541.1| putative F-box protein [Arabidopsis thaliana] gi|75264281|sp|Q9LVS9.1|FB340_ARATH RecName: Full=Probable F-box protein At5g47300 gi|8809613|dbj|BAA97164.1| unnamed protein product [Arabidopsis thaliana] gi|332008112|gb|AED95495.1| putative F-box protein [Arabidopsis thaliana]</td><td>380</td><td>416</td><td>4.00E-72</td><td>109.5</td><td>46.3</td><td>61.8</td><td>putative F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G47300.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:19198125-19199375 FORWARD LENGTH=416</td><td>380</td><td>416</td><td>9.00E-75</td><td>109.5</td><td>46.3</td><td>61.8</td></tr>
<tr><td>Rsa1.0_00102.1.g5055.t1</td><td>gb|AAF19803.1| RPS2 protein [Brassica oleracea]</td><td>906</td><td>907</td><td>0</td><td>100.1</td><td>90.5</td><td>95.5</td><td>RPS2 protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G26090.1 | Symbols: RPS2 | NB-ARC domain-containing disease resistance protein | chr4:13224596-13227325 FORWARD LENGTH=909</td><td>906</td><td>909</td><td>0</td><td>100.3</td><td>84.8</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00102.1.g5056.t1</td><td>gb|EOA13389.1| hypothetical protein CARUB_v10026431mg [Capsella rubella]</td><td>434</td><td>434</td><td>0</td><td>100.0</td><td>91.9</td><td>94.9</td><td>hypothetical protein CARUB_v10026431mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G57020.1 | Symbols: NMT1, ATNMT1 | myristoyl-CoA:protein N-myristoyltransferase | chr5:23075451-23076755 FORWARD LENGTH=434</td><td>434</td><td>434</td><td>0</td><td>100.0</td><td>91.2</td><td>95.2</td></tr>
<tr><td>Rsa1.0_00102.1.g5057.t1</td><td>ref|XP_002867580.1| hypothetical protein ARALYDRAFT_492204 [Arabidopsis lyrata subsp. lyrata] gi|297313416|gb|EFH43839.1| hypothetical protein ARALYDRAFT_492204 [Arabidopsis lyrata subsp. lyrata]</td><td>462</td><td>454</td><td>0</td><td>98.3</td><td>90.3</td><td>92.9</td><td>hypothetical protein ARALYDRAFT_492204</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G26100.1 | Symbols: CK1, CKL1 | casein kinase 1 | chr4:13227885-13230508 REVERSE LENGTH=450</td><td>462</td><td>450</td><td>0</td><td>97.4</td><td>88.7</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00102.1.g5058.t1</td><td>gb|AAM88865.2|AF527176_1 putative NPR1 [Brassica napus]</td><td>581</td><td>579</td><td>0</td><td>99.7</td><td>91.2</td><td>95.0</td><td>putative NPR1</td><td>gbpln</td><td>Brassica napus</td><td>AT1G64280.1 | Symbols: NPR1, SAI1, NIM1, ATNPR1 | regulatory protein (NPR1) | chr1:23853329-23855407 REVERSE LENGTH=593</td><td>581</td><td>593</td><td>0</td><td>102.1</td><td>69.7</td><td>82.8</td></tr>
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Rsa1.0_00102.1.g5059.t1	gb|AAA50234.1| nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707, partial [Arabidopsis thaliana]	371	382	1.00E-145	103.0	77.9	90.6	nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707, partial	gbpln	Arabidopsis thaliana	AT4G26110.1 | Symbols: NAP1;1, ATNAP1;1 | nucleosome assembly protein1;1 | chr4:13232712-13235502 FORWARD LENGTH=372	371	372	1.00E-148	100.3	77.9	90.6
Rsa1.0_00102.1.g5060.t1	gb|EOA16271.1| hypothetical protein CARUB_v10004416mg [Capsella rubella]	605	599	0	99.0	72.7	84.6	hypothetical protein CARUB_v10004416mg	gbpln	Capsella rubella	AT4G26120.1 | Symbols: | Ankyrin repeat family protein / BTB/POZ domain-containing protein | chr4:13236448-13238487 FORWARD LENGTH=600	605	600	0	99.2	70.9	80.5
Rsa1.0_00102.1.g5061.t1	gb|AAG52629.1|AC024261_16 unknown protein; 27363-23366 [Arabidopsis thaliana]	72	1036	1.00E-11	1438.9	56.9	65.3	unknown protein; 27363-23366	gbpln	Arabidopsis thaliana	AT1G51540.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:19115702-19117381 FORWARD LENGTH=415	72	415	3.00E-14	576.4	56.9	65.3
Rsa1.0_00102.1.g5062.t1	ref|XP_002867579.1| hypothetical protein ARALYDRAFT_492200 [Arabidopsis lyrata subsp. lyrata] gi|297313415|gb|EFH43838.1| hypothetical protein ARALYDRAFT_492200 [Arabidopsis lyrata subsp. lyrata]	290	284	1.00E-106	97.9	76.9	83.4	hypothetical protein ARALYDRAFT_492200	gbpln	Arabidopsis lyrata	AT4G26130.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G56980.1); Has 121 Blast hits to 116 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 113; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:13240403-13241263 REVERSE LENGTH=286	290	286	2.00E-96	98.6	76.2	83.1
Rsa1.0_00102.1.g5063.t2	ref|NP_849553.1| beta-galactosidase 12 [Arabidopsis thaliana] gi|75265630|sp|Q9SCV0.1|BGL12_ARATH RecName: Full=Beta-galactosidase 12; Short=Lactase 12; Flags: Precursor gi|6686896|emb|CAB64748.1| putative beta-galactosidase [Arabidopsis thaliana] gi|332659762|gb|AEE85162.1| beta-galactosidase 12 [Arabidopsis thaliana]	733	728	0	99.3	89.6	93.6	beta-galactosidase 12	gbpln	Arabidopsis thaliana	AT4G26140.1 | Symbols: BGAL12 | beta-galactosidase 12 | chr4:13243219-13247823 REVERSE LENGTH=728	733	728	0	99.3	89.6	93.6
Rsa1.0_00102.1.g5064.t1	gb|AAC95212.1| Mutator-like transposase [Arabidopsis thaliana]	906	915	1.00E-160	101.0	30.9	42.5	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	906	719	3.00E-36	79.4	14.6	27.0
Rsa1.0_00102.1.g5065.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	930	871	1.00E-101	93.7	31.7	48.7	Ulp1 protease family protein	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	930	673	5.00E-32	72.4	11.6	18.2
Rsa1.0_00102.1.g5066.t1	gb|EOA16889.1| hypothetical protein CARUB_v10005113mg [Capsella rubella]	330	361	1.00E-89	109.4	65.8	75.2	hypothetical protein CARUB_v10005113mg	gbpln	Capsella rubella	AT4G26150.1 | Symbols: CGA1, GATA22, GNL | cytokinin-responsive gata factor 1 | chr4:13253210-13254659 FORWARD LENGTH=352	330	352	1.00E-79	106.7	65.2	73.9
Rsa1.0_00102.1.g5067.t1	ref|NP_194346.1| thioredoxin-like 2-1 [Arabidopsis thaliana] gi|51702019|sp|Q8LEK4.2|TRL21_ARATH RecName: Full=Thioredoxin-like 2-1, chloroplastic; AltName: Full=Atypical cysteine/histidine-rich thioredoxin 1; Short=AtACHT1; Flags: Precursor gi|4538945|emb|CAB39681.1| putative thioredoxin [Arabidopsis thaliana] gi|7269467|emb|CAB79471.1| putative thioredoxin [Arabidopsis thaliana] gi|88196727|gb|ABD43006.1| At4g26160 [Arabidopsis thaliana] gi|332659765|gb|AEE85165.1| thioredoxin-like 2-1 [Arabidopsis thaliana]	215	221	3.00E-84	102.8	80.0	86.5	thioredoxin-like 2-1	gbpln	Arabidopsis thaliana	AT4G26160.1 | Symbols: ACHT1 | atypical CYS HIS rich thioredoxin 1 | chr4:13255296-13256632 FORWARD LENGTH=221	215	221	9.00E-87	102.8	80.0	86.5
Rsa1.0_00102.1.g5068.t10	gb|EOA26149.1| hypothetical protein CARUB_v10019585mg [Capsella rubella]	577	423	1.00E-29	73.3	19.4	26.2	hypothetical protein CARUB_v10019585mg	gbpln	Capsella rubella	AT4G26340.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:13324130-13325559 FORWARD LENGTH=419	577	419	5.00E-28	72.6	19.1	28.2
Rsa1.0_00102.1.g5069.t1	gb|EOA25784.1| hypothetical protein CARUB_v10019151mg, partial [Capsella rubella]	439	460	5.00E-79	104.8	44.2	57.9	hypothetical protein CARUB_v10019151mg, partial	gbpln	Capsella rubella	AT3G52680.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr3:19527075-19528838 FORWARD LENGTH=456	439	456	4.00E-80	103.9	43.5	59.0

Rsa1.0_00102.1.g5070.t1	gb|AAT00536.1| effector of transcription [Brassica napus]	390	440	1.00E-165	112.8	81.0	86.9	effector of transcription	gbpln	Brassica napus	AT4G26170.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 7 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; BEST Arabidopsis thaliana protein match is: effector of transcription2 (TAIR:AT5G56780.1); Has 75 Blast hits to 42 proteins in 17 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 0; Plants - 70; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr4:13256930-13259382 FORWARD LENGTH=506	390	506	3.00E-95	129.7	55.1	63.8
Rsa1.0_00102.1.g5071.t1	gb|EOA16979.1| hypothetical protein CARUB_v10005210mg [Capsella rubella]	357	333	1.00E-173	93.3	86.0	88.8	hypothetical protein CARUB_v10005210mg	gbpln	Capsella rubella	AT4G26180.1 | Symbols: | Mitochondrial substrate carrier family protein | chr4:13260263-13261887 REVERSE LENGTH=325	357	325	1.00E-169	91.0	83.5	86.8
Rsa1.0_00102.1.g5072.t1	gb|EOA17906.1| hypothetical protein CARUB_v10006315mg [Capsella rubella]	447	450	0	100.7	94.9	97.8	hypothetical protein CARUB_v10006315mg	gbpln	Capsella rubella	AT4G26200.1 | Symbols: ACS7, ATACS7 | 1-amino-cyclopropane-1-carboxylate synthase 7 | chr4:13275307-13276946 FORWARD LENGTH=447	447	447	0	100.0	95.5	98.0
Rsa1.0_00102.1.g5073.t1	#	#	#	#	#	#	#	–	----	----	AT3G55430.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr3:20549806-20552004 REVERSE LENGTH=449	139	449	6.00E-12	323.0	23.7	36.0
Rsa1.0_00102.1.g5074.t1	ref|NP_567741.2| galactinol synthase 6 [Arabidopsis thaliana] gi|75151964|sp|Q8H1S1.1|GOLS6_ARATH RecName: Full=Galactinol synthase 6; Short=AtGolS6; Short=GolS-6 gi|23296356|gb|AAN13051.1| galactinol synthase [Arabidopsis thaliana] gi|332659775|gb|AEE85175.1| galactinol synthase 6 [Arabidopsis thaliana]	338	336	1.00E-166	99.4	82.2	91.1	galactinol synthase 6	gbpln	Arabidopsis thaliana	AT4G26250.1 | Symbols: AtGolS6, GolS6 | galactinol synthase 6 | chr4:13289641-13291053 FORWARD LENGTH=336	338	336	1.00E-169	99.4	82.2	91.1
Rsa1.0_00102.1.g5075.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00102.1.g5076.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00102.1.g5077.t2	gb|EOA30274.1| hypothetical protein CARUB_v10013395mg [Capsella rubella]	617	546	8.00E-80	88.5	26.9	29.3	hypothetical protein CARUB_v10013395mg	gbpln	Capsella rubella	AT2G17700.1 | Symbols: | ACT-like protein tyrosine kinase family protein | chr2:7685778-7689278 REVERSE LENGTH=546	617	546	3.00E-80	88.5	26.6	28.7
Rsa1.0_00103.1.g5078.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00103.1.g5079.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1794	1213	0	67.6	34.2	44.0	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	1794	289	3.00E-71	16.1	7.2	10.0
Rsa1.0_00103.1.g5080.t2	ref|NP_192969.4| cytochrome P450, family 706, subfamily A, polypeptide 6 [Arabidopsis thaliana] gi|51536592|gb|AAU05534.1| At4g12320 [Arabidopsis thaliana] gi|332657714|gb|AEE83114.1| cytochrome P450, family 706, subfamily A, polypeptide 6 [Arabidopsis thaliana]	516	518	0	100.4	82.2	91.3	cytochrome P450, family 706, subfamily A, polypeptide 6	gbpln	Arabidopsis thaliana	AT4G12320.1 | Symbols: CYP706A6 | cytochrome P450, family 706, subfamily A, polypeptide 6 | chr4:7314939-7316647 REVERSE LENGTH=518	516	518	0	100.4	82.2	91.3
Rsa1.0_00103.1.g5081.t1	gb|EOA22327.1| hypothetical protein CARUB_v10002934mg [Capsella rubella]	165	163	2.00E-71	98.8	82.4	90.3	hypothetical protein CARUB_v10002934mg	gbpln	Capsella rubella	AT4G12410.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:7342956-7343429 REVERSE LENGTH=157	165	157	2.00E-71	95.2	80.6	88.5
Rsa1.0_00103.1.g5082.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00103.1.g5083.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00103.1.g5084.t1		#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00103.1.g5085.t1	ref|XP_002874771.1| hypothetical protein ARALYDRAFT_911635 [Arabidopsis lyrata subsp. lyrata] gi|297320608|gb|EFH51030.1| hypothetical protein ARALYDRAFT_911635 [Arabidopsis lyrata subsp. lyrata]	574	587	0	102.3	91.6	94.9	hypothetical protein ARALYDRAFT_911635	gbpln	Arabidopsis lyrata	AT4G12420.2 | Symbols: SKU5 | Cupredoxin superfamily protein | chr4:7349941-7352868 REVERSE LENGTH=587	574	587	0	102.3	90.8	94.4
Rsa1.0_00103.1.g5086.t2	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1609	1214	0	75.5	26.7	40.3	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	1609	295	1.00E-74	18.3	9.0	11.9
Rsa1.0_00103.1.g5087.t1	gb|AAC35532.1| contains similarity to proteases [Arabidopsis thaliana]	549	1392	1.00E-112	253.6	46.3	61.2	contains similarity to proteases	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	549	1262	2.00E-34	229.9	19.3	30.4

Rsa1.0_00103.1.g5088.t1	gb|ABA93904.1| transposon protein, putative, Mariner sub-class [Oryza sativa Japonica Group] gi|222616021|gb|EEE52153.1| hypothetical protein OsJ_33993 [Oryza sativa Japonica Group]	273	452	7.00E-57	165.6	42.9	66.7	transposon protein, putative, Mariner sub-class	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_00103.1.g5089.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00103.1.g5090.t1	ref|NP_192983.2| OSBP(oxysterol binding protein)-related protein 2B [Arabidopsis thaliana] gi|313471379|sp|Q9SU36.2|ORP2B_ARATH RecName: Full=Oxysterol-binding protein-related protein 2B; AltName: Full=OSBP-related protein 2B gi|332657735|gb|AEE83135.1| OSBP(oxysterol binding protein)-related protein 2B [Arabidopsis thaliana]	730	693	0	94.9	82.9	87.5	OSBP(oxysterol binding protein)-related protein 2B	gbpln	Arabidopsis thaliana	AT4G12460.1 | Symbols: ORP2B | OSBP(oxysterol binding protein)-related protein 2B | chr4:7391400-7396056 FORWARD LENGTH=693	730	693	0	94.9	82.9	87.5
Rsa1.0_00103.1.g5091.t1	ref|NP_192986.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|4725948|emb|CAB41719.1| pEARLI 1-like protein [Arabidopsis thaliana] gi|7267951|emb|CAB78292.1| pEARLI 1-like protein [Arabidopsis thaliana] gi|15450471|gb|AAK96529.1| AT4g12490/T1P17_80 [Arabidopsis thaliana] gi|16974459|gb|AAL31233.1| AT4g12490/T1P17_80 [Arabidopsis thaliana] gi|332657739|gb|AEE83139.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	166	182	4.00E-56	109.6	75.9	88.0	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT4G12490.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:7409830-7410378 REVERSE LENGTH=182	166	182	2.00E-58	109.6	75.9	88.0
Rsa1.0_00103.1.g5092.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00103.1.g5093.t1	gb|EOA22039.1| hypothetical protein CARUB_v10002564mg [Capsella rubella]	133	135	9.00E-50	101.5	86.5	92.5	hypothetical protein CARUB_v10002564mg	gbpln	Capsella rubella	AT4G12510.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:7417414-7417803 REVERSE LENGTH=129	133	129	5.00E-52	97.0	83.5	88.0
Rsa1.0_00103.1.g5094.t1	ref|NP_192990.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|4725952|emb|CAB41723.1| AIR1A-like protein [Arabidopsis thaliana] gi|7267955|emb|CAB78296.1| AIR1A-like protein [Arabidopsis thaliana] gi|89001069|gb|ABD59124.1| At4g12530 [Arabidopsis thaliana] gi|91806666|gb|ABE66060.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis thaliana] gi|332657743|gb|AEE83143.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	117	117	2.00E-43	100.0	81.2	87.2	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT4G12530.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:7428141-7428494 REVERSE LENGTH=117	117	117	4.00E-46	100.0	81.2	87.2
Rsa1.0_00103.1.g5095.t1	ref|XP_002863072.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297308883|gb|EFH39331.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	171	387	9.00E-14	226.3	24.0	31.0	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT5G48990.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19862340-19863458 FORWARD LENGTH=372	171	372	5.00E-16	217.5	24.0	32.7
Rsa1.0_00103.1.g5096.t1	gb|EOA22039.1| hypothetical protein CARUB_v10002564mg [Capsella rubella]	133	135	5.00E-49	101.5	85.0	91.7	hypothetical protein CARUB_v10002564mg	gbpln	Capsella rubella	AT4G12510.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:7417414-7417803 REVERSE LENGTH=129	133	129	3.00E-51	97.0	82.0	87.2
Rsa1.0_00103.1.g5097.t2	gb|AGC65584.1| GFP-CESA3ixr1-2 [Binary plant gene expression vector pKM24-MD1]	402	1344	0	334.3	85.3	88.3	GFP-CESA3ixr1-2	----	----	AT5G05170.1 | Symbols: CESA3, IXR1, ATCESA3, ATH-B, CEV1 | Cellulose synthase family protein | chr5:1530401-1535090 REVERSE LENGTH=1065	402	1065	0	264.9	85.3	88.3
Rsa1.0_00104.1.g5098.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	327	1489	4.00E-66	455.4	39.4	54.7	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	327	237	4.00E-25	72.5	19.9	32.7

Rsa1.0_00104.1.g5099.t1	gb|EOA13781.1| hypothetical protein CARUB_v10026881mg, partial [Capsella rubella]	291	297	1.00E-152	102.1	92.8	95.5	hypothetical protein CARUB_v10026881mg, partial	gbpln	Capsella rubella	AT5G60660.1 | Symbols: PIP2F, PIP2;4 | plasma membrane intrinsic protein 2;4 | chr5:24375673-24376939 REVERSE LENGTH=291	291	291	1.00E-148	100.0	89.0	91.8
Rsa1.0_00104.1.g5100.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5101.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5102.t1	ref|NP_200873.1| uncharacterized protein [Arabidopsis thaliana] gi|9759329|dbj|BAB09838.1| unnamed protein product [Arabidopsis thaliana] gi|55978853|gb|AAV68888.1| hypothetical protein AT5G60650 [Arabidopsis thaliana] gi|332009980|gb|AED97363.1| uncharacterized protein AT5G60650 [Arabidopsis thaliana]	74	147	1.00E-21	198.6	68.9	71.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G60650.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G28410.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:24374305-24374748 REVERSE LENGTH=147	74	147	2.00E-24	198.6	68.9	71.6
Rsa1.0_00104.1.g5103.t1	ref|XP_002866387.1| hypothetical protein ARALYDRAFT_496212 [Arabidopsis lyrata subsp. lyrata] gi|297312222|gb|EFH42646.1| hypothetical protein ARALYDRAFT_496212 [Arabidopsis lyrata subsp. lyrata]	600	597	0	99.5	85.8	90.7	hypothetical protein ARALYDRAFT_496212	gbpln	Arabidopsis lyrata	AT5G60640.1 | Symbols: ATPDIL1-4, PDI2, ATPDI2, PDIL1-4 | PDI-like 1-4 | chr5:24371141-24373993 REVERSE LENGTH=597	600	597	0	99.5	85.0	90.3
Rsa1.0_00104.1.g5104.t1	ref|NP_174811.1| protein pumilio 9 [Arabidopsis thaliana] gi|122244101|sp|Q1PFN9.1|PUM9_ARATH RecName: Full=Pumilio homolog 9; Short=APUM-9; Short=AtPUM9 gi|91805917|gb|ABE65687.1| pumilio/Puf RNA-binding domain-containing protein [Arabidopsis thaliana] gi|332193705|gb|AEE31826.1| protein pumilio 9 [Arabidopsis thaliana]	139	564	2.00E-16	405.8	28.1	35.3	protein pumilio 9	gbpln	Arabidopsis thaliana	AT1G35730.1 | Symbols: APUM9, PUM9 | pumilio 9 | chr1:13227324-13229796 REVERSE LENGTH=564	139	564	5.00E-19	405.8	28.1	35.3
Rsa1.0_00104.1.g5105.t2	ref|XP_002864695.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310530|gb|EFH40954.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	356	376	0	105.6	95.8	97.5	phospholipid/glycerol acyltransferase family protein	gbpln	Arabidopsis lyrata	AT5G60620.1 | Symbols: GPAT9 | glycerol-3-phosphate acyltransferase 9 | chr5:24367266-24369647 FORWARD LENGTH=376	356	376	0	105.6	94.7	97.5
Rsa1.0_00104.1.g5106.t1	ref|NP_192624.2| pumilio 11 [Arabidopsis thaliana] gi|313471422|sp|Q9LDW3.2|PUM11_ARATH RecName: Full=Pumilio homolog 11; Short=APUM-11; Short=AtPUM11 gi|332657281|gb|AEE82681.1| pumilio 11 [Arabidopsis thaliana]	524	556	1.00E-140	106.1	56.7	71.0	pumilio 11	gbpln	Arabidopsis thaliana	AT4G08840.1 | Symbols: APUM11, PUM11 | pumilio 11 | chr4:5631298-5633779 FORWARD LENGTH=556	524	556	1.00E-143	106.1	56.7	71.0
Rsa1.0_00104.1.g5107.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5108.t4	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5109.t1	ref|XP_002864693.1| hypothetical protein ARALYDRAFT_358267 [Arabidopsis lyrata subsp. lyrata] gi|297310528|gb|EFH40952.1| hypothetical protein ARALYDRAFT_358267 [Arabidopsis lyrata subsp. lyrata]	282	284	1.00E-138	100.7	87.6	90.4	hypothetical protein ARALYDRAFT_358267	gbpln	Arabidopsis lyrata	AT5G60590.2 | Symbols: | DHBP synthase RibB-like alpha/beta domain | chr5:24357066-24358443 FORWARD LENGTH=288	282	288	1.00E-136	102.1	85.1	88.3
Rsa1.0_00104.1.g5110.t1	ref|XP_002864692.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310527|gb|EFH40951.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	493	491	0	99.6	84.8	88.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G60580.3 | Symbols: | RING/U-box superfamily protein | chr5:24354298-24356706 FORWARD LENGTH=487	493	487	0	98.8	83.8	88.2
Rsa1.0_00104.1.g5111.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5112.t1	ref|XP_002864691.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297310526|gb|EFH40950.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	385	386	0	100.3	85.2	91.7	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT5G60570.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:24348713-24349894 FORWARD LENGTH=393	385	393	0	102.1	85.7	93.0
Rsa1.0_00104.1.g5113.t1	ref|XP_002864689.1| hypothetical protein ARALYDRAFT_919290 [Arabidopsis lyrata subsp. lyrata] gi|297310524|gb|EFH40948.1| hypothetical protein ARALYDRAFT_919290 [Arabidopsis lyrata subsp. lyrata]	401	407	0	101.5	87.5	93.5	hypothetical protein ARALYDRAFT_919290	gbpln	Arabidopsis lyrata	AT5G60550.1 | Symbols: GRIK2, ATSNAK1 | geminivirus rep interacting kinase 2 | chr5:24340135-24342356 FORWARD LENGTH=407	401	407	0	101.5	86.3	93.3

Rsa1.0_00104.1.g5114.t1	ref|NP_568922.1| Pyridoxal biosynthesis protein PDX2 [Arabidopsis thaliana] gi|75154761|sp|Q8LAD0.1|PDX2_ARATH RecName: Full=Pyridoxal biosynthesis protein PDX2; AltName: Full=Probable glutamine amidotransferase; Short=AtPDX2; AltName: Full=Protein EMBRYO DEFECTIVE 2407 gi|21593486|gb|AAM65453.1| imidazoleglycerol-phosphate synthase subunit H-like [Arabidopsis thaliana] gi|26449721|dbj|BAC41984.1| putative imidazoleglycerol-phosphate synthase subunit H [Arabidopsis thaliana] gi|28950813|gb|AAO63330.1| At5g60540 [Arabidopsis thaliana] gi|332009958|gb|AED97341.1| Pyridoxal biosynthesis protein PDX2 [Arabidopsis thaliana]	255	255	1.00E-131	100.0	91.8	95.7	Pyridoxal biosynthesis protein PDX2	gbpln	Arabidopsis thaliana	AT5G60540.1 | Symbols: EMB2407, ATPDX2, PDX2 | pyridoxine biosynthesis 2 | chr5:24336874-24338647 REVERSE LENGTH=255	255	255	1.00E-133	100.0	91.8	95.7
Rsa1.0_00104.1.g5115.t1	ref|NP_200861.1| late embryogenesis abundant protein-like protein [Arabidopsis thaliana] gi|9757755|dbj|BAB08236.1| unnamed protein product [Arabidopsis thaliana] gi|23308395|gb|AAN18167.1| At5g60530/muf9_180 [Arabidopsis thaliana] gi|332009957|gb|AED97340.1| late embryogenesis abundant protein-like protein [Arabidopsis thaliana]	420	439	1.00E-169	104.5	66.0	70.0	late embryogenesis abundant protein-like protein	gbpln	Arabidopsis thaliana	AT5G60530.1 | Symbols: | late embryogenesis abundant protein-related / LEA protein-related | chr5:24334197-24335685 REVERSE LENGTH=439	420	439	1.00E-171	104.5	66.0	70.0
Rsa1.0_00104.1.g5116.t1	gb|EOA14608.1| hypothetical protein CARUB_v10027860mg [Capsella rubella]	332	335	0	100.9	94.3	96.7	hypothetical protein CARUB_v10027860mg	gbpln	Capsella rubella	AT5G60520.1 | Symbols: | Late embryogenesis abundant (LEA) protein-related | chr5:24331787-24332947 REVERSE LENGTH=338	332	338	1.00E-172	101.8	91.9	95.8
Rsa1.0_00104.1.g5117.t1	gb|EOA12731.1| hypothetical protein CARUB_v10028181mg [Capsella rubella]	271	271	1.00E-130	100.0	79.3	90.4	hypothetical protein CARUB_v10028181mg	gbpln	Capsella rubella	AT5G60510.1 | Symbols: | Undecaprenyl pyrophosphate synthetase family protein | chr5:24330721-24331539 FORWARD LENGTH=272	271	272	1.00E-127	100.4	75.3	88.9
Rsa1.0_00104.1.g5118.t1	gb|EOA12731.1| hypothetical protein CARUB_v10028181mg [Capsella rubella]	271	271	1.00E-130	100.0	79.0	90.4	hypothetical protein CARUB_v10028181mg	gbpln	Capsella rubella	AT5G60510.1 | Symbols: | Undecaprenyl pyrophosphate synthetase family protein | chr5:24330721-24331539 FORWARD LENGTH=272	271	272	1.00E-128	100.4	76.8	88.6
Rsa1.0_00104.1.g5119.t1	ref|NP_200854.1| protein transport protein SEC61 subunit beta [Arabidopsis thaliana] gi|9757748|dbj|BAB08229.1| unnamed protein product [Arabidopsis thaliana] gi|26451290|dbj|BAC42746.1| protein transport protein subunit - like [Arabidopsis thaliana] gi|28973101|gb|AAO63875.1| putative protein transport protein subunit [Arabidopsis thaliana] gi|332009950|gb|AED97333.1| protein transport protein SEC61 subunit beta [Arabidopsis thaliana]	109	109	8.00E-32	100.0	88.1	93.6	protein transport protein SEC61 subunit beta	gbpln	Arabidopsis thaliana	AT5G60460.1 | Symbols: | Preprotein translocase Sec, Sec61-beta subunit protein | chr5:24317590-24317919 REVERSE LENGTH=109	109	109	1.00E-34	100.0	88.1	93.6
Rsa1.0_00104.1.g5120.t1	gb|ACR10266.1| sulfotransferase 5b [Brassica rapa subsp. pekinensis]	344	344	0	100.0	95.3	97.7	sulfotransferase 5b	gbpln	Brassica rapa	AT1G74090.1 | Symbols: SOT18, ATSOT18, ATST5B | desulfo-glucosinolate sulfotransferase 18 | chr1:27863003-27864055 FORWARD LENGTH=350	344	350	1.00E-167	101.7	83.1	89.8
Rsa1.0_00104.1.g5121.t1	gb|ACR10265.1| sulfotransferase 5a [Brassica rapa subsp. pekinensis]	337	338	0	100.3	95.8	97.3	sulfotransferase 5a	gbpln	Brassica rapa	AT1G74100.1 | Symbols: SOT16, ATSOT16, CORI-7, ATST5A | sulfotransferase 16 | chr1:27864489-27865505 REVERSE LENGTH=338	337	338	0	100.3	91.4	95.8
Rsa1.0_00104.1.g5122.t1	ref|NP_177551.1| cytochrome P450, family 78, subfamily A, polypeptide 10 [Arabidopsis thaliana] gi|12325138|gb|AAG52514.1|AC016662_8 putative cytochrome P-450; 4810-6511 [Arabidopsis thaliana] gi|91806081|gb|ABE65769.1| cytochrome P450 family protein [Arabidopsis thaliana] gi|332197430|gb|AEE35551.1| cytochrome P450, family 78, subfamily A, polypeptide 10 [Arabidopsis thaliana]	534	537	0	100.6	89.3	94.0	cytochrome P450, family 78, subfamily A, polypeptide 10	gbpln	Arabidopsis thaliana	AT1G74110.1 | Symbols: CYP78A10 | cytochrome P450, family 78, subfamily A, polypeptide 10 | chr1:27866667-27868368 REVERSE LENGTH=537	534	537	0	100.6	89.3	94.0

Rsa1.0_00104.1.g5123.t1	ref|NP_565080.1| Mitochondrial transcription termination factor family protein [Arabidopsis thaliana] gi|12323819|gb|AAG51878.1|AC079678_8 unknown protein; 33994-35331 [Arabidopsis thaliana] gi|332197431|gb|AEE35552.1| Mitochondrial transcription termination factor family protein [Arabidopsis thaliana]	445	445	0	100.0	75.1	87.2	Mitochondrial transcription termination factor family protein	gbpln	Arabidopsis thaliana	AT1G74120.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:27871923-27873260 REVERSE LENGTH=445	445	445	0	100.0	75.1	87.2
Rsa1.0_00104.1.g5124.t1	ref|XP_002887527.1| hypothetical protein ARALYDRAFT_316359 [Arabidopsis lyrata subsp. lyrata] gi|297333368|gb|EFH63786.1| hypothetical protein ARALYDRAFT_316359 [Arabidopsis lyrata subsp. lyrata]	313	323	1.00E-89	103.2	59.7	75.4	hypothetical protein ARALYDRAFT_316359	gbpln	Arabidopsis lyrata	AT1G74130.1 | Symbols: | Rhomboid-related intramembrane serine protease family protein | chr1:27873687-27875897 FORWARD LENGTH=322	313	322	1.00E-87	102.9	57.2	70.0
Rsa1.0_00104.1.g5125.t1	ref|XP_002887528.1| hypothetical protein ARALYDRAFT_316360 [Arabidopsis lyrata subsp. lyrata] gi|297333369|gb|EFH63787.1| hypothetical protein ARALYDRAFT_316360 [Arabidopsis lyrata subsp. lyrata]	591	567	0	95.9	73.8	81.0	hypothetical protein ARALYDRAFT_316360	gbpln	Arabidopsis lyrata	AT1G74150.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:27880528-27883626 FORWARD LENGTH=569	591	569	0	96.3	72.3	80.2
Rsa1.0_00104.1.g5126.t1	gb|EOA29006.1| hypothetical protein CARUB_v10025259mg [Capsella rubella]	1985	1761	0	88.7	40.5	53.9	hypothetical protein CARUB_v10025259mg	gbpln	Capsella rubella	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	1985	965	0	48.6	31.6	37.0
Rsa1.0_00104.1.g5127.t2	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	946	966	0	102.1	65.9	79.6	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	946	965	0	102.0	64.8	78.3
Rsa1.0_00104.1.g5128.t4	ref|NP_177558.4| receptor like protein 14 [Arabidopsis thaliana] gi|332197442|gb|AEE35563.1| receptor like protein 14 [Arabidopsis thaliana]	1120	976	0	87.1	52.1	60.0	receptor like protein 14	gbpln	Arabidopsis thaliana	AT1G74180.1 | Symbols: AtRLP14, RLP14 | receptor like protein 14 | chr1:27897197-27900908 REVERSE LENGTH=976	1120	976	0	87.1	52.1	60.0
Rsa1.0_00104.1.g5129.t1	ref|NP_177561.1| glycerophosphoryl diester phosphodiesterase [Arabidopsis thaliana] gi|12324904|gb|AAG52406.1|AC020579_8 putative glycerophosphodiester phosphodiesterase; 42559-40170 [Arabidopsis thaliana] gi|17381162|gb|AAL36393.1| putative glycerophosphodiester phosphodiesterase [Arabidopsis thaliana] gi|21592460|gb|AAM64411.1| putative glycerophosphodiester phosphodiesterase [Arabidopsis thaliana] gi|23296874|gb|AAN13192.1| putative glycerophosphodiester phosphodiesterase [Arabidopsis thaliana] gi|332197445|gb|AEE35566.1| glycerophosphoryl diester phosphodiesterase [Arabidopsis thaliana]	425	392	0	92.2	78.4	84.0	glycerophosphoryl diester phosphodiesterase	gbpln	Arabidopsis thaliana	AT1G74210.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr1:27910396-27912785 FORWARD LENGTH=392	425	392	0	92.2	78.4	84.0
Rsa1.0_00104.1.g5130.t1	ref|NP_177562.1| uncharacterized protein [Arabidopsis thaliana] gi|12324902|gb|AAG52404.1|AC020579_6 hypothetical protein; 38821-39856 [Arabidopsis thaliana] gi|332197446|gb|AEE35567.1| uncharacterized protein AT1G74220 [Arabidopsis thaliana]	305	316	3.00E-85	103.6	70.5	80.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G74220.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03630.1); Has 383 Blast hits to 347 proteins in 86 species: Archae - 0; Bacteria - 17; Metazoa - 87; Fungi - 65; Plants - 76; Viruses - 2; Other Eukaryotes - 136 (source: NCBI BLink). | chr1:27913099-27914134 REVERSE LENGTH=316	305	316	7.00E-88	103.6	70.5	80.7
Rsa1.0_00104.1.g5131.t1	gb|ABB97027.1| unknown [Brassica rapa]	285	208	1.00E-59	73.0	38.2	38.2	unknown	gbpln	Brassica rapa	AT1G74230.1 | Symbols: GR-RBP5 | glycine-rich RNA-binding protein 5 | chr1:27915346-27916857 FORWARD LENGTH=289	285	289	3.00E-58	101.4	36.8	38.2
Rsa1.0_00104.1.g5132.t1	ref|XP_002887533.1| hypothetical protein ARALYDRAFT_339621 [Arabidopsis lyrata subsp. lyrata] gi|297333374|gb|EFH63792.1| hypothetical protein ARALYDRAFT_339621 [Arabidopsis lyrata subsp. lyrata]	366	364	1.00E-175	99.5	88.8	94.0	hypothetical protein ARALYDRAFT_339621	gbpln	Arabidopsis lyrata	AT1G74240.1 | Symbols: | Mitochondrial substrate carrier family protein | chr1:27917437-27919987 FORWARD LENGTH=364	366	364	1.00E-172	99.5	87.7	93.7

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<tr><td>Rsa1.0_00104.1.g5133.t1</td><td>ref|NP_172188.1| 60S ribosomal protein L35a-1 [Arabidopsis thaliana] gi|297843500|ref|XP_002889631.1| 60S ribosomal protein L35a [Arabidopsis lyrata subsp. lyrata] gi|75174783|sp|Q9LMK0.1|R35A1_ARATH RecName: Full=60S ribosomal protein L35a-1 gi|8954039|gb|AAF82213.1|AC067971_21 Strong similarity to a ribosomal protein from Arabidopsis thaliana gb|AL161667. It contains a ribosomal protein L35Ae domain PF|01247 [Arabidopsis thaliana] gi|21555376|gb|AAM63844.1| ribosomal protein, putative [Arabidopsis thaliana] gi|26453120|dbj|BAC43636.1| unknown protein [Arabidopsis thaliana] gi|28416859|gb|AAO42960.1| At1g07070 [Arabidopsis thaliana] gi|297335473|gb|EFH65890.1| 60S ribosomal protein L35a [Arabidopsis lyrata subsp. lyrata] gi|332189953|gb|AEE28074.1| 60S ribosomal protein L35a-1 [Arabidopsis thaliana]</td><td>112</td><td>112</td><td>4.00E-57</td><td>100.0</td><td>96.4</td><td>99.1</td><td>60S ribosomal protein L35a-1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G07070.1 | Symbols: | Ribosomal protein L35Ae family protein | chr1:2168652-2169703 FORWARD LENGTH=112</td><td>112</td><td>112</td><td>6.00E-60</td><td>100.0</td><td>96.4</td><td>99.1</td></tr>
<tr><td>Rsa1.0_00104.1.g5134.t1</td><td>gb|EOA35326.1| hypothetical protein CARUB_v10020509mg [Capsella rubella]</td><td>363</td><td>367</td><td>1.00E-165</td><td>101.1</td><td>75.5</td><td>85.7</td><td>hypothetical protein CARUB_v10020509mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G74300.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:27935368-27936474 FORWARD LENGTH=346</td><td>363</td><td>346</td><td>1.00E-160</td><td>95.3</td><td>71.9</td><td>81.8</td></tr>
<tr><td>Rsa1.0_00104.1.g5135.t1</td><td>ref|XP_002888971.1| ATHSP101 [Arabidopsis lyrata subsp. lyrata] gi|297334812|gb|EFH65230.1| ATHSP101 [Arabidopsis lyrata subsp. lyrata]</td><td>913</td><td>911</td><td>0</td><td>99.8</td><td>95.5</td><td>98.7</td><td>ATHSP101</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G74310.1 | Symbols: ATHSP101, HSP101, HOT1 | heat shock protein 101 | chr1:27936715-27939862 REVERSE LENGTH=911</td><td>913</td><td>911</td><td>0</td><td>99.8</td><td>93.6</td><td>97.0</td></tr>
<tr><td>Rsa1.0_00104.1.g5136.t1</td><td>ref|NP_177572.2| protein kinase domain-containing protein [Arabidopsis thaliana] gi|20453122|gb|AAM19803.1| At1g74320/F1O17_1 [Arabidopsis thaliana] gi|22655288|gb|AAM98234.1| putative choline kinase [Arabidopsis thaliana] gi|30984574|gb|AAP42750.1| At1g74320 [Arabidopsis thaliana] gi|332197456|gb|AEE35577.1| protein kinase domain-containing protein [Arabidopsis thaliana]</td><td>345</td><td>350</td><td>0</td><td>101.4</td><td>89.6</td><td>93.6</td><td>protein kinase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G74320.1 | Symbols: | Protein kinase superfamily protein | chr1:27941192-27942903 FORWARD LENGTH=350</td><td>345</td><td>350</td><td>0</td><td>101.4</td><td>89.6</td><td>93.6</td></tr>
<tr><td>Rsa1.0_00104.1.g5137.t2</td><td>ref|NP_001154470.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|332197458|gb|AEE35579.1| protein kinase domain-containing protein [Arabidopsis thaliana]</td><td>663</td><td>690</td><td>0</td><td>104.1</td><td>86.4</td><td>92.3</td><td>protein kinase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G74330.2 | Symbols: | Protein kinase superfamily protein | chr1:27943535-27947109 REVERSE LENGTH=690</td><td>663</td><td>690</td><td>0</td><td>104.1</td><td>86.4</td><td>92.3</td></tr>
<tr><td>Rsa1.0_00104.1.g5138.t1</td><td>ref|NP_177575.1| intron maturase, type II-like protein [Arabidopsis thaliana] gi|12324793|gb|AAG52355.1|AC011765_7 putative type II intron maturase; 7603-5342 [Arabidopsis thaliana] gi|332197460|gb|AEE35581.1| intron maturase, type II-like protein [Arabidopsis thaliana]</td><td>879</td><td>753</td><td>0</td><td>85.7</td><td>70.5</td><td>76.1</td><td>intron maturase, type II-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G74350.1 | Symbols: | Intron maturase, type II family protein | chr1:27949022-27951283 REVERSE LENGTH=753</td><td>879</td><td>753</td><td>0</td><td>85.7</td><td>70.5</td><td>76.1</td></tr>
<tr><td>Rsa1.0_00104.1.g5139.t1</td><td>ref|NP_565084.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|264664459|sp|C0LGJ1.1|Y1743_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g74360; Flags: Precursor gi|224589485|gb|ACN59276.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332197461|gb|AEE35582.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]</td><td>1124</td><td>1106</td><td>0</td><td>98.4</td><td>84.2</td><td>91.0</td><td>putative LRR receptor-like serine/threonine-protein kinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G74360.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:27954299-27957911 FORWARD LENGTH=1106</td><td>1124</td><td>1106</td><td>0</td><td>98.4</td><td>84.2</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00104.1.g5140.t1</td><td>ref|XP_002888973.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297334814|gb|EFH65232.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>244</td><td>259</td><td>1.00E-114</td><td>106.1</td><td>83.6</td><td>91.8</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G74370.1 | Symbols: | RING/U-box superfamily protein | chr1:27958200-27958985 REVERSE LENGTH=261</td><td>244</td><td>261</td><td>1.00E-113</td><td>107.0</td><td>82.4</td><td>89.3</td></tr>
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Rsa1.0_00104.1.g5141.t1	ref|XP_002887538.1| galactosyl transferase GMA12/MNN10 family protein [Arabidopsis lyrata subsp. lyrata] gi|297333379|gb|EFH63797.1| galactosyl transferase GMA12/MNN10 family protein [Arabidopsis lyrata subsp. lyrata]	346	457	0	132.1	95.4	97.7	galactosyl transferase GMA12/MNN10 family protein	gbpln	Arabidopsis lyrata	AT1G74380.1 | Symbols: XXT5 | xyloglucan xylosyltransferase 5 | chr1:27959848-27961221 FORWARD LENGTH=457	346	457	0	132.1	94.8	97.4
Rsa1.0_00104.1.g5142.t1	ref|XP_002888974.1| exonuclease family protein [Arabidopsis lyrata subsp. lyrata] gi|297334815|gb|EFH65233.1| exonuclease family protein [Arabidopsis lyrata subsp. lyrata]	496	506	0	102.0	81.0	89.3	exonuclease family protein	gbpln	Arabidopsis lyrata	AT1G74390.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr1:27961760-27963826 REVERSE LENGTH=506	496	506	0	102.0	77.2	86.3
Rsa1.0_00104.1.g5143.t1	gb|EOA35690.1| hypothetical protein CARUB_v10020916mg [Capsella rubella]	223	223	1.00E-114	100.0	89.2	93.3	hypothetical protein CARUB_v10020916mg	gbpln	Capsella rubella	AT1G74410.1 | Symbols: | RING/U-box superfamily protein | chr1:27965723-27967681 FORWARD LENGTH=223	223	223	1.00E-112	100.0	90.1	93.3
Rsa1.0_00104.1.g5144.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5145.t1	ref|NP_177583.1| myb domain protein 95 [Arabidopsis thaliana] gi|6715434|gb|AAF26414.1|AF217205_1 putative transcription factor [Arabidopsis thaliana] gi|12324794|gb|AAG52356.1|AC011765_8 putative MYB family transcription factor; 31729-33438 [Arabidopsis thaliana] gi|26451798|dbj|BAC42993.1| putative transcription factor MYB95 [Arabidopsis thaliana] gi|28950825|gb|AAO63336.1| At1g74430 [Arabidopsis thaliana] gi|41619172|gb|AAS10040.1| MYB transcription factor [Arabidopsis thaliana] gi|332197470|gb|AEE35591.1| myb domain protein 95 [Arabidopsis thaliana]	279	271	5.00E-95	97.1	71.3	83.2	myb domain protein 95	gbpln	Arabidopsis thaliana	AT1G74430.1 | Symbols: MYB95, ATMYB95, ATMYBCP66 | myb domain protein 95 | chr1:27975409-27977118 FORWARD LENGTH=271	279	271	1.00E-97	97.1	71.3	83.2
Rsa1.0_00104.1.g5146.t1	ref|NP_177584.1| uncharacterized protein [Arabidopsis thaliana] gi|12324798|gb|AAG52360.1|AC011765_12 hypothetical protein; 36691-35528 [Arabidopsis thaliana] gi|332197471|gb|AEE35592.1| uncharacterized protein AT1G74440 [Arabidopsis thaliana]	206	208	2.00E-97	101.0	85.0	89.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G74440.1 | Symbols: | Protein of unknown function (DUF962) | chr1:27979208-27980371 REVERSE LENGTH=208	206	208	1.00E-100	101.0	85.0	89.3
Rsa1.0_00104.1.g5147.t1	ref|XP_002887541.1| hypothetical protein ARALYDRAFT_476579 [Arabidopsis lyrata subsp. lyrata] gi|297333382|gb|EFH63800.1| hypothetical protein ARALYDRAFT_476579 [Arabidopsis lyrata subsp. lyrata]	390	398	1.00E-175	102.1	81.5	92.3	hypothetical protein ARALYDRAFT_476579	gbpln	Arabidopsis lyrata	AT1G74450.1 | Symbols: | Protein of unknown function (DUF793) | chr1:27982737-27983930 FORWARD LENGTH=397	390	397	1.00E-176	101.8	81.3	91.8
Rsa1.0_00104.1.g5148.t1	gb|EOA34248.1| hypothetical protein CARUB_v10021759mg [Capsella rubella]	94	95	1.00E-24	101.1	60.6	79.8	hypothetical protein CARUB_v10021759mg	gbpln	Capsella rubella	AT1G74458.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; Has 9 Blast hits to 9 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 9; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27987071-27987551 FORWARD LENGTH=94	94	94	3.00E-26	100.0	60.6	77.7
Rsa1.0_00104.1.g5149.t1	gb|ABI63587.1| geranylgeranyl reductase [Brassica rapa subsp. pekinensis]	380	466	0	122.6	99.7	100.0	geranylgeranyl reductase	gbpln	Brassica rapa	AT1G74470.1 | Symbols: | Pyridine nucleotide-disulphide oxidoreductase family protein | chr1:27991248-27992845 FORWARD LENGTH=467	380	467	0	122.9	96.3	97.6
Rsa1.0_00104.1.g5150.t1	gb|EOA34041.1| hypothetical protein CARUB_v10021541mg [Capsella rubella]	283	298	3.00E-87	105.3	65.4	77.4	hypothetical protein CARUB_v10021541mg	gbpln	Capsella rubella	AT1G74480.1 | Symbols: | RWP-RK domain-containing protein | chr1:27993032-27994178 REVERSE LENGTH=298	283	298	2.00E-87	105.3	64.3	76.3
Rsa1.0_00104.1.g5151.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5152.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5153.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	226	1274	7.00E-35	563.7	39.8	52.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315	226	315	4.00E-32	139.4	35.8	47.8
Rsa1.0_00104.1.g5154.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5155.t1	gb|EOA35161.1| hypothetical protein CARUB_v10020300mg [Capsella rubella] gi|482570975|gb|EOA35163.1| hypothetical protein CARUB_v10020300mg [Capsella rubella]	458	444	0	96.9	77.1	82.8	hypothetical protein CARUB_v10020300mg	gbpln	Capsella rubella	AT1G74510.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:28006065-28007420 FORWARD LENGTH=451	458	451	0	98.5	79.3	84.1

Rsa1.0_00104.1.g5156.t1	ref|XP_002888983.1| hypothetical protein ARALYDRAFT_476589 [Arabidopsis lyrata subsp. lyrata] gi|297334824|gb|EFH65242.1| hypothetical protein ARALYDRAFT_476589 [Arabidopsis lyrata subsp. lyrata]	488	308	1.00E-124	63.1	49.6	53.9	hypothetical protein ARALYDRAFT_476589	gbpln	Arabidopsis lyrata	AT1G74530.3 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:28009723-28012044 REVERSE LENGTH=314	488	314	1.00E-120	64.3	48.8	53.1
Rsa1.0_00104.1.g5157.t1	ref|NP_177597.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75169839|sp|Q9CA58.1|PP120_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At1g74580 gi|12324819|gb|AAG52381.1|AC011765_33 hypothetical protein; 77097-79388 [Arabidopsis thaliana] gi|332197491|gb|AEE35612.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	764	763	0	99.9	86.5	95.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G74580.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:28020777-28023068 FORWARD LENGTH=763	764	763	0	99.9	86.5	95.0
Rsa1.0_00104.1.g5158.t1	gb|EOA34238.1| hypothetical protein CARUB_v10021750mg [Capsella rubella]	120	232	6.00E-44	193.3	72.5	85.8	hypothetical protein CARUB_v10021750mg	gbpln	Capsella rubella	AT1G74590.1 | Symbols: ATGSTU10, GSTU10 | glutathione S-transferase TAU 10 | chr1:28023887-28024666 REVERSE LENGTH=232	120	232	6.00E-45	193.3	70.8	84.2
Rsa1.0_00104.1.g5159.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00104.1.g5160.t1	ref|NP_177598.1| glutathione S-transferase TAU 10 [Arabidopsis thaliana] gi|75169838|sp|Q9CA57.1|GSTUA_ARATH RecName: Full=Glutathione S-transferase U10; Short=AtGSTU10; AltName: Full=GST class-tau member 10 gi|12324822|gb|AAG52384.1|AC011765_36 putative glutathione S-transferase; 80986-80207 [Arabidopsis thaliana] gi|21593631|gb|AAM65598.1| putative glutathione S-transferase [Arabidopsis thaliana] gi|26450308|dbj|BAC42270.1| putative glutathione S-transferase [Arabidopsis thaliana] gi|28973029|gb|AAO63839.1| putative glutathione transferase [Arabidopsis thaliana] gi|332197492|gb|AEE35613.1| glutathione S-transferase TAU 10 [Arabidopsis thaliana]	89	232	2.00E-32	260.7	78.7	88.8	glutathione S-transferase TAU 10	gbpln	Arabidopsis thaliana	AT1G74590.1 | Symbols: ATGSTU10, GSTU10 | glutathione S-transferase TAU 10 | chr1:28023887-28024666 REVERSE LENGTH=232	89	232	3.00E-35	260.7	78.7	88.8
Rsa1.0_00104.1.g5161.t1	ref|NP_177598.1| glutathione S-transferase TAU 10 [Arabidopsis thaliana] gi|75169838|sp|Q9CA57.1|GSTUA_ARATH RecName: Full=Glutathione S-transferase U10; Short=AtGSTU10; AltName: Full=GST class-tau member 10 gi|12324822|gb|AAG52384.1|AC011765_36 putative glutathione S-transferase; 80986-80207 [Arabidopsis thaliana] gi|21593631|gb|AAM65598.1| putative glutathione S-transferase [Arabidopsis thaliana] gi|26450308|dbj|BAC42270.1| putative glutathione S-transferase [Arabidopsis thaliana] gi|28973029|gb|AAO63839.1| putative glutathione transferase [Arabidopsis thaliana] gi|332197492|gb|AEE35613.1| glutathione S-transferase TAU 10 [Arabidopsis thaliana]	221	232	2.00E-96	105.0	81.0	88.2	glutathione S-transferase TAU 10	gbpln	Arabidopsis thaliana	AT1G74590.1 | Symbols: ATGSTU10, GSTU10 | glutathione S-transferase TAU 10 | chr1:28023887-28024666 REVERSE LENGTH=232	221	232	8.00E-99	105.0	81.0	88.2
Rsa1.0_00104.1.g5162.t1	ref|NP_177599.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75169837|sp|Q9CA56.1|PP121_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g74600, chloroplastic; Flags: Precursor gi|12324789|gb|AAG52351.1|AC011765_3 hypothetical protein; 84160-81473 [Arabidopsis thaliana] gi|332197493|gb|AEE35614.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	796	895	0	112.4	83.7	91.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G74600.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:28025153-28027840 REVERSE LENGTH=895	796	895	0	112.4	83.7	91.2
Rsa1.0_00104.1.g5163.t1	gb|ABD64930.1| hypothetical protein 24.t00076 [Brassica oleracea]	472	407	1.00E-10	86.2	19.5	28.6	hypothetical protein 24.t00076	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_00104.1.g5164.t3	gb|AAD25557.1|AC005850_14 Hypothetical protein [Arabidopsis thaliana]	293	404	1.00E-116	137.9	67.6	77.5	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G43722.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28730.1); Has 924 Blast hits to 912 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 222; Fungi - 31; Plants - 661; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:16496403-16497377 FORWARD LENGTH=324	293	324	1.00E-39	110.6	29.0	37.5
Rsa1.0_00105.1.g5165.t1	gb|EOA31254.1| hypothetical protein CARUB_v10014434mg [Capsella rubella]	263	259	1.00E-122	98.5	83.7	90.5	hypothetical protein CARUB_v10014434mg	gbpln	Capsella rubella	AT3G07565.1 | Symbols: | Protein of unknown function (DUF3755) | chr3:2413823-2415872 FORWARD LENGTH=258	263	258	1.00E-118	98.1	82.5	89.7
Rsa1.0_00105.1.g5166.t1	ref|NP_566313.2| Cytochrome b561/ferric reductase transmembrane with DOMON related domain [Arabidopsis thaliana] gi|110736322|dbj|BAF00131.1| hypothetical protein [Arabidopsis thaliana] gi|332641046|gb|AEE74567.1| Cytochrome b561/ferric reductase transmembrane with DOMON related domain [Arabidopsis thaliana]	370	369	1.00E-176	99.7	79.5	91.4	Cytochrome b561/ferric reductase transmembrane with DOMON related domain	gbpln	Arabidopsis thaliana	AT3G07570.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane with DOMON related domain | chr3:2418205-2420206 REVERSE LENGTH=369	370	369	1.00E-179	99.7	79.5	91.4
Rsa1.0_00105.1.g5167.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00105.1.g5168.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	592	536	2.00E-89	90.5	30.2	40.0	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	592	530	1.00E-51	89.5	15.4	19.1
Rsa1.0_00105.1.g5169.t1	ref|XP_002884659.1| At3g07580 [Arabidopsis lyrata subsp. lyrata] gi|297330499|gb|EFH60918.1| At3g07580 [Arabidopsis lyrata subsp. lyrata]	145	145	8.00E-54	100.0	73.1	80.7	At3g07580	gbpln	Arabidopsis lyrata	AT3G07580.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48335.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:2421177-2422661 REVERSE LENGTH=143	145	143	5.00E-54	98.6	70.3	78.6
Rsa1.0_00105.1.g5170.t1	gb|ABC00745.1| putative small nuclear ribonucleoprotein D1 [Brassica napus]	118	118	1.00E-58	100.0	99.2	100.0	putative small nuclear ribonucleoprotein D1	gbpln	Brassica napus	AT3G07590.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr3:2423146-2423958 FORWARD LENGTH=114	118	114	2.00E-49	96.6	80.5	82.2
Rsa1.0_00105.1.g5171.t1	dbj|BAB11200.1| copia-type polyprotein [Arabidopsis thaliana] gi|13872710|emb|CAC37622.1| polyprotein [Arabidopsis thaliana]	1415	1334	0	94.3	42.0	51.7	copia-type polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1415	1262	2.00E-79	89.2	11.7	18.6
Rsa1.0_00105.1.g5172.t6	ref|XP_002888593.1| meiotic asynaptic mutant 1 [Arabidopsis lyrata subsp. lyrata] gi|297334434|gb|EFH64852.1| meiotic asynaptic mutant 1 [Arabidopsis lyrata subsp. lyrata]	879	596	1.00E-32	67.8	12.7	15.5	meiotic asynaptic mutant 1	gbpln	Arabidopsis lyrata	AT1G67370.1 | Symbols: ASY1, ATASY1 | DNA-binding HORMA family protein | chr1:25239347-25243713 REVERSE LENGTH=596	879	596	1.00E-34	67.8	12.7	15.5
Rsa1.0_00105.1.g5173.t1	ref|XP_002882534.1| hypothetical protein ARALYDRAFT_896920 [Arabidopsis lyrata subsp. lyrata] gi|297328374|gb|EFH58793.1| hypothetical protein ARALYDRAFT_896920 [Arabidopsis lyrata subsp. lyrata]	571	699	1.00E-113	122.4	39.8	45.0	hypothetical protein ARALYDRAFT_896920	gbpln	Arabidopsis lyrata	AT3G07530.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Beta-Casp domain (InterPro:IPR022712); BEST Arabidopsis thaliana protein match is: cleavage and polyadenylation specificity factor 73 kDa subunit-II (TAIR:AT2G01730.1); Has 624 Blast hits to 615 proteins in 160 species: Archae - 54; Bacteria - 6; Metazoa - 333; Fungi - 44; Plants - 93; Viruses - 0; Other Eukaryotes - 94 (source: NCBI BLink). | chr3:2400793-2404280 FORWARD LENGTH=699	571	699	1.00E-108	122.4	37.5	42.6
Rsa1.0_00105.1.g5174.t1	ref|XP_002862875.1| hypothetical protein ARALYDRAFT_920182 [Arabidopsis lyrata subsp. lyrata] gi|297308637|gb|EFH39134.1| hypothetical protein ARALYDRAFT_920182 [Arabidopsis lyrata subsp. lyrata]	325	315	2.00E-27	96.9	29.5	40.3	hypothetical protein ARALYDRAFT_920182	gbpln	Arabidopsis lyrata	AT1G02770.1 | Symbols: | Protein of unknown function (DUF626) | chr1:605071-606624 REVERSE LENGTH=316	325	316	5.00E-29	97.2	25.2	39.7
Rsa1.0_00105.1.g5175.t1	gb|AAF67380.1| Hypothetical protein T15F17.l [Arabidopsis thaliana]	146	1141	3.00E-40	781.5	52.7	61.6	Hypothetical protein T15F17.l	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00105.1.g5176.t1	emb|CAN81763.1| hypothetical protein VITISV_026693 [Vitis vinifera]	164	179	1.00E-18	109.1	32.9	50.0	hypothetical protein VITISV_026693	gbpln	Vitis vinifera	#	#	#	#	#	#	#

Rsa1.0_00105.1.g5177.t1	gb|EOA29803.1| hypothetical protein CARUB_v10012897mg [Capsella rubella]	814	983	0	120.8	57.2	67.0	hypothetical protein CARUB_v10012897mg	gbpln	Capsella rubella	AT3G07610.1 | Symbols: IBM1 | Transcription factor jumonji (jmjC) domain-containing protein | chr3:2426148-2432876 FORWARD LENGTH=1027	814	1027	0	126.2	56.8	66.8
Rsa1.0_00105.1.g5178.t2	gb|AAD09508.1| ATFP4, partial [Arabidopsis thaliana]	177	179	1.00E-44	101.1	58.2	67.8	ATFP4, partial	gbpln	Arabidopsis thaliana	AT3G07600.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:2424300-2424954 REVERSE LENGTH=157	177	157	1.00E-46	88.7	58.2	67.8
Rsa1.0_00105.1.g5179.t1	gb|EOA29803.1| hypothetical protein CARUB_v10012897mg [Capsella rubella]	1011	983	0	97.2	49.3	58.3	hypothetical protein CARUB_v10012897mg	gbpln	Capsella rubella	AT3G07610.1 | Symbols: IBM1 | Transcription factor jumonji (jmjC) domain-containing protein | chr3:2426148-2432876 FORWARD LENGTH=1027	1011	1027	0	101.6	36.1	40.9
Rsa1.0_00105.1.g5180.t1	gb|AAM61395.1| putative P-protein: chorismate mutase, prephenate dehydratase [Arabidopsis thaliana]	382	381	0	99.7	89.0	95.0	putative P-protein: chorismate mutase, prephenate dehydratase	gbpln	Arabidopsis thaliana	AT3G07630.2 | Symbols: ADT2 | arogenate dehydratase 2 | chr3:2435457-2437530 FORWARD LENGTH=381	382	381	0	99.7	88.7	94.8
Rsa1.0_00105.1.g5181.t1	ref|NP_187422.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|42572309|ref|NP_974250.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|79313159|ref|NP_001030659.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|186509893|ref|NP_001118599.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|17433084|sp|Q9SSE5.1|COL9_ARATH RecName: Full=Zinc finger protein CONSTANS-LIKE 9 gi|6466948|gb|AAF13083.1|AC009176_10 unknown protein [Arabidopsis thaliana] gi|119360037|gb|ABL66747.1| At3g07650 [Arabidopsis thaliana] gi|222423327|dbj|BAH19639.1| AT3G07650 [Arabidopsis thaliana] gi|332641059|gb|AEE74580.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641060|gb|AEE74581.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641061|gb|AEE74582.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641062|gb|AEE74583.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana]	377	372	1.00E-175	98.7	84.6	88.9	zinc finger protein CONSTANS-LIKE 9	gbpln	Arabidopsis thaliana	AT3G07650.4 | Symbols: COL9 | CONSTANS-like 9 | chr3:2442494-2443901 FORWARD LENGTH=372	377	372	1.00E-178	98.7	84.6	88.9
Rsa1.0_00105.1.g5182.t1	ref|XP_002884662.1| hypothetical protein ARALYDRAFT_896937 [Arabidopsis lyrata subsp. lyrata] gi|297330502|gb|EFH60921.1| hypothetical protein ARALYDRAFT_896937 [Arabidopsis lyrata subsp. lyrata]	809	840	0	103.8	82.8	88.3	hypothetical protein ARALYDRAFT_896937	gbpln	Arabidopsis lyrata	AT3G07660.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr3:2445275-2450372 REVERSE LENGTH=841	809	841	0	104.0	81.1	87.0
Rsa1.0_00105.1.g5183.t1	ref|XP_002882544.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328384|gb|EFH58803.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	445	459	0	103.1	93.5	97.1	predicted protein	gbpln	Arabidopsis lyrata	AT3G07690.1 | Symbols: | 6-phosphogluconate dehydrogenase family protein | chr3:2457232-2459378 FORWARD LENGTH=466	445	466	0	104.7	93.7	96.9
Rsa1.0_00105.1.g5184.t1	gb|EOA29986.1| hypothetical protein CARUB_v10013091mg [Capsella rubella]	678	701	0	103.4	92.9	96.8	hypothetical protein CARUB_v10013091mg	gbpln	Capsella rubella	AT3G07700.2 | Symbols: | Protein kinase superfamily protein | chr3:2459696-2463241 REVERSE LENGTH=695	678	695	0	102.5	92.0	95.9
Rsa1.0_00105.1.g5185.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	177	329	1.00E-22	185.9	37.9	50.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	177	256	1.00E-14	144.6	23.7	31.6
Rsa1.0_00105.1.g5186.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	343	1225	2.00E-68	357.1	40.2	53.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	343	575	1.00E-42	167.6	28.0	47.8

Rsa1.0_00105.1.g5187.t1	ref|NP_566316.1| galactose oxidase/kelch repeat-containing protein [Arabidopsis thaliana] gi|6466955|gb|AAF13090.1|AC009176_17 unknown protein [Arabidopsis thaliana] gi|6648184|gb|AAF21182.1|AC013483_6 unknown protein [Arabidopsis thaliana] gi|11692832|gb|AAG40019.1|AF324668_1 MLP3.17 [Arabidopsis thaliana] gi|11993873|gb|AAG42920.1|AF329503_1 unknown protein [Arabidopsis thaliana] gi|14517448|gb|AAK62614.1| AT3g07720/F17A17_6 [Arabidopsis thaliana] gi|21280883|gb|AAM44920.1| unknown protein [Arabidopsis thaliana] gi|23507767|gb|AAN38687.1| At3g07720/F17A17_6 [Arabidopsis thaliana] gi|332641071|gb|AEE74592.1| galactose oxidase/kelch repeat-containing protein [Arabidopsis thaliana]	329	329	1.00E-170	100.0	86.9	93.3	galactose oxidase/kelch repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G07720.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:2465439-2467033 FORWARD LENGTH=329	329	329	1.00E-172	100.0	86.9	93.3
Rsa1.0_00105.1.g5188.t1	gb|EOA30367.1| hypothetical protein CARUB_v10013490mg [Capsella rubella]	488	507	1.00E-77	103.9	45.3	57.8	hypothetical protein CARUB_v10013490mg	gbpln	Capsella rubella	AT3G07730.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01170.1); Has 1299 Blast hits to 1149 proteins in 206 species: Archae - 3; Bacteria - 100; Metazoa - 453; Fungi - 114; Plants - 108; Viruses - 2; Other Eukaryotes - 519 (source: NCBI BLink). | chr3:2468185-2469606 FORWARD LENGTH=473	488	473	2.00E-73	96.9	44.7	58.0
Rsa1.0_00105.1.g5189.t2	gb|EOA30269.1| hypothetical protein CARUB_v10013390mg [Capsella rubella]	550	548	0	99.6	82.5	89.6	hypothetical protein CARUB_v10013390mg	gbpln	Capsella rubella	AT3G07740.1 | Symbols: ADA2A, ATADA2A, HAC10, HXA02, HXA2 | homolog of yeast ADA2 2A | chr3:2470014-2473062 REVERSE LENGTH=548	550	548	0	99.6	82.0	88.4
Rsa1.0_00105.1.g5190.t1	gb|EOA31153.1| hypothetical protein CARUB_v10014316mg [Capsella rubella]	285	287	1.00E-147	100.7	90.5	95.1	hypothetical protein CARUB_v10014316mg	gbpln	Capsella rubella	AT3G07750.2 | Symbols: | 3'-5'-exoribonuclease family protein | chr3:2473486-2475218 FORWARD LENGTH=286	285	286	1.00E-149	100.4	90.2	94.7
Rsa1.0_00105.1.g5191.t1	ref|XP_002882548.1| hypothetical protein ARALYDRAFT_896947 [Arabidopsis lyrata subsp. lyrata] gi|297328388|gb|EFH58807.1| hypothetical protein ARALYDRAFT_896947 [Arabidopsis lyrata subsp. lyrata]	142	140	1.00E-70	98.6	93.0	94.4	hypothetical protein ARALYDRAFT_896947	gbpln	Arabidopsis lyrata	AT3G07760.2 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr3:2476723-2477947 FORWARD LENGTH=125	142	125	2.00E-68	88.0	85.2	86.6
Rsa1.0_00105.1.g5192.t1	ref|XP_002882549.1| hypothetical protein ARALYDRAFT_896948 [Arabidopsis lyrata subsp. lyrata] gi|297328389|gb|EFH58808.1| hypothetical protein ARALYDRAFT_896948 [Arabidopsis lyrata subsp. lyrata]	804	799	0	99.4	88.7	94.0	hypothetical protein ARALYDRAFT_896948	gbpln	Arabidopsis lyrata	AT3G07770.1 | Symbols: Hsp89.1, AtHsp90.6, AtHsp90-6 | HEAT SHOCK PROTEIN 89.1 | chr3:2479611-2483970 FORWARD LENGTH=799	804	799	0	99.4	87.8	93.9
Rsa1.0_00105.1.g5193.t1	ref|NP_187436.1| protein DGCR14 [Arabidopsis thaliana] gi|6466961|gb|AAF13096.1|AC009176_23 hypothetical protein [Arabidopsis thaliana] gi|6648191|gb|AAF21189.1|AC013483_13 hypothetical protein [Arabidopsis thaliana] gi|332641083|gb|AEE74604.1| protein DGCR14-like protein [Arabidopsis thaliana]	488	508	0	104.1	84.2	89.5	protein DGCR14	gbpln	Arabidopsis thaliana	AT3G07790.1 | Symbols: | DGCR14-related | chr3:2487491-2489017 FORWARD LENGTH=508	488	508	0	104.1	84.2	89.5
Rsa1.0_00105.1.g5194.t1	gb|EOA31343.1| hypothetical protein CARUB_v10014517mg [Capsella rubella]	227	238	1.00E-108	104.8	86.3	91.2	hypothetical protein CARUB_v10014517mg	gbpln	Capsella rubella	AT3G07800.1 | Symbols: | Thymidine kinase | chr3:2489944-2490935 REVERSE LENGTH=238	227	238	1.00E-107	104.8	85.5	89.0
Rsa1.0_00105.1.g5195.t2	ref|XP_002882552.1| hypothetical protein ARALYDRAFT_478119 [Arabidopsis lyrata subsp. lyrata] gi|297328392|gb|EFH58811.1| hypothetical protein ARALYDRAFT_478119 [Arabidopsis lyrata subsp. lyrata]	512	495	0	96.7	88.1	90.2	hypothetical protein ARALYDRAFT_478119	gbpln	Arabidopsis lyrata	AT3G07810.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:2492875-2495102 FORWARD LENGTH=495	512	495	0	96.7	87.7	90.2
Rsa1.0_00105.1.g5196.t1	gb|ADJ68232.1| exo-polygalacturonase [Brassica rapa subsp. oleifera]	426	476	0	111.7	92.5	95.1	exo-polygalacturonase	gbpln	Brassica rapa	AT3G14040.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:4648607-4650226 REVERSE LENGTH=445	426	445	0	104.5	79.1	87.1

Rsa1.0_00105.1.g5197.t1	ref|XP_002884670.1| exopolygalacturonase [Arabidopsis lyrata subsp. lyrata] gi|297330510|gb|EFH60929.1| exopolygalacturonase [Arabidopsis lyrata subsp. lyrata]	543	449	1.00E-164	82.7	51.7	62.6	exopolygalacturonase	gbpln	Arabidopsis lyrata	AT3G14040.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:4648607-4650226 REVERSE LENGTH=445	543	445	1.00E-158	82.0	51.4	62.6
Rsa1.0_00105.1.g5198.t1	gb|EOA31341.1| hypothetical protein CARUB_v10014515mg [Capsella rubella]	237	238	1.00E-117	100.4	89.5	92.0	hypothetical protein CARUB_v10014515mg	gbpln	Capsella rubella	AT3G07880.1 | Symbols: SCN1 | Immunoglobulin E-set superfamily protein | chr3:2514175-2515544 FORWARD LENGTH=240	237	240	1.00E-114	101.3	85.7	89.9
Rsa1.0_00106.1.g5199.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00106.1.g5200.t1	gb|AAM60857.1| dihydrolipoamide S-acetyltransferase, putative [Arabidopsis thaliana]	457	464	0	101.5	85.3	90.2	dihydrolipoamide S-acetyltransferase, putative	gbpln	Arabidopsis thaliana	AT1G34430.1 | Symbols: EMB3003 | 2-oxoacid dehydrogenases acyltransferase family protein | chr1:12588027-12590084 REVERSE LENGTH=465	457	465	0	101.8	86.0	90.6
Rsa1.0_00106.1.g5201.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1410	1365	0	96.8	36.9	51.6	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1410	575	5.00E-65	40.8	11.3	18.2
Rsa1.0_00106.1.g5202.t3	ref|XP_002893821.1| At1g34380 [Arabidopsis lyrata subsp. lyrata] gi|297339663|gb|EFH70080.1| At1g34380 [Arabidopsis lyrata subsp. lyrata]	743	335	1.00E-162	45.1	38.6	41.6	At1g34380	gbpln	Arabidopsis lyrata	AT1G34380.2 | Symbols: | 5'-3' exonuclease family protein | chr1:12552839-12554299 REVERSE LENGTH=347	743	347	1.00E-163	46.7	39.0	42.4
Rsa1.0_00106.1.g5203.t1	ref|XP_002891100.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297336942|gb|EFH67359.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	457	505	0	110.5	78.1	86.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G34370.1 | Symbols: STOP1 | C2H2 and C2HC zinc fingers superfamily protein | chr1:12551002-12552501 FORWARD LENGTH=499	457	499	0	109.2	75.5	84.7
Rsa1.0_00106.1.g5204.t7	gb|EOA39503.1| hypothetical protein CARUB_v10008117mg [Capsella rubella]	1134	1204	0	106.2	50.3	62.3	hypothetical protein CARUB_v10008117mg	gbpln	Capsella rubella	AT1G34355.1 | Symbols: ATPS1, PS1 | forkhead-associated (FHA) domain-containing protein | chr1:12536497-12541730 FORWARD LENGTH=1477	1134	1477	0	130.2	47.3	58.5
Rsa1.0_00106.1.g5205.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00106.1.g5206.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00106.1.g5207.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00106.1.g5208.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	684	1103	1.00E-162	161.3	46.1	59.2	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00106.1.g5209.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	751	695	0	92.5	59.9	72.2	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	751	681	1.00E-21	90.7	5.9	9.9
Rsa1.0_00106.1.g5210.t1	gb|AAF79483.1|AC022492_27 F1L3.20 [Arabidopsis thaliana]	835	1188	0	142.3	45.4	56.2	F1L3.20	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	835	1262	1.00E-20	151.1	5.6	9.3
Rsa1.0_00106.1.g5211.t1	ref|XP_002891097.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336939|gb|EFH67356.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	544	529	0	97.2	80.0	87.1	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT1G34340.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:12530936-12534031 FORWARD LENGTH=530	544	530	0	97.4	79.8	87.1
Rsa1.0_00106.1.g5212.t1	ref|NP_174692.1| uncharacterized protein [Arabidopsis thaliana] gi|37202044|gb|AAQ89637.1| At1g34320 [Arabidopsis thaliana] gi|51970944|dbj|BAD44164.1| hypothetical protein [Arabidopsis thaliana] gi|51971088|dbj|BAD44236.1| hypothetical protein [Arabidopsis thaliana] gi|332193576|gb|AEE31697.1| uncharacterized protein AT1G34320 [Arabidopsis thaliana]	654	657	0	100.5	90.8	93.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G34320.1 | Symbols: | Protein of unknown function (DUF668) | chr1:12520713-12524046 FORWARD LENGTH=657	654	657	0	100.5	90.8	93.7
Rsa1.0_00106.1.g5213.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00106.1.g5214.t1	ref|NP_174690.1| lectin protein kinase-like protein [Arabidopsis thaliana] gi|75338636|sp|Q9XID3.1|Y1343_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300; Flags: Precursor gi|5091617|gb|AAD39605.1|AC007454_4 Contains similarity to gi|479356 protein kinase PK1 from Zea mays, is a member of the PF|00954 S-locus glycoprotein family and contains a PF|00069 Eukaryotic protein kinase domain [Arabidopsis thaliana] gi|19699084|gb|AAL90909.1| At1g34300/F23M19_5 [Arabidopsis thaliana] gi|24111429|gb|AAN46865.1| At1g34300/F23M19_5 [Arabidopsis thaliana] gi|332193573|gb|AEE31694.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	533	829	0	155.5	64.2	69.2	lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G34300.1 | Symbols: | lectin protein kinase family protein | chr1:12503450-12505939 FORWARD LENGTH=829	533	829	0	155.5	64.2	69.2
Rsa1.0_00106.1.g5215.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00106.1.g5216.t1	gb|AAD21699.1| Contains reverse transcriptase domain (rvt) PF|00078 [Arabidopsis thaliana]	448	1253	1.00E-57	279.7	33.7	50.9	Contains reverse transcriptase domain (rvt) PF|00078	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	448	289	1.00E-29	64.5	17.4	29.0
Rsa1.0_00106.1.g5217.t1	ref|NP_564443.1| exostosin-like protein [Arabidopsis thaliana] gi|5091619|gb|AAD39607.1|AC007454_6 F23M19.7 [Arabidopsis thaliana] gi|15450928|gb|AAK96735.1| Unknown protein [Arabidopsis thaliana] gi|20148711|gb|AAM10246.1| unknown protein [Arabidopsis thaliana] gi|332193570|gb|AEE31691.1| exostosin-like protein [Arabidopsis thaliana]	486	477	0	98.1	85.0	90.7	exostosin-like protein	gbpln	Arabidopsis thaliana	AT1G34270.1 | Symbols: | Exostosin family protein | chr1:12492571-12494514 REVERSE LENGTH=477	486	477	0	98.1	85.0	90.7
Rsa1.0_00106.1.g5218.t1	ref|XP_002891093.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336935|gb|EFH67352.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata]	1428	1450	0	101.5	78.3	85.4	phosphatidylinositol-4-phosphate 5-kinase family protein	gbpln	Arabidopsis lyrata	AT1G34260.1 | Symbols: FAB1D | FORMS APLOID AND BINUCLEATE CELLS 1A | chr1:12485967-12491799 FORWARD LENGTH=1456	1428	1456	0	102.0	77.0	84.5
Rsa1.0_00106.1.g5219.t1	gb|ACB59223.1| glutathione S-transferase [Brassica oleracea]	155	523	1.00E-24	337.4	34.2	44.5	glutathione S-transferase	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00107.1.g5220.t2	ref|NP_200453.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|42573694|ref|NP_974943.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262699|sp|Q9FM89.1|FDL38_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At5g56420 gi|10177841|dbj|BAB11270.1| unnamed protein product [Arabidopsis thaliana] gi|332009379|gb|AED96762.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|332009380|gb|AED96763.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	350	422	3.00E-38	120.6	35.4	56.0	F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G56420.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22850863-22852334 REVERSE LENGTH=422	350	422	8.00E-41	120.6	35.4	56.0
Rsa1.0_00107.1.g5221.t2	ref|XP_002870044.1| hypothetical protein ARALYDRAFT_493014 [Arabidopsis lyrata subsp. lyrata] gi|297315880|gb|EFH46303.1| hypothetical protein ARALYDRAFT_493014 [Arabidopsis lyrata subsp. lyrata]	432	431	0	99.8	81.9	90.3	hypothetical protein ARALYDRAFT_493014	gbpln	Arabidopsis lyrata	AT4G18470.1 | Symbols: SNI1 | negative regulator of systemic acquired resistance (SNI1) | chr4:10192984-10195511 FORWARD LENGTH=432	432	432	0	100.0	80.8	90.3
Rsa1.0_00107.1.g5222.t1	gb|EOA15623.1| hypothetical protein CARUB_v10005759mg [Capsella rubella]	208	203	2.00E-96	97.6	87.0	90.4	hypothetical protein CARUB_v10005759mg	gbpln	Capsella rubella	AT4G18460.1 | Symbols: | D-Tyr-tRNA(Tyr) deacylase family protein | chr4:10195763-10196679 REVERSE LENGTH=153	208	153	8.00E-81	73.6	68.8	73.1
Rsa1.0_00107.1.g5223.t1	gb|EOA17808.1| hypothetical protein CARUB_v10006206mg [Capsella rubella]	667	695	0	104.2	95.5	97.9	hypothetical protein CARUB_v10006206mg	gbpln	Capsella rubella	AT4G18465.1 | Symbols: | RNA helicase family protein | chr4:10197056-10201611 FORWARD LENGTH=695	667	695	0	104.2	94.5	97.3

Rsa1.0_00107.1.g5224.t1	ref|NP_193583.1| magnesium-chelatase subunit chlI [Arabidopsis thaliana] gi|117238|sp|P16127.1|CHLI1_ARATH RecName: Full=Magnesium-chelatase subunit ChlI-1, chloroplastic; Short=Mg-chelatase subunit I-1; AltName: Full=Mg-protoporphyrin IX chelatase subunit ChlI-1; AltName: Full=Protein CHLORINA 42; Flags: Precursor gi|1020100|emb|CAA62754.1| protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] gi|2832653|emb|CAA16728.1| protein ch-42 precursor, chloroplast [Arabidopsis thaliana] gi|4490290|emb|CAB38561.1| unnamed protein product [Arabidopsis thaliana] gi|7268641|emb|CAB78850.1| protein ch-42 precursor, chloroplast [Arabidopsis thaliana] gi|20260586|gb|AAM13191.1| protein ch-42 precursor, chloroplast [Arabidopsis thaliana] gi|33589664|gb|AAQ22598.1| At4g18480 [Arabidopsis thaliana] gi|110742552|dbj|BAE99191.1| protein ch-42 precursor [Arabidopsis thaliana] gi|195604748|gb|ACG24204.1| magnesium-chelatase subunit chlI [Zea mays] gi|332658651|gb|AEE84051.1| magnesium-chelatase subunit chlI [Arabidopsis thaliana] gi|228771|prf||1811226A ccsA gene	423	424	0	100.2	93.4	96.5	magnesium-chelatase subunit chlI	gbpln	Arabidopsis thaliana	AT4G18480.1 | Symbols: CHLI1, CH42, CH-42, CHL11, CHLI-1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:10201897-10203361 REVERSE LENGTH=424	423	424	0	100.2	93.4	96.5
Rsa1.0_00107.1.g5225.t2	gb|EOA15459.1| hypothetical protein CARUB_v10004153mg [Capsella rubella] gi|482551267|gb|EOA15460.1| hypothetical protein CARUB_v10004153mg [Capsella rubella]	809	814	0	100.6	63.7	73.8	hypothetical protein CARUB_v10004153mg	gbpln	Capsella rubella	AT4G18490.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot, shoot apex, embryo, flower, seed; EXPRESSED DURING: petal differentiation and expansion stage, E expanded cotyledon stage; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10204388-10208197 FORWARD LENGTH=755	809	755	0	93.3	62.4	70.8
Rsa1.0_00107.1.g5226.t4	ref|NP_197443.3| regulator of chromosome condensation-like protein with FYVE zinc finger domain [Arabidopsis thaliana] gi|332005320|gb|AED92703.1| regulator of chromosome condensation-like protein with FYVE zinc finger domain [Arabidopsis thaliana]	487	1105	3.00E-86	226.9	40.2	43.7	regulator of chromosome condensation-like protein with FYVE zinc finger domain	gbpln	Arabidopsis thaliana	AT5G19420.1 | Symbols: | Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain | chr5:6547945-6552866 REVERSE LENGTH=1105	487	1105	8.00E-89	226.9	40.2	43.7
Rsa1.0_00107.1.g5227.t2	gb|EOA15459.1| hypothetical protein CARUB_v10004153mg [Capsella rubella] gi|482551267|gb|EOA15460.1| hypothetical protein CARUB_v10004153mg [Capsella rubella]	344	814	2.00E-56	236.6	36.6	41.3	hypothetical protein CARUB_v10004153mg	gbpln	Capsella rubella	AT4G18490.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10204388-10208197 FORWARD LENGTH=756	344	756	2.00E-56	219.8	35.5	40.1
Rsa1.0_00107.1.g5228.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00107.1.g5229.t1	gb|EOA18754.1| hypothetical protein CARUB_v10007338mg [Capsella rubella]	108	112	7.00E-27	103.7	78.7	88.0	hypothetical protein CARUB_v10007338mg	gbpln	Capsella rubella	AT4G18501.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:10209311-10209640 FORWARD LENGTH=109	108	109	4.00E-25	100.9	70.4	82.4
Rsa1.0_00107.1.g5230.t1	ref|XP_002870040.1| hypothetical protein ARALYDRAFT_493008 [Arabidopsis lyrata subsp. lyrata] gi|297315876|gb|EFH46299.1| hypothetical protein ARALYDRAFT_493008 [Arabidopsis lyrata subsp. lyrata]	78	78	1.00E-16	100.0	71.8	83.3	hypothetical protein ARALYDRAFT_493008	gbpln	Arabidopsis lyrata	AT4G18510.1 | Symbols: CLE2 | CLAVATA3/ESR-related 2 | chr4:10212092-10212319 FORWARD LENGTH=75	78	75	4.00E-16	96.2	70.5	78.2
Rsa1.0_00107.1.g5231.t3	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1730	1213	0	70.1	24.4	37.2	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1730	626	2.00E-61	36.2	7.2	12.3
Rsa1.0_00107.1.g5232.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00107.1.g5233.t1	ref|NP_193588.5| uncharacterized protein [Arabidopsis thaliana] gi|332658658|gb|AEE84058.1| uncharacterized protein AT4G18530 [Arabidopsis thaliana]	399	389	0	97.5	82.0	88.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G18530.1 | Symbols: | Protein of unknown function (DUF707) | chr4:10217749-10220285 FORWARD LENGTH=389	399	389	0	97.5	82.0	88.0
Rsa1.0_00107.1.g5234.t1	gb|EOA16325.1| hypothetical protein CARUB_v10004475mg [Capsella rubella]	542	569	0	105.0	82.8	90.0	hypothetical protein CARUB_v10004475mg	gbpln	Capsella rubella	AT4G18540.1 | Symbols: | unknown protein; Has 209 Blast hits to 205 proteins in 54 species: Archae - 0; Bacteria - 17; Metazoa - 2; Fungi - 150; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:10221203-10223028 REVERSE LENGTH=520	542	520	0	95.9	75.3	81.4
Rsa1.0_00107.1.g5235.t1	ref|XP_002867985.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297313821|gb|EFH44244.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	434	418	0	96.3	83.6	89.6	lipase class 3 family protein	gbpln	Arabidopsis lyrata	AT4G18550.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:10225006-10226862 REVERSE LENGTH=419	434	419	0	96.5	81.3	88.5
Rsa1.0_00107.1.g5236.t1	gb|EOA17812.1| hypothetical protein CARUB_v10006210mg [Capsella rubella]	601	647	0	107.7	85.7	90.3	hypothetical protein CARUB_v10006210mg	gbpln	Capsella rubella	AT4G18570.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:10231439-10234534 FORWARD LENGTH=642	601	642	0	106.8	83.0	89.9
Rsa1.0_00107.1.g5237.t1	gb|EOA18306.1| hypothetical protein CARUB_v10006819mg [Capsella rubella]	144	130	3.00E-15	90.3	43.8	57.6	hypothetical protein CARUB_v10006819mg	gbpln	Capsella rubella	AT4G18580.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:10234853-10235524 REVERSE LENGTH=115	144	115	1.00E-16	79.9	44.4	52.1
Rsa1.0_00107.1.g5238.t1	ref|NP_567560.2| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|45773776|gb|AAS76692.1| At4g18590 [Arabidopsis thaliana] gi|46359785|gb|AAS88756.1| At4g18590 [Arabidopsis thaliana] gi|332658664|gb|AEE84064.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	106	106	7.00E-50	100.0	88.7	95.3	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT4G18590.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr4:10236524-10236940 FORWARD LENGTH=106	106	106	1.00E-52	100.0	88.7	95.3
Rsa1.0_00107.1.g5239.t1	ref|XP_002870034.1| pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata] gi|297315870|gb|EFH46293.1| pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata]	173	173	1.00E-87	100.0	90.8	95.4	pollen ole e 1 allergen and extensin family protein	gbpln	Arabidopsis lyrata	AT4G18596.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr4:10239114-10239728 FORWARD LENGTH=172	173	172	1.00E-89	99.4	91.3	96.0
Rsa1.0_00107.1.g5240.t1	gb|EOA15429.1| hypothetical protein CARUB_v10003966mg [Capsella rubella]	2174	2074	0	95.4	43.4	52.3	hypothetical protein CARUB_v10003966mg	gbpln	Capsella rubella	AT4G18600.1 | Symbols: WAVE5, ATSCAR-LIKE, SCARL | SCAR family protein | chr4:10239947-10247372 REVERSE LENGTH=2028	2174	2028	0	93.3	42.2	50.1
Rsa1.0_00107.1.g5241.t1	ref|XP_002870033.1| hypothetical protein ARALYDRAFT_914818 [Arabidopsis lyrata subsp. lyrata] gi|297315869|gb|EFH46292.1| hypothetical protein ARALYDRAFT_914818 [Arabidopsis lyrata subsp. lyrata]	194	191	5.00E-88	98.5	91.2	91.8	hypothetical protein ARALYDRAFT_914818	gbpln	Arabidopsis lyrata	AT4G18610.1 | Symbols: LSH9 | Protein of unknown function (DUF640) | chr4:10250794-10251369 FORWARD LENGTH=191	194	191	9.00E-90	98.5	90.7	91.8
Rsa1.0_00107.1.g5242.t1	gb|ABK28243.1| unknown [Arabidopsis thaliana]	315	297	5.00E-59	94.3	36.8	55.6	unknown	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	315	332	5.00E-59	105.4	35.9	54.3
Rsa1.0_00107.1.g5243.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00107.1.g5244.t1	gb|EOA15586.1| hypothetical protein CARUB_v10005444mg [Capsella rubella]	279	280	1.00E-121	100.4	76.3	85.3	hypothetical protein CARUB_v10005444mg	gbpln	Capsella rubella	AT4G18690.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G18680.1); Has 522 Blast hits to 522 proteins in 39 species: Archae - 0; Bacteria - 0; Metazoa - 9; Fungi - 0; Plants - 513; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:10282788-10283636 FORWARD LENGTH=282	279	282	4.00E-80	101.1	52.7	70.6
Rsa1.0_00107.1.g5245.t1	ref|NP_193602.4| leucine-rich repeat extensin-like protein 5 [Arabidopsis thaliana] gi|300681244|sp|Q9SN46.2|LRX5_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 5; Short=AtLRX5; Short=LRR/EXTENSIN5; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor gi|332658674|gb|AEE84074.1| leucine-rich repeat extensin-like protein 5 [Arabidopsis thaliana]	797	857	0	107.5	44.7	46.5	leucine-rich repeat extensin-like protein 5	gbpln	Arabidopsis thaliana	AT4G18670.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:10275918-10278491 REVERSE LENGTH=857	797	857	0	107.5	44.7	46.5

Rsa1.0_00107.1.g5246.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00107.1.g5247.t1	gb|EOA18865.1| hypothetical protein CARUB_v10007488mg, partial [Capsella rubella]	496	509	0	102.6	91.1	94.6	hypothetical protein CARUB_v10007488mg, partial	gbpln	Capsella rubella	AT4G18700.1 | Symbols: CIPK12, SnRK3.9, ATWL4, WL4 | CBL-interacting protein kinase 12 | chr4:10289110-10290579 REVERSE LENGTH=489	496	489	0	98.6	90.9	94.4
Rsa1.0_00107.1.g5248.t1	ref|XP_002870026.1| hypothetical protein ARALYDRAFT_914806 [Arabidopsis lyrata subsp. lyrata] gi|297315862|gb|EFH46285.1| hypothetical protein ARALYDRAFT_914806 [Arabidopsis lyrata subsp. lyrata]	375	380	0	101.3	98.9	99.7	hypothetical protein ARALYDRAFT_914806	gbpln	Arabidopsis lyrata	AT4G18710.1 | Symbols: BIN2, DWF12, UCU1, ATSK21, SK21 | Protein kinase superfamily protein | chr4:10296474-10298913 FORWARD LENGTH=380	375	380	0	101.3	98.7	99.7
Rsa1.0_00107.1.g5249.t1	ref|NP_191429.1| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|18415161|ref|NP_567563.1| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|30694822|ref|NP_568649.2| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|27735235|sp|P42794.2|RL112_ARATH RecName: Full=60S ribosomal protein L11-2; AltName: Full=L16 gi|11908058|gb|AAG41458.1|AF326876_1 putative ribosomal protein L11 [Arabidopsis thaliana] gi|12642874|gb|AAK00379.1|AF339697_1 putative ribosomal protein L11 [Arabidopsis thaliana] gi|14326537|gb|AAK60313.1|AF385722_1 AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|7630065|emb|CAB88287.1| ribosomal protein L11-like [Arabidopsis thaliana] gi|9758681|dbj|BAB09220.1| ribosomal protein L11-like [Arabidopsis thaliana] gi|14517470|gb|AAK62625.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|18700224|gb|AAL77722.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|21553372|gb|AAM62465.1| ribosomal protein L11, cytosolic [Arabidopsis thaliana] gi|21592421|gb|AAM64372.1| ribosomal protein L11, cytosolic [Arabidopsis thaliana] gi|22136574|gb|AAM91073.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|332007914|gb|AED95297.1|	182	182	1.00E-102	100.0	99.5	100.0	60S ribosomal protein L11-2	gbpln	Arabidopsis thaliana	AT5G45775.2 | Symbols: | Ribosomal L5P family protein | chr5:18565281-18566496 REVERSE LENGTH=182	182	182	1.00E-104	100.0	99.5	100.0
Rsa1.0_00107.1.g5250.t1	ref|NP_193609.2| Rho termination factor [Arabidopsis thaliana] gi|332658683|gb|AEE84083.1| Rho termination factor [Arabidopsis thaliana]	230	245	4.00E-65	106.5	66.1	77.4	Rho termination factor	gbpln	Arabidopsis thaliana	AT4G18740.1 | Symbols: | Rho termination factor | chr4:10303543-10304479 REVERSE LENGTH=245	230	245	1.00E-67	106.5	66.1	77.4
Rsa1.0_00107.1.g5251.t1	gb|EOA15340.1| hypothetical protein CARUB_v10004110mg [Capsella rubella]	869	872	0	100.3	86.7	92.6	hypothetical protein CARUB_v10004110mg	gbpln	Capsella rubella	AT4G18750.1 | Symbols: DOT4 | Pentatricopeptide repeat (PPR) superfamily protein | chr4:10304850-10307465 FORWARD LENGTH=871	869	871	0	100.2	85.7	91.4
Rsa1.0_00107.1.g5252.t1	gb|EOA16660.1| hypothetical protein CARUB_v10004846mg [Capsella rubella]	456	434	1.00E-169	95.2	76.3	83.8	hypothetical protein CARUB_v10004846mg	gbpln	Capsella rubella	AT4G18760.1 | Symbols: AtRLP51, RLP51 | receptor like protein 51 | chr4:10308163-10309458 REVERSE LENGTH=431	456	431	1.00E-167	94.5	71.7	78.7
Rsa1.0_00107.1.g5253.t1	gb|EOA18242.1| hypothetical protein CARUB_v10006734mg [Capsella rubella]	421	432	0	102.6	87.6	94.3	hypothetical protein CARUB_v10006734mg	gbpln	Capsella rubella	AT4G18770.1 | Symbols: MYB98, AtMYB98 | myb domain protein 98 | chr4:10311068-10312557 FORWARD LENGTH=427	421	427	0	101.4	86.9	93.1
Rsa1.0_00107.1.g5254.t1	ref|XP_002878577.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297324416|gb|EFH54836.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	639	796	1.00E-137	124.6	46.5	60.4	protein binding protein	gbpln	Arabidopsis lyrata	AT2G21850.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:9315268-9317908 FORWARD LENGTH=787	639	787	1.00E-139	123.2	46.5	59.5
Rsa1.0_00107.1.g5255.t3	ref|XP_002867975.1| hypothetical protein ARALYDRAFT_492979 [Arabidopsis lyrata subsp. lyrata] gi|297313811|gb|EFH44234.1| hypothetical protein ARALYDRAFT_492979 [Arabidopsis lyrata subsp. lyrata]	97	214	1.00E-40	220.6	86.6	92.8	hypothetical protein ARALYDRAFT_492979	gbpln	Arabidopsis lyrata	AT4G18800.1 | Symbols: ATHSGBP, ATRAB11B, ATRABA1D, RABA1d | RAB GTPase homolog A1D | chr4:10320156-10321339 REVERSE LENGTH=214	97	214	2.00E-43	220.6	86.6	92.8
Rsa1.0_00107.1.g5256.t1	gb|EOA17416.1| hypothetical protein CARUB_v10005719mg [Capsella rubella]	115	214	3.00E-59	186.1	96.5	98.3	hypothetical protein CARUB_v10005719mg	gbpln	Capsella rubella	AT4G18800.1 | Symbols: ATHSGBP, ATRAB11B, ATRABA1D, RABA1d | RAB GTPase homolog A1D | chr4:10320156-10321339 REVERSE LENGTH=214	115	214	6.00E-62	186.1	96.5	98.3

Rsa1.0_00107.1.g5257.t1	ref|NP_188381.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75274267|sp|Q9LUP4.1|FBK60_ARATH RecName: Full=Putative F-box/kelch-repeat protein At3g17540 gi|9294141|dbj|BAB02043.1| unnamed protein product [Arabidopsis thaliana] gi|332642445|gb|AEE75966.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	384	396	2.00E-82	103.1	49.0	65.1	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G17540.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6002783-6003973 FORWARD LENGTH=396	384	396	4.00E-85	103.1	49.0	65.1
Rsa1.0_00107.1.g5258.t1	gb|ABV89650.1| transcriptional repressor [Brassica rapa]	598	600	0	100.3	92.6	95.5	transcriptional repressor	gbpln	Brassica rapa	AT4G18810.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:10322622-10325735 REVERSE LENGTH=596	598	596	0	99.7	88.8	93.5
Rsa1.0_00107.1.g5259.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	372	1274	4.00E-57	342.5	37.9	54.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315	372	315	2.00E-41	84.7	26.1	37.4
Rsa1.0_00107.1.g5260.t1	gb|EOA15933.1| hypothetical protein CARUB_v10004027mg [Capsella rubella]	1093	1115	0	102.0	85.5	90.6	hypothetical protein CARUB_v10004027mg	gbpln	Capsella rubella	AT4G18820.1 | Symbols: | AAA-type ATPase family protein | chr4:10330371-10334090 FORWARD LENGTH=1097	1093	1097	0	100.4	84.7	89.5
Rsa1.0_00107.1.g5261.t1	ref|XP_002870022.1| ATOFP5/OFP5 [Arabidopsis lyrata subsp. lyrata] gi|297315858|gb|EFH46281.1| ATOFP5/OFP5 [Arabidopsis lyrata subsp. lyrata]	332	351	1.00E-155	105.7	83.1	92.5	ATOFP5/OFP5	gbpln	Arabidopsis lyrata	AT4G18830.1 | Symbols: ATOFP5, OFP5 | ovate family protein 5 | chr4:10337449-10338498 FORWARD LENGTH=349	332	349	1.00E-156	105.1	82.5	91.9
Rsa1.0_00107.1.g5262.t1	gb|EOA16398.1| hypothetical protein CARUB_v10004552mg [Capsella rubella]	538	537	0	99.8	81.4	90.7	hypothetical protein CARUB_v10004552mg	gbpln	Capsella rubella	AT4G18840.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr4:10338719-10340356 REVERSE LENGTH=545	538	545	0	101.3	76.2	84.8
Rsa1.0_00107.1.g5263.t1	ref|XP_002870008.1| hypothetical protein ARALYDRAFT_492961 [Arabidopsis lyrata subsp. lyrata] gi|297315844|gb|EFH46267.1| hypothetical protein ARALYDRAFT_492961 [Arabidopsis lyrata subsp. lyrata]	111	107	9.00E-35	96.4	71.2	77.5	hypothetical protein ARALYDRAFT_492961	gbpln	Arabidopsis lyrata	AT4G18980.1 | Symbols: AtS40-3 | AtS40-3 | chr4:10398973-10399293 FORWARD LENGTH=106	111	106	4.00E-34	95.5	70.3	75.7
Rsa1.0_00107.1.g5264.t1	gb|EOA17974.1| hypothetical protein CARUB_v10006389mg [Capsella rubella]	352	361	1.00E-172	102.6	87.5	93.5	hypothetical protein CARUB_v10006389mg	gbpln	Capsella rubella	AT4G18990.1 | Symbols: XTH29 | xyloglucan endotransglucosylase/hydrolase 29 | chr4:10401941-10404248 REVERSE LENGTH=357	352	357	1.00E-171	101.4	88.6	93.8
Rsa1.0_00107.1.g5265.t1	gb|EOA16327.1| hypothetical protein CARUB_v10004477mg [Capsella rubella]	782	566	0	72.4	59.7	66.0	hypothetical protein CARUB_v10004477mg	gbpln	Capsella rubella	AT4G19010.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr4:10411715-10414221 REVERSE LENGTH=566	782	566	0	72.4	59.8	66.0
Rsa1.0_00107.1.g5266.t1	ref|NP_193637.2| chromomethylase 2 [Arabidopsis thaliana] gi|322510132|sp|Q94F87.3|CMT2_ARATH RecName: Full=DNA (cytosine-5)-methyltransferase CMT2; AltName: Full=Chromomethylase 2; AltName: Full=Protein CHROMOMETHYLASE 2 gi|332658726|gb|AEE84126.1| chromomethylase 2 [Arabidopsis thaliana]	1104	1295	0	117.3	72.4	81.5	chromomethylase 2	gbpln	Arabidopsis thaliana	AT4G19020.1 | Symbols: CMT2 | chromomethylase 2 | chr4:10414526-10420936 FORWARD LENGTH=1295	1104	1295	0	117.3	72.4	81.5
Rsa1.0_00107.1.g5267.t3	ref|XP_002867959.1| hypothetical protein ARALYDRAFT_492951 [Arabidopsis lyrata subsp. lyrata] gi|297313795|gb|EFH44218.1| hypothetical protein ARALYDRAFT_492951 [Arabidopsis lyrata subsp. lyrata]	728	718	0	98.6	93.7	96.0	hypothetical protein ARALYDRAFT_492951	gbpln	Arabidopsis lyrata	AT4G19040.1 | Symbols: EDR2 | ENHANCED DISEASE RESISTANCE 2 | chr4:10431799-10437171 REVERSE LENGTH=718	728	718	0	98.6	93.4	95.7
Rsa1.0_00107.1.g5268.t3	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	535	1142	1.00E-115	213.5	42.4	54.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	535	575	2.00E-46	107.5	26.5	44.1
Rsa1.0_00107.1.g5269.t1	ref|NP_193641.1| putative disease resistance protein [Arabidopsis thaliana] gi|46395783|sp|Q84WD3.2|DRL26_ARATH RecName: Full=Probable disease resistance protein At4g19060 gi|2832635|emb|CAA16764.1| hypothetical protein [Arabidopsis thaliana] gi|7268701|emb|CAB78908.1| hypothetical protein [Arabidopsis thaliana] gi|63003754|gb|AAY25406.1| At4g19060 [Arabidopsis thaliana] gi|332658735|gb|AEE84135.1| putative disease resistance protein [Arabidopsis thaliana]	350	383	1.00E-109	109.4	61.1	72.3	putative disease resistance protein	gbpln	Arabidopsis thaliana	AT4G19060.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:10445082-10446233 REVERSE LENGTH=383	350	383	1.00E-112	109.4	61.1	72.3

Rsa1.0_00107.1.g5270.t1	emb|CAA16762.1| putative protein [Arabidopsis thaliana] gi|7268700|emb|CAB78907.1| putative protein [Arabidopsis thaliana]	1153	1405	0	121.9	67.7	81.0	putative protein	gbpln	Arabidopsis thaliana	AT4G19050.1 | Symbols: | NB-ARC domain-containing disease resistance protein | chr4:10440102-10443786 REVERSE LENGTH=1201	1153	1201	0	104.2	54.1	63.0
Rsa1.0_00107.1.g5271.t1	ref|XP_002867953.1| early-responsive to dehydration 3 [Arabidopsis lyrata subsp. lyrata] gi|297313789|gb|EFH44212.1| early-responsive to dehydration 3 [Arabidopsis lyrata subsp. lyrata]	600	600	0	100.0	94.7	98.5	early-responsive to dehydration 3	gbpln	Arabidopsis lyrata	AT4G19120.2 | Symbols: ERD3 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:10460665-10463034 REVERSE LENGTH=600	600	600	0	100.0	93.7	98.3
Rsa1.0_00107.1.g5272.t1	gb|EOA17088.1| hypothetical protein CARUB_v10005338mg [Capsella rubella]	287	304	1.00E-127	105.9	81.5	91.6	hypothetical protein CARUB_v10005338mg	gbpln	Capsella rubella	AT4G19140.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10469830-10471275 FORWARD LENGTH=303	287	303	1.00E-128	105.6	80.5	89.2
Rsa1.0_00107.1.g5273.t1	gb|EOA17266.1| hypothetical protein CARUB_v10005540mg [Capsella rubella]	254	258	6.00E-99	101.6	76.0	81.5	hypothetical protein CARUB_v10005540mg	gbpln	Capsella rubella	AT4G19150.1 | Symbols: | Ankyrin repeat family protein | chr4:10471578-10472677 REVERSE LENGTH=243	254	243	2.00E-96	95.7	75.2	79.9
Rsa1.0_00107.1.g5274.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1474	1491	0	101.2	61.3	75.3	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1474	1262	2.33E-156	85.6	17.2	24.1
Rsa1.0_00107.1.g5275.t1	ref|NP_974572.1| uncharacterized protein [Arabidopsis thaliana] gi|332658751|gb|AEE84151.1| uncharacterized protein AT4G19160 [Arabidopsis thaliana]	467	453	1.00E-178	97.0	73.4	81.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G19160.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:10477772-10479947 FORWARD LENGTH=453	467	453	1.00E-180	97.0	73.4	81.4
Rsa1.0_00107.1.g5276.t1	dbj|BAJ34120.1| unnamed protein product [Thellungiella halophila]	596	602	0	101.0	87.6	94.1	unnamed protein product	----	----	AT4G19170.1 | Symbols: NCED4, CCD4 | nine-cis-epoxycarotenoid dioxygenase 4 | chr4:10481835-10483622 FORWARD LENGTH=595	596	595	0	99.8	84.1	90.6
Rsa1.0_00107.1.g5277.t1	ref|XP_002867950.1| nucleoside phosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313786|gb|EFH44209.1| nucleoside phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	740	741	0	100.1	87.7	92.7	nucleoside phosphatase family protein	gbpln	Arabidopsis lyrata	AT4G19180.1 | Symbols: | GDA1/CD39 nucleoside phosphatase family protein | chr4:10485518-10487868 REVERSE LENGTH=740	740	740	0	100.0	86.9	92.4
Rsa1.0_00107.1.g5278.t1	gb|EOA16763.1| hypothetical protein CARUB_v10004980mg [Capsella rubella]	399	397	0	99.5	87.7	93.7	hypothetical protein CARUB_v10004980mg	gbpln	Capsella rubella	AT4G19185.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:10489201-10491488 REVERSE LENGTH=398	399	398	0	99.7	88.7	93.7
Rsa1.0_00107.1.g5279.t1	ref|XP_002869996.1| putative protein [Arabidopsis lyrata subsp. lyrata] gi|297315832|gb|EFH46255.1| putative protein [Arabidopsis lyrata subsp. lyrata]	574	1251	0	217.9	80.8	88.5	putative protein	gbpln	Arabidopsis lyrata	AT4G19190.1 | Symbols: | zinc knuckle (CCHC-type) family protein | chr4:10493323-10495969 FORWARD LENGTH=595	574	595	0	103.7	81.0	88.9
Rsa1.0_00107.1.g5280.t1	ref|XP_002869995.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297315831|gb|EFH46254.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	171	171	4.00E-19	100.0	59.6	60.8	expressed protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00107.1.g5281.t1	ref|XP_002869937.1| transcription initiation factor [Arabidopsis lyrata subsp. lyrata] gi|297315773|gb|EFH46196.1| transcription initiation factor [Arabidopsis lyrata subsp. lyrata]	431	483	1.00E-136	112.1	60.8	73.5	transcription initiation factor	gbpln	Arabidopsis lyrata	AT4G20340.1 | Symbols: | Transcription factor TFIIE, alpha subunit | chr4:10985011-10987748 FORWARD LENGTH=475	431	475	1.00E-133	110.2	62.9	76.1
Rsa1.0_00107.1.g5282.t1	ref|XP_002867886.1| hypothetical protein ARALYDRAFT_492835 [Arabidopsis lyrata subsp. lyrata] gi|297313722|gb|EFH44145.1| hypothetical protein ARALYDRAFT_492835 [Arabidopsis lyrata subsp. lyrata]	290	286	1.00E-114	98.6	74.1	85.9	hypothetical protein ARALYDRAFT_492835	gbpln	Arabidopsis lyrata	AT4G20330.1 | Symbols: | Transcription initiation factor TFIIE, beta subunit | chr4:10982683-10984039 REVERSE LENGTH=286	290	286	1.00E-111	98.6	73.1	84.5
Rsa1.0_00107.1.g5283.t1	gb|AGC70150.1| ABC transporter E family member 2 protein [Cardamine hirsuta]	605	605	0	100.0	97.0	99.0	ABC transporter E family member 2 protein	gbpln	Cardamine hirsuta	AT4G19210.1 | Symbols: ATRLI2, RLI2 | RNAse l inhibitor protein 2 | chr4:10501906-10504776 FORWARD LENGTH=605	605	605	0	100.0	96.2	98.5
Rsa1.0_00107.1.g5284.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	284	390	2.00E-38	137.3	29.6	43.0	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	284	289	4.00E-35	101.8	32.4	48.9

Rsa1.0_00107.1.g5285.t2	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1120	1214	0	108.4	48.3	64.1	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1120	626	6.00E-74	55.9	13.1	20.0
Rsa1.0_00107.1.g5286.t1	ref|NP_567581.1| abscisic acid 8'-hydroxylase 1 [Arabidopsis thaliana] gi|75306306|sp|Q949P1.1|ABAH1_ARATH RecName: Full=Abscisic acid 8'-hydroxylase 1; Short=ABA 8'-hydroxylase 1; AltName: Full=Cytochrome P450 707A1 gi|15293093|gb|AAK93657.1| putative cytochrome P450 protein [Arabidopsis thaliana] gi|20259299|gb|AAM14385.1| putative cytochrome P450 protein [Arabidopsis thaliana] gi|46401564|dbj|BAD16629.1| cytochrome P450 monooxygenase [Arabidopsis thaliana] gi|332658762|gb|AEE84162.1| abscisic acid 8'-hydroxylase 1 [Arabidopsis thaliana]	467	467	0	100.0	92.7	96.1	abscisic acid 8'-hydroxylase 1	gbpln	Arabidopsis thaliana	AT4G19230.1 | Symbols: CYP707A1 | cytochrome P450, family 707, subfamily A, polypeptide 1 | chr4:10521524-10523517 FORWARD LENGTH=467	467	467	0	100.0	92.7	96.1
Rsa1.0_00107.1.g5287.t1	gb|EOA17520.1| hypothetical protein CARUB_v10005853mg [Capsella rubella]	180	180	3.00E-71	100.0	72.2	83.9	hypothetical protein CARUB_v10005853mg	gbpln	Capsella rubella	AT4G19350.1 | Symbols: EMB3006 | embryo defective 3006 | chr4:10562214-10563676 REVERSE LENGTH=180	180	180	1.00E-67	100.0	66.1	81.7
Rsa1.0_00107.1.g5288.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00107.1.g5289.t1	gb|AAM62450.1| unknown [Arabidopsis thaliana]	167	160	3.00E-53	95.8	61.7	74.9	unknown	gbpln	Arabidopsis thaliana	AT4G19430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10598606-10599088 REVERSE LENGTH=160	167	160	2.00E-54	95.8	60.5	73.7
Rsa1.0_00107.1.g5290.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00108.1.g5291.t1	gb|EOA15965.1| hypothetical protein CARUB_v10004060mg [Capsella rubella]	968	996	0	102.9	86.3	92.4	hypothetical protein CARUB_v10004060mg	gbpln	Capsella rubella	AT4G20270.1 | Symbols: BAM3 | Leucine-rich receptor-like protein kinase family protein | chr4:10949822-10952924 FORWARD LENGTH=992	968	992	0	102.5	85.0	91.4
Rsa1.0_00108.1.g5292.t1	ref|XP_002869942.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315778|gb|EFH46201.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	212	211	2.00E-68	99.5	77.8	83.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G20280.1 | Symbols: TAF11 | TBP-associated factor 11 | chr4:10953792-10954664 FORWARD LENGTH=210	212	210	1.00E-67	99.1	76.4	83.5
Rsa1.0_00108.1.g5293.t1	gb|EOA16922.1| hypothetical protein CARUB_v10005146mg [Capsella rubella]	160	352	9.00E-31	220.0	60.6	66.3	hypothetical protein CARUB_v10005146mg	gbpln	Capsella rubella	AT4G20300.2 | Symbols: | Protein of unknown function (DUF1639) | chr4:10955813-10958865 FORWARD LENGTH=352	160	352	8.00E-33	220.0	61.9	68.1
Rsa1.0_00108.1.g5294.t1	gb|AAM63055.1| unknown [Arabidopsis thaliana]	187	174	1.00E-74	93.0	79.7	85.0	unknown	gbpln	Arabidopsis thaliana	AT4G20300.2 | Symbols: | Protein of unknown function (DUF1639) | chr4:10955813-10958865 FORWARD LENGTH=352	187	352	7.00E-77	188.2	79.7	84.5
Rsa1.0_00108.1.g5295.t1	ref|NP_001154255.1| Peptidase M50 family protein [Arabidopsis thaliana] gi|332658903|gb|AEE84303.1| Peptidase M50 family protein [Arabidopsis thaliana]	513	488	0	95.1	76.8	83.0	Peptidase M50 family protein	gbpln	Arabidopsis thaliana	AT4G20310.2 | Symbols: | Peptidase M50 family protein | chr4:10961639-10963690 FORWARD LENGTH=488	513	488	0	95.1	76.8	83.0
Rsa1.0_00108.1.g5296.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00108.1.g5297.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00108.1.g5298.t1	ref|NP_001078412.2| ribonuclease H2 subunit B [Arabidopsis thaliana] gi|332658907|gb|AEE84307.1| ribonuclease H2 subunit B domain-containing protein [Arabidopsis thaliana]	498	277	1.00E-125	55.6	44.6	47.0	ribonuclease H2 subunit B	gbpln	Arabidopsis thaliana	AT4G20325.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleus; CONTAINS InterPro DOMAIN/s: Ribonuclease H2, subunit B (InterPro:IPR019024); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10980124-10982426 FORWARD LENGTH=277	498	277	1.00E-127	55.6	44.6	47.0
Rsa1.0_00108.1.g5299.t1	gb|EOA18090.1| hypothetical protein CARUB_v10006542mg [Capsella rubella]	472	480	0	101.7	94.1	95.3	hypothetical protein CARUB_v10006542mg	gbpln	Capsella rubella	AT4G20360.1 | Symbols: ATRAB8D, ATRABE1B, RABE1b | RAB GTPase homolog E1B | chr4:10990036-10991466 FORWARD LENGTH=476	472	476	0	100.8	92.4	94.7

Rsa1.0_00108.1.g5300.t7	gb|ADK63407.1| zinc finger protein [Brassica rapa]	307	191	2.00E-94	62.2	58.6	59.3	zinc finger protein	gbpln	Brassica rapa	AT4G20380.7 | Symbols: LSD1 | LSD1 zinc finger family protein | chr4:11005012-11006438 FORWARD LENGTH=189	307	189	7.00E-71	61.6	49.2	53.7
Rsa1.0_00108.1.g5301.t1	sp|Q56XW8.2|FBL30_ARATH RecName: Full=F-box/LRR-repeat protein At1g48400	439	487	1.00E-106	110.9	51.7	66.5	RecName: Full=F-box/LRR-repeat protein At1g48400	----	----	AT1G48390.1 | Symbols: | RNI-like superfamily protein | chr1:17879448-17880903 REVERSE LENGTH=413	439	413	2.00E-86	94.1	49.7	60.4
Rsa1.0_00108.1.g5302.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00108.1.g5303.t1	sp|Q56XW8.2|FBL30_ARATH RecName: Full=F-box/LRR-repeat protein At1g48400	491	487	1.00E-145	99.2	62.5	73.7	RecName: Full=F-box/LRR-repeat protein At1g48400	----	----	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	491	513	1.00E-147	104.5	62.1	73.3
Rsa1.0_00108.1.g5304.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00108.1.g5305.t1	ref|XP_002869932.1| transcription factor jumonji family protein [Arabidopsis lyrata subsp. lyrata] gi|297315768|gb|EFH46191.1| transcription factor jumonji family protein [Arabidopsis lyrata subsp. lyrata]	980	948	0	96.7	76.1	83.5	transcription factor jumonji family protein	gbpln	Arabidopsis lyrata	AT4G20400.1 | Symbols: JMJ14, PKDM7B | JUMONJI 14 | chr4:11009004-11013588 FORWARD LENGTH=954	980	954	0	97.3	75.8	82.7
Rsa1.0_00108.1.g5306.t1	gb|EOA17129.1| hypothetical protein CARUB_v10005391mg [Capsella rubella]	291	291	1.00E-160	100.0	94.2	98.3	hypothetical protein CARUB_v10005391mg	gbpln	Capsella rubella	AT4G20410.1 | Symbols: GSNAP, GAMMA-SNAP | gamma-soluble NSF attachment protein | chr4:11014099-11016454 REVERSE LENGTH=291	291	291	1.00E-162	100.0	93.8	97.9
Rsa1.0_00108.1.g5307.t1	gb|ABA00707.1| putative tapetum-specific A3 [Brassica napus]	140	139	1.00E-48	99.3	72.9	81.4	putative tapetum-specific A3	gbpln	Brassica napus	AT4G20420.1 | Symbols: | Tapetum specific protein TAP35/TAP44 | chr4:11017041-11017469 FORWARD LENGTH=142	140	142	4.00E-35	101.4	62.1	74.3
Rsa1.0_00108.1.g5308.t1	ref|XP_002867881.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313717|gb|EFH44140.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]	850	857	0	100.8	89.8	94.6	subtilase family protein	gbpln	Arabidopsis lyrata	AT4G20430.1 | Symbols: | Subtilase family protein | chr4:11017656-11021105 REVERSE LENGTH=856	850	856	0	100.7	89.1	93.5
Rsa1.0_00108.1.g5309.t1	dbj|BAD43836.1| unknown protein [Arabidopsis thaliana]	215	254	6.00E-70	118.1	74.0	76.7	unknown protein	gbpln	Arabidopsis thaliana	AT5G44500.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr5:17927505-17928269 FORWARD LENGTH=254	215	254	4.00E-69	118.1	72.1	74.9
Rsa1.0_00108.1.g5310.t1	ref|NP_193779.2| putative UDP-arabinose 4-epimerase 3 [Arabidopsis thaliana] gi|332278213|sp|Q9SUN3.3|ARAE3_ARATH RecName: Full=Probable UDP-arabinose 4-epimerase 3; AltName: Full=UDP-D-xylose 4-epimerase 3 gi|332658935|gb|AEE84335.1| putative UDP-arabinose 4-epimerase 3 [Arabidopsis thaliana]	607	411	0	67.7	62.9	64.3	putative UDP-arabinose 4-epimerase 3	gbpln	Arabidopsis thaliana	AT4G20460.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:11029767-11031765 REVERSE LENGTH=411	607	411	0	67.7	62.9	64.3
Rsa1.0_00108.1.g5311.t1	ref|NP_193806.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75211707|sp|Q9SVH3.1|PP328_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g20740 gi|5262214|emb|CAB45840.1| putative protein [Arabidopsis thaliana] gi|7268870|emb|CAB79074.1| putative protein [Arabidopsis thaliana] gi|332658957|gb|AEE84357.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	975	727	0	74.6	59.6	64.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G20740.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr4:11126151-11128334 FORWARD LENGTH=727	975	727	0	74.6	59.6	64.7
Rsa1.0_00108.1.g5312.t1	gb|EOA18794.1| hypothetical protein CARUB_v10007408mg [Capsella rubella]	770	770	0	100.0	79.5	87.0	hypothetical protein CARUB_v10007408mg	gbpln	Capsella rubella	AT4G20770.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:11130762-11133086 REVERSE LENGTH=774	770	774	0	100.5	80.1	87.7
Rsa1.0_00108.1.g5313.t1	ref|NP_193810.1| calcium-binding protein CML42 [Arabidopsis thaliana] gi|75337714|sp|Q9SVG9.1|CML42_ARATH RecName: Full=Calcium-binding protein CML42; AltName: Full=Calmodulin-like protein 42 gi|5262218|emb|CAB45844.1| calcium-binding protein-like [Arabidopsis thaliana] gi|7268874|emb|CAB79078.1| calcium-binding protein-like [Arabidopsis thaliana] gi|26450755|dbj|BAC42486.1| putative calcium-binding protein [Arabidopsis thaliana] gi|28372940|gb|AAO39952.1| At4g20780 [Arabidopsis thaliana] gi|332658960|gb|AEE84360.1| calcium-binding protein CML42 [Arabidopsis thaliana]	191	191	8.00E-81	100.0	82.7	89.5	calcium-binding protein CML42	gbpln	Arabidopsis thaliana	AT4G20780.1 | Symbols: CML42 | calmodulin like 42 | chr4:11133309-11133884 REVERSE LENGTH=191	191	191	3.00E-83	100.0	82.7	89.5

Rsa1.0_00108.1.g5314.t1	gb|EOA18285.1| hypothetical protein CARUB_v10006784mg [Capsella rubella]	523	519	0	99.2	77.2	86.4	hypothetical protein CARUB_v10006784mg	gbpln	Capsella rubella	AT4G20790.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:11134775-11136423 REVERSE LENGTH=518	523	518	0	99.0	79.7	88.3
Rsa1.0_00108.1.g5315.t1	ref|XP_002869926.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315762|gb|EFH46185.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	527	529	0	100.4	76.1	87.1	FAD-binding domain-containing protein	gbpln	Arabidopsis lyrata	AT4G20800.1 | Symbols: | FAD-binding Berberine family protein | chr4:11139656-11141242 FORWARD LENGTH=528	527	528	0	100.2	75.5	85.6
Rsa1.0_00108.1.g5316.t1	ref|XP_002869926.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315762|gb|EFH46185.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	527	529	0	100.4	78.0	86.0	FAD-binding domain-containing protein	gbpln	Arabidopsis lyrata	AT4G20800.1 | Symbols: | FAD-binding Berberine family protein | chr4:11139656-11141242 FORWARD LENGTH=528	527	528	0	100.2	77.2	85.6
Rsa1.0_00108.1.g5317.t1	ref|NP_193814.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana] gi|5262222|emb|CAB45848.1| reticuline oxidase-like protein [Arabidopsis thaliana] gi|7268878|emb|CAB79082.1| reticuline oxidase-like protein [Arabidopsis thaliana] gi|332658964|gb|AEE84364.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana]	534	532	0	99.6	85.8	93.8	FAD-binding and BBE domain-containing protein	gbpln	Arabidopsis thaliana	AT4G20820.1 | Symbols: | FAD-binding Berberine family protein | chr4:11150160-11151758 FORWARD LENGTH=532	534	532	0	99.6	85.8	93.8
Rsa1.0_00108.1.g5318.t1	gb|EOA18748.1| hypothetical protein CARUB_v10007331mg [Capsella rubella]	511	555	0	108.6	81.2	91.0	hypothetical protein CARUB_v10007331mg	gbpln	Capsella rubella	AT4G20840.1 | Symbols: | FAD-binding Berberine family protein | chr4:11157916-11159535 FORWARD LENGTH=539	511	539	0	105.5	80.0	90.2
Rsa1.0_00108.1.g5319.t1	gb|EOA18748.1| hypothetical protein CARUB_v10007331mg [Capsella rubella]	577	555	0	96.2	72.1	82.8	hypothetical protein CARUB_v10007331mg	gbpln	Capsella rubella	AT4G20840.1 | Symbols: | FAD-binding Berberine family protein | chr4:11157916-11159535 FORWARD LENGTH=539	577	539	0	93.4	68.3	78.0
Rsa1.0_00108.1.g5320.t25	gb|EOA15904.1| hypothetical protein CARUB_v10003995mg [Capsella rubella]	1292	1384	0	107.1	89.2	94.5	hypothetical protein CARUB_v10003995mg	gbpln	Capsella rubella	AT4G20850.1 | Symbols: TPP2 | tripeptidyl peptidase ii | chr4:11160935-11169889 REVERSE LENGTH=1380	1292	1380	0	106.8	87.3	92.5
Rsa1.0_00108.1.g5321.t1	gb|EOA18805.1| hypothetical protein CARUB_v10007418mg [Capsella rubella]	522	523	0	100.2	85.4	92.5	hypothetical protein CARUB_v10007418mg	gbpln	Capsella rubella	AT4G20860.1 | Symbols: | FAD-binding Berberine family protein | chr4:11172726-11174318 FORWARD LENGTH=530	522	530	0	101.5	83.3	90.8
Rsa1.0_00108.1.g5322.t2	gb|EOA17348.1| hypothetical protein CARUB_v10005630mg [Capsella rubella]	239	237	1.00E-127	99.2	92.9	97.1	hypothetical protein CARUB_v10005630mg	gbpln	Capsella rubella	AT4G20870.1 | Symbols: FAH2, ATFAH2 | fatty acid hydroxylase 2 | chr4:11174620-11175878 REVERSE LENGTH=237	239	237	1.00E-130	99.2	92.5	97.1
Rsa1.0_00108.1.g5323.t1	ref|NP_193820.1| ethylene-responsive/regulated nuclear protein [Arabidopsis thaliana] gi|5262778|emb|CAB45883.1| ethylene-regulated transcript 2 (ERT2) [Arabidopsis thaliana] gi|7268884|emb|CAB79088.1| ethylene-regulated transcript 2 (ERT2) [Arabidopsis thaliana] gi|26452095|dbj|BAC43137.1| putative ethylene-regulated transcript 2 ERT2 [Arabidopsis thaliana] gi|332658971|gb|AEE84371.1| ethylene-responsive/regulated nuclear protein [Arabidopsis thaliana]	419	405	7.00E-73	96.7	59.4	67.3	ethylene-responsive/regulated nuclear protein	gbpln	Arabidopsis thaliana	AT4G20880.1 | Symbols: | ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2) | chr4:11179389-11180606 REVERSE LENGTH=405	419	405	2.00E-75	96.7	59.4	67.3
Rsa1.0_00108.1.g5324.t1	gb|EOA16631.1| hypothetical protein CARUB_v10004805mg [Capsella rubella]	447	445	0	99.6	94.9	95.7	hypothetical protein CARUB_v10004805mg	gbpln	Capsella rubella	AT4G20890.1 | Symbols: TUB9 | tubulin beta-9 chain | chr4:11182218-11183840 FORWARD LENGTH=444	447	444	0	99.3	94.6	95.5
Rsa1.0_00108.1.g5325.t1	gb|AAL05056.1|AF411383_1 HEN1 [Arabidopsis thaliana]	935	942	0	100.7	78.9	87.8	HEN1	gbpln	Arabidopsis thaliana	AT4G20910.2 | Symbols: HEN1 | double-stranded RNA binding protein-related / DsRBD protein-related | chr4:11186264-11190575 REVERSE LENGTH=942	935	942	0	100.7	78.8	87.7
Rsa1.0_00108.1.g5326.t2	ref|XP_002867868.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313704|gb|EFH44127.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	674	854	0	126.7	63.6	73.6	predicted protein	gbpln	Arabidopsis lyrata	AT4G20920.1 | Symbols: | double-stranded RNA-binding domain (DsRBD)-containing protein | chr4:11194177-11197577 REVERSE LENGTH=743	674	743	0	110.2	63.4	73.0
Rsa1.0_00108.1.g5327.t1	ref|XP_002867868.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313704|gb|EFH44127.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	927	854	0	92.1	64.6	74.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G20910.2 | Symbols: HEN1 | double-stranded RNA binding protein-related / DsRBD protein-related | chr4:11186264-11190575 REVERSE LENGTH=942	927	942	0	101.6	63.9	75.1

Rsa1.0_00108.1.g5328.t1	sp|C0LGQ9.1|Y4294_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g20940 gi|224589622|gb|ACN59344.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	1051	1037	0	98.7	90.4	94.8	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g20940 gi|224589622|gb|ACN59344.1| leucine-rich repeat receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT4G20940.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr4:11202728-11206038 FORWARD LENGTH=977	1051	977	0	93.0	69.7	73.8
Rsa1.0_00108.1.g5329.t1	gb|EOA17462.1| hypothetical protein CARUB_v10005784mg, partial [Capsella rubella]	189	196	2.00E-74	103.7	77.8	87.8	hypothetical protein CARUB_v10005784mg, partial	gbpln	Capsella rubella	AT4G20970.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:11215259-11216212 FORWARD LENGTH=190	189	190	8.00E-72	100.5	77.2	86.8
Rsa1.0_00108.1.g5330.t1	ref|XP_002869915.1| carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315751|gb|EFH46174.1| carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata]	261	267	1.00E-106	102.3	69.0	80.8	carbonic anhydrase family protein	gbpln	Arabidopsis lyrata	AT4G20990.1 | Symbols: ATACA4, ACA4 | alpha carbonic anhydrase 4 | chr4:11219772-11221126 FORWARD LENGTH=267	261	267	1.00E-107	102.3	69.0	79.3
Rsa1.0_00108.1.g5331.t1	ref|NP_189230.1| F-box protein [Arabidopsis thaliana] gi|75274193|sp|Q9LU90.1|FB188_ARATH RecName: Full=F-box protein At3g26010 gi|9279606|dbj|BAB01064.1| unnamed protein product [Arabidopsis thaliana] gi|91806483|gb|ABE65969.1| F-box family protein [Arabidopsis thaliana] gi|332643580|gb|AEE77101.1| F-box protein [Arabidopsis thaliana]	419	414	1.00E-109	98.8	53.2	66.6	F-box protein	gbpln	Arabidopsis thaliana	AT3G26010.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:9511901-9513145 FORWARD LENGTH=414	419	414	1.00E-111	98.8	53.2	66.6
Rsa1.0_00108.1.g5332.t1	ref|NP_193834.1| late embryogenesis abundant domain-containing protein [Arabidopsis thaliana] gi|5262792|emb|CAB45897.1| putative protein [Arabidopsis thaliana] gi|7268899|emb|CAB79102.1| putative protein [Arabidopsis thaliana] gi|18176126|gb|AAL59988.1| unknown protein [Arabidopsis thaliana] gi|21436217|gb|AAM51396.1| unknown protein [Arabidopsis thaliana] gi|332658988|gb|AEE84388.1| late embryogenesis abundant domain-containing protein [Arabidopsis thaliana]	242	266	1.00E-102	109.9	83.5	91.7	late embryogenesis abundant domain-containing protein	gbpln	Arabidopsis thaliana	AT4G21020.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr4:11228263-11229392 FORWARD LENGTH=266	242	266	1.00E-105	109.9	83.5	91.7
Rsa1.0_00108.1.g5333.t1	#	#	#	#	#	#	#	–	––––	––––	AT5G15450.1 | Symbols: APG6, CLPB3, CLPB-P | casein lytic proteinase B3 | chr5:5014399-5018255 REVERSE LENGTH=968	75	968	9.00E-13	1290.7	44.0	53.3
Rsa1.0_00108.1.g5334.t1	ref|XP_002869911.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315747|gb|EFH46170.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	250	223	1.00E-61	89.2	53.2	64.0	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT4G21050.1 | Symbols: | Dof-type zinc finger domain-containing protein | chr4:11238441-11239073 FORWARD LENGTH=210	250	210	5.00E-58	84.0	46.4	55.6
Rsa1.0_00108.1.g5335.t1	ref|XP_002869911.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315747|gb|EFH46170.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	244	223	6.00E-56	91.4	50.4	62.7	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT4G21050.1 | Symbols: | Dof-type zinc finger domain-containing protein | chr4:11238441-11239073 FORWARD LENGTH=210	244	210	2.00E-52	86.1	43.9	54.9
Rsa1.0_00108.1.g5336.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	250	478	1.00E-71	191.2	50.0	68.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	250	746	3.00E-64	298.4	42.4	59.6
Rsa1.0_00108.1.g5337.t1	ref|XP_002869911.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315747|gb|EFH46170.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	250	223	9.00E-64	89.2	54.0	64.8	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT4G21050.1 | Symbols: | Dof-type zinc finger domain-containing protein | chr4:11238441-11239073 FORWARD LENGTH=210	250	210	4.00E-59	84.0	46.4	56.0
Rsa1.0_00108.1.g5338.t1	ref|XP_002869911.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315747|gb|EFH46170.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	221	223	2.00E-58	100.9	59.7	70.1	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT4G21050.1 | Symbols: | Dof-type zinc finger domain-containing protein | chr4:11238441-11239073 FORWARD LENGTH=210	221	210	5.00E-54	95.0	50.7	58.4

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<tr><td>Rsa1.0_00108.1.g5339.t1</td><td>ref|XP_002869910.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315746|gb|EFH46169.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>126</td><td>741</td><td>5.00E-20</td><td>588.1</td><td>40.5</td><td>42.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G21060.1 | Symbols: | Galactosyltransferase family protein | chr4:11240730-11244860 FORWARD LENGTH=741</td><td>126</td><td>741</td><td>3.00E-21</td><td>588.1</td><td>40.5</td><td>42.1</td></tr>
<tr><td>Rsa1.0_00108.1.g5340.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00108.1.g5341.t1</td><td>ref|NP_001154260.1| Galactosyltransferase family protein [Arabidopsis thaliana] gi|221271910|sp|A7XDQ9.1|B3GTK_ARATH RecName: Full=Probable beta-1,3-galactosyltransferase 20 gi|150026533|gb|ABR58857.1| putative galactosyltransferase [Arabidopsis thaliana] gi|332658993|gb|AEE84393.1| Galactosyltransferase family protein [Arabidopsis thaliana]</td><td>682</td><td>684</td><td>0</td><td>100.3</td><td>89.7</td><td>95.3</td><td>Galactosyltransferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G21060.2 | Symbols: | Galactosyltransferase family protein | chr4:11242003-11244860 FORWARD LENGTH=684</td><td>682</td><td>684</td><td>0</td><td>100.3</td><td>89.7</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00108.1.g5342.t1</td><td>emb|CAB45902.1| putative protein (fragment) [Arabidopsis thaliana] gi|7268904|emb|CAB79107.1| putative protein (fragment) [Arabidopsis thaliana]</td><td>1525</td><td>1495</td><td>0</td><td>98.0</td><td>74.5</td><td>82.7</td><td>putative protein (fragment)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G21070.1 | Symbols: ATBRCA1, BRCA1 | breast cancer susceptibility1 | chr4:11248174-11252633 FORWARD LENGTH=941</td><td>1525</td><td>941</td><td>0</td><td>61.7</td><td>44.7</td><td>50.9</td></tr>
<tr><td>Rsa1.0_00108.1.g5343.t1</td><td>ref|NP_193841.2| ferredoxin 2 [Arabidopsis thaliana] gi|30685306|ref|NP_849415.1| ferredoxin 2 [Arabidopsis thaliana] gi|79325201|ref|NP_001031685.1| ferredoxin 2 [Arabidopsis thaliana] gi|19698259|dbj|BAB86773.1| MFDX2 precursor [Arabidopsis thaliana] gi|28192429|gb|AAL82812.1| adrenodoxin-like ferredoxin 1 [Arabidopsis thaliana] gi|28466923|gb|AAO44070.1| At4g21090 [Arabidopsis thaliana] gi|110743957|dbj|BAE99811.1| mitochondrial ferredoxin [Arabidopsis thaliana] gi|222424373|dbj|BAH20142.1| AT4G21090 [Arabidopsis thaliana] gi|332658998|gb|AEE84398.1| ferredoxin 2 [Arabidopsis thaliana] gi|332658999|gb|AEE84399.1| ferredoxin 2 [Arabidopsis thaliana] gi|332659000|gb|AEE84400.1| ferredoxin 2 [Arabidopsis thaliana]</td><td>208</td><td>197</td><td>1.00E-87</td><td>94.7</td><td>81.3</td><td>85.6</td><td>ferredoxin 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G21090.3 | Symbols: ATMFDX2, MFDX2 | MITOCHONDRIAL FERREDOXIN 2 | chr4:11256663-11258269 REVERSE LENGTH=197</td><td>208</td><td>197</td><td>5.00E-90</td><td>94.7</td><td>81.3</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00108.1.g5344.t1</td><td>gb|EOA18805.1| hypothetical protein CARUB_v10007418mg [Capsella rubella]</td><td>520</td><td>523</td><td>0</td><td>100.6</td><td>83.3</td><td>91.5</td><td>hypothetical protein CARUB_v10007418mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G20860.1 | Symbols: | FAD-binding Berberine family protein | chr4:11172726-11174318 FORWARD LENGTH=530</td><td>520</td><td>530</td><td>0</td><td>101.9</td><td>82.1</td><td>90.8</td></tr>
<tr><td>Rsa1.0_00108.1.g5345.t1</td><td>gb|EOA17579.1| hypothetical protein CARUB_v10005939mg [Capsella rubella]</td><td>145</td><td>145</td><td>9.00E-78</td><td>100.0</td><td>95.9</td><td>98.6</td><td>hypothetical protein CARUB_v10005939mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G21110.1 | Symbols: | G10 family protein | chr4:11267673-11268774 FORWARD LENGTH=145</td><td>145</td><td>145</td><td>2.00E-79</td><td>100.0</td><td>94.5</td><td>97.9</td></tr>
<tr><td>Rsa1.0_00108.1.g5346.t1</td><td>ref|XP_002867862.1| hypothetical protein ARALYDRAFT_492773 [Arabidopsis lyrata subsp. lyrata] gi|297313698|gb|EFH44121.1| hypothetical protein ARALYDRAFT_492773 [Arabidopsis lyrata subsp. lyrata]</td><td>241</td><td>246</td><td>4.00E-85</td><td>102.1</td><td>73.0</td><td>81.7</td><td>hypothetical protein ARALYDRAFT_492773</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G21140.1 | Symbols: | BEST Arabidopsis thaliana protein match is: copper ion binding (TAIR:AT4G05400.2); Has 41 Blast hits to 41 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr4:11277491-11278222 REVERSE LENGTH=243</td><td>241</td><td>243</td><td>3.00E-86</td><td>100.8</td><td>73.4</td><td>83.4</td></tr>
<tr><td>Rsa1.0_00108.1.g5347.t1</td><td>ref|NP_193847.2| ribophorin II (RPN2) family protein [Arabidopsis thaliana] gi|334186764|ref|NP_001190785.1| ribophorin II (RPN2) family protein [Arabidopsis thaliana] gi|75163691|sp|Q93Z16.1|RPN2_ARATH RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Protein HAPLESS 6; AltName: Full=Ribophorin II; Short=RPN-II; AltName: Full=Ribophorin-2; Flags: Precursor gi|16604454|gb|AAL24233.1| AT4g21150/F7J7_90 [Arabidopsis thaliana] gi|18958022|gb|AAL79584.1| AT4g21150/F7J7_90 [Arabidopsis thaliana] gi|332659008|gb|AEE84408.1| ribophorin II (RPN2) family protein [Arabidopsis thaliana] gi|332659010|gb|AEE84410.1| ribophorin II (RPN2) family protein [Arabidopsis thaliana]</td><td>684</td><td>691</td><td>0</td><td>101.0</td><td>89.8</td><td>94.9</td><td>ribophorin II (RPN2) family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G21150.3 | Symbols: HAP6 | ribophorin II (RPN2) family protein | chr4:11278646-11283599 FORWARD LENGTH=691</td><td>684</td><td>691</td><td>0</td><td>101.0</td><td>89.8</td><td>94.9</td></tr>
</table>

Rsa1.0_00108.1.g5348.t1	ref|XP_002869903.1| zac [Arabidopsis lyrata subsp. lyrata] gi|297315739|gb|EFH46162.1| zac [Arabidopsis lyrata subsp. lyrata]	312	332	1.00E-159	106.4	88.8	94.2	zac	gbpln	Arabidopsis lyrata	AT4G21160.4 | Symbols: ZAC | Calcium-dependent ARF-type GTPase activating protein family | chr4:11284694-11286532 FORWARD LENGTH=337	312	337	1.00E-160	108.0	87.8	94.2
Rsa1.0_00108.1.g5349.t1	sp|O49558.2|PP331_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g21170	580	585	0	100.9	76.9	84.3	RecName: Full=Pentatricopeptide repeat-containing protein At4g21170	----	----	AT4G21170.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:11286756-11288513 REVERSE LENGTH=551	580	551	0	95.0	69.7	77.2
Rsa1.0_00108.1.g5350.t1	ref|XP_002869902.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315738|gb|EFH46161.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	665	662	0	99.5	83.3	91.3	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT4G21180.1 | Symbols: ATERDJ2B | DnaJ / Sec63 Brl domains-containing protein | chr4:11289337-11292179 FORWARD LENGTH=661	665	661	0	99.4	82.7	90.1
Rsa1.0_00108.1.g5351.t1	ref|XP_002867860.1| EMB1417 [Arabidopsis lyrata subsp. lyrata] gi|297313696|gb|EFH44119.1| EMB1417 [Arabidopsis lyrata subsp. lyrata]	310	317	1.00E-150	102.3	91.6	94.8	EMB1417	gbpln	Arabidopsis lyrata	AT4G21190.1 | Symbols: emb1417 | Pentatricopeptide repeat (PPR) superfamily protein | chr4:11292493-11293763 REVERSE LENGTH=307	310	307	2.33E-156	99.0	87.1	90.6
Rsa1.0_00108.1.g5352.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00108.1.g5353.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00108.1.g5354.t2	ref|XP_002869899.1| phosphoprotein phosphatase/ protein kinase [Arabidopsis lyrata subsp. lyrata] gi|297315735|gb|EFH46158.1| phosphoprotein phosphatase/ protein kinase [Arabidopsis lyrata subsp. lyrata]	571	403	0	70.6	58.8	62.0	phosphoprotein phosphatase/ protein kinase	gbpln	Arabidopsis lyrata	AT4G21210.1 | Symbols: ATRP1, RP1 | PPDK regulatory protein | chr4:11307002-11308587 FORWARD LENGTH=403	571	403	0	70.6	58.3	62.2
Rsa1.0_00108.1.g5355.t2	ref|NP_974583.1| uncharacterized protein [Arabidopsis thaliana] gi|222423130|dbj|BAH19544.1| AT4G21215 [Arabidopsis thaliana] gi|332659027|gb|AEE84427.1| uncharacterized protein AT4G21215 [Arabidopsis thaliana]	200	199	4.00E-82	99.5	82.0	90.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G21215.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:11310890-11313421 REVERSE LENGTH=199	200	199	1.00E-84	99.5	82.0	90.5
Rsa1.0_00108.1.g5356.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	343	1555	1.00E-31	453.4	28.9	44.9	disease resistance protein	gbpln	Brassica rapa	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	343	303	2.00E-29	88.3	25.7	39.1
Rsa1.0_00108.1.g5357.t1	ref|XP_002867857.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313693|gb|EFH44116.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	640	642	0	100.3	82.8	90.2	kinase family protein	gbpln	Arabidopsis lyrata	AT4G21230.1 | Symbols: CRK27 | cysteine-rich RLK (RECEPTOR-like protein kinase) 27 | chr4:11319244-11321679 REVERSE LENGTH=642	640	642	0	100.3	82.0	88.9
Rsa1.0_00108.1.g5358.t1	ref|NP_566724.1| putative E3 ubiquitin-protein ligase XBAT35 [Arabidopsis thaliana] gi|122233562|sp|Q4FE47.1|XB35_ARATH RecName: Full=Putative E3 ubiquitin-protein ligase XBAT35; AltName: Full=Ankyrin repeat domain and RING finger-containing protein XBAT35; AltName: Full=Protein XB3 homolog 5 gi|70905085|gb|AAZ14068.1| At3g23280 [Arabidopsis thaliana] gi|332643225|gb|AEE76746.1| putative E3 ubiquitin-protein ligase XBAT35 [Arabidopsis thaliana]	435	462	1.00E-151	106.2	66.7	79.1	putative E3 ubiquitin-protein ligase XBAT35	gbpln	Arabidopsis thaliana	AT3G23280.1 | Symbols: XBAT35 | XB3 ortholog 5 in Arabidopsis thaliana | chr3:8321588-8324109 FORWARD LENGTH=462	435	462	1.00E-153	106.2	66.7	79.1
Rsa1.0_00108.1.g5359.t1	gb|EOA20168.1| hypothetical protein CARUB_v10000461mg [Capsella rubella]	623	626	0	100.5	86.4	91.2	hypothetical protein CARUB_v10000461mg	gbpln	Capsella rubella	AT5G16590.1 | Symbols: LRR1 | Leucine-rich repeat protein kinase family protein | chr5:5431862-5433921 FORWARD LENGTH=625	623	625	0	100.3	86.5	91.3
Rsa1.0_00108.1.g5360.t1	ref|XP_002871726.1| hypothetical protein ARALYDRAFT_909643 [Arabidopsis lyrata subsp. lyrata] gi|297317563|gb|EFH47985.1| hypothetical protein ARALYDRAFT_909643 [Arabidopsis lyrata subsp. lyrata]	313	320	1.00E-122	102.2	78.0	86.9	hypothetical protein ARALYDRAFT_909643	gbpln	Arabidopsis lyrata	AT5G16600.1 | Symbols: MYB43, AtMYB43 | myb domain protein 43 | chr5:5438291-5440214 FORWARD LENGTH=327	313	327	1.00E-125	104.5	79.6	88.5
Rsa1.0_00108.1.g5361.t1	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	660	1044	0	158.2	49.2	61.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	660	626	8.00E-28	94.8	11.1	17.9
Rsa1.0_00108.1.g5362.t1	gb|AAM64808.1| myb-related protein M4 [Arabidopsis thaliana]	352	350	1.00E-153	99.4	81.5	87.5	myb-related protein M4	gbpln	Arabidopsis thaliana	AT4G21440.1 | Symbols: ATMYB102, ATM4, MYB102 | MYB-like 102 | chr4:11418425-11419652 REVERSE LENGTH=350	352	350	1.00E-155	99.4	81.3	87.5
Rsa1.0_00108.1.g5363.t1	gb|EOA16902.1| hypothetical protein CARUB_v10005126mg, partial [Capsella rubella]	293	357	1.00E-143	121.8	90.8	94.2	hypothetical protein CARUB_v10005126mg, partial	gbpln	Capsella rubella	AT4G21450.1 | Symbols: | PapD-like superfamily protein | chr4:11426136-11428125 FORWARD LENGTH=295	293	295	1.00E-144	100.7	91.5	94.5

Rsa1.0_00108.1.g5364.t1	ref|XP_002869885.1| ATFMN [Arabidopsis lyrata subsp. lyrata] gi|297315721|gb|EFH46144.1| ATFMN [Arabidopsis lyrata subsp. lyrata]	381	380	0	99.7	92.9	96.6	ATFMN	gbpln	Arabidopsis lyrata	AT4G21470.1 | Symbols: ATFMN/FHY, FMN/FHY | riboflavin kinase/FMN hydrolase | chr4:11431284-11433197 FORWARD LENGTH=379	381	379	0	99.5	92.1	95.8
Rsa1.0_00108.1.g5365.t1	ref|XP_002867843.1| hypothetical protein ARALYDRAFT_914525 [Arabidopsis lyrata subsp. lyrata] gi|297313679|gb|EFH44102.1| hypothetical protein ARALYDRAFT_914525 [Arabidopsis lyrata subsp. lyrata]	234	222	3.00E-39	94.9	56.0	66.7	hypothetical protein ARALYDRAFT_914525	gbpln	Arabidopsis lyrata	AT4G21500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G05018.1); Has 20 Blast hits to 20 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr4:11441065-11441712 REVERSE LENGTH=215	234	215	1.00E-41	91.9	55.1	63.7
Rsa1.0_00108.1.g5366.t1	emb|CAA18501.1| Calcium-dependent serine/threonine protein kinase [Arabidopsis thaliana] gi|7270559|emb|CAB81516.1| Calcium-dependent serine/threonine protein kinase [Arabidopsis thaliana]	180	536	1.00E-26	297.8	37.2	45.6	Calcium-dependent serine/threonine protein kinase	gbpln	Arabidopsis thaliana	AT4G36070.1 | Symbols: CPK18 | calcium-dependent protein kinase 18 | chr4:17056907-17059595 REVERSE LENGTH=534	180	534	5.00E-28	296.7	36.1	43.3
Rsa1.0_00108.1.g5367.t1	gb|EOA16671.1| hypothetical protein CARUB_v10004860mg [Capsella rubella]	648	429	0	66.2	59.6	62.0	hypothetical protein CARUB_v10004860mg	gbpln	Capsella rubella	AT4G21520.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:11447514-11450377 REVERSE LENGTH=425	648	425	0	65.6	59.3	62.5
Rsa1.0_00108.1.g5368.t4	gb|EOA18651.1| hypothetical protein CARUB_v10007227mg [Capsella rubella]	821	777	0	94.6	81.2	86.4	hypothetical protein CARUB_v10007227mg	gbpln	Capsella rubella	AT4G21530.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:11450743-11455862 FORWARD LENGTH=777	821	777	0	94.6	81.6	87.2
Rsa1.0_00108.1.g5369.t1	gb|EOA16060.1| hypothetical protein CARUB_v10004192mg, partial [Capsella rubella]	765	776	0	101.4	59.5	69.0	hypothetical protein CARUB_v10004192mg, partial	gbpln	Capsella rubella	AT4G21550.1 | Symbols: VAL3 | VP1/ABI3-like 3 | chr4:11463104-11468486 FORWARD LENGTH=713	765	713	0	93.2	58.0	67.1
Rsa1.0_00108.1.g5370.t1	dbj|BAJ33668.1| unnamed protein product [Thellungiella halophila]	185	209	4.00E-95	113.0	95.1	97.3	unnamed protein product	----	----	AT4G21560.3 | Symbols: VPS28-1 | vacuolar protein sorting-associated protein 28 homolog 1 | chr4:11469037-11469666 REVERSE LENGTH=209	185	209	1.00E-96	113.0	94.1	97.3
Rsa1.0_00108.1.g5371.t1	dbj|BAJ34582.1| unnamed protein product [Thellungiella halophila]	294	294	1.00E-162	100.0	96.3	97.6	unnamed protein product	----	----	AT4G21570.1 | Symbols: | Protein of unknown function (DUF300) | chr4:11471126-11472269 REVERSE LENGTH=294	294	294	1.00E-159	100.0	91.5	95.6
Rsa1.0_00108.1.g5372.t1	sp|Q9SVX4.1|FB205_ARATH RecName: Full=F-box protein At3g57590 gi|4678288|emb|CAB41196.1| putative protein [Arabidopsis thaliana]	439	404	9.00E-78	92.0	42.1	54.0	RecName: Full=F-box protein At3g57590 gi|4678288|emb|CAB41196.1| putative protein	gbpln	Arabidopsis thaliana	AT3G57590.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:21330182-21331396 REVERSE LENGTH=404	439	404	4.00E-80	92.0	41.9	54.0
Rsa1.0_00108.1.g5373.t1	gb|EOA32879.1| hypothetical protein CARUB_v10016194mg [Capsella rubella]	388	431	4.00E-66	111.1	45.4	58.8	hypothetical protein CARUB_v10016194mg	gbpln	Capsella rubella	AT5G42430.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:16971312-16972499 REVERSE LENGTH=395	388	395	2.00E-71	101.8	45.6	58.0
Rsa1.0_00108.1.g5374.t1	ref|XP_002866486.1| BCL-2-associated athanogene 7 [Arabidopsis lyrata subsp. lyrata] gi|297312321|gb|EFH42745.1| BCL-2-associated athanogene 7 [Arabidopsis lyrata subsp. lyrata]	444	447	1.00E-158	100.7	73.9	84.2	BCL-2-associated athanogene 7	gbpln	Arabidopsis lyrata	AT5G62390.1 | Symbols: ATBAG7, BAG7 | BCL-2-associated athanogene 7 | chr5:25052377-25054170 REVERSE LENGTH=446	444	446	1.00E-158	100.5	72.5	84.0
Rsa1.0_00108.1.g5375.t1	gb|EOA16997.1| hypothetical protein CARUB_v10005235mg [Capsella rubella]	326	325	1.00E-169	99.7	91.7	94.8	hypothetical protein CARUB_v10005235mg	gbpln	Capsella rubella	AT4G21580.1 | Symbols: | oxidoreductase, zinc-binding dehydrogenase family protein | chr4:11475822-11477514 FORWARD LENGTH=325	326	325	1.00E-170	99.7	90.8	94.5
Rsa1.0_00108.1.g5376.t1	ref|XP_002869881.1| hypothetical protein ARALYDRAFT_492719 [Arabidopsis lyrata subsp. lyrata] gi|297315717|gb|EFH46140.1| hypothetical protein ARALYDRAFT_492719 [Arabidopsis lyrata subsp. lyrata]	307	299	1.00E-164	97.4	90.6	93.2	hypothetical protein ARALYDRAFT_492719	gbpln	Arabidopsis lyrata	AT4G21585.1 | Symbols: ENDO4 | endonuclease 4 | chr4:11477988-11479953 FORWARD LENGTH=299	307	299	1.00E-164	97.4	89.3	93.2
Rsa1.0_00108.1.g5377.t1	gb|EOA37991.1| hypothetical protein CARUB_v10009460mg [Capsella rubella]	374	377	1.00E-116	100.8	59.1	72.5	hypothetical protein CARUB_v10009460mg	gbpln	Capsella rubella	AT1G11270.2 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3785715-3786653 REVERSE LENGTH=312	374	312	1.00E-89	83.4	46.0	54.5
Rsa1.0_00108.1.g5378.t1	ref|NP_567633.2| Subtilase family protein [Arabidopsis thaliana] gi|27311663|gb|AAO00797.1| subtilisin proteinase - like [Arabidopsis thaliana] gi|332659085|gb|AEE84485.1| Subtilase family protein [Arabidopsis thaliana]	271	766	1.00E-120	282.7	80.8	87.8	Subtilase family protein	gbpln	Arabidopsis thaliana	AT4G21650.1 | Symbols: | Subtilase family protein | chr4:11501314-11504656 REVERSE LENGTH=766	271	766	1.00E-122	282.7	80.8	87.8
Rsa1.0_00109.1.g5379.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00109.1.g5380.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	368	940	5.00E-51	255.4	27.4	35.3	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5381.t5	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1399	940	6.00E-55	67.2	7.0	9.6	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5382.t1	ref|NP_179121.1| CCHC-type zinc knuckle protein [Arabidopsis thaliana] gi|4585917|gb|AAD25578.1| hypothetical protein [Arabidopsis thaliana] gi|330251280|gb|AEC06374.1| CCHC-type zinc knuckle protein [Arabidopsis thaliana]	459	474	2.00E-14	103.3	21.8	33.3	CCHC-type zinc knuckle protein	gbpln	Arabidopsis thaliana	AT2G15180.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:6588743-6590167 REVERSE LENGTH=474	459	474	4.00E-17	103.3	21.8	33.3
Rsa1.0_00109.1.g5383.t3	gb|ABD65084.1| hypothetical protein 27.t00096 [Brassica oleracea]	338	645	2.00E-38	190.8	37.6	51.5	hypothetical protein 27.t00096	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5384.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5385.t3	ref|NP_850114.1| FER-LIKE IRON DEFICIENCY-INDUCED transcription factor [Arabidopsis thaliana] gi|122242304|sp|Q0V7X4.1|FIT_ARATH RecName: Full=Transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR; AltName: Full=Basic helix-loop-helix protein 29; Short=AtbHLH29; Short=bHLH 29; AltName: Full=FER-LIKE REGULATOR OF IRON UPTAKE; AltName: Full=Transcription factor EN 43; AltName: Full=Transcription factor Fe-DEFICIENCY INDUCED TRANSCRIPTION FACTOR 1; AltName: Full=bHLH transcription factor bHLH029 gi|111074360|gb|ABH04553.1| At2g28160 [Arabidopsis thaliana] gi|225898152|dbj|BAH30406.1| hypothetical protein [Arabidopsis thaliana] gi|330252992|gb|AEC08086.1| FER-LIKE IRON DEFICIENCY-INDUCED transcription factor [Arabidopsis thaliana]	387	318	1.00E-145	82.2	67.4	73.9	FER-LIKE IRON DEFICIENCY-INDUCED transcription factor	gbpln	Arabidopsis thaliana	AT2G28160.1 | Symbols: FIT1, ATBHLH029, FRU, BHLH029, ATBHLH29, ATFIT1 | FER-like regulator of iron uptake | chr2:12004713-12005908 FORWARD LENGTH=318	387	318	1.00E-147	82.2	67.4	73.9
Rsa1.0_00109.1.g5386.t2	gb|ABW81058.1| atlantys transposase [Arabidopsis lyrata subsp. lyrata]	535	777	3.00E-18	145.2	9.2	14.6	atlantys transposase	gbpln	Arabidopsis lyrata	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	535	681	1.00E-18	127.3	7.5	13.1
Rsa1.0_00109.1.g5387.t1	sp|P21239.2|RUB1_BRANA RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor gi|289365|gb|AAA32979.1| 60-kDa chaperonin-60 alpha-polypeptide precursor, partial [Brassica napus]	616	546	0	88.6	85.6	86.4	RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor gi|289365|gb|AAA32979.1| 60-kDa chaperonin-60 alpha-polypeptide precursor, partial	gbpln	Brassica napus	AT2G28000.1 | Symbols: CPN60A, CH-CPN60A, SLP | chaperonin-60alpha | chr2:11926603-11929184 FORWARD LENGTH=586	616	586	0	95.1	81.3	84.1

Rsa1.0_00109.1.g5388.t1	gb|EOA28660.1| hypothetical protein CARUB_v10024882mg [Capsella rubella]	1142	1133	0	99.2	86.7	91.7	hypothetical protein CARUB_v10024882mg	gbpln	Capsella rubella	AT2G27900.2 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2451, C-terminal (InterPro:IPR019514), Vacuolar protein sorting-associated protein 54 (InterPro:IPR019515); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:11877654-11885238 FORWARD LENGTH=1124	1142	1124	0	98.4	86.7	91.3
Rsa1.0_00109.1.g5389.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5390.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5391.t1	ref|XP_002887565.1| hypothetical protein ARALYDRAFT_895360 [Arabidopsis lyrata subsp. lyrata] gi|297333406|gb|EFH63824.1| hypothetical protein ARALYDRAFT_895360 [Arabidopsis lyrata subsp. lyrata]	275	254	3.00E-92	92.4	68.0	76.4	hypothetical protein ARALYDRAFT_895360	gbpln	Arabidopsis lyrata	AT1G45063.2 | Symbols: | copper ion binding;electron carriers | chr1:17034068-17034886 REVERSE LENGTH=272	275	272	2.00E-87	98.9	61.5	73.8
Rsa1.0_00109.1.g5392.t2	ref|NP_180328.1| vacuolar protein-sorting-associated protein 4 [Arabidopsis thaliana] gi|13605797|gb|AAK32884.1|AF367297_1 F10A12.27/F10A12.27 [Arabidopsis thaliana] gi|3860272|gb|AAC73040.1| putative ATPase [Arabidopsis thaliana] gi|20147133|gb|AAM10283.1| F10A12.27/F10A12.27 [Arabidopsis thaliana] gi|20197659|gb|AAM15184.1| putative ATPase [Arabidopsis thaliana] gi|330252925|gb|AEC08019.1| suppressor of K+ transport growth defect1 protein [Arabidopsis thaliana]	437	435	0	99.5	94.3	95.9	vacuolar protein-sorting-associated protein 4	gbpln	Arabidopsis thaliana	AT2G27600.1 | Symbols: SKD1, VPS4, ATSKD1 | AAA-type ATPase family protein | chr2:11781226-11783730 FORWARD LENGTH=435	437	435	0	99.5	94.3	95.9
Rsa1.0_00109.1.g5393.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	300	1365	8.00E-49	455.0	35.7	49.7	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	ATMG01250.1 | Symbols: ORF102 | RNA-directed DNA polymerase (reverse transcriptase) | chrM:310514-310882 FORWARD LENGTH=122	300	122	4.00E-11	40.7	9.7	13.7
Rsa1.0_00109.1.g5394.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	479	1142	3.00E-73	238.4	39.7	57.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	479	575	1.00E-28	120.0	27.3	45.7
Rsa1.0_00109.1.g5395.t1	ref|XP_002878119.1| hypothetical protein ARALYDRAFT_907145 [Arabidopsis lyrata subsp. lyrata] gi|297822539|ref|XP_002879152.1| hypothetical protein ARALYDRAFT_901778 [Arabidopsis lyrata subsp. lyrata] gi|297323957|gb|EFH54378.1| hypothetical protein ARALYDRAFT_907145 [Arabidopsis lyrata subsp. lyrata] gi|297324991|gb|EFH55411.1| hypothetical protein ARALYDRAFT_901778 [Arabidopsis lyrata subsp. lyrata]	164	163	3.00E-60	99.4	73.2	85.4	hypothetical protein ARALYDRAFT_907145	gbpln	Arabidopsis lyrata	AT2G27580.2 | Symbols: | A20/AN1-like zinc finger family protein | chr2:11776640-11777131 REVERSE LENGTH=163	164	163	2.00E-59	99.4	73.8	85.4
Rsa1.0_00109.1.g5396.t9	emb|CAN66330.1| hypothetical protein VITISV_000598 [Vitis vinifera]	459	2691	8.00E-45	586.3	25.7	32.7	hypothetical protein VITISV_000598	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5397.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5398.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	657	1024	2.00E-61	155.9	24.4	36.4	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5399.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5400.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5401.t1	dbj|BAB11196.1| mutator-like transposase [Arabidopsis thaliana]	685	797	1.00E-107	116.4	38.8	57.4	mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00109.1.g5402.t6	gb|ABD65085.1| Ulp1 protease family protein [Brassica oleracea]	675	640	6.00E-42	94.8	21.5	30.2	Ulp1 protease family protein	gbpln	Brassica oleracea	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	675	921	5.00E-11	136.4	9.9	15.7
Rsa1.0_00110.1.g5403.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00110.1.g5404.t1	ref|XP_002884836.1| CPRD49 [Arabidopsis lyrata subsp. lyrata] gi|297330676|gb|EFH61095.1| CPRD49 [Arabidopsis lyrata subsp. lyrata]	256	256	1.00E-140	100.0	92.6	96.9	CPRD49	gbpln	Arabidopsis lyrata	AT3G11210.1 | Symbols: | SGNH hydrolase-type esterase superfamily protein | chr3:3511101-3512899 REVERSE LENGTH=256	256	256	1.00E-137	100.0	89.1	95.3
Rsa1.0_00110.1.g5405.t1	gb|EOA31316.1| hypothetical protein CARUB_v10014489mg [Capsella rubella]	248	246	1.00E-116	99.2	92.7	94.8	hypothetical protein CARUB_v10014489mg	gbpln	Capsella rubella	AT3G11200.1 | Symbols: AL2 | alfin-like 2 | chr3:3508387-3510418 REVERSE LENGTH=246	248	246	1.00E-111	99.2	91.5	95.2

<table>
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<tr><td>Rsa1.0_00110.1.g5407.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00110.1.g5408.t1</td><td>ref|XP_002884832.1| hypothetical protein ARALYDRAFT_478455 [Arabidopsis lyrata subsp. lyrata] gi|297330672|gb|EFH61091.1| hypothetical protein ARALYDRAFT_478455 [Arabidopsis lyrata subsp. lyrata]</td><td>345</td><td>375</td><td>1.00E-131</td><td>108.7</td><td>73.6</td><td>84.1</td><td>hypothetical protein ARALYDRAFT_478455</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11150.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:3492986-3494599 REVERSE LENGTH=371</td><td>345</td><td>371</td><td>1.00E-127</td><td>107.5</td><td>71.6</td><td>81.2</td></tr>
<tr><td>Rsa1.0_00110.1.g5409.t1</td><td>ref|XP_002884831.1| hypothetical protein ARALYDRAFT_478454 [Arabidopsis lyrata subsp. lyrata] gi|297330671|gb|EFH61090.1| hypothetical protein ARALYDRAFT_478454 [Arabidopsis lyrata subsp. lyrata]</td><td>1687</td><td>1702</td><td>0</td><td>100.9</td><td>95.3</td><td>96.4</td><td>hypothetical protein ARALYDRAFT_478454</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11130.1 | Symbols: | Clathrin, heavy chain | chr3:3482575-3491667 REVERSE LENGTH=1705</td><td>1687</td><td>1705</td><td>0</td><td>101.1</td><td>95.3</td><td>96.2</td></tr>
<tr><td>Rsa1.0_00110.1.g5410.t1</td><td>dbj|BAJ34637.1| unnamed protein product [Thellungiella halophila]</td><td>258</td><td>250</td><td>2.00E-96</td><td>96.9</td><td>79.5</td><td>88.4</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G11100.1 | Symbols: | sequence-specific DNA binding transcription factors | chr3:3476490-3477320 REVERSE LENGTH=249</td><td>258</td><td>249</td><td>2.00E-93</td><td>96.5</td><td>76.0</td><td>85.3</td></tr>
<tr><td>Rsa1.0_00110.1.g5411.t1</td><td>dbj|BAE98403.1| putative non-LTR reverse transcriptase [Arabidopsis thaliana]</td><td>160</td><td>278</td><td>1.00E-34</td><td>173.8</td><td>43.8</td><td>63.1</td><td>putative non-LTR reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332</td><td>160</td><td>332</td><td>1.00E-17</td><td>207.5</td><td>30.6</td><td>44.4</td></tr>
<tr><td>Rsa1.0_00110.1.g5412.t1</td><td>ref|NP_187719.1| receptor like protein 35 [Arabidopsis thaliana] gi|6016687|gb|AAF01514.1|AC009991_10 putative disease resistance protein [Arabidopsis thaliana] gi|12321885|gb|AAG50981.1|AC073395_23 disease resistance protein, putative; 7647-10478 [Arabidopsis thaliana] gi|332641479|gb|AEE75000.1| receptor like protein 35 [Arabidopsis thaliana]</td><td>523</td><td>943</td><td>1.00E-161</td><td>180.3</td><td>63.7</td><td>72.8</td><td>receptor like protein 35</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G11080.1 | Symbols: AtRLP35, RLP35 | receptor like protein 35 | chr3:3470481-3473312 FORWARD LENGTH=943</td><td>523</td><td>943</td><td>1.00E-164</td><td>180.3</td><td>63.7</td><td>72.8</td></tr>
<tr><td>Rsa1.0_00110.1.g5413.t1</td><td>gb|EOA29966.1| hypothetical protein CARUB_v10013078mg [Capsella rubella]</td><td>680</td><td>710</td><td>0</td><td>104.4</td><td>82.4</td><td>89.7</td><td>hypothetical protein CARUB_v10013078mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G11040.1 | Symbols: | Glycosyl hydrolase family 85 | chr3:3460143-3463312 FORWARD LENGTH=701</td><td>680</td><td>701</td><td>0</td><td>103.1</td><td>83.2</td><td>89.9</td></tr>
<tr><td>Rsa1.0_00110.1.g5414.t1</td><td>gb|ABV08790.1| DREB2B [Eutrema halophilum]</td><td>288</td><td>316</td><td>8.00E-86</td><td>109.7</td><td>68.4</td><td>80.6</td><td>DREB2B</td><td>gbpln</td><td>Eutrema halophilum</td><td>AT3G11020.1 | Symbols: DREB2B, DREB2 | DRE/CRT-binding protein 2B | chr3:3456009-3457001 FORWARD LENGTH=330</td><td>288</td><td>330</td><td>7.00E-78</td><td>114.6</td><td>62.8</td><td>77.8</td></tr>
<tr><td>Rsa1.0_00110.1.g5415.t1</td><td>gb|EOA29651.1| hypothetical protein CARUB_v10015153mg [Capsella rubella]</td><td>467</td><td>478</td><td>1.00E-167</td><td>102.4</td><td>67.5</td><td>76.4</td><td>hypothetical protein CARUB_v10015153mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G11000.1 | Symbols: | DCD (Development and Cell Death) domain protein | chr3:3448442-3450283 FORWARD LENGTH=488</td><td>467</td><td>488</td><td>1.00E-158</td><td>104.5</td><td>64.2</td><td>74.5</td></tr>
<tr><td>Rsa1.0_00110.1.g5416.t1</td><td>gb|EOA32919.1| hypothetical protein CARUB_v10016246mg, partial [Capsella rubella]</td><td>104</td><td>161</td><td>1.00E-42</td><td>154.8</td><td>89.4</td><td>93.3</td><td>hypothetical protein CARUB_v10016246mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G10985.1 | Symbols: SAG20, WI12, ATWI-12 | senescence associated gene 20 | chr3:3442776-3443108 FORWARD LENGTH=110</td><td>104</td><td>110</td><td>1.00E-41</td><td>105.8</td><td>86.5</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00110.1.g5417.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00110.1.g5418.t1</td><td>emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]</td><td>1527</td><td>1489</td><td>0</td><td>97.5</td><td>56.6</td><td>70.5</td><td>retrovirus-related like polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1527</td><td>1262</td><td>1.00E-165</td><td>82.6</td><td>18.5</td><td>24.4</td></tr>
<tr><td>Rsa1.0_00110.1.g5419.t1</td><td>ref|XP_002884824.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata] gi|297330664|gb|EFH61083.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata]</td><td>564</td><td>580</td><td>0</td><td>102.8</td><td>88.3</td><td>91.7</td><td>xanthine/uracil permease family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G10960.1 | Symbols: ATAZG1, AZG1 | AZA-guanine resistant1 | chr3:3424986-3426725 REVERSE LENGTH=579</td><td>564</td><td>579</td><td>0</td><td>102.7</td><td>88.1</td><td>91.1</td></tr>
<tr><td>Rsa1.0_00110.1.g5420.t1</td><td>emb|CAB39637.1| putative protein [Arabidopsis thaliana] gi|7267665|emb|CAB78093.1| putative protein [Arabidopsis thaliana] gi|91805577|gb|ABE65517.1| hypothetical protein At4g09700 [Arabidopsis thaliana]</td><td>404</td><td>371</td><td>6.00E-77</td><td>91.8</td><td>33.4</td><td>46.5</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G13450.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02000.1); Has 247 Blast hits to 243 proteins in 13 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 2; Plants - 243; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:5598739-5599923 REVERSE LENGTH=394</td><td>404</td><td>394</td><td>2.00E-25</td><td>97.5</td><td>16.8</td><td>24.8</td></tr>
</table>

Rsa1.0_00110.1.g5421.t1	gb|AAF01528.1|AC009991_24 hypothetical protein [Arabidopsis thaliana] gi|21618249|gb|AAM67299.1| unknown [Arabidopsis thaliana]	97	97	9.00E-29	100.0	76.3	86.6	hypothetical protein	gbpln	Arabidopsis thaliana	AT5G05300.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 8 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1570102-1570410 REVERSE LENGTH=102	97	102	2.00E-17	105.2	58.8	70.1
Rsa1.0_00110.1.g5422.t1	gb|AAL07333.1| superoxide dismutase [Raphanus sativus]	370	231	1.00E-133	62.4	61.9	61.9	superoxide dismutase	gbpln	Raphanus sativus	AT3G10920.1 | Symbols: MSD1, MEE33, ATMSD1 | manganese superoxide dismutase 1 | chr3:3418015-3419581 FORWARD LENGTH=231	370	231	1.00E-130	62.4	59.7	60.0
Rsa1.0_00110.1.g5423.t1	gb|EOA31384.1| hypothetical protein CARUB_v10014560mg [Capsella rubella]	227	226	1.00E-110	99.6	87.7	93.0	hypothetical protein CARUB_v10014560mg	gbpln	Capsella rubella	AT3G10915.2 | Symbols: | Reticulon family protein | chr3:3416101-3417497 REVERSE LENGTH=226	227	226	1.00E-112	99.6	86.8	93.8
Rsa1.0_00110.1.g5424.t1	ref|NP_187702.1| RING-H2 finger protein ATL72 [Arabidopsis thaliana] gi|68565331|sp|Q9SG96.1|ATL72_ARATH RecName: Full=RING-H2 finger protein ATL72 gi|6630539|gb|AAF19558.1|AC011708_1 putative RING zinc finger protein [Arabidopsis thaliana] gi|28466857|gb|AAO44037.1| At3g10910 [Arabidopsis thaliana] gi|110735947|dbj|BAE99948.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|332641448|gb|AEE74969.1| RING-H2 finger protein ATL72 [Arabidopsis thaliana]	185	181	4.00E-81	97.8	80.5	88.1	RING-H2 finger protein ATL72	gbpln	Arabidopsis thaliana	AT3G10910.1 | Symbols: | RING/U-box superfamily protein | chr3:3413068-3413613 REVERSE LENGTH=181	185	181	1.00E-83	97.8	80.5	88.1
Rsa1.0_00110.1.g5425.t1	ref|NP_187700.1| mannan endo-1,4-beta-mannosidase 3 [Arabidopsis thaliana] gi|75265804|sp|Q9SG94.1|MAN3_ARATH RecName: Full=Mannan endo-1,4-beta-mannosidase 3; AltName: Full=Beta-mannanase 3; AltName: Full=Endo-beta-1,4-mannanase 3; Short=AtMAN3; Flags: Precursor gi|6630541|gb|AAF19560.1|AC011708_3 putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana] gi|332641446|gb|AEE74967.1| mannan endo-1,4-beta-mannosidase 3 [Arabidopsis thaliana]	415	414	0	99.8	80.2	88.2	mannan endo-1,4-beta-mannosidase 3	gbpln	Arabidopsis thaliana	AT3G10890.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr3:3407455-3409000 REVERSE LENGTH=414	415	414	0	99.8	80.2	88.2
Rsa1.0_00110.1.g5426.t1	ref|XP_002884817.1| hypothetical protein ARALYDRAFT_478421 [Arabidopsis lyrata subsp. lyrata] gi|297330657|gb|EFH61076.1| hypothetical protein ARALYDRAFT_478421 [Arabidopsis lyrata subsp. lyrata]	272	275	1.00E-139	101.1	86.4	96.3	hypothetical protein ARALYDRAFT_478421	gbpln	Arabidopsis lyrata	AT3G10870.1 | Symbols: MES17, ATMES17 | methyl esterase 17 | chr3:3401228-3402612 REVERSE LENGTH=276	272	276	1.00E-138	101.5	87.1	96.0
Rsa1.0_00110.1.g5427.t1	gb|EOA31718.1| hypothetical protein CARUB_v10014926mg [Capsella rubella]	72	125	1.00E-33	173.6	94.4	100.0	hypothetical protein CARUB_v10014926mg	gbpln	Capsella rubella	AT3G10860.1 | Symbols: | Cytochrome b-c1 complex, subunit 8 protein | chr3:3399815-3400514 FORWARD LENGTH=72	72	72	1.00E-35	100.0	94.4	100.0
Rsa1.0_00110.1.g5428.t1	gb|EOA30394.1| hypothetical protein CARUB_v10013515mg [Capsella rubella]	555	498	1.00E-171	89.7	70.3	76.6	hypothetical protein CARUB_v10013515mg	gbpln	Capsella rubella	AT3G10810.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr3:3381848-3384227 REVERSE LENGTH=496	555	496	1.00E-173	89.4	71.2	77.5
Rsa1.0_00110.1.g5429.t1	dbj|BAJ34203.1| unnamed protein product [Thellungiella halophila]	630	677	0	107.5	76.3	83.2	unnamed protein product	----	----	AT3G10800.1 | Symbols: BZIP28 | Basic-leucine zipper (bZIP) transcription factor family protein | chr3:3379326-3381430 FORWARD LENGTH=675	630	675	0	107.1	72.5	81.3
Rsa1.0_00110.1.g5430.t1	ref|XP_002882696.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328536|gb|EFH58955.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	211	227	7.00E-80	107.6	69.7	84.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G10780.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr3:3375161-3376334 FORWARD LENGTH=217	211	217	2.00E-78	102.8	66.8	82.9
Rsa1.0_00110.1.g5431.t1	gb|EOA31000.1| hypothetical protein CARUB_v10014143mg [Capsella rubella]	276	334	7.00E-84	121.0	67.0	74.6	hypothetical protein CARUB_v10014143mg	gbpln	Capsella rubella	AT3G10770.2 | Symbols: | Single-stranded nucleic acid binding R3H protein | chr3:3372461-3374026 REVERSE LENGTH=325	276	325	4.00E-85	117.8	65.9	74.6
Rsa1.0_00110.1.g5432.t1	dbj|BAJ34024.1| unnamed protein product [Thellungiella halophila]	277	325	1.00E-105	117.3	83.8	85.9	unnamed protein product	----	----	AT3G10760.1 | Symbols: | Homeodomain-like superfamily protein | chr3:3369814-3370821 FORWARD LENGTH=335	277	335	1.00E-106	120.9	81.6	83.0

Rsa1.0_00110.1.g5433.t1	gb|EOA39317.1| hypothetical protein CARUB_v10012356mg, partial [Capsella rubella]	345	507	2.00E-46	147.0	45.8	62.6	hypothetical protein CARUB_v10012356mg, partial	gbpln	Capsella rubella	AT1G22000.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr1:7744189-7747123 FORWARD LENGTH=717	345	717	3.00E-40	207.8	42.9	58.6
Rsa1.0_00110.1.g5434.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00111.1.g5435.t1	ref|NP_850203.1| chaperonin CPN60-like 1 [Arabidopsis thaliana] gi|75301136|sp|Q8L7B5.1|CH60B_ARATH RecName: Full=Chaperonin CPN60-like 1, mitochondrial; AltName: Full=HSP60-like 1; Flags: Precursor gi|22531044|gb|AAM97026.1| mitochondrial chaperonin HSP60 [Arabidopsis thaliana] gi|23197790|gb|AAN15422.1| mitochondrial chaperonin HSP60 [Arabidopsis thaliana] gi|51968972|dbj|BAD43178.1| mitochondrial chaperonin (HSP60) [Arabidopsis thaliana] gi|330253705|gb|AEC08799.1| chaperonin CPN60-like 1 [Arabidopsis thaliana]	436	585	1.00E-101	134.2	52.3	60.6	chaperonin CPN60-like 1	gbpln	Arabidopsis thaliana	AT2G33210.1 | Symbols: HSP60-2 | heat shock protein 60-2 | chr2:14075093-14078568 REVERSE LENGTH=585	436	585	1.00E-103	134.2	52.3	60.6
Rsa1.0_00111.1.g5436.t1	gb|EOA28559.1| hypothetical protein CARUB_v10024776mg [Capsella rubella]	524	245	1.00E-125	46.8	42.2	43.5	hypothetical protein CARUB_v10024776mg	gbpln	Capsella rubella	AT2G33255.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:14098795-14100358 FORWARD LENGTH=245	524	245	1.00E-128	46.8	42.0	43.5
Rsa1.0_00111.1.g5437.t1	ref|NP_180861.1| receptor like protein 24 [Arabidopsis thaliana] gi|2924789|gb|AAC04918.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|20196994|gb|AAM14862.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|330253681|gb|AEC08775.1| receptor like protein 24 [Arabidopsis thaliana]	887	864	0	97.4	63.4	75.4	receptor like protein 24	gbpln	Arabidopsis thaliana	AT2G33020.1 | Symbols: AtRLP24, RLP24 | receptor like protein 24 | chr2:14013874-14016516 REVERSE LENGTH=864	887	864	0	97.4	63.4	75.4
Rsa1.0_00111.1.g5438.t1	gb|ACT33452.1| SU(VAR)3-9-like protein 2 [Brassica rapa subsp. pekinensis]	642	635	0	98.9	83.5	88.0	SU(VAR)3-9-like protein 2	gbpln	Brassica rapa	AT2G33290.1 | Symbols: SUVH2, SDG3, ATSUVH2 | SU(VAR)3-9 homolog 2 | chr2:14110078-14112033 FORWARD LENGTH=651	642	651	0	101.4	61.2	76.9
Rsa1.0_00111.1.g5439.t1	ref|XP_002880380.1| hypothetical protein ARALYDRAFT_481010 [Arabidopsis lyrata subsp. lyrata] gi|297326219|gb|EFH56639.1| hypothetical protein ARALYDRAFT_481010 [Arabidopsis lyrata subsp. lyrata]	811	800	0	98.6	74.6	83.5	hypothetical protein ARALYDRAFT_481010	gbpln	Arabidopsis lyrata	AT2G21450.1 | Symbols: CHR34 | chromatin remodeling 34 | chr2:9179622-9182356 REVERSE LENGTH=816	811	816	0	100.6	74.1	84.0
Rsa1.0_00111.1.g5440.t1	ref|XP_002880380.1| hypothetical protein ARALYDRAFT_481010 [Arabidopsis lyrata subsp. lyrata] gi|297326219|gb|EFH56639.1| hypothetical protein ARALYDRAFT_481010 [Arabidopsis lyrata subsp. lyrata]	165	800	2.00E-25	484.8	39.4	51.5	hypothetical protein ARALYDRAFT_481010	gbpln	Arabidopsis lyrata	AT2G21450.1 | Symbols: CHR34 | chromatin remodeling 34 | chr2:9179622-9182356 REVERSE LENGTH=816	165	816	1.00E-24	494.5	44.8	58.2
Rsa1.0_00111.1.g5441.t1	gb|EOA29418.1| hypothetical protein CARUB_v10025709mg, partial [Capsella rubella]	366	281	5.00E-56	76.8	30.1	34.2	hypothetical protein CARUB_v10025709mg, partial	gbpln	Capsella rubella	AT2G33030.1 | Symbols: AtRLP25, RLP25 | receptor like protein 25 | chr2:14017684-14018340 REVERSE LENGTH=218	366	218	6.00E-57	59.6	28.4	33.9
Rsa1.0_00111.1.g5442.t1	ref|XP_002881275.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327114|gb|EFH57534.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	613	595	0	97.1	82.4	88.1	C2 domain-containing protein	gbpln	Arabidopsis lyrata	AT2G33320.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:14119526-14121334 REVERSE LENGTH=602	613	602	0	98.2	80.3	86.9

Rsa1.0_00111.1.g5443.t1	ref|NP_850206.4| Pre-mRNA-processing factor 19-2 [Arabidopsis thaliana] gi|240254574|ref|NP_850207.4| Pre-mRNA-processing factor 19-2 [Arabidopsis thaliana] gi|288558844|sp|O22785.3|PR19B_ARATH RecName: Full=Pre-mRNA-processing factor 19 homolog 2; AltName: Full=MOS4-associated complex protein 3B; Short=MAC protein 3B; AltName: Full=Plant U-box protein 60; AltName: Full=U-box domain-containing protein 60 gi|226222620|gb|ACO38702.1| truncated MOS4-associated complex protein 3B [Arabidopsis thaliana] gi|330253723|gb|AEC08817.1| Pre-mRNA-processing factor 19-2 [Arabidopsis thaliana] gi|330253724|gb|AEC08818.1| Pre-mRNA-processing factor 19-2 [Arabidopsis thaliana]	525	525	0	100.0	93.5	97.1	Pre-mRNA-processing factor 19-2	gbpln	Arabidopsis thaliana	AT2G33340.2 | Symbols: MAC3B | MOS4-associated complex 3B | chr2:14126584-14131000 REVERSE LENGTH=525	525	525	0	100.0	93.5	97.1
Rsa1.0_00111.1.g5444.t1	ref|NP_001077999.1| CCT motif-containing protein [Arabidopsis thaliana] gi|60547735|gb|AAX23831.1| hypothetical protein At2g33350 [Arabidopsis thaliana] gi|330253727|gb|AEC08821.1| CCT motif-containing protein [Arabidopsis thaliana]	380	409	1.00E-131	107.6	73.7	81.3	CCT motif-containing protein	gbpln	Arabidopsis thaliana	AT2G33350.2 | Symbols: | CCT motif family protein | chr2:14134116-14136836 FORWARD LENGTH=409	380	409	1.00E-134	107.6	73.7	81.3
Rsa1.0_00111.1.g5445.t1	gb|ACG69528.1| caleosin CLO3-2 [Brassica napus]	239	239	1.00E-134	100.0	96.7	97.9	caleosin CLO3-2	gbpln	Brassica napus	AT2G33380.1 | Symbols: RD20, CLO-3 | Caleosin-related family protein | chr2:14144984-14146374 REVERSE LENGTH=236	239	236	1.00E-120	98.7	82.8	92.1
Rsa1.0_00111.1.g5446.t4	gb|EOA27327.1| hypothetical protein CARUB_v10023443mg [Capsella rubella]	381	377	0	99.0	86.1	92.9	hypothetical protein CARUB_v10023443mg	gbpln	Capsella rubella	AT2G33385.2 | Symbols: arpc2b | actin-related protein C2B | chr2:14147604-14149769 REVERSE LENGTH=374	381	374	0	98.2	83.7	91.9
Rsa1.0_00111.1.g5447.t1	ref|NP_180897.1| uncharacterized protein [Arabidopsis thaliana] gi|2459422|gb|AAB80657.1| unknown protein [Arabidopsis thaliana] gi|19310603|gb|AAL85032.1| unknown protein [Arabidopsis thaliana] gi|24030291|gb|AAN41317.1| unknown protein [Arabidopsis thaliana] gi|330253735|gb|AEC08829.1| uncharacterized protein AT2G33390 [Arabidopsis thaliana]	98	98	8.00E-27	100.0	84.7	88.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G33390.1 | Symbols: | unknown protein; Has 34 Blast hits to 34 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:14151714-14152698 FORWARD LENGTH=98	98	98	1.00E-29	100.0	84.7	88.8
Rsa1.0_00111.1.g5448.t1	ref|XP_002881282.1| hypothetical protein ARALYDRAFT_482283 [Arabidopsis lyrata subsp. lyrata] gi|297327121|gb|EFH57541.1| hypothetical protein ARALYDRAFT_482283 [Arabidopsis lyrata subsp. lyrata]	289	270	5.00E-85	93.4	64.0	75.1	hypothetical protein ARALYDRAFT_482283	gbpln	Arabidopsis lyrata	AT2G33400.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G04030.1); Has 3875 Blast hits to 2949 proteins in 323 species: Archae - 6; Bacteria - 281; Metazoa - 960; Fungi - 593; Plants - 281; Viruses - 98; Other Eukaryotes - 1656 (source: NCBI BLink). | chr2:14153331-14154401 REVERSE LENGTH=272	289	272	2.00E-80	94.1	67.5	75.8
Rsa1.0_00111.1.g5449.t1	gb|EOA27238.1| hypothetical protein CARUB_v10023347mg [Capsella rubella]	395	403	1.00E-154	102.0	82.5	85.1	hypothetical protein CARUB_v10023347mg	gbpln	Capsella rubella	AT2G33410.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:14156085-14157435 FORWARD LENGTH=404	395	404	1.00E-136	102.3	81.0	84.1
Rsa1.0_00111.1.g5450.t1	gb|EOA29220.1| hypothetical protein CARUB_v10025494mg [Capsella rubella]	1035	1044	0	100.9	91.4	95.0	hypothetical protein CARUB_v10025494mg	gbpln	Capsella rubella	AT2G33420.1 | Symbols: | Protein of unknown function (DUF810) | chr2:14158782-14162304 FORWARD LENGTH=1039	1035	1039	0	100.4	90.0	94.4
Rsa1.0_00111.1.g5451.t1	ref|XP_002879451.1| hypothetical protein ARALYDRAFT_482286 [Arabidopsis lyrata subsp. lyrata] gi|297325290|gb|EFH55710.1| hypothetical protein ARALYDRAFT_482286 [Arabidopsis lyrata subsp. lyrata]	356	219	1.00E-112	61.5	56.7	58.7	hypothetical protein ARALYDRAFT_482286	gbpln	Arabidopsis lyrata	AT2G33430.1 | Symbols: DAL1, DAL | differentiation and greening-like 1 | chr2:14162732-14164729 FORWARD LENGTH=219	356	219	1.00E-112	61.5	56.2	57.9
Rsa1.0_00111.1.g5452.t1	gb|EOA28019.1| hypothetical protein CARUB_v10024195mg [Capsella rubella]	143	166	7.00E-64	116.1	89.5	95.8	hypothetical protein CARUB_v10024195mg	gbpln	Capsella rubella	AT2G33450.1 | Symbols: | Ribosomal L28 family | chr2:14173620-14174380 FORWARD LENGTH=143	143	143	8.00E-66	100.0	89.5	95.1
Rsa1.0_00111.1.g5453.t1	gb|EOA29289.1| hypothetical protein CARUB_v10025564mg [Capsella rubella]	199	220	1.00E-74	110.6	78.4	85.4	hypothetical protein CARUB_v10025564mg	gbpln	Capsella rubella	AT2G33460.1 | Symbols: RIC1 | ROP-interactive CRIB motif-containing protein 1 | chr2:14174590-14175561 REVERSE LENGTH=224	199	224	8.00E-75	112.6	78.9	84.9

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<tr><td>Rsa1.0_00111.1.g5454.t1</td><td>ref|XP_002881284.1| hypothetical protein ARALYDRAFT_482291 [Arabidopsis lyrata subsp. lyrata] gi|297327123|gb|EFH57543.1| hypothetical protein ARALYDRAFT_482291 [Arabidopsis lyrata subsp. lyrata]</td><td>202</td><td>202</td><td>1.00E-109</td><td>100.0</td><td>93.6</td><td>97.5</td><td>hypothetical protein ARALYDRAFT_482291</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G33470.2 | Symbols: GLTP1 | glycolipid transfer protein 1 | chr2:14176599-14177950 REVERSE LENGTH=202</td><td>202</td><td>202</td><td>1.00E-108</td><td>100.0</td><td>90.6</td><td>96.0</td></tr>
<tr><td>Rsa1.0_00111.1.g5455.t16</td><td>gb|EOA27680.1| hypothetical protein CARUB_v10023833mg [Capsella rubella]</td><td>256</td><td>273</td><td>1.00E-90</td><td>106.6</td><td>76.6</td><td>87.1</td><td>hypothetical protein CARUB_v10023833mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G33480.1 | Symbols: ANAC041, NAC041 | NAC domain containing protein 41 | chr2:14181275-14182247 FORWARD LENGTH=268</td><td>256</td><td>268</td><td>2.00E-90</td><td>104.7</td><td>77.0</td><td>89.5</td></tr>
<tr><td>Rsa1.0_00111.1.g5456.t2</td><td>gb|EOA26568.1| hypothetical protein CARUB_v10022626mg [Capsella rubella]</td><td>276</td><td>853</td><td>5.00E-33</td><td>309.1</td><td>35.5</td><td>37.7</td><td>hypothetical protein CARUB_v10022626mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G31260.1 | Symbols: APG9, ATAPG9 | autophagy 9 (APG9) | chr2:13322291-13326293 REVERSE LENGTH=866</td><td>276</td><td>866</td><td>2.00E-34</td><td>313.8</td><td>35.1</td><td>37.0</td></tr>
<tr><td>Rsa1.0_00111.1.g5457.t1</td><td>ref|XP_002881291.1| hypothetical protein ARALYDRAFT_321088 [Arabidopsis lyrata subsp. lyrata] gi|297327130|gb|EFH57550.1| hypothetical protein ARALYDRAFT_321088 [Arabidopsis lyrata subsp. lyrata]</td><td>90</td><td>139</td><td>3.00E-33</td><td>154.4</td><td>78.9</td><td>90.0</td><td>hypothetical protein ARALYDRAFT_321088</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G33585.1 | Symbols: | unknown protein; Has 31 Blast hits to 31 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:14223403-14224167 REVERSE LENGTH=193</td><td>90</td><td>193</td><td>8.00E-36</td><td>214.4</td><td>75.6</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00111.1.g5458.t1</td><td>ref|NP_180917.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|2459446|gb|AAB80681.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gi|21536817|gb|AAM61149.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gi|21539439|gb|AAM53272.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gi|23197694|gb|AAN15374.1| putative cinnamoyl-CoA reductase [Arabidopsis thaliana] gi|330253763|gb|AEC08857.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]</td><td>321</td><td>321</td><td>1.00E-149</td><td>100.0</td><td>80.4</td><td>90.7</td><td>Rossmann-fold NAD(P)-binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G33590.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:14224622-14226365 FORWARD LENGTH=321</td><td>321</td><td>321</td><td>1.00E-152</td><td>100.0</td><td>80.4</td><td>90.7</td></tr>
<tr><td>Rsa1.0_00111.1.g5459.t1</td><td>ref|XP_002873095.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318932|gb|EFH49354.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>258</td><td>227</td><td>2.00E-27</td><td>88.0</td><td>34.5</td><td>45.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321</td><td>258</td><td>321</td><td>9.00E-26</td><td>124.4</td><td>27.9</td><td>40.7</td></tr>
<tr><td>Rsa1.0_00111.1.g5460.t1</td><td>gb|EOA27050.1| hypothetical protein CARUB_v10023146mg [Capsella rubella]</td><td>458</td><td>467</td><td>0</td><td>102.0</td><td>78.8</td><td>88.0</td><td>hypothetical protein CARUB_v10023146mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G33610.1 | Symbols: ATSWI3B, CHB2, SWI3B | switch subunit 3 | chr2:14229023-14231149 FORWARD LENGTH=469</td><td>458</td><td>469</td><td>0</td><td>102.4</td><td>77.5</td><td>86.5</td></tr>
<tr><td>Rsa1.0_00111.1.g5461.t5</td><td>gb|EOA27415.1| hypothetical protein CARUB_v10023550mg [Capsella rubella]</td><td>354</td><td>346</td><td>2.00E-98</td><td>97.7</td><td>63.3</td><td>69.2</td><td>hypothetical protein CARUB_v10023550mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G33620.4 | Symbols: | AT hook motif DNA-binding family protein | chr2:14234749-14236563 FORWARD LENGTH=351</td><td>354</td><td>351</td><td>1.00E-96</td><td>99.2</td><td>66.1</td><td>72.0</td></tr>
<tr><td>Rsa1.0_00111.1.g5462.t1</td><td>gb|EOA29301.1| hypothetical protein CARUB_v10025579mg [Capsella rubella]</td><td>501</td><td>501</td><td>0</td><td>100.0</td><td>87.4</td><td>91.2</td><td>hypothetical protein CARUB_v10025579mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G33670.1 | Symbols: MLO5, ATMLO5 | Seven transmembrane MLO family protein | chr2:14245138-14247879 FORWARD LENGTH=501</td><td>501</td><td>501</td><td>0</td><td>100.0</td><td>86.4</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00111.1.g5463.t1</td><td>ref|NP_180861.1| receptor like protein 24 [Arabidopsis thaliana] gi|2924789|gb|AAC04918.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|20196994|gb|AAM14862.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|330253681|gb|AEC08775.1| receptor like protein 24 [Arabidopsis thaliana]</td><td>881</td><td>864</td><td>0</td><td>98.1</td><td>64.9</td><td>75.5</td><td>receptor like protein 24</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G33020.1 | Symbols: AtRLP24, RLP24 | receptor like protein 24 | chr2:14013874-14016516 REVERSE LENGTH=864</td><td>881</td><td>864</td><td>0</td><td>98.1</td><td>64.9</td><td>75.5</td></tr>
<tr><td>Rsa1.0_00111.1.g5464.t1</td><td>gb|EOA28253.1| hypothetical protein CARUB_v10024446mg [Capsella rubella]</td><td>72</td><td>77</td><td>4.00E-27</td><td>106.9</td><td>88.9</td><td>91.7</td><td>hypothetical protein CARUB_v10024446mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G33690.1 | Symbols: | Late embryogenesis abundant protein, group 6 | chr2:14252199-14252414 FORWARD LENGTH=71</td><td>72</td><td>71</td><td>3.00E-28</td><td>98.6</td><td>86.1</td><td>90.3</td></tr>
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Rsa1.0_00111.1.g5465.t1	ref|NP_180926.1| putative protein phosphatase 2C 27 [Arabidopsis thaliana] gi|75220399|sp|P93006.1|P2C27_ARATH RecName: Full=Probable protein phosphatase 2C 27; Short=AtPP2C27 gi|1707015|gb|AAC69126.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|17979442|gb|AAL49863.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|20259093|gb|AAM14262.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|330253776|gb|AEC08870.1| putative protein phosphatase 2C 27 [Arabidopsis thaliana]	395	380	0	96.2	84.8	90.4	putative protein phosphatase 2C 27	gbpln	Arabidopsis thaliana	AT2G33700.1 | Symbols: | Protein phosphatase 2C family protein | chr2:14254200-14255784 FORWARD LENGTH=380	395	380	0	96.2	84.8	90.4
Rsa1.0_00111.1.g5466.t1	gb|EOA29237.1| hypothetical protein CARUB_v10025511mg [Capsella rubella]	198	214	1.00E-70	108.1	69.7	75.3	hypothetical protein CARUB_v10025511mg	gbpln	Capsella rubella	AT2G33710.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr2:14259271-14260652 REVERSE LENGTH=218	198	218	5.00E-64	110.1	70.2	77.8
Rsa1.0_00111.1.g5467.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1476	1491	0	101.0	57.2	72.6	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1476	1262	1.00E-137	85.5	15.5	22.3
Rsa1.0_00111.1.g5468.t1	ref|NP_180929.1| DEAD-box ATP-dependent RNA helicase 21 [Arabidopsis thaliana] gi|75319077|sp|P93008.1|RH21_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 21 gi|1707017|gb|AAC69128.1| putative U5 small nuclear ribonucleoprotein, an RNA helicase [Arabidopsis thaliana] gi|17473908|gb|AAL38370.1| putative U5 small nuclear ribonucleoprotein, an RNA helicase [Arabidopsis thaliana] gi|20259792|gb|AAM13243.1| putative U5 small nuclear ribonucleoprotein, an RNA helicase [Arabidopsis thaliana] gi|330253781|gb|AEC08875.1| DEAD-box ATP-dependent RNA helicase 21 [Arabidopsis thaliana]	706	733	0	103.8	81.7	83.3	DEAD-box ATP-dependent RNA helicase 21	gbpln	Arabidopsis thaliana	AT2G33730.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:14265679-14267880 REVERSE LENGTH=733	706	733	0	103.8	81.7	83.3
Rsa1.0_00111.1.g5469.t1	gb|EOA28781.1| hypothetical protein CARUB_v10025013mg [Capsella rubella]	285	349	8.00E-76	122.5	58.9	75.1	hypothetical protein CARUB_v10025013mg	gbpln	Capsella rubella	AT2G33750.2 | Symbols: ATPUP2, PUP2 | purine permease 2 | chr2:14271794-14273265 REVERSE LENGTH=347	285	347	4.00E-68	121.8	57.5	72.6
Rsa1.0_00111.1.g5470.t1	ref|NP_180932.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75101013|sp|P93011.1|PP182_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g33760 gi|1707020|gb|AAC69141.1| hypothetical protein [Arabidopsis thaliana] gi|330253787|gb|AEC08881.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	584	583	0	99.8	84.9	93.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G33760.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:14275800-14277551 FORWARD LENGTH=583	584	583	0	99.8	84.9	93.5
Rsa1.0_00111.1.g5471.t1	dbj|BAJ34336.1| unnamed protein product [Thellungiella halophila]	1004	896	0	89.2	73.7	78.2	unnamed protein product	----	----	AT2G33770.1 | Symbols: UBC24, ATUBC24, PHO2 | phosphate 2 | chr2:14277785-14281482 REVERSE LENGTH=907	1004	907	0	90.3	72.0	77.6
Rsa1.0_00111.1.g5472.t1	ref|XP_002893514.1| hypothetical protein ARALYDRAFT_473032 [Arabidopsis lyrata subsp. lyrata] gi|297339356|gb|EFH69773.1| hypothetical protein ARALYDRAFT_473032 [Arabidopsis lyrata subsp. lyrata]	562	578	0	102.8	64.6	75.3	hypothetical protein ARALYDRAFT_473032	gbpln	Arabidopsis lyrata	AT1G28240.1 | Symbols: | Protein of unknown function (DUF616) | chr1:9868521-9871798 REVERSE LENGTH=581	562	581	0	103.4	62.8	72.4
Rsa1.0_00111.1.g5473.t1	gb|EOA29043.1| hypothetical protein CARUB_v10025298mg [Capsella rubella]	219	256	7.00E-72	116.9	69.4	81.7	hypothetical protein CARUB_v10025298mg	gbpln	Capsella rubella	AT2G33790.1 | Symbols: ATAGP30, AGP30 | arabinogalactan protein 30 | chr2:14293862-14295237 REVERSE LENGTH=239	219	239	5.00E-74	109.1	70.8	81.3
Rsa1.0_00111.1.g5474.t1	ref|XP_002881312.1| hypothetical protein ARALYDRAFT_902475 [Arabidopsis lyrata subsp. lyrata] gi|297327151|gb|EFH57571.1| hypothetical protein ARALYDRAFT_902475 [Arabidopsis lyrata subsp. lyrata]	147	144	2.00E-60	98.0	83.7	89.8	hypothetical protein ARALYDRAFT_902475	gbpln	Arabidopsis lyrata	AT2G33855.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:14324717-14325151 REVERSE LENGTH=144	147	144	7.00E-55	98.0	79.6	89.1
Rsa1.0_00111.1.g5475.t1	gb|AAB62404.1| auxin response transcription factor 3 [Arabidopsis thaliana]	614	608	0	99.0	82.2	87.3	auxin response transcription factor 3	gbpln	Arabidopsis thaliana	AT2G33860.1 | Symbols: ETT, ARF3 | Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related | chr2:14325444-14328613 REVERSE LENGTH=608	614	608	0	99.0	81.3	86.3

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<tr><td>Rsa1.0_00111.1.g5477.t1</td><td>gb|AAB67617.1| putative SF16 protein {Helianthus annuus} [Arabidopsis thaliana]</td><td>115</td><td>249</td><td>4.00E-40</td><td>216.5</td><td>73.0</td><td>82.6</td><td>putative SF16 protein {Helianthus annuus}</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G33990.1 | Symbols: iqd9 | IQ-domain 9 | chr2:14360502-14361630 REVERSE LENGTH=263</td><td>115</td><td>263</td><td>7.00E-43</td><td>228.7</td><td>73.0</td><td>82.6</td></tr>
<tr><td>Rsa1.0_00111.1.g5478.t1</td><td>gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>616</td><td>1555</td><td>1.00E-109</td><td>252.4</td><td>31.5</td><td>40.6</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT2G34000.1 | Symbols: | RING/U-box superfamily protein | chr2:14365177-14365632 FORWARD LENGTH=151</td><td>616</td><td>151</td><td>2.00E-57</td><td>24.5</td><td>17.5</td><td>19.2</td></tr>
<tr><td>Rsa1.0_00111.1.g5479.t1</td><td>ref|NP_180950.2| calcium-binding EF-hand-containing protein [Arabidopsis thaliana] gi|330253814|gb|AEC08908.1| calcium-binding EF-hand-containing protein [Arabidopsis thaliana]</td><td>568</td><td>566</td><td>0</td><td>99.6</td><td>72.0</td><td>85.2</td><td>calcium-binding EF-hand-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34030.1 | Symbols: | Calcium-binding EF-hand family protein | chr2:14375086-14377364 REVERSE LENGTH=566</td><td>568</td><td>566</td><td>0</td><td>99.6</td><td>72.0</td><td>85.2</td></tr>
<tr><td>Rsa1.0_00111.1.g5480.t3</td><td>gb|EOA26361.1| hypothetical protein CARUB_v10022882mg, partial [Capsella rubella]</td><td>190</td><td>586</td><td>3.00E-33</td><td>308.4</td><td>43.2</td><td>45.3</td><td>hypothetical protein CARUB_v10022882mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G34040.2 | Symbols: | Apoptosis inhibitory protein 5 (API5) | chr2:14378571-14382246 REVERSE LENGTH=442</td><td>190</td><td>442</td><td>1.00E-35</td><td>232.6</td><td>42.6</td><td>44.7</td></tr>
<tr><td>Rsa1.0_00111.1.g5481.t1</td><td>gb|EOA27690.1| hypothetical protein CARUB_v10023843mg, partial [Capsella rubella]</td><td>252</td><td>271</td><td>8.00E-25</td><td>107.5</td><td>27.0</td><td>42.1</td><td>hypothetical protein CARUB_v10023843mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>252</td><td>303</td><td>6.00E-21</td><td>120.2</td><td>23.0</td><td>40.5</td></tr>
<tr><td>Rsa1.0_00111.1.g5482.t1</td><td>ref|NP_565779.1| trichome birefringence-like 37 protein [Arabidopsis thaliana] gi|20196907|gb|AAB67625.2| expressed protein [Arabidopsis thaliana] gi|21554400|gb|AAM63505.1| unknown [Arabidopsis thaliana] gi|330253819|gb|AEC08913.1| trichome birefringence-like 37 protein [Arabidopsis thaliana]</td><td>383</td><td>385</td><td>0</td><td>100.5</td><td>84.3</td><td>90.9</td><td>trichome birefringence-like 37 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34070.1 | Symbols: TBL37 | TRICHOME BIREFRINGENCE-LIKE 37 | chr2:14387631-14390160 REVERSE LENGTH=385</td><td>383</td><td>385</td><td>0</td><td>100.5</td><td>84.3</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00111.1.g5483.t1</td><td>ref|NP_565780.1| cysteine proteinase-like protein [Arabidopsis thaliana] gi|2342728|gb|AAB67626.1| cysteine proteinase [Arabidopsis thaliana] gi|330253821|gb|AEC08915.1| cysteine proteinase-like protein [Arabidopsis thaliana]</td><td>345</td><td>345</td><td>1.00E-177</td><td>100.0</td><td>85.5</td><td>91.3</td><td>cysteine proteinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34080.1 | Symbols: | Cysteine proteinases superfamily protein | chr2:14393431-14394777 REVERSE LENGTH=345</td><td>345</td><td>345</td><td>1.00E-180</td><td>100.0</td><td>85.5</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00111.1.g5484.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00111.1.g5485.t1</td><td>gb|EOA12750.1| hypothetical protein CARUB_v10028431mg [Capsella rubella]</td><td>469</td><td>423</td><td>1.00E-116</td><td>90.2</td><td>48.4</td><td>61.2</td><td>hypothetical protein CARUB_v10028431mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G56430.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:22853323-22854575 REVERSE LENGTH=360</td><td>469</td><td>360</td><td>1.00E-88</td><td>76.8</td><td>34.5</td><td>43.7</td></tr>
<tr><td>Rsa1.0_00111.1.g5486.t1</td><td>ref|NP_180961.1| Dof zinc finger protein DOF2.3 [Arabidopsis thaliana] gi|55583789|sp|O22967.1|CDF4_ARATH RecName: Full=Cyclic dof factor 4; AltName: Full=Dof zinc finger protein DOF2.3; Short=AtDOF2.3 gi|2342734|gb|AAB67632.1| putative DOF zinc finger protein [Arabidopsis thaliana] gi|34365615|gb|AAQ65119.1| At2g34140 [Arabidopsis thaliana] gi|62319965|dbj|BAD94068.1| putative DOF zinc finger protein [Arabidopsis thaliana] gi|330253829|gb|AEC08923.1| Dof zinc finger protein DOF2.3 [Arabidopsis thaliana]</td><td>167</td><td>170</td><td>1.00E-68</td><td>101.8</td><td>79.0</td><td>85.0</td><td>Dof zinc finger protein DOF2.3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34140.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr2:14414188-14414700 REVERSE LENGTH=170</td><td>167</td><td>170</td><td>4.00E-71</td><td>101.8</td><td>79.0</td><td>85.0</td></tr>
<tr><td>Rsa1.0_00111.1.g5487.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00111.1.g5488.t1</td><td>ref|XP_002883131.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297328971|gb|EFH59390.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]</td><td>175</td><td>175</td><td>5.00E-91</td><td>100.0</td><td>93.7</td><td>98.3</td><td>calcium-binding EF hand family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G18430.2 | Symbols: | Calcium-binding EF-hand family protein | chr3:6326180-6327476 FORWARD LENGTH=175</td><td>175</td><td>175</td><td>4.00E-93</td><td>100.0</td><td>93.1</td><td>98.3</td></tr>
<tr><td>Rsa1.0_00111.1.g5489.t1</td><td>ref|XP_002881326.1| CIPK13 [Arabidopsis lyrata subsp. lyrata] gi|297327165|gb|EFH57585.1| CIPK13 [Arabidopsis lyrata subsp. lyrata]</td><td>498</td><td>505</td><td>0</td><td>101.4</td><td>87.1</td><td>93.6</td><td>CIPK13</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G34180.1 | Symbols: CIPK13, SnRK3.7, WL2, ATWL2 | CBL-interacting protein kinase 13 | chr2:14430761-14432269 REVERSE LENGTH=502</td><td>498</td><td>502</td><td>0</td><td>100.8</td><td>85.7</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00111.1.g5490.t3</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<tr><td>Rsa1.0_00111.1.g5491.t1</td><td>gb|ABY58019.1| arm repeat containing protein 1 [Brassica oleracea var. viridis]</td><td>660</td><td>663</td><td>0</td><td>100.5</td><td>87.7</td><td>93.3</td><td>arm repeat containing protein 1</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G29340.1 | Symbols: PUB17, ATPUB17 | plant U-box 17 | chr1:10264412-10266601 FORWARD LENGTH=729</td><td>660</td><td>729</td><td>0</td><td>110.5</td><td>59.2</td><td>75.9</td></tr>
<tr><td>Rsa1.0_00111.1.g5492.t1</td><td>ref|XP_002881327.1| hypothetical protein ARALYDRAFT_321144 [Arabidopsis lyrata subsp. lyrata] gi|297327166|gb|EFH57586.1| hypothetical protein ARALYDRAFT_321144 [Arabidopsis lyrata subsp. lyrata]</td><td>829</td><td>865</td><td>0</td><td>104.3</td><td>71.5</td><td>80.6</td><td>hypothetical protein ARALYDRAFT_321144</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G29350.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr1:10268761-10273613 REVERSE LENGTH=831</td><td>829</td><td>831</td><td>0</td><td>100.2</td><td>65.3</td><td>76.7</td></tr>
<tr><td>Rsa1.0_00111.1.g5493.t1</td><td>gb|EOA27389.1| hypothetical protein CARUB_v10023519mg [Capsella rubella]</td><td>347</td><td>353</td><td>1.00E-180</td><td>101.7</td><td>88.5</td><td>94.8</td><td>hypothetical protein CARUB_v10023519mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G34260.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr2:14465899-14468416 FORWARD LENGTH=353</td><td>347</td><td>353</td><td>1.00E-174</td><td>101.7</td><td>87.9</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00111.1.g5494.t1</td><td>gb|EOA27733.1| hypothetical protein CARUB_v10023887mg [Capsella rubella]</td><td>224</td><td>258</td><td>4.00E-54</td><td>115.2</td><td>67.0</td><td>78.6</td><td>hypothetical protein CARUB_v10023887mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G34310.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G29530.1); Has 236 Blast hits to 216 proteins in 70 species: Archae - 0; Bacteria - 10; Metazoa - 74; Fungi - 47; Plants - 60; Viruses - 0; Other Eukaryotes - 45 (source: NCBI BLink). | chr2:14478564-14479812 REVERSE LENGTH=242</td><td>224</td><td>242</td><td>2.00E-54</td><td>108.0</td><td>57.6</td><td>70.1</td></tr>
<tr><td>Rsa1.0_00111.1.g5495.t1</td><td>ref|XP_002881332.1| hypothetical protein ARALYDRAFT_482377 [Arabidopsis lyrata subsp. lyrata] gi|297327171|gb|EFH57591.1| hypothetical protein ARALYDRAFT_482377 [Arabidopsis lyrata subsp. lyrata]</td><td>139</td><td>134</td><td>2.00E-39</td><td>96.4</td><td>62.6</td><td>74.8</td><td>hypothetical protein ARALYDRAFT_482377</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G34340.1 | Symbols: | Protein of unknown function, DUF584 | chr2:14489032-14489442 REVERSE LENGTH=136</td><td>139</td><td>136</td><td>4.00E-38</td><td>97.8</td><td>66.2</td><td>80.6</td></tr>
<tr><td>Rsa1.0_00111.1.g5496.t1</td><td>ref|XP_002879492.1| hypothetical protein ARALYDRAFT_321151 [Arabidopsis lyrata subsp. lyrata] gi|297325331|gb|EFH55751.1| hypothetical protein ARALYDRAFT_321151 [Arabidopsis lyrata subsp. lyrata]</td><td>525</td><td>2264</td><td>0</td><td>431.2</td><td>88.4</td><td>93.9</td><td>hypothetical protein ARALYDRAFT_321151</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G34350.1 | Symbols: | Nodulin-like / Major Facilitator Superfamily protein | chr2:14493624-14495644 FORWARD LENGTH=525</td><td>525</td><td>525</td><td>0</td><td>100.0</td><td>88.8</td><td>93.7</td></tr>
<tr><td>Rsa1.0_00111.1.g5497.t1</td><td>ref|XP_002879492.1| hypothetical protein ARALYDRAFT_321151 [Arabidopsis lyrata subsp. lyrata] gi|297325331|gb|EFH55751.1| hypothetical protein ARALYDRAFT_321151 [Arabidopsis lyrata subsp. lyrata]</td><td>524</td><td>2264</td><td>0</td><td>432.1</td><td>87.2</td><td>93.3</td><td>hypothetical protein ARALYDRAFT_321151</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G34355.1 | Symbols: | Major facilitator superfamily protein | chr2:14496376-14498311 FORWARD LENGTH=523</td><td>524</td><td>523</td><td>0</td><td>99.8</td><td>87.6</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00111.1.g5498.t1</td><td>gb|AAC26703.1| unknown protein [Arabidopsis thaliana] gi|20197167|gb|AAM14953.1| unknown protein [Arabidopsis thaliana]</td><td>384</td><td>459</td><td>1.00E-139</td><td>119.5</td><td>67.2</td><td>80.2</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34380.1 | Symbols: | Putative adipose-regulatory protein (Seipin) | chr2:14512777-14514306 FORWARD LENGTH=509</td><td>384</td><td>509</td><td>1.00E-141</td><td>132.6</td><td>67.2</td><td>80.2</td></tr>
<tr><td>Rsa1.0_00111.1.g5499.t1</td><td>ref|XP_002879496.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325335|gb|EFH55755.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>499</td><td>617</td><td>0</td><td>123.6</td><td>67.7</td><td>75.4</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G34400.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr2:14516226-14518186 FORWARD LENGTH=621</td><td>499</td><td>621</td><td>0</td><td>124.4</td><td>66.3</td><td>74.5</td></tr>
<tr><td>Rsa1.0_00111.1.g5500.t1</td><td>ref|NP_180988.3| O-acetyltransferase-like protein [Arabidopsis thaliana] gi|79324285|ref|NP_001031478.1| O-acetyltransferase-like protein [Arabidopsis thaliana] gi|51536464|gb|AAU05470.1| At2g34410 [Arabidopsis thaliana] gi|55733775|gb|AAV59284.1| At2g34410 [Arabidopsis thaliana] gi|62320442|dbj|BAD94920.1| hypothetical protein [Arabidopsis thaliana] gi|110737554|dbj|BAF00719.1| hypothetical protein [Arabidopsis thaliana] gi|222423437|dbj|BAH19689.1| AT2G34410 [Arabidopsis thaliana] gi|330253875|gb|AEC08969.1| O-acetyltransferase-like protein [Arabidopsis thaliana] gi|330253876|gb|AEC08970.1| O-acetyltransferase-like protein [Arabidopsis thaliana]</td><td>541</td><td>540</td><td>0</td><td>99.8</td><td>95.4</td><td>98.2</td><td>O-acetyltransferase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34410.2 | Symbols: | O-acetyltransferase family protein | chr2:14518719-14522053 FORWARD LENGTH=540</td><td>541</td><td>540</td><td>0</td><td>99.8</td><td>95.4</td><td>98.2</td></tr>
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Rsa1.0_00111.1.g5501.t1	sp|P13851.1|CB21_SINAL RecName: Full=Chlorophyll a-b binding protein 1, chloroplastic; AltName: Full=LHCII type I CAB-1; Short=LHCP; Flags: Precursor gi|21138|emb|CAA34459.1| unnamed protein product [Sinapis alba] gi|21140|emb|CAA33903.1| chlorophyll a/b-binding polypeptide [Sinapis alba]	266	266	1.00E-151	100.0	100.0	100.0	RecName: Full=Chlorophyll a-b binding protein 1, chloroplastic; AltName: Full=LHCII type I CAB-1; Short=LHCP; Flags: Precursor gi|21138|emb|CAA34459.1| unnamed protein product	gbpln	Sinapis alba	AT2G34430.1 | Symbols: LHB1B1, LHCB1.4 | light-harvesting chlorophyll-protein complex II subunit B1 | chr2:14524818-14525618 FORWARD LENGTH=266	266	266	1.00E-149	100.0	96.2	97.7
Rsa1.0_00111.1.g5502.t1	ref|XP_002879499.1| MADS-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297325338|gb|EFH55758.1| MADS-box family protein [Arabidopsis lyrata subsp. lyrata]	191	172	3.00E-69	90.1	70.7	77.5	MADS-box family protein	gbpln	Arabidopsis lyrata	AT2G34440.1 | Symbols: AGL29 | AGAMOUS-like 29 | chr2:14526950-14527468 FORWARD LENGTH=172	191	172	2.00E-70	90.1	69.1	78.5
Rsa1.0_00111.1.g5503.t1	ref|XP_002881335.1| high mobility group family protein [Arabidopsis lyrata subsp. lyrata] gi|297327174|gb|EFH57594.1| high mobility group family protein [Arabidopsis lyrata subsp. lyrata]	156	152	1.00E-57	97.4	78.8	83.3	high mobility group family protein	gbpln	Arabidopsis lyrata	AT2G34450.1 | Symbols: | HMG-box (high mobility group) DNA-binding family protein | chr2:14527918-14529448 REVERSE LENGTH=151	156	151	2.00E-59	96.8	76.9	83.3
Rsa1.0_00111.1.g5504.t1	ref|NP_565789.2| NAD(P)-binding Rossmann-fold-containing protein [Arabidopsis thaliana] gi|75151867|sp|Q8H124.1|Y2446_ARATH RecName: Full=Uncharacterized protein At2g34460, chloroplastic; Flags: Precursor gi|24030209|gb|AAN41284.1| unknown protein [Arabidopsis thaliana] gi|330253883|gb|AEC08977.1| NAD(P)-binding Rossmann-fold-containing protein [Arabidopsis thaliana]	288	280	1.00E-129	97.2	82.6	88.9	NAD(P)-binding Rossmann-fold-containing protein	gbpln	Arabidopsis thaliana	AT2G34460.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:14529635-14530732 FORWARD LENGTH=280	288	280	1.00E-131	97.2	82.6	88.9
Rsa1.0_00111.1.g5505.t1	ref|XP_002881336.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327175|gb|EFH57595.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	275	278	1.00E-138	101.1	88.0	89.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G34470.1 | Symbols: UREG, PSKF109 | urease accessory protein G | chr2:14530900-14532411 REVERSE LENGTH=275	275	275	1.00E-139	100.0	87.3	89.1
Rsa1.0_00111.1.g5506.t1	ref|NP_180995.1| 60S ribosomal protein L18a-2 [Arabidopsis thaliana] gi|297826909|ref|XP_002881337.1| 60S ribosomal protein L18A [Arabidopsis lyrata subsp. lyrata] gi|21431842|sp|P51418.2|R18A2_ARATH RecName: Full=60S ribosomal protein L18a-2 gi|3128228|gb|AAC26708.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|14596031|gb|AAK68743.1| Unknown protein [Arabidopsis thaliana] gi|20197170|gb|AAM14956.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|21539567|gb|AAM53336.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|23197736|gb|AAN15395.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|30102898|gb|AAP21367.1| At2g34480 [Arabidopsis thaliana] gi|297327176|gb|EFH57596.1| 60S ribosomal protein L18A [Arabidopsis lyrata subsp. lyrata] gi|330253886|gb|AEC08980.1| 60S ribosomal protein L18a-2 [Arabidopsis thaliana]	178	178	1.00E-100	100.0	98.3	100.0	60S ribosomal protein L18a-2	gbpln	Arabidopsis lyrata	AT2G34480.1 | Symbols: | Ribosomal protein L18ae/LX family protein | chr2:14532916-14534161 REVERSE LENGTH=178	178	178	1.00E-102	100.0	98.3	100.0
Rsa1.0_00111.1.g5507.t1	ref|NP_180997.1| cytochrome P450, family 710, subfamily A [Arabidopsis thaliana] gi|75278303|sp|O64697.1|C7101_ARATH RecName: Full=Cytochrome P450 710A1; AltName: Full=C-22 sterol desaturase gi|3128210|gb|AAC26690.1| putative cytochrome P450 [Arabidopsis thaliana] gi|20197156|gb|AAM14944.1| putative cytochrome P450 [Arabidopsis thaliana] gi|25083451|gb|AAN72080.1| putative cytochrome P450 [Arabidopsis thaliana] gi|34365731|gb|AAQ65177.1| At2g34500 [Arabidopsis thaliana] gi|84468537|dbj|BAE71351.1| CYP710 [Arabidopsis thaliana] gi|330253888|gb|AEC08982.1| cytochrome P450 710A1 [Arabidopsis thaliana]	502	495	0	98.6	82.7	89.4	cytochrome P450, family 710, subfamily A	gbpln	Arabidopsis thaliana	AT2G34500.1 | Symbols: CYP710A1 | cytochrome P450, family 710, subfamily A, polypeptide 1 | chr2:14539712-14541199 REVERSE LENGTH=495	502	495	0	98.6	82.7	89.4

Rsa1.0_00112.1.g5508.t1	gb|EOA38233.1| hypothetical protein CARUB_v10009715mg [Capsella rubella]	530	328	9.00E-15	61.9	10.8	12.5	hypothetical protein CARUB_v10009715mg	gbpln	Capsella rubella	AT1G62740.1 | Symbols: Hop2 | stress-inducible protein, putative | chr1:23231026-23233380 FORWARD LENGTH=571	530	571	2.00E-16	107.7	11.1	17.2
Rsa1.0_00112.1.g5509.t1	dbj|BAF01167.1| hypothetical protein [Arabidopsis thaliana]	992	1061	0	107.0	87.0	91.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G06900.1 | Symbols: | Insulinase (Peptidase family M16) family protein | chr1:2115155-2120635 REVERSE LENGTH=1024	992	1024	0	103.2	85.5	89.9
Rsa1.0_00112.1.g5510.t1	ref|NP_172172.2| nodulin MtN21 /EamA-like transporter protein [Arabidopsis thaliana] gi|145323764|ref|NP_001077471.1| nodulin MtN21 /EamA-like transporter protein [Arabidopsis thaliana] gi|75158873|sp|Q8RXL8.1|Y1689_ARATH RecName: Full=Uncharacterized membrane protein At1g06890 gi|19423946|gb|AAL87295.1| unknown protein [Arabidopsis thaliana] gi|21436373|gb|AAM51356.1| unknown protein [Arabidopsis thaliana] gi|332189927|gb|AEE28048.1| nodulin MtN21 /EamA-like transporter protein [Arabidopsis thaliana] gi|332189928|gb|AEE28049.1| nodulin MtN21 /EamA-like transporter protein [Arabidopsis thaliana]	379	357	0	94.2	90.5	92.9	nodulin MtN21 /EamA-like transporter protein	gbpln	Arabidopsis thaliana	AT1G06890.2 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:2111728-2114038 REVERSE LENGTH=357	379	357	0	94.2	90.5	92.9
Rsa1.0_00112.1.g5511.t1	gb|EOA38045.1| hypothetical protein CARUB_v10009515mg [Capsella rubella]	370	365	1.00E-155	98.6	77.8	84.3	hypothetical protein CARUB_v10009515mg	gbpln	Capsella rubella	AT1G06870.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr1:2108832-2110642 FORWARD LENGTH=367	370	367	1.00E-155	99.2	76.8	83.5
Rsa1.0_00112.1.g5512.t1	ref|NP_197389.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|332005241|gb|AED92624.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	263	295	1.00E-67	112.2	52.9	70.7	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	263	295	3.00E-70	112.2	52.9	70.7
Rsa1.0_00112.1.g5513.t1	gb|EOA39597.1| hypothetical protein CARUB_v10008222mg [Capsella rubella]	957	951	0	99.4	84.0	91.1	hypothetical protein CARUB_v10008222mg	gbpln	Capsella rubella	AT1G06840.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:2097854-2103208 REVERSE LENGTH=953	957	953	0	99.6	84.4	91.0
Rsa1.0_00112.1.g5514.t1	ref|NP_172168.1| monothiol glutaredoxin-S11 [Arabidopsis thaliana] gi|75191726|sp|Q9M9Y9.1|GRS11_ARATH RecName: Full=Monothiol glutaredoxin-S11; Short=AtGrxS11; AltName: Full=Protein ROXY 6 gi|7523711|gb|AAF63150.1|AC011001_20 Similar to glutaredoxin [Arabidopsis thaliana] gi|18252863|gb|AAL62358.1| glutaredoxin, putative [Arabidopsis thaliana] gi|21387059|gb|AAM47933.1| putative glutaredoxin [Arabidopsis thaliana] gi|21537263|gb|AAM61604.1| glutaredoxin, putative [Arabidopsis thaliana] gi|226348190|gb|ACO50411.1| glutaredoxin [Arabidopsis thaliana] gi|332189922|gb|AEE28043.1| monothiol glutaredoxin-S11 [Arabidopsis thaliana]	99	99	5.00E-49	100.0	97.0	100.0	monothiol glutaredoxin-S11	gbpln	Arabidopsis thaliana	AT1G06830.1 | Symbols: | Glutaredoxin family protein | chr1:2097189-2097488 FORWARD LENGTH=99	99	99	9.00E-52	100.0	97.0	100.0
Rsa1.0_00112.1.g5515.t1	gb|ACJ76846.1| chloroplast lipase protein [Brassica napus]	511	513	0	100.4	94.9	96.5	chloroplast lipase protein	gbpln	Brassica napus	AT1G06800.1 | Symbols: PLA-I{gamma}1 | alpha/beta-Hydrolases superfamily protein | chr1:2089538-2091443 REVERSE LENGTH=515	511	515	0	100.8	87.1	92.2
Rsa1.0_00112.1.g5516.t2	dbj|BAJ33712.1| unnamed protein product [Thellungiella halophila]	293	456	7.00E-94	155.6	70.0	74.4	unnamed protein product	----	----	AT1G05560.1 | Symbols: UGT1, UGT75B1 | UDP-glucosyltransferase 75B1 | chr1:1645674-1647083 REVERSE LENGTH=469	293	469	1.00E-86	160.1	66.2	73.4
Rsa1.0_00112.1.g5517.t1	ref|NP_973671.1| uncharacterized protein [Arabidopsis thaliana] gi|29028790|gb|AAO64774.1| At2g42395 [Arabidopsis thaliana] gi|110743081|dbj|BAE99433.1| hypothetical protein [Arabidopsis thaliana] gi|330255022|gb|AEC10116.1| uncharacterized protein AT2G42395 [Arabidopsis thaliana]	130	104	1.00E-21	80.0	36.9	45.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G42395.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17653566-17653980 REVERSE LENGTH=104	130	104	3.00E-24	80.0	36.9	45.4

Rsa1.0_00112.1.g5518.t1	ref|XP_002892525.1| hypothetical protein ARALYDRAFT_888225 [Arabidopsis lyrata subsp. lyrata] gi|297338367|gb|EFH68784.1| hypothetical protein ARALYDRAFT_888225 [Arabidopsis lyrata subsp. lyrata]	233	166	3.00E-11	71.2	15.9	24.0	hypothetical protein ARALYDRAFT_888225	gbpln	Arabidopsis lyrata	AT2G42395.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17653566-17653980 REVERSE LENGTH=104	233	104	3.00E-13	44.6	14.2	20.2
Rsa1.0_00112.1.g5519.t1	emb|CAA62296.1| component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]	131	133	2.00E-34	101.5	64.9	74.8	component of 6.1 kDa polypeptide of photosystem II reaction center	gbpln	Arabidopsis thaliana	AT2G30570.1 | Symbols: PSBW | photosystem II reaction center W | chr2:13019326-13020053 REVERSE LENGTH=133	131	133	7.00E-37	101.5	64.9	74.8
Rsa1.0_00112.1.g5520.t1	ref|XP_002889617.1| hypothetical protein ARALYDRAFT_470701 [Arabidopsis lyrata subsp. lyrata] gi|297335459|gb|EFH65876.1| hypothetical protein ARALYDRAFT_470701 [Arabidopsis lyrata subsp. lyrata]	675	595	0	88.1	68.7	74.4	hypothetical protein ARALYDRAFT_470701	gbpln	Arabidopsis lyrata	AT1G06780.2 | Symbols: GAUT6 | galacturonosyltransferase 6 | chr1:2083689-2086853 FORWARD LENGTH=602	675	602	0	89.2	68.9	74.1
Rsa1.0_00112.1.g5521.t1	ref|XP_002892358.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297338200|gb|EFH68617.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	349	440	1.00E-119	126.1	71.1	80.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G06770.1 | Symbols: DRIP1 | DREB2A-interacting protein 1 | chr1:2079222-2081707 REVERSE LENGTH=421	349	421	1.00E-120	120.6	72.8	80.5
Rsa1.0_00112.1.g5522.t1	ref|NP_180620.1| histone H1.2 [Arabidopsis thaliana] gi|121907|sp|P26569.1|H12_ARATH RecName: Full=Histone H1.2 gi|13430598|gb|AAK25921.1|AF360211_1 putative histone H1 protein [Arabidopsis thaliana] gi|16320|emb|CAA44316.1| Histone H1-2 [Arabidopsis thaliana] gi|14532870|gb|AAK64117.1| putative histone H1 protein [Arabidopsis thaliana] gi|20198329|gb|AAM15525.1| histone H1 [Arabidopsis thaliana] gi|21553923|gb|AAM63006.1| histone H1 [Arabidopsis thaliana] gi|330253325|gb|AEC08419.1| histone H1.2 [Arabidopsis thaliana]	251	273	1.00E-42	108.8	57.0	65.3	histone H1.2	gbpln	Arabidopsis thaliana	AT2G30620.1 | Symbols: | winged-helix DNA-binding transcription factor family protein | chr2:13045360-13046267 FORWARD LENGTH=273	251	273	3.00E-45	108.8	57.0	65.3
Rsa1.0_00112.1.g5523.t1	ref|XP_002889615.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335457|gb|EFH65874.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	486	490	0	100.8	89.7	93.8	pfkB-type carbohydrate kinase family protein	gbpln	Arabidopsis lyrata	AT1G06730.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr1:2067633-2070049 FORWARD LENGTH=488	486	488	0	100.4	87.7	92.4
Rsa1.0_00112.1.g5524.t1	ref|XP_002892356.1| hypothetical protein ARALYDRAFT_470695 [Arabidopsis lyrata subsp. lyrata] gi|297338198|gb|EFH68615.1| hypothetical protein ARALYDRAFT_470695 [Arabidopsis lyrata subsp. lyrata]	1170	1148	0	98.1	77.6	84.4	hypothetical protein ARALYDRAFT_470695	gbpln	Arabidopsis lyrata	AT1G06720.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:2060615-2067281 REVERSE LENGTH=1147	1170	1147	0	98.0	76.2	83.9
Rsa1.0_00112.1.g5525.t1	ref|NP_172156.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332189906|gb|AEE28027.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	952	997	0	104.7	81.6	88.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G06710.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:2056999-2060242 REVERSE LENGTH=997	952	997	0	104.7	81.6	88.9
Rsa1.0_00112.1.g5526.t1	gb|EOA38049.1| hypothetical protein CARUB_v10009518mg [Capsella rubella]	368	365	1.00E-177	99.2	86.4	91.3	hypothetical protein CARUB_v10009518mg	gbpln	Capsella rubella	AT1G06700.2 | Symbols: | Protein kinase superfamily protein | chr1:2052750-2054552 REVERSE LENGTH=361	368	361	1.00E-174	98.1	85.3	90.2
Rsa1.0_00112.1.g5527.t1	sp|P11594.2|PSBP_SINAL RecName: Full=Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; AltName: Full=23 kDa subunit of oxygen evolving system of photosystem II; AltName: Full=23 kDa thylakoid membrane protein; AltName: Full=OEC 23 kDa subunit; Flags: Precursor gi|21133|emb|CAA35081.1| oxygen-evolving complex of photosystem II [Sinapis alba]	263	260	1.00E-139	98.9	95.1	97.0	RecName: Full=Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; AltName: Full=23 kDa subunit of oxygen evolving system of photosystem II; AltName: Full=23 kDa thylakoid membrane protein; AltName: Full=OEC 23 kDa subunit; Flags: Precursor gi|21133|emb|CAA35081.1| oxygen-evolving complex of photosystem II	gbpln	Sinapis alba	AT1G06680.1 | Symbols: PSBP-1, OEE2, PSII-P, OE23 | photosystem II subunit P-1 | chr1:2047940-2049186 FORWARD LENGTH=263	263	263	1.00E-137	100.0	92.4	97.3

Rsa1.0_00112.1.g5528.t1	ref|XP_002889613.1| nuclear deih-boxhelicase [Arabidopsis lyrata subsp. lyrata] gi|297335455|gb|EFH65872.1| nuclear deih-boxhelicase [Arabidopsis lyrata subsp. lyrata]	1369	1580	0	115.4	72.0	81.5	nuclear deih-boxhelicase	gbpln	Arabidopsis lyrata	AT1G06670.1 | Symbols: NIH | nuclear DEIH-boxhelicase | chr1:2040567-2047333 FORWARD LENGTH=1576	1369	1576	0	115.1	71.2	81.6
Rsa1.0_00112.1.g5529.t1	ref|XP_002892352.1| hypothetical protein ARALYDRAFT_887868 [Arabidopsis lyrata subsp. lyrata] gi|297338194|gb|EFH68611.1| hypothetical protein ARALYDRAFT_887868 [Arabidopsis lyrata subsp. lyrata]	492	486	0	98.8	74.4	82.9	hypothetical protein ARALYDRAFT_887868	gbpln	Arabidopsis lyrata	AT1G06660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30820.2); Has 166 Blast hits to 144 proteins in 35 species: Archae - 0; Bacteria - 17; Metazoa - 13; Fungi - 20; Plants - 104; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr1:2037461-2040148 REVERSE LENGTH=481	492	481	0	97.8	73.0	81.7
Rsa1.0_00112.1.g5530.t1	ref|XP_002889612.1| hypothetical protein ARALYDRAFT_470684 [Arabidopsis lyrata subsp. lyrata] gi|297335454|gb|EFH65871.1| hypothetical protein ARALYDRAFT_470684 [Arabidopsis lyrata subsp. lyrata]	356	369	1.00E-164	103.7	76.7	88.2	hypothetical protein ARALYDRAFT_470684	gbpln	Arabidopsis lyrata	AT1G06650.2 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:2035909-2037186 FORWARD LENGTH=369	356	369	1.00E-162	103.7	75.6	86.5
Rsa1.0_00112.1.g5531.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	677	1239	0	183.0	47.6	54.7	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	677	1262	6.00E-61	186.4	18.5	26.7
Rsa1.0_00112.1.g5532.t1	ref|NP_172147.2| 1-aminocyclopropane-1-carboxylate oxidase-1 [Arabidopsis thaliana] gi|75297894|sp|Q84MB3.1|ACCH1_ARATH RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana] gi|332189889|gb|AEE28010.1| 1-aminocyclopropane-1-carboxylate oxidase-1 [Arabidopsis thaliana]	366	365	0	99.7	86.3	94.3	1-aminocyclopropane-1-carboxylate oxidase-1	gbpln	Arabidopsis thaliana	AT1G06620.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:2025618-2027094 FORWARD LENGTH=365	366	365	0	99.7	86.3	94.3
Rsa1.0_00112.1.g5533.t1	ref|XP_002892351.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297338193|gb|EFH68610.1| binding protein [Arabidopsis lyrata subsp. lyrata]	920	916	0	99.6	90.0	94.0	binding protein	gbpln	Arabidopsis lyrata	AT1G06590.1 | Symbols: | unknown protein; Has 380 Blast hits to 268 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 245; Fungi - 73; Plants - 49; Viruses - 0; Other Eukaryotes - 13 (source: NCBI BLink). | chr1:2016504-2024505 REVERSE LENGTH=916	920	916	0	99.6	89.5	93.3
Rsa1.0_00112.1.g5534.t1	gb|AFB74208.1| 4-hydroxyphenylpyruvate dioxygenase [Brassica napus]	469	445	0	94.9	84.6	87.6	4-hydroxyphenylpyruvate dioxygenase	gbpln	Brassica napus	AT1G06570.1 | Symbols: PDS1, HPD | phytoene desaturation 1 | chr1:2012015-2013543 REVERSE LENGTH=473	469	473	0	100.9	80.8	86.1
Rsa1.0_00112.1.g5535.t2	ref|NP_172143.3| NOL1/NOP2/sun-like protein [Arabidopsis thaliana] gi|30102680|gb|AAP21258.1| At1g06560 [Arabidopsis thaliana] gi|110743735|dbj|BAE99704.1| hypothetical protein [Arabidopsis thaliana] gi|332189884|gb|AEE28005.1| NOL1/NOP2/sun-like protein [Arabidopsis thaliana]	558	599	0	107.3	87.5	93.4	NOL1/NOP2/sun-like protein	gbpln	Arabidopsis thaliana	AT1G06560.1 | Symbols: | NOL1/NOP2/sun family protein | chr1:2007660-2011824 FORWARD LENGTH=599	558	599	0	107.3	87.5	93.4
Rsa1.0_00112.1.g5536.t1	ref|NP_172141.1| uncharacterized protein [Arabidopsis thaliana] gi|6692681|gb|AAF24815.1|AC007592_8 F12K11.13 [Arabidopsis thaliana] gi|20258790|gb|AAM13917.1| unknown protein [Arabidopsis thaliana] gi|332189882|gb|AEE28003.1| uncharacterized protein AT1G06540 [Arabidopsis thaliana]	116	125	3.00E-37	107.8	75.0	87.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G06540.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30930.1); Has 16 Blast hits to 16 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2002908-2003393 REVERSE LENGTH=125	116	125	4.00E-40	107.8	75.0	87.9
Rsa1.0_00112.1.g5537.t1	ref|NP_172140.1| tropomyosin-related protein [Arabidopsis thaliana] gi|6692690|gb|AAF24824.1|AC007592_17 F12K11.14 [Arabidopsis thaliana] gi|332189881|gb|AEE28002.1| tropomyosin-related protein [Arabidopsis thaliana]	510	323	1.00E-93	63.3	39.6	48.8	tropomyosin-related protein	gbpln	Arabidopsis thaliana	AT1G06530.1 | Symbols: | Tropomyosin-related | chr1:2001625-2002596 FORWARD LENGTH=323	510	323	3.00E-96	63.3	39.6	48.8
Rsa1.0_00112.1.g5538.t1	ref|XP_002892346.1| hypothetical protein ARALYDRAFT_887856 [Arabidopsis lyrata subsp. lyrata] gi|297338188|gb|EFH68605.1| hypothetical protein ARALYDRAFT_887856 [Arabidopsis lyrata subsp. lyrata]	603	584	0	96.8	83.6	89.1	hypothetical protein ARALYDRAFT_887856	gbpln	Arabidopsis lyrata	AT1G06520.1 | Symbols: ATGPAT1, GPAT1 | glycerol-3-phosphate acyltransferase 1 | chr1:1994170-1996067 REVERSE LENGTH=585	603	585	0	97.0	81.4	87.7

Rsa1.0_00112.1.g5539.t1	ref|NP_172138.2| uncharacterized protein [Arabidopsis thaliana] gi|27754366|gb|AAO22632.1| unknown protein [Arabidopsis thaliana] gi|28393897|gb|AAO42356.1| unknown protein [Arabidopsis thaliana] gi|332189879|gb|AEE28000.1| uncharacterized protein AT1G06510 [Arabidopsis thaliana]	247	277	1.00E-86	112.1	73.7	85.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G06510.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 376 Blast hits to 369 proteins in 152 species: Archae - 5; Bacteria - 113; Metazoa - 105; Fungi - 46; Plants - 27; Viruses - 2; Other Eukaryotes - 78 (source: NCBI BLink). | chr1:1992389-1993583 FORWARD LENGTH=277	247	277	4.00E-89	112.1	73.7	85.4
Rsa1.0_00112.1.g5540.t1	gb|ADK87343.1| callose synthase 7 [Arabidopsis thaliana]	1922	1933	0	100.6	89.4	94.6	callose synthase 7	gbpln	Arabidopsis thaliana	AT1G06490.1 | Symbols: ATGSL07, gsl07, atgsl7, GSL7 | glucan synthase-like 7 | chr1:1978762-1989295 FORWARD LENGTH=1958	1922	1958	0	101.9	89.4	94.6
Rsa1.0_00113.1.g5541.t1	gb|EOA17357.1| hypothetical protein CARUB_v10005638mg [Capsella rubella]	240	236	1.00E-117	98.3	86.7	92.9	hypothetical protein CARUB_v10005638mg	gbpln	Capsella rubella	AT4G28190.1 | Symbols: ULT1, ULT | Developmental regulator, ULTRAPETALA | chr4:13985753-13987050 FORWARD LENGTH=237	240	237	1.00E-119	98.8	87.1	92.9
Rsa1.0_00113.1.g5542.t1	ref|XP_002869514.1| hypothetical protein ARALYDRAFT_913700 [Arabidopsis lyrata subsp. lyrata] gi|297315350|gb|EFH45773.1| hypothetical protein ARALYDRAFT_913700 [Arabidopsis lyrata subsp. lyrata]	570	573	0	100.5	91.1	95.4	hypothetical protein ARALYDRAFT_913700	gbpln	Arabidopsis lyrata	AT4G28220.1 | Symbols: NDB1 | NAD(P)H dehydrogenase B1 | chr4:13993078-13995651 FORWARD LENGTH=571	570	571	0	100.2	88.9	94.6
Rsa1.0_00113.1.g5543.t1	gb|ABV89634.1| wound-responsive protein-related [Brassica rapa]	87	89	5.00E-35	102.3	90.8	94.3	wound-responsive protein-related	gbpln	Brassica rapa	AT4G28240.1 | Symbols: | Wound-responsive family protein | chr4:13997979-13998239 REVERSE LENGTH=86	87	86	2.00E-36	98.9	81.6	92.0
Rsa1.0_00113.1.g5544.t1	dbj|BAJ34284.1| unnamed protein product [Thellungiella halophila]	265	266	1.00E-142	100.4	92.1	97.0	unnamed protein product	----	----	AT4G28250.1 | Symbols: ATEXPB3, EXPB3, ATHEXP BETA 1.6 | expansin B3 | chr4:14000446-14001945 REVERSE LENGTH=264	265	264	1.00E-142	99.6	90.6	95.1
Rsa1.0_00113.1.g5545.t1	ref|NP_194555.1| uncharacterized protein [Arabidopsis thaliana] gi|145334149|ref|NP_001078455.1| uncharacterized protein [Arabidopsis thaliana] gi|7269680|emb|CAB79628.1| putative protein [Arabidopsis thaliana] gi|110742700|dbj|BAE99261.1| hypothetical protein [Arabidopsis thaliana] gi|332660060|gb|AEE85460.1| uncharacterized protein AT4G28260 [Arabidopsis thaliana] gi|332660061|gb|AEE85461.1| uncharacterized protein AT4G28260 [Arabidopsis thaliana]	120	516	4.00E-43	430.0	72.5	75.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G28260.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 50 Blast hits to 42 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14005048-14006762 FORWARD LENGTH=516	120	516	7.00E-46	430.0	72.5	75.8
Rsa1.0_00113.1.g5546.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00113.1.g5547.t1	ref|NP_194556.1| E3 ubiquitin-protein ligase RMA2 [Arabidopsis thaliana] gi|75279780|sp|P93030.1|RMA2_ARATH RecName: Full=E3 ubiquitin-protein ligase RMA2; AltName: Full=Protein RING membrane-anchor 2 gi|1773040|gb|AAC49830.1| RING zinc finger protein [Arabidopsis thaliana] gi|7269681|emb|CAB79629.1| putative protein [Arabidopsis thaliana] gi|27764994|gb|AAO23618.1| At4g28270 [Arabidopsis thaliana] gi|110742855|dbj|BAE99326.1| hypothetical protein [Arabidopsis thaliana] gi|332660062|gb|AEE85462.1| E3 ubiquitin-protein ligase RMA2 [Arabidopsis thaliana]	193	193	4.00E-87	100.0	80.8	88.6	E3 ubiquitin-protein ligase RMA2	gbpln	Arabidopsis thaliana	AT4G28270.1 | Symbols: ATRMA2, RMA2 | RING membrane-anchor 2 | chr4:14007614-14008195 REVERSE LENGTH=193	193	193	1.00E-89	100.0	80.8	88.6
Rsa1.0_00113.1.g5548.t5	gb|EOA16491.1| hypothetical protein CARUB_v10004649mg [Capsella rubella]	702	497	0	70.8	57.8	61.4	hypothetical protein CARUB_v10004649mg	gbpln	Capsella rubella	AT4G28300.1 | Symbols: | Protein of unknown function (DUF1421) | chr4:14014860-14016823 FORWARD LENGTH=496	702	496	0	70.7	58.1	62.3
Rsa1.0_00113.1.g5549.t1	ref|NP_567804.1| uncharacterized protein [Arabidopsis thaliana] gi|21553910|gb|AAM62993.1| unknown [Arabidopsis thaliana] gi|51972009|dbj|BAD44669.1| unknown protein [Arabidopsis thaliana] gi|105829831|gb|ABF74705.1| At4g28310 [Arabidopsis thaliana] gi|332660068|gb|AEE85468.1| uncharacterized protein AT4G28310 [Arabidopsis thaliana]	186	202	2.00E-29	108.6	52.7	65.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G28310.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:14017458-14018066 FORWARD LENGTH=202	186	202	9.00E-32	108.6	52.7	65.1

Rsa1.0_00113.1.g5550.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00113.1.g5551.t1	ref|NP_194974.1| uncharacterized protein [Arabidopsis thaliana] gi|4049350|emb|CAA22575.1| putative protein [Arabidopsis thaliana] gi|7270152|emb|CAB79965.1| putative protein [Arabidopsis thaliana] gi|15450373|gb|AAK96480.1| AT4g32480/F8B4_180 [Arabidopsis thaliana] gi|16974485|gb|AAL31246.1| AT4g32480/F8B4_180 [Arabidopsis thaliana] gi|332660667|gb|AEE86067.1| uncharacterized protein AT4G32480 [Arabidopsis thaliana]	300	287	1.00E-134	95.7	79.3	85.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32480.1 | Symbols: | Protein of unknown function (DUF506) | chr4:15676488-15677776 FORWARD LENGTH=287	300	287	1.00E-137	95.7	79.3	85.7
Rsa1.0_00113.1.g5552.t1	gb|EOA18034.1| hypothetical protein CARUB_v10006477mg, partial [Capsella rubella]	149	142	2.00E-51	95.3	71.1	79.9	hypothetical protein CARUB_v10006477mg, partial	gbpln	Capsella rubella	AT4G28395.1 | Symbols: ATA7, A7 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:14043991-14044728 FORWARD LENGTH=180	149	180	2.00E-53	120.8	71.8	78.5
Rsa1.0_00113.1.g5553.t1	ref|NP_567808.1| putative protein phosphatase 2C 58 [Arabidopsis thaliana] gi|75163673|sp|Q93YW5.1|P2C58_ARATH RecName: Full=Probable protein phosphatase 2C 58; Short=AtPP2C58 gi|16604585|gb|AAL24149.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|20258991|gb|AAM14211.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|332660081|gb|AEE85481.1| putative protein phosphatase 2C 58 [Arabidopsis thaliana]	264	283	1.00E-135	107.2	89.0	95.5	putative protein phosphatase 2C 58	gbpln	Arabidopsis thaliana	AT4G28400.1 | Symbols: | Protein phosphatase 2C family protein | chr4:14048499-14050118 FORWARD LENGTH=283	264	283	1.00E-138	107.2	89.0	95.5
Rsa1.0_00113.1.g5554.t1	gb|EOA19176.1| hypothetical protein CARUB_v10007855mg [Capsella rubella]	448	449	0	100.2	80.6	90.4	hypothetical protein CARUB_v10007855mg	gbpln	Capsella rubella	AT4G28410.1 | Symbols: | Tyrosine transaminase family protein | chr4:14052391-14054846 FORWARD LENGTH=447	448	447	0	99.8	80.4	89.1
Rsa1.0_00113.1.g5555.t1	gb|EOA17584.1| hypothetical protein CARUB_v10005945mg [Capsella rubella]	154	152	2.00E-68	98.7	85.1	88.3	hypothetical protein CARUB_v10005945mg	gbpln	Capsella rubella	AT4G28440.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr4:14060054-14060970 FORWARD LENGTH=153	154	153	6.00E-65	99.4	76.6	79.9
Rsa1.0_00113.1.g5556.t2	ref|XP_002867449.1| AT4g28450/F20O9_130 [Arabidopsis lyrata subsp. lyrata] gi|297313285|gb|EFH43708.1| AT4g28450/F20O9_130 [Arabidopsis lyrata subsp. lyrata]	452	452	0	100.0	86.9	92.9	AT4g28450/F20O9_130	gbpln	Arabidopsis lyrata	AT4G28450.1 | Symbols: | nucleotide binding;protein binding | chr4:14061724-14064582 REVERSE LENGTH=452	452	452	0	100.0	85.6	92.0
Rsa1.0_00113.1.g5557.t1	ref|NP_194575.2| uncharacterized protein [Arabidopsis thaliana] gi|91805615|gb|ABE65536.1| hypothetical protein At4g28460 [Arabidopsis thaliana] gi|332660089|gb|AEE85489.1| uncharacterized protein AT4G28460 [Arabidopsis thaliana]	73	72	2.00E-24	98.6	82.2	87.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G28460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; Has 8 Blast hits to 8 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14066083-14066301 FORWARD LENGTH=72	73	72	4.00E-27	98.6	82.2	87.7
Rsa1.0_00113.1.g5558.t1	ref|NP_194576.5| 26S proteasome regulatory subunit S2 1B [Arabidopsis thaliana] gi|75130218|sp|Q6XJG8.1|RPN1B_ARATH RecName: Full=26S proteasome non-ATPase regulatory subunit 2 1B; AltName: Full=26S proteasome regulatory subunit RPN1 B; Short=AtRPN1b; AltName: Full=26S proteasome regulatory subunit S2 1B gi|32700012|gb|AAP86656.1| 26S proteasome subunit RPN1b [Arabidopsis thaliana] gi|332660090|gb|AEE85490.1| 26S proteasome regulatory subunit S2 1B [Arabidopsis thaliana]	891	891	0	100.0	93.2	96.2	26S proteasome regulatory subunit S2 1B	gbpln	Arabidopsis thaliana	AT4G28470.1 | Symbols: RPN1B, ATRPN1B | 26S proteasome regulatory subunit S2 1B | chr4:14067082-14072357 REVERSE LENGTH=891	891	891	0	100.0	93.2	96.2
Rsa1.0_00113.1.g5559.t1	ref|XP_002869499.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata] gi|297315335|gb|EFH45758.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata]	322	344	1.00E-148	106.8	88.5	92.9	DNAJ heat shock family protein	gbpln	Arabidopsis lyrata	AT2G20560.1 | Symbols: | DNAJ heat shock family protein | chr2:8848353-8849815 REVERSE LENGTH=337	322	337	1.00E-150	104.7	83.9	89.1

<table>
<tr><td>Rsa1.0_00113.1.g5560.t1</td><td>ref|XP_002867447.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313283|gb|EFH43706.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>200</td><td>200</td><td>4.00E-95</td><td>100.0</td><td>82.0</td><td>90.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G46090.1 | Symbols: | Protein of unknown function (DUF679) | chr5:18693485-18694129 FORWARD LENGTH=214</td><td>200</td><td>214</td><td>5.00E-52</td><td>107.0</td><td>49.0</td><td>65.5</td></tr>
<tr><td>Rsa1.0_00113.1.g5561.t1</td><td>ref|NP_194579.1| NAC domain containing protein 73 [Arabidopsis thaliana] gi|2842493|emb|CAA16890.1| predicted protein [Arabidopsis thaliana] gi|7269704|emb|CAB79652.1| predicted protein [Arabidopsis thaliana] gi|67633762|gb|AAY78805.1| no apical meristem family protein [Arabidopsis thaliana] gi|332660095|gb|AEE85495.1| NAC domain containing protein 73 [Arabidopsis thaliana]</td><td>306</td><td>305</td><td>1.00E-141</td><td>99.7</td><td>85.9</td><td>90.5</td><td>NAC domain containing protein 73</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G28500.1 | Symbols: ANAC073, SND2, NAC073 | NAC domain containing protein 73 | chr4:14083014-14084266 FORWARD LENGTH=305</td><td>306</td><td>305</td><td>1.00E-144</td><td>99.7</td><td>85.9</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00113.1.g5562.t1</td><td>gb|EOA16916.1| hypothetical protein CARUB_v10005139mg [Capsella rubella]</td><td>349</td><td>353</td><td>1.00E-166</td><td>101.1</td><td>84.8</td><td>89.4</td><td>hypothetical protein CARUB_v10005139mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G28530.1 | Symbols: anac074, NAC074 | NAC domain containing protein 74 | chr4:14090725-14094603 REVERSE LENGTH=352</td><td>349</td><td>352</td><td>1.00E-154</td><td>100.9</td><td>85.1</td><td>89.4</td></tr>
<tr><td>Rsa1.0_00113.1.g5563.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00113.1.g5564.t1</td><td>ref|XP_002886265.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332105|gb|EFH62524.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>1183</td><td>1181</td><td>0</td><td>99.8</td><td>83.1</td><td>90.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G18760.1 | Symbols: CHR8 | chromatin remodeling 8 | chr2:8129154-8133502 FORWARD LENGTH=1187</td><td>1183</td><td>1187</td><td>0</td><td>100.3</td><td>83.9</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00113.1.g5565.t1</td><td>ref|NP_567812.1| casein kinase I-like 6 [Arabidopsis thaliana] gi|20466498|gb|AAM20566.1| protein kinase ADK1-like protein [Arabidopsis thaliana] gi|23198156|gb|AAN15605.1| protein kinase ADK1-like protein [Arabidopsis thaliana] gi|62996982|gb|AAY24535.1| casein kinase 1-like protein 6 [Arabidopsis thaliana] gi|332660103|gb|AEE85503.1| casein kinase I-like 6 [Arabidopsis thaliana]</td><td>481</td><td>479</td><td>0</td><td>99.6</td><td>91.7</td><td>95.4</td><td>casein kinase I-like 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G28540.1 | Symbols: CKL6, PAPK1 | casein kinase I-like 6 | chr4:14107284-14110511 FORWARD LENGTH=479</td><td>481</td><td>479</td><td>0</td><td>99.6</td><td>91.7</td><td>95.4</td></tr>
<tr><td>Rsa1.0_00114.1.g5566.t1</td><td>ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]</td><td>346</td><td>390</td><td>4.00E-50</td><td>112.7</td><td>35.3</td><td>47.4</td><td>hypothetical protein ARALYDRAFT_917455</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295</td><td>346</td><td>295</td><td>4.00E-39</td><td>85.3</td><td>27.2</td><td>43.6</td></tr>
<tr><td>Rsa1.0_00114.1.g5567.t1</td><td>gb|EOA38158.1| hypothetical protein CARUB_v10009634mg [Capsella rubella]</td><td>347</td><td>343</td><td>1.00E-139</td><td>98.8</td><td>77.8</td><td>86.5</td><td>hypothetical protein CARUB_v10009634mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G24267.1 | Symbols: | Protein of unknown function (DUF1664) | chr1:8604451-8607241 REVERSE LENGTH=343</td><td>347</td><td>343</td><td>1.00E-137</td><td>98.8</td><td>76.1</td><td>85.0</td></tr>
<tr><td>Rsa1.0_00114.1.g5568.t1</td><td>ref|XP_002514883.1| conserved hypothetical protein [Ricinus communis] gi|223545934|gb|EEF47437.1| conserved hypothetical protein [Ricinus communis]</td><td>222</td><td>269</td><td>7.00E-47</td><td>121.2</td><td>59.0</td><td>70.3</td><td>conserved hypothetical protein</td><td>gbpln</td><td>Ricinus communis</td><td>AT5G13090.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4153758-4154567 REVERSE LENGTH=269</td><td>222</td><td>269</td><td>4.00E-42</td><td>121.2</td><td>54.5</td><td>67.1</td></tr>
<tr><td>Rsa1.0_00114.1.g5569.t1</td><td>ref|XP_002893458.1| glucose-6-phosphate dehydrogenase 3 [Arabidopsis lyrata subsp. lyrata] gi|297339300|gb|EFH69717.1| glucose-6-phosphate dehydrogenase 3 [Arabidopsis lyrata subsp. lyrata]</td><td>591</td><td>601</td><td>0</td><td>101.7</td><td>87.6</td><td>92.9</td><td>glucose-6-phosphate dehydrogenase 3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G24280.1 | Symbols: G6PD3 | glucose-6-phosphate dehydrogenase 3 | chr1:8609495-8612383 FORWARD LENGTH=599</td><td>591</td><td>599</td><td>0</td><td>101.4</td><td>85.6</td><td>90.7</td></tr>
<tr><td>Rsa1.0_00114.1.g5570.t1</td><td>ref|NP_174062.1| kelch repeat-containing F-box protein [Arabidopsis thaliana] gi|374095396|sp|Q9FZJ3.2|FBK16_ARATH RecName: Full=Putative F-box/kelch-repeat protein At1g27420 gi|332192706|gb|AEE30827.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]</td><td>356</td><td>346</td><td>1.00E-119</td><td>97.2</td><td>64.0</td><td>73.9</td><td>kelch repeat-containing F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G27420.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9519108-9520520 FORWARD LENGTH=346</td><td>356</td><td>346</td><td>1.00E-122</td><td>97.2</td><td>64.0</td><td>73.9</td></tr>
</table>

Rsa1.0_00114.1.g5571.t1	gb|EOA37642.1| hypothetical protein CARUB_v10012120mg [Capsella rubella]	384	605	1.00E-176	157.6	86.2	91.9	hypothetical protein CARUB_v10012120mg	gbpln	Capsella rubella	AT1G24310.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; Has 2922 Blast hits to 2454 proteins in 263 species: Archae - 0; Bacteria - 57; Metazoa - 1043; Fungi - 654; Plants - 388; Viruses - 11; Other Eukaryotes - 769 (source: NCBI BLink). | chr1:8624192-8626179 FORWARD LENGTH=377	384	377	1.00E-164	98.2	82.6	87.0
Rsa1.0_00114.1.g5572.t1	ref|NP_201043.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75180621|sp|Q9LVA2.1|PP443_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g62370 gi|8809650|dbj|BAA97201.1| unnamed protein product [Arabidopsis thaliana] gi|332010218|gb|AED97601.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	83	982	2.00E-18	1183.1	51.8	56.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G62370.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:25041901-25044849 REVERSE LENGTH=982	83	982	3.00E-21	1183.1	51.8	56.6
Rsa1.0_00114.1.g5573.t1	gb|EOA39714.1| hypothetical protein CARUB_v10008359mg [Capsella rubella]	773	776	0	100.4	84.2	90.4	hypothetical protein CARUB_v10008359mg	gbpln	Capsella rubella	AT1G24330.1 | Symbols: | ARM repeat superfamily protein | chr1:8631779-8634835 FORWARD LENGTH=771	773	771	0	99.7	85.1	91.2
Rsa1.0_00114.1.g5574.t1	gb|EOA37163.1| hypothetical protein CARUB_v10010495mg [Capsella rubella]	164	166	8.00E-81	101.2	89.6	92.7	hypothetical protein CARUB_v10010495mg	gbpln	Capsella rubella	AT1G24350.1 | Symbols: | Acid phosphatase/vanadium-dependent haloperoxidase-related protein | chr1:8639098-8640313 REVERSE LENGTH=168	164	168	3.00E-83	102.4	89.6	92.7
Rsa1.0_00114.1.g5575.t1	ref|NP_564218.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|9743332|gb|AAF97956.1|AC000103_6 F21J9.10 [Arabidopsis thaliana] gi|21553664|gb|AAM62757.1| unknown [Arabidopsis thaliana] gi|24030317|gb|AAN41327.1| unknown protein [Arabidopsis thaliana] gi|332192409|gb|AEE30530.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	254	251	1.00E-134	98.8	92.1	96.1	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT1G24440.1 | Symbols: | RING/U-box superfamily protein | chr1:8662340-8663777 FORWARD LENGTH=251	254	251	1.00E-137	98.8	92.1	96.1
Rsa1.0_00114.1.g5576.t1	gb|EOA37586.1| hypothetical protein CARUB_v10011938mg [Capsella rubella]	1750	1772	0	101.3	75.0	85.6	hypothetical protein CARUB_v10011938mg	gbpln	Capsella rubella	AT1G24460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G31570.1); Has 181008 Blast hits to 85359 proteins in 3551 species: Archae - 3290; Bacteria - 48304; Metazoa - 70793; Fungi - 13943; Plants - 10118; Viruses - 785; Other Eukaryotes - 33775 (source: NCBI BLink). | chr1:8666072-8672338 FORWARD LENGTH=1807	1750	1807	0	103.3	75.3	85.0
Rsa1.0_00114.1.g5577.t1	ref|NP_173859.1| T-complex protein 1 subunit epsilon [Arabidopsis thaliana] gi|3024697|sp|O04450.1|TCPE_ARATH RecName: Full=T-complex protein 1 subunit epsilon; Short=TCP-1-epsilon; AltName: Full=CCT-epsilon gi|9743353|gb|AAF97977.1|AC000103_27 F21J9.17 [Arabidopsis thaliana] gi|19715605|gb|AAL91625.1| At1g24510/F21J9_150 [Arabidopsis thaliana] gi|23463047|gb|AAN33193.1| At1g24510/F21J9_150 [Arabidopsis thaliana] gi|332192420|gb|AEE30541.1| T-complex protein 1 subunit epsilon [Arabidopsis thaliana]	535	535	0	100.0	98.7	99.4	T-complex protein 1 subunit epsilon	gbpln	Arabidopsis thaliana	AT1G24510.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr1:8685504-8688101 REVERSE LENGTH=535	535	535	0	100.0	98.7	99.4
Rsa1.0_00114.1.g5578.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00114.1.g5579.t1	emb|CAA48292.1| bgp1 [Brassica rapa] gi|448272|prf||1916399A Bgp1 gene	117	119	5.00E-29	101.7	86.3	89.7	bgp1	gbpln	Brassica rapa	AT1G24520.1 | Symbols: BCP1 | homolog of Brassica campestris pollen protein 1 | chr1:8688699-8689058 FORWARD LENGTH=119	117	119	3.00E-30	101.7	78.6	88.0

Rsa1.0_00114.1.g5580.t8	ref|XP_002893444.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297339286|gb|EFH69703.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	887	418	1.00E-170	47.1	35.7	38.0	transducin family protein	gbpln	Arabidopsis lyrata	AT1G24530.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:8693287-8694543 FORWARD LENGTH=418	887	418	1.00E-168	47.1	35.6	37.8
Rsa1.0_00114.1.g5581.t1	ref|XP_002893439.1| F21J9.24 [Arabidopsis lyrata subsp. lyrata] gi|297339281|gb|EFH69698.1| F21J9.24 [Arabidopsis lyrata subsp. lyrata]	139	136	3.00E-47	97.8	85.6	88.5	F21J9.24	gbpln	Arabidopsis lyrata	AT1G67856.1 | Symbols: | RING/U-box superfamily protein | chr1:25442486-25442887 FORWARD LENGTH=133	139	133	6.00E-43	95.7	66.9	79.9
Rsa1.0_00114.1.g5582.t1	gb|EOA36370.1| hypothetical protein CARUB_v10010770mg [Capsella rubella]	80	87	5.00E-13	108.8	67.5	72.5	hypothetical protein CARUB_v10010770mg	gbpln	Capsella rubella	AT1G24575.1 | Symbols: | unknown protein; Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:8711211-8711477 REVERSE LENGTH=88	80	88	1.00E-15	110.0	65.0	73.8
Rsa1.0_00114.1.g5583.t1	gb|EMJ13006.1| hypothetical protein PRUPE_ppa009890mg [Prunus persica] gi|462409693|gb|EMJ15027.1| hypothetical protein PRUPE_ppa009892mg [Prunus persica]	63	273	3.00E-14	433.3	69.8	76.2	hypothetical protein PRUPE_ppa009890mg	gbpln	Prunus persica	AT1G58684.1 | Symbols: | Ribosomal protein S5 family protein | chr1:21770021-21771217 REVERSE LENGTH=284	63	284	3.00E-16	450.8	61.9	65.1
Rsa1.0_00114.1.g5584.t1	gb|EOA36376.1| hypothetical protein CARUB_v10010782mg [Capsella rubella]	84	82	1.00E-24	97.6	72.6	81.0	hypothetical protein CARUB_v10010782mg	gbpln	Capsella rubella	AT1G24577.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67910.2); Has 115 Blast hits to 115 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 115; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:8712758-8712985 REVERSE LENGTH=75	84	75	3.00E-23	89.3	64.3	70.2
Rsa1.0_00114.1.g5585.t1	ref|XP_002890702.1| hypothetical protein ARALYDRAFT_890210 [Arabidopsis lyrata subsp. lyrata] gi|297336544|gb|EFH66961.1| hypothetical protein ARALYDRAFT_890210 [Arabidopsis lyrata subsp. lyrata]	296	305	1.00E-132	103.0	82.8	89.2	hypothetical protein ARALYDRAFT_890210	gbpln	Arabidopsis lyrata	AT1G24590.1 | Symbols: DRNL, DRN-LIKE, SOB2, ESR2 | DORNROSCHEN-like | chr1:8714389-8715309 REVERSE LENGTH=306	296	306	1.00E-135	103.4	82.1	89.5
Rsa1.0_00114.1.g5586.t1	ref|XP_002893438.1| hypothetical protein ARALYDRAFT_890209 [Arabidopsis lyrata subsp. lyrata] gi|297339280|gb|EFH69697.1| hypothetical protein ARALYDRAFT_890209 [Arabidopsis lyrata subsp. lyrata]	75	72	3.00E-24	96.0	78.7	85.3	hypothetical protein ARALYDRAFT_890209	gbpln	Arabidopsis lyrata	AT1G24600.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67920.1); Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:8720375-8720593 FORWARD LENGTH=72	75	72	5.00E-24	96.0	73.3	80.0
Rsa1.0_00114.1.g5587.t3	ref|XP_002888898.1| hypothetical protein ARALYDRAFT_476423 [Arabidopsis lyrata subsp. lyrata] gi|297334739|gb|EFH65157.1| hypothetical protein ARALYDRAFT_476423 [Arabidopsis lyrata subsp. lyrata]	139	381	9.00E-34	274.1	53.2	58.3	hypothetical protein ARALYDRAFT_476423	gbpln	Arabidopsis lyrata	AT1G72880.1 | Symbols: | Survival protein SurE-like phosphatase/nucleotidase | chr1:27423678-27425928 REVERSE LENGTH=385	139	385	6.00E-36	277.0	52.5	56.1
Rsa1.0_00114.1.g5588.t1	ref|NP_173866.1| putative calcium-binding protein CML25 [Arabidopsis thaliana] gi|75334522|sp|Q9FYK2.1|CML25_ARATH RecName: Full=Probable calcium-binding protein CML25; AltName: Full=Calmodulin-like protein 25 gi|9743349|gb|AAF97973.1|AC000103_23 F21J9.28 [Arabidopsis thaliana] gi|91805849|gb|ABE65653.1| polcalcin [Arabidopsis thaliana] gi|332192433|gb|AEE30554.1| putative calcium-binding protein CML25 [Arabidopsis thaliana]	185	186	1.00E-89	100.5	90.3	94.1	putative calcium-binding protein CML25	gbpln	Arabidopsis thaliana	AT1G24620.1 | Symbols: | EF hand calcium-binding protein family | chr1:8723893-8724453 REVERSE LENGTH=186	185	186	5.00E-92	100.5	90.3	94.1
Rsa1.0_00114.1.g5589.t1	ref|XP_002893435.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297339277|gb|EFH69694.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	298	894	4.00E-74	300.0	54.0	65.1	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G24650.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:8734570-8737315 FORWARD LENGTH=886	298	886	1.00E-69	297.3	50.7	62.4
Rsa1.0_00114.1.g5590.t1	gb|EOA20525.1| hypothetical protein CARUB_v10000839mg [Capsella rubella]	205	484	6.00E-18	236.1	33.2	46.8	hypothetical protein CARUB_v10000839mg	gbpln	Capsella rubella	AT1G52030.1 | Symbols: MBP2, MBP1.2, F-ATMBP | myrosinase-binding protein 2 | chr1:19346090-19348282 REVERSE LENGTH=642	205	642	3.00E-19	313.2	31.7	47.8
Rsa1.0_00114.1.g5591.t1	dbj|BAJ33823.1| unnamed protein product [Thellungiella halophila]	212	209	1.00E-103	98.6	86.3	92.0	unnamed protein product	----	----	AT1G24625.1 | Symbols: ZFP7 | zinc finger protein 7 | chr1:8726009-8726638 REVERSE LENGTH=209	212	209	3.00E-94	98.6	83.0	89.2

Rsa1.0_00114.1.g5592.t1	gb|EOA36780.1| hypothetical protein CARUB_v10008078mg [Capsella rubella]	1802	1806	0	100.2	86.9	91.7	hypothetical protein CARUB_v10008078mg	gbpln	Capsella rubella	AT1G24706.1 | Symbols: THO2, AtTHO2 | THO2 | chr1:8742210-8755243 FORWARD LENGTH=1804	1802	1804	0	100.1	86.8	91.5
Rsa1.0_00114.1.g5593.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00114.1.g5594.t1	gb|EOA36221.1| hypothetical protein CARUB_v10010170mg [Capsella rubella]	238	236	1.00E-112	99.2	83.2	91.2	hypothetical protein CARUB_v10010170mg	gbpln	Capsella rubella	AT1G24735.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:8757977-8759448 FORWARD LENGTH=240	238	240	1.00E-113	100.8	80.7	87.8
Rsa1.0_00114.1.g5595.t3	ref|XP_002890697.1| At1g68060/T23K23_9 [Arabidopsis lyrata subsp. lyrata] gi|297336539|gb|EFH66956.1| At1g68060/T23K23_9 [Arabidopsis lyrata subsp. lyrata]	552	634	0	114.9	89.5	93.7	At1g68060/T23K23_9	gbpln	Arabidopsis lyrata	AT1G24764.1 | Symbols: ATMAP70-2, MAP70-2 | microtubule-associated proteins 70-2 | chr1:8760001-8763256 REVERSE LENGTH=634	552	634	0	114.9	88.9	93.7
Rsa1.0_00114.1.g5596.t3	ref|NP_173884.5| UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Arabidopsis thaliana] gi|334182837|ref|NP_173878.6| UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Arabidopsis thaliana] gi|332192446|gb|AEE30567.1| UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Arabidopsis thaliana] gi|332192452|gb|AEE30573.1| UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Arabidopsis thaliana]	350	369	2.33E-156	105.4	72.9	80.6	UDP-3-O-	gbpln	Arabidopsis thaliana	AT1G24880.1 | Symbols: | UDP-3-O-acyl N-acetylglycosamine deacetylase family protein | chr1:8776028-8783586 FORWARD LENGTH=369	350	369	1.00E-149	105.4	72.9	80.6
Rsa1.0_00114.1.g5597.t1	ref|XP_002890696.1| hypothetical protein ARALYDRAFT_472860 [Arabidopsis lyrata subsp. lyrata] gi|297336538|gb|EFH66955.1| hypothetical protein ARALYDRAFT_472860 [Arabidopsis lyrata subsp. lyrata]	278	277	1.00E-137	99.6	88.5	92.1	hypothetical protein ARALYDRAFT_472860	gbpln	Arabidopsis lyrata	AT1G25220.1 | Symbols: ASB1, TRP4, WEI7 | anthranilate synthase beta subunit 1 | chr1:8837430-8839478 REVERSE LENGTH=276	278	276	1.00E-140	99.3	88.5	91.7
Rsa1.0_00114.1.g5598.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00115.1.g5599.t1	dbj|BAJ34508.1| unnamed protein product [Thellungiella halophila]	497	502	0	101.0	88.7	94.2	unnamed protein product	----	----	AT4G21910.3 | Symbols: | MATE efflux family protein | chr4:11625821-11630964 REVERSE LENGTH=507	497	507	0	102.0	84.9	91.5
Rsa1.0_00115.1.g5600.t1	gb|EOA18828.1| hypothetical protein CARUB_v10007442mg [Capsella rubella]	117	119	4.00E-44	101.7	76.1	88.9	hypothetical protein CARUB_v10007442mg	gbpln	Capsella rubella	AT4G21902.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G04745.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:11619786-11620139 FORWARD LENGTH=117	117	117	6.00E-45	100.0	71.8	84.6
Rsa1.0_00115.1.g5601.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00115.1.g5602.t1	gb|EOA16303.1| hypothetical protein CARUB_v10004453mg [Capsella rubella]	583	578	0	99.1	80.8	87.3	hypothetical protein CARUB_v10004453mg	gbpln	Capsella rubella	AT4G21900.1 | Symbols: PRORP3 | proteinaceous RNase P 3 | chr4:11616567-11619349 REVERSE LENGTH=576	583	576	0	98.8	80.3	86.4
Rsa1.0_00115.1.g5603.t1	ref|XP_002867816.1| hypothetical protein ARALYDRAFT_354584 [Arabidopsis lyrata subsp. lyrata] gi|297313652|gb|EFH44075.1| hypothetical protein ARALYDRAFT_354584 [Arabidopsis lyrata subsp. lyrata]	272	388	8.00E-63	142.6	57.7	70.6	hypothetical protein ARALYDRAFT_354584	gbpln	Arabidopsis lyrata	AT4G21895.1 | Symbols: | DNA binding | chr4:11613523-11614242 REVERSE LENGTH=239	272	239	1.00E-49	87.9	41.9	54.0
Rsa1.0_00115.1.g5604.t1	ref|XP_002266891.1| PREDICTED: uncharacterized protein LOC100252085 [Vitis vinifera]	635	633	0	99.7	63.5	77.6	PREDICTED: uncharacterized protein LOC100252085	gbpln	Vitis vinifera	AT4G21890.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleus; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 7 growth stages; Has 14 Blast hits to 14 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11611874-11612674 REVERSE LENGTH=266	635	266	1.00E-132	41.9	37.8	39.8

Rsa1.0_00115.1.g5605.t2	ref|NP_193919.6| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|223635628|sp|O49711.2|PP335_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g21880, mitochondrial; Flags: Precursor gi|332659118|gb|AEE84518.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	818	843	0	103.1	70.0	79.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G21880.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:11605156-11610651 FORWARD LENGTH=843	818	843	0	103.1	70.0	79.3
Rsa1.0_00115.1.g5606.t1	gb|EOA17633.1| hypothetical protein CARUB_v10005998mg [Capsella rubella]	138	134	6.00E-54	97.1	75.4	86.2	hypothetical protein CARUB_v10005998mg	gbpln	Capsella rubella	AT4G21870.1 | Symbols: | HSP20-like chaperones superfamily protein | chr4:11603756-11604285 REVERSE LENGTH=134	138	134	5.00E-55	97.1	76.1	87.0
Rsa1.0_00115.1.g5607.t1	gb|EOA17443.1| hypothetical protein CARUB_v10005762mg [Capsella rubella]	254	202	6.00E-78	79.5	64.2	67.7	hypothetical protein CARUB_v10005762mg	gbpln	Capsella rubella	AT4G21860.3 | Symbols: MSRB2 | methionine sulfoxide reductase B 2 | chr4:11600238-11601507 REVERSE LENGTH=202	254	202	3.00E-76	79.5	61.4	65.7
Rsa1.0_00115.1.g5608.t1	gb|EOA15912.1| hypothetical protein CARUB_v10004007mg [Capsella rubella]	1354	1233	0	91.1	73.9	81.0	hypothetical protein CARUB_v10004007mg	gbpln	Capsella rubella	AT4G21820.1 | Symbols: | binding;calmodulin binding | chr4:11577558-11583871 FORWARD LENGTH=1255	1354	1255	0	92.7	56.4	62.7
Rsa1.0_00115.1.g5609.t1	ref|NP_193912.3| derlin-2.1 [Arabidopsis thaliana] gi|297799884|ref|XP_002867826.1| hypothetical protein ARALYDRAFT_492693 [Arabidopsis lyrata subsp. lyrata] gi|332278209|sp|Q8VZ96.3|DER21_ARATH RecName: Full=Derlin-2.1; AltName: Full=AtDerlin2-1 gi|17473759|gb|AAL38318.1| putative protein [Arabidopsis thaliana] gi|24899743|gb|AAN65086.1| putative protein [Arabidopsis thaliana] gi|297313662|gb|EFH44085.1| hypothetical protein ARALYDRAFT_492693 [Arabidopsis lyrata subsp. lyrata] gi|332659106|gb|AEE84506.1| derlin-2.1 [Arabidopsis thaliana]	244	244	1.00E-137	100.0	97.1	98.4	derlin-2.1	gbpln	Arabidopsis lyrata	AT4G21810.1 | Symbols: DER2.1 | DERLIN-2.1 | chr4:11575345-11577003 REVERSE LENGTH=244	244	244	1.00E-140	100.0	97.1	98.4
Rsa1.0_00115.1.g5610.t2	ref|NP_193911.1| XPA-binding protein 1 [Arabidopsis thaliana] gi|42572979|ref|NP_974586.1| XPA-binding protein 1 [Arabidopsis thaliana] gi|16930419|gb|AAL31895.1|AF419563_1 AT4g21800/F17L22_260 [Arabidopsis thaliana] gi|23505917|gb|AAN28818.1| At4g21800/F17L22_260 [Arabidopsis thaliana] gi|332659104|gb|AEE84504.1| XPA-binding protein 1 [Arabidopsis thaliana] gi|332659105|gb|AEE84505.1| XPA-binding protein 1 [Arabidopsis thaliana]	375	379	0	101.1	85.9	91.2	XPA-binding protein 1	gbpln	Arabidopsis thaliana	AT4G21800.2 | Symbols: QQT2 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:11573289-11574976 FORWARD LENGTH=379	375	379	0	101.1	85.9	91.2
Rsa1.0_00115.1.g5611.t2	ref|XP_002869863.1| hypothetical protein ARALYDRAFT_492696 [Arabidopsis lyrata subsp. lyrata] gi|297315699|gb|EFH46122.1| hypothetical protein ARALYDRAFT_492696 [Arabidopsis lyrata subsp. lyrata]	268	291	1.00E-127	108.6	86.6	91.4	hypothetical protein ARALYDRAFT_492696	gbpln	Arabidopsis lyrata	AT4G21790.1 | Symbols: TOM1, ATTOM1 | tobamovirus multiplication 1 | chr4:11569924-11572163 FORWARD LENGTH=291	268	291	1.00E-129	108.6	86.6	92.2
Rsa1.0_00115.1.g5612.t24	ref|NP_567635.1| uncharacterized protein [Arabidopsis thaliana] gi|4455286|emb|CAB36822.1| hypothetical protein [Arabidopsis thaliana] gi|7268975|emb|CAB81285.1| hypothetical protein [Arabidopsis thaliana] gi|21553952|gb|AAM63033.1| unknown [Arabidopsis thaliana] gi|26450234|dbj|BAC42234.1| unknown protein [Arabidopsis thaliana] gi|28827718|gb|AAO50703.1| unknown protein [Arabidopsis thaliana] gi|332659102|gb|AEE84502.1| uncharacterized protein AT4G21780 [Arabidopsis thaliana]	112	115	1.00E-37	102.7	75.0	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G21780.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:11567213-11567560 FORWARD LENGTH=115	112	115	2.00E-40	102.7	75.0	83.9

Rsa1.0_00115.1.g5613.t1	ref|NP_193908.1| RNA pseudourine synthase 6 [Arabidopsis thaliana] gi|75212600|sp|Q9SVS0.1|PUS6_ARATH RecName: Full=RNA pseudourine synthase 6, chloroplastic; AltName: Full=RNA pseudouridylate synthase 6; AltName: Full=RNA-uridine isomerase 6; Flags: Precursor gi|4455285|emb|CAB36821.1| hypothetical protein [Arabidopsis thaliana] gi|7268974|emb|CAB81284.1| hypothetical protein [Arabidopsis thaliana] gi|23296381|gb|AAN13057.1| unknown protein [Arabidopsis thaliana] gi|110741616|dbj|BAE98756.1| hypothetical protein [Arabidopsis thaliana] gi|332659101|gb|AEE84501.1| RNA pseudourine synthase 6 [Arabidopsis thaliana]	474	472	0	99.6	85.0	91.8	RNA pseudourine synthase 6	gbpln	Arabidopsis thaliana	AT4G21770.1 | Symbols: | Pseudouridine synthase family protein | chr4:11564028-11566345 REVERSE LENGTH=472	474	472	0	99.6	85.0	91.8
Rsa1.0_00115.1.g5614.t1	ref|XP_002869865.1| beta-glucosidase 47 [Arabidopsis lyrata subsp. lyrata] gi|297315701|gb|EFH46124.1| beta-glucosidase 47 [Arabidopsis lyrata subsp. lyrata]	529	523	0	98.9	80.5	86.8	beta-glucosidase 47	gbpln	Arabidopsis lyrata	AT4G21760.1 | Symbols: BGLU47 | beta-glucosidase 47 | chr4:11561229-11563871 FORWARD LENGTH=535	529	535	0	101.1	78.4	84.5
Rsa1.0_00115.1.g5615.t1	gb|EOA18374.1| hypothetical protein CARUB_v10006895mg [Capsella rubella]	739	762	0	103.1	87.4	92.0	hypothetical protein CARUB_v10006895mg	gbpln	Capsella rubella	AT4G21750.2 | Symbols: ATML1 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr4:11556965-11560243 FORWARD LENGTH=762	739	762	0	103.1	87.6	91.9
Rsa1.0_00115.1.g5616.t2	gb|EOA17556.1| hypothetical protein CARUB_v10005915mg [Capsella rubella]	169	162	1.00E-45	95.9	60.9	72.8	hypothetical protein CARUB_v10005915mg	gbpln	Capsella rubella	AT4G21745.1 | Symbols: | PAK-box/P21-Rho-binding family protein | chr4:11549340-11550415 FORWARD LENGTH=156	169	156	4.00E-42	92.3	60.4	69.8
Rsa1.0_00115.1.g5617.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00115.1.g5618.t1	ref|XP_002869843.1| hypothetical protein ARALYDRAFT_354556 [Arabidopsis lyrata subsp. lyrata] gi|297315679|gb|EFH46102.1| hypothetical protein ARALYDRAFT_354556 [Arabidopsis lyrata subsp. lyrata]	140	504	1.00E-51	360.0	75.7	80.0	hypothetical protein ARALYDRAFT_354556	gbpln	Arabidopsis lyrata	AT4G21740.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G30515.1); Has 20 Blast hits to 20 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11545926-11546396 FORWARD LENGTH=156	140	156	5.00E-49	111.4	74.3	80.0
Rsa1.0_00115.1.g5619.t1	ref|XP_002519046.1| conserved hypothetical protein [Ricinus communis] gi|223541709|gb|EEF43257.1| conserved hypothetical protein [Ricinus communis]	166	138	2.00E-45	83.1	59.0	69.9	conserved hypothetical protein	gbpln	Ricinus communis	AT4G21720.1 | Symbols: | unknown protein; Has 2692 Blast hits to 975 proteins in 186 species: Archae - 4; Bacteria - 460; Metazoa - 658; Fungi - 93; Plants - 1089; Viruses - 100; Other Eukaryotes - 288 (source: NCBI BLink). | chr4:11542561-11544274 FORWARD LENGTH=139	166	139	2.00E-45	83.7	65.1	72.9
Rsa1.0_00115.1.g5620.t1	ref|XP_002867829.1| hypothetical protein ARALYDRAFT_492703 [Arabidopsis lyrata subsp. lyrata] gi|297313665|gb|EFH44088.1| hypothetical protein ARALYDRAFT_492703 [Arabidopsis lyrata subsp. lyrata]	1189	1188	0	99.9	98.0	99.3	hypothetical protein ARALYDRAFT_492703	gbpln	Arabidopsis lyrata	AT4G21710.1 | Symbols: NRPB2, EMB1989, RPB2 | DNA-directed RNA polymerase family protein | chr4:11535684-11542200 REVERSE LENGTH=1188	1189	1188	0	99.9	97.8	99.2
Rsa1.0_00115.1.g5621.t1	sp|Q56XW8.2|FBL30_ARATH RecName: Full=F-box/LRR-repeat protein At1g48400	493	487	1.00E-148	98.8	62.3	73.8	RecName: Full=F-box/LRR-repeat protein At1g48400	----	----	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	493	513	1.00E-150	104.1	61.9	73.4
Rsa1.0_00115.1.g5622.t1	ref|NP_175273.1| F-box/RNI-like/FBD-like domain-containing protein [Arabidopsis thaliana] gi|5733869|gb|AAD49757.1|AC007932_5 Contains F-box domain PF|00646 [Arabidopsis thaliana] gi|332194164|gb|AEE32285.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	490	513	1.00E-154	104.7	63.3	74.3	F-box/RNI-like/FBD-like domain-containing protein	gbpln	Arabidopsis thaliana	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	490	513	1.00E-157	104.7	63.3	74.3
Rsa1.0_00115.1.g5623.t1	ref|NP_193901.1| uncharacterized protein [Arabidopsis thaliana] gi|4455278|emb|CAB36814.1| hypothetical protein [Arabidopsis thaliana] gi|7268967|emb|CAB81277.1| hypothetical protein [Arabidopsis thaliana] gi|332659091|gb|AEE84491.1| uncharacterized protein AT4G21700 [Arabidopsis thaliana]	923	962	0	104.2	78.3	86.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G21700.1 | Symbols: | Protein of unknown function (DUF2921) | chr4:11529956-11532844 FORWARD LENGTH=962	923	962	0	104.2	78.3	86.8
Rsa1.0_00115.1.g5624.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00115.1.g5625.t1	ref|XP_002867832.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297313668|gb|EFH44091.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	583	589	0	101.0	92.6	95.9	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT4G21680.1 | Symbols: NRT1.8 | NITRATE TRANSPORTER 1.8 | chr4:11517540-11519576 REVERSE LENGTH=589	583	589	0	101.0	90.6	94.5
Rsa1.0_00115.1.g5626.t1	ref|XP_002869873.1| hypothetical protein ARALYDRAFT_492708 [Arabidopsis lyrata subsp. lyrata] gi|297315709|gb|EFH46132.1| hypothetical protein ARALYDRAFT_492708 [Arabidopsis lyrata subsp. lyrata]	827	965	0	116.7	57.9	64.6	hypothetical protein ARALYDRAFT_492708	gbpln	Arabidopsis lyrata	AT4G21670.1 | Symbols: CPL1, FRY2, ATCPL1 | C-terminal domain phosphatase-like 1 | chr4:11511511-11516922 FORWARD LENGTH=967	827	967	0	116.9	61.5	72.4
Rsa1.0_00116.1.g5627.t1	gb|EOA18823.1| hypothetical protein CARUB_v10007437mg [Capsella rubella]	110	110	1.00E-38	100.0	84.5	90.9	hypothetical protein CARUB_v10007437mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00116.1.g5628.t1	ref|XP_002868886.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314722|gb|EFH45145.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	855	882	0	103.2	91.3	94.0	kinase family protein	gbpln	Arabidopsis lyrata	AT4G39110.1 | Symbols: | Malectin/receptor-like protein kinase family protein | chr4:18222483-18225119 REVERSE LENGTH=878	855	878	0	102.7	90.8	93.6
Rsa1.0_00116.1.g5629.t1	ref|XP_002868887.1| inositol monophosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314723|gb|EFH45146.1| inositol monophosphatase family protein [Arabidopsis lyrata subsp. lyrata]	347	346	1.00E-164	99.7	83.0	89.0	inositol monophosphatase family protein	gbpln	Arabidopsis lyrata	AT4G39120.1 | Symbols: IMPL2, HISN7 | myo-inositol monophosphatase like 2 | chr4:18225578-18227988 REVERSE LENGTH=375	347	375	1.00E-166	108.1	84.4	89.0
Rsa1.0_00116.1.g5630.t1	ref|NP_195625.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|30692196|ref|NP_849522.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|42573229|ref|NP_974711.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|42573231|ref|NP_974712.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|145334267|ref|NP_001078514.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|4914426|emb|CAB43629.1| putative protein [Arabidopsis thaliana] gi|7270897|emb|CAB80577.1| putative protein [Arabidopsis thaliana] gi|17065052|gb|AAL32680.1| putative protein [Arabidopsis thaliana] gi|22136224|gb|AAM91190.1| putative protein [Arabidopsis thaliana] gi|66865958|gb|AAY57613.1| RING finger family protein [Arabidopsis thaliana] gi|332661622|gb|AEE87022.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332661623|gb|AEE87023.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332661624|gb|AEE87024.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332661625|gb|AEE87025.1| RING/U-	426	429	0	100.7	83.8	87.8	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT4G39140.5 | Symbols: | RING/U-box superfamily protein | chr4:18229637-18231282 REVERSE LENGTH=429	426	429	0	100.7	83.8	87.8
Rsa1.0_00116.1.g5631.t1	ref|XP_002866831.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297312667|gb|EFH43090.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	601	600	1.00E-149	99.8	61.2	72.4	DNA binding protein	gbpln	Arabidopsis lyrata	AT4G39160.1 | Symbols: | Homeodomain-like superfamily protein | chr4:18236828-18239744 FORWARD LENGTH=601	601	601	1.00E-149	100.0	60.4	70.7
Rsa1.0_00116.1.g5632.t1	gb|EOA16166.1| hypothetical protein CARUB_v10004299mg [Capsella rubella]	613	672	0	109.6	88.1	93.3	hypothetical protein CARUB_v10004299mg	gbpln	Capsella rubella	AT4G39170.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr4:18240887-18243621 FORWARD LENGTH=614	613	614	0	100.2	87.9	93.3
Rsa1.0_00116.1.g5633.t1	ref|XP_002868891.1| hypothetical protein ARALYDRAFT_912375 [Arabidopsis lyrata subsp. lyrata] gi|297314727|gb|EFH45150.1| hypothetical protein ARALYDRAFT_912375 [Arabidopsis lyrata subsp. lyrata]	1060	551	0	52.0	42.8	46.1	hypothetical protein ARALYDRAFT_912375	gbpln	Arabidopsis lyrata	AT4G39180.1 | Symbols: SEC14, ATSEC14 | Sec14p-like phosphatidylinositol transfer family protein | chr4:18244006-18246673 REVERSE LENGTH=554	1060	554	0	52.3	43.0	45.9

<table>
<tr><td>Rsa1.0_00116.1.g5634.t1</td><td>ref|NP_195631.1| 40S ribosomal protein S25-4 [Arabidopsis thaliana] gi|30580493|sp|Q9T029.1|RS254_ARATH RecName: Full=40S ribosomal protein S25-4 gi|4914432|emb|CAB43635.1| ribosomal protein S25 [Arabidopsis thaliana] gi|7270903|emb|CAB80583.1| ribosomal protein S25 [Arabidopsis thaliana] gi|14335026|gb|AAK59777.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gi|16323232|gb|AAL15350.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gi|21553704|gb|AAM62797.1| ribosomal protein S25 [Arabidopsis thaliana] gi|332661636|gb|AEE87036.1| 40S ribosomal protein S25-4 [Arabidopsis thaliana] gi|482553510|gb|EOA17703.1| hypothetical protein CARUB_v10006075mg [Capsella rubella]</td><td>108</td><td>108</td><td>1.00E-55</td><td>100.0</td><td>100.0</td><td>100.0</td><td>40S ribosomal protein S25-4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G39200.1 | Symbols: | Ribosomal protein S25 family protein | chr4:18257464-18258464 FORWARD LENGTH=108</td><td>108</td><td>108</td><td>2.00E-58</td><td>100.0</td><td>100.0</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00116.1.g5635.t1</td><td>ref|NP_195633.1| protein RER1A [Arabidopsis thaliana] gi|6225938|sp|O48670.1|RER1A_ARATH RecName: Full=Protein RER1A; Short=AtRER1A gi|2865175|dbj|BAA24803.1| AtRer1A [Arabidopsis thaliana] gi|4914434|emb|CAB43637.1| AtRer1A [Arabidopsis thaliana] gi|7270905|emb|CAB80585.1| AtRer1A [Arabidopsis thaliana] gi|14994255|gb|AAK73262.1| AtRer1A [Arabidopsis thaliana] gi|21554242|gb|AAM63317.1| AtRer1A [Arabidopsis thaliana] gi|24030322|gb|AAN41329.1| putative AtRer1A protein [Arabidopsis thaliana] gi|332661639|gb|AEE87039.1| protein RER1A [Arabidopsis thaliana]</td><td>194</td><td>191</td><td>2.00E-98</td><td>98.5</td><td>91.2</td><td>93.3</td><td>protein RER1A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G39220.1 | Symbols: ATRER1A | Rer1 family protein | chr4:18264280-18265531 FORWARD LENGTH=191</td><td>194</td><td>191</td><td>1.00E-101</td><td>98.5</td><td>91.2</td><td>93.3</td></tr>
<tr><td>Rsa1.0_00116.1.g5636.t1</td><td>ref|NP_195634.1| NmrA-like negative transcriptional regulator family protein [Arabidopsis thaliana] gi|4914435|emb|CAB43638.1| NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana] gi|7270906|emb|CAB80586.1| NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana] gi|23297378|gb|AAN12954.1| putative NAD(P)H oxidoreductase, isoflavone reductase [Arabidopsis thaliana] gi|332661640|gb|AEE87040.1| NmrA-like negative transcriptional regulator family protein [Arabidopsis thaliana]</td><td>308</td><td>308</td><td>1.00E-157</td><td>100.0</td><td>87.3</td><td>92.9</td><td>NmrA-like negative transcriptional regulator family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G39230.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr4:18266024-18267604 REVERSE LENGTH=308</td><td>308</td><td>308</td><td>1.00E-160</td><td>100.0</td><td>87.3</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00116.1.g5637.t3</td><td>gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]</td><td>622</td><td>871</td><td>6.00E-70</td><td>140.0</td><td>32.0</td><td>49.8</td><td>Ulp1 protease family protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874</td><td>622</td><td>874</td><td>1.00E-42</td><td>140.5</td><td>15.6</td><td>23.5</td></tr>
<tr><td>Rsa1.0_00116.1.g5638.t1</td><td>ref|XP_002863918.1| hypothetical protein ARALYDRAFT_357086 [Arabidopsis lyrata subsp. lyrata] gi|297309753|gb|EFH40177.1| hypothetical protein ARALYDRAFT_357086 [Arabidopsis lyrata subsp. lyrata]</td><td>147</td><td>123</td><td>5.00E-17</td><td>83.7</td><td>28.6</td><td>37.4</td><td>hypothetical protein ARALYDRAFT_357086</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00116.1.g5639.t1</td><td>gb|AAC95212.1| Mutator-like transposase [Arabidopsis thaliana]</td><td>1039</td><td>915</td><td>1.00E-174</td><td>88.1</td><td>26.9</td><td>38.7</td><td>Mutator-like transposase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719</td><td>1039</td><td>719</td><td>4.00E-36</td><td>69.2</td><td>11.8</td><td>21.7</td></tr>
<tr><td>Rsa1.0_00116.1.g5640.t1</td><td>dbj|BAJ34207.1| unnamed protein product [Thellungiella halophila]</td><td>171</td><td>166</td><td>1.00E-41</td><td>97.1</td><td>47.4</td><td>48.5</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G39260.3 | Symbols: CCR1, ATGRP8, GR-RBP8, GRP8 | cold, circadian rhythm, and RNA binding 1 | chr4:18274166-18274958 REVERSE LENGTH=92</td><td>171</td><td>92</td><td>1.00E-43</td><td>53.8</td><td>48.0</td><td>50.9</td></tr>
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Rsa1.0_00116.1.g5641.t1	ref|NP_195541.2| uncharacterized protein [Arabidopsis thaliana] gi|22655230|gb|AAM98205.1| putative protein [Arabidopsis thaliana] gi|30102890|gb|AAP21363.1| At4g38290 [Arabidopsis thaliana] gi|51969484|dbj|BAD43434.1| putative protein [Arabidopsis thaliana] gi|51969630|dbj|BAD43507.1| putative protein [Arabidopsis thaliana] gi|51970242|dbj|BAD43813.1| putative protein [Arabidopsis thaliana] gi|332661509|gb|AEE86909.1| uncharacterized protein AT4G38280 [Arabidopsis thaliana]	153	170	6.00E-39	111.1	60.8	69.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G38280.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Integral membrane protein hemolysin-III homolog (TAIR:AT2G45250.1); Has 65 Blast hits to 65 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17942034-17942864 FORWARD LENGTH=170	153	170	2.00E-41	111.1	60.8	69.9
Rsa1.0_00116.1.g5642.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1529	1142	0	74.7	42.2	53.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1529	575	5.00E-68	37.6	9.9	15.1
Rsa1.0_00116.1.g5643.t1	gb|EOA16024.1| hypothetical protein CARUB_v10004149mg [Capsella rubella]	815	815	0	100.0	92.8	97.1	hypothetical protein CARUB_v10004149mg	gbpln	Capsella rubella	AT2G21790.1 | Symbols: R1, RNR1, CLS8, ATRNR1 | ribonucleotide reductase 1 | chr2:9293529-9297580 FORWARD LENGTH=816	815	816	0	100.1	91.0	96.2
Rsa1.0_00116.1.g5644.t1	ref|NP_568058.1| ubiquitin carboxyl-terminal hydrolase 27 [Arabidopsis thaliana] gi|75262796|sp|Q9FPS0.1|UBP27_ARATH RecName: Full=Ubiquitin carboxyl-terminal hydrolase 27; AltName: Full=Deubiquitinating enzyme 27; Short=AtUBP27; AltName: Full=Ubiquitin thioesterase 27; AltName: Full=Ubiquitin-specific-processing protease 27 gi|11993494|gb|AAG42765.1|AF302675_1 ubiquitin-specific protease 27 [Arabidopsis thaliana] gi|13877891|gb|AAK44023.1|AF370208_1 putative ubiquitin-specific protease UBP27 [Arabidopsis thaliana] gi|22136950|gb|AAM91704.1| putative ubiquitin-specific protease UBP27 [Arabidopsis thaliana] gi|332661662|gb|AEE87062.1| ubiquitin carboxyl-terminal hydrolase 27 [Arabidopsis thaliana]	494	494	0	100.0	75.7	86.2	ubiquitin carboxyl-terminal hydrolase 27	gbpln	Arabidopsis thaliana	AT4G39370.1 | Symbols: UBP27 | ubiquitin-specific protease 27 | chr4:18306392-18308625 FORWARD LENGTH=494	494	494	0	100.0	75.7	86.2
Rsa1.0_00116.1.g5645.t1	ref|NP_195648.1| uncharacterized protein [Arabidopsis thaliana] gi|5042154|emb|CAB44673.1| hypothetical protein [Arabidopsis thaliana] gi|7270922|emb|CAB80601.1| hypothetical protein [Arabidopsis thaliana] gi|332661664|gb|AEE87064.1| uncharacterized protein AT4G39380 [Arabidopsis thaliana]	508	518	1.00E-177	102.0	69.9	77.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G39380.1 | Symbols: | BEST Arabidopsis thaliana protein match is: TSL-kinase interacting protein 1 (TAIR:AT2G36960.3); Has 80 Blast hits to 74 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:18309628-18311874 REVERSE LENGTH=518	508	518	1.00E-179	102.0	69.9	77.4
Rsa1.0_00116.1.g5646.t1	ref|NP_568059.1| nucleotide sugar transporter-KT 1 [Arabidopsis thaliana] gi|30692341|ref|NP_849527.1| nucleotide sugar transporter-KT 1 [Arabidopsis thaliana] gi|20259516|gb|AAM13878.1| unknown protein [Arabidopsis thaliana] gi|23296523|gb|AAN13117.1| unknown protein [Arabidopsis thaliana] gi|332661666|gb|AEE87066.1| nucleotide sugar transporter-KT 1 [Arabidopsis thaliana] gi|332661667|gb|AEE87067.1| nucleotide sugar transporter-KT 1 [Arabidopsis thaliana]	336	337	1.00E-177	100.3	96.4	98.2	nucleotide sugar transporter-KT 1	gbpln	Arabidopsis thaliana	AT4G39390.2 | Symbols: ATNST-KT1, NST-K1 | nucleotide sugar transporter-KT 1 | chr4:18316278-18317854 FORWARD LENGTH=337	336	337	1.00E-179	100.3	96.4	98.2
Rsa1.0_00116.1.g5647.t2	gb|EOA16559.1| hypothetical protein CARUB_v10004718mg [Capsella rubella]	604	478	0	79.1	71.2	74.0	hypothetical protein CARUB_v10004718mg	gbpln	Capsella rubella	AT4G39660.1 | Symbols: AGT2 | alanine:glyoxylate aminotransferase 2 | chr4:18406797-18409262 FORWARD LENGTH=476	604	476	0	78.8	69.9	73.2
Rsa1.0_00116.1.g5648.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00116.1.g5649.t1	gb|EOA15353.1| hypothetical protein CARUB_v10004348mg [Capsella rubella]	603	640	0	106.1	72.1	79.9	hypothetical protein CARUB_v10004348mg	gbpln	Capsella rubella	AT4G39680.2 | Symbols: | SAP domain-containing protein | chr4:18414604-18416938 REVERSE LENGTH=633	603	633	0	105.0	70.3	78.8

Rsa1.0_00116.1.g5650.t1	ref|NP_568066.1| uncharacterized protein [Arabidopsis thaliana] gi|13605659|gb|AAK32823.1|AF361810_1 AT4g39690/T19P19_80 [Arabidopsis thaliana] gi|21700889|gb|AAM70568.1| AT4g39690/T19P19_80 [Arabidopsis thaliana] gi|23397147|gb|AAN31857.1| unknown protein [Arabidopsis thaliana] gi|332661705|gb|AEE87105.1| uncharacterized protein AT4G39690 [Arabidopsis thaliana]	633	650	0	102.7	76.8	86.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G39690.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 26 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Mitochondrial inner membrane protein Mitofilin (InterPro:IPR019133); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:18417755-18421633 FORWARD LENGTH=650	633	650	0	102.7	76.8	86.4
Rsa1.0_00116.1.g5651.t1	ref|XP_002868925.1| hypothetical protein ARALYDRAFT_490754 [Arabidopsis lyrata subsp. lyrata] gi|297314761|gb|EFH45184.1| hypothetical protein ARALYDRAFT_490754 [Arabidopsis lyrata subsp. lyrata]	294	287	1.00E-111	97.6	75.5	82.0	hypothetical protein ARALYDRAFT_490754	gbpln	Arabidopsis lyrata	AT4G39720.1 | Symbols: | VQ motif-containing protein | chr4:18429992-18430864 REVERSE LENGTH=290	294	290	1.00E-112	98.6	73.8	81.3
Rsa1.0_00116.1.g5652.t1	gb|AAK01359.1|AF314810_1 dehydration stress-induced protein [Brassica napus]	178	178	1.00E-100	100.0	98.9	98.9	dehydration stress-induced protein	gbpln	Brassica napus	AT4G39730.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr4:18432950-18433581 FORWARD LENGTH=181	178	181	1.00E-90	101.7	86.0	91.0
Rsa1.0_00116.1.g5653.t1	ref|XP_002863119.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308943|gb|EFH39378.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1157	1121	0	96.9	48.2	60.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189	1157	1189	0	102.8	46.9	59.9
Rsa1.0_00116.1.g5654.t1	ref|XP_002868926.1| electron transport SCO1/SenC family protein [Arabidopsis lyrata subsp. lyrata] gi|297314762|gb|EFH45185.1| electron transport SCO1/SenC family protein [Arabidopsis lyrata subsp. lyrata]	280	276	1.00E-123	98.6	77.5	86.8	electron transport SCO1/SenC family protein	gbpln	Arabidopsis lyrata	AT4G39740.1 | Symbols: | Thioredoxin superfamily protein | chr4:18435586-18437095 REVERSE LENGTH=276	280	276	1.00E-124	98.6	76.8	86.1
Rsa1.0_00116.1.g5655.t1	gb|AAM62525.1| unknown [Arabidopsis thaliana]	383	390	1.00E-124	101.8	61.4	73.6	unknown	gbpln	Arabidopsis thaliana	AT4G39753.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18440125-18441297 FORWARD LENGTH=390	383	390	1.00E-120	101.8	59.8	72.1
Rsa1.0_00116.1.g5656.t1	gb|EOA29201.1| hypothetical protein CARUB_v10025475mg [Capsella rubella]	346	420	1.00E-102	121.4	59.2	71.7	hypothetical protein CARUB_v10025475mg	gbpln	Capsella rubella	AT4G39753.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18440125-18441297 FORWARD LENGTH=390	346	390	4.00E-99	112.7	55.5	65.6
Rsa1.0_00116.1.g5657.t1	gb|AAM62525.1| unknown [Arabidopsis thaliana]	375	390	1.00E-130	104.0	64.3	75.5	unknown	gbpln	Arabidopsis thaliana	AT4G39753.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18440125-18441297 FORWARD LENGTH=390	375	390	1.00E-125	104.0	62.9	74.1
Rsa1.0_00116.1.g5658.t1	ref|NP_568071.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|125991857|sp|P0C2F9.1|FK105_ARATH RecName: Full=Putative F-box/kelch-repeat protein At4g39756 gi|332661715|gb|AEE87115.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	376	374	1.00E-147	99.5	71.0	80.3	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT4G39756.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18441756-18442880 FORWARD LENGTH=374	376	374	1.00E-149	99.5	71.0	80.3
Rsa1.0_00116.1.g5659.t1	ref|XP_002868927.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314763|gb|EFH45186.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	342	349	1.00E-179	102.0	88.6	94.7	predicted protein	gbpln	Arabidopsis lyrata	AT4G39770.1 | Symbols: TPPH | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr4:18449138-18451218 REVERSE LENGTH=349	342	349	1.00E-180	102.0	88.6	94.2
Rsa1.0_00116.1.g5660.t1	ref|NP_195688.1| ethylene-responsive transcription factor ERF060 [Arabidopsis thaliana] gi|75219968|sp|O65665.1|ERF60_ARATH RecName: Full=Ethylene-responsive transcription factor ERF060 gi|3080447|emb|CAA18764.1| putative protein [Arabidopsis thaliana] gi|7270962|emb|CAB80641.1| putative protein [Arabidopsis thaliana] gi|106879185|gb|ABF82622.1| At4g39780 [Arabidopsis thaliana] gi|332661718|gb|AEE87118.1| ethylene-responsive transcription factor ERF060 [Arabidopsis thaliana]	275	272	1.00E-117	98.9	77.5	84.4	ethylene-responsive transcription factor ERF060	gbpln	Arabidopsis thaliana	AT4G39780.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:18458216-18459034 REVERSE LENGTH=272	275	272	1.00E-120	98.9	77.5	84.4
Rsa1.0_00116.1.g5661.t1	gb|EOA17274.1| hypothetical protein CARUB_v10005547mg [Capsella rubella]	447	256	1.00E-114	57.3	47.0	49.2	hypothetical protein CARUB_v10005547mg	gbpln	Capsella rubella	AT4G39810.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:18474608-18475735 REVERSE LENGTH=255	447	255	1.00E-112	57.0	44.7	47.2

Rsa1.0_00116.1.g5662.t1	ref|XP_002868932.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314768|gb|EFH45191.1| binding protein [Arabidopsis lyrata subsp. lyrata]	387	412	1.00E-175	106.5	79.8	88.9	binding protein	gbpln	Arabidopsis lyrata	AT4G39820.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:18476698-18477924 REVERSE LENGTH=408	387	408	1.00E-177	105.4	79.6	88.1
Rsa1.0_00116.1.g5663.t1	gb|EOA14703.1| hypothetical protein CARUB_v10027980mg [Capsella rubella]	72	842	5.00E-12	1169.4	51.4	69.4	hypothetical protein CARUB_v10027980mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00116.1.g5664.t1	ref|XP_002866887.1| hypothetical protein ARALYDRAFT_490769 [Arabidopsis lyrata subsp. lyrata] gi|297312723|gb|EFH43146.1| hypothetical protein ARALYDRAFT_490769 [Arabidopsis lyrata subsp. lyrata]	445	449	1.00E-159	100.9	78.2	86.3	hypothetical protein ARALYDRAFT_490769	gbpln	Arabidopsis lyrata	AT4G39840.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 20719 Blast hits to 6096 proteins in 607 species: Archae - 22; Bacteria - 3243; Metazoa - 4364; Fungi - 2270; Plants - 237; Viruses - 128; Other Eukaryotes - 10455 (source: NCBI BLink). | chr4:18485268-18486623 FORWARD LENGTH=451	445	451	1.00E-154	101.3	80.2	88.8
Rsa1.0_00116.1.g5665.t26	gb|EOA24245.1| hypothetical protein CARUB_v10017480mg [Capsella rubella]	412	366	2.00E-82	88.8	41.5	54.1	hypothetical protein CARUB_v10017480mg	gbpln	Capsella rubella	AT5G54330.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22064993-22066063 FORWARD LENGTH=356	412	356	1.00E-78	86.4	40.0	53.2
Rsa1.0_00116.1.g5666.t1	gb|EOA24245.1| hypothetical protein CARUB_v10017480mg [Capsella rubella]	416	366	2.00E-82	88.0	38.2	48.8	hypothetical protein CARUB_v10017480mg	gbpln	Capsella rubella	AT5G52930.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21470370-21471449 FORWARD LENGTH=359	416	359	5.00E-82	86.3	36.5	46.2
Rsa1.0_00116.1.g5667.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00116.1.g5668.t1	gb|EOA17796.1| hypothetical protein CARUB_v10006190mg [Capsella rubella]	365	364	2.00E-99	99.7	54.8	67.9	hypothetical protein CARUB_v10006190mg	gbpln	Capsella rubella	AT2G21950.1 | Symbols: SKIP6 | SKP1 interacting partner 6 | chr2:9353526-9354644 REVERSE LENGTH=372	365	372	1.00E-48	101.9	36.4	50.7
Rsa1.0_00116.1.g5669.t2	ref|XP_002868935.1| hypothetical protein ARALYDRAFT_912479 [Arabidopsis lyrata subsp. lyrata] gi|297314771|gb|EFH45194.1| hypothetical protein ARALYDRAFT_912479 [Arabidopsis lyrata subsp. lyrata]	235	244	2.00E-92	103.8	79.1	84.3	hypothetical protein ARALYDRAFT_912479	gbpln	Arabidopsis lyrata	AT4G39900.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:18508569-18510289 REVERSE LENGTH=245	235	245	5.00E-93	104.3	75.3	80.9
Rsa1.0_00116.1.g5670.t1	ref|NP_568074.1| ubiquitin carboxyl-terminal hydrolase 3 [Arabidopsis thaliana] gi|62901126|sp|O24454.1|UBP3_ARATH RecName: Full=Ubiquitin carboxyl-terminal hydrolase 3; AltName: Full=Deubiquitinating enzyme 3; Short=AtUBP3; AltName: Full=Ubiquitin thioesterase 3; AltName: Full=Ubiquitin-specific-processing protease 3 gi|2347098|gb|AAB67966.1| ubiquitin-specific protease [Arabidopsis thaliana] gi|4490742|emb|CAB38904.1| ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana] gi|7271046|emb|CAB80654.1| ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana] gi|16604539|gb|AAL24275.1| AT4g39910/T5J17_80 [Arabidopsis thaliana] gi|18958042|gb|AAL79594.1| AT4g39910/T5J17_80 [Arabidopsis thaliana] gi|332661736|gb|AEE87136.1| ubiquitin carboxyl-terminal hydrolase 3 [Arabidopsis thaliana]	373	371	0	99.5	96.8	97.3	ubiquitin carboxyl-terminal hydrolase 3	gbpln	Arabidopsis thaliana	AT4G39910.1 | Symbols: ATUBP3, UBP3 | ubiquitin-specific protease 3 | chr4:18511858-18514139 REVERSE LENGTH=371	373	371	0	99.5	96.8	97.3

Rsa1.0_00116.1.g5671.t1	ref|NP_195704.1| Adenylyl-sulfate kinase 2 [Arabidopsis thaliana] gi|7387808|sp|O49196.1|KAP2_ARATH RecName: Full=Adenylyl-sulfate kinase 2, chloroplastic; AltName: Full=ATP adenosine-5'-phosphosulfate 3'-phosphotransferase; AltName: Full=Adenosine-5'-phosphosulfate kinase; Short=APS kinase; Flags: Precursor gi|18087563|gb|AAL58913.1|AF462823_1 AT4g39940/T5J17_110 [Arabidopsis thaliana] gi|2829133|gb|AAC39520.1| adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana] gi|4490745|emb|CAB38907.1| adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana] gi|7271049|emb|CAB80657.1| adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana] gi|20453397|gb|AAM19937.1| AT4g39940/T5J17_110 [Arabidopsis thaliana] gi|332661742|gb|AEE87142.1| Adenylyl-sulfate kinase 2 [Arabidopsis thaliana]	222	293	2.00E-91	132.0	79.3	85.6	Adenylyl-sulfate kinase 2	gbpln	Arabidopsis thaliana	AT4G39940.1 | Symbols: AKN2, APK2 | APS-kinase 2 | chr4:18519787-18521276 FORWARD LENGTH=293	222	293	7.00E-94	132.0	79.3	85.6
Rsa1.0_00116.1.g5672.t1	ref|NP_850025.1| 6-phosphofructokinase 5 [Arabidopsis thaliana] gi|75161510|sp|Q8VYN6.1|K6PF5_ARATH RecName: Full=6-phosphofructokinase 5, chloroplastic; Short=Phosphofructokinase 5; AltName: Full=Phosphohexokinase 5; Flags: Precursor gi|17979345|gb|AAL49898.1| putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase [Arabidopsis thaliana] gi|20466013|gb|AAM20228.1| putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase [Arabidopsis thaliana] gi|330252218|gb|AEC07312.1| 6-phosphofructokinase 5 [Arabidopsis thaliana]	511	537	0	105.1	84.1	90.2	6-phosphofructokinase 5	gbpln	Arabidopsis thaliana	AT2G22480.1 | Symbols: PFK5 | phosphofructokinase 5 | chr2:9545670-9548414 FORWARD LENGTH=537	511	537	0	105.1	84.1	90.2
Rsa1.0_00116.1.g5673.t1	ref|NP_568035.1| uncharacterized protein [Arabidopsis thaliana] gi|21554198|gb|AAM63277.1| unknown [Arabidopsis thaliana] gi|107738205|gb|ABF83661.1| At4g38100 [Arabidopsis thaliana] gi|332661478|gb|AEE86878.1| uncharacterized protein AT4G38100 [Arabidopsis thaliana]	204	193	5.00E-67	94.6	68.6	78.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G38100.1 | Symbols: | unknown protein; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01150.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17887033-17888177 REVERSE LENGTH=193	204	193	1.00E-69	94.6	68.6	78.9
Rsa1.0_00116.1.g5674.t1	ref|XP_002868948.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314784|gb|EFH45207.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	225	225	2.00E-88	100.0	76.9	84.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G38070.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:17876535-17882569 FORWARD LENGTH=1513	225	1513	3.00E-85	672.4	76.9	84.0
Rsa1.0_00116.1.g5675.t1	sp|P0CB23.1|Y4862_ARATH RecName: Full=Uncharacterized protein At4g38062	1018	1050	0	103.1	75.2	86.1	RecName: Full=Uncharacterized protein At4g38062	----	----	AT4G38070.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:17876535-17882569 FORWARD LENGTH=1513	1018	1513	0	148.6	74.6	85.5
Rsa1.0_00116.1.g5676.t1	ref|NP_195519.3| uncharacterized protein [Arabidopsis thaliana] gi|4467112|emb|CAB37546.1| putative protei [Arabidopsis thaliana] gi|7270789|emb|CAB80471.1| putative protein [Arabidopsis thaliana] gi|332661470|gb|AEE86870.1| uncharacterized protein AT4G38060 [Arabidopsis thaliana]	142	125	3.00E-42	88.0	70.4	77.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G38060.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65480.1); Has 63 Blast hits to 63 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17874002-17874379 REVERSE LENGTH=125	142	125	8.00E-45	88.0	70.4	77.5
Rsa1.0_00116.1.g5677.t1	gb|EOA16680.1| hypothetical protein CARUB_v10004872mg [Capsella rubella]	407	426	0	104.7	87.5	92.6	hypothetical protein CARUB_v10004872mg	gbpln	Capsella rubella	AT4G38040.1 | Symbols: | Exostosin family protein | chr4:17867501-17869131 FORWARD LENGTH=425	407	425	0	104.4	85.7	91.6
Rsa1.0_00116.1.g5678.t1	gb|EOA16170.1| hypothetical protein CARUB_v10004306mg [Capsella rubella]	665	668	0	100.5	82.3	90.2	hypothetical protein CARUB_v10004306mg	gbpln	Capsella rubella	AT4G38030.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr4:17863206-17866730 REVERSE LENGTH=667	665	667	0	100.3	81.8	89.2

Rsa1.0_00116.1.g5679.t1	ref|XP_002868953.1| elicitor-activated gene 3 [Arabidopsis lyrata subsp. lyrata] gi|297314789|gb|EFH45212.1| elicitor-activated gene 3 [Arabidopsis lyrata subsp. lyrata]	353	359	1.00E-178	101.7	91.8	97.2	elicitor-activated gene 3	gbpln	Arabidopsis lyrata	AT4G37990.1 | Symbols: ELI3-2, ELI3, ATCAD8, CAD-B2 | elicitor-activated gene 3-2 | chr4:17855964-17857388 FORWARD LENGTH=359	353	359	1.00E-178	101.7	90.4	96.6
Rsa1.0_00116.1.g5680.t1	dbj|BAJ33843.1| unnamed protein product [Thellungiella halophila]	357	358	1.00E-179	100.3	90.5	95.5	unnamed protein product	----	----	AT4G37980.1 | Symbols: ELI3-1, ELI3, ATCAD7, CAD7 | elicitor-activated gene 3-1 | chr4:17852670-17854302 FORWARD LENGTH=357	357	357	1.00E-174	100.0	85.7	92.4
Rsa1.0_00116.1.g5681.t11	ref|XP_002868957.1| hypothetical protein ARALYDRAFT_912531 [Arabidopsis lyrata subsp. lyrata] gi|297314793|gb|EFH45216.1| hypothetical protein ARALYDRAFT_912531 [Arabidopsis lyrata subsp. lyrata]	1330	665	0	50.0	33.3	37.7	hypothetical protein ARALYDRAFT_912531	gbpln	Arabidopsis lyrata	AT4G37950.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr4:17844792-17849156 FORWARD LENGTH=678	1330	678	0	51.0	31.4	38.1
Rsa1.0_00117.1.g5682.t1	ref|NP_178819.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|3327395|gb|AAC26677.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana] gi|330251037|gb|AEC06131.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	142	530	3.00E-11	373.2	23.2	27.5	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	142	530	9.00E-14	373.2	23.2	27.5
Rsa1.0_00117.1.g5683.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00117.1.g5684.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00117.1.g5685.t1	ref|NP_188965.1| ethylene-responsive transcription factor 1B [Arabidopsis thaliana] gi|57012702|sp|Q8LDC8.2|ERF92_ARATH RecName: Full=Ethylene-responsive transcription factor 1B; Short=AtERF1B; AltName: Full=Ethylene-responsive element-binding factor 1B; Short=EREBP-1B gi|16226399|gb|AAL16158.1|AF428390_1 AT3g23240/K14B15_13 [Arabidopsis thaliana] gi|4128208|gb|AAD03544.1| ethylene response factor 1 [Arabidopsis thaliana] gi|4128210|gb|AAD03545.1| ethylene response factor 1 [Arabidopsis thaliana] gi|7939534|dbj|BAA95737.1| ethylene response DNA binding protein-like [Arabidopsis thaliana] gi|22137228|gb|AAM91459.1| AT3g23240/K14B15_13 [Arabidopsis thaliana] gi|332643217|gb|AEE76738.1| ethylene-responsive transcription factor 1B [Arabidopsis thaliana]	210	218	1.00E-92	103.8	87.1	92.9	ethylene-responsive transcription factor 1B	gbpln	Arabidopsis thaliana	AT3G23240.1 | Symbols: ERF1, ATERF1 | ethylene response factor 1 | chr3:8295705-8296361 FORWARD LENGTH=218	210	218	4.00E-95	103.8	87.1	92.9
Rsa1.0_00117.1.g5686.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00117.1.g5687.t1	gb|EOA32154.1| hypothetical protein CARUB_v10015406mg [Capsella rubella]	136	143	4.00E-57	105.1	89.0	97.1	hypothetical protein CARUB_v10015406mg	gbpln	Capsella rubella	AT3G23230.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:8289647-8290066 REVERSE LENGTH=139	136	139	2.00E-56	102.2	90.4	94.9
Rsa1.0_00117.1.g5688.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1815	1274	0	70.2	31.7	41.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1815	575	3.00E-52	31.7	6.4	10.2
Rsa1.0_00117.1.g5689.t1	gb|EOA31669.1| hypothetical protein CARUB_v10014873mg [Capsella rubella]	137	141	6.00E-44	102.9	75.9	85.4	hypothetical protein CARUB_v10014873mg	gbpln	Capsella rubella	AT3G23220.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:8287969-8288388 FORWARD LENGTH=139	137	139	5.00E-38	101.5	76.6	81.8

Rsa1.0_00117.1.g5690.t1	ref|NP_188962.2| transcription factor bHLH34 [Arabidopsis thaliana] gi|75311556|sp|Q9LTC7.1|BH034_ARATH RecName: Full=Transcription factor bHLH34; AltName: Full=Basic helix-loop-helix protein 34; Short=AtbHLH34; Short=bHLH 34; AltName: Full=Transcription factor EN 135; AltName: Full=bHLH transcription factor bHLH034 gi|7939531|dbj|BAA95734.1| unnamed protein product [Arabidopsis thaliana] gi|20466416|gb|AAM20525.1| unknown protein [Arabidopsis thaliana] gi|22136350|gb|AAM91253.1| unknown protein [Arabidopsis thaliana] gi|332643214|gb|AEE76735.1| transcription factor bHLH34 [Arabidopsis thaliana]	314	320	3.00E-98	101.9	69.7	79.0	transcription factor bHLH34	gbpln	Arabidopsis thaliana	AT3G23210.1 | Symbols: bHLH34 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:8283255-8284915 REVERSE LENGTH=320	314	320	1.00E-101	101.9	69.7	79.0
Rsa1.0_00117.1.g5691.t1	ref|XP_002883411.1| hypothetical protein ARALYDRAFT_898831 [Arabidopsis lyrata subsp. lyrata] gi|297329251|gb|EFH59670.1| hypothetical protein ARALYDRAFT_898831 [Arabidopsis lyrata subsp. lyrata]	152	152	1.00E-71	100.0	92.1	96.1	hypothetical protein ARALYDRAFT_898831	gbpln	Arabidopsis lyrata	AT3G23200.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr3:8281659-8282603 FORWARD LENGTH=152	152	152	5.00E-74	100.0	91.4	96.1
Rsa1.0_00117.1.g5692.t1	ref|XP_002883410.1| hypothetical protein ARALYDRAFT_479832 [Arabidopsis lyrata subsp. lyrata] gi|297329250|gb|EFH59669.1| hypothetical protein ARALYDRAFT_479832 [Arabidopsis lyrata subsp. lyrata]	174	215	1.00E-29	123.6	54.0	67.2	hypothetical protein ARALYDRAFT_479832	gbpln	Arabidopsis lyrata	AT3G23190.1 | Symbols: | HR-like lesion-inducing protein-related | chr3:8279445-8280663 FORWARD LENGTH=216	174	216	2.00E-29	124.1	51.1	63.8
Rsa1.0_00117.1.g5693.t1	ref|NP_188959.3| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana] gi|7939528|dbj|BAA95731.1| HR-like lesion-inducing protein [Arabidopsis thaliana] gi|332643211|gb|AEE76732.1| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana]	217	217	8.00E-97	100.0	76.5	87.6	HR-like lesion-inducing protein-like protein	gbpln	Arabidopsis thaliana	AT3G23180.1 | Symbols: | HR-like lesion-inducing protein-related | chr3:8277131-8278396 FORWARD LENGTH=217	217	217	2.00E-99	100.0	76.5	87.6
Rsa1.0_00117.1.g5694.t1	ref|NP_683584.2| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana] gi|26450286|dbj|BAC42259.1| unknown protein [Arabidopsis thaliana] gi|28972991|gb|AAO63820.1| unknown protein [Arabidopsis thaliana] gi|29367154|gb|AAO72720.1| unknown protein [Arabidopsis thaliana] gi|61742709|gb|AAX55175.1| hypothetical protein At3g23175 [Arabidopsis thaliana] gi|332643210|gb|AEE76731.1| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana]	170	169	2.00E-19	99.4	27.6	32.4	HR-like lesion-inducing protein-like protein	gbpln	Arabidopsis thaliana	AT3G23175.1 | Symbols: | HR-like lesion-inducing protein-related | chr3:8274202-8274973 REVERSE LENGTH=169	170	169	7.00E-22	99.4	27.6	32.4
Rsa1.0_00117.1.g5695.t1	dbj|BAF00897.1| thylene receptor like protein [Arabidopsis thaliana]	127	773	1.00E-49	608.7	76.4	81.1	thylene receptor like protein	gbpln	Arabidopsis thaliana	AT3G23150.1 | Symbols: ETR2 | Signal transduction histidine kinase, hybrid-type, ethylene sensor | chr3:8255156-8257560 FORWARD LENGTH=773	127	773	3.00E-52	608.7	76.4	81.1
Rsa1.0_00117.1.g5696.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1373	1515	0	110.3	60.2	75.5	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1373	1262	1.00E-112	91.9	14.6	21.8
Rsa1.0_00117.1.g5697.t1	dbj|BAB84007.2| ethylene receptor [Brassica oleracea]	624	776	0	124.4	97.0	98.2	ethylene receptor	gbpln	Brassica oleracea	AT3G23150.1 | Symbols: ETR2 | Signal transduction histidine kinase, hybrid-type, ethylene sensor | chr3:8255156-8257560 FORWARD LENGTH=773	624	773	0	123.9	85.9	91.8
Rsa1.0_00117.1.g5698.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00117.1.g5699.t1	ref|XP_002870534.1| hypothetical protein ARALYDRAFT_493723 [Arabidopsis lyrata subsp. lyrata] gi|297316370|gb|EFH46793.1| hypothetical protein ARALYDRAFT_493723 [Arabidopsis lyrata subsp. lyrata]	253	225	2.00E-24	88.9	27.7	32.0	hypothetical protein ARALYDRAFT_493723	gbpln	Arabidopsis lyrata	AT5G37475.1 | Symbols: | Translation initiation factor eIF3 subunit | chr5:14866328-14867749 REVERSE LENGTH=225	253	225	3.00E-26	88.9	26.5	32.0
Rsa1.0_00117.1.g5700.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00117.1.g5701.t1	gb|EOA32767.1| hypothetical protein CARUB_v10016073mg [Capsella rubella]	203	205	5.00E-77	101.0	81.8	86.7	hypothetical protein CARUB_v10016073mg	gbpln	Capsella rubella	AT3G23130.1 | Symbols: SUP, FON1, FLO10 | C2H2 and C2HC zinc fingers superfamily protein | chr3:8242504-8243118 FORWARD LENGTH=204	203	204	4.00E-77	100.5	78.8	85.2
Rsa1.0_00117.1.g5702.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00117.1.g5703.t1	ref|NP_188951.2| DNA repair protein XRCC4 [Arabidopsis thaliana] gi|238479872|ref|NP_001154639.1| DNA repair protein XRCC4 [Arabidopsis thaliana] gi|85701292|sp|Q682V0.2|XRCC4_ARATH RecName: Full=DNA repair protein XRCC4 gi|9800643|gb|AAF91285.2|AF233528_1 putative double strand break repair protein [Arabidopsis thaliana] gi|9294200|dbj|BAB02102.1| unnamed protein product [Arabidopsis thaliana] gi|332643196|gb|AEE76717.1| DNA repair protein XRCC4 [Arabidopsis thaliana] gi|332643197|gb|AEE76718.1| DNA repair protein XRCC4 [Arabidopsis thaliana]	317	264	1.00E-109	83.3	65.9	72.2	DNA repair protein XRCC4	gbpln	Arabidopsis thaliana	AT3G23100.2 | Symbols: XRCC4 | homolog of human DNA ligase iv-binding protein XRCC4 | chr3:8220721-8221991 FORWARD LENGTH=264	317	264	1.00E-112	83.3	65.9	72.2
Rsa1.0_00117.1.g5704.t1	dbj|BAB02101.1| unnamed protein product [Arabidopsis thaliana]	163	374	8.00E-21	229.4	31.9	36.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G23090.2 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr3:8214533-8216137 REVERSE LENGTH=338	163	338	3.00E-23	207.4	31.9	36.8
Rsa1.0_00117.1.g5705.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00117.1.g5706.t1	ref|XP_002885543.1| hypothetical protein ARALYDRAFT_319027 [Arabidopsis lyrata subsp. lyrata] gi|297331383|gb|EFH61802.1| hypothetical protein ARALYDRAFT_319027 [Arabidopsis lyrata subsp. lyrata]	454	427	0	94.1	79.1	85.2	hypothetical protein ARALYDRAFT_319027	gbpln	Arabidopsis lyrata	AT4G14500.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:8334391-8337022 FORWARD LENGTH=433	454	433	0	95.4	74.0	81.1
Rsa1.0_00117.1.g5707.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00117.1.g5708.t11	ref|XP_002883396.1| hypothetical protein ARALYDRAFT_479814 [Arabidopsis lyrata subsp. lyrata] gi|297329236|gb|EFH59655.1| hypothetical protein ARALYDRAFT_479814 [Arabidopsis lyrata subsp. lyrata]	334	482	3.00E-30	144.3	31.7	41.9	hypothetical protein ARALYDRAFT_479814	gbpln	Arabidopsis lyrata	AT3G23060.1 | Symbols: | RING/U-box superfamily protein | chr3:8200868-8203116 FORWARD LENGTH=480	334	480	7.00E-32	143.7	29.9	37.7
Rsa1.0_00117.1.g5709.t1	dbj|BAJ33997.1| unnamed protein product [Thellungiella halophila]	241	239	1.00E-113	99.2	85.5	92.9	unnamed protein product	----	----	AT3G23050.1 | Symbols: IAA7, AXR2 | indole-3-acetic acid 7 | chr3:8194768-8196716 FORWARD LENGTH=243	241	243	1.00E-114	100.8	85.9	93.8
Rsa1.0_00118.1.g5710.t2	gb|EOA39639.1| hypothetical protein CARUB_v10008273mg [Capsella rubella]	567	879	1.00E-170	155.0	55.2	70.4	hypothetical protein CARUB_v10008273mg	gbpln	Capsella rubella	AT1G51820.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19237407-19241883 REVERSE LENGTH=885	567	885	1.00E-166	156.1	54.1	69.1
Rsa1.0_00118.1.g5711.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2035	1274	0	62.6	29.3	40.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT2G01740.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:326136-327815 REVERSE LENGTH=559	2035	559	0	27.5	20.3	23.3
Rsa1.0_00118.1.g5712.t1	ref|XP_002886329.1| hypothetical protein ARALYDRAFT_892929 [Arabidopsis lyrata subsp. lyrata] gi|297332170|gb|EFH62588.1| hypothetical protein ARALYDRAFT_892929 [Arabidopsis lyrata subsp. lyrata]	379	383	1.00E-178	101.1	82.6	88.4	hypothetical protein ARALYDRAFT_892929	gbpln	Arabidopsis lyrata	AT1G64720.1 | Symbols: CP5 | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:24046887-24048537 REVERSE LENGTH=385	379	385	1.00E-180	101.6	82.8	89.4
Rsa1.0_00118.1.g5713.t1	ref|NP_565275.1| uncharacterized protein [Arabidopsis thaliana] gi|75268025|sp|Q9ZU97.2|VAC14_ARATH RecName: Full=Protein VAC14 homolog gi|20197546|gb|AAD12702.2| expressed protein [Arabidopsis thaliana] gi|330250391|gb|AEC05485.1| uncharacterized protein AT2G01690 [Arabidopsis thaliana]	736	743	0	101.0	92.1	96.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G01690.1 | Symbols: | ARM repeat superfamily protein | chr2:309144-313499 REVERSE LENGTH=743	736	743	0	101.0	92.1	96.6
Rsa1.0_00118.1.g5714.t1	gb|EOA25668.1| hypothetical protein CARUB_v10019019mg [Capsella rubella]	208	227	2.00E-69	109.1	70.2	80.3	hypothetical protein CARUB_v10019019mg	gbpln	Capsella rubella	AT2G01610.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr2:274124-274792 REVERSE LENGTH=222	208	222	4.00E-65	106.7	68.8	78.8

Rsa1.0_00118.1.g5715.t1	ref|XP_002875082.1| hypothetical protein ARALYDRAFT_904366 [Arabidopsis lyrata subsp. lyrata] gi|297320920|gb|EFH51341.1| hypothetical protein ARALYDRAFT_904366 [Arabidopsis lyrata subsp. lyrata]	577	562	0	97.4	84.7	89.1	hypothetical protein ARALYDRAFT_904366	gbpln	Arabidopsis lyrata	AT2G01600.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr2:268975-272356 FORWARD LENGTH=571	577	571	0	99.0	83.2	88.6
Rsa1.0_00118.1.g5716.t1	ref|XP_002876764.1| hypothetical protein ARALYDRAFT_484074 [Arabidopsis lyrata subsp. lyrata] gi|297322602|gb|EFH53023.1| hypothetical protein ARALYDRAFT_484074 [Arabidopsis lyrata subsp. lyrata]	193	191	3.00E-76	99.0	82.9	94.3	hypothetical protein ARALYDRAFT_484074	gbpln	Arabidopsis lyrata	AT2G01580.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G07510.2); Has 129 Blast hits to 129 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 129; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:265181-265756 REVERSE LENGTH=191	193	191	9.00E-69	99.0	82.9	92.7
Rsa1.0_00118.1.g5717.t6	gb|ABD64940.1| hypothetical protein 24.t00018 [Brassica oleracea]	549	380	3.00E-56	69.2	24.6	34.6	hypothetical protein 24.t00018	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	549	302	4.00E-42	55.0	22.4	29.9
Rsa1.0_00118.1.g5718.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	395	442	1.00E-157	111.9	68.4	77.2	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	395	343	5.00E-32	86.8	14.9	20.0
Rsa1.0_00118.1.g5719.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	275	329	5.00E-40	119.6	37.1	50.5	unnamed protein product	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	275	575	4.00E-20	209.1	28.0	47.6
Rsa1.0_00118.1.g5720.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00118.1.g5721.t1	sp|Q5BN22.1|RGA2_BRACM RecName: Full=DELLA protein RGA2; AltName: Full=BrRGA2; AltName: Full=RGA-like protein 2 gi|60656561|gb|AAX33298.1| DELLA protein [Brassica rapa]	585	579	0	99.0	91.1	93.7	RecName: Full=DELLA protein RGA2; AltName: Full=BrRGA2; AltName: Full=RGA-like protein 2 gi|60656561|gb|AAX33298.1| DELLA protein	gbpln	Brassica rapa	AT2G01570.1 | Symbols: RGA1, RGA | GRAS family transcription factor family protein | chr2:255581-257344 REVERSE LENGTH=587	585	587	0	100.3	82.6	88.4
Rsa1.0_00118.1.g5722.t1	ref|XP_002875078.1| hypothetical protein ARALYDRAFT_322499 [Arabidopsis lyrata subsp. lyrata] gi|297320916|gb|EFH51337.1| hypothetical protein ARALYDRAFT_322499 [Arabidopsis lyrata subsp. lyrata]	135	137	4.00E-57	101.5	82.2	89.6	hypothetical protein ARALYDRAFT_322499	gbpln	Arabidopsis lyrata	AT1G70780.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23150.1); Has 143 Blast hits to 143 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 143; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26695462-26695975 REVERSE LENGTH=140	135	140	6.00E-35	103.7	53.3	68.9
Rsa1.0_00118.1.g5723.t1	gb|ADK63403.1| C2 domain-containing protein [Brassica rapa]	180	180	3.00E-96	100.0	93.3	97.2	C2 domain-containing protein	gbpln	Brassica rapa	AT2G01540.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:242297-243233 REVERSE LENGTH=180	180	180	9.00E-94	100.0	87.8	92.2
Rsa1.0_00118.1.g5724.t1	ref|XP_002870338.1| hypothetical protein ARALYDRAFT_493506 [Arabidopsis lyrata subsp. lyrata] gi|297316174|gb|EFH46597.1| hypothetical protein ARALYDRAFT_493506 [Arabidopsis lyrata subsp. lyrata]	151	151	2.00E-75	100.0	88.1	92.7	hypothetical protein ARALYDRAFT_493506	gbpln	Arabidopsis lyrata	AT2G01520.1 | Symbols: MLP328 | MLP-like protein 328 | chr2:235992-236881 FORWARD LENGTH=151	151	151	2.00E-77	100.0	86.8	93.4
Rsa1.0_00118.1.g5725.t1	#	#	#	#	#	#	#	-	----	----	AT2G01510.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:230752-232506 REVERSE LENGTH=584	134	584	1.00E-12	435.8	23.1	26.1

Rsa1.0_00118.1.g5726.t1	ref|NP_671764.1| protein CLAVATA3/ESR-related 16 [Arabidopsis thaliana] gi|75160477|sp|Q8S8M2.1|CLE16_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 16; Contains: RecName: Full=CLE16p; Flags: Precursor gi|20197403|gb|AAM15061.1|AC005560_22 CLE16, putative [Arabidopsis thaliana] gi|44917487|gb|AAS49068.1| At2g01505 [Arabidopsis thaliana] gi|330250368|gb|AEC05462.1| protein CLAVATA3/ESR-related 16 [Arabidopsis thaliana]		104	103	6.00E-25	99.0	56.7	66.3	protein CLAVATA3/ESR-related 16	gbpln	Arabidopsis thaliana	AT2G01505.1 | Symbols: CLE16 | CLAVATA3/ESR-RELATED 16 | chr2:228926-229237 REVERSE LENGTH=103		104	103	1.00E-27	99.0	56.7	66.3
Rsa1.0_00118.1.g5727.t2	ref|XP_002876753.1| HOS9/PFS2 [Arabidopsis lyrata subsp. lyrata] gi|297322591|gb|EFH53012.1| HOS9/PFS2 [Arabidopsis lyrata subsp. lyrata]		250	275	7.00E-70	110.0	63.2	72.8	HOS9/PFS2	gbpln	Arabidopsis lyrata	AT2G01500.1 | Symbols: PFS2, WOX6, HOS9 | Homeodomain-like superfamily protein | chr2:224470-225997 REVERSE LENGTH=271		250	271	5.00E-61	108.4	61.2	69.2
Rsa1.0_00118.1.g5728.t1	ref|XP_002875075.1| hypothetical protein ARALYDRAFT_484067 [Arabidopsis lyrata subsp. lyrata] gi|297320913|gb|EFH51334.1| hypothetical protein ARALYDRAFT_484067 [Arabidopsis lyrata subsp. lyrata]		284	284	1.00E-140	100.0	85.6	93.3	hypothetical protein ARALYDRAFT_484067	gbpln	Arabidopsis lyrata	AT2G01490.1 | Symbols: | phytanoyl-CoA dioxygenase (PhyH) family protein | chr2:221316-223187 FORWARD LENGTH=283		284	283	1.00E-140	99.6	84.2	91.9
Rsa1.0_00118.1.g5729.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00118.1.g5730.t1	ref|NP_178254.2| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|79316341|ref|NP_001030939.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|79316349|ref|NP_001030940.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|79316359|ref|NP_001030941.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|75327927|sp|Q84M93.1|MPK17_ARATH RecName: Full=Mitogen-activated protein kinase 17; Short=AtMPK17; Short=MAP kinase 17 gi|30102718|gb|AAP21277.1| At2g01450 [Arabidopsis thaliana] gi|110736492|dbj|BAF00214.1| putative MAP kinase [Arabidopsis thaliana] gi|222423803|dbj|BAH19867.1| AT2G01450 [Arabidopsis thaliana] gi|330250358|gb|AEC05452.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|330250359|gb|AEC05453.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|330250360|gb|AEC05454.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|330250361|gb|AEC05455.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana]		489	486	0	99.4	94.9	97.3	mitogen-activated protein kinase 17	gbpln	Arabidopsis thaliana	AT2G01450.4 | Symbols: ATMPK17, MPK17 | MAP kinase 17 | chr2:199722-202010 REVERSE LENGTH=486		489	486	0	99.4	94.9	97.3
Rsa1.0_00118.1.g5731.t1	dbj|BAJ34534.1| unnamed protein product [Thellungiella halophila]		122	201	4.00E-52	164.8	85.2	89.3	unnamed protein product	----	----	AT2G01430.1 | Symbols: ATHB17, ATHB-17, HB17 | homeobox-leucine zipper protein 17 | chr2:187798-190369 REVERSE LENGTH=275		122	275	2.00E-52	225.4	83.6	89.3
Rsa1.0_00119.1.g5732.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00119.1.g5733.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	

Rsa1.0_00119.1.g5734.t1	ref|NP_567581.1| abscisic acid 8'-hydroxylase 1 [Arabidopsis thaliana] gi|75306306|sp|Q949P1.1|ABAH1_ARATH RecName: Full=Abscisic acid 8'-hydroxylase 1; Short=ABA 8'-hydroxylase 1; AltName: Full=Cytochrome P450 707A1 gi|15293093|gb|AAK93657.1| putative cytochrome P450 protein [Arabidopsis thaliana] gi|20259299|gb|AAM14385.1| putative cytochrome P450 protein [Arabidopsis thaliana] gi|46401564|dbj|BAD16629.1| cytochrome P450 monooxygenase [Arabidopsis thaliana] gi|332658762|gb|AEE84162.1| abscisic acid 8'-hydroxylase 1 [Arabidopsis thaliana]	467	467	0	100.0	92.9	96.1	abscisic acid 8'-hydroxylase 1	gbpln	Arabidopsis thaliana	AT4G19230.1 | Symbols: CYP707A1 | cytochrome P450, family 707, subfamily A, polypeptide 1 | chr4:10521524-10523517 FORWARD LENGTH=467	467	467	0	100.0	92.9	96.1
Rsa1.0_00119.1.g5735.t1	ref|XP_002867948.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297313784|gb|EFH44207.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	873	919	0	105.3	80.3	88.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G19220.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:10505266-10508121 REVERSE LENGTH=932	873	932	0	106.8	77.8	86.8
Rsa1.0_00119.1.g5736.t1	ref|NP_193656.2| ABC transporter E family member 2 [Arabidopsis thaliana] gi|75330288|sp|Q8LPJ4.1|AB2E_ARATH RecName: Full=ABC transporter E family member 2; Short=ABC transporter ABCE.2; Short=AtABCE2; AltName: Full=RNase L inhibitor-like protein 2; Short=AtRLI2; Short=AthaRLI2 gi|20466462|gb|AAM20548.1| RNase L inhibitor-like protein [Arabidopsis thaliana] gi|23198180|gb|AAN15617.1| RNase L inhibitor-like protein [Arabidopsis thaliana] gi|110742163|dbj|BAE99009.1| RNase L inhibitor-like protein [Arabidopsis thaliana] gi|332658760|gb|AEE84160.1| ABC transporter E family member 2 [Arabidopsis thaliana]	578	605	0	104.7	97.4	98.8	ABC transporter E family member 2	gbpln	Arabidopsis thaliana	AT4G19210.1 | Symbols: ATRLI2, RLI2 | RNAse l inhibitor protein 2 | chr4:10501906-10504776 FORWARD LENGTH=605	578	605	0	104.7	97.4	98.8
Rsa1.0_00119.1.g5737.t1	ref|XP_002890942.1| hypothetical protein ARALYDRAFT_313748 [Arabidopsis lyrata subsp. lyrata] gi|297336784|gb|EFH67201.1| hypothetical protein ARALYDRAFT_313748 [Arabidopsis lyrata subsp. lyrata]	352	822	5.00E-28	233.5	16.2	17.3	hypothetical protein ARALYDRAFT_313748	gbpln	Arabidopsis lyrata	AT5G45400.1 | Symbols: RPA70C, ATRPA70C | Replication factor-A protein 1-related | chr5:18398990-18401644 FORWARD LENGTH=853	352	853	1.00E-30	242.3	16.2	17.3
Rsa1.0_00119.1.g5738.t1	gb|EOA30324.1| hypothetical protein CARUB_v10013451mg [Capsella rubella]	431	445	1.00E-109	103.2	51.0	61.3	hypothetical protein CARUB_v10013451mg	gbpln	Capsella rubella	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	431	472	1.00E-110	109.5	50.6	63.8
Rsa1.0_00119.1.g5739.t1	gb|EOA17088.1| hypothetical protein CARUB_v10005338mg [Capsella rubella]	169	304	2.00E-69	179.9	80.5	88.8	hypothetical protein CARUB_v10005338mg	gbpln	Capsella rubella	AT4G19140.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10469830-10471275 FORWARD LENGTH=303	169	303	7.00E-70	179.3	77.5	82.8
Rsa1.0_00119.1.g5740.t1	gb|EOA15986.1| hypothetical protein CARUB_v10004104mg [Capsella rubella]	760	879	0	115.7	69.9	81.6	hypothetical protein CARUB_v10004104mg	gbpln	Capsella rubella	AT4G19130.1 | Symbols: | Replication factor-A protein 1-related | chr4:10466618-10469092 REVERSE LENGTH=784	760	784	0	103.2	67.2	77.6
Rsa1.0_00119.1.g5741.t1	gb|EOA15853.1| hypothetical protein CARUB_v10007621mg [Capsella rubella]	600	600	0	100.0	91.2	96.3	hypothetical protein CARUB_v10007621mg	gbpln	Capsella rubella	AT4G19120.2 | Symbols: ERD3 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:10460665-10463034 REVERSE LENGTH=600	600	600	0	100.0	90.8	96.2
Rsa1.0_00119.1.g5742.t1	ref|NP_849407.1| putative serine/threonine protein kinase [Arabidopsis thaliana] gi|332658742|gb|AEE84142.1| putative serine/threonine protein kinase [Arabidopsis thaliana]	461	464	0	100.7	89.4	94.8	putative serine/threonine protein kinase	gbpln	Arabidopsis thaliana	AT4G19110.2 | Symbols: | Protein kinase superfamily protein | chr4:10454770-10457468 REVERSE LENGTH=464	461	464	0	100.7	89.4	94.8

Rsa1.0_00119.1.g5743.t1	ref|NP_193642.1| cadmium-induced protein AS8 [Arabidopsis thaliana] gi|1168863|sp|P42735.1|CDI8_ARATH RecName: Full=Cadmium-induced protein AS8 gi|534902|emb|CAA85363.1| cadmium induced protein [Arabidopsis thaliana] gi|2832634|emb|CAA16763.1| cadmium-induced protein [Arabidopsis thaliana] gi|7268702|emb|CAB78909.1| cadmium-induced protein [Arabidopsis thaliana] gi|18176472|gb|AAL60050.1| AT4g19070/F13C5_230 [Arabidopsis thaliana] gi|22655438|gb|AAM98311.1| At4g19070/F13C5_230 [Arabidopsis thaliana] gi|332658736|gb|AEE84136.1| cadmium-induced protein AS8 [Arabidopsis thaliana]	174	171	4.00E-71	98.3	82.2	88.5	cadmium-induced protein AS8	gbpln	Arabidopsis thaliana	AT4G19070.1 | Symbols: | Putative membrane lipoprotein | chr4:10446770-10448079 REVERSE LENGTH=171	174	171	2.00E-73	98.3	82.2	88.5
Rsa1.0_00119.1.g5744.t2	ref|XP_002867959.1| hypothetical protein ARALYDRAFT_492951 [Arabidopsis lyrata subsp. lyrata] gi|297313795|gb|EFH44218.1| hypothetical protein ARALYDRAFT_492951 [Arabidopsis lyrata subsp. lyrata]	725	718	0	99.0	92.7	96.0	hypothetical protein ARALYDRAFT_492951	gbpln	Arabidopsis lyrata	AT4G19040.1 | Symbols: EDR2 | ENHANCED DISEASE RESISTANCE 2 | chr4:10431799-10437171 REVERSE LENGTH=718	725	718	0	99.0	92.4	95.7
Rsa1.0_00119.1.g5745.t1	gb|EOA17974.1| hypothetical protein CARUB_v10006389mg [Capsella rubella]	353	361	1.00E-169	102.3	84.7	90.9	hypothetical protein CARUB_v10006389mg	gbpln	Capsella rubella	AT4G18990.1 | Symbols: XTH29 | xyloglucan endotransglucosylase/hydrolase 29 | chr4:10401941-10404248 REVERSE LENGTH=357	353	357	1.00E-169	101.1	86.4	92.9
Rsa1.0_00119.1.g5746.t1	ref|XP_002870008.1| hypothetical protein ARALYDRAFT_492961 [Arabidopsis lyrata subsp. lyrata] gi|297315844|gb|EFH46267.1| hypothetical protein ARALYDRAFT_492961 [Arabidopsis lyrata subsp. lyrata]	109	107	5.00E-36	98.2	71.6	81.7	hypothetical protein ARALYDRAFT_492961	gbpln	Arabidopsis lyrata	AT4G18980.1 | Symbols: AtS40-3 | AtS40-3 | chr4:10398973-10399293 FORWARD LENGTH=106	109	106	2.00E-36	97.2	70.6	78.9
Rsa1.0_00119.1.g5747.t1	emb|CAA16754.1| putative protein [Arabidopsis thaliana] gi|7268691|emb|CAB78899.1| putative protein [Arabidopsis thaliana]	360	626	0	173.9	90.8	95.8	putative protein	gbpln	Arabidopsis thaliana	AT4G18970.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr4:10389308-10390808 REVERSE LENGTH=361	360	361	0	100.3	90.8	95.8
Rsa1.0_00119.1.g5748.t1	ref|XP_002870009.1| hypothetical protein ARALYDRAFT_914774 [Arabidopsis lyrata subsp. lyrata] gi|297315845|gb|EFH46268.1| hypothetical protein ARALYDRAFT_914774 [Arabidopsis lyrata subsp. lyrata]	193	302	2.00E-85	156.5	89.6	92.7	hypothetical protein ARALYDRAFT_914774	gbpln	Arabidopsis lyrata	AT4G18960.1 | Symbols: AG | K-box region and MADS-box transcription factor family protein | chr4:10383917-10388272 FORWARD LENGTH=252	193	252	1.00E-87	130.6	88.6	92.7
Rsa1.0_00119.1.g5749.t1	gb|ABK28640.1| unknown [Arabidopsis thaliana]	268	248	4.00E-83	92.5	64.6	70.9	unknown	gbpln	Arabidopsis thaliana	AT4G18920.1 | Symbols: | Protein of unknown function (DUF1264) | chr4:10368784-10370086 FORWARD LENGTH=247	268	247	1.00E-85	92.2	64.6	70.9
Rsa1.0_00119.1.g5750.t1	ref|XP_002870013.1| hypothetical protein ARALYDRAFT_492969 [Arabidopsis lyrata subsp. lyrata] gi|297315849|gb|EFH46272.1| hypothetical protein ARALYDRAFT_492969 [Arabidopsis lyrata subsp. lyrata]	289	298	1.00E-151	103.1	91.7	96.9	hypothetical protein ARALYDRAFT_492969	gbpln	Arabidopsis lyrata	AT4G18910.1 | Symbols: NIP1;2, NLM2, ATNLM2 | NOD26-like intrinsic protein 1;2 | chr4:10366211-10368179 FORWARD LENGTH=294	289	294	1.00E-151	101.7	90.3	96.2
Rsa1.0_00119.1.g5751.t1	ref|NP_193624.1| BES1/BZR1 homolog 3 [Arabidopsis thaliana] gi|61211367|sp|O49404.1|BEH3_ARATH RecName: Full=BES1/BZR1 homolog protein 3 gi|2832617|emb|CAA16746.1| putative protein [Arabidopsis thaliana] gi|7268683|emb|CAB78891.1| putative protein [Arabidopsis thaliana] gi|21594000|gb|AAM65918.1| unknown [Arabidopsis thaliana] gi|26452712|dbj|BAC43438.1| unknown protein [Arabidopsis thaliana] gi|87116658|gb|ABD19693.1| At4g18890 [Arabidopsis thaliana] gi|332658702|gb|AEE84102.1| BES1/BZR1 homolog 3 [Arabidopsis thaliana]	276	284	1.00E-130	102.9	95.7	97.5	BES1/BZR1 homolog 3	gbpln	Arabidopsis thaliana	AT4G18890.1 | Symbols: BEH3 | BES1/BZR1 homolog 3 | chr4:10352774-10355259 FORWARD LENGTH=284	276	284	1.00E-132	102.9	95.7	97.5
Rsa1.0_00119.1.g5752.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00119.1.g5753.t1	gb|ADX69244.1| heat shock transcription factor A4a [Brassica napus]	386	389	0	100.8	92.7	95.6	heat shock transcription factor A4a	gbpln	Brassica napus	AT4G18880.1 | Symbols: AT-HSFA4A, HSF A4A | heat shock transcription factor A4A | chr4:10347769-10349051 REVERSE LENGTH=401	386	401	1.00E-172	103.9	84.5	90.4
Rsa1.0_00119.1.g5754.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00119.1.g5755.t1	ref|XP_002870027.1| hypothetical protein ARALYDRAFT_492990 [Arabidopsis lyrata subsp. lyrata] gi|297315863|gb|EFH46286.1| hypothetical protein ARALYDRAFT_492990 [Arabidopsis lyrata subsp. lyrata]	285	281	1.00E−113	98.6	72.6	82.5	hypothetical protein ARALYDRAFT_492990	gbpln	Arabidopsis lyrata	AT4G18690.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G18680.1); Has 522 Blast hits to 522 proteins in 39 species: Archae − 0; Bacteria − 0; Metazoa − 9; Fungi − 0; Plants − 513; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr4:10282788−10283636 FORWARD LENGTH=282	285	282	1.00E−111	98.9	70.9	82.1
Rsa1.0_00119.1.g5756.t1	emb|CAB37448.1| putative protein [Arabidopsis thaliana] gi|7268657|emb|CAB78865.1| putative protein [Arabidopsis thaliana]	418	472	1.00E−161	112.9	74.4	84.2	putative protein	gbpln	Arabidopsis thaliana	AT4G18630.1 | Symbols: | Protein of unknown function (DUF688) | chr4:10257178−10258734 FORWARD LENGTH=479	418	479	1.00E−163	114.6	73.9	83.5
Rsa1.0_00119.1.g5757.t1	emb|CAB10225.1| retrovirus−related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus−related like polyprotein [Arabidopsis thaliana]	1382	1489	0	107.7	46.7	64.5	retrovirus−related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1382	1262	3.00E−71	91.3	9.6	12.8
Rsa1.0_00119.1.g5758.t1	gb|EOA19044.1| hypothetical protein CARUB_v10007704mg [Capsella rubella]	189	191	2.00E−80	101.1	85.7	88.4	hypothetical protein CARUB_v10007704mg	gbpln	Capsella rubella	AT4G18610.1 | Symbols: LSH9 | Protein of unknown function (DUF640) | chr4:10250794−10251369 FORWARD LENGTH=191	189	191	5.00E−82	101.1	85.2	88.4
Rsa1.0_00119.1.g5759.t1	ref|XP_002870037.1| hypothetical protein ARALYDRAFT_493003 [Arabidopsis lyrata subsp. lyrata] gi|297315873|gb|EFH46296.1| hypothetical protein ARALYDRAFT_493003 [Arabidopsis lyrata subsp. lyrata]	606	636	0	105.0	80.4	85.8	hypothetical protein ARALYDRAFT_493003	gbpln	Arabidopsis lyrata	AT4G18570.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr4:10231439−10234534 FORWARD LENGTH=642	606	642	0	105.9	79.2	87.0
Rsa1.0_00119.1.g5760.t1	gb|EOA15507.1| hypothetical protein CARUB_v10004827mg [Capsella rubella]	391	440	0	112.5	84.4	92.3	hypothetical protein CARUB_v10004827mg	gbpln	Capsella rubella	AT4G18550.1 | Symbols: | alpha/beta−Hydrolases superfamily protein | chr4:10225006−10226862 REVERSE LENGTH=419	391	419	1.00E−179	107.2	78.5	84.9
Rsa1.0_00119.1.g5761.t1	gb|EOA16325.1| hypothetical protein CARUB_v10004475mg [Capsella rubella]	570	569	0	99.8	87.0	93.2	hypothetical protein CARUB_v10004475mg	gbpln	Capsella rubella	AT4G18540.1 | Symbols: | unknown protein; Has 209 Blast hits to 205 proteins in 54 species: Archae − 0; Bacteria − 17; Metazoa − 2; Fungi − 150; Plants − 40; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr4:10221203−10223028 REVERSE LENGTH=520	570	520	0	91.2	77.7	84.0
Rsa1.0_00119.1.g5762.t1	ref|NP_567176.2| XH/XS domain−containing protein [Arabidopsis thaliana] gi|332656471|gb|AEE81871.1| XH/XS domain−containing protein [Arabidopsis thaliana]	174	635	1.00E−29	364.9	47.1	64.4	XH/XS domain−containing protein	gbpln	Arabidopsis thaliana	AT4G00380.1 | Symbols: | XH/XS domain−containing protein | chr4:167959−170448 FORWARD LENGTH=635	174	635	4.00E−32	364.9	47.1	64.4
Rsa1.0_00119.1.g5763.t1	ref|NP_173043.1| XH/XS domain−containing protein [Arabidopsis thaliana] gi|6587797|gb|AAF18488.1|AC010924_1 Contains similarity to gb|AF136530 transcriptional regulator from Zea mays. ESTs gb|F14071, gb|Z26823, gb|AI998935 come from this gene [Arabidopsis thaliana] gi|332191261|gb|AEE29382.1| XH/XS domain−containing protein [Arabidopsis thaliana]	239	634	2.00E−56	265.3	47.7	63.2	XH/XS domain−containing protein	gbpln	Arabidopsis thaliana	AT1G15910.1 | Symbols: | XH/XS domain−containing protein | chr1:5465951−5468723 FORWARD LENGTH=634	239	634	5.00E−59	265.3	47.7	63.2
Rsa1.0_00119.1.g5764.t1	ref|NP_193588.5| uncharacterized protein [Arabidopsis thaliana] gi|332658658|gb|AEE84058.1| uncharacterized protein AT4G18530 [Arabidopsis thaliana]	403	389	0	96.5	78.7	84.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G18530.1 | Symbols: | Protein of unknown function (DUF707) | chr4:10217749−10220285 FORWARD LENGTH=389	403	389	0	96.5	78.7	84.9
Rsa1.0_00119.1.g5765.t1	gb|EOA16240.1| hypothetical protein CARUB_v10004383mg [Capsella rubella]	615	621	0	101.0	91.2	95.3	hypothetical protein CARUB_v10004383mg	gbpln	Capsella rubella	AT4G18520.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:10215250−10217103 REVERSE LENGTH=617	615	617	0	100.3	90.4	94.5
Rsa1.0_00119.1.g5766.t1	ref|XP_002870040.1| hypothetical protein ARALYDRAFT_493008 [Arabidopsis lyrata subsp. lyrata] gi|297315876|gb|EFH46299.1| hypothetical protein ARALYDRAFT_493008 [Arabidopsis lyrata subsp. lyrata]	78	78	1.00E−14	100.0	65.4	74.4	hypothetical protein ARALYDRAFT_493008	gbpln	Arabidopsis lyrata	AT4G18510.1 | Symbols: CLE2 | CLAVATA3/ESR−related 2 | chr4:10212092−10212319 FORWARD LENGTH=75	78	75	3.00E−14	96.2	70.5	75.6

Rsa1.0_00119.1.g5767.t2	gb|AAB61114.1| EST gb|ATTS0887 comes from this gene [Arabidopsis thaliana]	233	358	3.00E-38	153.6	41.2	45.1	EST gb|ATTS0887 comes from this gene	gbpln	Arabidopsis thaliana	AT1G69980.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 30 Blast hits to 30 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26356559-26357647 REVERSE LENGTH=205	233	205	1.00E-40	88.0	41.2	45.1
Rsa1.0_00119.1.g5768.t1	ref|XP_002870040.1| hypothetical protein ARALYDRAFT_493008 [Arabidopsis lyrata subsp. lyrata] gi|297315876|gb|EFH46299.1| hypothetical protein ARALYDRAFT_493008 [Arabidopsis lyrata subsp. lyrata]	78	78	3.00E-14	100.0	70.5	78.2	hypothetical protein ARALYDRAFT_493008	gbpln	Arabidopsis lyrata	AT4G18510.1 | Symbols: CLE2 | CLAVATA3/ESR-related 2 | chr4:10212092-10212319 FORWARD LENGTH=75	78	75	4.00E-15	96.2	70.5	78.2
Rsa1.0_00119.1.g5769.t1	ref|NP_001031665.1| uncharacterized protein [Arabidopsis thaliana] gi|98962121|gb|ABF59390.1| unknown protein [Arabidopsis thaliana] gi|332658655|gb|AEE84055.1| uncharacterized protein AT4G18501 [Arabidopsis thaliana]	113	109	6.00E-27	96.5	73.5	81.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G18501.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:10209311-10209640 FORWARD LENGTH=109	113	109	1.00E-29	96.5	73.5	81.4
Rsa1.0_00119.1.g5770.t1	ref|NP_001119007.2| uncharacterized protein [Arabidopsis thaliana] gi|332658653|gb|AEE84053.1| uncharacterized protein AT4G18490 [Arabidopsis thaliana]	773	755	0	97.7	69.2	79.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G18490.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot, shoot apex, embryo, flower, seed; EXPRESSED DURING: petal differentiation and expansion stage, E expanded cotyledon stage; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10204388-10208197 FORWARD LENGTH=755	773	755	0	97.7	69.2	79.4
Rsa1.0_00119.1.g5771.t1	ref|XP_002316838.1| predicted protein [Populus trichocarpa] gi|222859903|gb|EEE97450.1| predicted protein [Populus trichocarpa]	93	420	3.00E-27	451.6	63.4	71.0	predicted protein	gbpln	Populus trichocarpa	AT4G18480.1 | Symbols: CHLI1, CH42, CH-42, CHL11, CHLI-1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:10201897-10203361 REVERSE LENGTH=424	93	424	2.00E-27	455.9	69.9	72.0
Rsa1.0_00119.1.g5772.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1356	1274	0	94.0	41.7	56.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1356	575	1.00E-63	42.4	12.6	20.1
Rsa1.0_00119.1.g5773.t1	gb|EOA16437.1| hypothetical protein CARUB_v10004589mg [Capsella rubella]	60	523	1.00E-20	871.7	80.0	86.7	hypothetical protein CARUB_v10004589mg	gbpln	Capsella rubella	AT1G36280.2 | Symbols: | L-Aspartase-like family protein | chr1:13640600-13642908 FORWARD LENGTH=519	60	519	4.00E-23	865.0	80.0	85.0
Rsa1.0_00119.1.g5774.t1	ref|NP_193578.1| RAB GTPase homolog A1E [Arabidopsis thaliana] gi|297800216|ref|XP_002867992.1| hypothetical protein ARALYDRAFT_493018 [Arabidopsis lyrata subsp. lyrata] gi|75098755|sp|O49513.1|RAA1E_ARATH RecName: Full=Ras-related protein RABA1e; Short=AtRABA1e gi|2832648|emb|CAA16723.1| membrane-bound small GTP-binding -like protein [Arabidopsis thaliana] gi|7268636|emb|CAB78845.1| membrane-bound small GTP-binding-like protein [Arabidopsis thaliana] gi|38603932|gb|AAR24711.1| At4g18430 [Arabidopsis thaliana] gi|44681422|gb|AAS47651.1| At4g18430 [Arabidopsis thaliana] gi|297313828|gb|EFH44251.1| hypothetical protein ARALYDRAFT_493018 [Arabidopsis lyrata subsp. lyrata] gi|332658645|gb|AEE84045.1| RAB GTPase homolog A1E [Arabidopsis thaliana]	217	217	1.00E-122	100.0	97.7	99.1	RAB GTPase homolog A1E	gbpln	Arabidopsis lyrata	AT4G18430.1 | Symbols: AtRABA1e, RABA1e | RAB GTPase homolog A1E | chr4:10183903-10185223 REVERSE LENGTH=217	217	217	1.00E-125	100.0	97.7	99.1
Rsa1.0_00119.1.g5775.t1	emb|CAN73272.1| hypothetical protein VITISV_013115 [Vitis vinifera]	1021	1178	0	115.4	43.6	55.6	hypothetical protein VITISV_013115	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1021	1262	1.00E-123	123.6	21.3	30.4

Rsa1.0_00119.1.g5776.t1	gb|EOA17708.1| hypothetical protein CARUB_v10006080mg [Capsella rubella]	99	107	6.00E-31	108.1	69.7	73.7	hypothetical protein CARUB_v10006080mg	gbpln	Capsella rubella	AT4G18400.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10170024-10171221 REVERSE LENGTH=107	99	107	1.00E-33	108.1	69.7	73.7
Rsa1.0_00119.1.g5777.t1	dbj|BAJ33883.1| unnamed protein product [Thellungiella halophila]	253	379	3.00E-91	149.8	81.8	86.6	unnamed protein product	----	----	AT4G18390.2 | Symbols: TCP2 | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 2 | chr4:10163212-10164309 REVERSE LENGTH=365	253	365	4.00E-87	144.3	77.5	81.8
Rsa1.0_00119.1.g5778.t1	ref|XP_002868000.1| hypothetical protein ARALYDRAFT_914851 [Arabidopsis lyrata subsp. lyrata] gi|297313836|gb|EFH44259.1| hypothetical protein ARALYDRAFT_914851 [Arabidopsis lyrata subsp. lyrata]	115	112	5.00E-48	97.4	84.3	93.9	hypothetical protein ARALYDRAFT_914851	gbpln	Arabidopsis lyrata	AT4G18372.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr4:10151349-10151687 REVERSE LENGTH=112	115	112	3.00E-50	97.4	83.5	93.0
Rsa1.0_00119.1.g5779.t1	gb|EOA16863.1| hypothetical protein CARUB_v10005088mg [Capsella rubella]	368	368	0	100.0	98.4	99.5	hypothetical protein CARUB_v10005088mg	gbpln	Capsella rubella	AT4G18360.1 | Symbols: | Aldolase-type TIM barrel family protein | chr4:10146141-10148386 REVERSE LENGTH=368	368	368	0	100.0	97.3	98.6
Rsa1.0_00119.1.g5780.t1	ref|XP_002862798.1| hypothetical protein ARALYDRAFT_497292 [Arabidopsis lyrata subsp. lyrata] gi|297308526|gb|EFH39056.1| hypothetical protein ARALYDRAFT_497292 [Arabidopsis lyrata subsp. lyrata]	787	842	0	107.0	57.8	69.8	hypothetical protein ARALYDRAFT_497292	gbpln	Arabidopsis lyrata	AT1G71400.1 | Symbols: AtRLP12, RLP12 | receptor like protein 12 | chr1:26909905-26912448 FORWARD LENGTH=847	787	847	0	107.6	56.7	70.5
Rsa1.0_00119.1.g5781.t1	ref|NP_193569.1| 9-cis-epoxycarotenoid dioxygenase NCED2 [Arabidopsis thaliana] gi|75098750|sp|O49505.1|NCED2_ARATH RecName: Full=9-cis-epoxycarotenoid dioxygenase NCED2, chloroplastic; Short=AtNCED2; Flags: Precursor gi|2832640|emb|CAA16715.1| neoxanthin cleavage enzyme - like protein [Arabidopsis thaliana] gi|7268628|emb|CAB78837.1| neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana] gi|133778876|gb|ABO38778.1| At4g18350 [Arabidopsis thaliana] gi|332658630|gb|AEE84030.1| 9-cis-epoxycarotenoid dioxygenase NCED2 [Arabidopsis thaliana]	583	583	0	100.0	90.1	95.2	9-cis-epoxycarotenoid dioxygenase NCED2	gbpln	Arabidopsis thaliana	AT4G18350.1 | Symbols: NCED2, ATNCED2 | nine-cis-epoxycarotenoid dioxygenase 2 | chr4:10142672-10144423 FORWARD LENGTH=583	583	583	0	100.0	90.1	95.2
Rsa1.0_00119.1.g5782.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	234	1161	2.00E-53	496.2	42.3	56.4	F14N23.4	gbpln	Arabidopsis thaliana	AT5G16486.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:5383597-5384226 REVERSE LENGTH=209	234	209	3.00E-50	89.3	41.5	57.3
Rsa1.0_00119.1.g5783.t1	ref|NP_193568.2| glycosyl hydrolase family 17 protein [Arabidopsis thaliana] gi|21539539|gb|AAM53322.1| beta-1,3-glucanase-like protein [Arabidopsis thaliana] gi|24899809|gb|AAN65119.1| beta-1,3-glucanase-like protein [Arabidopsis thaliana] gi|332658629|gb|AEE84029.1| glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	956	397	0	41.5	37.1	39.4	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis thaliana	AT4G18340.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr4:10130245-10132019 REVERSE LENGTH=397	956	397	0	41.5	37.1	39.4
Rsa1.0_00119.1.g5784.t1	gb|EOA15399.1| hypothetical protein CARUB_v10006826mg [Capsella rubella]	282	537	1.00E-131	190.4	80.9	89.0	hypothetical protein CARUB_v10006826mg	gbpln	Capsella rubella	AT4G18260.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane protein family | chr4:10093524-10097337 REVERSE LENGTH=545	282	545	1.00E-130	193.3	79.1	88.7
Rsa1.0_00119.1.g5785.t2	gb|EOA16230.1| hypothetical protein CARUB_v10004372mg [Capsella rubella]	642	626	0	97.5	72.6	82.9	hypothetical protein CARUB_v10004372mg	gbpln	Capsella rubella	AT4G18250.1 | Symbols: | receptor serine/threonine kinase, putative | chr4:10087343-10091963 REVERSE LENGTH=853	642	853	0	132.9	68.4	80.5

Rsa1.0_00119.1.g5786.t1	ref|XP_002868006.1| hypothetical protein ARALYDRAFT_493043 [Arabidopsis lyrata subsp. lyrata] gi|297313842|gb|EFH44265.1| hypothetical protein ARALYDRAFT_493043 [Arabidopsis lyrata subsp. lyrata]	222	233	8.00E-99	105.0	79.3	83.8	hypothetical protein ARALYDRAFT_493043	gbpln	Arabidopsis lyrata	AT4G18230.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Oligosaccharide biosynthesis protein Alg14 like (InterPro:IPR013969); Has 640 Blast hits to 640 proteins in 277 species: Archae - 4; Bacteria - 281; Metazoa - 94; Fungi - 127; Plants - 57; Viruses - 0; Other Eukaryotes - 77 (source: NCBI BLink). | chr4:10080521-10081710 REVERSE LENGTH=233	222	233	9.00E-94	105.0	80.6	83.8
Rsa1.0_00119.1.g5787.t1	ref|XP_002870065.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297315901|gb|EFH46324.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	840	414	0	49.3	41.0	43.8	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT4G18180.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:10065626-10067317 FORWARD LENGTH=414	840	414	0	49.3	40.0	42.5
Rsa1.0_00119.1.g5788.t1	gb|ACI14393.1| WRKY28-1 transcription factor [Brassica napus]	313	312	1.00E-169	99.7	93.3	96.8	WRKY28-1 transcription factor	gbpln	Brassica napus	AT4G18170.1 | Symbols: WRKY28, ATWRKY28 | WRKY DNA-binding protein 28 | chr4:10061508-10062691 FORWARD LENGTH=318	313	318	1.00E-141	101.6	83.4	89.8
Rsa1.0_00119.1.g5789.t1	ref|XP_002870067.1| hypothetical protein ARALYDRAFT_914875 [Arabidopsis lyrata subsp. lyrata] gi|297315903|gb|EFH46326.1| hypothetical protein ARALYDRAFT_914875 [Arabidopsis lyrata subsp. lyrata]	447	438	0	98.0	82.6	87.7	hypothetical protein ARALYDRAFT_914875	gbpln	Arabidopsis lyrata	AT4G18160.1 | Symbols: KCO6, ATTPK3, ATKCO6, TPK3 | Ca2+ activated outward rectifying K+ channel 6 | chr4:10055696-10057546 FORWARD LENGTH=436	447	436	0	97.5	79.6	84.1
Rsa1.0_00119.1.g5790.t1	gb|EOA17641.1| hypothetical protein CARUB_v10006007mg [Capsella rubella]	150	133	1.00E-68	88.7	88.0	88.7	hypothetical protein CARUB_v10006007mg	gbpln	Capsella rubella	AT4G18100.1 | Symbols: | Ribosomal protein L32e | chr4:10035715-10036475 REVERSE LENGTH=133	150	133	6.00E-71	88.7	87.3	88.7
Rsa1.0_00119.1.g5791.t2	gb|EOA12313.1| hypothetical protein CARUB_v10007956mg [Capsella rubella]	1403	1409	0	100.4	84.5	91.0	hypothetical protein CARUB_v10007956mg	gbpln	Capsella rubella	AT2G07680.1 | Symbols: ATMRP11, MRP11, ABCC13 | multidrug resistance-associated protein 11 | chr2:3514774-3522491 FORWARD LENGTH=1404	1403	1404	0	100.1	84.3	90.3
Rsa1.0_00119.1.g5792.t2	ref|NP_850027.2| FAD-dependent oxidoreductase-like protein [Arabidopsis thaliana] gi|55740569|gb|AAV63877.1| hypothetical protein [Arabidopsis thaliana] gi|330252239|gb|AEC07333.1| FAD-dependent oxidoreductase-like protein [Arabidopsis thaliana]	683	420	0	61.5	50.7	54.6	FAD-dependent oxidoreductase-like protein	gbpln	Arabidopsis thaliana	AT2G22650.1 | Symbols: | FAD-dependent oxidoreductase family protein | chr2:9624703-9626931 REVERSE LENGTH=420	683	420	0	61.5	50.7	54.6
Rsa1.0_00119.1.g5793.t1	gb|EOA16930.1| hypothetical protein CARUB_v10005154mg [Capsella rubella]	351	351	0	100.0	94.9	98.0	hypothetical protein CARUB_v10005154mg	gbpln	Capsella rubella	AT4G18060.1 | Symbols: | SH3 domain-containing protein | chr4:10027668-10029662 REVERSE LENGTH=351	351	351	0	100.0	94.0	98.0
Rsa1.0_00119.1.g5794.t1	ref|XP_002870073.1| P-glycoprotein 9 [Arabidopsis lyrata subsp. lyrata] gi|297315909|gb|EFH46332.1| P-glycoprotein 9 [Arabidopsis lyrata subsp. lyrata]	1186	1239	0	104.5	79.9	84.7	P-glycoprotein 9	gbpln	Arabidopsis lyrata	AT4G18050.1 | Symbols: PGP9 | P-glycoprotein 9 | chr4:10022205-10027280 FORWARD LENGTH=1236	1186	1236	0	104.2	80.2	84.1
Rsa1.0_00119.1.g5795.t1	ref|XP_002868014.1| hypothetical protein ARALYDRAFT_493066 [Arabidopsis lyrata subsp. lyrata] gi|297313850|gb|EFH44273.1| hypothetical protein ARALYDRAFT_493066 [Arabidopsis lyrata subsp. lyrata]	206	235	2.00E-98	114.1	84.0	89.8	hypothetical protein ARALYDRAFT_493066	gbpln	Arabidopsis lyrata	AT4G18040.1 | Symbols: EIF4E, CUM1, AT.EIF4E1, eIF4E1 | eukaryotic translation initiation factor 4E | chr4:10016724-10018151 REVERSE LENGTH=235	206	235	9.00E-99	114.1	82.5	88.3

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<tr><td>Rsa1.0_00119.1.g5796.t1</td><td>ref|NP_567548.1| two-component response regulator-like APRR2 [Arabidopsis thaliana] gi|30684266|ref|NP_849403.1| two-component response regulator-like APRR2 [Arabidopsis thaliana] gi|145361326|ref|NP_849404.2| two-component response regulator-like APRR2 [Arabidopsis thaliana] gi|334186660|ref|NP_001190759.1| two-component response regulator-like APRR2 [Arabidopsis thaliana] gi|52783226|sp|Q6LA43.2|APRR2_ARATH RecName: Full=Two-component response regulator-like APRR2; AltName: Full=Pseudo-response regulator 2; AltName: Full=TOC2 protein gi|14326543|gb|AAK60316.1|AF385725_1 AT4g18020/T6K21_200 [Arabidopsis thaliana] gi|23506085|gb|AAN28902.1| At4g18020/T6K21_200 [Arabidopsis thaliana] gi|332658580|gb|AEE83980.1| two-component response regulator-like APRR2 [Arabidopsis thaliana] gi|332658581|gb|AEE83981.1| two-component response regulator-like APRR2 [Arabidopsis thaliana] gi|332658582|gb|AEE83982.1| two-component response regulator-like APRR2 [Arabidopsis thaliana] gi|332658585|gb|AEE83985.1| two-component response regulator-like APRR2 [Arabidopsis thaliana]</td><td>546</td><td>535</td><td>0</td><td>98.0</td><td>72.7</td><td>81.5</td><td>two-component response regulator-like APRR2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G18020.6 | Symbols: APRR2 | CheY-like two-component responsive regulator family protein | chr4:10003738-10006682 REVERSE LENGTH=535</td><td>546</td><td>535</td><td>0</td><td>98.0</td><td>72.7</td><td>81.5</td></tr>
<tr><td>Rsa1.0_00119.1.g5797.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00120.1.g5798.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00120.1.g5799.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00120.1.g5800.t1</td><td>ref|NP_193987.1| uncharacterized protein [Arabidopsis thaliana] gi|3892711|emb|CAA22161.1| putative protein [Arabidopsis thaliana] gi|7269102|emb|CAB79211.1| putative protein [Arabidopsis thaliana] gi|332659224|gb|AEE84624.1| uncharacterized protein AT4G22560 [Arabidopsis thaliana]</td><td>257</td><td>264</td><td>1.00E-110</td><td>102.7</td><td>82.1</td><td>89.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G22560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12450.1); Has 380 Blast hits to 380 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 6; Plants - 374; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11880178-11880972 FORWARD LENGTH=264</td><td>257</td><td>264</td><td>1.00E-113</td><td>102.7</td><td>82.1</td><td>89.1</td></tr>
<tr><td>Rsa1.0_00120.1.g5801.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00120.1.g5802.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00120.1.g5803.t2</td><td>ref|NP_196896.1| endonuclease VIII-like 3 [Arabidopsis thaliana] gi|10177658|dbj|BAB11120.1| unnamed protein product [Arabidopsis thaliana] gi|332004577|gb|AED91960.1| GRF zinc finger / zinc knuckle protein [Arabidopsis thaliana]</td><td>169</td><td>415</td><td>5.00E-23</td><td>245.6</td><td>32.5</td><td>35.5</td><td>endonuclease VIII-like 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G13920.1 | Symbols: | GRF zinc finger / Zinc knuckle protein | chr5:4485931-4487433 REVERSE LENGTH=415</td><td>169</td><td>415</td><td>2.00E-25</td><td>245.6</td><td>32.5</td><td>35.5</td></tr>
<tr><td>Rsa1.0_00120.1.g5804.t1</td><td>ref|NP_567662.1| OSBP(oxysterol binding protein)-related protein 2A [Arabidopsis thaliana] gi|75163969|sp|Q940Y1.1|ORP2A_ARATH RecName: Full=Oxysterol-binding protein-related protein 2A; AltName: Full=OSBP-related protein 2A gi|15450519|gb|AAK96552.1| AT4g22540/F7K2_120 [Arabidopsis thaliana] gi|24111447|gb|AAN46892.1| At4g22540/F7K2_120 [Arabidopsis thaliana] gi|332659220|gb|AEE84620.1| OSBP(oxysterol binding protein)-related protein 2A [Arabidopsis thaliana]</td><td>731</td><td>721</td><td>0</td><td>98.6</td><td>89.7</td><td>94.5</td><td>OSBP(oxysterol binding protein)-related protein 2A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G22540.1 | Symbols: ORP2A | OSBP(oxysterol binding protein)-related protein 2A | chr4:11860969-11866108 REVERSE LENGTH=721</td><td>731</td><td>721</td><td>0</td><td>98.6</td><td>89.7</td><td>94.5</td></tr>
<tr><td>Rsa1.0_00120.1.g5805.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<tr><td>Rsa1.0_00120.1.g5807.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00120.1.g5808.t1</td><td>ref|XP_002867770.1| hypothetical protein ARALYDRAFT_329378 [Arabidopsis lyrata subsp. lyrata] gi|297313606|gb|EFH44029.1| hypothetical protein ARALYDRAFT_329378 [Arabidopsis lyrata subsp. lyrata]</td><td>433</td><td>406</td><td>0</td><td>93.8</td><td>80.8</td><td>88.2</td><td>hypothetical protein ARALYDRAFT_329378</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G12560.2 | Symbols: CPR30 | F-box and associated interaction domains-containing protein | chr4:7441815-7443157 FORWARD LENGTH=413</td><td>433</td><td>413</td><td>1.00E-172</td><td>95.4</td><td>68.6</td><td>80.4</td></tr>
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Rsa1.0_00120.1.g5809.t1	ref|XP_002891749.1| hypothetical protein ARALYDRAFT_337498 [Arabidopsis lyrata subsp. lyrata] gi|297337591|gb|EFH68008.1| hypothetical protein ARALYDRAFT_337498 [Arabidopsis lyrata subsp. lyrata]	386	495	3.00E-76	128.2	46.6	60.6	hypothetical protein ARALYDRAFT_337498	gbpln	Arabidopsis lyrata	AT1G53360.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:19907517-19908548 FORWARD LENGTH=343	386	343	6.00E-76	88.9	45.9	55.4
Rsa1.0_00120.1.g5810.t1	sp|Q3ECR3.3|FB305_ARATH RecName: Full=Putative F-box protein At1g53360	399	384	8.00E-76	96.2	46.1	56.9	RecName: Full=Putative F-box protein At1g53360	----	----	AT1G53360.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:19907517-19908548 FORWARD LENGTH=343	399	343	3.00E-76	86.0	44.6	54.6
Rsa1.0_00120.1.g5811.t1	ref|XP_002869826.1| hypothetical protein ARALYDRAFT_914375 [Arabidopsis lyrata subsp. lyrata] gi|297315662|gb|EFH46085.1| hypothetical protein ARALYDRAFT_914375 [Arabidopsis lyrata subsp. lyrata]	247	246	1.00E-135	99.6	96.4	98.4	hypothetical protein ARALYDRAFT_914375	gbpln	Arabidopsis lyrata	AT4G12590.1 | Symbols: | Protein of unknown function DUF106, transmembrane | chr4:7451291-7452976 REVERSE LENGTH=246	247	246	1.00E-136	99.6	95.1	97.6
Rsa1.0_00120.1.g5812.t1	gb|EOA16792.1| hypothetical protein CARUB_v10005012mg [Capsella rubella]	636	388	1.00E-136	61.0	43.4	46.9	hypothetical protein CARUB_v10005012mg	gbpln	Capsella rubella	AT4G22360.1 | Symbols: | SWIB complex BAF60b domain-containing protein | chr4:11807811-11809660 FORWARD LENGTH=385	636	385	1.00E-137	60.5	44.0	47.6
Rsa1.0_00120.1.g5813.t1	sp|Q3ECR3.3|FB305_ARATH RecName: Full=Putative F-box protein At1g53360	411	384	4.00E-88	93.4	47.2	59.9	RecName: Full=Putative F-box protein At1g53360	----	----	AT1G53360.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:19907517-19908548 FORWARD LENGTH=343	411	343	7.00E-89	83.5	46.5	58.9
Rsa1.0_00120.1.g5814.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00120.1.g5815.t1	gb|EOA26092.1| hypothetical protein CARUB_v10019514mg [Capsella rubella]	412	421	1.00E-136	102.2	61.7	72.3	hypothetical protein CARUB_v10019514mg	gbpln	Capsella rubella	AT5G35600.1 | Symbols: HDA7 | histone deacetylase7 | chr5:13770121-13771712 REVERSE LENGTH=409	412	409	1.00E-137	99.3	61.2	72.1
Rsa1.0_00120.1.g5816.t1	gb|AAG51247.1|AC055769_6 copia-type polyprotein, putative; 28768-32772 [Arabidopsis thaliana]	1356	1334	0	98.4	68.7	81.6	copia-type polyprotein, putative; 28768-32772	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1356	1262	3.00E-97	93.1	13.1	21.4
Rsa1.0_00120.1.g5817.t2	ref|XP_002891749.1| hypothetical protein ARALYDRAFT_337498 [Arabidopsis lyrata subsp. lyrata] gi|297337591|gb|EFH68008.1| hypothetical protein ARALYDRAFT_337498 [Arabidopsis lyrata subsp. lyrata]	789	495	9.00E-77	62.7	23.3	31.1	hypothetical protein ARALYDRAFT_337498	gbpln	Arabidopsis lyrata	AT1G53360.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:19907517-19908548 FORWARD LENGTH=343	789	343	1.00E-76	43.5	22.6	29.3
Rsa1.0_00120.1.g5818.t1	gb|EOA21412.1| hypothetical protein CARUB_v10001785mg [Capsella rubella]	255	254	1.00E-122	99.6	85.5	91.8	hypothetical protein CARUB_v10001785mg	gbpln	Capsella rubella	AT4G05530.1 | Symbols: IBR1, SDRA | indole-3-butyric acid response 1 | chr4:2816462-2818074 FORWARD LENGTH=254	255	254	1.00E-124	99.6	85.1	91.0
Rsa1.0_00120.1.g5819.t1	ref|NP_193953.1| SufE/NifU family protein [Arabidopsis thaliana] gi|75098815|sp|O49627.1|ISU1_ARATH RecName: Full=Iron-sulfur cluster assembly protein 1; Short=AtISU1; Short=Protein ISCU-LIKE 1; AltName: Full=NifU-like N-terminal domain-containing protein ISU1; AltName: Full=NifU-like protein ISU1; Flags: Precursor gi|13605507|gb|AAK32747.1|AF361579_1 AT4g22220/T10I14_50 [Arabidopsis thaliana] gi|2832672|emb|CAA16772.1| nifU-like protein [Arabidopsis thaliana] gi|7269067|emb|CAB79177.1| nifU-like protein [Arabidopsis thaliana] gi|19548021|gb|AAL87374.1| AT4g22220/T10I14_50 [Arabidopsis thaliana] gi|82937831|emb|CAI29442.1| Fe-S scaffold protein 1 [Arabidopsis thaliana] gi|332659176|gb|AEE84576.1| SufE/NifU family protein [Arabidopsis thaliana]	170	167	1.00E-88	98.2	93.5	96.5	SufE/NifU family protein	gbpln	Arabidopsis thaliana	AT4G22220.1 | Symbols: ISU1, ATISU1 | SufE/NifU family protein | chr4:11759444-11760881 REVERSE LENGTH=167	170	167	5.00E-91	98.2	93.5	96.5
Rsa1.0_00120.1.g5820.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00120.1.g5821.t1	gb|ACG60672.1| unknown protein [Brassica oleracea var. alboglabra]	98	288	3.00E-12	293.9	38.8	64.3	unknown protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00120.1.g5822.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	389	1489	1.00E-138	382.8	62.2	74.0	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	389	237	3.00E-34	60.9	18.3	30.3

Rsa1.0_00120.1.g5823.t1	dbj|BAJ34508.1| unnamed protein product [Thellungiella halophila]	502	502	0	100.0	92.6	97.2	unnamed protein product	----	----	AT4G21910.3 | Symbols: | MATE efflux family protein | chr4:11625821-11630964 REVERSE LENGTH=507	502	507	0	101.0	87.8	94.0
Rsa1.0_00120.1.g5824.t1	ref|XP_002867816.1| hypothetical protein ARALYDRAFT_354584 [Arabidopsis lyrata subsp. lyrata] gi|297313652|gb|EFH44075.1| hypothetical protein ARALYDRAFT_354584 [Arabidopsis lyrata subsp. lyrata]	272	388	3.00E-60	142.6	53.7	66.2	hypothetical protein ARALYDRAFT_354584	gbpln	Arabidopsis lyrata	AT4G21895.1 | Symbols: | DNA binding | chr4:11613523-11614242 REVERSE LENGTH=239	272	239	3.00E-52	87.9	46.0	58.8
Rsa1.0_00120.1.g5825.t1	ref|XP_002867819.1| hypothetical protein ARALYDRAFT_492684 [Arabidopsis lyrata subsp. lyrata] gi|297313655|gb|EFH44078.1| hypothetical protein ARALYDRAFT_492684 [Arabidopsis lyrata subsp. lyrata]	136	131	9.00E-49	96.3	74.3	82.4	hypothetical protein ARALYDRAFT_492684	gbpln	Arabidopsis lyrata	AT4G21870.1 | Symbols: | HSP20-like chaperones superfamily protein | chr4:11603756-11604285 REVERSE LENGTH=134	136	134	1.00E-49	98.5	72.8	83.1
Rsa1.0_00120.1.g5826.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00120.1.g5827.t1	ref|NP_189011.2| transcription factor bHLH77 [Arabidopsis thaliana] gi|75311240|sp|Q9LK48.1|BH077_ARATH RecName: Full=Transcription factor bHLH77; AltName: Full=Basic helix-loop-helix protein 77; Short=AtbHLH77; Short=bHLH 77; AltName: Full=Transcription factor EN 87; AltName: Full=bHLH transcription factor bHLH077 gi|9293943|dbj|BAB01846.1| unnamed protein product [Arabidopsis thaliana] gi|17529310|gb|AAL38882.1| putative DNA-binding protein [Arabidopsis thaliana] gi|20465453|gb|AAM20186.1| putative DNA-binding protein [Arabidopsis thaliana] gi|332643281|gb|AEE76802.1| transcription factor bHLH77 [Arabidopsis thaliana]	82	371	1.00E-12	452.4	52.4	58.5	transcription factor bHLH77	gbpln	Arabidopsis thaliana	AT3G23690.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:8528933-8530655 REVERSE LENGTH=371	82	371	2.00E-15	452.4	52.4	58.5
Rsa1.0_00120.1.g5828.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	158	1555	2.00E-19	984.2	31.6	49.4	disease resistance protein	gbpln	Brassica rapa	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	158	170	5.00E-19	107.6	30.4	46.8
Rsa1.0_00120.1.g5829.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00120.1.g5830.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00120.1.g5831.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00120.1.g5832.t1	ref|NP_567638.1| peptide methionine sulfoxide reductase B9 [Arabidopsis thaliana] gi|75146721|sp|Q84JT6.1|MSRB9_ARATH RecName: Full=Peptide methionine sulfoxide reductase B9; Short=AtMSRB9; AltName: Full=Peptide-methionine (R)-S-oxide reductase gi|28393654|gb|AAO42245.1| unknown protein [Arabidopsis thaliana] gi|28973573|gb|AAO64111.1| unknown protein [Arabidopsis thaliana] gi|332659112|gb|AEE84512.1| peptide methionine sulfoxide reductase B9 [Arabidopsis thaliana]	144	143	1.00E-61	99.3	80.6	86.1	peptide methionine sulfoxide reductase B9	gbpln	Arabidopsis thaliana	AT4G21850.1 | Symbols: ATMSRB9, MSRB9 | methionine sulfoxide reductase B9 | chr4:11591378-11592138 REVERSE LENGTH=143	144	143	3.00E-64	99.3	80.6	86.1
Rsa1.0_00120.1.g5833.t1	ref|NP_567638.1| peptide methionine sulfoxide reductase B9 [Arabidopsis thaliana] gi|75146721|sp|Q84JT6.1|MSRB9_ARATH RecName: Full=Peptide methionine sulfoxide reductase B9; Short=AtMSRB9; AltName: Full=Peptide-methionine (R)-S-oxide reductase gi|28393654|gb|AAO42245.1| unknown protein [Arabidopsis thaliana] gi|28973573|gb|AAO64111.1| unknown protein [Arabidopsis thaliana] gi|332659112|gb|AEE84512.1| peptide methionine sulfoxide reductase B9 [Arabidopsis thaliana]	144	143	6.00E-62	99.3	81.3	86.1	peptide methionine sulfoxide reductase B9	gbpln	Arabidopsis thaliana	AT4G21850.1 | Symbols: ATMSRB9, MSRB9 | methionine sulfoxide reductase B9 | chr4:11591378-11592138 REVERSE LENGTH=143	144	143	2.00E-64	99.3	81.3	86.1

Rsa1.0_00120.1.g5834.t17	sp|P10978.1|POLX_TOBAC RecName: Full=Retrovirus-related Pol polyprotein from transposon TNT 1-94; Includes: RecName: Full=Protease; Includes: RecName: Full=Reverse transcriptase; Includes: RecName: Full=Endonuclease gi|20045|emb|CAA32025.1| unnamed protein product [Nicotiana tabacum]	467	1328	8.00E-33	284.4	20.1	29.1	RecName: Full=Retrovirus-related Pol polyprotein from transposon TNT 1-94; Includes: RecName: Full=Protease; Includes: RecName: Full=Reverse transcriptase; Includes: RecName: Full=Endonuclease gi|20045|emb|CAA32025.1| unnamed protein product	gbpln	Nicotiana tabacum	#	#	#	#	#	#	#
Rsa1.0_00120.1.g5835.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	189	1142	3.00E-22	604.2	34.4	54.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	189	292	2.00E-15	154.5	21.2	36.0
Rsa1.0_00121.1.g5836.t1	ref|NP_001031725.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|332659833|gb|AEE85233.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	430	452	0	105.1	87.0	92.3	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT4G26650.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:13445265-13447592 FORWARD LENGTH=452	430	452	0	105.1	87.0	92.3
Rsa1.0_00121.1.g5837.t1	ref|NP_567754.1| Tim17/Tim22/Tim23 pre-protein translocase of the mitochondrial outer membrane domain-containing protein [Arabidopsis thaliana] gi|75165412|sp|Q94EH2.1|TI222_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM22-2 gi|15294264|gb|AAK95309.1|AF410323_1 AT4g26670/F10M23_10 [Arabidopsis thaliana] gi|20857097|gb|AAM26699.1| AT4g26670/F10M23_10 [Arabidopsis thaliana] gi|21593873|gb|AAM65840.1| unknown [Arabidopsis thaliana] gi|89213239|gb|ABD64059.1| At4g26670 [Arabidopsis thaliana] gi|332659835|gb|AEE85235.1| mitochondrial import inner membrane translocase subunit TIM22-2 [Arabidopsis thaliana]	188	210	3.00E-82	111.7	82.4	86.7	Tim17/Tim22/Tim23 pre-protein translocase of the mitochondrial outer membrane domain-containing protein	gbpln	Arabidopsis thaliana	AT4G26670.1 | Symbols: | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr4:13452257-13453579 FORWARD LENGTH=210	188	210	1.00E-84	111.7	82.4	86.7
Rsa1.0_00121.1.g5838.t1	ref|XP_002867547.1| hypothetical protein ARALYDRAFT_913883 [Arabidopsis lyrata subsp. lyrata] gi|297313383|gb|EFH43806.1| hypothetical protein ARALYDRAFT_913883 [Arabidopsis lyrata subsp. lyrata]	61	61	1.00E-26	100.0	95.1	98.4	hypothetical protein ARALYDRAFT_913883	gbpln	Arabidopsis lyrata	AT3G11591.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:3663780-3663971 REVERSE LENGTH=63	61	63	1.00E-13	103.3	50.8	68.9
Rsa1.0_00121.1.g5839.t1	ref|XP_002869597.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315433|gb|EFH45856.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	527	538	0	102.1	80.6	88.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G26680.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:13454853-13456418 FORWARD LENGTH=521	527	521	0	98.9	79.5	88.6
Rsa1.0_00121.1.g5840.t1	ref|XP_002867546.1| MRH5/SHV3 [Arabidopsis lyrata subsp. lyrata] gi|297313382|gb|EFH43805.1| MRH5/SHV3 [Arabidopsis lyrata subsp. lyrata]	757	756	0	99.9	81.2	90.1	MRH5/SHV3	gbpln	Arabidopsis lyrata	AT4G26690.1 | Symbols: SHV3, MRH5, GPDL2 | PLC-like phosphodiesterase family protein | chr4:13456793-13459890 REVERSE LENGTH=759	757	759	0	100.3	80.2	90.0
Rsa1.0_00121.1.g5841.t1	ref|XP_002869596.1| hypothetical protein ARALYDRAFT_913880 [Arabidopsis lyrata subsp. lyrata] gi|297315432|gb|EFH45855.1| hypothetical protein ARALYDRAFT_913880 [Arabidopsis lyrata subsp. lyrata]	685	690	0	100.7	90.1	94.2	hypothetical protein ARALYDRAFT_913880	gbpln	Arabidopsis lyrata	AT4G26700.2 | Symbols: ATFIM1, FIM1 | fimbrin 1 | chr4:13463760-13467426 FORWARD LENGTH=687	685	687	0	100.3	88.9	93.6
Rsa1.0_00121.1.g5842.t1	ref|XP_002869595.1| hypothetical protein ARALYDRAFT_329014 [Arabidopsis lyrata subsp. lyrata] gi|297315431|gb|EFH45854.1| hypothetical protein ARALYDRAFT_329014 [Arabidopsis lyrata subsp. lyrata]	748	785	0	104.9	74.3	83.0	hypothetical protein ARALYDRAFT_329014	gbpln	Arabidopsis lyrata	AT5G55300.1 | Symbols: MGO1, TOP1ALPHA, TOP1 | DNA topoisomerase I alpha | chr5:22424837-22429045 REVERSE LENGTH=916	748	916	0	122.5	68.3	78.7

Rsa1.0_00121.1.g5843.t1	ref|XP_002867545.1| protein phosphatase x-1 [Arabidopsis lyrata subsp. lyrata] gi|297313381|gb|EFH43804.1| protein phosphatase x-1 [Arabidopsis lyrata subsp. lyrata]	303	305	1.00E-159	100.7	89.8	93.1	protein phosphatase x-1	gbpln	Arabidopsis lyrata	AT4G26720.1 | Symbols: PPX1, PPX-1 | protein phosphatase X 1 | chr4:13470397-13472154 REVERSE LENGTH=305	303	305	1.00E-161	100.7	89.4	92.7
Rsa1.0_00121.1.g5844.t1	gb|ACG69537.1| caleosin CLO1-5 [Brassica napus]	245	245	1.00E-138	100.0	96.7	97.1	caleosin CLO1-5	gbpln	Brassica napus	AT4G26740.1 | Symbols: ATS1, CLO1, ATPXG1 | seed gene 1 | chr4:13473791-13475278 REVERSE LENGTH=245	245	245	1.00E-136	100.0	92.7	96.3
Rsa1.0_00121.1.g5845.t1	ref|XP_002867543.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297313379|gb|EFH43802.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	419	421	0	100.5	87.4	91.6	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis lyrata	AT4G26750.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:13475848-13478382 REVERSE LENGTH=421	419	421	0	100.5	86.4	90.7
Rsa1.0_00121.1.g5846.t1	gb|EOA16304.1| hypothetical protein CARUB_v10004454mg [Capsella rubella]	580	578	0	99.7	88.1	93.1	hypothetical protein CARUB_v10004454mg	gbpln	Capsella rubella	AT4G26760.1 | Symbols: MAP65-2 | microtubule-associated protein 65-2 | chr4:13478834-13481300 REVERSE LENGTH=578	580	578	0	99.7	86.9	92.4
Rsa1.0_00121.1.g5847.t1	ref|XP_002869592.1| phosphatidate cytidylyltransferase/CDP-diglyceride synthetase [Arabidopsis lyrata subsp. lyrata] gi|297315428|gb|EFH45851.1| phosphatidate cytidylyltransferase/CDP-diglyceride synthetase [Arabidopsis lyrata subsp. lyrata]	536	471	0	87.9	79.7	82.3	phosphatidate cytidylyltransferase/CDP-diglyceride synthetase	gbpln	Arabidopsis lyrata	AT4G26770.1 | Symbols: | Phosphatidate cytidylyltransferase family protein | chr4:13482580-13484697 FORWARD LENGTH=471	536	471	0	87.9	79.3	81.7
Rsa1.0_00121.1.g5848.t1	ref|NP_567757.1| molecular chaperone GrpE [Arabidopsis thaliana] gi|21593024|gb|AAM64973.1| grpE like protein [Arabidopsis thaliana] gi|26451456|dbj|BAC42827.1| putative grpE protein [Arabidopsis thaliana] gi|29824143|gb|AAP04032.1| putative grpE protein [Arabidopsis thaliana] gi|332659851|gb|AEE85251.1| molecular chaperone GrpE [Arabidopsis thaliana]	324	327	1.00E-130	100.9	79.3	88.0	molecular chaperone GrpE	gbpln	Arabidopsis thaliana	AT4G26780.1 | Symbols: AR192 | Co-chaperone GrpE family protein | chr4:13485066-13486560 REVERSE LENGTH=327	324	327	1.00E-133	100.9	79.3	88.0
Rsa1.0_00121.1.g5849.t1	gb|EOA16926.1| hypothetical protein CARUB_v10005151mg [Capsella rubella] gi|482552734|gb|EOA16927.1| hypothetical protein CARUB_v10005151mg [Capsella rubella]	352	351	0	99.7	88.6	93.2	hypothetical protein CARUB_v10005151mg	gbpln	Capsella rubella	AT4G26790.2 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr4:13487859-13489149 FORWARD LENGTH=351	352	351	1.00E-180	99.7	84.4	90.3
Rsa1.0_00121.1.g5850.t1	sp|Q9SZ20.2|PP339_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g26800	500	514	1.00E-161	102.8	59.2	73.0	RecName: Full=Pentatricopeptide repeat-containing protein At4g26800	----	----	AT1G62680.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:23208247-23209893 REVERSE LENGTH=548	500	548	1.00E-129	109.6	46.4	67.6
Rsa1.0_00121.1.g5851.t1	gb|EOA15377.1| hypothetical protein CARUB_v10006096mg, partial [Capsella rubella]	103	103	4.00E-45	100.0	90.3	91.3	hypothetical protein CARUB_v10006096mg, partial	gbpln	Capsella rubella	AT4G26810.2 | Symbols: | SWIB/MDM2 domain superfamily protein | chr4:13492247-13492649 REVERSE LENGTH=106	103	106	3.00E-46	102.9	88.3	92.2
Rsa1.0_00121.1.g5852.t1	ref|NP_001045207.1| Os01g0918300 [Oryza sativa Japonica Group] gi|2501449|sp|P55857.1|SUMO1_ORYSJ RecName: Full=Small ubiquitin-related modifier 1; Short=OsSUMO1; AltName: Full=Ubiquitin-like protein SMT3 gi|1668773|emb|CAA67922.1| ubiquitin-like protein [Oryza sativa] gi|18146762|dbj|BAB82439.1| ubiquitin-related protein [Oryza sativa Japonica Group] gi|19386713|dbj|BAB86095.1| putative SUMO protein [Oryza sativa Japonica Group] gi|57900450|dbj|BAD87743.1| putative SUMO protein [Oryza sativa Japonica Group] gi|113534738|dbj|BAF07121.1| Os01g0918300 [Oryza sativa Japonica Group] gi|125528873|gb|EAY76987.1| hypothetical protein OsI_04943 [Oryza sativa Indica Group] gi|125573116|gb|EAZ14631.1| hypothetical protein OsJ_04555 [Oryza sativa Japonica Group] gi|149390685|gb|ABR25360.1| ubiquitin-like protein smt3 [Oryza sativa Indica Group] gi|215765122|dbj|BAG86819.1| unnamed protein product [Oryza sativa Japonica Group]	107	100	7.00E-45	93.5	85.0	86.0	Os01g0918300	gbpln	Oryza sativa	AT4G26840.1 | Symbols: SUM1, SUMO 1, SUMO1, ATSUMO1 | small ubiquitin-like modifier 1 | chr4:13497466-13498458 FORWARD LENGTH=100	107	100	2.00E-46	93.5	82.2	84.1

Rsa1.0_00121.1.g5853.t1	gb|AET14214.1| GDP-L-galactose phosphorylase [Brassica rapa subsp. chinensis]	435	434	0	99.8	97.5	99.1	GDP-L-galactose phosphorylase	gbpln	Brassica rapa	AT4G26850.1 | Symbols: VTC2 | mannose-1-phosphate guanylyltransferase (GDP)s;GDP-galactose:mannose-1-phosphate guanylyltransferases;GDP-galactose:glucose-1-phosphate guanylyltransferases;GDP-galactose:myoinositol-1- phosphate guanylyltransferases;glucose-1-phosphate guanylyltransferase | chr4:13499262-13501145 REVERSE LENGTH=442	435	442	0	101.6	90.8	95.4
Rsa1.0_00121.1.g5854.t1	ref|XP_002867537.1| AT4g26860/F10M23_200 [Arabidopsis lyrata subsp. lyrata] gi|297313373|gb|EFH43796.1| AT4g26860/F10M23_200 [Arabidopsis lyrata subsp. lyrata]	244	244	1.00E-131	100.0	91.4	96.3	AT4g26860/F10M23_200	gbpln	Arabidopsis lyrata	AT4G26860.1 | Symbols: | Predicted pyridoxal phosphate-dependent enzyme, YBL036C type | chr4:13503291-13504693 REVERSE LENGTH=244	244	244	1.00E-132	100.0	91.0	95.9
Rsa1.0_00121.1.g5855.t1	ref|NP_194419.2| mitogen-activated protein kinase kinase kinase 16 [Arabidopsis thaliana] gi|332659865|gb|AEE85265.1| mitogen-activated protein kinase kinase kinase 16 [Arabidopsis thaliana]	439	444	1.00E-175	101.1	73.1	83.8	mitogen-activated protein kinase kinase kinase 16	gbpln	Arabidopsis thaliana	AT4G26890.1 | Symbols: MAPKKK16 | mitogen-activated protein kinase kinase kinase 16 | chr4:13512072-13513406 FORWARD LENGTH=444	439	444	1.00E-178	101.1	73.1	83.8
Rsa1.0_00121.1.g5856.t1	gb|EOA15723.1| hypothetical protein CARUB_v10006625mg [Capsella rubella]	587	586	0	99.8	91.7	94.2	hypothetical protein CARUB_v10006625mg	gbpln	Capsella rubella	AT4G26900.1 | Symbols: AT-HF, HISN4 | HIS HF | chr4:13515514-13519608 FORWARD LENGTH=592	587	592	0	100.9	92.0	95.1
Rsa1.0_00121.1.g5857.t1	ref|XP_002866485.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297312320|gb|EFH42744.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	934	983	0	105.2	83.5	91.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G62370.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:25041901-25044849 REVERSE LENGTH=982	934	982	0	105.1	82.5	90.7
Rsa1.0_00121.1.g5858.t1	ref|XP_002869585.1| NADH:ubiquinone oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315421|gb|EFH45844.1| NADH:ubiquinone oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	196	184	2.00E-75	93.9	80.1	85.7	NADH:ubiquinone oxidoreductase family protein	gbpln	Arabidopsis lyrata	AT4G26965.1 | Symbols: | NADH:ubiquinone oxidoreductase, 17.2kDa subunit | chr4:13539717-13542041 FORWARD LENGTH=184	196	184	2.00E-75	93.9	78.6	84.2
Rsa1.0_00121.1.g5859.t1	gb|EOA18648.1| hypothetical protein CARUB_v10007224mg [Capsella rubella]	467	468	1.00E-175	100.2	71.3	79.0	hypothetical protein CARUB_v10007224mg	gbpln	Capsella rubella	AT4G26990.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54920.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13551150-13554253 REVERSE LENGTH=474	467	474	1.00E-178	101.5	72.2	82.0
Rsa1.0_00121.1.g5860.t1	ref|XP_002869583.1| hypothetical protein ARALYDRAFT_354097 [Arabidopsis lyrata subsp. lyrata] gi|297315419|gb|EFH45842.1| hypothetical protein ARALYDRAFT_354097 [Arabidopsis lyrata subsp. lyrata]	2537	2550	0	100.5	72.8	81.6	hypothetical protein ARALYDRAFT_354097	gbpln	Arabidopsis lyrata	AT4G27010.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ribosome 60S biogenesis N-terminal (InterPro:IPR021714); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G72270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13558943-13568296 FORWARD LENGTH=2374	2537	2374	0	93.6	67.1	75.9
Rsa1.0_00121.1.g5861.t1	ref|XP_002867528.1| hypothetical protein ARALYDRAFT_913846 [Arabidopsis lyrata subsp. lyrata] gi|297313364|gb|EFH43787.1| hypothetical protein ARALYDRAFT_913846 [Arabidopsis lyrata subsp. lyrata]	525	522	0	99.4	93.0	97.9	hypothetical protein ARALYDRAFT_913846	gbpln	Arabidopsis lyrata	AT4G27020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: vacuole; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54870.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr4:13568604-13571381 REVERSE LENGTH=523	525	523	0	99.6	91.8	96.6
Rsa1.0_00121.1.g5862.t1	ref|XP_002869582.1| hypothetical protein ARALYDRAFT_492093 [Arabidopsis lyrata subsp. lyrata] gi|297315418|gb|EFH45841.1| hypothetical protein ARALYDRAFT_492093 [Arabidopsis lyrata subsp. lyrata]	295	323	1.00E-143	109.5	84.4	91.9	hypothetical protein ARALYDRAFT_492093	gbpln	Arabidopsis lyrata	AT4G27030.1 | Symbols: FAD4, FADA | fatty acid desaturase A | chr4:13571951-13572922 FORWARD LENGTH=323	295	323	1.00E-144	109.5	83.7	91.5
Rsa1.0_00121.1.g5863.t1	gb|EOA17310.1| hypothetical protein CARUB_v10005583mg [Capsella rubella]	250	250	1.00E-138	100.0	95.2	97.6	hypothetical protein CARUB_v10005583mg	gbpln	Capsella rubella	AT4G27040.4 | Symbols: VPS22 | EAP30/Vps36 family protein | chr4:13573061-13574576 REVERSE LENGTH=250	250	250	1.00E-140	100.0	94.8	97.6

Rsa1.0_00121.1.g5864.t1	ref|NP_194436.2| Microtubule-associated protein TORTIFOLIA1 [Arabidopsis thaliana] gi|83288274|sp|Q9T041.2|MAPT_ARATH RecName: Full=Microtubule-associated protein TORTIFOLIA1; AltName: Full=Microtubule-associated protein SPIRAL2; AltName: Full=Protein CONVOLUTA gi|51870567|emb|CAC80696.2| TORTIFOLIA1 microtubule-associated protein [Arabidopsis thaliana] gi|53791209|dbj|BAD54701.1| microtubule associated protein SPIRAL2 [Arabidopsis thaliana] gi|332659895|gb|AEE85295.1| Microtubule-associated protein TORTIFOLIA1 [Arabidopsis thaliana]	869	864	0	99.4	88.4	93.0	Microtubule-associated protein TORTIFOLIA1	gbpln	Arabidopsis thaliana	AT4G27060.1 | Symbols: TOR1, SPR2, CN | ARM repeat superfamily protein | chr4:13581581-13585070 REVERSE LENGTH=864	869	864	0	99.4	88.4	93.0
Rsa1.0_00121.1.g5865.t1	gb|EOA17638.1| hypothetical protein CARUB_v10006004mg [Capsella rubella]	134	134	1.00E-67	100.0	97.8	100.0	hypothetical protein CARUB_v10006004mg	gbpln	Capsella rubella	AT4G27090.1 | Symbols: | Ribosomal protein L14 | chr4:13594104-13595187 REVERSE LENGTH=134	134	134	2.00E-69	100.0	97.0	99.3
Rsa1.0_00121.1.g5866.t1	ref|NP_001031730.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|332659901|gb|AEE85301.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	433	433	0	100.0	90.8	95.2	RabGAP/TBC domain-containing protein	gbpln	Arabidopsis thaliana	AT4G27100.2 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr4:13595845-13598620 FORWARD LENGTH=433	433	433	0	100.0	90.8	95.2
Rsa1.0_00121.1.g5867.t1	emb|CAB38841.1| putative protein [Arabidopsis thaliana] gi|7269564|emb|CAB79566.1| putative protein [Arabidopsis thaliana]	685	717	0	104.7	83.6	90.9	putative protein	gbpln	Arabidopsis thaliana	AT4G27110.1 | Symbols: COBL11 | COBRA-like protein 11 precursor | chr4:13599236-13601521 REVERSE LENGTH=668	685	668	0	97.5	80.7	87.7
Rsa1.0_00121.1.g5868.t1	gb|EOA17860.1| hypothetical protein CARUB_v10006265mg [Capsella rubella]	447	298	1.00E-129	66.7	61.1	63.3	hypothetical protein CARUB_v10006265mg	gbpln	Capsella rubella	AT4G27120.2 | Symbols: | CONTAINS InterPro DOMAIN/s: DDRGK domain (InterPro:IPR019153); Has 14775 Blast hits to 8764 proteins in 778 species: Archae - 29; Bacteria - 1878; Metazoa - 5164; Fungi - 1447; Plants - 582; Viruses - 164; Other Eukaryotes - 5511 (source: NCBI BLink). | chr4:13602210-13604227 REVERSE LENGTH=298	447	298	1.00E-120	66.7	60.0	61.1
Rsa1.0_00121.1.g5869.t1	gb|AAA63470.1| storage protein, partial [Raphanus sativus]	176	155	1.00E-84	88.1	86.4	86.4	storage protein, partial	gbpln	Raphanus sativus	AT4G27170.1 | Symbols: SESA4, AT2S4 | seed storage albumin 4 | chr4:13613637-13614137 FORWARD LENGTH=166	176	166	1.00E-53	94.3	61.9	73.3
Rsa1.0_00121.1.g5870.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00121.1.g5871.t1	gb|ABD65056.1| hypothetical protein 27.t00122 [Brassica oleracea]	237	239	9.00E-26	100.8	27.0	33.8	hypothetical protein 27.t00122	gbpln	Brassica oleracea	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	237	575	5.00E-15	242.6	20.7	32.5
Rsa1.0_00121.1.g5872.t1	gb|ABC87311.1| sporocyteless [Brassica juncea]	325	313	1.00E-154	96.3	88.9	91.4	sporocyteless	gbpln	Brassica juncea	AT4G27330.1 | Symbols: SPL, NZZ | sporocyteless (SPL) | chr4:13682327-13683459 REVERSE LENGTH=314	325	314	3.00E-98	96.6	68.3	74.2
Rsa1.0_00121.1.g5873.t1	ref|XP_002867510.1| hypothetical protein ARALYDRAFT_492065 [Arabidopsis lyrata subsp. lyrata] gi|297313346|gb|EFH43769.1| hypothetical protein ARALYDRAFT_492065 [Arabidopsis lyrata subsp. lyrata]	682	617	0	90.5	78.9	84.3	hypothetical protein ARALYDRAFT_492065	gbpln	Arabidopsis lyrata	AT4G27340.1 | Symbols: | Met-10+ like family protein | chr4:13687366-13690370 REVERSE LENGTH=619	682	619	0	90.8	79.9	84.9
Rsa1.0_00121.1.g5874.t1	#	#	#	#	#	#	#	-	----	----	AT5G45275.1 | Symbols: | Major facilitator superfamily protein | chr5:18334476-18337240 REVERSE LENGTH=570	139	570	5.00E-11	410.1	20.9	23.0
Rsa1.0_00121.1.g5875.t1	ref|XP_002867508.1| hypothetical protein ARALYDRAFT_492064 [Arabidopsis lyrata subsp. lyrata] gi|297313344|gb|EFH43767.1| hypothetical protein ARALYDRAFT_492064 [Arabidopsis lyrata subsp. lyrata]	282	278	2.33E-156	98.6	90.8	94.0	hypothetical protein ARALYDRAFT_492064	gbpln	Arabidopsis lyrata	AT4G27350.1 | Symbols: | Protein of unknown function (DUF1223) | chr4:13690979-13692621 REVERSE LENGTH=278	282	278	1.00E-147	98.6	89.4	93.3
Rsa1.0_00121.1.g5876.t1	gb|EOA18630.1| hypothetical protein CARUB_v10007205mg [Capsella rubella]	101	111	8.00E-45	109.9	86.1	90.1	hypothetical protein CARUB_v10007205mg	gbpln	Capsella rubella	AT4G27360.1 | Symbols: | Dynein light chain type 1 family protein | chr4:13694032-13694517 FORWARD LENGTH=103	101	103	3.00E-47	102.0	85.1	89.1
Rsa1.0_00121.1.g5877.t2	gb|EOA15928.1| hypothetical protein CARUB_v10004022mg [Capsella rubella]	1066	1140	0	106.9	77.5	85.6	hypothetical protein CARUB_v10004022mg	gbpln	Capsella rubella	AT4G27370.1 | Symbols: VIIIB, ATVIIIB | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13694881-13700780 REVERSE LENGTH=1134	1066	1134	0	106.4	77.0	84.7

Rsa1.0_00121.1.g5878.t1	gb|EOA15638.1| hypothetical protein CARUB_v10005882mg, partial [Capsella rubella]	103	173	8.00E-26	168.0	73.8	83.5	hypothetical protein CARUB_v10005882mg, partial	gbpln	Capsella rubella	AT4G27380.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13701340-13702953 FORWARD LENGTH=156	103	156	2.00E-21	151.5	66.0	79.6
Rsa1.0_00121.1.g5879.t1	gb|AAP35056.1| NAC-domain protein 485 [Brassica napus]	271	300	1.00E-137	110.7	90.8	93.7	NAC-domain protein 485	gbpln	Brassica napus	AT4G27410.2 | Symbols: RD26, ANAC072 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr4:13707928-13709013 REVERSE LENGTH=297	271	297	1.00E-134	109.6	87.5	91.1
Rsa1.0_00121.1.g5880.t1	ref|XP_002867504.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297313340|gb|EFH43763.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata]	641	639	0	99.7	82.4	90.0	abc transporter family protein	gbpln	Arabidopsis lyrata	AT4G27420.1 | Symbols: | ABC-2 type transporter family protein | chr4:13712434-13714797 REVERSE LENGTH=638	641	638	0	99.5	81.3	89.2
Rsa1.0_00122.1.g5881.t1	ref|XP_002867617.1| hypothetical protein ARALYDRAFT_354257 [Arabidopsis lyrata subsp. lyrata] gi|297313453|gb|EFH43876.1| hypothetical protein ARALYDRAFT_354257 [Arabidopsis lyrata subsp. lyrata]	739	758	0	102.6	85.1	92.8	hypothetical protein ARALYDRAFT_354257	gbpln	Arabidopsis lyrata	AT4G25270.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:12937253-12938836 REVERSE LENGTH=527	739	527	0	71.3	56.8	61.8
Rsa1.0_00122.1.g5882.t1	ref|XP_002867618.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297313454|gb|EFH43877.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	201	201	6.00E-94	100.0	83.1	92.5	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT4G25260.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:12936005-12936610 REVERSE LENGTH=201	201	201	2.00E-96	100.0	82.6	92.0
Rsa1.0_00122.1.g5883.t1	gb|EOA17786.1| hypothetical protein CARUB_v10006179mg [Capsella rubella]	138	68	3.00E-15	49.3	30.4	31.2	hypothetical protein CARUB_v10006179mg	gbpln	Capsella rubella	AT4G21105.1 | Symbols: | cytochrome-c oxidases;electron carriers | chr4:11266273-11266724 FORWARD LENGTH=68	138	68	1.00E-17	49.3	29.7	31.2
Rsa1.0_00122.1.g5884.t1	ref|NP_194255.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|4454013|emb|CAA23066.1| putative protein [Arabidopsis thaliana] gi|7269376|emb|CAB81336.1| putative protein [Arabidopsis thaliana] gi|28416607|gb|AAO42834.1| At4g25250 [Arabidopsis thaliana] gi|110743315|dbj|BAE99546.1| hypothetical protein [Arabidopsis thaliana] gi|332659631|gb|AEE85031.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	197	199	2.00E-54	101.0	59.4	75.6	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT4G25250.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:12934632-12935231 FORWARD LENGTH=199	197	199	6.00E-57	101.0	59.4	75.6
Rsa1.0_00122.1.g5885.t1	gb|AAM62643.1| ripening-related protein-like [Arabidopsis thaliana]	150	199	1.00E-58	132.7	76.7	87.3	ripening-related protein-like	gbpln	Arabidopsis thaliana	AT4G25250.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:12934632-12935231 FORWARD LENGTH=199	150	199	6.00E-61	132.7	76.0	86.7
Rsa1.0_00122.1.g5886.t1	gb|EOA16286.1| hypothetical protein CARUB_v10004433mg [Capsella rubella]	617	590	0	95.6	84.8	89.1	hypothetical protein CARUB_v10004433mg	gbpln	Capsella rubella	AT4G25240.1 | Symbols: SKS1 | SKU5 similar 1 | chr4:12930539-12933563 FORWARD LENGTH=589	617	589	0	95.5	84.1	88.7
Rsa1.0_00122.1.g5887.t1	gb|EOA15790.1| hypothetical protein CARUB_v10007136mg [Capsella rubella]	505	503	0	99.6	91.9	96.8	hypothetical protein CARUB_v10007136mg	gbpln	Capsella rubella	AT4G25220.1 | Symbols: RHS15 | root hair specific 15 | chr4:12921161-12922762 FORWARD LENGTH=504	505	504	0	99.8	87.7	92.7
Rsa1.0_00122.1.g5888.t1	ref|NP_194251.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana] gi|75201680|sp|Q9SB42.1|MDA1_ARATH RecName: Full=Mediator-associated protein 1 gi|13272449|gb|AAK17163.1|AF325095_1 putative protein [Arabidopsis thaliana] gi|4454009|emb|CAA23062.1| putative protein [Arabidopsis thaliana] gi|7269371|emb|CAB79430.1| putative protein [Arabidopsis thaliana] gi|225898811|dbj|BAH30536.1| hypothetical protein [Arabidopsis thaliana] gi|332659625|gb|AEE85025.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana]	377	368	8.00E-84	97.6	47.7	58.9	DNA-binding storekeeper protein-related transcriptional regulator	gbpln	Arabidopsis thaliana	AT4G25210.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr4:12918446-12919552 FORWARD LENGTH=368	377	368	2.00E-86	97.6	47.7	58.9

Rsa1.0_00122.1.g5889.t1	emb|CAA67022.1| LMW heat shock protein [Arabidopsis thaliana]	214	210	3.00E-91	98.1	80.4	90.2	LMW heat shock protein	gbpln	Arabidopsis thaliana	AT4G25200.1 | Symbols: ATHSP23.6-MITO, HSP23.6-MITO | mitochondrion-localized small heat shock protein 23.6 | chr4:12917089-12917858 FORWARD LENGTH=210	214	210	3.00E-85	98.1	76.6	85.5
Rsa1.0_00122.1.g5890.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00122.1.g5891.t1	ref|XP_002867620.1| hypothetical protein ARALYDRAFT_492315 [Arabidopsis lyrata subsp. lyrata] gi|297313456|gb|EFH43879.1| hypothetical protein ARALYDRAFT_492315 [Arabidopsis lyrata subsp. lyrata]	387	412	2.33E-156	106.5	77.3	88.1	hypothetical protein ARALYDRAFT_492315	gbpln	Arabidopsis lyrata	AT4G25190.1 | Symbols: QWRF7 | Family of unknown function (DUF566) | chr4:12914400-12916001 REVERSE LENGTH=394	387	394	1.00E-147	101.8	75.2	86.0
Rsa1.0_00122.1.g5892.t1	ref|XP_002867621.1| DNA-directed RNA polymerase [Arabidopsis lyrata subsp. lyrata] gi|297313457|gb|EFH43880.1| DNA-directed RNA polymerase [Arabidopsis lyrata subsp. lyrata]	316	315	1.00E-127	99.7	75.9	82.0	DNA-directed RNA polymerase	gbpln	Arabidopsis lyrata	AT4G25180.1 | Symbols: | RNA polymerase III RPC4 | chr4:12911746-12913907 REVERSE LENGTH=311	316	311	1.00E-113	98.4	70.9	76.9
Rsa1.0_00122.1.g5893.t1	ref|NP_201433.1| GATA transcription factor 5 [Arabidopsis thaliana] gi|42573812|ref|NP_975002.1| GATA transcription factor 5 [Arabidopsis thaliana] gi|71660777|sp|Q9FH57.1|GATA5_ARATH RecName: Full=GATA transcription factor 5 gi|10177426|dbj|BAB10711.1| GATA-binding transcription factor-like protein [Arabidopsis thaliana] gi|22531223|gb|AAM97115.1| GATA-binding transcription factor-like protein [Arabidopsis thaliana] gi|34098855|gb|AAQ56810.1| At5g66320 [Arabidopsis thaliana] gi|332010815|gb|AED98198.1| GATA transcription factor 5 [Arabidopsis thaliana] gi|332010816|gb|AED98199.1| GATA transcription factor 5 [Arabidopsis thaliana]	339	339	1.00E-127	100.0	76.7	85.5	GATA transcription factor 5	gbpln	Arabidopsis thaliana	AT5G66320.2 | Symbols: GATA5 | GATA transcription factor 5 | chr5:26496208-26497309 REVERSE LENGTH=339	339	339	1.00E-130	100.0	76.7	85.5
Rsa1.0_00122.1.g5894.t1	emb|CAA23058.1| putative protein [Arabidopsis thaliana] gi|7269367|emb|CAB79426.1| putative protein [Arabidopsis thaliana]	344	336	1.00E-155	97.7	80.2	87.8	putative protein	gbpln	Arabidopsis thaliana	AT4G25170.1 | Symbols: | Uncharacterised conserved protein (UCP012943) | chr4:12909740-12911389 FORWARD LENGTH=344	344	344	1.00E-150	100.0	76.7	84.3
Rsa1.0_00122.1.g5895.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00122.1.g5896.t1	ref|NP_565573.4| uncharacterized protein [Arabidopsis thaliana] gi|15724184|gb|AAL06484.1|AF411794_1 At2g24550/F25P17.15 [Arabidopsis thaliana] gi|20466816|gb|AAM20725.1| unknown protein [Arabidopsis thaliana] gi|23198218|gb|AAN15636.1| unknown protein [Arabidopsis thaliana] gi|330252497|gb|AEC07591.1| uncharacterized protein AT2G24550 [Arabidopsis thaliana]	255	245	1.00E-63	96.1	69.0	73.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G24550.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G31510.1); Has 219 Blast hits to 219 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 2; Plants - 184; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr2:10428060-10429051 REVERSE LENGTH=245	255	245	3.00E-66	96.1	69.0	73.7
Rsa1.0_00122.1.g5897.t1	gb|ACQ76799.1| WRKY transcription factor 17 [Brassica napus]	321	325	1.00E-144	101.2	91.9	94.7	WRKY transcription factor 17	gbpln	Brassica napus	AT2G24570.1 | Symbols: WRKY17, ATWRKY17 | WRKY DNA-binding protein 17 | chr2:10437676-10439222 REVERSE LENGTH=321	321	321	1.00E-139	100.0	82.9	89.1
Rsa1.0_00122.1.g5898.t1	gb|EOA27191.1| hypothetical protein CARUB_v10023301mg [Capsella rubella]	413	416	0	100.7	88.6	94.4	hypothetical protein CARUB_v10023301mg	gbpln	Capsella rubella	AT2G24580.1 | Symbols: | FAD-dependent oxidoreductase family protein | chr2:10444928-10446178 REVERSE LENGTH=416	413	416	0	100.7	87.7	93.9

Rsa1.0_00122.1.g5899.t3	ref|NP_180035.1| RNA recognition motif and CCHC-type zinc finger domain-containing protein [Arabidopsis thaliana] gi|75337303|sp|Q9SJA6.1|RZ22A_ARATH RecName: Full=Serine/arginine-rich splicing factor RSZ22A; AltName: Full=RS-containing zinc finger protein 22A; Short=At-RSZ22a; Short=At-RSZp22a gi|4572679|gb|AAD23894.1| putative RSZp22 splicing factor [Arabidopsis thaliana] gi|26450830|dbj|BAC42523.1| putative RSZp22 splicing factor [Arabidopsis thaliana] gi|28950713|gb|AAO63280.1| At2g24590 [Arabidopsis thaliana] gi|330252501|gb|AEC07595.1| serine/arginine-rich splicing factor RSZ22A [Arabidopsis thaliana]	245	196	3.00E-45	80.0	64.9	67.3	RNA recognition motif and CCHC-type zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT2G24590.1 | Symbols: RSZ22a, At-RSZ22a | RNA recognition motif and CCHC-type zinc finger domains containing protein | chr2:10449837-10450860 FORWARD LENGTH=196	245	196	9.00E-48	80.0	64.9	67.3
Rsa1.0_00122.1.g5900.t1	ref|NP_850056.1| cyclic nucleotide gated channel [Arabidopsis thaliana] gi|38503238|sp|Q9SJA4.2|CNG14_ARATH RecName: Full=Probable cyclic nucleotide-gated ion channel 14; AltName: Full=Cyclic nucleotide- and calmodulin-regulated ion channel 14 gi|110736217|dbj|BAF00079.1| putative cyclic nucleotide-regulated ion channel protein [Arabidopsis thaliana] gi|330252507|gb|AEC07601.1| cyclic nucleotide-gated channel 14 [Arabidopsis thaliana]	758	726	0	95.8	87.5	91.4	cyclic nucleotide gated channel	gbpln	Arabidopsis thaliana	AT2G24610.1 | Symbols: ATCNGC14, CNGC14 | cyclic nucleotide-gated channel 14 | chr2:10457105-10460351 FORWARD LENGTH=726	758	726	0	95.8	87.5	91.4
Rsa1.0_00122.1.g5901.t1	ref|NP_565576.1| ubiquitin carboxyl-terminal hydrolase 19 [Arabidopsis thaliana] gi|75265927|sp|Q9SJA1.2|UBP19_ARATH RecName: Full=Ubiquitin carboxyl-terminal hydrolase 19; AltName: Full=Deubiquitinating enzyme 19; Short=AtUBP19; AltName: Full=Ubiquitin thioesterase 19; AltName: Full=Ubiquitin-specific-processing protease 19 gi|13430806|gb|AAK26025.1|AF360315_1 putative ubiquitin carboxyl terminal hydrolase [Arabidopsis thaliana] gi|15810655|gb|AAL07252.1| putative ubiquitin carboxyl terminal hydrolase [Arabidopsis thaliana] gi|20197976|gb|AAD23896.2| putative ubiquitin carboxyl terminal hydrolase [Arabidopsis thaliana] gi|330252513|gb|AEC07607.1| ubiquitin carboxyl-terminal hydrolase 19 [Arabidopsis thaliana]	617	672	0	108.9	83.0	88.5	ubiquitin carboxyl-terminal hydrolase 19	gbpln	Arabidopsis thaliana	AT2G24640.1 | Symbols: UBP19 | ubiquitin-specific protease 19 | chr2:10475613-10479341 REVERSE LENGTH=672	617	672	0	108.9	83.0	88.5
Rsa1.0_00122.1.g5902.t2	gb|EOA27328.1| hypothetical protein CARUB_v10023444mg, partial [Capsella rubella]	577	378	1.00E-123	65.5	40.0	48.5	hypothetical protein CARUB_v10023444mg, partial	gbpln	Capsella rubella	AT4G00260.1 | Symbols: MEE45 | Transcriptional factor B3 family protein | chr4:114971-117051 FORWARD LENGTH=528	577	528	3.00E-93	91.5	32.2	41.1
Rsa1.0_00122.1.g5903.t2	ref|XP_002878782.1| hypothetical protein ARALYDRAFT_901047 [Arabidopsis lyrata subsp. lyrata] gi|297324621|gb|EFH55041.1| hypothetical protein ARALYDRAFT_901047 [Arabidopsis lyrata subsp. lyrata]	510	595	1.00E-169	116.7	64.5	78.4	hypothetical protein ARALYDRAFT_901047	gbpln	Arabidopsis lyrata	AT4G00260.1 | Symbols: MEE45 | Transcriptional factor B3 family protein | chr4:114971-117051 FORWARD LENGTH=528	510	528	1.00E-171	103.5	63.7	75.5
Rsa1.0_00122.1.g5904.t1	ref|XP_002880626.1| hypothetical protein ARALYDRAFT_901062 [Arabidopsis lyrata subsp. lyrata] gi|297326465|gb|EFH56885.1| hypothetical protein ARALYDRAFT_901062 [Arabidopsis lyrata subsp. lyrata]	485	631	1.00E-170	130.1	65.8	80.2	hypothetical protein ARALYDRAFT_901062	gbpln	Arabidopsis lyrata	AT4G00260.1 | Symbols: MEE45 | Transcriptional factor B3 family protein | chr4:114971-117051 FORWARD LENGTH=528	485	528	1.00E-154	108.9	62.5	75.1
Rsa1.0_00122.1.g5905.t1	ref|NP_180117.4| receptor like protein 21 [Arabidopsis thaliana] gi|330252611|gb|AEC07705.1| receptor like protein 21 [Arabidopsis thaliana]	1023	935	0	91.4	63.4	72.5	receptor like protein 21	gbpln	Arabidopsis thaliana	AT2G25470.1 | Symbols: AtRLP21, RLP21 | receptor like protein 21 | chr2:10838420-10841881 FORWARD LENGTH=935	1023	935	0	91.4	63.4	72.5
Rsa1.0_00122.1.g5906.t1	gb|EOA28688.1| hypothetical protein CARUB_v10024914mg [Capsella rubella]	171	215	3.00E-67	125.7	72.5	85.4	hypothetical protein CARUB_v10024914mg	gbpln	Capsella rubella	AT2G24840.1 | Symbols: AGL61, DIA | AGAMOUS-like 61 | chr2:10581082-10581876 FORWARD LENGTH=264	171	264	3.00E-69	154.4	73.7	84.2

Rsa1.0_00122.1.g5907.t1	ref|NP_565578.1| DnaJ/Hsp40 cysteine-rich domain-containing protein [Arabidopsis thaliana] gi|15294198|gb|AAK95276.1|AF410290_1 At2g24860/F27C12.22 [Arabidopsis thaliana] gi|20197874|gb|AAD23026.2| expressed protein [Arabidopsis thaliana] gi|20453299|gb|AAM19888.1| At2g24860/F27C12.22 [Arabidopsis thaliana] gi|21618127|gb|AAM67177.1| Tsi1-interacting protein TSIP1 [Arabidopsis thaliana] gi|51970710|dbj|BAD44047.1| unknown protein [Arabidopsis thaliana] gi|330252543|gb|AEC07637.1| DnaJ/Hsp40 cysteine-rich domain-containing protein [Arabidopsis thaliana]	148	144	1.00E-63	97.3	82.4	89.2	DnaJ/Hsp40 cysteine-rich domain-containing protein	gbpln	Arabidopsis thaliana	AT2G24860.1 | Symbols: | DnaJ/Hsp40 cysteine-rich domain superfamily protein | chr2:10587118-10588240 REVERSE LENGTH=144	148	144	3.00E-66	97.3	82.4	89.2
Rsa1.0_00122.1.g5908.t1	ref|XP_002878810.1| membrane-associated progesterone binding protein 2 [Arabidopsis lyrata subsp. lyrata] gi|297324649|gb|EFH55069.1| membrane-associated progesterone binding protein 2 [Arabidopsis lyrata subsp. lyrata]	100	100	9.00E-49	100.0	95.0	98.0	membrane-associated progesterone binding protein 2	gbpln	Arabidopsis lyrata	AT2G24940.1 | Symbols: AtMAPR2, MAPR2 | membrane-associated progesterone binding protein 2 | chr2:10609447-10609749 FORWARD LENGTH=100	100	100	4.00E-51	100.0	94.0	98.0
Rsa1.0_00122.1.g5909.t1	ref|NP_001118381.1| uncharacterized protein [Arabidopsis thaliana] gi|330252550|gb|AEC07644.1| uncharacterized protein AT2G24960 [Arabidopsis thaliana]	744	774	0	104.0	75.5	84.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G24960.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02210.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:10617263-10620034 FORWARD LENGTH=774	744	774	0	104.0	75.5	84.0
Rsa1.0_00122.1.g5910.t1	ref|NP_851100.1| Serine/threonine-protein kinase Rio1 [Arabidopsis thaliana] gi|9758721|dbj|BAB09107.1| SUDD-like protein [Arabidopsis thaliana] gi|51971891|dbj|BAD44610.1| unknown protein [Arabidopsis thaliana] gi|51972017|dbj|BAD44673.1| unknown protein [Arabidopsis thaliana] gi|332006786|gb|AED94169.1| Serine/threonine-protein kinase Rio1 [Arabidopsis thaliana]	540	531	0	98.3	88.7	92.8	Serine/threonine-protein kinase Rio1	gbpln	Arabidopsis thaliana	AT5G37350.1 | Symbols: | Serine/threonine-protein kinase Rio1 | chr5:14793037-14795828 FORWARD LENGTH=531	540	531	0	98.3	88.7	92.8
Rsa1.0_00122.1.g5911.t1	ref|XP_002886580.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332421|gb|EFH62839.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	179	275	5.00E-43	153.6	54.2	67.6	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00122.1.g5912.t1	gb|EOA35514.1| hypothetical protein CARUB_v10020721mg [Capsella rubella]	267	298	1.00E-38	111.6	37.8	55.4	hypothetical protein CARUB_v10020721mg	gbpln	Capsella rubella	AT1G66620.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr1:24852806-24854044 REVERSE LENGTH=313	267	313	2.00E-37	117.2	35.2	51.7
Rsa1.0_00122.1.g5913.t1	ref|NP_565582.1| aminotransferase-like, plant mobile domain-containing protein [Arabidopsis thaliana] gi|4559351|gb|AAD23012.1| expressed protein [Arabidopsis thaliana] gi|95147312|gb|ABF57291.1| At2g25010 [Arabidopsis thaliana] gi|330252555|gb|AEC07649.1| aminotransferase-like, plant mobile domain-containing protein [Arabidopsis thaliana]	512	509	0	99.4	91.0	95.5	aminotransferase-like, plant mobile domain-containing protein	gbpln	Arabidopsis thaliana	AT2G25010.1 | Symbols: | Aminotransferase-like, plant mobile domain family protein | chr2:10631691-10633547 FORWARD LENGTH=509	512	509	0	99.4	91.0	95.5
Rsa1.0_00122.1.g5914.t1	gb|EOA29374.1| hypothetical protein CARUB_v10025661mg [Capsella rubella]	815	809	0	99.3	77.9	88.0	hypothetical protein CARUB_v10025661mg	gbpln	Capsella rubella	AT2G25140.1 | Symbols: HSP98.7, CLPB-M, CLPB4 | casein lytic proteinase B4 | chr2:10697877-10701998 REVERSE LENGTH=964	815	964	0	118.3	69.2	78.7
Rsa1.0_00122.1.g5915.t1	dbj|BAJ34450.1| unnamed protein product [Thellungiella halophila]	317	356	1.00E-154	112.3	89.0	93.4	unnamed protein product	----	----	AT2G25070.1 | Symbols: | Protein phosphatase 2C family protein | chr2:10663517-10665366 REVERSE LENGTH=355	317	355	1.00E-156	112.0	84.9	89.9

Rsa1.0_00122.1.g5916.t1	ref|NP_180081.1| CBL-interacting serine/threonine-protein kinase 16 [Arabidopsis thaliana] gi|75337155|sp|Q9SEZ7.1|CIPKG_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 16; AltName: Full=SNF1-related kinase 3.18; AltName: Full=SOS2-like protein kinase PKS15 gi|14009298|gb|AAK50348.1| CBL-interacting protein kinase 16 [Arabidopsis thaliana] gi|116325944|gb|ABJ98573.1| At2g25090 [Arabidopsis thaliana] gi|330252562|gb|AEC07656.1| CBL-interacting serine/threonine-protein kinase 16 [Arabidopsis thaliana]	461	469	0	101.7	85.7	92.2	CBL-interacting serine/threonine-protein kinase 16	gbpln	Arabidopsis thaliana	AT2G25090.1 | Symbols: CIPK16, SnRK3.18 | CBL-interacting protein kinase 16 | chr2:10670542-10672610 REVERSE LENGTH=469	461	469	0	101.7	85.7	92.2
Rsa1.0_00123.1.g5917.t1	gb|EOA19387.1| hypothetical protein CARUB_v10000661mg [Capsella rubella]	500	539	1.00E-178	107.8	72.8	84.0	hypothetical protein CARUB_v10000661mg	gbpln	Capsella rubella	AT5G05240.1 | Symbols: | Uncharacterised conserved protein (UCP030365) | chr5:1554023-1556230 REVERSE LENGTH=530	500	530	1.00E-174	106.0	70.2	80.2
Rsa1.0_00123.1.g5918.t1	ref|XP_002871146.1| hypothetical protein ARALYDRAFT_487314 [Arabidopsis lyrata subsp. lyrata] gi|297316983|gb|EFH47405.1| hypothetical protein ARALYDRAFT_487314 [Arabidopsis lyrata subsp. lyrata]	371	365	1.00E-149	98.4	82.2	88.7	hypothetical protein ARALYDRAFT_487314	gbpln	Arabidopsis lyrata	AT5G05230.1 | Symbols: | RING/U-box superfamily protein | chr5:1551593-1553543 FORWARD LENGTH=363	371	363	1.00E-150	97.8	82.7	88.7
Rsa1.0_00123.1.g5919.t1	ref|XP_002871145.1| hypothetical protein ARALYDRAFT_908428 [Arabidopsis lyrata subsp. lyrata] gi|297316982|gb|EFH47404.1| hypothetical protein ARALYDRAFT_908428 [Arabidopsis lyrata subsp. lyrata]	138	183	5.00E-50	132.6	78.3	84.1	hypothetical protein ARALYDRAFT_908428	gbpln	Arabidopsis lyrata	AT5G05220.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:1550273-1550821 FORWARD LENGTH=182	138	182	4.00E-50	131.9	73.2	81.9
Rsa1.0_00123.1.g5920.t1	ref|NP_568150.1| aarF domain-containing protein kinase [Arabidopsis thaliana] gi|75261770|sp|Q9ASX5.1|Y5520_ARATH RecName: Full=Uncharacterized aarF domain-containing protein kinase At5g05200, chloroplastic; Flags: Precursor gi|13605575|gb|AAK32781.1|AF361613_1 AT5g05200/K2A11_7 [Arabidopsis thaliana] gi|14334952|gb|AAK59653.1| unknown protein [Arabidopsis thaliana] gi|16648993|gb|AAL24348.1| Unknown protein [Arabidopsis thaliana] gi|17104611|gb|AAL34194.1| unknown protein [Arabidopsis thaliana] gi|20259938|gb|AAM13316.1| unknown protein [Arabidopsis thaliana] gi|22137078|gb|AAM91384.1| At5g05200/K2A11_7 [Arabidopsis thaliana] gi|332003457|gb|AED90840.1| aarF domain-containing protein kinase [Arabidopsis thaliana]	565	540	0	95.6	85.8	90.3	aarF domain-containing protein kinase	gbpln	Arabidopsis thaliana	AT5G05200.1 | Symbols: | Protein kinase superfamily protein | chr5:1544206-1547082 REVERSE LENGTH=540	565	540	0	95.6	85.8	90.3
Rsa1.0_00123.1.g5921.t1	ref|XP_002871143.1| hypothetical protein ARALYDRAFT_908425 [Arabidopsis lyrata subsp. lyrata] gi|297316980|gb|EFH47402.1| hypothetical protein ARALYDRAFT_908425 [Arabidopsis lyrata subsp. lyrata]	630	591	0	93.8	63.2	71.6	hypothetical protein ARALYDRAFT_908425	gbpln	Arabidopsis lyrata	AT5G05190.1 | Symbols: | Protein of unknown function (DUF3133) | chr5:1541853-1543875 FORWARD LENGTH=615	630	615	0	97.6	65.2	73.8
Rsa1.0_00123.1.g5922.t1	gb|EOA20598.1| hypothetical protein CARUB_v10000908mg [Capsella rubella]	404	462	1.00E-128	114.4	65.8	78.7	hypothetical protein CARUB_v10000908mg	gbpln	Capsella rubella	AT5G05180.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G10880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1536924-1538318 FORWARD LENGTH=432	404	432	1.00E-121	106.9	63.6	77.7
Rsa1.0_00123.1.g5923.t1	gb|AFJ66186.1| hypothetical protein 11M19.5 [Arabidopsis halleri]	1416	1557	0	110.0	56.1	65.9	hypothetical protein 11M19.5	gbpln	Arabidopsis halleri	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1416	158	2.00E-31	11.2	4.9	6.1

Rsa1.0_00123.1.g5924.t1	ref|NP_196135.1| putative leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|75333868|sp|Q9FHK7.1|Y5516_ARATH RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At5g05160; Flags: Precursor gi|9759257|dbj|BAB09692.1| receptor-like protein kinase [Arabidopsis thaliana] gi|224589658|gb|ACN59361.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332003452|gb|AED90835.1| putative leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	633	640	0	101.1	90.7	95.1	putative leucine-rich repeat receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G05160.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:1528000-1530017 FORWARD LENGTH=640	633	640	0	101.1	90.7	95.1
Rsa1.0_00123.1.g5925.t2	ref|NP_196133.3| Transcription elongation factor (TFIIS) family protein [Arabidopsis thaliana] gi|75170631|sp|Q9FHK9.1|MD26B_ARATH RecName: Full=Probable mediator of RNA polymerase II transcription subunit 26b gi|9759255|dbj|BAB09690.1| unnamed protein product [Arabidopsis thaliana] gi|332003450|gb|AED90833.1| Transcription elongation factor (TFIIS) family protein [Arabidopsis thaliana]	445	436	0	98.0	78.4	84.9	Transcription elongation factor (TFIIS) family protein	gbpln	Arabidopsis thaliana	AT5G05140.1 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr5:1520353-1522297 FORWARD LENGTH=436	445	436	0	98.0	78.4	84.9
Rsa1.0_00123.1.g5926.t1	gb|EOA19963.1| hypothetical protein CARUB_v10000214mg [Capsella rubella]	849	846	0	99.6	85.3	91.6	hypothetical protein CARUB_v10000214mg	gbpln	Capsella rubella	AT5G05130.1 | Symbols: | DNA/RNA helicase protein | chr5:1512173-1514918 FORWARD LENGTH=862	849	862	0	101.5	85.2	91.5
Rsa1.0_00123.1.g5927.t1	ref|XP_002871138.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297316975|gb|EFH47397.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	172	204	4.00E-23	118.6	48.3	57.0	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G05120.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:1511232-1511837 FORWARD LENGTH=201	172	201	3.00E-23	116.9	44.2	55.8
Rsa1.0_00123.1.g5928.t1	dbj|BAJ34510.1| unnamed protein product [Thellungiella halophila]	271	270	1.00E-102	99.6	81.2	85.2	unnamed protein product	----	----	AT5G05090.1 | Symbols: | Homeodomain-like superfamily protein | chr5:1503393-1504193 FORWARD LENGTH=266	271	266	5.00E-93	98.2	77.1	81.5
Rsa1.0_00123.1.g5929.t2	ref|XP_002873191.1| ubiquitin-conjugating enzyme 18 [Arabidopsis lyrata subsp. lyrata] gi|297319028|gb|EFH49450.1| ubiquitin-conjugating enzyme 18 [Arabidopsis lyrata subsp. lyrata]	263	254	1.00E-126	96.6	87.5	90.5	ubiquitin-conjugating enzyme 18	gbpln	Arabidopsis lyrata	AT5G05080.2 | Symbols: UBC22, ATUBC22 | ubiquitin-conjugating enzyme 22 | chr5:1498727-1499972 REVERSE LENGTH=251	263	251	1.00E-124	95.4	85.2	88.6
Rsa1.0_00123.1.g5930.t2	ref|NP_196126.2| putative S-acyltransferase [Arabidopsis thaliana] gi|75251250|sp|Q5PNZ1.1|ZDH21_ARATH RecName: Full=Probable S-acyltransferase At5g05070; AltName: Full=Probable palmitoyltransferase At5g05070; AltName: Full=Zinc finger DHHC domain-containing protein At5g05070 gi|56381885|gb|AAV85661.1| At5g05070 [Arabidopsis thaliana] gi|332003441|gb|AED90824.1| putative S-acyltransferase [Arabidopsis thaliana]	375	413	1.00E-176	110.1	83.2	90.9	putative S-acyltransferase	gbpln	Arabidopsis thaliana	AT5G05070.1 | Symbols: | DHHC-type zinc finger family protein | chr5:1496896-1498441 FORWARD LENGTH=413	375	413	1.00E-179	110.1	83.2	90.9
Rsa1.0_00123.1.g5931.t2	ref|NP_197984.2| alpha-L-arabinofuranosidase 2 [Arabidopsis thaliana] gi|75248533|sp|Q8VZR2.1|ASD2_ARATH RecName: Full=Alpha-L-arabinofuranosidase 2; Short=AtASD2; AltName: Full=Beta-D-xylosidase; Flags: Precursor gi|17380938|gb|AAL36281.1| putative arabinosidase [Arabidopsis thaliana] gi|29824173|gb|AAP04047.1| unknown protein [Arabidopsis thaliana] gi|29825625|gb|AAO92262.1| alpha-L-arabinofuranosidase [Arabidopsis thaliana] gi|332006144|gb|AED93527.1| alpha-L-arabinofuranosidase 2 [Arabidopsis thaliana]	678	674	0	99.4	80.7	87.5	alpha-L-arabinofuranosidase 2	gbpln	Arabidopsis thaliana	AT5G26120.1 | Symbols: ATASD2, ASD2 | alpha-L-arabinofuranosidase 2 | chr5:9121835-9125399 REVERSE LENGTH=674	678	674	0	99.4	80.7	87.5
Rsa1.0_00123.1.g5932.t1	gb|EOA22393.1| hypothetical protein CARUB_v10003029mg [Capsella rubella]	529	526	0	99.4	88.8	93.2	hypothetical protein CARUB_v10003029mg	gbpln	Capsella rubella	AT5G05010.2 | Symbols: | clathrin adaptor complexes medium subunit family protein | chr5:1477137-1479872 FORWARD LENGTH=527	529	527	0	99.6	88.3	94.0
Rsa1.0_00123.1.g5933.t1	gb|EOA21162.1| hypothetical protein CARUB_v10001510mg [Capsella rubella]	314	313	1.00E-163	99.7	89.8	95.2	hypothetical protein CARUB_v10001510mg	gbpln	Capsella rubella	AT5G05000.1 | Symbols: TOC34, ATTOC34, OEP34 | translocon at the outer envelope membrane of chloroplasts 34 | chr5:1474262-1475772 REVERSE LENGTH=313	314	313	1.00E-160	99.7	87.3	93.9

Rsa1.0_00123.1.g5934.t1	gb|EOA20566.1| hypothetical protein CARUB_v10000878mg [Capsella rubella]	615	472	0	76.7	59.0	66.7	hypothetical protein CARUB_v10000878mg	gbpln	Capsella rubella	AT5G04990.1 | Symbols: SUN1, ATSUN1 | SAD1/UNC-84 domain protein 1 | chr5:1471698-1473770 REVERSE LENGTH=471	615	471	0	76.6	57.6	66.2
Rsa1.0_00123.1.g5935.t1	ref|XP_002873178.1| hypothetical protein ARALYDRAFT_487284 [Arabidopsis lyrata subsp. lyrata] gi|297319015|gb|EFH49437.1| hypothetical protein ARALYDRAFT_487284 [Arabidopsis lyrata subsp. lyrata]	599	616	0	102.8	81.3	85.1	hypothetical protein ARALYDRAFT_487284	gbpln	Arabidopsis lyrata	AT5G04970.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:1464262-1467001 REVERSE LENGTH=624	599	624	0	104.2	81.3	84.8
Rsa1.0_00123.1.g5936.t1	gb|EOA22839.1| hypothetical protein CARUB_v10003563mg [Capsella rubella]	360	321	1.00E-163	89.2	78.1	82.2	hypothetical protein CARUB_v10003563mg	gbpln	Capsella rubella	AT5G04950.1 | Symbols: NAS1, ATNAS1 | nicotianamine synthase 1 | chr5:1457876-1458838 REVERSE LENGTH=320	360	320	1.00E-165	88.9	77.8	82.2
Rsa1.0_00123.1.g5937.t1	ref|XP_002872136.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297317973|gb|EFH48395.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata]	113	498	2.00E-41	440.7	75.2	80.5	integral membrane transporter family protein	gbpln	Arabidopsis lyrata	AT5G25050.1 | Symbols: | Major facilitator superfamily protein | chr5:8632022-8633828 FORWARD LENGTH=499	113	499	1.00E-43	441.6	74.3	79.6
Rsa1.0_00123.1.g5938.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00123.1.g5939.t1	gb|EOA22636.1| hypothetical protein CARUB_v10003306mg [Capsella rubella]	662	664	0	100.3	81.3	90.0	hypothetical protein CARUB_v10003306mg	gbpln	Capsella rubella	AT5G04940.2 | Symbols: SUVH1 | SU(VAR)3-9 homolog 1 | chr5:1454616-1456628 REVERSE LENGTH=670	662	670	0	101.2	81.3	89.6
Rsa1.0_00123.1.g5940.t1	gb|EOA22636.1| hypothetical protein CARUB_v10003306mg [Capsella rubella]	665	664	0	99.8	81.7	89.0	hypothetical protein CARUB_v10003306mg	gbpln	Capsella rubella	AT5G04940.2 | Symbols: SUVH1 | SU(VAR)3-9 homolog 1 | chr5:1454616-1456628 REVERSE LENGTH=670	665	670	0	100.8	81.5	87.8
Rsa1.0_00123.1.g5941.t1	ref|XP_002871124.1| hypothetical protein ARALYDRAFT_908384 [Arabidopsis lyrata subsp. lyrata] gi|297316961|gb|EFH47383.1| hypothetical protein ARALYDRAFT_908384 [Arabidopsis lyrata subsp. lyrata]	1154	1161	0	100.6	92.5	95.7	hypothetical protein ARALYDRAFT_908384	gbpln	Arabidopsis lyrata	AT5G04930.1 | Symbols: ALA1 | aminophospholipid ATPase 1 | chr5:1445509-1449568 FORWARD LENGTH=1158	1154	1158	0	100.3	92.1	95.1
Rsa1.0_00123.1.g5942.t2	ref|NP_196112.1| vacuolar protein sorting-associated protein 36 [Arabidopsis thaliana] gi|75170174|sp|Q9FF81.1|VPS36_ARATH RecName: Full=Vacuolar protein sorting-associated protein 36; Short=AtVPS36; AltName: Full=ESCRT-II complex subunit VPS36 gi|10178031|dbj|BAB11514.1| unnamed protein product [Arabidopsis thaliana] gi|18175694|gb|AAL59912.1| unknown protein [Arabidopsis thaliana] gi|20465997|gb|AAM20220.1| unknown protein [Arabidopsis thaliana] gi|332003421|gb|AED90804.1| vacuolar protein sorting-associated protein 36 [Arabidopsis thaliana]	444	440	0	99.1	89.4	93.5	vacuolar protein sorting-associated protein 36	gbpln	Arabidopsis thaliana	AT5G04920.1 | Symbols: | EAP30/Vps36 family protein | chr5:1439172-1441545 REVERSE LENGTH=440	444	440	0	99.1	89.4	93.5
Rsa1.0_00123.1.g5943.t1	gb|EOA21537.1| hypothetical protein CARUB_v10001943mg [Capsella rubella]	213	215	5.00E-92	100.9	87.8	92.0	hypothetical protein CARUB_v10001943mg	gbpln	Capsella rubella	AT5G04910.1 | Symbols: | unknown protein; Has 71 Blast hits to 71 proteins in 36 species: Archae - 0; Bacteria - 0; Metazoa - 17; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink). | chr5:1437695-1438770 FORWARD LENGTH=222	213	222	4.00E-90	104.2	86.4	92.5
Rsa1.0_00123.1.g5944.t1	gb|EOA26425.1| hypothetical protein CARUB_v10024547mg [Capsella rubella]	517	509	0	98.5	91.7	95.0	hypothetical protein CARUB_v10024547mg	gbpln	Capsella rubella	AT2G26640.1 | Symbols: KCS11 | 3-ketoacyl-CoA synthase 11 | chr2:11330094-11331623 FORWARD LENGTH=509	517	509	0	98.5	90.9	95.4
Rsa1.0_00123.1.g5945.t1	ref|NP_680142.2| DEA(D/H)-box RNA helicase family protein [Arabidopsis thaliana] gi|10178028|dbj|BAB11511.1| ATP-dependent RNA helicase A-like protein [Arabidopsis thaliana] gi|332003418|gb|AED90801.1| DEA(D/H)-box RNA helicase family protein [Arabidopsis thaliana]	1165	1161	0	99.7	94.2	96.8	DEA(D/H)-box RNA helicase family protein	gbpln	Arabidopsis thaliana	AT5G04895.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr5:1428796-1434516 FORWARD LENGTH=1161	1165	1161	0	99.7	94.2	96.8
Rsa1.0_00123.1.g5946.t1	ref|XP_002871120.1| hypothetical protein ARALYDRAFT_487275 [Arabidopsis lyrata subsp. lyrata] gi|297316957|gb|EFH47379.1| hypothetical protein ARALYDRAFT_487275 [Arabidopsis lyrata subsp. lyrata]	384	366	2.00E-96	95.3	54.4	67.4	hypothetical protein ARALYDRAFT_487275	gbpln	Arabidopsis lyrata	AT5G04890.1 | Symbols: RTM2 | HSP20-like chaperones superfamily protein | chr5:1427217-1428390 FORWARD LENGTH=366	384	366	1.00E-79	95.3	53.4	64.3

Rsa1.0_00123.1.g5947.t4	ref|XP_002871119.1| glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata] gi|297316956|gb|EFH47378.1| glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata]	674	668	0	99.1	88.3	92.6	glycosyl hydrolase family 3 protein	gbpln	Arabidopsis lyrata	AT5G04885.1 | Symbols: | Glycosyl hydrolase family protein | chr5:1423369-1426628 FORWARD LENGTH=665	674	665	0	98.7	86.5	92.4
Rsa1.0_00123.1.g5948.t1	gb|AAX22255.1| At1g23470 [Arabidopsis thaliana]	160	169	5.00E-66	105.6	78.1	90.0	At1g23470	gbpln	Arabidopsis thaliana	AT1G29960.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr1:10494813-10495851 FORWARD LENGTH=169	160	169	1.00E-67	105.6	76.9	89.4
Rsa1.0_00123.1.g5949.t1	gb|ABE73345.1| putative calcium-dependent protein kinase 2 [Isatis tinctoria] gi|92110524|gb|ABE73346.1| putative calcium-dependent protein kinase 2 [Isatis tinctoria]	609	625	0	102.6	93.6	95.2	putative calcium-dependent protein kinase 2	gbpln	Isatis tinctoria	AT5G04870.1 | Symbols: CPK1, ATCPK1 | calcium dependent protein kinase 1 | chr5:1417015-1419877 REVERSE LENGTH=610	609	610	0	100.2	91.3	93.8
Rsa1.0_00123.1.g5950.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00123.1.g5951.t1	ref|XP_002873172.1| hypothetical protein ARALYDRAFT_487270 [Arabidopsis lyrata subsp. lyrata] gi|297319009|gb|EFH49431.1| hypothetical protein ARALYDRAFT_487270 [Arabidopsis lyrata subsp. lyrata]	758	770	0	101.6	79.9	86.3	hypothetical protein ARALYDRAFT_487270	gbpln	Arabidopsis lyrata	AT5G04860.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11760.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1411760-1414459 REVERSE LENGTH=782	758	782	0	103.2	80.7	88.3
Rsa1.0_00123.1.g5952.t1	gb|EOA21471.1| hypothetical protein CARUB_v10001863mg [Capsella rubella]	238	235	1.00E-120	98.7	92.4	95.8	hypothetical protein CARUB_v10001863mg	gbpln	Capsella rubella	AT5G04850.1 | Symbols: VPS60.2 | SNF7 family protein | chr5:1408246-1409806 REVERSE LENGTH=235	238	235	1.00E-120	98.7	90.8	95.4
Rsa1.0_00123.1.g5953.t3	dbj|BAB08988.1| unnamed protein product [Arabidopsis thaliana]	354	342	1.00E-134	96.6	75.1	82.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G04840.1 | Symbols: | bZIP protein | chr5:1406005-1407648 FORWARD LENGTH=307	354	307	1.00E-129	86.7	72.9	78.5
Rsa1.0_00123.1.g5954.t1	gb|EOA21611.1| hypothetical protein CARUB_v10002023mg [Capsella rubella]	193	194	1.00E-93	100.5	86.5	91.7	hypothetical protein CARUB_v10002023mg	gbpln	Capsella rubella	AT5G04830.2 | Symbols: | Nuclear transport factor 2 (NTF2) family protein | chr5:1402294-1403671 REVERSE LENGTH=178	193	178	3.00E-89	92.2	79.3	83.9
Rsa1.0_00123.1.g5955.t1	ref|NP_196102.1| ovate family protein 13 [Arabidopsis thaliana] gi|9758457|dbj|BAB08986.1| unnamed protein product [Arabidopsis thaliana] gi|17529322|gb|AAL38888.1| unknown protein [Arabidopsis thaliana] gi|21436369|gb|AAM51354.1| unknown protein [Arabidopsis thaliana] gi|21536974|gb|AAM61315.1| unknown [Arabidopsis thaliana] gi|332003407|gb|AED90790.1| ovate family protein 13 [Arabidopsis thaliana]	264	260	1.00E-107	98.5	81.4	87.1	ovate family protein 13	gbpln	Arabidopsis thaliana	AT5G04820.1 | Symbols: ATOFP13, OFP13 | ovate family protein 13 | chr5:1399685-1400467 FORWARD LENGTH=260	264	260	1.00E-109	98.5	81.4	87.1
Rsa1.0_00123.1.g5956.t1	ref|XP_002892396.1| hypothetical protein ARALYDRAFT_470757 [Arabidopsis lyrata subsp. lyrata] gi|297338238|gb|EFH68655.1| hypothetical protein ARALYDRAFT_470757 [Arabidopsis lyrata subsp. lyrata]	170	481	1.00E-63	282.9	72.4	82.4	hypothetical protein ARALYDRAFT_470757	gbpln	Arabidopsis lyrata	AT1G07360.1 | Symbols: | CCCH-type zinc fingerfamily protein with RNA-binding domain | chr1:2260562-2262795 REVERSE LENGTH=481	170	481	5.00E-66	282.9	72.4	82.4
Rsa1.0_00123.1.g5957.t1	ref|XP_002871115.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297316952|gb|EFH47374.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	947	942	0	99.5	88.4	91.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G04810.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:1390049-1393760 FORWARD LENGTH=952	947	952	0	100.5	87.8	91.6
Rsa1.0_00123.1.g5958.t1	ref|XP_002871114.1| 40S ribosomal protein S17 [Arabidopsis lyrata subsp. lyrata] gi|297316951|gb|EFH47373.1| 40S ribosomal protein S17 [Arabidopsis lyrata subsp. lyrata]	136	138	7.00E-65	101.5	92.6	94.1	40S ribosomal protein S17	gbpln	Arabidopsis lyrata	AT5G04800.4 | Symbols: | Ribosomal S17 family protein | chr5:1389217-1389642 FORWARD LENGTH=141	136	141	8.00E-65	103.7	91.2	93.4
Rsa1.0_00123.1.g5959.t1	gb|EOA21222.1| hypothetical protein CARUB_v10001570mg [Capsella rubella]	501	300	1.00E-134	59.9	48.1	50.9	hypothetical protein CARUB_v10001570mg	gbpln	Capsella rubella	AT5G04740.1 | Symbols: | ACT domain-containing protein | chr5:1368713-1371391 REVERSE LENGTH=301	501	301	1.00E-136	60.1	48.3	51.1
Rsa1.0_00123.1.g5960.t1	gb|EOA19982.1| hypothetical protein CARUB_v10000246mg [Capsella rubella]	804	812	0	101.0	80.6	89.9	hypothetical protein CARUB_v10000246mg	gbpln	Capsella rubella	AT5G04720.1 | Symbols: ADR1-L2 | ADR1-like 2 | chr5:1360748-1363665 FORWARD LENGTH=811	804	811	0	100.9	77.1	88.8
Rsa1.0_00123.1.g5961.t1	gb|EOA20384.1| hypothetical protein CARUB_v10000697mg [Capsella rubella]	525	529	0	100.8	91.0	94.9	hypothetical protein CARUB_v10000697mg	gbpln	Capsella rubella	AT5G04710.1 | Symbols: | Zn-dependent exopeptidases superfamily protein | chr5:1357273-1360128 REVERSE LENGTH=526	525	526	0	100.2	91.6	95.0

Rsa1.0_00123.1.g5962.t1	gb|EOA24093.1| hypothetical protein CARUB_v10017323mg, partial [Capsella rubella]	384	423	7.00E−91	110.2	51.6	68.0	hypothetical protein CARUB_v10017323mg, partial	gbpln	Capsella rubella	AT3G26010.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:9511901−9513145 FORWARD LENGTH=414	384	414	5.00E−93	107.8	51.6	68.5
Rsa1.0_00123.1.g5963.t1	ref|NP_189230.1| F−box protein [Arabidopsis thaliana] gi|75274193|sp|Q9LU90.1|FB188_ARATH RecName: Full=F−box protein At3g26010 gi|9279606|dbj|BAB01064.1| unnamed protein product [Arabidopsis thaliana] gi|91806483|gb|ABE65969.1| F−box family protein [Arabidopsis thaliana] gi|332643580|gb|AEE77101.1| F−box protein [Arabidopsis thaliana]	423	414	1.00E−112	97.9	52.0	68.1	F−box protein	gbpln	Arabidopsis thaliana	AT3G26010.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:9511901−9513145 FORWARD LENGTH=414	423	414	1.00E−115	97.9	52.0	68.1
Rsa1.0_00123.1.g5964.t1	ref|NP_189230.1| F−box protein [Arabidopsis thaliana] gi|75274193|sp|Q9LU90.1|FB188_ARATH RecName: Full=F−box protein At3g26010 gi|9279606|dbj|BAB01064.1| unnamed protein product [Arabidopsis thaliana] gi|91806483|gb|ABE65969.1| F−box family protein [Arabidopsis thaliana] gi|332643580|gb|AEE77101.1| F−box protein [Arabidopsis thaliana]	381	414	4.00E−93	108.7	53.3	68.5	F−box protein	gbpln	Arabidopsis thaliana	AT3G26010.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:9511901−9513145 FORWARD LENGTH=414	381	414	9.00E−96	108.7	53.3	68.5
Rsa1.0_00123.1.g5965.t2	ref|NP_187447.1| O−fucosyltransferase−like protein [Arabidopsis thaliana] gi|6648202|gb|AAF21200.1|AC013483_24 putative auxin−independent growth promoter [Arabidopsis thaliana] gi|332641096|gb|AEE74617.1| O−fucosyltransferase−like protein [Arabidopsis thaliana]	170	579	1.00E−22	340.6	31.2	34.7	O−fucosyltransferase−like protein	gbpln	Arabidopsis thaliana	AT3G07900.1 | Symbols: | O−fucosyltransferase family protein | chr3:2520826−2523008 FORWARD LENGTH=579	170	579	4.00E−25	340.6	31.2	34.7
Rsa1.0_00123.1.g5966.t1	ref|NP_568384.1| uncharacterized protein [Arabidopsis thaliana] gi|21593922|gb|AAM65887.1| unknown [Arabidopsis thaliana] gi|26453290|dbj|BAC43718.1| unknown protein [Arabidopsis thaliana] gi|28416873|gb|AAO42967.1| At5g19875 [Arabidopsis thaliana] gi|332005377|gb|AED92760.1| uncharacterized protein AT5G19875 [Arabidopsis thaliana]	123	123	6.00E−48	100.0	80.5	91.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G19875.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: endomembrane system; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G31940.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:6718412−6718783 FORWARD LENGTH=123	123	123	1.00E−50	100.0	80.5	91.9
Rsa1.0_00123.1.g5967.t1	gb|AAM60837.1| peroxidase [Arabidopsis thaliana]	344	329	1.00E−166	95.6	84.9	90.1	peroxidase	gbpln	Arabidopsis thaliana	AT5G19880.1 | Symbols: | Peroxidase superfamily protein | chr5:6720578−6722411 REVERSE LENGTH=329	344	329	1.00E−167	95.6	84.6	89.8
Rsa1.0_00123.1.g5968.t1	sp|Q42517.1|PERN_ARMRU RecName: Full=Peroxidase N; AltName: Full=Neutral peroxidase; Flags: Precursor gi|16096|emb|CAA40796.1| peroxidase [Armoracia rusticana]	324	327	1.00E−163	100.9	86.4	92.3	RecName: Full=Peroxidase N; AltName: Full=Neutral peroxidase; Flags: Precursor gi|16096|emb|CAA40796.1| peroxidase	gbpln	Armoracia rusticana	AT5G19890.1 | Symbols: | Peroxidase superfamily protein | chr5:6724372−6725877 REVERSE LENGTH=328	324	328	1.00E−163	101.2	85.2	92.6
Rsa1.0_00123.1.g5969.t1	ref|NP_197490.1| putative PRLI−interacting factor [Arabidopsis thaliana] gi|222422845|dbj|BAH19409.1| AT5G19900 [Arabidopsis thaliana] gi|332005380|gb|AED92763.1| putative PRLI−interacting factor [Arabidopsis thaliana]	466	494	1.00E−175	106.0	76.8	84.3	putative PRLI−interacting factor	gbpln	Arabidopsis thaliana	AT5G19900.1 | Symbols: | PRLI−interacting factor, putative | chr5:6728561−6730045 REVERSE LENGTH=494	466	494	1.00E−178	106.0	76.8	84.3
Rsa1.0_00123.1.g5970.t2	gb|EOA20119.1| hypothetical protein CARUB_v10000397mg [Capsella rubella]	828	668	0	80.7	53.9	59.8	hypothetical protein CARUB_v10000397mg	gbpln	Capsella rubella	AT5G19920.1 | Symbols: | Transducin/WD40 repeat−like superfamily protein | chr5:6733622−6737266 REVERSE LENGTH=656	828	656	0	79.2	42.6	46.3
Rsa1.0_00123.1.g5971.t18	ref|NP_568386.1| uncharacterized protein [Arabidopsis thaliana] gi|334187781|ref|NP_001190343.1| uncharacterized protein [Arabidopsis thaliana] gi|110738248|dbj|BAF01053.1| hypothetical protein [Arabidopsis thaliana] gi|332005384|gb|AED92767.1| uncharacterized protein AT5G19930 [Arabidopsis thaliana] gi|332005385|gb|AED92768.1| uncharacterized protein AT5G19930 [Arabidopsis thaliana]	667	288	1.00E−133	43.2	37.5	40.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G19930.2 | Symbols: | Protein of unknown function DUF92, transmembrane | chr5:6737872−6739283 REVERSE LENGTH=288	667	288	1.00E−136	43.2	37.5	40.3

Rsa1.0_00123.1.g5972.t1	gb|EOA21452.1| hypothetical protein CARUB_v10001836mg [Capsella rubella]	228	241	1.00E-108	105.7	86.8	92.5	hypothetical protein CARUB_v10001836mg	gbpln	Capsella rubella	AT5G19940.1 | Symbols: | Plastid-lipid associated protein PAP / fibrillin family protein | chr5:6739693-6740661 FORWARD LENGTH=239	228	239	1.00E-107	104.8	84.6	90.4
Rsa1.0_00123.1.g5973.t1	ref|XP_002873975.1| hypothetical protein ARALYDRAFT_488891 [Arabidopsis lyrata subsp. lyrata] gi|297319812|gb|EFH50234.1| hypothetical protein ARALYDRAFT_488891 [Arabidopsis lyrata subsp. lyrata]	448	445	0	99.3	74.1	81.5	hypothetical protein ARALYDRAFT_488891	gbpln	Arabidopsis lyrata	AT5G19950.2 | Symbols: | Domain of unknown function (DUF1767) | chr5:6741163-6743702 REVERSE LENGTH=443	448	443	0	98.9	73.4	81.3
Rsa1.0_00123.1.g5974.t1	gb|EOA21005.1| hypothetical protein CARUB_v10001340mg [Capsella rubella]	341	344	1.00E-155	100.9	83.6	88.6	hypothetical protein CARUB_v10001340mg	gbpln	Capsella rubella	AT5G19980.1 | Symbols: GONST4 | golgi nucleotide sugar transporter 4 | chr5:6749907-6750932 REVERSE LENGTH=341	341	341	1.00E-153	100.0	79.5	86.8
Rsa1.0_00123.1.g5975.t1	ref|NP_568389.1| regulatory particle triple-A ATPase 6A [Arabidopsis thaliana] gi|75168996|sp|Q9C5U3.1|PRS8A_ARATH RecName: Full=26S protease regulatory subunit 8 homolog A; AltName: Full=26S proteasome AAA-ATPase subunit RPT6a; AltName: Full=26S proteasome subunit 8 homolog A; AltName: Full=Regulatory particle triple-A ATPase subunit 6a gi|13537115|dbj|BAB40755.1| AtSUG1 [Arabidopsis thaliana] gi|17473854|gb|AAL38350.1| unknown protein [Arabidopsis thaliana] gi|32306505|gb|AAP78936.1| At5g19990 [Arabidopsis thaliana] gi|332005394|gb|AED92777.1| regulatory particle triple-A ATPase 6A [Arabidopsis thaliana]	420	419	0	99.8	98.6	99.3	regulatory particle triple-A ATPase 6A	gbpln	Arabidopsis thaliana	AT5G19990.1 | Symbols: RPT6A, ATSUG1 | regulatory particle triple-A ATPase 6A | chr5:6752144-6754918 FORWARD LENGTH=419	420	419	0	99.8	98.6	99.3
Rsa1.0_00123.1.g5976.t1	gb|ABD17866.1| etiolation seedling like-RAN2 small Ras GTP-binding nuclear protein [Brassica napus]	221	221	1.00E-127	100.0	98.6	99.5	etiolation seedling like-RAN2 small Ras GTP-binding nuclear protein	gbpln	Brassica napus	AT5G20010.1 | Symbols: RAN-1, RAN1, ATRAN1 | RAS-related nuclear protein-1 | chr5:6760364-6761747 FORWARD LENGTH=221	221	221	1.00E-126	100.0	95.0	98.2
Rsa1.0_00123.1.g5977.t1	ref|XP_002871925.1| SPX domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317762|gb|EFH48184.1| SPX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	255	257	1.00E-114	100.8	81.6	89.0	SPX domain-containing protein	gbpln	Arabidopsis lyrata	AT5G20150.1 | Symbols: ATSPX1, SPX1 | SPX domain gene 1 | chr5:6802429-6803367 FORWARD LENGTH=256	255	256	1.00E-116	100.4	81.6	89.8
Rsa1.0_00123.1.g5978.t1	ref|NP_680174.2| uncharacterized protein [Arabidopsis thaliana] gi|297812203|ref|XP_002873985.1| hypothetical protein ARALYDRAFT_488920 [Arabidopsis lyrata subsp. lyrata] gi|48310058|gb|AAT41745.1| At5g20165 [Arabidopsis thaliana] gi|50198835|gb|AAT70449.1| At5g20165 [Arabidopsis thaliana] gi|62318608|dbj|BAD95036.1| putative protein [Arabidopsis thaliana] gi|297319822|gb|EFH50244.1| hypothetical protein ARALYDRAFT_488920 [Arabidopsis lyrata subsp. lyrata] gi|332005422|gb|AED92805.1| uncharacterized protein AT5G20165 [Arabidopsis thaliana]	158	70	2.00E-32	44.3	42.4	43.0	uncharacterized protein	gbpln	Arabidopsis lyrata	AT5G20165.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1242 (InterPro:IPR009653); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:6805803-6806730 REVERSE LENGTH=70	158	70	6.00E-35	44.3	42.4	43.0
Rsa1.0_00123.1.g5979.t1	ref|XP_002871927.1| hypothetical protein ARALYDRAFT_488924 [Arabidopsis lyrata subsp. lyrata] gi|297317764|gb|EFH48186.1| hypothetical protein ARALYDRAFT_488924 [Arabidopsis lyrata subsp. lyrata]	286	287	1.00E-104	100.3	81.8	87.8	hypothetical protein ARALYDRAFT_488924	gbpln	Arabidopsis lyrata	AT5G20190.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:6814093-6815171 FORWARD LENGTH=290	286	290	1.00E-106	101.4	81.8	88.8
Rsa1.0_00123.1.g5980.t1	emb|CAN61043.1| hypothetical protein VITISV_037528 [Vitis vinifera]	83	183	1.00E-12	220.5	42.2	47.0	hypothetical protein VITISV_037528	gbpln	Vitis vinifera	AT4G26370.2 | Symbols: | antitermination NusB domain-containing protein | chr4:13334766-13336153 REVERSE LENGTH=248	83	248	4.00E-14	298.8	50.6	51.8
Rsa1.0_00123.1.g5981.t16	ref|XP_002871928.1| hypothetical protein ARALYDRAFT_488925 [Arabidopsis lyrata subsp. lyrata] gi|297317765|gb|EFH48187.1| hypothetical protein ARALYDRAFT_488925 [Arabidopsis lyrata subsp. lyrata]	745	762	0	102.3	70.5	80.7	hypothetical protein ARALYDRAFT_488925	gbpln	Arabidopsis lyrata	AT5G20200.1 | Symbols: | nucleoporin-related | chr5:6816776-6821620 FORWARD LENGTH=762	745	762	0	102.3	69.3	79.7

Rsa1.0_00123.1.g5982.t1	dbj|BAJ34551.1| unnamed protein product [Thellungiella halophila]	177	194	3.00E-61	109.6	76.3	83.6	unnamed protein product	----	----	AT5G20230.1 | Symbols: ATBCB, BCB, SAG14 | blue-copper-binding protein | chr5:6826626-6827408 FORWARD LENGTH=196	177	196	1.00E-62	110.7	76.3	84.7
Rsa1.0_00123.1.g5983.t1	gb|AAY63867.1| PISTILLATA [Brassica juncea]	203	208	1.00E-107	102.5	94.1	97.0	PISTILLATA	gbpln	Brassica juncea	AT5G20240.1 | Symbols: PI | K-box region and MADS-box transcription factor family protein | chr5:6829203-6831208 FORWARD LENGTH=208	203	208	1.00E-108	102.5	92.6	96.1
Rsa1.0_00123.1.g5984.t1	ref|NP_001190347.1| putative galactinol--sucrose galactosyltransferase 6 [Arabidopsis thaliana] gi|19699067|gb|AAL90901.1| AT5g20250/F5O24_140 [Arabidopsis thaliana] gi|23308457|gb|AAN18198.1| At5g20250/F5O24_140 [Arabidopsis thaliana] gi|110742681|dbj|BAE99252.1| seed imbitition protein-like [Arabidopsis thaliana] gi|332005438|gb|AED92821.1| putative galactinol--sucrose galactosyltransferase 6 [Arabidopsis thaliana]	870	844	0	97.0	81.3	86.9	putative galactinol--sucrose galactosyltransferase 6	gbpln	Arabidopsis thaliana	AT5G20250.4 | Symbols: DIN10 | Raffinose synthase family protein | chr5:6833730-6836635 FORWARD LENGTH=844	870	844	0	97.0	81.3	86.9
Rsa1.0_00123.1.g5985.t1	sp|Q3E9A4.3|GLYT5_ARATH RecName: Full=Probable glycosyltransferase At5g20260	1069	466	0	43.6	27.4	30.2	RecName: Full=Probable glycosyltransferase At5g20260	----	----	AT5G20260.1 | Symbols: | Exostosin family protein | chr5:6836806-6839532 REVERSE LENGTH=458	1069	458	0	42.8	27.4	30.2
Rsa1.0_00123.1.g5986.t1	sp|Q3E9A4.3|GLYT5_ARATH RecName: Full=Probable glycosyltransferase At5g20260	118	466	3.00E-33	394.9	64.4	70.3	RecName: Full=Probable glycosyltransferase At5g20260	----	----	AT5G20260.1 | Symbols: | Exostosin family protein | chr5:6836806-6839532 REVERSE LENGTH=458	118	458	6.00E-36	388.1	64.4	70.3
Rsa1.0_00123.1.g5987.t1	dbj|BAJ33817.1| unnamed protein product [Thellungiella halophila]	334	331	1.00E-173	99.1	91.0	94.6	unnamed protein product	----	----	AT5G20270.1 | Symbols: HHP1 | heptahelical transmembrane protein1 | chr5:6841025-6842656 REVERSE LENGTH=332	334	332	1.00E-174	99.4	87.1	91.6
Rsa1.0_00123.1.g5988.t1	ref|XP_002873988.1| ATSPS1F [Arabidopsis lyrata subsp. lyrata] gi|297319825|gb|EFH50247.1| ATSPS1F [Arabidopsis lyrata subsp. lyrata]	1045	1045	0	100.0	94.4	97.5	ATSPS1F	gbpln	Arabidopsis lyrata	AT5G20280.1 | Symbols: ATSPS1F, SPS1F | sucrose phosphate synthase 1F | chr5:6844994-6849997 REVERSE LENGTH=1043	1045	1043	0	99.8	94.4	97.3
Rsa1.0_00123.1.g5989.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00123.1.g5990.t1	gb|EOA13427.1| hypothetical protein CARUB_v10026466mg [Capsella rubella]	144	423	5.00E-15	293.8	36.1	44.4	hypothetical protein CARUB_v10026466mg	gbpln	Capsella rubella	AT5G62510.1 | Symbols: | F-box family protein | chr5:25095373-25096635 REVERSE LENGTH=420	144	420	4.00E-15	291.7	33.3	45.8
Rsa1.0_00123.1.g5991.t1	ref|NP_001105391.1| 40S ribosomal protein S8 [Zea mays] gi|6226702|sp|Q08069.2|RS8_MAIZE RecName: Full=40S ribosomal protein S8 gi|1498053|gb|AAB06330.1| ribosomal protein S8 [Zea mays] gi|194692698|gb|ACF80433.1| unknown [Zea mays] gi|195605614|gb|ACG24637.1| 40S ribosomal protein S8 [Zea mays] gi|413926193|gb|AFW66125.1| putative ribosomal protein S8e family protein [Zea mays] gi|413926197|gb|AFW66129.1| putative ribosomal protein S8e family protein [Zea mays] gi|413926198|gb|AFW66130.1| putative ribosomal protein S8e family protein [Zea mays] gi|413926206|gb|AFW66138.1| putative ribosomal protein S8e family protein [Zea mays] gi|413926210|gb|AFW66142.1| putative ribosomal protein S8e family protein [Zea mays]	226	221	1.00E-104	97.8	82.3	90.3	40S ribosomal protein S8	gbenv/gbpln	Zea mays	AT5G59240.1 | Symbols: | Ribosomal protein S8e family protein | chr5:23902626-23903670 REVERSE LENGTH=210	226	210	2.00E-98	92.9	77.4	82.7
Rsa1.0_00123.1.g5992.t1	ref|XP_002873990.1| hypothetical protein ARALYDRAFT_910069 [Arabidopsis lyrata subsp. lyrata] gi|297319827|gb|EFH50249.1| hypothetical protein ARALYDRAFT_910069 [Arabidopsis lyrata subsp. lyrata]	793	786	0	99.1	84.4	90.8	hypothetical protein ARALYDRAFT_910069	gbpln	Arabidopsis lyrata	AT5G20300.2 | Symbols: | Avirulence induced gene (AIG1) family protein | chr5:6853544-6856332 REVERSE LENGTH=793	793	793	0	100.0	83.6	89.0
Rsa1.0_00123.1.g5993.t1	gb|EOA22284.1| hypothetical protein CARUB_v10002882mg [Capsella rubella]	376	413	1.00E-153	109.8	75.5	84.0	hypothetical protein CARUB_v10002882mg	gbpln	Capsella rubella	AT5G20310.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr5:6857553-6859001 FORWARD LENGTH=394	376	394	1.00E-138	104.8	70.5	80.1
Rsa1.0_00123.1.g5994.t23	ref|XP_002873991.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319828|gb|EFH50250.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1689	1693	0	100.2	76.8	84.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G20320.1 | Symbols: DCL4, ATDCL4 | dicer-like 4 | chr5:6859571-6869068 REVERSE LENGTH=1702	1689	1702	0	100.8	76.9	84.7

Rsa1.0_00124.1.g5995.t1	gb|ABW17183.1| profilin [Raphanus sativus] gi|158122106|gb|ABW17189.1| profilin [Brassica juncea var. multiceps]	134	134	5.00E-73	100.0	99.3	100.0	profilin	gbpln	Brassica juncea	AT4G29340.1 | Symbols: PRF4 | profilin 4 | chr4:14447718-14448467 FORWARD LENGTH=134	134	134	3.00E-73	100.0	96.3	97.8
Rsa1.0_00124.1.g5996.t1	ref|XP_002869435.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297315271|gb|EFH45694.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	407	387	1.00E-120	95.1	58.7	71.7	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G29370.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:14455602-14456738 FORWARD LENGTH=378	407	378	1.00E-104	92.9	53.1	67.3
Rsa1.0_00124.1.g5997.t1	ref|XP_002867410.1| 60S ribosomal protein L28 [Arabidopsis lyrata subsp. lyrata] gi|297313246|gb|EFH43669.1| 60S ribosomal protein L28 [Arabidopsis lyrata subsp. lyrata]	143	143	2.00E-72	100.0	93.7	96.5	60S ribosomal protein L28	gbpln	Arabidopsis lyrata	AT4G29410.2 | Symbols: | Ribosomal L28e protein family | chr4:14468439-14469964 REVERSE LENGTH=143	143	143	2.00E-72	100.0	90.2	95.1
Rsa1.0_00124.1.g5998.t1	ref|XP_002867404.1| mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297313240|gb|EFH43663.1| mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata]	122	122	3.00E-60	100.0	92.6	95.9	mitochondrial ATP synthase g subunit family protein	gbpln	Arabidopsis lyrata	AT4G29480.1 | Symbols: | Mitochondrial ATP synthase subunit G protein | chr4:14486265-14487257 REVERSE LENGTH=122	122	122	6.00E-63	100.0	92.6	95.9
Rsa1.0_00124.1.g5999.t1	gb|EOA18714.1| hypothetical protein CARUB_v10007292mg [Capsella rubella]	375	386	0	102.9	92.5	95.7	hypothetical protein CARUB_v10007292mg	gbpln	Capsella rubella	AT4G29510.1 | Symbols: ATPRMT11, PRMT11, ATPRMT1B, PRMT1B | arginine methyltransferase 11 | chr4:14491739-14493752 FORWARD LENGTH=390	375	390	0	104.0	91.7	95.2
Rsa1.0_00124.1.g6000.t1	gb|EOA17036.1| hypothetical protein CARUB_v10005279mg [Capsella rubella]	311	317	1.00E-153	101.9	87.8	92.3	hypothetical protein CARUB_v10005279mg	gbpln	Capsella rubella	AT4G29590.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:14512736-14514404 REVERSE LENGTH=317	311	317	1.00E-154	101.9	87.8	92.3
Rsa1.0_00124.1.g6001.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00124.1.g6002.t1	gb|EOA31108.1| hypothetical protein CARUB_v10014260mg [Capsella rubella]	318	303	1.00E-118	95.3	70.4	79.9	hypothetical protein CARUB_v10014260mg	gbpln	Capsella rubella	AT2G19570.1 | Symbols: CDA1, AT-CDA1, DESZ | cytidine deaminase 1 | chr2:8470598-8471503 REVERSE LENGTH=301	318	301	1.00E-121	94.7	69.8	79.6
Rsa1.0_00124.1.g6003.t1	gb|EOA17360.1| hypothetical protein CARUB_v10005641mg [Capsella rubella]	244	235	1.00E-97	96.3	81.1	86.1	hypothetical protein CARUB_v10005641mg	gbpln	Capsella rubella	AT4G29670.1 | Symbols: ACHT2 | atypical CYS HIS rich thioredoxin 2 | chr4:14535772-14537108 REVERSE LENGTH=235	244	235	7.00E-96	96.3	78.3	85.2
Rsa1.0_00124.1.g6004.t1	ref|NP_194697.1| alkaline-phosphatase-like protein [Arabidopsis thaliana] gi|5123562|emb|CAB45328.1| nucleotide pyrophosphatase-like protein [Arabidopsis thaliana] gi|7269867|emb|CAB79726.1| nucleotide pyrophosphatase-like protein [Arabidopsis thaliana] gi|225898829|dbj|BAH30545.1| hypothetical protein [Arabidopsis thaliana] gi|332660261|gb|AEE85661.1| alkaline-phosphatase-like protein [Arabidopsis thaliana]	467	496	0	106.2	85.0	92.5	alkaline-phosphatase-like protein	gbpln	Arabidopsis thaliana	AT4G29680.1 | Symbols: | Alkaline-phosphatase-like family protein | chr4:14538067-14539557 REVERSE LENGTH=496	467	496	0	106.2	85.0	92.5
Rsa1.0_00124.1.g6005.t1	ref|XP_002867392.1| ATPAO5 [Arabidopsis lyrata subsp. lyrata] gi|297313228|gb|EFH43651.1| ATPAO5 [Arabidopsis lyrata subsp. lyrata]	521	536	0	102.9	83.9	91.7	ATPAO5	gbpln	Arabidopsis lyrata	AT4G29720.1 | Symbols: ATPAO5, PAO5 | polyamine oxidase 5 | chr4:14553456-14555057 REVERSE LENGTH=533	521	533	0	102.3	83.9	91.2
Rsa1.0_00124.1.g6006.t2	#	#	#	#	#	#	#	–	----	----	AT4G29735.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0197 (InterPro:IPR007915); Has 190 Blast hits to 190 proteins in 72 species: Archae - 0; Bacteria - 0; Metazoa - 133; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr4:14562962-14564277 REVERSE LENGTH=98	35	98	1.00E-10	280.0	85.7	94.3
Rsa1.0_00124.1.g6007.t1	ref|NP_849470.1| cytokinin dehydrogenase 4 [Arabidopsis thaliana] gi|332660270|gb|AEE85670.1| cytokinin dehydrogenase 4 [Arabidopsis thaliana]	412	428	0	103.9	87.6	92.5	cytokinin dehydrogenase 4	gbpln	Arabidopsis thaliana	AT4G29740.1 | Symbols: CKX4, ATCKX4 | cytokinin oxidase 4 | chr4:14566351-14568754 FORWARD LENGTH=428	412	428	0	103.9	87.6	92.5
Rsa1.0_00124.1.g6008.t1	ref|XP_002880655.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297326494|gb|EFH56914.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	412	462	0	112.1	83.5	92.7	transferase family protein	gbpln	Arabidopsis lyrata	AT2G25150.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr2:10702582-10704266 REVERSE LENGTH=461	412	461	0	111.9	82.0	91.7
Rsa1.0_00124.1.g6009.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00124.1.g6010.t1	gb|EOA28459.1| hypothetical protein CARUB_v10024668mg [Capsella rubella]	780	840	0	107.7	79.6	87.7	hypothetical protein CARUB_v10024668mg	gbpln	Capsella rubella	AT4G29750.1 | Symbols: | CRS1 / YhbY (CRM) domain-containing protein | chr4:14569728-14572962 FORWARD LENGTH=841	780	841	0	107.8	79.5	86.7
Rsa1.0_00124.1.g6011.t2	ref|XP_002880655.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297326494|gb|EFH56914.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	455	462	0	101.5	79.6	89.0	transferase family protein	gbpln	Arabidopsis lyrata	AT2G25150.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr2:10702582-10704266 REVERSE LENGTH=461	455	461	0	101.3	78.5	87.9
Rsa1.0_00124.1.g6012.t1	ref|XP_002869413.1| hypothetical protein ARALYDRAFT_913517 [Arabidopsis lyrata subsp. lyrata] gi|297315249|gb|EFH45672.1| hypothetical protein ARALYDRAFT_913517 [Arabidopsis lyrata subsp. lyrata]	462	461	0	99.8	78.1	85.7	hypothetical protein ARALYDRAFT_913517	gbpln	Arabidopsis lyrata	AT2G25150.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr2:10702582-10704266 REVERSE LENGTH=461	462	461	1.00E-158	99.8	61.0	75.5
Rsa1.0_00124.1.g6013.t1	ref|NP_567834.2| uncharacterized protein [Arabidopsis thaliana] gi|27754582|gb|AAO22738.1| unknown protein [Arabidopsis thaliana] gi|28973634|gb|AAO64139.1| unknown protein [Arabidopsis thaliana] gi|332660275|gb|AEE85675.1| uncharacterized protein AT4G29780 [Arabidopsis thaliana]	496	540	0	108.9	82.3	89.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G29780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12010.1); Has 945 Blast hits to 944 proteins in 87 species: Archae - 0; Bacteria - 0; Metazoa - 519; Fungi - 43; Plants - 365; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr4:14579859-14581481 FORWARD LENGTH=540	496	540	0	108.9	82.3	89.7
Rsa1.0_00124.1.g6014.t1	ref|XP_002869409.1| hypothetical protein ARALYDRAFT_491781 [Arabidopsis lyrata subsp. lyrata] gi|297315245|gb|EFH45668.1| hypothetical protein ARALYDRAFT_491781 [Arabidopsis lyrata subsp. lyrata]	1234	1210	0	98.1	83.5	89.1	hypothetical protein ARALYDRAFT_491781	gbpln	Arabidopsis lyrata	AT4G29790.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G19390.1); Has 538 Blast hits to 357 proteins in 124 species: Archae - 0; Bacteria - 74; Metazoa - 109; Fungi - 58; Plants - 105; Viruses - 2; Other Eukaryotes - 190 (source: NCBI BLink). | chr4:14584228-14590123 FORWARD LENGTH=1211	1234	1211	0	98.1	83.1	88.7
Rsa1.0_00124.1.g6015.t1	ref|XP_002869436.1| hypothetical protein ARALYDRAFT_913570 [Arabidopsis lyrata subsp. lyrata] gi|297315272|gb|EFH45695.1| hypothetical protein ARALYDRAFT_913570 [Arabidopsis lyrata subsp. lyrata]	399	386	5.00E-91	96.7	50.9	65.2	hypothetical protein ARALYDRAFT_913570	gbpln	Arabidopsis lyrata	AT5G39560.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:15841885-15843096 REVERSE LENGTH=403	399	403	3.00E-68	101.0	45.1	64.7
Rsa1.0_00124.1.g6016.t1	ref|NP_194714.1| uncharacterized protein [Arabidopsis thaliana] gi|4914409|emb|CAB43660.1| putative protein [Arabidopsis thaliana] gi|7269884|emb|CAB79743.1| putative protein [Arabidopsis thaliana] gi|88900368|gb|ABD57496.1| At4g29850 [Arabidopsis thaliana] gi|332660285|gb|AEE85685.1| uncharacterized protein AT4G29850 [Arabidopsis thaliana]	64	103	3.00E-27	160.9	93.8	96.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G29850.1 | Symbols: | Eukaryotic protein of unknown function (DUF872) | chr4:14601818-14602874 REVERSE LENGTH=103	64	103	5.00E-30	160.9	93.8	96.9
Rsa1.0_00124.1.g6017.t1	ref|XP_002869407.1| hypothetical protein ARALYDRAFT_491771 [Arabidopsis lyrata subsp. lyrata] gi|297315243|gb|EFH45666.1| hypothetical protein ARALYDRAFT_491771 [Arabidopsis lyrata subsp. lyrata]	161	173	3.00E-78	107.5	88.8	96.9	hypothetical protein ARALYDRAFT_491771	gbpln	Arabidopsis lyrata	AT4G29870.1 | Symbols: | Oligosaccharyltransferase complex/magnesium transporter family protein | chr4:14606012-14606530 FORWARD LENGTH=172	161	172	8.00E-79	106.8	87.0	94.4
Rsa1.0_00124.1.g6018.t1	ref|XP_002867383.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297313219|gb|EFH43642.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	368	369	1.00E-168	100.3	86.4	92.1	protein binding protein	gbpln	Arabidopsis lyrata	AT4G29880.1 | Symbols: PIRL7 | plant intracellular ras group-related LRR 7 | chr4:14607078-14608379 REVERSE LENGTH=373	368	373	1.00E-167	101.4	85.6	92.1
Rsa1.0_00124.1.g6019.t1	ref|XP_002869406.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315242|gb|EFH45665.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	453	422	0	93.2	75.5	83.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G29890.1 | Symbols: | choline monooxygenase, putative (CMO-like) | chr4:14608868-14610905 FORWARD LENGTH=422	453	422	0	93.2	74.2	82.6
Rsa1.0_00124.1.g6020.t1	gb|EOA18057.1| hypothetical protein CARUB_v10006503mg [Capsella rubella]	1062	1070	0	100.8	93.6	96.6	hypothetical protein CARUB_v10006503mg	gbpln	Capsella rubella	AT4G29900.1 | Symbols: ACA10, CIF1, ATACA10 | autoinhibited Ca(2+)-ATPase 10 | chr4:14611225-14618775 REVERSE LENGTH=1069	1062	1069	0	100.7	93.6	96.5
Rsa1.0_00124.1.g6021.t1	emb|CAN77253.1| hypothetical protein VITISV_020397 [Vitis vinifera]	112	215	1.00E-44	192.0	74.1	86.6	hypothetical protein VITISV_020397	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00124.1.g6022.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	744	1274	0	171.2	46.9	63.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	744	575	2.00E-68	77.3	23.0	36.0

<table>
<tr><td>Rsa1.0_00124.1.g6023.t1</td><td>gb|EOA17787.1| hypothetical protein CARUB_v10006180mg [Capsella rubella]</td><td>67</td><td>67</td><td>8.00E-30</td><td>100.0</td><td>94.0</td><td>97.0</td><td>hypothetical protein CARUB_v10006180mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G29905.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G57123.1); Has 73 Blast hits to 73 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14627227-14627430 REVERSE LENGTH=67</td><td>67</td><td>67</td><td>2.00E-31</td><td>100.0</td><td>91.0</td><td>95.5</td></tr>
<tr><td>Rsa1.0_00124.1.g6024.t1</td><td>ref|NP_194722.2| transcription factor bHLH27 [Arabidopsis thaliana] gi|26450533|dbj|BAC42379.1| putative bHLH transcription factor bHLH027 [Arabidopsis thaliana] gi|29028850|gb|AAO64804.1| At4g29930 [Arabidopsis thaliana] gi|51970544|dbj|BAD43964.1| bHLH transcription factor (bHLH027) - like protein [Arabidopsis thaliana] gi|51970694|dbj|BAD44039.1| bHLH transcription factor (bHLH027) - like protein [Arabidopsis thaliana] gi|110736372|dbj|BAF00155.1| bHLH transcription factor (bHLH027) - like protein [Arabidopsis thaliana] gi|332660294|gb|AEE85694.1| transcription factor bHLH27 [Arabidopsis thaliana]</td><td>325</td><td>254</td><td>1.00E-104</td><td>78.2</td><td>58.8</td><td>64.6</td><td>transcription factor bHLH27</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29930.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:14644108-14647449 FORWARD LENGTH=254</td><td>325</td><td>254</td><td>1.00E-107</td><td>78.2</td><td>58.8</td><td>64.6</td></tr>
<tr><td>Rsa1.0_00124.1.g6025.t1</td><td>ref|XP_002867376.1| hypothetical protein ARALYDRAFT_491757 [Arabidopsis lyrata subsp. lyrata] gi|297313212|gb|EFH43635.1| hypothetical protein ARALYDRAFT_491757 [Arabidopsis lyrata subsp. lyrata]</td><td>164</td><td>170</td><td>2.00E-60</td><td>103.7</td><td>79.3</td><td>87.2</td><td>hypothetical protein ARALYDRAFT_491757</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G29980.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf whorl, sepal, flower, seed; EXPRESSED DURING: petal differentiation and expansion stage, E expanded cotyledon stage; BEST Arabidopsis thaliana protein match is: Fasciclin-like arabinogalactan family protein (TAIR:AT1G30800.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:14665037-14665546 REVERSE LENGTH=169</td><td>164</td><td>169</td><td>2.00E-60</td><td>103.0</td><td>68.3</td><td>76.2</td></tr>
<tr><td>Rsa1.0_00124.1.g6026.t1</td><td>gb|EOA15663.1| hypothetical protein CARUB_v10006130mg [Capsella rubella]</td><td>90</td><td>90</td><td>2.00E-41</td><td>100.0</td><td>87.8</td><td>95.6</td><td>hypothetical protein CARUB_v10006130mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G30010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, plastid; EXPRESSED IN: 26 plant structures; EXPRESSED DURING: 15 growth stages; Has 39 Blast hits to 39 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14672947-14673219 FORWARD LENGTH=90</td><td>90</td><td>90</td><td>6.00E-42</td><td>100.0</td><td>84.4</td><td>93.3</td></tr>
<tr><td>Rsa1.0_00124.1.g6027.t3</td><td>ref|NP_567839.1| PA-domain containing subtilase family protein [Arabidopsis thaliana] gi|4938478|emb|CAB43837.1| proteinase-like protein [Arabidopsis thaliana] gi|7269902|emb|CAB80995.1| AT4g30020 [Arabidopsis thaliana] gi|22655014|gb|AAM98098.1| AT4g30020/F6G3_50 [Arabidopsis thaliana] gi|29028756|gb|AAO64757.1| AT4g30020/F6G3_50 [Arabidopsis thaliana] gi|110740572|dbj|BAE98391.1| hypothetical protein [Arabidopsis thaliana] gi|332660309|gb|AEE85709.1| PA-domain containing subtilase family protein [Arabidopsis thaliana]</td><td>781</td><td>816</td><td>0</td><td>104.5</td><td>91.4</td><td>96.7</td><td>PA-domain containing subtilase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G30020.1 | Symbols: | PA-domain containing subtilase family protein | chr4:14678251-14681762 FORWARD LENGTH=816</td><td>781</td><td>816</td><td>0</td><td>104.5</td><td>91.4</td><td>96.7</td></tr>
<tr><td>Rsa1.0_00124.1.g6028.t1</td><td>ref|NP_194735.2| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|17065050|gb|AAL32679.1| putative protein [Arabidopsis thaliana] gi|21387127|gb|AAM47967.1| putative protein [Arabidopsis thaliana] gi|332660313|gb|AEE85713.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]</td><td>402</td><td>401</td><td>0</td><td>99.8</td><td>88.3</td><td>95.0</td><td>Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G30060.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:14689420-14691519 REVERSE LENGTH=401</td><td>402</td><td>401</td><td>0</td><td>99.8</td><td>88.3</td><td>95.0</td></tr>
</table>

Rsa1.0_00124.1.g6029.t1	ref|XP_002869396.1| hypothetical protein ARALYDRAFT_491747 [Arabidopsis lyrata subsp. lyrata] gi|297315232|gb|EFH45655.1| hypothetical protein ARALYDRAFT_491747 [Arabidopsis lyrata subsp. lyrata]	189	127	1.00E−29	67.2	36.0	42.9	hypothetical protein ARALYDRAFT_491747	gbpln	Arabidopsis lyrata	AT4G30070.1 | Symbols: LCR59 | low-molecular-weight cysteine-rich 59 | chr4:14697549-14698315 FORWARD LENGTH=129	189	129	4.00E−28	68.3	34.9	42.3
Rsa1.0_00124.1.g6030.t1	ref|XP_002867369.1| hypothetical protein ARALYDRAFT_913475 [Arabidopsis lyrata subsp. lyrata] gi|297313205|gb|EFH43628.1| hypothetical protein ARALYDRAFT_913475 [Arabidopsis lyrata subsp. lyrata]	658	670	0	101.8	92.4	96.0	hypothetical protein ARALYDRAFT_913475	gbpln	Arabidopsis lyrata	AT4G30080.1 | Symbols: ARF16 | auxin response factor 16 | chr4:14703369-14705564 REVERSE LENGTH=670	658	670	0	101.8	92.4	95.9
Rsa1.0_00124.1.g6031.t1	ref|NP_194739.1| tRNA-splicing endonuclease positive effector-related protein [Arabidopsis thaliana] gi|4938486|emb|CAB43845.1| putative protein [Arabidopsis thaliana] gi|7269910|emb|CAB81003.1| putative protein [Arabidopsis thaliana] gi|332660321|gb|AEE85721.1| tRNA-splicing endonuclease positive effector-related protein [Arabidopsis thaliana]	1273	1311	0	103.0	87.5	92.3	tRNA-splicing endonuclease positive effector-related protein	gbpln	Arabidopsis thaliana	AT4G30100.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:14714191-14719335 FORWARD LENGTH=1311	1273	1311	0	103.0	87.5	92.3
Rsa1.0_00124.1.g6032.t1	ref|XP_002867367.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313203|gb|EFH43626.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	917	944	0	102.9	82.4	88.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G30110.1 | Symbols: HMA2, ATHMA2 | heavy metal atpase 2 | chr4:14720253-14724577 REVERSE LENGTH=951	917	951	0	103.7	80.6	87.7
Rsa1.0_00124.1.g6033.t1	gb|AFS33099.1| heavy metal ATPase transporter 3 [Camelina sativa]	160	761	8.00E−33	475.6	62.5	70.6	heavy metal ATPase transporter 3	gbpln	Camelina sativa	AT4G30110.1 | Symbols: HMA2, ATHMA2 | heavy metal atpase 2 | chr4:14720253-14724577 REVERSE LENGTH=951	160	951	1.00E−22	594.4	46.9	60.6
Rsa1.0_00124.1.g6034.t1	gb|EOA39894.1| hypothetical protein CARUB_v10008573mg [Capsella rubella]	1148	630	4.00E−99	54.9	17.6	25.4	hypothetical protein CARUB_v10008573mg	gbpln	Capsella rubella	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	1148	673	3.00E−63	58.6	11.8	17.3
Rsa1.0_00124.1.g6035.t1	gb|ABD64950.1| GRF zinc finger containing protein [Brassica oleracea]	99	180	1.00E−10	181.8	37.4	52.5	GRF zinc finger containing protein	gbpln	Brassica oleracea	AT5G15690.1 | Symbols: | zinc ion binding | chr5:5113823-5114402 REVERSE LENGTH=169	99	169	3.00E−12	170.7	34.3	49.5
Rsa1.0_00124.1.g6036.t1	gb|AAF78267.1|AC020576_11 Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene [Arabidopsis thaliana]	932	1206	0	129.4	44.8	63.7	Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	932	719	2.00E−41	77.1	15.7	25.8
Rsa1.0_00124.1.g6037.t1	gb|EOA18568.1| hypothetical protein CARUB_v10007127mg [Capsella rubella]	982	969	0	98.7	92.4	95.3	hypothetical protein CARUB_v10007127mg	gbpln	Capsella rubella	AT4G30160.1 | Symbols: VLN4, ATVLN4 | villin 4 | chr4:14754528-14759511 FORWARD LENGTH=974	982	974	0	99.2	92.0	95.0
Rsa1.0_00124.1.g6038.t1	ref|XP_002867366.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313202|gb|EFH43625.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	762	757	0	99.3	87.8	92.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G30110.1 | Symbols: HMA2, ATHMA2 | heavy metal atpase 2 | chr4:14720253-14724577 REVERSE LENGTH=951	762	951	0	124.8	67.7	80.2
Rsa1.0_00124.1.g6039.t1	gb|EOA17003.1| hypothetical protein CARUB_v10005239mg [Capsella rubella]	325	325	1.00E−170	100.0	91.1	95.1	hypothetical protein CARUB_v10005239mg	gbpln	Capsella rubella	AT4G30170.1 | Symbols: | Peroxidase family protein | chr4:14762922-14764482 FORWARD LENGTH=325	325	325	1.00E−168	100.0	89.5	94.2

Rsa1.0_00124.1.g6040.t1	ref|NP_194748.1| H(+)-ATPase 2 [Arabidopsis thaliana] gi|114335|sp|P19456.2|PMA2_ARATH RecName: Full=ATPase 2, plasma membrane-type; AltName: Full=Proton pump 2 gi|166629|gb|AAA32751.1| H+-ATPase [Arabidopsis thaliana] gi|5730129|emb|CAB52463.1| H+-transporting ATPase type 2, plasma membrane [Arabidopsis thaliana] gi|7269919|emb|CAB81012.1| H+-transporting ATPase type 2, plasma membrane [Arabidopsis thaliana] gi|14334804|gb|AAK59580.1| putative H+-transporting ATPase [Arabidopsis thaliana] gi|23397277|gb|AAN31920.1| putative H+-transporting ATPase type 2 [Arabidopsis thaliana] gi|25055009|gb|AAN71968.1| putative H+-transporting ATPase [Arabidopsis thaliana] gi|332660331|gb|AEE85731.1| H(+)-ATPase 2 [Arabidopsis thaliana]	924	948	0	102.6	91.3	95.6	H(+)-ATPase 2	gbpln	Arabidopsis thaliana	AT4G30190.1 | Symbols: AHA2, PMA2, HA2 | H(+)-ATPase 2 | chr4:14770820-14775920 REVERSE LENGTH=948	924	948	0	102.6	91.3	95.6
Rsa1.0_00125.1.g6041.t1	dbj|BAA22099.1| unnamed protein product [Arabidopsis thaliana]	637	642	0	100.8	57.5	71.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT1G52030.1 | Symbols: MBP2, MBP1.2, F-ATMBP | myrosinase-binding protein 2 | chr1:19346090-19348282 REVERSE LENGTH=642	637	642	0	100.8	57.5	71.7
Rsa1.0_00125.1.g6042.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00125.1.g6043.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00125.1.g6044.t1	gb|AAG50652.1|AC073433_4 transposase, putative [Arabidopsis thaliana]	90	659	5.00E-21	732.2	55.6	71.1	transposase, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00125.1.g6045.t1	ref|XP_002871180.1| ATHMOV34 [Arabidopsis lyrata subsp. lyrata] gi|297317017|gb|EFH47439.1| ATHMOV34 [Arabidopsis lyrata subsp. lyrata]	75	308	2.00E-14	410.7	60.0	65.3	ATHMOV34	gbpln	Arabidopsis lyrata	AT5G05780.1 | Symbols: RPN8A, AE3, ATHMOV34 | RP non-ATPase subunit 8A | chr5:1735862-1738176 FORWARD LENGTH=308	75	308	3.00E-16	410.7	57.3	64.0
Rsa1.0_00125.1.g6046.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1338	1475	0	110.2	62.3	77.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1338	1262	0	94.3	23.7	30.6
Rsa1.0_00125.1.g6047.t1	ref|NP_001189859.1| 26S proteasome regulatory subunit N8 [Arabidopsis thaliana] gi|332641502|gb|AEE75023.1| probable 26S proteasome non-ATPase regulatory subunit 8 [Arabidopsis thaliana]	261	307	4.00E-18	117.6	21.1	24.9	26S proteasome regulatory subunit N8	gbpln	Arabidopsis thaliana	AT3G11270.2 | Symbols: MEE34 | Mov34/MPN/PAD-1 family protein | chr3:3528989-3531317 FORWARD LENGTH=307	261	307	1.00E-20	117.6	21.1	24.9
Rsa1.0_00125.1.g6048.t1	gb|AAM63626.1| unknown [Arabidopsis thaliana]	205	208	1.00E-102	101.5	89.3	94.6	unknown	gbpln	Arabidopsis thaliana	AT1G52140.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G16330.1); Has 114 Blast hits to 114 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 114; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:19407559-19408185 REVERSE LENGTH=208	205	208	1.00E-104	101.5	88.8	94.6
Rsa1.0_00125.1.g6049.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	144	390	2.00E-31	270.8	46.5	66.0	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	144	295	4.00E-18	204.9	31.3	49.3

Rsa1.0_00125.1.g6050.t3	ref|NP_175627.1| homeobox-leucine zipper protein ATHB-15 [Arabidopsis thaliana] gi|75216693|sp|Q9ZU11.1|ATB15_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-15; AltName: Full=HD-ZIP protein ATHB-15; AltName: Full=Homeodomain transcription factor ATHB-15; AltName: Full=Protein CORONA; AltName: Full=Protein INCURVATA 4 gi|4220462|gb|AAD12689.1| Strong similarity to gb|Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF|00046 and bZIP PF|00170 domains [Arabidopsis thaliana] gi|16974581|gb|AAL31186.1| At1g52150/F5F19_21 [Arabidopsis thaliana] gi|19578319|emb|CAD28400.1| homeodomain-leucine zipper protein [Arabidopsis thaliana] gi|332194639|gb|AEE32760.1| homeobox-leucine zipper protein ATHB-15 [Arabidopsis thaliana]	628	836	0	133.1	67.0	70.7	homeobox-leucine zipper protein ATHB-15	gbpln	Arabidopsis thaliana	AT1G52150.1 | Symbols: ATHB-15, ATHB15, CNA, ICU4 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr1:19409913-19413961 REVERSE LENGTH=836	628	836	0	133.1	67.0	70.7
Rsa1.0_00125.1.g6051.t1	ref|XP_002880903.1| hypothetical protein ARALYDRAFT_901626 [Arabidopsis lyrata subsp. lyrata] gi|297326742|gb|EFH57162.1| hypothetical protein ARALYDRAFT_901626 [Arabidopsis lyrata subsp. lyrata]	1007	1014	0	100.7	69.4	79.9	hypothetical protein ARALYDRAFT_901626	gbpln	Arabidopsis lyrata	AT3G47580.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17532687-17535810 FORWARD LENGTH=1011	1007	1011	0	100.4	68.1	79.7
Rsa1.0_00125.1.g6052.t1	ref|NP_175627.1| homeobox-leucine zipper protein ATHB-15 [Arabidopsis thaliana] gi|75216693|sp|Q9ZU11.1|ATB15_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-15; AltName: Full=HD-ZIP protein ATHB-15; AltName: Full=Homeodomain transcription factor ATHB-15; AltName: Full=Protein CORONA; AltName: Full=Protein INCURVATA 4 gi|4220462|gb|AAD12689.1| Strong similarity to gb|Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF|00046 and bZIP PF|00170 domains [Arabidopsis thaliana] gi|16974581|gb|AAL31186.1| At1g52150/F5F19_21 [Arabidopsis thaliana] gi|19578319|emb|CAD28400.1| homeodomain-leucine zipper protein [Arabidopsis thaliana] gi|332194639|gb|AEE32760.1| homeobox-leucine zipper protein ATHB-15 [Arabidopsis thaliana]	845	836	0	98.9	95.3	96.9	homeobox-leucine zipper protein ATHB-15	gbpln	Arabidopsis thaliana	AT1G52150.1 | Symbols: ATHB-15, ATHB15, CNA, ICU4 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr1:19409913-19413961 REVERSE LENGTH=836	845	836	0	98.9	95.3	96.9
Rsa1.0_00125.1.g6053.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00125.1.g6054.t1	gb|AAN62481.1| phosphatidylinositol 3-kinase [Brassica napus]	109	813	1.00E-35	745.9	62.4	65.1	phosphatidylinositol 3-kinase	gbpln	Brassica napus	AT1G60490.1 | Symbols: ATVPS34, VPS34, PI3K | vacuolar protein sorting 34 | chr1:22285792-22290190 REVERSE LENGTH=814	109	814	2.00E-35	746.8	56.9	63.3
Rsa1.0_00125.1.g6055.t1	gb|EOA36300.1| hypothetical protein CARUB_v10010579mg [Capsella rubella]	145	145	3.00E-73	100.0	95.2	99.3	hypothetical protein CARUB_v10010579mg	gbpln	Capsella rubella	AT1G52230.1 | Symbols: PSAH2, PSAH-2, PSI-H | photosystem I subunit H2 | chr1:19454902-19455508 FORWARD LENGTH=145	145	145	6.00E-74	100.0	93.8	97.2
Rsa1.0_00125.1.g6056.t1	ref|XP_002894369.1| dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297340211|gb|EFH70628.1| dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata]	94	94	1.00E-46	100.0	96.8	97.9	dynein light chain type 1 family protein	gbpln	Arabidopsis lyrata	AT1G52240.2 | Symbols: ATROPGEF11, ROPGEF11, PIRF1 | RHO guanyl-nucleotide exchange factor 11 | chr1:19458844-19459235 REVERSE LENGTH=94	94	94	4.00E-49	100.0	95.7	97.9
Rsa1.0_00125.1.g6057.t1	ref|NP_175636.2| protein PDI-like 1-5 [Arabidopsis thaliana] gi|310947294|sp|A3KPF5.1|PDI15_ARATH RecName: Full=Protein disulfide isomerase-like 1-5; Short=AtPDIL1-5; AltName: Full=Protein disulfide isomerase 3; Short=AtPDI3; AltName: Full=Protein disulfide isomerase-like 3-1; Short=AtPDIL3-1; Flags: Precursor gi|126352280|gb|ABO09885.1| At1g52260 [Arabidopsis thaliana] gi|332194654|gb|AEE32775.1| protein PDI-like 1-5 [Arabidopsis thaliana]	249	537	1.00E-33	215.7	41.4	51.4	protein PDI-like 1-5	gbpln	Arabidopsis thaliana	AT1G52260.1 | Symbols: ATPDIL1-5, ATPDI3, PDI3, PDIL1-5 | PDI-like 1-5 | chr1:19460694-19463346 FORWARD LENGTH=537	249	537	4.00E-36	215.7	41.4	51.4

Rsa1.0_00125.1.g6058.t1	emb|CAB75932.1| putative protein [Arabidopsis thaliana]	1333	1339	0	100.5	54.5	71.2	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1333	1262	1.00E-107	94.7	15.1	23.6
Rsa1.0_00125.1.g6059.t1	gb|EOA36855.1| hypothetical protein CARUB_v10008802mg [Capsella rubella]	98	536	3.00E-41	546.9	83.7	89.8	hypothetical protein CARUB_v10008802mg	gbpln	Capsella rubella	AT1G52260.1 | Symbols: ATPDIL1-5, ATPDI3, PDI3, PDIL1-5 | PDI-like 1-5 | chr1:19460694-19463346 FORWARD LENGTH=537	98	537	2.00E-41	548.0	80.6	89.8
Rsa1.0_00125.1.g6060.t1	ref|NP_175638.1| RAB GTPase homolog G3D [Arabidopsis thaliana] gi|297852978|ref|XP_002894370.1| hypothetical protein ARALYDRAFT_474344 [Arabidopsis lyrata subsp. lyrata] gi|75169431|sp|Q9C820.1|RAG3D_ARATH RecName: Full=Ras-related protein RABG3d; Short=AtRABG3d; AltName: Full=Ras-related protein Rab72; Short=AtRab72 gi|12323132|gb|AAG51552.1|AC037424_17 GTP-binding protein RAB7D, putative; 63624-64923 [Arabidopsis thaliana] gi|15718410|dbj|BAB68372.1| AtRab72 [Arabidopsis thaliana] gi|18389228|gb|AAL67057.1| putative GTP-binding protein RAB7D [Arabidopsis thaliana] gi|20465885|gb|AAM20047.1| putative GTP-binding protein RAB7D [Arabidopsis thaliana] gi|297340212|gb|EFH70629.1| hypothetical protein ARALYDRAFT_474344 [Arabidopsis lyrata subsp. lyrata] gi|332194656|gb|AEE32777.1| RAB GTPase homolog G3D [Arabidopsis thaliana]	206	206	1.00E-115	100.0	97.6	99.0	RAB GTPase homolog G3D	gbpln	Arabidopsis lyrata	AT1G52280.1 | Symbols: AtRABG3d, RABG3d | RAB GTPase homolog G3D | chr1:19468150-19469449 REVERSE LENGTH=206	206	206	1.00E-117	100.0	97.6	99.0
Rsa1.0_00125.1.g6061.t1	ref|NP_175639.1| protein kinase-like protein [Arabidopsis thaliana] gi|75333493|sp|Q9C821.1|PEK15_ARATH RecName: Full=Proline-rich receptor-like protein kinase PERK15; AltName: Full=Proline-rich extensin-like receptor kinase 15; Short=AtPERK15 gi|12323130|gb|AAG51550.1|AC037424_15 protein kinase, putative; 60711-62822 [Arabidopsis thaliana] gi|44917591|gb|AAS49120.1| At1g52290 [Arabidopsis thaliana] gi|62320604|dbj|BAD95250.1| protein kinase [Arabidopsis thaliana] gi|332194657|gb|AEE32778.1| proline-rich receptor-like protein kinase PERK15 [Arabidopsis thaliana]	509	509	0	100.0	80.2	86.8	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G52290.1 | Symbols: | Protein kinase superfamily protein | chr1:19470251-19472362 REVERSE LENGTH=509	509	509	0	100.0	80.2	86.8
Rsa1.0_00125.1.g6062.t1	ref|NP_175640.1| 60S ribosomal protein L37-2 [Arabidopsis thaliana] gi|20143906|sp|Q43292.2|RL372_ARATH RecName: Full=60S ribosomal protein L37-2 gi|12323122|gb|AAG51542.1|AC037424_7 60S ribosomal protein L37, putative; 56921-57860 [Arabidopsis thaliana] gi|13877907|gb|AAK44031.1|AF370216_1 putative 60S ribosomal protein L37 [Arabidopsis thaliana] gi|21280805|gb|AAM44969.1| putative 60S ribosomal protein L37 [Arabidopsis thaliana] gi|222423584|dbj|BAH19761.1| AT1G52300 [Arabidopsis thaliana] gi|332194658|gb|AEE32779.1| 60S ribosomal protein L37-2 [Arabidopsis thaliana]	75	95	6.00E-30	126.7	97.3	97.3	60S ribosomal protein L37-2	gbpln	Arabidopsis thaliana	AT1G52300.1 | Symbols: | Zinc-binding ribosomal protein family protein | chr1:19475213-19476152 REVERSE LENGTH=95	75	95	9.00E-33	126.7	97.3	97.3
Rsa1.0_00125.1.g6063.t1	gb|EOA40057.1| hypothetical protein CARUB_v10008750mg [Capsella rubella] gi|482575871|gb|EOA40058.1| hypothetical protein CARUB_v10008750mg [Capsella rubella]	602	554	0	92.0	77.7	83.4	hypothetical protein CARUB_v10008750mg	gbpln	Capsella rubella	AT1G52310.1 | Symbols: | protein kinase family protein / C-type lectin domain-containing protein | chr1:19478401-19480462 FORWARD LENGTH=552	602	552	0	91.7	77.7	82.7

Rsa1.0_00125.1.g6064.t1	ref|NP_175645.1| coatomer subunit beta'-2 [Arabidopsis thaliana] gi|75169434|sp|Q9C827.1|COB22_ARATH RecName: Full=Coatomer subunit beta'-2; AltName: Full=Beta'-coat protein 2; Short=Beta'-COP 2 gi|12323125|gb|AAG51545.1|AC037424_10 coatomer complex subunit, putative; 33791-27676 [Arabidopsis thaliana] gi|332194671|gb|AEE32792.1| coatomer subunit beta'-2 [Arabidopsis thaliana]	938	926	0	98.7	92.3	96.2	coatomer subunit beta'-2	gbpln	Arabidopsis thaliana	AT1G52360.1 | Symbols: | Coatomer, beta' subunit | chr1:19499282-19505397 FORWARD LENGTH=926	938	926	0	98.7	92.3	96.2
Rsa1.0_00125.1.g6065.t1	#	#	#	#	#	#	#	-	----	----	AT1G52380.1 | Symbols: | NUP50 (Nucleoporin 50 kDa) protein | chr1:19509979-19511301 FORWARD LENGTH=440	113	440	2.00E-11	389.4	34.5	40.7
Rsa1.0_00125.1.g6066.t1	ref|XP_002894381.1| hypothetical protein ARALYDRAFT_892257 [Arabidopsis lyrata subsp. lyrata] gi|297340223|gb|EFH70640.1| hypothetical protein ARALYDRAFT_892257 [Arabidopsis lyrata subsp. lyrata]	391	721	3.00E-98	184.4	51.4	65.7	hypothetical protein ARALYDRAFT_892257	gbpln	Arabidopsis lyrata	AT1G52490.1 | Symbols: | CONTAINS InterPro DOMAIN/s: F-box domain, cyclin-like (InterPro:IPR001810), F-box domain, Skp2-like (InterPro:IPR022364), F-box associated domain, type 3 (InterPro:IPR013187), F-box associated interaction domain (InterPro:IPR017451); BEST Arabidopsis thaliana protein match is: F-box and associated interaction domains-containing protein (TAIR:AT1G32420.1); Has 1577 Blast hits to 1056 proteins in 31 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 1577; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:19556218-19559011 REVERSE LENGTH=513	391	513	1.00E-66	131.2	37.1	47.1
Rsa1.0_00125.1.g6067.t1	sp|Q9SSQ2.1|FB55_ARATH RecName: Full=F-box protein At1g52490 gi|5903056|gb|AAD55615.1|AC008016_25 F6D8.29 [Arabidopsis thaliana]	391	423	1.00E-96	108.2	50.9	62.9	RecName: Full=F-box protein At1g52490 gi|5903056|gb|AAD55615.1|AC008016_25 F6D8.29	gbpln	Arabidopsis thaliana	AT1G52490.1 | Symbols: | CONTAINS InterPro DOMAIN/s: F-box domain, cyclin-like (InterPro:IPR001810), F-box domain, Skp2-like (InterPro:IPR022364), F-box associated domain, type 3 (InterPro:IPR013187), F-box associated interaction domain (InterPro:IPR017451); BEST Arabidopsis thaliana protein match is: F-box and associated interaction domains-containing protein (TAIR:AT1G32420.1); Has 1577 Blast hits to 1056 proteins in 31 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 1577; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:19556218-19559011 REVERSE LENGTH=513	391	513	2.00E-66	131.2	37.3	45.8
Rsa1.0_00125.1.g6068.t1	ref|XP_002894388.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340230|gb|EFH70647.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	814	810	0	99.5	93.2	95.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G52570.1 | Symbols: PLDALPHA2 | phospholipase D alpha 2 | chr1:19583940-19586551 REVERSE LENGTH=810	814	810	0	99.5	93.0	95.7
Rsa1.0_00125.1.g6069.t1	gb|AAG50751.1|AC079733_19 polyprotein, putative [Arabidopsis thaliana]	268	1468	2.00E-31	547.8	23.5	28.7	polyprotein, putative	gbpln	Arabidopsis thaliana	AT1G52580.1 | Symbols: ATRBL5, RBL5 | RHOMBOID-like protein 5 | chr1:19587637-19588958 FORWARD LENGTH=309	268	309	4.00E-26	115.3	26.9	32.5
Rsa1.0_00125.1.g6070.t1	ref|NP_175669.1| signal peptidase, endoplasmic reticulum-type [Arabidopsis thaliana] gi|297847646|ref|XP_002891704.1| hypothetical protein ARALYDRAFT_474386 [Arabidopsis lyrata subsp. lyrata] gi|5903045|gb|AAD55604.1|AC008016_14 Similar to gb|AF108945 signal peptidase 18 kDa subunit from Homo sapiens. ESTs gb|H76629, gb|H76949 and gb|H76216 come from this gene [Arabidopsis thaliana] gi|17381152|gb|AAL36388.1| putative signal peptidase subunit [Arabidopsis thaliana] gi|20465737|gb|AAM20337.1| putative signal peptidase subunit [Arabidopsis thaliana] gi|21536563|gb|AAM60895.1| signal peptidase subunit, putative [Arabidopsis thaliana] gi|297337546|gb|EFH67963.1| hypothetical protein ARALYDRAFT_474386 [Arabidopsis lyrata subsp. lyrata] gi|332194707|gb|AEE32828.1| Peptidase S24/S26A/S26B/S26C family protein [Arabidopsis thaliana]	153	180	8.00E-77	117.6	94.1	96.1	signal peptidase, endoplasmic reticulum-type	gbpln	Arabidopsis lyrata	AT1G52600.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr1:19590612-19592486 FORWARD LENGTH=180	153	180	2.00E-79	117.6	94.1	96.1
Rsa1.0_00125.1.g6071.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00126.1.g6072.t1	gb|AAC62132.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	241	1137	5.00E-76	471.8	61.0	76.3	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	241	240	9.00E-12	99.6	20.3	34.4
Rsa1.0_00126.1.g6073.t1	ref|XP_002880460.1| homeobox-leucine zipper protein 9 [Arabidopsis lyrata subsp. lyrata] gi|297326299|gb|EFH56719.1| homeobox-leucine zipper protein 9 [Arabidopsis lyrata subsp. lyrata]	278	273	1.00E-121	98.2	83.8	89.9	homeobox-leucine zipper protein 9	gbpln	Arabidopsis lyrata	AT2G22800.1 | Symbols: HAT9 | Homeobox-leucine zipper protein family | chr2:9704949-9706048 REVERSE LENGTH=274	278	274	1.00E-112	98.6	82.4	88.8
Rsa1.0_00126.1.g6074.t1	gb|EOA28316.1| hypothetical protein CARUB_v10024517mg [Capsella rubella]	232	740	6.00E-17	319.0	34.9	46.6	hypothetical protein CARUB_v10024517mg	gbpln	Capsella rubella	AT4G37820.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G22795.1); Has 433572 Blast hits to 177005 proteins in 4263 species: Archae - 2016; Bacteria - 67591; Metazoa - 157995; Fungi - 49745; Plants - 22011; Viruses - 2192; Other Eukaryotes - 132022 (source: NCBI BLink). | chr4:17785692-17787290 FORWARD LENGTH=532	232	532	4.00E-17	229.3	34.1	45.7
Rsa1.0_00126.1.g6075.t1	ref|XP_002878634.1| hypothetical protein ARALYDRAFT_900728 [Arabidopsis lyrata subsp. lyrata] gi|297324473|gb|EFH54893.1| hypothetical protein ARALYDRAFT_900728 [Arabidopsis lyrata subsp. lyrata]	322	321	1.00E-104	99.7	67.4	78.6	hypothetical protein ARALYDRAFT_900728	gbpln	Arabidopsis lyrata	AT2G22790.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G67020.1); Has 111 Blast hits to 111 proteins in 33 species: Archae - 0; Bacteria - 44; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9695932-9696909 FORWARD LENGTH=325	322	325	6.00E-92	100.9	65.2	73.9
Rsa1.0_00126.1.g6076.t1	ref|XP_002880457.1| peroxisomal NAD-malate dehydrogenase 1 [Arabidopsis lyrata subsp. lyrata] gi|297326296|gb|EFH56716.1| peroxisomal NAD-malate dehydrogenase 1 [Arabidopsis lyrata subsp. lyrata]	353	354	0	100.3	95.2	96.9	peroxisomal NAD-malate dehydrogenase 1	gbpln	Arabidopsis lyrata	AT2G22780.1 | Symbols: PMDH1 | peroxisomal NAD-malate dehydrogenase 1 | chr2:9689995-9691923 REVERSE LENGTH=354	353	354	0	100.3	94.6	96.9
Rsa1.0_00126.1.g6077.t1	ref|XP_002878633.1| hypothetical protein ARALYDRAFT_481138 [Arabidopsis lyrata subsp. lyrata] gi|297324472|gb|EFH54892.1| hypothetical protein ARALYDRAFT_481138 [Arabidopsis lyrata subsp. lyrata]	323	321	1.00E-119	99.4	77.4	85.8	hypothetical protein ARALYDRAFT_481138	gbpln	Arabidopsis lyrata	AT2G22770.1 | Symbols: NAI1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:9684858-9686321 FORWARD LENGTH=320	323	320	1.00E-120	99.1	77.4	86.1
Rsa1.0_00126.1.g6078.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	714	1223	0	171.3	47.6	65.1	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	714	746	3.00E-84	104.5	24.1	32.6
Rsa1.0_00126.1.g6079.t1	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	944	1449	1.00E-134	153.5	33.1	48.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	944	746	2.00E-59	79.0	15.3	22.2
Rsa1.0_00126.1.g6080.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	581	530	9.00E-39	91.2	14.5	19.1	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00126.1.g6081.t1	emb|CAB39942.1| putative protein [Arabidopsis thaliana] gi|7267871|emb|CAB78214.1| putative protein [Arabidopsis thaliana]	175	473	3.00E-32	270.3	40.6	61.7	putative protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	175	295	3.00E-32	168.6	38.3	57.1
Rsa1.0_00126.1.g6082.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00126.1.g6083.t1	ref|NP_179861.2| transcription factor bHLH19 [Arabidopsis thaliana] gi|122231648|sp|Q1PF16.1|BH019_ARATH RecName: Full=Transcription factor bHLH19; AltName: Full=Basic helix-loop-helix protein 19; Short=AtbHLH19; Short=bHLH 19; AltName: Full=Transcription factor EN 26; AltName: Full=bHLH transcription factor bHLH019 gi|91806242|gb|ABE65849.1| basic helix-loop-helix family protein [Arabidopsis thaliana] gi|225898130|dbj|BAH30397.1| hypothetical protein [Arabidopsis thaliana] gi|330252257|gb|AEC07351.1| transcription factor bHLH19 [Arabidopsis thaliana]	296	295	1.00E-118	99.7	74.0	83.8	transcription factor bHLH19	gbpln	Arabidopsis thaliana	AT2G22760.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:9678012-9679165 FORWARD LENGTH=295	296	295	1.00E-121	99.7	74.0	83.8

Rsa1.0_00126.1.g6084.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	128	1307	1.00E-35	1021.1	55.5	75.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	128	1262	1.00E-21	985.9	36.7	54.7
Rsa1.0_00126.1.g6085.t1	gb|EOA28808.1| hypothetical protein CARUB_v10025041mg [Capsella rubella]	322	305	1.00E-128	94.7	73.0	82.3	hypothetical protein CARUB_v10025041mg	gbpln	Capsella rubella	AT2G22750.2 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:9672145-9673624 FORWARD LENGTH=305	322	305	1.00E-114	94.7	75.2	82.0
Rsa1.0_00126.1.g6086.t1	ref|XP_002880456.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326295|gb|EFH56715.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	780	808	0	103.6	61.0	72.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G22740.1 | Symbols: SUVH6, SDG23 | SU(VAR)3-9 homolog 6 | chr2:9664256-9666628 REVERSE LENGTH=790	780	790	0	101.3	60.1	71.7
Rsa1.0_00126.1.g6087.t1	ref|XP_002878630.1| hypothetical protein ARALYDRAFT_320107 [Arabidopsis lyrata subsp. lyrata] gi|297324469|gb|EFH54889.1| hypothetical protein ARALYDRAFT_320107 [Arabidopsis lyrata subsp. lyrata]	527	506	0	96.0	84.3	89.0	hypothetical protein ARALYDRAFT_320107	gbpln	Arabidopsis lyrata	AT2G22730.1 | Symbols: | Major facilitator superfamily protein | chr2:9660964-9663972 FORWARD LENGTH=510	527	510	0	96.8	82.5	87.3
Rsa1.0_00126.1.g6088.t1	ref|NP_973513.1| SPT2 chromatin protein [Arabidopsis thaliana] gi|110741100|dbj|BAE98644.1| hypothetical protein [Arabidopsis thaliana] gi|330252251|gb|AEC07345.1| SPT2 chromatin protein [Arabidopsis thaliana]	517	569	1.00E-164	110.1	72.5	82.2	SPT2 chromatin protein	gbpln	Arabidopsis thaliana	AT2G22720.3 | Symbols: | SPT2 chromatin protein | chr2:9658182-9660532 FORWARD LENGTH=569	517	569	1.00E-167	110.1	72.5	82.2
Rsa1.0_00126.1.g6089.t1	sp|Q9SAE1.2|C71BR_ARATH RecName: Full=Cytochrome P450 71B27	103	503	9.00E-38	488.3	73.8	84.5	RecName: Full=Cytochrome P450 71B27	----	----	AT1G13080.1 | Symbols: CYP71B2 | cytochrome P450, family 71, subfamily B, polypeptide 2 | chr1:4459212-4460807 FORWARD LENGTH=502	103	502	2.00E-37	487.4	78.6	89.3
Rsa1.0_00126.1.g6090.t1	gb|ABD65065.1| hypothetical protein 27.t00043 [Brassica oleracea]	117	117	4.00E-30	100.0	60.7	77.8	hypothetical protein 27.t00043	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00127.1.g6091.t1	gb|EOA16586.1| hypothetical protein CARUB_v10004752mg [Capsella rubella] gi|482552394|gb|EOA16587.1| hypothetical protein CARUB_v10004752mg [Capsella rubella] gi|482552395|gb|EOA16588.1| hypothetical protein CARUB_v10004752mg [Capsella rubella] gi|482552396|gb|EOA16589.1| hypothetical protein CARUB_v10004752mg [Capsella rubella]	432	464	1.00E-123	107.4	66.4	77.3	hypothetical protein CARUB_v10004752mg	gbpln	Capsella rubella	AT4G33740.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37820.1); Has 138092 Blast hits to 73110 proteins in 2951 species: Archae - 732; Bacteria - 17903; Metazoa - 48520; Fungi - 16808; Plants - 7078; Viruses - 1044; Other Eukaryotes - 46007 (source: NCBI BLink). | chr4:16187384-16188802 FORWARD LENGTH=472	432	472	1.00E-109	109.3	62.7	76.6
Rsa1.0_00127.1.g6092.t1	gb|EOA18047.1| hypothetical protein CARUB_v10006493mg [Capsella rubella]	172	173	1.00E-80	100.6	82.6	89.5	hypothetical protein CARUB_v10006493mg	gbpln	Capsella rubella	AT4G33730.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:16185098-16185616 FORWARD LENGTH=172	172	172	3.00E-79	100.0	82.6	88.4
Rsa1.0_00127.1.g6093.t1	ref|NP_195098.1| putative pathogenesis-related protein [Arabidopsis thaliana] gi|11692906|gb|AAG40056.1|AF324705_1 AT4g33720 [Arabidopsis thaliana] gi|11935187|gb|AAG42009.1|AF327419_1 putative pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|12642878|gb|AAK00381.1|AF339699_1 putative pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|3549674|emb|CAA20585.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|7270321|emb|CAB80089.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|14517484|gb|AAK62632.1| AT4g33720/T16L1_210 [Arabidopsis thaliana] gi|21593911|gb|AAM65876.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|22136566|gb|AAM91069.1| AT4g33720/T16L1_210 [Arabidopsis thaliana] gi|332660869|gb|AEE86269.1| putative pathogenesis-related protein [Arabidopsis thaliana]	165	163	1.00E-68	98.8	77.0	85.5	putative pathogenesis-related protein	gbpln	Arabidopsis thaliana	AT4G33720.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:16182813-16183304 FORWARD LENGTH=163	165	163	5.00E-71	98.8	77.0	85.5

Rsa1.0_00127.1.g6094.t1	ref|NP_195096.2| CBS domain-containing protein [Arabidopsis thaliana] gi|75248526|sp|Q8VZI2.1|Y4370_ARATH RecName: Full=DUF21 domain-containing protein At4g33700; AltName: Full=CBS domain-containing protein CBSDUF6 gi|17381276|gb|AAL36056.1| AT4g33700/T16L1_190 [Arabidopsis thaliana] gi|20856058|gb|AAM26645.1| AT4g33700/T16L1_190 [Arabidopsis thaliana] gi|332660867|gb|AEE86267.1| DUF21 domain-containing protein [Arabidopsis thaliana]	419	424	0	101.2	93.1	95.2	CBS domain-containing protein	gbpln	Arabidopsis thaliana	AT4G33700.1 | Symbols: | CBS domain-containing protein with a domain of unknown function (DUF21) | chr4:16176547-16179188 REVERSE LENGTH=424	419	424	0	101.2	93.1	95.2
Rsa1.0_00127.1.g6095.t1	ref|XP_002869199.1| AT4g33690/T16L1_180 [Arabidopsis lyrata subsp. lyrata] gi|297315035|gb|EFH45458.1| AT4g33690/T16L1_180 [Arabidopsis lyrata subsp. lyrata]	267	245	8.00E-82	91.8	62.5	67.8	AT4g33690/T16L1_180	gbpln	Arabidopsis lyrata	AT4G33690.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: pollen tube; Has 543 Blast hits to 512 proteins in 106 species: Archae - 0; Bacteria - 0; Metazoa - 281; Fungi - 54; Plants - 72; Viruses - 0; Other Eukaryotes - 136 (source: NCBI BLink). | chr4:16175198-16176137 FORWARD LENGTH=246	267	246	3.00E-77	92.1	60.3	65.2
Rsa1.0_00127.1.g6096.t1	ref|NP_567934.1| LL-diaminopimelate aminotransferase [Arabidopsis thaliana] gi|75163801|sp|Q93ZN9.1|DAPAT_ARATH RecName: Full=LL-diaminopimelate aminotransferase, chloroplastic; Short=AtDAP-AT; Short=DAP-AT; Short=DAP-aminotransferase; Short=LL-DAP-aminotransferase; AltName: Full=Protein ABERRANT GROWTH AND DEATH 2; Flags: Precursor gi|15912291|gb|AAL08279.1| AT4g33680/T16L1_170 [Arabidopsis thaliana] gi|17529044|gb|AAL38732.1| unknown protein [Arabidopsis thaliana] gi|21436149|gb|AAM51321.1| unknown protein [Arabidopsis thaliana] gi|41323503|gb|AAR99909.1| aminotransferase AGD2 [Arabidopsis thaliana] gi|332660865|gb|AEE86265.1| LL-diaminopimelate aminotransferase [Arabidopsis thaliana]	462	461	0	99.8	95.0	98.3	LL-diaminopimelate aminotransferase	gbpln	Arabidopsis thaliana	AT4G33680.1 | Symbols: AGD2 | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr4:16171847-16174630 REVERSE LENGTH=461	462	461	0	99.8	95.0	98.3
Rsa1.0_00127.1.g6097.t1	ref|NP_195093.1| D-threo-aldose 1-dehydrogenase [Arabidopsis thaliana] gi|75220139|sp|O81884.1|GALDH_ARATH RecName: Full=L-galactose dehydrogenase; Short=At-GalDH; Short=L-GalDH gi|3549669|emb|CAA20580.1| putative protein [Arabidopsis thaliana] gi|7270315|emb|CAB80084.1| putative protein [Arabidopsis thaliana] gi|15215698|gb|AAK91395.1| AT4g33670/T16L1_160 [Arabidopsis thaliana] gi|16555790|emb|CAD10386.1| L-galactose dehydrogenase [Arabidopsis thaliana] gi|19699264|gb|AAL90998.1| AT4g33670/T16L1_160 [Arabidopsis thaliana] gi|332660864|gb|AEE86264.1| L-galactose dehydrogenase [Arabidopsis thaliana]	318	319	1.00E-161	100.3	88.1	93.7	D-threo-aldose 1-dehydrogenase	gbpln	Arabidopsis thaliana	AT4G33670.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr4:16169670-16171446 REVERSE LENGTH=319	318	319	1.00E-163	100.3	88.1	93.7
Rsa1.0_00127.1.g6098.t1	ref|XP_002869200.1| hypothetical protein ARALYDRAFT_913046 [Arabidopsis lyrata subsp. lyrata] gi|297315036|gb|EFH45459.1| hypothetical protein ARALYDRAFT_913046 [Arabidopsis lyrata subsp. lyrata]	83	78	4.00E-22	94.0	72.3	80.7	hypothetical protein ARALYDRAFT_913046	gbpln	Arabidopsis lyrata	AT4G33666.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 11 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16169167-16169406 FORWARD LENGTH=79	83	79	2.00E-19	95.2	62.7	72.3
Rsa1.0_00127.1.g6099.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00127.1.g6100.t1	ref|XP_002865966.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata] gi|297311801|gb|EFH42225.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata]	427	455	2.00E-96	106.6	48.7	59.7	hypothetical protein ARALYDRAFT_357572	gbpln	Arabidopsis lyrata	AT1G32660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11811040-11812380 FORWARD LENGTH=446	427	446	5.00E-77	104.4	43.8	56.7
Rsa1.0_00127.1.g6101.t3	ref|NP_567931.1| dynamin-related protein 3A [Arabidopsis thaliana] gi|60392233|sp|Q8S944.2|DRP3A_ARATH RecName: Full=Dynamin-related protein 3A; AltName: Full=Dynamin-like protein 2; AltName: Full=Dynamin-like protein 2a gi|3549667|emb|CAA20578.1| Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana] gi|7270313|emb|CAB80082.1| Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana] gi|19032335|dbj|BAB85643.1| dynamin like protein 2a [Arabidopsis thaliana] gi|332660860|gb|AEE86260.1| dynamin-related protein 3A [Arabidopsis thaliana]	803	808	0	100.6	85.9	90.8	dynamin-related protein 3A	gbpln	Arabidopsis thaliana	AT4G33650.1 | Symbols: ADL2, DRP3A | dynamin-related protein 3A | chr4:16161073-16166587 FORWARD LENGTH=808	803	808	0	100.6	85.9	90.8
Rsa1.0_00127.1.g6102.t1	emb|CAA20577.1| putative protein [Arabidopsis thaliana] gi|7270312|emb|CAB80081.1| putative protein [Arabidopsis thaliana]	96	161	8.00E-37	167.7	78.1	79.2	putative protein	gbpln	Arabidopsis thaliana	AT4G33640.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16159727-16160211 REVERSE LENGTH=95	96	95	2.00E-39	99.0	78.1	79.2
Rsa1.0_00127.1.g6103.t1	ref|NP_001119110.1| uncharacterized protein [Arabidopsis thaliana] gi|332660856|gb|AEE86256.1| uncharacterized protein AT4G33625 [Arabidopsis thaliana]	193	199	2.00E-82	103.1	77.2	82.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G33625.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Golgi apparatus membrane protein TVP15 (InterPro:IPR013714); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16153114-16154543 REVERSE LENGTH=199	193	199	8.00E-85	103.1	77.2	82.4
Rsa1.0_00127.1.g6104.t1	ref|XP_002869203.1| Ulp1 protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297315039|gb|EFH45462.1| Ulp1 protease family protein [Arabidopsis lyrata subsp. lyrata]	807	777	0	96.3	74.2	82.0	Ulp1 protease family protein	gbpln	Arabidopsis lyrata	AT4G33620.1 | Symbols: | Cysteine proteinases superfamily protein | chr4:16147692-16152853 FORWARD LENGTH=783	807	783	0	97.0	74.0	80.8
Rsa1.0_00127.1.g6105.t1	gb|EOA18539.1| hypothetical protein CARUB_v10007093mg, partial [Capsella rubella]	147	160	6.00E-37	108.8	69.4	73.5	hypothetical protein CARUB_v10007093mg, partial	gbpln	Capsella rubella	AT4G33585.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; Has 3456 Blast hits to 2147 proteins in 337 species: Archae - 4; Bacteria - 491; Metazoa - 997; Fungi - 201; Plants - 1105; Viruses - 207; Other Eukaryotes - 451 (source: NCBI BLink). | chr4:16141778-16142257 REVERSE LENGTH=159	147	159	6.00E-28	108.2	56.5	62.6
Rsa1.0_00127.1.g6106.t2	ref|NP_195080.2| metallo-beta-lactamase family protein [Arabidopsis thaliana] gi|20260498|gb|AAM13147.1| putative protein [Arabidopsis thaliana] gi|28059392|gb|AAO30054.1| putative protein [Arabidopsis thaliana] gi|110740679|dbj|BAE98442.1| hypothetical protein [Arabidopsis thaliana] gi|332660843|gb|AEE86243.1| metallo-beta-lactamase family protein [Arabidopsis thaliana]	658	355	1.00E-148	54.0	37.4	41.3	metallo-beta-lactamase family protein	gbpln	Arabidopsis thaliana	AT4G33540.1 | Symbols: | metallo-beta-lactamase family protein | chr4:16130882-16133678 FORWARD LENGTH=355	658	355	1.00E-151	54.0	37.4	41.3
Rsa1.0_00127.1.g6107.t1	gb|EOA16000.1| hypothetical protein CARUB_v10004118mg [Capsella rubella]	861	855	0	99.3	90.0	94.4	hypothetical protein CARUB_v10004118mg	gbpln	Capsella rubella	AT4G33530.1 | Symbols: KUP5 | K+ uptake permease 5 | chr4:16126503-16130353 REVERSE LENGTH=855	861	855	0	99.3	90.0	94.7
Rsa1.0_00127.1.g6108.t1	ref|XP_002869211.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315047|gb|EFH45470.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	951	949	0	99.8	90.2	94.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G33520.2 | Symbols: PAA1, HMA6 | P-type ATP-ase 1 | chr4:16118993-16125849 FORWARD LENGTH=949	951	949	0	99.8	89.8	94.3

Rsa1.0_00127.1.g6109.t1	ref|NP_195077.1| phospho-2-dehydro-3-deoxyheptonate aldolase 2 [Arabidopsis thaliana] gi|21264400|sp|Q00218.2|AROG_ARATH RecName: Full=Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic; AltName: Full=3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2; AltName: Full=DAHP synthase 2; AltName: Full=Phospho-2-keto-3-deoxyheptonate aldolase 2; Flags: Precursor gi|13605635|gb|AAK32811.1|AF361798_1 AT4g33510/F17M5_270 [Arabidopsis thaliana] gi|4490318|emb|CAB38809.1| 2-dehydro-3-deoxyphosphoheptonate aldolase [Arabidopsis thaliana] gi|7270299|emb|CAB80068.1| 2-dehydro-3-deoxyphosphoheptonate aldolase [Arabidopsis thaliana] gi|21700887|gb|AAM70567.1| AT4g33510/F17M5_270 [Arabidopsis thaliana] gi|332660837|gb|AEE86237.1| phospho-2-dehydro-3-deoxyheptonate aldolase 2 [Arabidopsis thaliana]	509	507	0	99.6	93.5	96.9	phospho-2-dehydro-3-deoxyheptonate aldolase 2	gbpln	Arabidopsis thaliana	AT4G33510.1 | Symbols: DHS2 | 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase | chr4:16116496-16118549 FORWARD LENGTH=507	509	507	0	99.6	93.5	96.9
Rsa1.0_00127.1.g6110.t2	gb|EOA16026.1| hypothetical protein CARUB_v10004154mg [Capsella rubella]	581	813	7.00E-85	139.9	48.4	61.3	hypothetical protein CARUB_v10004154mg	gbpln	Capsella rubella	AT4G33500.1 | Symbols: | Protein phosphatase 2C family protein | chr4:16112835-16116243 REVERSE LENGTH=724	581	724	2.00E-73	124.6	41.0	49.2
Rsa1.0_00127.1.g6111.t1	gb|EOA17969.1| hypothetical protein CARUB_v10006384mg [Capsella rubella]	414	409	0	98.8	88.4	93.7	hypothetical protein CARUB_v10006384mg	gbpln	Capsella rubella	AT4G33495.1 | Symbols: RPD1 | Ubiquitin carboxyl-terminal hydrolase family protein | chr4:16111349-16112578 REVERSE LENGTH=409	414	409	0	98.8	88.6	93.5
Rsa1.0_00127.1.g6112.t1	ref|XP_002867175.1| hypothetical protein ARALYDRAFT_328390 [Arabidopsis lyrata subsp. lyrata] gi|297313011|gb|EFH43434.1| hypothetical protein ARALYDRAFT_328390 [Arabidopsis lyrata subsp. lyrata]	428	425	0	99.3	93.7	96.3	hypothetical protein ARALYDRAFT_328390	gbpln	Arabidopsis lyrata	AT4G33490.2 | Symbols: | Eukaryotic aspartyl protease family protein | chr4:16108781-16110679 REVERSE LENGTH=425	428	425	0	99.3	93.5	96.0
Rsa1.0_00127.1.g6113.t4	ref|XP_002867176.1| hypothetical protein ARALYDRAFT_491340 [Arabidopsis lyrata subsp. lyrata] gi|297313012|gb|EFH43435.1| hypothetical protein ARALYDRAFT_491340 [Arabidopsis lyrata subsp. lyrata]	346	336	1.00E-138	97.1	83.5	87.0	hypothetical protein ARALYDRAFT_491340	gbpln	Arabidopsis lyrata	AT4G33480.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3727 (InterPro:IPR022203); Has 348 Blast hits to 348 proteins in 78 species: Archae - 0; Bacteria - 101; Metazoa - 0; Fungi - 0; Plants - 183; Viruses - 0; Other Eukaryotes - 64 (source: NCBI BLink). | chr4:16105804-16108497 REVERSE LENGTH=336	346	336	1.00E-139	97.1	82.1	86.7
Rsa1.0_00127.1.g6114.t1	gb|EOA18366.1| hypothetical protein CARUB_v10006887mg [Capsella rubella]	426	437	0	102.6	89.0	93.9	hypothetical protein CARUB_v10006887mg	gbpln	Capsella rubella	AT4G33470.1 | Symbols: hda14, ATHDA14 | histone deacetylase 14 | chr4:16102774-16105439 REVERSE LENGTH=423	426	423	0	99.3	86.9	91.5
Rsa1.0_00127.1.g6115.t1	ref|NP_195072.2| ABC transporter I family member 10 [Arabidopsis thaliana] gi|75329129|sp|Q8H1R4.1|AB10I_ARATH RecName: Full=ABC transporter I family member 10, chloroplastic; Short=ABC transporter ABCI.10; Short=AtABCI10; AltName: Full=Non-intrinsic ABC protein 13; AltName: Full=Protein EMBRYO DEFECTIVE 2751; Flags: Precursor gi|23296450|gb|AAN13061.1| unknown protein [Arabidopsis thaliana] gi|37202112|gb|AAQ89671.1| At4g33460 [Arabidopsis thaliana] gi|62318881|dbj|BAD93954.1| hypothetical protein [Arabidopsis thaliana] gi|332660827|gb|AEE86227.1| ABC transporter I family member 10 [Arabidopsis thaliana]	359	271	1.00E-126	75.5	63.2	66.9	ABC transporter I family member 10	gbpln	Arabidopsis thaliana	AT4G33460.1 | Symbols: ATNAP13, EMB2751 | ABC transporter family protein | chr4:16098325-16100113 REVERSE LENGTH=271	359	271	1.00E-129	75.5	63.2	66.9
Rsa1.0_00127.1.g6116.t1	ref|XP_002867181.1| AtMYB69 [Arabidopsis lyrata subsp. lyrata] gi|297313017|gb|EFH43440.1| AtMYB69 [Arabidopsis lyrata subsp. lyrata]	250	250	1.00E-121	100.0	83.6	89.6	AtMYB69	gbpln	Arabidopsis lyrata	AT4G33450.1 | Symbols: ATMYB69, MYB69 | myb domain protein 69 | chr4:16095746-16096603 REVERSE LENGTH=250	250	250	1.00E-120	100.0	82.0	87.6

Rsa1.0_00127.1.g6117.t1	ref|NP_195070.2| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana] gi|27754320|gb|AAO22613.1| putative polygalacturonase [Arabidopsis thaliana] gi|28393881|gb|AAO42348.1| putative polygalacturonase [Arabidopsis thaliana] gi|332660825|gb|AEE86225.1| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	475	475	0	100.0	88.8	94.7	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	gbpln	Arabidopsis thaliana	AT4G33440.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:16092020-16094732 FORWARD LENGTH=475	475	475	0	100.0	88.8	94.7
Rsa1.0_00127.1.g6118.t1	gb|AFO67895.1| leucine-rich repeat receptor-like kinase (mitochondrion) [Brassica rapa subsp. oleifera]	611	632	0	103.4	98.0	98.5	leucine-rich repeat receptor-like kinase (mitochondrion)	gbpln	Brassica rapa	AT4G33430.1 | Symbols: BAK1, RKS10, SERK3, ELG, ATSERK3, ATBAK1 | BRI1-associated receptor kinase | chr4:16086654-16090288 REVERSE LENGTH=615	611	615	0	100.7	94.3	96.2
Rsa1.0_00127.1.g6119.t1	emb|CCJ34835.1| horseradish peroxidase isoenzyme HRP_6351 [Armoracia rusticana]	316	314	1.00E-156	99.4	84.5	91.1	horseradish peroxidase isoenzyme HRP_6351	gbpln	Armoracia rusticana	AT4G33420.1 | Symbols: | Peroxidase superfamily protein | chr4:16084856-16086105 FORWARD LENGTH=325	316	325	1.00E-158	102.8	84.5	90.8
Rsa1.0_00127.1.g6120.t1	ref|XP_002869215.1| signal peptide peptidase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315051|gb|EFH45474.1| signal peptide peptidase family protein [Arabidopsis lyrata subsp. lyrata]	372	372	0	100.0	94.1	98.4	signal peptide peptidase family protein	gbpln	Arabidopsis lyrata	AT4G33410.1 | Symbols: ATSPPL1, SPPL1 | SIGNAL PEPTIDE PEPTIDASE-LIKE 1 | chr4:16081640-16083119 FORWARD LENGTH=372	372	372	0	100.0	94.1	98.4
Rsa1.0_00127.1.g6121.t1	ref|NP_195066.1| Vacuolar import/degradation, Vid27-related protein [Arabidopsis thaliana] gi|4490307|emb|CAB38798.1| Dem-like protein [Arabidopsis thaliana] gi|7270288|emb|CAB80057.1| Dem-like protein [Arabidopsis thaliana] gi|20465423|gb|AAM20135.1| putative Dem protein [Arabidopsis thaliana] gi|28394003|gb|AAO42409.1| putative Dem protein [Arabidopsis thaliana] gi|332660820|gb|AEE86220.1| Vacuolar import/degradation, Vid27-related protein [Arabidopsis thaliana]	651	645	0	99.1	87.9	92.6	Vacuolar import/degradation, Vid27-related protein	gbpln	Arabidopsis thaliana	AT4G33400.1 | Symbols: | Vacuolar import/degradation, Vid27-related protein | chr4:16078189-16080410 REVERSE LENGTH=645	651	645	0	99.1	87.9	92.6
Rsa1.0_00127.1.g6122.t7	ref|XP_002869216.1| hypothetical protein ARALYDRAFT_491351 [Arabidopsis lyrata subsp. lyrata] gi|297315052|gb|EFH45475.1| hypothetical protein ARALYDRAFT_491351 [Arabidopsis lyrata subsp. lyrata]	1116	777	0	69.6	51.6	57.6	hypothetical protein ARALYDRAFT_491351	gbpln	Arabidopsis lyrata	AT4G33390.1 | Symbols: | Plant protein of unknown function (DUF827) | chr4:16075282-16077706 FORWARD LENGTH=779	1116	779	0	69.8	50.6	57.1
Rsa1.0_00127.1.g6123.t1	gb|EOA17218.1| hypothetical protein CARUB_v10005493mg [Capsella rubella]	279	269	1.00E-132	96.4	84.9	88.9	hypothetical protein CARUB_v10005493mg	gbpln	Capsella rubella	AT4G33350.1 | Symbols: | Tic22-like family protein | chr4:16064638-16066715 REVERSE LENGTH=268	279	268	1.00E-130	96.1	82.4	88.5
Rsa1.0_00127.1.g6124.t1	gb|EOA16266.1| hypothetical protein CARUB_v10004410mg [Capsella rubella]	593	604	0	101.9	89.5	94.6	hypothetical protein CARUB_v10004410mg	gbpln	Capsella rubella	AT4G33330.1 | Symbols: PGSIP3, GUX2 | plant glycogenin-like starch initiation protein 3 | chr4:16060142-16063061 REVERSE LENGTH=596	593	596	0	100.5	87.5	93.4
Rsa1.0_00127.1.g6125.t4	gb|ACP30606.1| disease resistance protein [Brassica rapa subsp. pekinensis]	943	836	0	88.7	46.8	48.3	disease resistance protein	gbpln	Brassica rapa	AT4G33300.2 | Symbols: ADR1-L1 | ADR1-like 1 | chr4:16051162-16054005 REVERSE LENGTH=816	943	816	0	86.5	37.4	43.5
Rsa1.0_00128.1.g6126.t1	ref|XP_002890867.1| hypothetical protein ARALYDRAFT_473263 [Arabidopsis lyrata subsp. lyrata] gi|297336709|gb|EFH67126.1| hypothetical protein ARALYDRAFT_473263 [Arabidopsis lyrata subsp. lyrata]	1627	1622	0	99.7	93.7	96.8	hypothetical protein ARALYDRAFT_473263	gbpln	Arabidopsis lyrata	AT1G30400.2 | Symbols: ATMRP1, EST1, ABCC1 | multidrug resistance-associated protein 1 | chr1:10728139-10737697 FORWARD LENGTH=1622	1627	1622	0	99.7	93.6	96.9
Rsa1.0_00128.1.g6127.t1	gb|ABU90830.1| pollen-expressed protein MF10 [Brassica rapa subsp. oleifera]	481	434	1.00E-174	90.2	76.3	80.0	pollen-expressed protein MF10	gbpln	Brassica rapa	AT3G28980.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10993403-10994925 REVERSE LENGTH=445	481	445	1.00E-129	92.5	55.5	70.5
Rsa1.0_00128.1.g6128.t1	ref|NP_174332.1| Phototropic-responsive NPH3-like protein [Arabidopsis thaliana] gi|166228367|sp|Q9S9Q9.2|Y1044_ARATH RecName: Full=BTB/POZ domain-containing protein At1g30440 gi|332193095|gb|AEE31216.1| Phototropic-responsive NPH3-like protein [Arabidopsis thaliana]	676	665	0	98.4	87.4	91.7	Phototropic-responsive NPH3-like protein	gbpln	Arabidopsis thaliana	AT1G30440.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr1:10759475-10762199 FORWARD LENGTH=665	676	665	0	98.4	87.4	91.7

Rsa1.0_00128.1.g6129.t1	gb|EOA30041.1| hypothetical protein CARUB_v10013147mg [Capsella rubella] gi|482565853|gb|EOA30042.1| hypothetical protein CARUB_v10013147mg [Capsella rubella] gi|482565854|gb|EOA30043.1| hypothetical protein CARUB_v10013147mg [Capsella rubella]	260	667	2.00E-57	256.5	41.5	50.4	hypothetical protein CARUB_v10013147mg	gbpln	Capsella rubella	AT3G06340.3 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr3:1920607-1922628 REVERSE LENGTH=673	260	673	2.00E-58	258.8	41.2	50.8
Rsa1.0_00128.1.g6130.t2	gb|EOA27117.1| hypothetical protein CARUB_v10023215mg [Capsella rubella]	186	446	4.00E-54	239.8	58.1	61.8	hypothetical protein CARUB_v10023215mg	gbpln	Capsella rubella	AT2G45730.1 | Symbols: | eukaryotic initiation factor 3 gamma subunit family protein | chr2:18836519-18839123 REVERSE LENGTH=446	186	446	3.00E-53	239.8	51.1	54.8
Rsa1.0_00128.1.g6131.t1	gb|EOA26321.1| hypothetical protein CARUB_v10025291mg [Capsella rubella]	134	553	1.00E-61	412.7	87.3	95.5	hypothetical protein CARUB_v10025291mg	gbpln	Capsella rubella	AT2G45720.2 | Symbols: | ARM repeat superfamily protein | chr2:18834468-18836129 FORWARD LENGTH=553	134	553	4.00E-64	412.7	88.1	94.0
Rsa1.0_00128.1.g6132.t1	ref|NP_174333.2| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|30691718|ref|NP_849731.1| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|30691724|ref|NP_849732.1| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|122209111|sp|Q2UVJ5.1|CCC1_ARATH RecName: Full=Cation-chloride cotransporter 1; Short=AtCCC1; AltName: Full=Protein HAPLESS 5 gi|83523648|emb|CAJ34849.1| cation chloride cotransporter [Arabidopsis thaliana] gi|110741532|dbj|BAE98715.1| putative cation-chloride co-transporter [Arabidopsis thaliana] gi|332193096|gb|AEE31217.1| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|332193097|gb|AEE31218.1| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|332193098|gb|AEE31219.1| cation-chloride co-transporter 1 [Arabidopsis thaliana]	973	975	0	100.2	93.1	95.1	cation-chloride co-transporter 1	gbpln	Arabidopsis thaliana	AT1G30450.2 | Symbols: CCC1, ATCCC1, HAP5 | cation-chloride co-transporter 1 | chr1:10762905-10769061 FORWARD LENGTH=975	973	975	0	100.2	93.1	95.1
Rsa1.0_00128.1.g6133.t1	ref|XP_002893618.1| hypothetical protein ARALYDRAFT_890588 [Arabidopsis lyrata subsp. lyrata] gi|297339460|gb|EFH69877.1| hypothetical protein ARALYDRAFT_890588 [Arabidopsis lyrata subsp. lyrata]	713	631	0	88.5	78.5	81.6	hypothetical protein ARALYDRAFT_890588	gbpln	Arabidopsis lyrata	AT1G30460.1 | Symbols: CPSF30, ATCPSF30 | cleavage and polyadenylation specificity factor 30 | chr1:10771469-10775323 REVERSE LENGTH=631	713	631	0	88.5	77.8	81.3
Rsa1.0_00128.1.g6134.t4	ref|NP_174335.4| SIT4 phosphatase-associated-like protein [Arabidopsis thaliana] gi|332193102|gb|AEE31223.1| SIT4 phosphatase-associated-like protein [Arabidopsis thaliana]	798	811	0	101.6	86.3	91.6	SIT4 phosphatase-associated-like protein	gbpln	Arabidopsis thaliana	AT1G30470.1 | Symbols: | SIT4 phosphatase-associated family protein | chr1:10779423-10786415 FORWARD LENGTH=811	798	811	0	101.6	86.3	91.6
Rsa1.0_00128.1.g6135.t1	ref|XP_002893626.1| hypothetical protein ARALYDRAFT_473274 [Arabidopsis lyrata subsp. lyrata] gi|297339468|gb|EFH69885.1| hypothetical protein ARALYDRAFT_473274 [Arabidopsis lyrata subsp. lyrata]	179	192	2.00E-22	107.3	51.4	62.6	hypothetical protein ARALYDRAFT_473274	gbpln	Arabidopsis lyrata	AT1G30475.1 | Symbols: | BEST Arabidopsis thaliana protein match is: embryo defective 1303 (TAIR:AT1G56200.1); Has 148 Blast hits to 148 proteins in 34 species: Archae - 0; Bacteria - 14; Metazoa - 63; Fungi - 0; Plants - 62; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr1:10788501-10789943 REVERSE LENGTH=191	179	191	2.00E-20	106.7	48.6	59.2
Rsa1.0_00128.1.g6136.t1	gb|EOA37969.1| hypothetical protein CARUB_v10009438mg [Capsella rubella]	424	382	1.00E-141	90.1	72.6	78.5	hypothetical protein CARUB_v10009438mg	gbpln	Capsella rubella	AT1G30480.1 | Symbols: DRT111 | D111/G-patch domain-containing protein | chr1:10790315-10792423 FORWARD LENGTH=387	424	387	1.00E-143	91.3	72.2	79.0
Rsa1.0_00128.1.g6137.t2	ref|NP_001078388.1| AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein [Arabidopsis thaliana] gi|332658025|gb|AEE83425.1| AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein [Arabidopsis thaliana]	184	548	1.00E-14	297.8	22.8	25.0	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	gbpln	Arabidopsis thaliana	AT4G14350.3 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr4:8256353-8259934 REVERSE LENGTH=548	184	548	4.00E-17	297.8	22.8	25.0
Rsa1.0_00128.1.g6138.t1	ref|XP_002868291.1| hypothetical protein ARALYDRAFT_915444 [Arabidopsis lyrata subsp. lyrata] gi|297314127|gb|EFH44550.1| hypothetical protein ARALYDRAFT_915444 [Arabidopsis lyrata subsp. lyrata]	451	456	0	101.1	88.2	90.7	hypothetical protein ARALYDRAFT_915444	gbpln	Arabidopsis lyrata	AT4G14340.1 | Symbols: CKI1, CKL11 | casein kinase I | chr4:8248532-8251668 REVERSE LENGTH=457	451	457	0	101.3	88.5	90.9

Rsa1.0_00128.1.g6139.t1	emb|CAB10212.1| kinesin like protein [Arabidopsis thaliana] gi|7268138|emb|CAB78475.1| kinesin like protein [Arabidopsis thaliana]	516	959	0	185.9	77.9	84.5	kinesin like protein	gbpln	Arabidopsis thaliana	AT4G14330.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:8244228-8247286 FORWARD LENGTH=869	516	869	0	168.4	77.9	84.5
Rsa1.0_00128.1.g6140.t1	gb|EOA15341.1| hypothetical protein CARUB_v10004114mg [Capsella rubella]	200	864	7.00E-85	432.0	82.0	90.5	hypothetical protein CARUB_v10004114mg	gbpln	Capsella rubella	AT4G14330.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:8244228-8247286 FORWARD LENGTH=869	200	869	5.00E-87	434.5	82.0	89.5
Rsa1.0_00128.1.g6141.t1	gb|AAK94425.1|AF398144_1 60S ribosomal protein L144 [Brassica rapa subsp. pekinensis]	105	119	2.00E-52	113.3	100.0	100.0	60S ribosomal protein L144	gbpln	Brassica rapa	AT4G14320.1 | Symbols: | Zinc-binding ribosomal protein family protein | chr4:8242684-8243805 REVERSE LENGTH=105	105	105	4.00E-53	100.0	96.2	97.1
Rsa1.0_00128.1.g6142.t1	ref|NP_001031638.1| uncharacterized protein [Arabidopsis thaliana] gi|332658017|gb|AEE83417.1| uncharacterized protein AT4G14315 [Arabidopsis thaliana]	61	59	2.00E-15	96.7	73.8	83.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G14315.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:8240994-8241173 FORWARD LENGTH=59	61	59	3.00E-18	96.7	73.8	83.6
Rsa1.0_00128.1.g6143.t1	ref|NP_193167.3| transducin/WD40 domain-containing protein-like protein [Arabidopsis thaliana] gi|332658016|gb|AEE83416.1| transducin/WD40 domain-containing protein-like protein [Arabidopsis thaliana]	845	893	0	105.7	80.4	87.1	transducin/WD40 domain-containing protein-like protein	gbpln	Arabidopsis thaliana	AT4G14310.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:8237137-8240324 REVERSE LENGTH=893	845	893	0	105.7	80.4	87.1
Rsa1.0_00128.1.g6144.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00128.1.g6145.t1	gb|EOA16593.1| hypothetical protein CARUB_v10004759mg, partial [Capsella rubella] gi|482552401|gb|EOA16594.1| hypothetical protein CARUB_v10004759mg, partial [Capsella rubella]	384	463	1.00E-122	120.6	72.1	76.8	hypothetical protein CARUB_v10004759mg, partial	gbpln	Capsella rubella	AT4G14300.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:8231179-8232785 FORWARD LENGTH=411	384	411	1.00E-117	107.0	69.8	74.5
Rsa1.0_00128.1.g6146.t2	ref|XP_002868296.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314132|gb|EFH44555.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	523	557	0	106.5	87.0	90.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G14290.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:8225547-8230057 REVERSE LENGTH=558	523	558	0	106.7	85.9	90.8
Rsa1.0_00128.1.g6147.t1	gb|EOA16558.1| hypothetical protein CARUB_v10004717mg [Capsella rubella]	472	478	0	101.3	85.0	90.7	hypothetical protein CARUB_v10004717mg	gbpln	Capsella rubella	AT4G14230.1 | Symbols: | CBS domain-containing protein with a domain of unknown function (DUF21) | chr4:8200850-8203130 REVERSE LENGTH=495	472	495	0	104.9	84.5	91.3
Rsa1.0_00128.1.g6148.t1	gb|EOA15685.1| hypothetical protein CARUB_v10006394mg [Capsella rubella]	141	134	2.00E-41	95.0	62.4	75.2	hypothetical protein CARUB_v10006394mg	gbpln	Capsella rubella	AT4G14225.1 | Symbols: | A20/AN1-like zinc finger family protein | chr4:8198777-8199202 FORWARD LENGTH=125	141	125	2.00E-40	88.7	57.4	66.0
Rsa1.0_00128.1.g6149.t1	ref|NP_193158.2| E3 ubiquitin-protein ligase RHF1A [Arabidopsis thaliana] gi|75339838|sp|Q4TU14.1|RHF1A_ARATH RecName: Full=E3 ubiquitin-protein ligase RHF1A; AltName: Full=RING-H2 zinc finger protein RHF1a gi|66865948|gb|AAY57608.1| RING finger family protein [Arabidopsis thaliana] gi|332657995|gb|AEE83395.1| E3 ubiquitin-protein ligase RHF1A [Arabidopsis thaliana]	316	371	1.00E-103	117.4	73.4	80.7	E3 ubiquitin-protein ligase RHF1A	gbpln	Arabidopsis thaliana	AT4G14220.1 | Symbols: RHF1A | RING-H2 group F1A | chr4:8196012-8198240 FORWARD LENGTH=371	316	371	1.00E-106	117.4	73.4	80.7
Rsa1.0_00128.1.g6150.t1	gb|ADT89708.1| chloroplast phytoene desaturase [Brassica napus] gi|315185067|gb|ADT89709.1| chloroplast phytoene desaturase [Brassica napus]	536	565	0	105.4	96.3	98.1	chloroplast phytoene desaturase	gbpln	Brassica napus	AT4G14210.1 | Symbols: PDS3, PDS, PDE226 | phytoene desaturase 3 | chr4:8190426-8194769 REVERSE LENGTH=566	536	566	0	105.6	91.6	97.0
Rsa1.0_00128.1.g6151.t1	ref|NP_190196.1| Histidyl-tRNA synthetase 1 [Arabidopsis thaliana] gi|3659909|gb|AAC61600.1| histidyl-tRNA synthetase [Arabidopsis thaliana] gi|7798998|emb|CAB90937.1| histidyl-tRNA synthetase [Arabidopsis thaliana] gi|15810389|gb|AAL07082.1| putative histidyl-tRNA synthetase [Arabidopsis thaliana] gi|21436315|gb|AAM51327.1| putative histidyl-tRNA synthetase [Arabidopsis thaliana] gi|332644592|gb|AEE78113.1| Histidyl-tRNA synthetase 1 [Arabidopsis thaliana]	490	486	0	99.2	90.4	93.9	Histidyl-tRNA synthetase 1	gbpln	Arabidopsis thaliana	AT3G46100.1 | Symbols: ATHRS1, HRS1 | Histidyl-tRNA synthetase 1 | chr3:16928444-16930984 REVERSE LENGTH=486	490	486	0	99.2	90.4	93.9

Rsa1.0_00128.1.g6152.t1	ref|XP_002870333.1| hypothetical protein ARALYDRAFT_493493 [Arabidopsis lyrata subsp. lyrata] gi|297316169|gb|EFH46592.1| hypothetical protein ARALYDRAFT_493493 [Arabidopsis lyrata subsp. lyrata]	781	763	0	97.7	90.5	94.6	hypothetical protein ARALYDRAFT_493493	gbpln	Arabidopsis lyrata	AT4G14160.2 | Symbols: | Sec23/Sec24 protein transport family protein | chr4:8167574-8173026 FORWARD LENGTH=772	781	772	0	98.8	87.2	91.8
Rsa1.0_00128.1.g6153.t1	ref|NP_680684.1| uncharacterized protein [Arabidopsis thaliana] gi|117168131|gb|ABK32148.1| At4g14145 [Arabidopsis thaliana] gi|332657981|gb|AEE83381.1| uncharacterized protein AT4G14145 [Arabidopsis thaliana]	120	134	4.00E-52	111.7	86.7	90.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G14145.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:8152499-8153091 REVERSE LENGTH=134	120	134	7.00E-55	111.7	86.7	90.8
Rsa1.0_00128.1.g6154.t1	ref|NP_195548.6| Patched family protein [Arabidopsis thaliana] gi|332661516|gb|AEE86916.1| Patched family protein [Arabidopsis thaliana]	1306	1273	0	97.5	86.4	92.2	Patched family protein	gbpln	Arabidopsis thaliana	AT4G38350.1 | Symbols: | Patched family protein | chr4:17958324-17966846 REVERSE LENGTH=1273	1306	1273	0	97.5	86.4	92.2
Rsa1.0_00128.1.g6155.t1	ref|NP_195551.5| mate efflux domain-containing protein [Arabidopsis thaliana] gi|325530113|sp|Q9SVE7.2|MATE3_ARATH RecName: Full=MATE efflux family protein 3, chloroplastic; AltName: Full=Protein DTX45; Flags: Precursor gi|332661521|gb|AEE86921.1| MATE efflux family protein 3 [Arabidopsis thaliana]	753	560	0	74.4	63.5	66.9	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT4G38380.1 | Symbols: | MATE efflux family protein | chr4:17971855-17974787 REVERSE LENGTH=560	753	560	0	74.4	63.5	66.9
Rsa1.0_00128.1.g6156.t1	ref|NP_198882.1| ATP synthase mitochondrial F1 complex assembly factor 2 [Arabidopsis thaliana] gi|14517426|gb|AAK62603.1| AT5g40660/MNF13_180 [Arabidopsis thaliana] gi|22655442|gb|AAM98313.1| At5g40660/MNF13_180 [Arabidopsis thaliana] gi|332007196|gb|AED94579.1| ATP12 protein-related [Arabidopsis thaliana]	68	325	9.00E-30	477.9	92.6	94.1	ATP synthase mitochondrial F1 complex assembly factor 2	gbpln	Arabidopsis thaliana	AT5G40660.1 | Symbols: | ATP12 protein-related | chr5:16283650-16285161 REVERSE LENGTH=325	68	325	1.00E-32	477.9	92.6	94.1
Rsa1.0_00128.1.g6157.t2	ref|NP_568041.1| ACT-like protein tyrosine kinase family protein [Arabidopsis thaliana] gi|332661531|gb|AEE86931.1| ACT-like protein tyrosine kinase family protein [Arabidopsis thaliana]	571	575	0	100.7	85.8	90.0	ACT-like protein tyrosine kinase family protein	gbpln	Arabidopsis thaliana	AT4G38470.1 | Symbols: | ACT-like protein tyrosine kinase family protein | chr4:17999432-18003551 FORWARD LENGTH=575	571	575	0	100.7	85.8	90.0
Rsa1.0_00128.1.g6158.t1	ref|NP_568042.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|332661532|gb|AEE86932.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	496	471	0	95.0	68.5	74.2	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G38480.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:18003957-18006002 FORWARD LENGTH=471	496	471	0	95.0	68.5	74.2
Rsa1.0_00128.1.g6159.t1	ref|NP_568043.1| uncharacterized protein [Arabidopsis thaliana] gi|15451094|gb|AAK96818.1| Unknown protein [Arabidopsis thaliana] gi|18377452|gb|AAL66892.1| unknown protein [Arabidopsis thaliana] gi|332661533|gb|AEE86933.1| uncharacterized protein AT4G38490 [Arabidopsis thaliana]	153	153	6.00E-39	100.0	63.4	74.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G38490.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:18006385-18007203 FORWARD LENGTH=153	153	153	2.00E-41	100.0	63.4	74.5
Rsa1.0_00128.1.g6160.t1	ref|NP_195564.2| putative protein phosphatase 2C 64 [Arabidopsis thaliana] gi|42573223|ref|NP_974708.1| putative protein phosphatase 2C 64 [Arabidopsis thaliana] gi|75251246|sp|Q5PNS9.1|P2C64_ARATH RecName: Full=Probable protein phosphatase 2C 64; Short=AtPP2C64 gi|56382009|gb|AAV85723.1| At4g38520 [Arabidopsis thaliana] gi|59958308|gb|AAX12864.1| At4g38520 [Arabidopsis thaliana] gi|332661541|gb|AEE86941.1| putative protein phosphatase 2C 64 [Arabidopsis thaliana] gi|332661542|gb|AEE86942.1| putative protein phosphatase 2C 64 [Arabidopsis thaliana]	378	400	0	105.8	88.1	93.1	putative protein phosphatase 2C 64	gbpln	Arabidopsis thaliana	AT4G38520.2 | Symbols: | Protein phosphatase 2C family protein | chr4:18015999-18017514 REVERSE LENGTH=400	378	400	0	105.8	88.1	93.1
Rsa1.0_00128.1.g6161.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00128.1.g6162.t2</td><td>ref|NP_195567.2| phospholipase like protein (PEARLI 4) [Arabidopsis thaliana] gi|13430740|gb|AAK25992.1|AF360282_1 putative Phospholipase [Arabidopsis thaliana] gi|23397110|gb|AAN31839.1| putative phospholipase [Arabidopsis thaliana] gi|25054999|gb|AAN71965.1| putative phospholipase [Arabidopsis thaliana] gi|332661545|gb|AEE86945.1| phospholipase like protein (PEARLI 4) [Arabidopsis thaliana]</td><td>601</td><td>612</td><td>0</td><td>101.8</td><td>76.2</td><td>84.7</td><td>phospholipase like protein (PEARLI 4)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G38550.1 | Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) family | chr4:18025886-18028546 FORWARD LENGTH=612</td><td>601</td><td>612</td><td>0</td><td>101.8</td><td>76.2</td><td>84.7</td></tr>
<tr><td>Rsa1.0_00128.1.g6163.t1</td><td>ref|XP_002866808.1| hypothetical protein ARALYDRAFT_327813 [Arabidopsis lyrata subsp. lyrata] gi|297312644|gb|EFH43067.1| hypothetical protein ARALYDRAFT_327813 [Arabidopsis lyrata subsp. lyrata]</td><td>522</td><td>520</td><td>1.00E-134</td><td>99.6</td><td>58.8</td><td>70.1</td><td>hypothetical protein ARALYDRAFT_327813</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38560.2 | Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) family | chr4:18029275-18031191 FORWARD LENGTH=523</td><td>522</td><td>523</td><td>1.00E-132</td><td>100.2</td><td>56.9</td><td>69.7</td></tr>
<tr><td>Rsa1.0_00128.1.g6164.t1</td><td>gb|AAM77369.1|AF521301_1 phosphatidylinositol synthase [Brassica napus]</td><td>226</td><td>227</td><td>1.00E-114</td><td>100.4</td><td>88.1</td><td>95.1</td><td>phosphatidylinositol synthase</td><td>gbpln</td><td>Brassica napus</td><td>AT4G38570.1 | Symbols: PIS2 | probable CDP-diacylglycerol--inositol 3-phosphatidyltransferase 2 | chr4:18031420-18033091 REVERSE LENGTH=225</td><td>226</td><td>225</td><td>1.00E-116</td><td>99.6</td><td>92.9</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00128.1.g6165.t1</td><td>gb|EOA15649.1| hypothetical protein CARUB_v10005941mg [Capsella rubella]</td><td>153</td><td>153</td><td>5.00E-82</td><td>100.0</td><td>96.1</td><td>100.0</td><td>hypothetical protein CARUB_v10005941mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G38580.1 | Symbols: ATFP6, HIPP26, FP6 | farnesylated protein 6 | chr4:18034596-18035693 FORWARD LENGTH=153</td><td>153</td><td>153</td><td>2.00E-84</td><td>100.0</td><td>96.1</td><td>99.3</td></tr>
<tr><td>Rsa1.0_00128.1.g6166.t1</td><td>ref|XP_002868849.1| hypothetical protein ARALYDRAFT_912310 [Arabidopsis lyrata subsp. lyrata] gi|297314685|gb|EFH45108.1| hypothetical protein ARALYDRAFT_912310 [Arabidopsis lyrata subsp. lyrata]</td><td>1890</td><td>1884</td><td>0</td><td>99.7</td><td>88.1</td><td>92.8</td><td>hypothetical protein ARALYDRAFT_912310</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38600.1 | Symbols: KAK, UPL3 | HEAT repeat ;HECT-domain (ubiquitin-transferase) | chr4:18041503-18049292 REVERSE LENGTH=1888</td><td>1890</td><td>1888</td><td>0</td><td>99.9</td><td>88.3</td><td>93.4</td></tr>
<tr><td>Rsa1.0_00128.1.g6167.t3</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00128.1.g6168.t1</td><td>ref|NP_195574.1| transcription repressor MYB4 [Arabidopsis thaliana] gi|56749359|sp|Q9SZP1.1|MYB4_ARATH RecName: Full=Transcription repressor MYB4; AltName: Full=Myb-related protein 4; Short=AtMYB4 gi|4467149|emb|CAB37518.1| putative transcription factor (MYB4) [Arabidopsis thaliana] gi|7270845|emb|CAB80526.1| putative transcription factor (MYB4) [Arabidopsis thaliana] gi|17979197|gb|AAL49837.1| putative transcription factor MYB4 [Arabidopsis thaliana] gi|21689787|gb|AAM67537.1| putative transcription factor MYB4 [Arabidopsis thaliana] gi|22655176|gb|AAM98178.1| putative transcription factor MYB4 [Arabidopsis thaliana] gi|30023754|gb|AAP13410.1| At4g38620 [Arabidopsis thaliana] gi|41619362|gb|AAS10085.1| MYB transcription factor [Arabidopsis thaliana] gi|332661555|gb|AEE86955.1| transcription repressor MYB4 [Arabidopsis thaliana]</td><td>288</td><td>282</td><td>1.00E-135</td><td>97.9</td><td>85.4</td><td>89.6</td><td>transcription repressor MYB4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G38620.1 | Symbols: ATMYB4, MYB4 | myb domain protein 4 | chr4:18053866-18054876 FORWARD LENGTH=282</td><td>288</td><td>282</td><td>1.00E-138</td><td>97.9</td><td>85.4</td><td>89.6</td></tr>
</table>

Rsa1.0_00128.1.g6169.t1	ref|NP_195575.1| 26S proteasome non-ATPase regulatory subunit 4 [Arabidopsis thaliana] gi|1709794|sp|P55034.1|PSMD4_ARATH RecName: Full=26S proteasome non-ATPase regulatory subunit 4; AltName: Full=26S proteasome regulatory subunit RPN10; AltName: Full=26S proteasome regulatory subunit S5A; AltName: Full=Multiubiquitin chain-binding protein 1; Short=AtMCB1; AltName: Full=Protein REGULATORY PARTICLE NON-ATPASE 10 gi|13430814|gb|AAK26029.1|AF360319_1 putative multiubiquitin chain binding protein MBP1 [Arabidopsis thaliana] gi|1165206|gb|AAA85583.1| MBP1 [Arabidopsis thaliana] gi|4467150|emb|CAB37519.1| multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana] gi|7270846|emb|CAB80527.1| multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana] gi|21281020|gb|AAM44937.1| putative multiubiquitin chain binding protein MBP1 [Arabidopsis thaliana] gi|110735112|gb|ABG89126.1| RPN10 [synthetic construct] gi|332661556|gb|AEE86956.1| 26S proteasome non-ATPase regulatory subunit 4 [Arabidopsis thaliana]	381	386	0	101.3	96.9	98.7	26S proteasome non-ATPase regulatory subunit 4	gbpln	Arabidopsis thaliana	AT4G38630.1 | Symbols: RPN10, MCB1, ATMCB1, MBP1 | regulatory particle non-ATPase 10 | chr4:18057357-18059459 REVERSE LENGTH=386	381	386	0	101.3	96.9	98.7
Rsa1.0_00128.1.g6170.t1	ref|NP_568045.1| Plasma-membrane choline transporter family protein [Arabidopsis thaliana] gi|16649077|gb|AAL24390.1| putative protein [Arabidopsis thaliana] gi|21387167|gb|AAM47987.1| putative protein [Arabidopsis thaliana] gi|332661557|gb|AEE86957.1| Plasma-membrane choline transporter family protein [Arabidopsis thaliana]	544	556	0	102.2	87.9	94.5	Plasma-membrane choline transporter family protein	gbpln	Arabidopsis thaliana	AT4G38640.1 | Symbols: | Plasma-membrane choline transporter family protein | chr4:18059884-18062091 REVERSE LENGTH=556	544	556	0	102.2	87.9	94.5
Rsa1.0_00128.1.g6171.t1	ref|XP_002866813.1| glycosyl hydrolase family 10 protein [Arabidopsis lyrata subsp. lyrata] gi|297312649|gb|EFH43072.1| glycosyl hydrolase family 10 protein [Arabidopsis lyrata subsp. lyrata]	565	562	0	99.5	85.1	91.9	glycosyl hydrolase family 10 protein	gbpln	Arabidopsis lyrata	AT4G38650.1 | Symbols: | Glycosyl hydrolase family 10 protein | chr4:18063377-18065769 FORWARD LENGTH=562	565	562	0	99.5	83.5	89.7
Rsa1.0_00128.1.g6172.t1	ref|XP_002868852.1| hypothetical protein ARALYDRAFT_912315 [Arabidopsis lyrata subsp. lyrata] gi|297314688|gb|EFH45111.1| hypothetical protein ARALYDRAFT_912315 [Arabidopsis lyrata subsp. lyrata]	354	345	1.00E-168	97.5	88.1	90.4	hypothetical protein ARALYDRAFT_912315	gbpln	Arabidopsis lyrata	AT4G38660.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr4:18066448-18067984 REVERSE LENGTH=345	354	345	1.00E-165	97.5	85.3	89.8
Rsa1.0_00128.1.g6173.t1	ref|NP_195581.1| 1-phosphatidylinositol phosphodiesterase-related protein [Arabidopsis thaliana] gi|4467156|emb|CAB37525.1| putative protein [Arabidopsis thaliana] gi|7270852|emb|CAB80533.1| putative protein [Arabidopsis thaliana] gi|17979229|gb|AAL49931.1| AT4g38690/F20M13_250 [Arabidopsis thaliana] gi|20147101|gb|AAM10267.1| AT4g38690/F20M13_250 [Arabidopsis thaliana] gi|332661565|gb|AEE86965.1| 1-phosphatidylinositol phosphodiesterase-related protein [Arabidopsis thaliana]	318	318	1.00E-176	100.0	93.4	95.9	1-phosphatidylinositol phosphodiesterase-related protein	gbpln	Arabidopsis thaliana	AT4G38690.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr4:18074743-18075699 REVERSE LENGTH=318	318	318	1.00E-179	100.0	93.4	95.9
Rsa1.0_00128.1.g6174.t1	ref|NP_001190956.1| glycine-rich protein [Arabidopsis thaliana] gi|332661568|gb|AEE86968.1| glycine-rich protein [Arabidopsis thaliana]	449	465	1.00E-123	103.6	71.7	78.2	glycine-rich protein	gbpln	Arabidopsis thaliana	AT4G38710.2 | Symbols: | glycine-rich protein | chr4:18078141-18080002 REVERSE LENGTH=465	449	465	1.00E-126	103.6	71.7	78.2
Rsa1.0_00128.1.g6175.t1	gb|EOA16996.1| hypothetical protein CARUB_v10005234mg [Capsella rubella]	341	326	1.00E-176	95.6	88.6	92.4	hypothetical protein CARUB_v10005234mg	gbpln	Capsella rubella	AT4G38730.1 | Symbols: | Protein of unknown function (DUF803) | chr4:18080484-18082305 REVERSE LENGTH=326	341	326	1.00E-176	95.6	87.1	90.9
Rsa1.0_00128.1.g6176.t1	gb|EOA15636.1| hypothetical protein CARUB_v10005879mg [Capsella rubella]	172	173	5.00E-90	100.6	93.6	95.9	hypothetical protein CARUB_v10005879mg	gbpln	Capsella rubella	AT4G38740.1 | Symbols: ROC1 | rotamase CYP 1 | chr4:18083620-18084138 REVERSE LENGTH=172	172	172	3.00E-91	100.0	92.4	95.3
Rsa1.0_00128.1.g6177.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00128.1.g6178.t1	ref|XP_002868862.1| hypothetical protein ARALYDRAFT_490641 [Arabidopsis lyrata subsp. lyrata] gi|297314698|gb|EFH45121.1| hypothetical protein ARALYDRAFT_490641 [Arabidopsis lyrata subsp. lyrata]	463	458	1.00E-81	98.9	31.1	33.7	hypothetical protein ARALYDRAFT_490641	gbpln	Arabidopsis lyrata	AT4G38770.1 | Symbols: PRP4, ATPRP4 | proline-rich protein 4 | chr4:18097009-18098448 REVERSE LENGTH=448	463	448	5.00E-78	96.8	31.1	33.7
Rsa1.0_00128.1.g6179.t1	ref|NP_178437.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75216181|sp|Q9ZQ74.1|PP146_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g03380, mitochondrial; Flags: Precursor gi|4335760|gb|AAD17437.1| unknown protein [Arabidopsis thaliana] gi|330250600|gb|AEC05694.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	67	689	2.00E-22	1028.4	73.1	83.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G03380.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:1028292-1030361 FORWARD LENGTH=689	67	689	3.00E-25	1028.4	73.1	83.6
Rsa1.0_00128.1.g6180.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00128.1.g6181.t1	gb|EOA17208.1| hypothetical protein CARUB_v10005480mg [Capsella rubella]	272	273	1.00E-152	100.4	97.4	99.3	hypothetical protein CARUB_v10005480mg	gbpln	Capsella rubella	AT4G38790.1 | Symbols: | ER lumen protein retaining receptor family protein | chr4:18111426-18112977 FORWARD LENGTH=273	272	273	1.00E-152	100.4	96.0	97.4
Rsa1.0_00128.1.g6182.t1	ref|XP_002868864.1| ATMTN1 [Arabidopsis lyrata subsp. lyrata] gi|297314700|gb|EFH45123.1| ATMTN1 [Arabidopsis lyrata subsp. lyrata]	259	266	1.00E-127	102.7	89.6	95.4	ATMTN1	gbpln	Arabidopsis lyrata	AT4G38800.1 | Symbols: ATMTN1, ATMTAN1, MTN1, MTAN1 | methylthioadenosine nucleosidase 1 | chr4:18113355-18114996 REVERSE LENGTH=267	259	267	1.00E-128	103.1	88.0	95.4
Rsa1.0_00128.1.g6183.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00128.1.g6184.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00129.1.g6185.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00129.1.g6186.t1	ref|XP_002873009.1| hypothetical protein ARALYDRAFT_486927 [Arabidopsis lyrata subsp. lyrata] gi|297318846|gb|EFH49268.1| hypothetical protein ARALYDRAFT_486927 [Arabidopsis lyrata subsp. lyrata]	184	454	2.00E-43	246.7	50.5	59.2	hypothetical protein ARALYDRAFT_486927	gbpln	Arabidopsis lyrata	AT5G01490.1 | Symbols: CAX4, ATCAX4 | cation exchanger 4 | chr5:195589-198465 FORWARD LENGTH=454	184	454	3.00E-44	246.7	49.5	55.4
Rsa1.0_00129.1.g6187.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00129.1.g6188.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	376	255	2.00E-59	67.8	33.5	43.6	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	376	302	7.00E-37	80.3	24.7	35.1
Rsa1.0_00129.1.g6189.t1	ref|NP_195758.1| transcription factor [Arabidopsis thaliana] gi|75337089|sp|Q9SDW0.1|TGT3A_ARATH RecName: Full=Trihelix transcription factor GT-3a; AltName: Full=Trihelix DNA-binding protein GT-3a gi|6573264|gb|AAF17610.1|AF206715_1 transcription factor GT-3a [Arabidopsis thaliana] gi|7320716|emb|CAB81921.1| transcription factor GT-3a [Arabidopsis thaliana] gi|30060335|gb|AAP13347.1| transcription factor GT-3a [Arabidopsis thaliana] gi|114050647|gb|ABI49473.1| At5g01380 [Arabidopsis thaliana] gi|332002951|gb|AED90334.1| trihelix transcription factor GT-3a [Arabidopsis thaliana]	311	323	1.00E-105	103.9	77.8	87.1	transcription factor	gbpln	Arabidopsis thaliana	AT5G01380.1 | Symbols: | Homeodomain-like superfamily protein | chr5:155784-157451 REVERSE LENGTH=323	311	323	1.00E-108	103.9	77.8	87.1
Rsa1.0_00129.1.g6190.t1	gb|EOA22576.1| hypothetical protein CARUB_v10003236mg [Capsella rubella]	364	134	1.00E-14	36.8	14.6	21.7	hypothetical protein CARUB_v10003236mg	gbpln	Capsella rubella	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	364	303	5.00E-15	83.2	14.6	21.7
Rsa1.0_00129.1.g6191.t1	ref|XP_002870931.1| hypothetical protein ARALYDRAFT_486945 [Arabidopsis lyrata subsp. lyrata] gi|297316768|gb|EFH47190.1| hypothetical protein ARALYDRAFT_486945 [Arabidopsis lyrata subsp. lyrata]	601	603	0	100.3	91.7	95.3	hypothetical protein ARALYDRAFT_486945	gbpln	Arabidopsis lyrata	AT5G01320.1 | Symbols: | Thiamine pyrophosphate dependent pyruvate decarboxylase family protein | chr5:129484-131625 REVERSE LENGTH=603	601	603	0	100.3	89.4	94.3
Rsa1.0_00129.1.g6192.t1	ref|XP_002873016.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297318853|gb|EFH49275.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	687	898	0	130.7	81.5	90.4	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT5G01310.1 | Symbols: APTX | APRATAXIN-like | chr5:125304-128960 FORWARD LENGTH=912	687	912	0	132.8	81.1	90.0

Rsa1.0_00129.1.g6193.t1	ref|NP_195745.1| alpha 1,4-glycosyltransferase family protein [Arabidopsis thaliana] gi|6759448|emb|CAB69853.1| putative protein [Arabidopsis thaliana] gi|51315396|gb|AAT99803.1| At5g01250 [Arabidopsis thaliana] gi|110738709|dbj|BAF01279.1| hypothetical protein [Arabidopsis thaliana] gi|332002934|gb|AED90317.1| alpha 1,4-glycosyltransferase family protein [Arabidopsis thaliana]	532	407	1.00E-176	76.5	58.3	65.0	alpha 1,4-glycosyltransferase family protein	gbpln	Arabidopsis thaliana	AT5G01250.1 | Symbols: | alpha 1,4-glycosyltransferase family protein | chr5:102370-103593 REVERSE LENGTH=407	532	407	1.00E-179	76.5	58.3	65.0
Rsa1.0_00129.1.g6194.t1	gb|EOA20516.1| hypothetical protein CARUB_v10000830mg [Capsella rubella]	496	488	0	98.4	93.8	95.4	hypothetical protein CARUB_v10000830mg	gbpln	Capsella rubella	AT5G01240.1 | Symbols: LAX1 | like AUXIN RESISTANT 1 | chr5:98228-101493 FORWARD LENGTH=488	496	488	0	98.4	91.9	94.6
Rsa1.0_00129.1.g6195.t1	gb|EOA21184.1| hypothetical protein CARUB_v10001529mg [Capsella rubella]	315	309	1.00E-173	98.1	93.3	96.5	hypothetical protein CARUB_v10001529mg	gbpln	Capsella rubella	AT5G01230.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:92789-95380 REVERSE LENGTH=309	315	309	1.00E-176	98.1	93.7	96.5
Rsa1.0_00129.1.g6196.t1	gb|EOA19296.1| hypothetical protein CARUB_v10002205mg [Capsella rubella]	155	148	5.00E-33	95.5	58.7	73.5	hypothetical protein CARUB_v10002205mg	gbpln	Capsella rubella	AT3G09032.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G01225.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:2757605-2758045 REVERSE LENGTH=146	155	146	5.00E-33	94.2	52.3	67.1
Rsa1.0_00129.1.g6197.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	1446	1489	0	103.0	54.6	69.3	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1446	1262	1.00E-150	87.3	18.4	24.1
Rsa1.0_00129.1.g6198.t1	gb|EOA20265.1| hypothetical protein CARUB_v10000567mg [Capsella rubella]	566	577	0	101.9	86.2	92.2	hypothetical protein CARUB_v10000567mg	gbpln	Capsella rubella	AT5G01180.1 | Symbols: PTR5, ATPTR5 | peptide transporter 5 | chr5:61257-63240 REVERSE LENGTH=570	566	570	0	100.7	85.5	91.7
Rsa1.0_00129.1.g6199.t1	ref|XP_002873024.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata] gi|297318861|gb|EFH49283.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	517	575	1.00E-157	111.2	68.9	78.7	glycine-rich protein	gbpln	Arabidopsis lyrata	AT5G01170.1 | Symbols: | Protein of unknown function (DUF740) | chr5:58315-60021 FORWARD LENGTH=568	517	568	1.00E-152	109.9	71.0	79.7
Rsa1.0_00129.1.g6200.t1	gb|EOA20910.1| hypothetical protein CARUB_v10001245mg [Capsella rubella]	360	361	1.00E-162	100.3	81.9	87.2	hypothetical protein CARUB_v10001245mg	gbpln	Capsella rubella	AT5G01160.1 | Symbols: | RING/U-box superfamily protein | chr5:54280-55727 FORWARD LENGTH=360	360	360	1.00E-159	100.0	80.0	86.1
Rsa1.0_00129.1.g6201.t1	gb|EOA20523.1| hypothetical protein CARUB_v10000837mg [Capsella rubella]	436	485	1.00E-143	111.2	65.8	79.4	hypothetical protein CARUB_v10000837mg	gbpln	Capsella rubella	AT5G01150.1 | Symbols: | Protein of unknown function (DUF674) | chr5:51988-53649 FORWARD LENGTH=501	436	501	1.00E-110	114.9	55.0	70.9
Rsa1.0_00129.1.g6202.t1	gb|EOA22313.1| hypothetical protein CARUB_v10002914mg [Capsella rubella]	500	513	0	102.6	74.2	86.2	hypothetical protein CARUB_v10002914mg	gbpln	Capsella rubella	AT5G01120.1 | Symbols: | Protein of unknown function (DUF674) | chr5:45281-46986 FORWARD LENGTH=510	500	510	0	102.0	71.8	83.0
Rsa1.0_00129.1.g6203.t1	gb|EMS60894.1| Polyubiquitin [Triticum urartu]	130	458	4.00E-50	352.3	78.5	81.5	Polyubiquitin	gbpln	Triticum urartu	AT1G65350.1 | Symbols: UBQ13 | ubiquitin 13 | chr1:24272518-24277275 REVERSE LENGTH=319	130	319	3.00E-52	245.4	78.5	81.5
Rsa1.0_00129.1.g6204.t1	gb|EOA35496.1| hypothetical protein CARUB_v10020702mg [Capsella rubella]	171	307	1.00E-27	179.5	33.9	40.9	hypothetical protein CARUB_v10020702mg	gbpln	Capsella rubella	AT1G70440.1 | Symbols: SRO3 | similar to RCD one 3 | chr1:26549354-26550520 REVERSE LENGTH=305	171	305	1.00E-28	178.4	32.2	40.9
Rsa1.0_00129.1.g6205.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00129.1.g6206.t1	ref|XP_002870942.1| hypothetical protein ARALYDRAFT_486969 [Arabidopsis lyrata subsp. lyrata] gi|297316779|gb|EFH47201.1| hypothetical protein ARALYDRAFT_486969 [Arabidopsis lyrata subsp. lyrata]	632	630	0	99.7	84.3	90.0	hypothetical protein ARALYDRAFT_486969	gbpln	Arabidopsis lyrata	AT5G01100.1 | Symbols: | O-fucosyltransferase family protein | chr5:34872-37756 REVERSE LENGTH=631	632	631	0	99.8	84.3	91.0
Rsa1.0_00129.1.g6207.t1	ref|XP_002870943.1| hypothetical protein ARALYDRAFT_324871 [Arabidopsis lyrata subsp. lyrata] gi|297316780|gb|EFH47202.1| hypothetical protein ARALYDRAFT_324871 [Arabidopsis lyrata subsp. lyrata]	76	79	1.00E-16	103.9	57.9	67.1	hypothetical protein ARALYDRAFT_324871	gbpln	Arabidopsis lyrata	AT5G01075.1 | Symbols: | Glycosyl hydrolase family 35 protein | chr5:27095-27423 REVERSE LENGTH=81	76	81	1.00E-15	106.6	57.9	69.7
Rsa1.0_00129.1.g6208.t1	gb|EOA21547.1| hypothetical protein CARUB_v10001956mg [Capsella rubella]	207	211	4.00E-87	101.9	82.1	87.4	hypothetical protein CARUB_v10001956mg	gbpln	Capsella rubella	AT5G01070.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:25094-25799 REVERSE LENGTH=206	207	206	1.00E-82	99.5	79.2	85.0

Rsa1.0_00129.1.g6209.t1	ref|NP_195726.1| Protein kinase protein with tetratricopeptide repeat domain [Arabidopsis thaliana] gi|6759429|emb|CAB69834.1| putative protein-kinase [Arabidopsis thaliana] gi|332002910|gb|AED90293.1| Protein kinase protein with tetratricopeptide repeat domain [Arabidopsis thaliana]	850	499	1.00E-148	58.7	30.0	33.9	Protein kinase protein with tetratricopeptide repeat domain	gbpln	Arabidopsis thaliana	AT5G01060.1 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr5:22740-24847 FORWARD LENGTH=499	850	499	1.00E-150	58.7	30.0	33.9
Rsa1.0_00129.1.g6210.t1	gb|EOA19354.1| hypothetical protein CARUB_v10000287mg [Capsella rubella] gi|482555163|gb|EOA19355.1| hypothetical protein CARUB_v10000287mg [Capsella rubella]	686	760	1.00E-167	110.8	57.7	68.4	hypothetical protein CARUB_v10000287mg	gbpln	Capsella rubella	AT5G01030.2 | Symbols: | Protein of unknown function (DUF3527) | chr5:10638-13003 FORWARD LENGTH=744	686	744	1.00E-166	108.5	58.0	69.2
Rsa1.0_00129.1.g6211.t1	gb|EOA20315.1| hypothetical protein CARUB_v10000622mg [Capsella rubella]	541	553	0	102.2	89.5	93.5	hypothetical protein CARUB_v10000622mg	gbpln	Capsella rubella	AT5G02010.1 | Symbols: ATROPGEF7, ROPGEF7 | RHO guanyl-nucleotide exchange factor 7 | chr5:383493-385698 FORWARD LENGTH=546	541	546	0	100.9	88.2	93.2
Rsa1.0_00129.1.g6212.t1	ref|NP_195822.1| uncharacterized protein [Arabidopsis thaliana] gi|7340676|emb|CAB82975.1| putative protein [Arabidopsis thaliana] gi|16648748|gb|AAL25566.1| AT5g02020/T7H20_70 [Arabidopsis thaliana] gi|20334906|gb|AAM16209.1| AT5g02020/T7H20_70 [Arabidopsis thaliana] gi|332003037|gb|AED90420.1| uncharacterized protein AT5G02020 [Arabidopsis thaliana]	150	149	3.00E-46	99.3	76.7	84.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G02020.1 | Symbols: SIS | Encodes a protein involved in salt tolerance, names SIS (Salt Induced Serine rich). | chr5:386557-387921 REVERSE LENGTH=149	150	149	9.00E-49	99.3	76.7	84.7
Rsa1.0_00129.1.g6213.t1	gb|EOA20156.1| hypothetical protein CARUB_v10000448mg [Capsella rubella]	579	637	0	110.0	84.6	90.2	hypothetical protein CARUB_v10000448mg	gbpln	Capsella rubella	AT5G02030.1 | Symbols: LSN, PNY, HB-6, BLR, RPL, BLH9, VAN | POX (plant homeobox) family protein | chr5:395754-398872 FORWARD LENGTH=575	579	575	0	99.3	83.8	87.6
Rsa1.0_00130.1.g6214.t1	#	#	#	#	#	#	#	–	----	----	AT1G54410.1 | Symbols: | dehydrin family protein | chr1:20310305-20310601 REVERSE LENGTH=98	95	98	4.00E-11	103.2	54.7	56.8
Rsa1.0_00130.1.g6215.t1	gb|AAA92823.1| cyclin dependent protein kinase homolog; similar to moth bean p34cdc2 protein, PIR Accession Number JQ2243 [Brassica napus]	303	294	1.00E-166	97.0	95.0	95.7	cyclin dependent protein kinase homolog; similar to moth bean p34cdc2 protein, PIR Accession Number JQ2243	gbpln	Brassica napus	AT3G48750.1 | Symbols: CDKA;1, CDC2AAT, CDK2, CDC2, CDC2A, CDKA1 | cell division control 2 | chr3:18072238-18074296 FORWARD LENGTH=294	303	294	1.00E-164	97.0	92.1	95.0
Rsa1.0_00130.1.g6216.t1	gb|ADK63397.1| DHHC type zinc finger protein [Brassica rapa]	450	441	0	98.0	90.9	92.4	DHHC type zinc finger protein	gbpln	Brassica rapa	AT3G48760.1 | Symbols: | DHHC-type zinc finger family protein | chr3:18075902-18078084 FORWARD LENGTH=476	450	476	0	105.8	84.4	88.9
Rsa1.0_00130.1.g6217.t1	gb|EOA15422.1| hypothetical protein CARUB_v10007751mg [Capsella rubella]	217	108	6.00E-26	49.8	29.0	36.9	hypothetical protein CARUB_v10007751mg	gbpln	Capsella rubella	AT4G02655.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G18486.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:1158876-1159241 FORWARD LENGTH=121	217	121	5.00E-24	55.8	27.6	38.7
Rsa1.0_00130.1.g6218.t1	gb|ABW97708.1| serine palmitoyltransferase long chain base subunit [Brassica rapa subsp. chinensis]	489	489	0	100.0	98.4	99.0	serine palmitoyltransferase long chain base subunit	gbpln	Brassica rapa	AT3G48780.1 | Symbols: ATSPT1, SPT1 | serine palmitoyltransferase 1 | chr3:18089346-18092276 FORWARD LENGTH=489	489	489	0	100.0	92.4	96.9
Rsa1.0_00130.1.g6219.t1	gb|EOA23885.1| hypothetical protein CARUB_v10017101mg [Capsella rubella]	484	489	0	101.0	81.8	90.7	hypothetical protein CARUB_v10017101mg	gbpln	Capsella rubella	AT3G48780.1 | Symbols: ATSPT1, SPT1 | serine palmitoyltransferase 1 | chr3:18089346-18092276 FORWARD LENGTH=489	484	489	0	101.0	81.0	90.1
Rsa1.0_00130.1.g6220.t1	ref|XP_002877632.1| hypothetical protein ARALYDRAFT_485234 [Arabidopsis lyrata subsp. lyrata] gi|297323470|gb|EFH53891.1| hypothetical protein ARALYDRAFT_485234 [Arabidopsis lyrata subsp. lyrata]	236	280	5.00E-83	118.6	78.4	86.4	hypothetical protein ARALYDRAFT_485234	gbpln	Arabidopsis lyrata	AT3G48800.1 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr3:18095825-18096661 REVERSE LENGTH=278	236	278	2.00E-80	117.8	78.4	86.0

<table>
<tr><td>Rsa1.0_00130.1.g6221.t1</td><td>ref|NP_190451.2| glycosyltransferase family 29 (sialyltransferase) protein [Arabidopsis thaliana] gi|19347711|gb|AAL85966.1| unknown protein [Arabidopsis thaliana] gi|22136812|gb|AAM91750.1| unknown protein [Arabidopsis thaliana] gi|332644938|gb|AEE78459.1| glycosyltransferase family 29 (sialyltransferase) protein [Arabidopsis thaliana]</td><td>811</td><td>440</td><td>0</td><td>54.3</td><td>41.2</td><td>44.0</td><td>glycosyltransferase family 29 (sialyltransferase) protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G48820.1 | Symbols: | Glycosyltransferase family 29 (sialyltransferase) family protein | chr3:18100106-18102852 REVERSE LENGTH=440</td><td>811</td><td>440</td><td>0</td><td>54.3</td><td>41.2</td><td>44.0</td></tr>
<tr><td>Rsa1.0_00130.1.g6222.t1</td><td>ref|XP_002875931.1| membrane-associated progesterone binding protein 3 [Arabidopsis lyrata subsp. lyrata] gi|297321769|gb|EFH52190.1| membrane-associated progesterone binding protein 3 [Arabidopsis lyrata subsp. lyrata]</td><td>191</td><td>232</td><td>4.00E-72</td><td>121.5</td><td>80.6</td><td>88.0</td><td>membrane-associated progesterone binding protein 3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G48890.1 | Symbols: ATMP2, ATMAPR3, MSBP2, MAPR3 | membrane-associated progesterone binding protein 3 | chr3:18129669-18131353 FORWARD LENGTH=233</td><td>191</td><td>233</td><td>4.00E-71</td><td>122.0</td><td>77.0</td><td>82.2</td></tr>
<tr><td>Rsa1.0_00130.1.g6223.t3</td><td>ref|XP_002863317.1| hypothetical protein ARALYDRAFT_497154 [Arabidopsis lyrata subsp. lyrata] gi|297309151|gb|EFH39576.1| hypothetical protein ARALYDRAFT_497154 [Arabidopsis lyrata subsp. lyrata]</td><td>397</td><td>403</td><td>0</td><td>101.5</td><td>86.9</td><td>91.7</td><td>hypothetical protein ARALYDRAFT_497154</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G12730.1 | Symbols: FLA2 | FASCICLIN-like arabinogalactan 2 | chr4:7491598-7492809 REVERSE LENGTH=403</td><td>397</td><td>403</td><td>0</td><td>101.5</td><td>86.6</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00130.1.g6224.t1</td><td>ref|XP_002872419.1| RNA polymerase III subunit RPC82 family protein [Arabidopsis lyrata subsp. lyrata] gi|297318256|gb|EFH48678.1| RNA polymerase III subunit RPC82 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>526</td><td>521</td><td>0</td><td>99.0</td><td>78.3</td><td>88.2</td><td>RNA polymerase III subunit RPC82 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G49000.1 | Symbols: | RNA polymerase III subunit RPC82 family protein | chr3:18162903-18165846 FORWARD LENGTH=523</td><td>526</td><td>523</td><td>0</td><td>99.4</td><td>77.8</td><td>88.2</td></tr>
<tr><td>Rsa1.0_00130.1.g6225.t1</td><td>gb|ABL97945.1| cold induced protein [Brassica rapa]</td><td>229</td><td>206</td><td>1.00E-113</td><td>90.0</td><td>88.2</td><td>88.6</td><td>cold induced protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G49010.3 | Symbols: ATBBC1, BBC1, RSU2 | breast basic conserved 1 | chr3:18166971-18168047 REVERSE LENGTH=206</td><td>229</td><td>206</td><td>1.00E-103</td><td>90.0</td><td>77.7</td><td>80.3</td></tr>
<tr><td>Rsa1.0_00130.1.g6226.t1</td><td>ref|NP_190471.1| FBD-associated F-box protein [Arabidopsis thaliana] gi|75337428|sp|Q9SMT9.1|FBD9_ARATH RecName: Full=FBD-associated F-box protein At3g49020 gi|6522564|emb|CAB62008.1| putative protein [Arabidopsis thaliana] gi|67633680|gb|AAY78764.1| F-box family protein [Arabidopsis thaliana] gi|111074508|gb|ABH04627.1| At3g49020 [Arabidopsis thaliana] gi|332644966|gb|AEE78487.1| FBD-associated F-box protein [Arabidopsis thaliana]</td><td>387</td><td>447</td><td>1.00E-129</td><td>115.5</td><td>63.0</td><td>76.0</td><td>FBD-associated F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G49020.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr3:18169079-18170660 FORWARD LENGTH=447</td><td>387</td><td>447</td><td>1.00E-131</td><td>115.5</td><td>63.0</td><td>76.0</td></tr>
<tr><td>Rsa1.0_00130.1.g6227.t1</td><td>ref|NP_566915.1| U-box domain-containing protein 32 [Arabidopsis thaliana] gi|75332032|sp|Q94A51.1|PUB32_ARATH RecName: Full=U-box domain-containing protein 32; AltName: Full=Plant U-box protein 32 gi|15215682|gb|AAK91387.1| AT3g49060/T2J13_100 [Arabidopsis thaliana] gi|28416483|gb|AAO42772.1| At3g49060/T2J13_100 [Arabidopsis thaliana] gi|51970634|dbj|BAD44009.1| unknown protein [Arabidopsis thaliana] gi|51970796|dbj|BAD44090.1| unknown protein [Arabidopsis thaliana] gi|332644973|gb|AEE78494.1| U-box domain-containing protein 32 [Arabidopsis thaliana]</td><td>821</td><td>805</td><td>0</td><td>98.1</td><td>85.9</td><td>91.7</td><td>U-box domain-containing protein 32</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G49060.1 | Symbols: | U-box domain-containing protein kinase family protein | chr3:18187386-18191878 REVERSE LENGTH=805</td><td>821</td><td>805</td><td>0</td><td>98.1</td><td>85.9</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00130.1.g6228.t1</td><td>gb|EOA24998.1| hypothetical protein CARUB_v10018295mg [Capsella rubella]</td><td>119</td><td>103</td><td>3.00E-49</td><td>86.6</td><td>83.2</td><td>84.9</td><td>hypothetical protein CARUB_v10018295mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G49100.1 | Symbols: | Signal recognition particle, SRP9/SRP14 subunit | chr3:18196944-18198298 FORWARD LENGTH=103</td><td>119</td><td>103</td><td>1.00E-51</td><td>86.6</td><td>82.4</td><td>84.0</td></tr>
<tr><td>Rsa1.0_00130.1.g6229.t1</td><td>ref|XP_002872085.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317922|gb|EFH48344.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>424</td><td>430</td><td>1.00E-133</td><td>101.4</td><td>58.5</td><td>72.9</td><td>transferase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23970.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:8096326-8097612 FORWARD LENGTH=428</td><td>424</td><td>428</td><td>1.00E-132</td><td>100.9</td><td>58.0</td><td>72.2</td></tr>
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Rsa1.0_00130.1.g6230.t1	ref|XP_002877656.1| hypothetical protein ARALYDRAFT_906195 [Arabidopsis lyrata subsp. lyrata] gi|297323494|gb|EFH53915.1| hypothetical protein ARALYDRAFT_906195 [Arabidopsis lyrata subsp. lyrata]	488	503	0	103.1	71.5	84.0	hypothetical protein ARALYDRAFT_906195	gbpln	Arabidopsis lyrata	AT3G49200.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr3:18235445-18237646 REVERSE LENGTH=507	488	507	0	103.9	70.5	83.6
Rsa1.0_00130.1.g6231.t1	gb|EOA26120.1| hypothetical protein CARUB_v10019546mg [Capsella rubella]	440	522	0	118.6	76.6	86.4	hypothetical protein CARUB_v10019546mg	gbpln	Capsella rubella	AT3G49190.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr3:18231988-18234376 REVERSE LENGTH=522	440	522	0	118.6	78.0	88.0
Rsa1.0_00130.1.g6232.t1	ref|XP_002875955.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321793|gb|EFH52214.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	568	598	0	105.3	82.9	90.0	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT3G49220.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:18249840-18253647 FORWARD LENGTH=598	568	598	0	105.3	82.9	90.1
Rsa1.0_00130.1.g6233.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00130.1.g6234.t1	ref|XP_002877660.1| hypothetical protein ARALYDRAFT_485283 [Arabidopsis lyrata subsp. lyrata] gi|297323498|gb|EFH53919.1| hypothetical protein ARALYDRAFT_485283 [Arabidopsis lyrata subsp. lyrata]	398	423	1.00E-172	106.3	76.6	88.2	hypothetical protein ARALYDRAFT_485283	gbpln	Arabidopsis lyrata	AT3G49250.1 | Symbols: DMS3, IDN1 | defective in meristem silencing 3 | chr3:18258613-18260803 REVERSE LENGTH=420	398	420	1.00E-164	105.5	73.9	85.7
Rsa1.0_00130.1.g6235.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00130.1.g6236.t1	ref|NP_566917.1| protein IQ-domain 21 [Arabidopsis thaliana] gi|42572619|ref|NP_974405.1| protein IQ-domain 21 [Arabidopsis thaliana] gi|13605619|gb|AAK32803.1|AF361635_1 AT3g49260/F2K15_120 [Arabidopsis thaliana] gi|21593446|gb|AAM65413.1| SF16-like protein [Arabidopsis thaliana] gi|23308403|gb|AAN18171.1| At3g49260/F2K15_120 [Arabidopsis thaliana] gi|39980284|gb|AAR32943.1| guard cell associated protein [Arabidopsis thaliana] gi|332644995|gb|AEE78516.1| protein IQ-domain 21 [Arabidopsis thaliana] gi|332644996|gb|AEE78517.1| protein IQ-domain 21 [Arabidopsis thaliana]	475	471	0	99.2	82.9	87.8	protein IQ-domain 21	gbpln	Arabidopsis thaliana	AT3G49260.2 | Symbols: iqd21 | IQ-domain 21 | chr3:18262755-18265859 FORWARD LENGTH=471	475	471	0	99.2	82.9	87.8
Rsa1.0_00130.1.g6237.t7	ref|XP_002877664.1| hypothetical protein ARALYDRAFT_906210 [Arabidopsis lyrata subsp. lyrata] gi|297323502|gb|EFH53923.1| hypothetical protein ARALYDRAFT_906210 [Arabidopsis lyrata subsp. lyrata]	908	460	0	50.7	44.8	46.5	hypothetical protein ARALYDRAFT_906210	gbpln	Arabidopsis lyrata	AT3G49310.1 | Symbols: | Major facilitator superfamily protein | chr3:18285084-18287991 REVERSE LENGTH=460	908	460	0	50.7	41.7	42.7
Rsa1.0_00130.1.g6238.t1	ref|XP_002877667.1| hypothetical protein ARALYDRAFT_348033 [Arabidopsis lyrata subsp. lyrata] gi|297323505|gb|EFH53926.1| hypothetical protein ARALYDRAFT_348033 [Arabidopsis lyrata subsp. lyrata]	341	341	1.00E-158	100.0	79.8	89.4	hypothetical protein ARALYDRAFT_348033	gbpln	Arabidopsis lyrata	AT3G49340.1 | Symbols: | Cysteine proteinases superfamily protein | chr3:18293347-18294577 REVERSE LENGTH=341	341	341	1.00E-157	100.0	78.0	88.3
Rsa1.0_00130.1.g6239.t1	ref|XP_002877670.1| hypothetical protein ARALYDRAFT_485296 [Arabidopsis lyrata subsp. lyrata] gi|297323508|gb|EFH53929.1| hypothetical protein ARALYDRAFT_485296 [Arabidopsis lyrata subsp. lyrata]	597	592	0	99.2	89.6	94.6	hypothetical protein ARALYDRAFT_485296	gbpln	Arabidopsis lyrata	AT5G24430.1 | Symbols: | Calcium-dependent protein kinase (CDPK) family protein | chr5:8339390-8342913 REVERSE LENGTH=594	597	594	0	99.5	85.9	92.0
Rsa1.0_00130.1.g6240.t1	#	#	#	#	#	#	#	-	----	----	AT3G49390.2 | Symbols: CID10 | CTC-interacting domain 10 | chr3:18314901-18317658 REVERSE LENGTH=353	39	353	2.00E-11	905.1	76.9	84.6

Rsa1.0_00130.1.g6241.t1	ref|NP_190508.1| CTC-interacting domain 10 protein [Arabidopsis thaliana] gi|79314662|ref|NP_001030833.1| CTC-interacting domain 10 protein [Arabidopsis thaliana] gi|12324442|gb|AAG52182.1|AC012329_9 putative RNA-binding protein; 38450-35693 [Arabidopsis thaliana] gi|6723409|emb|CAB66418.1| RNA-binding-like protein [Arabidopsis thaliana] gi|222424104|dbj|BAH20012.1| AT3G49390 [Arabidopsis thaliana] gi|332645014|gb|AEE78535.1| CTC-interacting domain 10 protein [Arabidopsis thaliana] gi|332645015|gb|AEE78536.1| CTC-interacting domain 10 protein [Arabidopsis thaliana]	302	353	1.00E-126	116.9	77.2	85.1	CTC-interacting domain 10 protein	gbpln	Arabidopsis thaliana	AT3G49390.2 | Symbols: CID10 | CTC-interacting domain 10 | chr3:18314901-18317658 REVERSE LENGTH=353	302	353	1.00E-128	116.9	77.2	85.1
Rsa1.0_00130.1.g6242.t1	gb|AAG52185.1|AC012329_12 putative splicing factor; 53460-55514 [Arabidopsis thaliana]	289	295	1.00E-106	102.1	84.1	87.2	putative splicing factor; 53460-55514	gbpln	Arabidopsis thaliana	AT3G49430.3 | Symbols: SRp34a, SR34a, At-SR34a | SER/ARG-rich protein 34A | chr3:18332668-18334829 FORWARD LENGTH=300	289	300	1.00E-108	103.8	84.1	87.2
Rsa1.0_00130.1.g6243.t1	ref|NP_192444.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|7267295|emb|CAB81077.1| putative protein [Arabidopsis thaliana] gi|332657108|gb|AEE82508.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	223	206	2.00E-30	92.4	43.0	54.3	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT4G05350.1 | Symbols: | RING/U-box superfamily protein | chr4:2726910-2727530 REVERSE LENGTH=206	223	206	5.00E-33	92.4	43.0	54.3
Rsa1.0_00131.1.g6244.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00131.1.g6245.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00131.1.g6246.t1	ref|XP_002882559.1| hypothetical protein ARALYDRAFT_478135 [Arabidopsis lyrata subsp. lyrata] gi|297328399|gb|EFH58818.1| hypothetical protein ARALYDRAFT_478135 [Arabidopsis lyrata subsp. lyrata]	383	383	0	100.0	89.8	93.5	hypothetical protein ARALYDRAFT_478135	gbpln	Arabidopsis lyrata	AT3G07940.1 | Symbols: | Calcium-dependent ARF-type GTPase activating protein family | chr3:2529542-2531368 FORWARD LENGTH=385	383	385	0	100.5	88.8	93.2
Rsa1.0_00131.1.g6247.t1	ref|XP_002882562.1| hypothetical protein ARALYDRAFT_896969 [Arabidopsis lyrata subsp. lyrata] gi|297328402|gb|EFH58821.1| hypothetical protein ARALYDRAFT_896969 [Arabidopsis lyrata subsp. lyrata]	305	304	1.00E-156	99.7	93.4	96.1	hypothetical protein ARALYDRAFT_896969	gbpln	Arabidopsis lyrata	AT3G07950.1 | Symbols: | rhomboid protein-related | chr3:2531982-2534277 FORWARD LENGTH=304	305	304	1.00E-157	99.7	92.1	95.7
Rsa1.0_00131.1.g6248.t1	ref|XP_002882563.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328403|gb|EFH58822.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata]	714	715	0	100.1	95.4	97.8	phosphatidylinositol-4-phosphate 5-kinase family protein	gbpln	Arabidopsis lyrata	AT3G07960.1 | Symbols: | Phosphatidylinositol-4-phosphate 5-kinase family protein | chr3:2535274-2538090 FORWARD LENGTH=715	714	715	0	100.1	94.8	97.6
Rsa1.0_00131.1.g6249.t6	gb|AFJ66186.1| hypothetical protein 11M19.5 [Arabidopsis halleri]	2683	1557	0	58.0	36.7	44.5	hypothetical protein 11M19.5	gbpln	Arabidopsis halleri	AT3G25270.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:9203934-9204965 REVERSE LENGTH=343	2683	343	4.00E-59	12.8	4.1	6.2
Rsa1.0_00131.1.g6250.t1	gb|EOA21051.1| hypothetical protein CARUB_v10001392mg [Capsella rubella]	310	334	5.00E-65	107.7	50.6	61.0	hypothetical protein CARUB_v10001392mg	gbpln	Capsella rubella	AT3G25080.1 | Symbols: | Protein of unknown function (DUF626) | chr3:9137105-9137892 FORWARD LENGTH=171	310	171	8.00E-40	55.2	30.0	36.5
Rsa1.0_00131.1.g6251.t1	ref|XP_002884676.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330516|gb|EFH60935.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	748	778	0	104.0	86.2	91.4	protein binding protein	gbpln	Arabidopsis lyrata	AT3G08020.1 | Symbols: | PHD finger family protein | chr3:2557753-2561534 REVERSE LENGTH=779	748	779	0	104.1	85.7	91.2
Rsa1.0_00131.1.g6252.t1	gb|EOA30873.1| hypothetical protein CARUB_v10014019mg [Capsella rubella]	365	365	0	100.0	93.2	98.1	hypothetical protein CARUB_v10014019mg	gbpln	Capsella rubella	AT3G08030.1 | Symbols: | Protein of unknown function, DUF642 | chr3:2564191-2565819 FORWARD LENGTH=365	365	365	0	100.0	91.8	97.3
Rsa1.0_00131.1.g6253.t1	ref|XP_002884678.1| hypothetical protein ARALYDRAFT_478146 [Arabidopsis lyrata subsp. lyrata] gi|297330518|gb|EFH60937.1| hypothetical protein ARALYDRAFT_478146 [Arabidopsis lyrata subsp. lyrata]	529	530	0	100.2	82.4	92.2	hypothetical protein ARALYDRAFT_478146	gbpln	Arabidopsis lyrata	AT3G08040.2 | Symbols: FRD3, MAN1, ATFRD3 | MATE efflux family protein | chr3:2566593-2569397 REVERSE LENGTH=526	529	526	0	99.4	81.5	91.1

Rsa1.0_00131.1.g6254.t1	ref|XP_002884680.1| hypothetical protein ARALYDRAFT_478147 [Arabidopsis lyrata subsp. lyrata] gi|297330520|gb|EFH60939.1| hypothetical protein ARALYDRAFT_478147 [Arabidopsis lyrata subsp. lyrata]	314	342	1.00E−116	108.9	75.2	83.4	hypothetical protein ARALYDRAFT_478147	gbpln	Arabidopsis lyrata	AT3G08500.1 | Symbols: MYB83, AtMYB83 | myb domain protein 83 | chr3:2576958-2578072 REVERSE LENGTH=343	314	343	1.00E−111	109.2	72.3	81.8
Rsa1.0_00131.1.g6255.t1	ref|NP_850540.1| E3 ubiquitin-protein ligase makorin [Arabidopsis thaliana] gi|42572319|ref|NP_974255.1| E3 ubiquitin-protein ligase makorin [Arabidopsis thaliana] gi|75323660|sp|Q6IDS6.1|C3H35_ARATH RecName: Full=E3 ubiquitin-protein ligase makorin; AltName: Full=Zinc finger CCCH domain-containing protein 35; Short=AtC3H35 gi|17979277|gb|AAL49864.1| unknown protein [Arabidopsis thaliana] gi|24030475|gb|AAN41388.1| unknown protein [Arabidopsis thaliana] gi|332641117|gb|AEE74638.1| E3 ubiquitin-protein ligase makorin [Arabidopsis thaliana] gi|332641118|gb|AEE74639.1| E3 ubiquitin-protein ligase makorin [Arabidopsis thaliana]	364	323	1.00E−142	88.7	69.8	75.3	E3 ubiquitin-protein ligase makorin	gbpln	Arabidopsis thaliana	AT3G08505.1 | Symbols: | zinc finger (CCCH-type/C3HC4-type RING finger) family protein | chr3:2580603-2582043 REVERSE LENGTH=323	364	323	1.00E−145	88.7	69.8	75.3
Rsa1.0_00131.1.g6256.t1	gb|AAD26119.1|AF108123_1 phosphoinositide-specific phospholipase C [Brassica napus]	582	581	0	99.8	94.3	97.1	phosphoinositide-specific phospholipase C	gbpln	Brassica napus	AT3G08510.2 | Symbols: ATPLC2, PLC2 | phospholipase C 2 | chr3:2582626-2585556 REVERSE LENGTH=581	582	581	0	99.8	91.1	95.4
Rsa1.0_00131.1.g6257.t1	dbj|BAJ33646.1| unnamed protein product [Thellungiella halophila]	527	533	0	101.1	94.7	98.3	unnamed protein product	----	----	AT3G08550.1 | Symbols: ELD1, ABI8, KOB1 | elongation defective 1 protein / ELD1 protein | chr3:2596513-2599515 FORWARD LENGTH=533	527	533	0	101.1	92.4	97.0
Rsa1.0_00131.1.g6258.t1	gb|EOA36510.1| hypothetical protein CARUB_v10011291mg [Capsella rubella]	176	353	7.00E−31	200.6	46.0	64.8	hypothetical protein CARUB_v10011291mg	gbpln	Capsella rubella	AT1G47790.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:17600004-17601173 REVERSE LENGTH=389	176	389	8.00E−32	221.0	46.6	63.1
Rsa1.0_00131.1.g6259.t1	gb|AAP21180.1| At3g08610 [Arabidopsis thaliana]	65	73	2.00E−29	112.3	95.4	96.9	At3g08610	gbpln	Arabidopsis thaliana	AT3G08610.1 | Symbols: | unknown protein; Has 40 Blast hits to 40 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2616435-2616768 REVERSE LENGTH=65	65	65	6.00E−32	100.0	95.4	96.9
Rsa1.0_00131.1.g6260.t1	ref|NP_187476.1| uncharacterized protein [Arabidopsis thaliana] gi|12322723|gb|AAG51347.1|AC012562_8 unknown protein; 33915-34928 [Arabidopsis thaliana] gi|19698961|gb|AAL91216.1| unknown protein [Arabidopsis thaliana] gi|22136296|gb|AAM91226.1| unknown protein [Arabidopsis thaliana] gi|332641136|gb|AEE74657.1| uncharacterized protein AT3G08640 [Arabidopsis thaliana]	351	337	1.00E−138	96.0	74.4	81.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G08640.1 | Symbols: | Protein of unknown function (DUF3411) | chr3:2622992-2624005 FORWARD LENGTH=337	351	337	1.00E−140	96.0	74.4	81.5
Rsa1.0_00131.1.g6261.t1	ref|NP_974256.1| ZIP metal ion transporter-like protein [Arabidopsis thaliana] gi|310947322|sp|Q9C9Z1.2|ZTP50_ARATH RecName: Full=Putative zinc transporter At3g08650 gi|332641138|gb|AEE74659.1| ZIP metal ion transporter-like protein [Arabidopsis thaliana]	81	619	9.00E−20	764.2	60.5	69.1	ZIP metal ion transporter-like protein	gbpln	Arabidopsis thaliana	AT3G08650.2 | Symbols: | ZIP metal ion transporter family | chr3:2624694-2627308 REVERSE LENGTH=619	81	619	2.00E−22	764.2	60.5	69.1
Rsa1.0_00131.1.g6262.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00131.1.g6263.t1	emb|CAA18485.1| putative protein [Arabidopsis thaliana] gi|3805857|emb|CAA21477.1| putative protein [Arabidopsis thaliana] gi|7270543|emb|CAB81500.1| putative protein [Arabidopsis thaliana]	222	527	2.00E−30	237.4	29.7	31.1	putative protein	gbpln	Arabidopsis thaliana	AT4G35910.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr4:17008817-17011014 REVERSE LENGTH=458	222	458	9.00E−33	206.3	29.7	31.1
Rsa1.0_00131.1.g6264.t1	gb|EOA30171.1| hypothetical protein CARUB_v10013288mg [Capsella rubella]	587	595	0	101.4	91.1	95.7	hypothetical protein CARUB_v10013288mg	gbpln	Capsella rubella	AT3G08650.2 | Symbols: | ZIP metal ion transporter family | chr3:2624694-2627308 REVERSE LENGTH=619	587	619	0	105.5	91.7	95.2

Rsa1.0_00131.1.g6265.t1	ref|NP_187480.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|42572323|ref|NP_974257.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|75333601|sp|Q9C9Y8.1|Y3868_ARATH RecName: Full=Probable inactive receptor kinase At3g08680; Flags: Precursor gi|12322735|gb|AAG51359.1|AC012562_20 putative protein kinase; 49514-51513 [Arabidopsis thaliana] gi|224589559|gb|ACN59313.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332641141|gb|AEE74662.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|332641142|gb|AEE74663.1| putative inactive receptor kinase [Arabidopsis thaliana]	621	640	0	103.1	85.7	91.3	putative inactive receptor kinase	gbpln	Arabidopsis thaliana	AT3G08680.2 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:2638591-2640590 FORWARD LENGTH=640	621	640	0	103.1	85.7	91.3
Rsa1.0_00131.1.g6266.t1	ref|NP_566331.1| ubiquitin-conjugating enzyme E2 11 [Arabidopsis thaliana] gi|334185174|ref|NP_001189841.1| ubiquitin-conjugating enzyme E2 11 [Arabidopsis thaliana] gi|297829396|ref|XP_002882580.1| ubiquitin-conjugating enzyme 11 [Arabidopsis lyrata subsp. lyrata] gi|12643427|sp|P35134.2|UBC11_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 11; AltName: Full=Ubiquitin carrier protein 11; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 11; AltName: Full=Ubiquitin-protein ligase 11 gi|12322738|gb|AAG51362.1|AC012562_23 putative ubiquitin conjugating enzyme; 52410-53412 [Arabidopsis thaliana] gi|17380790|gb|AAL36225.1| putative E2, ubiquitin-conjugating enzyme UBC11 [Arabidopsis thaliana] gi|20259611|gb|AAM14162.1| putative ubiquitin conjugating enzyme 11 (UBC11) [Arabidopsis thaliana] gi|21554241|gb|AAM63316.1| E2, ubiquitin-conjugating enzyme UBC11 [Arabidopsis thaliana] gi|66354432|gb|AAY44851.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|110736468|dbj|BAF00202.1| putative ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|297328420|gb|EFH58839.1| ubiquitin-conjugating enzyme 11 [Arabidopsis	148	148	2.00E-80	100.0	96.6	100.0	ubiquitin-conjugating enzyme E2 11	gbpln	Arabidopsis lyrata	AT3G08690.2 | Symbols: UBC11 | ubiquitin-conjugating enzyme 11 | chr3:2641487-2642489 FORWARD LENGTH=148	148	148	5.00E-83	100.0	96.6	100.0
Rsa1.0_00131.1.g6267.t1	ref|NP_187484.1| serine/threonine protein kinase 2 [Arabidopsis thaliana] gi|30680612|ref|NP_850543.1| serine/threonine protein kinase 2 [Arabidopsis thaliana] gi|21431798|sp|Q39030.2|KPK2_ARATH RecName: Full=Serine/threonine-protein kinase AtPK2/AtPK19; AltName: Full=Ribosomal-protein S6 kinase homolog 2 gi|12322721|gb|AAG51345.1|AC012562_6 putative ribosomal-protein S6 kinase (ATPK19); 61330-59548 [Arabidopsis thaliana] gi|13272447|gb|AAK17162.1|AF325094_1 putative ribosomal-protein S6 kinase (ATPK19) [Arabidopsis thaliana] gi|111074206|gb|ABH04476.1| At3g08720 [Arabidopsis thaliana] gi|222422905|dbj|BAH19439.1| AT3G08720 [Arabidopsis thaliana] gi|332641148|gb|AEE74669.1| serine/threonine protein kinase 2 [Arabidopsis thaliana] gi|332641149|gb|AEE74670.1| serine/threonine protein kinase 2 [Arabidopsis thaliana]	437	471	0	107.8	82.8	88.8	serine/threonine protein kinase 2	gbpln	Arabidopsis thaliana	AT3G08720.2 | Symbols: ATPK19, ATPK2 | serine/threonine protein kinase 2 | chr3:2648625-2650407 REVERSE LENGTH=471	437	471	0	107.8	82.8	88.8

Rsa1.0_00131.1.g6268.t1	gb|ACD79975.1| serine/threonine-protein kinase ATPK19/ATPK2 [Brassica rapa]	461	458	0	99.3	94.1	96.3	serine/threonine-protein kinase ATPK19/ATPK2	gbpln	Brassica rapa	AT3G08730.1 | Symbols: ATPK1, ATPK6, ATS6K1, PK6, PK1, S6K1 | protein-serine kinase 1 | chr3:2651581-2653363 REVERSE LENGTH=465	461	465	0	100.9	86.3	93.9
Rsa1.0_00131.1.g6269.t7	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00131.1.g6270.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00131.1.g6271.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00131.1.g6272.t1	gb|EOA32525.1| hypothetical protein CARUB_v10015806mg [Capsella rubella]	622	613	0	98.6	81.4	86.5	hypothetical protein CARUB_v10015806mg	gbpln	Capsella rubella	AT3G08790.1 | Symbols: | ENTH/VHS/GAT family protein | chr3:2667881-2671001 FORWARD LENGTH=607	622	607	0	97.6	81.8	86.2
Rsa1.0_00131.1.g6273.t1	ref|XP_002884700.1| RAPTOR1B [Arabidopsis lyrata subsp. lyrata] gi|297330540|gb|EFH60959.1| RAPTOR1B [Arabidopsis lyrata subsp. lyrata]	179	1344	6.00E-13	750.8	22.3	24.6	RAPTOR1B	gbpln	Arabidopsis lyrata	AT3G08850.1 | Symbols: RAPTOR1B, ATRAPTOR1B, RAPTOR1 | HEAT repeat ;WD domain, G-beta repeat protein protein | chr3:2686978-2694911 REVERSE LENGTH=1344	179	1344	2.00E-15	750.8	22.3	24.6
Rsa1.0_00131.1.g6274.t1	ref|NP_187499.1| concanavalin A-like lectin protein kinase-like protein [Arabidopsis thaliana] gi|75337552|sp|Q9SR87.1|LRK61_ARATH RecName: Full=Probable L-type lectin-domain containing receptor kinase VI.1; Short=LecRK-VI.1; Flags: Precursor gi|6403505|gb|AAF07845.1|AC010871_21 putative serine/threonine protein kinase [Arabidopsis thaliana] gi|332641168|gb|AEE74689.1| concanavalin A-like lectin protein kinase-like protein [Arabidopsis thaliana]	685	693	0	101.2	75.2	86.1	concanavalin A-like lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT3G08870.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:2700500-2702581 REVERSE LENGTH=693	685	693	0	101.2	75.2	86.1
Rsa1.0_00131.1.g6275.t3	ref|NP_187500.2| uncharacterized protein [Arabidopsis thaliana] gi|51969186|dbj|BAD43285.1| hypothetical protein [Arabidopsis thaliana] gi|51971667|dbj|BAD44498.1| hypothetical protein [Arabidopsis thaliana] gi|332641169|gb|AEE74690.1| uncharacterized protein AT3G08880 [Arabidopsis thaliana]	171	201	3.00E-70	117.5	80.1	90.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G08880.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G01570.1); Has 177 Blast hits to 175 proteins in 60 species: Archae - 4; Bacteria - 33; Metazoa - 18; Fungi - 11; Plants - 59; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink). | chr3:2703169-2704165 FORWARD LENGTH=201	171	201	1.00E-72	117.5	80.1	90.1
Rsa1.0_00131.1.g6276.t1	gb|EOA31033.1| hypothetical protein CARUB_v10014182mg [Capsella rubella]	320	324	1.00E-158	101.3	88.8	92.8	hypothetical protein CARUB_v10014182mg	gbpln	Capsella rubella	AT3G08910.1 | Symbols: | DNAJ heat shock family protein | chr3:2710402-2711811 REVERSE LENGTH=323	320	323	1.00E-159	100.9	88.4	93.1
Rsa1.0_00131.1.g6277.t1	ref|XP_002871919.1| phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317756|gb|EFH48178.1| phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata]	210	252	7.00E-85	120.0	75.7	84.8	phospholipase/carboxylesterase family protein	gbpln	Arabidopsis lyrata	AT5G20060.3 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:6776800-6779447 FORWARD LENGTH=252	210	252	1.00E-86	120.0	75.7	84.8
Rsa1.0_00131.1.g6278.t1	gb|EOA31912.1| hypothetical protein CARUB_v10015141mg [Capsella rubella]	716	523	0	73.0	57.4	62.2	hypothetical protein CARUB_v10015141mg	gbpln	Capsella rubella	AT3G09000.1 | Symbols: | proline-rich family protein | chr3:2746014-2748326 FORWARD LENGTH=541	716	541	0	75.6	58.4	63.5
Rsa1.0_00131.1.g6279.t1	ref|NP_566341.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|21537226|gb|AAM61567.1| putative receptor ser thr protein kinase [Arabidopsis thaliana] gi|332641187|gb|AEE74708.1| protein kinase domain-containing protein [Arabidopsis thaliana]	390	393	0	100.8	87.2	93.1	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G09010.1 | Symbols: | Protein kinase superfamily protein | chr3:2750285-2752086 FORWARD LENGTH=393	390	393	0	100.8	87.2	93.1
Rsa1.0_00131.1.g6280.t1	gb|EOA30698.1| hypothetical protein CARUB_v10013835mg [Capsella rubella]	396	409	0	103.3	83.3	92.2	hypothetical protein CARUB_v10013835mg	gbpln	Capsella rubella	AT3G09020.1 | Symbols: | alpha 1,4-glycosyltransferase family protein | chr3:2753307-2754542 FORWARD LENGTH=411	396	411	0	103.8	84.3	92.2
Rsa1.0_00131.1.g6281.t1	ref|NP_974262.1| uncharacterized protein [Arabidopsis thaliana] gi|48310269|gb|AAT41787.1| At3g09032 [Arabidopsis thaliana] gi|52627121|gb|AAU84687.1| At3g09032 [Arabidopsis thaliana] gi|332641190|gb|AEE74711.1| uncharacterized protein AT3G09032 [Arabidopsis thaliana]	136	146	2.00E-39	107.4	72.8	82.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G09032.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G01225.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:2757605-2758045 REVERSE LENGTH=146	136	146	6.00E-42	107.4	72.8	82.4

Rsa1.0_00131.1.g6282.t1	ref|NP_187517.1| uncharacterized protein [Arabidopsis thaliana] gi|5923670|gb|AAD56321.1|AC009326_8 unknown protein [Arabidopsis thaliana] gi|44681474|gb|AAS47677.1| At3g09050 [Arabidopsis thaliana] gi|62320254|dbj|BAD94528.1| hypothetical protein [Arabidopsis thaliana] gi|332641193|gb|AEE74714.1| uncharacterized protein AT3G09050 [Arabidopsis thaliana]	263	258	1.00E-107	98.1	80.2	87.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G09050.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 120 Blast hits to 120 proteins in 47 species: Archae - 4; Bacteria - 10; Metazoa - 33; Fungi - 2; Plants - 44; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr3:2764860-2765907 FORWARD LENGTH=258	263	258	1.00E-109	98.1	80.2	87.8
Rsa1.0_00131.1.g6283.t1	ref|XP_002884711.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297330551|gb|EFH60970.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	1090	1010	0	92.7	67.3	73.5	transducin family protein	gbpln	Arabidopsis lyrata	AT3G09080.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:2776259-2781785 REVERSE LENGTH=1026	1090	1026	0	94.1	66.8	74.0
Rsa1.0_00131.1.g6284.t1	gb|EOA32721.1| hypothetical protein CARUB_v10016025mg [Capsella rubella]	112	112	3.00E-54	100.0	92.9	96.4	hypothetical protein CARUB_v10016025mg	gbpln	Capsella rubella	AT3G09085.1 | Symbols: | Protein of unknown function (DUF962) | chr3:2782238-2782576 FORWARD LENGTH=112	112	112	8.00E-55	100.0	89.3	94.6
Rsa1.0_00131.1.g6285.t1	gb|EOA29845.1| hypothetical protein CARUB_v10012938mg [Capsella rubella]	884	896	0	101.4	88.9	93.4	hypothetical protein CARUB_v10012938mg	gbpln	Capsella rubella	AT3G09090.1 | Symbols: DEX1 | defective in exine formation protein (DEX1) | chr3:2782912-2787552 REVERSE LENGTH=896	884	896	0	101.4	88.0	92.9
Rsa1.0_00131.1.g6286.t1	ref|XP_002884720.1| 60S acidic ribosomal protein P0 [Arabidopsis lyrata subsp. lyrata] gi|297330560|gb|EFH60979.1| 60S acidic ribosomal protein P0 [Arabidopsis lyrata subsp. lyrata]	323	322	1.00E-152	99.7	82.4	84.5	60S acidic ribosomal protein P0	gbpln	Arabidopsis lyrata	AT3G09200.1 | Symbols: | Ribosomal protein L10 family protein | chr3:2823364-2825020 REVERSE LENGTH=320	323	320	1.00E-154	99.1	81.7	84.5
Rsa1.0_00131.1.g6287.t1	gb|EOA32588.1| hypothetical protein CARUB_v10015881mg [Capsella rubella]	332	329	1.00E-158	99.1	86.1	93.4	hypothetical protein CARUB_v10015881mg	gbpln	Capsella rubella	AT3G09210.1 | Symbols: PTAC13 | plastid transcriptionally active 13 | chr3:2825422-2826850 REVERSE LENGTH=333	332	333	1.00E-155	100.3	88.0	94.0
Rsa1.0_00131.1.g6288.t1	gb|AEI89705.1| transcription factor MYB1 protein [Brassica rapa subsp. chinensis]	399	387	0	97.0	88.2	89.5	transcription factor MYB1 protein	gbpln	Brassica rapa	AT3G09230.1 | Symbols: AtMYB1, MYB1 | myb domain protein 1 | chr3:2833460-2835134 FORWARD LENGTH=393	399	393	1.00E-144	98.5	68.7	76.9
Rsa1.0_00131.1.g6289.t1	ref|XP_002884723.1| hypothetical protein ARALYDRAFT_317726 [Arabidopsis lyrata subsp. lyrata] gi|297330563|gb|EFH60982.1| hypothetical protein ARALYDRAFT_317726 [Arabidopsis lyrata subsp. lyrata]	488	506	0	103.7	89.1	93.4	hypothetical protein ARALYDRAFT_317726	gbpln	Arabidopsis lyrata	AT3G09240.1 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr3:2835668-2837956 REVERSE LENGTH=477	488	477	0	97.7	85.7	89.5
Rsa1.0_00131.1.g6290.t1	ref|NP_566347.1| nuclear transport factor 2 (NTF2)-like protein [Arabidopsis thaliana] gi|6478918|gb|AAF14023.1|AC011436_7 unknown protein [Arabidopsis thaliana] gi|17380786|gb|AAL36223.1| unknown protein [Arabidopsis thaliana] gi|20259607|gb|AAM14160.1| unknown protein [Arabidopsis thaliana] gi|21592811|gb|AAM64760.1| unknown [Arabidopsis thaliana] gi|332641221|gb|AEE74742.1| nuclear transport factor 2 (NTF2)-like protein [Arabidopsis thaliana]	243	244	1.00E-118	100.4	84.4	91.8	nuclear transport factor 2 (NTF2)-like protein	gbpln	Arabidopsis thaliana	AT3G09250.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein | chr3:2839080-2840294 FORWARD LENGTH=244	243	244	1.00E-120	100.4	84.4	91.8
Rsa1.0_00131.1.g6291.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00131.1.g6292.t1	ref|XP_002884741.1| lipin family protein [Arabidopsis lyrata subsp. lyrata] gi|297330581|gb|EFH61000.1| lipin family protein [Arabidopsis lyrata subsp. lyrata]	834	875	0	104.9	85.0	90.6	lipin family protein	gbpln	Arabidopsis lyrata	AT3G09560.3 | Symbols: | Lipin family protein | chr3:2934953-2938673 REVERSE LENGTH=904	834	904	0	108.4	83.9	89.6
Rsa1.0_00131.1.g6293.t2	ref|XP_002882629.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297328469|gb|EFH58888.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	288	297	1.00E-113	103.1	79.2	84.7	myb family transcription factor	gbpln	Arabidopsis lyrata	AT3G09600.1 | Symbols: | Homeodomain-like superfamily protein | chr3:2946459-2948270 FORWARD LENGTH=298	288	298	1.00E-115	103.5	79.2	84.7
Rsa1.0_00131.1.g6294.t1	ref|XP_002882630.1| 60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata] gi|297328470|gb|EFH58889.1| 60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata]	406	406	0	100.0	94.8	97.5	60S ribosomal protein L4/L1	gbpln	Arabidopsis lyrata	AT3G09630.1 | Symbols: | Ribosomal protein L4/L1 family | chr3:2953813-2955444 FORWARD LENGTH=406	406	406	0	100.0	94.6	97.0
Rsa1.0_00131.1.g6295.t1	gb|EOA31293.1| hypothetical protein CARUB_v10014466mg [Capsella rubella]	271	251	1.00E-129	92.6	83.8	87.8	hypothetical protein CARUB_v10014466mg	gbpln	Capsella rubella	AT3G09640.2 | Symbols: APX2, APX1B | ascorbate peroxidase 2 | chr3:2956301-2958163 FORWARD LENGTH=251	271	251	1.00E-131	92.6	83.0	87.8

Rsa1.0_00131.1.g6296.t1	gb|EOA21773.1| hypothetical protein CARUB_v10002234mg [Capsella rubella]	136	136	7.00E-72	100.0	100.0	100.0	hypothetical protein CARUB_v10002234mg	gbpln	Capsella rubella	AT5G02960.1 | Symbols: | Ribosomal protein S12/S23 family protein | chr5:693280-694396 REVERSE LENGTH=142	136	142	7.00E-74	104.4	99.3	99.3
Rsa1.0_00131.1.g6297.t1	ref|NP_187580.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|79313171|ref|NP_001030665.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|6682247|gb|AAF23299.1|AC016661_24 unknown protein [Arabidopsis thaliana] gi|45237181|gb|AAS55571.1| At3g09690 [Arabidopsis thaliana] gi|110740722|dbj|BAE98461.1| hypothetical protein [Arabidopsis thaliana] gi|332641277|gb|AEE74798.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|332641278|gb|AEE74799.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana]	518	527	0	101.7	79.2	88.4	alpha/beta-hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G09690.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:2972356-2974592 FORWARD LENGTH=527	518	527	0	101.7	79.2	88.4
Rsa1.0_00131.1.g6298.t1	dbj|BAJ34352.1| unnamed protein product [Thellungiella halophila]	555	449	1.00E-176	80.9	62.7	67.6	unnamed protein product	----	----	AT3G09710.1 | Symbols: IQD1 | IQ-domain 1 | chr3:2976834-2978900 REVERSE LENGTH=454	555	454	1.00E-166	81.8	58.7	65.2
Rsa1.0_00131.1.g6299.t1	ref|NP_187583.2| DEAD-box ATP-dependent RNA helicase 57 [Arabidopsis thaliana] gi|75328099|sp|Q84TG1.1|RH57_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 57 gi|29028778|gb|AAO64768.1| At3g09720 [Arabidopsis thaliana] gi|110742885|dbj|BAE99340.1| RNA helicase like protein [Arabidopsis thaliana] gi|332641282|gb|AEE74803.1| DEAD-box ATP-dependent RNA helicase 57 [Arabidopsis thaliana]	542	541	0	99.8	87.3	93.5	DEAD-box ATP-dependent RNA helicase 57	gbpln	Arabidopsis thaliana	AT3G09720.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:2980483-2983268 REVERSE LENGTH=541	542	541	0	99.8	87.3	93.5
Rsa1.0_00131.1.g6300.t2	gb|AAF23302.1|AC016661_27 hypothetical protein [Arabidopsis thaliana]	412	405	1.00E-137	98.3	73.3	80.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G09730.1 | Symbols: | unknown protein; Has 1171 Blast hits to 1097 proteins in 212 species: Archae - 14; Bacteria - 83; Metazoa - 583; Fungi - 105; Plants - 149; Viruses - 14; Other Eukaryotes - 223 (source: NCBI BLink). | chr3:2984018-2986260 FORWARD LENGTH=397	412	397	1.00E-137	96.4	71.8	79.4
Rsa1.0_00131.1.g6301.t1	gb|EOA31812.1| hypothetical protein CARUB_v10015035mg [Capsella rubella]	70	73	3.00E-15	104.3	90.0	95.7	hypothetical protein CARUB_v10015035mg	gbpln	Capsella rubella	AT2G37120.1 | Symbols: | S1FA-like DNA-binding protein | chr2:15594250-15594815 REVERSE LENGTH=76	70	76	8.00E-14	108.6	75.7	88.6
Rsa1.0_00131.1.g6302.t2	gb|EOA29627.1| hypothetical protein CARUB_v10014405mg [Capsella rubella]	340	265	2.33E-156	77.9	75.0	77.1	hypothetical protein CARUB_v10014405mg	gbpln	Capsella rubella	AT3G09740.1 | Symbols: SYP71, ATSYP71 | syntaxin of plants 71 | chr3:2989615-2991354 FORWARD LENGTH=266	340	266	2.33E-156	78.2	74.7	77.1
Rsa1.0_00131.1.g6303.t1	gb|EOA30784.1| hypothetical protein CARUB_v10013928mg [Capsella rubella]	379	384	1.00E-139	101.3	68.3	73.4	hypothetical protein CARUB_v10013928mg	gbpln	Capsella rubella	AT3G09770.1 | Symbols: | RING/U-box superfamily protein | chr3:2996402-2997835 REVERSE LENGTH=388	379	388	1.00E-120	102.4	64.4	68.6
Rsa1.0_00131.1.g6304.t1	ref|XP_002884782.1| hypothetical protein ARALYDRAFT_317819 [Arabidopsis lyrata subsp. lyrata] gi|297330622|gb|EFH61041.1| hypothetical protein ARALYDRAFT_317819 [Arabidopsis lyrata subsp. lyrata]	79	79	1.00E-14	100.0	55.7	69.6	hypothetical protein ARALYDRAFT_317819	gbpln	Arabidopsis lyrata	AT3G10195.1 | Symbols: | Putative membrane lipoprotein | chr3:3156630-3156976 REVERSE LENGTH=81	79	81	2.00E-14	102.5	51.9	62.0
Rsa1.0_00131.1.g6305.t1	gb|EOA31328.1| hypothetical protein CARUB_v10014499mg [Capsella rubella]	143	243	1.00E-16	169.9	29.4	35.0	hypothetical protein CARUB_v10014499mg	gbpln	Capsella rubella	AT3G10220.1 | Symbols: | tubulin folding cofactor B | chr3:3161977-3164037 FORWARD LENGTH=243	143	243	1.00E-18	169.9	28.7	34.3
Rsa1.0_00131.1.g6306.t1	ref|NP_194099.1| SRPBCC ligand-binding domain-containing protein [Arabidopsis thaliana] gi|13605714|gb|AAK32850.1|AF361838_1 AT4g23680/F9D16_150 [Arabidopsis thaliana] gi|4454037|emb|CAA23034.1| putative major latex protein [Arabidopsis thaliana] gi|7269216|emb|CAB79323.1| putative major latex protein [Arabidopsis thaliana] gi|22655454|gb|AAM98319.1| At4g23680/F9D16_150 [Arabidopsis thaliana] gi|332659394|gb|AEE84794.1| SRPBCC ligand-binding domain-containing protein [Arabidopsis thaliana]	151	151	4.00E-68	100.0	80.1	90.1	SRPBCC ligand-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT4G23680.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:12336416-12337417 REVERSE LENGTH=151	151	151	1.00E-70	100.0	80.1	90.1

<table>
<tr><td>Rsa1.0_00131.1.g6307.t1</td><td>ref|XP_002875076.1| hypothetical protein ARALYDRAFT_904347 [Arabidopsis lyrata subsp. lyrata] gi|297320914|gb|EFH51335.1| hypothetical protein ARALYDRAFT_904347 [Arabidopsis lyrata subsp. lyrata]</td><td>151</td><td>151</td><td>7.00E-66</td><td>100.0</td><td>78.1</td><td>86.1</td><td>hypothetical protein ARALYDRAFT_904347</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G01520.1 | Symbols: MLP328 | MLP-like protein 328 | chr2:235992-236881 FORWARD LENGTH=151</td><td>151</td><td>151</td><td>3.00E-68</td><td>100.0</td><td>78.1</td><td>85.4</td></tr>
<tr><td>Rsa1.0_00131.1.g6308.t2</td><td>ref|NP_176271.1| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana] gi|332195602|gb|AEE33723.1| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana]</td><td>237</td><td>289</td><td>2.00E-44</td><td>121.9</td><td>38.4</td><td>55.3</td><td>RNA-directed DNA polymerase (reverse transcriptase)-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289</td><td>237</td><td>289</td><td>7.00E-47</td><td>121.9</td><td>38.4</td><td>55.3</td></tr>
<tr><td>Rsa1.0_00131.1.g6309.t1</td><td>ref|NP_566370.1| uncharacterized protein [Arabidopsis thaliana] gi|42572351|ref|NP_974271.1| uncharacterized protein [Arabidopsis thaliana] gi|15809982|gb|AAL06918.1| AT3g10250/F14P13_15 [Arabidopsis thaliana] gi|18958054|gb|AAL79600.1| AT3g10250/F14P13_15 [Arabidopsis thaliana] gi|21536630|gb|AAM60962.1| unknown [Arabidopsis thaliana] gi|222423631|dbj|BAH19784.1| AT3G10250 [Arabidopsis thaliana] gi|332641356|gb|AEE74877.1| uncharacterized protein AT3G10250 [Arabidopsis thaliana] gi|332641357|gb|AEE74878.1| uncharacterized protein AT3G10250 [Arabidopsis thaliana]</td><td>338</td><td>324</td><td>1.00E-148</td><td>95.9</td><td>83.7</td><td>88.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G10250.2 | Symbols: | Plant protein 1589 of unknown function | chr3:3168371-3170418 REVERSE LENGTH=324</td><td>338</td><td>324</td><td>1.00E-151</td><td>95.9</td><td>83.7</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00131.1.g6310.t1</td><td>gb|EOA30978.1| hypothetical protein CARUB_v10014124mg, partial [Capsella rubella]</td><td>574</td><td>337</td><td>1.00E-170</td><td>58.7</td><td>53.3</td><td>54.9</td><td>hypothetical protein CARUB_v10014124mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G10290.1 | Symbols: | Nucleotide-sugar transporter family protein | chr3:3183511-3185324 REVERSE LENGTH=355</td><td>574</td><td>355</td><td>1.00E-172</td><td>61.8</td><td>53.1</td><td>55.1</td></tr>
<tr><td>Rsa1.0_00131.1.g6311.t17</td><td>ref|NP_187641.2| putative calcium-binding protein CML49 [Arabidopsis thaliana] gi|75331395|sp|Q8W4L0.1|CML49_ARATH RecName: Full=Probable calcium-binding protein CML49; AltName: Full=Calmodulin-like protein 49 gi|17064844|gb|AAL32576.1| Unknown protein [Arabidopsis thaliana] gi|50897258|gb|AAT85768.1| At3g10300 [Arabidopsis thaliana] gi|332641365|gb|AEE74886.1| putative calcium-binding protein CML49 [Arabidopsis thaliana]</td><td>424</td><td>335</td><td>1.00E-106</td><td>79.0</td><td>46.5</td><td>48.6</td><td>putative calcium-binding protein CML49</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G10300.3 | Symbols: | Calcium-binding EF-hand family protein | chr3:3186436-3188071 FORWARD LENGTH=335</td><td>424</td><td>335</td><td>1.00E-108</td><td>79.0</td><td>46.5</td><td>48.6</td></tr>
<tr><td>Rsa1.0_00131.1.g6312.t1</td><td>ref|XP_002882663.1| anion-transporting ATPase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328503|gb|EFH58922.1| anion-transporting ATPase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>406</td><td>410</td><td>0</td><td>101.0</td><td>93.1</td><td>95.1</td><td>anion-transporting ATPase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G10350.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:3208310-3210678 FORWARD LENGTH=411</td><td>406</td><td>411</td><td>0</td><td>101.2</td><td>93.1</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00131.1.g6313.t3</td><td>ref|XP_002884791.1| hypothetical protein ARALYDRAFT_897214 [Arabidopsis lyrata subsp. lyrata] gi|297330631|gb|EFH61050.1| hypothetical protein ARALYDRAFT_897214 [Arabidopsis lyrata subsp. lyrata]</td><td>1076</td><td>1053</td><td>0</td><td>97.9</td><td>89.4</td><td>93.3</td><td>hypothetical protein ARALYDRAFT_897214</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G10380.1 | Symbols: SEC8, ATSEC8 | subunit of exocyst complex 8 | chr3:3219922-3228356 REVERSE LENGTH=1053</td><td>1076</td><td>1053</td><td>0</td><td>97.9</td><td>89.4</td><td>93.5</td></tr>
<tr><td>Rsa1.0_00131.1.g6314.t1</td><td>ref|NP_187652.1| carboxypeptidase [Arabidopsis thaliana] gi|20455475|sp|P32826.2|SCP49_ARATH RecName: Full=Serine carboxypeptidase-like 49; Flags: Precursor gi|12322792|gb|AAG51389.1|AC011560_21 putative serine carboxypeptidase precursor; 109294-111839 [Arabidopsis thaliana] gi|20147199|gb|AAM10315.1| AT3g10410/F13M14_32 [Arabidopsis thaliana] gi|23506193|gb|AAN31108.1| At3g10410/F13M14_32 [Arabidopsis thaliana] gi|332641381|gb|AEE74902.1| serine carboxypeptidase-like 49 [Arabidopsis thaliana]</td><td>521</td><td>516</td><td>0</td><td>99.0</td><td>81.8</td><td>87.3</td><td>carboxypeptidase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G10410.1 | Symbols: SCPL49, CPY | SERINE CARBOXYPEPTIDASE-LIKE 49 | chr3:3235518-3238063 REVERSE LENGTH=516</td><td>521</td><td>516</td><td>0</td><td>99.0</td><td>81.8</td><td>87.3</td></tr>
</table>

Rsa1.0_00131.1.g6315.t1	gb|EOA32369.1| hypothetical protein CARUB_v10015636mg [Capsella rubella]	639	688	0	107.7	90.6	94.4	hypothetical protein CARUB_v10015636mg	gbpln	Capsella rubella	AT3G10420.2 | Symbols: SPD1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:3239307-3242274 FORWARD LENGTH=684	639	684	0	107.0	91.1	94.2
Rsa1.0_00131.1.g6316.t1	ref|NP_187487.1| F-box protein [Arabidopsis thaliana] gi|75333597|sp|Q9C9Y4.1|FB136_ARATH RecName: Full=F-box protein At3g08750 gi|12322733|gb|AAG51357.1|AC012562_18 hypothetical protein; 68748-67639 [Arabidopsis thaliana] gi|67633624|gb|AAY78736.1| F-box family protein [Arabidopsis thaliana] gi|332641152|gb|AEE74673.1| F-box protein [Arabidopsis thaliana]	379	369	3.00E-95	97.4	53.0	66.2	F-box protein	gbpln	Arabidopsis thaliana	AT3G08750.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:2656716-2657825 REVERSE LENGTH=369	379	369	8.00E-98	97.4	53.0	66.2
Rsa1.0_00132.1.g6317.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	699	1529	1.00E-149	218.7	40.9	59.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	699	746	1.00E-46	106.7	18.2	28.3
Rsa1.0_00132.1.g6318.t1	ref|NP_192187.1| Ent-copalyl diphosphate synthase [Arabidopsis thaliana] gi|62900384|sp|Q38802.1|KSA_ARATH RecName: Full=Ent-copalyl diphosphate synthase, chloroplastic; Short=AtCPS; Short=Ent-CDP synthase; AltName: Full=Ent-kaurene synthase A; Short=KSA; AltName: Full=Protein GA REQUIRING 1; Flags: Precursor gi|571330|gb|AAA53632.1| ent-kaurene synthetase A [Arabidopsis thaliana] gi|4263508|gb|AAD15334.1| ent-kaurene synthetase A [Arabidopsis thaliana] gi|7269763|emb|CAB77763.1| ent-kaurene synthetase A-like protein [Arabidopsis thaliana] gi|332656829|gb|AEE82229.1| Ent-copalyl diphosphate synthase [Arabidopsis thaliana]	816	802	0	98.3	81.5	86.4	Ent-copalyl diphosphate synthase	gbpln	Arabidopsis thaliana	AT4G02780.1 | Symbols: GA1, ABC33, ATCPS1, CPS, CPS1 | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr4:1237881-1244766 REVERSE LENGTH=802	816	802	0	98.3	81.5	86.4
Rsa1.0_00132.1.g6319.t1	gb|EOA21585.1| hypothetical protein CARUB_v10001997mg [Capsella rubella]	207	202	1.00E-108	97.6	93.7	95.7	hypothetical protein CARUB_v10001997mg	gbpln	Capsella rubella	AT4G02770.1 | Symbols: PSAD-1 | photosystem I subunit D-1 | chr4:1229247-1229873 REVERSE LENGTH=208	207	208	1.00E-109	100.5	93.7	96.6
Rsa1.0_00132.1.g6320.t1	ref|NP_001190662.1| F-box protein [Arabidopsis thaliana] gi|332656827|gb|AEE82227.1| F-box protein [Arabidopsis thaliana]	459	551	1.00E-157	120.0	66.2	78.4	F-box protein	gbpln	Arabidopsis thaliana	AT4G02760.3 | Symbols: | RNI-like superfamily protein | chr4:1224336-1227857 REVERSE LENGTH=551	459	551	1.00E-160	120.0	66.2	78.4
Rsa1.0_00132.1.g6321.t1	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	670	1449	5.00E-45	216.3	14.8	21.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365	670	365	3.00E-28	54.5	8.5	12.1
Rsa1.0_00132.1.g6322.t1	ref|NP_192183.2| F-box protein SKIP17 [Arabidopsis thaliana] gi|122223794|sp|Q0WRC9.1|SKI17_ARATH RecName: Full=F-box protein SKIP17; AltName: Full=SKP1-interacting partner 17 gi|110736714|dbj|BAF00320.1| hypothetical protein [Arabidopsis thaliana] gi|332656823|gb|AEE82223.1| F-box protein SKIP17 [Arabidopsis thaliana]	509	479	1.00E-163	94.1	62.5	69.7	F-box protein SKIP17	gbpln	Arabidopsis thaliana	AT4G02740.1 | Symbols: | F-box/RNI-like superfamily protein | chr4:1217756-1220834 REVERSE LENGTH=479	509	479	1.00E-166	94.1	62.5	69.7
Rsa1.0_00132.1.g6323.t1	ref|XP_002888603.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334444|gb|EFH64862.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	126	718	1.00E-24	569.8	55.6	58.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G67510.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:25297477-25300184 REVERSE LENGTH=719	126	719	6.00E-27	570.6	54.8	58.7
Rsa1.0_00132.1.g6324.t1	ref|NP_849820.1| dormancy/auxin associated protein [Arabidopsis thaliana] gi|12321756|gb|AAG50916.1|AC069159_17 unknown protein [Arabidopsis thaliana] gi|332195242|gb|AEE33363.1| dormancy/auxin associated protein [Arabidopsis thaliana]	132	140	3.00E-54	106.1	88.6	94.7	dormancy/auxin associated protein	gbpln	Arabidopsis thaliana	AT1G56220.3 | Symbols: | Dormancy/auxin associated family protein | chr1:21043414-21044469 FORWARD LENGTH=140	132	140	6.00E-57	106.1	88.6	94.7

Rsa1.0_00132.1.g6325.t1	gb|EOA20700.1| hypothetical protein CARUB_v10001014mg [Capsella rubella]	376	429	3.00E-86	114.1	42.6	44.4	hypothetical protein CARUB_v10001014mg	gbpln	Capsella rubella	AT4G02720.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF926 (InterPro:IPR009269); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:1204545-1205813 REVERSE LENGTH=422	376	422	1.00E-79	112.2	40.4	43.6
Rsa1.0_00132.1.g6326.t1	ref|XP_002872822.1| hypothetical protein ARALYDRAFT_911940 [Arabidopsis lyrata subsp. lyrata] gi|297318659|gb|EFH49081.1| hypothetical protein ARALYDRAFT_911940 [Arabidopsis lyrata subsp. lyrata]	227	205	2.00E-72	90.3	67.0	70.5	hypothetical protein ARALYDRAFT_911940	gbpln	Arabidopsis lyrata	AT4G02715.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:1202170-1202787 REVERSE LENGTH=205	227	205	1.00E-71	90.3	66.1	70.5
Rsa1.0_00132.1.g6327.t1	gb|EOA19816.1| hypothetical protein CARUB_v10000062mg [Capsella rubella]	1147	1214	0	105.8	75.3	87.1	hypothetical protein CARUB_v10000062mg	gbpln	Capsella rubella	AT4G02710.1 | Symbols: | Kinase interacting (KIP1-like) family protein | chr4:1193516-1197061 REVERSE LENGTH=1111	1147	1111	0	96.9	69.0	78.7
Rsa1.0_00132.1.g6328.t1	gb|ABA01552.1| sulfate transporter [Raphanus sativus] gi|83026562|gb|ABB96299.1| sulfate transporter RSultr3.2A [Raphanus sativus]	629	651	0	103.5	98.6	98.9	sulfate transporter	gbpln	Raphanus sativus	AT4G02700.1 | Symbols: SULTR3;2 | sulfate transporter 3;2 | chr4:1189062-1193325 FORWARD LENGTH=646	629	646	0	102.7	87.3	94.0
Rsa1.0_00132.1.g6329.t1	gb|EOA21179.1| hypothetical protein CARUB_v10001524mg [Capsella rubella]	177	309	5.00E-17	174.6	25.4	29.4	hypothetical protein CARUB_v10001524mg	gbpln	Capsella rubella	AT4G02690.1 | Symbols: | Bax inhibitor-1 family protein | chr4:1186023-1187534 FORWARD LENGTH=248	177	248	3.00E-19	140.1	26.6	28.8
Rsa1.0_00132.1.g6330.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1378	1307	0	94.8	59.1	73.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1378	1262	1.00E-103	91.6	14.2	21.9
Rsa1.0_00132.1.g6331.t1	gb|EOA21998.1| hypothetical protein CARUB_v10002509mg [Capsella rubella]	253	650	2.00E-58	256.9	47.0	60.1	hypothetical protein CARUB_v10002509mg	gbpln	Capsella rubella	AT4G01740.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr4:753422-755456 FORWARD LENGTH=652	253	652	3.00E-59	257.7	46.6	58.1
Rsa1.0_00132.1.g6332.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	662	723	0	109.2	56.3	72.7	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	662	696	5.00E-44	105.1	20.7	38.5
Rsa1.0_00132.1.g6333.t1	gb|EOA19666.1| hypothetical protein CARUB_v10003318mg [Capsella rubella]	595	608	0	102.2	80.5	88.4	hypothetical protein CARUB_v10003318mg	gbpln	Capsella rubella	AT4G02650.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr4:1156539-1158543 FORWARD LENGTH=611	595	611	0	102.7	80.3	89.6
Rsa1.0_00132.1.g6334.t1	dbj|BAJ34632.1| unnamed protein product [Thellungiella halophila]	385	419	1.00E-160	108.8	86.8	92.2	unnamed protein product	----	----	AT4G02640.2 | Symbols: BZO2H1 | bZIP transcription factor family protein | chr4:1154031-1156085 FORWARD LENGTH=417	385	417	1.00E-160	108.3	83.4	90.6
Rsa1.0_00132.1.g6335.t1	ref|XP_002874905.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320742|gb|EFH51164.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	492	492	0	100.0	87.4	92.9	kinase family protein	gbpln	Arabidopsis lyrata	AT4G02630.1 | Symbols: | Protein kinase superfamily protein | chr4:1151683-1153161 FORWARD LENGTH=492	492	492	0	100.0	86.0	92.1

Rsa1.0_00132.1.g6336.t1	ref|NP_192171.1| V-type proton ATPase subunit F [Arabidopsis thaliana] gi|12585530|sp|Q9ZQX4.1|VATF_ARATH RecName: Full=V-type proton ATPase subunit F; Short=V-ATPase subunit F; AltName: Full=V-ATPase 14 kDa subunit; AltName: Full=Vacuolar H(+)-ATPase subunit F; AltName: Full=Vacuolar proton pump subunit F gi|3892056|gb|AAC78269.1| putative vacuolar ATPase [Arabidopsis thaliana] gi|7269022|emb|CAB80755.1| putative vacuolar ATPase [Arabidopsis thaliana] gi|17529086|gb|AAL38753.1| putative vacuolar ATPase [Arabidopsis thaliana] gi|21436129|gb|AAM51311.1| putative vacuolar ATPase [Arabidopsis thaliana] gi|21536536|gb|AAM60868.1| putative vacuolar ATPase [Arabidopsis thaliana] gi|332656805|gb|AEE82205.1| V-type proton ATPase subunit F [Arabidopsis thaliana]	128	128	3.00E-66	100.0	96.9	100.0	V-type proton ATPase subunit F	gbpln	Arabidopsis thaliana	AT4G02620.1 | Symbols: | vacuolar ATPase subunit F family protein | chr4:1149419-1151132 REVERSE LENGTH=128	128	128	6.00E-69	100.0	96.9	100.0
Rsa1.0_00132.1.g6337.t1	ref|NP_192170.1| tryptophan synthase alpha chain [Arabidopsis thaliana] gi|75097570|sp|O22765.2|TRPA1_ARATH RecName: Full=Tryptophan synthase alpha chain; AltName: Full=Indole synthase; AltName: Full=Indole-3-glycerol-phosphate lyase gi|3892048|gb|AAC78257.1| putative tryptophan synthase alpha 1-like protein [Arabidopsis thaliana] gi|7269021|emb|CAB80754.1| tryptophan synthase alpha 1-like protein [Arabidopsis thaliana] gi|26450413|dbj|BAC42321.1| putative tryptophan synthase alpha 1 [Arabidopsis thaliana] gi|29824243|gb|AAP04082.1| putative tryptophan synthase alpha 1 chain [Arabidopsis thaliana] gi|332656804|gb|AEE82204.1| tryptophan synthase alpha chain [Arabidopsis thaliana]	276	275	2.33E-156	99.6	93.8	96.7	tryptophan synthase alpha chain	gbpln	Arabidopsis thaliana	AT4G02610.1 | Symbols: | Aldolase-type TIM barrel family protein | chr4:1147662-1149217 FORWARD LENGTH=275	276	275	1.00E-148	99.6	93.8	96.7
Rsa1.0_00132.1.g6338.t1	ref|NP_192169.1| MLO-like protein 1 [Arabidopsis thaliana] gi|79324987|ref|NP_001031578.1| MLO-like protein 1 [Arabidopsis thaliana] gi|6166555|sp|O49621.1|MLO1_ARATH RecName: Full=MLO-like protein 1; Short=AtMlo1; AltName: Full=MLO protein homolog 1; Short=AtMlo-H1 gi|2765817|emb|CAB08605.1| AtMlo-h1 [Arabidopsis thaliana] gi|3892049|gb|AAC78258.1| AtMlo-h1 [Arabidopsis thaliana] gi|7269020|emb|CAB80753.1| AtMlo-h1-like protein [Arabidopsis thaliana] gi|18175953|gb|AAL59957.1| putative AtMlo-h1 protein [Arabidopsis thaliana] gi|21280825|gb|AAM45040.1| putative AtMlo-h1 protein [Arabidopsis thaliana] gi|332656802|gb|AEE82202.1| MLO-like protein 1 [Arabidopsis thaliana] gi|332656803|gb|AEE82203.1| MLO-like protein 1 [Arabidopsis thaliana]	538	526	0	97.8	85.9	90.5	MLO-like protein 1	gbpln	Arabidopsis thaliana	AT4G02600.2 | Symbols: MLO1, ATMLO1 | Seven transmembrane MLO family protein | chr4:1144141-1147156 FORWARD LENGTH=526	538	526	0	97.8	85.9	90.5
Rsa1.0_00132.1.g6339.t1	dbj|BAJ33851.1| unnamed protein product [Thellungiella halophila]	303	310	1.00E-144	102.3	92.1	94.1	unnamed protein product	----	----	AT4G02590.2 | Symbols: UNE12 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:1137968-1140306 REVERSE LENGTH=310	303	310	1.00E-140	102.3	91.4	93.1
Rsa1.0_00132.1.g6340.t1	gb|EOA22672.1| hypothetical protein CARUB_v10003375mg [Capsella rubella]	986	738	0	74.8	71.8	73.5	hypothetical protein CARUB_v10003375mg	gbpln	Capsella rubella	AT4G02570.4 | Symbols: CUL1 | cullin 1 | chr4:1129315-1133435 FORWARD LENGTH=738	986	738	0	74.8	71.2	73.1
Rsa1.0_00132.1.g6341.t1	#	#	#	#	#	#	#	-	----	----	AT2G21590.2 | Symbols: APL4 | Glucose-1-phosphate adenylyltransferase family protein | chr2:9239362-9242150 FORWARD LENGTH=523	203	523	3.00E-12	257.6	16.3	17.7
Rsa1.0_00133.1.g6342.t4	gb|EOA15720.1| hypothetical protein CARUB_v10006622mg, partial [Capsella rubella]	873	545	1.00E-129	62.4	28.9	39.5	hypothetical protein CARUB_v10006622mg, partial	gbpln	Capsella rubella	AT1G24650.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:8734570-8737315 FORWARD LENGTH=886	873	886	1.00E-112	101.5	27.8	36.9

Rsa1.0_00133.1.g6343.t1	gb|EOA36981.1| hypothetical protein CARUB_v10009953mg [Capsella rubella] gi|482572795|gb|EOA36982.1| hypothetical protein CARUB_v10009953mg [Capsella rubella] gi|482572796|gb|EOA36983.1| hypothetical protein CARUB_v10009953mg [Capsella rubella]	281	281	1.00E-150	100.0	95.0	97.5	hypothetical protein CARUB_v10009953mg	gbpln	Capsella rubella	AT1G22280.1 | Symbols: PAPP2C | phytochrome-associated protein phosphatase type 2C | chr1:7874236-7875496 FORWARD LENGTH=281	281	281	1.00E-151	100.0	93.2	97.2
Rsa1.0_00133.1.g6344.t1	gb|ADO95305.1| 14-3-3-like protein GF14 Epsilon [Eutrema salsugineum]	230	253	1.00E-116	110.0	93.9	96.5	14-3-3-like protein GF14 Epsilon	gbpln	Eutrema salsugineum	AT1G22300.2 | Symbols: GRF10, GF14 EPSILON | general regulatory factor 10 | chr1:7879244-7881103 REVERSE LENGTH=254	230	254	1.00E-117	110.4	93.9	96.1
Rsa1.0_00133.1.g6345.t1	ref|NP_173653.1| UDP-glucosyl transferase 85A2 [Arabidopsis thaliana] gi|75315975|sp|Q9ZWJ3.1|U85A2_ARATH RecName: Full=UDP-glycosyltransferase 85A2 gi|9392679|gb|AAF87256.1|AC068562_3 Identical to UDP-glucose glucosyltransferase from Arabidopsis thaliana gb|AB016819 and contains a UDP-glucosyl transferase PF|00201 domain. ESTs gb|T46254, gb|R83990, gb|H37246, gb|W43072, gb|R90721, gb|R90712, gb|AA712612, gb|AA404770 come from this gene [Arabidopsis thaliana] gi|12083244|gb|AAG48781.1|AF332418_1 putative UDP-glucose glucosyltransferase [Arabidopsis thaliana] gi|3928543|dbj|BAA34687.1| UDP-glucose glucosyltransferase [Arabidopsis thaliana] gi|332192111|gb|AEE30232.1| UDP-glucosyl transferase 85A2 [Arabidopsis thaliana]	480	481	0	100.2	78.3	88.5	UDP-glucosyl transferase 85A2	gbpln	Arabidopsis thaliana	AT1G22360.1 | Symbols: AtUGT85A2, UGT85A2 | UDP-glucosyl transferase 85A2 | chr1:7895068-7897527 REVERSE LENGTH=481	480	481	0	100.2	78.3	88.5
Rsa1.0_00133.1.g6346.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00133.1.g6347.t1	ref|XP_002890510.1| hypothetical protein ARALYDRAFT_472481 [Arabidopsis lyrata subsp. lyrata] gi|297336352|gb|EFH66769.1| hypothetical protein ARALYDRAFT_472481 [Arabidopsis lyrata subsp. lyrata]	521	527	0	101.2	92.9	97.1	hypothetical protein ARALYDRAFT_472481	gbpln	Arabidopsis lyrata	AT1G22410.1 | Symbols: | Class-II DAHP synthetase family protein | chr1:7912120-7914742 FORWARD LENGTH=527	521	527	0	101.2	92.1	96.7
Rsa1.0_00133.1.g6348.t1	ref|XP_002887733.1| GF14 omega [Arabidopsis lyrata subsp. lyrata] gi|297333574|gb|EFH63992.1| GF14 omega [Arabidopsis lyrata subsp. lyrata]	384	260	2.00E-90	67.7	43.5	46.9	GF14 omega	gbpln	Arabidopsis lyrata	AT1G78300.1 | Symbols: GRF2, 14-3-3OMEGA, GF14 OMEGA | general regulatory factor 2 | chr1:29461883-29463052 FORWARD LENGTH=259	384	259	5.00E-92	67.4	43.0	46.9
Rsa1.0_00133.1.g6349.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00133.1.g6350.t1	ref|NP_567645.1| alcohol dehydrogenase-like 5 [Arabidopsis thaliana] gi|42572985|ref|NP_974589.1| alcohol dehydrogenase-like 5 [Arabidopsis thaliana] gi|122223583|sp|Q0V7W6.1|ADHL5_ARATH RecName: Full=Alcohol dehydrogenase-like 5 gi|111074376|gb|ABH04561.1| At4g22110 [Arabidopsis thaliana] gi|332659151|gb|AEE84551.1| alcohol dehydrogenase-like 5 [Arabidopsis thaliana] gi|332659152|gb|AEE84552.1| alcohol dehydrogenase-like 5 [Arabidopsis thaliana]	549	389	0	70.9	58.8	65.0	alcohol dehydrogenase-like 5	gbpln	Arabidopsis thaliana	AT4G22110.2 | Symbols: | GroES-like zinc-binding dehydrogenase family protein | chr4:11711422-11713946 REVERSE LENGTH=389	549	389	0	70.9	58.8	65.0
Rsa1.0_00133.1.g6351.t1	ref|XP_002893233.1| hypothetical protein ARALYDRAFT_335492 [Arabidopsis lyrata subsp. lyrata] gi|297339075|gb|EFH69492.1| hypothetical protein ARALYDRAFT_335492 [Arabidopsis lyrata subsp. lyrata]	301	312	1.00E-125	103.7	83.4	90.4	hypothetical protein ARALYDRAFT_335492	gbpln	Arabidopsis lyrata	AT1G22490.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:7938448-7940489 REVERSE LENGTH=304	301	304	1.00E-126	101.0	82.1	87.4
Rsa1.0_00133.1.g6352.t1	ref|NP_001154357.1| uncharacterized protein [Arabidopsis thaliana] gi|332192131|gb|AEE30252.1| uncharacterized protein AT1G22520 [Arabidopsis thaliana]	97	179	3.00E-33	184.5	78.4	85.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G22520.2 | Symbols: | Domain of unknown function (DUF543) | chr1:7952996-7954304 REVERSE LENGTH=179	97	179	5.00E-36	184.5	78.4	85.6
Rsa1.0_00133.1.g6353.t1	gb|EOA37552.1| hypothetical protein CARUB_v10011811mg [Capsella rubella]	565	564	0	99.8	86.9	92.0	hypothetical protein CARUB_v10011811mg	gbpln	Capsella rubella	AT1G22570.1 | Symbols: | Major facilitator superfamily protein | chr1:7976620-7978573 REVERSE LENGTH=565	565	565	0	100.0	85.7	91.5

Rsa1.0_00133.1.g6354.t1	ref|XP_002893241.1| hypothetical protein ARALYDRAFT_472501 [Arabidopsis lyrata subsp. lyrata] gi|297339083|gb|EFH69500.1| hypothetical protein ARALYDRAFT_472501 [Arabidopsis lyrata subsp. lyrata]	911	911	0	100.0	92.8	96.3	hypothetical protein ARALYDRAFT_472501	gbpln	Arabidopsis lyrata	AT1G22620.1 | Symbols: ATSAC1 | Phosphoinositide phosphatase family protein | chr1:7997889-8002787 REVERSE LENGTH=912	911	912	0	100.1	92.2	96.0
Rsa1.0_00133.1.g6355.t1	gb|EOA36458.1| hypothetical protein CARUB_v10011037mg [Capsella rubella]	216	206	1.00E-109	95.4	89.4	94.0	hypothetical protein CARUB_v10011037mg	gbpln	Capsella rubella	AT1G22740.1 | Symbols: RAB7, ATRABG3B, RAB75, RABG3B | RAB GTPase homolog G3B | chr1:8049247-8050494 FORWARD LENGTH=203	216	203	1.00E-106	94.0	85.6	91.2
Rsa1.0_00133.1.g6356.t1	emb|CAB77996.1| putative protein [Arabidopsis thaliana] gi|7321060|emb|CAB82107.1| putative protein [Arabidopsis thaliana]	658	715	1.00E-104	108.7	31.5	42.4	putative protein	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	658	249	2.00E-63	37.8	18.4	24.2
Rsa1.0_00133.1.g6357.t1	ref|XP_002863918.1| hypothetical protein ARALYDRAFT_357086 [Arabidopsis lyrata subsp. lyrata] gi|297309753|gb|EFH40177.1| hypothetical protein ARALYDRAFT_357086 [Arabidopsis lyrata subsp. lyrata]	136	123	5.00E-18	90.4	36.0	43.4	hypothetical protein ARALYDRAFT_357086	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00133.1.g6358.t1	gb|AAC23765.1| Mutator-like transposase [Arabidopsis thaliana]	414	784	1.00E-128	189.4	54.1	71.5	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	414	719	2.00E-21	173.7	22.7	42.8
Rsa1.0_00133.1.g6359.t1	ref|NP_174690.1| lectin protein kinase-like protein [Arabidopsis thaliana] gi|75338636|sp|Q9XID3.1|Y1343_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300; Flags: Precursor gi|5091617|gb|AAD39605.1|AC007454_4 Contains similarity to gi|479356 protein kinase PK1 from Zea mays, is a member of the PF|00954 S-locus glycoprotein family and contains a PF|00069 Eukaryotic protein kinase domain [Arabidopsis thaliana] gi|19699084|gb|AAL90909.1| At1g34300/F23M19_5 [Arabidopsis thaliana] gi|24111429|gb|AAN46865.1| At1g34300/F23M19_5 [Arabidopsis thaliana] gi|332193573|gb|AEE31694.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	842	829	0	98.5	78.4	84.9	lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G34300.1 | Symbols: | lectin protein kinase family protein | chr1:12503450-12505939 FORWARD LENGTH=829	842	829	0	98.5	78.4	84.9
Rsa1.0_00133.1.g6360.t3	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1351	1475	0	109.2	57.0	73.6	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1351	1262	1.00E-161	93.4	20.9	26.6
Rsa1.0_00133.1.g6361.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00133.1.g6362.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00133.1.g6363.t1	ref|NP_174692.1| uncharacterized protein [Arabidopsis thaliana] gi|37202044|gb|AAQ89637.1| At1g34320 [Arabidopsis thaliana] gi|51970944|dbj|BAD44164.1| hypothetical protein [Arabidopsis thaliana] gi|51971088|dbj|BAD44236.1| hypothetical protein [Arabidopsis thaliana] gi|332193576|gb|AEE31697.1| uncharacterized protein AT1G34320 [Arabidopsis thaliana]	599	657	0	109.7	86.8	92.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G34320.1 | Symbols: | Protein of unknown function (DUF668) | chr1:12520713-12524046 FORWARD LENGTH=657	599	657	0	109.7	86.8	92.2
Rsa1.0_00133.1.g6364.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1441	1447	0	100.4	37.1	55.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1441	626	8.00E-57	43.4	9.9	15.3
Rsa1.0_00133.1.g6365.t1	ref|XP_002891097.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336939|gb|EFH67356.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	501	529	0	105.6	83.0	90.0	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT1G34340.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:12530936-12534031 FORWARD LENGTH=530	501	530	0	105.8	80.4	88.0
Rsa1.0_00133.1.g6366.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00133.1.g6367.t1	gb|ABD32665.1| Terpenoid cylases/protein prenyltransferase alpha-alpha toroid; Bacterial adhesion [Medicago truncatula]	330	426	1.00E-131	129.1	74.8	84.5	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid; Bacterial adhesion	gbpln	Medicago truncatula	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	330	343	3.00E-37	103.9	33.3	43.0
Rsa1.0_00134.1.g6368.t1	ref|NP_175386.2| presequence protease 2 [Arabidopsis thaliana] gi|30694606|ref|NP_850961.1| presequence protease 2 [Arabidopsis thaliana] gi|30694608|ref|NP_850962.1| presequence protease 2 [Arabidopsis thaliana] gi|75161392|sp|Q8VY06.1|PREP2_ARATH RecName: Full=Presequence protease 2, chloroplastic/mitochondrial; Short=AtPreP2; Short=PreP 2; AltName: Full=Zinc metalloprotease 2; Short=AtZnMP2; Flags: Precursor gi|18377704|gb|AAL67002.1| putative hydrogenase protein [Arabidopsis thaliana] gi|28393925|gb|AAO42370.1| putative hydrogenase [Arabidopsis thaliana] gi|332194330|gb|AEE32451.1| presequence protease 2 [Arabidopsis thaliana] gi|332194331|gb|AEE32452.1| presequence protease 2 [Arabidopsis thaliana] gi|332194332|gb|AEE32453.1| presequence protease 2 [Arabidopsis thaliana]	1088	1080	0	99.3	87.7	92.7	presequence protease 2	gbpln	Arabidopsis thaliana	AT1G49630.2 | Symbols: ATPREP2, PREP2 | presequence protease 2 | chr1:18368405-18375336 REVERSE LENGTH=1080	1088	1080	0	99.3	87.7	92.7
Rsa1.0_00134.1.g6369.t1	gb|EOA38477.1| hypothetical protein CARUB_v10010232mg, partial [Capsella rubella]	172	225	3.00E-45	130.8	72.1	82.6	hypothetical protein CARUB_v10010232mg, partial	gbpln	Capsella rubella	AT1G49620.1 | Symbols: KRP7, ICN6, ICK5 | Cyclin-dependent kinase inhibitor family protein | chr1:18365692-18366559 REVERSE LENGTH=195	172	195	2.00E-39	113.4	68.6	79.1
Rsa1.0_00134.1.g6370.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6371.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	355	530	2.00E-16	149.3	15.2	23.7	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6372.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6373.t2	gb|AAC13599.1| similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]	725	928	1.00E-126	128.0	35.3	48.8	similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31)	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	725	626	6.00E-37	86.3	16.0	25.5
Rsa1.0_00134.1.g6374.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6375.t2	gb|EOA40417.1| hypothetical protein CARUB_v10009142mg [Capsella rubella]	1064	443	0	41.6	36.7	37.8	hypothetical protein CARUB_v10009142mg	gbpln	Capsella rubella	AT1G49600.1 | Symbols: ATRBP47A, RBP47A | RNA-binding protein 47A | chr1:18357236-18360150 REVERSE LENGTH=445	1064	445	0	41.8	34.4	35.0
Rsa1.0_00134.1.g6376.t1	ref|XP_002891523.1| hypothetical protein ARALYDRAFT_474094 [Arabidopsis lyrata subsp. lyrata] gi|297337365|gb|EFH67782.1| hypothetical protein ARALYDRAFT_474094 [Arabidopsis lyrata subsp. lyrata]	213	242	1.00E-95	113.6	86.4	91.5	hypothetical protein ARALYDRAFT_474094	gbpln	Arabidopsis lyrata	AT1G49590.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr1:18354997-18356409 FORWARD LENGTH=242	213	242	5.00E-98	113.6	85.9	91.5
Rsa1.0_00134.1.g6377.t1	dbj|BAB09912.1| MADS-box protein-like [Arabidopsis thaliana]	267	368	2.00E-25	137.8	24.7	33.3	MADS-box protein-like	gbpln	Arabidopsis thaliana	AT5G49420.1 | Symbols: | MADS-box transcription factor family protein | chr5:20035166-20036170 REVERSE LENGTH=334	267	334	6.00E-28	125.1	24.7	33.3
Rsa1.0_00134.1.g6378.t1	ref|XP_002870580.1| hypothetical protein ARALYDRAFT_915957 [Arabidopsis lyrata subsp. lyrata] gi|297316416|gb|EFH46839.1| hypothetical protein ARALYDRAFT_915957 [Arabidopsis lyrata subsp. lyrata]	291	286	1.00E-103	98.3	62.5	75.9	hypothetical protein ARALYDRAFT_915957	gbpln	Arabidopsis lyrata	AT5G37890.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr5:15090512-15091822 REVERSE LENGTH=286	291	286	1.00E-101	98.3	58.1	73.5

Rsa1.0_00134.1.g6379.t1	ref|NP_564480.1| uncharacterized protein [Arabidopsis thaliana] gi|13605690|gb|AAK32838.1|AF361826_1 At1g42440/F7F22_7 [Arabidopsis thaliana] gi|22137072|gb|AAM91381.1| At1g42440/F7F22_7 [Arabidopsis thaliana] gi|23397226|gb|AAN31895.1| unknown protein [Arabidopsis thaliana] gi|332193797|gb|AEE31918.1| uncharacterized protein AT1G42440 [Arabidopsis thaliana]	235	793	6.00E−82	337.4	71.9	79.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G42440.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ribosome biogenesis; LOCATED IN: nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: AARP2CN (InterPro:IPR012948), Protein of unknown function DUF663 (InterPro:IPR007034); BEST Arabidopsis thaliana protein match is: P−loop containing nucleoside triphosphate hydrolases superfamily protein (TAIR:AT1G06720.1); Has 2741 Blast hits to 2088 proteins in 291 species: Archae − 2; Bacteria − 131; Metazoa − 833; Fungi − 650; Plants − 171; Viruses − 49; Other Eukaryotes − 905 (source: NCBI BLink). | chr1:15895528−15899939 REVERSE LENGTH=793	235	793	2.00E−84	337.4	71.9	79.1
Rsa1.0_00134.1.g6380.t1	gb|EOA37196.1| hypothetical protein CARUB_v10010637mg [Capsella rubella]	130	129	2.00E−55	99.2	83.8	92.3	hypothetical protein CARUB_v10010637mg	gbpln	Capsella rubella	AT1G49975.1 | Symbols: | INVOLVED IN: photosynthesis; LOCATED IN: photosystem I, chloroplast, thylakoid membrane; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Photosystem I reaction centre subunit N (InterPro:IPR008796); Has 34 Blast hits to 34 proteins in 14 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 34; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:18504845−18505431 FORWARD LENGTH=129	130	129	9.00E−58	99.2	84.6	89.2
Rsa1.0_00134.1.g6381.t1	ref|XP_002891550.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata] gi|297337392|gb|EFH67809.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata]	405	422	1.00E−112	104.2	57.3	70.1	hypothetical protein ARALYDRAFT_474131	gbpln	Arabidopsis lyrata	AT1G49990.1 | Symbols: | F−box family protein | chr1:18513696−18514988 FORWARD LENGTH=430	405	430	1.00E−111	106.2	57.3	69.6
Rsa1.0_00134.1.g6382.t1	ref|XP_002891550.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata] gi|297337392|gb|EFH67809.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata]	434	422	1.00E−109	97.2	53.5	66.8	hypothetical protein ARALYDRAFT_474131	gbpln	Arabidopsis lyrata	AT1G49990.1 | Symbols: | F−box family protein | chr1:18513696−18514988 FORWARD LENGTH=430	434	430	1.00E−108	99.1	52.8	67.3
Rsa1.0_00134.1.g6383.t1	ref|XP_002891550.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata] gi|297337392|gb|EFH67809.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata]	416	422	1.00E−113	101.4	57.9	70.9	hypothetical protein ARALYDRAFT_474131	gbpln	Arabidopsis lyrata	AT1G49990.1 | Symbols: | F−box family protein | chr1:18513696−18514988 FORWARD LENGTH=430	416	430	1.00E−112	103.4	57.9	70.9
Rsa1.0_00134.1.g6384.t1	ref|NP_175420.3| DNA polymerase kappa subunit [Arabidopsis thaliana] gi|46394839|gb|AAS91582.1| DNA−directed polymerase kappa [Arabidopsis thaliana] gi|332194382|gb|AEE32503.1| DNA polymerase kappa subunit [Arabidopsis thaliana]	1235	671	0	54.3	42.3	45.3	DNA polymerase kappa subunit	gbpln	Arabidopsis thaliana	AT1G49980.1 | Symbols: | DNA/RNA polymerases superfamily protein | chr1:18508026−18512111 FORWARD LENGTH=671	1235	671	0	54.3	42.3	45.3
Rsa1.0_00134.1.g6385.t1	ref|NP_175422.2| ribosomal RNA small subunit methyltransferase E [Arabidopsis thaliana] gi|49660069|gb|AAT68325.1| hypothetical protein At1g50000 [Arabidopsis thaliana] gi|55740521|gb|AAV63853.1| hypothetical protein At1g50000 [Arabidopsis thaliana] gi|332194384|gb|AEE32505.1| ribosomal RNA small subunit methyltransferase E [Arabidopsis thaliana]	308	296	1.00E−145	96.1	86.0	90.9	ribosomal RNA small subunit methyltransferase E	gbpln	Arabidopsis thaliana	AT1G50000.1 | Symbols: | methyltransferases | chr1:18515183−18517244 REVERSE LENGTH=296	308	296	1.00E−148	96.1	86.0	90.9

Rsa1.0_00134.1.g6386.t1	ref|NP_193232.1| tubulin alpha-6 chain [Arabidopsis thaliana] gi|267070|sp|P29511.1|TBA6_ARATH RecName: Full=Tubulin alpha-6 chain gi|166920|gb|AAA32892.1| TUA6 [Arabidopsis thaliana] gi|2244853|emb|CAB10275.1| tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana] gi|7268242|emb|CAB78538.1| tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana] gi|16604480|gb|AAL24246.1| AT4g14960/dl3520c [Arabidopsis thaliana] gi|17529124|gb|AAL38788.1| putative tubulin alpha-6 chain TUA6 [Arabidopsis thaliana] gi|18958026|gb|AAL79586.1| AT4g14960/dl3520c [Arabidopsis thaliana] gi|21436097|gb|AAM51249.1| putative tubulin alpha-6 chain TUA6 [Arabidopsis thaliana] gi|89514805|gb|ABD75335.1| tubulin alpha-1 chain [Brassica rapa subsp. oleifera] gi|332658130|gb|AEE83530.1| tubulin alpha-6 chain [Arabidopsis thaliana]	450	450	0	100.0	100.0	100.0	tubulin alpha-6 chain	gbpln	Arabidopsis thaliana	AT4G14960.2 | Symbols: TUA6 | Tubulin/FtsZ family protein | chr4:8548769-8550319 REVERSE LENGTH=450	450	450	0	100.0	100.0	100.0
Rsa1.0_00134.1.g6387.t1	dbj|BAJ34041.1| unnamed protein product [Thellungiella halophila]	212	212	5.00E-95	100.0	88.2	91.5	unnamed protein product	----	----	AT1G50020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 72 Blast hits to 72 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 72; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18520144-18521600 REVERSE LENGTH=209	212	209	1.00E-91	98.6	83.5	88.7
Rsa1.0_00134.1.g6388.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6389.t11	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	729	777	5.00E-27	106.6	15.2	25.1	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6390.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6391.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6392.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6393.t26	gb|AEH16576.1| target of rapamycin [Eutrema halophilum] gi|334855093|gb|AEH16577.1| target of rapamycin [Eutrema halophilum]	2482	2479	0	99.9	93.6	96.0	target of rapamycin	gbpln	Eutrema halophilum	AT1G50030.1 | Symbols: TOR | target of rapamycin | chr1:18522626-18539619 REVERSE LENGTH=2481	2482	2481	0	100.0	92.5	95.3
Rsa1.0_00134.1.g6394.t1	gb|AFW66445.1| ubiquitin2 [Zea mays]	384	535	1.00E-115	139.3	63.3	75.3	ubiquitin2	gbenv/gbpln	Zea mays	AT5G20620.1 | Symbols: UBQ4 | ubiquitin 4 | chr5:6973315-6974463 REVERSE LENGTH=382	384	382	1.00E-117	99.5	63.0	75.0
Rsa1.0_00134.1.g6395.t1	gb|EOA23612.1| hypothetical protein CARUB_v10016812mg [Capsella rubella]	475	651	1.00E-154	137.1	59.2	75.4	hypothetical protein CARUB_v10016812mg	gbpln	Capsella rubella	AT3G58930.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21778381-21780014 REVERSE LENGTH=482	475	482	1.00E-154	101.5	58.3	72.0
Rsa1.0_00134.1.g6396.t1	emb|CAN81876.1| hypothetical protein VITISV_034528 [Vitis vinifera]	559	1241	5.00E-42	222.0	24.7	36.5	hypothetical protein VITISV_034528	gbpln	Vitis vinifera	AT3G19680.1 | Symbols: | Protein of unknown function (DUF1005) | chr3:6840448-6842107 FORWARD LENGTH=491	559	491	2.00E-30	87.8	15.9	18.8
Rsa1.0_00134.1.g6397.t1	gb|EOA39631.1| hypothetical protein CARUB_v10008262mg, partial [Capsella rubella]	291	895	1.00E-92	307.6	59.8	68.7	hypothetical protein CARUB_v10008262mg, partial	gbpln	Capsella rubella	AT1G51890.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19274802-19278528 REVERSE LENGTH=876	291	876	1.00E-94	301.0	58.8	69.8
Rsa1.0_00134.1.g6398.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1342	1307	0	97.4	60.7	74.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1342	1262	3.00E-98	94.0	13.9	21.8
Rsa1.0_00134.1.g6399.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00134.1.g6400.t1	ref|XP_002891554.1| hypothetical protein ARALYDRAFT_474142 [Arabidopsis lyrata subsp. lyrata] gi|297337396|gb|EFH67813.1| hypothetical protein ARALYDRAFT_474142 [Arabidopsis lyrata subsp. lyrata]	162	161	5.00E-68	99.4	74.1	88.9	hypothetical protein ARALYDRAFT_474142	gbpln	Arabidopsis lyrata	AT1G50060.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr1:18551186-18552446 FORWARD LENGTH=161	162	161	1.00E-63	99.4	72.2	88.3

<table>
<tr><td>Rsa1.0_00134.1.g6401.t1</td><td>ref|NP_175431.1| branched-chain-amino-acid aminotransferase 6 [Arabidopsis thaliana] gi|26391671|sp|Q9LPM9.1|BCAT6_ARATH RecName: Full=Branched-chain-amino-acid aminotransferase 6; Short=Atbcat-6 gi|8569092|gb|AAF76437.1|AC015445_4 Strong similarity to branched-chain amino acid aminotransferase (BCAT2) from Solanum tuberosum gb|AF193846 and contains an Aminotransferase class IV domain PF|01063. ESTs gb|Z26805, gb|Z30511 come from this gene [Arabidopsis thaliana] gi|13810195|emb|CAC37393.1| branched-chain amino acid transaminase 6 [Arabidopsis thaliana] gi|332194395|gb|AEE32516.1| branched-chain-amino-acid aminotransferase 6 [Arabidopsis thaliana]</td><td>417</td><td>356</td><td>0</td><td>85.4</td><td>75.8</td><td>79.9</td><td>branched-chain-amino-acid aminotransferase 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G50110.1 | Symbols: | D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein | chr1:18558203-18560219 REVERSE LENGTH=356</td><td>417</td><td>356</td><td>0</td><td>85.4</td><td>75.8</td><td>79.9</td></tr>
<tr><td>Rsa1.0_00134.1.g6402.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00134.1.g6403.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00134.1.g6404.t1</td><td>gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]</td><td>1261</td><td>1413</td><td>0</td><td>112.1</td><td>53.4</td><td>68.7</td><td>Putative retroelement polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1261</td><td>1262</td><td>0</td><td>100.1</td><td>24.6</td><td>32.4</td></tr>
<tr><td>Rsa1.0_00134.1.g6405.t6</td><td>gb|EOA37992.1| hypothetical protein CARUB_v10009461mg [Capsella rubella]</td><td>544</td><td>377</td><td>1.00E-127</td><td>69.3</td><td>50.7</td><td>53.3</td><td>hypothetical protein CARUB_v10009461mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G50300.1 | Symbols: TAF15 | TBP-associated factor 15 | chr1:18628818-18631662 REVERSE LENGTH=372</td><td>544</td><td>372</td><td>1.00E-122</td><td>68.4</td><td>49.8</td><td>52.9</td></tr>
<tr><td>Rsa1.0_00134.1.g6406.t1</td><td>ref|NP_175085.1| porphobilinogen synthase [Arabidopsis thaliana] gi|13876503|gb|AAK43479.1|AC084807_4 delta-aminolevulinic acid dehydratase (Alad), putative [Arabidopsis thaliana] gi|332193910|gb|AEE32031.1| porphobilinogen synthase [Arabidopsis thaliana]</td><td>389</td><td>406</td><td>0</td><td>104.4</td><td>84.1</td><td>91.0</td><td>porphobilinogen synthase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G44318.1 | Symbols: hemb2 | Aldolase superfamily protein | chr1:16831016-16833916 FORWARD LENGTH=406</td><td>389</td><td>406</td><td>0</td><td>104.4</td><td>84.1</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00134.1.g6407.t1</td><td>gb|AAF97281.1|AC010164_3 Hypothetical protein [Arabidopsis thaliana] gi|12324507|gb|AAG52212.1|AC022288_11 putative gag-pol polyprotein; 76173-77576 [Arabidopsis thaliana]</td><td>384</td><td>467</td><td>1.00E-106</td><td>121.6</td><td>57.0</td><td>74.0</td><td>Hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00134.1.g6408.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00134.1.g6409.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00135.1.g6410.t1</td><td>gb|AAM62981.1| unknown [Arabidopsis thaliana]</td><td>110</td><td>114</td><td>7.00E-44</td><td>103.6</td><td>83.6</td><td>94.5</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G52680.1 | Symbols: | late embryogenesis abundant protein-related / LEA protein-related | chr1:19618419-19618961 REVERSE LENGTH=114</td><td>110</td><td>114</td><td>9.00E-46</td><td>103.6</td><td>82.7</td><td>92.7</td></tr>
<tr><td>Rsa1.0_00135.1.g6411.t1</td><td>gb|EOA37169.1| hypothetical protein CARUB_v10010503mg, partial [Capsella rubella]</td><td>135</td><td>163</td><td>1.00E-62</td><td>120.7</td><td>96.3</td><td>98.5</td><td>hypothetical protein CARUB_v10010503mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G52740.1 | Symbols: HTA9 | histone H2A protein 9 | chr1:19645409-19646221 FORWARD LENGTH=134</td><td>135</td><td>134</td><td>9.00E-65</td><td>99.3</td><td>96.3</td><td>98.5</td></tr>
<tr><td>Rsa1.0_00135.1.g6412.t1</td><td>ref|NP_175684.3| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|332194727|gb|AEE32848.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana]</td><td>617</td><td>633</td><td>0</td><td>102.6</td><td>85.3</td><td>91.4</td><td>alpha/beta-hydrolase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G52750.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:19646785-19649208 REVERSE LENGTH=633</td><td>617</td><td>633</td><td>0</td><td>102.6</td><td>85.3</td><td>91.4</td></tr>
<tr><td>Rsa1.0_00135.1.g6413.t1</td><td>gb|EOA39092.1| hypothetical protein CARUB_v10011835mg [Capsella rubella]</td><td>329</td><td>322</td><td>1.00E-172</td><td>97.9</td><td>87.8</td><td>92.1</td><td>hypothetical protein CARUB_v10011835mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G52760.1 | Symbols: LysoPL2 | lysophospholipase 2 | chr1:19651378-19652576 FORWARD LENGTH=332</td><td>329</td><td>332</td><td>1.00E-173</td><td>100.9</td><td>89.1</td><td>93.9</td></tr>
<tr><td>Rsa1.0_00135.1.g6414.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00135.1.g6415.t1</td><td>ref|NP_175686.1| phototropic-responsive NPH3-like protein [Arabidopsis thaliana] gi|12324646|gb|AAG52282.1|AC019018_19 putative non-phototropic hypocotyl; 25081-26618 [Arabidopsis thaliana] gi|27311773|gb|AAO00852.1| putative non-phototropic hypocotyl [Arabidopsis thaliana] gi|31376385|gb|AAP49519.1| At1g52770 [Arabidopsis thaliana] gi|332194729|gb|AEE32850.1| phototropic-responsive NPH3-like protein [Arabidopsis thaliana]</td><td>449</td><td>454</td><td>0</td><td>101.1</td><td>81.3</td><td>88.4</td><td>phototropic-responsive NPH3-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G52770.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr1:19656009-19657546 FORWARD LENGTH=454</td><td>449</td><td>454</td><td>0</td><td>101.1</td><td>81.3</td><td>88.4</td></tr>
<tr><td>Rsa1.0_00135.1.g6416.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>432</td><td>1142</td><td>1.00E-111</td><td>264.4</td><td>47.2</td><td>62.5</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>432</td><td>575</td><td>4.00E-44</td><td>133.1</td><td>28.9</td><td>46.3</td></tr>
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Rsa1.0_00135.1.g6417.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1774	1274	0	71.8	32.0	42.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1774	575	7.00E-63	32.4	9.3	14.3
Rsa1.0_00135.1.g6418.t1	gb|EOA39112.1| hypothetical protein CARUB_v10011888mg [Capsella rubella]	1059	1061	0	100.2	78.8	87.6	hypothetical protein CARUB_v10011888mg	gbpln	Capsella rubella	AT1G52780.1 | Symbols: | Protein of unknown function (DUF2921) | chr1:19658846-19662025 FORWARD LENGTH=1059	1059	1059	0	100.0	76.3	84.7
Rsa1.0_00135.1.g6419.t1	ref|NP_175688.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] gi|12324652|gb|AAG52288.1|AC019018_25 putative oxidoreductase; 32373-31266 [Arabidopsis thaliana] gi|332194731|gb|AEE32852.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	310	310	1.00E-171	100.0	91.6	96.5	oxidoreductase, 2OG-Fe(II) oxygenase family protein	gbpln	Arabidopsis thaliana	AT1G52790.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:19662194-19663301 REVERSE LENGTH=310	310	310	1.00E-174	100.0	91.6	96.5
Rsa1.0_00135.1.g6420.t1	ref|NP_175689.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] gi|12324655|gb|AAG52291.1|AC019018_28 putative oxidoreductase; 33116-34434 [Arabidopsis thaliana] gi|67633452|gb|AAY78650.1| oxidoreductase [Arabidopsis thaliana] gi|332194732|gb|AEE32853.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	324	314	1.00E-170	96.9	86.4	92.0	oxidoreductase, 2OG-Fe(II) oxygenase family protein	gbpln	Arabidopsis thaliana	AT1G52800.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:19664044-19665362 FORWARD LENGTH=314	324	314	1.00E-173	96.9	86.4	92.0
Rsa1.0_00135.1.g6421.t1	ref|NP_175690.1| 2-oxoglutarate-dependent dioxygenase-related protein [Arabidopsis thaliana] gi|12324657|gb|AAG52293.1|AC019018_30 putative oxidoreductase; 36199-37309 [Arabidopsis thaliana] gi|332194733|gb|AEE32854.1| 2-oxoglutarate-dependent dioxygenase-related protein [Arabidopsis thaliana]	321	289	1.00E-139	90.0	75.7	82.9	2-oxoglutarate-dependent dioxygenase-related protein	gbpln	Arabidopsis thaliana	AT1G52810.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:19667127-19668237 FORWARD LENGTH=289	321	289	1.00E-142	90.0	75.7	82.9
Rsa1.0_00135.1.g6422.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00135.1.g6423.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00135.1.g6424.t1	ref|NP_175691.1| putative 2-oxoglutarate-dependent dioxygenase [Arabidopsis thaliana] gi|12324633|gb|AAG52269.1|AC019018_6 putative oxidoreductase; 38288-39393 [Arabidopsis thaliana] gi|332194734|gb|AEE32855.1| putative 2-oxoglutarate-dependent dioxygenase [Arabidopsis thaliana]	314	317	1.00E-168	101.0	90.8	96.2	putative 2-oxoglutarate-dependent dioxygenase	gbpln	Arabidopsis thaliana	AT1G52820.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:19669216-19670321 FORWARD LENGTH=317	314	317	1.00E-170	101.0	90.8	96.2
Rsa1.0_00135.1.g6425.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00135.1.g6426.t1	ref|XP_002894404.1| hypothetical protein ARALYDRAFT_474409 [Arabidopsis lyrata subsp. lyrata] gi|297340246|gb|EFH70663.1| hypothetical protein ARALYDRAFT_474409 [Arabidopsis lyrata subsp. lyrata]	201	188	2.00E-75	93.5	73.1	81.1	hypothetical protein ARALYDRAFT_474409	gbpln	Arabidopsis lyrata	AT1G52830.1 | Symbols: IAA6, SHY1 | indole-3-acetic acid 6 | chr1:19672670-19673559 REVERSE LENGTH=189	201	189	1.00E-76	94.0	72.1	81.1
Rsa1.0_00135.1.g6427.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00135.1.g6428.t1	dbj|BAB02160.1| unnamed protein product [Arabidopsis thaliana] gi|15292885|gb|AAK92813.1| unknown protein [Arabidopsis thaliana] gi|21280913|gb|AAM45005.1| unknown protein [Arabidopsis thaliana]	296	415	1.00E-53	140.2	43.2	56.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	296	343	1.00E-27	115.9	31.8	41.9
Rsa1.0_00135.1.g6429.t1	gb|EOA37260.1| hypothetical protein CARUB_v10010820mg [Capsella rubella]	68	68	9.00E-30	100.0	95.6	98.5	hypothetical protein CARUB_v10010820mg	gbpln	Capsella rubella	AT1G52855.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G15534.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:19683137-19683343 REVERSE LENGTH=68	68	68	5.00E-32	100.0	94.1	97.1
Rsa1.0_00135.1.g6430.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00135.1.g6431.t1	ref|NP_564615.3| Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein [Arabidopsis thaliana] gi|12324641|gb|AAG52277.1|AC019018_14 unknown protein; 54928-56750 [Arabidopsis thaliana] gi|14326545|gb|AAK60317.1|AF385726_1 At1g52870/F14G24_14 [Arabidopsis thaliana] gi|25090145|gb|AAN72239.1| At1g52870/F14G24_14 [Arabidopsis thaliana] gi|332194741|gb|AEE32862.1| Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein [Arabidopsis thaliana]	362	366	0	101.1	89.0	94.8	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	gbpln	Arabidopsis thaliana	AT1G52870.2 | Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr1:19685856-19687678 FORWARD LENGTH=366	362	366	0	101.1	89.0	94.8
Rsa1.0_00135.1.g6432.t1	gb|EOA33105.1| hypothetical protein CARUB_v10016443mg [Capsella rubella]	107	107	4.00E-28	100.0	60.7	77.6	hypothetical protein CARUB_v10016443mg	gbpln	Capsella rubella	AT3G15518.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:5249221-5249541 FORWARD LENGTH=106	107	106	9.00E-31	99.1	62.6	77.6
Rsa1.0_00135.1.g6433.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1358	1307	0	96.2	60.6	75.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1358	1262	1.00E-101	92.9	14.7	21.8
Rsa1.0_00135.1.g6434.t1	gb|EOA38054.1| hypothetical protein CARUB_v10009524mg, partial [Capsella rubella]	321	363	1.00E-104	113.1	73.5	79.8	hypothetical protein CARUB_v10009524mg, partial	gbpln	Capsella rubella	AT1G52880.1 | Symbols: NAM, ANAC018, ATNAM, NARS2 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:19689285-19690430 REVERSE LENGTH=320	321	320	1.00E-100	99.7	72.9	77.9
Rsa1.0_00135.1.g6435.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00135.1.g6436.t1	gb|AAG00256.1|AC002130_21 F1N21.7 [Arabidopsis thaliana]	132	303	4.00E-17	229.5	29.5	36.4	F1N21.7	gbpln	Arabidopsis thaliana	AT5G33393.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:12656430-12658588 REVERSE LENGTH=435	132	435	1.00E-15	329.5	24.2	37.1
Rsa1.0_00135.1.g6437.t1	ref|XP_002894409.1| ANAC019 [Arabidopsis lyrata subsp. lyrata] gi|297340251|gb|EFH70668.1| ANAC019 [Arabidopsis lyrata subsp. lyrata]	314	320	1.00E-154	101.9	88.2	93.3	ANAC019	gbpln	Arabidopsis lyrata	AT1G52890.1 | Symbols: ANAC019, NAC019 | NAC domain containing protein 19 | chr1:19697292-19698444 REVERSE LENGTH=317	314	317	1.00E-149	101.0	84.4	90.8
Rsa1.0_00135.1.g6438.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00135.1.g6439.t1	gb|EOA39327.1| hypothetical protein CARUB_v10012368mg [Capsella rubella]	196	203	3.00E-90	103.6	83.2	90.8	hypothetical protein CARUB_v10012368mg	gbpln	Capsella rubella	AT1G52900.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr1:19702211-19702916 REVERSE LENGTH=199	196	199	1.00E-89	101.5	83.7	89.8
Rsa1.0_00135.1.g6440.t1	gb|EOA38605.1| hypothetical protein CARUB_v10010446mg [Capsella rubella]	175	175	4.00E-90	100.0	92.0	96.6	hypothetical protein CARUB_v10010446mg	gbpln	Capsella rubella	AT1G52910.1 | Symbols: | Protein of unknown function (DUF1218) | chr1:19708114-19709128 FORWARD LENGTH=175	175	175	4.00E-87	100.0	87.4	92.0
Rsa1.0_00135.1.g6441.t1	ref|XP_002894411.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340253|gb|EFH70670.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	657	410	0	62.4	54.5	58.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G52920.1 | Symbols: GCR2, GPCR | G protein coupled receptor | chr1:19709360-19711048 REVERSE LENGTH=410	657	410	0	62.4	52.7	57.5
Rsa1.0_00135.1.g6442.t1	dbj|BAJ33634.1| unnamed protein product [Thellungiella halophila]	248	512	1.00E-122	206.5	83.1	91.1	unnamed protein product	----	----	AT3G14680.1 | Symbols: CYP72A14 | cytochrome P450, family 72, subfamily A, polypeptide 14 | chr3:4934478-4936462 FORWARD LENGTH=512	248	512	1.00E-123	206.5	81.0	91.1
Rsa1.0_00136.1.g6443.t1	gb|EOA36640.1| hypothetical protein CARUB_v10011892mg [Capsella rubella]	719	1530	0	212.8	94.6	97.2	hypothetical protein CARUB_v10011892mg	gbpln	Capsella rubella	AT1G08730.1 | Symbols: XIC, ATXIC | Myosin family protein with Dil domain | chr1:2779963-2788325 FORWARD LENGTH=1538	719	1538	0	213.9	94.4	96.2
Rsa1.0_00136.1.g6444.t2	ref|NP_172347.2| F-box protein SKIP24 [Arabidopsis thaliana] gi|17529082|gb|AAL38751.1| unknown protein [Arabidopsis thaliana] gi|22136746|gb|AAM91692.1| unknown protein [Arabidopsis thaliana] gi|332190216|gb|AEE28337.1| F-box protein SKIP24 [Arabidopsis thaliana]	260	274	1.00E-109	105.4	79.2	88.5	F-box protein SKIP24	gbpln	Arabidopsis thaliana	AT1G08710.1 | Symbols: | F-box family protein | chr1:2771720-2773250 FORWARD LENGTH=274	260	274	1.00E-112	105.4	79.2	88.5
Rsa1.0_00136.1.g6445.t1	gb|EOA40330.1| hypothetical protein CARUB_v10009057mg [Capsella rubella]	442	467	0	105.7	88.7	93.9	hypothetical protein CARUB_v10009057mg	gbpln	Capsella rubella	AT1G08700.1 | Symbols: PS1 | Presenilin-1 | chr1:2769885-2771348 REVERSE LENGTH=453	442	453	0	102.5	84.8	91.4

Rsa1.0_00136.1.g6446.t1	ref|XP_002889709.1| hypothetical protein ARALYDRAFT_470937 [Arabidopsis lyrata subsp. lyrata] gi|297335551|gb|EFH65968.1| hypothetical protein ARALYDRAFT_470937 [Arabidopsis lyrata subsp. lyrata]	996	668	0	67.1	51.1	54.8	hypothetical protein ARALYDRAFT_470937	gbpln	Arabidopsis lyrata	AT1G08680.2 | Symbols: ZIGA4 | ARF GAP-like zinc finger-containing protein ZIGA4 | chr1:2762820-2768387 FORWARD LENGTH=648	996	648	0	65.1	49.8	53.7
Rsa1.0_00136.1.g6447.t1	gb|AAF86559.1|AC069252_18 F2E2.15 [Arabidopsis thaliana]	169	487	7.00E-18	288.2	35.5	56.2	F2E2.15	gbpln	Arabidopsis thaliana	AT1G22080.2 | Symbols: | Cysteine proteinases superfamily protein | chr1:7792404-7794089 REVERSE LENGTH=332	169	332	5.00E-20	196.4	34.3	52.7
Rsa1.0_00136.1.g6448.t1	gb|EOA38383.1| hypothetical protein CARUB_v10009932mg [Capsella rubella]	288	285	1.00E-155	99.0	91.0	96.2	hypothetical protein CARUB_v10009932mg	gbpln	Capsella rubella	AT1G08650.1 | Symbols: PPCK1, ATPPCK1 | phosphoenolpyruvate carboxylase kinase 1 | chr1:2752206-2753232 FORWARD LENGTH=284	288	284	1.00E-156	98.6	89.6	95.1
Rsa1.0_00136.1.g6449.t1	gb|EOA36952.1| hypothetical protein CARUB_v10009875mg [Capsella rubella]	287	299	1.00E-136	104.2	84.0	90.9	hypothetical protein CARUB_v10009875mg	gbpln	Capsella rubella	AT1G08640.1 | Symbols: CJD1 | Chloroplast J-like domain 1 | chr1:2748714-2751209 REVERSE LENGTH=294	287	294	1.00E-137	102.4	84.3	90.6
Rsa1.0_00136.1.g6450.t1	gb|EOA38078.1| hypothetical protein CARUB_v10009546mg [Capsella rubella]	358	358	0	100.0	90.5	94.7	hypothetical protein CARUB_v10009546mg	gbpln	Capsella rubella	AT1G08630.4 | Symbols: THA1 | threonine aldolase 1 | chr1:2743948-2745685 REVERSE LENGTH=358	358	358	0	100.0	89.1	94.7
Rsa1.0_00136.1.g6451.t1	ref|NP_172338.4| transcription factor jumonji and C5HC2 type zinc finger domain-containing protein [Arabidopsis thaliana] gi|334182398|ref|NP_001184940.1| transcription factor jumonji and C5HC2 type zinc finger domain-containing protein [Arabidopsis thaliana] gi|225897896|dbj|BAH30280.1| hypothetical protein [Arabidopsis thaliana] gi|332190197|gb|AEE28318.1| transcription factor jumonji and C5HC2 type zinc finger domain-containing protein [Arabidopsis thaliana] gi|332190198|gb|AEE28319.1| transcription factor jumonji and C5HC2 type zinc finger domain-containing protein [Arabidopsis thaliana]	1194	1209	0	101.3	80.5	88.4	transcription factor jumonji and C5HC2 type zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT1G08620.2 | Symbols: PKDM7D | Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein | chr1:2737554-2743370 FORWARD LENGTH=1209	1194	1209	0	101.3	80.5	88.4
Rsa1.0_00136.1.g6452.t19	ref|XP_002889705.1| ATRX/CHR20 [Arabidopsis lyrata subsp. lyrata] gi|297335547|gb|EFH65964.1| ATRX/CHR20 [Arabidopsis lyrata subsp. lyrata]	1510	1483	0	98.2	83.7	89.1	ATRX/CHR20	gbpln	Arabidopsis lyrata	AT1G08600.2 | Symbols: ATRX | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:2724562-2733431 FORWARD LENGTH=1479	1510	1479	0	97.9	82.8	87.7
Rsa1.0_00136.1.g6453.t1	ref|NP_172334.1| uncharacterized protein [Arabidopsis thaliana] gi|9802580|gb|AAF99782.1|AC003981_32 F22O13.6 [Arabidopsis thaliana] gi|38454044|gb|AAR20716.1| At1g08580 [Arabidopsis thaliana] gi|41349904|gb|AAS00337.1| At1g08580 [Arabidopsis thaliana] gi|332190190|gb|AEE28311.1| uncharacterized protein AT1G08580 [Arabidopsis thaliana]	168	123	1.00E-40	73.2	50.0	52.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G08580.1 | Symbols: | unknown protein; Has 39 Blast hits to 39 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr1:2715296-2716351 REVERSE LENGTH=123	168	123	4.00E-43	73.2	50.0	52.4
Rsa1.0_00136.1.g6454.t1	dbj|BAJ34000.1| unnamed protein product [Thellungiella halophila]	250	274	1.00E-106	109.6	84.0	90.4	unnamed protein product	----	----	AT1G08570.1 | Symbols: ACHT4 | atypical CYS HIS rich thioredoxin 4 | chr1:2713059-2714312 FORWARD LENGTH=275	250	275	1.00E-106	110.0	81.6	88.4
Rsa1.0_00136.1.g6455.t1	ref|XP_002892462.1| SYP111 [Arabidopsis lyrata subsp. lyrata] gi|297338304|gb|EFH68721.1| SYP111 [Arabidopsis lyrata subsp. lyrata]	306	310	1.00E-135	101.3	84.6	92.8	SYP111	gbpln	Arabidopsis lyrata	AT1G08560.1 | Symbols: SYP111, KN, ATSYP111 | syntaxin of plants 111 | chr1:2709778-2710710 REVERSE LENGTH=310	306	310	1.00E-135	101.3	84.0	92.5
Rsa1.0_00136.1.g6456.t1	gb|EOA40354.1| hypothetical protein CARUB_v10009082mg [Capsella rubella]	459	461	0	100.4	86.9	93.2	hypothetical protein CARUB_v10009082mg	gbpln	Capsella rubella	AT1G08550.2 | Symbols: NPQ1, AVDE1 | non-photochemical quenching 1 | chr1:2707462-2709387 FORWARD LENGTH=462	459	462	0	100.7	86.5	93.0
Rsa1.0_00136.1.g6457.t2	ref|NP_172329.2| uncharacterized protein [Arabidopsis thaliana] gi|110738913|dbj|BAF01378.1| hypothetical protein [Arabidopsis thaliana] gi|332190181|gb|AEE28302.1| uncharacterized protein AT1G08530 [Arabidopsis thaliana]	261	257	5.00E-79	98.5	67.8	78.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G08530.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G09995.2); Has 140 Blast hits to 140 proteins in 53 species: Archae - 0; Bacteria - 63; Metazoa - 0; Fungi - 0; Plants - 76; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:2701252-2702952 FORWARD LENGTH=257	261	257	1.00E-81	98.5	67.8	78.2

Rsa1.0_00136.1.g6458.t1	gb|EOA39742.1| hypothetical protein CARUB_v10008387mg [Capsella rubella]	755	758	0	100.4	89.8	94.2	hypothetical protein CARUB_v10008387mg	gbpln	Capsella rubella	AT1G08520.1 | Symbols: ALB1, ALB-1V, V157, PDE166, CHLD | ALBINA 1 | chr1:2696538-2700819 FORWARD LENGTH=760	755	760	0	100.7	90.2	94.6
Rsa1.0_00136.1.g6459.t1	gb|ABI18986.1| palmitoyl-ACP thioesterase [Brassica juncea]	411	411	0	100.0	92.2	95.4	palmitoyl-ACP thioesterase	gbpln	Brassica juncea	AT1G08510.1 | Symbols: FATB | fatty acyl-ACP thioesterases B | chr1:2691546-2693409 REVERSE LENGTH=412	411	412	0	100.2	88.3	93.2
Rsa1.0_00136.1.g6460.t1	ref|XP_002892460.1| hypothetical protein ARALYDRAFT_470910 [Arabidopsis lyrata subsp. lyrata] gi|297338302|gb|EFH68719.1| hypothetical protein ARALYDRAFT_470910 [Arabidopsis lyrata subsp. lyrata]	464	466	0	100.4	90.7	93.5	hypothetical protein ARALYDRAFT_470910	gbpln	Arabidopsis lyrata	AT1G08490.1 | Symbols: ATSUFS, SUFS, ATCPNIFS, ATNFS2, CPNIFS | chloroplastic NIFS-like cysteine desulfurase | chr1:2685980-2688547 REVERSE LENGTH=463	464	463	0	99.8	90.3	93.5
Rsa1.0_00136.1.g6461.t1	ref|NP_563819.1| uncharacterized protein [Arabidopsis thaliana] gi|15450427|gb|AAK96507.1| At1g08480/T27G7_10 [Arabidopsis thaliana] gi|16974435|gb|AAL31221.1| At1g08480/T27G7_10 [Arabidopsis thaliana] gi|332190176|gb|AEE28297.1| uncharacterized protein AT1G08480 [Arabidopsis thaliana]	138	142	2.00E-65	102.9	90.6	92.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G08480.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, plasma membrane, plastid, vacuole; EXPRESSED IN: 27 plant structures; EXPRESSED DURING: 15 growth stages; Has 39 Blast hits to 39 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2684340-2685395 FORWARD LENGTH=142	138	142	5.00E-68	102.9	90.6	92.8
Rsa1.0_00136.1.g6462.t1	gb|EOA37930.1| hypothetical protein CARUB_v10009397mg [Capsella rubella]	393	390	0	99.2	88.0	93.4	hypothetical protein CARUB_v10009397mg	gbpln	Capsella rubella	AT1G08470.1 | Symbols: SSL3 | strictosidine synthase-like 3 | chr1:2682262-2683977 REVERSE LENGTH=390	393	390	0	99.2	87.5	93.1
Rsa1.0_00136.1.g6463.t1	gb|EOA36256.1| hypothetical protein CARUB_v10010384mg [Capsella rubella]	168	188	2.00E-82	111.9	87.5	94.0	hypothetical protein CARUB_v10010384mg	gbpln	Capsella rubella	AT1G08465.1 | Symbols: YAB2 | Plant-specific transcription factor YABBY family protein | chr1:2676033-2679382 FORWARD LENGTH=184	168	184	3.00E-78	109.5	82.7	89.9
Rsa1.0_00136.1.g6464.t1	ref|XP_002889694.1| hypothetical protein ARALYDRAFT_334132 [Arabidopsis lyrata subsp. lyrata] gi|297335536|gb|EFH65953.1| hypothetical protein ARALYDRAFT_334132 [Arabidopsis lyrata subsp. lyrata]	508	501	0	98.6	86.2	90.9	hypothetical protein ARALYDRAFT_334132	gbpln	Arabidopsis lyrata	AT1G08440.1 | Symbols: | Aluminium activated malate transporter family protein | chr1:2663027-2665343 FORWARD LENGTH=501	508	501	0	98.6	85.0	90.6
Rsa1.0_00136.1.g6465.t1	ref|XP_003605992.1| Serine/threonine protein phosphatase [Medicago truncatula] gi|355507047|gb|AES88189.1| Serine/threonine protein phosphatase [Medicago truncatula]	120	875	1.00E-36	729.2	63.3	66.7	Serine/threonine protein phosphatase	gbpln	Medicago truncatula	AT2G27210.2 | Symbols: BSL3 | BRI1 suppressor 1 (BSU1)-like 3 | chr2:11630188-11636182 FORWARD LENGTH=1001	120	1001	4.00E-38	834.2	62.5	66.7
Rsa1.0_00136.1.g6466.t1	ref|NP_172316.2| RINT-1 / TIP-1 family protein [Arabidopsis thaliana] gi|26451304|dbj|BAC42753.1| unknown protein [Arabidopsis thaliana] gi|29824357|gb|AAP04139.1| unknown protein [Arabidopsis thaliana] gi|332190164|gb|AEE28285.1| RINT-1 / TIP-1 family protein [Arabidopsis thaliana]	800	804	0	100.5	79.0	86.5	RINT-1 / TIP-1 family protein	gbpln	Arabidopsis thaliana	AT1G08400.1 | Symbols: | RINT-1 / TIP-1 family | chr1:2643348-2646005 REVERSE LENGTH=804	800	804	0	100.5	79.0	86.5
Rsa1.0_00136.1.g6467.t1	gb|EOA37194.1| hypothetical protein CARUB_v10010612mg [Capsella rubella]	123	136	3.00E-43	110.6	74.8	78.0	hypothetical protein CARUB_v10010612mg	gbpln	Capsella rubella	AT1G08390.1 | Symbols: | unknown protein; Has 62 Blast hits to 62 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 34; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2642220-2643103 FORWARD LENGTH=137	123	137	3.00E-41	111.4	69.1	78.0
Rsa1.0_00136.1.g6468.t1	gb|EOA38046.1| hypothetical protein CARUB_v10009516mg [Capsella rubella]	368	365	1.00E-160	99.2	84.8	90.8	hypothetical protein CARUB_v10009516mg	gbpln	Capsella rubella	AT1G08370.1 | Symbols: DCP1, ATDCP1 | decapping 1 | chr1:2638355-2640367 FORWARD LENGTH=367	368	367	1.00E-153	99.7	83.7	91.0
Rsa1.0_00136.1.g6469.t1	gb|EOA38504.1| hypothetical protein CARUB_v10010278mg [Capsella rubella]	216	216	1.00E-107	100.0	95.8	99.1	hypothetical protein CARUB_v10010278mg	gbpln	Capsella rubella	AT1G08360.1 | Symbols: | Ribosomal protein L1p/L10e family | chr1:2636231-2637694 FORWARD LENGTH=216	216	216	1.00E-108	100.0	95.8	97.7
Rsa1.0_00136.1.g6470.t1	ref|NP_001077489.1| endomembrane protein 70-like protein [Arabidopsis thaliana] gi|332190159|gb|AEE28280.1| endomembrane protein 70-like protein [Arabidopsis thaliana]	610	589	0	96.6	82.5	88.4	endomembrane protein 70-like protein	gbpln	Arabidopsis thaliana	AT1G08350.2 | Symbols: | Endomembrane protein 70 protein family | chr1:2632970-2635605 REVERSE LENGTH=589	610	589	0	96.6	82.5	88.4

Rsa1.0_00136.1.g6471.t1	ref|NP_172310.1| Rho GTPase activating protein with PAK-box/P21-Rho-binding domain [Arabidopsis thaliana] gi|46931246|gb|AAT06427.1| At1g08340 [Arabidopsis thaliana] gi|48958519|gb|AAT47812.1| At1g08340 [Arabidopsis thaliana] gi|110736318|dbj|BAF00129.1| hypothetical protein [Arabidopsis thaliana] gi|332190157|gb|AEE28278.1| Rho GTPase activating protein with PAK-box/P21-Rho-binding domain [Arabidopsis thaliana]	321	331	1.00E-144	103.1	83.2	91.6	Rho GTPase activating protein with PAK-box/P21-Rho-binding domain	gbpln	Arabidopsis thaliana	AT1G08340.1 | Symbols: | Rho GTPase activating protein with PAK-box/P21-Rho-binding domain | chr1:2631308-2632669 FORWARD LENGTH=331	321	331	2.33E-156	103.1	83.2	91.6
Rsa1.0_00137.1.g6472.t1	ref|XP_002518059.1| arp2/3 complex 20 kD subunit, putative [Ricinus communis] gi|223542655|gb|EEF44192.1| arp2/3 complex 20 kD subunit, putative [Ricinus communis]	139	169	8.00E-66	121.6	95.0	99.3	arp2/3 complex 20 kD subunit, putative	gbpln	Ricinus communis	AT4G14147.1 | Symbols: ARPC4 | protein binding | chr4:8154079-8156246 REVERSE LENGTH=169	139	169	6.00E-68	121.6	97.1	97.8
Rsa1.0_00137.1.g6473.t1	ref|XP_002880292.1| ribonuclease P [Arabidopsis lyrata subsp. lyrata] gi|297326131|gb|EFH56551.1| ribonuclease P [Arabidopsis lyrata subsp. lyrata]	820	825	0	100.6	78.0	86.8	ribonuclease P	gbpln	Arabidopsis lyrata	AT2G47300.2 | Symbols: | ribonuclease Ps | chr2:19418733-19422076 FORWARD LENGTH=826	820	826	0	100.7	78.8	86.6
Rsa1.0_00137.1.g6474.t1	ref|NP_182265.1| histidine kinase CKI1 [Arabidopsis thaliana] gi|75097398|sp|O22267.1|CKI1_ARATH RecName: Full=Histidine kinase CKI1; AltName: Full=Protein CYTOKININ-INDEPENDENT 1 gi|1679803|dbj|BAA13416.1| histidine kinase homolog [Arabidopsis thaliana] gi|2529684|gb|AAC62867.1| putative histidine kinase [Arabidopsis thaliana] gi|330255746|gb|AEC10840.1| histidine kinase CKI1 [Arabidopsis thaliana]	1078	1122	0	104.1	66.5	76.3	histidine kinase CKI1	gbpln	Arabidopsis thaliana	AT2G47430.1 | Symbols: CKI1 | Signal transduction histidine kinase | chr2:19459167-19463122 REVERSE LENGTH=1122	1078	1122	0	104.1	66.5	76.3
Rsa1.0_00137.1.g6475.t1	ref|XP_002864881.1| hypothetical protein ARALYDRAFT_496593 [Arabidopsis lyrata subsp. lyrata] gi|297310716|gb|EFH41140.1| hypothetical protein ARALYDRAFT_496593 [Arabidopsis lyrata subsp. lyrata]	130	357	1.00E-25	274.6	48.5	55.4	hypothetical protein ARALYDRAFT_496593	gbpln	Arabidopsis lyrata	AT5G63990.1 | Symbols: | Inositol monophosphatase family protein | chr5:25613387-25615736 FORWARD LENGTH=357	130	357	4.00E-28	274.6	47.7	53.1
Rsa1.0_00137.1.g6476.t1	emb|CAA49513.1| beta-1,3-glucanase homologue [Brassica napus]	473	474	0	100.2	82.5	88.8	beta-1,3-glucanase homologue	gbpln	Brassica napus	AT4G14080.1 | Symbols: MEE48 | O-Glycosyl hydrolases family 17 protein | chr4:8118697-8120292 REVERSE LENGTH=478	473	478	0	101.1	81.2	90.3
Rsa1.0_00137.1.g6477.t2	emb|CAA96521.1| AMP-binding protein [Brassica napus]	750	701	0	93.5	89.5	91.3	AMP-binding protein	gbpln	Brassica napus	AT4G14070.1 | Symbols: AAE15 | acyl-activating enzyme 15 | chr4:8112122-8118039 REVERSE LENGTH=727	750	727	0	96.9	82.9	90.0
Rsa1.0_00137.1.g6478.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00137.1.g6479.t1	ref|XP_002868318.1| hypothetical protein ARALYDRAFT_330113 [Arabidopsis lyrata subsp. lyrata] gi|297314154|gb|EFH44577.1| hypothetical protein ARALYDRAFT_330113 [Arabidopsis lyrata subsp. lyrata]	167	1057	3.00E-92	632.9	96.4	98.2	hypothetical protein ARALYDRAFT_330113	gbpln	Arabidopsis lyrata	AT4G14040.1 | Symbols: EDA38, SBP2 | selenium-binding protein 2 | chr4:8100691-8102828 REVERSE LENGTH=487	167	487	5.00E-92	291.6	94.6	98.2
Rsa1.0_00137.1.g6480.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	134	1499	7.00E-34	1118.7	53.7	67.9	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00137.1.g6481.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00137.1.g6482.t1	gb|EOA17616.1| hypothetical protein CARUB_v10005981mg, partial [Capsella rubella]	117	139	2.00E-42	118.8	74.4	82.9	hypothetical protein CARUB_v10005981mg, partial	gbpln	Capsella rubella	AT4G14010.1 | Symbols: RALFL32 | ralf-like 32 | chr4:8093010-8093363 REVERSE LENGTH=117	117	117	1.00E-44	100.0	75.2	82.1
Rsa1.0_00137.1.g6483.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	260	1142	1.00E-12	439.2	13.5	20.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00137.1.g6484.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	807	1142	1.00E-172	141.5	40.1	51.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	807	626	5.00E-31	77.6	12.6	21.6
Rsa1.0_00137.1.g6485.t2	gb|EOA17132.1| hypothetical protein CARUB_v10005396mg [Capsella rubella]	953	290	1.00E-127	30.4	25.5	26.8	hypothetical protein CARUB_v10005396mg	gbpln	Capsella rubella	AT4G14000.1 | Symbols: | Putative methyltransferase family protein | chr4:8090851-8092347 FORWARD LENGTH=290	953	290	1.00E-129	30.4	25.7	26.8

Rsa1.0_00137.1.g6486.t1	gb|AAG52094.1|AC012680_5 putative Mutator-like transposase; 12516-14947 [Arabidopsis thaliana]	382	761	1.00E-118	199.2	57.9	72.3	putative Mutator-like transposase; 12516-14947	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00137.1.g6487.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00137.1.g6488.t1	gb|EOA16570.1| hypothetical protein CARUB_v10004729mg [Capsella rubella]	473	473	0	100.0	84.8	90.9	hypothetical protein CARUB_v10004729mg	gbpln	Capsella rubella	AT4G13980.1 | Symbols: AT-HSFA5, HSFA5 | winged-helix DNA-binding transcription factor family protein | chr4:8077519-8079247 REVERSE LENGTH=466	473	466	0	98.5	84.4	89.4
Rsa1.0_00137.1.g6489.t2	ref|XP_002868324.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314160|gb|EFH44583.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	795	776	0	97.6	83.0	88.7	zinc ion binding protein	gbpln	Arabidopsis lyrata	AT4G13970.1 | Symbols: | zinc ion binding | chr4:8070696-8074134 REVERSE LENGTH=778	795	778	0	97.9	82.9	87.4
Rsa1.0_00137.1.g6490.t1	gb|AAD25646.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	731	1461	1.00E-144	199.9	43.8	59.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00137.1.g6491.t1	gb|ABD65088.1| hypothetical protein 27.t00109 [Brassica oleracea]	668	1176	9.00E-88	176.0	27.1	38.8	hypothetical protein 27.t00109	gbpln	Brassica oleracea	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	668	452	1.00E-29	67.7	18.4	29.2
Rsa1.0_00138.1.g6492.t1	ref|XP_002867739.1| hypothetical protein ARALYDRAFT_492568 [Arabidopsis lyrata subsp. lyrata] gi|297313575|gb|EFH43998.1| hypothetical protein ARALYDRAFT_492568 [Arabidopsis lyrata subsp. lyrata]	566	557	0	98.4	78.3	85.5	hypothetical protein ARALYDRAFT_492568	gbpln	Arabidopsis lyrata	AT4G22980.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: Pyridoxal phosphate (PLP)-dependent transferases superfamily protein (TAIR:AT5G51920.1); Has 520 Blast hits to 468 proteins in 130 species: Archae - 5; Bacteria - 23; Metazoa - 99; Fungi - 131; Plants - 231; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink). | chr4:12043974-12045653 REVERSE LENGTH=559	566	559	0	98.8	74.7	83.4
Rsa1.0_00138.1.g6493.t2	ref|NP_001190805.1| SPX domain-containing membrane protein [Arabidopsis thaliana] gi|332659290|gb|AEE84690.1| SPX domain-containing membrane protein [Arabidopsis thaliana]	701	700	0	99.9	90.6	95.1	SPX domain-containing membrane protein	gbpln	Arabidopsis thaliana	AT4G22990.2 | Symbols: | Major Facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein | chr4:12048240-12050984 REVERSE LENGTH=700	701	700	0	99.9	90.6	95.1
Rsa1.0_00138.1.g6494.t2	ref|NP_001078433.1| UDP-galactose transporter 2 [Arabidopsis thaliana] gi|3292827|emb|CAA19817.1| putative protein [Arabidopsis thaliana] gi|7269148|emb|CAB79256.1| putative protein [Arabidopsis thaliana] gi|67764062|gb|AAY79163.1| Golgi-localized UDP-galactose transporter [Arabidopsis thaliana] gi|332659293|gb|AEE84693.1| UDP-galactose transporter 2 [Arabidopsis thaliana]	348	362	1.00E-160	104.0	86.2	91.7	UDP-galactose transporter 2	gbpln	Arabidopsis thaliana	AT4G23010.2 | Symbols: ATUTR2, UTR2 | UDP-galactose transporter 2 | chr4:12060318-12062486 REVERSE LENGTH=362	348	362	1.00E-163	104.0	86.2	91.7
Rsa1.0_00138.1.g6495.t1	ref|NP_001190807.1| uncharacterized protein [Arabidopsis thaliana] gi|332659296|gb|AEE84696.1| uncharacterized protein AT4G23020 [Arabidopsis thaliana]	404	452	2.00E-94	111.9	57.7	66.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G23020.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11780.1). | chr4:12066331-12068442 REVERSE LENGTH=452	404	452	5.00E-97	111.9	57.7	66.8
Rsa1.0_00138.1.g6496.t1	gb|EOA17838.1| hypothetical protein CARUB_v10006239mg [Capsella rubella]	507	509	0	100.4	90.1	94.5	hypothetical protein CARUB_v10006239mg	gbpln	Capsella rubella	AT4G23030.1 | Symbols: | MATE efflux family protein | chr4:12072857-12074365 FORWARD LENGTH=502	507	502	0	99.0	89.7	94.1
Rsa1.0_00138.1.g6497.t1	ref|NP_194037.2| protein IQ-domain 22 [Arabidopsis thaliana] gi|56693675|gb|AAW22634.1| calmodulin binding protein IQD22 [Arabidopsis thaliana] gi|332659301|gb|AEE84701.1| protein IQ-domain 22 [Arabidopsis thaliana]	503	484	0	96.2	79.3	84.9	protein IQ-domain 22	gbpln	Arabidopsis thaliana	AT4G23060.1 | Symbols: IQD22 | IQ-domain 22 | chr4:12087283-12090408 FORWARD LENGTH=484	503	484	0	96.2	79.3	84.9
Rsa1.0_00138.1.g6498.t1	ref|XP_002867733.1| rhomboid family protein [Arabidopsis lyrata subsp. lyrata] gi|297313569|gb|EFH43992.1| rhomboid family protein [Arabidopsis lyrata subsp. lyrata]	302	318	1.00E-125	105.3	83.4	85.8	rhomboid family protein	gbpln	Arabidopsis lyrata	AT4G23070.1 | Symbols: ATRBL7, RBL7 | RHOMBOID-like protein 7 | chr4:12090690-12092077 REVERSE LENGTH=313	302	313	1.00E-120	103.6	81.1	85.8
Rsa1.0_00138.1.g6499.t1	dbj|BAE98403.1| putative non-LTR reverse transcriptase [Arabidopsis thaliana]	143	278	7.00E-27	194.4	39.2	58.0	putative non-LTR reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	143	320	2.00E-14	223.8	30.8	49.0

Rsa1.0_00138.1.g6500.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1835	1213	0	66.1	35.1	46.2	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	1835	289	1.00E-72	15.7	7.4	10.1
Rsa1.0_00138.1.g6501.t1	gb|EOA27833.1| hypothetical protein CARUB_v10023990mg [Capsella rubella]	231	231	1.00E-118	100.0	87.9	92.6	hypothetical protein CARUB_v10023990mg	gbpln	Capsella rubella	AT4G11650.1 | Symbols: ATOSM34, OSM34 | osmotin 34 | chr4:7025127-7026113 REVERSE LENGTH=244	231	244	2.00E-70	105.6	57.1	68.0
Rsa1.0_00138.1.g6502.t1	emb|CAK24967.1| gamma-glutamylcysteine synthetase [Brassica napus]	518	514	0	99.2	95.2	96.7	gamma-glutamylcysteine synthetase	gbpln	Brassica napus	AT4G23100.3 | Symbols: GSH1 | glutamate-cysteine ligase | chr4:12103458-12106751 REVERSE LENGTH=522	518	522	0	100.8	91.7	95.0
Rsa1.0_00138.1.g6503.t2	ref|XP_004166549.1| PREDICTED: cysteine-rich receptor-like protein kinase 29-like [Cucumis sativus]	1296	1251	0	96.5	43.6	61.4	PREDICTED: cysteine-rich receptor-like protein kinase 29-like	gbpln	Cucumis sativus	AT4G23180.1 | Symbols: CRK10, RLK4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 | chr4:12138171-12140780 FORWARD LENGTH=669	1296	669	0	51.6	34.3	40.3
Rsa1.0_00138.1.g6504.t1	ref|XP_002869784.1| hypothetical protein ARALYDRAFT_492546 [Arabidopsis lyrata subsp. lyrata] gi|297315620|gb|EFH46043.1| hypothetical protein ARALYDRAFT_492546 [Arabidopsis lyrata subsp. lyrata]	665	662	0	99.5	81.5	88.0	hypothetical protein ARALYDRAFT_492546	gbpln	Arabidopsis lyrata	AT4G23180.1 | Symbols: CRK10, RLK4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 | chr4:12138171-12140780 FORWARD LENGTH=669	665	669	0	100.6	78.6	86.2
Rsa1.0_00138.1.g6505.t1	ref|XP_002867727.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313563|gb|EFH43986.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	652	674	0	103.4	61.8	73.5	predicted protein	gbpln	Arabidopsis lyrata	AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667	652	667	0	102.3	60.1	71.8
Rsa1.0_00138.1.g6506.t1	ref|XP_002877439.1| hypothetical protein ARALYDRAFT_484965 [Arabidopsis lyrata subsp. lyrata] gi|297323277|gb|EFH53698.1| hypothetical protein ARALYDRAFT_484965 [Arabidopsis lyrata subsp. lyrata]	861	678	0	78.7	49.2	55.6	hypothetical protein ARALYDRAFT_484965	gbpln	Arabidopsis lyrata	AT4G23130.2 | Symbols: CRK5, RLK6 | cysteine-rich RLK (RECEPTOR-like protein kinase) 5 | chr4:12117688-12120134 REVERSE LENGTH=663	861	663	0	77.0	48.2	56.4
Rsa1.0_00138.1.g6507.t1	ref|NP_849425.1| cysteine-rich receptor-like protein kinase 5 [Arabidopsis thaliana] gi|23296342|gb|AAN13047.1| putative protein kinase [Arabidopsis thaliana] gi|332659313|gb|AEE84713.1| cysteine-rich receptor-like protein kinase 5 [Arabidopsis thaliana]	666	663	0	99.5	67.6	78.7	cysteine-rich receptor-like protein kinase 5	gbpln	Arabidopsis thaliana	AT4G23130.2 | Symbols: CRK5, RLK6 | cysteine-rich RLK (RECEPTOR-like protein kinase) 5 | chr4:12117688-12120134 REVERSE LENGTH=663	666	663	0	99.5	67.6	78.7
Rsa1.0_00138.1.g6508.t1	sp|O65483.2|CRK24_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 24; Short=Cysteine-rich RLK24; Flags: Precursor	1285	636	0	49.5	35.0	40.5	RecName: Full=Cysteine-rich receptor-like protein kinase 24; Short=Cysteine-rich RLK24; Flags: Precursor	----	----	AT4G23290.2 | Symbols: CRK21 | cysteine-rich RLK (RECEPTOR-like protein kinase) 21 | chr4:12177910-12180810 REVERSE LENGTH=690	1285	690	0	53.7	33.3	38.8
Rsa1.0_00138.1.g6509.t1	gb|EOA16043.1| hypothetical protein CARUB_v10004176mg [Capsella rubella]	772	787	0	101.9	70.9	80.8	hypothetical protein CARUB_v10004176mg	gbpln	Capsella rubella	AT4G23310.1 | Symbols: CRK23 | cysteine-rich RLK (RECEPTOR-like protein kinase) 23 | chr4:12185737-12188763 FORWARD LENGTH=830	772	830	0	107.5	73.3	83.9
Rsa1.0_00138.1.g6510.t7	ref|NP_194062.1| putative cysteine-rich receptor-like protein kinase 23 [Arabidopsis thaliana] gi|75318568|sp|O65482.1|CRK23_ARATH RecName: Full=Putative cysteine-rich receptor-like protein kinase 23; Short=Cysteine-rich RLK23; Flags: Precursor gi|3021283|emb|CAA18478.1| serine/threonine kinase-like protein [Arabidopsis thaliana] gi|7269179|emb|CAB79286.1| serine/threonine kinase-like protein [Arabidopsis thaliana] gi|332659337|gb|AEE84737.1| putative cysteine-rich receptor-like protein kinase 23 [Arabidopsis thaliana]	1095	830	0	75.8	51.0	58.1	putative cysteine-rich receptor-like protein kinase 23	gbpln	Arabidopsis thaliana	AT4G23310.1 | Symbols: CRK23 | cysteine-rich RLK (RECEPTOR-like protein kinase) 23 | chr4:12185737-12188763 FORWARD LENGTH=830	1095	830	0	75.8	51.0	58.1
Rsa1.0_00138.1.g6511.t1	sp|O65483.2|CRK24_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 24; Short=Cysteine-rich RLK24; Flags: Precursor	1226	636	0	51.9	39.6	44.2	RecName: Full=Cysteine-rich receptor-like protein kinase 24; Short=Cysteine-rich RLK24; Flags: Precursor	----	----	AT4G23290.2 | Symbols: CRK21 | cysteine-rich RLK (RECEPTOR-like protein kinase) 21 | chr4:12177910-12180810 REVERSE LENGTH=690	1226	690	0	56.3	33.0	39.2
Rsa1.0_00138.1.g6512.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00138.1.g6513.t1	gb|EOA17073.1| hypothetical protein CARUB_v10005322mg [Capsella rubella]	304	306	1.00E-163	100.7	92.8	96.1	hypothetical protein CARUB_v10005322mg	gbpln	Capsella rubella	AT4G23730.1 | Symbols: | Galactose mutarotase-like superfamily protein | chr4:12362955-12364792 FORWARD LENGTH=306	304	306	1.00E-163	100.7	90.1	95.4

Rsa1.0_00138.1.g6514.t1	gb|ACC91242.1| leucine-rich repeat transmembrane protein kinase [Arabidopsis halleri]	631	636	0	100.8	84.9	92.1	leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis halleri	AT4G23740.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:12367063-12369159 FORWARD LENGTH=638	631	638	0	101.1	83.2	89.5
Rsa1.0_00138.1.g6515.t1	ref|XP_002869765.1| hypothetical protein ARALYDRAFT_492491 [Arabidopsis lyrata subsp. lyrata] gi|297315601|gb|EFH46024.1| hypothetical protein ARALYDRAFT_492491 [Arabidopsis lyrata subsp. lyrata]	312	340	1.00E-105	109.0	72.1	82.7	hypothetical protein ARALYDRAFT_492491	gbpln	Arabidopsis lyrata	AT4G23750.2 | Symbols: CRF2, TMO3 | cytokinin response factor 2 | chr4:12376751-12377782 FORWARD LENGTH=343	312	343	1.00E-107	109.9	70.8	80.1
Rsa1.0_00139.1.g6516.t1	gb|EOA35159.1| hypothetical protein CARUB_v10020298mg [Capsella rubella]	449	446	0	99.3	85.3	90.9	hypothetical protein CARUB_v10020298mg	gbpln	Capsella rubella	AT1G71980.1 | Symbols: | Protease-associated (PA) RING/U-box zinc finger family protein | chr1:27098250-27099881 FORWARD LENGTH=448	449	448	0	99.8	83.7	90.2
Rsa1.0_00139.1.g6517.t2	ref|XP_002318388.1| predicted protein [Populus trichocarpa] gi|222859061|gb|EEE96608.1| predicted protein [Populus trichocarpa]	137	529	3.00E-23	386.1	43.8	51.8	predicted protein	gbpln	Populus trichocarpa	AT5G64960.1 | Symbols: CDKC2, CDKC;2 | cyclin dependent kinase group C2 | chr5:25955497-25958427 FORWARD LENGTH=513	137	513	1.00E-22	374.5	39.4	52.6
Rsa1.0_00139.1.g6518.t1	gb|EOA35238.1| hypothetical protein CARUB_v10020397mg [Capsella rubella]	409	405	0	99.0	86.6	91.2	hypothetical protein CARUB_v10020397mg	gbpln	Capsella rubella	AT1G71990.1 | Symbols: FUT13, ATFUT13, FUCTC, FT4-M, ATFT4 | fucosyltransferase 13 | chr1:27100345-27102097 FORWARD LENGTH=401	409	401	0	98.0	85.8	91.2
Rsa1.0_00139.1.g6519.t1	gb|EOA34198.1| hypothetical protein CARUB_v10021707mg [Capsella rubella]	570	535	0	93.9	84.2	89.1	hypothetical protein CARUB_v10021707mg	gbpln	Capsella rubella	AT1G22650.1 | Symbols: | Plant neutral invertase family protein | chr1:8013529-8015647 REVERSE LENGTH=534	570	534	0	93.7	79.5	88.2
Rsa1.0_00139.1.g6520.t1	gb|EOA34875.1| hypothetical protein CARUB_v10022457mg [Capsella rubella]	307	384	4.00E-86	125.1	73.0	77.9	hypothetical protein CARUB_v10022457mg	gbpln	Capsella rubella	AT1G72010.1 | Symbols: | TCP family transcription factor | chr1:27107844-27108971 FORWARD LENGTH=375	307	375	4.00E-82	122.1	68.4	73.9
Rsa1.0_00139.1.g6521.t1	gb|EOA34662.1| hypothetical protein CARUB_v10022225mg [Capsella rubella]	96	96	1.00E-40	100.0	94.8	97.9	hypothetical protein CARUB_v10022225mg	gbpln	Capsella rubella	AT1G72020.1 | Symbols: | unknown protein; Has 52 Blast hits to 52 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 52; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27109521-27110327 REVERSE LENGTH=97	96	97	5.00E-42	101.0	87.5	92.7
Rsa1.0_00139.1.g6522.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00139.1.g6523.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00139.1.g6524.t1	ref|XP_002888857.1| deoxynucleoside kinase family [Arabidopsis lyrata subsp. lyrata] gi|297334698|gb|EFH65116.1| deoxynucleoside kinase family [Arabidopsis lyrata subsp. lyrata]	567	586	0	103.4	81.0	86.9	deoxynucleoside kinase family	gbpln	Arabidopsis lyrata	AT1G72040.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:27112159-27114248 REVERSE LENGTH=580	567	580	0	102.3	80.6	86.9
Rsa1.0_00139.1.g6525.t1	gb|EOA35884.1| hypothetical protein CARUB_v10021139mg [Capsella rubella]	183	131	3.00E-43	71.6	51.9	57.4	hypothetical protein CARUB_v10021139mg	gbpln	Capsella rubella	AT1G72070.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:27118851-27119608 REVERSE LENGTH=126	183	126	6.00E-41	68.9	51.9	56.8
Rsa1.0_00139.1.g6526.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00139.1.g6527.t1	ref|XP_002887411.1| radical SAM domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297333252|gb|EFH63670.1| radical SAM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	619	602	0	97.3	86.3	91.6	radical SAM domain-containing protein	gbpln	Arabidopsis lyrata	AT1G72090.1 | Symbols: | Methylthiotransferase | chr1:27123617-27126767 FORWARD LENGTH=601	619	601	0	97.1	84.5	89.8
Rsa1.0_00139.1.g6528.t1	dbj|BAJ33896.1| unnamed protein product [Thellungiella halophila]	285	467	1.00E-134	163.9	79.6	84.9	unnamed protein product	----	----	AT1G72110.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr1:27129253-27131354 REVERSE LENGTH=479	285	479	1.00E-135	168.1	77.9	87.0
Rsa1.0_00139.1.g6529.t1	ref|XP_002887414.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata] gi|297333255|gb|EFH63673.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata]	466	535	1.00E-169	114.8	71.0	79.0	hypothetical protein ARALYDRAFT_316182	gbpln	Arabidopsis lyrata	AT1G72130.1 | Symbols: | Major facilitator superfamily protein | chr1:27137201-27139223 FORWARD LENGTH=538	466	538	1.00E-167	115.5	68.7	77.5
Rsa1.0_00139.1.g6530.t1	ref|XP_002887416.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297333257|gb|EFH63675.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	732	534	0	73.0	56.4	61.6	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G72130.1 | Symbols: | Major facilitator superfamily protein | chr1:27137201-27139223 FORWARD LENGTH=538	732	538	0	73.5	52.9	61.3
Rsa1.0_00139.1.g6531.t2	gb|EOA34977.1| hypothetical protein CARUB_v10020065mg [Capsella rubella]	567	567	0	100.0	79.4	84.7	hypothetical protein CARUB_v10020065mg	gbpln	Capsella rubella	AT1G72150.1 | Symbols: PATL1 | PATELLIN 1 | chr1:27148558-27150652 FORWARD LENGTH=573	567	573	0	101.1	79.7	84.7

Rsa1.0_00139.1.g6532.t1	ref|NP_177366.1| transcription factor bHLH96 [Arabidopsis thaliana] gi|75308860|sp|Q9C7T4.1|BH096_ARATH RecName: Full=Transcription factor bHLH96; AltName: Full=Basic helix-loop-helix protein 96; Short=AtbHLH96; Short=bHLH 96; AltName: Full=Transcription factor EN 15; AltName: Full=bHLH transcription factor bHLH096 gi|12323671|gb|AAG51804.1|AC067754_20 unknown protein; 44011-46213 [Arabidopsis thaliana] gi|20520637|emb|CAD30833.1| basic-helix-loop-helix transcription factor [Arabidopsis thaliana] gi|28392970|gb|AAO41920.1| putative bHLH protein [Arabidopsis thaliana] gi|29824221|gb|AAP04071.1| putative bHLH protein [Arabidopsis thaliana] gi|332197168|gb|AEE35289.1| transcription factor bHLH96 [Arabidopsis thaliana]	324	320	1.00E-139	98.8	81.2	88.0	transcription factor bHLH96	gbpln	Arabidopsis thaliana	AT1G72210.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:27180066-27182268 FORWARD LENGTH=320	324	320	1.00E-142	98.8	81.2	88.0
Rsa1.0_00139.1.g6533.t1	ref|NP_177367.1| RING-H2 finger protein ATL54 [Arabidopsis thaliana] gi|68565207|sp|Q8LFY8.2|ATL54_ARATH RecName: Full=RING-H2 finger protein ATL54 gi|12323653|gb|AAG51786.1|AC067754_2 RING-H2 zinc finger protein ATL3, putative; 49574-48333 [Arabidopsis thaliana] gi|15529216|gb|AAK97702.1| At1g72220/T9N14_22 [Arabidopsis thaliana] gi|25141211|gb|AAN73300.1| At1g72220/T9N14_22 [Arabidopsis thaliana] gi|332197169|gb|AEE35290.1| RING-H2 finger protein ATL54 [Arabidopsis thaliana]	319	413	1.00E-102	129.5	70.5	80.6	RING-H2 finger protein ATL54	gbpln	Arabidopsis thaliana	AT1G72220.1 | Symbols: | RING/U-box superfamily protein | chr1:27184388-27185629 REVERSE LENGTH=413	319	413	1.00E-105	129.5	70.5	80.6
Rsa1.0_00139.1.g6534.t1	ref|XP_002887423.1| hypothetical protein ARALYDRAFT_476354 [Arabidopsis lyrata subsp. lyrata] gi|297333264|gb|EFH63682.1| hypothetical protein ARALYDRAFT_476354 [Arabidopsis lyrata subsp. lyrata]	176	181	1.00E-66	102.8	77.3	83.5	hypothetical protein ARALYDRAFT_476354	gbpln	Arabidopsis lyrata	AT1G72230.1 | Symbols: | Cupredoxin superfamily protein | chr1:27188287-27189093 FORWARD LENGTH=181	176	181	6.00E-68	102.8	75.6	82.4
Rsa1.0_00139.1.g6535.t1	gb|AAG51792.1|AC067754_8 hypothetical protein; 54117-54518 [Arabidopsis thaliana]	136	133	3.00E-27	97.8	72.1	79.4	hypothetical protein; 54117-54518	gbpln	Arabidopsis thaliana	AT1G72240.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22470.1); Has 65 Blast hits to 63 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27190211-27190573 FORWARD LENGTH=120	136	120	2.00E-27	88.2	65.4	72.8
Rsa1.0_00139.1.g6536.t1	gb|EOA35119.1| hypothetical protein CARUB_v10020240mg [Capsella rubella]	760	467	0	61.4	55.3	57.0	hypothetical protein CARUB_v10020240mg	gbpln	Capsella rubella	AT1G72280.1 | Symbols: AERO1, ERO1 | endoplasmic reticulum oxidoreductins 1 | chr1:27212039-27214506 REVERSE LENGTH=469	760	469	0	61.7	55.7	57.9
Rsa1.0_00139.1.g6537.t1	gb|AAQ54577.1| drought-induced protein [Raphanus sativus]	220	202	1.00E-112	91.8	90.5	90.9	drought-induced protein	gbpln	Raphanus sativus	AT1G72290.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27215852-27216499 FORWARD LENGTH=215	220	215	2.00E-68	97.7	60.9	70.0
Rsa1.0_00139.1.g6538.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1371	1459	0	106.4	54.7	70.7	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1371	1262	1.00E-109	92.0	14.4	20.4
Rsa1.0_00139.1.g6539.t1	dbj|BAB72020.1| water-soluble chlorophyll protein [Raphanus sativus var. niger] gi|404312339|dbj|BAM42883.1| water soluble chlorophyll-binding protein [Raphanus sativus var. raphanistroides]	222	222	1.00E-125	100.0	100.0	100.0	water-soluble chlorophyll protein	gbpln	Raphanus sativus	AT1G72290.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27215852-27216499 FORWARD LENGTH=215	222	215	7.00E-68	96.8	61.3	71.2
Rsa1.0_00139.1.g6540.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00139.1.g6541.t1	gb|ABA39633.1| Kunitz-type cysteine protease inhibitor [Brassica oleracea var. botrytis]	225	226	5.00E-67	100.4	62.7	73.3	Kunitz-type cysteine protease inhibitor	gbpln	Brassica oleracea	AT1G72290.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27215852-27216499 FORWARD LENGTH=215	225	215	6.00E-56	95.6	50.7	62.2

Rsa1.0_00139.1.g6542.t1	ref|XP_002887429.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333270|gb|EFH63688.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	101	101	3.00E-28	100.0	74.3	82.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G17285.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17300.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:5920895-5921287 FORWARD LENGTH=95	101	95	3.00E-18	94.1	46.5	62.4
Rsa1.0_00139.1.g6543.t1	gb|EOA33684.1| hypothetical protein CARUB_v10019867mg [Capsella rubella] gi|482569497|gb|EOA33685.1| hypothetical protein CARUB_v10019867mg [Capsella rubella]	729	729	0	100.0	82.9	90.1	hypothetical protein CARUB_v10019867mg	gbpln	Capsella rubella	AT1G72320.1 | Symbols: APUM23, PUM23 | pumilio 23 | chr1:27228984-27232580 REVERSE LENGTH=753	729	753	0	103.3	81.9	90.1
Rsa1.0_00139.1.g6544.t1	ref|XP_002881012.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326851|gb|EFH57271.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	280	290	2.00E-63	103.6	52.5	63.2	predicted protein	gbpln	Arabidopsis lyrata	ATCG00790.1 | Symbols: RPL16 | ribosomal protein L16 | chrC:81189-82652 REVERSE LENGTH=135	280	135	5.00E-55	48.2	35.0	40.4
Rsa1.0_00139.1.g6545.t1	gb|AAD25622.1|AC005287_24 Hypothetical protein [Arabidopsis thaliana]	487	224	9.00E-73	46.0	29.0	35.1	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	487	384	2.00E-64	78.9	25.9	31.0
Rsa1.0_00139.1.g6546.t1	gb|AAF79224.1|AC006917_9 F10B6.21 [Arabidopsis thaliana]	211	383	1.00E-26	181.5	28.0	45.5	F10B6.21	gbpln	Arabidopsis thaliana	AT2G35280.1 | Symbols: | F-box family protein | chr2:14859709-14860200 REVERSE LENGTH=163	211	163	1.00E-24	77.3	25.6	40.3
Rsa1.0_00139.1.g6547.t1	ref|XP_003606913.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula] gi|355507968|gb|AES89110.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula]	1928	1558	0	80.8	35.5	49.2	ATP-dependent DNA helicase PIF1	gbpln	Medicago truncatula	AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907-10814173 REVERSE LENGTH=337	1928	337	4.00E-66	17.5	7.0	9.6
Rsa1.0_00139.1.g6548.t1	gb|EOA35257.1| hypothetical protein CARUB_v10020426mg, partial [Capsella rubella]	390	392	0	100.5	92.1	95.1	hypothetical protein CARUB_v10020426mg, partial	gbpln	Capsella rubella	AT1G72340.1 | Symbols: | NagB/RpiA/CoA transferase-like superfamily protein | chr1:27236898-27238482 FORWARD LENGTH=382	390	382	0	97.9	92.3	94.4
Rsa1.0_00139.1.g6549.t1	gb|EOA34308.1| hypothetical protein CARUB_v10021825mg [Capsella rubella]	254	222	6.00E-62	87.4	52.4	60.6	hypothetical protein CARUB_v10021825mg	gbpln	Capsella rubella	AT1G72350.1 | Symbols: | MADS-box transcription factor family protein | chr1:27239273-27239947 REVERSE LENGTH=224	254	224	5.00E-61	88.2	52.8	60.2
Rsa1.0_00139.1.g6550.t1	ref|NP_001077812.1| ethylene-responsive transcription factor ERF073 [Arabidopsis thaliana] gi|12325282|gb|AAG52589.1|AC016529_20 putative AP2 domain transcription factor; 71325-70452 [Arabidopsis thaliana] gi|332197190|gb|AEE35311.1| ethylene-responsive transcription factor ERF073 [Arabidopsis thaliana]	246	262	1.00E-68	106.5	61.4	71.5	ethylene-responsive transcription factor ERF073	gbpln	Arabidopsis thaliana	AT1G72360.2 | Symbols: HRE1 | Integrase-type DNA-binding superfamily protein | chr1:27241904-27242777 FORWARD LENGTH=262	246	262	4.00E-71	106.5	61.4	71.5
Rsa1.0_00139.1.g6551.t1	sp|Q9ZSR8.1|RSSA_BRANA RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor-like protein; AltName: Full=p40 gi|3769681|gb|AAC97937.1| laminin receptor-like protein [Brassica napus]	294	292	1.00E-165	99.3	96.6	97.6	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor-like protein; AltName: Full=p40 gi|3769681|gb|AAC97937.1| laminin receptor-like protein	gbpln	Brassica napus	AT1G72370.1 | Symbols: P40, AP40, RP40, RPSAA | 40s ribosomal protein SA | chr1:27243148-27244842 REVERSE LENGTH=298	294	298	1.00E-143	101.4	88.4	90.8
Rsa1.0_00139.1.g6552.t1	gb|EOA33489.1| hypothetical protein CARUB_v10019669mg [Capsella rubella]	1312	1325	0	101.0	79.1	85.3	hypothetical protein CARUB_v10019669mg	gbpln	Capsella rubella	AT1G72390.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Spt20 family (InterPro:IPR021950); Has 8778 Blast hits to 7244 proteins in 477 species: Archae - 6; Bacteria - 326; Metazoa - 4198; Fungi - 1506; Plants - 923; Viruses - 22; Other Eukaryotes - 1797 (source: NCBI BLink). | chr1:27245455-27251218 FORWARD LENGTH=1325	1312	1325	0	101.0	78.6	85.4
Rsa1.0_00139.1.g6553.t1	ref|NP_001117589.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|332197199|gb|AEE35320.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]	204	201	2.00E-56	98.5	64.7	72.1	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT1G72416.3 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:27259125-27260109 REVERSE LENGTH=201	204	201	7.00E-59	98.5	64.7	72.1
Rsa1.0_00139.1.g6554.t1	emb|CAA07494.1| heat stress-induced protein [Brassica oleracea var. capitata] gi|3551243|dbj|BAA32820.1| Water-Soluble Chlorophyll Protein [Brassica oleracea var. botrytis]	231	218	7.00E-72	94.4	61.0	69.3	heat stress-induced protein	gbpln	Brassica oleracea	AT1G72290.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27215852-27216499 FORWARD LENGTH=215	231	215	2.00E-54	93.1	48.1	61.0

Rsa1.0_00139.1.g6555.t1	gb|EOA35672.1| hypothetical protein CARUB_v10020896mg [Capsella rubella]	207	228	1.00E-98	110.1	88.9	92.8	hypothetical protein CARUB_v10020896mg	gbpln	Capsella rubella	AT1G72420.1 | Symbols: | NADH:ubiquinone oxidoreductase intermediate-associated protein 30 | chr1:27261367-27263186 REVERSE LENGTH=228	207	228	2.00E-96	110.1	85.0	90.8
Rsa1.0_00139.1.g6556.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00139.1.g6557.t1	dbj|BAF63144.1| kinetochore protein [Crucihimalaya wallichii]	269	241	5.00E-62	89.6	51.3	62.8	kinetochore protein	gbpln	Crucihimalaya wallichii	AT5G35520.1 | Symbols: MIS12, ATMIS12 | minichromosome instability 12 (mis12)-like | chr5:13701396-13702925 FORWARD LENGTH=238	269	238	3.00E-58	88.5	48.7	61.3
Rsa1.0_00139.1.g6558.t1	gb|EOA34209.1| hypothetical protein CARUB_v10021718mg [Capsella rubella]	118	118	1.00E-60	100.0	94.9	99.2	hypothetical protein CARUB_v10021718mg	gbpln	Capsella rubella	AT1G72430.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:27265150-27265509 REVERSE LENGTH=119	118	119	4.00E-62	100.8	94.9	99.2
Rsa1.0_00139.1.g6559.t1	ref|XP_002888875.1| hypothetical protein ARALYDRAFT_316209 [Arabidopsis lyrata subsp. lyrata] gi|297334716|gb|EFH65134.1| hypothetical protein ARALYDRAFT_316209 [Arabidopsis lyrata subsp. lyrata]	1008	1029	0	102.1	81.9	87.7	hypothetical protein ARALYDRAFT_316209	gbpln	Arabidopsis lyrata	AT1G72440.1 | Symbols: EDA25, SWA2 | CCAAT-binding factor | chr1:27268325-27273596 REVERSE LENGTH=1043	1008	1043	0	103.5	74.2	80.6
Rsa1.0_00139.1.g6560.t1	ref|NP_565043.1| protein TIFY 11B [Arabidopsis thaliana] gi|75169694|sp|Q9C9E3.1|TI11B_ARATH RecName: Full=Protein TIFY 11B; AltName: Full=Jasmonate ZIM domain-containing protein 6 gi|12325268|gb|AAG52575.1|AC016529_6 unknown protein; 37093-38893 [Arabidopsis thaliana] gi|13877769|gb|AAK43962.1|AF370147_1 unknown protein [Arabidopsis thaliana] gi|16323402|gb|AAL15195.1| unknown protein [Arabidopsis thaliana] gi|21593614|gb|AAM65581.1| unknown [Arabidopsis thaliana] gi|332197205|gb|AEE35326.1| protein TIFY 11B [Arabidopsis thaliana]	275	269	1.00E-108	97.8	73.1	84.0	protein TIFY 11B	gbpln	Arabidopsis thaliana	AT1G72450.1 | Symbols: JAZ6, TIFY11B | jasmonate-zim-domain protein 6 | chr1:27274336-27276136 REVERSE LENGTH=269	275	269	1.00E-111	97.8	73.1	84.0
Rsa1.0_00139.1.g6561.t1	ref|XP_002888879.1| hypothetical protein ARALYDRAFT_895100 [Arabidopsis lyrata subsp. lyrata] gi|297334720|gb|EFH65138.1| hypothetical protein ARALYDRAFT_895100 [Arabidopsis lyrata subsp. lyrata]	491	509	0	103.7	80.9	85.5	hypothetical protein ARALYDRAFT_895100	gbpln	Arabidopsis lyrata	AT1G72480.1 | Symbols: | Lung seven transmembrane receptor family protein | chr1:27286304-27288339 REVERSE LENGTH=509	491	509	0	103.7	80.4	85.1
Rsa1.0_00139.1.g6562.t1	gb|EOA35532.1| hypothetical protein CARUB_v10020740mg [Capsella rubella]	287	288	1.00E-127	100.3	84.0	88.9	hypothetical protein CARUB_v10020740mg	gbpln	Capsella rubella	AT1G72490.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17400.1); Has 75 Blast hits to 75 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 4; Plants - 58; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:27289435-27290732 REVERSE LENGTH=287	287	287	1.00E-127	100.0	81.9	89.5
Rsa1.0_00139.1.g6563.t1	ref|XP_002888881.1| hypothetical protein ARALYDRAFT_476383 [Arabidopsis lyrata subsp. lyrata] gi|297334722|gb|EFH65140.1| hypothetical protein ARALYDRAFT_476383 [Arabidopsis lyrata subsp. lyrata]	756	757	0	100.1	88.6	93.9	hypothetical protein ARALYDRAFT_476383	gbpln	Arabidopsis lyrata	AT1G72500.1 | Symbols: | LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: von Willebrand factor, type A (InterPro:IPR002035); BEST Arabidopsis thaliana protein match is: inter-alpha-trypsin inhibitor heavy chain-related (TAIR:AT1G19110.1); Has 1407 Blast hits to 1406 proteins in 307 species: Archae - 6; Bacteria - 522; Metazoa - 484; Fungi - 59; Plants - 110; Viruses - 0; Other Eukaryotes - 226 (source: NCBI BLink). | chr1:27295336-27298556 REVERSE LENGTH=756	756	756	0	100.0	86.5	93.3
Rsa1.0_00139.1.g6564.t10	gb|AAO73529.1| gag-pol polyprotein [Glycine max]	1467	1577	0	107.5	43.4	60.1	gag-pol polyprotein	gbenv/gbpln	Glycine max	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1467	1262	1.00E-61	86.0	9.5	14.6
Rsa1.0_00139.1.g6565.t1	gb|AAF18631.1|AC006228_2 F5J5.2 [Arabidopsis thaliana]	425	463	7.00E-39	108.9	24.5	40.9	F5J5.2	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00140.1.g6566.t1	gb|EOA28259.1| hypothetical protein CARUB_v10024453mg [Capsella rubella]	75	75	2.00E-31	100.0	93.3	97.3	hypothetical protein CARUB_v10024453mg	gbpln	Capsella rubella	AT2G24040.1 | Symbols: | Low temperature and salt responsive protein family | chr2:10224028-10224531 FORWARD LENGTH=75	75	75	9.00E-33	100.0	89.3	94.7
Rsa1.0_00140.1.g6567.t1	gb|EOA18398.1| hypothetical protein CARUB_v10006936mg [Capsella rubella]	599	614	0	102.5	74.0	82.1	hypothetical protein CARUB_v10006936mg	gbpln	Capsella rubella	AT4G33430.1 | Symbols: BAK1, RKS10, SERK3, ELG, ATSERK3, ATBAK1 | BRI1-associated receptor kinase | chr4:16086654-16090288 REVERSE LENGTH=615	599	615	0	102.7	73.5	81.8

Rsa1.0_00140.1.g6568.t1	ref|XP_002878716.1| hypothetical protein ARALYDRAFT_481264 [Arabidopsis lyrata subsp. lyrata] gi|297324555|gb|EFH54975.1| hypothetical protein ARALYDRAFT_481264 [Arabidopsis lyrata subsp. lyrata]	316	292	1.00E−119	92.4	77.8	83.2	hypothetical protein ARALYDRAFT_481264	gbpln	Arabidopsis lyrata	AT2G24060.1 | Symbols: | Translation initiation factor 3 protein | chr2:10229453-10231390 FORWARD LENGTH=312	316	312	1.00E−117	98.7	73.1	78.8
Rsa1.0_00140.1.g6569.t2	gb|EOA29260.1| hypothetical protein CARUB_v10025534mg [Capsella rubella]	590	614	0	104.1	77.1	83.2	hypothetical protein CARUB_v10025534mg	gbpln	Capsella rubella	AT2G24070.2 | Symbols: QWRF4 | Family of unknown function (DUF566) | chr2:10231822-10233986 REVERSE LENGTH=609	590	609	0	103.2	73.9	80.7
Rsa1.0_00140.1.g6570.t1	ref|XP_002878721.1| ribosomal protein L35 [Arabidopsis lyrata subsp. lyrata] gi|297324560|gb|EFH54980.1| ribosomal protein L35 [Arabidopsis lyrata subsp. lyrata]	148	140	7.00E−54	94.6	79.1	83.8	ribosomal protein L35	gbpln	Arabidopsis lyrata	AT2G24090.1 | Symbols: | Ribosomal protein L35 | chr2:10242038-10243416 FORWARD LENGTH=145	148	145	1.00E−52	98.0	81.1	86.5
Rsa1.0_00140.1.g6571.t1	ref|NP_001118363.1| uncharacterized protein [Arabidopsis thaliana] gi|330252224|gb|AEC07318.1| uncharacterized protein AT2G22520 [Arabidopsis thaliana]	159	151	1.00E−27	95.0	49.7	64.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G22520.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: stem; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr2:9572066-9572623 FORWARD LENGTH=151	159	151	5.00E−30	95.0	49.7	64.2
Rsa1.0_00140.1.g6572.t1	gb|EOA29019.1| hypothetical protein CARUB_v10025273mg [Capsella rubella]	996	991	0	99.5	88.6	93.1	hypothetical protein CARUB_v10025273mg	gbpln	Capsella rubella	AT2G24120.1 | Symbols: PDE319, SCA3 | DNA/RNA polymerases superfamily protein | chr2:10249358-10254530 REVERSE LENGTH=993	996	993	0	99.7	88.1	92.0
Rsa1.0_00140.1.g6573.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00140.1.g6574.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00140.1.g6575.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	514	1274	4.00E−78	247.9	32.9	49.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	514	575	3.00E−47	111.9	26.7	43.4
Rsa1.0_00140.1.g6576.t1	#	#	#	#	#	#	#	–	----	----	AT3G50610.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66816.1); Has 125 Blast hits to 60 proteins in 16 species: Archae − 0; Bacteria − 2; Metazoa − 10; Fungi − 4; Plants − 97; Viruses − 0; Other Eukaryotes − 12 (source: NCBI BLink). | chr3:18779723-18780412 REVERSE LENGTH=229	130	229	7.00E−12	176.2	33.8	43.8
Rsa1.0_00140.1.g6577.t2	dbj|BAJ33647.1| unnamed protein product [Thellungiella halophila]	493	520	0	105.5	94.5	96.1	unnamed protein product	----	----	AT2G24200.2 | Symbols: | Cytosol aminopeptidase family protein | chr2:10287017-10289450 REVERSE LENGTH=520	493	520	0	105.5	91.5	95.5
Rsa1.0_00140.1.g6578.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00140.1.g6579.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00140.1.g6580.t1	ref|XP_002874699.1| hypothetical protein ARALYDRAFT_352228 [Arabidopsis lyrata subsp. lyrata] gi|297320536|gb|EFH50958.1| hypothetical protein ARALYDRAFT_352228 [Arabidopsis lyrata subsp. lyrata]	297	304	6.00E−78	102.4	52.9	66.7	hypothetical protein ARALYDRAFT_352228	gbpln	Arabidopsis lyrata	AT4G11580.1 | Symbols: | RNI-like superfamily protein | chr4:7006648-7007738 REVERSE LENGTH=333	297	333	6.00E−55	112.1	44.4	63.0
Rsa1.0_00140.1.g6581.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00140.1.g6582.t1	gb|EOA27318.1| hypothetical protein CARUB_v10023435mg [Capsella rubella]	359	378	1.00E−160	105.3	89.7	95.3	hypothetical protein CARUB_v10023435mg	gbpln	Capsella rubella	AT2G24220.2 | Symbols: PUP5 | purine permease 5 | chr2:10300603-10301688 FORWARD LENGTH=361	359	361	1.00E−159	100.6	84.1	89.4
Rsa1.0_00140.1.g6583.t1	gb|EOA28753.1| hypothetical protein CARUB_v10024985mg [Capsella rubella]	851	852	0	100.1	89.1	94.5	hypothetical protein CARUB_v10024985mg	gbpln	Capsella rubella	AT2G24230.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:10301979-10304540 REVERSE LENGTH=853	851	853	0	100.2	88.2	94.5
Rsa1.0_00140.1.g6584.t1	ref|XP_002893531.1| CYP705A24 [Arabidopsis lyrata subsp. lyrata] gi|297339373|gb|EFH69790.1| CYP705A24 [Arabidopsis lyrata subsp. lyrata]	549	518	0	94.4	69.9	80.5	CYP705A24	gbpln	Arabidopsis lyrata	AT1G28430.1 | Symbols: CYP705A24 | cytochrome P450, family 705, subfamily A, polypeptide 24 | chr1:9992986-9994642 REVERSE LENGTH=521	549	521	0	94.9	69.6	80.0

Rsa1.0_00140.1.g6585.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	388	387	1.00E-82	99.7	45.4	61.1	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	388	387	3.00E-85	99.7	45.4	61.1
Rsa1.0_00140.1.g6586.t1	gb|EOA29274.1| hypothetical protein CARUB_v10025549mg [Capsella rubella]	360	362	1.00E-104	100.6	58.6	69.7	hypothetical protein CARUB_v10025549mg	gbpln	Capsella rubella	AT2G24250.2 | Symbols: | Protein of unknown function (DUF295) | chr2:10313436-10314560 REVERSE LENGTH=374	360	374	1.00E-90	103.9	56.7	70.0
Rsa1.0_00140.1.g6587.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00140.1.g6588.t1	ref|XP_002880625.1| hypothetical protein ARALYDRAFT_901061 [Arabidopsis lyrata subsp. lyrata] gi|297326464|gb|EFH56884.1| hypothetical protein ARALYDRAFT_901061 [Arabidopsis lyrata subsp. lyrata]	392	365	1.00E-117	93.1	57.7	69.4	hypothetical protein ARALYDRAFT_901061	gbpln	Arabidopsis lyrata	AT1G64840.1 | Symbols: | Protein of unknown function (DUF295) | chr1:24094010-24095164 FORWARD LENGTH=384	392	384	1.00E-114	98.0	55.6	67.9
Rsa1.0_00140.1.g6589.t1	gb|EOA27399.1| hypothetical protein CARUB_v10023532mg [Capsella rubella]	157	351	3.00E-45	223.6	73.9	83.4	hypothetical protein CARUB_v10023532mg	gbpln	Capsella rubella	AT2G24260.1 | Symbols: LRL1 | LJRHL1-like 1 | chr2:10319646-10322177 REVERSE LENGTH=350	157	350	2.00E-44	222.9	66.2	73.9
Rsa1.0_00140.1.g6590.t1	dbj|BAJ34194.1| unnamed protein product [Thellungiella halophila]	496	496	0	100.0	99.0	99.8	unnamed protein product	----	----	AT2G24270.3 | Symbols: ALDH11A3 | aldehyde dehydrogenase 11A3 | chr2:10327325-10329601 REVERSE LENGTH=496	496	496	0	100.0	97.4	99.4
Rsa1.0_00141.1.g6591.t1	ref|NP_177473.1| serine carboxypeptidase-like 2 [Arabidopsis thaliana] gi|75169956|sp|Q9CAU3.1|SCP2_ARATH RecName: Full=Serine carboxypeptidase-like 2; Flags: Precursor gi|12324326|gb|AAG52135.1|AC010556_17 putative serine carboxypeptidase; 5659-8034 [Arabidopsis thaliana] gi|332197318|gb|AEE35439.1| serine carboxypeptidase-like 2 [Arabidopsis thaliana]	337	441	1.00E-139	130.9	69.4	78.0	serine carboxypeptidase-like 2	gbpln	Arabidopsis thaliana	AT1G73300.1 | Symbols: scpl2 | serine carboxypeptidase-like 2 | chr1:27559673-27562048 REVERSE LENGTH=441	337	441	1.00E-141	130.9	69.4	78.0
Rsa1.0_00141.1.g6592.t3	ref|NP_177471.1| serine carboxypeptidase-like 3 [Arabidopsis thaliana] gi|75169954|sp|Q9CAU1.1|SCP3_ARATH RecName: Full=Serine carboxypeptidase-like 3; Flags: Precursor gi|12324329|gb|AAG52138.1|AC010556_20 putative serine carboxypeptidase; 12385-14737 [Arabidopsis thaliana] gi|332197316|gb|AEE35437.1| serine carboxypeptidase-like 3 [Arabidopsis thaliana]	1569	441	1.00E-158	28.1	17.8	20.9	serine carboxypeptidase-like 3	gbpln	Arabidopsis thaliana	AT1G73280.1 | Symbols: scpl3 | serine carboxypeptidase-like 3 | chr1:27552970-27555322 REVERSE LENGTH=441	1569	441	1.00E-161	28.1	17.8	20.9
Rsa1.0_00141.1.g6593.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00141.1.g6594.t1	gb|EOA35721.1| hypothetical protein CARUB_v10020954mg [Capsella rubella]	279	208	4.00E-72	74.6	49.8	53.8	hypothetical protein CARUB_v10020954mg	gbpln	Capsella rubella	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410-27548057 REVERSE LENGTH=215	279	215	6.00E-70	77.1	46.6	52.0
Rsa1.0_00141.1.g6595.t1	gb|EOA37168.1| hypothetical protein CARUB_v10010502mg [Capsella rubella]	164	163	3.00E-70	99.4	82.9	87.8	hypothetical protein CARUB_v10010502mg	gbpln	Capsella rubella	AT1G17880.1 | Symbols: BTF3, ATBTF3 | basic transcription factor 3 | chr1:6152572-6153425 REVERSE LENGTH=165	164	165	6.00E-72	100.6	81.7	85.4
Rsa1.0_00141.1.g6596.t1	ref|NP_188443.2| F-box domain-containing protein [Arabidopsis thaliana] gi|257051013|sp|Q9LV26.2|FBL45_ARATH RecName: Full=Putative F-box/LRR-repeat protein At3g18150 gi|332642533|gb|AEE76054.1| F-box domain-containing protein [Arabidopsis thaliana]	176	456	5.00E-14	259.1	22.2	31.8	F-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	176	456	2.00E-16	259.1	22.2	31.8
Rsa1.0_00141.1.g6597.t1	ref|XP_002870999.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297316836|gb|EFH47258.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	430	458	3.00E-77	106.5	43.0	58.4	F-box family protein	gbpln	Arabidopsis lyrata	AT5G02910.1 | Symbols: | F-box/RNI-like superfamily protein | chr5:677120-678907 FORWARD LENGTH=458	430	458	3.00E-77	106.5	43.0	57.4
Rsa1.0_00141.1.g6598.t1	gb|EOA34775.1| hypothetical protein CARUB_v10022350mg [Capsella rubella]	266	265	1.00E-132	99.6	95.1	97.0	hypothetical protein CARUB_v10022350mg	gbpln	Capsella rubella	AT1G73190.1 | Symbols: ALPHA-TIP, TIP3;1 | Aquaporin-like superfamily protein | chr1:27522155-27523171 FORWARD LENGTH=268	266	268	1.00E-132	100.8	92.9	96.2

Rsa1.0_00141.1.g6599.t1	dbj|BAJ33996.1| unnamed protein product [Thellungiella halophila]	513	513	0	100.0	87.1	92.2	unnamed protein product	----	----	AT1G73180.1 | Symbols: | Eukaryotic translation initiation factor eIF2A family protein | chr1:27518335-27521432 FORWARD LENGTH=513	513	513	0	100.0	83.4	89.3
Rsa1.0_00141.1.g6600.t1	gb|AFK38622.1| unknown [Lotus japonicus]	63	65	2.00E-19	103.2	76.2	84.1	unknown	gbpln	Lotus japonicus	AT1G73177.1 | Symbols: BNS | bonsai | chr1:27516721-27517352 REVERSE LENGTH=63	63	63	5.00E-16	100.0	88.9	90.5
Rsa1.0_00141.1.g6601.t1	ref|NP_683490.1| protein CLAVATA3/ESR-related 1 [Arabidopsis thaliana] gi|122215278|sp|Q3ECD6.1|CLE1_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 1; Contains: RecName: Full=CLE1p; Flags: Precursor gi|332197300|gb|AEE35421.1| protein CLAVATA3/ESR-related 1 [Arabidopsis thaliana]	122	74	8.00E-13	60.7	30.3	31.1	protein CLAVATA3/ESR-related 1	gbpln	Arabidopsis thaliana	AT1G73165.1 | Symbols: CLE1 | CLAVATA3/ESR-RELATED 1 | chr1:27508725-27508949 REVERSE LENGTH=74	122	74	1.00E-15	60.7	30.3	31.1
Rsa1.0_00141.1.g6602.t1	ref|NP_683490.1| protein CLAVATA3/ESR-related 1 [Arabidopsis thaliana] gi|122215278|sp|Q3ECD6.1|CLE1_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 1; Contains: RecName: Full=CLE1p; Flags: Precursor gi|332197300|gb|AEE35421.1| protein CLAVATA3/ESR-related 1 [Arabidopsis thaliana]	75	74	3.00E-14	98.7	66.7	76.0	protein CLAVATA3/ESR-related 1	gbpln	Arabidopsis thaliana	AT1G73165.1 | Symbols: CLE1 | CLAVATA3/ESR-RELATED 1 | chr1:27508725-27508949 REVERSE LENGTH=74	75	74	4.00E-17	98.7	66.7	76.0
Rsa1.0_00141.1.g6603.t1	gb|EOA34026.1| hypothetical protein CARUB_v10021524mg [Capsella rubella]	489	484	0	99.0	83.2	90.4	hypothetical protein CARUB_v10021524mg	gbpln	Capsella rubella	AT1G73160.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:27506534-27507994 FORWARD LENGTH=486	489	486	0	99.4	84.7	89.8
Rsa1.0_00141.1.g6604.t1	ref|XP_002888909.1| hypothetical protein ARALYDRAFT_316265 [Arabidopsis lyrata subsp. lyrata] gi|297334750|gb|EFH65168.1| hypothetical protein ARALYDRAFT_316265 [Arabidopsis lyrata subsp. lyrata]	417	449	1.00E-131	107.7	65.9	73.4	hypothetical protein ARALYDRAFT_316265	gbpln	Arabidopsis lyrata	AT1G73150.1 | Symbols: GTE3 | global transcription factor group E3 | chr1:27504327-27505996 REVERSE LENGTH=461	417	461	1.00E-133	110.6	66.7	74.6
Rsa1.0_00141.1.g6605.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00141.1.g6606.t1	ref|XP_002871006.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297316843|gb|EFH47265.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	361	353	2.00E-66	97.8	42.4	59.3	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT2G44030.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:18220086-18221228 FORWARD LENGTH=380	361	380	2.00E-67	105.3	47.9	61.8
Rsa1.0_00141.1.g6607.t1	ref|NP_565056.1| histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3 [Arabidopsis thaliana] gi|30580525|sp|Q9C5P4.2|SUVH3_ARATH RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3; AltName: Full=Histone H3-K9 methyltransferase 3; Short=H3-K9-HMTase 3; AltName: Full=Protein SET DOMAIN GROUP 19; AltName: Full=Suppressor of variegation 3-9 homolog protein 3; Short=Su(var)3-9 homolog protein 3 gi|5903099|gb|AAD55657.1|AC008017_30 Unknown protein [Arabidopsis thaliana] gi|20466308|gb|AAM20471.1| unknown protein [Arabidopsis thaliana] gi|25083988|gb|AAN72148.1| unknown protein [Arabidopsis thaliana] gi|332197293|gb|AEE35414.1| histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3 [Arabidopsis thaliana]	673	669	0	99.4	83.4	90.5	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3	gbpln	Arabidopsis thaliana	AT1G73100.1 | Symbols: SUVH3, SDG19 | SU(VAR)3-9 homolog 3 | chr1:27491970-27493979 FORWARD LENGTH=669	673	669	0	99.4	83.4	90.5
Rsa1.0_00141.1.g6608.t1	ref|XP_002887470.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333311|gb|EFH63729.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1125	1122	0	99.7	79.6	88.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G73080.1 | Symbols: PEPR1, ATPEPR1 | PEP1 receptor 1 | chr1:27484513-27488021 FORWARD LENGTH=1123	1125	1123	0	99.8	78.0	87.7

Rsa1.0_00141.1.g6609.t1	ref|NP_565053.1| SNF7-like protein [Arabidopsis thaliana] gi|297839171|ref|XP_002887467.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|5903092|gb|AAD55650.1|AC008017_23 Highly similar to developmental protein DG1118 [Arabidopsis thaliana] gi|16648963|gb|AAL24333.1| Highly similar to developmental protein DG1118 [Arabidopsis thaliana] gi|20148689|gb|AAM10235.1| similar to developmental protein DG1118 [Arabidopsis thaliana] gi|297333308|gb|EFH63726.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|332197285|gb|AEE35406.1| SNF7-like protein [Arabidopsis thaliana] gi|482571541|gb|EOA35729.1| hypothetical protein CARUB_v10020963mg [Capsella rubella]	315	203	2.00E-44	64.4	27.6	28.3	SNF7-like protein	gbpln	Arabidopsis lyrata	AT1G73030.1 | Symbols: VPS46.2, CHMP1A | SNF7 family protein | chr1:27473938-27474848 FORWARD LENGTH=203	315	203	6.00E-47	64.4	27.6	28.3
Rsa1.0_00141.1.g6610.t1	ref|NP_565053.1| SNF7-like protein [Arabidopsis thaliana] gi|297839171|ref|XP_002887467.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|5903092|gb|AAD55650.1|AC008017_23 Highly similar to developmental protein DG1118 [Arabidopsis thaliana] gi|16648963|gb|AAL24333.1| Highly similar to developmental protein DG1118 [Arabidopsis thaliana] gi|20148689|gb|AAM10235.1| similar to developmental protein DG1118 [Arabidopsis thaliana] gi|297333308|gb|EFH63726.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|332197285|gb|AEE35406.1| SNF7-like protein [Arabidopsis thaliana] gi|482571541|gb|EOA35729.1| hypothetical protein CARUB_v10020963mg [Capsella rubella]	203	203	1.00E-113	100.0	99.0	99.0	SNF7-like protein	gbpln	Arabidopsis lyrata	AT1G73030.1 | Symbols: VPS46.2, CHMP1A | SNF7 family protein | chr1:27473938-27474848 FORWARD LENGTH=203	203	203	1.00E-115	100.0	99.0	99.0
Rsa1.0_00141.1.g6611.t1	gb|EOA33724.1| hypothetical protein CARUB_v10019915mg [Capsella rubella]	669	664	0	99.3	85.2	92.5	hypothetical protein CARUB_v10019915mg	gbpln	Capsella rubella	AT1G73020.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF590 (InterPro:IPR007632). | chr1:27469714-27473181 REVERSE LENGTH=665	669	665	0	99.4	84.5	92.1
Rsa1.0_00141.1.g6612.t1	ref|NP_181931.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75099812|sp|O80573.1|FBK45_ARATH RecName: Full=Putative F-box/kelch-repeat protein At2g44030 gi|3212860|gb|AAC23411.1| hypothetical protein [Arabidopsis thaliana] gi|330255269|gb|AEC10363.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	344	380	2.00E-64	110.5	50.3	64.2	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT2G44030.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:18220086-18221228 FORWARD LENGTH=380	344	380	5.00E-67	110.5	50.3	64.2
Rsa1.0_00141.1.g6613.t1	#	#	#	#	#	#	#	-	----	----	AT3G46050.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:16916072-16917184 FORWARD LENGTH=370	105	370	2.00E-12	352.4	31.4	39.0
Rsa1.0_00141.1.g6614.t2	ref|XP_002888903.1| hypothetical protein ARALYDRAFT_476432 [Arabidopsis lyrata subsp. lyrata] gi|297334744|gb|EFH65162.1| hypothetical protein ARALYDRAFT_476432 [Arabidopsis lyrata subsp. lyrata]	125	667	1.00E-18	533.6	36.8	40.8	hypothetical protein ARALYDRAFT_476432	gbpln	Arabidopsis lyrata	AT1G73020.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF590 (InterPro:IPR007632). | chr1:27469714-27473181 REVERSE LENGTH=665	125	665	1.00E-20	532.0	36.0	40.0

Rsa1.0_00141.1.g6615.t1	ref|XP_002871006.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297316843|gb|EFH47265.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	344	353	2.00E-65	102.6	45.3	61.6	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT2G44030.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:18220086-18221228 FORWARD LENGTH=380	344	380	7.00E-68	110.5	51.2	64.5
Rsa1.0_00141.1.g6616.t1	gb|EOA34748.1| hypothetical protein CARUB_v10022320mg [Capsella rubella]	600	691	0	115.2	56.7	60.8	hypothetical protein CARUB_v10022320mg	gbpln	Capsella rubella	AT1G72990.1 | Symbols: BGAL17 | beta-galactosidase 17 | chr1:27457480-27462168 REVERSE LENGTH=697	600	697	0	116.2	56.3	60.5
Rsa1.0_00141.1.g6617.t1	dbj|BAA77842.1| ACE [Arabidopsis thaliana]	596	594	0	99.7	93.8	96.3	ACE	gbpln	Arabidopsis thaliana	AT1G72970.1 | Symbols: HTH, EDA17 | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr1:27452872-27455706 FORWARD LENGTH=594	596	594	0	99.7	93.6	96.1
Rsa1.0_00141.1.g6618.t6	ref|XP_002887457.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333298|gb|EFH63716.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	393	436	1.00E-137	110.9	66.7	79.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G72890.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27429947-27431717 FORWARD LENGTH=438	393	438	1.00E-136	111.5	66.2	77.4
Rsa1.0_00142.1.g6619.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	208	441	5.00E-38	212.0	42.3	57.2	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	208	746	3.00E-27	358.7	28.8	38.9
Rsa1.0_00142.1.g6620.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00142.1.g6621.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00142.1.g6622.t1	ref|XP_002878665.1| CYP96A1 [Arabidopsis lyrata subsp. lyrata] gi|297324504|gb|EFH54924.1| CYP96A1 [Arabidopsis lyrata subsp. lyrata]	213	514	1.00E-96	241.3	78.4	86.9	CYP96A1	gbpln	Arabidopsis lyrata	AT2G23180.1 | Symbols: CYP96A1 | cytochrome P450, family 96, subfamily A, polypeptide 1 | chr2:9874953-9876503 FORWARD LENGTH=516	213	516	8.00E-98	242.3	77.5	86.4
Rsa1.0_00142.1.g6623.t3	ref|NP_179932.1| spermidine disinapoyl acyltransferase [Arabidopsis thaliana] gi|3242714|gb|AAC23766.1| putative anthranilate N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana] gi|330252366|gb|AEC07460.1| spermidine disinapoyl acyltransferase [Arabidopsis thaliana]	448	451	0	100.7	78.1	86.4	spermidine disinapoyl acyltransferase	gbpln	Arabidopsis thaliana	AT2G23510.1 | Symbols: SDT | spermidine disinapoyl acyltransferase | chr2:10011517-10013533 REVERSE LENGTH=451	448	451	0	100.7	78.1	86.4
Rsa1.0_00142.1.g6624.t1	gb|AAF87143.1|AC002423_8 T23E23.16 [Arabidopsis thaliana]	136	653	4.00E-24	480.1	39.7	50.7	T23E23.16	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	136	746	3.00E-18	548.5	31.6	38.2
Rsa1.0_00142.1.g6625.t1	ref|NP_001154368.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana] gi|332192539|gb|AEE30660.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana]	309	312	1.00E-135	101.0	76.7	86.4	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	gbpln	Arabidopsis thaliana	AT1G26200.1 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr1:9063471-9064914 REVERSE LENGTH=312	309	312	1.00E-138	101.0	76.7	86.4
Rsa1.0_00142.1.g6626.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00142.1.g6627.t1	gb|EOA38455.1| hypothetical protein CARUB_v10010121mg [Capsella rubella]	154	245	7.00E-76	159.1	92.2	95.5	hypothetical protein CARUB_v10010121mg	gbpln	Capsella rubella	AT1G31260.1 | Symbols: ZIP10 | zinc transporter 10 precursor | chr1:11175559-11177362 REVERSE LENGTH=364	154	364	6.00E-76	236.4	89.6	94.2
Rsa1.0_00142.1.g6628.t1	ref|NP_174411.2| putative zinc transporter 10 [Arabidopsis thaliana] gi|37090222|sp|Q8W245.2|ZIP10_ARATH RecName: Full=Probable zinc transporter 10; AltName: Full=ZRT/IRT-like protein 10; Flags: Precursor gi|6692132|gb|AAF24597.1|AC007654_13 T19E23.6 [Arabidopsis thaliana] gi|332193212|gb|AEE31333.1| putative zinc transporter 10 [Arabidopsis thaliana]	216	364	5.00E-79	168.5	67.1	82.4	putative zinc transporter 10	gbpln	Arabidopsis thaliana	AT1G31260.1 | Symbols: ZIP10 | zinc transporter 10 precursor | chr1:11175559-11177362 REVERSE LENGTH=364	216	364	2.00E-81	168.5	67.1	82.4
Rsa1.0_00142.1.g6629.t1	ref|XP_002891153.1| At1g31330/T19E23_1 [Arabidopsis lyrata subsp. lyrata] gi|297336995|gb|EFH67412.1| At1g31330/T19E23_1 [Arabidopsis lyrata subsp. lyrata]	218	220	1.00E-113	100.9	92.2	97.7	At1g31330/T19E23_1	gbpln	Arabidopsis lyrata	AT1G31330.1 | Symbols: PSAF | photosystem I subunit F | chr1:11215011-11215939 REVERSE LENGTH=221	218	221	1.00E-114	101.4	91.7	97.2
Rsa1.0_00142.1.g6630.t1	ref|XP_002307191.1| predicted protein [Populus trichocarpa] gi|118481405|gb|ABK92645.1| unknown [Populus trichocarpa] gi|118486039|gb|ABK94863.1| unknown [Populus trichocarpa] gi|222856640|gb|EEE94187.1| predicted protein [Populus trichocarpa]	155	157	3.00E-80	101.3	96.8	98.7	predicted protein	gbpln	Populus trichocarpa	AT1G31340.1 | Symbols: RUB1, NEDD8, ATRUB1 | related to ubiquitin 1 | chr1:11218076-11219417 REVERSE LENGTH=156	155	156	3.00E-82	100.6	97.4	98.7

<table>
<tr><td>Rsa1.0_00142.1.g6631.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00142.1.g6632.t1</td><td>ref|XP_002891150.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297336992|gb|EFH67409.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>380</td><td>385</td><td>1.00E-169</td><td>101.3</td><td>80.0</td><td>88.4</td><td>F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G31350.1 | Symbols: KUF1 | KAR-UP F-box 1 | chr1:11221519-11222706 REVERSE LENGTH=395</td><td>380</td><td>395</td><td>1.00E-166</td><td>103.9</td><td>80.5</td><td>89.2</td></tr>
<tr><td>Rsa1.0_00142.1.g6633.t2</td><td>gb|AAF19546.1|AC007190_14 F23N19.13 [Arabidopsis thaliana]</td><td>591</td><td>633</td><td>6.00E-87</td><td>107.1</td><td>38.1</td><td>50.9</td><td>F23N19.13</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>591</td><td>696</td><td>2.00E-14</td><td>117.8</td><td>6.9</td><td>11.2</td></tr>
<tr><td>Rsa1.0_00142.1.g6634.t1</td><td>ref|XP_002893846.1| RECQL2 [Arabidopsis lyrata subsp. lyrata] gi|297339688|gb|EFH70105.1| RECQL2 [Arabidopsis lyrata subsp. lyrata]</td><td>740</td><td>704</td><td>0</td><td>95.1</td><td>86.8</td><td>90.5</td><td>RECQL2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G31360.1 | Symbols: RECQL2, ATRECQ2, MED34 | RECQ helicase L2 | chr1:11232422-11237412 FORWARD LENGTH=705</td><td>740</td><td>705</td><td>0</td><td>95.3</td><td>86.6</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00142.1.g6635.t1</td><td>gb|EOA37829.1| hypothetical protein CARUB_v10011411mg [Capsella rubella]</td><td>569</td><td>570</td><td>0</td><td>100.2</td><td>81.4</td><td>87.7</td><td>hypothetical protein CARUB_v10011411mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G31430.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:11254025-11255737 REVERSE LENGTH=570</td><td>569</td><td>570</td><td>0</td><td>100.2</td><td>81.2</td><td>88.2</td></tr>
<tr><td>Rsa1.0_00142.1.g6636.t2</td><td>ref|NP_174429.1| SH3 domain-containing protein [Arabidopsis thaliana] gi|12322535|gb|AAG51264.1|AC027135_5 unknown protein [Arabidopsis thaliana] gi|16974676|gb|AAL32438.1|AF367773_1 SH3 domain-containing protein 1 [Arabidopsis thaliana] gi|19424043|gb|AAL87310.1| unknown protein [Arabidopsis thaliana] gi|21281229|gb|AAM45032.1| unknown protein [Arabidopsis thaliana] gi|332193235|gb|AEE31356.1| SH3 domain-containing protein [Arabidopsis thaliana]</td><td>439</td><td>439</td><td>0</td><td>100.0</td><td>86.6</td><td>91.8</td><td>SH3 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31440.1 | Symbols: | SH3 domain-containing protein | chr1:11256150-11258479 REVERSE LENGTH=439</td><td>439</td><td>439</td><td>0</td><td>100.0</td><td>86.6</td><td>91.8</td></tr>
<tr><td>Rsa1.0_00142.1.g6637.t2</td><td>ref|NP_174433.2| protein shoot gravitropism 2 (SGR2) [Arabidopsis thaliana] gi|16904659|dbj|BAB71959.1| shoot gravitropism 2 [Arabidopsis thaliana] gi|332193239|gb|AEE31360.1| protein shoot gravitropism 2 (SGR2) [Arabidopsis thaliana]</td><td>894</td><td>933</td><td>0</td><td>104.4</td><td>84.5</td><td>89.9</td><td>protein shoot gravitropism 2 (SGR2)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31480.1 | Symbols: SGR2 | shoot gravitropism 2 (SGR2) | chr1:11266225-11271527 FORWARD LENGTH=933</td><td>894</td><td>933</td><td>0</td><td>104.4</td><td>84.5</td><td>89.9</td></tr>
<tr><td>Rsa1.0_00142.1.g6638.t2</td><td>gb|EOA38144.1| hypothetical protein CARUB_v10009616mg [Capsella rubella]</td><td>359</td><td>346</td><td>1.00E-174</td><td>96.4</td><td>83.3</td><td>88.6</td><td>hypothetical protein CARUB_v10009616mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G31600.3 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:11313376-11315199 REVERSE LENGTH=431</td><td>359</td><td>431</td><td>1.00E-173</td><td>120.1</td><td>82.5</td><td>87.7</td></tr>
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<tr><td>Rsa1.0_00142.1.g6640.t1</td><td>dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]</td><td>66</td><td>341</td><td>3.00E-12</td><td>516.7</td><td>53.0</td><td>69.7</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00143.1.g6641.t1</td><td>ref|NP_187047.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|42572239|ref|NP_974214.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|42572241|ref|NP_974215.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|6223642|gb|AAF05856.1|AC011698_7 hypothetical protein [Arabidopsis thaliana] gi|26450645|dbj|BAC42434.1| unknown protein [Arabidopsis thaliana] gi|29028942|gb|AAO64850.1| At3g03970 [Arabidopsis thaliana] gi|332640498|gb|AEE74019.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332640499|gb|AEE74020.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332640500|gb|AEE74021.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]</td><td>279</td><td>554</td><td>6.00E-46</td><td>198.6</td><td>56.6</td><td>70.3</td><td>armadillo/beta-catenin-like repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G03970.2 | Symbols: | ARM repeat superfamily protein | chr3:1028144-1029891 REVERSE LENGTH=554</td><td>279</td><td>554</td><td>2.00E-48</td><td>198.6</td><td>56.6</td><td>70.3</td></tr>
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Rsa1.0_00143.1.g6642.t1	ref|NP_187048.1| 3-oxoacyl-[acyl-carrier protein] reductase [Arabidopsis thaliana] gi|6223643|gb|AAF05857.1|AC011698_8 putative short-chain type dehydrogenase/reductase [Arabidopsis thaliana] gi|332640501|gb|AEE74022.1| NAD(P)-binding Rossmann-fold domain-containing protein [Arabidopsis thaliana]	263	270	1.00E-127	102.7	86.7	92.0	3-oxoacyl-	gbpln	Arabidopsis thaliana	AT3G03980.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:1031786-1033081 FORWARD LENGTH=270	263	270	1.00E-129	102.7	86.7	92.0
Rsa1.0_00143.1.g6643.t1	gb|EOA24703.1| hypothetical protein CARUB_v10017981mg [Capsella rubella]	223	225	2.00E-88	100.9	74.0	82.1	hypothetical protein CARUB_v10017981mg	gbpln	Capsella rubella	AT3G53490.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G02720.1); Has 70 Blast hits to 70 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 70; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:19832666-19834024 FORWARD LENGTH=225	223	225	3.00E-81	100.9	69.5	81.6
Rsa1.0_00143.1.g6644.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	144	255	2.00E-22	177.1	47.9	59.7	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	144	302	3.00E-21	209.7	36.1	47.9
Rsa1.0_00143.1.g6645.t1	ref|NP_683376.1| uncharacterized protein [Arabidopsis thaliana] gi|332193870|gb|AEE31991.1| uncharacterized protein AT1G43722 [Arabidopsis thaliana]	452	324	3.00E-92	71.7	35.8	40.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G43722.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28730.1); Has 924 Blast hits to 912 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 222; Fungi - 31; Plants - 661; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:16496403-16497377 FORWARD LENGTH=324	452	324	8.00E-95	71.7	35.8	40.5
Rsa1.0_00143.1.g6646.t1	ref|XP_002877919.1| 60S ribosomal protein L12 [Arabidopsis lyrata subsp. lyrata] gi|297323757|gb|EFH54178.1| 60S ribosomal protein L12 [Arabidopsis lyrata subsp. lyrata]	166	166	1.00E-87	100.0	98.8	99.4	60S ribosomal protein L12	gbpln	Arabidopsis lyrata	AT3G53430.1 | Symbols: | Ribosomal protein L11 family protein | chr3:19809895-19810395 REVERSE LENGTH=166	166	166	5.00E-90	100.0	98.8	98.8
Rsa1.0_00143.1.g6647.t1	ref|NP_190908.1| uncharacterized protein [Arabidopsis thaliana] gi|6729491|emb|CAB67647.1| putative protein [Arabidopsis thaliana] gi|332645559|gb|AEE79080.1| uncharacterized protein AT3G53400 [Arabidopsis thaliana]	457	466	0	102.0	80.7	88.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G53400.1 | Symbols: | BEST Arabidopsis thaliana protein match is: conserved peptide upstream open reading frame 47 (TAIR:AT5G03190.1); Has 285 Blast hits to 285 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 279; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr3:19798526-19799926 FORWARD LENGTH=466	457	466	0	102.0	80.7	88.0
Rsa1.0_00143.1.g6648.t1	gb|EOA25167.1| hypothetical protein CARUB_v10018478mg [Capsella rubella]	539	561	0	104.1	88.9	92.2	hypothetical protein CARUB_v10018478mg	gbpln	Capsella rubella	AT3G53390.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:19792781-19796428 FORWARD LENGTH=558	539	558	0	103.5	89.1	92.6
Rsa1.0_00143.1.g6649.t1	gb|EOA25950.1| hypothetical protein CARUB_v10019339mg [Capsella rubella]	707	714	0	101.0	88.7	92.5	hypothetical protein CARUB_v10019339mg	gbpln	Capsella rubella	AT3G53380.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:19789204-19791351 REVERSE LENGTH=715	707	715	0	101.1	88.0	92.8
Rsa1.0_00143.1.g6650.t1	ref|XP_002877910.1| hypothetical protein ARALYDRAFT_323872 [Arabidopsis lyrata subsp. lyrata] gi|297323748|gb|EFH54169.1| hypothetical protein ARALYDRAFT_323872 [Arabidopsis lyrata subsp. lyrata]	309	280	1.00E-125	90.6	71.2	80.9	hypothetical protein ARALYDRAFT_323872	gbpln	Arabidopsis lyrata	AT3G53270.5 | Symbols: | Small nuclear RNA activating complex (SNAPc), subunit SNAP43 protein | chr3:19750406-19752168 REVERSE LENGTH=280	309	280	1.00E-124	90.6	70.2	78.0
Rsa1.0_00143.1.g6651.t1	gb|AAX22053.1| phenylalanine ammonia-lyase [Brassica napus] gi|60499703|gb|AAX22054.1| phenylalanine ammonia-lyase [Brassica napus]	724	724	0	100.0	98.2	99.4	phenylalanine ammonia-lyase	gbpln	Brassica napus	AT3G53260.1 | Symbols: PAL2, ATPAL2 | phenylalanine ammonia-lyase 2 | chr3:19744256-19746619 REVERSE LENGTH=717	724	717	0	99.0	94.5	96.5
Rsa1.0_00143.1.g6652.t1	ref|NP_198884.1| kelch repeat-containing protein [Arabidopsis thaliana] gi|9758096|dbj|BAB08540.1| unnamed protein product [Arabidopsis thaliana] gi|332007198|gb|AED94581.1| kelch repeat-containing protein [Arabidopsis thaliana]	303	415	4.00E-87	137.0	57.4	69.6	kelch repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G40680.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:16288754-16290001 FORWARD LENGTH=415	303	415	1.00E-89	137.0	57.4	69.6

Rsa1.0_00143.1.g6653.t1	ref|NP_566982.1| thioredoxin-like 3-3 [Arabidopsis thaliana] gi|75155215|sp|Q8LCH9.1|TRL33_ARATH RecName: Full=Thioredoxin-like 3-3 gi|21554669|gb|AAM63651.1| thioredoxin-like protein [Arabidopsis thaliana] gi|114050675|gb|ABI49487.1| At3g53220 [Arabidopsis thaliana] gi|332645528|gb|AEE79049.1| thioredoxin-like 3-3 [Arabidopsis thaliana]	118	126	3.00E-51	106.8	81.4	92.4	thioredoxin-like 3-3	gbpln	Arabidopsis thaliana	AT3G53220.1 | Symbols: | Thioredoxin superfamily protein | chr3:19722032-19722615 FORWARD LENGTH=126	118	126	5.00E-54	106.8	81.4	92.4
Rsa1.0_00143.1.g6654.t1	ref|XP_002877903.1| UDP-glucosyl transferase 73D1 [Arabidopsis lyrata subsp. lyrata] gi|297323741|gb|EFH54162.1| UDP-glucosyl transferase 73D1 [Arabidopsis lyrata subsp. lyrata]	117	507	1.00E-43	433.3	79.5	89.7	UDP-glucosyl transferase 73D1	gbpln	Arabidopsis lyrata	AT3G53150.1 | Symbols: UGT73D1 | UDP-glucosyl transferase 73D1 | chr3:19697736-19699259 REVERSE LENGTH=507	117	507	1.00E-45	433.3	76.1	89.7
Rsa1.0_00143.1.g6655.t1	ref|NP_190882.1| putative O-diphenol-O-methyl transferase [Arabidopsis thaliana] gi|14194165|gb|AAK56277.1|AF367289_1 AT3g53140/T4D2_70 [Arabidopsis thaliana] gi|6630734|emb|CAB64217.1| caffeic acid O-methyltransferase-like protein [Arabidopsis thaliana] gi|22137206|gb|AAM91448.1| AT3g53140/T4D2_70 [Arabidopsis thaliana] gi|332645520|gb|AEE79041.1| putative O-diphenol-O-methyl transferase [Arabidopsis thaliana]	363	359	0	98.9	90.9	94.5	putative O-diphenol-O-methyl transferase	gbpln	Arabidopsis thaliana	AT3G53140.1 | Symbols: | O-methyltransferase family protein | chr3:19695692-19697355 FORWARD LENGTH=359	363	359	0	98.9	90.9	94.5
Rsa1.0_00143.1.g6656.t1	ref|NP_850268.2| vacuolar protein-sorting-associated protein 37-2 [Arabidopsis thaliana] gi|122215039|sp|Q3EBL9.1|VP372_ARATH RecName: Full=Vacuolar protein-sorting-associated protein 37 homolog 2; Short=AtVPS37-2; AltName: Full=ESCRT-I complex subunit VPS37 homolog 2 gi|330254189|gb|AEC09283.1| vacuolar protein-sorting-associated protein 37-2 [Arabidopsis thaliana]	254	218	8.00E-97	85.8	70.9	78.7	vacuolar protein-sorting-associated protein 37-2	gbpln	Arabidopsis thaliana	AT2G36680.1 | Symbols: | Modifier of rudimentary (Mod(r)) protein | chr2:15368980-15370726 REVERSE LENGTH=218	254	218	2.00E-99	85.8	70.9	78.7
Rsa1.0_00143.1.g6657.t2	ref|XP_002877902.1| hypothetical protein ARALYDRAFT_906697 [Arabidopsis lyrata subsp. lyrata] gi|297323740|gb|EFH54161.1| hypothetical protein ARALYDRAFT_906697 [Arabidopsis lyrata subsp. lyrata]	121	217	8.00E-23	179.3	53.7	57.9	hypothetical protein ARALYDRAFT_906697	gbpln	Arabidopsis lyrata	AT3G53120.1 | Symbols: VPS37-1 | Modifier of rudimentary (Mod(r)) protein | chr3:19690729-19692490 REVERSE LENGTH=217	121	217	1.00E-24	179.3	52.1	57.9
Rsa1.0_00143.1.g6658.t1	ref|NP_190879.1| DEAD-box ATP-dependent RNA helicase 38 [Arabidopsis thaliana] gi|108861891|sp|Q93ZG7.2|RH38_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 38; AltName: Full=Low expression of osmotically-responsive genes 4 protein; AltName: Full=Protein CRYOPHYTE gi|6630731|emb|CAB64214.1| RNA helicase-like protein [Arabidopsis thaliana] gi|27311677|gb|AAO00804.1| RNA helicase -like protein [Arabidopsis thaliana] gi|31711900|gb|AAP68306.1| At3g53110 [Arabidopsis thaliana] gi|332645517|gb|AEE79038.1| DEAD-box ATP-dependent RNA helicase 38 [Arabidopsis thaliana]	497	496	0	99.8	88.1	93.8	DEAD-box ATP-dependent RNA helicase 38	gbpln	Arabidopsis thaliana	AT3G53110.1 | Symbols: LOS4 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:19687968-19690423 FORWARD LENGTH=496	497	496	0	99.8	88.1	93.8
Rsa1.0_00143.1.g6659.t1	ref|XP_002877901.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297323739|gb|EFH54160.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	351	351	0	100.0	90.0	93.7	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT3G53100.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:19684989-19686542 REVERSE LENGTH=351	351	351	0	100.0	88.3	93.2

Rsa1.0_00143.1.g6660.t1	ref|NP_190877.1| E3 ubiquitin-protein ligase UPL7 [Arabidopsis thaliana] gi|79314848|ref|NP_001030850.1| E3 ubiquitin-protein ligase UPL7 [Arabidopsis thaliana] gi|75265625|sp|Q9SCQ2.1|UPL7_ARATH RecName: Full=E3 ubiquitin-protein ligase UPL7; Short=Ubiquitin-protein ligase 7 gi|6630729|emb|CAB64212.1| putative protein [Arabidopsis thaliana] gi|332645514|gb|AEE79035.1| E3 ubiquitin-protein ligase UPL7 [Arabidopsis thaliana] gi|332645515|gb|AEE79036.1| E3 ubiquitin-protein ligase UPL7 [Arabidopsis thaliana]	1142	1142	0	100.0	89.6	95.2	E3 ubiquitin-protein ligase UPL7	gbpln	Arabidopsis thaliana	AT3G53090.2 | Symbols: UPL7 | ubiquitin-protein ligase 7 | chr3:19679273-19684453 FORWARD LENGTH=1142	1142	1142	0	100.0	89.6	95.2
Rsa1.0_00144.1.g6661.t1	gb|EOA23646.1| hypothetical protein CARUB_v10016844mg [Capsella rubella]	625	626	0	100.2	93.6	97.1	hypothetical protein CARUB_v10016844mg	gbpln	Capsella rubella	AT3G52850.1 | Symbols: VSR1, BP-80, ATELP, BP80, BP80B, ATELP1, ATVSR1, GFS1, VSR1;1, BP80-1;1 | vacuolar sorting receptor homolog 1 | chr3:19587999-19591690 FORWARD LENGTH=623	625	623	0	99.7	92.3	96.5
Rsa1.0_00144.1.g6662.t1	gb|EOA25450.1| hypothetical protein CARUB_v10018788mg [Capsella rubella]	156	156	2.00E-67	100.0	91.7	94.2	hypothetical protein CARUB_v10018788mg	gbpln	Capsella rubella	AT3G52860.1 | Symbols: | unknown protein; Has 86 Blast hits to 86 proteins in 36 species: Archae - 0; Bacteria - 2; Metazoa - 41; Fungi - 13; Plants - 26; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr3:19591998-19592741 REVERSE LENGTH=156	156	156	9.00E-67	100.0	88.5	92.9
Rsa1.0_00144.1.g6663.t1	gb|AAK72107.1| monodehydroascorbate reductase [Brassica rapa subsp. pekinensis]	434	434	0	100.0	98.8	100.0	monodehydroascorbate reductase	gbpln	Brassica rapa	AT3G52880.1 | Symbols: ATMDAR1, MDAR1 | monodehydroascorbate reductase 1 | chr3:19601477-19604366 REVERSE LENGTH=434	434	434	0	100.0	95.4	98.2
Rsa1.0_00144.1.g6664.t1	gb|EOA23462.1| hypothetical protein CARUB_v10016653mg [Capsella rubella]	829	935	0	112.8	83.7	89.0	hypothetical protein CARUB_v10016653mg	gbpln	Capsella rubella	AT3G52890.2 | Symbols: KIPK | KCBP-interacting protein kinase | chr3:19609150-19612032 FORWARD LENGTH=934	829	934	0	112.7	82.5	88.5
Rsa1.0_00144.1.g6665.t1	ref|NP_190858.1| uncharacterized protein [Arabidopsis thaliana] gi|7529714|emb|CAB86894.1| putative protein [Arabidopsis thaliana] gi|110738967|dbj|BAF01404.1| hypothetical protein [Arabidopsis thaliana] gi|332645486|gb|AEE79007.1| uncharacterized protein AT3G52900 [Arabidopsis thaliana]	164	164	7.00E-77	100.0	90.9	95.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G52900.1 | Symbols: | Family of unknown function (DUF662) | chr3:19613134-19613852 FORWARD LENGTH=164	164	164	2.00E-79	100.0	90.9	95.1
Rsa1.0_00144.1.g6666.t1	gb|EOA24133.1| hypothetical protein CARUB_v10017366mg, partial [Capsella rubella]	384	407	1.00E-150	106.0	83.9	89.3	hypothetical protein CARUB_v10017366mg, partial	gbpln	Capsella rubella	AT3G52910.1 | Symbols: AtGRF4, GRF4 | growth-regulating factor 4 | chr3:19616177-19618268 REVERSE LENGTH=380	384	380	1.00E-147	99.0	84.1	88.0
Rsa1.0_00144.1.g6667.t1	ref|NP_566974.1| uncharacterized protein [Arabidopsis thaliana] gi|21593825|gb|AAM65792.1| unknown [Arabidopsis thaliana] gi|332645489|gb|AEE79010.1| uncharacterized protein AT3G52920 [Arabidopsis thaliana]	165	180	4.00E-72	109.1	84.8	92.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G52920.1 | Symbols: | Family of unknown function (DUF662) | chr3:19624601-19625981 FORWARD LENGTH=180	165	180	2.00E-74	109.1	84.8	92.1
Rsa1.0_00144.1.g6668.t1	ref|XP_002877893.1| hypothetical protein ARALYDRAFT_906673 [Arabidopsis lyrata subsp. lyrata] gi|297323731|gb|EFH54152.1| hypothetical protein ARALYDRAFT_906673 [Arabidopsis lyrata subsp. lyrata]	358	358	0	100.0	98.3	99.2	hypothetical protein ARALYDRAFT_906673	gbpln	Arabidopsis lyrata	AT3G52930.1 | Symbols: | Aldolase superfamily protein | chr3:19627383-19628874 REVERSE LENGTH=358	358	358	0	100.0	97.8	98.9
Rsa1.0_00144.1.g6669.t1	gb|EOA24034.1| hypothetical protein CARUB_v10017251mg [Capsella rubella]	434	444	0	102.3	90.3	95.9	hypothetical protein CARUB_v10017251mg	gbpln	Capsella rubella	AT2G36530.1 | Symbols: LOS2, ENO2 | Enolase | chr2:15321081-15323786 REVERSE LENGTH=444	434	444	0	102.3	88.7	95.2

Rsa1.0_00144.1.g6670.t1	ref|NP_190863.3| CBS / octicosapeptide/Phox/Bemp1 domain-containing protein [Arabidopsis thaliana] gi|334185937|ref|NP_001190074.1| CBS / octicosapeptide/Phox/Bemp1 domain-containing protein [Arabidopsis thaliana] gi|75263848|sp|Q9LF97.1|Y3295_ARATH RecName: Full=CBS domain-containing protein CBSCBSPB3 gi|7529719|emb|CAB86899.1| putative protein [Arabidopsis thaliana] gi|332645495|gb|AEE79016.1| CBS / octicosapeptide/Phox/Bemp1 domain-containing protein [Arabidopsis thaliana] gi|332645496|gb|AEE79017.1| CBS / octicosapeptide/Phox/Bemp1 domain-containing protein [Arabidopsis thaliana]	538	556	0	103.3	77.3	84.8	CBS / octicosapeptide/Phox/Bemp1 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G52950.2 | Symbols: | CBS / octicosapeptide/Phox/Bemp1 (PB1) domains-containing protein | chr3:19634866-19636536 FORWARD LENGTH=556	538	556	0	103.3	77.3	84.8
Rsa1.0_00144.1.g6671.t1	ref|NP_190864.1| peroxiredoxin-2E [Arabidopsis thaliana] gi|143360522|sp|Q949U7.2|PRX2E_ARATH RecName: Full=Peroxiredoxin-2E, chloroplastic; AltName: Full=Peroxiredoxin IIE; AltName: Full=Thioredoxin reductase 2E; Flags: Precursor gi|7529720|emb|CAB86900.1| peroxiredoxin-like protein [Arabidopsis thaliana] gi|15451116|gb|AAK96829.1| peroxiredoxin-like protein [Arabidopsis thaliana] gi|18377484|gb|AAL66908.1| peroxiredoxin-like protein [Arabidopsis thaliana] gi|23297326|gb|AAN12942.1| putative peroxiredoxin [Arabidopsis thaliana] gi|332645497|gb|AEE79018.1| peroxiredoxin-2E [Arabidopsis thaliana]	231	234	1.00E-113	101.3	90.5	95.7	peroxiredoxin-2E	gbpln	Arabidopsis thaliana	AT3G52960.1 | Symbols: | Thioredoxin superfamily protein | chr3:19639699-19640403 FORWARD LENGTH=234	231	234	1.00E-116	101.3	90.5	95.7
Rsa1.0_00144.1.g6672.t1	ref|XP_002876178.1| hypothetical protein ARALYDRAFT_906680 [Arabidopsis lyrata subsp. lyrata] gi|297322016|gb|EFH52437.1| hypothetical protein ARALYDRAFT_906680 [Arabidopsis lyrata subsp. lyrata]	527	527	0	100.0	97.7	99.1	hypothetical protein ARALYDRAFT_906680	gbpln	Arabidopsis lyrata	AT3G52990.1 | Symbols: | Pyruvate kinase family protein | chr3:19649046-19652237 FORWARD LENGTH=527	527	527	0	100.0	97.5	99.2
Rsa1.0_00144.1.g6673.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	163	329	1.00E-12	201.8	23.3	33.7	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00144.1.g6674.t1	gb|EOA24470.1| hypothetical protein CARUB_v10017732mg [Capsella rubella]	307	298	1.00E-149	97.1	83.1	90.9	hypothetical protein CARUB_v10017732mg	gbpln	Capsella rubella	AT3G53000.1 | Symbols: AtPP2-A15, PP2-A15 | phloem protein 2-A15 | chr3:19654278-19655801 FORWARD LENGTH=300	307	300	1.00E-150	97.7	81.8	89.9
Rsa1.0_00144.1.g6675.t1	ref|NP_190869.3| uncharacterized protein [Arabidopsis thaliana] gi|110738676|dbj|BAF01263.1| hypothetical protein [Arabidopsis thaliana] gi|332645504|gb|AEE79025.1| uncharacterized protein AT3G53010 [Arabidopsis thaliana]	246	297	1.00E-121	120.7	84.1	90.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G53010.1 | Symbols: | Domain of unknown function (DUF303) | chr3:19656603-19657928 REVERSE LENGTH=297	246	297	1.00E-123	120.7	84.1	90.7
Rsa1.0_00144.1.g6676.t1	ref|XP_002335364.1| predicted protein [Populus trichocarpa] gi|222833671|gb|EEE72148.1| predicted protein [Populus trichocarpa]	193	155	1.00E-65	80.3	65.8	69.9	predicted protein	gbpln	Populus trichocarpa	AT3G53020.1 | Symbols: STV1, RPL24B, RPL24 | Ribosomal protein L24e family protein | chr3:19660749-19661912 REVERSE LENGTH=163	193	163	3.00E-67	84.5	69.4	72.0
Rsa1.0_00144.1.g6677.t1	ref|XP_002876180.1| hypothetical protein ARALYDRAFT_485678 [Arabidopsis lyrata subsp. lyrata] gi|297322018|gb|EFH52439.1| hypothetical protein ARALYDRAFT_485678 [Arabidopsis lyrata subsp. lyrata]	732	533	0	72.8	60.2	62.0	hypothetical protein ARALYDRAFT_485678	gbpln	Arabidopsis lyrata	AT3G53030.1 | Symbols: SRPK4 | ser/arg-rich protein kinase 4 | chr3:19662412-19664362 FORWARD LENGTH=529	732	529	0	72.3	59.2	61.2
Rsa1.0_00144.1.g6678.t1	gb|EOA24269.1| hypothetical protein CARUB_v10017511mg [Capsella rubella]	361	359	0	99.4	90.3	94.5	hypothetical protein CARUB_v10017511mg	gbpln	Capsella rubella	AT3G53140.1 | Symbols: | O-methyltransferase family protein | chr3:19695692-19697355 FORWARD LENGTH=359	361	359	0	99.4	90.6	93.9
Rsa1.0_00144.1.g6679.t1	ref|XP_002877903.1| UDP-glucosyl transferase 73D1 [Arabidopsis lyrata subsp. lyrata] gi|297323741|gb|EFH54162.1| UDP-glucosyl transferase 73D1 [Arabidopsis lyrata subsp. lyrata]	504	507	0	100.6	80.8	90.9	UDP-glucosyl transferase 73D1	gbpln	Arabidopsis lyrata	AT3G53150.1 | Symbols: UGT73D1 | UDP-glucosyl transferase 73D1 | chr3:19697736-19699259 REVERSE LENGTH=507	504	507	0	100.6	80.8	90.1

Rsa1.0_00144.1.g6680.t1	gb|AAD26953.1| putative non-LTR retrolelement reverse transcriptase [Arabidopsis thaliana]	334	323	3.00E-43	96.7	31.4	49.4	putative non-LTR retrolelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	334	295	3.00E-41	88.3	31.1	47.0
Rsa1.0_00144.1.g6681.t1	ref|XP_002877903.1| UDP-glucosyl transferase 73D1 [Arabidopsis lyrata subsp. lyrata] gi|297323741|gb|EFH54162.1| UDP-glucosyl transferase 73D1 [Arabidopsis lyrata subsp. lyrata]	501	507	0	101.2	85.2	93.2	UDP-glucosyl transferase 73D1	gbpln	Arabidopsis lyrata	AT3G53150.1 | Symbols: UGT73D1 | UDP-glucosyl transferase 73D1 | chr3:19697736-19699259 REVERSE LENGTH=507	501	507	0	101.2	84.2	92.6
Rsa1.0_00144.1.g6682.t1	ref|NP_190884.1| UDP-glucosyl transferase 73C7 [Arabidopsis thaliana] gi|75313289|sp|Q9SCP5.1|U73C7_ARATH RecName: Full=UDP-glycosyltransferase 73C7 gi|6630736|emb|CAB64219.1| glucosyltransferase-like protein [Arabidopsis thaliana] gi|50253526|gb|AAT71965.1| At3g53160 [Arabidopsis thaliana] gi|56381967|gb|AAV85702.1| At3g53160 [Arabidopsis thaliana] gi|332645522|gb|AEE79043.1| UDP-glucosyl transferase 73C7 [Arabidopsis thaliana]	490	490	0	100.0	82.9	89.8	UDP-glucosyl transferase 73C7	gbpln	Arabidopsis thaliana	AT3G53160.1 | Symbols: UGT73C7 | UDP-glucosyl transferase 73C7 | chr3:19702485-19703957 REVERSE LENGTH=490	490	490	0	100.0	82.9	89.8
Rsa1.0_00144.1.g6683.t1	ref|NP_190885.5| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana] gi|332645523|gb|AEE79044.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	454	499	0	109.9	86.1	93.2	tetratricopeptide repeat domain-containing protein	gbpln	Arabidopsis thaliana	AT3G53170.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:19704600-19706417 REVERSE LENGTH=499	454	499	0	109.9	86.1	93.2
Rsa1.0_00144.1.g6684.t1	ref|XP_002876191.1| hypothetical protein ARALYDRAFT_485693 [Arabidopsis lyrata subsp. lyrata] gi|297322029|gb|EFH52450.1| hypothetical protein ARALYDRAFT_485693 [Arabidopsis lyrata subsp. lyrata]	174	853	9.00E-71	490.2	77.6	83.9	hypothetical protein ARALYDRAFT_485693	gbpln	Arabidopsis lyrata	AT3G53180.1 | Symbols: | glutamate-ammonia ligases;catalytics;glutamate-ammonia ligases | chr3:19707068-19711188 FORWARD LENGTH=852	174	852	1.00E-72	489.7	76.4	83.3
Rsa1.0_00144.1.g6685.t1	#	#	#	#	#	#	#	-	----	----	AT4G26430.1 | Symbols: CSN6B | COP9 signalosome subunit 6B | chr4:13355229-13357326 FORWARD LENGTH=317	62	317	2.00E-12	511.3	50.0	51.6
Rsa1.0_00144.1.g6686.t1	emb|CAB64221.1| nodulin / glutamate-ammonia ligase-like protein [Arabidopsis thaliana]	667	845	0	126.7	85.2	90.7	nodulin / glutamate-ammonia ligase-like protein	gbpln	Arabidopsis thaliana	AT3G53180.1 | Symbols: | glutamate-ammonia ligases;catalytics;glutamate-ammonia ligases | chr3:19707068-19711188 FORWARD LENGTH=852	667	852	0	127.7	85.2	90.7
Rsa1.0_00145.1.g6687.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1341	1515	0	113.0	58.3	74.0	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1341	1262	1.00E-118	94.1	14.8	21.9
Rsa1.0_00145.1.g6688.t1	ref|NP_173264.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|6714296|gb|AAF25992.1|AC013354_11 F15H18.20 [Arabidopsis thaliana] gi|8671770|gb|AAF78376.1|AC069551_9 T10O22.25 [Arabidopsis thaliana] gi|21592585|gb|AAM64534.1| lipid transfer protein, putative [Arabidopsis thaliana] gi|91805803|gb|ABE65630.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis thaliana] gi|107738083|gb|ABF83631.1| At1g18280 [Arabidopsis thaliana] gi|332191576|gb|AEE29697.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	180	180	1.00E-51	100.0	66.7	76.1	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT1G18280.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:6294403-6295207 FORWARD LENGTH=180	180	180	5.00E-54	100.0	66.7	76.1

Rsa1.0_00145.1.g6689.t1	ref|NP_173265.1| uncharacterized protein [Arabidopsis thaliana] gi|6714297|gb|AAF25993.1|AC013354_12 F15H18.19 [Arabidopsis thaliana] gi|8671771|gb|AAF78377.1|AC069551_10 T10O22.26 [Arabidopsis thaliana] gi|52354129|gb|AAU44385.1| hypothetical protein AT1G18290 [Arabidopsis thaliana] gi|55740499|gb|AAV63842.1| hypothetical protein At1g18290 [Arabidopsis thaliana] gi|332191577|gb|AEE29698.1| uncharacterized protein AT1G18290 [Arabidopsis thaliana]	164	176	6.00E-66	107.3	81.1	90.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G18290.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: chloroplast; EXPRESSED IN: root; Has 94 Blast hits to 94 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 94; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6297436-6297966 FORWARD LENGTH=176	164	176	2.00E-68	107.3	81.1	90.2
Rsa1.0_00145.1.g6690.t1	ref|XP_002890268.1| hypothetical protein ARALYDRAFT_312784 [Arabidopsis lyrata subsp. lyrata] gi|297336110|gb|EFH66527.1| hypothetical protein ARALYDRAFT_312784 [Arabidopsis lyrata subsp. lyrata]	206	207	1.00E-101	100.5	85.9	91.3	hypothetical protein ARALYDRAFT_312784	gbpln	Arabidopsis lyrata	AT1G18300.1 | Symbols: atnudt4, NUDT4 | nudix hydrolase homolog 4 | chr1:6299841-6300799 FORWARD LENGTH=207	206	207	1.00E-101	100.5	84.0	90.8
Rsa1.0_00145.1.g6691.t1	ref|XP_002890269.1| At3g10110 [Arabidopsis lyrata subsp. lyrata] gi|297336111|gb|EFH66528.1| At3g10110 [Arabidopsis lyrata subsp. lyrata]	170	171	6.00E-69	100.6	82.9	91.8	At3g10110	gbpln	Arabidopsis lyrata	AT3G10110.1 | Symbols: MEE67 | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr3:3116225-3117378 FORWARD LENGTH=173	170	173	3.00E-71	101.8	84.1	92.4
Rsa1.0_00145.1.g6692.t1	ref|NP_683313.2| acyl-CoA N-acyltransferases-like protein [Arabidopsis thaliana] gi|332191583|gb|AEE29704.1| acyl-CoA N-acyltransferases-like protein [Arabidopsis thaliana]	294	269	1.00E-111	91.5	68.0	71.8	acyl-CoA N-acyltransferases-like protein	gbpln	Arabidopsis thaliana	AT1G18335.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr1:6309428-6311326 REVERSE LENGTH=269	294	269	1.00E-114	91.5	68.0	71.8
Rsa1.0_00145.1.g6693.t4	gb|AAW81736.1| Putative Acttin-related protein 4 (ARP4) [Brassica oleracea]	443	442	0	99.8	95.5	97.1	Putative Acttin-related protein 4 (ARP4)	gbpln	Brassica oleracea	AT1G18450.1 | Symbols: ATARP4, ARP4 | actin-related protein 4 | chr1:6348199-6351766 FORWARD LENGTH=441	443	441	0	99.5	94.6	98.2
Rsa1.0_00145.1.g6694.t2	gb|AAW81737.1| Putative finger family protein [Brassica oleracea]	434	467	0	107.6	88.7	93.5	Putative finger family protein	gbpln	Brassica oleracea	AT1G18470.1 | Symbols: | Transmembrane Fragile-X-F-associated protein | chr1:6356407-6360057 REVERSE LENGTH=467	434	467	0	107.6	88.5	93.5
Rsa1.0_00145.1.g6695.t1	gb|AAW81738.1| Putative [Brassica oleracea]	393	394	0	100.3	83.2	91.9	Putative	gbpln	Brassica oleracea	AT1G18480.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr1:6361639-6362814 FORWARD LENGTH=391	393	391	0	99.5	81.2	89.1
Rsa1.0_00145.1.g6696.t1	ref|XP_002890283.1| hypothetical protein ARALYDRAFT_889272 [Arabidopsis lyrata subsp. lyrata] gi|297336125|gb|EFH66542.1| hypothetical protein ARALYDRAFT_889272 [Arabidopsis lyrata subsp. lyrata]	272	272	1.00E-137	100.0	86.8	92.6	hypothetical protein ARALYDRAFT_889272	gbpln	Arabidopsis lyrata	AT1G18520.1 | Symbols: TET11 | tetraspanin11 | chr1:6375051-6376178 FORWARD LENGTH=271	272	271	1.00E-137	99.6	86.4	91.9
Rsa1.0_00145.1.g6697.t1	gb|EOA36227.1| hypothetical protein CARUB_v10010178mg [Capsella rubella]	234	234	1.00E-109	100.0	93.6	97.4	hypothetical protein CARUB_v10010178mg	gbpln	Capsella rubella	AT1G18540.1 | Symbols: | Ribosomal protein L6 family protein | chr1:6377448-6378548 REVERSE LENGTH=233	234	233	1.00E-108	99.6	93.6	97.0
Rsa1.0_00145.1.g6698.t1	gb|ACR48188.1| MYB domain protein 51-2 [Brassica rapa subsp. pekinensis]	328	333	1.00E-156	101.5	90.9	94.8	MYB domain protein 51-2	gbpln	Brassica rapa	AT1G18570.1 | Symbols: MYB51, AtMYB51, BW51A, BW51B, HIG1 | myb domain protein 51 | chr1:6389765-6391026 FORWARD LENGTH=352	328	352	1.00E-125	107.3	79.0	86.6
Rsa1.0_00145.1.g6699.t1	ref|NP_564057.4| alpha-1,4-galacturonosyltransferase [Arabidopsis thaliana] gi|75164846|sp|Q949Q1.1|GAUTB_ARATH RecName: Full=Probable galacturonosyltransferase 11 gi|15293067|gb|AAK93644.1| unknown protein [Arabidopsis thaliana] gi|17064736|gb|AAL32522.1| Unknown protein [Arabidopsis thaliana] gi|332191610|gb|AEE29731.1| probable galacturonosyltransferase 11 [Arabidopsis thaliana]	535	537	0	100.4	89.3	93.5	alpha-1,4-galacturonosyltransferase	gbpln	Arabidopsis thaliana	AT1G18580.1 | Symbols: GAUT11 | galacturonosyltransferase 11 | chr1:6396144-6398005 FORWARD LENGTH=537	535	537	0	100.4	89.3	93.5
Rsa1.0_00145.1.g6700.t1	ref|XP_002890286.1| hypothetical protein ARALYDRAFT_312807 [Arabidopsis lyrata subsp. lyrata] gi|297336128|gb|EFH66545.1| hypothetical protein ARALYDRAFT_312807 [Arabidopsis lyrata subsp. lyrata]	525	538	2.00E-99	102.5	32.2	34.3	hypothetical protein ARALYDRAFT_312807	gbpln	Arabidopsis lyrata	AT1G18580.1 | Symbols: GAUT11 | galacturonosyltransferase 11 | chr1:6396144-6398005 FORWARD LENGTH=537	525	537	1.00E-101	102.3	31.8	33.9
Rsa1.0_00145.1.g6701.t1	sp|P0C2G3.3|FB308_ARATH RecName: Full=Putative F-box protein At1g30925	393	523	7.00E-70	133.1	44.8	57.3	RecName: Full=Putative F-box protein At1g30925	----	----	AT1G30920.1 | Symbols: | F-box family protein | chr1:11004242-11005444 REVERSE LENGTH=400	393	400	8.00E-69	101.8	41.7	57.0

Rsa1.0_00145.1.g6702.t5	ref|NP_173296.3| galactose oxidase/kelch repeat domain-containing protein [Arabidopsis thaliana] gi|9795595|gb|AAF98413.1|AC026238_5 Hypothetical protein [Arabidopsis thaliana] gi|332191613|gb|AEE29734.1| galactose oxidase/kelch repeat domain-containing protein [Arabidopsis thaliana]	536	556	0	103.7	79.1	86.9	galactose oxidase/kelch repeat domain-containing protein	gbpln	Arabidopsis thaliana	AT1G18610.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:6405779-6408831 FORWARD LENGTH=556	536	556	0	103.7	79.1	86.9
Rsa1.0_00145.1.g6703.t1	ref|NP_194349.2| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|332659768|gb|AEE85168.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana]	624	1057	1.00E-126	169.4	33.0	38.0	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT4G26190.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr4:13262473-13266282 REVERSE LENGTH=1057	624	1057	1.00E-128	169.4	33.0	38.0
Rsa1.0_00145.1.g6704.t1	gb|EOA39586.1| hypothetical protein CARUB_v10008208mg [Capsella rubella]	815	973	0	119.4	67.7	77.7	hypothetical protein CARUB_v10008208mg	gbpln	Capsella rubella	AT1G18620.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74160.1); Has 1987 Blast hits to 1263 proteins in 207 species: Archae - 0; Bacteria - 172; Metazoa - 665; Fungi - 149; Plants - 271; Viruses - 6; Other Eukaryotes - 724 (source: NCBI BLink). | chr1:6410719-6414269 FORWARD LENGTH=978	815	978	0	120.0	68.8	78.9
Rsa1.0_00145.1.g6705.t2	ref|NP_173298.1| glycine-rich RNA-binding protein 6 [Arabidopsis thaliana] gi|75334552|sp|Q9FZ84.1|RBG6_ARATH RecName: Full=Glycine-rich RNA-binding protein 6, mitochondrial; Short=AtGR-RBP6; AltName: Full=AtRBG6; Flags: Precursor gi|9795594|gb|AAF98412.1|AC026238_4 Similar to glycine-rich RNA-binding proteins [Arabidopsis thaliana] gi|29029110|gb|AAO64934.1| At1g18630 [Arabidopsis thaliana] gi|110743184|dbj|BAE99483.1| hypothetical protein [Arabidopsis thaliana] gi|332191616|gb|AEE29737.1| glycine-rich RNA-binding protein 6 [Arabidopsis thaliana]	159	155	1.00E-46	97.5	57.2	66.7	glycine-rich RNA-binding protein 6	gbpln	Arabidopsis thaliana	AT1G18630.1 | Symbols: GR-RBP6 | glycine-rich RNA-binding protein 6 | chr1:6415226-6416283 FORWARD LENGTH=155	159	155	5.00E-49	97.5	57.2	66.7
Rsa1.0_00145.1.g6706.t1	gb|EOA27005.1| hypothetical protein CARUB_v10023099mg [Capsella rubella]	533	486	0	91.2	70.9	78.0	hypothetical protein CARUB_v10023099mg	gbpln	Capsella rubella	AT4G39280.2 | Symbols: | phenylalanyl-tRNA synthetase, putative / phenylalanine--tRNA ligase, putative | chr4:18280292-18284831 REVERSE LENGTH=485	533	485	0	91.0	71.5	79.5
Rsa1.0_00145.1.g6707.t1	gb|AAF97297.1|AC010164_19 Hypothetical protein [Arabidopsis thaliana]	122	308	8.00E-45	252.5	73.8	82.0	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00145.1.g6708.t1	ref|XP_002893006.1| hypothetical protein ARALYDRAFT_889285 [Arabidopsis lyrata subsp. lyrata] gi|297338848|gb|EFH69265.1| hypothetical protein ARALYDRAFT_889285 [Arabidopsis lyrata subsp. lyrata]	190	187	6.00E-75	98.4	83.7	86.8	hypothetical protein ARALYDRAFT_889285	gbpln	Arabidopsis lyrata	AT1G18650.1 | Symbols: PDCB3 | plasmodesmata callose-binding protein 3 | chr1:6419036-6420413 REVERSE LENGTH=184	190	184	6.00E-75	96.8	81.1	84.7
Rsa1.0_00145.1.g6709.t1	gb|EOA39803.1| hypothetical protein CARUB_v10008466mg [Capsella rubella]	704	699	0	99.3	86.9	91.2	hypothetical protein CARUB_v10008466mg	gbpln	Capsella rubella	AT1G18670.1 | Symbols: IBS1 | Protein kinase superfamily protein | chr1:6427242-6430696 REVERSE LENGTH=709	704	709	0	100.7	87.2	92.2
Rsa1.0_00145.1.g6710.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00145.1.g6711.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1525	1274	0	83.5	39.5	52.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1525	575	5.00E-56	37.7	10.2	15.7
Rsa1.0_00145.1.g6712.t1	ref|XP_002890304.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297336146|gb|EFH66563.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	577	587	0	101.7	90.3	93.6	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G18880.1 | Symbols: | Major facilitator superfamily protein | chr1:6520800-6523241 FORWARD LENGTH=587	577	587	0	101.7	89.9	93.2

Rsa1.0_00145.1.g6713.t1	ref|NP_173324.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|42571539|ref|NP_973860.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75151479|sp|Q8GYP6.1|PPR49_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g18900 gi|26450017|dbj|BAC42129.1| unknown protein [Arabidopsis thaliana] gi|28827402|gb|AAO50545.1| unknown protein [Arabidopsis thaliana] gi|332191657|gb|AEE29778.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332191658|gb|AEE29779.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	825	860	0	104.2	78.8	86.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G18900.2 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:6529778-6532360 FORWARD LENGTH=860	825	860	0	104.2	78.8	86.9
Rsa1.0_00145.1.g6714.t1	ref|XP_002890307.1| aminoacyl-tRNA synthetase family [Arabidopsis lyrata subsp. lyrata] gi|297336149|gb|EFH66566.1| aminoacyl-tRNA synthetase family [Arabidopsis lyrata subsp. lyrata]	783	761	0	97.2	79.7	85.1	aminoacyl-tRNA synthetase family	gbpln	Arabidopsis lyrata	AT1G18950.1 | Symbols: | DDT domain superfamily | chr1:6546539-6551549 FORWARD LENGTH=750	783	750	0	95.8	79.4	85.4
Rsa1.0_00145.1.g6715.t1	ref|NP_173330.1| myb-like HTH transcriptional regulator-like protein [Arabidopsis thaliana] gi|8778276|gb|AAF79285.1|AC068602_8 F14D16.11 [Arabidopsis thaliana] gi|225897944|dbj|BAH30304.1| hypothetical protein [Arabidopsis thaliana] gi|332191663|gb|AEE29784.1| myb-like HTH transcriptional regulator-like protein [Arabidopsis thaliana]	312	307	1.00E-131	98.4	84.9	91.0	myb-like HTH transcriptional regulator-like protein	gbpln	Arabidopsis thaliana	AT1G18960.1 | Symbols: | myb-like HTH transcriptional regulator family protein | chr1:6552854-6553940 FORWARD LENGTH=307	312	307	1.00E-134	98.4	84.9	91.0
Rsa1.0_00145.1.g6716.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00145.1.g6717.t1	dbj|BAJ34162.1| unnamed protein product [Thellungiella halophila]	282	294	1.00E-109	104.3	83.0	86.9	unnamed protein product	----	----	AT1G19000.2 | Symbols: | Homeodomain-like superfamily protein | chr1:6561335-6562684 REVERSE LENGTH=285	282	285	1.00E-101	101.1	79.8	84.4
Rsa1.0_00145.1.g6718.t1	ref|XP_002890309.1| hypothetical protein ARALYDRAFT_335156 [Arabidopsis lyrata subsp. lyrata] gi|297336151|gb|EFH66568.1| hypothetical protein ARALYDRAFT_335156 [Arabidopsis lyrata subsp. lyrata]	315	317	1.00E-113	100.6	72.4	82.5	hypothetical protein ARALYDRAFT_335156	gbpln	Arabidopsis lyrata	AT1G19010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74860.1); Has 337 Blast hits to 320 proteins in 97 species: Archae - 0; Bacteria - 14; Metazoa - 153; Fungi - 26; Plants - 76; Viruses - 0; Other Eukaryotes - 68 (source: NCBI BLink). | chr1:6565616-6567354 FORWARD LENGTH=319	315	319	1.00E-109	101.3	71.4	81.9
Rsa1.0_00145.1.g6719.t1	gb|AFK49462.1| unknown [Medicago truncatula]	64	307	8.00E-12	479.7	57.8	67.2	unknown	gbpln	Medicago truncatula	AT5G52660.2 | Symbols: | Homeodomain-like superfamily protein | chr5:21359423-21362037 REVERSE LENGTH=331	64	331	1.00E-13	517.2	53.1	54.7
Rsa1.0_00146.1.g6720.t1	ref|NP_197755.1| MTN3-like protein [Arabidopsis thaliana] gi|75100713|sp|O82587.1|SWT12_ARATH RecName: Full=Bidirectional sugar transporter SWEET12; Short=AtSWEET12; AltName: Full=MtN3-like protein gi|3747111|gb|AAC64192.1| MTN3 homolog [Arabidopsis thaliana] gi|8809694|dbj|BAA97235.1| MtN3-like protein [Arabidopsis thaliana] gi|15982723|gb|AAL09814.1| putative MtN3 protein [Arabidopsis thaliana] gi|16323440|gb|AAL15214.1| putative MtN3 protein [Arabidopsis thaliana] gi|21358848|gb|AAM47150.1| putative MtN3 protein [Arabidopsis thaliana] gi|332005812|gb|AED93195.1| bidirectional sugar transporter SWEET12 [Arabidopsis thaliana]	288	285	1.00E-143	99.0	87.5	92.4	MTN3-like protein	gbpln	Arabidopsis thaliana	AT5G23660.1 | Symbols: MTN3, SWEET12, AtSWEET12 | homolog of Medicago truncatula MTN3 | chr5:7971936-7973796 REVERSE LENGTH=285	288	285	2.33E-156	99.0	87.5	92.4
Rsa1.0_00146.1.g6721.t1	ref|XP_002874143.1| sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319980|gb|EFH50402.1| sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata]	265	287	8.00E-83	108.3	72.8	80.0	sterile alpha motif domain-containing protein	gbpln	Arabidopsis lyrata	AT5G23680.1 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr5:7985573-7986460 REVERSE LENGTH=295	265	295	1.00E-81	111.3	71.3	78.9
Rsa1.0_00146.1.g6722.t1	emb|CAB75484.1| putative protein [Arabidopsis thaliana]	639	851	1.00E-110	133.2	34.9	47.6	putative protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	639	575	4.00E-69	90.0	21.9	33.6

Rsa1.0_00146.1.g6723.t1	ref|NP_197758.2| Polynucleotide adenylyltransferase family protein [Arabidopsis thaliana] gi|332005816|gb|AED93199.1| Polynucleotide adenylyltransferase family protein [Arabidopsis thaliana]	532	527	0	99.1	84.2	91.9	Polynucleotide adenylyltransferase family protein	gbpln	Arabidopsis thaliana	AT5G23690.1 | Symbols: | Polynucleotide adenylyltransferase family protein | chr5:7987664-7990466 FORWARD LENGTH=527	532	527	0	99.1	84.2	91.9
Rsa1.0_00146.1.g6724.t1	ref|XP_002874144.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319981|gb|EFH50403.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	234	230	7.00E-87	98.3	68.8	81.6	DNA binding protein	gbpln	Arabidopsis lyrata	AT5G23710.1 | Symbols: | DNA binding;DNA-directed RNA polymerases | chr5:7996528-7997220 REVERSE LENGTH=230	234	230	1.00E-88	98.3	65.0	81.2
Rsa1.0_00146.1.g6725.t1	ref|NP_001031933.1| dual specificity protein phosphatase family protein [Arabidopsis thaliana] gi|332005821|gb|AED93204.1| dual specificity protein phosphatase family protein [Arabidopsis thaliana]	961	920	0	95.7	84.5	89.7	dual specificity protein phosphatase family protein	gbpln	Arabidopsis thaliana	AT5G23720.3 | Symbols: PHS1 | dual specificity protein phosphatase family protein | chr5:7998506-8002594 FORWARD LENGTH=920	961	920	0	95.7	84.5	89.7
Rsa1.0_00146.1.g6726.t1	ref|XP_002869362.1| 40S ribosomal protein S11 [Arabidopsis lyrata subsp. lyrata] gi|297315198|gb|EFH45621.1| 40S ribosomal protein S11 [Arabidopsis lyrata subsp. lyrata]	376	159	1.00E-84	42.3	39.4	41.0	40S ribosomal protein S11	gbpln	Arabidopsis lyrata	AT5G23750.2 | Symbols: | Remorin family protein | chr5:8010004-8011453 REVERSE LENGTH=201	376	201	1.00E-82	53.5	48.7	50.5
Rsa1.0_00146.1.g6727.t1	ref|XP_002334885.1| predicted protein [Populus trichocarpa] gi|222832333|gb|EEE70810.1| predicted protein [Populus trichocarpa]	103	105	7.00E-26	101.9	62.1	67.0	predicted protein	gbpln	Populus trichocarpa	AT5G23760.1 | Symbols: | Copper transport protein family | chr5:8013242-8014129 REVERSE LENGTH=103	103	103	2.00E-24	100.0	70.9	72.8
Rsa1.0_00146.1.g6728.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00146.1.g6729.t1	gb|EOA20340.1| hypothetical protein CARUB_v10000648mg [Capsella rubella]	535	544	0	101.7	85.6	92.0	hypothetical protein CARUB_v10000648mg	gbpln	Capsella rubella	AT5G23850.1 | Symbols: | Arabidopsis thaliana protein of unknown function (DUF821) | chr5:8038126-8040741 FORWARD LENGTH=542	535	542	0	101.3	85.8	92.0
Rsa1.0_00146.1.g6730.t1	gb|EOA20636.1| hypothetical protein CARUB_v10000948mg [Capsella rubella]	449	449	0	100.0	99.3	100.0	hypothetical protein CARUB_v10000948mg	gbpln	Capsella rubella	AT5G23860.2 | Symbols: TUB8 | tubulin beta 8 | chr5:8042962-8044528 FORWARD LENGTH=449	449	449	0	100.0	99.3	99.8
Rsa1.0_00146.1.g6731.t1	ref|NP_197775.3| Pectinacetylesterase family protein [Arabidopsis thaliana] gi|10176854|dbj|BAB10060.1| pectinacetylesterase [Arabidopsis thaliana] gi|332005844|gb|AED93227.1| Pectinacetylesterase family protein [Arabidopsis thaliana]	426	415	0	97.4	86.6	91.8	Pectinacetylesterase family protein	gbpln	Arabidopsis thaliana	AT5G23870.1 | Symbols: | Pectinacetylesterase family protein | chr5:8046309-8049999 REVERSE LENGTH=415	426	415	0	97.4	86.6	91.8
Rsa1.0_00146.1.g6732.t1	gb|EOA20032.1| hypothetical protein CARUB_v10000306mg [Capsella rubella]	739	739	0	100.0	94.5	97.2	hypothetical protein CARUB_v10000306mg	gbpln	Capsella rubella	AT5G23880.1 | Symbols: EMB1265, CPSF100, ESP5, ATCPSF100 | cleavage and polyadenylation specificity factor 100 | chr5:8052550-8058147 FORWARD LENGTH=739	739	739	0	100.0	93.8	97.3
Rsa1.0_00146.1.g6733.t2	ref|NP_197777.1| uncharacterized protein [Arabidopsis thaliana] gi|10176856|dbj|BAB10062.1| unnamed protein product [Arabidopsis thaliana] gi|332005846|gb|AED93229.1| uncharacterized protein AT5G23890 [Arabidopsis thaliana]	938	946	0	100.9	77.4	85.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G23890.1 | Symbols: | LOCATED IN: mitochondrion, chloroplast thylakoid membrane, chloroplast, plastid, chloroplast envelope; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: S-layer homology domain (InterPro:IPR001119); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G52410.2); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8058789-8063005 FORWARD LENGTH=946	938	946	0	100.9	77.4	85.9
Rsa1.0_00146.1.g6734.t1	ref|XP_002877641.1| ATBBC1 [Arabidopsis lyrata subsp. lyrata] gi|297323479|gb|EFH53900.1| ATBBC1 [Arabidopsis lyrata subsp. lyrata]	231	206	2.00E-98	89.2	74.0	81.0	ATBBC1	gbpln	Arabidopsis lyrata	AT5G23900.1 | Symbols: | Ribosomal protein L13e family protein | chr5:8064176-8065081 REVERSE LENGTH=206	231	206	8.00E-95	89.2	71.0	74.0
Rsa1.0_00146.1.g6735.t1	ref|NP_001119268.1| uncharacterized protein [Arabidopsis thaliana] gi|332005848|gb|AED93231.1| uncharacterized protein AT5G23903 [Arabidopsis thaliana]	124	141	3.00E-25	113.7	56.5	67.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G23903.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G07680.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:8066419-8067037 FORWARD LENGTH=141	124	141	5.00E-28	113.7	56.5	67.7

Rsa1.0_00146.1.g6736.t2	ref|NP_197779.4| ATP binding microtubule motor family protein [Arabidopsis thaliana] gi|332005850|gb|AED93233.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]	642	701	0	109.2	68.2	78.5	ATP binding microtubule motor family protein	gbpln	Arabidopsis thaliana	AT5G23910.1 | Symbols: | ATP binding microtubule motor family protein | chr5:8068452-8072723 FORWARD LENGTH=701	642	701	0	109.2	68.2	78.5
Rsa1.0_00146.1.g6737.t1	gb|EOA20599.1| hypothetical protein CARUB_v10000909mg [Capsella rubella]	456	462	0	101.3	74.1	84.6	hypothetical protein CARUB_v10000909mg	gbpln	Capsella rubella	AT5G23930.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr5:8074625-8075998 REVERSE LENGTH=457	456	457	0	100.2	73.2	82.7
Rsa1.0_00146.1.g6738.t1	ref|XP_002874154.1| EMB3009 [Arabidopsis lyrata subsp. lyrata] gi|297319991|gb|EFH50413.1| EMB3009 [Arabidopsis lyrata subsp. lyrata]	464	474	0	102.2	84.3	89.9	EMB3009	gbpln	Arabidopsis lyrata	AT5G23940.1 | Symbols: EMB3009, PEL3, DCR | HXXXD-type acyl-transferase family protein | chr5:8076616-8079677 REVERSE LENGTH=484	464	484	0	104.3	84.1	89.4
Rsa1.0_00146.1.g6739.t1	gb|ACN58564.1| (E)-beta-caryophyllene synthase [Arabidopsis lyrata subsp. petraea]	430	545	1.00E-148	126.7	57.9	63.7	(E)-beta-caryophyllene synthase	gbpln	Arabidopsis lyrata	AT5G23960.1 | Symbols: ATTPS21, TPS21 | terpene synthase 21 | chr5:8092969-8095128 FORWARD LENGTH=547	430	547	1.00E-144	127.2	55.6	63.3
Rsa1.0_00146.1.g6740.t5	ref|XP_002874158.1| hypothetical protein ARALYDRAFT_489258 [Arabidopsis lyrata subsp. lyrata] gi|297319995|gb|EFH50417.1| hypothetical protein ARALYDRAFT_489258 [Arabidopsis lyrata subsp. lyrata]	301	442	4.00E-38	146.8	29.6	30.6	hypothetical protein ARALYDRAFT_489258	gbpln	Arabidopsis lyrata	AT5G24000.1 | Symbols: | Protein of unknown function (DUF819) | chr5:8110380-8112692 REVERSE LENGTH=443	301	443	9.00E-40	147.2	29.2	30.2
Rsa1.0_00146.1.g6741.t1	gb|AAB81881.1| putative MuDR-A-like transposon protein [Arabidopsis thaliana] gi|7267510|emb|CAB77993.1| putative MuDR-A-like transposon protein [Arabidopsis thaliana]	695	761	0	109.5	54.0	66.9	putative MuDR-A-like transposon protein	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	695	785	1.00E-17	112.9	17.7	31.5
Rsa1.0_00146.1.g6742.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00146.1.g6743.t1	gb|ACN58564.1| (E)-beta-caryophyllene synthase [Arabidopsis lyrata subsp. petraea]	549	545	0	99.3	78.5	85.8	(E)-beta-caryophyllene synthase	gbpln	Arabidopsis lyrata	AT5G23960.1 | Symbols: ATTPS21, TPS21 | terpene synthase 21 | chr5:8092969-8095128 FORWARD LENGTH=547	549	547	0	99.6	77.2	86.2
Rsa1.0_00146.1.g6744.t2	ref|XP_002874158.1| hypothetical protein ARALYDRAFT_489258 [Arabidopsis lyrata subsp. lyrata] gi|297319995|gb|EFH50417.1| hypothetical protein ARALYDRAFT_489258 [Arabidopsis lyrata subsp. lyrata]	459	442	0	96.3	84.1	89.3	hypothetical protein ARALYDRAFT_489258	gbpln	Arabidopsis lyrata	AT5G24000.1 | Symbols: | Protein of unknown function (DUF819) | chr5:8110380-8112692 REVERSE LENGTH=443	459	443	0	96.5	84.3	88.7
Rsa1.0_00146.1.g6745.t1	ref|NP_197789.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|75334039|sp|Q9FLW0.1|Y5241_ARATH RecName: Full=Probable receptor-like protein kinase At5g24010; Flags: Precursor gi|9758225|dbj|BAB08724.1| receptor-protein kinase-like protein [Arabidopsis thaliana] gi|332005862|gb|AED93245.1| putative receptor-like protein kinase [Arabidopsis thaliana]	837	824	0	98.4	82.8	89.8	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G24010.1 | Symbols: | Protein kinase superfamily protein | chr5:8113910-8116384 FORWARD LENGTH=824	837	824	0	98.4	82.8	89.8
Rsa1.0_00146.1.g6746.t1	ref|XP_002872087.1| hypothetical protein ARALYDRAFT_910418 [Arabidopsis lyrata subsp. lyrata] gi|297317924|gb|EFH48346.1| hypothetical protein ARALYDRAFT_910418 [Arabidopsis lyrata subsp. lyrata]	326	326	1.00E-164	100.0	95.4	97.2	hypothetical protein ARALYDRAFT_910418	gbpln	Arabidopsis lyrata	AT5G24020.1 | Symbols: MIND, ARC11, ATMIND1 | septum site-determining protein (MIND) | chr5:8116731-8117711 FORWARD LENGTH=326	326	326	1.00E-165	100.0	94.8	96.9
Rsa1.0_00146.1.g6747.t1	gb|EOA20155.1| hypothetical protein CARUB_v10000447mg [Capsella rubella]	636	637	0	100.2	83.3	89.6	hypothetical protein CARUB_v10000447mg	gbpln	Capsella rubella	AT5G24030.1 | Symbols: SLAH3 | SLAC1 homologue 3 | chr5:8118618-8120993 REVERSE LENGTH=635	636	635	0	99.8	82.7	88.8
Rsa1.0_00147.1.g6748.t1	gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]	252	198	5.00E-32	78.6	30.2	38.5	hypothetical protein 27.t00041	gbpln	Brassica oleracea	AT2G35280.1 | Symbols: | F-box family protein | chr2:14859709-14860200 REVERSE LENGTH=163	252	163	5.00E-11	64.7	11.1	17.9

<table>
<tr><td>Rsa1.0_00147.1.g6749.t1</td><td>ref|NP_192822.1| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana] gi|3513727|gb|AAC33943.1| contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] gi|4539358|emb|CAB40052.1| putative protein [Arabidopsis thaliana] gi|7267782|emb|CAB81185.1| putative protein [Arabidopsis thaliana] gi|18176148|gb|AAL59992.1| unknown protein [Arabidopsis thaliana] gi|19699309|gb|AAL91265.1| AT4g10840/F25I24_50 [Arabidopsis thaliana] gi|24030472|gb|AAN41387.1| unknown protein [Arabidopsis thaliana] gi|332657533|gb|AEE82933.1| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana]</td><td>601</td><td>609</td><td>0</td><td>101.3</td><td>95.7</td><td>97.8</td><td>tetratricopeptide repeat domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G10840.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:6656614-6659033 FORWARD LENGTH=609</td><td>601</td><td>609</td><td>0</td><td>101.3</td><td>95.7</td><td>97.8</td></tr>
<tr><td>Rsa1.0_00147.1.g6750.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00147.1.g6751.t1</td><td>pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)</td><td>1639</td><td>1365</td><td>0</td><td>83.3</td><td>33.7</td><td>47.1</td><td>RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)</td><td>----</td><td>----</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1639</td><td>575</td><td>1.00E-74</td><td>35.1</td><td>10.5</td><td>17.4</td></tr>
<tr><td>Rsa1.0_00147.1.g6752.t1</td><td>ref|XP_002872545.1| WRKY DNA-binding protein 41 [Arabidopsis lyrata subsp. lyrata] gi|297318382|gb|EFH48804.1| WRKY DNA-binding protein 41 [Arabidopsis lyrata subsp. lyrata]</td><td>316</td><td>313</td><td>1.00E-121</td><td>99.1</td><td>73.4</td><td>79.7</td><td>WRKY DNA-binding protein 41</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G11070.1 | Symbols: WRKY41, AtWRKY41 | WRKY family transcription factor | chr4:6759303-6760763 FORWARD LENGTH=313</td><td>316</td><td>313</td><td>1.00E-122</td><td>99.1</td><td>73.1</td><td>83.2</td></tr>
<tr><td>Rsa1.0_00147.1.g6753.t1</td><td>ref|XP_002872546.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318383|gb|EFH48805.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>246</td><td>289</td><td>1.00E-40</td><td>117.5</td><td>51.2</td><td>62.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G11100.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G03060.1); Has 6010 Blast hits to 4873 proteins in 584 species: Archae - 88; Bacteria - 744; Metazoa - 2092; Fungi - 437; Plants - 321; Viruses - 9; Other Eukaryotes - 2319 (source: NCBI BLink). | chr4:6769036-6769976 FORWARD LENGTH=287</td><td>246</td><td>287</td><td>4.00E-35</td><td>116.7</td><td>48.4</td><td>61.4</td></tr>
<tr><td>Rsa1.0_00147.1.g6754.t1</td><td>ref|XP_002867886.1| hypothetical protein ARALYDRAFT_492835 [Arabidopsis lyrata subsp. lyrata] gi|297313722|gb|EFH44145.1| hypothetical protein ARALYDRAFT_492835 [Arabidopsis lyrata subsp. lyrata]</td><td>286</td><td>286</td><td>1.00E-114</td><td>100.0</td><td>75.9</td><td>84.6</td><td>hypothetical protein ARALYDRAFT_492835</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G20330.1 | Symbols: | Transcription initiation factor TFIIE, beta subunit | chr4:10982683-10984039 REVERSE LENGTH=286</td><td>286</td><td>286</td><td>1.00E-109</td><td>100.0</td><td>74.1</td><td>83.9</td></tr>
<tr><td>Rsa1.0_00147.1.g6755.t2</td><td>gb|EOA20031.1| hypothetical protein CARUB_v10000305mg [Capsella rubella]</td><td>992</td><td>740</td><td>0</td><td>74.6</td><td>65.4</td><td>69.2</td><td>hypothetical protein CARUB_v10000305mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G11160.1 | Symbols: | Translation initiation factor 2, small GTP-binding protein | chr4:6803846-6806726 FORWARD LENGTH=743</td><td>992</td><td>743</td><td>0</td><td>74.9</td><td>64.8</td><td>68.5</td></tr>
<tr><td>Rsa1.0_00147.1.g6756.t1</td><td>gb|AAC25101.1| putative transposase [Arabidopsis thaliana]</td><td>706</td><td>729</td><td>0</td><td>103.3</td><td>65.7</td><td>80.3</td><td>putative transposase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15020.2 | Symbols: | hAT transposon superfamily | chr4:8575806-8578372 FORWARD LENGTH=768</td><td>706</td><td>768</td><td>2.00E-99</td><td>108.8</td><td>33.3</td><td>53.7</td></tr>
<tr><td>Rsa1.0_00147.1.g6757.t1</td><td>ref|XP_002890328.1| hypothetical protein ARALYDRAFT_472154 [Arabidopsis lyrata subsp. lyrata] gi|297336170|gb|EFH66587.1| hypothetical protein ARALYDRAFT_472154 [Arabidopsis lyrata subsp. lyrata]</td><td>247</td><td>244</td><td>6.00E-89</td><td>98.8</td><td>68.4</td><td>75.7</td><td>hypothetical protein ARALYDRAFT_472154</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G19320.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:6679327-6680178 FORWARD LENGTH=247</td><td>247</td><td>247</td><td>2.00E-88</td><td>100.0</td><td>66.8</td><td>73.3</td></tr>
<tr><td>Rsa1.0_00147.1.g6758.t1</td><td>ref|XP_002872559.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297318396|gb|EFH48818.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata]</td><td>187</td><td>184</td><td>7.00E-70</td><td>98.4</td><td>65.2</td><td>79.1</td><td>disease resistance-responsive family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G11210.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr4:6832691-6833245 FORWARD LENGTH=184</td><td>187</td><td>184</td><td>8.00E-71</td><td>98.4</td><td>68.4</td><td>80.7</td></tr>
</table>

Rsa1.0_00147.1.g6759.t2	ref|XP_002874679.1| hypothetical protein ARALYDRAFT_489958 [Arabidopsis lyrata subsp. lyrata] gi|297320516|gb|EFH50938.1| hypothetical protein ARALYDRAFT_489958 [Arabidopsis lyrata subsp. lyrata]	916	924	0	100.9	80.2	88.9	hypothetical protein ARALYDRAFT_489958	gbpln	Arabidopsis lyrata	AT4G11230.1 | Symbols: | Riboflavin synthase-like superfamily protein | chr4:6840791-6845587 REVERSE LENGTH=941	916	941	0	102.7	80.7	88.5
Rsa1.0_00147.1.g6760.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00147.1.g6761.t1	emb|CAF06581.1| SGT1-like protein [Brassica oleracea]	151	354	1.00E-27	234.4	43.0	45.7	SGT1-like protein	gbpln	Brassica oleracea	AT4G11260.1 | Symbols: ATSGT1B, ETA3, RPR1, EDM1, SGT1B | phosphatase-related | chr4:6851515-6853719 REVERSE LENGTH=358	151	358	3.00E-28	237.1	41.1	44.4
Rsa1.0_00147.1.g6762.t1	ref|XP_002874909.1| ATCUL1 [Arabidopsis lyrata subsp. lyrata] gi|297320746|gb|EFH51168.1| ATCUL1 [Arabidopsis lyrata subsp. lyrata]	702	738	0	105.1	71.4	84.0	ATCUL1	gbpln	Arabidopsis lyrata	AT4G02570.4 | Symbols: CUL1 | cullin 1 | chr4:1129315-1133435 FORWARD LENGTH=738	702	738	0	105.1	70.1	83.0
Rsa1.0_00147.1.g6763.t1	dbj|BAJ33824.1| unnamed protein product [Thellungiella halophila]	359	358	0	99.7	92.5	96.1	unnamed protein product	----	----	AT4G11260.1 | Symbols: ATSGT1B, ETA3, RPR1, EDM1, SGT1B | phosphatase-related | chr4:6851515-6853719 REVERSE LENGTH=358	359	358	1.00E-174	99.7	89.1	93.6
Rsa1.0_00147.1.g6764.t1	emb|CAA57724.1| 1-aminocyclopropane-1-carboxylate synthase [Brassica oleracea]	488	491	0	100.6	92.2	96.1	1-aminocyclopropane-1-carboxylate synthase	gbpln	Brassica oleracea	AT4G11280.1 | Symbols: ACS6, ATACS6 | 1-aminocyclopropane-1-carboxylic acid (acc) synthase 6 | chr4:6864168-6865922 FORWARD LENGTH=495	488	495	0	101.4	91.0	95.5
Rsa1.0_00147.1.g6765.t1	ref|XP_002878134.1| hypothetical protein ARALYDRAFT_486159 [Arabidopsis lyrata subsp. lyrata] gi|297323972|gb|EFH54393.1| hypothetical protein ARALYDRAFT_486159 [Arabidopsis lyrata subsp. lyrata]	549	561	0	102.2	74.7	79.2	hypothetical protein ARALYDRAFT_486159	gbpln	Arabidopsis lyrata	AT3G57150.1 | Symbols: NAP57, AtNAP57, CBF5, AtCBF5 | homologue of NAP57 | chr3:21154255-21155952 REVERSE LENGTH=565	549	565	0	102.9	74.0	78.3
Rsa1.0_00148.1.g6766.t1	ref|XP_002892309.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297338151|gb|EFH68568.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	157	484	6.00E-26	308.3	42.7	48.4	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT1G05840.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:1762843-1766150 REVERSE LENGTH=485	157	485	8.00E-28	308.9	39.5	44.6
Rsa1.0_00148.1.g6767.t1	ref|XP_002891911.1| thylakoid lumen 18.3 kDa protein [Arabidopsis lyrata subsp. lyrata] gi|297337753|gb|EFH68170.1| thylakoid lumen 18.3 kDa protein [Arabidopsis lyrata subsp. lyrata]	284	285	1.00E-135	100.4	89.4	95.8	thylakoid lumen 18.3 kDa protein	gbpln	Arabidopsis lyrata	AT1G54780.1 | Symbols: TLP18.3 | thylakoid lumen 18.3 kDa protein | chr1:20439533-20440953 FORWARD LENGTH=285	284	285	1.00E-137	100.4	90.5	94.7
Rsa1.0_00148.1.g6768.t1	gb|EOA34273.1| hypothetical protein CARUB_v10021787mg [Capsella rubella]	289	336	1.00E-158	116.3	92.7	97.9	hypothetical protein CARUB_v10021787mg	gbpln	Capsella rubella	AT1G54870.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:20459011-20460417 FORWARD LENGTH=335	289	335	1.00E-160	115.9	92.7	97.2
Rsa1.0_00148.1.g6769.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00148.1.g6770.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	722	1023	1.00E-152	141.7	38.8	51.5	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	722	575	4.00E-32	79.6	8.7	13.2
Rsa1.0_00148.1.g6771.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	172	1142	2.00E-14	664.0	24.4	32.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00148.1.g6772.t1	ref|XP_002891931.1| hypothetical protein ARALYDRAFT_474773 [Arabidopsis lyrata subsp. lyrata] gi|297337773|gb|EFH68190.1| hypothetical protein ARALYDRAFT_474773 [Arabidopsis lyrata subsp. lyrata]	454	472	0	104.0	81.1	91.0	hypothetical protein ARALYDRAFT_474773	gbpln	Arabidopsis lyrata	AT1G54990.1 | Symbols: AXR4, RGR, RGR1 | alpha/beta-Hydrolases superfamily protein | chr1:20511565-20513489 FORWARD LENGTH=473	454	473	0	104.2	80.2	90.7
Rsa1.0_00148.1.g6773.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00148.1.g6774.t1	gb|AAO03558.1| lipoxygenase 1 [Brassica napus]	71	857	5.00E-29	1207.0	88.7	88.7	lipoxygenase 1	gbpln	Brassica napus	AT1G55020.1 | Symbols: LOX1, ATLOX1 | lipoxygenase 1 | chr1:20525798-20530143 FORWARD LENGTH=859	71	859	1.00E-25	1209.9	76.1	80.3
Rsa1.0_00148.1.g6775.t2	gb|AAO03558.1| lipoxygenase 1 [Brassica napus]	797	857	0	107.5	96.7	97.5	lipoxygenase 1	gbpln	Brassica napus	AT1G55020.1 | Symbols: LOX1, ATLOX1 | lipoxygenase 1 | chr1:20525798-20530143 FORWARD LENGTH=859	797	859	0	107.8	92.3	96.1
Rsa1.0_00148.1.g6776.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00148.1.g6777.t1	ref|NP_176019.1| uncharacterized protein [Arabidopsis thaliana] gi|12321753|gb|AAG50913.1|AC069159_14 unknown protein [Arabidopsis thaliana] gi|110741625|dbj|BAE98760.1| hypothetical protein [Arabidopsis thaliana] gi|332195244|gb|AEE33365.1| uncharacterized protein AT1G56230 [Arabidopsis thaliana]	751	752	0	100.1	85.6	92.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G56230.1 | Symbols: | Protein of unknown function (DUF1399) | chr1:21046111-21048959 REVERSE LENGTH=752	751	752	0	100.1	85.6	92.1
Rsa1.0_00148.1.g6778.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00148.1.g6779.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1361	1475	0	108.4	58.5	73.2	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1361	1262	1.00E-172	92.7	20.6	25.8
Rsa1.0_00148.1.g6780.t1	gb|EOA14487.1| hypothetical protein CARUB_v10027702mg [Capsella rubella]	190	187	3.00E-39	98.4	45.3	60.5	hypothetical protein CARUB_v10027702mg	gbpln	Capsella rubella	AT5G46980.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19065453-19066007 REVERSE LENGTH=184	190	184	6.00E-41	96.8	45.3	60.0
Rsa1.0_00148.1.g6781.t1	ref|XP_002894632.1| phloem protein 2-B13 [Arabidopsis lyrata subsp. lyrata] gi|297340474|gb|EFH70891.1| phloem protein 2-B13 [Arabidopsis lyrata subsp. lyrata]	282	281	1.00E-133	99.6	84.0	89.7	phloem protein 2-B13	gbpln	Arabidopsis lyrata	AT1G56250.1 | Symbols: AtPP2-B14, PP2-B14 | phloem protein 2-B14 | chr1:21061746-21062844 REVERSE LENGTH=282	282	282	1.00E-132	100.0	82.3	89.0
Rsa1.0_00148.1.g6782.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00148.1.g6783.t1	ref|XP_002894633.1| hypothetical protein ARALYDRAFT_474790 [Arabidopsis lyrata subsp. lyrata] gi|297340475|gb|EFH70892.1| hypothetical protein ARALYDRAFT_474790 [Arabidopsis lyrata subsp. lyrata]	126	126	2.00E-55	100.0	84.9	91.3	hypothetical protein ARALYDRAFT_474790	gbpln	Arabidopsis lyrata	AT1G56260.1 | Symbols: | unknown protein; Has 32 Blast hits to 32 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:21064647-21065577 REVERSE LENGTH=127	126	127	2.00E-56	100.8	83.3	90.5
Rsa1.0_00149.1.g6784.t1	ref|XP_002891618.1| hypothetical protein ARALYDRAFT_474227 [Arabidopsis lyrata subsp. lyrata] gi|297337460|gb|EFH67877.1| hypothetical protein ARALYDRAFT_474227 [Arabidopsis lyrata subsp. lyrata]	81	353	8.00E-12	435.8	46.9	60.5	hypothetical protein ARALYDRAFT_474227	gbpln	Arabidopsis lyrata	AT1G51120.1 | Symbols: | AP2/B3 transcription factor family protein | chr1:18938091-18939149 FORWARD LENGTH=352	81	352	2.00E-13	434.6	44.4	61.7
Rsa1.0_00149.1.g6785.t2	gb|EOA38742.1| hypothetical protein CARUB_v10010894mg [Capsella rubella]	405	423	0	104.4	92.3	96.8	hypothetical protein CARUB_v10010894mg	gbpln	Capsella rubella	AT1G50710.1 | Symbols: | unknown protein; Has 109 Blast hits to 109 proteins in 44 species: Archae - 0; Bacteria - 2; Metazoa - 61; Fungi - 8; Plants - 36; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:18784719-18787615 REVERSE LENGTH=423	405	423	0	104.4	92.6	96.5
Rsa1.0_00149.1.g6786.t2	gb|EOA36626.1| hypothetical protein CARUB_v10011864mg [Capsella rubella]	474	510	0	107.6	86.9	92.4	hypothetical protein CARUB_v10011864mg	gbpln	Capsella rubella	AT1G47600.1 | Symbols: BGLU34, TGG4 | beta glucosidase 34 | chr1:17491771-17494589 FORWARD LENGTH=511	474	511	0	107.8	81.9	88.0
Rsa1.0_00149.1.g6787.t1	ref|XP_002891595.1| hypothetical protein ARALYDRAFT_474208 [Arabidopsis lyrata subsp. lyrata] gi|297337437|gb|EFH67854.1| hypothetical protein ARALYDRAFT_474208 [Arabidopsis lyrata subsp. lyrata]	1041	1047	0	100.6	84.8	91.2	hypothetical protein ARALYDRAFT_474208	gbpln	Arabidopsis lyrata	AT1G50840.1 | Symbols: POLGAMMA2 | polymerase gamma 2 | chr1:18839277-18844313 FORWARD LENGTH=1050	1041	1050	0	100.9	83.3	90.9
Rsa1.0_00149.1.g6788.t1	ref|NP_175204.1| putative F-box protein [Arabidopsis thaliana] gi|75266610|sp|Q9SXA0.1|FB42_ARATH RecName: Full=Putative F-box protein At1g47730 gi|5668790|gb|AAD46016.1|AC007519_1 F16N3.1 [Arabidopsis thaliana] gi|9802591|gb|AAF99793.1|AC012463_10 T2E6.20 [Arabidopsis thaliana] gi|332194084|gb|AEE32205.1| putative F-box protein [Arabidopsis thaliana]	389	391	1.00E-101	100.5	53.0	68.4	putative F-box protein	gbpln	Arabidopsis thaliana	AT1G47730.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:17563931-17565106 REVERSE LENGTH=391	389	391	1.00E-104	100.5	53.0	68.4
Rsa1.0_00149.1.g6789.t1	gb|AFK13834.1| putative PIF1 DNA helicase/replication protein A1-like protein [Beta vulgaris subsp. vulgaris]	139	2037	2.00E-25	1465.5	41.0	59.7	putative PIF1 DNA helicase/replication protein A1-like protein	gbpln	Beta vulgaris	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	139	566	3.00E-18	407.2	31.7	51.8
Rsa1.0_00149.1.g6790.t1	ref|XP_002894282.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297340124|gb|EFH70541.1| binding protein [Arabidopsis lyrata subsp. lyrata]	774	821	0	106.1	83.9	89.8	binding protein	gbpln	Arabidopsis lyrata	AT1G50890.1 | Symbols: | ARM repeat superfamily protein | chr1:18862295-18865752 REVERSE LENGTH=821	774	821	0	106.1	83.7	90.6
Rsa1.0_00149.1.g6791.t1	ref|XP_002894283.1| hypothetical protein ARALYDRAFT_474212 [Arabidopsis lyrata subsp. lyrata] gi|297340125|gb|EFH70542.1| hypothetical protein ARALYDRAFT_474212 [Arabidopsis lyrata subsp. lyrata]	318	500	4.00E-91	157.2	60.7	66.4	hypothetical protein ARALYDRAFT_474212	gbpln	Arabidopsis lyrata	AT1G50910.1 | Symbols: | unknown protein; Has 1105 Blast hits to 802 proteins in 217 species: Archae - 2; Bacteria - 177; Metazoa - 445; Fungi - 210; Plants - 58; Viruses - 6; Other Eukaryotes - 207 (source: NCBI BLink). | chr1:18867083-18869839 REVERSE LENGTH=500	318	500	1.00E-90	157.2	59.4	65.1

Rsa1.0_00149.1.g6792.t3	ref|XP_002891601.1| hypothetical protein ARALYDRAFT_474213 [Arabidopsis lyrata subsp. lyrata] gi|297337443|gb|EFH67860.1| hypothetical protein ARALYDRAFT_474213 [Arabidopsis lyrata subsp. lyrata]	179	195	2.00E-60	108.9	76.0	85.5	hypothetical protein ARALYDRAFT_474213	gbpln	Arabidopsis lyrata	AT1G50930.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G20557.1); Has 215 Blast hits to 213 proteins in 63 species: Archae - 0; Bacteria - 2; Metazoa - 83; Fungi - 10; Plants - 45; Viruses - 5; Other Eukaryotes - 70 (source: NCBI BLink). | chr1:18876898-18877706 FORWARD LENGTH=196	179	196	3.00E-54	109.5	74.9	83.8
Rsa1.0_00149.1.g6793.t1	ref|XP_002891603.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337445|gb|EFH67862.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	332	336	1.00E-159	101.2	80.7	89.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G50960.1 | Symbols: ATGA2OX7, GA2OX7 | gibberellin 2-oxidase 7 | chr1:18889549-18891719 FORWARD LENGTH=336	332	336	1.00E-160	101.2	80.1	89.5
Rsa1.0_00149.1.g6794.t2	ref|XP_002891604.1| hypothetical protein ARALYDRAFT_892049 [Arabidopsis lyrata subsp. lyrata] gi|297337446|gb|EFH67863.1| hypothetical protein ARALYDRAFT_892049 [Arabidopsis lyrata subsp. lyrata]	228	491	2.00E-13	215.4	24.1	33.8	hypothetical protein ARALYDRAFT_892049	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00149.1.g6795.t1	gb|EOA36310.1| hypothetical protein CARUB_v10010618mg [Capsella rubella]	133	133	4.00E-67	100.0	96.2	98.5	hypothetical protein CARUB_v10010618mg	gbpln	Capsella rubella	AT1G51060.1 | Symbols: HTA10 | histone H2A 10 | chr1:18926948-18927443 FORWARD LENGTH=132	133	132	8.00E-67	99.2	94.0	97.0
Rsa1.0_00149.1.g6796.t1	ref|XP_002891614.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297337456|gb|EFH67873.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	228	226	1.00E-107	99.1	86.4	91.7	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT1G51070.1 | Symbols: bHLH115 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:18928018-18929513 FORWARD LENGTH=226	228	226	1.00E-107	99.1	85.5	91.2
Rsa1.0_00149.1.g6797.t1	ref|XP_002891618.1| hypothetical protein ARALYDRAFT_474227 [Arabidopsis lyrata subsp. lyrata] gi|297337460|gb|EFH67877.1| hypothetical protein ARALYDRAFT_474227 [Arabidopsis lyrata subsp. lyrata]	355	353	1.00E-143	99.4	74.6	83.4	hypothetical protein ARALYDRAFT_474227	gbpln	Arabidopsis lyrata	AT1G51120.1 | Symbols: | AP2/B3 transcription factor family protein | chr1:18938091-18939149 FORWARD LENGTH=352	355	352	1.00E-145	99.2	73.5	83.9
Rsa1.0_00149.1.g6798.t1	gb|EOA40599.1| hypothetical protein CARUB_v10009330mg [Capsella rubella]	397	402	1.00E-168	101.3	78.8	86.4	hypothetical protein CARUB_v10009330mg	gbpln	Capsella rubella	AT1G51130.1 | Symbols: | Nse4, component of Smc5/6 DNA repair complex | chr1:18939480-18941560 REVERSE LENGTH=403	397	403	1.00E-168	101.5	76.6	85.9
Rsa1.0_00149.1.g6799.t1	gb|EOA39251.1| hypothetical protein CARUB_v10012248mg [Capsella rubella]	563	570	0	101.2	91.8	95.0	hypothetical protein CARUB_v10012248mg	gbpln	Capsella rubella	AT1G51190.1 | Symbols: PLT2 | Integrase-type DNA-binding superfamily protein | chr1:18977517-18980305 FORWARD LENGTH=568	563	568	0	100.9	90.9	93.8
Rsa1.0_00149.1.g6800.t1	gb|EOA39443.1| hypothetical protein CARUB_v10012613mg [Capsella rubella]	345	345	1.00E-168	100.0	88.7	92.5	hypothetical protein CARUB_v10012613mg	gbpln	Capsella rubella	AT1G51220.1 | Symbols: WIP5 | WIP domain protein 5 | chr1:18989925-18992034 REVERSE LENGTH=337	345	337	1.00E-159	97.7	82.9	87.8
Rsa1.0_00149.1.g6801.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00149.1.g6802.t1	gb|EOA26685.1| hypothetical protein CARUB_v10022767mg [Capsella rubella]	708	691	0	97.6	76.7	85.5	hypothetical protein CARUB_v10022767mg	gbpln	Capsella rubella	AT2G22410.1 | Symbols: SLO1 | SLOW GROWTH 1 | chr2:9509035-9511080 FORWARD LENGTH=681	708	681	0	96.2	74.6	83.1
Rsa1.0_00149.1.g6803.t2	gb|EOA37613.1| hypothetical protein CARUB_v10012002mg [Capsella rubella]	555	376	0	67.7	60.5	64.3	hypothetical protein CARUB_v10012002mg	gbpln	Capsella rubella	AT1G51260.1 | Symbols: LPAT3 | lysophosphatidyl acyltransferase 3 | chr1:19003460-19005512 REVERSE LENGTH=376	555	376	0	67.7	60.5	63.8
Rsa1.0_00149.1.g6804.t2	gb|AFW19998.1| aluminum-activated citrate transporter [Brassica napus]	518	519	0	100.2	94.2	96.1	aluminum-activated citrate transporter	gbpln	Brassica napus	AT1G51340.2 | Symbols: | MATE efflux family protein | chr1:19032021-19034681 FORWARD LENGTH=515	518	515	0	99.4	90.0	93.4
Rsa1.0_00149.1.g6805.t2	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00149.1.g6806.t1	ref|NP_683417.1| uncharacterized protein [Arabidopsis thaliana] gi|89001065|gb|ABD59122.1| At1g51355 [Arabidopsis thaliana] gi|332194534|gb|AEE32655.1| uncharacterized protein AT1G51355 [Arabidopsis thaliana]	116	116	7.00E-27	100.0	70.7	81.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G51355.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G20898.1); Has 52 Blast hits to 52 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:19041475-19041825 FORWARD LENGTH=116	116	116	1.00E-29	100.0	70.7	81.0
Rsa1.0_00149.1.g6807.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	321	1274	1.00E-43	396.9	32.7	48.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	321	303	1.00E-43	94.4	34.0	46.7

Rsa1.0_00149.1.g6808.t1	gb|EOA28714.1| hypothetical protein CARUB_v10024942mg [Capsella rubella]	206	270	4.00E-64	131.1	64.6	78.6	hypothetical protein CARUB_v10024942mg	gbpln	Capsella rubella	AT2G31670.1 | Symbols: | Stress responsive alpha-beta barrel domain protein | chr2:13472699-13473490 REVERSE LENGTH=263	206	263	3.00E-64	127.7	61.7	77.2
Rsa1.0_00149.1.g6809.t1	gb|EOA33008.1| hypothetical protein CARUB_v10016338mg [Capsella rubella]	412	430	0	104.4	90.0	93.4	hypothetical protein CARUB_v10016338mg	gbpln	Capsella rubella	AT5G01990.1 | Symbols: | Auxin efflux carrier family protein | chr5:377373-379600 REVERSE LENGTH=431	412	431	0	104.6	89.1	93.7
Rsa1.0_00149.1.g6810.t1	ref|XP_002891638.1| hypothetical protein ARALYDRAFT_314503 [Arabidopsis lyrata subsp. lyrata] gi|297337480|gb|EFH67897.1| hypothetical protein ARALYDRAFT_314503 [Arabidopsis lyrata subsp. lyrata]	318	796	1.00E-178	250.3	94.0	97.5	hypothetical protein ARALYDRAFT_314503	gbpln	Arabidopsis lyrata	AT1G51410.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:19059885-19061424 FORWARD LENGTH=325	318	325	1.00E-178	102.2	95.0	98.7
Rsa1.0_00149.1.g6811.t1	ref|XP_002894316.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340158|gb|EFH70575.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	423	424	0	100.2	85.3	92.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G51420.1 | Symbols: ATSPP1, SPP1 | sucrose-phosphatase 1 | chr1:19064852-19066704 REVERSE LENGTH=423	423	423	0	100.0	84.6	92.4
Rsa1.0_00149.1.g6812.t1	gb|EOA36626.1| hypothetical protein CARUB_v10011864mg [Capsella rubella]	441	510	0	115.6	73.0	77.8	hypothetical protein CARUB_v10011864mg	gbpln	Capsella rubella	AT1G47600.1 | Symbols: BGLU34, TGG4 | beta glucosidase 34 | chr1:17491771-17494589 FORWARD LENGTH=511	441	511	0	115.9	71.4	76.2
Rsa1.0_00149.1.g6813.t1	gb|EOA36626.1| hypothetical protein CARUB_v10011864mg [Capsella rubella]	483	510	0	105.6	82.6	87.6	hypothetical protein CARUB_v10011864mg	gbpln	Capsella rubella	AT1G47600.1 | Symbols: BGLU34, TGG4 | beta glucosidase 34 | chr1:17491771-17494589 FORWARD LENGTH=511	483	511	0	105.8	80.5	85.7
Rsa1.0_00149.1.g6814.t1	dbj|BAJ33599.1| unnamed protein product [Thellungiella halophila]	760	694	0	91.3	81.2	84.7	unnamed protein product	----	----	AT1G51500.1 | Symbols: CER5, D3, ABCG12, WBC12, ATWBC12 | ABC-2 type transporter family protein | chr1:19097967-19100972 REVERSE LENGTH=687	760	687	0	90.4	80.4	83.9
Rsa1.0_00150.1.g6815.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6816.t1	gb|AAF99736.1|AC004557_15 F17L21.21 [Arabidopsis thaliana]	181	360	1.00E-34	198.9	40.9	49.2	F17L21.21	gbpln	Arabidopsis thaliana	AT1G27420.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9519108-9520520 FORWARD LENGTH=346	181	346	4.00E-37	191.2	40.9	49.2
Rsa1.0_00150.1.g6817.t1	ref|NP_564283.1| uncharacterized protein [Arabidopsis thaliana] gi|14423400|gb|AAK62382.1|AF386937_1 Unknown protein [Arabidopsis thaliana] gi|24899683|gb|AAN65056.1| Unknown protein [Arabidopsis thaliana] gi|26452099|dbj|BAC43139.1| unknown protein [Arabidopsis thaliana] gi|332192708|gb|AEE30829.1| uncharacterized protein AT1G27435 [Arabidopsis thaliana]	61	81	7.00E-17	132.8	68.9	72.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G27435.1 | Symbols: | unknown protein; Has 16 Blast hits to 16 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:9527956-9528814 REVERSE LENGTH=81	61	81	1.00E-19	132.8	68.9	72.1
Rsa1.0_00150.1.g6818.t1	ref|XP_004139852.1| PREDICTED: uncharacterized protein LOC101219957 [Cucumis sativus]	854	766	0	89.7	42.2	57.4	PREDICTED: uncharacterized protein LOC101219957	gbpln	Cucumis sativus	AT5G33406.1 | Symbols: | hAT dimerisation domain-containing protein / transposase-related | chr5:12676126-12678403 REVERSE LENGTH=509	854	509	1.00E-123	59.6	25.5	30.0
Rsa1.0_00150.1.g6819.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	387	627	5.00E-57	162.0	35.4	52.7	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6820.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6821.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6822.t1	gb|EOA40460.1| hypothetical protein CARUB_v10009184mg [Capsella rubella]	834	434	0	52.0	46.8	47.4	hypothetical protein CARUB_v10009184mg	gbpln	Capsella rubella	AT1G27440.1 | Symbols: GUT2, IRX10, ATGUT1 | Exostosin family protein | chr1:9529265-9531213 REVERSE LENGTH=412	834	412	0	49.4	46.2	47.2
Rsa1.0_00150.1.g6823.t1	ref|XP_002890730.1| lecithin:cholesterol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336572|gb|EFH66989.1| lecithin:cholesterol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	443	432	0	97.5	79.7	87.8	lecithin:cholesterol acyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G27480.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:9544607-9546168 FORWARD LENGTH=432	443	432	0	97.5	78.8	86.2
Rsa1.0_00150.1.g6824.t1	gb|EOA37527.1| hypothetical protein CARUB_v10011729mg [Capsella rubella]	174	174	1.00E-95	100.0	96.0	97.7	hypothetical protein CARUB_v10011729mg	gbpln	Capsella rubella	AT1G27530.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ubiquitin-conjugating enzyme/RWD-like (InterPro:IPR016135), Ubiquitin-fold modifier-conjugating enzyme 1 (InterPro:IPR014806); Has 269 Blast hits to 269 proteins in 110 species: Archae - 0; Bacteria - 0; Metazoa - 175; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink). | chr1:9562761-9563887 REVERSE LENGTH=174	174	174	5.00E-97	100.0	94.8	97.1
Rsa1.0_00150.1.g6825.t3	gb|EOA37898.1| hypothetical protein CARUB_v10009365mg [Capsella rubella]	417	395	1.00E-177	94.7	72.2	81.5	hypothetical protein CARUB_v10009365mg	gbpln	Capsella rubella	AT1G27600.2 | Symbols: IRX9-L, I9H | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:9604083-9605881 REVERSE LENGTH=394	417	394	1.00E-178	94.5	71.7	79.9

Rsa1.0_00150.1.g6826.t1	dbj|BAJ34257.1| unnamed protein product [Thellungiella halophila]	239	308	3.00E-97	128.9	91.6	94.1	unnamed protein product	----	----	AT1G27650.2 | Symbols: ATU2AF35A | U2 snRNP auxiliary factor small subunit, putative | chr1:9615302-9616042 FORWARD LENGTH=246	239	246	2.00E-93	102.9	86.2	89.1
Rsa1.0_00150.1.g6827.t4	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	460	703	1.00E-101	152.8	44.1	50.7	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6828.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6829.t1	ref|XP_004246844.1| PREDICTED: uncharacterized protein LOC101268024 [Solanum lycopersicum]	290	584	4.00E-37	201.4	31.0	43.4	PREDICTED: uncharacterized protein LOC101268024	gbpln	Solanum lycopersicum	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6830.t1	#	#	#	#	#	#	#	–	----	----	AT1G27710.2 | Symbols: | Glycine-rich protein family | chr1:9642550-9643188 FORWARD LENGTH=206	155	206	6.00E-11	132.9	26.5	28.4
Rsa1.0_00150.1.g6831.t4	ref|NP_174093.3| TBP-associated factor 4B [Arabidopsis thaliana] gi|38490051|gb|AAR21619.1| TATA-binding protein associated factor 4 [Arabidopsis thaliana] gi|332192748|gb|AEE30869.1| TBP-associated factor 4B [Arabidopsis thaliana]	716	720	1.00E-134	100.6	37.8	44.8	TBP-associated factor 4B	gbpln	Arabidopsis thaliana	AT1G27720.1 | Symbols: TAF4, TAF4B | TBP-associated factor 4B | chr1:9643351-9647376 REVERSE LENGTH=720	716	720	1.00E-137	100.6	37.8	44.8
Rsa1.0_00150.1.g6832.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6833.t1	ref|NP_174109.2| ATP-dependent DNA helicase Q-like 5 [Arabidopsis thaliana] gi|298289257|sp|Q0WVW7.2|RQL5_ARATH RecName: Full=ATP-dependent DNA helicase Q-like 5; AltName: Full=RecQ-like protein 5; Short=AtRecQ5; Short=AtRecQl5 gi|332192766|gb|AEE30887.1| ATP-dependent DNA helicase Q-like 5 [Arabidopsis thaliana]	904	911	0	100.8	83.0	88.8	ATP-dependent DNA helicase Q-like 5	gbpln	Arabidopsis thaliana	AT1G27880.1 | Symbols: | DEAD/DEAH box RNA helicase family protein | chr1:9708940-9713901 FORWARD LENGTH=911	904	911	0	100.8	83.0	88.8
Rsa1.0_00150.1.g6834.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	635	1486	1.00E-158	234.0	47.4	58.7	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	635	1262	6.00E-87	198.7	28.7	42.0
Rsa1.0_00150.1.g6835.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6836.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	2135	1501	0	70.3	36.6	46.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	2135	1262	1.00E-135	59.1	11.3	16.2
Rsa1.0_00150.1.g6837.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	537	414	1.00E-75	77.1	28.7	32.2	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00150.1.g6838.t1	gb|ABL97965.1| putative nuclear transport factor 2 [Brassica rapa]	123	123	2.00E-66	100.0	99.2	99.2	putative nuclear transport factor 2	gbpln	Brassica rapa	AT1G27970.1 | Symbols: NTF2B | nuclear transport factor 2B | chr1:9746921-9747787 FORWARD LENGTH=126	123	126	6.00E-68	102.4	96.7	99.2
Rsa1.0_00150.1.g6839.t1	ref|XP_002893503.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297339345|gb|EFH69762.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	364	428	1.00E-124	117.6	67.9	75.0	zinc finger (B-box type) family protein	gbpln	Arabidopsis lyrata	AT1G28050.1 | Symbols: | B-box type zinc finger protein with CCT domain | chr1:9775768-9777657 REVERSE LENGTH=433	364	433	1.00E-113	119.0	66.8	74.5
Rsa1.0_00151.1.g6840.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00151.1.g6841.t2	dbj|BAB02733.1| transposase-like protein [Arabidopsis thaliana]	452	554	3.00E-84	122.6	48.0	61.1	transposase-like protein	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	452	696	4.00E-17	154.0	16.6	27.9
Rsa1.0_00151.1.g6842.t3	ref|XP_002885200.1| methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331040|gb|EFH61459.1| methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	702	743	0	105.8	77.6	86.2	methyltransferase family protein	gbpln	Arabidopsis lyrata	AT3G17310.1 | Symbols: DRM3, AtDRM3 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:5909294-5912838 REVERSE LENGTH=710	702	710	0	101.1	77.2	85.6
Rsa1.0_00151.1.g6843.t1	ref|XP_002883056.1| hypothetical protein ARALYDRAFT_341872 [Arabidopsis lyrata subsp. lyrata] gi|297328896|gb|EFH59315.1| hypothetical protein ARALYDRAFT_341872 [Arabidopsis lyrata subsp. lyrata]	295	299	1.00E-113	101.4	66.4	77.6	hypothetical protein ARALYDRAFT_341872	gbpln	Arabidopsis lyrata	AT3G17350.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G50290.1); Has 203 Blast hits to 203 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 203; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5934111-5935276 FORWARD LENGTH=301	295	301	1.00E-113	102.0	66.8	76.3

Rsa1.0_00151.1.g6844.t1	ref|XP_002883056.1| hypothetical protein ARALYDRAFT_341872 [Arabidopsis lyrata subsp. lyrata] gi|297328896|gb|EFH59315.1| hypothetical protein ARALYDRAFT_341872 [Arabidopsis lyrata subsp. lyrata]	295	299	1.00E-110	101.4	66.1	77.6	hypothetical protein ARALYDRAFT_341872	gbpln	Arabidopsis lyrata	AT3G17350.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G50290.1); Has 203 Blast hits to 203 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 203; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5934111-5935276 FORWARD LENGTH=301	295	301	1.00E-108	102.0	65.4	75.6
Rsa1.0_00151.1.g6845.t1	gb|EOA29710.1| hypothetical protein CARUB_v10012795mg [Capsella rubella]	1930	2139	0	110.8	56.1	62.4	hypothetical protein CARUB_v10012795mg	gbpln	Capsella rubella	AT3G17360.1 | Symbols: POK1 | phragmoplast orienting kinesin 1 | chr3:5936108-5946205 FORWARD LENGTH=2066	1930	2066	0	107.0	51.2	56.7
Rsa1.0_00151.1.g6846.t1	ref|XP_002883060.1| hypothetical protein ARALYDRAFT_479217 [Arabidopsis lyrata subsp. lyrata] gi|297328900|gb|EFH59319.1| hypothetical protein ARALYDRAFT_479217 [Arabidopsis lyrata subsp. lyrata]	364	363	0	99.7	94.2	96.7	hypothetical protein ARALYDRAFT_479217	gbpln	Arabidopsis lyrata	AT3G17410.1 | Symbols: | Protein kinase superfamily protein | chr3:5956601-5958882 FORWARD LENGTH=364	364	364	0	100.0	91.5	94.8
Rsa1.0_00151.1.g6847.t2	gb|EOA30510.1| hypothetical protein CARUB_v10013633mg [Capsella rubella]	455	467	0	102.6	85.7	92.3	hypothetical protein CARUB_v10013633mg	gbpln	Capsella rubella	AT3G17420.1 | Symbols: GPK1 | glyoxysomal protein kinase 1 | chr3:5959462-5961313 REVERSE LENGTH=467	455	467	0	102.6	85.9	91.6
Rsa1.0_00151.1.g6848.t1	gb|EOA30815.1| hypothetical protein CARUB_v10013966mg [Capsella rubella]	316	375	7.00E-28	118.7	19.9	20.3	hypothetical protein CARUB_v10013966mg	gbpln	Capsella rubella	AT3G17430.1 | Symbols: | Nucleotide-sugar transporter family protein | chr3:5966597-5968962 FORWARD LENGTH=375	316	375	4.00E-30	118.7	19.6	20.3
Rsa1.0_00151.1.g6849.t1	gb|EOA29624.1| hypothetical protein CARUB_v10014402mg [Capsella rubella]	271	267	1.00E-138	98.5	91.9	95.6	hypothetical protein CARUB_v10014402mg	gbpln	Capsella rubella	AT3G17440.1 | Symbols: NPSN13, ATNPSN13 | novel plant snare 13 | chr3:5969909-5972290 REVERSE LENGTH=269	271	269	1.00E-140	99.3	91.5	96.3
Rsa1.0_00151.1.g6850.t1	gb|EOA29978.1| hypothetical protein CARUB_v10013083mg [Capsella rubella]	202	707	6.00E-12	350.0	17.8	20.8	hypothetical protein CARUB_v10013083mg	gbpln	Capsella rubella	AT3G17450.1 | Symbols: | hAT dimerisation domain-containing protein | chr3:5972793-5975684 REVERSE LENGTH=877	202	877	5.00E-14	434.2	17.3	20.8
Rsa1.0_00151.1.g6851.t1	ref|NP_188372.1| PHD finger family protein [Arabidopsis thaliana] gi|11994684|dbj|BAB02922.1| unnamed protein product [Arabidopsis thaliana] gi|332642435|gb|AEE75956.1| PHD finger family protein [Arabidopsis thaliana]	199	198	1.00E-35	99.5	46.2	58.3	PHD finger family protein	gbpln	Arabidopsis thaliana	AT3G17460.1 | Symbols: | PHD finger family protein | chr3:5976949-5977545 REVERSE LENGTH=198	199	198	4.00E-38	99.5	46.2	58.3
Rsa1.0_00151.1.g6852.t1	gb|EOA31043.1| hypothetical protein CARUB_v10014193mg [Capsella rubella]	324	323	1.00E-162	99.7	88.0	91.4	hypothetical protein CARUB_v10014193mg	gbpln	Capsella rubella	AT3G17465.1 | Symbols: RPL3P | ribosomal protein L3 plastid | chr3:5978059-5979572 REVERSE LENGTH=324	324	324	1.00E-159	100.0	85.8	89.8
Rsa1.0_00151.1.g6853.t1	ref|NP_188377.1| F-box associated protein [Arabidopsis thaliana] gi|332642440|gb|AEE75961.1| F-box associated protein [Arabidopsis thaliana]	397	438	2.00E-72	110.3	45.1	59.7	F-box associated protein	gbpln	Arabidopsis thaliana	AT3G17500.1 | Symbols: | F-box family protein | chr3:5986685-5988498 FORWARD LENGTH=438	397	438	6.00E-75	110.3	45.1	59.7
Rsa1.0_00151.1.g6854.t1	gb|EOA31989.1| hypothetical protein CARUB_v10015229mg, partial [Capsella rubella]	357	350	2.00E-57	98.0	42.9	58.3	hypothetical protein CARUB_v10015229mg, partial	gbpln	Capsella rubella	AT3G17500.1 | Symbols: | F-box family protein | chr3:5986685-5988498 FORWARD LENGTH=438	357	438	1.00E-64	122.7	45.4	60.5
Rsa1.0_00151.1.g6855.t1	ref|XP_002883067.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297328907|gb|EFH59326.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	392	385	5.00E-74	98.2	44.6	62.0	F-box family protein	gbpln	Arabidopsis lyrata	AT3G17500.1 | Symbols: | F-box family protein | chr3:5986685-5988498 FORWARD LENGTH=438	392	438	3.00E-75	111.7	45.9	60.7
Rsa1.0_00151.1.g6856.t2	ref|NP_566580.1| CBL-interacting serine/threonine-protein kinase 1 [Arabidopsis thaliana] gi|56748824|sp|Q8RWC9.2|CIPK1_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 1; AltName: Full=SNF1-related kinase 3.16; AltName: Full=SOS2-like protein kinase PKS13 gi|332642442|gb|AEE75963.1| CBL-interacting serine/threonine-protein kinase 1 [Arabidopsis thaliana]	661	444	0	67.2	61.3	64.6	CBL-interacting serine/threonine-protein kinase 1	gbpln	Arabidopsis thaliana	AT3G17510.1 | Symbols: CIPK1, SnRK3.16 | CBL-interacting protein kinase 1 | chr3:5989309-5992627 REVERSE LENGTH=444	661	444	0	67.2	61.3	64.6
Rsa1.0_00151.1.g6857.t1	ref|XP_002885215.1| late embryogenesis abundant domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297331055|gb|EFH61474.1| late embryogenesis abundant domain-containing protein [Arabidopsis lyrata subsp. lyrata]	296	299	1.00E-102	101.0	77.7	91.2	late embryogenesis abundant domain-containing protein	gbpln	Arabidopsis lyrata	AT3G17520.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr3:5999462-6000358 REVERSE LENGTH=298	296	298	1.00E-104	100.7	78.4	89.9

Rsa1.0_00151.1.g6858.t1	gb|EOA32842.1| hypothetical protein CARUB_v10016156mg [Capsella rubella]	80	80	2.00E-32	100.0	85.0	92.5	hypothetical protein CARUB_v10016156mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00151.1.g6859.t1	gb|AAD21699.1| Contains reverse transcriptase domain (rvt) PF|00078 [Arabidopsis thaliana]	146	1253	3.00E-32	858.2	48.6	67.1	Contains reverse transcriptase domain (rvt) PF|00078	gbpln	Arabidopsis thaliana	AT4G10613.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:6561039-6561479 FORWARD LENGTH=146	146	146	2.00E-34	100.0	47.3	61.6
Rsa1.0_00151.1.g6860.t1	ref|XP_002883069.1| hypothetical protein ARALYDRAFT_898099 [Arabidopsis lyrata subsp. lyrata] gi|297328909|gb|EFH59328.1| hypothetical protein ARALYDRAFT_898099 [Arabidopsis lyrata subsp. lyrata]	82	80	4.00E-36	97.6	90.2	92.7	hypothetical protein ARALYDRAFT_898099	gbpln	Arabidopsis lyrata	AT3G17580.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G48330.1); Has 40 Blast hits to 40 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6015276-6015518 FORWARD LENGTH=80	82	80	5.00E-34	97.6	80.5	82.9
Rsa1.0_00151.1.g6861.t1	ref|NP_001189918.1| chromatin structure-remodeling complex protein BSH [Arabidopsis thaliana] gi|332642451|gb|AEE75972.1| chromatin structure-remodeling complex protein BSH [Arabidopsis thaliana]	241	242	1.00E-124	100.4	90.0	95.9	chromatin structure-remodeling complex protein BSH	gbpln	Arabidopsis thaliana	AT3G17590.2 | Symbols: BSH | transcription regulatory protein SNF5, putative (BSH) | chr3:6017313-6019591 REVERSE LENGTH=242	241	242	1.00E-127	100.4	90.0	95.9
Rsa1.0_00151.1.g6862.t1	ref|XP_002885218.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331058|gb|EFH61477.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	159	158	3.00E-67	99.4	78.6	81.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G17600.1 | Symbols: IAA31 | indole-3-acetic acid inducible 31 | chr3:6020281-6021040 REVERSE LENGTH=158	159	158	1.00E-69	99.4	78.6	81.8
Rsa1.0_00151.1.g6863.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1474	1485	0	100.7	44.8	61.2	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	AT1G47350.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:17358447-17360722 REVERSE LENGTH=528	1474	528	1.00E-25	35.8	4.3	5.8
Rsa1.0_00152.1.g6864.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	230	1555	1.00E-65	676.1	55.2	69.1	disease resistance protein	gbpln	Brassica rapa	AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315	230	315	3.00E-24	137.0	32.6	42.2
Rsa1.0_00152.1.g6865.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00152.1.g6866.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00152.1.g6867.t1	ref|XP_002876738.1| 60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata] gi|297322576|gb|EFH52997.1| 60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata]	242	242	1.00E-131	100.0	96.3	97.1	60S ribosomal protein L7	gbpln	Arabidopsis lyrata	AT2G01250.1 | Symbols: | Ribosomal protein L30/L7 family protein | chr2:132943-134264 REVERSE LENGTH=242	242	242	1.00E-133	100.0	95.9	97.1
Rsa1.0_00152.1.g6868.t1	sp|Q9ZU43.2|RTNLO_ARATH RecName: Full=Reticulon-like protein B15; Short=AtRTNLB15	192	191	7.00E-65	99.5	70.8	83.3	RecName: Full=Reticulon-like protein B15; Short=AtRTNLB15	----	----	AT2G01240.1 | Symbols: | Reticulon family protein | chr2:128440-129256 REVERSE LENGTH=160	192	160	3.00E-36	83.3	38.0	47.9
Rsa1.0_00152.1.g6869.t1	sp|Q9ZU43.2|RTNLO_ARATH RecName: Full=Reticulon-like protein B15; Short=AtRTNLB15	323	191	2.00E-50	59.1	35.9	44.6	RecName: Full=Reticulon-like protein B15; Short=AtRTNLB15	----	----	AT2G01240.1 | Symbols: | Reticulon family protein | chr2:128440-129256 REVERSE LENGTH=160	323	160	2.00E-25	49.5	17.3	23.8
Rsa1.0_00152.1.g6870.t1	gb|EOA33848.1| hypothetical protein CARUB_v10021338mg [Capsella rubella]	451	659	3.00E-59	146.1	38.4	52.8	hypothetical protein CARUB_v10021338mg	gbpln	Capsella rubella	AT2G02030.1 | Symbols: | F-box family protein | chr2:482335-483829 FORWARD LENGTH=334	451	334	7.00E-37	74.1	22.4	37.7
Rsa1.0_00152.1.g6871.t1	gb|AAL86294.1| putative amino acid or GABA permease [Arabidopsis thaliana]	545	516	0	94.7	86.6	90.5	putative amino acid or GABA permease	gbpln	Arabidopsis thaliana	AT2G01170.1 | Symbols: BAT1 | bidirectional amino acid transporter 1 | chr2:102364-104462 REVERSE LENGTH=516	545	516	0	94.7	86.4	90.5
Rsa1.0_00152.1.g6872.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00152.1.g6873.t1	ref|NP_565253.1| putative E3 ubiquitin-protein ligase RHA2B [Arabidopsis thaliana] gi|51316550|sp|Q9ZU51.2|RHA2B_ARATH RecName: Full=Probable E3 ubiquitin-protein ligase RHA2B; AltName: Full=RING-H2 zinc finger protein RHA2b gi|3790571|gb|AAC68672.1| RING-H2 finger protein RHA2b [Arabidopsis thaliana] gi|20197589|gb|AAD14516.2| RING-H2 finger protein RHA2b [Arabidopsis thaliana] gi|98960889|gb|ABF58928.1| At2g01150 [Arabidopsis thaliana] gi|330250313|gb|AEC05407.1| putative E3 ubiquitin-protein ligase RHA2B [Arabidopsis thaliana]	153	147	4.00E-48	96.1	69.9	76.5	putative E3 ubiquitin-protein ligase RHA2B	gbpln	Arabidopsis thaliana	AT2G01150.1 | Symbols: RHA2B | RING-H2 finger protein 2B | chr2:100703-101146 FORWARD LENGTH=147	153	147	1.00E-50	96.1	69.9	76.5
Rsa1.0_00152.1.g6874.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00152.1.g6875.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	88	1231	1.00E-15	1398.9	50.0	62.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00152.1.g6876.t1	ref|NP_178224.1| fructose-bisphosphate aldolase, class I [Arabidopsis thaliana] gi|75268018|sp|Q9ZU52.1|ALFC3_ARATH RecName: Full=Probable fructose-bisphosphate aldolase 3, chloroplastic; Flags: Precursor gi|11762176|gb|AAG40366.1|AF325014_1 At2g01140 [Arabidopsis thaliana] gi|4262250|gb|AAD14543.1| putative aldolase [Arabidopsis thaliana] gi|21592330|gb|AAM64281.1| putative aldolase [Arabidopsis thaliana] gi|330250312|gb|AEC05406.1| fructose-bisphosphate aldolase 3 [Arabidopsis thaliana]	391	391	0	100.0	94.4	96.7	fructose-bisphosphate aldolase, class I	gbpln	Arabidopsis thaliana	AT2G01140.1 | Symbols: | Aldolase superfamily protein | chr2:95006-96491 REVERSE LENGTH=391	391	391	0	100.0	94.4	96.7
Rsa1.0_00152.1.g6877.t2	gb|EOA25931.1| hypothetical protein CARUB_v10019313mg [Capsella rubella]	179	417	4.00E-46	233.0	60.3	66.5	hypothetical protein CARUB_v10019313mg	gbpln	Capsella rubella	AT2G01120.1 | Symbols: ORC4, ATORC4 | origin recognition complex subunit 4 | chr2:85444-88027 FORWARD LENGTH=418	179	418	4.00E-45	233.5	58.1	64.2
Rsa1.0_00152.1.g6878.t7	gb|EOA24317.1| hypothetical protein CARUB_v10017557mg [Capsella rubella]	424	347	1.00E-164	81.8	71.9	75.7	hypothetical protein CARUB_v10017557mg	gbpln	Capsella rubella	AT2G01110.1 | Symbols: APG2, UNE3, PGA2, TATC | Sec-independent periplasmic protein translocase | chr2:83786-85088 REVERSE LENGTH=340	424	340	1.00E-159	80.2	70.8	74.3
Rsa1.0_00152.1.g6879.t1	gb|AAM62951.1| unknown [Arabidopsis thaliana]	523	543	0	103.8	79.5	87.8	unknown	gbpln	Arabidopsis thaliana	AT2G13690.1 | Symbols: | PRLI-interacting factor, putative | chr2:5706704-5708895 REVERSE LENGTH=544	523	544	0	104.0	79.2	87.2
Rsa1.0_00152.1.g6880.t1	gb|EOA30667.1| hypothetical protein CARUB_v10013805mg [Capsella rubella]	382	417	2.00E-93	109.2	52.4	67.0	hypothetical protein CARUB_v10013805mg	gbpln	Capsella rubella	AT3G20620.1 | Symbols: | F-box family protein-related | chr3:7198708-7199969 REVERSE LENGTH=391	382	391	2.00E-93	102.4	51.0	65.2
Rsa1.0_00152.1.g6881.t1	ref|NP_565251.1| uncharacterized protein [Arabidopsis thaliana] gi|30677872|ref|NP_849919.1| uncharacterized protein [Arabidopsis thaliana] gi|42570625|ref|NP_973386.1| uncharacterized protein [Arabidopsis thaliana] gi|6598625|gb|AAF18658.1| expressed protein [Arabidopsis thaliana] gi|18086561|gb|AAL57705.1| At2g01100/F23H14.7 [Arabidopsis thaliana] gi|21593516|gb|AAM65483.1| unknown [Arabidopsis thaliana] gi|21928015|gb|AAM78036.1| At2g01100/F23H14.7 [Arabidopsis thaliana] gi|222424050|dbj|BAH19986.1| AT2G01100 [Arabidopsis thaliana] gi|330250305|gb|AEC05399.1| uncharacterized protein AT2G01100 [Arabidopsis thaliana] gi|330250306|gb|AEC05400.1| uncharacterized protein AT2G01100 [Arabidopsis thaliana] gi|330250307|gb|AEC05401.1| uncharacterized protein AT2G01100 [Arabidopsis thaliana]	251	247	3.00E-58	98.4	64.9	77.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G01100.3 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:82245-82988 FORWARD LENGTH=247	251	247	9.00E-61	98.4	64.9	77.3
Rsa1.0_00152.1.g6882.t1	gb|AAM63085.1| putative ubiquinol--cytochrome-c reductase [Arabidopsis thaliana]	103	69	4.00E-28	67.0	59.2	63.1	putative ubiquinol--cytochrome-c reductase	gbpln	Arabidopsis thaliana	AT1G15120.1 | Symbols: | Ubiquinol-cytochrome C reductase hinge protein | chr1:5203091-5203897 FORWARD LENGTH=69	103	69	1.00E-30	67.0	59.2	63.1
Rsa1.0_00152.1.g6883.t1	gb|EOA36212.1| hypothetical protein CARUB_v10010136mg [Capsella rubella]	249	243	4.00E-58	97.6	59.0	69.5	hypothetical protein CARUB_v10010136mg	gbpln	Capsella rubella	AT1G15190.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr1:5227275-5228021 FORWARD LENGTH=248	249	248	3.00E-60	99.6	58.2	70.3
Rsa1.0_00152.1.g6884.t1	gb|AAK55661.1|AF378858_1 At2g01080/F23H14.5 [Arabidopsis thaliana] gi|16323356|gb|AAL15391.1| At2g01080/F23H14.5 [Arabidopsis thaliana]	299	231	2.00E-79	77.3	67.9	72.6	At2g01080/F23H14.5	gbpln	Arabidopsis thaliana	AT2G01080.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:78038-79176 FORWARD LENGTH=231	299	231	1.00E-81	77.3	67.2	71.9
Rsa1.0_00152.1.g6885.t1	gb|AAF18655.1| unknown protein [Arabidopsis thaliana]	122	467	1.00E-25	382.8	54.9	63.1	unknown protein	gbpln	Arabidopsis thaliana	AT2G01070.1 | Symbols: | Lung seven transmembrane receptor family protein | chr2:75596-77625 FORWARD LENGTH=496	122	496	1.00E-27	406.6	54.1	59.0
Rsa1.0_00152.1.g6886.t1	gb|EOA24516.1| hypothetical protein CARUB_v10017769mg [Capsella rubella]	288	286	1.00E-150	99.3	93.1	95.5	hypothetical protein CARUB_v10017769mg	gbpln	Capsella rubella	AT2G01060.1 | Symbols: | myb-like HTH transcriptional regulator family protein | chr2:73456-74902 REVERSE LENGTH=286	288	286	1.00E-150	99.3	91.7	94.8

Rsa1.0_00152.1.g6887.t1	ref|NP_568688.1| alpha−1,4−galacturonosyltransferase [Arabidopsis thaliana] gi|75163841|sp|Q93ZX7.1|GAUT4_ARATH RecName: Full=Probable galacturonosyltransferase 4; AltName: Full=Like glycosyl transferase 3 gi|15810327|gb|AAL07051.1| unknown protein [Arabidopsis thaliana] gi|20259235|gb|AAM14333.1| unknown protein [Arabidopsis thaliana] gi|332008188|gb|AED95571.1| probable galacturonosyltransferase 4 [Arabidopsis thaliana]	677	616	0	91.0	77.7	83.8	alpha−1,4−galacturonosyltransferase	gbpln	Arabidopsis thaliana	AT5G47780.1 | Symbols: GAUT4 | galacturonosyltransferase 4 | chr5:19347991−19350517 FORWARD LENGTH=616	677	616	0	91.0	77.7	83.8
Rsa1.0_00152.1.g6888.t1	gb|EMJ14562.1| hypothetical protein PRUPE_ppa026835mg, partial [Prunus persica]	787	740	0	94.0	65.9	77.5	hypothetical protein PRUPE_ppa026835mg, partial	gbpln	Prunus persica	AT5G59810.1 | Symbols: ATSBT5.4, SBT5.4 | Subtilase family protein | chr5:24096895−24100387 REVERSE LENGTH=778	787	778	0	98.9	62.8	75.3
Rsa1.0_00152.1.g6889.t1	gb|EOA15620.1| hypothetical protein CARUB_v10005755mg [Capsella rubella]	209	203	2.00E−58	97.1	59.3	70.8	hypothetical protein CARUB_v10005755mg	gbpln	Capsella rubella	AT4G15950.1 | Symbols: NRPD4, NRPE4, RDM2 | RNA polymerase II, Rpb4, core protein | chr4:9040743−9041994 FORWARD LENGTH=205	209	205	8.00E−57	98.1	57.4	72.2
Rsa1.0_00152.1.g6890.t1	gb|EOA14425.1| hypothetical protein CARUB_v10027627mg [Capsella rubella]	342	383	0	112.0	95.0	98.0	hypothetical protein CARUB_v10027627mg	gbpln	Capsella rubella	AT5G47770.1 | Symbols: FPS1 | farnesyl diphosphate synthase 1 | chr5:19345297−19347415 FORWARD LENGTH=384	342	384	0	112.3	93.9	96.8
Rsa1.0_00152.1.g6891.t3	#	#	#	#	#	#	#	–	――――	――――	#	#	#	#	#	#	#
Rsa1.0_00152.1.g6892.t1	gb|EOA13117.1| hypothetical protein CARUB_v10026139mg [Capsella rubella]	557	586	0	105.2	91.9	95.0	hypothetical protein CARUB_v10026139mg	gbpln	Capsella rubella	AT5G47750.1 | Symbols: D6PKL2, PK5 | D6 protein kinase like 2 | chr5:19339947−19341864 REVERSE LENGTH=586	557	586	0	105.2	91.9	94.8
Rsa1.0_00152.1.g6893.t1	gb|EOA15202.1| hypothetical protein CARUB_v10028591mg [Capsella rubella]	281	243	1.00E−105	86.5	67.3	74.4	hypothetical protein CARUB_v10028591mg	gbpln	Capsella rubella	AT5G47740.1 | Symbols: | Adenine nucleotide alpha hydrolases−like superfamily protein | chr5:19338688−19339683 FORWARD LENGTH=244	281	244	1.00E−104	86.8	65.8	73.3
Rsa1.0_00152.1.g6894.t1	gb|EOA13661.1| hypothetical protein CARUB_v10026730mg [Capsella rubella]	331	341	1.00E−174	103.0	88.2	93.7	hypothetical protein CARUB_v10026730mg	gbpln	Capsella rubella	AT5G47730.1 | Symbols: | Sec14p−like phosphatidylinositol transfer family protein | chr5:19334592−19336618 REVERSE LENGTH=341	331	341	1.00E−172	103.0	89.4	94.3
Rsa1.0_00152.1.g6895.t1	#	#	#	#	#	#	#	–	――――	――――	#	#	#	#	#	#	#
Rsa1.0_00152.1.g6896.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1849	2726	0	147.4	50.0	63.5	disease resistance protein	gbpln	Brassica rapa	AT5G47650.1 | Symbols: ATNUDT2, ATNUDX2, NUDT2 | nudix hydrolase homolog 2 | chr5:19310391−19312084 REVERSE LENGTH=278	1849	278	1.00E−143	15.0	13.0	13.8
Rsa1.0_00152.1.g6897.t1	gb|ABD64993.1| transcription factor Hap3b, putative [Brassica oleracea]	182	185	1.00E−72	101.6	72.5	73.1	transcription factor Hap3b, putative	gbpln	Brassica oleracea	AT5G47640.1 | Symbols: NF−YB2 | nuclear factor Y, subunit B2 | chr5:19309414−19309986 FORWARD LENGTH=190	182	190	2.00E−66	104.4	70.3	71.4
Rsa1.0_00152.1.g6898.t1	ref|NP_199574.1| acyl carrier protein 3 [Arabidopsis thaliana] gi|145334761|ref|NP_001078726.1| acyl carrier protein 3 [Arabidopsis thaliana] gi|75333808|sp|Q9FGJ4.1|ACPM3_ARATH RecName: Full=Acyl carrier protein 3, mitochondrial; AltName: Full=MtACP−3; Short=ACP; AltName: Full=NADH−ubiquinone oxidoreductase 9.6 kDa subunit; Flags: Precursor gi|9758791|dbj|BAB09089.1| acyl carrier protein−like [Arabidopsis thaliana] gi|17380990|gb|AAL36307.1| putative acyl carrier protein [Arabidopsis thaliana] gi|20466033|gb|AAM20351.1| putative acyl carrier protein [Arabidopsis thaliana] gi|332008159|gb|AED95542.1| acyl carrier protein 3 [Arabidopsis thaliana] gi|332008160|gb|AED95543.1| acyl carrier protein 3 [Arabidopsis thaliana]	127	131	7.00E−45	103.1	72.4	83.5	acyl carrier protein 3	gbpln	Arabidopsis thaliana	AT5G47630.2 | Symbols: mtACP3 | mitochondrial acyl carrier protein 3 | chr5:19306397−19306885 FORWARD LENGTH=131	127	131	1.00E−47	103.1	72.4	83.5
Rsa1.0_00152.1.g6899.t1	gb|ABD64996.1| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) containing protein [Brassica oleracea]	408	587	0	143.9	86.8	88.7	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) containing protein	gbpln	Brassica oleracea	AT5G47620.2 | Symbols: | RNA−binding (RRM/RBD/RNP motifs) family protein | chr5:19302548−19304278 REVERSE LENGTH=431	408	431	1.00E−172	105.6	79.2	86.3
Rsa1.0_00152.1.g6900.t1	gb|ABD64996.1| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) containing protein [Brassica oleracea]	178	587	4.00E−79	329.8	79.2	81.5	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) containing protein	gbpln	Brassica oleracea	AT5G47610.1 | Symbols: | RING/U−box superfamily protein | chr5:19301399−19301899 REVERSE LENGTH=166	178	166	4.00E−65	93.3	76.4	80.3
Rsa1.0_00152.1.g6901.t1	gb|EOA14220.1| hypothetical protein CARUB_v10027375mg [Capsella rubella]	125	125	6.00E−62	100.0	93.6	96.0	hypothetical protein CARUB_v10027375mg	gbpln	Capsella rubella	AT5G47570.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:19292869−19294666 REVERSE LENGTH=125	125	125	2.00E−57	100.0	93.6	95.2

Rsa1.0_00152.1.g6902.t1	gb|ABD64997.1| sodium-dicarboxylate cotransporter, putative [Brassica oleracea]	76	527	9.00E-28	693.4	73.7	75.0	sodium-dicarboxylate cotransporter, putative	gbpln	Brassica oleracea	AT5G47560.1 | Symbols: ATTDT, ATSDAT, TDT | tonoplast dicarboxylate transporter | chr5:19287895-19290347 REVERSE LENGTH=540	76	540	2.00E-25	710.5	64.5	69.7
Rsa1.0_00152.1.g6903.t1	ref|XP_002863336.1| ATSDAT [Arabidopsis lyrata subsp. lyrata] gi|297309171|gb|EFH39595.1| ATSDAT [Arabidopsis lyrata subsp. lyrata]	461	540	0	117.1	92.2	97.6	ATSDAT	gbpln	Arabidopsis lyrata	AT5G47560.1 | Symbols: ATTDT, ATSDAT, TDT | tonoplast dicarboxylate transporter | chr5:19287895-19290347 REVERSE LENGTH=540	461	540	0	117.1	90.9	96.7
Rsa1.0_00152.1.g6904.t1	gb|ABD64998.1| cystatin domain containing protein [Brassica oleracea]	108	148	2.00E-32	137.0	69.4	74.1	cystatin domain containing protein	gbpln	Brassica oleracea	AT5G47550.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:19286596-19286964 REVERSE LENGTH=122	108	122	7.00E-26	113.0	54.6	61.1
Rsa1.0_00152.1.g6905.t1	ref|XP_002863338.1| hypothetical protein ARALYDRAFT_916635 [Arabidopsis lyrata subsp. lyrata] gi|297309173|gb|EFH39597.1| hypothetical protein ARALYDRAFT_916635 [Arabidopsis lyrata subsp. lyrata]	343	343	0	100.0	95.9	99.1	hypothetical protein ARALYDRAFT_916635	gbpln	Arabidopsis lyrata	AT5G47540.1 | Symbols: | Mo25 family protein | chr5:19283265-19285328 REVERSE LENGTH=343	343	343	0	100.0	95.0	99.4
Rsa1.0_00152.1.g6906.t1	gb|ABD65002.1| hypothetical protein 26.t00022 [Brassica oleracea]	394	394	0	100.0	91.1	95.4	hypothetical protein 26.t00022	gbpln	Brassica oleracea	AT5G47530.1 | Symbols: | Auxin-responsive family protein | chr5:19281471-19282870 FORWARD LENGTH=395	394	395	0	100.3	79.7	86.8
Rsa1.0_00152.1.g6907.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	272	1142	4.00E-24	419.9	19.9	27.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT3G32050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14780.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:13067626-13068582 REVERSE LENGTH=175	272	175	6.00E-11	64.3	10.7	12.9
Rsa1.0_00152.1.g6908.t1	gb|ABD65003.1| Ras-related GTP-binding protein, putative [Brassica oleracea]	219	221	1.00E-120	100.9	97.3	99.1	Ras-related GTP-binding protein, putative	gbpln	Brassica oleracea	AT5G47520.1 | Symbols: AtRABA5a, RABA5a | RAB GTPase homolog A5A | chr5:19277596-19278366 REVERSE LENGTH=221	219	221	1.00E-120	100.9	95.0	97.7
Rsa1.0_00152.1.g6909.t2	gb|ABD64977.1| pectinesterase family protein [Brassica oleracea]	362	360	0	99.4	95.3	97.0	pectinesterase family protein	gbpln	Brassica oleracea	AT5G47500.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:19271262-19272845 REVERSE LENGTH=362	362	362	0	100.0	91.2	94.5
Rsa1.0_00152.1.g6910.t1	gb|ABD65007.1| integral membrane protein, putative [Brassica oleracea]	345	376	0	109.0	93.9	96.8	integral membrane protein, putative	gbpln	Brassica oleracea	AT5G47470.1 | Symbols: | Nodulin MtN21 /EamA-like transporter family protein | chr5:19254598-19256378 FORWARD LENGTH=364	345	364	1.00E-166	105.5	83.8	91.3
Rsa1.0_00152.1.g6911.t1	gb|ABD65008.1| PPR repeat containing protein [Brassica oleracea]	586	583	0	99.5	89.8	95.1	PPR repeat containing protein	gbpln	Brassica oleracea	AT5G47460.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:19252463-19254193 REVERSE LENGTH=576	586	576	0	98.3	82.1	89.2
Rsa1.0_00152.1.g6912.t5	gb|ABD64980.1| hypothetical protein 25.t00029 [Brassica oleracea]	192	109	2.00E-40	56.8	45.8	48.4	hypothetical protein 25.t00029	gbpln	Brassica oleracea	AT4G17310.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G47455.7); Has 164 Blast hits to 164 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 164; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:9686466-9686848 REVERSE LENGTH=99	192	99	1.00E-29	51.6	35.9	41.1
Rsa1.0_00152.1.g6913.t1	gb|ABD65010.1| tonoplast intrinsic protein, putative [Brassica oleracea]	243	250	1.00E-127	102.9	97.9	99.2	tonoplast intrinsic protein, putative	gbpln	Brassica oleracea	AT5G47450.1 | Symbols: ATTIP2;3, TIP2;3, DELTA-TIP3 | tonoplast intrinsic protein 2;3 | chr5:19248509-19249466 REVERSE LENGTH=250	243	250	1.00E-125	102.9	93.4	97.5
Rsa1.0_00153.1.g6914.t2	dbj|BAB02796.1| replication protein A1-like [Arabidopsis thaliana]	240	581	5.00E-59	242.1	42.9	62.1	replication protein A1-like	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	240	566	9.00E-61	235.8	42.9	69.6
Rsa1.0_00153.1.g6915.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00153.1.g6916.t1	ref|XP_002892967.1| hypothetical protein ARALYDRAFT_312744 [Arabidopsis lyrata subsp. lyrata] gi|297338809|gb|EFH69226.1| hypothetical protein ARALYDRAFT_312744 [Arabidopsis lyrata subsp. lyrata]	462	482	1.00E-152	104.3	67.1	75.3	hypothetical protein ARALYDRAFT_312744	gbpln	Arabidopsis lyrata	AT1G17790.1 | Symbols: | DNA-binding bromodomain-containing protein | chr1:6125532-6127276 REVERSE LENGTH=487	462	487	1.00E-152	105.4	66.7	74.7

Rsa1.0_00153.1.g6917.t1	gb|EOA39163.1| hypothetical protein CARUB_v10012112mg [Capsella rubella]	236	273	3.00E−75	115.7	68.2	79.2	hypothetical protein CARUB_v10012112mg	gbpln	Capsella rubella	AT1G17780.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G16575.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr1:6124095-6125166 FORWARD LENGTH=263	236	263	2.00E−69	111.4	64.0	73.7
Rsa1.0_00153.1.g6918.t1	ref|XP_002892966.1| cleavage stimulation factor 77 [Arabidopsis lyrata subsp. lyrata] gi|297338808|gb|EFH69225.1| cleavage stimulation factor 77 [Arabidopsis lyrata subsp. lyrata]	736	734	0	99.7	90.1	94.2	cleavage stimulation factor 77	gbpln	Arabidopsis lyrata	AT1G17760.1 | Symbols: CSTF77, ATCSTF77 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:6110208-6116271 REVERSE LENGTH=734	736	734	0	99.7	88.7	93.5
Rsa1.0_00153.1.g6919.t1	gb|EOA39905.1| hypothetical protein CARUB_v10008585mg [Capsella rubella]	580	625	0	107.8	85.3	91.6	hypothetical protein CARUB_v10008585mg	gbpln	Capsella rubella	AT1G17745.1 | Symbols: PGDH | D-3-phosphoglycerate dehydrogenase | chr1:6101157-6104979 FORWARD LENGTH=624	580	624	0	107.6	84.5	90.0
Rsa1.0_00153.1.g6920.t1	gb|EOA40186.1| hypothetical protein CARUB_v10008904mg [Capsella rubella]	510	506	0	99.2	93.3	95.5	hypothetical protein CARUB_v10008904mg	gbpln	Capsella rubella	AT1G17720.2 | Symbols: ATB BETA | Protein phosphatase 2A, regulatory subunit PR55 | chr1:6093949-6098065 REVERSE LENGTH=500	510	500	0	98.0	92.2	94.5
Rsa1.0_00153.1.g6921.t1	ref|XP_002892964.1| phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata] gi|297338806|gb|EFH69223.1| phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata]	280	284	1.00E−141	101.4	86.4	93.6	phosphoric monoester hydrolase	gbpln	Arabidopsis lyrata	AT1G17710.1 | Symbols: | Pyridoxal phosphate phosphatase-related protein | chr1:6090763-6091975 REVERSE LENGTH=279	280	279	1.00E−138	99.6	84.6	90.0
Rsa1.0_00153.1.g6922.t1	ref|XP_002892963.1| hypothetical protein ARALYDRAFT_471979 [Arabidopsis lyrata subsp. lyrata] gi|297338805|gb|EFH69222.1| hypothetical protein ARALYDRAFT_471979 [Arabidopsis lyrata subsp. lyrata]	745	748	0	100.4	80.9	89.5	hypothetical protein ARALYDRAFT_471979	gbpln	Arabidopsis lyrata	AT1G17690.1 | Symbols: NOF1 | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleus; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Digestive organ expansion factor, predicted (InterPro:IPR010678); Has 25006 Blast hits to 13379 proteins in 904 species: Archae − 102; Bacteria − 5571; Metazoa − 7448; Fungi − 3168; Plants − 1056; Viruses − 466; Other Eukaryotes − 7195 (source: NCBI BLink). | chr1:6082878-6088157 REVERSE LENGTH=754	745	754	0	101.2	81.1	89.9
Rsa1.0_00153.1.g6923.t1	gb|EOA37010.1| hypothetical protein CARUB_v10010038mg [Capsella rubella]	262	263	1.00E−107	100.4	84.0	91.6	hypothetical protein CARUB_v10010038mg	gbpln	Capsella rubella	AT1G17620.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr1:6062313-6063107 FORWARD LENGTH=264	262	264	7.00E−98	100.8	79.8	89.7
Rsa1.0_00153.1.g6924.t2	gb|ACP30555.1| disease resistance protein [Brassica rapa subsp. pekinensis]	546	1074	1.00E−143	196.7	52.2	69.2	disease resistance protein	gbpln	Brassica rapa	AT5G48770.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:19773277-19777242 REVERSE LENGTH=1190	546	1190	2.00E−90	217.9	39.4	51.8
Rsa1.0_00153.1.g6925.t1	ref|NP_173184.2| nucleoside diphosphate kinase-like protein [Arabidopsis thaliana] gi|332191462|gb|AEE29583.1| nucleoside diphosphate kinase-like protein [Arabidopsis thaliana]	176	181	9.00E−73	102.8	84.1	92.0	nucleoside diphosphate kinase-like protein	gbpln	Arabidopsis thaliana	AT1G17410.1 | Symbols: | Nucleoside diphosphate kinase family protein | chr1:5968627-5969780 REVERSE LENGTH=181	176	181	3.00E−75	102.8	84.1	92.0
Rsa1.0_00153.1.g6926.t1	gb|EOA38320.1| hypothetical protein CARUB_v10009828mg [Capsella rubella]	295	309	1.00E−120	104.7	80.7	85.8	hypothetical protein CARUB_v10009828mg	gbpln	Capsella rubella	AT1G17400.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G72490.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr1:5960920-5962245 REVERSE LENGTH=295	295	295	1.00E−117	100.0	85.8	90.8

Rsa1.0_00153.1.g6927.t1	ref|NP_564019.1| protein TIFY 11A [Arabidopsis thaliana] gi|75173855|sp|Q9LDU5.1|TI11A_ARATH RecName: Full=Protein TIFY 11A; AltName: Full=Jasmonate ZIM domain-containing protein 5 gi|8778483|gb|AAF79491.1|AC022492_35 F1L3.3 [Arabidopsis thaliana] gi|9665119|gb|AAF97303.1|AC007843_6 Hypothetical protein [Arabidopsis thaliana] gi|23306360|gb|AAN17407.1| expressed protein [Arabidopsis thaliana] gi|27311875|gb|AAO00903.1| expressed protein [Arabidopsis thaliana] gi|332191460|gb|AEE29581.1| protein TIFY 11A [Arabidopsis thaliana]	260	274	1.00E-88	105.4	72.7	81.9	protein TIFY 11A	gbpln	Arabidopsis thaliana	AT1G17380.1 | Symbols: JAZ5, TIFY11A | jasmonate-zim-domain protein 5 | chr1:5955654-5957070 REVERSE LENGTH=274	260	274	3.00E-91	105.4	72.7	81.9
Rsa1.0_00153.1.g6928.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00153.1.g6929.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1386	1459	0	105.3	52.5	70.1	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1386	1262	1.00E-114	91.1	14.1	20.5
Rsa1.0_00153.1.g6930.t1	ref|NP_173179.4| uncharacterized protein [Arabidopsis thaliana] gi|9665120|gb|AAF97304.1|AC007843_7 Hypothetical protein [Arabidopsis thaliana] gi|332191457|gb|AEE29578.1| uncharacterized protein AT1G17360 [Arabidopsis thaliana]	709	1061	1.00E-116	149.6	38.2	44.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G17360.1 | Symbols: | BEST Arabidopsis thaliana protein match is: COP1-interacting protein-related (TAIR:AT1G72410.1); Has 9949 Blast hits to 7480 proteins in 576 species: Archae - 12; Bacteria - 1007; Metazoa - 3636; Fungi - 982; Plants - 444; Viruses - 50; Other Eukaryotes - 3818 (source: NCBI BLink). | chr1:5947441-5951399 FORWARD LENGTH=1061	709	1061	1.00E-118	149.6	38.2	44.9
Rsa1.0_00153.1.g6931.t1	ref|NP_849679.1| SAUR-like auxin-responsive protein family [Arabidopsis thaliana] gi|9665126|gb|AAF97310.1|AC007843_13 Hypothetical protein [Arabidopsis thaliana] gi|26452787|dbj|BAC43474.1| unknown protein [Arabidopsis thaliana] gi|109946549|gb|ABG48453.1| At1g17345 [Arabidopsis thaliana] gi|332191454|gb|AEE29575.1| SAUR-like auxin-responsive protein family [Arabidopsis thaliana]	133	131	4.00E-51	98.5	75.2	85.7	SAUR-like auxin-responsive protein family	gbpln	Arabidopsis thaliana	AT1G17345.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:5940525-5940920 FORWARD LENGTH=131	133	131	1.00E-53	98.5	75.2	85.7
Rsa1.0_00153.1.g6932.t1	ref|NP_001185380.1| alanine aminotransferase 2 [Arabidopsis thaliana] gi|332197186|gb|AEE35307.1| alanine aminotransferase 2 [Arabidopsis thaliana]	52	553	4.00E-19	1063.5	88.5	90.4	alanine aminotransferase 2	gbpln	Arabidopsis thaliana	AT1G72330.3 | Symbols: ALAAT2 | alanine aminotransferase 2 | chr1:27233637-27236571 FORWARD LENGTH=553	52	553	7.00E-22	1063.5	88.5	90.4
Rsa1.0_00153.1.g6933.t1	ref|XP_002887430.1| ALAAT2 [Arabidopsis lyrata subsp. lyrata] gi|297333271|gb|EFH63689.1| ALAAT2 [Arabidopsis lyrata subsp. lyrata]	546	535	0	98.0	86.1	92.1	ALAAT2	gbpln	Arabidopsis lyrata	AT1G72330.1 | Symbols: ALAAT2 | alanine aminotransferase 2 | chr1:27233637-27236571 FORWARD LENGTH=540	546	540	0	98.9	86.3	92.5
Rsa1.0_00153.1.g6934.t1	ref|XP_002892943.1| hypothetical protein ARALYDRAFT_889130 [Arabidopsis lyrata subsp. lyrata] gi|297338785|gb|EFH69202.1| hypothetical protein ARALYDRAFT_889130 [Arabidopsis lyrata subsp. lyrata]	553	583	0	105.4	83.0	90.2	hypothetical protein ARALYDRAFT_889130	gbpln	Arabidopsis lyrata	AT1G17270.1 | Symbols: | O-fucosyltransferase family protein | chr1:5909443-5911624 REVERSE LENGTH=564	553	564	0	102.0	80.5	88.1
Rsa1.0_00153.1.g6935.t1	gb|EOA39598.1| hypothetical protein CARUB_v10008225mg [Capsella rubella]	944	947	0	100.3	90.7	95.9	hypothetical protein CARUB_v10008225mg	gbpln	Capsella rubella	AT1G17260.1 | Symbols: AHA10 | autoinhibited H(+)-ATPase isoform 10 | chr1:5904058-5908898 FORWARD LENGTH=947	944	947	0	100.3	91.2	96.1
Rsa1.0_00153.1.g6936.t1	gb|EOA37109.1| hypothetical protein CARUB_v10010315mg [Capsella rubella]	204	204	3.00E-97	100.0	83.8	93.1	hypothetical protein CARUB_v10010315mg	gbpln	Capsella rubella	AT1G17200.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr1:5878493-5879871 FORWARD LENGTH=204	204	204	3.00E-96	100.0	83.3	92.2
Rsa1.0_00153.1.g6937.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00153.1.g6938.t1	gb|EOA38496.1| hypothetical protein CARUB_v10010264mg [Capsella rubella]	219	218	1.00E-108	99.5	85.4	90.9	hypothetical protein CARUB_v10010264mg	gbpln	Capsella rubella	AT1G17190.1 | Symbols: ATGSTU26, GSTU26 | glutathione S-transferase tau 26 | chr1:5875452-5876375 FORWARD LENGTH=220	219	220	1.00E-109	100.5	84.0	90.0
Rsa1.0_00153.1.g6939.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00153.1.g6940.t1	ref|NP_001117300.1| VQ motif-containing protein [Arabidopsis thaliana] gi|98961981|gb|ABF59320.1| unknown protein [Arabidopsis thaliana] gi|332191429|gb|AEE29550.1| VQ motif-containing protein [Arabidopsis thaliana]	95	98	8.00E-38	103.2	83.2	89.5	VQ motif-containing protein	gbpln	Arabidopsis thaliana	AT1G17147.1 | Symbols: | VQ motif-containing protein | chr1:5863654-5863950 REVERSE LENGTH=98	95	98	1.00E-40	103.2	83.2	89.5

Rsa1.0_00153.1.g6941.t1	gb|EOA38153.1| hypothetical protein CARUB_v10009626mg [Capsella rubella]	333	344	1.00E-127	103.3	79.9	86.5	hypothetical protein CARUB_v10009626mg	gbpln	Capsella rubella	AT1G17140.2 | Symbols: ICR1, RIP1 | interactor of constitutive active rops 1 | chr1:5856740-5857861 REVERSE LENGTH=344	333	344	1.00E-126	103.3	79.0	85.6
Rsa1.0_00153.1.g6942.t1	ref|XP_002892935.1| ubiquitin-specific protease 15 [Arabidopsis lyrata subsp. lyrata] gi|297338777|gb|EFH69194.1| ubiquitin-specific protease 15 [Arabidopsis lyrata subsp. lyrata]	922	926	0	100.4	81.9	87.1	ubiquitin-specific protease 15	gbpln	Arabidopsis lyrata	AT1G17110.1 | Symbols: UBP15 | ubiquitin-specific protease 15 | chr1:5845816-5849889 REVERSE LENGTH=924	922	924	0	100.2	81.6	87.1
Rsa1.0_00153.1.g6943.t1	gb|EOA36893.1| hypothetical protein CARUB_v10011434mg [Capsella rubella]	94	92	1.00E-26	97.9	68.1	79.8	hypothetical protein CARUB_v10011434mg	gbpln	Capsella rubella	AT1G17090.2 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 7 growth stages; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5842464-5842745 REVERSE LENGTH=93	94	93	4.00E-24	98.9	66.0	76.6
Rsa1.0_00153.1.g6944.t1	gb|EOA38632.1| hypothetical protein CARUB_v10010518mg [Capsella rubella]	159	158	7.00E-72	99.4	84.9	93.1	hypothetical protein CARUB_v10010518mg	gbpln	Capsella rubella	AT1G17080.1 | Symbols: | Ribosomal protein L18ae family | chr1:5840458-5841536 REVERSE LENGTH=154	159	154	1.00E-71	96.9	85.5	91.2
Rsa1.0_00153.1.g6945.t1	sp|Q9SHG5.2|C72C1_ARATH RecName: Full=Cytochrome P450 72C1; AltName: Full=Protein CHIBI 2; AltName: Full=Protein DWARFISH WITH LOW FERTILITY; AltName: Full=Protein SHRINK 1; AltName: Full=Protein SUPPRESSOR OF PHYB-4 PROTEIN 7	515	519	0	100.8	89.3	94.6	RecName: Full=Cytochrome P450 72C1; AltName: Full=Protein CHIBI 2; AltName: Full=Protein DWARFISH WITH LOW FERTILITY; AltName: Full=Protein SHRINK 1; AltName: Full=Protein SUPPRESSOR OF PHYB-4 PROTEIN 7	----	----	AT1G17060.1 | Symbols: CYP72C1, SOB7 | cytochrome p450 72c1 | chr1:5832282-5835255 REVERSE LENGTH=476	515	476	0	92.4	82.1	86.8
Rsa1.0_00153.1.g6946.t1	gb|EOA37214.1| hypothetical protein CARUB_v10010695mg [Capsella rubella]	114	114	6.00E-56	100.0	91.2	94.7	hypothetical protein CARUB_v10010695mg	gbpln	Capsella rubella	AT1G16960.1 | Symbols: | Ubiquitin domain-containing protein | chr1:5799998-5800624 FORWARD LENGTH=114	114	114	9.00E-57	100.0	88.6	93.0
Rsa1.0_00153.1.g6947.t1	gb|EOA39391.1| hypothetical protein CARUB_v10012478mg [Capsella rubella]	59	93	8.00E-15	157.6	76.3	86.4	hypothetical protein CARUB_v10012478mg	gbpln	Capsella rubella	AT1G16950.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: stamen; EXPRESSED DURING: 4 anthesis; Has 17 Blast hits to 17 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5796083-5796364 FORWARD LENGTH=93	59	93	4.00E-16	157.6	72.9	83.1
Rsa1.0_00153.1.g6948.t1	ref|NP_173136.1| Ras-related protein RABA1b [Arabidopsis thaliana] gi|3024526|sp|Q39222.1|RAA1B_ARATH RecName: Full=Ras-related protein RABA1b; Short=AtRABA1b; AltName: Full=Ras-related protein Rab11; Short=AtRab11 gi|9802771|gb|AAF99840.1|AC051629_7 GTP-binding protein Rab11 [Arabidopsis thaliana] gi|451860|gb|AAA32872.1| small GTP-binding protein [Arabidopsis thaliana] gi|30102592|gb|AAP21214.1| At1g16920 [Arabidopsis thaliana] gi|110735723|dbj|BAE99841.1| hypothetical protein [Arabidopsis thaliana] gi|332191401|gb|AEE29522.1| Ras-related protein RABA1b [Arabidopsis thaliana]	216	216	1.00E-119	100.0	96.8	98.1	Ras-related protein RABA1b	gbpln	Arabidopsis thaliana	AT1G16920.1 | Symbols: RAB11, ATRABA1B, RABA1b | RAB GTPase homolog A1B | chr1:5787489-5789147 REVERSE LENGTH=216	216	216	1.00E-121	100.0	96.8	98.1
Rsa1.0_00153.1.g6949.t1	ref|XP_002892928.1| sugar binding protein [Arabidopsis lyrata subsp. lyrata] gi|297338770|gb|EFH69187.1| sugar binding protein [Arabidopsis lyrata subsp. lyrata]	442	424	1.00E-159	95.9	65.6	71.7	sugar binding protein	gbpln	Arabidopsis lyrata	AT1G16905.1 | Symbols: | Curculin-like (mannose-binding) lectin family protein | chr1:5782546-5783817 REVERSE LENGTH=423	442	423	1.00E-161	95.7	65.6	72.9
Rsa1.0_00153.1.g6950.t5	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00153.1.g6951.t1	ref|NP_173134.2| alpha-1,2-mannosyltransferase [Arabidopsis thaliana] gi|75173357|sp|Q9FZ49.1|ALG9_ARATH RecName: Full=Dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase; AltName: Full=Alpha-1,2-mannosyltransferase ALG9; AltName: Full=Asparagine-linked glycosylation protein 9; AltName: Full=Dol-P-Man:Man(8)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase gi|9802774|gb|AAF99843.1|AC051629_10 Hypothetical protein [Arabidopsis thaliana] gi|22655224|gb|AAM98202.1| Ser/Thr protein kinase, putative [Arabidopsis thaliana] gi|34098911|gb|AAQ56838.1| At1g16900 [Arabidopsis thaliana] gi|332191397|gb|AEE29518.1| Dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase [Arabidopsis thaliana]	571	570	0	99.8	90.5	96.5	alpha-1,2-mannosyltransferase	gbpln	Arabidopsis thaliana	AT1G16900.1 | Symbols: | Alg9-like mannosyltransferase family | chr1:5779262-5782303 REVERSE LENGTH=570	571	570	0	99.8	90.5	96.5
Rsa1.0_00153.1.g6952.t1	ref|XP_003633254.1| PREDICTED: ubiquitin-conjugating enzyme E2 36 [Vitis vinifera]	120	163	5.00E-65	135.8	100.0	100.0	PREDICTED: ubiquitin-conjugating enzyme E2 36	gbpln	Vitis vinifera	AT1G16890.2 | Symbols: UBC36, UBC13B | ubiquitin-conjugating enzyme 36 | chr1:5776550-5778327 REVERSE LENGTH=153	120	153	1.00E-67	127.5	100.0	100.0
Rsa1.0_00153.1.g6953.t1	gb|EOA38375.1| hypothetical protein CARUB_v10009908mg [Capsella rubella]	297	291	1.00E-139	98.0	86.5	89.9	hypothetical protein CARUB_v10009908mg	gbpln	Capsella rubella	AT1G16880.1 | Symbols: | uridylyltransferase-related | chr1:5773796-5776125 FORWARD LENGTH=290	297	290	1.00E-140	97.6	85.9	89.9
Rsa1.0_00153.1.g6954.t1	gb|EOA40305.1| hypothetical protein CARUB_v10009033mg [Capsella rubella]	476	474	0	99.6	88.9	93.3	hypothetical protein CARUB_v10009033mg	gbpln	Capsella rubella	AT1G16860.1 | Symbols: | Ubiquitin-specific protease family C19-related protein | chr1:5768280-5770183 FORWARD LENGTH=474	476	474	0	99.6	88.4	92.6
Rsa1.0_00153.1.g6955.t1	gb|EOA36658.1| hypothetical protein CARUB_v10011947mg [Capsella rubella]	150	144	1.00E-63	96.0	83.3	88.0	hypothetical protein CARUB_v10011947mg	gbpln	Capsella rubella	AT1G16790.1 | Symbols: | ribosomal protein-related | chr1:5744638-5745072 FORWARD LENGTH=144	150	144	1.00E-61	96.0	82.0	87.3
Rsa1.0_00153.1.g6956.t3	ref|NP_173120.1| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana] gi|332191372|gb|AEE29493.1| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana]	1095	758	0	69.2	60.1	64.0	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	gbpln	Arabidopsis thaliana	AT1G16760.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:5734234-5737307 FORWARD LENGTH=758	1095	758	0	69.2	60.1	64.0
Rsa1.0_00153.1.g6957.t1	gb|EOA36852.1| hypothetical protein CARUB_v10008799mg [Capsella rubella]	525	537	0	102.3	87.4	92.2	hypothetical protein CARUB_v10008799mg	gbpln	Capsella rubella	AT1G16750.1 | Symbols: | Protein of unknown function, DUF547 | chr1:5729221-5731689 REVERSE LENGTH=529	525	529	0	100.8	85.1	90.5
Rsa1.0_00153.1.g6958.t1	ref|NP_173118.1| Ribosomal protein L20 [Arabidopsis thaliana] gi|21554397|gb|AAM63502.1| ribosomal protein L20, putative [Arabidopsis thaliana] gi|88011169|gb|ABD38912.1| At1g16740 [Arabidopsis thaliana] gi|332191370|gb|AEE29491.1| Ribosomal protein L20 [Arabidopsis thaliana] gi|482574488|gb|EOA38675.1| hypothetical protein CARUB_v10010647mg [Capsella rubella]	64	126	1.00E-28	196.9	98.4	98.4	Ribosomal protein L20	gbpln	Arabidopsis thaliana	AT1G16740.1 | Symbols: | Ribosomal protein L20 | chr1:5727773-5728950 FORWARD LENGTH=126	64	126	2.00E-31	196.9	98.4	98.4
Rsa1.0_00154.1.g6959.t1	#	#	#	#	#	#	#	-	----	----	AT5G46730.2 | Symbols: | glycine-rich protein | chr5:18964030-18964902 FORWARD LENGTH=246	114	246	1.00E-10	215.8	22.8	23.7
Rsa1.0_00154.1.g6960.t1	gb|EOA14095.1| hypothetical protein CARUB_v10027235mg [Capsella rubella] gi|482549902|gb|EOA14096.1| hypothetical protein CARUB_v10027235mg [Capsella rubella]	174	175	2.00E-74	100.6	79.9	87.9	hypothetical protein CARUB_v10027235mg	gbpln	Capsella rubella	AT5G46720.1 | Symbols: | AIG2-like (avirulence induced gene) family protein | chr5:18959183-18959710 FORWARD LENGTH=175	174	175	5.00E-74	100.6	80.5	87.4
Rsa1.0_00154.1.g6961.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00154.1.g6962.t1	gb|EOA17250.1| hypothetical protein CARUB_v10005524mg, partial [Capsella rubella]	226	262	9.00E-88	115.9	71.7	81.4	hypothetical protein CARUB_v10005524mg, partial	gbpln	Capsella rubella	AT4G17900.1 | Symbols: | PLATZ transcription factor family protein | chr4:9946046-9947697 FORWARD LENGTH=227	226	227	3.00E-90	100.4	72.6	81.0

Rsa1.0_00154.1.g6963.t1	ref|NP_199482.1| Tetraspanin family protein [Arabidopsis thaliana] gi|75262522|sp|Q9FIQ5.1|TRN2_ARATH RecName: Full=Protein TORNADO 2; AltName: Full=Protein EKEKO; AltName: Full=TETRASPANIN-1 gi|9758506|dbj|BAB08914.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] gi|56381915|gb|AAV85676.1| At5g46700 [Arabidopsis thaliana] gi|110740669|dbj|BAE98437.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] gi|332008032|gb|AED95415.1| Tetraspanin family protein [Arabidopsis thaliana]	269	269	1.00E-127	100.0	90.7	95.9	Tetraspanin family protein	gbpln	Arabidopsis thaliana	AT5G46700.1 | Symbols: TET1, TRN2 | Tetraspanin family protein | chr5:18951035-18952439 FORWARD LENGTH=269	269	269	1.00E-130	100.0	90.7	95.9
Rsa1.0_00154.1.g6964.t1	ref|XP_002865171.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297311006|gb|EFH41430.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	334	290	1.00E-104	86.8	59.0	66.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G46650.1 | Symbols: | RING/U-box superfamily protein | chr5:18930443-18931312 FORWARD LENGTH=289	334	289	1.00E-105	86.5	57.5	65.9
Rsa1.0_00154.1.g6965.t2	gb|EOA13488.1| hypothetical protein CARUB_v10026550mg [Capsella rubella]	370	396	5.00E-97	107.0	65.9	75.7	hypothetical protein CARUB_v10026550mg	gbpln	Capsella rubella	AT5G46640.1 | Symbols: | AT hook motif DNA-binding family protein | chr5:18924670-18926292 FORWARD LENGTH=386	370	386	2.00E-88	104.3	65.1	74.3
Rsa1.0_00154.1.g6966.t1	ref|NP_199475.1| AP-2 complex subunit mu-1 [Arabidopsis thaliana] gi|297794577|ref|XP_002865173.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|2271477|gb|AAB88283.1| AP47/50p [Arabidopsis thaliana] gi|9758499|dbj|BAB08907.1| AP47/50p [Arabidopsis thaliana] gi|297311008|gb|EFH41432.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|332008024|gb|AED95407.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis thaliana]	439	438	0	99.8	99.3	99.8	AP-2 complex subunit mu-1	gbpln	Arabidopsis lyrata	AT5G46630.1 | Symbols: | Clathrin adaptor complexes medium subunit family protein | chr5:18920580-18923252 FORWARD LENGTH=438	439	438	0	99.8	99.3	99.8
Rsa1.0_00154.1.g6967.t1	ref|XP_002868934.1| hypothetical protein ARALYDRAFT_912478 [Arabidopsis lyrata subsp. lyrata] gi|297314770|gb|EFH45193.1| hypothetical protein ARALYDRAFT_912478 [Arabidopsis lyrata subsp. lyrata]	357	386	4.00E-68	108.1	47.3	61.1	hypothetical protein ARALYDRAFT_912478	gbpln	Arabidopsis lyrata	AT4G39580.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18385684-18386811 REVERSE LENGTH=375	357	375	1.00E-31	105.0	34.2	51.3
Rsa1.0_00154.1.g6968.t1	ref|NP_199466.1| ABC transporter B family member 7 [Arabidopsis thaliana] gi|75333860|sp|Q9FHF1.1|AB7B_ARATH RecName: Full=ABC transporter B family member 7; Short=ABC transporter ABCB.7; Short=AtABCB7; AltName: Full=Multidrug resistance protein 7; AltName: Full=P-glycoprotein 7 gi|10177591|dbj|BAB10822.1| multidrug resistance p-glycoprotein [Arabidopsis thaliana] gi|332008013|gb|AED95396.1| ABC transporter B family member 7 [Arabidopsis thaliana]	864	1248	0	144.4	79.9	88.7	ABC transporter B family member 7	gbpln	Arabidopsis thaliana	AT5G46540.1 | Symbols: PGP7 | P-glycoprotein 7 | chr5:18877192-18882347 REVERSE LENGTH=1248	864	1248	0	144.4	79.9	88.7
Rsa1.0_00154.1.g6969.t3	ref|NP_199465.4| AWPM-19-like protein [Arabidopsis thaliana] gi|332008012|gb|AED95395.1| AWPM-19-like protein [Arabidopsis thaliana]	286	157	3.00E-50	54.9	35.0	37.4	AWPM-19-like protein	gbpln	Arabidopsis thaliana	AT5G46530.1 | Symbols: | AWPM-19-like family protein | chr5:18875576-18876779 FORWARD LENGTH=157	286	157	8.00E-53	54.9	35.0	37.4
Rsa1.0_00154.1.g6970.t1	gb|ACP30561.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1110	1005	0	90.5	76.8	79.5	disease resistance protein	gbpln	Brassica rapa	AT5G46450.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18835618-18839546 FORWARD LENGTH=1123	1110	1123	0	101.2	57.8	71.0
Rsa1.0_00154.1.g6971.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	393	1274	6.00E-53	324.2	32.3	47.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	393	303	1.00E-47	77.1	29.3	40.7

Rsa1.0_00154.1.g6972.t1	ref|XP_002868793.1| hypothetical protein ARALYDRAFT_916529 [Arabidopsis lyrata subsp. lyrata] gi|297314629|gb|EFH45052.1| hypothetical protein ARALYDRAFT_916529 [Arabidopsis lyrata subsp. lyrata]	250	292	1.00E-77	116.8	60.4	76.0	hypothetical protein ARALYDRAFT_916529	gbpln	Arabidopsis lyrata	AT5G38280.1 | Symbols: PR5K | PR5-like receptor kinase | chr5:15293325-15295838 REVERSE LENGTH=665	250	665	2.00E-79	266.0	56.8	75.2
Rsa1.0_00154.1.g6973.t1	gb|ACP30585.1| disease resistance protein [Brassica rapa subsp. pekinensis]	803	1301	0	162.0	86.3	91.5	disease resistance protein	gbpln	Brassica rapa	AT5G46470.1 | Symbols: RPS6 | disease resistance protein (TIR-NBS-LRR class) family | chr5:18842701-18846809 FORWARD LENGTH=1127	803	1127	0	140.3	64.5	76.8
Rsa1.0_00154.1.g6974.t8	dbj|BAB11094.1| carboxy-terminal proteinase D1-like protein [Arabidopsis thaliana]	883	488	0	55.3	45.4	49.0	carboxy-terminal proteinase D1-like protein	gbpln	Arabidopsis thaliana	AT5G46390.2 | Symbols: | Peptidase S41 family protein | chr5:18816612-18819148 FORWARD LENGTH=489	883	489	0	55.4	45.2	48.7
Rsa1.0_00154.1.g6975.t1	ref|XP_002863403.1| hypothetical protein ARALYDRAFT_356363 [Arabidopsis lyrata subsp. lyrata] gi|297309238|gb|EFH39662.1| hypothetical protein ARALYDRAFT_356363 [Arabidopsis lyrata subsp. lyrata]	455	1047	3.00E-17	230.1	20.9	26.4	hypothetical protein ARALYDRAFT_356363	gbpln	Arabidopsis lyrata	AT5G46380.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr5:18813088-18815974 REVERSE LENGTH=607	455	607	3.00E-16	133.4	21.8	28.1
Rsa1.0_00154.1.g6976.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00154.1.g6977.t1	gb|EOA12518.1| hypothetical protein CARUB_v10026412mg [Capsella rubella]	443	440	0	99.3	75.2	85.8	hypothetical protein CARUB_v10026412mg	gbpln	Capsella rubella	AT5G46370.1 | Symbols: KCO2, ATTPK2, ATKCO2 | Ca2+ activated outward rectifying K+ channel 2 | chr5:18809623-18811720 REVERSE LENGTH=443	443	443	1.00E-172	100.0	70.4	82.2
Rsa1.0_00154.1.g6978.t1	gb|ACI14410.1| WRKY8-1 transcription factor [Brassica napus]	320	321	1.00E-165	100.3	89.4	94.1	WRKY8-1 transcription factor	gbpln	Brassica napus	AT5G46350.1 | Symbols: WRKY8, ATWRKY8 | WRKY DNA-binding protein 8 | chr5:18801403-18803901 REVERSE LENGTH=326	320	326	1.00E-120	101.9	76.3	85.0
Rsa1.0_00154.1.g6979.t1	ref|XP_002865197.1| flagellin-sensitive 2 [Arabidopsis lyrata subsp. lyrata] gi|297311032|gb|EFH41456.1| flagellin-sensitive 2 [Arabidopsis lyrata subsp. lyrata]	1171	1175	0	100.3	79.3	88.0	flagellin-sensitive 2	gbpln	Arabidopsis lyrata	AT5G46330.1 | Symbols: FLS2 | Leucine-rich receptor-like protein kinase family protein | chr5:18791802-18795407 FORWARD LENGTH=1173	1171	1173	0	100.2	78.1	87.4
Rsa1.0_00154.1.g6980.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00154.1.g6981.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00154.1.g6982.t1	ref|NP_199441.1| 3-oxoacyl-[acyl-carrier-protein] synthase I [Arabidopsis thaliana] gi|20141399|sp|P52410.2|KASC1_ARATH RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic; AltName: Full=Beta-ketoacyl-ACP synthase I; Short=KAS I; Flags: Precursor gi|10177710|dbj|BAB11084.1| 3-oxoacyl-[acyl-carrier-protein] synthase I precursor [Arabidopsis thaliana] gi|14335164|gb|AAK59862.1| AT5g46290/MPL12_7 [Arabidopsis thaliana] gi|20334810|gb|AAM16266.1| AT5g46290/MPL12_7 [Arabidopsis thaliana] gi|21593429|gb|AAM65396.1| 3-oxoacyl-(acyl-carrier-protein) synthase I precursor (beta-ketoacyl-acp synthase I) (KAS I) [Arabidopsis thaliana] gi|21703101|gb|AAM74493.1| AT5g46290/MPL12_7 [Arabidopsis thaliana] gi|332007980|gb|AED95363.1| 3-oxoacyl-[acyl-carrier-protein] synthase I [Arabidopsis thaliana]	406	473	0	116.5	96.3	98.3	3-oxoacyl-	gbpln	Arabidopsis thaliana	AT5G46290.1 | Symbols: KASI, KAS1 | 3-ketoacyl-acyl carrier protein synthase I | chr5:18774439-18776629 REVERSE LENGTH=473	406	473	0	116.5	96.3	98.3
Rsa1.0_00154.1.g6983.t1	ref|NP_851141.1| RNA-binding protein [Arabidopsis thaliana] gi|15215748|gb|AAK91419.1| AT5g46250/MPL12_3 [Arabidopsis thaliana] gi|23308375|gb|AAN18157.1| At5g46250/MPL12_3 [Arabidopsis thaliana] gi|332007974|gb|AED95357.1| RNA-binding protein [Arabidopsis thaliana]	418	422	1.00E-152	101.0	72.0	78.9	RNA-binding protein	gbpln	Arabidopsis thaliana	AT5G46250.1 | Symbols: | RNA-binding protein | chr5:18755388-18758056 FORWARD LENGTH=422	418	422	1.00E-155	101.0	72.0	78.9
Rsa1.0_00154.1.g6984.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00154.1.g6985.t1	ref|XP_002863415.1| hypothetical protein ARALYDRAFT_494350 [Arabidopsis lyrata subsp. lyrata] gi|297309250|gb|EFH39674.1| hypothetical protein ARALYDRAFT_494350 [Arabidopsis lyrata subsp. lyrata]	690	676	0	98.0	84.1	89.3	hypothetical protein ARALYDRAFT_494350	gbpln	Arabidopsis lyrata	AT5G46240.1 | Symbols: KAT1 | potassium channel in Arabidopsis thaliana 1 | chr5:18743652-18746561 REVERSE LENGTH=677	690	677	0	98.1	82.9	89.3

Rsa1.0_00154.1.g6986.t1	gb|EOA14036.1| hypothetical protein CARUB_v10027170mg [Capsella rubella]	144	197	2.00E-69	136.8	86.1	92.4	hypothetical protein CARUB_v10027170mg	gbpln	Capsella rubella	AT5G46230.1 | Symbols: | Protein of unknown function, DUF538 | chr5:18742593-18743024 REVERSE LENGTH=143	144	143	4.00E-68	99.3	82.6	90.3
Rsa1.0_00154.1.g6987.t3	gb|EOA23695.1| hypothetical protein CARUB_v10016902mg [Capsella rubella]	595	592	0	99.5	90.3	94.3	hypothetical protein CARUB_v10016902mg	gbpln	Capsella rubella	AT3G54860.1 | Symbols: ATVPS33, VPS33 | Sec1/munc18-like (SM) proteins superfamily | chr3:20324286-20329841 REVERSE LENGTH=592	595	592	0	99.5	89.4	93.8
Rsa1.0_00154.1.g6988.t1	gb|EOA14814.1| hypothetical protein CARUB_v10028121mg [Capsella rubella]	793	791	0	99.7	90.0	94.1	hypothetical protein CARUB_v10028121mg	gbpln	Capsella rubella	AT5G46210.1 | Symbols: CUL4, ATCUL4 | cullin4 | chr5:18731569-18736653 REVERSE LENGTH=792	793	792	0	99.9	89.5	93.4
Rsa1.0_00154.1.g6989.t2	ref|NP_851140.1| large subunit ribosomal protein L14 [Arabidopsis thaliana] gi|18140860|gb|AAL60452.1|AF402993_1 HUELLENLOS PARALOG [Arabidopsis thaliana] gi|16604452|gb|AAL24232.1| AT5g46160/MCL19_22 [Arabidopsis thaliana] gi|332007964|gb|AED95347.1| large subunit ribosomal protein L14 [Arabidopsis thaliana]	175	173	4.00E-83	98.9	92.0	94.3	large subunit ribosomal protein L14	gbpln	Arabidopsis thaliana	AT5G46160.1 | Symbols: | Ribosomal protein L14p/L23e family protein | chr5:18711456-18712341 REVERSE LENGTH=173	175	173	2.00E-85	98.9	92.0	94.3
Rsa1.0_00154.1.g6990.t1	ref|XP_002863424.1| LEM3 (ligand-effect modulator 3) family protein [Arabidopsis lyrata subsp. lyrata] gi|297309259|gb|EFH39683.1| LEM3 (ligand-effect modulator 3) family protein [Arabidopsis lyrata subsp. lyrata]	383	343	1.00E-166	89.6	80.9	85.1	LEM3 (ligand-effect modulator 3) family protein	gbpln	Arabidopsis lyrata	AT5G46150.1 | Symbols: | LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein | chr5:18708735-18710424 REVERSE LENGTH=343	383	343	1.00E-168	89.6	80.7	84.6
Rsa1.0_00154.1.g6991.t1	ref|XP_002863425.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297309260|gb|EFH39684.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	79	79	4.00E-31	100.0	82.3	89.9	expressed protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00154.1.g6992.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00154.1.g6993.t1	ref|NP_199420.1| protein kinase family protein [Arabidopsis thaliana] gi|9757728|dbj|BAB08253.1| serine/threonine protein kinase-like protein [Arabidopsis thaliana] gi|332007952|gb|AED95335.1| protein kinase family protein [Arabidopsis thaliana]	333	332	1.00E-138	99.7	80.8	89.5	protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G46080.1 | Symbols: | Protein kinase superfamily protein | chr5:18689723-18690721 REVERSE LENGTH=332	333	332	1.00E-141	99.7	80.8	89.5
Rsa1.0_00154.1.g6994.t1	ref|NP_199419.2| Guanylate-binding protein [Arabidopsis thaliana] gi|332007951|gb|AED95334.1| Guanylate-binding protein [Arabidopsis thaliana]	1074	1082	0	100.7	89.0	94.1	Guanylate-binding protein	gbpln	Arabidopsis thaliana	AT5G46070.1 | Symbols: | Guanylate-binding family protein | chr5:18683468-18688397 FORWARD LENGTH=1082	1074	1082	0	100.7	89.0	94.1
Rsa1.0_00155.1.g6995.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00155.1.g6996.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	1429	1534	0	107.3	66.6	78.6	F17L21.7	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1429	1262	1.00E-104	88.3	14.1	20.8
Rsa1.0_00155.1.g6997.t1	ref|XP_002466956.1| hypothetical protein SORBIDRAFT_01g017380 [Sorghum bicolor] gi|242039131|ref|XP_002466960.1| hypothetical protein SORBIDRAFT_01g017430 [Sorghum bicolor] gi|241920810|gb|EER93954.1| hypothetical protein SORBIDRAFT_01g017380 [Sorghum bicolor] gi|241920814|gb|EER93958.1| hypothetical protein SORBIDRAFT_01g017430 [Sorghum bicolor]	377	377	0	100.0	95.8	99.2	hypothetical protein SORBIDRAFT_01g017380	gbpln	Sorghum bicolor	AT5G09810.1 | Symbols: ACT7 | actin 7 | chr5:3052809-3054220 FORWARD LENGTH=377	377	377	0	100.0	94.7	98.4
Rsa1.0_00155.1.g6998.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00155.1.g6999.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1431	1491	0	104.2	67.2	80.2	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1431	1262	1.00E-125	88.2	15.2	22.0
Rsa1.0_00155.1.g7000.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00155.1.g7001.t1	ref|XP_002891032.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297336874|gb|EFH67291.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	643	639	0	99.4	89.0	93.6	dehydration-responsive family protein	gbpln	Arabidopsis lyrata	AT1G33170.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:12027262-12030397 FORWARD LENGTH=639	643	639	0	99.4	88.3	93.3

Rsa1.0_00155.1.g7002.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	831	1274	0	153.3	47.7	65.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	831	575	2.00E-49	69.2	19.0	28.9
Rsa1.0_00155.1.g7003.t1	gb|EOA39207.1| hypothetical protein CARUB_v10012177mg [Capsella rubella]	295	347	1.00E-157	117.6	91.5	94.2	hypothetical protein CARUB_v10012177mg	gbpln	Capsella rubella	AT1G33230.1 | Symbols: | TMPIT-like protein | chr1:12046844-12049794 FORWARD LENGTH=347	295	347	1.00E-158	117.6	90.2	93.6
Rsa1.0_00155.1.g7004.t1	ref|NP_174594.1| protein GT-2-like 1 [Arabidopsis thaliana] gi|332193452|gb|AEE31573.1| trihelix transcription factor GTL1 [Arabidopsis thaliana]	649	669	0	103.1	81.0	87.1	protein GT-2-like 1	gbpln	Arabidopsis thaliana	AT1G33240.1 | Symbols: AT-GTL1, AT-GTL2, GTL1 | GT-2-like 1 | chr1:12051859-12054320 REVERSE LENGTH=669	649	669	0	103.1	81.0	87.1
Rsa1.0_00155.1.g7005.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00155.1.g7006.t1	ref|XP_002893759.1| hypothetical protein ARALYDRAFT_890907 [Arabidopsis lyrata subsp. lyrata] gi|297339601|gb|EFH70018.1| hypothetical protein ARALYDRAFT_890907 [Arabidopsis lyrata subsp. lyrata]	511	548	0	107.2	85.7	90.8	hypothetical protein ARALYDRAFT_890907	gbpln	Arabidopsis lyrata	AT1G33250.1 | Symbols: | Protein of unknown function (DUF604) | chr1:12057524-12059346 REVERSE LENGTH=548	511	548	0	107.2	85.3	90.4
Rsa1.0_00155.1.g7007.t3	ref|XP_002883095.1| hypothetical protein ARALYDRAFT_898144 [Arabidopsis lyrata subsp. lyrata] gi|297328935|gb|EFH59354.1| hypothetical protein ARALYDRAFT_898144 [Arabidopsis lyrata subsp. lyrata]	354	837	1.00E-21	236.4	18.4	22.3	hypothetical protein ARALYDRAFT_898144	gbpln	Arabidopsis lyrata	AT3G17900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 45 Blast hits to 44 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 2; Plants - 39; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:6128983-6133069 FORWARD LENGTH=838	354	838	1.00E-23	236.7	17.8	21.2
Rsa1.0_00155.1.g7008.t1	ref|XP_002891037.1| hypothetical protein ARALYDRAFT_313871 [Arabidopsis lyrata subsp. lyrata] gi|297336879|gb|EFH67296.1| hypothetical protein ARALYDRAFT_313871 [Arabidopsis lyrata subsp. lyrata]	347	525	1.00E-172	151.3	85.9	90.2	hypothetical protein ARALYDRAFT_313871	gbpln	Arabidopsis lyrata	AT1G33260.1 | Symbols: | Protein kinase superfamily protein | chr1:12064796-12066114 FORWARD LENGTH=349	347	349	1.00E-172	100.6	84.1	90.2
Rsa1.0_00155.1.g7009.t1	gb|AAG51288.1|AC027035_11 protein kinase, putative [Arabidopsis thaliana]	177	528	1.00E-67	298.3	84.2	90.4	protein kinase, putative	gbpln	Arabidopsis thaliana	AT1G33265.1 | Symbols: | Transmembrane proteins 14C | chr1:12066662-12067820 FORWARD LENGTH=177	177	177	6.00E-69	100.0	84.2	90.4
Rsa1.0_00155.1.g7010.t1	ref|NP_174597.2| patatin-like phospholipase domain-containing protein [Arabidopsis thaliana] gi|38603808|gb|AAR24649.1| At1g33270 [Arabidopsis thaliana] gi|110742517|dbj|BAE99176.1| hypothetical protein [Arabidopsis thaliana] gi|332193457|gb|AEE31578.1| patatin-like phospholipase domain-containing protein [Arabidopsis thaliana]	367	369	1.00E-164	100.5	79.6	87.2	patatin-like phospholipase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G33270.1 | Symbols: | Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein | chr1:12068324-12070157 REVERSE LENGTH=369	367	369	1.00E-167	100.5	79.6	87.2
Rsa1.0_00155.1.g7011.t1	ref|NP_174599.1| putative stage III sporulation protein AA [Arabidopsis thaliana] gi|12322578|gb|AAG51292.1|AC027035_15 unknown protein [Arabidopsis thaliana] gi|48596989|gb|AAT46035.1| At1g33290 [Arabidopsis thaliana] gi|50198961|gb|AAT70483.1| At1g33290 [Arabidopsis thaliana] gi|332193460|gb|AEE31581.1| putative stage III sporulation protein AA [Arabidopsis thaliana]	370	379	0	102.4	94.1	97.3	putative stage III sporulation protein AA	gbpln	Arabidopsis thaliana	AT1G33290.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:12074125-12075989 FORWARD LENGTH=379	370	379	0	102.4	94.1	97.3
Rsa1.0_00155.1.g7012.t1	ref|NP_567663.1| HSP70-interacting protein 1 [Arabidopsis thaliana] gi|75331763|sp|Q93YR3.1|F10AL_ARATH RecName: Full=FAM10 family protein At4g22670 gi|16648867|gb|AAL24285.1| HSP associated protein like [Arabidopsis thaliana] gi|21593067|gb|AAM65016.1| HSP associated protein like [Arabidopsis thaliana] gi|28058906|gb|AAO29967.1| HSP associated protein like [Arabidopsis thaliana] gi|332659238|gb|AEE84638.1| HSP70-interacting protein 1 [Arabidopsis thaliana]	364	441	2.00E-70	121.2	44.2	53.8	HSP70-interacting protein 1	gbpln	Arabidopsis thaliana	AT4G22670.1 | Symbols: AtHip1, HIP1, TPR11 | HSP70-interacting protein 1 | chr4:11918236-11920671 FORWARD LENGTH=441	364	441	4.00E-73	121.2	44.2	53.8

Rsa1.0_00155.1.g7013.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00156.1.g7014.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00156.1.g7015.t1	gb|ACG60669.1| copia-type polyprotein-like protein [Brassica oleracea var. alboglabra]	182	196	2.00E-37	107.7	40.7	44.5	copia-type polyprotein-like protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00156.1.g7016.t1	ref|NP_174257.1| uncharacterized protein [Arabidopsis thaliana] gi|12323541|gb|AAG51753.1|AC068667_32 hypothetical protein; 98808-98386 [Arabidopsis thaliana] gi|28466825|gb|AAO44021.1| At1g29640 [Arabidopsis thaliana] gi|110743019|dbj|BAE99402.1| hypothetical protein [Arabidopsis thaliana] gi|332192993|gb|AEE31114.1| uncharacterized protein AT1G29640 [Arabidopsis thaliana]	136	140	2.00E-51	102.9	82.4	89.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G29640.1 | Symbols: | Protein of unknown function, DUF584 | chr1:10355959-10356381 REVERSE LENGTH=140	136	140	4.00E-54	102.9	82.4	89.0
Rsa1.0_00156.1.g7017.t2	ref|XP_002890823.1| hypothetical protein ARALYDRAFT_473168 [Arabidopsis lyrata subsp. lyrata] gi|297336665|gb|EFH67082.1| hypothetical protein ARALYDRAFT_473168 [Arabidopsis lyrata subsp. lyrata]	695	744	0	107.1	85.5	91.5	hypothetical protein ARALYDRAFT_473168	gbpln	Arabidopsis lyrata	AT1G29630.2 | Symbols: | 5'-3' exonuclease family protein | chr1:10349587-10353538 FORWARD LENGTH=735	695	735	0	105.8	82.6	89.8
Rsa1.0_00156.1.g7018.t2	ref|XP_002894487.1| hypothetical protein ARALYDRAFT_474562 [Arabidopsis lyrata subsp. lyrata] gi|297340329|gb|EFH70746.1| hypothetical protein ARALYDRAFT_474562 [Arabidopsis lyrata subsp. lyrata]	298	230	4.00E-34	77.2	23.8	29.5	hypothetical protein ARALYDRAFT_474562	gbpln	Arabidopsis lyrata	AT1G55080.1 | Symbols: MED9 | MED9; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G29580.1); Has 67203 Blast hits to 25757 proteins in 1293 species: Archae - 12; Bacteria - 4374; Metazoa - 24340; Fungi - 7940; Plants - 5927; Viruses - 273; Other Eukaryotes - 24337 (source: NCBI BLink). | chr1:20553121-20554174 REVERSE LENGTH=244	298	244	3.00E-34	81.9	22.5	28.5
Rsa1.0_00156.1.g7019.t1	gb|AAC63678.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	471	1216	5.00E-28	258.2	14.4	21.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	471	295	4.00E-21	62.6	12.5	19.1
Rsa1.0_00156.1.g7020.t2	ref|NP_190414.1| zinc finger CCCH domain-containing protein 43 [Arabidopsis thaliana] gi|62901491|sp|Q9STM4.1|C3H43_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 43; Short=AtC3H43; AltName: Full=Zinc finger CCCH domain-containing protein ZFN-like 6 gi|4678344|emb|CAB41154.1| putative protein [Arabidopsis thaliana] gi|194272236|gb|ACF37203.1| At3g48440 [Arabidopsis thaliana] gi|332644896|gb|AEE78417.1| zinc finger CCCH domain-containing protein 43 [Arabidopsis thaliana]	346	448	3.00E-18	129.5	16.8	21.1	zinc finger CCCH domain-containing protein 43	gbpln	Arabidopsis thaliana	AT3G48440.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr3:17941402-17943576 FORWARD LENGTH=448	346	448	8.00E-21	129.5	16.8	21.1
Rsa1.0_00156.1.g7021.t1	ref|NP_174252.1| translation initiation factor eIF-4E [Arabidopsis thaliana] gi|12323529|gb|AAG51741.1|AC068667_20 eukaryotic translation initiation factor 4E, putative; 82364-84055 [Arabidopsis thaliana] gi|332192986|gb|AEE31107.1| translation initiation factor eIF-4E [Arabidopsis thaliana]	496	285	1.00E-97	57.5	35.3	39.3	translation initiation factor eIF-4E	gbpln	Arabidopsis thaliana	AT1G29590.1 | Symbols: eIF4E3 | Eukaryotic initiation factor 4E protein | chr1:10339937-10341628 FORWARD LENGTH=285	496	285	1.00E-100	57.5	35.3	39.3
Rsa1.0_00156.1.g7022.t1	gb|EOA37333.1| hypothetical protein CARUB_v10011041mg [Capsella rubella]	133	139	2.00E-33	104.5	72.9	84.2	hypothetical protein CARUB_v10011041mg	gbpln	Capsella rubella	AT1G29540.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34330.1); Has 10 Blast hits to 10 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10327439-10327846 FORWARD LENGTH=135	133	135	6.00E-31	101.5	66.9	78.2
Rsa1.0_00156.1.g7023.t1	gb|EOA36216.1| hypothetical protein CARUB_v10010140mg [Capsella rubella]	183	242	3.00E-22	132.2	53.6	63.9	hypothetical protein CARUB_v10010140mg	gbpln	Capsella rubella	AT1G29530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34310.3); Has 84 Blast hits to 78 proteins in 24 species: Archae - 2; Bacteria - 4; Metazoa - 9; Fungi - 8; Plants - 55; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:10325553-10326651 REVERSE LENGTH=236	183	236	2.00E-20	129.0	51.4	59.6

Rsa1.0_00156.1.g7024.t1	gb|EOA37440.1| hypothetical protein CARUB_v10011510mg [Capsella rubella]	243	158	2.00E-72	65.0	60.9	62.1	hypothetical protein CARUB_v10011510mg	gbpln	Capsella rubella	AT1G29520.1 | Symbols: | AWPM-19-like family protein | chr1:10323735-10324525 FORWARD LENGTH=158	243	158	1.00E-73	65.0	60.1	61.7
Rsa1.0_00156.1.g7025.t1	gb|EOA17225.1| hypothetical protein CARUB_v10005500mg [Capsella rubella]	247	267	5.00E-95	108.1	79.4	89.9	hypothetical protein CARUB_v10005500mg	gbpln	Capsella rubella	AT5G32440.1 | Symbols: | Ubiquitin system component Cue protein | chr5:12077014-12078396 FORWARD LENGTH=264	247	264	8.00E-94	106.9	79.4	89.5
Rsa1.0_00156.1.g7026.t1	gb|EOA36053.1| hypothetical protein CARUB_v10008372mg [Capsella rubella] gi|482571867|gb|EOA36054.1| hypothetical protein CARUB_v10008372mg [Capsella rubella]	757	767	0	101.3	90.9	95.1	hypothetical protein CARUB_v10008372mg	gbpln	Capsella rubella	AT1G29470.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:10310424-10313369 REVERSE LENGTH=770	757	770	0	101.7	91.3	95.4
Rsa1.0_00156.1.g7027.t1	sp|Q0WP85.1|PP150_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g13420, mitochondrial; Flags: Precursor gi|110738270|dbj|BAF01064.1| hypothetical protein [Arabidopsis thaliana]	516	509	0	98.6	85.7	91.7	RecName: Full=Pentatricopeptide repeat-containing protein At2g13420, mitochondrial; Flags: Precursor gi|110738270|dbj|BAF01064.1| hypothetical protein	gbpln	Arabidopsis thaliana	AT1G52640.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:19608857-19610428 REVERSE LENGTH=523	516	523	9.00E-55	101.4	27.7	46.3
Rsa1.0_00156.1.g7028.t2	ref|NP_174756.2| uncharacterized protein [Arabidopsis thaliana] gi|332193648|gb|AEE31769.1| uncharacterized protein AT1G35220 [Arabidopsis thaliana]	1049	1005	0	95.8	87.9	91.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G35220.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 313 Blast hits to 185 proteins in 75 species: Archae - 0; Bacteria - 0; Metazoa - 200; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 46 (source: NCBI BLink). | chr1:12909293-12913916 FORWARD LENGTH=1005	1049	1005	0	95.8	87.9	91.0
Rsa1.0_00156.1.g7029.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	164	1231	7.00E-21	750.6	36.6	54.9	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	164	292	3.00E-11	178.0	18.3	31.1
Rsa1.0_00156.1.g7030.t1	gb|EOA14807.1| hypothetical protein CARUB_v10028114mg [Capsella rubella]	208	335	1.00E-26	161.1	28.8	32.7	hypothetical protein CARUB_v10028114mg	gbpln	Capsella rubella	AT5G64920.1 | Symbols: CIP8 | COP1-interacting protein 8 | chr5:25944338-25945342 REVERSE LENGTH=334	208	334	5.00E-29	160.6	27.9	31.3
Rsa1.0_00156.1.g7031.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00156.1.g7032.t1	ref|NP_174233.2| MEI2-like protein 5 [Arabidopsis thaliana] gi|30690716|ref|NP_849727.1| MEI2-like protein 5 [Arabidopsis thaliana] gi|75331078|sp|Q8VWF5.1|AML5_ARATH RecName: Full=Protein MEI2-like 5; Short=AML5; AltName: Full=MEI2-like protein 5 gi|17065074|gb|AAL32691.1| RNA-binding protein MEI2, putative [Arabidopsis thaliana] gi|17979281|gb|AAL49866.1| putative RNA-binding protein MEI2 [Arabidopsis thaliana] gi|20259101|gb|AAM14266.1| putative RNA-binding protein MEI2 [Arabidopsis thaliana] gi|332192961|gb|AEE31082.1| MEI2-like protein 5 [Arabidopsis thaliana] gi|332192962|gb|AEE31083.1| MEI2-like protein 5 [Arabidopsis thaliana]	707	800	0	113.2	76.8	84.2	MEI2-like protein 5	gbpln	Arabidopsis thaliana	AT1G29400.2 | Symbols: AML5, ML5 | MEI2-like protein 5 | chr1:10290393-10293696 REVERSE LENGTH=800	707	800	0	113.2	76.8	84.2
Rsa1.0_00156.1.g7033.t1	ref|XP_002893558.1| hypothetical protein ARALYDRAFT_473146 [Arabidopsis lyrata subsp. lyrata] gi|297339400|gb|EFH69817.1| hypothetical protein ARALYDRAFT_473146 [Arabidopsis lyrata subsp. lyrata]	164	841	1.00E-14	512.8	34.1	42.1	hypothetical protein ARALYDRAFT_473146	gbpln	Arabidopsis lyrata	AT1G29370.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr1:10278080-10283024 REVERSE LENGTH=831	164	831	9.00E-16	506.7	32.9	40.9
Rsa1.0_00156.1.g7034.t1	ref|XP_002889553.1| hypothetical protein ARALYDRAFT_470554 [Arabidopsis lyrata subsp. lyrata] gi|297335395|gb|EFH65812.1| hypothetical protein ARALYDRAFT_470554 [Arabidopsis lyrata subsp. lyrata]	362	367	4.00E-89	101.4	52.8	65.5	hypothetical protein ARALYDRAFT_470554	gbpln	Arabidopsis lyrata	AT1G05540.1 | Symbols: | Protein of unknown function (DUF295) | chr1:1639348-1640707 FORWARD LENGTH=367	362	367	2.00E-90	101.4	51.9	64.9
Rsa1.0_00156.1.g7035.t5	gb|EOA33021.1| hypothetical protein CARUB_v10016352mg, partial [Capsella rubella]	1009	886	1.00E-110	87.8	19.7	27.9	hypothetical protein CARUB_v10016352mg, partial	gbpln	Capsella rubella	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	1009	719	2.00E-24	71.3	8.8	15.1

Rsa1.0_00156.1.g7036.t1	ref|XP_002883806.1| hypothetical protein ARALYDRAFT_899599 [Arabidopsis lyrata subsp. lyrata] gi|297329646|gb|EFH60065.1| hypothetical protein ARALYDRAFT_899599 [Arabidopsis lyrata subsp. lyrata]	117	165	3.00E-16	141.0	41.0	57.3	hypothetical protein ARALYDRAFT_899599	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00156.1.g7037.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00156.1.g7038.t1	ref|XP_002894278.1| hypothetical protein ARALYDRAFT_337235 [Arabidopsis lyrata subsp. lyrata] gi|297340120|gb|EFH70537.1| hypothetical protein ARALYDRAFT_337235 [Arabidopsis lyrata subsp. lyrata]	160	800	2.00E-29	500.0	40.0	53.8	hypothetical protein ARALYDRAFT_337235	gbpln	Arabidopsis lyrata	AT2G07200.1 | Symbols: | Cysteine proteinases superfamily protein | chr2:2989205-2989878 FORWARD LENGTH=151	160	151	1.00E-15	94.4	21.3	34.4
Rsa1.0_00156.1.g7039.t1	ref|XP_002870431.1| hypothetical protein ARALYDRAFT_493607 [Arabidopsis lyrata subsp. lyrata] gi|297316267|gb|EFH46690.1| hypothetical protein ARALYDRAFT_493607 [Arabidopsis lyrata subsp. lyrata]	148	138	4.00E-19	93.2	35.8	48.6	hypothetical protein ARALYDRAFT_493607	gbpln	Arabidopsis lyrata	AT2G07505.1 | Symbols: | zinc ion binding | chr2:3125671-3126173 FORWARD LENGTH=143	148	143	6.00E-16	96.6	34.5	45.9
Rsa1.0_00156.1.g7040.t1	ref|XP_002894033.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339875|gb|EFH70292.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	104	83	2.00E-11	79.8	39.4	51.0	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00156.1.g7041.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00157.1.g7042.t1	ref|NP_172380.2| WRC, zf-4CXXC-R1 transcription factor and jumonji domain-containing protein [Arabidopsis thaliana] gi|42571415|ref|NP_973798.1| WRC, zf-4CXXC-R1 transcription factor and jumonji domain-containing protein [Arabidopsis thaliana] gi|222423917|dbj|BAH19922.1| AT1G09060 [Arabidopsis thaliana] gi|332190267|gb|AEE28388.1| WRC, zf-4CXXC-R1 transcription factor and jumonji domain-containing protein [Arabidopsis thaliana] gi|332190268|gb|AEE28389.1| WRC, zf-4CXXC-R1 transcription factor and jumonji domain-containing protein [Arabidopsis thaliana]	936	930	0	99.4	76.6	86.0	WRC, zf-4CXXC-R1 transcription factor and jumonji domain-containing protein	gbpln	Arabidopsis thaliana	AT1G09060.2 | Symbols: | Zinc finger, RING-type;Transcription factor jumonji/aspartyl beta-hydroxylase | chr1:2921235-2925212 REVERSE LENGTH=930	936	930	0	99.4	76.6	86.0
Rsa1.0_00157.1.g7043.t1	ref|NP_172378.1| uncharacterized protein [Arabidopsis thaliana] gi|332190265|gb|AEE28386.1| uncharacterized protein AT1G09040 [Arabidopsis thaliana]	859	911	0	106.1	67.1	76.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G09040.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; EXPRESSED IN: leaf; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G09050.1); Has 614 Blast hits to 567 proteins in 104 species: Archae - 2; Bacteria - 12; Metazoa - 344; Fungi - 31; Plants - 81; Viruses - 0; Other Eukaryotes - 144 (source: NCBI BLink). | chr1:2912362-2915174 FORWARD LENGTH=911	859	911	0	106.1	67.1	76.3
Rsa1.0_00157.1.g7044.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00157.1.g7045.t1	gb|AGA95983.1| sucrose non-fermenting 4 [Brassica rapa subsp. pekinensis]	483	482	0	99.8	95.0	97.7	sucrose non-fermenting 4	gbpln	Brassica rapa	AT1G09020.1 | Symbols: SNF4, ATSNF4 | homolog of yeast sucrose nonfermenting 4 | chr1:2900149-2904212 REVERSE LENGTH=487	483	487	0	100.8	93.4	97.1
Rsa1.0_00157.1.g7046.t1	dbj|BAE97370.1| endo-beta-mannosidase [Brassica oleracea]	932	946	0	101.5	89.3	94.1	endo-beta-mannosidase	gbpln	Brassica oleracea	AT1G09010.1 | Symbols: | glycoside hydrolase family 2 protein | chr1:2895259-2899287 REVERSE LENGTH=944	932	944	0	101.3	87.3	93.7

Rsa1.0_00157.1.g7047.t1	ref|NP_172373.3| plant glycogenin-like starch initiation protein 5 [Arabidopsis thaliana] gi|385178635|sp|F4HZC3.1|GUX5_ARATH RecName: Full=Putative UDP-glucuronate:xylan alpha-glucuronosyltransferase 5; Short=UDP-GlcA:xylan glucuronyltransferase 5; AltName: Full=Glycogenin-like protein 5; AltName: Full=Plant glycogenin-like starch initiation protein 5; AltName: Full=Protein GLUCURONIC ACID SUBSTITUTION OF XYLAN 5; Short=AtGUX5 gi|332190259|gb|AEE28380.1| plant glycogenin-like starch initiation protein 5 [Arabidopsis thaliana]	554	566	0	102.2	79.4	88.8	plant glycogenin-like starch initiation protein 5	gbpln	Arabidopsis thaliana	AT1G08990.1 | Symbols: PGSIP5 | plant glycogenin-like starch initiation protein 5 | chr1:2888753-2890753 FORWARD LENGTH=566	554	566	0	102.2	79.4	88.8
Rsa1.0_00157.1.g7048.t8	ref|NP_563830.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|79317421|ref|NP_001031006.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|117940144|sp|O04036.3|ERD6_ARATH RecName: Full=Sugar transporter ERD6; AltName: Full=Early-responsive to dehydration protein 6; AltName: Full=Sugar transporter-like protein 1 gi|3123712|dbj|BAA25989.1| ERD6 protein [Arabidopsis thaliana] gi|6686825|emb|CAB64732.1| putative sugar transporter [Arabidopsis thaliana] gi|30794056|gb|AAP40473.1| putative zinc finger protein ATZF1 [Arabidopsis thaliana] gi|332190249|gb|AEE28370.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|332190250|gb|AEE28371.1| sugar transporter ERD6 [Arabidopsis thaliana]	786	496	0	63.1	51.5	55.3	sugar transporter ERD6	gbpln	Arabidopsis thaliana	AT1G08930.2 | Symbols: ERD6 | Major facilitator superfamily protein | chr1:2873604-2876979 FORWARD LENGTH=496	786	496	0	63.1	51.5	55.3
Rsa1.0_00157.1.g7049.t1	ref|NP_563829.1| sugar transporter ERD6-like 3 [Arabidopsis thaliana] gi|75332302|sp|Q94KE0.1|ERDL3_ARATH RecName: Full=Sugar transporter ERD6-like 3; AltName: Full=Sugar transporter-like protein 2 gi|14194109|gb|AAK56249.1|AF367260_1 At1g08920/F7G19_20 [Arabidopsis thaliana] gi|22137064|gb|AAM91377.1| At1g08920/F7G19_20 [Arabidopsis thaliana] gi|169403716|emb|CAQ16329.1| hexose transporter-like protein [Arabidopsis thaliana] gi|332190246|gb|AEE28367.1| sugar transporter ERD6-like 3 [Arabidopsis thaliana]	470	470	0	100.0	90.0	94.7	sugar transporter ERD6-like 3	gbpln	Arabidopsis thaliana	AT1G08920.1 | Symbols: ESL1 | ERD (early response to dehydration) six-like 1 | chr1:2867446-2870360 FORWARD LENGTH=470	470	470	0	100.0	90.0	94.7
Rsa1.0_00157.1.g7050.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00157.1.g7051.t2	ref|XP_002889721.1| EMB3001 [Arabidopsis lyrata subsp. lyrata] gi|297335563|gb|EFH65980.1| EMB3001 [Arabidopsis lyrata subsp. lyrata]	760	836	0	110.0	50.4	58.7	EMB3001	gbpln	Arabidopsis lyrata	AT1G08910.1 | Symbols: EMB3001 | zinc ion binding;zinc ion binding | chr1:2856227-2860816 FORWARD LENGTH=829	760	829	0	109.1	49.1	57.2
Rsa1.0_00157.1.g7052.t1	ref|XP_002892475.1| hypothetical protein ARALYDRAFT_888122 [Arabidopsis lyrata subsp. lyrata] gi|297338317|gb|EFH68734.1| hypothetical protein ARALYDRAFT_888122 [Arabidopsis lyrata subsp. lyrata]	143	142	8.00E-73	99.3	97.2	97.9	hypothetical protein ARALYDRAFT_888122	gbpln	Arabidopsis lyrata	AT1G08880.1 | Symbols: HTA5, H2AXA, G-H2AX, GAMMA-H2AX | Histone superfamily protein | chr1:2847144-2847676 REVERSE LENGTH=142	143	142	2.00E-74	99.3	95.8	97.2
Rsa1.0_00157.1.g7053.t2	ref|XP_002892474.1| VAMP/synaptobrevin-associated protein 27-2 [Arabidopsis lyrata subsp. lyrata] gi|297338316|gb|EFH68733.1| VAMP/synaptobrevin-associated protein 27-2 [Arabidopsis lyrata subsp. lyrata]	615	386	1.00E-141	62.8	45.0	48.8	VAMP/synaptobrevin-associated protein 27-2	gbpln	Arabidopsis lyrata	AT1G08820.2 | Symbols: VAP27-2 | vamp/synaptobrevin-associated protein 27-2 | chr1:2821810-2824412 REVERSE LENGTH=386	615	386	1.00E-141	62.8	44.4	48.3
Rsa1.0_00157.1.g7054.t2	ref|XP_002892472.1| hypothetical protein ARALYDRAFT_470953 [Arabidopsis lyrata subsp. lyrata] gi|297338314|gb|EFH68731.1| hypothetical protein ARALYDRAFT_470953 [Arabidopsis lyrata subsp. lyrata]	941	1113	0	118.3	60.1	71.5	hypothetical protein ARALYDRAFT_470953	gbpln	Arabidopsis lyrata	AT1G08800.2 | Symbols: | Protein of unknown function, DUF593 | chr1:2813578-2817078 REVERSE LENGTH=1113	941	1113	0	118.3	50.9	61.0

Rsa1.0_00157.1.g7055.t1	ref|NP_172356.1| uncharacterized protein [Arabidopsis thaliana] gi|9802566|gb|AAF99768.1|AC003981_18 F22O13.28 [Arabidopsis thaliana] gi|55978689|gb|AAV68806.1| hypothetical protein AT1G08790 [Arabidopsis thaliana] gi|60547543|gb|AAX23735.1| hypothetical protein At1g08790 [Arabidopsis thaliana] gi|332190226|gb|AEE28347.1| uncharacterized protein AT1G08790 [Arabidopsis thaliana]	168	190	9.00E-57	113.1	82.7	87.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G08790.1 | Symbols: | Protein of unknown function (DUF1685) | chr1:2811989-2812646 FORWARD LENGTH=190	168	190	4.00E-59	113.1	82.7	87.5
Rsa1.0_00157.1.g7056.t1	ref|NP_563825.1| peptidase C13-like protein [Arabidopsis thaliana] gi|30680805|ref|NP_849616.1| peptidase C13-like protein [Arabidopsis thaliana] gi|42571407|ref|NP_973794.1| peptidase C13-like protein [Arabidopsis thaliana] gi|26450273|dbj|BAC42253.1| putative GPI-anchor transamidase [Arabidopsis thaliana] gi|332190220|gb|AEE28341.1| peptidase C13-like protein [Arabidopsis thaliana] gi|332190221|gb|AEE28342.1| peptidase C13-like protein [Arabidopsis thaliana] gi|332190222|gb|AEE28343.1| peptidase C13-like protein [Arabidopsis thaliana]	391	388	0	99.2	88.7	93.9	peptidase C13-like protein	gbpln	Arabidopsis thaliana	AT1G08750.3 | Symbols: | Peptidase C13 family | chr1:2801283-2804392 FORWARD LENGTH=388	391	388	0	99.2	88.7	93.9
Rsa1.0_00157.1.g7057.t2	gb|EOA36640.1| hypothetical protein CARUB_v10011892mg [Capsella rubella]	1857	1530	0	82.4	76.6	79.8	hypothetical protein CARUB_v10011892mg	gbpln	Capsella rubella	AT1G08730.1 | Symbols: XIC, ATXIC | Myosin family protein with Dil domain | chr1:2779963-2788325 FORWARD LENGTH=1538	1857	1538	0	82.8	76.7	79.8
Rsa1.0_00157.1.g7058.t1	gb|AAF86559.1|AC069252_18 F2E2.15 [Arabidopsis thaliana]	442	487	2.00E-80	110.2	41.0	53.6	F2E2.15	gbpln	Arabidopsis thaliana	AT3G19515.2 | Symbols: | CONTAINS InterPro DOMAIN/s: Apoptosis inhibitory 5 (InterPro:IPR008383); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23935.1); Has 546 Blast hits to 394 proteins in 84 species: Archae - 0; Bacteria - 3; Metazoa - 210; Fungi - 15; Plants - 143; Viruses - 0; Other Eukaryotes - 175 (source: NCBI BLink). | chr3:6766872-6771078 REVERSE LENGTH=805	442	805	1.00E-56	182.1	29.0	41.0
Rsa1.0_00157.1.g7059.t2	gb|EOA36256.1| hypothetical protein CARUB_v10010384mg [Capsella rubella]	182	188	6.00E-61	103.3	61.5	66.5	hypothetical protein CARUB_v10010384mg	gbpln	Capsella rubella	AT1G08465.1 | Symbols: YAB2 | Plant-specific transcription factor YABBY family protein | chr1:2676033-2679382 FORWARD LENGTH=184	182	184	6.00E-58	101.1	61.5	69.8
Rsa1.0_00157.1.g7060.t1	ref|NP_001184936.1| calreticulin-3 [Arabidopsis thaliana] gi|332190172|gb|AEE28293.1| calreticulin-3 [Arabidopsis thaliana]	396	399	0	100.8	92.2	94.7	calreticulin-3	gbpln	Arabidopsis thaliana	AT1G08450.3 | Symbols: CRT3 | calreticulin 3 | chr1:2668008-2671800 REVERSE LENGTH=399	396	399	0	100.8	92.2	94.7
Rsa1.0_00157.1.g7061.t1	ref|XP_002889694.1| hypothetical protein ARALYDRAFT_334132 [Arabidopsis lyrata subsp. lyrata] gi|297335536|gb|EFH65953.1| hypothetical protein ARALYDRAFT_334132 [Arabidopsis lyrata subsp. lyrata]	527	501	0	95.1	77.0	81.8	hypothetical protein ARALYDRAFT_334132	gbpln	Arabidopsis lyrata	AT1G08440.1 | Symbols: | Aluminium activated malate transporter family protein | chr1:2663027-2665343 FORWARD LENGTH=501	527	501	0	95.1	75.5	81.0
Rsa1.0_00157.1.g7062.t1	dbj|BAE97280.1| putative aluminum activated malate transporter [Brassica napus]	496	498	0	100.4	91.7	95.0	putative aluminum activated malate transporter	gbpln	Brassica napus	AT1G08430.1 | Symbols: ALMT1, ATALMT1 | aluminum-activated malate transporter 1 | chr1:2658800-2661029 FORWARD LENGTH=493	496	493	0	99.4	74.0	84.3
Rsa1.0_00157.1.g7063.t1	ref|NP_172318.1| serine/threonine-protein phosphatase BSL2 [Arabidopsis thaliana] gi|160359046|sp|Q9SJF0.2|BSL2_ARATH RecName: Full=Serine/threonine-protein phosphatase BSL2; AltName: Full=BSU1-like protein 2 gi|332190166|gb|AEE28287.1| serine/threonine-protein phosphatase BSL2 [Arabidopsis thaliana]	999	1018	0	101.9	92.4	95.3	serine/threonine-protein phosphatase BSL2	gbpln	Arabidopsis thaliana	AT1G08420.1 | Symbols: BSL2 | BRI1 suppressor 1 (BSU1)-like 2 | chr1:2649959-2656564 FORWARD LENGTH=1018	999	1018	0	101.9	92.4	95.3
Rsa1.0_00157.1.g7064.t1	gb|EOA36709.1| hypothetical protein CARUB_v10012258mg [Capsella rubella]	577	589	0	102.1	88.7	92.7	hypothetical protein CARUB_v10012258mg	gbpln	Capsella rubella	AT1G08410.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:2646307-2649106 FORWARD LENGTH=589	577	589	0	102.1	87.9	92.4
Rsa1.0_00157.1.g7065.t1	dbj|BAJ33638.1| unnamed protein product [Thellungiella halophila]	145	142	2.00E-67	97.9	89.0	93.1	unnamed protein product	----	----	AT1G08380.1 | Symbols: PSAO | photosystem I subunit O | chr1:2641004-2641739 REVERSE LENGTH=140	145	140	4.00E-69	96.6	89.0	91.0

Rsa1.0_00157.1.g7066.t1	ref|XP_002890493.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336335|gb|EFH66752.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	361	337	3.00E-66	93.4	44.0	56.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G22090.1 | Symbols: emb2204 | Protein of unknown function (DUF626) | chr1:7795721-7797252 FORWARD LENGTH=329	361	329	4.00E-64	91.1	41.3	55.4
Rsa1.0_00157.1.g7067.t1	dbj|BAJ33638.1| unnamed protein product [Thellungiella halophila]	80	142	2.00E-36	177.5	92.5	98.8	unnamed protein product	----	----	AT1G08380.1 | Symbols: PSAO | photosystem I subunit O | chr1:2641004-2641739 REVERSE LENGTH=140	80	140	7.00E-39	175.0	92.5	97.5
Rsa1.0_00157.1.g7068.t1	ref|XP_002889689.1| hypothetical protein ARALYDRAFT_470898 [Arabidopsis lyrata subsp. lyrata] gi|297335531|gb|EFH65948.1| hypothetical protein ARALYDRAFT_470898 [Arabidopsis lyrata subsp. lyrata]	361	368	1.00E-128	101.9	76.2	85.0	hypothetical protein ARALYDRAFT_470898	gbpln	Arabidopsis lyrata	AT1G08370.1 | Symbols: DCP1, ATDCP1 | decapping 1 | chr1:2638355-2640367 FORWARD LENGTH=367	361	367	1.00E-126	101.7	74.2	83.7
Rsa1.0_00157.1.g7069.t4	ref|NP_172308.2| esterase/lipase/thioesterase-like protein [Arabidopsis thaliana] gi|193211489|gb|ACF16164.1| At1g08310 [Arabidopsis thaliana] gi|332190151|gb|AEE28272.1| esterase/lipase/thioesterase-like protein [Arabidopsis thaliana]	583	315	1.00E-133	54.0	41.2	46.1	esterase/lipase/thioesterase-like protein	gbpln	Arabidopsis thaliana	AT1G08310.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:2619134-2620338 FORWARD LENGTH=315	583	315	1.00E-135	54.0	41.2	46.1
Rsa1.0_00157.1.g7070.t1	ref|NP_001077487.1| transmembrane amino acid transporter [Arabidopsis thaliana] gi|403399391|sp|F4HW02.1|GAT1_ARATH RecName: Full=GABA transporter 1; Short=AtGAT1; AltName: Full=Bidirectional amino acid transporter 1 gi|332190143|gb|AEE28264.1| GABA transporter 1 [Arabidopsis thaliana]	108	451	6.00E-48	417.6	86.1	90.7	transmembrane amino acid transporter	gbpln	Arabidopsis thaliana	AT1G08230.2 | Symbols: | Transmembrane amino acid transporter family protein | chr1:2583715-2586700 REVERSE LENGTH=451	108	451	1.00E-50	417.6	86.1	90.7
Rsa1.0_00157.1.g7071.t1	gb|EOA40374.1| hypothetical protein CARUB_v10009101mg [Capsella rubella]	370	453	1.00E-171	122.4	81.9	87.6	hypothetical protein CARUB_v10009101mg	gbpln	Capsella rubella	AT1G08230.2 | Symbols: | Transmembrane amino acid transporter family protein | chr1:2583715-2586700 REVERSE LENGTH=451	370	451	1.00E-163	121.9	80.0	85.4
Rsa1.0_00157.1.g7072.t1	gb|EOA40235.1| hypothetical protein CARUB_v10008955mg [Capsella rubella]	887	493	0	55.6	48.7	50.8	hypothetical protein CARUB_v10008955mg	gbpln	Capsella rubella	AT1G08210.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:2577119-2580581 REVERSE LENGTH=492	887	492	0	55.5	48.0	50.8
Rsa1.0_00157.1.g7073.t1	ref|XP_002892445.1| hypothetical protein ARALYDRAFT_888049 [Arabidopsis lyrata subsp. lyrata] gi|297338287|gb|EFH68704.1| hypothetical protein ARALYDRAFT_888049 [Arabidopsis lyrata subsp. lyrata]	110	111	2.00E-35	100.9	82.7	88.2	hypothetical protein ARALYDRAFT_888049	gbpln	Arabidopsis lyrata	AT1G08180.1 | Symbols: | unknown protein; Has 53 Blast hits to 53 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 52; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2564741-2565076 REVERSE LENGTH=111	110	111	1.00E-37	100.9	81.8	87.3
Rsa1.0_00157.1.g7074.t1	gb|EOA37085.1| hypothetical protein CARUB_v10010243mg [Capsella rubella]	209	222	6.00E-89	106.2	87.6	94.3	hypothetical protein CARUB_v10010243mg	gbpln	Capsella rubella	AT1G08160.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr1:2559672-2560337 REVERSE LENGTH=221	209	221	9.00E-88	105.7	85.2	92.8
Rsa1.0_00157.1.g7075.t1	gb|AEZ68614.1| high-affinity nitrate transporter [Brassica juncea]	530	530	0	100.0	97.9	99.4	high-affinity nitrate transporter	gbpln	Brassica juncea	AT1G08090.1 | Symbols: ATNRT2:1, NRT2, NRT2;1AT, ACH1, LIN1, ATNRT2.1, NRT2.1, NRT2:1 | nitrate transporter 2:1 | chr1:2524139-2525920 FORWARD LENGTH=530	530	530	0	100.0	94.0	97.0
Rsa1.0_00157.1.g7076.t1	ref|NP_172283.1| C3HC4-type RING finger-containing protein [Arabidopsis thaliana] gi|8778841|gb|AAF79840.1|AC026875_20 T6D22.13 [Arabidopsis thaliana] gi|332190114|gb|AEE28235.1| C3HC4-type RING finger-containing protein [Arabidopsis thaliana]	627	641	0	102.2	73.4	83.4	C3HC4-type RING finger-containing protein	gbpln	Arabidopsis thaliana	AT1G08050.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr1:2499088-2501311 REVERSE LENGTH=641	627	641	0	102.2	73.4	83.4
Rsa1.0_00157.1.g7077.t2	gb|EOA36703.1| hypothetical protein CARUB_v10012236mg [Capsella rubella]	103	140	1.00E-34	135.9	71.8	79.6	hypothetical protein CARUB_v10012236mg	gbpln	Capsella rubella	AT1G08035.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G28330.1); Has 10 Blast hits to 10 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2494772-2495149 FORWARD LENGTH=125	103	125	3.00E-35	121.4	73.8	84.5
Rsa1.0_00157.1.g7078.t1	gb|EOA36903.1| hypothetical protein CARUB_v10011453mg [Capsella rubella]	501	499	0	99.6	79.8	87.6	hypothetical protein CARUB_v10011453mg	gbpln	Capsella rubella	AT1G08030.1 | Symbols: TPST | tyrosylprotein sulfotransferase | chr1:2489575-2492741 REVERSE LENGTH=500	501	500	0	99.8	80.2	86.8

Rsa1.0_00157.1.g7079.t1	gb|EOA36949.1| hypothetical protein CARUB_v10009871mg [Capsella rubella] gi|482572763|gb|EOA36950.1| hypothetical protein CARUB_v10009871mg [Capsella rubella]	285	300	1.00E-91	105.3	67.0	75.4	hypothetical protein CARUB_v10009871mg	gbpln	Capsella rubella	AT1G08010.2 | Symbols: GATA11 | GATA transcription factor 11 | chr1:2486202-2487402 REVERSE LENGTH=303	285	303	5.00E-90	106.3	64.6	76.1
Rsa1.0_00157.1.g7080.t1	ref|XP_002889677.1| SIT4 phosphatase-associated family protein [Arabidopsis lyrata subsp. lyrata] gi|297335519|gb|EFH65936.1| SIT4 phosphatase-associated family protein [Arabidopsis lyrata subsp. lyrata]	796	805	0	101.1	87.7	92.6	SIT4 phosphatase-associated family protein	gbpln	Arabidopsis lyrata	AT1G07990.1 | Symbols: | SIT4 phosphatase-associated family protein | chr1:2477413-2482898 FORWARD LENGTH=802	796	802	0	100.8	86.8	92.1
Rsa1.0_00157.1.g7081.t1	gb|EOA38222.1| hypothetical protein CARUB_v10009702mg [Capsella rubella]	145	330	3.00E-40	227.6	76.6	86.9	hypothetical protein CARUB_v10009702mg	gbpln	Capsella rubella	AT1G07985.1 | Symbols: | Expressed protein | chr1:2475508-2475942 FORWARD LENGTH=144	145	144	7.00E-41	99.3	75.9	83.4
Rsa1.0_00157.1.g7082.t1	gb|AAF79822.1|AC026875_2 T6D22.2 [Arabidopsis thaliana]	462	967	0	209.3	97.2	98.3	T6D22.2	gbpln	Arabidopsis thaliana	AT5G60390.3 | Symbols: | GTP binding Elongation factor Tu family protein | chr5:24289226-24290675 FORWARD LENGTH=449	462	449	0	97.2	92.2	93.1
Rsa1.0_00157.1.g7083.t1	ref|XP_002865857.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311692|gb|EFH42116.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	128	142	8.00E-22	110.9	48.4	68.0	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00157.1.g7084.t1	gb|EOA38236.1| hypothetical protein CARUB_v10009719mg [Capsella rubella]	250	328	1.00E-129	131.2	87.6	94.0	hypothetical protein CARUB_v10009719mg	gbpln	Capsella rubella	AT1G07890.8 | Symbols: APX1, MEE6, CS1, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250	250	250	1.00E-131	100.0	88.4	94.0
Rsa1.0_00157.1.g7085.t1	ref|NP_001184932.1| putative serine/threonine-protein kinase RLCKVII [Arabidopsis thaliana] gi|332190074|gb|AEE28195.1| putative serine/threonine-protein kinase RLCKVII [Arabidopsis thaliana]	420	538	0	128.1	87.6	90.7	putative serine/threonine-protein kinase RLCKVII	gbpln	Arabidopsis thaliana	AT1G07870.2 | Symbols: | Protein kinase superfamily protein | chr1:2428942-2431843 REVERSE LENGTH=538	420	538	0	128.1	87.6	90.7
Rsa1.0_00157.1.g7086.t1	ref|XP_002892421.1| hypothetical protein ARALYDRAFT_470820 [Arabidopsis lyrata subsp. lyrata] gi|297338263|gb|EFH68680.1| hypothetical protein ARALYDRAFT_470820 [Arabidopsis lyrata subsp. lyrata]	166	132	2.00E-38	79.5	50.0	60.8	hypothetical protein ARALYDRAFT_470820	gbpln	Arabidopsis lyrata	AT1G07860.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Protein kinase superfamily protein (TAIR:AT1G07870.2); Has 7 Blast hits to 7 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2428942-2429431 REVERSE LENGTH=135	166	135	3.00E-36	81.3	50.6	56.0
Rsa1.0_00157.1.g7087.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_00157.1.g7088.t1	gb|EOA39923.1| hypothetical protein CARUB_v10008611mg [Capsella rubella]	454	612	1.00E-111	134.8	58.6	73.1	hypothetical protein CARUB_v10008611mg	gbpln	Capsella rubella	AT1G07705.2 | Symbols: | NOT2 / NOT3 / NOT5 family | chr1:2382090-2385856 FORWARD LENGTH=614	454	614	1.00E-110	135.2	57.7	72.9
Rsa1.0_00157.1.g7089.t1	gb|EOA25182.1| hypothetical protein CARUB_v10018494mg [Capsella rubella]	274	282	7.00E-39	102.9	36.5	50.7	hypothetical protein CARUB_v10018494mg	gbpln	Capsella rubella	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	274	303	2.00E-32	110.6	33.6	48.2
Rsa1.0_00158.1.g7090.t1	gb|EOA22207.1| hypothetical protein CARUB_v10002795mg [Capsella rubella]	361	352	2.33E-156	97.5	77.0	85.6	hypothetical protein CARUB_v10002795mg	gbpln	Capsella rubella	AT5G06920.1 | Symbols: FLA21 | FASCICLIN-like arabinogalactan protein 21 precursor | chr5:2142858-2143919 FORWARD LENGTH=353	361	353	2.33E-156	97.8	75.9	82.8
Rsa1.0_00158.1.g7091.t1	ref|NP_568727.1| cycloeucalenol cycloisomerase [Arabidopsis thaliana] gi|24211551|sp|Q9M643.1|CCI1_ARATH RecName: Full=Cycloeucalenol cycloisomerase; AltName: Full=Cycloeucalenol--obtusifoliol isomerase; AltName: Full=Cyclopropyl sterol isomerase gi|7715089|gb|AAF67863.1|AF216756_1 cyclopropyl isomerase [Arabidopsis thaliana] gi|107738422|gb|ABF83694.1| At5g50375 [Arabidopsis thaliana] gi|332008552|gb|AED95935.1| cycloeucalenol cycloisomerase [Arabidopsis thaliana]	282	280	1.00E-143	99.3	90.4	94.0	cycloeucalenol cycloisomerase	gbpln	Arabidopsis thaliana	AT5G50375.1 | Symbols: CPI1 | cyclopropyl isomerase | chr5:20511856-20513931 FORWARD LENGTH=280	282	280	1.00E-145	99.3	90.4	94.0
Rsa1.0_00158.1.g7092.t1	gb|ACG69524.1| steroleosin SLO1-3 [Brassica napus]	356	341	1.00E-180	95.8	91.0	93.0	steroleosin SLO1-3	gbpln	Brassica napus	AT5G50700.1 | Symbols: HSD1 | hydroxysteroid dehydrogenase 1 | chr5:20623259-20624995 REVERSE LENGTH=349	356	349	1.00E-163	98.0	80.9	87.9
Rsa1.0_00158.1.g7093.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00158.1.g7094.t1	ref|XP_002865818.1| hypothetical protein ARALYDRAFT_918095 [Arabidopsis lyrata subsp. lyrata] gi|297311653|gb|EFH42077.1| hypothetical protein ARALYDRAFT_918095 [Arabidopsis lyrata subsp. lyrata]	349	358	1.00E-136	102.6	79.7	84.5	hypothetical protein ARALYDRAFT_918095	gbpln	Arabidopsis lyrata	AT5G50570.2 | Symbols: SPL13A, SPL13 | Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein | chr5:20582555-20583791 REVERSE LENGTH=359	349	359	1.00E-136	102.9	79.1	84.0
Rsa1.0_00158.1.g7095.t3	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	949	1342	1.00E-138	141.4	30.5	43.1	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT5G50570.2 | Symbols: SPL13A, SPL13 | Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein | chr5:20582555-20583791 REVERSE LENGTH=359	949	359	1.00E-128	37.8	27.9	29.9
Rsa1.0_00158.1.g7096.t1	ref|NP_194222.1| protein transport protein sec61 subunit gamma-1 [Arabidopsis thaliana] gi|18423153|ref|NP_568728.1| protein transport protein sec61 subunit gamma-1 [Arabidopsis thaliana] gi|297795847|ref|XP_002865808.1| hypothetical protein ARALYDRAFT_495113 [Arabidopsis lyrata subsp. lyrata] gi|297799504|ref|XP_002867636.1| hypothetical protein ARALYDRAFT_492346 [Arabidopsis lyrata subsp. lyrata] gi|408407792|sp|P0DI74.1|S61G1_ARATH RecName: Full=Protein transport protein Sec61 subunit gamma-1 gi|408407793|sp|P0DI75.1|S61G2_ARATH RecName: Full=Protein transport protein Sec61 subunit gamma-2 gi|13877813|gb|AAK43984.1|AF370169_1 putative protein translocation complex Sec61 gamma chain [Arabidopsis thaliana] gi|4455235|emb|CAB36734.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana] gi|7269342|emb|CAB79401.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana] gi|9758755|dbj|BAB09131.1| protein translocation complex Sec61 gamma chain [Arabidopsis thaliana] gi|16323486|gb|AAL15237.1| putative	69	69	1.00E-30	100.0	100.0	100.0	protein transport protein sec61 subunit gamma-1	gbpln	Arabidopsis lyrata	AT5G50460.1 | Symbols: | secE/sec61-gamma protein transport protein | chr5:20552168-20552509 REVERSE LENGTH=69	69	69	2.00E-33	100.0	100.0	100.0
Rsa1.0_00158.1.g7097.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00158.1.g7098.t1	ref|NP_199888.1| reversibly glycosylated polypeptide 4 [Arabidopsis thaliana] gi|75180555|sp|Q9LUE6.1|RGP4_ARATH RecName: Full=Probable UDP-arabinopyranose mutase 4; AltName: Full=Reversibly glycosylated polypeptide 4; Short=AtRGP4; AltName: Full=UDP-L-arabinose mutase 4 gi|14326034|gb|AAK60126.1|AF329280_1 reversibly glycosylated polypeptide RGP-4 [Arabidopsis thaliana] reversibly glycosylated polypeptide gi|8777398|dbj|BAA96988.1| UDP-glucose:protein transglucosylase; reversibly glycosylated polypeptide [Arabidopsis thaliana] gi|28393265|gb|AAO42061.1| putative UDP-glucose:protein transglucosylase [Arabidopsis thaliana] gi|28827766|gb|AAO50727.1| putative UDP-glucose [Arabidopsis thaliana] gi|332008605|gb|AED95988.1| reversibly glycosylated polypeptide 4 [Arabidopsis thaliana]	362	364	0	100.6	93.9	96.4	reversibly glycosylated polypeptide 4	gbpln	Arabidopsis thaliana	AT5G50750.1 | Symbols: RGP4 | reversibly glycosylated polypeptide 4 | chr5:20641066-20642470 FORWARD LENGTH=364	362	364	0	100.6	93.9	96.4
Rsa1.0_00158.1.g7099.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00158.1.g7100.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	527	1307	0	248.0	65.5	78.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	527	1262	2.00E-98	239.5	32.8	52.8
Rsa1.0_00158.1.g7101.t1	gb|AAC95173.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	401	1200	1.00E-129	299.3	53.4	61.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00158.1.g7102.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00158.1.g7103.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	936	1164	1.00E-171	124.4	35.0	51.4	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	936	746	4.00E-54	79.7	14.6	21.9

Rsa1.0_00158.1.g7104.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00158.1.g7105.t2	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	328	1250	1.00E-69	381.1	47.0	64.3	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00158.1.g7106.t1	gb|EOA14070.1| hypothetical protein CARUB_v10027207mg [Capsella rubella]	169	184	6.00E-49	108.9	69.2	79.3	hypothetical protein CARUB_v10027207mg	gbpln	Capsella rubella	AT5G50760.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:20644780-20645331 FORWARD LENGTH=183	169	183	3.00E-51	108.3	72.2	84.6
Rsa1.0_00158.1.g7107.t1	sp|F4IMK4.2|MES19_ARATH RecName: Full=Putative methylesterase 19; Short=AtMES19	264	260	1.00E-111	98.5	73.5	83.0	RecName: Full=Putative methylesterase 19; Short=AtMES19	----	----	AT2G23560.1 | Symbols: ATMES7, MES7 | methyl esterase 7 | chr2:10029336-10030282 REVERSE LENGTH=260	264	260	1.00E-111	98.5	72.7	82.6
Rsa1.0_00158.1.g7108.t1	gb|EOA28827.1| hypothetical protein CARUB_v10025066mg [Capsella rubella]	173	200	5.00E-75	115.6	76.3	86.1	hypothetical protein CARUB_v10025066mg	gbpln	Capsella rubella	AT2G23550.1 | Symbols: ATMES6, MES6, ABE1 | methyl esterase 6 | chr2:10027813-10028767 REVERSE LENGTH=265	173	265	8.00E-76	153.2	76.9	82.7
Rsa1.0_00158.1.g7109.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	923	1352	1.00E-178	146.5	41.5	56.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	923	746	1.00E-87	80.8	19.0	25.2
Rsa1.0_00158.1.g7110.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	382	1529	2.00E-32	400.3	17.8	29.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00158.1.g7111.t1	ref|NP_567315.1| Mannose-P-dolichol utilization defect 1 protein [Arabidopsis thaliana] gi|75161427|sp|Q8VY63.1|MPU12_ARATH RecName: Full=Mannose-P-dolichol utilization defect 1 protein homolog 2 gi|18252961|gb|AAL62407.1| unknown protein [Arabidopsis thaliana] gi|21389665|gb|AAM48031.1| unknown protein [Arabidopsis thaliana] gi|332657164|gb|AEE82564.1| Mannose-P-dolichol utilization defect 1 protein [Arabidopsis thaliana]	246	235	1.00E-115	95.5	83.7	88.6	Mannose-P-dolichol utilization defect 1 protein	gbpln	Arabidopsis thaliana	AT4G07390.1 | Symbols: | Mannose-P-dolichol utilization defect 1 protein | chr4:4195750-4197317 FORWARD LENGTH=235	246	235	1.00E-118	95.5	83.7	88.6
Rsa1.0_00158.1.g7112.t1	dbj|BAB03143.1| ankyrin-like protein [Arabidopsis thaliana]	721	1100	1.00E-165	152.6	40.5	45.5	ankyrin-like protein	gbpln	Arabidopsis thaliana	AT3G12350.1 | Symbols: | F-box family protein | chr3:3931626-3933104 FORWARD LENGTH=422	721	422	1.00E-164	58.5	40.6	45.9
Rsa1.0_00158.1.g7113.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00159.1.g7114.t1	ref|XP_002879161.1| VHA-A1 [Arabidopsis lyrata subsp. lyrata] gi|297325000|gb|EFH55420.1| VHA-A1 [Arabidopsis lyrata subsp. lyrata]	2782	822	0	29.5	27.4	28.0	VHA-A1	gbpln	Arabidopsis lyrata	AT2G28520.1 | Symbols: VHA-A1 | vacuolar proton ATPase A1 | chr2:12210026-12215532 FORWARD LENGTH=817	2782	817	0	29.4	26.8	27.5
Rsa1.0_00159.1.g7115.t1	gb|EOA26342.1| hypothetical protein CARUB_v10022558mg, partial [Capsella rubella]	887	1034	0	116.6	71.5	82.4	hypothetical protein CARUB_v10022558mg, partial	gbpln	Capsella rubella	AT2G28540.2 | Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr2:12218652-12223594 FORWARD LENGTH=960	887	960	0	108.2	69.4	80.0
Rsa1.0_00159.1.g7116.t1	gb|EOA27271.1| hypothetical protein CARUB_v10023390mg, partial [Capsella rubella]	388	390	0	100.5	83.5	87.9	hypothetical protein CARUB_v10023390mg, partial	gbpln	Capsella rubella	AT2G28560.1 | Symbols: ATRAD51B, RAD51B | DNA repair (Rad51) family protein | chr2:12237052-12239086 REVERSE LENGTH=371	388	371	0	95.6	82.5	87.4
Rsa1.0_00159.1.g7117.t1	ref|NP_565675.1| uncharacterized protein [Arabidopsis thaliana] gi|4510404|gb|AAD21491.1| expressed protein [Arabidopsis thaliana] gi|89111822|gb|ABD60683.1| At2g28570 [Arabidopsis thaliana] gi|330253050|gb|AEC08144.1| uncharacterized protein AT2G28570 [Arabidopsis thaliana]	76	78	2.00E-12	102.6	69.7	81.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G28570.1 | Symbols: | unknown protein; Has 13 Blast hits to 13 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:12242064-12242300 FORWARD LENGTH=78	76	78	3.00E-15	102.6	69.7	81.6
Rsa1.0_00159.1.g7118.t1	ref|NP_850123.1| PsbP domain-containing protein 2 [Arabidopsis thaliana] gi|75161418|sp|Q8VY52.1|PPD2_ARATH RecName: Full=PsbP domain-containing protein 2, chloroplastic; AltName: Full=PsbP-related thylakoid lumenal protein 3; Flags: Precursor gi|18253015|gb|AAL62434.1| unknown protein [Arabidopsis thaliana] gi|22136412|gb|AAM91284.1| unknown protein [Arabidopsis thaliana] gi|330253054|gb|AEC08148.1| PsbP domain-containing protein 2 [Arabidopsis thaliana]	237	232	3.00E-93	97.9	76.8	82.7	PsbP domain-containing protein 2	gbpln	Arabidopsis thaliana	AT2G28605.1 | Symbols: | Photosystem II reaction center PsbP family protein | chr2:12254911-12255689 FORWARD LENGTH=232	237	232	8.00E-96	97.9	76.8	82.7

Rsa1.0_00159.1.g7119.t1	ref|XP_002879183.1| hypothetical protein ARALYDRAFT_481786 [Arabidopsis lyrata subsp. lyrata] gi|297325022|gb|EFH55442.1| hypothetical protein ARALYDRAFT_481786 [Arabidopsis lyrata subsp. lyrata]		103	107	3.00E-33	103.9	68.0	78.6	hypothetical protein ARALYDRAFT_481786	gbpln	Arabidopsis lyrata	AT2G28725.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G07795.1); Has 35 Blast hits to 35 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:12328605-12328943 FORWARD LENGTH=112		103	112	6.00E-33	108.7	65.0	75.7
Rsa1.0_00159.1.g7120.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]		103	248	1.00E-51	240.8	98.1	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103		103	103	6.00E-52	100.0	98.1	100.0
Rsa1.0_00159.1.g7121.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00159.1.g7122.t1	ref|XP_002879183.1| hypothetical protein ARALYDRAFT_481786 [Arabidopsis lyrata subsp. lyrata] gi|297325022|gb|EFH55442.1| hypothetical protein ARALYDRAFT_481786 [Arabidopsis lyrata subsp. lyrata]		170	107	2.00E-31	62.9	40.0	45.9	hypothetical protein ARALYDRAFT_481786	gbpln	Arabidopsis lyrata	AT2G28725.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G07795.1); Has 35 Blast hits to 35 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:12328605-12328943 FORWARD LENGTH=112		170	112	2.00E-32	65.9	40.0	45.3
Rsa1.0_00159.1.g7123.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]		103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103		103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_00159.1.g7124.t1	ref|XP_002881008.1| hypothetical protein ARALYDRAFT_320665 [Arabidopsis lyrata subsp. lyrata] gi|297326847|gb|EFH57267.1| hypothetical protein ARALYDRAFT_320665 [Arabidopsis lyrata subsp. lyrata]		796	795	0	99.9	85.6	92.3	hypothetical protein ARALYDRAFT_320665	gbpln	Arabidopsis lyrata	AT2G28780.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: inflorescence meristem, root, flower; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF939, bacterial (InterPro:IPR010343); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G09450.1); Has 671 Blast hits to 667 proteins in 305 species: Archae - 0; Bacteria - 588; Metazoa - 0; Fungi - 2; Plants - 66; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink). | chr2:12340099-12343281 REVERSE LENGTH=796		796	796	0	100.0	84.5	91.7
Rsa1.0_00159.1.g7125.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00159.1.g7126.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00159.1.g7127.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00159.1.g7128.t1	gb|AAO12209.1| thaumatin-like cytokinin-binding protein [Brassica oleracea]		252	250	1.00E-138	99.2	96.4	98.0	thaumatin-like cytokinin-binding protein	gbpln	Brassica oleracea	AT2G28790.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr2:12354664-12355413 REVERSE LENGTH=249		252	249	1.00E-124	98.8	85.3	91.3
Rsa1.0_00159.1.g7129.t1	gb|EOA27075.1| hypothetical protein CARUB_v10023172mg [Capsella rubella]		453	460	0	101.5	90.3	94.3	hypothetical protein CARUB_v10023172mg	gbpln	Capsella rubella	AT2G28800.1 | Symbols: ALB3 | 63 kDa inner membrane family protein | chr2:12356669-12359158 REVERSE LENGTH=462		453	462	0	102.0	89.6	93.6
Rsa1.0_00159.1.g7130.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]		294	1142	1.00E-58	388.4	49.0	67.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484		294	484	2.00E-22	164.6	22.8	32.3
Rsa1.0_00159.1.g7131.t2	ref|XP_002879112.1| cation/H+ exchanger [Arabidopsis lyrata subsp. lyrata] gi|297324951|gb|EFH55371.1| cation/H+ exchanger [Arabidopsis lyrata subsp. lyrata]		863	848	0	98.3	66.3	76.5	cation/H+ exchanger	gbpln	Arabidopsis lyrata	AT2G28180.1 | Symbols: ATCHX8, CHX8, CHX08 | Cation/hydrogen exchanger family protein | chr2:12010994-12013832 REVERSE LENGTH=847		863	847	0	98.1	65.0	75.8
Rsa1.0_00159.1.g7132.t1	ref|NP_850126.1| Dof zinc finger protein DOF2.2 [Arabidopsis thaliana] gi|55584015|sp|Q9ZV33.2|DOF22_ARATH RecName: Full=Dof zinc finger protein DOF2.2; Short=AtDOF2.2 gi|189339294|gb|ACD89067.1| At2g28810 [Arabidopsis thaliana] gi|330253082|gb|AEC08176.1| Dof zinc finger protein DOF2.2 [Arabidopsis thaliana]		338	340	1.00E-131	100.6	77.8	84.6	Dof zinc finger protein DOF2.2	gbpln	Arabidopsis thaliana	AT2G28810.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr2:12363681-12365080 FORWARD LENGTH=340		338	340	1.00E-133	100.6	77.8	84.6
Rsa1.0_00159.1.g7133.t1	gb|EOA26517.1| hypothetical protein CARUB_v10022571mg [Capsella rubella]		653	982	0	150.4	77.9	85.8	hypothetical protein CARUB_v10022571mg	gbpln	Capsella rubella	AT2G28830.1 | Symbols: PUB12, AtPUB12 | PLANT U-BOX 12 | chr2:12367001-12370608 REVERSE LENGTH=962		653	962	0	147.3	76.9	86.8
Rsa1.0_00159.1.g7134.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	

Rsa1.0_00159.1.g7135.t1	ref|XP_002881015.1| hypothetical protein ARALYDRAFT_481802 [Arabidopsis lyrata subsp. lyrata] gi|297326854|gb|EFH57274.1| hypothetical protein ARALYDRAFT_481802 [Arabidopsis lyrata subsp. lyrata]	136	157	6.00E-38	115.4	70.6	77.9	hypothetical protein ARALYDRAFT_481802	gbpln	Arabidopsis lyrata	AT2G28870.1 | Symbols: | unknown protein; Has 34 Blast hits to 34 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:12394363-12394833 REVERSE LENGTH=156	136	156	5.00E-39	114.7	73.5	80.9
Rsa1.0_00159.1.g7136.t1	ref|NP_850127.1| para-aminobenzoate synthetase [Arabidopsis thaliana] gi|20466065|gb|AAM19955.1| At2g28880/F8N16.17 [Arabidopsis thaliana] gi|27363398|gb|AAO11618.1| At2g28880/F8N16.17 [Arabidopsis thaliana] gi|52078130|tpg|DAA01457.1| TPA_exp: plastid aminodeoxychorismate synthase/glutamine amidotransferase [Arabidopsis thaliana] gi|330253090|gb|AEC08184.1| aminodeoxychorismate synthase [Arabidopsis thaliana]	941	919	0	97.7	80.3	86.6	para-aminobenzoate synthetase	gbpln	Arabidopsis thaliana	AT2G28880.1 | Symbols: emb1997, ADCS | para-aminobenzoate (PABA) synthase family protein | chr2:12398937-12403108 REVERSE LENGTH=919	941	919	0	97.7	80.3	86.6
Rsa1.0_00159.1.g7137.t1	ref|XP_002881020.1| hypothetical protein ARALYDRAFT_481806 [Arabidopsis lyrata subsp. lyrata] gi|297326859|gb|EFH57279.1| hypothetical protein ARALYDRAFT_481806 [Arabidopsis lyrata subsp. lyrata]	326	332	3.00E-76	101.8	70.2	78.8	hypothetical protein ARALYDRAFT_481806	gbpln	Arabidopsis lyrata	AT2G28910.1 | Symbols: CXIP4 | CAX interacting protein 4 | chr2:12415992-12416990 REVERSE LENGTH=332	326	332	3.00E-65	101.8	42.9	48.2
Rsa1.0_00159.1.g7138.t1	ref|XP_002879188.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297325027|gb|EFH55447.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	141	145	1.00E-55	102.8	81.6	87.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G28920.1 | Symbols: | RING/U-box superfamily protein | chr2:12418017-12418454 FORWARD LENGTH=145	141	145	5.00E-58	102.8	80.9	88.7
Rsa1.0_00159.1.g7139.t2	gb|EOA27190.1| hypothetical protein CARUB_v10023308mg [Capsella rubella]	418	414	0	99.0	90.7	95.2	hypothetical protein CARUB_v10023308mg	gbpln	Capsella rubella	AT2G28930.3 | Symbols: APK1B, PK1B | protein kinase 1B | chr2:12424551-12426565 FORWARD LENGTH=415	418	415	0	99.3	89.0	93.8
Rsa1.0_00159.1.g7140.t1	emb|CAA04385.1| Expansin [Brassica napus]	260	260	1.00E-145	100.0	96.2	98.5	Expansin	gbpln	Brassica napus	AT2G28950.1 | Symbols: ATEXPA6, ATEXP6, ATHEXP ALPHA 1.8, EXPA6 | expansin A6 | chr2:12431840-12433482 REVERSE LENGTH=257	260	257	1.00E-133	98.8	91.2	95.8
Rsa1.0_00159.1.g7141.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00159.1.g7142.t1	gb|AAG50886.1|AC025294_24 hypothetical protein [Arabidopsis thaliana]	264	629	5.00E-49	238.3	37.5	52.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	264	746	8.00E-36	282.6	31.4	43.9
Rsa1.0_00159.1.g7143.t1	gb|EOA28870.1| hypothetical protein CARUB_v10025114mg [Capsella rubella]	510	866	1.00E-121	169.8	44.9	53.5	hypothetical protein CARUB_v10025114mg	gbpln	Capsella rubella	AT2G28970.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:12443919-12448163 FORWARD LENGTH=786	510	786	1.00E-117	154.1	41.2	48.4
Rsa1.0_00159.1.g7144.t1	gb|EOA29069.1| hypothetical protein CARUB_v10025325mg [Capsella rubella]	887	882	0	99.4	83.4	90.0	hypothetical protein CARUB_v10025325mg	gbpln	Capsella rubella	AT2G29000.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:12460781-12465037 FORWARD LENGTH=872	887	872	0	98.3	57.7	72.9
Rsa1.0_00159.1.g7145.t1	ref|XP_002862803.1| rab5-interacting family protein [Arabidopsis lyrata subsp. lyrata] gi|297822627|ref|XP_002879196.1| rab5-interacting family protein [Arabidopsis lyrata subsp. lyrata] gi|297308535|gb|EFH39061.1| rab5-interacting family protein [Arabidopsis lyrata subsp. lyrata] gi|297325035|gb|EFH55455.1| rab5-interacting family protein [Arabidopsis lyrata subsp. lyrata]	133	132	6.00E-53	99.2	88.7	94.0	rab5-interacting family protein	gbpln	Arabidopsis lyrata	AT5G59410.1 | Symbols: | Rab5-interacting family protein | chr5:23959761-23960730 REVERSE LENGTH=130	133	130	8.00E-53	97.7	74.4	86.5
Rsa1.0_00159.1.g7146.t1	ref|XP_002881026.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297326865|gb|EFH57285.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	662	707	0	106.8	82.9	89.7	exostosin family protein	gbpln	Arabidopsis lyrata	AT2G29040.1 | Symbols: | Exostosin family protein | chr2:12472425-12474962 REVERSE LENGTH=720	662	720	0	108.8	81.9	89.3
Rsa1.0_00159.1.g7147.t2	gb|EOA28676.1| hypothetical protein CARUB_v10024900mg [Capsella rubella]	770	901	1.00E-169	117.0	37.5	49.4	hypothetical protein CARUB_v10024900mg	gbpln	Capsella rubella	AT2G29050.1 | Symbols: ATRBL1, RBL1 | RHOMBOID-like 1 | chr2:12478245-12480121 FORWARD LENGTH=389	770	389	5.00E-99	50.5	23.4	24.2
Rsa1.0_00159.1.g7148.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00159.1.g7149.t1	gb|EOA28710.1| hypothetical protein CARUB_v10024938mg [Capsella rubella]	720	715	0	99.3	71.3	83.3	hypothetical protein CARUB_v10024938mg	gbpln	Capsella rubella	AT2G29060.1 | Symbols: | GRAS family transcription factor | chr2:12481991-12484075 FORWARD LENGTH=694	720	694	0	96.4	70.1	81.0

Rsa1.0_00159.1.g7150.t1	ref|NP_973557.1| ubiquitin fusion degradation UFD1-like protein [Arabidopsis thaliana] gi|44917441|gb|AAS49045.1| At2g29070 [Arabidopsis thaliana] gi|45773886|gb|AAS76747.1| At2g29070 [Arabidopsis thaliana] gi|111609944|gb|ABH11522.1| UFD1c [synthetic construct] gi|330253112|gb|AEC08206.1| ubiquitin fusion degradation UFD1-like protein [Arabidopsis thaliana]	314	312	1.00E-151	99.4	84.7	90.4	ubiquitin fusion degradation UFD1-like protein	gbpln	Arabidopsis thaliana	AT2G29070.2 | Symbols: | Ubiquitin fusion degradation UFD1 family protein | chr2:12487797-12489335 FORWARD LENGTH=312	314	312	1.00E-154	99.4	84.7	90.4
Rsa1.0_00159.1.g7151.t1	gb|AAC33234.1| putative AAA-type ATPase [Arabidopsis thaliana]	795	807	0	101.5	88.6	93.3	putative AAA-type ATPase	gbpln	Arabidopsis thaliana	AT2G29080.1 | Symbols: ftsh3 | FTSH protease 3 | chr2:12489911-12492999 REVERSE LENGTH=809	795	809	0	101.8	88.6	93.3
Rsa1.0_00159.1.g7152.t1	gb|ABW74564.1| glutamate receptor 3 [Boechera divaricarpa]	921	954	0	103.6	71.4	81.7	glutamate receptor 3	gbpln	Boechera divaricarpa	AT2G29110.1 | Symbols: ATGLR2.8, GLR2.8 | glutamate receptor 2.8 | chr2:12506880-12510552 REVERSE LENGTH=947	921	947	0	102.8	71.2	80.3
Rsa1.0_00159.1.g7153.t1	gb|ABW74564.1| glutamate receptor 3 [Boechera divaricarpa]	882	954	0	108.2	70.4	82.0	glutamate receptor 3	gbpln	Boechera divaricarpa	AT2G29110.1 | Symbols: ATGLR2.8, GLR2.8 | glutamate receptor 2.8 | chr2:12506880-12510552 REVERSE LENGTH=947	882	947	0	107.4	70.1	80.6
Rsa1.0_00159.1.g7154.t1	gb|ABW74563.1| glutamate receptor 2 [Boechera divaricarpa]	835	959	0	114.9	76.3	85.6	glutamate receptor 2	gbpln	Boechera divaricarpa	AT2G29120.1 | Symbols: ATGLR2.7, GLR2.7 | glutamate receptor 2.7 | chr2:12511479-12515893 REVERSE LENGTH=952	835	952	0	114.0	75.0	84.7
Rsa1.0_00159.1.g7155.t1	ref|NP_172196.1| putative protein phosphatase 2C 2 [Arabidopsis thaliana] gi|75303253|sp|Q8RX37.1|P2C02_ARATH RecName: Full=Probable protein phosphatase 2C 2; Short=AtPP2C02; AltName: Full=Protein phosphatase AP2C2 gi|20258780|gb|AAM13912.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|332189963|gb|AEE28084.1| putative protein phosphatase 2C 2 [Arabidopsis thaliana] gi|333891315|gb|AEG21042.1| PP2C-type phosphatase AP2C2 [Arabidopsis thaliana]	68	380	2.00E-11	558.8	52.9	58.8	putative protein phosphatase 2C 2	gbpln	Arabidopsis thaliana	AT1G07160.1 | Symbols: | Protein phosphatase 2C family protein | chr1:2198155-2199678 REVERSE LENGTH=380	68	380	4.00E-14	558.8	52.9	58.8
Rsa1.0_00159.1.g7156.t2	gb|EOA18545.1| hypothetical protein CARUB_v10007102mg [Capsella rubella]	218	208	8.00E-30	95.4	41.7	52.8	hypothetical protein CARUB_v10007102mg	gbpln	Capsella rubella	AT5G37200.1 | Symbols: | RING/U-box superfamily protein | chr5:14727832-14728485 FORWARD LENGTH=217	218	217	1.00E-28	99.5	38.1	53.7
Rsa1.0_00159.1.g7157.t1	ref|NP_194638.1| Ribonuclease H-like protein [Arabidopsis thaliana] gi|4972055|emb|CAB43923.1| putative protein [Arabidopsis thaliana] gi|7269807|emb|CAB79667.1| putative protein [Arabidopsis thaliana] gi|67633766|gb|AAY78807.1| putative reverse transcriptase/RNA-dependent DNA polymerase [Arabidopsis thaliana] gi|332660185|gb|AEE85585.1| Ribonuclease H-like protein [Arabidopsis thaliana]	256	575	3.00E-11	224.6	16.0	23.4	Ribonuclease H-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	256	575	9.00E-14	224.6	16.0	23.4
Rsa1.0_00159.1.g7158.t1	#	#	#	#	#	#	#	-	----	----	AT2G29125.1 | Symbols: RTFL2, DVL13 | ROTUNDIFOLIA like 2 | chr2:12523472-12523819 FORWARD LENGTH=115	130	115	2.00E-11	88.5	52.3	58.5
Rsa1.0_00159.1.g7159.t1	gb|ABW81111.1| putative pumilio Mpt5 [Boechera divaricarpa]	961	975	0	101.5	83.8	89.0	putative pumilio Mpt5	gbpln	Boechera divaricarpa	AT2G29200.1 | Symbols: APUM1, PUM1 | pumilio 1 | chr2:12549483-12553185 REVERSE LENGTH=968	961	968	0	100.7	82.6	87.7
Rsa1.0_00159.1.g7160.t2	ref|NP_180491.1| tropine dehydrogenase [Arabidopsis thaliana] gi|3980418|gb|AAC95221.1| putative tropinone reductase [Arabidopsis thaliana] gi|18252899|gb|AAL62376.1| putative tropinone reductase [Arabidopsis thaliana] gi|23197854|gb|AAN15454.1| putative tropinone reductase [Arabidopsis thaliana] gi|330253136|gb|AEC08230.1| tropine dehydrogenase [Arabidopsis thaliana]	328	263	1.00E-104	80.2	56.4	61.0	tropine dehydrogenase	gbpln	Arabidopsis thaliana	AT2G29300.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:12588214-12589372 FORWARD LENGTH=263	328	263	1.00E-107	80.2	56.4	61.0
Rsa1.0_00159.1.g7161.t1	gb|AAD32759.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1324	1356	0	102.4	73.0	86.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1324	1262	1.00E-88	95.3	13.7	20.6
Rsa1.0_00159.1.g7162.t1	gb|ABW81050.1| tropinone-reductase-like35 [Arabidopsis lyrata subsp. lyrata]	262	262	1.00E-133	100.0	87.0	92.0	tropinone-reductase-like35	gbpln	Arabidopsis lyrata	AT2G29310.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:12590068-12591260 FORWARD LENGTH=262	262	262	1.00E-133	100.0	84.4	90.8

Rsa1.0_00160.1.g7163.t1	ref|NP_568670.1| mitochondrial carnitine/acylcarnitine carrier-like protein [Arabidopsis thaliana] gi|24211999|sp|Q93XM7.1|MCAT_ARATH RecName: Full=Mitochondrial carnitine/acylcarnitine carrier-like protein; AltName: Full=Carnitine/acylcarnitine translocase-like protein; Short=CAC-like protein; AltName: Full=Protein A BOUT DE SOUFFLE gi|13992452|emb|CAC38047.1| carnitine acyl carrier-like protein [Arabidopsis thaliana] gi|22531072|gb|AAM97040.1| carnitine/acylcarnitine translocase-like protein [Arabidopsis thaliana] gi|23197914|gb|AAN15484.1| carnitine/acylcarnitine translocase-like protein [Arabidopsis thaliana] gi|332008045|gb|AED95428.1| mitochondrial carnitine/acylcarnitine carrier-like protein [Arabidopsis thaliana]	300	300	1.00E-155	100.0	91.3	94.7	mitochondrial carnitine/acylcarnitine carrier-like protein	gbpln	Arabidopsis thaliana	AT5G46800.1 | Symbols: BOU | Mitochondrial substrate carrier family protein | chr5:18988779-18989810 REVERSE LENGTH=300	300	300	1.00E-158	100.0	91.3	94.7
Rsa1.0_00160.1.g7164.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	565	1231	1.00E-141	217.9	47.3	64.4	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	565	575	7.00E-78	101.8	30.8	45.8
Rsa1.0_00160.1.g7165.t1	gb|AAD21687.1| Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078 [Arabidopsis thaliana]	1297	1415	0	109.1	64.8	76.5	Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1297	1262	3.00E-86	97.3	12.9	20.0
Rsa1.0_00160.1.g7166.t2	gb|EOA13941.1| hypothetical protein CARUB_v10027058mg [Capsella rubella]	351	229	6.00E-82	65.2	43.6	47.9	hypothetical protein CARUB_v10027058mg	gbpln	Capsella rubella	AT5G46790.1 | Symbols: PYL1, RCAR12 | PYR1-like 1 | chr5:18984063-18984728 REVERSE LENGTH=221	351	221	2.00E-80	63.0	46.7	51.6
Rsa1.0_00160.1.g7167.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00160.1.g7168.t1	ref|XP_002865162.1| hypothetical protein ARALYDRAFT_916750 [Arabidopsis lyrata subsp. lyrata] gi|297310997|gb|EFH41421.1| hypothetical protein ARALYDRAFT_916750 [Arabidopsis lyrata subsp. lyrata]	229	233	3.00E-75	101.7	84.3	89.5	hypothetical protein ARALYDRAFT_916750	gbpln	Arabidopsis lyrata	AT5G46780.2 | Symbols: | VQ motif-containing protein | chr5:18979236-18979949 FORWARD LENGTH=237	229	237	3.00E-77	103.5	84.7	90.0
Rsa1.0_00160.1.g7169.t1	ref|XP_002863391.1| ARF-GAP domain 8 [Arabidopsis lyrata subsp. lyrata] gi|297309226|gb|EFH39650.1| ARF-GAP domain 8 [Arabidopsis lyrata subsp. lyrata]	401	405	0	101.0	85.0	91.5	ARF-GAP domain 8	gbpln	Arabidopsis lyrata	AT5G46750.1 | Symbols: AGD9 | ARF-GAP domain 9 | chr5:18969950-18971817 REVERSE LENGTH=402	401	402	0	100.2	84.0	91.0
Rsa1.0_00160.1.g7170.t1	ref|XP_002863392.1| ubiquitin-specific protease 21 [Arabidopsis lyrata subsp. lyrata] gi|297309227|gb|EFH39651.1| ubiquitin-specific protease 21 [Arabidopsis lyrata subsp. lyrata]	680	724	0	106.5	59.9	72.1	ubiquitin-specific protease 21	gbpln	Arabidopsis lyrata	AT5G46740.1 | Symbols: UBP21 | ubiquitin-specific protease 21 | chr5:18965410-18968492 REVERSE LENGTH=732	680	732	0	107.6	59.4	70.9
Rsa1.0_00160.1.g7171.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	183	341	2.00E-18	186.3	35.0	48.6	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00160.1.g7172.t1	ref|XP_002863397.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297309232|gb|EFH39656.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	712	711	0	99.9	92.6	95.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G46580.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:18897510-18899645 REVERSE LENGTH=711	712	711	0	99.9	90.9	95.9
Rsa1.0_00160.1.g7173.t1	gb|EOA13267.1| hypothetical protein CARUB_v10026296mg [Capsella rubella]	522	489	0	93.7	88.7	91.8	hypothetical protein CARUB_v10026296mg	gbpln	Capsella rubella	AT5G46570.1 | Symbols: BSK2 | BR-signaling kinase 2 | chr5:18894687-18897198 FORWARD LENGTH=489	522	489	0	93.7	88.9	92.0
Rsa1.0_00160.1.g7174.t1	ref|XP_002877631.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297323469|gb|EFH53890.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	1707	1902	0	111.4	79.2	89.0	ATP binding protein	gbpln	Arabidopsis lyrata	AT3G48770.1 | Symbols: | DNA binding;ATP binding | chr3:18079261-18086817 REVERSE LENGTH=1899	1707	1899	0	111.2	78.0	87.1

Rsa1.0_00160.1.g7175.t1	ref|NP_199468.5| uncharacterized protein [Arabidopsis thaliana] gi|332008015|gb|AED95398.1| uncharacterized protein AT5G46560 [Arabidopsis thaliana]	387	387	1.00E-163	100.0	76.2	86.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G46560.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Inner nuclear membrane protein MAN1 (InterPro:IPR018996); Has 58 Blast hits to 58 proteins in 29 species: Archae - 0; Bacteria - 4; Metazoa - 11; Fungi - 15; Plants - 20; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr5:18888061-18890090 FORWARD LENGTH=387	387	387	1.00E-166	100.0	76.2	86.6
Rsa1.0_00160.1.g7176.t1	ref|XP_002868325.1| hypothetical protein ARALYDRAFT_915512 [Arabidopsis lyrata subsp. lyrata] gi|297314161|gb|EFH44584.1| hypothetical protein ARALYDRAFT_915512 [Arabidopsis lyrata subsp. lyrata]	323	366	4.00E-53	113.3	48.9	59.1	hypothetical protein ARALYDRAFT_915512	gbpln	Arabidopsis lyrata	AT4G36840.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:17352166-17352882 FORWARD LENGTH=238	323	238	9.00E-44	73.7	35.9	44.6
Rsa1.0_00160.1.g7177.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1038	1555	0	149.8	89.3	93.2	disease resistance protein	gbpln	Brassica rapa	AT1G17600.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:6053026-6056572 REVERSE LENGTH=1049	1038	1049	0	101.1	83.2	88.4
Rsa1.0_00160.1.g7178.t1	ref|NP_173204.1| Disease resistance protein (TIR-NBS class) [Arabidopsis thaliana] gi|332191492|gb|AEE29613.1| Disease resistance protein (TIR-NBS class) [Arabidopsis thaliana]	416	420	0	101.0	78.8	89.9	Disease resistance protein (TIR-NBS class)	gbpln	Arabidopsis thaliana	AT1G17610.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:6056895-6058157 FORWARD LENGTH=420	416	420	0	101.0	78.8	89.9
Rsa1.0_00160.1.g7179.t9	gb|EOA17641.1| hypothetical protein CARUB_v10006007mg [Capsella rubella]	133	133	7.00E-71	100.0	97.7	100.0	hypothetical protein CARUB_v10006007mg	gbpln	Capsella rubella	AT4G18100.1 | Symbols: | Ribosomal protein L32e | chr4:10035715-10036475 REVERSE LENGTH=133	133	133	3.00E-73	100.0	97.0	100.0
Rsa1.0_00160.1.g7180.t1	gb|EOA15162.1| hypothetical protein CARUB_v10028539mg [Capsella rubella]	454	453	0	99.8	84.6	91.9	hypothetical protein CARUB_v10028539mg	gbpln	Capsella rubella	AT5G46410.1 | Symbols: SSP4 | SCP1-like small phosphatase 4 | chr5:18826007-18828156 FORWARD LENGTH=453	454	453	0	99.8	84.1	90.7
Rsa1.0_00160.1.g7181.t2	ref|XP_002865195.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297311030|gb|EFH41454.1| binding protein [Arabidopsis lyrata subsp. lyrata]	1025	1035	0	101.0	70.1	78.0	binding protein	gbpln	Arabidopsis lyrata	AT5G46400.1 | Symbols: AT PRP39-2, PRP39-2 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:18820032-18824522 FORWARD LENGTH=1036	1025	1036	0	101.1	70.2	78.1
Rsa1.0_00160.1.g7182.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00160.1.g7183.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00160.1.g7184.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00160.1.g7185.t2	ref|NP_001190533.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana] gi|75262547|sp|Q9FJC1.1|FBD31_ARATH RecName: Full=Putative FBD-associated F-box protein At5g53635 gi|9759202|dbj|BAB09739.1| heat shock transcription factor HSF30-like protein [Arabidopsis thaliana] gi|332009006|gb|AED96389.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana]	478	426	1.00E-110	89.1	49.0	60.7	F-box/RNI-like/FBD-like domains-containing protein	gbpln	Arabidopsis thaliana	AT5G53635.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:21785999-21787444 REVERSE LENGTH=426	478	426	1.00E-112	89.1	49.0	60.7
Rsa1.0_00160.1.g7186.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00160.1.g7187.t1	ref|NP_175207.1| protein agamous-like 102 [Arabidopsis thaliana] gi|9802597|gb|AAF99799.1|AC012463_16 T2E6.17 [Arabidopsis thaliana] gi|32402446|gb|AAN52805.1| MADS-box protein AGL102 [Arabidopsis thaliana] gi|332194088|gb|AEE32209.1| protein agamous-like 102 [Arabidopsis thaliana]	149	184	8.00E-25	123.5	43.6	61.1	protein agamous-like 102	gbpln	Arabidopsis thaliana	AT1G47760.1 | Symbols: AGL102 | AGAMOUS-like 102 | chr1:17572451-17573159 FORWARD LENGTH=184	149	184	2.00E-27	123.5	43.6	61.1
Rsa1.0_00160.1.g7188.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1551	1274	0	82.1	34.6	45.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1551	575	1.00E-52	37.1	10.4	16.6
Rsa1.0_00160.1.g7189.t1	gb|EOA16415.1| hypothetical protein CARUB_v10004569mg [Capsella rubella]	530	530	0	100.0	84.9	93.0	hypothetical protein CARUB_v10004569mg	gbpln	Capsella rubella	AT5G41480.1 | Symbols: EMB9, GLA1, ATDFA, DFA | Folylpolyglutamate synthetase family protein | chr5:16595967-16598523 FORWARD LENGTH=530	530	530	0	100.0	86.2	93.2
Rsa1.0_00160.1.g7190.t1	ref|XP_002863410.1| hypothetical protein ARALYDRAFT_494342 [Arabidopsis lyrata subsp. lyrata] gi|297309245|gb|EFH39669.1| hypothetical protein ARALYDRAFT_494342 [Arabidopsis lyrata subsp. lyrata]	193	70	8.00E-15	36.3	21.8	24.9	hypothetical protein ARALYDRAFT_494342	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#

Rsa1.0_00160.1.g7191.t1	gb|EOA13309.1| hypothetical protein CARUB_v10026344mg [Capsella rubella]	502	471	0	93.8	89.2	90.8	hypothetical protein CARUB_v10026344mg	gbpln	Capsella rubella	AT5G46290.1 | Symbols: KASI, KAS1 | 3-ketoacyl-acyl carrier protein synthase I | chr5:18774439-18776629 REVERSE LENGTH=473	502	473	0	94.2	89.2	90.8
Rsa1.0_00160.1.g7192.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00160.1.g7193.t1	#	#	#	#	#	#	#	–	----	----	AT5G49020.1 | Symbols: ATPRMT4A, PRMT4A | protein arginine methyltransferase 4A | chr5:19871341-19874683 FORWARD LENGTH=528	201	528	3.00E-11	262.7	20.9	30.3
Rsa1.0_00160.1.g7194.t1	ref|XP_002863413.1| hypothetical protein ARALYDRAFT_494345 [Arabidopsis lyrata subsp. lyrata] gi|297309248|gb|EFH39672.1| hypothetical protein ARALYDRAFT_494345 [Arabidopsis lyrata subsp. lyrata]	771	776	0	100.6	92.9	97.1	hypothetical protein ARALYDRAFT_494345	gbpln	Arabidopsis lyrata	AT5G46280.1 | Symbols: MCM3 | Minichromosome maintenance (MCM2/3/5) family protein | chr5:18769902-18773606 REVERSE LENGTH=776	771	776	0	100.6	91.8	96.2
Rsa1.0_00160.1.g7195.t1	ref|NP_851141.1| RNA-binding protein [Arabidopsis thaliana] gi|15215748|gb|AAK91419.1| AT5g46250/MPL12_3 [Arabidopsis thaliana] gi|23308375|gb|AAN18157.1| At5g46250/MPL12_3 [Arabidopsis thaliana] gi|332007974|gb|AED95357.1| RNA-binding protein [Arabidopsis thaliana]	408	422	1.00E-171	103.4	80.6	85.8	RNA-binding protein	gbpln	Arabidopsis thaliana	AT5G46250.1 | Symbols: | RNA-binding protein | chr5:18755388-18758056 FORWARD LENGTH=422	408	422	1.00E-174	103.4	80.6	85.8
Rsa1.0_00160.1.g7196.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1670	1365	0	81.7	31.3	44.0	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1670	575	2.00E-59	34.4	9.2	14.4
Rsa1.0_00161.1.g7197.t1	dbj|BAJ33922.1| unnamed protein product [Thellungiella halophila]	71	226	2.00E-16	318.3	57.7	59.2	unnamed protein product	----	----	AT1G04250.1 | Symbols: AXR3, IAA17 | AUX/IAA transcriptional regulator family protein | chr1:1136382-1138340 FORWARD LENGTH=229	71	229	5.00E-19	322.5	57.7	59.2
Rsa1.0_00161.1.g7198.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00161.1.g7199.t26	ref|XP_002889494.1| EIF2 gamma [Arabidopsis lyrata subsp. lyrata] gi|297335336|gb|EFH65753.1| EIF2 gamma [Arabidopsis lyrata subsp. lyrata]	601	465	1.00E-135	77.4	44.1	48.1	EIF2 gamma	gbpln	Arabidopsis lyrata	AT1G04170.1 | Symbols: EIF2 GAMMA | eukaryotic translation initiation factor 2 gamma subunit | chr1:1097423-1099702 FORWARD LENGTH=465	601	465	1.00E-137	77.4	43.9	48.1
Rsa1.0_00161.1.g7200.t1	ref|NP_181675.2| uncharacterized protein [Arabidopsis thaliana] gi|330254884|gb|AEC09978.1| uncharacterized protein AT2G41440 [Arabidopsis thaliana]	256	289	6.00E-58	112.9	55.9	66.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G41440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41470.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:17271792-17274065 FORWARD LENGTH=289	256	289	2.00E-60	112.9	55.9	66.4
Rsa1.0_00161.1.g7201.t1	dbj|BAJ34139.1| unnamed protein product [Thellungiella halophila]	70	158	2.00E-20	225.7	82.9	90.0	unnamed protein product	----	----	AT1G03850.2 | Symbols: | Glutaredoxin family protein | chr1:977233-977685 REVERSE LENGTH=150	70	150	2.00E-21	214.3	80.0	88.6
Rsa1.0_00161.1.g7202.t1	ref|NP_001184903.1| guanylate-binding protein [Arabidopsis thaliana] gi|332189498|gb|AEE27619.1| guanylate-binding protein [Arabidopsis thaliana]	1229	1013	0	82.4	62.4	70.3	guanylate-binding protein	gbpln	Arabidopsis thaliana	AT1G03830.2 | Symbols: | guanylate-binding family protein | chr1:962128-966622 REVERSE LENGTH=1013	1229	1013	0	82.4	62.4	70.3
Rsa1.0_00161.1.g7203.t1	ref|NP_171875.1| zinc finger CCCH domain-containing protein 2 [Arabidopsis thaliana] gi|75268098|sp|Q9ZWA1.1|C3H2_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 2; Short=AtC3H2; AltName: Full=Protein SOMNUS; Short=SOM gi|4204308|gb|AAD10689.1| Hypothetical protein [Arabidopsis thaliana] gi|332189493|gb|AEE27614.1| zinc finger CCCH domain-containing protein 2 [Arabidopsis thaliana]	394	393	1.00E-151	99.7	82.2	89.6	zinc finger CCCH domain-containing protein 2	gbpln	Arabidopsis thaliana	AT1G03790.1 | Symbols: SOM | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:954589-955770 FORWARD LENGTH=393	394	393	1.00E-154	99.7	82.2	89.6
Rsa1.0_00161.1.g7204.t1	ref|XP_002889465.1| por C [Arabidopsis lyrata subsp. lyrata] gi|297335307|gb|EFH65724.1| por C [Arabidopsis lyrata subsp. lyrata]	401	401	0	100.0	94.3	97.0	por C	gbpln	Arabidopsis lyrata	AT1G03630.1 | Symbols: POR C, PORC | protochlorophyllide oxidoreductase C | chr1:907699-909245 FORWARD LENGTH=401	401	401	0	100.0	94.0	96.8
Rsa1.0_00161.1.g7205.t1	ref|XP_002892171.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338013|gb|EFH68430.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	265	265	2.33E-156	100.0	94.0	96.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G03620.1 | Symbols: | ELMO/CED-12 family protein | chr1:904319-906013 REVERSE LENGTH=265	265	265	1.00E-149	100.0	94.0	96.2

Rsa1.0_00161.1.g7206.t1	ref|XP_002889464.1| hypothetical protein ARALYDRAFT_470333 [Arabidopsis lyrata subsp. lyrata] gi|297335306|gb|EFH65723.1| hypothetical protein ARALYDRAFT_470333 [Arabidopsis lyrata subsp. lyrata]	310	308	1.00E−153	99.4	88.1	92.9	hypothetical protein ARALYDRAFT_470333	gbpln	Arabidopsis lyrata	AT1G03610.1 | Symbols: | Protein of unknown function (DUF789) | chr1:901304−902672 FORWARD LENGTH=308	310	308	1.00E−155	99.4	87.4	92.6
Rsa1.0_00161.1.g7207.t1	ref|XP_002889463.1| photosystem II family protein [Arabidopsis lyrata subsp. lyrata] gi|297335305|gb|EFH65722.1| photosystem II family protein [Arabidopsis lyrata subsp. lyrata]	176	174	7.00E−72	98.9	86.4	92.6	photosystem II family protein	gbpln	Arabidopsis lyrata	AT1G03600.1 | Symbols: PSB27 | photosystem II family protein | chr1:898916−899440 FORWARD LENGTH=174	176	174	7.00E−72	98.9	84.1	90.9
Rsa1.0_00161.1.g7208.t1	ref|XP_002892170.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338012|gb|EFH68429.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	439	460	0	104.8	83.8	90.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G03590.1 | Symbols: | Protein phosphatase 2C family protein | chr1:894480−896257 REVERSE LENGTH=462	439	462	0	105.2	82.5	90.2
Rsa1.0_00161.1.g7209.t1	gb|EOA39421.1| hypothetical protein CARUB_v10012530mg [Capsella rubella]	283	283	1.00E−157	100.0	93.6	97.2	hypothetical protein CARUB_v10012530mg	gbpln	Capsella rubella	AT1G03550.1 | Symbols: | Secretory carrier membrane protein (SCAMP) family protein | chr1:885851−887778 REVERSE LENGTH=283	283	283	1.00E−154	100.0	95.4	98.6
Rsa1.0_00161.1.g7210.t1	ref|XP_002889462.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335304|gb|EFH65721.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata]	604	608	0	100.7	86.6	92.7	pentatricopeptide repeat−containing protein	gbpln	Arabidopsis lyrata	AT1G03540.1 | Symbols: | Pentatricopeptide repeat (PPR−like) superfamily protein | chr1:883782−885611 FORWARD LENGTH=609	604	609	0	100.8	85.6	91.9
Rsa1.0_00161.1.g7211.t1	ref|XP_002892165.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338007|gb|EFH68424.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata]	466	429	0	92.1	74.5	78.1	pentatricopeptide repeat−containing protein	gbpln	Arabidopsis lyrata	AT1G03510.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr1:876258−877547 REVERSE LENGTH=429	466	429	0	92.1	73.2	77.7
Rsa1.0_00161.1.g7212.t1	ref|XP_002889459.1| leucine−rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297335301|gb|EFH65718.1| leucine−rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	395	396	0	100.3	89.9	94.2	leucine−rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G03440.1 | Symbols: | Leucine−rich repeat (LRR) family protein | chr1:852681−853874 FORWARD LENGTH=397	395	397	0	100.5	88.6	93.4
Rsa1.0_00161.1.g7213.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00161.1.g7214.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00161.1.g7215.t1	ref|XP_002892158.1| hypothetical protein ARALYDRAFT_470313 [Arabidopsis lyrata subsp. lyrata] gi|297338000|gb|EFH68417.1| hypothetical protein ARALYDRAFT_470313 [Arabidopsis lyrata subsp. lyrata]	431	452	1.00E−155	104.9	76.8	83.1	hypothetical protein ARALYDRAFT_470313	gbpln	Arabidopsis lyrata	AT1G03350.1 | Symbols: | BSD domain−containing protein | chr1:822834−824246 REVERSE LENGTH=470	431	470	1.00E−153	109.0	75.6	82.1
Rsa1.0_00161.1.g7216.t1	gb|EOA38703.1| hypothetical protein CARUB_v10010754mg [Capsella rubella]	111	93	8.00E−44	83.8	82.9	83.8	hypothetical protein CARUB_v10010754mg	gbpln	Capsella rubella	AT1G03330.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:818161−819297 REVERSE LENGTH=93	111	93	1.00E−45	83.8	82.0	82.9
Rsa1.0_00161.1.g7217.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00161.1.g7218.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00161.1.g7219.t2	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00161.1.g7220.t1	ref|XP_002889446.1| EDGP precursor [Arabidopsis lyrata subsp. lyrata] gi|297335288|gb|EFH65705.1| EDGP precursor [Arabidopsis lyrata subsp. lyrata]	433	433	0	100.0	85.7	91.9	EDGP precursor	gbpln	Arabidopsis lyrata	AT1G03220.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:787143−788444 FORWARD LENGTH=433	433	433	0	100.0	83.8	91.2
Rsa1.0_00161.1.g7221.t1	ref|XP_002889446.1| EDGP precursor [Arabidopsis lyrata subsp. lyrata] gi|297335288|gb|EFH65705.1| EDGP precursor [Arabidopsis lyrata subsp. lyrata]	225	433	2.00E−57	192.4	55.1	64.9	EDGP precursor	gbpln	Arabidopsis lyrata	AT1G03220.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:787143−788444 FORWARD LENGTH=433	225	433	2.00E−58	192.4	54.2	64.0
Rsa1.0_00161.1.g7222.t1	ref|NP_189038.1| putative F−box protein [Arabidopsis thaliana] gi|75273446|sp|Q9LIR1.1|FB182_ARATH RecName: Full=Putative F−box protein At3g23960 gi|9294665|dbj|BAB03014.1| unnamed protein product [Arabidopsis thaliana] gi|332643318|gb|AEE76839.1| putative F−box protein [Arabidopsis thaliana]	340	402	1.00E−60	118.2	41.5	60.9	putative F−box protein	gbpln	Arabidopsis thaliana	AT3G23960.1 | Symbols: | F−box and associated interaction domains−containing protein | chr3:8657736−8658944 FORWARD LENGTH=402	340	402	3.00E−63	118.2	41.5	60.9
Rsa1.0_00161.1.g7223.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#

Rsa1.0_00161.1.g7224.t1	ref|XP_002889444.1| hypothetical protein ARALYDRAFT_470299 [Arabidopsis lyrata subsp. lyrata] gi|297335286|gb|EFH65703.1| hypothetical protein ARALYDRAFT_470299 [Arabidopsis lyrata subsp. lyrata]	758	758	0	100.0	96.6	98.2	hypothetical protein ARALYDRAFT_470299	gbpln	Arabidopsis lyrata	AT1G03190.2 | Symbols: ATXPD, UVH6 | RAD3-like DNA-binding helicase protein | chr1:775822-779863 FORWARD LENGTH=758	758	758	0	100.0	96.3	97.9
Rsa1.0_00161.1.g7225.t5	ref|XP_002889442.1| hypothetical protein ARALYDRAFT_470297 [Arabidopsis lyrata subsp. lyrata] gi|297335284|gb|EFH65701.1| hypothetical protein ARALYDRAFT_470297 [Arabidopsis lyrata subsp. lyrata]	294	263	1.00E-123	89.5	75.9	82.0	hypothetical protein ARALYDRAFT_470297	gbpln	Arabidopsis lyrata	AT1G03180.1 | Symbols: | unknown protein; Has 36 Blast hits to 36 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:773543-775179 FORWARD LENGTH=265	294	265	1.00E-124	90.1	75.2	81.6
Rsa1.0_00161.1.g7226.t1	gb|EOA37699.1| hypothetical protein CARUB_v10012407mg [Capsella rubella]	234	276	3.00E-84	117.9	76.1	82.9	hypothetical protein CARUB_v10012407mg	gbpln	Capsella rubella	AT1G03170.1 | Symbols: | Protein of unknown function (DUF3049) | chr1:769805-770527 FORWARD LENGTH=240	234	240	1.00E-81	102.6	72.2	79.9
Rsa1.0_00161.1.g7227.t4	gb|EOA39607.1| hypothetical protein CARUB_v10008235mg [Capsella rubella]	951	929	0	97.7	84.8	89.4	hypothetical protein CARUB_v10008235mg	gbpln	Capsella rubella	AT1G03160.1 | Symbols: FZL | FZO-like | chr1:761321-766053 FORWARD LENGTH=912	951	912	0	95.9	84.5	89.4
Rsa1.0_00161.1.g7228.t1	gb|EOA38906.1| hypothetical protein CARUB_v10011298mg [Capsella rubella]	426	425	0	99.8	87.3	93.4	hypothetical protein CARUB_v10011298mg	gbpln	Capsella rubella	AT1G03140.1 | Symbols: | splicing factor Prp18 family protein | chr1:754471-756223 REVERSE LENGTH=420	426	420	0	98.6	84.5	91.5
Rsa1.0_00161.1.g7229.t1	ref|NP_563675.1| transducin/WD-40 repeat-containing protein [Arabidopsis thaliana] gi|13877931|gb|AAK44043.1|AF370228_1 unknown protein [Arabidopsis thaliana] gi|16323464|gb|AAL15226.1| unknown protein [Arabidopsis thaliana] gi|332189411|gb|AEE27532.1| transducin/WD-40 repeat-containing protein [Arabidopsis thaliana]	405	427	0	105.4	81.7	89.6	transducin/WD-40 repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G03110.1 | Symbols: TRM82, AtTRM82 | Transducin/WD40 repeat-like superfamily protein | chr1:749359-751796 FORWARD LENGTH=427	405	427	0	105.4	81.7	89.6
Rsa1.0_00161.1.g7230.t2	ref|NP_171804.1| putative clathrin assembly protein [Arabidopsis thaliana] gi|46396022|sp|Q9SA65.1|CAP4_ARATH RecName: Full=Putative clathrin assembly protein At1g03050 gi|4587573|gb|AAD25804.1|AC006550_12 Similar to clathrin assembly protein gb|AF041374 (CALM) from Rattus norvegicus [Arabidopsis thaliana] gi|91805731|gb|ABE65594.1| clathrin assembly protein-like [Arabidopsis thaliana] gi|332189399|gb|AEE27520.1| putative clathrin assembly protein [Arabidopsis thaliana]	592	599	0	101.2	87.5	93.1	putative clathrin assembly protein	gbpln	Arabidopsis thaliana	AT1G03050.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:707726-709860 FORWARD LENGTH=599	592	599	0	101.2	87.5	93.1
Rsa1.0_00161.1.g7231.t1	gb|EOA40245.1| hypothetical protein CARUB_v10008963mg [Capsella rubella]	430	491	0	114.2	86.3	93.7	hypothetical protein CARUB_v10008963mg	gbpln	Capsella rubella	AT1G02970.1 | Symbols: WEE1, ATWEE1 | WEE1 kinase homolog | chr1:673408-676127 FORWARD LENGTH=500	430	500	0	116.3	85.6	94.0
Rsa1.0_00161.1.g7232.t1	ref|NP_849582.1| uncharacterized protein [Arabidopsis thaliana] gi|26452912|dbj|BAC43534.1| unknown protein [Arabidopsis thaliana] gi|29824301|gb|AAP04111.1| unknown protein [Arabidopsis thaliana] gi|332189384|gb|AEE27505.1| uncharacterized protein AT1G02960 [Arabidopsis thaliana]	498	471	1.00E-163	94.6	62.0	72.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G02960.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02965.1); Has 100 Blast hits to 99 proteins in 48 species: Archae - 0; Bacteria - 4; Metazoa - 26; Fungi - 13; Plants - 29; Viruses - 0; Other Eukaryotes - 28 (source: NCBI BLink). | chr1:667002-669773 REVERSE LENGTH=471	498	471	1.00E-166	94.6	62.0	72.7
Rsa1.0_00161.1.g7233.t1	ref|XP_002892135.1| hypothetical protein ARALYDRAFT_887439 [Arabidopsis lyrata subsp. lyrata] gi|297337977|gb|EFH68394.1| hypothetical protein ARALYDRAFT_887439 [Arabidopsis lyrata subsp. lyrata]	449	453	0	100.9	89.8	94.0	hypothetical protein ARALYDRAFT_887439	gbpln	Arabidopsis lyrata	AT1G02910.1 | Symbols: LPA1 | tetratricopeptide repeat (TPR)-containing protein | chr1:655749-658125 REVERSE LENGTH=453	449	453	0	100.9	87.8	93.1
Rsa1.0_00162.1.g7234.t3	ref|XP_002890545.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata] gi|297336387|gb|EFH66804.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata]	142	1130	4.00E-22	795.8	38.7	44.4	T-complex protein 11	gbpln	Arabidopsis lyrata	AT1G22930.2 | Symbols: | T-complex protein 11 | chr1:8118049-8121854 FORWARD LENGTH=1020	142	1020	5.00E-24	718.3	38.0	43.0
Rsa1.0_00162.1.g7235.t1	ref|XP_002875115.1| hypothetical protein ARALYDRAFT_484136 [Arabidopsis lyrata subsp. lyrata] gi|297320953|gb|EFH51374.1| hypothetical protein ARALYDRAFT_484136 [Arabidopsis lyrata subsp. lyrata]	77	77	4.00E-32	100.0	84.4	94.8	hypothetical protein ARALYDRAFT_484136	gbpln	Arabidopsis lyrata	AT2G02130.1 | Symbols: PDF2.3, LCR68 | low-molecular-weight cysteine-rich 68 | chr2:540071-540407 FORWARD LENGTH=77	77	77	7.00E-34	100.0	81.8	92.2

Rsa1.0_00162.1.g7236.t1	gb|AAM20729.1| unknown protein [Arabidopsis thaliana]	642	618	0	96.3	67.9	74.0	unknown protein	gbpln	Arabidopsis thaliana	AT2G02160.1 | Symbols: | CCCH-type zinc finger family protein | chr2:553407-555899 REVERSE LENGTH=669	642	669	0	104.2	67.3	73.2
Rsa1.0_00162.1.g7237.t1	ref|XP_002876802.1| hypothetical protein ARALYDRAFT_322556 [Arabidopsis lyrata subsp. lyrata] gi|297322640|gb|EFH53061.1| hypothetical protein ARALYDRAFT_322556 [Arabidopsis lyrata subsp. lyrata]	459	492	0	107.2	84.3	91.1	hypothetical protein ARALYDRAFT_322556	gbpln	Arabidopsis lyrata	AT2G02170.2 | Symbols: | Remorin family protein | chr2:556595-558610 REVERSE LENGTH=486	459	486	0	105.9	84.1	90.4
Rsa1.0_00162.1.g7238.t1	ref|XP_002875118.1| hypothetical protein ARALYDRAFT_484143 [Arabidopsis lyrata subsp. lyrata] gi|297320956|gb|EFH51377.1| hypothetical protein ARALYDRAFT_484143 [Arabidopsis lyrata subsp. lyrata]	302	308	1.00E-137	102.0	80.5	84.8	hypothetical protein ARALYDRAFT_484143	gbpln	Arabidopsis lyrata	AT2G02180.1 | Symbols: TOM3 | tobamovirus multiplication protein 3 | chr2:560976-562961 FORWARD LENGTH=303	302	303	1.00E-136	100.3	81.1	84.4
Rsa1.0_00162.1.g7239.t1	ref|NP_178330.1| phytosulfokin receptor 1 [Arabidopsis thaliana] gi|29428075|sp|Q9ZVR7.4|PSKR1_ARATH RecName: Full=Phytosulfokine receptor 1; Short=AtPSKR1; AltName: Full=Phytosulfokine LRR receptor kinase 1; Flags: Precursor gi|224589499|gb|ACN59283.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|330250464|gb|AEC05558.1| phytosulfokin receptor 1 [Arabidopsis thaliana]	905	1008	0	111.4	79.4	87.1	phytosulfokin receptor 1	gbpln	Arabidopsis thaliana	AT2G02220.1 | Symbols: ATPSKR1, PSKR1 | phytosulfokin receptor 1 | chr2:584098-587124 REVERSE LENGTH=1008	905	1008	0	111.4	79.4	87.1
Rsa1.0_00162.1.g7240.t1	ref|NP_178819.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|3327395|gb|AAC26677.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana] gi|330251037|gb|AEC06131.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	190	530	1.00E-17	278.9	27.9	36.3	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	190	530	5.00E-20	278.9	27.9	36.3
Rsa1.0_00162.1.g7241.t1	gb|EOA24287.1| hypothetical protein CARUB_v10017527mg, partial [Capsella rubella]	328	355	1.00E-113	108.2	63.7	75.3	hypothetical protein CARUB_v10017527mg, partial	gbpln	Capsella rubella	AT2G02230.1 | Symbols: AtPP2-B1, PP2-B1 | phloem protein 2-B1 | chr2:590393-591595 REVERSE LENGTH=336	328	336	1.00E-112	102.4	62.8	72.9
Rsa1.0_00162.1.g7242.t1	ref|XP_002876806.1| hypothetical protein ARALYDRAFT_322561 [Arabidopsis lyrata subsp. lyrata] gi|297322644|gb|EFH53065.1| hypothetical protein ARALYDRAFT_322561 [Arabidopsis lyrata subsp. lyrata]	277	317	1.00E-109	114.4	70.8	83.8	hypothetical protein ARALYDRAFT_322561	gbpln	Arabidopsis lyrata	AT2G02240.1 | Symbols: MEE66 | F-box family protein | chr2:592359-593602 REVERSE LENGTH=320	277	320	1.00E-110	115.5	70.4	82.7
Rsa1.0_00162.1.g7243.t5	ref|XP_002872697.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318534|gb|EFH48956.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	537	659	0	122.7	73.9	86.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G04540.1 | Symbols: CRK39 | cysteine-rich RLK (RECEPTOR-like protein kinase) 39 | chr4:2259580-2262138 FORWARD LENGTH=659	537	659	0	122.7	73.7	86.4
Rsa1.0_00162.1.g7244.t6	gb|AAC13599.1| similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]	612	928	1.00E-113	151.6	40.2	57.4	similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31)	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	612	295	4.00E-30	48.2	11.6	15.8
Rsa1.0_00162.1.g7245.t1	ref|NP_178107.1| chromosome transmission fidelity protein 1 [Arabidopsis thaliana] gi|12324592|gb|AAG52253.1|AC011717_21 putative helicase; 55525-51977 [Arabidopsis thaliana] gi|332198199|gb|AEE36320.1| RAD3-like DNA-binding helicase protein [Arabidopsis thaliana]	870	882	0	101.4	79.2	85.6	chromosome transmission fidelity protein 1	gbpln	Arabidopsis thaliana	AT1G79890.1 | Symbols: | RAD3-like DNA-binding helicase protein | chr1:30048655-30052203 FORWARD LENGTH=882	870	882	0	101.4	79.2	85.6
Rsa1.0_00162.1.g7246.t1	ref|XP_002876806.1| hypothetical protein ARALYDRAFT_322561 [Arabidopsis lyrata subsp. lyrata] gi|297322644|gb|EFH53065.1| hypothetical protein ARALYDRAFT_322561 [Arabidopsis lyrata subsp. lyrata]	205	317	1.00E-55	154.6	58.0	69.3	hypothetical protein ARALYDRAFT_322561	gbpln	Arabidopsis lyrata	AT2G02240.1 | Symbols: MEE66 | F-box family protein | chr2:592359-593602 REVERSE LENGTH=320	205	320	1.00E-56	156.1	58.0	67.8

Rsa1.0_00162.1.g7247.t1	ref|NP_178332.2| phloem protein 2–B2 [Arabidopsis thaliana] gi|334302847|sp|Q9ZVR5.2|PP2B2_ARATH RecName: Full=Putative F–box protein PP2–B2; AltName: Full=Protein PHLOEM PROTEIN 2–LIKE B2; Short=AtPP2–B2 gi|330250467|gb|AEC05561.1| phloem protein 2–B2 [Arabidopsis thaliana]	166	310	9.00E–60	186.7	68.7	82.5	phloem protein 2–B2	gbpln	Arabidopsis thaliana	AT2G02250.1 | Symbols: AtPP2–B2, PP2–B2 | phloem protein 2–B2 | chr2:594655–595825 REVERSE LENGTH=310	166	310	3.00E–62	186.7	68.7	82.5
Rsa1.0_00162.1.g7248.t1	gb|EOA26085.1| hypothetical protein CARUB_v10019504mg [Capsella rubella]	106	307	3.00E–36	289.6	67.0	82.1	hypothetical protein CARUB_v10019504mg	gbpln	Capsella rubella	AT2G02250.1 | Symbols: AtPP2–B2, PP2–B2 | phloem protein 2–B2 | chr2:594655–595825 REVERSE LENGTH=310	106	310	3.00E–37	292.5	71.7	83.0
Rsa1.0_00162.1.g7249.t1	gb|EOA25428.1| hypothetical protein CARUB_v10018760mg [Capsella rubella]	264	300	7.00E–47	113.6	41.7	54.5	hypothetical protein CARUB_v10018760mg	gbpln	Capsella rubella	AT2G02240.1 | Symbols: MEE66 | F–box family protein | chr2:592359–593602 REVERSE LENGTH=320	264	320	2.00E–44	121.2	40.5	56.4
Rsa1.0_00162.1.g7250.t1	gb|EOA25428.1| hypothetical protein CARUB_v10018760mg [Capsella rubella]	470	300	1.00E–124	63.8	45.5	52.6	hypothetical protein CARUB_v10018760mg	gbpln	Capsella rubella	AT2G02240.1 | Symbols: MEE66 | F–box family protein | chr2:592359–593602 REVERSE LENGTH=320	470	320	2.00E–94	68.1	35.1	44.5
Rsa1.0_00162.1.g7251.t1	gb|EOA25983.1| hypothetical protein CARUB_v10019372mg [Capsella rubella]	703	282	5.00E–38	40.1	11.9	15.8	hypothetical protein CARUB_v10019372mg	gbpln	Capsella rubella	AT2G02240.1 | Symbols: MEE66 | F–box family protein | chr2:592359–593602 REVERSE LENGTH=320	703	320	3.00E–39	45.5	12.8	15.4
Rsa1.0_00162.1.g7252.t1	gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]	194	863	2.00E–34	444.8	40.2	54.6	Ulp1 protease family protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00162.1.g7253.t1	#	#	#	#	#	#	#	–	––––	––––	AT2G02370.2 | Symbols: | SNARE associated Golgi protein family | chr2:621841–623084 FORWARD LENGTH=320	109	320	1.00E–12	293.6	44.0	56.9
Rsa1.0_00162.1.g7254.t1	ref|XP_002876816.1| phloem protein 2–B10 [Arabidopsis lyrata subsp. lyrata] gi|297322654|gb|EFH53075.1| phloem protein 2–B10 [Arabidopsis lyrata subsp. lyrata]	284	273	1.00E–91	96.1	61.6	73.6	phloem protein 2–B10	gbpln	Arabidopsis lyrata	AT2G02360.1 | Symbols: AtPP2–B10, PP2–B10 | phloem protein 2–B10 | chr2:619699–620736 REVERSE LENGTH=272	284	272	6.00E–89	95.8	58.1	70.1
Rsa1.0_00162.1.g7255.t2	ref|XP_002875121.1| hypothetical protein ARALYDRAFT_484153 [Arabidopsis lyrata subsp. lyrata] gi|297320959|gb|EFH51380.1| hypothetical protein ARALYDRAFT_484153 [Arabidopsis lyrata subsp. lyrata]	358	322	6.00E–88	89.9	53.4	62.0	hypothetical protein ARALYDRAFT_484153	gbpln	Arabidopsis lyrata	AT2G02370.2 | Symbols: | SNARE associated Golgi protein family | chr2:621841–623084 FORWARD LENGTH=320	358	320	6.00E–90	89.4	53.4	61.7
Rsa1.0_00162.1.g7256.t1	ref|XP_002875123.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320961|gb|EFH51382.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	170	227	2.00E–75	133.5	78.2	88.2	predicted protein	gbpln	Arabidopsis lyrata	AT2G02390.1 | Symbols: ATGSTZ1, GST18, GSTZ1 | glutathione S–transferase zeta 1 | chr2:629015–630955 FORWARD LENGTH=221	170	221	1.00E–77	130.0	78.8	88.2
Rsa1.0_00162.1.g7257.t1	ref|XP_002876817.1| cinnamoyl–CoA reductase family [Arabidopsis lyrata subsp. lyrata] gi|297322655|gb|EFH53076.1| cinnamoyl–CoA reductase family [Arabidopsis lyrata subsp. lyrata]	274	318	1.00E–142	116.1	88.7	94.2	cinnamoyl–CoA reductase family	gbpln	Arabidopsis lyrata	AT2G02400.1 | Symbols: | NAD(P)–binding Rossmann–fold superfamily protein | chr2:631413–632449 REVERSE LENGTH=318	274	318	1.00E–143	116.1	87.2	93.8
Rsa1.0_00162.1.g7258.t1	gb|EOA24407.1| hypothetical protein CARUB_v10017657mg [Capsella rubella]	309	320	1.00E–110	103.6	75.1	84.5	hypothetical protein CARUB_v10017657mg	gbpln	Capsella rubella	AT2G02540.1 | Symbols: ATHB21, ZFHD4, HB21, ZHD3 | homeobox protein 21 | chr2:684302–685234 FORWARD LENGTH=310	309	310	1.00E–111	100.3	75.1	83.8
Rsa1.0_00163.1.g7259.t4	gb|EOA38784.1| hypothetical protein CARUB_v10011034mg [Capsella rubella]	588	584	1.00E–173	99.3	65.5	75.3	hypothetical protein CARUB_v10011034mg	gbpln	Capsella rubella	AT1G15280.2 | Symbols: | CASC3/Barentsz eIF4AIII binding | chr1:5252538–5256214 FORWARD LENGTH=585	588	585	1.00E–161	99.5	64.1	73.3
Rsa1.0_00163.1.g7260.t1	gb|EOA38838.1| hypothetical protein CARUB_v10011179mg [Capsella rubella]	694	905	0	130.4	54.5	65.1	hypothetical protein CARUB_v10011179mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838–14323928 FORWARD LENGTH=696	694	696	1.00E–120	100.3	32.3	47.3
Rsa1.0_00163.1.g7261.t1	ref|XP_002892861.1| hypothetical protein ARALYDRAFT_312525 [Arabidopsis lyrata subsp. lyrata] gi|297338703|gb|EFH69120.1| hypothetical protein ARALYDRAFT_312525 [Arabidopsis lyrata subsp. lyrata]	354	357	2.00E–83	100.8	65.8	72.6	hypothetical protein ARALYDRAFT_312525	gbpln	Arabidopsis lyrata	AT1G15340.1 | Symbols: MBD10 | methyl–CPG–binding domain 10 | chr1:5275895–5277474 REVERSE LENGTH=384	354	384	1.00E–85	108.5	67.8	72.9

Rsa1.0_00163.1.g7262.t1	ref|NP_563972.1| uncharacterized protein [Arabidopsis thaliana] gi|30684315|ref|NP_849667.1| uncharacterized protein [Arabidopsis thaliana] gi|21617951|gb|AAM67001.1| unknown [Arabidopsis thaliana] gi|110742955|dbj|BAE99372.1| hypothetical protein [Arabidopsis thaliana] gi|332191186|gb|AEE29307.1| uncharacterized protein AT1G15350 [Arabidopsis thaliana] gi|332191187|gb|AEE29308.1| uncharacterized protein AT1G15350 [Arabidopsis thaliana]	215	154	2.00E−62	71.6	55.8	62.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G15350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G15770.2); Has 148 Blast hits to 148 proteins in 25 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 141; Viruses − 0; Other Eukaryotes − 7 (source: NCBI BLink). | chr1:5278481−5279486 REVERSE LENGTH=154	215	154	6.00E−65	71.6	55.8	62.8
Rsa1.0_00163.1.g7263.t2	ref|NP_172988.1| ethylene−responsive transcription factor WIN1 [Arabidopsis thaliana] gi|75338622|sp|Q9XI33.1|WIN1_ARATH RecName: Full=Ethylene−responsive transcription factor WIN1; AltName: Full=Protein SHINE 1; AltName: Full=Protein WAX INDUCER 1 gi|5103834|gb|AAD39664.1|AC007591_29 Similar to gb|AB008104 ethylene responsive element binding factor 2 from Arabidopsis thaliana and contains an PF|00847 AP2 domain. EST gb|AA728476 comes from this gene [Arabidopsis thaliana] gi|26450944|dbj|BAC42579.1| putative ethylene responsive element [Arabidopsis thaliana] gi|28950721|gb|AAO63284.1| At1g15360 [Arabidopsis thaliana] gi|38426898|gb|AAR20494.1| transcription factor wax inducer 1 [Arabidopsis thaliana] gi|332191189|gb|AEE29310.1| ethylene−responsive transcription factor WIN1 [Arabidopsis thaliana]	227	199	3.00E−73	87.7	70.0	75.8	ethylene−responsive transcription factor WIN1	gbpln	Arabidopsis thaliana	AT1G15360.1 | Symbols: SHN1, WIN1 | Integrase−type DNA−binding superfamily protein | chr1:5283609−5284506 FORWARD LENGTH=199	227	199	8.00E−76	87.7	70.0	75.8
Rsa1.0_00163.1.g7264.t1	gb|EOA38607.1| hypothetical protein CARUB_v10010450mg [Capsella rubella]	172	174	6.00E−86	101.2	91.3	94.8	hypothetical protein CARUB_v10010450mg	gbpln	Capsella rubella	AT1G15380.2 | Symbols: | Lactoylglutathione lyase / glyoxalase I family protein | chr1:5290955−5292287 FORWARD LENGTH=174	172	174	1.00E−85	101.2	89.0	93.0
Rsa1.0_00163.1.g7265.t1	ref|XP_002892864.1| hypothetical protein ARALYDRAFT_888930 [Arabidopsis lyrata subsp. lyrata] gi|297338706|gb|EFH69123.1| hypothetical protein ARALYDRAFT_888930 [Arabidopsis lyrata subsp. lyrata]	76	76	7.00E−20	100.0	64.5	71.1	hypothetical protein ARALYDRAFT_888930	gbpln	Arabidopsis lyrata	AT1G15385.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF761, plant (InterPro:IPR008480); Has 6 Blast hits to 6 proteins in 3 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 6; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:5292976−5293197 REVERSE LENGTH=73	76	73	3.00E−22	96.1	64.5	69.7
Rsa1.0_00163.1.g7266.t1	ref|NP_172994.1| uncharacterized protein [Arabidopsis thaliana] gi|5103841|gb|AAD39671.1|AC007591_36 F9L1.37 [Arabidopsis thaliana] gi|332191199|gb|AEE29320.1| uncharacterized protein AT1G15415 [Arabidopsis thaliana]	50	96	8.00E−16	192.0	82.0	94.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G15415.1 | Symbols: | The protein encoded by this gene was identified as a part of pollen proteome by mass spec analysis. It has weak homology to LEA (late embryo abundant) proteins. Encodes protein phosphatase 2A (PP2A) B'gamma subunit. Targeted to nucleus and cytosol. | chr1:5300931−5301412 REVERSE LENGTH=96	50	96	1.00E−18	192.0	82.0	94.0
Rsa1.0_00163.1.g7267.t1	ref|XP_002892867.1| hypothetical protein ARALYDRAFT_471743 [Arabidopsis lyrata subsp. lyrata] gi|297338709|gb|EFH69126.1| hypothetical protein ARALYDRAFT_471743 [Arabidopsis lyrata subsp. lyrata]	269	278	2.00E−95	103.3	82.9	91.1	hypothetical protein ARALYDRAFT_471743	gbpln	Arabidopsis lyrata	AT1G15420.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Small−subunit processome, Utp12 (InterPro:IPR007148); Has 764 Blast hits to 656 proteins in 193 species: Archae − 0; Bacteria − 42; Metazoa − 237; Fungi − 154; Plants − 85; Viruses − 23; Other Eukaryotes − 223 (source: NCBI BLink). | chr1:5301794−5303296 REVERSE LENGTH=278	269	278	2.00E−92	103.3	81.0	90.0
Rsa1.0_00163.1.g7268.t1	ref|XP_002890104.1| F9L1.39 [Arabidopsis lyrata subsp. lyrata] gi|297335946|gb|EFH66363.1| F9L1.39 [Arabidopsis lyrata subsp. lyrata]	248	249	1.00E−78	100.4	64.9	73.8	F9L1.39	gbpln	Arabidopsis lyrata	AT1G15430.2 | Symbols: | Protein of unknown function (DUF1644) | chr1:5305011−5305790 FORWARD LENGTH=259	248	259	5.00E−80	104.4	65.7	74.6
Rsa1.0_00163.1.g7269.t1	gb|EOA39629.1| hypothetical protein CARUB_v10008260mg [Capsella rubella]	881	900	0	102.2	90.6	95.7	hypothetical protein CARUB_v10008260mg	gbpln	Capsella rubella	AT1G15440.1 | Symbols: PWP2, ATPWP2 | periodic tryptophan protein 2 | chr1:5306159−5309460 REVERSE LENGTH=900	881	900	0	102.2	88.9	95.1
Rsa1.0_00163.1.g7270.t1	gb|EOA39910.1| hypothetical protein CARUB_v10008598mg [Capsella rubella]	617	618	0	100.2	90.9	94.8	hypothetical protein CARUB_v10008598mg	gbpln	Capsella rubella	AT1G15500.1 | Symbols: ATNTT2 | TLC ATP/ADP transporter | chr1:5326426−5328688 FORWARD LENGTH=618	617	618	0	100.2	91.1	94.7

<table>
<tr><td>Rsa1.0_00163.1.g7271.t8</td><td>gb|AAA51659.1| cyclin [Brassica napus]</td><td>463</td><td>434</td><td>0</td><td>93.7</td><td>79.9</td><td>84.7</td><td>cyclin</td><td>gbpln</td><td>Brassica napus</td><td>AT1G15570.1 | Symbols: CYCA2;3 | CYCLIN A2;3 | chr1:5363034-5365218 FORWARD LENGTH=450</td><td>463</td><td>450</td><td>0</td><td>97.2</td><td>76.7</td><td>84.2</td></tr>
<tr><td>Rsa1.0_00163.1.g7272.t1</td><td>gb|AET95910.1| AVP1-1 [Brassica rapa]</td><td>771</td><td>769</td><td>0</td><td>99.7</td><td>98.6</td><td>99.1</td><td>AVP1-1</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G15690.1 | Symbols: AVP1, ATAVP3, AVP-3, AtVHP1;1 | Inorganic H pyrophosphatase family protein | chr1:5399115-5402185 FORWARD LENGTH=770</td><td>771</td><td>770</td><td>0</td><td>99.9</td><td>95.3</td><td>98.2</td></tr>
<tr><td>Rsa1.0_00163.1.g7273.t1</td><td>gb|EOA37423.1| hypothetical protein CARUB_v10011380mg [Capsella rubella]</td><td>374</td><td>386</td><td>0</td><td>103.2</td><td>87.4</td><td>93.3</td><td>hypothetical protein CARUB_v10011380mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G15700.1 | Symbols: ATPC2 | ATPase, F1 complex, gamma subunit protein | chr1:5402629-5403789 REVERSE LENGTH=386</td><td>374</td><td>386</td><td>1.00E-178</td><td>103.2</td><td>87.2</td><td>92.8</td></tr>
<tr><td>Rsa1.0_00163.1.g7274.t4</td><td>gb|EOA39491.1| hypothetical protein CARUB_v10008096mg [Capsella rubella]</td><td>1381</td><td>1344</td><td>0</td><td>97.3</td><td>82.2</td><td>87.7</td><td>hypothetical protein CARUB_v10008096mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10440.1); Has 103701 Blast hits to 43153 proteins in 1828 species: Archae - 30; Bacteria - 7385; Metazoa - 38639; Fungi - 11531; Plants - 7727; Viruses - 307; Other Eukaryotes - 38082 (source: NCBI BLink). | chr1:5430446-5435921 REVERSE LENGTH=1335</td><td>1381</td><td>1335</td><td>0</td><td>96.7</td><td>81.7</td><td>87.3</td></tr>
<tr><td>Rsa1.0_00163.1.g7275.t1</td><td>ref|NP_001154344.1| uncharacterized protein [Arabidopsis thaliana] gi|240254082|ref|NP_563983.4| uncharacterized protein [Arabidopsis thaliana] gi|32815875|gb|AAP88334.1| At1g15860 [Arabidopsis thaliana] gi|332191253|gb|AEE29374.1| uncharacterized protein AT1G15860 [Arabidopsis thaliana] gi|332191254|gb|AEE29375.1| uncharacterized protein AT1G15860 [Arabidopsis thaliana]</td><td>281</td><td>227</td><td>4.00E-86</td><td>80.8</td><td>53.4</td><td>62.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G15860.2 | Symbols: | Domain of unknown function (DUF298) | chr1:5455055-5456741 FORWARD LENGTH=227</td><td>281</td><td>227</td><td>1.00E-88</td><td>80.8</td><td>53.4</td><td>62.6</td></tr>
<tr><td>Rsa1.0_00163.1.g7276.t1</td><td>gb|EOA36249.1| hypothetical protein CARUB_v10010239mg [Capsella rubella]</td><td>222</td><td>223</td><td>1.00E-111</td><td>100.5</td><td>91.4</td><td>95.5</td><td>hypothetical protein CARUB_v10010239mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G15880.1 | Symbols: GOS11, atgos11 | golgi snare 11 | chr1:5458718-5460089 REVERSE LENGTH=223</td><td>222</td><td>223</td><td>1.00E-112</td><td>100.5</td><td>91.0</td><td>94.6</td></tr>
<tr><td>Rsa1.0_00163.1.g7277.t1</td><td>gb|EOA36301.1| hypothetical protein CARUB_v10010589mg [Capsella rubella]</td><td>144</td><td>142</td><td>1.00E-71</td><td>98.6</td><td>95.1</td><td>97.2</td><td>hypothetical protein CARUB_v10010589mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G32060.2 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr2:13639228-13640104 REVERSE LENGTH=144</td><td>144</td><td>144</td><td>7.00E-63</td><td>100.0</td><td>87.5</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00163.1.g7278.t1</td><td>ref|NP_173046.2| aspartyl beta-hydroxylase N-terminal region domain-containing protein [Arabidopsis thaliana] gi|6587800|gb|AAF18491.1|AC010924_4 T24D18.4 [Arabidopsis thaliana] gi|332191266|gb|AEE29387.1| aspartyl beta-hydroxylase N-terminal region domain-containing protein [Arabidopsis thaliana]</td><td>918</td><td>990</td><td>0</td><td>107.8</td><td>61.2</td><td>72.4</td><td>aspartyl beta-hydroxylase N-terminal region domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G15940.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr1:5473672-5478050 FORWARD LENGTH=990</td><td>918</td><td>990</td><td>0</td><td>107.8</td><td>61.2</td><td>72.4</td></tr>
<tr><td>Rsa1.0_00163.1.g7279.t1</td><td>gb|EOA38128.1| hypothetical protein CARUB_v10009599mg [Capsella rubella]</td><td>364</td><td>349</td><td>1.00E-142</td><td>95.9</td><td>75.0</td><td>83.2</td><td>hypothetical protein CARUB_v10009599mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G15970.1 | Symbols: | DNA glycosylase superfamily protein | chr1:5486544-5488494 REVERSE LENGTH=352</td><td>364</td><td>352</td><td>1.00E-140</td><td>96.7</td><td>72.0</td><td>79.9</td></tr>
<tr><td>Rsa1.0_00163.1.g7280.t1</td><td>dbj|BAJ34597.1| unnamed protein product [Thellungiella halophila]</td><td>655</td><td>647</td><td>0</td><td>98.8</td><td>93.9</td><td>96.8</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G16030.1 | Symbols: Hsp70b | heat shock protein 70B | chr1:5502386-5504326 REVERSE LENGTH=646</td><td>655</td><td>646</td><td>0</td><td>98.6</td><td>92.2</td><td>96.0</td></tr>
<tr><td>Rsa1.0_00163.1.g7281.t1</td><td>gb|EOA33804.1| hypothetical protein CARUB_v10021275mg [Capsella rubella]</td><td>88</td><td>93</td><td>2.00E-28</td><td>105.7</td><td>71.6</td><td>87.5</td><td>hypothetical protein CARUB_v10021275mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G79660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16170.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:29976294-29976575 FORWARD LENGTH=93</td><td>88</td><td>93</td><td>1.00E-30</td><td>105.7</td><td>71.6</td><td>85.2</td></tr>
<tr><td>Rsa1.0_00163.1.g7282.t2</td><td>ref|XP_002890155.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297335997|gb|EFH66414.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>854</td><td>404</td><td>0</td><td>47.3</td><td>41.3</td><td>43.3</td><td>kelch repeat-containing F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G16250.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:5557214-5558697 FORWARD LENGTH=383</td><td>854</td><td>383</td><td>0</td><td>44.8</td><td>41.0</td><td>43.1</td></tr>
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Rsa1.0_00163.1.g7283.t1	ref|NP_173076.1| wall-associated receptor kinase-like 8 [Arabidopsis thaliana] gi|334182612|ref|NP_001185009.1| wall-associated receptor kinase-like 8 [Arabidopsis thaliana] gi|75265500|sp|Q9SA25.1|WAKLG_ARATH RecName: Full=Wall-associated receptor kinase-like 8; Flags: Precursor gi|4966347|gb|AAD34678.1|AC006341_6 Similar to gb|AJ012423 wall-associated kinase 2 from Arabidopsis thaliana [Arabidopsis thaliana] gi|110739498|dbj|BAF01658.1| putative wall-associated kinase [Arabidopsis thaliana] gi|332191306|gb|AEE29427.1| wall-associated receptor kinase-like 8 [Arabidopsis thaliana] gi|332191307|gb|AEE29428.1| wall-associated receptor kinase-like 8 [Arabidopsis thaliana]	720	720	0	100.0	80.0	87.9	wall-associated receptor kinase-like 8	gbpln	Arabidopsis thaliana	AT1G16260.2 | Symbols: | Wall-associated kinase family protein | chr1:5559708-5562018 REVERSE LENGTH=720	720	720	0	100.0	80.0	87.9
Rsa1.0_00163.1.g7284.t18	ref|XP_002892905.1| ATCHX1 [Arabidopsis lyrata subsp. lyrata] gi|297338747|gb|EFH69164.1| ATCHX1 [Arabidopsis lyrata subsp. lyrata]	1484	785	0	52.9	44.5	48.1	ATCHX1	gbpln	Arabidopsis lyrata	AT1G16380.1 | Symbols: ATCHX1, CHX1 | Cation/hydrogen exchanger family protein | chr1:5598453-5601367 REVERSE LENGTH=785	1484	785	0	52.9	44.1	47.6
Rsa1.0_00163.1.g7285.t1	ref|XP_002890162.1| hypothetical protein ARALYDRAFT_471835 [Arabidopsis lyrata subsp. lyrata] gi|297336004|gb|EFH66421.1| hypothetical protein ARALYDRAFT_471835 [Arabidopsis lyrata subsp. lyrata]	509	518	0	101.8	88.0	93.1	hypothetical protein ARALYDRAFT_471835	gbpln	Arabidopsis lyrata	AT1G16390.1 | Symbols: ATOCT3, 3-Oct | organic cation/carnitine transporter 3 | chr1:5602921-5604477 FORWARD LENGTH=518	509	518	0	101.8	87.2	92.9
Rsa1.0_00163.1.g7286.t1	gb|EOA37332.1| hypothetical protein CARUB_v10011040mg [Capsella rubella]	353	371	1.00E-125	105.1	66.0	79.6	hypothetical protein CARUB_v10011040mg	gbpln	Capsella rubella	AT1G16420.1 | Symbols: ATMC8, MC8 | metacaspase 8 | chr1:5612304-5613829 REVERSE LENGTH=381	353	381	1.00E-122	107.9	64.0	79.0
Rsa1.0_00163.1.g7287.t1	ref|XP_002892909.1| hypothetical protein ARALYDRAFT_889039 [Arabidopsis lyrata subsp. lyrata] gi|297338751|gb|EFH69168.1| hypothetical protein ARALYDRAFT_889039 [Arabidopsis lyrata subsp. lyrata]	1141	1038	0	91.0	77.5	83.1	hypothetical protein ARALYDRAFT_889039	gbpln	Arabidopsis lyrata	AT1G16480.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:5625843-5628656 REVERSE LENGTH=937	1141	937	0	82.1	72.3	76.6
Rsa1.0_00164.1.g7288.t1	gb|EOA19416.1| hypothetical protein CARUB_v10001181mg [Capsella rubella]	284	379	4.00E-43	133.5	29.2	32.0	hypothetical protein CARUB_v10001181mg	gbpln	Capsella rubella	AT5G01700.2 | Symbols: | Protein phosphatase 2C family protein | chr5:260848-262492 REVERSE LENGTH=382	284	382	2.00E-44	134.5	28.5	32.0
Rsa1.0_00164.1.g7289.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00164.1.g7290.t1	ref|NP_195794.1| Nuclear transport factor 2 (NTF2) family protein [Arabidopsis thaliana] gi|7329647|emb|CAB82744.1| putative protein [Arabidopsis thaliana] gi|19715593|gb|AAL91620.1| AT5g01740/T20L15_10 [Arabidopsis thaliana] gi|48310614|gb|AAT41853.1| At5g01740 [Arabidopsis thaliana] gi|332003002|gb|AED90385.1| Nuclear transport factor 2 (NTF2) family protein [Arabidopsis thaliana]	154	162	6.00E-60	105.2	73.4	77.3	Nuclear transport factor 2 (NTF2) family protein	gbpln	Arabidopsis thaliana	AT5G01740.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein | chr5:280793-281281 FORWARD LENGTH=162	154	162	2.00E-62	105.2	73.4	77.3
Rsa1.0_00164.1.g7291.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00164.1.g7292.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	200	442	2.00E-46	221.0	48.5	56.5	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	200	343	4.00E-21	171.5	27.0	35.0

Rsa1.0_00164.1.g7293.t1	ref|NP_850751.1| LURP-one-related 15 protein [Arabidopsis thaliana] gi|75181359|sp|Q9LZX1.1|LOR15_ARATH RecName: Full=Protein LURP-one-related 15 gi|13926237|gb|AAK49593.1|AF372877_1 AT5g01750/T20L15_20 [Arabidopsis thaliana] gi|7329648|emb|CAB82745.1| putative protein [Arabidopsis thaliana] gi|22655412|gb|AAM98298.1| At5g01750/T20L15_20 [Arabidopsis thaliana] gi|332003004|gb|AED90387.1| LURP-one-related 15 protein [Arabidopsis thaliana]	221	217	1.00E-107	98.2	83.7	90.5	LURP-one-related 15 protein	gbpln	Arabidopsis thaliana	AT5G01750.2 | Symbols: | Protein of unknown function (DUF567) | chr5:290034-291109 FORWARD LENGTH=217	221	217	1.00E-110	98.2	83.7	90.5
Rsa1.0_00164.1.g7294.t1	ref|XP_002872993.1| cbl-interacting protein kinase 15 [Arabidopsis lyrata subsp. lyrata] gi|297318830|gb|EFH49252.1| cbl-interacting protein kinase 15 [Arabidopsis lyrata subsp. lyrata]	426	423	0	99.3	80.3	89.9	cbl-interacting protein kinase 15	gbpln	Arabidopsis lyrata	AT5G01810.2 | Symbols: CIPK15, ATPK10, PKS3 | CBL-interacting protein kinase 15 | chr5:310460-311725 FORWARD LENGTH=421	426	421	0	98.8	80.5	89.9
Rsa1.0_00164.1.g7295.t1	ref|XP_002870896.1| hypothetical protein ARALYDRAFT_486886 [Arabidopsis lyrata subsp. lyrata] gi|297316733|gb|EFH47155.1| hypothetical protein ARALYDRAFT_486886 [Arabidopsis lyrata subsp. lyrata]	435	443	0	101.8	80.9	86.0	hypothetical protein ARALYDRAFT_486886	gbpln	Arabidopsis lyrata	AT5G01820.1 | Symbols: ATSR1, SnRK3.15, CIPK14, ATCIPK14, SR1 | serine/threonine protein kinase 1 | chr5:313423-314751 REVERSE LENGTH=442	435	442	0	101.6	80.9	86.2
Rsa1.0_00164.1.g7296.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00164.1.g7297.t1	ref|NP_195804.1| ovate family protein 1 [Arabidopsis thaliana] gi|7329657|emb|CAB82754.1| putative protein [Arabidopsis thaliana] gi|332003016|gb|AED90399.1| ovate family protein 1 [Arabidopsis thaliana]	267	270	8.00E-72	101.1	63.3	72.3	ovate family protein 1	gbpln	Arabidopsis thaliana	AT5G01840.1 | Symbols: ATOFP1, OFP1 | ovate family protein 1 | chr5:324552-325364 FORWARD LENGTH=270	267	270	2.00E-74	101.1	63.3	72.3
Rsa1.0_00164.1.g7298.t1	ref|XP_002872990.1| hypothetical protein ARALYDRAFT_324798 [Arabidopsis lyrata subsp. lyrata] gi|297318827|gb|EFH49249.1| hypothetical protein ARALYDRAFT_324798 [Arabidopsis lyrata subsp. lyrata]	341	337	1.00E-169	98.8	86.2	92.4	hypothetical protein ARALYDRAFT_324798	gbpln	Arabidopsis lyrata	AT5G01850.1 | Symbols: | Protein kinase superfamily protein | chr5:332829-334180 FORWARD LENGTH=333	341	333	1.00E-163	97.7	84.5	88.9
Rsa1.0_00164.1.g7299.t1	ref|XP_002872989.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297318826|gb|EFH49248.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	235	224	2.00E-79	95.3	74.9	81.3	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G01860.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:335630-336277 FORWARD LENGTH=215	235	215	1.00E-66	91.5	68.1	74.5
Rsa1.0_00164.1.g7300.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00164.1.g7301.t1	ref|NP_195808.1| RING-H2 finger protein ATL74 [Arabidopsis thaliana] gi|68565316|sp|Q9LZV8.1|ATL74_ARATH RecName: Full=RING-H2 finger protein ATL74 gi|7329661|emb|CAB82758.1| putative protein [Arabidopsis thaliana] gi|38454090|gb|AAR20739.1| At5g01880 [Arabidopsis thaliana] gi|38604016|gb|AAR24751.1| At5g01880 [Arabidopsis thaliana] gi|110738314|dbj|BAF01085.1| hypothetical protein [Arabidopsis thaliana] gi|332003021|gb|AED90404.1| RING-H2 finger protein ATL74 [Arabidopsis thaliana]	153	159	1.00E-59	103.9	85.6	91.5	RING-H2 finger protein ATL74	gbpln	Arabidopsis thaliana	AT5G01880.1 | Symbols: | RING/U-box superfamily protein | chr5:339017-339496 FORWARD LENGTH=159	153	159	5.00E-62	103.9	85.6	91.5
Rsa1.0_00164.1.g7302.t1	ref|XP_002870895.1| hypothetical protein ARALYDRAFT_486880 [Arabidopsis lyrata subsp. lyrata] gi|297316732|gb|EFH47154.1| hypothetical protein ARALYDRAFT_486880 [Arabidopsis lyrata subsp. lyrata]	953	968	0	101.6	78.7	87.1	hypothetical protein ARALYDRAFT_486880	gbpln	Arabidopsis lyrata	AT5G01890.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr5:341661-344650 REVERSE LENGTH=967	953	967	0	101.5	74.9	83.7
Rsa1.0_00164.1.g7303.t2	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	912	1342	0	147.1	37.1	48.7	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT2G30290.2 | Symbols: VSR2, AtVSR2 | VACUOLAR SORTING RECEPTOR 2 | chr2:12912569-12915781 REVERSE LENGTH=641	912	641	1.00E-168	70.3	30.8	32.8
Rsa1.0_00165.1.g7304.t1	ref|XP_002889555.1| glycosyl hydrolase family 20 protein [Arabidopsis lyrata subsp. lyrata] gi|297335397|gb|EFH65814.1| glycosyl hydrolase family 20 protein [Arabidopsis lyrata subsp. lyrata]	578	578	0	100.0	85.1	91.3	glycosyl hydrolase family 20 protein	gbpln	Arabidopsis lyrata	AT1G05590.1 | Symbols: HEXO2, ATHEX3 | beta-hexosaminidase 2 | chr1:1669871-1671686 FORWARD LENGTH=580	578	580	0	100.3	84.4	90.5

Rsa1.0_00165.1.g7305.t1	ref|XP_002878775.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324614|gb|EFH55034.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	290	208	4.00E-29	71.7	30.0	40.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G24850.1 | Symbols: | Domain of unknown function (DUF313) | chr3:9071105-9072184 FORWARD LENGTH=359	290	359	8.00E-29	123.8	25.2	36.2
Rsa1.0_00165.1.g7306.t1	ref|NP_563745.1| putative uridine nucleosidase 2 [Arabidopsis thaliana] gi|75154756|sp|Q8LAC4.1|URH2_ARATH RecName: Full=Probable uridine nucleosidase 2; AltName: Full=Uridine ribohydrolase 2 gi|21593497|gb|AAM65464.1| unknown [Arabidopsis thaliana] gi|25083300|gb|AAN72060.1| expressed protein [Arabidopsis thaliana] gi|30984540|gb|AAP42733.1| At1g05620 [Arabidopsis thaliana] gi|332189745|gb|AEE27866.1| putative uridine nucleosidase 2 [Arabidopsis thaliana]	323	322	1.00E-172	99.7	92.3	95.7	putative uridine nucleosidase 2	gbpln	Arabidopsis thaliana	AT1G05620.1 | Symbols: URH2 | uridine-ribohydrolase 2 | chr1:1679286-1681527 FORWARD LENGTH=322	323	322	1.00E-174	99.7	92.3	95.7
Rsa1.0_00165.1.g7307.t1	ref|XP_002892306.1| hypothetical protein ARALYDRAFT_887757 [Arabidopsis lyrata subsp. lyrata] gi|297338148|gb|EFH68565.1| hypothetical protein ARALYDRAFT_887757 [Arabidopsis lyrata subsp. lyrata]	394	394	0	100.0	84.8	92.6	hypothetical protein ARALYDRAFT_887757	gbpln	Arabidopsis lyrata	AT1G05650.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:1690264-1692126 REVERSE LENGTH=394	394	394	0	100.0	84.8	92.6
Rsa1.0_00165.1.g7308.t8	ref|NP_172054.3| Type I inositol-1,4,5-trisphosphate 5-phosphatase 13 [Arabidopsis thaliana] gi|332189747|gb|AEE27868.1| Type I inositol-1,4,5-trisphosphate 5-phosphatase 13 [Arabidopsis thaliana]	1386	1170	0	84.4	69.5	76.0	Type I inositol-1,4,5-trisphosphate 5-phosphatase 13	gbpln	Arabidopsis thaliana	AT1G05630.1 | Symbols: AT5PTASE13, 5PTASE13 | Endonuclease/exonuclease/phosphatase family protein | chr1:1682483-1687153 FORWARD LENGTH=1170	1386	1170	0	84.4	69.5	76.0
Rsa1.0_00165.1.g7309.t2	gb|EOA37125.1| hypothetical protein CARUB_v10010380mg, partial [Capsella rubella]	182	188	2.00E-74	103.3	76.9	80.2	hypothetical protein CARUB_v10010380mg, partial	gbpln	Capsella rubella	AT1G05720.1 | Symbols: | selenoprotein family protein | chr1:1717677-1718849 REVERSE LENGTH=163	182	163	2.00E-76	89.6	76.4	80.8
Rsa1.0_00165.1.g7310.t1	ref|XP_002889561.1| hypothetical protein ARALYDRAFT_470580 [Arabidopsis lyrata subsp. lyrata] gi|297335403|gb|EFH65820.1| hypothetical protein ARALYDRAFT_470580 [Arabidopsis lyrata subsp. lyrata]	149	149	3.00E-75	100.0	90.6	96.6	hypothetical protein ARALYDRAFT_470580	gbpln	Arabidopsis lyrata	AT1G05730.1 | Symbols: | Eukaryotic protein of unknown function (DUF842) | chr1:1719107-1720159 FORWARD LENGTH=149	149	149	3.00E-76	100.0	88.6	96.0
Rsa1.0_00165.1.g7311.t1	gb|EOA30157.1| hypothetical protein CARUB_v10013272mg [Capsella rubella]	569	600	4.00E-56	105.4	23.2	28.3	hypothetical protein CARUB_v10013272mg	gbpln	Capsella rubella	AT2G01280.1 | Symbols: MEE65 | Cyclin/Brf1-like TBP-binding protein | chr2:145676-148784 FORWARD LENGTH=548	569	548	7.00E-58	96.3	20.7	25.3
Rsa1.0_00165.1.g7312.t1	gb|EOA38495.1| hypothetical protein CARUB_v10010263mg [Capsella rubella]	217	218	1.00E-114	100.5	93.5	95.9	hypothetical protein CARUB_v10010263mg	gbpln	Capsella rubella	AT1G05810.1 | Symbols: ARA, ARA-1, ATRAB11D, ATRABA5E, RABA5E | RAB GTPase homolog A5E | chr1:1748314-1749350 FORWARD LENGTH=261	217	261	1.00E-115	120.3	92.6	97.2
Rsa1.0_00165.1.g7313.t1	ref|NP_172074.6| histone-lysine N-methyltransferase ATX2 [Arabidopsis thaliana] gi|240254020|ref|NP_001077464.4| histone-lysine N-methyltransferase ATX2 [Arabidopsis thaliana] gi|257096236|sp|P0CB22.1|ATX2_ARATH RecName: Full=Histone-lysine N-methyltransferase ATX2; AltName: Full=Protein SET DOMAIN GROUP 30; AltName: Full=Trithorax-homolog protein 2; Short=TRX-homolog protein 2 gi|332189779|gb|AEE27900.1| histone-lysine N-methyltransferase ATX2 [Arabidopsis thaliana] gi|332189780|gb|AEE27901.1| histone-lysine N-methyltransferase ATX2 [Arabidopsis thaliana]	1028	1083	0	105.4	83.9	90.4	histone-lysine N-methyltransferase ATX2	gbpln	Arabidopsis thaliana	AT1G05830.2 | Symbols: ATX2 | trithorax-like protein 2 | chr1:1754452-1761225 FORWARD LENGTH=1083	1028	1083	0	105.4	83.9	90.4
Rsa1.0_00165.1.g7314.t1	ref|XP_002892309.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297338151|gb|EFH68568.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	479	484	0	101.0	92.5	95.8	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT1G05840.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:1762843-1766150 REVERSE LENGTH=485	479	485	0	101.3	90.2	92.9
Rsa1.0_00165.1.g7315.t1	ref|XP_002892311.1| hypothetical protein ARALYDRAFT_470598 [Arabidopsis lyrata subsp. lyrata] gi|297338153|gb|EFH68570.1| hypothetical protein ARALYDRAFT_470598 [Arabidopsis lyrata subsp. lyrata]	160	187	8.00E-62	116.9	84.4	88.8	hypothetical protein ARALYDRAFT_470598	gbpln	Arabidopsis lyrata	AT1G05870.4 | Symbols: | Protein of unknown function (DUF1685) | chr1:1772454-1773228 REVERSE LENGTH=189	160	189	8.00E-63	118.1	81.9	88.8

Rsa1.0_00165.1.g7316.t2	ref|NP_973767.1| endonuclease III [Arabidopsis thaliana] gi|222423369|dbj|BAH19657.1| AT1G05900 [Arabidopsis thaliana] gi|332189795|gb|AEE27916.1| endonuclease III [Arabidopsis thaliana]	384	386	1.00E-157	100.5	75.0	81.5	endonuclease III	gbpln	Arabidopsis thaliana	AT1G05900.2 | Symbols: ATNTH2, NTH2 | endonuclease III 2 | chr1:1786896-1789502 FORWARD LENGTH=386	384	386	1.00E-160	100.5	75.0	81.5
Rsa1.0_00165.1.g7317.t1	ref|XP_002889576.1| hypothetical protein ARALYDRAFT_470606 [Arabidopsis lyrata subsp. lyrata] gi|297335418|gb|EFH65835.1| hypothetical protein ARALYDRAFT_470606 [Arabidopsis lyrata subsp. lyrata]	1214	1208	0	99.5	88.6	92.8	hypothetical protein ARALYDRAFT_470606	gbpln	Arabidopsis lyrata	AT1G05910.1 | Symbols: | cell division cycle protein 48-related / CDC48-related | chr1:1790796-1796503 FORWARD LENGTH=1210	1214	1210	0	99.7	88.1	92.0
Rsa1.0_00165.1.g7318.t1	ref|XP_002892313.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338155|gb|EFH68572.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	914	1634	0	178.8	46.8	53.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G05950.1 | Symbols: | unknown protein; Has 50 Blast hits to 45 proteins in 14 species: Archae - 5; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr1:1804573-1807471 REVERSE LENGTH=627	914	627	0	68.6	45.7	52.7
Rsa1.0_00165.1.g7319.t3	ref|XP_002892313.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338155|gb|EFH68572.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	938	1634	9.00E-67	174.2	15.2	17.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G05950.1 | Symbols: | unknown protein; Has 50 Blast hits to 45 proteins in 14 species: Archae - 5; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr1:1804573-1807471 REVERSE LENGTH=627	938	627	4.00E-64	66.8	15.1	17.6
Rsa1.0_00165.1.g7320.t1	ref|NP_683294.2| phosphoglycerate mutase-like protein [Arabidopsis thaliana] gi|332190397|gb|AEE28518.1| phosphoglycerate mutase-like protein [Arabidopsis thaliana]	206	231	1.00E-105	112.1	93.2	95.6	phosphoglycerate mutase-like protein	gbpln	Arabidopsis thaliana	AT1G09935.1 | Symbols: | Phosphoglycerate mutase family protein | chr1:3234060-3235530 REVERSE LENGTH=231	206	231	1.00E-107	112.1	93.2	95.6
Rsa1.0_00165.1.g7321.t1	gb|EOA36079.1| hypothetical protein CARUB_v10010176mg [Capsella rubella]	227	234	1.00E-102	103.1	80.6	86.3	hypothetical protein CARUB_v10010176mg	gbpln	Capsella rubella	AT1G09950.1 | Symbols: RAS1 | RESPONSE TO ABA AND SALT 1 | chr1:3240849-3241541 REVERSE LENGTH=230	227	230	1.00E-101	101.3	82.8	89.4
Rsa1.0_00165.1.g7322.t2	gb|AAG09191.1|AF175321_1 sucrose transporter SUT4 [Arabidopsis thaliana] gi|9957055|gb|AAG09192.1|AF175322_1 sucrose transporter SUT4 [Arabidopsis thaliana]	523	510	0	97.5	89.5	93.1	sucrose transporter SUT4	gbpln	Arabidopsis thaliana	AT1G09960.1 | Symbols: SUT4, ATSUT4, SUC4, ATSUC4 | sucrose transporter 4 | chr1:3244258-3246718 FORWARD LENGTH=510	523	510	0	97.5	89.3	92.9
Rsa1.0_00165.1.g7323.t1	ref|XP_002892542.1| hypothetical protein ARALYDRAFT_888257 [Arabidopsis lyrata subsp. lyrata] gi|297338384|gb|EFH68801.1| hypothetical protein ARALYDRAFT_888257 [Arabidopsis lyrata subsp. lyrata]	797	802	0	100.6	88.6	93.6	hypothetical protein ARALYDRAFT_888257	gbpln	Arabidopsis lyrata	AT1G09980.1 | Symbols: | Putative serine esterase family protein | chr1:3256541-3260866 REVERSE LENGTH=802	797	802	0	100.6	86.6	93.0
Rsa1.0_00165.1.g7324.t2	ref|XP_002889784.1| hypothetical protein ARALYDRAFT_888258 [Arabidopsis lyrata subsp. lyrata] gi|297335626|gb|EFH66043.1| hypothetical protein ARALYDRAFT_888258 [Arabidopsis lyrata subsp. lyrata]	479	491	0	102.5	81.4	88.7	hypothetical protein ARALYDRAFT_888258	gbpln	Arabidopsis lyrata	AT1G10010.1 | Symbols: AAP8, ATAAP8 | amino acid permease 8 | chr1:3265976-3268726 FORWARD LENGTH=475	479	475	0	99.2	74.9	85.4
Rsa1.0_00165.1.g7325.t1	ref|XP_004144665.1| PREDICTED: uncharacterized protein LOC101203090 isoform 1 [Cucumis sativus] gi|449453844|ref|XP_004144666.1| PREDICTED: uncharacterized protein LOC101203090 isoform 2 [Cucumis sativus] gi|449522819|ref|XP_004168423.1| PREDICTED: uncharacterized LOC101203090 [Cucumis sativus]	65	776	8.00E-12	1193.8	50.8	56.9	PREDICTED: uncharacterized protein LOC101203090 isoform 1	gbpln	Cucumis sativus	AT3G57880.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein | chr3:21431198-21433519 REVERSE LENGTH=773	65	773	5.00E-14	1189.2	47.7	55.4
Rsa1.0_00165.1.g7326.t1	ref|XP_002889784.1| hypothetical protein ARALYDRAFT_888258 [Arabidopsis lyrata subsp. lyrata] gi|297335626|gb|EFH66043.1| hypothetical protein ARALYDRAFT_888258 [Arabidopsis lyrata subsp. lyrata]	467	491	0	105.1	79.9	89.1	hypothetical protein ARALYDRAFT_888258	gbpln	Arabidopsis lyrata	AT1G10010.1 | Symbols: AAP8, ATAAP8 | amino acid permease 8 | chr1:3265976-3268726 FORWARD LENGTH=475	467	475	0	101.7	78.2	87.8
Rsa1.0_00166.1.g7327.t1	gb|ACR48185.1| MYB domain protein 34-2 [Brassica rapa subsp. pekinensis]	263	316	1.00E-110	120.2	77.6	86.3	MYB domain protein 34-2	gbpln	Brassica rapa	AT5G60890.1 | Symbols: ATMYB34, ATR1, MYB34 | myb domain protein 34 | chr5:24495029-24496220 FORWARD LENGTH=295	263	295	3.00E-94	112.2	71.9	79.5
Rsa1.0_00166.1.g7328.t1	dbj|BAJ33723.1| unnamed protein product [Thellungiella halophila]	430	417	0	97.0	88.1	93.5	unnamed protein product	----	----	AT5G65990.1 | Symbols: | Transmembrane amino acid transporter family protein | chr5:26394955-26396321 FORWARD LENGTH=427	430	427	0	99.3	87.2	93.7

Rsa1.0_00166.1.g7329.t1	ref|XP_002866421.1| complex 1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297312256|gb|EFH42680.1| complex 1 family protein [Arabidopsis lyrata subsp. lyrata]	87	87	3.00E-35	100.0	82.8	90.8	complex 1 family protein	gbpln	Arabidopsis lyrata	AT5G61220.1 | Symbols: | LYR family of Fe/S cluster biogenesis protein | chr5:24626057-24626320 REVERSE LENGTH=87	87	87	4.00E-37	100.0	80.5	89.7
Rsa1.0_00166.1.g7330.t1	ref|XP_002864727.1| hypothetical protein ARALYDRAFT_496281 [Arabidopsis lyrata subsp. lyrata] gi|297310562|gb|EFH40986.1| hypothetical protein ARALYDRAFT_496281 [Arabidopsis lyrata subsp. lyrata]	412	499	1.00E-122	121.1	70.1	80.8	hypothetical protein ARALYDRAFT_496281	gbpln	Arabidopsis lyrata	AT5G61260.1 | Symbols: | Plant calmodulin-binding protein-related | chr5:24637109-24638599 FORWARD LENGTH=496	412	496	1.00E-117	120.4	69.2	81.8
Rsa1.0_00166.1.g7331.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00166.1.g7332.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00166.1.g7333.t1	ref|NP_200971.1| uncharacterized protein [Arabidopsis thaliana] gi|91807084|gb|ABE66269.1| hypothetical protein At5g61630 [Arabidopsis thaliana] gi|332010116|gb|AED97499.1| uncharacterized protein AT5G61630 [Arabidopsis thaliana]	150	147	6.00E-67	98.0	88.0	91.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G61630.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G07490.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:24773803-24774502 REVERSE LENGTH=147	150	147	2.00E-69	98.0	88.0	91.3
Rsa1.0_00166.1.g7334.t1	ref|XP_002864744.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297310579|gb|EFH41003.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	309	321	1.00E-137	103.9	79.0	88.3	myb family transcription factor	gbpln	Arabidopsis lyrata	AT5G61620.1 | Symbols: | myb-like transcription factor family protein | chr5:24772383-24773507 FORWARD LENGTH=317	309	317	1.00E-131	102.6	75.4	86.4
Rsa1.0_00166.1.g7335.t1	gb|ADM89080.1| ethylene response factor 56 [Brassica napus]	243	219	4.00E-90	90.1	74.1	80.2	ethylene response factor 56	gbpln	Brassica napus	AT5G61600.1 | Symbols: ERF104 | ethylene response factor 104 | chr5:24766643-24767368 REVERSE LENGTH=241	243	241	1.00E-78	99.2	72.0	79.4
Rsa1.0_00166.1.g7336.t1	ref|NP_200964.2| U-box domain-containing protein 51 [Arabidopsis thaliana] gi|172045896|sp|Q9FKG5.2|PUB51_ARATH RecName: Full=U-box domain-containing protein 51; AltName: Full=Plant U-box protein 51; Includes: RecName: Full=E3 ubiquitin ligase; Includes: RecName: Full=Serine/threonine-protein kinase gi|332010105|gb|AED97488.1| U-box domain-containing protein 51 [Arabidopsis thaliana]	761	796	0	104.6	85.9	93.3	U-box domain-containing protein 51	gbpln	Arabidopsis thaliana	AT5G61560.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:24753476-24756506 FORWARD LENGTH=796	761	796	0	104.6	85.9	93.3
Rsa1.0_00166.1.g7337.t1	gb|EOA14619.1| hypothetical protein CARUB_v10027877mg [Capsella rubella]	813	849	0	104.4	83.9	91.4	hypothetical protein CARUB_v10027877mg	gbpln	Capsella rubella	AT5G61550.2 | Symbols: | U-box domain-containing protein kinase family protein | chr5:24748325-24751805 FORWARD LENGTH=860	813	860	0	105.8	80.3	89.4
Rsa1.0_00166.1.g7338.t1	ref|XP_002866440.1| hypothetical protein ARALYDRAFT_496310 [Arabidopsis lyrata subsp. lyrata] gi|297312275|gb|EFH42699.1| hypothetical protein ARALYDRAFT_496310 [Arabidopsis lyrata subsp. lyrata]	80	403	3.00E-14	503.8	52.5	62.5	hypothetical protein ARALYDRAFT_496310	gbpln	Arabidopsis lyrata	AT5G61510.1 | Symbols: | GroES-like zinc-binding alcohol dehydrogenase family protein | chr5:24737084-24738975 REVERSE LENGTH=406	80	406	7.00E-17	507.5	52.5	62.5
Rsa1.0_00166.1.g7339.t1	gb|EOA14619.1| hypothetical protein CARUB_v10027877mg [Capsella rubella]	858	849	0	99.0	88.8	93.9	hypothetical protein CARUB_v10027877mg	gbpln	Capsella rubella	AT5G61550.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:24748325-24751558 FORWARD LENGTH=845	858	845	0	98.5	84.3	92.2
Rsa1.0_00166.1.g7340.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00166.1.g7341.t1	gb|EOA12449.1| hypothetical protein CARUB_v10028614mg [Capsella rubella]	269	291	3.00E-39	108.2	40.9	59.1	hypothetical protein CARUB_v10028614mg	gbpln	Capsella rubella	AT5G61470.1 | Symbols: | C2H2-like zinc finger protein | chr5:24722870-24723784 FORWARD LENGTH=304	269	304	4.00E-39	113.0	42.8	61.7
Rsa1.0_00166.1.g7342.t1	gb|EOA14349.1| hypothetical protein CARUB_v10027529mg [Capsella rubella]	227	222	3.00E-84	97.8	74.9	87.7	hypothetical protein CARUB_v10027529mg	gbpln	Capsella rubella	AT5G51860.2 | Symbols: | K-box region and MADS-box transcription factor family protein | chr5:21081844-21084126 REVERSE LENGTH=202	227	202	9.00E-60	89.0	55.5	70.0
Rsa1.0_00166.1.g7343.t1	ref|XP_002866435.1| ANAC100/ATNAC5 [Arabidopsis lyrata subsp. lyrata] gi|297312270|gb|EFH42694.1| ANAC100/ATNAC5 [Arabidopsis lyrata subsp. lyrata]	384	336	1.00E-156	87.5	69.8	71.6	ANAC100/ATNAC5	gbpln	Arabidopsis lyrata	AT5G61430.1 | Symbols: ANAC100, ATNAC5, NAC100 | NAC domain containing protein 100 | chr5:24701328-24702553 REVERSE LENGTH=336	384	336	1.00E-158	87.5	69.3	71.1
Rsa1.0_00166.1.g7344.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1367	1307	0	95.6	59.9	74.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1367	1262	1.00E-96	92.3	14.0	21.5

Rsa1.0_00166.1.g7345.t1	dbj|BAM78213.1| Myb transcription factor BoMyb28-1 [Brassica oleracea var. viridis]	363	352	1.00E-172	97.0	85.4	89.5	Myb transcription factor BoMyb28-1	gbpln	Brassica oleracea	AT5G61420.2 | Symbols: MYB28, HAG1 | myb domain protein 28 | chr5:24689475-24690795 REVERSE LENGTH=366	363	366	1.00E-157	100.8	77.7	84.6
Rsa1.0_00166.1.g7346.t1	ref|XP_002866429.1| hypothetical protein ARALYDRAFT_919377 [Arabidopsis lyrata subsp. lyrata] gi|297312264|gb|EFH42688.1| hypothetical protein ARALYDRAFT_919377 [Arabidopsis lyrata subsp. lyrata]	311	325	1.00E-112	104.5	78.5	86.5	hypothetical protein ARALYDRAFT_919377	gbpln	Arabidopsis lyrata	AT5G61340.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26650.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:24662064-24663044 REVERSE LENGTH=326	311	326	1.00E-113	104.8	78.1	85.2
Rsa1.0_00166.1.g7347.t1	ref|XP_002864755.1| tudor domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310590|gb|EFH41014.1| tudor domain-containing protein [Arabidopsis lyrata subsp. lyrata]	985	983	0	99.8	89.8	94.5	tudor domain-containing protein	gbpln	Arabidopsis lyrata	AT5G61780.1 | Symbols: Tudor2, AtTudor2, TSN2 | TUDOR-SN protein 2 | chr5:24822012-24826641 FORWARD LENGTH=985	985	985	0	100.0	89.4	94.0
Rsa1.0_00166.1.g7348.t1	ref|XP_002866455.1| hypothetical protein ARALYDRAFT_496347 [Arabidopsis lyrata subsp. lyrata] gi|297312290|gb|EFH42714.1| hypothetical protein ARALYDRAFT_496347 [Arabidopsis lyrata subsp. lyrata]	953	1401	0	147.0	49.4	51.3	hypothetical protein ARALYDRAFT_496347	gbpln	Arabidopsis lyrata	AT5G61790.1 | Symbols: CNX1, ATCNX1 | calnexin 1 | chr5:24827394-24829642 REVERSE LENGTH=530	953	530	0	55.6	49.8	52.3
Rsa1.0_00166.1.g7349.t1	dbj|BAH04509.1| leafy-like protein [Raphanus sativus]	415	420	0	101.2	97.6	97.8	leafy-like protein	gbpln	Raphanus sativus	AT5G61850.1 | Symbols: LFY, LFY3 | floral meristem identity control protein LEAFY (LFY) | chr5:24844295-24846933 FORWARD LENGTH=420	415	420	1.00E-178	101.2	88.4	92.5
Rsa1.0_00166.1.g7350.t1	dbj|BAB08881.1| unnamed protein product [Arabidopsis thaliana]	1171	1134	0	96.8	38.7	47.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G61940.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr5:24868155-24872717 FORWARD LENGTH=1094	1171	1094	0	93.4	38.7	47.4
Rsa1.0_00167.1.g7351.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00167.1.g7352.t1	gb|AAM62517.1| unknown [Arabidopsis thaliana]	388	390	0	100.5	87.1	95.1	unknown	gbpln	Arabidopsis thaliana	AT1G76520.2 | Symbols: | Auxin efflux carrier family protein | chr1:28715384-28717289 FORWARD LENGTH=390	388	390	0	100.5	86.9	95.1
Rsa1.0_00167.1.g7353.t1	gb|EOA35411.1| hypothetical protein CARUB_v10020611mg, partial [Capsella rubella]	327	337	1.00E-167	103.1	86.5	92.4	hypothetical protein CARUB_v10020611mg, partial	gbpln	Capsella rubella	AT1G76570.1 | Symbols: | Chlorophyll A-B binding family protein | chr1:28729132-28730754 FORWARD LENGTH=327	327	327	1.00E-167	100.0	87.5	91.4
Rsa1.0_00167.1.g7354.t1	ref|XP_002887647.1| hypothetical protein ARALYDRAFT_895541 [Arabidopsis lyrata subsp. lyrata] gi|297333488|gb|EFH63906.1| hypothetical protein ARALYDRAFT_895541 [Arabidopsis lyrata subsp. lyrata]	964	1034	0	107.3	80.5	86.9	hypothetical protein ARALYDRAFT_895541	gbpln	Arabidopsis lyrata	AT1G76580.1 | Symbols: | Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein | chr1:28734600-28738451 FORWARD LENGTH=988	964	988	0	102.5	76.1	83.6
Rsa1.0_00167.1.g7355.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00167.1.g7356.t1	ref|NP_565136.1| uncharacterized protein [Arabidopsis thaliana] gi|12323985|gb|AAG51956.1|AC015450_17 unknown protein; 83277-83927 [Arabidopsis thaliana] gi|21592540|gb|AAM64489.1| unknown [Arabidopsis thaliana] gi|23197634|gb|AAN15344.1| Unknown protein [Arabidopsis thaliana] gi|332197742|gb|AEE35863.1| uncharacterized protein AT1G76600 [Arabidopsis thaliana]	208	216	6.00E-69	103.8	74.5	87.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G76600.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: nucleolus, nucleus; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21010.1); Has 220 Blast hits to 220 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 220; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:28746975-28747625 FORWARD LENGTH=216	208	216	2.00E-71	103.8	74.5	87.0
Rsa1.0_00167.1.g7357.t1	ref|XP_002881678.1| hypothetical protein ARALYDRAFT_903237 [Arabidopsis lyrata subsp. lyrata] gi|297327517|gb|EFH57937.1| hypothetical protein ARALYDRAFT_903237 [Arabidopsis lyrata subsp. lyrata]	169	159	1.00E-66	94.1	78.1	84.6	hypothetical protein ARALYDRAFT_903237	gbpln	Arabidopsis lyrata	AT1G76640.1 | Symbols: | Calcium-binding EF-hand family protein | chr1:28765324-28765803 REVERSE LENGTH=159	169	159	1.00E-66	94.1	77.5	83.4

Rsa1.0_00167.1.g7358.t1	gb|EOA33381.1| hypothetical protein CARUB_v10020307mg [Capsella rubella]	374	441	2.33E-156	117.9	82.9	88.0	hypothetical protein CARUB_v10020307mg	gbpln	Capsella rubella	AT1G76660.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT5G52430.1); Has 353 Blast hits to 231 proteins in 60 species: Archae - 0; Bacteria - 6; Metazoa - 57; Fungi - 22; Plants - 125; Viruses - 4; Other Eukaryotes - 139 (source: NCBI BLink). | chr1:28769157-28771036 REVERSE LENGTH=431	374	431	1.00E-142	115.2	80.2	84.5
Rsa1.0_00167.1.g7359.t1	dbj|BAJ33636.1| unnamed protein product [Thellungiella halophila]	372	374	0	100.5	92.2	96.2	unnamed protein product	----	----	AT1G76680.1 | Symbols: OPR1, ATOPR1 | 12-oxophytodienoate reductase 1 | chr1:28776982-28778271 FORWARD LENGTH=372	372	372	0	100.0	89.5	94.6
Rsa1.0_00167.1.g7360.t1	gb|EOA35314.1| hypothetical protein CARUB_v10020489mg [Capsella rubella]	375	374	0	99.7	90.7	95.7	hypothetical protein CARUB_v10020489mg	gbpln	Capsella rubella	AT1G76680.1 | Symbols: OPR1, ATOPR1 | 12-oxophytodienoate reductase 1 | chr1:28776982-28778271 FORWARD LENGTH=372	375	372	0	99.2	87.7	93.3
Rsa1.0_00167.1.g7361.t1	gb|EOA27962.1| hypothetical protein CARUB_v10024133mg [Capsella rubella]	229	185	5.00E-28	80.8	31.0	33.6	hypothetical protein CARUB_v10024133mg	gbpln	Capsella rubella	AT2G24020.1 | Symbols: | Uncharacterised BCR, YbaB family COG0718 | chr2:10217869-10219269 REVERSE LENGTH=182	229	182	4.00E-30	79.5	31.4	34.5
Rsa1.0_00167.1.g7362.t1	ref|NP_177801.1| uncharacterized protein [Arabidopsis thaliana] gi|75207334|sp|Q9SRD8.1|EC11_ARATH RecName: Full=Egg cell-secreted protein 1.1; Flags: Precursor gi|6143892|gb|AAF04438.1|AC010718_7 hypothetical protein; 47879-48355 [Arabidopsis thaliana] gi|52354237|gb|AAU44439.1| hypothetical protein AT1G76750 [Arabidopsis thaliana] gi|55740537|gb|AAV63861.1| hypothetical protein At1g76750 [Arabidopsis thaliana] gi|332197764|gb|AEE35885.1| uncharacterized protein AT1G76750 [Arabidopsis thaliana]	155	158	4.00E-61	101.9	74.8	86.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G76750.1 | Symbols: | Protein of unknown function (DUF1278) | chr1:28811107-28811583 FORWARD LENGTH=158	155	158	1.00E-63	101.9	74.8	86.5
Rsa1.0_00167.1.g7363.t3	ref|NP_177804.1| HSP20-like chaperone [Arabidopsis thaliana] gi|6143906|gb|AAF04452.1|AC010718_21 putative heat shock protein; 53413-59028 [Arabidopsis thaliana] gi|332197767|gb|AEE35888.1| HSP20-like chaperone [Arabidopsis thaliana]	5055	1871	2.00E-66	37.0	4.1	5.1	HSP20-like chaperone	gbpln	Arabidopsis thaliana	AT1G76780.1 | Symbols: | HSP20-like chaperones superfamily protein | chr1:28816641-28822256 FORWARD LENGTH=1871	5055	1871	5.00E-69	37.0	4.1	5.1
Rsa1.0_00167.1.g7364.t1	ref|NP_177806.1| vacuolar iron transporter-like protein [Arabidopsis thaliana] gi|75207331|sp|Q9SRD3.1|VITH2_ARATH RecName: Full=Vacuolar iron transporter homolog 2; AltName: Full=Protein NODULIN-LIKE 2 gi|6143895|gb|AAF04441.1|AC010718_10 nodulin-like protein; 66117-66707 [Arabidopsis thaliana] gi|48958481|gb|AAT47793.1| At1g76800 [Arabidopsis thaliana] gi|51972058|gb|AAU15133.1| At1g76800 [Arabidopsis thaliana] gi|332197769|gb|AEE35890.1| vacuolar iron transporter homolog 2 [Arabidopsis thaliana]	194	196	7.00E-87	101.0	91.2	96.9	vacuolar iron transporter-like protein	gbpln	Arabidopsis thaliana	AT1G76800.1 | Symbols: | Vacuolar iron transporter (VIT) family protein | chr1:28829345-28829935 FORWARD LENGTH=196	194	196	3.00E-89	101.0	91.2	96.9
Rsa1.0_00167.1.g7365.t1	gb|EOA33550.1| hypothetical protein CARUB_v10019670mg [Capsella rubella]	225	1301	5.00E-70	578.2	53.8	58.7	hypothetical protein CARUB_v10019670mg	gbpln	Capsella rubella	AT1G76810.1 | Symbols: | eukaryotic translation initiation factor 2 (eIF-2) family protein | chr1:28831366-28836310 REVERSE LENGTH=1294	225	1294	8.00E-72	575.1	52.9	58.7
Rsa1.0_00167.1.g7366.t3	gb|EOA33550.1| hypothetical protein CARUB_v10019670mg [Capsella rubella]	1258	1301	0	103.4	76.6	83.8	hypothetical protein CARUB_v10019670mg	gbpln	Capsella rubella	AT1G76810.1 | Symbols: | eukaryotic translation initiation factor 2 (eIF-2) family protein | chr1:28831366-28836310 REVERSE LENGTH=1294	1258	1294	0	102.9	77.1	82.9
Rsa1.0_00167.1.g7367.t1	ref|XP_002889106.1| hypothetical protein ARALYDRAFT_895567 [Arabidopsis lyrata subsp. lyrata] gi|297334947|gb|EFH65365.1| hypothetical protein ARALYDRAFT_895567 [Arabidopsis lyrata subsp. lyrata]	97	98	1.00E-44	101.0	94.8	95.9	hypothetical protein ARALYDRAFT_895567	gbpln	Arabidopsis lyrata	AT1G76860.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:28854594-28855637 REVERSE LENGTH=98	97	98	5.00E-47	101.0	93.8	95.9

Rsa1.0_00167.1.g7368.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00167.1.g7369.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00167.1.g7370.t1	ref|XP_002887660.1| hypothetical protein ARALYDRAFT_895569 [Arabidopsis lyrata subsp. lyrata] gi|297333501|gb|EFH63919.1| hypothetical protein ARALYDRAFT_895569 [Arabidopsis lyrata subsp. lyrata]	590	598	0	101.4	65.6	71.5	hypothetical protein ARALYDRAFT_895569	gbpln	Arabidopsis lyrata	AT1G76880.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr1:28865594-28867931 FORWARD LENGTH=603	590	603	0	102.2	64.9	71.5
Rsa1.0_00167.1.g7371.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00167.1.g7372.t1	emb|CAA05997.1| GT2 [Arabidopsis thaliana]	465	575	0	123.7	81.1	87.3	GT2	gbpln	Arabidopsis thaliana	AT1G76890.2 | Symbols: GT2, AT-GT2 | Duplicated homeodomain-like superfamily protein | chr1:28873211-28875203 REVERSE LENGTH=575	465	575	0	123.7	81.1	87.3
Rsa1.0_00168.1.g7373.t1	ref|XP_002871370.1| hypothetical protein ARALYDRAFT_325494 [Arabidopsis lyrata subsp. lyrata] gi|297317207|gb|EFH47629.1| hypothetical protein ARALYDRAFT_325494 [Arabidopsis lyrata subsp. lyrata]	601	621	0	103.3	88.5	95.0	hypothetical protein ARALYDRAFT_325494	gbpln	Arabidopsis lyrata	AT5G09420.1 | Symbols: ATTOC64-V, MTOM64, TOC64-V, OM64, AtmtOM64 | translocon at the outer membrane of chloroplasts 64-V | chr5:2928316-2931750 FORWARD LENGTH=603	601	603	0	100.3	86.2	94.0
Rsa1.0_00168.1.g7374.t1	ref|NP_196505.2| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|67633792|gb|AAY78820.1| hydrolase [Arabidopsis thaliana] gi|332004009|gb|AED91392.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana]	312	311	1.00E-171	99.7	92.9	97.4	alpha/beta-hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G09430.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:2932162-2933362 FORWARD LENGTH=311	312	311	1.00E-173	99.7	92.9	97.4
Rsa1.0_00168.1.g7375.t1	ref|XP_002871372.1| hypothetical protein ARALYDRAFT_487757 [Arabidopsis lyrata subsp. lyrata] gi|297317209|gb|EFH47631.1| hypothetical protein ARALYDRAFT_487757 [Arabidopsis lyrata subsp. lyrata]	298	281	1.00E-135	94.3	81.5	88.3	hypothetical protein ARALYDRAFT_487757	gbpln	Arabidopsis lyrata	AT5G64260.1 | Symbols: EXL2 | EXORDIUM like 2 | chr5:25703980-25704897 FORWARD LENGTH=305	298	305	1.00E-136	102.3	79.5	86.9
Rsa1.0_00168.1.g7376.t1	gb|EOA23045.1| hypothetical protein CARUB_v10003815mg [Capsella rubella]	407	331	1.00E-112	81.3	59.7	64.1	hypothetical protein CARUB_v10003815mg	gbpln	Capsella rubella	AT5G09460.1 | Symbols: | sequence-specific DNA binding transcription factors;transcription regulators | chr5:2944437-2945417 REVERSE LENGTH=326	407	326	1.00E-107	80.1	59.0	63.4
Rsa1.0_00168.1.g7377.t1	gb|EOA22044.1| hypothetical protein CARUB_v10002569mg [Capsella rubella]	149	139	3.00E-23	93.3	68.5	78.5	hypothetical protein CARUB_v10002569mg	gbpln	Capsella rubella	AT5G09480.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:2951181-2951615 REVERSE LENGTH=144	149	144	4.00E-19	96.6	52.3	57.0
Rsa1.0_00168.1.g7378.t1	gb|EOA21204.1| hypothetical protein CARUB_v10001551mg [Capsella rubella]	259	306	5.00E-73	118.1	72.2	83.4	hypothetical protein CARUB_v10001551mg	gbpln	Capsella rubella	AT5G09530.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:2960080-2961192 REVERSE LENGTH=370	259	370	2.00E-65	142.9	71.0	81.5
Rsa1.0_00168.1.g7379.t1	ref|XP_002873410.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319247|gb|EFH49669.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	284	286	6.00E-99	100.7	69.0	77.5	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT5G09540.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:2962422-2963264 REVERSE LENGTH=280	284	280	2.00E-97	98.6	66.5	75.7
Rsa1.0_00168.1.g7380.t1	gb|EOA22581.1| hypothetical protein CARUB_v10003247mg [Capsella rubella]	445	445	0	100.0	96.9	98.4	hypothetical protein CARUB_v10003247mg	gbpln	Capsella rubella	AT5G09550.1 | Symbols: | GDP dissociation inhibitor family protein / Rab GTPase activator family protein | chr5:2963850-2966465 FORWARD LENGTH=445	445	445	0	100.0	96.9	98.7
Rsa1.0_00168.1.g7381.t1	ref|NP_196519.1| Cox19-like CHCH family protein [Arabidopsis thaliana] gi|7671432|emb|CAB89373.1| putative protein [Arabidopsis thaliana] gi|26452406|dbj|BAC43288.1| unknown protein [Arabidopsis thaliana] gi|28372814|gb|AAO39889.1| At5g09570 [Arabidopsis thaliana] gi|332004028|gb|AED91411.1| Cox19-like CHCH family protein [Arabidopsis thaliana]	151	139	3.00E-47	92.1	64.2	77.5	Cox19-like CHCH family protein	gbpln	Arabidopsis thaliana	AT5G09570.1 | Symbols: | Cox19-like CHCH family protein | chr5:2970733-2971970 FORWARD LENGTH=139	151	139	1.00E-49	92.1	64.2	77.5
Rsa1.0_00168.1.g7382.t1	ref|XP_002871380.1| succinate dehydrogenase 3-1 [Arabidopsis lyrata subsp. lyrata] gi|297317217|gb|EFH47639.1| succinate dehydrogenase 3-1 [Arabidopsis lyrata subsp. lyrata]	211	213	6.00E-83	100.9	77.3	84.4	succinate dehydrogenase 3-1	gbpln	Arabidopsis lyrata	AT5G09600.3 | Symbols: SDH3-1 | succinate dehydrogenase 3-1 | chr5:2979220-2980527 FORWARD LENGTH=213	211	213	7.00E-83	100.9	75.8	83.9

<table>
<tr><td>Rsa1.0_00168.1.g7383.t1</td><td>ref|XP_002873411.1| hypothetical protein ARALYDRAFT_487778 [Arabidopsis lyrata subsp. lyrata] gi|297319248|gb|EFH49670.1| hypothetical protein ARALYDRAFT_487778 [Arabidopsis lyrata subsp. lyrata]</td><td>485</td><td>514</td><td>1.00E-166</td><td>106.0</td><td>75.1</td><td>80.0</td><td>hypothetical protein ARALYDRAFT_487778</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G09620.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr5:2983757-2985352 REVERSE LENGTH=531</td><td>485</td><td>531</td><td>1.00E-163</td><td>109.5</td><td>75.3</td><td>81.9</td></tr>
<tr><td>Rsa1.0_00168.1.g7384.t2</td><td>emb|CAM91988.1| sinapoylglucose:choline sinapoyltransferase [Brassica oleracea var. medullosa] gi|146189650|emb|CAM91990.1| sinapoylglucose:choline sinapoyltransferase [Brassica napus var. napus]</td><td>418</td><td>466</td><td>0</td><td>111.5</td><td>80.4</td><td>84.7</td><td>sinapoylglucose:choline sinapoyltransferase</td><td>gbpln</td><td>Brassica napus</td><td>AT5G09640.1 | Symbols: SNG2, SCPL19 | serine carboxypeptidase-like 19 | chr5:2988373-2990966 FORWARD LENGTH=465</td><td>418</td><td>465</td><td>0</td><td>111.2</td><td>78.7</td><td>85.9</td></tr>
<tr><td>Rsa1.0_00168.1.g7385.t1</td><td>ref|XP_002873413.1| inorganic pyrophosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319250|gb|EFH49672.1| inorganic pyrophosphatase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>299</td><td>299</td><td>1.00E-148</td><td>100.0</td><td>89.3</td><td>93.6</td><td>inorganic pyrophosphatase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G09650.1 | Symbols: AtPPa6, PPa6 | pyrophosphorylase 6 | chr5:2991331-2993117 REVERSE LENGTH=300</td><td>299</td><td>300</td><td>1.00E-151</td><td>100.3</td><td>90.3</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00168.1.g7386.t1</td><td>gb|EOA30902.1| hypothetical protein CARUB_v10014049mg [Capsella rubella]</td><td>359</td><td>358</td><td>0</td><td>99.7</td><td>92.5</td><td>96.9</td><td>hypothetical protein CARUB_v10014049mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G09660.1 | Symbols: PMDH2 | peroxisomal NAD-malate dehydrogenase 2 | chr5:2993645-2995551 REVERSE LENGTH=354</td><td>359</td><td>354</td><td>0</td><td>98.6</td><td>93.3</td><td>96.4</td></tr>
<tr><td>Rsa1.0_00168.1.g7387.t1</td><td>ref|NP_196535.1| beta-xylosidase 3 [Arabidopsis thaliana] gi|75264323|sp|Q9LXD6.1|BXL3_ARATH RecName: Full=Beta-D-xylosidase 3; Short=AtBXL3; AltName: Full=Alpha-L-arabinofuranosidase; Flags: Precursor gi|7671416|emb|CAB89357.1| beta-xylosidase-like protein [Arabidopsis thaliana] gi|9759004|dbj|BAB09531.1| beta-xylosidase [Arabidopsis thaliana] gi|15450735|gb|AAK96639.1| AT5g09730/F17I14_80 [Arabidopsis thaliana] gi|332004056|gb|AED91439.1| beta-xylosidase 3 [Arabidopsis thaliana]</td><td>970</td><td>773</td><td>0</td><td>79.7</td><td>63.9</td><td>70.4</td><td>beta-xylosidase 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G09730.1 | Symbols: BXL3, ATBXL3, XYL3, ATBX3, BX3 | beta-xylosidase 3 | chr5:3015319-3018226 REVERSE LENGTH=773</td><td>970</td><td>773</td><td>0</td><td>79.7</td><td>63.9</td><td>70.4</td></tr>
<tr><td>Rsa1.0_00168.1.g7388.t1</td><td>ref|XP_002873419.1| hypothetical protein ARALYDRAFT_487793 [Arabidopsis lyrata subsp. lyrata] gi|297319256|gb|EFH49678.1| hypothetical protein ARALYDRAFT_487793 [Arabidopsis lyrata subsp. lyrata]</td><td>445</td><td>441</td><td>0</td><td>99.1</td><td>93.0</td><td>94.4</td><td>hypothetical protein ARALYDRAFT_487793</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G09740.1 | Symbols: HAM2 | histone acetyltransferase of the MYST family 2 | chr5:3022141-3024711 REVERSE LENGTH=445</td><td>445</td><td>445</td><td>0</td><td>100.0</td><td>92.8</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00168.1.g7389.t1</td><td>ref|NP_196537.1| transcription factor HEC3 [Arabidopsis thaliana] gi|75311668|sp|Q9LXD8.1|HEC3_ARATH RecName: Full=Transcription factor HEC3; AltName: Full=Basic helix-loop-helix protein 43; Short=AtbHLH43; Short=bHLH 43; AltName: Full=Protein HECATE 3; AltName: Full=Transcription factor EN 119; AltName: Full=bHLH transcription factor bHLH043 gi|7671414|emb|CAB89355.1| putative protein [Arabidopsis thaliana] gi|9759006|dbj|BAB09533.1| unnamed protein product [Arabidopsis thaliana] gi|332004059|gb|AED91442.1| transcription factor HEC3 [Arabidopsis thaliana]</td><td>221</td><td>224</td><td>3.00E-58</td><td>101.4</td><td>73.3</td><td>81.0</td><td>transcription factor HEC3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G09750.1 | Symbols: HEC3 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:3026401-3027075 REVERSE LENGTH=224</td><td>221</td><td>224</td><td>1.00E-60</td><td>101.4</td><td>73.3</td><td>81.0</td></tr>
</table>

Rsa1.0_00168.1.g7390.t1	ref|NP_196538.1| Putative pectinesterase/pectinesterase inhibitor 51 [Arabidopsis thaliana] gi|75180831|sp|Q9LXD9.1|PME51_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 51; Includes: RecName: Full=Pectinesterase inhibitor 51; AltName: Full=Pectin methylesterase inhibitor 51; Includes: RecName: Full=Pectinesterase 51; Short=PE 51; AltName: Full=Pectin methylesterase 51; Short=AtPME51; Flags: Precursor gi|7671413|emb|CAB89354.1| pectin methylesterase-like protein [Arabidopsis thaliana] gi|17979183|gb|AAL49830.1| putative pectin methylesterase [Arabidopsis thaliana] gi|29824167|gb|AAP04044.1| putative pectin methylesterase [Arabidopsis thaliana] gi|332004060|gb|AED91443.1| Putative pectinesterase/pectinesterase inhibitor 51 [Arabidopsis thaliana]	536	551	0	102.8	81.5	87.9	Putative pectinesterase/pectinesterase inhibitor 51	gbpln	Arabidopsis thaliana	AT5G09760.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:3032446-3034364 FORWARD LENGTH=551	536	551	0	102.8	81.5	87.9
Rsa1.0_00168.1.g7391.t1	gb|EOA20839.1| hypothetical protein CARUB_v10001176mg [Capsella rubella]	388	380	0	97.9	83.2	90.7	hypothetical protein CARUB_v10001176mg	gbpln	Capsella rubella	AT5G09790.2 | Symbols: ATXR5, SDG15 | ARABIDOPSIS TRITHORAX-RELATED PROTEIN 5 | chr5:3039204-3040970 REVERSE LENGTH=379	388	379	0	97.7	83.2	89.9
Rsa1.0_00168.1.g7392.t1	ref|XP_002871385.1| hypothetical protein ARALYDRAFT_908929 [Arabidopsis lyrata subsp. lyrata] gi|297317222|gb|EFH47644.1| hypothetical protein ARALYDRAFT_908929 [Arabidopsis lyrata subsp. lyrata]	102	103	2.00E-31	101.0	77.5	86.3	hypothetical protein ARALYDRAFT_908929	gbpln	Arabidopsis lyrata	AT5G09805.1 | Symbols: IDL3 | inflorescence deficient in abscission (IDA)-like 3 | chr5:3047218-3047517 FORWARD LENGTH=99	102	99	4.00E-33	97.1	74.5	82.4
Rsa1.0_00168.1.g7393.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00168.1.g7394.t1	gb|AEN25580.1| actin 7 [Brassica rapa subsp. pekinensis]	375	377	0	100.5	98.1	99.2	actin 7	gbpln	Brassica rapa	AT5G09810.1 | Symbols: ACT7 | actin 7 | chr5:3052809-3054220 FORWARD LENGTH=377	375	377	0	100.5	97.6	98.9
Rsa1.0_00168.1.g7395.t1	ref|NP_568217.1| BolA-like family protein [Arabidopsis thaliana] gi|9758961|dbj|BAB09404.1| unnamed protein product [Arabidopsis thaliana] gi|21593245|gb|AAM65194.1| unknown [Arabidopsis thaliana] gi|27808606|gb|AAO24583.1| At5g09830 [Arabidopsis thaliana] gi|110736310|dbj|BAF00125.1| hypothetical protein [Arabidopsis thaliana] gi|332004070|gb|AED91453.1| BolA-like family protein [Arabidopsis thaliana]	94	93	5.00E-41	98.9	93.6	95.7	BolA-like family protein	gbpln	Arabidopsis thaliana	AT5G09830.1 | Symbols: | BolA-like family protein | chr5:3057816-3058769 REVERSE LENGTH=93	94	93	8.00E-44	98.9	93.6	95.7
Rsa1.0_00168.1.g7396.t1	ref|NP_196546.1| Putative endonuclease or glycosyl hydrolase [Arabidopsis thaliana] gi|9758962|dbj|BAB09405.1| unnamed protein product [Arabidopsis thaliana] gi|332004071|gb|AED91454.1| Putative endonuclease or glycosyl hydrolase [Arabidopsis thaliana]	883	924	0	104.6	66.7	79.4	Putative endonuclease or glycosyl hydrolase	gbpln	Arabidopsis thaliana	AT5G09840.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr5:3059027-3061970 FORWARD LENGTH=924	883	924	0	104.6	66.7	79.4
Rsa1.0_00168.1.g7397.t1	ref|NP_568218.1| Transcription elongation factor (TFIIS) family protein [Arabidopsis thaliana] gi|395406779|sp|F4KFC7.1|MD26C_ARATH RecName: Full=Probable mediator of RNA polymerase II transcription subunit 26c gi|332004072|gb|AED91455.1| Transcription elongation factor (TFIIS) family protein [Arabidopsis thaliana]	518	353	1.00E-147	68.1	53.7	59.3	Transcription elongation factor (TFIIS) family protein	gbpln	Arabidopsis thaliana	AT5G09850.1 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr5:3063488-3065221 REVERSE LENGTH=353	518	353	1.00E-150	68.1	53.7	59.3
Rsa1.0_00168.1.g7398.t1	gb|EOA18933.1| hypothetical protein CARUB_v10007564mg [Capsella rubella]	461	424	1.00E-134	92.0	57.9	69.8	hypothetical protein CARUB_v10007564mg	gbpln	Capsella rubella	AT1G05080.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:1459091-1460579 FORWARD LENGTH=439	461	439	1.00E-121	95.2	53.8	69.0
Rsa1.0_00168.1.g7399.t1	gb|AAG50751.1|AC079733_19 polyprotein, putative [Arabidopsis thaliana]	1436	1468	0	102.2	50.0	68.2	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1436	1262	1.00E-132	87.9	16.2	24.3

Rsa1.0_00168.1.g7400.t1	ref|XP_002871390.1| hypothetical protein ARALYDRAFT_908937 [Arabidopsis lyrata subsp. lyrata] gi|297317227|gb|EFH47649.1| hypothetical protein ARALYDRAFT_908937 [Arabidopsis lyrata subsp. lyrata]	89	103	2.00E−17	115.7	69.7	82.0	hypothetical protein ARALYDRAFT_908937	gbpln	Arabidopsis lyrata	AT5G09876.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 5 Blast hits to 5 proteins in 2 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 5; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr5:3079987−3080304 FORWARD LENGTH=105	89	105	2.00E−19	118.0	64.0	79.8
Rsa1.0_00168.1.g7401.t1	ref|XP_002873428.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319265|gb|EFH49687.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	504	520	0	103.2	81.5	88.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G09880.1 | Symbols: | Splicing factor, CC1−like | chr5:3081646−3085179 REVERSE LENGTH=527	504	527	0	104.6	80.6	88.7
Rsa1.0_00168.1.g7402.t1	gb|EOA19397.1| hypothetical protein CARUB_v10000967mg [Capsella rubella]	336	442	0	131.5	97.9	98.8	hypothetical protein CARUB_v10000967mg	gbpln	Capsella rubella	AT5G09900.2 | Symbols: EMB2107, RPN5A, MSA | 26S proteasome regulatory subunit, putative (RPN5) | chr5:3089462−3092434 REVERSE LENGTH=442	336	442	0	131.5	96.4	99.1
Rsa1.0_00169.1.g7403.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00169.1.g7404.t1	dbj|BAB08714.1| non−LTR retroelement reverse transcriptase−like protein [Arabidopsis thaliana]	1109	1197	4.00E−71	107.9	11.3	16.2	non−LTR retroelement reverse transcriptase−like protein	gbpln	Arabidopsis thaliana	AT2G06845.1 | Symbols: | Beta−galactosidase related protein | chr2:2754666−2756008 FORWARD LENGTH=315	1109	315	7.00E−23	28.4	6.2	8.2
Rsa1.0_00169.1.g7405.t1	ref|XP_002883483.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329323|gb|EFH59742.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	335	335	1.00E−162	100.0	79.7	89.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G24130.1 | Symbols: | Pectin lyase−like superfamily protein | chr3:8711663−8713361 REVERSE LENGTH=335	335	335	1.00E−163	100.0	78.8	88.7
Rsa1.0_00169.1.g7406.t1	ref|XP_002883481.1| hypothetical protein ARALYDRAFT_898955 [Arabidopsis lyrata subsp. lyrata] gi|297329321|gb|EFH59740.1| hypothetical protein ARALYDRAFT_898955 [Arabidopsis lyrata subsp. lyrata]	401	400	0	99.8	88.3	92.8	hypothetical protein ARALYDRAFT_898955	gbpln	Arabidopsis lyrata	AT3G24140.1 | Symbols: FMA | basic helix−loop−helix (bHLH) DNA−binding superfamily protein | chr3:8715525−8717772 REVERSE LENGTH=414	401	414	0	103.2	85.0	91.0
Rsa1.0_00169.1.g7407.t1	ref|XP_002883480.1| hypothetical protein ARALYDRAFT_479917 [Arabidopsis lyrata subsp. lyrata] gi|297329320|gb|EFH59739.1| hypothetical protein ARALYDRAFT_479917 [Arabidopsis lyrata subsp. lyrata]	323	347	1.00E−138	107.4	82.0	89.5	hypothetical protein ARALYDRAFT_479917	gbpln	Arabidopsis lyrata	AT3G24150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32295.1); Has 50 Blast hits to 50 proteins in 12 species: Archae − 0; Bacteria − 0; Metazoa − 7; Fungi − 0; Plants − 41; Viruses − 0; Other Eukaryotes − 2 (source: NCBI BLink). | chr3:8724273−8725586 REVERSE LENGTH=343	323	343	1.00E−135	106.2	79.9	87.3
Rsa1.0_00169.1.g7408.t3	ref|NP_189058.1| putative type 1 membrane protein [Arabidopsis thaliana] gi|4206765|gb|AAD11797.1| putative type 1 membrane protein [Arabidopsis thaliana] gi|11994235|dbj|BAB01357.1| unnamed protein product [Arabidopsis thaliana] gi|15450743|gb|AAK96643.1| AT3g24160/MUJ8_16 [Arabidopsis thaliana] gi|21537239|gb|AAM61580.1| type 1 membrane protein, putative [Arabidopsis thaliana] gi|22137144|gb|AAM91417.1| AT3g24160/MUJ8_16 [Arabidopsis thaliana] gi|332643343|gb|AEE76864.1| putative type 1 membrane protein [Arabidopsis thaliana]	382	364	1.00E−150	95.3	76.4	85.9	putative type 1 membrane protein	gbpln	Arabidopsis thaliana	AT3G24160.1 | Symbols: PMP | putative type 1 membrane protein | chr3:8726241−8729023 FORWARD LENGTH=364	382	364	1.00E−153	95.3	76.4	85.9
Rsa1.0_00169.1.g7409.t1	ref|XP_002883472.1| hypothetical protein ARALYDRAFT_898937 [Arabidopsis lyrata subsp. lyrata] gi|297329312|gb|EFH59731.1| hypothetical protein ARALYDRAFT_898937 [Arabidopsis lyrata subsp. lyrata]	345	295	5.00E−41	85.5	33.9	50.1	hypothetical protein ARALYDRAFT_898937	gbpln	Arabidopsis lyrata	AT3G24260.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Histone deacetylase interacting (InterPro:IPR013194); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G28870.1); Has 220 Blast hits to 218 proteins in 65 species: Archae − 7; Bacteria − 6; Metazoa − 43; Fungi − 2; Plants − 115; Viruses − 0; Other Eukaryotes − 47 (source: NCBI BLink). | chr3:8793837−8794961 REVERSE LENGTH=374	345	374	2.00E−32	108.4	28.7	42.0
Rsa1.0_00169.1.g7410.t1	gb|EOA30105.1| hypothetical protein CARUB_v10013216mg [Capsella rubella]	659	626	0	95.0	75.0	81.0	hypothetical protein CARUB_v10013216mg	gbpln	Capsella rubella	AT3G24210.1 | Symbols: | Ankyrin repeat family protein | chr3:8753712−8755627 REVERSE LENGTH=607	659	607	0	92.1	73.9	80.1

<table>
<tr><td>Rsa1.0_00169.1.g7411.t1</td><td>gb|EOA33758.1| hypothetical protein CARUB_v10019951mg [Capsella rubella]</td><td>188</td><td>634</td><td>1.00E-22</td><td>337.2</td><td>32.4</td><td>38.8</td><td>hypothetical protein CARUB_v10019951mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G63080.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:23388884-23390728 REVERSE LENGTH=614</td><td>188</td><td>614</td><td>4.00E-23</td><td>326.6</td><td>27.7</td><td>34.6</td></tr>
<tr><td>Rsa1.0_00169.1.g7412.t1</td><td>gb|AAM98191.1| unknown protein [Arabidopsis thaliana] gi|38603804|gb|AAR24647.1| At2g23330 [Arabidopsis thaliana] gi|110742535|dbj|BAE99183.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>256</td><td>776</td><td>1.00E-58</td><td>303.1</td><td>42.2</td><td>55.5</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>256</td><td>1262</td><td>3.00E-40</td><td>493.0</td><td>32.0</td><td>50.0</td></tr>
<tr><td>Rsa1.0_00169.1.g7413.t1</td><td>gb|AAL57176.1|AF343656_1 CLV3/ESR-related 19 [Brassica napus] gi|18033507|gb|AAL57178.1|AF343658_1 CLV3/ESR-related 19 [Brassica napus]</td><td>74</td><td>74</td><td>7.00E-23</td><td>100.0</td><td>75.7</td><td>83.8</td><td>CLV3/ESR-related 19</td><td>gbpln</td><td>Brassica napus</td><td>AT3G24225.1 | Symbols: CLE19, ESR19, ATCLE19 | CLAVATA3/ESR-RELATED 19 | chr3:8768948-8769172 FORWARD LENGTH=74</td><td>74</td><td>74</td><td>1.00E-23</td><td>100.0</td><td>73.0</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00169.1.g7414.t1</td><td>ref|XP_002883472.1| hypothetical protein ARALYDRAFT_898937 [Arabidopsis lyrata subsp. lyrata] gi|297329312|gb|EFH59731.1| hypothetical protein ARALYDRAFT_898937 [Arabidopsis lyrata subsp. lyrata]</td><td>404</td><td>295</td><td>4.00E-43</td><td>73.0</td><td>27.5</td><td>36.6</td><td>hypothetical protein ARALYDRAFT_898937</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G24260.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Histone deacetylase interacting (InterPro:IPR013194); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G28870.1); Has 220 Blast hits to 218 proteins in 65 species: Archae - 7; Bacteria - 6; Metazoa - 43; Fungi - 2; Plants - 115; Viruses - 0; Other Eukaryotes - 47 (source: NCBI BLink). | chr3:8793837-8794961 REVERSE LENGTH=374</td><td>404</td><td>374</td><td>2.00E-36</td><td>92.6</td><td>23.5</td><td>31.4</td></tr>
<tr><td>Rsa1.0_00169.1.g7415.t1</td><td>dbj|BAB03007.1| unnamed protein product [Arabidopsis thaliana]</td><td>862</td><td>1006</td><td>0</td><td>116.7</td><td>79.1</td><td>87.6</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G23900.3 | Symbols: | RNA recognition motif (RRM)-containing protein | chr3:8631941-8635852 REVERSE LENGTH=987</td><td>862</td><td>987</td><td>0</td><td>114.5</td><td>79.1</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00169.1.g7416.t1</td><td>gb|AAM65391.1| fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana]</td><td>423</td><td>420</td><td>1.00E-174</td><td>99.3</td><td>72.1</td><td>82.7</td><td>fatty acid elongase-like protein (cer2-like)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G23840.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:8611177-8612559 FORWARD LENGTH=420</td><td>423</td><td>420</td><td>1.00E-175</td><td>99.3</td><td>71.6</td><td>82.0</td></tr>
<tr><td>Rsa1.0_00169.1.g7417.t1</td><td>ref|NP_189024.1| UDP-D-glucuronate 4-epimerase 6 [Arabidopsis thaliana] gi|75311206|sp|Q9LIS3.1|GAE6_ARATH RecName: Full=UDP-glucuronate 4-epimerase 6; AltName: Full=UDP-glucuronic acid epimerase 6; Short=AtUGlcAE2 gi|13877895|gb|AAK44025.1|AF370210_1 putative NAD dependent epimerase [Arabidopsis thaliana] gi|9294651|dbj|BAB03000.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|15810205|gb|AAL07003.1| AT3g23820/F14O13_1 [Arabidopsis thaliana] gi|17065098|gb|AAL32703.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|22136952|gb|AAM91705.1| putative NAD dependent epimerase [Arabidopsis thaliana] gi|59668636|emb|CAI53858.1| UDP-D-glucuronate 4-epimerase [Arabidopsis thaliana] gi|332643297|gb|AEE76818.1| UDP-D-glucuronate 4-epimerase 6 [Arabidopsis thaliana] gi|385137880|gb|AFI41201.1| UDP-D-glucuronate 4-epimerase 6, partial [Arabidopsis thaliana]</td><td>458</td><td>460</td><td>0</td><td>100.4</td><td>93.7</td><td>96.7</td><td>UDP-D-glucuronate 4-epimerase 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G23820.1 | Symbols: GAE6 | UDP-D-glucuronate 4-epimerase 6 | chr3:8603645-8605027 FORWARD LENGTH=460</td><td>458</td><td>460</td><td>0</td><td>100.4</td><td>93.7</td><td>96.7</td></tr>
<tr><td>Rsa1.0_00169.1.g7418.t1</td><td>dbj|BAA97166.1| 40S ribosomal protein S19 [Arabidopsis thaliana]</td><td>209</td><td>244</td><td>3.00E-96</td><td>116.7</td><td>83.3</td><td>89.0</td><td>40S ribosomal protein S19</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G47320.1 | Symbols: RPS19 | ribosomal protein S19 | chr5:19203801-19204951 FORWARD LENGTH=212</td><td>209</td><td>212</td><td>1.00E-98</td><td>101.4</td><td>83.3</td><td>89.0</td></tr>
</table>

Rsa1.0_00169.1.g7419.t1	ref|NP_189023.1| adenosylhomocysteinase 2 [Arabidopsis thaliana] gi|61216850|sp|Q9LK36.1|SAHH2_ARATH RecName: Full=Adenosylhomocysteinase 2; Short=AdoHcyase 2; AltName: Full=S-adenosyl-L-homocysteine hydrolase 1; AltName: Full=SAH hydrolase 2 gi|9293955|dbj|BAB01858.1| S-adenosyl L-homocystein hydrolase [Arabidopsis thaliana] gi|16649037|gb|AAL24370.1| S-adenosyl L-homocystein hydrolase [Arabidopsis thaliana] gi|20260074|gb|AAM13384.1| S-adenosyl L-homocystein hydrolase [Arabidopsis thaliana] gi|23297630|gb|AAN12996.1| putative S-adenosyl-L-homocysteinase [Arabidopsis thaliana] gi|332643296|gb|AEE76817.1| adenosylhomocysteinase 2 [Arabidopsis thaliana]		485	485	0	100.0	98.6	98.8	adenosylhomocysteinase 2	gbpln	Arabidopsis thaliana	AT3G23810.1 | Symbols: SAHH2, ATSAHH2 | S-adenosyl-l-homocysteine (SAH) hydrolase 2 | chr3:8588013-8589671 REVERSE LENGTH=485	485	485	0	100.0	98.6	98.8
Rsa1.0_00169.1.g7420.t1	ref|NP_566740.1| protein ralf-like 24 [Arabidopsis thaliana] gi|75273714|sp|Q9LK37.1|RLF24_ARATH RecName: Full=Protein RALF-like 24; Flags: Precursor gi|9293954|dbj|BAB01857.1| unnamed protein product [Arabidopsis thaliana] gi|332643295|gb|AEE76816.1| protein ralf-like 24 [Arabidopsis thaliana]		113	118	8.00E-41	104.4	79.6	92.9	protein ralf-like 24	gbpln	Arabidopsis thaliana	AT3G23805.1 | Symbols: RALFL24 | ralf-like 24 | chr3:8586467-8586823 FORWARD LENGTH=118	113	118	1.00E-43	104.4	79.6	92.9
Rsa1.0_00169.1.g7421.t4	gb|ACP30604.1| disease resistance protein [Brassica rapa subsp. pekinensis]		132	1196	5.00E-38	906.1	56.8	62.1	disease resistance protein	gbpln	Brassica rapa	AT5G18370.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6085036-6088926 REVERSE LENGTH=1210	132	1210	6.00E-37	916.7	49.2	59.8
Rsa1.0_00169.1.g7422.t3	#	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00169.1.g7423.t1	gb|EOA32655.1| hypothetical protein CARUB_v10015952mg [Capsella rubella]		169	476	3.00E-91	281.7	92.3	97.0	hypothetical protein CARUB_v10015952mg	gbpln	Capsella rubella	AT3G23770.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr3:8565556-8567196 FORWARD LENGTH=476	169	476	6.00E-89	281.7	89.9	92.3
Rsa1.0_00169.1.g7424.t1	ref|XP_002864934.1| cyclin-dependent kinase C_2 [Arabidopsis lyrata subsp. lyrata] gi|297310769|gb|EFH41193.1| cyclin-dependent kinase C_2 [Arabidopsis lyrata subsp. lyrata]		503	514	0	102.2	86.5	92.2	cyclin-dependent kinase C_2	gbpln	Arabidopsis lyrata	AT5G64960.1 | Symbols: CDKC2, CDKC;2 | cyclin dependent kinase group C2 | chr5:25955497-25958427 FORWARD LENGTH=513	503	513	0	102.0	86.3	91.7
Rsa1.0_00169.1.g7425.t1	gb|EOA29782.1| hypothetical protein CARUB_v10012876mg [Capsella rubella]		1047	1051	0	100.4	85.6	90.8	hypothetical protein CARUB_v10012876mg	gbpln	Capsella rubella	AT3G23640.2 | Symbols: HGL1 | heteroglycan glucosidase 1 | chr3:8502355-8509358 FORWARD LENGTH=991	1047	991	0	94.7	82.5	87.9
Rsa1.0_00169.1.g7426.t1	ref|XP_002883444.1| hypothetical protein ARALYDRAFT_898886 [Arabidopsis lyrata subsp. lyrata] gi|297329284|gb|EFH59703.1| hypothetical protein ARALYDRAFT_898886 [Arabidopsis lyrata subsp. lyrata]		998	988	0	99.0	85.9	93.1	hypothetical protein ARALYDRAFT_898886	gbpln	Arabidopsis lyrata	AT3G23640.2 | Symbols: HGL1 | heteroglycan glucosidase 1 | chr3:8502355-8509358 FORWARD LENGTH=991	998	991	0	99.3	85.4	92.7
Rsa1.0_00169.1.g7427.t1	dbj|BAE43829.1| isopentenyltransferase [Brassica rapa subsp. pekinensis]		332	332	1.00E-172	100.0	93.1	95.5	isopentenyltransferase	gbpln	Brassica rapa	AT3G23630.1 | Symbols: ATIPT7, IPT7 | isopentenyltransferase 7 | chr3:8488878-8489867 FORWARD LENGTH=329	332	329	1.00E-169	99.1	86.7	92.5
Rsa1.0_00169.1.g7428.t1	gb|EOA31032.1| hypothetical protein CARUB_v10014181mg [Capsella rubella]		315	324	1.00E-154	102.9	84.8	91.1	hypothetical protein CARUB_v10014181mg	gbpln	Capsella rubella	AT3G23620.1 | Symbols: | Ribosomal RNA processing Brix domain protein | chr3:8480147-8481873 FORWARD LENGTH=314	315	314	2.33E-156	99.7	83.2	91.1
Rsa1.0_00169.1.g7429.t1	ref|XP_002875592.1| alcohol dehydrogenase [Arabidopsis lyrata subsp. lyrata] gi|297321430|gb|EFH51851.1| alcohol dehydrogenase [Arabidopsis lyrata subsp. lyrata]		447	272	1.00E-129	60.9	52.8	55.9	alcohol dehydrogenase	gbpln	Arabidopsis lyrata	AT3G42960.1 | Symbols: ATA1, ASD, TA1 | TAPETUM 1 | chr3:15018735-15019656 REVERSE LENGTH=272	447	272	1.00E-122	60.9	51.0	55.7
Rsa1.0_00170.1.g7430.t1	gb|AAM63020.1| unknown [Arabidopsis thaliana]		182	177	7.00E-54	97.3	71.4	83.5	unknown	gbpln	Arabidopsis thaliana	AT1G69760.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26920.1); Has 51 Blast hits to 51 proteins in 15 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 7; Plants - 29; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr1:26240094-26240627 REVERSE LENGTH=177	182	177	6.00E-55	97.3	70.3	83.0
Rsa1.0_00170.1.g7431.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]		1148	1223	0	106.5	26.9	34.9	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1148	746	1.00E-110	65.0	18.0	23.4

Rsa1.0_00170.1.g7432.t1	gb|AAG51175.1|AC079285_8 hypothetical protein [Arabidopsis thaliana]	98	135	4.00E-49	137.8	95.9	98.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G66590.1 | Symbols: ATCOX19-1, COX19-1 | cytochrome c oxidase 19-1 | chr1:24841191-24842157 FORWARD LENGTH=98	98	98	3.00E-51	100.0	95.9	98.0
Rsa1.0_00170.1.g7433.t1	ref|NP_564878.1| 60S ribosomal protein L10-3 [Arabidopsis thaliana] gi|297838747|ref|XP_002887255.1| 60S ribosomal protein L10 [Arabidopsis lyrata subsp. lyrata] gi|75249285|sp|Q93W22.1|RL103_ARATH RecName: Full=60S ribosomal protein L10-3 gi|14194141|gb|AAK56265.1|AF367276_1 At1g66580/T12I7_3 [Arabidopsis thaliana] gi|15777885|gb|AAL05903.1| At1g66580/T12I7_3 [Arabidopsis thaliana] gi|21593025|gb|AAM64974.1| 60S ribosomal protein L10, putative [Arabidopsis thaliana] gi|297333096|gb|EFH63514.1| 60S ribosomal protein L10 [Arabidopsis lyrata subsp. lyrata] gi|332196410|gb|AEE34531.1| 60S ribosomal protein L10-3 [Arabidopsis thaliana] gi|482569259|gb|EOA33447.1| hypothetical protein CARUB_v10020922mg [Capsella rubella]	221	221	1.00E-122	100.0	96.4	98.2	60S ribosomal protein L10-3	gbpln	Arabidopsis lyrata	AT1G66580.1 | Symbols: SAG24, RPL10C | senescence associated gene 24 | chr1:24839208-24840439 FORWARD LENGTH=221	221	221	1.00E-125	100.0	96.4	98.2
Rsa1.0_00170.1.g7434.t1	gb|AAK15323.1|AF332195_1 aminolevulinate dehydratase [Raphanus sativus]	426	426	0	100.0	99.1	99.3	aminolevulinate dehydratase	gbpln	Raphanus sativus	AT1G69740.2 | Symbols: HEMB1 | Aldolase superfamily protein | chr1:26232197-26234713 FORWARD LENGTH=430	426	430	0	100.9	93.4	96.7
Rsa1.0_00170.1.g7435.t2	gb|EMJ19697.1| hypothetical protein PRUPE_ppa012246mg [Prunus persica]	142	178	3.00E-63	125.4	82.4	90.8	hypothetical protein PRUPE_ppa012246mg	gbpln	Prunus persica	AT5G02960.1 | Symbols: | Ribosomal protein S12/S23 family protein | chr5:693280-694396 REVERSE LENGTH=142	142	142	3.00E-62	100.0	80.3	87.3
Rsa1.0_00170.1.g7436.t1	ref|XP_002887251.1| hypothetical protein ARALYDRAFT_476102 [Arabidopsis lyrata subsp. lyrata] gi|297333092|gb|EFH63510.1| hypothetical protein ARALYDRAFT_476102 [Arabidopsis lyrata subsp. lyrata]	189	184	4.00E-90	97.4	84.7	91.0	hypothetical protein ARALYDRAFT_476102	gbpln	Arabidopsis lyrata	AT1G69700.1 | Symbols: ATHVA22C, HVA22C | HVA22 homologue C | chr1:26220337-26221663 FORWARD LENGTH=184	189	184	1.00E-90	97.4	83.1	89.9
Rsa1.0_00170.1.g7437.t1	dbj|BAJ34416.1| unnamed protein product [Thellungiella halophila]	321	334	1.00E-126	104.0	89.4	92.2	unnamed protein product	----	----	AT1G69690.1 | Symbols: | TCP family transcription factor | chr1:26216449-26217426 FORWARD LENGTH=325	321	325	1.00E-112	101.2	81.9	87.5
Rsa1.0_00170.1.g7438.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00170.1.g7439.t1	gb|EOA30123.1| hypothetical protein CARUB_v10013233mg [Capsella rubella]	335	446	2.00E-15	133.1	11.3	13.1	hypothetical protein CARUB_v10013233mg	gbpln	Capsella rubella	AT3G02280.1 | Symbols: | Flavodoxin family protein | chr3:453646-457659 FORWARD LENGTH=623	335	623	3.00E-17	186.0	11.6	15.2
Rsa1.0_00170.1.g7440.t1	emb|CAB82966.1| putative protein [Arabidopsis thaliana]	707	705	0	99.7	77.2	86.6	putative protein	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	707	696	5.00E-70	98.4	26.6	45.5
Rsa1.0_00170.1.g7441.t1	ref|XP_002887249.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333090|gb|EFH63508.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	202	202	1.00E-102	100.0	88.6	96.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G69680.1 | Symbols: | Mog1/PsbP/DUF1795-like photosystem Ⅱ reaction center PsbP family protein | chr1:26205148-26206568 FORWARD LENGTH=202	202	202	1.00E-103	100.0	88.1	95.0
Rsa1.0_00170.1.g7442.t1	gb|EOA34585.1| hypothetical protein CARUB_v10022142mg, partial [Capsella rubella]	316	283	1.00E-113	89.6	63.0	72.5	hypothetical protein CARUB_v10022142mg, partial	gbpln	Capsella rubella	AT3G22080.1 | Symbols: | TRAF-like family protein | chr3:7777818-7781718 REVERSE LENGTH=648	316	648	1.00E-108	205.1	61.7	75.0
Rsa1.0_00170.1.g7443.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	581	1225	1.00E-90	210.8	39.8	55.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	581	575	7.00E-20	99.0	14.3	25.8
Rsa1.0_00170.1.g7444.t1	gb|EOA35611.1| hypothetical protein CARUB_v10020825mg [Capsella rubella]	260	259	1.00E-140	99.6	91.5	96.5	hypothetical protein CARUB_v10020825mg	gbpln	Capsella rubella	AT1G69640.1 | Symbols: SBH1 | sphingoid base hydroxylase 1 | chr1:26193933-26195466 REVERSE LENGTH=260	260	260	1.00E-134	100.0	92.3	96.5
Rsa1.0_00170.1.g7445.t2	gb|EOA34014.1| hypothetical protein CARUB_v10021514mg [Capsella rubella]	388	387	1.00E-141	99.7	68.6	78.6	hypothetical protein CARUB_v10021514mg	gbpln	Capsella rubella	AT1G26870.1 | Symbols: FEZ, ANAC009 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:9312856-9314983 FORWARD LENGTH=425	388	425	1.00E-125	109.5	63.7	73.5
Rsa1.0_00170.1.g7446.t1	gb|EOA35546.1| hypothetical protein CARUB_v10020752mg [Capsella rubella]	297	283	1.00E-104	95.3	58.9	70.0	hypothetical protein CARUB_v10020752mg	gbpln	Capsella rubella	AT1G66620.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr1:24852806-24854044 REVERSE LENGTH=313	297	313	1.00E-105	105.4	59.9	72.1

Rsa1.0_00170.1.g7447.t1	ref|NP_176835.1| E3 ubiquitin–protein ligase SINA–like 2 [Arabidopsis thaliana] gi|75169112|sp|Q9C6H3.1|SINL2_ARATH RecName: Full=E3 ubiquitin–protein ligase SINA–like 2; AltName: Full=Seven in absentia–like protein 2 gi|12322296|gb|AAG51178.1|AC079285_11 hypothetical protein [Arabidopsis thaliana] gi|332196416|gb|AEE34537.1| E3 ubiquitin–protein ligase SINA–like 2 [Arabidopsis thaliana]	169	313	5.00E–36	185.2	47.3	55.0	E3 ubiquitin–protein ligase SINA–like 2	gbpln	Arabidopsis thaliana	AT1G66620.1 | Symbols: | Protein with RING/U–box and TRAF–like domains | chr1:24852806–24854044 REVERSE LENGTH=313	169	313	2.00E–38	185.2	47.3	55.0
Rsa1.0_00170.1.g7448.t1	ref|NP_176835.1| E3 ubiquitin–protein ligase SINA–like 2 [Arabidopsis thaliana] gi|75169112|sp|Q9C6H3.1|SINL2_ARATH RecName: Full=E3 ubiquitin–protein ligase SINA–like 2; AltName: Full=Seven in absentia–like protein 2 gi|12322296|gb|AAG51178.1|AC079285_11 hypothetical protein [Arabidopsis thaliana] gi|332196416|gb|AEE34537.1| E3 ubiquitin–protein ligase SINA–like 2 [Arabidopsis thaliana]	297	313	1.00E–98	105.4	59.9	69.0	E3 ubiquitin–protein ligase SINA–like 2	gbpln	Arabidopsis thaliana	AT1G66620.1 | Symbols: | Protein with RING/U–box and TRAF–like domains | chr1:24852806–24854044 REVERSE LENGTH=313	297	313	1.00E–101	105.4	59.9	69.0
Rsa1.0_00170.1.g7449.t2	gb|EOA35904.1| hypothetical protein CARUB_v10021161mg [Capsella rubella]	133	120	3.00E–56	90.2	85.7	88.7	hypothetical protein CARUB_v10021161mg	gbpln	Capsella rubella	AT1G69620.1 | Symbols: RPL34 | ribosomal protein L34 | chr1:26189900–26191081 FORWARD LENGTH=119	133	119	3.00E–58	89.5	85.0	87.2
Rsa1.0_00170.1.g7450.t1	gb|EOA35643.1| hypothetical protein CARUB_v10020860mg [Capsella rubella]	251	245	1.00E–104	97.6	80.5	87.6	hypothetical protein CARUB_v10020860mg	gbpln	Capsella rubella	AT1G69600.1 | Symbols: ZFHD1, ATHB29, ZHD11 | zinc finger homeodomain 1 | chr1:26182470–26183198 FORWARD LENGTH=242	251	242	1.00E–104	96.4	76.9	84.1
Rsa1.0_00170.1.g7451.t1	gb|EOA33235.1| hypothetical protein CARUB_v10021295mg [Capsella rubella]	119	124	5.00E–37	104.2	68.1	77.3	hypothetical protein CARUB_v10021295mg	gbpln	Capsella rubella	AT1G69588.1 | Symbols: CLE45 | CLAVATA3/ESR–RELATED 45 | chr1:26178150–26178524 FORWARD LENGTH=124	119	124	3.00E–37	104.2	60.5	79.0
Rsa1.0_00170.1.g7452.t1	dbj|BAJ34568.1| unnamed protein product [Thellungiella halophila]	359	393	1.00E–147	109.5	80.5	85.2	unnamed protein product	----	----	AT1G69570.1 | Symbols: | Dof–type zinc finger DNA–binding family protein | chr1:26161771–26163230 REVERSE LENGTH=399	359	399	1.00E–137	111.1	76.9	83.8
Rsa1.0_00170.1.g7453.t1	ref|XP_002877070.1| hypothetical protein ARALYDRAFT_484564 [Arabidopsis lyrata subsp. lyrata] gi|297322908|gb|EFH53329.1| hypothetical protein ARALYDRAFT_484564 [Arabidopsis lyrata subsp. lyrata]	425	430	0	101.2	91.8	95.3	hypothetical protein ARALYDRAFT_484564	gbpln	Arabidopsis lyrata	AT3G27740.1 | Symbols: CARA | carbamoyl phosphate synthetase A | chr3:10281470–10283792 REVERSE LENGTH=430	425	430	0	101.2	91.3	94.8
Rsa1.0_00170.1.g7454.t1	ref|XP_002887243.1| MYB105 [Arabidopsis lyrata subsp. lyrata] gi|297333084|gb|EFH63502.1| MYB105 [Arabidopsis lyrata subsp. lyrata]	316	294	1.00E–115	93.0	67.4	73.7	MYB105	gbpln	Arabidopsis lyrata	AT1G69560.1 | Symbols: MYB105, LOF2, ATMYB105 | myb domain protein 105 | chr1:26157755–26158906 FORWARD LENGTH=330	316	330	1.00E–117	104.4	69.6	77.5
Rsa1.0_00170.1.g7455.t1	ref|NP_177113.3| protein agamous–like 94 [Arabidopsis thaliana] gi|41016522|dbj|BAD07477.1| MADS–box protein [Arabidopsis thaliana] gi|332196826|gb|AEE34947.1| protein agamous–like 94 [Arabidopsis thaliana]	386	344	1.00E–143	89.1	65.8	76.9	protein agamous–like 94	gbpln	Arabidopsis thaliana	AT1G69540.1 | Symbols: AGL94 | AGAMOUS–like 94 | chr1:26145306–26147159 REVERSE LENGTH=344	386	344	2.33E–156	89.1	65.8	76.9
Rsa1.0_00170.1.g7456.t1	gb|ACZ57921.1| expansin protein 1 [Brassica juncea] gi|283459396|gb|ADB22388.1| expansin [Brassica juncea]	248	249	1.00E–134	100.4	95.6	96.8	expansin protein 1	gbpln	Brassica juncea	AT1G69530.2 | Symbols: ATEXPA1, EXP1, AT–EXP1, ATEXP1, ATHEXP ALPHA 1.2, EXPA1 | expansin A1 | chr1:26142034–26143051 FORWARD LENGTH=250	248	250	1.00E–134	100.8	94.4	96.8
Rsa1.0_00171.1.g7457.t1	gb|EOA17434.1| hypothetical protein CARUB_v10005737mg [Capsella rubella]	189	208	3.00E–93	110.1	91.5	94.7	hypothetical protein CARUB_v10005737mg	gbpln	Capsella rubella	AT4G28830.1 | Symbols: | S–adenosyl–L–methionine–dependent methyltransferases superfamily protein | chr4:14232490–14233917 FORWARD LENGTH=208	189	208	3.00E–95	110.1	91.5	94.2
Rsa1.0_00171.1.g7458.t1	ref|XP_004139852.1| PREDICTED: uncharacterized protein LOC101219957 [Cucumis sativus]	870	766	0	88.0	43.6	59.3	PREDICTED: uncharacterized protein LOC101219957	gbpln	Cucumis sativus	AT5G33406.1 | Symbols: | hAT dimerisation domain–containing protein / transposase–related | chr5:12676126–12678403 REVERSE LENGTH=509	870	509	1.00E–143	58.5	27.4	32.5
Rsa1.0_00171.1.g7459.t2	ref|XP_002867436.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297313272|gb|EFH43695.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	139	173	6.00E–46	124.5	77.7	83.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G28820.1 | Symbols: | HIT–type Zinc finger family protein | chr4:14230815–14232287 REVERSE LENGTH=173	139	173	1.00E–47	124.5	78.4	82.7
Rsa1.0_00171.1.g7460.t1	gb|EOA15835.1| hypothetical protein CARUB_v10007459mg, partial [Capsella rubella]	475	453	2.00E–95	95.4	54.3	62.1	hypothetical protein CARUB_v10007459mg, partial	gbpln	Capsella rubella	AT4G28800.1 | Symbols: | basic helix–loop–helix (bHLH) DNA–binding superfamily protein | chr4:14221970–14224075 FORWARD LENGTH=445	475	445	1.00E–94	93.7	52.4	59.6
Rsa1.0_00171.1.g7461.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00171.1.g7462.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00171.1.g7463.t1	ref|NP_194607.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75212623|sp|Q9SVU5.1|GDL67_ARATH RecName: Full=GDSL esterase/lipase At4g28780; AltName: Full=Extracellular lipase At4g28780; Flags: Precursor gi|4218120|emb|CAA22974.1| Proline-rich APG-like protein [Arabidopsis thaliana] gi|7269733|emb|CAB81466.1| Proline-rich APG-like protein [Arabidopsis thaliana] gi|21592773|gb|AAM64722.1| Proline-rich APG-like protein [Arabidopsis thaliana] gi|27754717|gb|AAO22802.1| putative proline-rich APG protein [Arabidopsis thaliana] gi|28394103|gb|AAO42459.1| putative proline-rich APG protein [Arabidopsis thaliana] gi|332660143|gb|AEE85543.1| GDSL esterase/lipase [Arabidopsis thaliana]	366	367	0	100.3	93.2	94.8	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT4G28780.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr4:14215603-14217159 FORWARD LENGTH=367	366	367	0	100.3	93.2	94.8
Rsa1.0_00171.1.g7464.t1	gb|EOA17197.1| hypothetical protein CARUB_v10005468mg [Capsella rubella]	269	275	1.00E-113	102.2	84.8	91.4	hypothetical protein CARUB_v10005468mg	gbpln	Capsella rubella	AT4G28770.2 | Symbols: | Tetraspanin family protein | chr4:14212177-14213896 REVERSE LENGTH=325	269	325	1.00E-108	120.8	84.0	90.7
Rsa1.0_00171.1.g7465.t1	ref|XP_002869475.1| hypothetical protein ARALYDRAFT_491881 [Arabidopsis lyrata subsp. lyrata] gi|297315311|gb|EFH45734.1| hypothetical protein ARALYDRAFT_491881 [Arabidopsis lyrata subsp. lyrata]	894	924	0	103.4	77.6	84.1	hypothetical protein ARALYDRAFT_491881	gbpln	Arabidopsis lyrata	AT4G28760.2 | Symbols: | Protein of unknown function (DUF3741) | chr4:14208640-14211811 FORWARD LENGTH=924	894	924	0	103.4	77.0	84.0
Rsa1.0_00171.1.g7466.t1	ref|XP_002867438.1| hypothetical protein ARALYDRAFT_491882 [Arabidopsis lyrata subsp. lyrata] gi|297313274|gb|EFH43697.1| hypothetical protein ARALYDRAFT_491882 [Arabidopsis lyrata subsp. lyrata]	140	143	1.00E-46	102.1	85.0	90.7	hypothetical protein ARALYDRAFT_491882	gbpln	Arabidopsis lyrata	AT2G20260.1 | Symbols: PSAE-2 | photosystem I subunit E-2 | chr2:8736780-8737644 FORWARD LENGTH=145	140	145	2.00E-42	103.6	72.9	81.4
Rsa1.0_00171.1.g7467.t1	ref|NP_194602.2| glutaredoxin-C5 [Arabidopsis thaliana] gi|75151040|sp|Q8GWS0.1|GRXC5_ARATH RecName: Full=Glutaredoxin-C5, chloroplastic; Short=AtGrxC5; Flags: Precursor gi|26452363|dbj|BAC43267.1| unknown protein [Arabidopsis thaliana] gi|28372898|gb|AAO39931.1| At4g28730 [Arabidopsis thaliana] gi|332660135|gb|AEE85535.1| glutaredoxin-C5 [Arabidopsis thaliana]	177	174	3.00E-64	98.3	75.1	84.7	glutaredoxin-C5	gbpln	Arabidopsis thaliana	AT4G28730.1 | Symbols: | Glutaredoxin family protein | chr4:14199174-14200712 FORWARD LENGTH=174	177	174	1.00E-66	98.3	75.1	84.7
Rsa1.0_00171.1.g7468.t1	gb|EOA18198.1| hypothetical protein CARUB_v10006681mg [Capsella rubella]	426	426	0	100.0	91.8	95.8	hypothetical protein CARUB_v10006681mg	gbpln	Capsella rubella	AT4G28720.1 | Symbols: YUC8 | Flavin-binding monooxygenase family protein | chr4:14192688-14193968 FORWARD LENGTH=426	426	426	0	100.0	90.8	95.8
Rsa1.0_00171.1.g7469.t1	ref|NP_567266.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|5732057|gb|AAD48956.1|AF149414_5 contains similarity to a family of Arabidopsis thaliana predicted proteins, which have similarity to reverse transcriptases; see T14P8.10 (GB:AF069298) [Arabidopsis thaliana] gi|7267223|emb|CAB80830.1| AT4g04650 [Arabidopsis thaliana] gi|332657009|gb|AEE82409.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	267	332	1.00E-52	124.3	43.8	58.4	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	267	332	3.00E-55	124.3	43.8	58.4
Rsa1.0_00171.1.g7470.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00171.1.g7471.t1	sp|Q9C7F1.2|PPR61_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At1g28020	370	566	3.00E-90	153.0	46.2	61.1	RecName: Full=Putative pentatricopeptide repeat-containing protein At1g28020	----	----	AT1G28020.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:9768395-9771157 REVERSE LENGTH=612	370	612	8.00E-93	165.4	46.2	61.1
Rsa1.0_00171.1.g7472.t10	gb|EOA18420.1| hypothetical protein CARUB_v10006964mg [Capsella rubella]	1967	1510	0	76.8	68.5	73.0	hypothetical protein CARUB_v10006964mg	gbpln	Capsella rubella	AT4G28710.1 | Symbols: XIH, ATXIH | Myosin family protein with Dil domain | chr4:14172280-14181771 FORWARD LENGTH=1516	1967	1516	0	77.1	68.0	72.4

Rsa1.0_00171.1.g7473.t1	ref|XP_002869482.1| hypothetical protein ARALYDRAFT_491890 [Arabidopsis lyrata subsp. lyrata] gi|297315318|gb|EFH45741.1| hypothetical protein ARALYDRAFT_491890 [Arabidopsis lyrata subsp. lyrata]	113	109	5.00E-46	96.5	84.1	87.6	hypothetical protein ARALYDRAFT_491890	gbpln	Arabidopsis lyrata	AT4G28703.1 | Symbols: | RmlC-like cupins superfamily protein | chr4:14166365-14166798 FORWARD LENGTH=107	113	107	6.00E-47	94.7	80.5	83.2
Rsa1.0_00171.1.g7474.t1	ref|XP_002869483.1| hypothetical protein ARALYDRAFT_913645 [Arabidopsis lyrata subsp. lyrata] gi|297315319|gb|EFH45742.1| hypothetical protein ARALYDRAFT_913645 [Arabidopsis lyrata subsp. lyrata]	503	505	0	100.4	88.7	95.2	hypothetical protein ARALYDRAFT_913645	gbpln	Arabidopsis lyrata	AT4G28700.1 | Symbols: AMT1;4 | ammonium transporter 1;4 | chr4:14161681-14163195 FORWARD LENGTH=504	503	504	0	100.2	88.3	95.0
Rsa1.0_00171.1.g7475.t1	ref|XP_002869484.1| hypothetical protein ARALYDRAFT_328829 [Arabidopsis lyrata subsp. lyrata] gi|297315320|gb|EFH45743.1| hypothetical protein ARALYDRAFT_328829 [Arabidopsis lyrata subsp. lyrata]	339	437	3.00E-56	128.9	49.9	62.5	hypothetical protein ARALYDRAFT_328829	gbpln	Arabidopsis lyrata	AT4G28690.1 | Symbols: | BEST Arabidopsis thaliana protein match is: RPM1 interacting protein 13 (TAIR:AT2G20310.1); Has 455 Blast hits to 438 proteins in 127 species: Archae - 0; Bacteria - 18; Metazoa - 148; Fungi - 91; Plants - 136; Viruses - 3; Other Eukaryotes - 59 (source: NCBI BLink). | chr4:14159093-14160876 FORWARD LENGTH=448	339	448	5.00E-55	132.2	47.8	59.6
Rsa1.0_00171.1.g7476.t1	gb|EOA18065.1| hypothetical protein CARUB_v10006511mg [Capsella rubella]	1221	623	0	51.0	37.3	41.2	hypothetical protein CARUB_v10006511mg	gbpln	Capsella rubella	AT4G28670.1 | Symbols: | Protein kinase family protein with domain of unknown function (DUF26) | chr4:14151387-14153935 FORWARD LENGTH=625	1221	625	0	51.2	36.9	41.1
Rsa1.0_00171.1.g7477.t1	ref|XP_002869488.1| photosystem II reaction centre W family protein [Arabidopsis lyrata subsp. lyrata] gi|297315324|gb|EFH45747.1| photosystem II reaction centre W family protein [Arabidopsis lyrata subsp. lyrata]	202	183	3.00E-83	90.6	79.2	85.1	photosystem II reaction centre W family protein	gbpln	Arabidopsis lyrata	AT4G28660.2 | Symbols: PSB28 | photosystem II reaction center PSB28 protein | chr4:14150008-14150933 FORWARD LENGTH=198	202	198	3.00E-85	98.0	79.2	85.6
Rsa1.0_00172.1.g7478.t1	ref|NP_974068.1| uncharacterized protein [Arabidopsis thaliana] gi|332195780|gb|AEE33901.1| uncharacterized protein AT1G61900 [Arabidopsis thaliana]	152	413	4.00E-72	271.7	87.5	96.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G61900.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: anchored to plasma membrane, plasma membrane, anchored to membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30700.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:22882561-22884722 REVERSE LENGTH=413	152	413	1.00E-74	271.7	87.5	96.1
Rsa1.0_00172.1.g7479.t8	ref|NP_564788.1| uncharacterized protein [Arabidopsis thaliana] gi|3367524|gb|AAC28509.1| F8K4.12 [Arabidopsis thaliana] gi|110740269|dbj|BAF02031.1| hypothetical protein [Arabidopsis thaliana] gi|115311437|gb|ABI93899.1| At1g61930 [Arabidopsis thaliana] gi|332195783|gb|AEE33904.1| uncharacterized protein AT1G61930 [Arabidopsis thaliana]	201	203	2.00E-69	101.0	77.6	86.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G61930.1 | Symbols: | Protein of unknown function, DUF584 | chr1:22893218-22893829 FORWARD LENGTH=203	201	203	6.00E-72	101.0	77.6	86.6
Rsa1.0_00172.1.g7480.t1	gb|EOA33363.1| hypothetical protein CARUB_v10020262mg [Capsella rubella]	506	461	2.33E-156	91.1	54.5	68.4	hypothetical protein CARUB_v10020262mg	gbpln	Capsella rubella	AT1G62085.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:22948757-22950142 REVERSE LENGTH=461	506	461	1.00E-148	91.1	54.5	69.2
Rsa1.0_00172.1.g7481.t1	ref|XP_002888053.1| hypothetical protein ARALYDRAFT_475137 [Arabidopsis lyrata subsp. lyrata] gi|297333894|gb|EFH64312.1| hypothetical protein ARALYDRAFT_475137 [Arabidopsis lyrata subsp. lyrata]	420	419	1.00E-142	99.8	63.6	76.9	hypothetical protein ARALYDRAFT_475137	gbpln	Arabidopsis lyrata	AT1G62120.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:22960326-22961639 REVERSE LENGTH=437	420	437	1.00E-142	104.0	62.9	77.1
Rsa1.0_00172.1.g7482.t1	ref|XP_002886466.1| hypothetical protein ARALYDRAFT_893233 [Arabidopsis lyrata subsp. lyrata] gi|297332307|gb|EFH62725.1| hypothetical protein ARALYDRAFT_893233 [Arabidopsis lyrata subsp. lyrata]	436	473	1.00E-151	108.5	60.6	75.9	hypothetical protein ARALYDRAFT_893233	gbpln	Arabidopsis lyrata	AT1G61960.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:22902239-22903612 FORWARD LENGTH=457	436	457	1.00E-151	104.8	64.7	80.5

Rsa1.0_00172.1.g7483.t1	gb|AAC28522.1| Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi|485107 from Caenorhabditis elegans cosmid gb|U00049. This gene is continued from unannotated gene on BAC F19K23 gb|AC000375 [Arabidopsis thaliana]	65	684	1.00E-21	1052.3	84.6	87.7	Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi|485107 from Caenorhabditis elegans cosmid gb|U00049. This gene is continued from unannotated gene on BAC F19K23 gb|AC000375	gbpln	Arabidopsis thaliana	AT1G62045.1 | Symbols: | BEST Arabidopsis thaliana protein match is: ankyrin repeat family protein (TAIR:AT1G11740.1); Has 26 Blast hits to 26 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:22934905-22935108 REVERSE LENGTH=67	65	67	2.00E-23	103.1	84.6	87.7
Rsa1.0_00172.1.g7484.t1	ref|XP_002888042.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333883|gb|EFH64301.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	353	378	3.00E-87	107.1	56.1	66.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G19560.1 | Symbols: | F-box family protein | chr3:6793717-6794802 FORWARD LENGTH=361	353	361	6.00E-67	102.3	47.9	61.8
Rsa1.0_00172.1.g7485.t1	ref|XP_002875821.1| hypothetical protein ARALYDRAFT_485072 [Arabidopsis lyrata subsp. lyrata] gi|297321659|gb|EFH52080.1| hypothetical protein ARALYDRAFT_485072 [Arabidopsis lyrata subsp. lyrata]	217	433	4.00E-48	199.5	57.1	70.5	hypothetical protein ARALYDRAFT_485072	gbpln	Arabidopsis lyrata	AT1G62490.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:23130405-23131533 REVERSE LENGTH=334	217	334	2.00E-47	153.9	53.9	65.0
Rsa1.0_00172.1.g7486.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	430	1142	3.00E-76	265.6	36.5	55.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	430	575	2.00E-42	133.7	27.9	48.4
Rsa1.0_00172.1.g7487.t1	gb|EOA33271.1| hypothetical protein CARUB_v10022438mg [Capsella rubella]	144	145	3.00E-18	100.7	53.5	65.3	hypothetical protein CARUB_v10022438mg	gbpln	Capsella rubella	AT1G62225.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G62000.1); Has 41 Blast hits to 41 proteins in 5 species: Archae - 0; Bacteria - 2; Metazoa - 1; Fungi - 2; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:22989850-22990281 REVERSE LENGTH=143	144	143	1.00E-15	99.3	42.4	54.2
Rsa1.0_00172.1.g7488.t1	ref|XP_002886483.1| hypothetical protein ARALYDRAFT_338156 [Arabidopsis lyrata subsp. lyrata] gi|297332324|gb|EFH62742.1| hypothetical protein ARALYDRAFT_338156 [Arabidopsis lyrata subsp. lyrata]	663	1243	0	187.5	76.8	84.8	hypothetical protein ARALYDRAFT_338156	gbpln	Arabidopsis lyrata	AT1G62260.1 | Symbols: MEF9 | mitochondrial editing factor 9 | chr1:22997826-22999796 REVERSE LENGTH=656	663	656	0	98.9	76.6	84.5
Rsa1.0_00172.1.g7489.t1	ref|NP_001077757.1| SLAC1 homologue 4 [Arabidopsis thaliana] gi|322518637|sp|A8MRV9.1|SLAH4_ARATH RecName: Full=S-type anion channel SLAH4; AltName: Full=SLAC1-homolog protein 4 gi|332195822|gb|AEE33943.1| SLAC1 homologue 4 [Arabidopsis thaliana]	368	365	0	99.2	86.7	91.6	SLAC1 homologue 4	gbpln	Arabidopsis thaliana	AT1G62262.1 | Symbols: SLAH4 | SLAC1 homologue 4 | chr1:23000318-23001491 REVERSE LENGTH=365	368	365	0	99.2	86.7	91.6
Rsa1.0_00172.1.g7490.t1	emb|CAD40121.3| OSJNBa0061C06.5 [Oryza sativa Japonica Group]	360	621	7.00E-54	172.5	39.2	53.3	OSJNBa0061C06.5	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	360	1262	2.00E-23	350.6	22.8	32.2
Rsa1.0_00172.1.g7491.t1	ref|XP_002886482.1| C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297332323|gb|EFH62741.1| C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata]	381	385	0	101.0	82.4	88.5	C4-dicarboxylate transporter/malic acid transport family protein	gbpln	Arabidopsis lyrata	AT1G62280.1 | Symbols: SLAH1 | SLAC1 homologue 1 | chr1:23007309-23008540 REVERSE LENGTH=385	381	385	0	101.0	81.4	87.9
Rsa1.0_00172.1.g7492.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00172.1.g7493.t1	gb|ACI14403.1| WRKY6-1 transcription factor [Brassica napus]	550	553	0	100.5	94.4	96.0	WRKY6-1 transcription factor	gbpln	Brassica napus	AT1G62300.1 | Symbols: WRKY6, ATWRKY6 | WRKY family transcription factor | chr1:23016887-23019155 REVERSE LENGTH=553	550	553	0	100.5	84.9	90.7
Rsa1.0_00172.1.g7494.t1	ref|XP_002886476.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332317|gb|EFH62735.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1012	931	0	92.0	64.7	73.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G62310.1 | Symbols: | transcription factor jumonji (jmjC) domain-containing protein | chr1:23036039-23039301 REVERSE LENGTH=883	1012	883	0	87.3	62.9	71.5
Rsa1.0_00172.1.g7495.t1	gb|EOA33299.1| hypothetical protein CARUB_v10019839mg [Capsella rubella]	779	774	0	99.4	88.6	94.4	hypothetical protein CARUB_v10019839mg	gbpln	Capsella rubella	AT1G62320.1 | Symbols: | ERD (early-responsive to dehydration stress) family protein | chr1:23041668-23044855 REVERSE LENGTH=769	779	769	0	98.7	87.2	92.6

Rsa1.0_00173.1.g7496.t1	gb|EOA13765.1| hypothetical protein CARUB_v10026857mg [Capsella rubella]	255	303	5.00E-58	118.8	45.5	63.5	hypothetical protein CARUB_v10026857mg	gbpln	Capsella rubella	AT5G42670.1 | Symbols: | Agenet domain-containing protein | chr5:17108262-17110235 FORWARD LENGTH=294	255	294	5.00E-54	115.3	45.9	64.7
Rsa1.0_00173.1.g7497.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00173.1.g7498.t1	gb|EOA13765.1| hypothetical protein CARUB_v10026857mg [Capsella rubella]	288	303	6.00E-43	105.2	37.5	50.7	hypothetical protein CARUB_v10026857mg	gbpln	Capsella rubella	AT5G42670.1 | Symbols: | Agenet domain-containing protein | chr5:17108262-17110235 FORWARD LENGTH=294	288	294	3.00E-32	102.1	25.0	33.3
Rsa1.0_00173.1.g7499.t1	ref|NP_199081.1| Agenet domain-containing protein [Arabidopsis thaliana] gi|10177270|dbj|BAB10623.1| unnamed protein product [Arabidopsis thaliana] gi|332007462|gb|AED94845.1| Agenet domain-containing protein [Arabidopsis thaliana]	300	294	3.00E-49	98.0	36.0	52.3	Agenet domain-containing protein	gbpln	Arabidopsis thaliana	AT5G42670.1 | Symbols: | Agenet domain-containing protein | chr5:17108262-17110235 FORWARD LENGTH=294	300	294	9.00E-52	98.0	36.0	52.3
Rsa1.0_00173.1.g7500.t1	gb|AAT69582.1| putative polyprotein [Oryza sativa Japonica Group] gi|52353546|gb|AAU44112.1| putative polyprotein [Oryza sativa Japonica Group]	256	1256	3.00E-43	490.6	35.9	50.0	putative polyprotein	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	256	1262	5.00E-27	493.0	26.6	41.0
Rsa1.0_00173.1.g7501.t1	ref|NP_200023.1| putative dihydrodipicolinate reductase 3 [Arabidopsis thaliana] gi|75262543|sp|Q9FJ82.1|DAPB3_ARATH RecName: Full=Putative 4-hydroxy-tetrahydrodipicolinate reductase 3, chloroplastic; Short=HTPA reductase 3; Flags: Precursor gi|10177745|dbj|BAB11058.1| dihydrodipicolinate reductase-like protein [Arabidopsis thaliana] gi|124301156|gb|ABN04830.1| At5g52100 [Arabidopsis thaliana] gi|332008788|gb|AED96171.1| putative dihydrodipicolinate reductase 3 [Arabidopsis thaliana]	300	298	1.00E-166	99.3	97.0	98.3	putative dihydrodipicolinate reductase 3	gbpln	Arabidopsis thaliana	AT5G52100.1 | Symbols: crr1 | Dihydrodipicolinate reductase, bacterial/plant | chr5:21170203-21172107 FORWARD LENGTH=298	300	298	1.00E-169	99.3	97.0	98.3
Rsa1.0_00173.1.g7502.t1	ref|NP_200024.1| uncharacterized protein [Arabidopsis thaliana] gi|79330641|ref|NP_001032060.1| uncharacterized protein [Arabidopsis thaliana] gi|10177746|dbj|BAB11059.1| unnamed protein product [Arabidopsis thaliana] gi|117959001|gb|ABK59697.1| At5g52110 [Arabidopsis thaliana] gi|332008789|gb|AED96172.1| uncharacterized protein AT5G52110 [Arabidopsis thaliana] gi|332008790|gb|AED96173.1| uncharacterized protein AT5G52110 [Arabidopsis thaliana]	278	275	1.00E-136	98.9	83.8	92.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G52110.2 | Symbols: HCF208 | Protein of unknown function (DUF2930) | chr5:21172159-21173953 REVERSE LENGTH=275	278	275	1.00E-138	98.9	83.8	92.4
Rsa1.0_00173.1.g7503.t1	ref|XP_002865894.1| phloem protein 2-A14 [Arabidopsis lyrata subsp. lyrata] gi|297311729|gb|EFH42153.1| phloem protein 2-A14 [Arabidopsis lyrata subsp. lyrata]	419	287	1.00E-119	68.5	48.9	53.2	phloem protein 2-A14	gbpln	Arabidopsis lyrata	AT5G52120.1 | Symbols: AtPP2-A14, PP2-A14 | phloem protein 2-A14 | chr5:21176661-21180143 REVERSE LENGTH=291	419	291	1.00E-121	69.5	48.9	52.0
Rsa1.0_00173.1.g7504.t1	gb|EOA14892.1| hypothetical protein CARUB_v10028221mg [Capsella rubella]	97	96	3.00E-30	99.0	70.1	79.4	hypothetical protein CARUB_v10028221mg	gbpln	Capsella rubella	AT5G52160.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:21195140-21195430 FORWARD LENGTH=96	97	96	2.00E-30	99.0	73.2	82.5
Rsa1.0_00173.1.g7505.t1	ref|XP_002865900.1| sugar isomerase domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311735|gb|EFH42159.1| sugar isomerase domain-containing protein [Arabidopsis lyrata subsp. lyrata]	200	208	2.00E-86	104.0	82.0	90.0	sugar isomerase domain-containing protein	gbpln	Arabidopsis lyrata	AT5G52190.1 | Symbols: | Sugar isomerase (SIS) family protein | chr5:21201817-21202443 REVERSE LENGTH=208	200	208	2.00E-87	104.0	79.0	87.0
Rsa1.0_00173.1.g7506.t1	ref|XP_002865901.1| hypothetical protein ARALYDRAFT_918263 [Arabidopsis lyrata subsp. lyrata] gi|297311736|gb|EFH42160.1| hypothetical protein ARALYDRAFT_918263 [Arabidopsis lyrata subsp. lyrata]	192	185	7.00E-52	96.4	65.6	78.1	hypothetical protein ARALYDRAFT_918263	gbpln	Arabidopsis lyrata	AT5G52200.1 | Symbols: | phosphoprotein phosphatase inhibitors | chr5:21202818-21204719 REVERSE LENGTH=191	192	191	6.00E-53	99.5	69.8	80.7

Rsa1.0_00173.1.g7507.t1	ref|NP_200034.1| GTP-binding protein 1 [Arabidopsis thaliana] gi|30696156|ref|NP_851175.1| GTP-binding protein 1 [Arabidopsis thaliana] gi|1184981|gb|AAA87882.1| GTP-binding protein ATGB1 [Arabidopsis thaliana] gi|8885534|dbj|BAA97464.1| GTP-binding protein-like [Arabidopsis thaliana] gi|28416611|gb|AAO42836.1| At5g52210 [Arabidopsis thaliana] gi|110743285|dbj|BAE99533.1| GTP-binding protein-like [Arabidopsis thaliana] gi|332008801|gb|AED96184.1| GTP-binding protein 1 [Arabidopsis thaliana] gi|332008802|gb|AED96185.1| GTP-binding protein 1 [Arabidopsis thaliana]	205	205	1.00E-109	100.0	92.7	98.5	GTP-binding protein 1	gbpln	Arabidopsis thaliana	AT5G52210.2 | Symbols: ATARLB1, ATGB1, GB1 | GTP-binding protein 1 | chr5:21205567-21206840 FORWARD LENGTH=205	205	205	1.00E-112	100.0	92.7	98.5
Rsa1.0_00173.1.g7508.t1	gb|AAM64761.1| contains similarity to photomorphogenesis repressor protein [Arabidopsis thaliana]	342	385	1.00E-150	112.6	84.2	89.2	contains similarity to photomorphogenesis repressor protein	gbpln	Arabidopsis thaliana	AT5G52250.1 | Symbols: RUP1 | Transducin/WD40 repeat-like superfamily protein | chr5:21216898-21218055 FORWARD LENGTH=385	342	385	1.00E-152	112.6	83.9	88.9
Rsa1.0_00173.1.g7509.t1	ref|XP_002864161.1| hypothetical protein ARALYDRAFT_495295 [Arabidopsis lyrata subsp. lyrata] gi|297309996|gb|EFH40420.1| hypothetical protein ARALYDRAFT_495295 [Arabidopsis lyrata subsp. lyrata]	268	270	1.00E-113	100.7	81.0	91.0	hypothetical protein ARALYDRAFT_495295	gbpln	Arabidopsis lyrata	AT5G52260.1 | Symbols: AtMYB19, MYB19 | myb domain protein 19 | chr5:21220165-21221223 FORWARD LENGTH=268	268	268	1.00E-115	100.0	80.2	89.2
Rsa1.0_00173.1.g7510.t2	ref|NP_197389.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|332005241|gb|AED92624.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	206	295	4.00E-30	143.2	36.4	51.0	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	206	295	1.00E-32	143.2	36.4	51.0
Rsa1.0_00173.1.g7511.t1	gb|EOA13973.1| hypothetical protein CARUB_v10027102mg [Capsella rubella]	160	219	1.00E-57	136.9	68.8	75.0	hypothetical protein CARUB_v10027102mg	gbpln	Capsella rubella	AT5G52240.1 | Symbols: MSBP1, ATMP1, AtMAPR5 | membrane steroid binding protein 1 | chr5:21213121-21214557 FORWARD LENGTH=220	160	220	1.00E-59	137.5	67.5	75.0
Rsa1.0_00173.1.g7512.t1	gb|EOA13973.1| hypothetical protein CARUB_v10027102mg [Capsella rubella]	227	219	1.00E-72	96.5	65.6	74.0	hypothetical protein CARUB_v10027102mg	gbpln	Capsella rubella	AT5G52240.1 | Symbols: MSBP1, ATMP1, AtMAPR5 | membrane steroid binding protein 1 | chr5:21213121-21214557 FORWARD LENGTH=220	227	220	2.00E-73	96.9	63.9	70.9
Rsa1.0_00173.1.g7513.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00173.1.g7514.t3	ref|NP_200042.4| shortage in chiasmata 1 [Arabidopsis thaliana] gi|332008813|gb|AED96196.1| shortage in chiasmata 1 [Arabidopsis thaliana]	1606	1594	0	99.3	75.1	84.5	shortage in chiasmata 1	gbpln	Arabidopsis thaliana	AT5G52290.1 | Symbols: SHOC1 | shortage in chiasmata 1 | chr5:21230353-21236554 REVERSE LENGTH=1594	1606	1594	0	99.3	75.1	84.5
Rsa1.0_00173.1.g7515.t1	gb|EOA14447.1| hypothetical protein CARUB_v10027650mg [Capsella rubella]	593	634	1.00E-169	106.9	66.9	77.7	hypothetical protein CARUB_v10027650mg	gbpln	Capsella rubella	AT5G52300.1 | Symbols: RD29B, LTI65 | CAP160 protein | chr5:21237205-21239404 FORWARD LENGTH=619	593	619	1.00E-166	104.4	63.9	75.9
Rsa1.0_00173.1.g7516.t1	ref|XP_002865909.1| hypothetical protein ARALYDRAFT_495305 [Arabidopsis lyrata subsp. lyrata] gi|297311744|gb|EFH42168.1| hypothetical protein ARALYDRAFT_495305 [Arabidopsis lyrata subsp. lyrata] gi|482550326|gb|EOA14520.1| hypothetical protein CARUB_v10027750mg [Capsella rubella]	130	137	4.00E-67	105.4	96.2	96.2	hypothetical protein ARALYDRAFT_495305	gbpln	Arabidopsis lyrata	AT5G52360.1 | Symbols: ADF10 | actin depolymerizing factor 10 | chr5:21258157-21259229 REVERSE LENGTH=137	130	137	2.00E-67	105.4	93.1	94.6
Rsa1.0_00173.1.g7517.t1	ref|XP_002865910.1| zinc knuckle (CCHC-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297311745|gb|EFH42169.1| zinc knuckle (CCHC-type) family protein [Arabidopsis lyrata subsp. lyrata]	265	268	1.00E-109	101.1	85.7	91.7	zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis lyrata	AT5G52380.1 | Symbols: | VASCULAR-RELATED NAC-DOMAIN 6 | chr5:21261521-21263061 REVERSE LENGTH=268	265	268	1.00E-112	101.1	84.9	91.7
Rsa1.0_00173.1.g7518.t1	gb|EOA21683.1| hypothetical protein CARUB_v10002107mg [Capsella rubella]	140	171	1.00E-20	122.1	31.4	47.9	hypothetical protein CARUB_v10002107mg	gbpln	Capsella rubella	AT5G42965.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17236736-17237125 FORWARD LENGTH=129	140	129	2.00E-11	92.1	23.6	38.6
Rsa1.0_00173.1.g7519.t2	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1670	1213	0	72.6	35.5	46.3	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	1670	289	9.00E-70	17.3	7.7	10.8

Rsa1.0_00173.1.g7520.t1	ref|XP_002864167.1| hypothetical protein ARALYDRAFT_331608 [Arabidopsis lyrata subsp. lyrata] gi|297310002|gb|EFH40426.1| hypothetical protein ARALYDRAFT_331608 [Arabidopsis lyrata subsp. lyrata]	517	530	0	102.5	88.6	93.4	hypothetical protein ARALYDRAFT_331608	gbpln	Arabidopsis lyrata	AT5G52400.1 | Symbols: CYP715A1 | cytochrome P450, family 715, subfamily A, polypeptide 1 | chr5:21272949-21275509 FORWARD LENGTH=519	517	519	0	100.4	87.4	92.6
Rsa1.0_00173.1.g7521.t1	gb|EOA12724.1| hypothetical protein CARUB_v10028150mg [Capsella rubella]	274	267	7.00E-99	97.4	72.3	78.1	hypothetical protein CARUB_v10028150mg	gbpln	Capsella rubella	AT5G52440.1 | Symbols: HCF106 | Bacterial sec-independent translocation protein mttA/Hcf106 | chr5:21286896-21288613 FORWARD LENGTH=260	274	260	3.00E-96	94.9	70.4	76.6
Rsa1.0_00173.1.g7522.t1	ref|NP_190233.2| iron ion binding / oxidoreductase/ oxidoreductase protein [Arabidopsis thaliana] gi|332644644|gb|AEE78165.1| iron ion binding / oxidoreductase/ oxidoreductase protein [Arabidopsis thaliana]	334	330	1.00E-148	98.8	76.3	84.4	iron ion binding / oxidoreductase/ oxidoreductase protein	gbpln	Arabidopsis thaliana	AT3G46490.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:17115629-17119451 FORWARD LENGTH=330	334	330	1.00E-151	98.8	76.3	84.4
Rsa1.0_00173.1.g7523.t1	gb|ABL97978.1| metal ion binding [Brassica rapa]	135	139	2.00E-42	103.0	70.4	81.5	metal ion binding	gbpln	Brassica rapa	AT5G52760.1 | Symbols: | Copper transport protein family | chr5:21386919-21387540 FORWARD LENGTH=126	135	126	2.00E-34	93.3	64.4	75.6
Rsa1.0_00173.1.g7524.t1	gb|EOA25898.1| hypothetical protein CARUB_v10019277mg [Capsella rubella]	264	281	4.00E-86	106.4	62.9	77.3	hypothetical protein CARUB_v10019277mg	gbpln	Capsella rubella	AT3G53310.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr3:19766927-19768368 REVERSE LENGTH=286	264	286	2.00E-75	108.3	57.6	73.9
Rsa1.0_00173.1.g7525.t1	ref|XP_002864198.1| hypothetical protein ARALYDRAFT_495348 [Arabidopsis lyrata subsp. lyrata] gi|297310033|gb|EFH40457.1| hypothetical protein ARALYDRAFT_495348 [Arabidopsis lyrata subsp. lyrata]	212	169	5.00E-82	79.7	74.5	79.2	hypothetical protein ARALYDRAFT_495348	gbpln	Arabidopsis lyrata	AT5G52840.1 | Symbols: | NADH-ubiquinone oxidoreductase-related | chr5:21413718-21414794 FORWARD LENGTH=169	212	169	1.00E-83	79.7	75.0	77.8
Rsa1.0_00173.1.g7526.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00173.1.g7527.t1	ref|NP_200099.1| uncharacterized protein [Arabidopsis thaliana] gi|75171557|sp|Q9FLX4.1|MAKR5_ARATH RecName: Full=Probable membrane-associated kinase regulator 5 gi|10177101|dbj|BAB10435.1| unnamed protein product [Arabidopsis thaliana] gi|15028097|gb|AAK76579.1| unknown protein [Arabidopsis thaliana] gi|20258915|gb|AAM14151.1| unknown protein [Arabidopsis thaliana] gi|332008887|gb|AED96270.1| uncharacterized protein AT5G52870 [Arabidopsis thaliana]	317	326	4.00E-97	102.8	71.3	81.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G52870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G64080.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:21428191-21429367 REVERSE LENGTH=326	317	326	1.00E-99	102.8	71.3	81.7
Rsa1.0_00173.1.g7528.t1	ref|XP_002865936.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297311771|gb|EFH42195.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	819	830	0	101.3	91.9	95.7	ATP binding protein	gbpln	Arabidopsis lyrata	AT5G52882.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:21434155-21438362 REVERSE LENGTH=829	819	829	0	101.2	91.9	95.6
Rsa1.0_00173.1.g7529.t1	ref|XP_002891891.1| hypothetical protein ARALYDRAFT_337726 [Arabidopsis lyrata subsp. lyrata] gi|297337733|gb|EFH68150.1| hypothetical protein ARALYDRAFT_337726 [Arabidopsis lyrata subsp. lyrata]	183	183	2.00E-63	100.0	72.1	82.5	hypothetical protein ARALYDRAFT_337726	gbpln	Arabidopsis lyrata	AT1G54400.1 | Symbols: | HSP20-like chaperones superfamily protein | chr1:20307667-20308768 FORWARD LENGTH=183	183	183	4.00E-61	100.0	68.9	80.3
Rsa1.0_00173.1.g7530.t1	ref|NP_568780.1| uncharacterized protein [Arabidopsis thaliana] gi|75146673|sp|Q84JK8.1|MAKR6_ARATH RecName: Full=Probable membrane-associated kinase regulator 6 gi|28973707|gb|AAO64170.1| unknown protein [Arabidopsis thaliana] gi|29824227|gb|AAP04074.1| unknown protein [Arabidopsis thaliana] gi|110737043|dbj|BAF00476.1| hypothetical protein [Arabidopsis thaliana] gi|332008892|gb|AED96275.1| uncharacterized protein AT5G52900 [Arabidopsis thaliana]	230	235	4.00E-96	102.2	79.1	87.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G52900.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21452893-21453692 REVERSE LENGTH=235	230	235	1.00E-98	102.2	79.1	87.8
Rsa1.0_00173.1.g7531.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00173.1.g7532.t22	gb|EMJ28231.1| hypothetical protein PRUPE_ppa000670mg [Prunus persica]	1007	1029	0	102.2	42.7	59.4	hypothetical protein PRUPE_ppa000670mg	gbpln	Prunus persica	AT5G53010.1 | Symbols: | calcium-transporting ATPase, putative | chr5:21488899-21496537 REVERSE LENGTH=1049	1007	1049	0	104.2	37.0	42.6

Rsa1.0_00173.1.g7533.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	936	1356	0	144.9	55.2	71.6	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	936	1262	1.00E-79	134.8	18.2	29.2
Rsa1.0_00173.1.g7534.t1	ref|XP_002865952.1| hypothetical protein ARALYDRAFT_918370 [Arabidopsis lyrata subsp. lyrata] gi|297311787|gb|EFH42211.1| hypothetical protein ARALYDRAFT_918370 [Arabidopsis lyrata subsp. lyrata]	96	96	3.00E-39	100.0	80.2	88.5	hypothetical protein ARALYDRAFT_918370	gbpln	Arabidopsis lyrata	AT5G53045.1 | Symbols: | unknown protein; Has 122 Blast hits to 122 proteins in 57 species: Archae - 0; Bacteria - 0; Metazoa - 46; Fungi - 30; Plants - 41; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr5:21508603-21509538 REVERSE LENGTH=96	96	96	8.00E-42	100.0	80.2	88.5
Rsa1.0_00173.1.g7535.t2	ref|XP_002865953.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297311788|gb|EFH42212.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	405	396	0	97.8	83.2	89.4	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT5G53050.3 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:21510534-21513432 REVERSE LENGTH=396	405	396	1.00E-177	97.8	81.2	87.9
Rsa1.0_00173.1.g7536.t1	gb|EOA13332.1| hypothetical protein CARUB_v10026366mg [Capsella rubella]	240	460	3.00E-35	191.7	47.5	60.8	hypothetical protein CARUB_v10026366mg	gbpln	Capsella rubella	AT5G53635.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:21785999-21787444 REVERSE LENGTH=426	240	426	2.00E-33	177.5	44.6	56.7
Rsa1.0_00174.1.g7537.t1	gb|EOA38077.1| hypothetical protein CARUB_v10009545mg, partial [Capsella rubella]	305	358	1.00E-144	117.4	85.2	92.5	hypothetical protein CARUB_v10009545mg, partial	gbpln	Capsella rubella	AT1G45976.1 | Symbols: SBP1 | S-ribonuclease binding protein 1 | chr1:17199371-17200680 FORWARD LENGTH=325	305	325	1.00E-141	106.6	81.0	89.2
Rsa1.0_00174.1.g7538.t1	emb|CAB40051.1| putative protein [Arabidopsis thaliana] gi|7267781|emb|CAB81184.1| putative protein [Arabidopsis thaliana]	307	1294	3.00E-22	421.5	22.1	31.3	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00174.1.g7539.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	228	1142	2.00E-52	500.9	50.9	66.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	228	256	4.00E-18	112.3	24.1	30.7
Rsa1.0_00174.1.g7540.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00174.1.g7541.t1	ref|XP_002891331.1| hypothetical protein ARALYDRAFT_473862 [Arabidopsis lyrata subsp. lyrata] gi|297337173|gb|EFH67590.1| hypothetical protein ARALYDRAFT_473862 [Arabidopsis lyrata subsp. lyrata]	333	347	1.00E-156	104.2	86.8	91.6	hypothetical protein ARALYDRAFT_473862	gbpln	Arabidopsis lyrata	AT1G46264.1 | Symbols: AT-HSFB4, HSFB4, SCZ | heat shock transcription factor B4 | chr1:17224904-17226183 FORWARD LENGTH=348	333	348	1.00E-148	104.5	86.2	91.0
Rsa1.0_00174.1.g7542.t1	gb|EOA40316.1| hypothetical protein CARUB_v10009041mg [Capsella rubella]	215	470	5.00E-62	218.6	57.2	60.9	hypothetical protein CARUB_v10009041mg	gbpln	Capsella rubella	AT1G12680.1 | Symbols: PEPKR2 | phosphoenolpyruvate carboxylase-related kinase 2 | chr1:4320123-4322269 REVERSE LENGTH=470	215	470	3.00E-61	218.6	55.8	60.5
Rsa1.0_00174.1.g7543.t1	ref|XP_002889953.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335795|gb|EFH66212.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	113	123	8.00E-25	108.8	56.6	74.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G12663.1 | Symbols: | Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant thionin (PR-13) family with the following members: At1g66100, At5g36910, At1g72260, At2g15010, At1g12663, At1g12660. | chr1:4310969-4311457 FORWARD LENGTH=115	113	115	8.00E-24	101.8	49.6	69.0
Rsa1.0_00174.1.g7544.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00174.1.g7545.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00174.1.g7546.t1	gb|EOA38449.1| hypothetical protein CARUB_v10010093mg [Capsella rubella]	257	251	1.00E-110	97.7	81.7	87.9	hypothetical protein CARUB_v10010093mg	gbpln	Capsella rubella	AT1G46480.1 | Symbols: WOX4 | WUSCHEL related homeobox 4 | chr1:17236903-17237953 REVERSE LENGTH=251	257	251	1.00E-103	97.7	82.9	87.5
Rsa1.0_00174.1.g7547.t12	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	1422	657	1.00E-142	46.2	18.5	24.0	T14P8.10	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	1422	332	7.00E-72	23.3	9.6	12.4
Rsa1.0_00174.1.g7548.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1347	1307	0	97.0	59.2	73.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1347	1262	1.00E-100	93.7	14.0	23.2
Rsa1.0_00174.1.g7549.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00174.1.g7550.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00174.1.g7551.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00174.1.g7552.t1	ref|NP_564496.1| ethylene-responsive transcription factor RAP2-1 [Arabidopsis thaliana] gi|75245929|sp|Q8LC30.1|RAP21_ARATH RecName: Full=Ethylene-responsive transcription factor RAP2-1; AltName: Full=Protein RELATED TO APETALA2 1 gi|21555563|gb|AAM63886.1| AP2 domain containing protein RAP2.1 [Arabidopsis thaliana] gi|88900408|gb|ABD57516.1| At1g46768 [Arabidopsis thaliana] gi|332194008|gb|AEE32129.1| ethylene-responsive transcription factor RAP2-1 [Arabidopsis thaliana]	155	153	4.00E-54	98.7	76.1	81.3	ethylene-responsive transcription factor RAP2-1	gbpln	Arabidopsis thaliana	AT1G46768.1 | Symbols: RAP2.1 | related to AP2 1 | chr1:17266046-17266507 REVERSE LENGTH=153	155	153	1.00E-56	98.7	76.1	81.3
Rsa1.0_00174.1.g7553.t10	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1244	1142	0	91.8	40.5	53.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1244	575	6.00E-61	46.2	12.7	20.2
Rsa1.0_00174.1.g7554.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00175.1.g7555.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00175.1.g7556.t1	dbj|BAA23676.1| receptor kinase 1 [Brassica rapa subsp. oleifera]	805	847	0	105.2	87.6	92.2	receptor kinase 1	gbpln	Brassica rapa	AT1G65800.1 | Symbols: ARK2, RK2 | receptor kinase 2 | chr1:24473166-24476523 FORWARD LENGTH=847	805	847	0	105.2	76.3	86.2
Rsa1.0_00175.1.g7557.t1	gb|ACR10278.1| putative benzoate-CoA ligase [Brassica rapa subsp. pekinensis]	566	567	0	100.2	94.0	96.5	putative benzoate-CoA ligase	gbpln	Brassica rapa	AT1G65880.1 | Symbols: BZO1 | benzoyloxyglucosinolate 1 | chr1:24508633-24510737 REVERSE LENGTH=580	566	580	0	102.5	78.1	88.0
Rsa1.0_00175.1.g7558.t1	ref|XP_002886975.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332816|gb|EFH63234.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	846	845	0	99.9	74.6	85.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G65800.1 | Symbols: ARK2, RK2 | receptor kinase 2 | chr1:24473166-24476523 FORWARD LENGTH=847	846	847	0	100.1	75.8	86.1
Rsa1.0_00175.1.g7559.t1	gb|EOA35211.1| hypothetical protein CARUB_v10020361mg, partial [Capsella rubella]	410	419	0	102.2	84.6	92.0	hypothetical protein CARUB_v10020361mg, partial	gbpln	Capsella rubella	AT1G65900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 306 Blast hits to 306 proteins in 119 species: Archae - 19; Bacteria - 238; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink). | chr1:24516023-24518325 REVERSE LENGTH=408	410	408	0	99.5	84.9	91.2
Rsa1.0_00175.1.g7560.t1	gb|EOA35225.1| hypothetical protein CARUB_v10020383mg [Capsella rubella]	410	410	0	100.0	98.5	99.5	hypothetical protein CARUB_v10020383mg	gbpln	Capsella rubella	AT1G65930.1 | Symbols: cICDH | cytosolic NADP+-dependent isocitrate dehydrogenase | chr1:24539088-24541861 FORWARD LENGTH=410	410	410	0	100.0	97.8	99.3
Rsa1.0_00175.1.g7561.t2	ref|XP_002888468.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297334309|gb|EFH64727.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata]	533	550	0	103.2	82.7	89.1	ABC1 family protein	gbpln	Arabidopsis lyrata	AT1G65950.1 | Symbols: | Protein kinase superfamily protein | chr1:24546860-24551119 REVERSE LENGTH=551	533	551	0	103.4	83.1	88.9
Rsa1.0_00175.1.g7562.t1	gb|AAS79669.1| glutamate decarboxylase 2 [Brassica juncea]	494	494	0	100.0	97.6	99.0	glutamate decarboxylase 2	gbpln	Brassica juncea	AT1G65960.2 | Symbols: GAD2 | glutamate decarboxylase 2 | chr1:24552094-24557253 FORWARD LENGTH=494	494	494	0	100.0	92.1	96.2
Rsa1.0_00175.1.g7563.t1	gb|AAD33602.1|AF133302_1 type 2 peroxiredoxin [Brassica rapa subsp. pekinensis] gi|83032224|gb|ABB97029.1| unknown [Brassica rapa]	162	162	6.00E-86	100.0	95.7	100.0	type 2 peroxiredoxin	gbpln	Brassica rapa	AT1G65980.1 | Symbols: TPX1 | thioredoxin-dependent peroxidase 1 | chr1:24559524-24560753 REVERSE LENGTH=162	162	162	6.00E-88	100.0	95.7	98.8
Rsa1.0_00175.1.g7564.t1	ref|NP_178476.1| nonsense-mediated mRNA decay protein 3 [Arabidopsis thaliana] gi|4582430|gb|AAD24816.1| putative nonsense-mediated mRNA decay protein [Arabidopsis thaliana] gi|20466624|gb|AAM20629.1| putative nonsense-mediated mRNA decay protein [Arabidopsis thaliana] gi|22136400|gb|AAM91278.1| putative nonsense-mediated mRNA decay protein [Arabidopsis thaliana] gi|330250660|gb|AEC05754.1| nonsense-mediated mRNA decay protein 3 [Arabidopsis thaliana]	520	516	0	99.2	89.2	92.1	nonsense-mediated mRNA decay protein 3	gbpln	Arabidopsis thaliana	AT2G03820.1 | Symbols: | nonsense-mediated mRNA decay NMD3 family protein | chr2:1165149-1166699 REVERSE LENGTH=516	520	516	0	99.2	89.2	92.1

<table>
<tr><td>Rsa1.0_00175.1.g7565.t1</td><td>ref|NP_174707.1| DC1 domain-containing protein [Arabidopsis thaliana] gi|8778258|gb|AAF79267.1|AC023279_16 F12K21.20 [Arabidopsis thaliana] gi|12323862|gb|AAG51903.1|AC023913_11 hypothetical protein; 1917-109 [Arabidopsis thaliana] gi|332193597|gb|AEE31718.1| DC1 domain-containing protein [Arabidopsis thaliana]</td><td>704</td><td>602</td><td>1.00E-179</td><td>85.5</td><td>44.6</td><td>55.8</td><td>DC1 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G34480.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:12607276-12609084 FORWARD LENGTH=602</td><td>704</td><td>602</td><td>0</td><td>85.5</td><td>44.6</td><td>55.8</td></tr>
<tr><td>Rsa1.0_00175.1.g7566.t1</td><td>ref|NP_564865.1| Translation initiation factor eIF3 subunit [Arabidopsis thaliana] gi|334183669|ref|NP_001185326.1| Translation initiation factor eIF3 subunit [Arabidopsis thaliana] gi|12322607|gb|AAG51301.1|AC026480_8 unknown protein [Arabidopsis thaliana] gi|17380828|gb|AAL36101.1| unknown protein [Arabidopsis thaliana] gi|20259027|gb|AAM14229.1| unknown protein [Arabidopsis thaliana] gi|332196337|gb|AEE34458.1| Translation initiation factor eIF3 subunit [Arabidopsis thaliana] gi|332196338|gb|AEE34459.1| Translation initiation factor eIF3 subunit [Arabidopsis thaliana]</td><td>252</td><td>226</td><td>3.00E-82</td><td>89.7</td><td>71.4</td><td>79.0</td><td>Translation initiation factor eIF3 subunit</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G66070.2 | Symbols: | Translation initiation factor eIF3 subunit | chr1:24596194-24597520 REVERSE LENGTH=226</td><td>252</td><td>226</td><td>9.00E-85</td><td>89.7</td><td>71.4</td><td>79.0</td></tr>
<tr><td>Rsa1.0_00175.1.g7567.t1</td><td>ref|NP_564865.1| Translation initiation factor eIF3 subunit [Arabidopsis thaliana] gi|334183669|ref|NP_001185326.1| Translation initiation factor eIF3 subunit [Arabidopsis thaliana] gi|12322607|gb|AAG51301.1|AC026480_8 unknown protein [Arabidopsis thaliana] gi|17380828|gb|AAL36101.1| unknown protein [Arabidopsis thaliana] gi|20259027|gb|AAM14229.1| unknown protein [Arabidopsis thaliana] gi|332196337|gb|AEE34458.1| Translation initiation factor eIF3 subunit [Arabidopsis thaliana] gi|332196338|gb|AEE34459.1| Translation initiation factor eIF3 subunit [Arabidopsis thaliana]</td><td>179</td><td>226</td><td>7.00E-42</td><td>126.3</td><td>52.5</td><td>62.0</td><td>Translation initiation factor eIF3 subunit</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G66070.2 | Symbols: | Translation initiation factor eIF3 subunit | chr1:24596194-24597520 REVERSE LENGTH=226</td><td>179</td><td>226</td><td>3.00E-44</td><td>126.3</td><td>52.5</td><td>62.0</td></tr>
<tr><td>Rsa1.0_00175.1.g7568.t1</td><td>ref|XP_002888481.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334322|gb|EFH64740.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>354</td><td>349</td><td>1.00E-114</td><td>98.6</td><td>59.6</td><td>73.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G66110.1 | Symbols: | Family of unknown function (DUF577) | chr1:24609094-24610232 REVERSE LENGTH=338</td><td>354</td><td>338</td><td>1.00E-103</td><td>95.5</td><td>55.6</td><td>69.8</td></tr>
<tr><td>Rsa1.0_00175.1.g7569.t1</td><td>ref|NP_176787.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|12322603|gb|AAG51297.1|AC026480_4 oxidoreductase, putative [Arabidopsis thaliana] gi|332196344|gb|AEE34465.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]</td><td>412</td><td>364</td><td>0</td><td>88.3</td><td>73.3</td><td>81.6</td><td>Rossmann-fold NAD(P)-binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G66130.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:24615040-24616742 FORWARD LENGTH=364</td><td>412</td><td>364</td><td>0</td><td>88.3</td><td>73.3</td><td>81.6</td></tr>
<tr><td>Rsa1.0_00175.1.g7570.t1</td><td>gb|EOA35598.1| hypothetical protein CARUB_v10020811mg [Capsella rubella]</td><td>250</td><td>263</td><td>1.00E-80</td><td>105.2</td><td>76.0</td><td>85.2</td><td>hypothetical protein CARUB_v10020811mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G66140.1 | Symbols: ZFP4 | zinc finger protein 4 | chr1:24620063-24620845 REVERSE LENGTH=260</td><td>250</td><td>260</td><td>9.00E-80</td><td>104.0</td><td>78.4</td><td>86.8</td></tr>
<tr><td>Rsa1.0_00175.1.g7571.t1</td><td>ref|XP_002887010.1| hypothetical protein ARALYDRAFT_475717 [Arabidopsis lyrata subsp. lyrata] gi|297332851|gb|EFH63269.1| hypothetical protein ARALYDRAFT_475717 [Arabidopsis lyrata subsp. lyrata]</td><td>935</td><td>937</td><td>0</td><td>100.2</td><td>89.0</td><td>93.3</td><td>hypothetical protein ARALYDRAFT_475717</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G66150.1 | Symbols: TMK1 | transmembrane kinase 1 | chr1:24631503-24634415 FORWARD LENGTH=942</td><td>935</td><td>942</td><td>0</td><td>100.7</td><td>88.2</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00175.1.g7572.t1</td><td>ref|XP_002888489.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334330|gb|EFH64748.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>757</td><td>760</td><td>0</td><td>100.4</td><td>82.2</td><td>90.1</td><td>subtilase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G66210.1 | Symbols: | Subtilisin-like serine endopeptidase family protein | chr1:24665735-24668650 REVERSE LENGTH=759</td><td>757</td><td>759</td><td>0</td><td>100.3</td><td>81.5</td><td>90.1</td></tr>
<tr><td>Rsa1.0_00175.1.g7573.t1</td><td>ref|XP_002887016.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata] gi|297332857|gb|EFH63275.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>757</td><td>753</td><td>0</td><td>99.5</td><td>79.3</td><td>88.8</td><td>subtilase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G66220.1 | Symbols: | Subtilase family protein | chr1:24670536-24673661 FORWARD LENGTH=753</td><td>757</td><td>753</td><td>0</td><td>99.5</td><td>77.5</td><td>87.1</td></tr>
</table>

Rsa1.0_00175.1.g7574.t3	#	#	#	#	#	#	#	–	----	----	AT1G04510.1 | Symbols: MAC3A | MOS4-associated complex 3A | chr1:1226749-1230592 FORWARD LENGTH=523	177	523	3.00E-12	295.5	17.5	20.3
Rsa1.0_00175.1.g7575.t1	ref|XP_002887017.1| hypothetical protein ARALYDRAFT_894261 [Arabidopsis lyrata subsp. lyrata] gi|297332858|gb|EFH63276.1| hypothetical protein ARALYDRAFT_894261 [Arabidopsis lyrata subsp. lyrata]	282	288	1.00E-116	102.1	82.3	91.1	hypothetical protein ARALYDRAFT_894261	gbpln	Arabidopsis lyrata	AT1G66230.1 | Symbols: MYB20, AtMYB20 | myb domain protein 20 | chr1:24677322-24678246 FORWARD LENGTH=282	282	282	1.00E-107	100.0	77.7	88.7
Rsa1.0_00175.1.g7576.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00175.1.g7577.t1	ref|NP_199308.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262649|sp|Q9FLA2.1|FDL34_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g44950 gi|10177487|dbj|BAB10878.1| unnamed protein product [Arabidopsis thaliana] gi|332007796|gb|AED95179.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	470	438	7.00E-73	93.2	39.1	49.6	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G44950.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:18151665-18153164 FORWARD LENGTH=438	470	438	2.00E-75	93.2	39.1	49.6
Rsa1.0_00175.1.g7578.t1	ref|NP_199308.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262649|sp|Q9FLA2.1|FDL34_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g44950 gi|10177487|dbj|BAB10878.1| unnamed protein product [Arabidopsis thaliana] gi|332007796|gb|AED95179.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	551	438	3.00E-92	79.5	40.1	51.7	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G44950.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:18151665-18153164 FORWARD LENGTH=438	551	438	6.00E-95	79.5	40.1	51.7
Rsa1.0_00175.1.g7579.t1	ref|NP_199308.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262649|sp|Q9FLA2.1|FDL34_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g44950 gi|10177487|dbj|BAB10878.1| unnamed protein product [Arabidopsis thaliana] gi|332007796|gb|AED95179.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	570	438	1.00E-98	76.8	39.1	50.9	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G44950.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:18151665-18153164 FORWARD LENGTH=438	570	438	1.00E-101	76.8	39.1	50.9
Rsa1.0_00175.1.g7580.t1	ref|NP_199308.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262649|sp|Q9FLA2.1|FDL34_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g44950 gi|10177487|dbj|BAB10878.1| unnamed protein product [Arabidopsis thaliana] gi|332007796|gb|AED95179.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	567	438	9.00E-97	77.2	39.9	51.3	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G44950.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:18151665-18153164 FORWARD LENGTH=438	567	438	2.00E-99	77.2	39.9	51.3
Rsa1.0_00175.1.g7581.t1	gb|EOA35523.1| hypothetical protein CARUB_v10020732mg [Capsella rubella]	293	294	7.00E-85	100.3	66.2	76.5	hypothetical protein CARUB_v10020732mg	gbpln	Capsella rubella	AT1G66260.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:24695895-24697883 REVERSE LENGTH=295	293	295	9.00E-79	100.7	68.6	78.8
Rsa1.0_00175.1.g7582.t1	ref|XP_002888495.1| hypothetical protein ARALYDRAFT_475736 [Arabidopsis lyrata subsp. lyrata] gi|297334336|gb|EFH64754.1| hypothetical protein ARALYDRAFT_475736 [Arabidopsis lyrata subsp. lyrata]	422	416	0	98.6	84.8	88.2	hypothetical protein ARALYDRAFT_475736	gbpln	Arabidopsis lyrata	AT1G66330.2 | Symbols: | senescence-associated family protein | chr1:24729880-24732144 REVERSE LENGTH=417	422	417	0	98.8	84.4	88.6
Rsa1.0_00175.1.g7583.t1	sp|O49230.1|ETR1_BRAOL RecName: Full=Ethylene receptor 1 gi|2896029|gb|AAC39497.1| ethylene receptor [Brassica oleracea]	734	735	0	100.1	98.2	99.2	RecName: Full=Ethylene receptor 1 gi|2896029|gb|AAC39497.1| ethylene receptor	gbpln	Brassica oleracea	AT1G66340.1 | Symbols: ETR1, EIN1, ETR, AtETR1 | Signal transduction histidine kinase, hybrid-type, ethylene sensor | chr1:24734698-24737366 FORWARD LENGTH=738	734	738	0	100.5	96.0	98.2
Rsa1.0_00175.1.g7584.t1	gb|EOA33796.1| hypothetical protein CARUB_v10021265mg [Capsella rubella]	180	167	4.00E-60	92.8	66.1	71.1	hypothetical protein CARUB_v10021265mg	gbpln	Capsella rubella	AT1G66360.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:24751431-24752607 FORWARD LENGTH=174	180	174	4.00E-62	96.7	65.6	70.6

Rsa1.0_00175.1.g7585.t1	gb|ADP76651.1| MYB2 [Brassica oleracea var. botrytis]	168	247	3.00E-77	147.0	85.7	89.9	MYB2	gbpln	Brassica oleracea	AT1G66390.1 | Symbols: ATMYB90, PAP2, MYB90 | myb domain protein 90 | chr1:24764052-24765400 FORWARD LENGTH=249	168	249	1.00E-54	148.2	64.3	74.4
Rsa1.0_00176.1.g7586.t1	dbj|BAJ34079.1| unnamed protein product [Thellungiella halophila]	175	184	8.00E-79	105.1	86.9	93.1	unnamed protein product	----	----	AT5G67190.1 | Symbols: DEAR2 | DREB and EAR motif protein 2 | chr5:26809135-26809689 REVERSE LENGTH=184	175	184	2.00E-76	105.1	85.1	92.6
Rsa1.0_00176.1.g7587.t1	gb|AAN17412.1| putative protein [Arabidopsis thaliana] gi|25084238|gb|AAN72203.1| putative protein [Arabidopsis thaliana]	421	375	1.00E-176	89.1	75.3	81.5	putative protein	gbpln	Arabidopsis thaliana	AT5G67170.1 | Symbols: | SEC-C motif-containing protein / OTU-like cysteine protease family protein | chr5:26799851-26801763 FORWARD LENGTH=375	421	375	1.00E-173	89.1	72.0	78.1
Rsa1.0_00176.1.g7588.t1	ref|XP_002865022.1| hypothetical protein ARALYDRAFT_919995 [Arabidopsis lyrata subsp. lyrata] gi|297310857|gb|EFH41281.1| hypothetical protein ARALYDRAFT_919995 [Arabidopsis lyrata subsp. lyrata]	453	448	0	98.9	76.4	82.6	hypothetical protein ARALYDRAFT_919995	gbpln	Arabidopsis lyrata	AT5G67160.1 | Symbols: EPS1 | HXXXD-type acyl-transferase family protein | chr5:26797700-26799004 REVERSE LENGTH=434	453	434	1.00E-145	95.8	60.9	71.7
Rsa1.0_00176.1.g7589.t1	ref|XP_002866719.1| hypothetical protein ARALYDRAFT_920006 [Arabidopsis lyrata subsp. lyrata] gi|297312554|gb|EFH42978.1| hypothetical protein ARALYDRAFT_920006 [Arabidopsis lyrata subsp. lyrata]	128	128	2.00E-49	100.0	78.1	84.4	hypothetical protein ARALYDRAFT_920006	gbpln	Arabidopsis lyrata	AT5G67070.1 | Symbols: RALFL34 | ralf-like 34 | chr5:26768120-26768509 FORWARD LENGTH=129	128	129	7.00E-50	100.8	78.1	82.8
Rsa1.0_00176.1.g7590.t1	gb|EOA14640.1| hypothetical protein CARUB_v10027898mg [Capsella rubella]	207	242	5.00E-65	116.9	82.1	87.0	hypothetical protein CARUB_v10027898mg	gbpln	Capsella rubella	AT5G67060.1 | Symbols: HEC1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:26766276-26767001 FORWARD LENGTH=241	207	241	6.00E-66	116.4	79.2	84.1
Rsa1.0_00176.1.g7591.t3	ref|XP_002865030.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297310865|gb|EFH41289.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	470	479	0	101.9	83.4	91.5	lipase class 3 family protein	gbpln	Arabidopsis lyrata	AT5G67050.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:26759482-26761165 REVERSE LENGTH=477	470	477	0	101.5	80.6	90.6
Rsa1.0_00176.1.g7592.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1569	1352	0	86.2	44.0	58.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1569	746	1.00E-114	47.5	13.3	16.8
Rsa1.0_00176.1.g7593.t1	ref|XP_002888458.1| hypothetical protein ARALYDRAFT_338787 [Arabidopsis lyrata subsp. lyrata] gi|297334299|gb|EFH64717.1| hypothetical protein ARALYDRAFT_338787 [Arabidopsis lyrata subsp. lyrata]	267	278	2.00E-74	104.1	62.9	74.5	hypothetical protein ARALYDRAFT_338787	gbpln	Arabidopsis lyrata	AT5G66990.1 | Symbols: | RWP-RK domain-containing protein | chr5:26744257-26745362 REVERSE LENGTH=277	267	277	4.00E-74	103.7	61.4	74.2
Rsa1.0_00176.1.g7594.t1	ref|NP_569043.1| uncharacterized protein [Arabidopsis thaliana] gi|21593797|gb|AAM65764.1| unknown [Arabidopsis thaliana] gi|89111824|gb|ABD60684.1| At5g66985 [Arabidopsis thaliana] gi|332010904|gb|AED98287.1| uncharacterized protein AT5G66985 [Arabidopsis thaliana]	86	83	2.00E-23	96.5	66.3	75.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G66985.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26743412-26743663 FORWARD LENGTH=83	86	83	4.00E-26	96.5	66.3	75.6
Rsa1.0_00176.1.g7595.t1	dbj|BAJ33900.1| unnamed protein product [Thellungiella halophila]	425	626	1.00E-147	147.3	58.8	60.7	unnamed protein product	----	----	AT5G66760.1 | Symbols: SDH1-1 | succinate dehydrogenase 1-1 | chr5:26653776-26657224 FORWARD LENGTH=634	425	634	1.00E-147	149.2	57.2	60.5
Rsa1.0_00176.1.g7596.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00176.1.g7597.t1	gb|EOA29413.1| hypothetical protein CARUB_v10025704mg [Capsella rubella]	276	309	6.00E-22	112.0	17.4	25.4	hypothetical protein CARUB_v10025704mg	gbpln	Capsella rubella	AT2G30130.1 | Symbols: ASL5, LBD12, PCK1 | Lateral organ boundaries (LOB) domain family protein | chr2:12868740-12869684 FORWARD LENGTH=193	276	193	8.00E-23	69.9	18.1	27.9
Rsa1.0_00176.1.g7598.t3	dbj|BAJ33900.1| unnamed protein product [Thellungiella halophila]	1190	626	0	52.6	36.6	37.6	unnamed protein product	----	----	AT5G66760.1 | Symbols: SDH1-1 | succinate dehydrogenase 1-1 | chr5:26653776-26657224 FORWARD LENGTH=634	1190	634	0	53.3	35.5	37.6
Rsa1.0_00176.1.g7599.t1	gb|EOA13246.1| hypothetical protein CARUB_v10026275mg [Capsella rubella]	496	499	0	100.6	80.0	85.9	hypothetical protein CARUB_v10026275mg	gbpln	Capsella rubella	AT5G66730.1 | Symbols: | C2H2-like zinc finger protein | chr5:26641914-26643883 REVERSE LENGTH=500	496	500	0	100.8	78.6	84.5
Rsa1.0_00176.1.g7600.t1	ref|XP_002866744.1| hypothetical protein ARALYDRAFT_496930 [Arabidopsis lyrata subsp. lyrata] gi|297312579|gb|EFH43003.1| hypothetical protein ARALYDRAFT_496930 [Arabidopsis lyrata subsp. lyrata]	413	406	1.00E-165	98.3	74.3	82.6	hypothetical protein ARALYDRAFT_496930	gbpln	Arabidopsis lyrata	AT5G66710.1 | Symbols: | Protein kinase superfamily protein | chr5:26636609-26638564 FORWARD LENGTH=405	413	405	1.00E-162	98.1	71.4	81.6

Rsa1.0_00176.1.g7601.t1	ref|XP_002866745.1| hypothetical protein ARALYDRAFT_332898 [Arabidopsis lyrata subsp. lyrata] gi|297312580|gb|EFH43004.1| hypothetical protein ARALYDRAFT_332898 [Arabidopsis lyrata subsp. lyrata]	224	231	2.00E-86	103.1	81.7	88.8	hypothetical protein ARALYDRAFT_332898	gbpln	Arabidopsis lyrata	AT5G66700.1 | Symbols: HB53, HB-8, ATHB53 | homeobox 53 | chr5:26634406-26635762 FORWARD LENGTH=228	224	228	2.00E-86	101.8	81.3	87.5
Rsa1.0_00176.1.g7602.t1	ref|XP_002866746.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297312581|gb|EFH43005.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	473	481	0	101.7	81.4	90.7	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT5G66690.1 | Symbols: UGT72E2 | UDP-Glycosyltransferase superfamily protein | chr5:26625155-26626600 FORWARD LENGTH=481	473	481	0	101.7	80.5	90.3
Rsa1.0_00176.1.g7603.t1	ref|NP_569038.1| oligosaccharyltransferase complex subunit beta [Arabidopsis thaliana] gi|75164192|sp|Q944K2.1|OST48_ARATH RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit; Short=Oligosaccharyl transferase 48 kDa subunit; AltName: Full=Protein DEFECTIVE GLYCOSYLATION 1; Flags: Precursor gi|16226812|gb|AAL16268.1|AF428338_1 AT5g66680/MSN2_7 [Arabidopsis thaliana] gi|23297258|gb|AAN12926.1| putative dolichyl-di-phosphooligosaccharide glycotransferase (oligosaccharyltransferase) [Arabidopsis thaliana] gi|332010868|gb|AED98251.1| dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit [Arabidopsis thaliana]	435	437	0	100.5	96.1	99.1	oligosaccharyltransferase complex subunit beta	gbpln	Arabidopsis thaliana	AT5G66680.1 | Symbols: DGL1 | dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48kDa subunit family protein | chr5:26617840-26620581 REVERSE LENGTH=437	435	437	0	100.5	96.1	99.1
Rsa1.0_00176.1.g7604.t1	ref|XP_002865056.1| hypothetical protein ARALYDRAFT_496938 [Arabidopsis lyrata subsp. lyrata] gi|297310891|gb|EFH41315.1| hypothetical protein ARALYDRAFT_496938 [Arabidopsis lyrata subsp. lyrata]	319	320	1.00E-135	100.3	75.9	88.4	hypothetical protein ARALYDRAFT_496938	gbpln	Arabidopsis lyrata	AT5G66650.1 | Symbols: | Protein of unknown function (DUF607) | chr5:26603204-26604257 REVERSE LENGTH=321	319	321	1.00E-134	100.6	73.4	86.8
Rsa1.0_00176.1.g7605.t1	dbj|BAA97270.1| unnamed protein product [Arabidopsis thaliana]	522	451	1.00E-161	86.4	59.2	69.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G66640.1 | Symbols: DAR3 | DA1-related protein 3 | chr5:26599818-26601765 FORWARD LENGTH=450	522	450	1.00E-163	86.2	58.8	69.5
Rsa1.0_00176.1.g7606.t1	ref|NP_201463.1| protein DA1-related 6 [Arabidopsis thaliana] gi|75171127|sp|Q9FJX8.1|DAR6_ARATH RecName: Full=Protein DA1-related 6 gi|10177543|dbj|BAB10938.1| unnamed protein product [Arabidopsis thaliana] gi|332010857|gb|AED98240.1| protein DA1-related 6 [Arabidopsis thaliana]	531	644	1.00E-155	121.3	55.9	68.7	protein DA1-related 6	gbpln	Arabidopsis thaliana	AT5G66620.1 | Symbols: DAR6 | DA1-related protein 6 | chr5:26588585-26592006 FORWARD LENGTH=644	531	644	1.00E-158	121.3	55.9	68.7
Rsa1.0_00176.1.g7607.t3	ref|NP_201461.1| uncharacterized protein [Arabidopsis thaliana] gi|186532816|ref|NP_001119511.1| uncharacterized protein [Arabidopsis thaliana] gi|10177541|dbj|BAB10936.1| unnamed protein product [Arabidopsis thaliana] gi|61742773|gb|AAX55207.1| hypothetical protein At5g66600 [Arabidopsis thaliana] gi|332010850|gb|AED98233.1| uncharacterized protein AT5G66600 [Arabidopsis thaliana] gi|332010852|gb|AED98235.1| uncharacterized protein AT5G66600 [Arabidopsis thaliana]	575	614	0	106.8	77.6	84.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G66600.3 | Symbols: | Protein of unknown function, DUF547 | chr5:26575105-26578315 REVERSE LENGTH=614	575	614	0	106.8	77.6	84.7
Rsa1.0_00176.1.g7608.t1	ref|NP_001147033.1| pathogenesis-related protein PRB1-3 precursor [Zea mays] gi|195606704|gb|ACG25182.1| pathogenesis-related protein PRB1-3 precursor [Zea mays]	183	180	9.00E-96	98.4	93.4	95.1	pathogenesis-related protein PRB1-3 precursor	gbenv/gbpln	Zea mays	AT5G66590.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr5:26574255-26574812 FORWARD LENGTH=185	183	185	1.00E-84	101.1	85.2	90.2

Rsa1.0_00176.1.g7609.t1	ref|NP_201459.1| uncharacterized protein [Arabidopsis thaliana] gi|10177539|dbj|BAB10934.1| unnamed protein product [Arabidopsis thaliana] gi|28393574|gb|AAO42207.1| unknown protein [Arabidopsis thaliana] gi|28972979|gb|AAO63814.1| unknown protein [Arabidopsis thaliana] gi|332010848|gb|AED98231.1| uncharacterized protein AT5G66580 [Arabidopsis thaliana]	154	156	1.00E−62	101.3	84.4	89.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G66580.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N−terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G50800.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:26572724−26573194 FORWARD LENGTH=156	154	156	3.00E−65	101.3	84.4	89.0
Rsa1.0_00176.1.g7610.t1	gb|EOA13683.1| hypothetical protein CARUB_v10026754mg [Capsella rubella]	332	332	0	100.0	97.6	98.8	hypothetical protein CARUB_v10026754mg	gbpln	Capsella rubella	AT5G66570.1 | Symbols: PSBO−1, OEE1, OEE33, OE33, PSBO1, MSP−1 | PS II oxygen−evolving complex 1 | chr5:26568744−26570124 FORWARD LENGTH=332	332	332	0	100.0	96.7	98.2
Rsa1.0_00176.1.g7611.t2	ref|XP_002865060.1| hypothetical protein ARALYDRAFT_496951 [Arabidopsis lyrata subsp. lyrata] gi|297310895|gb|EFH41319.1| hypothetical protein ARALYDRAFT_496951 [Arabidopsis lyrata subsp. lyrata]	1398	522	0	37.3	29.8	32.8	hypothetical protein ARALYDRAFT_496951	gbpln	Arabidopsis lyrata	AT5G66540.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: rRNA processing; LOCATED IN: cytosol, nucleolus, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: U3 small nucleolar ribonucleoprotein complex, subunit Mpp10p (InterPro:IPR012173), Mpp10 protein (InterPro:IPR007151); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:26556653−26559310 REVERSE LENGTH=524	1398	524	0	37.5	29.5	32.4
Rsa1.0_00176.1.g7612.t2	gb|ABB45851.1| hypothetical protein [Eutrema halophilum]	1569	697	0	44.4	34.5	37.8	hypothetical protein	gbpln	Eutrema halophilum	AT3G47840.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr3:17651912−17654032 FORWARD LENGTH=706	1569	706	0	45.0	34.0	38.0
Rsa1.0_00176.1.g7613.t1	gb|ABB45850.1| hypothetical protein [Eutrema halophilum]	194	296	3.00E−53	152.6	63.9	72.2	hypothetical protein	gbpln	Eutrema halophilum	AT5G66450.1 | Symbols: | Phosphatidic acid phosphatase (PAP2) family protein | chr5:26534801−26535951 FORWARD LENGTH=286	194	286	2.00E−47	147.4	58.8	68.0
Rsa1.0_00177.1.g7614.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00177.1.g7615.t1	ref|NP_182302.1| nuclear transcription factor Y subunit B−5 [Arabidopsis thaliana] gi|75220231|sp|O82248.1|NFYB5_ARATH RecName: Full=Nuclear transcription factor Y subunit B−5; Short=AtNF−YB−5 gi|3738293|gb|AAC63635.1| putative CCAAT−box binding trancription factor [Arabidopsis thaliana] gi|28393159|gb|AAO42012.1| putative CCAAT−box binding trancription factor [Arabidopsis thaliana] gi|28827540|gb|AAO50614.1| putative CCAAT−box binding trancription factor [Arabidopsis thaliana] gi|330255796|gb|AEC10890.1| nuclear transcription factor Y subunit B−5 [Arabidopsis thaliana]	114	160	4.00E−57	140.4	91.2	95.6	nuclear transcription factor Y subunit B−5	gbpln	Arabidopsis thaliana	AT2G47810.1 | Symbols: NF−YB5 | nuclear factor Y, subunit B5 | chr2:19582938−19583420 REVERSE LENGTH=160	114	160	7.00E−60	140.4	91.2	95.6
Rsa1.0_00177.1.g7616.t1	pir||S65812 RNA−directed DNA polymerase (EC 2.7.7.49) (clone DW15) − Arabidopsis thaliana retrotransposon Ta11−1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	1796	1333	0	74.2	37.1	49.9	RNA−directed DNA polymerase (EC 2.7.7.49) (clone DW15) − Arabidopsis thaliana retrotransposon Ta11−1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1796	575	3.00E−85	32.0	9.2	14.6
Rsa1.0_00177.1.g7617.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00177.1.g7618.t1	ref|XP_002882009.1| hypothetical protein ARALYDRAFT_903981 [Arabidopsis lyrata subsp. lyrata] gi|297327848|gb|EFH58268.1| hypothetical protein ARALYDRAFT_903981 [Arabidopsis lyrata subsp. lyrata]	207	308	4.00E−13	148.8	17.9	18.8	hypothetical protein ARALYDRAFT_903981	gbpln	Arabidopsis lyrata	AT3G60800.1 | Symbols: | DHHC−type zinc finger family protein | chr3:22467486−22469273 REVERSE LENGTH=307	207	307	5.00E−13	148.3	15.5	17.9
Rsa1.0_00177.1.g7619.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_00177.1.g7620.t1	ref|XP_002880325.1| hypothetical protein ARALYDRAFT_483966 [Arabidopsis lyrata subsp. lyrata] gi|297326164|gb|EFH56584.1| hypothetical protein ARALYDRAFT_483966 [Arabidopsis lyrata subsp. lyrata]	739	789	0	106.8	73.3	81.6	hypothetical protein ARALYDRAFT_483966	gbpln	Arabidopsis lyrata	AT2G47820.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G09040.1). | chr2:19588122-19590629 FORWARD LENGTH=805	739	805	0	108.9	70.6	80.4
Rsa1.0_00177.1.g7621.t1	ref|NP_182304.2| metal tolerance protein C1 [Arabidopsis thaliana] gi|71151963|sp|Q8L725.1|MTPC1_ARATH RecName: Full=Metal tolerance protein C1; Short=AtMTPc1; AltName: Full=AtMTP6 gi|22655099|gb|AAM98140.1| unknown protein [Arabidopsis thaliana] gi|30387579|gb|AAP31955.1| At2g47830 [Arabidopsis thaliana] gi|330255799|gb|AEC10893.1| metal tolerance protein C1 [Arabidopsis thaliana]	458	471	0	102.8	82.5	86.9	metal tolerance protein C1	gbpln	Arabidopsis thaliana	AT2G47830.1 | Symbols: | Cation efflux family protein | chr2:19591094-19593973 REVERSE LENGTH=471	458	471	0	102.8	82.5	86.9
Rsa1.0_00177.1.g7622.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1345	1352	0	100.5	46.4	63.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1345	746	1.00E-100	55.5	13.7	18.8
Rsa1.0_00177.1.g7623.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00177.1.g7624.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	2084	1142	0	54.8	29.7	37.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2084	575	3.00E-75	27.6	8.3	13.5
Rsa1.0_00177.1.g7625.t1	ref|XP_002871294.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297317131|gb|EFH47553.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata]	401	404	0	100.7	81.5	88.5	mitochondrial transcription termination factor family protein	gbpln	Arabidopsis lyrata	AT5G07900.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr5:2520188-2521405 FORWARD LENGTH=405	401	405	0	101.0	79.6	87.8
Rsa1.0_00177.1.g7626.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00177.1.g7627.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00177.1.g7628.t1	gb|AAM64620.1| unknown [Arabidopsis thaliana]	138	128	5.00E-18	92.8	54.3	63.0	unknown	gbpln	Arabidopsis thaliana	AT2G47950.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root, flower; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G62990.1); Has 22 Blast hits to 22 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19624280-19624666 FORWARD LENGTH=128	138	128	5.00E-17	92.8	50.7	56.5
Rsa1.0_00177.1.g7629.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	185	1142	4.00E-30	617.3	43.8	58.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00177.1.g7630.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	140	704	2.00E-39	502.9	55.7	60.7	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00177.1.g7631.t1	ref|NP_180556.1| protein ELF4-like 1 [Arabidopsis thaliana] gi|75099965|sp|O80877.1|EF4L1_ARATH RecName: Full=Protein ELF4-LIKE 1 gi|3420056|gb|AAC31857.1| hypothetical protein [Arabidopsis thaliana] gi|49823506|gb|AAT68736.1| hypothetical protein At2g29950 [Arabidopsis thaliana] gi|61742622|gb|AAX55132.1| hypothetical protein At2g29950 [Arabidopsis thaliana] gi|330253232|gb|AEC08326.1| protein ELF4-like 1 [Arabidopsis thaliana]	138	125	7.00E-35	90.6	55.8	68.8	protein ELF4-like 1	gbpln	Arabidopsis thaliana	AT2G29950.1 | Symbols: ELF4-L1 | ELF4-like 1 | chr2:12767790-12768167 FORWARD LENGTH=125	138	125	2.00E-37	90.6	55.8	68.8
Rsa1.0_00177.1.g7632.t1	ref|XP_002879240.1| ATPDR3/PDR3 [Arabidopsis lyrata subsp. lyrata] gi|297325079|gb|EFH55499.1| ATPDR3/PDR3 [Arabidopsis lyrata subsp. lyrata]	1421	1428	0	100.5	91.1	96.1	ATPDR3/PDR3	gbpln	Arabidopsis lyrata	AT2G29940.1 | Symbols: PDR3, ATPDR3 | pleiotropic drug resistance 3 | chr2:12760139-12766455 FORWARD LENGTH=1426	1421	1426	0	100.4	90.5	95.7

Rsa1.0_00177.1.g7633.t1	emb|CAB75932.1| putative protein [Arabidopsis thaliana]	1633	1339	0	82.0	44.0	57.3	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1633	1262	1.00E-109	77.3	12.5	19.1
Rsa1.0_00178.1.g7634.t2	ref|XP_004249683.1| PREDICTED: mitochondrial import inner membrane translocase subunit TIM14-1-like [Solanum lycopersicum]	108	112	5.00E-46	103.7	82.4	89.8	PREDICTED: mitochondrial import inner membrane translocase subunit TIM14-1-like	gbpln	Solanum lycopersicum	AT2G35795.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr2:15042321-15043334 FORWARD LENGTH=112	108	112	4.00E-48	103.7	80.6	90.7
Rsa1.0_00178.1.g7635.t1	ref|XP_002871004.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297316841|gb|EFH47263.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	526	515	0	97.9	89.5	93.9	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT5G02970.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:695391-697412 FORWARD LENGTH=514	526	514	0	97.7	87.8	93.2
Rsa1.0_00178.1.g7636.t1	gb|EOA21773.1| hypothetical protein CARUB_v10002234mg [Capsella rubella]	136	136	7.00E-72	100.0	100.0	100.0	hypothetical protein CARUB_v10002234mg	gbpln	Capsella rubella	AT5G02960.1 | Symbols: | Ribosomal protein S12/S23 family protein | chr5:693280-694396 REVERSE LENGTH=142	136	142	7.00E-74	104.4	99.3	99.3
Rsa1.0_00178.1.g7637.t1	gb|EOA20616.1| hypothetical protein CARUB_v10000928mg [Capsella rubella]	456	456	0	100.0	75.9	87.1	hypothetical protein CARUB_v10000928mg	gbpln	Capsella rubella	AT5G02910.1 | Symbols: | F-box/RNI-like superfamily protein | chr5:677120-678907 FORWARD LENGTH=458	456	458	0	100.4	72.1	84.0
Rsa1.0_00178.1.g7638.t1	dbj|BAB02857.1| unnamed protein product [Arabidopsis thaliana]	797	507	3.00E-89	63.6	26.0	31.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G28410.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:10640152-10642071 REVERSE LENGTH=465	797	465	1.00E-91	58.3	26.0	31.7
Rsa1.0_00178.1.g7639.t1	gb|EOA20937.1| hypothetical protein CARUB_v10001270mg [Capsella rubella]	343	357	1.00E-130	104.1	70.0	81.0	hypothetical protein CARUB_v10001270mg	gbpln	Capsella rubella	AT5G02890.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:670207-671454 REVERSE LENGTH=353	343	353	1.00E-131	102.9	69.1	78.7
Rsa1.0_00178.1.g7640.t1	dbj|BAC42280.1| putative 60S ribosomal protein [Arabidopsis thaliana]	406	407	0	100.2	92.4	96.3	putative 60S ribosomal protein	gbpln	Arabidopsis thaliana	AT3G09630.1 | Symbols: | Ribosomal protein L4/L1 family | chr3:2953813-2955444 FORWARD LENGTH=406	406	406	0	100.0	92.9	96.8
Rsa1.0_00178.1.g7641.t1	gb|EOA20698.1| hypothetical protein CARUB_v10001011mg [Capsella rubella]	449	431	1.00E-134	96.0	73.1	78.8	hypothetical protein CARUB_v10001011mg	gbpln	Capsella rubella	AT5G02850.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:652159-653439 FORWARD LENGTH=426	449	426	1.00E-135	94.9	73.3	79.1
Rsa1.0_00178.1.g7642.t5	emb|CAB86038.1| putative protein [Arabidopsis thaliana]	302	307	1.00E-122	101.7	77.5	80.1	putative protein	gbpln	Arabidopsis thaliana	AT5G02840.3 | Symbols: LCL1 | LHY/CCA1-like 1 | chr5:648794-651204 FORWARD LENGTH=283	302	283	1.00E-119	93.7	75.5	78.8
Rsa1.0_00178.1.g7643.t1	gb|EOA19949.1| hypothetical protein CARUB_v10000200mg [Capsella rubella]	856	858	0	100.2	86.8	92.4	hypothetical protein CARUB_v10000200mg	gbpln	Capsella rubella	AT5G02830.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:644458-648421 REVERSE LENGTH=852	856	852	0	99.5	85.6	91.2
Rsa1.0_00178.1.g7644.t1	ref|NP_195902.1| DNA topoisomerase 6 subunit A [Arabidopsis thaliana] gi|297806215|ref|XP_002870991.1| hypothetical protein ARALYDRAFT_487058 [Arabidopsis lyrata subsp. lyrata] gi|75335684|sp|Q9LZ03.1|TOP6A_ARATH RecName: Full=DNA topoisomerase 6 subunit A; Short=AtTOP6A; AltName: Full=Meiotic recombination protein SPO11-3; Short=AtSPO11-3; AltName: Full=Protein BRASSINOSTEROID INSENSITIVE 5; AltName: Full=Protein ROOT HAIRLESS 2 gi|15488539|gb|AAL01152.1|AF323679_1 putative topoisomerase VI subunit A [Arabidopsis thaliana] gi|7413557|emb|CAB86036.1| meiosis specific-like protein [Arabidopsis thaliana] gi|12331186|emb|CAC24689.1| topoisomerase 6 subunit A [Arabidopsis thaliana] gi|114213517|gb|ABI54341.1| At5g02820 [Arabidopsis thaliana] gi|297316828|gb|EFH47250.1| hypothetical protein ARALYDRAFT_487058 [Arabidopsis lyrata subsp. lyrata] gi|332003139|gb|AED90522.1| DNA topoisomerase 6 subunit A [Arabidopsis thaliana]	429	427	0	99.5	93.2	94.9	DNA topoisomerase 6 subunit A	gbpln	Arabidopsis lyrata	AT5G02820.1 | Symbols: RHL2, BIN5 | Spo11/DNA topoisomerase VI, subunit A protein | chr5:642658-644123 FORWARD LENGTH=427	429	427	0	99.5	93.2	94.9
Rsa1.0_00178.1.g7645.t1	gb|ADA58346.1| pseudo-response regulator 7b [Brassica rapa]	705	704	0	99.9	93.2	94.9	pseudo-response regulator 7b	gbpln	Brassica rapa	AT5G02810.1 | Symbols: PRR7, APRR7 | pseudo-response regulator 7 | chr5:638283-641461 REVERSE LENGTH=727	705	727	0	103.1	85.2	89.2
Rsa1.0_00178.1.g7646.t1	dbj|BAB09991.1| mutator-like transposase-like [Arabidopsis thaliana]	689	825	0	119.7	57.9	73.1	mutator-like transposase-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00178.1.g7647.t1	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	1947	1274	0	65.4	31.3	43.2	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1947	575	1.00E−73	29.5	9.5	14.4
Rsa1.0_00178.1.g7648.t1	gb|EOA22009.1| hypothetical protein CARUB_v10002532mg [Capsella rubella]	752	746	0	99.2	83.4	90.4	hypothetical protein CARUB_v10002532mg	gbpln	Capsella rubella	AT5G47580.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17250.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:19294948−19297194 REVERSE LENGTH=748	752	748	0	99.5	82.3	91.1
Rsa1.0_00178.1.g7649.t1	ref|XP_002873065.1| hypothetical protein ARALYDRAFT_487051 [Arabidopsis lyrata subsp. lyrata] gi|297318902|gb|EFH49324.1| hypothetical protein ARALYDRAFT_487051 [Arabidopsis lyrata subsp. lyrata]	209	214	2.00E−76	102.4	84.2	87.6	hypothetical protein ARALYDRAFT_487051	gbpln	Arabidopsis lyrata	AT5G02770.1 | Symbols: | unknown protein; Has 469 Blast hits to 336 proteins in 126 species: Archae − 0; Bacteria − 54; Metazoa − 249; Fungi − 22; Plants − 47; Viruses − 0; Other Eukaryotes − 97 (source: NCBI BLink). | chr5:628101−629168 REVERSE LENGTH=214	209	214	1.00E−74	102.4	81.3	86.6
Rsa1.0_00178.1.g7650.t1	dbj|BAJ33929.1| unnamed protein product [Thellungiella halophila]	370	370	0	100.0	87.8	93.5	unnamed protein product	----	----	AT5G02760.1 | Symbols: | Protein phosphatase 2C family protein | chr5:625377−626817 FORWARD LENGTH=370	370	370	0	100.0	85.1	91.6
Rsa1.0_00178.1.g7651.t1	ref|NP_566063.1| uncharacterized protein [Arabidopsis thaliana] gi|3702339|gb|AAC62896.1| expressed protein [Arabidopsis thaliana] gi|18252159|gb|AAL61912.1| unknown protein [Arabidopsis thaliana] gi|21386927|gb|AAM47867.1| unknown protein [Arabidopsis thaliana] gi|330255547|gb|AEC10641.1| uncharacterized protein AT2G46080 [Arabidopsis thaliana]	176	347	6.00E−26	197.2	34.7	35.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G46080.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein BYPASS related (InterPro:IPR008511); BEST Arabidopsis thaliana protein match is: Protein of unknown function (DUF793) (TAIR:AT1G01550.2); Has 153 Blast hits to 139 proteins in 20 species: Archae − 0; Bacteria − 2; Metazoa − 1; Fungi − 0; Plants − 150; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr2:18948317−18949360 REVERSE LENGTH=347	176	347	2.00E−28	197.2	34.7	35.8
Rsa1.0_00178.1.g7652.t1	ref|XP_002870987.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297316824|gb|EFH47246.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	291	283	1.00E−119	97.3	84.5	89.3	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G02750.1 | Symbols: | RING/U−box superfamily protein | chr5:620101−620952 FORWARD LENGTH=283	291	283	1.00E−121	97.3	83.2	89.0
Rsa1.0_00178.1.g7653.t1	ref|XP_002870986.1| hypothetical protein ARALYDRAFT_487048 [Arabidopsis lyrata subsp. lyrata] gi|297316823|gb|EFH47245.1| hypothetical protein ARALYDRAFT_487048 [Arabidopsis lyrata subsp. lyrata]	239	228	3.00E−94	95.4	74.5	82.8	hypothetical protein ARALYDRAFT_487048	gbpln	Arabidopsis lyrata	AT5G02740.1 | Symbols: | Ribosomal protein S24e family protein | chr5:616517−618267 FORWARD LENGTH=228	239	228	2.00E−93	95.4	72.4	82.4
Rsa1.0_00178.1.g7654.t1	ref|NP_195893.1| allergen V5/Tpx−1−related family protein [Arabidopsis thaliana] gi|7413548|emb|CAB86027.1| pathogenesis related protein−like [Arabidopsis thaliana] gi|332003127|gb|AED90510.1| allergen V5/Tpx−1−related family protein [Arabidopsis thaliana]	192	205	9.00E−71	106.8	66.1	74.0	allergen V5/Tpx−1−related family protein	gbpln	Arabidopsis thaliana	AT5G02730.1 | Symbols: | CAP (Cysteine−rich secretory proteins, Antigen 5, and Pathogenesis−related 1 protein) superfamily protein | chr5:615610−616227 FORWARD LENGTH=205	192	205	3.00E−73	106.8	66.1	74.0
Rsa1.0_00178.1.g7655.t1	gb|EOA19661.1| hypothetical protein CARUB_v10003262mg [Capsella rubella]	172	227	4.00E−67	132.0	69.8	77.9	hypothetical protein CARUB_v10003262mg	gbpln	Capsella rubella	AT5G02720.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G53490.1); Has 47 Blast hits to 47 proteins in 13 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 47; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr5:613782−614313 REVERSE LENGTH=138	172	138	4.00E−60	80.2	62.8	71.5
Rsa1.0_00178.1.g7656.t1	gb|EOA21455.1| hypothetical protein CARUB_v10001846mg, partial [Capsella rubella]	178	211	4.00E−84	118.5	86.5	91.6	hypothetical protein CARUB_v10001846mg, partial	gbpln	Capsella rubella	AT5G02710.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0153 (InterPro:IPR005358); Has 240 Blast hits to 240 proteins in 73 species: Archae − 10; Bacteria − 110; Metazoa − 0; Fungi − 0; Plants − 25; Viruses − 0; Other Eukaryotes − 95 (source: NCBI BLink). | chr5:612628−613480 FORWARD LENGTH=176	178	176	6.00E−83	98.9	83.7	89.9

Rsa1.0_00178.1.g7657.t1	ref|XP_002873064.1| hypothetical protein ARALYDRAFT_487043 [Arabidopsis lyrata subsp. lyrata] gi|297318901|gb|EFH49323.1| hypothetical protein ARALYDRAFT_487043 [Arabidopsis lyrata subsp. lyrata]	159	158	2.00E-60	99.4	80.5	88.7	hypothetical protein ARALYDRAFT_487043	gbpln	Arabidopsis lyrata	AT5G02640.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G46300.1); Has 37 Blast hits to 37 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:594334-594819 REVERSE LENGTH=161	159	161	3.00E-61	101.3	78.0	86.2
Rsa1.0_00178.1.g7658.t1	dbj|BAE98405.1| ankyrin like protein [Arabidopsis thaliana]	525	524	0	99.8	91.4	96.2	ankyrin like protein	gbpln	Arabidopsis thaliana	AT5G02620.1 | Symbols: ANK1, ATANK1 | ankyrin-like1 | chr5:589666-591536 FORWARD LENGTH=524	525	524	0	99.8	91.6	96.4
Rsa1.0_00178.1.g7659.t1	ref|XP_002870982.1| 60S ribosomal protein L35 [Arabidopsis lyrata subsp. lyrata] gi|297316819|gb|EFH47241.1| 60S ribosomal protein L35 [Arabidopsis lyrata subsp. lyrata]	163	123	6.00E-57	75.5	69.3	73.0	60S ribosomal protein L35	gbpln	Arabidopsis lyrata	AT5G02610.1 | Symbols: | Ribosomal L29 family protein | chr5:587611-588547 FORWARD LENGTH=123	163	123	2.00E-58	75.5	68.7	72.4
Rsa1.0_00178.1.g7660.t2	ref|NP_568105.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|42573253|ref|NP_974723.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|21553967|gb|AAM63048.1| unknown [Arabidopsis thaliana] gi|26449554|dbj|BAC41903.1| unknown protein [Arabidopsis thaliana] gi|30725362|gb|AAP37703.1| At5g02600 [Arabidopsis thaliana] gi|62320791|dbj|BAD93718.1| hypothetical protein [Arabidopsis thaliana] gi|332003112|gb|AED90495.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|332003113|gb|AED90496.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana]	348	319	1.00E-123	91.7	73.6	78.7	heavy metal transport/detoxification domain-containing protein	gbpln	Arabidopsis thaliana	AT5G02600.1 | Symbols: NAKR1 | Heavy metal transport/detoxification superfamily protein | chr5:585713-586855 REVERSE LENGTH=319	348	319	1.00E-126	91.7	73.6	78.7
Rsa1.0_00178.1.g7661.t1	ref|NP_974722.1| uncharacterized protein [Arabidopsis thaliana] gi|332003109|gb|AED90492.1| uncharacterized protein AT5G02580 [Arabidopsis thaliana]	244	66	1.00E-22	27.0	20.1	20.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G02580.2 | Symbols: | Plant protein 1589 of unknown function | chr5:579965-580292 FORWARD LENGTH=66	244	66	4.00E-25	27.0	20.1	20.1
Rsa1.0_00179.1.g7662.t1	ref|XP_002882782.1| hypothetical protein ARALYDRAFT_478618 [Arabidopsis lyrata subsp. lyrata] gi|297328622|gb|EFH59041.1| hypothetical protein ARALYDRAFT_478618 [Arabidopsis lyrata subsp. lyrata]	174	180	1.00E-86	103.4	89.7	94.3	hypothetical protein ARALYDRAFT_478618	gbpln	Arabidopsis lyrata	AT3G12600.1 | Symbols: atnudt16, NUDT16 | nudix hydrolase homolog 16 | chr3:4004809-4005995 FORWARD LENGTH=180	174	180	2.00E-79	103.4	87.9	92.5
Rsa1.0_00179.1.g7663.t1	ref|XP_002884912.1| hypothetical protein ARALYDRAFT_897465 [Arabidopsis lyrata subsp. lyrata] gi|297330752|gb|EFH61171.1| hypothetical protein ARALYDRAFT_897465 [Arabidopsis lyrata subsp. lyrata]	652	650	0	99.7	96.5	98.0	hypothetical protein ARALYDRAFT_897465	gbpln	Arabidopsis lyrata	AT3G12580.1 | Symbols: HSP70, ATHSP70 | heat shock protein 70 | chr3:3991487-3993689 REVERSE LENGTH=650	652	650	0	99.7	96.8	98.3
Rsa1.0_00179.1.g7664.t1	dbj|BAB02264.1| unnamed protein product [Arabidopsis thaliana]	559	572	0	102.3	84.1	90.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G12540.1 | Symbols: | Protein of unknown function, DUF547 | chr3:3975246-3977247 FORWARD LENGTH=505	559	505	0	90.3	77.8	83.0
Rsa1.0_00179.1.g7665.t2	gb|ABB89769.1| At3g12520-like protein [Boechera stricta]	1133	678	0	59.8	51.5	54.5	At3g12520-like protein	gbpln	Boechera stricta	AT3G12520.1 | Symbols: SULTR4;2 | sulfate transporter 4;2 | chr3:3967976-3971891 REVERSE LENGTH=677	1133	677	0	59.8	51.1	55.0
Rsa1.0_00179.1.g7666.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00179.1.g7667.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	189	1311	5.00E-19	693.7	33.3	47.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	189	303	6.00E-16	160.3	32.8	49.7
Rsa1.0_00179.1.g7668.t1	sp|Q9AVB0.1|LECB_PHYAM RecName: Full=Lectin-B; AltName: Full=PL-B; Flags: Precursor gi|13537555|dbj|BAB40792.1| mitogen PL-B [Phytolacca americana]	261	361	3.00E-37	138.3	36.8	48.7	RecName: Full=Lectin-B; AltName: Full=PL-B; Flags: Precursor gi|13537555|dbj|BAB40792.1| mitogen PL-B	gbpln	Phytolacca americana	#	#	#	#	#	#	#
Rsa1.0_00179.1.g7669.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00179.1.g7670.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00179.1.g7671.t1</td><td>ref|NP_176758.1| glutathione S-transferase [Arabidopsis thaliana] gi|25991925|gb|AAN76990.1|AF461148_1 MAPEG-like protein [Arabidopsis thaliana] gi|14517464|gb|AAK62622.1| At1g65820/F1E22_4 [Arabidopsis thaliana] gi|17978909|gb|AAL47424.1| At1g65820/F1E22_4 [Arabidopsis thaliana] gi|21617891|gb|AAM66941.1| glutathione-s-transferase, putative [Arabidopsis thaliana] gi|332196306|gb|AEE34427.1| glutathione S-transferase [Arabidopsis thaliana]</td><td>270</td><td>146</td><td>2.00E-71</td><td>54.1</td><td>47.0</td><td>50.4</td><td>glutathione S-transferase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G65820.1 | Symbols: | microsomal glutathione s-transferase, putative | chr1:24485213-24486682 FORWARD LENGTH=146</td><td>270</td><td>146</td><td>5.00E-74</td><td>54.1</td><td>47.0</td><td>50.4</td></tr>
<tr><td>Rsa1.0_00179.1.g7672.t2</td><td>dbj|BAJ34153.1| unnamed protein product [Thellungiella halophila]</td><td>307</td><td>294</td><td>1.00E-112</td><td>95.8</td><td>78.5</td><td>82.4</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G12480.1 | Symbols: NF-YC11 | nuclear factor Y, subunit C11 | chr3:3958065-3960278 FORWARD LENGTH=293</td><td>307</td><td>293</td><td>1.00E-104</td><td>95.4</td><td>73.3</td><td>80.1</td></tr>
<tr><td>Rsa1.0_00179.1.g7673.t1</td><td>ref|XP_002884901.1| ATELC [Arabidopsis lyrata subsp. lyrata] gi|297330741|gb|EFH61160.1| ATELC [Arabidopsis lyrata subsp. lyrata]</td><td>398</td><td>397</td><td>0</td><td>99.7</td><td>85.7</td><td>91.2</td><td>ATELC</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G12400.1 | Symbols: ELC, ATELC | Ubiquitin-conjugating enzyme/RWD-like protein | chr3:3944600-3945796 REVERSE LENGTH=398</td><td>398</td><td>398</td><td>0</td><td>100.0</td><td>84.9</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00179.1.g7674.t1</td><td>gb|EOA31478.1| hypothetical protein CARUB_v10014664mg [Capsella rubella]</td><td>203</td><td>203</td><td>1.00E-83</td><td>100.0</td><td>91.6</td><td>96.1</td><td>hypothetical protein CARUB_v10014664mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G12390.1 | Symbols: | Nascent polypeptide-associated complex (NAC), alpha subunit family protein | chr3:3942344-3943595 FORWARD LENGTH=203</td><td>203</td><td>203</td><td>1.00E-78</td><td>100.0</td><td>86.2</td><td>91.1</td></tr>
<tr><td>Rsa1.0_00179.1.g7675.t1</td><td>gb|EOA32950.1| hypothetical protein CARUB_v10016278mg [Capsella rubella]</td><td>268</td><td>272</td><td>1.00E-104</td><td>101.5</td><td>82.1</td><td>86.9</td><td>hypothetical protein CARUB_v10016278mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G12320.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G06980.4); Has 102 Blast hits to 102 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 98; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr3:3924034-3925262 FORWARD LENGTH=269</td><td>268</td><td>269</td><td>1.00E-100</td><td>100.4</td><td>79.5</td><td>84.7</td></tr>
<tr><td>Rsa1.0_00179.1.g7676.t2</td><td>gb|AAM62762.1| 5,10-methylenetetrahydrofolate dehydrogenase:5,10-methenyltetrahydrofolate cyclohydrolase, putative [Arabidopsis thaliana]</td><td>508</td><td>299</td><td>1.00E-149</td><td>58.9</td><td>52.2</td><td>54.7</td><td>5,10-methylenetetrahydrofolate dehydrogenase:5,10-methenyltetrahydrofolate cyclohydrolase, putative</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G12290.1 | Symbols: | Amino acid dehydrogenase family protein | chr3:3919591-3921326 FORWARD LENGTH=299</td><td>508</td><td>299</td><td>1.00E-151</td><td>58.9</td><td>52.0</td><td>54.7</td></tr>
<tr><td>Rsa1.0_00179.1.g7677.t1</td><td>ref|XP_002884897.1| hypothetical protein ARALYDRAFT_897441 [Arabidopsis lyrata subsp. lyrata] gi|297330737|gb|EFH61156.1| hypothetical protein ARALYDRAFT_897441 [Arabidopsis lyrata subsp. lyrata]</td><td>132</td><td>190</td><td>6.00E-57</td><td>143.9</td><td>81.8</td><td>83.3</td><td>hypothetical protein ARALYDRAFT_897441</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G12300.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF667 (InterPro:IPR007714); Has 373 Blast hits to 371 proteins in 116 species: Archae - 0; Bacteria - 0; Metazoa - 213; Fungi - 4; Plants - 71; Viruses - 0; Other Eukaryotes - 85 (source: NCBI BLink). | chr3:3921787-3923092 REVERSE LENGTH=190</td><td>132</td><td>190</td><td>5.00E-59</td><td>143.9</td><td>81.1</td><td>83.3</td></tr>
<tr><td>Rsa1.0_00179.1.g7678.t1</td><td>gb|AFJ64573.1| retinoblastoma-related protein 1 [Brassica juncea]</td><td>1021</td><td>1017</td><td>0</td><td>99.6</td><td>86.4</td><td>92.4</td><td>retinoblastoma-related protein 1</td><td>gbpln</td><td>Brassica juncea</td><td>AT3G12280.2 | Symbols: RBR1 | retinoblastoma-related 1 | chr3:3913671-3918433 REVERSE LENGTH=1012</td><td>1021</td><td>1012</td><td>0</td><td>99.1</td><td>82.9</td><td>89.3</td></tr>
<tr><td>Rsa1.0_00179.1.g7679.t1</td><td>ref|NP_187835.2| protein arginine N-methyltransferase 3 [Arabidopsis thaliana] gi|122230175|sp|Q0WVD6.1|ANM3_ARATH RecName: Full=Probable protein arginine N-methyltransferase 3 gi|110741943|dbj|BAE98912.1| hypothetical protein [Arabidopsis thaliana] gi|332641657|gb|AEE75178.1| protein arginine N-methyltransferase 3 [Arabidopsis thaliana]</td><td>585</td><td>601</td><td>0</td><td>102.7</td><td>81.2</td><td>90.4</td><td>protein arginine N-methyltransferase 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G12270.1 | Symbols: ATPRMT3, PRMT3 | protein arginine methyltransferase 3 | chr3:3910642-3913122 FORWARD LENGTH=601</td><td>585</td><td>601</td><td>0</td><td>102.7</td><td>81.2</td><td>90.4</td></tr>
<tr><td>Rsa1.0_00179.1.g7680.t1</td><td>ref|XP_002884895.1| complex 1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297330735|gb|EFH61154.1| complex 1 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>133</td><td>133</td><td>2.00E-70</td><td>100.0</td><td>94.7</td><td>99.2</td><td>complex 1 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G12260.1 | Symbols: | LYR family of Fe/S cluster biogenesis protein | chr3:3909252-3910337 REVERSE LENGTH=133</td><td>133</td><td>133</td><td>2.00E-72</td><td>100.0</td><td>94.0</td><td>98.5</td></tr>
</table>

Rsa1.0_00179.1.g7681.t1	ref|NP_566415.3| transcription factor TGA6 [Arabidopsis thaliana] gi|42572393|ref|NP_974292.1| transcription factor TGA6 [Arabidopsis thaliana] gi|44888355|sp|Q39140.2|TGA6_ARATH RecName: Full=Transcription factor TGA6; AltName: Full=bZIP transcription factor 45; Short=AtbZIP45 gi|12322056|gb|AAG51079.1|AC069472_19 transcription factor HBP-1B-like; 31032-33264 [Arabidopsis thaliana] gi|14571607|emb|CAC42807.1| transcription factor TGA6 [Arabidopsis thaliana] gi|119360085|gb|ABL66771.1| At3g12250 [Arabidopsis thaliana] gi|225898635|dbj|BAH30448.1| hypothetical protein [Arabidopsis thaliana] gi|332641651|gb|AEE75172.1| transcription factor TGA6 [Arabidopsis thaliana] gi|332641652|gb|AEE75173.1| transcription factor TGA6 [Arabidopsis thaliana]	332	330	1.00E-172	99.4	95.2	97.0	transcription factor TGA6	gbpln	Arabidopsis thaliana	AT3G12250.2 | Symbols: TGA6, BZIP45 | TGACG motif-binding factor 6 | chr3:3906351-3908583 FORWARD LENGTH=330	332	330	1.00E-175	99.4	95.2	97.0
Rsa1.0_00179.1.g7682.t3	gb|EOA32081.1| hypothetical protein CARUB_v10015328mg [Capsella rubella]	684	435	1.00E-172	63.6	42.1	49.7	hypothetical protein CARUB_v10015328mg	gbpln	Capsella rubella	AT3G12240.1 | Symbols: SCPL15 | serine carboxypeptidase-like 15 | chr3:3902436-3904918 REVERSE LENGTH=436	684	436	1.00E-168	63.7	41.2	48.7
Rsa1.0_00179.1.g7683.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00179.1.g7684.t1	ref|NP_187823.1| RAB GTPase-like protein A4D [Arabidopsis thaliana] gi|297834018|ref|XP_002884891.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|75334990|sp|Q9LH50.1|RAA4D_ARATH RecName: Full=Ras-related protein RABA4d; Short=AtRABA4d gi|12322042|gb|AAG51065.1|AC069472_5 ras-related GTP-binding protein; 5118-4176 [Arabidopsis thaliana] gi|9294115|dbj|BAB01966.1| GTP-binding protein-like [Arabidopsis thaliana] gi|67633628|gb|AAY78738.1| Ras-related GTP-binding family protein [Arabidopsis thaliana] gi|297330731|gb|EFH61150.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|332641639|gb|AEE75160.1| RAB GTPase-like protein A4D [Arabidopsis thaliana] gi|482567210|gb|EOA31399.1| hypothetical protein CARUB_v10014578mg [Capsella rubella]	222	222	1.00E-126	100.0	98.2	99.5	RAB GTPase-like protein A4D	gbpln	Arabidopsis lyrata	AT3G12160.1 | Symbols: ATRABA4D, RABA4D | RAB GTPase homolog A4D | chr3:3879495-3880437 REVERSE LENGTH=222	222	222	1.00E-128	100.0	98.2	99.5
Rsa1.0_00179.1.g7685.t1	gb|EOA32726.1| hypothetical protein CARUB_v10016030mg, partial [Capsella rubella]	339	465	1.00E-136	137.2	75.2	85.8	hypothetical protein CARUB_v10016030mg, partial	gbpln	Capsella rubella	AT3G11840.1 | Symbols: PUB24 | plant U-box 24 | chr3:3736578-3738250 REVERSE LENGTH=470	339	470	1.00E-134	138.6	73.5	84.1
Rsa1.0_00179.1.g7686.t1	ref|NP_187789.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana] gi|6671939|gb|AAF23199.1|AC016795_12 putative T-complex protein 1, ETA subunit [Arabidopsis thaliana] gi|17979243|gb|AAL49938.1| AT3g11830/F26K24_12 [Arabidopsis thaliana] gi|20857172|gb|AAM26704.1| AT3g11830/F26K24_12 [Arabidopsis thaliana] gi|332641584|gb|AEE75105.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]	547	557	0	101.8	94.3	95.4	TCP-1/cpn60 chaperonin family protein	gbpln	Arabidopsis thaliana	AT3G11830.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:3732734-3736156 FORWARD LENGTH=557	547	557	0	101.8	94.3	95.4
Rsa1.0_00179.1.g7687.t2	ref|XP_002884867.1| SYP121 [Arabidopsis lyrata subsp. lyrata] gi|297330707|gb|EFH61126.1| SYP121 [Arabidopsis lyrata subsp. lyrata]	347	342	1.00E-148	98.6	86.2	89.9	SYP121	gbpln	Arabidopsis lyrata	AT3G11820.1 | Symbols: SYP121, AT-SYR1, ATSYP121, SYR1, ATSYR1, PEN1 | syntaxin of plants 121 | chr3:3729540-3730868 REVERSE LENGTH=346	347	346	1.00E-145	99.7	82.1	85.9

Rsa1.0_00179.1.g7688.t1	gb|EOA31323.1| hypothetical protein CARUB_v10014494mg [Capsella rubella]	245	244	1.00E-127	99.6	90.2	95.9	hypothetical protein CARUB_v10014494mg	gbpln	Capsella rubella	AT3G11800.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G44150.1); Has 74 Blast hits to 73 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 72; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:3726154-3727562 FORWARD LENGTH=246	245	246	1.00E-126	100.4	87.8	95.9
Rsa1.0_00179.1.g7689.t1	gb|EOA29650.1| hypothetical protein CARUB_v10015152mg [Capsella rubella]	151	154	3.00E-67	102.0	84.8	91.4	hypothetical protein CARUB_v10015152mg	gbpln	Capsella rubella	AT3G11780.1 | Symbols: | MD-2-related lipid recognition domain-containing protein / ML domain-containing protein | chr3:3724326-3725476 REVERSE LENGTH=153	151	153	3.00E-69	101.3	84.8	89.4
Rsa1.0_00179.1.g7690.t1	gb|EOA32890.1| hypothetical protein CARUB_v10016206mg [Capsella rubella]	194	194	1.00E-102	100.0	92.3	97.4	hypothetical protein CARUB_v10016206mg	gbpln	Capsella rubella	AT3G11740.1 | Symbols: | Protein of unknown function (DUF567) | chr3:3712427-3713389 FORWARD LENGTH=194	194	194	1.00E-102	100.0	89.2	96.4
Rsa1.0_00179.1.g7691.t2	gb|AAB04618.1| ypt-related protein [Brassica rapa subsp. oleifera]	244	206	1.00E-109	84.4	82.8	83.2	ypt-related protein	gbpln	Brassica rapa	AT3G11730.1 | Symbols: ATFP8, ATRABD1, RABD1 | Ras-related small GTP-binding family protein | chr3:3709490-3711397 REVERSE LENGTH=205	244	205	1.00E-109	84.0	82.0	83.2
Rsa1.0_00179.1.g7692.t4	ref|XP_002884860.1| hypothetical protein ARALYDRAFT_478517 [Arabidopsis lyrata subsp. lyrata] gi|297330700|gb|EFH61119.1| hypothetical protein ARALYDRAFT_478517 [Arabidopsis lyrata subsp. lyrata]	505	545	1.00E-179	107.9	68.5	80.6	hypothetical protein ARALYDRAFT_478517	gbpln	Arabidopsis lyrata	AT3G11720.3 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr3:3705991-3708721 REVERSE LENGTH=596	505	596	0	118.0	68.1	80.6
Rsa1.0_00179.1.g7693.t1	ref|XP_002882740.1| 2-cys peroxiredoxin, chloroplast [Arabidopsis lyrata subsp. lyrata] gi|297328580|gb|EFH58999.1| 2-cys peroxiredoxin, chloroplast [Arabidopsis lyrata subsp. lyrata]	263	266	1.00E-122	101.1	92.4	96.2	2-cys peroxiredoxin, chloroplast	gbpln	Arabidopsis lyrata	AT3G11630.1 | Symbols: | Thioredoxin superfamily protein | chr3:3672189-3673937 FORWARD LENGTH=266	263	266	1.00E-122	101.1	92.0	95.8
Rsa1.0_00179.1.g7694.t1	ref|XP_002884854.1| hypothetical protein ARALYDRAFT_897364 [Arabidopsis lyrata subsp. lyrata] gi|297330694|gb|EFH61113.1| hypothetical protein ARALYDRAFT_897364 [Arabidopsis lyrata subsp. lyrata]	369	312	1.00E-160	84.6	72.1	79.4	hypothetical protein ARALYDRAFT_897364	gbpln	Arabidopsis lyrata	AT3G11620.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:3669551-3671734 REVERSE LENGTH=312	369	312	1.00E-161	84.6	72.1	78.9
Rsa1.0_00179.1.g7695.t1	ref|NP_566393.1| uncharacterized protein [Arabidopsis thaliana] gi|6041814|gb|AAF02129.1|AC009918_1 hypothetical protein [Arabidopsis thaliana] gi|21553924|gb|AAM63007.1| unknown [Arabidopsis thaliana] gi|26450081|dbj|BAC42160.1| unknown protein [Arabidopsis thaliana] gi|28827726|gb|AAO50707.1| unknown protein [Arabidopsis thaliana] gi|332641551|gb|AEE75072.1| uncharacterized protein AT3G11600 [Arabidopsis thaliana]	119	117	1.00E-41	98.3	80.7	86.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G11600.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G06270.1); Has 171 Blast hits to 171 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 171; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3667337-3667690 FORWARD LENGTH=117	119	117	2.00E-44	98.3	80.7	86.6
Rsa1.0_00179.1.g7696.t1	ref|XP_002884852.1| hypothetical protein ARALYDRAFT_897360 [Arabidopsis lyrata subsp. lyrata] gi|297330692|gb|EFH61111.1| hypothetical protein ARALYDRAFT_897360 [Arabidopsis lyrata subsp. lyrata]	236	263	1.00E-102	111.4	83.1	87.3	hypothetical protein ARALYDRAFT_897360	gbpln	Arabidopsis lyrata	AT3G11580.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr3:3649165-3651271 REVERSE LENGTH=267	236	267	1.00E-100	113.1	81.8	85.2
Rsa1.0_00179.1.g7697.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00179.1.g7698.t1	gb|EOA32287.1| hypothetical protein CARUB_v10015549mg [Capsella rubella]	425	423	0	99.5	86.1	92.0	hypothetical protein CARUB_v10015549mg	gbpln	Capsella rubella	AT3G11570.1 | Symbols: TBL8 | TRICHOME BIREFRINGENCE-LIKE 8 | chr3:3645540-3647328 REVERSE LENGTH=427	425	427	0	100.5	87.5	92.9
Rsa1.0_00179.1.g7699.t1	gb|EOA32220.1| hypothetical protein CARUB_v10015479mg [Capsella rubella]	204	204	4.00E-90	100.0	87.7	94.1	hypothetical protein CARUB_v10015479mg	gbpln	Capsella rubella	AT3G11550.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr3:3638262-3639052 FORWARD LENGTH=204	204	204	6.00E-84	100.0	88.2	93.6
Rsa1.0_00179.1.g7700.t1	gb|EOA29834.1| hypothetical protein CARUB_v10012928mg [Capsella rubella]	907	913	0	100.7	94.7	97.6	hypothetical protein CARUB_v10012928mg	gbpln	Capsella rubella	AT3G11540.1 | Symbols: SPY | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:3632842-3637547 FORWARD LENGTH=914	907	914	0	100.8	94.6	97.2
Rsa1.0_00179.1.g7701.t6	gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	335	150	1.00E-80	44.8	44.2	44.5	cytoplasmic ribosomal protein S14	gbpln	Brassica napus	AT3G11510.1 | Symbols: | Ribosomal protein S11 family protein | chr3:3623757-3624866 REVERSE LENGTH=150	335	150	1.00E-74	44.8	39.7	40.9

Rsa1.0_00179.1.g7702.t1	ref|XP_002882839.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328679|gb|EFH59098.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	212	339	2.00E-55	159.9	58.5	72.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G11060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06545.1); Has 12 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3466303-3466944 REVERSE LENGTH=213	212	213	3.00E-54	100.5	53.8	67.9
Rsa1.0_00179.1.g7703.t1	gb|AAP57211.1| methyl transferase [Arabidopsis lyrata subsp. lyrata]	383	380	0	99.2	83.3	92.4	methyl transferase	gbpln	Arabidopsis lyrata	AT3G11480.1 | Symbols: BSMT1, ATBSMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:3614544-3617137 FORWARD LENGTH=379	383	379	0	99.0	82.0	90.9
Rsa1.0_00179.1.g7704.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	647	657	2.33E-156	101.5	42.7	56.0	T14P8.10	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	647	332	2.00E-54	51.3	16.7	24.3
Rsa1.0_00179.1.g7705.t1	ref|NP_187752.2| DnaJ homolog subfamily C member 2 [Arabidopsis thaliana] gi|332641527|gb|AEE75048.1| DnaJ and Myb-like DNA-binding domain-containing protein [Arabidopsis thaliana]	641	647	0	100.9	67.4	79.3	DnaJ homolog subfamily C member 2	gbpln	Arabidopsis thaliana	AT3G11450.1 | Symbols: | DnaJ domain ;Myb-like DNA-binding domain | chr3:3605459-3607402 REVERSE LENGTH=647	641	647	0	100.9	67.4	79.3
Rsa1.0_00179.1.g7706.t1	gb|EOA19642.1| hypothetical protein CARUB_v10003012mg [Capsella rubella]	397	390	4.00E-73	98.2	46.1	59.9	hypothetical protein CARUB_v10003012mg	gbpln	Capsella rubella	AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378	397	378	2.00E-75	95.2	44.8	58.2
Rsa1.0_00179.1.g7707.t1	ref|XP_002882730.1| hypothetical protein ARALYDRAFT_478479 [Arabidopsis lyrata subsp. lyrata] gi|297328570|gb|EFH58989.1| hypothetical protein ARALYDRAFT_478479 [Arabidopsis lyrata subsp. lyrata]	508	505	0	99.4	83.7	89.6	hypothetical protein ARALYDRAFT_478479	gbpln	Arabidopsis lyrata	AT3G11420.1 | Symbols: | Protein of unknown function (DUF604) | chr3:3591834-3594323 FORWARD LENGTH=505	508	505	0	99.4	82.1	89.6
Rsa1.0_00179.1.g7708.t1	ref|NP_187747.1| translation initiation factor eIF-3 subunit 4 [Arabidopsis thaliana] gi|12322907|gb|AAG51445.1|AC008153_18 putative eukaryotic translation initiation factor 3 subunit; 21071-22901 [Arabidopsis thaliana] gi|16226341|gb|AAL16140.1|AF428308_1 AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|9755847|emb|CAC01929.1| translation initiation factor 3, subunit g (eIF3g) [Arabidopsis thaliana] gi|18377870|gb|AAL67121.1| AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|22137220|gb|AAM91455.1| AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|332641520|gb|AEE75041.1| translation initiation factor eIF-3 subunit 4 [Arabidopsis thaliana]	293	294	1.00E-157	100.3	92.8	95.6	translation initiation factor eIF-3 subunit 4	gbpln	Arabidopsis thaliana	AT3G11400.1 | Symbols: EIF3G1, ATEIF3G1 | eukaryotic translation initiation factor 3G1 | chr3:3578536-3580366 FORWARD LENGTH=294	293	294	1.00E-160	100.3	92.8	95.6
Rsa1.0_00179.1.g7709.t1	ref|NP_001189860.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|332641518|gb|AEE75039.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	209	910	1.00E-115	435.4	94.3	96.2	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G11402.2 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:3573516-3577765 FORWARD LENGTH=910	209	910	1.00E-118	435.4	94.3	96.2
Rsa1.0_00179.1.g7710.t1	gb|EOA31992.1| hypothetical protein CARUB_v10015232mg [Capsella rubella]	711	749	0	105.3	56.7	70.3	hypothetical protein CARUB_v10015232mg	gbpln	Capsella rubella	AT3G11380.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:3564079-3565779 FORWARD LENGTH=541	711	541	1.00E-143	76.1	41.8	50.5
Rsa1.0_00179.1.g7711.t1	gb|EOA31992.1| hypothetical protein CARUB_v10015232mg [Capsella rubella]	724	749	0	103.5	56.8	73.1	hypothetical protein CARUB_v10015232mg	gbpln	Capsella rubella	AT3G11380.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:3564079-3565779 FORWARD LENGTH=541	724	541	1.00E-153	74.7	44.6	55.0

Rsa1.0_00179.1.g7712.t1	ref|XP_002882839.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328679|gb|EFH59098.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	393	339	2.00E-44	86.3	24.7	29.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G11060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06545.1); Has 12 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3466303-3466944 REVERSE LENGTH=213	393	213	2.00E-43	54.2	23.4	28.8
Rsa1.0_00179.1.g7713.t1	ref|XP_002864337.1| hypothetical protein ARALYDRAFT_495531 [Arabidopsis lyrata subsp. lyrata] gi|297310172|gb|EFH40596.1| hypothetical protein ARALYDRAFT_495531 [Arabidopsis lyrata subsp. lyrata]	183	204	4.00E-32	111.5	36.6	37.7	hypothetical protein ARALYDRAFT_495531	gbpln	Arabidopsis lyrata	AT5G54500.2 | Symbols: FQR1 | flavodoxin-like quinone reductase 1 | chr5:22124674-22126435 FORWARD LENGTH=244	183	244	3.00E-33	133.3	35.0	36.6
Rsa1.0_00179.1.g7714.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00179.1.g7715.t1	gb|AAG50968.1|AC073395_10 hypothetical protein; 91861-89496 [Arabidopsis thaliana]	537	537	0	100.0	78.2	86.0	hypothetical protein; 91861-89496	gbpln	Arabidopsis thaliana	AT3G11330.1 | Symbols: PIRL9 | plant intracellular ras group-related LRR 9 | chr3:3552330-3554695 REVERSE LENGTH=499	537	499	0	92.9	75.8	83.2
Rsa1.0_00179.1.g7716.t1	ref|NP_187740.2| nucleotide-sugar transporter-like protein [Arabidopsis thaliana] gi|75110965|sp|Q5XF09.1|PT311_ARATH RecName: Full=Probable sugar phosphate/phosphate translocator At3g11320 gi|53828521|gb|AAU94370.1| At3g11320 [Arabidopsis thaliana] gi|110735735|dbj|BAE99847.1| hypothetical protein [Arabidopsis thaliana] gi|332641508|gb|AEE75029.1| probable sugar phosphate/phosphate translocator [Arabidopsis thaliana] gi|385137878|gb|AFI41200.1| putative nucleotide-sugar transporter, partial [Arabidopsis thaliana]	311	308	1.00E-169	99.0	95.8	97.1	nucleotide-sugar transporter-like protein	gbpln	Arabidopsis thaliana	AT3G11320.1 | Symbols: | Nucleotide-sugar transporter family protein | chr3:3547017-3548539 REVERSE LENGTH=308	311	308	1.00E-172	99.0	95.8	97.1
Rsa1.0_00179.1.g7717.t1	ref|NP_001078135.1| yippee-like protein [Arabidopsis thaliana] gi|332641497|gb|AEE75018.1| yippee-like protein [Arabidopsis thaliana]	130	162	3.00E-65	124.6	92.3	95.4	yippee-like protein	gbpln	Arabidopsis thaliana	AT3G11230.2 | Symbols: | Yippee family putative zinc-binding protein | chr3:3516683-3518193 FORWARD LENGTH=162	130	162	7.00E-68	124.6	92.3	95.4
Rsa1.0_00179.1.g7718.t1	gb|EOA17856.1| hypothetical protein CARUB_v10006261mg [Capsella rubella]	505	488	1.00E-117	96.6	46.9	56.4	hypothetical protein CARUB_v10006261mg	gbpln	Capsella rubella	AT3G13590.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:4435316-4437334 REVERSE LENGTH=513	505	513	1.00E-118	101.6	45.3	56.6
Rsa1.0_00179.1.g7719.t1	gb|EOA31316.1| hypothetical protein CARUB_v10014489mg [Capsella rubella]	245	246	1.00E-119	100.4	94.3	97.1	hypothetical protein CARUB_v10014489mg	gbpln	Capsella rubella	AT3G11200.1 | Symbols: AL2 | alfin-like 2 | chr3:3508387-3510418 REVERSE LENGTH=246	245	246	1.00E-114	100.4	93.5	97.1
Rsa1.0_00179.1.g7720.t1	emb|CAB85467.1| chloroplast omega-3 fatty acid desaturase [Brassica juncea]	441	429	0	97.3	95.0	96.4	chloroplast omega-3 fatty acid desaturase	gbpln	Brassica juncea	AT3G11170.1 | Symbols: FAD7, FADD | fatty acid desaturase 7 | chr3:3499959-3502126 FORWARD LENGTH=446	441	446	0	101.1	90.2	93.7
Rsa1.0_00179.1.g7721.t1	ref|XP_002884831.1| hypothetical protein ARALYDRAFT_478454 [Arabidopsis lyrata subsp. lyrata] gi|297330671|gb|EFH61090.1| hypothetical protein ARALYDRAFT_478454 [Arabidopsis lyrata subsp. lyrata]	1724	1702	0	98.7	94.6	95.5	hypothetical protein ARALYDRAFT_478454	gbpln	Arabidopsis lyrata	AT3G11130.1 | Symbols: | Clathrin, heavy chain | chr3:3482575-3491667 REVERSE LENGTH=1705	1724	1705	0	98.9	94.5	95.4
Rsa1.0_00179.1.g7722.t1	gb|EOA24931.1| hypothetical protein CARUB_v10018222mg [Capsella rubella]	134	134	1.00E-37	100.0	59.7	69.4	hypothetical protein CARUB_v10018222mg	gbpln	Capsella rubella	AT5G36910.1 | Symbols: THI2.2 | thionin 2.2 | chr5:14562053-14562673 REVERSE LENGTH=134	134	134	7.00E-38	100.0	55.2	67.9
Rsa1.0_00179.1.g7723.t1	ref|XP_002882716.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297328556|gb|EFH58975.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	160	159	2.00E-60	99.4	75.0	84.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G11110.1 | Symbols: | RING/U-box superfamily protein | chr3:3479979-3480455 FORWARD LENGTH=158	160	158	4.00E-60	98.8	76.3	83.1
Rsa1.0_00179.1.g7724.t1	gb|AAF01520.1|AC009991_16 putative disease resistance protein [Arabidopsis thaliana]	892	957	0	107.3	63.8	75.2	putative disease resistance protein	gbpln	Arabidopsis thaliana	AT3G11080.1 | Symbols: AtRLP35, RLP35 | receptor like protein 35 | chr3:3470481-3473312 FORWARD LENGTH=943	892	943	0	105.7	64.6	75.7

Rsa1.0_00179.1.g7725.t2	ref|NP_187718.1| outer membrane OMP85-like protein [Arabidopsis thaliana] gi|6016688|gb|AAF01515.1|AC009991_11 unknown protein [Arabidopsis thaliana] gi|12321882|gb|AAG50978.1|AC073395_20 unknown protein; 4967-6981 [Arabidopsis thaliana] gi|20466221|gb|AAM20428.1| unknown protein [Arabidopsis thaliana] gi|25084079|gb|AAN72169.1| unknown protein [Arabidopsis thaliana] gi|332641478|gb|AEE74999.1| outer membrane OMP85-like protein [Arabidopsis thaliana]	547	520	0	95.1	78.1	86.7	outer membrane OMP85-like protein	gbpln	Arabidopsis thaliana	AT3G11070.1 | Symbols: | Outer membrane OMP85 family protein | chr3:3467801-3469815 FORWARD LENGTH=520	547	520	0	95.1	78.1	86.7
Rsa1.0_00179.1.g7726.t1	ref|XP_002882712.1| hypothetical protein ARALYDRAFT_317904 [Arabidopsis lyrata subsp. lyrata] gi|297328552|gb|EFH58971.1| hypothetical protein ARALYDRAFT_317904 [Arabidopsis lyrata subsp. lyrata]	356	355	1.00E-123	99.7	62.4	76.1	hypothetical protein ARALYDRAFT_317904	gbpln	Arabidopsis lyrata	AT2G24700.1 | Symbols: | Transcriptional factor B3 family protein | chr2:10513049-10515288 REVERSE LENGTH=555	356	555	3.00E-73	155.9	41.0	59.3
Rsa1.0_00179.1.g7727.t1	ref|XP_002882712.1| hypothetical protein ARALYDRAFT_317904 [Arabidopsis lyrata subsp. lyrata] gi|297328552|gb|EFH58971.1| hypothetical protein ARALYDRAFT_317904 [Arabidopsis lyrata subsp. lyrata]	189	355	8.00E-63	187.8	67.7	78.8	hypothetical protein ARALYDRAFT_317904	gbpln	Arabidopsis lyrata	AT4G31615.1 | Symbols: | Transcriptional factor B3 family protein | chr4:15320297-15322194 REVERSE LENGTH=487	189	487	2.00E-33	257.7	42.9	56.6
Rsa1.0_00179.1.g7728.t1	gb|ABV08790.1| DREB2B [Eutrema halophilum]	346	316	6.00E-90	91.3	60.7	73.1	DREB2B	gbpln	Eutrema halophilum	AT3G11020.1 | Symbols: DREB2B, DREB2 | DRE/CRT-binding protein 2B | chr3:3456009-3457001 FORWARD LENGTH=330	346	330	2.00E-80	95.4	59.2	71.4
Rsa1.0_00179.1.g7729.t1	gb|EOA31502.1| hypothetical protein CARUB_v10014688mg [Capsella rubella]	197	197	9.00E-96	100.0	85.8	91.9	hypothetical protein CARUB_v10014688mg	gbpln	Capsella rubella	AT3G10986.1 | Symbols: | Protein of unknown function (DUF567) | chr3:3444203-3445672 REVERSE LENGTH=197	197	197	1.00E-96	100.0	84.3	92.4
Rsa1.0_00179.1.g7730.t1	gb|EOA32919.1| hypothetical protein CARUB_v10016246mg, partial [Capsella rubella]	214	161	7.00E-75	75.2	65.0	71.0	hypothetical protein CARUB_v10016246mg, partial	gbpln	Capsella rubella	AT3G10985.1 | Symbols: SAG20, WI12, ATWI-12 | senescence associated gene 20 | chr3:3442776-3443108 FORWARD LENGTH=110	214	110	7.00E-43	51.4	43.0	46.3
Rsa1.0_00179.1.g7731.t1	ref|XP_002884818.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330658|gb|EFH61077.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	415	415	0	100.0	74.9	84.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G10890.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr3:3407455-3409000 REVERSE LENGTH=414	415	414	0	99.8	73.3	84.1
Rsa1.0_00179.1.g7732.t1	gb|EOA30817.1| hypothetical protein CARUB_v10013960mg [Capsella rubella]	354	377	1.00E-112	106.5	61.6	73.7	hypothetical protein CARUB_v10013960mg	gbpln	Capsella rubella	AT3G10820.2 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr3:3387358-3390693 FORWARD LENGTH=580	354	580	1.00E-112	163.8	62.1	73.2
Rsa1.0_00179.1.g7733.t1	ref|XP_002884814.1| hypothetical protein ARALYDRAFT_317879 [Arabidopsis lyrata subsp. lyrata] gi|297330654|gb|EFH61073.1| hypothetical protein ARALYDRAFT_317879 [Arabidopsis lyrata subsp. lyrata]	196	698	2.00E-78	356.1	68.9	79.6	hypothetical protein ARALYDRAFT_317879	gbpln	Arabidopsis lyrata	AT3G10815.1 | Symbols: | RING/U-box superfamily protein | chr3:3385009-3385608 REVERSE LENGTH=199	196	199	7.00E-79	101.5	75.0	84.2
Rsa1.0_00180.1.g7734.t1	ref|NP_199643.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|8978336|dbj|BAA98189.1| unnamed protein product [Arabidopsis thaliana] gi|332008268|gb|AED95651.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	682	977	0	143.3	54.3	64.5	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G48320.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:19581794-19584727 REVERSE LENGTH=977	682	977	0	143.3	54.3	64.5
Rsa1.0_00180.1.g7735.t1	ref|XP_002873089.1| hypothetical protein ARALYDRAFT_908205 [Arabidopsis lyrata subsp. lyrata] gi|297318926|gb|EFH49348.1| hypothetical protein ARALYDRAFT_908205 [Arabidopsis lyrata subsp. lyrata]	377	384	1.00E-114	101.9	73.2	80.1	hypothetical protein ARALYDRAFT_908205	gbpln	Arabidopsis lyrata	AT5G03380.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:832400-834301 REVERSE LENGTH=392	377	392	1.00E-115	104.0	73.5	81.2
Rsa1.0_00180.1.g7736.t2	ref|XP_002871033.1| hypothetical protein ARALYDRAFT_487117 [Arabidopsis lyrata subsp. lyrata] gi|297316870|gb|EFH47292.1| hypothetical protein ARALYDRAFT_487117 [Arabidopsis lyrata subsp. lyrata]	1051	636	0	60.5	39.8	46.1	hypothetical protein ARALYDRAFT_487117	gbpln	Arabidopsis lyrata	AT5G03420.1 | Symbols: | 5'-AMP-activated protein kinase-related | chr5:845641-848705 FORWARD LENGTH=598	1051	598	0	56.9	38.1	43.3

Rsa1.0_00180.1.g7737.t1	gb|EOA20483.1| hypothetical protein CARUB_v10000795mg [Capsella rubella]	501	498	0	99.4	91.8	95.6	hypothetical protein CARUB_v10000795mg	gbpln	Capsella rubella	AT5G03430.1 | Symbols: | phosphoadenosine phosphosulfate (PAPS) reductase family protein | chr5:849237-852867 REVERSE LENGTH=497	501	497	0	99.2	91.8	95.6
Rsa1.0_00180.1.g7738.t1	ref|XP_002871035.1| hypothetical protein ARALYDRAFT_487123 [Arabidopsis lyrata subsp. lyrata] gi|297316872|gb|EFH47294.1| hypothetical protein ARALYDRAFT_487123 [Arabidopsis lyrata subsp. lyrata]	112	88	6.00E-16	78.6	43.8	52.7	hypothetical protein ARALYDRAFT_487123	gbpln	Arabidopsis lyrata	AT5G03460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:864391-865509 FORWARD LENGTH=89	112	89	2.00E-18	79.5	43.8	52.7
Rsa1.0_00180.1.g7739.t1	ref|NP_179537.1| casein kinase I-like 5 [Arabidopsis thaliana] gi|4191777|gb|AAD10146.1| putative casein kinase I [Arabidopsis thaliana] gi|20466742|gb|AAM20688.1| putative casein kinase I [Arabidopsis thaliana] gi|21592384|gb|AAM64335.1| putative casein kinase I [Arabidopsis thaliana] gi|30387517|gb|AAP31924.1| At2g19470 [Arabidopsis thaliana] gi|62996980|gb|AAY24534.1| casein kinase 1-like protein 5 [Arabidopsis thaliana] gi|330251790|gb|AEC06884.1| casein kinase I-like 5 [Arabidopsis thaliana]	327	433	1.00E-134	132.4	71.6	78.6	casein kinase I-like 5	gbpln	Arabidopsis thaliana	AT2G19470.1 | Symbols: ckl5 | casein kinase I-like 5 | chr2:8433851-8436295 REVERSE LENGTH=433	327	433	1.00E-136	132.4	71.6	78.6
Rsa1.0_00180.1.g7740.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00180.1.g7741.t1	ref|NP_195971.1| C2H2-type zinc finger protein [Arabidopsis thaliana] gi|7378636|emb|CAB83312.1| putative protein [Arabidopsis thaliana] gi|51971385|dbj|BAD44357.1| unknown protein [Arabidopsis thaliana] gi|225898883|dbj|BAH30572.1| hypothetical protein [Arabidopsis thaliana] gi|332003233|gb|AED90616.1| C2H2-type zinc finger protein [Arabidopsis thaliana]	267	292	1.00E-104	109.4	78.7	86.9	C2H2-type zinc finger protein	gbpln	Arabidopsis thaliana	AT5G03510.1 | Symbols: | C2H2-type zinc finger family protein | chr5:880353-881231 FORWARD LENGTH=292	267	292	1.00E-107	109.4	78.7	86.9
Rsa1.0_00180.1.g7742.t1	gb|EOA22635.1| hypothetical protein CARUB_v10003305mg [Capsella rubella]	211	210	1.00E-111	99.5	95.3	96.2	hypothetical protein CARUB_v10003305mg	gbpln	Capsella rubella	AT5G03530.1 | Symbols: ATRAB ALPHA, ATRAB, ATRAB18B, ATRABC2A, RABC2A | RAB GTPase homolog C2A | chr5:885741-887061 REVERSE LENGTH=210	211	210	1.00E-113	99.5	95.3	96.7
Rsa1.0_00180.1.g7743.t1	gb|AEI26267.1| Exo70A1 [Brassica oleracea var. viridis]	638	638	0	100.0	98.4	99.7	Exo70A1	gbpln	Brassica oleracea	AT5G03540.1 | Symbols: ATEXO70A1, EXO70A1 | exocyst subunit exo70 family protein A1 | chr5:889606-893916 FORWARD LENGTH=638	638	638	0	100.0	94.8	98.1
Rsa1.0_00180.1.g7744.t1	dbj|BAH56827.1| AT5G03545 [Arabidopsis thaliana]	57	67	4.00E-17	117.5	78.9	87.7	AT5G03545	gbpln	Arabidopsis thaliana	AT5G03545.1 | Symbols: AT4, ATIPS2 | Expressed in response to phosphate starvation, this response is enhanced by the presence of IAA. | chr5:895047-895259 FORWARD LENGTH=70	57	70	3.00E-19	122.8	75.4	82.5
Rsa1.0_00180.1.g7745.t1	gb|EOA19909.1| hypothetical protein CARUB_v10000159mg [Capsella rubella]	898	937	0	104.3	86.3	91.8	hypothetical protein CARUB_v10000159mg	gbpln	Capsella rubella	AT5G03640.1 | Symbols: | Protein kinase superfamily protein | chr5:927915-930781 FORWARD LENGTH=926	898	926	0	103.1	85.2	90.3
Rsa1.0_00180.1.g7746.t1	gb|EOA19974.1| hypothetical protein CARUB_v10000235mg [Capsella rubella]	847	822	0	97.0	86.9	91.3	hypothetical protein CARUB_v10000235mg	gbpln	Capsella rubella	AT5G03650.1 | Symbols: SBE2.2 | starch branching enzyme 2.2 | chr5:931924-937470 FORWARD LENGTH=805	847	805	0	95.0	86.4	90.2
Rsa1.0_00180.1.g7747.t1	ref|XP_002871051.1| hypothetical protein ARALYDRAFT_487145 [Arabidopsis lyrata subsp. lyrata] gi|297316888|gb|EFH47310.1| hypothetical protein ARALYDRAFT_487145 [Arabidopsis lyrata subsp. lyrata]	152	173	7.00E-62	113.8	86.8	96.1	hypothetical protein ARALYDRAFT_487145	gbpln	Arabidopsis lyrata	AT5G03660.1 | Symbols: | Family of unknown function (DUF662) | chr5:938068-939811 FORWARD LENGTH=173	152	173	8.00E-63	113.8	85.5	94.7
Rsa1.0_00180.1.g7748.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00180.1.g7749.t2	ref|XP_002871052.1| hypothetical protein ARALYDRAFT_487147 [Arabidopsis lyrata subsp. lyrata] gi|297316889|gb|EFH47311.1| hypothetical protein ARALYDRAFT_487147 [Arabidopsis lyrata subsp. lyrata]	520	516	0	99.2	78.7	85.0	hypothetical protein ARALYDRAFT_487147	gbpln	Arabidopsis lyrata	AT5G03670.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G36420.1); Has 700 Blast hits to 624 proteins in 104 species: Archae - 0; Bacteria - 18; Metazoa - 333; Fungi - 60; Plants - 73; Viruses - 24; Other Eukaryotes - 192 (source: NCBI BLink). | chr5:947311-949898 FORWARD LENGTH=516	520	516	0	99.2	79.2	85.0

Rsa1.0_00180.1.g7750.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	129	1274	5.00E-18	987.6	40.3	54.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	129	303	9.00E-15	234.9	35.7	48.8
Rsa1.0_00180.1.g7751.t1	ref|NP_195988.1| trihelix DNA binding transcription factor [Arabidopsis thaliana] gi|75311735|sp|Q9LZS0.1|PTL_ARATH RecName: Full=Trihelix transcription factor PTL; AltName: Full=Trihelix DNA-binding protein PETAL LOSS gi|7340653|emb|CAB82933.1| GT2-like protein [Arabidopsis thaliana] gi|332003258|gb|AED90641.1| trihelix transcription factor PTLED96690 [Arabidopsis thaliana]	582	591	0	101.5	86.6	90.2	trihelix DNA binding transcription factor	gbpln	Arabidopsis thaliana	AT5G03680.1 | Symbols: PTL | Duplicated homeodomain-like superfamily protein | chr5:957858-960760 FORWARD LENGTH=591	582	591	0	101.5	86.6	90.2
Rsa1.0_00180.1.g7752.t1	ref|NP_195990.1| PAN domain-containing protein [Arabidopsis thaliana] gi|75181333|sp|Q9LZR8.1|Y5370_ARATH RecName: Full=PAN domain-containing protein At5g03700; Flags: Precursor gi|7340655|emb|CAB82935.1| S-receptor kinase-like protein [Arabidopsis thaliana] gi|332003261|gb|AED90644.1| PAN domain-containing protein [Arabidopsis thaliana]	810	482	0	59.5	48.1	51.5	PAN domain-containing protein	gbpln	Arabidopsis thaliana	AT5G03700.1 | Symbols: | D-mannose binding lectin protein with Apple-like carbohydrate-binding domain | chr5:965874-967322 REVERSE LENGTH=482	810	482	0	59.5	48.1	51.5
Rsa1.0_00180.1.g7753.t1	ref|XP_002873110.1| AT-HSFA3 [Arabidopsis lyrata subsp. lyrata] gi|297318947|gb|EFH49369.1| AT-HSFA3 [Arabidopsis lyrata subsp. lyrata]	407	413	0	101.5	85.7	90.7	AT-HSFA3	gbpln	Arabidopsis lyrata	AT5G03720.1 | Symbols: AT-HSFA3, HSFA3 | heat shock transcription factor A3 | chr5:971913-973683 REVERSE LENGTH=412	407	412	0	101.2	83.3	88.7
Rsa1.0_00180.1.g7754.t1	dbj|BAJ34040.1| unnamed protein product [Thellungiella halophila]	828	815	0	98.4	89.9	92.0	unnamed protein product	----	----	AT5G03730.1 | Symbols: CTR1, SIS1, AtCTR1 | Protein kinase superfamily protein | chr5:974958-979660 REVERSE LENGTH=821	828	821	0	99.2	89.1	92.1
Rsa1.0_00180.1.g7755.t1	gb|EOA21229.1| hypothetical protein CARUB_v10001577mg [Capsella rubella]	265	299	6.00E-74	112.8	68.3	79.2	hypothetical protein CARUB_v10001577mg	gbpln	Capsella rubella	AT5G03740.1 | Symbols: HD2C, HDT3 | histone deacetylase 2C | chr5:981994-983961 FORWARD LENGTH=294	265	294	4.00E-74	110.9	69.1	78.5
Rsa1.0_00180.1.g7756.t1	ref|XP_002873112.1| ATCSLA09 [Arabidopsis lyrata subsp. lyrata] gi|297318949|gb|EFH49371.1| ATCSLA09 [Arabidopsis lyrata subsp. lyrata]	305	534	1.00E-172	175.1	95.4	97.7	ATCSLA09	gbpln	Arabidopsis lyrata	AT5G03760.1 | Symbols: ATCSLA09, CSLA09, ATCSLA9, CSLA9, RAT4 | Nucleotide-diphospho-sugar transferases superfamily protein | chr5:985910-990087 REVERSE LENGTH=533	305	533	1.00E-174	174.8	95.7	97.4
Rsa1.0_00181.1.g7757.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00181.1.g7758.t1	ref|NP_188919.1| leucine-rich repeat extensin-like protein 6 [Arabidopsis thaliana] gi|75335502|sp|Q9LUI1.1|LRX6_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 6; Short=AtLRX6; Short=LRR/EXTENSIN6; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor gi|9279698|dbj|BAB01255.1| extensin protein-like [Arabidopsis thaliana] gi|219291096|gb|ACL13984.1| At3g22800 [Arabidopsis thaliana] gi|332643157|gb|AEE76678.1| leucine-rich repeat extensin-like protein 6 [Arabidopsis thaliana]	425	470	0	110.6	75.8	81.2	leucine-rich repeat extensin-like protein 6	gbpln	Arabidopsis thaliana	AT3G22800.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:8063063-8064475 REVERSE LENGTH=470	425	470	0	110.6	75.8	81.2
Rsa1.0_00181.1.g7759.t1	ref|NP_188918.2| kinase interacting KIP1-like protein [Arabidopsis thaliana] gi|9279697|dbj|BAB01254.1| centromere protein [Arabidopsis thaliana] gi|332643156|gb|AEE76677.1| kinase interacting KIP1-like protein [Arabidopsis thaliana]	1715	1728	0	100.8	83.4	91.8	kinase interacting KIP1-like protein	gbpln	Arabidopsis thaliana	AT3G22790.1 | Symbols: | Kinase interacting (KIP1-like) family protein | chr3:8052446-8057888 REVERSE LENGTH=1728	1715	1728	0	100.8	83.4	91.8
Rsa1.0_00181.1.g7760.t3	gb|EOA29996.1| hypothetical protein CARUB_v10013101mg [Capsella rubella]	308	693	1.00E-118	225.0	70.1	75.0	hypothetical protein CARUB_v10013101mg	gbpln	Capsella rubella	AT3G22780.1 | Symbols: TSO1, ATTSO1 | Tesmin/TSO1-like CXC domain-containing protein | chr3:8048927-8052058 FORWARD LENGTH=695	308	695	1.00E-119	225.6	68.5	74.4
Rsa1.0_00181.1.g7761.t1	ref|XP_002883376.1| hypothetical protein ARALYDRAFT_898758 [Arabidopsis lyrata subsp. lyrata] gi|297329216|gb|EFH59635.1| hypothetical protein ARALYDRAFT_898758 [Arabidopsis lyrata subsp. lyrata]	587	623	0	106.1	72.1	81.8	hypothetical protein ARALYDRAFT_898758	gbpln	Arabidopsis lyrata	AT3G22760.1 | Symbols: SOL1 | Tesmin/TSO1-like CXC domain-containing protein | chr3:8044622-8047381 FORWARD LENGTH=609	587	609	0	103.7	68.1	78.7

Rsa1.0_00181.1.g7762.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00181.1.g7763.t1	ref|XP_002885523.1| hypothetical protein ARALYDRAFT_898756 [Arabidopsis lyrata subsp. lyrata] gi|297331363|gb|EFH61782.1| hypothetical protein ARALYDRAFT_898756 [Arabidopsis lyrata subsp. lyrata]	381	378	0	99.2	93.7	97.9	hypothetical protein ARALYDRAFT_898756	gbpln	Arabidopsis lyrata	AT3G22750.1 | Symbols: | Protein kinase superfamily protein | chr3:8037364-8039096 REVERSE LENGTH=378	381	378	0	99.2	92.9	97.4
Rsa1.0_00181.1.g7764.t1	ref|NP_188905.1| putative rRNA-processing protein EBP2-like protein [Arabidopsis thaliana] gi|21362538|sp|Q9LUJ5.1|EBP2_ARATH RecName: Full=Probable rRNA-processing protein EBP2 homolog gi|9279684|dbj|BAB01241.1| nucleolar protein-like [Arabidopsis thaliana] gi|16604529|gb|AAL24270.1| AT3g22660/MWI23_3 [Arabidopsis thaliana] gi|24111281|gb|AAN46764.1| At3g22660/MWI23_3 [Arabidopsis thaliana] gi|332643141|gb|AEE76662.1| putative rRNA-processing protein EBP2-like protein [Arabidopsis thaliana]	298	293	1.00E-135	98.3	84.2	91.3	putative rRNA-processing protein EBP2-like protein	gbpln	Arabidopsis thaliana	AT3G22660.1 | Symbols: | rRNA processing protein-related | chr3:8016237-8017118 REVERSE LENGTH=293	298	293	1.00E-138	98.3	84.2	91.3
Rsa1.0_00181.1.g7765.t1	ref|NP_566714.1| cupin family protein [Arabidopsis thaliana] gi|9279682|dbj|BAB01239.1| unnamed protein product [Arabidopsis thaliana] gi|16604374|gb|AAL24193.1| AT3g22640/MWI23_1 [Arabidopsis thaliana] gi|19699204|gb|AAL90968.1| AT3g22640/MWI23_1 [Arabidopsis thaliana] gi|332643139|gb|AEE76660.1| cupin family protein [Arabidopsis thaliana]	485	486	1.00E-169	100.2	69.1	82.3	cupin family protein	gbpln	Arabidopsis thaliana	AT3G22640.1 | Symbols: PAP85 | cupin family protein | chr3:8011902-8013883 REVERSE LENGTH=486	485	486	1.00E-172	100.2	69.1	82.3
Rsa1.0_00181.1.g7766.t1	ref|XP_002865424.1| hypothetical protein ARALYDRAFT_494656 [Arabidopsis lyrata subsp. lyrata] gi|297311259|gb|EFH41683.1| hypothetical protein ARALYDRAFT_494656 [Arabidopsis lyrata subsp. lyrata]	177	379	2.00E-34	214.1	51.4	65.5	hypothetical protein ARALYDRAFT_494656	gbpln	Arabidopsis lyrata	AT5G43420.1 | Symbols: | RING/U-box superfamily protein | chr5:17451790-17452917 FORWARD LENGTH=375	177	375	9.00E-33	211.9	48.0	62.7
Rsa1.0_00181.1.g7767.t1	ref|XP_002885514.1| hypothetical protein ARALYDRAFT_898737 [Arabidopsis lyrata subsp. lyrata] gi|297331354|gb|EFH61773.1| hypothetical protein ARALYDRAFT_898737 [Arabidopsis lyrata subsp. lyrata]	204	204	1.00E-115	100.0	98.5	100.0	hypothetical protein ARALYDRAFT_898737	gbpln	Arabidopsis lyrata	AT3G22630.1 | Symbols: PBD1, PRCGB | 20S proteasome beta subunit D1 | chr3:8009709-8010774 REVERSE LENGTH=204	204	204	1.00E-116	100.0	97.5	99.5
Rsa1.0_00181.1.g7768.t1	gb|EOA32748.1| hypothetical protein CARUB_v10016053mg [Capsella rubella]	206	203	1.00E-79	98.5	76.2	84.0	hypothetical protein CARUB_v10016053mg	gbpln	Capsella rubella	AT3G22620.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:8008615-8009415 FORWARD LENGTH=203	206	203	1.00E-81	98.5	82.0	89.8
Rsa1.0_00181.1.g7769.t1	gb|EOA22856.1| hypothetical protein CARUB_v10003595mg [Capsella rubella]	135	141	2.00E-43	104.4	74.1	84.4	hypothetical protein CARUB_v10003595mg	gbpln	Capsella rubella	AT4G10910.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:6696933-6697343 FORWARD LENGTH=136	135	136	1.00E-43	100.7	71.9	79.3
Rsa1.0_00181.1.g7770.t1	ref|NP_566712.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|11994292|dbj|BAB01475.1| unnamed protein product [Arabidopsis thaliana] gi|15010698|gb|AAK74008.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] gi|18958062|gb|AAL79604.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] gi|84778474|dbj|BAE73264.1| xylogen like protein 8 [Arabidopsis thaliana] gi|332643136|gb|AEE76657.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	170	170	2.00E-65	100.0	80.6	85.9	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT3G22600.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:8006711-8007397 REVERSE LENGTH=170	170	170	6.00E-68	100.0	80.6	85.9

Rsa1.0_00181.1.g7771.t1	ref|NP_188895.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] gi|11994288|dbj|BAB01471.1| alanine acetyl transferase-like protein [Arabidopsis thaliana] gi|124301058|gb|ABN04781.1| At3g22560 [Arabidopsis thaliana] gi|332643132|gb|AEE76653.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana]	171	175	3.00E-77	102.3	80.7	88.9	GCN5-related N-acetyltransferase (GNAT) family protein	gbpln	Arabidopsis thaliana	AT3G22560.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr3:7998915-7999442 REVERSE LENGTH=175	171	175	1.00E-79	102.3	80.7	88.9
Rsa1.0_00181.1.g7772.t1	gb|EOA31246.1| hypothetical protein CARUB_v10014416mg [Capsella rubella]	262	263	1.00E-112	100.4	83.6	87.0	hypothetical protein CARUB_v10014416mg	gbpln	Capsella rubella	AT3G22550.1 | Symbols: | Protein of unknown function (DUF581) | chr3:7991827-7992805 REVERSE LENGTH=267	262	267	1.00E-112	101.9	83.6	87.4
Rsa1.0_00181.1.g7773.t1	ref|XP_002885507.1| hypothetical protein ARALYDRAFT_479772 [Arabidopsis lyrata subsp. lyrata] gi|297331347|gb|EFH61766.1| hypothetical protein ARALYDRAFT_479772 [Arabidopsis lyrata subsp. lyrata]	159	166	4.00E-62	104.4	83.6	88.1	hypothetical protein ARALYDRAFT_479772	gbpln	Arabidopsis lyrata	AT3G22530.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G14830.1); Has 77 Blast hits to 77 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 77; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7977774-7978370 REVERSE LENGTH=198	159	198	2.00E-63	124.5	84.3	88.1
Rsa1.0_00181.1.g7774.t1	ref|NP_188891.1| uncharacterized protein [Arabidopsis thaliana] gi|11994284|dbj|BAB01467.1| unnamed protein product [Arabidopsis thaliana] gi|17381094|gb|AAL36359.1| unknown protein [Arabidopsis thaliana] gi|20259295|gb|AAM14383.1| unknown protein [Arabidopsis thaliana] gi|332643128|gb|AEE76649.1| uncharacterized protein AT3G22520 [Arabidopsis thaliana]	595	600	0	100.8	80.3	87.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G22520.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast, chloroplast envelope; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G14840.1); Has 717 Blast hits to 703 proteins in 179 species: Archae - 14; Bacteria - 134; Metazoa - 141; Fungi - 74; Plants - 209; Viruses - 0; Other Eukaryotes - 145 (source: NCBI BLink). | chr3:7974984-7977406 FORWARD LENGTH=600	595	600	0	100.8	80.3	87.6
Rsa1.0_00181.1.g7775.t1	ref|XP_002885521.1| hypothetical protein ARALYDRAFT_318995 [Arabidopsis lyrata subsp. lyrata] gi|297331361|gb|EFH61780.1| hypothetical protein ARALYDRAFT_318995 [Arabidopsis lyrata subsp. lyrata]	448	383	5.00E-81	85.5	43.5	53.6	hypothetical protein ARALYDRAFT_318995	gbpln	Arabidopsis lyrata	AT3G22720.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8028961-8030097 REVERSE LENGTH=378	448	378	4.00E-76	84.4	41.1	52.5
Rsa1.0_00181.1.g7776.t1	ref|NP_680377.1| Transcription factor IIS protein [Arabidopsis thaliana] gi|332007413|gb|AED94796.1| Transcription factor IIS protein [Arabidopsis thaliana]	69	233	1.00E-13	337.7	63.8	76.8	Transcription factor IIS protein	gbpln	Arabidopsis thaliana	AT5G42325.1 | Symbols: | Transcription factor IIS protein | chr5:16924102-16924851 REVERSE LENGTH=233	69	233	2.00E-16	337.7	63.8	76.8
Rsa1.0_00181.1.g7777.t1	gb|EOA22909.1| hypothetical protein CARUB_v10003642mg [Capsella rubella]	329	282	1.00E-18	85.7	23.7	32.8	hypothetical protein CARUB_v10003642mg	gbpln	Capsella rubella	AT5G26950.1 | Symbols: AGL93 | AGAMOUS-like 93 | chr5:9483251-9484120 REVERSE LENGTH=289	329	289	3.00E-14	87.8	23.7	32.8
Rsa1.0_00181.1.g7778.t1	ref|NP_181801.1| F-box protein [Arabidopsis thaliana] gi|4512680|gb|AAD21734.1| hypothetical protein [Arabidopsis thaliana] gi|330255067|gb|AEC10161.1| F-box protein [Arabidopsis thaliana]	74	737	2.00E-16	995.9	63.5	74.3	F-box protein	gbpln	Arabidopsis thaliana	AT2G42730.1 | Symbols: | F-box family protein | chr2:17787454-17791218 REVERSE LENGTH=737	74	737	4.00E-19	995.9	63.5	74.3
Rsa1.0_00181.1.g7779.t1	gb|EOA32037.1| hypothetical protein CARUB_v10015281mg [Capsella rubella]	320	323	1.00E-126	100.9	78.1	84.7	hypothetical protein CARUB_v10015281mg	gbpln	Capsella rubella	AT3G22450.1 | Symbols: | Ribosomal L18p/L5e family protein | chr3:7962443-7963378 FORWARD LENGTH=311	320	311	1.00E-117	97.2	76.3	82.8
Rsa1.0_00181.1.g7780.t1	ref|NP_566709.1| FRIGIDA-like protein [Arabidopsis thaliana] gi|9293881|dbj|BAB01784.1| hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|15292673|gb|AAK92705.1| unknown protein [Arabidopsis thaliana] gi|20465585|gb|AAM20275.1| putative hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|21537354|gb|AAM61695.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|332643119|gb|AEE76640.1| FRIGIDA-like protein [Arabidopsis thaliana]	530	532	0	100.4	86.0	89.6	FRIGIDA-like protein	gbpln	Arabidopsis thaliana	AT3G22440.1 | Symbols: | FRIGIDA-like protein | chr3:7959854-7961886 FORWARD LENGTH=532	530	532	0	100.4	86.0	89.6

Rsa1.0_00181.1.g7781.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	143	442	3.00E-32	309.1	51.0	55.9	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	143	343	3.00E-19	239.9	28.7	33.6
Rsa1.0_00181.1.g7782.t1	gb|ABD64940.1| hypothetical protein 24.t00018 [Brassica oleracea]	250	380	3.00E-70	152.0	56.8	67.6	hypothetical protein 24.t00018	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	250	302	4.00E-54	120.8	48.0	65.6
Rsa1.0_00181.1.g7783.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00181.1.g7784.t2	ref|NP_850625.1| Imidazoleglycerol-phosphate dehydratase 1 [Arabidopsis thaliana] gi|462273|sp|P34047.1|HIS7A_ARATH RecName: Full=Imidazoleglycerol-phosphate dehydratase 1; Short=IGPD 1 gi|437213|gb|AAA93196.1| imidazoleglycerolphosphate dehydratase [Arabidopsis thaliana] gi|9293878|dbj|BAB01781.1| imidazoleglycerol-phosphate dehydratase [Arabidopsis thaliana] gi|21593529|gb|AAM65496.1| imidazoleglycerol-phosphate dehydratase [Arabidopsis thaliana] gi|26452644|dbj|BAC43405.1| putative imidazoleglycerolphosphate dehydratase [Arabidopsis thaliana] gi|51971000|dbj|BAD44192.1| imidazoleglycerolphosphate dehydratase [Arabidopsis thaliana] gi|332643116|gb|AEE76637.1| Imidazoleglycerol-phosphate dehydratase 1 [Arabidopsis thaliana]	311	270	1.00E-117	86.8	71.1	75.6	Imidazoleglycerol-phosphate dehydratase 1	gbpln	Arabidopsis thaliana	AT3G22425.2 | Symbols: IGPD | imidazoleglycerol-phosphate dehydratase | chr3:7951110-7952853 FORWARD LENGTH=270	311	270	1.00E-120	86.8	71.1	75.6
Rsa1.0_00182.1.g7785.t4	gb|AAG00239.1|AC002130_4 F1N21.6 [Arabidopsis thaliana]	834	901	0	108.0	51.1	64.1	F1N21.6	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00182.1.g7786.t1	gb|EOA14157.1| hypothetical protein CARUB_v10027303mg [Capsella rubella]	160	152	1.00E-21	95.0	35.6	56.3	hypothetical protein CARUB_v10027303mg	gbpln	Capsella rubella	AT5G33393.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:12656430-12658588 REVERSE LENGTH=435	160	435	1.00E-14	271.9	27.5	36.3
Rsa1.0_00182.1.g7787.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	564	1239	0	219.7	69.0	82.4	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	564	1262	2.00E-96	223.8	31.9	47.9
Rsa1.0_00182.1.g7788.t1	ref|XP_002871454.1| hypothetical protein ARALYDRAFT_487941 [Arabidopsis lyrata subsp. lyrata] gi|297317291|gb|EFH47713.1| hypothetical protein ARALYDRAFT_487941 [Arabidopsis lyrata subsp. lyrata]	208	223	6.00E-68	107.2	73.6	87.5	hypothetical protein ARALYDRAFT_487941	gbpln	Arabidopsis lyrata	AT5G11090.1 | Symbols: | serine-rich protein-related | chr5:3524796-3525449 FORWARD LENGTH=217	208	217	6.00E-70	104.3	73.1	85.1
Rsa1.0_00182.1.g7789.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00182.1.g7790.t1	gb|EOA19862.1| hypothetical protein CARUB_v10000113mg [Capsella rubella]	1041	1049	0	100.8	86.6	92.0	hypothetical protein CARUB_v10000113mg	gbpln	Capsella rubella	AT5G11110.1 | Symbols: SPS1, ATSPS2F, KNS2, SPS2F | sucrose phosphate synthase 2F | chr5:3536426-3540901 FORWARD LENGTH=1047	1041	1047	0	100.6	85.5	91.0
Rsa1.0_00182.1.g7791.t1	ref|NP_197913.4| putative glycosyltransferase [Arabidopsis thaliana] gi|292630776|sp|Q3E7Q9.2|GLYT6_ARATH RecName: Full=Probable glycosyltransferase At5g25310 gi|332006042|gb|AED93425.1| putative glycosyltransferase [Arabidopsis thaliana]	482	480	0	99.6	78.2	87.3	putative glycosyltransferase	gbpln	Arabidopsis thaliana	AT5G25310.1 | Symbols: | Exostosin family protein | chr5:8784820-8787235 FORWARD LENGTH=480	482	480	0	99.6	78.2	87.3
Rsa1.0_00182.1.g7792.t1	ref|NP_197914.1| ACT domain-containing protein [Arabidopsis thaliana] gi|332006043|gb|AED93426.1| ACT domain-containing protein [Arabidopsis thaliana]	498	500	0	100.4	90.2	94.4	ACT domain-containing protein	gbpln	Arabidopsis thaliana	AT5G25320.1 | Symbols: | ACT-like superfamily protein | chr5:8787403-8789530 REVERSE LENGTH=500	498	500	0	100.4	90.2	94.4
Rsa1.0_00182.1.g7793.t1	gb|AAD29058.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1750	1229	0	70.2	28.3	39.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G11590.1 | Symbols: | F-box associated ubiquitination effector family protein | chr4:7008603-7009796 FORWARD LENGTH=397	1750	397	7.00E-61	22.7	8.6	11.4

Rsa1.0_00182.1.g7794.t2	ref|XP_002872157.1| hypothetical protein ARALYDRAFT_489384 [Arabidopsis lyrata subsp. lyrata] gi|297317994|gb|EFH48416.1| hypothetical protein ARALYDRAFT_489384 [Arabidopsis lyrata subsp. lyrata]	343	366	1.00E-166	106.7	84.0	90.4	hypothetical protein ARALYDRAFT_489384	gbpln	Arabidopsis lyrata	AT5G25330.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:8791564-8792664 FORWARD LENGTH=366	343	366	1.00E-166	106.7	83.1	89.2
Rsa1.0_00182.1.g7795.t1	ref|XP_002872158.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317995|gb|EFH48417.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	210	208	2.00E-89	99.0	78.6	84.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G25340.1 | Symbols: | Ubiquitin-like superfamily protein | chr5:8793238-8794211 FORWARD LENGTH=208	210	208	2.00E-91	99.0	78.6	84.3
Rsa1.0_00182.1.g7796.t1	ref|NP_197917.1| EIN3-binding F-box protein 2 [Arabidopsis thaliana] gi|75325708|sp|Q708Y0.1|EBF2_ARATH RecName: Full=EIN3-binding F-box protein 2 gi|38705081|gb|AAR27072.1| EIN3-binding F-box protein 2 [Arabidopsis thaliana] gi|40641627|emb|CAE75865.1| F-box protein [Arabidopsis thaliana] gi|110735710|dbj|BAE99835.1| leucine-rich repeats containing protein [Arabidopsis thaliana] gi|332006046|gb|AED93429.1| EIN3-binding F-box protein 2 [Arabidopsis thaliana]	638	623	0	97.6	81.8	89.8	EIN3-binding F-box protein 2	gbpln	Arabidopsis thaliana	AT5G25350.1 | Symbols: EBF2 | EIN3-binding F box protein 2 | chr5:8794842-8796882 REVERSE LENGTH=623	638	623	0	97.6	81.8	89.8
Rsa1.0_00182.1.g7797.t2	ref|NP_197919.1| phospholipase D zeta [Arabidopsis thaliana] gi|20138932|sp|P58766.1|PLDZ1_ARATH RecName: Full=Phospholipase D zeta; Short=AtPLDzeta; Short=PLD zeta gi|332006049|gb|AED93432.1| phospholipase D zeta [Arabidopsis thaliana]	822	820	0	99.8	87.2	93.7	phospholipase D zeta	gbpln	Arabidopsis thaliana	AT5G25370.1 | Symbols: PLDALPHA3 | phospholipase D alpha 3 | chr5:8804240-8807547 REVERSE LENGTH=820	822	820	0	99.8	87.2	93.7
Rsa1.0_00182.1.g7798.t1	ref|XP_002874259.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320096|gb|EFH50518.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	602	547	0	90.9	78.4	82.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G65550.1 | Symbols: | Xanthine/uracil permease family protein | chr1:24367694-24370800 REVERSE LENGTH=541	602	541	0	89.9	76.9	82.1
Rsa1.0_00182.1.g7799.t1	gb|EOA22417.1| hypothetical protein CARUB_v10003060mg, partial [Capsella rubella]	671	658	0	98.1	89.1	93.4	hypothetical protein CARUB_v10003060mg, partial	gbpln	Capsella rubella	AT5G25430.1 | Symbols: | HCO3-transporter family | chr5:8851251-8854259 FORWARD LENGTH=671	671	671	0	100.0	89.0	93.1
Rsa1.0_00182.1.g7800.t1	ref|NP_197928.1| uncharacterized protein [Arabidopsis thaliana] gi|14423450|gb|AAK62407.1|AF386962_1 Unknown protein [Arabidopsis thaliana] gi|30725566|gb|AAP37805.1| At5g25460 [Arabidopsis thaliana] gi|332006063|gb|AED93446.1| uncharacterized protein AT5G25460 [Arabidopsis thaliana]	367	369	0	100.5	91.8	96.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G25460.1 | Symbols: | Protein of unknown function, DUF642 | chr5:8863430-8865394 FORWARD LENGTH=369	367	369	0	100.5	91.8	96.7
Rsa1.0_00182.1.g7801.t1	gb|AAM62513.1| DNA methyltransferase PMT1-like protein [Arabidopsis thaliana]	403	383	0	95.0	80.6	86.4	DNA methyltransferase PMT1-like protein	gbpln	Arabidopsis thaliana	AT5G25480.1 | Symbols: DNMT2, AtDNMT2 | DNA methyltransferase-2 | chr5:8870069-8872199 REVERSE LENGTH=383	403	383	0	95.0	80.1	86.1
Rsa1.0_00182.1.g7802.t1	ref|NP_197931.1| Ran BP2/NZF zinc finger-like protein [Arabidopsis thaliana] gi|26452848|dbj|BAC43503.1| unknown protein [Arabidopsis thaliana] gi|28973315|gb|AAO63982.1| unknown protein [Arabidopsis thaliana] gi|332006071|gb|AED93454.1| Ran BP2/NZF zinc finger-like protein [Arabidopsis thaliana]	169	170	5.00E-64	100.6	82.8	87.0	Ran BP2/NZF zinc finger-like protein	gbpln	Arabidopsis thaliana	AT5G25490.1 | Symbols: | Ran BP2/NZF zinc finger-like superfamily protein | chr5:8876639-8877339 FORWARD LENGTH=170	169	170	2.00E-66	100.6	82.8	87.0
Rsa1.0_00182.1.g7803.t1	ref|XP_002872168.1| hypothetical protein ARALYDRAFT_910610 [Arabidopsis lyrata subsp. lyrata] gi|297318005|gb|EFH48427.1| hypothetical protein ARALYDRAFT_910610 [Arabidopsis lyrata subsp. lyrata]	414	420	0	101.4	81.9	89.6	hypothetical protein ARALYDRAFT_910610	gbpln	Arabidopsis lyrata	AT5G25500.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8881118-8882380 FORWARD LENGTH=420	414	420	0	101.4	80.2	88.4
Rsa1.0_00182.1.g7804.t1	gb|EOA20475.1| hypothetical protein CARUB_v10000786mg [Capsella rubella]	493	501	0	101.6	86.4	91.7	hypothetical protein CARUB_v10000786mg	gbpln	Capsella rubella	AT5G25510.1 | Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr5:8882728-8884325 REVERSE LENGTH=500	493	500	0	101.4	85.2	89.0
Rsa1.0_00182.1.g7805.t1	gb|EOA19885.1| hypothetical protein CARUB_v10000133mg [Capsella rubella]	1096	1004	0	91.6	63.0	69.8	hypothetical protein CARUB_v10000133mg	gbpln	Capsella rubella	AT5G25520.2 | Symbols: | SPOC domain / Transcription elongation factor S-II protein | chr5:8885550-8889484 FORWARD LENGTH=997	1096	997	0	91.0	61.0	67.7

Rsa1.0_00182.1.g7806.t1	ref|XP_002874268.1| hypothetical protein ARALYDRAFT_910614 [Arabidopsis lyrata subsp. lyrata] gi|297320105|gb|EFH50527.1| hypothetical protein ARALYDRAFT_910614 [Arabidopsis lyrata subsp. lyrata]	175	182	3.00E-48	104.0	69.7	80.0	hypothetical protein ARALYDRAFT_910614	gbpln	Arabidopsis lyrata	AT5G25540.1 | Symbols: CID6 | CTC-interacting domain 6 | chr5:8891770-8892362 REVERSE LENGTH=175	175	175	6.00E-46	100.0	62.3	73.7
Rsa1.0_00182.1.g7807.t1	gb|EOA22854.1| hypothetical protein CARUB_v10003584mg [Capsella rubella]	421	429	0	101.9	80.0	84.6	hypothetical protein CARUB_v10003584mg	gbpln	Capsella rubella	AT5G25550.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:8894179-8895480 FORWARD LENGTH=433	421	433	0	102.9	78.1	83.1
Rsa1.0_00182.1.g7808.t1	ref|NP_568475.1| uncharacterized protein [Arabidopsis thaliana] gi|42573475|ref|NP_974834.1| uncharacterized protein [Arabidopsis thaliana] gi|21592308|gb|AAM64259.1| unknown [Arabidopsis thaliana] gi|94807656|gb|ABF47125.1| At5g25570 [Arabidopsis thaliana] gi|332006083|gb|AED93466.1| uncharacterized protein AT5G25570 [Arabidopsis thaliana] gi|332006084|gb|AED93467.1| uncharacterized protein AT5G25570 [Arabidopsis thaliana]	98	99	4.00E-39	101.0	82.7	92.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G25570.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:8901832-8902891 FORWARD LENGTH=99	98	99	7.00E-42	101.0	82.7	92.9
Rsa1.0_00182.1.g7809.t1	ref|XP_002872175.1| hypothetical protein ARALYDRAFT_489418 [Arabidopsis lyrata subsp. lyrata] gi|297318012|gb|EFH48434.1| hypothetical protein ARALYDRAFT_489418 [Arabidopsis lyrata subsp. lyrata]	421	402	1.00E-151	95.5	71.0	81.2	hypothetical protein ARALYDRAFT_489418	gbpln	Arabidopsis lyrata	AT5G25580.1 | Symbols: | BEST Arabidopsis thaliana protein match is: DDT domain superfamily (TAIR:AT1G18950.1); Has 178 Blast hits to 178 proteins in 75 species: Archae - 0; Bacteria - 4; Metazoa - 51; Fungi - 33; Plants - 60; Viruses - 1; Other Eukaryotes - 29 (source: NCBI BLink). | chr5:8903550-8906108 FORWARD LENGTH=405	421	405	1.00E-149	96.2	68.4	77.7
Rsa1.0_00182.1.g7810.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00182.1.g7811.t1	gb|AAQ57584.1| BURP domain-containing protein [Brassica napus]	387	387	0	100.0	96.9	97.9	BURP domain-containing protein	gbpln	Brassica napus	AT5G25610.1 | Symbols: RD22, ATRD22 | BURP domain-containing protein | chr5:8914498-8916684 REVERSE LENGTH=392	387	392	0	101.3	87.6	92.0
Rsa1.0_00182.1.g7812.t1	gb|EOA33837.1| hypothetical protein CARUB_v10021318mg, partial [Capsella rubella]	134	290	2.00E-20	216.4	43.3	57.5	hypothetical protein CARUB_v10021318mg, partial	gbpln	Capsella rubella	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	134	332	5.00E-15	247.8	29.9	39.6
Rsa1.0_00182.1.g7813.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1027	1213	0	118.1	34.4	50.0	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1027	626	3.00E-65	61.0	14.3	23.0
Rsa1.0_00183.1.g7814.t1	ref|XP_002881770.1| hypothetical protein ARALYDRAFT_903451 [Arabidopsis lyrata subsp. lyrata] gi|297327609|gb|EFH58029.1| hypothetical protein ARALYDRAFT_903451 [Arabidopsis lyrata subsp. lyrata]	198	491	3.00E-86	248.0	91.9	93.9	hypothetical protein ARALYDRAFT_903451	gbpln	Arabidopsis lyrata	AT2G41370.1 | Symbols: BOP2 | Ankyrin repeat family protein / BTB/POZ domain-containing protein | chr2:17238019-17240203 REVERSE LENGTH=491	198	491	3.00E-88	248.0	89.4	91.4
Rsa1.0_00183.1.g7815.t2	ref|XP_002879921.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297325760|gb|EFH56180.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	170	408	6.00E-37	240.0	44.1	53.5	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT2G41330.1 | Symbols: | Glutaredoxin family protein | chr2:17227067-17228275 FORWARD LENGTH=402	170	402	2.00E-38	236.5	43.5	52.4
Rsa1.0_00183.1.g7816.t1	gb|EOA27848.1| hypothetical protein CARUB_v10024006mg [Capsella rubella]	210	225	4.00E-95	107.1	88.1	91.9	hypothetical protein CARUB_v10024006mg	gbpln	Capsella rubella	AT2G41310.1 | Symbols: ATRR3, ARR8, RR3 | response regulator 3 | chr2:17222280-17223536 FORWARD LENGTH=225	210	225	3.00E-95	107.1	89.0	92.9
Rsa1.0_00183.1.g7817.t1	ref|XP_002881767.1| hypothetical protein ARALYDRAFT_321816 [Arabidopsis lyrata subsp. lyrata] gi|297327606|gb|EFH58026.1| hypothetical protein ARALYDRAFT_321816 [Arabidopsis lyrata subsp. lyrata]	369	370	0	100.3	88.1	95.1	hypothetical protein ARALYDRAFT_321816	gbpln	Arabidopsis lyrata	AT2G41300.1 | Symbols: SSL1 | strictosidine synthase-like 1 | chr2:17214312-17216292 REVERSE LENGTH=394	369	394	1.00E-171	106.8	77.0	81.6
Rsa1.0_00183.1.g7818.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	295	255	3.00E-66	86.4	45.4	59.7	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	295	302	8.00E-52	102.4	41.7	60.7
Rsa1.0_00183.1.g7819.t1	ref|XP_002881766.1| hypothetical protein ARALYDRAFT_483200 [Arabidopsis lyrata subsp. lyrata] gi|297327605|gb|EFH58025.1| hypothetical protein ARALYDRAFT_483200 [Arabidopsis lyrata subsp. lyrata]	375	376	0	100.3	83.5	89.9	hypothetical protein ARALYDRAFT_483200	gbpln	Arabidopsis lyrata	AT2G41290.1 | Symbols: SSL2 | strictosidine synthase-like 2 | chr2:17210599-17212904 REVERSE LENGTH=376	375	376	1.00E-180	100.3	81.6	89.6

Rsa1.0_00183.1.g7820.t1	ref|XP_002879917.1| hypothetical protein ARALYDRAFT_903435 [Arabidopsis lyrata subsp. lyrata] gi|297325756|gb|EFH56176.1| hypothetical protein ARALYDRAFT_903435 [Arabidopsis lyrata subsp. lyrata]	246	272	1.00E-15	110.6	43.5	48.4	hypothetical protein ARALYDRAFT_903435	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00183.1.g7821.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00183.1.g7822.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00183.1.g7823.t1	gb|EOA28546.1| hypothetical protein CARUB_v10024770mg [Capsella rubella]	772	772	0	100.0	93.7	96.5	hypothetical protein CARUB_v10024770mg	gbpln	Capsella rubella	AT2G41210.1 | Symbols: PIP5K5 | phosphatidylinositol- 4-phosphate 5-kinase 5 | chr2:17173627-17176575 FORWARD LENGTH=772	772	772	0	100.0	93.4	96.8
Rsa1.0_00183.1.g7824.t1	gb|EOA26862.1| hypothetical protein CARUB_v10022954mg [Capsella rubella]	525	538	0	102.5	84.6	90.1	hypothetical protein CARUB_v10022954mg	gbpln	Capsella rubella	AT2G41190.1 | Symbols: | Transmembrane amino acid transporter family protein | chr2:17167561-17170145 REVERSE LENGTH=536	525	536	0	102.1	84.2	90.5
Rsa1.0_00183.1.g7825.t1	ref|XP_002879913.1| hypothetical protein ARALYDRAFT_483187 [Arabidopsis lyrata subsp. lyrata] gi|297325752|gb|EFH56172.1| hypothetical protein ARALYDRAFT_483187 [Arabidopsis lyrata subsp. lyrata]	140	140	3.00E-55	100.0	81.4	87.1	hypothetical protein ARALYDRAFT_483187	gbpln	Arabidopsis lyrata	AT2G41180.1 | Symbols: | VQ motif-containing protein | chr2:17165242-17165667 FORWARD LENGTH=141	140	141	5.00E-55	100.7	80.0	86.4
Rsa1.0_00183.1.g7826.t2	gb|EOA27338.1| hypothetical protein CARUB_v10023454mg [Capsella rubella]	390	373	1.00E-166	95.6	73.6	82.6	hypothetical protein CARUB_v10023454mg	gbpln	Capsella rubella	AT2G41170.1 | Symbols: | F-box family protein | chr2:17159310-17160845 REVERSE LENGTH=371	390	371	1.00E-164	95.1	75.4	83.1
Rsa1.0_00183.1.g7827.t1	ref|NP_850346.1| Ubiquitin-associated (UBA) protein [Arabidopsis thaliana] gi|19347848|gb|AAL86004.1| unknown protein [Arabidopsis thaliana] gi|22136996|gb|AAM91727.1| unknown protein [Arabidopsis thaliana] gi|330254845|gb|AEC09939.1| Ubiquitin-associated (UBA) protein [Arabidopsis thaliana]	290	287	1.00E-137	99.0	85.2	91.7	Ubiquitin-associated (UBA) protein	gbpln	Arabidopsis thaliana	AT2G41160.1 | Symbols: | Ubiquitin-associated (UBA) protein | chr2:17156314-17158687 REVERSE LENGTH=287	290	287	1.00E-139	99.0	85.2	91.7
Rsa1.0_00183.1.g7828.t1	ref|XP_002879912.1| hypothetical protein ARALYDRAFT_483184 [Arabidopsis lyrata subsp. lyrata] gi|297325751|gb|EFH56171.1| hypothetical protein ARALYDRAFT_483184 [Arabidopsis lyrata subsp. lyrata]	393	405	0	103.1	80.9	89.3	hypothetical protein ARALYDRAFT_483184	gbpln	Arabidopsis lyrata	AT2G41150.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G56750.1); Has 127 Blast hits to 127 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 117; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr2:17153851-17155633 FORWARD LENGTH=404	393	404	0	102.8	79.4	88.0
Rsa1.0_00183.1.g7829.t1	gb|EOA26799.1| hypothetical protein CARUB_v10022894mg [Capsella rubella]	592	576	0	97.3	91.6	93.8	hypothetical protein CARUB_v10022894mg	gbpln	Capsella rubella	AT2G41140.1 | Symbols: CRK1, ATCRK1, ATCBK3 | CDPK-related kinase 1 | chr2:17150492-17153378 FORWARD LENGTH=576	592	576	0	97.3	90.9	93.9
Rsa1.0_00183.1.g7830.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00183.1.g7831.t1	ref|XP_002879910.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297325749|gb|EFH56169.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	253	253	1.00E-117	100.0	93.3	97.2	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT2G41130.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:17143360-17144686 FORWARD LENGTH=253	253	253	1.00E-119	100.0	92.9	97.2
Rsa1.0_00183.1.g7832.t1	gb|EOA26357.1| hypothetical protein CARUB_v10022804mg [Capsella rubella]	690	650	0	94.2	78.4	84.9	hypothetical protein CARUB_v10022804mg	gbpln	Capsella rubella	AT2G41080.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:17132857-17134554 FORWARD LENGTH=565	690	565	0	81.9	69.6	75.2
Rsa1.0_00183.1.g7833.t1	ref|XP_002879906.1| hypothetical protein ARALYDRAFT_483175 [Arabidopsis lyrata subsp. lyrata] gi|297325745|gb|EFH56165.1| hypothetical protein ARALYDRAFT_483175 [Arabidopsis lyrata subsp. lyrata]	280	262	1.00E-110	93.6	78.2	82.9	hypothetical protein ARALYDRAFT_483175	gbpln	Arabidopsis lyrata	AT2G41070.2 | Symbols: EEL, ATBZIP12, DPBF4 | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:17131249-17132208 FORWARD LENGTH=262	280	262	1.00E-111	93.6	78.9	83.2
Rsa1.0_00183.1.g7834.t1	ref|XP_002881756.1| PQ-loop repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297327595|gb|EFH58015.1| PQ-loop repeat family protein [Arabidopsis lyrata subsp. lyrata]	383	380	0	99.2	86.2	91.9	PQ-loop repeat family protein	gbpln	Arabidopsis lyrata	AT2G41050.1 | Symbols: | PQ-loop repeat family protein / transmembrane family protein | chr2:17123388-17125622 REVERSE LENGTH=376	383	376	0	98.2	84.3	89.8

Rsa1.0_00183.1.g7835.t1	ref|NP_181632.5| DHHC-type zinc finger-containing protein [Arabidopsis thaliana] gi|374095470|sp|O80685.3|ZDHC4_ARATH RecName: Full=Probable S-acyltransferase At2g40990; AltName: Full=Probable palmitoyltransferase At2g40990; AltName: Full=Zinc finger DHHC domain-containing protein At2g40990 gi|330254816|gb|AEC09910.1| probable S-acyltransferas [Arabidopsis thaliana]	394	411	1.00E-179	104.3	83.5	89.8	DHHC-type zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT2G40990.1 | Symbols: | DHHC-type zinc finger family protein | chr2:17105097-17106773 REVERSE LENGTH=411	394	411	0	104.3	83.5	89.8
Rsa1.0_00183.1.g7836.t2	gb|AAN72059.1| unknown protein [Arabidopsis thaliana] gi|30725514|gb|AAP37779.1| At2g40980 [Arabidopsis thaliana]	1329	698	0	52.5	45.2	48.8	unknown protein	gbpln	Arabidopsis thaliana	AT2G40980.1 | Symbols: | Protein kinase superfamily protein | chr2:17102090-17104443 FORWARD LENGTH=617	1329	617	0	46.4	32.7	35.3
Rsa1.0_00183.1.g7837.t1	ref|NP_181630.1| myb family transcription factor [Arabidopsis thaliana] gi|2623311|gb|AAB86457.1| unknown protein [Arabidopsis thaliana] gi|18252893|gb|AAL62373.1| unknown protein [Arabidopsis thaliana] gi|20197124|gb|AAM14927.1| unknown protein [Arabidopsis thaliana] gi|23197780|gb|AAN15417.1| unknown protein [Arabidopsis thaliana] gi|330254814|gb|AEC09908.1| myb family transcription factor [Arabidopsis thaliana]	264	248	2.00E-87	93.9	75.8	81.4	myb family transcription factor	gbpln	Arabidopsis thaliana	AT2G40970.1 | Symbols: MYBC1 | Homeodomain-like superfamily protein | chr2:17097772-17098518 REVERSE LENGTH=248	264	248	5.00E-90	93.9	75.8	81.4
Rsa1.0_00184.1.g7838.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00184.1.g7839.t1	ref|NP_564190.1| polyketide cyclase/dehydrase and lipid transport-like protein [Arabidopsis thaliana] gi|2829899|gb|AAC00607.1| similar to ripening-induced protein, gp|AJ001449|2465015 and major#latex protein, gp|X91961|1107495 [Arabidopsis thaliana] gi|14517378|gb|AAK62580.1| At1g23130/T26J12_10 [Arabidopsis thaliana] gi|15450533|gb|AAK96444.1| At1g23130/T26J12_10 [Arabidopsis thaliana] gi|332192222|gb|AEE30343.1| polyketide cyclase/dehydrase and lipid transport-like protein [Arabidopsis thaliana]	161	160	4.00E-52	99.4	60.2	78.3	polyketide cyclase/dehydrase and lipid transport-like protein	gbpln	Arabidopsis thaliana	AT1G23130.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:8200434-8200997 FORWARD LENGTH=160	161	160	1.00E-54	99.4	60.2	78.3
Rsa1.0_00184.1.g7840.t1	gb|AAF98181.1|AC000107_4 F17F8.5 [Arabidopsis thaliana]	389	872	8.00E-46	224.2	27.0	37.8	F17F8.5	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	389	746	4.00E-40	191.8	24.2	33.4
Rsa1.0_00184.1.g7841.t3	ref|NP_173724.2| uncharacterized protein [Arabidopsis thaliana] gi|186478778|ref|NP_001117336.1| uncharacterized protein [Arabidopsis thaliana] gi|186478780|ref|NP_001117337.1| uncharacterized protein [Arabidopsis thaliana] gi|334182781|ref|NP_001185068.1| uncharacterized protein [Arabidopsis thaliana] gi|334182783|ref|NP_001185069.1| uncharacterized protein [Arabidopsis thaliana] gi|49823472|gb|AAT68719.1| hypothetical protein At1g23110 [Arabidopsis thaliana] gi|332192216|gb|AEE30337.1| uncharacterized protein AT1G23110 [Arabidopsis thaliana] gi|332192217|gb|AEE30338.1| uncharacterized protein AT1G23110 [Arabidopsis thaliana] gi|332192218|gb|AEE30339.1| uncharacterized protein AT1G23110 [Arabidopsis thaliana] gi|332192219|gb|AEE30340.1| uncharacterized protein AT1G23110 [Arabidopsis thaliana] gi|332192220|gb|AEE30341.1| uncharacterized protein AT1G23110 [Arabidopsis thaliana]	396	248	1.00E-124	62.6	55.6	57.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23110.4 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G70900.1). | chr1:8196608-8197665 REVERSE LENGTH=248	396	248	1.00E-126	62.6	55.6	57.3

Rsa1.0_00184.1.g7842.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	581	1197	1.00E-122	206.0	46.3	59.4	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	581	575	3.00E-64	99.0	29.4	45.4
Rsa1.0_00184.1.g7843.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00184.1.g7844.t1	gb|EOA39173.1| hypothetical protein CARUB_v10012133mg [Capsella rubella]	631	631	0	100.0	95.6	97.6	hypothetical protein CARUB_v10012133mg	gbpln	Capsella rubella	AT1G23090.1 | Symbols: AST91, SULTR3;3 | sulfate transporter 91 | chr1:8185238-8188954 REVERSE LENGTH=631	631	631	0	100.0	94.3	97.0
Rsa1.0_00184.1.g7845.t1	ref|NP_001077584.1| auxin efflux carrier component 7 [Arabidopsis thaliana] gi|222423080|dbj|BAH19520.1| AT1G23080 [Arabidopsis thaliana] gi|332192213|gb|AEE30334.1| auxin efflux carrier component 7 [Arabidopsis thaliana]	601	615	0	102.3	91.0	94.3	auxin efflux carrier component 7	gbpln	Arabidopsis thaliana	AT1G23080.3 | Symbols: PIN7 | Auxin efflux carrier family protein | chr1:8180768-8183406 REVERSE LENGTH=615	601	615	0	102.3	91.0	94.3
Rsa1.0_00184.1.g7846.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00184.1.g7847.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00184.1.g7848.t1	ref|XP_002893258.1| hypothetical protein ARALYDRAFT_472556 [Arabidopsis lyrata subsp. lyrata] gi|297339100|gb|EFH69517.1| hypothetical protein ARALYDRAFT_472556 [Arabidopsis lyrata subsp. lyrata]	382	364	1.00E-101	95.3	60.7	71.2	hypothetical protein ARALYDRAFT_472556	gbpln	Arabidopsis lyrata	AT1G23060.1 | Symbols: | BEST Arabidopsis thaliana protein match is: TPX2 (targeting protein for Xklp2) protein family (TAIR:AT1G70950.1); Has 449 Blast hits to 419 proteins in 98 species: Archae - 0; Bacteria - 40; Metazoa - 139; Fungi - 21; Plants - 158; Viruses - 3; Other Eukaryotes - 88 (source: NCBI BLink). | chr1:8170946-8172739 REVERSE LENGTH=367	382	367	1.00E-97	96.1	61.0	72.5
Rsa1.0_00184.1.g7849.t1	ref|XP_002867009.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297312845|gb|EFH43268.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	317	376	9.00E-79	118.6	48.6	50.8	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT4G36530.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:17240120-17241770 REVERSE LENGTH=378	317	378	4.00E-76	119.2	47.3	50.2
Rsa1.0_00184.1.g7850.t1	ref|NP_568013.1| uncharacterized protein [Arabidopsis thaliana] gi|11762152|gb|AAG40354.1|AF325002_1 AT4g37020 [Arabidopsis thaliana] gi|110736928|dbj|BAF00421.1| hypothetical protein [Arabidopsis thaliana] gi|332661336|gb|AEE86736.1| uncharacterized protein AT4G37020 [Arabidopsis thaliana]	124	212	1.00E-27	171.0	61.3	69.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G37020.1 | Symbols: | BEST Arabidopsis thaliana protein match is: eukaryotic initiation factor 4A-III (TAIR:AT3G19760.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17445778-17447135 FORWARD LENGTH=212	124	212	2.00E-30	171.0	61.3	69.4
Rsa1.0_00184.1.g7851.t1	ref|NP_001031868.1| 14-3-3-like protein GF14 lambda [Arabidopsis thaliana] gi|332004159|gb|AED91542.1| 14-3-3-like protein GF14 lambda [Arabidopsis thaliana]	137	246	4.00E-18	179.6	32.1	35.0	14-3-3-like protein GF14 lambda	gbpln	Arabidopsis thaliana	AT5G10450.2 | Symbols: GRF6, AFT1, 14-3-3lambda | G-box regulating factor 6 | chr5:3284452-3286261 REVERSE LENGTH=246	137	246	1.00E-20	179.6	32.1	35.0
Rsa1.0_00184.1.g7852.t1	ref|NP_564187.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|2462823|gb|AAB72158.1| unknown [Arabidopsis thaliana] gi|2829907|gb|AAC00615.1| Unknown protein [Arabidopsis thaliana] gi|98960877|gb|ABF58922.1| At1g23040 [Arabidopsis thaliana] gi|110738822|dbj|BAF01334.1| predicted GPI-anchored protein [Arabidopsis thaliana] gi|332192205|gb|AEE30326.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	144	144	1.00E-38	100.0	81.3	86.8	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT1G23040.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:8165025-8165459 FORWARD LENGTH=144	144	144	3.00E-41	100.0	81.3	86.8
Rsa1.0_00184.1.g7853.t1	ref|XP_002890550.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297336392|gb|EFH66809.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	599	612	0	102.2	85.5	92.8	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT1G23030.1 | Symbols: | ARM repeat superfamily protein | chr1:8156745-8158842 FORWARD LENGTH=612	599	612	0	102.2	84.5	91.8
Rsa1.0_00184.1.g7854.t1	gb|ADK47027.1| coronatine insensitive 1 [Brassica rapa subsp. chinensis]	429	596	0	138.9	76.0	83.9	coronatine insensitive 1	gbpln	Brassica rapa	AT2G39940.1 | Symbols: COI1 | RNI-like superfamily protein | chr2:16672848-16675486 REVERSE LENGTH=592	429	592	1.00E-170	138.0	71.1	80.2
Rsa1.0_00184.1.g7855.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1419	1475	0	103.9	59.1	73.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1419	1262	0	88.9	22.1	28.3
Rsa1.0_00184.1.g7856.t5	gb|EOA29164.1| hypothetical protein CARUB_v10025431mg [Capsella rubella]	754	312	1.00E-108	41.4	26.4	31.4	hypothetical protein CARUB_v10025431mg	gbpln	Capsella rubella	AT2G27670.1 | Symbols: | Domain of unknown function DUF220 | chr2:11801568-11802891 REVERSE LENGTH=293	754	293	1.00E-99	38.9	24.8	29.3
Rsa1.0_00184.1.g7857.t1	gb|EOA39878.1| hypothetical protein CARUB_v10008554mg, partial [Capsella rubella]	84	641	1.00E-11	763.1	45.2	51.2	hypothetical protein CARUB_v10008554mg, partial	gbpln	Capsella rubella	AT1G23170.2 | Symbols: | Protein of unknown function DUF2359, transmembrane | chr1:8212724-8215516 FORWARD LENGTH=615	84	615	7.00E-13	732.1	41.7	48.8

Rsa1.0_00184.1.g7858.t1	gb|EOA38639.1| hypothetical protein CARUB_v10010544mg, partial [Capsella rubella]	112	154	2.00E-58	137.5	97.3	99.1	hypothetical protein CARUB_v10010544mg, partial	gbpln	Capsella rubella	AT1G22840.1 | Symbols: CYTC-1, ATCYTC-A | CYTOCHROME C-1 | chr1:8079384-8080286 FORWARD LENGTH=114	112	114	3.00E-59	101.8	94.6	97.3
Rsa1.0_00185.1.g7859.t1	ref|XP_002888096.1| hypothetical protein ARALYDRAFT_475199 [Arabidopsis lyrata subsp. lyrata] gi|297333937|gb|EFH64355.1| hypothetical protein ARALYDRAFT_475199 [Arabidopsis lyrata subsp. lyrata]	425	425	0	100.0	93.6	95.8	hypothetical protein ARALYDRAFT_475199	gbpln	Arabidopsis lyrata	AT1G61240.4 | Symbols: | Protein of unknown function (DUF707) | chr1:22582537-22585050 FORWARD LENGTH=425	425	425	0	100.0	92.5	95.8
Rsa1.0_00185.1.g7860.t1	emb|CAC19877.1| long chain acyl-CoA synthetase [Brassica napus]	131	693	5.00E-46	529.0	68.7	77.9	long chain acyl-CoA synthetase	gbpln	Brassica napus	AT1G77590.1 | Symbols: LACS9 | long chain acyl-CoA synthetase 9 | chr1:29148501-29151776 REVERSE LENGTH=691	131	691	2.00E-38	527.5	54.2	71.0
Rsa1.0_00185.1.g7861.t1	ref|NP_176320.1| secretory carrier-associated membrane protein 3 [Arabidopsis thaliana] gi|75185088|sp|Q9M5P2.1|SCAM3_ARATH RecName: Full=Secretory carrier-associated membrane protein 3; Short=AtSC3; Short=Secretory carrier membrane protein 3 gi|7109228|gb|AAF36686.1|AF225920_1 secretory carrier membrane protein [Arabidopsis thaliana] gi|15027863|gb|AAK76462.1| putative secretory carrier membrane protein [Arabidopsis thaliana] gi|19310673|gb|AAL85067.1| putative secretory carrier membrane protein [Arabidopsis thaliana] gi|21555163|gb|AAM63793.1| secretory carrier membrane protein [Arabidopsis thaliana] gi|332195690|gb|AEE33811.1| secretory carrier-associated membrane protein 3 [Arabidopsis thaliana]	292	289	1.00E-152	99.0	90.4	94.9	secretory carrier-associated membrane protein 3	gbpln	Arabidopsis thaliana	AT1G61250.1 | Symbols: SC3 | secretory carrier 3 | chr1:22586035-22588664 FORWARD LENGTH=289	292	289	1.00E-155	99.0	90.4	94.9
Rsa1.0_00185.1.g7862.t1	ref|NP_176328.1| putative FBD-associated F-box protein [Arabidopsis thaliana] gi|75219848|sp|O64787.1|FBD4_ARATH RecName: Full=Putative FBD-associated F-box protein At1g61330 gi|3056597|gb|AAC13908.1|AAC13908 T1F9.18 [Arabidopsis thaliana] gi|332195700|gb|AEE33821.1| putative FBD-associated F-box protein [Arabidopsis thaliana]	398	447	1.00E-102	112.3	51.8	68.1	putative FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT1G61330.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr1:22622975-22624527 FORWARD LENGTH=447	398	447	1.00E-104	112.3	51.8	68.1
Rsa1.0_00185.1.g7863.t1	ref|XP_002888090.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297333931|gb|EFH64349.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	182	186	1.00E-65	102.2	75.8	86.8	F-box family protein	gbpln	Arabidopsis lyrata	AT1G61340.1 | Symbols: | F-box family protein | chr1:22628526-22629741 FORWARD LENGTH=185	182	185	4.00E-68	101.6	76.4	86.3
Rsa1.0_00185.1.g7864.t2	ref|NP_564775.1| protein S-domain-1 29 [Arabidopsis thaliana] gi|75099194|sp|O64782.1|SD129_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase SD1-29; AltName: Full=S-domain-1 (SD1) receptor kinase 29; Short=SD1-29; Flags: Precursor gi|3056592|gb|AAC13903.1|AAC13903 T1F9.13 [Arabidopsis thaliana] gi|19699075|gb|AAL90905.1| At1g61380/T1F9_13 [Arabidopsis thaliana] gi|23308469|gb|AAN18204.1| At1g61380/T1F9_13 [Arabidopsis thaliana] gi|332195708|gb|AEE33829.1| G-type lectin S-receptor-like serine/threonine-protein kinase SD1-29 [Arabidopsis thaliana]	1306	805	0	61.6	49.1	54.3	protein S-domain-1 29	gbpln	Arabidopsis thaliana	AT1G61380.1 | Symbols: SD1-29 | S-domain-1 29 | chr1:22646277-22649401 REVERSE LENGTH=805	1306	805	0	61.6	49.1	54.3
Rsa1.0_00185.1.g7865.t1	ref|XP_002888077.1| hypothetical protein ARALYDRAFT_475164 [Arabidopsis lyrata subsp. lyrata] gi|297333918|gb|EFH64336.1| hypothetical protein ARALYDRAFT_475164 [Arabidopsis lyrata subsp. lyrata]	417	417	0	100.0	87.3	93.8	hypothetical protein ARALYDRAFT_475164	gbpln	Arabidopsis lyrata	AT1G61630.1 | Symbols: ATENT7, ENT7 | equilibrative nucleoside transporter 7 | chr1:22744207-22746111 FORWARD LENGTH=417	417	417	0	100.0	86.6	93.5
Rsa1.0_00185.1.g7866.t1	ref|XP_002886526.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297332367|gb|EFH62785.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata]	577	619	0	107.3	75.9	87.3	ABC1 family protein	gbpln	Arabidopsis lyrata	AT1G61640.1 | Symbols: | Protein kinase superfamily protein | chr1:22746629-22749053 REVERSE LENGTH=621	577	621	0	107.6	75.0	86.7

Rsa1.0_00185.1.g7867.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	97	1231	5.00E-15	1269.1	50.5	67.0	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00185.1.g7868.t1	dbj|BAB03186.1| En/Spm transposon protein-like [Arabidopsis thaliana]	909	1516	5.00E-79	166.8	21.9	32.6	En/Spm transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00185.1.g7869.t1	ref|NP_564782.1| transcription factor bHLH112 [Arabidopsis thaliana] gi|75306605|sp|Q94JL3.1|BH112_ARATH RecName: Full=Transcription factor bHLH112; AltName: Full=Basic helix-loop-helix protein 112; Short=AtbHLH112; Short=bHLH 112; AltName: Full=Transcription factor EN 64; AltName: Full=bHLH transcription factor bHLH112 gi|14190499|gb|AAK55730.1|AF380649_1 At1g61660/T13M11_21 [Arabidopsis thaliana] gi|21360529|gb|AAM47380.1| At1g61660/T13M11_21 [Arabidopsis thaliana] gi|332195746|gb|AEE33867.1| transcription factor bHLH112 [Arabidopsis thaliana]	534	393	1.00E-167	73.6	57.5	63.1	transcription factor bHLH112	gbpln	Arabidopsis thaliana	AT1G61660.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:22754003-22756171 REVERSE LENGTH=393	534	393	1.00E-170	73.6	57.5	63.1
Rsa1.0_00185.1.g7870.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00185.1.g7871.t1	gb|AAT06463.1| At3g44205 [Arabidopsis thaliana]	92	277	8.00E-13	301.1	37.0	44.6	At3g44205	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00185.1.g7872.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00185.1.g7873.t1	gb|AAM63037.1| unknown [Arabidopsis thaliana]	157	157	1.00E-74	100.0	91.7	95.5	unknown	gbpln	Arabidopsis thaliana	AT1G61667.1 | Symbols: | Protein of unknown function, DUF538 | chr1:22767674-22768269 FORWARD LENGTH=156	157	156	9.00E-77	99.4	86.6	89.8
Rsa1.0_00185.1.g7874.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00185.1.g7875.t1	gb|EOA35046.1| hypothetical protein CARUB_v10020152mg [Capsella rubella]	515	514	0	99.8	84.9	91.5	hypothetical protein CARUB_v10020152mg	gbpln	Capsella rubella	AT1G61670.1 | Symbols: | Lung seven transmembrane receptor family protein | chr1:22770132-22772258 FORWARD LENGTH=513	515	513	0	99.6	83.9	91.7
Rsa1.0_00185.1.g7876.t1	ref|NP_176377.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|3367532|gb|AAC28517.1| Strong similarity to unknown protein T28M21.21 gi|2088661 from A. thaliana BAC gb|AF002109 [Arabidopsis thaliana] gi|332195773|gb|AEE33894.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	624	814	0	130.4	59.0	72.0	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G61840.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:22847389-22849833 FORWARD LENGTH=814	624	814	0	130.4	59.0	72.0
Rsa1.0_00185.1.g7877.t1	ref|NP_176362.3| phosphoinositide binding protein [Arabidopsis thaliana] gi|38564274|gb|AAR23716.1| At1g61690 [Arabidopsis thaliana] gi|62319901|dbj|BAD93965.1| hypothetical protein [Arabidopsis thaliana] gi|332195755|gb|AEE33876.1| phosphoinositide binding protein [Arabidopsis thaliana]	1093	1171	0	107.1	80.2	88.3	phosphoinositide binding protein	gbpln	Arabidopsis thaliana	AT1G61690.1 | Symbols: | phosphoinositide binding | chr1:22782825-22786782 REVERSE LENGTH=1171	1093	1171	0	107.1	80.2	88.3
Rsa1.0_00185.1.g7878.t1	gb|ABK20909.1| unknown [Picea sitchensis] gi|116781551|gb|ABK22149.1| unknown [Picea sitchensis] gi|116789545|gb|ABK25286.1| unknown [Picea sitchensis]	71	71	2.00E-32	100.0	94.4	98.6	unknown	gbpln	Picea sitchensis	AT1G61700.1 | Symbols: | RNA polymerases N / 8 kDa subunit | chr1:22787105-22788112 FORWARD LENGTH=71	71	71	9.00E-35	100.0	91.5	97.2
Rsa1.0_00185.1.g7879.t1	gb|ACY30421.1| C.BANa [Brassica napus]	351	338	1.00E-165	96.3	83.8	90.9	C.BANa	gbpln	Brassica napus	AT1G61720.1 | Symbols: BAN | NAD(P)-binding Rossmann-fold superfamily protein | chr1:22791326-22792757 REVERSE LENGTH=340	351	340	1.00E-144	96.9	74.1	84.0
Rsa1.0_00185.1.g7880.t1	ref|NP_564784.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana] gi|4508074|gb|AAD21418.1| Unknown protein [Arabidopsis thaliana] gi|222424594|dbj|BAH20252.1| AT1G61730 [Arabidopsis thaliana] gi|332195759|gb|AEE33880.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana]	332	376	4.00E-86	113.3	59.6	73.2	DNA-binding storekeeper protein-related transcriptional regulator	gbpln	Arabidopsis thaliana	AT1G61730.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:22793447-22794577 REVERSE LENGTH=376	332	376	1.00E-88	113.3	59.6	73.2

Rsa1.0_00185.1.g7881.t1	ref|NP_176367.1| Sulfite exporter TauE/SafE family protein [Arabidopsis thaliana] gi|13272465|gb|AAK17171.1|AF325103_1 unknown protein [Arabidopsis thaliana] gi|4508075|gb|AAD21419.1| Unknown protein [Arabidopsis thaliana] gi|111074464|gb|ABH04605.1| At1g61740 [Arabidopsis thaliana] gi|332195760|gb|AEE33881.1| Sulfite exporter TauE/SafE family protein [Arabidopsis thaliana]	203	458	6.00E-94	225.6	90.1	95.1	Sulfite exporter TauE/SafE family protein	gbpln	Arabidopsis thaliana	AT1G61740.1 | Symbols: | Sulfite exporter TauE/SafE family protein | chr1:22798365-22801020 REVERSE LENGTH=458	203	458	2.00E-96	225.6	90.1	95.1
Rsa1.0_00186.1.g7882.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00186.1.g7883.t3	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1733	1274	0	73.5	38.8	49.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1733	575	7.00E-55	33.2	9.7	14.4
Rsa1.0_00186.1.g7884.t1	dbj|BAB02844.1| unnamed protein product [Arabidopsis thaliana]	491	565	0	115.1	80.7	89.0	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G21820.1 | Symbols: ATXR2, SDG36 | histone-lysine N-methyltransferase ATXR2 | chr3:7688629-7691444 REVERSE LENGTH=473	491	473	0	96.3	80.7	88.8
Rsa1.0_00186.1.g7885.t1	ref|NP_188815.2| UDP-glucosyl transferase 71B6 [Arabidopsis thaliana] gi|75311545|sp|Q9LSY6.1|U71B6_ARATH RecName: Full=UDP-glycosyltransferase 71B6; AltName: Full=Abscisic acid glycosyltransferase gi|11994645|dbj|BAB02840.1| UTP-glucose glucosyltransferase [Arabidopsis thaliana] gi|332643030|gb|AEE76551.1| UDP-glucosyl transferase 71B6 [Arabidopsis thaliana]	459	479	0	104.4	74.3	83.0	UDP-glucosyl transferase 71B6	gbpln	Arabidopsis thaliana	AT3G21780.1 | Symbols: UGT71B6 | UDP-glucosyl transferase 71B6 | chr3:7675051-7676490 REVERSE LENGTH=479	459	479	0	104.4	74.3	83.0
Rsa1.0_00186.1.g7886.t1	gb|ACT35472.1| peroxidase 30, partial [Brassica rapa]	333	354	0	106.3	95.2	97.0	peroxidase 30, partial	gbpln	Brassica rapa	AT3G21770.1 | Symbols: | Peroxidase superfamily protein | chr3:7673345-7674661 FORWARD LENGTH=329	333	329	1.00E-172	98.8	87.1	91.9
Rsa1.0_00186.1.g7887.t1	ref|XP_002883317.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329157|gb|EFH59576.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	486	485	0	99.8	80.5	89.7	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT3G21760.1 | Symbols: HYR1 | UDP-Glycosyltransferase superfamily protein | chr3:7667099-7668556 FORWARD LENGTH=485	486	485	0	99.8	78.8	89.5
Rsa1.0_00186.1.g7888.t1	gb|EOA33162.1| hypothetical protein CARUB_v100153260mg, partial [Capsella rubella]	208	362	5.00E-65	174.0	54.8	62.0	hypothetical protein CARUB_v100153260mg, partial	gbpln	Capsella rubella	AT3G21750.1 | Symbols: UGT71B1 | UDP-glucosyl transferase 71B1 | chr3:7664565-7665986 FORWARD LENGTH=473	208	473	8.00E-65	227.4	52.4	61.1
Rsa1.0_00186.1.g7889.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00186.1.g7890.t1	ref|XP_002885464.1| hypothetical protein ARALYDRAFT_318914 [Arabidopsis lyrata subsp. lyrata] gi|297331304|gb|EFH61723.1| hypothetical protein ARALYDRAFT_318914 [Arabidopsis lyrata subsp. lyrata]	338	337	1.00E-170	99.7	84.0	92.6	hypothetical protein ARALYDRAFT_318914	gbpln	Arabidopsis lyrata	AT3G21740.1 | Symbols: APO4 | Arabidopsis thaliana protein of unknown function (DUF794) | chr3:7662542-7663638 REVERSE LENGTH=337	338	337	1.00E-169	99.7	81.1	92.3
Rsa1.0_00186.1.g7891.t1	ref|XP_002883316.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329156|gb|EFH59575.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	231	476	4.00E-40	206.1	38.5	51.5	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT3G21750.1 | Symbols: UGT71B1 | UDP-glucosyl transferase 71B1 | chr3:7664565-7665986 FORWARD LENGTH=473	231	473	2.00E-38	204.8	37.2	48.1
Rsa1.0_00186.1.g7892.t1	sp|P25248.1|ACEA_BRANA RecName: Full=Isocitrate lyase; Short=ICL; Short=Isocitrase; Short=Isocitratase gi|167144|gb|AAA32992.1| isocitrate lyase [Brassica napus] gi|255220|gb|AAB23208.1| isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] gi|447142|prf||1913424A isocitrate lyase	565	576	0	101.9	99.5	99.8	RecName: Full=Isocitrate lyase; Short=ICL; Short=Isocitrase; Short=Isocitratase gi|167144|gb|AAA32992.1| isocitrate lyase	gbpln	Brassica napus	AT3G21720.1 | Symbols: ICL | isocitrate lyase | chr3:7652789-7655873 REVERSE LENGTH=576	565	576	0	101.9	95.6	98.4
Rsa1.0_00186.1.g7893.t1	ref|NP_850622.1| Ras-related small GTP-binding family protein [Arabidopsis thaliana] gi|11994637|dbj|BAB02832.1| unnamed protein product [Arabidopsis thaliana] gi|22316556|emb|CAD44270.1| monomeric G-protein [Arabidopsis thaliana] gi|332643018|gb|AEE76539.1| Ras-related small GTP-binding family protein [Arabidopsis thaliana]	286	292	1.00E-133	102.1	89.2	93.7	Ras-related small GTP-binding family protein	gbpln	Arabidopsis thaliana	AT3G21700.3 | Symbols: SGP2 | Ras-related small GTP-binding family protein | chr3:7644581-7646190 FORWARD LENGTH=292	286	292	1.00E-135	102.1	89.2	93.7

Rsa1.0_00186.1.g7894.t1	ref|XP_002883313.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297329153|gb|EFH59572.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	140	506	2.00E-66	361.4	91.4	94.3	mate efflux family protein	gbpln	Arabidopsis lyrata	AT3G21690.1 | Symbols: | MATE efflux family protein | chr3:7638750-7641861 FORWARD LENGTH=506	140	506	3.00E-68	361.4	90.7	93.6
Rsa1.0_00186.1.g7895.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00186.1.g7896.t1	dbj|BAJ34540.1| unnamed protein product [Thellungiella halophila]	323	505	1.00E-156	156.3	90.7	93.5	unnamed protein product	----	----	AT3G21690.1 | Symbols: | MATE efflux family protein | chr3:7638750-7641861 FORWARD LENGTH=506	323	506	1.00E-152	156.7	89.5	92.6
Rsa1.0_00186.1.g7897.t1	ref|NP_188806.1| mate efflux domain-containing protein [Arabidopsis thaliana] gi|11994404|dbj|BAB02363.1| unnamed protein product [Arabidopsis thaliana] gi|51536586|gb|AAU05531.1| At3g21690 [Arabidopsis thaliana] gi|332643017|gb|AEE76538.1| mate efflux domain-containing protein [Arabidopsis thaliana]	188	506	1.00E-93	269.1	89.9	94.7	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT3G21690.1 | Symbols: | MATE efflux family protein | chr3:7638750-7641861 FORWARD LENGTH=506	188	506	5.00E-96	269.1	89.9	94.7
Rsa1.0_00186.1.g7898.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00186.1.g7899.t2	gb|AAD08951.1| putative reverse transcriptase [Arabidopsis thaliana] gi|20197043|gb|AAM14892.1| putative reverse transcriptase [Arabidopsis thaliana]	397	1412	4.00E-47	355.7	28.2	40.6	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	397	746	1.00E-35	187.9	18.4	21.2
Rsa1.0_00186.1.g7900.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00186.1.g7901.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00186.1.g7902.t1	gb|EOA30183.1| hypothetical protein CARUB_v10013300mg [Capsella rubella]	589	589	0	100.0	90.0	95.1	hypothetical protein CARUB_v10013300mg	gbpln	Capsella rubella	AT3G21670.1 | Symbols: | Major facilitator superfamily protein | chr3:7626942-7628954 REVERSE LENGTH=590	589	590	0	100.2	91.2	95.2
Rsa1.0_00186.1.g7903.t1	ref|XP_002885457.1| protein phosphatase 2A B [Arabidopsis lyrata subsp. lyrata] gi|297331297|gb|EFH61716.1| protein phosphatase 2A B [Arabidopsis lyrata subsp. lyrata]	506	542	0	107.1	89.3	93.5	protein phosphatase 2A B	gbpln	Arabidopsis lyrata	AT3G21650.1 | Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr3:7621680-7623412 REVERSE LENGTH=546	506	546	0	107.9	87.9	92.7
Rsa1.0_00187.1.g7904.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7905.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7906.t2	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	772	498	3.00E-73	64.5	24.0	32.6	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	772	336	2.00E-24	43.5	8.4	12.6
Rsa1.0_00187.1.g7907.t1	gb|EOA19880.1| hypothetical protein CARUB_v10000130mg [Capsella rubella] gi|482555689|gb|EOA19881.1| hypothetical protein CARUB_v10000130mg [Capsella rubella]	1009	1009	0	100.0	80.9	88.9	hypothetical protein CARUB_v10000130mg	gbpln	Capsella rubella	AT4G00700.1 | Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr4:286260-289369 FORWARD LENGTH=1006	1009	1006	0	99.7	79.6	88.4
Rsa1.0_00187.1.g7908.t1	ref|XP_002875018.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320855|gb|EFH51277.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	491	490	0	99.8	93.7	97.8	kinase family protein	gbpln	Arabidopsis lyrata	AT4G00710.1 | Symbols: BSK3 | BR-signaling kinase 3 | chr4:290807-293096 FORWARD LENGTH=489	491	489	0	99.6	92.1	96.3
Rsa1.0_00187.1.g7909.t1	sp|O04160.2|KSGT_BRANA RecName: Full=Shaggy-related protein kinase theta; AltName: Full=ASK-theta gi|2569950|emb|CAA73214.1| shaggy-like protein kinase tetha [Brassica napus]	474	468	0	98.7	93.2	96.0	RecName: Full=Shaggy-related protein kinase theta; AltName: Full=ASK-theta gi|2569950|emb|CAA73214.1| shaggy-like protein kinase tetha	gbpln	Brassica napus	AT4G00720.1 | Symbols: ATSK32, ASKTHETA, SK32 | shaggy-like protein kinase 32 | chr4:294116-297002 REVERSE LENGTH=472	474	472	0	99.6	90.9	93.5
Rsa1.0_00187.1.g7910.t1	dbj|BAJ34339.1| unnamed protein product [Thellungiella halophila]	823	795	0	96.6	86.5	90.0	unnamed protein product	----	----	AT4G00730.1 | Symbols: ANL2, AHDP | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr4:299741-304103 REVERSE LENGTH=802	823	802	0	97.4	85.8	90.2
Rsa1.0_00187.1.g7911.t1	ref|XP_002872931.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318768|gb|EFH49190.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	457	470	0	102.8	77.7	86.2	UBX domain-containing protein	gbpln	Arabidopsis lyrata	AT4G00752.1 | Symbols: | UBX domain-containing protein | chr4:317771-320793 REVERSE LENGTH=469	457	469	0	102.6	76.8	86.0

Rsa1.0_00187.1.g7912.t1	gb|AAC26240.1| contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]	370	1322	2.00E-16	357.3	19.7	28.1	contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7913.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7914.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7915.t1	ref|XP_002872909.1| hypothetical protein ARALYDRAFT_490459 [Arabidopsis lyrata subsp. lyrata] gi|297318746|gb|EFH49168.1| hypothetical protein ARALYDRAFT_490459 [Arabidopsis lyrata subsp. lyrata]	259	259	1.00E-105	100.0	76.1	85.7	hypothetical protein ARALYDRAFT_490459	gbpln	Arabidopsis lyrata	AT4G01110.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G01453.1); Has 273 Blast hits to 272 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 273; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:480176-481056 REVERSE LENGTH=261	259	261	1.00E-105	100.8	75.7	84.9
Rsa1.0_00187.1.g7916.t1	gb|EOA20942.1| hypothetical protein CARUB_v10001278mg [Capsella rubella]	353	355	0	100.6	98.6	99.4	hypothetical protein CARUB_v10001278mg	gbpln	Capsella rubella	AT4G01100.1 | Symbols: ADNT1 | adenine nucleotide transporter 1 | chr4:477411-479590 FORWARD LENGTH=352	353	352	0	99.7	94.1	97.5
Rsa1.0_00187.1.g7917.t1	ref|NP_192018.1| uncharacterized protein [Arabidopsis thaliana] gi|7267606|emb|CAB80918.1| hypothetical protein [Arabidopsis thaliana] gi|17979014|gb|AAL47466.1| AT4g01090/F2N1_13 [Arabidopsis thaliana] gi|20334762|gb|AAM16242.1| AT4g01090/F2N1_13 [Arabidopsis thaliana] gi|222424660|dbj|BAH20284.1| AT4G01090 [Arabidopsis thaliana] gi|332656580|gb|AEE81980.1| uncharacterized protein AT4G01090 [Arabidopsis thaliana]	594	714	0	120.2	74.9	82.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G01090.1 | Symbols: | Protein of unknown function (DUF3133) | chr4:470834-473248 REVERSE LENGTH=714	594	714	0	120.2	74.9	82.5
Rsa1.0_00187.1.g7918.t1	dbj|BAJ34074.1| unnamed protein product [Thellungiella halophila]	481	480	0	99.8	82.7	89.4	unnamed protein product	----	----	AT4G01070.1 | Symbols: GT72B1, UGT72B1 | UDP-Glycosyltransferase superfamily protein | chr4:461858-463300 REVERSE LENGTH=480	481	480	0	99.8	78.6	87.9
Rsa1.0_00187.1.g7919.t2	ref|XP_002874998.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297320835|gb|EFH51257.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	165	79	4.00E-24	47.9	33.3	38.2	myb family transcription factor	gbpln	Arabidopsis lyrata	AT4G01060.2 | Symbols: ETC3, CPL3 | CAPRICE-like MYB3 | chr4:460534-460967 FORWARD LENGTH=74	165	74	1.00E-25	44.8	32.7	37.0
Rsa1.0_00187.1.g7920.t6	ref|NP_192013.1| glycosyl hydrolase family 18 protein [Arabidopsis thaliana] gi|7267601|emb|CAB80913.1| hypothetical protein [Arabidopsis thaliana] gi|332656572|gb|AEE81972.1| glycosyl hydrolase family 18 protein [Arabidopsis thaliana]	426	430	0	100.9	86.2	92.0	glycosyl hydrolase family 18 protein	gbpln	Arabidopsis thaliana	AT4G01040.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr4:453383-455407 FORWARD LENGTH=430	426	430	0	100.9	86.2	92.0
Rsa1.0_00187.1.g7921.t1	dbj|BAJ34300.1| unnamed protein product [Thellungiella halophila]	193	192	7.00E-98	99.5	88.6	93.8	unnamed protein product	----	----	AT4G01026.1 | Symbols: PYL7, RCAR2 | PYR1-like 7 | chr4:447180-448109 FORWARD LENGTH=211	193	211	7.00E-97	109.3	86.0	90.7
Rsa1.0_00187.1.g7922.t2	gb|EOA20065.1| hypothetical protein CARUB_v10000339mg [Capsella rubella]	330	710	1.00E-126	215.2	66.7	74.2	hypothetical protein CARUB_v10000339mg	gbpln	Capsella rubella	AT4G01010.1 | Symbols: ATCNGC13, CNGC13 | cyclic nucleotide-gated channel 13 | chr4:434569-437242 REVERSE LENGTH=696	330	696	1.00E-123	210.9	66.1	72.1
Rsa1.0_00187.1.g7923.t1	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	607	1250	0	205.9	55.4	66.4	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	607	1262	3.00E-89	207.9	26.9	42.3
Rsa1.0_00187.1.g7924.t1	pir||T10541 cyclic nucleotide gated channel homolog F3I3.30 - Arabidopsis thaliana	423	698	0	165.0	91.7	94.3	cyclic nucleotide gated channel homolog F3I3.30 - Arabidopsis thaliana	----	----	AT4G01010.1 | Symbols: ATCNGC13, CNGC13 | cyclic nucleotide-gated channel 13 | chr4:434569-437242 REVERSE LENGTH=696	423	696	0	164.5	91.7	94.3
Rsa1.0_00187.1.g7925.t1	dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	219	1098	5.00E-27	501.4	30.1	40.2	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7926.t5	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7927.t1	gb|EOA19940.1| hypothetical protein CARUB_v10000192mg [Capsella rubella]	419	876	3.00E-55	209.1	29.4	34.8	hypothetical protein CARUB_v10000192mg	gbpln	Capsella rubella	AT4G00990.1 | Symbols: | Transcription factor jumonji (jmjC) domain-containing protein | chr4:427035-431535 FORWARD LENGTH=840	419	840	2.00E-53	200.5	23.4	27.7
Rsa1.0_00187.1.g7928.t2	ref|XP_002875004.1| transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297320841|gb|EFH51263.1| transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata]	865	841	0	97.2	60.6	70.5	transcription factor jumonji domain-containing protein	gbpln	Arabidopsis lyrata	AT4G00990.1 | Symbols: | Transcription factor jumonji (jmjC) domain-containing protein | chr4:427035-431535 FORWARD LENGTH=840	865	840	0	97.1	59.7	69.9

Rsa1.0_00187.1.g7929.t1	gb|EOA19940.1| hypothetical protein CARUB_v10000192mg [Capsella rubella]	856	876	0	102.3	63.3	75.0	hypothetical protein CARUB_v10000192mg	gbpln	Capsella rubella	AT4G00990.1 | Symbols: | Transcription factor jumonji (jmjC) domain-containing protein | chr4:427035-431535 FORWARD LENGTH=840	856	840	0	98.1	45.4	52.1
Rsa1.0_00187.1.g7930.t1	ref|XP_002872891.1| GAMMA-TIP3/TIP1_3 [Arabidopsis lyrata subsp. lyrata] gi|297318728|gb|EFH49150.1| GAMMA-TIP3/TIP1_3 [Arabidopsis lyrata subsp. lyrata]	252	252	1.00E-130	100.0	94.8	97.2	GAMMA-TIP3/TIP1_3	gbpln	Arabidopsis lyrata	AT4G01470.1 | Symbols: GAMMA-TIP3, TIP1;3, ATTIP1.3 | tonoplast intrinsic protein 1;3 | chr4:625092-625850 REVERSE LENGTH=252	252	252	1.00E-131	100.0	94.4	96.8
Rsa1.0_00187.1.g7931.t1	dbj|BAF00422.1| hypothetical protein [Arabidopsis thaliana]	149	95	1.00E-11	63.8	24.2	27.5	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7932.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00187.1.g7933.t1	gb|EOA20915.1| hypothetical protein CARUB_v10001250mg [Capsella rubella]	391	360	1.00E-138	92.1	60.6	68.3	hypothetical protein CARUB_v10001250mg	gbpln	Capsella rubella	AT4G01450.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:608586-610487 FORWARD LENGTH=343	391	343	1.00E-137	87.7	61.4	68.5
Rsa1.0_00187.1.g7934.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00188.1.g7935.t1	ref|NP_567802.1| putative wound-responsive protein [Arabidopsis thaliana] gi|297799150|ref|XP_002867459.1| hypothetical protein ARALYDRAFT_491951 [Arabidopsis lyrata subsp. lyrata] gi|15215820|gb|AAK91455.1| AT4g28240/F26K10_120 [Arabidopsis thaliana] gi|21554087|gb|AAM63168.1| putative wound induced protein [Arabidopsis thaliana] gi|22530932|gb|AAM96970.1| putative wound-induced protein [Arabidopsis thaliana] gi|297313295|gb|EFH43718.1| hypothetical protein ARALYDRAFT_491951 [Arabidopsis lyrata subsp. lyrata] gi|332660057|gb|AEE85457.1| putative wound-responsive protein [Arabidopsis thaliana]	86	86	2.00E-35	100.0	82.6	95.3	putative wound-responsive protein	gbpln	Arabidopsis lyrata	AT4G28240.1 | Symbols: | Wound-responsive family protein | chr4:13997979-13998239 REVERSE LENGTH=86	86	86	3.00E-38	100.0	82.6	95.3
Rsa1.0_00188.1.g7936.t1	gb|EOA15467.1| hypothetical protein CARUB_v10004327mg [Capsella rubella]	656	653	0	99.5	78.7	88.6	hypothetical protein CARUB_v10004327mg	gbpln	Capsella rubella	AT4G28200.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: RNA processing; LOCATED IN: intracellular; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: RNA-processing protein, HAT helix (InterPro:IPR003107), U3 small nucleolar RNA-associated protein 6 (InterPro:IPR013949); Has 492 Blast hits to 480 proteins in 206 species: Archae - 0; Bacteria - 2; Metazoa - 128; Fungi - 191; Plants - 60; Viruses - 0; Other Eukaryotes - 111 (source: NCBI BLink). | chr4:13987808-13990422 REVERSE LENGTH=648	656	648	0	98.8	76.8	86.6
Rsa1.0_00188.1.g7937.t1	ref|XP_002867464.1| hypothetical protein ARALYDRAFT_491962 [Arabidopsis lyrata subsp. lyrata] gi|297313300|gb|EFH43723.1| hypothetical protein ARALYDRAFT_491962 [Arabidopsis lyrata subsp. lyrata]	287	278	1.00E-106	96.9	76.0	83.3	hypothetical protein ARALYDRAFT_491962	gbpln	Arabidopsis lyrata	AT4G28140.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:13974905-13975783 REVERSE LENGTH=292	287	292	1.00E-109	101.7	75.3	82.2
Rsa1.0_00188.1.g7938.t1	ref|NP_194537.7| tetratricopeptide repeat domain protein [Arabidopsis thaliana] gi|332660036|gb|AEE85436.1| tetratricopeptide repeat domain protein [Arabidopsis thaliana]	1756	1819	0	103.6	83.8	89.2	tetratricopeptide repeat domain protein	gbpln	Arabidopsis thaliana	AT4G28080.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:13948993-13957840 REVERSE LENGTH=1819	1756	1819	0	103.6	83.8	89.2
Rsa1.0_00188.1.g7939.t1	ref|XP_002869522.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297315358|gb|EFH45781.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	322	359	1.00E-150	111.5	82.3	89.1	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT4G28040.5 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:13940881-13942201 FORWARD LENGTH=359	322	359	1.00E-151	111.5	81.4	89.1

Rsa1.0_00188.1.g7940.t2	ref|NP_194533.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|42573063|ref|NP_974628.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|79325295|ref|NP_001031735.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|79325300|ref|NP_001031736.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|186514305|ref|NP_001119071.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75208263|sp|Q9SUD5.1|WTR36_ARATH RecName: Full=WAT1-related protein At4g28040 gi|13899061|gb|AAK48952.1|AF370525_1 Medicago nodulin N21-like protein [Arabidopsis thaliana] gi|4455363|emb|CAB36773.1| Medicago nodulin N21-like protein [Arabidopsis thaliana] gi|7269658|emb|CAB79606.1| Medicago nodulin N21-like protein [Arabidopsis thaliana] gi|20148375|gb|AAM10078.1| Medicago nodulin N21-like protein [Arabidopsis thaliana] gi|222424181|dbj|BAH20049.1| AT4G28040 [Arabidopsis thaliana] gi|332660026|gb|AEE85426.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]	238	359	5.00E-50	150.8	41.2	45.0	nodulin MtN21 /EamA-like transporter family protein	gbpln	Arabidopsis thaliana	AT4G28040.5 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:13940881-13942201 FORWARD LENGTH=359	238	359	2.00E-52	150.8	41.2	45.0
Rsa1.0_00188.1.g7941.t1	ref|NP_567793.1| uncharacterized protein [Arabidopsis thaliana] gi|44917569|gb|AAS49109.1| At4g28020 [Arabidopsis thaliana] gi|110741672|dbj|BAE98782.1| hypothetical protein [Arabidopsis thaliana] gi|332660021|gb|AEE85421.1| uncharacterized protein AT4G28020 [Arabidopsis thaliana]	346	351	1.00E-177	101.4	87.6	93.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G28020.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0066 (InterPro:IPR001378); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13933389-13935249 REVERSE LENGTH=351	346	351	1.00E-179	101.4	87.6	93.4
Rsa1.0_00188.1.g7942.t1	gb|EOA15737.1| hypothetical protein CARUB_v10006764mg [Capsella rubella]	307	830	6.00E-42	270.4	34.2	40.1	hypothetical protein CARUB_v10006764mg	gbpln	Capsella rubella	AT4G28000.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13925456-13929280 FORWARD LENGTH=830	307	830	1.00E-43	270.4	33.6	40.1
Rsa1.0_00188.1.g7943.t1	ref|NP_567792.1| SLAC1 homologue 2 [Arabidopsis thaliana] gi|75167715|sp|Q9ASQ7.1|SLAH2_ARATH RecName: Full=S-type anion channel SLAH2; AltName: Full=SLAC1-homolog protein 2 gi|13605877|gb|AAK32924.1|AF367337_1 AT4g27970/T13J8_80 [Arabidopsis thaliana] gi|25090193|gb|AAN72249.1| At4g27970/T13J8_80 [Arabidopsis thaliana] gi|332660015|gb|AEE85415.1| SLAC1 homologue 2 [Arabidopsis thaliana]	545	519	0	95.2	77.4	84.8	SLAC1 homologue 2	gbpln	Arabidopsis thaliana	AT4G27970.1 | Symbols: SLAH2 | SLAC1 homologue 2 | chr4:13918290-13920122 REVERSE LENGTH=519	545	519	0	95.2	77.4	84.8
Rsa1.0_00188.1.g7944.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00188.1.g7945.t1	ref|NP_849462.1| SUMO-conjugating enzyme UBC9 [Arabidopsis thaliana] gi|464986|sp|P35132.1|UBC9_ARATH RecName: Full=SUMO-conjugating enzyme UBC9; AltName: Full=UBCAT4B; AltName: Full=Ubiquitin carrier protein 9; AltName: Full=Ubiquitin-conjugating enzyme E2 9; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa; AltName: Full=Ubiquitin-protein ligase 9 gi|297884|emb|CAA78714.1| ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] gi|349211|gb|AAA32894.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|600391|emb|CAA51201.1| ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] gi|4455355|emb|CAB36765.1| ubiquitin-protein ligase UBC9 [Arabidopsis thaliana] gi|7269650|emb|CAB79598.1| ubiquitin-protein ligase UBC9 [Arabidopsis thaliana] gi|23297139|gb|AAN13102.1| E2 ubiquitin-conjugating enzyme 9 (UBC9) [Arabidopsis thaliana] gi|332660013|gb|AEE85413.1| SUMO-conjugating enzyme UBC9 [Arabidopsis thaliana] gi|482553405|gb|EOA17598.1| hypothetical protein CARUB_v10005960mg [Capsella rubella] gi|482553406|gb|EOA17599.1| hypothetical protein	148	148	7.00E-81	100.0	98.6	98.6	SUMO-conjugating enzyme UBC9	gbpln	Arabidopsis thaliana	AT4G27960.1 | Symbols: UBC9 | ubiquitin conjugating enzyme 9 | chr4:13916065-13917203 REVERSE LENGTH=148	148	148	2.00E-83	100.0	98.6	98.6
Rsa1.0_00188.1.g7946.t1	ref|NP_194524.2| ethylene-responsive transcription factor CRF4 [Arabidopsis thaliana] gi|334302779|sp|Q9SUE3.2|CRF4_ARATH RecName: Full=Ethylene-responsive transcription factor CRF4; AltName: Full=Protein CYTOKININ RESPONSE FACTOR 4 gi|192571732|gb|ACF04811.1| At4g27950 [Arabidopsis thaliana] gi|332660012|gb|AEE85412.1| ethylene-responsive transcription factor CRF4 [Arabidopsis thaliana]	322	335	1.00E-122	104.0	74.2	84.2	ethylene-responsive transcription factor CRF4	gbpln	Arabidopsis thaliana	AT4G27950.1 | Symbols: CRF4 | cytokinin response factor 4 | chr4:13909732-13910739 REVERSE LENGTH=335	322	335	1.00E-124	104.0	74.2	84.2
Rsa1.0_00188.1.g7947.t1	ref|XP_002879579.1| sucrose-phosphatase 1 [Arabidopsis lyrata subsp. lyrata] gi|297325418|gb|EFH55838.1| sucrose-phosphatase 1 [Arabidopsis lyrata subsp. lyrata]	188	422	8.00E-90	224.5	86.2	89.9	sucrose-phosphatase 1	gbpln	Arabidopsis lyrata	AT2G35840.3 | Symbols: | Sucrose-6F-phosphate phosphohydrolase family protein | chr2:15053952-15055776 FORWARD LENGTH=422	188	422	1.00E-90	224.5	85.1	89.9
Rsa1.0_00188.1.g7948.t1	ref|NP_567790.1| manganese tracking factor for mitochondrial SOD2 [Arabidopsis thaliana] gi|75306049|sp|Q944H5.1|MTM1_ARATH RecName: Full=Mitochondrial carrier protein MTM1; AltName: Full=Manganese tracking factor for mitochondrial SOD2 gi|16226567|gb|AAL16202.1|AF428433_1 AT4g27940/T13J8_50 [Arabidopsis thaliana] gi|21553497|gb|AAM62590.1| unknown [Arabidopsis thaliana] gi|21928061|gb|AAM78059.1| AT4g27940/T13J8_50 [Arabidopsis thaliana] gi|332660011|gb|AEE85411.1| manganese tracking factor for mitochondrial SOD2 [Arabidopsis thaliana]	407	413	0	101.5	79.6	86.2	manganese tracking factor for mitochondrial SOD2	gbpln	Arabidopsis thaliana	AT4G27940.1 | Symbols: ATMTM1, MTM1 | manganese tracking factor for mitochondrial SOD2 | chr4:13904745-13907036 FORWARD LENGTH=413	407	413	0	101.5	79.6	86.2

Rsa1.0_00188.1.g7949.t1	ref|NP_194519.1| CCT motif family protein [Arabidopsis thaliana] gi|30687777|ref|NP_849461.1| CCT motif family protein [Arabidopsis thaliana] gi|4455349|emb|CAB36759.1| putative protein [Arabidopsis thaliana] gi|7269644|emb|CAB79592.1| putative protein [Arabidopsis thaliana] gi|17064786|gb|AAL32547.1| putative protein [Arabidopsis thaliana] gi|20259898|gb|AAM13296.1| putative protein [Arabidopsis thaliana] gi|332660006|gb|AEE85406.1| CCT motif family protein [Arabidopsis thaliana] gi|332660007|gb|AEE85407.1| CCT motif family protein [Arabidopsis thaliana]	261	261	1.00E−107	100.0	80.5	88.1	CCT motif family protein	gbpln	Arabidopsis thaliana	AT4G27900.2 | Symbols: | CCT motif family protein | chr4:13890858−13892777 FORWARD LENGTH=261	261	261	1.00E−109	100.0	80.5	88.1
Rsa1.0_00188.1.g7950.t1	gb|EMJ19910.1| hypothetical protein PRUPE_ppa008943mg [Prunus persica]	66	313	3.00E−23	474.2	74.2	80.3	hypothetical protein PRUPE_ppa008943mg	gbpln	Prunus persica	AT4G27880.1 | Symbols: | Protein with RING/U−box and TRAF−like domains | chr4:13883623−13884927 FORWARD LENGTH=327	66	327	2.00E−25	495.5	77.3	81.8
Rsa1.0_00188.1.g7951.t1	ref|XP_004149777.1| PREDICTED: uncharacterized protein LOC101210214 [Cucumis sativus]	583	803	1.00E−35	137.7	13.9	20.6	PREDICTED: uncharacterized protein LOC101210214	gbpln	Cucumis sativus	AT4G27860.1 | Symbols: | vacuolar iron transporter (VIT) family protein | chr4:13873808−13876240 FORWARD LENGTH=611	583	611	8.00E−38	104.8	14.2	21.6
Rsa1.0_00188.1.g7952.t1	ref|NP_194504.2| yippee−like protein [Arabidopsis thaliana] gi|122209321|sp|Q2V3E2.1|YIPL5_ARATH RecName: Full=Protein yippee−like At4g27740 gi|110738581|dbj|BAF01216.1| hypothetical protein [Arabidopsis thaliana] gi|332659987|gb|AEE85387.1| yippee−like protein [Arabidopsis thaliana]	105	105	5.00E−51	100.0	91.4	96.2	yippee−like protein	gbpln	Arabidopsis thaliana	AT4G27740.1 | Symbols: | Yippee family putative zinc−binding protein | chr4:13839148−13839616 FORWARD LENGTH=105	105	105	9.00E−54	100.0	91.4	96.2
Rsa1.0_00188.1.g7953.t1	ref|XP_002869552.1| hypothetical protein ARALYDRAFT_492020 [Arabidopsis lyrata subsp. lyrata] gi|297315388|gb|EFH45811.1| hypothetical protein ARALYDRAFT_492020 [Arabidopsis lyrata subsp. lyrata]	62	62	6.00E−24	100.0	87.1	96.8	hypothetical protein ARALYDRAFT_492020	gbpln	Arabidopsis lyrata	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:13813124−13813312 FORWARD LENGTH=62	62	62	1.00E−26	100.0	85.5	96.8
Rsa1.0_00188.1.g7954.t4	ref|XP_002869553.1| hypothetical protein ARALYDRAFT_913767 [Arabidopsis lyrata subsp. lyrata] gi|297315389|gb|EFH45812.1| hypothetical protein ARALYDRAFT_913767 [Arabidopsis lyrata subsp. lyrata]	62	62	3.00E−24	100.0	87.1	93.5	hypothetical protein ARALYDRAFT_913767	gbpln	Arabidopsis lyrata	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:13813124−13813312 FORWARD LENGTH=62	62	62	8.00E−27	100.0	88.7	93.5
Rsa1.0_00188.1.g7955.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	AT2G02520.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr2:676771−678145 REVERSE LENGTH=211	81	211	2.00E−12	260.5	39.5	49.4
Rsa1.0_00188.1.g7956.t1	ref|XP_002869552.1| hypothetical protein ARALYDRAFT_492020 [Arabidopsis lyrata subsp. lyrata] gi|297315388|gb|EFH45811.1| hypothetical protein ARALYDRAFT_492020 [Arabidopsis lyrata subsp. lyrata]	67	62	2.00E−20	92.5	77.6	83.6	hypothetical protein ARALYDRAFT_492020	gbpln	Arabidopsis lyrata	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:13813124−13813312 FORWARD LENGTH=62	67	62	5.00E−23	92.5	76.1	83.6
Rsa1.0_00188.1.g7957.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_00188.1.g7958.t1	ref|XP_002869552.1| hypothetical protein ARALYDRAFT_492020 [Arabidopsis lyrata subsp. lyrata] gi|297315388|gb|EFH45811.1| hypothetical protein ARALYDRAFT_492020 [Arabidopsis lyrata subsp. lyrata]	67	62	1.00E-21	92.5	80.6	85.1	hypothetical protein ARALYDRAFT_492020	gbpln	Arabidopsis lyrata	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13813124-13813312 FORWARD LENGTH=62	67	62	3.00E-24	92.5	79.1	85.1
Rsa1.0_00189.1.g7959.t1	gb|AAL36413.1| putative peptide transporter protein [Arabidopsis thaliana]	122	582	4.00E-49	477.0	75.4	86.1	putative peptide transporter protein	gbpln	Arabidopsis thaliana	AT5G46050.1 | Symbols: ATPTR3, PTR3 | peptide transporter 3 | chr5:18675062-18679071 REVERSE LENGTH=582	122	582	1.00E-44	477.0	74.6	86.1
Rsa1.0_00189.1.g7960.t1	gb|EOA14228.1| hypothetical protein CARUB_v10027385mg [Capsella rubella]	124	120	2.00E-41	96.8	80.6	86.3	hypothetical protein CARUB_v10027385mg	gbpln	Capsella rubella	AT5G46030.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF701, zinc-binding putative (InterPro:IPR007808); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:18670531-18671138 FORWARD LENGTH=120	124	120	1.00E-39	96.8	79.0	86.3
Rsa1.0_00189.1.g7961.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00189.1.g7962.t1	ref|XP_002522509.1| 28 kDa heat- and acid-stable phosphoprotein, putative [Ricinus communis] gi|223538200|gb|EEF39809.1| 28 kDa heat- and acid-stable phosphoprotein, putative [Ricinus communis]	163	164	3.00E-54	100.6	75.5	85.3	28 kDa heat- and acid-stable phosphoprotein, putative	gbpln	Ricinus communis	AT5G46020.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Casein kinase substrate, phosphoprotein PP28 (InterPro:IPR019380); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:18663075-18664629 REVERSE LENGTH=164	163	164	2.00E-55	100.6	87.7	93.3
Rsa1.0_00189.1.g7963.t1	ref|NP_199410.2| WUSCHEL-related homeobox 8 [Arabidopsis thaliana] gi|61217284|sp|Q6X7J5.1|WOX8_ARATH RecName: Full=WUSCHEL-related homeobox 8 gi|37955180|gb|AAP37138.1| WOX8 protein [Arabidopsis thaliana] gi|332007940|gb|AED95323.1| WUSCHEL-related homeobox 8 [Arabidopsis thaliana]	309	325	1.00E-111	105.2	70.6	79.6	WUSCHEL-related homeobox 8	gbpln	Arabidopsis thaliana	AT5G45980.1 | Symbols: WOX8, STPL | WUSCHEL related homeobox 8 | chr5:18648921-18650698 FORWARD LENGTH=325	309	325	1.00E-114	105.2	70.6	79.6
Rsa1.0_00189.1.g7964.t1	emb|CAA16721.1| MuDR transposable element - like protein [Arabidopsis thaliana] gi|7268634|emb|CAB78843.1| MuDR transposable element-like protein [Arabidopsis thaliana]	541	633	1.00E-160	117.0	51.6	66.7	MuDR transposable element - like protein	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	541	785	6.00E-13	145.1	17.4	34.2
Rsa1.0_00189.1.g7965.t1	dbj|BAB09034.1| unnamed protein product [Arabidopsis thaliana]	164	154	4.00E-34	93.9	44.5	64.6	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G15690.1 | Symbols: | zinc ion binding | chr5:5113823-5114402 REVERSE LENGTH=169	164	169	2.00E-18	103.0	28.0	42.1
Rsa1.0_00189.1.g7966.t1	gb|EOA14025.1| hypothetical protein CARUB_v10027157mg [Capsella rubella]	187	201	9.00E-85	107.5	80.2	82.4	hypothetical protein CARUB_v10027157mg	gbpln	Capsella rubella	AT5G45970.1 | Symbols: ARAC2, RAC2, ROP7, ATRAC2, ATROP7 | RAC-like 2 | chr5:18643761-18645758 FORWARD LENGTH=201	187	201	8.00E-87	107.5	80.2	81.8
Rsa1.0_00189.1.g7967.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00189.1.g7968.t2	ref|XP_002522519.1| zinc finger protein, putative [Ricinus communis] gi|223538210|gb|EEF39819.1| zinc finger protein, putative [Ricinus communis]	621	297	2.00E-82	47.8	24.6	30.8	zinc finger protein, putative	gbpln	Ricinus communis	AT5G45960.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:18637174-18640319 REVERSE LENGTH=375	621	375	4.00E-63	60.4	18.4	19.3
Rsa1.0_00189.1.g7969.t1	gb|EOA13600.1| hypothetical protein CARUB_v10026665mg [Capsella rubella]	261	357	5.00E-62	136.8	44.1	47.1	hypothetical protein CARUB_v10026665mg	gbpln	Capsella rubella	AT5G45950.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:18634155-18636512 FORWARD LENGTH=357	261	357	5.00E-61	136.8	41.4	46.7
Rsa1.0_00189.1.g7970.t1	ref|NP_199406.1| nudix hydrolase 11 [Arabidopsis thaliana] gi|68565910|sp|Q8LET2.2|NUD11_ARATH RecName: Full=Nudix hydrolase 11; Short=AtNUDT11; AltName: Full=Coenzyme A diphosphatase NUDT11 gi|9758941|dbj|BAB09322.1| unnamed protein product [Arabidopsis thaliana] gi|332007934|gb|AED95317.1| nudix hydrolase 11 [Arabidopsis thaliana]	221	222	1.00E-103	100.5	84.2	91.4	nudix hydrolase 11	gbpln	Arabidopsis thaliana	AT5G45940.1 | Symbols: atnudt11, NUDT11 | nudix hydrolase homolog 11 | chr5:18629665-18630597 REVERSE LENGTH=222	221	222	1.00E-105	100.5	84.2	91.4

Rsa1.0_00189.1.g7971.t1	gb|AAM98163.1| magnesium chelatase subunit of protochlorophyllide reductase [Arabidopsis thaliana]	420	418	0	99.5	87.4	92.9	magnesium chelatase subunit of protochlorophyllide reductase	gbpln	Arabidopsis thaliana	AT5G45930.1 | Symbols: CHLI2, CHL I2, CHLI-2 | magnesium chelatase i2 | chr5:18628095-18629565 FORWARD LENGTH=418	420	418	0	99.5	87.6	93.1
Rsa1.0_00189.1.g7972.t1	ref|XP_002865219.1| hypothetical protein ARALYDRAFT_916858 [Arabidopsis lyrata subsp. lyrata] gi|297311054|gb|EFH41478.1| hypothetical protein ARALYDRAFT_916858 [Arabidopsis lyrata subsp. lyrata]	697	697	0	100.0	86.9	91.4	hypothetical protein ARALYDRAFT_916858	gbpln	Arabidopsis lyrata	AT5G45900.1 | Symbols: APG7, ATAPG7, ATG7, ATATG7 | ThiF family protein | chr5:18615304-18618436 FORWARD LENGTH=697	697	697	0	100.0	87.2	91.7
Rsa1.0_00189.1.g7973.t1	gb|AAD53011.1|AF089848_1 senescence-specific cysteine protease [Brassica napus]	346	346	0	100.0	94.5	96.0	senescence-specific cysteine protease	gbpln	Brassica napus	AT5G45890.1 | Symbols: SAG12 | senescence-associated gene 12 | chr5:18613300-18614759 FORWARD LENGTH=346	346	346	0	100.0	86.7	92.8
Rsa1.0_00189.1.g7974.t1	ref|NP_001031546.1| uncharacterized protein [Arabidopsis thaliana] gi|330255535|gb|AEC10629.1| uncharacterized protein AT2G45990 [Arabidopsis thaliana]	123	263	2.00E-14	213.8	35.8	43.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G45990.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:18919402-18921043 FORWARD LENGTH=263	123	263	3.00E-17	213.8	35.8	43.1
Rsa1.0_00189.1.g7975.t1	emb|CAN77974.1| hypothetical protein VITISV_006175 [Vitis vinifera]	256	1501	6.00E-78	586.3	57.8	72.3	hypothetical protein VITISV_006175	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00189.1.g7976.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00189.1.g7977.t1	ref|NP_567562.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] gi|44681468|gb|AAS47674.1| At4g18596 [Arabidopsis thaliana] gi|62320348|dbj|BAD94719.1| pollen-specific protein - like [Arabidopsis thaliana] gi|332658666|gb|AEE84066.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana]	174	172	6.00E-84	98.9	87.4	94.3	pollen Ole e 1 allergen and extensin family protein	gbpln	Arabidopsis thaliana	AT4G18596.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr4:10239114-10239728 FORWARD LENGTH=172	174	172	3.00E-86	98.9	87.4	94.3
Rsa1.0_00190.1.g7978.t1	sp|P93820.3|Y1439_ARATH RecName: Full=BTB/POZ domain-containing protein At1g04390	989	1002	0	101.3	86.1	92.2	RecName: Full=BTB/POZ domain-containing protein At1g04390	----	----	AT1G04390.1 | Symbols: | BTB/POZ domain-containing protein | chr1:1179678-1183615 REVERSE LENGTH=849	989	849	0	85.8	38.6	41.2
Rsa1.0_00190.1.g7979.t1	gb|ADU19845.1| cryptochrome 2b [Brassica napus] gi|327082233|gb|AEA29691.1| cryptochrome 2b [Brassica napus]	601	575	0	95.7	90.3	92.7	cryptochrome 2b	gbpln	Brassica napus	AT1G04400.1 | Symbols: CRY2, FHA, AT-PHH1, PHH1, ATCRY2 | cryptochrome 2 | chr1:1185719-1187901 REVERSE LENGTH=612	601	612	0	101.8	83.4	88.2
Rsa1.0_00190.1.g7980.t1	gb|AGB34187.1| malate dehydrogenase [Brassica oleracea]	332	332	0	100.0	99.4	99.7	malate dehydrogenase	gbpln	Brassica oleracea	AT1G04410.1 | Symbols: | Lactate/malate dehydrogenase family protein | chr1:1189418-1191267 REVERSE LENGTH=332	332	332	0	100.0	96.1	98.8
Rsa1.0_00190.1.g7981.t1	ref|XP_002889502.1| aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335344|gb|EFH65761.1| aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata]	419	412	0	98.3	82.3	88.8	aldo/keto reductase family protein	gbpln	Arabidopsis lyrata	AT1G04420.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr1:1191634-1193699 FORWARD LENGTH=412	419	412	0	98.3	81.6	88.1
Rsa1.0_00190.1.g7982.t1	gb|EOA38884.1| hypothetical protein CARUB_v10011254mg [Capsella rubella]	622	623	0	100.2	92.3	97.6	hypothetical protein CARUB_v10011254mg	gbpln	Capsella rubella	AT1G04430.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:1198860-1201301 FORWARD LENGTH=623	622	623	0	100.2	92.1	96.9
Rsa1.0_00190.1.g7983.t1	gb|EOA36675.1| hypothetical protein CARUB_v10012017mg [Capsella rubella]	468	468	0	100.0	87.4	92.9	hypothetical protein CARUB_v10012017mg	gbpln	Capsella rubella	AT1G04440.1 | Symbols: CKL13 | casein kinase like 13 | chr1:1202815-1205664 FORWARD LENGTH=468	468	468	0	100.0	86.5	93.4
Rsa1.0_00190.1.g7984.t1	ref|XP_002889506.1| hypothetical protein ARALYDRAFT_470423 [Arabidopsis lyrata subsp. lyrata] gi|297335348|gb|EFH65765.1| hypothetical protein ARALYDRAFT_470423 [Arabidopsis lyrata subsp. lyrata]	175	154	2.00E-34	88.0	46.9	57.7	hypothetical protein ARALYDRAFT_470423	gbpln	Arabidopsis lyrata	AT1G04445.1 | Symbols: | C2H2-like zinc finger protein | chr1:1207344-1207862 FORWARD LENGTH=172	175	172	1.00E-29	98.3	46.3	60.0
Rsa1.0_00190.1.g7985.t1	gb|EOA39245.1| hypothetical protein CARUB_v10012233mg [Capsella rubella]	1031	1032	0	100.1	87.2	91.9	hypothetical protein CARUB_v10012233mg	gbpln	Capsella rubella	AT1G04470.1 | Symbols: | Protein of unknown function (DUF810) | chr1:1211177-1214591 REVERSE LENGTH=1035	1031	1035	0	100.4	86.2	91.9
Rsa1.0_00190.1.g7986.t1	gb|EOA31608.1| hypothetical protein CARUB_v10014805mg, partial [Capsella rubella]	140	161	1.00E-74	115.0	99.3	100.0	hypothetical protein CARUB_v10014805mg, partial	gbpln	Capsella rubella	AT3G04400.1 | Symbols: emb2171 | Ribosomal protein L14p/L23e family protein | chr3:1167339-1168308 FORWARD LENGTH=140	140	140	1.00E-76	100.0	99.3	100.0

Rsa1.0_00190.1.g7987.t1	gb|AAB70425.1| EST gb|T21788 comes from this gene [Arabidopsis thaliana]	413	412	1.00E-103	99.8	56.7	70.7	EST gb|T21788 comes from this gene	gbpln	Arabidopsis thaliana	AT1G04490.2 | Symbols: | Protein of unknown function (DUF3527) | chr1:1218020-1219325 REVERSE LENGTH=401	413	401	1.00E-106	97.1	56.4	70.7
Rsa1.0_00190.1.g7988.t3	ref|NP_171944.2| CCT motif-containing protein [Arabidopsis thaliana] gi|91805737|gb|ABE65597.1| zinc finger CONSTANS-like protein [Arabidopsis thaliana] gi|225897874|dbj|BAH30269.1| hypothetical protein [Arabidopsis thaliana] gi|332189584|gb|AEE27705.1| CCT motif-containing protein [Arabidopsis thaliana]	380	386	1.00E-169	101.6	82.6	87.6	CCT motif-containing protein	gbpln	Arabidopsis thaliana	AT1G04500.1 | Symbols: | CCT motif family protein | chr1:1221757-1224235 REVERSE LENGTH=386	380	386	1.00E-172	101.6	82.6	87.6
Rsa1.0_00190.1.g7989.t1	gb|EOA40141.1| hypothetical protein CARUB_v10008852mg [Capsella rubella]	531	522	0	98.3	90.0	94.7	hypothetical protein CARUB_v10008852mg	gbpln	Capsella rubella	AT1G04510.1 | Symbols: MAC3A | MOS4-associated complex 3A | chr1:1226749-1230592 FORWARD LENGTH=523	531	523	0	98.5	89.5	93.8
Rsa1.0_00190.1.g7990.t1	ref|NP_171946.2| cysteine-rich repeat secretory protein 3 [Arabidopsis thaliana] gi|75127023|sp|Q6NM73.1|CRR3_ARATH RecName: Full=Cysteine-rich repeat secretory protein 3; Flags: Precursor gi|38566686|gb|AAR24233.1| At1g04520 [Arabidopsis thaliana] gi|45592918|gb|AAS68113.1| At1g04520 [Arabidopsis thaliana] gi|332189588|gb|AEE27709.1| cysteine-rich repeat secretory protein 3 [Arabidopsis thaliana]	286	307	1.00E-123	107.3	86.0	90.2	cysteine-rich repeat secretory protein 3	gbpln	Arabidopsis thaliana	AT1G04520.1 | Symbols: PDLP2 | plasmodesmata-located protein 2 | chr1:1231852-1233787 FORWARD LENGTH=307	286	307	1.00E-126	107.3	86.0	90.2
Rsa1.0_00190.1.g7991.t1	ref|XP_002892222.1| hypothetical protein ARALYDRAFT_470433 [Arabidopsis lyrata subsp. lyrata] gi|297338064|gb|EFH68481.1| hypothetical protein ARALYDRAFT_470433 [Arabidopsis lyrata subsp. lyrata]	299	308	1.00E-114	103.0	75.6	84.9	hypothetical protein ARALYDRAFT_470433	gbpln	Arabidopsis lyrata	AT1G04530.1 | Symbols: TPR4 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1234456-1235895 REVERSE LENGTH=310	299	310	1.00E-114	103.7	73.9	83.6
Rsa1.0_00190.1.g7992.t1	ref|NP_171948.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana] gi|332189590|gb|AEE27711.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana]	598	601	0	100.5	75.9	83.8	calcium-dependent lipid-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G04540.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:1237256-1239061 FORWARD LENGTH=601	598	601	0	100.5	75.9	83.8
Rsa1.0_00190.1.g7993.t2	ref|XP_002889513.1| hypothetical protein ARALYDRAFT_470436 [Arabidopsis lyrata subsp. lyrata] gi|297335355|gb|EFH65772.1| hypothetical protein ARALYDRAFT_470436 [Arabidopsis lyrata subsp. lyrata]	233	239	9.00E-94	102.6	85.4	93.6	hypothetical protein ARALYDRAFT_470436	gbpln	Arabidopsis lyrata	AT1G04550.2 | Symbols: IAA12, BDL | AUX/IAA transcriptional regulator family protein | chr1:1240582-1241810 FORWARD LENGTH=239	233	239	4.00E-95	102.6	85.0	92.7
Rsa1.0_00190.1.g7994.t1	gb|EOA39346.1| hypothetical protein CARUB_v10012389mg [Capsella rubella]	184	184	3.00E-92	100.0	90.8	95.7	hypothetical protein CARUB_v10012389mg	gbpln	Capsella rubella	AT1G04560.1 | Symbols: | AWPM-19-like family protein | chr1:1245070-1245888 FORWARD LENGTH=186	184	186	4.00E-93	101.1	89.7	95.7
Rsa1.0_00190.1.g7995.t1	ref|XP_002892226.1| hypothetical protein ARALYDRAFT_887628 [Arabidopsis lyrata subsp. lyrata] gi|297338068|gb|EFH68485.1| hypothetical protein ARALYDRAFT_887628 [Arabidopsis lyrata subsp. lyrata]	534	542	0	101.5	83.9	91.9	hypothetical protein ARALYDRAFT_887628	gbpln	Arabidopsis lyrata	AT1G04570.1 | Symbols: | Major facilitator superfamily protein | chr1:1246859-1248600 REVERSE LENGTH=542	534	542	0	101.5	85.2	92.1
Rsa1.0_00190.1.g7996.t1	ref|NP_563711.1| aldehyde oxidase 4 [Arabidopsis thaliana] gi|62899864|sp|Q7G191.2|ALDO4_ARATH RecName: Full=Benzaldehyde dehydrogenase (NAD(+)); AltName: Full=Aldehyde oxidase 4; Short=AO-4; Short=AtAO-4; Short=AtAO2; AltName: Full=Indole-3-acetaldehyde oxidase; Short=IAA oxidase gi|6759368|dbj|BAA90299.1| aldehyde oxidase [Arabidopsis thaliana] gi|332189596|gb|AEE27717.1| aldehyde oxidase 4 [Arabidopsis thaliana]	1373	1337	0	97.4	84.3	90.9	aldehyde oxidase 4	gbpln	Arabidopsis thaliana	AT1G04580.1 | Symbols: AAO4, ATAO-4, ATAO2, AO4 | aldehyde oxidase 4 | chr1:1252212-1257510 REVERSE LENGTH=1337	1373	1337	0	97.4	84.3	90.9

Rsa1.0_00190.1.g7997.t1	ref|XP_002892228.1| EMB2748 [Arabidopsis lyrata subsp. lyrata] gi|297338070|gb|EFH68487.1| EMB2748 [Arabidopsis lyrata subsp. lyrata]	772	395	1.00E-159	51.2	36.9	40.4	EMB2748	gbpln	Arabidopsis lyrata	AT1G04590.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Pentatricopeptide repeat (PPR) superfamily protein (TAIR:AT4G21190.1); Has 111 Blast hits to 111 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 109; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:1258760-1261411 REVERSE LENGTH=381	772	381	1.00E-157	49.4	36.7	40.0
Rsa1.0_00190.1.g7998.t1	gb|EOA36577.1| hypothetical protein CARUB_v10011757mg [Capsella rubella]	436	436	0	100.0	94.3	97.7	hypothetical protein CARUB_v10011757mg	gbpln	Capsella rubella	AT1G04610.1 | Symbols: YUC3 | YUCCA 3 | chr1:1279524-1281331 FORWARD LENGTH=437	436	437	0	100.2	93.3	97.5
Rsa1.0_00190.1.g7999.t5	ref|NP_565761.1| NADH dehydrogenase [Arabidopsis thaliana] gi|297823115|ref|XP_002879440.1| hypothetical protein ARALYDRAFT_482258 [Arabidopsis lyrata subsp. lyrata] gi|75219577|sp|O49313.1|NDADB_ARATH RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-B gi|2924772|gb|AAC04901.1| expressed protein [Arabidopsis thaliana] gi|17529030|gb|AAL38725.1| unknown protein [Arabidopsis thaliana] gi|20259081|gb|AAM14256.1| unknown protein [Arabidopsis thaliana] gi|21618056|gb|AAM67106.1| unknown [Arabidopsis thaliana] gi|297325279|gb|EFH55699.1| hypothetical protein ARALYDRAFT_482258 [Arabidopsis lyrata subsp. lyrata] gi|330253707|gb|AEC08801.1| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-B [Arabidopsis thaliana]	143	143	6.00E-77	100.0	99.3	100.0	NADH dehydrogenase	gbpln	Arabidopsis lyrata	AT2G33220.1 | Symbols: | GRIM-19 protein | chr2:14078974-14079929 FORWARD LENGTH=143	143	143	2.00E-79	100.0	99.3	100.0
Rsa1.0_00190.1.g8000.t1	gb|AAB80636.1| Contains similarity to Mycobacterium LIPB gene (gb|Q104041) [Arabidopsis thaliana]	386	333	1.00E-168	86.3	76.2	81.3	Contains similarity to Mycobacterium LIPB gene (gb|Q104041)	gbpln	Arabidopsis thaliana	AT1G04640.2 | Symbols: LIP2 | lipoyltransferase 2 | chr1:1292541-1293248 FORWARD LENGTH=235	386	235	1.00E-125	60.9	55.2	57.8
Rsa1.0_00190.1.g8001.t1	ref|NP_171959.2| uncharacterized protein [Arabidopsis thaliana] gi|332189608|gb|AEE27729.1| uncharacterized protein AT1G04650 [Arabidopsis thaliana]	982	997	0	101.5	81.7	89.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G04650.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:1294893-1298903 REVERSE LENGTH=997	982	997	0	101.5	81.7	89.6
Rsa1.0_00190.1.g8002.t1	ref|XP_002892235.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338077|gb|EFH68494.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	196	207	2.00E-19	105.6	24.0	27.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G04660.1 | Symbols: | glycine-rich protein | chr1:1300668-1301306 REVERSE LENGTH=212	196	212	3.00E-21	108.2	24.0	26.5
Rsa1.0_00190.1.g8003.t1	ref|NP_171961.1| uncharacterized protein [Arabidopsis thaliana] gi|55978673|gb|AAV68798.1| hypothetical protein AT1G04670 [Arabidopsis thaliana] gi|60547523|gb|AAX23725.1| hypothetical protein At1g04670 [Arabidopsis thaliana] gi|332189610|gb|AEE27731.1| uncharacterized protein AT1G04670 [Arabidopsis thaliana]	94	126	2.00E-38	134.0	90.4	93.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G04670.1 | Symbols: | unknown protein; Has 40 Blast hits to 40 proteins in 14 species: Archae - 2; Bacteria - 5; Metazoa - 1; Fungi - 2; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1301985-1302532 FORWARD LENGTH=126	94	126	3.00E-41	134.0	90.4	93.6
Rsa1.0_00190.1.g8004.t1	ref|NP_563715.1| putative pectate lyase 1 [Arabidopsis thaliana] gi|32129844|sp|Q940Q1.2|PEL1_ARATH RecName: Full=Probable pectate lyase 1; AltName: Full=Pectate lyase A1; Flags: Precursor gi|2494113|gb|AAB80622.1| Strong similarity to Musa pectate lyase (gb|X92943). ESTs gb|AA042458, gb|ATTS4502, gb|N38552 come from this gene [Arabidopsis thaliana] gi|18086433|gb|AAL57671.1| At1g04680/T1G11_6 [Arabidopsis thaliana] gi|21593312|gb|AAM65261.1| putative pectate lyase A11 [Arabidopsis thaliana] gi|332189611|gb|AEE27732.1| putative pectate lyase 1 [Arabidopsis thaliana]	431	431	0	100.0	94.2	97.4	putative pectate lyase 1	gbpln	Arabidopsis thaliana	AT1G04680.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:1304052-1307780 REVERSE LENGTH=431	431	431	0	100.0	94.2	97.4

Rsa1.0_00190.1.g8005.t1	ref|XP_002889520.1| hypothetical protein ARALYDRAFT_470455 [Arabidopsis lyrata subsp. lyrata] gi|297335362|gb|EFH65779.1| hypothetical protein ARALYDRAFT_470455 [Arabidopsis lyrata subsp. lyrata]	466	328	0	70.4	69.1	70.2	hypothetical protein ARALYDRAFT_470455	gbpln	Arabidopsis lyrata	AT1G04690.1 | Symbols: KAB1, KV-BETA1 | potassium channel beta subunit 1 | chr1:1313662-1315420 FORWARD LENGTH=328	466	328	0	70.4	68.9	70.2
Rsa1.0_00190.1.g8006.t1	ref|XP_002889521.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335363|gb|EFH65780.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	1015	1043	0	102.8	83.3	89.1	kinase family protein	gbpln	Arabidopsis lyrata	AT1G04700.1 | Symbols: | PB1 domain-containing protein tyrosine kinase | chr1:1316919-1320653 FORWARD LENGTH=1042	1015	1042	0	102.7	82.7	88.8
Rsa1.0_00190.1.g8007.t1	gb|EOA39837.1| hypothetical protein CARUB_v10008506mg [Capsella rubella]	672	671	0	99.9	93.0	97.5	hypothetical protein CARUB_v10008506mg	gbpln	Capsella rubella	AT1G50920.1 | Symbols: | Nucleolar GTP-binding protein | chr1:18870555-18872570 FORWARD LENGTH=671	672	671	0	99.9	90.8	96.3
Rsa1.0_00190.1.g8008.t2	ref|NP_171966.2| chromosome transmission fidelity protein 18 [Arabidopsis thaliana] gi|332189616|gb|AEE27737.1| chromosome transmission fidelity protein 18 [Arabidopsis thaliana]	958	943	0	98.4	85.1	91.0	chromosome transmission fidelity protein 18	gbpln	Arabidopsis thaliana	AT1G04730.1 | Symbols: CTF18 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:1325385-1331086 REVERSE LENGTH=943	958	943	0	98.4	85.1	91.0
Rsa1.0_00190.1.g8009.t2	gb|EOA37088.1| hypothetical protein CARUB_v10010251mg [Capsella rubella]	267	219	1.00E-108	82.0	80.1	82.0	hypothetical protein CARUB_v10010251mg	gbpln	Capsella rubella	AT1G04750.1 | Symbols: VAMP7B, VAMP721, ATVAMP721, AT VAMP7B | vesicle-associated membrane protein 721 | chr1:1331857-1333426 REVERSE LENGTH=219	267	219	1.00E-110	82.0	80.1	82.0
Rsa1.0_00190.1.g8010.t1	gb|AAF40459.1|AC004809_17 Strong similarity to the beta-9 tubulin gene (178 gene product) gb|AF060248 [Arabidopsis thaliana]	298	364	1.00E-151	122.1	89.9	93.3	Strong similarity to the beta-9 tubulin gene (178 gene product) gb|AF060248	gbpln	Arabidopsis thaliana	AT1G04770.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1336564-1337767 REVERSE LENGTH=303	298	303	1.00E-153	101.7	89.9	93.3
Rsa1.0_00190.1.g8011.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00190.1.g8012.t1	ref|NP_563716.3| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|26451052|dbj|BAC42631.1| unknown protein [Arabidopsis thaliana] gi|332189622|gb|AEE27743.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	750	664	0	88.5	76.1	80.3	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G04780.1 | Symbols: | Ankyrin repeat family protein | chr1:1340891-1342965 REVERSE LENGTH=664	750	664	0	88.5	76.1	80.3
Rsa1.0_00190.1.g8013.t2	ref|XP_002889524.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297335366|gb|EFH65783.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	671	634	1.00E-175	94.5	60.2	69.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G04790.1 | Symbols: | RING/U-box superfamily protein | chr1:1345469-1348143 FORWARD LENGTH=634	671	634	1.00E-176	94.5	61.0	69.4
Rsa1.0_00190.1.g8014.t1	ref|XP_002892243.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338085|gb|EFH68502.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	190	198	3.00E-13	104.2	18.9	22.6	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00190.1.g8015.t1	ref|NP_974195.1| F-box protein [Arabidopsis thaliana] gi|332198353|gb|AEE36474.1| F-box protein [Arabidopsis thaliana]	413	462	1.00E-102	111.9	53.5	65.9	F-box protein	gbpln	Arabidopsis thaliana	AT1G80960.3 | Symbols: | F-box and Leucine Rich Repeat domains containing protein | chr1:30416065-30418220 FORWARD LENGTH=462	413	462	1.00E-105	111.9	53.5	65.9
Rsa1.0_00190.1.g8016.t2	ref|XP_002892245.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338087|gb|EFH68504.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	1047	664	0	63.4	50.4	55.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G04840.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1362867-1364962 REVERSE LENGTH=665	1047	665	0	63.5	50.0	55.1
Rsa1.0_00190.1.g8017.t1	ref|NP_171980.1| high mobility group-box and ARID domain-binding domain-containing protein [Arabidopsis thaliana] gi|75192516|sp|Q9MAT6.1|HMG15_ARATH RecName: Full=High mobility group B protein 15; AltName: Full=Nucleosome/chromatin assembly factor group D 15 gi|7211978|gb|AAF40449.1|AC004809_7 Contains similarity to the high mobility group family PF|00505 [Arabidopsis thaliana] gi|56236040|gb|AAV84476.1| At1g04880 [Arabidopsis thaliana] gi|56790208|gb|AAW30021.1| At1g04880 [Arabidopsis thaliana] gi|225897878|dbj|BAH30271.1| hypothetical protein [Arabidopsis thaliana] gi|332189634|gb|AEE27755.1| high mobility group B protein 15 [Arabidopsis thaliana]	420	448	1.00E-160	106.7	73.8	84.3	high mobility group-box and ARID domain-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G04880.1 | Symbols: | HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain | chr1:1376106-1378264 REVERSE LENGTH=448	420	448	1.00E-163	106.7	73.8	84.3

Rsa1.0_00190.1.g8018.t1	gb|EOA38922.1| hypothetical protein CARUB_v10011320mg [Capsella rubella]	532	568	0	106.8	73.1	84.0	hypothetical protein CARUB_v10011320mg	gbpln	Capsella rubella	AT1G04890.1 | Symbols: | Protein of unknown function, DUF593 | chr1:1381116-1382546 REVERSE LENGTH=411	532	411	1.00E-144	77.3	57.5	62.4
Rsa1.0_00190.1.g8019.t1	ref|XP_002889527.1| hypothetical protein ARALYDRAFT_470475 [Arabidopsis lyrata subsp. lyrata] gi|297335369|gb|EFH65786.1| hypothetical protein ARALYDRAFT_470475 [Arabidopsis lyrata subsp. lyrata]	448	447	0	99.8	92.2	95.8	hypothetical protein ARALYDRAFT_470475	gbpln	Arabidopsis lyrata	AT1G04900.1 | Symbols: | Protein of unknown function (DUF185) | chr1:1383912-1387561 FORWARD LENGTH=442	448	442	0	98.7	91.7	94.6
Rsa1.0_00190.1.g8020.t2	ref|XP_002892251.1| hypothetical protein ARALYDRAFT_470476 [Arabidopsis lyrata subsp. lyrata] gi|297338093|gb|EFH68510.1| hypothetical protein ARALYDRAFT_470476 [Arabidopsis lyrata subsp. lyrata]	541	519	0	95.9	88.7	91.3	hypothetical protein ARALYDRAFT_470476	gbpln	Arabidopsis lyrata	AT1G04910.1 | Symbols: | O-fucosyltransferase family protein | chr1:1388101-1391074 REVERSE LENGTH=519	541	519	0	95.9	88.5	90.8
Rsa1.0_00190.1.g8021.t1	ref|NP_180843.2| proline-rich uncharacterized protein [Arabidopsis thaliana] gi|26450185|dbj|BAC42211.1| unknown protein [Arabidopsis thaliana] gi|28827576|gb|AAO50632.1| unknown protein [Arabidopsis thaliana] gi|330253655|gb|AEC08749.1| proline-rich uncharacterized protein [Arabidopsis thaliana]	342	337	2.00E-77	98.5	53.2	62.9	proline-rich uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G32840.1 | Symbols: | proline-rich family protein | chr2:13933101-13934836 REVERSE LENGTH=337	342	337	5.00E-80	98.5	53.2	62.9
Rsa1.0_00190.1.g8022.t1	ref|XP_002889528.1| hypothetical protein ARALYDRAFT_887669 [Arabidopsis lyrata subsp. lyrata] gi|297335370|gb|EFH65787.1| hypothetical protein ARALYDRAFT_887669 [Arabidopsis lyrata subsp. lyrata]	273	273	1.00E-125	100.0	86.8	91.2	hypothetical protein ARALYDRAFT_887669	gbpln	Arabidopsis lyrata	AT1G04940.1 | Symbols: TIC20 | translocon at the inner envelope membrane of chloroplasts 20 | chr1:1399588-1400616 FORWARD LENGTH=274	273	274	1.00E-126	100.4	85.7	90.5
Rsa1.0_00190.1.g8023.t1	gb|EOA40075.1| hypothetical protein CARUB_v10008770mg [Capsella rubella]	867	547	0	63.1	53.6	56.7	hypothetical protein CARUB_v10008770mg	gbpln	Capsella rubella	AT1G04950.3 | Symbols: TAFII59, TAF6, ATTAF6 | TATA BOX ASSOCIATED FACTOR II 59 | chr1:1403606-1407184 REVERSE LENGTH=549	867	549	0	63.3	53.7	56.9
Rsa1.0_00190.1.g8024.t1	ref|XP_002863818.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297309653|gb|EFH40077.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	400	412	1.00E-180	103.0	84.0	90.3	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT5G42130.1 | Symbols: | Mitochondrial substrate carrier family protein | chr5:16835572-16836810 REVERSE LENGTH=412	400	412	0	103.0	83.3	91.0
Rsa1.0_00190.1.g8025.t1	gb|EOA40204.1| hypothetical protein CARUB_v10008924mg [Capsella rubella]	365	502	0	137.5	87.7	93.4	hypothetical protein CARUB_v10008924mg	gbpln	Capsella rubella	AT1G04970.1 | Symbols: | lipid-binding serum glycoprotein family protein | chr1:1411216-1413431 FORWARD LENGTH=488	365	488	0	133.7	85.5	91.0
Rsa1.0_00190.1.g8026.t1	ref|XP_002892256.1| hypothetical protein ARALYDRAFT_470488 [Arabidopsis lyrata subsp. lyrata] gi|297338098|gb|EFH68515.1| hypothetical protein ARALYDRAFT_470488 [Arabidopsis lyrata subsp. lyrata]	333	442	7.00E-88	132.7	50.8	55.9	hypothetical protein ARALYDRAFT_470488	gbpln	Arabidopsis lyrata	AT1G04980.1 | Symbols: ATPDIL2-2, ATPDI10, PDI10, PDIL2-2 | PDI-like 2-2 | chr1:1413869-1416120 REVERSE LENGTH=447	333	447	6.00E-89	134.2	50.2	55.0
Rsa1.0_00190.1.g8027.t1	ref|XP_002879672.1| hypothetical protein ARALYDRAFT_345475 [Arabidopsis lyrata subsp. lyrata] gi|297325511|gb|EFH55931.1| hypothetical protein ARALYDRAFT_345475 [Arabidopsis lyrata subsp. lyrata]	201	232	8.00E-27	115.4	38.8	54.2	hypothetical protein ARALYDRAFT_345475	gbpln	Arabidopsis lyrata	AT2G37435.1 | Symbols: | Cystatin/monellin superfamily protein | chr2:15709823-15710528 FORWARD LENGTH=171	201	171	1.00E-27	85.1	32.8	48.8
Rsa1.0_00190.1.g8028.t1	ref|NP_171990.3| protein disulfide-isomerase A6 [Arabidopsis thaliana] gi|310947346|sp|Q9MAU6.2|PDI22_ARATH RecName: Full=Protein disulfide-isomerase like 2-2; Short=AtPDIL2-2; AltName: Full=Protein disulfide-isomerase 10; Short=PDI10; AltName: Full=Protein disulfide-isomerase like 5-1; Short=AtPDIL5-1; Flags: Precursor gi|332189652|gb|AEE27773.1| protein disulfide-isomerase like 2-2 [Arabidopsis thaliana]	444	447	0	100.7	88.3	93.0	protein disulfide-isomerase A6	gbpln	Arabidopsis thaliana	AT1G04980.1 | Symbols: ATPDIL2-2, ATPDI10, PDI10, PDIL2-2 | PDI-like 2-2 | chr1:1413869-1416120 REVERSE LENGTH=447	444	447	0	100.7	88.3	93.0
Rsa1.0_00190.1.g8029.t1	ref|XP_002889536.1| MAPKKK18 [Arabidopsis lyrata subsp. lyrata] gi|297335378|gb|EFH65795.1| MAPKKK18 [Arabidopsis lyrata subsp. lyrata]	334	341	1.00E-167	102.1	86.5	93.1	MAPKKK18	gbpln	Arabidopsis lyrata	AT1G05100.1 | Symbols: MAPKKK18 | mitogen-activated protein kinase kinase kinase 18 | chr1:1469679-1470698 FORWARD LENGTH=339	334	339	1.00E-165	101.5	84.1	90.7

Rsa1.0_00190.1.g8030.t1	ref|NP_172004.1| Helicase protein with RING/U-box domain [Arabidopsis thaliana] gi|332189671|gb|AEE27792.1| Helicase protein with RING/U-box domain [Arabidopsis thaliana]	867	833	0	96.1	78.1	84.7	Helicase protein with RING/U-box domain	gbpln	Arabidopsis thaliana	AT1G05120.1 | Symbols: | Helicase protein with RING/U-box domain | chr1:1471624-1476067 REVERSE LENGTH=833	867	833	0	96.1	78.1	84.7
Rsa1.0_00190.1.g8031.t1	gb|EOA39063.1| hypothetical protein CARUB_v10011717mg [Capsella rubella]	442	448	0	101.4	81.2	87.1	hypothetical protein CARUB_v10011717mg	gbpln	Capsella rubella	AT1G05140.1 | Symbols: | Peptidase M50 family protein | chr1:1482681-1484006 FORWARD LENGTH=441	442	441	0	99.8	84.6	91.0
Rsa1.0_00190.1.g8032.t2	ref|NP_172004.1| Helicase protein with RING/U-box domain [Arabidopsis thaliana] gi|332189671|gb|AEE27792.1| Helicase protein with RING/U-box domain [Arabidopsis thaliana]	796	833	0	104.6	73.1	82.2	Helicase protein with RING/U-box domain	gbpln	Arabidopsis thaliana	AT1G05120.1 | Symbols: | Helicase protein with RING/U-box domain | chr1:1471624-1476067 REVERSE LENGTH=833	796	833	0	104.6	73.1	82.2
Rsa1.0_00190.1.g8033.t1	gb|EOA37664.1| hypothetical protein CARUB_v10012243mg [Capsella rubella]	806	808	0	100.2	92.2	95.4	hypothetical protein CARUB_v10012243mg	gbpln	Capsella rubella	AT1G05150.1 | Symbols: | Calcium-binding tetratricopeptide family protein | chr1:1484280-1486706 REVERSE LENGTH=808	806	808	0	100.2	91.3	94.5
Rsa1.0_00190.1.g8034.t1	ref|NP_172008.1| Ent-kaurenoic acid oxidase 1 [Arabidopsis thaliana] gi|5915848|sp|O23051.1|KAO1_ARATH RecName: Full=Ent-kaurenoic acid oxidase 1; Short=AtKAO1; AltName: Full=Cytochrome P450 88A3 gi|2388581|gb|AAB71462.1| Similar to Zea DWARF3 (gb|U32579) [Arabidopsis thaliana] gi|110737917|dbj|BAF00896.1| cytochrome P450 like protein [Arabidopsis thaliana] gi|115646749|gb|ABJ17104.1| At1g05160 [Arabidopsis thaliana] gi|332189675|gb|AEE27796.1| Ent-kaurenoic acid oxidase 1 [Arabidopsis thaliana]	871	490	0	56.3	49.0	51.9	Ent-kaurenoic acid oxidase 1	gbpln	Arabidopsis thaliana	AT1G05160.1 | Symbols: CYP88A3, ATKAO1, KAO1 | cytochrome P450, family 88, subfamily A, polypeptide 3 | chr1:1487640-1489828 REVERSE LENGTH=490	871	490	0	56.3	49.0	51.9
Rsa1.0_00190.1.g8035.t4	gb|EOA37082.1| hypothetical protein CARUB_v10010237mg [Capsella rubella]	456	223	1.00E-113	48.9	44.3	45.4	hypothetical protein CARUB_v10010237mg	gbpln	Capsella rubella	AT1G05190.1 | Symbols: emb2394 | Ribosomal protein L6 family | chr1:1502515-1503738 REVERSE LENGTH=223	456	223	1.00E-114	48.9	43.6	45.4
Rsa1.0_00190.1.g8036.t1	ref|NP_172900.2| Ankyrin repeat family protein [Arabidopsis thaliana] gi|7262691|gb|AAF43949.1|AC012188_26 Contains similarity to a hypothetical protein from Arabidopsis thaliana gb|AF080119.1 and contains Ankyrin PF|00023 repeats [Arabidopsis thaliana] gi|332191048|gb|AEE29169.1| Ankyrin repeat family protein [Arabidopsis thaliana]	171	441	2.00E-27	257.9	38.6	46.2	Ankyrin repeat family protein	gbpln	Arabidopsis thaliana	AT1G14480.1 | Symbols: | Ankyrin repeat family protein | chr1:4956404-4957888 FORWARD LENGTH=441	171	441	6.00E-30	257.9	38.6	46.2
Rsa1.0_00190.1.g8037.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00191.1.g8038.t1	ref|XP_002867990.1| hypothetical protein ARALYDRAFT_914837 [Arabidopsis lyrata subsp. lyrata] gi|297313826|gb|EFH44249.1| hypothetical protein ARALYDRAFT_914837 [Arabidopsis lyrata subsp. lyrata]	305	304	1.00E-114	99.7	73.4	82.3	hypothetical protein ARALYDRAFT_914837	gbpln	Arabidopsis lyrata	AT4G18450.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:10190250-10191161 REVERSE LENGTH=303	305	303	1.00E-110	99.3	70.8	80.7
Rsa1.0_00191.1.g8039.t1	gb|EOA16437.1| hypothetical protein CARUB_v10004589mg [Capsella rubella]	540	523	0	96.9	84.3	91.3	hypothetical protein CARUB_v10004589mg	gbpln	Capsella rubella	AT1G36280.1 | Symbols: | L-Aspartase-like family protein | chr1:13640600-13642908 FORWARD LENGTH=527	540	527	0	97.6	85.0	91.5
Rsa1.0_00191.1.g8040.t1	gb|EOA17406.1| hypothetical protein CARUB_v10005708mg [Capsella rubella]	216	217	1.00E-109	100.5	87.5	94.0	hypothetical protein CARUB_v10005708mg	gbpln	Capsella rubella	AT4G18430.1 | Symbols: AtRABA1e, RABA1e | RAB GTPase homolog A1E | chr4:10183903-10185223 REVERSE LENGTH=217	216	217	1.00E-112	100.5	87.5	94.0
Rsa1.0_00191.1.g8041.t1	ref|XP_002867993.1| hypothetical protein ARALYDRAFT_914840 [Arabidopsis lyrata subsp. lyrata] gi|297313829|gb|EFH44252.1| hypothetical protein ARALYDRAFT_914840 [Arabidopsis lyrata subsp. lyrata]	223	213	1.00E-110	95.5	87.0	89.2	hypothetical protein ARALYDRAFT_914840	gbpln	Arabidopsis lyrata	AT4G18425.1 | Symbols: | Protein of unknown function (DUF679) | chr4:10181421-10182062 REVERSE LENGTH=213	223	213	1.00E-111	95.5	85.7	87.9
Rsa1.0_00191.1.g8042.t1	ref|NP_001154252.1| uncharacterized protein [Arabidopsis thaliana] gi|332658643|gb|AEE84043.1| uncharacterized protein AT4G18422 [Arabidopsis thaliana]	81	88	7.00E-25	108.6	79.0	84.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G18422.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 0 Blast hits to 0 proteins in 0 species (source: NCBI BLink). | chr4:10176264-10176530 REVERSE LENGTH=88	81	88	1.00E-27	108.6	79.0	84.0

Rsa1.0_00191.1.g8043.t1	gb|EOA17708.1| hypothetical protein CARUB_v10006080mg [Capsella rubella]	139	107	2.00E-32	77.0	61.2	66.9	hypothetical protein CARUB_v10006080mg	gbpln	Capsella rubella	AT4G18400.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10170024-10171221 REVERSE LENGTH=107	139	107	8.00E-31	77.0	61.2	66.2
Rsa1.0_00191.1.g8044.t1	dbj|BAJ33883.1| unnamed protein product [Thellungiella halophila]	387	379	1.00E-150	97.9	82.2	86.0	unnamed protein product	----	----	AT4G18390.2 | Symbols: TCP2 | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 2 | chr4:10163212-10164309 REVERSE LENGTH=365	387	365	1.00E-138	94.3	75.7	79.1
Rsa1.0_00191.1.g8045.t1	gb|EOA16709.1| hypothetical protein CARUB_v10004910mg, partial [Capsella rubella]	382	418	1.00E-165	109.4	82.5	88.5	hypothetical protein CARUB_v10004910mg, partial	gbpln	Capsella rubella	AT4G18380.2 | Symbols: | F-box family protein | chr4:10157957-10159099 FORWARD LENGTH=380	382	380	1.00E-161	99.5	82.2	88.5
Rsa1.0_00191.1.g8046.t1	ref|NP_193572.1| KH domain-containing protein [Arabidopsis thaliana] gi|15214341|sp|P58223.1|Y4837_ARATH RecName: Full=KH domain-containing protein At4g18375 gi|22136632|gb|AAM91635.1| unknown protein [Arabidopsis thaliana] gi|332658636|gb|AEE84036.1| KH domain-containing protein [Arabidopsis thaliana]	601	606	0	100.8	65.6	77.7	KH domain-containing protein	gbpln	Arabidopsis thaliana	AT4G18375.2 | Symbols: | RNA-binding KH domain-containing protein | chr4:10152825-10155125 FORWARD LENGTH=606	601	606	0	100.8	65.6	77.7
Rsa1.0_00191.1.g8047.t1	gb|EOA18560.1| hypothetical protein CARUB_v10007117mg [Capsella rubella]	112	109	1.00E-49	97.3	88.4	93.8	hypothetical protein CARUB_v10007117mg	gbpln	Capsella rubella	AT4G18372.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr4:10151349-10151687 REVERSE LENGTH=112	112	112	7.00E-51	100.0	85.7	92.9
Rsa1.0_00191.1.g8048.t1	ref|XP_002870050.1| hypothetical protein ARALYDRAFT_493027 [Arabidopsis lyrata subsp. lyrata] gi|297315886|gb|EFH46309.1| hypothetical protein ARALYDRAFT_493027 [Arabidopsis lyrata subsp. lyrata]	319	320	1.00E-134	100.3	79.0	84.6	hypothetical protein ARALYDRAFT_493027	gbpln	Arabidopsis lyrata	AT4G18370.1 | Symbols: DEG5, DEGP5, HHOA | DEGP protease 5 | chr4:10149235-10151051 FORWARD LENGTH=323	319	323	1.00E-126	101.3	74.6	80.9
Rsa1.0_00191.1.g8049.t1	ref|XP_002868001.1| hypothetical protein ARALYDRAFT_914854 [Arabidopsis lyrata subsp. lyrata] gi|297313837|gb|EFH44260.1| hypothetical protein ARALYDRAFT_914854 [Arabidopsis lyrata subsp. lyrata]	400	368	1.00E-169	92.0	74.0	78.8	hypothetical protein ARALYDRAFT_914854	gbpln	Arabidopsis lyrata	AT4G18360.1 | Symbols: | Aldolase-type TIM barrel family protein | chr4:10146141-10148386 REVERSE LENGTH=368	400	368	1.00E-171	92.0	73.8	78.5
Rsa1.0_00191.1.g8050.t1	ref|NP_193569.1| 9-cis-epoxycarotenoid dioxygenase NCED2 [Arabidopsis thaliana] gi|75098750|sp|O49505.1|NCED2_ARATH RecName: Full=9-cis-epoxycarotenoid dioxygenase NCED2, chloroplastic; Short=AtNCED2; Flags: Precursor gi|2832640|emb|CAA16715.1| neoxanthin cleavage enzyme - like protein [Arabidopsis thaliana] gi|7268628|emb|CAB78837.1| neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana] gi|133778876|gb|ABO38778.1| At4g18350 [Arabidopsis thaliana] gi|332658630|gb|AEE84030.1| 9-cis-epoxycarotenoid dioxygenase NCED2 [Arabidopsis thaliana]	580	583	0	100.5	88.3	93.6	9-cis-epoxycarotenoid dioxygenase NCED2	gbpln	Arabidopsis thaliana	AT4G18350.1 | Symbols: NCED2, ATNCED2 | nine-cis-epoxycarotenoid dioxygenase 2 | chr4:10142672-10144423 FORWARD LENGTH=583	580	583	0	100.5	88.3	93.6

Rsa1.0_00191.1.g8051.t1	ref|NP_193550.1| putative calcium-activated outward-rectifying potassium channel 6 [Arabidopsis thaliana] gi|38605078|sp|Q9SVV6.1|TPK3_ARATH RecName: Full=Two-pore potassium channel 3; Short=AtTPK3; AltName: Full=Calcium-activated outward-rectifying potassium channel 6; Short=AtKCO6 gi|5817002|emb|CAB53657.1| potassium channel-like protein [Arabidopsis thaliana] gi|7268609|emb|CAB78818.1| potassium channel-like protein [Arabidopsis thaliana] gi|332658605|gb|AEE84005.1| putative calcium-activated outward-rectifying potassium channel 6 [Arabidopsis thaliana]	172	436	5.00E-31	253.5	44.8	48.8	putative calcium-activated outward-rectifying potassium channel 6	gbpln	Arabidopsis thaliana	AT4G18160.1 | Symbols: KCO6, ATTPK3, ATKCO6, TPK3 | Ca2+ activated outward rectifying K+ channel 6 | chr4:10055696-10057546 FORWARD LENGTH=436	172	436	2.00E-33	253.5	44.8	48.8
Rsa1.0_00191.1.g8052.t1	ref|XP_002870067.1| hypothetical protein ARALYDRAFT_914875 [Arabidopsis lyrata subsp. lyrata] gi|297315903|gb|EFH46326.1| hypothetical protein ARALYDRAFT_914875 [Arabidopsis lyrata subsp. lyrata]	447	438	0	98.0	81.7	87.0	hypothetical protein ARALYDRAFT_914875	gbpln	Arabidopsis lyrata	AT4G18160.1 | Symbols: KCO6, ATTPK3, ATKCO6, TPK3 | Ca2+ activated outward rectifying K+ channel 6 | chr4:10055696-10057546 FORWARD LENGTH=436	447	436	0	97.5	81.0	85.9
Rsa1.0_00191.1.g8053.t1	ref|XP_002870069.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315905|gb|EFH46328.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	792	802	0	101.3	77.7	86.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G18150.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr4:10050211-10053790 FORWARD LENGTH=758	792	758	0	95.7	68.2	77.4
Rsa1.0_00191.1.g8054.t1	ref|NP_193547.4| phytochrome E [Arabidopsis thaliana] gi|332278136|sp|P42498.2|PHYE_ARATH RecName: Full=Phytochrome E gi|332658600|gb|AEE84000.1| phytochrome E [Arabidopsis thaliana]	1106	1112	0	100.5	89.8	94.3	phytochrome E	gbpln	Arabidopsis thaliana	AT4G18130.1 | Symbols: PHYE | phytochrome E | chr4:10042312-10045948 REVERSE LENGTH=1112	1106	1112	0	100.5	89.8	94.3
Rsa1.0_00191.1.g8055.t1	gb|EOA16128.1| hypothetical protein CARUB_v10004261mg [Capsella rubella]	717	706	0	98.5	72.2	79.2	hypothetical protein CARUB_v10004261mg	gbpln	Capsella rubella	AT4G18120.2 | Symbols: AML3, ML3 | MEI2-like 3 | chr4:10038878-10041950 FORWARD LENGTH=730	717	730	0	101.8	67.9	75.5
Rsa1.0_00191.1.g8056.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00191.1.g8057.t1	gb|EOA17641.1| hypothetical protein CARUB_v10006007mg [Capsella rubella]	133	133	2.00E-71	100.0	99.2	100.0	hypothetical protein CARUB_v10006007mg	gbpln	Capsella rubella	AT4G18100.1 | Symbols: | Ribosomal protein L32e | chr4:10035715-10036475 REVERSE LENGTH=133	133	133	6.00E-74	100.0	98.5	100.0
Rsa1.0_00191.1.g8058.t1	gb|ADK94607.1| translation initiation factor eIF4E.a [Brassica rapa] gi|430007156|gb|AGA20262.1| eukaryotic translation initiation factor eIF4E.a [Brassica napus] gi|459284110|gb|AGG54049.1| eukaryotic translation initiation factor 4E.a [Brassica rapa subsp. pekinensis]	230	228	1.00E-113	99.1	87.0	90.0	translation initiation factor eIF4E.a	gbpln	Brassica napus	AT4G18040.1 | Symbols: EIF4E, CUM1, AT.EIF4E1, eIF4E1 | eukaryotic translation initiation factor 4E | chr4:10016724-10018151 REVERSE LENGTH=235	230	235	1.00E-103	102.2	83.0	88.7
Rsa1.0_00191.1.g8059.t1	ref|NP_193537.2| putative methyltransferase PMT14 [Arabidopsis thaliana] gi|75250016|sp|Q94EJ6.1|PMTE_ARATH RecName: Full=Probable methyltransferase PMT14 gi|15294146|gb|AAK95250.1|AF410264_1 AT4g18030/T6K21_210 [Arabidopsis thaliana] gi|24797056|gb|AAN64540.1| At4g18030/T6K21_210 [Arabidopsis thaliana] gi|332658586|gb|AEE83986.1| putative methyltransferase PMT14 [Arabidopsis thaliana]	621	621	0	100.0	89.7	94.0	putative methyltransferase PMT14	gbpln	Arabidopsis thaliana	AT4G18030.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:10012850-10015267 REVERSE LENGTH=621	621	621	0	100.0	89.7	94.0
Rsa1.0_00191.1.g8060.t2	ref|XP_002868017.1| pseudo-response regulator 2 [Arabidopsis lyrata subsp. lyrata] gi|297313853|gb|EFH44276.1| pseudo-response regulator 2 [Arabidopsis lyrata subsp. lyrata]	511	533	0	104.3	78.3	85.3	pseudo-response regulator 2	gbpln	Arabidopsis lyrata	AT4G18020.6 | Symbols: APRR2 | CheY-like two-component responsive regulator family protein | chr4:10003738-10006682 REVERSE LENGTH=535	511	535	0	104.7	78.7	86.5
Rsa1.0_00191.1.g8061.t1	ref|XP_002868018.1| hypothetical protein ARALYDRAFT_914893 [Arabidopsis lyrata subsp. lyrata] gi|297313854|gb|EFH44277.1| hypothetical protein ARALYDRAFT_914893 [Arabidopsis lyrata subsp. lyrata]	631	646	0	102.4	87.6	92.1	hypothetical protein ARALYDRAFT_914893	gbpln	Arabidopsis lyrata	AT4G18010.1 | Symbols: IP5PII, AT5PTASE2, 5PTASE2 | myo-inositol polyphosphate 5-phosphatase 2 | chr4:9991194-9994099 REVERSE LENGTH=646	631	646	0	102.4	87.2	91.3
Rsa1.0_00191.1.g8062.t1	ref|XP_002865175.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311010|gb|EFH41434.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	497	489	0	98.4	83.9	90.5	kinase family protein	gbpln	Arabidopsis lyrata	AT5G46570.1 | Symbols: BSK2 | BR-signaling kinase 2 | chr5:18894687-18897198 FORWARD LENGTH=489	497	489	0	98.4	83.1	90.5

Rsa1.0_00191.1.g8063.t1	gb|EOA15827.1| hypothetical protein CARUB_v10007390mg, partial [Capsella rubella]	289	262	1.00E-117	90.7	72.3	79.2	hypothetical protein CARUB_v10007390mg, partial	gbpln	Capsella rubella	AT4G17980.1 | Symbols: anac071, NAC071 | NAC domain containing protein 71 | chr4:9978850-9980038 REVERSE LENGTH=262	289	262	1.00E-110	90.7	69.9	76.1
Rsa1.0_00191.1.g8064.t1	gb|EOA17564.1| hypothetical protein CARUB_v10005925mg [Capsella rubella]	164	158	1.00E-65	96.3	76.2	84.8	hypothetical protein CARUB_v10005925mg	gbpln	Capsella rubella	AT4G17960.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G46620.1); Has 46 Blast hits to 45 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:9971154-9972227 FORWARD LENGTH=154	164	154	3.00E-67	93.9	78.7	83.5
Rsa1.0_00191.1.g8065.t1	ref|NP_567546.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|15451060|gb|AAK96801.1| putative protein [Arabidopsis thaliana] gi|20148333|gb|AAM10057.1| putative protein [Arabidopsis thaliana] gi|119657370|tpd|FAA00284.1| TPA: AT-hook motif nuclear localized protein 13 [Arabidopsis thaliana] gi|332658571|gb|AEE83971.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	431	439	1.00E-126	101.9	69.4	78.4	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT4G17950.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:9967295-9969007 REVERSE LENGTH=439	431	439	1.00E-129	101.9	69.4	78.4
Rsa1.0_00191.1.g8066.t1	gb|EOA17188.1| hypothetical protein CARUB_v10005460mg [Capsella rubella]	243	276	8.00E-83	113.6	77.4	86.8	hypothetical protein CARUB_v10005460mg	gbpln	Capsella rubella	AT4G17940.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:9965787-9966778 FORWARD LENGTH=274	243	274	9.00E-81	112.8	75.3	84.4
Rsa1.0_00191.1.g8067.t1	ref|XP_002868029.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297313865|gb|EFH44288.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	299	294	1.00E-129	98.3	78.3	83.6	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G17920.1 | Symbols: | RING/U-box superfamily protein | chr4:9963221-9964090 REVERSE LENGTH=289	299	289	1.00E-130	96.7	80.6	86.0
Rsa1.0_00191.1.g8068.t1	emb|CAA17134.1| putative protein [Arabidopsis thaliana] gi|7268543|emb|CAB78793.1| putative protein [Arabidopsis thaliana]	305	1208	1.00E-137	396.1	77.4	85.6	putative protein	gbpln	Arabidopsis thaliana	AT4G17905.1 | Symbols: ATL4H | RING/U-box superfamily protein | chr4:9948853-9949785 REVERSE LENGTH=310	305	310	1.00E-139	101.6	78.0	86.2
Rsa1.0_00191.1.g8069.t1	gb|EOA17250.1| hypothetical protein CARUB_v10005524mg, partial [Capsella rubella]	227	262	1.00E-123	115.4	92.1	97.4	hypothetical protein CARUB_v10005524mg, partial	gbpln	Capsella rubella	AT4G17900.1 | Symbols: | PLATZ transcription factor family protein | chr4:9946046-9947697 FORWARD LENGTH=227	227	227	1.00E-125	100.0	91.6	96.0
Rsa1.0_00191.1.g8070.t2	emb|CAA18234.1| putative protein [Arabidopsis thaliana] gi|7269488|emb|CAB79491.1| putative protein [Arabidopsis thaliana]	884	1141	4.00E-99	129.1	19.6	26.7	putative protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	884	626	4.00E-38	70.8	10.5	16.5
Rsa1.0_00191.1.g8071.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00191.1.g8072.t1	ref|NP_567543.1| putative ADP-ribosylation factor GTPase-activating protein AGD8 [Arabidopsis thaliana] gi|75244593|sp|Q8H100.1|AGD8_ARATH RecName: Full=Probable ADP-ribosylation factor GTPase-activating protein AGD8; Short=ARF GAP AGD8; AltName: Full=Protein ARF-GAP DOMAIN 8; Short=AtAGD8 gi|24030421|gb|AAN41368.1| unknown protein [Arabidopsis thaliana] gi|51970716|dbj|BAD44050.1| unknown protein [Arabidopsis thaliana] gi|51971433|dbj|BAD44381.1| unknown protein [Arabidopsis thaliana] gi|62319827|dbj|BAD93852.1| hypothetical protein [Arabidopsis thaliana] gi|62320091|dbj|BAD94263.1| hypothetical protein [Arabidopsis thaliana] gi|110739292|dbj|BAF01559.1| hypothetical protein [Arabidopsis thaliana] gi|332658561|gb|AEE83961.1| putative ADP-ribosylation factor GTPase-activating protein AGD8 [Arabidopsis thaliana]	414	413	0	99.8	86.7	93.0	putative ADP-ribosylation factor GTPase-activating protein AGD8	gbpln	Arabidopsis thaliana	AT4G17890.1 | Symbols: AGD8 | ARF-GAP domain 8 | chr4:9937121-9939146 FORWARD LENGTH=413	414	413	0	99.8	86.7	93.0
Rsa1.0_00191.1.g8073.t1	gb|ABD65632.1| basic helix-loop-helix (bHLH) family transcription factor [Brassica oleracea]	599	586	0	97.8	85.0	89.8	basic helix-loop-helix (bHLH) family transcription factor	gbpln	Brassica oleracea	AT4G17880.1 | Symbols: | Basic helix-loop-helix (bHLH) DNA-binding family protein | chr4:9933702-9935471 REVERSE LENGTH=589	599	589	0	98.3	72.5	81.3
Rsa1.0_00191.1.g8074.t1	gb|ABD65631.1| Streptomyces cyclase/dehydrase family protein [Brassica oleracea]	124	281	3.00E-49	226.6	75.0	76.6	Streptomyces cyclase/dehydrase family protein	gbpln	Brassica oleracea	AT4G17870.1 | Symbols: PYR1, RCAR11 | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:9928792-9929367 FORWARD LENGTH=191	124	191	7.00E-47	154.0	67.7	71.8

Rsa1.0_00191.1.g8075.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00191.1.g8076.t1	gb|ABD65621.1| hypothetical protein 23.t00063 [Brassica oleracea]	262	360	1.00E-111	137.4	83.2	89.3	hypothetical protein 23.t00063	gbpln	Brassica oleracea	AT4G17850.1 | Symbols: | BEST Arabidopsis thaliana protein match is: RING/FYVE/PHD zinc finger superfamily protein (TAIR:AT3G02890.1); Has 200 Blast hits to 194 proteins in 51 species: Archae - 0; Bacteria - 0; Metazoa - 61; Fungi - 11; Plants - 116; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr4:9922990-9923850 FORWARD LENGTH=187	262	187	1.00E-33	71.4	36.6	46.9
Rsa1.0_00191.1.g8077.t1	gb|ABD65620.1| hypothetical protein 23.t00062 [Brassica oleracea]	225	200	3.00E-75	88.9	68.0	74.7	hypothetical protein 23.t00062	gbpln	Brassica oleracea	AT4G17850.1 | Symbols: | BEST Arabidopsis thaliana protein match is: RING/FYVE/PHD zinc finger superfamily protein (TAIR:AT3G02890.1); Has 200 Blast hits to 194 proteins in 51 species: Archae - 0; Bacteria - 0; Metazoa - 61; Fungi - 11; Plants - 116; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr4:9922990-9923850 FORWARD LENGTH=187	225	187	1.00E-26	83.1	28.9	40.0
Rsa1.0_00191.1.g8078.t1	gb|ABD65619.1| hypothetical protein 23.t00061 [Brassica oleracea]	220	223	2.00E-98	101.4	84.5	88.6	hypothetical protein 23.t00061	gbpln	Brassica oleracea	AT4G17850.1 | Symbols: | BEST Arabidopsis thaliana protein match is: RING/FYVE/PHD zinc finger superfamily protein (TAIR:AT3G02890.1); Has 200 Blast hits to 194 proteins in 51 species: Archae - 0; Bacteria - 0; Metazoa - 61; Fungi - 11; Plants - 116; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr4:9922990-9923850 FORWARD LENGTH=187	220	187	1.00E-18	85.0	25.0	35.0
Rsa1.0_00191.1.g8079.t1	gb|ABD65626.1| hypothetical protein 23.t00040 [Brassica oleracea]	404	409	0	101.2	92.8	95.0	hypothetical protein 23.t00040	gbpln	Brassica oleracea	AT4G17840.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Abortive infection protein (InterPro:IPR003675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35260.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9918222-9920190 REVERSE LENGTH=422	404	422	0	104.5	89.1	93.3
Rsa1.0_00191.1.g8080.t1	gb|ABD65616.1| zinc finger (C2H2 type) containing protein [Brassica oleracea]	206	196	2.00E-94	95.1	84.5	85.9	zinc finger (C2H2 type) containing protein	gbpln	Brassica oleracea	AT4G17810.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr4:9906918-9907532 FORWARD LENGTH=204	206	204	1.00E-87	99.0	79.6	84.5
Rsa1.0_00191.1.g8081.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1868	1274	0	68.2	31.3	41.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1868	575	3.00E-67	30.8	8.9	14.7
Rsa1.0_00191.1.g8082.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2011	1274	0	63.4	31.3	42.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2011	575	1.00E-71	28.6	8.9	13.6
Rsa1.0_00192.1.g8083.t1	ref|XP_002871317.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317154|gb|EFH47576.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	243	313	1.00E-30	128.8	33.3	43.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321	243	321	2.00E-30	132.1	34.2	44.4
Rsa1.0_00192.1.g8084.t1	gb|AAR13701.1| protein kinase [Brassica oleracea]	268	353	1.00E-110	131.7	73.9	82.1	protein kinase	gbpln	Brassica oleracea	AT5G07620.1 | Symbols: | Protein kinase superfamily protein | chr5:2407401-2409066 REVERSE LENGTH=359	268	359	1.00E-110	134.0	70.1	76.5
Rsa1.0_00192.1.g8085.t1	gb|AAR15502.1| F-box protein [Arabidopsis arenosa]	441	421	1.00E-149	95.5	64.9	76.0	F-box protein	gbpln	Arabidopsis arenosa	AT5G07610.1 | Symbols: | F-box family protein | chr5:2406068-2407330 FORWARD LENGTH=420	441	420	1.00E-150	95.2	63.7	75.5
Rsa1.0_00192.1.g8086.t2	ref|XP_002871277.1| hypothetical protein ARALYDRAFT_487594 [Arabidopsis lyrata subsp. lyrata] gi|297317114|gb|EFH47536.1| hypothetical protein ARALYDRAFT_487594 [Arabidopsis lyrata subsp. lyrata]	100	111	8.00E-12	111.0	41.0	45.0	hypothetical protein ARALYDRAFT_487594	gbpln	Arabidopsis lyrata	AT5G07572.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:2396913-2397263 FORWARD LENGTH=116	100	116	5.00E-14	116.0	43.0	52.0

Rsa1.0_00192.1.g8087.t1	ref|XP_002871277.1| hypothetical protein ARALYDRAFT_487594 [Arabidopsis lyrata subsp. lyrata] gi|297317114|gb|EFH47536.1| hypothetical protein ARALYDRAFT_487594 [Arabidopsis lyrata subsp. lyrata]	190	111	5.00E-14	58.4	27.4	28.9	hypothetical protein ARALYDRAFT_487594	gbpln	Arabidopsis lyrata	AT5G07572.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:2396913-2397263 FORWARD LENGTH=116	190	116	2.00E-13	61.1	24.7	26.8
Rsa1.0_00192.1.g8088.t1	emb|CAA64800.1| oleosin-like protein [Brassica napus]	168	207	1.00E-48	123.2	75.6	82.1	oleosin-like protein	gbpln	Brassica napus	AT5G07530.2 | Symbols: GRP17, ATGRP17, ATGRP-7 | glycine rich protein 17 | chr5:2382629-2384495 REVERSE LENGTH=512	168	512	2.00E-29	304.8	36.9	45.8
Rsa1.0_00192.1.g8089.t1	emb|CAA64800.1| oleosin-like protein [Brassica napus]	233	207	2.00E-42	88.8	50.6	58.4	oleosin-like protein	gbpln	Brassica napus	AT5G07530.2 | Symbols: GRP17, ATGRP17, ATGRP-7 | glycine rich protein 17 | chr5:2382629-2384495 REVERSE LENGTH=512	233	512	2.00E-39	219.7	33.0	39.1
Rsa1.0_00192.1.g8090.t1	gb|AAR15475.1| hypothetical protein Op_7490 [Olimarabidopsis pumila]	150	150	9.00E-71	100.0	86.0	92.7	hypothetical protein Op_7490	gbpln	Olimarabidopsis pumila	AT5G07490.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61630.1); Has 50 Blast hits to 50 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:2370248-2371003 FORWARD LENGTH=149	150	149	7.00E-73	99.3	86.7	92.7
Rsa1.0_00192.1.g8091.t1	gb|AAR15424.1| Cu2+ plastocyanin-like [Sisymbrium irio]	194	195	6.00E-90	100.5	82.5	88.1	Cu2+ plastocyanin-like	gbpln	Sisymbrium irio	AT5G07475.1 | Symbols: | Cupredoxin superfamily protein | chr5:2364827-2365536 REVERSE LENGTH=192	194	192	3.00E-86	99.0	78.4	86.1
Rsa1.0_00192.1.g8092.t1	gb|AAR15472.1| peptide methionine sulfoxide reductase [Olimarabidopsis pumila]	184	202	8.00E-82	109.8	76.6	86.4	peptide methionine sulfoxide reductase	gbpln	Olimarabidopsis pumila	AT5G07470.1 | Symbols: PMSR3, ATMSRA3 | peptidemethionine sulfoxide reductase 3 | chr5:2362760-2364286 REVERSE LENGTH=202	184	202	4.00E-81	109.8	75.0	83.2
Rsa1.0_00192.1.g8093.t1	gb|AAR15472.1| peptide methionine sulfoxide reductase [Olimarabidopsis pumila]	195	202	1.00E-80	103.6	73.3	82.1	peptide methionine sulfoxide reductase	gbpln	Olimarabidopsis pumila	AT5G07470.1 | Symbols: PMSR3, ATMSRA3 | peptidemethionine sulfoxide reductase 3 | chr5:2362760-2364286 REVERSE LENGTH=202	195	202	4.00E-80	103.6	71.8	79.5
Rsa1.0_00192.1.g8094.t1	gb|AAR15486.1| peptide methionine sulfoxide reductase [Arabidopsis arenosa]	144	202	8.00E-51	140.3	73.6	81.9	peptide methionine sulfoxide reductase	gbpln	Arabidopsis arenosa	AT5G07470.1 | Symbols: PMSR3, ATMSRA3 | peptidemethionine sulfoxide reductase 3 | chr5:2362760-2364286 REVERSE LENGTH=202	144	202	2.00E-52	140.3	72.9	80.6
Rsa1.0_00192.1.g8095.t1	gb|AAR15485.1| peptide methionine sulfoxide reductase [Arabidopsis arenosa]	221	221	1.00E-106	100.0	81.4	91.4	peptide methionine sulfoxide reductase	gbpln	Arabidopsis arenosa	AT5G07460.1 | Symbols: PMSR2, ATMSRA2 | peptidemethionine sulfoxide reductase 2 | chr5:2360844-2361885 REVERSE LENGTH=218	221	218	1.00E-106	98.6	81.4	90.5
Rsa1.0_00192.1.g8096.t1	ref|NP_196361.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|186521018|ref|NP_001119183.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|297806777|ref|XP_002871272.1| hypothetical protein ARALYDRAFT_487575 [Arabidopsis lyrata subsp. lyrata] gi|12229806|sp|Q38946.1|DHE2_ARATH RecName: Full=Glutamate dehydrogenase 2; Short=GDH 2 gi|1336084|gb|AAB01222.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|7576182|emb|CAB87933.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|297317109|gb|EFH47531.1| hypothetical protein ARALYDRAFT_487575 [Arabidopsis lyrata subsp. lyrata] gi|332003774|gb|AED91157.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|332003775|gb|AED91158.1| glutamate dehydrogenase 2 [Arabidopsis thaliana]	90	411	7.00E-34	456.7	74.4	75.6	glutamate dehydrogenase 2	gbpln	Arabidopsis lyrata	AT5G07440.2 | Symbols: GDH2 | glutamate dehydrogenase 2 | chr5:2356153-2358012 FORWARD LENGTH=411	90	411	1.00E-36	456.7	74.4	75.6
Rsa1.0_00192.1.g8097.t1	gb|AAR15485.1| peptide methionine sulfoxide reductase [Arabidopsis arenosa]	223	221	1.00E-100	99.1	77.1	87.9	peptide methionine sulfoxide reductase	gbpln	Arabidopsis arenosa	AT5G07460.1 | Symbols: PMSR2, ATMSRA2 | peptidemethionine sulfoxide reductase 2 | chr5:2360844-2361885 REVERSE LENGTH=218	223	218	1.00E-100	97.8	76.2	87.0
Rsa1.0_00192.1.g8098.t1	gb|EOA20446.1| hypothetical protein CARUB_v10000757mg, partial [Capsella rubella]	411	509	0	123.8	96.6	99.8	hypothetical protein CARUB_v10000757mg, partial	gbpln	Capsella rubella	AT5G07440.2 | Symbols: GDH2 | glutamate dehydrogenase 2 | chr5:2356153-2358012 FORWARD LENGTH=411	411	411	0	100.0	96.4	99.8

Rsa1.0_00192.1.g8099.t1	ref|NP_196360.1| putative pectinesterase 50 [Arabidopsis thaliana] gi|75180992|sp|Q9LY17.1|PME50_ARATH RecName: Full=Probable pectinesterase 50; Short=PE 50; AltName: Full=Pectin methylesterase 50; Short=AtPME50; Flags: Precursor gi|7576181|emb|CAB87932.1| pectin methyl-esterase-like protein [Arabidopsis thaliana] gi|332003773|gb|AED91156.1| putative pectinesterase 50 [Arabidopsis thaliana]	361	361	0	100.0	89.8	96.4	putative pectinesterase 50	gbpln	Arabidopsis thaliana	AT5G07430.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:2352549-2354069 FORWARD LENGTH=361	361	361	0	100.0	89.8	96.4
Rsa1.0_00192.1.g8100.t1	ref|XP_002873307.1| respiratory burst oxidase protein A [Arabidopsis lyrata subsp. lyrata] gi|297319144|gb|EFH49566.1| respiratory burst oxidase protein A [Arabidopsis lyrata subsp. lyrata]	831	897	0	107.9	68.8	81.3	respiratory burst oxidase protein A	gbpln	Arabidopsis lyrata	AT5G07390.1 | Symbols: ATRBOHA, RBOHA | respiratory burst oxidase homolog A | chr5:2336063-2339728 REVERSE LENGTH=902	831	902	0	108.5	68.0	81.0
Rsa1.0_00192.1.g8101.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	708	1231	0	173.9	48.3	65.7	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	708	575	1.00E-102	81.2	29.0	44.2
Rsa1.0_00192.1.g8102.t1	gb|EOA19890.1| hypothetical protein CARUB_v10000137mg [Capsella rubella]	990	991	0	100.1	89.3	95.6	hypothetical protein CARUB_v10000137mg	gbpln	Capsella rubella	AT5G07350.1 | Symbols: Tudor1, AtTudor1, TSN1 | TUDOR-SN protein 1 | chr5:2320344-2324892 REVERSE LENGTH=991	990	991	0	100.1	88.9	94.8
Rsa1.0_00192.1.g8103.t1	gb|ABK28684.1| unknown [Arabidopsis thaliana]	255	264	1.00E-102	103.5	85.5	89.4	unknown	gbpln	Arabidopsis thaliana	AT5G07310.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:2305684-2306660 FORWARD LENGTH=263	255	263	1.00E-105	103.1	85.5	89.4
Rsa1.0_00192.1.g8104.t2	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	458	1213	1.00E-111	264.8	45.9	59.6	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	458	746	7.00E-42	162.9	23.4	35.6
Rsa1.0_00192.1.g8105.t2	ref|XP_002871263.1| hypothetical protein ARALYDRAFT_487555 [Arabidopsis lyrata subsp. lyrata] gi|297317100|gb|EFH47522.1| hypothetical protein ARALYDRAFT_487555 [Arabidopsis lyrata subsp. lyrata]	585	587	0	100.3	87.9	93.3	hypothetical protein ARALYDRAFT_487555	gbpln	Arabidopsis lyrata	AT5G07300.1 | Symbols: BON2 | Calcium-dependent phospholipid-binding Copine family protein | chr5:2299996-2303040 FORWARD LENGTH=586	585	586	0	100.2	87.7	93.5
Rsa1.0_00192.1.g8106.t1	gb|EOA20989.1| hypothetical protein CARUB_v10001321mg [Capsella rubella]	324	346	1.00E-110	106.8	67.0	75.9	hypothetical protein CARUB_v10001321mg	gbpln	Capsella rubella	AT5G07250.1 | Symbols: ATRBL3, RBL3 | RHOMBOID-like protein 3 | chr5:2274437-2275935 REVERSE LENGTH=346	324	346	1.00E-104	106.8	66.4	75.0
Rsa1.0_00192.1.g8107.t1	ref|XP_002871260.1| IQ-domain 24 [Arabidopsis lyrata subsp. lyrata] gi|297317097|gb|EFH47519.1| IQ-domain 24 [Arabidopsis lyrata subsp. lyrata]	370	401	1.00E-120	108.4	75.1	80.8	IQ-domain 24	gbpln	Arabidopsis lyrata	AT5G07240.1 | Symbols: IQD24 | IQ-domain 24 | chr5:2272028-2274051 FORWARD LENGTH=401	370	401	1.00E-118	108.4	73.8	80.0
Rsa1.0_00192.1.g8108.t2	ref|NP_196338.1| putative two-component response regulator ARR21 [Arabidopsis thaliana] gi|7546699|emb|CAB87277.1| putative protein [Arabidopsis thaliana] gi|332003739|gb|AED91122.1| putative two-component response regulator ARR21 [Arabidopsis thaliana]	734	621	1.00E-156	84.6	39.2	46.0	putative two-component response regulator ARR21	gbpln	Arabidopsis thaliana	AT5G07210.1 | Symbols: ARR21, RR21 | response regulator 21 | chr5:2252237-2256018 FORWARD LENGTH=621	734	621	1.00E-159	84.6	39.2	46.0
Rsa1.0_00192.1.g8109.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00192.1.g8110.t1	gb|EOA22960.1| hypothetical protein CARUB_v10003698mg, partial [Capsella rubella]	217	165	6.00E-29	76.0	33.2	45.2	hypothetical protein CARUB_v10003698mg, partial	gbpln	Capsella rubella	AT5G03495.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:873804-875025 REVERSE LENGTH=226	217	226	5.00E-25	104.1	32.3	45.2
Rsa1.0_00192.1.g8111.t1	gb|EMT25720.1| TATA-box-binding protein 2 [Aegilops tauschii]	129	260	3.00E-48	201.6	75.2	82.9	TATA-box-binding protein 2	gbpln	Aegilops tauschii	AT3G13445.1 | Symbols: TBP1, TFIID-1 | TATA binding protein 1 | chr3:4380317-4381869 FORWARD LENGTH=200	129	200	6.00E-51	155.0	74.4	83.7
Rsa1.0_00192.1.g8112.t1	ref|XP_002871223.1| hypothetical protein ARALYDRAFT_908591 [Arabidopsis lyrata subsp. lyrata] gi|297317060|gb|EFH47482.1| hypothetical protein ARALYDRAFT_908591 [Arabidopsis lyrata subsp. lyrata]	370	368	1.00E-180	99.5	84.1	90.3	hypothetical protein ARALYDRAFT_908591	gbpln	Arabidopsis lyrata	AT5G06610.1 | Symbols: | Protein of unknown function (DUF620) | chr5:2029953-2033620 FORWARD LENGTH=368	370	368	0	99.5	82.4	90.3
Rsa1.0_00192.1.g8113.t1	dbj|BAJ34172.1| unnamed protein product [Thellungiella halophila]	1140	1115	0	97.8	93.9	96.2	unnamed protein product	----	----	AT5G06600.1 | Symbols: UBP12 | ubiquitin-specific protease 12 | chr5:2019545-2027834 REVERSE LENGTH=1116	1140	1116	0	97.9	93.2	95.5

Rsa1.0_00192.1.g8114.t1	ref|NP_196275.1| alpha/beta hydrolase fold-containing protein [Arabidopsis thaliana] gi|30681513|ref|NP_850782.1| alpha/beta hydrolase fold-containing protein [Arabidopsis thaliana] gi|75333783|sp|Q9FG13.1|CXE15_ARATH RecName: Full=Probable carboxylesterase 15; AltName: Full=AtCXE15 gi|10178113|dbj|BAB11406.1| unnamed protein product [Arabidopsis thaliana] gi|26452184|dbj|BAC43180.1| unknown protein [Arabidopsis thaliana] gi|30725374|gb|AAP37709.1| At5g06570 [Arabidopsis thaliana] gi|332003652|gb|AED91035.1| probable carboxylesterase 15 [Arabidopsis thaliana] gi|332003653|gb|AED91036.1| alpha/beta hydrolase fold-containing protein [Arabidopsis thaliana]	216	329	2.00E-29	152.3	28.2	32.9	alpha/beta hydrolase fold-containing protein	gbpln	Arabidopsis thaliana	AT5G06570.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:2008075-2011013 REVERSE LENGTH=329	216	329	7.00E-32	152.3	28.2	32.9
Rsa1.0_00192.1.g8115.t1	ref|NP_196265.1| Glutaredoxin family protein [Arabidopsis thaliana] gi|9758427|dbj|BAB08969.1| unnamed protein product [Arabidopsis thaliana] gi|332003638|gb|AED91021.1| Glutaredoxin family protein [Arabidopsis thaliana]	246	239	1.00E-113	97.2	82.9	91.9	Glutaredoxin family protein	gbpln	Arabidopsis thaliana	AT5G06470.1 | Symbols: | Glutaredoxin family protein | chr5:1974659-1975378 REVERSE LENGTH=239	246	239	1.00E-115	97.2	82.9	91.9
Rsa1.0_00192.1.g8116.t1	ref|NP_196263.1| DnaQ-like exonuclease domain-containing protein [Arabidopsis thaliana] gi|73921148|sp|Q9FNG3.1|Y5645_ARATH RecName: Full=Uncharacterized protein At5g06450 gi|9758425|dbj|BAB08967.1| unnamed protein product [Arabidopsis thaliana] gi|19347954|gb|AAL86312.1| unknown protein [Arabidopsis thaliana] gi|21436419|gb|AAM51410.1| unknown protein [Arabidopsis thaliana] gi|332003636|gb|AED91019.1| DnaQ-like exonuclease domain-containing protein [Arabidopsis thaliana]	200	206	2.00E-89	103.0	84.0	91.0	DnaQ-like exonuclease domain-containing protein	gbpln	Arabidopsis thaliana	AT5G06450.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:1967869-1968489 REVERSE LENGTH=206	200	206	8.00E-92	103.0	84.0	91.0
Rsa1.0_00192.1.g8117.t3	ref|XP_002873256.1| hypothetical protein ARALYDRAFT_487451 [Arabidopsis lyrata subsp. lyrata] gi|297319093|gb|EFH49515.1| hypothetical protein ARALYDRAFT_487451 [Arabidopsis lyrata subsp. lyrata]	667	480	1.00E-128	72.0	37.9	45.3	hypothetical protein ARALYDRAFT_487451	gbpln	Arabidopsis lyrata	AT5G06440.3 | Symbols: | BEST Arabidopsis thaliana protein match is: Polyketide cyclase/dehydrase and lipid transport superfamily protein (TAIR:AT3G11720.3); Has 157 Blast hits to 155 proteins in 41 species: Archae - 0; Bacteria - 6; Metazoa - 5; Fungi - 6; Plants - 99; Viruses - 0; Other Eukaryotes - 41 (source: NCBI BLink). | chr5:1964641-1966807 REVERSE LENGTH=479	667	479	1.00E-127	71.8	37.5	45.0
Rsa1.0_00192.1.g8118.t1	dbj|BAB08961.1| unnamed protein product [Arabidopsis thaliana]	442	465	0	105.2	89.4	93.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G06390.1 | Symbols: FLA17 | FASCICLIN-like arabinogalactan protein 17 precursor | chr5:1952939-1955047 FORWARD LENGTH=458	442	458	0	103.6	89.1	93.0
Rsa1.0_00192.1.g8119.t1	ref|XP_002873253.1| NC domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319090|gb|EFH49512.1| NC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	202	259	5.00E-99	128.2	86.1	88.6	NC domain-containing protein	gbpln	Arabidopsis lyrata	AT5G06370.1 | Symbols: | NC domain-containing protein-related | chr5:1947299-1948432 REVERSE LENGTH=259	202	259	1.00E-101	128.2	86.1	87.6
Rsa1.0_00192.1.g8120.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00192.1.g8121.t2	dbj|BAJ34098.1| unnamed protein product [Thellungiella halophila]	235	235	1.00E-105	100.0	87.2	94.0	unnamed protein product	----	----	AT5G06320.1 | Symbols: NHL3 | NDR1/HIN1-like 3 | chr5:1931016-1931711 REVERSE LENGTH=231	235	231	2.00E-97	98.3	83.0	89.4
Rsa1.0_00192.1.g8122.t1	ref|XP_002871317.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317154|gb|EFH47576.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	245	313	6.00E-24	127.8	30.6	44.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321	245	321	4.00E-23	131.0	26.5	37.6
Rsa1.0_00192.1.g8123.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	649	1529	1.00E-139	235.6	37.4	52.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	649	746	1.00E-97	114.9	27.7	38.4
Rsa1.0_00193.1.g8124.t1	dbj|BAJ34509.1| unnamed protein product [Thellungiella halophila]	280	284	1.00E-113	101.4	82.5	87.5	unnamed protein product	----	----	AT4G00950.1 | Symbols: MEE47 | Protein of unknown function (DUF688) | chr4:405984-407087 REVERSE LENGTH=291	280	291	1.00E-100	103.9	75.7	85.0
Rsa1.0_00193.1.g8125.t1	gb|EOA36597.1| hypothetical protein CARUB_v10011796mg [Capsella rubella]	561	572	0	102.0	68.3	78.6	hypothetical protein CARUB_v10011796mg	gbpln	Capsella rubella	AT1G43245.1 | Symbols: | SET domain-containing protein | chr1:16308982-16310883 REVERSE LENGTH=558	561	558	0	99.5	66.7	76.1

Rsa1.0_00193.1.g8126.t1	gb|EOA21258.1| hypothetical protein CARUB_v10001609mg [Capsella rubella] gi|482557067|gb|EOA21259.1| hypothetical protein CARUB_v10001609mg [Capsella rubella]	283	292	1.00E−105	103.2	73.9	82.7	hypothetical protein CARUB_v10001609mg	gbpln	Capsella rubella	AT4G00940.1 | Symbols: | Dof−type zinc finger DNA−binding family protein | chr4:403320−404204 REVERSE LENGTH=294	283	294	1.00E−102	103.9	67.1	74.6
Rsa1.0_00193.1.g8127.t1	ref|NP_179553.1| F−box protein [Arabidopsis thaliana] gi|75216815|sp|Q9ZUN0.1|FB113_ARATH RecName: Full=Putative F−box protein At2g19630 gi|4191792|gb|AAD10161.1| hypothetical protein [Arabidopsis thaliana] gi|330251810|gb|AEC06904.1| F−box protein [Arabidopsis thaliana]	308	297	4.00E−23	96.4	26.6	34.7	F−box protein	gbpln	Arabidopsis thaliana	AT2G19630.1 | Symbols: | F−box and associated interaction domains−containing protein | chr2:8490217−8491110 REVERSE LENGTH=297	308	297	1.00E−25	96.4	26.6	34.7
Rsa1.0_00193.1.g8128.t1	gb|EOA23025.1| hypothetical protein CARUB_v10003790mg [Capsella rubella]	484	485	0	100.2	83.5	91.7	hypothetical protein CARUB_v10003790mg	gbpln	Capsella rubella	AT4G00910.1 | Symbols: | Aluminium activated malate transporter family protein | chr4:389370−391287 REVERSE LENGTH=497	484	497	0	102.7	84.5	90.9
Rsa1.0_00193.1.g8129.t1	ref|XP_002875007.1| hypothetical protein ARALYDRAFT_490474 [Arabidopsis lyrata subsp. lyrata] gi|297320844|gb|EFH51266.1| hypothetical protein ARALYDRAFT_490474 [Arabidopsis lyrata subsp. lyrata]	255	263	1.00E−122	103.1	86.3	91.4	hypothetical protein ARALYDRAFT_490474	gbpln	Arabidopsis lyrata	AT4G00905.1 | Symbols: | NC domain−containing protein−related | chr4:387865−389060 FORWARD LENGTH=263	255	263	1.00E−123	103.1	85.1	92.2
Rsa1.0_00193.1.g8130.t1	ref|NP_191999.1| Ca2+−transporting ATPase [Arabidopsis thaliana] gi|12230024|sp|O23087.1|ECA2_ARATH RecName: Full=Calcium−transporting ATPase 2, endoplasmic reticulum−type gi|2252852|gb|AAB62850.1| similar to the cation transport ATPases family [Arabidopsis thaliana] gi|4185853|emb|CAA10659.1| Ca2+−ATPase [Arabidopsis thaliana] gi|7267429|emb|CAB80899.1| Ca2+−transporting ATPase−like protein [Arabidopsis thaliana] gi|332656553|gb|AEE81953.1| calcium−transporting ATPase 2 [Arabidopsis thaliana]	1058	1054	0	99.6	93.2	96.2	Ca2+−transporting ATPase	gbpln	Arabidopsis thaliana	AT4G00900.1 | Symbols: ECA2, ATECA2 | ER−type Ca2+−ATPase 2 | chr4:382690−386226 REVERSE LENGTH=1054	1058	1054	0	99.6	93.2	96.2
Rsa1.0_00193.1.g8131.t1	ref|XP_002880980.1| hypothetical protein ARALYDRAFT_901765 [Arabidopsis lyrata subsp. lyrata] gi|297326819|gb|EFH57239.1| hypothetical protein ARALYDRAFT_901765 [Arabidopsis lyrata subsp. lyrata]	302	356	5.00E−83	117.9	55.3	67.9	hypothetical protein ARALYDRAFT_901765	gbpln	Arabidopsis lyrata	AT5G47300.1 | Symbols: | F−box and associated interaction domains−containing protein | chr5:19198125−19199375 FORWARD LENGTH=416	302	416	3.00E−81	137.7	53.6	70.2
Rsa1.0_00193.1.g8132.t1	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	327	1274	9.00E−50	389.6	39.1	50.5	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H−like superfamily protein | chr1:3263877−3264788 REVERSE LENGTH=303	327	303	7.00E−42	92.7	32.4	49.5
Rsa1.0_00193.1.g8133.t1	ref|XP_002883182.1| pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329022|gb|EFH59441.1| pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	472	477	0	101.1	86.4	92.4	pseudouridine synthase family protein	gbpln	Arabidopsis lyrata	AT3G19440.1 | Symbols: | Pseudouridine synthase family protein | chr3:6740778−6743132 FORWARD LENGTH=477	472	477	0	101.1	84.7	91.5

Rsa1.0_00193.1.g8134.t1	ref|NP_188576.1| cinnamyl alcohol dehydrogenase 4 [Arabidopsis thaliana] gi|1345655|sp|P48523.1|CADH4_ARATH RecName: Full=Cinnamyl alcohol dehydrogenase 4; Short=AtCAD4; AltName: Full=Cinnamyl alcohol dehydrogenase C gi|13877997|gb|AAK44076.1|AF370261_1 putative cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|757535|emb|CAA83508.1| cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|11994468|dbj|BAB02470.1| cinnamyl alcohol dehydrogenase 2 [Arabidopsis thaliana] gi|17104723|gb|AAL34250.1| putative cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|31880041|gb|AAP59434.1| cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|169635512|emb|CAP09010.1| cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|169635514|emb|CAP09011.1| cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|169635516|emb|CAP09012.1| cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|169635518|emb|CAP09013.1| cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|169635520|emb|CAP09014.1|	365	365	0	100.0	93.4	96.4	cinnamyl alcohol dehydrogenase 4	gbpln	Arabidopsis thaliana	AT3G19450.1 | Symbols: CAD4, ATCAD4, CAD, CAD-C | GroES-like zinc-binding alcohol dehydrogenase family protein | chr3:6744859-6747005 FORWARD LENGTH=365	365	365	0	100.0	93.4	96.4
Rsa1.0_00193.1.g8135.t1	ref|NP_566635.1| reticulon-like protein B11 [Arabidopsis thaliana] gi|75274072|sp|Q9LT71.1|RTNLK_ARATH RecName: Full=Reticulon-like protein B11; Short=AtRTNLB11 gi|11994469|dbj|BAB02471.1| unnamed protein product [Arabidopsis thaliana] gi|26449615|dbj|BAC41933.1| unknown protein [Arabidopsis thaliana] gi|28950723|gb|AAO63285.1| At3g19460 [Arabidopsis thaliana] gi|332642721|gb|AEE76242.1| reticulon-like protein B11 [Arabidopsis thaliana]	196	200	1.00E-81	102.0	78.6	88.3	reticulon-like protein B11	gbpln	Arabidopsis thaliana	AT3G19460.1 | Symbols: | Reticulon family protein | chr3:6747600-6748904 FORWARD LENGTH=200	196	200	4.00E-84	102.0	78.6	88.3
Rsa1.0_00193.1.g8136.t1	ref|XP_002885310.1| ATNHD1 [Arabidopsis lyrata subsp. lyrata] gi|297331150|gb|EFH61569.1| ATNHD1 [Arabidopsis lyrata subsp. lyrata]	580	575	0	99.1	90.2	94.8	ATNHD1	gbpln	Arabidopsis lyrata	AT3G19490.1 | Symbols: ATNHD1, NHD1 | sodium:hydrogen antiporter 1 | chr3:6754875-6758127 REVERSE LENGTH=576	580	576	0	99.3	88.3	94.0
Rsa1.0_00193.1.g8137.t2	gb|AAM61088.1| unknown [Arabidopsis thaliana]	256	270	1.00E-104	105.5	76.2	82.4	unknown	gbpln	Arabidopsis thaliana	AT3G19500.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:6759289-6760893 REVERSE LENGTH=270	256	270	1.00E-106	105.5	75.8	82.4
Rsa1.0_00193.1.g8138.t1	ref|NP_188582.1| homeobox protein HAT3.1 [Arabidopsis thaliana] gi|148886602|sp|Q04996.3|HAT31_ARATH RecName: Full=Homeobox protein HAT3.1 gi|26449313|dbj|BAC41784.1| putative homeobox protein HAT3.1 [Arabidopsis thaliana] gi|29029042|gb|AAO64900.1| At3g19510 [Arabidopsis thaliana] gi|332642729|gb|AEE76250.1| homeobox protein HAT3.1 [Arabidopsis thaliana]	695	723	0	104.0	69.2	79.7	homeobox protein HAT3.1	gbpln	Arabidopsis thaliana	AT3G19510.1 | Symbols: HAT3.1 | Homeodomain-like protein with RING/FYVE/PHD-type zinc finger domain | chr3:6763205-6766049 REVERSE LENGTH=723	695	723	0	104.0	69.2	79.7
Rsa1.0_00193.1.g8139.t1	gb|EOA30442.1| hypothetical protein CARUB_v10013565mg [Capsella rubella]	471	484	0	102.8	89.8	93.8	hypothetical protein CARUB_v10013565mg	gbpln	Capsella rubella	AT3G19540.1 | Symbols: | Protein of unknown function (DUF620) | chr3:6780762-6782633 FORWARD LENGTH=485	471	485	0	103.0	89.6	93.6
Rsa1.0_00193.1.g8140.t1	ref|XP_002885314.1| hypothetical protein ARALYDRAFT_479468 [Arabidopsis lyrata subsp. lyrata] gi|297331154|gb|EFH61573.1| hypothetical protein ARALYDRAFT_479468 [Arabidopsis lyrata subsp. lyrata]	110	110	2.00E-41	100.0	78.2	86.4	hypothetical protein ARALYDRAFT_479468	gbpln	Arabidopsis lyrata	AT3G19550.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; Has 36 Blast hits to 36 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6787462-6788165 REVERSE LENGTH=110	110	110	3.00E-43	100.0	76.4	83.6

Rsa1.0_00193.1.g8141.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	1101	1534	0	139.3	70.0	81.2	F17L21.7	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1101	1262	2.00E-96	114.6	17.3	26.6
Rsa1.0_00193.1.g8142.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00193.1.g8143.t1	ref|NP_188589.1| Amino acid permease family protein [Arabidopsis thaliana] gi|75311166|sp|Q9LH39.1|PHSD_ARATH RecName: Full=Probable polyamine transporter At3g19553 gi|9294126|dbj|BAB01977.1| unnamed protein product [Arabidopsis thaliana] gi|332642736|gb|AEE76257.1| Amino acid permease family protein [Arabidopsis thaliana]	453	479	0	105.7	92.9	96.7	Amino acid permease family protein	gbpln	Arabidopsis thaliana	AT3G19553.1 | Symbols: | Amino acid permease family protein | chr3:6790988-6792507 REVERSE LENGTH=479	453	479	0	105.7	92.9	96.7
Rsa1.0_00193.1.g8144.t1	ref|XP_002883191.1| hypothetical protein ARALYDRAFT_898339 [Arabidopsis lyrata subsp. lyrata] gi|297329031|gb|EFH59450.1| hypothetical protein ARALYDRAFT_898339 [Arabidopsis lyrata subsp. lyrata]	381	360	3.00E-84	94.5	49.6	64.3	hypothetical protein ARALYDRAFT_898339	gbpln	Arabidopsis lyrata	AT3G19560.1 | Symbols: | F-box family protein | chr3:6793717-6794802 FORWARD LENGTH=361	381	361	3.00E-77	94.8	44.9	59.3
Rsa1.0_00193.1.g8145.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00193.1.g8146.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	247	1142	1.00E-42	462.3	37.7	50.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	247	575	2.00E-22	232.8	26.3	41.3
Rsa1.0_00193.1.g8147.t1	sp|Q9CA02.1|FB198_ARATH RecName: Full=F-box protein At3g49510 gi|12324446|gb|AAG52186.1|AC012329_13 unknown protein; 74683-75849 [Arabidopsis thaliana] gi|33589708|gb|AAQ22620.1| At3g49510 [Arabidopsis thaliana] gi|110735675|dbj|BAE99818.1| hypothetical protein [Arabidopsis thaliana]	470	388	2.00E-69	82.6	37.0	49.4	RecName: Full=F-box protein At3g49510 gi|12324446|gb|AAG52186.1|AC012329_13 unknown protein; 74683-75849	gbpln	Arabidopsis thaliana	AT3G49510.1 | Symbols: | F-box family protein | chr3:18353891-18356508 FORWARD LENGTH=662	470	662	5.00E-69	140.9	34.7	46.6
Rsa1.0_00193.1.g8148.t2	sp|Q9CA02.1|FB198_ARATH RecName: Full=F-box protein At3g49510 gi|12324446|gb|AAG52186.1|AC012329_13 unknown protein; 74683-75849 [Arabidopsis thaliana] gi|33589708|gb|AAQ22620.1| At3g49510 [Arabidopsis thaliana] gi|110735675|dbj|BAE99818.1| hypothetical protein [Arabidopsis thaliana]	377	388	9.00E-75	102.9	46.9	63.9	RecName: Full=F-box protein At3g49510 gi|12324446|gb|AAG52186.1|AC012329_13 unknown protein; 74683-75849	gbpln	Arabidopsis thaliana	AT3G49510.1 | Symbols: | F-box family protein | chr3:18353891-18356508 FORWARD LENGTH=662	377	662	3.00E-75	175.6	44.6	61.0
Rsa1.0_00193.1.g8149.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00193.1.g8150.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00193.1.g8151.t1	ref|XP_002883191.1| hypothetical protein ARALYDRAFT_898339 [Arabidopsis lyrata subsp. lyrata] gi|297329031|gb|EFH59450.1| hypothetical protein ARALYDRAFT_898339 [Arabidopsis lyrata subsp. lyrata]	367	360	2.00E-72	98.1	47.7	63.8	hypothetical protein ARALYDRAFT_898339	gbpln	Arabidopsis lyrata	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	367	395	6.00E-69	107.6	45.5	62.4
Rsa1.0_00193.1.g8152.t1	gb|ABI74621.1| C2H2 zinc finger protein 1 [Eutrema halophilum] gi|312282663|dbj|BAJ34197.1| unnamed protein product [Thellungiella halophila]	285	276	5.00E-83	96.8	72.3	80.0	C2H2 zinc finger protein 1	gbpln	Eutrema halophilum	AT3G19580.2 | Symbols: AZF2, ZF2 | zinc-finger protein 2 | chr3:6803293-6804114 REVERSE LENGTH=273	285	273	5.00E-83	95.8	73.3	80.7
Rsa1.0_00193.1.g8153.t1	ref|NP_001118664.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|9294424|dbj|BAB02544.1| unnamed protein product [Arabidopsis thaliana] gi|332642743|gb|AEE76264.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana]	308	307	4.00E-93	99.7	59.4	72.4	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G19595.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr3:6808585-6809508 REVERSE LENGTH=307	308	307	1.00E-95	99.7	59.4	72.4
Rsa1.0_00193.1.g8154.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00194.1.g8155.t1	dbj|BAJ33811.1| unnamed protein product [Thellungiella halophila]	328	213	1.00E-105	64.9	56.7	59.8	unnamed protein product	----	----	AT3G03190.1 | Symbols: ATGSTF11, ATGSTF6, GSTF11 | glutathione S-transferase F11 | chr3:735071-735877 FORWARD LENGTH=214	328	214	4.00E-97	65.2	51.8	55.5

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<tr><td>Rsa1.0_00194.1.g8156.t1</td><td>ref|XP_002882276.1| hypothetical protein ARALYDRAFT_477563 [Arabidopsis lyrata subsp. lyrata] gi|297328116|gb|EFH58535.1| hypothetical protein ARALYDRAFT_477563 [Arabidopsis lyrata subsp. lyrata]</td><td>130</td><td>130</td><td>2.00E-67</td><td>100.0</td><td>93.8</td><td>99.2</td><td>hypothetical protein ARALYDRAFT_477563</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G03160.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular protein transport; LOCATED IN: endomembrane system, integral to membrane, endoplasmic reticulum; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: B-cell receptor-associated 31-like (InterPro:IPR008417); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G17190.1); Has 102 Blast hits to 102 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 102; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:729876-730268 FORWARD LENGTH=130</td><td>130</td><td>130</td><td>4.00E-70</td><td>100.0</td><td>93.8</td><td>99.2</td></tr>
<tr><td>Rsa1.0_00194.1.g8157.t1</td><td>gb|AAP37967.1| seed specific protein Bn15D1B [Brassica napus]</td><td>119</td><td>120</td><td>4.00E-58</td><td>100.8</td><td>95.8</td><td>96.6</td><td>seed specific protein Bn15D1B</td><td>gbpln</td><td>Brassica napus</td><td>AT3G03150.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G17165.1); Has 39 Blast hits to 39 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:727733-729357 REVERSE LENGTH=121</td><td>119</td><td>121</td><td>5.00E-50</td><td>101.7</td><td>80.7</td><td>86.6</td></tr>
<tr><td>Rsa1.0_00194.1.g8158.t1</td><td>gb|EOA32118.1| hypothetical protein CARUB_v10015369mg [Capsella rubella]</td><td>755</td><td>761</td><td>0</td><td>100.8</td><td>80.9</td><td>86.5</td><td>hypothetical protein CARUB_v10015369mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G03140.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr3:724348-727093 FORWARD LENGTH=769</td><td>755</td><td>769</td><td>0</td><td>101.9</td><td>79.3</td><td>85.8</td></tr>
<tr><td>Rsa1.0_00194.1.g8159.t1</td><td>gb|EOA31520.1| hypothetical protein CARUB_v10014710mg [Capsella rubella]</td><td>212</td><td>192</td><td>1.00E-102</td><td>90.6</td><td>87.3</td><td>89.2</td><td>hypothetical protein CARUB_v10014710mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G03120.1 | Symbols: ATARFB1C, ARFB1C | ADP-ribosylation factor B1C | chr3:717345-718914 FORWARD LENGTH=192</td><td>212</td><td>192</td><td>1.00E-104</td><td>90.6</td><td>86.8</td><td>89.6</td></tr>
<tr><td>Rsa1.0_00194.1.g8160.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>2341</td><td>1274</td><td>0</td><td>54.4</td><td>23.5</td><td>32.4</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G03110.1 | Symbols: XPO1B, CRM1B | exportin 1B | chr3:708966-716879 FORWARD LENGTH=1076</td><td>2341</td><td>1076</td><td>0</td><td>46.0</td><td>16.5</td><td>19.9</td></tr>
<tr><td>Rsa1.0_00194.1.g8161.t8</td><td>ref|XP_002882274.1| hypothetical protein ARALYDRAFT_896304 [Arabidopsis lyrata subsp. lyrata] gi|297328114|gb|EFH58533.1| hypothetical protein ARALYDRAFT_896304 [Arabidopsis lyrata subsp. lyrata]</td><td>475</td><td>1076</td><td>0</td><td>226.5</td><td>73.7</td><td>83.4</td><td>hypothetical protein ARALYDRAFT_896304</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G03110.1 | Symbols: XPO1B, CRM1B | exportin 1B | chr3:708966-716879 FORWARD LENGTH=1076</td><td>475</td><td>1076</td><td>0</td><td>226.5</td><td>72.8</td><td>82.9</td></tr>
<tr><td>Rsa1.0_00194.1.g8162.t1</td><td>ref|NP_566192.1| putative NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 [Arabidopsis thaliana] gi|12644540|sp|Q9M9M9.1|NDUAC_ARATH RecName: Full=Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 gi|6714426|gb|AAF26114.1|AC012328_17 unknown protein [Arabidopsis thaliana] gi|13878173|gb|AAK44164.1|AF370349_1 unknown protein [Arabidopsis thaliana] gi|17104529|gb|AAL34153.1| unknown protein [Arabidopsis thaliana] gi|21593289|gb|AAM65238.1| probable NADH-ubiquinone oxidoreductase subunit B17.2 (Complex I-B17.2) (CI-B17.2) [Arabidopsis thaliana] gi|332640380|gb|AEE73901.1| putative NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 [Arabidopsis thaliana]</td><td>159</td><td>159</td><td>7.00E-86</td><td>100.0</td><td>94.3</td><td>98.1</td><td>putative NADH dehydrogenase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G03100.1 | Symbols: | NADH:ubiquinone oxidoreductase, 17.2kDa subunit | chr3:705564-707578 REVERSE LENGTH=159</td><td>159</td><td>159</td><td>2.00E-88</td><td>100.0</td><td>94.3</td><td>98.1</td></tr>
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Rsa1.0_00194.1.g8163.t1	ref|NP_186959.2| D-xylose-proton symporter-like 1 [Arabidopsis thaliana] gi|75329736|sp|Q8L6Z8.1|XYLL1_ARATH RecName: Full=D-xylose-proton symporter-like 1 gi|22655210|gb|AAM98195.1| unknown protein [Arabidopsis thaliana] gi|34098871|gb|AAQ56818.1| At3g03090 [Arabidopsis thaliana] gi|332640379|gb|AEE73900.1| D-xylose-proton symporter-like 1 [Arabidopsis thaliana]	505	503	0	99.6	86.5	93.3	D-xylose-proton symporter-like 1	gbpln	Arabidopsis thaliana	AT3G03090.1 | Symbols: AtVGT1, VGT1 | vacuolar glucose transporter 1 | chr3:700749-704579 REVERSE LENGTH=503	505	503	0	99.6	86.5	93.3
Rsa1.0_00194.1.g8164.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00194.1.g8165.t1	gb|EOA32971.1| hypothetical protein CARUB_v10016301mg [Capsella rubella]	345	350	1.00E-171	101.4	84.1	91.9	hypothetical protein CARUB_v10016301mg	gbpln	Capsella rubella	AT3G03080.1 | Symbols: | Zinc-binding dehydrogenase family protein | chr3:698530-700278 REVERSE LENGTH=350	345	350	1.00E-171	101.4	83.8	90.7
Rsa1.0_00194.1.g8166.t1	ref|XP_002884357.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330197|gb|EFH60616.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	352	351	1.00E-173	99.7	83.2	90.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G03080.1 | Symbols: | Zinc-binding dehydrogenase family protein | chr3:698530-700278 REVERSE LENGTH=350	352	350	1.00E-174	99.4	83.2	90.6
Rsa1.0_00194.1.g8167.t1	ref|XP_002882270.1| hypothetical protein ARALYDRAFT_340454 [Arabidopsis lyrata subsp. lyrata] gi|297328110|gb|EFH58529.1| hypothetical protein ARALYDRAFT_340454 [Arabidopsis lyrata subsp. lyrata]	618	642	0	103.9	91.4	95.0	hypothetical protein ARALYDRAFT_340454	gbpln	Arabidopsis lyrata	AT3G03060.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:692188-695424 FORWARD LENGTH=628	618	628	0	101.6	89.8	93.9
Rsa1.0_00194.1.g8168.t1	gb|EOA29758.1| hypothetical protein CARUB_v10012847mg [Capsella rubella]	1159	1147	0	99.0	95.6	97.6	hypothetical protein CARUB_v10012847mg	gbpln	Capsella rubella	AT3G03050.1 | Symbols: CSLD3, KJK, ATCSLD3 | cellulose synthase-like D3 | chr3:687873-691629 FORWARD LENGTH=1145	1159	1145	0	98.8	94.3	96.5
Rsa1.0_00194.1.g8169.t1	ref|XP_002884336.1| phosphatase 2C family protein [Arabidopsis lyrata subsp. lyrata] gi|297330176|gb|EFH60595.1| phosphatase 2C family protein [Arabidopsis lyrata subsp. lyrata]	462	490	0	106.1	85.3	91.6	phosphatase 2C family protein	gbpln	Arabidopsis lyrata	AT3G02750.2 | Symbols: | Protein phosphatase 2C family protein | chr3:593601-595457 REVERSE LENGTH=492	462	492	0	106.5	83.5	89.8
Rsa1.0_00194.1.g8170.t1	gb|AAF36996.1|AF236092_1 isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase [Brassica oleracea var. botrytis]	310	281	2.33E-156	90.6	87.4	88.7	isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	gbpln	Brassica oleracea	AT3G02780.1 | Symbols: IPP2, IPIAT1, IDI2 | isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase 2 | chr3:602578-604648 REVERSE LENGTH=284	310	284	1.00E-135	91.6	82.9	84.5
Rsa1.0_00194.1.g8171.t1	dbj|BAJ34455.1| unnamed protein product [Thellungiella halophila]	105	105	2.00E-51	100.0	97.1	100.0	unnamed protein product	----	----	AT3G02790.1 | Symbols: | zinc finger (C2H2 type) family protein | chr3:604926-605243 FORWARD LENGTH=105	105	105	1.00E-52	100.0	96.2	97.1
Rsa1.0_00194.1.g8172.t1	ref|NP_186929.2| tyrosine specific protein phosphatase-like protein [Arabidopsis thaliana] gi|51969092|dbj|BAD43238.1| unknown protein [Arabidopsis thaliana] gi|332640340|gb|AEE73861.1| atypical dual-specificity phosphatase [Arabidopsis thaliana]	215	203	1.00E-82	94.4	70.2	76.3	tyrosine specific protein phosphatase-like protein	gbpln	Arabidopsis thaliana	AT3G02800.1 | Symbols: | Tyrosine phosphatase family protein | chr3:606638-607704 REVERSE LENGTH=203	215	203	4.00E-85	94.4	70.2	76.3
Rsa1.0_00194.1.g8173.t1	ref|NP_186930.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|6728981|gb|AAF26979.1|AC018363_24 putative protein kinase [Arabidopsis thaliana] gi|28393294|gb|AAO42074.1| putative protein kinase [Arabidopsis thaliana] gi|28827262|gb|AAO50475.1| putative protein kinase [Arabidopsis thaliana] gi|332640341|gb|AEE73862.1| protein kinase domain-containing protein [Arabidopsis thaliana]	468	558	0	119.2	82.3	90.4	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G02810.1 | Symbols: | Protein kinase superfamily protein | chr3:608729-610785 REVERSE LENGTH=558	468	558	0	119.2	82.3	90.4
Rsa1.0_00194.1.g8174.t1	ref|NP_186931.2| CCHC-type zinc knuckle protein [Arabidopsis thaliana] gi|26453004|dbj|BAC43578.1| putative CCHC-type zinc finger protein [Arabidopsis thaliana] gi|106879191|gb|ABF82625.1| At3g02820 [Arabidopsis thaliana] gi|332640342|gb|AEE73863.1| CCHC-type zinc knuckle protein [Arabidopsis thaliana]	300	282	1.00E-128	94.0	78.7	84.7	CCHC-type zinc knuckle protein	gbpln	Arabidopsis thaliana	AT3G02820.1 | Symbols: | zinc knuckle (CCHC-type) family protein | chr3:611573-613294 FORWARD LENGTH=282	300	282	1.00E-130	94.0	78.7	84.7

Rsa1.0_00194.1.g8175.t1	ref|NP_566183.1| zinc finger CCCH domain-containing protein 33 [Arabidopsis thaliana] gi|62901378|sp|Q8GXX7.1|C3H33_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 33; Short=AtC3H33; AltName: Full=Zinc finger CCCH domain-containing protein ZFN1 gi|26451016|dbj|BAC42614.1| putative zinc finger protein 1 zfn1 [Arabidopsis thaliana] gi|109134113|gb|ABG25055.1| At3g02830 [Arabidopsis thaliana] gi|332640343|gb|AEE73864.1| zinc finger CCCH domain-containing protein 33 [Arabidopsis thaliana]	376	397	0	105.6	88.8	92.3	zinc finger CCCH domain-containing protein 33	gbpln	Arabidopsis thaliana	AT3G02830.1 | Symbols: ZFN1 | zinc finger protein 1 | chr3:614075-615916 FORWARD LENGTH=397	376	397	0	105.6	88.8	92.3
Rsa1.0_00194.1.g8176.t1	ref|NP_566184.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|6728978|gb|AAF26976.1|AC018363_21 unknown protein [Arabidopsis thaliana] gi|26452125|dbj|BAC43151.1| unknown protein [Arabidopsis thaliana] gi|27311855|gb|AAO00893.1| expressed protein [Arabidopsis thaliana] gi|30725622|gb|AAP37833.1| At3g02840 [Arabidopsis thaliana] gi|332640344|gb|AEE73865.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	386	379	1.00E-159	98.2	77.7	86.8	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G02840.1 | Symbols: | ARM repeat superfamily protein | chr3:618480-619619 FORWARD LENGTH=379	386	379	1.00E-161	98.2	77.7	86.8
Rsa1.0_00194.1.g8177.t1	gb|EOA29886.1| hypothetical protein CARUB_v10012982mg [Capsella rubella]	833	830	0	99.6	90.8	94.0	hypothetical protein CARUB_v10012982mg	gbpln	Capsella rubella	AT3G02850.1 | Symbols: SKOR | STELAR K+ outward rectifier | chr3:619701-623473 REVERSE LENGTH=828	833	828	0	99.4	90.5	93.5
Rsa1.0_00194.1.g8178.t1	ref|XP_002884343.1| hypothetical protein ARALYDRAFT_477531 [Arabidopsis lyrata subsp. lyrata] gi|297330183|gb|EFH60602.1| hypothetical protein ARALYDRAFT_477531 [Arabidopsis lyrata subsp. lyrata]	271	271	1.00E-139	100.0	91.9	95.9	hypothetical protein ARALYDRAFT_477531	gbpln	Arabidopsis lyrata	AT3G02870.1 | Symbols: VTC4 | Inositol monophosphatase family protein | chr3:627742-629682 REVERSE LENGTH=271	271	271	1.00E-140	100.0	91.9	95.6
Rsa1.0_00195.1.g8179.t1	gb|EOA30625.1| hypothetical protein CARUB_v10013760mg, partial [Capsella rubella]	332	429	3.00E-61	129.2	47.0	59.0	hypothetical protein CARUB_v10013760mg, partial	gbpln	Capsella rubella	AT3G17570.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6009413-6010558 FORWARD LENGTH=381	332	381	1.00E-61	114.8	47.6	59.3
Rsa1.0_00195.1.g8180.t1	ref|XP_003521839.1| PREDICTED: translation initiation factor eIF-2B subunit alpha-like [Glycine max]	64	382	1.00E-18	596.9	70.3	73.4	PREDICTED: translation initiation factor eIF-2B subunit alpha-like	gbenv/gbpln	Glycine max	AT1G72340.1 | Symbols: | NagB/RpiA/CoA transferase-like superfamily protein | chr1:27236898-27238482 FORWARD LENGTH=382	64	382	3.00E-21	596.9	70.3	73.4
Rsa1.0_00195.1.g8181.t1	ref|XP_002883069.1| hypothetical protein ARALYDRAFT_898099 [Arabidopsis lyrata subsp. lyrata] gi|297328909|gb|EFH59328.1| hypothetical protein ARALYDRAFT_898099 [Arabidopsis lyrata subsp. lyrata]	82	80	2.00E-35	97.6	89.0	92.7	hypothetical protein ARALYDRAFT_898099	gbpln	Arabidopsis lyrata	AT3G17580.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G48330.1); Has 40 Blast hits to 40 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6015276-6015518 FORWARD LENGTH=80	82	80	3.00E-34	97.6	80.5	84.1
Rsa1.0_00195.1.g8182.t1	ref|NP_850605.1| transcription factor HY5-like protein [Arabidopsis thaliana] gi|55976199|sp|Q8W191.1|HYH_ARATH RecName: Full=Transcription factor HY5-like; AltName: Full=HY5 homolog gi|18042111|gb|AAL57834.1|AF453477_1 HY5-like protein [Arabidopsis thaliana] gi|51969022|dbj|BAD43203.1| bZip transcription factor AtbZip64 [Arabidopsis thaliana] gi|51969188|dbj|BAD43286.1| bZip transcription factor AtbZip64 [Arabidopsis thaliana] gi|332642454|gb|AEE75975.1| transcription factor HY5-like protein [Arabidopsis thaliana]	150	149	2.00E-60	99.3	86.7	90.0	transcription factor HY5-like protein	gbpln	Arabidopsis thaliana	AT3G17609.2 | Symbols: HYH | HY5-homolog | chr3:6023971-6024585 FORWARD LENGTH=149	150	149	6.00E-63	99.3	86.7	90.0
Rsa1.0_00195.1.g8183.t1	dbj|BAB02051.1| unnamed protein product [Arabidopsis thaliana]	339	506	1.00E-151	149.3	83.2	91.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G17611.1 | Symbols: ATRBL14, RBL14 | RHOMBOID-like protein 14 | chr3:6024946-6026173 FORWARD LENGTH=334	339	334	1.00E-151	98.5	83.2	91.2

Rsa1.0_00195.1.g8184.t1	gb|EOA29911.1| hypothetical protein CARUB_v10013004mg [Capsella rubella] gi|482565723|gb|EOA29912.1| hypothetical protein CARUB_v10013004mg [Capsella rubella]	800	800	0	100.0	89.8	95.6	hypothetical protein CARUB_v10013004mg	gbpln	Capsella rubella	AT3G17630.1 | Symbols: ATCHX19, CHX19 | cation/H+ exchanger 19 | chr3:6029201-6031773 FORWARD LENGTH=800	800	800	0	100.0	89.6	95.0
Rsa1.0_00195.1.g8185.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00195.1.g8186.t1	ref|NP_179323.1| protein SUPPRESSOR OF NIM1 1 [Arabidopsis thaliana] gi|75272519|sp|Q8LL17.1|SON1_ARATH RecName: Full=Protein SUPPRESSOR OF NIM1 1 gi|22023774|gb|AAM89220.1|AF472589_1 suppressor of nim1-1 [Arabidopsis thaliana] gi|330251518|gb|AEC06612.1| protein SUPPRESSOR OF NIM1 1 [Arabidopsis thaliana]	364	370	1.00E-101	101.6	58.0	71.7	protein SUPPRESSOR OF NIM1 1	gbpln	Arabidopsis thaliana	AT2G17310.1 | Symbols: SON1 | F-box and associated interaction domains-containing protein | chr2:7531212-7532324 FORWARD LENGTH=370	364	370	1.00E-104	101.6	58.0	71.7
Rsa1.0_00195.1.g8187.t1	ref|NP_179323.1| protein SUPPRESSOR OF NIM1 1 [Arabidopsis thaliana] gi|75272519|sp|Q8LL17.1|SON1_ARATH RecName: Full=Protein SUPPRESSOR OF NIM1 1 gi|22023774|gb|AAM89220.1|AF472589_1 suppressor of nim1-1 [Arabidopsis thaliana] gi|330251518|gb|AEC06612.1| protein SUPPRESSOR OF NIM1 1 [Arabidopsis thaliana]	306	370	9.00E-75	120.9	52.3	65.0	protein SUPPRESSOR OF NIM1 1	gbpln	Arabidopsis thaliana	AT2G17310.1 | Symbols: SON1 | F-box and associated interaction domains-containing protein | chr2:7531212-7532324 FORWARD LENGTH=370	306	370	2.00E-77	120.9	52.3	65.0
Rsa1.0_00195.1.g8188.t1	ref|XP_002883075.1| hypothetical protein ARALYDRAFT_479246 [Arabidopsis lyrata subsp. lyrata] gi|297328915|gb|EFH59334.1| hypothetical protein ARALYDRAFT_479246 [Arabidopsis lyrata subsp. lyrata]	710	714	0	100.6	92.3	95.9	hypothetical protein ARALYDRAFT_479246	gbpln	Arabidopsis lyrata	AT3G17650.1 | Symbols: YSL5, PDE321 | YELLOW STRIPE like 5 | chr3:6034307-6037087 FORWARD LENGTH=714	710	714	0	100.6	91.8	95.6
Rsa1.0_00195.1.g8189.t1	ref|XP_002883076.1| ARF-GAP domain 15 [Arabidopsis lyrata subsp. lyrata] gi|297328916|gb|EFH59335.1| ARF-GAP domain 15 [Arabidopsis lyrata subsp. lyrata]	256	253	1.00E-121	98.8	80.9	85.9	ARF-GAP domain 15	gbpln	Arabidopsis lyrata	AT3G17660.1 | Symbols: AGD15 | ARF-GAP domain 15 | chr3:6037717-6039092 FORWARD LENGTH=232	256	232	1.00E-118	90.6	78.9	84.0
Rsa1.0_00195.1.g8190.t1	ref|XP_002883077.1| hypothetical protein ARALYDRAFT_479249 [Arabidopsis lyrata subsp. lyrata] gi|297328917|gb|EFH59336.1| hypothetical protein ARALYDRAFT_479249 [Arabidopsis lyrata subsp. lyrata]	122	136	2.00E-52	111.5	83.6	91.0	hypothetical protein ARALYDRAFT_479249	gbpln	Arabidopsis lyrata	AT3G17668.1 | Symbols: ENA | DnaJ/Hsp40 cysteine-rich domain superfamily protein | chr3:6039640-6040324 FORWARD LENGTH=135	122	135	2.00E-53	110.7	81.1	88.5
Rsa1.0_00195.1.g8191.t11	ref|NP_188396.2| cyclic nucleotide gated channel 19 [Arabidopsis thaliana] gi|38503200|sp|Q9LDR2.1|CNG19_ARATH RecName: Full=Putative cyclic nucleotide-gated ion channel 19; AltName: Full=Cyclic nucleotide-binding transporter 2 gi|8131900|gb|AAF73129.1|AF148542_1 cyclic nucleotide-binding transporter 2 [Arabidopsis thaliana] gi|9294159|dbj|BAB02061.1| cyclic nucleotide and calmodulin-regulated ion channel protein-like [Arabidopsis thaliana] gi|332642472|gb|AEE75993.1| cyclic nucleotide gated channel 19 [Arabidopsis thaliana]	1405	729	0	51.9	41.6	45.0	cyclic nucleotide gated channel 19	gbpln	Arabidopsis thaliana	AT3G17690.1 | Symbols: ATCNGC19, CNGC19 | cyclic nucleotide gated channel 19 | chr3:6045382-6048339 FORWARD LENGTH=729	1405	729	0	51.9	41.6	45.0
Rsa1.0_00195.1.g8192.t1	ref|XP_002884782.1| hypothetical protein ARALYDRAFT_317819 [Arabidopsis lyrata subsp. lyrata] gi|297330622|gb|EFH61041.1| hypothetical protein ARALYDRAFT_317819 [Arabidopsis lyrata subsp. lyrata]	73	79	2.00E-11	108.2	57.5	69.9	hypothetical protein ARALYDRAFT_317819	gbpln	Arabidopsis lyrata	AT3G10195.1 | Symbols: | Putative membrane lipoprotein | chr3:3156630-3156976 REVERSE LENGTH=81	73	81	3.00E-11	111.0	52.1	63.0

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<tr><td>Rsa1.0_00195.1.g8193.t1</td><td>ref|NP_566585.1| cyclic nucleotide gated channel [Arabidopsis thaliana]
gi|38503198|sp|Q9LD37.1|CNG20_ARATH RecName: Full=Probable cyclic nucleotide-gated ion channel 20, chloroplastic; AltName: Full=Cyclic nucleotide-binding transporter 1; Flags: Precursor
gi|8131898|gb|AAF73128.1|AF148541_1 cyclic nucleotide-binding transporter 1 [Arabidopsis thaliana]
gi|8131901|gb|AAF73130.1|AF148542_2 cyclic nucleotide-binding transporter 1 [Arabidopsis thaliana]
gi|9294160|dbj|BAB02062.1| unnamed protein product [Arabidopsis thaliana]
gi|332642473|gb|AEE75994.1| cyclic nucleotide-binding transporter 1 [Arabidopsis thaliana]</td><td>760</td><td>764</td><td>0</td><td>100.5</td><td>88.2</td><td>92.6</td><td>cyclic nucleotide gated channel</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G17700.1 | Symbols: CNBT1, CNGC20, ATCNGC20 | cyclic nucleotide-binding transporter 1 | chr3:6049074-6052449 FORWARD LENGTH=764</td><td>760</td><td>764</td><td>0</td><td>100.5</td><td>88.2</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00195.1.g8194.t1</td><td>gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1621</td><td>1352</td><td>0</td><td>83.4</td><td>42.8</td><td>57.0</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>1621</td><td>746</td><td>1.00E-107</td><td>46.0</td><td>11.6</td><td>14.8</td></tr>
<tr><td>Rsa1.0_00195.1.g8195.t1</td><td>ref|NP_188403.1| glutamate decarboxylase 5 [Arabidopsis thaliana]
gi|238479801|ref|NP_001154621.1| glutamate decarboxylase 5 [Arabidopsis thaliana]
gi|75311525|sp|Q9LSH2.1|DCE5_ARATH RecName: Full=Glutamate decarboxylase 5; Short=GAD 5
gi|9294589|dbj|BAB02870.1| glutamate decarboxylase [Arabidopsis thaliana]
gi|332642482|gb|AEE76003.1| glutamate decarboxylase 5 [Arabidopsis thaliana]
gi|332642483|gb|AEE76004.1| glutamate decarboxylase 5 [Arabidopsis thaliana]</td><td>490</td><td>494</td><td>0</td><td>100.8</td><td>93.7</td><td>97.1</td><td>glutamate decarboxylase 5</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G17760.2 | Symbols: GAD5 | glutamate decarboxylase 5 | chr3:6078893-6080838 REVERSE LENGTH=494</td><td>490</td><td>494</td><td>0</td><td>100.8</td><td>93.7</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00195.1.g8196.t2</td><td>gb|EOA32502.1| hypothetical protein CARUB_v10015783mg [Capsella rubella]</td><td>511</td><td>398</td><td>1.00E-119</td><td>77.9</td><td>45.4</td><td>54.4</td><td>hypothetical protein CARUB_v10015783mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G16740.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:5699476-5700651 FORWARD LENGTH=391</td><td>511</td><td>391</td><td>1.00E-115</td><td>76.5</td><td>43.4</td><td>54.2</td></tr>
<tr><td>Rsa1.0_00195.1.g8197.t1</td><td>ref|XP_002891431.1| hypothetical protein ARALYDRAFT_473983 [Arabidopsis lyrata subsp. lyrata]
gi|297337273|gb|EFH67690.1| hypothetical protein ARALYDRAFT_473983 [Arabidopsis lyrata subsp. lyrata]</td><td>129</td><td>129</td><td>6.00E-60</td><td>100.0</td><td>89.1</td><td>92.2</td><td>hypothetical protein ARALYDRAFT_473983</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G48440.1 | Symbols: | B-cell receptor-associated 31-like | chr1:17907075-17908327 FORWARD LENGTH=129</td><td>129</td><td>129</td><td>6.00E-62</td><td>100.0</td><td>87.6</td><td>91.5</td></tr>
<tr><td>Rsa1.0_00195.1.g8198.t1</td><td>gb|ABW82644.1| purple acid phosphatase 17 [Brassica napus]
gi|158905970|gb|ABW82645.1| purple acid phosphatase 17 [Brassica napus]
gi|295854825|gb|ADG45869.1| purple acid phosphatase 17 isoform 2 [Brassica oleracea var. viridis]
gi|295854833|gb|ADG45873.1| purple acid phosphatase 17 isoform 2 [Brassica oleracea var. viridis]</td><td>311</td><td>333</td><td>0</td><td>107.1</td><td>98.1</td><td>99.4</td><td>purple acid phosphatase 17</td><td>gbpln</td><td>Brassica napus</td><td>AT3G17790.1 | Symbols: ATACP5, ATPAP17, PAP17 | purple acid phosphatase 17 | chr3:6089779-6090988 FORWARD LENGTH=338</td><td>311</td><td>338</td><td>1.00E-168</td><td>108.7</td><td>87.5</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00195.1.g8199.t1</td><td>ref|NP_188408.1| pyrimidine 1 [Arabidopsis thaliana]
gi|9294485|dbj|BAB02704.1| senescencs-related protein; dihydroorotate dehydrogenase-like protein [Arabidopsis thaliana]
gi|14334712|gb|AAK59534.1| putative dehydrogenase [Arabidopsis thaliana]
gi|16323430|gb|AAL15209.1| putative dehydrogenase [Arabidopsis thaliana]
gi|24850451|gb|AAN64919.1| putative dehydrogenase [Arabidopsis thaliana]
gi|332642489|gb|AEE76010.1| pyrimidine 1 [Arabidopsis thaliana]</td><td>425</td><td>426</td><td>0</td><td>100.2</td><td>91.8</td><td>96.5</td><td>pyrimidine 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G17810.1 | Symbols: PYD1 | pyrimidine 1 | chr3:6094279-6096289 FORWARD LENGTH=426</td><td>425</td><td>426</td><td>0</td><td>100.2</td><td>91.8</td><td>96.5</td></tr>
<tr><td>Rsa1.0_00195.1.g8200.t1</td><td>dbj|BAA04994.1| glutamine synthetase [Raphanus sativus]</td><td>354</td><td>354</td><td>0</td><td>100.0</td><td>96.6</td><td>99.2</td><td>glutamine synthetase</td><td>gbpln</td><td>Raphanus sativus</td><td>AT3G17820.1 | Symbols: ATGSKB6, GLN1.3, GLN1;3 | glutamine synthetase 1.3 | chr3:6097503-6099408 FORWARD LENGTH=354</td><td>354</td><td>354</td><td>0</td><td>100.0</td><td>92.9</td><td>96.9</td></tr>
</table>

Rsa1.0_00195.1.g8201.t1	ref|XP_002883091.1| hypothetical protein ARALYDRAFT_479268 [Arabidopsis lyrata subsp. lyrata] gi|297328931|gb|EFH59350.1| hypothetical protein ARALYDRAFT_479268 [Arabidopsis lyrata subsp. lyrata]	631	639	0	101.3	83.7	89.5	hypothetical protein ARALYDRAFT_479268	gbpln	Arabidopsis lyrata	AT3G17840.1 | Symbols: RLK902 | receptor-like kinase 902 | chr3:6106092-6108430 FORWARD LENGTH=647	631	647	0	102.5	82.7	89.1
Rsa1.0_00195.1.g8202.t1	ref|XP_002885231.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331071|gb|EFH61490.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	414	1327	7.00E-54	320.5	34.8	39.1	predicted protein	gbpln	Arabidopsis lyrata	AT3G17850.1 | Symbols: | Protein kinase superfamily protein | chr3:6109854-6116245 REVERSE LENGTH=1296	414	1296	2.00E-51	313.0	32.4	37.2
Rsa1.0_00195.1.g8203.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00195.1.g8204.t2	ref|NP_188457.1| zinc finger protein-like protein [Arabidopsis thaliana] gi|20453199|gb|AAM19839.1| AT3g18290/MIE15_8 [Arabidopsis thaliana] gi|29028750|gb|AAO64754.1| At3g18290/MIE15_8 [Arabidopsis thaliana] gi|332642556|gb|AEE76077.1| zinc finger protein-like protein [Arabidopsis thaliana]	1253	1254	0	100.1	89.4	93.2	zinc finger protein-like protein	gbpln	Arabidopsis thaliana	AT3G18290.1 | Symbols: EMB2454, BTS | zinc finger protein-related | chr3:6274308-6280174 FORWARD LENGTH=1254	1253	1254	0	100.1	89.4	93.2
Rsa1.0_00195.1.g8205.t1	ref|NP_188458.1| uncharacterized protein [Arabidopsis thaliana] gi|11994092|dbj|BAB01095.1| unnamed protein product [Arabidopsis thaliana] gi|40822865|gb|AAR92245.1| At3g18295 [Arabidopsis thaliana] gi|45752678|gb|AAS76237.1| At3g18295 [Arabidopsis thaliana] gi|332642558|gb|AEE76079.1| uncharacterized protein AT3G18295 [Arabidopsis thaliana]	181	216	3.00E-41	119.3	66.9	75.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G18295.1 | Symbols: | Protein of unknown function (DUF1639) | chr3:6281268-6282000 FORWARD LENGTH=216	181	216	1.00E-43	119.3	66.9	75.7
Rsa1.0_00195.1.g8206.t2	gb|EOA29997.1| hypothetical protein CARUB_v10013102mg [Capsella rubella]	686	692	0	100.9	88.8	94.2	hypothetical protein CARUB_v10013102mg	gbpln	Capsella rubella	AT3G18350.1 | Symbols: | Plant protein of unknown function (DUF639) | chr3:6297524-6300500 FORWARD LENGTH=692	686	692	0	100.9	89.2	94.8
Rsa1.0_00195.1.g8207.t1	gb|EOA32835.1| hypothetical protein CARUB_v10016148mg [Capsella rubella]	279	268	4.00E-67	96.1	68.8	77.8	hypothetical protein CARUB_v10016148mg	gbpln	Capsella rubella	AT3G18360.1 | Symbols: | VQ motif-containing protein | chr3:6300827-6301684 REVERSE LENGTH=285	279	285	8.00E-67	102.2	68.5	77.8
Rsa1.0_00195.1.g8208.t1	gb|EOA30946.1| hypothetical protein CARUB_v10014092mg [Capsella rubella]	344	346	1.00E-157	100.6	83.1	87.2	hypothetical protein CARUB_v10014092mg	gbpln	Capsella rubella	AT3G18380.3 | Symbols: | sequence-specific DNA binding transcription factors;sequence-specific DNA binding | chr3:6311002-6313181 REVERSE LENGTH=346	344	346	1.00E-158	100.6	82.6	87.5
Rsa1.0_00195.1.g8209.t1	ref|XP_002885255.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331095|gb|EFH61514.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	296	314	1.00E-141	106.1	89.5	93.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G18400.1 | Symbols: anac058, NAC058 | NAC domain containing protein 58 | chr3:6318745-6320593 REVERSE LENGTH=314	296	314	1.00E-143	106.1	89.2	92.9
Rsa1.0_00195.1.g8210.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00195.1.g8211.t1	ref|XP_002883130.1| hypothetical protein ARALYDRAFT_479342 [Arabidopsis lyrata subsp. lyrata] gi|297328970|gb|EFH59389.1| hypothetical protein ARALYDRAFT_479342 [Arabidopsis lyrata subsp. lyrata]	106	106	3.00E-55	100.0	97.2	100.0	hypothetical protein ARALYDRAFT_479342	gbpln	Arabidopsis lyrata	AT3G18410.2 | Symbols: | Complex I subunit NDUFS6 | chr3:6323203-6323761 FORWARD LENGTH=106	106	106	3.00E-57	100.0	96.2	99.1
Rsa1.0_00195.1.g8212.t2	gb|EOA30007.1| hypothetical protein CARUB_v10013111mg [Capsella rubella]	1303	690	0	53.0	50.1	51.3	hypothetical protein CARUB_v10013111mg	gbpln	Capsella rubella	AT3G18480.1 | Symbols: AtCASP, CASP | CCAAT-displacement protein alternatively spliced product | chr3:6336924-6341596 FORWARD LENGTH=689	1303	689	0	52.9	49.9	51.1
Rsa1.0_00195.1.g8213.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00195.1.g8214.t1	dbj|BAJ33681.1| unnamed protein product [Thellungiella halophila]	505	502	0	99.4	85.7	91.7	unnamed protein product	----	----	AT3G18490.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:6349090-6350592 REVERSE LENGTH=500	505	500	0	99.0	83.6	90.7
Rsa1.0_00196.1.g8215.t1	gb|EOA31118.1| hypothetical protein CARUB_v10014278mg [Capsella rubella]	304	299	1.00E-130	98.4	81.3	88.2	hypothetical protein CARUB_v10014278mg	gbpln	Capsella rubella	AT3G07350.1 | Symbols: | Protein of unknown function (DUF506) | chr3:2347674-2348570 FORWARD LENGTH=298	304	298	1.00E-132	98.0	81.3	88.8
Rsa1.0_00196.1.g8216.t1	ref|XP_002862652.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297308299|gb|EFH38910.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	451	460	0	102.0	87.4	92.7	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT3G07360.1 | Symbols: PUB9, ATPUB9 | plant U-box 9 | chr3:2354884-2356613 FORWARD LENGTH=460	451	460	0	102.0	87.4	92.9
Rsa1.0_00196.1.g8217.t1	gb|EOA31335.1| hypothetical protein CARUB_v10014508mg [Capsella rubella]	232	241	6.00E-81	103.9	70.3	78.9	hypothetical protein CARUB_v10014508mg	gbpln	Capsella rubella	AT3G07390.1 | Symbols: AIR12 | auxin-responsive family protein | chr3:2365452-2366273 FORWARD LENGTH=273	232	273	2.00E-80	117.7	70.3	78.9

Rsa1.0_00196.1.g8218.t1	ref|XP_002884647.1| hypothetical protein ARALYDRAFT_896904 [Arabidopsis lyrata subsp. lyrata] gi|297330487|gb|EFH60906.1| hypothetical protein ARALYDRAFT_896904 [Arabidopsis lyrata subsp. lyrata]	213	217	1.00E-113	101.9	96.2	99.1	hypothetical protein ARALYDRAFT_896904	gbpln	Arabidopsis lyrata	AT3G07410.1 | Symbols: AtRABA5b, RABA5b | RAB GTPase homolog A5B | chr3:2372485-2373482 REVERSE LENGTH=217	213	217	1.00E-115	101.9	95.8	98.6
Rsa1.0_00196.1.g8219.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00196.1.g8220.t1	gb|EOA31586.1| hypothetical protein CARUB_v10014780mg [Capsella rubella]	167	171	4.00E-66	102.4	74.3	84.4	hypothetical protein CARUB_v10014780mg	gbpln	Capsella rubella	AT3G07460.1 | Symbols: | Protein of unknown function, DUF538 | chr3:2384837-2385617 REVERSE LENGTH=177	167	177	1.00E-63	106.0	72.5	83.8
Rsa1.0_00196.1.g8221.t1	ref|NP_187405.1| calmodulin-like protein 3 [Arabidopsis thaliana] gi|297829300|ref|XP_002882532.1| ARF-GAP domain 11 [Arabidopsis lyrata subsp. lyrata] gi|75337571|sp|Q9SRR7.1|CML3_ARATH RecName: Full=Calmodulin-like protein 3 gi|6041859|gb|AAF02168.1|AC009853_28 putative calmodulin [Arabidopsis thaliana] gi|297328372|gb|EFH58791.1| ARF-GAP domain 11 [Arabidopsis lyrata subsp. lyrata] gi|332641028|gb|AEE74549.1| calmodulin-like protein 3 [Arabidopsis thaliana]	149	153	5.00E-63	102.7	89.9	97.3	calmodulin-like protein 3	gbpln	Arabidopsis lyrata	AT3G07490.1 | Symbols: AGD11 | ARF-GAP domain 11 | chr3:2391189-2391650 FORWARD LENGTH=153	149	153	1.00E-65	102.7	89.9	97.3
Rsa1.0_00196.1.g8222.t1	gb|EOA31112.1| hypothetical protein CARUB_v10014265mg [Capsella rubella]	288	302	5.00E-55	104.9	37.8	39.6	hypothetical protein CARUB_v10014265mg	gbpln	Capsella rubella	AT3G07560.1 | Symbols: APM2, PEX13 | peroxin 13 | chr3:2411616-2413310 REVERSE LENGTH=304	288	304	3.00E-57	105.6	37.8	39.9
Rsa1.0_00196.1.g8223.t1	ref|XP_002882536.1| hypothetical protein ARALYDRAFT_478080 [Arabidopsis lyrata subsp. lyrata] gi|297328376|gb|EFH58795.1| hypothetical protein ARALYDRAFT_478080 [Arabidopsis lyrata subsp. lyrata]	230	251	1.00E-101	109.1	83.5	90.4	hypothetical protein ARALYDRAFT_478080	gbpln	Arabidopsis lyrata	AT3G07565.1 | Symbols: | Protein of unknown function (DUF3755) | chr3:2413823-2415872 FORWARD LENGTH=258	230	258	1.00E-100	112.2	80.4	90.4
Rsa1.0_00196.1.g8224.t1	gb|EOA30840.1| hypothetical protein CARUB_v10013985mg [Capsella rubella]	370	369	1.00E-171	99.7	78.6	86.8	hypothetical protein CARUB_v10013985mg	gbpln	Capsella rubella	AT3G07570.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane with DOMON related domain | chr3:2418205-2420206 REVERSE LENGTH=369	370	369	1.00E-173	99.7	79.2	86.2
Rsa1.0_00196.1.g8225.t1	ref|XP_002884658.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330498|gb|EFH60917.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	251	467	6.00E-77	186.1	57.0	65.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G07570.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane with DOMON related domain | chr3:2418205-2420206 REVERSE LENGTH=369	251	369	9.00E-79	147.0	57.0	64.5
Rsa1.0_00196.1.g8226.t1	ref|NP_566313.2| Cytochrome b561/ferric reductase transmembrane with DOMON related domain [Arabidopsis thaliana] gi|110736322|dbj|BAF00131.1| hypothetical protein [Arabidopsis thaliana] gi|332641046|gb|AEE74567.1| Cytochrome b561/ferric reductase transmembrane with DOMON related domain [Arabidopsis thaliana]	424	369	1.00E-140	87.0	61.8	69.1	Cytochrome b561/ferric reductase transmembrane with DOMON related domain	gbpln	Arabidopsis thaliana	AT3G07570.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane with DOMON related domain | chr3:2418205-2420206 REVERSE LENGTH=369	424	369	1.00E-143	87.0	61.8	69.1
Rsa1.0_00196.1.g8227.t1	gb|ABC00745.1| putative small nuclear ribonucleoprotein D1 [Brassica napus]	159	118	7.00E-60	74.2	74.2	74.2	putative small nuclear ribonucleoprotein D1	gbpln	Brassica napus	AT3G07590.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr3:2423146-2423958 FORWARD LENGTH=114	159	114	3.00E-49	71.7	59.1	61.0
Rsa1.0_00196.1.g8228.t1	ref|NP_187419.1| putative glycosyltransferase [Arabidopsis thaliana] gi|75207507|sp|Q9SSE8.1|GLYT1_ARATH RecName: Full=Probable glycosyltransferase At3g07620 gi|6466945|gb|AAF13080.1|AC009176_7 hypothetical protein [Arabidopsis thaliana] gi|332641055|gb|AEE74576.1| putative glycosyltransferase [Arabidopsis thaliana]	601	470	0	78.2	66.4	68.2	putative glycosyltransferase	gbpln	Arabidopsis thaliana	AT3G07620.1 | Symbols: | Exostosin family protein | chr3:2433267-2434988 REVERSE LENGTH=470	601	470	0	78.2	66.4	68.2

Rsa1.0_00196.1.g8229.t2	ref|NP_187422.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|42572309|ref|NP_974250.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|79313159|ref|NP_001030659.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|186509893|ref|NP_001118599.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|17433084|sp|Q9SSE5.1|COL9_ARATH RecName: Full=Zinc finger protein CONSTANS-LIKE 9 gi|6466948|gb|AAF13083.1|AC009176_10 unknown protein [Arabidopsis thaliana] gi|119360037|gb|ABL66747.1| At3g07650 [Arabidopsis thaliana] gi|222423327|dbj|BAH19639.1| AT3G07650 [Arabidopsis thaliana] gi|332641059|gb|AEE74580.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641060|gb|AEE74581.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641061|gb|AEE74582.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641062|gb|AEE74583.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana]	366	372	1.00E-178	101.6	84.4	90.4	zinc finger protein CONSTANS-LIKE 9	gbpln	Arabidopsis thaliana	AT3G07650.4 | Symbols: COL9 | CONSTANS-like 9 | chr3:2442494-2443901 FORWARD LENGTH=372	366	372	0	101.6	84.4	90.4
Rsa1.0_00196.1.g8230.t1	gb|EOA29878.1| hypothetical protein CARUB_v10012975mg [Capsella rubella]	837	838	0	100.1	81.1	86.7	hypothetical protein CARUB_v10012975mg	gbpln	Capsella rubella	AT3G07660.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr3:2445275-2450372 REVERSE LENGTH=841	837	841	0	100.5	81.0	86.6
Rsa1.0_00196.1.g8231.t3	gb|EOA30367.1| hypothetical protein CARUB_v10013490mg [Capsella rubella]	608	507	7.00E-54	83.4	27.3	36.5	hypothetical protein CARUB_v10013490mg	gbpln	Capsella rubella	AT3G07730.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01170.1); Has 1299 Blast hits to 1149 proteins in 206 species: Archae - 3; Bacteria - 100; Metazoa - 453; Fungi - 114; Plants - 108; Viruses - 2; Other Eukaryotes - 519 (source: NCBI BLink). | chr3:2468185-2469606 FORWARD LENGTH=473	608	473	1.00E-54	77.8	26.8	35.2
Rsa1.0_00196.1.g8232.t1	ref|NP_566318.1| 3'-5'-exoribonuclease family protein [Arabidopsis thaliana] gi|30680427|ref|NP_850537.1| 3'-5'-exoribonuclease family protein [Arabidopsis thaliana] gi|11762184|gb|AAG40370.1|AF325018_1 AT3g07750 [Arabidopsis thaliana] gi|26453010|dbj|BAC43581.1| putative 3' exoribonuclease [Arabidopsis thaliana] gi|56744222|gb|AAW28551.1| At3g07750 [Arabidopsis thaliana] gi|332641077|gb|AEE74598.1| 3'-5'-exoribonuclease family protein [Arabidopsis thaliana] gi|332641078|gb|AEE74599.1| 3'-5'-exoribonuclease family protein [Arabidopsis thaliana]	288	286	1.00E-151	99.3	92.4	95.8	3'-5'-exoribonuclease family protein	gbpln	Arabidopsis thaliana	AT3G07750.2 | Symbols: | 3'-5'-exoribonuclease family protein | chr3:2473486-2475218 FORWARD LENGTH=286	288	286	1.00E-153	99.3	92.4	95.8
Rsa1.0_00196.1.g8233.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00196.1.g8234.t1	ref|XP_002882548.1| hypothetical protein ARALYDRAFT_896947 [Arabidopsis lyrata subsp. lyrata] gi|297328388|gb|EFH58807.1| hypothetical protein ARALYDRAFT_896947 [Arabidopsis lyrata subsp. lyrata]	145	140	7.00E-67	96.6	87.6	88.3	hypothetical protein ARALYDRAFT_896947	gbpln	Arabidopsis lyrata	AT3G07760.2 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr3:2476723-2477947 FORWARD LENGTH=125	145	125	1.00E-66	86.2	82.1	82.1
Rsa1.0_00196.1.g8235.t3	gb|EOA32302.1| hypothetical protein CARUB_v10015564mg [Capsella rubella]	774	799	0	103.2	90.4	95.1	hypothetical protein CARUB_v10015564mg	gbpln	Capsella rubella	AT3G07770.1 | Symbols: Hsp89.1, AtHsp90.6, AtHsp90-6 | HEAT SHOCK PROTEIN 89.1 | chr3:2479611-2483970 FORWARD LENGTH=799	774	799	0	103.2	89.1	94.3
Rsa1.0_00196.1.g8236.t1	gb|EOA30228.1| hypothetical protein CARUB_v10013350mg [Capsella rubella] gi|482566040|gb|EOA30229.1| hypothetical protein CARUB_v10013350mg [Capsella rubella]	550	566	0	102.9	85.6	91.1	hypothetical protein CARUB_v10013350mg	gbpln	Capsella rubella	AT3G07780.1 | Symbols: OBE1 | Protein of unknown function (DUF1423) | chr3:2485104-2486876 FORWARD LENGTH=566	550	566	0	102.9	84.4	91.5

Rsa1.0_00196.1_g8237.t1	ref|XP_002882551.1| hypothetical protein ARALYDRAFT_478116 [Arabidopsis lyrata subsp. lyrata] gi|297328391|gb|EFH58810.1| hypothetical protein ARALYDRAFT_478116 [Arabidopsis lyrata subsp. lyrata]	502	503	0	100.2	86.1	91.0	hypothetical protein ARALYDRAFT_478116	gbpln	Arabidopsis lyrata	AT3G07790.1 | Symbols: | DGCR14-related | chr3:2487491-2489017 FORWARD LENGTH=508	502	508	0	101.2	85.9	91.0
Rsa1.0_00196.1_g8238.t1	gb|EOA31343.1| hypothetical protein CARUB_v10014517mg [Capsella rubella]	220	238	1.00E-108	108.2	86.4	93.6	hypothetical protein CARUB_v10014517mg	gbpln	Capsella rubella	AT3G07800.1 | Symbols: | Thymidine kinase | chr3:2489944-2490935 REVERSE LENGTH=238	220	238	1.00E-108	108.2	85.0	91.8
Rsa1.0_00196.1_g8239.t2	ref|XP_002882552.1| hypothetical protein ARALYDRAFT_478119 [Arabidopsis lyrata subsp. lyrata] gi|297328392|gb|EFH58811.1| hypothetical protein ARALYDRAFT_478119 [Arabidopsis lyrata subsp. lyrata]	511	495	0	96.9	85.7	88.6	hypothetical protein ARALYDRAFT_478119	gbpln	Arabidopsis lyrata	AT3G07810.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:2492875-2495102 FORWARD LENGTH=495	511	495	0	96.9	85.1	88.5
Rsa1.0_00196.1_g8240.t1	ref|XP_002884668.1| polygalacturonase 3 [Arabidopsis lyrata subsp. lyrata] gi|297330508|gb|EFH60927.1| polygalacturonase 3 [Arabidopsis lyrata subsp. lyrata]	379	391	0	103.2	89.7	95.3	polygalacturonase 3	gbpln	Arabidopsis lyrata	AT3G07820.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:2496597-2498028 REVERSE LENGTH=391	379	391	0	103.2	89.2	95.3
Rsa1.0_00196.1_g8241.t1	gb|EOA35006.1| hypothetical protein CARUB_v10020105mg, partial [Capsella rubella]	508	542	0	106.7	81.1	89.2	hypothetical protein CARUB_v10020105mg, partial	gbpln	Capsella rubella	AT2G03820.1 | Symbols: | nonsense-mediated mRNA decay NMD3 family protein | chr2:1165149-1166699 REVERSE LENGTH=516	508	516	0	101.6	80.7	89.2
Rsa1.0_00197.1_g8242.t1	ref|NP_172408.2| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|3482912|gb|AAC33197.1| Hypothetical protein [Arabidopsis thaliana] gi|48310224|gb|AAT41778.1| At1g09370 [Arabidopsis thaliana] gi|332190313|gb|AEE28434.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	170	174	2.00E-43	102.4	54.1	71.2	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT1G09370.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:3024901-3025425 FORWARD LENGTH=174	170	174	8.00E-46	102.4	54.1	71.2
Rsa1.0_00197.1_g8243.t1	gb|EOA38007.1| hypothetical protein CARUB_v10009476mg [Capsella rubella]	385	373	0	96.9	82.1	87.5	hypothetical protein CARUB_v10009476mg	gbpln	Capsella rubella	AT1G09380.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:3026351-3029322 REVERSE LENGTH=374	385	374	0	97.1	82.6	88.8
Rsa1.0_00197.1_g8244.t1	ref|XP_002889747.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335589|gb|EFH66006.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	661	370	1.00E-154	56.0	38.6	41.9	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT1G09390.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:3031264-3033415 FORWARD LENGTH=370	661	370	1.00E-157	56.0	38.9	41.6
Rsa1.0_00197.1_g8245.t1	ref|NP_172412.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|193806401|sp|Q56XI1.2|PPR25_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g09410 gi|3482916|gb|AAC33201.1| Hypothetical protein [Arabidopsis thaliana] gi|91805759|gb|ABE65608.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332190317|gb|AEE28438.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	266	705	1.00E-40	265.0	41.0	51.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G09410.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:3035443-3037560 FORWARD LENGTH=705	266	705	3.00E-43	265.0	41.0	51.5
Rsa1.0_00197.1_g8246.t1	ref|XP_002892506.1| hypothetical protein ARALYDRAFT_311987 [Arabidopsis lyrata subsp. lyrata] gi|297338348|gb|EFH68765.1| hypothetical protein ARALYDRAFT_311987 [Arabidopsis lyrata subsp. lyrata]	461	481	0	104.3	89.4	94.4	hypothetical protein ARALYDRAFT_311987	gbpln	Arabidopsis lyrata	AT1G09440.1 | Symbols: | Protein kinase superfamily protein | chr1:3045513-3047393 REVERSE LENGTH=466	461	466	0	101.1	88.7	94.1
Rsa1.0_00197.1_g8247.t1	ref|NP_172417.2| carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana] gi|332190324|gb|AEE28445.1| carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana]	300	330	7.00E-84	110.0	76.3	83.3	carbohydrate-binding X8 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G09460.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr1:3053901-3055090 FORWARD LENGTH=330	300	330	2.00E-86	110.0	76.3	83.3

Rsa1.0_00197.1.g8248.t1	ref|XP_002892507.1| hypothetical protein ARALYDRAFT_471040 [Arabidopsis lyrata subsp. lyrata] gi|297338349|gb|EFH68766.1| hypothetical protein ARALYDRAFT_471040 [Arabidopsis lyrata subsp. lyrata]	357	336	1.00E-152	94.1	80.7	86.0	hypothetical protein ARALYDRAFT_471040	gbpln	Arabidopsis lyrata	AT1G09470.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: cotyledon; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26770.1); Has 55019 Blast hits to 30094 proteins in 2088 species: Archae - 730; Bacteria - 6553; Metazoa - 28961; Fungi - 4800; Plants - 2559; Viruses - 111; Other Eukaryotes - 11305 (source: NCBI BLink). | chr1:3055391-3056931 REVERSE LENGTH=336	357	336	1.00E-154	94.1	80.1	85.7
Rsa1.0_00197.1.g8249.t1	gb|ACP20258.1| cinnamyl-alcohol dehydrogenase [Brassica rapa subsp. oleifera]	295	322	1.00E-155	109.2	92.5	96.6	cinnamyl-alcohol dehydrogenase	gbpln	Brassica rapa	AT1G09480.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:3057975-3060661 FORWARD LENGTH=369	295	369	1.00E-133	125.1	78.0	89.8
Rsa1.0_00197.1.g8250.t1	dbj|BAJ33939.1| unnamed protein product [Thellungiella halophila]	322	336	1.00E-151	104.3	79.8	89.4	unnamed protein product	----	----	AT1G09490.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:3064172-3065815 FORWARD LENGTH=322	322	322	1.00E-148	100.0	79.5	87.0
Rsa1.0_00197.1.g8251.t1	gb|ACP20258.1| cinnamyl-alcohol dehydrogenase [Brassica rapa subsp. oleifera]	329	322	1.00E-152	97.9	83.3	88.4	cinnamyl-alcohol dehydrogenase	gbpln	Brassica rapa	AT1G09490.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:3064172-3065815 FORWARD LENGTH=322	329	322	1.00E-145	97.9	77.2	86.0
Rsa1.0_00197.1.g8252.t1	gb|EOA36734.1| hypothetical protein CARUB_v10012528mg [Capsella rubella]	244	266	8.00E-69	109.0	58.2	72.1	hypothetical protein CARUB_v10012528mg	gbpln	Capsella rubella	AT1G09520.1 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Zinc finger, PHD-type, conserved site (InterPro:IPR019786); BEST Arabidopsis thaliana protein match is: PHD finger family protein (TAIR:AT3G17460.1); Has 56 Blast hits to 56 proteins in 17 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 4; Plants - 46; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr1:3071248-3072030 REVERSE LENGTH=260	244	260	1.00E-69	106.6	61.5	74.6
Rsa1.0_00197.1.g8253.t1	emb|CAA16721.1| MuDR transposable element - like protein [Arabidopsis thaliana] gi|7268634|emb|CAB78843.1| MuDR transposable element-like protein [Arabidopsis thaliana]	323	633	5.00E-68	196.0	39.6	50.2	MuDR transposable element - like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00197.1.g8254.t1	ref|XP_002889756.1| hypothetical protein ARALYDRAFT_471048 [Arabidopsis lyrata subsp. lyrata] gi|297335598|gb|EFH66015.1| hypothetical protein ARALYDRAFT_471048 [Arabidopsis lyrata subsp. lyrata]	507	522	0	103.0	81.3	88.2	hypothetical protein ARALYDRAFT_471048	gbpln	Arabidopsis lyrata	AT1G09530.2 | Symbols: PIF3, POC1, PAP3 | phytochrome interacting factor 3 | chr1:3077216-3079367 FORWARD LENGTH=524	507	524	0	103.4	81.1	87.2
Rsa1.0_00197.1.g8255.t1	gb|EOA38027.1| hypothetical protein CARUB_v10009497mg [Capsella rubella]	351	369	1.00E-171	105.1	88.3	93.7	hypothetical protein CARUB_v10009497mg	gbpln	Capsella rubella	AT1G09540.1 | Symbols: MYB61, ATMYB61 | myb domain protein 61 | chr1:3086333-3087689 FORWARD LENGTH=366	351	366	1.00E-165	104.3	87.2	91.7
Rsa1.0_00197.1.g8256.t1	ref|XP_002892509.1| hypothetical protein ARALYDRAFT_311997 [Arabidopsis lyrata subsp. lyrata] gi|297338351|gb|EFH68768.1| hypothetical protein ARALYDRAFT_311997 [Arabidopsis lyrata subsp. lyrata]	346	363	1.00E-153	104.9	78.9	84.7	hypothetical protein ARALYDRAFT_311997	gbpln	Arabidopsis lyrata	AT1G09550.1 | Symbols: | Pectinacetylesterase family protein | chr1:3089733-3092254 REVERSE LENGTH=388	346	388	1.00E-151	112.1	77.5	83.5
Rsa1.0_00197.1.g8257.t1	gb|EOA38478.1| hypothetical protein CARUB_v10010233mg [Capsella rubella]	217	225	1.00E-104	103.7	86.2	88.9	hypothetical protein CARUB_v10010233mg	gbpln	Capsella rubella	AT1G09560.1 | Symbols: GLP5 | germin-like protein 5 | chr1:3093896-3094639 FORWARD LENGTH=219	217	219	1.00E-105	100.9	85.3	88.5
Rsa1.0_00197.1.g8258.t1	dbj|BAA99410.1| phytochrome A [Armoracia rusticana]	1121	1122	0	100.1	95.2	97.9	phytochrome A	gbpln	Armoracia rusticana	AT1G09570.1 | Symbols: PHYA, FHY2, FRE1, HY8 | phytochrome A | chr1:3095498-3099216 REVERSE LENGTH=1122	1121	1122	0	100.1	95.4	98.3
Rsa1.0_00197.1.g8259.t1	ref|XP_002892511.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338353|gb|EFH68770.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	297	293	1.00E-137	98.7	82.8	90.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G09575.1 | Symbols: | Protein of unknown function (DUF607) | chr1:3101851-3102832 REVERSE LENGTH=292	297	292	1.00E-136	98.3	82.5	90.2
Rsa1.0_00197.1.g8260.t2	gb|EOA38463.1| hypothetical protein CARUB_v10010159mg, partial [Capsella rubella]	214	238	8.00E-98	111.2	80.8	91.6	hypothetical protein CARUB_v10010159mg, partial	gbpln	Capsella rubella	AT1G09580.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:3104657-3106092 FORWARD LENGTH=217	214	217	1.00E-98	101.4	79.9	90.2
Rsa1.0_00197.1.g8261.t1	ref|XP_002889760.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata] gi|297335602|gb|EFH66019.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata]	164	164	2.00E-87	100.0	97.0	98.2	60S ribosomal protein L21	gbpln	Arabidopsis lyrata	AT1G09690.1 | Symbols: | Translation protein SH3-like family protein | chr1:3136407-3137430 REVERSE LENGTH=164	164	164	2.00E-89	100.0	96.3	97.6
Rsa1.0_00197.1.g8262.t1	gb|AAC33218.1| Similar to cdc2 protein kinases [Arabidopsis thaliana]	967	967	0	100.0	78.6	86.0	Similar to cdc2 protein kinases	gbpln	Arabidopsis thaliana	AT1G09600.1 | Symbols: | Protein kinase superfamily protein | chr1:3108617-3111318 FORWARD LENGTH=714	967	714	0	73.8	55.3	61.4

Rsa1.0_00197.1.g8263.t1	ref|XP_002892512.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297338354|gb|EFH68771.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	1083	1091	0	100.7	92.3	96.7	ATP binding protein	gbpln	Arabidopsis lyrata	AT1G09620.1 | Symbols: | ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases | chr1:3113077-3116455 REVERSE LENGTH=1091	1083	1091	0	100.7	88.4	94.4
Rsa1.0_00197.1.g8264.t1	ref|NP_001147252.1| ras-related protein Rab11C [Zea mays] gi|195609118|gb|ACG26389.1| ras-related protein Rab11C [Zea mays]	218	217	1.00E-119	99.5	96.8	98.2	ras-related protein Rab11C	gbenv/gbpln	Zea mays	AT1G09630.1 | Symbols: ATRAB11C, ATRABA2A, ATRAB-A2A, RAB-A2A, RAB11c | RAB GTPase 11C | chr1:3118350-3119571 REVERSE LENGTH=217	218	217	1.00E-119	99.5	94.5	97.7
Rsa1.0_00197.1.g8265.t2	ref|NP_563848.1| elongation factor EF-1 gamma subunit [Arabidopsis thaliana] gi|13626364|sp|O04487.1|EF1G1_ARATH RecName: Full=Probable elongation factor 1-gamma 1; Short=EF-1-gamma 1; AltName: Full=eEF-1B gamma 1 gi|2160158|gb|AAB60721.1| Similar to elongation factor 1-gamma (gb|EF1G_XENLA). ESTs gb|T20564,gb|T45940,gb|T04527 come from this gene [Arabidopsis thaliana] gi|222424502|dbj|BAH20206.1| AT1G09640 [Arabidopsis thaliana] gi|332190351|gb|AEE28472.1| elongation factor EF-1 gamma subunit [Arabidopsis thaliana]	425	414	0	97.4	87.1	91.5	elongation factor EF-1 gamma subunit	gbpln	Arabidopsis thaliana	AT1G09640.1 | Symbols: | Translation elongation factor EF1B, gamma chain | chr1:3120162-3122152 FORWARD LENGTH=414	425	414	0	97.4	87.1	91.5
Rsa1.0_00197.1.g8266.t1	ref|XP_002889763.1| hypothetical protein ARALYDRAFT_888210 [Arabidopsis lyrata subsp. lyrata] gi|297335605|gb|EFH66022.1| hypothetical protein ARALYDRAFT_888210 [Arabidopsis lyrata subsp. lyrata]	105	105	6.00E-28	100.0	70.5	72.4	hypothetical protein ARALYDRAFT_888210	gbpln	Arabidopsis lyrata	AT1G09645.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G57765.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:3123155-3124347 FORWARD LENGTH=106	105	106	2.00E-30	101.0	76.2	85.7
Rsa1.0_00197.1.g8267.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00197.1.g8268.t1	ref|XP_002892515.1| hypothetical protein ARALYDRAFT_471067 [Arabidopsis lyrata subsp. lyrata] gi|297338357|gb|EFH68774.1| hypothetical protein ARALYDRAFT_471067 [Arabidopsis lyrata subsp. lyrata]	300	298	1.00E-137	99.3	86.3	90.7	hypothetical protein ARALYDRAFT_471067	gbpln	Arabidopsis lyrata	AT1G09660.1 | Symbols: | RNA-binding KH domain-containing protein | chr1:3128032-3130791 REVERSE LENGTH=298	300	298	1.00E-138	99.3	84.7	90.3
Rsa1.0_00197.1.g8269.t1	gb|EOA36110.1| hypothetical protein CARUB_v10011501mg, partial [Capsella rubella]	174	175	1.00E-71	100.6	78.2	86.8	hypothetical protein CARUB_v10011501mg, partial	gbpln	Capsella rubella	AT1G09665.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr1:3133095-3133674 FORWARD LENGTH=165	174	165	2.00E-71	94.8	73.0	79.3
Rsa1.0_00197.1.g8270.t1	ref|XP_002892516.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338358|gb|EFH68775.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	600	607	0	101.2	84.5	90.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G09680.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:3134107-3135930 REVERSE LENGTH=607	600	607	0	101.2	83.8	90.0
Rsa1.0_00198.1.g8271.t1	gb|EOA15681.1| hypothetical protein CARUB_v10006371mg [Capsella rubella]	160	494	2.00E-35	308.8	53.1	67.5	hypothetical protein CARUB_v10006371mg	gbpln	Capsella rubella	AT4G26000.1 | Symbols: PEP | RNA-binding KH domain-containing protein | chr4:13197280-13199539 FORWARD LENGTH=495	160	495	1.00E-35	309.4	53.8	68.1
Rsa1.0_00198.1.g8272.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00198.1.g8273.t2	ref|XP_002867585.1| hypothetical protein ARALYDRAFT_354188 [Arabidopsis lyrata subsp. lyrata] gi|297313421|gb|EFH43844.1| hypothetical protein ARALYDRAFT_354188 [Arabidopsis lyrata subsp. lyrata]	345	392	3.00E-97	113.6	67.0	75.1	hypothetical protein ARALYDRAFT_354188	gbpln	Arabidopsis lyrata	AT4G25990.1 | Symbols: CIL | CCT motif family protein | chr4:13191937-13193543 REVERSE LENGTH=394	345	394	4.00E-94	114.2	62.9	71.0
Rsa1.0_00198.1.g8274.t6	ref|NP_194328.1| peroxidase 43 [Arabidopsis thaliana] gi|7433052|pir||T04253 peroxidase homolog F20B18.90 - Arabidopsis thaliana gi|4538927|emb|CAB39663.1| putative peroxidase [Arabidopsis thaliana] gi|7269449|emb|CAB79453.1| putative peroxidase [Arabidopsis thaliana] gi|332659739|gb|AEE85139.1| peroxidase 43 [Arabidopsis thaliana]	326	371	1.00E-171	113.8	87.7	95.4	peroxidase 43	gbpln	Arabidopsis thaliana	AT4G25980.1 | Symbols: | Peroxidase superfamily protein | chr4:13189393-13191507 FORWARD LENGTH=371	326	371	1.00E-173	113.8	87.7	95.4

Rsa1.0_00198.1.g8275.t1	emb|CAA71277.1| P-glycoprotein-2 [Arabidopsis thaliana] gi|2108254|emb|CAA71276.1| P-glycoprotein-2 [Arabidopsis thaliana] gi|4538925|emb|CAB39661.1| P-glycoprotein-2 (pgp2) [Arabidopsis thaliana] gi|7269447|emb|CAB79451.1| P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]	1234	1233	0	99.9	92.1	96.5	P-glycoprotein-2	gbpln	Arabidopsis thaliana	AT4G25960.1 | Symbols: PGP2 | P-glycoprotein 2 | chr4:13177438-13183425 FORWARD LENGTH=1273	1234	1273	0	103.2	92.1	96.5
Rsa1.0_00198.1.g8276.t3	ref|XP_002867586.1| hypothetical protein ARALYDRAFT_492222 [Arabidopsis lyrata subsp. lyrata] gi|297313422|gb|EFH43845.1| hypothetical protein ARALYDRAFT_492222 [Arabidopsis lyrata subsp. lyrata]	108	108	4.00E-50	100.0	93.5	99.1	hypothetical protein ARALYDRAFT_492222	gbpln	Arabidopsis lyrata	AT4G25950.1 | Symbols: VATG3 | vacuolar ATP synthase G3 | chr4:13173815-13174324 REVERSE LENGTH=108	108	108	5.00E-51	100.0	91.7	96.3
Rsa1.0_00198.1.g8277.t1	ref|NP_567735.1| NifU-like protein 3 [Arabidopsis thaliana] gi|75147908|sp|Q84RQ7.1|NIFU3_ARATH RecName: Full=NifU-like protein 3, chloroplastic; Short=AtCNfu3; Short=AtCnfU-IVa; Flags: Precursor gi|28207820|emb|CAD55560.1| NFU3 protein [Arabidopsis thaliana] gi|88196759|gb|ABD43022.1| At4g25910 [Arabidopsis thaliana] gi|222423670|dbj|BAH19802.1| AT4G25910 [Arabidopsis thaliana] gi|332659732|gb|AEE85132.1| NifU-like protein 3 [Arabidopsis thaliana]	237	236	1.00E-113	99.6	87.3	93.2	NifU-like protein 3	gbpln	Arabidopsis thaliana	AT4G25910.1 | Symbols: NFU3, ATCNFU3 | NFU domain protein 3 | chr4:13164128-13165094 FORWARD LENGTH=236	237	236	1.00E-116	99.6	87.3	93.2
Rsa1.0_00198.1.g8278.t2	gb|EOA16987.1| hypothetical protein CARUB_v10005219mg [Capsella rubella]	316	332	1.00E-145	105.1	80.4	88.9	hypothetical protein CARUB_v10005219mg	gbpln	Capsella rubella	AT4G25900.1 | Symbols: | Galactose mutarotase-like superfamily protein | chr4:13161487-13163397 FORWARD LENGTH=318	316	318	1.00E-141	100.6	77.8	87.0
Rsa1.0_00198.1.g8279.t1	gb|EOA15920.1| hypothetical protein CARUB_v10004014mg [Capsella rubella]	1159	1171	0	101.0	81.5	88.9	hypothetical protein CARUB_v10004014mg	gbpln	Capsella rubella	AT4G38120.1 | Symbols: | ARM repeat superfamily protein | chr4:17888668-17896060 REVERSE LENGTH=1165	1159	1165	0	100.5	81.1	88.4
Rsa1.0_00198.1.g8280.t1	ref|XP_002869646.1| hypothetical protein ARALYDRAFT_913980 [Arabidopsis lyrata subsp. lyrata] gi|297315482|gb|EFH45905.1| hypothetical protein ARALYDRAFT_913980 [Arabidopsis lyrata subsp. lyrata]	779	858	0	110.1	81.3	87.3	hypothetical protein ARALYDRAFT_913980	gbpln	Arabidopsis lyrata	AT4G25880.1 | Symbols: APUM6, PUM6 | pumilio 6 | chr4:13155518-13159078 FORWARD LENGTH=861	779	861	0	110.5	80.2	86.5
Rsa1.0_00198.1.g8281.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1394	1365	0	97.9	44.8	61.3	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1394	575	6.00E-90	41.2	13.7	21.2
Rsa1.0_00198.1.g8282.t1	gb|EOA16782.1| hypothetical protein CARUB_v10005002mg [Capsella rubella] gi|482552590|gb|EOA16783.1| hypothetical protein CARUB_v10005002mg [Capsella rubella]	380	391	0	102.9	91.6	95.3	hypothetical protein CARUB_v10005002mg	gbpln	Capsella rubella	AT4G25870.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:13149831-13151737 REVERSE LENGTH=389	380	389	0	102.4	90.8	95.0
Rsa1.0_00198.1.g8283.t14	gb|EOA17897.1| hypothetical protein CARUB_v10006306mg [Capsella rubella]	116	118	3.00E-41	101.7	74.1	81.9	hypothetical protein CARUB_v10006306mg	gbpln	Capsella rubella	AT4G25845.1 | Symbols: | BEST Arabidopsis thaliana protein match is: OSBP(oxysterol binding protein)-related protein 4B (TAIR:AT4G25850.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:13142270-13142632 FORWARD LENGTH=120	116	120	4.00E-44	103.4	73.3	83.6
Rsa1.0_00198.1.g8284.t1	gb|EOA16463.1| hypothetical protein CARUB_v10004616mg [Capsella rubella]	507	507	0	100.0	80.1	87.2	hypothetical protein CARUB_v10004616mg	gbpln	Capsella rubella	AT4G25835.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13136117-13137637 FORWARD LENGTH=506	507	506	0	99.8	79.7	86.2
Rsa1.0_00198.1.g8285.t1	ref|XP_002869651.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|341958571|sp|D7MFW5.1|CSPL4_ARALL RecName: Full=CASP-like protein ARALYDRAFT_657503 gi|297315487|gb|EFH45910.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	175	175	4.00E-81	100.0	82.9	90.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G25830.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:13133727-13134790 FORWARD LENGTH=175	175	175	3.00E-83	100.0	82.9	90.9

Rsa1.0_00198.1.g8286.t1	gb|EOA17900.1| hypothetical protein CARUB_v10006309mg [Capsella rubella]	284	289	1.00E−144	101.8	87.0	92.6	hypothetical protein CARUB_v10006309mg	gbpln	Capsella rubella	AT4G25820.1 | Symbols: XTR9, XTH14, ATXTH14 | xyloglucan endotransglucosylase/hydrolase 14 | chr4:13130349-13131615 FORWARD LENGTH=287	284	287	1.00E−135	101.1	82.7	90.1
Rsa1.0_00198.1.g8287.t1	ref|NP_194311.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|38605152|sp|Q38910.1|XTH23_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 23; Short=At-XTH23; Short=XTH-23; Flags: Precursor gi|1244758|gb|AAB18367.1| xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] gi|4539299|emb|CAB39602.1| xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana] gi|7269432|emb|CAB79436.1| xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana] gi|332659717|gb|AEE85117.1| probable xyloglucan endotransglucosylase/hydrolase protein 23 [Arabidopsis thaliana]	281	286	1.00E−151	101.8	91.5	95.7	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT4G25810.1 | Symbols: XTR6, XTH23 | xyloglucan endotransglycosylase 6 | chr4:13128694-13129715 FORWARD LENGTH=286	281	286	1.00E−154	101.8	91.5	95.7
Rsa1.0_00198.1.g8288.t1	ref|XP_002869655.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315491|gb|EFH45914.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	589	600	0	101.9	77.1	86.4	calmodulin-binding protein	gbpln	Arabidopsis lyrata	AT4G25800.2 | Symbols: | Calmodulin-binding protein | chr4:13125224-13127765 FORWARD LENGTH=601	589	601	0	102.0	75.6	84.7
Rsa1.0_00198.1.g8289.t1	gb|EOA18029.1| hypothetical protein CARUB_v10006471mg [Capsella rubella]	209	208	1.00E−103	99.5	89.0	92.3	hypothetical protein CARUB_v10006471mg	gbpln	Capsella rubella	AT4G25790.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:13122248-13123290 REVERSE LENGTH=210	209	210	2.00E−93	100.5	84.7	89.5
Rsa1.0_00198.1.g8290.t1	ref|XP_002869656.1| hypothetical protein ARALYDRAFT_492242 [Arabidopsis lyrata subsp. lyrata] gi|297315492|gb|EFH45915.1| hypothetical protein ARALYDRAFT_492242 [Arabidopsis lyrata subsp. lyrata]	204	190	2.00E−78	93.1	69.6	80.9	hypothetical protein ARALYDRAFT_492242	gbpln	Arabidopsis lyrata	AT4G25780.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:13121107-13121679 FORWARD LENGTH=190	204	190	6.00E−79	93.1	68.6	79.4
Rsa1.0_00198.1.g8291.t1	ref|XP_002867591.1| hypothetical protein ARALYDRAFT_492243 [Arabidopsis lyrata subsp. lyrata] gi|297313427|gb|EFH43850.1| hypothetical protein ARALYDRAFT_492243 [Arabidopsis lyrata subsp. lyrata]	419	418	0	99.8	85.4	90.5	hypothetical protein ARALYDRAFT_492243	gbpln	Arabidopsis lyrata	AT4G25770.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:13117821-13119982 REVERSE LENGTH=418	419	418	0	99.8	85.4	90.0
Rsa1.0_00198.1.g8292.t1	ref|NP_567728.1| glutamine dumper 2 [Arabidopsis thaliana] gi|75266435|sp|Q9SW07.1|GDU2_ARATH RecName: Full=Protein GLUTAMINE DUMPER 2 gi|4539294|emb|CAB39597.1| hypothetical protein [Arabidopsis thaliana] gi|7269426|emb|CAB81386.1| hypothetical protein [Arabidopsis thaliana] gi|332659710|gb|AEE85110.1| glutamine dumper 2 [Arabidopsis thaliana]	138	129	3.00E−53	93.5	74.6	81.9	glutamine dumper 2	gbpln	Arabidopsis thaliana	AT4G25760.1 | Symbols: ATGDU2, GDU2 | glutamine dumper 2 | chr4:13116149-13116538 FORWARD LENGTH=129	138	129	7.00E−56	93.5	74.6	81.9
Rsa1.0_00198.1.g8293.t1	gb|EOA13969.1| hypothetical protein CARUB_v10027094mg, partial [Capsella rubella]	181	220	2.00E−75	121.5	86.2	90.1	hypothetical protein CARUB_v10027094mg, partial	gbpln	Capsella rubella	AT4G25740.1 | Symbols: | RNA binding Plectin/S10 domain-containing protein | chr4:13107488-13108751 REVERSE LENGTH=177	181	177	1.00E−70	97.8	88.4	91.2
Rsa1.0_00198.1.g8294.t1	gb|EOA17044.1| hypothetical protein CARUB_v10005281mg [Capsella rubella]	324	317	1.00E−148	97.8	79.9	87.7	hypothetical protein CARUB_v10005281mg	gbpln	Capsella rubella	AT4G25720.1 | Symbols: ATQC, QC, QCT | glutaminyl cyclase | chr4:13099929-13102470 REVERSE LENGTH=320	324	320	1.00E−140	98.8	77.2	85.2
Rsa1.0_00198.1.g8295.t1	gb|ACS45170.1| beta-carotene hydroxylase [Brassica rapa subsp. pekinensis]	296	306	2.33E−156	103.4	90.2	93.6	beta-carotene hydroxylase	gbpln	Brassica rapa	AT4G25700.1 | Symbols: BETA-OHASE 1, B1, chy1, BCH1 | beta-hydroxylase 1 | chr4:13094142-13095866 REVERSE LENGTH=310	296	310	1.00E−136	104.7	81.1	88.5
Rsa1.0_00198.1.g8296.t1	emb|CAB43698.1| hypothetical protein [Arabidopsis thaliana] gi|7269417|emb|CAB81377.1| hypothetical protein [Arabidopsis thaliana]	307	247	7.00E−86	80.5	58.0	62.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G25670.2 | Symbols: | unknown protein; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25690.2). | chr4:13085431-13085997 REVERSE LENGTH=188	307	188	1.00E−70	61.2	46.9	50.8

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<tr><td>Rsa1.0_00198.1.g8297.t1</td><td>gb|EOA17297.1| hypothetical protein CARUB_v10005569mg [Capsella rubella]</td><td>252</td><td>252</td><td>1.00E-126</td><td>100.0</td><td>86.5</td><td>92.5</td><td>hypothetical protein CARUB_v10005569mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25680.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr4:13088425-13089952 FORWARD LENGTH=252</td><td>252</td><td>252</td><td>1.00E-127</td><td>100.0</td><td>86.5</td><td>92.5</td></tr>
<tr><td>Rsa1.0_00198.1.g8298.t1</td><td>emb|CAB43698.1| hypothetical protein [Arabidopsis thaliana] gi|7269417|emb|CAB81377.1| hypothetical protein [Arabidopsis thaliana]</td><td>235</td><td>247</td><td>9.00E-92</td><td>105.1</td><td>80.9</td><td>87.2</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25670.2 | Symbols: | unknown protein; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25690.2). | chr4:13085431-13085997 REVERSE LENGTH=188</td><td>235</td><td>188</td><td>2.00E-78</td><td>80.0</td><td>65.5</td><td>70.2</td></tr>
<tr><td>Rsa1.0_00198.1.g8299.t1</td><td>ref|NP_194296.1| PPPDE putative thiol peptidase family protein [Arabidopsis thaliana] gi|4914458|emb|CAB43697.1| putative protein [Arabidopsis thaliana] gi|7269416|emb|CAB81376.1| putative protein [Arabidopsis thaliana] gi|25082894|gb|AAN72011.1| putative protein [Arabidopsis thaliana] gi|33942049|gb|AAQ55277.1| At4g25660 [Arabidopsis thaliana] gi|332659690|gb|AEE85090.1| PPPDE putative thiol peptidase family protein [Arabidopsis thaliana]</td><td>246</td><td>255</td><td>1.00E-120</td><td>103.7</td><td>83.7</td><td>92.3</td><td>PPPDE putative thiol peptidase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25660.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr4:13083677-13084989 FORWARD LENGTH=255</td><td>246</td><td>255</td><td>1.00E-123</td><td>103.7</td><td>83.7</td><td>92.3</td></tr>
<tr><td>Rsa1.0_00198.1.g8300.t1</td><td>ref|NP_567725.1| ACD1-like protein [Arabidopsis thaliana] gi|15983402|gb|AAL11569.1|AF424575_1 AT4g25650/L73G19_30 [Arabidopsis thaliana] gi|15810259|gb|AAL07017.1| unknown protein [Arabidopsis thaliana] gi|37962888|gb|AAR05798.1| LLS1-like protein [Arabidopsis thaliana] gi|332659688|gb|AEE85088.1| ACD1-like protein [Arabidopsis thaliana]</td><td>539</td><td>536</td><td>0</td><td>99.4</td><td>82.4</td><td>88.5</td><td>ACD1-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25650.1 | Symbols: ACD1-LIKE, PTC52, TIC55-IV | ACD1-like | chr4:13081021-13083153 REVERSE LENGTH=536</td><td>539</td><td>536</td><td>0</td><td>99.4</td><td>82.4</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00198.1.g8301.t1</td><td>dbj|BAJ33972.1| unnamed protein product [Thellungiella halophila]</td><td>489</td><td>488</td><td>0</td><td>99.8</td><td>89.8</td><td>95.1</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G25640.1 | Symbols: ATDTX35, FFT, DTX35 | detoxifying efflux carrier 35 | chr4:13076953-13078965 REVERSE LENGTH=488</td><td>489</td><td>488</td><td>0</td><td>99.8</td><td>91.2</td><td>95.9</td></tr>
<tr><td>Rsa1.0_00198.1.g8302.t1</td><td>ref|NP_567724.1| rRNA 2'-O-methyltransferase fibrillarin 2 [Arabidopsis thaliana] gi|67461067|sp|Q94AH9.2|MD36A_ARATH RecName: Full=Mediator of RNA polymerase II transcription subunit 36a; AltName: Full=Fibrillarin-like protein 2; AltName: Full=rRNA 2'-O-methyltransferase fibrillarin 2 gi|9965655|gb|AAG10104.1|AF233444_1 fibrillarin 2 [Arabidopsis thaliana] gi|4914455|emb|CAB43694.1| fibrillarin-like protein [Arabidopsis thaliana] gi|7269413|emb|CAB81373.1| fibrillarin-like protein [Arabidopsis thaliana] gi|9965796|gb|AAG10153.1| fibrillarin 2 [Arabidopsis thaliana] gi|21536840|gb|AAM61172.1| fibrillarin 2 (AtFib2) [Arabidopsis thaliana] gi|23297150|gb|AAN13105.1| fibrillarin 2 (AtFib2) [Arabidopsis thaliana] gi|332659685|gb|AEE85085.1| rRNA 2'-O-methyltransferase fibrillarin 2 [Arabidopsis thaliana]</td><td>313</td><td>320</td><td>1.00E-133</td><td>102.2</td><td>73.8</td><td>76.4</td><td>rRNA 2'-O-methyltransferase fibrillarin 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25630.1 | Symbols: FIB2, ATFIB2 | fibrillarin 2 | chr4:13074239-13076205 FORWARD LENGTH=320</td><td>313</td><td>320</td><td>1.00E-136</td><td>102.2</td><td>73.8</td><td>76.4</td></tr>
<tr><td>Rsa1.0_00198.1.g8303.t1</td><td>ref|NP_194292.2| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|26449762|dbj|BAC42004.1| unknown protein [Arabidopsis thaliana] gi|28951011|gb|AAO63429.1| At4g25620 [Arabidopsis thaliana] gi|332659684|gb|AEE85084.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]</td><td>457</td><td>449</td><td>1.00E-154</td><td>98.2</td><td>72.6</td><td>79.2</td><td>hydroxyproline-rich glycoprotein family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25620.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:13067447-13069296 REVERSE LENGTH=449</td><td>457</td><td>449</td><td>1.00E-157</td><td>98.2</td><td>72.6</td><td>79.2</td></tr>
<tr><td>Rsa1.0_00198.1.g8304.t2</td><td>ref|NP_194291.2| C2H2-like zinc finger protein [Arabidopsis thaliana] gi|19698895|gb|AAL91183.1| unknown protein [Arabidopsis thaliana] gi|23198356|gb|AAN15705.1| unknown protein [Arabidopsis thaliana] gi|332659682|gb|AEE85082.1| C2H2-like zinc finger protein [Arabidopsis thaliana]</td><td>628</td><td>586</td><td>0</td><td>93.3</td><td>74.2</td><td>81.5</td><td>C2H2-like zinc finger protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25610.1 | Symbols: | C2H2-like zinc finger protein | chr4:13063801-13066860 FORWARD LENGTH=586</td><td>628</td><td>586</td><td>0</td><td>93.3</td><td>74.2</td><td>81.5</td></tr>
</table>

Rsa1.0_00198.1.g8305.t2	ref|NP_194290.2| Oxoglutarate/iron-dependent oxygenase [Arabidopsis thaliana] gi|26451153|dbj|BAC42680.1| unknown protein [Arabidopsis thaliana] gi|29893542|gb|AAP06823.1| unknown protein [Arabidopsis thaliana] gi|332659681|gb|AEE85081.1| Oxoglutarate/iron-dependent oxygenase [Arabidopsis thaliana]	269	291	1.00E-96	108.2	65.4	71.7	Oxoglutarate/iron-dependent oxygenase	gbpln	Arabidopsis thaliana	AT4G25600.1 | Symbols: | Oxoglutarate/iron-dependent oxygenase | chr4:13060712-13062359 FORWARD LENGTH=291	269	291	4.00E-99	108.2	65.4	71.7
Rsa1.0_00198.1.g8306.t1	gb|EOA18372.1| hypothetical protein CARUB_v10006893mg [Capsella rubella]	170	137	2.00E-69	80.6	76.5	78.2	hypothetical protein CARUB_v10006893mg	gbpln	Capsella rubella	AT4G25590.1 | Symbols: ADF7 | actin depolymerizing factor 7 | chr4:13059137-13060050 REVERSE LENGTH=137	170	137	9.00E-71	80.6	75.9	77.6
Rsa1.0_00198.1.g8307.t1	ref|NP_194286.1| transcription factor LAF1 [Arabidopsis thaliana] gi|55976604|sp|Q9M0K4.2|LAF1_ARATH RecName: Full=Transcription factor LAF1; AltName: Full=Myb-related protein 18; Short=AtMYB18; AltName: Full=Protein LONG AFTER FAR-RED LIGHT 1 gi|2980794|emb|CAA18170.1| myb-like protein [Arabidopsis thaliana] gi|41619336|gb|AAS10079.1| MYB transcription factor [Arabidopsis thaliana] gi|332659677|gb|AEE85077.1| transcription factor LAF1 [Arabidopsis thaliana]	273	283	1.00E-106	103.7	74.0	82.4	transcription factor LAF1	gbpln	Arabidopsis thaliana	AT4G25560.1 | Symbols: AtMYB18, MYB18 | myb domain protein 18 | chr4:13052555-13053573 FORWARD LENGTH=283	273	283	1.00E-108	103.7	74.0	82.4
Rsa1.0_00198.1.g8308.t1	gb|EOA17453.1| hypothetical protein CARUB_v10005772mg [Capsella rubella]	200	200	1.00E-113	100.0	97.5	99.0	hypothetical protein CARUB_v10005772mg	gbpln	Capsella rubella	AT4G25550.1 | Symbols: | Cleavage/polyadenylation specificity factor, 25kDa subunit | chr4:13048519-13050873 FORWARD LENGTH=200	200	200	1.00E-114	100.0	95.5	98.0
Rsa1.0_00198.1.g8309.t1	ref|XP_002865885.1| hypothetical protein ARALYDRAFT_495266 [Arabidopsis lyrata subsp. lyrata] gi|297311720|gb|EFH42144.1| hypothetical protein ARALYDRAFT_495266 [Arabidopsis lyrata subsp. lyrata]	119	440	1.00E-33	369.7	54.6	58.8	hypothetical protein ARALYDRAFT_495266	gbpln	Arabidopsis lyrata	AT4G25440.1 | Symbols: ZFWD1 | zinc finger WD40 repeat protein 1 | chr4:13007107-13009381 REVERSE LENGTH=430	119	430	1.00E-35	361.3	56.3	59.7
Rsa1.0_00198.1.g8310.t2	ref|NP_849443.2| nudix hydrolase 10 [Arabidopsis thaliana] gi|68565889|sp|Q6NPD7.1|NUD10_ARATH RecName: Full=Nudix hydrolase 10; Short=AtNUDT10; AltName: Full=ADP-ribose pyrophosphatase; AltName: Full=NADH pyrophosphatase gi|38564312|gb|AAR23735.1| At4g25434 [Arabidopsis thaliana] gi|38604044|gb|AAR24765.1| At4g25434 [Arabidopsis thaliana] gi|332659658|gb|AEE85058.1| nudix hydrolase 10 [Arabidopsis thaliana]	278	277	1.00E-133	99.6	85.3	90.3	nudix hydrolase 10	gbpln	Arabidopsis thaliana	AT4G25434.1 | Symbols: ATNUDT10, NUDT10 | nudix hydrolase homolog 10 | chr4:13004043-13005771 REVERSE LENGTH=277	278	277	1.00E-136	99.6	85.3	90.3
Rsa1.0_00198.1.g8311.t1	ref|XP_002867610.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313446|gb|EFH43869.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	114	114	1.00E-41	100.0	72.8	84.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G25433.1 | Symbols: | peptidoglycan-binding LysM domain-containing protein | chr4:13001463-13001795 REVERSE LENGTH=110	114	110	2.00E-43	96.5	72.8	82.5
Rsa1.0_00198.1.g8312.t1	gb|EOA14349.1| hypothetical protein CARUB_v10027529mg [Capsella rubella]	219	222	4.00E-77	101.4	70.3	84.9	hypothetical protein CARUB_v10027529mg	gbpln	Capsella rubella	AT5G51860.2 | Symbols: | K-box region and MADS-box transcription factor family protein | chr5:21081844-21084126 REVERSE LENGTH=202	219	202	2.00E-58	92.2	58.0	72.6
Rsa1.0_00198.1.g8313.t1	ref|NP_194273.2| uncharacterized protein [Arabidopsis thaliana] gi|332659656|gb|AEE85056.1| uncharacterized protein AT4G25430 [Arabidopsis thaliana]	176	459	5.00E-39	260.8	56.8	73.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G25430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G51850.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12998571-13000211 FORWARD LENGTH=459	176	459	2.00E-41	260.8	56.8	73.3
Rsa1.0_00198.1.g8314.t1	dbj|BAM73279.1| gibberellin 20 oxidase 1 [Raphanus sativus]	380	381	0	100.3	85.5	91.8	gibberellin 20 oxidase 1	gbpln	Raphanus sativus	AT4G25420.1 | Symbols: GA5, GA20OX1, AT2301, ATGA20OX1 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:12990982-12992409 REVERSE LENGTH=377	380	377	0	99.2	85.3	90.0

Rsa1.0_00199.1.g8315.t1	ref|NP_199137.2| uncharacterized protein [Arabidopsis thaliana] gi|332007543|gb|AED94926.1| uncharacterized protein AT5G43230 [Arabidopsis thaliana]	598	848	0	141.8	55.5	59.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G43230.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01810.3); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:17349125-17352747 FORWARD LENGTH=848	598	848	0	141.8	55.5	59.4
Rsa1.0_00199.1.g8316.t1	emb|CAB81573.1| putative protein [Arabidopsis thaliana]	356	510	7.00E-22	143.3	18.5	27.5	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8317.t1	ref|NP_199135.1| endo/excinuclease amino terminal domain-containing protein [Arabidopsis thaliana] gi|10177383|dbj|BAB10584.1| unnamed protein product [Arabidopsis thaliana] gi|332007541|gb|AED94924.1| endo/excinuclease amino terminal domain-containing protein [Arabidopsis thaliana]	183	170	7.00E-70	92.9	73.2	81.4	endo/excinuclease amino terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT5G43210.1 | Symbols: | Excinuclease ABC, C subunit, N-terminal | chr5:17347567-17348379 FORWARD LENGTH=170	183	170	3.00E-72	92.9	73.2	81.4
Rsa1.0_00199.1.g8318.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8319.t1	dbj|BAE98403.1| putative non-LTR reverse transcriptase [Arabidopsis thaliana]	286	278	2.00E-52	97.2	39.9	54.9	putative non-LTR reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	286	295	3.00E-49	103.1	36.4	50.3
Rsa1.0_00199.1.g8320.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8321.t2	ref|XP_002865450.1| hypothetical protein ARALYDRAFT_917371 [Arabidopsis lyrata subsp. lyrata] gi|297311285|gb|EFH41709.1| hypothetical protein ARALYDRAFT_917371 [Arabidopsis lyrata subsp. lyrata]	94	91	1.00E-36	96.8	81.9	85.1	hypothetical protein ARALYDRAFT_917371	gbpln	Arabidopsis lyrata	AT5G43150.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:17325076-17325689 FORWARD LENGTH=91	94	91	2.00E-36	96.8	78.7	85.1
Rsa1.0_00199.1.g8322.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	147	1231	2.00E-25	837.4	42.9	58.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365	147	365	4.00E-13	248.3	29.9	48.3
Rsa1.0_00199.1.g8323.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8324.t2	gb|AAF63106.1|AC006423_7 Hypothetical protein [Arabidopsis thaliana]	506	570	2.00E-12	112.6	14.0	25.3	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8325.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	742	1838	0	247.7	54.3	69.3	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8326.t1	ref|NP_199127.3| TBP-associated factor 4 [Arabidopsis thaliana] gi|38490053|gb|AAR21620.1| TATA-binding protein associated factor 4b [Arabidopsis thaliana] gi|110738778|dbj|BAF01312.1| hypothetical protein [Arabidopsis thaliana] gi|332007530|gb|AED94913.1| TBP-associated factor 4 [Arabidopsis thaliana]	1036	823	0	79.4	65.0	68.8	TBP-associated factor 4	gbpln	Arabidopsis thaliana	AT5G43130.1 | Symbols: TAF4, TAF4B | TBP-associated factor 4 | chr5:17315608-17321144 REVERSE LENGTH=823	1036	823	0	79.4	65.0	68.8

Rsa1.0_00199.1.g8327.t1	ref|NP_199115.1| regulatory particle triple-A ATPase 4A [Arabidopsis thaliana] gi|75337115|sp|Q9SEI3.1|PS10A_ARATH RecName: Full=26S protease regulatory subunit 10B homolog A; AltName: Full=26S proteasome AAA-ATPase subunit RPT4a; AltName: Full=26S proteasome subunit 10B homolog A; AltName: Full=Regulatory particle triple-A ATPase subunit 4a gi|6652884|gb|AAF22524.1|AF123393_1 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gi|13937183|gb|AAK50085.1|AF372945_1 AT5g43010/MBD2_21 [Arabidopsis thaliana] gi|9758590|dbj|BAB09203.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gi|18700262|gb|AAL77741.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] gi|332007517|gb|AED94900.1| regulatory particle triple-A ATPase 4A [Arabidopsis thaliana] gi|482549284|gb|EOA13478.1| hypothetical protein CARUB_v10026536mg [Capsella rubella]	399	399	0	100.0	97.5	99.5	regulatory particle triple-A ATPase 4A	gbpln	Arabidopsis thaliana	AT5G43010.1 | Symbols: RPT4A | regulatory particle triple-A ATPase 4A | chr5:17248563-17251014 REVERSE LENGTH=399	399	399	0	100.0	97.5	99.5
Rsa1.0_00199.1.g8328.t1	emb|CAN61630.1| hypothetical protein VITISV_003191 [Vitis vinifera]	1083	1208	0	111.5	41.5	61.0	hypothetical protein VITISV_003191	gbpln	Vitis vinifera	ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145	1083	145	2.00E-26	13.4	5.0	7.0
Rsa1.0_00199.1.g8329.t1	gb|AAM15254.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	322	930	2.00E-25	288.8	24.8	36.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT2G14000.1 | Symbols: | Arabidopsis retrotransposon ORF-1 protein | chr2:5884600-5885985 REVERSE LENGTH=346	322	346	1.00E-13	107.5	11.2	19.9
Rsa1.0_00199.1.g8330.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8331.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8332.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8333.t1	ref|NP_568607.1| B-cell receptor-associated 31-like protein [Arabidopsis thaliana] gi|15450826|gb|AAK96684.1| Unknown protein [Arabidopsis thaliana] gi|88196723|gb|ABD43004.1| At5g42570 [Arabidopsis thaliana] gi|332007447|gb|AED94830.1| B-cell receptor-associated 31-like protein [Arabidopsis thaliana]	218	218	1.00E-112	100.0	93.1	95.4	B-cell receptor-associated 31-like protein	gbpln	Arabidopsis thaliana	AT5G42570.1 | Symbols: | B-cell receptor-associated 31-like | chr5:17021459-17022497 REVERSE LENGTH=218	218	218	1.00E-115	100.0	93.1	95.4
Rsa1.0_00199.1.g8334.t3	ref|NP_567695.1| ATP binding microtubule motor family protein [Arabidopsis thaliana] gi|332659458|gb|AEE84858.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]	1180	1004	0	85.1	52.5	64.0	ATP binding microtubule motor family protein	gbpln	Arabidopsis thaliana	AT4G24170.1 | Symbols: | ATP binding microtubule motor family protein | chr4:12543206-12546805 FORWARD LENGTH=1004	1180	1004	0	85.1	52.5	64.0
Rsa1.0_00199.1.g8335.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8336.t1	gb|AGB34186.1| allene oxide synthase [Brassica oleracea]	529	529	0	100.0	95.5	97.2	allene oxide synthase	gbpln	Brassica oleracea	AT5G42650.1 | Symbols: AOS, CYP74A, DDE2 | allene oxide synthase | chr5:17097803-17099359 REVERSE LENGTH=518	529	518	0	97.9	82.6	90.0
Rsa1.0_00199.1.g8337.t1	ref|NP_180318.1| dephospho-CoA kinase [Arabidopsis thaliana] gi|30683542|ref|NP_850102.1| dephospho-CoA kinase [Arabidopsis thaliana] gi|4314391|gb|AAD15601.1| unknown protein [Arabidopsis thaliana] gi|110737255|dbj|BAF00575.1| hypothetical protein [Arabidopsis thaliana] gi|117168209|gb|ABK32187.1| At2g27490 [Arabidopsis thaliana] gi|330252908|gb|AEC08002.1| dephospho-CoA kinase [Arabidopsis thaliana] gi|330252909|gb|AEC08003.1| dephospho-CoA kinase [Arabidopsis thaliana]	72	232	6.00E-21	322.2	70.8	77.8	dephospho-CoA kinase	gbpln	Arabidopsis thaliana	AT2G27490.2 | Symbols: ATCOAE | dephospho-CoA kinase family | chr2:11748087-11749009 REVERSE LENGTH=232	72	232	9.00E-24	322.2	70.8	77.8
Rsa1.0_00199.1.g8338.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	654	1142	3.00E-65	174.6	19.0	24.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	654	484	6.00E-26	74.0	12.2	17.9
Rsa1.0_00199.1.g8339.t1	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	505	521	8.00E-30	103.2	14.9	20.8	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#

Rsa1.0_00199.1.g8340.t1	ref|NP_178356.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|3184287|gb|AAC18934.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana] gi|330250497|gb|AEC05591.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	139	211	8.00E-34	151.8	48.2	66.9	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT2G02520.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr2:676771-678145 REVERSE LENGTH=211	139	211	2.00E-36	151.8	48.2	66.9
Rsa1.0_00199.1.g8341.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	384	1274	8.00E-73	331.8	40.9	58.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	384	575	7.00E-31	149.7	31.3	49.0
Rsa1.0_00199.1.g8342.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8343.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8344.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8345.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	593	940	6.00E-66	158.5	20.7	26.0	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8346.t1	gb|AAF79797.1|AC020646_20 T32E20.30 [Arabidopsis thaliana]	1365	1397	0	102.3	48.8	65.7	T32E20.30	gbpln	Arabidopsis thaliana	AT1G67020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf; Has 72 Blast hits to 72 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 72; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25011008-25012987 REVERSE LENGTH=659	1365	659	1.00E-14	48.3	2.3	3.8
Rsa1.0_00199.1.g8347.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00199.1.g8348.t2	gb|AAZ41811.1| 01P13-1 [Brassica rapa subsp. pekinensis]	1241	1545	0	124.5	61.9	77.6	01P13-1	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1241	1262	3.00E-70	101.7	12.8	19.0
Rsa1.0_00199.1.g8349.t1	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	176	1453	6.00E-73	825.6	73.9	84.7	polyprotein	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	176	240	3.00E-57	136.4	57.4	73.9
Rsa1.0_00199.1.g8350.t1	gb|AAZ66952.1| 117M18_33 [Brassica rapa]	658	681	6.00E-81	103.5	27.4	35.4	117M18_33	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	658	1262	7.00E-23	191.8	8.2	14.1
Rsa1.0_00200.1.g8351.t1	ref|YP_717161.1| hypothetical protein BrnapMp064 [Brassica napus] gi|353526385|ref|YP_004927457.1| orf448 (mitochondrion) [Brassica oleracea] gi|353526703|ref|YP_004927873.1| orf448 (mitochondrion) [Brassica rapa subsp. oleifera] gi|353531385|ref|YP_004927776.1| orf448 (mitochondrion) [Brassica juncea] gi|37591108|dbj|BAC98910.1| hypothetical protein [Brassica napus] gi|335354891|gb|AEH43447.1| orf448 [Brassica rapa subsp. oleifera] gi|335354930|gb|AEH43485.1| orf448 [Brassica oleracea] gi|335355118|gb|AEH43671.1| orf448 [Brassica juncea] gi|339511319|emb|CBX48374.1| unnamed protein product [Brassica napus]	126	448	4.00E-28	355.6	46.8	48.4	hypothetical protein BrnapMp064	gbpln	Brassica juncea	#	#	#	#	#	#	#
Rsa1.0_00200.1.g8352.t1	ref|XP_002331327.1| predicted protein [Populus trichocarpa] gi|222873910|gb|EEF11041.1| predicted protein [Populus trichocarpa]	78	596	1.00E-16	764.1	56.4	60.3	predicted protein	gbpln	Populus trichocarpa	AT1G53510.1 | Symbols: ATMPK18, MPK18 | mitogen-activated protein kinase 18 | chr1:19970961-19974158 REVERSE LENGTH=615	78	615	2.00E-19	788.5	56.4	61.5
Rsa1.0_00200.1.g8353.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00200.1.g8354.t2	ref|NP_001031695.1| PHD finger and bromo-adjacent homology domain-containing protein [Arabidopsis thaliana] gi|62321730|dbj|BAD95354.1| receptor like protein [Arabidopsis thaliana] gi|332659163|gb|AEE84563.1| PHD finger and bromo-adjacent homology domain-containing protein [Arabidopsis thaliana]	255	224	1.00E-124	87.8	82.7	83.9	PHD finger and bromo-adjacent homology domain-containing protein	gbpln	Arabidopsis thaliana	AT4G22140.2 | Symbols: EBS | PHD finger family protein / bromo-adjacent homology (BAH) domain-containing protein | chr4:11728093-11730230 REVERSE LENGTH=224	255	224	1.00E-126	87.8	82.7	83.9

Rsa1.0_00200.1.g8355.t1	gb|EOA18522.1| hypothetical protein CARUB_v10007075mg [Capsella rubella]	389	401	1.00E-107	103.1	57.1	69.9	hypothetical protein CARUB_v10007075mg	gbpln	Capsella rubella	AT4G22180.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr4:11738574-11739782 FORWARD LENGTH=402	389	402	1.00E-110	103.3	56.3	70.4
Rsa1.0_00200.1.g8356.t1	ref|NP_567650.2| uncharacterized protein [Arabidopsis thaliana] gi|20466282|gb|AAM20458.1| unknown protein [Arabidopsis thaliana] gi|22136352|gb|AAM91254.1| unknown protein [Arabidopsis thaliana] gi|332659170|gb|AEE84570.1| uncharacterized protein AT4G22190 [Arabidopsis thaliana]	350	387	1.00E-109	110.6	73.1	80.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G22190.1 | Symbols: | unknown protein; Has 283 Blast hits to 154 proteins in 44 species: Archae - 0; Bacteria - 2; Metazoa - 24; Fungi - 12; Plants - 48; Viruses - 0; Other Eukaryotes - 197 (source: NCBI BLink). | chr4:11742102-11743265 REVERSE LENGTH=387	350	387	1.00E-112	110.6	73.1	80.0
Rsa1.0_00200.1.g8357.t1	ref|XP_002867780.1| hypothetical protein ARALYDRAFT_492641 [Arabidopsis lyrata subsp. lyrata] gi|297313616|gb|EFH44039.1| hypothetical protein ARALYDRAFT_492641 [Arabidopsis lyrata subsp. lyrata]	656	214	1.00E-72	32.6	24.1	25.6	hypothetical protein ARALYDRAFT_492641	gbpln	Arabidopsis lyrata	AT4G22250.1 | Symbols: | RING/U-box superfamily protein | chr4:11767685-11768329 REVERSE LENGTH=214	656	214	4.00E-69	32.6	23.3	25.5
Rsa1.0_00200.1.g8358.t1	gb|EOA16917.1| hypothetical protein CARUB_v10005140mg [Capsella rubella]	196	353	5.00E-39	180.1	43.4	44.4	hypothetical protein CARUB_v10005140mg	gbpln	Capsella rubella	AT4G22260.1 | Symbols: IM, IM1 | Alternative oxidase family protein | chr4:11769967-11772350 REVERSE LENGTH=351	196	351	7.00E-40	179.1	42.3	43.9
Rsa1.0_00200.1.g8359.t1	gb|EOA16620.1| hypothetical protein CARUB_v10004790mg [Capsella rubella]	439	443	0	100.9	88.4	92.7	hypothetical protein CARUB_v10004790mg	gbpln	Capsella rubella	AT4G22270.1 | Symbols: MRB1, ATMRB1 | Protein of unknown function (DUF3537) | chr4:11773396-11775782 FORWARD LENGTH=437	439	437	0	99.5	84.1	90.0
Rsa1.0_00200.1.g8360.t1	ref|XP_002868681.1| hypothetical protein ARALYDRAFT_916271 [Arabidopsis lyrata subsp. lyrata] gi|297314517|gb|EFH44940.1| hypothetical protein ARALYDRAFT_916271 [Arabidopsis lyrata subsp. lyrata]	1097	1168	0	106.5	90.1	94.8	hypothetical protein ARALYDRAFT_916271	gbpln	Arabidopsis lyrata	AT4G10320.1 | Symbols: | tRNA synthetase class I (I, L, M and V) family protein | chr4:6397526-6404509 REVERSE LENGTH=1190	1097	1190	0	108.5	81.6	90.2
Rsa1.0_00200.1.g8361.t1	ref|XP_002868681.1| hypothetical protein ARALYDRAFT_916271 [Arabidopsis lyrata subsp. lyrata] gi|297314517|gb|EFH44940.1| hypothetical protein ARALYDRAFT_916271 [Arabidopsis lyrata subsp. lyrata]	1104	1168	0	105.8	90.1	94.7	hypothetical protein ARALYDRAFT_916271	gbpln	Arabidopsis lyrata	AT4G10320.1 | Symbols: | tRNA synthetase class I (I, L, M and V) family protein | chr4:6397526-6404509 REVERSE LENGTH=1190	1104	1190	0	107.8	83.6	91.3
Rsa1.0_00200.1.g8362.t1	gb|EOA18195.1| hypothetical protein CARUB_v10006678mg [Capsella rubella]	435	417	1.00E-147	95.9	63.0	73.8	hypothetical protein CARUB_v10006678mg	gbpln	Capsella rubella	AT4G22280.1 | Symbols: | F-box/RNI-like superfamily protein | chr4:11776054-11777517 REVERSE LENGTH=415	435	415	1.00E-131	95.4	60.2	71.0
Rsa1.0_00200.1.g8363.t1	ref|XP_002883939.1| hypothetical protein ARALYDRAFT_899844 [Arabidopsis lyrata subsp. lyrata] gi|297329779|gb|EFH60198.1| hypothetical protein ARALYDRAFT_899844 [Arabidopsis lyrata subsp. lyrata]	161	1439	4.00E-12	893.8	23.6	24.8	hypothetical protein ARALYDRAFT_899844	gbpln	Arabidopsis lyrata	AT2G42550.1 | Symbols: | Protein kinase superfamily protein | chr2:17713196-17714230 FORWARD LENGTH=344	161	344	9.00E-14	213.7	21.7	29.2
Rsa1.0_00200.1.g8364.t1	gb|EOA16644.1| hypothetical protein CARUB_v10004819mg [Capsella rubella]	444	442	0	99.5	91.4	95.3	hypothetical protein CARUB_v10004819mg	gbpln	Capsella rubella	AT4G22290.1 | Symbols: | Ubiquitin-specific protease family C19-related protein | chr4:11783199-11785730 REVERSE LENGTH=445	444	445	0	100.2	90.8	94.4
Rsa1.0_00200.1.g8365.t1	gb|EOA17233.1| hypothetical protein CARUB_v10005506mg [Capsella rubella]	263	266	1.00E-119	101.1	83.7	88.2	hypothetical protein CARUB_v10005506mg	gbpln	Capsella rubella	AT4G22300.1 | Symbols: SOBER1 | carboxylesterases | chr4:11787560-11789252 REVERSE LENGTH=262	263	262	1.00E-120	99.6	81.7	88.2
Rsa1.0_00200.1.g8366.t1	ref|XP_002869829.1| hypothetical protein ARALYDRAFT_492636 [Arabidopsis lyrata subsp. lyrata] gi|297315665|gb|EFH46088.1| hypothetical protein ARALYDRAFT_492636 [Arabidopsis lyrata subsp. lyrata]	108	108	5.00E-51	100.0	88.0	95.4	hypothetical protein ARALYDRAFT_492636	gbpln	Arabidopsis lyrata	AT4G22310.1 | Symbols: | Uncharacterised protein family (UPF0041) | chr4:11791443-11792638 FORWARD LENGTH=108	108	108	1.00E-53	100.0	87.0	95.4
Rsa1.0_00200.1.g8367.t1	ref|XP_002867776.1| hypothetical protein ARALYDRAFT_492635 [Arabidopsis lyrata subsp. lyrata] gi|297313612|gb|EFH44035.1| hypothetical protein ARALYDRAFT_492635 [Arabidopsis lyrata subsp. lyrata]	210	234	3.00E-53	111.4	66.2	81.0	hypothetical protein ARALYDRAFT_492635	gbpln	Arabidopsis lyrata	AT4G22320.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G55210.1). | chr4:11793129-11794596 REVERSE LENGTH=237	210	237	5.00E-50	112.9	63.8	81.0
Rsa1.0_00200.1.g8368.t1	gb|EOA17285.1| hypothetical protein CARUB_v10005555mg [Capsella rubella]	255	255	1.00E-148	100.0	98.4	99.2	hypothetical protein CARUB_v10005555mg	gbpln	Capsella rubella	AT4G22330.1 | Symbols: ATCES1 | Alkaline phytoceramidase (aPHC) | chr4:11798483-11799549 FORWARD LENGTH=255	255	255	1.00E-149	100.0	97.3	98.8

Rsa1.0_00200.1.g8369.t1	ref|XP_002867774.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313610|gb|EFH44033.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	491	506	0	103.1	92.9	95.9	ubiquitin carboxyl-terminal hydrolase family protein	gbpln	Arabidopsis lyrata	AT4G22350.1 | Symbols: | Ubiquitin C-terminal hydrolases superfamily protein | chr4:11804073-11806939 REVERSE LENGTH=510	491	510	0	103.9	92.7	94.7
Rsa1.0_00200.1.g8370.t1	ref|XP_002869827.1| hypothetical protein ARALYDRAFT_492627 [Arabidopsis lyrata subsp. lyrata] gi|297315663|gb|EFH46086.1| hypothetical protein ARALYDRAFT_492627 [Arabidopsis lyrata subsp. lyrata]	367	370	1.00E-147	100.8	82.6	88.0	hypothetical protein ARALYDRAFT_492627	gbpln	Arabidopsis lyrata	AT4G22360.1 | Symbols: | SWIB complex BAF60b domain-containing protein | chr4:11807811-11809660 FORWARD LENGTH=385	367	385	1.00E-148	104.9	81.5	86.1
Rsa1.0_00200.1.g8371.t1	gb|EOA17661.1| hypothetical protein CARUB_v10006030mg [Capsella rubella]	123	123	5.00E-40	100.0	73.2	79.7	hypothetical protein CARUB_v10006030mg	gbpln	Capsella rubella	AT4G22490.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:11849933-11850295 REVERSE LENGTH=120	123	120	4.00E-39	97.6	62.6	69.1
Rsa1.0_00200.1.g8372.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00200.1.g8373.t1	gb|AAD21687.1| Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078 [Arabidopsis thaliana]	264	1415	1.00E-102	536.0	68.2	79.2	Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078	gbpln	Arabidopsis thaliana	AT5G48050.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G34070.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19472661-19473770 REVERSE LENGTH=369	264	369	1.00E-18	139.8	19.3	36.4
Rsa1.0_00200.1.g8374.t1	ref|XP_002867764.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297313600|gb|EFH44023.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata]	97	721	4.00E-25	743.3	60.8	64.9	oxysterol-binding family protein	gbpln	Arabidopsis lyrata	AT4G22540.4 | Symbols: ORP2A | OSBP(oxysterol binding protein)-related protein 2A | chr4:11860969-11863886 REVERSE LENGTH=510	97	510	1.00E-27	525.8	59.8	64.9
Rsa1.0_00200.1.g8375.t1	gb|EOA17503.1| hypothetical protein CARUB_v10005836mg [Capsella rubella]	183	183	8.00E-99	100.0	98.4	100.0	hypothetical protein CARUB_v10005836mg	gbpln	Capsella rubella	AT4G22570.1 | Symbols: APT3 | adenine phosphoribosyl transferase 3 | chr4:11882310-11885250 REVERSE LENGTH=183	183	183	1.00E-101	100.0	98.4	100.0
Rsa1.0_00200.1.g8376.t1	ref|NP_193991.1| uncharacterized protein [Arabidopsis thaliana] gi|3892715|emb|CAA22165.1| hypothetical protein [Arabidopsis thaliana] gi|7269106|emb|CAB79215.1| hypothetical protein [Arabidopsis thaliana] gi|93007376|gb|ABE97191.1| hypothetical protein At4g22600 [Arabidopsis thaliana] gi|332659229|gb|AEE84629.1| uncharacterized protein AT4G22600 [Arabidopsis thaliana]	363	273	2.00E-37	75.2	27.3	39.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G22600.1 | Symbols: | unknown protein; Has 26 Blast hits to 26 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11900211-11901032 REVERSE LENGTH=273	363	273	5.00E-40	75.2	27.3	39.1
Rsa1.0_00200.1.g8377.t1	ref|NP_193991.1| uncharacterized protein [Arabidopsis thaliana] gi|3892715|emb|CAA22165.1| hypothetical protein [Arabidopsis thaliana] gi|7269106|emb|CAB79215.1| hypothetical protein [Arabidopsis thaliana] gi|93007376|gb|ABE97191.1| hypothetical protein At4g22600 [Arabidopsis thaliana] gi|332659229|gb|AEE84629.1| uncharacterized protein AT4G22600 [Arabidopsis thaliana]	376	273	4.00E-20	72.6	19.1	25.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G22600.1 | Symbols: | unknown protein; Has 26 Blast hits to 26 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11900211-11901032 REVERSE LENGTH=273	376	273	1.00E-22	72.6	19.1	25.5
Rsa1.0_00200.1.g8378.t1	gb|EOA16835.1| hypothetical protein CARUB_v10005056mg [Capsella rubella]	359	377	0	105.0	91.6	95.5	hypothetical protein CARUB_v10005056mg	gbpln	Capsella rubella	AT4G22590.1 | Symbols: TPPG | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr4:11893707-11895371 REVERSE LENGTH=377	359	377	0	105.0	90.3	95.3
Rsa1.0_00200.1.g8379.t1	gb|EOA37612.1| hypothetical protein CARUB_v10012000mg [Capsella rubella]	510	562	1.00E-80	110.2	35.9	55.3	hypothetical protein CARUB_v10012000mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	510	566	7.00E-81	111.0	34.1	55.7
Rsa1.0_00200.1.g8380.t1	dbj|BAB11364.1| helicase [Arabidopsis thaliana]	561	1523	1.00E-112	271.5	34.9	44.6	helicase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00201.1.g8381.t1	ref|XP_002882044.1| hypothetical protein ARALYDRAFT_904051 [Arabidopsis lyrata subsp. lyrata] gi|297327883|gb|EFH58303.1| hypothetical protein ARALYDRAFT_904051 [Arabidopsis lyrata subsp. lyrata]	255	265	1.00E-95	103.9	75.7	84.7	hypothetical protein ARALYDRAFT_904051	gbpln	Arabidopsis lyrata	AT2G45980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G00355.2); Has 93 Blast hits to 90 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 93; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18917680-18918569 REVERSE LENGTH=256	255	256	4.00E-94	100.4	73.3	80.8
Rsa1.0_00201.1.g8382.t1	ref|XP_002880212.1| hypothetical protein ARALYDRAFT_904052 [Arabidopsis lyrata subsp. lyrata] gi|297326051|gb|EFH56471.1| hypothetical protein ARALYDRAFT_904052 [Arabidopsis lyrata subsp. lyrata]	269	268	1.00E-137	99.6	92.9	96.3	hypothetical protein ARALYDRAFT_904052	gbpln	Arabidopsis lyrata	AT2G45990.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 312 Blast hits to 312 proteins in 90 species: Archae - 0; Bacteria - 131; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 114 (source: NCBI BLink). | chr2:18919402-18921043 FORWARD LENGTH=268	269	268	1.00E-137	99.6	91.4	95.2
Rsa1.0_00201.1.g8383.t1	ref|XP_002882045.1| hypothetical protein ARALYDRAFT_483745 [Arabidopsis lyrata subsp. lyrata] gi|297327884|gb|EFH58304.1| hypothetical protein ARALYDRAFT_483745 [Arabidopsis lyrata subsp. lyrata]	206	206	9.00E-86	100.0	77.7	86.4	hypothetical protein ARALYDRAFT_483745	gbpln	Arabidopsis lyrata	AT2G46000.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Mesoderm development candidate 2 (InterPro:IPR019330); Has 31 Blast hits to 31 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 5; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18921194-18922047 REVERSE LENGTH=208	206	208	6.00E-76	101.0	79.1	85.9
Rsa1.0_00201.1.g8384.t1	gb|EOA26811.1| hypothetical protein CARUB_v10022904mg [Capsella rubella]	535	560	1.00E-179	104.7	64.3	77.0	hypothetical protein CARUB_v10022904mg	gbpln	Capsella rubella	AT2G46040.1 | Symbols: | ARID/BRIGHT DNA-binding domain;ELM2 domain protein | chr2:18935684-18937807 REVERSE LENGTH=562	535	562	1.00E-179	105.0	64.5	77.0
Rsa1.0_00201.1.g8385.t1	gb|EOA28383.1| hypothetical protein CARUB_v10024588mg [Capsella rubella]	559	583	0	104.3	77.3	87.1	hypothetical protein CARUB_v10024588mg	gbpln	Capsella rubella	AT2G46050.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr2:18939262-18941034 FORWARD LENGTH=590	559	590	0	105.5	75.0	85.9
Rsa1.0_00201.1.g8386.t1	ref|XP_002882047.1| hypothetical protein ARALYDRAFT_483751 [Arabidopsis lyrata subsp. lyrata] gi|297327886|gb|EFH58306.1| hypothetical protein ARALYDRAFT_483751 [Arabidopsis lyrata subsp. lyrata]	812	808	0	99.5	86.8	93.3	hypothetical protein ARALYDRAFT_483751	gbpln	Arabidopsis lyrata	AT2G46060.1 | Symbols: | transmembrane protein-related | chr2:18941355-18945000 REVERSE LENGTH=807	812	807	0	99.4	84.6	92.2
Rsa1.0_00201.1.g8387.t1	ref|XP_002882049.1| hypothetical protein ARALYDRAFT_322261 [Arabidopsis lyrata subsp. lyrata] gi|297327888|gb|EFH58308.1| hypothetical protein ARALYDRAFT_322261 [Arabidopsis lyrata subsp. lyrata]	372	406	0	109.1	94.9	96.8	hypothetical protein ARALYDRAFT_322261	gbpln	Arabidopsis lyrata	AT2G46070.1 | Symbols: ATMPK12, MAPK12, MPK12 | mitogen-activated protein kinase 12 | chr2:18946134-18947770 REVERSE LENGTH=372	372	372	0	100.0	91.9	93.5
Rsa1.0_00201.1.g8388.t1	ref|XP_002882050.1| hypothetical protein ARALYDRAFT_904061 [Arabidopsis lyrata subsp. lyrata] gi|297327889|gb|EFH58309.1| hypothetical protein ARALYDRAFT_904061 [Arabidopsis lyrata subsp. lyrata]	97	347	3.00E-32	357.7	69.1	75.3	hypothetical protein ARALYDRAFT_904061	gbpln	Arabidopsis lyrata	AT2G46080.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein BYPASS related (InterPro:IPR008511); BEST Arabidopsis thaliana protein match is: Protein of unknown function (DUF793) (TAIR:AT1G01550.2); Has 153 Blast hits to 139 proteins in 20 species: Archae - 0; Bacteria - 2; Metazoa - 1; Fungi - 0; Plants - 150; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18948317-18949360 REVERSE LENGTH=347	97	347	2.00E-34	357.7	68.0	74.2

Rsa1.0_00201.1.g8389.t3	ref|NP_182134.2| Nuclear transport factor 2 (NTF2) family protein [Arabidopsis thaliana] gi|48310194|gb|AAT41772.1| At2g46100 [Arabidopsis thaliana] gi|50198900|gb|AAT70469.1| At2g46100 [Arabidopsis thaliana] gi|330255549|gb|AEC10643.1| Nuclear transport factor 2 (NTF2) family protein [Arabidopsis thaliana]	246	240	1.00E-110	97.6	82.9	88.2	Nuclear transport factor 2 (NTF2) family protein	gbpln	Arabidopsis thaliana	AT2G46100.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein | chr2:18953326-18954467 FORWARD LENGTH=240	246	240	1.00E-113	97.6	82.9	88.2
Rsa1.0_00201.1.g8390.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	293	329	7.00E-57	112.3	42.7	54.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	293	292	6.00E-32	99.7	28.7	44.0
Rsa1.0_00201.1.g8391.t1	ref|XP_004295930.1| PREDICTED: uncharacterized protein LOC101294643 [Fragaria vesca subsp. vesca]	97	2166	8.00E-11	2233.0	45.4	52.6	PREDICTED: uncharacterized protein LOC101294643	gbpln	Fragaria vesca	AT4G22970.2 | Symbols: ESP | homolog of separase | chr4:12033703-12043572 REVERSE LENGTH=2177	97	2177	2.00E-12	2244.3	48.5	58.8
Rsa1.0_00201.1.g8392.t1	ref|NP_198207.1| uncharacterized protein [Arabidopsis thaliana] gi|332006430|gb|AED93813.1| uncharacterized protein AT5G28550 [Arabidopsis thaliana]	147	286	3.00E-25	194.6	39.5	51.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G28550.1 | Symbols: | BEST Arabidopsis thaliana protein match is: homolog of separase (TAIR:AT4G22970.2); Has 25 Blast hits to 25 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:10557722-10559779 REVERSE LENGTH=286	147	286	9.00E-28	194.6	39.5	51.0
Rsa1.0_00201.1.g8393.t1	ref|XP_002880219.1| hypothetical protein ARALYDRAFT_483759 [Arabidopsis lyrata subsp. lyrata] gi|297326058|gb|EFH56478.1| hypothetical protein ARALYDRAFT_483759 [Arabidopsis lyrata subsp. lyrata]	166	166	2.00E-81	100.0	91.0	95.2	hypothetical protein ARALYDRAFT_483759	gbpln	Arabidopsis lyrata	AT2G46140.1 | Symbols: | Late embryogenesis abundant protein | chr2:18959163-18960362 FORWARD LENGTH=166	166	166	8.00E-84	100.0	91.0	95.2
Rsa1.0_00201.1.g8394.t1	ref|NP_182138.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|3702334|gb|AAC62891.1| hypothetical protein [Arabidopsis thaliana] gi|21805750|gb|AAM76770.1| hypothetical protein [Arabidopsis thaliana] gi|50058829|gb|AAT69159.1| hypothetical protein At2g46150 [Arabidopsis thaliana] gi|330255555|gb|AEC10649.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	220	221	1.00E-95	100.5	79.1	87.7	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT2G46150.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:18961424-18962089 FORWARD LENGTH=221	220	221	4.00E-98	100.5	79.1	87.7
Rsa1.0_00201.1.g8395.t1	gb|EOA27826.1| hypothetical protein CARUB_v10023982mg, partial [Capsella rubella]	211	233	3.00E-89	110.4	87.7	90.0	hypothetical protein CARUB_v10023982mg, partial	gbpln	Capsella rubella	AT2G46160.1 | Symbols: | RING/U-box superfamily protein | chr2:18963109-18963753 FORWARD LENGTH=214	211	214	2.00E-86	101.4	86.7	89.1
Rsa1.0_00201.1.g8396.t1	gb|EOA27748.1| hypothetical protein CARUB_v10023902mg [Capsella rubella]	263	255	1.00E-116	97.0	83.3	88.6	hypothetical protein CARUB_v10023902mg	gbpln	Capsella rubella	AT2G46170.1 | Symbols: | Reticulon family protein | chr2:18965410-18966940 FORWARD LENGTH=255	263	255	1.00E-118	97.0	82.9	87.5
Rsa1.0_00201.1.g8397.t1	ref|XP_002882054.1| hypothetical protein ARALYDRAFT_483767 [Arabidopsis lyrata subsp. lyrata] gi|297327893|gb|EFH58313.1| hypothetical protein ARALYDRAFT_483767 [Arabidopsis lyrata subsp. lyrata]	387	385	0	99.5	81.7	89.7	hypothetical protein ARALYDRAFT_483767	gbpln	Arabidopsis lyrata	AT2G46200.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:18974864-18976646 REVERSE LENGTH=382	387	382	0	98.7	80.9	89.7
Rsa1.0_00201.1.g8398.t1	emb|CAA11857.1| delta-8 sphingolipid desaturase [Brassica napus]	449	449	0	100.0	96.9	98.7	delta-8 sphingolipid desaturase	gbpln	Brassica napus	AT2G46210.1 | Symbols: | Fatty acid/sphingolipid desaturase | chr2:18977542-18978891 FORWARD LENGTH=449	449	449	0	100.0	90.9	96.4
Rsa1.0_00201.1.g8399.t1	gb|AAB03378.1| transcription factor [Brassica napus]	377	376	0	99.7	91.8	95.5	transcription factor	gbpln	Brassica napus	AT2G46270.1 | Symbols: GBF3 | G-box binding factor 3 | chr2:19000859-19002901 FORWARD LENGTH=382	377	382	1.00E-170	101.3	85.4	89.1
Rsa1.0_00201.1.g8400.t1	ref|NP_182153.2| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|91806363|gb|ABE65909.1| unknown [Arabidopsis thaliana] gi|330255579|gb|AEC10673.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	254	252	6.00E-92	99.2	76.4	86.6	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT2G46300.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:19008392-19009247 FORWARD LENGTH=252	254	252	2.00E-94	99.2	76.4	86.6
Rsa1.0_00201.1.g8401.t1	gb|EOA27621.1| hypothetical protein CARUB_v10023769mg [Capsella rubella]	301	290	1.00E-80	96.3	62.1	70.8	hypothetical protein CARUB_v10023769mg	gbpln	Capsella rubella	AT2G46310.1 | Symbols: CRF5 | cytokinin response factor 5 | chr2:19011614-19012498 FORWARD LENGTH=294	301	294	1.00E-82	97.7	64.5	72.4

Rsa1.0_00201.1.g8402.t1	gb|EOA27354.1| hypothetical protein CARUB_v10023475mg [Capsella rubella]	378	367	1.00E-174	97.1	83.9	86.5	hypothetical protein CARUB_v10023475mg	gbpln	Capsella rubella	AT2G46320.1 | Symbols: | Mitochondrial substrate carrier family protein | chr2:19015998-19018020 FORWARD LENGTH=361	378	361	1.00E-177	95.5	84.7	89.2
Rsa1.0_00201.1.g8403.t1	ref|NP_566070.3| arabinogalactan protein 16 [Arabidopsis thaliana] gi|297828351|ref|XP_002882058.1| hypothetical protein ARALYDRAFT_483786 [Arabidopsis lyrata subsp. lyrata] gi|75100629|sp|O82337.1|AGP16_ARATH RecName: Full=Arabinogalactan peptide 16; Short=AG-peptide 16; Flags: Precursor gi|10880509|gb|AAG24284.1|AF195897_1 arabinogalactan protein [Arabidopsis thaliana] gi|15294170|gb|AAK95262.1|AF410276_1 At2g46330/F11C10.2 [Arabidopsis thaliana] gi|4559376|gb|AAD23036.1| expressed protein [Arabidopsis thaliana] gi|20197373|gb|AAM15047.1| expressed protein [Arabidopsis thaliana] gi|20453295|gb|AAM19886.1| At2g46330/F11C10.2 [Arabidopsis thaliana] gi|21553759|gb|AAM62852.1| unknown [Arabidopsis thaliana] gi|297327897|gb|EFH58317.1| hypothetical protein ARALYDRAFT_483786 [Arabidopsis lyrata subsp. lyrata] gi|330255586|gb|AEC10680.1| arabinogalactan protein 16 [Arabidopsis thaliana]	73	73	6.00E-29	100.0	93.2	95.9	arabinogalactan protein 16	gbpln	Arabidopsis lyrata	AT2G46330.1 | Symbols: AGP16, ATAGP16 | arabinogalactan protein 16 | chr2:19018730-19019108 REVERSE LENGTH=73	73	73	1.00E-31	100.0	93.2	95.9
Rsa1.0_00201.1.g8404.t2	ref|NP_182157.2| protein SUPPRESSOR OF PHYA-105 1 [Arabidopsis thaliana] gi|75337885|sp|Q9SYX2.1|SPA1_ARATH RecName: Full=Protein SUPPRESSOR OF PHYA-105 1 gi|4809171|gb|AAD30124.1|AF135455_1 phytochrome A supressor spa1 [Arabidopsis thaliana] gi|330255587|gb|AEC10681.1| protein SUPPRESSOR OF PHYA-105 1 [Arabidopsis thaliana]	1052	1029	0	97.8	81.7	88.4	protein SUPPRESSOR OF PHYA-105 1	gbpln	Arabidopsis thaliana	AT2G46340.1 | Symbols: SPA1 | SPA (suppressor of phyA-105) protein family | chr2:19022572-19026821 REVERSE LENGTH=1029	1052	1029	0	97.8	81.7	88.4
Rsa1.0_00201.1.g8405.t1	ref|NP_188381.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75274267|sp|Q9LUP4.1|FBK60_ARATH RecName: Full=Putative F-box/kelch-repeat protein At3g17540 gi|9294141|dbj|BAB02043.1| unnamed protein product [Arabidopsis thaliana] gi|332642445|gb|AEE75966.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	390	396	9.00E-77	101.5	47.4	63.8	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G17540.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6002783-6003973 FORWARD LENGTH=396	390	396	2.00E-79	101.5	47.4	63.8
Rsa1.0_00201.1.g8406.t1	ref|NP_182159.1| uncharacterized protein [Arabidopsis thaliana] gi|4559379|gb|AAD23039.1| hypothetical protein [Arabidopsis thaliana] gi|18491281|gb|AAL69465.1| At2g46360/F11C10.5 [Arabidopsis thaliana] gi|330255588|gb|AEC10682.1| uncharacterized protein AT2G46360 [Arabidopsis thaliana]	93	97	2.00E-28	104.3	78.5	87.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G46360.1 | Symbols: | unknown protein; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19028507-19028800 FORWARD LENGTH=97	93	97	3.00E-31	104.3	78.5	87.1
Rsa1.0_00201.1.g8407.t1	gb|EOA26758.1| hypothetical protein CARUB_v10022844mg, partial [Capsella rubella]	579	605	0	104.5	90.2	95.5	hypothetical protein CARUB_v10022844mg, partial	gbpln	Capsella rubella	AT2G46370.4 | Symbols: JAR1 | Auxin-responsive GH3 family protein | chr2:19034233-19036369 FORWARD LENGTH=586	579	586	0	101.2	90.0	95.7
Rsa1.0_00201.1.g8408.t1	gb|EOA28441.1| hypothetical protein CARUB_v10024648mg [Capsella rubella]	125	133	1.00E-21	106.4	49.6	64.0	hypothetical protein CARUB_v10024648mg	gbpln	Capsella rubella	AT2G46375.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G61660.1); Has 12 Blast hits to 12 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19037958-19038329 FORWARD LENGTH=123	125	123	6.00E-23	98.4	44.0	54.4

<table>
<tr><td>Rsa1.0_00201.1.g8409.t2</td><td>ref|NP_182161.3| uncharacterized protein [Arabidopsis thaliana] gi|110741891|dbj|BAE98887.1| hypothetical protein [Arabidopsis thaliana] gi|330255594|gb|AEC10688.1| uncharacterized protein AT2G46380 [Arabidopsis thaliana]</td><td>679</td><td>768</td><td>0</td><td>113.1</td><td>70.4</td><td>79.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46380.1 | Symbols: | Protein of unknown function (DUF3133) | chr2:19039377-19042171 FORWARD LENGTH=768</td><td>679</td><td>768</td><td>0</td><td>113.1</td><td>70.4</td><td>79.1</td></tr>
<tr><td>Rsa1.0_00201.1.g8410.t1</td><td>gb|ADM32893.1| WRKY46 [Brassica rapa subsp. chinensis]</td><td>300</td><td>285</td><td>1.00E-128</td><td>95.0</td><td>81.7</td><td>85.7</td><td>WRKY46</td><td>gbpln</td><td>Brassica rapa</td><td>AT2G46400.1 | Symbols: WRKY46, ATWRKY46 | WRKY DNA-binding protein 46 | chr2:19043676-19044754 REVERSE LENGTH=295</td><td>300</td><td>295</td><td>1.00E-116</td><td>98.3</td><td>73.7</td><td>82.7</td></tr>
<tr><td>Rsa1.0_00201.1.g8411.t1</td><td>ref|NP_182164.1| transcription factor CPC [Arabidopsis thaliana] gi|75317955|sp|O22059.1|CPC_ARATH RecName: Full=Transcription factor CPC; AltName: Full=Protein CAPRICE gi|2346966|dbj|BAA21917.1| CPC [Arabidopsis thaliana] gi|4559383|gb|AAD23043.1| putative MYB family transcription factor [Arabidopsis thaliana] gi|18491257|gb|AAL69453.1| At2g46410/F11C10.10 [Arabidopsis thaliana] gi|41618962|gb|AAS09991.1| MYB transcription factor [Arabidopsis thaliana] gi|330255597|gb|AEC10691.1| transcription factor CPC [Arabidopsis thaliana]</td><td>85</td><td>94</td><td>6.00E-39</td><td>110.6</td><td>94.1</td><td>97.6</td><td>transcription factor CPC</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46410.1 | Symbols: CPC | Homeodomain-like superfamily protein | chr2:19049315-19050185 REVERSE LENGTH=94</td><td>85</td><td>94</td><td>1.00E-41</td><td>110.6</td><td>94.1</td><td>97.6</td></tr>
<tr><td>Rsa1.0_00201.1.g8412.t2</td><td>ref|NP_566074.1| uncharacterized protein [Arabidopsis thaliana] gi|15450511|gb|AAK96548.1| At2g46420/F11C10.11 [Arabidopsis thaliana] gi|20197824|gb|AAD23044.2| expressed protein [Arabidopsis thaliana] gi|27363256|gb|AAO11547.1| At2g46420/F11C10.11 [Arabidopsis thaliana] gi|330255598|gb|AEC10692.1| uncharacterized protein AT2G46420 [Arabidopsis thaliana]</td><td>344</td><td>363</td><td>1.00E-175</td><td>105.5</td><td>90.4</td><td>94.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46420.1 | Symbols: | Plant protein 1589 of unknown function | chr2:19054891-19056830 FORWARD LENGTH=363</td><td>344</td><td>363</td><td>1.00E-177</td><td>105.5</td><td>90.4</td><td>94.5</td></tr>
<tr><td>Rsa1.0_00201.1.g8413.t1</td><td>ref|XP_002880240.1| ATCNGC3 [Arabidopsis lyrata subsp. lyrata] gi|297326079|gb|EFH56499.1| ATCNGC3 [Arabidopsis lyrata subsp. lyrata]</td><td>727</td><td>704</td><td>0</td><td>96.8</td><td>82.8</td><td>88.6</td><td>ATCNGC3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46430.2 | Symbols: ATCNGC3, CNGC3, CNGC3.C | cyclic nucleotide gated channel 3 | chr2:19058472-19061273 FORWARD LENGTH=706</td><td>727</td><td>706</td><td>0</td><td>97.1</td><td>81.8</td><td>88.0</td></tr>
<tr><td>Rsa1.0_00201.1.g8414.t3</td><td>ref|NP_850455.4| OxaA/YidC-like membrane insertion protein [Arabidopsis thaliana] gi|330255606|gb|AEC10700.1| OxaA/YidC-like membrane insertion protein [Arabidopsis thaliana]</td><td>395</td><td>186</td><td>2.00E-34</td><td>47.1</td><td>25.1</td><td>30.1</td><td>OxaA/YidC-like membrane insertion protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46455.1 | Symbols: | OxaA/YidC-like membrane insertion protein | chr2:19069844-19070833 REVERSE LENGTH=186</td><td>395</td><td>186</td><td>5.00E-37</td><td>47.1</td><td>25.1</td><td>30.1</td></tr>
<tr><td>Rsa1.0_00201.1.g8415.t2</td><td>gb|EOA29241.1| hypothetical protein CARUB_v10025515mg, partial [Capsella rubella]</td><td>677</td><td>646</td><td>0</td><td>95.4</td><td>64.0</td><td>72.8</td><td>hypothetical protein CARUB_v10025515mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G46480.1 | Symbols: GAUT2, LGT2 | galacturonosyltransferase 2 | chr2:19076405-19078386 REVERSE LENGTH=528</td><td>677</td><td>528</td><td>0</td><td>78.0</td><td>59.5</td><td>67.8</td></tr>
<tr><td>Rsa1.0_00201.1.g8416.t1</td><td>ref|NP_182172.1| uncharacterized protein [Arabidopsis thaliana] gi|4415930|gb|AAD20160.1| unknown protein [Arabidopsis thaliana] gi|17979199|gb|AAL49838.1| unknown protein [Arabidopsis thaliana] gi|20197822|gb|AAM15264.1| unknown protein [Arabidopsis thaliana] gi|21436075|gb|AAM51238.1| unknown protein [Arabidopsis thaliana] gi|330255610|gb|AEC10704.1| uncharacterized protein AT2G46490 [Arabidopsis thaliana]</td><td>129</td><td>134</td><td>1.00E-38</td><td>103.9</td><td>73.6</td><td>82.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46490.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35110.1); Has 34 Blast hits to 34 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19079457-19079861 FORWARD LENGTH=134</td><td>129</td><td>134</td><td>2.00E-41</td><td>103.9</td><td>73.6</td><td>82.2</td></tr>
<tr><td>Rsa1.0_00201.1.g8417.t1</td><td>ref|XP_002882072.1| hypothetical protein ARALYDRAFT_904117 [Arabidopsis lyrata subsp. lyrata] gi|297327911|gb|EFH58331.1| hypothetical protein ARALYDRAFT_904117 [Arabidopsis lyrata subsp. lyrata]</td><td>142</td><td>148</td><td>2.00E-46</td><td>104.2</td><td>71.1</td><td>87.3</td><td>hypothetical protein ARALYDRAFT_904117</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46505.1 | Symbols: SDH4 | succinate dehydrogenase subunit 4 | chr2:19090013-19090468 REVERSE LENGTH=151</td><td>142</td><td>151</td><td>2.00E-46</td><td>106.3</td><td>64.8</td><td>86.6</td></tr>
<tr><td>Rsa1.0_00201.1.g8418.t1</td><td>ref|XP_002882073.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297327912|gb|EFH58332.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]</td><td>490</td><td>563</td><td>0</td><td>114.9</td><td>78.0</td><td>86.7</td><td>basic helix-loop-helix family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46510.1 | Symbols: ATAIB, AIB | ABA-inducible BHLH-type transcription factor | chr2:19091187-19092887 REVERSE LENGTH=566</td><td>490</td><td>566</td><td>1.00E-122</td><td>115.5</td><td>42.2</td><td>47.8</td></tr>
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Rsa1.0_00201.1.g8419.t1	ref|XP_002880249.1| hypothetical protein ARALYDRAFT_904119 [Arabidopsis lyrata subsp. lyrata] gi|297326088|gb|EFH56508.1| hypothetical protein ARALYDRAFT_904119 [Arabidopsis lyrata subsp. lyrata]	962	972	0	101.0	86.5	94.4	hypothetical protein ARALYDRAFT_904119	gbpln	Arabidopsis lyrata	AT2G46520.1 | Symbols: | cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative | chr2:19096867-19099785 FORWARD LENGTH=972	962	972	0	101.0	84.7	92.5
Rsa1.0_00201.1.g8420.t1	gb|AAC35532.1| contains similarity to proteases [Arabidopsis thaliana]	1105	1392	0	126.0	44.3	54.6	contains similarity to proteases	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	1105	240	2.00E-55	21.7	9.0	11.4
Rsa1.0_00201.1.g8421.t2	gb|AFD01310.1| auxin response factor 11 [Brassica rapa subsp. pekinensis]	359	584	1.00E-109	162.7	55.2	56.5	auxin response factor 11	gbpln	Brassica rapa	AT2G46530.1 | Symbols: ARF11 | auxin response factor 11 | chr2:19104993-19108029 FORWARD LENGTH=601	359	601	1.00E-104	167.4	53.2	55.4
Rsa1.0_00201.1.g8422.t1	gb|EOA29267.1| hypothetical protein CARUB_v10025541mg [Capsella rubella]	122	174	1.00E-30	142.6	73.8	82.0	hypothetical protein CARUB_v10025541mg	gbpln	Capsella rubella	AT2G46535.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF688 (InterPro:IPR007789); BEST Arabidopsis thaliana protein match is: Protein of unknown function (DUF688) (TAIR:AT3G61840.1); Has 48 Blast hits to 48 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19109698-19110320 FORWARD LENGTH=175	122	175	1.00E-29	143.4	71.3	77.9
Rsa1.0_00201.1.g8423.t1	ref|NP_566079.1| uncharacterized protein [Arabidopsis thaliana] gi|15215610|gb|AAK91350.1| F11C10.23/F11C10.23 [Arabidopsis thaliana] gi|20197774|gb|AAD20165.2| expressed protein [Arabidopsis thaliana] gi|20334882|gb|AAM16197.1| At2g46540/F11C10.23 [Arabidopsis thaliana] gi|21554416|gb|AAM63521.1| unknown [Arabidopsis thaliana] gi|330255624|gb|AEC10718.1| uncharacterized protein AT2G46540 [Arabidopsis thaliana]	65	65	5.00E-27	100.0	96.9	98.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G46540.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 16 growth stages; Has 42 Blast hits to 42 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19110687-19111681 REVERSE LENGTH=65	65	65	7.00E-30	100.0	96.9	98.5
Rsa1.0_00201.1.g8424.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00201.1.g8425.t1	gb|AAM98127.1| expressed protein [Arabidopsis thaliana] gi|25083763|gb|AAN72116.1| expressed protein [Arabidopsis thaliana]	379	397	1.00E-144	104.7	76.5	82.6	expressed protein	gbpln	Arabidopsis thaliana	AT2G46550.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G01240.3); Has 72 Blast hits to 68 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 71; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19112264-19113457 REVERSE LENGTH=397	379	397	2.33E-156	104.7	76.5	82.3
Rsa1.0_00201.1.g8426.t1	ref|NP_182179.3| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] gi|330255627|gb|AEC10721.1| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	2445	2513	0	102.8	82.2	89.0	transducin family protein / WD-40 repeat family protein	gbpln	Arabidopsis thaliana	AT2G46560.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr2:19115570-19125856 REVERSE LENGTH=2513	2445	2513	0	102.8	82.2	89.0
Rsa1.0_00201.1.g8427.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00202.1.g8428.t1	ref|NP_189304.2| protein kinase family protein [Arabidopsis thaliana] gi|332643680|gb|AEE77201.1| protein kinase family protein [Arabidopsis thaliana]	375	380	1.00E-176	101.3	83.7	90.4	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G26700.1 | Symbols: | Protein kinase superfamily protein | chr3:9810669-9812356 FORWARD LENGTH=380	375	380	1.00E-179	101.3	83.7	90.4
Rsa1.0_00202.1.g8429.t1	ref|XP_002875334.1| hypothetical protein ARALYDRAFT_484443 [Arabidopsis lyrata subsp. lyrata] gi|297321172|gb|EFH51593.1| hypothetical protein ARALYDRAFT_484443 [Arabidopsis lyrata subsp. lyrata]	267	267	1.00E-135	100.0	91.4	94.0	hypothetical protein ARALYDRAFT_484443	gbpln	Arabidopsis lyrata	AT3G26710.1 | Symbols: CCB1 | cofactor assembly of complex C | chr3:9813550-9814606 FORWARD LENGTH=267	267	267	1.00E-136	100.0	90.3	94.4
Rsa1.0_00202.1.g8430.t1	ref|NP_189307.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|11994306|dbj|BAB01736.1| unnamed protein product [Arabidopsis thaliana] gi|18377743|gb|AAL67021.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|27754738|gb|AAO22812.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|332643684|gb|AEE77205.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	759	772	0	101.7	79.2	84.6	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G26730.1 | Symbols: | RING/U-box superfamily protein | chr3:9823770-9827270 FORWARD LENGTH=772	759	772	0	101.7	79.2	84.6

Rsa1.0_00202.1.g8431.t1	gb|ABV89628.1| light regulated protein-like protein [Brassica rapa]	142	138	7.00E-52	97.2	84.5	88.0	light regulated protein-like protein	gbpln	Brassica rapa	AT3G26740.1 | Symbols: CCL | CCR-like | chr3:9827868-9828461 FORWARD LENGTH=141	142	141	1.00E-40	99.3	68.3	76.8
Rsa1.0_00202.1.g8432.t1	ref|XP_002875343.1| auxin signaling F-box 2 [Arabidopsis lyrata subsp. lyrata] gi|297321181|gb|EFH51602.1| auxin signaling F-box 2 [Arabidopsis lyrata subsp. lyrata]	575	575	0	100.0	92.2	97.6	auxin signaling F-box 2	gbpln	Arabidopsis lyrata	AT3G26810.1 | Symbols: AFB2 | auxin signaling F-box 2 | chr3:9868342-9870464 FORWARD LENGTH=575	575	575	0	100.0	92.0	97.4
Rsa1.0_00202.1.g8433.t1	ref|XP_002512872.1| translocon-associated protein, beta subunit precursor, putative [Ricinus communis] gi|223547883|gb|EEF49375.1| translocon-associated protein, beta subunit precursor, putative [Ricinus communis]	237	208	2.00E-55	87.8	43.9	59.5	translocon-associated protein, beta subunit precursor, putative	gbpln	Ricinus communis	AT5G14030.4 | Symbols: | translocon-associated protein beta (TRAPB) family protein | chr5:4526878-4528253 FORWARD LENGTH=195	237	195	6.00E-54	82.3	44.3	59.5
Rsa1.0_00202.1.g8434.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00202.1.g8435.t1	ref|NP_566801.1| acyltransferase-like protein [Arabidopsis thaliana] gi|75335577|sp|Q9LW26.1|Y3684_ARATH RecName: Full=Acyltransferase-like protein At3g26840, chloroplastic; Flags: Precursor gi|13430466|gb|AAK25855.1|AF360145_1 unknown protein [Arabidopsis thaliana] gi|9279674|dbj|BAB01231.1| unnamed protein product [Arabidopsis thaliana] gi|15810663|gb|AAL07256.1| unknown protein [Arabidopsis thaliana] gi|332643700|gb|AEE77221.1| acyltransferase-like protein [Arabidopsis thaliana]	671	701	0	104.5	78.1	87.0	acyltransferase-like protein	gbpln	Arabidopsis thaliana	AT3G26840.1 | Symbols: | Esterase/lipase/thioesterase family protein | chr3:9892808-9896154 FORWARD LENGTH=701	671	701	0	104.5	78.1	87.0
Rsa1.0_00202.1.g8436.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00202.1.g8437.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00202.1.g8438.t4	ref|XP_002875348.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321186|gb|EFH51607.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	720	695	0	96.5	71.9	82.9	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G26840.1 | Symbols: | Esterase/lipase/thioesterase family protein | chr3:9892808-9896154 FORWARD LENGTH=701	720	701	0	97.4	71.9	82.5
Rsa1.0_00202.1.g8439.t1	ref|XP_002875348.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321186|gb|EFH51607.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	659	695	0	105.5	73.4	84.7	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G26840.1 | Symbols: | Esterase/lipase/thioesterase family protein | chr3:9892808-9896154 FORWARD LENGTH=701	659	701	0	106.4	73.6	84.1
Rsa1.0_00202.1.g8440.t2	ref|XP_002875348.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321186|gb|EFH51607.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	538	695	0	129.2	73.2	84.0	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G26840.1 | Symbols: | Esterase/lipase/thioesterase family protein | chr3:9892808-9896154 FORWARD LENGTH=701	538	701	0	130.3	73.2	83.6
Rsa1.0_00202.1.g8441.t2	ref|XP_002877001.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297322839|gb|EFH53260.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	785	616	0	78.5	53.0	56.9	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis lyrata	AT3G26910.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr3:9915338-9918511 REVERSE LENGTH=608	785	608	0	77.5	51.7	56.3
Rsa1.0_00202.1.g8442.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00202.1.g8443.t1	ref|XP_002877005.1| dsRNA-binding protein 3 [Arabidopsis lyrata subsp. lyrata] gi|297322843|gb|EFH53264.1| dsRNA-binding protein 3 [Arabidopsis lyrata subsp. lyrata]	378	356	1.00E-132	94.2	69.8	75.4	dsRNA-binding protein 3	gbpln	Arabidopsis lyrata	AT3G26932.2 | Symbols: DRB3 | dsRNA-binding protein 3 | chr3:9930460-9931714 REVERSE LENGTH=359	378	359	1.00E-130	95.0	67.5	73.0
Rsa1.0_00202.1.g8444.t2	gb|EOA24039.1| hypothetical protein CARUB_v10017257mg [Capsella rubella]	445	443	0	99.6	93.0	96.4	hypothetical protein CARUB_v10017257mg	gbpln	Capsella rubella	AT3G26935.1 | Symbols: | DHHC-type zinc finger family protein | chr3:9933001-9935218 REVERSE LENGTH=443	445	443	0	99.6	93.3	96.2
Rsa1.0_00202.1.g8445.t1	dbj|BAC67214.1| protein kinase CDG1 [Arabidopsis thaliana]	420	431	1.00E-103	102.6	49.3	61.0	protein kinase CDG1	gbpln	Arabidopsis thaliana	AT3G26940.1 | Symbols: CDG1 | Protein kinase superfamily protein | chr3:9936707-9938936 REVERSE LENGTH=432	420	432	1.00E-106	102.9	49.3	61.0
Rsa1.0_00202.1.g8446.t1	ref|XP_002890104.1| F9L1.39 [Arabidopsis lyrata subsp. lyrata] gi|297335946|gb|EFH66363.1| F9L1.39 [Arabidopsis lyrata subsp. lyrata]	174	249	4.00E-49	143.1	56.3	70.7	F9L1.39	gbpln	Arabidopsis lyrata	AT1G15430.2 | Symbols: | Protein of unknown function (DUF1644) | chr1:5305011-5305790 FORWARD LENGTH=259	174	259	1.00E-49	148.9	55.2	70.7

Rsa1.0_00202.1.g8447.t2	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	254	1311	4.00E-17	516.1	33.9	52.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	254	170	2.00E-14	66.9	18.9	26.0
Rsa1.0_00203.1.g8448.t1	ref|NP_001189903.1| phospholipase/carboxylesterase family protein [Arabidopsis thaliana] gi|332642188|gb|AEE75709.1| phospholipase/carboxylesterase family protein [Arabidopsis thaliana]	248	274	1.00E-129	110.5	93.5	95.2	phospholipase/carboxylesterase family protein	gbpln	Arabidopsis thaliana	AT3G15650.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:5306006-5307764 FORWARD LENGTH=274	248	274	1.00E-132	110.5	93.5	95.2
Rsa1.0_00203.1.g8449.t1	gb|EOA31587.1| hypothetical protein CARUB_v10014783mg [Capsella rubella]	166	169	8.00E-77	101.8	83.7	91.6	hypothetical protein CARUB_v10014783mg	gbpln	Capsella rubella	AT3G15660.2 | Symbols: ATGRX4, GRX4 | glutaredoxin 4 | chr3:5308134-5309383 REVERSE LENGTH=169	166	169	7.00E-78	101.8	82.5	91.0
Rsa1.0_00203.1.g8450.t1	dbj|BAB88877.1| late embryogenesis-abundant protein [Brassica napus]	229	226	1.00E-102	98.7	92.1	94.3	late embryogenesis-abundant protein	gbpln	Brassica napus	AT3G15670.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr3:5310141-5310901 REVERSE LENGTH=225	229	225	1.00E-88	98.3	84.7	90.0
Rsa1.0_00203.1.g8451.t1	ref|NP_188189.1| Ran BP2/NZF zinc finger-like protein [Arabidopsis thaliana] gi|11994340|dbj|BAB02299.1| zinc finger protein-like; Ser/Thr protein kinase-like protein [Arabidopsis thaliana] gi|89274153|gb|ABD65597.1| At3g15680 [Arabidopsis thaliana] gi|332642192|gb|AEE75713.1| Ran BP2/NZF zinc finger-like protein [Arabidopsis thaliana]	164	164	3.00E-75	100.0	91.5	94.5	Ran BP2/NZF zinc finger-like protein	gbpln	Arabidopsis thaliana	AT3G15680.1 | Symbols: | Ran BP2/NZF zinc finger-like superfamily protein | chr3:5315437-5316048 FORWARD LENGTH=164	164	164	9.00E-78	100.0	91.5	94.5
Rsa1.0_00203.1.g8452.t1	ref|XP_002882958.1| hypothetical protein ARALYDRAFT_479023 [Arabidopsis lyrata subsp. lyrata] gi|297328798|gb|EFH59217.1| hypothetical protein ARALYDRAFT_479023 [Arabidopsis lyrata subsp. lyrata]	293	263	1.00E-111	89.8	72.4	80.2	hypothetical protein ARALYDRAFT_479023	gbpln	Arabidopsis lyrata	AT3G15690.2 | Symbols: | Single hybrid motif superfamily protein | chr3:5317108-5319435 FORWARD LENGTH=263	293	263	1.00E-112	89.8	71.7	80.5
Rsa1.0_00203.1.g8453.t1	gb|EOA33124.1| hypothetical protein CARUB_v10016462mg [Capsella rubella]	66	451	9.00E-11	683.3	54.5	59.1	hypothetical protein CARUB_v10016462mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00203.1.g8454.t1	gb|EOA33124.1| hypothetical protein CARUB_v10016462mg [Capsella rubella]	398	451	0	113.3	83.7	87.9	hypothetical protein CARUB_v10016462mg	gbpln	Capsella rubella	AT3G15700.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:5321136-5322376 REVERSE LENGTH=375	398	375	0	94.2	83.7	87.7
Rsa1.0_00203.1.g8455.t1	ref|XP_002885105.1| hypothetical protein ARALYDRAFT_479026 [Arabidopsis lyrata subsp. lyrata] gi|297330945|gb|EFH61364.1| hypothetical protein ARALYDRAFT_479026 [Arabidopsis lyrata subsp. lyrata]	180	180	3.00E-87	100.0	88.3	95.0	hypothetical protein ARALYDRAFT_479026	gbpln	Arabidopsis lyrata	AT1G52600.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr1:19590612-19592486 FORWARD LENGTH=180	180	180	1.00E-89	100.0	89.4	93.9
Rsa1.0_00203.1.g8456.t1	sp|P55939.2|PLDA2_BRAOC RecName: Full=Phospholipase D alpha 2; Short=PLD 2; AltName: Full=Choline phosphatase 2; AltName: Full=Phosphatidylcholine-hydrolyzing phospholipase D 2; Flags: Precursor gi|3639087|gb|AAC78486.1| phospholipase D2 [Brassica oleracea var. capitata] gi|3924621|gb|AAC79125.1| phospholipase D [Brassica oleracea var. capitata] gi|4324971|gb|AAD17209.1| phospholipase D2 [Brassica oleracea var. capitata]	811	812	0	100.1	97.4	99.5	RecName: Full=Phospholipase D alpha 2; Short=PLD 2; AltName: Full=Choline phosphatase 2; AltName: Full=Phosphatidylcholine-hydrolyzing phospholipase D 2; Flags: Precursor gi|3639087|gb|AAC78486.1| phospholipase D2	gbpln	Brassica oleracea	AT3G15730.1 | Symbols: PLDALPHA1, PLD | phospholipase D alpha 1 | chr3:5330835-5333474 FORWARD LENGTH=810	811	810	0	99.9	90.9	96.9
Rsa1.0_00203.1.g8457.t1	ref|XP_002882960.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328800|gb|EFH59219.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	146	135	6.00E-47	92.5	71.2	77.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G15760.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52565.1); Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5337734-5338219 FORWARD LENGTH=135	146	135	6.00E-43	92.5	67.8	74.0

Rsa1.0_00203.1.g8458.t1	ref|NP_188199.1| uncharacterized protein [Arabidopsis thaliana] gi|11994350|dbj|BAB02309.1| unnamed protein product [Arabidopsis thaliana] gi|17065466|gb|AAL32887.1| Unknown protein [Arabidopsis thaliana] gi|20148569|gb|AAM10175.1| unknown protein [Arabidopsis thaliana] gi|332642205|gb|AEE75726.1| uncharacterized protein AT3G15780 [Arabidopsis thaliana]	129	117	2.00E-24	90.7	69.8	74.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52550.1); Has 20 Blast hits to 20 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5341434-5342351 FORWARD LENGTH=117	129	117	4.00E-27	90.7	69.8	74.4
Rsa1.0_00203.1.g8459.t1	ref|XP_002882963.1| hypothetical protein ARALYDRAFT_897878 [Arabidopsis lyrata subsp. lyrata] gi|297328803|gb|EFH59222.1| hypothetical protein ARALYDRAFT_897878 [Arabidopsis lyrata subsp. lyrata]	273	255	6.00E-92	93.4	72.2	79.5	hypothetical protein ARALYDRAFT_897878	gbpln	Arabidopsis lyrata	AT3G15790.1 | Symbols: MBD11, ATMBD11 | methyl-CPG-binding domain 11 | chr3:5343209-5344386 FORWARD LENGTH=254	273	254	2.00E-85	93.0	68.9	77.7
Rsa1.0_00203.1.g8460.t1	gb|EOA30744.1| hypothetical protein CARUB_v10013884mg [Capsella rubella]	394	397	0	100.8	81.0	86.5	hypothetical protein CARUB_v10013884mg	gbpln	Capsella rubella	AT3G15800.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr3:5345051-5346988 FORWARD LENGTH=399	394	399	0	101.3	77.9	82.0
Rsa1.0_00203.1.g8461.t1	ref|XP_002882965.1| hypothetical protein ARALYDRAFT_897881 [Arabidopsis lyrata subsp. lyrata] gi|297328805|gb|EFH59224.1| hypothetical protein ARALYDRAFT_897881 [Arabidopsis lyrata subsp. lyrata]	289	301	1.00E-118	104.2	75.8	84.1	hypothetical protein ARALYDRAFT_897881	gbpln	Arabidopsis lyrata	AT3G15820.1 | Symbols: ROD1 | phosphatidic acid phosphatase-related / PAP2-related | chr3:5351217-5353573 FORWARD LENGTH=301	289	301	1.00E-118	104.2	74.0	83.0
Rsa1.0_00203.1.g8462.t1	ref|NP_188207.1| uncharacterized protein [Arabidopsis thaliana] gi|52354305|gb|AAU44473.1| hypothetical protein AT3G15860 [Arabidopsis thaliana] gi|55740627|gb|AAV63906.1| hypothetical protein At3g15860 [Arabidopsis thaliana] gi|332642217|gb|AEE75738.1| uncharacterized protein AT3G15860 [Arabidopsis thaliana]	166	170	3.00E-84	102.4	88.0	94.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15860.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: pollen tube; CONTAINS InterPro DOMAIN/s: Plant self-incompatibility S1 (InterPro:IPR010264); BEST Arabidopsis thaliana protein match is: Plant self-incompatibility protein S1 family (TAIR:AT5G26090.1); Has 19 Blast hits to 16 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5361207-5361719 REVERSE LENGTH=170	166	170	1.00E-86	102.4	88.0	94.0
Rsa1.0_00203.1.g8463.t1	ref|NP_188048.1| pectinesterase 3 [Arabidopsis thaliana] gi|229891485|sp|O49006.2|PME3_ARATH RecName: Full=Pectinesterase/pectinesterase inhibitor 3; Includes: RecName: Full=Pectinesterase inhibitor 3; AltName: Full=Pectin methylesterase inhibitor 3; Includes: RecName: Full=Pectinesterase 3; Short=PE 3; AltName: Full=Pectin methylesterase 27; Short=AtPME27; AltName: Full=Pectin methylesterase 3; Flags: Precursor gi|9279579|dbj|BAB01037.1| pectinesterase [Arabidopsis thaliana] gi|14335010|gb|AAK59769.1| AT3g14310/MLN21_9 [Arabidopsis thaliana] gi|15529256|gb|AAK97722.1| AT3g14310/MLN21_9 [Arabidopsis thaliana] gi|23506059|gb|AAN28889.1| At3g14310/MLN21_9 [Arabidopsis thaliana] gi|332641979|gb|AEE75500.1| pectinesterase 3 [Arabidopsis thaliana]	592	592	0	100.0	89.0	94.1	pectinesterase 3	gbpln	Arabidopsis thaliana	AT3G14310.1 | Symbols: ATPME3, PME3 | pectin methylesterase 3 | chr3:4772214-4775095 REVERSE LENGTH=592	592	592	0	100.0	89.0	94.1
Rsa1.0_00203.1.g8464.t1	ref|NP_851003.2| Topless-related protein 4 [Arabidopsis thaliana] gi|298352695|sp|Q27GK7.2|TPR4_ARATH RecName: Full=Topless-related protein 4; AltName: Full=WUS-interacting protein 2 gi|332642219|gb|AEE75740.1| Topless-related protein 4 [Arabidopsis thaliana]	1124	1135	0	101.0	93.1	96.4	Topless-related protein 4	gbpln	Arabidopsis thaliana	AT3G15880.1 | Symbols: WSIP2, TPR4 | WUS-interacting protein 2 | chr3:5364792-5371869 REVERSE LENGTH=1135	1124	1135	0	101.0	93.1	96.4
Rsa1.0_00203.1.g8465.t1	ref|XP_002882968.1| hypothetical protein ARALYDRAFT_479045 [Arabidopsis lyrata subsp. lyrata] gi|297328808|gb|EFH59227.1| hypothetical protein ARALYDRAFT_479045 [Arabidopsis lyrata subsp. lyrata]	345	359	1.00E-153	104.1	78.3	88.4	hypothetical protein ARALYDRAFT_479045	gbpln	Arabidopsis lyrata	AT3G15890.1 | Symbols: | Protein kinase superfamily protein | chr3:5374389-5376114 FORWARD LENGTH=361	345	361	1.00E-153	104.6	76.5	87.2

Rsa1.0_00203.1_g8466.t1	ref|XP_002885114.1| hypothetical protein ARALYDRAFT_479046 [Arabidopsis lyrata subsp. lyrata] gi|297330954|gb|EFH61373.1| hypothetical protein ARALYDRAFT_479046 [Arabidopsis lyrata subsp. lyrata]	140	140	2.00E−44	100.0	72.9	80.7	hypothetical protein ARALYDRAFT_479046	gbpln	Arabidopsis lyrata	AT3G15900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 26 Blast hits to 26 proteins in 10 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 26; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:5376356−5376972 REVERSE LENGTH=141	140	141	9.00E−47	100.7	65.7	72.9
Rsa1.0_00203.1_g8467.t1	ref|XP_002885115.1| phox domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330955|gb|EFH61374.1| phox domain−containing protein [Arabidopsis lyrata subsp. lyrata]	700	757	0	108.1	81.7	89.1	phox domain−containing protein	gbpln	Arabidopsis lyrata	AT3G15920.1 | Symbols: | Phox (PX) domain−containing protein | chr3:5383768−5386955 REVERSE LENGTH=755	700	755	0	107.9	80.6	88.6
Rsa1.0_00203.1_g8468.t1	dbj|BAB02877.1| unnamed protein product [Arabidopsis thaliana]	649	695	0	107.1	81.2	88.6	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G15930.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:5387444−5389690 FORWARD LENGTH=687	649	687	0	105.9	81.2	88.6
Rsa1.0_00203.1_g8469.t1	dbj|BAB02797.1| unnamed protein product [Arabidopsis thaliana]	280	345	2.00E−45	123.2	38.9	50.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G13280.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:4295327−4297000 REVERSE LENGTH=383	280	383	1.00E−28	136.8	32.9	47.1
Rsa1.0_00203.1_g8470.t1	ref|NP_188216.2| DNA topoisomerase−like protein [Arabidopsis thaliana] gi|9294600|dbj|BAB02881.1| unnamed protein product [Arabidopsis thaliana] gi|21539511|gb|AAM53308.1| unknown protein [Arabidopsis thaliana] gi|24899759|gb|AAN65094.1| unknown protein [Arabidopsis thaliana] gi|332642230|gb|AEE75751.1| DNA topoisomerase−like protein [Arabidopsis thaliana]	744	772	0	103.8	76.7	85.5	DNA topoisomerase−like protein	gbpln	Arabidopsis thaliana	AT3G15950.1 | Symbols: NAI2 | DNA topoisomerase−related | chr3:5397783−5402610 REVERSE LENGTH=772	744	772	0	103.8	76.7	85.5
Rsa1.0_00203.1_g8471.t1	ref|NP_188217.4| mismatched DNA binding / ATP binding protein [Arabidopsis thaliana] gi|332642232|gb|AEE75753.1| mismatched DNA binding / ATP binding protein [Arabidopsis thaliana]	492	490	2.00E−65	99.6	28.5	40.0	mismatched DNA binding / ATP binding protein	gbpln	Arabidopsis thaliana	AT3G15960.1 | Symbols: | mismatched DNA binding;ATP binding | chr3:5404000−5406461 REVERSE LENGTH=490	492	490	6.00E−68	99.6	28.5	40.0
Rsa1.0_00203.1_g8472.t1	gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]	226	543	2.00E−41	240.3	38.1	58.4	hypothetical protein CARUB_v10015730mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:19725483−19728007 FORWARD LENGTH=566	226	566	2.00E−41	250.4	39.4	59.3
Rsa1.0_00204.1_g8473.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838−20266 [Arabidopsis thaliana]	196	1142	2.00E−31	582.7	41.8	58.7	reverse transcriptase, putative; 16838−20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H−like superfamily protein | chr2:14484959−14485837 FORWARD LENGTH=292	196	292	5.00E−12	149.0	29.6	49.5
Rsa1.0_00204.1_g8474.t1	ref|XP_002893408.1| hypothetical protein ARALYDRAFT_472786 [Arabidopsis lyrata subsp. lyrata] gi|297339250|gb|EFH69667.1| hypothetical protein ARALYDRAFT_472786 [Arabidopsis lyrata subsp. lyrata]	356	351	1.00E−180	98.6	86.2	92.4	hypothetical protein ARALYDRAFT_472786	gbpln	Arabidopsis lyrata	AT1G26320.1 | Symbols: | Zinc−binding dehydrogenase family protein | chr1:9105240−9107029 FORWARD LENGTH=351	356	351	0	98.6	86.0	91.9
Rsa1.0_00204.1_g8475.t1	ref|XP_002893407.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339249|gb|EFH69666.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1275	1194	0	93.6	67.4	76.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G26330.1 | Symbols: | DNA binding | chr1:9107625−9113520 FORWARD LENGTH=1189	1275	1189	0	93.3	65.3	74.8
Rsa1.0_00204.1_g8476.t1	gb|EOA37106.1| hypothetical protein CARUB_v10010310mg [Capsella rubella]	188	205	3.00E−62	109.0	60.6	64.4	hypothetical protein CARUB_v10010310mg	gbpln	Capsella rubella	AT1G26340.1 | Symbols: B5 #6, ATCB5−A, CB5−A | cytochrome B5 isoform A | chr1:9113992−9114755 FORWARD LENGTH=135	188	135	2.00E−62	71.8	58.5	63.8
Rsa1.0_00204.1_g8477.t1	gb|ABD65606.1| hypothetical protein 23.t00002 [Brassica oleracea]	367	433	3.00E−73	118.0	48.5	62.9	hypothetical protein 23.t00002	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00204.1_g8478.t1	gb|EOA39748.1| hypothetical protein CARUB_v10008395mg [Capsella rubella]	682	717	0	105.1	80.5	89.3	hypothetical protein CARUB_v10008395mg	gbpln	Capsella rubella	AT1G26370.1 | Symbols: | RNA helicase family protein | chr1:9122030−9125368 REVERSE LENGTH=717	682	717	0	105.1	80.2	89.3
Rsa1.0_00204.1_g8479.t1	ref|XP_002890663.1| FAD−binding domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297336505|gb|EFH66922.1| FAD−binding domain−containing protein [Arabidopsis lyrata subsp. lyrata]	529	530	0	100.2	86.8	94.1	FAD−binding domain−containing protein	gbpln	Arabidopsis lyrata	AT1G26390.1 | Symbols: | FAD−binding Berberine family protein | chr1:9130164−9131756 REVERSE LENGTH=530	529	530	0	100.2	83.0	91.1

Rsa1.0_00204.1.g8480.t1	ref|NP_173966.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana] gi|9797756|gb|AAF98574.1|AC013427_17 Contains weak similarity to berberine bridge enzyme (bbe1) from Berberis stolonifera gb|AF049347 and contains a FAD binding PF|01565 domain [Arabidopsis thaliana] gi|332192567|gb|AEE30688.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana]	527	529	0	100.4	83.1	90.7	FAD-binding and BBE domain-containing protein	gbpln	Arabidopsis thaliana	AT1G26420.1 | Symbols: | FAD-binding Berberine family protein | chr1:9141715-9143304 REVERSE LENGTH=529	527	529	0	100.4	83.1	90.7
Rsa1.0_00204.1.g8481.t1	ref|XP_002890658.1| ATUPS5 [Arabidopsis lyrata subsp. lyrata] gi|297336500|gb|EFH66917.1| ATUPS5 [Arabidopsis lyrata subsp. lyrata]	410	410	0	100.0	87.1	93.7	ATUPS5	gbpln	Arabidopsis lyrata	AT1G26440.2 | Symbols: ATUPS5, UPS5 | ureide permease 5 | chr1:9144109-9145673 REVERSE LENGTH=413	410	413	0	100.7	86.6	93.4
Rsa1.0_00204.1.g8482.t1	dbj|BAB01155.1| unnamed protein product [Arabidopsis thaliana] gi|49823524|gb|AAT68745.1| hypothetical protein At3g17200 [Arabidopsis thaliana] gi|60547763|gb|AAX23845.1| hypothetical protein At3g17200 [Arabidopsis thaliana]	308	310	8.00E-58	100.6	37.0	51.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	308	746	3.00E-36	242.2	26.9	36.4
Rsa1.0_00204.1.g8483.t1	ref|XP_002893403.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297339245|gb|EFH69662.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	623	630	0	101.1	83.8	92.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G26460.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:9151816-9154407 FORWARD LENGTH=630	623	630	0	101.1	83.3	92.5
Rsa1.0_00204.1.g8484.t1	gb|EOA36298.1| hypothetical protein CARUB_v10010577mg, partial [Capsella rubella]	146	146	5.00E-48	100.0	84.2	87.0	hypothetical protein CARUB_v10010577mg, partial	gbpln	Capsella rubella	AT1G26470.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: regulation of transcription; LOCATED IN: nucleus, H4/H2A histone acetyltransferase complex; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: CT20 (InterPro:IPR012423); Has 60 Blast hits to 60 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 26; Fungi - 2; Plants - 30; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:9155134-9156036 FORWARD LENGTH=133	146	133	7.00E-45	91.1	83.6	87.0
Rsa1.0_00204.1.g8485.t1	gb|EOA36455.1| hypothetical protein CARUB_v10011021mg [Capsella rubella]	267	268	1.00E-147	100.4	94.4	98.9	hypothetical protein CARUB_v10011021mg	gbpln	Capsella rubella	AT1G26480.1 | Symbols: GRF12, GF14 IOTA | general regulatory factor 12 | chr1:9156573-9157845 REVERSE LENGTH=268	267	268	1.00E-149	100.4	94.0	98.5
Rsa1.0_00204.1.g8486.t1	gb|EOA39416.1| hypothetical protein CARUB_v10012523mg [Capsella rubella]	528	499	0	94.5	79.9	87.3	hypothetical protein CARUB_v10012523mg	gbpln	Capsella rubella	AT1G26500.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:9158380-9159897 FORWARD LENGTH=505	528	505	0	95.6	78.0	84.8
Rsa1.0_00204.1.g8487.t1	ref|NP_173974.3| Cobalamin biosynthesis CobW-like protein [Arabidopsis thaliana] gi|63147374|gb|AAY34160.1| At1g26520 [Arabidopsis thaliana] gi|332192579|gb|AEE30700.1| Cobalamin biosynthesis CobW-like protein [Arabidopsis thaliana]	365	374	0	102.5	89.0	94.2	Cobalamin biosynthesis CobW-like protein	gbpln	Arabidopsis thaliana	AT1G26520.1 | Symbols: | Cobalamin biosynthesis CobW-like protein | chr1:9163448-9165594 REVERSE LENGTH=374	365	374	0	102.5	89.0	94.2
Rsa1.0_00204.1.g8488.t1	gb|ACJ86035.1| unknown [Medicago truncatula] gi|388515981|gb|AFK46052.1| unknown [Medicago truncatula]	127	144	1.00E-51	113.4	90.6	93.7	unknown	gbpln	Medicago truncatula	AT1G26550.1 | Symbols: | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | chr1:9171800-9172716 FORWARD LENGTH=142	127	142	7.00E-48	111.8	83.5	84.3
Rsa1.0_00204.1.g8489.t1	ref|NP_173978.1| beta glucosidase 40 [Arabidopsis thaliana] gi|75309954|sp|Q9FZE0.1|BGL40_ARATH RecName: Full=Beta-glucosidase 40; Short=AtBGLU40; Flags: Precursor gi|9797746|gb|AAF98564.1|AC013427_7 Strong similarity to beta-glucosidase (BGQ60) from Hordeum vulgare gb|L41869 and is a member of the Glycosyl hydrolase PF|00232 family. ESTs gb|AV561121, gb|AV565991 come from this gene [Arabidopsis thaliana] gi|15028209|gb|AAK76601.1| putative beta-glucosidase [Arabidopsis thaliana] gi|23296824|gb|AAN13179.1| putative beta-glucosidase [Arabidopsis thaliana] gi|332192583|gb|AEE30704.1| beta glucosidase 40 [Arabidopsis thaliana]	493	510	0	103.4	93.3	95.7	beta glucosidase 40	gbpln	Arabidopsis thaliana	AT1G26560.1 | Symbols: BGLU40 | beta glucosidase 40 | chr1:9178513-9181726 FORWARD LENGTH=510	493	510	0	103.4	93.3	95.7

Rsa1.0_00204.1.g8490.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00204.1.g8491.t1	ref|NP_173979.1| UDP-glucose dehydrogenase 1 [Arabidopsis thaliana] gi|9797743|gb|AAF98561.1|AC013427_4 Strong similarity to UDP-Glucose 6-Dehydrogenase from Glycine max gb|6136119 and is a member of the UDP-glucose/GDP-mannose dehydrogenase PF|00984 family. ESTs gb|AV566422, gb|AV555903 come from this gene [Arabidopsis thaliana] gi|17979522|gb|AAL50096.1| At1g26570/T1K7_6 [Arabidopsis thaliana] gi|23506003|gb|AAN28861.1| At1g26570/T1K7_6 [Arabidopsis thaliana] gi|332192584|gb|AEE30705.1| UDP-glucose dehydrogenase 1 [Arabidopsis thaliana]	479	481	0	100.4	91.2	96.5	UDP-glucose dehydrogenase 1	gbpln	Arabidopsis thaliana	AT1G26570.1 | Symbols: UGD1, ATUGD1 | UDP-glucose dehydrogenase 1 | chr1:9182801-9184246 FORWARD LENGTH=481	479	481	0	100.4	91.2	96.5
Rsa1.0_00204.1.g8492.t1	gb|EOA40241.1| hypothetical protein CARUB_v10008961mg [Capsella rubella] gi|482576055|gb|EOA40242.1| hypothetical protein CARUB_v10008961mg [Capsella rubella]	379	492	1.00E-134	129.8	68.3	78.4	hypothetical protein CARUB_v10008961mg	gbpln	Capsella rubella	AT1G26580.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: ELM2 domain-containing protein (TAIR:AT2G03470.1); Has 161 Blast hits to 161 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 4; Plants - 156; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:9185620-9187213 FORWARD LENGTH=493	379	493	1.00E-137	130.1	68.3	78.6
Rsa1.0_00204.1.g8493.t1	ref|NP_173981.1| C2H2-like zinc finger protein [Arabidopsis thaliana] gi|9797741|gb|AAF98559.1|AC013427_2 Contains similarity to C2H2 zinc finger protein (PEThy;ZPT4-2) from Petunia hybrida gb|AB000456 and contains three Zinc finger (C2H2 type) PF|00096 motifs [Arabidopsis thaliana] gi|225897970|dbj|BAH30317.1| hypothetical protein [Arabidopsis thaliana] gi|332192586|gb|AEE30707.1| C2H2-like zinc finger protein [Arabidopsis thaliana]	293	361	2.00E-36	123.2	47.1	57.0	C2H2-like zinc finger protein	gbpln	Arabidopsis thaliana	AT1G26590.1 | Symbols: | C2H2-like zinc finger protein | chr1:9189624-9190709 FORWARD LENGTH=361	293	361	6.00E-39	123.2	47.1	57.0
Rsa1.0_00204.1.g8494.t1	ref|NP_564251.1| protein CLAVATA3/ESR-related 9 [Arabidopsis thaliana] gi|313471278|sp|Q9FZE4.2|CLE9_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 9; Contains: RecName: Full=CLE9p; Flags: Precursor gi|332192587|gb|AEE30708.1| protein CLAVATA3/ESR-related 9 [Arabidopsis thaliana]	114	120	6.00E-34	105.3	69.3	79.8	protein CLAVATA3/ESR-related 9	gbpln	Arabidopsis thaliana	AT1G26600.1 | Symbols: CLE9 | CLAVATA3/ESR-RELATED 9 | chr1:9191684-9192046 FORWARD LENGTH=120	114	120	9.00E-37	105.3	69.3	79.8
Rsa1.0_00204.1.g8495.t1	dbj|BAF73724.1| pentatricopeptide repeat protein [Raphanus sativus]	143	687	4.00E-42	480.4	63.6	72.0	pentatricopeptide repeat protein	gbpln	Raphanus sativus	AT1G63630.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:23587298-23588220 FORWARD LENGTH=257	143	257	9.00E-26	179.7	37.8	52.4
Rsa1.0_00204.1.g8496.t1	gb|ADK92391.1| C2H2 zinc finger transcription factor [Brassica rapa subsp. chinensis]	457	452	0	98.9	87.3	91.5	C2H2 zinc finger transcription factor	gbpln	Brassica rapa	AT1G26610.1 | Symbols: | C2H2-like zinc finger protein | chr1:9193735-9195102 FORWARD LENGTH=455	457	455	1.00E-178	99.6	78.1	84.7
Rsa1.0_00204.1.g8497.t1	ref|XP_002890651.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336493|gb|EFH66910.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	808	861	0	106.6	74.0	81.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G26620.1 | Symbols: | Plant protein of unknown function (DUF863) | chr1:9195838-9198719 REVERSE LENGTH=867	808	867	0	107.3	71.5	80.6
Rsa1.0_00204.1.g8498.t1	gb|AAR91929.1| eukaryotic translation initiation factor-5A [Brassica napus]	159	159	2.00E-82	100.0	95.6	96.9	eukaryotic translation initiation factor-5A	gbpln	Brassica napus	AT1G26630.1 | Symbols: FBR12, ATELF5A-2, ELF5A-2 | Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) protein | chr1:9205968-9207098 FORWARD LENGTH=159	159	159	7.00E-79	100.0	87.4	94.3
Rsa1.0_00204.1.g8499.t1	ref|XP_002890650.1| aspartate/glutamate/uridylate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336492|gb|EFH66909.1| aspartate/glutamate/uridylate kinase family protein [Arabidopsis lyrata subsp. lyrata]	333	330	1.00E-171	99.1	91.3	94.3	aspartate/glutamate/uridylate kinase family protein	gbpln	Arabidopsis lyrata	AT1G26640.1 | Symbols: | Amino acid kinase family protein | chr1:9207620-9209766 REVERSE LENGTH=332	333	332	1.00E-171	99.7	89.8	94.6

<table>
<tr><td>Rsa1.0_00204.1.g8500.t1</td><td>ref|XP_002893390.1| hypothetical protein ARALYDRAFT_472743 [Arabidopsis lyrata subsp. lyrata] gi|297339232|gb|EFH69649.1| hypothetical protein ARALYDRAFT_472743 [Arabidopsis lyrata subsp. lyrata]</td><td>339</td><td>335</td><td>1.00E-166</td><td>98.8</td><td>84.7</td><td>92.9</td><td>hypothetical protein ARALYDRAFT_472743</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G26650.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G69430.1); Has 205 Blast hits to 204 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 205; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:9210335-9211342 FORWARD LENGTH=335</td><td>339</td><td>335</td><td>1.00E-168</td><td>98.8</td><td>84.7</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00204.1.g8501.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00204.1.g8502.t1</td><td>gb|AAB88009.1| heat shock cognate protein HSC70 [Brassica napus]</td><td>648</td><td>645</td><td>0</td><td>99.5</td><td>95.5</td><td>97.7</td><td>heat shock cognate protein HSC70</td><td>gbpln</td><td>Brassica napus</td><td>AT5G02500.1 | Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 | heat shock cognate protein 70-1 | chr5:554055-556334 REVERSE LENGTH=651</td><td>648</td><td>651</td><td>0</td><td>100.5</td><td>96.0</td><td>98.3</td></tr>
<tr><td>Rsa1.0_00204.1.g8503.t1</td><td>gb|EOA37780.1| hypothetical protein CARUB_v10012647mg [Capsella rubella]</td><td>178</td><td>757</td><td>6.00E-58</td><td>425.3</td><td>64.6</td><td>75.3</td><td>hypothetical protein CARUB_v10012647mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G17690.1 | Symbols: NOF1 | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleus; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Digestive organ expansion factor, predicted (InterPro:IPR010678); Has 25006 Blast hits to 13379 proteins in 904 species: Archae - 102; Bacteria - 5571; Metazoa - 7448; Fungi - 3168; Plants - 1056; Viruses - 466; Other Eukaryotes - 7195 (source: NCBI BLink). | chr1:6082878-6088157 REVERSE LENGTH=754</td><td>178</td><td>754</td><td>8.00E-58</td><td>423.6</td><td>61.2</td><td>74.7</td></tr>
<tr><td>Rsa1.0_00205.1.g8504.t1</td><td>ref|NP_194322.2| uncharacterized protein [Arabidopsis thaliana] gi|23296353|gb|AAN13050.1| unknown protein [Arabidopsis thaliana] gi|332659733|gb|AEE85133.1| uncharacterized protein AT4G25920 [Arabidopsis thaliana]</td><td>570</td><td>390</td><td>6.00E-68</td><td>68.4</td><td>24.7</td><td>31.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25920.1 | Symbols: | Protein of unknown function (DUF295) | chr4:13165475-13166841 FORWARD LENGTH=390</td><td>570</td><td>390</td><td>2.00E-70</td><td>68.4</td><td>24.7</td><td>31.4</td></tr>
<tr><td>Rsa1.0_00205.1.g8505.t1</td><td>ref|NP_194322.2| uncharacterized protein [Arabidopsis thaliana] gi|23296353|gb|AAN13050.1| unknown protein [Arabidopsis thaliana] gi|332659733|gb|AEE85133.1| uncharacterized protein AT4G25920 [Arabidopsis thaliana]</td><td>376</td><td>390</td><td>1.00E-119</td><td>103.7</td><td>61.2</td><td>75.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25920.1 | Symbols: | Protein of unknown function (DUF295) | chr4:13165475-13166841 FORWARD LENGTH=390</td><td>376</td><td>390</td><td>1.00E-122</td><td>103.7</td><td>61.2</td><td>75.5</td></tr>
<tr><td>Rsa1.0_00205.1.g8506.t1</td><td>ref|NP_194330.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana] gi|4538929|emb|CAB39665.1| putative nucleic acid binding protein [Arabidopsis thaliana] gi|7269451|emb|CAB79455.1| putative nucleic acid binding protein [Arabidopsis thaliana] gi|15810499|gb|AAL07137.1| putative nucleic acid binding protein [Arabidopsis thaliana] gi|20466386|gb|AAM20510.1| putative nucleic acid binding protein [Arabidopsis thaliana] gi|21280915|gb|AAM45112.1| putative nucleic acid binding protein [Arabidopsis thaliana] gi|332659742|gb|AEE85142.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana]</td><td>480</td><td>495</td><td>0</td><td>103.1</td><td>79.4</td><td>87.5</td><td>RNA-binding KH domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26000.1 | Symbols: PEP | RNA-binding KH domain-containing protein | chr4:13197280-13199539 FORWARD LENGTH=495</td><td>480</td><td>495</td><td>0</td><td>103.1</td><td>79.4</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00205.1.g8507.t1</td><td>ref|NP_001119059.1| uncharacterized protein [Arabidopsis thaliana] gi|332659750|gb|AEE85150.1| uncharacterized protein AT4G26055 [Arabidopsis thaliana]</td><td>62</td><td>62</td><td>8.00E-21</td><td>100.0</td><td>79.0</td><td>88.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26055.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G57080.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13214098-13214429 REVERSE LENGTH=62</td><td>62</td><td>62</td><td>1.00E-23</td><td>100.0</td><td>79.0</td><td>88.7</td></tr>
</table>

Rsa1.0_00205.1.g8508.t1	ref|NP_194336.1| ribosomal protein L18ae family protein [Arabidopsis thaliana] gi|4538935|emb|CAB39671.1| putative protein [Arabidopsis thaliana] gi|7269457|emb|CAB79461.1| putative protein [Arabidopsis thaliana] gi|106879161|gb|ABF82610.1| At4g26060 [Arabidopsis thaliana] gi|332659751|gb|AEE85151.1| ribosomal protein L18ae family protein [Arabidopsis thaliana]	135	133	7.00E-63	98.5	86.7	91.9	ribosomal protein L18ae family protein	gbpln	Arabidopsis thaliana	AT4G26060.1 | Symbols: | Ribosomal protein L18ae family | chr4:13214972-13215955 REVERSE LENGTH=133	135	133	2.00E-65	98.5	86.7	91.9
Rsa1.0_00205.1.g8509.t1	dbj|BAJ34574.1| unnamed protein product [Thellungiella halophila]	424	439	0	103.5	91.5	95.8	unnamed protein product	----	----	AT4G26080.1 | Symbols: ABI1, AtABI1 | Protein phosphatase 2C family protein | chr4:13220231-13221828 REVERSE LENGTH=434	424	434	0	102.4	86.6	91.5
Rsa1.0_00205.1.g8510.t1	gb|AAA50234.1| nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707, partial [Arabidopsis thaliana]	361	382	1.00E-135	105.8	80.6	92.0	nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707, partial	gbpln	Arabidopsis thaliana	AT4G26110.1 | Symbols: NAP1;1, ATNAP1;1 | nucleosome assembly protein1;1 | chr4:13232712-13235502 FORWARD LENGTH=372	361	372	1.00E-137	103.0	80.6	92.0
Rsa1.0_00205.1.g8511.t1	gb|EOA18191.1| hypothetical protein CARUB_v10006670mg [Capsella rubella]	335	337	1.00E-164	100.6	84.2	89.9	hypothetical protein CARUB_v10006670mg	gbpln	Capsella rubella	AT5G23790.1 | Symbols: AtGolS5, GolS5 | galactinol synthase 5 | chr5:8020183-8021597 REVERSE LENGTH=333	335	333	1.00E-166	99.4	83.0	89.9
Rsa1.0_00205.1.g8512.t1	ref|XP_002869622.1| mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297315458|gb|EFH45881.1| mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata]	313	122	5.00E-46	39.0	31.6	32.3	mitochondrial ATP synthase g subunit family protein	gbpln	Arabidopsis lyrata	AT4G26210.2 | Symbols: | Mitochondrial ATP synthase subunit G protein | chr4:13282370-13283118 FORWARD LENGTH=122	313	122	2.00E-47	39.0	30.7	32.3
Rsa1.0_00205.1.g8513.t1	ref|XP_002867571.1| arginyl-tRNA synthetase [Arabidopsis lyrata subsp. lyrata] gi|297313407|gb|EFH43830.1| arginyl-tRNA synthetase [Arabidopsis lyrata subsp. lyrata]	594	590	0	99.3	83.8	91.6	arginyl-tRNA synthetase	gbpln	Arabidopsis lyrata	AT4G26300.1 | Symbols: emb1027 | Arginyl-tRNA synthetase, class Ic | chr4:13308400-13313109 REVERSE LENGTH=642	594	642	0	108.1	83.5	91.2
Rsa1.0_00205.1.g8514.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00205.1.g8515.t2	ref|XP_002864440.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310275|gb|EFH40699.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	469	448	1.00E-147	95.5	54.2	66.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G56190.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:22742563-22744909 FORWARD LENGTH=441	469	441	1.00E-148	94.0	53.1	65.7
Rsa1.0_00205.1.g8516.t1	ref|NP_194393.3| DEK domain-containing chromatin associated protein [Arabidopsis thaliana] gi|79325273|ref|NP_001031724.1| DEK domain-containing chromatin associated protein [Arabidopsis thaliana] gi|4938501|emb|CAB43859.1| putative protein [Arabidopsis thaliana] gi|7269515|emb|CAB79518.1| putative protein [Arabidopsis thaliana] gi|332659828|gb|AEE85228.1| DEK domain-containing chromatin associated protein [Arabidopsis thaliana] gi|332659829|gb|AEE85229.1| DEK domain-containing chromatin associated protein [Arabidopsis thaliana]	867	763	1.00E-170	88.0	42.9	47.8	DEK domain-containing chromatin associated protein	gbpln	Arabidopsis thaliana	AT4G26630.2 | Symbols: | DEK domain-containing chromatin associated protein | chr4:13430873-13434877 REVERSE LENGTH=763	867	763	1.00E-173	88.0	42.9	47.8
Rsa1.0_00205.1.g8517.t5	gb|EOA16243.1| hypothetical protein CARUB_v10004390mg [Capsella rubella]	99	615	1.00E-22	621.2	62.6	67.7	hypothetical protein CARUB_v10004390mg	gbpln	Capsella rubella	AT4G26640.2 | Symbols: WRKY20, AtWRKY20 | WRKY family transcription factor family protein | chr4:13437298-13440693 REVERSE LENGTH=557	99	557	1.00E-24	562.6	71.7	78.8
Rsa1.0_00205.1.g8518.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	493	490	2.00E-73	99.4	33.9	54.6	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	493	566	3.00E-75	114.8	32.7	54.6
Rsa1.0_00205.1.g8519.t1	gb|AAG51081.1|AC027032_1 hypothetical protein [Arabidopsis thaliana]	932	1678	0	180.0	35.6	47.1	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	932	344	1.00E-71	36.9	15.0	20.4
Rsa1.0_00205.1.g8520.t1	gb|EOA16575.1| hypothetical protein CARUB_v10004740mg [Capsella rubella]	59	467	3.00E-23	791.5	84.7	88.1	hypothetical protein CARUB_v10004740mg	gbpln	Capsella rubella	AT4G26650.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:13445265-13447592 FORWARD LENGTH=452	59	452	1.00E-25	766.1	83.1	88.1
Rsa1.0_00205.1.g8521.t1	gb|EOA17427.1| hypothetical protein CARUB_v10005731mg [Capsella rubella]	208	210	3.00E-94	101.0	86.1	92.8	hypothetical protein CARUB_v10005731mg	gbpln	Capsella rubella	AT4G26670.1 | Symbols: | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr4:13452257-13453579 FORWARD LENGTH=210	208	210	2.00E-96	101.0	87.5	91.8

Rsa1.0_00205.1.g8522.t1	ref|XP_002867547.1| hypothetical protein ARALYDRAFT_913883 [Arabidopsis lyrata subsp. lyrata] gi|297313383|gb|EFH43806.1| hypothetical protein ARALYDRAFT_913883 [Arabidopsis lyrata subsp. lyrata]	61	61	2.00E-24	100.0	90.2	93.4	hypothetical protein ARALYDRAFT_913883	gbpln	Arabidopsis lyrata	AT3G11591.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:3663780-3663971 REVERSE LENGTH=63	61	63	9.00E-13	103.3	49.2	67.2
Rsa1.0_00205.1.g8523.t3	ref|XP_002867534.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313370|gb|EFH43793.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	588	407	1.00E-149	69.2	46.6	47.8	galactosyltransferase family protein	gbpln	Arabidopsis lyrata	AT4G26940.1 | Symbols: | Galactosyltransferase family protein | chr4:13529911-13532387 REVERSE LENGTH=407	588	407	1.00E-150	69.2	45.9	47.6
Rsa1.0_00205.1.g8524.t1	dbj|BAF00377.1| hypothetical protein [Arabidopsis thaliana]	116	138	4.00E-25	119.0	68.1	72.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G26960.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54970.1); Has 22 Blast hits to 22 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:13538923-13539653 REVERSE LENGTH=156	116	156	7.00E-28	134.5	69.8	75.9
Rsa1.0_00205.1.g8525.t2	ref|XP_002869585.1| NADH:ubiquinone oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315421|gb|EFH45844.1| NADH:ubiquinone oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	163	184	5.00E-70	112.9	91.4	95.1	NADH:ubiquinone oxidoreductase family protein	gbpln	Arabidopsis lyrata	AT4G26965.1 | Symbols: | NADH:ubiquinone oxidoreductase, 17.2kDa subunit | chr4:13539717-13542041 FORWARD LENGTH=184	163	184	3.00E-70	112.9	89.6	93.3
Rsa1.0_00205.1.g8526.t1	gb|EOA16728.1| hypothetical protein CARUB_v10004931mg [Capsella rubella]	418	413	1.00E-148	98.8	72.0	76.3	hypothetical protein CARUB_v10004931mg	gbpln	Capsella rubella	AT4G27000.1 | Symbols: ATRBP45C | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:13554983-13557763 REVERSE LENGTH=415	418	415	1.00E-147	99.3	72.5	76.3
Rsa1.0_00205.1.g8527.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	178	1142	2.00E-32	641.6	45.5	53.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	178	292	9.00E-13	164.0	25.8	44.4
Rsa1.0_00205.1.g8528.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00205.1.g8529.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00205.1.g8530.t1	ref|NP_194433.1| fatty acid desaturase A [Arabidopsis thaliana] gi|4455226|emb|CAB36549.1| putative protein [Arabidopsis thaliana] gi|7269556|emb|CAB79558.1| putative protein [Arabidopsis thaliana] gi|332659886|gb|AEE85286.1| fatty acid desaturase A [Arabidopsis thaliana]	290	323	1.00E-120	111.4	74.5	83.4	fatty acid desaturase A	gbpln	Arabidopsis thaliana	AT4G27030.1 | Symbols: FAD4, FADA | fatty acid desaturase A | chr4:13571951-13572922 FORWARD LENGTH=323	290	323	1.00E-122	111.4	74.5	83.4
Rsa1.0_00205.1.g8531.t1	gb|EOA18002.1| hypothetical protein CARUB_v10006437mg [Capsella rubella]	294	313	1.00E-150	106.5	88.1	93.2	hypothetical protein CARUB_v10006437mg	gbpln	Capsella rubella	AT4G27030.1 | Symbols: FAD4, FADA | fatty acid desaturase A | chr4:13571951-13572922 FORWARD LENGTH=323	294	323	1.00E-147	109.9	86.1	92.9
Rsa1.0_00205.1.g8532.t1	gb|EOA15725.1| hypothetical protein CARUB_v10006633mg, partial [Capsella rubella]	161	483	2.00E-31	300.0	43.5	64.0	hypothetical protein CARUB_v10006633mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	161	566	8.00E-18	351.6	30.4	52.8
Rsa1.0_00205.1.g8533.t1	#	#	#	#	#	#	#	-	----	----	AT4G28890.1 | Symbols: | RING/U-box superfamily protein | chr4:14256437-14257735 REVERSE LENGTH=432	73	432	3.00E-11	591.8	43.8	47.9
Rsa1.0_00205.1.g8534.t2	gb|EOA33328.1| hypothetical protein CARUB_v10022104mg [Capsella rubella]	278	298	1.00E-104	107.2	68.0	79.5	hypothetical protein CARUB_v10022104mg	gbpln	Capsella rubella	AT5G65370.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr5:26121708-26122749 FORWARD LENGTH=295	278	295	1.00E-105	106.1	65.8	77.0

Rsa1.0_00205.1.g8535.t1	ref|NP_567765.2| protein PDI-like 5-4 [Arabidopsis thaliana] gi|75213708|sp|Q9T042.1|PDI54_ARATH RecName: Full=Protein disulfide-isomerase 5-4; Short=AtPDIL5-4; AltName: Full=Protein disulfide-isomerase 7; Short=PDI7; AltName: Full=Protein disulfide-isomerase 8-2; Short=AtPDIL8-2; Flags: Precursor gi|4490704|emb|CAB38838.1| putative protein [Arabidopsis thaliana] gi|7269561|emb|CAB79563.1| putative protein [Arabidopsis thaliana] gi|15450832|gb|AAK96687.1| putative protein [Arabidopsis thaliana] gi|20259836|gb|AAM13265.1| putative protein [Arabidopsis thaliana] gi|332659897|gb|AEE85297.1| protein PDI-like 5-4 [Arabidopsis thaliana]	503	480	0	95.4	82.9	89.7	protein PDI-like 5-4	gbpln	Arabidopsis thaliana	AT4G27080.1 | Symbols: ATPDIL5-4, ATPDI7, PDI7, PDIL5-4 | PDI-like 5-4 | chr4:13589156-13593335 FORWARD LENGTH=480	503	480	0	95.4	82.9	89.7
Rsa1.0_00205.1.g8536.t1	gb|EOA17638.1| hypothetical protein CARUB_v10006004mg [Capsella rubella]	134	134	3.00E-67	100.0	97.0	99.3	hypothetical protein CARUB_v10006004mg	gbpln	Capsella rubella	AT4G27090.1 | Symbols: | Ribosomal protein L14 | chr4:13594104-13595187 REVERSE LENGTH=134	134	134	7.00E-69	100.0	96.3	98.5
Rsa1.0_00205.1.g8537.t1	emb|CAB38841.1| putative protein [Arabidopsis thaliana] gi|7269564|emb|CAB79566.1| putative protein [Arabidopsis thaliana]	820	717	0	87.4	69.5	75.1	putative protein	gbpln	Arabidopsis thaliana	AT4G27110.1 | Symbols: COBL11 | COBRA-like protein 11 precursor | chr4:13599236-13601521 REVERSE LENGTH=668	820	668	0	81.5	64.6	69.8
Rsa1.0_00205.1.g8538.t1	sp|P27740.1|2SSB_BRANA RecName: Full=Napin-B; AltName: Full=1.7S seed storage protein; Contains: RecName: Full=Napin-B small chain; Contains: RecName: Full=Napin-B large chain; Flags: Precursor gi|17835|emb|CAA41150.1| napin [Brassica napus]	174	178	4.00E-56	102.3	71.8	82.2	RecName: Full=Napin-B; AltName: Full=1.7S seed storage protein; Contains: RecName: Full=Napin-B small chain; Contains: RecName: Full=Napin-B large chain; Flags: Precursor gi|17835|emb|CAA41150.1| napin	gbpln	Brassica napus	AT4G27170.1 | Symbols: SESA4, AT2S4 | seed storage albumin 4 | chr4:13613637-13614137 FORWARD LENGTH=166	174	166	4.00E-52	95.4	59.2	72.4
Rsa1.0_00205.1.g8539.t1	ref|XP_002869569.1| hypothetical protein ARALYDRAFT_913814 [Arabidopsis lyrata subsp. lyrata] gi|297315405|gb|EFH45828.1| hypothetical protein ARALYDRAFT_913814 [Arabidopsis lyrata subsp. lyrata]	178	191	2.00E-46	107.3	55.6	61.8	hypothetical protein ARALYDRAFT_913814	gbpln	Arabidopsis lyrata	AT4G27310.1 | Symbols: | B-box type zinc finger family protein | chr4:13675853-13676616 FORWARD LENGTH=223	178	223	3.00E-45	125.3	57.9	67.4
Rsa1.0_00205.1.g8540.t1	gb|AAD22702.1| putative TNP1-like transposon protein [Arabidopsis thaliana]	187	531	7.00E-49	284.0	51.9	71.1	putative TNP1-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00205.1.g8541.t1	gb|EOA17257.1| hypothetical protein CARUB_v10005532mg [Capsella rubella]	213	260	3.00E-71	122.1	79.3	82.6	hypothetical protein CARUB_v10005532mg	gbpln	Capsella rubella	AT4G27320.1 | Symbols: ATPHOS34, PHOS34 | Adenine nucleotide alpha hydrolases-like superfamily protein | chr4:13678860-13680717 REVERSE LENGTH=260	213	260	2.00E-71	122.1	78.4	81.2
Rsa1.0_00205.1.g8542.t1	sp|Q9LUJ6.1|FB176_ARATH RecName: Full=Putative F-box protein At3g22650 gi|9279683|dbj|BAB01240.1| unnamed protein product [Arabidopsis thaliana]	447	383	1.00E-46	85.7	30.4	47.2	RecName: Full=Putative F-box protein At3g22650 gi|9279683|dbj|BAB01240.1| unnamed protein product	gbpln	Arabidopsis thaliana	AT3G22650.1 | Symbols: ATSFL61, SFL61, CEG | F-box and associated interaction domains-containing protein | chr3:8014809-8015960 FORWARD LENGTH=372	447	372	6.00E-43	83.2	29.1	45.4
Rsa1.0_00205.1.g8543.t1	gb|ADE43101.1| restricted tev movement 3 [Arabidopsis thaliana] gi|302608327|emb|CBW45911.1| RTM3 protein [Arabidopsis thaliana] gi|302608852|emb|CBW45917.1| RTM3 protein [Arabidopsis thaliana] gi|302608858|emb|CBW45920.1| RTM3 protein [Arabidopsis thaliana] gi|302608870|emb|CBW45926.1| RTM3 protein [Arabidopsis thaliana] gi|302608876|emb|CBW45929.1| RTM3 protein [Arabidopsis thaliana] gi|302608878|emb|CBW45930.1| RTM3 protein [Arabidopsis thaliana] gi|302608888|emb|CBW45935.1| RTM3 protein [Arabidopsis thaliana] gi|302608892|emb|CBW45937.1| RTM3 protein [Arabidopsis thaliana]	84	301	1.00E-23	358.3	72.6	85.7	restricted tev movement 3	gbpln	Arabidopsis thaliana	AT3G58350.1 | Symbols: RTM3 | RESTRICTED TEV MOVEMENT 3 | chr3:21591618-21592836 REVERSE LENGTH=301	84	301	6.00E-26	358.3	71.4	84.5
Rsa1.0_00205.1.g8544.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00205.1.g8545.t3	gb|ABJ88950.2| glyoxalase I [Arachis hypogaea]	280	187	6.00E-35	66.8	32.5	33.6	glyoxalase I	gbpln	Arachis hypogaea	AT1G64100.2 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:23791585-23795563 FORWARD LENGTH=806	280	806	2.00E-37	287.9	27.1	33.9

Rsa1.0_00205.1.g8546.t1	ref|NP_200248.1| late embryogenesis abundant protein-like protein [Arabidopsis thaliana] gi|10257484|dbj|BAB10109.1| root cap protein 2-like protein [Arabidopsis thaliana] gi|71143048|gb|AAZ23915.1| At5g54370 [Arabidopsis thaliana] gi|332009106|gb|AED96489.1| late embryogenesis abundant protein-like protein [Arabidopsis thaliana]	338	337	1.00E-130	99.7	66.9	78.7	late embryogenesis abundant protein-like protein	gbpln	Arabidopsis thaliana	AT5G54370.1 | Symbols: | Late embryogenesis abundant (LEA) protein-related | chr5:22075334-22076567 FORWARD LENGTH=337	338	337	1.00E-132	99.7	66.9	78.7
Rsa1.0_00205.1.g8547.t1	ref|NP_194478.3| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|186514118|ref|NP_001119069.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|332659947|gb|AEE85347.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|332659948|gb|AEE85348.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]	421	421	0	100.0	90.5	94.8	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	gbpln	Arabidopsis thaliana	AT4G27480.2 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:13736835-13738317 REVERSE LENGTH=421	421	421	0	100.0	90.5	94.8
Rsa1.0_00205.1.g8548.t1	ref|XP_002869559.1| hypothetical protein ARALYDRAFT_328945 [Arabidopsis lyrata subsp. lyrata] gi|297315395|gb|EFH45818.1| hypothetical protein ARALYDRAFT_328945 [Arabidopsis lyrata subsp. lyrata]	621	617	0	99.4	77.8	86.8	hypothetical protein ARALYDRAFT_328945	gbpln	Arabidopsis lyrata	AT4G27500.1 | Symbols: PPI1 | proton pump interactor 1 | chr4:13743614-13745900 FORWARD LENGTH=612	621	612	0	98.6	75.0	83.7
Rsa1.0_00205.1.g8549.t1	ref|XP_002869558.1| hypothetical protein ARALYDRAFT_492040 [Arabidopsis lyrata subsp. lyrata] gi|297315394|gb|EFH45817.1| hypothetical protein ARALYDRAFT_492040 [Arabidopsis lyrata subsp. lyrata]	131	132	2.00E-34	100.8	63.4	80.9	hypothetical protein ARALYDRAFT_492040	gbpln	Arabidopsis lyrata	AT4G27530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G53895.1); Has 14 Blast hits to 14 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:13752640-13753122 FORWARD LENGTH=130	131	130	6.00E-37	99.2	61.1	79.4
Rsa1.0_00205.1.g8550.t1	gb|EOA33547.1| hypothetical protein CARUB_v10019666mg [Capsella rubella]	1368	1348	0	98.5	59.1	72.4	hypothetical protein CARUB_v10019666mg	gbpln	Capsella rubella	AT1G65010.1 | Symbols: | Plant protein of unknown function (DUF827) | chr1:24149543-24154024 FORWARD LENGTH=1345	1368	1345	0	98.3	58.9	72.4
Rsa1.0_00206.1.g8551.t12	ref|XP_002869986.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315822|gb|EFH46245.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	2563	1044	0	40.7	37.1	38.7	protein binding protein	gbpln	Arabidopsis lyrata	AT4G19490.2 | Symbols: ATVPS54, VPS54 | VPS54 | chr4:10616017-10622934 FORWARD LENGTH=1034	2563	1034	0	40.3	36.5	38.1
Rsa1.0_00206.1.g8552.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00206.1.g8553.t1	gb|EOA18464.1| hypothetical protein CARUB_v10007010mg [Capsella rubella]	723	364	1.00E-47	50.3	13.7	15.9	hypothetical protein CARUB_v10007010mg	gbpln	Capsella rubella	AT4G19570.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:10665516-10667192 FORWARD LENGTH=558	723	558	2.00E-49	77.2	13.7	17.0
Rsa1.0_00206.1.g8554.t1	ref|NP_193694.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|2853086|emb|CAA16936.1| putative protein [Arabidopsis thaliana] gi|7268755|emb|CAB78961.1| putative protein [Arabidopsis thaliana] gi|332658802|gb|AEE84202.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]	525	345	3.00E-60	65.7	20.2	23.0	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT4G19590.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:10671199-10672290 FORWARD LENGTH=345	525	345	6.00E-63	65.7	20.2	23.0
Rsa1.0_00206.1.g8555.t1	ref|NP_193696.3| nucleotide/nucleic acid binding protein [Arabidopsis thaliana] gi|332658804|gb|AEE84204.1| nucleotide/nucleic acid binding protein [Arabidopsis thaliana]	1563	816	0	52.2	37.5	43.1	nucleotide/nucleic acid binding protein	gbpln	Arabidopsis thaliana	AT4G19610.1 | Symbols: | nucleotide binding;nucleic acid binding;RNA binding | chr4:10677482-10681623 FORWARD LENGTH=816	1563	816	0	52.2	37.5	43.1
Rsa1.0_00206.1.g8556.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00206.1.g8557.t3	gb|EOA17450.1| hypothetical protein CARUB_v10005769mg [Capsella rubella]	864	201	1.00E-105	23.3	21.8	22.1	hypothetical protein CARUB_v10005769mg	gbpln	Capsella rubella	AT4G19640.1 | Symbols: ARA7, ARA-7, ATRABF2B, ATRAB5B, RABF2B, ATRAB-F2B, RAB-F2B | Ras-related small GTP-binding family protein | chr4:10687441-10689449 REVERSE LENGTH=200	864	200	1.00E-106	23.1	21.4	21.9

Rsa1.0_00206.1.g8558.t1	ref|XP_002867929.1| hypothetical protein ARALYDRAFT_492902 [Arabidopsis lyrata subsp. lyrata] gi|297313765|gb|EFH44188.1| hypothetical protein ARALYDRAFT_492902 [Arabidopsis lyrata subsp. lyrata]	268	268	1.00E-135	100.0	87.7	93.3	hypothetical protein ARALYDRAFT_492902	gbpln	Arabidopsis lyrata	AT4G19645.2 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr4:10689941-10691298 REVERSE LENGTH=268	268	268	1.00E-134	100.0	85.4	91.8
Rsa1.0_00206.1.g8559.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00206.1.g8560.t1	gb|EOA16280.1| hypothetical protein CARUB_v10004425mg [Capsella rubella]	579	592	0	102.2	83.8	91.9	hypothetical protein CARUB_v10004425mg	gbpln	Capsella rubella	AT4G19650.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr4:10691674-10695166 FORWARD LENGTH=575	579	575	0	99.3	72.0	78.4
Rsa1.0_00206.1.g8561.t1	ref|XP_002867927.1| hypothetical protein ARALYDRAFT_354789 [Arabidopsis lyrata subsp. lyrata] gi|297313763|gb|EFH44186.1| hypothetical protein ARALYDRAFT_354789 [Arabidopsis lyrata subsp. lyrata]	767	777	0	101.3	68.8	80.1	hypothetical protein ARALYDRAFT_354789	gbpln	Arabidopsis lyrata	AT3G18100.1 | Symbols: MYB4R1, AtMYB4R1 | myb domain protein 4r1 | chr3:6200689-6204583 FORWARD LENGTH=847	767	847	0	110.4	62.3	74.6
Rsa1.0_00206.1.g8562.t1	dbj|BAJ34281.1| unnamed protein product [Thellungiella halophila]	675	588	0	87.1	75.1	79.9	unnamed protein product	----	----	AT4G19660.1 | Symbols: NPR4, ATNPR4 | NPR1-like protein 4 | chr4:10696266-10698243 REVERSE LENGTH=574	675	574	0	85.0	67.9	74.2
Rsa1.0_00206.1.g8563.t1	ref|XP_002867925.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297313761|gb|EFH44184.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	543	532	0	98.0	85.1	91.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G19670.2 | Symbols: | RING/U-box superfamily protein | chr4:10699383-10701342 REVERSE LENGTH=532	543	532	0	98.0	84.0	91.0
Rsa1.0_00206.1.g8564.t1	ref|NP_001031670.1| Fe(2+) transport protein 2 [Arabidopsis thaliana] gi|37079162|sp|O81850.1|IRT2_ARATH RecName: Full=Fe(2+) transport protein 2; AltName: Full=Fe(II) transport protein 2; AltName: Full=Iron-regulated transporter 2; Flags: Precursor gi|3250677|emb|CAA19685.1| putative Fe(II) transport protein [Arabidopsis thaliana] gi|7268764|emb|CAB78970.1| putative Fe(II) transport protein [Arabidopsis thaliana] gi|56461764|gb|AAV91338.1| At4g19680 [Arabidopsis thaliana] gi|332658815|gb|AEE84215.1| Fe(2+) transport protein 2 [Arabidopsis thaliana]	359	350	1.00E-172	97.5	85.5	90.8	Fe(2+) transport protein 2	gbpln	Arabidopsis thaliana	AT4G19680.2 | Symbols: IRT2 | iron regulated transporter 2 | chr4:10703385-10704621 FORWARD LENGTH=350	359	350	1.00E-174	97.5	85.5	90.8
Rsa1.0_00206.1.g8565.t1	gb|EOA18607.1| hypothetical protein CARUB_v10007180mg [Capsella rubella]	339	345	1.00E-161	101.8	83.5	90.9	hypothetical protein CARUB_v10007180mg	gbpln	Capsella rubella	AT4G19690.2 | Symbols: IRT1 | iron-regulated transporter 1 | chr4:10707487-10708723 FORWARD LENGTH=347	339	347	1.00E-158	102.4	82.3	89.7
Rsa1.0_00206.1.g8566.t1	#	#	#	#	#	#	#	-	----	----	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	93	170	6.00E-13	182.8	41.9	63.4
Rsa1.0_00206.1.g8567.t1	gb|EOA18607.1| hypothetical protein CARUB_v10007180mg [Capsella rubella]	345	345	0	100.0	90.7	95.7	hypothetical protein CARUB_v10007180mg	gbpln	Capsella rubella	AT4G19690.2 | Symbols: IRT1 | iron-regulated transporter 1 | chr4:10707487-10708723 FORWARD LENGTH=347	345	347	1.00E-176	100.6	90.7	95.4
Rsa1.0_00206.1.g8568.t1	gb|EOA18607.1| hypothetical protein CARUB_v10007180mg [Capsella rubella]	345	345	0	100.0	90.4	96.5	hypothetical protein CARUB_v10007180mg	gbpln	Capsella rubella	AT4G19690.2 | Symbols: IRT1 | iron-regulated transporter 1 | chr4:10707487-10708723 FORWARD LENGTH=347	345	347	1.00E-176	100.6	89.3	95.4
Rsa1.0_00207.1.g8569.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00207.1.g8570.t1	ref|NP_200248.1| late embryogenesis abundant protein-like protein [Arabidopsis thaliana] gi|10257484|dbj|BAB10109.1| root cap protein 2-like protein [Arabidopsis thaliana] gi|71143048|gb|AAZ23915.1| At5g54370 [Arabidopsis thaliana] gi|332009106|gb|AED96489.1| late embryogenesis abundant protein-like protein [Arabidopsis thaliana]	337	337	0	100.0	92.0	97.6	late embryogenesis abundant protein-like protein	gbpln	Arabidopsis thaliana	AT5G54370.1 | Symbols: | Late embryogenesis abundant (LEA) protein-related | chr5:22075334-22076567 FORWARD LENGTH=337	337	337	0	100.0	92.0	97.6
Rsa1.0_00207.1.g8571.t1	gb|EOA12897.1| hypothetical protein CARUB_v10025871mg [Capsella rubella]	837	860	0	102.7	84.3	90.0	hypothetical protein CARUB_v10025871mg	gbpln	Capsella rubella	AT5G54380.1 | Symbols: THE1 | protein kinase family protein | chr5:22077313-22079880 REVERSE LENGTH=855	837	855	0	102.2	85.1	90.8
Rsa1.0_00207.1.g8572.t1	ref|XP_002864334.1| hypothetical protein ARALYDRAFT_918574 [Arabidopsis lyrata subsp. lyrata] gi|297310169|gb|EFH40593.1| hypothetical protein ARALYDRAFT_918574 [Arabidopsis lyrata subsp. lyrata]	251	247	1.00E-76	98.4	78.1	84.9	hypothetical protein ARALYDRAFT_918574	gbpln	Arabidopsis lyrata	AT5G54430.1 | Symbols: ATPHOS32, PHOS32 | Adenine nucleotide alpha hydrolases-like superfamily protein | chr5:22097563-22099693 REVERSE LENGTH=242	251	242	5.00E-78	96.4	77.7	83.7
Rsa1.0_00207.1.g8573.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00207.1.g8574.t1	gb|EOA14018.1| hypothetical protein CARUB_v10027151mg [Capsella rubella]	194	204	1.00E−104	105.2	96.9	99.0	hypothetical protein CARUB_v10027151mg	gbpln	Capsella rubella	AT5G54500.1 | Symbols: FQR1 | flavodoxin-like quinone reductase 1 | chr5:22124674-22126256 FORWARD LENGTH=204	194	204	1.00E−104	105.2	93.8	97.4
Rsa1.0_00207.1.g8575.t1	ref|XP_002871167.1| exonuclease family protein [Arabidopsis lyrata subsp. lyrata] gi|297317004|gb|EFH47426.1| exonuclease family protein [Arabidopsis lyrata subsp. lyrata]	97	464	8.00E−24	478.4	60.8	76.3	exonuclease family protein	gbpln	Arabidopsis lyrata	AT5G05540.1 | Symbols: SDN2 | small RNA degrading nuclease 2 | chr5:1636419-1638759 FORWARD LENGTH=466	97	466	2.00E−25	480.4	58.8	77.3
Rsa1.0_00207.1.g8576.t1	ref|NP_200262.1| indole-3-acetic acid-amido synthetase GH3.6 [Arabidopsis thaliana] gi|62900334|sp|Q9LSQ4.1|GH36_ARATH RecName: Full=Indole-3-acetic acid-amido synthetase GH3.6; AltName: Full=Auxin-responsive GH3-like protein 6; Short=AtGH3-6; AltName: Full=Protein DWARF IN LIGHT 1; Short=DFL-1 gi|8885594|dbj|BAA97524.1| auxin-responsive-like protein [Arabidopsis thaliana] gi|11041726|dbj|BAB17304.1| auxin-responsive GH3 homologue [Arabidopsis thaliana] gi|59958336|gb|AAX12878.1| At5g54510 [Arabidopsis thaliana] gi|209414530|gb|ACI46505.1| At5g54510 [Arabidopsis thaliana] gi|332009121|gb|AED96504.1| indole-3-acetic acid-amido synthetase GH3.6 [Arabidopsis thaliana]	612	612	0	100.0	93.6	96.9	indole-3-acetic acid-amido synthetase GH3.6	gbpln	Arabidopsis thaliana	AT5G54510.1 | Symbols: GH3.6, DFL1 | Auxin-responsive GH3 family protein | chr5:22131321-22133564 REVERSE LENGTH=612	612	612	0	100.0	93.6	96.9
Rsa1.0_00207.1.g8577.t1	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	818	1250	1.00E−179	152.8	38.8	44.3	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	818	1262	2.00E−65	154.3	16.7	27.4
Rsa1.0_00207.1.g8578.t1	gb|EOA14680.1| hypothetical protein CARUB_v10027952mg [Capsella rubella]	450	450	0	100.0	78.9	88.0	hypothetical protein CARUB_v10027952mg	gbpln	Capsella rubella	AT5G54520.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:22146781-22149089 REVERSE LENGTH=457	450	457	0	101.6	80.7	89.1
Rsa1.0_00207.1.g8579.t1	ref|XP_002864345.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310180|gb|EFH40604.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	157	156	2.00E−68	99.4	83.4	89.2	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT5G54580.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:22171332-22172656 FORWARD LENGTH=156	157	156	3.00E−70	99.4	82.8	88.5
Rsa1.0_00207.1.g8580.t1	ref|NP_680435.1| uncharacterized protein [Arabidopsis thaliana] gi|17380702|gb|AAL36181.1| unknown protein [Arabidopsis thaliana] gi|20465573|gb|AAM20269.1| unknown protein [Arabidopsis thaliana] gi|332009130|gb|AED96513.1| uncharacterized protein AT5G54585 [Arabidopsis thaliana]	125	132	2.00E−43	105.6	82.4	91.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54585.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:22175688-22176509 FORWARD LENGTH=132	125	132	3.00E−46	105.6	82.4	91.2
Rsa1.0_00207.1.g8581.t2	gb|ABY47994.1| carotenoid cleavage dioxygenase 1 [Rosa x damascena]	107	552	4.00E−30	515.9	57.0	61.7	carotenoid cleavage dioxygenase 1	gbpln	Rosa x	AT3G63520.1 | Symbols: CCD1, ATCCD1, ATNCED1, NCED1 | carotenoid cleavage dioxygenase 1 | chr3:23452940-23455896 FORWARD LENGTH=538	107	538	6.00E−32	502.8	57.9	61.7
Rsa1.0_00207.1.g8582.t2	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	246	1555	4.00E−22	632.1	30.1	43.1	disease resistance protein	gbpln	Brassica rapa	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	246	303	7.00E−21	123.2	27.2	42.3
Rsa1.0_00207.1.g8583.t1	ref|XP_002864347.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310182|gb|EFH40606.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	439	437	0	99.5	87.9	92.9	kinase family protein	gbpln	Arabidopsis lyrata	AT5G54590.2 | Symbols: CRLK1 | Protein kinase superfamily protein | chr5:22180480-22182698 FORWARD LENGTH=440	439	440	0	100.2	88.2	93.2
Rsa1.0_00207.1.g8584.t2	ref|NP_200273.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|332009136|gb|AED96519.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	529	431	1.00E−132	81.5	42.9	49.7	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G54620.1 | Symbols: | Ankyrin repeat family protein | chr5:22187761-22189746 REVERSE LENGTH=431	529	431	1.00E−134	81.5	42.9	49.7
Rsa1.0_00207.1.g8585.t2	ref|XP_002866054.1| hypothetical protein ARALYDRAFT_495546 [Arabidopsis lyrata subsp. lyrata] gi|297311889|gb|EFH42313.1| hypothetical protein ARALYDRAFT_495546 [Arabidopsis lyrata subsp. lyrata]	840	902	0	107.4	80.6	86.7	hypothetical protein ARALYDRAFT_495546	gbpln	Arabidopsis lyrata	AT5G54650.2 | Symbols: Fh5, ATFH5 | formin homology5 | chr5:22197856-22201649 REVERSE LENGTH=900	840	900	0	107.1	79.0	85.4

Rsa1.0_00207.1.g8586.t2	ref|NP_568811.1| kinesin 3 [Arabidopsis thaliana] gi|1170621|sp|P46875.1|ATK3_ARATH RecName: Full=Kinesin-3; AltName: Full=Kinesin-like protein C gi|1438844|dbj|BAA04674.1| heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana] gi|27808616|gb|AAO24588.1| At5g54670 [Arabidopsis thaliana] gi|110736249|dbj|BAF00095.1| heavy chain polypeptide of kinesin like protein [Arabidopsis thaliana] gi|332009142|gb|AED96525.1| kinesin 3 [Arabidopsis thaliana]	65	754	1.00E-18	1160.0	78.5	83.1	kinesin 3	gbpln	Arabidopsis thaliana	AT5G54670.1 | Symbols: ATK3, KATC | kinesin 3 | chr5:22209912-22213843 FORWARD LENGTH=754	65	754	2.00E-21	1160.0	78.5	83.1
Rsa1.0_00207.1.g8587.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00207.1.g8588.t1	ref|NP_200279.1| transcription factor ILR3 [Arabidopsis thaliana] gi|297792933|ref|XP_002864351.1| hypothetical protein ARALYDRAFT_495549 [Arabidopsis lyrata subsp. lyrata] gi|75309075|sp|Q9FH37.1|ILR3_ARATH RecName: Full=Transcription factor ILR3; AltName: Full=Basic helix-loop-helix protein 105; Short=AtbHLH105; Short=bHLH 105; AltName: Full=Protein IAA-LEUCINE RESISTANT 3; AltName: Full=Transcription factor EN 133; AltName: Full=bHLH transcription factor bHLH105 gi|20127111|gb|AAM10964.1|AF488629_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|10176795|dbj|BAB09934.1| unnamed protein product [Arabidopsis thaliana] gi|15451010|gb|AAK96776.1| Unknown protein [Arabidopsis thaliana] gi|25084222|gb|AAN72200.1| Unknown protein [Arabidopsis thaliana] gi|297310186|gb|EFH40610.1| hypothetical protein ARALYDRAFT_495549 [Arabidopsis lyrata subsp. lyrata] gi|332009143|gb|AED96526.1| transcription factor ILR3 [Arabidopsis thaliana]	178	234	2.00E-30	131.5	50.6	58.4	transcription factor ILR3	gbpln	Arabidopsis lyrata	AT5G54680.1 | Symbols: ILR3, bHLH105 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:22217270-22218993 FORWARD LENGTH=234	178	234	6.00E-33	131.5	50.6	58.4
Rsa1.0_00207.1.g8589.t1	ref|XP_002866055.1| GAUT12/IRX8/LGT6 [Arabidopsis lyrata subsp. lyrata] gi|297311890|gb|EFH42314.1| GAUT12/IRX8/LGT6 [Arabidopsis lyrata subsp. lyrata]	513	535	0	104.3	95.7	98.1	GAUT12/IRX8/LGT6	gbpln	Arabidopsis lyrata	AT5G54690.1 | Symbols: GAUT12, LGT6, IRX8 | galacturonosyltransferase 12 | chr5:22219435-22221769 REVERSE LENGTH=535	513	535	0	104.3	95.7	98.1
Rsa1.0_00207.1.g8590.t1	gb|EOA25229.1| hypothetical protein CARUB_v10018542mg [Capsella rubella]	488	431	1.00E-155	88.3	61.1	72.1	hypothetical protein CARUB_v10018542mg	gbpln	Capsella rubella	AT5G50140.1 | Symbols: | Ankyrin repeat family protein | chr5:20395856-20398197 FORWARD LENGTH=535	488	535	1.00E-132	109.6	53.5	68.6
Rsa1.0_00207.1.g8591.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00207.1.g8592.t1	dbj|BAJ34327.1| unnamed protein product [Thellungiella halophila]	112	112	3.00E-54	100.0	91.1	97.3	unnamed protein product	----	----	AT5G54940.2 | Symbols: | Translation initiation factor SUI1 family protein | chr5:22308420-22308758 REVERSE LENGTH=112	112	112	1.00E-55	100.0	90.2	96.4
Rsa1.0_00207.1.g8593.t1	ref|NP_200308.1| uncharacterized protein [Arabidopsis thaliana] gi|9758277|dbj|BAB08776.1| unnamed protein product [Arabidopsis thaliana] gi|117168079|gb|ABK32122.1| At5g54970 [Arabidopsis thaliana] gi|332009181|gb|AED96564.1| uncharacterized protein AT5G54970 [Arabidopsis thaliana]	118	125	1.00E-32	105.9	72.9	80.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54970.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G26960.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:22313271-22313648 FORWARD LENGTH=125	118	125	2.00E-35	105.9	72.9	80.5
Rsa1.0_00207.1.g8594.t1	gb|EOA14046.1| hypothetical protein CARUB_v10027181mg [Capsella rubella]	110	193	2.00E-44	175.5	85.5	90.0	hypothetical protein CARUB_v10027181mg	gbpln	Capsella rubella	AT5G54980.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr5:22315799-22316560 FORWARD LENGTH=194	110	194	1.00E-44	176.4	81.8	89.1
Rsa1.0_00207.1.g8595.t1	gb|EOA13786.1| hypothetical protein CARUB_v10026879mg [Capsella rubella]	278	298	1.00E-134	107.2	87.8	93.2	hypothetical protein CARUB_v10026879mg	gbpln	Capsella rubella	AT5G55000.2 | Symbols: FIP2 | potassium channel tetramerisation domain-containing protein / pentapeptide repeat-containing protein | chr5:22318644-22321599 FORWARD LENGTH=298	278	298	1.00E-136	107.2	88.1	93.5

Rsa1.0_00207.1.g8596.t1	dbj|BAB10576.1| unnamed protein product [Arabidopsis thaliana]	568	581	1.00E-179	102.3	79.2	84.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G55020.1 | Symbols: ATMYB120, MYB120 | myb domain protein 120 | chr5:22324599-22326248 REVERSE LENGTH=523	568	523	1.00E-144	92.1	66.7	71.0
Rsa1.0_00207.1.g8597.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00207.1.g8598.t1	gb|EOA13535.1| hypothetical protein CARUB_v10026598mg [Capsella rubella]	377	378	0	100.3	84.1	92.6	hypothetical protein CARUB_v10026598mg	gbpln	Capsella rubella	AT5G55050.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:22337745-22339741 FORWARD LENGTH=376	377	376	1.00E-179	99.7	84.6	93.4
Rsa1.0_00207.1.g8599.t1	gb|EOA13535.1| hypothetical protein CARUB_v10026598mg [Capsella rubella]	376	378	1.00E-174	100.5	79.8	90.7	hypothetical protein CARUB_v10026598mg	gbpln	Capsella rubella	AT5G55050.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:22337745-22339741 FORWARD LENGTH=376	376	376	1.00E-169	100.0	80.3	91.8
Rsa1.0_00207.1.g8600.t1	gb|EOA13535.1| hypothetical protein CARUB_v10026598mg [Capsella rubella]	319	378	1.00E-114	118.5	66.1	78.1	hypothetical protein CARUB_v10026598mg	gbpln	Capsella rubella	AT5G55050.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:22337745-22339741 FORWARD LENGTH=376	319	376	1.00E-109	117.9	67.1	78.4
Rsa1.0_00207.1.g8601.t1	gb|EOA13041.1| hypothetical protein CARUB_v10026040mg [Capsella rubella]	635	660	0	103.9	80.9	89.0	hypothetical protein CARUB_v10026040mg	gbpln	Capsella rubella	AT5G55060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G58510.1); Has 223 Blast hits to 218 proteins in 80 species: Archae - 0; Bacteria - 2; Metazoa - 117; Fungi - 6; Plants - 65; Viruses - 0; Other Eukaryotes - 33 (source: NCBI BLink). | chr5:22342079-22346400 FORWARD LENGTH=662	635	662	0	104.3	81.9	88.2
Rsa1.0_00207.1.g8602.t1	emb|CAA11553.1| 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]	465	462	0	99.4	92.5	95.7	2-oxoglutarate dehydrogenase E2 subunit	gbpln	Arabidopsis thaliana	AT5G55070.1 | Symbols: | Dihydrolipoamide succinyltransferase | chr5:22347637-22350409 FORWARD LENGTH=464	465	464	0	99.8	92.0	94.6
Rsa1.0_00208.1.g8603.t1	gb|EOA22057.1| hypothetical protein CARUB_v10002597mg, partial [Capsella rubella]	61	221	1.00E-15	362.3	67.2	72.1	hypothetical protein CARUB_v10002597mg, partial	gbpln	Capsella rubella	AT5G23350.1 | Symbols: | GRAM domain-containing protein / ABA-responsive protein-related | chr5:7858545-7859387 REVERSE LENGTH=280	61	280	2.00E-16	459.0	63.9	67.2
Rsa1.0_00208.1.g8604.t1	gb|AAD26943.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	708	1454	1.00E-133	205.4	32.3	38.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT2G47250.1 | Symbols: | RNA helicase family protein | chr2:19399923-19402981 REVERSE LENGTH=729	708	729	1.00E-113	103.0	30.6	39.1
Rsa1.0_00208.1.g8605.t1	gb|EOA21466.1| hypothetical protein CARUB_v10001858mg [Capsella rubella]	244	236	6.00E-86	96.7	77.0	86.9	hypothetical protein CARUB_v10001858mg	gbpln	Capsella rubella	AT5G23420.1 | Symbols: HMGB6 | high-mobility group box 6 | chr5:7888712-7890111 REVERSE LENGTH=241	244	241	6.00E-69	98.8	61.1	70.1
Rsa1.0_00208.1.g8606.t1	ref|XP_002866559.1| F-box/LRR-repeat protein At5g63520 [Arabidopsis lyrata subsp. lyrata] gi|297312394|gb|EFH42818.1| F-box/LRR-repeat protein At5g63520 [Arabidopsis lyrata subsp. lyrata]	488	526	0	107.8	68.9	80.1	F-box/LRR-repeat protein At5g63520	gbpln	Arabidopsis lyrata	AT5G63520.1 | Symbols: | CONTAINS InterPro DOMAIN/s: F-box domain, Skp2-like (InterPro:IPR022364), FIST C domain (InterPro:IPR019494), FIST domain, N-terminal (InterPro:IPR013702); Has 137 Blast hits to 137 proteins in 56 species: Archae - 0; Bacteria - 88; Metazoa - 6; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr5:25426300-25429093 REVERSE LENGTH=519	488	519	0	106.4	67.8	79.3
Rsa1.0_00208.1.g8607.t1	gb|EOA15135.1| hypothetical protein CARUB_v10028510mg [Capsella rubella]	112	120	3.00E-41	107.1	75.0	83.9	hypothetical protein CARUB_v10028510mg	gbpln	Capsella rubella	AT5G52975.1 | Symbols: | Protein of unknown function (DUF1278) | chr5:21481514-21481879 FORWARD LENGTH=121	112	121	2.00E-42	108.0	75.0	83.0
Rsa1.0_00208.1.g8608.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00208.1.g8609.t1	gb|ABV89629.1| lipoic acid synthase-like protein [Brassica rapa]	154	155	3.00E-57	100.6	80.5	84.4	lipoic acid synthase-like protein	gbpln	Brassica rapa	AT5G23440.1 | Symbols: FTRA1 | ferredoxin/thioredoxin reductase subunit A (variable subunit) 1 | chr5:7903230-7903778 REVERSE LENGTH=182	154	182	8.00E-54	118.2	75.3	87.7
Rsa1.0_00208.1.g8610.t1	ref|XP_002874132.1| ATLCBK1 [Arabidopsis lyrata subsp. lyrata] gi|297319969|gb|EFH50391.1| ATLCBK1 [Arabidopsis lyrata subsp. lyrata]	743	763	0	102.7	89.1	94.5	ATLCBK1	gbpln	Arabidopsis lyrata	AT5G23450.2 | Symbols: ATLCBK1, LCBK1 | long-chain base (LCB) kinase 1 | chr5:7905041-7908960 REVERSE LENGTH=763	743	763	0	102.7	89.0	94.3
Rsa1.0_00208.1.g8611.t1	ref|XP_002872058.1| hypothetical protein ARALYDRAFT_351368 [Arabidopsis lyrata subsp. lyrata] gi|297317895|gb|EFH48317.1| hypothetical protein ARALYDRAFT_351368 [Arabidopsis lyrata subsp. lyrata]	511	604	1.00E-141	118.2	63.4	75.9	hypothetical protein ARALYDRAFT_351368	gbpln	Arabidopsis lyrata	AT5G23480.1 | Symbols: | SWIB/MDM2 domain;Plus-3;GYF | chr5:7916314-7919155 FORWARD LENGTH=570	511	570	1.00E-133	111.5	60.5	73.4
Rsa1.0_00208.1.g8612.t1	gb|EOA20507.1| hypothetical protein CARUB_v10000821mg [Capsella rubella]	528	490	0	92.8	78.2	84.7	hypothetical protein CARUB_v10000821mg	gbpln	Capsella rubella	AT5G23580.1 | Symbols: CDPK9, ATCDPK9, CPK12, ATCPK12 | calmodulin-like domain protein kinase 9 | chr5:7950388-7952433 REVERSE LENGTH=490	528	490	0	92.8	78.6	84.5

<table>
<tr><td>Rsa1.0_00208.1.g8613.t1</td><td>gb|EOA20507.1| hypothetical protein CARUB_v10000821mg [Capsella rubella]</td><td>502</td><td>490</td><td>0</td><td>97.6</td><td>77.5</td><td>86.3</td><td>hypothetical protein CARUB_v10000821mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G23580.1 | Symbols: CDPK9, ATCDPK9, CPK12, ATCPK12 | calmodulin-like domain protein kinase 9 | chr5:7950388-7952433 REVERSE LENGTH=490</td><td>502</td><td>490</td><td>0</td><td>97.6</td><td>75.3</td><td>83.7</td></tr>
<tr><td>Rsa1.0_00208.1.g8614.t1</td><td>gb|EOA20507.1| hypothetical protein CARUB_v10000821mg [Capsella rubella]</td><td>487</td><td>490</td><td>0</td><td>100.6</td><td>83.0</td><td>89.9</td><td>hypothetical protein CARUB_v10000821mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G23580.1 | Symbols: CDPK9, ATCDPK9, CPK12, ATCPK12 | calmodulin-like domain protein kinase 9 | chr5:7950388-7952433 REVERSE LENGTH=490</td><td>487</td><td>490</td><td>0</td><td>100.6</td><td>82.3</td><td>89.5</td></tr>
<tr><td>Rsa1.0_00208.1.g8615.t1</td><td>dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>1580</td><td>1491</td><td>0</td><td>94.4</td><td>55.6</td><td>69.9</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1580</td><td>1262</td><td>1.00E-136</td><td>79.9</td><td>14.8</td><td>21.5</td></tr>
<tr><td>Rsa1.0_00208.1.g8616.t1</td><td>gb|EOA33603.1| hypothetical protein CARUB_v10019755mg [Capsella rubella]</td><td>978</td><td>902</td><td>0</td><td>92.2</td><td>54.4</td><td>69.5</td><td>hypothetical protein CARUB_v10019755mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G58390.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:21690962-21693891 REVERSE LENGTH=907</td><td>978</td><td>907</td><td>0</td><td>92.7</td><td>50.7</td><td>66.0</td></tr>
<tr><td>Rsa1.0_00208.1.g8617.t1</td><td>ref|NP_001031931.2| uncharacterized protein [Arabidopsis thaliana] gi|332005808|gb|AED93191.1| uncharacterized protein AT5G23610 [Arabidopsis thaliana]</td><td>531</td><td>500</td><td>1.00E-117</td><td>94.2</td><td>46.9</td><td>61.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G23610.2 | Symbols: | INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: SWITCH1 (TAIR:AT5G51330.1); Has 173 Blast hits to 168 proteins in 34 species: Archae - 3; Bacteria - 10; Metazoa - 6; Fungi - 2; Plants - 115; Viruses - 0; Other Eukaryotes - 37 (source: NCBI BLink). | chr5:7957641-7959968 REVERSE LENGTH=500</td><td>531</td><td>500</td><td>1.00E-119</td><td>94.2</td><td>46.9</td><td>61.2</td></tr>
<tr><td>Rsa1.0_00208.1.g8618.t5</td><td>ref|XP_002872065.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317902|gb|EFH48324.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>455</td><td>327</td><td>5.00E-73</td><td>71.9</td><td>33.0</td><td>42.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23650.1 | Symbols: | Homeodomain-like transcriptional regulator | chr5:7969812-7971019 FORWARD LENGTH=337</td><td>455</td><td>337</td><td>3.00E-75</td><td>74.1</td><td>33.4</td><td>42.2</td></tr>
<tr><td>Rsa1.0_00208.1.g8619.t1</td><td>ref|NP_974827.1| Pectinacetylesterase family protein [Arabidopsis thaliana] gi|222423206|dbj|BAH19580.1| AT5G23870 [Arabidopsis thaliana] gi|332005843|gb|AED93226.1| Pectinacetylesterase family protein [Arabidopsis thaliana]</td><td>568</td><td>451</td><td>0</td><td>79.4</td><td>58.3</td><td>63.2</td><td>Pectinacetylesterase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G23870.3 | Symbols: | Pectinacetylesterase family protein | chr5:8046060-8049999 REVERSE LENGTH=451</td><td>568</td><td>451</td><td>0</td><td>79.4</td><td>58.3</td><td>63.2</td></tr>
<tr><td>Rsa1.0_00208.1.g8620.t1</td><td>gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]</td><td>375</td><td>1453</td><td>1.00E-108</td><td>387.5</td><td>50.4</td><td>58.7</td><td>polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240</td><td>375</td><td>240</td><td>1.00E-53</td><td>64.0</td><td>26.7</td><td>33.9</td></tr>
<tr><td>Rsa1.0_00208.1.g8621.t1</td><td>ref|XP_002870649.1| hypothetical protein ARALYDRAFT_355852 [Arabidopsis lyrata subsp. lyrata] gi|297316485|gb|EFH46908.1| hypothetical protein ARALYDRAFT_355852 [Arabidopsis lyrata subsp. lyrata]</td><td>706</td><td>634</td><td>1.00E-127</td><td>89.8</td><td>42.1</td><td>53.1</td><td>hypothetical protein ARALYDRAFT_355852</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G41690.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:16670126-16674189 REVERSE LENGTH=567</td><td>706</td><td>567</td><td>1.00E-112</td><td>80.3</td><td>38.2</td><td>49.9</td></tr>
<tr><td>Rsa1.0_00208.1.g8622.t1</td><td>ref|NP_197782.1| BAHD acyltransferase DCR [Arabidopsis thaliana] gi|75170176|sp|Q9FF86.1|DCR_ARATH RecName: Full=BAHD acyltransferase DCR; AltName: Full=Protein DEFECTIVE IN CUTICULAR RIDGES; AltName: Full=Protein PERMEABLE LEAVES 3 gi|10176861|dbj|BAB10067.1| acyltransferase [Arabidopsis thaliana] gi|22135843|gb|AAM91107.1| AT5g23940/MRO11_2 [Arabidopsis thaliana] gi|23397255|gb|AAN31909.1| putative acyltransferase [Arabidopsis thaliana] gi|24111347|gb|AAN46797.1| At5g23940/MRO11_2 [Arabidopsis thaliana] gi|332005853|gb|AED93236.1| BAHD acyltransferase DCR [Arabidopsis thaliana]</td><td>473</td><td>484</td><td>0</td><td>102.3</td><td>85.2</td><td>91.3</td><td>BAHD acyltransferase DCR</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G23940.1 | Symbols: EMB3009, PEL3, DCR | HXXXD-type acyl-transferase family protein | chr5:8076616-8079677 REVERSE LENGTH=484</td><td>473</td><td>484</td><td>0</td><td>102.3</td><td>85.2</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00208.1.g8623.t1</td><td>gb|EOA22500.1| hypothetical protein CARUB_v10003155mg, partial [Capsella rubella]</td><td>459</td><td>1112</td><td>0</td><td>242.3</td><td>83.9</td><td>91.7</td><td>hypothetical protein CARUB_v10003155mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G23980.1 | Symbols: ATFRO4, FRO4 | ferric reduction oxidase 4 | chr5:8098167-8101282 REVERSE LENGTH=699</td><td>459</td><td>699</td><td>0</td><td>152.3</td><td>84.1</td><td>91.1</td></tr>
<tr><td>Rsa1.0_00209.1.g8624.t1</td><td>gb|EOA27051.1| hypothetical protein CARUB_v10023147mg, partial [Capsella rubella]</td><td>432</td><td>467</td><td>0</td><td>108.1</td><td>78.2</td><td>87.3</td><td>hypothetical protein CARUB_v10023147mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G28590.1 | Symbols: | Protein kinase superfamily protein | chr2:12249835-12251490 FORWARD LENGTH=424</td><td>432</td><td>424</td><td>0</td><td>98.1</td><td>77.5</td><td>85.9</td></tr>
<tr><td>Rsa1.0_00209.1.g8625.t16</td><td>gb|AAC33958.1| contains similarity to Zea mays embryogenesis transmembrane protein (GB:X97570) [Arabidopsis thaliana]</td><td>488</td><td>417</td><td>1.00E-129</td><td>85.5</td><td>54.5</td><td>65.2</td><td>contains similarity to Zea mays embryogenesis transmembrane protein (GB:X97570)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G11000.1 | Symbols: | Ankyrin repeat family protein | chr4:6731020-6732464 FORWARD LENGTH=406</td><td>488</td><td>406</td><td>2.00E-98</td><td>83.2</td><td>44.9</td><td>57.2</td></tr>
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Rsa1.0_00209.1.g8626.t2	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	948	627	3.00E-66	66.1	20.6	33.5	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00209.1.g8627.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1303	2301	0	176.6	46.1	58.3	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1303	1262	3.00E-92	96.9	13.4	19.5
Rsa1.0_00209.1.g8628.t4	ref|XP_002879871.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325710|gb|EFH56130.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	233	582	1.00E-102	249.8	81.1	83.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G40460.1 | Symbols: | Major facilitator superfamily protein | chr2:16897123-16901171 FORWARD LENGTH=583	233	583	8.00E-95	250.2	79.0	83.3
Rsa1.0_00209.1.g8629.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	810	1024	2.00E-76	126.4	20.7	27.9	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00209.1.g8630.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	908	1311	1.00E-117	144.4	34.6	46.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	908	303	6.00E-28	33.4	10.5	16.2
Rsa1.0_00209.1.g8631.t1	gb|AAC62785.1| F11O4.11 [Arabidopsis thaliana] gi|7268192|emb|CAB77719.1| putative transposon protein [Arabidopsis thaliana]	557	577	7.00E-62	103.6	33.2	46.1	F11O4.11	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	557	361	2.00E-16	64.8	7.5	11.3
Rsa1.0_00209.1.g8632.t1	gb|EOA27812.1| hypothetical protein CARUB_v10023966mg [Capsella rubella]	240	237	5.00E-99	98.8	81.7	88.3	hypothetical protein CARUB_v10023966mg	gbpln	Capsella rubella	AT2G28605.1 | Symbols: | Photosystem II reaction center PsbP family protein | chr2:12254911-12255689 FORWARD LENGTH=232	240	232	9.00E-97	96.7	76.3	81.7
Rsa1.0_00209.1.g8633.t2	ref|NP_173321.4| Isochorismate synthase 2 [Arabidopsis thaliana] gi|205830866|sp|Q9M9V6.2|ICS2_ARATH RecName: Full=Isochorismate synthase 2, chloroplastic; Short=AtIcs2; AltName: Full=Isochorismate mutase 2; AltName: Full=menF-like protein 2; Flags: Precursor gi|183229349|gb|ACC60228.1| isochorismate synthase 2 [Arabidopsis thaliana] gi|332191652|gb|AEE29773.1| Isochorismate synthase 2 [Arabidopsis thaliana]	352	562	4.00E-61	159.7	35.5	42.3	Isochorismate synthase 2	gbpln	Arabidopsis thaliana	AT1G18870.1 | Symbols: ICS2, ATICS2 | isochorismate synthase 2 | chr1:6515486-6519176 FORWARD LENGTH=562	352	562	9.00E-64	159.7	35.5	42.3
Rsa1.0_00209.1.g8634.t1	ref|NP_175703.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|12324642|gb|AAG52278.1|AC019018_15 putative replication protein; 94555-97079 [Arabidopsis thaliana] gi|332194750|gb|AEE32871.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	507	566	1.00E-76	111.6	33.9	55.6	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	507	566	3.00E-79	111.6	33.9	55.6
Rsa1.0_00209.1.g8635.t1	gb|AAD32757.1| putative helicase [Arabidopsis thaliana]	1270	1241	0	97.7	26.8	35.8	putative helicase	gbpln	Arabidopsis thaliana	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	1270	344	4.00E-61	27.1	9.4	12.8
Rsa1.0_00209.1.g8636.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00209.1.g8637.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00209.1.g8638.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00209.1.g8639.t1	ref|XP_002879170.1| hypothetical protein ARALYDRAFT_481772 [Arabidopsis lyrata subsp. lyrata] gi|297325009|gb|EFH55429.1| hypothetical protein ARALYDRAFT_481772 [Arabidopsis lyrata subsp. lyrata]	194	242	1.00E-66	124.7	74.2	80.4	hypothetical protein ARALYDRAFT_481772	gbpln	Arabidopsis lyrata	AT2G28610.1 | Symbols: PRS, WOX3, PRS1 | Homeodomain-like superfamily protein | chr2:12262115-12263286 FORWARD LENGTH=244	194	244	5.00E-68	125.8	74.7	81.4
Rsa1.0_00209.1.g8640.t1	ref|XP_002892051.1| CYP86A4 [Arabidopsis lyrata subsp. lyrata] gi|297337893|gb|EFH68310.1| CYP86A4 [Arabidopsis lyrata subsp. lyrata]	59	554	3.00E-17	939.0	71.2	79.7	CYP86A4	gbpln	Arabidopsis lyrata	AT1G01600.1 | Symbols: CYP86A4 | cytochrome P450, family 86, subfamily A, polypeptide 4 | chr1:219200-220994 FORWARD LENGTH=554	59	554	1.00E-19	939.0	71.2	79.7
Rsa1.0_00209.1.g8641.t2	gb|AAC95170.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	269	916	7.00E-11	340.5	13.0	20.4	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00210.1.g8642.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00210.1.g8643.t1	ref|NP_199276.1| alpha-barbatene synthase [Arabidopsis thaliana] gi|254810224|sp|Q4KSH9.2|BARS_ARATH RecName: Full=Alpha-barbatene synthase; Short=AtBS; AltName: Full=Beta-chamigrene synthase; AltName: Full=Terpendeoid synthase 11; Short=AtTPS11; AltName: Full=Thujopsene synthase gi|126352284|gb|ABO09887.1| At5g44630 [Arabidopsis thaliana] gi|332007757|gb|AED95140.1| alpha-barbatene synthase [Arabidopsis thaliana]	499	557	0	111.6	70.9	81.6	alpha-barbatene synthase	gbpln	Arabidopsis thaliana	AT5G44630.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr5:18003280-18005616 FORWARD LENGTH=557	499	557	0	111.6	70.9	81.6
Rsa1.0_00210.1.g8644.t1	gb|ABA96113.2| retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa Japonica Group]	526	676	1.00E-122	128.5	47.5	62.2	retrotransposon protein, putative, Ty1-copia subclass	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	526	1262	2.00E-19	239.9	9.9	13.7
Rsa1.0_00210.1.g8645.t1	ref|NP_199276.1| alpha-barbatene synthase [Arabidopsis thaliana] gi|254810224|sp|Q4KSH9.2|BARS_ARATH RecName: Full=Alpha-barbatene synthase; Short=AtBS; AltName: Full=Beta-chamigrene synthase; AltName: Full=Terpendeoid synthase 11; Short=AtTPS11; AltName: Full=Thujopsene synthase gi|126352284|gb|ABO09887.1| At5g44630 [Arabidopsis thaliana] gi|332007757|gb|AED95140.1| alpha-barbatene synthase [Arabidopsis thaliana]	502	557	0	111.0	70.5	82.3	alpha-barbatene synthase	gbpln	Arabidopsis thaliana	AT5G44630.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr5:18003280-18005616 FORWARD LENGTH=557	502	557	0	111.0	70.5	82.3
Rsa1.0_00210.1.g8646.t1	ref|NP_199275.1| cytochrome P450, family 706, subfamily A, polypeptide 3 [Arabidopsis thaliana] gi|8953760|dbj|BAA98115.1| flavonoid 3',5'-hydroxylase-like; cytochrome P450 [Arabidopsis thaliana] gi|332007756|gb|AED95139.1| cytochrome P450, family 706, subfamily A, polypeptide 3 [Arabidopsis thaliana]	518	519	0	100.2	77.2	89.2	cytochrome P450, family 706, subfamily A, polypeptide 3	gbpln	Arabidopsis thaliana	AT5G44620.1 | Symbols: CYP706A3 | cytochrome P450, family 706, subfamily A, polypeptide 3 | chr5:17997908-17999539 REVERSE LENGTH=519	518	519	0	100.2	77.2	89.2
Rsa1.0_00210.1.g8647.t1	ref|XP_002863555.1| minichromosome maintenance family protein [Arabidopsis lyrata subsp. lyrata] gi|297309390|gb|EFH39814.1| minichromosome maintenance family protein [Arabidopsis lyrata subsp. lyrata]	830	830	0	100.0	97.0	98.3	minichromosome maintenance family protein	gbpln	Arabidopsis lyrata	AT5G44635.1 | Symbols: MCM6 | minichromosome maintenance (MCM2/3/5) family protein | chr5:18006431-18010542 REVERSE LENGTH=831	830	831	0	100.1	96.5	98.6
Rsa1.0_00210.1.g8648.t3	gb|EOA14938.1| hypothetical protein CARUB_v10028282mg [Capsella rubella]	352	284	3.00E-58	80.7	37.2	44.6	hypothetical protein CARUB_v10028282mg	gbpln	Capsella rubella	AT5G44650.1 | Symbols: CEST, AtCEST | Encodes a chloroplast protein that induces tolerance to multiple environmental stresses and reduces photooxidative damage. | chr5:18013396-18015292 FORWARD LENGTH=280	352	280	1.00E-59	79.5	36.9	44.9
Rsa1.0_00210.1.g8649.t1	gb|EOA14735.1| hypothetical protein CARUB_v10028028mg [Capsella rubella]	357	360	1.00E-151	100.8	82.6	91.6	hypothetical protein CARUB_v10028028mg	gbpln	Capsella rubella	AT5G44660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G20190.1); Has 944 Blast hits to 462 proteins in 141 species: Archae - 2; Bacteria - 370; Metazoa - 161; Fungi - 102; Plants - 64; Viruses - 6; Other Eukaryotes - 239 (source: NCBI BLink). | chr5:18015810-18017081 FORWARD LENGTH=423	357	423	1.00E-141	118.5	81.2	89.6
Rsa1.0_00210.1.g8650.t1	ref|NP_199280.1| uncharacterized protein [Arabidopsis thaliana] gi|13605503|gb|AAK32745.1|AF361577_1 AT5g44670/K15C23_12 [Arabidopsis thaliana] gi|8953765|dbj|BAA98120.1| unnamed protein product [Arabidopsis thaliana] gi|25090160|gb|AAN72243.1| At5g44670/K15C23_12 [Arabidopsis thaliana] gi|332007762|gb|AED95145.1| uncharacterized protein AT5G44670 [Arabidopsis thaliana]	543	519	0	95.6	80.5	87.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G44670.1 | Symbols: | Domain of unknown function (DUF23) | chr5:18019209-18021266 REVERSE LENGTH=519	543	519	0	95.6	80.5	87.8
Rsa1.0_00210.1.g8651.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	297	1142	4.00E-43	384.5	40.1	54.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00210.1.g8652.t2	gb|AAF69161.1|AC007915_13 F27F5.19 [Arabidopsis thaliana]	1284	1309	0	101.9	43.8	59.5	F27F5.19	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1284	1262	1.00E-161	98.3	21.7	28.0

Rsa1.0_00210.1.g8653.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00210.1.g8654.t1	ref|NP_565299.1| putative DNA-binding protein [Arabidopsis thaliana] gi|15027927|gb|AAK76494.1| putative helicase [Arabidopsis thaliana] gi|20197343|gb|AAM15033.1| putative helicase [Arabidopsis thaliana] gi|20197741|gb|AAD17447.2| putative helicase [Arabidopsis thaliana] gi|20259169|gb|AAM14300.1| putative helicase [Arabidopsis thaliana] gi|330250587|gb|AEC05681.1| putative DNA-binding protein [Arabidopsis thaliana]	81	639	7.00E-17	788.9	56.8	60.5	putative DNA-binding protein	gbpln	Arabidopsis thaliana	AT2G03270.1 | Symbols: | DNA-binding protein, putative | chr2:994071-995990 FORWARD LENGTH=639	81	639	1.00E-19	788.9	56.8	60.5
Rsa1.0_00210.1.g8655.t1	ref|NP_178819.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|3327395|gb|AAC26677.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana] gi|330251037|gb|AEC06131.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	448	530	3.00E-41	118.3	17.0	21.4	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	448	530	8.00E-44	118.3	17.0	21.4
Rsa1.0_00210.1.g8656.t2	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	497	1864	1.00E-83	375.1	39.2	52.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00210.1.g8657.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	647	1365	1.00E-141	211.0	43.1	60.1	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	647	575	5.00E-79	88.9	26.9	43.0
Rsa1.0_00210.1.g8658.t1	ref|NP_197284.1| peroxidase 57 [Arabidopsis thaliana] gi|26397647|sp|Q43729.1|PER57_ARATH RecName: Full=Peroxidase 57; Short=Atperox P57; AltName: Full=ATP13a; AltName: Full=PRXR10; Flags: Precursor gi|1402900|emb|CAA66966.1| peroxidase [Arabidopsis thaliana] gi|1429219|emb|CAA67312.1| peroxidase ATP13a [Arabidopsis thaliana] gi|9759059|dbj|BAB09581.1| peroxidase [Arabidopsis thaliana] gi|31745133|gb|AAO22769.2| putative peroxidase [Arabidopsis thaliana] gi|42494609|gb|AAS17635.1| peroxidase ATP13A [Arabidopsis thaliana] gi|332005091|gb|AED92474.1| peroxidase 57 [Arabidopsis thaliana]	317	313	1.00E-113	98.7	64.7	76.7	peroxidase 57	gbpln	Arabidopsis thaliana	AT5G17820.1 | Symbols: | Peroxidase superfamily protein | chr5:5888195-5890101 REVERSE LENGTH=313	317	313	1.00E-116	98.7	64.7	76.7
Rsa1.0_00211.1.g8659.t1	ref|XP_002866894.1| hypothetical protein ARALYDRAFT_912482 [Arabidopsis lyrata subsp. lyrata] gi|297312730|gb|EFH43153.1| hypothetical protein ARALYDRAFT_912482 [Arabidopsis lyrata subsp. lyrata]	336	350	1.00E-126	104.2	74.1	85.4	hypothetical protein ARALYDRAFT_912482	gbpln	Arabidopsis lyrata	AT4G39920.1 | Symbols: POR, TFC C | C-CAP/cofactor C-like domain-containing protein | chr4:18515882-18516919 FORWARD LENGTH=345	336	345	1.00E-128	102.7	74.7	84.2
Rsa1.0_00211.1.g8660.t1	dbj|BAJ34631.1| unnamed protein product [Thellungiella halophila]	214	213	1.00E-107	99.5	95.8	98.6	unnamed protein product	----	----	AT4G39890.1 | Symbols: AtRABH1c, RABH1c | RAB GTPase homolog H1C | chr4:18506112-18507459 FORWARD LENGTH=214	214	214	1.00E-103	100.0	90.2	94.9
Rsa1.0_00211.1.g8661.t1	gb|AAM63197.1| unknown [Arabidopsis thaliana]	178	178	4.00E-83	100.0	87.6	94.4	unknown	gbpln	Arabidopsis thaliana	AT4G39880.1 | Symbols: | Ribosomal protein L23/L15e family protein | chr4:18504601-18505137 FORWARD LENGTH=178	178	178	3.00E-78	100.0	87.6	93.8
Rsa1.0_00211.1.g8662.t1	gb|EOA16799.1| hypothetical protein CARUB_v10005018mg [Capsella rubella]	397	387	1.00E-157	97.5	78.1	85.4	hypothetical protein CARUB_v10005018mg	gbpln	Capsella rubella	AT4G39870.2 | Symbols: | TLD-domain containing nucleolar protein | chr4:18502234-18504275 FORWARD LENGTH=394	397	394	1.00E-156	99.2	78.3	86.1
Rsa1.0_00211.1.g8663.t1	ref|XP_002866889.1| hypothetical protein ARALYDRAFT_912474 [Arabidopsis lyrata subsp. lyrata] gi|297312725|gb|EFH43148.1| hypothetical protein ARALYDRAFT_912474 [Arabidopsis lyrata subsp. lyrata]	303	297	1.00E-140	98.0	86.1	90.4	hypothetical protein ARALYDRAFT_912474	gbpln	Arabidopsis lyrata	AT4G39860.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G22270.1); Has 152 Blast hits to 146 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 146; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:18499909-18501472 FORWARD LENGTH=299	303	299	1.00E-136	98.7	86.1	89.8
Rsa1.0_00211.1.g8664.t1	dbj|BAB02797.1| unnamed protein product [Arabidopsis thaliana]	302	345	2.00E-32	114.2	29.1	42.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G13280.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:4295327-4297000 REVERSE LENGTH=383	302	383	2.00E-18	126.8	18.5	28.1

Rsa1.0_00211.1.g8665.t1	ref|XP_002866888.1| peroxisomal abc transporter [Arabidopsis lyrata subsp. lyrata] gi|297312724|gb|EFH43147.1| peroxisomal abc transporter [Arabidopsis lyrata subsp. lyrata]	1339	1337	0	99.9	93.2	96.3	peroxisomal abc transporter	gbpln	Arabidopsis lyrata	AT4G39850.2 | Symbols: PXA1 | peroxisomal ABC transporter 1 | chr4:18489220-18496762 FORWARD LENGTH=1338	1339	1338	0	99.9	92.9	95.9
Rsa1.0_00211.1.g8666.t1	ref|NP_195693.1| putative L-ascorbate oxidase [Arabidopsis thaliana] gi|3080452|emb|CAA18769.1| putative L-ascorbate oxidase [Arabidopsis thaliana] gi|7271038|emb|CAB80646.1| putative L-ascorbate oxidase [Arabidopsis thaliana] gi|51536490|gb|AAU05483.1| At4g39830 [Arabidopsis thaliana] gi|53850489|gb|AAU95421.1| At4g39830 [Arabidopsis thaliana] gi|332661724|gb|AEE87124.1| putative L-ascorbate oxidase [Arabidopsis thaliana]	581	582	0	100.2	85.7	91.6	putative L-ascorbate oxidase	gbpln	Arabidopsis thaliana	AT4G39830.1 | Symbols: | Cupredoxin superfamily protein | chr4:18479103-18481184 FORWARD LENGTH=582	581	582	0	100.2	85.7	91.6
Rsa1.0_00211.1.g8667.t1	gb|EOA17274.1| hypothetical protein CARUB_v10005547mg [Capsella rubella]	255	256	1.00E-131	100.4	91.8	96.9	hypothetical protein CARUB_v10005547mg	gbpln	Capsella rubella	AT4G39810.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:18474608-18475735 REVERSE LENGTH=255	255	255	1.00E-132	100.0	89.4	95.7
Rsa1.0_00211.1.g8668.t2	ref|XP_002866884.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312720|gb|EFH43143.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	121	132	2.00E-48	109.1	81.8	84.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G39795.1 | Symbols: | Protein of unknown function (DUF581) | chr4:18466621-18467325 FORWARD LENGTH=126	121	126	4.00E-45	104.1	73.6	80.2
Rsa1.0_00211.1.g8669.t6	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	503	1142	9.00E-89	227.0	31.8	40.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	503	575	6.00E-30	114.3	11.1	17.3
Rsa1.0_00211.1.g8670.t1	ref|NP_195651.1| putative WRKY transcription factor 13 [Arabidopsis thaliana] gi|29839686|sp|Q9SVB7.1|WRK13_ARATH RecName: Full=Probable WRKY transcription factor 13; AltName: Full=WRKY DNA-binding protein 13 gi|15991730|gb|AAL13042.1|AF421153_1 WRKY transcription factor 13 [Arabidopsis thaliana] gi|5042157|emb|CAB44676.1| putative WRKY DNA-binding protein [Arabidopsis thaliana] gi|7270925|emb|CAB80604.1| putative WRKY DNA-binding protein [Arabidopsis thaliana] gi|225898873|dbj|BAH30567.1| hypothetical protein [Arabidopsis thaliana] gi|332661671|gb|AEE87071.1| putative WRKY transcription factor 13 [Arabidopsis thaliana]	233	304	4.00E-75	130.5	72.1	78.1	putative WRKY transcription factor 13	gbpln	Arabidopsis thaliana	AT4G39410.1 | Symbols: WRKY13, ATWRKY13 | WRKY DNA-binding protein 13 | chr4:18332937-18334789 REVERSE LENGTH=304	233	304	1.00E-77	130.5	72.1	78.1
Rsa1.0_00211.1.g8671.t1	ref|NP_195644.1| uncharacterized protein [Arabidopsis thaliana] gi|75213705|sp|Q9T039.1|EC14_ARATH RecName: Full=Egg cell-secreted protein 1.4; Flags: Precursor gi|4914446|emb|CAB43649.1| hypothetical protein [Arabidopsis thaliana] gi|7270918|emb|CAB80597.1| hypothetical protein [Arabidopsis thaliana] gi|91805627|gb|ABE65542.1| hypothetical protein At4g39340 [Arabidopsis thaliana] gi|332661658|gb|AEE87058.1| uncharacterized protein AT4G39340 [Arabidopsis thaliana]	127	127	1.00E-52	100.0	83.5	90.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G39340.1 | Symbols: | Protein of unknown function (DUF1278) | chr4:18293129-18293512 REVERSE LENGTH=127	127	127	2.00E-55	100.0	83.5	90.6
Rsa1.0_00211.1.g8672.t1	gb|EOA16882.1| hypothetical protein CARUB_v10005116mg [Capsella rubella]	360	360	0	100.0	91.4	97.8	hypothetical protein CARUB_v10005116mg	gbpln	Capsella rubella	AT4G39330.1 | Symbols: ATCAD9, CAD9 | cinnamyl alcohol dehydrogenase 9 | chr4:18291268-18292772 FORWARD LENGTH=360	360	360	0	100.0	90.8	97.2
Rsa1.0_00211.1.g8673.t1	ref|XP_002866840.1| hypothetical protein ARALYDRAFT_912391 [Arabidopsis lyrata subsp. lyrata] gi|297312676|gb|EFH43099.1| hypothetical protein ARALYDRAFT_912391 [Arabidopsis lyrata subsp. lyrata]	135	173	2.00E-36	128.1	73.3	80.0	hypothetical protein ARALYDRAFT_912391	gbpln	Arabidopsis lyrata	AT4G39320.1 | Symbols: | microtubule-associated protein-related | chr4:18289102-18289702 FORWARD LENGTH=166	135	166	1.00E-34	123.0	70.4	76.3

<table>
<tr><td>Rsa1.0_00211.1.g8674.t1</td><td>ref|XP_002866838.1| hypothetical protein ARALYDRAFT_490704 [Arabidopsis lyrata subsp. lyrata] gi|297312674|gb|EFH43097.1| hypothetical protein ARALYDRAFT_490704 [Arabidopsis lyrata subsp. lyrata]</td><td>960</td><td>864</td><td>0</td><td>90.0</td><td>73.8</td><td>80.1</td><td>hypothetical protein ARALYDRAFT_490704</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G39270.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:18276874-18279710 FORWARD LENGTH=864</td><td>960</td><td>864</td><td>0</td><td>90.0</td><td>71.7</td><td>78.3</td></tr>
<tr><td>Rsa1.0_00211.1.g8675.t1</td><td>ref|NP_195635.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75213699|sp|Q9T031.1|FBK96_ARATH RecName: Full=F-box/kelch-repeat protein At4g39240 gi|13877533|gb|AAK43844.1|AF370467_1 putative protein [Arabidopsis thaliana] gi|4914436|emb|CAB43639.1| putative protein [Arabidopsis thaliana] gi|7270907|emb|CAB80587.1| putative protein [Arabidopsis thaliana] gi|22136486|gb|AAM91321.1| putative protein [Arabidopsis thaliana] gi|332661642|gb|AEE87042.1| F-box/kelch-repeat protein [Arabidopsis thaliana]</td><td>359</td><td>375</td><td>1.00E-114</td><td>104.5</td><td>59.3</td><td>72.7</td><td>F-box/kelch-repeat protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G39240.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18269599-18270726 REVERSE LENGTH=375</td><td>359</td><td>375</td><td>1.00E-117</td><td>104.5</td><td>59.3</td><td>72.7</td></tr>
<tr><td>Rsa1.0_00211.1.g8676.t1</td><td>ref|NP_195635.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75213699|sp|Q9T031.1|FBK96_ARATH RecName: Full=F-box/kelch-repeat protein At4g39240 gi|13877533|gb|AAK43844.1|AF370467_1 putative protein [Arabidopsis thaliana] gi|4914436|emb|CAB43639.1| putative protein [Arabidopsis thaliana] gi|7270907|emb|CAB80587.1| putative protein [Arabidopsis thaliana] gi|22136486|gb|AAM91321.1| putative protein [Arabidopsis thaliana] gi|332661642|gb|AEE87042.1| F-box/kelch-repeat protein [Arabidopsis thaliana]</td><td>380</td><td>375</td><td>1.00E-125</td><td>98.7</td><td>60.3</td><td>75.0</td><td>F-box/kelch-repeat protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G39240.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18269599-18270726 REVERSE LENGTH=375</td><td>380</td><td>375</td><td>1.00E-128</td><td>98.7</td><td>60.3</td><td>75.0</td></tr>
<tr><td>Rsa1.0_00211.1.g8677.t1</td><td>ref|XP_002866837.1| hypothetical protein ARALYDRAFT_490696 [Arabidopsis lyrata subsp. lyrata] gi|297312673|gb|EFH43096.1| hypothetical protein ARALYDRAFT_490696 [Arabidopsis lyrata subsp. lyrata]</td><td>115</td><td>89</td><td>1.00E-31</td><td>77.4</td><td>67.8</td><td>73.0</td><td>hypothetical protein ARALYDRAFT_490696</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G39235.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G05570.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:18268514-18269034 FORWARD LENGTH=86</td><td>115</td><td>86</td><td>3.00E-32</td><td>74.8</td><td>65.2</td><td>69.6</td></tr>
<tr><td>Rsa1.0_00211.1.g8678.t1</td><td>ref|NP_195633.1| protein RER1A [Arabidopsis thaliana] gi|6225938|sp|O48670.1|RER1A_ARATH RecName: Full=Protein RER1A; Short=AtRER1A gi|2865175|dbj|BAA24803.1| AtRer1A [Arabidopsis thaliana] gi|4914434|emb|CAB43637.1| AtRer1A [Arabidopsis thaliana] gi|7270905|emb|CAB80585.1| AtRer1A [Arabidopsis thaliana] gi|14994255|gb|AAK73262.1| AtRer1A [Arabidopsis thaliana] gi|21554242|gb|AAM63317.1| AtRer1A [Arabidopsis thaliana] gi|24030322|gb|AAN41329.1| putative AtRer1A protein [Arabidopsis thaliana] gi|332661639|gb|AEE87039.1| protein RER1A [Arabidopsis thaliana</td><td>191</td><td>191</td><td>3.00E-94</td><td>100.0</td><td>91.1</td><td>94.2</td><td>protein RER1A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G39220.1 | Symbols: ATRER1A | Rer1 family protein | chr4:18264280-18265531 FORWARD LENGTH=191</td><td>191</td><td>191</td><td>1.00E-96</td><td>100.0</td><td>91.1</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00211.1.g8679.t1</td><td>dbj|BAJ34261.1| unnamed protein product [Thellungiella halophila]</td><td>523</td><td>521</td><td>0</td><td>99.6</td><td>92.0</td><td>95.0</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G39210.1 | Symbols: APL3 | Glucose-1-phosphate adenylyltransferase family protein | chr4:18260332-18263181 FORWARD LENGTH=521</td><td>523</td><td>521</td><td>0</td><td>99.6</td><td>90.1</td><td>94.8</td></tr>
</table>

Rsa1.0_00211.1.g8680.t1	ref|NP_195631.1| 40S ribosomal protein S25-4 [Arabidopsis thaliana] gi|30580493|sp|Q9T029.1|RS254_ARATH RecName: Full=40S ribosomal protein S25-4 gi|4914432|emb|CAB43635.1| ribosomal protein S25 [Arabidopsis thaliana] gi|7270903|emb|CAB80583.1| ribosomal protein S25 [Arabidopsis thaliana] gi|14335026|gb|AAK59777.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gi|16323232|gb|AAL15350.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gi|21553704|gb|AAM62797.1| ribosomal protein S25 [Arabidopsis thaliana] gi|332661636|gb|AEE87036.1| 40S ribosomal protein S25-4 [Arabidopsis thaliana] gi|482553510|gb|EOA17703.1| hypothetical protein CARUB_v10006075mg [Capsella rubella]	108	108	1.00E-55	100.0	100.0	100.0	40S ribosomal protein S25-4	gbpln	Arabidopsis thaliana	AT4G39200.1 | Symbols: | Ribosomal protein S25 family protein | chr4:18257464-18258464 FORWARD LENGTH=108	108	108	2.00E-58	100.0	100.0	100.0
Rsa1.0_00211.1.g8681.t1	ref|NP_195630.1| uncharacterized protein [Arabidopsis thaliana] gi|4914431|emb|CAB43634.1| hypothetical protein [Arabidopsis thaliana] gi|7270902|emb|CAB80582.1| hypothetical protein [Arabidopsis thaliana] gi|52354433|gb|AAU44537.1| hypothetical protein AT4G39190 [Arabidopsis thaliana] gi|332661635|gb|AEE87035.1| uncharacterized protein AT4G39190 [Arabidopsis thaliana]	275	277	1.00E-93	100.7	70.5	82.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G39190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G21560.1); Has 5536 Blast hits to 3562 proteins in 401 species: Archae - 12; Bacteria - 497; Metazoa - 1363; Fungi - 374; Plants - 149; Viruses - 22; Other Eukaryotes - 3119 (source: NCBI BLink). | chr4:18252032-18252865 REVERSE LENGTH=277	275	277	4.00E-96	100.7	70.5	82.9
Rsa1.0_00211.1.g8682.t2	gb|EOA18818.1| hypothetical protein CARUB_v10007432mg [Capsella rubella]	519	556	0	107.1	71.3	80.3	hypothetical protein CARUB_v10007432mg	gbpln	Capsella rubella	AT4G39180.1 | Symbols: SEC14, ATSEC14 | Sec14p-like phosphatidylinositol transfer family protein | chr4:18244006-18246673 REVERSE LENGTH=554	519	554	0	106.7	70.9	79.8
Rsa1.0_00211.1.g8683.t1	ref|XP_002866831.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297312667|gb|EFH43090.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	537	600	1.00E-151	111.7	66.1	76.9	DNA binding protein	gbpln	Arabidopsis lyrata	AT4G39160.1 | Symbols: | Homeodomain-like superfamily protein | chr4:18236828-18239744 FORWARD LENGTH=601	537	601	1.00E-147	111.9	63.9	74.9
Rsa1.0_00211.1.g8684.t1	ref|NP_195625.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|30692196|ref|NP_849522.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|42573229|ref|NP_974711.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|42573231|ref|NP_974712.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|145334267|ref|NP_001078514.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|4914426|emb|CAB43629.1| putative protein [Arabidopsis thaliana] gi|7270897|emb|CAB80577.1| putative protein [Arabidopsis thaliana] gi|17065052|gb|AAL32680.1| putative protein [Arabidopsis thaliana] gi|22136224|gb|AAM91190.1| putative protein [Arabidopsis thaliana] gi|66865958|gb|AAY57613.1| RING finger family protein [Arabidopsis thaliana] gi|332661622|gb|AEE87022.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332661623|gb|AEE87023.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332661624|gb|AEE87024.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332661625|gb|AEE87025.1| RING/U-	313	429	1.00E-127	137.1	80.2	87.2	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT4G39140.5 | Symbols: | RING/U-box superfamily protein | chr4:18229637-18231282 REVERSE LENGTH=429	313	429	1.00E-129	137.1	80.2	87.2
Rsa1.0_00211.1.g8685.t1	ref|XP_002868886.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314722|gb|EFH45145.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	854	882	0	103.3	91.2	94.4	kinase family protein	gbpln	Arabidopsis lyrata	AT4G39110.1 | Symbols: | Malectin/receptor-like protein kinase family protein | chr4:18222483-18225119 REVERSE LENGTH=878	854	878	0	102.8	91.0	93.9

Rsa1.0_00211.1.g8686.t1	ref|NP_195616.2| Kinesin motor family protein [Arabidopsis thaliana] gi|16902294|dbj|BAB71852.1| kinesin-related protein [Arabidopsis thaliana] gi|23297817|gb|AAN13032.1| putative kinesin protein [Arabidopsis thaliana] gi|332661612|gb|AEE87012.1| Kinesin motor family protein [Arabidopsis thaliana]	1056	1055	0	99.9	88.6	92.9	Kinesin motor family protein	gbpln	Arabidopsis thaliana	AT4G39050.1 | Symbols: | Kinesin motor family protein | chr4:18193462-18200148 FORWARD LENGTH=1055	1056	1055	0	99.9	88.6	92.9
Rsa1.0_00211.1.g8687.t1	ref|NP_195615.1| putative RNA-binding protein containing KH domain protein [Arabidopsis thaliana] gi|4539323|emb|CAB38824.1| putative protein [Arabidopsis thaliana] gi|7270887|emb|CAB80567.1| putative protein [Arabidopsis thaliana] gi|26452052|dbj|BAC43116.1| unknown protein [Arabidopsis thaliana] gi|28950859|gb|AAO63353.1| At4g39040 [Arabidopsis thaliana] gi|332661610|gb|AEE87010.1| putative RNA-binding protein containing KH domain [Arabidopsis thaliana]	286	296	6.00E-85	103.5	69.9	78.7	putative RNA-binding protein containing KH domain protein	gbpln	Arabidopsis thaliana	AT4G39040.1 | Symbols: | RNA-binding CRS1 / YhbY (CRM) domain protein | chr4:18189249-18190535 REVERSE LENGTH=296	286	296	2.00E-87	103.5	69.9	78.7
Rsa1.0_00211.1.g8688.t1	ref|XP_002887270.1| hypothetical protein ARALYDRAFT_894796 [Arabidopsis lyrata subsp. lyrata] gi|297333111|gb|EFH63529.1| hypothetical protein ARALYDRAFT_894796 [Arabidopsis lyrata subsp. lyrata]	345	177	7.00E-21	51.3	15.7	18.3	hypothetical protein ARALYDRAFT_894796	gbpln	Arabidopsis lyrata	AT1G70040.1 | Symbols: | Protein of unknown function (DUF1163) | chr1:26381233-26381908 FORWARD LENGTH=193	345	193	5.00E-22	55.9	14.8	17.7
Rsa1.0_00211.1.g8689.t1	ref|XP_002868879.1| hypothetical protein ARALYDRAFT_912358 [Arabidopsis lyrata subsp. lyrata] gi|297314715|gb|EFH45138.1| hypothetical protein ARALYDRAFT_912358 [Arabidopsis lyrata subsp. lyrata]	466	509	0	109.2	91.4	95.5	hypothetical protein ARALYDRAFT_912358	gbpln	Arabidopsis lyrata	AT4G36220.1 | Symbols: FAH1, CYP84A1 | ferulic acid 5-hydroxylase 1 | chr4:17137584-17139619 REVERSE LENGTH=520	466	520	0	111.6	63.5	81.8
Rsa1.0_00211.1.g8690.t1	ref|XP_004148537.1| PREDICTED: DNA-binding protein HEXBP-like [Cucumis sativus] gi|449519884|ref|XP_004166964.1| PREDICTED: DNA-binding protein HEXBP-like [Cucumis sativus]	246	260	6.00E-93	105.7	70.3	81.3	PREDICTED: DNA-binding protein HEXBP-like	gbpln	Cucumis sativus	AT1G75560.2 | Symbols: | zinc knuckle (CCHC-type) family protein | chr1:28371420-28372717 REVERSE LENGTH=257	246	257	4.00E-68	104.5	53.3	68.7
Rsa1.0_00211.1.g8691.t1	ref|XP_002868877.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata] gi|297314713|gb|EFH45136.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata]	491	491	0	100.0	82.3	89.6	glycosyl hydrolase family 9 protein	gbpln	Arabidopsis lyrata	AT4G39000.1 | Symbols: AtGH9B17, GH9B17 | glycosyl hydrolase 9B17 | chr4:18171722-18173797 REVERSE LENGTH=493	491	493	0	100.4	80.7	90.2
Rsa1.0_00211.1.g8692.t1	ref|XP_002868874.1| hypothetical protein ARALYDRAFT_490667 [Arabidopsis lyrata subsp. lyrata] gi|297314710|gb|EFH45133.1| hypothetical protein ARALYDRAFT_490667 [Arabidopsis lyrata subsp. lyrata]	393	393	0	100.0	96.7	99.0	hypothetical protein ARALYDRAFT_490667	gbpln	Arabidopsis lyrata	AT4G38970.1 | Symbols: FBA2 | fructose-bisphosphate aldolase 2 | chr4:18163714-18165659 REVERSE LENGTH=398	393	398	0	101.3	97.2	99.2
Rsa1.0_00211.1.g8693.t1	gb|EOA17498.1| hypothetical protein CARUB_v10005832mg [Capsella rubella]	180	183	1.00E-91	101.7	92.2	96.1	hypothetical protein CARUB_v10005832mg	gbpln	Capsella rubella	AT4G38960.1 | Symbols: | B-box type zinc finger family protein | chr4:18161576-18163045 FORWARD LENGTH=183	180	183	3.00E-93	101.7	91.7	95.0
Rsa1.0_00211.1.g8694.t1	ref|XP_002868873.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] gi|297314709|gb|EFH45132.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	595	836	1.00E-106	140.5	35.8	42.2	kinesin motor family protein	gbpln	Arabidopsis lyrata	AT4G38950.2 | Symbols: | ATP binding microtubule motor family protein | chr4:18154606-18158461 REVERSE LENGTH=836	595	836	1.00E-108	140.5	35.6	41.8
Rsa1.0_00211.1.g8695.t1	ref|XP_002866825.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297312661|gb|EFH43084.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	366	368	1.00E-156	100.5	76.2	83.9	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	366	370	1.00E-151	101.1	73.0	81.4
Rsa1.0_00211.1.g8696.t1	ref|XP_002313006.1| predicted protein [Populus trichocarpa] gi|222849414|gb|EEE86961.1| predicted protein [Populus trichocarpa]	164	207	6.00E-85	126.2	100.0	100.0	predicted protein	gbpln	Populus trichocarpa	AT4G34720.1 | Symbols: AVA-P1, VHA-C1, ATVHA-C1 | ATPase, F0/V0 complex, subunit C protein | chr4:16568223-16569165 REVERSE LENGTH=164	164	164	4.00E-87	100.0	100.0	100.0
Rsa1.0_00211.1.g8697.t1	gb|ABU63288.1| GAGA-motif binding transcriptional activator, partial [Cardamine pratensis]	269	275	1.00E-127	102.2	82.2	91.4	GAGA-motif binding transcriptional activator, partial	gbpln	Cardamine pratensis	AT4G38910.2 | Symbols: BPC5 | basic pentacysteine 5 | chr4:18145478-18146429 REVERSE LENGTH=283	269	283	1.00E-120	105.2	78.4	88.5

Rsa1.0_00211.1.g8698.t1	ref|NP_849520.1| basic leucine zipper transcription factor-like protein [Arabidopsis thaliana] gi|79326483|ref|NP_001031810.1| basic leucine zipper transcription factor-like protein [Arabidopsis thaliana] gi|23297471|gb|AAN12977.1| unknown protein [Arabidopsis thaliana] gi|332661589|gb|AEE86989.1| basic leucine zipper transcription factor-like protein [Arabidopsis thaliana] gi|332661590|gb|AEE86990.1| basic leucine zipper transcription factor-like protein [Arabidopsis thaliana]	492	547	1.00E-170	111.2	75.2	84.1	basic leucine zipper transcription factor-like protein	gbpln	Arabidopsis thaliana	AT4G38900.3 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:18139564-18141520 REVERSE LENGTH=547	492	547	1.00E-173	111.2	75.2	84.1
Rsa1.0_00211.1.g8699.t1	gb|EOA15659.1| hypothetical protein CARUB_v10006088mg [Capsella rubella]	104	105	4.00E-51	101.0	96.2	99.0	hypothetical protein CARUB_v10006088mg	gbpln	Capsella rubella	AT4G38860.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:18130357-18130674 FORWARD LENGTH=105	104	105	4.00E-53	101.0	95.2	98.1
Rsa1.0_00212.1.g8700.t1	gb|EOA34319.1| hypothetical protein CARUB_v10021839mg [Capsella rubella]	585	901	0	154.0	63.6	75.0	hypothetical protein CARUB_v10021839mg	gbpln	Capsella rubella	AT1G66910.1 | Symbols: | Protein kinase superfamily protein | chr1:24961634-24963941 REVERSE LENGTH=666	585	666	0	113.8	61.9	72.3
Rsa1.0_00212.1.g8701.t1	ref|NP_193380.3| pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] gi|223635634|sp|O23491.2|PP315_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g16470 gi|332658358|gb|AEE83758.1| pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	518	501	0	96.7	65.8	76.8	pentatricopeptide (PPR) repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G16470.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:9287862-9289541 REVERSE LENGTH=501	518	501	0	96.7	65.8	76.8
Rsa1.0_00212.1.g8702.t1	gb|EOA15472.1| hypothetical protein CARUB_v10004447mg [Capsella rubella]	581	582	0	100.2	94.5	97.8	hypothetical protein CARUB_v10004447mg	gbpln	Capsella rubella	AT4G16480.1 | Symbols: ATINT4, INT4 | inositol transporter 4 | chr4:9291246-9293083 FORWARD LENGTH=582	581	582	0	100.2	94.7	97.1
Rsa1.0_00212.1.g8703.t1	gb|EOA15494.1| hypothetical protein CARUB_v10004739mg [Capsella rubella]	469	468	0	99.8	92.5	96.4	hypothetical protein CARUB_v10004739mg	gbpln	Capsella rubella	AT4G16490.1 | Symbols: | ARM repeat superfamily protein | chr4:9293891-9295530 REVERSE LENGTH=472	469	472	0	100.6	93.0	96.8
Rsa1.0_00212.1.g8704.t1	gb|AAO22603.1| putative cysteine proteinase inhibitor [Arabidopsis thaliana]	111	117	5.00E-16	105.4	37.8	50.5	putative cysteine proteinase inhibitor	gbpln	Arabidopsis thaliana	AT4G16500.1 | Symbols: | Cystatin/monellin superfamily protein | chr4:9301530-9301883 REVERSE LENGTH=117	111	117	3.00E-18	105.4	36.9	49.5
Rsa1.0_00212.1.g8705.t1	gb|AAO22603.1| putative cysteine proteinase inhibitor [Arabidopsis thaliana]	69	117	2.00E-14	169.6	59.4	73.9	putative cysteine proteinase inhibitor	gbpln	Arabidopsis thaliana	AT4G16500.1 | Symbols: | Cystatin/monellin superfamily protein | chr4:9301530-9301883 REVERSE LENGTH=117	69	117	3.00E-17	169.6	59.4	72.5
Rsa1.0_00212.1.g8706.t1	gb|EOA17680.1| hypothetical protein CARUB_v10006049mg [Capsella rubella]	111	118	2.00E-22	106.3	66.7	78.4	hypothetical protein CARUB_v10006049mg	gbpln	Capsella rubella	AT4G16500.1 | Symbols: | Cystatin/monellin superfamily protein | chr4:9301530-9301883 REVERSE LENGTH=117	111	117	2.00E-24	105.4	45.9	60.4
Rsa1.0_00212.1.g8707.t1	gb|EOA17672.1| hypothetical protein CARUB_v10006041mg [Capsella rubella]	241	121	8.00E-53	50.2	43.2	44.4	hypothetical protein CARUB_v10006041mg	gbpln	Capsella rubella	AT4G16520.2 | Symbols: ATG8F | Ubiquitin-like superfamily protein | chr4:9306882-9308113 REVERSE LENGTH=121	241	121	1.00E-54	50.2	42.7	44.0
Rsa1.0_00212.1.g8708.t1	gb|EOA28276.1| hypothetical protein CARUB_v10024470mg [Capsella rubella] gi|482564087|gb|EOA28277.1| hypothetical protein CARUB_v10024470mg [Capsella rubella]	56	56	2.00E-15	100.0	62.5	89.3	hypothetical protein CARUB_v10024470mg	gbpln	Capsella rubella	AT2G35736.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25225.1). | chr2:15023084-15023254 REVERSE LENGTH=56	56	56	1.00E-17	100.0	60.7	83.9
Rsa1.0_00212.1.g8709.t1	gb|AAA33006.1| napin prepropeptide [Brassica napus]	175	178	2.00E-80	101.7	92.0	94.3	napin prepropeptide	gbpln	Brassica napus	AT4G27170.1 | Symbols: SESA4, AT2S4 | seed storage albumin 4 | chr4:13613637-13614137 FORWARD LENGTH=166	175	166	9.00E-56	94.9	63.4	74.3
Rsa1.0_00212.1.g8710.t2	gb|EOA16489.1| hypothetical protein CARUB_v10004647mg [Capsella rubella]	265	497	2.00E-89	187.5	63.4	74.3	hypothetical protein CARUB_v10004647mg	gbpln	Capsella rubella	AT4G16550.1 | Symbols: | HSP20-like chaperone | chr4:9318442-9324254 REVERSE LENGTH=743	265	743	5.00E-91	280.4	62.6	74.3
Rsa1.0_00212.1.g8711.t1	dbj|BAJ33622.1| unnamed protein product [Thellungiella halophila]	454	481	0	105.9	86.8	91.4	unnamed protein product	----	----	AT4G15900.1 | Symbols: PRL1 | pleiotropic regulatory locus 1 | chr4:9023775-9027443 FORWARD LENGTH=486	454	486	0	107.0	84.4	90.7
Rsa1.0_00212.1.g8712.t1	gb|EOA16489.1| hypothetical protein CARUB_v10004647mg [Capsella rubella]	264	497	7.00E-89	188.3	62.1	73.1	hypothetical protein CARUB_v10004647mg	gbpln	Capsella rubella	AT4G16550.1 | Symbols: | HSP20-like chaperone | chr4:9318442-9324254 REVERSE LENGTH=743	264	743	5.00E-91	281.4	61.4	74.2
Rsa1.0_00212.1.g8713.t1	gb|EOA16489.1| hypothetical protein CARUB_v10004647mg [Capsella rubella]	231	497	1.00E-60	215.2	53.2	68.8	hypothetical protein CARUB_v10004647mg	gbpln	Capsella rubella	AT2G03020.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr2:882927-884081 REVERSE LENGTH=255	231	255	5.00E-63	110.4	52.4	66.7
Rsa1.0_00212.1.g8714.t1	ref|XP_002868119.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297313955|gb|EFH44378.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	491	499	0	101.6	85.7	91.4	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT4G16563.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr4:9329933-9331432 REVERSE LENGTH=499	491	499	0	101.6	84.5	90.8

Rsa1.0_00212.1.g8715.t4	ref|XP_002868115.1| histidine triad family protein [Arabidopsis lyrata subsp. lyrata] gi|297313951|gb|EFH44374.1| histidine triad family protein [Arabidopsis lyrata subsp. lyrata]	235	146	6.00E-70	62.1	53.2	57.0	histidine triad family protein	gbpln	Arabidopsis lyrata	AT4G16566.1 | Symbols: HINT4 | histidine triad nucleotide-binding 4 | chr4:9334873-9335884 REVERSE LENGTH=146	235	146	1.00E-71	62.1	52.3	57.0
Rsa1.0_00212.1.g8716.t1	ref|XP_002870146.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315982|gb|EFH46405.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	700	729	0	104.1	83.1	88.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G16570.1 | Symbols: ATPRMT7, PRMT7 | protein arginine methyltransferase 7 | chr4:9336815-9340692 FORWARD LENGTH=724	700	724	0	103.4	82.9	87.4
Rsa1.0_00212.1.g8717.t1	gb|EOA16566.1| hypothetical protein CARUB_v10004725mg [Capsella rubella]	472	475	0	100.6	84.5	89.6	hypothetical protein CARUB_v10004725mg	gbpln	Capsella rubella	AT4G16580.1 | Symbols: | Protein phosphatase 2C family protein | chr4:9341152-9342555 REVERSE LENGTH=467	472	467	0	98.9	84.3	88.6
Rsa1.0_00212.1.g8718.t1	sp|Q84W54.1|CSLA1_ARATH RecName: Full=Probable mannan synthase 1; AltName: Full=Cellulose synthase-like protein A1; Short=AtCslA1 gi|28393622|gb|AAO42230.1| putative cellulose synthase [Arabidopsis thaliana]	554	553	0	99.8	89.7	95.5	RecName: Full=Probable mannan synthase 1; AltName: Full=Cellulose synthase-like protein A1; Short=AtCslA1 gi|28393622|gb|AAO42230.1| putative cellulose synthase	gbpln	Arabidopsis thaliana	AT1G24070.1 | Symbols: ATCSLA10, CSLA10 | cellulose synthase-like A10 | chr1:8516437-8519734 REVERSE LENGTH=552	554	552	0	99.6	68.4	82.7
Rsa1.0_00212.1.g8719.t1	ref|NP_193393.4| GT8-glycogenin domain-containing protein [Arabidopsis thaliana] gi|385178636|sp|F4JMI5.1|GUX7_ARATH RecName: Full=Putative glucuronosyltransferase PGSIP7; AltName: Full=Glycogenin-like protein 7; AltName: Full=Plant glycogenin-like starch initiation protein 7 gi|332658375|gb|AEE83775.1| putative glucuronosyltransferase PGSIP7 [Arabidopsis thaliana]	493	494	0	100.2	88.4	93.5	GT8-glycogenin domain-containing protein	gbpln	Arabidopsis thaliana	AT4G16600.1 | Symbols: | Nucleotide-diphospho-sugar transferases superfamily protein | chr4:9350039-9352707 FORWARD LENGTH=494	493	494	0	100.2	88.4	93.5
Rsa1.0_00212.1.g8720.t1	ref|XP_002868113.1| hypothetical protein ARALYDRAFT_493215 [Arabidopsis lyrata subsp. lyrata] gi|297313949|gb|EFH44372.1| hypothetical protein ARALYDRAFT_493215 [Arabidopsis lyrata subsp. lyrata]	196	201	5.00E-66	102.6	73.0	82.1	hypothetical protein ARALYDRAFT_493215	gbpln	Arabidopsis lyrata	AT4G16610.1 | Symbols: | C2H2-like zinc finger protein | chr4:9354568-9355182 REVERSE LENGTH=204	196	204	5.00E-67	104.1	75.0	82.7
Rsa1.0_00212.1.g8721.t1	ref|NP_193397.1| matrix metalloprotease domain-containing protein [Arabidopsis thaliana] gi|2245019|emb|CAB10439.1| proteinase like protein [Arabidopsis thaliana] gi|7268414|emb|CAB78706.1| proteinase like protein [Arabidopsis thaliana] gi|332658379|gb|AEE83779.1| matrix metalloprotease domain-containing protein [Arabidopsis thaliana]	628	364	1.00E-160	58.0	45.1	49.0	matrix metalloprotease domain-containing protein	gbpln	Arabidopsis thaliana	AT4G16640.1 | Symbols: | Matrixin family protein | chr4:9367396-9368490 REVERSE LENGTH=364	628	364	1.00E-163	58.0	45.1	49.0
Rsa1.0_00212.1.g8722.t1	ref|XP_002870141.1| hypothetical protein ARALYDRAFT_493211 [Arabidopsis lyrata subsp. lyrata] gi|297315977|gb|EFH46400.1| hypothetical protein ARALYDRAFT_493211 [Arabidopsis lyrata subsp. lyrata]	542	549	0	101.3	93.5	95.9	hypothetical protein ARALYDRAFT_493211	gbpln	Arabidopsis lyrata	AT4G16650.1 | Symbols: | O-fucosyltransferase family protein | chr4:9372727-9375910 FORWARD LENGTH=549	542	549	0	101.3	92.3	95.2
Rsa1.0_00212.1.g8723.t1	ref|NP_567510.1| hypoxia up-regulated 1 [Arabidopsis thaliana] gi|378548353|sp|F4JMJ1.1|HSP7R_ARATH RecName: Full=Heat shock 70 kDa protein 17; AltName: Full=Heat shock protein 70-17; Short=AtHsp70-17; Flags: Precursor gi|332658381|gb|AEE83781.1| heat shock 70 kDa protein 17 [Arabidopsis thaliana]	859	867	0	100.9	89.6	94.4	hypoxia up-regulated 1	gbpln	Arabidopsis thaliana	AT4G16660.1 | Symbols: | heat shock protein 70 (Hsp 70) family protein | chr4:9377225-9381232 FORWARD LENGTH=867	859	867	0	100.9	89.6	94.4
Rsa1.0_00213.1.g8724.t1	ref|NP_187488.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|12322736|gb|AAG51360.1|AC012562_21 putative protein kinase; 70907-69052 [Arabidopsis thaliana] gi|194294570|gb|ACF40324.1| At3g08760 [Arabidopsis thaliana] gi|222424853|dbj|BAH20378.1| AT3G08760 [Arabidopsis thaliana] gi|332641153|gb|AEE74674.1| protein kinase domain-containing protein [Arabidopsis thaliana]	570	557	0	97.7	89.5	93.3	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G08760.1 | Symbols: ATSIK | Protein kinase superfamily protein | chr3:2658129-2659984 REVERSE LENGTH=557	570	557	0	97.7	89.5	93.3

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<tr><td>Rsa1.0_00213.1.g8725.t1</td><td>gb|ACD79975.1| serine/threonine-protein kinase ATPK19/ATPK2 [Brassica rapa]</td><td>822</td><td>458</td><td>0</td><td>55.7</td><td>50.7</td><td>52.1</td><td>serine/threonine-protein kinase ATPK19/ATPK2</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G08730.1 | Symbols: ATPK1, ATPK6, ATS6K1, PK6, PK1, S6K1 | protein-serine kinase 1 | chr3:2651581-2653363 REVERSE LENGTH=465</td><td>822</td><td>465</td><td>0</td><td>56.6</td><td>47.6</td><td>51.7</td></tr>
<tr><td>Rsa1.0_00213.1.g8726.t1</td><td>ref|NP_187484.1| serine/threonine protein kinase 2 [Arabidopsis thaliana] gi|30680612|ref|NP_850543.1| serine/threonine protein kinase 2 [Arabidopsis thaliana] gi|21431798|sp|Q39030.2|KPK2_ARATH RecName: Full=Serine/threonine-protein kinase AtPK2/AtPK19; AltName: Full=Ribosomal-protein S6 kinase homolog 2 gi|12322721|gb|AAG51345.1|AC012562_6 putative ribosomal-protein S6 kinase (ATPK19); 61330-59548 [Arabidopsis thaliana] gi|13272447|gb|AAK17162.1|AF325094_1 putative ribosomal-protein S6 kinase (ATPK19) [Arabidopsis thaliana] gi|111074206|gb|ABH04476.1| At3g08720 [Arabidopsis thaliana] gi|222422905|dbj|BAH19439.1| AT3G08720 [Arabidopsis thaliana] gi|332641148|gb|AEE74669.1| serine/threonine protein kinase 2 [Arabidopsis thaliana] gi|332641149|gb|AEE74670.1| serine/threonine protein kinase 2 [Arabidopsis thaliana]</td><td>449</td><td>471</td><td>0</td><td>104.9</td><td>86.6</td><td>94.2</td><td>serine/threonine protein kinase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G08720.2 | Symbols: ATPK19, ATPK2 | serine/threonine protein kinase 2 | chr3:2648625-2650407 REVERSE LENGTH=471</td><td>449</td><td>471</td><td>0</td><td>104.9</td><td>86.6</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00213.1.g8727.t1</td><td>ref|NP_566331.1| ubiquitin-conjugating enzyme E2 11 [Arabidopsis thaliana] gi|334185174|ref|NP_001189841.1| ubiquitin-conjugating enzyme E2 11 [Arabidopsis thaliana] gi|297829396|ref|XP_002882580.1| ubiquitin-conjugating enzyme 11 [Arabidopsis lyrata subsp. lyrata] gi|12643427|sp|P35134.2|UBC11_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 11; AltName: Full=Ubiquitin carrier protein 11; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 11; AltName: Full=Ubiquitin-protein ligase 11 gi|12322738|gb|AAG51362.1|AC012562_23 putative ubiquitin conjugating enzyme; 52410-53412 [Arabidopsis thaliana] gi|17380790|gb|AAL36225.1| putative E2, ubiquitin-conjugating enzyme UBC11 [Arabidopsis thaliana] gi|20259611|gb|AAM14162.1| putative ubiquitin conjugating enzyme 11 (UBC11) [Arabidopsis thaliana] gi|21554241|gb|AAM63316.1| E2, ubiquitin-conjugating enzyme UBC11 [Arabidopsis thaliana] gi|66354432|gb|AAY44851.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|110736468|dbj|BAF00202.1| putative ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|297328420|gb|EFH58839.1| ubiquitin-conjugating enzyme 11 [Arabidopsis</td><td>254</td><td>148</td><td>6.00E-82</td><td>58.3</td><td>57.1</td><td>58.3</td><td>ubiquitin-conjugating enzyme E2 11</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G08690.2 | Symbols: UBC11 | ubiquitin-conjugating enzyme 11 | chr3:2641487-2642489 FORWARD LENGTH=148</td><td>254</td><td>148</td><td>2.00E-84</td><td>58.3</td><td>57.1</td><td>58.3</td></tr>
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<tr><td>Rsa1.0_00213.1.g8729.t1</td><td>gb|EOA30227.1| hypothetical protein CARUB_v10013349mg [Capsella rubella]</td><td>555</td><td>567</td><td>0</td><td>102.2</td><td>87.6</td><td>93.3</td><td>hypothetical protein CARUB_v10013349mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G08670.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G51540.1); Has 48380 Blast hits to 29827 proteins in 1356 species: Archae - 46; Bacteria - 5589; Metazoa - 17361; Fungi - 13192; Plants - 2237; Viruses - 905; Other Eukaryotes - 9050 (source: NCBI BLink). | chr3:2633946-2636536 FORWARD LENGTH=567</td><td>555</td><td>567</td><td>0</td><td>102.2</td><td>86.7</td><td>91.4</td></tr>
<tr><td>Rsa1.0_00213.1.g8730.t1</td><td>ref|NP_195254.1| C2H2-like zinc finger protein [Arabidopsis thaliana] gi|75318572|sp|O65499.1|ZAT3_ARATH RecName: Full=Zinc finger protein ZAT3; AltName: Full=Protein DUO1-ACTIVATED ZINC FINGER 2 gi|3080422|emb|CAA18741.1| putative zinc-finger protein [Arabidopsis thaliana] gi|7270480|emb|CAB80245.1| putative zinc-finger protein [Arabidopsis thaliana] gi|91806770|gb|ABE66112.1| zinc finger family protein [Arabidopsis thaliana] gi|225898853|dbj|BAH30557.1| hypothetical protein [Arabidopsis thaliana] gi|332661089|gb|AEE86489.1| C2H2-like zinc finger protein [Arabidopsis thaliana]</td><td>289</td><td>284</td><td>1.00E-117</td><td>98.3</td><td>77.2</td><td>83.0</td><td>C2H2-like zinc finger protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G35280.1 | Symbols: | C2H2-like zinc finger protein | chr4:16787429-16788283 REVERSE LENGTH=284</td><td>289</td><td>284</td><td>1.00E-119</td><td>98.3</td><td>77.2</td><td>83.0</td></tr>
<tr><td>Rsa1.0_00213.1.g8731.t1</td><td>gb|EOA30171.1| hypothetical protein CARUB_v10013288mg [Capsella rubella]</td><td>581</td><td>595</td><td>0</td><td>102.4</td><td>87.1</td><td>90.5</td><td>hypothetical protein CARUB_v10013288mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G08650.2 | Symbols: | ZIP metal ion transporter family | chr3:2624694-2627308 REVERSE LENGTH=619</td><td>581</td><td>619</td><td>0</td><td>106.5</td><td>87.6</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00213.1.g8732.t1</td><td>gb|ABW81126.1| short chain dehydrogenase-21 [Boechera divaricarpa]</td><td>264</td><td>261</td><td>1.00E-131</td><td>98.9</td><td>87.1</td><td>92.0</td><td>short chain dehydrogenase-21</td><td>gbpln</td><td>Boechera divaricarpa</td><td>AT1G07440.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:2286436-2287665 REVERSE LENGTH=266</td><td>264</td><td>266</td><td>1.00E-101</td><td>100.8</td><td>66.3</td><td>81.1</td></tr>
<tr><td>Rsa1.0_00213.1.g8733.t1</td><td>gb|EOA32200.1| hypothetical protein CARUB_v10015456mg [Capsella rubella]</td><td>328</td><td>337</td><td>1.00E-132</td><td>102.7</td><td>79.3</td><td>86.3</td><td>hypothetical protein CARUB_v10015456mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G08630.1 | Symbols: | Protein of unknown function (DUF3411) | chr3:2620943-2621962 FORWARD LENGTH=339</td><td>328</td><td>339</td><td>1.00E-132</td><td>103.4</td><td>78.4</td><td>85.7</td></tr>
<tr><td>Rsa1.0_00213.1.g8734.t1</td><td>gb|EOA31180.1| hypothetical protein CARUB_v10014346mg [Capsella rubella]</td><td>283</td><td>281</td><td>1.00E-149</td><td>99.3</td><td>92.6</td><td>96.5</td><td>hypothetical protein CARUB_v10014346mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G08620.1 | Symbols: | RNA-binding KH domain-containing protein | chr3:2617925-2620314 FORWARD LENGTH=283</td><td>283</td><td>283</td><td>1.00E-140</td><td>100.0</td><td>90.8</td><td>95.4</td></tr>
<tr><td>Rsa1.0_00213.1.g8735.t1</td><td>gb|AAP21180.1| At3g08610 [Arabidopsis thaliana]</td><td>65</td><td>73</td><td>1.00E-29</td><td>112.3</td><td>96.9</td><td>98.5</td><td>At3g08610</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G08610.1 | Symbols: | unknown protein; Has 40 Blast hits to 40 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2616435-2616768 REVERSE LENGTH=65</td><td>65</td><td>65</td><td>3.00E-32</td><td>100.0</td><td>96.9</td><td>98.5</td></tr>
<tr><td>Rsa1.0_00213.1.g8736.t1</td><td>ref|XP_002882573.1| hypothetical protein ARALYDRAFT_478161 [Arabidopsis lyrata subsp. lyrata] gi|297328413|gb|EFH58832.1| hypothetical protein ARALYDRAFT_478161 [Arabidopsis lyrata subsp. lyrata]</td><td>322</td><td>315</td><td>1.00E-101</td><td>97.8</td><td>73.3</td><td>82.6</td><td>hypothetical protein ARALYDRAFT_478161</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G08600.1 | Symbols: | Protein of unknown function (DUF1191) | chr3:2612646-2613596 FORWARD LENGTH=316</td><td>322</td><td>316</td><td>1.00E-102</td><td>98.1</td><td>70.2</td><td>78.0</td></tr>
<tr><td>Rsa1.0_00213.1.g8737.t1</td><td>dbj|BAJ33789.1| unnamed protein product [Thellungiella halophila]</td><td>593</td><td>560</td><td>0</td><td>94.4</td><td>88.0</td><td>91.7</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G08590.2 | Symbols: | Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent | chr3:2608683-2611237 REVERSE LENGTH=560</td><td>593</td><td>560</td><td>0</td><td>94.4</td><td>86.5</td><td>90.7</td></tr>
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Rsa1.0_00213.1.g8738.t1	ref|NP_187467.1| elongation defective 1 protein / ELD1 protein [Arabidopsis thaliana] gi|12322724|gb|AAG51348.1|AC012562_9 hypothetical protein; 7436-10438 [Arabidopsis thaliana] gi|23452834|gb|AAN33186.1| elongation defective 1 [Arabidopsis thaliana] gi|332641124|gb|AEE74645.1| elongation defective 1 protein / ELD1 protein [Arabidopsis thaliana]	301	533	2.00E-61	177.1	47.8	51.2	elongation defective 1 protein / ELD1 protein	gbpln	Arabidopsis thaliana	AT3G08550.1 | Symbols: ELD1, ABI8, KOB1 | elongation defective 1 protein / ELD1 protein | chr3:2596513-2599515 FORWARD LENGTH=533	301	533	5.00E-64	177.1	47.8	51.2
Rsa1.0_00213.1.g8739.t1	ref|XP_002884683.1| hypothetical protein ARALYDRAFT_896987 [Arabidopsis lyrata subsp. lyrata] gi|297330523|gb|EFH60942.1| hypothetical protein ARALYDRAFT_896987 [Arabidopsis lyrata subsp. lyrata]	1710	1703	0	99.6	87.1	92.5	hypothetical protein ARALYDRAFT_896987	gbpln	Arabidopsis lyrata	AT3G08530.1 | Symbols: | Clathrin, heavy chain | chr3:2587171-2595411 REVERSE LENGTH=1703	1710	1703	0	99.6	86.8	92.4
Rsa1.0_00213.1.g8740.t1	gb|EOA30191.1| hypothetical protein CARUB_v10013310mg [Capsella rubella]	582	584	0	100.3	93.3	96.7	hypothetical protein CARUB_v10013310mg	gbpln	Capsella rubella	AT3G08510.2 | Symbols: ATPLC2, PLC2 | phospholipase C 2 | chr3:2582626-2585556 REVERSE LENGTH=581	582	581	0	99.8	93.0	95.9
Rsa1.0_00213.1.g8741.t1	ref|XP_002882569.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328409|gb|EFH58828.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	65	63	1.00E-10	96.9	80.0	84.6	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00213.1.g8742.t1	ref|XP_002884680.1| hypothetical protein ARALYDRAFT_478147 [Arabidopsis lyrata subsp. lyrata] gi|297330520|gb|EFH60939.1| hypothetical protein ARALYDRAFT_478147 [Arabidopsis lyrata subsp. lyrata]	338	342	1.00E-148	101.2	83.7	90.8	hypothetical protein ARALYDRAFT_478147	gbpln	Arabidopsis lyrata	AT3G08500.1 | Symbols: MYB83, AtMYB83 | myb domain protein 83 | chr3:2576958-2578072 REVERSE LENGTH=343	338	343	1.00E-145	101.5	80.2	89.3
Rsa1.0_00213.1.g8743.t1	ref|NP_187462.1| uncharacterized protein [Arabidopsis thaliana] gi|12321556|gb|AAG50832.1|AC074395_6 hypothetical protein [Arabidopsis thaliana] gi|49660145|gb|AAT68363.1| hypothetical protein At3g08490 [Arabidopsis thaliana] gi|50058945|gb|AAT69217.1| hypothetical protein At3g08490 [Arabidopsis thaliana] gi|332641115|gb|AEE74636.1| uncharacterized protein AT3G08490 [Arabidopsis thaliana]	304	271	1.00E-111	89.1	64.1	74.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G08490.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Late embryogenesis abundant protein, group 2 (TAIR:AT3G24600.1); Has 161 Blast hits to 158 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 161; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2574105-2575125 REVERSE LENGTH=271	304	271	1.00E-114	89.1	64.1	74.7
Rsa1.0_00213.1.g8744.t1	ref|XP_002884678.1| hypothetical protein ARALYDRAFT_478146 [Arabidopsis lyrata subsp. lyrata] gi|297330518|gb|EFH60937.1| hypothetical protein ARALYDRAFT_478146 [Arabidopsis lyrata subsp. lyrata]	531	530	0	99.8	79.8	89.5	hypothetical protein ARALYDRAFT_478146	gbpln	Arabidopsis lyrata	AT3G08040.2 | Symbols: FRD3, MAN1, ATFRD3 | MATE efflux family protein | chr3:2566593-2569397 REVERSE LENGTH=526	531	526	0	99.1	79.7	89.5
Rsa1.0_00213.1.g8745.t1	gb|EOA30873.1| hypothetical protein CARUB_v10014019mg [Capsella rubella]	364	365	1.00E-176	100.3	87.1	91.2	hypothetical protein CARUB_v10014019mg	gbpln	Capsella rubella	AT3G08030.1 | Symbols: | Protein of unknown function, DUF642 | chr3:2564191-2565819 FORWARD LENGTH=365	364	365	1.00E-175	100.3	86.3	90.1
Rsa1.0_00213.1.g8746.t1	gb|EOA31641.1| hypothetical protein CARUB_v10014853mg [Capsella rubella]	149	146	5.00E-53	98.0	76.5	85.2	hypothetical protein CARUB_v10014853mg	gbpln	Capsella rubella	AT3G08000.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:2555034-2555829 REVERSE LENGTH=143	149	143	2.00E-54	96.0	75.2	84.6
Rsa1.0_00213.1.g8747.t1	gb|EOA30533.1| hypothetical protein CARUB_v10013654mg [Capsella rubella]	461	460	0	99.8	88.9	92.4	hypothetical protein CARUB_v10013654mg	gbpln	Capsella rubella	AT3G07990.1 | Symbols: SCPL27 | serine carboxypeptidase-like 27 | chr3:2552544-2554644 FORWARD LENGTH=459	461	459	0	99.6	87.0	92.0
Rsa1.0_00213.1.g8748.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00213.1.g8749.t1	ref|XP_002882564.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328404|gb|EFH58823.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	438	439	0	100.2	85.2	91.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G07970.1 | Symbols: QRT2 | Pectin lyase-like superfamily protein | chr3:2541006-2543370 FORWARD LENGTH=439	438	439	0	100.2	83.8	91.1
Rsa1.0_00213.1.g8750.t1	ref|XP_002882562.1| hypothetical protein ARALYDRAFT_896969 [Arabidopsis lyrata subsp. lyrata] gi|297328402|gb|EFH58821.1| hypothetical protein ARALYDRAFT_896969 [Arabidopsis lyrata subsp. lyrata]	304	304	1.00E-158	100.0	94.1	96.7	hypothetical protein ARALYDRAFT_896969	gbpln	Arabidopsis lyrata	AT3G07950.1 | Symbols: | rhomboid protein-related | chr3:2531982-2534277 FORWARD LENGTH=304	304	304	1.00E-158	100.0	92.1	95.7

Rsa1.0_00213.1.g8751.t1	ref|XP_002882559.1| hypothetical protein ARALYDRAFT_478135 [Arabidopsis lyrata subsp. lyrata] gi|297328399|gb|EFH58818.1| hypothetical protein ARALYDRAFT_478135 [Arabidopsis lyrata subsp. lyrata]	406	383	0	94.3	86.0	88.9	hypothetical protein ARALYDRAFT_478135	gbpln	Arabidopsis lyrata	AT3G07940.1 | Symbols: | Calcium-dependent ARF-type GTPase activating protein family | chr3:2529542-2531368 FORWARD LENGTH=385	406	385	0	94.8	85.0	88.9
Rsa1.0_00213.1.g8752.t1	gb|EIE18866.1| hypothetical protein COCSUDRAFT_26086 [Coccomyxa subellipsoidea C-169]	73	75	8.00E-21	102.7	63.0	82.2	hypothetical protein COCSUDRAFT_26086	gbpln	Coccomyxa subellipsoidea	AT3G07910.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Reactive oxygen species modulator 1 (InterPro:IPR018450); Has 192 Blast hits to 192 proteins in 80 species: Archae - 0; Bacteria - 0; Metazoa - 139; Fungi - 6; Plants - 39; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr3:2523367-2524048 REVERSE LENGTH=74	73	74	5.00E-19	101.4	79.5	89.0
Rsa1.0_00213.1.g8753.t1	ref|XP_002882556.1| hypothetical protein ARALYDRAFT_478129 [Arabidopsis lyrata subsp. lyrata] gi|297328396|gb|EFH58815.1| hypothetical protein ARALYDRAFT_478129 [Arabidopsis lyrata subsp. lyrata]	556	572	0	102.9	82.9	88.3	hypothetical protein ARALYDRAFT_478129	gbpln	Arabidopsis lyrata	AT3G07900.1 | Symbols: | O-fucosyltransferase family protein | chr3:2520826-2523008 FORWARD LENGTH=579	556	579	0	104.1	82.9	88.7
Rsa1.0_00214.1.g8754.t2	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1335	1496	0	112.1	57.9	72.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1335	1262	1.00E-109	94.5	14.5	20.7
Rsa1.0_00214.1.g8755.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00214.1.g8756.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00214.1.g8757.t1	gb|EOA32081.1| hypothetical protein CARUB_v10015328mg [Capsella rubella]	434	435	1.00E-170	100.2	67.3	79.3	hypothetical protein CARUB_v10015328mg	gbpln	Capsella rubella	AT3G12240.1 | Symbols: SCPL15 | serine carboxypeptidase-like 15 | chr3:3902436-3904918 REVERSE LENGTH=436	434	436	1.00E-167	100.5	64.3	77.4
Rsa1.0_00214.1.g8758.t1	ref|NP_191964.2| digalactosyldiacylglycerol synthase 2 [Arabidopsis thaliana] gi|75161985|sp|Q8W1S1.1|DGDG2_ARATH RecName: Full=Digalactosyldiacylglycerol synthase 2, chloroplastic gi|18141112|gb|AAL60504.1|AF421193_1 digalactosyldiacylglycerol synthase [Arabidopsis thaliana] gi|33589694|gb|AAQ22613.1| At4g00550 [Arabidopsis thaliana] gi|110736406|dbj|BAF00170.1| digalactosyldiacylglycerol synthase [Arabidopsis thaliana] gi|332656498|gb|AEE81898.1| digalactosyldiacylglycerol synthase 2 [Arabidopsis thaliana]	475	473	0	99.6	87.8	93.3	digalactosyldiacylglycerol synthase 2	gbpln	Arabidopsis thaliana	AT4G00550.1 | Symbols: DGD2 | digalactosyl diacylglycerol deficient 2 | chr4:238154-240019 REVERSE LENGTH=473	475	473	0	99.6	87.8	93.3
Rsa1.0_00214.1.g8759.t1	ref|XP_002872940.1| hypothetical protein ARALYDRAFT_912183 [Arabidopsis lyrata subsp. lyrata] gi|297318777|gb|EFH49199.1| hypothetical protein ARALYDRAFT_912183 [Arabidopsis lyrata subsp. lyrata]	607	607	0	100.0	93.4	96.7	hypothetical protein ARALYDRAFT_912183	gbpln	Arabidopsis lyrata	AT4G00570.1 | Symbols: NAD-ME2 | NAD-dependent malic enzyme 2 | chr4:242817-246522 REVERSE LENGTH=607	607	607	0	100.0	92.6	96.5
Rsa1.0_00214.1.g8760.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00214.1.g8761.t1	emb|CBI40290.3| unnamed protein product [Vitis vinifera]	66	185	3.00E-21	280.3	71.2	75.8	unnamed protein product	gbpln	Vitis vinifera	AT4G00585.1 | Symbols: | unknown protein; Has 47 Blast hits to 47 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 7; Plants - 33; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:251157-252284 REVERSE LENGTH=88	66	88	5.00E-22	133.3	71.2	74.2
Rsa1.0_00214.1.g8762.t1	ref|XP_002875021.1| hypothetical protein ARALYDRAFT_490508 [Arabidopsis lyrata subsp. lyrata] gi|297320858|gb|EFH51280.1| hypothetical protein ARALYDRAFT_490508 [Arabidopsis lyrata subsp. lyrata]	407	407	0	100.0	83.8	90.4	hypothetical protein ARALYDRAFT_490508	gbpln	Arabidopsis lyrata	AT4G00590.1 | Symbols: | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr4:252835-254880 FORWARD LENGTH=408	407	408	0	100.2	82.6	89.4

Rsa1.0_00214.1.g8763.t1	ref|NP_191971.1| Amino acid dehydrogenase family protein [Arabidopsis thaliana] gi|3047116|gb|AAC13627.1| F6N23.26 gene product [Arabidopsis thaliana] gi|7267401|emb|CAB80871.1| putative tetrahydrofolate synthase [Arabidopsis thaliana] gi|16649149|gb|AAL24426.1| Unknown protein [Arabidopsis thaliana] gi|23197716|gb|AAN15385.1| Unknown protein [Arabidopsis thaliana] gi|332656510|gb|AEE81910.1| Amino acid dehydrogenase family protein [Arabidopsis thaliana]	348	360	1.00E-169	103.4	83.9	91.4	Amino acid dehydrogenase family protein	gbpln	Arabidopsis thaliana	AT4G00620.1 | Symbols: | Amino acid dehydrogenase family protein | chr4:259265-260788 REVERSE LENGTH=360	348	360	1.00E-171	103.4	83.9	91.4
Rsa1.0_00214.1.g8764.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00214.1.g8765.t1	gb|AFP47629.1| nitrile-specifier protein [Schouwia purpurea]	508	467	0	91.9	70.9	80.9	nitrile-specifier protein	gbpln	Schouwia purpurea	AT3G16400.2 | Symbols: ATMLP-470 | nitrile specifier protein 1 | chr3:5566516-5568330 FORWARD LENGTH=470	508	470	0	92.5	67.5	78.3
Rsa1.0_00214.1.g8766.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00214.1.g8767.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	181	1501	2.00E-34	829.3	48.1	63.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	181	1262	2.00E-16	697.2	25.4	47.0
Rsa1.0_00214.1.g8768.t1	ref|NP_191975.2| DEAD-box ATP-dependent RNA helicase 8 [Arabidopsis thaliana] gi|30678703|ref|NP_849535.1| DEAD-box ATP-dependent RNA helicase 8 [Arabidopsis thaliana] gi|75330763|sp|Q8RXK6.1|RH8_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 8 gi|19423939|gb|AAL87312.1| putative RNA helicase [Arabidopsis thaliana] gi|21280839|gb|AAM45033.1| putative RNA helicase [Arabidopsis thaliana] gi|332656515|gb|AEE81915.1| DEAD-box ATP-dependent RNA helicase 8 [Arabidopsis thaliana] gi|332656516|gb|AEE81916.1| DEAD-box ATP-dependent RNA helicase 8 [Arabidopsis thaliana]	547	505	0	92.3	85.2	87.6	DEAD-box ATP-dependent RNA helicase 8	gbpln	Arabidopsis thaliana	AT4G00660.1 | Symbols: RH8, ATRH8 | RNAhelicase-like 8 | chr4:274638-277438 FORWARD LENGTH=505	547	505	0	92.3	85.2	87.6
Rsa1.0_00214.1.g8769.t1	ref|NP_191976.2| Remorin family protein [Arabidopsis thaliana] gi|48310044|gb|AAT41742.1| At4g00670 [Arabidopsis thaliana] gi|54606860|gb|AAV34778.1| At4g00670 [Arabidopsis thaliana] gi|332656517|gb|AEE81917.1| Remorin family protein [Arabidopsis thaliana]	117	123	3.00E-39	105.1	72.6	85.5	Remorin family protein	gbpln	Arabidopsis thaliana	AT4G00670.1 | Symbols: | Remorin family protein | chr4:278434-279170 REVERSE LENGTH=123	117	123	5.00E-42	105.1	72.6	85.5
Rsa1.0_00214.1.g8770.t1	ref|XP_002872934.1| hypothetical protein ARALYDRAFT_490501 [Arabidopsis lyrata subsp. lyrata] gi|297318771|gb|EFH49193.1| hypothetical protein ARALYDRAFT_490501 [Arabidopsis lyrata subsp. lyrata]	139	140	3.00E-69	100.7	89.2	96.4	hypothetical protein ARALYDRAFT_490501	gbpln	Arabidopsis lyrata	AT4G00680.1 | Symbols: ADF8 | actin depolymerizing factor 8 | chr4:279780-280608 REVERSE LENGTH=140	139	140	7.00E-72	100.7	89.2	96.4
Rsa1.0_00214.1.g8771.t1	ref|XP_002875018.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320855|gb|EFH51277.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	459	490	0	106.8	94.3	97.6	kinase family protein	gbpln	Arabidopsis lyrata	AT4G00710.1 | Symbols: BSK3 | BR-signaling kinase 3 | chr4:290807-293096 FORWARD LENGTH=489	459	489	0	106.5	93.2	96.7
Rsa1.0_00214.1.g8772.t1	ref|XP_002872933.1| hypothetical protein ARALYDRAFT_490498 [Arabidopsis lyrata subsp. lyrata] gi|297318770|gb|EFH49192.1| hypothetical protein ARALYDRAFT_490498 [Arabidopsis lyrata subsp. lyrata]	484	472	0	97.5	91.5	94.4	hypothetical protein ARALYDRAFT_490498	gbpln	Arabidopsis lyrata	AT4G00720.1 | Symbols: ATSK32, ASKTHETA, SK32 | shaggy-like protein kinase 32 | chr4:294116-297002 REVERSE LENGTH=472	484	472	0	97.5	90.9	94.2
Rsa1.0_00214.1.g8773.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00214.1.g8774.t1	ref|XP_002875016.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297320853|gb|EFH51275.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	338	380	1.00E-128	112.4	68.9	80.5	F-box family protein	gbpln	Arabidopsis lyrata	AT4G00755.2 | Symbols: | F-box family protein | chr4:325294-326787 FORWARD LENGTH=377	338	377	1.00E-127	111.5	68.0	79.6

Rsa1.0_00214.1.g8775.t2	ref|NP_567185.1| F−box protein [Arabidopsis thaliana] gi|30678731|ref|NP_849277.1| F−box protein [Arabidopsis thaliana] gi|75246091|sp|Q8LG03.1|FB345_ARATH RecName: Full=F−box protein At4g00755 gi|21536774|gb|AAM61106.1| unknown [Arabidopsis thaliana] gi|332656531|gb|AEE81931.1| F−box protein [Arabidopsis thaliana] gi|332656532|gb|AEE81932.1| F−box protein [Arabidopsis thaliana]	585	377	1.00E−107	64.4	36.4	44.1	F−box protein	gbpln	Arabidopsis thaliana	AT4G00755.2 | Symbols: | F−box family protein | chr4:325294−326787 FORWARD LENGTH=377	585	377	1.00E−110	64.4	36.4	44.1
Rsa1.0_00215.1.g8776.t1	ref|NP_564284.1| adenine phosphoribosyltransferase 1 [Arabidopsis thaliana] gi|38503396|sp|P31166.2|APT1_ARATH RecName: Full=Adenine phosphoribosyltransferase 1, chloroplastic; Short=APRT 1; Flags: Precursor gi|21536559|gb|AAM60891.1| adenine phosphoribosyltransferase 1, APRT [Arabidopsis thaliana] gi|332192710|gb|AEE30831.1| adenine phosphoribosyltransferase 1 [Arabidopsis thaliana]	242	243	2.00E−97	100.4	79.8	86.8	adenine phosphoribosyltransferase 1	gbpln	Arabidopsis thaliana	AT1G27450.1 | Symbols: APT1, ATAPT1 | adenine phosphoribosyl transferase 1 | chr1:9532042−9533807 FORWARD LENGTH=243	242	243	1.00E−100	100.4	79.8	86.8
Rsa1.0_00215.1.g8777.t1	ref|NP_564285.1| no pollen germination related 1 protein [Arabidopsis thaliana] gi|9802536|gb|AAF99738.1|AC004557_17 F17L21.25 [Arabidopsis thaliana] gi|16226498|gb|AAL16183.1|AF428415_1 At1g27460/F17L21_26 [Arabidopsis thaliana] gi|33589668|gb|AAQ22600.1| At1g27460/F17L21_26 [Arabidopsis thaliana] gi|332192713|gb|AEE30834.1| no pollen germination related 1 protein [Arabidopsis thaliana]	709	694	0	97.9	82.7	90.8	no pollen germination related 1 protein	gbpln	Arabidopsis thaliana	AT1G27460.1 | Symbols: NPGR1 | no pollen germination related 1 | chr1:9534977−9537424 FORWARD LENGTH=694	709	694	0	97.9	82.7	90.8
Rsa1.0_00215.1.g8778.t1	ref|NP_001117365.1| uncharacterized protein [Arabidopsis thaliana] gi|98961611|gb|ABF59135.1| unknown protein [Arabidopsis thaliana] gi|332192714|gb|AEE30835.1| uncharacterized protein AT1G27461 [Arabidopsis thaliana]	388	354	1.00E−138	91.2	67.5	76.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G27461.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr1:9537948−9539012 REVERSE LENGTH=354	388	354	1.00E−140	91.2	67.5	76.8
Rsa1.0_00215.1.g8779.t5	ref|XP_002893471.1| hypothetical protein ARALYDRAFT_472955 [Arabidopsis lyrata subsp. lyrata] gi|297339313|gb|EFH69730.1| hypothetical protein ARALYDRAFT_472955 [Arabidopsis lyrata subsp. lyrata]	671	645	0	96.1	77.8	86.3	hypothetical protein ARALYDRAFT_472955	gbpln	Arabidopsis lyrata	AT1G27500.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr1:9551629−9553654 REVERSE LENGTH=650	671	650	0	96.9	78.2	86.7
Rsa1.0_00215.1.g8780.t1	ref|XP_002893472.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339314|gb|EFH69731.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	646	647	0	100.2	77.4	86.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G27510.1 | Symbols: | Protein of unknown function (DUF3506) | chr1:9554945−9558293 REVERSE LENGTH=651	646	651	0	100.8	74.0	83.9
Rsa1.0_00215.1.g8781.t1	gb|EOA37527.1| hypothetical protein CARUB_v10011729mg [Capsella rubella]	174	174	3.00E−97	100.0	98.3	98.9	hypothetical protein CARUB_v10011729mg	gbpln	Capsella rubella	AT1G27530.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ubiquitin−conjugating enzyme/RWD−like (InterPro:IPR016135), Ubiquitin−fold modifier−conjugating enzyme 1 (InterPro:IPR014806); Has 269 Blast hits to 269 proteins in 110 species: Archae − 0; Bacteria − 0; Metazoa − 175; Fungi − 0; Plants − 42; Viruses − 0; Other Eukaryotes − 52 (source: NCBI BLink). | chr1:9562761−9563887 REVERSE LENGTH=174	174	174	1.00E−98	100.0	97.1	98.3
Rsa1.0_00215.1.g8782.t7	ref|XP_002890733.1| T17H3.9 [Arabidopsis lyrata subsp. lyrata] gi|297336575|gb|EFH66992.1| T17H3.9 [Arabidopsis lyrata subsp. lyrata]	246	1290	1.00E−110	524.4	79.7	84.6	T17H3.9	gbpln	Arabidopsis lyrata	AT1G27590.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3453 (InterPro:IPR021850); BEST Arabidopsis thaliana protein match is: phosphatidylinositol 3− and 4−kinase family protein (TAIR:AT1G27570.1); Has 109 Blast hits to 109 proteins in 38 species: Archae − 0; Bacteria − 0; Metazoa − 65; Fungi − 4; Plants − 38; Viruses − 0; Other Eukaryotes − 2 (source: NCBI BLink). | chr1:9592293−9593912 FORWARD LENGTH=264	246	264	1.00E−110	107.3	79.7	83.7
Rsa1.0_00215.1.g8783.t1	gb|EOA30313.1| hypothetical protein CARUB_v10013439mg, partial [Capsella rubella]	464	530	0	114.2	82.5	91.2	hypothetical protein CARUB_v10013439mg, partial	gbpln	Capsella rubella	AT2G18193.1 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:7917621−7919184 REVERSE LENGTH=495	464	495	0	106.7	80.2	87.7

Rsa1.0_00215.1.g8784.t1	gb|EOA37898.1| hypothetical protein CARUB_v10009365mg [Capsella rubella]	385	395	0	102.6	84.4	91.7	hypothetical protein CARUB_v10009365mg	gbpln	Capsella rubella	AT1G27600.2 | Symbols: IRX9-L, I9H | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:9604083-9605881 REVERSE LENGTH=394	385	394	0	102.3	83.6	90.6
Rsa1.0_00215.1.g8785.t1	ref|XP_002890739.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336581|gb|EFH66998.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	442	442	0	100.0	83.9	91.2	transferase family protein	gbpln	Arabidopsis lyrata	AT1G27620.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:9608444-9610432 FORWARD LENGTH=442	442	442	0	100.0	83.9	90.7
Rsa1.0_00215.1.g8786.t1	gb|EOA38290.1| hypothetical protein CARUB_v10009784mg [Capsella rubella]	363	317	2.33E-156	87.3	78.5	83.2	hypothetical protein CARUB_v10009784mg	gbpln	Capsella rubella	AT1G27630.1 | Symbols: CYCT1;3 | cyclin T 1;3 | chr1:9611647-9613967 FORWARD LENGTH=317	363	317	1.00E-148	87.3	77.7	82.4
Rsa1.0_00215.1.g8787.t1	dbj|BAJ34257.1| unnamed protein product [Thellungiella halophila]	293	308	1.00E-117	105.1	83.6	89.4	unnamed protein product	----	----	AT1G27650.1 | Symbols: ATU2AF35A | U2 snRNP auxiliary factor small subunit, putative | chr1:9615152-9616042 FORWARD LENGTH=296	293	296	1.00E-116	101.0	81.2	87.4
Rsa1.0_00215.1.g8788.t1	ref|XP_002890742.1| hypothetical protein ARALYDRAFT_472970 [Arabidopsis lyrata subsp. lyrata] gi|297336584|gb|EFH67001.1| hypothetical protein ARALYDRAFT_472970 [Arabidopsis lyrata subsp. lyrata]	443	449	0	101.4	87.1	92.1	hypothetical protein ARALYDRAFT_472970	gbpln	Arabidopsis lyrata	AT1G27660.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:9621701-9625666 FORWARD LENGTH=453	443	453	0	102.3	86.9	92.8
Rsa1.0_00215.1.g8789.t1	gb|EOA36870.1| hypothetical protein CARUB_v10008862mg [Capsella rubella]	114	519	1.00E-27	455.3	55.3	63.2	hypothetical protein CARUB_v10008862mg	gbpln	Capsella rubella	AT1G27680.1 | Symbols: APL2 | ADPGLC-PPase large subunit | chr1:9631630-9634450 FORWARD LENGTH=518	114	518	1.00E-29	454.4	53.5	63.2
Rsa1.0_00215.1.g8790.t1	#	#	#	#	#	#	#	-	----	----	AT1G27695.2 | Symbols: | glycine-rich protein | chr1:9639214-9640002 FORWARD LENGTH=91	86	91	2.00E-11	105.8	89.5	95.3
Rsa1.0_00215.1.g8791.t1	ref|XP_002893486.1| hypothetical protein ARALYDRAFT_472976 [Arabidopsis lyrata subsp. lyrata] gi|297339328|gb|EFH69745.1| hypothetical protein ARALYDRAFT_472976 [Arabidopsis lyrata subsp. lyrata]	292	297	1.00E-138	101.7	85.3	91.4	hypothetical protein ARALYDRAFT_472976	gbpln	Arabidopsis lyrata	AT1G27700.1 | Symbols: | Syntaxin/t-SNARE family protein | chr1:9640394-9641752 REVERSE LENGTH=297	292	297	1.00E-136	101.7	83.6	89.7
Rsa1.0_00215.1.g8792.t1	gb|AAK92721.1| putative actin protein [Arabidopsis thaliana]	160	421	2.00E-11	263.1	22.5	27.5	putative actin protein	gbpln	Arabidopsis thaliana	AT3G33520.1 | Symbols: ATARP6, ARP6, SUF3, ESD1 | actin-related protein 6 | chr3:14093791-14095476 REVERSE LENGTH=421	160	421	6.00E-14	263.1	22.5	27.5
Rsa1.0_00215.1.g8793.t2	gb|AAF24959.1|AC012375_22 T22C5.18 [Arabidopsis thaliana]	203	265	1.00E-63	130.5	69.5	74.9	T22C5.18	gbpln	Arabidopsis thaliana	AT1G27730.1 | Symbols: STZ, ZAT10 | salt tolerance zinc finger | chr1:9648302-9648985 REVERSE LENGTH=227	203	227	8.00E-66	111.8	69.5	74.9
Rsa1.0_00215.1.g8794.t1	ref|NP_564293.1| transcription factor bHLH54 [Arabidopsis thaliana] gi|75301354|sp|Q8LEG1.1|BH054_ARATH RecName: Full=Transcription factor bHLH54; AltName: Full=Basic helix-loop-helix protein 54; Short=AtbHLH54; Short=bHLH 54; AltName: Full=Transcription factor EN 114; AltName: Full=bHLH transcription factor bHLH054 gi|21553570|gb|AAM62663.1| unknown [Arabidopsis thaliana] gi|225897974|dbj|BAH30319.1| hypothetical protein [Arabidopsis thaliana] gi|332192750|gb|AEE30871.1| transcription factor bHLH54 [Arabidopsis thaliana]	254	258	1.00E-121	101.6	87.4	92.1	transcription factor bHLH54	gbpln	Arabidopsis thaliana	AT1G27740.1 | Symbols: RSL4 | root hair defective 6-like 4 | chr1:9654753-9655806 FORWARD LENGTH=258	254	258	1.00E-124	101.6	87.4	92.1
Rsa1.0_00215.1.g8795.t1	ref|NP_001077611.1| Ubiquitin system component Cue protein [Arabidopsis thaliana] gi|332192752|gb|AEE30873.1| Ubiquitin system component Cue protein [Arabidopsis thaliana]	934	873	0	93.5	79.6	84.2	Ubiquitin system component Cue protein	gbpln	Arabidopsis thaliana	AT1G27752.1 | Symbols: | Ubiquitin system component Cue protein | chr1:9662250-9667318 FORWARD LENGTH=873	934	873	0	93.5	79.6	84.2
Rsa1.0_00215.1.g8796.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	336	1491	2.00E-68	443.8	40.8	55.1	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	336	237	3.00E-20	70.5	18.8	28.6
Rsa1.0_00215.1.g8797.t1	gb|EOA39804.1| hypothetical protein CARUB_v10008467mg [Capsella rubella]	133	699	7.00E-67	525.6	95.5	97.0	hypothetical protein CARUB_v10008467mg	gbpln	Capsella rubella	AT1G27900.1 | Symbols: | RNA helicase family protein | chr1:9715615-9720346 REVERSE LENGTH=700	133	700	2.00E-68	526.3	94.7	96.2
Rsa1.0_00215.1.g8798.t1	gb|EOA39726.1| hypothetical protein CARUB_v10008370mg [Capsella rubella]	770	768	0	99.7	90.9	95.1	hypothetical protein CARUB_v10008370mg	gbpln	Capsella rubella	AT1G27910.1 | Symbols: PUB45, ATPUB45 | plant U-box 45 | chr1:9720962-9723975 REVERSE LENGTH=768	770	768	0	99.7	90.5	95.5

Rsa1.0_00215.1.g8799.t1	ref|NP_850204.2| Haloacid dehalogenase-like hydrolase [Arabidopsis thaliana] gi|20196855|gb|AAM14806.1| unknown protein [Arabidopsis thaliana] gi|330253712|gb|AEC08806.1| Haloacid dehalogenase-like hydrolase [Arabidopsis thaliana]	169	245	6.00E-38	145.0	52.7	58.0	Haloacid dehalogenase-like hydrolase	gbpln	Arabidopsis thaliana	AT2G33255.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:14098795-14100358 FORWARD LENGTH=245	169	245	2.00E-40	145.0	52.7	58.0
Rsa1.0_00215.1.g8800.t1	ref|XP_002890752.1| hypothetical protein ARALYDRAFT_890328 [Arabidopsis lyrata subsp. lyrata] gi|297336594|gb|EFH67011.1| hypothetical protein ARALYDRAFT_890328 [Arabidopsis lyrata subsp. lyrata]	183	197	1.00E-67	107.7	75.4	86.3	hypothetical protein ARALYDRAFT_890328	gbpln	Arabidopsis lyrata	AT1G27950.1 | Symbols: LTPG1 | glycosylphosphatidylinositol-anchored lipid protein transfer 1 | chr1:9740740-9741991 FORWARD LENGTH=193	183	193	1.00E-66	105.5	73.2	82.5
Rsa1.0_00215.1.g8801.t1	ref|XP_002893496.1| evolutionarily conserved C-terminal region 9 [Arabidopsis lyrata subsp. lyrata] gi|297339338|gb|EFH69755.1| evolutionarily conserved C-terminal region 9 [Arabidopsis lyrata subsp. lyrata]	536	559	1.00E-175	104.3	68.5	75.7	evolutionarily conserved C-terminal region 9	gbpln	Arabidopsis lyrata	AT1G27960.1 | Symbols: ECT9 | evolutionarily conserved C-terminal region 9 | chr1:9742359-9745648 REVERSE LENGTH=539	536	539	1.00E-173	100.6	66.8	75.6
Rsa1.0_00215.1.g8802.t7	ref|XP_002890754.1| pyridoxal-dependent decarboxylase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336596|gb|EFH67013.1| pyridoxal-dependent decarboxylase family protein [Arabidopsis lyrata subsp. lyrata]	578	544	0	94.1	86.0	90.0	pyridoxal-dependent decarboxylase family protein	gbpln	Arabidopsis lyrata	AT1G27980.1 | Symbols: DPL1, ATDPL1 | dihydrosphingosine phosphate lyase | chr1:9748812-9752618 FORWARD LENGTH=544	578	544	0	94.1	85.6	89.6
Rsa1.0_00215.1.g8803.t1	ref|XP_002893503.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297339345|gb|EFH69762.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	424	428	1.00E-161	100.9	75.0	82.8	zinc finger (B-box type) family protein	gbpln	Arabidopsis lyrata	AT1G28050.1 | Symbols: | B-box type zinc finger protein with CCT domain | chr1:9775768-9777657 REVERSE LENGTH=433	424	433	1.00E-154	102.1	74.5	82.1
Rsa1.0_00215.1.g8804.t1	gb|EOA39702.1| hypothetical protein CARUB_v10008347mg [Capsella rubella]	759	787	0	103.7	76.4	85.4	hypothetical protein CARUB_v10008347mg	gbpln	Capsella rubella	AT1G28060.1 | Symbols: | Pre-mRNA-splicing factor 3 | chr1:9779167-9782486 FORWARD LENGTH=786	759	786	0	103.6	75.8	84.1
Rsa1.0_00215.1.g8805.t1	ref|NP_174128.1| uncharacterized protein [Arabidopsis thaliana] gi|12323005|gb|AAG51495.1|AC069471_26 hypothetical protein [Arabidopsis thaliana] gi|44681470|gb|AAS47675.1| At1g28070 [Arabidopsis thaliana] gi|62318580|dbj|BAD94977.1| hypothetical protein [Arabidopsis thaliana] gi|332192787|gb|AEE30908.1| uncharacterized protein AT1G28070 [Arabidopsis thaliana]	176	176	3.00E-46	100.0	65.3	77.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G28070.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G33510.1); Has 85 Blast hits to 77 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 85; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:9783082-9783864 FORWARD LENGTH=176	176	176	1.00E-48	100.0	65.3	77.3
Rsa1.0_00215.1.g8806.t1	ref|XP_002890758.1| hypothetical protein ARALYDRAFT_313512 [Arabidopsis lyrata subsp. lyrata] gi|297336600|gb|EFH67017.1| hypothetical protein ARALYDRAFT_313512 [Arabidopsis lyrata subsp. lyrata]	264	296	2.00E-91	112.1	72.7	80.3	hypothetical protein ARALYDRAFT_313512	gbpln	Arabidopsis lyrata	AT1G28080.1 | Symbols: | RING finger protein | chr1:9789826-9790918 FORWARD LENGTH=291	264	291	2.00E-85	110.2	65.5	75.0
Rsa1.0_00215.1.g8807.t2	gb|EOA37308.1| hypothetical protein CARUB_v10010972mg [Capsella rubella]	457	459	0	100.4	94.1	96.9	hypothetical protein CARUB_v10010972mg	gbpln	Capsella rubella	AT1G28110.2 | Symbols: SCPL45 | serine carboxypeptidase-like 45 | chr1:9804153-9806832 REVERSE LENGTH=461	457	461	0	100.9	92.8	96.3
Rsa1.0_00215.1.g8808.t1	dbj|BAB10652.1| cell cycle control crn (crooked neck) protein-like [Arabidopsis thaliana]	127	665	1.00E-25	523.6	47.2	52.8	cell cycle control crn (crooked neck) protein-like	gbpln	Arabidopsis thaliana	AT5G41770.1 | Symbols: | crooked neck protein, putative / cell cycle protein, putative | chr5:16718021-16720936 FORWARD LENGTH=705	127	705	3.00E-28	555.1	47.2	52.8
Rsa1.0_00216.1.g8809.t2	ref|NP_195180.1| NmrA-like negative transcriptional regulator family protein [Arabidopsis thaliana] gi|3641839|emb|CAA18833.1| isoflavone reductase-like protein [Arabidopsis thaliana] gi|7270404|emb|CAB80171.1| isoflavone reductase-like protein [Arabidopsis thaliana] gi|332660990|gb|AEE86390.1| NmrA-like negative transcriptional regulator family protein [Arabidopsis thaliana]	227	306	4.00E-27	134.8	30.0	35.7	NmrA-like negative transcriptional regulator family protein	gbpln	Arabidopsis thaliana	AT4G34540.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr4:16500506-16501932 FORWARD LENGTH=306	227	306	1.00E-29	134.8	30.0	35.7

<table>
<tr><td>Rsa1.0_00216.1.g8810.t1</td><td>ref|NP_174345.1| hercules receptor kinase 2 [Arabidopsis thaliana] gi|75336895|sp|Q9SA72.1|Y1357_ARATH RecName: Full=Probable receptor-like protein kinase At1g30570; Flags: Precursor gi|4587513|gb|AAD25744.1|AC007060_2 Contains eukaryotic protein kinase domain PF|00069 [Arabidopsis thaliana] gi|332193124|gb|AEE31245.1| hercules receptor kinase 2 [Arabidopsis thaliana]</td><td>854</td><td>849</td><td>0</td><td>99.4</td><td>85.2</td><td>91.0</td><td>hercules receptor kinase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30570.1 | Symbols: HERK2 | hercules receptor kinase 2 | chr1:10828933-10831482 FORWARD LENGTH=849</td><td>854</td><td>849</td><td>0</td><td>99.4</td><td>85.2</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00216.1.g8811.t1</td><td>ref|NP_174346.1| GTP-binding protein [Arabidopsis thaliana] gi|4587514|gb|AAD25745.1|AC007060_3 Similar to WO8E3.3 gi|3880615 putative GTP-binding protein from C. elegans cosmid gb|Z92773. EST gb|AA597331 comes from this gene [Arabidopsis thaliana] gi|109134111|gb|ABG25054.1| At1g30580 [Arabidopsis thaliana] gi|332193125|gb|AEE31246.1| GTP-binding protein [Arabidopsis thaliana]</td><td>394</td><td>394</td><td>0</td><td>100.0</td><td>93.7</td><td>97.2</td><td>GTP-binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30580.1 | Symbols: | GTP binding | chr1:10831953-10835454 REVERSE LENGTH=394</td><td>394</td><td>394</td><td>0</td><td>100.0</td><td>93.7</td><td>97.2</td></tr>
<tr><td>Rsa1.0_00216.1.g8812.t1</td><td>ref|NP_174348.1| subtilase-like protein [Arabidopsis thaliana] gi|4587516|gb|AAD25747.1|AC007060_5 Strong similarity to gb|U80583 proteinase TMP from Lycopersicon esculentum and is a member of the PF|00082 subtilase family [Arabidopsis thaliana] gi|18175992|gb|AAL59964.1| putative serine proteinase [Arabidopsis thaliana] gi|20465293|gb|AAM20050.1| putative serine proteinase [Arabidopsis thaliana] gi|332193127|gb|AEE31248.1| subtilase-like protein [Arabidopsis thaliana]</td><td>833</td><td>832</td><td>0</td><td>99.9</td><td>88.8</td><td>94.7</td><td>subtilase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30600.1 | Symbols: | Subtilase family protein | chr1:10841341-10844906 REVERSE LENGTH=832</td><td>833</td><td>832</td><td>0</td><td>99.9</td><td>88.8</td><td>94.7</td></tr>
<tr><td>Rsa1.0_00216.1.g8813.t1</td><td>ref|NP_001185117.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332193129|gb|AEE31250.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]</td><td>922</td><td>978</td><td>0</td><td>106.1</td><td>79.7</td><td>87.6</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30610.2 | Symbols: EMB2279 | pentatricopeptide (PPR) repeat-containing protein | chr1:10846676-10850517 FORWARD LENGTH=978</td><td>922</td><td>978</td><td>0</td><td>106.1</td><td>79.7</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00216.1.g8814.t1</td><td>ref|XP_002890881.1| EMB2279 [Arabidopsis lyrata subsp. lyrata] gi|297336723|gb|EFH67140.1| EMB2279 [Arabidopsis lyrata subsp. lyrata]</td><td>73</td><td>913</td><td>1.00E-12</td><td>1250.7</td><td>49.3</td><td>53.4</td><td>EMB2279</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30610.1 | Symbols: EMB88, EMB2279 | pentatricopeptide (PPR) repeat-containing protein | chr1:10846676-10850517 FORWARD LENGTH=1006</td><td>73</td><td>1006</td><td>3.00E-15</td><td>1378.1</td><td>49.3</td><td>53.4</td></tr>
<tr><td>Rsa1.0_00216.1.g8815.t1</td><td>gb|AAF19546.1|AC007190_14 F23N19.13 [Arabidopsis thaliana]</td><td>565</td><td>633</td><td>1.00E-154</td><td>112.0</td><td>50.4</td><td>69.2</td><td>F23N19.13</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>565</td><td>696</td><td>1.00E-29</td><td>123.2</td><td>23.7</td><td>41.8</td></tr>
<tr><td>Rsa1.0_00216.1.g8816.t1</td><td>ref|XP_002890883.1| hypothetical protein ARALYDRAFT_890616 [Arabidopsis lyrata subsp. lyrata] gi|297336725|gb|EFH67142.1| hypothetical protein ARALYDRAFT_890616 [Arabidopsis lyrata subsp. lyrata]</td><td>420</td><td>418</td><td>0</td><td>99.5</td><td>96.2</td><td>97.6</td><td>hypothetical protein ARALYDRAFT_890616</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30620.2 | Symbols: HSR8, MUR4, UXE1 | NAD(P)-binding Rossmann-fold superfamily protein | chr1:10855496-10857970 FORWARD LENGTH=419</td><td>420</td><td>419</td><td>0</td><td>99.8</td><td>94.8</td><td>97.4</td></tr>
<tr><td>Rsa1.0_00216.1.g8817.t1</td><td>gb|EOA38367.1| hypothetical protein CARUB_v10009903mg [Capsella rubella]</td><td>294</td><td>292</td><td>1.00E-161</td><td>99.3</td><td>93.9</td><td>96.9</td><td>hypothetical protein CARUB_v10009903mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30630.1 | Symbols: | Coatomer epsilon subunit | chr1:10858546-10860173 REVERSE LENGTH=292</td><td>294</td><td>292</td><td>1.00E-163</td><td>99.3</td><td>93.9</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00216.1.g8818.t2</td><td>ref|XP_002890884.1| hypothetical protein ARALYDRAFT_313702 [Arabidopsis lyrata subsp. lyrata] gi|297336726|gb|EFH67143.1| hypothetical protein ARALYDRAFT_313702 [Arabidopsis lyrata subsp. lyrata]</td><td>562</td><td>564</td><td>0</td><td>100.4</td><td>91.8</td><td>96.1</td><td>hypothetical protein ARALYDRAFT_313702</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30640.1 | Symbols: | Protein kinase family protein | chr1:10861297-10864700 FORWARD LENGTH=562</td><td>562</td><td>562</td><td>0</td><td>100.0</td><td>89.1</td><td>93.2</td></tr>
<tr><td>Rsa1.0_00216.1.g8819.t1</td><td>ref|XP_002890885.1| WRKY DNA-binding protein 14 [Arabidopsis lyrata subsp. lyrata] gi|297336727|gb|EFH67144.1| WRKY DNA-binding protein 14 [Arabidopsis lyrata subsp. lyrata]</td><td>405</td><td>425</td><td>1.00E-164</td><td>104.9</td><td>81.5</td><td>88.1</td><td>WRKY DNA-binding protein 14</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30650.1 | Symbols: WRKY14, ATWRKY14, AR411 | WRKY DNA-binding protein 14 | chr1:10868612-10870973 FORWARD LENGTH=430</td><td>405</td><td>430</td><td>1.00E-167</td><td>106.2</td><td>81.0</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00216.1.g8820.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00216.1.g8821.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00216.1.g8822.t1</td><td>gb|EOA39325.1| hypothetical protein CARUB_v10012366mg [Capsella rubella]</td><td>710</td><td>715</td><td>0</td><td>100.7</td><td>83.7</td><td>91.4</td><td>hypothetical protein CARUB_v10012366mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30680.1 | Symbols: | toprim domain-containing protein | chr1:10881665-10886060 FORWARD LENGTH=709</td><td>710</td><td>709</td><td>0</td><td>99.9</td><td>82.8</td><td>88.6</td></tr>
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Rsa1.0_00216.1.g8823.t1	ref|XP_002890888.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336730|gb|EFH67147.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	563	546	0	97.0	70.9	80.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G30690.2 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:10888284-10890085 FORWARD LENGTH=540	563	540	0	95.9	71.4	80.6
Rsa1.0_00216.1.g8824.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00216.1.g8825.t1	gb|EOA40123.1| hypothetical protein CARUB_v10008825mg [Capsella rubella]	530	530	0	100.0	86.2	92.3	hypothetical protein CARUB_v10008825mg	gbpln	Capsella rubella	AT1G30700.1 | Symbols: | FAD-binding Berberine family protein | chr1:10892623-10894437 FORWARD LENGTH=527	530	527	0	99.4	85.3	93.0
Rsa1.0_00216.1.g8826.t1	gb|EOA39278.1| hypothetical protein CARUB_v10012287mg [Capsella rubella]	531	531	0	100.0	88.1	93.6	hypothetical protein CARUB_v10012287mg	gbpln	Capsella rubella	AT1G30710.1 | Symbols: | FAD-binding Berberine family protein | chr1:10895280-10896875 FORWARD LENGTH=531	531	531	0	100.0	86.3	92.7
Rsa1.0_00216.1.g8827.t1	ref|NP_174364.2| F-box domain-containing protein [Arabidopsis thaliana] gi|302425247|sp|Q9SY17.2|FB314_ARATH RecName: Full=Probable F-box protein At1g30780 gi|332193150|gb|AEE31271.1| F-box domain-containing protein [Arabidopsis thaliana]	142	482	1.00E-39	339.4	66.9	75.4	F-box domain-containing protein	gbpln	Arabidopsis thaliana	AT1G30780.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:10923919-10926561 REVERSE LENGTH=482	142	482	4.00E-42	339.4	66.9	75.4
Rsa1.0_00216.1.g8828.t2	gb|EOA39649.1| hypothetical protein CARUB_v10008288mg, partial [Capsella rubella]	830	855	0	103.0	85.4	91.6	hypothetical protein CARUB_v10008288mg, partial	gbpln	Capsella rubella	AT1G30810.2 | Symbols: | Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein | chr1:10938139-10941505 REVERSE LENGTH=819	830	819	0	98.7	84.8	90.1
Rsa1.0_00216.1.g8829.t1	ref|NP_001031120.1| uncharacterized protein [Arabidopsis thaliana] gi|186479080|ref|NP_001117392.1| uncharacterized protein [Arabidopsis thaliana] gi|332193156|gb|AEE31277.1| uncharacterized protein AT1G30814 [Arabidopsis thaliana] gi|332193158|gb|AEE31279.1| uncharacterized protein AT1G30814 [Arabidopsis thaliana]	291	305	3.00E-41	104.8	40.5	53.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G30814.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:10942826-10944225 REVERSE LENGTH=305	291	305	9.00E-44	104.8	40.5	53.3
Rsa1.0_00217.1.g8830.t2	ref|XP_002883160.1| hypothetical protein ARALYDRAFT_479423 [Arabidopsis lyrata subsp. lyrata] gi|297329000|gb|EFH59419.1| hypothetical protein ARALYDRAFT_479423 [Arabidopsis lyrata subsp. lyrata]	2789	2771	0	99.4	82.6	89.3	hypothetical protein ARALYDRAFT_479423	gbpln	Arabidopsis lyrata	AT3G19050.1 | Symbols: POK2 | phragmoplast orienting kinesin 2 | chr3:6578047-6590106 FORWARD LENGTH=2771	2789	2771	0	99.4	82.5	89.1
Rsa1.0_00217.1.g8831.t5	ref|NP_188538.1| SWIB complex BAF60b domain-containing protein [Arabidopsis thaliana] gi|332642670|gb|AEE76191.1| SWIB complex BAF60b domain-containing protein [Arabidopsis thaliana]	505	462	1.00E-172	91.5	69.9	77.0	SWIB complex BAF60b domain-containing protein	gbpln	Arabidopsis thaliana	AT3G19080.1 | Symbols: | SWIB complex BAF60b domain-containing protein | chr3:6596082-6598667 FORWARD LENGTH=462	505	462	1.00E-175	91.5	69.9	77.0
Rsa1.0_00217.1.g8832.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1436	1515	0	105.5	57.7	73.6	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1436	1262	7.00E-95	87.9	12.5	18.5
Rsa1.0_00217.1.g8833.t1	gb|EOA32461.1| hypothetical protein CARUB_v10015738mg [Capsella rubella]	442	456	0	103.2	81.9	88.7	hypothetical protein CARUB_v10015738mg	gbpln	Capsella rubella	AT3G19090.1 | Symbols: | RNA-binding protein | chr3:6601466-6603709 FORWARD LENGTH=455	442	455	0	102.9	80.8	87.3
Rsa1.0_00217.1.g8834.t1	ref|XP_002862200.1| hypothetical protein ARALYDRAFT_921091 [Arabidopsis lyrata subsp. lyrata] gi|297307451|gb|EFH38458.1| hypothetical protein ARALYDRAFT_921091 [Arabidopsis lyrata subsp. lyrata]	418	417	0	99.8	93.1	97.4	hypothetical protein ARALYDRAFT_921091	gbpln	Arabidopsis lyrata	AT3G19100.1 | Symbols: | Protein kinase superfamily protein | chr3:6605681-6608980 FORWARD LENGTH=599	418	599	0	143.3	92.6	96.7
Rsa1.0_00217.1.g8835.t2	gb|EOA30594.1| hypothetical protein CARUB_v10013726mg [Capsella rubella]	436	438	1.00E-157	100.5	67.9	73.4	hypothetical protein CARUB_v10013726mg	gbpln	Capsella rubella	AT3G19130.1 | Symbols: ATRBP47B, RBP47B | RNA-binding protein 47B | chr3:6611398-6613823 REVERSE LENGTH=435	436	435	1.00E-158	99.8	67.9	74.3

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<tr><td>Rsa1.0_00217.1.g8836.t1</td><td>ref|NP_188546.1| cyclin-dependent kinase inhibitor 6 [Arabidopsis thaliana] gi|152032530|sp|Q0WNX9.2|KRP6_ARATH RecName: Full=Cyclin-dependent kinase inhibitor 6; AltName: Full=Cyclin-dependent kinase inhibitor p22ack1; AltName: Full=Inhibitor/interactor of CDK protein 4; AltName: Full=KIP-related protein 6 gi|8789105|gb|AAF77612.2|AF106705_1 cyclin dependent kinase inhibitor [Arabidopsis thaliana] gi|9294616|dbj|BAB02955.1| unnamed protein product [Arabidopsis thaliana] gi|14422295|emb|CAC41620.1| cyclin-dependent kinase inhibitor 6 [Arabidopsis thaliana] gi|149944321|gb|ABR46203.1| At3g19150 [Arabidopsis thaliana] gi|332642677|gb|AEE76198.1| cyclin-dependent kinase inhibitor 6 [Arabidopsis thaliana]</td><td>178</td><td>196</td><td>3.00E-19</td><td>110.1</td><td>52.2</td><td>63.5</td><td>cyclin-dependent kinase inhibitor 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19150.1 | Symbols: KRP6, ICK4, ACK1 | KIP-related protein 6 | chr3:6616628-6617655 REVERSE LENGTH=196</td><td>178</td><td>196</td><td>1.00E-21</td><td>110.1</td><td>52.2</td><td>63.5</td></tr>
<tr><td>Rsa1.0_00217.1.g8837.t3</td><td>ref|XP_002883164.1| hypothetical protein ARALYDRAFT_318673 [Arabidopsis lyrata subsp. lyrata] gi|297329004|gb|EFH59423.1| hypothetical protein ARALYDRAFT_318673 [Arabidopsis lyrata subsp. lyrata]</td><td>810</td><td>835</td><td>0</td><td>103.1</td><td>82.8</td><td>88.3</td><td>hypothetical protein ARALYDRAFT_318673</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G19180.1 | Symbols: ARC6H, PARC6, ATCDP1, CDP1 | paralog of ARC6 | chr3:6632810-6636953 FORWARD LENGTH=819</td><td>810</td><td>819</td><td>0</td><td>101.1</td><td>82.0</td><td>87.7</td></tr>
<tr><td>Rsa1.0_00217.1.g8838.t2</td><td>gb|ADU79134.1| autophagy-related protein 2 [Arabidopsis thaliana]</td><td>1879</td><td>1892</td><td>0</td><td>100.7</td><td>82.1</td><td>89.1</td><td>autophagy-related protein 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19190.1 | Symbols: ATATG2, ATG2 | autophagy 2 | chr3:6639879-6648274 FORWARD LENGTH=1839</td><td>1879</td><td>1839</td><td>0</td><td>97.9</td><td>79.4</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00217.1.g8839.t1</td><td>ref|NP_188551.1| uncharacterized protein [Arabidopsis thaliana] gi|9294623|dbj|BAB02962.1| unnamed protein product [Arabidopsis thaliana] gi|61742707|gb|AAX55174.1| hypothetical protein At3g19200 [Arabidopsis thaliana] gi|332642686|gb|AEE76207.1| uncharacterized protein AT3G19200 [Arabidopsis thaliana]</td><td>149</td><td>143</td><td>5.00E-57</td><td>96.0</td><td>79.9</td><td>84.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19200.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G34419.1); Has 51 Blast hits to 51 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6649478-6650006 REVERSE LENGTH=143</td><td>149</td><td>143</td><td>1.00E-59</td><td>96.0</td><td>79.9</td><td>84.6</td></tr>
<tr><td>Rsa1.0_00217.1.g8840.t7</td><td>ref|XP_002885300.1| hypothetical protein ARALYDRAFT_479436 [Arabidopsis lyrata subsp. lyrata] gi|297331140|gb|EFH61559.1| hypothetical protein ARALYDRAFT_479436 [Arabidopsis lyrata subsp. lyrata]</td><td>954</td><td>910</td><td>0</td><td>95.4</td><td>85.7</td><td>89.5</td><td>hypothetical protein ARALYDRAFT_479436</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G19210.1 | Symbols: ATRAD54, CHR25, RAD54 | homolog of RAD54 | chr3:6652799-6658876 REVERSE LENGTH=910</td><td>954</td><td>910</td><td>0</td><td>95.4</td><td>86.0</td><td>89.3</td></tr>
<tr><td>Rsa1.0_00217.1.g8841.t1</td><td>gb|EOA31498.1| hypothetical protein CARUB_v10014684mg [Capsella rubella]</td><td>191</td><td>198</td><td>1.00E-87</td><td>103.7</td><td>84.8</td><td>90.6</td><td>hypothetical protein CARUB_v10014684mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G19220.1 | Symbols: CYO1, SCO2 | protein disulfide isomerases | chr3:6659207-6660488 FORWARD LENGTH=187</td><td>191</td><td>187</td><td>5.00E-87</td><td>97.9</td><td>83.2</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00217.1.g8842.t1</td><td>ref|NP_188554.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|332642690|gb|AEE76211.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]</td><td>517</td><td>519</td><td>0</td><td>100.4</td><td>82.0</td><td>89.0</td><td>leucine-rich repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19230.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:6661088-6663519 REVERSE LENGTH=519</td><td>517</td><td>519</td><td>0</td><td>100.4</td><td>82.0</td><td>89.0</td></tr>
<tr><td>Rsa1.0_00217.1.g8843.t1</td><td>gb|EOA30075.1| hypothetical protein CARUB_v10013181mg [Capsella rubella]</td><td>636</td><td>646</td><td>0</td><td>101.6</td><td>87.6</td><td>93.9</td><td>hypothetical protein CARUB_v10013181mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G19240.1 | Symbols: | Vacuolar import/degradation, Vid27-related protein | chr3:6664383-6666423 FORWARD LENGTH=648</td><td>636</td><td>648</td><td>0</td><td>101.9</td><td>86.6</td><td>93.6</td></tr>
<tr><td>Rsa1.0_00218.1.g8844.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00218.1.g8845.t4</td><td>ref|NP_196926.2| protoporphyrinogen oxidase [Arabidopsis thaliana] gi|18700121|gb|AAL77672.1| AT5g14220/MUA22_22 [Arabidopsis thaliana] gi|20856027|gb|AAM26644.1| AT5g14220/MUA22_22 [Arabidopsis thaliana] gi|332004618|gb|AED92001.1| protoporphyrinogen oxidase [Arabidopsis thaliana]</td><td>538</td><td>508</td><td>0</td><td>94.4</td><td>85.9</td><td>88.7</td><td>protoporphyrinogen oxidase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14220.1 | Symbols: HEMG2, MEE61, PPO2 | Flavin containing amine oxidoreductase family | chr5:4583506-4587369 REVERSE LENGTH=508</td><td>538</td><td>508</td><td>0</td><td>94.4</td><td>85.9</td><td>88.7</td></tr>
<tr><td>Rsa1.0_00218.1.g8846.t1</td><td>ref|NP_196925.2| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|224589671|gb|ACN59367.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332004617|gb|AED92000.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]</td><td>776</td><td>775</td><td>0</td><td>99.9</td><td>86.2</td><td>90.6</td><td>leucine-rich repeat protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14210.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:4578503-4581374 REVERSE LENGTH=775</td><td>776</td><td>775</td><td>0</td><td>99.9</td><td>86.2</td><td>90.6</td></tr>
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Rsa1.0_00218.1.g8847.t1	ref|NP_568295.2| triacylglycerol lipase 2 [Arabidopsis thaliana] gi|75322727|sp|Q67ZU1.1|LIP2_ARATH RecName: Full=Triacylglycerol lipase 2; Flags: Precursor gi|51970194|dbj|BAD43789.1| unnamed protein product [Arabidopsis thaliana] gi|332004613|gb|AED91996.1| triacylglycerol lipase 2 [Arabidopsis thaliana]	455	418	0	91.9	73.8	80.4	triacylglycerol lipase 2	gbpln	Arabidopsis thaliana	AT5G14180.1 | Symbols: MPL1 | Myzus persicae-induced lipase 1 | chr5:4571442-4574413 REVERSE LENGTH=418	455	418	0	91.9	73.8	80.4
Rsa1.0_00218.1.g8848.t1	gb|EOA20357.1| hypothetical protein CARUB_v10000669mg [Capsella rubella] gi|482556166|gb|EOA20358.1| hypothetical protein CARUB_v10000669mg [Capsella rubella] gi|482556167|gb|EOA20359.1| hypothetical protein CARUB_v10000669mg [Capsella rubella]	549	536	0	97.6	82.7	87.1	hypothetical protein CARUB_v10000669mg	gbpln	Capsella rubella	AT5G14170.1 | Symbols: CHC1 | SWIB/MDM2 domain superfamily protein | chr5:4568696-4570444 REVERSE LENGTH=534	549	534	0	97.3	83.2	87.4
Rsa1.0_00218.1.g8849.t1	gb|EOA21047.1| hypothetical protein CARUB_v10001386mg [Capsella rubella]	322	335	1.00E-139	104.0	76.4	84.2	hypothetical protein CARUB_v10001386mg	gbpln	Capsella rubella	AT5G14130.1 | Symbols: | Peroxidase superfamily protein | chr5:4558862-4560028 REVERSE LENGTH=330	322	330	1.00E-139	102.5	75.8	84.2
Rsa1.0_00218.1.g8850.t1	dbj|BAJ34083.1| unnamed protein product [Thellungiella halophila]	580	579	0	99.8	88.8	94.0	unnamed protein product	----	----	AT5G14120.1 | Symbols: | Major facilitator superfamily protein | chr5:4556308-4558447 FORWARD LENGTH=579	580	579	0	99.8	87.9	94.3
Rsa1.0_00218.1.g8851.t1	gb|ACG47680.1| hypothetical protein [Zea mays] gi|413946083|gb|AFW78732.1| hypothetical protein ZEAMMB73_647957 [Zea mays]	56	72	2.00E-17	128.6	78.6	85.7	hypothetical protein	gbenv/gbpln	Zea mays	AT5G14105.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4552169-4552901 REVERSE LENGTH=76	56	76	7.00E-16	135.7	66.1	69.6
Rsa1.0_00218.1.g8852.t1	ref|NP_196914.1| ABC transporter I family member 11 [Arabidopsis thaliana] gi|75330013|sp|Q8LEF6.1|AB11I_ARATH RecName: Full=ABC transporter I family member 11, chloroplastic; Short=ABC transporter ABCI.11; Short=AtABCI11; AltName: Full=Non-intrinsic ABC protein 14; Flags: Precursor gi|21553579|gb|AAM62672.1| contains similarity to ABC transporter, ATP-binding protein [Arabidopsis thaliana] gi|26452494|dbj|BAC43332.1| unknown protein [Arabidopsis thaliana] gi|29824157|gb|AAP04039.1| putative ABC transporter family protein [Arabidopsis thaliana] gi|332004604|gb|AED91987.1| ABC transporter I family member 11 [Arabidopsis thaliana]	275	278	1.00E-131	101.1	91.3	94.2	ABC transporter I family member 11	gbpln	Arabidopsis thaliana	AT5G14100.1 | Symbols: ATNAP14, NAP14 | non-intrinsic ABC protein 14 | chr5:4549706-4551632 REVERSE LENGTH=278	275	278	1.00E-134	101.1	91.3	94.2
Rsa1.0_00218.1.g8853.t1	gb|EOA20940.1| hypothetical protein CARUB_v10001273mg [Capsella rubella]	409	357	1.00E-135	87.3	63.1	70.2	hypothetical protein CARUB_v10001273mg	gbpln	Capsella rubella	AT5G14090.1 | Symbols: | unknown protein; Has 56 Blast hits to 56 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 46; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr5:4547230-4549214 FORWARD LENGTH=358	409	358	1.00E-137	87.5	63.1	71.4
Rsa1.0_00218.1.g8854.t1	ref|XP_002873646.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319483|gb|EFH49905.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	640	634	0	99.1	87.8	93.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G14080.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:4543265-4545256 REVERSE LENGTH=634	640	634	0	99.1	86.6	92.3
Rsa1.0_00218.1.g8855.t1	gb|EOA21767.1| hypothetical protein CARUB_v10002222mg [Capsella rubella]	134	140	1.00E-57	104.5	84.3	91.0	hypothetical protein CARUB_v10002222mg	gbpln	Capsella rubella	AT5G14070.1 | Symbols: ROXY2 | Thioredoxin superfamily protein | chr5:4541915-4542337 FORWARD LENGTH=140	134	140	5.00E-60	104.5	84.3	90.3

Rsa1.0_00218.1.g8856.t1	ref|NP_196909.1| U3 small nucleolar RNA-associated protein 18-like protein [Arabidopsis thaliana] gi|17366762|sp|Q9FMU5.1|UTP18_ARATH RecName: Full=U3 small nucleolar RNA-associated protein 18 homolog gi|9757786|dbj|BAB08284.1| unnamed protein product [Arabidopsis thaliana] gi|18700147|gb|AAL77685.1| AT5g14050/MUA22_5 [Arabidopsis thaliana] gi|22137238|gb|AAM91464.1| AT5g14050/MUA22_5 [Arabidopsis thaliana] gi|332004598|gb|AED91981.1| U3 small nucleolar RNA-associated protein 18-like protein [Arabidopsis thaliana]	526	546	0	103.8	81.0	88.4	U3 small nucleolar RNA-associated protein 18-like protein	gbpln	Arabidopsis thaliana	AT5G14050.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:4533539-4535179 FORWARD LENGTH=546	526	546	0	103.8	81.0	88.4
Rsa1.0_00218.1.g8857.t1	gb|EOA20732.1| hypothetical protein CARUB_v10001054mg [Capsella rubella]	422	419	0	99.3	85.1	89.1	hypothetical protein CARUB_v10001054mg	gbpln	Capsella rubella	AT5G13730.1 | Symbols: SIG4, SIGD | sigma factor 4 | chr5:4429132-4430744 REVERSE LENGTH=419	422	419	0	99.3	83.9	88.2
Rsa1.0_00218.1.g8858.t1	ref|NP_196876.1| uncharacterized protein [Arabidopsis thaliana] gi|9758038|dbj|BAB08699.1| unnamed protein product [Arabidopsis thaliana] gi|23297285|gb|AAN12932.1| unknown protein [Arabidopsis thaliana] gi|332004549|gb|AED91932.1| uncharacterized protein AT5G13720 [Arabidopsis thaliana]	264	262	1.00E-106	99.2	81.4	87.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G13720.1 | Symbols: | Uncharacterised protein family (UPF0114) | chr5:4427960-4429029 FORWARD LENGTH=262	264	262	1.00E-109	99.2	81.4	87.5
Rsa1.0_00218.1.g8859.t1	ref|XP_002873623.1| aba-overly sensitive 1 [Arabidopsis lyrata subsp. lyrata] gi|297319460|gb|EFH49882.1| aba-overly sensitive 1 [Arabidopsis lyrata subsp. lyrata]	1306	1317	0	100.8	87.7	93.1	aba-overly sensitive 1	gbpln	Arabidopsis lyrata	AT5G13680.1 | Symbols: ELO2, ABO1 | IKI3 family protein | chr5:4410522-4415471 REVERSE LENGTH=1319	1306	1319	0	101.0	87.8	93.0
Rsa1.0_00218.1.g8860.t1	ref|NP_196871.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75171811|sp|Q9FNA5.1|WTR39_ARATH RecName: Full=WAT1-related protein At5g13670 gi|9758033|dbj|BAB08694.1| unnamed protein product [Arabidopsis thaliana] gi|21536666|gb|AAM60998.1| nodulin-like protein [Arabidopsis thaliana] gi|332004543|gb|AED91926.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]	358	377	1.00E-165	105.3	81.3	88.8	nodulin MtN21 /EamA-like transporter family protein	gbpln	Arabidopsis thaliana	AT5G13670.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:4407205-4408955 REVERSE LENGTH=377	358	377	1.00E-167	105.3	81.3	88.8
Rsa1.0_00218.1.g8861.t2	ref|XP_002871578.1| elongation factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297317415|gb|EFH47837.1| elongation factor family protein [Arabidopsis lyrata subsp. lyrata]	694	675	0	97.3	94.1	95.4	elongation factor family protein	gbpln	Arabidopsis lyrata	AT5G13650.1 | Symbols: | elongation factor family protein | chr5:4397821-4402364 FORWARD LENGTH=675	694	675	0	97.3	93.7	95.2
Rsa1.0_00218.1.g8862.t1	ref|XP_002871577.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317414|gb|EFH47836.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	675	672	0	99.6	91.4	94.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G13640.1 | Symbols: ATPDAT, PDAT, PDAT1 | phospholipid:diacylglycerol acyltransferase | chr5:4393529-4397213 FORWARD LENGTH=671	675	671	0	99.4	90.2	94.2
Rsa1.0_00218.1.g8863.t1	gb|EOA22855.1| hypothetical protein CARUB_v10003585mg [Capsella rubella]	290	318	1.00E-68	109.7	49.7	65.2	hypothetical protein CARUB_v10003585mg	gbpln	Capsella rubella	AT5G13620.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49290.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4385385-4386373 REVERSE LENGTH=301	290	301	2.00E-62	103.8	49.7	64.1
Rsa1.0_00218.1.g8864.t1	ref|NP_196865.1| uncharacterized protein [Arabidopsis thaliana] gi|9758026|dbj|BAB08687.1| unnamed protein product [Arabidopsis thaliana] gi|22022566|gb|AAM83240.1| AT5g13610/MSH12_7 [Arabidopsis thaliana] gi|23308429|gb|AAN18184.1| At5g13610/MSH12_7 [Arabidopsis thaliana] gi|332004534|gb|AED91917.1| uncharacterized protein AT5G13610 [Arabidopsis thaliana]	403	402	1.00E-157	99.8	74.2	81.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G13610.1 | Symbols: | Protein of unknown function (DUF155) | chr5:4383073-4384808 FORWARD LENGTH=402	403	402	1.00E-160	99.8	74.2	81.9
Rsa1.0_00218.1.g8865.t1	gb|EOA22003.1| hypothetical protein CARUB_v10002526mg [Capsella rubella]	572	591	0	103.3	75.0	84.3	hypothetical protein CARUB_v10002526mg	gbpln	Capsella rubella	AT5G13600.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr5:4380432-4382497 FORWARD LENGTH=591	572	591	0	103.3	74.5	83.0

Rsa1.0_00218.1.g8866.t1	ref|XP_002873619.1| hypothetical protein ARALYDRAFT_909311 [Arabidopsis lyrata subsp. lyrata] gi|297319456|gb|EFH49878.1| hypothetical protein ARALYDRAFT_909311 [Arabidopsis lyrata subsp. lyrata]	1078	1217	0	112.9	65.0	75.5	hypothetical protein ARALYDRAFT_909311	gbpln	Arabidopsis lyrata	AT5G13590.1 | Symbols: | unknown protein; Has 150 Blast hits to 121 proteins in 42 species: Archae - 0; Bacteria - 8; Metazoa - 80; Fungi - 5; Plants - 17; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink). | chr5:4374718-4378647 REVERSE LENGTH=1168	1078	1168	0	108.3	62.8	73.7
Rsa1.0_00218.1.g8867.t1	ref|XP_002871574.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297317411|gb|EFH47833.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata]	728	726	0	99.7	91.5	95.1	abc transporter family protein	gbpln	Arabidopsis lyrata	AT5G13580.1 | Symbols: | ABC-2 type transporter family protein | chr5:4370879-4373062 FORWARD LENGTH=727	728	727	0	99.9	90.9	94.6
Rsa1.0_00218.1.g8868.t1	ref|NP_001190304.1| mRNA-decapping enzyme subunit 2 [Arabidopsis thaliana] gi|332004530|gb|AED91913.1| mRNA-decapping enzyme subunit 2 [Arabidopsis thaliana]	84	386	5.00E-26	459.5	81.0	84.5	mRNA-decapping enzyme subunit 2	gbpln	Arabidopsis thaliana	AT5G13570.2 | Symbols: DCP2 | decapping 2 | chr5:4367532-4369992 FORWARD LENGTH=386	84	386	8.00E-29	459.5	81.0	84.5
Rsa1.0_00218.1.g8869.t1	ref|XP_002873618.1| hypothetical protein ARALYDRAFT_909308 [Arabidopsis lyrata subsp. lyrata] gi|297319455|gb|EFH49877.1| hypothetical protein ARALYDRAFT_909308 [Arabidopsis lyrata subsp. lyrata]	679	679	0	100.0	87.2	92.5	hypothetical protein ARALYDRAFT_909308	gbpln	Arabidopsis lyrata	AT5G13560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G37370.1); Has 12055 Blast hits to 8846 proteins in 811 species: Archae - 217; Bacteria - 1046; Metazoa - 6104; Fungi - 1115; Plants - 528; Viruses - 14; Other Eukaryotes - 3031 (source: NCBI BLink). | chr5:4361579-4366318 REVERSE LENGTH=679	679	679	0	100.0	86.7	92.6
Rsa1.0_00218.1.g8870.t4	ref|XP_002882782.1| hypothetical protein ARALYDRAFT_478618 [Arabidopsis lyrata subsp. lyrata] gi|297328622|gb|EFH59041.1| hypothetical protein ARALYDRAFT_478618 [Arabidopsis lyrata subsp. lyrata]	176	180	2.00E-78	102.3	80.1	87.5	hypothetical protein ARALYDRAFT_478618	gbpln	Arabidopsis lyrata	AT3G12600.1 | Symbols: atnudt16, NUDT16 | nudix hydrolase homolog 16 | chr3:4004809-4005995 FORWARD LENGTH=180	176	180	3.00E-71	102.3	79.0	86.9
Rsa1.0_00218.1.g8871.t1	gb|EOA20189.1| hypothetical protein CARUB_v10000485mg [Capsella rubella]	611	616	0	100.8	87.9	94.3	hypothetical protein CARUB_v10000485mg	gbpln	Capsella rubella	AT5G13520.1 | Symbols: | peptidase M1 family protein | chr5:4342117-4344571 REVERSE LENGTH=616	611	616	0	100.8	87.4	93.9
Rsa1.0_00218.1.g8872.t1	ref|XP_002871572.1| ribosomal protein L10 family protein [Arabidopsis lyrata subsp. lyrata] gi|297317409|gb|EFH47831.1| ribosomal protein L10 family protein [Arabidopsis lyrata subsp. lyrata]	221	220	1.00E-109	99.5	92.3	94.6	ribosomal protein L10 family protein	gbpln	Arabidopsis lyrata	AT5G13510.1 | Symbols: | Ribosomal protein L10 family protein | chr5:4341294-4341956 FORWARD LENGTH=220	221	220	1.00E-111	99.5	92.3	94.6
Rsa1.0_00218.1.g8873.t1	ref|NP_196854.1| uncharacterized protein [Arabidopsis thaliana] gi|30684435|ref|NP_850813.1| uncharacterized protein [Arabidopsis thaliana] gi|42573361|ref|NP_974777.1| uncharacterized protein [Arabidopsis thaliana] gi|9955542|emb|CAC05427.1| putative protein [Arabidopsis thaliana] gi|19699009|gb|AAL91240.1| putative protein [Arabidopsis thaliana] gi|21594054|gb|AAM65972.1| unknown [Arabidopsis thaliana] gi|23198096|gb|AAN15575.1| putative protein [Arabidopsis thaliana] gi|332004520|gb|AED91903.1| uncharacterized protein AT5G13500 [Arabidopsis thaliana] gi|332004521|gb|AED91904.1| uncharacterized protein AT5G13500 [Arabidopsis thaliana] gi|332004522|gb|AED91905.1| uncharacterized protein AT5G13500 [Arabidopsis thaliana]	264	358	1.00E-137	135.6	89.8	95.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G13500.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25265.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:4338676-4340827 FORWARD LENGTH=358	264	358	1.00E-139	135.6	89.8	95.5
Rsa1.0_00218.1.g8874.t1	ref|XP_002871570.1| hypothetical protein ARALYDRAFT_488169 [Arabidopsis lyrata subsp. lyrata] gi|297317407|gb|EFH47829.1| hypothetical protein ARALYDRAFT_488169 [Arabidopsis lyrata subsp. lyrata]	380	384	0	101.1	91.8	95.3	hypothetical protein ARALYDRAFT_488169	gbpln	Arabidopsis lyrata	AT5G13490.2 | Symbols: AAC2 | ADP/ATP carrier 2 | chr5:4336034-4337379 FORWARD LENGTH=385	380	385	0	101.3	87.9	93.2
Rsa1.0_00218.1.g8875.t1	gb|EOA22855.1| hypothetical protein CARUB_v10003585mg [Capsella rubella]	259	318	3.00E-58	122.8	47.5	60.6	hypothetical protein CARUB_v10003585mg	gbpln	Capsella rubella	AT5G13620.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49290.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4385385-4386373 REVERSE LENGTH=301	259	301	4.00E-58	116.2	47.9	60.2

Rsa1.0_00218.1.g8876.t1	ref|XP_002871569.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317406|gb|EFH47828.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	165	163	1.00E-43	98.8	57.6	64.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G13470.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4318562-4319720 FORWARD LENGTH=159	165	159	3.00E-45	96.4	61.2	69.1
Rsa1.0_00218.1.g8877.t1	gb|ABL97953.1| hydrogen-transporting ATP synthase [Brassica rapa]	244	244	1.00E-135	100.0	97.5	98.4	hydrogen-transporting ATP synthase	gbpln	Brassica rapa	AT5G13450.1 | Symbols: ATP5 | delta subunit of Mt ATP synthase | chr5:4310558-4311941 REVERSE LENGTH=238	244	238	1.00E-119	97.5	84.4	90.6
Rsa1.0_00218.1.g8878.t1	ref|XP_002873613.1| hypothetical protein ARALYDRAFT_488163 [Arabidopsis lyrata subsp. lyrata] gi|297319450|gb|EFH49872.1| hypothetical protein ARALYDRAFT_488163 [Arabidopsis lyrata subsp. lyrata]	272	274	1.00E-147	100.7	93.0	97.4	hypothetical protein ARALYDRAFT_488163	gbpln	Arabidopsis lyrata	AT5G13430.1 | Symbols: | Ubiquinol-cytochrome C reductase iron-sulfur subunit | chr5:4305414-4307399 REVERSE LENGTH=272	272	272	1.00E-145	100.0	91.9	95.6
Rsa1.0_00218.1.g8879.t1	ref|XP_002873613.1| hypothetical protein ARALYDRAFT_488163 [Arabidopsis lyrata subsp. lyrata] gi|297319450|gb|EFH49872.1| hypothetical protein ARALYDRAFT_488163 [Arabidopsis lyrata subsp. lyrata]	271	274	1.00E-141	101.1	92.6	96.3	hypothetical protein ARALYDRAFT_488163	gbpln	Arabidopsis lyrata	AT5G13430.1 | Symbols: | Ubiquinol-cytochrome C reductase iron-sulfur subunit | chr5:4305414-4307399 REVERSE LENGTH=272	271	272	1.00E-141	100.4	93.4	95.6
Rsa1.0_00218.1.g8880.t1	ref|XP_002873611.1| hypothetical protein ARALYDRAFT_488161 [Arabidopsis lyrata subsp. lyrata] gi|297319448|gb|EFH49870.1| hypothetical protein ARALYDRAFT_488161 [Arabidopsis lyrata subsp. lyrata]	440	436	0	99.1	92.3	94.8	hypothetical protein ARALYDRAFT_488161	gbpln	Arabidopsis lyrata	AT5G13420.1 | Symbols: | Aldolase-type TIM barrel family protein | chr5:4302080-4304212 REVERSE LENGTH=438	440	438	0	99.5	92.5	95.2
Rsa1.0_00218.1.g8881.t1	ref|XP_002871567.1| hypothetical protein ARALYDRAFT_488158 [Arabidopsis lyrata subsp. lyrata] gi|297317404|gb|EFH47826.1| hypothetical protein ARALYDRAFT_488158 [Arabidopsis lyrata subsp. lyrata]	1135	1123	0	98.9	87.4	94.1	hypothetical protein ARALYDRAFT_488158	gbpln	Arabidopsis lyrata	AT5G13390.1 | Symbols: NEF1 | no exine formation 1 | chr5:4292809-4296572 FORWARD LENGTH=1123	1135	1123	0	98.9	86.9	93.7
Rsa1.0_00218.1.g8882.t1	ref|NP_196838.1| uncharacterized protein [Arabidopsis thaliana] gi|7529289|emb|CAB86641.1| putative protein [Arabidopsis thaliana] gi|332004499|gb|AED91882.1| uncharacterized protein AT5G13340 [Arabidopsis thaliana]	650	242	9.00E-70	37.2	27.8	29.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G13340.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10890.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4277939-4279397 REVERSE LENGTH=242	650	242	2.00E-72	37.2	27.8	29.7
Rsa1.0_00218.1.g8883.t1	dbj|BAJ34121.1| unnamed protein product [Thellungiella halophila]	234	231	6.00E-80	98.7	79.5	82.9	unnamed protein product	----	----	AT5G13330.1 | Symbols: Rap2.6L | related to AP2 6l | chr5:4272384-4274461 FORWARD LENGTH=212	234	212	4.00E-65	90.6	55.6	59.8
Rsa1.0_00219.1.g8884.t1	gb|AEX20385.1| cytochrome P450 family 78 subfamily A polypeptide 8 [Brassica napus]	450	534	0	118.7	89.8	94.2	cytochrome P450 family 78 subfamily A polypeptide 8	gbpln	Brassica napus	AT1G01190.1 | Symbols: CYP78A8 | cytochrome P450, family 78, subfamily A, polypeptide 8 | chr1:83045-84864 REVERSE LENGTH=535	450	535	0	118.9	88.0	92.9
Rsa1.0_00219.1.g8885.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	109	329	6.00E-17	301.8	35.8	52.3	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00219.1.g8886.t4	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1362	1529	1.00E-168	112.3	30.3	45.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1362	746	5.00E-54	54.8	10.4	14.1
Rsa1.0_00219.1.g8887.t2	gb|EOA38549.1| hypothetical protein CARUB_v10010354mg [Capsella rubella]	243	195	2.00E-64	80.2	68.7	71.2	hypothetical protein CARUB_v10010354mg	gbpln	Capsella rubella	AT1G01160.2 | Symbols: GIF2 | GRF1-interacting factor 2 | chr1:72583-73883 FORWARD LENGTH=229	243	229	3.00E-64	94.2	69.1	73.7
Rsa1.0_00219.1.g8888.t1	ref|XP_002266993.1| PREDICTED: uncharacterized protein LOC100264313 [Vitis vinifera]	97	453	6.00E-12	467.0	39.2	55.7	PREDICTED: uncharacterized protein LOC100264313	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00219.1.g8889.t1	gb|EOA40404.1| hypothetical protein CARUB_v10009130mg [Capsella rubella]	445	447	0	100.4	91.9	95.3	hypothetical protein CARUB_v10009130mg	gbpln	Capsella rubella	AT1G01140.1 | Symbols: CIPK9, SnRK3.12, PKS6 | CBL-interacting protein kinase 9 | chr1:64398-67512 REVERSE LENGTH=447	445	447	0	100.4	92.4	95.5
Rsa1.0_00219.1.g8890.t1	gb|EOA39259.1| hypothetical protein CARUB_v10012263mg [Capsella rubella]	520	528	0	101.5	94.0	96.9	hypothetical protein CARUB_v10012263mg	gbpln	Capsella rubella	AT1G01120.1 | Symbols: KCS1 | 3-ketoacyl-CoA synthase 1 | chr1:57392-58978 REVERSE LENGTH=528	520	528	0	101.5	94.6	96.7
Rsa1.0_00219.1.g8891.t1	gb|AAM64427.1| acidic ribosomal protein, putative [Arabidopsis thaliana]	114	112	1.00E-34	98.2	86.8	88.6	acidic ribosomal protein, putative	gbpln	Arabidopsis thaliana	AT4G00810.2 | Symbols: | 60S acidic ribosomal protein family | chr4:346179-346957 REVERSE LENGTH=113	114	113	4.00E-37	99.1	86.0	89.5

Rsa1.0_00219.1.g8892.t2	gb|EOA40477.1| hypothetical protein CARUB_v10009201mg [Capsella rubella]	447	430	0	96.2	89.5	91.7	hypothetical protein CARUB_v10009201mg	gbpln	Capsella rubella	AT1G01090.1 | Symbols: PDH-E1 ALPHA | pyruvate dehydrogenase E1 alpha | chr1:47705-49166 REVERSE LENGTH=428	447	428	0	95.7	87.0	91.1
Rsa1.0_00219.1.g8893.t3	ref|XP_002889387.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297335229|gb|EFH65646.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	367	361	1.00E-141	98.4	65.1	77.7	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT1G01070.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:38898-40877 REVERSE LENGTH=365	367	365	1.00E-142	99.5	65.9	79.6
Rsa1.0_00219.1.g8894.t2	gb|EOA30236.1| hypothetical protein CARUB_v10013358mg [Capsella rubella]	282	564	1.00E-28	200.0	25.2	35.5	hypothetical protein CARUB_v10013358mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	282	735	5.00E-25	260.6	25.2	34.4
Rsa1.0_00219.1.g8895.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00219.1.g8896.t1	gb|AAF06087.1|AC007918_11 Similar to gi|4325351 T25H8.2 TNP2 protein homolog from Arabidopsis thaliana BAC gb|AF128394 [Arabidopsis thaliana]	271	1121	3.00E-24	413.7	26.2	34.7	Similar to gi|4325351 T25H8.2 TNP2 protein homolog from Arabidopsis thaliana BAC gb|AF128394	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00219.1.g8897.t1	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	650	1864	5.00E-60	286.8	28.0	45.1	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00220.1.g8898.t1	gb|EOA17641.1| hypothetical protein CARUB_v10006007mg [Capsella rubella]	133	133	2.00E-71	100.0	99.2	100.0	hypothetical protein CARUB_v10006007mg	gbpln	Capsella rubella	AT4G18100.1 | Symbols: | Ribosomal protein L32e | chr4:10035715-10036475 REVERSE LENGTH=133	133	133	6.00E-74	100.0	98.5	100.0
Rsa1.0_00220.1.g8899.t1	ref|XP_002884509.1| hypothetical protein ARALYDRAFT_477824 [Arabidopsis lyrata subsp. lyrata] gi|297330349|gb|EFH60768.1| hypothetical protein ARALYDRAFT_477824 [Arabidopsis lyrata subsp. lyrata]	751	786	0	104.7	61.1	71.4	hypothetical protein ARALYDRAFT_477824	gbpln	Arabidopsis lyrata	AT3G05360.1 | Symbols: AtRLP30, RLP30 | receptor like protein 30 | chr3:1530900-1533260 REVERSE LENGTH=786	751	786	0	104.7	61.1	72.6
Rsa1.0_00220.1.g8900.t2	gb|EOA17179.1| hypothetical protein CARUB_v10005450mg [Capsella rubella]	233	278	1.00E-25	119.3	54.1	63.1	hypothetical protein CARUB_v10005450mg	gbpln	Capsella rubella	AT4G18070.4 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G29530.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10030839-10032329 FORWARD LENGTH=262	233	262	2.00E-20	112.4	29.6	35.6
Rsa1.0_00220.1.g8901.t1	gb|AGI37652.1| translation initiation factor eIF4E.c5 [Brassica rapa subsp. pekinensis]	270	234	1.00E-115	86.7	78.9	80.4	translation initiation factor eIF4E.c5	gbpln	Brassica rapa	AT4G18040.1 | Symbols: EIF4E, CUM1, AT.EIF4E1, eIF4E1 | eukaryotic translation initiation factor 4E | chr4:10016724-10018151 REVERSE LENGTH=235	270	235	1.00E-104	87.0	72.2	76.3
Rsa1.0_00220.1.g8902.t1	ref|NP_567546.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|15451060|gb|AAK96801.1| putative protein [Arabidopsis thaliana] gi|20148333|gb|AAM10057.1| putative protein [Arabidopsis thaliana] gi|119657370|tpd|FAA00284.1| TPA: AT-hook motif nuclear localized protein 13 [Arabidopsis thaliana] gi|332658571|gb|AEE83971.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	288	439	1.00E-101	152.4	74.3	81.9	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT4G17950.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:9967295-9969007 REVERSE LENGTH=439	288	439	1.00E-103	152.4	74.3	81.9
Rsa1.0_00220.1.g8903.t1	gb|EOA17188.1| hypothetical protein CARUB_v10005460mg [Capsella rubella]	254	276	1.00E-79	108.7	77.2	84.6	hypothetical protein CARUB_v10005460mg	gbpln	Capsella rubella	AT4G17940.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:9965787-9966778 FORWARD LENGTH=274	254	274	3.00E-81	107.9	74.0	83.9
Rsa1.0_00220.1.g8904.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	224	672	9.00E-39	300.0	33.0	46.0	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00220.1.g8905.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	614	1231	1.00E-179	200.5	49.7	67.1	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	614	575	6.00E-99	93.6	31.9	50.0
Rsa1.0_00220.1.g8906.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00220.1.g8907.t1	gb|EOA18343.1| hypothetical protein CARUB_v10006864mg [Capsella rubella]	89	345	1.00E-42	387.6	87.6	95.5	hypothetical protein CARUB_v10006864mg	gbpln	Capsella rubella	AT4G17785.1 | Symbols: MYB39 | myb domain protein 39 | chr4:9881867-9883368 REVERSE LENGTH=360	89	360	2.00E-45	404.5	87.6	95.5
Rsa1.0_00220.1.g8908.t1	gb|ABD65167.1| myb family transcription factor [Brassica oleracea]	197	337	1.00E-57	171.1	59.4	64.5	myb family transcription factor	gbpln	Brassica oleracea	AT4G17785.1 | Symbols: MYB39 | myb domain protein 39 | chr4:9881867-9883368 REVERSE LENGTH=360	197	360	1.00E-58	182.7	57.9	68.5

Rsa1.0_00220.1.g8909.t1	ref|NP_193506.2| homeobox-leucine zipper protein HDG4 [Arabidopsis thaliana] gi|75329764|sp|Q8L7H4.1|HDG4_ARATH RecName: Full=Homeobox-leucine zipper protein HDG4; AltName: Full=HD-ZIP protein HDG4; AltName: Full=Homeodomain GLABRA 2-like protein 4; AltName: Full=Homeodomain transcription factor HDG4; AltName: Full=Protein HOMEODOMAIN GLABROUS 4 gi|22136630|gb|AAM91634.1| putative GLABRA2 protein [Arabidopsis thaliana] gi|332658537|gb|AEE83937.1| homeobox-leucine zipper protein HDG4 [Arabidopsis thaliana]	734	709	0	96.6	63.2	77.1	homeobox-leucine zipper protein HDG4	gbpln	Arabidopsis thaliana	AT4G17710.1 | Symbols: HDG4 | homeodomain GLABROUS 4 | chr4:9856327-9859288 REVERSE LENGTH=709	734	709	0	96.6	63.2	77.1
Rsa1.0_00220.1.g8910.t1	dbj|BAJ34541.1| unnamed protein product [Thellungiella halophila]	296	302	1.00E-127	102.0	79.1	85.5	unnamed protein product	----	----	AT4G17695.1 | Symbols: KAN3 | Homeodomain-like superfamily protein | chr4:9848134-9850698 REVERSE LENGTH=322	296	322	1.00E-111	108.8	76.4	83.8
Rsa1.0_00220.1.g8911.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00220.1.g8912.t1	gb|ABD65075.1| kinase domain containing protein [Brassica oleracea]	396	396	0	100.0	90.7	94.4	kinase domain containing protein	gbpln	Brassica oleracea	AT4G17660.1 | Symbols: | Protein kinase superfamily protein | chr4:9831401-9833006 FORWARD LENGTH=388	396	388	0	98.0	78.5	86.9
Rsa1.0_00220.1.g8913.t1	gb|AAF02855.1|AC009324_4 Similar to retrotransposon proteins [Arabidopsis thaliana]	219	1522	4.00E-26	695.0	26.0	30.6	Similar to retrotransposon proteins	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00220.1.g8914.t1	gb|ABD65071.1| GATA zinc finger containing protein [Brassica oleracea]	530	508	0	95.8	84.2	87.7	GATA zinc finger containing protein	gbpln	Brassica oleracea	AT4G17570.3 | Symbols: GATA26 | GATA transcription factor 26 | chr4:9784329-9786974 REVERSE LENGTH=514	530	514	0	97.0	77.2	83.0
Rsa1.0_00220.1.g8915.t1	gb|ABD65070.1| plastid ribosomal protein L19, putative [Brassica oleracea]	211	224	4.00E-93	106.2	90.0	93.4	plastid ribosomal protein L19, putative	gbpln	Brassica oleracea	AT4G17560.1 | Symbols: | Ribosomal protein L19 family protein | chr4:9780343-9781752 FORWARD LENGTH=225	211	225	2.00E-82	106.6	82.9	88.6
Rsa1.0_00220.1.g8916.t1	gb|ABD65069.1| transporter, putative [Brassica oleracea]	534	539	0	100.9	92.3	95.1	transporter, putative	gbpln	Brassica oleracea	AT4G17550.1 | Symbols: | Major facilitator superfamily protein | chr4:9777938-9779738 REVERSE LENGTH=544	534	544	0	101.9	89.5	93.8
Rsa1.0_00220.1.g8917.t1	gb|EOA14024.1| hypothetical protein CARUB_v10027156mg [Capsella rubella]	202	202	1.00E-115	100.0	99.5	99.5	hypothetical protein CARUB_v10027156mg	gbpln	Capsella rubella	AT5G47200.1 | Symbols: ATRABD2B, ATRAB1A, RAB1A | RAB GTPase homolog 1A | chr5:19167029-19168718 FORWARD LENGTH=202	202	202	1.00E-117	100.0	99.0	99.0
Rsa1.0_00220.1.g8918.t1	gb|ABD65067.1| nuclear RNA binding protein, putative [Brassica oleracea]	377	367	1.00E-162	97.3	89.4	91.0	nuclear RNA binding protein, putative	gbpln	Brassica oleracea	AT4G17520.1 | Symbols: | Hyaluronan / mRNA binding family | chr4:9771496-9773313 FORWARD LENGTH=360	377	360	1.00E-120	95.5	70.0	76.7
Rsa1.0_00220.1.g8919.t1	ref|NP_567530.4| ethylene-responsive transcription factor 1A [Arabidopsis thaliana] gi|21264420|sp|O80337.2|EF100_ARATH RecName: Full=Ethylene-responsive transcription factor 1A; Short=AtERF1A; AltName: Full=Ethylene-responsive element-binding factor 1A; Short=EREBP-1A gi|16648795|gb|AAL25588.1| AT4g17500/dl4785w [Arabidopsis thaliana] gi|17064914|gb|AAL32611.1| Unknown protein [Arabidopsis thaliana] gi|27311945|gb|AAO00938.1| Unknown protein [Arabidopsis thaliana] gi|332658503|gb|AEE83903.1| ethylene-responsive transcription factor 1A [Arabidopsis thaliana]	257	268	1.00E-94	104.3	78.6	83.7	ethylene-responsive transcription factor 1A	gbpln	Arabidopsis thaliana	AT4G17500.1 | Symbols: ATERF-1, ERF-1 | ethylene responsive element binding factor 1 | chr4:9759405-9760211 FORWARD LENGTH=268	257	268	3.00E-97	104.3	78.6	83.7
Rsa1.0_00220.1.g8920.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00220.1.g8921.t1	gb|ABD65051.1| ethylene responsive element binding factor, putative [Brassica oleracea]	284	290	1.00E-131	102.1	87.7	93.0	ethylene responsive element binding factor, putative	gbpln	Brassica oleracea	AT4G17490.1 | Symbols: ATERF6, ERF-6-6, ERF6 | ethylene responsive element binding factor 6 | chr4:9752973-9753821 REVERSE LENGTH=282	284	282	9.00E-99	99.3	71.5	79.6
Rsa1.0_00220.1.g8922.t1	ref|NP_567528.2| PPPDE putative thiol peptidase-like protein [Arabidopsis thaliana] gi|57012715|sp|Q93VG8.1|PPDEX_ARATH RecName: Full=DeSI-like protein At4g17486 gi|14194147|gb|AAK56268.1|AF367279_1 AT4g17486/AT4g17486 [Arabidopsis thaliana] gi|15777887|gb|AAL05904.1| AT4g17486/AT4g17486 [Arabidopsis thaliana] gi|332658500|gb|AEE83900.1| PPPDE putative thiol peptidase-like protein [Arabidopsis thaliana]	227	224	1.00E-110	98.7	88.1	92.5	PPPDE putative thiol peptidase-like protein	gbpln	Arabidopsis thaliana	AT4G17486.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr4:9749992-9751201 REVERSE LENGTH=224	227	224	1.00E-112	98.7	88.1	92.5

Rsa1.0_00220.1.g8923.t1	gb|ABD65081.1| palmitoyl protein thioesterase family protein [Brassica oleracea]	295	298	1.00E-157	101.0	90.2	93.6	palmitoyl protein thioesterase family protein	gbpln	Brassica oleracea	AT4G17483.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:9747375-9748892 REVERSE LENGTH=300	295	300	1.00E-139	101.7	79.0	87.5
Rsa1.0_00220.1.g8924.t1	dbj|BAB09501.1| unnamed protein product [Arabidopsis thaliana]	386	312	1.00E-28	80.8	23.8	36.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT4G03728.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:1652242-1652976 REVERSE LENGTH=141	386	141	2.00E-15	36.5	9.6	15.0
Rsa1.0_00220.1.g8925.t1	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	286	1089	4.00E-40	380.8	35.0	50.3	transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00221.1.g8926.t1	ref|NP_182273.1| fumarate hydratase, class II [Arabidopsis thaliana] gi|145331433|ref|NP_001078075.1| fumarate hydratase, class II [Arabidopsis thaliana] gi|39931311|sp|P93033.2|FUM1_ARATH RecName: Full=Fumarate hydratase 1, mitochondrial; Short=Fumarase 1; Flags: Precursor gi|2443751|gb|AAB71399.1| fumarase [Arabidopsis thaliana] gi|2529676|gb|AAC62859.1| putative fumarase [Arabidopsis thaliana] gi|15809968|gb|AAL06911.1| At2g47510/T30B22.19 [Arabidopsis thaliana] gi|17064768|gb|AAL32538.1| putative fumarase [Arabidopsis thaliana] gi|28059023|gb|AAO29979.1| putative fumarase [Arabidopsis thaliana] gi|330255758|gb|AEC10852.1| fumarate hydratase, class II [Arabidopsis thaliana] gi|330255759|gb|AEC10853.1| fumarate hydratase 1 [Arabidopsis thaliana]	498	492	0	98.8	96.0	97.2	fumarate hydratase, class II	gbpln	Arabidopsis thaliana	AT2G47510.2 | Symbols: FUM1 | fumarase 1 | chr2:19498614-19502020 FORWARD LENGTH=492	498	492	0	98.8	96.0	97.2
Rsa1.0_00221.1.g8927.t1	gb|AAC31157.1| ethylene response sensor [Brassica oleracea]	613	613	0	100.0	99.3	99.7	ethylene response sensor	gbpln	Brassica oleracea	AT2G40940.1 | Symbols: ERS1, ERS | ethylene response sensor 1 | chr2:17084635-17086819 REVERSE LENGTH=613	613	613	0	100.0	94.8	97.2
Rsa1.0_00221.1.g8928.t1	ref|XP_002880311.1| pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata] gi|297326150|gb|EFH56570.1| pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata]	162	174	2.00E-77	107.4	89.5	94.4	pollen ole e 1 allergen and extensin family protein	gbpln	Arabidopsis lyrata	AT2G47540.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr2:19505901-19506504 FORWARD LENGTH=173	162	173	1.00E-79	106.8	89.5	93.2
Rsa1.0_00221.1.g8929.t1	gb|AAK84428.1| papillar cell-specific pectin methylesterase-like protein [Brassica napus]	562	562	0	100.0	95.7	98.4	papillar cell-specific pectin methylesterase-like protein	gbpln	Brassica napus	AT2G47550.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr2:19509024-19511604 FORWARD LENGTH=560	562	560	0	99.6	88.3	94.5
Rsa1.0_00221.1.g8930.t1	ref|NP_191828.1| RING-H2 finger protein ATL5 [Arabidopsis thaliana] gi|68565315|sp|Q9LZJ6.1|ATL5_ARATH RecName: Full=RING-H2 finger protein ATL5 gi|7362749|emb|CAB83119.1| RING-H2 zinc finger protein ATL5 [Arabidopsis thaliana] gi|32189289|gb|AAP75799.1| At3g62690 [Arabidopsis thaliana] gi|110736661|dbj|BAF00294.1| RING-H2 zinc finger protein ATL5 [Arabidopsis thaliana] gi|332646859|gb|AEE80380.1| RING-H2 finger protein ATL5 [Arabidopsis thaliana]	222	257	2.00E-65	115.8	71.2	83.8	RING-H2 finger protein ATL5	gbpln	Arabidopsis thaliana	AT3G62690.1 | Symbols: ATL5 | AtL5 | chr3:23185829-23186602 REVERSE LENGTH=257	222	257	7.00E-68	115.8	71.2	83.8
Rsa1.0_00221.1.g8931.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00221.1.g8932.t1	ref|NP_182280.1| spliceosomal protein U1A [Arabidopsis thaliana] gi|75319458|sp|Q39244.1|RU1A_ARATH RecName: Full=U1 small nuclear ribonucleoprotein A; Short=U1 snRNP protein A gi|1050430|emb|CAA90283.1| U1snRNP-specific protein [Arabidopsis thaliana] gi|2529669|gb|AAC62852.1| small nuclear ribonucleoprotein U1A [Arabidopsis thaliana] gi|15450591|gb|AAK96567.1| At2g47580/T30B22.12 [Arabidopsis thaliana] gi|16649011|gb|AAL24357.1| small nuclear ribonucleoprotein U1A [Arabidopsis thaliana] gi|20259986|gb|AAM13340.1| small nuclear ribonucleoprotein U1A [Arabidopsis thaliana] gi|22655484|gb|AAM98334.1| At2g47580/T30B22.12 [Arabidopsis thaliana] gi|330255767|gb|AEC10861.1| spliceosomal protein U1A [Arabidopsis thaliana]	282	250	1.00E-99	88.7	69.1	75.5	spliceosomal protein U1A	gbpln	Arabidopsis thaliana	AT2G47580.1 | Symbols: U1A | spliceosomal protein U1A | chr2:19517229-19518686 FORWARD LENGTH=250	282	250	1.00E-102	88.7	69.1	75.5
Rsa1.0_00221.1.g8933.t1	ref|XP_002880314.1| photolyase/blue-light receptor 2 [Arabidopsis lyrata subsp. lyrata] gi|297326153|gb|EFH56573.1| photolyase/blue-light receptor 2 [Arabidopsis lyrata subsp. lyrata]	443	448	0	101.1	87.6	93.0	photolyase/blue-light receptor 2	gbpln	Arabidopsis lyrata	AT2G47590.1 | Symbols: PHR2 | photolyase/blue-light receptor 2 | chr2:19521888-19523732 FORWARD LENGTH=447	443	447	0	100.9	86.5	91.6
Rsa1.0_00221.1.g8934.t1	ref|XP_002882124.1| hypothetical protein ARALYDRAFT_904236 [Arabidopsis lyrata subsp. lyrata] gi|297327963|gb|EFH58383.1| hypothetical protein ARALYDRAFT_904236 [Arabidopsis lyrata subsp. lyrata]	535	539	0	100.7	90.7	95.3	hypothetical protein ARALYDRAFT_904236	gbpln	Arabidopsis lyrata	AT2G47600.1 | Symbols: ATMHX, MHX1, ATMHX1, MHX | magnesium/proton exchanger | chr2:19524518-19526828 REVERSE LENGTH=539	535	539	0	100.7	90.3	95.3
Rsa1.0_00221.1.g8935.t1	gb|EOA27436.1| hypothetical protein CARUB_v10023573mg [Capsella rubella]	377	338	1.00E-142	89.7	69.5	72.4	hypothetical protein CARUB_v10023573mg	gbpln	Capsella rubella	AT3G62870.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr3:23242862-23244273 REVERSE LENGTH=256	377	256	1.00E-141	67.9	64.5	66.3
Rsa1.0_00221.1.g8936.t1	ref|XP_002882126.1| hypothetical protein ARALYDRAFT_904242 [Arabidopsis lyrata subsp. lyrata] gi|297327965|gb|EFH58385.1| hypothetical protein ARALYDRAFT_904242 [Arabidopsis lyrata subsp. lyrata]	209	205	2.00E-76	98.1	70.3	80.4	hypothetical protein ARALYDRAFT_904242	gbpln	Arabidopsis lyrata	AT2G47670.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr2:19544131-19544757 REVERSE LENGTH=208	209	208	2.00E-72	99.5	73.2	85.2
Rsa1.0_00221.1.g8937.t4	gb|EOA26511.1| hypothetical protein CARUB_v10022564mg [Capsella rubella]	1013	1010	0	99.7	84.9	91.1	hypothetical protein CARUB_v10022564mg	gbpln	Capsella rubella	AT2G47680.1 | Symbols: | zinc finger (CCCH type) helicase family protein | chr2:19545828-19550871 REVERSE LENGTH=1015	1013	1015	0	100.2	85.2	91.6
Rsa1.0_00221.1.g8938.t1	ref|XP_002882128.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297327967|gb|EFH58387.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	376	351	1.00E-142	93.4	71.3	78.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G47700.1 | Symbols: RFI2 | RING/U-box superfamily protein | chr2:19552506-19554351 REVERSE LENGTH=358	376	358	1.00E-142	95.2	71.3	78.2
Rsa1.0_00221.1.g8939.t1	dbj|BAJ33672.1| unnamed protein product [Thellungiella halophila]	162	162	9.00E-80	100.0	87.7	93.2	unnamed protein product	----	----	AT2G47710.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr2:19555045-19555956 REVERSE LENGTH=162	162	162	5.00E-79	100.0	84.6	92.6
Rsa1.0_00221.1.g8940.t1	dbj|BAJ33833.1| unnamed protein product [Thellungiella halophila]	215	215	1.00E-103	100.0	83.3	90.7	unnamed protein product	----	----	AT2G47730.1 | Symbols: ATGSTF8, ATGSTF5, GST6, GSTF8 | glutathione S-transferase phi 8 | chr2:19558213-19559266 FORWARD LENGTH=263	215	263	4.00E-99	122.3	77.7	87.9
Rsa1.0_00221.1.g8941.t1	ref|XP_002867794.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297313630|gb|EFH44053.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata]	82	501	5.00E-13	611.0	46.3	47.6	glycosyl hydrolase family 1 protein	gbpln	Arabidopsis lyrata	AT4G22100.1 | Symbols: BGLU3 | beta glucosidase 2 | chr4:11707370-11709932 REVERSE LENGTH=507	82	507	3.00E-15	618.3	47.6	54.9
Rsa1.0_00221.1.g8942.t3	gb|ACJ68117.1| putative indole-3-acetic acid-amido synthetase [Brassica napus]	646	594	0	92.0	84.4	86.5	putative indole-3-acetic acid-amido synthetase	gbpln	Brassica napus	AT2G47750.1 | Symbols: GH3.9 | putative indole-3-acetic acid-amido synthetase GH3.9 | chr2:19560307-19562974 REVERSE LENGTH=585	646	585	0	90.6	79.6	84.7
Rsa1.0_00221.1.g8943.t4	ref|XP_002882131.1| At2g47760/F17A22.15 [Arabidopsis lyrata subsp. lyrata] gi|297327970|gb|EFH58390.1| At2g47760/F17A22.15 [Arabidopsis lyrata subsp. lyrata]	416	439	1.00E-128	105.5	61.3	66.3	At2g47760/F17A22.15	gbpln	Arabidopsis lyrata	AT2G47760.3 | Symbols: ALG3, AtALG3 | asparagine-linked glycosylation 3 | chr2:19565933-19568221 REVERSE LENGTH=380	416	380	1.00E-129	91.3	59.9	65.1

Rsa1.0_00221.1.g8944.t1	ref|NP_182299.1| Rubber elongation factor protein (REF) [Arabidopsis thaliana] gi|14424099|sp|O82246.1|Y2778_ARATH RecName: Full=REF/SRPP-like protein At2g47780 gi|3738291|gb|AAC63633.1| unknown protein [Arabidopsis thaliana] gi|23306436|gb|AAN17445.1| unknown protein [Arabidopsis thaliana] gi|25084024|gb|AAN72157.1| unknown protein [Arabidopsis thaliana] gi|330255793|gb|AEC10887.1| Rubber elongation factor protein (REF) [Arabidopsis thaliana]		224	235	6.00E-95	104.9	79.5	86.6	Rubber elongation factor protein (REF)	gbpln	Arabidopsis thaliana	AT2G47780.1 | Symbols: | Rubber elongation factor protein (REF) | chr2:19570076-19570864 FORWARD LENGTH=235	224	235	2.00E-97	104.9	79.5	86.6
Rsa1.0_00221.1.g8945.t1	ref|NP_182302.1| nuclear transcription factor Y subunit B-5 [Arabidopsis thaliana] gi|75220231|sp|O82248.1|NFYB5_ARATH RecName: Full=Nuclear transcription factor Y subunit B-5; Short=AtNF-YB-5 gi|3738293|gb|AAC63635.1| putative CCAAT-box binding trancription factor [Arabidopsis thaliana] gi|28393159|gb|AAO42012.1| putative CCAAT-box binding trancription factor [Arabidopsis thaliana] gi|28827540|gb|AAO50614.1| putative CCAAT-box binding trancription factor [Arabidopsis thaliana] gi|330255796|gb|AEC10890.1| nuclear transcription factor Y subunit B-5 [Arabidopsis thaliana]		516	160	4.00E-61	31.0	21.7	23.1	nuclear transcription factor Y subunit B-5	gbpln	Arabidopsis thaliana	AT2G47810.1 | Symbols: NF-YB5 | nuclear factor Y, subunit B5 | chr2:19582938-19583420 REVERSE LENGTH=160	516	160	1.00E-63	31.0	21.7	23.1
Rsa1.0_00221.1.g8946.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00221.1.g8947.t1	gb|EOA27039.1| hypothetical protein CARUB_v10023134mg [Capsella rubella]		458	471	0	102.8	78.2	85.4	hypothetical protein CARUB_v10023134mg	gbpln	Capsella rubella	AT2G47850.3 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr2:19595953-19598119 FORWARD LENGTH=468	458	468	1.00E-180	102.2	77.9	84.9
Rsa1.0_00221.1.g8948.t1	ref|XP_002863057.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297824891|ref|XP_002880328.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297308863|gb|EFH39316.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297326167|gb|EFH56587.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]		103	103	8.00E-48	100.0	89.3	95.1	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT2G47870.1 | Symbols: | Thioredoxin superfamily protein | chr2:19603339-19603650 FORWARD LENGTH=103	103	103	5.00E-48	100.0	85.4	92.2
Rsa1.0_00221.1.g8949.t1	ref|NP_182309.1| glutaredoxin-C13 [Arabidopsis thaliana] gi|297790318|ref|XP_002863058.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297824893|ref|XP_002880329.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|75100580|sp|O82255.1|GRC13_ARATH RecName: Full=Glutaredoxin-C13; Short=AtGrxC13; AltName: Full=Protein ROXY 9 gi|3738300|gb|AAC63642.1| putative glutaredoxin [Arabidopsis thaliana] gi|20197557|gb|AAM15127.1| putative glutaredoxin [Arabidopsis thaliana] gi|21554200|gb|AAM63279.1| putative glutaredoxin [Arabidopsis thaliana] gi|62320234|dbj|BAD94488.1| putative glutaredoxin [Arabidopsis thaliana] gi|90962952|gb|ABE02400.1| At2g47880 [Arabidopsis thaliana] gi|226348196|gb|ACO50414.1| glutaredoxin [Arabidopsis thaliana] gi|297308864|gb|EFH39317.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297326168|gb|EFH56588.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|330255810|gb|AEC10904.1| glutaredoxin-C13 [Arabidopsis thaliana]		102	102	5.00E-49	100.0	93.1	98.0	glutaredoxin-C13	gbpln	Arabidopsis lyrata	AT2G47880.1 | Symbols: | Glutaredoxin family protein | chr2:19605124-19605432 FORWARD LENGTH=102	102	102	8.00E-52	100.0	93.1	98.0
Rsa1.0_00221.1.g8950.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00221.1.g8951.t1	ref|XP_002880330.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297326169|gb|EFH56589.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	334	324	1.00E-119	97.0	70.1	80.5	zinc finger (B-box type) family protein	gbpln	Arabidopsis lyrata	AT2G47890.1 | Symbols: | B-box type zinc finger protein with CCT domain | chr2:19608245-19609476 FORWARD LENGTH=332	334	332	1.00E-118	99.4	70.1	80.2
Rsa1.0_00221.1.g8952.t1	ref|XP_002880334.1| hypothetical protein ARALYDRAFT_904269 [Arabidopsis lyrata subsp. lyrata] gi|297326173|gb|EFH56593.1| hypothetical protein ARALYDRAFT_904269 [Arabidopsis lyrata subsp. lyrata]	153	226	3.00E-37	147.7	64.1	70.6	hypothetical protein ARALYDRAFT_904269	gbpln	Arabidopsis lyrata	AT2G47920.1 | Symbols: | Kinase interacting (KIP1-like) family protein | chr2:19616003-19616761 FORWARD LENGTH=225	153	225	7.00E-39	147.1	60.1	69.3
Rsa1.0_00221.1.g8953.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1601	2301	0	143.7	61.5	71.4	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1601	1262	1.00E-108	78.8	11.9	18.4
Rsa1.0_00221.1.g8954.t1	ref|NP_566117.1| uncharacterized protein [Arabidopsis thaliana] gi|16226796|gb|AAL16264.1|AF428334_1 At2g47960/T9J23.10 [Arabidopsis thaliana] gi|18377797|gb|AAL67048.1| unknown protein [Arabidopsis thaliana] gi|20197311|gb|AAC63650.2| expressed protein [Arabidopsis thaliana] gi|20197565|gb|AAM15133.1| expressed protein [Arabidopsis thaliana] gi|21281259|gb|AAM45021.1| unknown protein [Arabidopsis thaliana] gi|330255823|gb|AEC10917.1| uncharacterized protein AT2G47960 [Arabidopsis thaliana]	444	442	0	99.5	88.1	92.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G47960.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF974 (InterPro:IPR010378); Has 285 Blast hits to 284 proteins in 126 species: Archae - 0; Bacteria - 0; Metazoa - 150; Fungi - 68; Plants - 32; Viruses - 0; Other Eukaryotes - 35 (source: NCBI BLink). | chr2:19625631-19628869 FORWARD LENGTH=442	444	442	0	99.5	88.1	92.1
Rsa1.0_00222.1.g8955.t1	ref|XP_002881751.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297327590|gb|EFH58010.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	660	724	0	109.7	82.1	87.4	bZIP transcription factor family protein	gbpln	Arabidopsis lyrata	AT2G40950.1 | Symbols: BZIP17 | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:17087823-17090326 REVERSE LENGTH=721	660	721	0	109.2	81.4	87.3
Rsa1.0_00222.1.g8956.t1	ref|NP_565945.1| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|75160519|sp|Q8S8T8.1|PCR10_ARATH RecName: Full=Protein PLANT CADMIUM RESISTANCE 10; Short=AtPCR10 gi|20196932|gb|AAM14839.1| Expressed protein [Arabidopsis thaliana] gi|21537314|gb|AAM61655.1| unknown [Arabidopsis thaliana] gi|117958399|gb|ABK59670.1| At2g40935 [Arabidopsis thaliana] gi|330254808|gb|AEC09902.1| PLAC8 domain-containing protein [Arabidopsis thaliana]	186	190	3.00E-83	102.2	83.9	90.3	PLAC8 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G40935.1 | Symbols: | PLAC8 family protein | chr2:17083199-17084216 FORWARD LENGTH=190	186	190	1.00E-85	102.2	83.9	90.3
Rsa1.0_00222.1.g8957.t1	gb|EOA27257.1| hypothetical protein CARUB_v10023376mg [Capsella rubella]	393	393	0	100.0	83.2	90.3	hypothetical protein CARUB_v10023376mg	gbpln	Capsella rubella	AT2G40900.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr2:17063396-17065514 REVERSE LENGTH=394	393	394	0	100.3	85.0	91.1
Rsa1.0_00222.1.g8958.t1	ref|NP_181616.3| 4-alpha-glucanotransferase [Arabidopsis thaliana] gi|75158841|sp|Q8RXD9.1|DPE2_ARATH RecName: Full=4-alpha-glucanotransferase DPE2; AltName: Full=Amylomaltase; AltName: Full=Disproportionating enzyme; Short=D-enzyme; AltName: Full=Protein DISPROPORTIONATING ENZYME 2 gi|19698937|gb|AAL91204.1| 4-alpha-glucanotransferase [Arabidopsis thaliana] gi|34098849|gb|AAQ56807.1| At2g40840 [Arabidopsis thaliana] gi|330254795|gb|AEC09889.1| 4-alpha-glucanotransferase DPE2 [Arabidopsis thaliana]	953	955	0	100.2	91.5	95.2	4-alpha-glucanotransferase	gbpln	Arabidopsis thaliana	AT2G40840.1 | Symbols: DPE2 | disproportionating enzyme 2 | chr2:17045368-17050779 FORWARD LENGTH=955	953	955	0	100.2	91.5	95.2
Rsa1.0_00222.1.g8959.t1	gb|EOA27483.1| hypothetical protein CARUB_v10023620mg [Capsella rubella]	327	327	1.00E-129	100.0	79.5	87.2	hypothetical protein CARUB_v10023620mg	gbpln	Capsella rubella	AT2G40830.3 | Symbols: RHC1A | RING-H2 finger C1A | chr2:17043642-17044628 FORWARD LENGTH=328	327	328	1.00E-129	100.3	78.9	85.3

Rsa1.0_00222.1.g8960.t1	ref|NP_181614.7| uncharacterized protein [Arabidopsis thaliana] gi|330254791|gb|AEC09885.1| uncharacterized protein AT2G40820 [Arabidopsis thaliana]	493	492	0	99.8	86.8	93.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G40820.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT3G56480.1); Has 203 Blast hits to 195 proteins in 64 species: Archae - 3; Bacteria - 13; Metazoa - 26; Fungi - 15; Plants - 101; Viruses - 0; Other Eukaryotes - 45 (source: NCBI BLink). | chr2:17036768-17039474 REVERSE LENGTH=492	493	492	0	99.8	86.8	93.3
Rsa1.0_00222.1.g8961.t1	ref|NP_181612.1| uncharacterized protein [Arabidopsis thaliana] gi|17473709|gb|AAL38308.1| unknown protein [Arabidopsis thaliana] gi|20148507|gb|AAM10144.1| unknown protein [Arabidopsis thaliana] gi|330254786|gb|AEC09880.1| uncharacterized protein AT2G40800 [Arabidopsis thaliana]	365	377	1.00E-167	103.3	86.0	92.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G40800.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G56430.1); Has 43 Blast hits to 43 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:17024653-17026769 REVERSE LENGTH=377	365	377	1.00E-169	103.3	86.0	92.1
Rsa1.0_00222.1.g8962.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00222.1.g8963.t1	dbj|BAJ33964.1| unnamed protein product [Thellungiella halophila]	336	338	1.00E-144	100.6	75.9	84.2	unnamed protein product	----	----	AT2G40750.1 | Symbols: WRKY54, ATWRKY54 | WRKY DNA-binding protein 54 | chr2:17000636-17002354 REVERSE LENGTH=346	336	346	1.00E-132	103.0	71.7	81.0
Rsa1.0_00222.1.g8964.t1	gb|EOA28303.1| hypothetical protein CARUB_v10024501mg [Capsella rubella]	624	610	0	97.8	86.7	91.0	hypothetical protein CARUB_v10024501mg	gbpln	Capsella rubella	AT2G40700.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:16976783-16979392 FORWARD LENGTH=609	624	609	0	97.6	85.7	91.0
Rsa1.0_00222.1.g8965.t1	gb|EOA26998.1| hypothetical protein CARUB_v10023092mg [Capsella rubella]	386	489	1.00E-172	126.7	83.7	90.2	hypothetical protein CARUB_v10023092mg	gbpln	Capsella rubella	AT2G40660.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr2:16966011-16968866 FORWARD LENGTH=389	386	389	1.00E-164	100.8	81.3	88.9
Rsa1.0_00222.1.g8966.t1	emb|CAB06697.1| b-Zip DNA binding protein [Arabidopsis thaliana]	373	367	1.00E-158	98.4	81.5	85.8	b-Zip DNA binding protein	gbpln	Arabidopsis thaliana	AT2G40620.1 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:16954804-16956872 REVERSE LENGTH=367	373	367	1.00E-160	98.4	81.5	85.5
Rsa1.0_00222.1.g8967.t1	ref|NP_181593.1| expansin A8 [Arabidopsis thaliana] gi|20138147|sp|O22874.1|EXPA8_ARATH RecName: Full=Expansin-A8; Short=AtEXPA8; AltName: Full=Alpha-expansin-8; Short=At-EXP8; Short=AtEx8; AltName: Full=Ath-ExpAlpha-1.11; Flags: Precursor gi|2651297|gb|AAB87577.1| putative expansin [Arabidopsis thaliana] gi|21555274|gb|AAM63821.1| Alpha-expansin 8 precursor (At-EXP8) (AtEx8) (Ath-ExpAlpha-1.11) [Arabidopsis thaliana] gi|110737287|dbj|BAF00590.1| Expansin [Arabidopsis thaliana] gi|330254760|gb|AEC09854.1| expansin A8 [Arabidopsis thaliana]	257	253	1.00E-132	98.4	90.3	93.8	expansin A8	gbpln	Arabidopsis thaliana	AT2G40610.1 | Symbols: ATEXPA8, EXP8, ATEXP8, ATHEXP ALPHA 1.11, EXPA8 | expansin A8 | chr2:16949121-16950472 REVERSE LENGTH=253	257	253	1.00E-135	98.4	90.3	93.8
Rsa1.0_00222.1.g8968.t1	ref|NP_030605.2| appr-1-p processing enzyme family protein [Arabidopsis thaliana] gi|24030242|gb|AAN41297.1| unknown protein [Arabidopsis thaliana] gi|330254759|gb|AEC09853.1| appr-1-p processing enzyme family protein [Arabidopsis thaliana]	142	257	2.00E-65	181.0	84.5	91.5	appr-1-p processing enzyme family protein	gbpln	Arabidopsis thaliana	AT2G40600.1 | Symbols: | appr-1-p processing enzyme family protein | chr2:16947012-16948537 REVERSE LENGTH=257	142	257	7.00E-68	181.0	84.5	91.5
Rsa1.0_00222.1.g8969.t1	ref|XP_002892188.1| hypothetical protein ARALYDRAFT_887556 [Arabidopsis lyrata subsp. lyrata] gi|297338030|gb|EFH68447.1| hypothetical protein ARALYDRAFT_887556 [Arabidopsis lyrata subsp. lyrata]	264	357	1.00E-37	135.2	32.2	41.7	hypothetical protein ARALYDRAFT_887556	gbpln	Arabidopsis lyrata	AT1G03490.1 | Symbols: ANAC006, NAC006 | NAC domain containing protein 6 | chr1:871874-872906 FORWARD LENGTH=281	264	281	3.00E-27	106.4	21.2	26.1
Rsa1.0_00222.1.g8970.t1	gb|EOA28443.1| hypothetical protein CARUB_v10024650mg [Capsella rubella]	778	795	0	102.2	92.0	96.5	hypothetical protein CARUB_v10024650mg	gbpln	Capsella rubella	AT2G40540.2 | Symbols: KT2, ATKT2, SHY3, KUP2, ATKUP2, TRK2 | potassium transporter 2 | chr2:16931445-16934516 FORWARD LENGTH=794	778	794	0	102.1	91.6	96.3

Rsa1.0_00222.1.g8971.t1	ref|NP_565935.1| uncharacterized protein [Arabidopsis thaliana] gi|2651304|gb|AAB87584.1| expressed protein [Arabidopsis thaliana] gi|88900366|gb|ABD57495.1| At2g40530 [Arabidopsis thaliana] gi|330254750|gb|AEC09844.1| uncharacterized protein AT2G40530 [Arabidopsis thaliana]	101	105	1.00E-22	104.0	72.3	80.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G40530.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf apex, inflorescence meristem, petal, flower; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:16927600-16927917 FORWARD LENGTH=105	101	105	2.00E-25	104.0	72.3	80.2
Rsa1.0_00222.1.g8972.t1	gb|EOA26742.1| hypothetical protein CARUB_v10022828mg [Capsella rubella]	510	619	0	121.4	74.9	82.9	hypothetical protein CARUB_v10022828mg	gbpln	Capsella rubella	AT3G56320.1 | Symbols: | PAP/OAS1 substrate-binding domain superfamily | chr3:20886193-20888624 REVERSE LENGTH=603	510	603	0	118.2	65.3	76.7
Rsa1.0_00222.1.g8973.t1	ref|XP_002892188.1| hypothetical protein ARALYDRAFT_887556 [Arabidopsis lyrata subsp. lyrata] gi|297338030|gb|EFH68447.1| hypothetical protein ARALYDRAFT_887556 [Arabidopsis lyrata subsp. lyrata]	549	357	1.00E-37	65.0	15.7	20.6	hypothetical protein ARALYDRAFT_887556	gbpln	Arabidopsis lyrata	AT1G03490.1 | Symbols: ANAC006, NAC006 | NAC domain containing protein 6 | chr1:871874-872906 FORWARD LENGTH=281	549	281	3.00E-27	51.2	10.0	12.6
Rsa1.0_00222.1.g8974.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00222.1.g8975.t1	ref|XP_002881725.1| hypothetical protein ARALYDRAFT_903340 [Arabidopsis lyrata subsp. lyrata] gi|297327564|gb|EFH57984.1| hypothetical protein ARALYDRAFT_903340 [Arabidopsis lyrata subsp. lyrata]	198	192	8.00E-57	97.0	75.3	83.3	hypothetical protein ARALYDRAFT_903340	gbpln	Arabidopsis lyrata	AT2G40475.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G56260.2); Has 477 Blast hits to 219 proteins in 41 species: Archae - 0; Bacteria - 4; Metazoa - 91; Fungi - 61; Plants - 144; Viruses - 0; Other Eukaryotes - 177 (source: NCBI BLink). | chr2:16907222-16907803 REVERSE LENGTH=193	198	193	5.00E-51	97.5	73.7	80.8
Rsa1.0_00222.1.g8976.t1	gb|AAC33963.1| contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]	1542	1633	0	105.9	47.1	64.3	contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19)	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1542	1262	1.00E-178	81.8	19.6	26.1
Rsa1.0_00222.1.g8977.t1	ref|XP_002878835.1| hypothetical protein ARALYDRAFT_901144 [Arabidopsis lyrata subsp. lyrata] gi|297324674|gb|EFH55094.1| hypothetical protein ARALYDRAFT_901144 [Arabidopsis lyrata subsp. lyrata]	200	200	1.00E-77	100.0	70.5	84.5	hypothetical protein ARALYDRAFT_901144	gbpln	Arabidopsis lyrata	AT2G40450.1 | Symbols: | BTB/POZ domain-containing protein | chr2:16892024-16892790 REVERSE LENGTH=209	200	209	1.00E-59	104.5	62.0	76.5
Rsa1.0_00222.1.g8978.t2	ref|XP_002879870.1| hypothetical protein ARALYDRAFT_483101 [Arabidopsis lyrata subsp. lyrata] gi|297325709|gb|EFH56129.1| hypothetical protein ARALYDRAFT_483101 [Arabidopsis lyrata subsp. lyrata]	158	158	2.00E-75	100.0	86.1	94.3	hypothetical protein ARALYDRAFT_483101	gbpln	Arabidopsis lyrata	AT2G40435.1 | Symbols: | BEST Arabidopsis thaliana protein match is: transcription regulators (TAIR:AT3G56220.1); Has 289 Blast hits to 289 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 289; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:16887048-16888407 FORWARD LENGTH=158	158	158	2.00E-75	100.0	84.2	92.4
Rsa1.0_00222.1.g8979.t1	gb|EOA29100.1| hypothetical protein CARUB_v10025367mg, partial [Capsella rubella]	385	381	1.00E-152	99.0	74.3	83.9	hypothetical protein CARUB_v10025367mg, partial	gbpln	Capsella rubella	AT2G40430.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Tumour suppressor protein Gltscr2 (InterPro:IPR011211), P60-like (InterPro:IPR011687). | chr2:16879466-16882365 REVERSE LENGTH=441	385	441	1.00E-141	114.5	74.0	83.6
Rsa1.0_00222.1.g8980.t1	ref|NP_973649.1| Ca(2+)-dependent nuclease-like protein [Arabidopsis thaliana] gi|330254731|gb|AEC09825.1| Ca(2+)-dependent nuclease-like protein [Arabidopsis thaliana]	333	332	1.00E-171	99.7	88.3	94.3	Ca(2+)-dependent nuclease-like protein	gbpln	Arabidopsis thaliana	AT2G40410.2 | Symbols: | Staphylococcal nuclease homologue | chr2:16873509-16875215 FORWARD LENGTH=332	333	332	1.00E-173	99.7	88.3	94.3
Rsa1.0_00222.1.g8981.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00222.1.g8982.t1	gb|EOA26978.1| hypothetical protein CARUB_v10023075mg [Capsella rubella]	496	496	0	100.0	88.3	94.0	hypothetical protein CARUB_v10023075mg	gbpln	Capsella rubella	AT2G40390.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64190.1); Has 75 Blast hits to 75 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:16867385-16868961 FORWARD LENGTH=496	496	496	0	100.0	89.3	93.5

Rsa1.0_00222.1.g8983.t1	gb|EOA28822.1| hypothetical protein CARUB_v10025061mg [Capsella rubella]	214	213	8.00E-84	99.5	89.7	94.9	hypothetical protein CARUB_v10025061mg	gbpln	Capsella rubella	AT2G40380.1 | Symbols: PRA1.B2 | prenylated RAB acceptor 1.B2 | chr2:16864734-16865375 REVERSE LENGTH=213	214	213	1.00E-85	99.5	89.7	94.4
Rsa1.0_00222.1.g8984.t1	gb|EOA26796.1| hypothetical protein CARUB_v10022891mg [Capsella rubella]	578	579	0	100.2	93.1	95.3	hypothetical protein CARUB_v10022891mg	gbpln	Capsella rubella	AT2G40370.1 | Symbols: LAC5 | laccase 5 | chr2:16858192-16860593 REVERSE LENGTH=580	578	580	0	100.3	92.2	95.2
Rsa1.0_00222.1.g8985.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00222.1.g8986.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00222.1.g8987.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00222.1.g8988.t1	ref|XP_002881715.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata] gi|297327554|gb|EFH57974.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata]	217	215	9.00E-81	99.1	71.0	81.6	bet v I allergen family protein	gbpln	Arabidopsis lyrata	AT2G40330.1 | Symbols: PYL6, RCAR9 | PYR1-like 6 | chr2:16845177-16845824 REVERSE LENGTH=215	217	215	2.00E-81	99.1	70.0	78.8
Rsa1.0_00223.1.g8989.t1	ref|NP_565255.1| Lipid phosphate phosphatase 1 [Arabidopsis thaliana] gi|41017426|sp|Q9ZU49.2|LPP1_ARATH RecName: Full=Lipid phosphate phosphatase 1; Short=AtLPP1; AltName: Full=Phosphatidic acid phosphatase 1; Short=AtPAP1; AltName: Full=Prenyl diphosphate phosphatase gi|14020927|dbj|BAB47575.1| phosphatidic acid phosphatase [Arabidopsis thaliana] gi|20197584|gb|AAD14518.2| putative phosphatidic acid phosphatase [Arabidopsis thaliana] gi|330250318|gb|AEC05412.1| Lipid phosphate phosphatase 1 [Arabidopsis thaliana]	298	327	1.00E-157	109.7	87.9	93.6	Lipid phosphate phosphatase 1	gbpln	Arabidopsis thaliana	AT2G01180.1 | Symbols: ATPAP1, PAP1, LPP1, ATLPP1 | phosphatidic acid phosphatase 1 | chr2:107182-108555 REVERSE LENGTH=327	298	327	1.00E-159	109.7	87.9	93.6
Rsa1.0_00223.1.g8990.t1	gb|AAL86294.1| putative amino acid or GABA permease [Arabidopsis thaliana]	517	516	0	99.8	93.0	96.3	putative amino acid or GABA permease	gbpln	Arabidopsis thaliana	AT2G01170.1 | Symbols: BAT1 | bidirectional amino acid transporter 1 | chr2:102364-104462 REVERSE LENGTH=516	517	516	0	99.8	92.8	96.3
Rsa1.0_00223.1.g8991.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00223.1.g8992.t1	ref|NP_565253.1| putative E3 ubiquitin-protein ligase RHA2B [Arabidopsis thaliana] gi|51316550|sp|Q9ZU51.2|RHA2B_ARATH RecName: Full=Probable E3 ubiquitin-protein ligase RHA2B; AltName: Full=RING-H2 zinc finger protein RHA2b gi|3790571|gb|AAC68672.1| RING-H2 finger protein RHA2b [Arabidopsis thaliana] gi|20197589|gb|AAD14516.2| RING-H2 finger protein RHA2b [Arabidopsis thaliana] gi|98960889|gb|ABF58928.1| At2g01150 [Arabidopsis thaliana] gi|330250313|gb|AEC05407.1| putative E3 ubiquitin-protein ligase RHA2B [Arabidopsis thaliana]	152	147	2.00E-49	96.7	73.7	77.0	putative E3 ubiquitin-protein ligase RHA2B	gbpln	Arabidopsis thaliana	AT2G01150.1 | Symbols: RHA2B | RING-H2 finger protein 2B | chr2:100703-101146 FORWARD LENGTH=147	152	147	6.00E-52	96.7	73.7	77.0
Rsa1.0_00223.1.g8993.t1	dbj|BAB11200.1| copia-type polyprotein [Arabidopsis thaliana] gi|13872710|emb|CAC37622.1| polyprotein [Arabidopsis thaliana]	1131	1334	0	117.9	69.8	83.0	copia-type polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1131	1262	3.00E-83	111.6	14.9	22.4
Rsa1.0_00223.1.g8994.t1	gb|EOA23425.1| hypothetical protein CARUB_v10016608mg [Capsella rubella]	1131	1118	0	98.9	84.4	90.6	hypothetical protein CARUB_v10016608mg	gbpln	Capsella rubella	AT2G01130.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr2:88847-94635 REVERSE LENGTH=1113	1131	1113	0	98.4	83.0	89.7
Rsa1.0_00223.1.g8995.t1	gb|EOA25931.1| hypothetical protein CARUB_v10019313mg [Capsella rubella]	413	417	0	101.0	91.0	95.2	hypothetical protein CARUB_v10019313mg	gbpln	Capsella rubella	AT2G01120.1 | Symbols: ORC4, ATORC4 | origin recognition complex subunit 4 | chr2:85444-88027 FORWARD LENGTH=418	413	418	0	101.2	88.9	93.9
Rsa1.0_00223.1.g8996.t1	gb|EOA24317.1| hypothetical protein CARUB_v10017557mg [Capsella rubella]	350	347	1.00E-163	99.1	87.1	91.4	hypothetical protein CARUB_v10017557mg	gbpln	Capsella rubella	AT2G01110.1 | Symbols: APG2, UNE3, PGA2, TATC | Sec-independent periplasmic protein translocase | chr2:83786-85088 REVERSE LENGTH=340	350	340	1.00E-158	97.1	86.6	90.9
Rsa1.0_00223.1.g8997.t1	ref|XP_003609124.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula] gi|355510179|gb|AES91321.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula]	1657	1558	0	94.0	40.4	55.8	ATP-dependent DNA helicase PIF1	gbpln	Medicago truncatula	AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907-10814173 REVERSE LENGTH=337	1657	337	3.00E-73	20.3	8.3	11.4
Rsa1.0_00223.1.g8998.t1	gb|EOA39027.1| hypothetical protein CARUB_v10011597mg [Capsella rubella]	186	186	1.00E-15	100.0	28.0	48.4	hypothetical protein CARUB_v10011597mg	gbpln	Capsella rubella	AT5G53910.1 | Symbols: | RING/U-box superfamily protein | chr5:21890643-21891335 FORWARD LENGTH=230	186	230	4.00E-11	123.7	14.0	19.9

Rsa1.0_00223.1.g8999.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	583	484	5.00E-90	83.0	28.0	34.5	hypothetical protein 27.t00116	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	583	566	2.00E-14	97.1	16.1	30.7
Rsa1.0_00223.1.g9000.t1	ref|XP_002875058.1| hypothetical protein ARALYDRAFT_484014 [Arabidopsis lyrata subsp. lyrata] gi|297320896|gb|EFH51317.1| hypothetical protein ARALYDRAFT_484014 [Arabidopsis lyrata subsp. lyrata]	222	231	6.00E-80	104.1	66.7	71.2	hypothetical protein ARALYDRAFT_484014	gbpln	Arabidopsis lyrata	AT2G01080.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:78038-79176 FORWARD LENGTH=231	222	231	7.00E-82	104.1	66.2	71.2
Rsa1.0_00223.1.g9001.t1	ref|NP_178217.3| lung seven transmembrane receptor-like protein [Arabidopsis thaliana] gi|330250300|gb|AEC05394.1| lung seven transmembrane receptor-like protein [Arabidopsis thaliana]	500	496	0	99.2	85.2	90.8	lung seven transmembrane receptor-like protein	gbpln	Arabidopsis thaliana	AT2G01070.1 | Symbols: | Lung seven transmembrane receptor family protein | chr2:75596-77625 FORWARD LENGTH=496	500	496	0	99.2	85.2	90.8
Rsa1.0_00223.1.g9002.t1	gb|EOA24516.1| hypothetical protein CARUB_v10017769mg [Capsella rubella]	287	286	1.00E-142	99.7	89.2	92.7	hypothetical protein CARUB_v10017769mg	gbpln	Capsella rubella	AT2G01060.1 | Symbols: | myb-like HTH transcriptional regulator family protein | chr2:73456-74902 REVERSE LENGTH=286	287	286	1.00E-143	99.7	88.5	92.3
Rsa1.0_00223.1.g9003.t1	gb|EOA12493.1| hypothetical protein CARUB_v10026096mg [Capsella rubella]	637	614	0	96.4	85.4	91.2	hypothetical protein CARUB_v10026096mg	gbpln	Capsella rubella	AT5G47780.1 | Symbols: GAUT4 | galacturonosyltransferase 4 | chr5:19347991-19350517 FORWARD LENGTH=616	637	616	0	96.7	85.9	91.1
Rsa1.0_00223.1.g9004.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00223.1.g9005.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00223.1.g9006.t1	gb|EOA39558.1| hypothetical protein CARUB_v10008175mg [Capsella rubella]	1055	1024	0	97.1	87.1	92.1	hypothetical protein CARUB_v10008175mg	gbpln	Capsella rubella	AT1G03370.1 | Symbols: | C2 calcium/lipid-binding and GRAM domain containing protein | chr1:830968-834996 FORWARD LENGTH=1020	1055	1020	0	96.7	85.6	90.4
Rsa1.0_00223.1.g9007.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1834	1838	0	100.2	42.9	56.9	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00223.1.g9008.t2	ref|XP_002308735.1| predicted protein [Populus trichocarpa] gi|222854711|gb|EEE92258.1| predicted protein [Populus trichocarpa]	919	542	1.00E-131	59.0	29.7	37.4	predicted protein	gbpln	Populus trichocarpa	AT5G60710.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr5:24410953-24414849 REVERSE LENGTH=704	919	704	3.00E-31	76.6	12.4	19.9
Rsa1.0_00223.1.g9009.t1	gb|EOA23919.1| hypothetical protein CARUB_v10017134mg, partial [Capsella rubella]	444	477	0	107.4	88.7	93.0	hypothetical protein CARUB_v10017134mg, partial	gbpln	Capsella rubella	AT5G47810.1 | Symbols: PFK2 | phosphofructokinase 2 | chr5:19356569-19357989 REVERSE LENGTH=444	444	444	0	100.0	88.1	93.0
Rsa1.0_00223.1.g9010.t1	dbj|BAJ34459.1| unnamed protein product [Thellungiella halophila]	571	562	0	98.4	88.1	92.6	unnamed protein product	----	----	AT5G47800.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr5:19354171-19356126 FORWARD LENGTH=559	571	559	0	97.9	85.6	92.3
Rsa1.0_00223.1.g9011.t1	ref|NP_199590.1| SMAD/FHA domain-containing protein [Arabidopsis thaliana] gi|10177915|dbj|BAB11326.1| unnamed protein product [Arabidopsis thaliana] gi|18700141|gb|AAL77682.1| AT5g47790/MCA23_11 [Arabidopsis thaliana] gi|33589742|gb|AAQ22637.1| At5g47790/MCA23_11 [Arabidopsis thaliana] gi|332008189|gb|AED95572.1| SMAD/FHA domain-containing protein [Arabidopsis thaliana]	375	369	1.00E-170	98.4	84.3	87.7	SMAD/FHA domain-containing protein	gbpln	Arabidopsis thaliana	AT5G47790.1 | Symbols: | SMAD/FHA domain-containing protein | chr5:19351396-19352579 FORWARD LENGTH=369	375	369	1.00E-173	98.4	84.3	87.7
Rsa1.0_00224.1.g9012.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00224.1.g9013.t1	ref|XP_002873602.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297319439|gb|EFH49861.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	314	295	1.00E-130	93.9	75.2	84.1	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT5G13170.1 | Symbols: SAG29, SWEET15, AtSWEET15 | senescence-associated gene 29 | chr5:4181331-4183171 REVERSE LENGTH=292	314	292	1.00E-128	93.0	74.5	82.5
Rsa1.0_00224.1.g9014.t1	ref|XP_002871549.1| avrPphB susceptible 1 [Arabidopsis lyrata subsp. lyrata] gi|297317386|gb|EFH47808.1| avrPphB susceptible 1 [Arabidopsis lyrata subsp. lyrata]	456	456	0	100.0	95.2	98.0	avrPphB susceptible 1	gbpln	Arabidopsis lyrata	AT5G13160.1 | Symbols: PBS1 | Protein kinase superfamily protein | chr5:4176854-4179682 FORWARD LENGTH=456	456	456	0	100.0	95.0	98.2
Rsa1.0_00224.1.g9015.t1	ref|XP_002873601.1| ATEXO70C1 [Arabidopsis lyrata subsp. lyrata] gi|297319438|gb|EFH49860.1| ATEXO70C1 [Arabidopsis lyrata subsp. lyrata]	640	650	0	101.6	82.7	87.8	ATEXO70C1	gbpln	Arabidopsis lyrata	AT5G13150.1 | Symbols: ATEXO70C1, EXO70C1 | exocyst subunit exo70 family protein C1 | chr5:4172969-4174930 REVERSE LENGTH=653	640	653	0	102.0	80.5	86.7
Rsa1.0_00224.1.g9016.t1	ref|XP_002873600.1| hypothetical protein ARALYDRAFT_488130 [Arabidopsis lyrata subsp. lyrata] gi|297319437|gb|EFH49859.1| hypothetical protein ARALYDRAFT_488130 [Arabidopsis lyrata subsp. lyrata]	231	267	4.00E-85	115.6	81.8	88.3	hypothetical protein ARALYDRAFT_488130	gbpln	Arabidopsis lyrata	AT5G13140.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:4170688-4171744 REVERSE LENGTH=267	231	267	1.00E-81	115.6	77.5	84.0

Rsa1.0_00224.1.g9017.t1	ref|XP_002871548.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297317385|gb|EFH47807.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	873	710	0	81.3	54.5	61.3	ATP binding protein	gbpln	Arabidopsis lyrata	AT5G13130.1 | Symbols: | Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein | chr5:4166755-4170324 FORWARD LENGTH=708	873	708	0	81.1	54.6	61.7
Rsa1.0_00224.1.g9018.t1	gb|AAM63489.1| unknown [Arabidopsis thaliana]	268	272	1.00E-62	101.5	61.6	72.0	unknown	gbpln	Arabidopsis thaliana	AT5G13090.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4153758-4154567 REVERSE LENGTH=269	268	269	3.00E-63	100.4	61.2	71.3
Rsa1.0_00224.1.g9019.t1	gb|ACI14409.1| WRKY75-1 transcription factor [Brassica napus]	147	147	5.00E-68	100.0	86.4	89.8	WRKY75-1 transcription factor	gbpln	Brassica napus	AT5G13080.1 | Symbols: WRKY75, ATWRKY75 | WRKY DNA-binding protein 75 | chr5:4149928-4151019 REVERSE LENGTH=145	147	145	5.00E-65	98.6	87.8	91.2
Rsa1.0_00224.1.g9020.t1	ref|NP_196810.5| ARMADILLO BTB protein 1 [Arabidopsis thaliana] gi|325529879|sp|B7U179.1|ABAP1_ARATH RecName: Full=ARMADILLO BTB ARABIDOPSIS PROTEIN 1; Short=ABAP1 gi|213391123|gb|ACJ46331.1| ABAP1 [Arabidopsis thaliana] gi|332004463|gb|AED91846.1| ARMADILLO BTB protein 1 [Arabidopsis thaliana]	708	737	0	104.1	85.6	92.7	ARMADILLO BTB protein 1	gbpln	Arabidopsis thaliana	AT5G13060.1 | Symbols: ABAP1 | ARMADILLO BTB protein 1 | chr5:4142958-4146952 FORWARD LENGTH=737	708	737	0	104.1	85.6	92.7
Rsa1.0_00224.1.g9021.t2	emb|CAC05433.1| 5-formyltetrahydrofolate cyclo-ligase-like protein [Arabidopsis thaliana]	260	287	1.00E-111	110.4	80.0	85.4	5-formyltetrahydrofolate cyclo-ligase-like protein	gbpln	Arabidopsis thaliana	AT5G13050.1 | Symbols: 5-FCL | 5-formyltetrahydrofolate cycloligase | chr5:4136912-4138711 REVERSE LENGTH=277	260	277	1.00E-112	106.5	79.6	85.0
Rsa1.0_00224.1.g9022.t1	gb|EOA20163.1| hypothetical protein CARUB_v10000455mg [Capsella rubella]	636	633	0	99.5	90.1	95.0	hypothetical protein CARUB_v10000455mg	gbpln	Capsella rubella	AT5G13030.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0061 (InterPro:IPR003846); Has 5046 Blast hits to 4997 proteins in 1211 species: Archae - 8; Bacteria - 2327; Metazoa - 120; Fungi - 134; Plants - 48; Viruses - 0; Other Eukaryotes - 2409 (source: NCBI BLink). | chr5:4133216-4136461 FORWARD LENGTH=633	636	633	0	99.5	88.8	93.7
Rsa1.0_00224.1.g9023.t1	ref|NP_196804.6| callose synthase [Arabidopsis thaliana] gi|357529555|sp|Q9LXT9.3|CALS3_ARATH RecName: Full=Callose synthase 3; AltName: Full=1,3-beta-glucan synthase; AltName: Full=Protein GLUCAN SYNTHASE-LIKE 12 gi|332004456|gb|AED91839.1| callose synthase [Arabidopsis thaliana]	1957	1955	0	99.9	96.1	98.0	callose synthase	gbpln	Arabidopsis thaliana	AT5G13000.1 | Symbols: ATGSL12, gsl12 | glucan synthase-like 12 | chr5:4110445-4121202 REVERSE LENGTH=1955	1957	1955	0	99.9	96.1	98.0
Rsa1.0_00224.1.g9024.t1	ref|XP_002873592.1| hypothetical protein ARALYDRAFT_488115 [Arabidopsis lyrata subsp. lyrata] gi|297319429|gb|EFH49851.1| hypothetical protein ARALYDRAFT_488115 [Arabidopsis lyrata subsp. lyrata]	83	80	4.00E-22	96.4	65.1	74.7	hypothetical protein ARALYDRAFT_488115	gbpln	Arabidopsis lyrata	AT5G12990.1 | Symbols: CLE40 | CLAVATA3/ESR-RELATED 40 | chr5:4109234-4109768 REVERSE LENGTH=80	83	80	4.00E-19	96.4	61.4	69.9
Rsa1.0_00224.1.g9025.t1	ref|XP_002873591.1| hypothetical protein ARALYDRAFT_909249 [Arabidopsis lyrata subsp. lyrata] gi|297319428|gb|EFH49850.1| hypothetical protein ARALYDRAFT_909249 [Arabidopsis lyrata subsp. lyrata]	293	308	1.00E-114	105.1	71.7	81.9	hypothetical protein ARALYDRAFT_909249	gbpln	Arabidopsis lyrata	AT5G12980.1 | Symbols: | Cell differentiation, Rcd1-like protein | chr5:4105562-4108139 REVERSE LENGTH=311	293	311	1.00E-115	106.1	70.6	81.6
Rsa1.0_00224.1.g9026.t1	gb|EOA22845.1| hypothetical protein CARUB_v10003573mg [Capsella rubella]	769	769	0	100.0	95.6	98.7	hypothetical protein CARUB_v10003573mg	gbpln	Capsella rubella	AT5G12970.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein | chr5:4102992-4105301 FORWARD LENGTH=769	769	769	0	100.0	95.2	98.4

Rsa1.0_00224.1.g9027.t1	ref|NP_196799.1| uncharacterized protein [Arabidopsis thaliana] gi|7630051|emb|CAB88259.1| putative protein [Arabidopsis thaliana] gi|26451123|dbj|BAC42665.1| unknown protein [Arabidopsis thaliana] gi|332004451|gb|AED91834.1| uncharacterized protein AT5G12950 [Arabidopsis thaliana]	133	861	6.00E-46	647.4	74.4	83.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G12950.1 | Symbols: | Putative glycosyl hydrolase of unknown function (DUF1680) | chr5:4093117-4096806 FORWARD LENGTH=861	133	861	1.00E-48	647.4	74.4	83.5
Rsa1.0_00224.1.g9028.t1	ref|XP_002871534.1| hypothetical protein ARALYDRAFT_909242 [Arabidopsis lyrata subsp. lyrata] gi|297317371|gb|EFH47793.1| hypothetical protein ARALYDRAFT_909242 [Arabidopsis lyrata subsp. lyrata]	375	371	1.00E-172	98.9	79.2	88.8	hypothetical protein ARALYDRAFT_909242	gbpln	Arabidopsis lyrata	AT5G12940.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:4087782-4088897 FORWARD LENGTH=371	375	371	1.00E-172	98.9	77.3	88.0
Rsa1.0_00224.1.g9029.t1	ref|XP_002871534.1| hypothetical protein ARALYDRAFT_909242 [Arabidopsis lyrata subsp. lyrata] gi|297317371|gb|EFH47793.1| hypothetical protein ARALYDRAFT_909242 [Arabidopsis lyrata subsp. lyrata]	376	371	1.00E-165	98.7	76.9	85.1	hypothetical protein ARALYDRAFT_909242	gbpln	Arabidopsis lyrata	AT5G12940.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:4087782-4088897 FORWARD LENGTH=371	376	371	1.00E-164	98.7	75.0	84.0
Rsa1.0_00224.1.g9030.t2	dbj|BAB09269.1| unnamed protein product [Arabidopsis thaliana]	257	422	4.00E-28	164.2	26.8	36.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	257	295	7.00E-17	114.8	25.7	33.9
Rsa1.0_00224.1.g9031.t1	ref|XP_002873586.1| hypothetical protein ARALYDRAFT_488108 [Arabidopsis lyrata subsp. lyrata] gi|297319423|gb|EFH49845.1| hypothetical protein ARALYDRAFT_488108 [Arabidopsis lyrata subsp. lyrata]	1078	559	0	51.9	44.9	47.9	hypothetical protein ARALYDRAFT_488108	gbpln	Arabidopsis lyrata	AT5G12900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G12330.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4072151-4074445 REVERSE LENGTH=562	1078	562	0	52.1	45.1	48.0
Rsa1.0_00224.1.g9032.t1	ref|NP_196792.1| proline-rich family protein [Arabidopsis thaliana] gi|7630044|emb|CAB88252.1| putative protein [Arabidopsis thaliana] gi|38566520|gb|AAR24150.1| At5g12880 [Arabidopsis thaliana] gi|40823652|gb|AAR92296.1| At5g12880 [Arabidopsis thaliana] gi|332004442|gb|AED91825.1| proline-rich family protein [Arabidopsis thaliana]	76	73	5.00E-25	96.1	81.6	82.9	proline-rich family protein	gbpln	Arabidopsis thaliana	AT5G12880.1 | Symbols: | proline-rich family protein | chr5:4068714-4068935 REVERSE LENGTH=73	76	73	8.00E-28	96.1	81.6	82.9
Rsa1.0_00224.1.g9033.t1	ref|XP_002871525.1| hypothetical protein ARALYDRAFT_488087 [Arabidopsis lyrata subsp. lyrata] gi|297317362|gb|EFH47784.1| hypothetical protein ARALYDRAFT_488087 [Arabidopsis lyrata subsp. lyrata]	377	1581	1.00E-63	419.4	52.0	61.0	hypothetical protein ARALYDRAFT_488087	gbpln	Arabidopsis lyrata	AT5G12400.1 | Symbols: | DNA binding;zinc ion binding;DNA binding | chr5:4013813-4021018 FORWARD LENGTH=1602	377	1602	2.00E-64	424.9	50.1	59.7
Rsa1.0_00224.1.g9034.t1	ref|XP_002873568.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319405|gb|EFH49827.1| binding protein [Arabidopsis lyrata subsp. lyrata]	191	167	2.00E-71	87.4	73.3	79.6	binding protein	gbpln	Arabidopsis lyrata	AT5G12390.1 | Symbols: FIS1B | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:4010948-4011950 REVERSE LENGTH=167	191	167	2.00E-72	87.4	73.3	78.5
Rsa1.0_00224.1.g9035.t1	ref|XP_002871524.1| hypothetical protein ARALYDRAFT_488086 [Arabidopsis lyrata subsp. lyrata] gi|297317361|gb|EFH47783.1| hypothetical protein ARALYDRAFT_488086 [Arabidopsis lyrata subsp. lyrata]	294	315	2.33E-156	107.1	87.1	91.2	hypothetical protein ARALYDRAFT_488086	gbpln	Arabidopsis lyrata	AT5G12380.1 | Symbols: ANNAT8 | annexin 8 | chr5:4009223-4010687 FORWARD LENGTH=316	294	316	1.00E-144	107.5	84.7	88.8
Rsa1.0_00224.1.g9036.t4	gb|EOA22673.1| hypothetical protein CARUB_v10003376mg [Capsella rubella]	827	825	0	99.8	92.1	95.6	hypothetical protein CARUB_v10003376mg	gbpln	Capsella rubella	AT5G12370.2 | Symbols: SEC10 | exocyst complex component sec10 | chr5:4003002-4008445 REVERSE LENGTH=825	827	825	0	99.8	91.8	95.3

Rsa1.0_00224.1.g9037.t1	ref|XP_002873566.1| hypothetical protein ARALYDRAFT_488082 [Arabidopsis lyrata subsp. lyrata] gi|297319403|gb|EFH49825.1| hypothetical protein ARALYDRAFT_488082 [Arabidopsis lyrata subsp. lyrata]	190	196	8.00E-80	103.2	76.8	86.8	hypothetical protein ARALYDRAFT_488082	gbpln	Arabidopsis lyrata	AT5G12360.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14190.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4000890-4002248 REVERSE LENGTH=194	190	194	9.00E-73	102.1	77.9	85.8
Rsa1.0_00224.1.g9038.t2	gb|EOA19846.1| hypothetical protein CARUB_v10000094mg [Capsella rubella]	1063	1075	0	101.1	92.3	96.0	hypothetical protein CARUB_v10000094mg	gbpln	Capsella rubella	AT5G12350.1 | Symbols: | Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain | chr5:3995789-4000545 FORWARD LENGTH=1075	1063	1075	0	101.1	92.4	95.5
Rsa1.0_00224.1.g9039.t1	gb|EOA22373.1| hypothetical protein CARUB_v10003004mg [Capsella rubella]	548	461	1.00E-161	84.1	57.1	63.7	hypothetical protein CARUB_v10003004mg	gbpln	Capsella rubella	AT5G12330.4 | Symbols: LRP1 | Lateral root primordium (LRP) protein-related | chr5:3987677-3989408 REVERSE LENGTH=407	548	407	1.00E-163	74.3	59.1	64.1
Rsa1.0_00224.1.g9040.t1	dbj|BAJ08162.1| ankyrin repeats protein [Brassica rapa subsp. chinensis]	144	144	2.00E-72	100.0	94.4	95.8	ankyrin repeats protein	gbpln	Brassica rapa	AT5G12320.1 | Symbols: | ankyrin repeat family protein | chr5:3982762-3983899 FORWARD LENGTH=144	144	144	5.00E-69	100.0	86.1	93.8
Rsa1.0_00224.1.g9041.t2	ref|XP_002873563.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297319400|gb|EFH49822.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	305	252	2.00E-87	82.6	59.7	66.6	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G12310.1 | Symbols: | RING/U-box superfamily protein | chr5:3980485-3982093 REVERSE LENGTH=254	305	254	9.00E-89	83.3	60.7	66.2
Rsa1.0_00224.1.g9042.t1	ref|XP_002871521.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317358|gb|EFH47780.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	627	631	0	100.6	78.1	87.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G12260.1 | Symbols: | BEST Arabidopsis thaliana protein match is: glycosyltransferase family protein 2 (TAIR:AT5G60700.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3966417-3968684 FORWARD LENGTH=624	627	624	0	99.5	77.4	86.6
Rsa1.0_00224.1.g9043.t1	dbj|BAJ34332.1| unnamed protein product [Thellungiella halophila]	448	450	0	100.4	98.7	99.3	unnamed protein product	----	----	AT5G12250.1 | Symbols: TUB6 | beta-6 tubulin | chr5:3961317-3962971 REVERSE LENGTH=449	448	449	0	100.2	98.0	98.7
Rsa1.0_00224.1.g9044.t2	ref|NP_001190294.1| uncharacterized protein [Arabidopsis thaliana] gi|34365673|gb|AAQ65148.1| At5g12240 [Arabidopsis thaliana] gi|51969328|dbj|BAD43356.1| unnamed protein product [Arabidopsis thaliana] gi|332004399|gb|AED91782.1| uncharacterized protein AT5G12240 [Arabidopsis thaliana]	121	114	1.00E-37	94.2	71.1	81.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G12240.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages. | chr5:3959120-3960777 REVERSE LENGTH=114	121	114	2.00E-40	94.2	71.1	81.0
Rsa1.0_00224.1.g9045.t1	gb|AAR20782.1| At5g12230 [Arabidopsis thaliana] gi|44681434|gb|AAS47657.1| At5g12230 [Arabidopsis thaliana]	239	238	1.00E-52	99.6	64.9	73.6	At5g12230	gbpln	Arabidopsis thaliana	AT5G12230.1 | Symbols: MED19A | MED19A; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19480.2); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3953915-3955285 REVERSE LENGTH=221	239	221	5.00E-55	92.5	65.3	74.1
Rsa1.0_00224.1.g9046.t1	ref|NP_568259.1| RAB geranylgeranyl transferase beta subunit 1 [Arabidopsis thaliana] gi|28466947|gb|AAO44082.1| At5g12210 [Arabidopsis thaliana] gi|28466951|gb|AAO44084.1| At4g26580 [Arabidopsis thaliana] gi|110743899|dbj|BAE99784.1| Rab geranylgeranyltransferase, beta subunit [Arabidopsis thaliana] gi|332004391|gb|AED91774.1| RAB geranylgeranyl transferase beta subunit 1 [Arabidopsis thaliana]	323	321	1.00E-164	99.4	89.5	95.4	RAB geranylgeranyl transferase beta subunit 1	gbpln	Arabidopsis thaliana	AT5G12210.1 | Symbols: AtRGTB1, RGTB1 | RAB geranylgeranyl transferase beta subunit 1 | chr5:3947254-3949595 FORWARD LENGTH=321	323	321	1.00E-167	99.4	89.5	95.4
Rsa1.0_00224.1.g9047.t1	ref|XP_002873555.1| dihydropyrimidinase [Arabidopsis lyrata subsp. lyrata] gi|297319392|gb|EFH49814.1| dihydropyrimidinase [Arabidopsis lyrata subsp. lyrata]	540	531	0	98.3	92.0	95.0	dihydropyrimidinase	gbpln	Arabidopsis lyrata	AT5G12200.1 | Symbols: PYD2 | pyrimidine 2 | chr5:3941700-3944727 REVERSE LENGTH=531	540	531	0	98.3	90.9	94.8
Rsa1.0_00224.1.g9048.t1	gb|EOA23032.1| hypothetical protein CARUB_v10003798mg [Capsella rubella]	124	124	9.00E-62	100.0	91.9	95.2	hypothetical protein CARUB_v10003798mg	gbpln	Capsella rubella	AT5G12190.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:3940731-3941105 REVERSE LENGTH=124	124	124	3.00E-64	100.0	91.1	95.2
Rsa1.0_00224.1.g9049.t1	gb|EOA22225.1| hypothetical protein CARUB_v10002812mg [Capsella rubella]	523	530	0	101.3	96.7	98.5	hypothetical protein CARUB_v10002812mg	gbpln	Capsella rubella	AT5G12180.1 | Symbols: CPK17 | calcium-dependent protein kinase 17 | chr5:3937136-3939323 FORWARD LENGTH=528	523	528	0	101.0	96.2	98.1

Rsa1.0_00224.1.g9050.t1	gb|EOA19967.1| hypothetical protein CARUB_v10000228mg [Capsella rubella]	836	829	0	99.2	87.2	91.6	hypothetical protein CARUB_v10000228mg	gbpln	Capsella rubella	AT5G12150.1 | Symbols: | Rho GTPase activation protein (RhoGAP) with PH domain | chr5:3924393-3930100 REVERSE LENGTH=827	836	827	0	98.9	88.3	92.7
Rsa1.0_00224.1.g9051.t1	gb|AAQ03209.1|AF408862_1 phytocystatin [Brassica rapa subsp. pekinensis]	101	101	3.00E-48	100.0	95.0	95.0	phytocystatin	gbpln	Brassica rapa	AT5G12140.1 | Symbols: ATCYS1, CYS1 | cystatin-1 | chr5:3923295-3923936 REVERSE LENGTH=101	101	101	5.00E-48	100.0	86.1	94.1
Rsa1.0_00224.1.g9052.t1	ref|NP_568257.1| TerC integral membrane domain-containing protein [Arabidopsis thaliana] gi|332004383|gb|AED91766.1| protein pigment defective 149 [Arabidopsis thaliana]	368	384	1.00E-169	104.3	86.7	92.9	TerC integral membrane domain-containing protein	gbpln	Arabidopsis thaliana	AT5G12130.1 | Symbols: PDE149, ATTERC | integral membrane TerC family protein | chr5:3919613-3922154 FORWARD LENGTH=384	368	384	1.00E-172	104.3	86.7	92.9
Rsa1.0_00224.1.g9053.t1	gb|EOA20213.1| hypothetical protein CARUB_v10000507mg [Capsella rubella]	601	605	0	100.7	76.4	85.2	hypothetical protein CARUB_v10000507mg	gbpln	Capsella rubella	AT5G12120.1 | Symbols: | Ubiquitin-associated/translation elongation factor EF1B protein | chr5:3916229-3918088 REVERSE LENGTH=619	601	619	0	103.0	75.2	83.7
Rsa1.0_00224.1.g9054.t1	gb|EOA19454.1| hypothetical protein CARUB_v10001845mg, partial [Capsella rubella]	229	240	1.00E-102	104.8	86.9	93.0	hypothetical protein CARUB_v10001845mg, partial	gbpln	Capsella rubella	AT5G12110.1 | Symbols: | Glutathione S-transferase, C-terminal-like;Translation elongation factor EF1B/ribosomal protein S6 | chr5:3914483-3915732 FORWARD LENGTH=228	229	228	1.00E-99	99.6	85.6	90.0
Rsa1.0_00224.1.g9055.t1	ref|NP_196771.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75171712|sp|Q9FMQ1.1|PP376_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g12100, mitochondrial; Flags: Precursor gi|9759377|dbj|BAB10028.1| unnamed protein product [Arabidopsis thaliana] gi|28973713|gb|AAO64173.1| unknown protein [Arabidopsis thaliana] gi|29824237|gb|AAP04079.1| unknown protein [Arabidopsis thaliana] gi|110737169|dbj|BAF00534.1| hypothetical protein [Arabidopsis thaliana] gi|332004380|gb|AED91763.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	824	816	0	99.0	80.0	87.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G12100.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:3911388-3913838 FORWARD LENGTH=816	824	816	0	99.0	80.0	87.9
Rsa1.0_00224.1.g9056.t1	ref|XP_002873549.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319386|gb|EFH49808.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	744	732	0	98.4	83.5	90.3	mechanosensitive ion channel domain-containing protein	gbpln	Arabidopsis lyrata	AT5G12080.3 | Symbols: MSL10, ATMSL10 | mechanosensitive channel of small conductance-like 10 | chr5:3898182-3900923 REVERSE LENGTH=734	744	734	0	98.7	82.4	89.7
Rsa1.0_00224.1.g9057.t1	ref|XP_002871510.1| hypothetical protein ARALYDRAFT_488048 [Arabidopsis lyrata subsp. lyrata] gi|297317347|gb|EFH47769.1| hypothetical protein ARALYDRAFT_488048 [Arabidopsis lyrata subsp. lyrata]	350	364	1.00E-109	104.0	78.3	85.4	hypothetical protein ARALYDRAFT_488048	gbpln	Arabidopsis lyrata	AT5G12050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13980.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3890213-3891301 FORWARD LENGTH=362	350	362	1.00E-111	103.4	78.3	84.9
Rsa1.0_00225.1.g9058.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00225.1.g9059.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00225.1.g9060.t1	gb|AAD20646.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	345	1040	3.00E-77	301.4	39.7	47.8	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00225.1.g9061.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00225.1.g9062.t1	gb|AAB48344.1| reverse transcriptase, partial [Arabidopsis thaliana]	369	199	2.00E-39	53.9	20.6	26.8	reverse transcriptase, partial	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	369	303	3.00E-30	82.1	19.5	26.8
Rsa1.0_00225.1.g9063.t1	ref|NP_174523.2| nitrate transporter 1.5 [Arabidopsis thaliana] gi|310947340|sp|Q9LQL2.2|PTR14_ARATH RecName: Full=Nitrate transporter 1.5 gi|332193367|gb|AEE31488.1| nitrate transporter 1.5 [Arabidopsis thaliana]	604	614	0	101.7	90.6	94.9	nitrate transporter 1.5	gbpln	Arabidopsis thaliana	AT1G32450.1 | Symbols: NRT1.5 | nitrate transporter 1.5 | chr1:11715337-11719807 REVERSE LENGTH=614	604	614	0	101.7	90.6	94.9

Rsa1.0_00225.1.g9064.t1	ref|NP_564401.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|193806407|sp|P0C7R0.1|PPR69_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g32415, mitochondrial; Flags: Precursor gi|332193363|gb|AEE31484.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	787	761	0	96.7	83.9	90.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G32415.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:11695611-11697896 FORWARD LENGTH=761	787	761	0	96.7	83.9	90.9
Rsa1.0_00225.1.g9065.t1	ref|NP_564400.1| vacuolar protein sorting-associated protein 55-like protein [Arabidopsis thaliana] gi|30692698|ref|NP_849741.1| vacuolar protein sorting-associated protein 55-like protein [Arabidopsis thaliana] gi|145324108|ref|NP_001077643.1| vacuolar protein sorting-associated protein 55-like protein [Arabidopsis thaliana] gi|145324110|ref|NP_001077644.1| vacuolar protein sorting-associated protein 55-like protein [Arabidopsis thaliana] gi|145324112|ref|NP_001077645.1| vacuolar protein sorting-associated protein 55-like protein [Arabidopsis thaliana] gi|75167725|sp|Q9AST6.1|VSP55_ARATH RecName: Full=Vacuolar protein sorting-associated protein 55 homolog gi|13605734|gb|AAK32860.1|AF361848_1 At1g32410/F5D14_6 [Arabidopsis thaliana] gi|17978901|gb|AAL47420.1| At1g32410/F5D14_6 [Arabidopsis thaliana] gi|51972031|dbj|BAD44680.1| unknown protein [Arabidopsis thaliana] gi|110741330|dbj|BAF02215.1| hypothetical protein [Arabidopsis thaliana] gi|332193358|gb|AEE31479.1| vacuolar protein sorting-associated protein 55-like protein [Arabidopsis thaliana] gi|332193359|gb|AEE31480.1| vacuolar protein sorting-associated	140	140	2.00E-66	100.0	90.7	95.0	vacuolar protein sorting-associated protein 55-like protein	gbpln	Arabidopsis thaliana	AT1G32410.5 | Symbols: | Vacuolar protein sorting 55 (VPS55) family protein | chr1:11694398-11695297 FORWARD LENGTH=140	140	140	5.00E-69	100.0	90.7	95.0
Rsa1.0_00225.1.g9066.t1	dbj|BAJ34310.1| unnamed protein product [Thellungiella halophila]	278	280	1.00E-129	100.7	92.1	96.4	unnamed protein product	----	----	AT1G32400.3 | Symbols: TOM2A | tobamovirus multiplication 2A | chr1:11689393-11690873 REVERSE LENGTH=280	278	280	1.00E-129	100.7	89.9	95.3
Rsa1.0_00225.1.g9067.t1	ref|NP_174578.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana] gi|378405165|sp|Q9MAP1.2|FB33_ARATH RecName: Full=Putative F-box protein At1g33020 gi|332193429|gb|AEE31550.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana]	417	548	2.00E-82	131.4	46.0	57.6	F-box and associated interaction domain-containing protein	gbpln	Arabidopsis thaliana	AT1G33020.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11962746-11964832 FORWARD LENGTH=548	417	548	4.00E-85	131.4	46.0	57.6
Rsa1.0_00225.1.g9068.t2	emb|CAA22150.1| hypothetical protein [Arabidopsis thaliana] gi|7269091|emb|CAB79200.1| hypothetical protein [Arabidopsis thaliana]	201	457	2.00E-33	227.4	34.3	40.3	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00225.1.g9069.t1	ref|XP_002890988.1| ribose-phosphate pyrophosphokinase 2 [Arabidopsis lyrata subsp. lyrata] gi|297336830|gb|EFH67247.1| ribose-phosphate pyrophosphokinase 2 [Arabidopsis lyrata subsp. lyrata]	394	400	0	101.5	95.4	98.5	ribose-phosphate pyrophosphokinase 2	gbpln	Arabidopsis lyrata	AT1G32380.1 | Symbols: PRS2 | phosphoribosyl pyrophosphate (PRPP) synthase 2 | chr1:11682033-11684229 FORWARD LENGTH=400	394	400	0	101.5	95.4	98.5
Rsa1.0_00225.1.g9070.t1	ref|NP_564397.1| tobamovirus multiplication 2B protein [Arabidopsis thaliana] gi|21594393|gb|AAM66003.1| unknown [Arabidopsis thaliana] gi|332193350|gb|AEE31471.1| tobamovirus multiplication 2B protein [Arabidopsis thaliana]	121	131	2.00E-55	108.3	93.4	98.3	tobamovirus multiplication 2B protein	gbpln	Arabidopsis thaliana	AT1G32370.2 | Symbols: TOM2B, TTM1 | tobamovirus multiplication 2B | chr1:11677005-11678088 FORWARD LENGTH=131	121	131	4.00E-58	108.3	93.4	98.3
Rsa1.0_00225.1.g9071.t1	ref|XP_002890985.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297336827|gb|EFH67244.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	387	385	1.00E-162	99.5	84.8	88.9	zinc finger (CCCH-type) family protein	gbpln	Arabidopsis lyrata	AT1G32360.1 | Symbols: | Zinc finger (CCCH-type) family protein | chr1:11673325-11675162 FORWARD LENGTH=384	387	384	1.00E-164	99.2	84.2	88.6

Rsa1.0_00225.1.g9072.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00225.1.g9073.t1	gb|AAC19267.1| T14P8.13 [Arabidopsis thaliana]	161	423	5.00E-11	262.7	34.8	52.2	T14P8.13	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00225.1.g9074.t1	ref|XP_002887975.1| hypothetical protein ARALYDRAFT_893153 [Arabidopsis lyrata subsp. lyrata] gi|297333816|gb|EFH64234.1| hypothetical protein ARALYDRAFT_893153 [Arabidopsis lyrata subsp. lyrata]	380	381	1.00E-158	100.3	73.9	83.2	hypothetical protein ARALYDRAFT_893153	gbpln	Arabidopsis lyrata	AT1G77520.1 | Symbols: | O-methyltransferase family protein | chr1:29130557-29132007 FORWARD LENGTH=381	380	381	1.00E-157	100.3	69.5	79.7
Rsa1.0_00225.1.g9075.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	263	1142	1.00E-34	434.2	33.5	49.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	263	292	9.00E-21	111.0	24.7	41.4
Rsa1.0_00226.1.g9076.t1	dbj|BAA77394.1| SAE1-S9-protein [Brassica rapa]	246	255	2.00E-55	103.7	45.5	54.1	SAE1-S9-protein	gbpln	Brassica rapa	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	246	295	9.00E-53	119.9	39.8	50.8
Rsa1.0_00226.1.g9077.t1	ref|XP_002864336.1| pinoid-binding protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297310171|gb|EFH40595.1| pinoid-binding protein 1 [Arabidopsis lyrata subsp. lyrata]	131	131	7.00E-60	100.0	85.5	91.6	pinoid-binding protein 1	gbpln	Arabidopsis lyrata	AT5G54490.1 | Symbols: PBP1 | pinoid-binding protein 1 | chr5:22121458-22121841 FORWARD LENGTH=127	131	127	2.00E-60	96.9	84.0	90.8
Rsa1.0_00226.1.g9078.t1	ref|NP_173378.1| Kelch repeat-containing protein [Arabidopsis thaliana] gi|122215562|sp|Q3ED93.1|Y1946_ARATH RecName: Full=Kelch repeat-containing protein At1g19460 gi|332191733|gb|AEE29854.1| Kelch repeat-containing protein [Arabidopsis thaliana]	410	416	9.00E-76	101.5	43.7	60.5	Kelch repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G19460.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:6738484-6739734 FORWARD LENGTH=416	410	416	2.00E-78	101.5	43.7	60.5
Rsa1.0_00226.1.g9079.t1	ref|XP_002866044.1| hypothetical protein ARALYDRAFT_495528 [Arabidopsis lyrata subsp. lyrata] gi|297311879|gb|EFH42303.1| hypothetical protein ARALYDRAFT_495528 [Arabidopsis lyrata subsp. lyrata]	201	209	1.00E-46	104.0	59.7	69.7	hypothetical protein ARALYDRAFT_495528	gbpln	Arabidopsis lyrata	AT5G54470.1 | Symbols: | B-box type zinc finger family protein | chr5:22114584-22115315 REVERSE LENGTH=215	201	215	5.00E-47	107.0	61.7	70.1
Rsa1.0_00226.1.g9080.t1	gb|EOA13904.1| hypothetical protein CARUB_v10027020mg [Capsella rubella]	242	241	2.00E-85	99.6	83.1	87.6	hypothetical protein CARUB_v10027020mg	gbpln	Capsella rubella	AT5G54430.1 | Symbols: ATPHOS32, PHOS32 | Adenine nucleotide alpha hydrolases-like superfamily protein | chr5:22097563-22099693 REVERSE LENGTH=242	242	242	3.00E-84	100.0	84.3	88.8
Rsa1.0_00226.1.g9081.t1	ref|XP_002866042.1| hypothetical protein ARALYDRAFT_331786 [Arabidopsis lyrata subsp. lyrata] gi|297311877|gb|EFH42301.1| hypothetical protein ARALYDRAFT_331786 [Arabidopsis lyrata subsp. lyrata]	1277	1259	0	98.6	91.8	95.5	hypothetical protein ARALYDRAFT_331786	gbpln	Arabidopsis lyrata	AT5G54440.1 | Symbols: CLUB, AtTRS130 | CLUB | chr5:22100056-22107695 FORWARD LENGTH=1259	1277	1259	0	98.6	91.3	95.1
Rsa1.0_00226.1.g9082.t1	ref|XP_002864329.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310164|gb|EFH40588.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	293	292	1.00E-154	99.7	91.5	96.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G54400.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:22090680-22091998 FORWARD LENGTH=292	293	292	1.00E-157	99.7	91.1	96.2
Rsa1.0_00226.1.g9083.t1	gb|AAB94051.1| PAP-specific phosphatase [Arabidopsis thaliana]	367	373	0	101.6	90.2	95.4	PAP-specific phosphatase	gbpln	Arabidopsis thaliana	AT5G54390.1 | Symbols: AHL, ATAHL, HL | HAL2-like | chr5:22086133-22087586 FORWARD LENGTH=373	367	373	0	101.6	89.6	94.8
Rsa1.0_00226.1.g9084.t1	ref|NP_563720.1| putative protein arginine N-methyltransferase 4.2 [Arabidopsis thaliana] gi|75336166|sp|Q9MAT5.1|ANM10_ARATH RecName: Full=Protein arginine N-methyltransferase PRMT10 gi|7211979|gb|AAF40450.1|AC004809_8 Similar to protein arginine N-methyltransferase from Rattus norvegicus gb|U60882. ESTs gb|Z30908 and gb|Z29205 come from this gene [Arabidopsis thaliana] gi|22135775|gb|AAM91044.1| At1g04870/F13M7_12 [Arabidopsis thaliana] gi|332189633|gb|AEE27754.1| putative protein arginine N-methyltransferase 4.2 [Arabidopsis thaliana]	381	383	0	100.5	85.8	90.6	putative protein arginine N-methyltransferase 4.2	gbpln	Arabidopsis thaliana	AT1G04870.2 | Symbols: PRMT10, ATPRMT10 | protein arginine methyltransferase 10 | chr1:1373485-1375598 REVERSE LENGTH=383	381	383	0	100.5	85.8	90.6
Rsa1.0_00226.1.g9085.t1	gb|EOA13308.1| hypothetical protein CARUB_v10026343mg [Capsella rubella]	467	471	0	100.9	75.8	85.0	hypothetical protein CARUB_v10026343mg	gbpln	Capsella rubella	AT5G42240.1 | Symbols: scpl42 | serine carboxypeptidase-like 42 | chr5:16888717-16890931 FORWARD LENGTH=473	467	473	0	101.3	74.5	82.9

Rsa1.0_00226.1.g9086.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00226.1.g9087.t1	ref|NP_200248.1| late embryogenesis abundant protein–like protein [Arabidopsis thaliana] gi|10257484|dbj|BAB10109.1| root cap protein 2–like protein [Arabidopsis thaliana] gi|71143048|gb|AAZ23915.1| At5g54370 [Arabidopsis thaliana] gi|332009106|gb|AED96489.1| late embryogenesis abundant protein–like protein [Arabidopsis thaliana]	337	337	0	100.0	93.8	97.9	late embryogenesis abundant protein–like protein	gbpln	Arabidopsis thaliana	AT5G54370.1 | Symbols: | Late embryogenesis abundant (LEA) protein–related | chr5:22075334–22076567 FORWARD LENGTH=337	337	337	0	100.0	93.8	97.9
Rsa1.0_00226.1.g9088.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00226.1.g9089.t1	gb|EOA12434.1| hypothetical protein CARUB_v10028316mg [Capsella rubella]	482	480	0	99.6	85.9	90.7	hypothetical protein CARUB_v10028316mg	gbpln	Capsella rubella	AT5G54310.1 | Symbols: NEV, AGD5 | ARF–GAP domain 5 | chr5:22057262–22061066 REVERSE LENGTH=483	482	483	0	100.2	83.6	88.8
Rsa1.0_00226.1.g9090.t1	ref|NP_200241.1| uncharacterized protein [Arabidopsis thaliana] gi|9759503|dbj|BAB10753.1| cotton fiber expressed protein 1–like protein [Arabidopsis thaliana] gi|20466706|gb|AAM20670.1| cotton fiber expressed protein 1–like protein [Arabidopsis thaliana] gi|23198238|gb|AAN15646.1| cotton fiber expressed protein 1–like protein [Arabidopsis thaliana] gi|332009099|gb|AED96482.1| uncharacterized protein AT5G54300 [Arabidopsis thaliana]	327	326	1.00E–103	99.7	66.4	75.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54300.1 | Symbols: | Protein of unknown function (DUF761) | chr5:22054270–22055342 REVERSE LENGTH=326	327	326	1.00E–105	99.7	66.4	75.8
Rsa1.0_00226.1.g9091.t1	ref|NP_001190537.1| cytochrome c–type biogenesis ccda–like chloroplastic protein [Arabidopsis thaliana] gi|332009098|gb|AED96481.1| cytochrome c–type biogenesis ccda–like chloroplastic protein [Arabidopsis thaliana]	353	355	1.00E–161	100.6	89.8	95.2	cytochrome c–type biogenesis ccda–like chloroplastic protein	gbpln	Arabidopsis thaliana	AT5G54290.2 | Symbols: CcdA | cytochrome c biogenesis protein family | chr5:22051097–22053923 FORWARD LENGTH=355	353	355	1.00E–164	100.6	89.8	95.2
Rsa1.0_00226.1.g9092.t2	ref|XP_002866036.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311871|gb|EFH42295.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1204	1219	0	101.2	89.9	94.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G54280.2 | Symbols: ATM2, ATMYOS1, ATM4 | myosin 2 | chr5:22039606–22045592 REVERSE LENGTH=1220	1204	1220	0	101.3	89.8	94.1
Rsa1.0_00226.1.g9093.t1	ref|NP_200238.1| light–harvesting chlorophyll B–binding protein 3 [Arabidopsis thaliana] gi|4741952|gb|AAD28773.1|AF134126_1 Lhcb3 protein [Arabidopsis thaliana] gi|5002210|gb|AAD37362.1|AF143691_1 type III chlorophyll a/b binding protein [Arabidopsis thaliana] gi|13605754|gb|AAK32870.1|AF361858_1 AT5g54270/MDK4_9 [Arabidopsis thaliana] gi|13926339|gb|AAK49633.1|AF372917_1 AT5g54270/MDK4_9 [Arabidopsis thaliana] gi|9759500|dbj|BAB10750.1| Lhcb3 chlorophyll a/b binding protein [Arabidopsis thaliana] gi|16323262|gb|AAL15365.1| AT5g54270/MDK4_9 [Arabidopsis thaliana] gi|332009094|gb|AED96477.1| light–harvesting chlorophyll B–binding protein 3 [Arabidopsis thaliana]	265	265	1.00E–150	100.0	98.9	99.2	light–harvesting chlorophyll B–binding protein 3	gbpln	Arabidopsis thaliana	AT5G54270.1 | Symbols: LHCB3, LHCB3*1 | light–harvesting chlorophyll B–binding protein 3 | chr5:22038424–22039383 FORWARD LENGTH=265	265	265	1.00E–152	100.0	98.9	99.2
Rsa1.0_00226.1.g9094.t1	ref|XP_002864331.1| hypothetical protein ARALYDRAFT_495522 [Arabidopsis lyrata subsp. lyrata] gi|297310166|gb|EFH40590.1| hypothetical protein ARALYDRAFT_495522 [Arabidopsis lyrata subsp. lyrata]	369	369	1.00E–114	100.0	58.8	72.9	hypothetical protein ARALYDRAFT_495522	gbpln	Arabidopsis lyrata	AT5G54450.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22108273–22109379 REVERSE LENGTH=368	369	368	1.00E–116	99.7	60.7	71.8
Rsa1.0_00227.1.g9095.t1	ref|XP_002876320.1| hypothetical protein ARALYDRAFT_485995 [Arabidopsis lyrata subsp. lyrata] gi|297322158|gb|EFH52579.1| hypothetical protein ARALYDRAFT_485995 [Arabidopsis lyrata subsp. lyrata]	185	139	2.00E–44	75.1	55.1	61.6	hypothetical protein ARALYDRAFT_485995	gbpln	Arabidopsis lyrata	AT3G55646.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G39855.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae – 798; Bacteria – 22429; Metazoa – 974; Fungi – 991; Plants – 531; Viruses – 0; Other Eukaryotes – 9610 (source: NCBI BLink). | chr3:20645087–20646148 FORWARD LENGTH=146	185	146	7.00E–42	78.9	55.7	62.7

Rsa1.0_00227.1.g9096.t1	gb|EOA24465.1| hypothetical protein CARUB_v10017721mg [Capsella rubella]	245	302	1.00E−139	123.3	98.8	99.6	hypothetical protein CARUB_v10017721mg	gbpln	Capsella rubella	AT3G55620.1 | Symbols: emb1624 | Translation initiation factor IF6 | chr3:20634581−20636312 FORWARD LENGTH=245	245	245	1.00E−140	100.0	97.6	99.6
Rsa1.0_00227.1.g9097.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00227.1.g9098.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00227.1.g9099.t1	gb|AAK01361.1|AF314812_1 delta 1−pyrroline−5−carboxylate synthetase B [Brassica napus]	726	727	0	100.1	93.7	96.4	delta 1−pyrroline−5−carboxylate synthetase B	gbpln	Brassica napus	AT3G55610.1 | Symbols: P5CS2 | delta 1−pyrroline−5−carboxylate synthase 2 | chr3:20624278−20628989 REVERSE LENGTH=726	726	726	0	100.0	91.2	95.3
Rsa1.0_00227.1.g9100.t1	ref|NP_567025.1| Mitochondrial glycoprotein family protein [Arabidopsis thaliana] gi|21554314|gb|AAM63419.1| unknown [Arabidopsis thaliana] gi|30102600|gb|AAP21218.1| At3g55605 [Arabidopsis thaliana] gi|110743885|dbj|BAE99777.1| hypothetical protein [Arabidopsis thaliana] gi|332645886|gb|AEE79407.1| Mitochondrial glycoprotein family protein [Arabidopsis thaliana]	252	258	4.00E−98	102.4	79.0	86.1	Mitochondrial glycoprotein family protein	gbpln	Arabidopsis thaliana	AT3G55605.1 | Symbols: | Mitochondrial glycoprotein family protein | chr3:20622668−20623889 FORWARD LENGTH=258	252	258	1.00E−100	102.4	79.0	86.1
Rsa1.0_00227.1.g9101.t1	ref|XP_002878040.1| hypothetical protein ARALYDRAFT_906983 [Arabidopsis lyrata subsp. lyrata] gi|297323878|gb|EFH54299.1| hypothetical protein ARALYDRAFT_906983 [Arabidopsis lyrata subsp. lyrata]	81	139	4.00E−33	171.6	82.7	87.7	hypothetical protein ARALYDRAFT_906983	gbpln	Arabidopsis lyrata	AT3G55570.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41761.1); Has 128 Blast hits to 128 proteins in 12 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 128; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:20610166−20610671 REVERSE LENGTH=109	81	109	5.00E−35	134.6	82.7	86.4
Rsa1.0_00227.1.g9102.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033−105622 [Arabidopsis thaliana]	1566	1557	0	99.4	40.9	58.9	reverse transcriptase, putative; 100033−105622	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chrM:90883−91347 REVERSE LENGTH=154	1566	154	3.00E−34	9.8	4.3	6.4
Rsa1.0_00227.1.g9103.t1	ref|XP_002878039.1| hypothetical protein ARALYDRAFT_906980 [Arabidopsis lyrata subsp. lyrata] gi|297323877|gb|EFH54298.1| hypothetical protein ARALYDRAFT_906980 [Arabidopsis lyrata subsp. lyrata]	303	308	1.00E−125	101.7	87.8	94.4	hypothetical protein ARALYDRAFT_906980	gbpln	Arabidopsis lyrata	AT3G55560.1 | Symbols: AGF2, AHL15 | AT−hook protein of GA feedback 2 | chr3:20604904−20605836 REVERSE LENGTH=310	303	310	1.00E−127	102.3	87.8	94.4
Rsa1.0_00227.1.g9104.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	117	149	3.00E−16	127.4	40.2	56.4	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00227.1.g9105.t1	gb|EOA23348.1| hypothetical protein CARUB_v10019451mg [Capsella rubella]	638	682	0	106.9	87.1	92.3	hypothetical protein CARUB_v10019451mg	gbpln	Capsella rubella	AT3G55550.1 | Symbols: | Concanavalin A−like lectin protein kinase family protein | chr3:20600019−20602073 REVERSE LENGTH=684	638	684	0	107.2	86.8	91.8
Rsa1.0_00227.1.g9106.t1	dbj|BAB02146.1| copia retroelement pol polyprotein−like [Arabidopsis thaliana]	350	526	1.00E−13	150.3	10.0	12.9	copia retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00227.1.g9107.t1	ref|XP_002876307.1| hypothetical protein ARALYDRAFT_906973 [Arabidopsis lyrata subsp. lyrata] gi|297322145|gb|EFH52566.1| hypothetical protein ARALYDRAFT_906973 [Arabidopsis lyrata subsp. lyrata]	88	80	8.00E−21	90.9	59.1	68.2	hypothetical protein ARALYDRAFT_906973	gbpln	Arabidopsis lyrata	AT3G55515.1 | Symbols: DVL8, RTFL7 | ROTUNDIFOLIA like 7 | chr3:20590923−20591162 FORWARD LENGTH=79	88	79	3.00E−22	89.8	55.7	70.5
Rsa1.0_00227.1.g9108.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00227.1.g9109.t1	ref|XP_002876306.1| hypothetical protein ARALYDRAFT_485977 [Arabidopsis lyrata subsp. lyrata] gi|297322144|gb|EFH52565.1| hypothetical protein ARALYDRAFT_485977 [Arabidopsis lyrata subsp. lyrata]	415	601	1.00E−81	144.8	41.7	48.0	hypothetical protein ARALYDRAFT_485977	gbpln	Arabidopsis lyrata	AT3G55510.1 | Symbols: RBL | Noc2p family | chr3:20579232−20582124 FORWARD LENGTH=594	415	594	5.00E−83	143.1	41.7	47.5
Rsa1.0_00227.1.g9110.t1	ref|XP_002878036.1| ATEXPA16 [Arabidopsis lyrata subsp. lyrata] gi|297323874|gb|EFH54295.1| ATEXPA16 [Arabidopsis lyrata subsp. lyrata]	260	260	1.00E−137	100.0	90.4	95.0	ATEXPA16	gbpln	Arabidopsis lyrata	AT3G55500.1 | Symbols: ATEXPA16, EXP16, ATEXP16, ATHEXP ALPHA 1.7, EXPA16 | expansin A16 | chr3:20575073−20576102 REVERSE LENGTH=260	260	260	1.00E−138	100.0	89.2	94.6
Rsa1.0_00227.1.g9111.t1	gb|EOA24879.1| hypothetical protein CARUB_v10018170mg [Capsella rubella]	154	155	9.00E−73	100.6	86.4	92.9	hypothetical protein CARUB_v10018170mg	gbpln	Capsella rubella	AT3G55470.2 | Symbols: | Calcium−dependent lipid−binding (CaLB domain) family protein | chr3:20564356−20566092 FORWARD LENGTH=155	154	155	7.00E−75	100.6	85.1	93.5
Rsa1.0_00227.1.g9112.t2	gb|EOA24419.1| hypothetical protein CARUB_v10017670mg, partial [Capsella rubella]	350	315	4.00E−45	90.0	51.4	52.9	hypothetical protein CARUB_v10017670mg, partial	gbpln	Capsella rubella	AT3G55460.1 | Symbols: SCL30, At−SCL30 | SC35−like splicing factor 30 | chr3:20561024−20563502 FORWARD LENGTH=262	350	262	4.00E−26	74.9	18.0	20.6

Rsa1.0_00228.1.g9113.t1	emb|CAB85500.1| putative protein [Arabidopsis thaliana]	420	837	1.00E-106	199.3	54.0	62.6	putative protein	gbpln	Arabidopsis thaliana	AT5G03800.1 | Symbols: EMB175, emb1899, EMB166 | Pentatricopeptide repeat (PPR) superfamily protein | chr5:1010894-1013584 REVERSE LENGTH=896	420	896	1.00E-108	213.3	54.0	62.6
Rsa1.0_00228.1.g9114.t1	gb|EOA19541.1| hypothetical protein CARUB_v10002513mg [Capsella rubella]	177	353	5.00E-65	199.4	67.8	73.4	hypothetical protein CARUB_v10002513mg	gbpln	Capsella rubella	AT5G03810.1 | Symbols: | GDSL-like Lipase/Acylhydrolase family protein | chr5:1013939-1015345 REVERSE LENGTH=353	177	353	9.00E-61	199.4	61.6	70.1
Rsa1.0_00228.1.g9115.t1	ref|XP_002873117.1| hypothetical protein ARALYDRAFT_487163 [Arabidopsis lyrata subsp. lyrata] gi|166065101|gb|ABY79195.1| At5g03840-like protein [Arabidopsis lyrata] gi|297318954|gb|EFH49376.1| hypothetical protein ARALYDRAFT_487163 [Arabidopsis lyrata subsp. lyrata]	179	177	1.00E-88	98.9	90.5	95.5	hypothetical protein ARALYDRAFT_487163	gbpln	Arabidopsis lyrata	AT5G03840.1 | Symbols: TFL1, TFL-1 | PEBP (phosphatidylethanolamine-binding protein) family protein | chr5:1024760-1025796 REVERSE LENGTH=177	179	177	4.00E-90	98.9	89.4	95.0
Rsa1.0_00228.1.g9116.t1	gb|EOA31777.1| hypothetical protein CARUB_v10014999mg, partial [Capsella rubella]	64	92	4.00E-28	143.8	98.4	100.0	hypothetical protein CARUB_v10014999mg, partial	gbpln	Capsella rubella	AT5G64140.1 | Symbols: RPS28 | ribosomal protein S28 | chr5:25667529-25667723 REVERSE LENGTH=64	64	64	2.00E-30	100.0	98.4	100.0
Rsa1.0_00228.1.g9117.t1	gb|EOA29177.1| hypothetical protein CARUB_v10025449mg [Capsella rubella]	195	535	2.00E-63	274.4	59.5	64.1	hypothetical protein CARUB_v10025449mg	gbpln	Capsella rubella	AT2G31865.2 | Symbols: PARG2 | poly(ADP-ribose) glycohydrolase 2 | chr2:13546790-13549472 REVERSE LENGTH=532	195	532	4.00E-63	272.8	57.9	62.1
Rsa1.0_00228.1.g9118.t1	gb|EOA30214.1| hypothetical protein CARUB_v10013336mg [Capsella rubella]	99	571	8.00E-13	576.8	53.5	56.6	hypothetical protein CARUB_v10013336mg	gbpln	Capsella rubella	AT3G12200.2 | Symbols: Nek7 | NIMA-related kinase 7 | chr3:3887173-3890550 REVERSE LENGTH=581	99	581	2.00E-14	586.9	48.5	54.5
Rsa1.0_00228.1.g9119.t1	sp|P13244.1|MASY_BRANA RecName: Full=Malate synthase, glyoxysomal gi|167150|gb|AAA32996.1| malate synthase (EC 4.1.3.2) [Brassica napus]	561	561	0	100.0	97.3	99.1	RecName: Full=Malate synthase, glyoxysomal gi|167150|gb|AAA32996.1| malate synthase (EC 4.1.3.2)	gbpln	Brassica napus	AT5G03860.2 | Symbols: MLS | malate synthase | chr5:1032276-1034527 REVERSE LENGTH=562	561	562	0	100.2	94.8	98.6
Rsa1.0_00228.1.g9120.t1	ref|NP_196007.1| Glutaredoxin family protein [Arabidopsis thaliana] gi|7406397|emb|CAB85507.1| putative protein [Arabidopsis thaliana] gi|9758016|dbj|BAB08613.1| unnamed protein product [Arabidopsis thaliana] gi|332003282|gb|AED90665.1| Glutaredoxin family protein [Arabidopsis thaliana]	363	384	1.00E-155	105.8	83.7	90.1	Glutaredoxin family protein	gbpln	Arabidopsis thaliana	AT5G03870.1 | Symbols: | Glutaredoxin family protein | chr5:1035813-1036967 REVERSE LENGTH=384	363	384	1.00E-157	105.8	83.7	90.1
Rsa1.0_00228.1.g9121.t1	dbj|BAJ34555.1| unnamed protein product [Thellungiella halophila]	525	523	0	99.6	89.3	94.7	unnamed protein product	----	----	AT5G03900.2 | Symbols: | Iron-sulphur cluster biosynthesis family protein | chr5:1048338-1051869 FORWARD LENGTH=523	525	523	0	99.6	85.3	92.0
Rsa1.0_00228.1.g9122.t1	gb|EOA22053.1| hypothetical protein CARUB_v10002593mg [Capsella rubella]	154	158	5.00E-66	102.6	82.5	90.9	hypothetical protein CARUB_v10002593mg	gbpln	Capsella rubella	AT5G03905.1 | Symbols: | Iron-sulphur cluster biosynthesis family protein | chr5:1052728-1054041 FORWARD LENGTH=158	154	158	3.00E-63	102.6	78.6	87.7
Rsa1.0_00228.1.g9123.t1	gb|EOA22946.1| hypothetical protein CARUB_v10003682mg [Capsella rubella]	567	564	0	99.5	87.7	94.0	hypothetical protein CARUB_v10003682mg	gbpln	Capsella rubella	AT5G03940.1 | Symbols: FFC, 54CP, CPSRP54, SRP54CP | chloroplast signal recognition particle 54 kDa subunit | chr5:1060265-1063257 REVERSE LENGTH=564	567	564	0	99.5	87.1	92.6
Rsa1.0_00228.1.g9124.t1	ref|XP_002873125.1| IQ-domain 12 [Arabidopsis lyrata subsp. lyrata] gi|297318962|gb|EFH49384.1| IQ-domain 12 [Arabidopsis lyrata subsp. lyrata]	379	403	1.00E-147	106.3	81.0	88.9	IQ-domain 12	gbpln	Arabidopsis lyrata	AT5G03960.1 | Symbols: IQD12 | IQ-domain 12 | chr5:1068333-1069683 REVERSE LENGTH=403	379	403	1.00E-149	106.3	80.2	89.7
Rsa1.0_00228.1.g9125.t1	gb|ABD65606.1| hypothetical protein 23.t00002 [Brassica oleracea]	493	433	5.00E-64	87.8	33.9	45.4	hypothetical protein 23.t00002	gbpln	Brassica oleracea	AT3G61090.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:22609094-22609822 REVERSE LENGTH=180	493	180	7.00E-12	36.5	7.7	13.2
Rsa1.0_00228.1.g9126.t1	gb|ABD65606.1| hypothetical protein 23.t00002 [Brassica oleracea]	486	433	4.00E-64	89.1	34.6	46.5	hypothetical protein 23.t00002	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00228.1.g9127.t1	ref|NP_178368.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|3184275|gb|AAC18922.1| putative reverse transcriptase [Arabidopsis thaliana] gi|330250513|gb|AEC05607.1| RNase H domain-containing protein [Arabidopsis thaliana]	161	365	1.00E-36	226.7	47.8	60.2	RNase H domain-containing protein	gbpln	Arabidopsis thaliana	AT2G02650.1 | Symbols: | Ribonuclease H-like superfamily protein | chr2:735411-736546 FORWARD LENGTH=365	161	365	4.00E-39	226.7	47.8	60.2
Rsa1.0_00228.1.g9128.t1	gb|ABA70759.1| baby boom interacting protein 1B [Brassica napus]	258	711	1.00E-98	275.6	69.0	72.5	baby boom interacting protein 1B	gbpln	Brassica napus	AT1G73360.1 | Symbols: HDG11, EDT1, ATHDG11 | homeodomain GLABROUS 11 | chr1:27578893-27581820 REVERSE LENGTH=722	258	722	7.00E-86	279.8	63.6	67.8

Rsa1.0_00228.1.g9129.t1	ref|NP_196024.1| triacylglycerol lipase SDP1 [Arabidopsis thaliana] gi|75181222|sp|Q9LZA6.1|SDP1_ARATH RecName: Full=Triacylglycerol lipase SDP1; AltName: Full=Protein SUGAR-DEPENDENT 1 gi|7406414|emb|CAB85524.1| putative protein [Arabidopsis thaliana] gi|22531263|gb|AAM97135.1| putative protein [Arabidopsis thaliana] gi|332003304|gb|AED90687.1| triacylglycerol lipase SDP1 [Arabidopsis thaliana]	778	825	0	106.0	87.1	91.4	triacylglycerol lipase SDP1	gbpln	Arabidopsis thaliana	AT5G04040.1 | Symbols: SDP1 | Patatin-like phospholipase family protein | chr5:1090346-1093003 FORWARD LENGTH=825	778	825	0	106.0	87.1	91.4
Rsa1.0_00228.1.g9130.t2	ref|NP_196028.2| uncharacterized protein [Arabidopsis thaliana] gi|38603900|gb|AAR24695.1| At5g04080 [Arabidopsis thaliana] gi|41349906|gb|AAS00338.1| At5g04080 [Arabidopsis thaliana] gi|332003311|gb|AED90694.1| uncharacterized protein AT5G04080 [Arabidopsis thaliana]	66	63	4.00E-21	95.5	78.8	84.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G04080.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 9 growth stages; Has 115 Blast hits to 115 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 5; Plants - 110; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:1104815-1105186 FORWARD LENGTH=63	66	63	7.00E-24	95.5	78.8	84.8
Rsa1.0_00228.1.g9131.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	494	1274	2.00E-97	257.9	39.1	56.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	494	575	1.00E-54	116.4	30.2	45.1
Rsa1.0_00228.1.g9132.t1	ref|XP_002871076.1| phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis lyrata subsp. lyrata] gi|297316913|gb|EFH47335.1| phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis lyrata subsp. lyrata]	238	238	1.00E-122	100.0	90.3	94.5	phosphoglycerate/bisphosphoglycerate mutase family protein	gbpln	Arabidopsis lyrata	AT5G04120.1 | Symbols: | Phosphoglycerate mutase family protein | chr5:1120091-1121605 FORWARD LENGTH=238	238	238	1.00E-123	100.0	88.7	94.1
Rsa1.0_00228.1.g9133.t1	gb|ABD65606.1| hypothetical protein 23.t00002 [Brassica oleracea]	390	433	2.00E-41	111.0	34.1	49.2	hypothetical protein 23.t00002	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00228.1.g9134.t1	gb|ABD65606.1| hypothetical protein 23.t00002 [Brassica oleracea]	399	433	4.00E-63	108.5	42.6	55.6	hypothetical protein 23.t00002	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00228.1.g9135.t1	ref|NP_568133.1| DNA gyrase subunit B [Arabidopsis thaliana] gi|75165162|sp|Q94BZ7.1|GYRBM_ARATH RecName: Full=DNA gyrase subunit B, mitochondrial; Flags: Precursor gi|14517374|gb|AAK62578.1| AT3g10270/F14P13_13 [Arabidopsis thaliana] gi|22655426|gb|AAM98305.1| At3g10270/F14P13_13 [Arabidopsis thaliana] gi|332003319|gb|AED90702.1| DNA gyrase subunit B [Arabidopsis thaliana]	978	732	0	74.8	63.8	66.5	DNA gyrase subunit B	gbpln	Arabidopsis thaliana	AT5G04130.1 | Symbols: GYRB2 | DNA GYRASE B2 | chr5:1122084-1128031 REVERSE LENGTH=732	978	732	0	74.8	63.8	66.5
Rsa1.0_00228.1.g9136.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00228.1.g9137.t1	ref|NP_196040.1| metacaspase 9 [Arabidopsis thaliana] gi|75263209|sp|Q9FYE1.1|MCA9_ARATH RecName: Full=Metacaspase-9; Short=AtMC9; Contains: RecName: Full=Metacaspase-9 subunit p20; Contains: RecName: Full=Metacaspase-9 subunit p10; AltName: Full=Metacaspase 2f; Short=AtMCP2f gi|9955575|emb|CAC05502.1| latex-abundant protein-like [Arabidopsis thaliana] gi|17380712|gb|AAL36186.1| putative latex-abundant protein [Arabidopsis thaliana] gi|20259063|gb|AAM14247.1| putative latex-abundant protein [Arabidopsis thaliana] gi|32482824|gb|AAP84712.1| metacaspase 9 [Arabidopsis thaliana] gi|37788561|gb|AAP44522.1| metacaspase 9 precurser [Arabidopsis thaliana] gi|332003327|gb|AED90710.1| metacaspase 9 [Arabidopsis thaliana]	322	325	1.00E-162	100.9	86.3	93.2	metacaspase 9	gbpln	Arabidopsis thaliana	AT5G04200.1 | Symbols: AtMC9, MC9 | metacaspase 9 | chr5:1153893-1154870 FORWARD LENGTH=325	322	325	1.00E-165	100.9	86.3	93.2
Rsa1.0_00229.1.g9138.t1	gb|AAC33963.1| contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]	1346	1633	0	121.3	49.4	62.2	contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19)	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1346	1262	1.00E-165	93.8	21.2	27.3

Rsa1.0_00229.1.g9139.t1	ref|NP_001189585.1| zinc binding motif and SET domain-containing protein [Arabidopsis thaliana] gi|306526268|sp|O64827.3|SUVR5_ARATH RecName: Full=Histone-lysine N-methyltransferase SUVR5; AltName: Full=C2H2 zinc finger-SET histone methyltransferase; Short=Protein C2H2 SET; AltName: Full=Protein SET DOMAIN GROUP 6; AltName: Full=Suppressor of variegation 3-9-related protein 5; Short=Su(var)3-9-related protein 5 gi|227204171|dbj|BAH56937.1| AT2G23740 [Arabidopsis thaliana] gi|330252390|gb|AEC07484.1| zinc binding motif and SET domain-containing protein [Arabidopsis thaliana]	1370	1382	0	100.9	76.0	83.6	zinc binding motif and SET domain-containing protein	gbpln	Arabidopsis thaliana	AT2G23740.2 | Symbols: | nucleic acid binding;sequence-specific DNA binding transcription factors;zinc ion binding | chr2:10098213-10103229 FORWARD LENGTH=1382	1370	1382	0	100.9	76.0	83.6
Rsa1.0_00229.1.g9140.t1	ref|NP_179950.1| uncharacterized protein [Arabidopsis thaliana] gi|20197175|gb|AAC17092.2| unknown protein [Arabidopsis thaliana] gi|330252388|gb|AEC07482.1| uncharacterized protein AT2G23700 [Arabidopsis thaliana]	682	707	0	103.7	83.3	90.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G23700.1 | Symbols: | Protein of unknown function, DUF547 | chr2:10076624-10079849 REVERSE LENGTH=707	682	707	0	103.7	83.3	90.6
Rsa1.0_00229.1.g9141.t1	gb|EOA25391.1| hypothetical protein CARUB_v10018723mg [Capsella rubella]	157	156	6.00E-63	99.4	74.5	83.4	hypothetical protein CARUB_v10018723mg	gbpln	Capsella rubella	AT1G64100.2 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:23791585-23795563 FORWARD LENGTH=806	157	806	6.00E-46	513.4	54.1	68.8
Rsa1.0_00229.1.g9142.t1	gb|EOA25391.1| hypothetical protein CARUB_v10018723mg [Capsella rubella]	157	156	9.00E-63	99.4	72.6	84.1	hypothetical protein CARUB_v10018723mg	gbpln	Capsella rubella	AT1G64100.2 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:23791585-23795563 FORWARD LENGTH=806	157	806	2.00E-45	513.4	52.2	68.8
Rsa1.0_00229.1.g9143.t1	ref|XP_002883241.1| hypothetical protein ARALYDRAFT_479561 [Arabidopsis lyrata subsp. lyrata] gi|297329081|gb|EFH59500.1| hypothetical protein ARALYDRAFT_479561 [Arabidopsis lyrata subsp. lyrata]	369	385	8.00E-99	104.3	49.1	63.4	hypothetical protein ARALYDRAFT_479561	gbpln	Arabidopsis lyrata	AT3G20370.1 | Symbols: | TRAF-like family protein | chr3:7105481-7107079 FORWARD LENGTH=379	369	379	2.00E-96	102.7	47.4	60.7
Rsa1.0_00229.1.g9144.t1	gb|EOA28028.1| hypothetical protein CARUB_v10024204mg [Capsella rubella]	164	164	3.00E-71	100.0	85.4	91.5	hypothetical protein CARUB_v10024204mg	gbpln	Capsella rubella	AT2G23690.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 7 plant structures; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37240.1); Has 243 Blast hits to 243 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 241; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:10072297-10072788 FORWARD LENGTH=163	164	163	4.00E-73	99.4	88.4	92.1
Rsa1.0_00229.1.g9145.t1	ref|NP_565556.1| synechocystis YCF37-like protein [Arabidopsis thaliana] gi|3152615|gb|AAC17094.1| expressed protein [Arabidopsis thaliana] gi|16648702|gb|AAL25543.1| At2g23670/F26B6.32 [Arabidopsis thaliana] gi|20197003|gb|AAM14867.1| expressed protein [Arabidopsis thaliana] gi|20334912|gb|AAM16212.1| At2g23670/F26B6.32 [Arabidopsis thaliana] gi|206748360|gb|ACI22363.1| YCF37-like protein [Arabidopsis thaliana] gi|330252384|gb|AEC07478.1| synechocystis YCF37-like protein [Arabidopsis thaliana]	162	167	3.00E-71	103.1	86.4	88.3	synechocystis YCF37-like protein	gbpln	Arabidopsis thaliana	AT2G23670.1 | Symbols: YCF37 | homolog of Synechocystis YCF37 | chr2:10063307-10063810 REVERSE LENGTH=167	162	167	1.00E-73	103.1	86.4	88.3
Rsa1.0_00229.1.g9146.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00229.1.g9147.t1	ref|XP_002880519.1| LOB domain family protein [Arabidopsis lyrata subsp. lyrata] gi|297326358|gb|EFH56778.1| LOB domain family protein [Arabidopsis lyrata subsp. lyrata]	309	311	1.00E-138	100.6	85.8	91.9	LOB domain family protein	gbpln	Arabidopsis lyrata	AT2G23660.2 | Symbols: LBD10 | LOB domain-containing protein 10 | chr2:10060242-10061177 REVERSE LENGTH=311	309	311	1.00E-137	100.6	85.1	91.3
Rsa1.0_00229.1.g9148.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00229.1.g9149.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00229.1.g9150.t1	gb|EOA29060.1| hypothetical protein CARUB_v10025315mg [Capsella rubella]	539	540	0	100.2	87.4	94.1	hypothetical protein CARUB_v10025315mg	gbpln	Capsella rubella	AT2G23630.1 | Symbols: sks16 | SKU5 similar 16 | chr2:10052581-10055311 REVERSE LENGTH=541	539	541	0	100.4	87.2	93.7
Rsa1.0_00229.1.g9151.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00230.1.g9152.t1	ref|NP_566156.2| putative translation factor [Arabidopsis thaliana] gi|6091731|gb|AAF03443.1|AC010797_19 hypothetical protein [Arabidopsis thaliana] gi|19310491|gb|AAL84979.1| At3g1920/F28J7.25 [Arabidopsis thaliana] gi|23505865|gb|AAN28792.1| At3g1920/F28J7.25 [Arabidopsis thaliana] gi|332640214|gb|AEE73735.1| Sua5/YciO/YrdC domain-containing protein [Arabidopsis thaliana]	296	307	1.00E-148	103.7	88.2	92.6	putative translation factor	gbpln	Arabidopsis thaliana	AT3G01920.1 | Symbols: | DHBP synthase RibB-like alpha/beta domain | chr3:317449-319001 FORWARD LENGTH=307	296	307	1.00E-151	103.7	88.2	92.6
Rsa1.0_00230.1.g9153.t1	sp|P41128.1|RL131_BRANA RecName: Full=60S ribosomal protein L13-1; AltName: Full=Cold-induced protein C24A gi|398918|emb|CAA80341.1| cold induced protein (BnC24A) [Brassica napus]	206	206	1.00E-113	100.0	97.6	98.5	RecName: Full=60S ribosomal protein L13-1; AltName: Full=Cold-induced protein C24A gi|398918|emb|CAA80341.1| cold induced protein (BnC24A)	gbpln	Brassica napus	AT3G49010.3 | Symbols: ATBBC1, BBC1, RSU2 | breast basic conserved 1 | chr3:18166971-18168047 REVERSE LENGTH=206	206	206	1.00E-104	100.0	86.4	90.3
Rsa1.0_00230.1.g9154.t1	gb|EOA21517.1| hypothetical protein CARUB_v10001929mg [Capsella rubella]	244	219	1.00E-108	89.8	79.9	84.0	hypothetical protein CARUB_v10001929mg	gbpln	Capsella rubella	AT5G19830.1 | Symbols: | Peptidyl-tRNA hydrolase family protein | chr5:6703383-6705125 FORWARD LENGTH=219	244	219	1.00E-109	89.8	79.1	84.0
Rsa1.0_00230.1.g9155.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	979	1529	0	156.2	54.3	72.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	979	746	1.00E-110	76.2	20.9	27.1
Rsa1.0_00230.1.g9156.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	503	1529	7.00E-69	304.0	29.2	43.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	503	530	3.00E-15	105.4	8.3	13.1
Rsa1.0_00230.1.g9157.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00230.1.g9158.t1	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	204	1449	6.00E-42	710.3	42.6	62.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	204	746	1.00E-29	365.7	38.7	59.8
Rsa1.0_00230.1.g9159.t1	ref|NP_190481.1| peroxidase 34 [Arabidopsis thaliana] gi|25453220|sp|Q9SMU8.1|PER34_ARATH RecName: Full=Peroxidase 34; Short=Atperox P34; AltName: Full=ATPCb; Flags: Precursor gi|11908066|gb|AAG41462.1|AF326880_1 putative peroxidase [Arabidopsis thaliana] gi|12642880|gb|AAK00382.1|AF339700_1 putative peroxidase [Arabidopsis thaliana] gi|16930431|gb|AAL31901.1|AF419569_1 AT3g49120/T2J13_40 [Arabidopsis thaliana] gi|6522554|emb|CAB61998.1| peroxidase [Arabidopsis thaliana] gi|19310513|gb|AAL84990.1| AT3g49120/T2J13_40 [Arabidopsis thaliana] gi|21593509|gb|AAM65476.1| peroxidase [Arabidopsis thaliana] gi|332644980|gb|AEE78501.1| peroxidase 34 [Arabidopsis thaliana]	449	353	0	78.6	72.4	74.6	peroxidase 34	gbpln	Arabidopsis thaliana	AT3G49120.1 | Symbols: ATPERX34, PERX34, PRXCB, ATPCB, PRX34 | peroxidase CB | chr3:18207819-18210041 FORWARD LENGTH=353	449	353	0	78.6	72.4	74.6
Rsa1.0_00230.1.g9160.t1	gb|EOA22500.1| hypothetical protein CARUB_v10003155mg, partial [Capsella rubella]	577	1112	0	192.7	64.1	73.0	hypothetical protein CARUB_v10003155mg, partial	gbpln	Capsella rubella	AT5G23980.1 | Symbols: ATFRO4, FRO4 | ferric reduction oxidase 4 | chr5:8098167-8101282 REVERSE LENGTH=699	577	699	0	121.1	62.9	71.2
Rsa1.0_00230.1.g9161.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	520	1225	1.00E-65	235.6	25.2	37.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	520	575	3.00E-28	110.6	12.7	20.6
Rsa1.0_00230.1.g9162.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	402	1142	1.00E-60	284.1	30.1	38.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	402	575	3.00E-25	143.0	17.7	29.1
Rsa1.0_00230.1.g9163.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	1509	1072	1.00E-158	71.0	17.3	23.0	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	1509	289	9.00E-75	19.2	8.9	12.5
Rsa1.0_00230.1.g9164.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00230.1.g9165.t9	gb|EOA25470.1| hypothetical protein CARUB_v10018807mg [Capsella rubella]	1763	684	0	38.8	33.7	35.7	hypothetical protein CARUB_v10018807mg	gbpln	Capsella rubella	AT3G49142.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:18215788-18217848 REVERSE LENGTH=686	1763	686	0	38.9	33.6	35.8

Rsa1.0_00230.1.g9166.t1	ref|NP_001118381.1| uncharacterized protein [Arabidopsis thaliana] gi|330252550|gb|AEC07644.1| uncharacterized protein AT2G24960 [Arabidopsis thaliana]	131	774	3.00E-51	590.8	77.9	86.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G24960.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02210.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:10617263-10620034 FORWARD LENGTH=774	131	774	7.00E-54	590.8	77.9	86.3
Rsa1.0_00230.1.g9167.t1	ref|NP_190485.1| pyruvate kinase [Arabidopsis thaliana] gi|75183756|sp|Q9M3B6.1|PKP4_ARATH RecName: Full=Plastidial pyruvate kinase 4, chloroplastic; Short=PKp4; Flags: Precursor gi|6723386|emb|CAB66395.1| pyruvate kinase-like protein [Arabidopsis thaliana] gi|18176182|gb|AAL59999.1| putative pyruvate kinase [Arabidopsis thaliana] gi|20465435|gb|AAM20177.1| putative pyruvate kinase [Arabidopsis thaliana] gi|332644985|gb|AEE78506.1| pyruvate kinase family protein [Arabidopsis thaliana]	710	710	0	100.0	77.9	85.9	pyruvate kinase	gbpln	Arabidopsis thaliana	AT3G49160.1 | Symbols: | pyruvate kinase family protein | chr3:18222132-18224415 REVERSE LENGTH=710	710	710	0	100.0	77.9	85.9
Rsa1.0_00230.1.g9168.t1	ref|XP_002875954.1| hypothetical protein ARALYDRAFT_485276 [Arabidopsis lyrata subsp. lyrata] gi|297321792|gb|EFH52213.1| hypothetical protein ARALYDRAFT_485276 [Arabidopsis lyrata subsp. lyrata]	440	438	0	99.5	80.2	88.6	hypothetical protein ARALYDRAFT_485276	gbpln	Arabidopsis lyrata	AT3G49180.1 | Symbols: RID3 | Transducin/WD40 repeat-like superfamily protein | chr3:18229810-18231874 FORWARD LENGTH=438	440	438	0	99.5	78.2	88.9
Rsa1.0_00230.1.g9169.t2	ref|NP_190489.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana] gi|6723390|emb|CAB66399.1| putative protein [Arabidopsis thaliana] gi|332644989|gb|AEE78510.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana]	410	507	0	123.7	79.8	88.5	O-acyltransferase (WSD1-like) family protein	gbpln	Arabidopsis thaliana	AT3G49200.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr3:18235445-18237646 REVERSE LENGTH=507	410	507	0	123.7	79.8	88.5
Rsa1.0_00230.1.g9170.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00230.1.g9171.t1	ref|NP_190489.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana] gi|6723390|emb|CAB66399.1| putative protein [Arabidopsis thaliana] gi|332644989|gb|AEE78510.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana]	84	507	3.00E-22	603.6	71.4	82.1	O-acyltransferase (WSD1-like) family protein	gbpln	Arabidopsis thaliana	AT3G49200.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr3:18235445-18237646 REVERSE LENGTH=507	84	507	5.00E-25	603.6	71.4	82.1
Rsa1.0_00230.1.g9172.t1	ref|NP_190490.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana] gi|6723391|emb|CAB66400.1| putative protein [Arabidopsis thaliana] gi|332644990|gb|AEE78511.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana]	416	518	0	124.5	83.9	91.1	O-acyltransferase (WSD1-like) family protein	gbpln	Arabidopsis thaliana	AT3G49210.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr3:18238216-18241161 REVERSE LENGTH=518	416	518	0	124.5	83.9	91.1
Rsa1.0_00231.1.g9173.t1	ref|XP_002871102.1| hypothetical protein ARALYDRAFT_487239 [Arabidopsis lyrata subsp. lyrata] gi|297316939|gb|EFH47361.1| hypothetical protein ARALYDRAFT_487239 [Arabidopsis lyrata subsp. lyrata]	914	1997	0	218.5	61.5	70.0	hypothetical protein ARALYDRAFT_487239	gbpln	Arabidopsis lyrata	AT5G04560.2 | Symbols: DME | HhH-GPD base excision DNA repair family protein | chr5:1309786-1318091 FORWARD LENGTH=1987	914	1987	0	217.4	60.0	69.3
Rsa1.0_00231.1.g9174.t1	ref|NP_200114.3| Ribonuclease P protein subunit P38-like protein [Arabidopsis thaliana] gi|8809591|dbj|BAA97142.1| unnamed protein product [Arabidopsis thaliana] gi|332008907|gb|AED96290.1| Ribonuclease P protein subunit P38-like protein [Arabidopsis thaliana]	690	720	0	104.3	78.3	87.0	Ribonuclease P protein subunit P38-like protein	gbpln	Arabidopsis thaliana	AT5G53020.1 | Symbols: | Ribonuclease P protein subunit P38-related | chr5:21499899-21502235 FORWARD LENGTH=720	690	720	0	104.3	78.3	87.0

Rsa1.0_00231.1.g9175.t1	ref|NP_568783.1| PP2A regulatory subunit TAP46 [Arabidopsis thaliana] gi|83305913|sp|Q8LDQ4.2|TAP46_ARATH RecName: Full=PP2A regulatory subunit TAP46; AltName: Full=2A phosphatase-associated protein of 46 kDa gi|5107033|gb|AAD39930.1|AF133708_1 PP2A regulatory subunit [Arabidopsis thaliana] gi|28393350|gb|AAO42099.1| putative PP2A regulatory subunit [Arabidopsis thaliana] gi|29824349|gb|AAP04135.1| putative PP2A regulatory subunit [Arabidopsis thaliana] gi|332008905|gb|AED96288.1| PP2A regulatory subunit TAP46 [Arabidopsis thaliana]	405	405	0	100.0	92.1	96.0	PP2A regulatory subunit TAP46	gbpln	Arabidopsis thaliana	AT5G53000.1 | Symbols: TAP46 | 2A phosphatase associated protein of 46 kD | chr5:21485654-21487869 REVERSE LENGTH=405	405	405	0	100.0	92.1	96.0
Rsa1.0_00231.1.g9176.t1	gb|EOA13841.1| hypothetical protein CARUB_v10026944mg [Capsella rubella]	263	274	1.00E-104	104.2	77.9	86.7	hypothetical protein CARUB_v10026944mg	gbpln	Capsella rubella	AT5G52990.1 | Symbols: | SNARE-like superfamily protein | chr5:21484188-21485006 FORWARD LENGTH=272	263	272	1.00E-106	103.4	76.8	86.7
Rsa1.0_00231.1.g9177.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00231.1.g9178.t1	ref|NP_200110.1| uncharacterized protein [Arabidopsis thaliana] gi|8809587|dbj|BAA97138.1| unnamed protein product [Arabidopsis thaliana] gi|46518365|gb|AAS99664.1| At5g52980 [Arabidopsis thaliana] gi|48310362|gb|AAT41806.1| At5g52980 [Arabidopsis thaliana] gi|110743071|dbj|BAE99428.1| hypothetical protein [Arabidopsis thaliana] gi|332008903|gb|AED96286.1| uncharacterized protein AT5G52980 [Arabidopsis thaliana]	238	222	1.00E-105	93.3	83.2	87.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G52980.1 | Symbols: | CONTAINS InterPro DOMAIN/s: ATPase, vacuolar ER assembly factor, Vma12 (InterPro:IPR021013); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:21482329-21483642 REVERSE LENGTH=222	238	222	1.00E-108	93.3	83.2	87.8
Rsa1.0_00231.1.g9179.t1	ref|NP_200108.1| uncharacterized protein [Arabidopsis thaliana] gi|8809585|dbj|BAA97136.1| unnamed protein product [Arabidopsis thaliana] gi|21553436|gb|AAM62529.1| unknown [Arabidopsis thaliana] gi|26449336|dbj|BAC41795.1| unknown protein [Arabidopsis thaliana] gi|28372880|gb|AAO39922.1| At5g52960 [Arabidopsis thaliana] gi|332008899|gb|AED96282.1| uncharacterized protein AT5G52960 [Arabidopsis thaliana]	163	170	6.00E-73	104.3	87.1	92.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G52960.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3143 (InterPro:IPR021489); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:21477250-21478269 FORWARD LENGTH=170	163	170	2.00E-75	104.3	87.1	92.0
Rsa1.0_00231.1.g9180.t1	gb|AAF79797.1|AC020646_20 T32E20.30 [Arabidopsis thaliana]	188	1397	1.00E-19	743.1	26.6	33.5	T32E20.30	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00231.1.g9181.t1	ref|NP_200104.1| pyruvate kinase [Arabidopsis thaliana] gi|75309198|sp|Q9FLW9.1|PKP2_ARATH RecName: Full=Plastidial pyruvate kinase 2; Short=PKp2; AltName: Full=Plastidial pyruvate kinase 1; Short=PKP1; AltName: Full=Pyruvate kinase III; AltName: Full=Pyruvate kinase isozyme B1, chloroplastic; Short=PKP-BETA1; Short=Plastidic pyruvate kinase beta subunit 1; Flags: Precursor gi|10177106|dbj|BAB10440.1| pyruvate kinase [Arabidopsis thaliana] gi|21536743|gb|AAM61075.1| pyruvate kinase [Arabidopsis thaliana] gi|332008895|gb|AED96278.1| pyruvate kinase [Arabidopsis thaliana]	583	579	0	99.3	94.9	97.1	pyruvate kinase	gbpln	Arabidopsis thaliana	AT5G52920.1 | Symbols: PKP1, PKP-BETA1, PKP2 | plastidic pyruvate kinase beta subunit 1 | chr5:21463680-21466612 FORWARD LENGTH=579	583	579	0	99.3	94.9	97.1
Rsa1.0_00231.1.g9182.t1	gb|EOA12459.1| hypothetical protein CARUB_v10025761mg [Capsella rubella]	1172	1185	0	101.1	82.8	89.3	hypothetical protein CARUB_v10025761mg	gbpln	Capsella rubella	AT5G52910.1 | Symbols: ATIM | timeless family protein | chr5:21457774-21463159 REVERSE LENGTH=1141	1172	1141	0	97.4	80.8	87.2
Rsa1.0_00231.1.g9183.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00231.1.g9184.t1	dbj|BAB10438.1| unnamed protein product [Arabidopsis thaliana]	231	236	5.00E-96	102.2	81.0	86.6	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G52900.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21452893-21453692 REVERSE LENGTH=235	231	235	1.00E-97	101.7	80.5	86.1

Rsa1.0_00231.1.g9185.t1	#	#	#	#	#	#	-	----	----	AT3G17365.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:5947144-5948766 REVERSE LENGTH=239	107	239	2.00E-11	223.4	28.0	32.7	
Rsa1.0_00231.1.g9186.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1486	1365	0	91.9	41.4	55.6	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1486	575	7.00E-87	38.7	12.2	17.8
Rsa1.0_00231.1.g9187.t1	ref|NP_200101.2| AT hook motif-containing protein [Arabidopsis thaliana] gi|57222118|gb|AAW38966.1| At5g52890 [Arabidopsis thaliana] gi|57222216|gb|AAW39015.1| At5g52890 [Arabidopsis thaliana] gi|332008890|gb|AED96273.1| AT hook motif-containing protein [Arabidopsis thaliana]	373	357	2.00E-79	95.7	46.6	52.0	AT hook motif-containing protein	gbpln	Arabidopsis thaliana	AT5G52890.1 | Symbols: | AT hook motif-containing protein | chr5:21445040-21446197 REVERSE LENGTH=357	373	357	6.00E-82	95.7	46.6	52.0
Rsa1.0_00231.1.g9188.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00231.1.g9189.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00232.1.g9190.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00232.1.g9191.t1	gb|ABK28184.1| unknown [Arabidopsis thaliana]	351	488	3.00E-15	139.0	12.0	18.8	unknown	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00232.1.g9192.t1	ref|XP_002883436.1| hypothetical protein ARALYDRAFT_479868 [Arabidopsis lyrata subsp. lyrata] gi|297329276|gb|EFH59695.1| hypothetical protein ARALYDRAFT_479868 [Arabidopsis lyrata subsp. lyrata]	1310	1309	0	99.9	89.1	94.7	hypothetical protein ARALYDRAFT_479868	gbpln	Arabidopsis lyrata	AT3G23590.1 | Symbols: RFR1, MED33A | REF4-related 1 | chr3:8467638-8473469 FORWARD LENGTH=1309	1310	1309	0	99.9	89.2	94.5
Rsa1.0_00232.1.g9193.t6	ref|XP_002883478.1| hypothetical protein ARALYDRAFT_479911 [Arabidopsis lyrata subsp. lyrata] gi|297329318|gb|EFH59737.1| hypothetical protein ARALYDRAFT_479911 [Arabidopsis lyrata subsp. lyrata]	1255	950	0	75.7	67.4	70.4	hypothetical protein ARALYDRAFT_479911	gbpln	Arabidopsis lyrata	AT3G24180.2 | Symbols: | Beta-glucosidase, GBA2 type family protein | chr3:8735011-8741147 REVERSE LENGTH=950	1255	950	0	75.7	67.2	70.5
Rsa1.0_00232.1.g9194.t7	ref|XP_002883439.1| dual specificity protein phosphatase [Arabidopsis lyrata subsp. lyrata] gi|297329279|gb|EFH59698.1| dual specificity protein phosphatase [Arabidopsis lyrata subsp. lyrata]	338	203	1.00E-84	60.1	43.8	48.2	dual specificity protein phosphatase	gbpln	Arabidopsis lyrata	AT3G23610.2 | Symbols: DSPTP1 | dual specificity protein phosphatase 1 | chr3:8478280-8479641 FORWARD LENGTH=201	338	201	3.00E-86	59.5	43.8	47.6
Rsa1.0_00232.1.g9195.t1	gb|EOA31032.1| hypothetical protein CARUB_v10014181mg [Capsella rubella]	344	324	1.00E-150	94.2	77.3	84.0	hypothetical protein CARUB_v10014181mg	gbpln	Capsella rubella	AT3G23620.1 | Symbols: | Ribosomal RNA processing Brix domain protein | chr3:8480147-8481873 FORWARD LENGTH=314	344	314	1.00E-141	91.3	75.6	84.0
Rsa1.0_00232.1.g9196.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00232.1.g9197.t1	dbj|BAE43829.1| isopentenyltransferase [Brassica rapa subsp. pekinensis]	332	332	1.00E-179	100.0	96.1	97.6	isopentenyltransferase	gbpln	Brassica rapa	AT3G23630.1 | Symbols: ATIPT7, IPT7 | isopentenyltransferase 7 | chr3:8488878-8489867 FORWARD LENGTH=329	332	329	1.00E-169	99.1	86.7	91.0
Rsa1.0_00232.1.g9198.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00232.1.g9199.t1	gb|EOA28939.1| hypothetical protein CARUB_v10025187mg [Capsella rubella]	408	752	1.00E-12	184.3	8.6	13.2	hypothetical protein CARUB_v10025187mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00232.1.g9200.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00233.1.g9201.t3	ref|XP_002864410.1| hypothetical protein ARALYDRAFT_357817 [Arabidopsis lyrata subsp. lyrata] gi|297310245|gb|EFH40669.1| hypothetical protein ARALYDRAFT_357817 [Arabidopsis lyrata subsp. lyrata]	1811	1781	0	98.3	61.7	72.1	hypothetical protein ARALYDRAFT_357817	gbpln	Arabidopsis lyrata	AT5G55820.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Inner centromere protein, ARK-binding region (InterPro:IPR005635); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:22586287-22594035 FORWARD LENGTH=1826	1811	1826	0	100.8	46.2	52.8
Rsa1.0_00233.1.g9202.t1	gb|EOA25654.1| hypothetical protein CARUB_v10019004mg [Capsella rubella]	263	240	1.00E-101	91.3	71.9	79.5	hypothetical protein CARUB_v10019004mg	gbpln	Capsella rubella	AT5G55810.1 | Symbols: AtNMNAT, NMNAT | nicotinate/nicotinamide mononucleotide adenyltransferase | chr5:22584229-22586239 REVERSE LENGTH=238	263	238	1.00E-104	90.5	71.5	78.7

Rsa1.0_00233.1.g9203.t1	ref|NP_565474.1| uncharacterized protein [Arabidopsis thaliana] gi|20198088|gb|AAM15393.1| Expressed protein [Arabidopsis thaliana] gi|30794122|gb|AAP40503.1| unknown protein [Arabidopsis thaliana] gi|56236118|gb|AAV84515.1| At2g20515 [Arabidopsis thaliana] gi|89001021|gb|ABD59100.1| At2g20515 [Arabidopsis thaliana] gi|330251927|gb|AEC07021.1| uncharacterized protein AT2G20515 [Arabidopsis thaliana]	225	155	5.00E−72	68.9	57.3	61.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G20515.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 7 growth stages; Has 71 Blast hits to 71 proteins in 14 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 71; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr2:8839041−8839595 REVERSE LENGTH=155	225	155	2.00E−74	68.9	57.3	61.8
Rsa1.0_00233.1.g9204.t1	gb|EOA13175.1| hypothetical protein CARUB_v10026199mg [Capsella rubella]	467	540	0	115.6	88.9	95.3	hypothetical protein CARUB_v10026199mg	gbpln	Capsella rubella	AT5G55760.1 | Symbols: SRT1 | sirtuin 1 | chr5:22567282−22570716 FORWARD LENGTH=473	467	473	0	101.3	88.2	95.7
Rsa1.0_00233.1.g9205.t1	gb|EOA13191.1| hypothetical protein CARUB_v10026217mg [Capsella rubella]	536	531	0	99.1	89.9	94.4	hypothetical protein CARUB_v10026217mg	gbpln	Capsella rubella	AT5G55700.1 | Symbols: BMY6, BAM4 | beta−amylase 4 | chr5:22551873−22554702 FORWARD LENGTH=531	536	531	0	99.1	89.2	93.8
Rsa1.0_00233.1.g9206.t1	ref|NP_200380.1| MADS−box protein AGL47 [Arabidopsis thaliana] gi|9758603|dbj|BAB09236.1| unnamed protein product [Arabidopsis thaliana] gi|32402392|gb|AAN52778.1| MADS−box protein AGL47 [Arabidopsis thaliana] gi|109946439|gb|ABG48398.1| At5g55690 [Arabidopsis thaliana] gi|332009285|gb|AED96668.1| MADS−box protein AGL47 [Arabidopsis thaliana]	273	277	1.00E−111	101.5	72.9	82.8	MADS−box protein AGL47	gbpln	Arabidopsis thaliana	AT5G55690.1 | Symbols: | MADS−box transcription factor family protein | chr5:22548790−22549623 REVERSE LENGTH=277	273	277	1.00E−114	101.5	72.9	82.8
Rsa1.0_00233.1.g9207.t1	sp|Q9LHD3.2|FB190_ARATH RecName: Full=F−box protein At3g28330	479	397	2.00E−91	82.9	43.4	54.3	RecName: Full=F−box protein At3g28330	----	----	AT3G28223.1 | Symbols: | F−box family protein | chr3:10527669−10528921 REVERSE LENGTH=391	479	391	5.00E−80	81.6	38.8	48.6
Rsa1.0_00233.1.g9208.t1	ref|NP_200378.1| RNA recognition motif−containing protein [Arabidopsis thaliana] gi|9758601|dbj|BAB09234.1| unnamed protein product [Arabidopsis thaliana] gi|332009282|gb|AED96665.1| RNA recognition motif−containing protein [Arabidopsis thaliana]	656	710	0	108.2	75.8	83.7	RNA recognition motif−containing protein	gbpln	Arabidopsis thaliana	AT5G55670.1 | Symbols: | RNA−binding (RRM/RBD/RNP motifs) family protein | chr5:22544669−22546801 REVERSE LENGTH=710	656	710	0	108.2	75.8	83.7
Rsa1.0_00233.1.g9209.t2	ref|NP_199643.1| cysteine/histidine−rich C1 domain−containing protein [Arabidopsis thaliana] gi|8978336|dbj|BAA98189.1| unnamed protein product [Arabidopsis thaliana] gi|332008268|gb|AED95651.1| cysteine/histidine−rich C1 domain−containing protein [Arabidopsis thaliana]	662	977	1.00E−133	147.6	36.0	42.4	cysteine/histidine−rich C1 domain−containing protein	gbpln	Arabidopsis thaliana	AT5G48320.1 | Symbols: | Cysteine/Histidine−rich C1 domain family protein | chr5:19581794−19584727 REVERSE LENGTH=977	662	977	1.00E−136	147.6	36.0	42.4
Rsa1.0_00233.1.g9210.t1	gb|EOA36883.1| hypothetical protein CARUB_v10008966mg [Capsella rubella]	211	491	8.00E−46	232.7	44.1	48.3	hypothetical protein CARUB_v10008966mg	gbpln	Capsella rubella	AT1G11880.1 | Symbols: | transferases, transferring hexosyl groups | chr1:4007909−4010327 REVERSE LENGTH=489	211	489	4.00E−47	231.8	44.5	49.3
Rsa1.0_00233.1.g9211.t1	gb|AAM64705.1| outward rectifying potassium channel KCO [Arabidopsis thaliana]	370	363	1.00E−168	98.1	84.9	92.4	outward rectifying potassium channel KCO	gbpln	Arabidopsis thaliana	AT5G55630.2 | Symbols: KCO1, TPK1 | Outward rectifying potassium channel protein | chr5:22531718−22532893 FORWARD LENGTH=363	370	363	1.00E−171	98.1	84.9	92.2
Rsa1.0_00233.1.g9212.t1	ref|NP_197207.1| Flavonoid 3−O−glucosyltransferase [Arabidopsis thaliana] gi|75311137|sp|Q9LFJ8.1|U78D2_ARATH RecName: Full=UDP−glycosyltransferase 78D2; AltName: Full=Anthocyanin 3−O−glucosyltransferase; AltName: Full=Flavonol 3−O−glucosyltransferase.; AltName: Full=UDP glucose:flavonoid 3−O−glucosyltransferase gi|9755706|emb|CAC01718.1| UDP glucose:flavonoid 3−o−glucosyltransferase−like protein [Arabidopsis thaliana] gi|18252199|gb|AAL61932.1| UDP glucose:flavonoid 3−o−glucosyltransferase−like protein [Arabidopsis thaliana] gi|22136122|gb|AAM91139.1| UDP glucose:flavonoid 3−o−glucosyltransferase−like protein [Arabidopsis thaliana] gi|332004994|gb|AED92377.1| Flavonoid 3−O−glucosyltransferase [Arabidopsis thaliana]	446	460	0	103.1	73.1	84.5	Flavonoid 3−O−glucosyltransferase	gbpln	Arabidopsis thaliana	AT5G17050.1 | Symbols: UGT78D2 | UDP−glucosyl transferase 78D2 | chr5:5607828−5609392 REVERSE LENGTH=460	446	460	0	103.1	73.1	84.5

Rsa1.0_00233.1.g9213.t1	ref|XP_002892315.1| hypothetical protein ARALYDRAFT_887793 [Arabidopsis lyrata subsp. lyrata] gi|297338157|gb|EFH68574.1| hypothetical protein ARALYDRAFT_887793 [Arabidopsis lyrata subsp. lyrata]	432	434	0	100.5	80.8	88.7	hypothetical protein ARALYDRAFT_887793	gbpln	Arabidopsis lyrata	AT1G06000.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:1820495-1821802 REVERSE LENGTH=435	432	435	0	100.7	78.5	88.0
Rsa1.0_00233.1.g9214.t1	gb|EOA12607.1| hypothetical protein CARUB_v10027338mg, partial [Capsella rubella]	100	140	5.00E-42	140.0	84.0	92.0	hypothetical protein CARUB_v10027338mg, partial	gbpln	Capsella rubella	AT5G55620.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G09950.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:22530373-22530678 FORWARD LENGTH=101	100	101	3.00E-39	101.0	85.0	90.0
Rsa1.0_00233.1.g9215.t1	ref|XP_002866105.1| hypothetical protein ARALYDRAFT_495647 [Arabidopsis lyrata subsp. lyrata] gi|297311940|gb|EFH42364.1| hypothetical protein ARALYDRAFT_495647 [Arabidopsis lyrata subsp. lyrata]	651	664	0	102.0	81.7	89.4	hypothetical protein ARALYDRAFT_495647	gbpln	Arabidopsis lyrata	AT5G55600.3 | Symbols: | agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein | chr5:22522232-22524796 REVERSE LENGTH=663	651	663	0	101.8	81.7	88.6
Rsa1.0_00233.1.g9216.t1	ref|XP_002864399.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297310234|gb|EFH40658.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata]	503	493	0	98.0	87.9	91.5	mitochondrial transcription termination factor family protein	gbpln	Arabidopsis lyrata	AT5G55580.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr5:22515601-22517408 FORWARD LENGTH=496	503	496	0	98.6	86.3	90.7
Rsa1.0_00233.1.g9217.t1	gb|EOA14704.1| hypothetical protein CARUB_v10027981mg [Capsella rubella]	356	562	1.00E-112	157.9	63.5	69.1	hypothetical protein CARUB_v10027981mg	gbpln	Capsella rubella	AT4G26640.2 | Symbols: WRKY20, AtWRKY20 | WRKY family transcription factor family protein | chr4:13437298-13440693 REVERSE LENGTH=557	356	557	1.00E-111	156.5	57.6	65.4
Rsa1.0_00233.1.g9218.t1	ref|NP_200367.2| putative serine/threonine-protein kinase WNK11 [Arabidopsis thaliana] gi|75323650|sp|Q6ICW6.1|WNK11_ARATH RecName: Full=Probable serine/threonine-protein kinase WNK11; Short=AtWNK11; AltName: Full=Protein kinase with no lysine 11 gi|48596991|gb|AAT46036.1| At5g55560 [Arabidopsis thaliana] gi|50198956|gb|AAT70481.1| At5g55560 [Arabidopsis thaliana] gi|332009266|gb|AED96649.1| putative serine/threonine-protein kinase WNK11 [Arabidopsis thaliana]	311	314	1.00E-149	101.0	83.3	88.1	putative serine/threonine-protein kinase WNK11	gbpln	Arabidopsis thaliana	AT5G55560.1 | Symbols: | Protein kinase superfamily protein | chr5:22506477-22507757 REVERSE LENGTH=314	311	314	1.00E-152	101.0	83.3	88.1
Rsa1.0_00233.1.g9219.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00234.1.g9220.t2	gb|EOA15965.1| hypothetical protein CARUB_v10004060mg [Capsella rubella]	997	996	0	99.9	88.4	93.9	hypothetical protein CARUB_v10004060mg	gbpln	Capsella rubella	AT4G20270.1 | Symbols: BAM3 | Leucine-rich receptor-like protein kinase family protein | chr4:10949822-10952924 FORWARD LENGTH=992	997	992	0	99.5	87.3	92.5
Rsa1.0_00234.1.g9221.t1	gb|EOA18090.1| hypothetical protein CARUB_v10006542mg [Capsella rubella]	376	480	0	127.7	100.0	100.0	hypothetical protein CARUB_v10006542mg	gbpln	Capsella rubella	AT4G20360.1 | Symbols: ATRAB8D, ATRABE1B, RABE1b | RAB GTPase homolog E1B | chr4:10990036-10991466 FORWARD LENGTH=476	376	476	0	126.6	97.6	99.2
Rsa1.0_00234.1.g9222.t1	ref|NP_199269.1| vacuolar protein sorting-associated protein 2-2 [Arabidopsis thaliana] gi|226698193|sp|Q0WTY4.2|VPS2B_ARATH RecName: Full=Vacuolar protein sorting-associated protein 2 homolog 2; Short=AtVPS2-2; AltName: Full=Charged multivesicular body protein 2 homolog 2; AltName: Full=ESCRT-III complex subunit VPS2 homolog 2 gi|332007740|gb|AED95123.1| vacuolar protein sorting-associated protein 2-2 [Arabidopsis thaliana]	276	222	8.00E-95	80.4	70.3	72.5	vacuolar protein sorting-associated protein 2-2	gbpln	Arabidopsis thaliana	AT5G44560.1 | Symbols: VPS2.2 | SNF7 family protein | chr5:17946081-17948222 FORWARD LENGTH=222	276	222	2.00E-97	80.4	70.3	72.5
Rsa1.0_00234.1.g9223.t1	gb|ADK63407.1| zinc finger protein [Brassica rapa]	61	191	1.00E-14	313.1	83.6	90.2	zinc finger protein	gbpln	Brassica rapa	#	#	#	#	#	#	#

Rsa1.0_00234.1.g9224.t4	ref|XP_002869933.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|341958556|sp|D7MFJ8.1|CSPLC_ARALL RecName: Full=CASP-like protein ARALYDRAFT_492822 gi|297315769|gb|EFH46192.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata]	197	197	9.00E-81	100.0	82.2	88.3	integral membrane family protein	gbpln	Arabidopsis lyrata	AT4G20390.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:11007068-11007869 FORWARD LENGTH=197	197	197	6.00E-78	100.0	83.8	89.8
Rsa1.0_00234.1.g9225.t2	gb|EOA17129.1| hypothetical protein CARUB_v10005391mg [Capsella rubella]	139	291	4.00E-40	209.4	61.2	66.2	hypothetical protein CARUB_v10005391mg	gbpln	Capsella rubella	AT4G20410.1 | Symbols: GSNAP, GAMMA-SNAP | gamma-soluble NSF attachment protein | chr4:11014099-11016454 REVERSE LENGTH=291	139	291	3.00E-42	209.4	61.2	66.2
Rsa1.0_00234.1.g9226.t1	gb|ABA00707.1| putative tapetum-specific A3 [Brassica napus]	132	139	3.00E-46	105.3	75.8	84.8	putative tapetum-specific A3	gbpln	Brassica napus	AT4G20420.1 | Symbols: | Tapetum specific protein TAP35/TAP44 | chr4:11017041-11017469 FORWARD LENGTH=142	132	142	1.00E-38	107.6	66.7	78.0
Rsa1.0_00234.1.g9227.t1	dbj|BAD43836.1| unknown protein [Arabidopsis thaliana]	249	254	2.00E-73	102.0	68.7	72.3	unknown protein	gbpln	Arabidopsis thaliana	AT5G44500.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr5:17927505-17928269 FORWARD LENGTH=254	249	254	4.00E-72	102.0	65.9	69.5
Rsa1.0_00234.1.g9228.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1786	1374	0	76.9	39.8	51.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1786	575	1.00E-147	32.2	13.4	18.1
Rsa1.0_00234.1.g9229.t1	ref|NP_193779.2| putative UDP-arabinose 4-epimerase 3 [Arabidopsis thaliana] gi|332278213|sp|Q9SUN3.3|ARAE3_ARATH RecName: Full=Probable UDP-arabinose 4-epimerase 3; AltName: Full=UDP-D-xylose 4-epimerase 3 gi|332658935|gb|AEE84335.1| putative UDP-arabinose 4-epimerase 3 [Arabidopsis thaliana]	411	411	0	100.0	95.1	97.6	putative UDP-arabinose 4-epimerase 3	gbpln	Arabidopsis thaliana	AT4G20460.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:11029767-11031765 REVERSE LENGTH=411	411	411	0	100.0	95.1	97.6
Rsa1.0_00234.1.g9230.t1	gb|EOA18170.1| hypothetical protein CARUB_v10006646mg [Capsella rubella]	185	189	3.00E-79	102.2	82.2	89.7	hypothetical protein CARUB_v10006646mg	gbpln	Capsella rubella	AT4G20780.1 | Symbols: CML42 | calmodulin like 42 | chr4:11133309-11133884 REVERSE LENGTH=191	185	191	8.00E-81	103.2	80.5	88.6
Rsa1.0_00234.1.g9231.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1005	1365	0	135.8	47.3	64.1	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1005	575	1.00E-88	57.2	17.6	27.4
Rsa1.0_00234.1.g9232.t1	#	#	#	#	#	#	#	-	----	----	AT1G71720.1 | Symbols: | Nucleic acid-binding proteins superfamily | chr1:26983744-26985893 FORWARD LENGTH=500	149	500	2.00E-12	335.6	33.6	38.9
Rsa1.0_00234.1.g9233.t1	gb|EOA18748.1| hypothetical protein CARUB_v10007331mg [Capsella rubella]	531	555	0	104.5	76.6	88.3	hypothetical protein CARUB_v10007331mg	gbpln	Capsella rubella	AT4G20840.1 | Symbols: | FAD-binding Berberine family protein | chr4:11157916-11159535 FORWARD LENGTH=539	531	539	0	101.5	77.8	86.8
Rsa1.0_00234.1.g9234.t1	ref|XP_002863368.1| farnesyl diphosphate synthase short form [Arabidopsis lyrata subsp. lyrata] gi|297309203|gb|EFH39627.1| farnesyl diphosphate synthase short form [Arabidopsis lyrata subsp. lyrata]	111	343	4.00E-27	309.0	52.3	57.7	farnesyl diphosphate synthase short form	gbpln	Arabidopsis lyrata	AT5G47770.1 | Symbols: FPS1 | farnesyl diphosphate synthase 1 | chr5:19345297-19347415 FORWARD LENGTH=384	111	384	8.00E-30	345.9	52.3	57.7
Rsa1.0_00234.1.g9235.t1	emb|CAA75349.1| ERT2 [Arabidopsis thaliana]	362	407	4.00E-43	112.4	36.7	40.6	ERT2	gbpln	Arabidopsis thaliana	AT4G20880.1 | Symbols: | ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2) | chr4:11179389-11180606 REVERSE LENGTH=405	362	405	5.00E-45	111.9	33.1	35.4
Rsa1.0_00234.1.g9236.t1	gb|EOA16631.1| hypothetical protein CARUB_v10004805mg [Capsella rubella]	445	445	0	100.0	98.2	99.3	hypothetical protein CARUB_v10004805mg	gbpln	Capsella rubella	AT4G20890.1 | Symbols: TUB9 | tubulin beta-9 chain | chr4:11182218-11183840 FORWARD LENGTH=444	445	444	0	99.8	97.8	98.4
Rsa1.0_00234.1.g9237.t3	ref|XP_002867829.1| hypothetical protein ARALYDRAFT_492703 [Arabidopsis lyrata subsp. lyrata] gi|297313665|gb|EFH44088.1| hypothetical protein ARALYDRAFT_492703 [Arabidopsis lyrata subsp. lyrata]	1228	1188	0	96.7	88.7	92.4	hypothetical protein ARALYDRAFT_492703	gbpln	Arabidopsis lyrata	AT4G21710.1 | Symbols: NRPB2, EMB1989, RPB2 | DNA-directed RNA polymerase family protein | chr4:11535684-11542200 REVERSE LENGTH=1188	1228	1188	0	96.7	88.7	92.3
Rsa1.0_00234.1.g9238.t1	ref|XP_002869872.1| gibberellin 3-oxidase 3 [Arabidopsis lyrata subsp. lyrata] gi|297315708|gb|EFH46131.1| gibberellin 3-oxidase 3 [Arabidopsis lyrata subsp. lyrata]	489	348	1.00E-166	71.2	58.1	62.4	gibberellin 3-oxidase 3	gbpln	Arabidopsis lyrata	AT4G21690.1 | Symbols: ATGA3OX3, GA3OX3 | gibberellin 3-oxidase 3 | chr4:11527229-11529060 FORWARD LENGTH=349	489	349	1.00E-167	71.4	57.9	62.6
Rsa1.0_00234.1.g9239.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1720	2301	0	133.8	45.6	59.5	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1720	1262	6.00E-83	73.4	9.8	14.9

Rsa1.0_00234.1.g9240.t1	dbj|BAJ34582.1| unnamed protein product [Thellungiella halophila]	294	294	1.00E-167	100.0	98.3	99.3	unnamed protein product	----	----	AT4G21570.1 | Symbols: | Protein of unknown function (DUF300) | chr4:11471126-11472269 REVERSE LENGTH=294	294	294	1.00E-162	100.0	93.2	97.3
Rsa1.0_00234.1.g9241.t1	gb|AAD48972.1|AF162444_4 contains similarity to S. cerevisiae vacuolar protein sorting-associated protein VPS28 (GB:U39205) [Arabidopsis thaliana] gi|7267259|emb|CAB81042.1| AT4g05000 [Arabidopsis thaliana]	212	209	1.00E-102	98.6	84.4	92.5	contains similarity to S. cerevisiae vacuolar protein sorting-associated protein VPS28 (GB:U39205)	gbpln	Arabidopsis thaliana	AT4G05000.2 | Symbols: VPS28-1 | Vacuolar protein sorting-associated protein VPS28 family protein | chr4:2563953-2564585 FORWARD LENGTH=210	212	210	1.00E-104	99.1	84.9	92.9
Rsa1.0_00234.1.g9242.t1	ref|NP_001190787.1| Diacylglycerol kinase family protein [Arabidopsis thaliana] gi|487523611|sp|F2Y4A3.1|SPHK2_ARATH RecName: Full=Sphingosine kinase 2 gi|325656782|gb|ADZ38930.1| sphingosine kinase 2 [Arabidopsis thaliana] gi|332659064|gb|AEE84464.1| Diacylglycerol kinase family protein [Arabidopsis thaliana]	478	481	0	100.6	77.8	89.7	Diacylglycerol kinase family protein	gbpln	Arabidopsis thaliana	AT4G21534.1 | Symbols: | Diacylglycerol kinase family protein | chr4:11456230-11458820 FORWARD LENGTH=481	478	481	0	100.6	77.8	89.7
Rsa1.0_00234.1.g9243.t1	gb|EOA16902.1| hypothetical protein CARUB_v10005126mg, partial [Capsella rubella]	289	357	1.00E-139	123.5	91.0	94.1	hypothetical protein CARUB_v10005126mg, partial	gbpln	Capsella rubella	AT4G21450.1 | Symbols: | PapD-like superfamily protein | chr4:11426136-11428125 FORWARD LENGTH=295	289	295	1.00E-139	102.1	92.7	94.8
Rsa1.0_00234.1.g9244.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00234.1.g9245.t1	ref|XP_002867846.1| hypothetical protein ARALYDRAFT_492740 [Arabidopsis lyrata subsp. lyrata] gi|297313682|gb|EFH44105.1| hypothetical protein ARALYDRAFT_492740 [Arabidopsis lyrata subsp. lyrata]	346	350	1.00E-134	101.2	76.9	84.4	hypothetical protein ARALYDRAFT_492740	gbpln	Arabidopsis lyrata	AT4G21440.1 | Symbols: ATMYB102, ATM4, MYB102 | MYB-like 102 | chr4:11418425-11419652 REVERSE LENGTH=350	346	350	1.00E-136	101.2	76.9	84.4
Rsa1.0_00234.1.g9246.t1	ref|NP_193872.2| cysteine-rich receptor-like protein kinase 29 [Arabidopsis thaliana] gi|75330985|sp|Q8S9L6.1|CRK29_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 29; Short=Cysteine-rich RLK29; Flags: Precursor gi|18650594|gb|AAL75897.1| AT4g21410/T6K22_140 [Arabidopsis thaliana] gi|332659049|gb|AEE84449.1| cysteine-rich receptor-like protein kinase 29 [Arabidopsis thaliana]	430	679	1.00E-172	157.9	74.2	81.6	cysteine-rich receptor-like protein kinase 29	gbpln	Arabidopsis thaliana	AT4G21410.1 | Symbols: CRK29 | cysteine-rich RLK (RECEPTOR-like protein kinase) 29 | chr4:11402463-11405025 REVERSE LENGTH=679	430	679	1.00E-175	157.9	74.2	81.6
Rsa1.0_00234.1.g9247.t1	ref|XP_002869900.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315736|gb|EFH46159.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	184	338	1.00E-98	183.7	90.8	96.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G21200.1 | Symbols: ATGA2OX8, GA2OX8 | gibberellin 2-oxidase 8 | chr4:11302751-11306601 FORWARD LENGTH=338	184	338	1.00E-100	183.7	90.2	95.1
Rsa1.0_00234.1.g9248.t1	ref|XP_002869900.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315736|gb|EFH46159.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	159	338	1.00E-74	212.6	84.3	89.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G21200.3 | Symbols: ATGA2OX8, GA2OX8 | gibberellin 2-oxidase 8 | chr4:11302751-11304032 FORWARD LENGTH=181	159	181	3.00E-75	113.8	81.8	88.7
Rsa1.0_00235.1.g9249.t1	gb|AFI23585.1| vernalization 2 [Brassica oleracea var. italica] gi|384597743|gb|AFI23588.1| vernalization 2 [Brassica oleracea var. italica]	295	425	4.00E-52	144.1	46.8	57.3	vernalization 2	gbpln	Brassica oleracea	AT4G16845.2 | Symbols: VRN2 | VEFS-Box of polycomb protein | chr4:9477246-9479725 FORWARD LENGTH=380	295	380	1.00E-42	128.8	42.0	53.6
Rsa1.0_00235.1.g9250.t1	ref|XP_002868098.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297313934|gb|EFH44357.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	165	461	4.00E-52	279.4	72.7	80.6	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis lyrata	AT4G16790.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:9451747-9453168 REVERSE LENGTH=473	165	473	4.00E-52	286.7	72.1	78.2
Rsa1.0_00235.1.g9251.t1	ref|NP_567515.1| lipase class 3 family protein [Arabidopsis thaliana] gi|374095438|sp|O23522.2|PLA14_ARATH RecName: Full=Phospholipase A1-Ibeta2, chloroplastic; Flags: Precursor gi|332658408|gb|AEE83808.1| phospholipase A1-Ibeta2 [Arabidopsis thaliana]	280	517	1.00E-109	184.6	71.8	75.4	lipase class 3 family protein	gbpln	Arabidopsis thaliana	AT4G16820.1 | Symbols: PLA-I[beta]2 | alpha/beta-Hydrolases superfamily protein | chr4:9467563-9469116 FORWARD LENGTH=517	280	517	1.00E-111	184.6	71.8	75.4
Rsa1.0_00235.1.g9252.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1392	1213	0	87.1	32.2	48.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1392	626	6.00E-65	45.0	9.2	16.1

Rsa1.0_00235.1.g9253.t1	ref|XP_002885228.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297331068|gb|EFH61487.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	439	371	1.00E-105	84.5	49.7	61.3	F-box family protein	gbpln	Arabidopsis lyrata	AT3G19470.2 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6749766-6750914 FORWARD LENGTH=382	439	382	1.00E-102	87.0	47.6	60.1
Rsa1.0_00235.1.g9254.t1	gb|AFI23585.1| vernalization 2 [Brassica oleracea var. italica] gi|384597743|gb|AFI23588.1| vernalization 2 [Brassica oleracea var. italica]	468	425	1.00E-110	90.8	48.9	60.7	vernalization 2	gbpln	Brassica oleracea	AT4G16845.1 | Symbols: VRN2 | VEFS-Box of polycomb protein | chr4:9476708-9479725 FORWARD LENGTH=440	468	440	5.00E-93	94.0	43.6	54.9
Rsa1.0_00235.1.g9255.t1	ref|XP_002868098.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297313934|gb|EFH44357.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	478	461	1.00E-147	96.4	69.9	78.9	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis lyrata	AT4G16790.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:9451747-9453168 REVERSE LENGTH=473	478	473	1.00E-149	99.0	71.1	79.7
Rsa1.0_00235.1.g9256.t1	ref|NP_193411.1| homeobox-leucine zipper protein HAT4 [Arabidopsis thaliana] gi|462281|sp|Q05466.1|HAT4_ARATH RecName: Full=Homeobox-leucine zipper protein HAT4; AltName: Full=HD-ZIP protein ATHB-2; AltName: Full=Homeodomain transcription factor ATHB-2; AltName: Full=Homeodomain-leucine zipper protein HAT4; Short=HD-ZIP protein 4 gi|14030725|gb|AAK53037.1|AF375453_1 AT4g16780/dl4415w [Arabidopsis thaliana] gi|16180|emb|CAA48246.1| Athb-2 [Arabidopsis thaliana] gi|16332|emb|CAA48248.1| DNA binding protein [Arabidopsis thaliana] gi|2245033|emb|CAB10452.1| DNA-binding homeotic protein Athb-2 [Arabidopsis thaliana] gi|7268428|emb|CAB78720.1| DNA-binding homeotic protein Athb-2 [Arabidopsis thaliana] gi|19548073|gb|AAL87400.1| AT4g16780/dl4415w [Arabidopsis thaliana] gi|332658403|gb|AEE83803.1| homeobox-leucine zipper protein HAT4 [Arabidopsis thaliana]	271	284	1.00E-126	104.8	90.4	92.6	homeobox-leucine zipper protein HAT4	gbpln	Arabidopsis thaliana	AT4G16780.1 | Symbols: ATHB-2, HAT4, ATHB2, HB-2 | homeobox protein 2 | chr4:9449291-9450604 FORWARD LENGTH=284	271	284	1.00E-128	104.8	90.4	92.6
Rsa1.0_00235.1.g9257.t2	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	676	536	7.00E-87	79.3	23.1	30.5	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	676	530	1.00E-50	78.4	12.3	15.5
Rsa1.0_00235.1.g9258.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	474	1486	0	313.5	69.6	82.5	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	474	1262	1.00E-122	266.2	41.4	63.1
Rsa1.0_00235.1.g9259.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00235.1.g9260.t2	emb|CAB96197.1| hypothetical protein [Capsella rubella]	322	315	1.00E-124	97.8	68.6	75.8	hypothetical protein	gbpln	Capsella rubella	AT4G16770.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:9434571-9437168 REVERSE LENGTH=325	322	325	1.00E-127	100.9	68.0	75.5
Rsa1.0_00235.1.g9261.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00235.1.g9262.t1	gb|EOA16175.1| hypothetical protein CARUB_v10004312mg [Capsella rubella]	664	664	0	100.0	93.4	97.1	hypothetical protein CARUB_v10004312mg	gbpln	Capsella rubella	AT4G16760.1 | Symbols: ACX1, ATACX1 | acyl-CoA oxidase 1 | chr4:9424930-9428689 REVERSE LENGTH=664	664	664	0	100.0	92.6	97.4

Rsa1.0_00235.1.g9263.t1	ref|NP_193408.1| ethylene-responsive transcription factor ERF039 [Arabidopsis thaliana] gi|75337675|sp|Q9SUK8.1|ERF39_ARATH RecName: Full=Ethylene-responsive transcription factor ERF039 gi|5302798|emb|CAB46040.1| apetala2 domain TINY like protein [Arabidopsis thaliana] gi|7268425|emb|CAB78717.1| apetala2 domain TINY like protein [Arabidopsis thaliana] gi|44021914|gb|AAS46629.1| At4g16750 [Arabidopsis thaliana] gi|48479340|gb|AAT44941.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|58652080|gb|AAW80865.1| At4g16750 [Arabidopsis thaliana] gi|332658397|gb|AEE83797.1| ethylene-responsive transcription factor ERF039 [Arabidopsis thaliana]	181	179	2.00E-71	98.9	82.9	90.1	ethylene-responsive transcription factor ERF039	gbpln	Arabidopsis thaliana	AT4G16750.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:9421121-9421660 REVERSE LENGTH=179	181	179	8.00E-74	98.9	82.9	90.1
Rsa1.0_00235.1.g9264.t1	gb|EOA19151.1| hypothetical protein CARUB_v10007826mg [Capsella rubella]	547	545	0	99.6	85.7	93.1	hypothetical protein CARUB_v10007826mg	gbpln	Capsella rubella	AT4G16745.1 | Symbols: | Exostosin family protein | chr4:9412185-9414053 FORWARD LENGTH=542	547	542	0	99.1	86.1	94.3
Rsa1.0_00235.1.g9265.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	927	1274	0	137.4	50.1	66.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	927	575	3.00E-71	62.0	18.7	29.2
Rsa1.0_00235.1.g9266.t1	sp|P0CJ43.1|OCISB_ARATH RecName: Full=(E)-beta-ocimene synthase, chloroplastic; AltName: Full=(E,E)-alpha-farnesene synthase; AltName: Full=Terpenoid synthase 2; Short=AtTPS02; Flags: Precursor	591	589	0	99.7	78.2	85.8	RecName: Full=(E)-beta-ocimene synthase, chloroplastic; AltName: Full=(E,E)-alpha-farnesene synthase; AltName: Full=Terpenoid synthase 2; Short=AtTPS02; Flags: Precursor	----	----	AT4G16730.1 | Symbols: TPS02 | terpene synthase 02 | chr4:9403119-9406003 FORWARD LENGTH=539	591	539	0	91.2	71.2	78.3
Rsa1.0_00235.1.g9267.t1	ref|NP_193405.1| 60S ribosomal protein L15-1 [Arabidopsis thaliana] gi|297800374|ref|XP_002868071.1| 60S ribosomal protein L15 [Arabidopsis lyrata subsp. lyrata] gi|3122673|sp|O23515.1|RL151_ARATH RecName: Full=60S ribosomal protein L15-1 gi|13878179|gb|AAK44167.1|AF370352_1 putative ribosomal protein [Arabidopsis thaliana] gi|2245027|emb|CAB10447.1| ribosomal protein [Arabidopsis thaliana] gi|7268422|emb|CAB78714.1| ribosomal protein [Arabidopsis thaliana] gi|16604446|gb|AAL24229.1| AT4g16720/dl4385c [Arabidopsis thaliana] gi|19715591|gb|AAL91619.1| AT4g16720/dl4385c [Arabidopsis thaliana] gi|21592436|gb|AAM64387.1| ribosomal protein [Arabidopsis thaliana] gi|22136774|gb|AAM91731.1| putative ribosomal protein [Arabidopsis thaliana] gi|23505795|gb|AAN28757.1| At4g16720/dl4385c [Arabidopsis thaliana] gi|297313907|gb|EFH44330.1| 60S ribosomal protein L15 [Arabidopsis lyrata subsp. lyrata] gi|332658391|gb|AEE83791.1| 60S ribosomal protein L15-1 [Arabidopsis thaliana]	204	204	1.00E-113	100.0	99.5	100.0	60S ribosomal protein L15-1	gbpln	Arabidopsis lyrata	AT4G16720.1 | Symbols: | Ribosomal protein L23/L15e family protein | chr4:9400156-9401315 REVERSE LENGTH=204	204	204	1.00E-115	100.0	99.5	100.0

Rsa1.0_00235.1.g9268.t1	ref|NP_193404.1| beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana] gi|30683771|ref|NP_849397.1| beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana] gi|2245026|emb|CAB10446.1| hypothetical protein [Arabidopsis thaliana] gi|7268421|emb|CAB78713.1| hypothetical protein [Arabidopsis thaliana] gi|33589780|gb|AAQ22656.1| At4g16710 [Arabidopsis thaliana] gi|110739298|dbj|BAF01562.1| hypothetical protein [Arabidopsis thaliana] gi|332658389|gb|AEE83789.1| glycosyltransferase family protein 28 [Arabidopsis thaliana] gi|332658390|gb|AEE83790.1| beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]	178	176	3.00E-85	98.9	88.8	92.7	beta-1,4-N-acetylglucosaminyltransferase	gbpln	Arabidopsis thaliana	AT4G16710.2 | Symbols: | glycosyltransferase family protein 28 | chr4:9398818-9399618 FORWARD LENGTH=176	178	176	1.00E-87	98.9	88.8	92.7
Rsa1.0_00235.1.g9269.t1	ref|NP_193403.2| phosphatidylserine decarboxylase [Arabidopsis thaliana] gi|29468598|gb|AAO38842.1| phosphatidylserine decarboxylase [Arabidopsis thaliana] gi|109946625|gb|ABG48491.1| At4g16700 [Arabidopsis thaliana] gi|332658388|gb|AEE83788.1| phosphatidylserine decarboxylase [Arabidopsis thaliana]	446	453	0	101.6	86.3	92.6	phosphatidylserine decarboxylase	gbpln	Arabidopsis thaliana	AT4G16700.1 | Symbols: PSD1 | phosphatidylserine decarboxylase 1 | chr4:9395815-9398261 REVERSE LENGTH=453	446	453	0	101.6	86.3	92.6
Rsa1.0_00235.1.g9270.t1	ref|NP_849396.1| uncharacterized protein [Arabidopsis thaliana] gi|26451302|dbj|BAC42752.1| unknown protein [Arabidopsis thaliana] gi|332658386|gb|AEE83786.1| uncharacterized protein AT4G16695 [Arabidopsis thaliana]	53	57	6.00E-18	107.5	92.5	96.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G16695.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 21 Blast hits to 21 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:9394259-9395251 FORWARD LENGTH=57	53	57	1.00E-20	107.5	92.5	96.2
Rsa1.0_00235.1.g9271.t1	sp|Q2V0W1.1|PPD_RAPSA RecName: Full=Pheophorbidase; Short=RsPPD gi|83699291|dbj|BAE54383.1| pheophorbidase [Raphanus sativus]	263	263	1.00E-148	100.0	98.1	98.1	RecName: Full=Pheophorbidase; Short=RsPPD gi|83699291|dbj|BAE54383.1| pheophorbidase	gbpln	Raphanus sativus	AT4G16690.1 | Symbols: ATMES16, MES16 | methyl esterase 16 | chr4:9392405-9393424 REVERSE LENGTH=262	263	262	1.00E-128	99.6	82.9	89.0
Rsa1.0_00235.1.g9272.t1	gb|EOA15451.1| hypothetical protein CARUB_v10004093mg [Capsella rubella]	847	915	0	108.0	75.4	86.0	hypothetical protein CARUB_v10004093mg	gbpln	Capsella rubella	AT1G32490.1 | Symbols: EMB2733, ESP3 | RNA helicase family protein | chr1:11742356-11749286 REVERSE LENGTH=1044	847	1044	0	123.3	58.6	73.2
Rsa1.0_00235.1.g9273.t1	gb|AAO41942.1| unknown protein [Arabidopsis thaliana]	439	429	1.00E-163	97.7	77.7	84.1	unknown protein	gbpln	Arabidopsis thaliana	AT4G16670.1 | Symbols: | Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region | chr4:9385326-9387570 FORWARD LENGTH=429	439	429	1.00E-166	97.7	77.9	84.3
Rsa1.0_00236.1.g9274.t1	ref|NP_173137.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana] gi|75263252|sp|Q9FZ52.1|FDL3_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g16930 gi|9802769|gb|AAF99838.1|AC051629_5 Hypothetical protein [Arabidopsis thaliana] gi|332191402|gb|AEE29523.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana]	90	449	3.00E-14	498.9	57.8	72.2	F-box/RNI-like/FBD-like domains-containing protein	gbpln	Arabidopsis thaliana	AT1G16930.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:5789987-5791534 FORWARD LENGTH=449	90	449	4.00E-17	498.9	57.8	72.2
Rsa1.0_00236.1.g9275.t2	ref|NP_173137.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana] gi|75263252|sp|Q9FZ52.1|FDL3_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g16930 gi|9802769|gb|AAF99838.1|AC051629_5 Hypothetical protein [Arabidopsis thaliana] gi|332191402|gb|AEE29523.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana]	494	449	1.00E-152	90.9	58.5	67.0	F-box/RNI-like/FBD-like domains-containing protein	gbpln	Arabidopsis thaliana	AT1G16930.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:5789987-5791534 FORWARD LENGTH=449	494	449	1.00E-155	90.9	58.5	67.0

Rsa1.0_00236.1.g9276.t1	ref|NP_173137.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana] gi|75263252|sp|Q9FZ52.1|FDL3_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g16930 gi|9802769|gb|AAF99838.1|AC051629_5 Hypothetical protein [Arabidopsis thaliana] gi|332191402|gb|AEE29523.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana]	446	449	0	100.7	77.1	87.7	F-box/RNI-like/FBD-like domains-containing protein	gbpln	Arabidopsis thaliana	AT1G16930.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:5789987-5791534 FORWARD LENGTH=449	446	449	0	100.7	77.1	87.7
Rsa1.0_00236.1.g9277.t1	ref|NP_173137.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana] gi|75263252|sp|Q9FZ52.1|FDL3_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g16930 gi|9802769|gb|AAF99838.1|AC051629_5 Hypothetical protein [Arabidopsis thaliana] gi|332191402|gb|AEE29523.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana]	863	449	0	52.0	38.7	43.6	F-box/RNI-like/FBD-like domains-containing protein	gbpln	Arabidopsis thaliana	AT1G16930.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:5789987-5791534 FORWARD LENGTH=449	863	449	0	52.0	38.7	43.6
Rsa1.0_00236.1.g9278.t1	ref|XP_002890194.1| hypothetical protein ARALYDRAFT_889088 [Arabidopsis lyrata subsp. lyrata] gi|297336036|gb|EFH66453.1| hypothetical protein ARALYDRAFT_889088 [Arabidopsis lyrata subsp. lyrata]	102	93	3.00E-32	91.2	71.6	78.4	hypothetical protein ARALYDRAFT_889088	gbpln	Arabidopsis lyrata	AT1G16950.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: stamen; EXPRESSED DURING: 4 anthesis; Has 17 Blast hits to 17 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5796083-5796364 FORWARD LENGTH=93	102	93	9.00E-34	91.2	70.6	77.5
Rsa1.0_00236.1.g9279.t1	gb|EOA39908.1| hypothetical protein CARUB_v10008595mg [Capsella rubella]	683	620	0	90.8	79.4	85.9	hypothetical protein CARUB_v10008595mg	gbpln	Capsella rubella	AT1G16970.1 | Symbols: KU70, ATKU70 | KU70 homolog | chr1:5801159-5805724 REVERSE LENGTH=621	683	621	0	90.9	79.2	85.5
Rsa1.0_00236.1.g9280.t1	ref|XP_002890196.1| hypothetical protein ARALYDRAFT_312668 [Arabidopsis lyrata subsp. lyrata] gi|297336038|gb|EFH66455.1| hypothetical protein ARALYDRAFT_312668 [Arabidopsis lyrata subsp. lyrata]	866	842	0	97.2	78.2	86.7	hypothetical protein ARALYDRAFT_312668	gbpln	Arabidopsis lyrata	AT1G16980.1 | Symbols: ATTPS2, TPS2 | trehalose-phosphatase/synthase 2 | chr1:5807311-5811488 FORWARD LENGTH=821	866	821	0	94.8	76.4	85.3
Rsa1.0_00236.1.g9281.t1	ref|XP_002890196.1| hypothetical protein ARALYDRAFT_312668 [Arabidopsis lyrata subsp. lyrata] gi|297336038|gb|EFH66455.1| hypothetical protein ARALYDRAFT_312668 [Arabidopsis lyrata subsp. lyrata]	817	842	0	103.1	78.5	87.8	hypothetical protein ARALYDRAFT_312668	gbpln	Arabidopsis lyrata	AT1G16980.1 | Symbols: ATTPS2, TPS2 | trehalose-phosphatase/synthase 2 | chr1:5807311-5811488 FORWARD LENGTH=821	817	821	0	100.5	76.4	86.3
Rsa1.0_00236.1.g9282.t1	ref|XP_002887744.1| RHM1/ROL1 [Arabidopsis lyrata subsp. lyrata] gi|297333585|gb|EFH64003.1| RHM1/ROL1 [Arabidopsis lyrata subsp. lyrata]	672	669	0	99.6	92.4	96.7	RHM1/ROL1	gbpln	Arabidopsis lyrata	AT1G78570.1 | Symbols: RHM1, ROL1, ATRHM1 | rhamnose biosynthesis 1 | chr1:29550110-29552207 FORWARD LENGTH=669	672	669	0	99.6	91.8	96.7
Rsa1.0_00236.1.g9283.t1	gb|EOA38725.1| hypothetical protein CARUB_v10010858mg [Capsella rubella]	240	357	5.00E-70	148.8	52.1	55.8	hypothetical protein CARUB_v10010858mg	gbpln	Capsella rubella	AT1G17010.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:5817667-5819183 FORWARD LENGTH=361	240	361	1.00E-69	150.4	50.0	55.0
Rsa1.0_00236.1.g9284.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1493	2301	0	154.1	66.3	78.6	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1493	1262	1.00E-110	84.5	14.2	21.5
Rsa1.0_00236.1.g9285.t1	ref|XP_002890199.1| hypothetical protein ARALYDRAFT_334969 [Arabidopsis lyrata subsp. lyrata] gi|297336041|gb|EFH66458.1| hypothetical protein ARALYDRAFT_334969 [Arabidopsis lyrata subsp. lyrata]	502	501	0	99.8	88.0	93.4	hypothetical protein ARALYDRAFT_334969	gbpln	Arabidopsis lyrata	AT1G17030.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G47010.2); Has 70 Blast hits to 70 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:5822487-5824424 FORWARD LENGTH=502	502	502	0	100.0	87.6	93.6

Rsa1.0_00236.1.g9286.t2	gb|EOA37410.1| hypothetical protein CARUB_v10011338mg [Capsella rubella]	688	673	0	97.8	80.2	87.4	hypothetical protein CARUB_v10011338mg	gbpln	Capsella rubella	AT1G17040.1 | Symbols: SHA, ATSHA, STATLA | SH2 domain protein A | chr1:5825109-5828056 FORWARD LENGTH=641	688	641	0	93.2	76.7	83.7
Rsa1.0_00236.1.g9287.t1	gb|EOA40503.1| hypothetical protein CARUB_v10009229mg [Capsella rubella]	420	424	0	101.0	89.8	95.0	hypothetical protein CARUB_v10009229mg	gbpln	Capsella rubella	AT1G17050.1 | Symbols: SPS2 | solanesyl diphosphate synthase 2 | chr1:5829289-5831215 FORWARD LENGTH=417	420	417	0	99.3	88.3	93.1
Rsa1.0_00236.1.g9288.t1	sp|Q9SHG5.2|C72C1_ARATH RecName: Full=Cytochrome P450 72C1; AltName: Full=Protein CHIBI 2; AltName: Full=Protein DWARFISH WITH LOW FERTILITY; AltName: Full=Protein SHRINK 1; AltName: Full=Protein SUPPRESSOR OF PHYB-4 PROTEIN 7	519	519	0	100.0	92.3	96.1	RecName: Full=Cytochrome P450 72C1; AltName: Full=Protein CHIBI 2; AltName: Full=Protein DWARFISH WITH LOW FERTILITY; AltName: Full=Protein SHRINK 1; AltName: Full=Protein SUPPRESSOR OF PHYB-4 PROTEIN 7	----	----	AT1G17060.1 | Symbols: CYP72C1, SOB7 | cytochrome p450 72c1 | chr1:5832282-5835255 REVERSE LENGTH=476	519	476	0	91.7	85.4	89.0
Rsa1.0_00236.1.g9289.t1	ref|NP_173150.1| tuftelin-interacting protein 11 [Arabidopsis thaliana] gi|5734758|gb|AAD50023.1|AC007651_18 Similar to tuftelin-interacting protein [Arabidopsis thaliana] gi|332191416|gb|AEE29537.1| GC-rich sequence DNA-binding factor-like protein with tuftelin interacting domain [Arabidopsis thaliana]	840	849	0	101.1	84.2	90.4	tuftelin-interacting protein 11	gbpln	Arabidopsis thaliana	AT1G17070.1 | Symbols: | GC-rich sequence DNA-binding factor-like protein with Tuftelin interacting domain | chr1:5837653-5840202 FORWARD LENGTH=849	840	849	0	101.1	84.2	90.4
Rsa1.0_00236.1.g9290.t1	dbj|BAJ33660.1| unnamed protein product [Thellungiella halophila]	230	254	1.00E-107	110.4	80.4	84.8	unnamed protein product	----	----	AT1G17100.1 | Symbols: | SOUL heme-binding family protein | chr1:5844766-5845539 FORWARD LENGTH=232	230	232	1.00E-105	100.9	76.5	83.9
Rsa1.0_00236.1.g9291.t1	gb|EOA39021.1| hypothetical protein CARUB_v10011568mg [Capsella rubella]	893	938	0	105.0	83.2	88.5	hypothetical protein CARUB_v10011568mg	gbpln	Capsella rubella	AT1G17110.1 | Symbols: UBP15 | ubiquitin-specific protease 15 | chr1:5845816-5849889 REVERSE LENGTH=924	893	924	0	103.5	83.7	88.0
Rsa1.0_00236.1.g9292.t1	ref|NP_173156.1| uncharacterized protein [Arabidopsis thaliana] gi|5734754|gb|AAD50019.1|AC007651_14 Unknown protein [Arabidopsis thaliana] gi|44681362|gb|AAS47621.1| At1g17130 [Arabidopsis thaliana] gi|45773888|gb|AAS76748.1| At1g17130 [Arabidopsis thaliana] gi|110737612|dbj|BAF00747.1| hypothetical protein [Arabidopsis thaliana] gi|332191424|gb|AEE29545.1| uncharacterized protein AT1G17130 [Arabidopsis thaliana]	336	331	1.00E-162	98.5	89.0	92.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G17130.1 | Symbols: | Family of unknown function (DUF572) | chr1:5854264-5856472 FORWARD LENGTH=331	336	331	1.00E-164	98.5	89.0	92.6
Rsa1.0_00236.1.g9293.t1	gb|EOA38153.1| hypothetical protein CARUB_v10009626mg [Capsella rubella]	345	344	1.00E-143	99.7	79.4	88.1	hypothetical protein CARUB_v10009626mg	gbpln	Capsella rubella	AT1G17140.2 | Symbols: ICR1, RIP1 | interactor of constitutive active rops 1 | chr1:5856740-5857861 REVERSE LENGTH=344	345	344	1.00E-142	99.7	80.3	90.4
Rsa1.0_00236.1.g9294.t1	ref|XP_002892936.1| hypothetical protein ARALYDRAFT_471915 [Arabidopsis lyrata subsp. lyrata] gi|297338778|gb|EFH69195.1| hypothetical protein ARALYDRAFT_471915 [Arabidopsis lyrata subsp. lyrata]	337	334	1.00E-135	99.1	75.7	86.6	hypothetical protein ARALYDRAFT_471915	gbpln	Arabidopsis lyrata	AT1G17145.1 | Symbols: | RING/U-box superfamily protein | chr1:5860351-5862241 REVERSE LENGTH=335	337	335	1.00E-136	99.4	76.3	86.6
Rsa1.0_00236.1.g9295.t1	ref|XP_002892937.1| hypothetical protein ARALYDRAFT_471916 [Arabidopsis lyrata subsp. lyrata] gi|297338779|gb|EFH69196.1| hypothetical protein ARALYDRAFT_471916 [Arabidopsis lyrata subsp. lyrata]	91	98	9.00E-40	107.7	91.2	93.4	hypothetical protein ARALYDRAFT_471916	gbpln	Arabidopsis lyrata	AT1G17147.1 | Symbols: | VQ motif-containing protein | chr1:5863654-5863950 REVERSE LENGTH=98	91	98	4.00E-41	107.7	87.9	93.4
Rsa1.0_00236.1.g9296.t1	ref|XP_002890206.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297336048|gb|EFH66465.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	580	401	1.00E-123	69.1	36.0	44.8	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT1G17150.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:5865707-5867495 FORWARD LENGTH=402	580	402	1.00E-118	69.3	33.8	43.3
Rsa1.0_00236.1.g9297.t1	gb|EOA37961.1| hypothetical protein CARUB_v10009429mg [Capsella rubella]	377	383	1.00E-178	101.6	85.9	91.2	hypothetical protein CARUB_v10009429mg	gbpln	Capsella rubella	AT1G17160.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr1:5867678-5869215 FORWARD LENGTH=379	377	379	1.00E-179	100.5	85.7	91.0
Rsa1.0_00236.1.g9298.t1	ref|XP_002890207.1| hypothetical protein ARALYDRAFT_471920 [Arabidopsis lyrata subsp. lyrata] gi|297336049|gb|EFH66466.1| hypothetical protein ARALYDRAFT_471920 [Arabidopsis lyrata subsp. lyrata]	205	218	1.00E-90	106.3	79.0	86.3	hypothetical protein ARALYDRAFT_471920	gbpln	Arabidopsis lyrata	AT1G17170.1 | Symbols: ATGSTU24, GST, GSTU24 | glutathione S-transferase TAU 24 | chr1:5869895-5870691 FORWARD LENGTH=218	205	218	5.00E-92	106.3	77.6	86.3

Rsa1.0_00236.1.g9299.t1	ref|NP_173160.1| glutathione S-transferase TAU 24 [Arabidopsis thaliana] gi|75337229|sp|Q9SHH6.1|GSTUO_ARATH RecName: Full=Glutathione S-transferase U24; Short=AtGSTU24; AltName: Full=GST class-tau member 24 gi|5734751|gb|AAD50016.1|AC007651_11 Putative glutathione transferase [Arabidopsis thaliana] gi|45752760|gb|AAS76278.1| At1g17170 [Arabidopsis thaliana] gi|332191433|gb|AEE29554.1| glutathione S-transferase TAU 24 [Arabidopsis thaliana]	105	218	1.00E-49	207.6	88.6	93.3	glutathione S-transferase TAU 24	gbpln	Arabidopsis thaliana	AT1G17170.1 | Symbols: ATGSTU24, GST, GSTU24 | glutathione S-transferase TAU 24 | chr1:5869895-5870691 FORWARD LENGTH=218	105	218	2.00E-52	207.6	88.6	93.3
Rsa1.0_00237.1.g9300.t1	gb|EOA16153.1| hypothetical protein CARUB_v10004291mg [Capsella rubella]	696	676	0	97.1	83.3	90.2	hypothetical protein CARUB_v10004291mg	gbpln	Capsella rubella	AT4G33630.2 | Symbols: EX1 | Protein of unknown function (DUF3506) | chr4:16155560-16159094 FORWARD LENGTH=684	696	684	0	98.3	83.5	91.1
Rsa1.0_00237.1.g9301.t2	ref|NP_001119110.1| uncharacterized protein [Arabidopsis thaliana] gi|332660856|gb|AEE86256.1| uncharacterized protein AT4G33625 [Arabidopsis thaliana]	197	199	4.00E-83	101.0	74.1	83.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G33625.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Golgi apparatus membrane protein TVP15 (InterPro:IPR013714); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16153114-16154543 REVERSE LENGTH=199	197	199	1.00E-85	101.0	74.1	83.8
Rsa1.0_00237.1.g9302.t1	gb|ACP30605.1| disease resistance protein [Brassica rapa subsp. pekinensis]	803	860	0	107.1	84.2	87.4	disease resistance protein	gbpln	Brassica rapa	AT1G61190.1 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr1:22557602-22560687 FORWARD LENGTH=967	803	967	0	120.4	63.5	74.7
Rsa1.0_00237.1.g9303.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00237.1.g9304.t1	gb|EOA14669.1| hypothetical protein CARUB_v10027941mg [Capsella rubella]	572	579	0	101.2	64.7	78.1	hypothetical protein CARUB_v10027941mg	gbpln	Capsella rubella	AT5G51470.1 | Symbols: | Auxin-responsive GH3 family protein | chr5:20907287-20909340 FORWARD LENGTH=581	572	581	0	101.6	64.5	77.8
Rsa1.0_00237.1.g9305.t1	gb|AAF79324.1|AC002304_17 F14J16.29 [Arabidopsis thaliana]	145	143	5.00E-34	98.6	63.4	70.3	F14J16.29	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00237.1.g9306.t1	gb|EOA19007.1| hypothetical protein CARUB_v10007658mg [Capsella rubella]	462	454	0	98.3	79.4	89.6	hypothetical protein CARUB_v10007658mg	gbpln	Capsella rubella	AT4G33590.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G33600.1); Has 126 Blast hits to 126 proteins in 35 species: Archae - 0; Bacteria - 12; Metazoa - 0; Fungi - 21; Plants - 62; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink). | chr4:16142585-16143985 REVERSE LENGTH=466	462	466	0	100.9	80.3	90.7
Rsa1.0_00237.1.g9307.t1	ref|NP_567928.1| beta carbonic anhydrase 5 [Arabidopsis thaliana] gi|14334478|gb|AAK59437.1| putative carbonate dehydratase [Arabidopsis thaliana] gi|21594039|gb|AAM65957.1| carbonate dehydratase-like protein [Arabidopsis thaliana] gi|21689751|gb|AAM67519.1| putative carbonate dehydratase [Arabidopsis thaliana] gi|62321082|dbj|BAD94173.1| carbonate dehydratase - like protein [Arabidopsis thaliana] gi|332660848|gb|AEE86248.1| beta carbonic anhydrase 5 [Arabidopsis thaliana]	248	301	1.00E-124	121.4	86.7	91.9	beta carbonic anhydrase 5	gbpln	Arabidopsis thaliana	AT4G33580.1 | Symbols: ATBCA5, BCA5 | beta carbonic anhydrase 5 | chr4:16139406-16141363 FORWARD LENGTH=301	248	301	1.00E-127	121.4	86.7	91.9
Rsa1.0_00237.1.g9308.t1	ref|XP_002869206.1| hypothetical protein ARALYDRAFT_328381 [Arabidopsis lyrata subsp. lyrata] gi|297315042|gb|EFH45465.1| hypothetical protein ARALYDRAFT_328381 [Arabidopsis lyrata subsp. lyrata]	300	315	1.00E-82	105.0	66.0	78.0	hypothetical protein ARALYDRAFT_328381	gbpln	Arabidopsis lyrata	AT4G33565.1 | Symbols: | RING/U-box superfamily protein | chr4:16136821-16137924 FORWARD LENGTH=367	300	367	1.00E-79	122.3	64.7	76.0
Rsa1.0_00237.1.g9309.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00237.1.g9310.t3	emb|CAB38802.1| putative protein [Arabidopsis thaliana] gi|7270292|emb|CAB80061.1| putative protein [Arabidopsis thaliana]	301	462	6.00E-73	153.5	46.2	50.5	putative protein	gbpln	Arabidopsis thaliana	AT4G33440.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:16092020-16094732 FORWARD LENGTH=475	301	475	5.00E-75	157.8	45.5	48.8

Rsa1.0_00237.1.g9311.t1	gb|ACF23029.1| ST63-2 [Eutrema halophilum]	97	90	2.00E-30	92.8	68.0	79.4	ST63-2	gbpln	Eutrema halophilum	AT4G33467.2 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:16101691-16102084 REVERSE LENGTH=101	97	101	8.00E-32	104.1	71.1	85.6
Rsa1.0_00237.1.g9312.t2	dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	96	1098	2.00E-18	1143.8	45.8	54.2	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00237.1.g9313.t1	ref|NP_195070.2| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana] gi|27754320|gb|AAO22613.1| putative polygalacturonase [Arabidopsis thaliana] gi|28393881|gb|AAO42348.1| putative polygalacturonase [Arabidopsis thaliana] gi|332660825|gb|AEE86225.1| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	473	475	0	100.4	89.6	95.3	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	gbpln	Arabidopsis thaliana	AT4G33440.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:16092020-16094732 FORWARD LENGTH=475	473	475	0	100.4	89.6	95.3
Rsa1.0_00237.1.g9314.t1	gb|AFO67895.1| leucine-rich repeat receptor-like kinase (mitochondrion) [Brassica rapa subsp. oleifera]	615	632	0	102.8	95.3	97.1	leucine-rich repeat receptor-like kinase (mitochondrion)	gbpln	Brassica rapa	AT4G33430.1 | Symbols: BAK1, RKS10, SERK3, ELG, ATSERK3, ATBAK1 | BRI1-associated receptor kinase | chr4:16086654-16090288 REVERSE LENGTH=615	615	615	0	100.0	94.6	96.6
Rsa1.0_00237.1.g9315.t1	gb|EOA15571.1| hypothetical protein CARUB_v10005237mg [Capsella rubella]	304	325	1.00E-160	106.9	87.5	94.4	hypothetical protein CARUB_v10005237mg	gbpln	Capsella rubella	AT4G33420.1 | Symbols: | Peroxidase superfamily protein | chr4:16084856-16086105 FORWARD LENGTH=325	304	325	1.00E-162	106.9	88.2	93.8
Rsa1.0_00237.1.g9316.t1	gb|EOA16846.1| hypothetical protein CARUB_v10005069mg [Capsella rubella]	373	372	0	99.7	91.7	97.1	hypothetical protein CARUB_v10005069mg	gbpln	Capsella rubella	AT4G33410.1 | Symbols: ATSPPL1, SPPL1 | SIGNAL PEPTIDE PEPTIDASE-LIKE 1 | chr4:16081640-16083119 FORWARD LENGTH=372	373	372	0	99.7	91.4	97.3
Rsa1.0_00237.1.g9317.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00237.1.g9318.t1	gb|EOA18471.1| hypothetical protein CARUB_v10007017mg [Capsella rubella]	689	791	0	114.8	71.0	82.9	hypothetical protein CARUB_v10007017mg	gbpln	Capsella rubella	AT4G33390.1 | Symbols: | Plant protein of unknown function (DUF827) | chr4:16075282-16077706 FORWARD LENGTH=779	689	779	2.33E-156	113.1	46.0	57.2
Rsa1.0_00237.1.g9319.t2	gb|EOA18933.1| hypothetical protein CARUB_v10007564mg [Capsella rubella]	459	424	1.00E-131	92.4	59.0	70.4	hypothetical protein CARUB_v10007564mg	gbpln	Capsella rubella	AT1G05080.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:1459091-1460579 FORWARD LENGTH=439	459	439	1.00E-111	95.6	51.6	66.7
Rsa1.0_00237.1.g9320.t1	ref|XP_002867184.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313020|gb|EFH43443.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	335	343	1.00E-175	102.4	88.1	95.5	predicted protein	gbpln	Arabidopsis lyrata	AT4G33360.1 | Symbols: FLDH | NAD(P)-binding Rossmann-fold superfamily protein | chr4:16067989-16069374 REVERSE LENGTH=344	335	344	1.00E-174	102.7	85.4	94.6
Rsa1.0_00237.1.g9321.t1	ref|NP_680758.3| non-specific lipid-transfer protein 11 [Arabidopsis thaliana] gi|122209302|sp|Q2V3C1.1|NLTPB_ARATH RecName: Full=Non-specific lipid-transfer protein 11; Short=LTP 11; Flags: Precursor gi|332660811|gb|AEE86211.1| non-specific lipid-transfer protein 11 [Arabidopsis thaliana]	120	119	6.00E-43	99.2	71.7	83.3	non-specific lipid-transfer protein 11	gbpln	Arabidopsis thaliana	AT4G33355.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:16067097-16067568 FORWARD LENGTH=119	120	119	1.00E-45	99.2	71.7	83.3
Rsa1.0_00237.1.g9322.t1	emb|CAB38786.1| hypothetical protein [Arabidopsis thaliana] gi|7270276|emb|CAB80045.1| hypothetical protein [Arabidopsis thaliana]	671	461	1.00E-133	68.7	39.5	44.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G33280.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr4:16047357-16049310 REVERSE LENGTH=337	671	337	1.00E-132	50.2	35.2	40.5
Rsa1.0_00237.1.g9323.t1	ref|XP_002867190.1| CDC20.1 [Arabidopsis lyrata subsp. lyrata] gi|297313026|gb|EFH43449.1| CDC20.1 [Arabidopsis lyrata subsp. lyrata]	455	456	0	100.2	93.2	96.0	CDC20.1	gbpln	Arabidopsis lyrata	AT4G33270.1 | Symbols: CDC20.1 | Transducin family protein / WD-40 repeat family protein | chr4:16044545-16046590 REVERSE LENGTH=457	455	457	0	100.4	93.4	96.3
Rsa1.0_00237.1.g9324.t1	ref|XP_002867193.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313029|gb|EFH43452.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	603	609	0	101.0	84.6	91.4	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT4G33230.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr4:16026591-16028754 REVERSE LENGTH=609	603	609	0	101.0	82.6	90.2
Rsa1.0_00237.1.g9325.t1	gb|AAF97281.1|AC010164_3 Hypothetical protein [Arabidopsis thaliana] gi|12324507|gb|AAG52212.1|AC022288_11 putative gag-pol polyprotein; 76173-77576 [Arabidopsis thaliana]	423	467	1.00E-139	110.4	58.4	74.9	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00237.1.g9326.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00237.1.g9327.t1	ref|XP_002867194.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313030|gb|EFH43453.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	967	990	0	102.4	90.2	94.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G33210.1 | Symbols: SLOMO | F-box family protein | chr4:16015971-16020697 REVERSE LENGTH=990	967	990	0	102.4	89.9	94.6
Rsa1.0_00237.1.g9328.t1	ref|XP_002867195.1| hypothetical protein ARALYDRAFT_913100 [Arabidopsis lyrata subsp. lyrata] gi|297313031|gb|EFH43454.1| hypothetical protein ARALYDRAFT_913100 [Arabidopsis lyrata subsp. lyrata]	1532	1522	0	99.3	88.5	93.3	hypothetical protein ARALYDRAFT_913100	gbpln	Arabidopsis lyrata	AT4G33200.1 | Symbols: XI-I, ATXI-I, XI-15 | myosin, putative | chr4:16002768-16014792 REVERSE LENGTH=1522	1532	1522	0	99.3	88.3	93.0
Rsa1.0_00237.1.g9329.t1	ref|XP_002869220.1| hypothetical protein ARALYDRAFT_491367 [Arabidopsis lyrata subsp. lyrata] gi|297315056|gb|EFH45479.1| hypothetical protein ARALYDRAFT_491367 [Arabidopsis lyrata subsp. lyrata]	307	308	1.00E-164	100.3	90.6	95.4	hypothetical protein ARALYDRAFT_491367	gbpln	Arabidopsis lyrata	AT4G33180.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:16000282-16002055 FORWARD LENGTH=307	307	307	1.00E-164	100.0	89.3	93.5
Rsa1.0_00237.1.g9330.t1	ref|NP_567915.3| F-box only protein 13 [Arabidopsis thaliana] gi|334302802|sp|Q9SMZ3.2|FBX13_ARATH RecName: Full=F-box only protein 13 gi|332660785|gb|AEE86185.1| F-box only protein 13 [Arabidopsis thaliana]	412	457	1.00E-163	110.9	73.3	84.0	F-box only protein 13	gbpln	Arabidopsis thaliana	AT4G33160.1 | Symbols: | F-box family protein | chr4:15994160-15995533 FORWARD LENGTH=457	412	457	1.00E-166	110.9	73.3	84.0
Rsa1.0_00237.1.g9331.t1	ref|XP_002869238.1| hypothetical protein ARALYDRAFT_491409 [Arabidopsis lyrata subsp. lyrata] gi|297315074|gb|EFH45497.1| hypothetical protein ARALYDRAFT_491409 [Arabidopsis lyrata subsp. lyrata]	182	157	4.00E-56	86.3	55.5	68.7	hypothetical protein ARALYDRAFT_491409	gbpln	Arabidopsis lyrata	AT4G32870.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:15862168-15862641 FORWARD LENGTH=157	182	157	1.00E-57	86.3	54.9	69.2
Rsa1.0_00237.1.g9332.t1	ref|NP_195012.2| uncharacterized protein [Arabidopsis thaliana] gi|38566612|gb|AAR24196.1| At4g32860 [Arabidopsis thaliana] gi|40824060|gb|AAR92334.1| At4g32860 [Arabidopsis thaliana] gi|332660736|gb|AEE86136.1| uncharacterized protein AT4G32860 [Arabidopsis thaliana]	195	199	2.00E-90	102.1	84.1	91.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32860.1 | Symbols: | unknown protein; Has 46 Blast hits to 46 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15856710-15857309 REVERSE LENGTH=199	195	199	8.00E-93	102.1	84.1	91.8
Rsa1.0_00237.1.g9333.t1	gb|EOA15715.1| hypothetical protein CARUB_v10006567mg [Capsella rubella]	320	228	2.00E-67	71.3	45.9	49.4	hypothetical protein CARUB_v10006567mg	gbpln	Capsella rubella	AT4G32800.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:15819812-15820477 FORWARD LENGTH=221	320	221	7.00E-69	69.1	45.3	49.4
Rsa1.0_00237.1.g9334.t2	gb|AFB74210.1| tocopherol cyclase [Brassica napus]	504	490	0	97.2	93.7	95.0	tocopherol cyclase	gbpln	Brassica napus	AT4G32770.1 | Symbols: VTE1, ATSDX1 | tocopherol cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose export defective 1 (SXD1) | chr4:15804981-15807790 FORWARD LENGTH=488	504	488	0	96.8	87.1	91.3
Rsa1.0_00237.1.g9335.t1	ref|NP_195002.2| ENTH/VHS/GAT family protein [Arabidopsis thaliana] gi|21539459|gb|AAM53282.1| putative protein [Arabidopsis thaliana] gi|23197650|gb|AAN15352.1| putative protein [Arabidopsis thaliana] gi|332660714|gb|AEE86114.1| ENTH/VHS/GAT family protein [Arabidopsis thaliana]	651	675	0	103.7	87.9	91.2	ENTH/VHS/GAT family protein	gbpln	Arabidopsis thaliana	AT4G32760.1 | Symbols: | ENTH/VHS/GAT family protein | chr4:15799376-15803832 FORWARD LENGTH=675	651	675	0	103.7	87.9	91.2
Rsa1.0_00237.1.g9336.t1	ref|NP_974718.1| myb-related protein 3R-1 [Arabidopsis thaliana] gi|332660712|gb|AEE86112.1| myb-related protein 3R-1 [Arabidopsis thaliana]	936	995	0	106.3	76.8	83.8	myb-related protein 3R-1	gbpln	Arabidopsis thaliana	AT4G32730.2 | Symbols: PC-MYB1, MYB3R-1, ATMYB3R-1, ATMYB3R1 | Homeodomain-like protein | chr4:15791039-15795643 FORWARD LENGTH=995	936	995	0	106.3	76.8	83.8
Rsa1.0_00237.1.g9337.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00237.1.g9338.t2	ref|NP_194991.1| Potassium channel KAT3 [Arabidopsis thaliana] gi|44888078|sp|P92960.1|KAT3_ARATH RecName: Full=Potassium channel KAT3; AltName: Full=AKT4; AltName: Full=AtKC1; AltName: Full=Potassium channel TKC gi|1708777|emb|CAB05669.1| potassium channel [Arabidopsis thaliana] gi|3063705|emb|CAA18596.1| potassium channel protein [Arabidopsis thaliana] gi|4090537|gb|AAC98810.1| K+ inward rectifying channel protein [Arabidopsis thaliana] gi|4098949|gb|AAD00503.1| K+ inward rectifying channel [Arabidopsis thaliana] gi|7270169|emb|CAB79982.1| potassium channel protein AtKC [Arabidopsis thaliana] gi|15529218|gb|AAK97703.1| AT4g32650/F4D11_150 [Arabidopsis thaliana] gi|27777708|gb|AAO23890.1| At4g32650/F4D11_150 [Arabidopsis thaliana] gi|332660697|gb|AEE86097.1| Potassium channel KAT3 [Arabidopsis thaliana]	685	662	0	96.6	80.7	88.0	Potassium channel KAT3	gbpln	Arabidopsis thaliana	AT4G32650.1 | Symbols: ATKC1, KAT3, KC1, AtLKT1 | potassium channel in Arabidopsis thaliana 3 | chr4:15751482-15754797 REVERSE LENGTH=662	685	662	0	96.6	80.7	88.0
Rsa1.0_00237.1.g9339.t1	emb|CAA18600.1| putative protein [Arabidopsis thaliana] gi|7270165|emb|CAB79978.1| putative protein [Arabidopsis thaliana]	300	557	3.00E-59	185.7	77.7	86.0	putative protein	gbpln	Arabidopsis thaliana	AT4G32610.1 | Symbols: | copper ion binding | chr4:15728376-15729897 REVERSE LENGTH=315	300	315	7.00E-62	105.0	77.3	86.3
Rsa1.0_00237.1.g9340.t5	ref|XP_002869264.1| hypothetical protein ARALYDRAFT_491464 [Arabidopsis lyrata subsp. lyrata] gi|297315100|gb|EFH45523.1| hypothetical protein ARALYDRAFT_491464 [Arabidopsis lyrata subsp. lyrata]	923	920	0	99.7	72.9	75.7	hypothetical protein ARALYDRAFT_491464	gbpln	Arabidopsis lyrata	AT4G32551.1 | Symbols: LUG, RON2 | LisH dimerisation motif;WD40/YVTN repeat-like-containing domain | chr4:15707863-15713359 FORWARD LENGTH=931	923	931	0	100.9	72.6	75.8
Rsa1.0_00237.1.g9341.t3	ref|NP_180132.1| V-type H+-transporting ATPase 21kDa proteolipid subunit [Arabidopsis thaliana] gi|4874301|gb|AAD31363.1| putative vacuolar ATP synthase proteolipid subunit [Arabidopsis thaliana] gi|21536776|gb|AAM61108.1| putative vacuolar ATP synthase proteolipid subunit [Arabidopsis thaliana] gi|109946567|gb|ABG48462.1| At2g25610 [Arabidopsis thaliana] gi|330252630|gb|AEC07724.1| ATPase, F0/V0 complex, subunit C protein [Arabidopsis thaliana]	347	178	3.00E-89	51.3	49.9	50.7	V-type H+-transporting ATPase 21kDa proteolipid subunit	gbpln	Arabidopsis thaliana	AT2G25610.1 | Symbols: | ATPase, F0/V0 complex, subunit C protein | chr2:10901585-10902494 REVERSE LENGTH=178	347	178	9.00E-92	51.3	49.9	50.7
Rsa1.0_00237.1.g9342.t1	gb|EOA16174.1| hypothetical protein CARUB_v10004311mg, partial [Capsella rubella]	653	666	0	102.0	90.4	94.3	hypothetical protein CARUB_v10004311mg, partial	gbpln	Capsella rubella	AT4G32510.1 | Symbols: | HCO3- transporter family | chr4:15685903-15688811 REVERSE LENGTH=673	653	673	0	103.1	89.6	94.0
Rsa1.0_00238.1.g9343.t1	gb|EOA28992.1| hypothetical protein CARUB_v10025243mg [Capsella rubella]	159	119	7.00E-13	74.8	27.0	37.1	hypothetical protein CARUB_v10025243mg	gbpln	Capsella rubella	AT3G55430.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr3:20549806-20552004 REVERSE LENGTH=449	159	449	9.00E-13	282.4	20.8	30.2
Rsa1.0_00238.1.g9344.t1	gb|EOA17998.1| hypothetical protein CARUB_v10006433mg [Capsella rubella]	119	119	3.00E-58	100.0	95.8	97.5	hypothetical protein CARUB_v10006433mg	gbpln	Capsella rubella	AT5G56710.1 | Symbols: | Ribosomal protein L31e family protein | chr5:22944003-22944767 REVERSE LENGTH=119	119	119	3.00E-60	100.0	94.1	97.5
Rsa1.0_00238.1.g9345.t1	ref|NP_178239.1| uncharacterized protein [Arabidopsis thaliana] gi|4262237|gb|AAD14530.1| predicted by genscan and genefinder [Arabidopsis thaliana] gi|17529142|gb|AAL38797.1| unknown protein [Arabidopsis thaliana] gi|21436241|gb|AAM51259.1| unknown protein [Arabidopsis thaliana] gi|49660101|gb|AAT68341.1| hypothetical protein At2g01300 [Arabidopsis thaliana] gi|60547691|gb|AAX23809.1| hypothetical protein At2g01300 [Arabidopsis thaliana] gi|330250336|gb|AEC05430.1| uncharacterized protein AT2G01300 [Arabidopsis thaliana]	141	156	3.00E-56	110.6	81.6	86.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G01300.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15010.1); Has 73 Blast hits to 73 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:151221-151691 REVERSE LENGTH=156	141	156	7.00E-59	110.6	81.6	86.5

Rsa1.0_00238.1.g9346.t1	ref|NP_178248.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546783|sp|Q9ZU29.2|PP139_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g01390 gi|330250351|gb|AEC05445.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	203	577	5.00E-75	284.2	69.0	76.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G01390.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:172256-174137 FORWARD LENGTH=577	203	577	2.00E-77	284.2	69.0	76.4
Rsa1.0_00238.1.g9347.t1	gb|EOA17840.1| hypothetical protein CARUB_v10006241mg, partial [Capsella rubella]	279	230	2.00E-34	82.4	35.1	49.8	hypothetical protein CARUB_v10006241mg, partial	gbpln	Capsella rubella	AT4G11310.1 | Symbols: | Papain family cysteine protease | chr4:6883594-6885318 FORWARD LENGTH=364	279	364	7.00E-20	130.5	28.7	42.3
Rsa1.0_00238.1.g9348.t2	dbj|BAA96887.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	610	1140	1.00E-59	186.9	22.8	35.4	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00238.1.g9349.t1	gb|AAC67205.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	699	1413	5.00E-64	202.1	23.2	30.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	699	237	3.00E-15	33.9	6.9	12.0
Rsa1.0_00238.1.g9350.t1	ref|XP_002870216.1| hypothetical protein ARALYDRAFT_915224 [Arabidopsis lyrata subsp. lyrata] gi|297316052|gb|EFH46475.1| hypothetical protein ARALYDRAFT_915224 [Arabidopsis lyrata subsp. lyrata]	200	185	3.00E-44	92.5	47.5	63.0	hypothetical protein ARALYDRAFT_915224	gbpln	Arabidopsis lyrata	AT4G15715.1 | Symbols: | Proteinase inhibitor I25, cystatin, conserved region | chr4:8945317-8945673 FORWARD LENGTH=118	200	118	6.00E-32	59.0	30.0	39.5
Rsa1.0_00238.1.g9351.t1	ref|NP_178248.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546783|sp|Q9ZU29.2|PP139_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g01390 gi|330250351|gb|AEC05445.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	354	577	2.33E-156	163.0	73.7	82.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G01390.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:172256-174137 FORWARD LENGTH=577	354	577	1.00E-149	163.0	73.7	82.5
Rsa1.0_00238.1.g9352.t1	gb|EOA22812.1| hypothetical protein CARUB_v10003530mg [Capsella rubella]	258	288	7.00E-82	111.6	62.4	73.3	hypothetical protein CARUB_v10003530mg	gbpln	Capsella rubella	AT1G45063.2 | Symbols: | copper ion binding;electron carriers | chr1:17034068-17034886 REVERSE LENGTH=272	258	272	3.00E-73	105.4	57.4	69.8
Rsa1.0_00238.1.g9353.t1	gb|EOA23655.1| hypothetical protein CARUB_v10016856mg [Capsella rubella]	560	612	0	109.3	89.6	92.3	hypothetical protein CARUB_v10016856mg	gbpln	Capsella rubella	AT2G01420.1 | Symbols: PIN4, ATPIN4 | Auxin efflux carrier family protein | chr2:180478-183199 REVERSE LENGTH=612	560	612	0	109.3	88.9	92.9
Rsa1.0_00238.1.g9354.t1	ref|NP_174108.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|12320885|gb|AAG50576.1|AC079280_7 hypothetical protein [Arabidopsis thaliana] gi|332192765|gb|AEE30886.1| RNase H domain-containing protein [Arabidopsis thaliana]	137	213	6.00E-11	155.5	27.0	40.1	RNase H domain-containing protein	gbpln	Arabidopsis thaliana	AT1G27870.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr1:9706657-9707298 REVERSE LENGTH=213	137	213	2.00E-13	155.5	27.0	40.1
Rsa1.0_00238.1.g9355.t1	ref|WP_001871707.1| hypothetical protein [Streptococcus agalactiae] gi|77173851|gb|EAO76897.1| hypothetical protein SAI_2423 [Streptococcus agalactiae H36B]	417	181	3.00E-17	43.4	10.8	12.0	hypothetical protein	gbbct	Streptococcus agalactiae	#	#	#	#	#	#	#
Rsa1.0_00238.1.g9356.t1	ref|XP_002876750.1| hypothetical protein ARALYDRAFT_346639 [Arabidopsis lyrata subsp. lyrata] gi|297322588|gb|EFH53009.1| hypothetical protein ARALYDRAFT_346639 [Arabidopsis lyrata subsp. lyrata]	380	201	4.00E-54	52.9	28.4	30.5	hypothetical protein ARALYDRAFT_346639	gbpln	Arabidopsis lyrata	AT2G01430.1 | Symbols: ATHB17, ATHB-17, HB17 | homeobox-leucine zipper protein 17 | chr2:187798-190369 REVERSE LENGTH=275	380	275	2.00E-54	72.4	27.6	30.0
Rsa1.0_00238.1.g9357.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00238.1.g9358.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00238.1.g9359.t1	ref|NP_178253.3| ATP-dependent DNA helicase RecG [Arabidopsis thaliana] gi|330250357|gb|AEC05451.1| DEAD/DEAH box RNA helicase family protein [Arabidopsis thaliana]	980	973	0	99.3	82.6	90.7	ATP-dependent DNA helicase RecG	gbpln	Arabidopsis thaliana	AT2G01440.1 | Symbols: | DEAD/DEAH box RNA helicase family protein | chr2:193950-199056 REVERSE LENGTH=973	980	973	0	99.3	82.6	90.7
Rsa1.0_00238.1.g9360.t1	gb|EOA24893.1| hypothetical protein CARUB_v10018184mg [Capsella rubella]	151	151	5.00E-76	100.0	88.1	94.7	hypothetical protein CARUB_v10018184mg	gbpln	Capsella rubella	AT2G01520.1 | Symbols: MLP328 | MLP-like protein 328 | chr2:235992-236881 FORWARD LENGTH=151	151	151	4.00E-78	100.0	88.1	94.0
Rsa1.0_00238.1.g9361.t1	gb|EOA36058.1| hypothetical protein CARUB_v10008394mg [Capsella rubella]	129	743	1.00E-15	576.0	41.9	45.7	hypothetical protein CARUB_v10008394mg	gbpln	Capsella rubella	AT1G17980.1 | Symbols: PAPS1 | poly(A) polymerase 1 | chr1:6187742-6191418 REVERSE LENGTH=713	129	713	4.00E-14	552.7	38.0	41.1

Rsa1.0_00238.1.g9362.t1	gb|ADK63403.1| C2 domain-containing protein [Brassica rapa]	181	180	1.00E-95	99.4	91.2	96.1	C2 domain-containing protein	gbpln	Brassica rapa	AT2G01540.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:242297-243233 REVERSE LENGTH=180	181	180	1.00E-94	99.4	88.4	92.8
Rsa1.0_00239.1.g9363.t1	ref|XP_002885164.1| hypothetical protein ARALYDRAFT_897993 [Arabidopsis lyrata subsp. lyrata] gi|297331004|gb|EFH61423.1| hypothetical protein ARALYDRAFT_897993 [Arabidopsis lyrata subsp. lyrata]	623	683	0	109.6	78.7	85.6	hypothetical protein ARALYDRAFT_897993	gbpln	Arabidopsis lyrata	AT3G16730.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Non-SMC condensin II complex, subunit H2-like (InterPro:IPR009378); Has 249 Blast hits to 211 proteins in 82 species: Archae - 0; Bacteria - 0; Metazoa - 145; Fungi - 8; Plants - 30; Viruses - 0; Other Eukaryotes - 66 (source: NCBI BLink). | chr3:5695633-5698863 REVERSE LENGTH=683	623	683	0	109.6	78.0	85.6
Rsa1.0_00239.1.g9364.t1	ref|XP_002883022.1| hypothetical protein ARALYDRAFT_479140 [Arabidopsis lyrata subsp. lyrata] gi|297328862|gb|EFH59281.1| hypothetical protein ARALYDRAFT_479140 [Arabidopsis lyrata subsp. lyrata]	259	304	1.00E-50	117.4	54.8	63.3	hypothetical protein ARALYDRAFT_479140	gbpln	Arabidopsis lyrata	AT3G16720.1 | Symbols: ATL2, TL2 | TOXICOS EN LEVADURA 2 | chr3:5692880-5693794 FORWARD LENGTH=304	259	304	9.00E-52	117.4	53.3	62.5
Rsa1.0_00239.1.g9365.t1	ref|XP_002883022.1| hypothetical protein ARALYDRAFT_479140 [Arabidopsis lyrata subsp. lyrata] gi|297328862|gb|EFH59281.1| hypothetical protein ARALYDRAFT_479140 [Arabidopsis lyrata subsp. lyrata]	198	304	3.00E-40	153.5	44.9	49.0	hypothetical protein ARALYDRAFT_479140	gbpln	Arabidopsis lyrata	AT3G16720.1 | Symbols: ATL2, TL2 | TOXICOS EN LEVADURA 2 | chr3:5692880-5693794 FORWARD LENGTH=304	198	304	9.00E-42	153.5	42.9	47.5
Rsa1.0_00239.1.g9366.t1	ref|XP_002883022.1| hypothetical protein ARALYDRAFT_479140 [Arabidopsis lyrata subsp. lyrata] gi|297328862|gb|EFH59281.1| hypothetical protein ARALYDRAFT_479140 [Arabidopsis lyrata subsp. lyrata]	285	304	2.00E-41	106.7	36.5	44.9	hypothetical protein ARALYDRAFT_479140	gbpln	Arabidopsis lyrata	AT3G16720.1 | Symbols: ATL2, TL2 | TOXICOS EN LEVADURA 2 | chr3:5692880-5693794 FORWARD LENGTH=304	285	304	2.00E-42	106.7	35.4	43.2
Rsa1.0_00239.1.g9367.t1	ref|XP_002883021.1| hypothetical protein ARALYDRAFT_479138 [Arabidopsis lyrata subsp. lyrata] gi|297328861|gb|EFH59280.1| hypothetical protein ARALYDRAFT_479138 [Arabidopsis lyrata subsp. lyrata]	490	504	0	102.9	68.2	80.4	hypothetical protein ARALYDRAFT_479138	gbpln	Arabidopsis lyrata	AT3G16710.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:5690020-5691543 FORWARD LENGTH=507	490	507	0	103.5	68.6	80.2
Rsa1.0_00239.1.g9368.t1	ref|XP_002883020.1| fumarylacetoacetate hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328860|gb|EFH59279.1| fumarylacetoacetate hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	225	226	1.00E-119	100.4	92.9	96.9	fumarylacetoacetate hydrolase family protein	gbpln	Arabidopsis lyrata	AT3G16700.1 | Symbols: | Fumarylacetoacetate (FAA) hydrolase family | chr3:5687809-5689664 FORWARD LENGTH=224	225	224	1.00E-121	99.6	91.1	96.0
Rsa1.0_00239.1.g9369.t1	gb|EOA31331.1| hypothetical protein CARUB_v10014504mg, partial [Capsella rubella]	231	242	1.00E-110	104.8	85.3	92.2	hypothetical protein CARUB_v10014504mg, partial	gbpln	Capsella rubella	AT3G16690.1 | Symbols: SWEET16, AtSWEET16 | Nodulin MtN3 family protein | chr3:5684563-5686425 REVERSE LENGTH=230	231	230	1.00E-112	99.6	84.8	92.2
Rsa1.0_00239.1.g9370.t1	gb|EOA31400.1| hypothetical protein CARUB_v10014579mg, partial [Capsella rubella]	188	222	5.00E-29	118.1	37.2	46.8	hypothetical protein CARUB_v10014579mg, partial	gbpln	Capsella rubella	AT3G16660.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr3:5676904-5677788 FORWARD LENGTH=180	188	180	6.00E-30	95.7	37.2	46.8
Rsa1.0_00239.1.g9371.t1	sp|Q944W6.1|TCTP_BRAOL RecName: Full=Translationally-controlled tumor protein homolog; Short=TCTP gi|16033628|gb|AAL13303.1|AF418663_1 translationally controlled tumor protein [Brassica oleracea]	168	168	2.00E-86	100.0	93.5	96.4	RecName: Full=Translationally-controlled tumor protein homolog; Short=TCTP gi|16033628|gb|AAL13303.1|AF418663_1 translationally controlled tumor protein	gbpln	Brassica oleracea	AT3G16640.1 | Symbols: TCTP | translationally controlled tumor protein | chr3:5669709-5670729 REVERSE LENGTH=168	168	168	4.00E-86	100.0	89.9	94.6
Rsa1.0_00239.1.g9372.t1	ref|XP_002885159.1| ATKINESIN-13A/KINESIN-13A [Arabidopsis lyrata subsp. lyrata] gi|297330999|gb|EFH61418.1| ATKINESIN-13A/KINESIN-13A [Arabidopsis lyrata subsp. lyrata]	789	783	0	99.2	91.3	94.7	ATKINESIN-13A/KINESIN-13A	gbpln	Arabidopsis lyrata	AT3G16630.2 | Symbols: ATKINESIN-13A, KINESIN-13A | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:5662660-5667261 REVERSE LENGTH=794	789	794	0	100.6	91.6	94.7
Rsa1.0_00239.1.g9373.t1	ref|XP_002875029.1| hypothetical protein ARALYDRAFT_912211 [Arabidopsis lyrata subsp. lyrata] gi|297320866|gb|EFH51288.1| hypothetical protein ARALYDRAFT_912211 [Arabidopsis lyrata subsp. lyrata]	567	653	1.00E-115	115.2	45.0	54.0	hypothetical protein ARALYDRAFT_912211	gbpln	Arabidopsis lyrata	AT3G16010.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr3:5434142-5436244 FORWARD LENGTH=642	567	642	2.00E-94	113.2	37.4	46.2

Rsa1.0_00239.1.g9374.t1	ref|XP_002885144.1| hypothetical protein ARALYDRAFT_479112 [Arabidopsis lyrata subsp. lyrata] gi|297330984|gb|EFH61403.1| hypothetical protein ARALYDRAFT_479112 [Arabidopsis lyrata subsp. lyrata]	286	345	9.00E-76	120.6	70.6	77.6	hypothetical protein ARALYDRAFT_479112	gbpln	Arabidopsis lyrata	AT3G16510.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:5617112-5618194 REVERSE LENGTH=360	286	360	8.00E-68	125.9	66.1	73.8
Rsa1.0_00239.1.g9375.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1460	1491	0	102.1	65.4	78.6	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1460	1262	1.00E-143	86.4	16.4	23.4
Rsa1.0_00239.1.g9376.t1	dbj|BAJ34060.1| unnamed protein product [Thellungiella halophila]	231	270	1.00E-107	116.9	85.7	90.0	unnamed protein product	----	----	AT3G16500.1 | Symbols: PAP1, IAA26 | phytochrome-associated protein 1 | chr3:5612801-5614208 REVERSE LENGTH=269	231	269	1.00E-103	116.5	82.3	86.6
Rsa1.0_00239.1.g9377.t1	ref|XP_002885142.1| IQ-domain 26 [Arabidopsis lyrata subsp. lyrata] gi|297330982|gb|EFH61401.1| IQ-domain 26 [Arabidopsis lyrata subsp. lyrata]	391	390	0	99.7	89.8	93.4	IQ-domain 26	gbpln	Arabidopsis lyrata	AT3G16490.1 | Symbols: IQD26 | IQ-domain 26 | chr3:5603962-5605489 REVERSE LENGTH=389	391	389	0	99.5	89.8	92.8
Rsa1.0_00239.1.g9378.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	700	536	2.00E-94	76.6	30.6	42.7	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	700	530	3.00E-52	75.7	13.7	17.3
Rsa1.0_00239.1.g9379.t1	emb|CAA72271.1| jasmonate inducible protein [Brassica napus]	452	680	0	150.4	75.4	84.5	jasmonate inducible protein	gbpln	Brassica napus	AT3G16460.2 | Symbols: | Mannose-binding lectin superfamily protein | chr3:5593029-5595522 FORWARD LENGTH=705	452	705	1.00E-156	156.0	63.9	77.2
Rsa1.0_00239.1.g9380.t1	ref|XP_002883008.1| hypothetical protein ARALYDRAFT_479101 [Arabidopsis lyrata subsp. lyrata] gi|297328848|gb|EFH59267.1| hypothetical protein ARALYDRAFT_479101 [Arabidopsis lyrata subsp. lyrata]	300	300	1.00E-143	100.0	83.3	92.0	hypothetical protein ARALYDRAFT_479101	gbpln	Arabidopsis lyrata	AT3G16440.1 | Symbols: ATMLP-300B, MEE36, MLP-300B | myrosinase-binding protein-like protein-300B | chr3:5586087-5587541 FORWARD LENGTH=300	300	300	1.00E-140	100.0	83.0	92.0
Rsa1.0_00239.1.g9381.t1	ref|XP_002883007.1| hypothetical protein ARALYDRAFT_897956 [Arabidopsis lyrata subsp. lyrata] gi|297328847|gb|EFH59266.1| hypothetical protein ARALYDRAFT_897956 [Arabidopsis lyrata subsp. lyrata]	92	298	4.00E-31	323.9	69.6	82.6	hypothetical protein ARALYDRAFT_897956	gbpln	Arabidopsis lyrata	AT3G16450.3 | Symbols: | Mannose-binding lectin superfamily protein | chr3:5588593-5589792 FORWARD LENGTH=300	92	300	9.00E-33	326.1	66.3	79.3
Rsa1.0_00240.1.g9382.t1	gb|ADA60971.1| stylish [Brassica rapa subsp. pekinensis]	361	363	1.00E-149	100.6	85.3	88.6	stylish	gbpln	Brassica rapa	AT3G51060.1 | Symbols: STY1, SRS1 | Lateral root primordium (LRP) protein-related | chr3:18964606-18966130 FORWARD LENGTH=370	361	370	1.00E-143	102.5	85.6	91.4
Rsa1.0_00240.1.g9383.t1	ref|XP_002877786.1| hypothetical protein ARALYDRAFT_485457 [Arabidopsis lyrata subsp. lyrata] gi|297323624|gb|EFH54045.1| hypothetical protein ARALYDRAFT_485457 [Arabidopsis lyrata subsp. lyrata]	226	231	1.00E-107	102.2	82.3	90.3	hypothetical protein ARALYDRAFT_485457	gbpln	Arabidopsis lyrata	AT3G51040.3 | Symbols: RTH | RTE1-homolog | chr3:18952281-18953060 REVERSE LENGTH=231	226	231	1.00E-105	102.2	79.6	88.9
Rsa1.0_00240.1.g9384.t1	gb|EOA24308.1| hypothetical protein CARUB_v10017549mg, partial [Capsella rubella]	559	351	1.00E-170	62.8	50.1	53.7	hypothetical protein CARUB_v10017549mg, partial	gbpln	Capsella rubella	AT3G51000.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:18945258-18946499 REVERSE LENGTH=323	559	323	1.00E-169	57.8	49.4	53.1
Rsa1.0_00240.1.g9385.t1	gb|AAK43926.1|AF370607_1 putative mitochondrial protein [Arabidopsis thaliana] gi|4835244|emb|CAB42922.1| putative mitochondrial protein [Arabidopsis thaliana] gi|20856863|gb|AAM26687.1| AT3g50930/F18B3_210 [Arabidopsis thaliana]	538	534	0	99.3	67.1	76.6	putative mitochondrial protein	gbpln	Arabidopsis thaliana	AT3G50930.1 | Symbols: BCS1 | cytochrome BC1 synthesis | chr3:18929817-18931547 FORWARD LENGTH=576	538	576	0	107.1	67.1	76.6
Rsa1.0_00240.1.g9386.t1	gb|EOA22499.1| hypothetical protein CARUB_v10003154mg [Capsella rubella]	146	143	1.00E-25	97.9	56.8	65.8	hypothetical protein CARUB_v10003154mg	gbpln	Capsella rubella	AT5G17280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Oxidoreductase-like, N-terminal (InterPro:IPR019180); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5686355-5686762 FORWARD LENGTH=135	146	135	1.00E-27	92.5	56.2	65.8
Rsa1.0_00240.1.g9387.t1	gb|EOA22340.1| hypothetical protein CARUB_v10002957mg [Capsella rubella]	484	503	0	103.9	79.1	86.2	hypothetical protein CARUB_v10002957mg	gbpln	Capsella rubella	AT5G17240.1 | Symbols: SDG40 | SET domain group 40 | chr5:5666854-5668849 FORWARD LENGTH=491	484	491	0	101.4	77.9	86.0
Rsa1.0_00240.1.g9388.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00240.1.g9389.t1	gb|EOA39894.1| hypothetical protein CARUB_v10008573mg [Capsella rubella]	1014	630	1.00E-81	62.1	17.3	24.1	hypothetical protein CARUB_v10008573mg	gbpln	Capsella rubella	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	1014	673	3.00E-63	66.4	13.7	19.5
Rsa1.0_00240.1.g9390.t1	emb|CAB80843.1| hypothetical protein [Arabidopsis thaliana]	170	381	5.00E-21	224.1	27.1	43.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G04775.1 | Symbols: | zinc ion binding | chr4:2431120-2431695 FORWARD LENGTH=150	170	150	2.00E-23	88.2	27.1	43.5
Rsa1.0_00240.1.g9391.t1	gb|AAF78267.1|AC020576_11 Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene [Arabidopsis thaliana]	942	1206	0	128.0	46.8	63.9	Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	942	719	3.00E-33	76.3	13.9	23.9
Rsa1.0_00240.1.g9392.t1	gb|AAM62787.1| phytoene synthase [Arabidopsis thaliana]	415	422	0	101.7	89.4	92.3	phytoene synthase	gbpln	Arabidopsis thaliana	AT5G17230.2 | Symbols: PSY | PHYTOENE SYNTHASE | chr5:5659839-5662087 REVERSE LENGTH=422	415	422	0	101.7	89.4	92.3
Rsa1.0_00240.1.g9393.t1	dbj|BAJ34302.1| unnamed protein product [Thellungiella halophila]	213	214	1.00E-107	100.5	86.9	94.4	unnamed protein product	----	----	AT5G17220.1 | Symbols: ATGSTF12, GST26, TT19, GSTF12 | glutathione S-transferase phi 12 | chr5:5658528-5659322 FORWARD LENGTH=214	213	214	1.00E-105	100.5	84.0	93.4
Rsa1.0_00240.1.g9394.t1	ref|XP_002871754.1| hypothetical protein ARALYDRAFT_488583 [Arabidopsis lyrata subsp. lyrata] gi|297317591|gb|EFH48013.1| hypothetical protein ARALYDRAFT_488583 [Arabidopsis lyrata subsp. lyrata]	211	212	8.00E-80	100.5	68.7	80.1	hypothetical protein ARALYDRAFT_488583	gbpln	Arabidopsis lyrata	AT5G17210.1 | Symbols: | Protein of unknown function (DUF1218) | chr5:5656519-5657970 FORWARD LENGTH=209	211	209	2.00E-78	99.1	66.4	78.7
Rsa1.0_00240.1.g9395.t1	gb|EOA22760.1| hypothetical protein CARUB_v10003473mg [Capsella rubella]	428	422	1.00E-177	98.6	70.1	82.2	hypothetical protein CARUB_v10003473mg	gbpln	Capsella rubella	AT5G17200.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:5653524-5655336 REVERSE LENGTH=421	428	421	1.00E-179	98.4	71.3	81.1
Rsa1.0_00240.1.g9396.t1	ref|NP_197221.1| uncharacterized protein [Arabidopsis thaliana] gi|10177064|dbj|BAB10506.1| unnamed protein product [Arabidopsis thaliana] gi|17381008|gb|AAL36316.1| unknown protein [Arabidopsis thaliana] gi|21280895|gb|AAM45077.1| unknown protein [Arabidopsis thaliana] gi|110741078|dbj|BAE98633.1| hypothetical protein [Arabidopsis thaliana] gi|332005011|gb|AED92394.1| uncharacterized protein AT5G17190 [Arabidopsis thaliana] gi|482555310|gb|EOA19502.1| hypothetical protein CARUB_v10002249mg [Capsella rubella]	130	130	3.00E-68	100.0	96.2	99.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G17190.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular protein transport; LOCATED IN: endomembrane system, integral to membrane, endoplasmic reticulum; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: B-cell receptor-associated 31-like (InterPro:IPR008417); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03160.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5652310-5652702 FORWARD LENGTH=130	130	130	5.00E-71	100.0	96.2	99.2
Rsa1.0_00240.1.g9397.t1	gb|EOA21343.1| hypothetical protein CARUB_v10001706mg [Capsella rubella]	277	271	1.00E-135	97.8	89.5	93.5	hypothetical protein CARUB_v10001706mg	gbpln	Capsella rubella	AT5G17170.1 | Symbols: ENH1 | rubredoxin family protein | chr5:5649335-5650975 FORWARD LENGTH=271	277	271	1.00E-132	97.8	89.5	93.9
Rsa1.0_00240.1.g9398.t1	ref|XP_002873814.1| hypothetical protein ARALYDRAFT_488576 [Arabidopsis lyrata subsp. lyrata] gi|297319651|gb|EFH50073.1| hypothetical protein ARALYDRAFT_488576 [Arabidopsis lyrata subsp. lyrata]	601	568	1.00E-136	94.5	61.2	68.4	hypothetical protein ARALYDRAFT_488576	gbpln	Arabidopsis lyrata	AT5G17160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03130.1); Has 14330 Blast hits to 10381 proteins in 896 species: Archae - 94; Bacteria - 2881; Metazoa - 4019; Fungi - 1576; Plants - 515; Viruses - 110; Other Eukaryotes - 5135 (source: NCBI BLink). | chr5:5639843-5642427 REVERSE LENGTH=569	601	569	1.00E-134	94.7	59.7	68.4
Rsa1.0_00240.1.g9399.t1	gb|EOA20368.1| hypothetical protein CARUB_v10000682mg [Capsella rubella]	352	533	4.00E-63	151.4	53.1	63.9	hypothetical protein CARUB_v10000682mg	gbpln	Capsella rubella	AT5G17160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03130.1); Has 14330 Blast hits to 10381 proteins in 896 species: Archae - 94; Bacteria - 2881; Metazoa - 4019; Fungi - 1576; Plants - 515; Viruses - 110; Other Eukaryotes - 5135 (source: NCBI BLink). | chr5:5639843-5642427 REVERSE LENGTH=569	352	569	5.00E-65	161.6	50.3	58.5

Rsa1.0_00240.1.g9400.t1	ref|NP_197207.1| Flavonoid 3-O-glucosyltransferase [Arabidopsis thaliana] gi|75311137|sp|Q9LFJ8.1|U78D2_ARATH RecName: Full=UDP-glycosyltransferase 78D2; AltName: Full=Anthocyanin 3-O-glucosyltransferase; AltName: Full=Flavonol 3-O-glucosyltransferase.; AltName: Full=UDP glucose:flavonoid 3-O-glucosyltransferase gi|9755706|emb|CAC01718.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|18252199|gb|AAL61932.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|22136122|gb|AAM91139.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|332004994|gb|AED92377.1| Flavonoid 3-O-glucosyltransferase [Arabidopsis thaliana]	761	460	0	60.4	45.9	51.6	Flavonoid 3-O-glucosyltransferase	gbpln	Arabidopsis thaliana	AT5G17050.1 | Symbols: UGT78D2 | UDP-glucosyl transferase 78D2 | chr5:5607828-5609392 REVERSE LENGTH=460	761	460	0	60.4	45.9	51.6
Rsa1.0_00240.1.g9401.t1	ref|NP_197207.1| Flavonoid 3-O-glucosyltransferase [Arabidopsis thaliana] gi|75311137|sp|Q9LFJ8.1|U78D2_ARATH RecName: Full=UDP-glycosyltransferase 78D2; AltName: Full=Anthocyanin 3-O-glucosyltransferase; AltName: Full=Flavonol 3-O-glucosyltransferase.; AltName: Full=UDP glucose:flavonoid 3-O-glucosyltransferase gi|9755706|emb|CAC01718.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|18252199|gb|AAL61932.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|22136122|gb|AAM91139.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|332004994|gb|AED92377.1| Flavonoid 3-O-glucosyltransferase [Arabidopsis thaliana]	460	460	0	100.0	78.9	87.8	Flavonoid 3-O-glucosyltransferase	gbpln	Arabidopsis thaliana	AT5G17050.1 | Symbols: UGT78D2 | UDP-glucosyl transferase 78D2 | chr5:5607828-5609392 REVERSE LENGTH=460	460	460	0	100.0	78.9	87.8
Rsa1.0_00240.1.g9402.t1	ref|XP_002871746.1| hypothetical protein ARALYDRAFT_909689 [Arabidopsis lyrata subsp. lyrata] gi|297317583|gb|EFH48005.1| hypothetical protein ARALYDRAFT_909689 [Arabidopsis lyrata subsp. lyrata]	1087	1076	0	99.0	95.1	97.1	hypothetical protein ARALYDRAFT_909689	gbpln	Arabidopsis lyrata	AT5G17020.1 | Symbols: XPO1A, ATCRM1, ATXPO1, XPO1, HIT2 | exportin 1A | chr5:5594904-5602467 FORWARD LENGTH=1075	1087	1075	0	98.9	94.5	96.5
Rsa1.0_00240.1.g9403.t1	ref|XP_002873804.1| sugar transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297319641|gb|EFH50063.1| sugar transporter family protein [Arabidopsis lyrata subsp. lyrata]	493	502	0	101.8	89.0	92.9	sugar transporter family protein	gbpln	Arabidopsis lyrata	AT5G17010.3 | Symbols: | Major facilitator superfamily protein | chr5:5587851-5592332 REVERSE LENGTH=503	493	503	0	102.0	89.7	92.9
Rsa1.0_00240.1.g9404.t1	gb|AAD48963.1|AF147263_5 contains similarity to transposases [Arabidopsis thaliana] gi|7267311|emb|CAB81093.1| AT4g05510 [Arabidopsis thaliana]	288	604	6.00E-50	209.7	33.7	39.9	contains similarity to transposases	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	288	696	2.00E-15	241.7	17.0	29.2
Rsa1.0_00240.1.g9405.t2	ref|XP_002873800.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319637|gb|EFH50059.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	348	346	1.00E-175	99.4	85.6	91.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G16960.1 | Symbols: | Zinc-binding dehydrogenase family protein | chr5:5574537-5575884 REVERSE LENGTH=346	348	346	1.00E-173	99.4	83.6	89.9
Rsa1.0_00240.1.g9406.t4	ref|NP_197195.2| AAA-type ATPase family protein [Arabidopsis thaliana] gi|19424059|gb|AAL87351.1| unknown protein [Arabidopsis thaliana] gi|22136966|gb|AAM91712.1| unknown protein [Arabidopsis thaliana] gi|332004976|gb|AED92359.1| AAA-type ATPase family protein [Arabidopsis thaliana]	655	644	0	98.3	83.8	88.1	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT5G16930.1 | Symbols: | AAA-type ATPase family protein | chr5:5568578-5571565 FORWARD LENGTH=644	655	644	0	98.3	83.8	88.1

Rsa1.0_00240.1.g9407.t1	gb|ABK28699.1| unknown [Arabidopsis thaliana]	257	257	4.00E-95	100.0	73.9	82.5	unknown	gbpln	Arabidopsis thaliana	AT5G16920.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr5:5567084-5567854 FORWARD LENGTH=256	257	256	2.00E-97	99.6	73.9	82.5
Rsa1.0_00240.1.g9408.t1	ref|XP_002871742.1| hypothetical protein ARALYDRAFT_488554 [Arabidopsis lyrata subsp. lyrata] gi|297317579|gb|EFH48001.1| hypothetical protein ARALYDRAFT_488554 [Arabidopsis lyrata subsp. lyrata]	1139	1143	0	100.4	89.8	95.0	hypothetical protein ARALYDRAFT_488554	gbpln	Arabidopsis lyrata	AT5G16910.1 | Symbols: ATCSLD2, CSLD2 | cellulose-synthase like D2 | chr5:5561679-5565290 FORWARD LENGTH=1145	1139	1145	0	100.5	89.0	94.7
Rsa1.0_00241.1.g9409.t1	ref|NP_178530.2| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|50058853|gb|AAT69171.1| hypothetical protein At2g04500 [Arabidopsis thaliana] gi|330250746|gb|AEC05840.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	135	495	6.00E-15	366.7	41.5	60.7	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G04500.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:1568492-1569979 FORWARD LENGTH=495	135	495	1.00E-17	366.7	41.5	60.7
Rsa1.0_00241.1.g9410.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00241.1.g9411.t1	ref|XP_002883420.1| hypothetical protein ARALYDRAFT_479845 [Arabidopsis lyrata subsp. lyrata] gi|297329260|gb|EFH59679.1| hypothetical protein ARALYDRAFT_479845 [Arabidopsis lyrata subsp. lyrata]	616	614	0	99.7	92.4	95.5	hypothetical protein ARALYDRAFT_479845	gbpln	Arabidopsis lyrata	AT3G23300.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:8333521-8335902 FORWARD LENGTH=611	616	611	0	99.2	91.9	95.9
Rsa1.0_00241.1.g9412.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00241.1.g9413.t4	gb|EOA30221.1| hypothetical protein CARUB_v10013343mg [Capsella rubella]	533	568	0	106.6	85.6	89.5	hypothetical protein CARUB_v10013343mg	gbpln	Capsella rubella	AT3G23310.1 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr3:8339799-8343355 FORWARD LENGTH=568	533	568	0	106.6	84.8	88.2
Rsa1.0_00241.1.g9414.t1	gb|AAF79687.1|AC022314_28 F9C16.9 [Arabidopsis thaliana]	891	946	0	106.2	52.0	64.6	F9C16.9	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	891	719	2.00E-20	80.7	13.0	24.9
Rsa1.0_00241.1.g9415.t1	gb|AAF88011.1| Hypothetical protein T10I18.4 [Arabidopsis thaliana]	129	156	7.00E-28	120.9	49.6	66.7	Hypothetical protein T10I18.4	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00241.1.g9416.t2	ref|XP_004245305.1| PREDICTED: uncharacterized protein At3g23325-like [Solanum lycopersicum]	130	87	2.00E-45	66.9	65.4	66.9	PREDICTED: uncharacterized protein At3g23325-like	gbpln	Solanum lycopersicum	AT3G23325.1 | Symbols: | Splicing factor 3B subunit 5/RDS3 complex subunit 10 | chr3:8345808-8346856 FORWARD LENGTH=87	130	87	3.00E-47	66.9	64.6	66.2
Rsa1.0_00241.1.g9417.t4	ref|XP_002883423.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329263|gb|EFH59682.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	1085	679	0	62.6	55.4	59.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G23330.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:8347200-8349347 FORWARD LENGTH=715	1085	715	0	65.9	56.3	60.5
Rsa1.0_00241.1.g9418.t2	gb|EOA32666.1| hypothetical protein CARUB_v10015964mg [Capsella rubella]	258	264	1.00E-105	102.3	74.4	83.7	hypothetical protein CARUB_v10015964mg	gbpln	Capsella rubella	AT3G23360.1 | Symbols: | Protein phosphatase 2C family protein | chr3:8355257-8356381 REVERSE LENGTH=260	258	260	1.00E-106	100.8	74.4	83.3
Rsa1.0_00241.1.g9419.t1	ref|XP_002883427.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297329267|gb|EFH59686.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	615	785	1.00E-173	127.6	61.5	76.1	nucleic acid binding protein	gbpln	Arabidopsis lyrata	AT3G23370.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:8357613-8360792 FORWARD LENGTH=811	615	811	1.00E-138	131.9	48.9	60.8
Rsa1.0_00241.1.g9420.t1	gb|EOA32791.1| hypothetical protein CARUB_v10016101mg [Capsella rubella]	171	205	1.00E-49	119.9	73.7	83.0	hypothetical protein CARUB_v10016101mg	gbpln	Capsella rubella	AT3G23380.1 | Symbols: RIC5 | ROP-interactive CRIB motif-containing protein 5 | chr3:8373947-8374708 FORWARD LENGTH=193	171	193	7.00E-48	112.9	70.8	81.9
Rsa1.0_00241.1.g9421.t1	gb|AAK94425.1|AF398144_1 60S ribosomal protein L144 [Brassica rapa subsp. pekinensis]	105	119	2.00E-52	113.3	100.0	100.0	60S ribosomal protein L144	gbpln	Brassica rapa	AT4G14320.1 | Symbols: | Zinc-binding ribosomal protein family protein | chr4:8242684-8243805 REVERSE LENGTH=105	105	105	4.00E-53	100.0	96.2	97.1
Rsa1.0_00241.1.g9422.t1	dbj|BAJ34097.1| unnamed protein product [Thellungiella halophila]	279	282	1.00E-130	101.1	88.2	94.3	unnamed protein product	----	----	AT3G23400.1 | Symbols: FIB4 | Plastid-lipid associated protein PAP / fibrillin family protein | chr3:8376636-8378225 REVERSE LENGTH=284	279	284	1.00E-109	101.8	80.3	85.3

Rsa1.0_00241.1.g9423.t1	ref|XP_002883430.1| hypothetical protein ARALYDRAFT_479855 [Arabidopsis lyrata subsp. lyrata] gi|297329270|gb|EFH59689.1| hypothetical protein ARALYDRAFT_479855 [Arabidopsis lyrata subsp. lyrata]	744	743	0	99.9	84.8	91.4	hypothetical protein ARALYDRAFT_479855	gbpln	Arabidopsis lyrata	AT3G23410.1 | Symbols: ATFAO3, FAO3 | fatty alcohol oxidase 3 | chr3:8382860-8386024 FORWARD LENGTH=746	744	746	0	100.3	82.7	90.6
Rsa1.0_00241.1.g9424.t1	gb|EOA29920.1| hypothetical protein CARUB_v10013014mg [Capsella rubella]	784	785	0	100.1	92.3	96.2	hypothetical protein CARUB_v10013014mg	gbpln	Capsella rubella	AT3G23430.1 | Symbols: PHO1, ATPHO1 | phosphate 1 | chr3:8387818-8393242 REVERSE LENGTH=782	784	782	0	99.7	88.3	93.0
Rsa1.0_00242.1.g9425.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00242.1.g9426.t1	gb|EOA39560.1| hypothetical protein CARUB_v10008178mg [Capsella rubella]	178	1022	2.00E-69	574.2	74.7	82.0	hypothetical protein CARUB_v10008178mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	178	1019	4.00E-65	572.5	73.6	80.9
Rsa1.0_00242.1.g9427.t1	gb|AAD32756.1| putative replication protein A1 [Arabidopsis thaliana]	451	458	1.00E-66	101.6	31.9	53.0	putative replication protein A1	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	451	566	2.00E-67	125.5	33.3	57.0
Rsa1.0_00242.1.g9428.t4	gb|EOA39560.1| hypothetical protein CARUB_v10008178mg [Capsella rubella]	2256	1022	0	45.3	22.4	24.7	hypothetical protein CARUB_v10008178mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	2256	1019	0	45.2	22.0	24.9
Rsa1.0_00242.1.g9429.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	994	1142	1.00E-160	114.9	30.0	41.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	994	575	1.00E-42	57.8	12.9	20.9
Rsa1.0_00242.1.g9430.t2	gb|AAD28663.1| hypothetical protein [Arabidopsis thaliana]	359	356	1.00E-19	99.2	18.9	32.6	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00242.1.g9431.t1	gb|AAD20433.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	127	889	5.00E-40	700.0	58.3	75.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00242.1.g9432.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	960	704	1.00E-101	73.3	21.4	24.3	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00242.1.g9433.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	617	723	1.00E-174	117.2	53.5	68.6	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	617	696	3.00E-41	112.8	20.9	37.9
Rsa1.0_00242.1.g9434.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00242.1.g9435.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00242.1.g9436.t1	gb|EOA38810.1| hypothetical protein CARUB_v10011128mg [Capsella rubella]	216	1008	1.00E-84	466.7	74.1	83.3	hypothetical protein CARUB_v10011128mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	216	1019	5.00E-67	471.8	61.6	71.3
Rsa1.0_00242.1.g9437.t2	gb|EOA38810.1| hypothetical protein CARUB_v10011128mg [Capsella rubella]	593	1008	0	170.0	74.9	84.5	hypothetical protein CARUB_v10011128mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	593	1019	0	171.8	73.7	84.0
Rsa1.0_00242.1.g9438.t1	pir||E85079 hypothetical protein AT4g08070 [imported] - Arabidopsis thaliana gi|5724773|gb|AAD48077.1|AF160183_4 contains similarity to Antirrhinum majus hypothetical protein TNP2 (GB:X57297); may be a pseudogene [Arabidopsis thaliana] gi|7267447|emb|CAB81144.1| AT4g08070 [Arabidopsis thaliana]	99	767	3.00E-33	774.7	68.7	76.8	hypothetical protein AT4g08070	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00242.1.g9439.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00242.1.g9440.t1	gb|ABD65060.1| hypothetical protein 27.t00039 [Brassica oleracea]	157	1367	1.00E-80	870.7	92.4	94.9	hypothetical protein 27.t00039	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00243.1.g9441.t1	gb|EOA13979.1| hypothetical protein CARUB_v10027111mg [Capsella rubella]	201	217	6.00E-60	108.0	66.7	78.1	hypothetical protein CARUB_v10027111mg	gbpln	Capsella rubella	AT5G48657.2 | Symbols: | defense protein-related | chr5:19734120-19735516 REVERSE LENGTH=219	201	219	8.00E-58	109.0	65.7	77.1
Rsa1.0_00243.1.g9442.t1	ref|XP_002865657.1| hypothetical protein ARALYDRAFT_494930 [Arabidopsis lyrata subsp. lyrata] gi|297311492|gb|EFH41916.1| hypothetical protein ARALYDRAFT_494930 [Arabidopsis lyrata subsp. lyrata]	199	203	5.00E-68	102.0	78.9	83.4	hypothetical protein ARALYDRAFT_494930	gbpln	Arabidopsis lyrata	AT5G48655.3 | Symbols: | RING/U-box superfamily protein | chr5:19731575-19732486 REVERSE LENGTH=203	199	203	8.00E-69	102.0	76.9	80.9
Rsa1.0_00243.1.g9443.t1	dbj|BAB10698.1| RNA-binding protein-like [Arabidopsis thaliana]	503	461	1.00E-125	91.7	57.1	66.4	RNA-binding protein-like	gbpln	Arabidopsis thaliana	AT5G48650.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr5:19727279-19729533 FORWARD LENGTH=458	503	458	1.00E-125	91.1	56.5	65.8

Rsa1.0_00243.1.g9444.t2	gb|EOA13886.1| hypothetical protein CARUB_v10026989mg [Capsella rubella]	271	252	1.00E-125	93.0	81.5	88.9	hypothetical protein CARUB_v10026989mg	gbpln	Capsella rubella	AT5G48640.1 | Symbols: | Cyclin family protein | chr5:19723653-19725641 REVERSE LENGTH=253	271	253	1.00E-126	93.4	81.9	88.6
Rsa1.0_00243.1.g9445.t1	gb|EOA13279.1| hypothetical protein CARUB_v10026310mg [Capsella rubella] gi|482549086|gb|EOA13280.1| hypothetical protein CARUB_v10026310mg [Capsella rubella]	465	484	1.00E-133	104.1	65.4	77.6	hypothetical protein CARUB_v10026310mg	gbpln	Capsella rubella	AT5G48610.1 | Symbols: | unknown protein; Has 43043 Blast hits to 23768 proteins in 1327 species: Archae - 108; Bacteria - 3952; Metazoa - 17076; Fungi - 3614; Plants - 1643; Viruses - 204; Other Eukaryotes - 16446 (source: NCBI BLink). | chr5:19712614-19714861 FORWARD LENGTH=354	465	354	2.00E-72	76.1	42.4	50.5
Rsa1.0_00243.1.g9446.t1	gb|EOA13641.1| hypothetical protein CARUB_v10026712mg [Capsella rubella]	343	345	1.00E-152	100.6	81.6	87.8	hypothetical protein CARUB_v10026712mg	gbpln	Capsella rubella	AT5G48590.1 | Symbols: | Protein of unknown function (DUF760) | chr5:19698476-19699771 FORWARD LENGTH=344	343	344	1.00E-150	100.3	78.4	85.1
Rsa1.0_00243.1.g9447.t1	ref|NP_199669.1| FK506-binding protein 2-2 [Arabidopsis thaliana] gi|23396587|sp|Q38936.2|FK152_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP15-2; Short=PPIase FKBP15-2; AltName: Full=15 kDa FK506-binding protein; Short=15 kDa FKBP; AltName: Full=FK506-binding protein 15-2; Short=AtFKBP15-2; AltName: Full=FK506-binding protein 2-2; AltName: Full=Immunophilin FKBP15-2; AltName: Full=Rotamase; Flags: Precursor gi|13877793|gb|AAK43974.1|AF370159_1 putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|10177348|dbj|BAB10691.1| peptidyl-prolyl cis-trans isomerase-like protein [Arabidopsis thaliana] gi|16323516|gb|AAL15252.1| putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|21553433|gb|AAM62526.1| peptidyl-prolyl cis-trans isomerase-like protein [Arabidopsis thaliana] gi|332008308|gb|AED95691.1| FK506-binding protein 2-2 [Arabidopsis thaliana]	176	163	2.00E-68	92.6	79.0	82.4	FK506-binding protein 2-2	gbpln	Arabidopsis thaliana	AT5G48580.1 | Symbols: FKBP15-2 | FK506- and rapamycin-binding protein 15 kD-2 | chr5:19696156-19697304 REVERSE LENGTH=163	176	163	9.00E-71	92.6	79.0	82.4
Rsa1.0_00243.1.g9448.t1	ref|XP_002865651.1| hypothetical protein ARALYDRAFT_494919 [Arabidopsis lyrata subsp. lyrata] gi|297311486|gb|EFH41910.1| hypothetical protein ARALYDRAFT_494919 [Arabidopsis lyrata subsp. lyrata]	573	570	0	99.5	89.0	94.9	hypothetical protein ARALYDRAFT_494919	gbpln	Arabidopsis lyrata	AT5G48570.1 | Symbols: ROF2, ATFKBP65, FKBP65 | FKBP-type peptidyl-prolyl cis-trans isomerase family protein | chr5:19690746-19693656 REVERSE LENGTH=578	573	578	0	100.9	87.1	93.9
Rsa1.0_00243.1.g9449.t1	gb|AAM10957.1|AF488610_1 putative bHLH transcription factor [Arabidopsis thaliana]	417	498	1.00E-143	119.4	76.3	80.3	putative bHLH transcription factor	gbpln	Arabidopsis thaliana	AT5G48560.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:19684160-19686871 FORWARD LENGTH=498	417	498	1.00E-144	119.4	74.1	78.9
Rsa1.0_00243.1.g9450.t1	ref|XP_002863905.1| histidine triad family protein [Arabidopsis lyrata subsp. lyrata] gi|297309740|gb|EFH40164.1| histidine triad family protein [Arabidopsis lyrata subsp. lyrata]	195	198	6.00E-92	101.5	90.3	92.3	histidine triad family protein	gbpln	Arabidopsis lyrata	AT5G48545.1 | Symbols: HINT3 | histidine triad nucleotide-binding 3 | chr5:19676228-19677945 FORWARD LENGTH=197	195	197	1.00E-90	101.0	88.2	90.3
Rsa1.0_00243.1.g9451.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00243.1.g9452.t1	ref|XP_002865649.1| hypothetical protein ARALYDRAFT_494916 [Arabidopsis lyrata subsp. lyrata] gi|297311484|gb|EFH41908.1| hypothetical protein ARALYDRAFT_494916 [Arabidopsis lyrata subsp. lyrata]	261	263	1.00E-134	100.8	88.5	93.5	hypothetical protein ARALYDRAFT_494916	gbpln	Arabidopsis lyrata	AT5G48540.1 | Symbols: | receptor-like protein kinase-related family protein | chr5:19669096-19669887 REVERSE LENGTH=263	261	263	1.00E-133	100.8	86.6	92.0
Rsa1.0_00243.1.g9453.t1	ref|XP_002882529.1| hypothetical protein ARALYDRAFT_896908 [Arabidopsis lyrata subsp. lyrata] gi|297328369|gb|EFH58788.1| hypothetical protein ARALYDRAFT_896908 [Arabidopsis lyrata subsp. lyrata]	236	235	1.00E-104	99.6	83.1	90.3	hypothetical protein ARALYDRAFT_896908	gbpln	Arabidopsis lyrata	AT3G07440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48530.1); Has 37 Blast hits to 37 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:2381411-2382902 FORWARD LENGTH=235	236	235	1.00E-103	99.6	80.1	89.4

Rsa1.0_00243.1.g9454.t1	ref|NP_199663.2| uncharacterized protein [Arabidopsis thaliana] gi|110737416|dbj|BAF00652.1| hypothetical protein [Arabidopsis thaliana] gi|332008298|gb|AED95681.1| uncharacterized protein AT5G48520 [Arabidopsis thaliana]	636	617	0	97.0	93.7	95.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G48520.1 | Symbols: | unknown protein; Has 609 Blast hits to 593 proteins in 129 species: Archae − 0; Bacteria − 41; Metazoa − 390; Fungi − 40; Plants − 64; Viruses − 0; Other Eukaryotes − 74 (source: NCBI BLink). | chr5:19661407−19666147 FORWARD LENGTH=617	636	617	0	97.0	93.7	95.6
Rsa1.0_00243.1.g9455.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00243.1.g9456.t1	ref|NP_568700.1| uncharacterized protein [Arabidopsis thaliana] gi|21553505|gb|AAM62598.1| unknown [Arabidopsis thaliana] gi|27754391|gb|AAO22644.1| unknown protein [Arabidopsis thaliana] gi|28393943|gb|AAO42379.1| unknown protein [Arabidopsis thaliana] gi|332008295|gb|AED95678.1| uncharacterized protein AT5G48500 [Arabidopsis thaliana]	166	167	2.00E−68	100.6	84.9	90.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G48500.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10930.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:19653235−19654017 FORWARD LENGTH=167	166	167	6.00E−71	100.6	84.9	90.4
Rsa1.0_00243.1.g9457.t1	gb|EOA12589.1| hypothetical protein CARUB_v10027068mg, partial [Capsella rubella]	166	226	2.00E−43	136.1	65.7	76.5	hypothetical protein CARUB_v10027068mg, partial	gbpln	Capsella rubella	AT5G48480.1 | Symbols: | Lactoylglutathione lyase / glyoxalase I family protein | chr5:19644814−19645658 FORWARD LENGTH=166	166	166	1.00E−44	100.0	65.7	74.7
Rsa1.0_00243.1.g9458.t2	dbj|BAA96967.1| unnamed protein product [Arabidopsis thaliana]	275	364	1.00E−65	132.4	53.1	59.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G48470.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:19641810−19644127 FORWARD LENGTH=397	275	397	2.00E−65	144.4	53.1	59.3
Rsa1.0_00243.1.g9459.t1	ref|NP_186837.1| uncharacterized protein [Arabidopsis thaliana] gi|6091728|gb|AAF03440.1|AC010797_16 hypothetical protein [Arabidopsis thaliana] gi|6513943|gb|AAF14847.1|AC011664_29 hypothetical protein [Arabidopsis thaliana] gi|332640208|gb|AEE73729.1| uncharacterized protein AT3G01880 [Arabidopsis thaliana]	987	592	0	60.0	38.6	45.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01880.1 | Symbols: | Plant protein of unknown function (DUF946) | chr3:307782−309560 FORWARD LENGTH=592	987	592	0	60.0	38.6	45.1
Rsa1.0_00243.1.g9460.t1	gb|ABO71664.1| ZIP4/SPO22 [Arabidopsis thaliana]	978	936	0	95.7	84.9	90.3	ZIP4/SPO22	gbpln	Arabidopsis thaliana	AT5G48390.1 | Symbols: ATZIP4 | Tetratricopeptide repeat (TPR)−like superfamily protein | chr5:19612078−19615363 FORWARD LENGTH=936	978	936	0	95.7	84.9	90.2
Rsa1.0_00243.1.g9461.t1	gb|EOA13159.1| hypothetical protein CARUB_v10026179mg [Capsella rubella]	597	556	0	93.1	80.7	85.8	hypothetical protein CARUB_v10026179mg	gbpln	Capsella rubella	AT5G48385.1 | Symbols: | FRIGIDA−like protein | chr5:19609471−19611712 FORWARD LENGTH=558	597	558	0	93.5	80.1	85.1
Rsa1.0_00243.1.g9462.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	296	441	2.00E−67	149.0	43.6	62.2	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr3:8789471−8793208 FORWARD LENGTH=746	296	746	1.00E−54	252.0	35.8	49.7
Rsa1.0_00243.1.g9463.t1	dbj|BAJ33754.1| unnamed protein product [Thellungiella halophila]	624	622	0	99.7	84.1	89.4	unnamed protein product	----	----	AT5G48380.1 | Symbols: BIR1 | BAK1−interacting receptor−like kinase 1 | chr5:19604584−19606532 REVERSE LENGTH=620	624	620	0	99.4	79.2	87.7
Rsa1.0_00243.1.g9464.t1	dbj|BAA98193.1| unnamed protein product [Arabidopsis thaliana]	816	780	0	95.6	62.9	74.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G48360.1 | Symbols: | Actin−binding FH2 (formin homology 2) family protein | chr5:19595716−19598331 FORWARD LENGTH=782	816	782	0	95.8	63.0	74.6
Rsa1.0_00243.1.g9465.t1	ref|XP_002863889.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309724|gb|EFH40148.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	494	515	0	104.3	66.8	75.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G48340.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:19590785−19592487 FORWARD LENGTH=510	494	510	0	103.2	66.2	75.1
Rsa1.0_00243.1.g9466.t2	ref|XP_003528812.1| PREDICTED: 60S ribosomal protein L5−like [Glycine max]	322	298	1.00E−136	92.5	73.0	82.3	PREDICTED: 60S ribosomal protein L5−like	gbenv/gbpln	Glycine max	AT5G39740.2 | Symbols: RPL5B | ribosomal protein L5 B | chr5:15903484−15905185 FORWARD LENGTH=301	322	301	1.00E−135	93.5	72.7	80.4

Rsa1.0_00243.1.g9467.t1	ref|NP_001190489.1| uncharacterized protein [Arabidopsis thaliana] gi|332008267|gb|AED95650.1| uncharacterized protein AT5G48310 [Arabidopsis thaliana]	1139	1129	0	99.1	80.2	87.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G48310.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24610.1). | chr5:19574961-19580362 REVERSE LENGTH=1129	1139	1129	0	99.1	80.2	87.7
Rsa1.0_00244.1.g9468.t1	gb|EOA28312.1| hypothetical protein CARUB_v10024512mg [Capsella rubella]	306	595	1.00E-161	194.4	86.3	95.4	hypothetical protein CARUB_v10024512mg	gbpln	Capsella rubella	AT2G47040.1 | Symbols: VGD1 | Plant invertase/pectin methylesterase inhibitor superfamily | chr2:19328186-19330060 REVERSE LENGTH=595	306	595	1.00E-163	194.4	85.9	95.4
Rsa1.0_00244.1.g9469.t1	ref|XP_002882100.1| P-glycoprotein 4, P-glycoprotein4 [Arabidopsis lyrata subsp. lyrata] gi|297327939|gb|EFH58359.1| P-glycoprotein 4, P-glycoprotein4 [Arabidopsis lyrata subsp. lyrata]	1287	1286	0	99.9	93.2	97.4	P-glycoprotein 4, P-glycoprotein4	gbpln	Arabidopsis lyrata	AT2G47000.1 | Symbols: MDR4, PGP4, ABCB4, ATPGP4 | ATP binding cassette subfamily B4 | chr2:19310008-19314750 REVERSE LENGTH=1286	1287	1286	0	99.9	93.2	97.3
Rsa1.0_00244.1.g9470.t1	gb|ADB93654.2| indole-3-acetic acid inducible 20 [Arabidopsis thaliana]	165	164	2.00E-59	99.4	74.5	78.8	indole-3-acetic acid inducible 20	gbpln	Arabidopsis thaliana	AT2G46990.1 | Symbols: IAA20 | indole-3-acetic acid inducible 20 | chr2:19307861-19308869 FORWARD LENGTH=175	165	175	1.00E-59	106.1	80.6	84.8
Rsa1.0_00244.1.g9471.t1	ref|XP_002862757.1| hypothetical protein ARALYDRAFT_497309 [Arabidopsis lyrata subsp. lyrata] gi|297308467|gb|EFH39015.1| hypothetical protein ARALYDRAFT_497309 [Arabidopsis lyrata subsp. lyrata]	308	312	1.00E-126	101.3	84.4	89.6	hypothetical protein ARALYDRAFT_497309	gbpln	Arabidopsis lyrata	AT2G46870.1 | Symbols: NGA1 | AP2/B3-like transcriptional factor family protein | chr2:19261313-19262245 FORWARD LENGTH=310	308	310	1.00E-126	100.6	84.4	88.3
Rsa1.0_00244.1.g9472.t1	ref|XP_002880270.1| hypothetical protein ARALYDRAFT_483853 [Arabidopsis lyrata subsp. lyrata] gi|297326109|gb|EFH56529.1| hypothetical protein ARALYDRAFT_483853 [Arabidopsis lyrata subsp. lyrata]	207	216	1.00E-115	104.3	97.1	98.1	hypothetical protein ARALYDRAFT_483853	gbpln	Arabidopsis lyrata	AT2G46860.1 | Symbols: AtPPa3, PPa3 | pyrophosphorylase 3 | chr2:19253843-19255060 FORWARD LENGTH=216	207	216	1.00E-116	104.3	96.1	97.6
Rsa1.0_00244.1.g9473.t3	ref|NP_190471.1| FBD-associated F-box protein [Arabidopsis thaliana] gi|75337428|sp|Q9SMT9.1|FBD9_ARATH RecName: Full=FBD-associated F-box protein At3g49020 gi|6522564|emb|CAB62008.1| putative protein [Arabidopsis thaliana] gi|67633680|gb|AAY78764.1| F-box family protein [Arabidopsis thaliana] gi|111074508|gb|ABH04627.1| At3g49020 [Arabidopsis thaliana] gi|332644966|gb|AEE78487.1| FBD-associated F-box protein [Arabidopsis thaliana]	397	447	3.00E-98	112.6	57.2	68.5	FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT3G49020.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr3:18169079-18170660 FORWARD LENGTH=447	397	447	1.00E-101	112.6	57.2	68.5
Rsa1.0_00244.1.g9474.t4	gb|AAC33963.1| contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]	1430	1633	0	114.2	64.4	74.2	contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19)	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1430	1262	1.00E-173	88.3	20.4	27.1
Rsa1.0_00244.1.g9475.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00244.1.g9476.t1	gb|EOA28676.1| hypothetical protein CARUB_v10024900mg [Capsella rubella]	1332	901	0	67.6	55.4	61.4	hypothetical protein CARUB_v10024900mg	gbpln	Capsella rubella	AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907-10814173 REVERSE LENGTH=337	1332	337	6.00E-72	25.3	10.4	13.9
Rsa1.0_00244.1.g9477.t3	ref|XP_002863367.1| hypothetical protein ARALYDRAFT_356287 [Arabidopsis lyrata subsp. lyrata] gi|297309202|gb|EFH39626.1| hypothetical protein ARALYDRAFT_356287 [Arabidopsis lyrata subsp. lyrata]	277	426	2.00E-39	153.8	35.0	42.6	hypothetical protein ARALYDRAFT_356287	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00244.1.g9478.t1	gb|EMT02183.1| hypothetical protein F775_04897 [Aegilops tauschii]	376	765	3.00E-21	203.5	12.2	14.1	hypothetical protein F775_04897	gbpln	Aegilops tauschii	#	#	#	#	#	#	#
Rsa1.0_00244.1.g9479.t1	gb|EOA27989.1| hypothetical protein CARUB_v10024165mg [Capsella rubella]	168	175	5.00E-41	104.2	65.5	72.0	hypothetical protein CARUB_v10024165mg	gbpln	Capsella rubella	AT2G46820.2 | Symbols: PTAC8, TMP14, PSAP, PSI-P | photosystem I P subunit | chr2:19243729-19244870 FORWARD LENGTH=174	168	174	2.00E-30	103.6	59.5	67.9
Rsa1.0_00244.1.g9480.t1	ref|XP_002880266.1| hypothetical protein ARALYDRAFT_904152 [Arabidopsis lyrata subsp. lyrata] gi|297326105|gb|EFH56525.1| hypothetical protein ARALYDRAFT_904152 [Arabidopsis lyrata subsp. lyrata]	273	354	3.00E-83	129.7	69.6	79.1	hypothetical protein ARALYDRAFT_904152	gbpln	Arabidopsis lyrata	AT2G46810.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:19239694-19242373 FORWARD LENGTH=371	273	371	1.00E-85	135.9	69.6	79.9

Rsa1.0_00244.1.g9481.t1	gb|AAO83658.1| cation-efflux transporter [Brassica juncea]	386	387	0	100.3	92.0	92.7	cation-efflux transporter	gbpln	Brassica juncea	AT2G46800.2 | Symbols: ZAT, ATMTP1, MTP1, ZAT1, ATCDF1 | zinc transporter of Arabidopsis thaliana | chr2:19238128-19239324 FORWARD LENGTH=398	386	398	1.00E-172	103.1	84.7	88.9
Rsa1.0_00244.1.g9482.t1	dbj|BAJ34373.1| unnamed protein product [Thellungiella halophila]	472	486	0	103.0	76.3	85.2	unnamed protein product	----	----	AT2G46790.1 | Symbols: APRR9, PRR9, TL1 | pseudo-response regulator 9 | chr2:19232874-19234901 FORWARD LENGTH=468	472	468	0	99.2	72.9	82.0
Rsa1.0_00244.1.g9483.t1	ref|NP_182201.4| RNA-binding (RRM/RBD/RNP motifs) family protein [Arabidopsis thaliana] gi|63003880|gb|AAY25469.1| At2g46780 [Arabidopsis thaliana] gi|330255657|gb|AEC10751.1| RNA-binding (RRM/RBD/RNP motifs) family protein [Arabidopsis thaliana]	323	336	1.00E-120	104.0	84.5	88.9	RNA-binding (RRM/RBD/RNP motifs) family protein	gbpln	Arabidopsis thaliana	AT2G46780.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:19229516-19231043 FORWARD LENGTH=336	323	336	1.00E-122	104.0	84.5	88.9
Rsa1.0_00244.1.g9484.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00244.1.g9485.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00244.1.g9486.t1	ref|NP_182200.2| NAC domain-containing protein 43 [Arabidopsis thaliana] gi|97180062|sp|Q84WP6.2|NAC43_ARATH RecName: Full=NAC domain-containing protein 43; Short=ANAC043; AltName: Full=Protein EMBRYO DEFECTIVE 2301; AltName: Full=Protein NAC SECONDARY WALL THICKENING PROMOTING FACTOR 1 gi|56550701|gb|AAV97804.1| At2g46770 [Arabidopsis thaliana] gi|330255656|gb|AEC10750.1| NAC domain-containing protein 43 [Arabidopsis thaliana]	367	365	0	99.5	85.8	91.3	NAC domain-containing protein 43	gbpln	Arabidopsis thaliana	AT2G46770.1 | Symbols: NST1, EMB2301, ANAC043 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr2:19220917-19222822 REVERSE LENGTH=365	367	365	0	99.5	85.8	91.3
Rsa1.0_00245.1.g9487.t2	ref|XP_002864780.1| hypothetical protein ARALYDRAFT_496402 [Arabidopsis lyrata subsp. lyrata] gi|297310615|gb|EFH41039.1| hypothetical protein ARALYDRAFT_496402 [Arabidopsis lyrata subsp. lyrata]	416	771	1.00E-138	185.3	70.0	74.8	hypothetical protein ARALYDRAFT_496402	gbpln	Arabidopsis lyrata	AT5G62260.1 | Symbols: | AT hook motif DNA-binding family protein | chr5:25009331-25011348 FORWARD LENGTH=404	416	404	1.00E-139	97.1	70.2	75.2
Rsa1.0_00245.1.g9488.t1	ref|XP_002864781.1| hypothetical protein ARALYDRAFT_332462 [Arabidopsis lyrata subsp. lyrata] gi|297310616|gb|EFH41040.1| hypothetical protein ARALYDRAFT_332462 [Arabidopsis lyrata subsp. lyrata]	244	235	1.00E-112	96.3	87.3	91.8	hypothetical protein ARALYDRAFT_332462	gbpln	Arabidopsis lyrata	AT5G62280.1 | Symbols: | Protein of unknown function (DUF1442) | chr5:25017165-25017985 FORWARD LENGTH=236	244	236	1.00E-106	96.7	87.3	92.2
Rsa1.0_00245.1.g9489.t1	ref|NP_001119478.1| nucleotide-sensitive chloride conductance regulator family protein [Arabidopsis thaliana] gi|332010209|gb|AED97592.1| chloride conductance regulatory protein ICln [Arabidopsis thaliana]	230	228	2.00E-96	99.1	83.9	90.4	nucleotide-sensitive chloride conductance regulator family protein	gbpln	Arabidopsis thaliana	AT5G62290.2 | Symbols: | nucleotide-sensitive chloride conductance regulator (ICln) family protein | chr5:25019568-25020972 FORWARD LENGTH=228	230	228	6.00E-99	99.1	83.9	90.4
Rsa1.0_00245.1.g9490.t1	gb|AAM67138.1| ripening-related protein-like [Arabidopsis thaliana]	198	202	6.00E-44	102.0	54.5	69.2	ripening-related protein-like	gbpln	Arabidopsis thaliana	AT5G62350.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:25037504-25038112 FORWARD LENGTH=202	198	202	9.00E-40	102.0	54.0	69.7
Rsa1.0_00245.1.g9491.t1	gb|EOA14032.1| hypothetical protein CARUB_v10027165mg [Capsella rubella]	201	199	1.00E-91	99.0	82.1	89.6	hypothetical protein CARUB_v10027165mg	gbpln	Capsella rubella	AT5G62350.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:25037504-25038112 FORWARD LENGTH=202	201	202	1.00E-86	100.5	73.6	81.1
Rsa1.0_00245.1.g9492.t1	gb|ABD65000.1| hypothetical protein 26.t00020 [Brassica oleracea]	293	302	2.00E-62	103.1	48.8	60.4	hypothetical protein 26.t00020	gbpln	Brassica oleracea	AT5G41220.1 | Symbols: ATGSTT3, GST10C, GSTT3 | glutathione S-transferase THETA 3 | chr5:16494560-16496969 REVERSE LENGTH=590	293	590	3.00E-22	201.4	30.4	43.3
Rsa1.0_00245.1.g9493.t1	ref|NP_201044.1| NAC-domain protein 101 [Arabidopsis thaliana] gi|8809651|dbj|BAA97202.1| NAM (no apical meristem)-like protein [Arabidopsis thaliana] gi|67633908|gb|AAY78878.1| no apical meristem family protein [Arabidopsis thaliana] gi|111074488|gb|ABH04617.1| At5g62380 [Arabidopsis thaliana] gi|332010219|gb|AED97602.1| NAC-domain protein 101 [Arabidopsis thaliana]	350	348	1.00E-177	99.4	91.4	94.3	NAC-domain protein 101	gbpln	Arabidopsis thaliana	AT5G62380.1 | Symbols: VND6, ANAC101, NAC101 | NAC-domain protein 101 | chr5:25050684-25051858 FORWARD LENGTH=348	350	348	1.00E-179	99.4	91.4	94.3
Rsa1.0_00245.1.g9494.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00245.1.g9495.t1	ref|XP_002864795.1| aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310630|gb|EFH41054.1| aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata]	316	316	1.00E−173	100.0	91.8	95.9	aldo/keto reductase family protein	gbpln	Arabidopsis lyrata	AT5G62420.1 | Symbols: | NAD(P)−linked oxidoreductase superfamily protein | chr5:25064835−25066111 FORWARD LENGTH=316	316	316	1.00E−175	100.0	92.1	95.6
Rsa1.0_00245.1.g9496.t1	dbj|BAJ34539.1| unnamed protein product [Thellungiella halophila]	297	307	1.00E−135	103.4	83.2	90.6	unnamed protein product	----	----	AT5G62430.1 | Symbols: CDF1 | cycling DOF factor 1 | chr5:25069298−25070787 REVERSE LENGTH=298	297	298	1.00E−131	100.3	78.1	87.9
Rsa1.0_00245.1.g9497.t1	ref|XP_002866491.1| hypothetical protein ARALYDRAFT_496421 [Arabidopsis lyrata subsp. lyrata] gi|297312326|gb|EFH42750.1| hypothetical protein ARALYDRAFT_496421 [Arabidopsis lyrata subsp. lyrata]	194	203	9.00E−68	104.6	72.7	77.3	hypothetical protein ARALYDRAFT_496421	gbpln	Arabidopsis lyrata	AT5G62440.1 | Symbols: | Protein of unknown function (DUF3223) | chr5:25072620−25073917 REVERSE LENGTH=202	194	202	1.00E−69	104.1	72.2	77.3
Rsa1.0_00245.1.g9498.t2	gb|EOA13766.1| hypothetical protein CARUB_v10026858mg [Capsella rubella]	319	303	3.00E−91	95.0	67.1	71.2	hypothetical protein CARUB_v10026858mg	gbpln	Capsella rubella	AT5G62460.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:25075545−25077072 FORWARD LENGTH=307	319	307	5.00E−93	96.2	69.0	74.0
Rsa1.0_00245.1.g9499.t1	dbj|BAJ34253.1| unnamed protein product [Thellungiella halophila]	346	355	1.00E−168	102.6	87.0	91.9	unnamed protein product	----	----	AT5G62470.2 | Symbols: MYB96 | myb domain protein 96 | chr5:25079434−25080858 REVERSE LENGTH=352	346	352	1.00E−161	101.7	84.1	89.0
Rsa1.0_00245.1.g9500.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838−20266 [Arabidopsis thaliana]	145	1142	2.00E−13	787.6	30.3	46.9	reverse transcriptase, putative; 16838−20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00245.1.g9501.t1	gb|EOA17213.1| hypothetical protein CARUB_v10005487mg [Capsella rubella]	271	271	1.00E−119	100.0	80.8	90.8	hypothetical protein CARUB_v10005487mg	gbpln	Capsella rubella	AT4G28360.1 | Symbols: | Ribosomal protein L22p/L17e family protein | chr4:14029294−14030926 REVERSE LENGTH=271	271	271	1.00E−121	100.0	80.4	91.5
Rsa1.0_00245.1.g9502.t1	gb|EOA14913.1| hypothetical protein CARUB_v10028253mg [Capsella rubella]	189	168	2.00E−70	88.9	72.5	79.4	hypothetical protein CARUB_v10028253mg	gbpln	Capsella rubella	AT5G62490.1 | Symbols: ATHVA22B, HVA22B | HVA22 homologue B | chr5:25090206−25091345 FORWARD LENGTH=167	189	167	3.00E−72	88.4	72.5	79.4
Rsa1.0_00245.1.g9503.t1	gb|AAF63110.1|AC006423_11 putative retroelement pol polyprotein [Arabidopsis thaliana]	613	1150	1.00E−135	187.6	40.0	54.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00245.1.g9504.t1	ref|XP_002864798.1| ATEB1B [Arabidopsis lyrata subsp. lyrata] gi|297310633|gb|EFH41057.1| ATEB1B [Arabidopsis lyrata subsp. lyrata]	278	288	1.00E−140	103.6	86.0	91.7	ATEB1B	gbpln	Arabidopsis lyrata	AT5G62500.1 | Symbols: ATEB1B, ATEB1, EB1B | end binding protein 1B | chr5:25092929−25095006 FORWARD LENGTH=293	278	293	1.00E−142	105.4	86.3	91.0
Rsa1.0_00245.1.g9505.t4	gb|EOA14515.1| hypothetical protein CARUB_v10027743mg [Capsella rubella]	426	316	1.00E−134	74.2	56.1	61.3	hypothetical protein CARUB_v10027743mg	gbpln	Capsella rubella	AT5G62520.1 | Symbols: SRO5 | similar to RCD one 5 | chr5:25098071−25099264 FORWARD LENGTH=309	426	309	1.00E−132	72.5	55.4	61.0
Rsa1.0_00246.1.g9506.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	173	442	6.00E−59	255.5	61.8	75.7	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase−derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae − 0; Bacteria − 0; Metazoa − 28; Fungi − 8; Plants − 388; Viruses − 0; Other Eukaryotes − 27 (source: NCBI BLink). | chr2:5736603−5737847 FORWARD LENGTH=343	173	343	4.00E−33	198.3	34.1	43.9
Rsa1.0_00246.1.g9507.t1	ref|NP_193436.2| expansin−like B1 [Arabidopsis thaliana] gi|22095652|sp|O23547.2|EXLB1_ARATH RecName: Full=Expansin−like B1; Short=At−EXPR1; Short=AtEXLB1; Short=AtEXPR1; AltName: Full=Ath−ExpBeta−3.1; Flags: Precursor gi|29028846|gb|AAO64802.1| At4g17030 [Arabidopsis thaliana] gi|110736418|dbj|BAF00176.1| Expansin−like protein [Arabidopsis thaliana] gi|332658441|gb|AEE83841.1| expansin−like B1 [Arabidopsis thaliana]	230	250	1.00E−101	108.7	81.7	86.5	expansin−like B1	gbpln	Arabidopsis thaliana	AT4G17030.1 | Symbols: ATEXLB1, EXPR, AT−EXPR, ATEXPR1, ATHEXP BETA 3.1, EXLB1 | expansin−like B1 | chr4:9581817−9583181 REVERSE LENGTH=250	230	250	1.00E−103	108.7	81.7	86.5
Rsa1.0_00246.1.g9508.t1	ref|XP_002868088.1| hypothetical protein ARALYDRAFT_493172 [Arabidopsis lyrata subsp. lyrata] gi|297313924|gb|EFH44347.1| hypothetical protein ARALYDRAFT_493172 [Arabidopsis lyrata subsp. lyrata]	307	305	1.00E−156	99.3	94.5	97.1	hypothetical protein ARALYDRAFT_493172	gbpln	Arabidopsis lyrata	AT4G17040.1 | Symbols: CLPR4 | CLP protease R subunit 4 | chr4:9586740−9589297 REVERSE LENGTH=305	307	305	1.00E−158	99.3	93.8	96.4
Rsa1.0_00246.1.g9509.t1	gb|EOA16651.1| hypothetical protein CARUB_v10004844mg [Capsella rubella]	420	434	1.00E−162	103.3	84.5	90.2	hypothetical protein CARUB_v10004844mg	gbpln	Capsella rubella	AT4G17060.1 | Symbols: FIP2 | FRIGIDA interacting protein 2 | chr4:9593721−9594653 REVERSE LENGTH=310	420	310	1.00E−111	73.8	58.1	62.6

Rsa1.0_00246.1.g9510.t1	ref|XP_002868086.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313922|gb|EFH44345.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	345	342	1.00E-166	99.1	83.8	89.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G17070.1 | Symbols: | peptidyl-prolyl cis-trans isomerases | chr4:9595523-9598066 REVERSE LENGTH=343	345	343	1.00E-168	99.4	84.3	88.7
Rsa1.0_00246.1.g9511.t1	gb|ACK37362.1| MORN [Brassica rapa subsp. pekinensis]	500	502	0	100.4	93.4	94.8	MORN	gbpln	Brassica rapa	AT4G17080.1 | Symbols: | Histone H3 K4-specific methyltransferase SET7/9 family protein | chr4:9601570-9603815 FORWARD LENGTH=513	500	513	0	102.6	84.6	88.8
Rsa1.0_00246.1.g9512.t1	dbj|BAJ34236.1| unnamed protein product [Thellungiella halophila]	559	548	0	98.0	90.9	94.3	unnamed protein product	----	----	AT4G17090.1 | Symbols: CT-BMY, BAM3, BMY8 | chloroplast beta-amylase | chr4:9605266-9607250 REVERSE LENGTH=548	559	548	0	98.0	89.8	93.2
Rsa1.0_00246.1.g9513.t1	ref|NP_193450.1| RAB GTPase homolog B1C [Arabidopsis thaliana] gi|297800394|ref|XP_002868081.1| hypothetical protein ARALYDRAFT_493160 [Arabidopsis lyrata subsp. lyrata] gi|75279776|sp|P92963.1|RAB1C_ARATH RecName: Full=Ras-related protein RABB1c; Short=AtRABB1c; AltName: Full=Ras-related protein Rab2A; Short=AtRab2A gi|1765896|emb|CAA70498.1| Rab2-like protein [Arabidopsis thaliana] gi|5281023|emb|CAB45962.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|7268468|emb|CAB80988.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|27311815|gb|AAO00873.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|30023652|gb|AAP13359.1| At4g17170 [Arabidopsis thaliana] gi|297313917|gb|EFH44340.1| hypothetical protein ARALYDRAFT_493160 [Arabidopsis lyrata subsp. lyrata] gi|332658457|gb|AEE83857.1| RAB GTPase homolog B1C [Arabidopsis thaliana] gi|482553233|gb|EOA17426.1| hypothetical protein CARUB_v10005730mg [Capsella rubella]	211	211	1.00E-120	100.0	98.6	100.0	RAB GTPase homolog B1C	gbpln	Arabidopsis lyrata	AT4G17170.1 | Symbols: AT-RAB2, ATRABB1C, ATRAB2A, RAB2A, RABB1C, ATRAB-B1B, RAB-B1B | RAB GTPase homolog B1C | chr4:9644908-9646220 REVERSE LENGTH=211	211	211	1.00E-123	100.0	98.6	100.0
Rsa1.0_00246.1.g9514.t1	gb|ABD65105.1| glycosyl hydrolase family protein [Brassica oleracea]	478	475	0	99.4	95.8	97.5	glycosyl hydrolase family protein	gbpln	Brassica oleracea	AT4G17180.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr4:9646541-9648045 FORWARD LENGTH=475	478	475	0	99.4	87.9	92.7
Rsa1.0_00246.1.g9515.t1	gb|ABD65106.1| ubiquitin family protein [Brassica oleracea]	452	863	0	190.9	83.6	90.5	ubiquitin family protein	gbpln	Brassica oleracea	AT4G17210.1 | Symbols: | Plant protein of unknown function (DUF827) | chr4:9652585-9654257 REVERSE LENGTH=527	452	527	1.00E-170	116.6	72.6	83.6
Rsa1.0_00246.1.g9516.t1	gb|ABD65106.1| ubiquitin family protein [Brassica oleracea]	367	863	1.00E-180	235.1	86.6	89.6	ubiquitin family protein	gbpln	Brassica oleracea	AT4G06599.1 | Symbols: | ubiquitin family protein | chr4:3666079-3667495 REVERSE LENGTH=340	367	340	1.00E-154	92.6	74.7	79.8
Rsa1.0_00246.1.g9517.t1	gb|ABD65108.1| hypothetical protein 31.t00008 [Brassica oleracea]	156	157	2.00E-69	100.6	89.1	91.0	hypothetical protein 31.t00008	gbpln	Brassica oleracea	AT4G17215.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr4:9655884-9656425 FORWARD LENGTH=150	156	150	4.00E-52	96.2	73.1	79.5
Rsa1.0_00246.1.g9518.t1	gb|ABD65109.1| Myosin II heavy chain-like domain containing protein [Brassica oleracea]	499	508	0	101.8	90.6	92.6	Myosin II heavy chain-like domain containing protein	gbpln	Brassica oleracea	AT4G17220.1 | Symbols: ATMAP70-5, MAP70-5 | microtubule-associated proteins 70-5 | chr4:9657008-9659405 REVERSE LENGTH=513	499	513	0	102.8	85.6	92.8
Rsa1.0_00246.1.g9519.t1	gb|ABD65111.1| hypothetical protein 31.t00013 [Brassica oleracea]	338	335	1.00E-149	99.1	92.6	95.9	hypothetical protein 31.t00013	gbpln	Brassica oleracea	AT4G17240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 8 growth stages; Has 1142 Blast hits to 1055 proteins in 252 species: Archae - 22; Bacteria - 318; Metazoa - 248; Fungi - 96; Plants - 59; Viruses - 3; Other Eukaryotes - 396 (source: NCBI BLink). | chr4:9666799-9668292 REVERSE LENGTH=343	338	343	1.00E-148	101.5	85.8	92.6
Rsa1.0_00246.1.g9520.t1	gb|ABD65113.1| hypothetical protein 31.t00019 [Brassica oleracea]	455	418	0	91.9	82.9	85.5	hypothetical protein 31.t00019	gbpln	Brassica oleracea	AT2G31290.2 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr2:13344151-13345398 FORWARD LENGTH=415	455	415	0	91.2	74.3	80.0

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<tr><td>Rsa1.0_00246.1.g9521.t1</td><td>ref|NP_193457.5| uncharacterized protein [Arabidopsis thaliana] gi|332658466|gb|AEE83866.1| uncharacterized protein AT4G17240 [Arabidopsis thaliana]</td><td>94</td><td>343</td><td>1.00E-18</td><td>364.9</td><td>50.0</td><td>56.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G17240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 8 growth stages; Has 1142 Blast hits to 1055 proteins in 252 species: Archae - 22; Bacteria - 318; Metazoa - 248; Fungi - 96; Plants - 59; Viruses - 3; Other Eukaryotes - 396 (source: NCBI BLink). | chr4:9666799-9668292 REVERSE LENGTH=343</td><td>94</td><td>343</td><td>2.00E-21</td><td>364.9</td><td>50.0</td><td>56.4</td></tr>
<tr><td>Rsa1.0_00246.1.g9522.t1</td><td>gb|ABD65113.1| hypothetical protein 31.t00019 [Brassica oleracea]</td><td>152</td><td>418</td><td>4.00E-64</td><td>275.0</td><td>88.2</td><td>89.5</td><td>hypothetical protein 31.t00019</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G31290.2 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr2:13344151-13345398 FORWARD LENGTH=415</td><td>152</td><td>415</td><td>5.00E-66</td><td>273.0</td><td>80.3</td><td>84.9</td></tr>
<tr><td>Rsa1.0_00246.1.g9523.t1</td><td>gb|ABD65114.1| L-lactate dehydrogenase, putative [Brassica oleracea]</td><td>350</td><td>350</td><td>0</td><td>100.0</td><td>95.1</td><td>98.0</td><td>L-lactate dehydrogenase, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17260.1 | Symbols: | Lactate/malate dehydrogenase family protein | chr4:9674057-9675309 FORWARD LENGTH=353</td><td>350</td><td>353</td><td>0</td><td>100.9</td><td>92.0</td><td>96.0</td></tr>
<tr><td>Rsa1.0_00246.1.g9524.t1</td><td>gb|ABD65115.1| hypothetical protein 31.t00023 [Brassica oleracea]</td><td>402</td><td>380</td><td>0</td><td>94.5</td><td>90.8</td><td>93.3</td><td>hypothetical protein 31.t00023</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17280.1 | Symbols: | Auxin-responsive family protein | chr4:9678887-9680277 REVERSE LENGTH=402</td><td>402</td><td>402</td><td>0</td><td>100.0</td><td>90.3</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00246.1.g9525.t2</td><td>ref|XP_002870111.1| hypothetical protein ARALYDRAFT_914989 [Arabidopsis lyrata subsp. lyrata] gi|297315947|gb|EFH46370.1| hypothetical protein ARALYDRAFT_914989 [Arabidopsis lyrata subsp. lyrata]</td><td>580</td><td>567</td><td>0</td><td>97.8</td><td>88.3</td><td>92.4</td><td>hypothetical protein ARALYDRAFT_914989</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G17300.1 | Symbols: NS1, OVA8, ATNS1 | Class II aminoacyl-tRNA and biotin synthetases superfamily protein | chr4:9681558-9684833 FORWARD LENGTH=567</td><td>580</td><td>567</td><td>0</td><td>97.8</td><td>88.4</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00246.1.g9526.t1</td><td>gb|ABD65120.1| Tonoplast intrinsic protein, putative [Brassica oleracea]</td><td>239</td><td>250</td><td>1.00E-123</td><td>104.6</td><td>98.7</td><td>98.7</td><td>Tonoplast intrinsic protein, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47450.1 | Symbols: ATTIP2;3, TIP2;3, DELTA-TIP3 | tonoplast intrinsic protein 2;3 | chr5:19248509-19249466 REVERSE LENGTH=250</td><td>239</td><td>250</td><td>1.00E-122</td><td>104.6</td><td>92.9</td><td>97.9</td></tr>
<tr><td>Rsa1.0_00246.1.g9527.t1</td><td>ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]</td><td>926</td><td>966</td><td>0</td><td>104.3</td><td>51.2</td><td>67.2</td><td>leucine-rich repeat family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G58190.1 | Symbols: AtRLP9, RLP9 | receptor like protein 9 | chr1:21540720-21544330 FORWARD LENGTH=932</td><td>926</td><td>932</td><td>0</td><td>100.6</td><td>52.4</td><td>68.0</td></tr>
<tr><td>Rsa1.0_00246.1.g9528.t1</td><td>gb|EOA17308.1| hypothetical protein CARUB_v10005581mg [Capsella rubella]</td><td>239</td><td>250</td><td>1.00E-122</td><td>104.6</td><td>96.7</td><td>98.3</td><td>hypothetical protein CARUB_v10005581mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G47450.1 | Symbols: ATTIP2;3, TIP2;3, DELTA-TIP3 | tonoplast intrinsic protein 2;3 | chr5:19248509-19249466 REVERSE LENGTH=250</td><td>239</td><td>250</td><td>1.00E-122</td><td>104.6</td><td>92.1</td><td>97.5</td></tr>
<tr><td>Rsa1.0_00246.1.g9529.t1</td><td>ref|NP_193466.2| uncharacterized protein [Arabidopsis thaliana] gi|54606846|gb|AAV34771.1| At4g17350 [Arabidopsis thaliana] gi|98960971|gb|ABF58969.1| At4g17350 [Arabidopsis thaliana] gi|332658479|gb|AEE83879.1| uncharacterized protein AT4G17350 [Arabidopsis thaliana]</td><td>406</td><td>405</td><td>0</td><td>99.8</td><td>88.2</td><td>92.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G17350.1 | Symbols: | Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region | chr4:9701582-9703358 FORWARD LENGTH=405</td><td>406</td><td>405</td><td>0</td><td>99.8</td><td>88.2</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00246.1.g9530.t1</td><td>gb|EOA15683.1| hypothetical protein CARUB_v10006392mg [Capsella rubella]</td><td>334</td><td>328</td><td>1.00E-180</td><td>98.2</td><td>90.7</td><td>93.7</td><td>hypothetical protein CARUB_v10006392mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G17360.1 | Symbols: | Formyl transferase | chr4:9703698-9705468 REVERSE LENGTH=328</td><td>334</td><td>328</td><td>0</td><td>98.2</td><td>90.4</td><td>92.8</td></tr>
<tr><td>Rsa1.0_00246.1.g9531.t1</td><td>gb|ABD65123.1| hypothetical protein 31.t00039 [Brassica oleracea]</td><td>889</td><td>862</td><td>0</td><td>97.0</td><td>68.6</td><td>70.0</td><td>hypothetical protein 31.t00039</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17410.1 | Symbols: | DWNN domain, a CCHC-type zinc finger | chr4:9716360-9721642 FORWARD LENGTH=826</td><td>889</td><td>826</td><td>0</td><td>92.9</td><td>57.8</td><td>63.3</td></tr>
<tr><td>Rsa1.0_00246.1.g9532.t1</td><td>ref|XP_002974570.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii] gi|300157465|gb|EFJ24090.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii]</td><td>604</td><td>516</td><td>1.00E-40</td><td>85.4</td><td>38.2</td><td>44.7</td><td>hypothetical protein SELMODRAFT_442529</td><td>gbpln</td><td>Selaginella moellendorffii</td><td>AT4G13390.1 | Symbols: | Proline-rich extensin-like family protein | chr4:7783856-7785145 FORWARD LENGTH=429</td><td>604</td><td>429</td><td>1.00E-37</td><td>71.0</td><td>53.6</td><td>59.3</td></tr>
<tr><td>Rsa1.0_00247.1.g9533.t2</td><td>ref|NP_850863.1| cytokinin dehydrogenase 7 [Arabidopsis thaliana] gi|66773939|sp|Q9FUJ1.1|CKX7_ARATH RecName: Full=Cytokinin dehydrogenase 7; AltName: Full=Cytokinin oxidase 7; Short=AtCKX5; Short=AtCKX7; Short=CKO7 gi|11120514|gb|AAG30908.1|AF303981_1 cytokinin oxidase [Arabidopsis thaliana] gi|29294045|gb|AAO73882.1| FAD-linked oxidoreductase family [Arabidopsis thaliana] gi|332005568|gb|AED92951.1| cytokinin dehydrogenase 7 [Arabidopsis thaliana]</td><td>459</td><td>524</td><td>0</td><td>114.2</td><td>82.4</td><td>88.0</td><td>cytokinin dehydrogenase 7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G21482.1 | Symbols: CKX7, ATCKX5 | cytokinin oxidase 7 | chr5:7226842-7230052 FORWARD LENGTH=524</td><td>459</td><td>524</td><td>0</td><td>114.2</td><td>82.4</td><td>88.0</td></tr>
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Rsa1.0_00247.1.g9534.t2	ref|XP_002871975.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317812|gb|EFH48234.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	443	218	4.00E-97	49.2	44.0	46.7	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT5G21430.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:7222294-7223400 FORWARD LENGTH=218	443	218	1.00E-97	49.2	42.9	46.0
Rsa1.0_00247.1.g9535.t1	ref|NP_850861.2| CBL-interacting serine/threonine-protein kinase 26 [Arabidopsis thaliana] gi|189082529|sp|Q84VQ3.2|CIPKQ_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 26; AltName: Full=SNF1-related kinase 3.26; AltName: Full=SOS2-like protein kinase PKS26 gi|332005565|gb|AED92948.1| CBL-interacting serine/threonine-protein kinase 26 [Arabidopsis thaliana]	441	439	0	99.5	91.8	95.7	CBL-interacting serine/threonine-protein kinase 26	gbpln	Arabidopsis thaliana	AT5G21326.1 | Symbols: | Ca2+regulated serine-threonine protein kinase family protein | chr5:7218081-7221743 FORWARD LENGTH=439	441	439	0	99.5	91.8	95.7
Rsa1.0_00247.1.g9536.t1	ref|XP_004251248.1| PREDICTED: calmodulin-like isoform 1 [Solanum lycopersicum]	149	180	4.00E-80	120.8	100.0	100.0	PREDICTED: calmodulin-like isoform 1	gbpln	Solanum lycopersicum	AT2G27030.3 | Symbols: CAM5 | calmodulin 5 | chr2:11532069-11534176 FORWARD LENGTH=181	149	181	6.00E-82	121.5	98.7	100.0
Rsa1.0_00247.1.g9537.t1	ref|NP_850859.2| SNF1-like protein kinase [Arabidopsis thaliana] gi|75160582|sp|Q8S9D1.1|PP395_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g21222; AltName: Full=SNF1-like protein kinase AtC401 gi|19071860|dbj|BAB85674.1| SNF1-like protein kinase [Arabidopsis thaliana] gi|332005563|gb|AED92946.1| pentatricopeptide repeat and serine/threonine kinase domain-containing protein [Arabidopsis thaliana]	839	831	0	99.0	85.8	90.9	SNF1-like protein kinase	gbpln	Arabidopsis thaliana	AT5G21222.1 | Symbols: | protein kinase family protein | chr5:7209422-7213700 FORWARD LENGTH=831	839	831	0	99.0	85.8	90.9
Rsa1.0_00247.1.g9538.t1	ref|XP_002871972.1| AMP-activated protein kinase [Arabidopsis lyrata subsp. lyrata] gi|297317809|gb|EFH48231.1| AMP-activated protein kinase [Arabidopsis lyrata subsp. lyrata]	322	319	1.00E-140	99.1	84.8	88.2	AMP-activated protein kinase	gbpln	Arabidopsis lyrata	AT5G21170.2 | Symbols: AKINBETA1 | 5'-AMP-activated protein kinase beta-2 subunit protein | chr5:7205718-7208239 FORWARD LENGTH=320	322	320	1.00E-142	99.4	84.5	88.5
Rsa1.0_00247.1.g9539.t1	ref|XP_002874032.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319869|gb|EFH50291.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	859	838	0	97.6	77.6	85.1	La domain-containing protein	gbpln	Arabidopsis lyrata	AT5G21160.1 | Symbols: | LA RNA-binding protein | chr5:7199191-7203879 REVERSE LENGTH=826	859	826	0	96.2	75.9	83.5
Rsa1.0_00247.1.g9540.t1	ref|XP_002871971.1| PAZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317808|gb|EFH48230.1| PAZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	906	902	0	99.6	73.1	84.4	PAZ domain-containing protein	gbpln	Arabidopsis lyrata	AT5G21150.1 | Symbols: AGO9 | Argonaute family protein | chr5:7193472-7198113 FORWARD LENGTH=896	906	896	0	98.9	73.4	85.1
Rsa1.0_00247.1.g9541.t1	gb|EOA21152.1| hypothetical protein CARUB_v10001499mg [Capsella rubella]	321	315	1.00E-152	98.1	82.9	89.1	hypothetical protein CARUB_v10001499mg	gbpln	Capsella rubella	AT5G21140.1 | Symbols: emb1379 | embryo defective 1379 | chr5:7187416-7189521 REVERSE LENGTH=312	321	312	1.00E-148	97.2	82.2	88.2
Rsa1.0_00247.1.g9542.t1	gb|EOA20396.1| hypothetical protein CARUB_v10000708mg [Capsella rubella]	557	524	1.00E-159	94.1	60.7	70.0	hypothetical protein CARUB_v10000708mg	gbpln	Capsella rubella	AT5G21120.1 | Symbols: EIL2 | ETHYLENE-INSENSITIVE3-like 2 | chr5:7182629-7184185 FORWARD LENGTH=518	557	518	1.00E-151	93.0	57.6	67.0
Rsa1.0_00247.1.g9543.t1	dbj|BAG50513.1| ascorbic acid oxidase [Brassica rapa subsp. chinensis]	535	577	0	107.9	93.8	96.4	ascorbic acid oxidase	gbpln	Brassica rapa	AT5G21105.1 | Symbols: | Plant L-ascorbate oxidase | chr5:7172727-7177409 FORWARD LENGTH=588	535	588	0	109.9	83.7	90.5
Rsa1.0_00247.1.g9544.t1	gb|AAF20931.1|AF206721_1 ascorbate oxidase [Brassica juncea]	574	574	0	100.0	80.7	87.1	ascorbate oxidase	gbpln	Brassica juncea	AT5G21100.1 | Symbols: | Plant L-ascorbate oxidase | chr5:7168312-7170719 FORWARD LENGTH=573	574	573	0	99.8	76.3	84.8
Rsa1.0_00247.1.g9545.t1	gb|AAF20931.1|AF206721_1 ascorbate oxidase [Brassica juncea]	572	574	0	100.3	92.7	96.2	ascorbate oxidase	gbpln	Brassica juncea	AT5G21100.1 | Symbols: | Plant L-ascorbate oxidase | chr5:7168312-7170719 FORWARD LENGTH=573	572	573	0	100.2	80.2	88.1

Rsa1.0_00247.1.g9546.t1	ref|NP_197608.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|11762126|gb|AAG40341.1|AF324989_1 AT5g21090 [Arabidopsis thaliana] gi|13899097|gb|AAK48970.1|AF370543_1 Unknown protein [Arabidopsis thaliana] gi|20148427|gb|AAM10104.1| unknown protein [Arabidopsis thaliana] gi|27311823|gb|AAO00877.1| Unknown protein [Arabidopsis thaliana] gi|29294060|gb|AAO73897.1| leucine rich repeat protein (LRP), putative [Arabidopsis thaliana] gi|30023686|gb|AAP13376.1| At5g21090 [Arabidopsis thaliana] gi|222424256|dbj|BAH20085.1| AT5G21090 [Arabidopsis thaliana] gi|332005547|gb|AED92930.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	209	218	1.00E-100	104.3	89.5	93.3	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G21090.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:7164758-7166904 FORWARD LENGTH=218	209	218	1.00E-102	104.3	89.5	93.3
Rsa1.0_00247.1.g9547.t1	gb|EOA21314.1| hypothetical protein CARUB_v10001673mg [Capsella rubella]	226	278	1.00E-118	123.0	96.5	98.2	hypothetical protein CARUB_v10001673mg	gbpln	Capsella rubella	AT5G21070.1 | Symbols: | unknown protein; Has 115 Blast hits to 115 proteins in 34 species: Archae - 1; Bacteria - 36; Metazoa - 0; Fungi - 0; Plants - 60; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr5:7156356-7157490 FORWARD LENGTH=225	226	225	1.00E-120	99.6	95.6	97.3
Rsa1.0_00247.1.g9548.t4	gb|EOA22042.1| hypothetical protein CARUB_v10002567mg [Capsella rubella]	374	378	1.00E-180	101.1	86.4	92.2	hypothetical protein CARUB_v10002567mg	gbpln	Capsella rubella	AT5G21060.2 | Symbols: | Glyceraldehyde-3-phosphate dehydrogenase-like family protein | chr5:7149153-7152745 REVERSE LENGTH=378	374	378	1.00E-178	101.1	84.8	89.8
Rsa1.0_00247.1.g9549.t1	ref|NP_197604.1| uncharacterized protein [Arabidopsis thaliana] gi|332005541|gb|AED92924.1| uncharacterized protein AT5G21050 [Arabidopsis thaliana]	346	355	1.00E-150	102.6	80.1	86.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G21050.1 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 8 growth stages; CONTAINS InterPro DOMAIN/s: Hyccin (InterPro:IPR018619); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64090.1); Has 206 Blast hits to 206 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 145; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr5:7147890-7148957 FORWARD LENGTH=355	346	355	1.00E-153	102.6	80.1	86.4
Rsa1.0_00247.1.g9550.t1	gb|EOA22287.1| hypothetical protein CARUB_v10002885mg [Capsella rubella]	543	540	0	99.4	79.7	85.8	hypothetical protein CARUB_v10002885mg	gbpln	Capsella rubella	AT5G21040.2 | Symbols: FBX2 | F-box protein 2 | chr5:7145058-7146677 REVERSE LENGTH=539	543	539	0	99.3	83.1	89.7
Rsa1.0_00247.1.g9551.t1	ref|XP_002874028.1| PAZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319865|gb|EFH50287.1| PAZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1081	848	0	78.4	57.9	65.0	PAZ domain-containing protein	gbpln	Arabidopsis lyrata	AT5G21150.1 | Symbols: AGO9 | Argonaute family protein | chr5:7193472-7198113 FORWARD LENGTH=896	1081	896	0	82.9	54.2	64.5
Rsa1.0_00247.1.g9552.t1	ref|XP_002874026.1| hypothetical protein ARALYDRAFT_489009 [Arabidopsis lyrata subsp. lyrata] gi|297319863|gb|EFH50285.1| hypothetical protein ARALYDRAFT_489009 [Arabidopsis lyrata subsp. lyrata]	808	810	0	100.2	90.0	94.6	hypothetical protein ARALYDRAFT_489009	gbpln	Arabidopsis lyrata	AT5G20980.2 | Symbols: ATMS3, MS3 | methionine synthase 3 | chr5:7124397-7128353 REVERSE LENGTH=812	808	812	0	100.5	91.1	95.3
Rsa1.0_00247.1.g9553.t1	ref|NP_197597.1| heat shock family protein [Arabidopsis thaliana] gi|332005531|gb|AED92914.1| heat shock family protein [Arabidopsis thaliana]	278	249	1.00E-90	89.6	67.3	76.6	heat shock family protein	gbpln	Arabidopsis thaliana	AT5G20970.1 | Symbols: | HSP20-like chaperones superfamily protein | chr5:7123132-7124001 FORWARD LENGTH=249	278	249	3.00E-93	89.6	67.3	76.6
Rsa1.0_00247.1.g9554.t2	dbj|BAE93768.1| aldehyde oxidase [Brassica rapa subsp. pekinensis]	1374	1349	0	98.2	92.1	95.4	aldehyde oxidase	gbpln	Brassica rapa	AT5G20960.2 | Symbols: AAO1, AO1, ATAO, AT-AO1, AOalpha, AtAO1 | aldehyde oxidase 1 | chr5:7116783-7122338 FORWARD LENGTH=1368	1374	1368	0	99.6	83.1	91.4
Rsa1.0_00248.1.g9555.t1	gb|EOA23232.1| hypothetical protein CARUB_v10016925mg [Capsella rubella]	74	578	1.00E-20	781.1	68.9	75.7	hypothetical protein CARUB_v10016925mg	gbpln	Capsella rubella	AT4G22760.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:11960553-11962289 FORWARD LENGTH=578	74	578	2.00E-21	781.1	64.9	74.3

Rsa1.0_00248.1.g9556.t1	ref|NP_194008.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|2827554|emb|CAA16562.1| putative DNA binding protein [Arabidopsis thaliana] gi|7269124|emb|CAB79232.1| putative DNA binding protein [Arabidopsis thaliana] gi|21537115|gb|AAM61456.1| putative DNA binding protein [Arabidopsis thaliana] gi|111074368|gb|ABH04557.1| At4g22770 [Arabidopsis thaliana] gi|119657348|tpd|FAA00273.1| TPA: AT-hook motif nuclear localized protein 2 [Arabidopsis thaliana] gi|225898799|dbj|BAH30530.1| hypothetical protein [Arabidopsis thaliana] gi|332659256|gb|AEE84656.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	330	334	1.00E-135	101.2	82.4	88.2	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT4G22770.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:11963879-11965439 REVERSE LENGTH=334	330	334	1.00E-137	101.2	82.4	88.2
Rsa1.0_00248.1.g9557.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1402	1515	0	108.1	60.8	75.4	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1402	1262	1.00E-104	90.0	14.0	20.7
Rsa1.0_00248.1.g9558.t1	ref|XP_002867750.1| hypothetical protein ARALYDRAFT_492590 [Arabidopsis lyrata subsp. lyrata] gi|297313586|gb|EFH44009.1| hypothetical protein ARALYDRAFT_492590 [Arabidopsis lyrata subsp. lyrata]	462	449	0	97.2	86.8	91.1	hypothetical protein ARALYDRAFT_492590	gbpln	Arabidopsis lyrata	AT4G22780.1 | Symbols: ACR7 | ACT domain repeat 7 | chr4:11968696-11970956 REVERSE LENGTH=449	462	449	0	97.2	86.8	90.7
Rsa1.0_00248.1.g9559.t1	gb|EOA16509.1| hypothetical protein CARUB_v10004667mg [Capsella rubella]	491	492	0	100.2	81.5	89.4	hypothetical protein CARUB_v10004667mg	gbpln	Capsella rubella	AT4G22790.1 | Symbols: | MATE efflux family protein | chr4:11975153-11976628 REVERSE LENGTH=491	491	491	0	100.0	79.0	87.6
Rsa1.0_00248.1.g9560.t1	ref|XP_002869805.1| hypothetical protein ARALYDRAFT_492588 [Arabidopsis lyrata subsp. lyrata] gi|297315641|gb|EFH46064.1| hypothetical protein ARALYDRAFT_492588 [Arabidopsis lyrata subsp. lyrata]	324	319	1.00E-111	98.5	85.8	88.3	hypothetical protein ARALYDRAFT_492588	gbpln	Arabidopsis lyrata	AT4G22810.1 | Symbols: | Predicted AT-hook DNA-binding family protein | chr4:11984432-11985406 FORWARD LENGTH=324	324	324	1.00E-113	100.0	86.4	89.2
Rsa1.0_00248.1.g9561.t1	ref|NP_194013.1| zinc finger A20 and AN1 domain-containing stress-associated protein 9 [Arabidopsis thaliana] gi|42572995|ref|NP_974594.1| zinc finger A20 and AN1 domain-containing stress-associated protein 9 [Arabidopsis thaliana] gi|75318397|sp|O49663.1|SAP9_ARATH RecName: Full=Zinc finger A20 and AN1 domain-containing stress-associated protein 9; Short=AtSAP9 gi|2827559|emb|CAA16567.1| predicted protein [Arabidopsis thaliana] gi|3292808|emb|CAA19798.1| putative protein [Arabidopsis thaliana] gi|7269129|emb|CAB79237.1| predicted protein [Arabidopsis thaliana] gi|25082838|gb|AAN72006.1| predicted protein [Arabidopsis thaliana] gi|30102906|gb|AAP21371.1| At4g22820 [Arabidopsis thaliana] gi|332659261|gb|AEE84661.1| zinc finger A20 and AN1 domain-containing stress-associated protein 9 [Arabidopsis thaliana] gi|332659262|gb|AEE84662.1| zinc finger A20 and AN1 domain-containing stress-associated protein 9 [Arabidopsis thaliana]	172	176	2.00E-72	102.3	85.5	89.0	zinc finger A20 and AN1 domain-containing stress-associated protein 9	gbpln	Arabidopsis thaliana	AT4G22820.2 | Symbols: | A20/AN1-like zinc finger family protein | chr4:11987871-11988401 REVERSE LENGTH=176	172	176	8.00E-75	102.3	85.5	89.0
Rsa1.0_00248.1.g9562.t2	ref|XP_002867746.1| bile acid:sodium symporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297313582|gb|EFH44005.1| bile acid:sodium symporter family protein [Arabidopsis lyrata subsp. lyrata]	414	406	0	98.1	86.7	93.0	bile acid:sodium symporter family protein	gbpln	Arabidopsis lyrata	AT4G22840.1 | Symbols: | Sodium Bile acid symporter family | chr4:11991636-11993676 REVERSE LENGTH=409	414	409	0	98.8	86.0	92.0
Rsa1.0_00248.1.g9563.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00248.1.g9564.t1	ref|NP_194017.3| Cell cycle regulated microtubule associated protein [Arabidopsis thaliana] gi|66792640|gb|AAY56422.1| At4g22860 [Arabidopsis thaliana] gi|332659268|gb|AEE84668.1| Cell cycle regulated microtubule associated protein [Arabidopsis thaliana]	523	509	0	97.3	71.5	78.6	Cell cycle regulated microtubule associated protein	gbpln	Arabidopsis thaliana	AT4G22860.1 | Symbols: | Cell cycle regulated microtubule associated protein | chr4:11997735-12001281 FORWARD LENGTH=509	523	509	0	97.3	71.5	78.6
Rsa1.0_00248.1.g9565.t1	gb|ABY89681.1| anthocyanidin synthase 1 protein [Brassica rapa subsp. oleifera] gi|166798273|gb|ABY89682.1| anthocyanidin synthase 2 protein [Brassica rapa subsp. oleifera] gi|288551983|gb|ADC53481.1| anthoncyanidin synthase [Brassica rapa var. purpuraria]	357	358	0	100.3	93.3	96.9	anthocyanidin synthase 1 protein	gbpln	Brassica rapa	AT4G22880.2 | Symbols: LDOX, TDS4, TT18, ANS | leucoanthocyanidin dioxygenase | chr4:12004905-12006059 REVERSE LENGTH=356	357	356	0	99.7	89.4	94.1
Rsa1.0_00248.1.g9566.t1	ref|NP_567672.1| PGR5-like protein 1A [Arabidopsis thaliana] gi|30685973|ref|NP_849422.1| PGR5-like protein 1A [Arabidopsis thaliana] gi|30685977|ref|NP_849423.1| PGR5-like protein 1A [Arabidopsis thaliana] gi|75151862|sp|Q8H112.1|PGL1A_ARATH RecName: Full=PGR5-like protein 1A, chloroplastic; AltName: Full=Ferredoxin-plastoquinone reductase 1; Flags: Precursor gi|24030260|gb|AAN41305.1| unknown protein [Arabidopsis thaliana] gi|332659274|gb|AEE84674.1| PGR5-like protein 1A [Arabidopsis thaliana] gi|332659275|gb|AEE84675.1| PGR5-like protein 1A [Arabidopsis thaliana] gi|332659276|gb|AEE84676.1| PGR5-like protein 1A [Arabidopsis thaliana]	325	324	1.00E-164	99.7	88.9	95.1	PGR5-like protein 1A	gbpln	Arabidopsis thaliana	AT4G22890.2 | Symbols: PGR5-LIKE A | PGR5-LIKE A | chr4:12007157-12009175 FORWARD LENGTH=324	325	324	1.00E-167	99.7	88.9	95.1
Rsa1.0_00248.1.g9567.t1	ref|XP_002869799.1| hypothetical protein ARALYDRAFT_914316 [Arabidopsis lyrata subsp. lyrata] gi|297315635|gb|EFH46058.1| hypothetical protein ARALYDRAFT_914316 [Arabidopsis lyrata subsp. lyrata]	342	342	1.00E-155	100.0	83.0	88.6	hypothetical protein ARALYDRAFT_914316	gbpln	Arabidopsis lyrata	AT4G22900.1 | Symbols: | Protein of unknown function (DUF1191) | chr4:12010221-12011252 FORWARD LENGTH=343	342	343	1.00E-157	100.3	81.6	88.9
Rsa1.0_00248.1.g9568.t1	ref|NP_198226.1| pre-mRNA-splicing factor SYF1 [Arabidopsis thaliana] gi|7682783|gb|AAF67364.1| Hypothetical protein T32B20.g [Arabidopsis thaliana] gi|332006447|gb|AED93830.1| tetratricopeptide repeat (TPR)-like superfamily protein [Arabidopsis thaliana]	105	917	1.00E-13	873.3	49.5	62.9	pre-mRNA-splicing factor SYF1	gbpln	Arabidopsis thaliana	AT5G28740.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:10780774-10783772 FORWARD LENGTH=917	105	917	2.00E-16	873.3	49.5	62.9
Rsa1.0_00248.1.g9569.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00248.1.g9570.t1	ref|XP_002869798.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297315634|gb|EFH46057.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	459	476	0	103.7	88.5	93.7	WD-40 repeat family protein	gbpln	Arabidopsis lyrata	AT4G22910.1 | Symbols: FZR2, CCS52A1 | FIZZY-related 2 | chr4:12012743-12015663 FORWARD LENGTH=483	459	483	0	105.2	88.7	93.5
Rsa1.0_00248.1.g9571.t1	gb|EOA17219.1| hypothetical protein CARUB_v10005494mg [Capsella rubella]	268	268	1.00E-129	100.0	83.6	89.9	hypothetical protein CARUB_v10005494mg	gbpln	Capsella rubella	AT4G22920.1 | Symbols: ATNYE1, NYE1 | non-yellowing 1 | chr4:12016776-12017969 REVERSE LENGTH=268	268	268	1.00E-130	100.0	82.1	89.6
Rsa1.0_00248.1.g9572.t1	gb|EOA16740.1| hypothetical protein CARUB_v10004941mg, partial [Capsella rubella]	511	409	0	80.0	70.1	71.8	hypothetical protein CARUB_v10004941mg, partial	gbpln	Capsella rubella	AT4G22930.1 | Symbols: PYR4, DHOASE | pyrimidin 4 | chr4:12019315-12021200 FORWARD LENGTH=377	511	377	0	73.8	67.5	70.1
Rsa1.0_00248.1.g9573.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00248.1.g9574.t3	gb|EOA16739.1| hypothetical protein CARUB_v10004941mg, partial [Capsella rubella]	158	386	1.00E-71	244.3	81.0	83.5	hypothetical protein CARUB_v10004941mg, partial	gbpln	Capsella rubella	AT4G22930.1 | Symbols: PYR4, DHOASE | pyrimidin 4 | chr4:12019315-12021200 FORWARD LENGTH=377	158	377	1.00E-72	238.6	79.1	81.6
Rsa1.0_00248.1.g9575.t6	gb|EOA15611.1| hypothetical protein CARUB_v10005697mg [Capsella rubella]	63	220	2.00E-24	349.2	88.9	93.7	hypothetical protein CARUB_v10005697mg	gbpln	Capsella rubella	AT4G22950.1 | Symbols: AGL19, GL19 | AGAMOUS-like 19 | chr4:12023946-12027421 REVERSE LENGTH=219	63	219	3.00E-27	347.6	88.9	93.7
Rsa1.0_00248.1.g9576.t1	ref|NP_567383.1| uncharacterized protein [Arabidopsis thaliana] gi|21553726|gb|AAM62819.1| unknown [Arabidopsis thaliana] gi|110738711|dbj|BAF01280.1| hypothetical protein [Arabidopsis thaliana] gi|332657659|gb|AEE83059.1| uncharacterized protein AT4G11860 [Arabidopsis thaliana]	532	682	1.00E-108	128.2	51.5	64.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G11860.1 | Symbols: | Protein of unknown function (DUF544) | chr4:7134237-7138361 REVERSE LENGTH=682	532	682	1.00E-111	128.2	51.5	64.7

Rsa1.0_00248.1.g9577.t1	ref|XP_002867740.1| hypothetical protein ARALYDRAFT_492569 [Arabidopsis lyrata subsp. lyrata] gi|297313576|gb|EFH43999.1| hypothetical protein ARALYDRAFT_492569 [Arabidopsis lyrata subsp. lyrata]	746	2186	1.00E-134	293.0	33.2	40.6	hypothetical protein ARALYDRAFT_492569	gbpln	Arabidopsis lyrata	AT4G22970.2 | Symbols: ESP | homolog of separase | chr4:12033703-12043572 REVERSE LENGTH=2177	746	2177	1.00E-132	291.8	32.3	39.8
Rsa1.0_00248.1.g9578.t2	ref|XP_004152730.1| PREDICTED: uncharacterized protein LOC101204257 [Cucumis sativus] gi|449496008|ref|XP_004160010.1| PREDICTED: uncharacterized LOC101204257 [Cucumis sativus]	982	1025	0	104.4	71.8	83.5	PREDICTED: uncharacterized protein LOC101204257	gbpln	Cucumis sativus	AT4G23000.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr4:12055241-12060028 FORWARD LENGTH=1015	982	1015	0	103.4	52.1	56.2
Rsa1.0_00248.1.g9579.t1	ref|NP_001078433.1| UDP-galactose transporter 2 [Arabidopsis thaliana] gi|3292827|emb|CAA19817.1| putative protein [Arabidopsis thaliana] gi|7269148|emb|CAB79256.1| putative protein [Arabidopsis thaliana] gi|67764062|gb|AAY79163.1| Golgi-localized UDP-galactose transporter [Arabidopsis thaliana] gi|332659293|gb|AEE84693.1| UDP-galactose transporter 2 [Arabidopsis thaliana]	301	362	1.00E-149	120.3	92.7	94.4	UDP-galactose transporter 2	gbpln	Arabidopsis thaliana	AT4G23010.2 | Symbols: ATUTR2, UTR2 | UDP-galactose transporter 2 | chr4:12060318-12062486 REVERSE LENGTH=362	301	362	1.00E-152	120.3	92.7	94.4
Rsa1.0_00248.1.g9580.t1	gb|EOA17838.1| hypothetical protein CARUB_v10006239mg [Capsella rubella]	236	509	1.00E-114	215.7	90.3	94.9	hypothetical protein CARUB_v10006239mg	gbpln	Capsella rubella	AT4G23030.1 | Symbols: | MATE efflux family protein | chr4:12072857-12074365 FORWARD LENGTH=502	236	502	1.00E-111	212.7	87.3	91.9
Rsa1.0_00248.1.g9581.t1	ref|NP_567676.1| PAS domain-containing protein tyrosine kinase family protein [Arabidopsis thaliana] gi|15810437|gb|AAL07106.1| putative serine/threonine kinase [Arabidopsis thaliana] gi|332659299|gb|AEE84699.1| PAS domain-containing protein tyrosine kinase family protein [Arabidopsis thaliana]	734	735	0	100.1	83.5	89.5	PAS domain-containing protein tyrosine kinase family protein	gbpln	Arabidopsis thaliana	AT4G23050.1 | Symbols: | PAS domain-containing protein tyrosine kinase family protein | chr4:12080112-12083708 FORWARD LENGTH=735	734	735	0	100.1	83.5	89.5
Rsa1.0_00248.1.g9582.t1	ref|NP_194037.2| protein IQ-domain 22 [Arabidopsis thaliana] gi|56693675|gb|AAW22634.1| calmodulin binding protein IQD22 [Arabidopsis thaliana] gi|332659301|gb|AEE84701.1| protein IQ-domain 22 [Arabidopsis thaliana]	644	484	1.00E-173	75.2	55.6	60.6	protein IQ-domain 22	gbpln	Arabidopsis thaliana	AT4G23060.1 | Symbols: IQD22 | IQ-domain 22 | chr4:12087283-12090408 FORWARD LENGTH=484	644	484	1.00E-176	75.2	55.6	60.6
Rsa1.0_00249.1.g9583.t1	gb|AAD32759.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	193	1356	9.00E-76	702.6	65.8	86.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	193	240	2.00E-22	124.4	33.7	50.8
Rsa1.0_00249.1.g9584.t12	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1872	1223	0	65.3	23.6	31.9	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1872	746	1.00E-47	39.9	5.3	6.5
Rsa1.0_00249.1.g9585.t1	gb|ABD65091.1| hypothetical protein 31.t00049 [Brassica oleracea]	476	530	7.00E-96	111.3	44.1	60.1	hypothetical protein 31.t00049	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00249.1.g9586.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	182	441	1.00E-36	242.3	43.4	64.3	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	182	746	5.00E-30	409.9	36.3	51.6
Rsa1.0_00249.1.g9587.t1	gb|EOA30096.1| hypothetical protein CARUB_v10013206mg [Capsella rubella]	631	629	0	99.7	83.5	90.6	hypothetical protein CARUB_v10013206mg	gbpln	Capsella rubella	AT2G17525.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:7624178-7626058 FORWARD LENGTH=626	631	626	0	99.2	82.1	90.3
Rsa1.0_00249.1.g9588.t1	ref|XP_002884065.1| hypothetical protein ARALYDRAFT_343373 [Arabidopsis lyrata subsp. lyrata] gi|297329905|gb|EFH60324.1| hypothetical protein ARALYDRAFT_343373 [Arabidopsis lyrata subsp. lyrata]	437	1056	0	241.6	91.5	95.9	hypothetical protein ARALYDRAFT_343373	gbpln	Arabidopsis lyrata	AT2G17530.3 | Symbols: | Protein kinase superfamily protein | chr2:7626518-7628624 FORWARD LENGTH=440	437	440	0	100.7	91.1	95.9

Rsa1.0_00249.1.g9589.t1	gb|EOA31017.1| hypothetical protein CARUB_v10014165mg [Capsella rubella] gi|482566829|gb|EOA31018.1| hypothetical protein CARUB_v10014165mg [Capsella rubella]	284	329	2.00E-72	115.8	70.4	79.9	hypothetical protein CARUB_v10014165mg	gbpln	Capsella rubella	AT2G17540.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G35510.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:7630662-7631489 REVERSE LENGTH=275	284	275	5.00E-55	96.8	58.1	66.2
Rsa1.0_00249.1.g9590.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00249.1.g9591.t1	ref|XP_002886120.1| hypothetical protein ARALYDRAFT_343376 [Arabidopsis lyrata subsp. lyrata] gi|297331960|gb|EFH62379.1| hypothetical protein ARALYDRAFT_343376 [Arabidopsis lyrata subsp. lyrata]	787	781	0	99.2	83.1	89.5	hypothetical protein ARALYDRAFT_343376	gbpln	Arabidopsis lyrata	AT2G17550.1 | Symbols: | unknown protein; Has 264 Blast hits to 258 proteins in 65 species: Archae - 5; Bacteria - 5; Metazoa - 66; Fungi - 16; Plants - 107; Viruses - 0; Other Eukaryotes - 65 (source: NCBI BLink). | chr2:7634495-7637212 REVERSE LENGTH=779	787	779	0	99.0	83.5	89.7
Rsa1.0_00249.1.g9592.t1	ref|XP_002886121.1| hypothetical protein ARALYDRAFT_480649 [Arabidopsis lyrata subsp. lyrata] gi|297331961|gb|EFH62380.1| hypothetical protein ARALYDRAFT_480649 [Arabidopsis lyrata subsp. lyrata]	137	143	3.00E-50	104.4	78.8	90.5	hypothetical protein ARALYDRAFT_480649	gbpln	Arabidopsis lyrata	AT2G17560.2 | Symbols: HMGB4, NFD4, NFD04 | high mobility group B4 | chr2:7642486-7643468 REVERSE LENGTH=138	137	138	4.00E-51	100.7	74.5	88.3
Rsa1.0_00249.1.g9593.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00249.1.g9594.t1	gb|AAF78267.1|AC020576_11 Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene [Arabidopsis thaliana]	977	1206	0	123.4	43.6	57.2	Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	977	719	2.00E-35	73.6	12.6	21.0
Rsa1.0_00249.1.g9595.t14	gb|AAF78272.1|AC020576_16 Contains similarity to a putative protein T32A11_100 gi|7413627 from Arabidopsis thaliana BAC T32A11 gb|AL138653 [Arabidopsis thaliana]	1538	1075	1.00E-74	69.9	11.4	16.8	Contains similarity to a putative protein T32A11_100 gi|7413627 from Arabidopsis thaliana BAC T32A11 gb|AL138653	gbpln	Arabidopsis thaliana	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	1538	673	9.00E-52	43.8	9.3	13.7
Rsa1.0_00249.1.g9596.t1	ref|XP_002884068.1| undecaprenyl pyrophosphate synthetase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329908|gb|EFH60327.1| undecaprenyl pyrophosphate synthetase family protein [Arabidopsis lyrata subsp. lyrata]	277	296	1.00E-133	106.9	84.1	92.4	undecaprenyl pyrophosphate synthetase family protein	gbpln	Arabidopsis lyrata	AT2G17570.1 | Symbols: | Undecaprenyl pyrophosphate synthetase family protein | chr2:7645086-7645973 FORWARD LENGTH=295	277	295	1.00E-132	106.5	83.8	91.7
Rsa1.0_00249.1.g9597.t2	ref|XP_002884073.1| AMP-dependent synthetase and ligase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329913|gb|EFH60332.1| AMP-dependent synthetase and ligase family protein [Arabidopsis lyrata subsp. lyrata]	565	596	0	105.5	87.8	92.2	AMP-dependent synthetase and ligase family protein	gbpln	Arabidopsis lyrata	AT2G17650.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr2:7671041-7672936 FORWARD LENGTH=603	565	603	0	106.7	86.9	93.5
Rsa1.0_00249.1.g9598.t1	ref|NP_179357.1| RPM1-interacting protein 4-like protein [Arabidopsis thaliana] gi|11762120|gb|AAG40338.1|AF324986_1 At2g17660 [Arabidopsis thaliana] gi|115646839|gb|ABJ17136.1| At2g17660 [Arabidopsis thaliana] gi|330251568|gb|AEC06662.1| RPM1-interacting protein 4-like protein [Arabidopsis thaliana]	69	69	1.00E-29	100.0	92.8	97.1	RPM1-interacting protein 4-like protein	gbpln	Arabidopsis thaliana	AT2G17660.1 | Symbols: | RPM1-interacting protein 4 (RIN4) family protein | chr2:7673359-7673568 FORWARD LENGTH=69	69	69	2.00E-32	100.0	92.8	97.1
Rsa1.0_00249.1.g9599.t1	ref|XP_002887164.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333005|gb|EFH63423.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	127	360	2.00E-37	283.5	59.1	79.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G68170.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:25551925-25554258 FORWARD LENGTH=356	127	356	9.00E-40	280.3	59.1	78.0

Rsa1.0_00249.1.g9600.t4	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1007	1274	1.00E-142	126.5	25.1	34.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1007	626	7.00E-35	62.2	11.4	18.5
Rsa1.0_00250.1.g9601.t1	gb|ABV21212.1| Ty1_Copia-element protein [Arabidopsis thaliana]	529	438	1.00E-82	82.8	32.3	45.4	Ty1_Copia-element protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	529	746	4.00E-56	141.0	28.5	42.9
Rsa1.0_00250.1.g9602.t1	ref|XP_002875082.1| hypothetical protein ARALYDRAFT_904366 [Arabidopsis lyrata subsp. lyrata] gi|297320920|gb|EFH51341.1| hypothetical protein ARALYDRAFT_904366 [Arabidopsis lyrata subsp. lyrata]	576	562	0	97.6	85.2	89.6	hypothetical protein ARALYDRAFT_904366	gbpln	Arabidopsis lyrata	AT2G01600.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr2:268975-272356 FORWARD LENGTH=571	576	571	0	99.1	85.9	90.8
Rsa1.0_00250.1.g9603.t1	ref|NP_190144.1| RING/U-box protein with C6HC-type zinc finger [Arabidopsis thaliana] gi|6996261|emb|CAB75487.1| putative protein [Arabidopsis thaliana] gi|332644525|gb|AEE78046.1| RING/U-box protein with C6HC-type zinc finger [Arabidopsis thaliana]	432	408	1.00E-108	94.4	46.3	61.1	RING/U-box protein with C6HC-type zinc finger	gbpln	Arabidopsis thaliana	AT3G45580.1 | Symbols: | RING/U-box protein with C6HC-type zinc finger | chr3:16729989-16731511 REVERSE LENGTH=408	432	408	1.00E-111	94.4	46.3	61.1
Rsa1.0_00250.1.g9604.t1	ref|XP_002875081.1| hypothetical protein ARALYDRAFT_346658 [Arabidopsis lyrata subsp. lyrata] gi|297320919|gb|EFH51340.1| hypothetical protein ARALYDRAFT_346658 [Arabidopsis lyrata subsp. lyrata]	156	167	3.00E-60	107.1	82.1	90.4	hypothetical protein ARALYDRAFT_346658	gbpln	Arabidopsis lyrata	AT2G01590.1 | Symbols: CRR3 | chlororespiratory reduction 3 | chr2:266675-267379 FORWARD LENGTH=174	156	174	6.00E-58	111.5	77.6	88.5
Rsa1.0_00250.1.g9605.t2	sp|Q9ZSR8.1|RSSA_BRANA RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor-like protein; AltName: Full=p40 gi|3769681|gb|AAC97937.1| laminin receptor-like protein [Brassica napus]	231	292	5.00E-37	126.4	39.8	42.0	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor-like protein; AltName: Full=p40 gi|3769681|gb|AAC97937.1| laminin receptor-like protein	gbpln	Brassica napus	AT1G72370.2 | Symbols: P40, AP40, RP40, RPSAA | 40s ribosomal protein SA | chr1:27243148-27244842 REVERSE LENGTH=294	231	294	2.00E-36	127.3	39.4	42.4
Rsa1.0_00250.1.g9606.t1	ref|NP_565780.1| cysteine proteinase-like protein [Arabidopsis thaliana] gi|2342728|gb|AAB67626.1| cysteine proteinase [Arabidopsis thaliana] gi|330253821|gb|AEC08915.1| cysteine proteinase-like protein [Arabidopsis thaliana]	238	345	1.00E-76	145.0	59.2	70.6	cysteine proteinase-like protein	gbpln	Arabidopsis thaliana	AT2G34080.1 | Symbols: | Cysteine proteinases superfamily protein | chr2:14393431-14394777 REVERSE LENGTH=345	238	345	3.00E-79	145.0	59.2	70.6
Rsa1.0_00250.1.g9607.t2	gb|ADK63403.1| C2 domain-containing protein [Brassica rapa]	193	180	1.00E-96	93.3	90.2	91.2	C2 domain-containing protein	gbpln	Brassica rapa	AT2G01540.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:242297-243233 REVERSE LENGTH=180	193	180	1.00E-92	93.3	82.9	86.5
Rsa1.0_00250.1.g9608.t1	ref|XP_002875076.1| hypothetical protein ARALYDRAFT_904347 [Arabidopsis lyrata subsp. lyrata] gi|297320914|gb|EFH51335.1| hypothetical protein ARALYDRAFT_904347 [Arabidopsis lyrata subsp. lyrata]	184	151	1.00E-70	82.1	71.7	76.6	hypothetical protein ARALYDRAFT_904347	gbpln	Arabidopsis lyrata	AT2G01520.1 | Symbols: MLP328 | MLP-like protein 328 | chr2:235992-236881 FORWARD LENGTH=151	184	151	9.00E-73	82.1	71.7	76.1
Rsa1.0_00250.1.g9609.t1	gb|EOA29259.1| hypothetical protein CARUB_v10025533mg, partial [Capsella rubella]	248	293	5.00E-65	118.1	55.2	65.3	hypothetical protein CARUB_v10025533mg, partial	gbpln	Capsella rubella	AT1G34070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48050.1); Has 648 Blast hits to 647 proteins in 29 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 25; Plants - 607; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12402283-12403209 FORWARD LENGTH=308	248	308	2.00E-54	124.2	46.4	57.3
Rsa1.0_00250.1.g9610.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00250.1.g9611.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00250.1.g9612.t1	ref|XP_002870668.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297316504|gb|EFH46927.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	439	466	0	106.2	76.5	84.5	WD-40 repeat family protein	gbpln	Arabidopsis lyrata	AT5G40880.1 | Symbols: | WD-40 repeat family protein / zfwd3 protein (ZFWD3) | chr5:16379481-16381205 FORWARD LENGTH=472	439	472	0	107.5	74.0	83.1
Rsa1.0_00250.1.g9613.t1	gb|EOA24970.1| hypothetical protein CARUB_v10018267mg [Capsella rubella]	107	115	1.00E-21	107.5	62.6	66.4	hypothetical protein CARUB_v10018267mg	gbpln	Capsella rubella	AT2G01505.1 | Symbols: CLE16 | CLAVATA3/ESR-RELATED 16 | chr2:228926-229237 REVERSE LENGTH=103	107	103	1.00E-23	96.3	49.5	57.9

Rsa1.0_00250.1.g9614.t1	ref|XP_002875075.1| hypothetical protein ARALYDRAFT_484067 [Arabidopsis lyrata subsp. lyrata] gi|297320913|gb|EFH51334.1| hypothetical protein ARALYDRAFT_484067 [Arabidopsis lyrata subsp. lyrata]	300	284	1.00E-145	94.7	86.7	91.7	hypothetical protein ARALYDRAFT_484067	gbpln	Arabidopsis lyrata	AT2G01490.1 | Symbols: | phytanoyl-CoA dioxygenase (PhyH) family protein | chr2:221316-223187 FORWARD LENGTH=283	300	283	1.00E-147	94.3	85.7	90.7
Rsa1.0_00250.1.g9615.t1	gb|EOA25557.1| hypothetical protein CARUB_v10018910mg [Capsella rubella]	952	962	0	101.1	94.6	96.7	hypothetical protein CARUB_v10018910mg	gbpln	Capsella rubella	AT2G01460.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:206136-211765 FORWARD LENGTH=955	952	955	0	100.3	94.0	96.2
Rsa1.0_00250.1.g9616.t1	ref|NP_178254.2| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|79316341|ref|NP_001030939.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|79316349|ref|NP_001030940.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|79316359|ref|NP_001030941.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|75327927|sp|Q84M93.1|MPK17_ARATH RecName: Full=Mitogen-activated protein kinase 17; Short=AtMPK17; Short=MAP kinase 17 gi|30102718|gb|AAP21277.1| At2g01450 [Arabidopsis thaliana] gi|110736492|dbj|BAF00214.1| putative MAP kinase [Arabidopsis thaliana] gi|222423803|dbj|BAH19867.1| AT2G01450 [Arabidopsis thaliana] gi|330250358|gb|AEC05452.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|330250359|gb|AEC05453.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|330250360|gb|AEC05454.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana] gi|330250361|gb|AEC05455.1| mitogen-activated protein kinase 17 [Arabidopsis thaliana]	509	486	0	95.5	90.2	92.5	mitogen-activated protein kinase 17	gbpln	Arabidopsis thaliana	AT2G01450.4 | Symbols: ATMPK17, MPK17 | MAP kinase 17 | chr2:199722-202010 REVERSE LENGTH=486	509	486	0	95.5	90.2	92.5
Rsa1.0_00250.1.g9617.t1	ref|XP_002876750.1| hypothetical protein ARALYDRAFT_346639 [Arabidopsis lyrata subsp. lyrata] gi|297322588|gb|EFH53009.1| hypothetical protein ARALYDRAFT_346639 [Arabidopsis lyrata subsp. lyrata]	196	201	4.00E-98	102.6	92.3	94.9	hypothetical protein ARALYDRAFT_346639	gbpln	Arabidopsis lyrata	AT2G01430.1 | Symbols: ATHB17, ATHB-17, HB17 | homeobox-leucine zipper protein 17 | chr2:187798-190369 REVERSE LENGTH=275	196	275	1.00E-95	140.3	89.3	92.9
Rsa1.0_00250.1.g9618.t1	ref|NP_565261.1| auxin efflux carrier component 4 [Arabidopsis thaliana] gi|7109715|gb|AAF36769.1| auxin transporter splice variant b [Arabidopsis thaliana] gi|20197401|gb|AAC67319.2| putative auxin transport protein [Arabidopsis thaliana] gi|20197591|gb|AAM15143.1| putative auxin transport protein [Arabidopsis thaliana] gi|330250354|gb|AEC05448.1| auxin efflux carrier component 4 [Arabidopsis thaliana]	601	612	0	101.8	90.8	93.7	auxin efflux carrier component 4	gbpln	Arabidopsis thaliana	AT2G01420.1 | Symbols: PIN4, ATPIN4 | Auxin efflux carrier family protein | chr2:180478-183199 REVERSE LENGTH=612	601	612	0	101.8	90.8	93.7
Rsa1.0_00250.1.g9619.t1	ref|XP_002875071.1| hypothetical protein ARALYDRAFT_322483 [Arabidopsis lyrata subsp. lyrata] gi|297320909|gb|EFH51330.1| hypothetical protein ARALYDRAFT_322483 [Arabidopsis lyrata subsp. lyrata]	151	142	2.00E-51	94.0	72.2	81.5	hypothetical protein ARALYDRAFT_322483	gbpln	Arabidopsis lyrata	AT2G01400.1 | Symbols: | unknown protein; Has 19 Blast hits to 19 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:174315-175080 FORWARD LENGTH=146	151	146	8.00E-53	96.7	74.8	84.8
Rsa1.0_00250.1.g9620.t1	gb|EOA24307.1| hypothetical protein CARUB_v10017548mg [Capsella rubella]	353	351	0	99.4	93.8	97.2	hypothetical protein CARUB_v10017548mg	gbpln	Capsella rubella	AT2G01350.1 | Symbols: QPT | quinolinate phoshoribosyltransferase | chr2:165332-167209 REVERSE LENGTH=348	353	348	0	98.6	90.9	94.9

Rsa1.0_00250.1.g9621.t1	ref|NP_178243.2| uncharacterized protein [Arabidopsis thaliana] gi|62867641|gb|AAY17424.1| At2g01340 [Arabidopsis thaliana] gi|94442481|gb|ABF19028.1| At2g01340 [Arabidopsis thaliana] gi|110741090|dbj|BAE98639.1| hypothetical protein [Arabidopsis thaliana] gi|330250344|gb|AEC05438.1| uncharacterized protein AT2G01340 [Arabidopsis thaliana]	221	215	2.00E-87	97.3	82.8	86.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G01340.1 | Symbols: At17.1 | Encodes a protein whose expression is responsive to nematode infection. | chr2:164014-165068 FORWARD LENGTH=215	221	215	6.00E-90	97.3	82.8	86.9
Rsa1.0_00250.1.g9622.t2	gb|EOA23654.1| hypothetical protein CARUB_v10016855mg [Capsella rubella]	376	612	4.00E-64	162.8	45.5	49.2	hypothetical protein CARUB_v10016855mg	gbpln	Capsella rubella	AT2G01330.2 | Symbols: | nucleotide binding | chr2:158417-160755 REVERSE LENGTH=611	376	611	3.00E-64	162.5	44.7	49.5
Rsa1.0_00250.1.g9623.t6	ref|XP_002876742.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297322580|gb|EFH53001.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata]	1123	729	0	64.9	58.3	61.4	abc transporter family protein	gbpln	Arabidopsis lyrata	AT2G01320.2 | Symbols: | ABC-2 type transporter family protein | chr2:154487-158063 REVERSE LENGTH=727	1123	727	0	64.7	57.7	61.0
Rsa1.0_00250.1.g9624.t1	ref|NP_178239.1| uncharacterized protein [Arabidopsis thaliana] gi|4262237|gb|AAD14530.1| predicted by genscan and genefinder [Arabidopsis thaliana] gi|17529142|gb|AAL38797.1| unknown protein [Arabidopsis thaliana] gi|21436241|gb|AAM51259.1| unknown protein [Arabidopsis thaliana] gi|49660101|gb|AAT68341.1| hypothetical protein At2g01300 [Arabidopsis thaliana] gi|60547691|gb|AAX23809.1| hypothetical protein At2g01300 [Arabidopsis thaliana] gi|330250336|gb|AEC05430.1| uncharacterized protein AT2G01300 [Arabidopsis thaliana]	155	156	1.00E-66	100.6	83.2	89.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G01300.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15010.1); Has 73 Blast hits to 73 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:151221-151691 REVERSE LENGTH=156	155	156	3.00E-69	100.6	83.2	89.0
Rsa1.0_00250.1.g9625.t1	ref|NP_178238.1| ribose 5-phosphate isomerase A [Arabidopsis thaliana] gi|6226027|sp|Q9ZU38.1|RPIA_ARATH RecName: Full=Probable ribose-5-phosphate isomerase; AltName: Full=Phosphoriboisomerase gi|4262236|gb|AAD14529.1| putative ribose 5-phosphate isomerase [Arabidopsis thaliana] gi|15809810|gb|AAL06833.1| At2g01290/F10A8.17 [Arabidopsis thaliana] gi|17978867|gb|AAL47405.1| At2g01290/F10A8.17 [Arabidopsis thaliana] gi|91805381|gb|ABE65420.1| unknown [Arabidopsis thaliana] gi|330250335|gb|AEC05429.1| ribose 5-phosphate isomerase A [Arabidopsis thaliana]	268	265	1.00E-128	98.9	87.7	92.9	ribose 5-phosphate isomerase A	gbpln	Arabidopsis thaliana	AT2G01290.1 | Symbols: RPI2 | ribose-5-phosphate isomerase 2 | chr2:149192-149989 REVERSE LENGTH=265	268	265	1.00E-131	98.9	87.7	92.9
Rsa1.0_00250.1.g9626.t4	gb|EOA25149.1| hypothetical protein CARUB_v10018459mg [Capsella rubella]	256	259	1.00E-122	101.2	84.8	91.0	hypothetical protein CARUB_v10018459mg	gbpln	Capsella rubella	AT2G01275.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:142610-143809 REVERSE LENGTH=259	256	259	1.00E-118	101.2	83.6	91.4
Rsa1.0_00250.1.g9627.t1	ref|NP_565258.1| quiescin-sulfhydryl oxidase 2 [Arabidopsis thaliana] gi|75339028|sp|Q9ZU40.2|QSOX2_ARATH RecName: Full=Sulfhydryl oxidase 2; AltName: Full=Quiescin-sulfhydryl oxidase 2; Short=AtQSOX2; Flags: Precursor gi|19699314|gb|AAL91267.1| At2g01270/F10A8.15 [Arabidopsis thaliana] gi|20197588|gb|AAD14527.2| expressed protein [Arabidopsis thaliana] gi|21928041|gb|AAM78049.1| At2g01270/F10A8.15 [Arabidopsis thaliana] gi|24030200|gb|AAN41280.1| unknown protein [Arabidopsis thaliana] gi|330250331|gb|AEC05425.1| quiescin-sulfhydryl oxidase 2 [Arabidopsis thaliana]	506	495	0	97.8	85.4	93.1	quiescin-sulfhydryl oxidase 2	gbpln	Arabidopsis thaliana	AT2G01270.1 | Symbols: AtQSOX2, QSOX2 | quiescin-sulfhydryl oxidase 2 | chr2:139457-142141 FORWARD LENGTH=495	506	495	0	97.8	85.4	93.1

Rsa1.0_00250.1.g9628.t1	ref|NP_565257.1| uncharacterized protein [Arabidopsis thaliana] gi|20197590|gb|AAD14526.2| predicted by genscan and genefinder [Arabidopsis thaliana] gi|30725294|gb|AAP37669.1| At2g01260 [Arabidopsis thaliana] gi|110736023|dbj|BAE99984.1| hypothetical protein [Arabidopsis thaliana] gi|330250328|gb|AEC05422.1| uncharacterized protein AT2G01260 [Arabidopsis thaliana]	380	369	1.00E-143	97.1	74.7	80.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G01260.1 | Symbols: | Protein of unknown function (DUF789) | chr2:135494-137504 REVERSE LENGTH=369	380	369	2.33E-156	97.1	74.7	80.5
Rsa1.0_00250.1.g9629.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	1581	1557	0	98.5	44.3	58.9	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1581	575	1.00E-54	36.4	6.8	10.9
Rsa1.0_00251.1.g9630.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	196	1142	1.00E-31	582.7	42.3	59.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9631.t1	ref|XP_002874383.1| ATGID1C/GID1C [Arabidopsis lyrata subsp. lyrata] gi|297320220|gb|EFH50642.1| ATGID1C/GID1C [Arabidopsis lyrata subsp. lyrata]	343	344	0	100.3	92.7	96.2	ATGID1C/GID1C	gbpln	Arabidopsis lyrata	AT5G27320.1 | Symbols: ATGID1C, GID1C | alpha/beta-Hydrolases superfamily protein | chr5:9629254-9630746 FORWARD LENGTH=344	343	344	0	100.3	92.7	95.3
Rsa1.0_00251.1.g9632.t1	ref|NP_198085.1| Prefoldin chaperone subunit family protein [Arabidopsis thaliana] gi|332006290|gb|AED93673.1| Prefoldin chaperone subunit family protein [Arabidopsis thaliana]	603	628	0	104.1	71.1	84.6	Prefoldin chaperone subunit family protein	gbpln	Arabidopsis thaliana	AT5G27330.1 | Symbols: | Prefoldin chaperone subunit family protein | chr5:9632997-9634883 REVERSE LENGTH=628	603	628	0	104.1	71.1	84.6
Rsa1.0_00251.1.g9633.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	805	1274	0	158.3	57.5	71.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	805	575	8.00E-36	71.4	16.6	25.7
Rsa1.0_00251.1.g9634.t1	ref|XP_002874378.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320215|gb|EFH50637.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	69	463	2.00E-21	671.0	71.0	82.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G27360.1 | Symbols: SFP2 | Major facilitator superfamily protein | chr5:9657119-9662425 FORWARD LENGTH=478	69	478	2.00E-23	692.8	69.6	82.6
Rsa1.0_00251.1.g9635.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1741	1213	0	69.7	26.4	38.8	unknown protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	1741	295	4.00E-79	16.9	8.4	11.7
Rsa1.0_00251.1.g9636.t1	gb|ACX70133.1| glutathione synthetase [Brassica rapa subsp. chinensis]	459	478	0	104.1	94.1	96.7	glutathione synthetase	gbpln	Brassica rapa	AT5G27380.1 | Symbols: GSH2, GSHB | glutathione synthetase 2 | chr5:9668211-9670912 REVERSE LENGTH=539	459	539	0	117.4	83.9	92.2
Rsa1.0_00251.1.g9637.t2	ref|XP_002872273.1| protein translocase [Arabidopsis lyrata subsp. lyrata] gi|297318110|gb|EFH48532.1| protein translocase [Arabidopsis lyrata subsp. lyrata]	314	314	1.00E-148	100.0	82.2	87.3	protein translocase	gbpln	Arabidopsis lyrata	AT5G27395.1 | Symbols: | Mitochondrial inner membrane translocase complex, subunit Tim44-related protein | chr5:9671845-9674085 REVERSE LENGTH=313	314	313	1.00E-147	99.7	81.2	86.0
Rsa1.0_00251.1.g9638.t1	ref|NP_198091.2| Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein [Arabidopsis thaliana] gi|332006298|gb|AED93681.1| Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein [Arabidopsis thaliana]	238	241	2.00E-87	101.3	76.1	80.7	Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein	gbpln	Arabidopsis thaliana	AT5G27390.1 | Symbols: | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | chr5:9674634-9676118 REVERSE LENGTH=241	238	241	6.00E-90	101.3	76.1	80.7
Rsa1.0_00251.1.g9639.t1	ref|XP_002874375.1| hypothetical protein ARALYDRAFT_910844 [Arabidopsis lyrata subsp. lyrata] gi|297320212|gb|EFH50634.1| hypothetical protein ARALYDRAFT_910844 [Arabidopsis lyrata subsp. lyrata]	367	369	0	100.5	85.0	91.0	hypothetical protein ARALYDRAFT_910844	gbpln	Arabidopsis lyrata	AT5G27400.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:9676362-9678285 FORWARD LENGTH=369	367	369	1.00E-177	100.5	82.0	89.1
Rsa1.0_00251.1.g9640.t1	ref|NP_001190410.1| branched-chain-amino-acid aminotransferase-like protein 2 [Arabidopsis thaliana] gi|332006301|gb|AED93684.1| branched-chain-amino-acid aminotransferase-like protein 2 [Arabidopsis thaliana]	558	936	0	167.7	92.8	96.4	branched-chain-amino-acid aminotransferase-like protein 2	gbpln	Arabidopsis thaliana	AT5G27410.2 | Symbols: | D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein | chr5:9676362-9682468 FORWARD LENGTH=936	558	936	0	167.7	92.8	96.4
Rsa1.0_00251.1.g9641.t1	ref|XP_002874373.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297320210|gb|EFH50632.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	253	370	6.00E-85	146.2	62.5	73.1	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G27420.1 | Symbols: CNI1, ATL31 | carbon/nitrogen insensitive 1 | chr5:9684119-9685225 FORWARD LENGTH=368	253	368	3.00E-86	145.5	62.8	71.5

Rsa1.0_00251.1.g9642.t1	ref|NP_198094.1| E3 ubiquitin-protein ligase ATL31 [Arabidopsis thaliana] gi|68565208|sp|Q8LGA5.2|ATL31_ARATH RecName: Full=E3 ubiquitin-protein ligase ATL31; AltName: Full=Protein CARBON/NITROGEN INSENSITIVE 1; AltName: Full=Protein SUPER SURVIVAL 1; AltName: Full=RING-H2 finger protein ATL31; Flags: Precursor gi|110742271|dbj|BAE99061.1| RING-H2 zinc finger protein-like [Arabidopsis thaliana] gi|332006302|gb|AED93685.1| E3 ubiquitin-protein ligase ATL31 [Arabidopsis thaliana]	295	368	1.00E-75	124.7	53.2	63.1	E3 ubiquitin-protein ligase ATL31	gbpln	Arabidopsis thaliana	AT5G27420.1 | Symbols: CNI1, ATL31 | carbon/nitrogen insensitive 1 | chr5:9684119-9685225 FORWARD LENGTH=368	295	368	3.00E-78	124.7	53.2	63.1
Rsa1.0_00251.1.g9643.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9644.t1	gb|EOA21694.1| hypothetical protein CARUB_v10002121mg [Capsella rubella] gi|482557503|gb|EOA21695.1| hypothetical protein CARUB_v10002121mg [Capsella rubella]	167	167	3.00E-90	100.0	94.6	98.8	hypothetical protein CARUB_v10002121mg	gbpln	Capsella rubella	AT5G27430.1 | Symbols: | Signal peptidase subunit | chr5:9687470-9689185 FORWARD LENGTH=167	167	167	1.00E-92	100.0	94.6	98.8
Rsa1.0_00251.1.g9645.t1	ref|XP_002877486.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323324|gb|EFH53745.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	196	362	8.00E-41	184.7	48.0	53.6	predicted protein	gbpln	Arabidopsis lyrata	AT2G34280.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:14470335-14471510 REVERSE LENGTH=391	196	391	2.00E-32	199.5	41.8	50.5
Rsa1.0_00251.1.g9646.t1	ref|XP_002872268.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297318105|gb|EFH48527.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	299	321	1.00E-120	107.4	70.9	74.6	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT5G27520.1 | Symbols: PNC2 | peroxisomal adenine nucleotide carrier 2 | chr5:9714664-9716244 REVERSE LENGTH=321	299	321	1.00E-122	107.4	70.9	74.2
Rsa1.0_00251.1.g9647.t8	gb|EOA20124.1| hypothetical protein CARUB_v10000404mg, partial [Capsella rubella]	619	664	0	107.3	84.2	90.5	hypothetical protein CARUB_v10000404mg, partial	gbpln	Capsella rubella	AT5G27540.2 | Symbols: MIRO1 | MIRO-related GTP-ase 1 | chr5:9722816-9727112 FORWARD LENGTH=648	619	648	0	104.7	83.5	90.1
Rsa1.0_00251.1.g9648.t1	gb|EOA23059.1| hypothetical protein CARUB_v10003829mg [Capsella rubella]	698	698	0	100.0	88.7	95.4	hypothetical protein CARUB_v10003829mg	gbpln	Capsella rubella	AT5G27600.1 | Symbols: LACS7, ATLACS7 | long-chain acyl-CoA synthetase 7 | chr5:9742616-9746795 FORWARD LENGTH=700	698	700	0	100.3	87.1	94.3
Rsa1.0_00251.1.g9649.t1	ref|NP_198113.2| protein ALWAYS EARLY 1 [Arabidopsis thaliana] gi|296439606|sp|Q6A331.2|ALY1_ARATH RecName: Full=Protein ALWAYS EARLY 1; Short=AtALY1 gi|225898943|dbj|BAH30602.1| hypothetical protein [Arabidopsis thaliana] gi|332006323|gb|AED93706.1| protein ALWAYS EARLY 1 [Arabidopsis thaliana]	1054	971	0	92.1	59.5	68.7	protein ALWAYS EARLY 1	gbpln	Arabidopsis thaliana	AT5G27610.1 | Symbols: ATALY1, ALY1 | DIRP ;Myb-like DNA-binding domain | chr5:9764852-9769706 FORWARD LENGTH=971	1054	971	0	92.1	59.5	68.7
Rsa1.0_00251.1.g9650.t1	gb|EOA20680.1| hypothetical protein CARUB_v10000993mg [Capsella rubella]	432	435	0	100.7	87.0	93.5	hypothetical protein CARUB_v10000993mg	gbpln	Capsella rubella	AT5G27660.1 | Symbols: | Trypsin family protein with PDZ domain | chr5:9789835-9792235 REVERSE LENGTH=428	432	428	0	99.1	78.9	86.6
Rsa1.0_00251.1.g9651.t1	ref|NP_198119.1| histone H2A 7 [Arabidopsis thaliana] gi|75306451|sp|Q94F49.1|H2A5_ARATH RecName: Full=Probable histone H2A.5; AltName: Full=HTA7 gi|14326516|gb|AAK60303.1|AF385711_1 AT5g27670/F15A18_130 [Arabidopsis thaliana] gi|18700220|gb|AAL77720.1| AT5g27670/F15A18_130 [Arabidopsis thaliana] gi|332006330|gb|AED93713.1| histone H2A 7 [Arabidopsis thaliana]	155	150	2.00E-66	96.8	83.2	89.0	histone H2A 7	gbpln	Arabidopsis thaliana	AT5G27670.1 | Symbols: HTA7 | histone H2A 7 | chr5:9792807-9793365 REVERSE LENGTH=150	155	150	5.00E-69	96.8	83.2	89.0
Rsa1.0_00251.1.g9652.t14	gb|AAO52679.1| putative DNA helicase RecQsim [Brassica napus]	949	880	0	92.7	75.8	79.8	putative DNA helicase RecQsim	gbpln	Brassica napus	AT5G27680.1 | Symbols: RECQSIM | RECQ helicase SIM | chr5:9794244-9798637 REVERSE LENGTH=858	949	858	0	90.4	70.1	75.3
Rsa1.0_00251.1.g9653.t1	gb|EOA21887.1| hypothetical protein CARUB_v10002364mg [Capsella rubella]	82	82	9.00E-40	100.0	93.9	97.6	hypothetical protein CARUB_v10002364mg	gbpln	Capsella rubella	AT5G27700.1 | Symbols: | Ribosomal protein S21e | chr5:9807541-9808048 REVERSE LENGTH=82	82	82	2.00E-42	100.0	93.9	97.6
Rsa1.0_00251.1.g9654.t1	sp|Q43582.1|LSM4_TOBAC RecName: Full=Probable U6 snRNA-associated Sm-like protein LSm4; AltName: Full=Glycine-rich protein 10; Short=GRP 10 gi|790473|emb|CAA58702.1| unnamed protein product [Nicotiana tabacum]	134	146	1.00E-50	109.0	73.1	74.6	RecName: Full=Probable U6 snRNA-associated Sm-like protein LSm4; AltName: Full=Glycine-rich protein 10; Short=GRP 10 gi|790473|emb|CAA58702.1| unnamed protein product	gbpln	Nicotiana tabacum	AT5G27720.1 | Symbols: emb1644 | Small nuclear ribonucleoprotein family protein | chr5:9815904-9817304 FORWARD LENGTH=129	134	129	3.00E-50	96.3	67.2	67.2

Rsa1.0_00251.1.g9655.t2	ref|NP_198126.1| replication factor C subunit 3/5 [Arabidopsis thaliana] gi|18389268|gb|AAL67077.1| putative replication factor C [Arabidopsis thaliana] gi|20259637|gb|AAM14175.1| putative replication factor C [Arabidopsis thaliana] gi|332006337|gb|AED93720.1| protein embryo defective 161 [Arabidopsis thaliana]	432	354	0	81.9	75.0	75.9	replication factor C subunit 3/5	gbpln	Arabidopsis thaliana	AT5G27740.1 | Symbols: EMB161, EMB2775, EMB251, RFC3 | ATPase family associated with various cellular activities (AAA) | chr5:9823831-9826869 FORWARD LENGTH=354	432	354	0	81.9	75.0	75.9
Rsa1.0_00251.1.g9656.t1	dbj|BAJ34418.1| unnamed protein product [Thellungiella halophila]	126	124	3.00E-50	98.4	92.1	95.2	unnamed protein product	----	----	AT3G05560.3 | Symbols: | Ribosomal L22e protein family | chr3:1614641-1615204 FORWARD LENGTH=124	126	124	1.00E-51	98.4	90.5	94.4
Rsa1.0_00251.1.g9657.t2	ref|NP_001190413.1| uncharacterized protein [Arabidopsis thaliana] gi|332006350|gb|AED93733.1| uncharacterized protein AT5G27830 [Arabidopsis thaliana]	420	322	1.00E-129	76.7	58.6	63.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G27830.4 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Folate receptor, conserved region (InterPro:IPR018143). | chr5:9861203-9862742 FORWARD LENGTH=322	420	322	1.00E-131	76.7	58.6	63.8
Rsa1.0_00251.1.g9658.t1	ref|XP_002872257.1| hypothetical protein ARALYDRAFT_489548 [Arabidopsis lyrata subsp. lyrata] gi|297318094|gb|EFH48516.1| hypothetical protein ARALYDRAFT_489548 [Arabidopsis lyrata subsp. lyrata]	371	318	1.00E-177	85.7	81.7	83.0	hypothetical protein ARALYDRAFT_489548	gbpln	Arabidopsis lyrata	AT5G27840.2 | Symbols: TOPP8 | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:9863465-9864828 REVERSE LENGTH=324	371	324	1.00E-179	87.3	81.4	82.7
Rsa1.0_00251.1.g9659.t1	ref|NP_187210.1| 60S ribosomal protein L18-2 [Arabidopsis thaliana] gi|21431838|sp|P42791.2|RL182_ARATH RecName: Full=60S ribosomal protein L18-2 gi|6714451|gb|AAF26138.1|AC011620_14 putative 60S ribosomal protein L18 [Arabidopsis thaliana] gi|14335090|gb|AAK59824.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gi|16974509|gb|AAL31164.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gi|332640742|gb|AEE74263.1| 60S ribosomal protein L18-2 [Arabidopsis thaliana]	187	187	3.00E-96	100.0	94.7	96.8	60S ribosomal protein L18-2	gbpln	Arabidopsis thaliana	AT3G05590.1 | Symbols: RPL18 | ribosomal protein L18 | chr3:1621511-1622775 FORWARD LENGTH=187	187	187	1.00E-98	100.0	94.7	96.8
Rsa1.0_00251.1.g9660.t1	ref|NP_198138.2| uncharacterized protein [Arabidopsis thaliana] gi|238481400|ref|NP_001154743.1| uncharacterized protein [Arabidopsis thaliana] gi|332006354|gb|AED93737.1| uncharacterized protein AT5G27860 [Arabidopsis thaliana] gi|332006355|gb|AED93738.1| uncharacterized protein AT5G27860 [Arabidopsis thaliana]	180	177	2.00E-37	98.3	52.2	54.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G27860.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: pollen tube; Has 23049 Blast hits to 11981 proteins in 648 species: Archae - 2; Bacteria - 589; Metazoa - 13464; Fungi - 1977; Plants - 1635; Viruses - 89; Other Eukaryotes - 5293 (source: NCBI BLink). | chr5:9875068-9876442 REVERSE LENGTH=177	180	177	9.00E-40	98.3	52.2	54.4
Rsa1.0_00251.1.g9661.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9662.t1	ref|NP_198139.1| pectinesterase 28 [Arabidopsis thaliana] gi|122214224|sp|Q3E8Z8.1|PME28_ARATH RecName: Full=Putative pectinesterase/pectinesterase inhibitor 28; Includes: RecName: Full=Pectinesterase inhibitor 28; AltName: Full=Pectin methylesterase inhibitor 28; Includes: RecName: Full=Pectinesterase 28; Short=PE 28; AltName: Full=Pectin methylesterase 28; Short=AtPME28 gi|332006356|gb|AED93739.1| pectinesterase 28 [Arabidopsis thaliana]	688	732	0	106.4	73.3	84.2	pectinesterase 28	gbpln	Arabidopsis thaliana	AT5G27870.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:9878991-9881806 REVERSE LENGTH=732	688	732	0	106.4	73.3	84.2
Rsa1.0_00251.1.g9663.t1	gb|EOA22296.1| hypothetical protein CARUB_v10002897mg [Capsella rubella]	295	278	3.00E-68	94.2	54.2	64.4	hypothetical protein CARUB_v10002897mg	gbpln	Capsella rubella	AT5G27880.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:9885908-9886744 FORWARD LENGTH=278	295	278	7.00E-71	94.2	53.6	64.7
Rsa1.0_00251.1.g9664.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9665.t1	ref|XP_002874340.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320177|gb|EFH50599.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	104	144	4.00E-15	138.5	49.0	57.7	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#

Rsa1.0_00251.1.g9666.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9667.t1	ref|XP_002874340.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320177|gb|EFH50599.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	94	144	3.00E-14	153.2	52.1	59.6	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9668.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9669.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9670.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00251.1.g9671.t1	ref|XP_002872252.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297318089|gb|EFH48511.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	642	642	0	100.0	86.1	92.5	F-box family protein	gbpln	Arabidopsis lyrata	AT5G27920.1 | Symbols: | F-box family protein | chr5:9942063-9944507 REVERSE LENGTH=642	642	642	0	100.0	84.6	91.9
Rsa1.0_00251.1.g9672.t1	ref|XP_002872242.1| hypothetical protein ARALYDRAFT_489519 [Arabidopsis lyrata subsp. lyrata] gi|297318079|gb|EFH48501.1| hypothetical protein ARALYDRAFT_489519 [Arabidopsis lyrata subsp. lyrata]	1031	991	0	96.1	85.1	88.7	hypothetical protein ARALYDRAFT_489519	gbpln	Arabidopsis lyrata	AT5G26860.1 | Symbols: LON_ARA_ARA, LON1 | lon protease 1 | chr5:9451183-9456631 FORWARD LENGTH=940	1031	940	0	91.2	82.0	85.4
Rsa1.0_00251.1.g9673.t1	gb|EOA22321.1| hypothetical protein CARUB_v10002922mg [Capsella rubella]	694	713	0	102.7	88.6	93.7	hypothetical protein CARUB_v10002922mg	gbpln	Capsella rubella	AT5G26830.1 | Symbols: | Threonyl-tRNA synthetase | chr5:9437351-9441568 FORWARD LENGTH=709	694	709	0	102.2	86.2	91.9
Rsa1.0_00251.1.g9674.t1	ref|XP_002886961.1| hypothetical protein ARALYDRAFT_894161 [Arabidopsis lyrata subsp. lyrata] gi|297332802|gb|EFH63220.1| hypothetical protein ARALYDRAFT_894161 [Arabidopsis lyrata subsp. lyrata]	283	299	5.00E-41	105.7	42.0	55.5	hypothetical protein ARALYDRAFT_894161	gbpln	Arabidopsis lyrata	AT1G23950.5 | Symbols: | Protein of unknown function (DUF626) | chr1:8469712-8471353 REVERSE LENGTH=343	283	343	1.00E-23	121.2	35.3	51.9
Rsa1.0_00251.1.g9675.t2	ref|NP_198033.2| putative pectinesterase 52 [Arabidopsis thaliana] gi|229891479|sp|O04953.2|PME52_ARATH RecName: Full=Putative pectinesterase 52; Short=PE 52; AltName: Full=Pectin methylesterase 52; Short=AtPME52; Flags: Precursor gi|332006225|gb|AED93608.1| putative pectinesterase 52 [Arabidopsis thaliana]	336	293	1.00E-117	87.2	64.3	73.8	putative pectinesterase 52	gbpln	Arabidopsis thaliana	AT5G26810.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:9430952-9432969 FORWARD LENGTH=293	336	293	1.00E-119	87.2	64.3	73.8
Rsa1.0_00251.1.g9676.t1	ref|NP_198032.2| uncharacterized protein [Arabidopsis thaliana] gi|48310023|gb|AAT41738.1| At5g26800 [Arabidopsis thaliana] gi|50198830|gb|AAT70447.1| At5g26800 [Arabidopsis thaliana] gi|332006223|gb|AED93606.1| uncharacterized protein AT5G26800 [Arabidopsis thaliana]	111	112	3.00E-44	100.9	81.1	88.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G26800.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; CONTAINS InterPro DOMAIN/s: IGR protein motif (InterPro:IPR019083); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G05810.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9425224-9426485 FORWARD LENGTH=112	111	112	5.00E-47	100.9	81.1	88.3
Rsa1.0_00251.1.g9677.t1	ref|XP_002872235.1| hypothetical protein ARALYDRAFT_489512 [Arabidopsis lyrata subsp. lyrata] gi|297318072|gb|EFH48494.1| hypothetical protein ARALYDRAFT_489512 [Arabidopsis lyrata subsp. lyrata]	110	66	5.00E-16	60.0	41.8	44.5	hypothetical protein ARALYDRAFT_489512	gbpln	Arabidopsis lyrata	AT5G26790.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06475.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:9423151-9423357 FORWARD LENGTH=68	110	68	1.00E-13	61.8	44.5	47.3
Rsa1.0_00252.1.g9678.t1	gb|EOA14861.1| hypothetical protein CARUB_v10028186mg [Capsella rubella]	153	149	2.00E-66	97.4	82.4	90.8	hypothetical protein CARUB_v10028186mg	gbpln	Capsella rubella	AT5G59040.1 | Symbols: COPT3 | copper transporter 3 | chr5:23836724-23837179 FORWARD LENGTH=151	153	151	4.00E-63	98.7	83.0	90.2
Rsa1.0_00252.1.g9679.t2	ref|XP_002875373.1| hypothetical protein ARALYDRAFT_322858 [Arabidopsis lyrata subsp. lyrata] gi|297321211|gb|EFH51632.1| hypothetical protein ARALYDRAFT_322858 [Arabidopsis lyrata subsp. lyrata]	272	1047	1.00E-43	384.9	36.0	39.7	hypothetical protein ARALYDRAFT_322858	gbpln	Arabidopsis lyrata	AT3G27325.2 | Symbols: | hydrolases, acting on ester bonds | chr3:10095956-10102087 FORWARD LENGTH=1121	272	1121	1.00E-45	412.1	35.3	39.3
Rsa1.0_00252.1.g9680.t1	ref|XP_002865336.1| helicase domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311171|gb|EFH41595.1| helicase domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1238	1251	0	101.1	74.7	84.0	helicase domain-containing protein	gbpln	Arabidopsis lyrata	AT1G33390.1 | Symbols: ATFAS4, FAS4 | RNA helicase family protein | chr1:12099738-12104108 REVERSE LENGTH=1237	1238	1237	0	99.9	73.8	83.1

<table>
<tr><td>Rsa1.0_00252.1.g9681.t1</td><td>ref|XP_002875372.1| hypothetical protein ARALYDRAFT_484517 [Arabidopsis lyrata subsp. lyrata] gi|297321210|gb|EFH51631.1| hypothetical protein ARALYDRAFT_484517 [Arabidopsis lyrata subsp. lyrata]</td><td>448</td><td>460</td><td>0</td><td>102.7</td><td>87.9</td><td>92.0</td><td>hypothetical protein ARALYDRAFT_484517</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G27320.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:10090307-10092391 FORWARD LENGTH=460</td><td>448</td><td>460</td><td>0</td><td>102.7</td><td>87.9</td><td>91.5</td></tr>
<tr><td>Rsa1.0_00252.1.g9682.t1</td><td>ref|XP_002875371.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321209|gb|EFH51630.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>443</td><td>479</td><td>0</td><td>108.1</td><td>73.6</td><td>84.9</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189</td><td>443</td><td>1189</td><td>1.00E-145</td><td>268.4</td><td>59.4</td><td>74.0</td></tr>
<tr><td>Rsa1.0_00252.1.g9683.t1</td><td>ref|NP_189363.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana] gi|9294220|dbj|BAB02122.1| unnamed protein product [Arabidopsis thaliana] gi|48310204|gb|AAT41774.1| At3g27270 [Arabidopsis thaliana] gi|52218804|gb|AAU29472.1| At3g27270 [Arabidopsis thaliana] gi|332643765|gb|AEE77286.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana]</td><td>344</td><td>249</td><td>1.00E-106</td><td>72.4</td><td>54.1</td><td>58.4</td><td>TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G27270.1 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr3:10073315-10074064 FORWARD LENGTH=249</td><td>344</td><td>249</td><td>1.00E-109</td><td>72.4</td><td>54.1</td><td>58.4</td></tr>
<tr><td>Rsa1.0_00252.1.g9684.t3</td><td>gb|AAC26234.1| contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]</td><td>903</td><td>940</td><td>0</td><td>104.1</td><td>47.1</td><td>61.4</td><td>contains similarity to maize transposon MuDR (GB:M76978)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00252.1.g9685.t1</td><td>ref|XP_002877435.1| hypothetical protein ARALYDRAFT_905750 [Arabidopsis lyrata subsp. lyrata] gi|297323273|gb|EFH53694.1| hypothetical protein ARALYDRAFT_905750 [Arabidopsis lyrata subsp. lyrata]</td><td>171</td><td>175</td><td>1.00E-33</td><td>102.3</td><td>42.7</td><td>58.5</td><td>hypothetical protein ARALYDRAFT_905750</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00252.1.g9686.t1</td><td>ref|NP_189361.1| uncharacterized protein [Arabidopsis thaliana] gi|9294218|dbj|BAB02120.1| unnamed protein product [Arabidopsis thaliana] gi|46931316|gb|AAT06462.1| At3g27250 [Arabidopsis thaliana] gi|62320492|dbj|BAD95032.1| hypothetical protein [Arabidopsis thaliana] gi|332643762|gb|AEE77283.1| uncharacterized protein AT3G27250 [Arabidopsis thaliana]</td><td>277</td><td>282</td><td>1.00E-122</td><td>101.8</td><td>78.3</td><td>87.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G27250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40800.1); Has 104 Blast hits to 104 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:10061633-10062481 FORWARD LENGTH=282</td><td>277</td><td>282</td><td>1.00E-124</td><td>101.8</td><td>78.3</td><td>87.4</td></tr>
<tr><td>Rsa1.0_00252.1.g9687.t1</td><td>ref|XP_002509561.1| cytochrome C1, putative [Ricinus communis] gi|223549460|gb|EEF50948.1| cytochrome C1, putative [Ricinus communis]</td><td>309</td><td>310</td><td>1.00E-160</td><td>100.3</td><td>86.4</td><td>93.5</td><td>cytochrome C1, putative</td><td>gbpln</td><td>Ricinus communis</td><td>AT3G27240.1 | Symbols: | Cytochrome C1 family | chr3:10056144-10058370 REVERSE LENGTH=307</td><td>309</td><td>307</td><td>1.00E-161</td><td>99.4</td><td>95.8</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00252.1.g9688.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00252.1.g9689.t1</td><td>ref|NP_565406.1| LysM domain-containing GPI-anchored protein 2 [Arabidopsis thaliana] gi|38257899|sp|O23006.1|LYM2_ARATH RecName: Full=LysM domain-containing GPI-anchored protein 2; AltName: Full=Chitin elicitor-binding protein LYM2; Short=CEBiP LYM2; Flags: Precursor gi|16226689|gb|AAL16233.1|AF428464_1 delta-8 sphingolipid desaturase [Arabidopsis thaliana] gi|15810365|gb|AAL07070.1| unknown protein [Arabidopsis thaliana] gi|21928083|gb|AAM78070.1| At2g17120 [Arabidopsis thaliana] gi|330251493|gb|AEC06587.1| LysM domain-containing GPI-anchored protein 2 [Arabidopsis thaliana]</td><td>111</td><td>350</td><td>3.00E-32</td><td>315.3</td><td>67.6</td><td>73.0</td><td>LysM domain-containing GPI-anchored protein 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17120.1 | Symbols: LYM2 | lysm domain GPI-anchored protein 2 precursor | chr2:7459156-7460648 FORWARD LENGTH=350</td><td>111</td><td>350</td><td>5.00E-35</td><td>315.3</td><td>67.6</td><td>73.0</td></tr>
</table>

Rsa1.0_00252.1.g9690.t1	ref|XP_002877027.1| hypothetical protein ARALYDRAFT_484504 [Arabidopsis lyrata subsp. lyrata] gi|297322865|gb|EFH53286.1| hypothetical protein ARALYDRAFT_484504 [Arabidopsis lyrata subsp. lyrata]	246	241	2.00E−68	98.0	73.6	80.5	hypothetical protein ARALYDRAFT_484504	gbpln	Arabidopsis lyrata	AT3G27210.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40860.1); Has 133 Blast hits to 98 proteins in 25 species: Archae − 0; Bacteria − 6; Metazoa − 32; Fungi − 7; Plants − 70; Viruses − 0; Other Eukaryotes − 18 (source: NCBI BLink). | chr3:10045458-10047222 REVERSE LENGTH=234	246	234	8.00E−65	95.1	69.1	75.6
Rsa1.0_00252.1.g9691.t1	gb|EOA24837.1| hypothetical protein CARUB_v10018126mg [Capsella rubella]	160	171	2.00E−56	106.9	65.6	71.3	hypothetical protein CARUB_v10018126mg	gbpln	Capsella rubella	AT3G27200.1 | Symbols: | Cupredoxin superfamily protein | chr3:10043738-10044340 REVERSE LENGTH=174	160	174	8.00E−58	108.8	63.8	70.6
Rsa1.0_00252.1.g9692.t1	gb|EOA23905.1| hypothetical protein CARUB_v10017120mg [Capsella rubella]	483	483	0	100.0	94.0	96.5	hypothetical protein CARUB_v10017120mg	gbpln	Capsella rubella	AT3G27190.1 | Symbols: UKL2 | uridine kinase-like 2 | chr3:10039504-10042917 REVERSE LENGTH=483	483	483	0	100.0	93.6	96.7
Rsa1.0_00252.1.g9693.t1	gb|EOA23519.1| hypothetical protein CARUB_v10016713mg [Capsella rubella]	783	779	0	99.5	91.7	95.5	hypothetical protein CARUB_v10016713mg	gbpln	Capsella rubella	AT3G27170.1 | Symbols: CLC-B, ATCLC-B | chloride channel B | chr3:10024147-10026921 FORWARD LENGTH=780	783	780	0	99.6	91.2	94.8
Rsa1.0_00252.1.g9694.t1	gb|EOA23280.1| hypothetical protein CARUB_v10018089mg [Capsella rubella]	188	183	6.00E−58	97.3	71.8	77.1	hypothetical protein CARUB_v10018089mg	gbpln	Capsella rubella	AT3G27160.1 | Symbols: GHS1 | Ribosomal protein S21 family protein | chr3:10017531-10018854 FORWARD LENGTH=183	188	183	8.00E−56	97.3	72.3	76.6
Rsa1.0_00252.1.g9695.t1	gb|EOA25852.1| hypothetical protein CARUB_v10019230mg [Capsella rubella]	411	420	0	102.2	81.3	89.3	hypothetical protein CARUB_v10019230mg	gbpln	Capsella rubella	AT3G27150.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:10009692-10010960 REVERSE LENGTH=422	411	422	0	102.7	80.8	89.1
Rsa1.0_00252.1.g9696.t2	gb|EOA25231.1| hypothetical protein CARUB_v10018544mg [Capsella rubella]	675	667	0	98.8	86.5	90.7	hypothetical protein CARUB_v10018544mg	gbpln	Capsella rubella	AT3G27120.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:10000248-10003265 REVERSE LENGTH=476	675	476	0	70.5	64.6	67.3
Rsa1.0_00252.1.g9697.t1	ref|NP_189345.1| DCD (Development and Cell Death) domain protein [Arabidopsis thaliana] gi|9279632|dbj|BAB01090.1| unnamed protein product [Arabidopsis thaliana] gi|16604450|gb|AAL24231.1| AT3g27090/MOJ10_18 [Arabidopsis thaliana] gi|21655279|gb|AAM65351.1| AT3g27090/MOJ10_18 [Arabidopsis thaliana] gi|332643744|gb|AEE77265.1| DCD (Development and Cell Death) domain protein [Arabidopsis thaliana]	284	296	1.00E−128	104.2	84.9	89.1	DCD (Development and Cell Death) domain protein	gbpln	Arabidopsis thaliana	AT3G27090.1 | Symbols: | DCD (Development and Cell Death) domain protein | chr3:9990020-9991407 FORWARD LENGTH=296	284	296	1.00E−130	104.2	84.9	89.1
Rsa1.0_00252.1.g9698.t1	ref|XP_002877017.1| TOM20-3 [Arabidopsis lyrata subsp. lyrata] gi|297322855|gb|EFH53276.1| TOM20-3 [Arabidopsis lyrata subsp. lyrata]	199	202	2.00E−68	101.5	62.3	77.9	TOM20-3	gbpln	Arabidopsis lyrata	AT3G27080.1 | Symbols: TOM20-3 | translocase of outer membrane 20 kDa subunit 3 | chr3:9985212-9986560 REVERSE LENGTH=202	199	202	1.00E−69	101.5	62.8	75.4
Rsa1.0_00252.1.g9699.t1	gb|EOA25773.1| hypothetical protein CARUB_v10019136mg [Capsella rubella]	332	332	0	100.0	94.6	96.7	hypothetical protein CARUB_v10019136mg	gbpln	Capsella rubella	AT3G27060.1 | Symbols: TSO2, ATTSO2 | Ferritin/ribonucleotide reductase-like family protein | chr3:9979971-9981057 REVERSE LENGTH=332	332	332	0	100.0	94.6	97.0
Rsa1.0_00253.1.g9700.t1	gb|EOA33645.1| hypothetical protein CARUB_v100198120mg [Capsella rubella]	800	814	0	101.8	86.1	91.4	hypothetical protein CARUB_v100198120mg	gbpln	Capsella rubella	AT1G76350.1 | Symbols: | Plant regulator RWP-RK family protein | chr1:28640143-28642817 FORWARD LENGTH=808	800	808	0	101.0	86.5	91.6
Rsa1.0_00253.1.g9701.t1	ref|XP_002889077.1| hypothetical protein ARALYDRAFT_476789 [Arabidopsis lyrata subsp. lyrata] gi|297334918|gb|EFH65336.1| hypothetical protein ARALYDRAFT_476789 [Arabidopsis lyrata subsp. lyrata]	423	506	0	119.6	81.6	88.9	hypothetical protein ARALYDRAFT_476789	gbpln	Arabidopsis lyrata	AT1G76360.1 | Symbols: | Protein kinase superfamily protein | chr1:28643242-28646483 REVERSE LENGTH=484	423	484	0	114.4	81.3	88.7
Rsa1.0_00253.1.g9702.t1	ref|XP_002889078.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334919|gb|EFH65337.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	364	381	0	104.7	86.5	92.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G76370.1 | Symbols: | Protein kinase superfamily protein | chr1:28648660-28650239 REVERSE LENGTH=381	364	381	0	104.7	84.9	91.5
Rsa1.0_00253.1.g9703.t1	ref|XP_002889079.1| hypothetical protein ARALYDRAFT_476793 [Arabidopsis lyrata subsp. lyrata] gi|297334920|gb|EFH65338.1| hypothetical protein ARALYDRAFT_476793 [Arabidopsis lyrata subsp. lyrata]	598	591	0	98.8	70.4	78.8	hypothetical protein ARALYDRAFT_476793	gbpln	Arabidopsis lyrata	AT1G76380.1 | Symbols: | DNA-binding bromodomain-containing protein | chr1:28651416-28654536 REVERSE LENGTH=579	598	579	0	96.8	67.9	76.6

<table>
<tr><td>Rsa1.0_00253.1.g9704.t1</td><td>ref|XP_002887635.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297333476|gb|EFH63894.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]</td><td>810</td><td>811</td><td>0</td><td>100.1</td><td>85.9</td><td>92.5</td><td>armadillo/beta-catenin repeat family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G76390.2 | Symbols: | ARM repeat superfamily protein | chr1:28655914-28658531 FORWARD LENGTH=811</td><td>810</td><td>811</td><td>0</td><td>100.1</td><td>85.4</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00253.1.g9705.t1</td><td>ref|NP_177766.1| Ribophorin I [Arabidopsis thaliana] gi|75204631|sp|Q9SFX3.1|OST1A_ARATH RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1A; AltName: Full=Ribophorin IA; Short=RPN-IA; AltName: Full=Ribophorin-1A; Flags: Precursor gi|6554479|gb|AAF16661.1|AC012394_10 putative ribophorin I (dolichyl-diphosphooligosaccharide-protein glycosyltransferase); 43789-46748 [Arabidopsis thaliana] gi|19698901|gb|AAL91186.1| putative dolichyl-diphosphooligosaccharide-protein glycosyltransferase [Arabidopsis thaliana] gi|22136202|gb|AAM91179.1| putative dolichyl-diphosphooligosaccharide-protein glycosyltransferase [Arabidopsis thaliana] gi|22655006|gb|AAM98094.1| At1g76400/F15M4_10 [Arabidopsis thaliana] gi|332197714|gb|AEE35835.1| Ribophorin I [Arabidopsis thaliana]</td><td>616</td><td>614</td><td>0</td><td>99.7</td><td>89.6</td><td>95.3</td><td>Ribophorin I</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G76400.1 | Symbols: | Ribophorin I | chr1:28658713-28661672 REVERSE LENGTH=614</td><td>616</td><td>614</td><td>0</td><td>99.7</td><td>89.6</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00253.1.g9706.t2</td><td>ref|XP_002887636.1| hypothetical protein ARALYDRAFT_476797 [Arabidopsis lyrata subsp. lyrata] gi|297333477|gb|EFH63895.1| hypothetical protein ARALYDRAFT_476797 [Arabidopsis lyrata subsp. lyrata]</td><td>168</td><td>167</td><td>1.00E-85</td><td>99.4</td><td>89.3</td><td>92.3</td><td>hypothetical protein ARALYDRAFT_476797</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G76405.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G20816.1); Has 52 Blast hits to 52 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:28661994-28663673 FORWARD LENGTH=167</td><td>168</td><td>167</td><td>1.00E-87</td><td>99.4</td><td>88.1</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00253.1.g9707.t1</td><td>ref|XP_002887637.1| hypothetical protein ARALYDRAFT_316562 [Arabidopsis lyrata subsp. lyrata] gi|297333478|gb|EFH63896.1| hypothetical protein ARALYDRAFT_316562 [Arabidopsis lyrata subsp. lyrata]</td><td>186</td><td>186</td><td>4.00E-80</td><td>100.0</td><td>79.0</td><td>88.2</td><td>hypothetical protein ARALYDRAFT_316562</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G76410.1 | Symbols: ATL8 | RING/U-box superfamily protein | chr1:28668915-28669472 FORWARD LENGTH=185</td><td>186</td><td>185</td><td>1.00E-75</td><td>99.5</td><td>80.1</td><td>87.1</td></tr>
<tr><td>Rsa1.0_00253.1.g9708.t1</td><td>ref|NP_177769.1| putative inorganic phosphate transporter 1-9 [Arabidopsis thaliana] gi|75313014|sp|Q9S735.1|PHT19_ARATH RecName: Full=Probable inorganic phosphate transporter 1-9; Short=AtPht1;9; AltName: Full=H(+)/Pi cotransporter gi|6554476|gb|AAF16658.1|AC012394_7 putative phosphate transporter; 23587-26346 [Arabidopsis thaliana] gi|12323970|gb|AAG51941.1|AC015450_2 putative phosphate transporter; 18176-15417 [Arabidopsis thaliana] gi|30725322|gb|AAP37683.1| At1g76430 [Arabidopsis thaliana] gi|110736507|dbj|BAF00221.1| putative phosphate transporter [Arabidopsis thaliana] gi|332197719|gb|AEE35840.1| putative inorganic phosphate transporter 1-9 [Arabidopsis thaliana]</td><td>536</td><td>532</td><td>0</td><td>99.3</td><td>79.7</td><td>86.9</td><td>putative inorganic phosphate transporter 1-9</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G76430.1 | Symbols: PHT1;9 | phosphate transporter 1;9 | chr1:28679115-28681874 REVERSE LENGTH=532</td><td>536</td><td>532</td><td>0</td><td>99.3</td><td>79.7</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00253.1.g9709.t2</td><td>ref|XP_002889083.1| hypothetical protein ARALYDRAFT_476800 [Arabidopsis lyrata subsp. lyrata] gi|297334924|gb|EFH65342.1| hypothetical protein ARALYDRAFT_476800 [Arabidopsis lyrata subsp. lyrata]</td><td>287</td><td>531</td><td>1.00E-139</td><td>185.0</td><td>86.4</td><td>91.3</td><td>hypothetical protein ARALYDRAFT_476800</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G76430.1 | Symbols: PHT1;9 | phosphate transporter 1;9 | chr1:28679115-28681874 REVERSE LENGTH=532</td><td>287</td><td>532</td><td>1.00E-141</td><td>185.4</td><td>86.1</td><td>90.2</td></tr>
</table>

Rsa1.0_00253.1.g9710.t1	ref|XP_002889083.1| hypothetical protein ARALYDRAFT_476800 [Arabidopsis lyrata subsp. lyrata] gi|297334924|gb|EFH65342.1| hypothetical protein ARALYDRAFT_476800 [Arabidopsis lyrata subsp. lyrata]	237	531	1.00E-113	224.1	85.7	89.5	hypothetical protein ARALYDRAFT_476800	gbpln	Arabidopsis lyrata	AT1G76430.1 | Symbols: PHT1;9 | phosphate transporter 1;9 | chr1:28679115-28681874 REVERSE LENGTH=532	237	532	1.00E-116	224.5	85.2	88.6
Rsa1.0_00253.1.g9711.t1	ref|XP_002889084.1| hypothetical protein ARALYDRAFT_476801 [Arabidopsis lyrata subsp. lyrata] gi|297334925|gb|EFH65343.1| hypothetical protein ARALYDRAFT_476801 [Arabidopsis lyrata subsp. lyrata]	139	141	2.00E-63	101.4	86.3	92.8	hypothetical protein ARALYDRAFT_476801	gbpln	Arabidopsis lyrata	AT1G76440.3 | Symbols: | HSP20-like chaperones superfamily protein | chr1:28682371-28682999 REVERSE LENGTH=143	139	143	2.00E-62	102.9	82.0	88.5
Rsa1.0_00253.1.g9712.t1	ref|XP_002887640.1| hypothetical protein ARALYDRAFT_895527 [Arabidopsis lyrata subsp. lyrata] gi|297333481|gb|EFH63899.1| hypothetical protein ARALYDRAFT_895527 [Arabidopsis lyrata subsp. lyrata]	467	494	0	105.8	80.5	89.5	hypothetical protein ARALYDRAFT_895527	gbpln	Arabidopsis lyrata	AT2G33630.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:14236951-14238734 REVERSE LENGTH=480	467	480	1.00E-140	102.8	51.6	68.7
Rsa1.0_00253.1.g9713.t1	ref|NP_565131.1| PsbP domain-containing protein 3 [Arabidopsis thaliana] gi|18203439|sp|Q9S720.2|PPD3_ARATH RecName: Full=PsbP domain-containing protein 3, chloroplastic; AltName: Full=OEC23-like protein 2; Flags: Precursor gi|32815945|gb|AAP88357.1| At1g76450 [Arabidopsis thaliana] gi|110742837|dbj|BAE99317.1| hypothetical protein [Arabidopsis thaliana] gi|332197723|gb|AEE35844.1| PsbP domain-containing protein 3 [Arabidopsis thaliana]	261	247	1.00E-116	94.6	80.8	86.6	PsbP domain-containing protein 3	gbpln	Arabidopsis thaliana	AT1G76450.1 | Symbols: | Photosystem II reaction center PsbP family protein | chr1:28684618-28686109 FORWARD LENGTH=247	261	247	1.00E-118	94.6	80.8	86.6
Rsa1.0_00253.1.g9714.t1	ref|NP_565132.2| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|332197724|gb|AEE35845.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	339	285	1.00E-121	84.1	71.1	75.2	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT1G76460.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:28686932-28688506 REVERSE LENGTH=285	339	285	1.00E-124	84.1	71.1	75.2
Rsa1.0_00253.1.g9715.t1	gb|EOA35402.1| hypothetical protein CARUB_v10020605mg, partial [Capsella rubella]	333	339	1.00E-151	101.8	77.5	88.0	hypothetical protein CARUB_v10020605mg, partial	gbpln	Capsella rubella	AT1G76470.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:28689955-28691405 REVERSE LENGTH=325	333	325	1.00E-145	97.6	78.4	88.0
Rsa1.0_00253.1.g9716.t1	emb|CAA48611.1| hydroxymethylglutaryl-CoA reductase (NADPH) [Raphanus sativus]	572	573	0	100.2	98.3	99.1	hydroxymethylglutaryl-CoA reductase (NADPH)	gbpln	Raphanus sativus	AT1G76490.1 | Symbols: HMG1, HMGR1, AtHMGR1 | hydroxy methylglutaryl CoA reductase 1 | chr1:28695801-28698206 FORWARD LENGTH=642	572	642	0	112.2	89.7	94.1
Rsa1.0_00253.1.g9717.t1	emb|CAA48611.1| hydroxymethylglutaryl-CoA reductase (NADPH) [Raphanus sativus]	100	573	6.00E-35	573.0	70.0	73.0	hydroxymethylglutaryl-CoA reductase (NADPH)	gbpln	Raphanus sativus	AT1G76490.1 | Symbols: HMG1, HMGR1, AtHMGR1 | hydroxy methylglutaryl CoA reductase 1 | chr1:28695801-28698206 FORWARD LENGTH=642	100	642	3.00E-37	642.0	69.0	73.0
Rsa1.0_00253.1.g9718.t1	emb|CAA48611.1| hydroxymethylglutaryl-CoA reductase (NADPH) [Raphanus sativus]	471	573	0	121.7	84.5	87.9	hydroxymethylglutaryl-CoA reductase (NADPH)	gbpln	Raphanus sativus	AT1G76490.1 | Symbols: HMG1, HMGR1, AtHMGR1 | hydroxy methylglutaryl CoA reductase 1 | chr1:28695801-28698206 FORWARD LENGTH=642	471	642	0	136.3	83.7	90.9
Rsa1.0_00253.1.g9719.t1	ref|XP_002887643.1| hypothetical protein ARALYDRAFT_476807 [Arabidopsis lyrata subsp. lyrata] gi|297333484|gb|EFH63902.1| hypothetical protein ARALYDRAFT_476807 [Arabidopsis lyrata subsp. lyrata]	290	289	1.00E-100	99.7	81.0	87.6	hypothetical protein ARALYDRAFT_476807	gbpln	Arabidopsis lyrata	AT1G76500.1 | Symbols: SOB3, AHL29 | Predicted AT-hook DNA-binding family protein | chr1:28705532-28706440 FORWARD LENGTH=302	290	302	3.00E-93	104.1	76.2	83.1

Rsa1.0_00253.1.g9720.t1	ref|NP_177777.3| ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis thaliana] gi|42572131|ref|NP_974156.1| ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis thaliana] gi|122229971|sp|Q0WNR6.1|ARID5_ARATH RecName: Full=AT-rich interactive domain-containing protein 5; Short=ARID domain-containing protein 5 gi|110738615|dbj|BAF01233.1| putative DNA-binding protein [Arabidopsis thaliana] gi|222424365|dbj|BAH20138.1| AT1G76510 [Arabidopsis thaliana] gi|332197730|gb|AEE35851.1| ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis thaliana] gi|332197731|gb|AEE35852.1| ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis thaliana]	404	434	1.00E-174	107.4	81.2	88.6	ARID/BRIGHT DNA-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G76510.2 | Symbols: | ARID/BRIGHT DNA-binding domain-containing protein | chr1:28708927-28712498 REVERSE LENGTH=434	404	434	1.00E-177	107.4	81.2	88.6
Rsa1.0_00253.1.g9721.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00253.1.g9722.t2	gb|AAM62517.1| unknown [Arabidopsis thaliana]	384	390	0	101.6	87.5	95.3	unknown	gbpln	Arabidopsis thaliana	AT1G76520.2 | Symbols: | Auxin efflux carrier family protein | chr1:28715384-28717289 FORWARD LENGTH=390	384	390	0	101.6	87.2	95.3
Rsa1.0_00253.1.g9723.t1	gb|EOA33990.1| hypothetical protein CARUB_v10021486mg [Capsella rubella]	313	313	1.00E-171	100.0	91.7	96.5	hypothetical protein CARUB_v10021486mg	gbpln	Capsella rubella	AT1G76540.1 | Symbols: CDKB2;1 | cyclin-dependent kinase B2;1 | chr1:28720554-28722351 REVERSE LENGTH=313	313	313	1.00E-173	100.0	90.7	96.8
Rsa1.0_00253.1.g9724.t1	gb|EOA34911.1| hypothetical protein CARUB_v10019988mg [Capsella rubella]	617	617	0	100.0	95.3	97.9	hypothetical protein CARUB_v10019988mg	gbpln	Capsella rubella	AT1G76550.1 | Symbols: | Phosphofructokinase family protein | chr1:28722900-28726929 REVERSE LENGTH=617	617	617	0	100.0	94.7	97.4
Rsa1.0_00253.1.g9725.t1	ref|XP_002887645.1| hypothetical protein ARALYDRAFT_895539 [Arabidopsis lyrata subsp. lyrata] gi|297333486|gb|EFH63904.1| hypothetical protein ARALYDRAFT_895539 [Arabidopsis lyrata subsp. lyrata]	141	135	7.00E-52	95.7	75.9	84.4	hypothetical protein ARALYDRAFT_895539	gbpln	Arabidopsis lyrata	AT1G76560.1 | Symbols: CP12-3 | CP12 domain-containing protein 3 | chr1:28728285-28728689 FORWARD LENGTH=134	141	134	1.00E-51	95.0	73.0	81.6
Rsa1.0_00253.1.g9726.t1	sp|Q3EA38.2|FDL48_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At4g13965	427	427	1.00E-68	100.0	43.8	58.5	RecName: Full=Putative F-box/FBD/LRR-repeat protein At4g13965	----	----	AT4G00160.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:63465-65365 FORWARD LENGTH=453	427	453	1.00E-66	106.1	41.0	55.5
Rsa1.0_00253.1.g9727.t1	ref|XP_002887647.1| hypothetical protein ARALYDRAFT_895541 [Arabidopsis lyrata subsp. lyrata] gi|297333488|gb|EFH63906.1| hypothetical protein ARALYDRAFT_895541 [Arabidopsis lyrata subsp. lyrata]	1022	1034	0	101.2	77.9	85.9	hypothetical protein ARALYDRAFT_895541	gbpln	Arabidopsis lyrata	AT1G76580.1 | Symbols: | Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein | chr1:28734600-28738451 FORWARD LENGTH=988	1022	988	0	96.7	72.8	81.4
Rsa1.0_00253.1.g9728.t1	gb|EOA34127.1| hypothetical protein CARUB_v10021628mg [Capsella rubella]	159	164	2.00E-36	103.1	55.3	66.7	hypothetical protein CARUB_v10021628mg	gbpln	Capsella rubella	AT3G55252.1 | Symbols: | Plant self-incompatibility protein S1 family | chr3:20480799-20481299 REVERSE LENGTH=166	159	166	1.00E-23	104.4	38.4	50.3
Rsa1.0_00253.1.g9729.t3	dbj|BAJ34637.1| unnamed protein product [Thellungiella halophila]	275	250	3.00E-21	90.9	21.5	23.6	unnamed protein product	----	----	AT3G11100.1 | Symbols: | sequence-specific DNA binding transcription factors | chr3:3476490-3477320 REVERSE LENGTH=249	275	249	7.00E-23	90.5	20.7	23.6
Rsa1.0_00253.1.g9730.t1	ref|XP_002887651.1| hypothetical protein ARALYDRAFT_476820 [Arabidopsis lyrata subsp. lyrata] gi|297333492|gb|EFH63910.1| hypothetical protein ARALYDRAFT_476820 [Arabidopsis lyrata subsp. lyrata]	527	526	0	99.8	79.7	86.5	hypothetical protein ARALYDRAFT_476820	gbpln	Arabidopsis lyrata	AT1G76620.1 | Symbols: | Protein of unknown function, DUF547 | chr1:28756787-28759131 FORWARD LENGTH=527	527	527	0	100.0	82.2	90.1
Rsa1.0_00253.1.g9731.t1	ref|NP_001185412.1| superkiller protein 3-like protein [Arabidopsis thaliana] gi|332197746|gb|AEE35867.1| superkiller protein 3 [Arabidopsis thaliana]	1171	1168	0	99.7	90.3	94.8	superkiller protein 3-like protein	gbpln	Arabidopsis thaliana	AT1G76630.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:28759699-28765042 FORWARD LENGTH=1168	1171	1168	0	99.7	90.3	94.8
Rsa1.0_00253.1.g9732.t1	ref|XP_002881678.1| hypothetical protein ARALYDRAFT_903237 [Arabidopsis lyrata subsp. lyrata] gi|297327517|gb|EFH57937.1| hypothetical protein ARALYDRAFT_903237 [Arabidopsis lyrata subsp. lyrata]	169	159	4.00E-72	94.1	83.4	87.6	hypothetical protein ARALYDRAFT_903237	gbpln	Arabidopsis lyrata	AT1G76640.1 | Symbols: | Calcium-binding EF-hand family protein | chr1:28765324-28765803 REVERSE LENGTH=159	169	159	8.00E-72	94.1	81.7	85.8

Rsa1.0_00253.1.g9733.t1	ref|NP_177791.1| calcium-binding protein CML38 [Arabidopsis thaliana] gi|334183948|ref|NP_001185413.1| calcium-binding protein CML38 [Arabidopsis thaliana] gi|75337561|sp|Q9SRE6.1|CML38_ARATH RecName: Full=Calcium-binding protein CML38; AltName: Full=Calmodulin-like protein 38 gi|6143901|gb|AAF04447.1|AC010718_16 putative calmodulin; 4214-3681 [Arabidopsis thaliana] gi|27311631|gb|AAO00781.1| putative calmodulin [Arabidopsis thaliana] gi|30102892|gb|AAP21364.1| At1g76650 [Arabidopsis thaliana] gi|332197748|gb|AEE35869.1| calcium-binding protein CML38 [Arabidopsis thaliana] gi|332197750|gb|AEE35871.1| calcium-binding protein CML38 [Arabidopsis thaliana]	178	177	4.00E-76	99.4	82.0	89.3	calcium-binding protein CML38	gbpln	Arabidopsis thaliana	AT1G76650.3 | Symbols: CML38 | calmodulin-like 38 | chr1:28766909-28767442 REVERSE LENGTH=177	178	177	1.00E-78	99.4	82.0	89.3
Rsa1.0_00253.1.g9734.t1	ref|XP_002889094.1| hypothetical protein ARALYDRAFT_476825 [Arabidopsis lyrata subsp. lyrata] gi|297334935|gb|EFH65353.1| hypothetical protein ARALYDRAFT_476825 [Arabidopsis lyrata subsp. lyrata]	410	440	1.00E-173	107.3	85.1	87.8	hypothetical protein ARALYDRAFT_476825	gbpln	Arabidopsis lyrata	AT1G76660.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT5G52430.1); Has 353 Blast hits to 231 proteins in 60 species: Archae - 0; Bacteria - 6; Metazoa - 57; Fungi - 22; Plants - 125; Viruses - 4; Other Eukaryotes - 139 (source: NCBI BLink). | chr1:28769157-28771036 REVERSE LENGTH=431	410	431	1.00E-173	105.1	83.4	86.6
Rsa1.0_00253.1.g9735.t1	dbj|BAJ33722.1| unnamed protein product [Thellungiella halophila]	345	348	0	100.9	94.2	98.0	unnamed protein product	----	----	AT1G76670.1 | Symbols: | Nucleotide-sugar transporter family protein | chr1:28772890-28774569 REVERSE LENGTH=347	345	347	1.00E-179	100.6	90.4	95.9
Rsa1.0_00253.1.g9736.t1	ref|NP_177797.2| histone-lysine N-methyltransferase ASHH1 [Arabidopsis thaliana] gi|42572135|ref|NP_974158.1| histone-lysine N-methyltransferase ASHH1 [Arabidopsis thaliana] gi|75243465|sp|Q84WW6.1|ASHH1_ARATH RecName: Full=Histone-lysine N-methyltransferase ASHH1; AltName: Full=ASH1 homolog 1; AltName: Full=Protein SET DOMAIN GROUP 26 gi|25054844|gb|AAN71912.1| unknown protein [Arabidopsis thaliana] gi|225898088|dbj|BAH30376.1| hypothetical protein [Arabidopsis thaliana] gi|332197758|gb|AEE35879.1| histone-lysine N-methyltransferase ASHH1 [Arabidopsis thaliana] gi|332197759|gb|AEE35880.1| histone-lysine N-methyltransferase ASHH1 [Arabidopsis thaliana]	848	492	0	58.0	44.3	47.2	histone-lysine N-methyltransferase ASHH1	gbpln	Arabidopsis thaliana	AT1G76710.2 | Symbols: ASHH1 | SET domain group 26 | chr1:28789887-28792371 REVERSE LENGTH=492	848	492	0	58.0	44.3	47.2
Rsa1.0_00253.1.g9737.t1	gb|AAC35532.1| contains similarity to proteases [Arabidopsis thaliana]	1309	1392	0	106.3	57.2	71.4	contains similarity to proteases	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1309	1262	2.00E-83	96.4	13.4	20.1
Rsa1.0_00253.1.g9738.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00254.1.g9739.t1	gb|EOA31423.1| hypothetical protein CARUB_v10014603mg [Capsella rubella]	219	215	2.00E-90	98.2	77.6	87.2	hypothetical protein CARUB_v10014603mg	gbpln	Capsella rubella	AT2G18550.1 | Symbols: HB-2, ATHB21, HB21 | homeobox protein 21 | chr2:8049663-8051213 REVERSE LENGTH=220	219	220	1.00E-91	100.5	75.8	87.2
Rsa1.0_00254.1.g9740.t1	ref|XP_002866997.1| hypothetical protein ARALYDRAFT_490965 [Arabidopsis lyrata subsp. lyrata] gi|297312833|gb|EFH43256.1| hypothetical protein ARALYDRAFT_490965 [Arabidopsis lyrata subsp. lyrata]	557	567	0	101.8	73.1	81.1	hypothetical protein ARALYDRAFT_490965	gbpln	Arabidopsis lyrata	AT4G36690.4 | Symbols: ATU2AF65A | U2 snRNP auxilliary factor, large subunit, splicing factor | chr4:17294139-17297609 REVERSE LENGTH=551	557	551	0	98.9	70.6	79.2
Rsa1.0_00254.1.g9741.t1	gb|EOA30658.1| hypothetical protein CARUB_v10013794mg [Capsella rubella]	429	420	0	97.9	80.2	86.2	hypothetical protein CARUB_v10013794mg	gbpln	Capsella rubella	AT2G18520.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:8034036-8035292 REVERSE LENGTH=418	429	418	0	97.4	78.1	84.8

Rsa1.0_00254.1.g9742.t1	ref|XP_002886178.1| hypothetical protein ARALYDRAFT_480759 [Arabidopsis lyrata subsp. lyrata] gi|297332018|gb|EFH62437.1| hypothetical protein ARALYDRAFT_480759 [Arabidopsis lyrata subsp. lyrata]	366	364	1.00E−118	99.5	68.9	73.0	hypothetical protein ARALYDRAFT_480759	gbpln	Arabidopsis lyrata	AT2G18510.1 | Symbols: emb2444 | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:8031554−8033517 REVERSE LENGTH=363	366	363	1.00E−120	99.2	68.6	73.0
Rsa1.0_00254.1.g9743.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838−20266 [Arabidopsis thaliana]	2044	1142	0	55.9	27.9	37.2	reverse transcriptase, putative; 16838−20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	2044	575	8.00E−92	28.1	9.2	15.2
Rsa1.0_00254.1.g9744.t1	ref|XP_002866083.1| hypothetical protein ARALYDRAFT_495611 [Arabidopsis lyrata subsp. lyrata] gi|297311918|gb|EFH42342.1| hypothetical protein ARALYDRAFT_495611 [Arabidopsis lyrata subsp. lyrata]	386	386	0	100.0	95.9	97.2	hypothetical protein ARALYDRAFT_495611	gbpln	Arabidopsis lyrata	AT5G55250.1 | Symbols: IAMT1 | IAA carboxylmethyltransferase 1 | chr5:22407589−22410854 REVERSE LENGTH=386	386	386	0	100.0	93.8	97.2
Rsa1.0_00254.1.g9745.t1	ref|NP_200335.1| peroxygenase 2 [Arabidopsis thaliana] gi|75171505|sp|Q9FLN9.1|PXG2_ARATH RecName: Full=Peroxygenase 2; Short=AtPXG2; AltName: Full=Caleosin-2; AltName: Full=Embryo-specific protein 2; AltName: Full=Putative embryo-specific protein 1 (ATS2) gi|9758121|dbj|BAB08593.1| embryo-specific protein 1; Ca2+-binding EF-hand protein-like [Arabidopsis thaliana] gi|28393110|gb|AAO41988.1| putative embryo-specific protein 1 (ATS1) [Arabidopsis thaliana] gi|28827436|gb|AAO50562.1| putative embryo-specific protein 1 (ATS1) [Arabidopsis thaliana] gi|332009221|gb|AED96604.1| peroxygenase 2 [Arabidopsis thaliana]	243	243	1.00E−128	100.0	89.7	95.1	peroxygenase 2	gbpln	Arabidopsis thaliana	AT5G55240.1 | Symbols: ATPXG2 | ARABIDOPSIS THALIANA PEROXYGENASE 2 | chr5:22405963−22407158 FORWARD LENGTH=243	243	243	1.00E−130	100.0	89.7	95.1
Rsa1.0_00254.1.g9746.t1	ref|XP_002864385.1| atmap65−1 [Arabidopsis lyrata subsp. lyrata] gi|297310220|gb|EFH40644.1| atmap65−1 [Arabidopsis lyrata subsp. lyrata]	588	587	0	99.8	93.2	96.6	atmap65−1	gbpln	Arabidopsis lyrata	AT5G55230.1 | Symbols: ATMAP65−1, MAP65−1 | microtubule-associated proteins 65−1 | chr5:22402716−22405182 FORWARD LENGTH=587	588	587	0	99.8	92.3	96.4
Rsa1.0_00254.1.g9747.t1	ref|XP_002864384.1| trigger factor type chaperone family protein [Arabidopsis lyrata subsp. lyrata] gi|297310219|gb|EFH40643.1| trigger factor type chaperone family protein [Arabidopsis lyrata subsp. lyrata]	66	551	3.00E−12	834.8	66.7	69.7	trigger factor type chaperone family protein	gbpln	Arabidopsis lyrata	AT5G55220.1 | Symbols: | trigger factor type chaperone family protein | chr5:22397677−22400678 FORWARD LENGTH=547	66	547	2.00E−14	828.8	63.6	69.7
Rsa1.0_00254.1.g9748.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00254.1.g9749.t1	ref|NP_200332.1| uncharacterized protein [Arabidopsis thaliana] gi|9758118|dbj|BAB08590.1| unnamed protein product [Arabidopsis thaliana] gi|194708822|gb|ACF88495.1| At5g55210 [Arabidopsis thaliana] gi|332009217|gb|AED96600.1| uncharacterized protein AT5G55210 [Arabidopsis thaliana]	162	168	3.00E−64	103.7	85.8	92.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G55210.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G22320.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:22396707−22397374 REVERSE LENGTH=168	162	168	1.00E−66	103.7	85.8	92.0
Rsa1.0_00254.1.g9750.t1	ref|XP_002864383.1| hypothetical protein ARALYDRAFT_495605 [Arabidopsis lyrata subsp. lyrata] gi|297310218|gb|EFH40642.1| hypothetical protein ARALYDRAFT_495605 [Arabidopsis lyrata subsp. lyrata]	294	302	1.00E−122	102.7	77.6	87.1	hypothetical protein ARALYDRAFT_495605	gbpln	Arabidopsis lyrata	AT5G55200.1 | Symbols: | Co-chaperone GrpE family protein | chr5:22394705−22396335 FORWARD LENGTH=302	294	302	1.00E−122	102.7	77.2	87.4
Rsa1.0_00254.1.g9751.t1	gb|EMJ23759.1| hypothetical protein PRUPE_ppa008371mg [Prunus persica]	221	335	1.00E−130	151.6	98.6	99.5	hypothetical protein PRUPE_ppa008371mg	gbpln	Prunus persica	AT5G55190.1 | Symbols: RAN3, ATRAN3 | RAN GTPase 3 | chr5:22392285−22393957 FORWARD LENGTH=221	221	221	1.00E−130	100.0	98.6	99.5
Rsa1.0_00254.1.g9752.t1	emb|CAA67923.1| ubiquitin-like protein [Arabidopsis thaliana]	103	104	1.00E−45	101.0	88.3	93.2	ubiquitin-like protein	gbpln	Arabidopsis thaliana	AT5G55160.1 | Symbols: SUM2, SUMO 2, SUMO2, ATSUMO2 | small ubiquitin-like modifier 2 | chr5:22383747−22384772 REVERSE LENGTH=103	103	103	4.00E−46	100.0	85.4	90.3

Rsa1.0_00254.1.g9753.t1	ref|NP_568821.1| large subunit ribosomal protein L30 [Arabidopsis thaliana] gi|21617966|gb|AAM67016.1| unknown [Arabidopsis thaliana] gi|88011076|gb|ABD38899.1| At5g55140 [Arabidopsis thaliana] gi|332009208|gb|AED96591.1| large subunit ribosomal protein L30 [Arabidopsis thaliana]	109	109	2.00E-53	100.0	93.6	96.3	large subunit ribosomal protein L30	gbpln	Arabidopsis thaliana	AT5G55140.1 | Symbols: | ribosomal protein L30 family protein | chr5:22381370-22381787 FORWARD LENGTH=109	109	109	3.00E-56	100.0	93.6	96.3
Rsa1.0_00254.1.g9754.t1	ref|NP_680438.1| uncharacterized protein [Arabidopsis thaliana] gi|91807044|gb|ABE66249.1| hypothetical protein At5g55135 [Arabidopsis thaliana] gi|332009207|gb|AED96590.1| uncharacterized protein AT5G55135 [Arabidopsis thaliana]	103	112	7.00E-28	108.7	64.1	74.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G55135.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:22379959-22380386 FORWARD LENGTH=112	103	112	1.00E-30	108.7	64.1	74.8
Rsa1.0_00254.1.g9755.t1	dbj|BAJ33776.1| unnamed protein product [Thellungiella halophila]	409	466	0	113.9	88.0	93.6	unnamed protein product	----	----	AT5G55130.1 | Symbols: CNX5, SIR1 | co-factor for nitrate, reductase and xanthine dehydrogenase 5 | chr5:22373374-22376028 REVERSE LENGTH=464	409	464	0	113.4	86.8	91.9
Rsa1.0_00254.1.g9756.t1	gb|EOA14782.1| hypothetical protein CARUB_v10028082mg [Capsella rubella]	142	76	2.00E-28	53.5	46.5	49.3	hypothetical protein CARUB_v10028082mg	gbpln	Capsella rubella	AT5G55125.2 | Symbols: | Ribosomal protein L31 | chr5:22372737-22372967 FORWARD LENGTH=76	142	76	4.00E-28	53.5	39.4	40.8
Rsa1.0_00254.1.g9757.t1	ref|XP_002864375.1| hypothetical protein ARALYDRAFT_918651 [Arabidopsis lyrata subsp. lyrata] gi|297310210|gb|EFH40634.1| hypothetical protein ARALYDRAFT_918651 [Arabidopsis lyrata subsp. lyrata]	156	429	3.00E-28	275.0	42.9	44.9	hypothetical protein ARALYDRAFT_918651	gbpln	Arabidopsis lyrata	AT5G55120.1 | Symbols: VTC5 | galactose-1-phosphate guanylyltransferase (GDP)s;GDP-D-glucose phosphorylases;quercetin 4'-O-glucosyltransferases | chr5:22369515-22371709 FORWARD LENGTH=431	156	431	5.00E-30	276.3	42.3	44.2
Rsa1.0_00254.1.g9758.t1	ref|XP_002864374.1| stigma-specific Stig1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297310209|gb|EFH40633.1| stigma-specific Stig1 family protein [Arabidopsis lyrata subsp. lyrata]	165	163	6.00E-71	98.8	82.4	90.3	stigma-specific Stig1 family protein	gbpln	Arabidopsis lyrata	AT5G55110.1 | Symbols: | Stigma-specific Stig1 family protein | chr5:22367870-22368361 FORWARD LENGTH=163	165	163	5.00E-71	98.8	80.6	89.1
Rsa1.0_00254.1.g9759.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00255.1.g9760.t2	ref|XP_002875262.1| hypothetical protein ARALYDRAFT_484318 [Arabidopsis lyrata subsp. lyrata] gi|297321100|gb|EFH51521.1| hypothetical protein ARALYDRAFT_484318 [Arabidopsis lyrata subsp. lyrata]	374	389	0	104.0	86.6	91.4	hypothetical protein ARALYDRAFT_484318	gbpln	Arabidopsis lyrata	AT3G25585.4 | Symbols: AAPT2, ATAAPT2 | aminoalcoholphosphotransferase | chr3:9295856-9298271 FORWARD LENGTH=389	374	389	0	104.0	85.6	91.2
Rsa1.0_00255.1.g9761.t1	gb|EOA24080.1| hypothetical protein CARUB_v10017307mg [Capsella rubella]	387	429	1.00E-142	110.9	77.5	84.0	hypothetical protein CARUB_v10017307mg	gbpln	Capsella rubella	AT3G25590.1 | Symbols: | unknown protein; Has 149 Blast hits to 140 proteins in 44 species: Archae - 0; Bacteria - 6; Metazoa - 40; Fungi - 6; Plants - 39; Viruses - 0; Other Eukaryotes - 58 (source: NCBI BLink). | chr3:9302271-9303542 FORWARD LENGTH=423	387	423	1.00E-139	109.3	78.3	85.3
Rsa1.0_00255.1.g9762.t1	ref|NP_189189.1| phospholipid-transporting ATPase 10 [Arabidopsis thaliana] gi|12229653|sp|Q9LI83.1|ALA10_ARATH RecName: Full=Phospholipid-transporting ATPase 10; Short=AtALA10; AltName: Full=Aminophospholipid flippase 10 gi|11994751|dbj|BAB03080.1| P-type transporting ATPase [Arabidopsis thaliana] gi|332643521|gb|AEE77042.1| phospholipid-transporting ATPase 10 [Arabidopsis thaliana]	1202	1202	0	100.0	94.7	97.1	phospholipid-transporting ATPase 10	gbpln	Arabidopsis thaliana	AT3G25610.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr3:9308942-9313353 REVERSE LENGTH=1202	1202	1202	0	100.0	94.7	97.1
Rsa1.0_00255.1.g9763.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00255.1.g9764.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00255.1.g9765.t1	ref|XP_002875266.1| hypothetical protein ARALYDRAFT_904728 [Arabidopsis lyrata subsp. lyrata] gi|297321104|gb|EFH51525.1| hypothetical protein ARALYDRAFT_904728 [Arabidopsis lyrata subsp. lyrata]	264	266	1.00E-121	100.8	86.4	95.1	hypothetical protein ARALYDRAFT_904728	gbpln	Arabidopsis lyrata	AT3G25640.1 | Symbols: | Protein of unknown function, DUF617 | chr3:9333775-9334578 FORWARD LENGTH=267	264	267	1.00E-120	101.1	84.5	94.3
Rsa1.0_00255.1.g9766.t1	gb|EOA23779.1| hypothetical protein CARUB_v10016991mg [Capsella rubella]	108	534	1.00E-11	494.4	33.3	37.0	hypothetical protein CARUB_v10016991mg	gbpln	Capsella rubella	AT3G25660.1 | Symbols: | Amidase family protein | chr3:9339640-9342044 REVERSE LENGTH=537	108	537	2.00E-14	497.2	33.3	37.0

Rsa1.0_00255.1.g9767.t1	gb|EOA24019.1| hypothetical protein CARUB_v10017234mg [Capsella rubella]	450	452	0	100.4	87.1	92.9	hypothetical protein CARUB_v10017234mg	gbpln	Capsella rubella	AT3G25700.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:9358937-9360295 FORWARD LENGTH=452	450	452	0	100.4	84.9	90.4
Rsa1.0_00255.1.g9768.t1	ref|NP_189199.1| transcription factor AIG1 [Arabidopsis thaliana] gi|75311510|sp|Q9LS08.1|BH032_ARATH RecName: Full=Transcription factor AIG1; Short=AtAIG1; AltName: Full=Basic helix-loop-helix protein 32; Short=AtbHLH32; Short=bHLH 32; AltName: Full=Protein TARGET OF MOOPTEROS 5; AltName: Full=Transcription factor EN 54; AltName: Full=bHLH transcription factor bHLH032 gi|7939557|dbj|BAA95758.1| DNA-binding protein-like [Arabidopsis thaliana] gi|16604444|gb|AAL24228.1| AT3g25710/K13N2_1 [Arabidopsis thaliana] gi|18958020|gb|AAL79583.1| AT3g25710/K13N2_1 [Arabidopsis thaliana] gi|21592500|gb|AAM64450.1| putative HLH DNA-binding protein [Arabidopsis thaliana] gi|76589372|gb|ABA54263.1| ABA-regulated protein AIG1 [Arabidopsis thaliana] gi|332643535|gb|AEE77056.1| transcription factor AIG1 [Arabidopsis thaliana]	332	344	1.00E-145	103.6	85.2	90.4	transcription factor AIG1	gbpln	Arabidopsis thaliana	AT3G25710.1 | Symbols: BHLH32, ATAIG1, TMO5 | basic helix-loop-helix 32 | chr3:9369598-9371096 FORWARD LENGTH=344	332	344	1.00E-148	103.6	85.2	90.4
Rsa1.0_00255.1.g9769.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00255.1.g9770.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00255.1.g9771.t3	gb|AAG50751.1|AC079733_19 polyprotein, putative [Arabidopsis thaliana]	1319	1468	0	111.3	46.8	66.4	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1319	1262	1.00E-115	95.7	15.5	23.8
Rsa1.0_00255.1.g9772.t1	gb|EOA38964.1| hypothetical protein CARUB_v10011383mg [Capsella rubella]	331	511	1.00E-101	154.4	57.7	70.7	hypothetical protein CARUB_v10011383mg	gbpln	Capsella rubella	AT1G28430.1 | Symbols: CYP705A24 | cytochrome P450, family 705, subfamily A, polypeptide 24 | chr1:9992986-9994642 REVERSE LENGTH=521	331	521	1.00E-101	157.4	57.7	72.5
Rsa1.0_00255.1.g9773.t1	gb|ABD65028.1| hypothetical protein 26.t00082 [Brassica oleracea]	133	220	2.00E-12	165.4	28.6	33.1	hypothetical protein 26.t00082	gbpln	Brassica oleracea	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	133	384	2.00E-13	288.7	23.3	27.8
Rsa1.0_00255.1.g9774.t3	gb|AAC35532.1| contains similarity to proteases [Arabidopsis thaliana]	1286	1392	0	108.2	30.3	39.9	contains similarity to proteases	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1286	1262	1.00E-79	98.1	12.2	19.1
Rsa1.0_00255.1.g9775.t1	ref|NP_566781.1| Copper transport protein family [Arabidopsis thaliana] gi|21592740|gb|AAM64689.1| unknown [Arabidopsis thaliana] gi|88900374|gb|ABD57499.1| At3g25855 [Arabidopsis thaliana] gi|332643558|gb|AEE77079.1| Copper transport protein family [Arabidopsis thaliana]	85	112	3.00E-23	131.8	75.3	84.7	Copper transport protein family	gbpln	Arabidopsis thaliana	AT3G25855.1 | Symbols: | Copper transport protein family | chr3:9459608-9460267 REVERSE LENGTH=112	85	112	4.00E-26	131.8	75.3	84.7
Rsa1.0_00255.1.g9776.t1	gb|EOA24857.1| hypothetical protein CARUB_v10018148mg [Capsella rubella]	161	163	2.00E-49	101.2	73.3	80.7	hypothetical protein CARUB_v10018148mg	gbpln	Capsella rubella	AT3G25870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G13360.1); Has 50 Blast hits to 50 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9463665-9464177 REVERSE LENGTH=170	161	170	6.00E-45	105.6	70.8	75.8
Rsa1.0_00255.1.g9777.t2	gb|AAG03119.1|AC004133_13 F5A9.24 [Arabidopsis thaliana]	286	1254	6.00E-39	438.5	28.3	38.5	F5A9.24	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	286	154	2.00E-18	53.8	15.0	20.6
Rsa1.0_00255.1.g9778.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00256.1.g9779.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00256.1.g9780.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00256.1.g9781.t1	ref|XP_002868207.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314043|gb|EFH44466.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	437	436	1.00E-145	99.8	63.6	76.9	transferase family protein	gbpln	Arabidopsis lyrata	AT4G15400.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr4:8812121-8813428 REVERSE LENGTH=435	437	435	1.00E-145	99.5	62.0	75.7
Rsa1.0_00256.1.g9782.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00256.1.g9783.t1	ref|NP_179876.1| serine carboxypeptidase-like 12 [Arabidopsis thaliana] gi|75100032|sp|O81009.1|SCP12_ARATH RecName: Full=Serine carboxypeptidase-like 12; Flags: Precursor gi|3445209|gb|AAC32439.1| putative serine carboxypeptidase I [Arabidopsis thaliana] gi|330252279|gb|AEC07373.1| serine carboxypeptidase-like 12 [Arabidopsis thaliana]	264	435	1.00E-110	164.8	72.7	87.5	serine carboxypeptidase-like 12	gbpln	Arabidopsis thaliana	AT2G22920.2 | Symbols: SCPL12 | serine carboxypeptidase-like 12 | chr2:9753938-9757420 FORWARD LENGTH=435	264	435	1.00E-113	164.8	72.7	87.5
Rsa1.0_00256.1.g9784.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1370	1307	0	95.4	60.4	74.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1370	1262	1.00E-100	92.1	13.6	21.7
Rsa1.0_00256.1.g9785.t1	ref|XP_002880473.1| hypothetical protein ARALYDRAFT_481174 [Arabidopsis lyrata subsp. lyrata] gi|297326312|gb|EFH56732.1| hypothetical protein ARALYDRAFT_481174 [Arabidopsis lyrata subsp. lyrata]	337	334	1.00E-179	99.1	90.2	94.7	hypothetical protein ARALYDRAFT_481174	gbpln	Arabidopsis lyrata	AT2G23030.1 | Symbols: SNRK2-9, SNRK2.9 | SNF1-related protein kinase 2.9 | chr2:9803753-9806603 REVERSE LENGTH=339	337	339	1.00E-178	100.6	89.6	94.1
Rsa1.0_00256.1.g9786.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00256.1.g9787.t1	ref|NP_179887.1| Phototropic-responsive NPH3-like protein [Arabidopsis thaliana] gi|75274987|sp|O64814.1|NPY4_ARATH RecName: Full=BTB/POZ domain-containing protein NPY4; AltName: Full=Protein NAKED PINS IN YUC MUTANTS 4 gi|3169178|gb|AAC17821.1| hypothetical protein [Arabidopsis thaliana] gi|21805663|gb|AAM76746.1| hypothetical protein [Arabidopsis thaliana] gi|26450059|dbj|BAC42149.1| unknown protein [Arabidopsis thaliana] gi|28973417|gb|AAO64033.1| unknown protein [Arabidopsis thaliana] gi|61742600|gb|AAX55121.1| hypothetical protein At2g23050 [Arabidopsis thaliana] gi|330252306|gb|AEC07400.1| BTB/POZ domain-containing protein NPY4 [Arabidopsis thaliana]	479	481	0	100.4	85.2	91.9	Phototropic-responsive NPH3-like protein	gbpln	Arabidopsis thaliana	AT2G23050.1 | Symbols: NPY4 | Phototropic-responsive NPH3 family protein | chr2:9810785-9812468 FORWARD LENGTH=481	479	481	0	100.4	85.2	91.9
Rsa1.0_00256.1.g9788.t1	ref|XP_002880477.1| hypothetical protein ARALYDRAFT_900772 [Arabidopsis lyrata subsp. lyrata] gi|297326316|gb|EFH56736.1| hypothetical protein ARALYDRAFT_900772 [Arabidopsis lyrata subsp. lyrata]	401	412	0	102.7	89.8	94.8	hypothetical protein ARALYDRAFT_900772	gbpln	Arabidopsis lyrata	AT2G23060.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr2:9812839-9814633 REVERSE LENGTH=413	401	413	0	103.0	88.5	93.8
Rsa1.0_00256.1.g9789.t1	ref|XP_002891097.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336939|gb|EFH67356.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	178	529	9.00E-37	297.2	43.8	48.3	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT1G34340.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:12530936-12534031 FORWARD LENGTH=530	178	530	6.00E-39	297.8	44.4	47.8
Rsa1.0_00256.1.g9790.t3	gb|EOA31029.1| hypothetical protein CARUB_v10014175mg [Capsella rubella]	181	326	3.00E-22	180.1	38.7	47.5	hypothetical protein CARUB_v10014175mg	gbpln	Capsella rubella	AT3G06060.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:1828296-1830160 REVERSE LENGTH=326	181	326	1.00E-24	180.1	36.5	47.0
Rsa1.0_00256.1.g9791.t1	ref|NP_177970.1| cytochrome P450, family 708, subfamily A, polypeptide 3 [Arabidopsis thaliana] gi|17473541|gb|AAL38249.1| similar to cytochrome P450 [Arabidopsis thaliana] gi|30387575|gb|AAP31953.1| At1g78490 [Arabidopsis thaliana] gi|332197991|gb|AEE36112.1| cytochrome P450, family 708, subfamily A, polypeptide 3 [Arabidopsis thaliana]	481	479	1.00E-179	99.6	63.2	78.2	cytochrome P450, family 708, subfamily A, polypeptide 3	gbpln	Arabidopsis thaliana	AT1G78490.1 | Symbols: CYP708A3 | cytochrome P450, family 708, subfamily A, polypeptide 3 | chr1:29528349-29530391 FORWARD LENGTH=479	481	479	0	99.6	63.2	78.2
Rsa1.0_00256.1.g9792.t2	emb|CAD12663.1| casein kinase II alpha subunit [Sinapis alba]	419	414	0	98.8	93.3	95.7	casein kinase II alpha subunit	gbpln	Sinapis alba	AT2G23070.1 | Symbols: | Protein kinase superfamily protein | chr2:9824162-9826871 REVERSE LENGTH=432	419	432	0	103.1	89.7	92.4
Rsa1.0_00256.1.g9793.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_00256.1.g9794.t2</td><td>ref|NP_564860.3| putative expansin-B2 [Arabidopsis thaliana] gi|20138423|sp|Q9SHY6.2|EXPB2_ARATH RecName: Full=Putative expansin-B2; Short=At-EXPB2; Short=AtEXPB2; AltName: Full=Ath-ExpBeta-1.4; AltName: Full=Beta-expansin-2; Flags: Precursor gi|332196289|gb|AEE34410.1| putative expansin-B2 [Arabidopsis thaliana]</td><td>321</td><td>273</td><td>1.00E-103</td><td>85.0</td><td>56.4</td><td>62.6</td><td>putative expansin-B2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G65680.1 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | expansin B2 | chr1:24427266-24428399 FORWARD LENGTH=273</td><td>321</td><td>273</td><td>1.00E-106</td><td>85.0</td><td>56.4</td><td>62.6</td></tr>
<tr><td>Rsa1.0_00256.1.g9795.t1</td><td>ref|NP_179895.6| RING/U-box domain and ARM repeat-containing protein [Arabidopsis thaliana] gi|330252323|gb|AEC07417.1| RING/U-box domain and ARM repeat-containing protein [Arabidopsis thaliana]</td><td>772</td><td>829</td><td>0</td><td>107.4</td><td>88.3</td><td>92.2</td><td>RING/U-box domain and ARM repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G23140.1 | Symbols: | RING/U-box superfamily protein with ARM repeat domain | chr2:9845696-9849105 REVERSE LENGTH=829</td><td>772</td><td>829</td><td>0</td><td>107.4</td><td>88.3</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00257.1.g9796.t1</td><td>ref|XP_002888863.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297334704|gb|EFH65122.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>359</td><td>426</td><td>1.00E-120</td><td>118.7</td><td>73.3</td><td>80.2</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G72220.1 | Symbols: | RING/U-box superfamily protein | chr1:27184388-27185629 REVERSE LENGTH=413</td><td>359</td><td>413</td><td>1.00E-122</td><td>115.0</td><td>73.5</td><td>80.8</td></tr>
<tr><td>Rsa1.0_00257.1.g9797.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00257.1.g9798.t1</td><td>ref|NP_177366.1| transcription factor bHLH96 [Arabidopsis thaliana] gi|75308860|sp|Q9C7T4.1|BH096_ARATH RecName: Full=Transcription factor bHLH96; AltName: Full=Basic helix-loop-helix protein 96; Short=AtbHLH96; Short=bHLH 96; AltName: Full=Transcription factor EN 15; AltName: Full=bHLH transcription factor bHLH096 gi|12323671|gb|AAG51804.1|AC067754_20 unknown protein; 44011-46213 [Arabidopsis thaliana] gi|20520637|emb|CAD30833.1| basic-helix-loop-helix transcription factor [Arabidopsis thaliana] gi|28392970|gb|AAO41920.1| putative bHLH protein [Arabidopsis thaliana] gi|29824221|gb|AAP04071.1| putative bHLH protein [Arabidopsis thaliana] gi|332197168|gb|AEE35289.1| transcription factor bHLH96 [Arabidopsis thaliana]</td><td>318</td><td>320</td><td>1.00E-132</td><td>100.6</td><td>79.9</td><td>88.4</td><td>transcription factor bHLH96</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G72210.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:27180066-27182268 FORWARD LENGTH=320</td><td>318</td><td>320</td><td>1.00E-135</td><td>100.6</td><td>79.9</td><td>88.4</td></tr>
<tr><td>Rsa1.0_00257.1.g9799.t1</td><td>ref|XP_002888862.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297334703|gb|EFH65121.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>403</td><td>403</td><td>1.00E-171</td><td>100.0</td><td>77.7</td><td>85.1</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G72200.1 | Symbols: | RING/U-box superfamily protein | chr1:27169935-27171149 REVERSE LENGTH=404</td><td>403</td><td>404</td><td>1.00E-171</td><td>100.2</td><td>76.7</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00257.1.g9800.t1</td><td>ref|XP_002888862.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297334703|gb|EFH65121.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>310</td><td>403</td><td>1.00E-106</td><td>130.0</td><td>67.4</td><td>79.0</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G72200.1 | Symbols: | RING/U-box superfamily protein | chr1:27169935-27171149 REVERSE LENGTH=404</td><td>310</td><td>404</td><td>1.00E-107</td><td>130.3</td><td>66.1</td><td>78.4</td></tr>
<tr><td>Rsa1.0_00257.1.g9801.t1</td><td>gb|EOA35070.1| hypothetical protein CARUB_v10020182mg [Capsella rubella]</td><td>239</td><td>496</td><td>4.00E-80</td><td>207.5</td><td>61.9</td><td>63.6</td><td>hypothetical protein CARUB_v10020182mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G72160.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:27153823-27155609 REVERSE LENGTH=490</td><td>239</td><td>490</td><td>3.00E-82</td><td>205.0</td><td>61.5</td><td>63.2</td></tr>
<tr><td>Rsa1.0_00257.1.g9802.t1</td><td>gb|EOA34977.1| hypothetical protein CARUB_v10020065mg [Capsella rubella]</td><td>557</td><td>567</td><td>0</td><td>101.8</td><td>81.7</td><td>87.1</td><td>hypothetical protein CARUB_v10020065mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G72150.1 | Symbols: PATL1 | PATELLIN 1 | chr1:27148558-27150652 FORWARD LENGTH=573</td><td>557</td><td>573</td><td>0</td><td>102.9</td><td>76.5</td><td>82.2</td></tr>
<tr><td>Rsa1.0_00257.1.g9803.t1</td><td>ref|NP_177359.1| putative peptide/nitrate transporter [Arabidopsis thaliana] gi|75169388|sp|Q9C7U1.1|PTR25_ARATH RecName: Full=Probable peptide/nitrate transporter At1g72140 gi|12323658|gb|AAG51791.1|AC067754_7 peptide transporter PTR2-B, putative; 5822-8291 [Arabidopsis thaliana] gi|50897244|gb|AAT85761.1| At1g72140 [Arabidopsis thaliana] gi|332197159|gb|AEE35280.1| probable peptide/nitrate transporter [Arabidopsis thaliana]</td><td>553</td><td>555</td><td>0</td><td>100.4</td><td>81.4</td><td>90.6</td><td>putative peptide/nitrate transporter</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G72140.1 | Symbols: | Major facilitator superfamily protein | chr1:27141877-27144346 FORWARD LENGTH=555</td><td>553</td><td>555</td><td>0</td><td>100.4</td><td>81.4</td><td>90.6</td></tr>
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Rsa1.0_00257.1.g9804.t1	ref|XP_002887414.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata] gi|297333255|gb|EFH63673.1| hypothetical protein ARALYDRAFT_316182 [Arabidopsis lyrata subsp. lyrata]	529	535	0	101.1	79.4	88.5	hypothetical protein ARALYDRAFT_316182	gbpln	Arabidopsis lyrata	AT1G72130.1 | Symbols: | Major facilitator superfamily protein | chr1:27137201-27139223 FORWARD LENGTH=538	529	538	0	101.7	77.1	87.7
Rsa1.0_00257.1.g9805.t3	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	402	484	8.00E-47	120.4	29.6	36.3	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00258.1.g9806.t1	ref|XP_002893211.1| hypothetical protein ARALYDRAFT_472444 [Arabidopsis lyrata subsp. lyrata] gi|297339053|gb|EFH69470.1| hypothetical protein ARALYDRAFT_472444 [Arabidopsis lyrata subsp. lyrata]	273	290	3.00E-77	106.2	72.9	81.0	hypothetical protein ARALYDRAFT_472444	gbpln	Arabidopsis lyrata	AT1G22110.1 | Symbols: | structural constituent of ribosome | chr1:7801625-7802473 REVERSE LENGTH=282	273	282	5.00E-77	103.3	71.8	82.1
Rsa1.0_00258.1.g9807.t1	ref|NP_564162.1| Endoplasmic reticulum vesicle transporter protein [Arabidopsis thaliana] gi|9454530|gb|AAF87853.1|AC073942_7 Contains similarity to a PR00989 protein from Homo sapiens gi|7959731. EST gb|AI995648 comes from this gene [Arabidopsis thaliana] gi|13878151|gb|AAK44153.1|AF370338_1 unknown protein [Arabidopsis thaliana] gi|21281042|gb|AAM44956.1| unknown protein [Arabidopsis thaliana] gi|21553754|gb|AAM62847.1| unknown [Arabidopsis thaliana] gi|332192089|gb|AEE30210.1| Endoplasmic reticulum vesicle transporter protein [Arabidopsis thaliana]	382	386	0	101.0	93.7	98.2	Endoplasmic reticulum vesicle transporter protein	gbpln	Arabidopsis thaliana	AT1G22200.1 | Symbols: | Endoplasmic reticulum vesicle transporter protein | chr1:7837857-7840602 REVERSE LENGTH=386	382	386	0	101.0	93.7	98.2
Rsa1.0_00258.1.g9808.t1	ref|XP_002890499.1| hypothetical protein ARALYDRAFT_313108 [Arabidopsis lyrata subsp. lyrata] gi|297336341|gb|EFH66758.1| hypothetical protein ARALYDRAFT_313108 [Arabidopsis lyrata subsp. lyrata]	314	329	1.00E-151	104.8	84.1	90.8	hypothetical protein ARALYDRAFT_313108	gbpln	Arabidopsis lyrata	AT1G22210.1 | Symbols: TPPC | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:7841518-7843812 FORWARD LENGTH=320	314	320	1.00E-153	101.9	83.4	90.4
Rsa1.0_00258.1.g9809.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00258.1.g9810.t3	gb|EOA38282.1| hypothetical protein CARUB_v10009775mg [Capsella rubella]	427	318	1.00E-119	74.5	52.2	60.0	hypothetical protein CARUB_v10009775mg	gbpln	Capsella rubella	AT1G22220.1 | Symbols: | F-box family protein | chr1:7846694-7847638 FORWARD LENGTH=314	427	314	1.00E-114	73.5	52.0	58.5
Rsa1.0_00258.1.g9811.t1	ref|NP_173644.2| uncharacterized protein [Arabidopsis thaliana] gi|9454525|gb|AAF87848.1|AC073942_2 Contains similarity to a hypothetical protein T11I11.11 gi|6587865 from Arabidopsis thaliana BAC gb|AC012680 [Arabidopsis thaliana] gi|26450950|dbj|BAC42582.1| unknown protein [Arabidopsis thaliana] gi|332192095|gb|AEE30216.1| uncharacterized protein AT1G22250 [Arabidopsis thaliana]	182	200	2.00E-64	109.9	72.0	84.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G22250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G78170.1); Has 64 Blast hits to 64 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7858961-7859648 FORWARD LENGTH=200	182	200	6.00E-67	109.9	72.0	84.1
Rsa1.0_00258.1.g9812.t1	gb|ACN73532.1| 1433-1 [Brassica napus] gi|224981571|gb|ACN73533.1| 1433-1 [Brassica napus]	833	253	1.00E-133	30.4	29.4	29.9	1433-1	gbpln	Brassica napus	AT1G22300.2 | Symbols: GRF10, GF14 EPSILON | general regulatory factor 10 | chr1:7879244-7881103 REVERSE LENGTH=254	833	254	1.00E-129	30.5	28.3	29.7
Rsa1.0_00258.1.g9813.t1	ref|XP_002890509.1| hypothetical protein ARALYDRAFT_313119 [Arabidopsis lyrata subsp. lyrata] gi|297336351|gb|EFH66768.1| hypothetical protein ARALYDRAFT_313119 [Arabidopsis lyrata subsp. lyrata]	270	291	2.00E-93	107.8	77.8	83.3	hypothetical protein ARALYDRAFT_313119	gbpln	Arabidopsis lyrata	AT1G22330.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:7886693-7889241 FORWARD LENGTH=291	270	291	1.00E-89	107.8	78.1	83.3
Rsa1.0_00258.1.g9814.t2	gb|EOA22419.1| hypothetical protein CARUB_v10003062mg [Capsella rubella]	194	1160	4.00E-53	597.9	50.5	51.0	hypothetical protein CARUB_v10003062mg	gbpln	Capsella rubella	AT5G04930.1 | Symbols: ALA1 | aminophospholipid ATPase 1 | chr5:1445509-1449568 FORWARD LENGTH=1158	194	1158	2.00E-55	596.9	50.5	51.0
Rsa1.0_00258.1.g9815.t1	gb|EOA37563.1| hypothetical protein CARUB_v10011877mg [Capsella rubella]	483	486	0	100.6	80.3	90.7	hypothetical protein CARUB_v10011877mg	gbpln	Capsella rubella	AT1G22380.1 | Symbols: AtUGT85A3, UGT85A3 | UDP-glucosyl transferase 85A3 | chr1:7900522-7902332 REVERSE LENGTH=488	483	488	0	101.0	80.1	88.4

Rsa1.0_00258.1.g9816.t1	ref|NP_173656.1| cytokinin-O-glucosyltransferase 2 [Arabidopsis thaliana] gi|66774037|sp|Q9SK82.1|U85A1_ARATH RecName: Full=UDP-glycosyltransferase 85A1; AltName: Full=Cytokinin-O-glucosyltransferase 2; AltName: Full=Zeatin O-glucosyltransferase 2; Short=AtZOG2 gi|6587848|gb|AAF18537.1|AC006551_23 Putative UDP-glucose glucosyltransferase [Arabidopsis thaliana] gi|19698985|gb|AAL91228.1| putative UDP-glucose glucosyltransferase [Arabidopsis thaliana] gi|31376401|gb|AAP49527.1| At1g22400 [Arabidopsis thaliana] gi|332192116|gb|AEE30237.1| cytokinin-O-glucosyltransferase 2 [Arabidopsis thaliana]	488	489	0	100.2	75.8	88.7	cytokinin-O-glucosyltransferase 2	gbpln	Arabidopsis thaliana	AT1G22400.1 | Symbols: UGT85A1, ATUGT85A1 | UDP-Glycosyltransferase superfamily protein | chr1:7903851-7906607 REVERSE LENGTH=489	488	489	0	100.2	75.8	88.7
Rsa1.0_00258.1.g9817.t1	ref|XP_002893224.1| UDP-glucosyl transferase 85A1 [Arabidopsis lyrata subsp. lyrata] gi|297339066|gb|EFH69483.1| UDP-glucosyl transferase 85A1 [Arabidopsis lyrata subsp. lyrata]	488	486	0	99.6	79.3	88.5	UDP-glucosyl transferase 85A1	gbpln	Arabidopsis lyrata	AT1G22400.1 | Symbols: UGT85A1, ATUGT85A1 | UDP-Glycosyltransferase superfamily protein | chr1:7903851-7906607 REVERSE LENGTH=489	488	489	0	100.2	78.3	87.9
Rsa1.0_00259.1.g9818.t1	gb|EOA33354.1| hypothetical protein CARUB_v10020212mg [Capsella rubella]	67	481	2.00E-17	717.9	65.7	71.6	hypothetical protein CARUB_v10020212mg	gbpln	Capsella rubella	AT1G70580.4 | Symbols: AOAT2, GGT2 | alanine-2-oxoglutarate aminotransferase 2 | chr1:26613222-26615845 FORWARD LENGTH=481	67	481	7.00E-20	717.9	64.2	71.6
Rsa1.0_00259.1.g9819.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00259.1.g9820.t1	dbj|BAH59426.1| putative disease resistance protein [Arabidopsis thaliana]	1285	1217	0	94.7	66.0	74.9	putative disease resistance protein	gbpln	Arabidopsis thaliana	AT5G45250.1 | Symbols: RPS4 | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18321914-18326022 REVERSE LENGTH=1217	1285	1217	0	94.7	65.9	74.9
Rsa1.0_00259.1.g9821.t1	ref|NP_199337.2| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332007837|gb|AED95220.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	690	812	1.00E-100	117.7	33.8	46.8	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G45240.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:18313706-18319089 FORWARD LENGTH=812	690	812	1.00E-103	117.7	33.8	46.8
Rsa1.0_00259.1.g9822.t1	gb|AAC63844.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1854	1231	0	66.4	40.8	50.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337-69884 REVERSE LENGTH=515	1854	515	1.00E-120	27.8	12.7	16.3
Rsa1.0_00259.1.g9823.t1	ref|XP_002863506.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309341|gb|EFH39765.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	165	1168	2.00E-62	707.9	72.1	81.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G45230.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18302147-18308303 REVERSE LENGTH=1231	165	1231	8.00E-54	746.1	64.2	76.4
Rsa1.0_00259.1.g9824.t1	ref|XP_002863510.1| hypothetical protein ARALYDRAFT_494460 [Arabidopsis lyrata subsp. lyrata] gi|297309345|gb|EFH39769.1| hypothetical protein ARALYDRAFT_494460 [Arabidopsis lyrata subsp. lyrata]	1072	1188	0	110.8	60.5	70.5	hypothetical protein ARALYDRAFT_494460	gbpln	Arabidopsis lyrata	AT5G45230.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18302147-18308303 REVERSE LENGTH=1231	1072	1231	0	114.8	59.9	70.1
Rsa1.0_00259.1.g9825.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00259.1.g9826.t1	gb|EOA14759.1| hypothetical protein CARUB_v10028056mg [Capsella rubella]	359	270	3.00E-49	75.2	26.7	32.3	hypothetical protein CARUB_v10028056mg	gbpln	Capsella rubella	AT1G51270.3 | Symbols: | structural molecules;transmembrane receptors;structural molecules | chr1:19007577-19011225 FORWARD LENGTH=637	359	637	1.00E-36	177.4	19.2	28.1
Rsa1.0_00259.1.g9827.t1	gb|ACB59223.1| glutathione S-transferase [Brassica oleracea]	177	523	2.00E-28	295.5	43.5	55.4	glutathione S-transferase	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00259.1.g9828.t1	dbj|BAB11392.1| unnamed protein product [Arabidopsis thaliana]	545	583	0	107.0	89.0	92.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G45190.1 | Symbols: | Cyclin family protein | chr5:18277808-18280733 REVERSE LENGTH=579	545	579	0	106.2	88.4	92.3
Rsa1.0_00259.1.g9829.t1	ref|XP_002865280.1| hypothetical protein ARALYDRAFT_494469 [Arabidopsis lyrata subsp. lyrata] gi|297311115|gb|EFH41539.1| hypothetical protein ARALYDRAFT_494469 [Arabidopsis lyrata subsp. lyrata]	586	586	0	100.0	82.1	88.6	hypothetical protein ARALYDRAFT_494469	gbpln	Arabidopsis lyrata	AT5G45110.1 | Symbols: NPR3, ATNPR3 | NPR1-like protein 3 | chr5:18229319-18231334 FORWARD LENGTH=586	586	586	0	100.0	83.8	91.1
Rsa1.0_00259.1.g9830.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00259.1.g9831.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00259.1.g9832.t1	ref|XP_002880000.1| hypothetical protein ARALYDRAFT_483365 [Arabidopsis lyrata subsp. lyrata] gi|297325839|gb|EFH56259.1| hypothetical protein ARALYDRAFT_483365 [Arabidopsis lyrata subsp. lyrata]	263	838	5.00E-29	318.6	28.1	31.2	hypothetical protein ARALYDRAFT_483365	gbpln	Arabidopsis lyrata	AT2G42700.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: vesicle-mediated transport, vesicle docking involved in exocytosis; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Sec1-like protein (InterPro:IPR001619). | chr2:17778464-17782034 FORWARD LENGTH=867	263	867	4.00E-31	329.7	28.1	30.8
Rsa1.0_00259.1.g9833.t1	gb|AAB88009.1| heat shock cognate protein HSC70 [Brassica napus]	650	645	0	99.2	95.7	98.3	heat shock cognate protein HSC70	gbpln	Brassica napus	AT5G02500.1 | Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 | heat shock cognate protein 70-1 | chr5:554055-556334 REVERSE LENGTH=651	650	651	0	100.2	94.9	97.7
Rsa1.0_00259.1.g9834.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00260.1.g9835.t2	ref|XP_002868593.1| hypothetical protein ARALYDRAFT_916060 [Arabidopsis lyrata subsp. lyrata] gi|297314429|gb|EFH44852.1| hypothetical protein ARALYDRAFT_916060 [Arabidopsis lyrata subsp. lyrata]	265	522	1.00E-120	197.0	75.8	78.9	hypothetical protein ARALYDRAFT_916060	gbpln	Arabidopsis lyrata	AT5G41460.1 | Symbols: | Protein of unknown function (DUF604) | chr5:16589724-16592197 REVERSE LENGTH=524	265	524	1.00E-121	197.7	75.8	78.5
Rsa1.0_00260.1.g9836.t1	dbj|BAJ33952.1| unnamed protein product [Thellungiella halophila]	595	597	0	100.3	86.4	90.3	unnamed protein product	----	----	AT5G41410.1 | Symbols: BEL1 | POX (plant homeobox) family protein | chr5:16580424-16583770 FORWARD LENGTH=611	595	611	0	102.7	81.5	89.1
Rsa1.0_00260.1.g9837.t1	gb|ABK28735.1| unknown [Arabidopsis thaliana]	274	265	1.00E-112	96.7	76.6	79.2	unknown	gbpln	Arabidopsis thaliana	AT5G41390.1 | Symbols: | PLAC8 family protein | chr5:16565576-16567253 FORWARD LENGTH=264	274	264	1.00E-114	96.4	76.3	78.8
Rsa1.0_00260.1.g9838.t1	ref|XP_002868599.1| hypothetical protein ARALYDRAFT_493840 [Arabidopsis lyrata subsp. lyrata] gi|297314435|gb|EFH44858.1| hypothetical protein ARALYDRAFT_493840 [Arabidopsis lyrata subsp. lyrata]	308	308	1.00E-120	100.0	81.2	86.7	hypothetical protein ARALYDRAFT_493840	gbpln	Arabidopsis lyrata	AT5G41380.1 | Symbols: | CCT motif family protein | chr5:16562129-16563553 REVERSE LENGTH=307	308	307	1.00E-118	99.7	77.6	84.7
Rsa1.0_00260.1.g9839.t1	ref|XP_002870640.1| DNA repair and transcription factor XPB1 [Arabidopsis lyrata subsp. lyrata] gi|297316476|gb|EFH46899.1| DNA repair and transcription factor XPB1 [Arabidopsis lyrata subsp. lyrata]	768	767	0	99.9	91.4	95.7	DNA repair and transcription factor XPB1	gbpln	Arabidopsis lyrata	AT5G41370.1 | Symbols: XPB1, ATXPB1 | homolog of xeroderma pigmentosum complementation group B 1 | chr5:16551337-16555792 FORWARD LENGTH=767	768	767	0	99.9	92.7	95.8
Rsa1.0_00260.1.g9840.t1	ref|XP_002868602.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297314438|gb|EFH44861.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	214	212	1.00E-101	99.1	86.4	92.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G41350.1 | Symbols: | RING/U-box superfamily protein | chr5:16542026-16543092 REVERSE LENGTH=212	214	212	1.00E-103	99.1	86.0	92.5
Rsa1.0_00260.1.g9841.t1	gb|EOA35717.1| hypothetical protein CARUB_v10020943mg, partial [Capsella rubella]	186	214	6.00E-93	115.1	89.2	94.6	hypothetical protein CARUB_v10020943mg, partial	gbpln	Capsella rubella	AT1G63800.1 | Symbols: UBC5 | ubiquitin-conjugating enzyme 5 | chr1:23667888-23669003 REVERSE LENGTH=185	186	185	1.00E-92	99.5	87.6	94.1
Rsa1.0_00260.1.g9842.t1	ref|NP_198949.1| BTB/POZ domain with WD40/YVTN repeat-containing protein [Arabidopsis thaliana] gi|75171793|sp|Q9FN67.1|Y5133_ARATH RecName: Full=BTB/POZ domain-containing protein At5g41330 gi|9758042|dbj|BAB08505.1| unnamed protein product [Arabidopsis thaliana] gi|54606858|gb|AAV34777.1| At5g41330 [Arabidopsis thaliana] gi|110741213|dbj|BAF02157.1| hypothetical protein [Arabidopsis thaliana] gi|110741215|dbj|BAF02158.1| hypothetical protein [Arabidopsis thaliana] gi|332007283|gb|AED94666.1| BTB/POZ domain with WD40/YVTN repeat-containing protein [Arabidopsis thaliana]	450	458	0	101.8	82.4	91.6	BTB/POZ domain with WD40/YVTN repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G41330.1 | Symbols: | BTB/POZ domain with WD40/YVTN repeat-like protein | chr5:16536452-16537828 REVERSE LENGTH=458	450	458	0	101.8	82.4	91.6
Rsa1.0_00260.1.g9843.t1	ref|NP_198948.1| uncharacterized protein [Arabidopsis thaliana] gi|9758041|dbj|BAB08504.1| unnamed protein product [Arabidopsis thaliana] gi|332007282|gb|AED94665.1| uncharacterized protein AT5G41320 [Arabidopsis thaliana]	449	515	1.00E-102	114.7	60.6	71.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G41320.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:16534442-16535989 FORWARD LENGTH=515	449	515	1.00E-105	114.7	60.6	71.9
Rsa1.0_00260.1.g9844.t1	ref|XP_002870642.1| hypothetical protein ARALYDRAFT_493847 [Arabidopsis lyrata subsp. lyrata] gi|297316478|gb|EFH46901.1| hypothetical protein ARALYDRAFT_493847 [Arabidopsis lyrata subsp. lyrata]	627	637	0	101.6	84.7	90.0	hypothetical protein ARALYDRAFT_493847	gbpln	Arabidopsis lyrata	AT5G41315.1 | Symbols: GL3, MYC6.2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:16529457-16532866 FORWARD LENGTH=637	627	637	0	101.6	84.4	89.5

Rsa1.0_00260.1.g9845.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1522	1274	0	83.7	26.3	35.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	1522	303	1.00E-37	19.9	6.4	9.2
Rsa1.0_00260.1.g9846.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00261.1.g9847.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00261.1.g9848.t1	ref|NP_201459.1| uncharacterized protein [Arabidopsis thaliana] gi|10177539|dbj|BAB10934.1| unnamed protein product [Arabidopsis thaliana] gi|28393574|gb|AAO42207.1| unknown protein [Arabidopsis thaliana] gi|28972979|gb|AAO63814.1| unknown protein [Arabidopsis thaliana] gi|332010848|gb|AED98231.1| uncharacterized protein AT5G66580 [Arabidopsis thaliana]	147	156	1.00E-53	106.1	81.0	85.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G66580.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G50800.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:26572724-26573194 FORWARD LENGTH=156	147	156	3.00E-56	106.1	81.0	85.7
Rsa1.0_00261.1.g9849.t2	gb|EOA13097.1| hypothetical protein CARUB_v10026104mg [Capsella rubella]	582	608	0	104.5	77.1	84.5	hypothetical protein CARUB_v10026104mg	gbpln	Capsella rubella	AT5G66600.4 | Symbols: | Protein of unknown function, DUF547 | chr5:26575105-26578315 REVERSE LENGTH=629	582	629	0	108.1	78.7	85.4
Rsa1.0_00261.1.g9850.t1	ref|XP_002866745.1| hypothetical protein ARALYDRAFT_332898 [Arabidopsis lyrata subsp. lyrata] gi|297312580|gb|EFH43004.1| hypothetical protein ARALYDRAFT_332898 [Arabidopsis lyrata subsp. lyrata]	231	231	3.00E-86	100.0	81.0	85.7	hypothetical protein ARALYDRAFT_332898	gbpln	Arabidopsis lyrata	AT5G66700.1 | Symbols: HB53, HB-8, ATHB53 | homeobox 53 | chr5:26634406-26635762 FORWARD LENGTH=228	231	228	4.00E-85	98.7	79.2	84.4
Rsa1.0_00261.1.g9851.t1	gb|EOA13246.1| hypothetical protein CARUB_v10026275mg [Capsella rubella]	544	499	0	91.7	71.5	77.2	hypothetical protein CARUB_v10026275mg	gbpln	Capsella rubella	AT5G66730.1 | Symbols: | C2H2-like zinc finger protein | chr5:26641914-26643883 REVERSE LENGTH=500	544	500	0	91.9	72.2	77.0
Rsa1.0_00261.1.g9852.t1	ref|NP_201475.4| uncharacterized protein [Arabidopsis thaliana] gi|332010875|gb|AED98258.1| uncharacterized protein AT5G66740 [Arabidopsis thaliana]	369	370	0	100.3	93.0	96.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G66740.1 | Symbols: | Protein of unknown function (DUF620) | chr5:26647114-26648558 FORWARD LENGTH=370	369	370	0	100.3	93.0	96.5
Rsa1.0_00261.1.g9853.t2	gb|EOA12951.1| hypothetical protein CARUB_v10025933mg [Capsella rubella]	659	760	0	115.3	82.4	88.0	hypothetical protein CARUB_v10025933mg	gbpln	Capsella rubella	AT5G66850.1 | Symbols: MAPKKK5 | mitogen-activated protein kinase kinase kinase 5 | chr5:26695965-26699159 REVERSE LENGTH=716	659	716	0	108.6	81.6	86.8
Rsa1.0_00261.1.g9854.t13	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1399	1449	1.00E-101	103.6	24.4	37.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1399	626	4.00E-44	44.7	8.7	14.4
Rsa1.0_00261.1.g9855.t1	gb|EOA13733.1| hypothetical protein CARUB_v10026811mg [Capsella rubella]	319	313	1.00E-112	98.1	72.7	80.3	hypothetical protein CARUB_v10026811mg	gbpln	Capsella rubella	AT5G66870.1 | Symbols: ASL1, LBD36 | ASYMMETRIC LEAVES 2-like 1 | chr5:26706621-26707562 FORWARD LENGTH=313	319	313	1.00E-111	98.1	74.6	81.5
Rsa1.0_00261.1.g9856.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00261.1.g9857.t1	ref|XP_002865045.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310880|gb|EFH41304.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	418	421	0	100.7	77.3	88.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G66890.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:26712944-26714383 REVERSE LENGTH=415	418	415	0	99.3	77.0	87.8
Rsa1.0_00261.1.g9858.t1	ref|XP_002866726.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312561|gb|EFH42985.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	544	543	0	99.8	86.6	90.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G66920.1 | Symbols: sks17 | SKU5 similar 17 | chr5:26722963-26725370 FORWARD LENGTH=546	544	546	0	100.4	89.3	93.9
Rsa1.0_00261.1.g9859.t1	gb|EOA14640.1| hypothetical protein CARUB_v10027898mg [Capsella rubella]	231	242	7.00E-77	104.8	84.4	89.2	hypothetical protein CARUB_v10027898mg	gbpln	Capsella rubella	AT5G67060.1 | Symbols: HEC1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:26766276-26767001 FORWARD LENGTH=241	231	241	6.00E-78	104.3	87.0	89.2
Rsa1.0_00261.1.g9860.t1	ref|XP_002866719.1| hypothetical protein ARALYDRAFT_920006 [Arabidopsis lyrata subsp. lyrata] gi|297312554|gb|EFH42978.1| hypothetical protein ARALYDRAFT_920006 [Arabidopsis lyrata subsp. lyrata]	130	128	2.00E-43	98.5	76.9	84.6	hypothetical protein ARALYDRAFT_920006	gbpln	Arabidopsis lyrata	AT5G67070.1 | Symbols: RALFL34 | ralf-like 34 | chr5:26768120-26768509 FORWARD LENGTH=129	130	129	3.00E-44	99.2	73.8	80.0
Rsa1.0_00261.1.g9861.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	417	1274	5.00E-76	305.5	38.6	58.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	417	303	6.00E-40	72.7	26.1	36.5
Rsa1.0_00261.1.g9862.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00261.1.g9863.t4	emb|CAA18107.1| LTR retrotransposon like protein [Arabidopsis thaliana] gi|7269049|emb|CAB79159.1| LTR retrotransposon like protein [Arabidopsis thaliana]	551	1109	1.00E-66	201.3	29.9	37.7	LTR retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	551	1262	6.00E-37	229.0	19.1	28.3
Rsa1.0_00261.1.g9864.t1	emb|CCD74510.1| unknown, partial [Arabidopsis halleri subsp. halleri]	219	300	9.00E-31	137.0	35.6	44.3	unknown, partial	gbpln	Arabidopsis halleri	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	219	303	4.00E-33	138.4	36.5	52.1
Rsa1.0_00261.1.g9865.t5	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1093	1485	0	135.9	39.9	53.2	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850	1093	850	1.00E-72	77.8	12.4	13.9
Rsa1.0_00261.1.g9866.t1	dbj|BAB69682.1| receptor kinase 3 [Brassica rapa]	297	847	1.00E-111	285.2	69.7	78.1	receptor kinase 3	gbpln	Brassica rapa	AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850	297	850	3.00E-80	286.2	49.2	66.7
Rsa1.0_00261.1.g9867.t1	gb|EOA37218.1| hypothetical protein CARUB_v10010700mg [Capsella rubella]	203	112	2.00E-11	55.2	17.2	17.7	hypothetical protein CARUB_v10010700mg	gbpln	Capsella rubella	AT5G44270.1 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr5:17833636-17835740 FORWARD LENGTH=309	203	309	2.00E-13	152.2	16.7	17.2
Rsa1.0_00262.1.g9868.t1	gb|EOA26386.1| hypothetical protein CARUB_v10023505mg [Capsella rubella]	330	358	3.00E-13	108.5	15.2	24.8	hypothetical protein CARUB_v10023505mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00262.1.g9869.t9	#	#	#	#	#	#	#	–	----	----	AT3G02880.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:634819-636982 FORWARD LENGTH=627	544	627	5.00E-11	115.3	5.5	6.3
Rsa1.0_00262.1.g9870.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00262.1.g9871.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00262.1.g9872.t1	ref|XP_002892212.1| hypothetical protein ARALYDRAFT_470414 [Arabidopsis lyrata subsp. lyrata] gi|297338054|gb|EFH68471.1| hypothetical protein ARALYDRAFT_470414 [Arabidopsis lyrata subsp. lyrata]	355	346	1.00E-159	97.5	80.0	88.5	hypothetical protein ARALYDRAFT_470414	gbpln	Arabidopsis lyrata	AT1G04380.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:1177142-1178384 REVERSE LENGTH=345	355	345	1.00E-156	97.2	76.9	85.9
Rsa1.0_00262.1.g9873.t1	gb|EOA38791.1| hypothetical protein CARUB_v10011057mg [Capsella rubella]	138	130	7.00E-45	94.2	81.9	89.1	hypothetical protein CARUB_v10011057mg	gbpln	Capsella rubella	AT1G04370.1 | Symbols: ATERF14, ERF14 | Ethylene-responsive element binding factor 14 | chr1:1175177-1175578 FORWARD LENGTH=133	138	133	1.00E-45	96.4	76.8	83.3
Rsa1.0_00262.1.g9874.t1	ref|XP_002892211.1| hypothetical protein ARALYDRAFT_887598 [Arabidopsis lyrata subsp. lyrata] gi|297338053|gb|EFH68470.1| hypothetical protein ARALYDRAFT_887598 [Arabidopsis lyrata subsp. lyrata]	369	382	1.00E-148	103.5	78.6	85.4	hypothetical protein ARALYDRAFT_887598	gbpln	Arabidopsis lyrata	AT1G04360.1 | Symbols: | RING/U-box superfamily protein | chr1:1167507-1168652 REVERSE LENGTH=381	369	381	1.00E-140	103.3	77.8	85.6
Rsa1.0_00262.1.g9875.t1	ref|XP_002889500.1| hypothetical protein ARALYDRAFT_470412 [Arabidopsis lyrata subsp. lyrata] gi|297335342|gb|EFH65759.1| hypothetical protein ARALYDRAFT_470412 [Arabidopsis lyrata subsp. lyrata]	346	361	1.00E-151	104.3	77.2	87.0	hypothetical protein ARALYDRAFT_470412	gbpln	Arabidopsis lyrata	AT1G04350.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:1165296-1166538 FORWARD LENGTH=360	346	360	1.00E-151	104.0	75.7	85.8
Rsa1.0_00262.1.g9876.t1	ref|XP_002869619.1| ATGOLS6 [Arabidopsis lyrata subsp. lyrata] gi|297315455|gb|EFH45878.1| ATGOLS6 [Arabidopsis lyrata subsp. lyrata]	329	333	1.00E-165	101.2	85.4	91.2	ATGOLS6	gbpln	Arabidopsis lyrata	AT5G23790.1 | Symbols: AtGolS5, GolS5 | galactinol synthase 5 | chr5:8020183-8021597 REVERSE LENGTH=333	329	333	1.00E-167	101.2	84.2	90.9
Rsa1.0_00262.1.g9877.t1	ref|NP_171929.1| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana] gi|2341039|gb|AAB70443.1| Similar to Nicotiana lesion-inducing ORF (gb|U66269) [Arabidopsis thaliana] gi|17979509|gb|AAL50090.1| At1g04340/F19P19_23 [Arabidopsis thaliana] gi|20147297|gb|AAM10362.1| At1g04340/F19P19_23 [Arabidopsis thaliana] gi|332189565|gb|AEE27686.1| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana]	162	159	2.00E-73	98.1	89.5	93.2	HR-like lesion-inducing protein-like protein	gbpln	Arabidopsis thaliana	AT1G04340.1 | Symbols: | HR-like lesion-inducing protein-related | chr1:1163345-1164737 REVERSE LENGTH=159	162	159	8.00E-76	98.1	89.5	93.2

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<tr><td>Rsa1.0_00262.1.g9878.t1</td><td>ref|NP_171928.1| uncharacterized protein [Arabidopsis thaliana] gi|2341040|gb|AAB70444.1| EST gb|H76414 comes from this gene [Arabidopsis thaliana] gi|38454052|gb|AAR20720.1| At1g04330 [Arabidopsis thaliana] gi|38603978|gb|AAR24732.1| At1g04330 [Arabidopsis thaliana] gi|332189564|gb|AEE27685.1| uncharacterized protein AT1G04330 [Arabidopsis thaliana]</td><td>98</td><td>100</td><td>2.00E−39</td><td>102.0</td><td>86.7</td><td>90.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G04330.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23170.1); Has 74 Blast hits to 74 proteins in 6 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 74; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:1161584−1161886 REVERSE LENGTH=100</td><td>98</td><td>100</td><td>3.00E−42</td><td>102.0</td><td>86.7</td><td>90.8</td></tr>
<tr><td>Rsa1.0_00262.1.g9879.t1</td><td>ref|XP_002892208.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338050|gb|EFH68467.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>643</td><td>652</td><td>0</td><td>101.4</td><td>78.8</td><td>85.4</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G04310.1 | Symbols: ERS2 | ethylene response sensor 2 | chr1:1155116−1157125 REVERSE LENGTH=645</td><td>643</td><td>645</td><td>0</td><td>100.3</td><td>77.6</td><td>84.3</td></tr>
<tr><td>Rsa1.0_00262.1.g9880.t1</td><td>ref|XP_002892207.1| hypothetical protein ARALYDRAFT_470409 [Arabidopsis lyrata subsp. lyrata] gi|297338049|gb|EFH68466.1| hypothetical protein ARALYDRAFT_470409 [Arabidopsis lyrata subsp. lyrata]</td><td>1082</td><td>1071</td><td>0</td><td>99.0</td><td>78.7</td><td>85.8</td><td>hypothetical protein ARALYDRAFT_470409</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G04300.1 | Symbols: | TRAF−like superfamily protein | chr1:1148818−1153895 REVERSE LENGTH=1074</td><td>1082</td><td>1074</td><td>0</td><td>99.3</td><td>77.8</td><td>85.8</td></tr>
<tr><td>Rsa1.0_00262.1.g9881.t1</td><td>ref|XP_002892206.1| thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338048|gb|EFH68465.1| thioesterase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>134</td><td>155</td><td>1.00E−51</td><td>115.7</td><td>81.3</td><td>88.8</td><td>thioesterase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G04290.1 | Symbols: | Thioesterase superfamily protein | chr1:1147721−1148352 REVERSE LENGTH=155</td><td>134</td><td>155</td><td>2.00E−52</td><td>115.7</td><td>79.9</td><td>85.8</td></tr>
<tr><td>Rsa1.0_00262.1.g9882.t1</td><td>gb|EOA39428.1| hypothetical protein CARUB_v10012550mg [Capsella rubella]</td><td>535</td><td>538</td><td>0</td><td>100.6</td><td>82.8</td><td>90.3</td><td>hypothetical protein CARUB_v10012550mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G04280.1 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:1143643−1146541 REVERSE LENGTH=534</td><td>535</td><td>534</td><td>0</td><td>99.8</td><td>79.6</td><td>88.2</td></tr>
<tr><td>Rsa1.0_00262.1.g9883.t1</td><td>gb|EOA36082.1| hypothetical protein CARUB_v10010394mg, partial [Capsella rubella]</td><td>152</td><td>186</td><td>1.00E−81</td><td>122.4</td><td>98.7</td><td>100.0</td><td>hypothetical protein CARUB_v10010394mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G04270.1 | Symbols: RPS15 | cytosolic ribosomal protein S15 | chr1:1141852−1142960 REVERSE LENGTH=152</td><td>152</td><td>152</td><td>8.00E−84</td><td>100.0</td><td>99.3</td><td>99.3</td></tr>
<tr><td>Rsa1.0_00262.1.g9884.t1</td><td>ref|XP_002889499.1| hypothetical protein ARALYDRAFT_470401 [Arabidopsis lyrata subsp. lyrata] gi|297335341|gb|EFH65758.1| hypothetical protein ARALYDRAFT_470401 [Arabidopsis lyrata subsp. lyrata]</td><td>230</td><td>229</td><td>1.00E−105</td><td>99.6</td><td>82.6</td><td>86.5</td><td>hypothetical protein ARALYDRAFT_470401</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G04250.1 | Symbols: AXR3, IAA17 | AUX/IAA transcriptional regulator family protein | chr1:1136382−1138340 FORWARD LENGTH=229</td><td>230</td><td>229</td><td>1.00E−108</td><td>99.6</td><td>82.2</td><td>85.7</td></tr>
<tr><td>Rsa1.0_00262.1.g9885.t1</td><td>gb|AAD21699.1| Contains reverse transcriptase domain (rvt) PF|00078 [Arabidopsis thaliana]</td><td>341</td><td>1253</td><td>2.00E−37</td><td>367.4</td><td>26.7</td><td>41.3</td><td>Contains reverse transcriptase domain (rvt) PF|00078</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G60720.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr1:22357072−22357941 FORWARD LENGTH=289</td><td>341</td><td>289</td><td>2.00E−38</td><td>84.8</td><td>27.6</td><td>41.9</td></tr>
<tr><td>Rsa1.0_00262.1.g9886.t1</td><td>ref|NP_171920.1| auxin−responsive protein IAA3 [Arabidopsis thaliana] gi|12643742|sp|Q38822.1|IAA3_ARATH RecName: Full=Auxin−responsive protein IAA3; AltName: Full=Indoleacetic acid−induced protein 3; AltName: Full=Short hypocotyl; AltName: Full=Suppressor of HY2 gi|12083196|gb|AAG48757.1|AF332393_1 auxin−induced protein IAA3 [Arabidopsis thaliana] gi|972911|gb|AAC49045.1| IAA3 [Arabidopsis thaliana] gi|1903369|gb|AAB70452.1| Match to Arabidopsis IAA3 (gb|U18406). EST gb|T04296 comes from this gene [Arabidopsis thaliana] gi|17381102|gb|AAL36363.1| putative auxin−induced protein IAA3 [Arabidopsis thaliana] gi|164604668|gb|ABY61894.1| At1g04240 [Arabidopsis thaliana] gi|164604670|gb|ABY61895.1| At1g04240 [Arabidopsis thaliana] gi|164604672|gb|ABY61896.1| At1g04240 [Arabidopsis thaliana] gi|164604674|gb|ABY61897.1| At1g04240 [Arabidopsis thaliana] gi|164604676|gb|ABY61898.1| At1g04240 [Arabidopsis thaliana] gi|164604678|gb|ABY61899.1| At1g04240 [Arabidopsis thaliana] gi|164604682|gb|ABY61901.1| At1g04240 [Arabidopsis thaliana]</td><td>186</td><td>189</td><td>7.00E−87</td><td>101.6</td><td>84.9</td><td>91.9</td><td>auxin−responsive protein IAA3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G04240.1 | Symbols: SHY2, IAA3 | AUX/IAA transcriptional regulator family protein | chr1:1128564−1129319 REVERSE LENGTH=189</td><td>186</td><td>189</td><td>3.00E−89</td><td>101.6</td><td>84.9</td><td>91.9</td></tr>
</table>

Rsa1.0_00262.1.g9887.t1	ref|XP_002892201.1| hypothetical protein ARALYDRAFT_470398 [Arabidopsis lyrata subsp. lyrata] gi|297338043|gb|EFH68460.1| hypothetical protein ARALYDRAFT_470398 [Arabidopsis lyrata subsp. lyrata]	273	524	1.00E-130	191.9	84.6	88.6	hypothetical protein ARALYDRAFT_470398	gbpln	Arabidopsis lyrata	AT1G04220.1 | Symbols: KCS2 | 3-ketoacyl-CoA synthase 2 | chr1:1119853-1122483 REVERSE LENGTH=528	273	528	1.00E-131	193.4	82.8	87.9
Rsa1.0_00262.1.g9888.t1	ref|XP_002889497.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297335339|gb|EFH65756.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	1132	1115	0	98.5	80.1	86.1	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G04210.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:1114696-1119383 FORWARD LENGTH=1112	1132	1112	0	98.2	80.0	86.7
Rsa1.0_00262.1.g9889.t1	gb|EOA36813.1| hypothetical protein CARUB_v10008423mg [Capsella rubella]	739	733	0	99.2	91.1	94.6	hypothetical protein CARUB_v10008423mg	gbpln	Capsella rubella	AT1G04200.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Dymeclin (InterPro:IPR019142); Has 395 Blast hits to 389 proteins in 117 species: Archae - 0; Bacteria - 0; Metazoa - 262; Fungi - 21; Plants - 68; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink). | chr1:1109676-1113875 FORWARD LENGTH=732	739	732	0	99.1	91.7	94.5
Rsa1.0_00262.1.g9890.t1	ref|XP_002889495.1| flavin-containing monooxygenase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335337|gb|EFH65754.1| flavin-containing monooxygenase family protein [Arabidopsis lyrata subsp. lyrata]	422	421	0	99.8	94.8	97.9	flavin-containing monooxygenase family protein	gbpln	Arabidopsis lyrata	AT1G04180.1 | Symbols: YUC9 | YUCCA 9 | chr1:1104623-1105988 FORWARD LENGTH=421	422	421	0	99.8	94.3	97.4
Rsa1.0_00262.1.g9891.t1	gb|EOA40138.1| hypothetical protein CARUB_v10008849mg, partial [Capsella rubella]	465	523	0	112.5	96.6	98.9	hypothetical protein CARUB_v10008849mg, partial	gbpln	Capsella rubella	AT1G04170.1 | Symbols: EIF2 GAMMA | eukaryotic translation initiation factor 2 gamma subunit | chr1:1097423-1099702 FORWARD LENGTH=465	465	465	0	100.0	96.6	98.7
Rsa1.0_00263.1.g9892.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00263.1.g9893.t1	gb|AEI17372.1| Knox-like protein 1 [Arabidopsis lyrata]	72	388	3.00E-35	538.9	94.4	95.8	Knox-like protein 1	gbpln	Arabidopsis lyrata	AT4G08150.1 | Symbols: KNAT1, BP, BP1 | KNOTTED-like from Arabidopsis thaliana | chr4:5147969-5150610 REVERSE LENGTH=398	72	398	7.00E-38	552.8	94.4	94.4
Rsa1.0_00263.1.g9894.t19	dbj|BAB03186.1| En/Spm transposon protein-like [Arabidopsis thaliana]	1470	1516	0	103.1	34.6	41.2	En/Spm transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00263.1.g9895.t2	gb|ACS28249.1| BREVIPEDICELLUS [Brassica rapa]	262	383	1.00E-132	146.2	95.4	96.6	BREVIPEDICELLUS	gbpln	Brassica rapa	AT4G08150.1 | Symbols: KNAT1, BP, BP1 | KNOTTED-like from Arabidopsis thaliana | chr4:5147969-5150610 REVERSE LENGTH=398	262	398	1.00E-119	151.9	87.0	92.4
Rsa1.0_00263.1.g9896.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00263.1.g9897.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00263.1.g9898.t1	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	331	1044	6.00E-13	315.4	13.0	19.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00263.1.g9899.t1	ref|NP_192558.2| OSBP(oxysterol binding protein)-related protein 1C [Arabidopsis thaliana] gi|75154096|sp|Q8L751.1|ORP1C_ARATH RecName: Full=Oxysterol-binding protein-related protein 1C; AltName: Full=OSBP-related protein 1C gi|22654958|gb|AAM98072.1| AT4g08180/T12G13_20 [Arabidopsis thaliana] gi|332657206|gb|AEE82606.1| OSBP(oxysterol binding protein)-related protein 1C [Arabidopsis thaliana]	786	814	0	103.6	87.3	92.2	OSBP(oxysterol binding protein)-related protein 1C	gbpln	Arabidopsis thaliana	AT4G08180.1 | Symbols: ORP1C | OSBP(oxysterol binding protein)-related protein 1C | chr4:5169727-5173360 FORWARD LENGTH=814	786	814	0	103.6	87.3	92.2
Rsa1.0_00263.1.g9900.t1	ref|NP_192563.2| glycine-rich protein [Arabidopsis thaliana] gi|18252943|gb|AAL62398.1| unknown protein [Arabidopsis thaliana] gi|23198028|gb|AAN15541.1| unknown protein [Arabidopsis thaliana] gi|332657210|gb|AEE82610.1| glycine-rich protein [Arabidopsis thaliana]	117	113	1.00E-35	96.6	84.6	85.5	glycine-rich protein	gbpln	Arabidopsis thaliana	AT4G08230.1 | Symbols: | glycine-rich protein | chr4:5188047-5189574 REVERSE LENGTH=113	117	113	2.00E-38	96.6	84.6	85.5
Rsa1.0_00263.1.g9901.t1	gb|ACB98704.1| phospholipase D gamma 1 [Brassica oleracea var. capitata]	818	859	0	105.0	76.9	84.5	phospholipase D gamma 1	gbpln	Brassica oleracea	AT4G11850.1 | Symbols: PLDGAMMA1, MEE54 | phospholipase D gamma 1 | chr4:7129352-7132937 REVERSE LENGTH=858	818	858	0	104.9	76.8	85.0

Rsa1.0_00263.1.g9902.t1	ref|XP_002872384.1| hypothetical protein ARALYDRAFT_489738 [Arabidopsis lyrata subsp. lyrata] gi|297318221|gb|EFH48643.1| hypothetical protein ARALYDRAFT_489738 [Arabidopsis lyrata subsp. lyrata]	133	136	5.00E-55	102.3	85.0	91.7	hypothetical protein ARALYDRAFT_489738	gbpln	Arabidopsis lyrata	AT4G08240.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:5194713-5195756 FORWARD LENGTH=136	133	136	7.00E-56	102.3	83.5	88.0
Rsa1.0_00263.1.g9903.t1	ref|NP_568713.1| uncharacterized protein [Arabidopsis thaliana] gi|16604643|gb|AAL24114.1| unknown protein [Arabidopsis thaliana] gi|23296703|gb|AAN13151.1| unknown protein [Arabidopsis thaliana] gi|332008476|gb|AED95859.1| uncharacterized protein AT5G49820 [Arabidopsis thaliana]	469	497	0	106.0	88.7	93.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G49820.1 | Symbols: EMB1879, RUS6 | Protein of unknown function, DUF647 | chr5:20246753-20249432 REVERSE LENGTH=497	469	497	0	106.0	88.7	93.2
Rsa1.0_00263.1.g9904.t1	ref|NP_192575.3| global transcription factor group A2 [Arabidopsis thaliana] gi|374095445|sp|Q9STN3.2|SPT51_ARATH RecName: Full=Putative transcription elongation factor SPT5 homolog 1 gi|332657229|gb|AEE82629.1| global transcription factor group A2 [Arabidopsis thaliana]	1042	1041	0	99.9	88.2	92.3	global transcription factor group A2	gbpln	Arabidopsis thaliana	AT4G08350.1 | Symbols: GTA02, GTA2 | global transcription factor group A2 | chr4:5286351-5292072 FORWARD LENGTH=1041	1042	1041	0	99.9	88.2	92.3
Rsa1.0_00263.1.g9905.t1	ref|XP_002893426.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339268|gb|EFH69685.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	293	384	1.00E-42	131.1	28.7	32.1	predicted protein	gbpln	Arabidopsis lyrata	AT3G20370.1 | Symbols: | TRAF-like family protein | chr3:7105481-7107079 FORWARD LENGTH=379	293	379	1.00E-41	129.4	26.6	30.4
Rsa1.0_00263.1.g9906.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00263.1.g9907.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	262	1142	2.00E-30	435.9	30.5	43.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	262	484	1.00E-15	184.7	16.8	25.2
Rsa1.0_00263.1.g9908.t1	ref|XP_002872397.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318234|gb|EFH48656.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	267	243	1.00E-125	91.0	82.0	86.9	BTB/POZ domain-containing protein	gbpln	Arabidopsis lyrata	AT4G08455.1 | Symbols: | BTB/POZ domain-containing protein | chr4:5375891-5376922 FORWARD LENGTH=243	267	243	1.00E-126	91.0	80.9	86.5
Rsa1.0_00263.1.g9909.t1	ref|XP_002874536.1| hypothetical protein ARALYDRAFT_489753 [Arabidopsis lyrata subsp. lyrata] gi|297320373|gb|EFH50795.1| hypothetical protein ARALYDRAFT_489753 [Arabidopsis lyrata subsp. lyrata]	280	277	6.00E-94	98.9	63.6	72.5	hypothetical protein ARALYDRAFT_489753	gbpln	Arabidopsis lyrata	AT4G08460.3 | Symbols: | Protein of unknown function (DUF1644) | chr4:5377378-5378202 REVERSE LENGTH=274	280	274	2.00E-89	97.9	63.2	69.6
Rsa1.0_00263.1.g9910.t1	ref|NP_194047.2| cysteine-rich receptor-like protein kinase 8 [Arabidopsis thaliana] gi|332659317|gb|AEE84717.1| cysteine-rich receptor-like protein kinase 8 [Arabidopsis thaliana]	104	1262	8.00E-29	1213.5	58.7	76.9	cysteine-rich receptor-like protein kinase 8	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	104	1262	1.00E-31	1213.5	58.7	76.9
Rsa1.0_00263.1.g9911.t1	emb|CAA08997.1| MAP3K beta 1 protein kinase [Brassica napus]	619	575	0	92.9	70.8	78.2	MAP3K beta 1 protein kinase	gbpln	Brassica napus	AT4G08500.1 | Symbols: MEKK1, ATMEKK1, MAPKKK8, ARAKIN | MAPK/ERK kinase kinase 1 | chr4:5404272-5407062 REVERSE LENGTH=608	619	608	0	98.2	65.9	74.5
Rsa1.0_00263.1.g9912.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00263.1.g9913.t1	ref|XP_002872399.1| hypothetical protein ARALYDRAFT_489756 [Arabidopsis lyrata subsp. lyrata] gi|297318236|gb|EFH48658.1| hypothetical protein ARALYDRAFT_489756 [Arabidopsis lyrata subsp. lyrata]	461	551	1.00E-106	119.5	61.0	71.6	hypothetical protein ARALYDRAFT_489756	gbpln	Arabidopsis lyrata	AT4G08510.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G36990.1); Has 888 Blast hits to 321 proteins in 121 species: Archae - 0; Bacteria - 120; Metazoa - 86; Fungi - 24; Plants - 79; Viruses - 0; Other Eukaryotes - 579 (source: NCBI BLink). | chr4:5411023-5413016 FORWARD LENGTH=551	461	551	1.00E-107	119.5	59.9	70.5
Rsa1.0_00263.1.g9914.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00263.1.g9915.t1	ref|XP_002872399.1| hypothetical protein ARALYDRAFT_489756 [Arabidopsis lyrata subsp. lyrata] gi|297318236|gb|EFH48658.1| hypothetical protein ARALYDRAFT_489756 [Arabidopsis lyrata subsp. lyrata]	376	551	4.00E-94	146.5	62.5	73.1	hypothetical protein ARALYDRAFT_489756	gbpln	Arabidopsis lyrata	AT4G08510.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G36990.1); Has 888 Blast hits to 321 proteins in 121 species: Archae - 0; Bacteria - 120; Metazoa - 86; Fungi - 24; Plants - 79; Viruses - 0; Other Eukaryotes - 579 (source: NCBI BLink). | chr4:5411023-5413016 FORWARD LENGTH=551	376	551	3.00E-95	146.5	60.6	71.3
Rsa1.0_00264.1.g9916.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00264.1.g9917.t1	ref|NP_564941.1| protein IDA [Arabidopsis thaliana] gi|75154765|sp|Q8LAD7.1|IDA_ARATH RecName: Full=Protein IDA; AltName: Full=Protein INFLORESCENCE DEFICIENT IN ABSCISSION; Flags: Precursor gi|21593468|gb|AAM65435.1| unknown [Arabidopsis thaliana] gi|94807658|gb|ABF47126.1| At1g68765 [Arabidopsis thaliana] gi|332196716|gb|AEE34837.1| protein IDA [Arabidopsis thaliana]	75	77	1.00E-19	102.7	78.7	86.7	protein IDA	gbpln	Arabidopsis thaliana	AT1G68765.1 | Symbols: IDA | Putative membrane lipoprotein | chr1:25830157-25830390 REVERSE LENGTH=77	75	77	2.00E-22	102.7	78.7	86.7
Rsa1.0_00264.1.g9918.t1	ref|XP_002888681.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334522|gb|EFH64940.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	431	430	0	99.8	84.7	92.3	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G68780.1 | Symbols: | RNI-like superfamily protein | chr1:25831881-25833335 REVERSE LENGTH=432	431	432	0	100.2	84.5	92.1
Rsa1.0_00264.1.g9919.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00264.1.g9920.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00264.1.g9921.t1	ref|XP_002888683.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334524|gb|EFH64942.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	254	121	8.00E-25	47.6	24.0	26.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G68795.1 | Symbols: CLE12 | CLAVATA3/ESR-RELATED 12 | chr1:25841079-25841435 REVERSE LENGTH=118	254	118	3.00E-26	46.5	23.6	25.6
Rsa1.0_00264.1.g9922.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00264.1.g9923.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	566	1274	1.00E-112	225.1	41.0	57.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	566	575	7.00E-77	101.6	30.0	49.3
Rsa1.0_00264.1.g9924.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	713	1307	1.00E-149	183.3	43.1	54.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	713	1262	9.00E-56	177.0	17.5	27.9
Rsa1.0_00264.1.g9925.t1	ref|XP_002887206.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297333047|gb|EFH63465.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	353	360	1.00E-160	102.0	87.8	91.2	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT1G68810.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:25861289-25862882 FORWARD LENGTH=368	353	368	1.00E-160	104.2	88.7	91.5
Rsa1.0_00264.1.g9926.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	383	1231	3.00E-93	321.4	46.0	63.2	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	383	575	2.00E-52	150.1	29.2	48.3
Rsa1.0_00264.1.g9927.t3	ref|NP_564945.1| Transmembrane Fragile-X-F-associated protein [Arabidopsis thaliana] gi|13878073|gb|AAK44114.1|AF370299_1 unknown protein [Arabidopsis thaliana] gi|17104741|gb|AAL34259.1| unknown protein [Arabidopsis thaliana] gi|332196722|gb|AEE34843.1| Transmembrane Fragile-X-F-associated protein [Arabidopsis thaliana]	476	468	0	98.3	93.7	96.4	Transmembrane Fragile-X-F-associated protein	gbpln	Arabidopsis thaliana	AT1G68820.1 | Symbols: | Transmembrane Fragile-X-F-associated protein | chr1:25865852-25868800 FORWARD LENGTH=468	476	468	0	98.3	93.7	96.4
Rsa1.0_00264.1.g9928.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00264.1.g9929.t1	ref|NP_001077795.1| protein ROTUNDIFOLIA like 15 [Arabidopsis thaliana] gi|238479011|ref|NP_001154459.1| protein ROTUNDIFOLIA like 15 [Arabidopsis thaliana] gi|37955430|gb|AAP13820.1| DVL5 [Arabidopsis thaliana] gi|332196723|gb|AEE34844.1| protein ROTUNDIFOLIA like 15 [Arabidopsis thaliana] gi|332196724|gb|AEE34845.1| protein ROTUNDIFOLIA like 15 [Arabidopsis thaliana]	46	46	1.00E-16	100.0	95.7	95.7	protein ROTUNDIFOLIA like 15	gbpln	Arabidopsis thaliana	AT1G68825.2 | Symbols: DVL5, RTFL15 | ROTUNDIFOLIA like 15 | chr1:25869946-25870086 REVERSE LENGTH=46	46	46	2.00E-19	100.0	95.7	95.7
Rsa1.0_00264.1.g9930.t1	gb|EOA34625.1| hypothetical protein CARUB_v10022188mg [Capsella rubella]	561	564	0	100.5	93.4	96.6	hypothetical protein CARUB_v10022188mg	gbpln	Capsella rubella	AT1G68830.1 | Symbols: STN7 | STT7 homolog STN7 | chr1:25872654-25875473 REVERSE LENGTH=562	561	562	0	100.2	92.2	96.8
Rsa1.0_00264.1.g9931.t1	ref|XP_002888686.1| hypothetical protein ARALYDRAFT_315905 [Arabidopsis lyrata subsp. lyrata] gi|297334527|gb|EFH64945.1| hypothetical protein ARALYDRAFT_315905 [Arabidopsis lyrata subsp. lyrata]	514	140	4.00E-39	27.2	17.3	20.4	hypothetical protein ARALYDRAFT_315905	gbpln	Arabidopsis lyrata	AT1G68845.1 | Symbols: | unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25882434-25882918 FORWARD LENGTH=138	514	138	2.00E-34	26.8	16.1	19.3

Rsa1.0_00264.1.g9932.t1	ref|NP_564948.1| peroxidase 11 [Arabidopsis thaliana] gi|25453204|sp|Q96519.1|PER11_ARATH RecName: Full=Peroxidase 11; Short=Atperox P11; AltName: Full=ATP23a/ATP23b; Flags: Precursor gi|12323216|gb|AAG51588.1|AC011665_9 peroxidase ATP23a [Arabidopsis thaliana] gi|12324132|gb|AAG52033.1|AC011914_3 peroxidase ATP23a; 12312-13683 [Arabidopsis thaliana] gi|1620371|emb|CAA70035.1| peroxidase ATP23a [Arabidopsis thaliana] gi|332196729|gb|AEE34850.1| peroxidase 11 [Arabidopsis thaliana]	335	336	0	100.3	92.2	96.4	peroxidase 11	gbpln	Arabidopsis thaliana	AT1G68850.1 | Symbols: | Peroxidase superfamily protein | chr1:25883806-25885177 REVERSE LENGTH=336	335	336	0	100.3	92.2	96.4
Rsa1.0_00264.1.g9933.t1	gb|EOA33892.1| hypothetical protein CARUB_v10021384mg [Capsella rubella]	146	149	9.00E-41	102.1	72.6	81.5	hypothetical protein CARUB_v10021384mg	gbpln	Capsella rubella	AT1G68870.1 | Symbols: ATSOFL2, SOFL2 | SOB five-like 2 | chr1:25889117-25889560 FORWARD LENGTH=147	146	147	1.00E-40	100.7	74.0	80.8
Rsa1.0_00265.1.g9934.t1	ref|XP_002878191.1| hypothetical protein ARALYDRAFT_907288 [Arabidopsis lyrata subsp. lyrata] gi|297324029|gb|EFH54450.1| hypothetical protein ARALYDRAFT_907288 [Arabidopsis lyrata subsp. lyrata]	214	195	2.00E-73	91.1	65.4	76.6	hypothetical protein ARALYDRAFT_907288	gbpln	Arabidopsis lyrata	AT3G58150.1 | Symbols: | Optic atrophy 3 protein (OPA3) | chr3:21532947-21534072 REVERSE LENGTH=194	214	194	2.00E-75	90.7	65.0	78.0
Rsa1.0_00265.1.g9935.t1	ref|XP_002876459.1| hypothetical protein ARALYDRAFT_907290 [Arabidopsis lyrata subsp. lyrata] gi|297322297|gb|EFH52718.1| hypothetical protein ARALYDRAFT_907290 [Arabidopsis lyrata subsp. lyrata]	1241	1249	0	100.6	87.0	93.6	hypothetical protein ARALYDRAFT_907290	gbpln	Arabidopsis lyrata	AT3G58160.1 | Symbols: XIJ, ATXIJ, ATMYOS3, MYA3, XI-16 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:21534797-21541877 FORWARD LENGTH=1242	1241	1242	0	100.1	86.4	93.0
Rsa1.0_00265.1.g9936.t1	ref|NP_191378.1| LOB domain-containing protein 29 [Arabidopsis thaliana] gi|29428017|sp|Q9M2J7.1|LBD29_ARATH RecName: Full=LOB domain-containing protein 29; AltName: Full=ASYMMETRIC LEAVES 2-like protein 16; Short=AS2-like protein 16 gi|17227168|gb|AAL38038.1|AF447893_1 LOB DOMAIN 29 [Arabidopsis thaliana] gi|6735331|emb|CAB68157.1| putative protein [Arabidopsis thaliana] gi|94442495|gb|ABF19035.1| At3g58190 [Arabidopsis thaliana] gi|219807108|dbj|BAH10560.1| ASYMMETRIC LEAVES2-like 16 protein [Arabidopsis thaliana] gi|332646231|gb|AEE79752.1| LOB domain-containing protein 29 [Arabidopsis thaliana]	216	218	1.00E-100	100.9	83.3	88.9	LOB domain-containing protein 29	gbpln	Arabidopsis thaliana	AT3G58190.1 | Symbols: LBD29, ASL16 | lateral organ boundaries-domain 29 | chr3:21548716-21549488 REVERSE LENGTH=218	216	218	1.00E-102	100.9	83.3	88.9
Rsa1.0_00265.1.g9937.t1	ref|XP_002876187.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322025|gb|EFH52446.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	118	155	4.00E-25	131.4	53.4	67.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G53080.1 | Symbols: | D-galactoside/L-rhamnose binding SUEL lectin protein | chr3:19678013-19678578 FORWARD LENGTH=155	118	155	3.00E-27	131.4	55.9	69.5
Rsa1.0_00265.1.g9938.t1	gb|EOA36691.1| hypothetical protein CARUB_v10012096mg [Capsella rubella]	331	327	1.00E-120	98.8	64.4	77.3	hypothetical protein CARUB_v10012096mg	gbpln	Capsella rubella	AT5G43690.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273-17547268 FORWARD LENGTH=331	331	331	1.00E-122	100.0	65.9	77.6
Rsa1.0_00265.1.g9939.t2	gb|EOA25716.1| hypothetical protein CARUB_v10019067mg [Capsella rubella]	191	494	1.00E-36	258.6	46.6	66.5	hypothetical protein CARUB_v10019067mg	gbpln	Capsella rubella	AT3G58410.1 | Symbols: | TRAF-like family protein | chr3:21604871-21606229 REVERSE LENGTH=328	191	328	3.00E-37	171.7	41.4	50.8
Rsa1.0_00265.1.g9940.t2	ref|NP_191400.1| TRAF-like family protein [Arabidopsis thaliana] gi|6735353|emb|CAB68179.1| putative protein [Arabidopsis thaliana] gi|332646257|gb|AEE79778.1| TRAF-like family protein [Arabidopsis thaliana]	323	328	1.00E-108	101.5	64.1	77.1	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G58410.1 | Symbols: | TRAF-like family protein | chr3:21604871-21606229 REVERSE LENGTH=328	323	328	1.00E-111	101.5	64.1	77.1
Rsa1.0_00265.1.g9941.t1	ref|NP_191400.1| TRAF-like family protein [Arabidopsis thaliana] gi|6735353|emb|CAB68179.1| putative protein [Arabidopsis thaliana] gi|332646257|gb|AEE79778.1| TRAF-like family protein [Arabidopsis thaliana]	192	328	6.00E-59	170.8	58.9	70.3	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G58410.1 | Symbols: | TRAF-like family protein | chr3:21604871-21606229 REVERSE LENGTH=328	192	328	2.00E-61	170.8	58.9	70.3
Rsa1.0_00265.1.g9942.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00265.1.g9943.t2	gb|EOA25745.1| hypothetical protein CARUB_v10019107mg [Capsella rubella]	563	577	0	102.5	86.9	92.0	hypothetical protein CARUB_v10019107mg	gbpln	Capsella rubella	AT3G58480.1 | Symbols: | calmodulin-binding family protein | chr3:21629341-21631853 FORWARD LENGTH=575	563	575	0	102.1	85.6	91.3

Rsa1.0_00265.1.g9944.t6	gb|EOA19018.1| hypothetical protein CARUB_v10007669mg [Capsella rubella]	668	882	1.00E-116	132.0	37.4	40.0	hypothetical protein CARUB_v10007669mg	gbpln	Capsella rubella	AT4G12780.2 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:7512200-7516655 FORWARD LENGTH=894	668	894	1.00E-114	133.8	32.3	34.1
Rsa1.0_00265.1.g9945.t1	gb|EOA15602.1| hypothetical protein CARUB_v10005649mg [Capsella rubella]	63	232	3.00E-18	368.3	82.5	88.9	hypothetical protein CARUB_v10005649mg	gbpln	Capsella rubella	AT4G26220.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:13284179-13285146 FORWARD LENGTH=232	63	232	1.00E-19	368.3	82.5	88.9
Rsa1.0_00265.1.g9946.t1	ref|XP_002275766.1| PREDICTED: auxilin-related protein 2-like [Vitis vinifera]	402	949	8.00E-77	236.1	33.3	35.3	PREDICTED: auxilin-related protein 2-like	gbpln	Vitis vinifera	AT4G12770.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:7506736-7511408 REVERSE LENGTH=891	402	891	9.00E-74	221.6	38.3	42.8
Rsa1.0_00265.1.g9947.t1	ref|NP_567066.1| serine/threonine-protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] gi|297820682|ref|XP_002878224.1| protein phosphatase 2A-3 [Arabidopsis lyrata subsp. lyrata] gi|1352664|sp|P48578.1|PP2A3_ARATH RecName: Full=Serine/threonine-protein phosphatase PP2A-3 catalytic subunit; AltName: Full=Protein phosphatase 2A isoform 3 gi|473259|gb|AAA64941.1| Ser/Thr protein phosphatase [Arabidopsis thaliana] gi|4204949|gb|AAD10855.1| serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana] gi|15810367|gb|AAL07071.1| putative phosphoprotein phosphatase 2A isoform 4 [Arabidopsis thaliana] gi|16209682|gb|AAL14399.1| AT3g58500/F14P22_90 [Arabidopsis thaliana] gi|21360431|gb|AAM47331.1| AT3g58500/F14P22_90 [Arabidopsis thaliana] gi|297324062|gb|EFH54483.1| protein phosphatase 2A-3 [Arabidopsis lyrata subsp. lyrata] gi|332646269|gb|AEE79790.1| serine/threonine-protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] gi|482560231|gb|EOA24422.1| hypothetical protein CARUB_v10017673mg [Capsella rubella]	346	313	1.00E-171	90.5	85.5	87.9	serine/threonine-protein phosphatase PP2A-3 catalytic subunit	gbpln	Arabidopsis lyrata	AT3G58500.1 | Symbols: PP2A-4 | protein phosphatase 2A-4 | chr3:21635503-21638911 REVERSE LENGTH=313	346	313	1.00E-174	90.5	85.5	87.9
Rsa1.0_00265.1.g9948.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00265.1.g9949.t1	ref|NP_191414.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|6735372|emb|CAB68193.1| putative protein [Arabidopsis thaliana] gi|26453160|dbj|BAC43656.1| GPI-anchored protein [Arabidopsis thaliana] gi|28372968|gb|AAO39966.1| At3g58550 [Arabidopsis thaliana] gi|332646277|gb|AEE79798.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	166	177	2.00E-77	106.6	83.7	93.4	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT3G58550.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:21649506-21650233 REVERSE LENGTH=177	166	177	7.00E-80	106.6	83.7	93.4
Rsa1.0_00265.1.g9950.t1	gb|EOA23679.1| hypothetical protein CARUB_v10016885mg [Capsella rubella]	601	600	0	99.8	92.7	95.8	hypothetical protein CARUB_v10016885mg	gbpln	Capsella rubella	AT3G58580.1 | Symbols: | DNAse I-like superfamily protein | chr3:21660866-21663697 REVERSE LENGTH=603	601	603	0	100.3	92.2	96.3
Rsa1.0_00265.1.g9951.t1	gb|AAD48963.1|AF147263_5 contains similarity to transposases [Arabidopsis thaliana] gi|7267311|emb|CAB81093.1| AT4g05510 [Arabidopsis thaliana]	76	604	3.00E-14	794.7	53.9	64.5	contains similarity to transposases	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00265.1.g9952.t1	ref|XP_002876469.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322307|gb|EFH52728.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	755	741	0	98.1	76.8	84.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G58590.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:21666262-21668487 FORWARD LENGTH=741	755	741	0	98.1	76.3	83.8
Rsa1.0_00265.1.g9953.t1	ref|XP_002878229.1| hypothetical protein ARALYDRAFT_486311 [Arabidopsis lyrata subsp. lyrata] gi|297324067|gb|EFH54488.1| hypothetical protein ARALYDRAFT_486311 [Arabidopsis lyrata subsp. lyrata]	289	297	1.00E-131	102.8	90.3	93.8	hypothetical protein ARALYDRAFT_486311	gbpln	Arabidopsis lyrata	AT3G58600.1 | Symbols: | Adaptin ear-binding coat-associated protein 1 NECAP-1 | chr3:21668746-21670999 REVERSE LENGTH=302	289	302	1.00E-129	104.5	89.3	93.1

Rsa1.0_00265.1.g9954.t1	gb|EOA23697.1| hypothetical protein CARUB_v10016904mg [Capsella rubella]	587	591	0	100.7	93.0	96.8	hypothetical protein CARUB_v10016904mg	gbpln	Capsella rubella	AT3G58610.3 | Symbols: | ketol-acid reductoisomerase | chr3:21671561-21674639 FORWARD LENGTH=591	587	591	0	100.7	94.5	97.3
Rsa1.0_00265.1.g9955.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00265.1.g9956.t1	ref|NP_191424.5| uncharacterized protein [Arabidopsis thaliana] gi|6735382|emb|CAB68203.1| putative protein [Arabidopsis thaliana] gi|332646290|gb|AEE79811.1| uncharacterized protein AT3G58650 [Arabidopsis thaliana]	661	820	0	124.1	79.6	88.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G58650.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 8 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26910.1); Has 2350 Blast hits to 1412 proteins in 248 species: Archae - 0; Bacteria - 487; Metazoa - 577; Fungi - 236; Plants - 184; Viruses - 4; Other Eukaryotes - 862 (source: NCBI BLink). | chr3:21696349-21699219 REVERSE LENGTH=820	661	820	0	124.1	79.6	88.7
Rsa1.0_00265.1.g9957.t1	ref|NP_191425.1| ribosomal protein L1p/L10e family protein [Arabidopsis thaliana] gi|7630061|emb|CAB88283.1| putative protein [Arabidopsis thaliana] gi|17979349|gb|AAL49900.1| unknown protein [Arabidopsis thaliana] gi|332646291|gb|AEE79812.1| ribosomal protein L1p/L10e family protein [Arabidopsis thaliana]	411	446	1.00E-140	108.5	69.8	80.5	ribosomal protein L1p/L10e family protein	gbpln	Arabidopsis thaliana	AT3G58660.1 | Symbols: | Ribosomal protein L1p/L10e family | chr3:21701574-21702914 FORWARD LENGTH=446	411	446	1.00E-143	108.5	69.8	80.5
Rsa1.0_00265.1.g9958.t1	gb|EOA24666.1| hypothetical protein CARUB_v10017939mg [Capsella rubella] gi|482560476|gb|EOA24667.1| hypothetical protein CARUB_v10017939mg [Capsella rubella]	242	242	1.00E-135	100.0	95.0	97.5	hypothetical protein CARUB_v10017939mg	gbpln	Capsella rubella	AT3G58670.3 | Symbols: | Protein of unknown function (DUF1637) | chr3:21703693-21705314 REVERSE LENGTH=242	242	242	1.00E-133	100.0	92.6	96.3
Rsa1.0_00265.1.g9959.t2	gb|EOA24914.1| hypothetical protein CARUB_v10018205mg [Capsella rubella]	167	142	4.00E-68	85.0	80.2	83.2	hypothetical protein CARUB_v10018205mg	gbpln	Capsella rubella	AT3G58680.1 | Symbols: MBF1B, ATMBF1B | multiprotein bridging factor 1B | chr3:21707367-21708625 FORWARD LENGTH=142	167	142	8.00E-68	85.0	77.2	82.0
Rsa1.0_00265.1.g9960.t1	ref|NP_191429.1| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|18415161|ref|NP_567563.1| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|30694822|ref|NP_568649.2| 60S ribosomal protein L11-2 [Arabidopsis thaliana] gi|27735235|sp|P42794.2|RL112_ARATH RecName: Full=60S ribosomal protein L11-2; AltName: Full=L16 gi|11908058|gb|AAG41458.1|AF326876_1 putative ribosomal protein L11 [Arabidopsis thaliana] gi|12642874|gb|AAK00379.1|AF339697_1 putative ribosomal protein L11 [Arabidopsis thaliana] gi|14326537|gb|AAK60313.1|AF385722_1 AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|7630065|emb|CAB88287.1| ribosomal protein L11-like [Arabidopsis thaliana] gi|9758681|dbj|BAB09220.1| ribosomal protein L11-like [Arabidopsis thaliana] gi|14517470|gb|AAK62625.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|18700224|gb|AAL77722.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|21553372|gb|AAM62465.1| ribosomal protein L11, cytosolic [Arabidopsis thaliana] gi|21592421|gb|AAM64372.1| ribosomal protein L11, cytosolic [Arabidopsis thaliana] gi|22136574|gb|AAM91073.1| AT4g18730/F28A21_140 [Arabidopsis thaliana] gi|332007914|gb|AED95297.1|	182	182	1.00E-101	100.0	98.9	100.0	60S ribosomal protein L11-2	gbpln	Arabidopsis thaliana	AT5G45775.2 | Symbols: | Ribosomal L5P family protein | chr5:18565281-18566496 REVERSE LENGTH=182	182	182	1.00E-104	100.0	98.9	100.0

Rsa1.0_00265.1.g9961.t1	ref|NP_567073.2| putative WRKY transcription factor 69 [Arabidopsis thaliana] gi|29839599|sp|Q93WV5.1|WRK69_ARATH RecName: Full=Probable WRKY transcription factor 69; AltName: Full=WRKY DNA-binding protein 69 gi|15991736|gb|AAL13045.1|AF421156_1 WRKY transcription factor 69 [Arabidopsis thaliana] gi|332646300|gb|AEE79821.1| putative WRKY transcription factor 69 [Arabidopsis thaliana]	278	271	1.00E-122	97.5	86.7	90.3	putative WRKY transcription factor 69	gbpln	Arabidopsis thaliana	AT3G58710.2 | Symbols: WRKY69, ATWRKY69 | WRKY DNA-binding protein 69 | chr3:21715192-21716766 FORWARD LENGTH=271	278	271	1.00E-124	97.5	86.7	90.3
Rsa1.0_00265.1.g9962.t1	gb|EOA24594.1| hypothetical protein CARUB_v10017860mg [Capsella rubella]	261	261	1.00E-143	100.0	97.3	97.7	hypothetical protein CARUB_v10017860mg	gbpln	Capsella rubella	AT3G58730.1 | Symbols: | vacuolar ATP synthase subunit D (VATD) / V-ATPase D subunit / vacuolar proton pump D subunit (VATPD) | chr3:21718495-21719280 REVERSE LENGTH=261	261	261	1.00E-144	100.0	96.2	97.7
Rsa1.0_00265.1.g9963.t3	dbj|BAJ34181.1| unnamed protein product [Thellungiella halophila]	488	508	0	104.1	79.5	86.3	unnamed protein product	----	----	AT3G58750.1 | Symbols: CSY2 | citrate synthase 2 | chr3:21724564-21727458 REVERSE LENGTH=514	488	514	0	105.3	77.5	85.7
Rsa1.0_00265.1.g9964.t1	ref|XP_002876477.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322315|gb|EFH52736.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	468	474	0	101.3	90.2	93.6	predicted protein	gbpln	Arabidopsis lyrata	AT3G58760.1 | Symbols: | Integrin-linked protein kinase family | chr3:21728756-21731740 FORWARD LENGTH=471	468	471	0	100.6	88.9	92.7
Rsa1.0_00266.1.g9965.t1	ref|XP_002865872.1| 1-amino-cyclopropane-1-carboxylate synthase 12 [Arabidopsis lyrata subsp. lyrata] gi|297311707|gb|EFH42131.1| 1-amino-cyclopropane-1-carboxylate synthase 12 [Arabidopsis lyrata subsp. lyrata]	510	495	0	97.1	88.2	92.7	1-amino-cyclopropane-1-carboxylate synthase 12	gbpln	Arabidopsis lyrata	AT5G51690.1 | Symbols: ACS12 | 1-amino-cyclopropane-1-carboxylate synthase 12 | chr5:20999015-21000957 REVERSE LENGTH=495	510	495	0	97.1	87.1	92.2
Rsa1.0_00266.1.g9966.t1	dbj|BAB11237.1| unnamed protein product [Arabidopsis thaliana]	329	325	3.00E-49	98.8	63.2	70.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G51680.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:20997591-20998755 FORWARD LENGTH=343	329	343	2.00E-47	104.3	57.1	63.5
Rsa1.0_00266.1.g9967.t1	ref|XP_002864121.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309956|gb|EFH40380.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	460	474	0	103.0	89.1	93.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G51670.1 | Symbols: | Protein of unknown function (DUF668) | chr5:20993560-20995096 FORWARD LENGTH=474	460	474	0	103.0	88.5	93.0
Rsa1.0_00266.1.g9968.t1	ref|NP_201383.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75170571|sp|Q9FH87.1|PP447_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At5g65820 gi|9758569|dbj|BAB09050.1| unnamed protein product [Arabidopsis thaliana] gi|332010728|gb|AED98111.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	118	637	2.00E-47	539.8	78.8	90.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G65820.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:26339876-26341789 REVERSE LENGTH=637	118	637	4.00E-50	539.8	78.8	90.7
Rsa1.0_00266.1.g9969.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00266.1.g9970.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00266.1.g9971.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1292	1459	0	112.9	57.9	73.8	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1292	1262	2.00E-97	97.7	13.6	19.5
Rsa1.0_00266.1.g9972.t1	ref|NP_199977.1| uncharacterized protein [Arabidopsis thaliana] gi|9758206|dbj|BAB08680.1| unnamed protein product [Arabidopsis thaliana] gi|13122292|dbj|BAB32887.1| leaf-senescence-related protein [Arabidopsis thaliana] gi|19424021|gb|AAL87282.1| unknown protein [Arabidopsis thaliana] gi|22136926|gb|AAM91807.1| unknown protein [Arabidopsis thaliana] gi|332008727|gb|AED96110.1| uncharacterized protein AT5G51640 [Arabidopsis thaliana]	466	501	0	107.5	85.0	92.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G51640.1 | Symbols: YLS7, TBL17 | Plant protein of unknown function (DUF828) | chr5:20975401-20977378 REVERSE LENGTH=501	466	501	0	107.5	85.0	92.1
Rsa1.0_00266.1.g9973.t1	gb|EOA13428.1| hypothetical protein CARUB_v10026469mg [Capsella rubella]	401	423	1.00E-119	105.5	69.3	79.3	hypothetical protein CARUB_v10026469mg	gbpln	Capsella rubella	AT5G51590.1 | Symbols: | AT hook motif DNA-binding family protein | chr5:20956863-20958929 REVERSE LENGTH=419	401	419	1.00E-112	104.5	70.3	78.1
Rsa1.0_00266.1.g9974.t5	gb|EOA17792.1| hypothetical protein CARUB_v10006186mg [Capsella rubella]	550	405	1.00E-103	73.6	38.7	45.5	hypothetical protein CARUB_v10006186mg	gbpln	Capsella rubella	AT5G56800.1 | Symbols: | Protein with RNI-like/FBD-like domains | chr5:22972989-22974208 FORWARD LENGTH=344	550	344	8.00E-62	62.5	22.0	26.7

Rsa1.0_00266.1.g9975.t1	dbj|BAB10837.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	606	1462	3.00E-50	241.3	19.3	32.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	606	237	1.00E-24	39.1	9.7	15.8
Rsa1.0_00266.1.g9976.t1	ref|NP_199968.1| protein EXORDIUM like 3 [Arabidopsis thaliana] gi|16226762|gb|AAL16255.1|AF428325_1 AT5g51550/K17N15_10 [Arabidopsis thaliana] gi|9758197|dbj|BAB08671.1| unnamed protein product [Arabidopsis thaliana] gi|332008714|gb|AED96097.1| protein EXORDIUM like 3 [Arabidopsis thaliana]	337	337	1.00E-178	100.0	94.1	96.1	protein EXORDIUM like 3	gbpln	Arabidopsis thaliana	AT5G51550.1 | Symbols: EXL3 | EXORDIUM like 3 | chr5:20939793-20940806 REVERSE LENGTH=337	337	337	1.00E-180	100.0	94.1	96.1
Rsa1.0_00266.1.g9977.t1	ref|NP_199965.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|9758194|dbj|BAB08668.1| ripening-related protein-like [Arabidopsis thaliana] gi|67633876|gb|AAY78862.1| invertase [Arabidopsis thaliana] gi|332008710|gb|AED96093.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	204	204	6.00E-94	100.0	82.8	90.2	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT5G51520.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:20925980-20926594 FORWARD LENGTH=204	204	204	2.00E-96	100.0	82.8	90.2
Rsa1.0_00266.1.g9978.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00266.1.g9979.t1	gb|EOA14518.1| hypothetical protein CARUB_v10027747mg [Capsella rubella]	635	538	0	84.7	67.7	71.8	hypothetical protein CARUB_v10027747mg	gbpln	Capsella rubella	AT5G51490.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:20913680-20915606 REVERSE LENGTH=536	635	536	0	84.4	68.2	73.4
Rsa1.0_00266.1.g9980.t1	ref|XP_002864114.1| hypothetical protein ARALYDRAFT_918182 [Arabidopsis lyrata subsp. lyrata] gi|297309949|gb|EFH40373.1| hypothetical protein ARALYDRAFT_918182 [Arabidopsis lyrata subsp. lyrata]	596	592	0	99.3	80.4	87.9	hypothetical protein ARALYDRAFT_918182	gbpln	Arabidopsis lyrata	AT5G51480.1 | Symbols: SKS2 | SKU5 similar 2 | chr5:20910433-20913153 FORWARD LENGTH=592	596	592	0	99.3	79.2	87.1
Rsa1.0_00267.1.g9981.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	591	1225	1.00E-172	207.3	50.8	68.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	591	626	8.00E-21	105.9	15.7	26.9
Rsa1.0_00267.1.g9982.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	433	1142	9.00E-31	263.7	18.0	29.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	433	256	5.00E-30	59.1	19.9	29.8
Rsa1.0_00267.1.g9983.t1	ref|NP_001154616.1| uncharacterized protein [Arabidopsis thaliana] gi|332641874|gb|AEE75395.1| uncharacterized protein AT3G13677 [Arabidopsis thaliana]	112	76	5.00E-23	67.9	47.3	49.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G13677.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 24 Blast hits to 24 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4476296-4476611 FORWARD LENGTH=76	112	76	9.00E-26	67.9	47.3	49.1
Rsa1.0_00267.1.g9984.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9985.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9986.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9987.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9988.t1	gb|EOA29826.1| hypothetical protein CARUB_v10012921mg [Capsella rubella]	934	932	0	99.8	92.6	95.9	hypothetical protein CARUB_v10012921mg	gbpln	Capsella rubella	AT2G05170.1 | Symbols: ATVPS11, VPS11 | vacuolar protein sorting 11 | chr2:1870020-1873278 FORWARD LENGTH=932	934	932	0	99.8	91.4	95.1
Rsa1.0_00267.1.g9989.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9990.t10	gb|AAD50007.1|AC007651_2 Similar to mudrA protein [Arabidopsis thaliana]	469	622	6.00E-32	132.6	17.1	21.1	Similar to mudrA protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9991.t1	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	144	954	3.00E-27	662.5	47.9	60.4	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9992.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00267.1.g9993.t1	ref|NP_001154316.1| calcineurin-like metallo-phosphoesterase-like protein [Arabidopsis thaliana] gi|332189946|gb|AEE28067.1| calcineurin-like metallo-phosphoesterase-like protein [Arabidopsis thaliana]	104	400	1.00E-24	384.6	55.8	59.6	calcineurin-like metallo-phosphoesterase-like protein	gbpln	Arabidopsis thaliana	AT1G07010.3 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr1:2152949-2154968 FORWARD LENGTH=400	104	400	2.00E-27	384.6	55.8	59.6
Rsa1.0_00267.1.g9994.t1	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	112	703	8.00E-39	627.7	83.9	88.4	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9995.t1	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	159	1089	3.00E-16	684.9	25.2	34.0	transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9996.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	707	695	0	98.3	57.0	68.3	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	707	681	2.00E-25	96.3	9.5	14.7
Rsa1.0_00267.1.g9997.t11	emb|CAN78623.1| hypothetical protein VITISV_010098 [Vitis vinifera]	1943	905	7.00E-74	46.6	8.5	12.2	hypothetical protein VITISV_010098	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00267.1.g9998.t1	ref|XP_002865287.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311122|gb|EFH41546.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	355	329	1.00E-133	92.7	68.7	75.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G45070.1 | Symbols: AtPP2-A8, PP2-A8 | phloem protein 2-A8 | chr5:18187899-18189362 REVERSE LENGTH=354	355	354	2.00E-77	99.7	43.9	64.8
Rsa1.0_00267.1.g9999.t1	gb|AAD17351.1| contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana] gi|7267432|emb|CAB77944.1| putative polyprotein [Arabidopsis thaliana]	656	1138	1.00E-169	173.5	50.9	59.5	contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1)	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	656	158	4.00E-24	24.1	8.4	12.2
Rsa1.0_00267.1.g10000.t1	gb|AAD17351.1| contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana] gi|7267432|emb|CAB77944.1| putative polyprotein [Arabidopsis thaliana]	506	1138	2.00E-89	224.9	40.3	52.8	contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00267.1.g10001.t1	ref|XP_002889521.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335363|gb|EFH65780.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	57	1043	8.00E-13	1829.8	56.1	64.9	kinase family protein	gbpln	Arabidopsis lyrata	AT1G04700.1 | Symbols: | PB1 domain-containing protein tyrosine kinase | chr1:1316919-1320653 FORWARD LENGTH=1042	57	1042	8.00E-15	1828.1	54.4	63.2
Rsa1.0_00267.1.g10002.t3	ref|NP_172041.2| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana] gi|75301121|sp|Q8L706.1|SYT5_ARATH RecName: Full=Synaptotagmin-5; AltName: Full=NTMC2T2.1; AltName: Full=Synaptotagmin E gi|22655178|gb|AAM98179.1| Ca2+-dependent lipid-binding protein, putative [Arabidopsis thaliana] gi|31711980|gb|AAP68346.1| At1g05500 [Arabidopsis thaliana] gi|110737090|dbj|BAF00497.1| putative Ca2+-dependent lipid-binding protein [Arabidopsis thaliana] gi|332189725|gb|AEE27846.1| synaptotagmin-5 [Arabidopsis thaliana]	208	560	6.00E-66	269.2	64.4	69.2	calcium-dependent lipid-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G05500.1 | Symbols: SYTE, ATSYTE, NTMC2TYPE2.1, NTMC2T2.1, SYT5 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:1625098-1628940 FORWARD LENGTH=560	208	560	2.00E-68	269.2	64.4	69.2

Rsa1.0_00267.1.g10003.t1	ref|NP_568825.1| beta-(1,2)-xylosyltransferase [Arabidopsis thaliana] gi|17369167|sp|Q9LDH0.1|XYLT_ARATH RecName: Full=Beta-(1,2)-xylosyltransferase gi|15724166|gb|AAL06475.1|AF411785_1 AT5g55500/MTE17_21 [Arabidopsis thaliana] gi|7671513|emb|CAB89489.1| beta1,2-Xylosyltransferase [Arabidopsis thaliana] gi|7768105|emb|CAB90610.1| beta1,2-xylosyltransferase [Arabidopsis thaliana] gi|9758182|dbj|BAB08567.1| unnamed protein product [Arabidopsis thaliana] gi|23505973|gb|AAN28846.1| At5g55500/MTE17_21 [Arabidopsis thaliana] gi|332009252|gb|AED96635.1| beta-(1,2)-xylosyltransferase [Arabidopsis thaliana]	166	534	1.00E-27	321.7	33.1	41.0	beta-(1,2)-xylosyltransferase	gbpln	Arabidopsis thaliana	AT5G55500.1 | Symbols: ATXYLT, XYLT | beta-1,2-xylosyltransferase | chr5:22482386-22484417 FORWARD LENGTH=534	166	534	5.00E-30	321.7	33.1	41.0
Rsa1.0_00267.1.g10004.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1269	1475	0	116.2	54.9	69.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1269	1262	1.00E-162	99.4	21.9	29.3
Rsa1.0_00268.1.g10005.t1	gb|EOA13182.1| hypothetical protein CARUB_v10026208mg [Capsella rubella]	484	534	0	110.3	74.8	85.7	hypothetical protein CARUB_v10026208mg	gbpln	Capsella rubella	AT5G50990.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:20739453-20741281 FORWARD LENGTH=534	484	534	0	110.3	75.0	84.9
Rsa1.0_00268.1.g10006.t1	ref|NP_199903.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|9758237|dbj|BAB08736.1| unnamed protein product [Arabidopsis thaliana] gi|58652072|gb|AAW80861.1| At5g50900 [Arabidopsis thaliana] gi|190576485|gb|ACE79043.1| At5g50900 [Arabidopsis thaliana] gi|332008624|gb|AED96007.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	535	555	0	103.7	80.0	89.2	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G50900.1 | Symbols: | ARM repeat superfamily protein | chr5:20705051-20706718 REVERSE LENGTH=555	535	555	0	103.7	80.0	89.2
Rsa1.0_00268.1.g10007.t1	ref|NP_199902.1| lipase domain-containing protein [Arabidopsis thaliana] gi|9758236|dbj|BAB08735.1| unnamed protein product [Arabidopsis thaliana] gi|332008623|gb|AED96006.1| lipase domain-containing protein [Arabidopsis thaliana]	413	408	0	98.8	84.7	91.0	lipase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G50890.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:20702684-20704235 FORWARD LENGTH=408	413	408	0	98.8	84.7	91.0
Rsa1.0_00268.1.g10008.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00268.1.g10009.t1	ref|XP_002870549.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316385|gb|EFH46808.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	584	614	1.00E-161	105.1	55.0	69.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G37650.1 | Symbols: | Family of unknown function (DUF577) | chr5:14954011-14955834 REVERSE LENGTH=607	584	607	1.00E-154	103.9	52.9	67.6
Rsa1.0_00268.1.g10010.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	518	1838	8.00E-56	354.8	31.3	49.4	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00268.1.g10011.t1	gb|AAD20101.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	775	764	6.00E-30	98.6	11.6	16.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00268.1.g10012.t1	ref|XP_002870549.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316385|gb|EFH46808.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	446	614	1.00E-82	137.7	37.4	46.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G37650.1 | Symbols: | Family of unknown function (DUF577) | chr5:14954011-14955834 REVERSE LENGTH=607	446	607	8.00E-81	136.1	37.0	45.1
Rsa1.0_00268.1.g10013.t1	ref|XP_002872029.1| methylthioalkylmalate synthase a [Arabidopsis lyrata subsp. lyrata] gi|98985860|emb|CAJ55515.1| methylthioalkylmalate synthase a [Arabidopsis lyrata subsp. lyrata] gi|297317866|gb|EFH48288.1| methylthioalkylmalate synthase a [Arabidopsis lyrata subsp. lyrata]	633	507	1.00E-169	80.1	44.9	49.8	methylthioalkylmalate synthase a	gbpln	Arabidopsis lyrata	AT5G23010.1 | Symbols: MAM1, IMS3 | methylthioalkylmalate synthase 1 | chr5:7703173-7706769 FORWARD LENGTH=506	633	506	1.00E-170	79.9	44.7	49.8
Rsa1.0_00268.1.g10014.t5	dbj|BAJ34206.1| unnamed protein product [Thellungiella halophila]	623	366	0	58.7	55.2	55.5	unnamed protein product	----	----	AT5G50850.1 | Symbols: MAB1 | Transketolase family protein | chr5:20689671-20692976 FORWARD LENGTH=363	623	363	0	58.3	53.9	54.6
Rsa1.0_00268.1.g10015.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00268.1.g10016.t1	dbj|BAD93953.1| hypothetical protein [Arabidopsis thaliana]	182	260	1.00E-17	142.9	24.7	24.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G25500.2 | Symbols: | Plasma-membrane choline transporter family protein | chr1:8955437-8957793 REVERSE LENGTH=488	182	488	6.00E-20	268.1	24.7	24.7

Rsa1.0_00268.1.g10017.t1	gb|EOA14605.1| hypothetical protein CARUB_v10027856mg [Capsella rubella]	388	406	1.00E-153	104.6	76.5	87.4	hypothetical protein CARUB_v10027856mg	gbpln	Capsella rubella	AT5G50840.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Taxilin (InterPro:IPR019132); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:20685903-20688739 FORWARD LENGTH=404	388	404	1.00E-152	104.1	76.5	86.6
Rsa1.0_00268.1.g10018.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	164	1142	4.00E-20	696.3	32.9	47.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	164	292	3.00E-13	178.0	24.4	42.7
Rsa1.0_00268.1.g10019.t1	emb|CAM59671.1| parvulin-type peptidyl-prolyl cis/trans isomerase [Lotus japonicus] gi|388496576|gb|AFK36354.1| unknown [Lotus japonicus]	87	122	8.00E-12	140.2	41.4	43.7	parvulin-type peptidyl-prolyl cis/trans isomerase	gbpln	Lotus japonicus	AT2G18040.1 | Symbols: PIN1AT | peptidylprolyl cis/trans isomerase, NIMA-interacting 1 | chr2:7842346-7843537 FORWARD LENGTH=119	87	119	2.00E-13	136.8	40.2	42.5
Rsa1.0_00268.1.g10020.t1	gb|EOA14430.1| hypothetical protein CARUB_v10027633mg [Capsella rubella]	273	268	3.00E-89	98.2	75.8	82.8	hypothetical protein CARUB_v10027633mg	gbpln	Capsella rubella	AT5G50830.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; Has 4984 Blast hits to 3288 proteins in 342 species: Archae - 12; Bacteria - 257; Metazoa - 1366; Fungi - 452; Plants - 199; Viruses - 77; Other Eukaryotes - 2621 (source: NCBI BLink). | chr5:20683452-20684549 FORWARD LENGTH=281	273	281	4.00E-86	102.9	73.6	82.1
Rsa1.0_00269.1.g10021.t1	gb|AAZ67609.1| 80A08_24 [Brassica rapa subsp. pekinensis]	315	475	4.00E-13	150.8	22.9	26.3	80A08_24	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00269.1.g10022.t1	ref|XP_002869011.1| hypothetical protein ARALYDRAFT_490932 [Arabidopsis lyrata subsp. lyrata] gi|297314847|gb|EFH45270.1| hypothetical protein ARALYDRAFT_490932 [Arabidopsis lyrata subsp. lyrata]	217	256	3.00E-94	118.0	76.5	85.7	hypothetical protein ARALYDRAFT_490932	gbpln	Arabidopsis lyrata	AT4G37150.1 | Symbols: ATMES9, MES9 | methyl esterase 9 | chr4:17492985-17494057 REVERSE LENGTH=256	217	256	1.00E-94	118.0	75.1	82.9
Rsa1.0_00269.1.g10023.t1	gb|EOA18087.1| hypothetical protein CARUB_v10006539mg [Capsella rubella]	540	540	0	100.0	92.0	95.9	hypothetical protein CARUB_v10006539mg	gbpln	Capsella rubella	AT4G37160.1 | Symbols: sks15 | SKU5 similar 15 | chr4:17494820-17497124 REVERSE LENGTH=541	540	541	0	100.2	91.7	95.6
Rsa1.0_00269.1.g10024.t1	ref|NP_849513.1| myb family transcription factor [Arabidopsis thaliana] gi|332661362|gb|AEE86762.1| myb family transcription factor [Arabidopsis thaliana]	254	363	4.00E-82	142.9	74.0	83.5	myb family transcription factor	gbpln	Arabidopsis thaliana	AT4G37180.2 | Symbols: | Homeodomain-like superfamily protein | chr4:17504648-17506107 FORWARD LENGTH=363	254	363	1.00E-84	142.9	74.0	83.5
Rsa1.0_00269.1.g10025.t1	ref|NP_195436.1| uncharacterized protein [Arabidopsis thaliana] gi|4006861|emb|CAB16779.1| tubulin-like protein [Arabidopsis thaliana] gi|7270668|emb|CAB80385.1| tubulin-like protein [Arabidopsis thaliana] gi|71143064|gb|AAZ23923.1| At4g37190 [Arabidopsis thaliana] gi|194306666|gb|ACF41946.1| At4g37190 [Arabidopsis thaliana] gi|332661364|gb|AEE86764.1| uncharacterized protein AT4G37190 [Arabidopsis thaliana]	550	562	0	102.2	85.8	92.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G37190.1 | Symbols: | LOCATED IN: cytosol, plasma membrane; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Beta tubulin, autoregulation binding site (InterPro:IPR013838), Misato Segment II, myosin-like (InterPro:IPR019605), Tubulin/FtsZ, N-terminal (InterPro:IPR019746); Has 345 Blast hits to 341 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 131; Fungi - 140; Plants - 55; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink). | chr4:17507155-17509512 FORWARD LENGTH=562	550	562	0	102.2	85.8	92.4
Rsa1.0_00269.1.g10026.t1	ref|XP_002866983.1| hypothetical protein ARALYDRAFT_328078 [Arabidopsis lyrata subsp. lyrata] gi|297312819|gb|EFH43242.1| hypothetical protein ARALYDRAFT_328078 [Arabidopsis lyrata subsp. lyrata]	319	328	1.00E-152	102.8	85.3	91.5	hypothetical protein ARALYDRAFT_328078	gbpln	Arabidopsis lyrata	AT5G66570.1 | Symbols: PSBO-1, OEE1, OEE33, OE33, PSBO1, MSP-1 | PS II oxygen-evolving complex 1 | chr5:26568744-26570124 FORWARD LENGTH=332	319	332	1.00E-136	104.1	75.2	81.8

Rsa1.0_00269.1.g10027.t1	gb|EOA15637.1| hypothetical protein CARUB_v10005881mg [Capsella rubella]	177	173	3.00E-68	97.7	80.8	85.9	hypothetical protein CARUB_v10005881mg	gbpln	Capsella rubella	AT4G37240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G23690.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17524546-17525052 FORWARD LENGTH=168	177	168	2.00E-65	94.9	78.0	84.7
Rsa1.0_00269.1.g10028.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00269.1.g10029.t1	ref|XP_002869018.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|297314854|gb|EFH45277.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata]	360	297	1.00E-148	82.5	72.5	75.0	GNS1/SUR4 membrane family protein	gbpln	Arabidopsis lyrata	AT4G36830.1 | Symbols: HOS3-1 | GNS1/SUR4 membrane protein family | chr4:17349511-17350380 FORWARD LENGTH=289	360	289	1.00E-143	80.3	69.7	72.5
Rsa1.0_00269.1.g10030.t1	gb|EOA16793.1| hypothetical protein CARUB_v10005013mg, partial [Capsella rubella]	344	388	1.00E-154	112.8	78.2	86.6	hypothetical protein CARUB_v10005013mg, partial	gbpln	Capsella rubella	AT4G36820.1 | Symbols: | Protein of unknown function (DUF607) | chr4:17346889-17347994 FORWARD LENGTH=338	344	338	1.00E-149	98.3	74.4	85.5
Rsa1.0_00269.1.g10031.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00269.1.g10032.t1	gb|AAD18103.1| putative calmodulin-binding protein [Arabidopsis thaliana] gi|40823412|gb|AAR92281.1| At2g24300 [Arabidopsis thaliana] gi|46518419|gb|AAS99691.1| At2g24300 [Arabidopsis thaliana]	71	503	2.00E-22	708.5	85.9	90.1	putative calmodulin-binding protein	gbpln	Arabidopsis thaliana	AT2G24300.1 | Symbols: | Calmodulin-binding protein | chr2:10341431-10343457 FORWARD LENGTH=552	71	552	6.00E-25	777.5	85.9	90.1
Rsa1.0_00269.1.g10033.t1	gb|EOA24339.1| hypothetical protein CARUB_v10017576mg [Capsella rubella]	167	341	1.00E-46	204.2	70.7	80.8	hypothetical protein CARUB_v10017576mg	gbpln	Capsella rubella	AT3G59990.4 | Symbols: MAP2B | methionine aminopeptidase 2B | chr3:22155921-22158551 REVERSE LENGTH=439	167	439	1.00E-43	262.9	67.1	73.1
Rsa1.0_00269.1.g10034.t1	gb|ACI16426.1| RUB1-conjugation enzyme [Brassica juncea]	185	185	1.00E-103	100.0	96.8	98.4	RUB1-conjugation enzyme	gbpln	Brassica juncea	AT4G36800.2 | Symbols: RCE1 | RUB1 conjugating enzyme 1 | chr4:17341237-17342148 REVERSE LENGTH=184	185	184	1.00E-104	99.5	96.8	98.4
Rsa1.0_00269.1.g10035.t1	sp|Q94A43.1|BEH2_ARATH RecName: Full=BES1/BZR1 homolog protein 2 gi|15215731|gb|AAK91411.1| AT4g36780/C7A10_580 [Arabidopsis thaliana] gi|20453269|gb|AAM19873.1| AT4g36780/C7A10_580 [Arabidopsis thaliana]	312	318	1.00E-137	101.9	89.1	91.7	RecName: Full=BES1/BZR1 homolog protein 2 gi|15215731|gb|AAK91411.1| AT4g36780/C7A10_580	gbpln	Arabidopsis thaliana	AT4G36780.1 | Symbols: BEH2 | BES1/BZR1 homolog 2 | chr4:17332989-17334212 REVERSE LENGTH=265	312	265	3.00E-77	84.9	58.0	59.3
Rsa1.0_00269.1.g10036.t1	gb|EOA16414.1| hypothetical protein CARUB_v10004567mg, partial [Capsella rubella]	251	531	1.00E-123	211.6	84.9	88.8	hypothetical protein CARUB_v10004567mg, partial	gbpln	Capsella rubella	AT4G36380.1 | Symbols: ROT3 | Cytochrome P450 superfamily protein | chr4:17187973-17192202 REVERSE LENGTH=524	251	524	1.00E-124	208.8	85.3	88.8
Rsa1.0_00269.1.g10037.t1	ref|NP_568001.1| beta-galactosidase 3 [Arabidopsis thaliana] gi|75202767|sp|Q9SCV9.1|BGAL3_ARATH RecName: Full=Beta-galactosidase 3; Short=Lactase 3; Flags: Precursor gi|6686878|emb|CAB64739.1| putative beta-galactosidase [Arabidopsis thaliana] gi|15810493|gb|AAL07134.1| putative beta-galactosidase [Arabidopsis thaliana] gi|20259271|gb|AAM14371.1| putative beta-galactosidase [Arabidopsis thaliana] gi|332661246|gb|AEE86646.1| beta-galactosidase 3 [Arabidopsis thaliana]	856	856	0	100.0	93.9	97.5	beta-galactosidase 3	gbpln	Arabidopsis thaliana	AT4G36360.1 | Symbols: BGAL3 | beta-galactosidase 3 | chr4:17176840-17181143 REVERSE LENGTH=856	856	856	0	100.0	93.9	97.5

<table>
<tr><td>Rsa1.0_00269.1.g10038.t1</td><td>ref|NP_176033.1| purple acid phosphatase 6 [Arabidopsis thaliana] gi|75268138|sp|Q9C510.1|PPA6_ARATH RecName: Full=Purple acid phosphatase 6; Flags: Precursor gi|12321764|gb|AAG50924.1|AC069159_25 purple acid phosphatase, putative [Arabidopsis thaliana] gi|12323034|gb|AAG51511.1|AC058785_14 purple acid phosphatase, putative [Arabidopsis thaliana] gi|91805975|gb|ABE65716.1| calcineurin-like phosphoesterase family protein [Arabidopsis thaliana] gi|111074186|gb|ABH04466.1| At1g56360 [Arabidopsis thaliana] gi|332195262|gb|AEE33383.1| purple acid phosphatase 6 [Arabidopsis thaliana]</td><td>460</td><td>466</td><td>0</td><td>101.3</td><td>84.1</td><td>90.2</td><td>purple acid phosphatase 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G56360.1 | Symbols: PAP6, ATPAP6 | purple acid phosphatase 6 | chr1:21098603-21100842 REVERSE LENGTH=466</td><td>460</td><td>466</td><td>0</td><td>101.3</td><td>84.1</td><td>90.2</td></tr>
<tr><td>Rsa1.0_00269.1.g10039.t13</td><td>ref|XP_002867022.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312858|gb|EFH43281.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>180</td><td>631</td><td>6.00E-32</td><td>350.6</td><td>45.0</td><td>50.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36290.1 | Symbols: CRT1 | compromised recognition of TCV 1 | chr4:17169669-17173187 REVERSE LENGTH=635</td><td>180</td><td>635</td><td>7.00E-32</td><td>352.8</td><td>39.4</td><td>48.9</td></tr>
<tr><td>Rsa1.0_00269.1.g10040.t1</td><td>gb|ADA60974.1| stylish 2b [Brassica rapa subsp. pekinensis]</td><td>310</td><td>321</td><td>1.00E-132</td><td>103.5</td><td>93.5</td><td>96.5</td><td>stylish 2b</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G36260.1 | Symbols: STY2, SRS2 | Lateral root primordium (LRP) protein-related | chr4:17155705-17157006 REVERSE LENGTH=322</td><td>310</td><td>322</td><td>1.00E-115</td><td>103.9</td><td>84.5</td><td>89.4</td></tr>
<tr><td>Rsa1.0_00269.1.g10041.t1</td><td>ref|XP_002867032.1| hypothetical protein ARALYDRAFT_491017 [Arabidopsis lyrata subsp. lyrata] gi|297312868|gb|EFH43291.1| hypothetical protein ARALYDRAFT_491017 [Arabidopsis lyrata subsp. lyrata]</td><td>370</td><td>376</td><td>0</td><td>101.6</td><td>85.4</td><td>90.8</td><td>hypothetical protein ARALYDRAFT_491017</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36160.1 | Symbols: ANAC076, VND2, NAC076 | NAC domain containing protein 76 | chr4:17110877-17112891 REVERSE LENGTH=377</td><td>370</td><td>377</td><td>0</td><td>101.9</td><td>85.4</td><td>90.3</td></tr>
<tr><td>Rsa1.0_00269.1.g10042.t1</td><td>ref|XP_002869043.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata] gi|297314879|gb|EFH45302.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata]</td><td>258</td><td>258</td><td>1.00E-144</td><td>100.0</td><td>97.3</td><td>99.2</td><td>60S ribosomal protein L8</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36130.1 | Symbols: | Ribosomal protein L2 family | chr4:17097613-17098656 FORWARD LENGTH=258</td><td>258</td><td>258</td><td>2.33E-156</td><td>100.0</td><td>96.5</td><td>99.2</td></tr>
<tr><td>Rsa1.0_00269.1.g10043.t1</td><td>ref|XP_002869044.1| hypothetical protein ARALYDRAFT_491020 [Arabidopsis lyrata subsp. lyrata] gi|297314880|gb|EFH45303.1| hypothetical protein ARALYDRAFT_491020 [Arabidopsis lyrata subsp. lyrata]</td><td>108</td><td>104</td><td>3.00E-47</td><td>96.3</td><td>82.4</td><td>89.8</td><td>hypothetical protein ARALYDRAFT_491020</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36110.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:17090031-17090345 FORWARD LENGTH=104</td><td>108</td><td>104</td><td>4.00E-49</td><td>96.3</td><td>82.4</td><td>88.9</td></tr>
<tr><td>Rsa1.0_00269.1.g10044.t1</td><td>gb|AAL91266.1| AT4g36060/T19K4_190 [Arabidopsis thaliana] gi|23308269|gb|AAN18104.1| At4g36060/T19K4_190 [Arabidopsis thaliana]</td><td>132</td><td>268</td><td>3.00E-17</td><td>203.0</td><td>34.8</td><td>43.9</td><td>AT4g36060/T19K4_190</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G36060.2 | Symbols: bHLH11 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:17055521-17056567 FORWARD LENGTH=268</td><td>132</td><td>268</td><td>6.00E-20</td><td>203.0</td><td>34.8</td><td>43.9</td></tr>
<tr><td>Rsa1.0_00269.1.g10045.t1</td><td>ref|XP_002869044.1| hypothetical protein ARALYDRAFT_491020 [Arabidopsis lyrata subsp. lyrata] gi|297314880|gb|EFH45303.1| hypothetical protein ARALYDRAFT_491020 [Arabidopsis lyrata subsp. lyrata]</td><td>103</td><td>104</td><td>1.00E-47</td><td>101.0</td><td>88.3</td><td>93.2</td><td>hypothetical protein ARALYDRAFT_491020</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36110.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:17090031-17090345 FORWARD LENGTH=104</td><td>103</td><td>104</td><td>1.00E-49</td><td>101.0</td><td>88.3</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00269.1.g10046.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>312</td><td>1274</td><td>1.00E-53</td><td>408.3</td><td>38.5</td><td>54.2</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>312</td><td>303</td><td>2.00E-40</td><td>97.1</td><td>35.3</td><td>49.0</td></tr>
<tr><td>Rsa1.0_00269.1.g10047.t1</td><td>ref|NP_195331.2| calcium-dependent protein kinase 18 [Arabidopsis thaliana] gi|122244077|sp|Q1PE17.1|CDPKI_ARATH RecName: Full=Calcium-dependent protein kinase 18 gi|91806778|gb|ABE66116.1| calcium-dependent protein kinase family protein/CDPK family protein [Arabidopsis thaliana] gi|332661210|gb|AEE86610.1| calcium-dependent protein kinase 18 [Arabidopsis thaliana]</td><td>541</td><td>534</td><td>0</td><td>98.7</td><td>87.8</td><td>91.9</td><td>calcium-dependent protein kinase 18</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G36070.1 | Symbols: CPK18 | calcium-dependent protein kinase 18 | chr4:17056907-17059595 REVERSE LENGTH=534</td><td>541</td><td>534</td><td>0</td><td>98.7</td><td>87.8</td><td>91.9</td></tr>
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<tr><td>Rsa1.0_00269.1.g10048.t1</td><td>ref|XP_002869046.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297314882|gb|EFH45305.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]</td><td>261</td><td>266</td><td>4.00E-74</td><td>101.9</td><td>64.0</td><td>73.2</td><td>basic helix-loop-helix family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36060.2 | Symbols: bHLH11 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:17055521-17056567 FORWARD LENGTH=268</td><td>261</td><td>268</td><td>8.00E-75</td><td>102.7</td><td>59.0</td><td>69.3</td></tr>
<tr><td>Rsa1.0_00269.1.g10049.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00269.1.g10050.t1</td><td>ref|XP_002867040.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297312876|gb|EFH43299.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]</td><td>652</td><td>669</td><td>0</td><td>102.6</td><td>89.3</td><td>94.9</td><td>armadillo/beta-catenin repeat family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G36030.1 | Symbols: ARO3 | armadillo repeat only 3 | chr4:17045084-17047096 REVERSE LENGTH=670</td><td>652</td><td>670</td><td>0</td><td>102.8</td><td>89.3</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00269.1.g10051.t1</td><td>ref|NP_195326.1| cellular nucleic acid-binding protein [Arabidopsis thaliana] gi|75318587|sp|O65639.1|CSP1_ARATH RecName: Full=Cold shock protein 1; Short=AtCSP1; AltName: Full=Cold shock domain-containing protein 1 gi|3036806|emb|CAA18496.1| glycine-rich protein [Arabidopsis thaliana] gi|7270554|emb|CAB81511.1| glycine-rich protein [Arabidopsis thaliana] gi|110741941|dbj|BAE98911.1| glycine-rich protein [Arabidopsis thaliana] gi|332661203|gb|AEE86603.1| cold shock protein 1 [Arabidopsis thaliana]</td><td>265</td><td>299</td><td>3.00E-84</td><td>112.8</td><td>70.6</td><td>80.0</td><td>cellular nucleic acid-binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G36020.1 | Symbols: CSDP1 | cold shock domain protein 1 | chr4:17043443-17044342 REVERSE LENGTH=299</td><td>265</td><td>299</td><td>1.00E-86</td><td>112.8</td><td>70.6</td><td>80.0</td></tr>
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<tr><td>Rsa1.0_00269.1.g10053.t1</td><td>ref|NP_179371.1| Rac-like GTP-binding protein ARAC1 [Arabidopsis thaliana] gi|145328750|ref|NP_001077910.1| Rac-like GTP-binding protein ARAC1 [Arabidopsis thaliana] gi|2500190|sp|Q38902.1|RAC1_ARATH RecName: Full=Rac-like GTP-binding protein ARAC1; AltName: Full=GTPase protein ROP3; Flags: Precursor gi|7211191|gb|AAF40237.1|AF115466_1 Arac1 [Arabidopsis thaliana] gi|1292908|gb|AAC49851.1| GTP binding protein [Arabidopsis thaliana] gi|4097563|gb|AAD00113.1| ATGP2 [Arabidopsis thaliana] gi|20260294|gb|AAM13045.1| unknown protein [Arabidopsis thaliana] gi|23198370|gb|AAN15712.1| unknown protein [Arabidopsis thaliana] gi|330251595|gb|AEC06689.1| Rac-like GTP-binding protein ARAC1 [Arabidopsis thaliana] gi|330251596|gb|AEC06690.1| Rac-like GTP-binding protein ARAC1 [Arabidopsis thaliana]</td><td>197</td><td>197</td><td>1.00E-110</td><td>100.0</td><td>98.5</td><td>99.5</td><td>Rac-like GTP-binding protein ARAC1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17800.2 | Symbols: ARAC1, ATGP2, ATRAC1, ROP3, ATROP3 | Arabidopsis RAC-like 1 | chr2:7740313-7741942 FORWARD LENGTH=197</td><td>197</td><td>197</td><td>1.00E-112</td><td>100.0</td><td>98.5</td><td>99.5</td></tr>
<tr><td>Rsa1.0_00269.1.g10054.t1</td><td>ref|XP_002869049.1| hypothetical protein ARALYDRAFT_491042 [Arabidopsis lyrata subsp. lyrata] gi|297314885|gb|EFH45308.1| hypothetical protein ARALYDRAFT_491042 [Arabidopsis lyrata subsp. lyrata]</td><td>361</td><td>352</td><td>3.00E-84</td><td>97.5</td><td>66.5</td><td>74.2</td><td>hypothetical protein ARALYDRAFT_491042</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G35940.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G17787.1). | chr4:17021672-17023593 FORWARD LENGTH=395</td><td>361</td><td>395</td><td>2.00E-69</td><td>109.4</td><td>56.0</td><td>68.7</td></tr>
<tr><td>Rsa1.0_00269.1.g10055.t1</td><td>gb|EOA17076.1| hypothetical protein CARUB_v10005325mg [Capsella rubella]</td><td>297</td><td>306</td><td>1.00E-135</td><td>103.0</td><td>82.8</td><td>89.6</td><td>hypothetical protein CARUB_v10005325mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G35930.1 | Symbols: | F-box family protein | chr4:17019482-17020744 FORWARD LENGTH=321</td><td>297</td><td>321</td><td>1.00E-131</td><td>108.1</td><td>83.5</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00269.1.g10056.t1</td><td>ref|XP_004308303.1| PREDICTED: uncharacterized protein LOC101292460 [Fragaria vesca subsp. vesca]</td><td>713</td><td>689</td><td>0</td><td>96.6</td><td>70.1</td><td>80.9</td><td>PREDICTED: uncharacterized protein LOC101292460</td><td>gbpln</td><td>Fragaria vesca</td><td>AT3G17450.1 | Symbols: | hAT dimerisation domain-containing protein | chr3:5972793-5975684 REVERSE LENGTH=877</td><td>713</td><td>877</td><td>2.00E-43</td><td>123.0</td><td>17.3</td><td>30.4</td></tr>
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Rsa1.0_00269.1.g10057.t1	ref|NP_195317.2| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|30690528|ref|NP_849503.1| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|42570170|ref|NP_849504.2| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|75154155|sp|Q8L7E9.1|MCAC1_ARATH RecName: Full=Protein MID1-COMPLEMENTING ACTIVITY 1 gi|22530910|gb|AAM96959.1| putative protein [Arabidopsis thaliana] gi|28059788|gb|AAO30093.1| putative protein [Arabidopsis thaliana] gi|124484595|dbj|BAF46389.1| Mca1 [Arabidopsis thaliana] gi|222423156|dbj|BAH19557.1| AT4G35920 [Arabidopsis thaliana] gi|332661189|gb|AEE86589.1| protein MID1-complementing activity 1 [Arabidopsis thaliana] gi|332661190|gb|AEE86590.1| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|332661191|gb|AEE86591.1| PLAC8 domain-containing protein [Arabidopsis thaliana]	407	421	0	103.4	88.2	93.9	PLAC8 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G35920.2 | Symbols: MCA1 | PLAC8 family protein | chr4:17012106-17014192 REVERSE LENGTH=421	407	421	0	103.4	88.2	93.9
Rsa1.0_00269.1.g10058.t2	ref|XP_002867048.1| hypothetical protein ARALYDRAFT_491048 [Arabidopsis lyrata subsp. lyrata] gi|297312884|gb|EFH43307.1| hypothetical protein ARALYDRAFT_491048 [Arabidopsis lyrata subsp. lyrata]	99	77	1.00E-28	77.8	70.7	74.7	hypothetical protein ARALYDRAFT_491048	gbpln	Arabidopsis lyrata	AT4G35905.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF343 (InterPro:IPR005651); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17007284-17008067 REVERSE LENGTH=77	99	77	9.00E-31	77.8	69.7	73.7
Rsa1.0_00269.1.g10059.t1	ref|XP_002869051.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314887|gb|EFH45310.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	259	282	5.00E-90	108.9	77.2	84.6	predicted protein	gbpln	Arabidopsis lyrata	AT4G35900.1 | Symbols: FD, FD-1, atbzip14 | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:17004746-17005952 FORWARD LENGTH=285	259	285	2.00E-87	110.0	75.3	83.4
Rsa1.0_00269.1.g10060.t1	# #	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00269.1.g10061.t1	ref|NP_567991.1| winged-helix DNA-binding transcription factor family protein [Arabidopsis thaliana] gi|13877889|gb|AAK44022.1|AF370207_1 unknown protein [Arabidopsis thaliana] gi|22136918|gb|AAM91803.1| unknown protein [Arabidopsis thaliana] gi|332661185|gb|AEE86585.1| winged-helix DNA-binding transcription factor family protein [Arabidopsis thaliana]	483	523	1.00E-142	108.3	68.1	77.6	winged-helix DNA-binding transcription factor family protein	gbpln	Arabidopsis thaliana	AT4G35890.1 | Symbols: | winged-helix DNA-binding transcription factor family protein | chr4:16997433-17000410 FORWARD LENGTH=523	483	523	1.00E-145	108.3	68.1	77.6
Rsa1.0_00269.1.g10062.t1	gb|EOA17424.1| hypothetical protein CARUB_v10005728mg [Capsella rubella]	211	211	1.00E-120	100.0	99.1	99.5	hypothetical protein CARUB_v10005728mg	gbpln	Capsella rubella	AT4G35860.1 | Symbols: ATRABB1B, ATGB2, ATRAB2C, GB2 | GTP-binding 2 | chr4:16987118-16988839 REVERSE LENGTH=211	211	211	1.00E-121	100.0	97.2	99.1
Rsa1.0_00269.1.g10063.t1	ref|XP_002869057.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297314893|gb|EFH45316.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	236	236	1.00E-118	100.0	89.8	93.6	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G35840.1 | Symbols: | RING/U-box superfamily protein | chr4:16981083-16982266 FORWARD LENGTH=236	236	236	1.00E-120	100.0	88.6	93.6
Rsa1.0_00269.1.g10064.t1	# #	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00269.1.g10065.t1	dbj|BAJ34379.1| unnamed protein product [Thellungiella halophila]	862	860	0	99.8	88.4	93.6	unnamed protein product	----	----	AT4G35790.2 | Symbols: ATPLDDELTA, PLDDELTA | phospholipase D delta | chr4:16955774-16959875 REVERSE LENGTH=857	862	857	0	99.4	84.8	92.1
Rsa1.0_00269.1.g10066.t1	dbj|BAJ34379.1| unnamed protein product [Thellungiella halophila]	124	860	3.00E-28	693.5	48.4	53.2	unnamed protein product	----	----	AT4G35790.2 | Symbols: ATPLDDELTA, PLDDELTA | phospholipase D delta | chr4:16955774-16959875 REVERSE LENGTH=857	124	857	5.00E-29	691.1	45.2	50.0

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<tr><td>Rsa1.0_00270.1.g10067.t1</td><td>gb|AAF65512.1| ADP-ribosylation factor [Capsicum annuum] gi|37791223|gb|AAR03592.1| ARF-like small GTPase [Brassica juncea] gi|482560625|gb|EOA24816.1| hypothetical protein CARUB_v10018102mg [Capsella rubella] gi|482564310|gb|EOA28500.1| hypothetical protein CARUB_v10024713mg [Capsella rubella]</td><td>181</td><td>181</td><td>1.00E-102</td><td>100.0</td><td>100.0</td><td>100.0</td><td>ADP-ribosylation factor</td><td>gbpln</td><td>Brassica juncea</td><td>AT3G62290.3 | Symbols: ARFA1E | ADP-ribosylation factor A1E | chr3:23052287-23053545 FORWARD LENGTH=181</td><td>181</td><td>181</td><td>1.00E-104</td><td>100.0</td><td>99.4</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00270.1.g10068.t1</td><td>gb|EOA23568.1| hypothetical protein CARUB_v10016761mg [Capsella rubella]</td><td>731</td><td>703</td><td>0</td><td>96.2</td><td>90.4</td><td>92.1</td><td>hypothetical protein CARUB_v10016761mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G62270.1 | Symbols: | HCO3-transporter family | chr3:23042528-23045633 REVERSE LENGTH=703</td><td>731</td><td>703</td><td>0</td><td>96.2</td><td>89.9</td><td>92.3</td></tr>
<tr><td>Rsa1.0_00270.1.g10069.t4</td><td>ref|XP_002878445.1| hypothetical protein ARALYDRAFT_486731 [Arabidopsis lyrata subsp. lyrata] gi|297324283|gb|EFH54704.1| hypothetical protein ARALYDRAFT_486731 [Arabidopsis lyrata subsp. lyrata]</td><td>309</td><td>384</td><td>4.00E-65</td><td>124.3</td><td>42.4</td><td>47.9</td><td>hypothetical protein ARALYDRAFT_486731</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G62260.2 | Symbols: | Protein phosphatase 2C family protein | chr3:23038516-23040391 REVERSE LENGTH=384</td><td>309</td><td>384</td><td>6.00E-67</td><td>124.3</td><td>42.4</td><td>47.2</td></tr>
<tr><td>Rsa1.0_00270.1.g10070.t2</td><td>ref|XP_004151860.1| PREDICTED: SUMO-conjugating enzyme SCE1-like [Cucumis sativus]</td><td>174</td><td>160</td><td>6.00E-77</td><td>92.0</td><td>79.9</td><td>84.5</td><td>PREDICTED: SUMO-conjugating enzyme SCE1-like</td><td>gbpln</td><td>Cucumis sativus</td><td>AT3G57870.1 | Symbols: AHUS5, EMB1637, SCE1, SCE1A, ATSCE1 | sumo conjugation enzyme 1 | chr3:21428831-21430110 REVERSE LENGTH=160</td><td>174</td><td>160</td><td>2.00E-75</td><td>92.0</td><td>75.9</td><td>82.2</td></tr>
<tr><td>Rsa1.0_00270.1.g10071.t1</td><td>ref|NP_191784.1| ubiquitin-40S ribosomal protein S27a-3 [Arabidopsis thaliana] gi|302393706|sp|P59233.2|R27AC_ARATH RecName: Full=Ubiquitin-40S ribosomal protein S27a-3; Contains: RecName: Full=Ubiquitin; Contains: RecName: Full=40S ribosomal protein S27a-3; Flags: Precursor gi|166934|gb|AAA32906.1| ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] gi|6899935|emb|CAB71885.1| ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] gi|15529190|gb|AAK97689.1| AT3g62250/T17J13_210 [Arabidopsis thaliana] gi|21537196|gb|AAM61537.1| ubiquitin extension protein UBQ5 [Arabidopsis thaliana] gi|22655050|gb|AAM98116.1| At3g62250/T17J13_210 [Arabidopsis thaliana] gi|110742096|dbj|BAE98979.1| ubiquitin extension protein [Arabidopsis thaliana] gi|332646806|gb|AEE80327.1| ubiquitin-40S ribosomal protein S27a-3 [Arabidopsis thaliana]</td><td>157</td><td>157</td><td>1.00E-85</td><td>100.0</td><td>98.7</td><td>99.4</td><td>ubiquitin-40S ribosomal protein S27a-3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G62250.1 | Symbols: UBQ5 | ubiquitin 5 | chr3:23037138-23037611 FORWARD LENGTH=157</td><td>157</td><td>157</td><td>3.00E-88</td><td>100.0</td><td>98.7</td><td>99.4</td></tr>
<tr><td>Rsa1.0_00270.1.g10072.t1</td><td>gb|EOA28377.1| hypothetical protein CARUB_v10024582mg [Capsella rubella]</td><td>462</td><td>464</td><td>1.00E-141</td><td>100.4</td><td>56.1</td><td>71.6</td><td>hypothetical protein CARUB_v10024582mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G62230.1 | Symbols: | F-box family protein | chr3:23031589-23032974 FORWARD LENGTH=461</td><td>462</td><td>461</td><td>1.00E-114</td><td>99.8</td><td>45.9</td><td>64.1</td></tr>
<tr><td>Rsa1.0_00270.1.g10073.t1</td><td>gb|EOA24104.1| hypothetical protein CARUB_v10017335mg, partial [Capsella rubella]</td><td>349</td><td>417</td><td>1.00E-162</td><td>119.5</td><td>82.5</td><td>89.7</td><td>hypothetical protein CARUB_v10017335mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G62220.1 | Symbols: | Protein kinase superfamily protein | chr3:23029276-23030864 REVERSE LENGTH=361</td><td>349</td><td>361</td><td>1.00E-162</td><td>103.4</td><td>81.7</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00270.1.g10074.t1</td><td>ref|NP_191777.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|6899928|emb|CAB71878.1| putative protein [Arabidopsis thaliana] gi|124301092|gb|ABN04798.1| At3g62180 [Arabidopsis thaliana] gi|332646798|gb|AEE80319.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]</td><td>215</td><td>215</td><td>5.00E-94</td><td>100.0</td><td>80.0</td><td>87.9</td><td>plant invertase/pectin methylesterase inhibitor domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G62180.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:23019832-23020479 REVERSE LENGTH=215</td><td>215</td><td>215</td><td>2.00E-96</td><td>100.0</td><td>80.0</td><td>87.9</td></tr>
</table>

Rsa1.0_00270.1.g10075.t1	sp|P41510.1|PME_BRANA RecName: Full=Probable pectinesterase/pectinesterase inhibitor; Includes: RecName: Full=Pectinesterase inhibitor; AltName: Full=Pectin methylesterase inhibitor; Includes: RecName: Full=Pectinesterase; Short=PE; AltName: Full=Pectin methylesterase; Flags: Precursor gi|17784|emb|CAA39658.1| Bp19 [Brassica napus]	575	584	0	101.6	83.1	92.2	RecName: Full=Probable pectinesterase/pectinesterase inhibitor; Includes: RecName: Full=Pectinesterase inhibitor; AltName: Full=Pectin methylesterase inhibitor; Includes: RecName: Full=Pectinesterase; Short=PE; AltName: Full=Pectin methylesterase; Flags: Precursor gi|17784|emb|CAA39658.1| Bp19	gbpln	Brassica napus	AT3G62170.1 | Symbols: VGDH2 | VANGUARD 1 homolog 2 | chr3:23016495-23018337 REVERSE LENGTH=588	575	588	0	102.3	83.7	91.7
Rsa1.0_00270.1.g10076.t1	gb|EOA23181.1| hypothetical protein CARUB_v10018117mg [Capsella rubella]	172	174	5.00E-78	101.2	92.4	95.9	hypothetical protein CARUB_v10018117mg	gbpln	Capsella rubella	AT3G62100.1 | Symbols: IAA30 | indole-3-acetic acid inducible 30 | chr3:22995835-22996593 FORWARD LENGTH=172	172	172	2.00E-75	100.0	89.5	95.3
Rsa1.0_00270.1.g10077.t1	ref|NP_191765.2| Pectinacetylesterase family protein [Arabidopsis thaliana] gi|28392968|gb|AAO41919.1| putative pectinacetylesterase [Arabidopsis thaliana] gi|28827554|gb|AAO50621.1| putative pectinacetylesterase [Arabidopsis thaliana] gi|332646781|gb|AEE80302.1| Pectinacetylesterase family protein [Arabidopsis thaliana]	416	419	0	100.7	88.9	93.3	Pectinacetylesterase family protein	gbpln	Arabidopsis thaliana	AT3G62060.1 | Symbols: | Pectinacetylesterase family protein | chr3:22980123-22982734 FORWARD LENGTH=419	416	419	0	100.7	88.9	93.3
Rsa1.0_00270.1.g10078.t1	gb|EOA23175.1| hypothetical protein CARUB_v10017856mg [Capsella rubella]	260	262	1.00E-127	100.8	87.3	92.7	hypothetical protein CARUB_v10017856mg	gbpln	Capsella rubella	AT3G62030.1 | Symbols: ROC4 | rotamase CYP 4 | chr3:22973708-22975139 FORWARD LENGTH=260	260	260	1.00E-127	100.0	86.5	92.7
Rsa1.0_00270.1.g10079.t1	gb|EOA24918.1| hypothetical protein CARUB_v10018209mg [Capsella rubella]	109	141	7.00E-28	129.4	51.4	63.3	hypothetical protein CARUB_v10018209mg	gbpln	Capsella rubella	AT3G62050.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:22978305-22978944 FORWARD LENGTH=157	109	157	5.00E-30	144.0	52.3	63.3
Rsa1.0_00270.1.g10080.t1	gb|EOA25822.1| hypothetical protein CARUB_v10019191mg [Capsella rubella]	89	118	3.00E-27	132.6	71.9	75.3	hypothetical protein CARUB_v10019191mg	gbpln	Capsella rubella	AT3G61980.1 | Symbols: | serine protease inhibitor, Kazal-type family protein | chr3:22956344-22956697 REVERSE LENGTH=117	89	117	3.00E-28	131.5	65.2	70.8
Rsa1.0_00270.1.g10081.t1	ref|XP_002878424.1| serine protease inhibitor, Kazal-type family protein [Arabidopsis lyrata subsp. lyrata] gi|297324262|gb|EFH54683.1| serine protease inhibitor, Kazal-type family protein [Arabidopsis lyrata subsp. lyrata]	95	117	9.00E-22	123.2	58.9	70.5	serine protease inhibitor, Kazal-type family protein	gbpln	Arabidopsis lyrata	AT3G61980.1 | Symbols: | serine protease inhibitor, Kazal-type family protein | chr3:22956344-22956697 REVERSE LENGTH=117	95	117	4.00E-22	123.2	54.7	68.4
Rsa1.0_00270.1.g10082.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00270.1.g10083.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	461	1225	1.00E-90	265.7	39.7	52.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	461	575	1.00E-54	124.7	29.3	45.6
Rsa1.0_00270.1.g10084.t1	ref|NP_191756.1| B3 domain-containing transcription factor NGA2 [Arabidopsis thaliana] gi|75182616|sp|Q9M268.1|NGA2_ARATH RecName: Full=B3 domain-containing transcription factor NGA2; AltName: Full=Protein NGATHA 2 gi|6899895|emb|CAB71904.1| RAV-like protein [Arabidopsis thaliana] gi|108385265|gb|ABF85768.1| At3g61970 [Arabidopsis thaliana] gi|227060687|gb|ACP18972.1| NGATHA2 [Arabidopsis thaliana] gi|332646767|gb|AEE80288.1| B3 domain-containing transcription factor NGA2 [Arabidopsis thaliana]	318	299	1.00E-127	94.0	77.7	84.9	B3 domain-containing transcription factor NGA2	gbpln	Arabidopsis thaliana	AT3G61970.1 | Symbols: NGA2 | AP2/B3-like transcriptional factor family protein | chr3:22951829-22952728 FORWARD LENGTH=299	318	299	1.00E-129	94.0	77.7	84.9
Rsa1.0_00270.1.g10085.t1	gb|EOA25299.1| hypothetical protein CARUB_v10018614mg [Capsella rubella]	319	360	1.00E-109	112.9	73.4	81.8	hypothetical protein CARUB_v10018614mg	gbpln	Capsella rubella	AT3G61950.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:22939661-22941332 FORWARD LENGTH=358	319	358	1.00E-106	112.2	72.4	82.1
Rsa1.0_00271.1.g10086.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00271.1.g10087.t1	gb|EOA13117.1| hypothetical protein CARUB_v10026139mg [Capsella rubella]	572	586	0	102.4	90.4	94.6	hypothetical protein CARUB_v10026139mg	gbpln	Capsella rubella	AT5G47750.1 | Symbols: D6PKL2, PK5 | D6 protein kinase like 2 | chr5:19339947-19341864 REVERSE LENGTH=586	572	586	0	102.4	90.9	94.8

Rsa1.0_00271.1.g10088.t1	ref|XP_002865104.1| hypothetical protein ARALYDRAFT_494188 [Arabidopsis lyrata subsp. lyrata] gi|297310939|gb|EFH41363.1| hypothetical protein ARALYDRAFT_494188 [Arabidopsis lyrata subsp. lyrata]	247	242	4.00E-80	98.0	69.2	81.4	hypothetical protein ARALYDRAFT_494188	gbpln	Arabidopsis lyrata	AT5G47740.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr5:19338688-19339683 FORWARD LENGTH=244	247	244	2.00E-80	98.8	63.6	76.5
Rsa1.0_00271.1.g10089.t2	gb|EOA13661.1| hypothetical protein CARUB_v10026730mg [Capsella rubella]	327	341	1.00E-171	104.3	88.4	93.3	hypothetical protein CARUB_v10026730mg	gbpln	Capsella rubella	AT5G47730.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr5:19334592-19336618 REVERSE LENGTH=341	327	341	1.00E-168	104.3	89.0	93.6
Rsa1.0_00271.1.g10090.t1	gb|ABD64985.1| C2 domain containing protein [Brassica oleracea]	165	168	1.00E-84	101.8	96.4	97.6	C2 domain containing protein	gbpln	Brassica oleracea	AT5G47710.2 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr5:19330470-19331178 FORWARD LENGTH=166	165	166	9.00E-86	100.6	92.1	97.6
Rsa1.0_00271.1.g10091.t1	gb|EOA40410.1| hypothetical protein CARUB_v10009137mg [Capsella rubella]	447	445	1.00E-153	99.6	68.2	77.2	hypothetical protein CARUB_v10009137mg	gbpln	Capsella rubella	AT1G01690.1 | Symbols: ATPRD3, PRD3 | putative recombination initiation defects 3 | chr1:249242-252221 FORWARD LENGTH=449	447	449	1.00E-132	100.4	60.9	69.4
Rsa1.0_00271.1.g10092.t1	gb|ABD64989.1| hypothetical protein 26.t00005 [Brassica oleracea]	1649	1681	0	101.9	80.5	88.3	hypothetical protein 26.t00005	gbpln	Brassica oleracea	AT5G47690.3 | Symbols: | binding | chr5:19317899-19327014 FORWARD LENGTH=1607	1649	1607	0	97.5	78.7	85.0
Rsa1.0_00271.1.g10093.t1	ref|NP_568687.1| nudix hydrolase 2 [Arabidopsis thaliana] gi|68565924|sp|Q94B74.1|NUDT2_ARATH RecName: Full=Nudix hydrolase 2; Short=AtNUDT2; AltName: Full=ADP-ribose pyrophosphatase; AltName: Full=NADH pyrophosphatase gi|14596037|gb|AAK68746.1| MutT domain protein-like [Arabidopsis thaliana] gi|17978727|gb|AAL47357.1| MutT domain protein-like [Arabidopsis thaliana] gi|332008163|gb|AED95546.1| nudix hydrolase 2 [Arabidopsis thaliana]	333	278	1.00E-124	83.5	64.6	69.7	nudix hydrolase 2	gbpln	Arabidopsis thaliana	AT5G47650.1 | Symbols: ATNUDT2, ATNUDX2, NUDT2 | nudix hydrolase homolog 2 | chr5:19310391-19312084 REVERSE LENGTH=278	333	278	1.00E-127	83.5	64.6	69.7
Rsa1.0_00271.1.g10094.t1	gb|ABD64968.1| hypothetical protein 25.t00005 [Brassica oleracea]	251	299	1.00E-106	119.1	82.1	88.0	hypothetical protein 25.t00005	gbpln	Brassica oleracea	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	251	264	5.00E-88	105.2	64.5	78.1
Rsa1.0_00271.1.g10095.t1	gb|ABD64967.1| hypothetical protein 25.t00004 [Brassica oleracea]	149	149	2.00E-66	100.0	84.6	91.3	hypothetical protein 25.t00004	gbpln	Brassica oleracea	AT5G47600.1 | Symbols: | HSP20-like chaperones superfamily protein | chr5:19299945-19300456 REVERSE LENGTH=131	149	131	3.00E-41	87.9	53.7	64.4
Rsa1.0_00271.1.g10096.t20	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	1379	1164	1.00E-161	84.4	24.3	36.3	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT5G47635.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:19307281-19307849 REVERSE LENGTH=164	1379	164	2.00E-66	11.9	9.2	10.2
Rsa1.0_00271.1.g10097.t1	gb|ABD64960.1| zinc finger, C3HC4 type (RING finger) containing protein [Brassica oleracea]	176	218	2.00E-75	123.9	78.4	81.3	zinc finger, C3HC4 type (RING finger) containing protein	gbpln	Brassica oleracea	AT5G47610.1 | Symbols: | RING/U-box superfamily protein | chr5:19301399-19301899 REVERSE LENGTH=166	176	166	1.00E-67	94.3	70.5	77.8
Rsa1.0_00271.1.g10098.t1	gb|ABD64966.1| hypothetical protein 25.t00003 [Brassica oleracea]	259	259	1.00E-135	100.0	91.9	96.9	hypothetical protein 25.t00003	gbpln	Brassica oleracea	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	259	264	7.00E-89	101.9	64.5	76.1
Rsa1.0_00271.1.g10099.t1	gb|ABD64967.1| hypothetical protein 25.t00004 [Brassica oleracea]	150	149	4.00E-70	99.3	87.3	94.7	hypothetical protein 25.t00004	gbpln	Brassica oleracea	AT5G47600.1 | Symbols: | HSP20-like chaperones superfamily protein | chr5:19299945-19300456 REVERSE LENGTH=131	150	131	3.00E-43	87.3	50.7	63.3
Rsa1.0_00271.1.g10100.t1	gb|ABD64967.1| hypothetical protein 25.t00004 [Brassica oleracea]	150	149	2.00E-50	99.3	64.0	68.7	hypothetical protein 25.t00004	gbpln	Brassica oleracea	AT5G47600.1 | Symbols: | HSP20-like chaperones superfamily protein | chr5:19299945-19300456 REVERSE LENGTH=131	150	131	1.00E-30	87.3	41.3	50.0
Rsa1.0_00271.1.g10101.t1	gb|ABD64968.1| hypothetical protein 25.t00005 [Brassica oleracea]	266	299	1.00E-111	112.4	84.6	88.7	hypothetical protein 25.t00005	gbpln	Brassica oleracea	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	266	264	3.00E-86	99.2	59.8	71.4
Rsa1.0_00271.1.g10102.t1	gb|ABD64969.1| hypothetical protein 25.t00006 [Brassica oleracea]	197	134	4.00E-56	68.0	54.8	56.3	hypothetical protein 25.t00006	gbpln	Brassica oleracea	AT5G47570.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19292869-19294666 REVERSE LENGTH=125	197	125	9.00E-47	63.5	51.8	52.8
Rsa1.0_00271.1.g10103.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00271.1.g10104.t1	ref|XP_002863336.1| ATSDAT [Arabidopsis lyrata subsp. lyrata] gi|297309171|gb|EFH39595.1| ATSDAT [Arabidopsis lyrata subsp. lyrata]	541	540	0	99.8	90.2	94.6	ATSDAT	gbpln	Arabidopsis lyrata	AT5G47560.1 | Symbols: ATTDT, ATSDAT, TDT | tonoplast dicarboxylate transporter | chr5:19287895-19290347 REVERSE LENGTH=540	541	540	0	99.8	89.3	94.3

Rsa1.0_00271.1.g10105.t1	gb|ADD10748.1| phytocystatin 5 [Brassica rapa subsp. pekinensis]	121	120	1.00E−44	99.2	82.6	90.1	phytocystatin 5	gbpln	Brassica rapa	AT5G47550.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:19286596-19286964 REVERSE LENGTH=122	121	122	1.00E−35	100.8	58.7	70.2
Rsa1.0_00271.1.g10106.t1	gb|ABD64974.1| MO25 protein −related [Brassica oleracea]	340	340	0	100.0	98.8	99.4	MO25 protein −related	gbpln	Brassica oleracea	AT5G47540.1 | Symbols: | Mo25 family protein | chr5:19283265-19285328 REVERSE LENGTH=343	340	343	0	100.9	95.6	98.2
Rsa1.0_00271.1.g10107.t1	gb|ABD64975.1| Ras family GTP−binding protein [Brassica oleracea]	222	221	1.00E−123	99.5	97.3	98.6	Ras family GTP−binding protein	gbpln	Brassica oleracea	AT5G47520.1 | Symbols: AtRABA5a, RABA5a | RAB GTPase homolog A5A | chr5:19277596-19278366 REVERSE LENGTH=221	222	221	1.00E−121	99.5	94.1	97.7
Rsa1.0_00272.1.g10108.t1	dbj|BAA83905.1| SRK13 [Brassica oleracea]	878	854	1.00E−178	97.3	42.0	57.3	SRK13	gbpln	Brassica oleracea	AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850	878	850	1.00E−174	96.8	41.2	56.3
Rsa1.0_00272.1.g10109.t1	gb|AFJ66186.1| hypothetical protein 11M19.5 [Arabidopsis halleri]	268	1557	3.00E−70	581.0	54.1	66.8	hypothetical protein 11M19.5	gbpln	Arabidopsis halleri	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10110.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10111.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10112.t1	gb|AAG52024.1|AC022456_5 Tam1 transposon protein TNP2, putative; 12762−16371 [Arabidopsis thaliana]	316	887	5.00E−28	280.7	21.2	25.9	Tam1 transposon protein TNP2, putative; 12762−16371	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10113.t5	gb|AAC69114.1| putative gag−protease polyprotein [Arabidopsis thaliana]	584	627	6.00E−17	107.4	15.4	24.3	putative gag−protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10114.t1	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	1755	1274	0	72.6	29.6	41.0	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1755	575	7.00E−46	32.8	8.0	13.3
Rsa1.0_00272.1.g10115.t3	ref|XP_002893979.1| CYCA1_1 [Arabidopsis lyrata subsp. lyrata] gi|297339821|gb|EFH70238.1| CYCA1_1 [Arabidopsis lyrata subsp. lyrata]	437	467	0	106.9	83.1	88.6	CYCA1_1	gbpln	Arabidopsis lyrata	AT1G44110.1 | Symbols: CYCA1;1 | Cyclin A1;1 | chr1:16775035-16777182 REVERSE LENGTH=460	437	460	0	105.3	80.8	86.7
Rsa1.0_00272.1.g10116.t2	ref|XP_002888606.1| ALDH3H1 [Arabidopsis lyrata subsp. lyrata] gi|297334447|gb|EFH64865.1| ALDH3H1 [Arabidopsis lyrata subsp. lyrata]	505	484	0	95.8	84.6	91.5	ALDH3H1	gbpln	Arabidopsis lyrata	AT1G44170.2 | Symbols: ALDH3H1, ALDH4 | aldehyde dehydrogenase 3H1 | chr1:16796564-16800031 REVERSE LENGTH=484	505	484	0	95.8	84.2	91.9
Rsa1.0_00272.1.g10117.t1	gb|EOA38139.1| hypothetical protein CARUB_v10009610mg [Capsella rubella]	301	347	7.00E−31	115.3	18.9	24.9	hypothetical protein CARUB_v10009610mg	gbpln	Capsella rubella	AT1G44191.1 | Symbols: | ECA1 gametogenesis related family protein | chr1:16813654-16814733 REVERSE LENGTH=359	301	359	1.00E−18	119.3	14.0	17.6
Rsa1.0_00272.1.g10118.t1	ref|NP_175092.1| photosystem II 22 kDa protein [Arabidopsis thaliana] gi|17380270|sp|Q9XF91.1|PSBS_ARATH RecName: Full=Photosystem II 22 kDa protein, chloroplastic; AltName: Full=CP22; Flags: Precursor gi|4741962|gb|AAD28778.1|AF134131_1 PsbS protein [Arabidopsis thaliana] gi|13876505|gb|AAK43481.1|AC084807_6 photosystem II 22kDa protein, putative [Arabidopsis thaliana] gi|62320751|dbj|BAD95419.1| Photosystem II chlorophyll−binding protein PsbS [Arabidopsis thaliana] gi|332193918|gb|AEE32039.1| photosystem II 22 kDa protein [Arabidopsis thaliana]	265	265	1.00E−122	100.0	95.1	96.6	photosystem II 22 kDa protein	gbpln	Arabidopsis thaliana	AT1G44575.1 | Symbols: NPQ4, PSBS | Chlorophyll A−B binding family protein | chr1:16871768-16873194 FORWARD LENGTH=265	265	265	1.00E−125	100.0	95.1	96.6
Rsa1.0_00272.1.g10119.t1	gb|EOA38028.1| hypothetical protein CARUB_v10009499mg [Capsella rubella]	359	369	1.00E−176	102.8	90.0	95.0	hypothetical protein CARUB_v10009499mg	gbpln	Capsella rubella	AT1G44750.2 | Symbols: ATPUP11, PUP11 | purine permease 11 | chr1:16893825-16895168 FORWARD LENGTH=367	359	367	1.00E−171	102.2	90.0	95.3
Rsa1.0_00272.1.g10120.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838−20266 [Arabidopsis thaliana]	465	1142	1.00E−122	245.6	50.1	64.9	reverse transcriptase, putative; 16838−20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	465	575	3.00E−57	123.7	32.3	53.3
Rsa1.0_00272.1.g10121.t1	ref|XP_004153378.1| PREDICTED: uncharacterized protein LOC101218423 [Cucumis sativus]	386	207	2.00E−13	53.6	10.6	15.8	PREDICTED: uncharacterized protein LOC101218423	gbpln	Cucumis sativus	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10122.t1	gb|AAG51228.1|AC035249_3 Tam3−like transposon protein; 93317−95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT−element transposase, putative [Arabidopsis thaliana]	723	723	0	100.0	56.0	71.8	Tam3−like transposon protein; 93317−95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	723	696	3.00E−54	96.3	24.1	41.9

Rsa1.0_00272.1.g10123.t1	ref|NP_175105.2| YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein [Arabidopsis thaliana] gi|26451543|dbj|BAC42869.1| unknown protein [Arabidopsis thaliana] gi|28973135|gb|AAO63892.1| unknown protein [Arabidopsis thaliana] gi|332193936|gb|AEE32057.1| YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein [Arabidopsis thaliana]	311	307	1.00E-144	98.7	83.9	89.7	YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein	gbpln	Arabidopsis thaliana	AT1G44835.1 | Symbols: | YbaK/aminoacyl-tRNA synthetase-associated domain | chr1:16939909-16942337 FORWARD LENGTH=307	311	307	2.33E-156	98.7	83.9	89.7
Rsa1.0_00272.1.g10124.t1	ref|XP_002891303.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297337145|gb|EFH67562.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	165	935	8.00E-51	566.7	72.1	84.2	ATP binding protein	gbpln	Arabidopsis lyrata	AT1G44900.1 | Symbols: MCM2, ATMCM2 | minichromosome maintenance (MCM2/3/5) family protein | chr1:16970291-16974457 FORWARD LENGTH=936	165	936	6.00E-53	567.3	72.7	84.8
Rsa1.0_00272.1.g10125.t4	ref|XP_002888245.1| hypothetical protein ARALYDRAFT_475439 [Arabidopsis lyrata subsp. lyrata] gi|297334086|gb|EFH64504.1| hypothetical protein ARALYDRAFT_475439 [Arabidopsis lyrata subsp. lyrata]	2158	2607	0	120.8	70.3	79.9	hypothetical protein ARALYDRAFT_475439	gbpln	Arabidopsis lyrata	AT1G58250.1 | Symbols: SAB | Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain | chr1:21587317-21601373 REVERSE LENGTH=2607	2158	2607	0	120.8	69.6	79.6
Rsa1.0_00272.1.g10126.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10127.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10128.t1	gb|EOA39875.1| hypothetical protein CARUB_v10008552mg [Capsella rubella]	649	642	0	98.9	91.8	95.8	hypothetical protein CARUB_v10008552mg	gbpln	Capsella rubella	AT1G45150.1 | Symbols: | unknown protein; Has 219 Blast hits to 202 proteins in 78 species: Archae - 0; Bacteria - 166; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr1:17077615-17082330 REVERSE LENGTH=643	649	643	0	99.1	90.6	94.8
Rsa1.0_00272.1.g10129.t1	ref|XP_002871511.1| hypothetical protein ARALYDRAFT_350399 [Arabidopsis lyrata subsp. lyrata] gi|297317348|gb|EFH47770.1| hypothetical protein ARALYDRAFT_350399 [Arabidopsis lyrata subsp. lyrata]	353	1202	3.00E-96	340.5	51.8	69.4	hypothetical protein ARALYDRAFT_350399	gbpln	Arabidopsis lyrata	AT5G12090.1 | Symbols: | Protein kinase superfamily protein | chr5:3909703-3910877 FORWARD LENGTH=369	353	369	7.00E-85	104.5	47.0	60.1
Rsa1.0_00272.1.g10130.t1	gb|EOA39275.1| hypothetical protein CARUB_v10012282mg [Capsella rubella]	1014	1060	0	104.5	83.4	88.9	hypothetical protein CARUB_v10012282mg	gbpln	Capsella rubella	AT1G45160.2 | Symbols: | Protein kinase superfamily protein | chr1:17083814-17090277 REVERSE LENGTH=1067	1014	1067	0	105.2	82.8	89.5
Rsa1.0_00272.1.g10131.t1	gb|EOA39964.1| hypothetical protein CARUB_v10008653mg, partial [Capsella rubella]	519	593	0	114.3	79.4	86.3	hypothetical protein CARUB_v10008653mg, partial	gbpln	Capsella rubella	AT1G45207.2 | Symbols: | Remorin family protein | chr1:17130703-17133548 REVERSE LENGTH=555	519	555	0	106.9	79.0	85.7
Rsa1.0_00272.1.g10132.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00272.1.g10133.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	1370	1486	0	108.5	23.2	28.3	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1370	1262	1.00E-118	92.1	15.0	22.2
Rsa1.0_00273.1.g10134.t1	emb|CAA07573.1| src2-like protein [Arabidopsis thaliana]	305	324	1.00E-104	106.2	70.5	74.8	src2-like protein	gbpln	Arabidopsis thaliana	AT1G09070.1 | Symbols: SRC2, (AT)SRC2 | soybean gene regulated by cold-2 | chr1:2927767-2928741 FORWARD LENGTH=324	305	324	1.00E-106	106.2	70.2	74.4
Rsa1.0_00273.1.g10135.t2	ref|NP_001184945.1| ATP-dependent Clp protease proteolytic subunit-related protein 3 [Arabidopsis thaliana] gi|332190278|gb|AEE28399.1| ATP-dependent Clp protease proteolytic subunit-related protein 3 [Arabidopsis thaliana]	321	370	1.00E-169	115.3	92.2	95.3	ATP-dependent Clp protease proteolytic subunit-related protein 3	gbpln	Arabidopsis thaliana	AT1G09130.3 | Symbols: | ATP-dependent caseinolytic (Clp) protease/crotonase family protein | chr1:2939731-2942217 REVERSE LENGTH=370	321	370	1.00E-172	115.3	92.2	95.3
Rsa1.0_00273.1.g10136.t1	ref|NP_563837.1| F-box protein PP2-B15 [Arabidopsis thaliana] gi|334302842|sp|O80494.2|P2B15_ARATH RecName: Full=F-box protein PP2-B15; AltName: Full=Protein PHLOEM PROTEIN 2-LIKE B15; Short=AtPP2-B15 gi|332190282|gb|AEE28403.1| F-box protein PP2-B15 [Arabidopsis thaliana]	292	289	1.00E-123	99.0	76.4	83.6	F-box protein PP2-B15	gbpln	Arabidopsis thaliana	AT1G09155.1 | Symbols: AtPP2-B15, PP2-B15 | phloem protein 2-B15 | chr1:2949831-2950842 REVERSE LENGTH=289	292	289	1.00E-126	99.0	76.4	83.6
Rsa1.0_00273.1.g10137.t2	dbj|BAJ34364.1| unnamed protein product [Thellungiella halophila]	431	428	0	99.3	91.2	95.6	unnamed protein product	----	----	AT1G09160.1 | Symbols: | Protein phosphatase 2C family protein | chr1:2953199-2955059 REVERSE LENGTH=428	431	428	0	99.3	88.9	94.2
Rsa1.0_00273.1.g10138.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00273.1.g10139.t1	gb|EOA37562.1| hypothetical protein CARUB_v10011869mg [Capsella rubella]	550	545	0	99.1	79.5	87.3	hypothetical protein CARUB_v10011869mg	gbpln	Capsella rubella	AT1G09195.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; CONTAINS InterPro DOMAIN/s: Metal-dependent phosphohydrolase, HD subdomain (InterPro:IPR006674), Ppx/GppA phosphatase (InterPro:IPR003695). | chr1:2968137-2971457 REVERSE LENGTH=600	550	600	0	109.1	76.2	85.5
Rsa1.0_00273.1.g10140.t1	ref|XP_002894638.1| secretion-associated ras [Arabidopsis lyrata subsp. lyrata] gi|297340480|gb|EFH70897.1| secretion-associated ras [Arabidopsis lyrata subsp. lyrata]	226	210	1.00E-102	92.9	82.7	85.8	secretion-associated ras	gbpln	Arabidopsis lyrata	AT1G56330.1 | Symbols: SAR1, ATSAR1, ATSARA1B, ATSAR1B, SAR1B | secretion-associated RAS 1B | chr1:21086845-21088478 REVERSE LENGTH=193	226	193	1.00E-101	85.4	81.0	82.7
Rsa1.0_00273.1.g10141.t1	tpg|DAA55311.1| TPA: histone H3.2 [Zea mays]	136	245	1.00E-72	180.1	100.0	100.0	TPA: histone H3.2	gbenv/gbpln	Zea mays	AT5G65360.1 | Symbols: | Histone superfamily protein | chr5:26120099-26120509 REVERSE LENGTH=136	136	136	5.00E-74	100.0	100.0	100.0
Rsa1.0_00273.1.g10142.t5	gb|AAM63796.1| putative calcium-binding protein, calreticulin [Arabidopsis thaliana]	450	424	0	94.2	84.2	88.0	putative calcium-binding protein, calreticulin	gbpln	Arabidopsis thaliana	AT1G09210.1 | Symbols: CRT1b, AtCRT1b | calreticulin 1b | chr1:2973217-2976655 REVERSE LENGTH=424	450	424	0	94.2	84.0	87.8
Rsa1.0_00273.1.g10143.t1	gb|EOA37676.1| hypothetical protein CARUB_v10012313mg [Capsella rubella]	490	506	0	103.3	83.9	90.8	hypothetical protein CARUB_v10012313mg	gbpln	Capsella rubella	AT1G09220.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:2977952-2979466 REVERSE LENGTH=504	490	504	0	102.9	83.3	91.0
Rsa1.0_00273.1.g10144.t1	gb|ABO21639.1| importin alpha-like protein [Brassica napus] gi|126572504|gb|ABO21640.1| importin alpha-like protein [Brassica napus]	540	542	0	100.4	97.0	98.7	importin alpha-like protein	gbpln	Brassica napus	AT1G09270.2 | Symbols: IMPA-4 | importin alpha isoform 4 | chr1:2994506-2997833 FORWARD LENGTH=538	540	538	0	99.6	92.6	96.1
Rsa1.0_00273.1.g10145.t2	ref|XP_002892498.1| hypothetical protein ARALYDRAFT_471019 [Arabidopsis lyrata subsp. lyrata] gi|297338340|gb|EFH68757.1| hypothetical protein ARALYDRAFT_471019 [Arabidopsis lyrata subsp. lyrata]	488	348	1.00E-145	71.3	55.5	59.6	hypothetical protein ARALYDRAFT_471019	gbpln	Arabidopsis lyrata	AT1G09290.1 | Symbols: | unknown protein; Has 73 Blast hits to 71 proteins in 26 species: Archae - 0; Bacteria - 0; Metazoa - 5; Fungi - 11; Plants - 54; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr1:3001682-3003715 REVERSE LENGTH=348	488	348	1.00E-147	71.3	55.7	59.4
Rsa1.0_00273.1.g10146.t1	ref|XP_002889741.1| hypothetical protein ARALYDRAFT_471021 [Arabidopsis lyrata subsp. lyrata] gi|297335583|gb|EFH66000.1| hypothetical protein ARALYDRAFT_471021 [Arabidopsis lyrata subsp. lyrata]	478	480	0	100.4	89.7	95.2	hypothetical protein ARALYDRAFT_471021	gbpln	Arabidopsis lyrata	AT1G09300.1 | Symbols: | Metallopeptidase M24 family protein | chr1:3003981-3008131 FORWARD LENGTH=493	478	493	0	103.1	88.5	94.8
Rsa1.0_00273.1.g10147.t1	ref|NP_563841.1| uncharacterized protein [Arabidopsis thaliana] gi|13194796|gb|AAK15560.1|AF348589_1 unknown protein [Arabidopsis thaliana] gi|4337175|gb|AAD18096.1| ESTs gb|T20589, gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457, gb|T20921, gb|AA042762 and gb|AA720210 come from this gene [Arabidopsis thaliana] gi|15028183|gb|AAK76588.1| unknown protein [Arabidopsis thaliana] gi|19310813|gb|AAL85137.1| unknown protein [Arabidopsis thaliana] gi|21536763|gb|AAM61095.1| unknown [Arabidopsis thaliana] gi|332190307|gb|AEE28428.1| uncharacterized protein AT1G09310 [Arabidopsis thaliana]	168	179	5.00E-76	106.5	86.9	95.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G09310.1 | Symbols: | Protein of unknown function, DUF538 | chr1:3009109-3009648 FORWARD LENGTH=179	168	179	2.00E-78	106.5	86.9	95.2
Rsa1.0_00273.1.g10148.t1	gb|EOA39357.1| hypothetical protein CARUB_v10012409mg [Capsella rubella]	185	185	3.00E-94	100.0	94.6	96.2	hypothetical protein CARUB_v10012409mg	gbpln	Capsella rubella	AT1G09330.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF846, eukaryotic (InterPro:IPR008564); Has 518 Blast hits to 518 proteins in 206 species: Archae - 0; Bacteria - 0; Metazoa - 193; Fungi - 145; Plants - 73; Viruses - 0; Other Eukaryotes - 107 (source: NCBI BLink). | chr1:3013003-3014903 REVERSE LENGTH=186	185	186	3.00E-96	100.5	94.1	96.2

<table>
<tr><td>Rsa1.0_00273.1.g10149.t1</td><td>ref|XP_002889763.1| hypothetical protein ARALYDRAFT_888210 [Arabidopsis lyrata subsp. lyrata] gi|297335605|gb|EFH66022.1| hypothetical protein ARALYDRAFT_888210 [Arabidopsis lyrata subsp. lyrata]</td><td>218</td><td>105</td><td>4.00E-28</td><td>48.2</td><td>35.3</td><td>37.6</td><td>hypothetical protein ARALYDRAFT_888210</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G09645.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G57765.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:3123155-3124347 FORWARD LENGTH=106</td><td>218</td><td>106</td><td>2.00E-30</td><td>48.6</td><td>34.9</td><td>37.2</td></tr>
<tr><td>Rsa1.0_00273.1.g10150.t2</td><td>ref|XP_002892515.1| hypothetical protein ARALYDRAFT_471067 [Arabidopsis lyrata subsp. lyrata] gi|297338357|gb|EFH68774.1| hypothetical protein ARALYDRAFT_471067 [Arabidopsis lyrata subsp. lyrata]</td><td>317</td><td>298</td><td>1.00E-148</td><td>94.0</td><td>83.3</td><td>88.6</td><td>hypothetical protein ARALYDRAFT_471067</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G09660.1 | Symbols: | RNA-binding KH domain-containing protein | chr1:3128032-3130791 REVERSE LENGTH=298</td><td>317</td><td>298</td><td>1.00E-148</td><td>94.0</td><td>81.7</td><td>87.7</td></tr>
<tr><td>Rsa1.0_00273.1.g10151.t1</td><td>ref|XP_002889760.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata] gi|297335602|gb|EFH66019.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata]</td><td>164</td><td>164</td><td>1.00E-88</td><td>100.0</td><td>98.2</td><td>98.8</td><td>60S ribosomal protein L21</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G09690.1 | Symbols: | Translation protein SH3-like family protein | chr1:3136407-3137430 REVERSE LENGTH=164</td><td>164</td><td>164</td><td>2.00E-90</td><td>100.0</td><td>97.0</td><td>98.2</td></tr>
<tr><td>Rsa1.0_00273.1.g10152.t2</td><td>gb|AAT77417.1| dsRNA-binding protein LH2 [Brassica oleracea var. capitata]</td><td>295</td><td>278</td><td>1.00E-124</td><td>94.2</td><td>85.8</td><td>88.5</td><td>dsRNA-binding protein LH2</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G09700.1 | Symbols: HYL1, DRB1 | dsRNA-binding domain-like superfamily protein | chr1:3137960-3140118 REVERSE LENGTH=419</td><td>295</td><td>419</td><td>1.00E-111</td><td>142.0</td><td>74.2</td><td>82.0</td></tr>
<tr><td>Rsa1.0_00273.1.g10153.t1</td><td>ref|NP_001184951.1| putative ubiquitin-like-specific protease 2B [Arabidopsis thaliana] gi|357529069|sp|Q8L7S0.3|ULP2B_ARATH RecName: Full=Probable ubiquitin-like-specific protease 2B gi|215400502|gb|ACJ66287.1| EL5 SUMO protease [Arabidopsis thaliana] gi|332190365|gb|AEE28486.1| putative ubiquitin-like-specific protease 2B [Arabidopsis thaliana]</td><td>978</td><td>931</td><td>0</td><td>95.2</td><td>70.3</td><td>77.2</td><td>putative ubiquitin-like-specific protease 2B</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G09730.2 | Symbols: | Cysteine proteinases superfamily protein | chr1:3148017-3154236 REVERSE LENGTH=931</td><td>978</td><td>931</td><td>0</td><td>95.2</td><td>70.3</td><td>77.2</td></tr>
<tr><td>Rsa1.0_00273.1.g10154.t1</td><td>ref|NP_172445.2| adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana] gi|29028798|gb|AAO64778.1| At1g09740 [Arabidopsis thaliana] gi|110736422|dbj|BAF00178.1| putative ER6 protein [Arabidopsis thaliana] gi|332190366|gb|AEE28487.1| adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana]</td><td>154</td><td>171</td><td>7.00E-60</td><td>111.0</td><td>79.2</td><td>85.7</td><td>adenine nucleotide alpha hydrolases-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G09740.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr1:3154603-3155834 FORWARD LENGTH=171</td><td>154</td><td>171</td><td>2.00E-62</td><td>111.0</td><td>79.2</td><td>85.7</td></tr>
<tr><td>Rsa1.0_00273.1.g10155.t1</td><td>gb|EOA40162.1| hypothetical protein CARUB_v10008880mg [Capsella rubella]</td><td>452</td><td>513</td><td>0</td><td>113.5</td><td>81.4</td><td>88.5</td><td>hypothetical protein CARUB_v10008880mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G09750.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:3157541-3158960 FORWARD LENGTH=449</td><td>452</td><td>449</td><td>0</td><td>99.3</td><td>83.4</td><td>89.2</td></tr>
<tr><td>Rsa1.0_00273.1.g10156.t1</td><td>emb|CAA48890.1| U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana]</td><td>255</td><td>249</td><td>1.00E-123</td><td>97.6</td><td>86.7</td><td>94.1</td><td>U2 small nuclear ribonucleoprotein A'</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G09760.1 | Symbols: U2A' | U2 small nuclear ribonucleoprotein A | chr1:3159476-3161603 REVERSE LENGTH=249</td><td>255</td><td>249</td><td>1.00E-126</td><td>97.6</td><td>86.7</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00273.1.g10157.t1</td><td>ref|NP_172448.1| cell division cycle 5-like protein [Arabidopsis thaliana] gi|288561907|sp|P92948.2|CDC5L_ARATH RecName: Full=Cell division cycle 5-like protein; Short=Cdc5-like protein; AltName: Full=Atypical R2R3-MYB transcription factor CDC5; AltName: Full=MOS4-associated complex protein 1; Short=MAC protein 1; AltName: Full=Protein MYB DOMAIN CELL DIVISION CYCLE 5; Short=AtMYBCD5 gi|2160167|gb|AAB60730.1| Identical to A. thaliana Myb-like protein (gb|D58424) [Arabidopsis thaliana] gi|20260316|gb|AAM13056.1| putative Myb DNA-binding protein [Arabidopsis thaliana] gi|31711768|gb|AAP68240.1| At1g09770 [Arabidopsis thaliana] gi|332190369|gb|AEE28490.1| cell division cycle 5-like protein [Arabidopsis thaliana]</td><td>836</td><td>844</td><td>0</td><td>101.0</td><td>89.5</td><td>94.9</td><td>cell division cycle 5-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G09770.1 | Symbols: ATCDC5, CDC5, ATMYBCDC5 | cell division cycle 5 | chr1:3162002-3165122 FORWARD LENGTH=844</td><td>836</td><td>844</td><td>0</td><td>101.0</td><td>89.5</td><td>94.9</td></tr>
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<tr><td>Rsa1.0_00273.1.g10158.t1</td><td>ref|NP_563852.1| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 [Arabidopsis thaliana] gi|30316342|sp|O04499.3|PMG1_ARATH RecName: Full=2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1; Short=BPG-independent PGAM 1; Short=Phosphoglyceromutase 1; AltName: Full=PGAM-I 1 gi|21592310|gb|AAM64261.1| putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Arabidopsis thaliana] gi|23297457|gb|AAN12974.1| putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Arabidopsis thaliana] gi|23397261|gb|AAN31912.1| putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Arabidopsis thaliana] gi|332190370|gb|AEE28491.1| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 [Arabidopsis thaliana]</td><td>557</td><td>557</td><td>0</td><td>100.0</td><td>94.1</td><td>97.3</td><td>2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G09780.1 | Symbols: | Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent | chr1:3165550-3167812 REVERSE LENGTH=557</td><td>557</td><td>557</td><td>0</td><td>100.0</td><td>94.1</td><td>97.3</td></tr>
<tr><td>Rsa1.0_00273.1.g10159.t1</td><td>gb|EOA38932.1| hypothetical protein CARUB_v10011331mg [Capsella rubella]</td><td>436</td><td>442</td><td>0</td><td>101.4</td><td>76.1</td><td>84.9</td><td>hypothetical protein CARUB_v10011331mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G09790.1 | Symbols: COBL6 | COBRA-like protein 6 precursor | chr1:3168568-3170819 REVERSE LENGTH=454</td><td>436</td><td>454</td><td>0</td><td>104.1</td><td>72.2</td><td>81.7</td></tr>
<tr><td>Rsa1.0_00273.1.g10160.t1</td><td>ref|XP_002889771.1| hypothetical protein ARALYDRAFT_334263 [Arabidopsis lyrata subsp. lyrata] gi|297335613|gb|EFH66030.1| hypothetical protein ARALYDRAFT_334263 [Arabidopsis lyrata subsp. lyrata]</td><td>623</td><td>128</td><td>3.00E-44</td><td>20.5</td><td>16.5</td><td>18.0</td><td>hypothetical protein ARALYDRAFT_334263</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G09812.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58007.2); Has 93 Blast hits to 93 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 93; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:3187817-3188580 FORWARD LENGTH=128</td><td>623</td><td>128</td><td>1.00E-45</td><td>20.5</td><td>16.1</td><td>18.0</td></tr>
<tr><td>Rsa1.0_00273.1.g10161.t1</td><td>ref|NP_172454.1| phosphoribosylamine--glycine ligase [Arabidopsis thaliana] gi|12644306|sp|P52420.2|PUR2_ARATH RecName: Full=Phosphoribosylamine--glycine ligase, chloroplastic; AltName: Full=Glycinamide ribonucleotide synthetase; Short=GARS; AltName: Full=Phosphoribosylglycinamide synthetase; Flags: Precursor gi|2160174|gb|AAB60737.1| Identical to A. thaliana PUR2 (gb|X74766). ESTs gb|ATTS3927,gb|N96446 come from this gene [Arabidopsis thaliana] gi|15292773|gb|AAK92755.1| putative phosphoribosylglycinamide synthetase [Arabidopsis thaliana] gi|20259251|gb|AAM14361.1| putative phosphoribosylglycinamide synthetase [Arabidopsis thaliana] gi|332190379|gb|AEE28500.1| phosphoribosylamine--glycine ligase [Arabidopsis thaliana]</td><td>534</td><td>532</td><td>0</td><td>99.6</td><td>88.0</td><td>92.1</td><td>phosphoribosylamine--glycine ligase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G09830.1 | Symbols: | Glycinamide ribonucleotide (GAR) synthetase | chr1:3192783-3194936 REVERSE LENGTH=532</td><td>534</td><td>532</td><td>0</td><td>99.6</td><td>88.0</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00273.1.g10162.t1</td><td>gb|EOA40520.1| hypothetical protein CARUB_v10009250mg [Capsella rubella]</td><td>422</td><td>421</td><td>0</td><td>99.8</td><td>94.8</td><td>96.9</td><td>hypothetical protein CARUB_v10009250mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G09840.6 | Symbols: ATSK41, SK41 | shaggy-like protein kinase 41 | chr1:3196114-3199524 REVERSE LENGTH=421</td><td>422</td><td>421</td><td>0</td><td>99.8</td><td>94.3</td><td>96.7</td></tr>
<tr><td>Rsa1.0_00273.1.g10163.t2</td><td>ref|XP_002892532.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338374|gb|EFH68791.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>695</td><td>664</td><td>0</td><td>95.5</td><td>82.9</td><td>89.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G09880.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr1:3208828-3211653 REVERSE LENGTH=631</td><td>695</td><td>631</td><td>0</td><td>90.8</td><td>77.4</td><td>84.2</td></tr>
<tr><td>Rsa1.0_00273.1.g10164.t1</td><td>ref|XP_002892536.1| hypothetical protein ARALYDRAFT_312036 [Arabidopsis lyrata subsp. lyrata] gi|297338378|gb|EFH68795.1| hypothetical protein ARALYDRAFT_312036 [Arabidopsis lyrata subsp. lyrata]</td><td>247</td><td>259</td><td>9.00E-94</td><td>104.9</td><td>71.3</td><td>83.8</td><td>hypothetical protein ARALYDRAFT_312036</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G09932.2 | Symbols: | Phosphoglycerate mutase family protein | chr1:3230716-3232924 REVERSE LENGTH=253</td><td>247</td><td>253</td><td>5.00E-96</td><td>102.4</td><td>69.2</td><td>81.4</td></tr>
<tr><td>Rsa1.0_00273.1.g10165.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00273.1.g10166.t1</td><td>gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>1478</td><td>2301</td><td>0</td><td>155.7</td><td>67.4</td><td>79.4</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1478</td><td>1262</td><td>1.00E-109</td><td>85.4</td><td>13.1</td><td>20.8</td></tr>
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Rsa1.0_00273.1.g10167.t1	ref|NP_172499.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|4914330|gb|AAD32878.1|AC005489_16 F14N23.16 [Arabidopsis thaliana] gi|117168053|gb|ABK32109.1| At1g10280 [Arabidopsis thaliana] gi|332190440|gb|AEE28561.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]	415	412	0	99.3	88.4	94.2	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	gbpln	Arabidopsis thaliana	AT1G10280.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:3366795-3368739 REVERSE LENGTH=412	415	412	0	99.3	88.4	94.2
Rsa1.0_00273.1.g10168.t1	gb|AAF22291.1|AF180732_1 dynamin-like protein 6 [Arabidopsis thaliana]	922	914	0	99.1	92.6	97.1	dynamin-like protein 6	gbpln	Arabidopsis thaliana	AT1G10290.1 | Symbols: ADL6, DRP2A | dynamin-like protein 6 | chr1:3370774-3377120 FORWARD LENGTH=914	922	914	0	99.1	92.5	97.0
Rsa1.0_00273.1.g10169.t1	ref|NP_563866.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|4914333|gb|AAD32881.1|AC005489_19 F14N23.19 [Arabidopsis thaliana] gi|51971537|dbj|BAD44433.1| unknown protein [Arabidopsis thaliana] gi|107738340|gb|ABF83679.1| At1g10310 [Arabidopsis thaliana] gi|332190443|gb|AEE28564.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]	252	242	1.00E-126	96.0	89.3	93.7	Rossmann-fold NAD(P)-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G10310.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:3381733-3383874 REVERSE LENGTH=242	252	242	1.00E-128	96.0	89.3	93.7
Rsa1.0_00273.1.g10170.t2	ref|NP_172503.1| zinc finger CCCH domain-containing protein 5 [Arabidopsis thaliana] gi|229621703|sp|Q9SY74.2|C3H5_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 5; Short=AtC3H5 gi|332190444|gb|AEE28565.1| zinc finger CCCH domain-containing protein 5 [Arabidopsis thaliana]	751	757	0	100.8	66.0	73.9	zinc finger CCCH domain-containing protein 5	gbpln	Arabidopsis thaliana	AT1G10320.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:3384164-3388373 REVERSE LENGTH=757	751	757	0	100.8	66.0	73.9
Rsa1.0_00273.1.g10171.t1	ref|NP_563867.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|4914336|gb|AAD32884.1|AC005489_22 F14N23.22 [Arabidopsis thaliana] gi|13937240|gb|AAK50112.1|AF372975_1 At1g10340/F14N23_22 [Arabidopsis thaliana] gi|19548017|gb|AAL87372.1| At1g10340/F14N23_22 [Arabidopsis thaliana] gi|332190446|gb|AEE28567.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	578	578	0	100.0	73.5	81.1	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G10340.1 | Symbols: | Ankyrin repeat family protein | chr1:3390475-3392481 REVERSE LENGTH=578	578	578	0	100.0	73.5	81.1
Rsa1.0_00273.1.g10172.t1	ref|NP_172506.1| putative DNAJ heat-shock protein [Arabidopsis thaliana] gi|4914337|gb|AAD32885.1|AC005489_23 F14N23.23 [Arabidopsis thaliana] gi|13430680|gb|AAK25962.1|AF360252_1 putative heat-shock protein [Arabidopsis thaliana] gi|14532888|gb|AAK64126.1| putative heat-shock protein [Arabidopsis thaliana] gi|332190448|gb|AEE28569.1| putative DNAJ heat-shock protein [Arabidopsis thaliana]	622	349	1.00E-129	56.1	39.9	44.1	putative DNAJ heat-shock protein	gbpln	Arabidopsis thaliana	AT1G10350.1 | Symbols: | DNAJ heat shock family protein | chr1:3393595-3394860 REVERSE LENGTH=349	622	349	1.00E-132	56.1	39.9	44.1
Rsa1.0_00273.1.g10173.t1	ref|NP_563869.1| Vps51/Vps67 family (components of vesicular transport) protein [Arabidopsis thaliana] gi|332190452|gb|AEE28573.1| Vps51/Vps67 family (components of vesicular transport) protein [Arabidopsis thaliana]	758	754	0	99.5	93.8	97.4	Vps51/Vps67 family (components of vesicular transport) protein	gbpln	Arabidopsis thaliana	AT1G10385.1 | Symbols: | Vps51/Vps67 family (components of vesicular transport) protein | chr1:3403224-3405856 FORWARD LENGTH=754	758	754	0	99.5	93.8	97.4

Rsa1.0_00273.1.g10174.t1	ref|NP_172510.2| Nucleoporin autopeptidase [Arabidopsis thaliana] gi|79317517|ref|NP_001031018.1| Nucleoporin autopeptidase [Arabidopsis thaliana] gi|19310423|gb|AAL84948.1| At1g10390/F14N23_29 [Arabidopsis thaliana] gi|27764948|gb|AAO23595.1| At1g10390/F14N23_29 [Arabidopsis thaliana] gi|110742211|dbj|BAE99032.1| hypothetical protein [Arabidopsis thaliana] gi|332190453|gb|AEE28574.1| Nucleoporin autopeptidase [Arabidopsis thaliana] gi|332190454|gb|AEE28575.1| Nucleoporin autopeptidase [Arabidopsis thaliana]	1032	1041	0	100.9	84.9	90.9	Nucleoporin autopeptidase	gbpln	Arabidopsis thaliana	AT1G10390.2 | Symbols: | Nucleoporin autopeptidase | chr1:3407265-3412045 REVERSE LENGTH=1041	1032	1041	0	100.9	84.9	90.9
Rsa1.0_00273.1.g10175.t1	ref|NP_172511.3| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75213386|sp|Q9SY84.1|U90A2_ARATH RecName: Full=UDP-glycosyltransferase 90A2 gi|4914344|gb|AAD32892.1|AC005489_30 F14N23.30 [Arabidopsis thaliana] gi|332190455|gb|AEE28576.1| UDP-glycosyltransferase 90A2 [Arabidopsis thaliana]	466	467	0	100.2	86.1	91.4	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT1G10400.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:3414869-3416358 REVERSE LENGTH=467	466	467	0	100.2	86.1	91.4
Rsa1.0_00273.1.g10176.t1	ref|XP_002892573.1| hypothetical protein ARALYDRAFT_888316 [Arabidopsis lyrata subsp. lyrata] gi|297338415|gb|EFH68832.1| hypothetical protein ARALYDRAFT_888316 [Arabidopsis lyrata subsp. lyrata]	257	258	1.00E-102	100.4	80.5	86.8	hypothetical protein ARALYDRAFT_888316	gbpln	Arabidopsis lyrata	AT1G10470.1 | Symbols: ARR4, MEE7, ATRR1, IBC7 | response regulator 4 | chr1:3442624-3443759 REVERSE LENGTH=259	257	259	4.00E-96	100.8	80.9	86.0
Rsa1.0_00273.1.g10177.t1	gb|ABD65629.1| hypothetical protein 23.t00046 [Brassica oleracea]	109	147	2.00E-35	134.9	62.4	73.4	hypothetical protein 23.t00046	gbpln	Brassica oleracea	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	109	746	2.00E-16	684.4	39.4	48.6
Rsa1.0_00273.1.g10178.t1	ref|XP_002889811.1| zinc finger protein 5, ZFP5 [Arabidopsis lyrata subsp. lyrata] gi|297335653|gb|EFH66070.1| zinc finger protein 5, ZFP5 [Arabidopsis lyrata subsp. lyrata]	205	205	1.00E-82	100.0	85.4	91.7	zinc finger protein 5, ZFP5	gbpln	Arabidopsis lyrata	AT1G10480.1 | Symbols: ZFP5 | zinc finger protein 5 | chr1:3449734-3450369 FORWARD LENGTH=211	205	211	5.00E-83	102.9	83.4	91.2
Rsa1.0_00273.1.g10179.t1	gb|EOA36696.1| hypothetical protein CARUB_v10012139mg [Capsella rubella]	1027	1028	0	100.1	92.1	96.5	hypothetical protein CARUB_v10012139mg	gbpln	Capsella rubella	AT1G10490.1 | Symbols: | Domain of unknown function (DUF1726) ;Putative ATPase (DUF699) | chr1:3453589-3459925 FORWARD LENGTH=1028	1027	1028	0	100.1	91.4	96.2
Rsa1.0_00273.1.g10180.t1	dbj|BAJ34349.1| unnamed protein product [Thellungiella halophila]	179	177	3.00E-86	98.9	89.9	92.2	unnamed protein product	----	----	AT1G10500.1 | Symbols: ATCPISCA, CPISCA | chloroplast-localized ISCA-like protein | chr1:3460160-3461340 REVERSE LENGTH=180	179	180	1.00E-77	100.6	83.8	88.3
Rsa1.0_00273.1.g10181.t1	ref|XP_002889813.1| EMB2004 [Arabidopsis lyrata subsp. lyrata] gi|297335655|gb|EFH66072.1| EMB2004 [Arabidopsis lyrata subsp. lyrata]	611	605	0	99.0	90.7	94.1	EMB2004	gbpln	Arabidopsis lyrata	AT1G10510.1 | Symbols: emb2004 | RNI-like superfamily protein | chr1:3461771-3465590 FORWARD LENGTH=605	611	605	0	99.0	90.0	93.8
Rsa1.0_00273.1.g10182.t1	ref|NP_172522.2| DNA polymerase lambda subunit [Arabidopsis thaliana] gi|12053869|emb|CAC21394.1| DNA polymerase lambda [Arabidopsis thaliana] gi|91805767|gb|ABE65612.1| DNA polymerase lambda [Arabidopsis thaliana] gi|304440990|gb|ADM33939.1| DNA pol lambda [Arabidopsis thaliana] gi|332190467|gb|AEE28588.1| DNA polymerase lambda subunit [Arabidopsis thaliana]	531	529	0	99.6	85.5	91.9	DNA polymerase lambda subunit	gbpln	Arabidopsis thaliana	AT1G10520.1 | Symbols: | DNA polymerase lambda (POLL) | chr1:3465964-3469248 FORWARD LENGTH=529	531	529	0	99.6	85.5	91.9
Rsa1.0_00273.1.g10183.t7	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	1337	1752	0	131.0	42.6	56.5	putative protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	1337	566	2.00E-30	42.3	7.3	12.3
Rsa1.0_00274.1.g10184.t1	gb|ABD65624.1| hypothetical protein 23.t00036 [Brassica oleracea]	913	842	1.00E-120	92.2	34.6	50.8	hypothetical protein 23.t00036	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	913	673	1.00E-34	73.7	11.0	16.1
Rsa1.0_00274.1.g10185.t1	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	167	326	7.00E-16	195.2	34.1	52.1	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10186.t1	gb|AFO66528.1| putative eukaryotic translation initiation factor SUI1 family protein [Brassica napus]	223	704	7.00E-72	315.7	57.0	69.1	putative eukaryotic translation initiation factor SUI1 family protein	gbpln	Brassica napus	AT2G24700.1 | Symbols: | Transcriptional factor B3 family protein | chr2:10513049-10515288 REVERSE LENGTH=555	223	555	8.00E-35	248.9	36.8	56.5

Rsa1.0_00274.1.g10187.t2	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	503	915	1.00E-139	181.9	47.3	66.2	F22O13.21	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	503	719	9.00E-29	142.9	20.7	35.4
Rsa1.0_00274.1.g10188.t3	ref|XP_002892938.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338780|gb|EFH69197.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	181	380	5.00E-15	209.9	19.9	26.0	pfkB-type carbohydrate kinase family protein	gbpln	Arabidopsis lyrata	AT1G17160.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr1:5867678-5869215 FORWARD LENGTH=379	181	379	9.00E-17	209.4	19.9	25.4
Rsa1.0_00274.1.g10189.t3	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	451	326	6.00E-24	72.3	15.5	24.8	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10190.t3	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	465	1024	1.00E-38	220.2	25.4	33.8	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10191.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	186	1231	3.00E-44	661.8	53.2	71.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	186	575	6.00E-18	309.1	37.1	58.1
Rsa1.0_00274.1.g10192.t1	gb|AAL60579.1|AF454957_1 senescence-associated cysteine protease [Brassica oleracea]	463	460	0	99.4	96.1	97.6	senescence-associated cysteine protease	gbpln	Brassica oleracea	AT5G43060.1 | Symbols: | Granulin repeat cysteine protease family protein | chr5:17269784-17272117 REVERSE LENGTH=463	463	463	0	100.0	87.0	92.2
Rsa1.0_00274.1.g10193.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10194.t2	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1388	1223	0	88.1	40.8	54.5	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1388	746	2.00E-94	53.7	13.5	17.1
Rsa1.0_00274.1.g10195.t1	ref|XP_002863700.1| hypothetical protein ARALYDRAFT_494701 [Arabidopsis lyrata subsp. lyrata] gi|297309535|gb|EFH39959.1| hypothetical protein ARALYDRAFT_494701 [Arabidopsis lyrata subsp. lyrata]	677	669	0	98.8	86.4	90.7	hypothetical protein ARALYDRAFT_494701	gbpln	Arabidopsis lyrata	AT5G43020.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:17255426-17257742 REVERSE LENGTH=669	677	669	0	98.8	86.0	90.0
Rsa1.0_00274.1.g10196.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	962	1142	0	118.7	34.6	43.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	962	626	2.00E-37	65.1	10.9	18.7
Rsa1.0_00274.1.g10197.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10198.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10199.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10200.t1	gb|AAG50652.1|AC073433_4 transposase, putative [Arabidopsis thaliana]	204	659	2.00E-47	323.0	49.0	64.7	transposase, putative	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	204	696	1.00E-17	341.2	27.5	46.1
Rsa1.0_00274.1.g10201.t1	ref|NP_199115.1| regulatory particle triple-A ATPase 4A [Arabidopsis thaliana] gi|75337115|sp|Q9SEI3.1|PS10A_ARATH RecName: Full=26S protease regulatory subunit 10B homolog A; AltName: Full=26S proteasome AAA-ATPase subunit RPT4a; AltName: Full=26S proteasome subunit 10B homolog A; AltName: Full=Regulatory particle triple-A ATPase subunit 4a gi|6652884|gb|AAF22524.1|AF123393_1 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gi|13937183|gb|AAK50085.1|AF372945_1 AT5g43010/MBD2_21 [Arabidopsis thaliana] gi|9758590|dbj|BAB09203.1| 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] gi|18700262|gb|AAL77741.1| AT5g43010/MBD2_21 [Arabidopsis thaliana] gi|332007517|gb|AED94900.1| regulatory particle triple-A ATPase 4A [Arabidopsis thaliana] gi|482549284|gb|EOA13478.1| hypothetical protein CARUB_v10026536mg [Capsella rubella]	399	399	0	100.0	97.5	99.2	regulatory particle triple-A ATPase 4A	gbpln	Arabidopsis thaliana	AT5G43010.1 | Symbols: RPT4A | regulatory particle triple-A ATPase 4A | chr5:17248563-17251014 REVERSE LENGTH=399	399	399	0	100.0	97.5	99.2
Rsa1.0_00274.1.g10202.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	987	1529	0	154.9	53.2	69.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	987	746	1.00E-113	75.6	20.5	27.2
Rsa1.0_00274.1.g10203.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00274.1.g10204.t1	gb|AAD25557.1|AC005850_14 Hypothetical protein [Arabidopsis thaliana]	415	404	3.00E-51	97.3	25.5	30.6	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G43722.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28730.1); Has 924 Blast hits to 912 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 222; Fungi - 31; Plants - 661; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:16496403-16497377 FORWARD LENGTH=324	415	324	8.00E-20	78.1	12.5	19.3
Rsa1.0_00274.1.g10205.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	483	723	1.00E-103	149.7	41.2	53.6	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	483	696	4.00E-13	144.1	13.9	23.0
Rsa1.0_00274.1.g10206.t1	ref|NP_974873.1| THO complex, subunit 5 [Arabidopsis thaliana] gi|332007505|gb|AED94888.1| THO complex, subunit 5 [Arabidopsis thaliana]	821	819	0	99.8	85.5	91.6	THO complex, subunit 5	gbpln	Arabidopsis thaliana	AT5G42920.2 | Symbols: THO5, AtTHO5 | THO complex, subunit 5 | chr5:17206310-17209522 REVERSE LENGTH=819	821	819	0	99.8	85.5	91.6
Rsa1.0_00274.1.g10207.t1	ref|NP_199105.1| abscisic acid-insensitive 5-like protein 8 [Arabidopsis thaliana] gi|75309215|sp|Q9FMM7.1|AI5L8_ARATH RecName: Full=ABSCISIC ACID-INSENSITIVE 5-like protein 8; AltName: Full=bZIP transcription factor 15; Short=AtbZIP15 gi|9758580|dbj|BAB09193.1| abscisic acid responsive elements-binding factor-like protein [Arabidopsis thaliana] gi|18656051|emb|CAD11866.1| basic leucine zipper transcription factor [Arabidopsis thaliana] gi|332007503|gb|AED94886.1| abscisic acid-insensitive 5-like protein 8 [Arabidopsis thaliana]	404	370	2.00E-82	91.6	50.2	63.1	abscisic acid-insensitive 5-like protein 8	gbpln	Arabidopsis thaliana	AT5G42910.1 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr5:17203908-17205211 FORWARD LENGTH=370	404	370	4.00E-85	91.6	50.2	63.1
Rsa1.0_00274.1.g10208.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10209.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00274.1.g10210.t1	ref|XP_002863724.1| hypothetical protein ARALYDRAFT_356828 [Arabidopsis lyrata subsp. lyrata] gi|297309559|gb|EFH39983.1| hypothetical protein ARALYDRAFT_356828 [Arabidopsis lyrata subsp. lyrata]	223	253	7.00E-72	113.5	71.7	78.0	hypothetical protein ARALYDRAFT_356828	gbpln	Arabidopsis lyrata	AT5G42900.2 | Symbols: | cold regulated gene 27 | chr5:17198366-17199712 REVERSE LENGTH=246	223	246	1.00E-71	110.3	73.5	79.8
Rsa1.0_00275.1.g10211.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	323	1611	6.00E-94	498.8	52.3	68.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00275.1.g10212.t1	gb|EOA28594.1| hypothetical protein CARUB_v10024814mg [Capsella rubella]	435	436	0	100.2	93.6	97.9	hypothetical protein CARUB_v10024814mg	gbpln	Capsella rubella	AT2G45310.1 | Symbols: GAE4 | UDP-D-glucuronate 4-epimerase 4 | chr2:18682652-18683965 FORWARD LENGTH=437	435	437	0	100.5	91.7	95.9
Rsa1.0_00275.1.g10213.t1	gb|EOA27266.1| hypothetical protein CARUB_v10023386mg [Capsella rubella]	393	391	0	99.5	84.5	91.9	hypothetical protein CARUB_v10023386mg	gbpln	Capsella rubella	AT2G45320.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 10 growth stages; Has 45 Blast hits to 45 proteins in 16 species: Archae - 0; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18684182-18686107 REVERSE LENGTH=392	393	392	0	99.7	83.7	91.9
Rsa1.0_00275.1.g10214.t1	ref|XP_002868031.1| hypothetical protein ARALYDRAFT_354960 [Arabidopsis lyrata subsp. lyrata] gi|297313867|gb|EFH44290.1| hypothetical protein ARALYDRAFT_354960 [Arabidopsis lyrata subsp. lyrata]	464	746	0	160.8	87.3	92.7	hypothetical protein ARALYDRAFT_354960	gbpln	Arabidopsis lyrata	AT4G17910.1 | Symbols: | transferases, transferring acyl groups | chr4:9951322-9953689 REVERSE LENGTH=434	464	434	0	93.5	78.4	84.1
Rsa1.0_00275.1.g10215.t1	ref|XP_002882010.1| hypothetical protein ARALYDRAFT_903982 [Arabidopsis lyrata subsp. lyrata] gi|297327849|gb|EFH58269.1| hypothetical protein ARALYDRAFT_903982 [Arabidopsis lyrata subsp. lyrata]	364	442	1.00E-124	121.4	62.9	72.3	hypothetical protein ARALYDRAFT_903982	gbpln	Arabidopsis lyrata	AT1G10270.1 | Symbols: GRP23 | glutamine-rich protein 23 | chr1:3363535-3366276 FORWARD LENGTH=913	364	913	1.00E-69	250.8	43.4	63.5

Rsa1.0_00275.1.g10216.t1	ref|XP_002880177.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326016|gb|EFH56436.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	438	455	1.00E-175	103.9	74.7	83.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G10270.1 | Symbols: GRP23 | glutamine-rich protein 23 | chr1:3363535-3366276 FORWARD LENGTH=913	438	913	8.00E-78	208.4	39.5	56.2
Rsa1.0_00275.1.g10217.t1	gb|AAC02664.1| polyprotein [Arabidopsis thaliana]	382	1451	1.00E-140	379.8	65.2	79.1	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	382	1262	1.00E-55	330.4	27.0	43.7
Rsa1.0_00275.1.g10218.t1	ref|NP_567151.1| 40S ribosomal protein S13-2 [Arabidopsis thaliana] gi|27808638|sp|P59224.1|RS132_ARATH RecName: Full=40S ribosomal protein S13-2 gi|13877541|gb|AAK43848.1|AF370471_1 similar to ribosomal protein S13 [Arabidopsis thaliana] gi|6521012|dbj|BAA88058.1| cytoplasmic ribosomal protein S13 [Arabidopsis thaliana] gi|15982874|gb|AAL09784.1| AT4g00100/F6N15_7 [Arabidopsis thaliana] gi|21593617|gb|AAM65584.1| putative ribosomal protein S13 [Arabidopsis thaliana] gi|30102866|gb|AAP21351.1| At4g00100 [Arabidopsis thaliana] gi|332656423|gb|AEE81823.1| 40S ribosomal protein S13-2 [Arabidopsis thaliana]	164	151	2.00E-62	92.1	79.3	80.5	40S ribosomal protein S13-2	gbpln	Arabidopsis thaliana	AT4G00100.1 | Symbols: ATRPS13A, RPS13, PFL2, RPS13A | ribosomal protein S13A | chr4:37172-38123 FORWARD LENGTH=151	164	151	9.00E-65	92.1	79.3	80.5
Rsa1.0_00275.1.g10219.t1	gb|EOA18130.1| hypothetical protein CARUB_v10006591mg [Capsella rubella]	138	256	4.00E-11	185.5	29.7	43.5	hypothetical protein CARUB_v10006591mg	gbpln	Capsella rubella	AT2G33160.1 | Symbols: | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein | chr2:14053404-14056246 FORWARD LENGTH=664	138	664	5.00E-12	481.2	26.1	42.8
Rsa1.0_00275.1.g10220.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00275.1.g10221.t1	ref|NP_182089.1| agamous-like MADS-box protein AGL6 [Arabidopsis thaliana] gi|1351899|sp|P29386.2|AGL6_ARATH RecName: Full=Agamous-like MADS-box protein AGL6 gi|1019925|gb|AAA79328.1| transcription factor [Arabidopsis thaliana] gi|2979564|gb|AAC06173.1| MADS-box protein (AGL6) [Arabidopsis thaliana] gi|91806361|gb|ABE65908.1| MADS-box protein [Arabidopsis thaliana] gi|330255488|gb|AEC10582.1| agamous-like MADS-box protein AGL6 [Arabidopsis thaliana] gi|399140006|gb|AFP23735.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140008|gb|AFP23736.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140020|gb|AFP23742.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140022|gb|AFP23743.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140026|gb|AFP23745.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140028|gb|AFP23746.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140030|gb|AFP23747.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140034|gb|AFP23749.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140044|gb|AFP23754.1| AGAMOUS-like protein 6 [Arabidopsis thaliana] gi|399140048|gb|AFP23756.1| AGAMOUS-like protein 6 [Arabidopsis	211	252	8.00E-66	119.4	59.7	66.8	agamous-like MADS-box protein AGL6	gbpln	Arabidopsis thaliana	AT2G45650.1 | Symbols: AGL6 | AGAMOUS-like 6 | chr2:18804453-18806291 FORWARD LENGTH=252	211	252	3.00E-68	119.4	59.7	66.8
Rsa1.0_00275.1.g10222.t1	gb|AAB41526.1| transcription factor SaMADS A [Sinapis alba]	213	213	1.00E-119	100.0	99.5	99.5	transcription factor SaMADS A	gbpln	Sinapis alba	AT2G45660.1 | Symbols: AGL20, SOC1, ATSOC1 | AGAMOUS-like 20 | chr2:18807799-18810193 REVERSE LENGTH=214	213	214	1.00E-111	100.5	96.2	99.1
Rsa1.0_00275.1.g10223.t1	ref|XP_002283163.1| PREDICTED: mRNA cap guanine-N7 methyltransferase 1 [Vitis vinifera] gi|302143175|emb|CBI20470.3| unnamed protein product [Vitis vinifera]	156	372	1.00E-22	238.5	32.7	40.4	PREDICTED: mRNA cap guanine-N7 methyltransferase 1	gbpln	Vitis vinifera	AT3G20650.2 | Symbols: | mRNA capping enzyme family protein | chr3:7221168-7223939 REVERSE LENGTH=369	156	369	1.00E-20	236.5	36.5	41.7

Rsa1.0_00275.1.g10224.t1	ref|XP_002882025.1| hypothetical protein ARALYDRAFT_483703 [Arabidopsis lyrata subsp. lyrata] gi|297327864|gb|EFH58284.1| hypothetical protein ARALYDRAFT_483703 [Arabidopsis lyrata subsp. lyrata]	526	528	0	100.4	83.1	89.7	hypothetical protein ARALYDRAFT_483703	gbpln	Arabidopsis lyrata	AT2G45670.1 | Symbols: | calcineurin B subunit-related | chr2:18815070-18818382 REVERSE LENGTH=539	526	539	0	102.5	82.7	90.1
Rsa1.0_00275.1.g10225.t1	gb|AAZ20121.1| putative shrunken seed protein [Brassica napus]	366	366	1.00E-175	100.0	86.9	91.8	putative shrunken seed protein	gbpln	Brassica napus	AT2G45690.1 | Symbols: SSE1, SSE, PEX16, ATPEX16 | shrunken seed protein (SSE1) | chr2:18823465-18825601 REVERSE LENGTH=367	366	367	1.00E-166	100.3	79.2	88.0
Rsa1.0_00275.1.g10226.t2	ref|NP_001078064.1| ubiquitin-related modifier 1-1 [Arabidopsis thaliana] gi|229557933|sp|A0MDQ1.2|URM11_ARATH RecName: Full=Ubiquitin-related modifier 1 homolog 1 gi|62318675|dbj|BAD95172.1| hypothetical protein [Arabidopsis thaliana] gi|98961773|gb|ABF59216.1| unknown protein [Arabidopsis thaliana] gi|330255494|gb|AEC10588.1| ubiquitin-related modifier 1-1 [Arabidopsis thaliana]	99	101	4.00E-44	102.0	89.9	97.0	ubiquitin-related modifier 1-1	gbpln	Arabidopsis thaliana	AT2G45695.1 | Symbols: | Ubiquitin related modifier 1 | chr2:18826043-18826744 FORWARD LENGTH=101	99	101	7.00E-47	102.0	89.9	97.0
Rsa1.0_00275.1.g10227.t1	ref|XP_002880193.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297326032|gb|EFH56452.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	550	553	0	100.5	86.7	92.4	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT2G45720.2 | Symbols: | ARM repeat superfamily protein | chr2:18834468-18836129 FORWARD LENGTH=553	550	553	0	100.5	86.9	92.0
Rsa1.0_00275.1.g10228.t2	gb|EOA27117.1| hypothetical protein CARUB_v10023215mg [Capsella rubella]	447	446	0	99.8	81.4	87.5	hypothetical protein CARUB_v10023215mg	gbpln	Capsella rubella	AT2G45730.1 | Symbols: | eukaryotic initiation factor 3 gamma subunit family protein | chr2:18836519-18839123 REVERSE LENGTH=446	447	446	0	99.8	83.4	89.5
Rsa1.0_00275.1.g10229.t1	ref|XP_002880194.1| peroxisomal biogenesis factor 11 family protein [Arabidopsis lyrata subsp. lyrata] gi|297326033|gb|EFH56453.1| peroxisomal biogenesis factor 11 family protein [Arabidopsis lyrata subsp. lyrata]	238	236	1.00E-126	99.2	94.1	95.4	peroxisomal biogenesis factor 11 family protein	gbpln	Arabidopsis lyrata	AT2G45740.3 | Symbols: PEX11D | peroxin 11D | chr2:18839865-18841102 FORWARD LENGTH=236	238	236	1.00E-127	99.2	92.9	95.0
Rsa1.0_00275.1.g10230.t1	ref|XP_002882032.1| hypothetical protein ARALYDRAFT_483714 [Arabidopsis lyrata subsp. lyrata] gi|297327871|gb|EFH58291.1| hypothetical protein ARALYDRAFT_483714 [Arabidopsis lyrata subsp. lyrata]	204	200	3.00E-75	98.0	70.6	83.8	hypothetical protein ARALYDRAFT_483714	gbpln	Arabidopsis lyrata	AT2G45760.1 | Symbols: BAP2, BAL | BON association protein 2 | chr2:18847125-18847748 REVERSE LENGTH=207	204	207	1.00E-77	101.5	71.1	82.4
Rsa1.0_00275.1.g10231.t1	ref|XP_002872639.1| bile acid:sodium symporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297318476|gb|EFH48898.1| bile acid:sodium symporter family protein [Arabidopsis lyrata subsp. lyrata]	408	409	0	100.2	89.0	93.9	bile acid:sodium symporter family protein	gbpln	Arabidopsis lyrata	AT4G12030.2 | Symbols: BAT5, BASS5 | bile acid transporter 5 | chr4:7210981-7212713 FORWARD LENGTH=407	408	407	0	99.8	89.0	94.1
Rsa1.0_00275.1.g10232.t1	ref|NP_192933.2| PGR5-like protein 1B [Arabidopsis thaliana] gi|75151402|sp|Q8GYC7.1|PGL1B_ARATH RecName: Full=PGR5-like protein 1B, chloroplastic; AltName: Full=Ferredoxin-plastoquinone reductase 2; Flags: Precursor gi|26450517|dbj|BAC42372.1| unknown protein [Arabidopsis thaliana] gi|28950891|gb|AAO63369.1| At4g11960 [Arabidopsis thaliana] gi|332657674|gb|AEE83074.1| PGR5-like protein 1B [Arabidopsis thaliana]	322	313	1.00E-156	97.2	88.8	92.9	PGR5-like protein 1B	gbpln	Arabidopsis thaliana	AT4G11960.1 | Symbols: PGRL1B | PGR5-like B | chr4:7175340-7177709 REVERSE LENGTH=313	322	313	1.00E-158	97.2	88.8	92.9
Rsa1.0_00275.1.g10233.t1	gb|EOA18445.1| hypothetical protein CARUB_v10006988mg [Capsella rubella]	697	683	0	98.0	54.4	69.0	hypothetical protein CARUB_v10006988mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	697	696	3.00E-41	99.9	22.4	39.3
Rsa1.0_00275.1.g10234.t1	gb|EOA20561.1| hypothetical protein CARUB_v10000874mg [Capsella rubella]	484	473	0	97.7	81.4	86.4	hypothetical protein CARUB_v10000874mg	gbpln	Capsella rubella	AT4G11920.1 | Symbols: CCS52A2, FZR1 | cell cycle switch protein 52 A2 | chr4:7160618-7163257 REVERSE LENGTH=475	484	475	0	98.1	81.6	86.8
Rsa1.0_00275.1.g10235.t1	ref|XP_002863072.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297308883|gb|EFH39331.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	379	387	1.00E-100	102.1	54.6	68.6	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT5G48980.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19860724-19861923 FORWARD LENGTH=399	379	399	1.00E-100	105.3	53.6	68.9

Rsa1.0_00275.1.g10236.t1	ref|XP_002863072.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297308883|gb|EFH39331.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	338	387	2.00E-87	114.5	54.7	67.8	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT5G48990.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19862340-19863458 FORWARD LENGTH=372	338	372	3.00E-88	110.1	54.7	66.6
Rsa1.0_00275.1.g10237.t1	ref|NP_199710.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75170772|sp|Q9FI71.1|FK121_ARATH RecName: Full=F-box/kelch-repeat protein At5g48990 gi|10177189|dbj|BAB10323.1| unnamed protein product [Arabidopsis thaliana] gi|18175611|gb|AAL59896.1| unknown protein [Arabidopsis thaliana] gi|21689859|gb|AAM67490.1| unknown protein [Arabidopsis thaliana] gi|332008370|gb|AED95753.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	289	372	2.00E-61	128.7	50.9	59.5	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT5G48990.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19862340-19863458 FORWARD LENGTH=372	289	372	6.00E-64	128.7	50.9	59.5
Rsa1.0_00275.1.g10238.t1	ref|NP_195670.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75210846|sp|Q9SV98.1|FK103_ARATH RecName: Full=Putative F-box/kelch-repeat protein At4g39600 gi|5042176|emb|CAB44695.1| putative protein [Arabidopsis thaliana] gi|7270944|emb|CAB80623.1| putative protein [Arabidopsis thaliana] gi|332661692|gb|AEE87092.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	236	367	3.00E-61	155.5	50.4	64.8	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT4G39600.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18389436-18390539 REVERSE LENGTH=367	236	367	8.00E-64	155.5	50.4	64.8
Rsa1.0_00275.1.g10239.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00275.1.g10240.t1	gb|EOA21319.1| hypothetical protein CARUB_v10001681mg [Capsella rubella]	261	272	1.00E-121	104.2	81.2	86.2	hypothetical protein CARUB_v10001681mg	gbpln	Capsella rubella	AT4G11910.1 | Symbols: | INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: non-yellowing 1 (TAIR:AT4G22920.1); Has 206 Blast hits to 202 proteins in 67 species: Archae - 0; Bacteria - 86; Metazoa - 0; Fungi - 0; Plants - 118; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:7156435-7157839 FORWARD LENGTH=271	261	271	1.00E-121	103.8	82.4	86.6
Rsa1.0_00276.1.g10241.t1	ref|NP_192145.1| uncharacterized protein [Arabidopsis thaliana] gi|3193298|gb|AAC19282.1| T14P8.17 [Arabidopsis thaliana] gi|7268996|emb|CAB80729.1| putative protein [Arabidopsis thaliana] gi|332656759|gb|AEE82159.1| uncharacterized protein AT4G02360 [Arabidopsis thaliana]	150	154	3.00E-61	102.7	80.0	84.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G02360.1 | Symbols: | Protein of unknown function, DUF538 | chr4:1041179-1041643 FORWARD LENGTH=154	150	154	9.00E-64	102.7	80.0	84.0
Rsa1.0_00276.1.g10242.t1	ref|NP_567228.1| putative epoxide hydrolase [Arabidopsis thaliana] gi|3193297|gb|AAC19281.1| T14P8.15 [Arabidopsis thaliana] gi|7268994|emb|CAB80727.1| AT4g02340 [Arabidopsis thaliana] gi|20856515|gb|AAM26670.1| AT4g02340/T14P8_15 [Arabidopsis thaliana] gi|23308303|gb|AAN18121.1| At4g02340/T14P8_15 [Arabidopsis thaliana] gi|332656757|gb|AEE82157.1| putative epoxide hydrolase [Arabidopsis thaliana]	315	324	1.00E-163	102.9	87.0	94.3	putative epoxide hydrolase	gbpln	Arabidopsis thaliana	AT4G02340.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:1035722-1037403 FORWARD LENGTH=324	315	324	1.00E-165	102.9	87.0	94.3

Rsa1.0_00276.1.g10243.t2	ref|NP_567227.1| pectinesterase 41 [Arabidopsis thaliana] gi|229891482|sp|Q8RXK7.2|PME41_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 41; Includes: RecName: Full=Pectinesterase inhibitor 41; AltName: Full=Pectin methylesterase inhibitor 41; Includes: RecName: Full=Pectinesterase 41; Short=PE 41; AltName: Full=AtPMEpcrB; AltName: Full=Pectin methylesterase 41; Short=AtPME41; Flags: Precursor gi|3193296|gb|AAC19280.1| T14P8.14 [Arabidopsis thaliana] gi|7268993|emb|CAB80726.1| AT4g02330 [Arabidopsis thaliana] gi|23297461|gb|AAN12975.1| unknown protein [Arabidopsis thaliana] gi|332656756|gb|AEE82156.1| pectinesterase 41 [Arabidopsis thaliana]	1046	573	0	54.8	49.3	51.9	pectinesterase 41	gbpln	Arabidopsis thaliana	AT4G02330.1 | Symbols: ATPMEPCRB | Plant invertase/pectin methylesterase inhibitor superfamily | chr4:1032479-1034928 FORWARD LENGTH=573	1046	573	0	54.8	49.3	51.9
Rsa1.0_00276.1.g10244.t1	ref|XP_002889264.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335105|gb|EFH65523.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	233	619	4.00E-35	265.7	33.5	42.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G16120.1 | Symbols: WAKL1 | wall associated kinase-like 1 | chr1:5522639-5524983 FORWARD LENGTH=730	233	730	4.00E-36	313.3	33.0	42.5
Rsa1.0_00276.1.g10245.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00276.1.g10246.t1	gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]	176	863	2.00E-63	490.3	68.8	80.7	Ulp1 protease family protein	gbpln	Brassica oleracea	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	176	921	3.00E-25	523.3	42.0	55.7
Rsa1.0_00276.1.g10247.t1	gb|ACG60684.1| maize transposon MuDR-like protein [Brassica oleracea var. alboglabra]	384	622	7.00E-61	162.0	31.0	48.7	maize transposon MuDR-like protein	gbpln	Brassica oleracea	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	384	719	2.00E-16	187.2	11.5	18.8
Rsa1.0_00276.1.g10248.t1	gb|AAC28197.1| contains similarity to reverse transcriptases [Arabidopsis thaliana] gi|7267156|emb|CAB77868.1| putative reverse transcriptase [Arabidopsis thaliana]	257	1077	5.00E-20	419.1	23.7	33.9	contains similarity to reverse transcriptases	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00276.1.g10249.t1	gb|EOA20378.1| hypothetical protein CARUB_v10000691mg [Capsella rubella]	503	530	0	105.4	75.9	88.3	hypothetical protein CARUB_v10000691mg	gbpln	Capsella rubella	AT4G02320.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr4:1022725-1026118 REVERSE LENGTH=518	503	518	0	103.0	74.4	83.9
Rsa1.0_00276.1.g10250.t1	gb|ACJ68111.1| pectinesterase [Brassica napus]	521	521	0	100.0	88.5	91.9	pectinesterase	gbpln	Brassica napus	AT4G02300.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr4:1009366-1013034 REVERSE LENGTH=532	521	532	0	102.1	68.1	81.2
Rsa1.0_00276.1.g10251.t1	ref|XP_002872847.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata] gi|297318684|gb|EFH49106.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata]	480	511	0	106.5	91.3	95.6	glycosyl hydrolase family 9 protein	gbpln	Arabidopsis lyrata	AT4G02290.1 | Symbols: AtGH9B13, GH9B13 | glycosyl hydrolase 9B13 | chr4:1002654-1005125 REVERSE LENGTH=516	480	516	0	107.5	90.2	95.0
Rsa1.0_00276.1.g10252.t1	ref|NP_192137.1| sucrose synthase 3 [Arabidopsis thaliana] gi|75264545|sp|Q9M111.1|SUS3_ARATH RecName: Full=Sucrose synthase 3; Short=AtSUS3; AltName: Full=Sucrose-UDP glucosyltransferase 3 gi|7268988|emb|CAB80721.1| putative sucrose synthetase [Arabidopsis thaliana] gi|15293135|gb|AAK93678.1| putative sucrose synthetase [Arabidopsis thaliana] gi|15982721|gb|AAL09730.1| AT4g02280/T2H3_8 [Arabidopsis thaliana] gi|23296413|gb|AAN13112.1| putative sucrose synthetase [Arabidopsis thaliana] gi|332656750|gb|AEE82150.1| sucrose synthase 3 [Arabidopsis thaliana]	801	809	0	101.0	92.3	96.9	sucrose synthase 3	gbpln	Arabidopsis thaliana	AT4G02280.1 | Symbols: SUS3, ATSUS3 | sucrose synthase 3 | chr4:995166-998719 FORWARD LENGTH=809	801	809	0	101.0	92.3	96.9
Rsa1.0_00276.1.g10253.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1179	1365	0	115.8	44.1	60.6	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1179	575	1.00E-61	48.8	13.5	21.6

Rsa1.0_00276.1.g10254.t8	ref|XP_002874925.1| hypothetical protein ARALYDRAFT_490346 [Arabidopsis lyrata subsp. lyrata] gi|297320762|gb|EFH51184.1| hypothetical protein ARALYDRAFT_490346 [Arabidopsis lyrata subsp. lyrata]	906	883	0	97.5	83.1	86.1	hypothetical protein ARALYDRAFT_490346	gbpln	Arabidopsis lyrata	AT4G02260.2 | Symbols: RSH1, AT-RSH1 | RELA/SPOT homolog 1 | chr4:985451-991178 FORWARD LENGTH=883	906	883	0	97.5	82.6	86.0
Rsa1.0_00276.1.g10255.t1	gb|AAT41847.1| At4g02250 [Arabidopsis thaliana]	184	184	6.00E-91	100.0	89.1	95.7	At4g02250	gbpln	Arabidopsis thaliana	AT4G02250.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:983970-984523 FORWARD LENGTH=160	184	160	9.00E-75	87.0	76.6	83.2
Rsa1.0_00276.1.g10256.t1	gb|EOA31438.1| hypothetical protein CARUB_v10014622mg [Capsella rubella]	199	210	5.00E-95	105.5	88.4	91.5	hypothetical protein CARUB_v10014622mg	gbpln	Capsella rubella	AT3G16780.1 | Symbols: | Ribosomal protein L19e family protein | chr3:5708982-5710249 FORWARD LENGTH=209	199	209	1.00E-95	105.0	86.4	89.9
Rsa1.0_00277.1.g10257.t2	gb|EOA25402.1| hypothetical protein CARUB_v10018734mg [Capsella rubella]	312	285	1.00E-77	91.3	47.1	62.2	hypothetical protein CARUB_v10018734mg	gbpln	Capsella rubella	AT4G30640.1 | Symbols: | RNI-like superfamily protein | chr4:14952670-14953682 FORWARD LENGTH=301	312	301	8.00E-76	96.5	46.8	58.0
Rsa1.0_00277.1.g10258.t1	gb|EOA33864.1| hypothetical protein CARUB_v10021355mg, partial [Capsella rubella]	397	750	2.00E-51	188.9	29.7	41.6	hypothetical protein CARUB_v10021355mg, partial	gbpln	Capsella rubella	AT1G77340.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:29068620-29069828 REVERSE LENGTH=402	397	402	2.00E-47	101.3	31.0	44.8
Rsa1.0_00277.1.g10259.t1	ref|XP_002869367.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297315203|gb|EFH45626.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	284	301	1.00E-129	106.0	77.8	87.7	F-box family protein	gbpln	Arabidopsis lyrata	AT4G30640.1 | Symbols: | RNI-like superfamily protein | chr4:14952670-14953682 FORWARD LENGTH=301	284	301	1.00E-128	106.0	75.0	86.3
Rsa1.0_00277.1.g10260.t1	gb|AAT11798.1| salt and low temperature response protein [Brassica rapa subsp. pekinensis]	74	74	2.00E-33	100.0	95.9	100.0	salt and low temperature response protein	gbpln	Brassica rapa	AT4G30650.1 | Symbols: | Low temperature and salt responsive protein family | chr4:14954403-14954698 FORWARD LENGTH=73	74	73	2.00E-31	98.6	89.2	94.6
Rsa1.0_00277.1.g10261.t1	gb|EOA15666.1| hypothetical protein CARUB_v10006167mg [Capsella rubella]	75	74	6.00E-29	98.7	85.3	94.7	hypothetical protein CARUB_v10006167mg	gbpln	Capsella rubella	AT4G30660.2 | Symbols: | Low temperature and salt responsive protein family | chr4:14955470-14955944 FORWARD LENGTH=74	75	74	2.00E-30	98.7	80.0	93.3
Rsa1.0_00277.1.g10262.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00277.1.g10263.t1	ref|XP_002871796.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317633|gb|EFH48055.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	266	277	1.00E-71	104.1	52.6	67.7	predicted protein	gbpln	Arabidopsis lyrata	AT4G29770.2 | Symbols: | Target of trans acting-siR480/255. | chr4:14575718-14577465 FORWARD LENGTH=329	266	329	5.00E-73	123.7	51.1	66.9
Rsa1.0_00277.1.g10264.t1	ref|XP_002867334.1| hypothetical protein ARALYDRAFT_353746 [Arabidopsis lyrata subsp. lyrata] gi|297313170|gb|EFH43593.1| hypothetical protein ARALYDRAFT_353746 [Arabidopsis lyrata subsp. lyrata]	791	745	0	94.2	78.6	84.3	hypothetical protein ARALYDRAFT_353746	gbpln	Arabidopsis lyrata	AT2G24050.1 | Symbols: eIFiso4G2 | MIF4G domain-containing protein / MA3 domain-containing protein | chr2:10225500-10228456 REVERSE LENGTH=747	791	747	0	94.4	66.6	76.9
Rsa1.0_00277.1.g10265.t1	ref|NP_194799.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75208664|sp|Q9SUH6.1|PP341_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g30700; AltName: Full=Protein DYW9 gi|5725434|emb|CAB52443.1| putative protein [Arabidopsis thaliana] gi|7269971|emb|CAB79788.1| putative protein [Arabidopsis thaliana] gi|332660398|gb|AEE85798.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	793	792	0	99.9	84.7	91.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G30700.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:14962617-14964995 REVERSE LENGTH=792	793	792	0	99.9	84.7	91.7
Rsa1.0_00277.1.g10266.t1	ref|NP_194800.1| uncharacterized protein [Arabidopsis thaliana] gi|5725435|emb|CAB52444.1| putative protein [Arabidopsis thaliana] gi|7269972|emb|CAB79789.1| putative protein [Arabidopsis thaliana] gi|27311861|gb|AAO00896.1| putative protein [Arabidopsis thaliana] gi|110742694|dbj|BAE99258.1| hypothetical protein [Arabidopsis thaliana] gi|332660399|gb|AEE85799.1| uncharacterized protein AT4G30710 [Arabidopsis thaliana]	646	644	0	99.7	84.8	91.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G30710.1 | Symbols: QWRF8 | Family of unknown function (DUF566) | chr4:14965538-14967881 REVERSE LENGTH=644	646	644	0	99.7	84.8	91.0

Rsa1.0_00277.1.g10267.t1	ref|XP_002867329.1| hypothetical protein ARALYDRAFT_913400 [Arabidopsis lyrata subsp. lyrata] gi|297313165|gb|EFH43588.1| hypothetical protein ARALYDRAFT_913400 [Arabidopsis lyrata subsp. lyrata]	153	157	1.00E−71	102.6	85.6	95.4	hypothetical protein ARALYDRAFT_913400	gbpln	Arabidopsis lyrata	AT4G30770.1 | Symbols: | Putative membrane lipoprotein | chr4:14986140-14986613 REVERSE LENGTH=157	153	157	3.00E−65	102.6	84.3	92.8
Rsa1.0_00277.1.g10268.t1	gb|EOA16289.1| hypothetical protein CARUB_v10004435mg [Capsella rubella]	564	586	0	103.9	86.3	91.3	hypothetical protein CARUB_v10004435mg	gbpln	Capsella rubella	AT4G30780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24100.1); Has 109 Blast hits to 109 proteins in 18 species: Archae − 0; Bacteria − 0; Metazoa − 1; Fungi − 0; Plants − 95; Viruses − 0; Other Eukaryotes − 13 (source: NCBI BLink). | chr4:14990523-14992855 FORWARD LENGTH=589	564	589	0	104.4	85.8	91.3
Rsa1.0_00277.1.g10269.t1	ref|NP_194808.1| uncharacterized protein [Arabidopsis thaliana] gi|5725443|emb|CAB52452.1| putative protein [Arabidopsis thaliana] gi|7269980|emb|CAB79797.1| putative protein [Arabidopsis thaliana] gi|332660409|gb|AEE85809.1| uncharacterized protein AT4G30790 [Arabidopsis thaliana]	1123	1148	0	102.2	87.3	93.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G30790.1 | Symbols: | INVOLVED IN: autophagy; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Autophagy-related protein 17 (InterPro:IPR007240), Autophagy-related protein 11 (InterPro:IPR019460); Has 8793 Blast hits to 6268 proteins in 570 species: Archae − 89; Bacteria − 657; Metazoa − 4844; Fungi − 808; Plants − 441; Viruses − 15; Other Eukaryotes − 1939 (source: NCBI BLink). | chr4:14993383-14997785 REVERSE LENGTH=1148	1123	1148	0	102.2	87.3	93.7
Rsa1.0_00277.1.g10270.t1	ref|XP_002869361.1| hypothetical protein ARALYDRAFT_491673 [Arabidopsis lyrata subsp. lyrata] gi|297315197|gb|EFH45620.1| hypothetical protein ARALYDRAFT_491673 [Arabidopsis lyrata subsp. lyrata]	477	479	0	100.4	84.5	90.6	hypothetical protein ARALYDRAFT_491673	gbpln	Arabidopsis lyrata	AT4G30810.1 | Symbols: scpl29 | serine carboxypeptidase-like 29 | chr4:15003474-15006017 FORWARD LENGTH=479	477	479	0	100.4	83.2	90.4
Rsa1.0_00277.1.g10271.t1	ref|NP_567854.1| carboxypeptidase D [Arabidopsis thaliana] gi|75332010|sp|Q949Q7.1|SCP29_ARATH RecName: Full=Serine carboxypeptidase-like 29; Flags: Precursor gi|15293049|gb|AAK93635.1| putative serine carboxypeptidase II [Arabidopsis thaliana] gi|22136958|gb|AAM91708.1| putative serine carboxypeptidase II [Arabidopsis thaliana] gi|332660411|gb|AEE85811.1| serine carboxypeptidase-like 29 [Arabidopsis thaliana]	472	479	0	101.5	82.6	90.0	carboxypeptidase D	gbpln	Arabidopsis thaliana	AT4G30810.1 | Symbols: scpl29 | serine carboxypeptidase-like 29 | chr4:15003474-15006017 FORWARD LENGTH=479	472	479	0	101.5	82.6	90.0
Rsa1.0_00277.1.g10272.t1	ref|XP_002869359.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315195|gb|EFH45618.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	885	906	0	102.4	84.3	91.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G30825.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:15009605-15012319 FORWARD LENGTH=904	885	904	0	102.1	81.4	88.5
Rsa1.0_00277.1.g10273.t1	ref|NP_194814.2| heptahelical transmembrane protein2 [Arabidopsis thaliana] gi|42573093|ref|NP_974643.1| heptahelical transmembrane protein2 [Arabidopsis thaliana] gi|30385618|gb|AAP23168.1| HHP2 [Arabidopsis thaliana] gi|60543323|gb|AAX22259.1| At4g30850 [Arabidopsis thaliana] gi|94442447|gb|ABF19011.1| At4g30850 [Arabidopsis thaliana] gi|332660419|gb|AEE85819.1| heptahelical transmembrane protein2 [Arabidopsis thaliana] gi|332660420|gb|AEE85820.1| heptahelical transmembrane protein2 [Arabidopsis thaliana]	362	358	1.00E−179	98.9	87.3	90.3	heptahelical transmembrane protein2	gbpln	Arabidopsis thaliana	AT4G30850.2 | Symbols: HHP2 | heptahelical transmembrane protein2 | chr4:15020540-15022278 REVERSE LENGTH=358	362	358	0	98.9	87.3	90.3
Rsa1.0_00277.1.g10274.t1	gb|AAP37971.1| seed specific protein Bn15D18B [Brassica napus]	109	109	2.00E−50	100.0	92.7	94.5	seed specific protein Bn15D18B	gbpln	Brassica napus	AT4G30880.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:15035229-15035750 FORWARD LENGTH=109	109	109	5.00E−48	100.0	82.6	90.8
Rsa1.0_00277.1.g10275.t1	gb|EOA16186.1| hypothetical protein CARUB_v10004326mg [Capsella rubella]	606	551	0	90.9	72.1	76.9	hypothetical protein CARUB_v10004326mg	gbpln	Capsella rubella	AT4G30890.3 | Symbols: UBP24 | ubiquitin-specific protease 24 | chr4:15036383-15038825 REVERSE LENGTH=551	606	551	0	90.9	70.8	75.4

Rsa1.0_00277.1.g10276.t1	ref|XP_002869355.1| hypothetical protein ARALYDRAFT_913382 [Arabidopsis lyrata subsp. lyrata] gi|297315191|gb|EFH45614.1| hypothetical protein ARALYDRAFT_913382 [Arabidopsis lyrata subsp. lyrata]	314	320	1.00E-170	101.9	91.4	95.5	hypothetical protein ARALYDRAFT_913382	gbpln	Arabidopsis lyrata	AT4G30900.2 | Symbols: | DNAse I-like superfamily protein | chr4:15040021-15042203 FORWARD LENGTH=316	314	316	1.00E-169	100.6	89.8	94.3
Rsa1.0_00277.1.g10277.t1	ref|XP_002867321.1| cytosol aminopeptidase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313157|gb|EFH43580.1| cytosol aminopeptidase family protein [Arabidopsis lyrata subsp. lyrata]	583	583	0	100.0	93.3	96.4	cytosol aminopeptidase family protein	gbpln	Arabidopsis lyrata	AT4G30920.1 | Symbols: | Cytosol aminopeptidase family protein | chr4:15046589-15049304 REVERSE LENGTH=583	583	583	0	100.0	92.8	96.1
Rsa1.0_00277.1.g10278.t4	ref|XP_002888202.1| ZCF125 [Arabidopsis lyrata subsp. lyrata] gi|297334043|gb|EFH64461.1| ZCF125 [Arabidopsis lyrata subsp. lyrata]	167	827	2.00E-50	495.2	59.9	62.3	ZCF125	gbpln	Arabidopsis lyrata	AT1G59540.1 | Symbols: ZCF125 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:21874083-21879382 FORWARD LENGTH=823	167	823	9.00E-52	492.8	58.7	61.7
Rsa1.0_00277.1.g10279.t1	ref|NP_567861.1| 50S ribosomal protein L21 [Arabidopsis thaliana] gi|29839556|sp|Q8L9A0.1|RM21_ARATH RecName: Full=50S ribosomal protein L21, mitochondrial; Flags: Precursor gi|12641613|emb|CAC27453.1| putative ribosomal protein L21 [Arabidopsis thaliana] gi|21595368|gb|AAM66095.1| unknown [Arabidopsis thaliana] gi|29028852|gb|AAO64805.1| At4g30930 [Arabidopsis thaliana] gi|110736393|dbj|BAF00165.1| hypothetical protein [Arabidopsis thaliana] gi|225898835|dbj|BAH30548.1| hypothetical protein [Arabidopsis thaliana] gi|332660431|gb|AEE85831.1| 50S ribosomal protein L21 [Arabidopsis thaliana]	259	270	1.00E-105	104.2	82.6	88.0	50S ribosomal protein L21	gbpln	Arabidopsis thaliana	AT4G30930.1 | Symbols: NFD1 | Ribosomal protein L21 | chr4:15050170-15051630 REVERSE LENGTH=270	259	270	1.00E-107	104.2	82.6	88.0
Rsa1.0_00277.1.g10280.t1	emb|CAB43840.1| hypothetical protein [Arabidopsis thaliana] gi|7269905|emb|CAB80998.1| hypothetical protein [Arabidopsis thaliana]	124	150	3.00E-14	121.0	42.7	62.1	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G30050.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf whorl, sepal, flower; EXPRESSED DURING: petal differentiation and expansion stage; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14687206-14687607 REVERSE LENGTH=133	124	133	7.00E-17	107.3	42.7	62.1
Rsa1.0_00277.1.g10281.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00277.1.g10282.t1	sp|P48627.1|FAD6C_BRANA RecName: Full=Omega-6 fatty acid desaturase, chloroplastic; Flags: Precursor gi|457631|gb|AAA50157.1| omega-6 desaturase [Brassica napus]	445	443	0	99.6	96.2	97.3	RecName: Full=Omega-6 fatty acid desaturase, chloroplastic; Flags: Precursor gi|457631|gb|AAA50157.1| omega-6 desaturase	gbpln	Brassica napus	AT4G30950.1 | Symbols: FAD6, FADC, SFD4 | fatty acid desaturase 6 | chr4:15057278-15059673 REVERSE LENGTH=448	445	448	0	100.7	91.7	95.5
Rsa1.0_00277.1.g10283.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00277.1.g10284.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00278.1.g10285.t4	ref|XP_002868324.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314160|gb|EFH44583.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	620	776	0	125.2	76.6	84.5	zinc ion binding protein	gbpln	Arabidopsis lyrata	AT4G13970.1 | Symbols: | zinc ion binding | chr4:8070696-8074134 REVERSE LENGTH=778	620	778	0	125.5	76.5	83.4
Rsa1.0_00278.1.g10286.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1463	1496	0	102.3	56.5	71.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1463	1262	1.00E-138	86.3	16.3	23.6
Rsa1.0_00278.1.g10287.t3	ref|XP_004289565.1| PREDICTED: uncharacterized protein LOC101298842 [Fragaria vesca subsp. vesca]	84	688	3.00E-25	819.0	59.5	64.3	PREDICTED: uncharacterized protein LOC101298842	gbpln	Fragaria vesca	AT1G65910.1 | Symbols: anac028, NAC028 | NAC domain containing protein 28 | chr1:24520933-24524108 REVERSE LENGTH=631	84	631	1.00E-27	751.2	58.3	64.3
Rsa1.0_00278.1.g10288.t1	gb|EOA38131.1| hypothetical protein CARUB_v10009602mg [Capsella rubella]	370	349	1.00E-177	94.3	85.4	88.6	hypothetical protein CARUB_v10009602mg	gbpln	Capsella rubella	AT1G54320.1 | Symbols: | LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein | chr1:20275732-20277793 REVERSE LENGTH=349	370	349	1.00E-177	94.3	84.9	87.6

Rsa1.0_00278.1.g10289.t1	ref|NP_201396.4| uncharacterized protein [Arabidopsis thaliana] gi|332010748|gb|AED98131.1| uncharacterized protein AT5G65950 [Arabidopsis thaliana]	1220	1190	0	97.5	82.9	88.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G65950.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1683, C-terminal (InterPro:IPR012880), Foie gras liver health family 1 (InterPro:IPR021773); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26380290-26384960 FORWARD LENGTH=1190	1220	1190	0	97.5	82.9	88.9
Rsa1.0_00278.1.g10290.t1	ref|XP_002894564.1| hypothetical protein ARALYDRAFT_474687 [Arabidopsis lyrata subsp. lyrata] gi|297340406|gb|EFH70823.1| hypothetical protein ARALYDRAFT_474687 [Arabidopsis lyrata subsp. lyrata]	378	385	1.00E-170	101.9	80.2	87.3	hypothetical protein ARALYDRAFT_474687	gbpln	Arabidopsis lyrata	AT1G56180.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G27290.1); Has 436 Blast hits to 436 proteins in 83 species: Archae - 0; Bacteria - 153; Metazoa - 0; Fungi - 0; Plants - 160; Viruses - 0; Other Eukaryotes - 123 (source: NCBI BLink). | chr1:21026243-21028047 REVERSE LENGTH=389	378	389	1.00E-172	102.9	79.4	87.6
Rsa1.0_00278.1.g10291.t1	ref|NP_176012.1| myb domain protein 72 [Arabidopsis thaliana] gi|6056369|gb|AAF02833.1|AC009894_4 Putative transcription factor [Arabidopsis thaliana] gi|12321743|gb|AAG50903.1|AC069159_4 Myb-family transcription factor, putative [Arabidopsis thaliana] gi|332195231|gb|AEE33352.1| myb domain protein 72 [Arabidopsis thaliana]	309	296	1.00E-104	95.8	68.6	78.3	myb domain protein 72	gbpln	Arabidopsis thaliana	AT1G56160.1 | Symbols: ATMYB72, MYB72 | myb domain protein 72 | chr1:21022384-21023444 FORWARD LENGTH=296	309	296	1.00E-106	95.8	68.6	78.3
Rsa1.0_00278.1.g10292.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00278.1.g10293.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00278.1.g10294.t2	ref|NP_567034.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|75163665|sp|Q93YU6.1|TRM51_ARATH RecName: Full=tRNA (guanine(37)-N1)-methyltransferase 1; AltName: Full=M1G-methyltransferase 1; AltName: Full=tRNA [GM37] methyltransferase 1; AltName: Full=tRNA methyltransferase 5 homolog 1 gi|16604635|gb|AAL24110.1| unknown protein [Arabidopsis thaliana] gi|28393917|gb|AAO42366.1| unknown protein [Arabidopsis thaliana] gi|332645959|gb|AEE79480.1| tRNA (guanine(37)-N1)-methyltransferase 1 [Arabidopsis thaliana]	270	468	3.00E-15	173.3	14.4	15.2	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT3G56120.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:20823243-20826357 FORWARD LENGTH=468	270	468	8.00E-18	173.3	14.4	15.2
Rsa1.0_00278.1.g10295.t1	ref|NP_564709.2| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|264664587|sp|C0LGH3.2|Y5614_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g56140; Flags: Precursor gi|332195227|gb|AEE33348.1| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana]	1034	1033	0	99.9	87.3	93.4	Leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT1G56140.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:21001708-21007725 REVERSE LENGTH=1033	1034	1033	0	99.9	87.3	93.4
Rsa1.0_00278.1.g10296.t9	ref|XP_002894562.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297340404|gb|EFH70821.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	1033	1031	0	99.8	80.5	88.8	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G56130.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:20994931-21000887 REVERSE LENGTH=1032	1033	1032	0	99.9	78.9	87.6
Rsa1.0_00278.1.g10297.t1	ref|XP_002894559.1| hypothetical protein ARALYDRAFT_474678 [Arabidopsis lyrata subsp. lyrata] gi|297340401|gb|EFH70818.1| hypothetical protein ARALYDRAFT_474678 [Arabidopsis lyrata subsp. lyrata]	462	522	0	113.0	81.8	84.6	hypothetical protein ARALYDRAFT_474678	gbpln	Arabidopsis lyrata	AT1G56110.1 | Symbols: NOP56 | homolog of nucleolar protein NOP56 | chr1:20984544-20986893 REVERSE LENGTH=522	462	522	0	113.0	82.0	85.1

Rsa1.0_00278.1.g10298.t1	gb|AAC26234.1| contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]	579	940	3.00E-95	162.3	31.8	40.9	contains similarity to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00278.1.g10299.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00278.1.g10300.t1	ref|NP_564708.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana] gi|21592954|gb|AAM64904.1| unknown [Arabidopsis thaliana] gi|109946435|gb|ABG48396.1| At1g56090 [Arabidopsis thaliana] gi|110738830|dbj|BAF01338.1| hypothetical protein [Arabidopsis thaliana] gi|332195220|gb|AEE33341.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	252	272	1.00E-91	107.9	75.8	86.5	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G56090.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:20977989-20979185 REVERSE LENGTH=272	252	272	3.00E-94	107.9	75.8	86.5
Rsa1.0_00278.1.g10301.t1	gb|ABA18089.1| actin-related protein 6 [Olimarabidopsis pumila]	430	423	0	98.4	83.3	89.5	actin-related protein 6	gbpln	Olimarabidopsis pumila	AT3G33520.1 | Symbols: ATARP6, ARP6, SUF3, ESD1 | actin-related protein 6 | chr3:14093791-14095476 REVERSE LENGTH=421	430	421	0	97.9	85.6	91.2
Rsa1.0_00278.1.g10302.t2	ref|XP_002891769.1| hypothetical protein ARALYDRAFT_474506 [Arabidopsis lyrata subsp. lyrata] gi|297337611|gb|EFH68028.1| hypothetical protein ARALYDRAFT_474506 [Arabidopsis lyrata subsp. lyrata]	519	508	0	97.9	76.1	79.6	hypothetical protein ARALYDRAFT_474506	gbpln	Arabidopsis lyrata	AT1G53720.1 | Symbols: ATCYP59, CYP59 | cyclophilin 59 | chr1:20057012-20059508 FORWARD LENGTH=506	519	506	0	97.5	73.6	78.4
Rsa1.0_00278.1.g10303.t1	ref|XP_002894549.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340391|gb|EFH70808.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	318	318	1.00E-153	100.0	85.5	89.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G56010.2 | Symbols: NAC1, ANAC022 | NAC domain containing protein 1 | chr1:20946852-20949144 REVERSE LENGTH=324	318	324	1.00E-154	101.9	84.6	88.7
Rsa1.0_00278.1.g10304.t4	gb|AAT38562.1| chloroplast serine acetyltransferase [Thlaspi goesingense]	326	319	1.00E-147	97.9	81.3	87.7	chloroplast serine acetyltransferase	gbpln	Thlaspi goesingense	AT1G55920.1 | Symbols: ATSERAT2;1, SAT5, SAT1, SERAT2;1 | serine acetyltransferase 2;1 | chr1:20912378-20913322 FORWARD LENGTH=314	326	314	2.33E-156	96.3	79.1	86.2
Rsa1.0_00278.1.g10305.t1	ref|XP_002891861.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297337703|gb|EFH68120.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	426	401	1.00E-176	94.1	72.5	80.0	zinc ion binding protein	gbpln	Arabidopsis lyrata	AT1G55915.1 | Symbols: | zinc ion binding | chr1:20907663-20909429 FORWARD LENGTH=404	426	404	1.00E-178	94.8	73.0	79.8
Rsa1.0_00278.1.g10306.t1	ref|NP_198562.1| uncharacterized protein [Arabidopsis thaliana] gi|10177785|dbj|BAB10967.1| unnamed protein product [Arabidopsis thaliana] gi|332006807|gb|AED94190.1| uncharacterized protein AT5G37460 [Arabidopsis thaliana]	527	622	1.00E-132	118.0	51.0	71.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G37460.1 | Symbols: | Family of unknown function (DUF577) | chr5:14858494-14860362 REVERSE LENGTH=622	527	622	1.00E-135	118.0	51.0	71.0
Rsa1.0_00278.1.g10307.t1	dbj|BAK52341.1| S9 Tyrosyl aminopeptidase [Raphanus sativus]	684	685	0	100.1	95.2	97.5	S9 Tyrosyl aminopeptidase	gbpln	Raphanus sativus	AT5G36210.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:14248202-14253272 REVERSE LENGTH=730	684	730	0	106.7	89.5	95.0
Rsa1.0_00278.1.g10308.t1	ref|NP_564703.1| zinc transporter 11 [Arabidopsis thaliana] gi|37090404|sp|Q94EG9.1|ZIP11_ARATH RecName: Full=Zinc transporter 11; AltName: Full=ZRT/IRT-like protein 11; Flags: Precursor gi|15294274|gb|AAK95314.1|AF410328_1 At1g55910/F14J16_22 [Arabidopsis thaliana] gi|18369839|gb|AAL67952.1|AF367763_1 putative metal transporter ZIP11 [Arabidopsis thaliana] gi|18369841|gb|AAL67953.1|AF367764_1 putative metal transporter ZIP11 [Arabidopsis thaliana] gi|20147287|gb|AAM10357.1| At1g55910/F14J16_22 [Arabidopsis thaliana] gi|332195197|gb|AEE33318.1| zinc transporter 11 [Arabidopsis thaliana]	326	326	1.00E-152	100.0	83.1	88.3	zinc transporter 11	gbpln	Arabidopsis thaliana	AT1G55910.1 | Symbols: ZIP11 | zinc transporter 11 precursor | chr1:20906161-20907225 FORWARD LENGTH=326	326	326	1.00E-155	100.0	83.1	88.3

Rsa1.0_00278.1.g10309.t1	ref|NP_175986.2| mitochondrial import inner membrane translocase subunit TIM50 [Arabidopsis thaliana] gi|75161466|sp|Q8VYE2.1|TIM50_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM50; AltName: Full=Protein EMBRYO DEFECTIVE 1860; Flags: Precursor gi|18175981|gb|AAL59962.1| unknown protein [Arabidopsis thaliana] gi|21689895|gb|AAM67508.1| unknown protein [Arabidopsis thaliana] gi|332195195|gb|AEE33316.1| mitochondrial import inner membrane translocase subunit TIM50 [Arabidopsis thaliana]	381	376	1.00E-148	98.7	75.6	82.4	mitochondrial import inner membrane translocase subunit TIM50	gbpln	Arabidopsis thaliana	AT1G55900.1 | Symbols: TIM50, emb1860 | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:20903163-20905420 FORWARD LENGTH=376	381	376	1.00E-151	98.7	75.6	82.4
Rsa1.0_00278.1.g10310.t1	gb|EOA36706.1| hypothetical protein CARUB_v10012240mg [Capsella rubella]	728	732	0	100.5	81.6	88.7	hypothetical protein CARUB_v10012240mg	gbpln	Capsella rubella	AT1G55850.1 | Symbols: ATCSLE1, CSLE1 | cellulose synthase like E1 | chr1:20876752-20879414 FORWARD LENGTH=729	728	729	0	100.1	82.7	90.1
Rsa1.0_00278.1.g10311.t2	ref|NP_175980.1| sec.4-like phosphatidylinositol transfer protein [Arabidopsis thaliana] gi|16930447|gb|AAL31909.1|AF419577_1 At1g55840/F14J16_2 [Arabidopsis thaliana] gi|19310517|gb|AAL84992.1| At1g55840/F14J16_2 [Arabidopsis thaliana] gi|332195185|gb|AEE33306.1| sec.4-like phosphatidylinositol transfer protein [Arabidopsis thaliana]	328	325	1.00E-175	99.1	89.9	94.8	sec.4-like phosphatidylinositol transfer protein	gbpln	Arabidopsis thaliana	AT1G55840.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:20873891-20876018 FORWARD LENGTH=325	328	325	1.00E-177	99.1	89.9	94.8
Rsa1.0_00278.1.g10312.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	640	1274	3.00E-88	199.1	23.4	31.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	ATMG01250.1 | Symbols: ORF102 | RNA-directed DNA polymerase (reverse transcriptase) | chrM:310514-310882 FORWARD LENGTH=122	640	122	9.00E-24	19.1	7.7	8.8
Rsa1.0_00278.1.g10313.t1	gb|EOA40331.1| hypothetical protein CARUB_v10009058mg [Capsella rubella]	444	466	0	105.0	93.7	95.7	hypothetical protein CARUB_v10009058mg	gbpln	Capsella rubella	AT1G55810.3 | Symbols: UKL3 | uridine kinase-like 3 | chr1:20861273-20864003 FORWARD LENGTH=466	444	466	0	105.0	93.9	96.6
Rsa1.0_00278.1.g10314.t1	ref|NP_564702.2| BolA-like-like protein [Arabidopsis thaliana] gi|51968914|dbj|BAD43149.1| BolA like protein [Arabidopsis thaliana] gi|332195178|gb|AEE33299.1| BolA-like-like protein [Arabidopsis thaliana]	161	160	9.00E-59	99.4	79.5	85.1	BolA-like-like protein	gbpln	Arabidopsis thaliana	AT1G55805.1 | Symbols: | BolA-like family protein | chr1:20858956-20859438 REVERSE LENGTH=160	161	160	3.00E-61	99.4	79.5	85.1
Rsa1.0_00278.1.g10315.t1	ref|XP_002894530.1| hypothetical protein ARALYDRAFT_892585 [Arabidopsis lyrata subsp. lyrata] gi|297340372|gb|EFH70789.1| hypothetical protein ARALYDRAFT_892585 [Arabidopsis lyrata subsp. lyrata]	492	480	5.00E-60	97.6	30.1	35.2	hypothetical protein ARALYDRAFT_892585	gbpln	Arabidopsis lyrata	AT1G55790.1 | Symbols: | Domain of unknown function (DUF2431) | chr1:20852685-20856069 REVERSE LENGTH=515	492	515	3.00E-40	104.7	16.7	20.9
Rsa1.0_00278.1.g10316.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00278.1.g10317.t1	ref|NP_564700.2| uncharacterized protein [Arabidopsis thaliana] gi|332195175|gb|AEE33296.1| uncharacterized protein AT1G55790 [Arabidopsis thaliana]	152	515	9.00E-44	338.8	63.2	75.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G55790.1 | Symbols: | Domain of unknown function (DUF2431) | chr1:20852685-20856069 REVERSE LENGTH=515	152	515	3.00E-46	338.8	63.2	75.7
Rsa1.0_00278.1.g10318.t1	ref|XP_002894528.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297340370|gb|EFH70787.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	175	175	5.00E-63	100.0	76.0	86.9	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT1G55770.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:20851039-20851566 REVERSE LENGTH=175	175	175	2.00E-61	100.0	72.6	84.0
Rsa1.0_00278.1.g10319.t1	ref|NP_175972.1| BTB/POZ domain-containing protein [Arabidopsis thaliana] gi|75271590|sp|Q680K8.1|Y1576_ARATH RecName: Full=BTB/POZ domain-containing protein At1g55760 gi|51969392|dbj|BAD43388.1| unknown protein [Arabidopsis thaliana] gi|51969860|dbj|BAD43622.1| unknown protein [Arabidopsis thaliana] gi|63147370|gb|AAY34158.1| At1g55760 [Arabidopsis thaliana] gi|332195173|gb|AEE33294.1| BTB/POZ domain-containing protein [Arabidopsis thaliana]	329	329	1.00E-180	100.0	90.9	97.0	BTB/POZ domain-containing protein	gbpln	Arabidopsis thaliana	AT1G55760.1 | Symbols: | BTB/POZ domain-containing protein | chr1:20847117-20848507 REVERSE LENGTH=329	329	329	0	100.0	90.9	97.0

Rsa1.0_00278.1.g10320.t1	gb|EOA23321.1| hypothetical protein CARUB_v10019219mg [Capsella rubella]	437	444	1.00E-116	101.6	53.1	62.9	hypothetical protein CARUB_v10019219mg	gbpln	Capsella rubella	AT2G40920.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17072586-17074012 REVERSE LENGTH=436	437	436	9.00E-72	99.8	38.2	51.9
Rsa1.0_00278.1.g10321.t3	gb|AAD48963.1|AF147263_5 contains similarity to transposases [Arabidopsis thaliana] gi|7267311|emb|CAB81093.1| AT4g05510 [Arabidopsis thaliana]	592	604	0	102.0	58.8	72.1	contains similarity to transposases	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	592	696	3.00E-47	117.6	19.8	33.1
Rsa1.0_00279.1.g10322.t1	dbj|BAJ33681.1| unnamed protein product [Thellungiella halophila]	491	502	0	102.2	85.9	92.1	unnamed protein product	----	----	AT3G18490.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:6349090-6350592 REVERSE LENGTH=500	491	500	0	101.8	81.5	90.8
Rsa1.0_00279.1.g10323.t1	gb|EOA30478.1| hypothetical protein CARUB_v10013601mg [Capsella rubella]	449	477	0	106.2	83.3	90.4	hypothetical protein CARUB_v10013601mg	gbpln	Capsella rubella	AT3G18500.3 | Symbols: | DNAse I-like superfamily protein | chr3:6352544-6355297 FORWARD LENGTH=449	449	449	0	100.0	78.8	87.3
Rsa1.0_00279.1.g10324.t1	ref|NP_188480.1| uncharacterized protein [Arabidopsis thaliana] gi|26450999|dbj|BAC42606.1| unknown protein [Arabidopsis thaliana] gi|28416737|gb|AAO42899.1| At3g18510 [Arabidopsis thaliana] gi|332642587|gb|AEE76108.1| uncharacterized protein AT3G18510 [Arabidopsis thaliana]	67	67	3.00E-26	100.0	86.6	92.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G18510.1 | Symbols: | unknown protein; Has 15 Blast hits to 15 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 15; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6355711-6355984 FORWARD LENGTH=67	67	67	5.00E-29	100.0	86.6	92.5
Rsa1.0_00279.1.g10325.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00279.1.g10326.t2	ref|NP_001185366.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|332196988|gb|AEE35109.1| protein kinase domain-containing protein [Arabidopsis thaliana]	207	425	7.00E-51	205.3	46.4	52.7	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G70740.2 | Symbols: | Protein kinase superfamily protein | chr1:26673847-26675651 REVERSE LENGTH=425	207	425	2.00E-53	205.3	46.4	52.7
Rsa1.0_00279.1.g10327.t2	gb|EOA30252.1| hypothetical protein CARUB_v10013374mg [Capsella rubella]	541	556	0	102.8	86.3	93.2	hypothetical protein CARUB_v10013374mg	gbpln	Capsella rubella	AT3G18520.1 | Symbols: HDA15, ATHDA15 | histone deacetylase 15 | chr3:6361605-6365367 FORWARD LENGTH=552	541	552	0	102.0	86.0	93.7
Rsa1.0_00279.1.g10328.t1	ref|XP_002883140.1| hypothetical protein ARALYDRAFT_898225 [Arabidopsis lyrata subsp. lyrata] gi|297328980|gb|EFH59399.1| hypothetical protein ARALYDRAFT_898225 [Arabidopsis lyrata subsp. lyrata]	169	195	4.00E-41	115.4	62.7	73.4	hypothetical protein ARALYDRAFT_898225	gbpln	Arabidopsis lyrata	AT3G18560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49000.1); Has 95 Blast hits to 95 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 95; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6393984-6394571 FORWARD LENGTH=195	169	195	2.00E-40	115.4	59.8	71.6
Rsa1.0_00279.1.g10329.t1	gb|EOA33015.1| hypothetical protein CARUB_v10016346mg [Capsella rubella]	165	166	1.00E-61	100.6	78.8	88.5	hypothetical protein CARUB_v10016346mg	gbpln	Capsella rubella	AT3G18570.1 | Symbols: | Oleosin family protein | chr3:6396072-6396572 REVERSE LENGTH=166	165	166	2.00E-63	100.6	78.8	87.9
Rsa1.0_00279.1.g10330.t1	ref|NP_188488.1| single-strand DNA-binding protein [Arabidopsis thaliana] gi|9294319|dbj|BAB02216.1| unnamed protein product [Arabidopsis thaliana] gi|332642598|gb|AEE76119.1| single-strand DNA-binding protein [Arabidopsis thaliana]	216	217	2.00E-96	100.5	85.2	90.7	single-strand DNA-binding protein	gbpln	Arabidopsis thaliana	AT3G18580.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr3:6396940-6398068 REVERSE LENGTH=217	216	217	7.00E-99	100.5	85.2	90.7
Rsa1.0_00279.1.g10331.t1	gb|ABL97946.1| copper ion binding/electron transporter [Brassica rapa]	188	203	5.00E-66	108.0	75.5	85.1	copper ion binding/electron transporter	gbpln	Brassica rapa	AT3G18590.1 | Symbols: ENODL5, AtENODL5 | early nodulin-like protein 5 | chr3:6398670-6399337 FORWARD LENGTH=188	188	188	4.00E-65	100.0	76.6	86.2
Rsa1.0_00279.1.g10332.t1	ref|NP_188490.1| DEAD-box ATP-dependent RNA helicase 51 [Arabidopsis thaliana] gi|75335038|sp|Q9LIH9.1|RH51_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 51 gi|9294321|dbj|BAB02218.1| DEAD-box ATP-dependent RNA helicase [Arabidopsis thaliana] gi|17979083|gb|AAL49809.1| putative DEAD box helicase protein [Arabidopsis thaliana] gi|20465335|gb|AAM20071.1| putative DEAD box helicase protein [Arabidopsis thaliana] gi|332642600|gb|AEE76121.1| DEAD-box ATP-dependent RNA helicase 51 [Arabidopsis thaliana]	742	568	0	76.5	63.1	68.9	DEAD-box ATP-dependent RNA helicase 51	gbpln	Arabidopsis thaliana	AT3G18600.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:6399724-6403007 REVERSE LENGTH=568	742	568	0	76.5	63.1	68.9

<table>
<tr><td>Rsa1.0_00279.1.g10333.t2</td><td>ref|NP_188491.1| nucleolin [Arabidopsis thaliana] gi|122225307|sp|Q1PEP5.1|NUCL2_ARATH RecName: Full=Nucleolin 2; AltName: Full=Protein NUCLEOLIN LIKE 2; Short=AtNUC-L2; AltName: Full=Protein PARALLEL LIKE 1; Short=AtPARLL1 gi|91806437|gb|ABE65946.1| nucleolin [Arabidopsis thaliana] gi|332642601|gb|AEE76122.1| nucleolin like 2 [Arabidopsis thaliana]</td><td>597</td><td>636</td><td>6.00E-78</td><td>106.5</td><td>56.6</td><td>69.0</td><td>nucleolin</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G18610.1 | Symbols: PARLL1, ATNUC-L2, NUC-L2 | nucleolin like 2 | chr3:6404270-6407822 REVERSE LENGTH=636</td><td>597</td><td>636</td><td>2.00E-80</td><td>106.5</td><td>56.6</td><td>69.0</td></tr>
<tr><td>Rsa1.0_00279.1.g10334.t3</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00279.1.g10335.t2</td><td>gb|EOA13744.1| hypothetical protein CARUB_v10026820mg [Capsella rubella]</td><td>115</td><td>310</td><td>5.00E-33</td><td>269.6</td><td>72.2</td><td>80.9</td><td>hypothetical protein CARUB_v10026820mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G08640.2 | Symbols: FLS1 | flavonol synthase 1 | chr5:2804009-2805175 FORWARD LENGTH=336</td><td>115</td><td>336</td><td>3.00E-23</td><td>292.2</td><td>53.0</td><td>69.6</td></tr>
<tr><td>Rsa1.0_00279.1.g10336.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00279.1.g10337.t1</td><td>ref|XP_002874638.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297320475|gb|EFH50897.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>231</td><td>230</td><td>5.00E-66</td><td>99.6</td><td>64.5</td><td>72.7</td><td>PHD finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G10600.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr4:6547934-6548647 REVERSE LENGTH=237</td><td>231</td><td>237</td><td>4.00E-67</td><td>102.6</td><td>63.2</td><td>71.0</td></tr>
<tr><td>Rsa1.0_00279.1.g10338.t1</td><td>gb|EOA30017.1| hypothetical protein CARUB_v10013117mg [Capsella rubella]</td><td>314</td><td>686</td><td>3.00E-55</td><td>218.5</td><td>41.7</td><td>56.4</td><td>hypothetical protein CARUB_v10013117mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G18610.1 | Symbols: PARLL1, ATNUC-L2, NUC-L2 | nucleolin like 2 | chr3:6404270-6407822 REVERSE LENGTH=636</td><td>314</td><td>636</td><td>5.00E-55</td><td>202.5</td><td>41.1</td><td>55.7</td></tr>
<tr><td>Rsa1.0_00279.1.g10339.t1</td><td>ref|NP_188492.2| putative S-acyltransferase [Arabidopsis thaliana] gi|75273387|sp|Q9LIH7.1|ZDHC7_ARATH RecName: Full=Probable S-acyltransferase At3g18620; AltName: Full=Probable palmitoyltransferase At3g18620; AltName: Full=Zinc finger DHHC domain-containing protein At3g18620 gi|9294323|dbj|BAB02220.1| unnamed protein product [Arabidopsis thaliana] gi|19424025|gb|AAL87266.1| unknown protein [Arabidopsis thaliana] gi|21281223|gb|AAM45051.1| unknown protein [Arabidopsis thaliana] gi|332642602|gb|AEE76123.1| putative S-acyltransferase [Arabidopsis thaliana]</td><td>390</td><td>345</td><td>1.00E-174</td><td>88.5</td><td>74.9</td><td>80.8</td><td>putative S-acyltransferase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G18620.1 | Symbols: | DHHC-type zinc finger family protein | chr3:6408849-6410716 FORWARD LENGTH=345</td><td>390</td><td>345</td><td>1.00E-176</td><td>88.5</td><td>74.9</td><td>80.8</td></tr>
<tr><td>Rsa1.0_00279.1.g10340.t1</td><td>ref|XP_002885267.1| uracil DNA glycosylase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331107|gb|EFH61526.1| uracil DNA glycosylase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>327</td><td>329</td><td>1.00E-154</td><td>100.6</td><td>85.3</td><td>90.8</td><td>uracil DNA glycosylase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G18630.1 | Symbols: ATUNG, UNG | uracil dna glycosylase | chr3:6411325-6413002 REVERSE LENGTH=330</td><td>327</td><td>330</td><td>1.00E-154</td><td>100.9</td><td>83.8</td><td>89.9</td></tr>
<tr><td>Rsa1.0_00279.1.g10341.t1</td><td>ref|NP_188495.1| protein agamous-like 103 [Arabidopsis thaliana] gi|9293888|dbj|BAB01791.1| unnamed protein product [Arabidopsis thaliana] gi|119360153|gb|ABL66805.1| At3g18650 [Arabidopsis thaliana] gi|332642605|gb|AEE76126.1| protein agamous-like 103 [Arabidopsis thaliana]</td><td>370</td><td>386</td><td>9.00E-81</td><td>104.3</td><td>51.4</td><td>62.7</td><td>protein agamous-like 103</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G18650.1 | Symbols: AGL103 | AGAMOUS-like 103 | chr3:6417344-6418504 REVERSE LENGTH=386</td><td>370</td><td>386</td><td>2.00E-83</td><td>104.3</td><td>51.4</td><td>62.7</td></tr>
<tr><td>Rsa1.0_00279.1.g10342.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>356</td><td>1274</td><td>8.00E-49</td><td>357.9</td><td>30.9</td><td>46.3</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>356</td><td>303</td><td>7.00E-48</td><td>85.1</td><td>32.6</td><td>45.8</td></tr>
<tr><td>Rsa1.0_00279.1.g10343.t1</td><td>ref|XP_002885271.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331111|gb|EFH61530.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>632</td><td>605</td><td>0</td><td>95.7</td><td>81.3</td><td>86.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G18670.1 | Symbols: | Ankyrin repeat family protein | chr3:6424135-6426471 REVERSE LENGTH=598</td><td>632</td><td>598</td><td>0</td><td>94.6</td><td>78.0</td><td>83.1</td></tr>
<tr><td>Rsa1.0_00280.1.g10344.t1</td><td>ref|XP_002871027.1| hypothetical protein ARALYDRAFT_487104 [Arabidopsis lyrata subsp. lyrata] gi|297316864|gb|EFH47286.1| hypothetical protein ARALYDRAFT_487104 [Arabidopsis lyrata subsp. lyrata]</td><td>345</td><td>350</td><td>1.00E-160</td><td>101.4</td><td>84.3</td><td>91.6</td><td>hypothetical protein ARALYDRAFT_487104</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G03330.2 | Symbols: | Cysteine proteinases superfamily protein | chr5:807728-809608 FORWARD LENGTH=356</td><td>345</td><td>356</td><td>1.00E-159</td><td>103.2</td><td>85.5</td><td>93.0</td></tr>
<tr><td>Rsa1.0_00280.1.g10345.t1</td><td>gb|EOA20730.1| hypothetical protein CARUB_v10001049mg [Capsella rubella]</td><td>424</td><td>420</td><td>0</td><td>99.1</td><td>84.7</td><td>91.0</td><td>hypothetical protein CARUB_v10001049mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G03320.1 | Symbols: | Protein kinase superfamily protein | chr5:802759-804242 FORWARD LENGTH=420</td><td>424</td><td>420</td><td>0</td><td>99.1</td><td>82.5</td><td>89.2</td></tr>
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Rsa1.0_00280.1.g10346.t1	ref|NP_195951.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|7378611|emb|CAB83287.1| putative protein [Arabidopsis thaliana] gi|9757782|dbj|BAB08391.1| unnamed protein product [Arabidopsis thaliana] gi|45752614|gb|AAS76205.1| At5g03310 [Arabidopsis thaliana] gi|52218822|gb|AAU29481.1| At5g03310 [Arabidopsis thaliana] gi|332003200|gb|AED90583.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	106	114	7.00E-47	107.5	87.7	91.5	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT5G03310.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:799302-799646 REVERSE LENGTH=114	106	114	1.00E-49	107.5	87.7	91.5
Rsa1.0_00280.1.g10347.t1	gb|EOA20984.1| hypothetical protein CARUB_v10001331mg [Capsella rubella]	345	345	0	100.0	97.4	99.1	hypothetical protein CARUB_v10001331mg	gbpln	Capsella rubella	AT5G03300.1 | Symbols: ADK2 | adenosine kinase 2 | chr5:796573-798997 FORWARD LENGTH=345	345	345	0	100.0	97.1	99.1
Rsa1.0_00280.1.g10348.t1	ref|XP_002871023.1| hypothetical protein ARALYDRAFT_487101 [Arabidopsis lyrata subsp. lyrata] gi|297316860|gb|EFH47282.1| hypothetical protein ARALYDRAFT_487101 [Arabidopsis lyrata subsp. lyrata]	335	373	1.00E-178	111.3	94.6	96.7	hypothetical protein ARALYDRAFT_487101	gbpln	Arabidopsis lyrata	AT5G03290.1 | Symbols: IDH-V | isocitrate dehydrogenase V | chr5:794043-795939 FORWARD LENGTH=374	335	374	1.00E-176	111.6	94.3	97.3
Rsa1.0_00280.1.g10349.t1	dbj|BAJ33707.1| unnamed protein product [Thellungiella halophila]	1380	1297	0	94.0	84.7	89.1	unnamed protein product	----	----	AT5G03280.1 | Symbols: EIN2, PIR2, CKR1, ERA3, ORE3, ORE2, ATEIN2 | NRAMP metal ion transporter family protein | chr5:788589-793066 FORWARD LENGTH=1294	1380	1294	0	93.8	82.2	86.9
Rsa1.0_00280.1.g10350.t1	gb|EOA20218.1| hypothetical protein CARUB_v10000520mg, partial [Capsella rubella]	561	598	0	106.6	94.1	97.1	hypothetical protein CARUB_v10000520mg, partial	gbpln	Capsella rubella	AT5G03260.1 | Symbols: LAC11 | laccase 11 | chr5:777198-779338 REVERSE LENGTH=557	561	557	0	99.3	92.3	95.7
Rsa1.0_00280.1.g10351.t1	ref|NP_195945.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana] gi|75264441|sp|Q9LYW0.1|Y5325_ARATH RecName: Full=BTB/POZ domain-containing protein At5g03250 gi|7413602|emb|CAB86092.1| photoreceptor-interacting protein-like [Arabidopsis thaliana] gi|9757776|dbj|BAB08385.1| non-phototropic hypocotyl-like protein [Arabidopsis thaliana] gi|110741901|dbj|BAE98892.1| photoreceptor-interacting like protein [Arabidopsis thaliana] gi|332003194|gb|AED90577.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana]	586	592	0	101.0	88.2	93.5	Phototropic-responsive NPH3 family protein	gbpln	Arabidopsis thaliana	AT5G03250.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr5:774591-776855 FORWARD LENGTH=592	586	592	0	101.0	88.2	93.5
Rsa1.0_00280.1.g10352.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00280.1.g10353.t1	gb|EOA20766.1| hypothetical protein CARUB_v10001095mg, partial [Capsella rubella]	382	407	0	106.5	100.0	100.0	hypothetical protein CARUB_v10001095mg, partial	gbpln	Capsella rubella	AT5G20620.1 | Symbols: UBQ4 | ubiquitin 4 | chr5:6973315-6974463 REVERSE LENGTH=382	382	382	0	100.0	100.0	100.0
Rsa1.0_00280.1.g10354.t1	gb|EOA21689.1| hypothetical protein CARUB_v10002114mg [Capsella rubella]	177	169	4.00E-62	95.5	77.4	84.2	hypothetical protein CARUB_v10002114mg	gbpln	Capsella rubella	AT5G03230.1 | Symbols: | Protein of unknown function, DUF584 | chr5:769636-770136 FORWARD LENGTH=166	177	166	2.00E-59	93.8	75.1	82.5

Rsa1.0_00280.1.g10355.t1	ref|NP_001078525.1| Mediator complex, subunit Med7 [Arabidopsis thaliana] gi|145357596|ref|NP_195970.2| Mediator complex, subunit Med7 [Arabidopsis thaliana] gi|334187401|ref|NP_001190215.1| Mediator complex, subunit Med7 [Arabidopsis thaliana] gi|75181253|sp|Q9LZD7.1|MED7B_ARATH RecName: Full=Mediator of RNA polymerase II transcription subunit 7b gi|7378634|emb|CAB83310.1| transcriptional co-activator-like protein [Arabidopsis thaliana] gi|19715581|gb|AAL91616.1| At5g03505/C320EPL23M [Arabidopsis thaliana] gi|20453355|gb|AAM19916.1| At5g03505/C320EPL23M [Arabidopsis thaliana] gi|222424056|dbj|BAH19989.1| AT5G03500 [Arabidopsis thaliana] gi|332003230|gb|AED90613.1| Mediator complex, subunit Med7 [Arabidopsis thaliana] gi|332003231|gb|AED90614.1| Mediator complex, subunit Med7 [Arabidopsis thaliana] gi|332003232|gb|AED90615.1| Mediator complex, subunit Med7 [Arabidopsis thaliana]	202	168	2.00E-58	83.2	66.8	71.8	Mediator complex, subunit Med7	gbpln	Arabidopsis thaliana	AT5G03500.3 | Symbols: | Mediator complex, subunit Med7 | chr5:876673-877660 REVERSE LENGTH=168	202	168	8.00E-61	83.2	66.8	71.8
Rsa1.0_00280.1.g10356.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00280.1.g10357.t1	ref|XP_002873081.1| hypothetical protein ARALYDRAFT_908186 [Arabidopsis lyrata subsp. lyrata] gi|297318918|gb|EFH49340.1| hypothetical protein ARALYDRAFT_908186 [Arabidopsis lyrata subsp. lyrata]	136	65	1.00E-15	47.8	30.1	35.3	hypothetical protein ARALYDRAFT_908186	gbpln	Arabidopsis lyrata	AT5G03210.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 7 growth stages; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:763070-763258 REVERSE LENGTH=62	136	62	1.00E-15	45.6	27.9	30.9
Rsa1.0_00280.1.g10358.t8	ref|NP_195940.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|75311709|sp|Q9LYW5.1|LUL1_ARATH RecName: Full=Probable E3 ubiquitin-protein ligase LUL1; AltName: Full=Protein LOG2-LIKE UBIQUITIN LIGASE 1; AltName: Full=RING finger protein 370 gi|7413597|emb|CAB86087.1| putative protein [Arabidopsis thaliana] gi|9757771|dbj|BAB08380.1| RING zinc finger protein-like [Arabidopsis thaliana] gi|108385412|gb|ABF85785.1| At5g03200 [Arabidopsis thaliana] gi|332003186|gb|AED90569.1| probable E3 ubiquitin-protein ligase LUL1 [Arabidopsis thaliana]	334	337	8.00E-87	100.9	57.5	68.6	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G03200.1 | Symbols: | RING/U-box superfamily protein | chr5:760450-761667 REVERSE LENGTH=337	334	337	2.00E-89	100.9	57.5	68.6
Rsa1.0_00280.1.g10359.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00280.1.g10360.t1	gb|EOA20532.1| hypothetical protein CARUB_v10000846mg [Capsella rubella]	484	482	0	99.6	84.3	87.8	hypothetical protein CARUB_v10000846mg	gbpln	Capsella rubella	AT5G03160.1 | Symbols: ATP58IPK, P58IPK | homolog of mamallian P58IPK | chr5:750286-752671 FORWARD LENGTH=482	484	482	0	99.6	86.0	90.3
Rsa1.0_00280.1.g10361.t1	ref|XP_002871015.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297316852|gb|EFH47274.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	513	505	0	98.4	87.9	90.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G03150.1 | Symbols: JKD | C2H2-like zinc finger protein | chr5:745849-748678 FORWARD LENGTH=503	513	503	0	98.1	88.1	91.4
Rsa1.0_00280.1.g10362.t1	ref|NP_195928.1| dolichyldiphosphatase [Arabidopsis thaliana] gi|38564298|gb|AAR23728.1| At5g03080 [Arabidopsis thaliana] gi|46402486|gb|AAS92345.1| At5g03080 [Arabidopsis thaliana] gi|110737805|dbj|BAF00841.1| hypothetical protein [Arabidopsis thaliana] gi|332003171|gb|AED90554.1| lipid phosphate phosphatase gamma [Arabidopsis thaliana]	296	226	8.00E-23	76.4	18.6	19.9	dolichyldiphosphatase	gbpln	Arabidopsis thaliana	AT5G03080.1 | Symbols: | Phosphatidic acid phosphatase (PAP2) family protein | chr5:721976-722656 FORWARD LENGTH=226	296	226	2.00E-25	76.4	18.6	19.9

Rsa1.0_00280.1.g10363.t1	ref|XP_002870990.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316827|gb|EFH47249.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	496	468	9.00E-99	94.4	47.4	58.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G02700.1 | Symbols: | F-box/RNI-like superfamily protein | chr5:609381-611679 REVERSE LENGTH=456	496	456	1.00E-100	91.9	45.8	58.9
Rsa1.0_00280.1.g10364.t1	ref|XP_002877865.1| hypothetical protein ARALYDRAFT_906617 [Arabidopsis lyrata subsp. lyrata] gi|297323703|gb|EFH54124.1| hypothetical protein ARALYDRAFT_906617 [Arabidopsis lyrata subsp. lyrata]	326	345	5.00E-82	105.8	54.6	68.1	hypothetical protein ARALYDRAFT_906617	gbpln	Arabidopsis lyrata	AT1G20320.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:7033846-7034874 REVERSE LENGTH=342	326	342	4.00E-38	104.9	30.4	48.2
Rsa1.0_00280.1.g10365.t1	ref|XP_002877864.1| hypothetical protein ARALYDRAFT_906616 [Arabidopsis lyrata subsp. lyrata] gi|297323702|gb|EFH54123.1| hypothetical protein ARALYDRAFT_906616 [Arabidopsis lyrata subsp. lyrata]	274	284	2.00E-89	103.6	65.3	74.5	hypothetical protein ARALYDRAFT_906616	gbpln	Arabidopsis lyrata	AT2G04930.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:1733638-1734471 REVERSE LENGTH=277	274	277	3.00E-44	101.1	42.0	56.9
Rsa1.0_00280.1.g10366.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00280.1.g10367.t1	ref|XP_002877865.1| hypothetical protein ARALYDRAFT_906617 [Arabidopsis lyrata subsp. lyrata] gi|297323703|gb|EFH54124.1| hypothetical protein ARALYDRAFT_906617 [Arabidopsis lyrata subsp. lyrata]	315	345	4.00E-82	109.5	54.9	68.9	hypothetical protein ARALYDRAFT_906617	gbpln	Arabidopsis lyrata	AT1G20320.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:7033846-7034874 REVERSE LENGTH=342	315	342	1.00E-33	108.6	30.2	45.7
Rsa1.0_00280.1.g10368.t2	ref|XP_002865011.1| hypothetical protein ARALYDRAFT_496871 [Arabidopsis lyrata subsp. lyrata] gi|297310846|gb|EFH41270.1| hypothetical protein ARALYDRAFT_496871 [Arabidopsis lyrata subsp. lyrata]	222	403	1.00E-39	181.5	37.8	39.6	hypothetical protein ARALYDRAFT_496871	gbpln	Arabidopsis lyrata	AT5G67290.1 | Symbols: | FAD-dependent oxidoreductase family protein | chr5:26848419-26849755 REVERSE LENGTH=406	222	406	6.00E-42	182.9	37.8	39.6
Rsa1.0_00280.1.g10369.t1	ref|XP_002877864.1| hypothetical protein ARALYDRAFT_906616 [Arabidopsis lyrata subsp. lyrata] gi|297323702|gb|EFH54123.1| hypothetical protein ARALYDRAFT_906616 [Arabidopsis lyrata subsp. lyrata]	275	284	1.00E-100	103.3	70.2	79.3	hypothetical protein ARALYDRAFT_906616	gbpln	Arabidopsis lyrata	AT2G04930.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:1733638-1734471 REVERSE LENGTH=277	275	277	2.00E-46	100.7	43.6	57.1
Rsa1.0_00280.1.g10370.t1	ref|NP_195927.2| importin alpha isoform 9 [Arabidopsis thaliana] gi|332003170|gb|AED90553.1| importin alpha isoform 9 [Arabidopsis thaliana]	408	519	1.00E-179	127.2	81.1	86.3	importin alpha isoform 9	gbpln	Arabidopsis thaliana	AT5G03070.1 | Symbols: IMPA-9 | importin alpha isoform 9 | chr5:718468-721395 REVERSE LENGTH=519	408	519	0	127.2	81.1	86.3
Rsa1.0_00280.1.g10371.t1	ref|XP_002873074.1| hypothetical protein ARALYDRAFT_487079 [Arabidopsis lyrata subsp. lyrata] gi|297318911|gb|EFH49333.1| hypothetical protein ARALYDRAFT_487079 [Arabidopsis lyrata subsp. lyrata]	244	292	5.00E-22	119.7	36.9	53.3	hypothetical protein ARALYDRAFT_487079	gbpln	Arabidopsis lyrata	AT5G03060.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11100.2); Has 14506 Blast hits to 10808 proteins in 1083 species: Archae - 280; Bacteria - 2737; Metazoa - 4707; Fungi - 940; Plants - 571; Viruses - 106; Other Eukaryotes - 5165 (source: NCBI BLink). | chr5:716722-717678 REVERSE LENGTH=292	244	292	3.00E-23	119.7	38.1	53.3
Rsa1.0_00281.1.g10372.t2	ref|NP_187424.1| rubisco methyltransferase-like protein [Arabidopsis thaliana] gi|6466950|gb|AAF13085.1|AC009176_12 putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Arabidopsis thaliana] gi|6648179|gb|AAF21177.1|AC013483_1 putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Arabidopsis thaliana] gi|15028205|gb|AAK76599.1| putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Arabidopsis thaliana] gi|19310671|gb|AAL85066.1| putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Arabidopsis thaliana] gi|332641064|gb|AEE74585.1| rubisco methyltransferase-like protein [Arabidopsis thaliana]	121	504	1.00E-20	416.5	53.7	60.3	rubisco methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT3G07670.1 | Symbols: | Rubisco methyltransferase family protein | chr3:2451651-2454617 FORWARD LENGTH=504	121	504	2.00E-23	416.5	53.7	60.3
Rsa1.0_00281.1.g10373.t3	gb|EOA17249.1| hypothetical protein CARUB_v10005523mg [Capsella rubella]	261	262	1.00E-137	100.4	94.6	98.5	hypothetical protein CARUB_v10005523mg	gbpln	Capsella rubella	AT4G34670.1 | Symbols: | Ribosomal protein S3Ae | chr4:16548724-16550222 FORWARD LENGTH=262	261	262	1.00E-137	100.4	93.5	96.9

Rsa1.0_00281.1.g10374.t1	dbj|BAJ33857.1| unnamed protein product [Thellungiella halophila]	263	269	1.00E-122	102.3	87.1	91.3	unnamed protein product	----	----	AT4G34680.2 | Symbols: GATA3 | GATA transcription factor 3 | chr4:16553700-16554610 FORWARD LENGTH=269	263	269	1.00E-110	102.3	81.0	87.5
Rsa1.0_00281.1.g10375.t1	gb|EOA17609.1| hypothetical protein CARUB_v10005980mg, partial [Capsella rubella]	117	140	2.00E-61	119.7	95.7	99.1	hypothetical protein CARUB_v10005980mg, partial	gbpln	Capsella rubella	AT4G34700.1 | Symbols: CIB22, AtCIB22 | LYR family of Fe/S cluster biogenesis protein | chr4:16556874-16558362 FORWARD LENGTH=117	117	117	9.00E-64	100.0	96.6	98.3
Rsa1.0_00281.1.g10376.t1	gb|AAF26435.1| arginine decarboxylase [Brassica juncea]	697	680	0	97.6	89.5	92.7	arginine decarboxylase	gbpln	Brassica juncea	AT4G34710.2 | Symbols: ADC2, SPE2, ATADC2 | arginine decarboxylase 2 | chr4:16560315-16562450 REVERSE LENGTH=711	697	711	0	102.0	86.1	92.7
Rsa1.0_00281.1.g10377.t1	ref|XP_002313006.1| predicted protein [Populus trichocarpa] gi|222849414|gb|EEE86961.1| predicted protein [Populus trichocarpa]	164	207	6.00E-85	126.2	100.0	100.0	predicted protein	gbpln	Populus trichocarpa	AT4G34720.1 | Symbols: AVA-P1, VHA-C1, ATVHA-C1 | ATPase, F0/V0 complex, subunit C protein | chr4:16568223-16569165 REVERSE LENGTH=164	164	164	4.00E-87	100.0	100.0	100.0
Rsa1.0_00281.1.g10378.t1	ref|NP_001147174.1| SAUR9 - auxin-responsive SAUR family member [Zea mays] gi|195608008|gb|ACG25834.1| SAUR9 - auxin-responsive SAUR family member [Zea mays]	107	107	5.00E-54	100.0	94.4	99.1	SAUR9 - auxin-responsive SAUR family member	gbenv/gbpln	Zea mays	AT4G34760.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:16582471-16582794 REVERSE LENGTH=107	107	107	2.00E-55	100.0	92.5	97.2
Rsa1.0_00281.1.g10379.t1	gb|EOA15376.1| hypothetical protein CARUB_v10006095mg [Capsella rubella]	105	104	3.00E-48	99.0	90.5	93.3	hypothetical protein CARUB_v10006095mg	gbpln	Capsella rubella	AT4G34770.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:16591352-16591666 FORWARD LENGTH=104	105	104	2.00E-50	99.0	90.5	92.4
Rsa1.0_00281.1.g10380.t1	gb|AAD26953.1| putative non-LTR retrolelement reverse transcriptase [Arabidopsis thaliana]	305	323	3.00E-66	105.9	44.9	57.7	putative non-LTR retrolelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	305	332	4.00E-65	108.9	40.3	55.1
Rsa1.0_00281.1.g10381.t1	ref|XP_002869125.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297314961|gb|EFH45384.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	93	94	1.00E-44	101.1	96.8	98.9	auxin-responsive family protein	gbpln	Arabidopsis lyrata	AT4G34800.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:16596860-16597144 FORWARD LENGTH=94	93	94	6.00E-47	101.1	95.7	98.9
Rsa1.0_00281.1.g10382.t2	gb|EOA18631.1| hypothetical protein CARUB_v10007206mg [Capsella rubella]	100	104	2.00E-40	104.0	83.0	90.0	hypothetical protein CARUB_v10007206mg	gbpln	Capsella rubella	AT4G34810.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:16599104-16599421 FORWARD LENGTH=105	100	105	1.00E-41	105.0	86.0	91.0
Rsa1.0_00281.1.g10383.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00281.1.g10384.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	102	1555	4.00E-14	1524.5	46.1	61.8	disease resistance protein	gbpln	Brassica rapa	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	102	170	1.00E-11	166.7	33.3	50.0
Rsa1.0_00281.1.g10385.t1	ref|XP_002869114.1| actin binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314950|gb|EFH45373.1| actin binding protein [Arabidopsis lyrata subsp. lyrata]	142	141	9.00E-71	99.3	89.4	96.5	actin binding protein	gbpln	Arabidopsis lyrata	AT4G34970.1 | Symbols: ADF9 | actin depolymerizing factor 9 | chr4:16653784-16654593 FORWARD LENGTH=141	142	141	5.00E-73	99.3	88.7	96.5
Rsa1.0_00281.1.g10386.t1	ref|XP_002867098.1| hypothetical protein ARALYDRAFT_491159 [Arabidopsis lyrata subsp. lyrata] gi|297312934|gb|EFH43357.1| hypothetical protein ARALYDRAFT_491159 [Arabidopsis lyrata subsp. lyrata]	728	764	0	104.9	94.5	97.8	hypothetical protein ARALYDRAFT_491159	gbpln	Arabidopsis lyrata	AT4G34980.1 | Symbols: SLP2 | subtilisin-like serine protease 2 | chr4:16656929-16659223 REVERSE LENGTH=764	728	764	0	104.9	93.8	97.7
Rsa1.0_00281.1.g10387.t1	ref|XP_002867097.1| AtMYB32 [Arabidopsis lyrata subsp. lyrata] gi|297312933|gb|EFH43356.1| AtMYB32 [Arabidopsis lyrata subsp. lyrata]	275	278	1.00E-108	101.1	78.5	84.4	AtMYB32	gbpln	Arabidopsis lyrata	AT4G34990.1 | Symbols: AtMYB32, MYB32 | myb domain protein 32 | chr4:16661370-16662289 REVERSE LENGTH=274	275	274	1.00E-110	99.6	76.7	82.9
Rsa1.0_00281.1.g10388.t1	gb|AEO78932.1| ascorbate peroxidase [Brassica oleracea var. italica]	287	287	1.00E-159	100.0	97.6	99.0	ascorbate peroxidase	gbpln	Brassica oleracea	AT4G35000.1 | Symbols: APX3 | ascorbate peroxidase 3 | chr4:16665007-16667541 REVERSE LENGTH=287	287	287	1.00E-147	100.0	89.5	95.5
Rsa1.0_00281.1.g10389.t1	ref|NP_567973.1| beta-galactosidase 11 [Arabidopsis thaliana] gi|75202765|sp|Q9SCV1.1|BGL11_ARATH RecName: Full=Beta-galactosidase 11; Short=Lactase 11; Flags: Precursor gi|6686894|emb|CAB64747.1| putative beta-galactosidase [Arabidopsis thaliana] gi|332661046|gb|AEE86446.1| beta-galactosidase 11 [Arabidopsis thaliana]	844	845	0	100.1	89.3	94.9	beta-galactosidase 11	gbpln	Arabidopsis thaliana	AT4G35010.1 | Symbols: BGAL11 | beta-galactosidase 11 | chr4:16668075-16671974 REVERSE LENGTH=845	844	845	0	100.1	89.3	94.9
Rsa1.0_00281.1.g10390.t1	ref|XP_002869110.1| hypothetical protein ARALYDRAFT_491149 [Arabidopsis lyrata subsp. lyrata] gi|297314946|gb|EFH45369.1| hypothetical protein ARALYDRAFT_491149 [Arabidopsis lyrata subsp. lyrata]	239	265	2.00E-88	110.9	76.2	83.7	hypothetical protein ARALYDRAFT_491149	gbpln	Arabidopsis lyrata	AT4G35070.1 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr4:16694488-16695387 FORWARD LENGTH=265	239	265	6.00E-90	110.9	74.9	85.4
Rsa1.0_00281.1.g10391.t1	gb|AAF71742.1|AF248491_1 catalase [Raphanus sativus]	485	492	0	101.4	99.8	99.8	catalase	gbpln	Raphanus sativus	AT4G35090.1 | Symbols: CAT2 | catalase 2 | chr4:16700937-16703215 REVERSE LENGTH=492	485	492	0	101.4	98.1	99.4

Rsa1.0_00281.1.g10392.t1	gb|AAG30607.1|AF314656_1 aquaporin [Brassica oleracea]	281	281	1.00E−153	100.0	95.4	96.1	aquaporin	gbpln	Brassica oleracea	AT4G35100.2 | Symbols: PIP3 | plasma membrane intrinsic protein 3 | chr4:16708672−16709958 FORWARD LENGTH=280	281	280	1.00E−155	99.6	95.0	96.8
Rsa1.0_00281.1.g10393.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	AT4G33090.1 | Symbols: APM1, ATAPM1 | aminopeptidase M1 | chr4:15965915−15970418 REVERSE LENGTH=879	238	879	3.00E−12	369.3	18.5	23.9
Rsa1.0_00281.1.g10394.t1	ref|XP_002869107.1| kelch repeat−containing F−box family protein [Arabidopsis lyrata subsp. lyrata] gi|297314943|gb|EFH45366.1| kelch repeat−containing F−box family protein [Arabidopsis lyrata subsp. lyrata]	419	413	5.00E−71	98.6	44.6	59.4	kelch repeat−containing F−box family protein	gbpln	Arabidopsis lyrata	AT4G35120.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:16716806−16718017 FORWARD LENGTH=389	419	389	2.00E−57	92.8	40.3	52.3
Rsa1.0_00281.1.g10395.t1	gb|AAQ01577.1| O−methyltransferase−like protein [Brassica rapa subsp. pekinensis]	106	158	3.00E−53	149.1	96.2	99.1	O−methyltransferase−like protein	gbpln	Brassica rapa	AT4G35160.1 | Symbols: | O−methyltransferase family protein | chr4:16730989−16732808 REVERSE LENGTH=382	106	382	4.00E−53	360.4	89.6	96.2
Rsa1.0_00282.1.g10396.t2	ref|NP_197803.1| Squalene monooxygenase 1,1 [Arabidopsis thaliana] gi|11467948|sp|O65404.2|ERG11_ARATH RecName: Full=Squalene monooxygenase 1,1; AltName: Full=Squalene epoxidase 1,1; Short=SE 1,1 gi|9757924|dbj|BAB08406.1| squalene monooxygenase [Arabidopsis thaliana] gi|222422883|dbj|BAH19428.1| AT5G24150 [Arabidopsis thaliana] gi|332005879|gb|AED93262.1| Squalene monooxygenase 1,1 [Arabidopsis thaliana]	517	516	0	99.8	77.9	87.8	Squalene monooxygenase 1,1	gbpln	Arabidopsis thaliana	AT5G24150.1 | Symbols: SQP1, SQE5 | FAD/NAD(P)−binding oxidoreductase family protein | chr5:8172594−8175395 REVERSE LENGTH=516	517	516	0	99.8	77.9	87.8
Rsa1.0_00282.1.g10397.t1	ref|XP_002874172.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320009|gb|EFH50431.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	120	519	3.00E−15	432.5	34.2	39.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G24160.1 | Symbols: SQE6 | squalene monoxygenase 6 | chr5:8183291−8186601 REVERSE LENGTH=517	120	517	8.00E−18	430.8	34.2	38.3
Rsa1.0_00282.1.g10398.t1	gb|EOA21899.1| hypothetical protein CARUB_v10002380mg [Capsella rubella]	81	75	4.00E−30	92.6	86.4	90.1	hypothetical protein CARUB_v10002380mg	gbpln	Capsella rubella	AT5G24165.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G23885.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:8188622−8189087 FORWARD LENGTH=75	81	75	4.00E−31	92.6	82.7	88.9
Rsa1.0_00282.1.g10399.t1	ref|NP_197811.2| lipase class 3−related protein [Arabidopsis thaliana] gi|26453202|dbj|BAC43675.1| unknown protein [Arabidopsis thaliana] gi|28950935|gb|AAO63391.1| At5g24230 [Arabidopsis thaliana] gi|332005890|gb|AED93273.1| lipase class 3−related protein [Arabidopsis thaliana]	367	369	0	100.5	92.4	96.2	lipase class 3−related protein	gbpln	Arabidopsis thaliana	AT5G24230.1 | Symbols: | Lipase class 3−related protein | chr5:8229182−8230841 FORWARD LENGTH=369	367	369	0	100.5	92.4	96.2
Rsa1.0_00282.1.g10400.t1	ref|XP_002880544.1| hypothetical protein ARALYDRAFT_900901 [Arabidopsis lyrata subsp. lyrata] gi|297326383|gb|EFH56803.1| hypothetical protein ARALYDRAFT_900901 [Arabidopsis lyrata subsp. lyrata]	216	277	2.00E−18	128.2	38.0	48.1	hypothetical protein ARALYDRAFT_900901	gbpln	Arabidopsis lyrata	AT2G24080.1 | Symbols: | Protein of unknown function (DUF295) | chr2:10237604−10238779 REVERSE LENGTH=374	216	374	3.00E−11	173.1	16.7	20.4
Rsa1.0_00282.1.g10401.t1	gb|AAM63232.1| unknown [Arabidopsis thaliana]	245	289	2.00E−58	118.0	52.2	64.5	unknown	gbpln	Arabidopsis thaliana	AT2G01660.1 | Symbols: PDLP6 | plasmodesmata−located protein 6 | chr2:290973−292496 REVERSE LENGTH=288	245	288	1.00E−60	117.6	52.2	64.5
Rsa1.0_00282.1.g10402.t1	gb|EOA24506.1| hypothetical protein CARUB_v10017762mg [Capsella rubella]	265	287	2.00E−58	108.3	46.8	62.3	hypothetical protein CARUB_v10017762mg	gbpln	Capsella rubella	AT2G01660.2 | Symbols: PDLP6 | plasmodesmata−located protein 6 | chr2:291717−292496 REVERSE LENGTH=259	265	259	8.00E−61	97.7	48.3	65.7
Rsa1.0_00282.1.g10403.t1	gb|EOA38519.1| hypothetical protein CARUB_v10010308mg [Capsella rubella]	157	206	3.00E−13	131.2	36.3	51.6	hypothetical protein CARUB_v10010308mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00282.1.g10404.t1	dbj|BAB08928.1| unnamed protein product [Arabidopsis thaliana]	161	552	3.00E−12	342.9	21.1	22.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G24450.1 | Symbols: | Transcription factor IIIC, subunit 5 | chr5:8348780−8353130 FORWARD LENGTH=554	161	554	1.00E−14	344.1	21.1	22.4

Rsa1.0_00282.1.g10405.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1116	1501	0	134.5	52.7	65.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1116	1262	1.00E-132	113.1	21.1	30.6
Rsa1.0_00282.1.g10406.t3	gb|ACP30619.1| disease resistance protein [Brassica rapa subsp. pekinensis]	819	889	0	108.5	61.2	73.3	disease resistance protein	gbpln	Brassica rapa	AT1G59620.1 | Symbols: CW9 | Disease resistance protein (CC-NBS-LRR class) family | chr1:21902627-21905527 FORWARD LENGTH=842	819	842	0	102.8	55.4	68.1
Rsa1.0_00282.1.g10407.t1	gb|AAC02664.1| polyprotein [Arabidopsis thaliana]	1428	1451	0	101.6	62.0	74.6	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1428	1262	1.00E-102	88.4	13.7	20.4
Rsa1.0_00282.1.g10408.t1	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	215	910	5.00E-25	423.3	23.7	30.7	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G24350.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Secretory pathway Sec39 (InterPro:IPR013244). | chr5:8301537-8310746 FORWARD LENGTH=2396	215	2396	7.00E-12	1114.4	18.1	22.3
Rsa1.0_00282.1.g10409.t3	gb|AEM36350.1| At1g58602 [Arabidopsis thaliana]	1131	1133	0	100.2	53.1	68.4	At1g58602	gbpln	Arabidopsis thaliana	AT1G58602.2 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr1:21760167-21763765 FORWARD LENGTH=1138	1131	1138	0	100.6	52.9	68.3
Rsa1.0_00282.1.g10410.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00282.1.g10411.t1	ref|NP_197833.2| Transcription factor IIIC, subunit 5 [Arabidopsis thaliana] gi|332005929|gb|AED93312.1| Transcription factor IIIC, subunit 5 [Arabidopsis thaliana]	588	554	0	94.2	75.5	83.3	Transcription factor IIIC, subunit 5	gbpln	Arabidopsis thaliana	AT5G24450.1 | Symbols: | Transcription factor IIIC, subunit 5 | chr5:8348780-8353130 FORWARD LENGTH=554	588	554	0	94.2	75.5	83.3
Rsa1.0_00282.1.g10412.t3	gb|EOA20292.1| hypothetical protein CARUB_v10000600mg [Capsella rubella]	93	561	1.00E-18	603.2	48.4	55.9	hypothetical protein CARUB_v10000600mg	gbpln	Capsella rubella	AT5G24470.1 | Symbols: APRR5, PRR5 | pseudo-response regulator 5 | chr5:8356204-8358873 REVERSE LENGTH=667	93	667	8.00E-21	717.2	52.7	64.5
Rsa1.0_00282.1.g10413.t1	gb|ADA58345.1| pseudo-response regulator 5b [Brassica rapa]	483	628	0	130.0	82.0	87.2	pseudo-response regulator 5b	gbpln	Brassica rapa	AT5G24470.1 | Symbols: APRR5, PRR5 | pseudo-response regulator 5 | chr5:8356204-8358873 REVERSE LENGTH=667	483	667	0	138.1	76.0	82.6
Rsa1.0_00282.1.g10414.t1	ref|XP_002874202.1| hypothetical protein ARALYDRAFT_326742 [Arabidopsis lyrata subsp. lyrata] gi|297320039|gb|EFH50461.1| hypothetical protein ARALYDRAFT_326742 [Arabidopsis lyrata subsp. lyrata]	341	305	2.00E-67	89.4	54.0	62.2	hypothetical protein ARALYDRAFT_326742	gbpln	Arabidopsis lyrata	AT5G24500.1 | Symbols: | unknown protein; Has 133 Blast hits to 129 proteins in 40 species: Archae - 2; Bacteria - 0; Metazoa - 60; Fungi - 5; Plants - 29; Viruses - 0; Other Eukaryotes - 37 (source: NCBI BLink). | chr5:8367468-8368715 REVERSE LENGTH=334	341	334	5.00E-66	97.9	49.0	58.7
Rsa1.0_00282.1.g10415.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00282.1.g10416.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1352	1475	0	109.1	57.9	72.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1352	1262	0	93.3	22.9	30.0
Rsa1.0_00282.1.g10417.t1	ref|NP_197841.1| downy mildew resistance 6 protein / oxidoreductase [Arabidopsis thaliana] gi|14423476|gb|AAK62420.1|AF386975_1 flavanone 3-hydroxylase-like protein [Arabidopsis thaliana] gi|10177853|dbj|BAB11205.1| flavanone 3-hydroxylase-like protein [Arabidopsis thaliana] gi|20148253|gb|AAM10017.1| flavanone 3-hydroxylase-like protein [Arabidopsis thaliana] gi|332005939|gb|AED93322.1| downy mildew resistance 6 protein / oxidoreductase [Arabidopsis thaliana]	341	341	0	100.0	88.6	94.7	downy mildew resistance 6 protein / oxidoreductase	gbpln	Arabidopsis thaliana	AT5G24530.1 | Symbols: DMR6 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:8378964-8383154 FORWARD LENGTH=341	341	341	0	100.0	88.6	94.7
Rsa1.0_00283.1.g10418.t1	gb|EOA13779.1| hypothetical protein CARUB_v10026873mg [Capsella rubella]	280	299	1.00E-116	106.8	82.9	92.9	hypothetical protein CARUB_v10026873mg	gbpln	Capsella rubella	AT5G53400.1 | Symbols: BOB1 | HSP20-like chaperones superfamily protein | chr5:21661588-21663383 FORWARD LENGTH=304	280	304	1.00E-115	108.6	81.4	91.1
Rsa1.0_00283.1.g10419.t2	gb|AAG03119.1|AC004133_13 F5A9.24 [Arabidopsis thaliana]	1450	1254	0	86.5	34.1	45.2	F5A9.24	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1450	575	4.00E-43	39.7	6.5	9.5

Rsa1.0_00283.1.g10420.t1	ref|NP_568793.1| CCT motif family protein [Arabidopsis thaliana] gi|20466574|gb|AAM20604.1| putative protein [Arabidopsis thaliana] gi|23198144|gb|AAN15599.1| putative protein [Arabidopsis thaliana] gi|332008967|gb|AED96350.1| CCT motif family protein [Arabidopsis thaliana]	273	264	1.00E-125	96.7	82.1	89.4	CCT motif family protein	gbpln	Arabidopsis thaliana	AT5G53420.1 | Symbols: | CCT motif family protein | chr5:21673683-21675469 FORWARD LENGTH=264	273	264	1.00E-127	96.7	82.1	89.4
Rsa1.0_00283.1.g10421.t1	ref|NP_200156.1| uncharacterized protein [Arabidopsis thaliana] gi|8843773|dbj|BAA97321.1| unnamed protein product [Arabidopsis thaliana] gi|332008971|gb|AED96354.1| uncharacterized protein AT5G53440 [Arabidopsis thaliana]	1090	1181	0	108.3	50.2	56.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G53440.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:21683679-21687970 REVERSE LENGTH=1181	1090	1181	0	108.3	50.2	56.2
Rsa1.0_00283.1.g10422.t1	gb|EOA12453.1| hypothetical protein CARUB_v10025734mg [Capsella rubella]	2206	2208	0	100.1	94.0	97.1	hypothetical protein CARUB_v10025734mg	gbpln	Capsella rubella	AT5G53460.3 | Symbols: GLT1 | NADH-dependent glutamate synthase 1 | chr5:21700518-21709629 FORWARD LENGTH=2208	2206	2208	0	100.1	93.7	96.5
Rsa1.0_00283.1.g10423.t1	ref|XP_002865975.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297311810|gb|EFH42234.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	583	654	0	112.2	77.5	85.8	WD-40 repeat family protein	gbpln	Arabidopsis lyrata	AT5G53500.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:21726167-21728524 REVERSE LENGTH=654	583	654	0	112.2	77.4	85.8
Rsa1.0_00283.1.g10424.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00283.1.g10425.t1	ref|XP_002864247.1| ATOPT9 [Arabidopsis lyrata subsp. lyrata] gi|297310082|gb|EFH40506.1| ATOPT9 [Arabidopsis lyrata subsp. lyrata]	741	741	0	100.0	89.3	95.1	ATOPT9	gbpln	Arabidopsis lyrata	AT5G53510.1 | Symbols: ATOPT9, OPT9 | oligopeptide transporter 9 | chr5:21738849-21742082 FORWARD LENGTH=741	741	741	0	100.0	88.8	95.4
Rsa1.0_00283.1.g10426.t1	ref|XP_002864248.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310083|gb|EFH40507.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	739	739	0	100.0	88.0	95.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G53520.1 | Symbols: ATOPT8, OPT8 | oligopeptide transporter 8 | chr5:21743450-21745981 FORWARD LENGTH=733	739	733	0	99.2	87.1	94.6
Rsa1.0_00283.1.g10427.t1	gb|EOA12739.1| hypothetical protein CARUB_v10028247mg [Capsella rubella]	431	436	1.00E-110	101.2	54.3	68.9	hypothetical protein CARUB_v10028247mg	gbpln	Capsella rubella	AT1G51370.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:19045615-19047141 FORWARD LENGTH=435	431	435	1.00E-112	100.9	53.1	68.4
Rsa1.0_00283.1.g10428.t2	gb|EOA13468.1| hypothetical protein CARUB_v10026523mg [Capsella rubella]	403	402	1.00E-165	99.8	71.2	80.9	hypothetical protein CARUB_v10026523mg	gbpln	Capsella rubella	AT5G53540.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:21749561-21751099 REVERSE LENGTH=403	403	403	1.00E-165	100.0	69.0	78.4
Rsa1.0_00283.1.g10429.t1	ref|NP_200226.4| uncharacterized protein [Arabidopsis thaliana] gi|332009076|gb|AED96459.1| uncharacterized protein AT5G54150 [Arabidopsis thaliana]	184	160	1.00E-51	87.0	53.8	62.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54148.1); Has 103 Blast hits to 99 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr5:21977461-21978237 REVERSE LENGTH=160	184	160	4.00E-54	87.0	53.8	62.0
Rsa1.0_00283.1.g10430.t2	gb|EOA16742.1| hypothetical protein CARUB_v10004943mg [Capsella rubella]	361	408	1.00E-168	113.0	81.4	87.3	hypothetical protein CARUB_v10004943mg	gbpln	Capsella rubella	AT4G27585.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr4:13766984-13769832 REVERSE LENGTH=411	361	411	1.00E-167	113.9	80.9	87.8
Rsa1.0_00283.1.g10431.t1	gb|EOA14373.1| hypothetical protein CARUB_v10027559mg [Capsella rubella]	101	130	6.00E-19	128.7	69.3	74.3	hypothetical protein CARUB_v10027559mg	gbpln	Capsella rubella	AT5G54095.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27580.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21952868-21953369 REVERSE LENGTH=135	101	135	4.00E-13	133.7	42.6	42.6

Rsa1.0_00283.1.g10432.t1	ref|NP_200212.1| glycosyltransferase domain-containing protein [Arabidopsis thaliana] gi|75171779|sp|Q9FN26.1|U79B6_ARATH RecName: Full=UDP-glycosyltransferase 79B6 gi|10177263|dbj|BAB10731.1| flavonol 3-O-glucosyltransferase-like protein [Arabidopsis thaliana] gi|56236076|gb|AAV84494.1| At5g54010 [Arabidopsis thaliana] gi|56790204|gb|AAW30019.1| At5g54010 [Arabidopsis thaliana] gi|332009055|gb|AED96438.1| UDP-glycosyltransferase 79B6 [Arabidopsis thaliana]	371	453	0	122.1	85.4	92.2	glycosyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G54010.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:21919819-21921180 REVERSE LENGTH=453	371	453	0	122.1	85.4	92.2
Rsa1.0_00284.1.g10433.t1	gb|EOA17212.1| hypothetical protein CARUB_v10005485mg [Capsella rubella]	240	271	1.00E-114	112.9	84.6	94.2	hypothetical protein CARUB_v10005485mg	gbpln	Capsella rubella	AT4G37470.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:17617045-17618363 REVERSE LENGTH=270	240	270	1.00E-113	112.5	82.5	93.8
Rsa1.0_00284.1.g10434.t1	ref|NP_001118516.1| RAB GTPase activator protein [Arabidopsis thaliana] gi|330255185|gb|AEC10279.1| RAB GTPase activator protein [Arabidopsis thaliana]	740	743	0	100.4	84.7	89.9	RAB GTPase activator protein	gbpln	Arabidopsis thaliana	AT2G43490.4 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr2:18055106-18058179 REVERSE LENGTH=743	740	743	0	100.4	84.7	89.9
Rsa1.0_00284.1.g10435.t1	gb|EOA29017.1| hypothetical protein CARUB_v10025271mg [Capsella rubella]	505	540	1.00E-174	106.9	79.6	85.5	hypothetical protein CARUB_v10025271mg	gbpln	Capsella rubella	AT2G43970.1 | Symbols: | RNA-binding protein | chr2:18205535-18208031 REVERSE LENGTH=545	505	545	1.00E-167	107.9	74.5	81.6
Rsa1.0_00284.1.g10436.t1	ref|XP_002881944.1| inositol 1,3,4-trisphosphate 5/6-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297327783|gb|EFH58203.1| inositol 1,3,4-trisphosphate 5/6-kinase family protein [Arabidopsis lyrata subsp. lyrata]	491	490	0	99.8	86.8	92.1	inositol 1,3,4-trisphosphate 5/6-kinase family protein	gbpln	Arabidopsis lyrata	AT2G43980.1 | Symbols: AtITPK4, ITPK4 | inositol 1,3,4-trisphosphate 5/6-kinase 4 | chr2:18208437-18211604 REVERSE LENGTH=488	491	488	0	99.4	85.1	90.6
Rsa1.0_00284.1.g10437.t1	ref|NP_181927.1| uncharacterized protein [Arabidopsis thaliana] gi|3212856|gb|AAC23407.1| hypothetical protein [Arabidopsis thaliana] gi|330255265|gb|AEC10359.1| uncharacterized protein AT2G43990 [Arabidopsis thaliana]	550	632	1.00E-175	114.9	74.4	81.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G43990.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; Has 1419 Blast hits to 494 proteins in 144 species: Archae - 0; Bacteria - 300; Metazoa - 246; Fungi - 102; Plants - 31; Viruses - 2; Other Eukaryotes - 738 (source: NCBI BLink). | chr2:18211974-18213872 FORWARD LENGTH=632	550	632	1.00E-177	114.9	74.4	81.1
Rsa1.0_00284.1.g10438.t1	ref|XP_002880077.1| hypothetical protein ARALYDRAFT_483519 [Arabidopsis lyrata subsp. lyrata] gi|297325916|gb|EFH56336.1| hypothetical protein ARALYDRAFT_483519 [Arabidopsis lyrata subsp. lyrata]	198	209	1.00E-66	105.6	69.7	79.3	hypothetical protein ARALYDRAFT_483519	gbpln	Arabidopsis lyrata	AT2G44000.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:18214627-18215256 FORWARD LENGTH=209	198	209	1.00E-61	105.6	68.2	79.3
Rsa1.0_00284.1.g10439.t1	gb|EOA28560.1| hypothetical protein CARUB_v10024778mg [Capsella rubella]	101	100	8.00E-38	99.0	78.2	86.1	hypothetical protein CARUB_v10024778mg	gbpln	Capsella rubella	AT2G44010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G59880.1); Has 18 Blast hits to 18 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18216879-18217184 FORWARD LENGTH=101	101	101	1.00E-38	100.0	77.2	85.1
Rsa1.0_00284.1.g10440.t1	ref|XP_002881945.1| hypothetical protein ARALYDRAFT_903808 [Arabidopsis lyrata subsp. lyrata] gi|297327784|gb|EFH58204.1| hypothetical protein ARALYDRAFT_903808 [Arabidopsis lyrata subsp. lyrata]	448	508	0	113.4	91.3	97.1	hypothetical protein ARALYDRAFT_903808	gbpln	Arabidopsis lyrata	AT2G44020.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr2:18217737-18219260 REVERSE LENGTH=507	448	507	0	113.2	90.8	96.9
Rsa1.0_00284.1.g10441.t1	gb|EOA24733.1| hypothetical protein CARUB_v10018009mg [Capsella rubella]	215	214	1.00E-107	99.5	91.2	96.3	hypothetical protein CARUB_v10018009mg	gbpln	Capsella rubella	AT2G44065.2 | Symbols: | Ribosomal protein L2 family | chr2:18228860-18230368 FORWARD LENGTH=214	215	214	1.00E-109	99.5	89.8	95.8
Rsa1.0_00284.1.g10442.t6	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1134	1342	0	118.3	47.5	64.9	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1134	1262	1.00E-48	111.3	9.4	13.9
Rsa1.0_00284.1.g10443.t2	gb|ACP30623.1| disease resistance protein [Brassica rapa subsp. pekinensis]	884	1262	1.00E-142	142.8	43.4	53.2	disease resistance protein	gbpln	Brassica rapa	AT5G18370.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6085036-6088926 REVERSE LENGTH=1210	884	1210	1.00E-98	136.9	35.3	49.1

Rsa1.0_00284.1.g10444.t1	gb|EOA17608.1| hypothetical protein CARUB_v10005968mg [Capsella rubella] gi|482557559|gb|EOA21751.1| hypothetical protein CARUB_v10002207mg [Capsella rubella]	146	146	1.00E-74	100.0	92.5	95.9	hypothetical protein CARUB_v10005968mg	gbpln	Capsella rubella	AT5G18380.1 | Symbols: | Ribosomal protein S5 domain 2-like superfamily protein | chr5:6090253-6090693 REVERSE LENGTH=146	146	146	2.00E-76	100.0	91.8	95.9
Rsa1.0_00284.1.g10445.t1	gb|EOA22127.1| hypothetical protein CARUB_v10002685mg, partial [Capsella rubella]	268	313	1.00E-118	116.8	82.5	89.9	hypothetical protein CARUB_v10002685mg, partial	gbpln	Capsella rubella	AT5G18400.3 | Symbols: | Cytokine-induced anti-apoptosis inhibitor 1, Fe-S biogenesis | chr5:6092955-6094876 REVERSE LENGTH=272	268	272	1.00E-108	101.5	79.5	88.1
Rsa1.0_00284.1.g10446.t1	gb|EOA20665.1| hypothetical protein CARUB_v10000977mg [Capsella rubella]	455	440	0	96.7	77.4	86.6	hypothetical protein CARUB_v10000977mg	gbpln	Capsella rubella	AT5G18420.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2363 (InterPro:IPR019312); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:6105638-6109337 REVERSE LENGTH=441	455	441	0	96.9	77.1	86.6
Rsa1.0_00284.1.g10447.t1	ref|NP_001078603.1| uncharacterized protein [Arabidopsis thaliana] gi|145358174|ref|NP_197345.2| uncharacterized protein [Arabidopsis thaliana] gi|60547897|gb|AAX23912.1| hypothetical protein At5g18440 [Arabidopsis thaliana] gi|71905555|gb|AAZ52755.1| hypothetical protein At5g18440 [Arabidopsis thaliana] gi|71905557|gb|AAZ52756.1| hypothetical protein At5g18440 [Arabidopsis thaliana] gi|332005180|gb|AED92563.1| uncharacterized protein AT5G18440 [Arabidopsis thaliana] gi|332005181|gb|AED92564.1| uncharacterized protein AT5G18440 [Arabidopsis thaliana]	411	470	1.00E-107	114.4	63.0	71.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G18440.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nuclear fragile X mental retardation-interacting protein 1, conserved region (InterPro:IPR019496); Has 1333 Blast hits to 1211 proteins in 205 species: Archae - 0; Bacteria - 137; Metazoa - 339; Fungi - 162; Plants - 70; Viruses - 6; Other Eukaryotes - 619 (source: NCBI BLink). | chr5:6113092-6115748 FORWARD LENGTH=470	411	470	1.00E-109	114.4	63.0	71.8
Rsa1.0_00284.1.g10448.t1	ref|XP_002873895.1| hypothetical protein ARALYDRAFT_909855 [Arabidopsis lyrata subsp. lyrata] gi|297319732|gb|EFH50154.1| hypothetical protein ARALYDRAFT_909855 [Arabidopsis lyrata subsp. lyrata]	304	310	1.00E-121	102.0	77.0	85.9	hypothetical protein ARALYDRAFT_909855	gbpln	Arabidopsis lyrata	AT5G18450.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:6116097-6117020 REVERSE LENGTH=307	304	307	1.00E-120	101.0	76.6	83.6
Rsa1.0_00284.1.g10449.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00284.1.g10450.t1	gb|EOA20676.1| hypothetical protein CARUB_v10000988mg [Capsella rubella]	434	437	0	100.7	89.6	92.6	hypothetical protein CARUB_v10000988mg	gbpln	Capsella rubella	AT5G18460.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:6123205-6126505 FORWARD LENGTH=430	434	430	0	99.1	86.9	90.1
Rsa1.0_00284.1.g10451.t1	ref|NP_175273.1| F-box/RNI-like/FBD-like domain-containing protein [Arabidopsis thaliana] gi|5733869|gb|AAD49757.1|AC007932_5 Contains F-box domain PF|00646 [Arabidopsis thaliana] gi|332194164|gb|AEE32285.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	512	513	1.00E-124	100.2	53.1	64.5	F-box/RNI-like/FBD-like domain-containing protein	gbpln	Arabidopsis thaliana	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	512	513	1.00E-126	100.2	53.1	64.5
Rsa1.0_00284.1.g10452.t1	ref|XP_002873898.1| hypothetical protein ARALYDRAFT_909860 [Arabidopsis lyrata subsp. lyrata] gi|297319735|gb|EFH50157.1| hypothetical protein ARALYDRAFT_909860 [Arabidopsis lyrata subsp. lyrata]	551	553	0	100.4	87.1	93.3	hypothetical protein ARALYDRAFT_909860	gbpln	Arabidopsis lyrata	AT5G18490.1 | Symbols: | Plant protein of unknown function (DUF946) | chr5:6134275-6136554 REVERSE LENGTH=553	551	553	0	100.4	86.6	92.7
Rsa1.0_00284.1.g10453.t6	dbj|BAD98296.1| glutamate dehydrogenase [Brassica oleracea]	278	260	8.00E-58	93.5	41.4	42.8	glutamate dehydrogenase	gbpln	Brassica oleracea	AT5G18170.1 | Symbols: GDH1 | glutamate dehydrogenase 1 | chr5:6006172-6008248 FORWARD LENGTH=411	278	411	5.00E-59	147.8	40.6	42.4
Rsa1.0_00284.1.g10454.t1	gb|EOA20522.1| hypothetical protein CARUB_v10000836mg [Capsella rubella]	493	485	0	98.4	93.1	95.9	hypothetical protein CARUB_v10000836mg	gbpln	Capsella rubella	AT5G18500.2 | Symbols: | Protein kinase superfamily protein | chr5:6139263-6141283 FORWARD LENGTH=484	493	484	0	98.2	92.1	95.3
Rsa1.0_00284.1.g10455.t1	gb|EOA20650.1| hypothetical protein CARUB_v10000963mg [Capsella rubella]	446	443	0	99.3	93.0	96.9	hypothetical protein CARUB_v10000963mg	gbpln	Capsella rubella	AT5G18520.1 | Symbols: | Lung seven transmembrane receptor family protein | chr5:6145027-6146349 FORWARD LENGTH=440	446	440	0	98.7	93.3	96.4

Rsa1.0_00284.1.g10456.t1	ref|NP_974804.4| protein serine/threonine kinase [Arabidopsis thaliana] gi|332005192|gb|AED92575.1| protein serine/threonine kinase [Arabidopsis thaliana]	1602	1639	0	102.3	87.3	92.0	protein serine/threonine kinase	gbpln	Arabidopsis thaliana	AT5G18525.1 | Symbols: | protein serine/threonine kinases;protein tyrosine kinases;ATP binding;protein kinases | chr5:6146932-6153658 REVERSE LENGTH=1639	1602	1639	0	102.3	87.3	92.0
Rsa1.0_00284.1.g10457.t1	gb|EOA20563.1| hypothetical protein CARUB_v10000876mg [Capsella rubella]	449	473	1.00E-172	105.3	77.5	85.1	hypothetical protein CARUB_v10000876mg	gbpln	Capsella rubella	AT5G18550.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr5:6160515-6162729 FORWARD LENGTH=465	449	465	1.00E-173	103.6	79.7	85.7
Rsa1.0_00284.1.g10458.t1	ref|NP_197357.2| ethylene response factor PUCHI [Arabidopsis thaliana] gi|334302788|sp|Q6J9Q2.2|ERF86_ARATH RecName: Full=Ethylene-responsive transcription factor ERF086 gi|332005196|gb|AED92579.1| ethylene response factor PUCHI [Arabidopsis thaliana]	318	348	1.00E-145	109.4	87.4	91.5	ethylene response factor PUCHI	gbpln	Arabidopsis thaliana	AT5G18560.1 | Symbols: PUCHI | Integrase-type DNA-binding superfamily protein | chr5:6164859-6165905 REVERSE LENGTH=348	318	348	1.00E-148	109.4	87.4	91.5
Rsa1.0_00284.1.g10459.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00284.1.g10460.t3	gb|EOA20539.1| hypothetical protein CARUB_v10000854mg [Capsella rubella]	167	480	7.00E-25	287.4	34.7	35.9	hypothetical protein CARUB_v10000854mg	gbpln	Capsella rubella	AT5G18580.1 | Symbols: FASS, TON2, EMB40, FS1, GDO, FASS 2 | tonneau 2 (TON2) | chr5:6175154-6178214 FORWARD LENGTH=480	167	480	3.00E-27	287.4	34.7	35.9
Rsa1.0_00284.1.g10461.t1	ref|XP_002873905.1| kelch repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319742|gb|EFH50164.1| kelch repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	712	709	0	99.6	88.5	93.3	kelch repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G18590.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:6178516-6182186 REVERSE LENGTH=708	712	708	0	99.4	88.9	94.1
Rsa1.0_00284.1.g10462.t1	gb|EOA21854.1| hypothetical protein CARUB_v10002321mg [Capsella rubella]	102	102	2.00E-50	100.0	93.1	100.0	hypothetical protein CARUB_v10002321mg	gbpln	Capsella rubella	AT5G18600.1 | Symbols: | Thioredoxin superfamily protein | chr5:6183466-6183774 REVERSE LENGTH=102	102	102	7.00E-53	100.0	94.1	98.0
Rsa1.0_00285.1.g10463.t1	ref|NP_001031828.1| putative glycosyltransferase [Arabidopsis thaliana] gi|292630778|sp|Q9FFN2.2|GLYT3_ARATH RecName: Full=Probable glycosyltransferase At5g03795 gi|332003272|gb|AED90655.1| putative glycosyltransferase [Arabidopsis thaliana]	192	518	4.00E-47	269.8	68.2	77.6	putative glycosyltransferase	gbpln	Arabidopsis thaliana	AT5G03795.1 | Symbols: | Exostosin family protein | chr5:1007554-1010373 REVERSE LENGTH=518	192	518	1.00E-49	269.8	68.2	77.6
Rsa1.0_00285.1.g10464.t1	gb|EOA19541.1| hypothetical protein CARUB_v10002513mg [Capsella rubella]	297	353	1.00E-130	118.9	75.1	84.2	hypothetical protein CARUB_v10002513mg	gbpln	Capsella rubella	AT5G03810.1 | Symbols: | GDSL-like Lipase/Acylhydrolase family protein | chr5:1013939-1015345 REVERSE LENGTH=353	297	353	1.00E-132	118.9	75.1	84.5
Rsa1.0_00285.1.g10465.t2	ref|XP_002873122.1| hypothetical protein ARALYDRAFT_487166 [Arabidopsis lyrata subsp. lyrata] gi|297318959|gb|EFH49381.1| hypothetical protein ARALYDRAFT_487166 [Arabidopsis lyrata subsp. lyrata]	380	336	1.00E-138	88.4	71.3	75.8	hypothetical protein ARALYDRAFT_487166	gbpln	Arabidopsis lyrata	AT5G03880.1 | Symbols: | Thioredoxin family protein | chr5:1038674-1041453 REVERSE LENGTH=339	380	339	1.00E-135	89.2	69.5	73.9
Rsa1.0_00285.1.g10466.t1	gb|EOA21663.1| hypothetical protein CARUB_v10002084mg [Capsella rubella]	173	178	9.00E-65	102.9	74.0	83.8	hypothetical protein CARUB_v10002084mg	gbpln	Capsella rubella	AT5G03890.1 | Symbols: | unknown protein; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G10120.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1047150-1047689 FORWARD LENGTH=179	173	179	2.00E-59	103.5	73.4	80.3
Rsa1.0_00285.1.g10467.t1	ref|XP_002871068.1| sugar-dependent1 [Arabidopsis lyrata subsp. lyrata] gi|297316905|gb|EFH47327.1| sugar-dependent1 [Arabidopsis lyrata subsp. lyrata]	774	824	0	106.5	87.7	92.5	sugar-dependent1	gbpln	Arabidopsis lyrata	AT5G04040.1 | Symbols: SDP1 | Patatin-like phospholipase family protein | chr5:1090346-1093003 FORWARD LENGTH=825	774	825	0	106.6	87.7	92.5
Rsa1.0_00285.1.g10468.t2	ref|NP_196028.2| uncharacterized protein [Arabidopsis thaliana] gi|38603900|gb|AAR24695.1| At5g04080 [Arabidopsis thaliana] gi|41349906|gb|AAS00338.1| At5g04080 [Arabidopsis thaliana] gi|332003311|gb|AED90694.1| uncharacterized protein AT5G04080 [Arabidopsis thaliana]	66	63	2.00E-15	95.5	63.6	71.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G04080.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 9 growth stages; Has 115 Blast hits to 115 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 5; Plants - 110; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:1104815-1105186 FORWARD LENGTH=63	66	63	3.00E-18	95.5	63.6	71.2

Rsa1.0_00285.1.g10469.t1	gb|EOA20379.1| hypothetical protein CARUB_v10000692mg [Capsella rubella]	500	530	1.00E-161	106.0	64.6	76.0	hypothetical protein CARUB_v10000692mg	gbpln	Capsella rubella	AT5G04110.1 | Symbols: GYRB3 | DNA GYRASE B3 | chr5:1110757-1114112 REVERSE LENGTH=546	500	546	1.00E-150	109.2	60.4	73.6
Rsa1.0_00285.1.g10470.t1	ref|NP_568133.1| DNA gyrase subunit B [Arabidopsis thaliana] gi|75165162|sp|Q94BZ7.1|GYRBM_ARATH RecName: Full=DNA gyrase subunit B, mitochondrial; Flags: Precursor gi|14517374|gb|AAK62578.1| AT3g10270/F14P13_13 [Arabidopsis thaliana] gi|22655426|gb|AAM98305.1| At3g10270/F14P13_13 [Arabidopsis thaliana] gi|332003319|gb|AED90702.1| DNA gyrase subunit B [Arabidopsis thaliana]	708	732	0	103.4	89.5	93.8	DNA gyrase subunit B	gbpln	Arabidopsis thaliana	AT5G04130.1 | Symbols: GYRB2 | DNA GYRASE B2 | chr5:1122084-1128031 REVERSE LENGTH=732	708	732	0	103.4	89.5	93.8
Rsa1.0_00285.1.g10471.t1	dbj|BAJ34136.1| unnamed protein product [Thellungiella halophila]	264	272	1.00E-103	103.0	78.8	86.4	unnamed protein product	----	----	AT5G04150.1 | Symbols: BHLH101 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:1138559-1139476 REVERSE LENGTH=240	264	240	4.00E-80	90.9	69.7	77.3
Rsa1.0_00285.1.g10472.t1	ref|XP_002871083.1| hypothetical protein ARALYDRAFT_908309 [Arabidopsis lyrata subsp. lyrata] gi|297316920|gb|EFH47342.1| hypothetical protein ARALYDRAFT_908309 [Arabidopsis lyrata subsp. lyrata]	352	345	1.00E-167	98.0	84.4	87.2	hypothetical protein ARALYDRAFT_908309	gbpln	Arabidopsis lyrata	AT5G04250.2 | Symbols: | Cysteine proteinases superfamily protein | chr5:1176397-1178492 FORWARD LENGTH=345	352	345	1.00E-169	98.0	83.8	88.1
Rsa1.0_00285.1.g10473.t3	ref|XP_002871084.1| hypothetical protein ARALYDRAFT_487209 [Arabidopsis lyrata subsp. lyrata] gi|297316921|gb|EFH47343.1| hypothetical protein ARALYDRAFT_487209 [Arabidopsis lyrata subsp. lyrata]	402	307	1.00E-109	76.4	60.7	64.2	hypothetical protein ARALYDRAFT_487209	gbpln	Arabidopsis lyrata	AT5G04280.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain | chr5:1192461-1195413 FORWARD LENGTH=310	402	310	1.00E-106	77.1	60.2	63.9
Rsa1.0_00285.1.g10474.t1	ref|NP_196051.2| pectate lyase family protein [Arabidopsis thaliana] gi|332003342|gb|AED90725.1| pectate lyase family protein [Arabidopsis thaliana]	525	518	0	98.7	87.4	91.8	pectate lyase family protein	gbpln	Arabidopsis thaliana	AT5G04310.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:1203356-1207352 REVERSE LENGTH=518	525	518	0	98.7	87.4	91.8
Rsa1.0_00285.1.g10475.t1	ref|XP_002872217.1| hypothetical protein ARALYDRAFT_910715 [Arabidopsis lyrata subsp. lyrata] gi|297318054|gb|EFH48476.1| hypothetical protein ARALYDRAFT_910715 [Arabidopsis lyrata subsp. lyrata]	86	81	3.00E-11	94.2	43.0	47.7	hypothetical protein ARALYDRAFT_910715	gbpln	Arabidopsis lyrata	AT5G26717.1 | Symbols: | Putative membrane lipoprotein | chr5:9284612-9284857 FORWARD LENGTH=81	86	81	3.00E-12	94.2	39.5	46.5
Rsa1.0_00285.1.g10476.t12	ref|XP_002871086.1| hypothetical protein ARALYDRAFT_487213 [Arabidopsis lyrata subsp. lyrata] gi|297316923|gb|EFH47345.1| hypothetical protein ARALYDRAFT_487213 [Arabidopsis lyrata subsp. lyrata]	647	413	1.00E-134	63.8	42.8	48.5	hypothetical protein ARALYDRAFT_487213	gbpln	Arabidopsis lyrata	AT5G04320.2 | Symbols: | Shugoshin C terminus | chr5:1209613-1212376 FORWARD LENGTH=470	647	470	1.00E-135	72.6	43.3	49.6
Rsa1.0_00285.1.g10477.t2	ref|NP_196057.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|332003350|gb|AED90733.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	500	396	0	79.2	62.2	69.0	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G04370.1 | Symbols: NAMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:1232027-1233888 FORWARD LENGTH=396	500	396	0	79.2	62.2	69.0
Rsa1.0_00285.1.g10478.t1	ref|NP_196059.1| C2H2-type zinc finger protein [Arabidopsis thaliana] gi|28392998|gb|AAO41934.1| putative zinc finger transcription factor [Arabidopsis thaliana] gi|28827440|gb|AAO50564.1| putative zinc finger transcription factor [Arabidopsis thaliana] gi|332003354|gb|AED90737.1| C2H2-type zinc finger protein [Arabidopsis thaliana]	368	362	1.00E-147	98.4	78.5	84.5	C2H2-type zinc finger protein	gbpln	Arabidopsis thaliana	AT5G04390.1 | Symbols: | C2H2-type zinc finger family protein | chr5:1239166-1240254 FORWARD LENGTH=362	368	362	1.00E-150	98.4	78.5	84.5
Rsa1.0_00285.1.g10479.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1987	1274	0	64.1	35.8	46.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1987	575	1.00E-65	28.9	8.9	13.6

Rsa1.0_00285.1.g10480.t1	ref|XP_002871092.1| hypothetical protein ARALYDRAFT_908325 [Arabidopsis lyrata subsp. lyrata] gi|297316929|gb|EFH47351.1| hypothetical protein ARALYDRAFT_908325 [Arabidopsis lyrata subsp. lyrata]	570	568	0	99.6	80.0	87.7	hypothetical protein ARALYDRAFT_908325	gbpln	Arabidopsis lyrata	AT5G04410.1 | Symbols: NAC2, anac078 | NAC domain containing protein 2 | chr5:1243980-1246416 FORWARD LENGTH=567	570	567	0	99.5	77.4	85.6
Rsa1.0_00285.1.g10481.t1	ref|NP_196062.1| kelch repeat-containing protein [Arabidopsis thaliana] gi|79326940|ref|NP_001031832.1| kelch repeat-containing protein [Arabidopsis thaliana] gi|79326969|ref|NP_001031833.1| kelch repeat-containing protein [Arabidopsis thaliana] gi|7406446|emb|CAB85548.1| putative protein [Arabidopsis thaliana] gi|53850551|gb|AAU95452.1| At5g04420 [Arabidopsis thaliana] gi|63003778|gb|AAY25418.1| At5g04420 [Arabidopsis thaliana] gi|222424058|dbj|BAH19990.1| AT5G04420 [Arabidopsis thaliana] gi|332003357|gb|AED90740.1| kelch repeat-containing protein [Arabidopsis thaliana] gi|332003358|gb|AED90741.1| kelch repeat-containing protein [Arabidopsis thaliana] gi|332003359|gb|AED90742.1| kelch repeat-containing protein [Arabidopsis thaliana]	505	514	0	101.8	88.3	92.1	kelch repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G04420.3 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:1246867-1249455 REVERSE LENGTH=514	505	514	0	101.8	88.3	92.1
Rsa1.0_00285.1.g10482.t1	gb|EOA21054.1| hypothetical protein CARUB_v10001394mg [Capsella rubella]	243	334	1.00E-106	137.4	79.8	83.1	hypothetical protein CARUB_v10001394mg	gbpln	Capsella rubella	AT5G04430.2 | Symbols: BTR1, BTR1L | binding to TOMV RNA 1L (long form) | chr5:1250602-1253523 REVERSE LENGTH=334	243	334	1.00E-108	137.4	79.8	82.7
Rsa1.0_00286.1.g10483.t1	ref|XP_002869911.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315747|gb|EFH46170.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	166	223	2.00E-21	134.3	39.8	48.2	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT4G21050.1 | Symbols: | Dof-type zinc finger domain-containing protein | chr4:11238441-11239073 FORWARD LENGTH=210	166	210	1.00E-15	126.5	27.7	37.3
Rsa1.0_00286.1.g10484.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00286.1.g10485.t1	ref|XP_002869910.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315746|gb|EFH46169.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	81	741	4.00E-21	914.8	64.2	67.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G21060.1 | Symbols: | Galactosyltransferase family protein | chr4:11240730-11244860 FORWARD LENGTH=741	81	741	3.00E-22	914.8	61.7	65.4
Rsa1.0_00286.1.g10486.t1	gb|EOA17786.1| hypothetical protein CARUB_v10006179mg [Capsella rubella]	68	68	1.00E-31	100.0	98.5	100.0	hypothetical protein CARUB_v10006179mg	gbpln	Capsella rubella	AT4G21105.1 | Symbols: | cytochrome-c oxidases;electron carriers | chr4:11266273-11266724 FORWARD LENGTH=68	68	68	6.00E-34	100.0	95.6	100.0
Rsa1.0_00286.1.g10487.t1	gb|EOA17579.1| hypothetical protein CARUB_v10005939mg [Capsella rubella]	145	145	9.00E-77	100.0	95.2	98.6	hypothetical protein CARUB_v10005939mg	gbpln	Capsella rubella	AT4G21110.1 | Symbols: | G10 family protein | chr4:11267673-11268774 FORWARD LENGTH=145	145	145	7.00E-79	100.0	94.5	97.9
Rsa1.0_00286.1.g10488.t1	ref|XP_002869906.1| hypothetical protein ARALYDRAFT_329490 [Arabidopsis lyrata subsp. lyrata] gi|297315742|gb|EFH46165.1| hypothetical protein ARALYDRAFT_329490 [Arabidopsis lyrata subsp. lyrata]	597	599	0	100.3	89.3	95.5	hypothetical protein ARALYDRAFT_329490	gbpln	Arabidopsis lyrata	AT4G21120.1 | Symbols: AAT1, CAT1 | amino acid transporter 1 | chr4:11270318-11273775 FORWARD LENGTH=594	597	594	0	99.5	88.3	94.0
Rsa1.0_00286.1.g10489.t3	ref|NP_193847.2| ribophorin II (RPN2) family protein [Arabidopsis thaliana] gi|334186764|ref|NP_001190785.1| ribophorin II (RPN2) family protein [Arabidopsis thaliana] gi|75163691|sp|Q93Z16.1|RPN2_ARATH RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Protein HAPLESS 6; AltName: Full=Ribophorin II; Short=RPN-II; AltName: Full=Ribophorin-2; Flags: Precursor gi|16604454|gb|AAL24233.1| AT4g21150/F7J7_90 [Arabidopsis thaliana] gi|18958022|gb|AAL79584.1| AT4g21150/F7J7_90 [Arabidopsis thaliana] gi|332659008|gb|AEE84408.1| ribophorin II (RPN2) family protein [Arabidopsis thaliana] gi|332659010|gb|AEE84410.1| ribophorin II (RPN2) family protein [Arabidopsis thaliana]	686	691	0	100.7	87.2	91.8	ribophorin II (RPN2) family protein	gbpln	Arabidopsis thaliana	AT4G21150.3 | Symbols: HAP6 | ribophorin II (RPN2) family protein | chr4:11278646-11283599 FORWARD LENGTH=691	686	691	0	100.7	87.2	91.8

Rsa1.0_00286.1.g10490.t1	gb|AAM65970.1| putative GTPase activating protein [Arabidopsis thaliana]	339	337	1.00E−173	99.4	87.6	92.6	putative GTPase activating protein	gbpln	Arabidopsis thaliana	AT4G21160.4 | Symbols: ZAC | Calcium-dependent ARF-type GTPase activating protein family | chr4:11284694-11286532 FORWARD LENGTH=337	339	337	1.00E−174	99.4	87.3	92.3
Rsa1.0_00286.1.g10491.t1	gb|EOA17090.1| hypothetical protein CARUB_v10005340mg [Capsella rubella]	291	304	1.00E−138	104.5	84.2	90.7	hypothetical protein CARUB_v10005340mg	gbpln	Capsella rubella	AT4G21190.1 | Symbols: emb1417 | Pentatricopeptide repeat (PPR) superfamily protein | chr4:11292493-11293763 REVERSE LENGTH=307	291	307	1.00E−133	105.5	78.0	84.2
Rsa1.0_00286.1.g10492.t1	ref|NP_001078417.1| cytochrome c oxidase biogenesis protein Cmc1-like protein [Arabidopsis thaliana] gi|145333595|ref|NP_001078418.1| cytochrome c oxidase biogenesis protein Cmc1-like protein [Arabidopsis thaliana] gi|110743950|dbj|BAE99808.1| hypothetical protein [Arabidopsis thaliana] gi|332659018|gb|AEE84418.1| cytochrome c oxidase biogenesis protein Cmc1-like protein [Arabidopsis thaliana] gi|332659019|gb|AEE84419.1| cytochrome c oxidase biogenesis protein Cmc1-like protein [Arabidopsis thaliana]	80	80	5.00E−35	100.0	92.5	95.0	cytochrome c oxidase biogenesis protein Cmc1-like protein	gbpln	Arabidopsis thaliana	AT4G21192.2 | Symbols: | Cytochrome c oxidase biogenesis protein Cmc1-like | chr4:11294563-11295192 FORWARD LENGTH=80	80	80	8.00E−38	100.0	92.5	95.0
Rsa1.0_00286.1.g10493.t2	gb|EOA15848.1| hypothetical protein CARUB_v10007608mg [Capsella rubella]	269	338	7.00E−96	125.7	60.6	62.8	hypothetical protein CARUB_v10007608mg	gbpln	Capsella rubella	AT4G21200.1 | Symbols: ATGA2OX8, GA2OX8 | gibberellin 2-oxidase 8 | chr4:11302751-11306601 FORWARD LENGTH=338	269	338	3.00E−98	125.7	60.2	62.8
Rsa1.0_00286.1.g10494.t2	ref|NP_974583.1| uncharacterized protein [Arabidopsis thaliana] gi|222423130|dbj|BAH19544.1| AT4G21215 [Arabidopsis thaliana] gi|332659027|gb|AEE84427.1| uncharacterized protein AT4G21215 [Arabidopsis thaliana]	197	199	5.00E−81	101.0	81.2	88.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G21215.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:11310890-11313421 REVERSE LENGTH=199	197	199	2.00E−83	101.0	81.2	88.8
Rsa1.0_00286.1.g10495.t1	gb|EOA17156.1| hypothetical protein CARUB_v10005424mg [Capsella rubella]	288	286	1.00E−158	99.3	93.8	98.3	hypothetical protein CARUB_v10005424mg	gbpln	Capsella rubella	AT4G21320.1 | Symbols: HSA32 | Aldolase-type TIM barrel family protein | chr4:11340492-11341732 FORWARD LENGTH=286	288	286	1.00E−160	99.3	93.4	97.9
Rsa1.0_00286.1.g10496.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00286.1.g10497.t1	ref|NP_567624.1| Subtilase family protein [Arabidopsis thaliana] gi|332659040|gb|AEE84440.1| Subtilase family protein [Arabidopsis thaliana]	802	803	0	100.1	70.7	80.9	Subtilase family protein	gbpln	Arabidopsis thaliana	AT4G21323.1 | Symbols: | Subtilase family protein | chr4:11342494-11345632 FORWARD LENGTH=803	802	803	0	100.1	70.7	80.9
Rsa1.0_00286.1.g10498.t1	emb|CCI61494.1| unnamed protein product [Arabidopsis halleri]	750	756	0	100.8	67.9	80.8	unnamed protein product	gbpln	Arabidopsis halleri	AT4G21326.1 | Symbols: ATSBT3.12, SBT3.12 | subtilase 3.12 | chr4:11346685-11349653 FORWARD LENGTH=754	750	754	0	100.5	66.9	81.1
Rsa1.0_00286.1.g10499.t1	gb|ABV21217.1| At4g21410 [Arabidopsis thaliana]	625	679	0	108.6	78.6	87.2	At4g21410	gbpln	Arabidopsis thaliana	AT4G21410.1 | Symbols: CRK29 | cysteine-rich RLK (RECEPTOR-like protein kinase) 29 | chr4:11402463-11405025 REVERSE LENGTH=679	625	679	0	108.6	78.7	87.2
Rsa1.0_00286.1.g10500.t1	ref|XP_002867848.1| hypothetical protein ARALYDRAFT_914534 [Arabidopsis lyrata subsp. lyrata] gi|297313684|gb|EFH44107.1| hypothetical protein ARALYDRAFT_914534 [Arabidopsis lyrata subsp. lyrata]	1000	937	0	93.7	71.7	79.3	hypothetical protein ARALYDRAFT_914534	gbpln	Arabidopsis lyrata	AT4G21430.1 | Symbols: B160 | Zinc finger, RING-type;Transcription factor jumonji/aspartyl beta-hydroxylase | chr4:11407835-11412159 REVERSE LENGTH=927	1000	927	0	92.7	70.7	77.9
Rsa1.0_00287.1.g10501.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	572	627	6.00E−42	109.6	24.5	39.9	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00287.1.g10502.t1	ref|XP_002894513.1| WRKY10 [Arabidopsis lyrata subsp. lyrata] gi|297340355|gb|EFH70772.1| WRKY10 [Arabidopsis lyrata subsp. lyrata]	202	495	3.00E−38	245.0	50.0	65.8	WRKY10	gbpln	Arabidopsis lyrata	AT1G55600.1 | Symbols: WRKY10, ATWRKY10, MINI3 | WRKY DNA-binding protein 10 | chr1:20774049-20776293 REVERSE LENGTH=485	202	485	6.00E−38	240.1	51.5	68.3
Rsa1.0_00287.1.g10503.t1	ref|XP_002894389.1| hypothetical protein ARALYDRAFT_474385 [Arabidopsis lyrata subsp. lyrata] gi|297340231|gb|EFH70648.1| hypothetical protein ARALYDRAFT_474385 [Arabidopsis lyrata subsp. lyrata]	168	172	5.00E−87	102.4	95.2	97.6	hypothetical protein ARALYDRAFT_474385	gbpln	Arabidopsis lyrata	AT1G52590.1 | Symbols: | Putative thiol-disulphide oxidoreductase DCC | chr1:19589224-19590231 REVERSE LENGTH=172	168	172	3.00E−89	102.4	94.6	97.0
Rsa1.0_00287.1.g10504.t1	gb|EOA37169.1| hypothetical protein CARUB_v10010503mg, partial [Capsella rubella]	135	163	8.00E−61	120.7	94.1	97.0	hypothetical protein CARUB_v10010503mg, partial	gbpln	Capsella rubella	AT1G52740.1 | Symbols: HTA9 | histone H2A protein 9 | chr1:19645409-19646221 FORWARD LENGTH=134	135	134	4.00E−63	99.3	94.1	97.0
Rsa1.0_00287.1.g10505.t1	gb|ABA94365.1| retrotransposon protein, putative, unclassified [Oryza sativa Japonica Group]	1171	1064	1.00E−163	90.9	25.1	31.3	retrotransposon protein, putative, unclassified	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1171	1262	3.00E−76	107.8	14.3	22.4

Rsa1.0_00287.1.g10506.t1	ref|XP_002891715.1| phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297337557|gb|EFH67974.1| phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	432	456	1.00E-128	105.6	59.7	70.1	phototropic-responsive NPH3 family protein	gbpln	Arabidopsis lyrata	AT1G52770.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr1:19656009-19657546 FORWARD LENGTH=454	432	454	1.00E-130	105.1	60.0	70.8
Rsa1.0_00287.1.g10507.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00287.1.g10508.t1	dbj|BAB11196.1| mutator-like transposase [Arabidopsis thaliana]	399	797	2.00E-22	199.7	16.5	25.1	mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00287.1.g10509.t1	gb|EOA38369.1| hypothetical protein CARUB_v10009902mg [Capsella rubella]	329	292	1.00E-150	88.8	80.9	82.7	hypothetical protein CARUB_v10009902mg	gbpln	Capsella rubella	AT1G53000.1 | Symbols: KDSB | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:19745330-19747133 REVERSE LENGTH=290	329	290	1.00E-145	88.1	80.9	83.6
Rsa1.0_00287.1.g10510.t1	dbj|BAC42437.1| putative ubiquitin-conjugating enzyme [Arabidopsis thaliana] gi|29028948|gb|AAO64853.1| At1g53020 [Arabidopsis thaliana]	441	543	1.00E-166	123.1	73.2	84.1	putative ubiquitin-conjugating enzyme	gbpln	Arabidopsis thaliana	AT1G53025.1 | Symbols: | Ubiquitin-conjugating enzyme family protein | chr1:19757072-19759474 REVERSE LENGTH=543	441	543	1.00E-169	123.1	73.2	84.1
Rsa1.0_00287.1.g10511.t1	gb|EOA24465.1| hypothetical protein CARUB_v10017721mg [Capsella rubella]	446	302	1.00E-113	67.7	43.5	48.9	hypothetical protein CARUB_v10017721mg	gbpln	Capsella rubella	AT3G55620.1 | Symbols: emb1624 | Translation initiation factor IF6 | chr3:20634581-20636312 FORWARD LENGTH=245	446	245	1.00E-113	54.9	42.8	48.9
Rsa1.0_00287.1.g10512.t1	emb|CAN80991.1| hypothetical protein VITISV_021529 [Vitis vinifera]	227	1033	2.00E-51	455.1	53.7	66.5	hypothetical protein VITISV_021529	gbpln	Vitis vinifera	AT3G29785.1 | Symbols: | unknown protein; Has 90 Blast hits to 90 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:11612357-11612686 REVERSE LENGTH=109	227	109	2.00E-28	48.0	26.0	31.3
Rsa1.0_00287.1.g10513.t1	dbj|BAJ34063.1| unnamed protein product [Thellungiella halophila]	263	267	1.00E-127	101.5	84.4	92.0	unnamed protein product	----	----	AT3G01980.4 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:327747-328833 REVERSE LENGTH=266	263	266	1.00E-124	101.1	79.1	87.8
Rsa1.0_00287.1.g10514.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00287.1.g10515.t1	gb|EOA38074.1| hypothetical protein CARUB_v10009543mg, partial [Capsella rubella]	252	358	6.00E-12	142.1	13.9	15.1	hypothetical protein CARUB_v10009543mg, partial	gbpln	Capsella rubella	AT1G16560.4 | Symbols: | Per1-like family protein | chr1:5669234-5670343 FORWARD LENGTH=287	252	287	3.00E-14	113.9	13.9	15.1
Rsa1.0_00287.1.g10516.t1	ref|NP_175712.2| uncharacterized protein [Arabidopsis thaliana] gi|42571845|ref|NP_974013.1| uncharacterized protein [Arabidopsis thaliana] gi|110738523|dbj|BAF01187.1| hypothetical protein [Arabidopsis thaliana] gi|332194761|gb|AEE32882.1| uncharacterized protein AT1G53040 [Arabidopsis thaliana] gi|332194762|gb|AEE32883.1| uncharacterized protein AT1G53040 [Arabidopsis thaliana]	536	540	0	100.7	89.2	95.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G53040.2 | Symbols: | Protein of unknown function (DUF616) | chr1:19764567-19766870 REVERSE LENGTH=540	536	540	0	100.7	89.2	95.1
Rsa1.0_00287.1.g10517.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00287.1.g10518.t1	ref|NP_175713.1| protein kinase-like protein [Arabidopsis thaliana] gi|9454540|gb|AAF87863.1|AC022520_7 similar to cdc2 protein kinase [Arabidopsis thaliana] gi|332194763|gb|AEE32884.1| protein kinase-like protein [Arabidopsis thaliana]	674	694	0	103.0	91.5	95.4	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G53050.1 | Symbols: | Protein kinase superfamily protein | chr1:19772574-19775531 FORWARD LENGTH=694	674	694	0	103.0	91.5	95.4
Rsa1.0_00287.1.g10519.t3	ref|XP_002894424.1| hypothetical protein ARALYDRAFT_474430 [Arabidopsis lyrata subsp. lyrata] gi|297340266|gb|EFH70683.1| hypothetical protein ARALYDRAFT_474430 [Arabidopsis lyrata subsp. lyrata]	424	406	1.00E-180	95.8	74.3	80.4	hypothetical protein ARALYDRAFT_474430	gbpln	Arabidopsis lyrata	AT1G53100.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:19786990-19788504 REVERSE LENGTH=423	424	423	0	99.8	74.5	81.4
Rsa1.0_00287.1.g10520.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	579	1164	1.00E-109	201.0	35.9	51.3	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	579	746	2.00E-48	128.8	21.9	34.0
Rsa1.0_00287.1.g10521.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	81	341	8.00E-12	421.0	44.4	50.6	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00288.1.g10522.t1	gb|EOA14818.1| hypothetical protein CARUB_v10028127mg [Capsella rubella]	662	1261	0	190.5	67.1	78.2	hypothetical protein CARUB_v10028127mg	gbpln	Capsella rubella	AT3G42670.1 | Symbols: CHR38, CLSY | chromatin remodeling 38 | chr3:14755906-14760085 REVERSE LENGTH=1256	662	1256	0	189.7	67.2	79.0

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<tr><td>Rsa1.0_00288.1.g10523.t1</td><td>ref|NP_567526.4| uncharacterized protein [Arabidopsis thaliana] gi|16323155|gb|AAL15312.1| AT4g17250/dl4660w [Arabidopsis thaliana] gi|23506021|gb|AAN28870.1| At4g17250/dl4660w [Arabidopsis thaliana] gi|332658469|gb|AEE83869.1| uncharacterized protein AT4G17250 [Arabidopsis thaliana]</td><td>730</td><td>741</td><td>0</td><td>101.5</td><td>80.5</td><td>88.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G17250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G47580.1); Has 31 Blast hits to 31 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:9671104-9673329 FORWARD LENGTH=741</td><td>730</td><td>741</td><td>0</td><td>101.5</td><td>80.5</td><td>88.9</td></tr>
<tr><td>Rsa1.0_00288.1.g10524.t1</td><td>gb|EOA14157.1| hypothetical protein CARUB_v10027303mg [Capsella rubella]</td><td>160</td><td>152</td><td>3.00E-25</td><td>95.0</td><td>37.5</td><td>60.0</td><td>hypothetical protein CARUB_v10027303mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G33393.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:12656430-12658588 REVERSE LENGTH=435</td><td>160</td><td>435</td><td>1.00E-14</td><td>271.9</td><td>26.9</td><td>39.4</td></tr>
<tr><td>Rsa1.0_00288.1.g10525.t1</td><td>gb|AAC26234.1| contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]</td><td>946</td><td>940</td><td>0</td><td>99.4</td><td>55.2</td><td>68.3</td><td>contains similarity to maize transposon MuDR (GB:M76978)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00288.1.g10526.t2</td><td>ref|XP_002870111.1| hypothetical protein ARALYDRAFT_914989 [Arabidopsis lyrata subsp. lyrata] gi|297315947|gb|EFH46370.1| hypothetical protein ARALYDRAFT_914989 [Arabidopsis lyrata subsp. lyrata]</td><td>562</td><td>567</td><td>0</td><td>100.9</td><td>91.6</td><td>96.1</td><td>hypothetical protein ARALYDRAFT_914989</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G17300.1 | Symbols: NS1, OVA8, ATNS1 | Class II aminoacyl-tRNA and biotin synthetases superfamily protein | chr4:9681558-9684833 FORWARD LENGTH=567</td><td>562</td><td>567</td><td>0</td><td>100.9</td><td>91.1</td><td>95.4</td></tr>
<tr><td>Rsa1.0_00288.1.g10527.t1</td><td>ref|XP_002870115.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297315951|gb|EFH46374.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>152</td><td>166</td><td>7.00E-58</td><td>109.2</td><td>73.7</td><td>83.6</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G17245.1 | Symbols: | RING/U-box superfamily protein | chr4:9669383-9669883 FORWARD LENGTH=166</td><td>152</td><td>166</td><td>9.00E-59</td><td>109.2</td><td>72.4</td><td>82.9</td></tr>
<tr><td>Rsa1.0_00288.1.g10528.t1</td><td>ref|NP_568685.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|30695248|ref|NP_851149.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|17528972|gb|AAL38696.1| putative RNA-binding protein [Arabidopsis thaliana] gi|23297042|gb|AAN13229.1| putative RNA-binding protein [Arabidopsis thaliana] gi|332008155|gb|AED95538.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|332008156|gb|AED95539.1| RNA recognition motif-containing protein [Arabidopsis thaliana]</td><td>390</td><td>431</td><td>1.00E-122</td><td>110.5</td><td>64.4</td><td>75.6</td><td>RNA recognition motif-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G47620.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:19302548-19304278 REVERSE LENGTH=431</td><td>390</td><td>431</td><td>1.00E-124</td><td>110.5</td><td>64.4</td><td>75.6</td></tr>
<tr><td>Rsa1.0_00288.1.g10529.t2</td><td>gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1331</td><td>1501</td><td>0</td><td>112.8</td><td>55.4</td><td>70.7</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1331</td><td>1262</td><td>1.00E-100</td><td>94.8</td><td>15.0</td><td>21.0</td></tr>
<tr><td>Rsa1.0_00288.1.g10530.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00288.1.g10531.t1</td><td>dbj|BAJ33904.1| unnamed protein product [Thellungiella halophila]</td><td>526</td><td>532</td><td>0</td><td>101.1</td><td>89.7</td><td>94.7</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G17230.1 | Symbols: SCL13 | SCARECROW-like 13 | chr4:9661218-9662807 REVERSE LENGTH=529</td><td>526</td><td>529</td><td>0</td><td>100.6</td><td>85.7</td><td>91.1</td></tr>
<tr><td>Rsa1.0_00288.1.g10532.t1</td><td>gb|ABD65130.1| hypothetical protein 40.t00005 [Brassica oleracea]</td><td>510</td><td>530</td><td>0</td><td>103.9</td><td>80.0</td><td>86.9</td><td>hypothetical protein 40.t00005</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17210.1 | Symbols: | Plant protein of unknown function (DUF827) | chr4:9652585-9654257 REVERSE LENGTH=527</td><td>510</td><td>527</td><td>0</td><td>103.3</td><td>75.5</td><td>86.3</td></tr>
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Rsa1.0_00288.1.g10533.t2	ref|NP_193450.1| RAB GTPase homolog B1C [Arabidopsis thaliana] gi|297800394|ref|XP_002868081.1| hypothetical protein ARALYDRAFT_493160 [Arabidopsis lyrata subsp. lyrata] gi|75279776|sp|P92963.1|RAB1C_ARATH RecName: Full=Ras-related protein RABB1c; Short=AtRABB1c; AltName: Full=Ras-related protein Rab2A; Short=AtRab2A gi|1765896|emb|CAA70498.1| Rab2-like protein [Arabidopsis thaliana] gi|5281023|emb|CAB45962.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|7268468|emb|CAB80988.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|27311815|gb|AAO00873.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|30023652|gb|AAP13359.1| At4g17170 [Arabidopsis thaliana] gi|297313917|gb|EFH44340.1| hypothetical protein ARALYDRAFT_493160 [Arabidopsis lyrata subsp. lyrata] gi|332658457|gb|AEE83857.1| RAB GTPase homolog B1C [Arabidopsis thaliana] gi|482553233|gb|EOA17426.1| hypothetical protein CARUB_v10005730mg [Capsella rubella]	230	211	1.00E-113	91.7	88.3	90.4	RAB GTPase homolog B1C	gbpln	Arabidopsis lyrata	AT4G17170.1 | Symbols: AT-RAB2, ATRABB1C, ATRAB2A, RAB2A, RABB1C, ATRAB-B1B, RAB-B1B | RAB GTPase homolog B1C | chr4:9644908-9646220 REVERSE LENGTH=211	230	211	1.00E-115	91.7	88.3	90.4
Rsa1.0_00288.1.g10534.t1	ref|XP_002870121.1| hypothetical protein ARALYDRAFT_915007 [Arabidopsis lyrata subsp. lyrata] gi|297315957|gb|EFH46380.1| hypothetical protein ARALYDRAFT_915007 [Arabidopsis lyrata subsp. lyrata]	513	501	0	97.7	77.4	84.2	hypothetical protein ARALYDRAFT_915007	gbpln	Arabidopsis lyrata	AT4G17150.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:9638591-9641648 FORWARD LENGTH=502	513	502	0	97.9	78.0	84.2
Rsa1.0_00288.1.g10535.t6	ref|NP_001190747.1| pleckstrin homology (PH) domain-containing protein [Arabidopsis thaliana] gi|332658453|gb|AEE83853.1| pleckstrin homology (PH) domain-containing protein [Arabidopsis thaliana]	4236	4219	0	99.6	88.3	93.5	pleckstrin homology (PH) domain-containing protein	gbpln	Arabidopsis thaliana	AT4G17140.3 | Symbols: | pleckstrin homology (PH) domain-containing protein | chr4:9613617-9636618 REVERSE LENGTH=4219	4236	4219	0	99.6	88.3	93.5
Rsa1.0_00288.1.g10536.t1	ref|XP_002870122.1| hypothetical protein ARALYDRAFT_329817 [Arabidopsis lyrata subsp. lyrata] gi|297315958|gb|EFH46381.1| hypothetical protein ARALYDRAFT_329817 [Arabidopsis lyrata subsp. lyrata]	59	57	1.00E-20	96.6	88.1	93.2	hypothetical protein ARALYDRAFT_329817	gbpln	Arabidopsis lyrata	AT4G17085.1 | Symbols: | Putative membrane lipoprotein | chr4:9604527-9604804 FORWARD LENGTH=57	59	57	1.00E-22	96.6	88.1	91.5
Rsa1.0_00288.1.g10537.t1	gb|EOA16451.1| hypothetical protein CARUB_v10004606mg [Capsella rubella]	440	513	0	116.6	86.8	92.5	hypothetical protein CARUB_v10004606mg	gbpln	Capsella rubella	AT4G17080.1 | Symbols: | Histone H3 K4-specific methyltransferase SET7/9 family protein | chr4:9601570-9603815 FORWARD LENGTH=513	440	513	0	116.6	86.4	92.3
Rsa1.0_00288.1.g10538.t1	ref|XP_002868086.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313922|gb|EFH44345.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	337	342	1.00E-175	101.5	88.1	94.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G17070.1 | Symbols: | peptidyl-prolyl cis-trans isomerases | chr4:9595523-9598066 REVERSE LENGTH=343	337	343	1.00E-175	101.8	88.1	93.8
Rsa1.0_00288.1.g10539.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00288.1.g10540.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_00288.1.g10541.t1</td><td>ref|NP_564041.2| homeobox-leucine zipper protein HDG12 [Arabidopsis thaliana] gi|75264044|sp|Q9LMT8.1|HDG12_ARATH RecName: Full=Homeobox-leucine zipper protein HDG12; AltName: Full=HD-ZIP protein HDG12; AltName: Full=Homeodomain GLABRA 2-like protein 12; AltName: Full=Homeodomain transcription factor HDG12; AltName: Full=Protein HOMEODOMAIN GLABROUS 12 gi|9665069|gb|AAF97271.1|AC034106_14 Strong similarity to meristem L1 layer homeobox protein (ATML1) from Arabidopsis thaliana gb|U37589 and contains Transposase PF|01527, Homeobox PF|00046, and START PF|01852 domains. EST gb|AI995645 comes from this gene [Arabidopsis thaliana] gi|225897942|dbj|BAH30303.1| hypothetical protein [Arabidopsis thaliana] gi|332191531|gb|AEE29652.1| homeobox-leucine zipper protein HDG12 [Arabidopsis thaliana]</td><td>139</td><td>687</td><td>2.00E-40</td><td>494.2</td><td>63.3</td><td>71.9</td><td>homeobox-leucine zipper protein HDG12</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G17920.1 | Symbols: HDG12 | homeodomain GLABROUS 12 | chr1:6162214-6165033 REVERSE LENGTH=687</td><td>139</td><td>687</td><td>4.00E-43</td><td>494.2</td><td>63.3</td><td>71.9</td></tr>
<tr><td>Rsa1.0_00288.1.g10542.t1</td><td>dbj|BAC42864.1| unknown protein [Arabidopsis thaliana]</td><td>387</td><td>434</td><td>1.00E-130</td><td>112.1</td><td>79.3</td><td>87.1</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G17060.1 | Symbols: FIP2 | FRIGIDA interacting protein 2 | chr4:9593721-9594653 REVERSE LENGTH=310</td><td>387</td><td>310</td><td>7.00E-85</td><td>80.1</td><td>53.5</td><td>58.9</td></tr>
<tr><td>Rsa1.0_00289.1.g10543.t2</td><td>gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]</td><td>260</td><td>1485</td><td>2.00E-44</td><td>571.2</td><td>33.1</td><td>40.0</td><td>hypothetical protein PRUPE_ppa017790mg</td><td>gbpln</td><td>Prunus persica</td><td>ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158</td><td>260</td><td>158</td><td>5.00E-15</td><td>60.8</td><td>13.5</td><td>19.6</td></tr>
<tr><td>Rsa1.0_00289.1.g10544.t1</td><td>ref|NP_849388.1| tubulin alpha-6 chain [Arabidopsis thaliana] gi|222422983|dbj|BAH19475.1| AT4G14960 [Arabidopsis thaliana] gi|332658129|gb|AEE83529.1| tubulin alpha-6 chain [Arabidopsis thaliana]</td><td>390</td><td>427</td><td>0</td><td>109.5</td><td>98.7</td><td>99.0</td><td>tubulin alpha-6 chain</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G14960.1 | Symbols: TUA6 | Tubulin/FtsZ family protein | chr4:8548753-8550319 REVERSE LENGTH=427</td><td>390</td><td>427</td><td>0</td><td>109.5</td><td>98.7</td><td>99.0</td></tr>
<tr><td>Rsa1.0_00289.1.g10545.t1</td><td>gb|EOA37944.1| hypothetical protein CARUB_v10009411mg [Capsella rubella]</td><td>389</td><td>387</td><td>0</td><td>99.5</td><td>94.6</td><td>97.9</td><td>hypothetical protein CARUB_v10009411mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G49970.1 | Symbols: CLPR1, NCLPP5, SVR2 | CLP protease proteolytic subunit 1 | chr1:18501936-18504462 REVERSE LENGTH=387</td><td>389</td><td>387</td><td>0</td><td>99.5</td><td>93.6</td><td>97.4</td></tr>
<tr><td>Rsa1.0_00289.1.g10546.t1</td><td>gb|AAF76447.1|AC015445_14 Identical to permease homolog (At PER-X) partial cds gb|U83501 and contains a Xanthine/Uracil Permease PF|00860 domain. EST gb|AA712474 comes from this gene [Arabidopsis thaliana]</td><td>522</td><td>529</td><td>0</td><td>101.3</td><td>94.1</td><td>97.3</td><td>Identical to permease homolog (At PER-X) partial cds gb|U83501 and contains a Xanthine/Uracil Permease PF|00860 domain. EST gb|AA712474 comes from this gene</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G49960.1 | Symbols: | Xanthine/uracil permease family protein | chr1:18498700-18501699 FORWARD LENGTH=526</td><td>522</td><td>526</td><td>0</td><td>100.8</td><td>94.6</td><td>97.9</td></tr>
<tr><td>Rsa1.0_00289.1.g10547.t1</td><td>gb|EOA36147.1| hypothetical protein CARUB_v10009836mg [Capsella rubella]</td><td>292</td><td>307</td><td>2.00E-79</td><td>105.1</td><td>68.8</td><td>82.9</td><td>hypothetical protein CARUB_v10009836mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G49950.1 | Symbols: TRB1, ATTRB1 | telomere repeat binding factor 1 | chr1:18494439-18496713 REVERSE LENGTH=300</td><td>292</td><td>300</td><td>5.00E-75</td><td>102.7</td><td>64.0</td><td>78.8</td></tr>
<tr><td>Rsa1.0_00289.1.g10548.t1</td><td>gb|EOA38178.1| hypothetical protein CARUB_v10009656mg [Capsella rubella]</td><td>339</td><td>339</td><td>0</td><td>100.0</td><td>93.8</td><td>97.9</td><td>hypothetical protein CARUB_v10009656mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G49910.1 | Symbols: BUB3.2 | Transducin/WD40 repeat-like superfamily protein | chr1:18479025-18481271 FORWARD LENGTH=339</td><td>339</td><td>339</td><td>0</td><td>100.0</td><td>93.5</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00289.1.g10549.t2</td><td>ref|XP_002891526.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata] gi|297337368|gb|EFH67785.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata]</td><td>398</td><td>824</td><td>8.00E-65</td><td>207.0</td><td>34.4</td><td>47.2</td><td>hypothetical protein ARALYDRAFT_337115</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452</td><td>398</td><td>452</td><td>1.00E-42</td><td>113.6</td><td>22.6</td><td>32.7</td></tr>
<tr><td>Rsa1.0_00289.1.g10550.t1</td><td>ref|NP_175473.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75178225|sp|Q9LPS8.1|U79B5_ARATH RecName: Full=UDP-glycosyltransferase 79B5 gi|9454554|gb|AAF87877.1|AC012561_10 Putative glucosyl transferase [Arabidopsis thaliana] gi|12322328|gb|AAG51184.1|AC079279_5 UDP rhamnose: anthocyanidin-3-glucoside rhamnosyltransferase, putative [Arabidopsis thaliana] gi|332194445|gb|AEE32566.1| UDP-glycosyltransferase 79B5 [Arabidopsis thaliana]</td><td>442</td><td>448</td><td>0</td><td>101.4</td><td>78.7</td><td>86.4</td><td>UDP-glycosyltransferase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G50580.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:18730831-18732177 FORWARD LENGTH=448</td><td>442</td><td>448</td><td>0</td><td>101.4</td><td>78.7</td><td>86.4</td></tr>
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Rsa1.0_00289.1.g10551.t1	gb|AAG60167.1|AC074110_5 hypothetical protein [Arabidopsis thaliana]	559	722	0	129.2	76.7	82.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G49890.1 | Symbols: QWRF2 | Family of unknown function (DUF566) | chr1:18470282−18473463 FORWARD LENGTH=659	559	659	0	117.9	76.7	82.6
Rsa1.0_00289.1.g10552.t2	gb|AAM63908.1| unknown [Arabidopsis thaliana]	224	190	1.00E−90	84.8	75.9	78.6	unknown	gbpln	Arabidopsis thaliana	AT1G49880.1 | Symbols: Erv1 | Erv1/Alr family protein | chr1:18464081−18465914 FORWARD LENGTH=191	224	191	4.00E−91	85.3	75.9	78.6
Rsa1.0_00289.1.g10553.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1616	1213	0	75.1	23.8	35.1	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I−like superfamily protein | chr1:16528880−16531065 REVERSE LENGTH=626	1616	626	1.00E−65	38.7	11.0	17.9
Rsa1.0_00289.1.g10554.t1	ref|NP_175409.1| uncharacterized protein [Arabidopsis thaliana] gi|12323598|gb|AAG51774.1|AC079674_7 hypothetical protein; 28681−31893 [Arabidopsis thaliana] gi|332194364|gb|AEE32485.1| uncharacterized protein AT1G49870 [Arabidopsis thaliana]	835	828	0	99.2	82.8	89.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G49870.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; Has 6518 Blast hits to 5022 proteins in 522 species: Archae − 49; Bacteria − 635; Metazoa − 3264; Fungi − 379; Plants − 242; Viruses − 9; Other Eukaryotes − 1940 (source: NCBI BLink). | chr1:18460345−18463557 FORWARD LENGTH=828	835	828	0	99.2	82.8	89.0
Rsa1.0_00290.1.g10555.t1	ref|XP_002870829.1| hypothetical protein ARALYDRAFT_494099 [Arabidopsis lyrata subsp. lyrata] gi|297316665|gb|EFH47088.1| hypothetical protein ARALYDRAFT_494099 [Arabidopsis lyrata subsp. lyrata]	476	476	0	100.0	88.9	95.2	hypothetical protein ARALYDRAFT_494099	gbpln	Arabidopsis lyrata	AT5G38710.1 | Symbols: | Methylenetetrahydrofolate reductase family protein | chr5:15501340−15503899 FORWARD LENGTH=476	476	476	0	100.0	89.1	96.0
Rsa1.0_00290.1.g10556.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00290.1.g10557.t1	ref|NP_198688.2| uncharacterized protein [Arabidopsis thaliana] gi|26450395|dbj|BAC42312.1| unknown protein [Arabidopsis thaliana] gi|29824303|gb|AAP04112.1| unknown protein [Arabidopsis thaliana] gi|332006970|gb|AED94353.1| uncharacterized protein AT5G38720 [Arabidopsis thaliana]	324	306	1.00E−78	94.4	58.6	70.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G38720.1 | Symbols: | unknown protein; Has 13419 Blast hits to 9093 proteins in 698 species: Archae − 38; Bacteria − 1038; Metazoa − 4949; Fungi − 1086; Plants − 485; Viruses − 44; Other Eukaryotes − 5779 (source: NCBI BLink). | chr5:15508417−15510472 REVERSE LENGTH=306	324	306	3.00E−81	94.4	58.6	70.7
Rsa1.0_00290.1.g10558.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	421	442	1.00E−168	105.0	67.9	78.4	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase−derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae − 0; Bacteria − 0; Metazoa − 28; Fungi − 8; Plants − 388; Viruses − 0; Other Eukaryotes − 27 (source: NCBI BLink). | chr2:5736603−5737847 FORWARD LENGTH=343	421	343	6.00E−34	81.5	14.7	18.5
Rsa1.0_00290.1.g10559.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	247	258	3.00E−54	104.5	52.6	66.8	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483−17578391 REVERSE LENGTH=302	247	302	1.00E−45	122.3	49.8	67.6
Rsa1.0_00290.1.g10560.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00290.1.g10561.t1	ref|NP_198689.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana] gi|75171307|sp|Q9FKR3.1|PP404_ARATH RecName: Full=Pentatricopeptide repeat−containing protein At5g38730 gi|10176899|dbj|BAB10131.1| unnamed protein product [Arabidopsis thaliana] gi|332006971|gb|AED94354.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana]	695	596	0	85.8	73.4	80.3	pentatricopeptide repeat−containing protein	gbpln	Arabidopsis thaliana	AT5G38730.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr5:15510901−15512691 FORWARD LENGTH=596	695	596	0	85.8	73.4	80.3
Rsa1.0_00290.1.g10562.t1	ref|NP_198716.1| putative receptor−like protein kinase [Arabidopsis thaliana] gi|75333906|sp|Q9FID8.1|Y5900_ARATH RecName: Full=Putative receptor−like protein kinase At5g39000; Flags: Precursor gi|10177545|dbj|BAB10824.1| receptor−like protein kinase [Arabidopsis thaliana] gi|332007002|gb|AED94385.1| putative receptor−like protein kinase [Arabidopsis thaliana]	884	873	0	98.8	69.7	82.0	putative receptor−like protein kinase	gbpln	Arabidopsis thaliana	AT5G39000.1 | Symbols: | Malectin/receptor−like protein kinase family protein | chr5:15611860−15614481 FORWARD LENGTH=873	884	873	0	98.8	69.7	82.0

Rsa1.0_00290.1.g10563.t1	ref|NP_198716.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|75333906|sp|Q9FID8.1|Y5900_ARATH RecName: Full=Putative receptor-like protein kinase At5g39000; Flags: Precursor gi|10177545|dbj|BAB10824.1| receptor-like protein kinase [Arabidopsis thaliana] gi|332007002|gb|AED94385.1| putative receptor-like protein kinase [Arabidopsis thaliana]	830	873	0	105.2	69.9	80.5	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G39000.1 | Symbols: | Malectin/receptor-like protein kinase family protein | chr5:15611860-15614481 FORWARD LENGTH=873	830	873	0	105.2	69.9	80.5
Rsa1.0_00290.1.g10564.t1	ref|XP_002870805.1| ATTAP2 [Arabidopsis lyrata subsp. lyrata] gi|297316641|gb|EFH47064.1| ATTAP2 [Arabidopsis lyrata subsp. lyrata]	641	644	0	100.5	92.8	96.6	ATTAP2	gbpln	Arabidopsis lyrata	AT5G39040.1 | Symbols: ALS1, ATTAP2, TAP2 | transporter associated with antigen processing protein 2 | chr5:15625660-15629621 FORWARD LENGTH=644	641	644	0	100.5	92.7	96.6
Rsa1.0_00290.1.g10565.t1	gb|EOA16596.1| hypothetical protein CARUB_v10004762mg [Capsella rubella]	468	462	0	98.7	74.4	87.6	hypothetical protein CARUB_v10004762mg	gbpln	Capsella rubella	AT5G39050.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:15634596-15636005 FORWARD LENGTH=469	468	469	0	100.2	75.6	86.1
Rsa1.0_00290.1.g10566.t1	ref|XP_002868739.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314575|gb|EFH44998.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	222	223	1.00E-109	100.5	88.3	93.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G39110.1 | Symbols: | RmlC-like cupins superfamily protein | chr5:15657802-15658584 REVERSE LENGTH=222	222	222	1.00E-109	100.0	84.2	91.9
Rsa1.0_00290.1.g10567.t1	ref|NP_198738.2| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] gi|28393576|gb|AAO42208.1| unknown protein [Arabidopsis thaliana] gi|28973005|gb|AAO63827.1| unknown protein [Arabidopsis thaliana] gi|332007026|gb|AED94409.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	333	330	1.00E-173	99.1	89.8	94.6	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis thaliana	AT5G39220.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:15705913-15708039 FORWARD LENGTH=330	333	330	1.00E-176	99.1	89.8	94.6
Rsa1.0_00290.1.g10568.t1	ref|XP_002868736.1| hypothetical protein ARALYDRAFT_916399 [Arabidopsis lyrata subsp. lyrata] gi|297314572|gb|EFH44995.1| hypothetical protein ARALYDRAFT_916399 [Arabidopsis lyrata subsp. lyrata]	121	114	2.00E-29	94.2	65.3	76.9	hypothetical protein ARALYDRAFT_916399	gbpln	Arabidopsis lyrata	AT5G39240.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G29370.1); Has 15 Blast hits to 15 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 15; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:15712683-15713003 REVERSE LENGTH=106	121	106	1.00E-30	87.6	64.5	72.7
Rsa1.0_00290.1.g10569.t1	ref|NP_198741.1| F-box family protein [Arabidopsis thaliana] gi|75262644|sp|Q9FL82.1|FB270_ARATH RecName: Full=F-box protein At5g39250 gi|9758854|dbj|BAB09380.1| unnamed protein product [Arabidopsis thaliana] gi|20259549|gb|AAM13894.1| unknown protein [Arabidopsis thaliana] gi|21689711|gb|AAM67477.1| unknown protein [Arabidopsis thaliana] gi|332007029|gb|AED94412.1| F-box family protein [Arabidopsis thaliana]	251	252	1.00E-123	100.4	84.1	92.8	F-box family protein	gbpln	Arabidopsis thaliana	AT5G39250.1 | Symbols: | F-box family protein | chr5:15724860-15725618 FORWARD LENGTH=252	251	252	1.00E-125	100.4	84.1	92.8
Rsa1.0_00290.1.g10570.t1	sp|Q9FL80.3|EXP22_ARATH RecName: Full=Expansin-A22; Short=AtEXPA22; AltName: Full=Alpha-expansin-22; Short=At-EXP22; Short=AtEx22; AltName: Full=Ath-ExpAlpha-1.15; Flags: Precursor	273	279	1.00E-119	102.2	75.8	86.1	RecName: Full=Expansin-A22; Short=AtEXPA22; AltName: Full=Alpha-expansin-22; Short=At-EXP22; Short=AtEx22; AltName: Full=Ath-ExpAlpha-1.15; Flags: Precursor	----	----	AT5G39270.1 | Symbols: ATEXPA22, EXP22, ATEXP22, ATHEXP ALPHA 1.15, EXPA22 | expansin A22 | chr5:15729118-15730150 REVERSE LENGTH=263	273	263	1.00E-118	96.3	74.0	82.8
Rsa1.0_00291.1.g10571.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00291.1.g10572.t1	ref|XP_002887249.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333090|gb|EFH63508.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	203	202	7.00E-98	99.5	85.2	93.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G69680.1 | Symbols: | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | chr1:26205148-26206568 FORWARD LENGTH=202	203	202	2.00E-98	99.5	83.3	91.6
Rsa1.0_00291.1.g10573.t1	gb|EOA36886.1| hypothetical protein CARUB_v10008981mg, partial [Capsella rubella]	472	486	0	103.0	73.9	83.7	hypothetical protein CARUB_v10008981mg, partial	gbpln	Capsella rubella	AT1G28760.1 | Symbols: | Uncharacterized conserved protein (DUF2215) | chr1:10103158-10104588 FORWARD LENGTH=476	472	476	0	100.8	72.5	83.5
Rsa1.0_00291.1.g10574.t1	gb|EOA34585.1| hypothetical protein CARUB_v10022142mg, partial [Capsella rubella]	316	283	1.00E-104	89.6	57.6	70.6	hypothetical protein CARUB_v10022142mg, partial	gbpln	Capsella rubella	AT3G22080.1 | Symbols: | TRAF-like family protein | chr3:7777818-7781718 REVERSE LENGTH=648	316	648	1.00E-104	205.1	59.8	73.1
Rsa1.0_00291.1.g10575.t1	ref|NP_188846.2| TRAF-like family protein [Arabidopsis thaliana] gi|332643066|gb|AEE76587.1| TRAF-like family protein [Arabidopsis thaliana]	339	648	1.00E-97	191.2	54.3	67.8	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G22080.1 | Symbols: | TRAF-like family protein | chr3:7777818-7781718 REVERSE LENGTH=648	339	648	1.00E-100	191.2	54.3	67.8

Rsa1.0_00291.1.g10576.t1	gb|EOA35904.1| hypothetical protein CARUB_v10021161mg [Capsella rubella]	120	120	7.00E-59	100.0	95.0	98.3	hypothetical protein CARUB_v10021161mg	gbpln	Capsella rubella	AT1G69620.1 | Symbols: RPL34 | ribosomal protein L34 | chr1:26189900-26191081 FORWARD LENGTH=119	120	119	1.00E-60	99.2	93.3	96.7
Rsa1.0_00291.1.g10577.t1	gb|EOA33235.1| hypothetical protein CARUB_v10021295mg [Capsella rubella]	124	124	2.00E-42	100.0	67.7	78.2	hypothetical protein CARUB_v10021295mg	gbpln	Capsella rubella	AT1G69588.1 | Symbols: CLE45 | CLAVATA3/ESR-RELATED 45 | chr1:26178150-26178524 FORWARD LENGTH=124	124	124	5.00E-43	100.0	62.1	80.6
Rsa1.0_00291.1.g10578.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00291.1.g10579.t1	dbj|BAJ34568.1| unnamed protein product [Thellungiella halophila]	391	393	1.00E-164	100.5	81.6	86.4	unnamed protein product	----	----	AT1G69570.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr1:26161771-26163230 REVERSE LENGTH=399	391	399	1.00E-150	102.0	77.5	85.2
Rsa1.0_00291.1.g10580.t1	ref|XP_002887243.1| MYB105 [Arabidopsis lyrata subsp. lyrata] gi|297333084|gb|EFH63502.1| MYB105 [Arabidopsis lyrata subsp. lyrata]	296	294	1.00E-128	99.3	75.7	83.1	MYB105	gbpln	Arabidopsis lyrata	AT1G69560.1 | Symbols: MYB105, LOF2, ATMYB105 | myb domain protein 105 | chr1:26157755-26158906 FORWARD LENGTH=330	296	330	1.00E-124	111.5	72.3	80.7
Rsa1.0_00291.1.g10581.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00291.1.g10582.t11	ref|XP_002863569.1| hypothetical protein ARALYDRAFT_917150 [Arabidopsis lyrata subsp. lyrata] gi|297309404|gb|EFH39828.1| hypothetical protein ARALYDRAFT_917150 [Arabidopsis lyrata subsp. lyrata]	1419	1177	0	82.9	35.0	44.8	hypothetical protein ARALYDRAFT_917150	gbpln	Arabidopsis lyrata	AT5G44510.1 | Symbols: TAO1 | target of AVRB operation1 | chr5:17929673-17934188 REVERSE LENGTH=1187	1419	1187	0	83.7	34.2	44.8
Rsa1.0_00291.1.g10583.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00291.1.g10584.t2	ref|XP_002863569.1| hypothetical protein ARALYDRAFT_917150 [Arabidopsis lyrata subsp. lyrata] gi|297309404|gb|EFH39828.1| hypothetical protein ARALYDRAFT_917150 [Arabidopsis lyrata subsp. lyrata]	971	1177	0	121.2	49.7	64.1	hypothetical protein ARALYDRAFT_917150	gbpln	Arabidopsis lyrata	AT5G44510.1 | Symbols: TAO1 | target of AVRB operation1 | chr5:17929673-17934188 REVERSE LENGTH=1187	971	1187	0	122.2	48.4	64.0
Rsa1.0_00291.1.g10585.t1	dbj|BAJ34610.1| unnamed protein product [Thellungiella halophila]	265	272	1.00E-131	102.6	89.1	93.2	unnamed protein product	----	----	AT1G69490.1 | Symbols: NAP, ANAC029, ATNAP | NAC-like, activated by AP3/PI | chr1:26122233-26123222 FORWARD LENGTH=268	265	268	1.00E-132	101.1	88.7	91.7
Rsa1.0_00291.1.g10586.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	313	1274	1.00E-74	407.0	47.6	63.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	313	303	2.00E-49	96.8	36.7	52.4
Rsa1.0_00291.1.g10587.t1	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	1035	1453	0	140.4	59.8	72.8	polyprotein	gbpln	Arabidopsis thaliana	ATMG00820.1 | Symbols: ORF170 | Reverse transcriptase (RNA-dependent DNA polymerase) | chrM:228573-229085 REVERSE LENGTH=170	1035	170	3.00E-38	16.4	7.1	9.4
Rsa1.0_00291.1.g10588.t1	ref|NP_177103.1| argonaute-like protein [Arabidopsis thaliana] gi|75169275|sp|Q9C793.1|AGO7_ARATH RecName: Full=Protein argonaute 7; AltName: Full=Protein ZIPPY gi|12597784|gb|AAG60096.1|AC073178_7 pinhead-like protein [Arabidopsis thaliana] gi|37528855|gb|AAQ92355.1| ZIPPY [Arabidopsis thaliana] gi|332196804|gb|AEE34925.1| protein argonaute 7 (protein ZIPPY) [Arabidopsis thaliana]	978	990	0	101.2	84.9	90.1	argonaute-like protein	gbpln	Arabidopsis thaliana	AT1G69440.1 | Symbols: AGO7, ZIP | Argonaute family protein | chr1:26101565-26105016 REVERSE LENGTH=990	978	990	0	101.2	84.9	90.1
Rsa1.0_00291.1.g10589.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00291.1.g10590.t1	ref|XP_002867758.1| hypothetical protein ARALYDRAFT_914352 [Arabidopsis lyrata subsp. lyrata] gi|297313594|gb|EFH44017.1| hypothetical protein ARALYDRAFT_914352 [Arabidopsis lyrata subsp. lyrata]	424	272	7.00E-42	64.2	27.1	35.1	hypothetical protein ARALYDRAFT_914352	gbpln	Arabidopsis lyrata	AT4G22600.1 | Symbols: | unknown protein; Has 26 Blast hits to 26 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11900211-11901032 REVERSE LENGTH=273	424	273	3.00E-42	64.4	26.7	36.1
Rsa1.0_00291.1.g10591.t1	gb|AAZ23773.1| plastid division regulator MinE [Brassica napus]	132	224	3.00E-64	169.7	92.4	97.0	plastid division regulator MinE	gbpln	Brassica napus	AT1G69390.1 | Symbols: ATMINE1, MINE1, ARC12 | homologue of bacterial MinE 1 | chr1:26084721-26086284 FORWARD LENGTH=229	132	229	1.00E-65	173.5	89.4	94.7
Rsa1.0_00291.1.g10592.t2	ref|XP_002887231.1| hypothetical protein ARALYDRAFT_894718 [Arabidopsis lyrata subsp. lyrata] gi|297333072|gb|EFH63490.1| hypothetical protein ARALYDRAFT_894718 [Arabidopsis lyrata subsp. lyrata]	322	319	1.00E-141	99.1	82.3	88.5	hypothetical protein ARALYDRAFT_894718	gbpln	Arabidopsis lyrata	AT1G69370.1 | Symbols: CM3, cm-3 | chorismate mutase 3 | chr1:26080098-26081559 FORWARD LENGTH=316	322	316	1.00E-141	98.1	79.5	86.3

Rsa1.0_00291.1.g10593.t1	ref|XP_002887226.1| hypothetical protein ARALYDRAFT_894705 [Arabidopsis lyrata subsp. lyrata] gi|297333067|gb|EFH63485.1| hypothetical protein ARALYDRAFT_894705 [Arabidopsis lyrata subsp. lyrata]	409	446	1.00E-100	109.0	51.1	66.7	hypothetical protein ARALYDRAFT_894705	gbpln	Arabidopsis lyrata	AT1G69250.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr1:26033163-26035301 FORWARD LENGTH=427	409	427	4.00E-97	104.4	50.4	67.5
Rsa1.0_00292.1.g10594.t1	ref|XP_002881620.1| yellow-leaf-specific gene 5 [Arabidopsis lyrata subsp. lyrata] gi|297327459|gb|EFH57879.1| yellow-leaf-specific gene 5 [Arabidopsis lyrata subsp. lyrata]	398	398	0	100.0	89.2	95.5	yellow-leaf-specific gene 5	gbpln	Arabidopsis lyrata	AT2G38860.2 | Symbols: YLS5 | Class I glutamine amidotransferase-like superfamily protein | chr2:16233629-16235207 REVERSE LENGTH=398	398	398	0	100.0	88.7	94.7
Rsa1.0_00292.1.g10595.t1	ref|NP_001031074.1| high mobility group B2 protein [Arabidopsis thaliana] gi|297845040|ref|XP_002890401.1| hypothetical protein ARALYDRAFT_472301 [Arabidopsis lyrata subsp. lyrata] gi|297336243|gb|EFH66660.1| hypothetical protein ARALYDRAFT_472301 [Arabidopsis lyrata subsp. lyrata] gi|332191886|gb|AEE30007.1| high mobility group B2 protein [Arabidopsis thaliana]	144	142	4.00E-65	98.6	91.0	95.1	high mobility group B2 protein	gbpln	Arabidopsis lyrata	AT1G20693.2 | Symbols: HMGB2, HMG BETA 1, NFD2, NFD02 | high mobility group B2 | chr1:7177282-7178487 FORWARD LENGTH=142	144	142	1.00E-67	98.6	91.0	95.1
Rsa1.0_00292.1.g10596.t1	ref|NP_001077570.1| high mobility group B3 protein [Arabidopsis thaliana] gi|332191890|gb|AEE30011.1| high mobility group B3 protein [Arabidopsis thaliana]	104	140	9.00E-29	134.6	75.0	80.8	high mobility group B3 protein	gbpln	Arabidopsis thaliana	AT1G20696.3 | Symbols: HMGB3, NFD3, NFD03 | high mobility group B3 | chr1:7179825-7181170 FORWARD LENGTH=140	104	140	1.00E-31	134.6	75.0	80.8
Rsa1.0_00292.1.g10597.t4	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1478	910	0	61.6	27.0	36.4	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1478	626	1.00E-109	42.4	13.2	18.6
Rsa1.0_00292.1.g10598.t1	ref|XP_002865328.1| molybdenum cofactor sulfurase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311163|gb|EFH41587.1| molybdenum cofactor sulfurase family protein [Arabidopsis lyrata subsp. lyrata]	102	308	1.00E-13	302.0	45.1	50.0	molybdenum cofactor sulfurase family protein	gbpln	Arabidopsis lyrata	AT5G44720.1 | Symbols: | Molybdenum cofactor sulfurase family protein | chr5:18043086-18045275 FORWARD LENGTH=308	102	308	1.00E-15	302.0	44.1	48.0
Rsa1.0_00292.1.g10599.t1	ref|XP_002890402.1| hypothetical protein ARALYDRAFT_472304 [Arabidopsis lyrata subsp. lyrata] gi|297336244|gb|EFH66661.1| hypothetical protein ARALYDRAFT_472304 [Arabidopsis lyrata subsp. lyrata]	143	141	4.00E-55	98.6	79.7	88.8	hypothetical protein ARALYDRAFT_472304	gbpln	Arabidopsis lyrata	AT1G20696.3 | Symbols: HMGB3, NFD3, NFD03 | high mobility group B3 | chr1:7179825-7181170 FORWARD LENGTH=140	143	140	2.00E-56	97.9	78.3	88.8
Rsa1.0_00292.1.g10600.t1	gb|EOA39693.1| hypothetical protein CARUB_v10008332mg [Capsella rubella]	801	801	0	100.0	84.8	92.8	hypothetical protein CARUB_v10008332mg	gbpln	Capsella rubella	AT1G20780.1 | Symbols: PUB44, ATPUB44, SAUL1 | senescence-associated E3 ubiquitin ligase 1 | chr1:7217812-7220609 FORWARD LENGTH=801	801	801	0	100.0	84.8	91.5
Rsa1.0_00292.1.g10601.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1464	1475	0	100.8	60.6	74.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1464	1262	0	86.2	22.5	29.0
Rsa1.0_00292.1.g10602.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00292.1.g10603.t1	gb|ABK56013.1| zinc finger protein [Brassica rapa]	199	196	3.00E-95	98.5	90.5	95.0	zinc finger protein	gbpln	Brassica rapa	AT1G20823.1 | Symbols: | RING/U-box superfamily protein | chr1:7238880-7239473 FORWARD LENGTH=197	199	197	4.00E-83	99.0	82.4	86.4
Rsa1.0_00292.1.g10604.t1	ref|XP_002890413.1| hypothetical protein ARALYDRAFT_472321 [Arabidopsis lyrata subsp. lyrata] gi|297336255|gb|EFH66672.1| hypothetical protein ARALYDRAFT_472321 [Arabidopsis lyrata subsp. lyrata]	300	357	1.00E-143	119.0	82.0	87.0	hypothetical protein ARALYDRAFT_472321	gbpln	Arabidopsis lyrata	AT1G20850.1 | Symbols: XCP2 | xylem cysteine peptidase 2 | chr1:7252208-7253537 FORWARD LENGTH=356	300	356	1.00E-140	118.7	78.7	82.7
Rsa1.0_00292.1.g10605.t1	ref|XP_002893135.1| hypothetical protein ARALYDRAFT_472323 [Arabidopsis lyrata subsp. lyrata] gi|297338977|gb|EFH69394.1| hypothetical protein ARALYDRAFT_472323 [Arabidopsis lyrata subsp. lyrata]	453	465	1.00E-161	102.6	69.5	82.8	hypothetical protein ARALYDRAFT_472323	gbpln	Arabidopsis lyrata	AT1G20870.1 | Symbols: | HSP20-like chaperones superfamily protein | chr1:7259287-7260775 REVERSE LENGTH=463	453	463	1.00E-162	102.2	67.8	81.0

Rsa1.0_00292.1.g10606.t1	ref|XP_002885269.1| hypothetical protein ARALYDRAFT_479371 [Arabidopsis lyrata subsp. lyrata] gi|297331109|gb|EFH61528.1| hypothetical protein ARALYDRAFT_479371 [Arabidopsis lyrata subsp. lyrata]	182	363	4.00E-20	199.5	30.2	34.1	hypothetical protein ARALYDRAFT_479371	gbpln	Arabidopsis lyrata	AT3G18650.1 | Symbols: AGL103 | AGAMOUS-like 103 | chr3:6417344-6418504 REVERSE LENGTH=386	182	386	6.00E-20	212.1	29.1	33.5
Rsa1.0_00292.1.g10607.t1	gb|EOA38418.1| hypothetical protein CARUB_v10009992mg [Capsella rubella]	189	274	4.00E-66	145.0	68.8	74.1	hypothetical protein CARUB_v10009992mg	gbpln	Capsella rubella	AT1G20880.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:7262879-7264834 REVERSE LENGTH=274	189	274	3.00E-66	145.0	65.6	72.0
Rsa1.0_00292.1.g10608.t1	gb|EOA36255.1| hypothetical protein CARUB_v10010341mg [Capsella rubella]	194	197	6.00E-59	101.5	59.8	67.0	hypothetical protein CARUB_v10010341mg	gbpln	Capsella rubella	AT1G20890.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76480.2); Has 33 Blast hits to 33 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7266088-7267060 REVERSE LENGTH=197	194	197	1.00E-60	101.5	59.8	66.5
Rsa1.0_00292.1.g10609.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	514	467	1.00E-140	90.9	48.6	60.3	hypothetical protein 31.t00031	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	514	566	3.00E-80	110.1	32.9	55.1
Rsa1.0_00292.1.g10610.t1	gb|ABD65101.1| hypothetical protein 31.t00082 [Brassica oleracea]	247	226	2.00E-46	91.5	40.1	57.5	hypothetical protein 31.t00082	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00292.1.g10611.t1	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	964	1453	1.00E-147	150.7	33.0	39.3	polyprotein	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	964	240	2.00E-53	24.9	11.5	13.8
Rsa1.0_00293.1.g10612.t1	dbj|BAB17226.1| myrosinase [Raphanus sativus]	545	548	0	100.6	96.9	97.6	myrosinase	gbpln	Raphanus sativus	AT5G26000.1 | Symbols: TGG1, BGLU38 | thioglucoside glucohydrolase 1 | chr5:9079678-9082347 REVERSE LENGTH=541	545	541	0	99.3	68.3	78.7
Rsa1.0_00293.1.g10613.t1	ref|NP_001185258.1| DNA-binding bromodomain-containing protein [Arabidopsis thaliana] gi|332195366|gb|AEE33487.1| DNA-binding bromodomain-containing protein [Arabidopsis thaliana]	226	573	7.00E-52	253.5	52.2	63.3	DNA-binding bromodomain-containing protein	gbpln	Arabidopsis thaliana	AT1G58025.3 | Symbols: | DNA-binding bromodomain-containing protein | chr1:21458219-21461757 REVERSE LENGTH=573	226	573	2.00E-54	253.5	52.2	63.3
Rsa1.0_00293.1.g10614.t1	gb|ABS83902.1| pheres1 [Arabidopsis lyrata] gi|154690693|gb|ABS83919.1| pheres1 [Arabidopsis lyrata] gi|154690709|gb|ABS83927.1| pheres1 [Arabidopsis lyrata]	141	274	2.00E-22	194.3	39.7	55.3	pheres1	gbpln	Arabidopsis lyrata	AT5G26650.1 | Symbols: AGL36 | AGAMOUS-like 36 | chr5:9343785-9344885 FORWARD LENGTH=366	141	366	2.00E-24	259.6	39.7	53.2
Rsa1.0_00293.1.g10615.t1	gb|AAX68547.1| myrosinase [Brassica rapa var. parachinensis]	161	548	9.00E-43	340.4	59.0	64.6	myrosinase	gbpln	Brassica rapa	AT5G25980.2 | Symbols: TGG2, BGLU37 | glucoside glucohydrolase 2 | chr5:9072730-9075477 FORWARD LENGTH=547	161	547	1.00E-36	339.8	47.2	55.9
Rsa1.0_00293.1.g10616.t1	gb|ABS83897.1| pheres1 [Arabidopsis lyrata]	265	269	2.00E-28	101.5	37.0	52.5	pheres1	gbpln	Arabidopsis lyrata	AT5G26650.1 | Symbols: AGL36 | AGAMOUS-like 36 | chr5:9343785-9344885 FORWARD LENGTH=366	265	366	2.00E-29	138.1	28.3	38.9
Rsa1.0_00293.1.g10617.t1	gb|EOA12793.1| hypothetical protein CARUB_v10025741mg [Capsella rubella]	1111	1478	0	133.0	83.3	88.7	hypothetical protein CARUB_v10025741mg	gbpln	Capsella rubella	AT5G67100.1 | Symbols: ICU2 | DNA-directed DNA polymerases | chr5:26776994-26785104 FORWARD LENGTH=1524	1111	1524	0	137.2	82.6	88.7
Rsa1.0_00293.1.g10618.t1	ref|XP_002865027.1| hypothetical protein ARALYDRAFT_496889 [Arabidopsis lyrata subsp. lyrata] gi|297310862|gb|EFH41286.1| hypothetical protein ARALYDRAFT_496889 [Arabidopsis lyrata subsp. lyrata]	194	206	4.00E-69	106.2	78.4	82.0	hypothetical protein ARALYDRAFT_496889	gbpln	Arabidopsis lyrata	AT5G67110.1 | Symbols: ALC | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:26785332-26786338 REVERSE LENGTH=210	194	210	2.00E-70	108.2	77.3	81.4
Rsa1.0_00293.1.g10619.t2	ref|XP_002868988.1| CYP91A2 [Arabidopsis lyrata subsp. lyrata] gi|297314824|gb|EFH45247.1| CYP91A2 [Arabidopsis lyrata subsp. lyrata]	375	500	1.00E-120	133.3	66.9	75.7	CYP91A2	gbpln	Arabidopsis lyrata	AT4G37430.1 | Symbols: CYP91A2, CYP81F1 | cytochrome P450, family 91, subfamily A, polypeptide 2 | chr4:17597242-17598829 FORWARD LENGTH=500	375	500	1.00E-111	133.3	58.4	65.3

Rsa1.0_00293.1.g10620.t1	ref|NP_850879.1| transcription factor MYB86 [Arabidopsis thaliana] gi|56749347|sp|Q8LPH6.1|MYB86_ARATH RecName: Full=Transcription factor MYB86; AltName: Full=Myb homolog 4; Short=AtMyb4; AltName: Full=Myb-related protein 86; Short=AtMYB86 gi|20466622|gb|AAM20628.1| transcription factor ATMYB4 [Arabidopsis thaliana] gi|30984580|gb|AAP42753.1| At5g26655 [Arabidopsis thaliana] gi|41619424|gb|AAS10099.1| MYB transcription factor [Arabidopsis thaliana] gi|332006197|gb|AED93580.1| transcription factor MYB86 [Arabidopsis thaliana]	340	352	1.00E-148	103.5	80.9	85.9	transcription factor MYB86	gbpln	Arabidopsis thaliana	AT5G26660.1 | Symbols: ATMYB86, MYB86 | myb domain protein 86 | chr5:9331775-9333044 REVERSE LENGTH=352	340	352	1.00E-150	103.5	80.9	85.9
Rsa1.0_00293.1.g10621.t1	ref|XP_002872226.1| heavy-metal-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318063|gb|EFH48485.1| heavy-metal-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata]	125	114	9.00E-31	91.2	63.2	79.2	heavy-metal-associated domain-containing protein	gbpln	Arabidopsis lyrata	AT5G26690.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:9310905-9311411 FORWARD LENGTH=114	125	114	3.00E-32	91.2	61.6	78.4
Rsa1.0_00293.1.g10622.t1	gb|EOA22223.1| hypothetical protein CARUB_v10002810mg [Capsella rubella]	217	216	9.00E-90	99.5	75.1	85.3	hypothetical protein CARUB_v10002810mg	gbpln	Capsella rubella	AT5G26700.1 | Symbols: | RmlC-like cupins superfamily protein | chr5:9308439-9309548 REVERSE LENGTH=213	217	213	4.00E-90	98.2	73.7	82.9
Rsa1.0_00293.1.g10623.t1	ref|NP_850874.1| glutamyl-tRNA synthetase [Arabidopsis thaliana] gi|3435196|gb|AAC36469.1| glutamyl-tRNA synthetase [Arabidopsis thaliana] gi|20466252|gb|AAM20443.1| glutamyl-tRNA synthetase [Arabidopsis thaliana] gi|23198080|gb|AAN15567.1| glutamyl-tRNA synthetase [Arabidopsis thaliana] gi|110740992|dbj|BAE98590.1| glutamyl-tRNA synthetase [Arabidopsis thaliana] gi|332006190|gb|AED93573.1| glutamyl/glutaminyl-tRNA synthetase, class Ic [Arabidopsis thaliana]	732	719	0	98.2	85.7	92.1	glutamyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT5G26710.1 | Symbols: | Glutamyl/glutaminyl-tRNA synthetase, class Ic | chr5:9305673-9308247 FORWARD LENGTH=719	732	719	0	98.2	85.7	92.1
Rsa1.0_00293.1.g10624.t1	ref|XP_002872223.1| hypothetical protein ARALYDRAFT_489490 [Arabidopsis lyrata subsp. lyrata] gi|297318060|gb|EFH48482.1| hypothetical protein ARALYDRAFT_489490 [Arabidopsis lyrata subsp. lyrata]	115	135	5.00E-15	117.4	59.1	70.4	hypothetical protein ARALYDRAFT_489490	gbpln	Arabidopsis lyrata	AT5G26720.1 | Symbols: | unknown protein; Has 15 Blast hits to 15 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 15; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:9304105-9304509 FORWARD LENGTH=134	115	134	4.00E-17	116.5	60.0	72.2
Rsa1.0_00293.1.g10625.t1	ref|NP_850872.1| Fasciclin-like arabinogalactan family protein [Arabidopsis thaliana] gi|332006188|gb|AED93571.1| Fasciclin-like arabinogalactan family protein [Arabidopsis thaliana]	110	268	8.00E-34	243.6	80.9	85.5	Fasciclin-like arabinogalactan family protein	gbpln	Arabidopsis thaliana	AT5G26730.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr5:9300422-9301990 FORWARD LENGTH=268	110	268	1.00E-36	243.6	80.9	85.5
Rsa1.0_00293.1.g10626.t1	gb|EOA19490.1| hypothetical protein CARUB_v10002163mg, partial [Capsella rubella]	103	158	1.00E-35	153.4	73.8	86.4	hypothetical protein CARUB_v10002163mg, partial	gbpln	Capsella rubella	AT3G05936.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:1774062-1774403 REVERSE LENGTH=113	103	113	2.00E-25	109.7	56.3	73.8
Rsa1.0_00293.1.g10627.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1557	2726	0	175.1	57.8	73.7	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1557	158	5.00E-34	10.1	4.6	5.4
Rsa1.0_00293.1.g10628.t1	gb|EOA20719.1| hypothetical protein CARUB_v10001039mg [Capsella rubella]	424	422	0	99.5	95.3	97.6	hypothetical protein CARUB_v10001039mg	gbpln	Capsella rubella	AT5G26740.3 | Symbols: | Protein of unknown function (DUF300) | chr5:9292436-9294407 FORWARD LENGTH=422	424	422	0	99.5	94.6	97.4
Rsa1.0_00293.1.g10629.t1	emb|CAA09196.1| RNA helicase [Arabidopsis thaliana]	740	748	0	101.1	89.7	93.8	RNA helicase	gbpln	Arabidopsis thaliana	AT5G26742.2 | Symbols: emb1138 | DEAD box RNA helicase (RH3) | chr5:9285540-9288871 REVERSE LENGTH=748	740	748	0	101.1	89.3	93.5
Rsa1.0_00293.1.g10630.t1	gb|EOA19326.1| hypothetical protein CARUB_v10003355mg [Capsella rubella]	86	84	9.00E-11	97.7	44.2	54.7	hypothetical protein CARUB_v10003355mg	gbpln	Capsella rubella	AT5G26673.1 | Symbols: | Putative membrane lipoprotein | chr5:9279309-9279611 FORWARD LENGTH=100	86	100	6.00E-12	116.3	44.2	50.0
Rsa1.0_00293.1.g10631.t1	emb|CAA09196.1| RNA helicase [Arabidopsis thaliana]	139	748	2.00E-27	538.1	75.5	79.1	RNA helicase	gbpln	Arabidopsis thaliana	AT5G26742.1 | Symbols: emb1138 | DEAD box RNA helicase (RH3) | chr5:9285540-9288871 REVERSE LENGTH=747	139	747	4.00E-23	537.4	74.8	78.4

Rsa1.0_00293.1.g10632.t1	gb|EOA19326.1| hypothetical protein CARUB_v10003355mg [Capsella rubella]	86	84	8.00E-11	97.7	44.2	54.7	hypothetical protein CARUB_v10003355mg	gbpln	Capsella rubella	AT5G26717.1 | Symbols: | Putative membrane lipoprotein | chr5:9284612-9284857 FORWARD LENGTH=81	86	81	1.00E-11	94.2	37.2	46.5
Rsa1.0_00293.1.g10633.t1	gb|EOA19326.1| hypothetical protein CARUB_v10003355mg [Capsella rubella]	86	84	1.00E-10	97.7	44.2	54.7	hypothetical protein CARUB_v10003355mg	gbpln	Capsella rubella	AT5G26717.1 | Symbols: | Putative membrane lipoprotein | chr5:9284612-9284857 FORWARD LENGTH=81	86	81	9.00E-12	94.2	38.4	46.5
Rsa1.0_00293.1.g10634.t1	gb|EOA23342.1| hypothetical protein CARUB_v10019413mg [Capsella rubella]	530	381	2.00E-67	71.9	30.0	41.5	hypothetical protein CARUB_v10019413mg	gbpln	Capsella rubella	AT3G28270.1 | Symbols: | Protein of unknown function (DUF677) | chr3:10538725-10539849 FORWARD LENGTH=374	530	374	8.00E-63	70.6	28.5	42.6
Rsa1.0_00293.1.g10635.t2	gb|EOA23342.1| hypothetical protein CARUB_v10019413mg [Capsella rubella]	766	381	3.00E-69	49.7	19.8	30.2	hypothetical protein CARUB_v10019413mg	gbpln	Capsella rubella	AT3G28270.1 | Symbols: | Protein of unknown function (DUF677) | chr3:10538725-10539849 FORWARD LENGTH=374	766	374	2.00E-64	48.8	19.2	29.1
Rsa1.0_00293.1.g10636.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00293.1.g10637.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00293.1.g10638.t1	gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]	455	543	3.00E-63	119.3	31.2	45.7	hypothetical protein CARUB_v10015730mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	455	566	6.00E-64	124.4	29.7	48.4
Rsa1.0_00293.1.g10639.t1	gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]	199	198	2.00E-50	99.5	53.8	70.9	hypothetical protein 27.t00041	gbpln	Brassica oleracea	AT2G35280.1 | Symbols: | F-box family protein | chr2:14859709-14860200 REVERSE LENGTH=163	199	163	7.00E-11	81.9	17.1	28.6
Rsa1.0_00293.1.g10640.t2	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	489	490	1.00E-85	100.2	38.0	58.3	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	489	566	2.00E-84	115.7	35.4	60.3
Rsa1.0_00293.1.g10641.t1	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	1700	1752	0	103.1	49.3	63.2	putative protein	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1700	331	7.00E-71	19.5	8.0	11.4
Rsa1.0_00293.1.g10642.t15	ref|NP_197952.2| small RNA degrading nuclease 5 [Arabidopsis thaliana] gi|215274964|sp|Q8L7M4.2|SDN5_ARATH RecName: Full=Small RNA degrading nuclease 5 gi|332006106|gb|AED93489.1| small RNA degrading nuclease 5 [Arabidopsis thaliana]	957	567	0	59.2	47.3	51.8	small RNA degrading nuclease 5	gbpln	Arabidopsis thaliana	AT5G25800.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:8979761-8982724 REVERSE LENGTH=567	957	567	0	59.2	47.3	51.8
Rsa1.0_00293.1.g10643.t1	gb|EOA20503.1| hypothetical protein CARUB_v10000816mg, partial [Capsella rubella]	383	491	9.00E-80	128.2	52.2	65.0	hypothetical protein CARUB_v10000816mg, partial	gbpln	Capsella rubella	AT5G25790.1 | Symbols: | Tesmin/TSO1-like CXC domain-containing protein | chr5:8977233-8979181 REVERSE LENGTH=459	383	459	7.00E-82	119.8	52.2	64.5
Rsa1.0_00293.1.g10644.t1	ref|XP_002874282.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320119|gb|EFH50541.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	576	402	1.00E-169	69.8	50.7	57.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G25770.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:8969308-8971806 REVERSE LENGTH=418	576	418	1.00E-169	72.6	48.4	55.6
Rsa1.0_00293.1.g10645.t15	ref|XP_002874282.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320119|gb|EFH50541.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	725	402	1.00E-160	55.4	37.2	42.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G25770.3 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:8969308-8971806 REVERSE LENGTH=421	725	421	1.00E-161	58.1	36.8	42.6
Rsa1.0_00293.1.g10646.t1	gb|EOA20666.1| hypothetical protein CARUB_v10000978mg, partial [Capsella rubella]	424	439	0	103.5	83.7	89.6	hypothetical protein CARUB_v10000978mg, partial	gbpln	Capsella rubella	AT5G25620.2 | Symbols: YUC6 | Flavin-binding monooxygenase family protein | chr5:8935312-8938200 REVERSE LENGTH=426	424	426	0	100.5	84.2	89.6
Rsa1.0_00293.1.g10647.t1	gb|AAQ57584.1| BURP domain-containing protein [Brassica napus]	387	387	0	100.0	92.2	96.4	BURP domain-containing protein	gbpln	Brassica napus	AT5G25610.1 | Symbols: RD22, ATRD22 | BURP domain-containing protein | chr5:8914498-8916684 REVERSE LENGTH=392	387	392	0	101.3	87.1	92.0
Rsa1.0_00293.1.g10648.t1	ref|NP_568475.1| uncharacterized protein [Arabidopsis thaliana] gi|42573475|ref|NP_974834.1| uncharacterized protein [Arabidopsis thaliana] gi|21592308|gb|AAM64259.1| unknown [Arabidopsis thaliana] gi|94807656|gb|ABF47125.1| At5g25570 [Arabidopsis thaliana] gi|332006083|gb|AED93466.1| uncharacterized protein AT5G25570 [Arabidopsis thaliana] gi|332006084|gb|AED93467.1| uncharacterized protein AT5G25570 [Arabidopsis thaliana]	215	99	3.00E-19	46.0	24.7	26.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G25570.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:8901832-8902891 FORWARD LENGTH=99	215	99	1.00E-21	46.0	24.7	26.5
Rsa1.0_00293.1.g10649.t3	ref|XP_002872173.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297318010|gb|EFH48432.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	306	308	1.00E-148	100.7	84.0	90.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G25560.1 | Symbols: | CHY-type/CTCHY-type/RING-type Zinc finger protein | chr5:8899486-8901391 FORWARD LENGTH=308	306	308	1.00E-149	100.7	83.0	91.2

Rsa1.0_00293.1.g10650.t1	gb|EOA21958.1| hypothetical protein CARUB_v10002457mg [Capsella rubella]	331	339	1.00E-163	102.4	88.5	94.0	hypothetical protein CARUB_v10002457mg	gbpln	Capsella rubella	AT5G25530.1 | Symbols: | DNAJ heat shock family protein | chr5:8889665-8890954 REVERSE LENGTH=347	331	347	1.00E-164	104.8	88.2	93.4
Rsa1.0_00293.1.g10651.t1	ref|XP_002874266.1| hypothetical protein ARALYDRAFT_489409 [Arabidopsis lyrata subsp. lyrata] gi|297320103|gb|EFH50525.1| hypothetical protein ARALYDRAFT_489409 [Arabidopsis lyrata subsp. lyrata]	490	499	0	101.8	84.7	92.2	hypothetical protein ARALYDRAFT_489409	gbpln	Arabidopsis lyrata	AT5G25510.1 | Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr5:8882728-8884325 REVERSE LENGTH=500	490	500	0	102.0	84.7	92.2
Rsa1.0_00293.1.g10652.t1	ref|XP_002874263.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320100|gb|EFH50522.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	278	280	1.00E-79	100.7	57.2	69.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G25470.2 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:8865854-8867234 REVERSE LENGTH=280	278	280	4.00E-79	100.7	55.0	68.3
Rsa1.0_00293.1.g10653.t2	ref|XP_002872166.1| hypothetical protein ARALYDRAFT_910605 [Arabidopsis lyrata subsp. lyrata] gi|297318003|gb|EFH48425.1| hypothetical protein ARALYDRAFT_910605 [Arabidopsis lyrata subsp. lyrata]	435	369	0	84.8	76.1	81.4	hypothetical protein ARALYDRAFT_910605	gbpln	Arabidopsis lyrata	AT5G25460.1 | Symbols: | Protein of unknown function, DUF642 | chr5:8863430-8865394 FORWARD LENGTH=369	435	369	0	84.8	76.1	81.1
Rsa1.0_00293.1.g10654.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00293.1.g10655.t1	ref|NP_197927.1| ubiquinol-cytochrome c reductase subunit 7 [Arabidopsis thaliana] gi|403399498|sp|F4JWS8.1|QCR72_ARATH RecName: Full=Cytochrome b-c1 complex subunit 7-2; AltName: Full=Complex III subunit VII gi|332006061|gb|AED93444.1| ubiquinol-cytochrome c reductase subunit 7 [Arabidopsis thaliana]	144	122	1.00E-54	84.7	77.1	81.9	ubiquinol-cytochrome c reductase subunit 7	gbpln	Arabidopsis thaliana	AT5G25450.1 | Symbols: | Cytochrome bd ubiquinol oxidase, 14kDa subunit | chr5:8857036-8857849 FORWARD LENGTH=122	144	122	4.00E-57	84.7	77.1	81.9
Rsa1.0_00293.1.g10656.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00293.1.g10657.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00294.1.g10658.t1	gb|EOA12915.1| hypothetical protein CARUB_v10025891mg [Capsella rubella]	299	828	1.00E-112	276.9	66.6	79.3	hypothetical protein CARUB_v10025891mg	gbpln	Capsella rubella	AT5G55390.2 | Symbols: EDM2 | ENHANCED DOWNY MILDEW 2 | chr5:22448152-22454414 REVERSE LENGTH=1297	299	1297	1.00E-52	433.8	43.1	59.5
Rsa1.0_00294.1.g10659.t1	ref|NP_199617.1| C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein [Arabidopsis thaliana] gi|10177757|dbj|BAB11070.1| phosphoribosylanthranilate transferase-like protein [Arabidopsis thaliana] gi|332008232|gb|AED95615.1| C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein [Arabidopsis thaliana]	1080	1036	0	95.9	86.4	89.8	C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT5G48060.1 | Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr5:19475296-19478878 FORWARD LENGTH=1036	1080	1036	0	95.9	86.4	89.8
Rsa1.0_00294.1.g10660.t1	ref|NP_199615.1| ubiquitin carboxyl-terminal hydrolase-like protein [Arabidopsis thaliana] gi|10177755|dbj|BAB11068.1| unnamed protein product [Arabidopsis thaliana] gi|55740679|gb|AAV63932.1| hypothetical protein At5g48040 [Arabidopsis thaliana] gi|332008230|gb|AED95613.1| ubiquitin carboxyl-terminal hydrolase-like protein [Arabidopsis thaliana]	426	422	1.00E-177	99.1	73.9	81.2	ubiquitin carboxyl-terminal hydrolase-like protein	gbpln	Arabidopsis thaliana	AT5G48040.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr5:19470461-19471729 FORWARD LENGTH=422	426	422	1.00E-179	99.1	73.9	81.2
Rsa1.0_00294.1.g10661.t1	ref|NP_568690.1| gametophytic factor 2 [Arabidopsis thaliana] gi|26452200|dbj|BAC43188.1| putative DnaJ protein [Arabidopsis thaliana] gi|332008229|gb|AED95612.1| gametophytic factor 2 [Arabidopsis thaliana]	454	456	0	100.4	83.7	90.7	gametophytic factor 2	gbpln	Arabidopsis thaliana	AT5G48030.1 | Symbols: GFA2 | gametophytic factor 2 | chr5:19466298-19469753 REVERSE LENGTH=456	454	456	0	100.4	83.7	90.7
Rsa1.0_00294.1.g10662.t1	ref|XP_002865589.1| hypothetical protein ARALYDRAFT_917648 [Arabidopsis lyrata subsp. lyrata] gi|297311424|gb|EFH41848.1| hypothetical protein ARALYDRAFT_917648 [Arabidopsis lyrata subsp. lyrata]	360	355	0	98.6	93.9	96.7	hypothetical protein ARALYDRAFT_917648	gbpln	Arabidopsis lyrata	AT5G48020.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:19462888-19464790 REVERSE LENGTH=355	360	355	0	98.6	90.3	93.6

Rsa1.0_00294.1.g10663.t1	ref|XP_002863846.1| small molecular weight G-protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297309681|gb|EFH40105.1| small molecular weight G-protein 1 [Arabidopsis lyrata subsp. lyrata]	223	223	1.00E-121	100.0	94.6	96.9	small molecular weight G-protein 1	gbpln	Arabidopsis lyrata	AT5G47960.1 | Symbols: SMG1, ATRABA4C, RABA4C | RAB GTPase homolog A4C | chr5:19421533-19422473 REVERSE LENGTH=223	223	223	1.00E-123	100.0	94.6	96.4
Rsa1.0_00294.1.g10664.t3	ref|XP_002865581.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311416|gb|EFH41840.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	734	755	0	102.9	64.4	74.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G47940.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19409407-19411893 REVERSE LENGTH=749	734	749	0	102.0	63.4	73.7
Rsa1.0_00294.1.g10665.t2	gb|EOA24972.1| hypothetical protein CARUB_v10018269mg, partial [Capsella rubella]	84	115	3.00E-42	136.9	97.6	100.0	hypothetical protein CARUB_v10018269mg, partial	gbpln	Capsella rubella	AT3G61110.1 | Symbols: ARS27A, RS27A | ribosomal protein S27 | chr3:22611710-22612632 FORWARD LENGTH=86	84	86	8.00E-44	102.4	96.4	100.0
Rsa1.0_00294.1.g10666.t1	gb|EOA14052.1| hypothetical protein CARUB_v10027188mg [Capsella rubella]	168	191	2.00E-62	113.7	78.0	88.7	hypothetical protein CARUB_v10027188mg	gbpln	Capsella rubella	AT5G47920.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19403458-19404021 REVERSE LENGTH=187	168	187	2.00E-64	111.3	79.2	88.7
Rsa1.0_00294.1.g10667.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00294.1.g10668.t1	gb|EOA12295.1| hypothetical protein CARUB_v10007974mg [Capsella rubella]	923	921	0	99.8	90.9	95.7	hypothetical protein CARUB_v10007974mg	gbpln	Capsella rubella	AT5G47910.1 | Symbols: RBOHD, ATRBOHD | respiratory burst oxidase homologue D | chr5:19397585-19401768 FORWARD LENGTH=921	923	921	0	99.8	91.5	95.7
Rsa1.0_00294.1.g10669.t3	ref|NP_199601.2| uncharacterized protein [Arabidopsis thaliana] gi|332008203|gb|AED95586.1| uncharacterized protein AT5G47900 [Arabidopsis thaliana]	472	440	0	93.2	82.4	86.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G47900.1 | Symbols: | Protein of unknown function (DUF1624) | chr5:19392408-19394963 FORWARD LENGTH=440	472	440	0	93.2	82.4	86.4
Rsa1.0_00294.1.g10670.t1	ref|XP_002863829.1| hypothetical protein ARALYDRAFT_494832 [Arabidopsis lyrata subsp. lyrata] gi|297309664|gb|EFH40088.1| hypothetical protein ARALYDRAFT_494832 [Arabidopsis lyrata subsp. lyrata]	98	97	1.00E-42	99.0	85.7	95.9	hypothetical protein ARALYDRAFT_494832	gbpln	Arabidopsis lyrata	AT5G47890.1 | Symbols: | NADH-ubiquinone oxidoreductase B8 subunit, putative | chr5:19388806-19390409 FORWARD LENGTH=97	98	97	6.00E-45	99.0	84.7	94.9
Rsa1.0_00294.1.g10671.t1	gb|ADE87483.1| eukaryotic release factor 1-1 [Brassica oleracea var. botrytis]	404	434	0	107.4	98.8	99.3	eukaryotic release factor 1-1	gbpln	Brassica oleracea	AT5G47880.2 | Symbols: ERF1-1 | eukaryotic release factor 1-1 | chr5:19386555-19387865 REVERSE LENGTH=436	404	436	0	107.9	93.8	97.3
Rsa1.0_00294.1.g10672.t1	gb|EOA13902.1| hypothetical protein CARUB_v10027018mg [Capsella rubella]	206	242	4.00E-90	117.5	79.6	86.4	hypothetical protein CARUB_v10027018mg	gbpln	Capsella rubella	AT5G47870.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: cobalt ion binding (TAIR:AT1G71310.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19384555-19385808 REVERSE LENGTH=199	206	199	5.00E-84	96.6	79.6	84.5
Rsa1.0_00294.1.g10673.t1	ref|NP_199597.1| uncharacterized protein [Arabidopsis thaliana] gi|10177922|dbj|BAB11333.1| unnamed protein product [Arabidopsis thaliana] gi|16648766|gb|AAL25574.1| AT5g47860/MCA23_20 [Arabidopsis thaliana] gi|22655374|gb|AAM98279.1| At5g47860/MCA23_20 [Arabidopsis thaliana] gi|332008198|gb|AED95581.1| uncharacterized protein AT5G47860 [Arabidopsis thaliana]	767	431	0	56.2	50.1	52.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G47860.1 | Symbols: | Protein of unknown function (DUF1350) | chr5:19381656-19384310 FORWARD LENGTH=431	767	431	0	56.2	50.1	52.3
Rsa1.0_00294.1.g10674.t2	dbj|BAB11330.1| unnamed protein product [Arabidopsis thaliana]	200	202	3.00E-80	101.0	77.5	84.5	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G47830.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:19373013-19374300 REVERSE LENGTH=173	200	173	3.00E-78	86.5	74.5	79.5

Rsa1.0_00294.1.g10675.t1	ref|NP_199593.2| kinesin family member 4/7/21/27 [Arabidopsis thaliana] gi|30695302|ref|NP_851151.1| kinesin family member 4/7/21/27 [Arabidopsis thaliana] gi|27260890|gb|AAN86114.1| kinesin-like protein [Arabidopsis thaliana] gi|27260892|gb|AAN86115.1| kinesin-like protein [Arabidopsis thaliana] gi|332008192|gb|AED95575.1| kinesin family member 4/7/21/27 [Arabidopsis thaliana] gi|332008193|gb|AED95576.1| kinesin family member 4/7/21/27 [Arabidopsis thaliana]	1034	1035	0	100.1	91.8	96.1	kinesin family member 4/7/21/27	gbpln	Arabidopsis thaliana	AT5G47820.2 | Symbols: FRA1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:19366505-19372229 FORWARD LENGTH=1035	1034	1035	0	100.1	91.8	96.1
Rsa1.0_00294.1.g10676.t1	gb|EOA23614.1| hypothetical protein CARUB_v10016814mg [Capsella rubella]	621	650	0	104.7	73.6	80.7	hypothetical protein CARUB_v10016814mg	gbpln	Capsella rubella	AT3G32940.1 | Symbols: | RNA-binding KH domain-containing protein | chr3:13491089-13493630 REVERSE LENGTH=607	621	607	0	97.7	72.5	79.2
Rsa1.0_00294.1.g10677.t2	ref|NP_197514.2| SOUL heme-binding protein [Arabidopsis thaliana] gi|17473811|gb|AAL38336.1| unknown protein [Arabidopsis thaliana] gi|23197728|gb|AAN15391.1| unknown protein [Arabidopsis thaliana] gi|332005416|gb|AED92799.1| SOUL heme-binding protein [Arabidopsis thaliana]	509	378	1.00E-179	74.3	62.1	66.6	SOUL heme-binding protein	gbpln	Arabidopsis thaliana	AT5G20140.1 | Symbols: | SOUL heme-binding family protein | chr5:6799047-6800892 REVERSE LENGTH=378	509	378	0	74.3	62.1	66.6
Rsa1.0_00294.1.g10678.t1	sp|Q9LHK4.1|AB8B_ARATH RecName: Full=Putative ABC transporter B family member 8; Short=ABC transporter ABCB.8; Short=AtABCB8; AltName: Full=P-glycoprotein 8; AltName: Full=Putative multidrug resistance protein 22 gi|9294508|dbj|BAB02613.1| P-glycoprotein; multi-drug resistance related; ABC transporter-like protein [Arabidopsis thaliana]	1243	1241	0	99.8	84.4	92.6	RecName: Full=Putative ABC transporter B family member 8; Short=ABC transporter ABCB.8; Short=AtABCB8; AltName: Full=P-glycoprotein 8; AltName: Full=Putative multidrug resistance protein 22 gi|9294508|dbj|BAB02613.1| P-glycoprotein; multi-drug resistance related; ABC transporter-like protein	gbpln	Arabidopsis thaliana	AT3G28345.1 | Symbols: | ABC transporter family protein | chr3:10593921-10598775 REVERSE LENGTH=1240	1243	1240	0	99.8	49.7	71.2
Rsa1.0_00294.1.g10679.t1	ref|XP_002877232.1| ATPDR10/PDR10 [Arabidopsis lyrata subsp. lyrata] gi|297323070|gb|EFH53491.1| ATPDR10/PDR10 [Arabidopsis lyrata subsp. lyrata]	287	1387	1.00E-125	483.3	78.7	86.4	ATPDR10/PDR10	gbpln	Arabidopsis lyrata	AT3G30842.1 | Symbols: PDR10, ATPDR10 | pleiotropic drug resistance 10 | chr3:12593959-12600432 REVERSE LENGTH=1406	287	1406	1.00E-120	489.9	75.3	85.4
Rsa1.0_00294.1.g10680.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1677	1213	0	72.3	31.7	44.2	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1677	626	1.00E-82	37.3	10.0	15.0
Rsa1.0_00294.1.g10681.t1	sp|Q7PC85.1|AB38G_ARATH RecName: Full=ABC transporter G family member 38; Short=ABC transporter ABCG.38; Short=AtABCG38; AltName: Full=Probable pleiotropic drug resistance protein 10 gi|28144356|tpg|DAA00878.1| TPA_exp: PDR10 ABC transporter [Arabidopsis thaliana]	1101	1418	0	128.8	83.9	91.5	RecName: Full=ABC transporter G family member 38; Short=ABC transporter ABCG.38; Short=AtABCG38; AltName: Full=Probable pleiotropic drug resistance protein 10 gi|28144356|tpg|DAA00878.1| TPA_exp: PDR10 ABC transporter	gbpln	Arabidopsis thaliana	AT3G30842.1 | Symbols: PDR10, ATPDR10 | pleiotropic drug resistance 10 | chr3:12593959-12600432 REVERSE LENGTH=1406	1101	1406	0	127.7	80.5	88.6
Rsa1.0_00294.1.g10682.t1	ref|XP_002875560.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321398|gb|EFH51819.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	893	495	0	55.4	50.6	52.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G30841.1 | Symbols: | Cofactor-independent phosphoglycerate mutase | chr3:12591595-12593401 FORWARD LENGTH=495	893	495	0	55.4	50.1	52.5
Rsa1.0_00294.1.g10683.t1	gb|ACA63477.1| proline dehydrogenase [Brassica napus]	498	498	0	100.0	96.8	98.8	proline dehydrogenase	gbpln	Brassica napus	AT3G30775.1 | Symbols: ERD5, PRODH, AT-POX, ATPOX, ATPDH, PRO1 | Methylenetetrahydrofolate reductase family protein | chr3:12448880-12451126 REVERSE LENGTH=499	498	499	0	100.2	90.4	95.6
Rsa1.0_00294.1.g10684.t3	gb|AAC95354.1| receptor-like protein kinase [Arabidopsis thaliana]	373	684	9.00E-32	183.4	19.6	23.1	receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT4G23250.1 | Symbols: EMB1290, DUF26-21, RKC1, CRK17 | kinases;protein kinases | chr4:12162004-12167026 REVERSE LENGTH=1035	373	1035	6.00E-34	277.5	19.0	22.3
Rsa1.0_00295.1.g10685.t1	gb|EOA15180.1| hypothetical protein CARUB_v10028566mg [Capsella rubella]	354	348	1.00E-163	98.3	81.1	89.0	hypothetical protein CARUB_v10028566mg	gbpln	Capsella rubella	AT5G59520.1 | Symbols: ZIP2 | ZRT/IRT-like protein 2 | chr5:23991447-23992762 REVERSE LENGTH=353	354	353	1.00E-164	99.7	84.7	92.4

Rsa1.0_00295.1.g10686.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	139	1311	3.00E-11	943.2	32.4	48.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00295.1.g10687.t1	ref|XP_002866333.1| hypothetical protein ARALYDRAFT_496082 [Arabidopsis lyrata subsp. lyrata] gi|297312168|gb|EFH42592.1| hypothetical protein ARALYDRAFT_496082 [Arabidopsis lyrata subsp. lyrata]	263	266	1.00E-125	101.1	84.4	91.6	hypothetical protein ARALYDRAFT_496082	gbpln	Arabidopsis lyrata	AT5G59490.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:23982922-23984419 REVERSE LENGTH=266	263	266	1.00E-120	101.1	84.4	91.6
Rsa1.0_00295.1.g10688.t1	ref|NP_200755.1| mannose-P-dolichol utilization defect 1 protein-like protein [Arabidopsis thaliana] gi|12644539|sp|Q9LTI3.1|MPU11_ARATH RecName: Full=Mannose-P-dolichol utilization defect 1 protein homolog 1 gi|8885552|dbj|BAA97482.1| unnamed protein product [Arabidopsis thaliana] gi|332009810|gb|AED97193.1| mannose-P-dolichol utilization defect 1 protein-like protein [Arabidopsis thaliana]	243	239	1.00E-103	98.4	76.5	87.2	mannose-P-dolichol utilization defect 1 protein-like protein	gbpln	Arabidopsis thaliana	AT5G59470.1 | Symbols: | Mannose-P-dolichol utilization defect 1 protein | chr5:23978611-23979414 FORWARD LENGTH=239	243	239	1.00E-106	98.4	76.5	87.2
Rsa1.0_00295.1.g10689.t1	gb|EOA14099.1| hypothetical protein CARUB_v10027239mg [Capsella rubella]	161	173	8.00E-48	107.5	73.3	82.0	hypothetical protein CARUB_v10027239mg	gbpln	Capsella rubella	AT5G59460.1 | Symbols: | scarecrow-like transcription factor 11 (SCL11) | chr5:23976968-23978291 REVERSE LENGTH=172	161	172	9.00E-41	106.8	70.2	78.9
Rsa1.0_00295.1.g10690.t1	ref|XP_002864630.1| hypothetical protein ARALYDRAFT_919168 [Arabidopsis lyrata subsp. lyrata] gi|297310465|gb|EFH40889.1| hypothetical protein ARALYDRAFT_919168 [Arabidopsis lyrata subsp. lyrata]	229	233	3.00E-71	101.7	67.7	78.2	hypothetical protein ARALYDRAFT_919168	gbpln	Arabidopsis lyrata	AT5G59380.1 | Symbols: MBD6, ATMBD6 | methyl-CPG-binding domain 6 | chr5:23952321-23953485 FORWARD LENGTH=225	229	225	3.00E-67	98.3	62.0	73.8
Rsa1.0_00295.1.g10691.t1	gb|EOA15091.1| hypothetical protein CARUB_v10028459mg [Capsella rubella]	377	377	0	100.0	98.7	99.5	hypothetical protein CARUB_v10028459mg	gbpln	Capsella rubella	AT3G46520.1 | Symbols: ACT12 | actin-12 | chr3:17128567-17129981 FORWARD LENGTH=377	377	377	0	100.0	98.7	99.5
Rsa1.0_00295.1.g10692.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00295.1.g10693.t1	ref|NP_200743.1| uncharacterized protein [Arabidopsis thaliana] gi|8885541|dbj|BAA97471.1| unnamed protein product [Arabidopsis thaliana] gi|28973705|gb|AAO64169.1| unknown protein [Arabidopsis thaliana] gi|29824225|gb|AAP04073.1| unknown protein [Arabidopsis thaliana] gi|110737229|dbj|BAF00562.1| hypothetical protein [Arabidopsis thaliana] gi|332009791|gb|AED97174.1| uncharacterized protein AT5G59350 [Arabidopsis thaliana]	277	287	4.00E-93	103.6	77.3	82.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G59350.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:23941132-23941995 FORWARD LENGTH=287	277	287	1.00E-95	103.6	77.3	82.7
Rsa1.0_00295.1.g10694.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00295.1.g10695.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00295.1.g10696.t1	gb|AAC79110.1| putative polyprotein of LTR transposon [Arabidopsis thaliana] gi|7269781|emb|CAB77781.1| putative polyprotein of LTR transposon [Arabidopsis thaliana]	507	1456	1.00E-110	287.2	37.1	43.0	putative polyprotein of LTR transposon	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	507	1262	4.00E-47	248.9	20.1	28.4
Rsa1.0_00295.1.g10697.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	2022	1365	0	67.5	28.7	39.3	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT5G59340.1 | Symbols: WOX2 | WUSCHEL related homeobox 2 | chr5:23933408-23934627 REVERSE LENGTH=260	2022	260	1.00E-106	12.9	9.4	10.5
Rsa1.0_00295.1.g10698.t1	ref|NP_568902.2| ubiquitin carrier protein 7 [Arabidopsis thaliana] gi|28973769|gb|AAO64200.1| putative E2, ubiquitin-conjugating enzyme UBC7 [Arabidopsis thaliana] gi|332009785|gb|AED97168.1| ubiquitin carrier protein 7 [Arabidopsis thaliana]	194	203	8.00E-85	104.6	76.3	77.3	ubiquitin carrier protein 7	gbpln	Arabidopsis thaliana	AT5G59300.1 | Symbols: UBC7, ATUBC7 | ubiquitin carrier protein 7 | chr5:23919868-23921304 REVERSE LENGTH=203	194	203	3.00E-87	104.6	76.3	77.3
Rsa1.0_00295.1.g10699.t1	ref|XP_002866324.1| UDP-glucuronic acid decarboxylase [Arabidopsis lyrata subsp. lyrata] gi|297312159|gb|EFH42583.1| UDP-glucuronic acid decarboxylase [Arabidopsis lyrata subsp. lyrata]	343	342	0	99.7	96.2	98.3	UDP-glucuronic acid decarboxylase	gbpln	Arabidopsis lyrata	AT5G59290.2 | Symbols: UXS3, ATUXS3 | UDP-glucuronic acid decarboxylase 3 | chr5:23915814-23917998 REVERSE LENGTH=357	343	357	0	104.1	95.6	98.0

Rsa1.0_00295.1.g10700.t1	ref|XP_002864606.1| hypothetical protein ARALYDRAFT_358128 [Arabidopsis lyrata subsp. lyrata] gi|297310441|gb|EFH40865.1| hypothetical protein ARALYDRAFT_358128 [Arabidopsis lyrata subsp. lyrata]	200	251	8.00E-16	125.5	21.0	31.0	hypothetical protein ARALYDRAFT_358128	gbpln	Arabidopsis lyrata	AT1G35890.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:13341300-13341953 FORWARD LENGTH=171	200	171	1.00E-10	85.5	12.0	16.5
Rsa1.0_00295.1.g10701.t1	ref|XP_002888042.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333883|gb|EFH64301.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	360	378	1.00E-90	105.0	55.0	68.1	predicted protein	gbpln	Arabidopsis lyrata	AT3G16740.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:5699476-5700651 FORWARD LENGTH=391	360	391	1.00E-69	108.6	46.1	64.4
Rsa1.0_00295.1.g10702.t7	ref|XP_002866314.1| DNA-directed RNA polymerase II [Arabidopsis lyrata subsp. lyrata] gi|297312149|gb|EFH42573.1| DNA-directed RNA polymerase II [Arabidopsis lyrata subsp. lyrata] gi|482549900|gb|EOA14094.1| hypothetical protein CARUB_v10027231mg [Capsella rubella]	465	176	3.00E-61	37.8	25.8	26.9	DNA-directed RNA polymerase II	gbpln	Arabidopsis lyrata	AT5G59180.1 | Symbols: NRPB7 | DNA-directed RNA polymerase II | chr5:23883499-23884976 FORWARD LENGTH=176	465	176	2.00E-62	37.8	25.2	26.7
Rsa1.0_00295.1.g10703.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00295.1.g10704.t1	sp|Q9FIF0.3|LRK22_ARATH RecName: Full=Putative L-type lectin-domain containing receptor kinase II.2; Short=LecRK-II.2; Flags: Precursor	700	694	0	99.1	75.0	84.7	RecName: Full=Putative L-type lectin-domain containing receptor kinase II.2; Short=LecRK-II.2; Flags: Precursor	----	----	AT5G59260.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:23907901-23909925 REVERSE LENGTH=674	700	674	0	96.3	72.7	81.4
Rsa1.0_00296.1.g10705.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00296.1.g10706.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00296.1.g10707.t1	gb|ABD65112.1| hypothetical protein 31.t00014 [Brassica oleracea]	144	122	6.00E-37	84.7	56.9	68.1	hypothetical protein 31.t00014	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00296.1.g10708.t3	gb|EOA26404.1| hypothetical protein CARUB_v10023766mg [Capsella rubella]	340	291	1.00E-103	85.6	75.3	79.4	hypothetical protein CARUB_v10023766mg	gbpln	Capsella rubella	AT2G37340.1 | Symbols: RSZ33, ATRSZ33, RS2Z33, AT-RS2Z33 | arginine/serine-rich zinc knuckle-containing protein 33 | chr2:15670372-15672331 REVERSE LENGTH=290	340	290	1.00E-104	85.3	75.6	78.8
Rsa1.0_00296.1.g10709.t4	gb|EOA27940.1| hypothetical protein CARUB_v10024110mg [Capsella rubella]	171	194	2.00E-42	113.5	72.5	80.1	hypothetical protein CARUB_v10024110mg	gbpln	Capsella rubella	AT2G37300.1 | Symbols: | unknown protein; Has 93 Blast hits to 62 proteins in 29 species: Archae - 0; Bacteria - 6; Metazoa - 13; Fungi - 19; Plants - 25; Viruses - 0; Other Eukaryotes - 30 (source: NCBI BLink). | chr2:15662845-15663547 REVERSE LENGTH=169	171	169	7.00E-38	98.8	69.6	76.6
Rsa1.0_00296.1.g10710.t1	gb|ACH99805.1| WRKY44 transcription factor [Brassica napus]	420	421	0	100.2	89.0	93.8	WRKY44 transcription factor	gbpln	Brassica napus	AT2G37260.1 | Symbols: TTG2, ATWRKY44, WRKY44, DSL1 | WRKY family transcription factor family protein | chr2:15645277-15646792 FORWARD LENGTH=429	420	429	0	102.1	80.7	88.3
Rsa1.0_00296.1.g10711.t1	gb|AAF19700.1|AC008047_7 F2K11.25 [Arabidopsis thaliana]	357	471	1.00E-121	131.9	66.1	75.1	F2K11.25	gbpln	Arabidopsis thaliana	AT1G62620.1 | Symbols: | Flavin-binding monooxygenase family protein | chr1:23182678-23184864 FORWARD LENGTH=450	357	450	1.00E-110	126.1	51.5	58.3
Rsa1.0_00296.1.g10712.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	152	1529	6.00E-29	1005.9	42.1	59.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	152	295	2.00E-18	194.1	33.6	48.7
Rsa1.0_00296.1.g10713.t1	ref|XP_003563399.1| PREDICTED: LOW QUALITY PROTEIN: polyubiquitin-C-like [Brachypodium distachyon]	440	535	2.00E-74	121.6	39.5	51.4	PREDICTED: LOW QUALITY PROTEIN: polyubiquitin-C-like	gbpln	Brachypodium distachyon	AT4G05320.4 | Symbols: UBQ10 | polyubiquitin 10 | chr4:2718559-2719932 FORWARD LENGTH=457	440	457	2.00E-75	103.9	39.5	51.4
Rsa1.0_00296.1.g10714.t1	ref|XP_002879658.1| ADK/ATPADK1 [Arabidopsis lyrata subsp. lyrata] gi|297325497|gb|EFH55917.1| ADK/ATPADK1 [Arabidopsis lyrata subsp. lyrata]	282	284	1.00E-150	100.7	93.3	96.8	ADK/ATPADK1	gbpln	Arabidopsis lyrata	AT2G37250.1 | Symbols: ADK, ATPADK1 | adenosine kinase | chr2:15641991-15643318 FORWARD LENGTH=284	282	284	1.00E-151	100.7	92.6	96.8
Rsa1.0_00296.1.g10715.t1	ref|XP_002868566.1| hypothetical protein ARALYDRAFT_493781 [Arabidopsis lyrata subsp. lyrata] gi|297314402|gb|EFH44825.1| hypothetical protein ARALYDRAFT_493781 [Arabidopsis lyrata subsp. lyrata]	669	668	0	99.9	98.1	99.1	hypothetical protein ARALYDRAFT_493781	gbpln	Arabidopsis lyrata	AT5G42020.1 | Symbols: BIP, BIP2 | Heat shock protein 70 (Hsp 70) family protein | chr5:16807697-16810480 REVERSE LENGTH=668	669	668	0	99.9	97.5	99.1
Rsa1.0_00296.1.g10716.t1	gb|EOA29094.1| hypothetical protein CARUB_v10025361mg [Capsella rubella]	752	757	0	100.7	87.2	93.0	hypothetical protein CARUB_v10025361mg	gbpln	Capsella rubella	AT2G37230.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:15637177-15639450 REVERSE LENGTH=757	752	757	0	100.7	87.1	92.8

Rsa1.0_00296.1.g10717.t1	ref|XP_002881497.1| hypothetical protein ARALYDRAFT_482714 [Arabidopsis lyrata subsp. lyrata] gi|297327336|gb|EFH57756.1| hypothetical protein ARALYDRAFT_482714 [Arabidopsis lyrata subsp. lyrata]	287	289	1.00E-114	100.7	80.1	85.4	hypothetical protein ARALYDRAFT_482714	gbpln	Arabidopsis lyrata	AT2G37220.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:15634980-15636331 REVERSE LENGTH=289	287	289	1.00E-109	100.7	78.0	85.0
Rsa1.0_00296.1.g10718.t1	ref|XP_002881496.1| hypothetical protein ARALYDRAFT_482713 [Arabidopsis lyrata subsp. lyrata] gi|297327335|gb|EFH57755.1| hypothetical protein ARALYDRAFT_482713 [Arabidopsis lyrata subsp. lyrata]	208	215	1.00E-111	103.4	93.8	96.6	hypothetical protein ARALYDRAFT_482713	gbpln	Arabidopsis lyrata	AT2G37210.1 | Symbols: | lysine decarboxylase family protein | chr2:15624253-15626834 REVERSE LENGTH=215	208	215	1.00E-114	103.4	93.8	96.6
Rsa1.0_00296.1.g10719.t1	ref|NP_850279.1| uncharacterized protein [Arabidopsis thaliana] gi|62867605|gb|AAY17406.1| At2g37195 [Arabidopsis thaliana] gi|66841340|gb|AAY57307.1| At2g37195 [Arabidopsis thaliana] gi|110743680|dbj|BAE99677.1| hypothetical protein [Arabidopsis thaliana] gi|330254271|gb|AEC09365.1| uncharacterized protein AT2G37195 [Arabidopsis thaliana]	143	133	7.00E-56	93.0	83.9	87.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G37195.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 23 Blast hits to 23 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15620370-15621464 FORWARD LENGTH=133	143	133	2.00E-58	93.0	83.9	87.4
Rsa1.0_00296.1.g10720.t1	gb|EOA19281.1| hypothetical protein CARUB_v10001944mg [Capsella rubella]	234	215	3.00E-59	91.9	55.1	65.0	hypothetical protein CARUB_v10001944mg	gbpln	Capsella rubella	AT4G03570.1 | Symbols: | Cystatin/monellin superfamily protein | chr4:1590413-1594105 REVERSE LENGTH=347	234	347	7.00E-39	148.3	32.5	38.0
Rsa1.0_00296.1.g10721.t1	gb|EOA28926.1| hypothetical protein CARUB_v10025173mg [Capsella rubella]	166	166	3.00E-87	100.0	97.6	99.4	hypothetical protein CARUB_v10025173mg	gbpln	Capsella rubella	AT3G53430.1 | Symbols: | Ribosomal protein L11 family protein | chr3:19809895-19810395 REVERSE LENGTH=166	166	166	6.00E-89	100.0	96.4	98.8
Rsa1.0_00296.1.g10722.t1	dbj|BAA92261.1| Plasma membrane aquaporin 2c [Raphanus sativus]	283	283	1.00E-160	100.0	100.0	100.0	Plasma membrane aquaporin 2c	gbpln	Raphanus sativus	AT2G37170.1 | Symbols: PIP2B, PIP2;2 | plasma membrane intrinsic protein 2 | chr2:15613624-15614791 REVERSE LENGTH=285	283	285	1.00E-156	100.7	95.4	97.5
Rsa1.0_00296.1.g10723.t1	gb|EOA26868.1| hypothetical protein CARUB_v10022961mg [Capsella rubella] gi|482562679|gb|EOA26869.1| hypothetical protein CARUB_v10022961mg [Capsella rubella] gi|482562680|gb|EOA26870.1| hypothetical protein CARUB_v10022961mg [Capsella rubella]	532	536	0	100.8	74.2	82.3	hypothetical protein CARUB_v10022961mg	gbpln	Capsella rubella	AT2G37150.2 | Symbols: | RING/U-box superfamily protein | chr2:15603748-15605988 REVERSE LENGTH=546	532	546	0	102.6	76.1	83.6
Rsa1.0_00297.1.g10724.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00297.1.g10725.t1	gb|EOA32755.1| hypothetical protein CARUB_v10016060mg [Capsella rubella]	469	394	2.00E-73	84.0	40.9	49.7	hypothetical protein CARUB_v10016060mg	gbpln	Capsella rubella	AT3G20030.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6990254-6991462 FORWARD LENGTH=402	469	402	3.00E-74	85.7	39.2	49.9
Rsa1.0_00297.1.g10726.t1	gb|ABD64968.1| hypothetical protein 25.t00005 [Brassica oleracea]	164	299	1.00E-16	182.3	39.0	51.8	hypothetical protein 25.t00005	gbpln	Brassica oleracea	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	164	264	2.00E-17	161.0	34.8	53.0
Rsa1.0_00297.1.g10727.t1	ref|NP_001031995.1| defensin-like protein 115 [Arabidopsis thaliana] gi|122209222|sp|Q2V321.1|DF115_ARATH RecName: Full=Defensin-like protein 115; Flags: Precursor gi|332007401|gb|AED94784.1| defensin-like protein 115 [Arabidopsis thaliana]	143	81	1.00E-10	56.6	24.5	30.1	defensin-like protein 115	gbpln	Arabidopsis thaliana	AT5G42232.1 | Symbols: | Defensin-like (DEFL) family protein | chr5:16884962-16885309 FORWARD LENGTH=81	143	81	4.00E-13	56.6	24.5	30.1
Rsa1.0_00297.1.g10728.t6	gb|EOA17867.1| hypothetical protein CARUB_v10006272mg [Capsella rubella]	484	511	0	105.6	77.3	85.3	hypothetical protein CARUB_v10006272mg	gbpln	Capsella rubella	AT4G22860.1 | Symbols: | Cell cycle regulated microtubule associated protein | chr4:11997735-12001281 FORWARD LENGTH=509	484	509	0	105.2	76.0	84.3
Rsa1.0_00297.1.g10729.t1	gb|EOA17219.1| hypothetical protein CARUB_v10005494mg [Capsella rubella]	265	268	1.00E-118	101.1	81.5	88.7	hypothetical protein CARUB_v10005494mg	gbpln	Capsella rubella	AT4G22920.1 | Symbols: ATNYE1, NYE1 | non-yellowing 1 | chr4:12016776-12017969 REVERSE LENGTH=268	265	268	1.00E-117	101.1	78.5	86.4
Rsa1.0_00297.1.g10730.t1	gb|EOA17219.1| hypothetical protein CARUB_v10005494mg [Capsella rubella]	263	268	1.00E-129	101.9	86.3	93.2	hypothetical protein CARUB_v10005494mg	gbpln	Capsella rubella	AT4G22920.1 | Symbols: ATNYE1, NYE1 | non-yellowing 1 | chr4:12016776-12017969 REVERSE LENGTH=268	263	268	1.00E-128	101.9	84.4	92.4
Rsa1.0_00297.1.g10731.t1	emb|CAA09731.1| receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	635	667	0	105.0	69.3	81.3	receptor-like protein kinase, RLK3	gbpln	Arabidopsis thaliana	AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667	635	667	0	105.0	69.1	80.6
Rsa1.0_00297.1.g10732.t1	dbj|BAJ33736.1| unnamed protein product [Thellungiella halophila]	154	403	1.00E-51	261.7	66.2	76.6	unnamed protein product	----	----	AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667	154	667	5.00E-53	433.1	63.6	76.6

Rsa1.0_00297.1.g10733.t1	ref|NP_194050.2| cysteine-rich receptor-like protein kinase 11 [Arabidopsis thaliana] gi|152013437|sp|Q9ZP16.2|CRK11_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 11; Short=Cysteine-rich RLK11; AltName: Full=Receptor-like protein kinase 3; Flags: Precursor gi|332659320|gb|AEE84720.1| cysteine-rich receptor-like protein kinase 11 [Arabidopsis thaliana]	667	667	0	100.0	69.6	78.1	cysteine-rich receptor-like protein kinase 11	gbpln	Arabidopsis thaliana	AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667	667	667	0	100.0	69.6	78.1
Rsa1.0_00297.1.g10734.t1	emb|CAA09731.1| receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	677	667	0	98.5	71.0	81.2	receptor-like protein kinase, RLK3	gbpln	Arabidopsis thaliana	AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667	677	667	0	98.5	70.8	80.6
Rsa1.0_00297.1.g10735.t1	ref|NP_194026.1| agamous-like MADS-box protein AGL19 [Arabidopsis thaliana] gi|12229640|sp|O82743.1|AGL19_ARATH RecName: Full=Agamous-like MADS-box protein AGL19 gi|11545543|gb|AAG37901.1|AF312664_1 MADS-box protein AGL19 [Arabidopsis thaliana] gi|3292820|emb|CAA19810.1| putative MADS Box / AGL protein [Arabidopsis thaliana] gi|7269142|emb|CAB79250.1| putative MADS Box / AGL protein [Arabidopsis thaliana] gi|23296476|gb|AAN13066.1| putative MADS box AGL protein [Arabidopsis thaliana] gi|332659284|gb|AEE84684.1| agamous-like MADS-box protein AGL19 [Arabidopsis thaliana]	221	219	4.00E-91	99.1	81.0	86.9	agamous-like MADS-box protein AGL19	gbpln	Arabidopsis thaliana	AT4G22950.1 | Symbols: AGL19, GL19 | AGAMOUS-like 19 | chr4:12023946-12027421 REVERSE LENGTH=219	221	219	1.00E-93	99.1	81.0	86.9
Rsa1.0_00297.1.g10736.t1	ref|NP_196651.1| serine/threonine-protein phosphatase 7 inactive-like protein [Arabidopsis thaliana] gi|75173991|sp|Q9LEV0.1|PPP7I_ARATH RecName: Full=Serine/threonine-protein phosphatase 7 inactive homolog gi|8979724|emb|CAB96845.1| serine/threonine protein phosphatase-like protein [Arabidopsis thaliana] gi|332004224|gb|AED91607.1| serine/threonine-protein phosphatase 7 inactive-like protein [Arabidopsis thaliana]	95	600	2.00E-34	631.6	73.7	81.1	serine/threonine-protein phosphatase 7 inactive-like protein	gbpln	Arabidopsis thaliana	AT5G10900.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:3436413-3439221 REVERSE LENGTH=600	95	600	4.00E-37	631.6	73.7	81.1
Rsa1.0_00297.1.g10737.t1	ref|NP_194029.1| uncharacterized protein [Arabidopsis thaliana] gi|3292823|emb|CAA19813.1| putative protein [Arabidopsis thaliana] gi|7269145|emb|CAB79253.1| putative protein [Arabidopsis thaliana] gi|52354393|gb|AAU44517.1| hypothetical protein AT4G22980 [Arabidopsis thaliana] gi|332659288|gb|AEE84688.1| uncharacterized protein AT4G22980 [Arabidopsis thaliana]	121	559	1.00E-43	462.0	78.5	83.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G22980.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: Pyridoxal phosphate (PLP)-dependent transferases superfamily protein (TAIR:AT5G51920.1); Has 520 Blast hits to 468 proteins in 130 species: Archae - 5; Bacteria - 23; Metazoa - 99; Fungi - 131; Plants - 231; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink). | chr4:12043974-12045653 REVERSE LENGTH=559	121	559	3.00E-46	462.0	78.5	83.5
Rsa1.0_00297.1.g10738.t1	gb|EOA16250.1| hypothetical protein CARUB_v10004396mg, partial [Capsella rubella]	565	612	0	108.3	76.6	85.8	hypothetical protein CARUB_v10004396mg, partial	gbpln	Capsella rubella	AT4G22980.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: Pyridoxal phosphate (PLP)-dependent transferases superfamily protein (TAIR:AT5G51920.1); Has 520 Blast hits to 468 proteins in 130 species: Archae - 5; Bacteria - 23; Metazoa - 99; Fungi - 131; Plants - 231; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink). | chr4:12043974-12045653 REVERSE LENGTH=559	565	559	0	98.9	76.6	85.3
Rsa1.0_00298.1.g10739.t1	gb|AAC23763.1| hypothetical protein [Arabidopsis thaliana]	389	705	1.00E-40	181.2	23.9	30.1	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	389	249	4.00E-20	64.0	16.7	21.3
Rsa1.0_00298.1.g10740.t1	dbj|BAB01350.1| Mutator-like transposase [Arabidopsis thaliana]	738	811	1.00E-152	109.9	38.3	52.2	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	738	719	8.00E-21	97.4	16.4	29.5

Rsa1.0_00298.1.g10741.t1	dbj|BAB01349.1| En/Spm-like transposon protein-like [Arabidopsis thaliana]	725	714	9.00E-73	98.5	30.2	41.8	En/Spm-like transposon protein-like	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	725	249	7.00E-31	34.3	10.6	14.8
Rsa1.0_00298.1.g10742.t5	ref|XP_002892977.1| nucleotidyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338819|gb|EFH69236.1| nucleotidyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	708	716	0	101.1	81.5	86.9	nucleotidyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G17980.1 | Symbols: PAPS1 | poly(A) polymerase 1 | chr1:6187742-6191418 REVERSE LENGTH=713	708	713	0	100.7	79.4	85.0
Rsa1.0_00298.1.g10743.t1	gb|EOA36865.1| hypothetical protein CARUB_v10008857mg [Capsella rubella]	418	521	1.00E-154	124.6	63.4	76.1	hypothetical protein CARUB_v10008857mg	gbpln	Capsella rubella	AT5G26830.1 | Symbols: | Threonyl-tRNA synthetase | chr5:9437351-9441568 FORWARD LENGTH=709	418	709	1.00E-148	169.6	59.1	73.2
Rsa1.0_00298.1.g10744.t1	ref|XP_002890254.1| hypothetical protein ARALYDRAFT_889207 [Arabidopsis lyrata subsp. lyrata] gi|297336096|gb|EFH66513.1| hypothetical protein ARALYDRAFT_889207 [Arabidopsis lyrata subsp. lyrata]	247	248	1.00E-117	100.4	84.2	91.1	hypothetical protein ARALYDRAFT_889207	gbpln	Arabidopsis lyrata	AT1G17950.1 | Symbols: ATMYB52, BW52, MYB52 | myb domain protein 52 | chr1:6177764-6179063 FORWARD LENGTH=249	247	249	1.00E-118	100.8	83.8	90.7
Rsa1.0_00298.1.g10745.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00298.1.g10746.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00298.1.g10747.t1	ref|XP_002892968.1| hypothetical protein ARALYDRAFT_889192 [Arabidopsis lyrata subsp. lyrata] gi|297338810|gb|EFH69227.1| hypothetical protein ARALYDRAFT_889192 [Arabidopsis lyrata subsp. lyrata]	773	797	0	103.1	79.3	87.6	hypothetical protein ARALYDRAFT_889192	gbpln	Arabidopsis lyrata	AT1G17820.1 | Symbols: | Putative integral membrane protein conserved region (DUF2404) | chr1:6131751-6135115 REVERSE LENGTH=803	773	803	0	103.9	78.1	87.1
Rsa1.0_00298.1.g10748.t1	ref|NP_173223.1| putative aquaporin TIP3-2 [Arabidopsis thaliana] gi|32363213|sp|O22588.1|TIP32_ARATH RecName: Full=Probable aquaporin TIP3-2; AltName: Full=Beta-tonoplast intrinsic protein; Short=Beta-TIP; AltName: Full=Tonoplast intrinsic protein 3-2; Short=AtTIP3;2 gi|9665059|gb|AAF97261.1|AC034106_4 Identical to beta-tonoplast intrinsic protein (beta-TIP) from Arabidopsis thaliana gb|AF026275 and contains a MIP (major intrinsic protein) PF|00230 domain. ESTs gb|R64952, gb|AI999191 come from this gene [Arabidopsis thaliana] gi|2605714|gb|AAB84183.1| beta-tonoplast intrinsic protein [Arabidopsis thaliana] gi|110737967|dbj|BAF00920.1| hypothetical protein [Arabidopsis thaliana] gi|332191518|gb|AEE29639.1| putative aquaporin TIP3-2 [Arabidopsis thaliana]	225	267	1.00E-104	118.7	90.2	95.6	putative aquaporin TIP3-2	gbpln	Arabidopsis thaliana	AT1G17810.1 | Symbols: BETA-TIP | beta-tonoplast intrinsic protein | chr1:6130209-6131442 FORWARD LENGTH=267	225	267	1.00E-106	118.7	90.2	95.6
Rsa1.0_00298.1.g10749.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	428	1024	7.00E-73	239.3	32.0	42.5	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00298.1.g10750.t2	ref|XP_002892965.1| ATB beta [Arabidopsis lyrata subsp. lyrata] gi|297338807|gb|EFH69224.1| ATB beta [Arabidopsis lyrata subsp. lyrata]	197	506	1.00E-105	256.9	94.4	95.9	ATB beta	gbpln	Arabidopsis lyrata	AT1G17720.1 | Symbols: ATB BETA | Protein phosphatase 2A, regulatory subunit PR55 | chr1:6093949-6098065 REVERSE LENGTH=501	197	501	1.00E-107	254.3	94.4	95.9
Rsa1.0_00298.1.g10751.t1	gb|AAD15532.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	215	1274	7.00E-42	592.6	40.5	53.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	215	921	4.00E-25	428.4	26.5	40.0
Rsa1.0_00298.1.g10752.t1	gb|ACP30556.1| disease resistance protein [Brassica rapa subsp. pekinensis]	519	522	0	100.6	79.4	86.5	disease resistance protein	gbpln	Brassica rapa	AT1G72870.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27421086-27422999 FORWARD LENGTH=512	519	512	9.00E-59	98.7	34.9	50.1
Rsa1.0_00298.1.g10753.t3	gb|ACP30589.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1080	1104	0	102.2	85.2	88.5	disease resistance protein	gbpln	Brassica rapa	AT5G48770.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:19773277-19777242 REVERSE LENGTH=1190	1080	1190	0	110.2	45.6	60.3
Rsa1.0_00298.1.g10754.t2	ref|XP_002890235.1| hypothetical protein ARALYDRAFT_889165 [Arabidopsis lyrata subsp. lyrata] gi|297336077|gb|EFH66494.1| hypothetical protein ARALYDRAFT_889165 [Arabidopsis lyrata subsp. lyrata]	1495	1520	0	101.7	88.0	93.0	hypothetical protein ARALYDRAFT_889165	gbpln	Arabidopsis lyrata	AT1G17580.1 | Symbols: MYA1, ATMYA1, XI-1 | myosin 1 | chr1:6039453-6049309 FORWARD LENGTH=1520	1495	1520	0	101.7	87.7	92.7
Rsa1.0_00298.1.g10755.t1	gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]	480	543	3.00E-75	113.1	36.5	56.0	hypothetical protein CARUB_v10015730mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	480	566	2.00E-75	117.9	37.1	61.9

Rsa1.0_00298.1.g10756.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1535	1213	1.00E-175	79.0	24.8	36.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1535	626	8.00E-49	40.8	7.1	11.9
Rsa1.0_00298.1.g10757.t1	ref|NP_200559.1| uncharacterized protein [Arabidopsis thaliana] gi|9758312|dbj|BAB08786.1| unnamed protein product [Arabidopsis thaliana] gi|91805711|gb|ABE65584.1| hypothetical protein At5g57510 [Arabidopsis thaliana] gi|332009526|gb|AED96909.1| uncharacterized protein AT5G57510 [Arabidopsis thaliana]	131	130	3.00E-51	99.2	81.7	88.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G57510.1 | Symbols: | unknown protein; Has 27 Blast hits to 27 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:23289164-23289556 REVERSE LENGTH=130	131	130	7.00E-54	99.2	81.7	88.5
Rsa1.0_00298.1.g10758.t1	ref|NP_173197.2| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana] gi|51969566|dbj|BAD43475.1| putative protein kinase [Arabidopsis thaliana] gi|332191482|gb|AEE29603.1| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana]	652	728	0	111.7	82.7	89.3	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	gbpln	Arabidopsis thaliana	AT1G17540.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:6029551-6032641 REVERSE LENGTH=728	652	728	0	111.7	82.7	89.3
Rsa1.0_00298.1.g10759.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00298.1.g10760.t1	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	743	915	1.00E-134	123.1	32.7	44.5	F22O13.21	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	743	719	2.00E-34	96.8	17.0	29.7
Rsa1.0_00298.1.g10761.t1	gb|EOA29684.1| hypothetical protein CARUB_v10016007mg [Capsella rubella]	128	134	6.00E-15	104.7	32.0	46.1	hypothetical protein CARUB_v10016007mg	gbpln	Capsella rubella	AT2G07505.1 | Symbols: | zinc ion binding | chr2:3125671-3126173 FORWARD LENGTH=143	128	143	8.00E-14	111.7	26.6	31.3
Rsa1.0_00298.1.g10762.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	738	871	1.00E-169	118.0	51.2	63.8	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	738	874	1.00E-23	118.4	11.1	17.1
Rsa1.0_00298.1.g10763.t1	gb|ACN58564.1| (E)-beta-caryophyllene synthase [Arabidopsis lyrata subsp. petraea]	441	545	1.00E-153	123.6	58.3	63.5	(E)-beta-caryophyllene synthase	gbpln	Arabidopsis lyrata	AT5G23960.1 | Symbols: ATTPS21, TPS21 | terpene synthase 21 | chr5:8092969-8095128 FORWARD LENGTH=547	441	547	1.00E-148	124.0	56.0	63.5
Rsa1.0_00298.1.g10764.t1	#	#	#	#	#	#	#	–	----	----	AT1G53250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53800.1); Has 11909 Blast hits to 7704 proteins in 757 species: Archae - 51; Bacteria - 1338; Metazoa - 4550; Fungi - 987; Plants - 464; Viruses - 24; Other Eukaryotes - 4495 (source: NCBI BLink). | chr1:19857468-19859156 FORWARD LENGTH=371	345	371	1.00E-10	107.5	10.1	12.5
Rsa1.0_00298.1.g10765.t1	ref|XP_002892947.1| hypothetical protein ARALYDRAFT_889143 [Arabidopsis lyrata subsp. lyrata] gi|297338789|gb|EFH69206.1| hypothetical protein ARALYDRAFT_889143 [Arabidopsis lyrata subsp. lyrata]	446	419	0	93.9	83.6	86.1	hypothetical protein ARALYDRAFT_889143	gbpln	Arabidopsis lyrata	AT1G17370.1 | Symbols: UBP1B | oligouridylate binding protein 1B | chr1:5951842-5954825 REVERSE LENGTH=419	446	419	0	93.9	83.0	85.7
Rsa1.0_00298.1.g10766.t1	dbj|BAF01585.1| hypothetical protein [Arabidopsis thaliana]	192	565	6.00E-39	294.3	39.6	49.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G17340.1 | Symbols: | Phosphoinositide phosphatase family protein | chr1:5934129-5938391 FORWARD LENGTH=785	192	785	2.00E-41	408.9	39.6	49.0
Rsa1.0_00298.1.g10767.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00298.1.g10768.t1	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	1053	190	1.00E-32	18.0	8.0	8.9	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00298.1.g10769.t1	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	806	954	2.00E-56	118.4	18.6	25.6	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00299.1.g10770.t1	ref|XP_002889130.1| hypothetical protein ARALYDRAFT_895606 [Arabidopsis lyrata subsp. lyrata] gi|297334971|gb|EFH65389.1| hypothetical protein ARALYDRAFT_895606 [Arabidopsis lyrata subsp. lyrata]	471	511	0	108.5	94.3	97.7	hypothetical protein ARALYDRAFT_895606	gbpln	Arabidopsis lyrata	AT1G77210.2 | Symbols: STP14 | sugar transporter 14 | chr1:29009036-29010980 REVERSE LENGTH=504	471	504	0	107.0	93.6	97.0
Rsa1.0_00299.1.g10771.t1	ref|XP_002887672.1| hypothetical protein ARALYDRAFT_895607 [Arabidopsis lyrata subsp. lyrata] gi|297333513|gb|EFH63931.1| hypothetical protein ARALYDRAFT_895607 [Arabidopsis lyrata subsp. lyrata]	500	484	0	96.8	87.2	92.4	hypothetical protein ARALYDRAFT_895607	gbpln	Arabidopsis lyrata	AT1G77220.1 | Symbols: | Protein of unknown function (DUF300) | chr1:29013232-29015530 FORWARD LENGTH=484	500	484	0	96.8	87.8	92.0

Rsa1.0_00299.1.g10772.t1	emb|CAA64328.1| amp-binding protein [Brassica napus]	545	552	0	101.3	88.8	95.0	amp-binding protein	gbpln	Brassica napus	AT1G77240.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr1:29017958-29019595 REVERSE LENGTH=545	545	545	0	100.0	84.6	91.9
Rsa1.0_00299.1.g10773.t1	gb|EOA35031.1| hypothetical protein CARUB_v10020138mg [Capsella rubella]	537	525	1.00E-174	97.8	63.5	72.1	hypothetical protein CARUB_v10020138mg	gbpln	Capsella rubella	AT1G77250.1 | Symbols: | RING/FYVE/PHD-type zinc finger family protein | chr1:29020444-29022938 REVERSE LENGTH=522	537	522	1.00E-163	97.2	61.5	70.2
Rsa1.0_00299.1.g10774.t1	ref|NP_565153.1| putative methyltransferase PMT10 [Arabidopsis thaliana] gi|75250280|sp|Q94KE1.1|PMTA_ARATH RecName: Full=Probable methyltransferase PMT10 gi|14194107|gb|AAK56248.1|AF367259_1 At1g77260/T14N5_19 [Arabidopsis thaliana] gi|20334726|gb|AAM16224.1| At1g77260/T14N5_19 [Arabidopsis thaliana] gi|332197834|gb|AEE35955.1| putative methyltransferase PMT10 [Arabidopsis thaliana]	672	655	0	97.5	84.7	89.3	putative methyltransferase PMT10	gbpln	Arabidopsis thaliana	AT1G77260.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:29023961-29026699 REVERSE LENGTH=655	672	655	0	97.5	84.7	89.3
Rsa1.0_00299.1.g10775.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00299.1.g10776.t1	ref|NP_177852.2| adenine nucleotide alpha hydrolases-domain containing protein kinase [Arabidopsis thaliana] gi|332197836|gb|AEE35957.1| adenine nucleotide alpha hydrolases-domain containing protein kinase [Arabidopsis thaliana]	688	794	0	115.4	81.5	88.8	adenine nucleotide alpha hydrolases-domain containing protein kinase	gbpln	Arabidopsis thaliana	AT1G77280.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:29031468-29035882 REVERSE LENGTH=794	688	794	0	115.4	81.5	88.8
Rsa1.0_00299.1.g10777.t1	gb|EOA33259.1| hypothetical protein CARUB_v10022136mg [Capsella rubella]	266	266	2.33E-156	100.0	94.7	98.9	hypothetical protein CARUB_v10022136mg	gbpln	Capsella rubella	AT1G77290.2 | Symbols: | Glutathione S-transferase family protein | chr1:29038917-29039815 FORWARD LENGTH=266	266	266	2.33E-156	100.0	92.9	98.1
Rsa1.0_00299.1.g10778.t14	ref|NP_177854.6| histone-lysine N-methyltransferase SETD2 [Arabidopsis thaliana] gi|157734196|gb|ABV68921.1| SDG8 [Arabidopsis thaliana] gi|332197839|gb|AEE35960.1| histone-lysine N-methyltransferase SETD2 [Arabidopsis thaliana]	1783	1805	0	101.2	69.7	78.4	histone-lysine N-methyltransferase SETD2	gbpln	Arabidopsis thaliana	AT1G77300.1 | Symbols: EFS, SDG8, CCR1, ASHH2, LAZ2 | histone methyltransferases(H3-K4 specific);histone methyltransferases(H3-K36 specific) | chr1:29040160-29048810 REVERSE LENGTH=1805	1783	1805	0	101.2	69.7	78.4
Rsa1.0_00299.1.g10779.t1	ref|NP_177855.4| uncharacterized protein [Arabidopsis thaliana] gi|332197841|gb|AEE35962.1| uncharacterized protein AT1G77310 [Arabidopsis thaliana]	668	717	0	107.3	66.2	77.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G77310.1 | Symbols: | BEST Arabidopsis thaliana protein match is: wound-responsive family protein (TAIR:AT1G21610.1); Has 493 Blast hits to 482 proteins in 163 species: Archae - 0; Bacteria - 100; Metazoa - 172; Fungi - 66; Plants - 65; Viruses - 7; Other Eukaryotes - 83 (source: NCBI BLink). | chr1:29051671-29056179 FORWARD LENGTH=717	668	717	0	107.3	66.2	77.7
Rsa1.0_00299.1.g10780.t1	ref|XP_002887677.1| MEI1 protein [Arabidopsis lyrata subsp. lyrata] gi|297333518|gb|EFH63936.1| MEI1 protein [Arabidopsis lyrata subsp. lyrata]	1002	970	0	96.8	76.9	83.3	MEI1 protein	gbpln	Arabidopsis lyrata	AT1G77320.1 | Symbols: MEI1 | transcription coactivators | chr1:29056740-29062710 FORWARD LENGTH=972	1002	972	0	97.0	76.3	82.6
Rsa1.0_00299.1.g10781.t1	gb|EOA40087.1| hypothetical protein CARUB_v10008781mg [Capsella rubella]	325	544	6.00E-70	167.4	42.5	52.6	hypothetical protein CARUB_v10008781mg	gbpln	Capsella rubella	AT1G21660.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:7605924-7608835 FORWARD LENGTH=523	325	523	3.00E-71	160.9	41.5	52.6
Rsa1.0_00299.1.g10782.t1	gb|AAM62803.1| amino acid carrier, putative [Arabidopsis thaliana]	477	476	0	99.8	92.0	95.6	amino acid carrier, putative	gbpln	Arabidopsis thaliana	AT1G77380.1 | Symbols: AAP3, ATAAP3 | amino acid permease 3 | chr1:29075201-29077252 REVERSE LENGTH=476	477	476	0	99.8	91.8	95.4
Rsa1.0_00300.1.g10783.t1	sp|Q9LJF9.3|FDL44_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	446	434	1.00E-118	97.3	54.0	70.6	RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	----	----	AT3G26930.1 | Symbols: | Protein with RNI-like/FBD-like domains | chr3:9925931-9927351 FORWARD LENGTH=409	446	409	7.00E-97	91.7	48.7	60.1
Rsa1.0_00300.1.g10784.t1	sp|Q9LJF9.3|FDL44_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	163	434	2.00E-41	266.3	58.9	75.5	RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	----	----	AT3G26922.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:9922858-9923891 FORWARD LENGTH=306	163	306	3.00E-39	187.7	54.0	69.3
Rsa1.0_00300.1.g10785.t1	gb|EOA24039.1| hypothetical protein CARUB_v10017257mg [Capsella rubella]	446	443	0	99.3	89.9	95.7	hypothetical protein CARUB_v10017257mg	gbpln	Capsella rubella	AT3G26935.1 | Symbols: | DHHC-type zinc finger family protein | chr3:9933001-9935218 REVERSE LENGTH=443	446	443	0	99.3	89.7	94.8
Rsa1.0_00300.1.g10786.t1	ref|XP_002877007.1| hypothetical protein ARALYDRAFT_484482 [Arabidopsis lyrata subsp. lyrata] gi|297322845|gb|EFH53266.1| hypothetical protein ARALYDRAFT_484482 [Arabidopsis lyrata subsp. lyrata]	441	432	1.00E-119	98.0	57.1	68.3	hypothetical protein ARALYDRAFT_484482	gbpln	Arabidopsis lyrata	AT3G26940.1 | Symbols: CDG1 | Protein kinase superfamily protein | chr3:9936707-9938936 REVERSE LENGTH=432	441	432	1.00E-118	98.0	56.7	68.9

Rsa1.0_00300.1.g10787.t1	gb|EOA23750.1| hypothetical protein CARUB_v10016962mg [Capsella rubella]	545	551	0	101.1	85.3	92.3	hypothetical protein CARUB_v10016962mg	gbpln	Capsella rubella	AT3G26950.1 | Symbols: | unknown protein; Has 27 Blast hits to 27 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9941202-9943411 REVERSE LENGTH=548	545	548	0	100.6	84.8	91.6
Rsa1.0_00300.1.g10788.t2	gb|EOA23822.1| hypothetical protein CARUB_v10017036mg [Capsella rubella]	538	513	0	95.4	77.7	85.3	hypothetical protein CARUB_v10017036mg	gbpln	Capsella rubella	AT3G26990.1 | Symbols: | ENTH/VHS family protein | chr3:9948426-9951557 REVERSE LENGTH=513	538	513	0	95.4	79.2	85.7
Rsa1.0_00300.1.g10789.t1	ref|XP_002875350.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] gi|297321188|gb|EFH51609.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	109	120	3.00E-48	110.1	85.3	88.1	ubiquitin family protein	gbpln	Arabidopsis lyrata	AT3G26980.1 | Symbols: MUB4 | membrane-anchored ubiquitin-fold protein 4 precursor | chr3:9946467-9947444 REVERSE LENGTH=120	109	120	3.00E-50	110.1	85.3	87.2
Rsa1.0_00300.1.g10790.t1	gb|EOA24831.1| hypothetical protein CARUB_v10018119mg [Capsella rubella]	172	174	1.00E-73	101.2	80.2	90.7	hypothetical protein CARUB_v10018119mg	gbpln	Capsella rubella	AT3G26960.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr3:9944859-9945459 REVERSE LENGTH=174	172	174	5.00E-72	101.2	76.2	86.0
Rsa1.0_00300.1.g10791.t2	dbj|BAJ34017.1| unnamed protein product [Thellungiella halophila]	366	389	0	106.3	97.8	98.9	unnamed protein product	----	----	AT3G27000.1 | Symbols: ARP2, ATARP2, WRM | actin related protein 2 | chr3:9952787-9955784 REVERSE LENGTH=389	366	389	0	106.3	97.5	98.9
Rsa1.0_00300.1.g10792.t1	gb|EOA23265.1| hypothetical protein CARUB_v10017630mg [Capsella rubella]	328	328	1.00E-115	100.0	75.3	82.3	hypothetical protein CARUB_v10017630mg	gbpln	Capsella rubella	AT3G27010.1 | Symbols: AT-TCP20, PCF1, TCP20, ATTCP20 | TEOSINTE BRANCHED 1, cycloidea, PCF (TCP)-domain family protein 20 | chr3:9957810-9958754 REVERSE LENGTH=314	328	314	1.00E-107	95.7	74.7	79.9
Rsa1.0_00300.1.g10793.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1222	1274	0	104.3	43.0	58.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1222	575	1.00E-54	47.1	11.5	17.3
Rsa1.0_00300.1.g10794.t1	ref|XP_002875353.1| hypothetical protein ARALYDRAFT_347067 [Arabidopsis lyrata subsp. lyrata] gi|297321191|gb|EFH51612.1| hypothetical protein ARALYDRAFT_347067 [Arabidopsis lyrata subsp. lyrata]	280	296	1.00E-75	105.7	60.7	75.4	hypothetical protein ARALYDRAFT_347067	gbpln	Arabidopsis lyrata	AT3G27025.1 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9969735-9971084 FORWARD LENGTH=289	280	289	3.00E-78	103.2	59.6	73.2
Rsa1.0_00300.1.g10795.t1	ref|XP_002533319.1| phosphatidylinositol-4-phosphate 5-kinase, putative [Ricinus communis] gi|223526863|gb|EEF29076.1| phosphatidylinositol-4-phosphate 5-kinase, putative [Ricinus communis]	219	1569	9.00E-25	716.4	27.9	35.6	phosphatidylinositol-4-phosphate 5-kinase, putative	gbpln	Ricinus communis	AT1G34260.1 | Symbols: FAB1D | FORMS APLOID AND BINUCLEATE CELLS 1A | chr1:12485967-12491799 FORWARD LENGTH=1456	219	1456	1.00E-24	664.8	26.9	37.9
Rsa1.0_00300.1.g10796.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00300.1.g10797.t1	ref|XP_002875353.1| hypothetical protein ARALYDRAFT_347067 [Arabidopsis lyrata subsp. lyrata] gi|297321191|gb|EFH51612.1| hypothetical protein ARALYDRAFT_347067 [Arabidopsis lyrata subsp. lyrata]	178	296	1.00E-13	166.3	23.6	29.8	hypothetical protein ARALYDRAFT_347067	gbpln	Arabidopsis lyrata	AT3G27025.1 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9969735-9971084 FORWARD LENGTH=289	178	289	4.00E-15	162.4	23.0	25.3
Rsa1.0_00300.1.g10798.t1	ref|XP_002877012.1| hypothetical protein ARALYDRAFT_322830 [Arabidopsis lyrata subsp. lyrata] gi|297322850|gb|EFH53271.1| hypothetical protein ARALYDRAFT_322830 [Arabidopsis lyrata subsp. lyrata]	69	142	3.00E-27	205.8	89.9	95.7	hypothetical protein ARALYDRAFT_322830	gbpln	Arabidopsis lyrata	AT3G27030.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3339 (InterPro:IPR021775); BEST Arabidopsis thaliana protein match is: Protein of unknown function (DUF 3339) (TAIR:AT5G40970.1); Has 538 Blast hits to 271 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 534; Viruses - 4; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9972508-9974225 REVERSE LENGTH=142	69	142	1.00E-29	205.8	88.4	95.7
Rsa1.0_00300.1.g10799.t1	gb|EOA25773.1| hypothetical protein CARUB_v10019136mg [Capsella rubella]	331	332	0	100.3	97.0	97.9	hypothetical protein CARUB_v10019136mg	gbpln	Capsella rubella	AT3G27060.1 | Symbols: TSO2, ATTSO2 | Ferritin/ribonucleotide reductase-like family protein | chr3:9979971-9981057 REVERSE LENGTH=332	331	332	0	100.3	97.0	98.2

Rsa1.0_00300.1.g10800.t2	ref|NP_189345.1| DCD (Development and Cell Death) domain protein [Arabidopsis thaliana] gi|9279632|dbj|BAB01090.1| unnamed protein product [Arabidopsis thaliana] gi|16604450|gb|AAL24231.1| AT3g27090/MOJ10_18 [Arabidopsis thaliana] gi|21655279|gb|AAM65351.1| AT3g27090/MOJ10_18 [Arabidopsis thaliana] gi|332643744|gb|AEE77265.1| DCD (Development and Cell Death) domain protein [Arabidopsis thaliana]	340	296	1.00E-130	87.1	73.2	77.4	DCD (Development and Cell Death) domain protein	gbpln	Arabidopsis thaliana	AT3G27090.1 | Symbols: | DCD (Development and Cell Death) domain protein | chr3:9990020-9991407 FORWARD LENGTH=296	340	296	1.00E-133	87.1	73.2	77.4
Rsa1.0_00300.1.g10801.t1	ref|NP_189346.2| enhancer of yellow 2 transcription factor [Arabidopsis thaliana] gi|37202032|gb|AAQ89631.1| At3g27100 [Arabidopsis thaliana] gi|51969380|dbj|BAD43382.1| hypothetical protein [Arabidopsis thaliana] gi|332643745|gb|AEE77266.1| enhancer of yellow 2 transcription factor [Arabidopsis thaliana]	102	115	3.00E-22	112.7	61.8	63.7	enhancer of yellow 2 transcription factor	gbpln	Arabidopsis thaliana	AT3G27100.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Transcription factor, enhancer of yellow 2 (InterPro:IPR018783); Has 288 Blast hits to 288 proteins in 94 species: Archae - 0; Bacteria - 0; Metazoa - 197; Fungi - 20; Plants - 51; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink). | chr3:9994743-9995923 REVERSE LENGTH=115	102	115	5.00E-25	112.7	61.8	63.7
Rsa1.0_00300.1.g10802.t1	ref|XP_002875358.1| peptidase M48 family protein [Arabidopsis lyrata subsp. lyrata] gi|297321196|gb|EFH51617.1| peptidase M48 family protein [Arabidopsis lyrata subsp. lyrata]	331	344	1.00E-159	103.9	88.2	93.1	peptidase M48 family protein	gbpln	Arabidopsis lyrata	AT3G27110.2 | Symbols: | Peptidase family M48 family protein | chr3:9998006-9999892 FORWARD LENGTH=344	331	344	1.00E-162	103.9	88.2	92.7
Rsa1.0_00300.1.g10803.t1	gb|EOA25852.1| hypothetical protein CARUB_v10019230mg [Capsella rubella]	434	420	0	96.8	74.4	83.9	hypothetical protein CARUB_v10019230mg	gbpln	Capsella rubella	AT3G27150.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:10009692-10010960 REVERSE LENGTH=422	434	422	0	97.2	74.2	82.0
Rsa1.0_00300.1.g10804.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00301.1.g10805.t1	ref|XP_002873746.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319583|gb|EFH50005.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	435	427	0	98.2	89.4	93.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G15860.1 | Symbols: ATPCME, PCME | prenylcysteine methylesterase | chr5:5178676-5181263 REVERSE LENGTH=427	435	427	0	98.2	89.2	93.1
Rsa1.0_00301.1.g10806.t1	dbj|BAJ33807.1| unnamed protein product [Thellungiella halophila]	186	190	3.00E-80	102.2	83.9	90.9	unnamed protein product	----	----	AT5G15830.1 | Symbols: AtbZIP3, bZIP3 | basic leucine-zipper 3 | chr5:5168591-5169151 FORWARD LENGTH=186	186	186	2.00E-71	100.0	82.8	87.6
Rsa1.0_00301.1.g10807.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	847	1274	0	150.4	49.6	65.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	847	575	6.00E-65	67.9	20.2	32.5
Rsa1.0_00301.1.g10808.t1	gb|EOA21044.1| hypothetical protein CARUB_v10001383mg [Capsella rubella]	382	336	2.00E-53	88.0	46.6	56.5	hypothetical protein CARUB_v10001383mg	gbpln	Capsella rubella	AT5G15820.1 | Symbols: | RING/U-box superfamily protein | chr5:5161787-5162833 FORWARD LENGTH=348	382	348	9.00E-52	91.1	43.7	54.2
Rsa1.0_00301.1.g10809.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00301.1.g10810.t1	ref|XP_002873741.1| hypothetical protein ARALYDRAFT_488422 [Arabidopsis lyrata subsp. lyrata] gi|297319578|gb|EFH50000.1| hypothetical protein ARALYDRAFT_488422 [Arabidopsis lyrata subsp. lyrata]	319	363	3.00E-78	113.8	55.5	60.8	hypothetical protein ARALYDRAFT_488422	gbpln	Arabidopsis lyrata	AT5G15780.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:5144898-5146297 REVERSE LENGTH=401	319	401	2.00E-78	125.7	46.7	49.8

Rsa1.0_00301.1.g10811.t1	ref|NP_197081.1| glucose-6-phosphate acetyltransferase 1 [Arabidopsis thaliana] gi|75174187|sp|Q9LFU9.1|GNA1_ARATH RecName: Full=Glucosamine 6-phosphate N-acetyltransferase; AltName: Full=Glucose-6-phosphate acetyltransferase 1; Short=AtGNA1; AltName: Full=Phosphoglucosamine acetylase; AltName: Full=Phosphoglucosamine transacetylase; AltName: Full=Protein LIGNESCENS gi|383875481|pdb|3T90|A Chain A, Crystal Structure Of Glucosamine-6-Phosphate N-Acetyltransferase From Arabidopsis Thaliana gi|9755622|emb|CAC01776.1| acetyltransferase-like protein [Arabidopsis thaliana] gi|332004820|gb|AED92203.1| glucose-6-phosphate acetyltransferase 1 [Arabidopsis thaliana]	159	149	2.00E-64	93.7	74.8	84.3	glucose-6-phosphate acetyltransferase 1	gbpln	Arabidopsis thaliana	AT5G15770.1 | Symbols: AtGNA1, GNA1 | glucose-6-phosphate acetyltransferase 1 | chr5:5144093-5144542 REVERSE LENGTH=149	159	149	6.00E-67	93.7	74.8	84.3
Rsa1.0_00301.1.g10812.t1	ref|XP_002871682.1| RNA-binding S4 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317519|gb|EFH47941.1| RNA-binding S4 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	183	182	9.00E-91	99.5	88.5	92.3	RNA-binding S4 domain-containing protein	gbpln	Arabidopsis lyrata	AT5G15750.1 | Symbols: | Alpha-L RNA-binding motif/Ribosomal protein S4 family protein | chr5:5141449-5142701 FORWARD LENGTH=182	183	182	1.00E-91	99.5	86.3	91.8
Rsa1.0_00301.1.g10813.t1	ref|XP_002873738.1| GDSL-motif lipase 7 [Arabidopsis lyrata subsp. lyrata] gi|297319575|gb|EFH49997.1| GDSL-motif lipase 7 [Arabidopsis lyrata subsp. lyrata]	367	364	1.00E-176	99.2	81.5	90.7	GDSL-motif lipase 7	gbpln	Arabidopsis lyrata	AT5G15720.1 | Symbols: GLIP7 | GDSL-motif lipase 7 | chr5:5124684-5126155 REVERSE LENGTH=364	367	364	1.00E-176	99.2	79.0	87.7
Rsa1.0_00301.1.g10814.t1	ref|XP_002873737.1| DNA-directed RNA polymerase [Arabidopsis lyrata subsp. lyrata] gi|297319574|gb|EFH49996.1| DNA-directed RNA polymerase [Arabidopsis lyrata subsp. lyrata]	1021	1009	0	98.8	81.0	85.7	DNA-directed RNA polymerase	gbpln	Arabidopsis lyrata	AT5G15700.2 | Symbols: | DNA/RNA polymerases superfamily protein | chr5:5115572-5121609 REVERSE LENGTH=1051	1021	1051	0	102.9	80.6	85.0
Rsa1.0_00301.1.g10815.t1	ref|NP_197072.3| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332004808|gb|AED92191.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	2150	2153	0	100.1	96.1	98.5	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G15680.1 | Symbols: | ARM repeat superfamily protein | chr5:5101188-5110793 REVERSE LENGTH=2153	2150	2153	0	100.1	96.1	98.5
Rsa1.0_00301.1.g10816.t1	ref|NP_192896.1| F-box protein [Arabidopsis thaliana] gi|75266803|sp|Q9T0C7.1|FB231_ARATH RecName: Full=F-box protein At4g11590 gi|4539450|emb|CAB39930.1| putative protein [Arabidopsis thaliana] gi|7267859|emb|CAB78202.1| putative protein [Arabidopsis thaliana] gi|332657628|gb|AEE83028.1| F-box protein [Arabidopsis thaliana]	399	397	9.00E-84	99.5	48.9	63.7	F-box protein	gbpln	Arabidopsis thaliana	AT4G11590.1 | Symbols: | F-box associated ubiquitination effector family protein | chr4:7008603-7009796 FORWARD LENGTH=397	399	397	2.00E-86	99.5	48.9	63.7
Rsa1.0_00301.1.g10817.t1	ref|NP_192896.1| F-box protein [Arabidopsis thaliana] gi|75266803|sp|Q9T0C7.1|FB231_ARATH RecName: Full=F-box protein At4g11590 gi|4539450|emb|CAB39930.1| putative protein [Arabidopsis thaliana] gi|7267859|emb|CAB78202.1| putative protein [Arabidopsis thaliana] gi|332657628|gb|AEE83028.1| F-box protein [Arabidopsis thaliana]	415	397	1.00E-80	95.7	45.5	59.0	F-box protein	gbpln	Arabidopsis thaliana	AT4G11590.1 | Symbols: | F-box associated ubiquitination effector family protein | chr4:7008603-7009796 FORWARD LENGTH=397	415	397	3.00E-83	95.7	45.5	59.0
Rsa1.0_00301.1.g10818.t1	gb|EOA20905.1| hypothetical protein CARUB_v10001241mg [Capsella rubella]	363	363	0	100.0	97.2	98.3	hypothetical protein CARUB_v10001241mg	gbpln	Capsella rubella	AT5G15650.1 | Symbols: RGP2, ATRGP2 | reversibly glycosylated polypeptide 2 | chr5:5092203-5094093 FORWARD LENGTH=360	363	360	0	99.2	96.7	98.3
Rsa1.0_00301.1.g10819.t1	ref|XP_002893723.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339565|gb|EFH69982.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	407	385	1.00E-117	94.6	56.0	66.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G32430.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11704932-11706325 REVERSE LENGTH=380	407	380	1.00E-110	93.4	51.8	62.9

Rsa1.0_00301.1.g10820.t2	ref|NP_197067.2| COBRA-like protein 4 [Arabidopsis thaliana] gi|34222647|sp|Q9LFW3.2|COBL4_ARATH RecName: Full=COBRA-like protein 4; Flags: Precursor gi|48525349|gb|AAT44976.1| At5g15630 [Arabidopsis thaliana] gi|56790214|gb|AAW30024.1| At5g15630 [Arabidopsis thaliana] gi|332004803|gb|AED92186.1| COBRA-like protein 4 [Arabidopsis thaliana]	435	431	0	99.1	88.5	92.9	COBRA-like protein 4	gbpln	Arabidopsis thaliana	AT5G15630.1 | Symbols: COBL4, IRX6 | COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family | chr5:5084842-5086545 FORWARD LENGTH=431	435	431	0	99.1	88.5	92.9
Rsa1.0_00301.1.g10821.t1	gb|AAM64731.1| nitrilase associated protein-like [Arabidopsis thaliana]	109	127	1.00E-31	116.5	79.8	82.6	nitrilase associated protein-like	gbpln	Arabidopsis thaliana	AT5G15600.1 | Symbols: SP1L4 | SPIRAL1-like4 | chr5:5078405-5078863 FORWARD LENGTH=127	109	127	2.00E-34	116.5	79.8	82.6
Rsa1.0_00301.1.g10822.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00301.1.g10823.t1	gb|EOA19910.1| hypothetical protein CARUB_v10000160mg [Capsella rubella]	909	931	0	102.4	81.6	88.3	hypothetical protein CARUB_v10000160mg	gbpln	Capsella rubella	AT5G15580.1 | Symbols: LNG1 | longifolia1 | chr5:5068495-5071930 REVERSE LENGTH=927	909	927	0	102.0	81.2	88.0
Rsa1.0_00301.1.g10824.t1	ref|XP_002871671.1| hypothetical protein ARALYDRAFT_909531 [Arabidopsis lyrata subsp. lyrata] gi|297317508|gb|EFH47930.1| hypothetical protein ARALYDRAFT_909531 [Arabidopsis lyrata subsp. lyrata]	376	380	1.00E-157	101.1	74.7	84.3	hypothetical protein ARALYDRAFT_909531	gbpln	Arabidopsis lyrata	AT5G15570.1 | Symbols: | Bromodomain transcription factor | chr5:5066851-5067996 FORWARD LENGTH=381	376	381	1.00E-157	101.3	72.3	81.4
Rsa1.0_00301.1.g10825.t1	ref|NP_197059.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|9755810|emb|CAC01754.1| putative protein [Arabidopsis thaliana] gi|17381110|gb|AAL36367.1| unknown protein [Arabidopsis thaliana] gi|20258961|gb|AAM14196.1| unknown protein [Arabidopsis thaliana] gi|332004793|gb|AED92176.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	369	433	1.00E-157	117.3	75.3	81.8	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G15550.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:5059051-5062003 REVERSE LENGTH=433	369	433	1.00E-160	117.3	75.3	81.8
Rsa1.0_00301.1.g10826.t1	ref|XP_002873731.1| sister chromatid cohesion 2 [Arabidopsis lyrata subsp. lyrata] gi|297319568|gb|EFH49990.1| sister chromatid cohesion 2 [Arabidopsis lyrata subsp. lyrata]	1847	1847	0	100.0	86.4	91.6	sister chromatid cohesion 2	gbpln	Arabidopsis lyrata	AT5G15540.1 | Symbols: EMB2773, ATSCC2, SCC2 | PHD finger family protein | chr5:5047887-5057411 REVERSE LENGTH=1846	1847	1846	0	99.9	85.6	91.1
Rsa1.0_00301.1.g10827.t1	ref|NP_197055.2| TPX2 (targeting protein for Xklp2) family protein [Arabidopsis thaliana] gi|332004787|gb|AED92170.1| TPX2 (targeting protein for Xklp2) family protein [Arabidopsis thaliana]	507	497	0	98.0	75.7	82.8	TPX2 (targeting protein for Xklp2) family protein	gbpln	Arabidopsis thaliana	AT5G15510.1 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr5:5034120-5036614 FORWARD LENGTH=497	507	497	0	98.0	75.7	82.8
Rsa1.0_00301.1.g10828.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00301.1.g10829.t1	gb|EOA20540.1| hypothetical protein CARUB_v10000855mg [Capsella rubella] gi|482556349|gb|EOA20541.1| hypothetical protein CARUB_v10000855mg [Capsella rubella] gi|482556350|gb|EOA20542.1| hypothetical protein CARUB_v10000855mg [Capsella rubella]	481	480	0	99.8	97.9	99.2	hypothetical protein CARUB_v10000855mg	gbpln	Capsella rubella	AT5G15490.1 | Symbols: | UDP-glucose 6-dehydrogenase family protein | chr5:5027872-5029314 REVERSE LENGTH=480	481	480	0	99.8	96.7	99.0
Rsa1.0_00301.1.g10830.t1	gb|EOA19903.1| hypothetical protein CARUB_v10000151mg [Capsella rubella]	967	971	0	100.4	94.6	97.2	hypothetical protein CARUB_v10000151mg	gbpln	Capsella rubella	AT5G15450.1 | Symbols: APG6, CLPB3, CLPB-P | casein lytic proteinase B3 | chr5:5014399-5018255 REVERSE LENGTH=968	967	968	0	100.1	94.3	97.0
Rsa1.0_00301.1.g10831.t1	ref|XP_002871665.1| hypothetical protein ARALYDRAFT_488388 [Arabidopsis lyrata subsp. lyrata] gi|297317502|gb|EFH47924.1| hypothetical protein ARALYDRAFT_488388 [Arabidopsis lyrata subsp. lyrata]	428	478	1.00E-119	111.7	66.1	76.9	hypothetical protein ARALYDRAFT_488388	gbpln	Arabidopsis lyrata	AT5G15430.1 | Symbols: | Plant calmodulin-binding protein-related | chr5:5010180-5011616 FORWARD LENGTH=478	428	478	1.00E-113	111.7	63.8	76.4

Rsa1.0_00301.1.g10832.t1	ref|NP_568313.2| putative ubiquitin conjugation factor E4 [Arabidopsis thaliana] gi|75174048|sp|Q9LF41.1|UBE4_ARATH RecName: Full=Probable ubiquitin conjugation factor E4; AltName: Full=Plant U-box protein 1; AltName: Full=U-box domain-containing protein 1; AltName: Full=Ubiquitin-fusion degradation protein 2-like; Short=UB fusion protein 2-like gi|9755795|emb|CAC01739.1| ubiquitin-fusion degradation protein-like [Arabidopsis thaliana] gi|332004773|gb|AED92156.1| putative ubiquitin conjugation factor E4 [Arabidopsis thaliana]	1042	1038	0	99.6	92.0	95.5	putative ubiquitin conjugation factor E4	gbpln	Arabidopsis thaliana	AT5G15400.1 | Symbols: | U-box domain-containing protein | chr5:4997764-5002907 REVERSE LENGTH=1038	1042	1038	0	99.6	92.0	95.5
Rsa1.0_00301.1.g10833.t1	ref|XP_002882199.1| hypothetical protein ARALYDRAFT_477417 [Arabidopsis lyrata subsp. lyrata] gi|297328039|gb|EFH58458.1| hypothetical protein ARALYDRAFT_477417 [Arabidopsis lyrata subsp. lyrata]	501	564	0	112.6	75.6	82.4	hypothetical protein ARALYDRAFT_477417	gbpln	Arabidopsis lyrata	AT3G01120.1 | Symbols: MTO1, CGS, ATCYS1, CGS1 | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr3:39234-41865 REVERSE LENGTH=563	501	563	0	112.4	74.5	81.4
Rsa1.0_00301.1.g10834.t1	dbj|BAJ34432.1| unnamed protein product [Thellungiella halophila]	315	326	1.00E-142	103.5	84.4	88.6	unnamed protein product	----	----	AT5G15310.1 | Symbols: ATMYB16, ATMIXTA, MYB16 | myb domain protein 16 | chr5:4974894-4976106 FORWARD LENGTH=326	315	326	1.00E-140	103.5	83.2	88.3
Rsa1.0_00301.1.g10835.t1	ref|NP_197032.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75180846|sp|Q9LXF4.1|PP384_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g15280 gi|7671497|emb|CAB89338.1| putative protein [Arabidopsis thaliana] gi|332004760|gb|AED92143.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	1234	1227	0	99.4	72.9	83.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G15280.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:4962293-4965976 FORWARD LENGTH=1227	1234	1227	0	99.4	72.9	83.5
Rsa1.0_00301.1.g10836.t1	gb|EOA20603.1| hypothetical protein CARUB_v10000919mg, partial [Capsella rubella]	426	460	0	108.0	87.8	93.0	hypothetical protein CARUB_v10000919mg, partial	gbpln	Capsella rubella	AT5G15240.1 | Symbols: | Transmembrane amino acid transporter family protein | chr5:4947762-4950211 FORWARD LENGTH=423	426	423	0	99.3	85.7	92.5
Rsa1.0_00301.1.g10837.t1	ref|NP_197027.1| gibberellin-regulated protein 4 [Arabidopsis thaliana] gi|21431771|sp|P46690.2|GASA4_ARATH RecName: Full=Gibberellin-regulated protein 4; AltName: Full=GAST1 protein homolog 4; Flags: Precursor gi|13430574|gb|AAK25909.1|AF360199_1 putative GASA4 protein [Arabidopsis thaliana] gi|2764941|emb|CAA66909.1| GASA4 [Arabidopsis thaliana] gi|7671492|emb|CAB89333.1| GASA4 [Arabidopsis thaliana] gi|14532848|gb|AAK64106.1| putative GASA4 protein [Arabidopsis thaliana] gi|16209676|gb|AAL14396.1| AT5g15230/F8M21_120 [Arabidopsis thaliana] gi|332004749|gb|AED92132.1| gibberellin-regulated protein 4 [Arabidopsis thaliana]	106	106	8.00E-46	100.0	82.1	88.7	gibberellin-regulated protein 4	gbpln	Arabidopsis thaliana	AT5G15230.1 | Symbols: GASA4 | GAST1 protein homolog 4 | chr5:4945017-4946025 FORWARD LENGTH=106	106	106	1.00E-48	100.0	82.1	88.7
Rsa1.0_00301.1.g10838.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00301.1.g10839.t2	ref|NP_568310.1| large subunit ribosomal protein L27 [Arabidopsis thaliana] gi|15081777|gb|AAK82543.1| AT5g15220/F8M21_110 [Arabidopsis thaliana] gi|18958058|gb|AAL79602.1| AT5g15220/F8M21_110 [Arabidopsis thaliana] gi|332004748|gb|AED92131.1| large subunit ribosomal protein L27 [Arabidopsis thaliana]	135	154	1.00E-25	114.1	58.5	63.7	large subunit ribosomal protein L27	gbpln	Arabidopsis thaliana	AT5G15220.1 | Symbols: | Ribosomal protein L27 family protein | chr5:4941466-4942133 REVERSE LENGTH=154	135	154	2.00E-28	114.1	58.5	63.7
Rsa1.0_00301.1.g10840.t1	gb|EOA21599.1| hypothetical protein CARUB_v10002009mg [Capsella rubella]	197	197	1.00E-109	100.0	98.5	100.0	hypothetical protein CARUB_v10002009mg	gbpln	Capsella rubella	AT5G15200.1 | Symbols: | Ribosomal protein S4 | chr5:4935124-4936334 REVERSE LENGTH=198	197	198	1.00E-105	100.5	92.9	94.9

Rsa1.0_00301.1.g10841.t1	ref|NP_197023.2| uncharacterized protein [Arabidopsis thaliana] gi|30685234|ref|NP_850823.1| uncharacterized protein [Arabidopsis thaliana] gi|26453158|dbj|BAC43655.1| unknown protein [Arabidopsis thaliana] gi|28416855|gb|AAO42958.1| At5g15190 [Arabidopsis thaliana] gi|332004743|gb|AED92126.1| uncharacterized protein AT5G15190 [Arabidopsis thaliana] gi|332004744|gb|AED92127.1| uncharacterized protein AT5G15190 [Arabidopsis thaliana]	121	116	2.00E-40	95.9	71.1	80.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G15190.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; Has 7 Blast hits to 7 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:4933148-4933498 REVERSE LENGTH=116	121	116	3.00E-43	95.9	71.1	80.2
Rsa1.0_00301.1.g10842.t1	ref|NP_197022.1| peroxidase 56 [Arabidopsis thaliana] gi|26397870|sp|Q9LXG3.1|PER56_ARATH RecName: Full=Peroxidase 56; Short=Atperox P56; AltName: Full=ATP33; Flags: Precursor gi|7671487|emb|CAB89328.1| prx10 peroxidase-like protein [Arabidopsis thaliana] gi|18176159|gb|AAL59994.1| putative prx10 peroxidase [Arabidopsis thaliana] gi|23296746|gb|AAN13160.1| putative prx10 peroxidase [Arabidopsis thaliana] gi|110736795|dbj|BAF00358.1| prx10 peroxidase - like protein [Arabidopsis thaliana] gi|332004742|gb|AED92125.1| peroxidase 56 [Arabidopsis thaliana]	330	329	1.00E-159	99.7	83.0	89.1	peroxidase 56	gbpln	Arabidopsis thaliana	AT5G15180.1 | Symbols: | Peroxidase superfamily protein | chr5:4930561-4932211 FORWARD LENGTH=329	330	329	1.00E-161	99.7	83.0	89.1
Rsa1.0_00301.1.g10843.t1	ref|NP_197020.1| protein banquo 2 [Arabidopsis thaliana] gi|297811653|ref|XP_002873710.1| bHLH family protein [Arabidopsis lyrata subsp. lyrata] gi|7671485|emb|CAB89326.1| putative protein [Arabidopsis thaliana] gi|26452783|dbj|BAC43472.1| unknown protein [Arabidopsis thaliana] gi|28973111|gb|AAO63880.1| putative bHLH protein [Arabidopsis thaliana] gi|297319547|gb|EFH49969.1| bHLH family protein [Arabidopsis lyrata subsp. lyrata] gi|332004740|gb|AED92123.1| protein banquo 2 [Arabidopsis thaliana]	93	94	4.00E-33	101.1	77.4	81.7	protein banquo 2	gbpln	Arabidopsis lyrata	AT5G15160.1 | Symbols: BNQ2, BHLH134 | BANQUO 2 | chr5:4921487-4922553 REVERSE LENGTH=94	93	94	6.00E-36	101.1	77.4	81.7
Rsa1.0_00301.1.g10844.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00301.1.g10845.t1	ref|NP_001154201.1| HSP20-like chaperone [Arabidopsis thaliana] gi|332656774|gb|AEE82174.1| HSP20-like chaperone [Arabidopsis thaliana]	115	240	1.00E-40	208.7	75.7	83.5	HSP20-like chaperone	gbpln	Arabidopsis thaliana	AT4G02450.2 | Symbols: | HSP20-like chaperones superfamily protein | chr4:1073987-1075765 REVERSE LENGTH=240	115	240	2.00E-43	208.7	75.7	83.5
Rsa1.0_00301.1.g10846.t1	ref|NP_568309.2| homeobox-leucine zipper protein HAT7 [Arabidopsis thaliana] gi|90101578|sp|Q00466.4|HAT7_ARATH RecName: Full=Homeobox-leucine zipper protein HAT7; AltName: Full=HD-ZIP protein ATHB-3; AltName: Full=Homeodomain transcription factor ATHB-3; AltName: Full=Homeodomain-leucine zipper protein HAT7; Short=HD-ZIP protein 7 gi|110738603|dbj|BAF01227.1| homeobox protein [Arabidopsis thaliana] gi|199589350|gb|ACH90466.1| At5g15150 [Arabidopsis thaliana] gi|332004739|gb|AED92122.1| homeobox-leucine zipper protein HAT7 [Arabidopsis thaliana]	286	314	1.00E-143	109.8	93.7	96.9	homeobox-leucine zipper protein HAT7	gbpln	Arabidopsis thaliana	AT5G15150.1 | Symbols: ATHB-3, HAT7, ATHB3, HB-3 | homeobox 3 | chr5:4913951-4915609 REVERSE LENGTH=314	286	314	2.33E-156	109.8	93.7	96.9
Rsa1.0_00301.1.g10847.t1	ref|XP_002871650.1| WRKY DNA-binding protein 72 [Arabidopsis lyrata subsp. lyrata] gi|297317487|gb|EFH47909.1| WRKY DNA-binding protein 72 [Arabidopsis lyrata subsp. lyrata]	607	555	0	91.4	64.6	69.9	WRKY DNA-binding protein 72	gbpln	Arabidopsis lyrata	AT5G15130.1 | Symbols: WRKY72, ATWRKY72 | WRKY DNA-binding protein 72 | chr5:4904426-4906879 FORWARD LENGTH=548	607	548	0	90.3	64.4	69.4
Rsa1.0_00301.1.g10848.t1	gb|ABK28696.1| unknown [Arabidopsis thaliana]	481	473	0	98.3	83.0	90.0	unknown	gbpln	Arabidopsis thaliana	AT5G15110.1 | Symbols: | Pectate lyase family protein | chr5:4895966-4897682 FORWARD LENGTH=472	481	472	0	98.1	83.0	90.0
Rsa1.0_00301.1.g10849.t1	gb|ABB97031.1| unknown [Brassica rapa]	276	276	1.00E-150	100.0	95.3	97.5	unknown	gbpln	Brassica rapa	AT5G15090.2 | Symbols: VDAC3 | voltage dependent anion channel 3 | chr5:4889641-4891389 REVERSE LENGTH=274	276	274	1.00E-129	99.3	80.1	89.9

Rsa1.0_00301.1.g10850.t1	gb|EOA20679.1| hypothetical protein CARUB_v10000991mg [Capsella rubella]	441	436	0	98.9	90.5	92.3	hypothetical protein CARUB_v10000991mg	gbpln	Capsella rubella	AT5G15050.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:4871820-4873454 REVERSE LENGTH=434	441	434	0	98.4	89.3	91.8
Rsa1.0_00301.1.g10851.t1	ref|XP_002873701.1| hypothetical protein ARALYDRAFT_488346 [Arabidopsis lyrata subsp. lyrata] gi|297319538|gb|EFH49960.1| hypothetical protein ARALYDRAFT_488346 [Arabidopsis lyrata subsp. lyrata]	1352	1372	0	101.5	83.1	89.3	hypothetical protein ARALYDRAFT_488346	gbpln	Arabidopsis lyrata	AT5G15020.2 | Symbols: SNL2 | SIN3-like 2 | chr5:4859408-4865569 REVERSE LENGTH=1355	1352	1355	0	100.2	81.7	88.6
Rsa1.0_00301.1.g10852.t2	ref|NP_197002.1| esterase/lipase/thioesterase family protein [Arabidopsis thaliana] gi|9755665|emb|CAC01817.1| lysophospholipase-like protein [Arabidopsis thaliana] gi|67633802|gb|AAY78825.1| esterase/lipase/thioesterase family protein [Arabidopsis thaliana] gi|332004715|gb|AED92098.1| esterase/lipase/thioesterase family protein [Arabidopsis thaliana]	328	327	1.00E-176	99.7	91.5	95.1	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis thaliana	AT5G14980.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:4849600-4850583 FORWARD LENGTH=327	328	327	1.00E-179	99.7	91.5	95.1
Rsa1.0_00301.1.g10853.t1	gb|EOA20959.1| hypothetical protein CARUB_v10001291mg [Capsella rubella]	352	352	1.00E-133	100.0	70.7	80.1	hypothetical protein CARUB_v10001291mg	gbpln	Capsella rubella	AT5G14960.1 | Symbols: DEL2, E2L1, E2FD | DP-E2F-like 2 | chr5:4843966-4846373 FORWARD LENGTH=359	352	359	1.00E-130	102.0	67.6	77.6
Rsa1.0_00301.1.g10854.t1	gb|EOA19830.1| hypothetical protein CARUB_v10000075mg [Capsella rubella]	1171	1171	0	100.0	92.0	95.8	hypothetical protein CARUB_v10000075mg	gbpln	Capsella rubella	AT5G14950.1 | Symbols: GMII, ATGMII | golgi alpha-mannosidase II | chr5:4837484-4841792 REVERSE LENGTH=1173	1171	1173	0	100.2	90.9	95.1
Rsa1.0_00301.1.g10855.t1	ref|NP_196998.1| major facilitator protein [Arabidopsis thaliana] gi|75174167|sp|Q9LFR1.1|PTR50_ARATH RecName: Full=Probable peptide/nitrate transporter At5g14940 gi|9755661|emb|CAC01813.1| oligopeptide transporter-like protein [Arabidopsis thaliana] gi|332004711|gb|AED92094.1| probable peptide/nitrate transporter [Arabidopsis thaliana]	545	552	0	101.3	87.2	92.1	major facilitator protein	gbpln	Arabidopsis thaliana	AT5G14940.1 | Symbols: | Major facilitator superfamily protein | chr5:4831748-4834312 REVERSE LENGTH=552	545	552	0	101.3	87.2	92.1
Rsa1.0_00301.1.g10856.t1	ref|XP_002871636.1| heavy-metal-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317473|gb|EFH47895.1| heavy-metal-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata]	181	178	4.00E-81	98.3	87.8	91.2	heavy-metal-associated domain-containing protein	gbpln	Arabidopsis lyrata	AT5G14910.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:4823815-4825196 FORWARD LENGTH=178	181	178	6.00E-81	98.3	85.6	90.1
Rsa1.0_00301.1.g10857.t1	ref|NP_196993.2| NHL domain-containing protein [Arabidopsis thaliana] gi|332004703|gb|AED92086.1| NHL domain-containing protein [Arabidopsis thaliana]	174	754	4.00E-80	433.3	79.9	86.8	NHL domain-containing protein	gbpln	Arabidopsis thaliana	AT5G14890.1 | Symbols: | NHL domain-containing protein | chr5:4818056-4821534 FORWARD LENGTH=754	174	754	2.00E-82	433.3	79.9	86.8
Rsa1.0_00301.1.g10858.t1	ref|NP_196992.1| Potassium transporter 8 [Arabidopsis thaliana] gi|38503205|sp|Q9M7J9.2|POT8_ARATH RecName: Full=Potassium transporter 8; Short=AtHAK8; Short=AtPOT8 gi|9755756|emb|CAC01887.1| putative cation transport protein [Arabidopsis thaliana] gi|332004702|gb|AED92085.1| Potassium transporter 8 [Arabidopsis thaliana]	1223	781	0	63.9	59.9	61.2	Potassium transporter 8	gbpln	Arabidopsis thaliana	AT5G14880.1 | Symbols: | Potassium transporter family protein | chr5:4814244-4817667 FORWARD LENGTH=781	1223	781	0	63.9	59.9	61.2
Rsa1.0_00301.1.g10859.t2	gb|EOA20341.1| hypothetical protein CARUB_v10000649mg [Capsella rubella]	549	543	0	98.9	82.0	88.3	hypothetical protein CARUB_v10000649mg	gbpln	Capsella rubella	AT5G14850.1 | Symbols: | Alg9-like mannosyltransferase family | chr5:4802099-4804977 REVERSE LENGTH=548	549	548	0	99.8	82.0	88.2

<table>
<tr><td>Rsa1.0_00301.1.g10860.t1</td><td>ref|NP_196983.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|9755747|emb|CAC01878.1| putative protein [Arabidopsis thaliana] gi|20260678|gb|AAM13237.1| putative protein [Arabidopsis thaliana] gi|21618131|gb|AAM67181.1| unknown [Arabidopsis thaliana] gi|24899827|gb|AAN65128.1| putative protein [Arabidopsis thaliana] gi|62320934|dbj|BAD93942.1| hypothetical protein [Arabidopsis thaliana] gi|332004694|gb|AED92077.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]</td><td>342</td><td>346</td><td>1.00E-158</td><td>101.2</td><td>84.2</td><td>93.3</td><td>armadillo/beta-catenin-like repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14790.1 | Symbols: | ARM repeat superfamily protein | chr5:4784058-4785508 FORWARD LENGTH=346</td><td>342</td><td>346</td><td>1.00E-161</td><td>101.2</td><td>84.2</td><td>93.3</td></tr>
<tr><td>Rsa1.0_00302.1.g10861.t1</td><td>ref|XP_002872033.1| hypothetical protein ARALYDRAFT_910314 [Arabidopsis lyrata subsp. lyrata] gi|297317870|gb|EFH48292.1| hypothetical protein ARALYDRAFT_910314 [Arabidopsis lyrata subsp. lyrata]</td><td>311</td><td>281</td><td>1.00E-114</td><td>90.4</td><td>65.9</td><td>75.2</td><td>hypothetical protein ARALYDRAFT_910314</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23070.1 | Symbols: | Thymidine kinase | chr5:7741979-7742827 FORWARD LENGTH=282</td><td>311</td><td>282</td><td>1.00E-112</td><td>90.7</td><td>65.9</td><td>74.6</td></tr>
<tr><td>Rsa1.0_00302.1.g10862.t1</td><td>gb|EOA19907.1| hypothetical protein CARUB_v10000157mg [Capsella rubella]</td><td>939</td><td>946</td><td>0</td><td>100.7</td><td>84.1</td><td>90.0</td><td>hypothetical protein CARUB_v10000157mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G23080.1 | Symbols: TGH | SWAP (Suppressor-of-White-APricot)/surp domain-containing protein | chr5:7743226-7748889 REVERSE LENGTH=930</td><td>939</td><td>930</td><td>0</td><td>99.0</td><td>82.6</td><td>87.8</td></tr>
<tr><td>Rsa1.0_00302.1.g10863.t1</td><td>ref|XP_002872035.1| hypothetical protein ARALYDRAFT_910318 [Arabidopsis lyrata subsp. lyrata] gi|297317872|gb|EFH48294.1| hypothetical protein ARALYDRAFT_910318 [Arabidopsis lyrata subsp. lyrata]</td><td>262</td><td>278</td><td>1.00E-101</td><td>106.1</td><td>82.1</td><td>86.3</td><td>hypothetical protein ARALYDRAFT_910318</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23100.1 | Symbols: | Protein of unknown function, DUF617 | chr5:7753557-7754390 FORWARD LENGTH=277</td><td>262</td><td>277</td><td>4.00E-99</td><td>105.7</td><td>80.2</td><td>84.4</td></tr>
<tr><td>Rsa1.0_00302.1.g10864.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00302.1.g10865.t1</td><td>ref|XP_002872036.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297317873|gb|EFH48295.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>4704</td><td>4711</td><td>0</td><td>100.1</td><td>90.6</td><td>94.9</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23110.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr5:7758307-7775509 FORWARD LENGTH=4706</td><td>4704</td><td>4706</td><td>0</td><td>100.0</td><td>90.0</td><td>94.6</td></tr>
<tr><td>Rsa1.0_00302.1.g10866.t1</td><td>ref|XP_002872037.1| HCF136 [Arabidopsis lyrata subsp. lyrata] gi|297317874|gb|EFH48296.1| HCF136 [Arabidopsis lyrata subsp. lyrata]</td><td>403</td><td>393</td><td>0</td><td>97.5</td><td>91.1</td><td>94.5</td><td>HCF136</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23120.1 | Symbols: HCF136 | photosystem II stability/assembly factor, chloroplast (HCF136) | chr5:7778154-7780463 FORWARD LENGTH=403</td><td>403</td><td>403</td><td>0</td><td>100.0</td><td>93.5</td><td>96.5</td></tr>
<tr><td>Rsa1.0_00302.1.g10867.t1</td><td>gb|EOA20773.1| hypothetical protein CARUB_v10001102mg [Capsella rubella]</td><td>398</td><td>405</td><td>1.00E-135</td><td>101.8</td><td>72.4</td><td>81.2</td><td>hypothetical protein CARUB_v10001102mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G23130.1 | Symbols: | Peptidoglycan-binding LysM domain-containing protein | chr5:7781475-7783333 FORWARD LENGTH=397</td><td>398</td><td>397</td><td>1.00E-137</td><td>99.7</td><td>72.1</td><td>79.6</td></tr>
<tr><td>Rsa1.0_00302.1.g10868.t2</td><td>ref|XP_002872039.1| hypothetical protein ARALYDRAFT_910322 [Arabidopsis lyrata subsp. lyrata] gi|297317876|gb|EFH48298.1| hypothetical protein ARALYDRAFT_910322 [Arabidopsis lyrata subsp. lyrata]</td><td>282</td><td>237</td><td>1.00E-117</td><td>84.0</td><td>77.7</td><td>80.1</td><td>hypothetical protein ARALYDRAFT_910322</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23140.1 | Symbols: CLPP2, NCLPP7 | nuclear-encoded CLP protease P7 | chr5:7783811-7784826 FORWARD LENGTH=241</td><td>282</td><td>241</td><td>1.00E-117</td><td>85.5</td><td>77.3</td><td>80.5</td></tr>
<tr><td>Rsa1.0_00302.1.g10869.t1</td><td>ref|NP_178545.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|4544429|gb|AAD22338.1| unknown protein [Arabidopsis thaliana] gi|55740549|gb|AAV63867.1| hypothetical protein At2g04680 [Arabidopsis thaliana] gi|330250761|gb|AEC05855.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]</td><td>697</td><td>657</td><td>0</td><td>94.3</td><td>58.8</td><td>69.2</td><td>cysteine/histidine-rich C1 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G04680.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:1640188-1642161 FORWARD LENGTH=657</td><td>697</td><td>657</td><td>0</td><td>94.3</td><td>58.8</td><td>69.2</td></tr>
<tr><td>Rsa1.0_00302.1.g10870.t3</td><td>ref|XP_002872040.1| enhancer of ag-4 2 [Arabidopsis lyrata subsp. lyrata] gi|297317877|gb|EFH48299.1| enhancer of ag-4 2 [Arabidopsis lyrata subsp. lyrata]</td><td>1369</td><td>1398</td><td>0</td><td>102.1</td><td>58.3</td><td>62.9</td><td>enhancer of ag-4 2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23150.1 | Symbols: HUA2 | Tudor/PWWP/MBT domain-containing protein | chr5:7786173-7792080 FORWARD LENGTH=1392</td><td>1369</td><td>1392</td><td>0</td><td>101.7</td><td>57.6</td><td>62.5</td></tr>
<tr><td>Rsa1.0_00302.1.g10871.t1</td><td>gb|EOA21003.1| hypothetical protein CARUB_v10001338mg [Capsella rubella]</td><td>403</td><td>344</td><td>1.00E-132</td><td>85.4</td><td>64.0</td><td>72.0</td><td>hypothetical protein CARUB_v10001338mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G23170.1 | Symbols: | Protein kinase superfamily protein | chr5:7798411-7799436 REVERSE LENGTH=341</td><td>403</td><td>341</td><td>1.00E-121</td><td>84.6</td><td>65.3</td><td>71.5</td></tr>
<tr><td>Rsa1.0_00302.1.g10872.t1</td><td>ref|XP_002874114.1| CYP86B1 [Arabidopsis lyrata subsp. lyrata] gi|297319951|gb|EFH50373.1| CYP86B1 [Arabidopsis lyrata subsp. lyrata]</td><td>560</td><td>559</td><td>0</td><td>99.8</td><td>92.1</td><td>95.2</td><td>CYP86B1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23190.1 | Symbols: CYP86B1 | cytochrome P450, family 86, subfamily B, polypeptide 1 | chr5:7803478-7805659 REVERSE LENGTH=559</td><td>560</td><td>559</td><td>0</td><td>99.8</td><td>91.6</td><td>95.5</td></tr>
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Rsa1.0_00302.1.g10873.t2	ref|XP_002872042.1| hypothetical protein ARALYDRAFT_489175 [Arabidopsis lyrata subsp. lyrata] gi|297317879|gb|EFH48301.1| hypothetical protein ARALYDRAFT_489175 [Arabidopsis lyrata subsp. lyrata]	500	398	0	79.6	67.6	71.6	hypothetical protein ARALYDRAFT_489175	gbpln	Arabidopsis lyrata	AT5G23200.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G08270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7807319-7808988 FORWARD LENGTH=399	500	399	0	79.8	67.4	71.6
Rsa1.0_00302.1.g10874.t1	ref|NP_197715.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] gi|10177813|dbj|BAB11179.1| unnamed protein product [Arabidopsis thaliana] gi|134031908|gb|ABO45691.1| At5g23240 [Arabidopsis thaliana] gi|332005757|gb|AED93140.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	470	465	0	98.9	83.8	91.1	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT5G23240.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:7826857-7828534 REVERSE LENGTH=465	470	465	0	98.9	83.8	91.1
Rsa1.0_00302.1.g10875.t1	ref|NP_197716.1| Succinyl-CoA ligase [GDP-forming] subunit alpha-2 [Arabidopsis thaliana] gi|56754629|sp|Q8LAD2.2|SUCA2_ARATH RecName: Full=Succinyl-CoA ligase [ADP-forming] subunit alpha-2, mitochondrial; AltName: Full=Succinyl-CoA synthetase subunit alpha-2; Short=SCS-alpha-2; Flags: Precursor gi|10177814|dbj|BAB11180.1| succinyl-CoA synthetase, alpha subunit [Arabidopsis thaliana] gi|20260190|gb|AAM12993.1| succinyl-CoA synthetase, alpha subunit [Arabidopsis thaliana] gi|21387045|gb|AAM47926.1| succinyl-CoA synthetase alpha subunit [Arabidopsis thaliana] gi|332005758|gb|AED93141.1| Succinyl-CoA ligase [GDP-forming] subunit alpha-2 [Arabidopsis thaliana]	342	341	1.00E-180	99.7	93.3	95.3	Succinyl-CoA ligase	gbpln	Arabidopsis thaliana	AT5G23250.1 | Symbols: | Succinyl-CoA ligase, alpha subunit | chr5:7830460-7832491 FORWARD LENGTH=341	342	341	0	99.7	93.3	95.3
Rsa1.0_00302.1.g10876.t2	gb|ABY59774.1| MADS-box DNA-binding domain transcription factor [Brassica napus] gi|317141590|gb|ADV03947.1| MADS DNA domain binding transcription factor BnaC.TT16a [Brassica napus] gi|317141607|gb|ADV03949.1| MADS DNA domain binding transcription factor BolC.TT16a [Brassica oleracea]	241	242	1.00E-128	100.4	96.7	97.5	MADS-box DNA-binding domain transcription factor	gbpln	Brassica napus	AT5G23260.2 | Symbols: TT16, ABS, AGL32 | K-box region and MADS-box transcription factor family protein | chr5:7836442-7838340 FORWARD LENGTH=252	241	252	1.00E-110	104.6	82.6	92.1
Rsa1.0_00302.1.g10877.t1	ref|XP_002872047.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317884|gb|EFH48306.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	527	517	0	98.1	80.1	88.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G23270.1 | Symbols: STP11, ATSTP11 | sugar transporter 11 | chr5:7839132-7840874 FORWARD LENGTH=514	527	514	0	97.5	79.1	87.3
Rsa1.0_00302.1.g10878.t1	gb|ABB97033.1| unknown [Brassica rapa]	263	249	1.00E-105	94.7	86.3	88.6	unknown	gbpln	Brassica rapa	AT5G23280.1 | Symbols: | TCP family transcription factor | chr5:7843017-7843769 FORWARD LENGTH=250	263	250	2.00E-89	95.1	72.2	77.9
Rsa1.0_00302.1.g10879.t1	gb|EOA21748.1| hypothetical protein CARUB_v10002195mg [Capsella rubella]	152	151	6.00E-71	99.3	90.8	95.4	hypothetical protein CARUB_v10002195mg	gbpln	Capsella rubella	AT5G23290.1 | Symbols: PFD5 | prefoldin 5 | chr5:7846144-7847428 FORWARD LENGTH=151	152	151	2.00E-73	99.3	90.8	95.4
Rsa1.0_00302.1.g10880.t1	gb|EOA20609.1| hypothetical protein CARUB_v10000920mg [Capsella rubella]	471	460	0	97.7	88.7	90.7	hypothetical protein CARUB_v10000920mg	gbpln	Capsella rubella	AT5G23300.1 | Symbols: PYRD | pyrimidine d | chr5:7847792-7850243 REVERSE LENGTH=460	471	460	0	97.7	87.9	90.4
Rsa1.0_00302.1.g10881.t3	gb|ABR24272.1| iron-containing superoxide dismutase [Brassica napus]	296	263	1.00E-135	88.9	82.4	85.1	iron-containing superoxide dismutase	gbpln	Brassica napus	AT5G23310.1 | Symbols: FSD3 | Fe superoxide dismutase 3 | chr5:7850624-7852241 FORWARD LENGTH=263	296	263	1.00E-127	88.9	81.1	85.1
Rsa1.0_00302.1.g10882.t1	ref|XP_002872053.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297317890|gb|EFH48312.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	406	405	0	99.8	91.1	97.3	protein binding protein	gbpln	Arabidopsis lyrata	AT5G23340.1 | Symbols: | RNI-like superfamily protein | chr5:7856314-7857983 FORWARD LENGTH=405	406	405	0	99.8	91.1	96.8
Rsa1.0_00302.1.g10883.t1	ref|XP_002874124.1| hypothetical protein ARALYDRAFT_489196 [Arabidopsis lyrata subsp. lyrata] gi|297319961|gb|EFH50383.1| hypothetical protein ARALYDRAFT_489196 [Arabidopsis lyrata subsp. lyrata]	118	218	9.00E-27	184.7	56.8	62.7	hypothetical protein ARALYDRAFT_489196	gbpln	Arabidopsis lyrata	AT5G23370.1 | Symbols: | GRAM domain-containing protein / ABA-responsive protein-related | chr5:7863542-7864201 REVERSE LENGTH=219	118	219	4.00E-29	185.6	55.9	62.7

Rsa1.0_00302.1.g10884.t1	ref|XP_002874125.1| hypothetical protein ARALYDRAFT_910349 [Arabidopsis lyrata subsp. lyrata] gi|297319962|gb|EFH50384.1| hypothetical protein ARALYDRAFT_910349 [Arabidopsis lyrata subsp. lyrata]	214	219	1.00E-100	102.3	86.0	91.1	hypothetical protein ARALYDRAFT_910349	gbpln	Arabidopsis lyrata	AT5G23370.1 | Symbols: | GRAM domain-containing protein / ABA-responsive protein-related | chr5:7863542-7864201 REVERSE LENGTH=219	214	219	1.00E-101	102.3	85.5	90.7
Rsa1.0_00303.1.g10885.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00303.1.g10886.t1	gb|EOA20937.1| hypothetical protein CARUB_v10001270mg [Capsella rubella]	358	357	1.00E-148	99.7	74.3	84.9	hypothetical protein CARUB_v10001270mg	gbpln	Capsella rubella	AT5G02890.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:670207-671454 REVERSE LENGTH=353	358	353	1.00E-147	98.6	73.7	83.0
Rsa1.0_00303.1.g10887.t1	ref|XP_002870997.1| ubiquitin-protein ligase 4 [Arabidopsis lyrata subsp. lyrata] gi|297316834|gb|EFH47256.1| ubiquitin-protein ligase 4 [Arabidopsis lyrata subsp. lyrata]	1486	1509	0	101.5	83.2	90.0	ubiquitin-protein ligase 4	gbpln	Arabidopsis lyrata	AT5G02880.1 | Symbols: UPL4 | ubiquitin-protein ligase 4 | chr5:662643-668847 FORWARD LENGTH=1502	1486	1502	0	101.1	81.6	88.7
Rsa1.0_00303.1.g10888.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00303.1.g10889.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00303.1.g10890.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00303.1.g10891.t1	gb|ADA58342.1| pseudo-response regulator 7a [Brassica rapa]	710	725	0	102.1	83.2	84.6	pseudo-response regulator 7a	gbpln	Brassica rapa	AT5G02810.1 | Symbols: PRR7, APRR7 | pseudo-response regulator 7 | chr5:638283-641461 REVERSE LENGTH=727	710	727	0	102.4	82.4	87.9
Rsa1.0_00303.1.g10892.t1	gb|AAG16628.1| protein serine/threonine kinase BNK1 [Brassica napus]	376	376	0	100.0	96.0	98.1	protein serine/threonine kinase BNK1	gbpln	Brassica napus	AT5G02800.1 | Symbols: | Protein kinase superfamily protein | chr5:635545-637374 REVERSE LENGTH=378	376	378	0	100.5	93.9	97.1
Rsa1.0_00303.1.g10893.t5	emb|CAB86032.1| putative protein [Arabidopsis thaliana]	236	245	1.00E-113	103.8	83.5	91.9	putative protein	gbpln	Arabidopsis thaliana	AT5G02780.1 | Symbols: GSTL1 | glutathione transferase lambda 1 | chr5:630957-632485 FORWARD LENGTH=237	236	237	1.00E-115	100.4	83.5	91.9
Rsa1.0_00303.1.g10894.t1	ref|NP_195897.1| uncharacterized protein [Arabidopsis thaliana] gi|14190431|gb|AAK55696.1|AF378893_1 AT5g02770/F9G14_80 [Arabidopsis thaliana] gi|7413552|emb|CAB86031.1| putative protein [Arabidopsis thaliana] gi|15215889|gb|AAK91488.1| AT5g02770/F9G14_80 [Arabidopsis thaliana] gi|62320777|dbj|BAD95440.1| putative protein [Arabidopsis thaliana] gi|332003132|gb|AED90515.1| uncharacterized protein AT5G02770 [Arabidopsis thaliana]	205	214	6.00E-62	104.4	75.6	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G02770.1 | Symbols: | unknown protein; Has 469 Blast hits to 336 proteins in 126 species: Archae - 0; Bacteria - 54; Metazoa - 249; Fungi - 22; Plants - 47; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink). | chr5:628101-629168 REVERSE LENGTH=214	205	214	2.00E-64	104.4	75.6	83.9
Rsa1.0_00303.1.g10895.t1	dbj|BAJ33929.1| unnamed protein product [Thellungiella halophila]	367	370	0	100.8	89.4	94.8	unnamed protein product	----	----	AT5G02760.1 | Symbols: | Protein phosphatase 2C family protein | chr5:625377-626817 FORWARD LENGTH=370	367	370	0	100.8	84.5	92.1
Rsa1.0_00303.1.g10896.t1	ref|NP_195895.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|26451566|dbj|BAC42880.1| unknown protein [Arabidopsis thaliana] gi|28973295|gb|AAO63972.1| unknown protein [Arabidopsis thaliana] gi|332003130|gb|AED90513.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	285	283	1.00E-116	99.3	83.2	88.8	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G02750.1 | Symbols: | RING/U-box superfamily protein | chr5:620101-620952 FORWARD LENGTH=283	285	283	1.00E-118	99.3	83.2	88.8
Rsa1.0_00303.1.g10897.t1	ref|XP_002870982.1| 60S ribosomal protein L35 [Arabidopsis lyrata subsp. lyrata] gi|297316819|gb|EFH47241.1| 60S ribosomal protein L35 [Arabidopsis lyrata subsp. lyrata]	123	123	1.00E-57	100.0	92.7	99.2	60S ribosomal protein L35	gbpln	Arabidopsis lyrata	AT5G02610.1 | Symbols: | Ribosomal L29 family protein | chr5:587611-588547 FORWARD LENGTH=123	123	123	2.00E-59	100.0	91.9	98.4

Rsa1.0_00303.1.g10898.t1	ref|NP_568105.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|42573253|ref|NP_974723.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|21553967|gb|AAM63048.1| unknown [Arabidopsis thaliana] gi|26449554|dbj|BAC41903.1| unknown protein [Arabidopsis thaliana] gi|30725362|gb|AAP37703.1| At5g02600 [Arabidopsis thaliana] gi|62320791|dbj|BAD93718.1| hypothetical protein [Arabidopsis thaliana] gi|332003112|gb|AED90495.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|332003113|gb|AED90496.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana]	265	319	4.00E-97	120.4	81.1	88.7	heavy metal transport/detoxification domain-containing protein	gbpln	Arabidopsis thaliana	AT5G02600.1 | Symbols: NAKR1 | Heavy metal transport/detoxification superfamily protein | chr5:585713-586855 REVERSE LENGTH=319	265	319	1.00E-99	120.4	81.1	88.7
Rsa1.0_00303.1.g10899.t2	ref|XP_002873062.1| hypothetical protein ARALYDRAFT_908126 [Arabidopsis lyrata subsp. lyrata] gi|297318899|gb|EFH49321.1| hypothetical protein ARALYDRAFT_908126 [Arabidopsis lyrata subsp. lyrata]	249	99	3.00E-13	39.8	21.7	24.5	hypothetical protein ARALYDRAFT_908126	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00303.1.g10900.t1	ref|NP_195876.1| histone H2A 12 [Arabidopsis thaliana] gi|75311717|sp|Q9LZ46.1|H2A4_ARATH RecName: Full=Probable histone H2A.4; AltName: Full=HTA12 gi|7413645|emb|CAB85993.1| putative protein [Arabidopsis thaliana] gi|21553646|gb|AAM62739.1| histone H2A [Arabidopsis thaliana] gi|98961093|gb|ABF59030.1| At5g02560 [Arabidopsis thaliana] gi|332003106|gb|AED90489.1| histone H2A 12 [Arabidopsis thaliana]	154	153	2.00E-65	99.4	89.0	91.6	histone H2A 12	gbpln	Arabidopsis thaliana	AT5G02560.1 | Symbols: HTA12 | histone H2A 12 | chr5:575437-576456 FORWARD LENGTH=153	154	153	6.00E-68	99.4	89.0	91.6
Rsa1.0_00303.1.g10901.t1	gb|AAN62481.1| phosphatidylinositol 3-kinase [Brassica napus]	196	813	5.00E-15	414.8	20.4	20.9	phosphatidylinositol 3-kinase	gbpln	Brassica napus	AT1G60490.1 | Symbols: ATVPS34, VPS34, PI3K | vacuolar protein sorting 34 | chr1:22285792-22290190 REVERSE LENGTH=814	196	814	1.00E-15	415.3	18.4	20.4
Rsa1.0_00303.1.g10902.t1	ref|XP_002873060.1| hypothetical protein ARALYDRAFT_487033 [Arabidopsis lyrata subsp. lyrata] gi|297318897|gb|EFH49319.1| hypothetical protein ARALYDRAFT_487033 [Arabidopsis lyrata subsp. lyrata]	74	76	2.00E-22	102.7	79.7	89.2	hypothetical protein ARALYDRAFT_487033	gbpln	Arabidopsis lyrata	AT5G02550.1 | Symbols: | unknown protein; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:573247-573477 REVERSE LENGTH=76	74	76	4.00E-20	102.7	79.7	89.2
Rsa1.0_00303.1.g10903.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	723	1142	9.00E-60	158.0	19.9	28.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	723	575	2.00E-29	79.5	13.8	24.1
Rsa1.0_00303.1.g10904.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00303.1.g10905.t1	ref|XP_002870977.1| hypothetical protein ARALYDRAFT_349549 [Arabidopsis lyrata subsp. lyrata] gi|297316814|gb|EFH47236.1| hypothetical protein ARALYDRAFT_349549 [Arabidopsis lyrata subsp. lyrata]	379	503	3.00E-94	132.7	63.3	76.0	hypothetical protein ARALYDRAFT_349549	gbpln	Arabidopsis lyrata	AT5G02520.1 | Symbols: | CONTAINS InterPro DOMAIN/s: SANT associated (InterPro:IPR015216); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT1G58210.1); Has 842 Blast hits to 736 proteins in 154 species: Archae - 2; Bacteria - 99; Metazoa - 236; Fungi - 52; Plants - 90; Viruses - 0; Other Eukaryotes - 363 (source: NCBI BLink). | chr5:561325-563840 FORWARD LENGTH=598	379	598	7.00E-58	157.8	40.4	48.5
Rsa1.0_00303.1.g10906.t1	ref|NP_195866.1| Dof zinc finger protein DOF5.1 [Arabidopsis thaliana] gi|55583994|sp|Q9LZ56.1|DOF51_ARATH RecName: Full=Dof zinc finger protein DOF5.1; Short=AtDOF5.1 gi|7413635|emb|CAB85983.1| putative zinc finger protein [Arabidopsis thaliana] gi|225898877|dbj|BAH30569.1| hypothetical protein [Arabidopsis thaliana] gi|332003091|gb|AED90474.1| Dof zinc finger protein DOF5.1 [Arabidopsis thaliana]	407	399	1.00E-128	98.0	81.3	86.0	Dof zinc finger protein DOF5.1	gbpln	Arabidopsis thaliana	AT5G02460.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr5:539549-541058 REVERSE LENGTH=399	407	399	1.00E-131	98.0	81.3	86.0

Rsa1.0_00303.1.g10907.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	534	1274	1.00E-100	238.6	39.5	58.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	534	575	2.00E-63	107.7	32.0	50.7
Rsa1.0_00304.1.g10908.t1	gb|EOA38966.1| hypothetical protein CARUB_v10011390mg [Capsella rubella]	1177	1373	0	116.7	92.9	96.2	hypothetical protein CARUB_v10011390mg	gbpln	Capsella rubella	AT1G18270.2 | Symbols: | ketose-bisphosphate aldolase class-Ⅱ family protein | chr1:6283634-6293772 REVERSE LENGTH=1374	1177	1374	0	116.7	93.1	96.3
Rsa1.0_00304.1.g10909.t1	gb|EOA38833.1| hypothetical protein CARUB_v10011169mg [Capsella rubella]	243	260	1.00E-49	107.0	65.8	77.0	hypothetical protein CARUB_v10011169mg	gbpln	Capsella rubella	AT1G18265.1 | Symbols: | Protein of unknown function, DUF593 | chr1:6282338-6283180 REVERSE LENGTH=280	243	280	3.00E-50	115.2	62.1	72.4
Rsa1.0_00304.1.g10910.t1	ref|XP_002884501.1| hypothetical protein ARALYDRAFT_477820 [Arabidopsis lyrata subsp. lyrata] gi|297330341|gb|EFH60760.1| hypothetical protein ARALYDRAFT_477820 [Arabidopsis lyrata subsp. lyrata]	101	445	9.00E-25	440.6	59.4	66.3	hypothetical protein ARALYDRAFT_477820	gbpln	Arabidopsis lyrata	AT3G05320.1 | Symbols: | O-fucosyltransferase family protein | chr3:1513558-1514895 REVERSE LENGTH=445	101	445	6.00E-27	440.6	58.4	65.3
Rsa1.0_00304.1.g10911.t1	gb|EOA39835.1| hypothetical protein CARUB_v10008501mg [Capsella rubella]	678	677	0	99.9	92.2	96.0	hypothetical protein CARUB_v10008501mg	gbpln	Capsella rubella	AT1G18260.1 | Symbols: | HCP-like superfamily protein | chr1:6279047-6282008 REVERSE LENGTH=678	678	678	0	100.0	93.2	96.6
Rsa1.0_00304.1.g10912.t1	gb|EOA36086.1| hypothetical protein CARUB_v10010474mg [Capsella rubella]	178	170	7.00E-82	95.5	87.6	92.1	hypothetical protein CARUB_v10010474mg	gbpln	Capsella rubella	AT1G18210.2 | Symbols: | Calcium-binding EF-hand family protein | chr1:6268273-6268785 REVERSE LENGTH=170	178	170	1.00E-80	95.5	79.8	83.7
Rsa1.0_00304.1.g10913.t1	gb|EOA38883.1| hypothetical protein CARUB_v10011252mg [Capsella rubella]	656	670	0	102.1	81.6	89.2	hypothetical protein CARUB_v10011252mg	gbpln	Capsella rubella	AT1G18190.1 | Symbols: GC2 | golgin candidate 2 | chr1:6257963-6261325 REVERSE LENGTH=668	656	668	0	101.8	81.6	87.7
Rsa1.0_00304.1.g10914.t1	ref|XP_002890265.1| hypothetical protein ARALYDRAFT_889231 [Arabidopsis lyrata subsp. lyrata] gi|297336107|gb|EFH66524.1| hypothetical protein ARALYDRAFT_889231 [Arabidopsis lyrata subsp. lyrata]	292	305	1.00E-154	104.5	90.8	94.9	hypothetical protein ARALYDRAFT_889231	gbpln	Arabidopsis lyrata	AT1G18180.1 | Symbols: | Protein of unknown function (DUF1295) | chr1:6255903-6257737 FORWARD LENGTH=305	292	305	1.00E-151	104.5	89.4	94.5
Rsa1.0_00304.1.g10915.t3	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1000	1250	0	125.0	36.5	44.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1000	1262	6.00E-82	126.2	16.7	24.9
Rsa1.0_00304.1.g10916.t1	ref|XP_002890263.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336105|gb|EFH66522.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	991	996	0	100.5	88.8	92.6	kinase family protein	gbpln	Arabidopsis lyrata	AT1G18160.1 | Symbols: | Protein kinase superfamily protein | chr1:6249126-6253835 FORWARD LENGTH=992	991	992	0	100.1	87.9	92.1
Rsa1.0_00304.1.g10917.t1	gb|EOA28172.1| hypothetical protein CARUB_v10024362mg [Capsella rubella]	96	110	1.00E-20	114.6	52.1	71.9	hypothetical protein CARUB_v10024362mg	gbpln	Capsella rubella	AT2G32765.1 | Symbols: SUM5, SUMO5, ATSUMO5 | small ubiquitinrelated modifier 5 | chr2:13894968-13895399 FORWARD LENGTH=108	96	108	3.00E-21	112.5	49.0	70.8
Rsa1.0_00304.1.g10918.t1	gb|EOA39977.1| hypothetical protein CARUB_v10008665mg [Capsella rubella]	507	587	0	115.8	93.5	95.9	hypothetical protein CARUB_v10008665mg	gbpln	Capsella rubella	AT1G18150.3 | Symbols: ATMPK8 | Protein kinase superfamily protein | chr1:6244641-6247582 REVERSE LENGTH=589	507	589	0	116.2	93.1	95.9
Rsa1.0_00304.1.g10919.t3	gb|ACO57702.1| epithiospecifier modifier [Brassica rapa subsp. pekinensis] gi|226444219|gb|ACO57706.1| epithiospecifier modifier [Brassica rapa subsp. pekinensis]	365	386	1.00E-157	105.8	71.8	83.0	epithiospecifier modifier	gbpln	Brassica rapa	AT3G14210.1 | Symbols: ESM1 | epithiospecifier modifier 1 | chr3:4729886-4731562 FORWARD LENGTH=392	365	392	1.00E-158	107.4	72.3	83.0
Rsa1.0_00304.1.g10920.t1	gb|EOA38819.1| hypothetical protein CARUB_v10011138mg [Capsella rubella]	107	173	5.00E-48	161.7	86.0	91.6	hypothetical protein CARUB_v10011138mg	gbpln	Capsella rubella	AT1G18100.1 | Symbols: E12A11, MFT | PEBP (phosphatidylethanolamine-binding protein) family protein | chr1:6228049-6230110 REVERSE LENGTH=173	107	173	8.00E-51	161.7	86.0	91.6
Rsa1.0_00304.1.g10921.t1	sp|Q39336.1|GBLP_BRANA RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein gi|563335|emb|CAA83924.1| guanine nucleotide regulatory protein [Brassica napus]	327	327	1.00E-180	100.0	95.7	97.9	RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein gi|563335|emb|CAA83924.1| guanine nucleotide regulatory protein	gbpln	Brassica napus	AT1G18080.1 | Symbols: ATARCA, RACK1A_AT, RACK1A | Transducin/WD40 repeat-like superfamily protein | chr1:6222325-6223901 FORWARD LENGTH=327	327	327	0	100.0	94.2	97.2
Rsa1.0_00304.1.g10922.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	548	1529	1.00E-94	279.0	36.9	54.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	548	746	2.00E-57	136.1	27.6	41.8

Rsa1.0_00304.1.g10923.t1	ref|NP_173247.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|79318119|ref|NP_001031063.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|21539549|gb|AAM53327.1| putative guanine nucleotide regulatory protein [Arabidopsis thaliana] gi|31711944|gb|AAP68328.1| At1g18070 [Arabidopsis thaliana] gi|332191549|gb|AEE29670.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|332191550|gb|AEE29671.1| Translation elongation factor EF1A/initiation factor IF2gamma family protein [Arabidopsis thaliana]	562	532	0	94.7	83.5	88.8	G1 to S phase transition protein	gbpln	Arabidopsis thaliana	AT1G18070.2 | Symbols: | Translation elongation factor EF1A/initiation factor IF2gamma family protein | chr1:6214236-6218211 REVERSE LENGTH=532	562	532	0	94.7	83.5	88.8
Rsa1.0_00304.1.g10924.t2	ref|XP_002892982.1| hypothetical protein ARALYDRAFT_472022 [Arabidopsis lyrata subsp. lyrata] gi|297338824|gb|EFH69241.1| hypothetical protein ARALYDRAFT_472022 [Arabidopsis lyrata subsp. lyrata]	468	533	1.00E-150	113.9	54.3	57.5	hypothetical protein ARALYDRAFT_472022	gbpln	Arabidopsis lyrata	AT1G18070.2 | Symbols: | Translation elongation factor EF1A/initiation factor IF2gamma family protein | chr1:6214236-6218211 REVERSE LENGTH=532	468	532	1.00E-152	113.7	53.8	57.5
Rsa1.0_00304.1.g10925.t1	ref|XP_002892982.1| hypothetical protein ARALYDRAFT_472022 [Arabidopsis lyrata subsp. lyrata] gi|297338824|gb|EFH69241.1| hypothetical protein ARALYDRAFT_472022 [Arabidopsis lyrata subsp. lyrata]	208	533	5.00E-37	256.3	38.5	40.4	hypothetical protein ARALYDRAFT_472022	gbpln	Arabidopsis lyrata	AT1G18070.2 | Symbols: | Translation elongation factor EF1A/initiation factor IF2gamma family protein | chr1:6214236-6218211 REVERSE LENGTH=532	208	532	6.00E-39	255.8	38.5	39.9
Rsa1.0_00304.1.g10926.t1	ref|XP_002890258.1| hypothetical protein ARALYDRAFT_312763 [Arabidopsis lyrata subsp. lyrata] gi|297336100|gb|EFH66517.1| hypothetical protein ARALYDRAFT_312763 [Arabidopsis lyrata subsp. lyrata]	363	341	1.00E-164	93.9	79.3	84.8	hypothetical protein ARALYDRAFT_312763	gbpln	Arabidopsis lyrata	AT1G18030.1 | Symbols: | Protein phosphatase 2C family protein | chr1:6204400-6206678 FORWARD LENGTH=351	363	351	1.00E-166	96.7	80.4	86.0
Rsa1.0_00304.1.g10927.t1	ref|XP_002862798.1| hypothetical protein ARALYDRAFT_497292 [Arabidopsis lyrata subsp. lyrata] gi|297308526|gb|EFH39056.1| hypothetical protein ARALYDRAFT_497292 [Arabidopsis lyrata subsp. lyrata]	840	842	0	100.2	54.2	66.5	hypothetical protein ARALYDRAFT_497292	gbpln	Arabidopsis lyrata	AT1G71400.1 | Symbols: AtRLP12, RLP12 | receptor like protein 12 | chr1:26909905-26912448 FORWARD LENGTH=847	840	847	0	100.8	54.0	67.9
Rsa1.0_00304.1.g10928.t1	ref|XP_002892977.1| nucleotidyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338819|gb|EFH69236.1| nucleotidyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	170	716	9.00E-33	421.2	54.1	64.1	nucleotidyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G17980.1 | Symbols: PAPS1 | poly(A) polymerase 1 | chr1:6187742-6191418 REVERSE LENGTH=713	170	713	2.00E-31	419.4	51.2	61.2
Rsa1.0_00304.1.g10929.t1	ref|XP_002887372.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata] gi|297333213|gb|EFH63631.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata]	838	832	0	99.3	54.3	67.3	hypothetical protein ARALYDRAFT_476271	gbpln	Arabidopsis lyrata	AT1G71400.1 | Symbols: AtRLP12, RLP12 | receptor like protein 12 | chr1:26909905-26912448 FORWARD LENGTH=847	838	847	0	101.1	54.4	68.4
Rsa1.0_00305.1.g10930.t1	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	210	1463	3.00E-33	696.7	33.3	42.4	F5J5.1	gbpln	Arabidopsis thaliana	AT3G19340.1 | Symbols: | Protein of unknown function (DUF3754) | chr3:6701387-6704071 REVERSE LENGTH=487	210	487	2.00E-24	231.9	23.8	26.7
Rsa1.0_00305.1.g10931.t2	ref|NP_187629.3| centromeric protein E [Arabidopsis thaliana] gi|332641347|gb|AEE74868.1| kinesin motor protein-related protein [Arabidopsis thaliana]	1298	1273	0	98.1	56.0	63.3	centromeric protein E	gbpln	Arabidopsis thaliana	AT3G10180.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:3146393-3154644 REVERSE LENGTH=1273	1298	1273	0	98.1	56.0	63.3
Rsa1.0_00305.1.g10932.t1	ref|XP_002889329.1| hypothetical protein ARALYDRAFT_470049 [Arabidopsis lyrata subsp. lyrata] gi|297335171|gb|EFH65588.1| hypothetical protein ARALYDRAFT_470049 [Arabidopsis lyrata subsp. lyrata]	205	226	4.00E-89	110.2	78.0	85.9	hypothetical protein ARALYDRAFT_470049	gbpln	Arabidopsis lyrata	AT1G02180.1 | Symbols: | ferredoxin-related | chr1:413619-414505 REVERSE LENGTH=226	205	226	2.00E-88	110.2	76.1	83.4
Rsa1.0_00305.1.g10933.t1	ref|XP_002892021.1| hypothetical protein ARALYDRAFT_470051 [Arabidopsis lyrata subsp. lyrata] gi|297337863|gb|EFH68280.1| hypothetical protein ARALYDRAFT_470051 [Arabidopsis lyrata subsp. lyrata]	72	90	6.00E-27	125.0	95.8	95.8	hypothetical protein ARALYDRAFT_470051	gbpln	Arabidopsis lyrata	AT1G02160.1 | Symbols: | Cox19 family protein (CHCH motif) | chr1:410803-411383 FORWARD LENGTH=71	72	71	1.00E-27	98.6	93.1	94.4

<table>
<tr><td>Rsa1.0_00305.1.g10934.t1</td><td>gb|EOA38945.1| hypothetical protein CARUB_v10011354mg [Capsella rubella]</td><td>508</td><td>524</td><td>0</td><td>103.1</td><td>88.2</td><td>93.3</td><td>hypothetical protein CARUB_v10011354mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G02150.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:408779-410433 FORWARD LENGTH=524</td><td>508</td><td>524</td><td>0</td><td>103.1</td><td>87.0</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00305.1.g10935.t1</td><td>ref|NP_001077448.1| alpha-1,6-mannosyltransferase [Arabidopsis thaliana] gi|347662308|sp|A8MR93.1|ALG12_ARATH RecName: Full=Dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase; AltName: Full=Alpha-1,6-mannosyltransferase ALG12; AltName: Full=Asparagine-linked glycosylation protein 12; AltName: Full=EMS-mutagenized BRI1 suppressor 4 gi|332189270|gb|AEE27391.1| alpha-1,6-mannosyltransferase [Arabidopsis thaliana]</td><td>501</td><td>497</td><td>0</td><td>99.2</td><td>88.2</td><td>94.2</td><td>alpha-1,6-mannosyltransferase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G02145.3 | Symbols: ALG12, EBS4 | homolog of asparagine-linked glycosylation 12 | chr1:404627-408485 FORWARD LENGTH=497</td><td>501</td><td>497</td><td>0</td><td>99.2</td><td>88.2</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00305.1.g10936.t1</td><td>ref|XP_004133763.1| PREDICTED: protein mago nashi homolog isoform 1 [Cucumis sativus] gi|449478034|ref|XP_004155202.1| PREDICTED: protein mago nashi homolog isoform 1 [Cucumis sativus]</td><td>135</td><td>193</td><td>1.00E-65</td><td>143.0</td><td>88.9</td><td>91.9</td><td>PREDICTED: protein mago nashi homolog isoform 1</td><td>gbpln</td><td>Cucumis sativus</td><td>AT1G02140.1 | Symbols: MEE63, MAGO, HAP1 | mago nashi family protein | chr1:403467-404401 REVERSE LENGTH=150</td><td>135</td><td>150</td><td>6.00E-66</td><td>111.1</td><td>85.9</td><td>91.1</td></tr>
<tr><td>Rsa1.0_00305.1.g10937.t1</td><td>gb|EOA39880.1| hypothetical protein CARUB_v10008556mg [Capsella rubella]</td><td>571</td><td>641</td><td>0</td><td>112.3</td><td>79.7</td><td>87.4</td><td>hypothetical protein CARUB_v10008556mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G02120.1 | Symbols: VAD1 | GRAM domain family protein | chr1:395761-399720 FORWARD LENGTH=598</td><td>571</td><td>598</td><td>0</td><td>104.7</td><td>77.8</td><td>86.0</td></tr>
<tr><td>Rsa1.0_00305.1.g10938.t1</td><td>ref|XP_002892031.1| hypothetical protein ARALYDRAFT_470069 [Arabidopsis lyrata subsp. lyrata] gi|297337873|gb|EFH68290.1| hypothetical protein ARALYDRAFT_470069 [Arabidopsis lyrata subsp. lyrata]</td><td>324</td><td>323</td><td>1.00E-104</td><td>99.7</td><td>64.5</td><td>69.4</td><td>hypothetical protein ARALYDRAFT_470069</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G02065.1 | Symbols: SPL8 | squamosa promoter binding protein-like 8 | chr1:365625-367149 FORWARD LENGTH=333</td><td>324</td><td>333</td><td>1.00E-100</td><td>102.8</td><td>64.8</td><td>70.4</td></tr>
<tr><td>Rsa1.0_00305.1.g10939.t1</td><td>gb|EOA37457.1| hypothetical protein CARUB_v10011557mg [Capsella rubella]</td><td>239</td><td>267</td><td>1.00E-80</td><td>111.7</td><td>67.8</td><td>79.9</td><td>hypothetical protein CARUB_v10011557mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G01990.1 | Symbols: | unknown protein; Has 32 Blast hits to 32 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:343462-344199 REVERSE LENGTH=245</td><td>239</td><td>245</td><td>7.00E-81</td><td>102.5</td><td>68.6</td><td>77.8</td></tr>
<tr><td>Rsa1.0_00305.1.g10940.t1</td><td>ref|XP_002892034.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297337876|gb|EFH68293.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>404</td><td>409</td><td>1.00E-168</td><td>101.2</td><td>75.2</td><td>84.7</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01970.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:338538-339905 FORWARD LENGTH=409</td><td>404</td><td>409</td><td>1.00E-170</td><td>101.2</td><td>74.5</td><td>84.4</td></tr>
<tr><td>Rsa1.0_00305.1.g10941.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00305.1.g10942.t1</td><td>ref|XP_002881817.1| phospholipase D beta 1 [Arabidopsis lyrata subsp. lyrata] gi|297327656|gb|EFH58076.1| phospholipase D beta 1 [Arabidopsis lyrata subsp. lyrata]</td><td>1067</td><td>1087</td><td>0</td><td>101.9</td><td>87.3</td><td>89.7</td><td>phospholipase D beta 1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G42010.1 | Symbols: PLDBETA1, PLDBETA | phospholipase D beta 1 | chr2:17533018-17537990 REVERSE LENGTH=1083</td><td>1067</td><td>1083</td><td>0</td><td>101.5</td><td>86.1</td><td>89.0</td></tr>
<tr><td>Rsa1.0_00305.1.g10943.t1</td><td>ref|XP_002892038.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337880|gb|EFH68297.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>757</td><td>774</td><td>0</td><td>102.2</td><td>83.9</td><td>89.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01900.1 | Symbols: ATSBT1.1, SBTI1.1 | subtilase family protein | chr1:310332-313011 FORWARD LENGTH=774</td><td>757</td><td>774</td><td>0</td><td>102.2</td><td>84.1</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00305.1.g10944.t1</td><td>ref|NP_563638.1| uncharacterized protein [Arabidopsis thaliana] gi|8671850|gb|AAF78413.1|AC009273_19T1N6.26 [Arabidopsis thaliana] gi|16648714|gb|AAL25549.1| At1g01840/T1N6_19 [Arabidopsis thaliana] gi|20453347|gb|AAM19912.1| At1g01840/T1N6_19 [Arabidopsis thaliana] gi|332189222|gb|AEE27343.1| uncharacterized protein AT1G01840 [Arabidopsis thaliana]</td><td>153</td><td>152</td><td>3.00E-53</td><td>99.3</td><td>73.9</td><td>83.0</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G01840.1 | Symbols: | unknown protein; Has 23 Blast hits to 23 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:303650-304108 FORWARD LENGTH=152</td><td>153</td><td>152</td><td>9.00E-56</td><td>99.3</td><td>73.9</td><td>83.0</td></tr>
<tr><td>Rsa1.0_00305.1.g10945.t1</td><td>ref|XP_002889350.1| hypothetical protein ARALYDRAFT_470092 [Arabidopsis lyrata subsp. lyrata] gi|297335192|gb|EFH65609.1| hypothetical protein ARALYDRAFT_470092 [Arabidopsis lyrata subsp. lyrata]</td><td>570</td><td>569</td><td>0</td><td>99.8</td><td>87.0</td><td>93.3</td><td>hypothetical protein ARALYDRAFT_470092</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01830.1 | Symbols: | ARM repeat superfamily protein | chr1:298717-300441 REVERSE LENGTH=574</td><td>570</td><td>574</td><td>0</td><td>100.7</td><td>86.3</td><td>93.5</td></tr>
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Rsa1.0_00305.1.g10946.t1	ref|NP_563635.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|13878161|gb|AAK44158.1|AF370343_1 putative carbonyl reductase [Arabidopsis thaliana] gi|22136772|gb|AAM91730.1| putative carbonyl reductase [Arabidopsis thaliana] gi|222423734|dbj|BAH19833.1| AT1G01800 [Arabidopsis thaliana] gi|332189215|gb|AEE27336.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]	295	295	1.00E-147	100.0	86.4	93.9	Rossmann-fold NAD(P)-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G01800.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:293396-294888 FORWARD LENGTH=295	295	295	1.00E-150	100.0	86.4	93.9
Rsa1.0_00305.1.g10947.t2	ref|XP_002892042.1| hypothetical protein ARALYDRAFT_311263 [Arabidopsis lyrata subsp. lyrata] gi|297337884|gb|EFH68301.1| hypothetical protein ARALYDRAFT_311263 [Arabidopsis lyrata subsp. lyrata]	946	1171	0	123.8	76.2	78.9	hypothetical protein ARALYDRAFT_311263	gbpln	Arabidopsis lyrata	AT1G01790.1 | Symbols: KEA1, ATKEA1 | K+ efflux antiporter 1 | chr1:284781-290869 FORWARD LENGTH=1193	946	1193	0	126.1	75.6	78.2
Rsa1.0_00305.1.g10948.t1	ref|XP_002892042.1| hypothetical protein ARALYDRAFT_311263 [Arabidopsis lyrata subsp. lyrata] gi|297337884|gb|EFH68301.1| hypothetical protein ARALYDRAFT_311263 [Arabidopsis lyrata subsp. lyrata]	1100	1171	0	106.5	85.5	90.6	hypothetical protein ARALYDRAFT_311263	gbpln	Arabidopsis lyrata	AT1G01790.1 | Symbols: KEA1, ATKEA1 | K+ efflux antiporter 1 | chr1:284781-290869 FORWARD LENGTH=1193	1100	1193	0	108.5	84.0	89.8
Rsa1.0_00305.1.g10949.t1	gb|AAF78411.1|AC009273_17 Contains similarity to mRNA for transcription factor L2 from Arabidopsis thaliana gb|X91398. It contains LIM domain containing proteins PF|00412. ESTs gb|T13084 and gb|T42925 come from this gene [Arabidopsis thaliana]	202	261	1.00E-108	129.2	94.1	96.5	Contains similarity to mRNA for transcription factor L2 from Arabidopsis thaliana gb|X91398. It contains LIM domain containing proteins PF|00412. ESTs gb|T13084 and gb|T42925 come from this gene	gbpln	Arabidopsis thaliana	AT1G01780.1 | Symbols: | GATA type zinc finger transcription factor family protein | chr1:282919-284082 FORWARD LENGTH=205	202	205	1.00E-110	101.5	94.1	96.5
Rsa1.0_00305.1.g10950.t2	ref|XP_002888820.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata] gi|297334661|gb|EFH65079.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata]	139	395	2.00E-20	284.2	33.8	34.5	glycosyltransferase family 14 protein	gbpln	Arabidopsis lyrata	AT1G71070.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:26807440-26809152 REVERSE LENGTH=395	139	395	3.00E-22	284.2	33.1	33.8
Rsa1.0_00305.1.g10951.t1	ref|XP_002889353.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335195|gb|EFH65612.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	392	399	1.00E-169	101.8	79.1	86.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G01760.1 | Symbols: | adenosine deaminases;RNA binding;RNA binding;adenosine deaminases | chr1:276412-278448 REVERSE LENGTH=420	392	420	1.00E-167	107.1	77.3	84.9
Rsa1.0_00305.1.g10952.t1	gb|EOA37536.1| hypothetical protein CARUB_v10011760mg [Capsella rubella]	140	140	9.00E-73	100.0	94.3	96.4	hypothetical protein CARUB_v10011760mg	gbpln	Capsella rubella	AT1G01750.1 | Symbols: ADF11 | actin depolymerizing factor 11 | chr1:275528-276126 FORWARD LENGTH=140	140	140	1.00E-74	100.0	92.9	96.4
Rsa1.0_00305.1.g10953.t1	ref|NP_171679.1| tetratricopeptide repeat domain-containing protein kinase [Arabidopsis thaliana] gi|334182219|ref|NP_001184886.1| protein kinase protein with tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana] gi|332189208|gb|AEE27329.1| tetratricopeptide repeat domain-containing protein kinase [Arabidopsis thaliana] gi|332189209|gb|AEE27330.1| protein kinase protein with tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana]	484	483	0	99.8	78.1	84.9	tetratricopeptide repeat domain-containing protein kinase	gbpln	Arabidopsis thaliana	AT1G01740.2 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr1:272111-274239 REVERSE LENGTH=483	484	483	0	99.8	78.1	84.9
Rsa1.0_00305.1.g10954.t1	gb|AAP35054.1| NAC-domain protein 18 [Brassica napus]	292	285	1.00E-148	97.6	94.2	95.9	NAC-domain protein 18	gbpln	Brassica napus	AT1G01720.1 | Symbols: ATAF1, ANAC002 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:268471-269514 FORWARD LENGTH=289	292	289	1.00E-145	99.0	87.0	92.5
Rsa1.0_00305.1.g10955.t1	dbj|BAJ33966.1| unnamed protein product [Thellungiella halophila]	192	431	1.00E-105	224.5	94.3	99.0	unnamed protein product	----	----	AT1G01710.1 | Symbols: | Acyl-CoA thioesterase family protein | chr1:262950-266029 FORWARD LENGTH=427	192	427	1.00E-101	222.4	88.5	94.3

<table>
<tr><td>Rsa1.0_00306.1.g10956.t2</td><td>gb|AAD21687.1| Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078 [Arabidopsis thaliana]</td><td>1309</td><td>1415</td><td>0</td><td>108.1</td><td>60.0</td><td>72.7</td><td>Strong similarity to gi|3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb|AF080119 and is a member of the reverse transcriptase family PF|00078</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1309</td><td>1262</td><td>9.00E-97</td><td>96.4</td><td>13.8</td><td>20.4</td></tr>
<tr><td>Rsa1.0_00306.1.g10957.t1</td><td>ref|XP_002866395.1| hypothetical protein ARALYDRAFT_496228 [Arabidopsis lyrata subsp. lyrata] gi|297312230|gb|EFH42654.1| hypothetical protein ARALYDRAFT_496228 [Arabidopsis lyrata subsp. lyrata]</td><td>260</td><td>284</td><td>1.00E-74</td><td>109.2</td><td>70.0</td><td>80.0</td><td>hypothetical protein ARALYDRAFT_496228</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G60800.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:24461116-24462464 REVERSE LENGTH=283</td><td>260</td><td>283</td><td>5.00E-73</td><td>108.8</td><td>66.9</td><td>77.7</td></tr>
<tr><td>Rsa1.0_00306.1.g10958.t1</td><td>gb|EOA19622.1| hypothetical protein CARUB_v10002949mg [Capsella rubella]</td><td>214</td><td>333</td><td>2.00E-67</td><td>155.6</td><td>70.6</td><td>78.0</td><td>hypothetical protein CARUB_v10002949mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G23000.1 | Symbols: RAX1, MYB37, ATMYB37 | myb domain protein 37 | chr5:7696234-7697712 FORWARD LENGTH=329</td><td>214</td><td>329</td><td>7.00E-55</td><td>153.7</td><td>61.7</td><td>71.5</td></tr>
<tr><td>Rsa1.0_00306.1.g10959.t1</td><td>ref|XP_002874104.1| hypothetical protein ARALYDRAFT_351315 [Arabidopsis lyrata subsp. lyrata] gi|297319941|gb|EFH50363.1| hypothetical protein ARALYDRAFT_351315 [Arabidopsis lyrata subsp. lyrata]</td><td>199</td><td>238</td><td>4.00E-95</td><td>119.6</td><td>86.9</td><td>92.5</td><td>hypothetical protein ARALYDRAFT_351315</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G22930.1 | Symbols: | Protein of unknown function (DUF1635) | chr5:7668229-7669315 REVERSE LENGTH=238</td><td>199</td><td>238</td><td>5.00E-95</td><td>119.6</td><td>85.9</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00306.1.g10960.t1</td><td>gb|EOA22938.1| hypothetical protein CARUB_v10003674mg [Capsella rubella]</td><td>800</td><td>799</td><td>0</td><td>99.9</td><td>74.6</td><td>85.4</td><td>hypothetical protein CARUB_v10003674mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G22910.1 | Symbols: ATCHX9, CHX9 | cation/H+ exchanger 9 | chr5:7660927-7663829 REVERSE LENGTH=800</td><td>800</td><td>800</td><td>0</td><td>100.0</td><td>73.8</td><td>85.8</td></tr>
<tr><td>Rsa1.0_00306.1.g10961.t1</td><td>gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]</td><td>1562</td><td>1213</td><td>0</td><td>77.7</td><td>29.4</td><td>42.4</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1562</td><td>626</td><td>5.00E-69</td><td>40.1</td><td>9.3</td><td>14.1</td></tr>
<tr><td>Rsa1.0_00306.1.g10962.t1</td><td>ref|XP_002874102.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297319939|gb|EFH50361.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>375</td><td>368</td><td>1.00E-143</td><td>98.1</td><td>69.3</td><td>80.8</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G22890.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:7653541-7654662 REVERSE LENGTH=373</td><td>375</td><td>373</td><td>1.00E-145</td><td>99.5</td><td>69.9</td><td>80.5</td></tr>
<tr><td>Rsa1.0_00306.1.g10963.t1</td><td>ref|XP_003606631.1| Histone H2B [Medicago truncatula] gi|355507686|gb|AES88828.1| Histone H2B [Medicago truncatula]</td><td>143</td><td>147</td><td>2.00E-60</td><td>102.8</td><td>86.7</td><td>91.6</td><td>Histone H2B</td><td>gbpln</td><td>Medicago truncatula</td><td>AT3G45980.1 | Symbols: H2B, HTB9 | Histone superfamily protein | chr3:16897492-16897944 REVERSE LENGTH=150</td><td>143</td><td>150</td><td>2.00E-59</td><td>104.9</td><td>88.1</td><td>90.2</td></tr>
<tr><td>Rsa1.0_00306.1.g10964.t1</td><td>gb|EOA21878.1| hypothetical protein CARUB_v10002354mg [Capsella rubella]</td><td>69</td><td>88</td><td>1.00E-31</td><td>127.5</td><td>98.6</td><td>100.0</td><td>hypothetical protein CARUB_v10002354mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G22875.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 32 Blast hits to 32 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr5:7651307-7651603 FORWARD LENGTH=69</td><td>69</td><td>69</td><td>1.00E-32</td><td>100.0</td><td>92.8</td><td>98.6</td></tr>
<tr><td>Rsa1.0_00306.1.g10965.t1</td><td>ref|NP_197676.2| aspartyl protease family protein [Arabidopsis thaliana] gi|110736370|dbj|BAF00154.1| protease-like protein [Arabidopsis thaliana] gi|332005704|gb|AED93087.1| aspartyl protease family protein [Arabidopsis thaliana]</td><td>492</td><td>493</td><td>0</td><td>100.2</td><td>92.1</td><td>96.5</td><td>aspartyl protease family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22850.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:7633717-7636298 REVERSE LENGTH=493</td><td>492</td><td>493</td><td>0</td><td>100.2</td><td>92.1</td><td>96.5</td></tr>
<tr><td>Rsa1.0_00306.1.g10966.t1</td><td>ref|NP_196209.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] gi|75262507|sp|Q9FI96.1|U76C3_ARATH RecName: Full=UDP-glycosyltransferase 76C3 gi|10177563|dbj|BAB10795.1| glucuronosyl transferase-like protein [Arabidopsis thaliana] gi|332003554|gb|AED90937.1| UDP-glycosyltransferase 76C3 [Arabidopsis thaliana]</td><td>442</td><td>450</td><td>0</td><td>101.8</td><td>77.8</td><td>86.9</td><td>UDP-glucoronosyl/UDP-glucosyl transferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G05900.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1774513-1776381 FORWARD LENGTH=450</td><td>442</td><td>450</td><td>0</td><td>101.8</td><td>77.8</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00306.1.g10967.t1</td><td>gb|AAM60872.1| serine protein kinase-like protein [Arabidopsis thaliana]</td><td>538</td><td>538</td><td>0</td><td>100.0</td><td>85.3</td><td>91.6</td><td>serine protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22840.1 | Symbols: | Protein kinase superfamily protein | chr5:7631103-7633103 REVERSE LENGTH=538</td><td>538</td><td>538</td><td>0</td><td>100.0</td><td>85.1</td><td>91.6</td></tr>
</table>

Rsa1.0_00306.1.g10968.t1	ref|XP_002872021.1| hypothetical protein ARALYDRAFT_489136 [Arabidopsis lyrata subsp. lyrata] gi|297317858|gb|EFH48280.1| hypothetical protein ARALYDRAFT_489136 [Arabidopsis lyrata subsp. lyrata]	466	456	0	97.9	85.6	89.5	hypothetical protein ARALYDRAFT_489136	gbpln	Arabidopsis lyrata	AT5G22830.1 | Symbols: ATMGT10, GMN10, MGT10, MRS2-11 | magnesium (Mg) transporter 10 | chr5:7627676-7630633 FORWARD LENGTH=459	466	459	0	98.5	85.4	89.1
Rsa1.0_00306.1.g10969.t1	ref|XP_002874089.1| hypothetical protein ARALYDRAFT_910273 [Arabidopsis lyrata subsp. lyrata] gi|297319926|gb|EFH50348.1| hypothetical protein ARALYDRAFT_910273 [Arabidopsis lyrata subsp. lyrata]	376	393	1.00E-102	104.5	56.1	67.8	hypothetical protein ARALYDRAFT_910273	gbpln	Arabidopsis lyrata	AT5G22791.2 | Symbols: | F-box family protein | chr5:7603579-7604771 REVERSE LENGTH=355	376	355	9.00E-99	94.4	55.1	65.7
Rsa1.0_00306.1.g10970.t1	ref|XP_002874089.1| hypothetical protein ARALYDRAFT_910273 [Arabidopsis lyrata subsp. lyrata] gi|297319926|gb|EFH50348.1| hypothetical protein ARALYDRAFT_910273 [Arabidopsis lyrata subsp. lyrata]	409	393	1.00E-120	96.1	55.5	67.5	hypothetical protein ARALYDRAFT_910273	gbpln	Arabidopsis lyrata	AT5G22791.2 | Symbols: | F-box family protein | chr5:7603579-7604771 REVERSE LENGTH=355	409	355	1.00E-109	86.8	53.3	63.1
Rsa1.0_00306.1.g10971.t1	ref|XP_002872017.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317854|gb|EFH48276.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	654	926	1.00E-164	141.6	43.6	46.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G53350.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:19903899-19907515 FORWARD LENGTH=927	654	927	3.00E-85	141.7	27.5	36.7
Rsa1.0_00306.1.g10972.t1	gb|EOA20677.1| hypothetical protein CARUB_v10000989mg [Capsella rubella]	425	436	0	102.6	85.9	91.3	hypothetical protein CARUB_v10000989mg	gbpln	Capsella rubella	AT5G22790.1 | Symbols: RER1 | reticulata-related 1 | chr5:7599395-7601573 REVERSE LENGTH=433	425	433	0	101.9	84.5	90.6
Rsa1.0_00306.1.g10973.t16	ref|XP_002874085.1| hypothetical protein ARALYDRAFT_489126 [Arabidopsis lyrata subsp. lyrata] gi|297319922|gb|EFH50344.1| hypothetical protein ARALYDRAFT_489126 [Arabidopsis lyrata subsp. lyrata]	1088	1016	0	93.4	86.8	90.0	hypothetical protein ARALYDRAFT_489126	gbpln	Arabidopsis lyrata	AT5G22780.1 | Symbols: | Adaptor protein complex AP-2, alpha subunit | chr5:7590100-7597828 REVERSE LENGTH=1013	1088	1013	0	93.1	86.5	89.8
Rsa1.0_00306.1.g10974.t1	ref|XP_002874083.1| hypothetical protein ARALYDRAFT_489123 [Arabidopsis lyrata subsp. lyrata] gi|297319920|gb|EFH50342.1| hypothetical protein ARALYDRAFT_489123 [Arabidopsis lyrata subsp. lyrata]	534	534	0	100.0	97.9	99.4	hypothetical protein ARALYDRAFT_489123	gbpln	Arabidopsis lyrata	AT5G22740.1 | Symbols: ATCSLA02, CSLA02, ATCSLA2, CSLA2 | cellulose synthase-like A02 | chr5:7555379-7559866 REVERSE LENGTH=534	534	534	0	100.0	97.6	99.4
Rsa1.0_00306.1.g10975.t1	gb|AAF19546.1|AC007190_14 F23N19.13 [Arabidopsis thaliana]	238	633	8.00E-43	266.0	38.2	45.0	F23N19.13	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00306.1.g10976.t1	ref|NP_001078614.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262764|sp|Q9FNJ5.1|FDL31_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At5g22660 gi|10178240|dbj|BAB11672.1| unnamed protein product [Arabidopsis thaliana] gi|332005678|gb|AED93061.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	429	450	1.00E-132	104.9	62.9	77.4	F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G22660.2 | Symbols: | FBD, F-box, Skp2-like and Leucine Rich Repeat domains containing protein | chr5:7536328-7537853 REVERSE LENGTH=450	429	450	1.00E-135	104.9	62.9	77.4
Rsa1.0_00306.1.g10977.t1	ref|NP_851056.1| histone deacetylase HDT2 [Arabidopsis thaliana] gi|73919940|sp|Q56WH4.2|HDT2_ARATH RecName: Full=Histone deacetylase HDT2; AltName: Full=HD-tuins protein 2; AltName: Full=Histone deacetylase 2b gi|10178239|dbj|BAB11671.1| histone deacetylase-like protein [Arabidopsis thaliana] gi|16649047|gb|AAL24375.1| histone deacetylase-like protein [Arabidopsis thaliana] gi|19310471|gb|AAL84970.1| AT5g22650/MDJ22_7 [Arabidopsis thaliana] gi|21689603|gb|AAM67423.1| AT5g22650/MDJ22_7 [Arabidopsis thaliana] gi|332005675|gb|AED93058.1| histone deacetylase HDT2 [Arabidopsis thaliana]	269	306	7.00E-53	113.8	56.5	68.4	histone deacetylase HDT2	gbpln	Arabidopsis thaliana	AT5G22650.1 | Symbols: HD2B, HDT02, HDT2, ATHD2B, HDA4, HD2, ATHD2 | histone deacetylase 2B | chr5:7534120-7536054 FORWARD LENGTH=306	269	306	2.00E-55	113.8	56.5	68.4
Rsa1.0_00306.1.g10978.t1	ref|XP_002872014.1| EMB1211 [Arabidopsis lyrata subsp. lyrata] gi|297317851|gb|EFH48273.1| EMB1211 [Arabidopsis lyrata subsp. lyrata]	910	867	0	95.3	76.3	83.2	EMB1211	gbpln	Arabidopsis lyrata	AT5G22640.1 | Symbols: emb1211 | MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein | chr5:7529423-7533641 FORWARD LENGTH=871	910	871	0	95.7	75.6	83.3

Rsa1.0_00306.1.g10979.t1	ref|XP_002872013.1| prephenate dehydratase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317850|gb|EFH48272.1| prephenate dehydratase family protein [Arabidopsis lyrata subsp. lyrata]	432	433	0	100.2	93.3	95.8	prephenate dehydratase family protein	gbpln	Arabidopsis lyrata	AT5G22630.1 | Symbols: ADT5 | arogenate dehydratase 5 | chr5:7524645-7525922 FORWARD LENGTH=425	432	425	0	98.4	91.4	93.8
Rsa1.0_00307.1.g10980.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00307.1.g10981.t1	ref|XP_002884997.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330837|gb|EFH61256.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	412	412	0	100.0	98.3	99.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G13920.1 | Symbols: EIF4A1, RH4, TIF4A1 | eukaryotic translation initiation factor 4A1 | chr3:4592635-4594128 REVERSE LENGTH=412	412	412	0	100.0	97.8	99.8
Rsa1.0_00307.1.g10982.t2	ref|XP_002884998.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330838|gb|EFH61257.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	442	443	1.00E-128	100.2	55.4	73.1	DNA binding protein	gbpln	Arabidopsis lyrata	AT3G13940.1 | Symbols: | DNA binding;DNA-directed RNA polymerases | chr3:4600647-4602412 REVERSE LENGTH=442	442	442	1.00E-128	100.0	54.5	71.9
Rsa1.0_00307.1.g10983.t1	gb|EOA30723.1| hypothetical protein CARUB_v10013860mg [Capsella rubella]	386	403	1.00E-161	104.4	79.5	87.6	hypothetical protein CARUB_v10013860mg	gbpln	Capsella rubella	AT3G13960.1 | Symbols: AtGRF5, GRF5 | growth-regulating factor 5 | chr3:4608526-4610160 FORWARD LENGTH=397	386	397	1.00E-144	102.8	78.5	85.5
Rsa1.0_00307.1.g10984.t1	ref|NP_188014.1| uncharacterized protein [Arabidopsis thaliana] gi|11994369|dbj|BAB02328.1| unnamed protein product [Arabidopsis thaliana] gi|332641926|gb|AEE75447.1| uncharacterized protein AT3G13980 [Arabidopsis thaliana]	360	357	1.00E-101	99.2	71.1	80.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G13980.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G54200.1); Has 1485 Blast hits to 418 proteins in 98 species: Archae - 0; Bacteria - 6; Metazoa - 246; Fungi - 61; Plants - 107; Viruses - 6; Other Eukaryotes - 1059 (source: NCBI BLink). | chr3:4619189-4620262 REVERSE LENGTH=357	360	357	1.00E-104	99.2	71.1	80.0
Rsa1.0_00307.1.g10985.t1	ref|NP_188015.2| uncharacterized protein [Arabidopsis thaliana] gi|22022592|gb|AAM83252.1| AT3g13990/MDC16_11 [Arabidopsis thaliana] gi|23308471|gb|AAN18205.1| At3g13990/MDC16_11 [Arabidopsis thaliana] gi|332641927|gb|AEE75448.1| uncharacterized protein AT3G13990 [Arabidopsis thaliana]	865	848	0	98.0	71.9	78.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G13990.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr3:4625708-4630383 REVERSE LENGTH=848	865	848	0	98.0	71.9	78.7
Rsa1.0_00307.1.g10986.t1	ref|NP_188016.2| protein Brevis radix-like 2 [Arabidopsis thaliana] gi|42572427|ref|NP_974309.1| protein Brevis radix-like 2 [Arabidopsis thaliana] gi|75151461|sp|Q8GYL9.1|BRXL2_ARATH RecName: Full=Protein Brevis radix-like 2; Short=AtBRXL2 gi|26450131|dbj|BAC42185.1| unknown protein [Arabidopsis thaliana] gi|115311461|gb|ABI93911.1| At3g14000 [Arabidopsis thaliana] gi|332641929|gb|AEE75450.1| protein Brevis radix-like 2 [Arabidopsis thaliana] gi|332641930|gb|AEE75451.1| protein Brevis radix-like 2 [Arabidopsis thaliana]	363	374	1.00E-162	103.0	85.1	92.3	protein Brevis radix-like 2	gbpln	Arabidopsis thaliana	AT3G14000.2 | Symbols: ATBRXL2, BRX-LIKE2 | DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein | chr3:4631170-4633353 REVERSE LENGTH=374	363	374	1.00E-164	103.0	85.1	92.3
Rsa1.0_00307.1.g10987.t6	ref|NP_566471.1| CTC-interacting domain 4 protein [Arabidopsis thaliana] gi|145332387|ref|NP_001078150.1| CTC-interacting domain 4 protein [Arabidopsis thaliana] gi|145332389|ref|NP_001078151.1| CTC-interacting domain 4 protein [Arabidopsis thaliana] gi|15028199|gb|AAK76596.1| unknown protein [Arabidopsis thaliana] gi|19310731|gb|AAL85096.1| unknown protein [Arabidopsis thaliana] gi|332641931|gb|AEE75452.1| CTC-interacting domain 4 protein [Arabidopsis thaliana] gi|332641932|gb|AEE75453.1| CTC-interacting domain 4 protein [Arabidopsis thaliana] gi|332641933|gb|AEE75454.1| CTC-interacting domain 4 protein [Arabidopsis thaliana]	616	595	0	96.6	66.2	76.1	CTC-interacting domain 4 protein	gbpln	Arabidopsis thaliana	AT3G14010.3 | Symbols: CID4 | CTC-interacting domain 4 | chr3:4637164-4640691 FORWARD LENGTH=595	616	595	0	96.6	66.2	76.1
Rsa1.0_00307.1.g10988.t1	ref|XP_002882866.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328706|gb|EFH59125.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	296	315	1.00E-101	106.4	76.7	81.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G14020.1 | Symbols: NF-YA6 | nuclear factor Y, subunit A6 | chr3:4642968-4644301 FORWARD LENGTH=308	296	308	4.00E-96	104.1	73.3	79.7

Rsa1.0_00307.1.g10989.t1	ref|XP_002885007.1| hypothetical protein ARALYDRAFT_478815 [Arabidopsis lyrata subsp. lyrata] gi|297330847|gb|EFH61266.1| hypothetical protein ARALYDRAFT_478815 [Arabidopsis lyrata subsp. lyrata]	153	125	2.00E-40	81.7	55.6	60.8	hypothetical protein ARALYDRAFT_478815	gbpln	Arabidopsis lyrata	AT3G14060.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G54120.1); Has 30 Blast hits to 30 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4657174-4657551 REVERSE LENGTH=125	153	125	3.00E-42	81.7	54.9	60.8
Rsa1.0_00307.1.g10990.t1	ref|NP_566473.2| Subtilase family protein [Arabidopsis thaliana] gi|11994380|dbj|BAB02339.1| cucumisin-like serine protease; subtilisin-like protease [Arabidopsis thaliana] gi|44917461|gb|AAS49055.1| At3g14067 [Arabidopsis thaliana] gi|45773916|gb|AAS76762.1| At3g14067 [Arabidopsis thaliana] gi|110738008|dbj|BAF00939.1| putative subtilisin-like serine proteinase [Arabidopsis thaliana] gi|332641940|gb|AEE75461.1| Subtilase family protein [Arabidopsis thaliana]	774	777	0	100.4	89.3	93.4	Subtilase family protein	gbpln	Arabidopsis thaliana	AT3G14067.1 | Symbols: | Subtilase family protein | chr3:4658421-4660754 REVERSE LENGTH=777	774	777	0	100.4	89.3	93.4
Rsa1.0_00307.1.g10991.t1	ref|NP_566475.1| lipase class 3 family protein [Arabidopsis thaliana] gi|334185334|ref|NP_001189887.1| lipase class 3 family protein [Arabidopsis thaliana] gi|15146181|gb|AAK83574.1| AT3g14070/MAG2_2 [Arabidopsis thaliana] gi|27764916|gb|AAO23579.1| At3g14070/MAG2_2 [Arabidopsis thaliana] gi|332641942|gb|AEE75463.1| lipase class 3 family protein [Arabidopsis thaliana] gi|332641943|gb|AEE75464.1| lipase class 3 family protein [Arabidopsis thaliana]	593	642	0	108.3	86.2	90.4	lipase class 3 family protein	gbpln	Arabidopsis thaliana	AT3G14075.2 | Symbols: | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | chr3:4663819-4666338 REVERSE LENGTH=642	593	642	0	108.3	86.2	90.4
Rsa1.0_00307.1.g10992.t1	dbj|BAB02972.1| unnamed protein product [Arabidopsis thaliana]	120	118	1.00E-53	98.3	90.0	93.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G14080.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr3:4667717-4668989 FORWARD LENGTH=128	120	128	5.00E-55	106.7	87.5	93.3
Rsa1.0_00307.1.g10993.t1	ref|XP_002882868.1| hypothetical protein ARALYDRAFT_478823 [Arabidopsis lyrata subsp. lyrata] gi|297328708|gb|EFH59127.1| hypothetical protein ARALYDRAFT_478823 [Arabidopsis lyrata subsp. lyrata]	422	430	0	101.9	93.4	95.0	hypothetical protein ARALYDRAFT_478823	gbpln	Arabidopsis lyrata	AT3G14100.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:4673027-4675950 FORWARD LENGTH=427	422	427	0	101.2	92.2	93.8
Rsa1.0_00307.1.g10994.t1	gb|EOA32951.1| hypothetical protein CARUB_v10016280mg [Capsella rubella]	1125	1077	0	95.7	86.1	91.1	hypothetical protein CARUB_v10016280mg	gbpln	Capsella rubella	AT3G14120.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: transport; LOCATED IN: nuclear pore; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nuclear pore protein 84/107 (InterPro:IPR007252); Has 271 Blast hits to 268 proteins in 107 species: Archae - 0; Bacteria - 0; Metazoa - 138; Fungi - 69; Plants - 52; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr3:4677993-4685455 FORWARD LENGTH=1077	1125	1077	0	95.7	85.6	90.5
Rsa1.0_00307.1.g10995.t1	gb|EOA31941.1| hypothetical protein CARUB_v10015180mg [Capsella rubella]	439	363	0	82.7	72.9	80.0	hypothetical protein CARUB_v10015180mg	gbpln	Capsella rubella	AT3G14130.1 | Symbols: | Aldolase-type TIM barrel family protein | chr3:4685844-4687852 REVERSE LENGTH=363	439	363	0	82.7	72.2	79.5
Rsa1.0_00307.1.g10996.t1	ref|XP_002885018.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330858|gb|EFH61277.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	97	68	4.00E-18	70.1	49.5	54.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G54070.1 | Symbols: | Dormancy/auxin associated family protein | chr1:20182683-20183242 FORWARD LENGTH=123	97	123	7.00E-11	126.8	46.4	55.7
Rsa1.0_00307.1.g10997.t1	ref|XP_002882871.1| At3g14190 [Arabidopsis lyrata subsp. lyrata] gi|297328711|gb|EFH59130.1| At3g14190 [Arabidopsis lyrata subsp. lyrata]	157	193	1.00E-40	122.9	58.6	70.1	At3g14190	gbpln	Arabidopsis lyrata	AT3G14190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12360.1); Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4710907-4711790 FORWARD LENGTH=193	157	193	4.00E-41	122.9	56.7	68.8

Rsa1.0_00307.1.g10998.t1	ref|NP_188036.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|9294648|dbj|BAB02987.1| unnamed protein product [Arabidopsis thaliana] gi|20268707|gb|AAM14057.1| unknown protein [Arabidopsis thaliana] gi|21689885|gb|AAM67503.1| unknown protein [Arabidopsis thaliana] gi|110743929|dbj|BAE99798.1| hypothetical protein [Arabidopsis thaliana] gi|332641964|gb|AEE75485.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]	215	230	4.00E-79	107.0	76.7	86.0	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT3G14200.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr3:4712881-4714361 REVERSE LENGTH=230	215	230	1.00E-81	107.0	76.7	86.0
Rsa1.0_00307.1.g10999.t1	gb|EOA32569.1| hypothetical protein CARUB_v10015859mg [Capsella rubella]	805	804	0	99.9	83.5	89.7	hypothetical protein CARUB_v10015859mg	gbpln	Capsella rubella	AT3G14205.1 | Symbols: | Phosphoinositide phosphatase family protein | chr3:4716008-4720524 REVERSE LENGTH=808	805	808	0	100.4	83.2	89.3
Rsa1.0_00307.1.g11000.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00307.1.g11001.t1	ref|XP_002882874.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328714|gb|EFH59133.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata]	1747	1789	0	102.4	88.5	92.7	phosphatidylinositol-4-phosphate 5-kinase family protein	gbpln	Arabidopsis lyrata	AT3G14270.1 | Symbols: FAB1B | phosphatidylinositol-4-phosphate 5-kinase family protein | chr3:4754624-4761185 FORWARD LENGTH=1791	1747	1791	0	102.5	87.5	92.2
Rsa1.0_00307.1.g11002.t1	ref|XP_002885030.1| hypothetical protein ARALYDRAFT_478845 [Arabidopsis lyrata subsp. lyrata] gi|297330870|gb|EFH61289.1| hypothetical protein ARALYDRAFT_478845 [Arabidopsis lyrata subsp. lyrata]	140	141	2.00E-58	100.7	81.4	87.9	hypothetical protein ARALYDRAFT_478845	gbpln	Arabidopsis lyrata	AT3G14280.1 | Symbols: | unknown protein; Has 51 Blast hits to 51 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4761654-4762286 REVERSE LENGTH=141	140	141	8.00E-59	100.7	79.3	86.4
Rsa1.0_00307.1.g11003.t1	gb|EOA32869.1| hypothetical protein CARUB_v10016184mg [Capsella rubella]	484	576	1.00E-155	119.0	55.2	71.7	hypothetical protein CARUB_v10016184mg	gbpln	Capsella rubella	AT1G53840.1 | Symbols: ATPME1, PME1 | pectin methylesterase 1 | chr1:20101533-20103458 FORWARD LENGTH=586	484	586	1.00E-101	121.1	40.5	59.5
Rsa1.0_00307.1.g11004.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00307.1.g11005.t1	ref|NP_188048.1| pectinesterase 3 [Arabidopsis thaliana] gi|229891485|sp|O49006.2|PME3_ARATH RecName: Full=Pectinesterase/pectinesterase inhibitor 3; Includes: RecName: Full=Pectinesterase inhibitor 3; AltName: Full=Pectin methylesterase inhibitor 3; Includes: RecName: Full=Pectinesterase 3; Short=PE 3; AltName: Full=Pectin methylesterase 27; Short=AtPME27; AltName: Full=Pectin methylesterase 3; Flags: Precursor gi|9279579|dbj|BAB01037.1| pectinesterase [Arabidopsis thaliana] gi|14335010|gb|AAK59769.1| AT3g14310/MLN21_9 [Arabidopsis thaliana] gi|15529256|gb|AAK97722.1| AT3g14310/MLN21_9 [Arabidopsis thaliana] gi|23506059|gb|AAN28889.1| At3g14310/MLN21_9 [Arabidopsis thaliana] gi|332641979|gb|AEE75500.1| pectinesterase 3 [Arabidopsis thaliana]	592	592	0	100.0	90.9	95.1	pectinesterase 3	gbpln	Arabidopsis thaliana	AT3G14310.1 | Symbols: ATPME3, PME3 | pectin methylesterase 3 | chr3:4772214-4775095 REVERSE LENGTH=592	592	592	0	100.0	90.9	95.1
Rsa1.0_00307.1.g11006.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00307.1.g11007.t1	dbj|BAB01039.1| unnamed protein product [Arabidopsis thaliana]	662	717	0	108.3	77.9	86.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G14330.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:4779688-4782451 REVERSE LENGTH=710	662	710	0	107.3	77.9	86.3

Rsa1.0_00307.1.g11008.t1	ref|NP_188052.2| STRUBBELIG-receptor family 7 protein [Arabidopsis thaliana] gi|75335505|sp|Q9LUL4.1|SRF7_ARATH RecName: Full=Protein STRUBBELIG-RECEPTOR FAMILY 7; AltName: Full=Leucine-rich repeat receptor kinase-like protein SRF7; Flags: Precursor gi|9279582|dbj|BAB01040.1| serine/threonine protein kinase-like protein [Arabidopsis thaliana] gi|41323413|gb|AAR99875.1| strubbelig receptor family 7 [Arabidopsis thaliana] gi|209529813|gb|ACI49801.1| At3g14350 [Arabidopsis thaliana] gi|224589565|gb|ACN59316.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332641984|gb|AEE75505.1| STRUBBELIG-receptor family 7 protein [Arabidopsis thaliana]	728	717	0	98.5	84.2	90.5	STRUBBELIG-receptor family 7 protein	gbpln	Arabidopsis thaliana	AT3G14350.1 | Symbols: SRF7 | STRUBBELIG-receptor family 7 | chr3:4783115-4786999 REVERSE LENGTH=717	728	717	0	98.5	84.2	90.5
Rsa1.0_00307.1.g11009.t2	dbj|BAB10837.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1464	1462	0	99.9	66.2	77.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1464	1262	1.00E-133	86.2	16.0	23.4
Rsa1.0_00307.1.g11010.t1	gb|AAF79677.1|AC022314_18 F9C16.26 [Arabidopsis thaliana]	229	1902	2.00E-31	830.6	31.0	42.8	F9C16.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00308.1.g11011.t1	gb|EOA29213.1| hypothetical protein CARUB_v10025487mg [Capsella rubella]	186	213	5.00E-32	114.5	37.1	37.6	hypothetical protein CARUB_v10025487mg	gbpln	Capsella rubella	AT2G35990.1 | Symbols: | Putative lysine decarboxylase family protein | chr2:15114070-15116647 FORWARD LENGTH=213	186	213	2.00E-34	114.5	37.1	37.6
Rsa1.0_00308.1.g11012.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00308.1.g11013.t1	gb|EOA29213.1| hypothetical protein CARUB_v10025487mg [Capsella rubella]	79	213	2.00E-31	269.6	87.3	87.3	hypothetical protein CARUB_v10025487mg	gbpln	Capsella rubella	AT2G35990.1 | Symbols: | Putative lysine decarboxylase family protein | chr2:15114070-15116647 FORWARD LENGTH=213	79	213	8.00E-33	269.6	84.8	86.1
Rsa1.0_00308.1.g11014.t1	ref|XP_002862184.1| hypothetical protein ARALYDRAFT_497554 [Arabidopsis lyrata subsp. lyrata] gi|297823411|ref|XP_002879588.1| hypothetical protein ARALYDRAFT_482571 [Arabidopsis lyrata subsp. lyrata] gi|297307418|gb|EFH38442.1| hypothetical protein ARALYDRAFT_497554 [Arabidopsis lyrata subsp. lyrata] gi|297325427|gb|EFH55847.1| hypothetical protein ARALYDRAFT_482571 [Arabidopsis lyrata subsp. lyrata]	336	330	1.00E-134	98.2	72.6	78.3	hypothetical protein ARALYDRAFT_497554	gbpln	Arabidopsis lyrata	AT2G36000.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr2:15117181-15118182 FORWARD LENGTH=333	336	333	1.00E-128	99.1	72.9	79.2
Rsa1.0_00308.1.g11015.t1	ref|XP_002879589.1| E2F transcription factor-3 [Arabidopsis lyrata subsp. lyrata] gi|297325428|gb|EFH55848.1| E2F transcription factor-3 [Arabidopsis lyrata subsp. lyrata]	481	486	0	101.0	81.9	87.1	E2F transcription factor-3	gbpln	Arabidopsis lyrata	AT2G36010.1 | Symbols: E2F3, ATE2FA | E2F transcription factor 3 | chr2:15119688-15122893 FORWARD LENGTH=483	481	483	0	100.4	80.0	85.2
Rsa1.0_00308.1.g11016.t1	ref|XP_002881422.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata] gi|297327261|gb|EFH57681.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata]	259	258	1.00E-124	99.6	88.0	93.1	abscisic acid-responsive HVA22 family protein	gbpln	Arabidopsis lyrata	AT2G36020.1 | Symbols: HVA22J | HVA22-like protein J | chr2:15123424-15125140 REVERSE LENGTH=258	259	258	1.00E-126	99.6	87.3	92.7
Rsa1.0_00308.1.g11017.t1	ref|XP_002862872.1| hypothetical protein ARALYDRAFT_920186 [Arabidopsis lyrata subsp. lyrata] gi|297308632|gb|EFH39131.1| hypothetical protein ARALYDRAFT_920186 [Arabidopsis lyrata subsp. lyrata]	186	184	7.00E-61	98.9	76.9	85.5	hypothetical protein ARALYDRAFT_920186	gbpln	Arabidopsis lyrata	AT2G36026.1 | Symbols: | Ovate family protein | chr2:15127265-15127816 FORWARD LENGTH=183	186	183	3.00E-59	98.4	75.8	84.4
Rsa1.0_00308.1.g11018.t1	ref|XP_002881423.1| ATOFP15/OFP15 [Arabidopsis lyrata subsp. lyrata] gi|297327262|gb|EFH57682.1| ATOFP15/OFP15 [Arabidopsis lyrata subsp. lyrata]	265	259	2.00E-89	97.7	76.6	84.9	ATOFP15/OFP15	gbpln	Arabidopsis lyrata	AT2G36050.1 | Symbols: ATOFP15, OFP15 | ovate family protein 15 | chr2:15135852-15136637 REVERSE LENGTH=261	265	261	9.00E-76	98.5	73.2	81.9

Rsa1.0_00308.1.g11019.t1	ref|NP_850260.1| B3 domain-containing protein [Arabidopsis thaliana] gi|75151444|sp|Q8GYJ2.1|Y2608_ARATH RecName: Full=B3 domain-containing protein At2g36080; AltName: Full=Protein AUXIN RESPONSIVE FACTOR 31 gi|26450255|dbj|BAC42244.1| putative RAV2-like DNA binding protein [Arabidopsis thaliana] gi|330254110|gb|AEC09204.1| B3 domain-containing protein [Arabidopsis thaliana]	221	244	2.00E-95	110.4	87.3	91.4	B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G36080.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr2:15148612-15151411 REVERSE LENGTH=244	221	244	7.00E-98	110.4	87.3	91.4
Rsa1.0_00308.1.g11020.t1	ref|XP_002879591.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297325430|gb|EFH55850.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	316	313	1.00E-129	99.1	75.6	86.1	F-box family protein	gbpln	Arabidopsis lyrata	AT2G36090.1 | Symbols: | F-box family protein | chr2:15158631-15159584 FORWARD LENGTH=317	316	317	1.00E-130	100.3	75.9	86.1
Rsa1.0_00308.1.g11021.t1	sp|P0DI49.1|CASP_RAPRA RecName: Full=Casparian strip membrane protein 1	191	207	7.00E-76	108.4	82.7	89.0	RecName: Full=Casparian strip membrane protein 1	----	----	AT2G36100.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr2:15159744-15160669 REVERSE LENGTH=206	191	206	3.00E-75	107.9	77.5	85.3
Rsa1.0_00308.1.g11022.t1	sp|P0DI49.1|CASP_RAPRA RecName: Full=Casparian strip membrane protein 1	207	207	3.00E-93	100.0	92.8	96.6	RecName: Full=Casparian strip membrane protein 1	----	----	AT2G36100.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr2:15159744-15160669 REVERSE LENGTH=206	207	206	2.00E-86	99.5	81.2	90.3
Rsa1.0_00308.1.g11023.t1	ref|XP_002869958.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata] gi|297315794|gb|EFH46217.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata]	367	428	1.00E-106	116.6	62.1	75.2	hypothetical protein ARALYDRAFT_914664	gbpln	Arabidopsis lyrata	AT4G19940.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:10806195-10807430 FORWARD LENGTH=411	367	411	1.00E-102	112.0	56.1	71.4
Rsa1.0_00308.1.g11024.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00308.1.g11025.t1	ref|XP_002869958.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata] gi|297315794|gb|EFH46217.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata]	425	428	1.00E-119	100.7	56.9	70.6	hypothetical protein ARALYDRAFT_914664	gbpln	Arabidopsis lyrata	AT4G19930.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:10803558-10804853 FORWARD LENGTH=431	425	431	1.00E-106	101.4	55.3	66.8
Rsa1.0_00308.1.g11026.t1	gb|EOA29179.1| hypothetical protein CARUB_v10025451mg [Capsella rubella]	164	164	2.00E-89	100.0	96.3	98.8	hypothetical protein CARUB_v10025451mg	gbpln	Capsella rubella	AT2G36130.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr2:15166863-15168259 FORWARD LENGTH=164	164	164	2.00E-90	100.0	94.5	97.6
Rsa1.0_00308.1.g11027.t2	gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	150	5.00E-80	100.0	98.7	99.3	cytoplasmic ribosomal protein S14	gbpln	Brassica napus	AT3G11510.1 | Symbols: | Ribosomal protein S11 family protein | chr3:3623757-3624866 REVERSE LENGTH=150	150	150	3.00E-75	100.0	89.3	92.0
Rsa1.0_00308.1.g11028.t1	ref|XP_002881429.1| ATCWINV4 [Arabidopsis lyrata subsp. lyrata] gi|297327268|gb|EFH57688.1| ATCWINV4 [Arabidopsis lyrata subsp. lyrata]	588	591	0	100.5	87.1	94.4	ATCWINV4	gbpln	Arabidopsis lyrata	AT2G36190.1 | Symbols: AtcwINV4, cwINV4 | cell wall invertase 4 | chr2:15174951-15177785 REVERSE LENGTH=591	588	591	0	100.5	84.2	91.2
Rsa1.0_00308.1.g11029.t1	ref|NP_181162.2| kinesin family member 11 [Arabidopsis thaliana] gi|322510039|sp|P82266.2|K125_ARATH RecName: Full=Probable 125 kDa kinesin-related protein gi|330254121|gb|AEC09215.1| kinesin family member 11 [Arabidopsis thaliana]	1009	1009	0	100.0	91.5	96.1	kinesin family member 11	gbpln	Arabidopsis thaliana	AT2G36200.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:15180078-15185189 REVERSE LENGTH=1009	1009	1009	0	100.0	91.5	96.1
Rsa1.0_00308.1.g11030.t1	ref|XP_002880228.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297326067|gb|EFH56487.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	105	561	6.00E-32	534.3	65.7	69.5	BTB/POZ domain-containing protein	gbpln	Arabidopsis lyrata	AT2G46260.1 | Symbols: | BTB/POZ/Kelch-associated protein | chr2:18996111-18998463 FORWARD LENGTH=561	105	561	1.00E-34	534.3	65.7	69.5
Rsa1.0_00309.1.g11031.t1	gb|EOA25658.1| hypothetical protein CARUB_v10019009mg, partial [Capsella rubella]	72	81	5.00E-14	112.5	58.3	65.3	hypothetical protein CARUB_v10019009mg, partial	gbpln	Capsella rubella	AT3G25655.1 | Symbols: IDL1 | inflorescence deficient in abscission (IDA)-like 1 | chr3:9337709-9337969 REVERSE LENGTH=86	72	86	3.00E-13	119.4	51.4	56.9
Rsa1.0_00309.1.g11032.t1	ref|XP_002875266.1| hypothetical protein ARALYDRAFT_904728 [Arabidopsis lyrata subsp. lyrata] gi|297321104|gb|EFH51525.1| hypothetical protein ARALYDRAFT_904728 [Arabidopsis lyrata subsp. lyrata]	261	266	1.00E-123	101.9	89.7	95.0	hypothetical protein ARALYDRAFT_904728	gbpln	Arabidopsis lyrata	AT3G25640.1 | Symbols: | Protein of unknown function, DUF617 | chr3:9333775-9334578 FORWARD LENGTH=267	261	267	1.00E-124	102.3	88.1	95.4
Rsa1.0_00309.1.g11033.t1	gb|EOA20114.1| hypothetical protein CARUB_v10000393mg, partial [Capsella rubella]	137	670	2.00E-42	489.1	69.3	78.1	hypothetical protein CARUB_v10000393mg, partial	gbpln	Capsella rubella	AT5G10900.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:3436413-3439221 REVERSE LENGTH=600	137	600	2.00E-38	438.0	67.9	75.2

Rsa1.0_00309.1.g11034.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00309.1.g11035.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00309.1.g11036.t1	ref|XP_002876921.1| hypothetical protein ARALYDRAFT_904727 [Arabidopsis lyrata subsp. lyrata] gi|297322759|gb|EFH53180.1| hypothetical protein ARALYDRAFT_904727 [Arabidopsis lyrata subsp. lyrata]	670	671	0	100.1	92.1	96.0	hypothetical protein ARALYDRAFT_904727	gbpln	Arabidopsis lyrata	AT3G25620.2 | Symbols: | ABC-2 type transporter family protein | chr3:9316677-9319505 REVERSE LENGTH=672	670	672	0	100.3	91.9	95.2
Rsa1.0_00309.1.g11037.t1	gb|EOA24080.1| hypothetical protein CARUB_v10017307mg [Capsella rubella]	406	429	1.00E-133	105.7	72.7	78.1	hypothetical protein CARUB_v10017307mg	gbpln	Capsella rubella	AT3G25590.1 | Symbols: | unknown protein; Has 149 Blast hits to 140 proteins in 44 species: Archae - 0; Bacteria - 6; Metazoa - 40; Fungi - 6; Plants - 39; Viruses - 0; Other Eukaryotes - 58 (source: NCBI BLink). | chr3:9302271-9303542 FORWARD LENGTH=423	406	423	1.00E-130	104.2	72.7	78.6
Rsa1.0_00309.1.g11038.t2	ref|XP_002875262.1| hypothetical protein ARALYDRAFT_484318 [Arabidopsis lyrata subsp. lyrata] gi|297321100|gb|EFH51521.1| hypothetical protein ARALYDRAFT_484318 [Arabidopsis lyrata subsp. lyrata]	368	389	0	105.7	85.3	92.7	hypothetical protein ARALYDRAFT_484318	gbpln	Arabidopsis lyrata	AT3G25585.4 | Symbols: AAPT2, ATAAPT2 | aminoalcoholphosphotransferase | chr3:9295856-9298271 FORWARD LENGTH=389	368	389	0	105.7	85.1	92.4
Rsa1.0_00309.1.g11039.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00309.1.g11040.t2	gb|EOA23613.1| hypothetical protein CARUB_v10016813mg [Capsella rubella]	607	651	0	107.2	90.6	94.6	hypothetical protein CARUB_v10016813mg	gbpln	Capsella rubella	AT3G25560.1 | Symbols: NIK2 | NSP-interacting kinase 2 | chr3:9279682-9282560 REVERSE LENGTH=635	607	635	0	104.6	89.6	94.4
Rsa1.0_00309.1.g11041.t1	gb|ABD65060.1| hypothetical protein 27.t00039 [Brassica oleracea]	1468	1367	0	93.1	59.4	72.5	hypothetical protein 27.t00039	gbpln	Brassica oleracea	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	1468	344	2.00E-88	23.4	11.4	14.0
Rsa1.0_00310.1.g11042.t1	ref|XP_002873545.1| 17.6 kDa class II heat shock protein [Arabidopsis lyrata subsp. lyrata] gi|297319382|gb|EFH49804.1| 17.6 kDa class II heat shock protein [Arabidopsis lyrata subsp. lyrata]	155	154	1.00E-71	99.4	94.2	97.4	17.6 kDa class II heat shock protein	gbpln	Arabidopsis lyrata	AT5G12020.1 | Symbols: HSP17.6II | 17.6 kDa class II heat shock protein | chr5:3882409-3882876 REVERSE LENGTH=155	155	155	1.00E-72	100.0	94.2	97.4
Rsa1.0_00310.1.g11043.t1	ref|NP_191711.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75183498|sp|Q9M316.1|PP292_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g61520, mitochondrial; Flags: Precursor gi|6850843|emb|CAB71082.1| putative protein [Arabidopsis thaliana] gi|332646696|gb|AEE80217.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	766	766	0	100.0	73.0	83.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G61520.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:22768974-22771274 REVERSE LENGTH=766	766	766	0	100.0	73.0	83.8
Rsa1.0_00310.1.g11044.t1	gb|AFO66517.1| putative kinase [Brassica napus]	456	1266	0	277.6	83.1	90.8	putative kinase	gbpln	Brassica napus	AT5G12010.1 | Symbols: | unknown protein; INVOLVED IN: response to salt stress; LOCATED IN: chloroplast, plasma membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G29780.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3877975-3879483 REVERSE LENGTH=502	456	502	0	110.1	79.6	87.1
Rsa1.0_00310.1.g11045.t2	ref|XP_002873544.1| kinase [Arabidopsis lyrata subsp. lyrata] gi|297319381|gb|EFH49803.1| kinase [Arabidopsis lyrata subsp. lyrata]	892	700	0	78.5	62.8	69.3	kinase	gbpln	Arabidopsis lyrata	AT5G12000.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr5:3874151-3876780 REVERSE LENGTH=701	892	701	0	78.6	61.9	68.5
Rsa1.0_00310.1.g11046.t1	gb|AFO66519.1| putative ABC superfamily ATP binding cassette transporter [Brassica napus]	106	356	7.00E-40	335.8	77.4	84.0	putative ABC superfamily ATP binding cassette transporter	gbpln	Brassica napus	AT5G11970.1 | Symbols: | Protein of unknown function (DUF3511) | chr5:3863289-3863606 REVERSE LENGTH=105	106	105	5.00E-41	99.1	78.3	84.9
Rsa1.0_00310.1.g11047.t2	gb|EOA20897.1| hypothetical protein CARUB_v10001232mg, partial [Capsella rubella]	355	364	1.00E-178	102.5	92.7	94.9	hypothetical protein CARUB_v10001232mg, partial	gbpln	Capsella rubella	AT5G11960.1 | Symbols: | Protein of unknown function (DUF803) | chr5:3858852-3861462 REVERSE LENGTH=344	355	344	1.00E-177	96.9	91.8	94.1
Rsa1.0_00310.1.g11048.t1	ref|XP_002871507.1| hypothetical protein ARALYDRAFT_488037 [Arabidopsis lyrata subsp. lyrata] gi|297317344|gb|EFH47766.1| hypothetical protein ARALYDRAFT_488037 [Arabidopsis lyrata subsp. lyrata]	206	217	1.00E-112	105.3	97.6	99.0	hypothetical protein ARALYDRAFT_488037	gbpln	Arabidopsis lyrata	AT5G11950.2 | Symbols: | Putative lysine decarboxylase family protein | chr5:3855072-3856815 FORWARD LENGTH=216	206	216	1.00E-114	104.9	95.6	98.1

Rsa1.0_00310.1.g11049.t2	gb|ACP30564.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1214	1084	0	89.3	72.1	78.6	disease resistance protein	gbpln	Brassica rapa	AT5G36930.2 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:14567771-14571916 REVERSE LENGTH=1191	1214	1191	0	98.1	48.3	62.2
Rsa1.0_00310.1.g11050.t1	ref|XP_002871506.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317343|gb|EFH47765.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]	762	762	0	100.0	73.5	86.5	subtilase family protein	gbpln	Arabidopsis lyrata	AT5G11940.1 | Symbols: | Subtilase family protein | chr5:3849283-3852417 FORWARD LENGTH=762	762	762	0	100.0	72.8	86.6
Rsa1.0_00310.1.g11051.t1	ref|XP_002871506.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317343|gb|EFH47765.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]	760	762	0	100.3	74.2	86.2	subtilase family protein	gbpln	Arabidopsis lyrata	AT5G11940.1 | Symbols: | Subtilase family protein | chr5:3849283-3852417 FORWARD LENGTH=762	760	762	0	100.3	73.4	85.8
Rsa1.0_00310.1.g11052.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	427	1555	2.00E-72	364.2	33.3	46.8	disease resistance protein	gbpln	Brassica rapa	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	427	303	2.00E-41	71.0	25.5	36.1
Rsa1.0_00310.1.g11053.t1	gb|AFO66501.1| putative harpin-induced 1 [Brassica napus]	283	284	1.00E-123	100.4	89.0	91.9	putative harpin-induced 1	gbpln	Brassica napus	AT5G11890.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (TAIR:AT1G17620.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3831770-3832633 FORWARD LENGTH=287	283	287	1.00E-117	101.4	83.0	88.7
Rsa1.0_00310.1.g11054.t1	ref|NP_196746.2| sterile alpha motif and leucine zipper containing kinase AZK [Arabidopsis thaliana] gi|18700075|gb|AAL77650.1| AT5g11850/F14F18_20 [Arabidopsis thaliana] gi|332004344|gb|AED91727.1| protein kinase superfamily protein [Arabidopsis thaliana]	900	880	0	97.8	86.9	91.6	sterile alpha motif and leucine zipper containing kinase AZK	gbpln	Arabidopsis thaliana	AT5G11850.1 | Symbols: | Protein kinase superfamily protein | chr5:3816632-3821024 REVERSE LENGTH=880	900	880	0	97.8	86.9	91.6
Rsa1.0_00310.1.g11055.t1	ref|XP_002873531.1| hypothetical protein ARALYDRAFT_488020 [Arabidopsis lyrata subsp. lyrata] gi|297319368|gb|EFH49790.1| hypothetical protein ARALYDRAFT_488020 [Arabidopsis lyrata subsp. lyrata]	166	174	5.00E-64	104.8	71.1	80.1	hypothetical protein ARALYDRAFT_488020	gbpln	Arabidopsis lyrata	AT5G11830.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:3812520-3813044 REVERSE LENGTH=174	166	174	2.00E-65	104.8	69.3	80.7
Rsa1.0_00310.1.g11056.t1	ref|NP_196743.1| self-incompatibility S1 family protein [Arabidopsis thaliana] gi|7573396|emb|CAB87700.1| putative protein [Arabidopsis thaliana] gi|332004341|gb|AED91724.1| self-incompatibility S1 family protein [Arabidopsis thaliana]	172	175	3.00E-68	101.7	72.7	82.0	self-incompatibility S1 family protein	gbpln	Arabidopsis thaliana	AT5G11820.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:3810649-3811176 REVERSE LENGTH=175	172	175	1.00E-70	101.7	72.7	82.0
Rsa1.0_00310.1.g11057.t1	gb|EOA22292.1| hypothetical protein CARUB_v10002889mg [Capsella rubella]	581	596	0	102.6	87.1	91.4	hypothetical protein CARUB_v10002889mg	gbpln	Capsella rubella	AT5G11800.1 | Symbols: KEA6, ATKEA6 | K+ efflux antiporter 6 | chr5:3803635-3808069 REVERSE LENGTH=597	581	597	0	102.8	84.5	87.8
Rsa1.0_00310.1.g11058.t1	ref|NP_568251.1| protein N-MYC downregulated-like 2 [Arabidopsis thaliana] gi|13605684|gb|AAK32835.1|AF361823_1 AT5g11790/T22P22_180 [Arabidopsis thaliana] gi|16323346|gb|AAL15386.1| AT5g11790/T22P22_180 [Arabidopsis thaliana] gi|332004338|gb|AED91721.1| protein N-MYC downregulated-like 2 [Arabidopsis thaliana]	344	344	0	100.0	95.1	97.1	protein N-MYC downregulated-like 2	gbpln	Arabidopsis thaliana	AT5G11790.1 | Symbols: NDL2 | N-MYC downregulated-like 2 | chr5:3799682-3802496 FORWARD LENGTH=344	344	344	0	100.0	95.1	97.1
Rsa1.0_00311.1.g11059.t1	ref|XP_002863417.1| hypothetical protein ARALYDRAFT_916814 [Arabidopsis lyrata subsp. lyrata] gi|297309252|gb|EFH39676.1| hypothetical protein ARALYDRAFT_916814 [Arabidopsis lyrata subsp. lyrata]	778	791	0	101.7	90.6	95.8	hypothetical protein ARALYDRAFT_916814	gbpln	Arabidopsis lyrata	AT5G46210.1 | Symbols: CUL4, ATCUL4 | cullin4 | chr5:18731569-18736653 REVERSE LENGTH=792	778	792	0	101.8	90.0	95.0
Rsa1.0_00311.1.g11060.t1	ref|XP_002865203.1| hypothetical protein ARALYDRAFT_494352 [Arabidopsis lyrata subsp. lyrata] gi|297311038|gb|EFH41462.1| hypothetical protein ARALYDRAFT_494352 [Arabidopsis lyrata subsp. lyrata]	465	462	0	99.4	85.2	92.9	hypothetical protein ARALYDRAFT_494352	gbpln	Arabidopsis lyrata	AT5G46220.1 | Symbols: | Protein of unknown function (DUF616) | chr5:18738827-18741964 FORWARD LENGTH=462	465	462	0	99.4	83.9	91.6

Rsa1.0_00311.1.g11061.t1	gb|EOA14036.1| hypothetical protein CARUB_v10027170mg [Capsella rubella]	141	197	2.00E-64	139.7	82.3	92.9	hypothetical protein CARUB_v10027170mg	gbpln	Capsella rubella	AT5G46230.1 | Symbols: | Protein of unknown function, DUF538 | chr5:18742593-18743024 REVERSE LENGTH=143	141	143	2.00E-63	101.4	78.7	88.7
Rsa1.0_00311.1.g11062.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1400	1501	0	107.2	60.6	75.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1400	1262	1.00E-142	90.1	16.9	23.6
Rsa1.0_00311.1.g11063.t1	ref|XP_002863413.1| hypothetical protein ARALYDRAFT_494345 [Arabidopsis lyrata subsp. lyrata] gi|297309248|gb|EFH39672.1| hypothetical protein ARALYDRAFT_494345 [Arabidopsis lyrata subsp. lyrata]	776	776	0	100.0	93.0	96.9	hypothetical protein ARALYDRAFT_494345	gbpln	Arabidopsis lyrata	AT5G46280.1 | Symbols: MCM3 | Minichromosome maintenance (MCM2/3/5) family protein | chr5:18769902-18773606 REVERSE LENGTH=776	776	776	0	100.0	91.9	96.0
Rsa1.0_00311.1.g11064.t1	ref|NP_199441.1| 3-oxoacyl-[acyl-carrier-protein] synthase I [Arabidopsis thaliana] gi|20141399|sp|P52410.2|KASC1_ARATH RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic; AltName: Full=Beta-ketoacyl-ACP synthase I; Short=KAS I; Flags: Precursor gi|10177710|dbj|BAB11084.1| 3-oxoacyl-[acyl-carrier-protein] synthase I precursor [Arabidopsis thaliana] gi|14335164|gb|AAK59862.1| AT5g46290/MPL12_7 [Arabidopsis thaliana] gi|20334810|gb|AAM16266.1| AT5g46290/MPL12_7 [Arabidopsis thaliana] gi|21593429|gb|AAM65396.1| 3-oxoacyl-(acyl-carrier-protein) synthase I precursor (beta-ketoacyl-acp synthase I) (KAS I) [Arabidopsis thaliana] gi|21703101|gb|AAM74493.1| AT5g46290/MPL12_7 [Arabidopsis thaliana] gi|332007980|gb|AED95363.1| 3-oxoacyl-[acyl-carrier-protein] synthase I [Arabidopsis thaliana]	493	473	0	95.9	86.4	86.8	3-oxoacyl-	gbpln	Arabidopsis thaliana	AT5G46290.1 | Symbols: KASI, KAS1 | 3-ketoacyl-acyl carrier protein synthase I | chr5:18774439-18776629 REVERSE LENGTH=473	493	473	0	95.9	86.4	86.8
Rsa1.0_00311.1.g11065.t1	ref|XP_002877500.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323338|gb|EFH53759.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	121	136	4.00E-12	112.4	25.6	40.5	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00311.1.g11066.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00311.1.g11067.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00311.1.g11068.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00311.1.g11069.t1	gb|EOA26027.1| hypothetical protein CARUB_v10019435mg [Capsella rubella]	333	595	6.00E-44	178.7	28.5	39.0	hypothetical protein CARUB_v10019435mg	gbpln	Capsella rubella	AT1G47350.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:17358447-17360722 REVERSE LENGTH=528	333	528	4.00E-13	158.6	11.1	16.8
Rsa1.0_00311.1.g11070.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00311.1.g11071.t1	gb|ACI14410.1| WRKY8-1 transcription factor [Brassica napus]	576	321	3.00E-77	55.7	25.7	29.2	WRKY8-1 transcription factor	gbpln	Brassica napus	AT5G46350.1 | Symbols: WRKY8, ATWRKY8 | WRKY DNA-binding protein 8 | chr5:18801403-18803901 REVERSE LENGTH=326	576	326	2.00E-71	56.6	25.3	29.9
Rsa1.0_00311.1.g11072.t1	dbj|BAB10743.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	858	1109	0	129.3	51.6	67.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	858	1262	1.00E-138	147.1	27.0	37.6
Rsa1.0_00312.1.g11073.t1	ref|XP_002870430.1| tRNA pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297316266|gb|EFH46689.1| tRNA pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	409	420	0	102.7	86.3	91.9	tRNA pseudouridine synthase family protein	gbpln	Arabidopsis lyrata	AT5G35400.1 | Symbols: | Pseudouridine synthase family protein | chr5:13599416-13602240 REVERSE LENGTH=420	409	420	0	102.7	84.4	91.2
Rsa1.0_00312.1.g11074.t1	ref|NP_198389.2| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|263505488|sp|C0LGU0.1|RLK_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase RLK; Flags: Precursor gi|224589687|gb|ACN59375.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332006579|gb|AED93962.1| probable LRR receptor-like serine/threonine-protein kinase RLK [Arabidopsis thaliana]	677	662	0	97.8	76.8	85.1	leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT5G35390.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:13596918-13598976 FORWARD LENGTH=662	677	662	0	97.8	76.8	85.1

Rsa1.0_00312.1.g11075.t1	ref|XP_002870429.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297316265|gb|EFH46688.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	716	737	0	102.9	79.1	87.7	kinase family protein	gbpln	Arabidopsis lyrata	AT5G35380.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr5:13593429-13596293 REVERSE LENGTH=731	716	731	0	102.1	78.1	87.2
Rsa1.0_00312.1.g11076.t2	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	1212	1123	0	92.7	52.9	58.6	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1212	1262	2.00E-57	104.1	13.5	21.0
Rsa1.0_00312.1.g11077.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00312.1.g11078.t3	ref|XP_002869784.1| hypothetical protein ARALYDRAFT_492546 [Arabidopsis lyrata subsp. lyrata] gi|297315620|gb|EFH46043.1| hypothetical protein ARALYDRAFT_492546 [Arabidopsis lyrata subsp. lyrata]	500	662	1.00E-152	132.4	51.4	56.2	hypothetical protein ARALYDRAFT_492546	gbpln	Arabidopsis lyrata	AT4G23180.1 | Symbols: CRK10, RLK4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 | chr4:12138171-12140780 FORWARD LENGTH=669	500	669	1.00E-155	133.8	51.0	56.4
Rsa1.0_00312.1.g11079.t1	ref|XP_002870426.1| hypothetical protein ARALYDRAFT_915661 [Arabidopsis lyrata subsp. lyrata] gi|297316262|gb|EFH46685.1| hypothetical protein ARALYDRAFT_915661 [Arabidopsis lyrata subsp. lyrata]	260	278	2.00E-93	106.9	65.8	76.5	hypothetical protein ARALYDRAFT_915661	gbpln	Arabidopsis lyrata	AT5G35330.3 | Symbols: MBD02 | methyl-CPG-binding domain protein 02 | chr5:13523725-13525270 REVERSE LENGTH=272	260	272	3.00E-94	104.6	65.0	76.2
Rsa1.0_00312.1.g11080.t1	ref|XP_002870422.1| hypothetical protein ARALYDRAFT_915653 [Arabidopsis lyrata subsp. lyrata] gi|297316258|gb|EFH46681.1| hypothetical protein ARALYDRAFT_915653 [Arabidopsis lyrata subsp. lyrata]	560	547	0	97.7	86.4	89.8	hypothetical protein ARALYDRAFT_915653	gbpln	Arabidopsis lyrata	AT5G35200.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr5:13462463-13465581 REVERSE LENGTH=544	560	544	0	97.1	85.9	89.8
Rsa1.0_00312.1.g11081.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00312.1.g11082.t20	ref|XP_002868408.1| adenylate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314244|gb|EFH44667.1| adenylate kinase family protein [Arabidopsis lyrata subsp. lyrata]	457	595	0	130.2	91.2	95.6	adenylate kinase family protein	gbpln	Arabidopsis lyrata	AT5G35170.1 | Symbols: | adenylate kinase family protein | chr5:13419278-13423482 FORWARD LENGTH=588	457	588	0	128.7	90.2	95.2
Rsa1.0_00312.1.g11083.t1	gb|AFK13856.1| Ty3/gypsy retrotransposon protein [Beta vulgaris subsp. vulgaris]	1579	1631	0	103.3	46.5	62.9	Ty3/gypsy retrotransposon protein	gbpln	Beta vulgaris	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1579	158	2.00E-37	10.0	4.6	6.0
Rsa1.0_00313.1.g11084.t1	ref|XP_002876359.1| hypothetical protein ARALYDRAFT_348712 [Arabidopsis lyrata subsp. lyrata] gi|297322197|gb|EFH52618.1| hypothetical protein ARALYDRAFT_348712 [Arabidopsis lyrata subsp. lyrata]	290	362	1.00E-122	124.8	71.0	83.4	hypothetical protein ARALYDRAFT_348712	gbpln	Arabidopsis lyrata	AT2G40580.1 | Symbols: | Protein kinase superfamily protein | chr2:16943964-16944899 FORWARD LENGTH=311	290	311	1.00E-44	107.2	39.3	55.9
Rsa1.0_00313.1.g11085.t2	ref|XP_002878078.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323916|gb|EFH54337.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	524	602	0	114.9	72.7	84.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G56320.1 | Symbols: | PAP/OAS1 substrate-binding domain superfamily | chr3:20886193-20888624 REVERSE LENGTH=603	524	603	0	115.1	72.5	83.8
Rsa1.0_00313.1.g11086.t1	gb|EOA28112.1| hypothetical protein CARUB_v10024308mg [Capsella rubella]	175	131	2.00E-60	74.9	65.1	65.7	hypothetical protein CARUB_v10024308mg	gbpln	Capsella rubella	AT2G40510.1 | Symbols: | Ribosomal protein S26e family protein | chr2:16918506-16919623 FORWARD LENGTH=133	175	133	9.00E-63	76.0	65.1	65.7
Rsa1.0_00313.1.g11087.t1	ref|XP_002876363.1| hypothetical protein ARALYDRAFT_907078 [Arabidopsis lyrata subsp. lyrata] gi|297322201|gb|EFH52622.1| hypothetical protein ARALYDRAFT_907078 [Arabidopsis lyrata subsp. lyrata]	224	233	5.00E-82	104.0	79.0	86.6	hypothetical protein ARALYDRAFT_907078	gbpln	Arabidopsis lyrata	AT3G56360.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G05250.1); Has 45 Blast hits to 45 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:20896641-20897342 FORWARD LENGTH=233	224	233	1.00E-81	104.0	76.8	86.2

Rsa1.0_00313.1.g11088.t1	ref|NP_567037.1| two-component response regulator ARR17 [Arabidopsis thaliana] gi|51316089|sp|Q9FPR6.1|ARR17_ARATH RecName: Full=Two-component response regulator ARR17 gi|11870071|gb|AAG40613.1|AF305722_1 response regulator 17 [Arabidopsis thaliana] gi|332645994|gb|AEE79515.1| two-component response regulator ARR17 [Arabidopsis thaliana]	127	153	3.00E-54	120.5	89.8	93.7	two-component response regulator ARR17	gbpln	Arabidopsis thaliana	AT3G56380.1 | Symbols: ARR17, RR17 | response regulator 17 | chr3:20905480-20906368 FORWARD LENGTH=153	127	153	6.00E-57	120.5	89.8	93.7
Rsa1.0_00313.1.g11089.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00313.1.g11090.t2	ref|XP_002876365.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322203|gb|EFH52624.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	260	268	4.00E-79	103.1	64.2	74.6	predicted protein	gbpln	Arabidopsis lyrata	AT2G40740.1 | Symbols: WRKY55, ATWRKY55 | WRKY DNA-binding protein 55 | chr2:16997177-16999276 FORWARD LENGTH=292	260	292	3.00E-62	112.3	55.4	69.2
Rsa1.0_00313.1.g11091.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00313.1.g11092.t1	gb|ACQ76810.1| WRKY transcription factor 70 [Brassica napus]	268	276	1.00E-107	103.0	77.6	86.6	WRKY transcription factor 70	gbpln	Brassica napus	AT3G56400.1 | Symbols: WRKY70, ATWRKY70 | WRKY DNA-binding protein 70 | chr3:20909082-20910409 REVERSE LENGTH=294	268	294	5.00E-93	109.7	67.2	78.7
Rsa1.0_00313.1.g11093.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00313.1.g11094.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	447	1142	1.00E-113	255.5	48.3	64.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	447	575	1.00E-36	128.6	28.4	47.9
Rsa1.0_00313.1.g11095.t1	gb|EOA24904.1| hypothetical protein CARUB_v10018194mg [Capsella rubella]	130	147	5.00E-67	113.1	96.9	99.2	hypothetical protein CARUB_v10018194mg	gbpln	Capsella rubella	AT3G56490.1 | Symbols: HIT3, HINT1 | HIS triad family protein 3 | chr3:20941532-20943129 FORWARD LENGTH=147	130	147	1.00E-69	113.1	97.7	98.5
Rsa1.0_00313.1.g11096.t1	ref|NP_191209.1| serine-rich protein-like protein [Arabidopsis thaliana] gi|7594528|emb|CAB88053.1| putative protein [Arabidopsis thaliana] gi|332646007|gb|AEE79528.1| serine-rich protein-like protein [Arabidopsis thaliana]	111	110	2.00E-37	99.1	77.5	81.1	serine-rich protein-like protein	gbpln	Arabidopsis thaliana	AT3G56500.1 | Symbols: | serine-rich protein-related | chr3:20943638-20943970 FORWARD LENGTH=110	111	110	3.00E-40	99.1	77.5	81.1
Rsa1.0_00313.1.g11097.t1	ref|XP_002878090.1| hypothetical protein ARALYDRAFT_486092 [Arabidopsis lyrata subsp. lyrata] gi|297323928|gb|EFH54349.1| hypothetical protein ARALYDRAFT_486092 [Arabidopsis lyrata subsp. lyrata]	151	256	2.00E-20	169.5	32.5	34.4	hypothetical protein ARALYDRAFT_486092	gbpln	Arabidopsis lyrata	AT3G56510.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:20944348-20946235 REVERSE LENGTH=257	151	257	2.00E-21	170.2	31.1	33.8
Rsa1.0_00313.1.g11098.t1	ref|XP_002878093.1| hypothetical protein ARALYDRAFT_486095 [Arabidopsis lyrata subsp. lyrata] gi|297323931|gb|EFH54352.1| hypothetical protein ARALYDRAFT_486095 [Arabidopsis lyrata subsp. lyrata]	538	301	1.00E-53	55.9	20.4	24.7	hypothetical protein ARALYDRAFT_486095	gbpln	Arabidopsis lyrata	AT3G56530.1 | Symbols: anac064, NAC064 | NAC domain containing protein 64 | chr3:20948911-20950045 REVERSE LENGTH=319	538	319	1.00E-50	59.3	21.9	26.4
Rsa1.0_00313.1.g11099.t1	#	#	#	#	#	#	#	–	----	----	AT1G75950.1 | Symbols: SKP1, ASK1, ATSKP1, SKP1A, UIP1 | S phase kinase-associated protein 1 | chr1:28516715-28517454 FORWARD LENGTH=160	128	160	8.00E-13	125.0	26.6	28.1
Rsa1.0_00313.1.g11100.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00314.1.g11101.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00314.1.g11102.t1	dbj|BAD11207.1| multidrug resistance-associated protein [Thlaspi caerulescens]	1496	1514	0	101.2	88.6	92.8	multidrug resistance-associated protein	gbpln	Thlaspi caerulescens	AT3G13080.1 | Symbols: ATMRP3, MRP3, ABCC3 | multidrug resistance-associated protein 3 | chr3:4196019-4201250 REVERSE LENGTH=1514	1496	1514	0	101.2	86.8	92.4
Rsa1.0_00314.1.g11103.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00314.1.g11104.t1	ref|XP_002884940.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330780|gb|EFH61199.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	661	660	0	99.8	88.7	92.6	CBS domain-containing protein	gbpln	Arabidopsis lyrata	AT3G13070.1 | Symbols: | CBS domain-containing protein / transporter associated domain-containing protein | chr3:4191511-4195112 REVERSE LENGTH=661	661	661	0	100.0	89.6	92.6
Rsa1.0_00314.1.g11105.t1	ref|NP_566443.1| lipid-binding START domain-containing protein [Arabidopsis thaliana] gi|14334998|gb|AAK59763.1| At3g13062 [Arabidopsis thaliana] gi|22137180|gb|AAM91435.1| At3g13062 [Arabidopsis thaliana] gi|332641767|gb|AEE75288.1| lipid-binding START domain-containing protein [Arabidopsis thaliana]	478	403	1.00E-177	84.3	60.0	64.0	lipid-binding START domain-containing protein	gbpln	Arabidopsis thaliana	AT3G13062.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr3:4184777-4186795 FORWARD LENGTH=403	478	403	1.00E-180	84.3	60.0	64.0

Rsa1.0_00314.1.g11106.t1	ref|XP_002879596.1| 40S ribosomal protein S14 [Arabidopsis lyrata subsp. lyrata] gi|297325435|gb|EFH55855.1| 40S ribosomal protein S14 [Arabidopsis lyrata subsp. lyrata]	188	151	3.00E-17	80.3	25.5	26.6	40S ribosomal protein S14	gbpln	Arabidopsis lyrata	AT3G11510.1 | Symbols: | Ribosomal protein S11 family protein | chr3:3623757-3624866 REVERSE LENGTH=150	188	150	1.00E-19	79.8	25.5	26.6
Rsa1.0_00314.1.g11107.t1	gb|EOA32797.1| hypothetical protein CARUB_v10016107mg [Capsella rubella]	502	500	0	99.6	83.9	90.8	hypothetical protein CARUB_v10016107mg	gbpln	Capsella rubella	AT3G13050.1 | Symbols: | Major facilitator superfamily protein | chr3:4176866-4178868 FORWARD LENGTH=500	502	500	0	99.6	83.7	90.6
Rsa1.0_00314.1.g11108.t1	gb|EOA30570.1| hypothetical protein CARUB_v10013698mg [Capsella rubella]	431	446	1.00E-177	103.5	79.6	86.5	hypothetical protein CARUB_v10013698mg	gbpln	Capsella rubella	AT3G13040.2 | Symbols: | myb-like HTH transcriptional regulator family protein | chr3:4172415-4174456 REVERSE LENGTH=449	431	449	1.00E-176	104.2	79.4	86.3
Rsa1.0_00314.1.g11109.t1	ref|NP_187908.1| hAT dimerization domain-containing protein [Arabidopsis thaliana] gi|15795134|dbj|BAB02512.1| transposase-like protein [Arabidopsis thaliana] gi|332641756|gb|AEE75277.1| hAT dimerization domain-containing protein [Arabidopsis thaliana]	590	605	0	102.5	60.5	75.9	hAT dimerization domain-containing protein	gbpln	Arabidopsis thaliana	AT3G13020.1 | Symbols: | hAT transposon superfamily protein | chr3:4166995-4168917 REVERSE LENGTH=605	590	605	0	102.5	60.5	75.9
Rsa1.0_00314.1.g11110.t1	dbj|BAJ33667.1| unnamed protein product [Thellungiella halophila]	575	590	0	102.6	89.2	93.0	unnamed protein product	----	----	AT3G13000.2 | Symbols: | Protein of unknown function, DUF547 | chr3:4158214-4160989 REVERSE LENGTH=582	575	582	0	101.2	87.7	92.7
Rsa1.0_00314.1.g11111.t1	ref|XP_002882800.1| histone acetyltransferase 5 [Arabidopsis lyrata subsp. lyrata] gi|297328640|gb|EFH59059.1| histone acetyltransferase 5 [Arabidopsis lyrata subsp. lyrata]	1649	1657	0	100.5	81.4	87.1	histone acetyltransferase 5	gbpln	Arabidopsis lyrata	AT3G12980.1 | Symbols: HAC5, ATHPCAT4 | histone acetyltransferase of the CBP family 5 | chr3:4146919-4154495 FORWARD LENGTH=1670	1649	1670	0	101.3	80.8	87.5
Rsa1.0_00314.1.g11112.t1	ref|NP_001030683.2| no apical meristem-domain containing transcriptional regulator [Arabidopsis thaliana] gi|15795128|dbj|BAB02506.1| NAM (no apical meristem) protein-like [Arabidopsis thaliana] gi|332641748|gb|AEE75269.1| no apical meristem-domain containing transcriptional regulator [Arabidopsis thaliana]	275	279	1.00E-125	101.5	79.6	86.9	no apical meristem-domain containing transcriptional regulator	gbpln	Arabidopsis thaliana	AT3G12977.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr3:4143832-4145860 FORWARD LENGTH=279	275	279	1.00E-128	101.5	79.6	86.9
Rsa1.0_00314.1.g11113.t1	ref|XP_002884935.1| hypothetical protein ARALYDRAFT_897507 [Arabidopsis lyrata subsp. lyrata] gi|297330775|gb|EFH61194.1| hypothetical protein ARALYDRAFT_897507 [Arabidopsis lyrata subsp. lyrata]	325	385	3.00E-97	118.5	72.6	79.1	hypothetical protein ARALYDRAFT_897507	gbpln	Arabidopsis lyrata	AT3G12970.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G56020.1); Has 2408 Blast hits to 418 proteins in 91 species: Archae - 0; Bacteria - 41; Metazoa - 198; Fungi - 63; Plants - 125; Viruses - 13; Other Eukaryotes - 1968 (source: NCBI BLink). | chr3:4141329-4142474 REVERSE LENGTH=381	325	381	2.00E-99	117.2	74.5	80.0
Rsa1.0_00314.1.g11114.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00314.1.g11115.t1	ref|XP_002884932.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330772|gb|EFH61191.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	342	333	1.00E-135	97.4	74.0	81.9	protein binding protein	gbpln	Arabidopsis lyrata	AT3G12920.1 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr3:4122127-4123323 REVERSE LENGTH=335	342	335	1.00E-137	98.0	73.7	82.2
Rsa1.0_00314.1.g11116.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00314.1.g11117.t1	ref|XP_002882795.1| transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297328635|gb|EFH59054.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	304	303	1.00E-142	99.7	83.6	89.5	transcription factor	gbpln	Arabidopsis lyrata	AT3G12910.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr3:4109417-4110648 FORWARD LENGTH=303	304	303	1.00E-140	99.7	81.3	87.8
Rsa1.0_00314.1.g11118.t1	ref|XP_002882794.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297328634|gb|EFH59053.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	360	357	0	99.2	86.9	93.1	oxidoreductase	gbpln	Arabidopsis lyrata	AT3G12900.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:4104576-4106112 FORWARD LENGTH=357	360	357	0	99.2	85.3	92.2
Rsa1.0_00314.1.g11119.t1	ref|XP_002882793.1| hypothetical protein ARALYDRAFT_478650 [Arabidopsis lyrata subsp. lyrata] gi|297328633|gb|EFH59052.1| hypothetical protein ARALYDRAFT_478650 [Arabidopsis lyrata subsp. lyrata]	250	251	1.00E-113	100.4	80.0	88.4	hypothetical protein ARALYDRAFT_478650	gbpln	Arabidopsis lyrata	AT3G12890.1 | Symbols: ASML2 | activator of spomin::LUC2 | chr3:4099223-4100277 FORWARD LENGTH=251	250	251	1.00E-114	100.4	78.8	87.2
Rsa1.0_00315.1.g11120.t1	gb|EOA27345.1| hypothetical protein CARUB_v10023459mg [Capsella rubella]	284	372	1.00E-126	131.0	85.9	90.8	hypothetical protein CARUB_v10023459mg	gbpln	Capsella rubella	AT2G46590.2 | Symbols: DAG2 | Dof-type zinc finger DNA-binding family protein | chr2:19133166-19134905 FORWARD LENGTH=369	284	369	1.00E-115	129.9	85.2	90.5

<table>
<tr><td>Rsa1.0_00315.1.g11121.t4</td><td>ref|NP_182185.2| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|330255636|gb|AEC10730.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana]</td><td>483</td><td>491</td><td>0</td><td>101.7</td><td>86.5</td><td>91.7</td><td>P-loop containing nucleoside triphosphate hydrolase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46620.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:19139071-19140546 REVERSE LENGTH=491</td><td>483</td><td>491</td><td>0</td><td>101.7</td><td>86.5</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00315.1.g11122.t1</td><td>ref|NP_182186.1| uncharacterized protein [Arabidopsis thaliana] gi|3831447|gb|AAC69930.1| putative extensin [Arabidopsis thaliana] gi|20197778|gb|AAM15241.1| putative extensin [Arabidopsis thaliana] gi|330255637|gb|AEC10731.1| uncharacterized protein AT2G46630 [Arabidopsis thaliana]</td><td>372</td><td>394</td><td>1.00E-101</td><td>105.9</td><td>73.1</td><td>79.0</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46630.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 110095 Blast hits to 59224 proteins in 2216 species: Archae - 177; Bacteria - 15429; Metazoa - 38345; Fungi - 18843; Plants - 13341; Viruses - 3084; Other Eukaryotes - 20876 (source: NCBI BLink). | chr2:19145529-19146713 FORWARD LENGTH=394</td><td>372</td><td>394</td><td>1.00E-103</td><td>105.9</td><td>73.1</td><td>79.0</td></tr>
<tr><td>Rsa1.0_00315.1.g11123.t1</td><td>ref|NP_001078070.1| uncharacterized protein [Arabidopsis thaliana] gi|330255639|gb|AEC10733.1| uncharacterized protein AT2G46640 [Arabidopsis thaliana]</td><td>268</td><td>281</td><td>2.00E-88</td><td>104.9</td><td>69.4</td><td>79.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46640.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 11 growth stages; Has 26 Blast hits to 26 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:19148792-19150751 FORWARD LENGTH=281</td><td>268</td><td>281</td><td>6.00E-91</td><td>104.9</td><td>69.4</td><td>79.9</td></tr>
<tr><td>Rsa1.0_00315.1.g11124.t1</td><td>ref|XP_002880257.1| B5 #1 [Arabidopsis lyrata subsp. lyrata] gi|297326096|gb|EFH56516.1| B5 #1 [Arabidopsis lyrata subsp. lyrata]</td><td>134</td><td>132</td><td>6.00E-63</td><td>98.5</td><td>86.6</td><td>91.8</td><td>B5 #1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46650.1 | Symbols: B5 #1, ATCB5-C, CB5-C | cytochrome B5 isoform C | chr2:19151807-19152394 FORWARD LENGTH=132</td><td>134</td><td>132</td><td>9.00E-59</td><td>98.5</td><td>86.6</td><td>92.5</td></tr>
<tr><td>Rsa1.0_00315.1.g11125.t1</td><td>ref|XP_002882080.1| CYP78A6 [Arabidopsis lyrata subsp. lyrata] gi|297327919|gb|EFH58339.1| CYP78A6 [Arabidopsis lyrata subsp. lyrata]</td><td>449</td><td>530</td><td>0</td><td>118.0</td><td>91.1</td><td>95.5</td><td>CYP78A6</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46660.1 | Symbols: CYP78A6 | cytochrome P450, family 78, subfamily A, polypeptide 6 | chr2:19153602-19155417 REVERSE LENGTH=530</td><td>449</td><td>530</td><td>0</td><td>118.0</td><td>90.4</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00315.1.g11126.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT5G64840.1 | Symbols: GCN5, ATGCN5 | general control non-repressible 5 | chr5:25916956-25919693 REVERSE LENGTH=692</td><td>91</td><td>692</td><td>7.00E-11</td><td>760.4</td><td>35.2</td><td>39.6</td></tr>
<tr><td>Rsa1.0_00315.1.g11127.t1</td><td>ref|NP_182191.1| homeobox-leucine zipper protein ATHB-7 [Arabidopsis thaliana] gi|21431751|sp|P46897.2|ATHB7_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-7; AltName: Full=HD-ZIP protein ATHB-7; AltName: Full=Homeodomain transcription factor ATHB-7 gi|3831442|gb|AAC69925.1| homeodomain transcription factor (ATHB-7) [Arabidopsis thaliana] gi|15027939|gb|AAK76500.1| putative homeodomain transcription factor ATHB-7 [Arabidopsis thaliana] gi|20259175|gb|AAM14303.1| putative homeodomain transcription factor protein ATHB-7 [Arabidopsis thaliana] gi|330255645|gb|AEC10739.1| homeobox-leucine zipper protein ATHB-7 [Arabidopsis thaliana]</td><td>255</td><td>258</td><td>1.00E-107</td><td>101.2</td><td>81.2</td><td>86.3</td><td>homeobox-leucine zipper protein ATHB-7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46680.1 | Symbols: ATHB-7, ATHB7, HB-7 | homeobox 7 | chr2:19165777-19166773 REVERSE LENGTH=258</td><td>255</td><td>258</td><td>1.00E-110</td><td>101.2</td><td>81.2</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00315.1.g11128.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00315.1.g11129.t1</td><td>gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]</td><td>1788</td><td>1213</td><td>0</td><td>67.8</td><td>24.0</td><td>35.2</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1788</td><td>626</td><td>5.00E-78</td><td>35.0</td><td>8.2</td><td>12.8</td></tr>
<tr><td>Rsa1.0_00315.1.g11130.t1</td><td>ref|XP_002880259.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297326098|gb|EFH56518.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]</td><td>122</td><td>121</td><td>7.00E-58</td><td>99.2</td><td>89.3</td><td>92.6</td><td>auxin-responsive family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46690.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:19180904-19181269 FORWARD LENGTH=121</td><td>122</td><td>121</td><td>2.00E-60</td><td>99.2</td><td>89.3</td><td>93.4</td></tr>
<tr><td>Rsa1.0_00315.1.g11131.t2</td><td>ref|XP_002880260.1| hypothetical protein ARALYDRAFT_483835 [Arabidopsis lyrata subsp. lyrata] gi|297326099|gb|EFH56519.1| hypothetical protein ARALYDRAFT_483835 [Arabidopsis lyrata subsp. lyrata]</td><td>468</td><td>455</td><td>0</td><td>97.2</td><td>81.4</td><td>88.0</td><td>hypothetical protein ARALYDRAFT_483835</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46710.1 | Symbols: | Rho GTPase activating protein with PAK-box/P21-Rho-binding domain | chr2:19192105-19194656 FORWARD LENGTH=455</td><td>468</td><td>455</td><td>0</td><td>97.2</td><td>80.8</td><td>88.0</td></tr>
<tr><td>Rsa1.0_00315.1.g11132.t1</td><td>gb|EOA28887.1| hypothetical protein CARUB_v10025132mg, partial [Capsella rubella]</td><td>600</td><td>469</td><td>0</td><td>78.2</td><td>68.2</td><td>72.5</td><td>hypothetical protein CARUB_v10025132mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G46720.1 | Symbols: HIC, KCS13 | 3-ketoacyl-CoA synthase 13 | chr2:19198821-19200221 FORWARD LENGTH=466</td><td>600</td><td>466</td><td>0</td><td>77.7</td><td>68.0</td><td>72.8</td></tr>
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Rsa1.0_00315.1.g11133.t1	emb|CAZ68131.1| FAD-binding domain-containing protein [Arabidopsis halleri subsp. halleri]	591	594	0	100.5	85.4	90.7	FAD-binding domain-containing protein	gbpln	Arabidopsis halleri	AT2G46740.1 | Symbols: | D-arabinono-1,4-lactone oxidase family protein | chr2:19205182-19207455 REVERSE LENGTH=590	591	590	0	99.8	84.9	90.2
Rsa1.0_00316.1.g11134.t1	gb|ACQ76807.1| WRKY transcription factor 42 [Brassica napus]	519	519	0	100.0	92.5	96.0	WRKY transcription factor 42	gbpln	Brassica napus	AT4G04450.1 | Symbols: WRKY42, AtWRKY42 | WRKY family transcription factor | chr4:2218379-2221113 FORWARD LENGTH=528	519	528	0	101.7	76.9	83.8
Rsa1.0_00316.1.g11135.t1	ref|NP_192345.4| uncharacterized protein [Arabidopsis thaliana] gi|332656984|gb|AEE82384.1| uncharacterized protein AT4G04360 [Arabidopsis thaliana]	179	176	3.00E-81	98.3	89.4	91.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G04360.1 | Symbols: | Protein of unknown function (DUF1068) | chr4:2133142-2133866 REVERSE LENGTH=176	179	176	1.00E-83	98.3	89.4	91.6
Rsa1.0_00316.1.g11136.t1	ref|NP_192344.1| leucyl-tRNA synthetase [Arabidopsis thaliana] gi|4982478|gb|AAD36946.1|AF069441_6 putative leucyl tRNA synthetase [Arabidopsis thaliana] gi|7267192|emb|CAB77903.1| putative leucyl tRNA synthetase [Arabidopsis thaliana] gi|19310531|gb|AAL84999.1| AT4g04350/T19B17_7 [Arabidopsis thaliana] gi|25090241|gb|AAN72260.1| At4g04350/T19B17_7 [Arabidopsis thaliana] gi|332656983|gb|AEE82383.1| tRNA synthetase class I (I, L, M and V) family protein [Arabidopsis thaliana]	964	973	0	100.9	92.2	95.7	leucyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT4G04350.1 | Symbols: EMB2369 | tRNA synthetase class I (I, L, M and V) family protein | chr4:2128129-2133030 FORWARD LENGTH=973	964	973	0	100.9	92.2	95.7
Rsa1.0_00316.1.g11137.t1	#	#	#	#	#	#	#	-	----	----	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	235	422	6.00E-11	179.6	12.3	16.6
Rsa1.0_00316.1.g11138.t1	ref|NP_189112.1| uncharacterized protein [Arabidopsis thaliana] gi|9279797|dbj|BAB01218.1| unnamed protein product [Arabidopsis thaliana] gi|332643415|gb|AEE76936.1| uncharacterized protein AT3G24690 [Arabidopsis thaliana]	156	158	1.00E-44	101.3	70.5	81.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G24690.1 | Symbols: | BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT1G27090.1); Has 51 Blast hits to 50 proteins in 15 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:9020738-9021290 FORWARD LENGTH=158	156	158	4.00E-47	101.3	70.5	81.4
Rsa1.0_00316.1.g11139.t1	gb|EOA20015.1| hypothetical protein CARUB_v10000278mg [Capsella rubella]	771	772	0	100.1	89.0	95.3	hypothetical protein CARUB_v10000278mg	gbpln	Capsella rubella	AT4G04340.1 | Symbols: | ERD (early-responsive to dehydration stress) family protein | chr4:2123235-2126624 FORWARD LENGTH=772	771	772	0	100.1	88.3	95.5
Rsa1.0_00316.1.g11140.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00316.1.g11141.t6	ref|NP_192341.2| malonyl-CoA decarboxylase [Arabidopsis thaliana] gi|30794100|gb|AAP40492.1| putative malonyl-CoA decarboxylase [Arabidopsis thaliana] gi|110739288|dbj|BAF01557.1| malonyl-CoA decarboxylase like protein [Arabidopsis thaliana] gi|332656977|gb|AEE82377.1| malonyl-CoA decarboxylase [Arabidopsis thaliana]	601	518	0	86.2	76.9	80.0	malonyl-CoA decarboxylase	gbpln	Arabidopsis thaliana	AT4G04320.1 | Symbols: | malonyl-CoA decarboxylase family protein | chr4:2113565-2116525 FORWARD LENGTH=518	601	518	0	86.2	76.9	80.0
Rsa1.0_00316.1.g11142.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00316.1.g11143.t1	ref|NP_198403.1| 40S ribosomal protein S3-3 [Arabidopsis thaliana] gi|75170994|sp|Q9FJA6.1|RS33_ARATH RecName: Full=40S ribosomal protein S3-3 gi|9758155|dbj|BAB08712.1| 40S ribosomal protein S3 [Arabidopsis thaliana] gi|16604318|gb|AAL24165.1| AT5g35530/MOK9_14 [Arabidopsis thaliana] gi|20466075|gb|AAM19959.1| AT5g35530/MOK9_14 [Arabidopsis thaliana] gi|332006595|gb|AED93978.1| 40S ribosomal protein S3-3 [Arabidopsis thaliana]	95	248	3.00E-16	261.1	44.2	53.7	40S ribosomal protein S3-3	gbpln	Arabidopsis thaliana	AT5G35530.1 | Symbols: | Ribosomal protein S3 family protein | chr5:13710355-13712192 REVERSE LENGTH=248	95	248	6.00E-19	261.1	44.2	53.7
Rsa1.0_00316.1.g11144.t1	ref|XP_002872684.1| plant UBX domain-containing protein 4 [Arabidopsis lyrata subsp. lyrata] gi|297318521|gb|EFH48943.1| plant UBX domain-containing protein 4 [Arabidopsis lyrata subsp. lyrata]	313	306	1.00E-139	97.8	87.5	91.7	plant UBX domain-containing protein 4	gbpln	Arabidopsis lyrata	AT4G04210.1 | Symbols: PUX4 | plant UBX domain containing protein 4 | chr4:2030391-2031670 FORWARD LENGTH=303	313	303	1.00E-136	96.8	85.0	89.8
Rsa1.0_00316.1.g11145.t1	gb|AAD32950.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	599	773	1.00E-106	129.0	34.1	45.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	599	575	2.00E-39	96.0	13.5	20.4

Rsa1.0_00316.1.g11146.t1	ref|WP_000519654.1| hypothetical protein, partial [Streptococcus agalactiae]	198	183	3.00E-16	92.4	27.3	36.9	hypothetical protein, partial	gbbct	Streptococcus agalactiae	#	#	#	#	#	#	#
Rsa1.0_00316.1.g11147.t1	gb|EOA39327.1| hypothetical protein CARUB_v10012368mg [Capsella rubella]	207	203	1.00E-81	98.1	72.9	82.6	hypothetical protein CARUB_v10012368mg	gbpln	Capsella rubella	AT1G52900.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr1:19702211-19702916 REVERSE LENGTH=199	207	199	5.00E-83	96.1	73.9	84.5
Rsa1.0_00316.1.g11148.t1	ref|XP_002874793.1| hypothetical protein ARALYDRAFT_911683 [Arabidopsis lyrata subsp. lyrata] gi|297320630|gb|EFH51052.1| hypothetical protein ARALYDRAFT_911683 [Arabidopsis lyrata subsp. lyrata]	187	184	2.00E-72	98.4	79.7	87.2	hypothetical protein ARALYDRAFT_911683	gbpln	Arabidopsis lyrata	AT1G06920.1 | Symbols: ATOFP4, OFP4 | ovate family protein 4 | chr1:2124854-2125801 REVERSE LENGTH=315	187	315	4.00E-14	168.4	18.7	27.8
Rsa1.0_00316.1.g11149.t1	sp|Q94FZ9.1|PAP1_BRACM RecName: Full=Plastid lipid-associated protein 1, chloroplastic; Flags: Precursor gi|14248554|gb|AAK57564.1| plastid-lipid associated protein PAP1 [Brassica rapa subsp. oleifera]	330	327	1.00E-152	99.1	89.4	92.1	RecName: Full=Plastid lipid-associated protein 1, chloroplastic; Flags: Precursor gi|14248554|gb|AAK57564.1| plastid-lipid associated protein PAP1	gbpln	Brassica rapa	AT4G04020.1 | Symbols: FIB | fibrillin | chr4:1932161-1933546 FORWARD LENGTH=318	330	318	1.00E-147	96.4	78.5	86.1
Rsa1.0_00316.1.g11150.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00316.1.g11151.t1	ref|NP_680579.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|52354369|gb|AAU44505.1| hypothetical protein AT4G03965 [Arabidopsis thaliana] gi|55740645|gb|AAV63915.1| hypothetical protein At4g03965 [Arabidopsis thaliana] gi|332656962|gb|AEE82362.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	205	209	7.00E-82	102.0	79.5	86.3	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT4G03965.1 | Symbols: | RING/U-box superfamily protein | chr4:1889576-1890205 FORWARD LENGTH=209	205	209	2.00E-84	102.0	79.5	86.3
Rsa1.0_00316.1.g11152.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00317.1.g11153.t2	gb|AAF67366.1| Hypothetical protein T32B20.i [Arabidopsis thaliana]	381	724	2.00E-69	190.0	43.3	58.8	Hypothetical protein T32B20.i	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00317.1.g11154.t3	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	1044	703	0	67.3	54.5	55.8	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00317.1.g11155.t1	gb|ABD65100.1| hypothetical protein 31.t00077 [Brassica oleracea]	426	391	6.00E-62	91.8	33.3	37.8	hypothetical protein 31.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00317.1.g11156.t1	gb|EOA31081.1| hypothetical protein CARUB_v10014232mg [Capsella rubella]	341	310	3.00E-95	90.9	56.9	68.3	hypothetical protein CARUB_v10014232mg	gbpln	Capsella rubella	AT5G48670.1 | Symbols: FEM111, AGL80 | AGAMOUS-like 80 | chr5:19738825-19739790 REVERSE LENGTH=321	341	321	8.00E-90	94.1	52.2	61.3
Rsa1.0_00317.1.g11157.t7	ref|XP_002893865.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339707|gb|EFH70124.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	716	654	0	91.3	71.6	78.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G04540.1 | Symbols: CRK39 | cysteine-rich RLK (RECEPTOR-like protein kinase) 39 | chr4:2259580-2262138 FORWARD LENGTH=659	716	659	0	92.0	69.7	77.7
Rsa1.0_00317.1.g11158.t1	ref|XP_002873484.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319321|gb|EFH49743.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	131	603	4.00E-18	460.3	38.9	46.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G10900.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:3436413-3439221 REVERSE LENGTH=600	131	600	3.00E-16	458.0	39.7	46.6
Rsa1.0_00317.1.g11159.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00317.1.g11160.t1	emb|CAB10249.1| replication control protein 1 like [Arabidopsis thaliana] gi|7268176|emb|CAB78512.1| replication control protein 1 like [Arabidopsis thaliana]	505	771	0	152.7	63.2	67.9	replication control protein 1 like	gbpln	Arabidopsis thaliana	AT4G14700.1 | Symbols: ATORC1A, ORC1A | origin recognition complex 1 | chr4:8422236-8424665 FORWARD LENGTH=809	505	809	0	160.2	63.2	67.9
Rsa1.0_00317.1.g11161.t1	ref|XP_002870293.1| hypothetical protein ARALYDRAFT_330043 [Arabidopsis lyrata subsp. lyrata] gi|297316129|gb|EFH46552.1| hypothetical protein ARALYDRAFT_330043 [Arabidopsis lyrata subsp. lyrata]	108	317	1.00E-54	293.5	93.5	95.4	hypothetical protein ARALYDRAFT_330043	gbpln	Arabidopsis lyrata	AT4G14695.1 | Symbols: | Uncharacterised protein family (UPF0041) | chr4:8419833-8420845 FORWARD LENGTH=109	108	109	1.00E-55	100.9	92.6	95.4
Rsa1.0_00317.1.g11162.t1	ref|XP_002871839.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297317676|gb|EFH48098.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	490	478	2.00E-86	97.6	43.9	54.9	F-box family protein	gbpln	Arabidopsis lyrata	AT5G18770.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:6261426-6263172 FORWARD LENGTH=481	490	481	2.00E-87	98.2	41.8	54.1

Rsa1.0_00317.1.g11163.t1	gb|EOA21838.1| hypothetical protein CARUB_v10002305mg [Capsella rubella]	108	108	7.00E−51	100.0	88.0	94.4	hypothetical protein CARUB_v10002305mg	gbpln	Capsella rubella	AT4G05590.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0041 (InterPro:IPR005336); BEST Arabidopsis thaliana protein match is: Uncharacterised protein family (UPF0041) (TAIR:AT4G22310.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:2907176−2908297 FORWARD LENGTH=108	108	108	3.00E−53	100.0	87.0	93.5
Rsa1.0_00317.1.g11164.t1	ref|XP_002872670.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318507|gb|EFH48929.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	428	444	0	103.7	84.1	90.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G22290.1 | Symbols: | Ubiquitin−specific protease family C19−related protein | chr4:11783199−11785730 REVERSE LENGTH=445	428	445	1.00E−180	104.0	75.5	85.3
Rsa1.0_00317.1.g11165.t1	ref|XP_002872671.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318508|gb|EFH48930.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	858	815	0	95.0	70.3	78.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G37150.1 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:14701330−14704562 FORWARD LENGTH=839	858	839	0	97.8	63.2	75.3
Rsa1.0_00317.1.g11166.t1	ref|XP_002874790.1| short−chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320627|gb|EFH51049.1| short−chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	255	254	1.00E−135	99.6	94.1	96.9	short−chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT4G05530.1 | Symbols: IBR1, SDRA | indole−3−butyric acid response 1 | chr4:2816462−2818074 FORWARD LENGTH=254	255	254	1.00E−136	99.6	93.3	96.1
Rsa1.0_00317.1.g11167.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00317.1.g11168.t1	gb|EOA20335.1| hypothetical protein CARUB_v10000641mg [Capsella rubella]	546	545	0	99.8	94.3	96.9	hypothetical protein CARUB_v10000641mg	gbpln	Capsella rubella	AT4G05520.1 | Symbols: ATEHD2, EHD2 | EPS15 homology domain 2 | chr4:2804522−2807833 FORWARD LENGTH=546	546	546	0	100.0	92.9	96.5
Rsa1.0_00317.1.g11169.t1	gb|EOA23178.1| hypothetical protein CARUB_v10018008mg [Capsella rubella]	57	214	4.00E−17	375.4	73.7	86.0	hypothetical protein CARUB_v10018008mg	gbpln	Capsella rubella	AT3G19790.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 32 Blast hits to 26 proteins in 8 species: Archae − 0; Bacteria − 0; Metazoa − 13; Fungi − 2; Plants − 14; Viruses − 0; Other Eukaryotes − 3 (source: NCBI BLink). | chr3:6874937−6875440 REVERSE LENGTH=167	57	167	1.00E−12	293.0	50.9	71.9
Rsa1.0_00317.1.g11170.t1	ref|XP_002874792.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320629|gb|EFH51051.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	491	453	0	92.3	73.7	79.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G03820.1 | Symbols: | Protein of unknown function (DUF3537) | chr4:1772114−1774380 REVERSE LENGTH=437	491	437	1.00E−174	89.0	60.9	65.0
Rsa1.0_00317.1.g11171.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00317.1.g11172.t7	gb|EOA27719.1| hypothetical protein CARUB_v10023871mg [Capsella rubella]	370	262	7.00E−46	70.8	28.6	34.1	hypothetical protein CARUB_v10023871mg	gbpln	Capsella rubella	AT4G01560.1 | Symbols: MEE49 | Ribosomal RNA processing Brix domain protein | chr4:677266−679164 REVERSE LENGTH=343	370	343	2.00E−17	92.7	17.6	25.7
Rsa1.0_00317.1.g11173.t1	gb|EOA25808.1| hypothetical protein CARUB_v10019176mg [Capsella rubella]	291	204	1.00E−53	70.1	38.8	49.1	hypothetical protein CARUB_v10019176mg	gbpln	Capsella rubella	AT4G04090.1 | Symbols: | BTB/POZ domain−containing protein | chr4:1964980−1965650 FORWARD LENGTH=192	291	192	4.00E−48	66.0	34.7	45.4
Rsa1.0_00317.1.g11174.t1	ref|NP_192328.2| uncharacterized protein [Arabidopsis thaliana] gi|42572827|ref|NP_974510.1| uncharacterized protein [Arabidopsis thaliana] gi|114050681|gb|ABI49490.1| At4g04190 [Arabidopsis thaliana] gi|332656971|gb|AEE82371.1| uncharacterized protein AT4G04190 [Arabidopsis thaliana] gi|332656972|gb|AEE82372.1| uncharacterized protein AT4G04190 [Arabidopsis thaliana]	171	184	5.00E−84	107.6	90.1	93.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G04190.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr4:2024873−2026330 FORWARD LENGTH=184	171	184	2.00E−86	107.6	90.1	93.6
Rsa1.0_00317.1.g11175.t1	gb|ABK96017.1| unknown [Populus trichocarpa]	182	305	7.00E−66	167.6	73.1	83.0	unknown	gbpln	Populus trichocarpa	AT4G22150.1 | Symbols: PUX3 | plant UBX domain−containing protein 3 | chr4:11731272−11732800 REVERSE LENGTH=367	182	367	8.00E−63	201.6	74.2	80.2
Rsa1.0_00318.1.g11176.t1	gb|AAC23640.1| CER1−like protein [Arabidopsis thaliana]	606	635	0	104.8	82.8	89.8	CER1−like protein	gbpln	Arabidopsis thaliana	AT2G37700.1 | Symbols: | Fatty acid hydroxylase superfamily | chr2:15810581−15814176 REVERSE LENGTH=613	606	613	0	101.2	81.0	88.0

Rsa1.0_00318.1.g11177.t1	dbj|BAB01155.1| unnamed protein product [Arabidopsis thaliana] gi|49823524|gb|AAT68745.1| hypothetical protein At3g17200 [Arabidopsis thaliana] gi|60547763|gb|AAX23845.1| hypothetical protein At3g17200 [Arabidopsis thaliana]	136	310	2.00E-30	227.9	41.9	61.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	136	746	3.00E-16	548.5	30.9	36.8
Rsa1.0_00318.1.g11178.t1	gb|AAC23640.1| CER1-like protein [Arabidopsis thaliana]	635	635	0	100.0	79.1	87.7	CER1-like protein	gbpln	Arabidopsis thaliana	AT2G37700.1 | Symbols: | Fatty acid hydroxylase superfamily | chr2:15810581-15814176 REVERSE LENGTH=613	635	613	0	96.5	78.1	86.6
Rsa1.0_00318.1.g11179.t1	ref|NP_181305.2| phosphoribosylaminoimidazole carboxylase [Arabidopsis thaliana] gi|28973715|gb|AAO64174.1| putative phosphoribosylaminoimidazole carboxylase [Arabidopsis thaliana] gi|30793959|gb|AAP40431.1| putative phosphoribosylaminoimidazole carboxylase [Arabidopsis thaliana] gi|110737176|dbj|BAF00537.1| phosphoribosylaminoimidazole carboxylase like protein [Arabidopsis thaliana] gi|330254341|gb|AEC09435.1| phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative [Arabidopsis thaliana]	640	642	0	100.3	88.3	94.2	phosphoribosylaminoimidazole carboxylase	gbpln	Arabidopsis thaliana	AT2G37690.1 | Symbols: | phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative | chr2:15806111-15810240 FORWARD LENGTH=642	640	642	0	100.3	88.3	94.2
Rsa1.0_00318.1.g11180.t1	ref|NP_181304.2| uncharacterized protein [Arabidopsis thaliana] gi|297827323|ref|XP_002881544.1| far-red elongated hypocotyl 1 [Arabidopsis lyrata subsp. lyrata] gi|297327383|gb|EFH57803.1| far-red elongated hypocotyl 1 [Arabidopsis lyrata subsp. lyrata] gi|330254340|gb|AEC09434.1| uncharacterized protein AT2G37680 [Arabidopsis thaliana]	215	215	1.00E-121	100.0	96.7	98.6	uncharacterized protein	gbpln	Arabidopsis lyrata	AT2G37680.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Vacuolar import/degradation protein Vid24 (InterPro:IPR018618); Has 318 Blast hits to 317 proteins in 131 species: Archae - 0; Bacteria - 0; Metazoa - 80; Fungi - 184; Plants - 51; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr2:15803500-15805515 REVERSE LENGTH=215	215	215	1.00E-124	100.0	96.7	98.6
Rsa1.0_00318.1.g11181.t1	dbj|BAJ34134.1| unnamed protein product [Thellungiella halophila]	166	191	1.00E-66	115.1	81.3	88.6	unnamed protein product	----	----	AT2G37678.1 | Symbols: FHY1, PAT3, FRY1 | far-red elongated hypocotyl 1 | chr2:15801689-15802696 REVERSE LENGTH=202	166	202	5.00E-64	121.7	80.1	88.6
Rsa1.0_00318.1.g11182.t1	ref|XP_002881542.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297327381|gb|EFH57801.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	897	911	0	101.6	84.7	91.9	WD-40 repeat family protein	gbpln	Arabidopsis lyrata	AT2G37670.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:15797384-15800536 REVERSE LENGTH=903	897	903	0	100.7	83.5	90.2
Rsa1.0_00318.1.g11183.t2	gb|EOA27487.1| hypothetical protein CARUB_v10023624mg [Capsella rubella]	335	326	1.00E-157	97.3	82.7	88.7	hypothetical protein CARUB_v10023624mg	gbpln	Capsella rubella	AT2G37660.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:15795481-15796977 REVERSE LENGTH=325	335	325	1.00E-158	97.0	83.0	89.9
Rsa1.0_00318.1.g11184.t1	ref|XP_002874288.1| hypothetical protein ARALYDRAFT_351609 [Arabidopsis lyrata subsp. lyrata] gi|297320125|gb|EFH50547.1| hypothetical protein ARALYDRAFT_351609 [Arabidopsis lyrata subsp. lyrata]	151	413	6.00E-53	273.5	61.6	70.2	hypothetical protein ARALYDRAFT_351609	gbpln	Arabidopsis lyrata	AT5G25960.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:9062917-9065011 REVERSE LENGTH=352	151	352	2.00E-52	233.1	58.3	69.5
Rsa1.0_00318.1.g11185.t1	ref|XP_002881518.1| hypothetical protein ARALYDRAFT_345496 [Arabidopsis lyrata subsp. lyrata] gi|297327357|gb|EFH57777.1| hypothetical protein ARALYDRAFT_345496 [Arabidopsis lyrata subsp. lyrata]	116	161	9.00E-34	138.8	75.0	83.6	hypothetical protein ARALYDRAFT_345496	gbpln	Arabidopsis lyrata	AT2G37610.1 | Symbols: | unknown protein; Has 21 Blast hits to 21 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15776869-15777673 REVERSE LENGTH=161	116	161	1.00E-32	138.8	69.8	77.6
Rsa1.0_00318.1.g11186.t1	gb|EOA28156.1| hypothetical protein CARUB_v10024358mg [Capsella rubella]	112	112	1.00E-50	100.0	94.6	94.6	hypothetical protein CARUB_v10024358mg	gbpln	Capsella rubella	AT3G53740.4 | Symbols: | Ribosomal protein L36e family protein | chr3:19913921-19914813 REVERSE LENGTH=112	112	112	3.00E-52	100.0	92.0	94.6
Rsa1.0_00318.1.g11187.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00318.1.g11188.t1	ref|XP_002879686.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325525|gb|EFH55945.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	307	326	1.00E-118	106.2	78.5	85.3	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT2G37590.1 | Symbols: ATDOF2.4, DOF2.4 | DNA binding with one finger 2.4 | chr2:15769292-15770497 FORWARD LENGTH=330	307	330	1.00E-116	107.5	76.9	85.0
Rsa1.0_00318.1.g11189.t1	ref|XP_004253326.1| PREDICTED: xylosyltransferase-like [Solanum lycopersicum]	144	384	1.00E-12	266.7	26.4	29.2	PREDICTED: xylosyltransferase-like	gbpln	Solanum lycopersicum	AT2G37585.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr2:15765864-15767722 FORWARD LENGTH=384	144	384	4.00E-15	266.7	26.4	29.2

Rsa1.0_00318.1.g11190.t1	gb|EOA27799.1| hypothetical protein CARUB_v10023951mg [Capsella rubella]	236	241	5.00E-68	102.1	74.2	80.1	hypothetical protein CARUB_v10023951mg	gbpln	Capsella rubella	AT2G37580.1 | Symbols: | RING/U-box superfamily protein | chr2:15764745-15765452 FORWARD LENGTH=235	236	235	3.00E-60	99.6	60.6	66.5
Rsa1.0_00318.1.g11191.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	188	248	4.00E-50	131.9	52.1	52.1	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	188	103	6.00E-50	54.8	52.1	52.1
Rsa1.0_00318.1.g11192.t1	gb|EOA27401.1| hypothetical protein CARUB_v10023534mg, partial [Capsella rubella]	321	350	1.00E-172	109.0	90.3	95.0	hypothetical protein CARUB_v10023534mg, partial	gbpln	Capsella rubella	AT2G37540.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:15751695-15753820 REVERSE LENGTH=321	321	321	1.00E-163	100.0	82.6	91.9
Rsa1.0_00318.1.g11193.t1	ref|NP_181288.4| acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein [Arabidopsis thaliana] gi|330254317|gb|AEC09411.1| acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein [Arabidopsis thaliana]	865	829	0	95.8	77.2	85.0	acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT2G37520.1 | Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain | chr2:15745033-15749615 REVERSE LENGTH=829	865	829	0	95.8	77.2	85.0
Rsa1.0_00318.1.g11194.t1	gb|EOA28737.1| hypothetical protein CARUB_v10024966mg [Capsella rubella]	599	468	0	78.1	67.6	71.5	hypothetical protein CARUB_v10024966mg	gbpln	Capsella rubella	AT2G37500.1 | Symbols: | arginine biosynthesis protein ArgJ family | chr2:15739904-15742689 REVERSE LENGTH=468	599	468	0	78.1	67.4	70.6
Rsa1.0_00318.1.g11195.t1	gb|EOA28737.1| hypothetical protein CARUB_v10024966mg [Capsella rubella]	66	468	1.00E-18	709.1	71.2	75.8	hypothetical protein CARUB_v10024966mg	gbpln	Capsella rubella	AT2G37500.1 | Symbols: | arginine biosynthesis protein ArgJ family | chr2:15739904-15742689 REVERSE LENGTH=468	66	468	9.00E-21	709.1	68.2	77.3
Rsa1.0_00318.1.g11196.t1	dbj|BAD95109.1| hypothetical protein [Arabidopsis thaliana]	189	194	6.00E-62	102.6	77.2	87.3	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G37480.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G53670.2); Has 186 Blast hits to 186 proteins in 35 species: Archae - 0; Bacteria - 2; Metazoa - 14; Fungi - 7; Plants - 154; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr2:15738645-15739579 FORWARD LENGTH=194	189	194	1.00E-63	102.6	76.7	87.3
Rsa1.0_00318.1.g11197.t1	gb|EOA27577.1| hypothetical protein CARUB_v10023716mg [Capsella rubella]	298	302	1.00E-133	101.3	77.5	87.6	hypothetical protein CARUB_v10023716mg	gbpln	Capsella rubella	AT4G02850.1 | Symbols: | phenazine biosynthesis PhzC/PhzF family protein | chr4:1266535-1268569 REVERSE LENGTH=306	298	306	1.00E-115	102.7	69.5	82.6
Rsa1.0_00319.1.g11198.t2	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1326	1307	0	98.6	57.5	74.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1326	1262	2.00E-96	95.2	13.5	21.3
Rsa1.0_00319.1.g11199.t2	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1427	1459	0	102.2	61.9	75.4	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1427	1262	1.00E-107	88.4	13.5	19.3
Rsa1.0_00319.1.g11200.t1	ref|XP_002894142.1| hypothetical protein ARALYDRAFT_337011 [Arabidopsis lyrata subsp. lyrata] gi|297339984|gb|EFH70401.1| hypothetical protein ARALYDRAFT_337011 [Arabidopsis lyrata subsp. lyrata]	540	569	0	105.4	74.4	84.1	hypothetical protein ARALYDRAFT_337011	gbpln	Arabidopsis lyrata	AT1G48870.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:18072325-18074457 REVERSE LENGTH=593	540	593	0	109.8	74.8	84.1
Rsa1.0_00319.1.g11201.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11202.t1	ref|XP_004159727.1| PREDICTED: SKP1-like protein 1A-like [Cucumis sativus]	183	155	2.00E-51	84.7	60.1	72.1	PREDICTED: SKP1-like protein 1A-like	gbpln	Cucumis sativus	AT4G34210.1 | Symbols: ASK11, SK11 | SKP1-like 11 | chr4:16379003-16379461 FORWARD LENGTH=152	183	152	4.00E-53	83.1	57.4	69.4
Rsa1.0_00319.1.g11203.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	2112	1838	0	87.0	32.8	41.6	F5M15.26	gbpln	Arabidopsis thaliana	AT1G36390.2 | Symbols: | Co-chaperone GrpE family protein | chr1:13701811-13703524 REVERSE LENGTH=279	2112	279	5.00E-86	13.2	7.6	9.1
Rsa1.0_00319.1.g11204.t1	gb|EOA23471.1| hypothetical protein CARUB_v10016663mg [Capsella rubella]	966	911	2.00E-12	94.3	5.5	8.4	hypothetical protein CARUB_v10016663mg	gbpln	Capsella rubella	AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957	966	957	7.00E-15	99.1	5.7	9.6
Rsa1.0_00319.1.g11205.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11206.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11207.t1	gb|EMT03939.1| SKP1-like protein 1B [Aegilops tauschii]	124	164	4.00E-44	132.3	67.7	83.9	SKP1-like protein 1B	gbpln	Aegilops tauschii	AT1G75950.1 | Symbols: SKP1, ASK1, ATSKP1, SKP1A, UIP1 | S phase kinase-associated protein 1 | chr1:28516715-28517454 FORWARD LENGTH=160	124	160	6.00E-44	129.0	68.5	85.5
Rsa1.0_00319.1.g11208.t1	ref|XP_002890353.1| ATPUP14 [Arabidopsis lyrata subsp. lyrata] gi|297336195|gb|EFH66612.1| ATPUP14 [Arabidopsis lyrata subsp. lyrata]	380	393	4.00E-68	103.4	42.9	57.6	ATPUP14	gbpln	Arabidopsis lyrata	AT1G19770.1 | Symbols: ATPUP14, PUP14 | purine permease 14 | chr1:6832426-6833702 FORWARD LENGTH=393	380	393	8.00E-66	103.4	43.2	57.1
Rsa1.0_00319.1.g11209.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00319.1.g11210.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2137	1274	0	59.6	28.7	38.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G48790.1 | Symbols: AMSH1 | associated molecule with the SH3 domain of STAM 1 | chr1:18043925-18047427 REVERSE LENGTH=507	2137	507	0	23.7	20.2	21.2
Rsa1.0_00319.1.g11211.t1	ref|XP_002891453.1| hypothetical protein ARALYDRAFT_474016 [Arabidopsis lyrata subsp. lyrata] gi|297337295|gb|EFH67712.1| hypothetical protein ARALYDRAFT_474016 [Arabidopsis lyrata subsp. lyrata]	255	252	1.00E-103	98.8	83.9	86.7	hypothetical protein ARALYDRAFT_474016	gbpln	Arabidopsis lyrata	AT1G48780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G18300.1); Has 89 Blast hits to 89 proteins in 11 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 86; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:18041989-18042744 FORWARD LENGTH=251	255	251	1.00E-105	98.4	82.7	85.5
Rsa1.0_00319.1.g11212.t4	gb|ACC38383.1| putative GH3-like protein [Brassica juncea]	703	592	0	84.2	48.4	53.6	putative GH3-like protein	gbpln	Brassica juncea	AT1G23160.1 | Symbols: | Auxin-responsive GH3 family protein | chr1:8209232-8211325 FORWARD LENGTH=578	703	578	1.00E-172	82.2	41.8	50.6
Rsa1.0_00319.1.g11213.t1	gb|ACG60669.1| copia-type polyprotein-like protein [Brassica oleracea var. alboglabra]	90	196	4.00E-37	217.8	81.1	86.7	copia-type polyprotein-like protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11214.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11215.t1	gb|AAZ41811.1| 01P13-1 [Brassica rapa subsp. pekinensis]	982	1545	0	157.3	59.2	69.3	01P13-1	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	982	1262	1.00E-93	128.5	19.7	29.2
Rsa1.0_00319.1.g11216.t1	ref|NP_190309.1| uncharacterized protein [Arabidopsis thaliana] gi|30692831|ref|NP_850661.1| uncharacterized protein [Arabidopsis thaliana] gi|30692834|ref|NP_850662.1| uncharacterized protein [Arabidopsis thaliana] gi|6706134|emb|CAB61971.2| putative protein [Arabidopsis thaliana] gi|17528938|gb|AAL38679.1| unknown protein [Arabidopsis thaliana] gi|20465945|gb|AAM20158.1| unknown protein [Arabidopsis thaliana] gi|110740818|dbj|BAE98506.1| hypothetical protein [Arabidopsis thaliana] gi|332644737|gb|AEE78258.1| uncharacterized protein AT3G47250 [Arabidopsis thaliana] gi|332644738|gb|AEE78259.1| uncharacterized protein AT3G47250 [Arabidopsis thaliana] gi|332644739|gb|AEE78260.1| uncharacterized protein AT3G47250 [Arabidopsis thaliana]	498	480	1.00E-109	96.4	43.0	58.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G47250.3 | Symbols: | Plant protein of unknown function (DUF247) | chr3:17400124-17401566 REVERSE LENGTH=480	498	480	1.00E-112	96.4	43.0	58.0
Rsa1.0_00319.1.g11217.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1112	1270	0	114.2	49.6	65.5	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1112	575	2.00E-83	51.7	15.5	25.6
Rsa1.0_00319.1.g11218.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11219.t1	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	399	695	0	174.2	85.2	88.0	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11220.t1	emb|CAN76528.1| hypothetical protein VITISV_017594 [Vitis vinifera]	405	477	1.00E-24	117.8	25.4	37.8	hypothetical protein VITISV_017594	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11221.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11222.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00319.1.g11223.t1	ref|NP_188458.1| uncharacterized protein [Arabidopsis thaliana] gi|11994092|dbj|BAB01095.1| unnamed protein product [Arabidopsis thaliana] gi|40822865|gb|AAR92245.1| At3g18295 [Arabidopsis thaliana] gi|45752678|gb|AAS76237.1| At3g18295 [Arabidopsis thaliana] gi|332642558|gb|AEE76079.1| uncharacterized protein AT3G18295 [Arabidopsis thaliana]	166	216	3.00E-42	130.1	73.5	83.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G18295.1 | Symbols: | Protein of unknown function (DUF1639) | chr3:6281268-6282000 FORWARD LENGTH=216	166	216	1.00E-44	130.1	73.5	83.1

<table>
<tr><td>Rsa1.0_00319.1.g11224.t1</td><td>ref|NP_175301.1| Auxin-responsive GH3 family protein [Arabidopsis thaliana] gi|12597807|gb|AAG60118.1|AC073555_2 auxin-regulated protein, putative [Arabidopsis thaliana] gi|38566604|gb|AAR24192.1| At1g48690 [Arabidopsis thaliana] gi|40824047|gb|AAR92331.1| At1g48690 [Arabidopsis thaliana] gi|332194216|gb|AEE32337.1| Auxin-responsive GH3 family protein [Arabidopsis thaliana]</td><td>124</td><td>190</td><td>5.00E-46</td><td>153.2</td><td>71.8</td><td>86.3</td><td>Auxin-responsive GH3 family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G48690.1 | Symbols: | Auxin-responsive GH3 family protein | chr1:18009105-18009878 REVERSE LENGTH=190</td><td>124</td><td>190</td><td>9.00E-49</td><td>153.2</td><td>71.8</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00320.1.g11225.t1</td><td>ref|XP_002883181.1| hypothetical protein ARALYDRAFT_479458 [Arabidopsis lyrata subsp. lyrata] gi|297329021|gb|EFH59440.1| hypothetical protein ARALYDRAFT_479458 [Arabidopsis lyrata subsp. lyrata]</td><td>606</td><td>599</td><td>0</td><td>98.8</td><td>87.0</td><td>91.1</td><td>hypothetical protein ARALYDRAFT_479458</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G19420.1 | Symbols: ATPEN2, PEN2 | PTEN 2 | chr3:6731824-6735354 FORWARD LENGTH=611</td><td>606</td><td>611</td><td>0</td><td>100.8</td><td>88.4</td><td>92.7</td></tr>
<tr><td>Rsa1.0_00320.1.g11226.t2</td><td>gb|AAL60578.1|AF454956_1 senescence-associated cysteine protease [Brassica oleracea]</td><td>440</td><td>445</td><td>0</td><td>101.1</td><td>76.4</td><td>83.0</td><td>senescence-associated cysteine protease</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G19390.1 | Symbols: | Granulin repeat cysteine protease family protein | chr3:6723024-6724768 FORWARD LENGTH=452</td><td>440</td><td>452</td><td>0</td><td>102.7</td><td>72.0</td><td>84.1</td></tr>
<tr><td>Rsa1.0_00320.1.g11227.t1</td><td>gb|AAL60578.1|AF454956_1 senescence-associated cysteine protease [Brassica oleracea]</td><td>121</td><td>445</td><td>1.00E-37</td><td>367.8</td><td>60.3</td><td>68.6</td><td>senescence-associated cysteine protease</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G19390.1 | Symbols: | Granulin repeat cysteine protease family protein | chr3:6723024-6724768 FORWARD LENGTH=452</td><td>121</td><td>452</td><td>6.00E-38</td><td>373.6</td><td>58.7</td><td>79.3</td></tr>
<tr><td>Rsa1.0_00320.1.g11228.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00320.1.g11229.t1</td><td>gb|ABV89622.1| U-box domain-containing protein [Brassica rapa]</td><td>418</td><td>417</td><td>0</td><td>99.8</td><td>95.5</td><td>97.8</td><td>U-box domain-containing protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G19380.1 | Symbols: PUB25 | plant U-box 25 | chr3:6714602-6715867 REVERSE LENGTH=421</td><td>418</td><td>421</td><td>0</td><td>100.7</td><td>87.3</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00320.1.g11230.t1</td><td>ref|NP_566631.1| zinc finger CCCH domain-containing protein 39 [Arabidopsis thaliana] gi|75274079|sp|Q9LT81.1|C3H39_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 39; Short=AtC3H39 gi|11994458|dbj|BAB02460.1| unnamed protein product [Arabidopsis thaliana] gi|14335094|gb|AAK59826.1| AT3g19360/MLD14_8 [Arabidopsis thaliana] gi|19548069|gb|AAL87398.1| AT3g19360/MLD14_8 [Arabidopsis thaliana] gi|332642708|gb|AEE76229.1| zinc finger CCCH domain-containing protein 39 [Arabidopsis thaliana]</td><td>368</td><td>386</td><td>1.00E-130</td><td>104.9</td><td>70.4</td><td>78.0</td><td>zinc finger CCCH domain-containing protein 39</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19360.1 | Symbols: | Zinc finger (CCCH-type) family protein | chr3:6707544-6708864 FORWARD LENGTH=386</td><td>368</td><td>386</td><td>1.00E-133</td><td>104.9</td><td>70.4</td><td>78.0</td></tr>
<tr><td>Rsa1.0_00320.1.g11231.t1</td><td>ref|XP_002883174.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329014|gb|EFH59433.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>122</td><td>113</td><td>3.00E-19</td><td>92.6</td><td>43.4</td><td>55.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G34110.1 | Symbols: PAB2, PABP2, ATPAB2 | poly(A) binding protein 2 | chr4:16336732-16339892 FORWARD LENGTH=629</td><td>122</td><td>629</td><td>1.00E-18</td><td>515.6</td><td>37.7</td><td>46.7</td></tr>
<tr><td>Rsa1.0_00320.1.g11232.t1</td><td>ref|XP_002883170.1| hypothetical protein ARALYDRAFT_479444 [Arabidopsis lyrata subsp. lyrata] gi|297329010|gb|EFH59429.1| hypothetical protein ARALYDRAFT_479444 [Arabidopsis lyrata subsp. lyrata]</td><td>401</td><td>432</td><td>1.00E-144</td><td>107.7</td><td>79.8</td><td>84.3</td><td>hypothetical protein ARALYDRAFT_479444</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G19290.1 | Symbols: ABF4, AREB2 | ABRE binding factor 4 | chr3:6687956-6689784 FORWARD LENGTH=431</td><td>401</td><td>431</td><td>1.00E-139</td><td>107.5</td><td>81.0</td><td>85.0</td></tr>
<tr><td>Rsa1.0_00320.1.g11233.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>125</td><td>1142</td><td>9.00E-19</td><td>913.6</td><td>44.8</td><td>57.6</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00320.1.g11234.t1</td><td>ref|NP_188557.1| LAG1 longevity assurance homolog 2 [Arabidopsis thaliana] gi|62900623|sp|Q9LJK3.1|LAG12_ARATH RecName: Full=LAG1 longevity assurance homolog 2; Short=LAG1 homolog 2 gi|9294628|dbj|BAB02967.1| unnamed protein product [Arabidopsis thaliana] gi|21537198|gb|AAM61539.1| longevity factor-like protein [Arabidopsis thaliana] gi|26451114|dbj|BAC42661.1| putative longevity factor [Arabidopsis thaliana] gi|30725356|gb|AAP37700.1| At3g19260 [Arabidopsis thaliana] gi|332642693|gb|AEE76214.1| LAG1 longevity assurance homolog 2 [Arabidopsis thaliana]</td><td>301</td><td>296</td><td>1.00E-145</td><td>98.3</td><td>84.7</td><td>90.4</td><td>LAG1 longevity assurance homolog 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19260.1 | Symbols: LAG1 HOMOLOG 2, LOH2 | LAG1 homologue 2 | chr3:6669448-6671257 REVERSE LENGTH=296</td><td>301</td><td>296</td><td>1.00E-148</td><td>98.3</td><td>84.7</td><td>90.4</td></tr>
</table>

Rsa1.0_00320.1.g11235.t1	ref|NP_191881.1| F-box/kelch-repeat protein SKIP30 [Arabidopsis thaliana] gi|7523404|emb|CAB86423.1| putative protein [Arabidopsis thaliana] gi|21593314|gb|AAM65263.1| unknown [Arabidopsis thaliana] gi|110738141|dbj|BAF01002.1| hypothetical protein [Arabidopsis thaliana] gi|332646928|gb|AEE80449.1| F-box/kelch-repeat protein SKIP30 [Arabidopsis thaliana]	349	345	1.00E-164	98.9	80.8	90.5	F-box/kelch-repeat protein SKIP30	gbpln	Arabidopsis thaliana	AT3G63220.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:23357540-23358577 REVERSE LENGTH=345	349	345	1.00E-167	98.9	80.8	90.5
Rsa1.0_00320.1.g11236.t1	dbj|BAB11243.1| unnamed protein product [Arabidopsis thaliana]	242	485	1.00E-72	200.4	56.6	69.0	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G51740.1 | Symbols: | Peptidase family M48 family protein | chr5:21017110-21018987 FORWARD LENGTH=442	242	442	4.00E-75	182.6	56.6	69.0
Rsa1.0_00320.1.g11237.t1	ref|XP_002885297.1| ATIPT8 [Arabidopsis lyrata subsp. lyrata] gi|297331137|gb|EFH61556.1| ATIPT8 [Arabidopsis lyrata subsp. lyrata]	324	334	1.00E-135	103.1	73.1	86.1	ATIPT8	gbpln	Arabidopsis lyrata	AT3G19160.1 | Symbols: ATIPT8, PGA22, IPT8 | ATP/ADP isopentenyltransferases | chr3:6621993-6623236 REVERSE LENGTH=330	324	330	1.00E-133	101.9	71.0	84.0
Rsa1.0_00320.1.g11238.t1	gb|EOA30594.1| hypothetical protein CARUB_v10013726mg [Capsella rubella]	431	438	1.00E-180	101.6	81.0	87.5	hypothetical protein CARUB_v10013726mg	gbpln	Capsella rubella	AT3G19130.1 | Symbols: ATRBP47B, RBP47B | RNA-binding protein 47B | chr3:6611398-6613823 REVERSE LENGTH=435	431	435	1.00E-180	100.9	81.0	88.6
Rsa1.0_00320.1.g11239.t4	ref|NP_188541.1| putative calcium-dependent protein kinase [Arabidopsis thaliana] gi|75335080|sp|Q9LJL9.1|CAMK2_ARATH RecName: Full=CDPK-related kinase 2; Short=AtCRK2; AltName: Full=Calcium/calmodulin-dependent protein kinase 2 gi|16904216|gb|AAL30815.1|AF435447_1 calcium/calmodulin-dependent protein kinase CaMK2 [Arabidopsis thaliana] gi|9294612|dbj|BAB02951.1| calcium-dependent protein kinase [Arabidopsis thaliana] gi|16604466|gb|AAL24239.1| AT3g19100/MVI11_1 [Arabidopsis thaliana] gi|18958024|gb|AAL79585.1| AT3g19100/MVI11_1 [Arabidopsis thaliana] gi|332642673|gb|AEE76194.1| CDPK-related kinase 2 [Arabidopsis thaliana]	200	599	6.00E-76	299.5	74.5	81.0	putative calcium-dependent protein kinase	gbpln	Arabidopsis thaliana	AT3G19100.1 | Symbols: | Protein kinase superfamily protein | chr3:6605681-6608980 FORWARD LENGTH=599	200	599	2.00E-78	299.5	74.5	81.0
Rsa1.0_00320.1.g11240.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00320.1.g11241.t1	ref|NP_174552.1| transcription initiation factor TFIID subunit 1-A [Arabidopsis thaliana] gi|75157524|sp|Q8LRK9.1|TAF1A_ARATH RecName: Full=Transcription initiation factor TFIID subunit 1-A; Short=AtTAF1a; AltName: Full=TAFII250-A gi|21105767|gb|AAM34782.1|AF510669_1 HAF1 [Arabidopsis thaliana] gi|332193403|gb|AEE31524.1| transcription initiation factor TFIID subunit 1-A [Arabidopsis thaliana]	1759	1919	0	109.1	76.0	83.9	transcription initiation factor TFIID subunit 1-A	gbpln	Arabidopsis thaliana	AT1G32750.1 | Symbols: HAF01, HAF1, HAC13, GTD1, TAF1 | HAC13 protein (HAC13) | chr1:11846385-11856261 REVERSE LENGTH=1919	1759	1919	0	109.1	76.0	83.9
Rsa1.0_00320.1.g11242.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	546	1365	1.00E-111	250.0	45.2	60.1	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	546	575	1.00E-57	105.3	28.0	42.9
Rsa1.0_00320.1.g11243.t1	ref|XP_002885291.1| hypothetical protein ARALYDRAFT_479421 [Arabidopsis lyrata subsp. lyrata] gi|297331131|gb|EFH61550.1| hypothetical protein ARALYDRAFT_479421 [Arabidopsis lyrata subsp. lyrata]	60	60	1.00E-19	100.0	81.7	90.0	hypothetical protein ARALYDRAFT_479421	gbpln	Arabidopsis lyrata	AT3G19030.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: pyridoxine biosynthetic process, homoserine biosynthetic process; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49500.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6564117-6564299 REVERSE LENGTH=60	60	60	2.00E-21	100.0	80.0	88.3
Rsa1.0_00321.1.g11244.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00321.1.g11245.t1	ref|XP_002884196.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330036|gb|EFH60455.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata]	402	402	0	100.0	93.5	97.0	catalytic/ coenzyme binding protein	gbpln	Arabidopsis lyrata	AT2G20360.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:8786070-8789098 FORWARD LENGTH=402	402	402	0	100.0	93.3	96.5
Rsa1.0_00321.1.g11246.t1	gb|EOA30119.1| hypothetical protein CARUB_v10013229mg [Capsella rubella]	603	621	0	103.0	90.0	94.0	hypothetical protein CARUB_v10013229mg	gbpln	Capsella rubella	AT2G20370.1 | Symbols: KAM1, MUR3 | Exostosin family protein | chr2:8792355-8794214 FORWARD LENGTH=619	603	619	0	102.7	89.7	94.5
Rsa1.0_00321.1.g11247.t2	ref|XP_002886277.1| hypothetical protein ARALYDRAFT_480866 [Arabidopsis lyrata subsp. lyrata] gi|297332117|gb|EFH62536.1| hypothetical protein ARALYDRAFT_480866 [Arabidopsis lyrata subsp. lyrata]	252	183	4.00E-73	72.6	61.5	65.9	hypothetical protein ARALYDRAFT_480866	gbpln	Arabidopsis lyrata	AT2G20390.1 | Symbols: | unknown protein; Has 50 Blast hits to 50 proteins in 18 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:8796475-8798142 REVERSE LENGTH=183	252	183	6.00E-74	72.6	61.1	65.5
Rsa1.0_00321.1.g11248.t1	ref|NP_179630.2| myb-like HTH transcriptional regulator-like protein [Arabidopsis thaliana] gi|26451666|dbj|BAC42929.1| unknown protein [Arabidopsis thaliana] gi|29824287|gb|AAP04104.1| unknown protein [Arabidopsis thaliana] gi|330251909|gb|AEC07003.1| myb-like HTH transcriptional regulator-like protein [Arabidopsis thaliana]	364	397	8.00E-84	109.1	56.9	69.5	myb-like HTH transcriptional regulator-like protein	gbpln	Arabidopsis thaliana	AT2G20400.1 | Symbols: | myb-like HTH transcriptional regulator family protein | chr2:8799624-8801621 FORWARD LENGTH=397	364	397	2.00E-86	109.1	56.9	69.5
Rsa1.0_00321.1.g11249.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00321.1.g11250.t1	ref|XP_002884202.1| hypothetical protein ARALYDRAFT_480870 [Arabidopsis lyrata subsp. lyrata] gi|297330042|gb|EFH60461.1| hypothetical protein ARALYDRAFT_480870 [Arabidopsis lyrata subsp. lyrata]	421	421	0	100.0	96.9	98.3	hypothetical protein ARALYDRAFT_480870	gbpln	Arabidopsis lyrata	AT2G20420.1 | Symbols: | ATP citrate lyase (ACL) family protein | chr2:8805574-8807858 FORWARD LENGTH=421	421	421	0	100.0	95.7	98.1
Rsa1.0_00321.1.g11251.t4	gb|EOA40254.1| hypothetical protein CARUB_v10008975mg [Capsella rubella]	462	487	1.00E-113	105.4	56.3	64.3	hypothetical protein CARUB_v10008975mg	gbpln	Capsella rubella	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	462	513	1.00E-109	111.0	55.0	64.5
Rsa1.0_00321.1.g11252.t1	ref|NP_179633.2| ROP-interactive CRIB motif-containing protein 6 [Arabidopsis thaliana] gi|91806212|gb|ABE65834.1| p21-rho-binding domain-containing protein [Arabidopsis thaliana] gi|330251912|gb|AEC07006.1| ROP-interactive CRIB motif-containing protein 6 [Arabidopsis thaliana]	200	212	9.00E-71	106.0	76.0	86.0	ROP-interactive CRIB motif-containing protein 6	gbpln	Arabidopsis thaliana	AT2G20430.1 | Symbols: RIC6 | ROP-interactive CRIB motif-containing protein 6 | chr2:8808667-8809781 REVERSE LENGTH=212	200	212	3.00E-73	106.0	76.0	86.0
Rsa1.0_00321.1.g11253.t1	ref|NP_179634.2| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|238479300|ref|NP_001154525.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|330251913|gb|AEC07007.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|330251914|gb|AEC07008.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	418	425	0	101.7	90.9	94.3	RabGAP/TBC domain-containing protein	gbpln	Arabidopsis thaliana	AT2G20440.2 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr2:8811034-8813251 REVERSE LENGTH=425	418	425	0	101.7	90.9	94.3
Rsa1.0_00321.1.g11254.t1	gb|EOA32203.1| hypothetical protein CARUB_v10015460mg [Capsella rubella]	571	566	0	99.1	94.7	97.0	hypothetical protein CARUB_v10015460mg	gbpln	Capsella rubella	AT2G20470.1 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr2:8826277-8829497 REVERSE LENGTH=569	571	569	0	99.6	93.5	96.1
Rsa1.0_00321.1.g11255.t1	ref|XP_002884205.1| EDA27/NOP10 [Arabidopsis lyrata subsp. lyrata] gi|297330045|gb|EFH60464.1| EDA27/NOP10 [Arabidopsis lyrata subsp. lyrata]	64	64	5.00E-27	100.0	92.2	95.3	EDA27/NOP10	gbpln	Arabidopsis lyrata	AT2G20490.1 | Symbols: NOP10, EDA27 | nucleolar RNA-binding Nop10p family protein | chr2:8831897-8832723 FORWARD LENGTH=64	64	64	2.00E-29	100.0	90.6	95.3
Rsa1.0_00321.1.g11256.t1	ref|XP_002890726.1| hypothetical protein ARALYDRAFT_472944 [Arabidopsis lyrata subsp. lyrata] gi|297336568|gb|EFH66985.1| hypothetical protein ARALYDRAFT_472944 [Arabidopsis lyrata subsp. lyrata]	320	422	1.00E-144	131.9	78.1	87.8	hypothetical protein ARALYDRAFT_472944	gbpln	Arabidopsis lyrata	AT1G27410.1 | Symbols: | DNA repair metallo-beta-lactamase family protein | chr1:9517226-9518743 FORWARD LENGTH=422	320	422	1.00E-145	131.9	77.5	87.2

Rsa1.0_00321.1.g11257.t1	gb|EOA31139.1| hypothetical protein CARUB_v10014301mg, partial [Capsella rubella]	274	290	1.00E-122	105.8	82.1	89.8	hypothetical protein CARUB_v10014301mg, partial	gbpln	Capsella rubella	AT2G20495.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Serine-threonine protein kinase 19 (InterPro:IPR018865); Has 155 Blast hits to 154 proteins in 53 species: Archae - 0; Bacteria - 0; Metazoa - 95; Fungi - 5; Plants - 34; Viruses - 0; Other Eukaryotes - 21 (source: NCBI BLink). | chr2:8833180-8835034 FORWARD LENGTH=282	274	282	1.00E-120	102.9	81.4	89.4
Rsa1.0_00321.1.g11258.t1	gb|EOA28746.1| hypothetical protein CARUB_v10024977mg [Capsella rubella]	463	473	0	102.2	77.5	87.7	hypothetical protein CARUB_v10024977mg	gbpln	Capsella rubella	AT2G36070.1 | Symbols: ATTIM44-2, TIM44-2 | translocase inner membrane subunit 44-2 | chr2:15145119-15147895 REVERSE LENGTH=469	463	469	0	101.3	76.7	88.6
Rsa1.0_00321.1.g11259.t2	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	625	703	3.00E-57	112.5	17.4	20.6	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00321.1.g11260.t1	ref|XP_002891886.1| hypothetical protein ARALYDRAFT_474703 [Arabidopsis lyrata subsp. lyrata] gi|297337728|gb|EFH68145.1| hypothetical protein ARALYDRAFT_474703 [Arabidopsis lyrata subsp. lyrata]	215	204	5.00E-39	94.9	43.3	47.4	hypothetical protein ARALYDRAFT_474703	gbpln	Arabidopsis lyrata	AT5G48920.1 | Symbols: TED7 | tracheary element differentiation-related 7 | chr5:19835405-19836022 FORWARD LENGTH=205	215	205	1.00E-37	95.3	41.4	45.1
Rsa1.0_00321.1.g11261.t1	ref|XP_002894568.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297340410|gb|EFH70827.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	424	433	0	102.1	94.3	97.2	transferase family protein	gbpln	Arabidopsis lyrata	AT5G48930.1 | Symbols: HCT | hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase | chr5:19836654-19838092 REVERSE LENGTH=433	424	433	0	102.1	93.9	97.2
Rsa1.0_00321.1.g11262.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00321.1.g11263.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00321.1.g11264.t1	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	1411	1643	0	116.4	35.1	44.2	gag/pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1411	1262	2.00E-69	89.4	10.1	15.3
Rsa1.0_00321.1.g11265.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00322.1.g11266.t2	gb|EOA19063.1| hypothetical protein CARUB_v10007728mg [Capsella rubella]	572	575	0	100.5	85.7	93.7	hypothetical protein CARUB_v10007728mg	gbpln	Capsella rubella	AT4G12680.1 | Symbols: | unknown protein; INVOLVED IN: vegetative to reproductive phase transition of meristem; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40640.1); Has 103 Blast hits to 103 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 103; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:7475104-7478174 FORWARD LENGTH=575	572	575	0	100.5	85.3	92.7
Rsa1.0_00322.1.g11267.t1	dbj|BAJ33770.1| unnamed protein product [Thellungiella halophila]	416	416	0	100.0	94.5	95.9	unnamed protein product	----	----	AT5G57630.1 | Symbols: CIPK21, SnRK3.4 | CBL-interacting protein kinase 21 | chr5:23341092-23343143 REVERSE LENGTH=416	416	416	0	100.0	93.0	96.2
Rsa1.0_00322.1.g11268.t1	ref|NP_680450.1| SCP-like extracellular protein domain-containing protein [Arabidopsis thaliana] gi|9758324|dbj|BAB08798.1| unnamed protein product [Arabidopsis thaliana] gi|28058747|gb|AAO29948.1| Unknown protein [Arabidopsis thaliana] gi|30023648|gb|AAP13357.1| At5g57625 [Arabidopsis thaliana] gi|110742530|dbj|BAE99181.1| pathogenesis-related protein - like [Arabidopsis thaliana] gi|332009544|gb|AED96927.1| SCP-like extracellular protein domain-containing protein [Arabidopsis thaliana]	205	207	7.00E-96	101.0	88.8	93.7	SCP-like extracellular protein domain-containing protein	gbpln	Arabidopsis thaliana	AT5G57625.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr5:23337865-23338577 FORWARD LENGTH=207	205	207	2.00E-98	101.0	88.8	93.7
Rsa1.0_00322.1.g11269.t1	gb|EOA13676.1| hypothetical protein CARUB_v10026749mg [Capsella rubella]	333	335	1.00E-168	100.6	90.7	95.2	hypothetical protein CARUB_v10026749mg	gbpln	Capsella rubella	AT5G57620.1 | Symbols: MYB36, AtMYB36 | myb domain protein 36 | chr5:23334904-23336388 FORWARD LENGTH=333	333	333	1.00E-166	100.0	89.8	91.9
Rsa1.0_00322.1.g11270.t1	gb|EOA15115.1| hypothetical protein CARUB_v10028490mg [Capsella rubella]	1057	1061	0	100.4	80.6	86.3	hypothetical protein CARUB_v10028490mg	gbpln	Capsella rubella	AT5G57610.1 | Symbols: | Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain | chr5:23325307-23329099 FORWARD LENGTH=1054	1057	1054	0	99.7	79.3	84.6

Rsa1.0_00322.1.g11271.t2	ref|NP_200561.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|38605471|sp|Q9FKL9.1|XTH12_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 12; Short=At-XTH12; Short=XTH-12; Flags: Precursor gi|9758314|dbj|BAB08788.1| xyloglucan endotransglycosylase [Arabidopsis thaliana] gi|16323043|gb|AAL15256.1| AT5g57530/MUA2_10 [Arabidopsis thaliana] gi|21360435|gb|AAM47333.1| AT5g57530/MUA2_10 [Arabidopsis thaliana] gi|332009528|gb|AED96911.1| probable xyloglucan endotransglucosylase/hydrolase protein 12 [Arabidopsis thaliana]	147	285	1.00E-55	193.9	72.1	75.5	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT5G57530.1 | Symbols: XTH12, AtXTH12 | xyloglucan endotransglucosylase/hydrolase 12 | chr5:23300469-23301549 REVERSE LENGTH=285	147	285	3.00E-58	193.9	72.1	75.5
Rsa1.0_00322.1.g11272.t1	gb|EOA14023.1| hypothetical protein CARUB_v10027155mg [Capsella rubella]	149	202	7.00E-67	135.6	94.0	96.0	hypothetical protein CARUB_v10027155mg	gbpln	Capsella rubella	AT5G57520.1 | Symbols: ZFP2, ATZFP2 | zinc finger protein 2 | chr5:23296019-23296471 FORWARD LENGTH=150	149	150	5.00E-66	100.7	90.6	94.6
Rsa1.0_00322.1.g11273.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	759	1365	0	179.8	44.7	61.3	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	759	575	3.00E-83	75.8	23.5	39.3
Rsa1.0_00322.1.g11274.t1	emb|CAN80919.1| hypothetical protein VITISV_002640 [Vitis vinifera]	1483	1450	0	97.8	47.7	64.7	hypothetical protein VITISV_002640	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1483	1262	1.00E-137	85.1	16.0	23.3
Rsa1.0_00322.1.g11275.t1	ref|XP_002866209.1| transferase, transferring glycosyl groups [Arabidopsis lyrata subsp. lyrata] gi|297312044|gb|EFH42468.1| transferase, transferring glycosyl groups [Arabidopsis lyrata subsp. lyrata]	319	318	1.00E-169	99.7	93.4	96.6	transferase, transferring glycosyl groups	gbpln	Arabidopsis lyrata	AT5G57500.1 | Symbols: | Galactosyltransferase family protein | chr5:23286406-23287525 REVERSE LENGTH=318	319	318	1.00E-169	99.7	92.8	95.6
Rsa1.0_00322.1.g11276.t1	gb|EOA13842.1| hypothetical protein CARUB_v10026945mg [Capsella rubella]	258	274	1.00E-114	106.2	84.1	88.4	hypothetical protein CARUB_v10026945mg	gbpln	Capsella rubella	AT5G57490.1 | Symbols: VDAC4, ATVDAC4 | voltage dependent anion channel 4 | chr5:23283895-23285335 REVERSE LENGTH=274	258	274	1.00E-113	106.2	82.2	86.8
Rsa1.0_00322.1.g11277.t1	gb|EOA14383.1| hypothetical protein CARUB_v10027577mg [Capsella rubella]	476	521	0	109.5	85.9	91.6	hypothetical protein CARUB_v10027577mg	gbpln	Capsella rubella	AT5G57480.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:23279406-23280968 REVERSE LENGTH=520	476	520	0	109.2	84.9	90.8
Rsa1.0_00322.1.g11278.t1	ref|XP_002864518.1| hypothetical protein ARALYDRAFT_495846 [Arabidopsis lyrata subsp. lyrata] gi|297310353|gb|EFH40777.1| hypothetical protein ARALYDRAFT_495846 [Arabidopsis lyrata subsp. lyrata]	642	642	0	100.0	93.0	96.0	hypothetical protein ARALYDRAFT_495846	gbpln	Arabidopsis lyrata	AT5G57460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 166 Blast hits to 166 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 112; Fungi - 4; Plants - 36; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink). | chr5:23275321-23277261 FORWARD LENGTH=646	642	646	0	100.6	92.8	96.1
Rsa1.0_00322.1.g11279.t17	ref|XP_002866205.1| hypothetical protein ARALYDRAFT_495841 [Arabidopsis lyrata subsp. lyrata] gi|297312040|gb|EFH42464.1| hypothetical protein ARALYDRAFT_495841 [Arabidopsis lyrata subsp. lyrata]	737	375	1.00E-170	50.9	42.3	44.0	hypothetical protein ARALYDRAFT_495841	gbpln	Arabidopsis lyrata	AT5G57410.3 | Symbols: | Afadin/alpha-actinin-binding protein | chr5:23264351-23267641 REVERSE LENGTH=391	737	391	1.00E-168	53.1	42.1	44.1
Rsa1.0_00322.1.g11280.t1	gb|AFP19440.1| VIN3-3 [Raphanus sativus]	550	550	0	100.0	93.8	96.0	VIN3-3	gbpln	Raphanus sativus	AT5G57380.1 | Symbols: VIN3 | Fibronectin type III domain-containing protein | chr5:23246538-23249289 REVERSE LENGTH=620	550	620	1.00E-156	112.7	49.1	54.0
Rsa1.0_00322.1.g11281.t1	gb|EOA13735.1| hypothetical protein CARUB_v10026813mg [Capsella rubella]	290	312	1.00E-158	107.6	95.5	97.9	hypothetical protein CARUB_v10026813mg	gbpln	Capsella rubella	AT5G57330.1 | Symbols: | Galactose mutarotase-like superfamily protein | chr5:23218392-23220664 FORWARD LENGTH=312	290	312	1.00E-158	107.6	94.1	97.2
Rsa1.0_00322.1.g11282.t1	gb|EOA15125.1| hypothetical protein CARUB_v10028500mg [Capsella rubella]	952	982	0	103.2	86.0	93.3	hypothetical protein CARUB_v10028500mg	gbpln	Capsella rubella	AT5G57320.1 | Symbols: VLN5 | villin, putative | chr5:23212690-23217549 FORWARD LENGTH=962	952	962	0	101.1	86.2	93.4
Rsa1.0_00322.1.g11283.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00322.1.g11284.t1	ref|XP_002864509.1| hypothetical protein ARALYDRAFT_495827 [Arabidopsis lyrata subsp. lyrata] gi|297310344|gb|EFH40768.1| hypothetical protein ARALYDRAFT_495827 [Arabidopsis lyrata subsp. lyrata]	286	289	1.00E-147	101.0	90.2	95.8	hypothetical protein ARALYDRAFT_495827	gbpln	Arabidopsis lyrata	AT5G57280.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:23204533-23206485 FORWARD LENGTH=289	286	289	1.00E-144	101.0	87.1	94.4
Rsa1.0_00322.1.g11285.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00322.1.g11286.t1	gb|EOA13053.1| hypothetical protein CARUB_v10026053mg [Capsella rubella]	643	655	0	101.9	93.6	96.4	hypothetical protein CARUB_v10026053mg	gbpln	Capsella rubella	AT5G57090.1 | Symbols: EIR1, WAV6, ATPIN2, PIN2, AGR, AGR1 | Auxin efflux carrier family protein | chr5:23100765-23104456 FORWARD LENGTH=647	643	647	0	100.6	90.7	94.6
Rsa1.0_00322.1.g11287.t1	ref|NP_200518.1| uncharacterized protein [Arabidopsis thaliana] gi|8843810|dbj|BAA97358.1| unnamed protein product [Arabidopsis thaliana] gi|91807056|gb|ABE66255.1| hypothetical protein At5g57080 [Arabidopsis thaliana] gi|332009461|gb|AED96844.1| uncharacterized protein AT5G57080 [Arabidopsis thaliana]	62	62	5.00E-18	100.0	75.8	85.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G57080.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G26055.1); Has 14 Blast hits to 14 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:23098959-23099368 FORWARD LENGTH=62	62	62	7.00E-21	100.0	75.8	85.5
Rsa1.0_00322.1.g11288.t1	ref|NP_001147026.1| glyoxalase/bleomycin resistance protein/dioxygenase [Zea mays] gi|195606588|gb|ACG25124.1| glyoxalase/bleomycin resistance protein/dioxygenase [Zea mays]	190	193	1.00E-101	101.6	93.2	97.4	glyoxalase/bleomycin resistance protein/dioxygenase	gbenv/gbpln	Zea mays	AT5G57040.1 | Symbols: | Lactoylglutathione lyase / glyoxalase I family protein | chr5:23084035-23085116 REVERSE LENGTH=197	190	197	5.00E-94	103.7	86.8	92.1
Rsa1.0_00322.1.g11289.t2	gb|EOA12919.1| hypothetical protein CARUB_v10025897mg, partial [Capsella rubella]	996	816	0	81.9	69.6	74.9	hypothetical protein CARUB_v10025897mg, partial	gbpln	Capsella rubella	AT5G57035.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:23080743-23083819 FORWARD LENGTH=789	996	789	0	79.2	68.9	74.5
Rsa1.0_00323.1.g11290.t1	gb|EOA24256.1| hypothetical protein CARUB_v10017497mg [Capsella rubella]	199	364	5.00E-71	182.9	71.9	77.9	hypothetical protein CARUB_v10017497mg	gbpln	Capsella rubella	AT3G30340.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:11956626-11958969 FORWARD LENGTH=364	199	364	5.00E-70	182.9	67.3	77.9
Rsa1.0_00323.1.g11291.t2	gb|EOA25673.1| hypothetical protein CARUB_v10019025mg [Capsella rubella]	467	458	0	98.1	85.7	92.9	hypothetical protein CARUB_v10019025mg	gbpln	Capsella rubella	AT3G30390.2 | Symbols: | Transmembrane amino acid transporter family protein | chr3:11977112-11978827 REVERSE LENGTH=460	467	460	0	98.5	86.7	92.3
Rsa1.0_00323.1.g11292.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00323.1.g11293.t1	gb|EOA25426.1| hypothetical protein CARUB_v10018758mg [Capsella rubella]	153	147	5.00E-48	96.1	64.7	75.2	hypothetical protein CARUB_v10018758mg	gbpln	Capsella rubella	AT3G30460.1 | Symbols: | RING/U-box superfamily protein | chr3:12104433-12104876 FORWARD LENGTH=147	153	147	1.00E-49	96.1	62.1	74.5
Rsa1.0_00323.1.g11294.t1	gb|ABV89624.1| early responsive to dehydration 5 dehydrogenase [Brassica rapa]	498	498	0	100.0	89.6	94.6	early responsive to dehydration 5 dehydrogenase	gbpln	Brassica rapa	AT3G30775.1 | Symbols: ERD5, PRODH, AT-POX, ATPOX, ATPDH, PRO1 | Methylenetetrahydrofolate reductase family protein | chr3:12448880-12451126 REVERSE LENGTH=499	498	499	0	100.2	87.6	93.2
Rsa1.0_00323.1.g11295.t1	ref|XP_002875563.1| hypothetical protein ARALYDRAFT_484754 [Arabidopsis lyrata subsp. lyrata] gi|297321401|gb|EFH51822.1| hypothetical protein ARALYDRAFT_484754 [Arabidopsis lyrata subsp. lyrata]	251	248	1.00E-113	98.8	85.3	89.6	hypothetical protein ARALYDRAFT_484754	gbpln	Arabidopsis lyrata	AT3G32930.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 57 Blast hits to 57 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:13489595-13490704 FORWARD LENGTH=249	251	249	1.00E-115	99.2	85.7	90.4
Rsa1.0_00323.1.g11296.t2	ref|NP_199593.2| kinesin family member 4/7/21/27 [Arabidopsis thaliana] gi|30695302|ref|NP_851151.1| kinesin family member 4/7/21/27 [Arabidopsis thaliana] gi|27260890|gb|AAN86114.1| kinesin-like protein [Arabidopsis thaliana] gi|27260892|gb|AAN86115.1| kinesin-like protein [Arabidopsis thaliana] gi|332008192|gb|AED95575.1| kinesin family member 4/7/21/27 [Arabidopsis thaliana] gi|332008193|gb|AED95576.1| kinesin family member 4/7/21/27 [Arabidopsis thaliana]	1075	1035	0	96.3	87.8	92.0	kinesin family member 4/7/21/27	gbpln	Arabidopsis thaliana	AT5G47820.2 | Symbols: FRA1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:19366505-19372229 FORWARD LENGTH=1035	1075	1035	0	96.3	87.8	92.0

Rsa1.0_00323.1.g11297.t2	ref|XP_002863827.1| hypothetical protein ARALYDRAFT_917605 [Arabidopsis lyrata subsp. lyrata] gi|297309662|gb|EFH40086.1| hypothetical protein ARALYDRAFT_917605 [Arabidopsis lyrata subsp. lyrata]	276	296	1.00E-108	107.2	80.8	85.9	hypothetical protein ARALYDRAFT_917605	gbpln	Arabidopsis lyrata	AT5G47840.1 | Symbols: AMK2 | adenosine monophosphate kinase | chr5:19375488-19378058 FORWARD LENGTH=283	276	283	1.00E-103	102.5	76.8	82.2
Rsa1.0_00323.1.g11298.t1	ref|XP_002865570.1| hypothetical protein ARALYDRAFT_331197 [Arabidopsis lyrata subsp. lyrata] gi|297311405|gb|EFH41829.1| hypothetical protein ARALYDRAFT_331197 [Arabidopsis lyrata subsp. lyrata]	757	753	0	99.5	72.4	80.2	hypothetical protein ARALYDRAFT_331197	gbpln	Arabidopsis lyrata	AT5G47850.1 | Symbols: CCR4 | CRINKLY4 related 4 | chr5:19378803-19381058 REVERSE LENGTH=751	757	751	0	99.2	71.9	79.7
Rsa1.0_00323.1.g11299.t1	gb|EOA13902.1| hypothetical protein CARUB_v10027018mg [Capsella rubella]	211	242	3.00E-85	114.7	75.4	83.4	hypothetical protein CARUB_v10027018mg	gbpln	Capsella rubella	AT5G47870.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: cobalt ion binding (TAIR:AT1G71310.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19384555-19385808 REVERSE LENGTH=199	211	199	5.00E-81	94.3	74.4	80.1
Rsa1.0_00323.1.g11300.t1	ref|NP_199118.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|9757830|dbj|BAB08267.1| CHP-rich zinc finger protein-like [Arabidopsis thaliana] gi|332007520|gb|AED94903.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	482	551	1.00E-117	114.3	47.9	61.4	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G43040.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:17263965-17265620 REVERSE LENGTH=551	482	551	1.00E-119	114.3	47.9	61.4
Rsa1.0_00323.1.g11301.t1	gb|EOA35650.1| hypothetical protein CARUB_v10020872mg [Capsella rubella]	469	240	1.00E-108	51.2	40.9	47.1	hypothetical protein CARUB_v10020872mg	gbpln	Capsella rubella	AT1G65520.1 | Symbols: ATECI1, ECI1, ECHIC, PEC11 | delta(3), delta(2)-enoyl CoA isomerase 1 | chr1:24361171-24361893 REVERSE LENGTH=240	469	240	1.00E-108	51.2	40.3	46.5
Rsa1.0_00323.1.g11302.t1	ref|XP_002863829.1| hypothetical protein ARALYDRAFT_494832 [Arabidopsis lyrata subsp. lyrata] gi|297309664|gb|EFH40088.1| hypothetical protein ARALYDRAFT_494832 [Arabidopsis lyrata subsp. lyrata]	85	97	1.00E-27	114.1	69.4	72.9	hypothetical protein ARALYDRAFT_494832	gbpln	Arabidopsis lyrata	AT5G47890.1 | Symbols: | NADH-ubiquinone oxidoreductase B8 subunit, putative | chr5:19388806-19390409 FORWARD LENGTH=97	85	97	1.00E-29	114.1	67.1	71.8
Rsa1.0_00323.1.g11303.t1	gb|EOA14052.1| hypothetical protein CARUB_v10027188mg [Capsella rubella]	182	191	4.00E-78	104.9	86.8	95.1	hypothetical protein CARUB_v10027188mg	gbpln	Capsella rubella	AT5G47920.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19403458-19404021 REVERSE LENGTH=187	182	187	6.00E-77	102.7	84.1	94.0
Rsa1.0_00323.1.g11304.t1	gb|EOA16169.1| hypothetical protein CARUB_v10004305mg [Capsella rubella]	140	670	1.00E-16	478.6	37.9	46.4	hypothetical protein CARUB_v10004305mg	gbpln	Capsella rubella	AT4G29050.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr4:14314870-14316879 REVERSE LENGTH=669	140	669	9.00E-18	477.9	31.4	38.6
Rsa1.0_00323.1.g11305.t5	gb|EOA24972.1| hypothetical protein CARUB_v10018269mg, partial [Capsella rubella]	84	115	3.00E-42	136.9	97.6	100.0	hypothetical protein CARUB_v10018269mg, partial	gbpln	Capsella rubella	AT3G61110.1 | Symbols: ARS27A, RS27A | ribosomal protein S27 | chr3:22611710-22612632 FORWARD LENGTH=86	84	86	8.00E-44	102.4	96.4	100.0
Rsa1.0_00323.1.g11306.t1	dbj|BAB02625.1| unnamed protein product [Arabidopsis thaliana]	506	420	6.00E-84	83.0	38.5	50.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G28223.1 | Symbols: | F-box family protein | chr3:10527669-10528921 REVERSE LENGTH=391	506	391	1.00E-68	77.3	33.2	45.3
Rsa1.0_00323.1.g11307.t1	dbj|BAB02625.1| unnamed protein product [Arabidopsis thaliana]	424	420	1.00E-90	99.1	47.4	61.6	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G28223.1 | Symbols: | F-box family protein | chr3:10527669-10528921 REVERSE LENGTH=391	424	391	4.00E-75	92.2	42.7	55.0
Rsa1.0_00323.1.g11308.t1	gb|EOA13259.1| hypothetical protein CARUB_v10026289mg [Capsella rubella]	495	490	0	99.0	86.7	91.3	hypothetical protein CARUB_v10026289mg	gbpln	Capsella rubella	AT5G48150.2 | Symbols: PAT1 | GRAS family transcription factor | chr5:19522497-19524053 REVERSE LENGTH=490	495	490	0	99.0	86.7	91.5

Rsa1.0_00323.1.g11309.t1	ref|NP_199627.1| OBERON 2 protein [Arabidopsis thaliana] gi|79330131|ref|NP_001032031.1| OBERON 2 protein [Arabidopsis thaliana] gi|75180552|sp|Q9LUB7.1|OBE2_ARATH RecName: Full=Protein OBERON 2; AltName: Full=Potyvirus VPg-interacting protein 1 gi|8777406|dbj|BAA96996.1| unnamed protein product [Arabidopsis thaliana] gi|222424758|dbj|BAH20332.1| AT5G48160 [Arabidopsis thaliana] gi|332008243|gb|AED95626.1| OBERON 2 protein [Arabidopsis thaliana] gi|332008244|gb|AED95627.1| OBERON 2 protein [Arabidopsis thaliana]	584	574	0	98.3	83.7	89.6	OBERON 2 protein	gbpln	Arabidopsis thaliana	AT5G48160.2 | Symbols: OBE2 | Protein of unknown function (DUF1423) | chr5:19528019-19529820 REVERSE LENGTH=574	584	574	0	98.3	83.7	89.6
Rsa1.0_00323.1.g11310.t1	ref|XP_002865614.1| hypothetical protein ARALYDRAFT_494871 [Arabidopsis lyrata subsp. lyrata] gi|297311449|gb|EFH41873.1| hypothetical protein ARALYDRAFT_494871 [Arabidopsis lyrata subsp. lyrata]	156	156	9.00E-77	100.0	91.0	94.9	hypothetical protein ARALYDRAFT_494871	gbpln	Arabidopsis lyrata	AT5G48170.1 | Symbols: SLY2 | F-box family protein | chr5:19532729-19533202 REVERSE LENGTH=157	156	157	3.00E-77	100.6	89.1	93.6
Rsa1.0_00323.1.g11311.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	699	1161	1.00E-110	166.1	31.6	46.9	F14N23.4	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	699	626	1.00E-63	89.6	17.9	30.8
Rsa1.0_00323.1.g11312.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	612	530	2.00E-36	86.6	13.4	18.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G32613.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr5:12263255-12265041 FORWARD LENGTH=457	612	457	4.00E-12	74.7	6.0	8.3
Rsa1.0_00323.1.g11313.t1	ref|NP_199635.2| uncharacterized protein [Arabidopsis thaliana] gi|332008257|gb|AED95640.1| uncharacterized protein AT5G48240 [Arabidopsis thaliana]	316	309	1.00E-125	97.8	75.9	87.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G48240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1665 (InterPro:IPR012459); Has 402 Blast hits to 382 proteins in 162 species: Archae - 0; Bacteria - 4; Metazoa - 139; Fungi - 111; Plants - 54; Viruses - 1; Other Eukaryotes - 93 (source: NCBI BLink). | chr5:19559301-19561153 FORWARD LENGTH=309	316	309	1.00E-128	97.8	75.9	87.7
Rsa1.0_00323.1.g11314.t1	ref|XP_002863882.1| hypothetical protein ARALYDRAFT_494878 [Arabidopsis lyrata subsp. lyrata] gi|297309717|gb|EFH40141.1| hypothetical protein ARALYDRAFT_494878 [Arabidopsis lyrata subsp. lyrata]	99	310	4.00E-38	313.1	83.8	88.9	hypothetical protein ARALYDRAFT_494878	gbpln	Arabidopsis lyrata	AT5G48240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1665 (InterPro:IPR012459); Has 402 Blast hits to 382 proteins in 162 species: Archae - 0; Bacteria - 4; Metazoa - 139; Fungi - 111; Plants - 54; Viruses - 1; Other Eukaryotes - 93 (source: NCBI BLink). | chr5:19559301-19561153 FORWARD LENGTH=309	99	309	7.00E-40	312.1	79.8	86.9
Rsa1.0_00323.1.g11315.t1	ref|NP_199638.1| uncharacterized protein [Arabidopsis thaliana] gi|8777417|dbj|BAA97007.1| unnamed protein product [Arabidopsis thaliana] gi|71905601|gb|AAZ52778.1| hypothetical protein At5g48270 [Arabidopsis thaliana] gi|91805693|gb|ABE65575.1| hypothetical protein At5g48270 [Arabidopsis thaliana] gi|332008261|gb|AED95644.1| uncharacterized protein AT5G48270 [Arabidopsis thaliana]	320	322	1.00E-161	100.6	86.6	92.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G48270.1 | Symbols: | Plant protein of unknown function (DUF868) | chr5:19564744-19565712 REVERSE LENGTH=322	320	322	1.00E-164	100.6	86.6	92.8
Rsa1.0_00323.1.g11316.t1	gb|EOA20463.1| hypothetical protein CARUB_v10000776mg, partial [Capsella rubella]	449	503	1.00E-108	112.0	55.9	68.6	hypothetical protein CARUB_v10000776mg, partial	gbpln	Capsella rubella	AT5G03780.1 | Symbols: TRFL10 | TRF-like 10 | chr5:999266-1000947 REVERSE LENGTH=420	449	420	1.00E-106	93.5	52.6	63.5

Rsa1.0_00323.1.g11317.t2	ref|XP_002863886.1| hypothetical protein ARALYDRAFT_331241 [Arabidopsis lyrata subsp. lyrata] gi|297309721|gb|EFH40145.1| hypothetical protein ARALYDRAFT_331241 [Arabidopsis lyrata subsp. lyrata]	96	114	6.00E-15	118.8	43.8	51.0	hypothetical protein ARALYDRAFT_331241	gbpln	Arabidopsis lyrata	AT5G48335.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G07580.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:19588083-19589366 FORWARD LENGTH=114	96	114	2.00E-16	118.8	42.7	49.0
Rsa1.0_00323.1.g11318.t2	ref|NP_199648.1| thioesterase family protein [Arabidopsis thaliana] gi|8978341|dbj|BAA98194.1| unnamed protein product [Arabidopsis thaliana] gi|53749132|gb|AAU90051.1| At5g48370 [Arabidopsis thaliana] gi|55733743|gb|AAV59268.1| At5g48370 [Arabidopsis thaliana] gi|110742181|dbj|BAE99018.1| hypothetical protein [Arabidopsis thaliana] gi|332008276|gb|AED95659.1| thioesterase family protein [Arabidopsis thaliana]	442	438	0	99.1	88.5	90.7	thioesterase family protein	gbpln	Arabidopsis thaliana	AT5G48370.1 | Symbols: | Thioesterase/thiol ester dehydrase-isomerase superfamily protein | chr5:19598666-19600512 REVERSE LENGTH=438	442	438	0	99.1	88.5	90.7
Rsa1.0_00323.1.g11319.t1	dbj|BAC56855.1| gamma-glutamyl transferase [Raphanus sativus]	543	575	0	105.9	88.0	93.4	gamma-glutamyl transferase	gbpln	Raphanus sativus	AT4G39640.2 | Symbols: GGT1 | gamma-glutamyl transpeptidase 1 | chr4:18400608-18402861 FORWARD LENGTH=572	543	572	0	105.3	83.4	90.8
Rsa1.0_00323.1.g11320.t1	ref|XP_002863896.1| ATGLR1.3 [Arabidopsis lyrata subsp. lyrata] gi|297309731|gb|EFH40155.1| ATGLR1.3 [Arabidopsis lyrata subsp. lyrata]	877	861	0	98.2	69.1	79.6	ATGLR1.3	gbpln	Arabidopsis lyrata	AT5G48410.1 | Symbols: ATGLR1.3, GLR1.3 | glutamate receptor 1.3 | chr5:19620316-19623277 FORWARD LENGTH=860	877	860	0	98.1	67.3	79.5
Rsa1.0_00323.1.g11321.t1	ref|XP_002863896.1| ATGLR1.3 [Arabidopsis lyrata subsp. lyrata] gi|297309731|gb|EFH40155.1| ATGLR1.3 [Arabidopsis lyrata subsp. lyrata]	880	861	0	97.8	70.3	79.9	ATGLR1.3	gbpln	Arabidopsis lyrata	AT5G48410.1 | Symbols: ATGLR1.3, GLR1.3 | glutamate receptor 1.3 | chr5:19620316-19623277 FORWARD LENGTH=860	880	860	0	97.7	69.4	79.9
Rsa1.0_00323.1.g11322.t1	ref|NP_186837.1| uncharacterized protein [Arabidopsis thaliana] gi|6091728|gb|AAF03440.1|AC010797_16 hypothetical protein [Arabidopsis thaliana] gi|6513943|gb|AAF14847.1|AC011664_29 hypothetical protein [Arabidopsis thaliana] gi|332640208|gb|AEE73729.1| uncharacterized protein AT3G01880 [Arabidopsis thaliana]	498	592	1.00E-124	118.9	43.4	49.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01880.1 | Symbols: | Plant protein of unknown function (DUF946) | chr3:307782-309560 FORWARD LENGTH=592	498	592	1.00E-127	118.9	43.4	49.0
Rsa1.0_00323.1.g11323.t1	ref|XP_002865634.1| hypothetical protein ARALYDRAFT_494897 [Arabidopsis lyrata subsp. lyrata] gi|297311469|gb|EFH41893.1| hypothetical protein ARALYDRAFT_494897 [Arabidopsis lyrata subsp. lyrata]	403	406	0	100.7	81.6	89.8	hypothetical protein ARALYDRAFT_494897	gbpln	Arabidopsis lyrata	AT5G48430.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:19627892-19629112 REVERSE LENGTH=406	403	406	0	100.7	77.2	87.6
Rsa1.0_00323.1.g11324.t1	gb|EOA31586.1| hypothetical protein CARUB_v10014780mg [Capsella rubella]	173	171	3.00E-54	98.8	59.0	76.3	hypothetical protein CARUB_v10014780mg	gbpln	Capsella rubella	AT3G07460.1 | Symbols: | Protein of unknown function, DUF538 | chr3:2384837-2385617 REVERSE LENGTH=177	173	177	8.00E-54	102.3	56.6	72.8
Rsa1.0_00323.1.g11325.t1	dbj|BAD44609.1| fimbrin 2 [Arabidopsis thaliana]	640	654	0	102.2	93.6	96.7	fimbrin 2	gbpln	Arabidopsis thaliana	AT5G48460.1 | Symbols: | Actin binding Calponin homology (CH) domain-containing protein | chr5:19636225-19639365 REVERSE LENGTH=654	640	654	0	102.2	93.6	96.9
Rsa1.0_00323.1.g11326.t1	ref|NP_568697.1| uncharacterized protein [Arabidopsis thaliana] gi|98960899|gb|ABF58933.1| At5g48470 [Arabidopsis thaliana] gi|332008291|gb|AED95674.1| uncharacterized protein AT5G48470 [Arabidopsis thaliana]	397	397	0	100.0	86.6	94.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G48470.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19641810-19644127 FORWARD LENGTH=397	397	397	0	100.0	86.6	94.0
Rsa1.0_00323.1.g11327.t1	gb|EOA12589.1| hypothetical protein CARUB_v10027068mg, partial [Capsella rubella]	188	226	4.00E-41	120.2	58.0	67.0	hypothetical protein CARUB_v10027068mg, partial	gbpln	Capsella rubella	AT5G48480.1 | Symbols: | Lactoylglutathione lyase / glyoxalase I family protein | chr5:19644814-19645658 FORWARD LENGTH=166	188	166	4.00E-39	88.3	54.3	63.8
Rsa1.0_00323.1.g11328.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00323.1.g11329.t1	ref|NP_568700.1| uncharacterized protein [Arabidopsis thaliana] gi|21553505|gb|AAM62598.1| unknown [Arabidopsis thaliana] gi|27754391|gb|AAO22644.1| unknown protein [Arabidopsis thaliana] gi|28393943|gb|AAO42379.1| unknown protein [Arabidopsis thaliana] gi|332008295|gb|AED95678.1| uncharacterized protein AT5G48500 [Arabidopsis thaliana]	146	167	6.00E-49	114.4	76.0	82.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G48500.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10930.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19653235-19654017 FORWARD LENGTH=167	146	167	2.00E-51	114.4	76.0	82.9
Rsa1.0_00323.1.g11330.t1	ref|XP_002865649.1| hypothetical protein ARALYDRAFT_494916 [Arabidopsis lyrata subsp. lyrata] gi|297311484|gb|EFH41908.1| hypothetical protein ARALYDRAFT_494916 [Arabidopsis lyrata subsp. lyrata]	340	263	2.00E-81	77.4	47.6	52.4	hypothetical protein ARALYDRAFT_494916	gbpln	Arabidopsis lyrata	AT5G48540.1 | Symbols: | receptor-like protein kinase-related family protein | chr5:19669096-19669887 REVERSE LENGTH=263	340	263	3.00E-81	77.4	45.0	48.8
Rsa1.0_00324.1.g11331.t1	ref|XP_002878010.1| hypothetical protein ARALYDRAFT_485918 [Arabidopsis lyrata subsp. lyrata] gi|297323848|gb|EFH54269.1| hypothetical protein ARALYDRAFT_485918 [Arabidopsis lyrata subsp. lyrata]	342	346	1.00E-127	101.2	82.2	89.5	hypothetical protein ARALYDRAFT_485918	gbpln	Arabidopsis lyrata	AT3G54990.1 | Symbols: SMZ | Integrase-type DNA-binding superfamily protein | chr3:20373718-20376522 REVERSE LENGTH=346	342	346	1.00E-127	101.2	81.3	89.5
Rsa1.0_00324.1.g11332.t1	ref|XP_002876279.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322117|gb|EFH52538.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	855	850	0	99.4	72.2	83.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G54980.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:20370293-20372848 FORWARD LENGTH=851	855	851	0	99.5	70.2	83.0
Rsa1.0_00324.1.g11333.t1	ref|XP_002878009.1| hypothetical protein ARALYDRAFT_324027 [Arabidopsis lyrata subsp. lyrata] gi|297323847|gb|EFH54268.1| hypothetical protein ARALYDRAFT_324027 [Arabidopsis lyrata subsp. lyrata]	385	359	1.00E-152	93.2	74.0	81.0	hypothetical protein ARALYDRAFT_324027	gbpln	Arabidopsis lyrata	AT3G54970.1 | Symbols: | D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein | chr3:20368329-20370070 REVERSE LENGTH=353	385	353	1.00E-153	91.7	73.8	79.7
Rsa1.0_00324.1.g11334.t2	dbj|BAJ33696.1| unnamed protein product [Thellungiella halophila]	578	572	0	99.0	91.2	93.9	unnamed protein product	----	----	AT3G54960.1 | Symbols: ATPDIL1-3, PDI1, ATPDI1, PDIL1-3 | PDI-like 1-3 | chr3:20363514-20366822 REVERSE LENGTH=579	578	579	0	100.2	86.5	90.8
Rsa1.0_00324.1.g11335.t1	ref|XP_002878007.1| hypothetical protein ARALYDRAFT_485912 [Arabidopsis lyrata subsp. lyrata] gi|297323845|gb|EFH54266.1| hypothetical protein ARALYDRAFT_485912 [Arabidopsis lyrata subsp. lyrata]	504	504	0	100.0	85.9	92.1	hypothetical protein ARALYDRAFT_485912	gbpln	Arabidopsis lyrata	AT3G54950.1 | Symbols: PLP7, PLA IIIA | patatin-like protein 6 | chr3:20359076-20360774 REVERSE LENGTH=488	504	488	0	96.8	85.3	91.3
Rsa1.0_00324.1.g11336.t1	ref|NP_567010.5| Papain family cysteine protease [Arabidopsis thaliana] gi|17979125|gb|AAL49820.1| putative cysteine proteinase [Arabidopsis thaliana] gi|332645795|gb|AEE79316.1| Papain family cysteine protease [Arabidopsis thaliana]	364	367	0	100.8	83.2	92.3	Papain family cysteine protease	gbpln	Arabidopsis thaliana	AT3G54940.2 | Symbols: | Papain family cysteine protease | chr3:20354402-20356127 FORWARD LENGTH=367	364	367	0	100.8	83.2	92.3
Rsa1.0_00324.1.g11337.t1	gb|EOA23878.1| hypothetical protein CARUB_v10017093mg [Capsella rubella] gi|482559688|gb|EOA23879.1| hypothetical protein CARUB_v10017093mg [Capsella rubella]	491	491	0	100.0	89.8	93.9	hypothetical protein CARUB_v10017093mg	gbpln	Capsella rubella	AT3G54930.1 | Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr3:20351084-20352659 REVERSE LENGTH=497	491	497	0	101.2	89.8	93.9
Rsa1.0_00324.1.g11338.t1	gb|AAQ87025.1| pectate lyase-like protein [Brassica napus]	492	500	0	101.6	92.1	94.7	pectate lyase-like protein	gbpln	Brassica napus	AT3G54920.1 | Symbols: PMR6 | Pectin lyase-like superfamily protein | chr3:20345311-20348477 FORWARD LENGTH=501	492	501	0	101.8	80.9	87.4
Rsa1.0_00324.1.g11339.t1	gb|EOA24113.1| hypothetical protein CARUB_v10017345mg [Capsella rubella]	376	414	2.00E-97	110.1	56.9	72.1	hypothetical protein CARUB_v10017345mg	gbpln	Capsella rubella	AT4G10400.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:6446335-6447715 REVERSE LENGTH=409	376	409	1.00E-81	108.8	51.3	65.2
Rsa1.0_00324.1.g11340.t1	gb|EOA24113.1| hypothetical protein CARUB_v10017345mg [Capsella rubella]	417	414	1.00E-138	99.3	63.5	78.2	hypothetical protein CARUB_v10017345mg	gbpln	Capsella rubella	AT4G10400.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:6446335-6447715 REVERSE LENGTH=409	417	409	1.00E-117	98.1	56.1	71.0
Rsa1.0_00324.1.g11341.t1	gb|EOA25157.1| hypothetical protein CARUB_v10018468mg [Capsella rubella]	718	731	0	101.8	88.7	94.2	hypothetical protein CARUB_v10018468mg	gbpln	Capsella rubella	AT3G54800.2 | Symbols: | Pleckstrin homology (PH) and lipid-binding START domains-containing protein | chr3:20286378-20289880 FORWARD LENGTH=733	718	733	0	102.1	88.3	94.4

<table>
<tr><td>Rsa1.0_00324.1.g11342.t1</td><td>ref|XP_002878000.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297323838|gb|EFH54259.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]</td><td>262</td><td>760</td><td>1.00E-89</td><td>290.1</td><td>64.5</td><td>67.9</td><td>armadillo/beta-catenin repeat family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G54790.2 | Symbols: | ARM repeat superfamily protein | chr3:20281830-20284255 REVERSE LENGTH=724</td><td>262</td><td>724</td><td>1.00E-91</td><td>276.3</td><td>64.1</td><td>67.6</td></tr>
<tr><td>Rsa1.0_00324.1.g11343.t1</td><td>gb|AAM61280.1| RNA binding protein-like [Arabidopsis thaliana]</td><td>303</td><td>261</td><td>1.00E-100</td><td>86.1</td><td>64.4</td><td>70.0</td><td>RNA binding protein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G54770.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:20273863-20275827 REVERSE LENGTH=261</td><td>303</td><td>261</td><td>1.00E-102</td><td>86.1</td><td>64.0</td><td>70.0</td></tr>
<tr><td>Rsa1.0_00324.1.g11344.t25</td><td>ref|XP_002877997.1| hypothetical protein ARALYDRAFT_485881 [Arabidopsis lyrata subsp. lyrata] gi|297323835|gb|EFH54256.1| hypothetical protein ARALYDRAFT_485881 [Arabidopsis lyrata subsp. lyrata]</td><td>624</td><td>608</td><td>0</td><td>97.4</td><td>77.6</td><td>86.1</td><td>hypothetical protein ARALYDRAFT_485881</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G54750.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages. | chr3:20264833-20268416 REVERSE LENGTH=590</td><td>624</td><td>590</td><td>0</td><td>94.6</td><td>74.5</td><td>84.5</td></tr>
<tr><td>Rsa1.0_00324.1.g11345.t1</td><td>ref|NP_001078285.1| uncharacterized protein [Arabidopsis thaliana] gi|7258378|emb|CAB77594.1| putative protein [Arabidopsis thaliana] gi|332645755|gb|AEE79276.1| uncharacterized protein AT3G54740 [Arabidopsis thaliana]</td><td>418</td><td>438</td><td>0</td><td>104.8</td><td>80.1</td><td>88.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G54740.2 | Symbols: | Protein of unknown function, DUF593 | chr3:20262949-20264466 FORWARD LENGTH=438</td><td>418</td><td>438</td><td>0</td><td>104.8</td><td>80.1</td><td>88.3</td></tr>
<tr><td>Rsa1.0_00324.1.g11346.t1</td><td>ref|XP_002877996.1| hypothetical protein ARALYDRAFT_485877 [Arabidopsis lyrata subsp. lyrata] gi|297323834|gb|EFH54255.1| hypothetical protein ARALYDRAFT_485877 [Arabidopsis lyrata subsp. lyrata]</td><td>707</td><td>705</td><td>0</td><td>99.7</td><td>85.6</td><td>92.4</td><td>hypothetical protein ARALYDRAFT_485877</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G54720.1 | Symbols: AMP1, COP2, HPT, PT, MFO1 | Peptidase M28 family protein | chr3:20254852-20257815 REVERSE LENGTH=705</td><td>707</td><td>705</td><td>0</td><td>99.7</td><td>85.6</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00324.1.g11347.t1</td><td>ref|XP_002877995.1| inorganic phosphate transporter 1-7 /Pi cotransporter [Arabidopsis lyrata subsp. lyrata] gi|297323833|gb|EFH54254.1| inorganic phosphate transporter 1-7 /Pi cotransporter [Arabidopsis lyrata subsp. lyrata]</td><td>531</td><td>533</td><td>0</td><td>100.4</td><td>90.0</td><td>94.0</td><td>inorganic phosphate transporter 1-7 /Pi cotransporter</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G54700.1 | Symbols: PHT1;7 | phosphate transporter 1;7 | chr3:20248463-20250070 REVERSE LENGTH=535</td><td>531</td><td>535</td><td>0</td><td>100.8</td><td>89.8</td><td>93.8</td></tr>
<tr><td>Rsa1.0_00324.1.g11348.t2</td><td>ref|NP_001190092.1| structural maintenance of chromosomes 1 [Arabidopsis thaliana] gi|332645744|gb|AEE79265.1| structural maintenance of chromosomes 1 [Arabidopsis thaliana]</td><td>1271</td><td>1239</td><td>0</td><td>97.5</td><td>85.3</td><td>91.0</td><td>structural maintenance of chromosomes 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G54670.3 | Symbols: TTN8 | Structural maintenance of chromosomes (SMC) family protein | chr3:20235818-20243701 FORWARD LENGTH=1239</td><td>1271</td><td>1239</td><td>0</td><td>97.5</td><td>85.3</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00324.1.g11349.t1</td><td>gb|AAK27157.1|AF349449_1 glutathione reductase [Brassica juncea]</td><td>563</td><td>564</td><td>0</td><td>100.2</td><td>95.4</td><td>97.3</td><td>glutathione reductase</td><td>gbpln</td><td>Brassica juncea</td><td>AT3G54660.1 | Symbols: GR, EMB2360, ATGR2 | glutathione reductase | chr3:20230356-20233100 REVERSE LENGTH=565</td><td>563</td><td>565</td><td>0</td><td>100.4</td><td>90.2</td><td>95.6</td></tr>
<tr><td>Rsa1.0_00324.1.g11350.t1</td><td>ref|NP_567005.2| F-box/LRR-repeat protein 17 [Arabidopsis thaliana] gi|75331246|sp|Q8W104.1|FBL17_ARATH RecName: Full=F-box/LRR-repeat protein 17; AltName: Full=F-box-like protein 17 gi|18087570|gb|AAL58916.1|AF462827_1 AT3g54650/T5N23_10 [Arabidopsis thaliana] gi|22655356|gb|AAM98270.1| At3g54650/T5N23_10 [Arabidopsis thaliana] gi|332645740|gb|AEE79261.1| F-box/LRR-repeat protein 17 [Arabidopsis thaliana]</td><td>578</td><td>593</td><td>0</td><td>102.6</td><td>84.3</td><td>91.9</td><td>F-box/LRR-repeat protein 17</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G54650.1 | Symbols: FBL17 | RNI-like superfamily protein | chr3:20226004-20228882 REVERSE LENGTH=593</td><td>578</td><td>593</td><td>0</td><td>102.6</td><td>84.3</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00324.1.g11351.t1</td><td>emb|CAH56477.1| tryptophan synthase, alpha subunit (TSA1) [Isatis tinctoria] gi|52673242|emb|CAH56478.1| tryptophan synthase, alpha subunit (TSA1) [Isatis tinctoria]</td><td>311</td><td>311</td><td>1.00E-157</td><td>100.0</td><td>92.9</td><td>96.8</td><td>tryptophan synthase, alpha subunit (TSA1)</td><td>gbpln</td><td>Isatis tinctoria</td><td>AT3G54640.1 | Symbols: TSA1, TRP3 | tryptophan synthase alpha chain | chr3:20223331-20225303 REVERSE LENGTH=312</td><td>311</td><td>312</td><td>1.00E-156</td><td>100.3</td><td>91.3</td><td>96.8</td></tr>
<tr><td>Rsa1.0_00324.1.g11352.t1</td><td>ref|XP_002877991.1| kinetochore protein [Arabidopsis lyrata subsp. lyrata] gi|297323829|gb|EFH54250.1| kinetochore protein [Arabidopsis lyrata subsp. lyrata]</td><td>568</td><td>567</td><td>0</td><td>99.8</td><td>68.3</td><td>81.3</td><td>kinetochore protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G54630.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Kinetochore protein Ndc80 (InterPro:IPR005550); Has 24780 Blast hits to 15608 proteins in 1321 species: Archae - 545; Bacteria - 2969; Metazoa - 12597; Fungi - 2181; Plants - 1581; Viruses - 39; Other Eukaryotes - 4868 (source: NCBI BLink). | chr3:20221195-20222901 REVERSE LENGTH=568</td><td>568</td><td>568</td><td>0</td><td>100.0</td><td>66.9</td><td>80.5</td></tr>
</table>

Rsa1.0_00324.1.g11353.t1	dbj|BAJ34147.1| unnamed protein product [Thellungiella halophila]	374	402	1.00E-129	107.5	80.2	85.3	unnamed protein product	----	----	AT3G54620.1 | Symbols: ATBZIP25, BZO2H4, BZIP25 | basic leucine zipper 25 | chr3:20218085-20220341 REVERSE LENGTH=403	374	403	1.00E-115	107.8	73.8	79.9
Rsa1.0_00324.1.g11354.t1	#	#	#	#	#	#	#	-	----	----	AT3G54610.1 | Symbols: HAT1, GCN5, HAG1, HAC3, HAG01, BGT | histone acetyltransferase of the GNAT family 1 | chr3:20213593-20217375 FORWARD LENGTH=568	53	568	1.00E-10	1071.7	49.1	52.8
Rsa1.0_00324.1.g11355.t1	ref|XP_002974570.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii] gi|300157465|gb|EFJ24090.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii]	828	516	4.00E-39	62.3	31.4	38.3	hypothetical protein SELMODRAFT_442529	gbpln	Selaginella moellendorffii	AT3G54590.1 | Symbols: ATHRGP1, HRGP1 | hydroxyproline-rich glycoprotein | chr3:20206223-20208472 FORWARD LENGTH=699	828	699	1.00E-17	84.4	6.5	7.6
Rsa1.0_00324.1.g11356.t1	gb|AAD29058.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	324	1229	2.00E-67	379.3	37.7	52.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	324	575	2.00E-37	177.5	31.5	45.4
Rsa1.0_00324.1.g11357.t1	ref|XP_002974570.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii] gi|300157465|gb|EFJ24090.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii]	757	516	2.00E-38	68.2	35.4	40.0	hypothetical protein SELMODRAFT_442529	gbpln	Selaginella moellendorffii	AT3G54590.1 | Symbols: ATHRGP1, HRGP1 | hydroxyproline-rich glycoprotein | chr3:20206223-20208472 FORWARD LENGTH=699	757	699	8.00E-17	92.3	6.9	7.8
Rsa1.0_00324.1.g11358.t1	ref|NP_001141633.1| uncharacterized protein LOC100273753 [Zea mays] gi|242065684|ref|XP_002454131.1| hypothetical protein SORBIDRAFT_04g025140 [Sorghum bicolor] gi|194705342|gb|ACF86755.1| unknown [Zea mays] gi|195605334|gb|ACG24497.1| histone H2A variant 1 [Zea mays] gi|195605602|gb|ACG24631.1| histone H2A variant 1 [Zea mays] gi|195624562|gb|ACG34111.1| histone H2A variant 1 [Zea mays] gi|241933962|gb|EES07107.1| hypothetical protein SORBIDRAFT_04g025140 [Sorghum bicolor] gi|414864935|tpg|DAA43492.1| TPA: histone H2A [Zea mays]	137	138	5.00E-62	100.7	87.6	94.2	uncharacterized protein LOC100273753	gbpln	Sorghum bicolor	AT3G54560.1 | Symbols: HTA11 | histone H2A 11 | chr3:20196532-20197466 FORWARD LENGTH=136	137	136	2.00E-63	99.3	94.9	97.1
Rsa1.0_00324.1.g11359.t1	ref|XP_002876258.1| ATGCN4 [Arabidopsis lyrata subsp. lyrata] gi|297322096|gb|EFH52517.1| ATGCN4 [Arabidopsis lyrata subsp. lyrata]	718	723	0	100.7	89.6	95.5	ATGCN4	gbpln	Arabidopsis lyrata	AT3G54540.1 | Symbols: ATGCN4, GCN4 | general control non-repressible 4 | chr3:20190393-20192564 FORWARD LENGTH=723	718	723	0	100.7	89.6	94.8
Rsa1.0_00325.1.g11360.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	441	530	1.00E-42	120.2	21.5	27.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G32613.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr5:12263255-12265041 FORWARD LENGTH=457	441	457	8.00E-11	103.6	11.8	17.5
Rsa1.0_00325.1.g11361.t1	ref|XP_002889996.1| hypothetical protein ARALYDRAFT_888685 [Arabidopsis lyrata subsp. lyrata] gi|297335838|gb|EFH66255.1| hypothetical protein ARALYDRAFT_888685 [Arabidopsis lyrata subsp. lyrata]	345	344	0	99.7	92.5	95.9	hypothetical protein ARALYDRAFT_888685	gbpln	Arabidopsis lyrata	AT1G13260.1 | Symbols: RAV1, EDF4 | related to ABI3/VP1 1 | chr1:4542386-4543420 FORWARD LENGTH=344	345	344	0	99.7	90.7	94.8
Rsa1.0_00325.1.g11362.t1	ref|XP_002892738.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297338580|gb|EFH68997.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	308	303	1.00E-140	98.4	83.1	90.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G13290.1 | Symbols: DOT5, WIP6 | C2H2-like zinc finger protein | chr1:4550366-4551527 REVERSE LENGTH=302	308	302	1.00E-142	98.1	83.8	90.3
Rsa1.0_00325.1.g11363.t1	gb|EOA36651.1| hypothetical protein CARUB_v10011925mg [Capsella rubella]	312	344	1.00E-131	110.3	82.4	85.6	hypothetical protein CARUB_v10011925mg	gbpln	Capsella rubella	AT1G13300.1 | Symbols: HRS1 | myb-like transcription factor family protein | chr1:4556977-4558591 FORWARD LENGTH=344	312	344	1.00E-129	110.3	82.4	85.9
Rsa1.0_00325.1.g11364.t2	gb|EOA39103.1| hypothetical protein CARUB_v10011847mg [Capsella rubella]	240	226	1.00E-115	94.2	87.5	91.3	hypothetical protein CARUB_v10011847mg	gbpln	Capsella rubella	AT1G13330.1 | Symbols: AHP2 | Arabidopsis Hop2 homolog | chr1:4568008-4569410 FORWARD LENGTH=226	240	226	1.00E-113	94.2	83.8	90.8
Rsa1.0_00325.1.g11365.t1	ref|XP_002892743.1| hypothetical protein ARALYDRAFT_471490 [Arabidopsis lyrata subsp. lyrata] gi|297338585|gb|EFH69002.1| hypothetical protein ARALYDRAFT_471490 [Arabidopsis lyrata subsp. lyrata]	420	410	1.00E-161	97.6	74.8	84.0	hypothetical protein ARALYDRAFT_471490	gbpln	Arabidopsis lyrata	AT1G13340.1 | Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr1:4569622-4571043 REVERSE LENGTH=409	420	409	1.00E-157	97.4	72.1	83.3

<table>
<tr><td>Rsa1.0_00325.1.g11366.t1</td><td>ref|NP_683304.1| uncharacterized protein [Arabidopsis thaliana] gi|9958057|gb|AAG09546.1|AC011810_5 Unknown Protein [Arabidopsis thaliana] gi|27754364|gb|AAO22631.1| unknown protein [Arabidopsis thaliana] gi|28393909|gb|AAO42362.1| unknown protein [Arabidopsis thaliana] gi|332190884|gb|AEE29005.1| uncharacterized protein AT1G13360 [Arabidopsis thaliana]</td><td>176</td><td>194</td><td>7.00E-64</td><td>110.2</td><td>79.5</td><td>86.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G13360.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G25870.1); Has 69 Blast hits to 69 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4577229-4577813 REVERSE LENGTH=194</td><td>176</td><td>194</td><td>3.00E-66</td><td>110.2</td><td>79.5</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00325.1.g11367.t1</td><td>ref|XP_002892745.1| hypothetical protein ARALYDRAFT_471492 [Arabidopsis lyrata subsp. lyrata] gi|297338587|gb|EFH69004.1| hypothetical protein ARALYDRAFT_471492 [Arabidopsis lyrata subsp. lyrata]</td><td>188</td><td>188</td><td>4.00E-88</td><td>100.0</td><td>89.9</td><td>94.7</td><td>hypothetical protein ARALYDRAFT_471492</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G13380.1 | Symbols: | Protein of unknown function (DUF1218) | chr1:4589218-4590362 REVERSE LENGTH=188</td><td>188</td><td>188</td><td>6.00E-89</td><td>100.0</td><td>89.4</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00325.1.g11368.t1</td><td>gb|EOA38616.1| hypothetical protein CARUB_v10010468mg [Capsella rubella]</td><td>161</td><td>171</td><td>4.00E-42</td><td>106.2</td><td>65.8</td><td>73.9</td><td>hypothetical protein CARUB_v10010468mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G13390.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G68490.1); Has 114 Blast hits to 114 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 114; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4592829-4593549 REVERSE LENGTH=176</td><td>161</td><td>176</td><td>3.00E-42</td><td>109.3</td><td>65.2</td><td>72.7</td></tr>
<tr><td>Rsa1.0_00325.1.g11369.t1</td><td>gb|EOA37285.1| hypothetical protein CARUB_v10010898mg [Capsella rubella]</td><td>167</td><td>245</td><td>4.00E-40</td><td>146.7</td><td>54.5</td><td>59.3</td><td>hypothetical protein CARUB_v10010898mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G13400.1 | Symbols: NUB, JGL | C2H2 and C2HC zinc fingers superfamily protein | chr1:4597784-4598911 FORWARD LENGTH=207</td><td>167</td><td>207</td><td>3.00E-40</td><td>124.0</td><td>59.9</td><td>64.7</td></tr>
<tr><td>Rsa1.0_00325.1.g11370.t10</td><td>ref|NP_172644.1| arogenate dehydratase 1 [Arabidopsis thaliana] gi|75265511|sp|Q9SA96.1|AROD1_ARATH RecName: Full=Arogenate dehydratase/prephenate dehydratase 1, chloroplastic; Short=AtADT1; Short=AtPDT1; Flags: Precursor gi|4835776|gb|AAD30242.1|AC007296_3 Similar to gi|2392772 T32N15.11 putative chloroplast prephenate dehydratase from Arabidopsis thaliana BAC gb|AC002534 and is a member of the PF|00800 Prephenate dehydratase family. ESTs gb|T21562 and gb|T21062 come from this gene [Arabidopsis thaliana] gi|89340486|gb|ABD67752.1| arogenate dehydratase isoform 3 [Arabidopsis thaliana] gi|332190665|gb|AEE28786.1| arogenate dehydratase 1 [Arabidopsis thaliana]</td><td>892</td><td>392</td><td>0</td><td>43.9</td><td>36.7</td><td>39.0</td><td>arogenate dehydratase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G11790.1 | Symbols: ADT1 | arogenate dehydratase 1 | chr1:3981476-3984962 FORWARD LENGTH=392</td><td>892</td><td>392</td><td>0</td><td>43.9</td><td>36.7</td><td>39.0</td></tr>
<tr><td>Rsa1.0_00325.1.g11371.t1</td><td>ref|XP_002889895.1| hypothetical protein ARALYDRAFT_471318 [Arabidopsis lyrata subsp. lyrata] gi|297335737|gb|EFH66154.1| hypothetical protein ARALYDRAFT_471318 [Arabidopsis lyrata subsp. lyrata]</td><td>532</td><td>536</td><td>0</td><td>100.8</td><td>83.3</td><td>90.6</td><td>hypothetical protein ARALYDRAFT_471318</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G11770.1 | Symbols: | FAD-binding Berberine family protein | chr1:3975679-3977289 FORWARD LENGTH=536</td><td>532</td><td>536</td><td>0</td><td>100.8</td><td>82.9</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00325.1.g11372.t1</td><td>ref|XP_002892655.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338497|gb|EFH68914.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>238</td><td>414</td><td>5.00E-94</td><td>173.9</td><td>74.8</td><td>84.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G11755.1 | Symbols: LEW1 | Undecaprenyl pyrophosphate synthetase family protein | chr1:3969987-3971488 REVERSE LENGTH=254</td><td>238</td><td>254</td><td>3.00E-95</td><td>106.7</td><td>73.1</td><td>85.3</td></tr>
<tr><td>Rsa1.0_00325.1.g11373.t1</td><td>gb|EOA37537.1| hypothetical protein CARUB_v10011779mg [Capsella rubella]</td><td>567</td><td>595</td><td>0</td><td>104.9</td><td>75.0</td><td>83.4</td><td>hypothetical protein CARUB_v10011779mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G11740.1 | Symbols: | ankyrin repeat family protein | chr1:3963317-3966824 REVERSE LENGTH=644</td><td>567</td><td>644</td><td>0</td><td>113.6</td><td>73.4</td><td>81.8</td></tr>
<tr><td>Rsa1.0_00325.1.g11374.t1</td><td>gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>882</td><td>1496</td><td>0</td><td>169.6</td><td>58.8</td><td>74.7</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>882</td><td>1262</td><td>1.00E-138</td><td>143.1</td><td>26.4</td><td>37.6</td></tr>
<tr><td>Rsa1.0_00326.1.g11375.t1</td><td>gb|EOA39854.1| hypothetical protein CARUB_v10008528mg [Capsella rubella]</td><td>119</td><td>659</td><td>1.00E-11</td><td>553.8</td><td>37.8</td><td>41.2</td><td>hypothetical protein CARUB_v10008528mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G49890.1 | Symbols: QWRF2 | Family of unknown function (DUF566) | chr1:18470282-18473463 FORWARD LENGTH=659</td><td>119</td><td>659</td><td>7.00E-13</td><td>553.8</td><td>36.1</td><td>39.5</td></tr>
<tr><td>Rsa1.0_00326.1.g11376.t1</td><td>gb|ABD65150.1| hypothetical protein 40.t00029 [Brassica oleracea]</td><td>298</td><td>311</td><td>1.00E-109</td><td>104.4</td><td>75.8</td><td>82.6</td><td>hypothetical protein 40.t00029</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17680.1 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr4:9842903-9844095 REVERSE LENGTH=314</td><td>298</td><td>314</td><td>8.00E-94</td><td>105.4</td><td>65.1</td><td>75.2</td></tr>
<tr><td>Rsa1.0_00326.1.g11377.t1</td><td>gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]</td><td>88</td><td>1231</td><td>1.00E-15</td><td>1398.9</td><td>51.1</td><td>62.5</td><td>Very similar to retrotransposon reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00326.1.g11378.t1	gb|ABD65149.1| hypothetical protein 40.t00027 [Brassica oleracea]	157	168	3.00E-57	107.0	81.5	89.2	hypothetical protein 40.t00027	gbpln	Brassica oleracea	AT4G17670.1 | Symbols: | Protein of unknown function (DUF581) | chr4:9833948-9834663 REVERSE LENGTH=159	157	159	3.00E-46	101.3	72.0	80.9
Rsa1.0_00326.1.g11379.t1	gb|EOA17294.1| hypothetical protein CARUB_v10005567mg [Capsella rubella]	253	253	1.00E-117	100.0	84.2	89.7	hypothetical protein CARUB_v10005567mg	gbpln	Capsella rubella	AT4G17650.1 | Symbols: | Polyketide cyclase / dehydrase and lipid transport protein | chr4:9827749-9829443 FORWARD LENGTH=256	253	256	1.00E-106	101.2	81.8	88.5
Rsa1.0_00326.1.g11380.t1	ref|NP_193499.1| casein kinase 2 subunit beta' [Arabidopsis thaliana] gi|729882|sp|P40229.1|CSK2C_ARATH RecName: Full=Casein kinase II subunit beta'; Short=CK II beta' gi|467975|gb|AAA53234.1| casein kinase II beta subunit CKB2 [Arabidopsis thaliana] gi|2245122|emb|CAB10544.1| casein kinase II beta chain CKB2 [Arabidopsis thaliana] gi|7268516|emb|CAB78767.1| casein kinase II beta chain CKB2 [Arabidopsis thaliana] gi|21554030|gb|AAM63111.1| casein kinase II beta chain CKB2 [Arabidopsis thaliana] gi|26453134|dbj|BAC43643.1| putative casein kinase II beta chain CKB2 [Arabidopsis thaliana] gi|28950839|gb|AAO63343.1| At4g17640 [Arabidopsis thaliana] gi|332658527|gb|AEE83927.1| casein kinase 2 subunit beta' [Arabidopsis thaliana]	284	282	1.00E-140	99.3	84.9	90.1	casein kinase 2 subunit beta'	gbpln	Arabidopsis thaliana	AT4G17640.1 | Symbols: CKB2 | casein kinase II beta chain 2 | chr4:9825438-9826988 FORWARD LENGTH=282	284	282	1.00E-143	99.3	84.9	90.1
Rsa1.0_00326.1.g11381.t1	gb|EOA16382.1| hypothetical protein CARUB_v10004533mg [Capsella rubella]	539	543	0	100.7	81.1	86.6	hypothetical protein CARUB_v10004533mg	gbpln	Capsella rubella	AT4G17620.2 | Symbols: | glycine-rich protein | chr4:9822005-9824859 FORWARD LENGTH=544	539	544	0	100.9	76.8	84.4
Rsa1.0_00326.1.g11382.t1	ref|XP_002870095.1| hypothetical protein ARALYDRAFT_914947 [Arabidopsis lyrata subsp. lyrata] gi|297315931|gb|EFH46354.1| hypothetical protein ARALYDRAFT_914947 [Arabidopsis lyrata subsp. lyrata]	460	213	1.00E-115	46.3	44.3	44.8	hypothetical protein ARALYDRAFT_914947	gbpln	Arabidopsis lyrata	AT4G17615.1 | Symbols: CBL1, ATCBL1, SCABP5 | calcineurin B-like protein 1 | chr4:9817142-9818995 FORWARD LENGTH=213	460	213	1.00E-117	46.3	43.9	44.8
Rsa1.0_00326.1.g11383.t3	ref|XP_002868048.1| tRNA/rRNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313884|gb|EFH44307.1| tRNA/rRNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	1820	1852	0	101.8	86.7	92.6	tRNA/rRNA methyltransferase family protein	gbpln	Arabidopsis lyrata	AT4G17610.1 | Symbols: | tRNA/rRNA methyltransferase (SpoU) family protein | chr4:9805652-9814910 REVERSE LENGTH=1850	1820	1850	0	101.6	87.0	92.7
Rsa1.0_00326.1.g11384.t1	ref|NP_178730.2| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|330250943|gb|AEC06037.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	835	820	0	98.2	79.2	84.9	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G07170.1 | Symbols: | ARM repeat superfamily protein | chr2:2975565-2978692 FORWARD LENGTH=820	835	820	0	98.2	79.2	84.9
Rsa1.0_00326.1.g11385.t1	gb|AAM63191.1| putative cell wall-plasma membrane disconnecting CLCT protein (AIR1A) [Arabidopsis thaliana]	200	111	4.00E-20	55.5	26.5	37.0	putative cell wall-plasma membrane disconnecting CLCT protein (AIR1A)	gbpln	Arabidopsis thaliana	AT4G12550.1 | Symbols: AIR1 | Auxin-Induced in Root cultures 1 | chr4:7439176-7439511 FORWARD LENGTH=111	200	111	3.00E-22	55.5	26.0	37.0
Rsa1.0_00326.1.g11386.t1	dbj|BAJ34326.1| unnamed protein product [Thellungiella halophila]	503	516	0	102.6	84.5	90.3	unnamed protein product	----	----	AT4G17570.3 | Symbols: GATA26 | GATA transcription factor 26 | chr4:9784329-9786974 REVERSE LENGTH=514	503	514	0	102.2	83.1	89.7
Rsa1.0_00326.1.g11387.t1	ref|NP_193490.1| putative F-box protein [Arabidopsis thaliana] gi|122214541|sp|Q3EA00.1|FB235_ARATH RecName: Full=Putative F-box protein At4g17565 gi|332658511|gb|AEE83911.1| putative F-box protein [Arabidopsis thaliana]	372	378	1.00E-101	101.6	53.8	68.3	putative F-box protein	gbpln	Arabidopsis thaliana	AT4G17565.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr4:9782508-9783644 REVERSE LENGTH=378	372	378	1.00E-103	101.6	53.8	68.3
Rsa1.0_00326.1.g11388.t1	ref|XP_002868054.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313890|gb|EFH44313.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	145	335	5.00E-29	231.0	46.2	46.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G17550.1 | Symbols: | Major facilitator superfamily protein | chr4:9777938-9779738 REVERSE LENGTH=544	145	544	2.00E-31	375.2	46.2	46.9

Rsa1.0_00326.1.g11389.t1	ref|NP_193487.2| uncharacterized protein [Arabidopsis thaliana] gi|20260466|gb|AAM13131.1| unknown protein [Arabidopsis thaliana] gi|28059310|gb|AAO30046.1| unknown protein [Arabidopsis thaliana] gi|332658508|gb|AEE83908.1| uncharacterized protein AT4G17540 [Arabidopsis thaliana]	255	294	2.00E-92	115.3	76.5	83.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G17540.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9775982-9777765 FORWARD LENGTH=294	255	294	6.00E-95	115.3	76.5	83.1
Rsa1.0_00326.1.g11390.t1	gb|ABD65068.1| GTP-binding protein, putative [Brassica oleracea]	202	202	1.00E-115	100.0	99.0	99.5	GTP-binding protein, putative	gbpln	Brassica oleracea	AT4G17530.1 | Symbols: RAB1C, ATRAB1C, ATRABD2C | RAB GTPase homolog 1C | chr4:9773721-9775424 REVERSE LENGTH=202	202	202	1.00E-115	100.0	98.0	98.5
Rsa1.0_00326.1.g11391.t1	gb|ABD65067.1| nuclear RNA binding protein, putative [Brassica oleracea]	345	367	1.00E-129	106.4	79.7	84.6	nuclear RNA binding protein, putative	gbpln	Brassica oleracea	AT4G17520.1 | Symbols: | Hyaluronan / mRNA binding family | chr4:9771496-9773313 FORWARD LENGTH=360	345	360	1.00E-112	104.3	70.1	79.4
Rsa1.0_00326.1.g11392.t1	gb|EOA15862.1| hypothetical protein CARUB_v10007723mg [Capsella rubella]	232	234	1.00E-122	100.9	90.9	95.7	hypothetical protein CARUB_v10007723mg	gbpln	Capsella rubella	AT4G17510.1 | Symbols: UCH3 | ubiquitin C-terminal hydrolase 3 | chr4:9767114-9768648 REVERSE LENGTH=234	232	234	1.00E-124	100.9	89.2	97.0
Rsa1.0_00326.1.g11393.t1	ref|NP_567530.4| ethylene-responsive transcription factor 1A [Arabidopsis thaliana] gi|21264420|sp|O80337.2|EF100_ARATH RecName: Full=Ethylene-responsive transcription factor 1A; Short=AtERF1A; AltName: Full=Ethylene-responsive element-binding factor 1A; Short=EREBP-1A gi|16648795|gb|AAL25588.1| AT4g17500/dl4785w [Arabidopsis thaliana] gi|17064914|gb|AAL32611.1| Unknown protein [Arabidopsis thaliana] gi|27311945|gb|AAO00938.1| Unknown protein [Arabidopsis thaliana] gi|332658503|gb|AEE83903.1| ethylene-responsive transcription factor 1A [Arabidopsis thaliana]	206	268	1.00E-84	130.1	83.5	89.3	ethylene-responsive transcription factor 1A	gbpln	Arabidopsis thaliana	AT4G17500.1 | Symbols: ATERF-1, ERF-1 | ethylene responsive element binding factor 1 | chr4:9759405-9760211 FORWARD LENGTH=268	206	268	4.00E-87	130.1	83.5	89.3
Rsa1.0_00326.1.g11394.t1	ref|XP_002884514.1| hypothetical protein ARALYDRAFT_317406 [Arabidopsis lyrata subsp. lyrata] gi|297330354|gb|EFH60773.1| hypothetical protein ARALYDRAFT_317406 [Arabidopsis lyrata subsp. lyrata]	168	896	4.00E-30	533.3	51.8	60.1	hypothetical protein ARALYDRAFT_317406	gbpln	Arabidopsis lyrata	AT3G05470.1 | Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr3:1579667-1582547 REVERSE LENGTH=884	168	884	3.00E-31	526.2	51.2	59.5
Rsa1.0_00326.1.g11395.t1	gb|ABD65051.1| ethylene responsive element binding factor, putative [Brassica oleracea]	294	290	1.00E-103	98.6	76.2	83.0	ethylene responsive element binding factor, putative	gbpln	Brassica oleracea	AT4G17490.1 | Symbols: ATERF6, ERF-6-6, ERF6 | ethylene responsive element binding factor 6 | chr4:9752973-9753821 REVERSE LENGTH=282	294	282	1.00E-100	95.9	70.1	79.6
Rsa1.0_00326.1.g11396.t2	gb|ABD65098.1| palmitoyl protein thioesterase family protein [Brassica oleracea]	298	300	1.00E-158	100.7	91.3	94.6	palmitoyl protein thioesterase family protein	gbpln	Brassica oleracea	AT4G17480.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:9745313-9746847 REVERSE LENGTH=304	298	304	1.00E-130	102.0	73.5	84.9
Rsa1.0_00326.1.g11397.t2	gb|ABD65097.1| homeobox-leucine zipper protein hat1, putative [Brassica oleracea]	272	273	1.00E-149	100.4	96.0	97.4	homeobox-leucine zipper protein hat1, putative	gbpln	Brassica oleracea	AT4G17460.1 | Symbols: HAT1 | Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein | chr4:9739862-9740983 FORWARD LENGTH=282	272	282	1.00E-140	103.7	93.0	96.0
Rsa1.0_00326.1.g11398.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00326.1.g11399.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1478	1496	0	101.2	57.2	72.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1478	1262	1.00E-140	85.4	15.8	22.5
Rsa1.0_00326.1.g11400.t1	ref|XP_002881770.1| hypothetical protein ARALYDRAFT_903451 [Arabidopsis lyrata subsp. lyrata] gi|297327609|gb|EFH58029.1| hypothetical protein ARALYDRAFT_903451 [Arabidopsis lyrata subsp. lyrata]	191	491	2.00E-87	257.1	82.2	82.7	hypothetical protein ARALYDRAFT_903451	gbpln	Arabidopsis lyrata	AT2G41370.1 | Symbols: BOP2 | Ankyrin repeat family protein / BTB/POZ domain-containing protein | chr2:17238019-17240203 REVERSE LENGTH=491	191	491	1.00E-88	257.1	80.6	82.7
Rsa1.0_00326.1.g11401.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1559	1274	0	81.7	44.7	57.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1559	575	1.00E-72	36.9	11.9	18.2
Rsa1.0_00327.1.g11402.t3	dbj|BAA37167.1| cytochrome P450 [Arabidopsis thaliana]	824	524	1.00E-111	63.6	25.8	27.1	cytochrome P450	gbpln	Arabidopsis thaliana	AT4G36380.1 | Symbols: ROT3 | Cytochrome P450 superfamily protein | chr4:17187973-17192202 REVERSE LENGTH=524	824	524	1.00E-108	63.6	25.7	26.9
Rsa1.0_00327.1.g11403.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00327.1.g11404.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	230	258	1.00E-72	112.2	62.6	73.5	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	230	302	9.00E-42	131.3	47.4	65.2
Rsa1.0_00327.1.g11405.t4	ref|NP_568004.1| putative ubiquitin-conjugating enzyme E2 17 [Arabidopsis thaliana] gi|75318090|sp|O23239.1|UBC17_ARATH RecName: Full=Probable ubiquitin-conjugating enzyme E2 17; AltName: Full=Ubiquitin carrier protein 17 gi|2464941|emb|CAB16814.1| ubiquitin-conjugating enzyme [Arabidopsis thaliana] gi|2801446|gb|AAC39326.1| ubiquitin-conjugating enzyme 17 [Arabidopsis thaliana] gi|7270589|emb|CAB80307.1| ubiquitin-conjugating enzyme [Arabidopsis thaliana] gi|21593655|gb|AAM65622.1| E2, ubiquitin-conjugating enzyme 17 (UBC17) [Arabidopsis thaliana] gi|66354444|gb|AAY44857.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|332661253|gb|AEE86653.1| putative ubiquitin-conjugating enzyme E2 17 [Arabidopsis thaliana] gi|482553365|gb|EOA17558.1| hypothetical protein CARUB_v10005917mg [Capsella rubella]	161	161	4.00E-80	100.0	92.5	96.9	putative ubiquitin-conjugating enzyme E2 17	gbpln	Arabidopsis thaliana	AT4G36410.1 | Symbols: UBC17 | ubiquitin-conjugating enzyme 17 | chr4:17201969-17202890 FORWARD LENGTH=161	161	161	2.00E-82	100.0	92.5	96.9
Rsa1.0_00327.1.g11406.t1	gb|EOA17517.1| hypothetical protein CARUB_v10005850mg [Capsella rubella]	175	180	1.00E-68	102.9	80.6	89.1	hypothetical protein CARUB_v10005850mg	gbpln	Capsella rubella	AT4G36420.1 | Symbols: | Ribosomal protein L12 family protein | chr4:17203718-17204257 REVERSE LENGTH=179	175	179	4.00E-59	102.3	76.6	86.3
Rsa1.0_00327.1.g11407.t1	emb|CCJ34843.1| horseradish peroxidase isoenzyme HRP_08562.1 [Armoracia rusticana]	331	331	1.00E-168	100.0	90.0	94.9	horseradish peroxidase isoenzyme HRP_08562.1	gbpln	Armoracia rusticana	AT4G36430.1 | Symbols: | Peroxidase superfamily protein | chr4:17204648-17205917 REVERSE LENGTH=331	331	331	1.00E-169	100.0	89.4	94.0
Rsa1.0_00327.1.g11408.t1	gb|ACH61906.1| serine palmitoyltransferase long chain base subunit [Brassica rapa subsp. chinensis] gi|197311352|gb|ACH61907.1| serine palmitoyltransferase long chain base subunit [Brassica rapa subsp. chinensis]	480	482	0	100.4	97.3	98.8	serine palmitoyltransferase long chain base subunit	gbpln	Brassica rapa	AT4G36480.2 | Symbols: ATLCB1, LCB1, EMB2779, FBR11 | long-chain base1 | chr4:17218598-17221124 FORWARD LENGTH=482	480	482	0	100.4	91.5	95.4
Rsa1.0_00327.1.g11409.t1	ref|NP_195365.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|4006915|emb|CAB16845.1| hypothetical protein [Arabidopsis thaliana] gi|7270595|emb|CAB80313.1| hypothetical protein [Arabidopsis thaliana] gi|48427662|gb|AAT42380.1| At4g36470 [Arabidopsis thaliana] gi|110741629|dbj|BAE98762.1| hypothetical protein [Arabidopsis thaliana] gi|332661259|gb|AEE86659.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	341	371	1.00E-150	108.8	80.6	85.9	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT4G36470.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:17215128-17216475 REVERSE LENGTH=371	341	371	1.00E-153	108.8	80.6	85.9
Rsa1.0_00327.1.g11410.t1	ref|NP_195368.1| uncharacterized protein [Arabidopsis thaliana] gi|2464932|emb|CAB16811.1| putative protein [Arabidopsis thaliana] gi|7270598|emb|CAB80316.1| putative protein [Arabidopsis thaliana] gi|28393196|gb|AAO42028.1| unknown protein [Arabidopsis thaliana] gi|28827518|gb|AAO50603.1| unknown protein [Arabidopsis thaliana] gi|332661263|gb|AEE86663.1| uncharacterized protein AT4G36500 [Arabidopsis thaliana]	122	122	4.00E-54	100.0	93.4	95.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G36500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G18210.1); Has 50 Blast hits to 50 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17226139-17226507 REVERSE LENGTH=122	122	122	7.00E-57	100.0	93.4	95.1
Rsa1.0_00327.1.g11411.t1	ref|NP_849508.1| transcription factor BEE 2 [Arabidopsis thaliana] gi|332661270|gb|AEE86670.1| transcription factor BEE 2 [Arabidopsis thaliana]	270	302	1.00E-121	111.9	84.8	91.1	transcription factor BEE 2	gbpln	Arabidopsis thaliana	AT4G36540.2 | Symbols: BEE2 | BR enhanced expression 2 | chr4:17243699-17244965 FORWARD LENGTH=302	270	302	1.00E-124	111.9	84.8	91.1

Rsa1.0_00327.1.g11412.t1	ref|XP_002867008.1| U-box domain-containing protein 5 [Arabidopsis lyrata subsp. lyrata] gi|297312844|gb|EFH43267.1| U-box domain-containing protein 5 [Arabidopsis lyrata subsp. lyrata]	521	751	4.00E-76	144.1	31.3	36.7	U-box domain-containing protein 5	gbpln	Arabidopsis lyrata	AT4G36550.1 | Symbols: | ARM repeat superfamily protein | chr4:17245400-17247926 REVERSE LENGTH=718	521	718	6.00E-73	137.8	29.8	34.5
Rsa1.0_00327.1.g11413.t1	gb|EOA15655.1| hypothetical protein CARUB_v10006084mg, partial [Capsella rubella]	75	105	2.00E-31	140.0	86.7	90.7	hypothetical protein CARUB_v10006084mg, partial	gbpln	Capsella rubella	AT1G75250.1 | Symbols: ATRL6, RSM3, RL6 | RAD-like 6 | chr1:28245073-28245453 REVERSE LENGTH=126	75	126	3.00E-25	168.0	58.7	81.3
Rsa1.0_00327.1.g11414.t1	gb|EOA18974.1| hypothetical protein CARUB_v10007612mg [Capsella rubella]	221	212	5.00E-84	95.9	81.4	88.2	hypothetical protein CARUB_v10007612mg	gbpln	Capsella rubella	AT4G36620.1 | Symbols: GATA19 | GATA transcription factor 19 | chr4:17268906-17269662 REVERSE LENGTH=211	221	211	3.00E-83	95.5	81.9	86.0
Rsa1.0_00327.1.g11415.t5	ref|XP_002886383.1| hypothetical protein ARALYDRAFT_474974 [Arabidopsis lyrata subsp. lyrata] gi|297332224|gb|EFH62642.1| hypothetical protein ARALYDRAFT_474974 [Arabidopsis lyrata subsp. lyrata]	992	1049	0	105.7	84.0	90.7	hypothetical protein ARALYDRAFT_474974	gbpln	Arabidopsis lyrata	AT1G63810.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nrap protein (InterPro:IPR005554); Has 396 Blast hits to 382 proteins in 182 species: Archae - 3; Bacteria - 2; Metazoa - 142; Fungi - 146; Plants - 43; Viruses - 0; Other Eukaryotes - 60 (source: NCBI BLink). | chr1:23669690-23675542 REVERSE LENGTH=1053	992	1053	0	106.1	82.8	89.6
Rsa1.0_00327.1.g11416.t1	gb|EOA15961.1| hypothetical protein CARUB_v10004058mg [Capsella rubella]	1001	1000	0	99.9	92.2	96.6	hypothetical protein CARUB_v10004058mg	gbpln	Capsella rubella	AT4G36630.1 | Symbols: EMB2754 | Vacuolar sorting protein 39 | chr4:17272088-17276524 REVERSE LENGTH=1000	1001	1000	0	99.9	91.4	96.5
Rsa1.0_00327.1.g11417.t1	gb|EOA18681.1| hypothetical protein CARUB_v10007257mg [Capsella rubella]	284	293	1.00E-136	103.2	81.3	89.4	hypothetical protein CARUB_v10007257mg	gbpln	Capsella rubella	AT4G36640.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr4:17277187-17278447 REVERSE LENGTH=294	284	294	1.00E-132	103.5	77.5	88.0
Rsa1.0_00327.1.g11418.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00327.1.g11419.t1	gb|EOA16387.1| hypothetical protein CARUB_v10004541mg, partial [Capsella rubella]	511	540	0	105.7	87.1	91.4	hypothetical protein CARUB_v10004541mg, partial	gbpln	Capsella rubella	AT4G36650.1 | Symbols: ATPBRP, PBRP | plant-specific TFIIB-related protein | chr4:17283283-17285527 REVERSE LENGTH=503	511	503	0	98.4	86.7	91.2
Rsa1.0_00327.1.g11420.t1	ref|NP_195384.5| uncharacterized protein [Arabidopsis thaliana] gi|45752648|gb|AAS76222.1| At4g36660 [Arabidopsis thaliana] gi|45773768|gb|AAS76688.1| At4g36660 [Arabidopsis thaliana] gi|332661284|gb|AEE86684.1| uncharacterized protein AT4G36660 [Arabidopsis thaliana]	187	179	5.00E-60	95.7	67.9	71.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G36660.1 | Symbols: | Protein of unknown function (DUF1195) | chr4:17285953-17287281 REVERSE LENGTH=179	187	179	2.00E-62	95.7	67.9	71.7
Rsa1.0_00327.1.g11421.t1	gb|EOA18172.1| hypothetical protein CARUB_v10006648mg [Capsella rubella]	506	493	0	97.4	92.1	95.7	hypothetical protein CARUB_v10006648mg	gbpln	Capsella rubella	AT4G36670.1 | Symbols: | Major facilitator superfamily protein | chr4:17287680-17289483 REVERSE LENGTH=493	506	493	0	97.4	91.3	95.3
Rsa1.0_00327.1.g11422.t1	ref|XP_002871167.1| exonuclease family protein [Arabidopsis lyrata subsp. lyrata] gi|297317004|gb|EFH47426.1| exonuclease family protein [Arabidopsis lyrata subsp. lyrata]	267	464	1.00E-37	173.8	43.1	58.4	exonuclease family protein	gbpln	Arabidopsis lyrata	AT5G05540.1 | Symbols: SDN2 | small RNA degrading nuclease 2 | chr5:1636419-1638759 FORWARD LENGTH=466	267	466	3.00E-39	174.5	37.8	50.9
Rsa1.0_00327.1.g11423.t1	ref|XP_002889482.1| hypothetical protein ARALYDRAFT_333714 [Arabidopsis lyrata subsp. lyrata] gi|297335324|gb|EFH65741.1| hypothetical protein ARALYDRAFT_333714 [Arabidopsis lyrata subsp. lyrata]	147	671	8.00E-77	456.5	87.8	95.2	hypothetical protein ARALYDRAFT_333714	gbpln	Arabidopsis lyrata	AT1G03910.2 | Symbols: | EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Cactin protein, cactus-binding domain, C-terminal (InterPro:IPR019134), Cactin, central region (InterPro:IPR018816); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G36815.2). | chr1:996432-1000231 FORWARD LENGTH=716	147	716	4.00E-79	487.1	87.8	95.2
Rsa1.0_00327.1.g11424.t1	gb|EOA35181.1| hypothetical protein CARUB_v10020326mg [Capsella rubella]	156	430	5.00E-67	275.6	76.3	83.3	hypothetical protein CARUB_v10020326mg	gbpln	Capsella rubella	AT1G77840.1 | Symbols: | Translation initiation factor IF2/IF5 | chr1:29269087-29270400 FORWARD LENGTH=437	156	437	7.00E-68	280.1	75.0	82.1
Rsa1.0_00327.1.g11425.t1	ref|NP_195388.2| cupin family protein [Arabidopsis thaliana] gi|332661291|gb|AEE86691.1| cupin family protein [Arabidopsis thaliana]	327	522	1.00E-122	159.6	69.7	78.9	cupin family protein	gbpln	Arabidopsis thaliana	AT4G36700.1 | Symbols: | RmlC-like cupins superfamily protein | chr4:17298443-17300337 REVERSE LENGTH=522	327	522	1.00E-124	159.6	69.7	78.9
Rsa1.0_00328.1.g11426.t1	gb|AAC63372.1| lipid transfer protein [Brassica oleracea]	118	118	4.00E-53	100.0	90.7	96.6	lipid transfer protein	gbpln	Brassica oleracea	AT2G38540.1 | Symbols: LP1, LTP1, ATLTP1 | lipid transfer protein 1 | chr2:16130418-16130893 FORWARD LENGTH=118	118	118	2.00E-45	100.0	72.9	88.1
Rsa1.0_00328.1.g11427.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00328.1.g11428.t1	ref|XP_002881569.1| hypothetical protein ARALYDRAFT_482825 [Arabidopsis lyrata subsp. lyrata] gi|297327408|gb|EFH57828.1| hypothetical protein ARALYDRAFT_482825 [Arabidopsis lyrata subsp. lyrata]	466	463	0	99.4	88.2	92.9	hypothetical protein ARALYDRAFT_482825	gbpln	Arabidopsis lyrata	AT2G38170.1 | Symbols: CAX1, ATCAX1, RCI4 | cation exchanger 1 | chr2:15989429-15993178 REVERSE LENGTH=463	466	463	0	99.4	87.1	92.7

Rsa1.0_00328.1.g11429.t1	ref|XP_002881567.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327406|gb|EFH57826.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	687	750	1.00E-168	109.2	41.5	46.0	predicted protein	gbpln	Arabidopsis lyrata	AT2G38150.1 | Symbols: | alpha 1,4-glycosyltransferase family protein | chr2:15981700-15982917 REVERSE LENGTH=405	687	405	1.00E-168	59.0	40.9	46.1
Rsa1.0_00328.1.g11430.t1	gb|ACZ67478.1| auxin resistant 1 protein [Brassica rapa subsp. oleifera]	488	493	0	101.0	96.3	98.8	auxin resistant 1 protein	gbpln	Brassica rapa	AT2G38120.1 | Symbols: AUX1, WAV5, PIR1, MAP1 | Transmembrane amino acid transporter family protein | chr2:15973493-15976792 FORWARD LENGTH=485	488	485	0	99.4	94.3	96.3
Rsa1.0_00328.1.g11431.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	193	1142	9.00E-48	591.7	54.9	63.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	193	256	1.00E-17	132.6	28.5	39.9
Rsa1.0_00328.1.g11432.t1	gb|AGC91763.1| glycerol-3-phosphate acyltransferase 6 [Brassica napus]	501	501	0	100.0	96.4	99.0	glycerol-3-phosphate acyltransferase 6	gbpln	Brassica napus	AT2G38110.1 | Symbols: ATGPAT6, GPAT6 | glycerol-3-phosphate acyltransferase 6 | chr2:15952816-15955364 REVERSE LENGTH=501	501	501	0	100.0	92.6	96.8
Rsa1.0_00328.1.g11433.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00328.1.g11434.t1	gb|EOA27596.1| hypothetical protein CARUB_v10023736mg [Capsella rubella]	298	299	1.00E-159	100.3	90.9	94.3	hypothetical protein CARUB_v10023736mg	gbpln	Capsella rubella	AT2G38090.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr2:15945278-15946775 FORWARD LENGTH=298	298	298	1.00E-156	100.0	93.0	95.6
Rsa1.0_00328.1.g11435.t1	ref|NP_565881.1| laccase-4 [Arabidopsis thaliana] gi|75318640|sp|O80434.2|LAC4_ARATH RecName: Full=Laccase-4; AltName: Full=Benzenediol:oxygen oxidoreductase 4; AltName: Full=Diphenol oxidase 4; AltName: Full=Protein IRREGULAR XYLEM 12; AltName: Full=Urishiol oxidase 4; Flags: Precursor gi|15450603|gb|AAK96573.1| At2g38080/T8P21 [Arabidopsis thaliana] gi|17380634|gb|AAL36080.1| At2g38080/T8P21 [Arabidopsis thaliana] gi|17473886|gb|AAL38363.1| putative diphenol oxidase [Arabidopsis thaliana] gi|20196985|gb|AAC27158.2| putative diphenol oxidase [Arabidopsis thaliana] gi|21387103|gb|AAM47955.1| putative diphenol oxidase [Arabidopsis thaliana] gi|330254393|gb|AEC09487.1| laccase-4 [Arabidopsis thaliana]	559	558	0	99.8	94.1	97.1	laccase-4	gbpln	Arabidopsis thaliana	AT2G38080.1 | Symbols: IRX12, LAC4, ATLMCO4, LMCO4 | Laccase/Diphenol oxidase family protein | chr2:15934540-15937352 FORWARD LENGTH=558	559	558	0	99.8	94.1	97.1
Rsa1.0_00328.1.g11436.t1	gb|EOA26744.1| hypothetical protein CARUB_v10022830mg [Capsella rubella]	611	618	0	101.1	67.6	74.6	hypothetical protein CARUB_v10022830mg	gbpln	Capsella rubella	AT2G38070.1 | Symbols: | Protein of unknown function (DUF740) | chr2:15928737-15930596 FORWARD LENGTH=619	611	619	1.00E-169	101.3	66.8	74.5
Rsa1.0_00328.1.g11437.t1	ref|XP_002881562.1| hypothetical protein ARALYDRAFT_482813 [Arabidopsis lyrata subsp. lyrata] gi|297327401|gb|EFH57821.1| hypothetical protein ARALYDRAFT_482813 [Arabidopsis lyrata subsp. lyrata]	577	517	0	89.6	77.1	81.1	hypothetical protein ARALYDRAFT_482813	gbpln	Arabidopsis lyrata	AT2G38060.1 | Symbols: PHT4;2 | phosphate transporter 4;2 | chr2:15922727-15925623 REVERSE LENGTH=512	577	512	0	88.7	76.6	80.8
Rsa1.0_00328.1.g11438.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00328.1.g11439.t1	ref|XP_002881561.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327400|gb|EFH57820.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	260	261	1.00E-125	100.4	83.1	91.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G38050.1 | Symbols: DET2, DWF6, ATDET2 | 3-oxo-5-alpha-steroid 4-dehydrogenase family protein | chr2:15921303-15922176 REVERSE LENGTH=262	260	262	1.00E-123	100.8	80.4	90.0
Rsa1.0_00328.1.g11440.t2	gb|EOA28982.1| hypothetical protein CARUB_v10025234mg [Capsella rubella]	253	756	1.00E-129	298.8	93.7	96.8	hypothetical protein CARUB_v10025234mg	gbpln	Capsella rubella	AT2G38010.1 | Symbols: | Neutral/alkaline non-lysosomal ceramidase | chr2:15906862-15909867 FORWARD LENGTH=757	253	757	1.00E-127	299.2	90.1	94.9
Rsa1.0_00328.1.g11441.t1	ref|XP_002879721.1| ribosome biogenesis regulatory protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297325560|gb|EFH55980.1| ribosome biogenesis regulatory protein family protein [Arabidopsis lyrata subsp. lyrata]	319	324	1.00E-156	101.6	86.8	92.2	ribosome biogenesis regulatory protein family protein	gbpln	Arabidopsis lyrata	AT2G37990.1 | Symbols: | ribosome biogenesis regulatory protein (RRS1) family protein | chr2:15900713-15903028 FORWARD LENGTH=318	319	318	1.00E-156	99.7	85.6	91.5
Rsa1.0_00329.1.g11442.t1	ref|XP_002273725.1| PREDICTED: uncharacterized protein LOC100248761 [Vitis vinifera] gi|298205155|emb|CBI17214.3| unnamed protein product [Vitis vinifera]	259	413	1.00E-105	159.5	73.7	79.9	PREDICTED: uncharacterized protein LOC100248761	gbpln	Vitis vinifera	AT1G04850.1 | Symbols: | ubiquitin-associated (UBA)/TS-N domain-containing protein | chr1:1365311-1368706 REVERSE LENGTH=413	259	413	1.00E-105	159.5	83.0	86.9

Rsa1.0_00329.1.g11443.t1	ref|NP_171980.1| high mobility group-box and ARID domain-binding domain-containing protein [Arabidopsis thaliana] gi|75192516|sp|Q9MAT6.1|HMG15_ARATH RecName: Full=High mobility group B protein 15; AltName: Full=Nucleosome/chromatin assembly factor group D 15 gi|7211978|gb|AAF40449.1|AC004809_7 Contains similarity to the high mobility group family PF|00505 [Arabidopsis thaliana] gi|56236040|gb|AAV84476.1| At1g04880 [Arabidopsis thaliana] gi|56790208|gb|AAW30021.1| At1g04880 [Arabidopsis thaliana] gi|225897878|dbj|BAH30271.1| hypothetical protein [Arabidopsis thaliana] gi|332189634|gb|AEE27755.1| high mobility group B protein 15 [Arabidopsis thaliana]	453	448	1.00E-167	98.9	72.6	82.3	high mobility group-box and ARID domain-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G04880.1 | Symbols: | HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain | chr1:1376106-1378264 REVERSE LENGTH=448	453	448	1.00E-170	98.9	72.6	82.3
Rsa1.0_00329.1.g11444.t1	ref|NP_177131.1| wall-associated receptor kinase-like 9 [Arabidopsis thaliana] gi|75333576|sp|Q9C9L5.1|WAKLH_ARATH RecName: Full=Wall-associated receptor kinase-like 9; Flags: Precursor gi|12325200|gb|AAG52551.1|AC013289_18 putative protein kinase; 39563-42199 [Arabidopsis thaliana] gi|332196847|gb|AEE34968.1| wall-associated receptor kinase-like 9 [Arabidopsis thaliana]	710	792	0	111.5	56.3	71.0	wall-associated receptor kinase-like 9	gbpln	Arabidopsis thaliana	AT1G69730.1 | Symbols: | Wall-associated kinase family protein | chr1:26228703-26231339 REVERSE LENGTH=792	710	792	0	111.5	56.3	71.0
Rsa1.0_00329.1.g11445.t2	gb|EOA29941.1| hypothetical protein CARUB_v10013039mg [Capsella rubella]	418	755	1.00E-114	180.6	59.8	73.9	hypothetical protein CARUB_v10013039mg	gbpln	Capsella rubella	AT4G31110.1 | Symbols: | Wall-associated kinase family protein | chr4:15127257-15129880 FORWARD LENGTH=793	418	793	1.00E-111	189.7	57.4	71.8
Rsa1.0_00329.1.g11446.t1	gb|EOA38824.1| hypothetical protein CARUB_v10011153mg [Capsella rubella]	400	636	1.00E-158	159.0	73.0	81.5	hypothetical protein CARUB_v10011153mg	gbpln	Capsella rubella	AT1G04945.3 | Symbols: | HIT-type Zinc finger family protein | chr1:1399588-1402651 FORWARD LENGTH=644	400	644	1.00E-156	161.0	72.8	80.8
Rsa1.0_00329.1.g11447.t1	gb|ABV89666.1| zinc finger an1-like family protein [Brassica rapa]	138	168	1.00E-52	121.7	74.6	78.3	zinc finger an1-like family protein	gbpln	Brassica rapa	AT1G51200.4 | Symbols: | A20/AN1-like zinc finger family protein | chr1:18985690-18986211 FORWARD LENGTH=173	138	173	1.00E-44	125.4	68.8	73.2
Rsa1.0_00329.1.g11448.t1	ref|XP_002872936.1| hypothetical protein ARALYDRAFT_490506 [Arabidopsis lyrata subsp. lyrata] gi|297318773|gb|EFH49195.1| hypothetical protein ARALYDRAFT_490506 [Arabidopsis lyrata subsp. lyrata]	334	361	1.00E-114	108.1	68.0	78.1	hypothetical protein ARALYDRAFT_490506	gbpln	Arabidopsis lyrata	AT4G00620.1 | Symbols: | Amino acid dehydrogenase family protein | chr4:259265-260788 REVERSE LENGTH=360	334	360	1.00E-116	107.8	67.4	77.2
Rsa1.0_00329.1.g11449.t1	gb|EOA40075.1| hypothetical protein CARUB_v10008770mg [Capsella rubella]	552	547	0	99.1	82.4	88.2	hypothetical protein CARUB_v10008770mg	gbpln	Capsella rubella	AT1G04950.3 | Symbols: TAFII59, TAF6, ATTAF6 | TATA BOX ASSOCIATED FACTOR II 59 | chr1:1403606-1407184 REVERSE LENGTH=549	552	549	0	99.5	82.8	87.5
Rsa1.0_00329.1.g11450.t1	ref|XP_002892257.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338099|gb|EFH68516.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	193	193	4.00E-83	100.0	84.5	91.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G04985.1 | Symbols: | unknown protein; Has 37 Blast hits to 37 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1416563-1418291 REVERSE LENGTH=193	193	193	3.00E-85	100.0	85.0	91.2
Rsa1.0_00329.1.g11451.t1	ref|NP_563726.1| clathrin coat assembly protein AP180 [Arabidopsis thaliana] gi|46396061|sp|Q9ZVN6.1|AP180_ARATH RecName: Full=Clathrin coat assembly protein AP180; Short=At-AP180; AltName: Full=Clathrin coat-associated protein AP180 gi|4056423|gb|AAC97997.1| Similar to clathrin assembly protein gb|X68878 (AP180) from Rattus norvegicus. EST gb|W43552 comes from this gene [Arabidopsis thaliana] gi|26450013|dbj|BAC42127.1| putative clathrin protein [Arabidopsis thaliana] gi|28827746|gb|AAO50717.1| putative clathrin [Arabidopsis thaliana] gi|332189659|gb|AEE27780.1| clathrin coat assembly protein AP180 [Arabidopsis thaliana]	907	653	0	72.0	52.0	56.9	clathrin coat assembly protein AP180	gbpln	Arabidopsis thaliana	AT1G05020.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:1435384-1437345 REVERSE LENGTH=653	907	653	0	72.0	52.0	56.9

Rsa1.0_00329.1.g11452.t1	ref|XP_002892263.1| ATGTF2H2/GTF2H2 [Arabidopsis lyrata subsp. lyrata] gi|297338105|gb|EFH68522.1| ATGTF2H2/GTF2H2 [Arabidopsis lyrata subsp. lyrata]	423	421	0	99.5	92.9	96.2	ATGTF2H2/GTF2H2	gbpln	Arabidopsis lyrata	AT1G05055.1 | Symbols: ATGTF2H2, GTF2H2 | general transcription factor Ⅱ H2 | chr1:1448913-1450852 REVERSE LENGTH=421	423	421	0	99.5	92.4	96.2	
Rsa1.0_00329.1.g11453.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00329.1.g11454.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00329.1.g11455.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00329.1.g11456.t1	emb|CAB45838.1| hypothetical protein [Arabidopsis thaliana] gi|7268868|emb|CAB79072.1| hypothetical protein [Arabidopsis thaliana]	678	758	0	111.8	73.7	83.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G20720.1 | Symbols: | dentin sialophosphoprotein-related | chr4:11105409-11107841 FORWARD LENGTH=729	678	729	0	107.5	73.7	83.8	
Rsa1.0_00329.1.g11457.t6	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00329.1.g11458.t1	gb|EOA37664.1| hypothetical protein CARUB_v10012243mg [Capsella rubella]	826	808	0	97.8	85.7	91.6	hypothetical protein CARUB_v10012243mg	gbpln	Capsella rubella	AT1G05150.1 | Symbols: | Calcium-binding tetratricopeptide family protein | chr1:1484280-1486706 REVERSE LENGTH=808	826	808	0	97.8	84.9	91.2	
Rsa1.0_00329.1.g11459.t1	gb|ABV89645.1| auxin resistant 1 [Brassica rapa]	521	522	0	100.2	90.8	95.8	auxin resistant 1	gbpln	Brassica rapa	AT1G05180.1 | Symbols: AXR1 | NAD(P)-binding Rossmann-fold superfamily protein | chr1:1498357-1501775 REVERSE LENGTH=540	521	540	0	103.6	89.4	94.6	
Rsa1.0_00329.1.g11460.t1	ref|XP_002889539.1| hypothetical protein ARALYDRAFT_470516 [Arabidopsis lyrata subsp. lyrata] gi|297335381|gb|EFH65798.1| hypothetical protein ARALYDRAFT_470516 [Arabidopsis lyrata subsp. lyrata]	165	168	1.00E-66	101.8	78.8	83.6	hypothetical protein ARALYDRAFT_470516	gbpln	Arabidopsis lyrata	AT1G05210.1 | Symbols: | Transmembrane protein 97, predicted | chr1:1510469-1511485 FORWARD LENGTH=168	165	168	6.00E-67	101.8	77.0	82.4	
Rsa1.0_00329.1.g11461.t1	gb|EOA39455.1| hypothetical protein CARUB_v10012652mg [Capsella rubella]	340	320	1.00E-140	94.1	72.6	82.9	hypothetical protein CARUB_v10012652mg	gbpln	Capsella rubella	AT1G05250.1 | Symbols: | Peroxidase superfamily protein | chr1:1525924-1527169 REVERSE LENGTH=325	340	325	1.00E-130	95.6	64.1	76.8	
Rsa1.0_00329.1.g11462.t1	gb|EOA39455.1| hypothetical protein CARUB_v10012652mg [Capsella rubella]	332	320	2.33E-156	96.4	76.5	86.4	hypothetical protein CARUB_v10012652mg	gbpln	Capsella rubella	AT1G05250.1 | Symbols: | Peroxidase superfamily protein | chr1:1525924-1527169 REVERSE LENGTH=325	332	325	1.00E-133	97.9	66.9	77.7	
Rsa1.0_00329.1.g11463.t1	gb|EOA37749.1| hypothetical protein CARUB_v10012564mg [Capsella rubella]	363	375	1.00E-162	103.3	79.6	89.5	hypothetical protein CARUB_v10012564mg	gbpln	Capsella rubella	AT1G05270.1 | Symbols: | TraB family protein | chr1:1531806-1534305 REVERSE LENGTH=371	363	371	1.00E-158	102.2	78.8	88.2	
Rsa1.0_00329.1.g11464.t1	ref|XP_002892278.1| hypothetical protein ARALYDRAFT_887710 [Arabidopsis lyrata subsp. lyrata] gi|297338120|gb|EFH68537.1| hypothetical protein ARALYDRAFT_887710 [Arabidopsis lyrata subsp. lyrata]	430	462	0	107.4	82.6	91.4	hypothetical protein ARALYDRAFT_887710	gbpln	Arabidopsis lyrata	AT1G05280.1 | Symbols: | Protein of unknown function (DUF604) | chr1:1535444-1537414 REVERSE LENGTH=461	430	461	0	107.2	81.4	90.0	
Rsa1.0_00329.1.g11465.t1	ref|NP_172038.4| Type Ⅰ inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Arabidopsis thaliana] gi|259016256|sp|Q9LR47.2|IP5P3_ARATH RecName: Full=Type Ⅰ inositol 1,4,5-trisphosphate 5-phosphatase CVP2; AltName: Full=Protein COTYLEDON VASCULAR PATTERN 2 gi|332189723|gb|AEE27844.1| Type Ⅰ inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Arabidopsis thaliana]	608	617	0	101.5	96.1	97.7	Type Ⅰ inositol-1,4,5-trisphosphate 5-phosphatase CVP2	gbpln	Arabidopsis thaliana	AT1G05470.1 | Symbols: CVP2 | DNAse Ⅰ-like superfamily protein | chr1:1608558-1611291 REVERSE LENGTH=617	608	617	0	101.5	96.1	97.7	
Rsa1.0_00329.1.g11466.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00329.1.g11467.t1	ref|NP_563741.1| sec23/sec24-like transport protein [Arabidopsis thaliana] gi|25090173|gb|AAN72246.1| At1g05520/T25N20_16 [Arabidopsis thaliana] gi|332189727|gb|AEE27848.1| sec23/sec24-like transport protein [Arabidopsis thaliana]	770	783	0	101.7	91.6	95.6	sec23/sec24-like transport protein	gbpln	Arabidopsis thaliana	AT1G05520.1 | Symbols: | Sec23/Sec24 protein transport family protein | chr1:1631126-1635703 REVERSE LENGTH=783	770	783	0	101.7	91.6	95.6	
Rsa1.0_00329.1.g11468.t1	ref|NP_001184912.1| uncharacterized protein [Arabidopsis thaliana] gi|332189732|gb|AEE27853.1| uncharacterized protein AT1G05550 [Arabidopsis thaliana]	351	385	1.00E-120	109.7	64.7	74.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G05550.3 | Symbols: | Protein of unknown function (DUF295) | chr1:1641229-1643748 REVERSE LENGTH=385	351	385	1.00E-123	109.7	64.7	74.4	
Rsa1.0_00329.1.g11469.t1	ref|XP_002889553.1| hypothetical protein ARALYDRAFT_470554 [Arabidopsis lyrata subsp. lyrata] gi|297335395|gb|EFH65812.1| hypothetical protein ARALYDRAFT_470554 [Arabidopsis lyrata subsp. lyrata]	438	367	1.00E-143	83.8	58.9	66.2	hypothetical protein ARALYDRAFT_470554	gbpln	Arabidopsis lyrata	AT1G05540.1 | Symbols: | Protein of unknown function (DUF295) | chr1:1639348-1640707 FORWARD LENGTH=367	438	367	2.33E-156	83.8	57.8	66.0	

Rsa1.0_00329.1.g11470.t1	ref|XP_002889557.1| inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335399|gb|EFH65816.1| inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	322	322	1.00E-169	100.0	89.8	94.7	inosine-uridine preferring nucleoside hydrolase family protein	gbpln	Arabidopsis lyrata	AT1G05620.1 | Symbols: URH2 | uridine-ribohydrolase 2 | chr1:1679286-1681527 FORWARD LENGTH=322	322	322	1.00E-171	100.0	90.1	94.1
Rsa1.0_00329.1.g11471.t2	ref|NP_001030976.1| Type I inositol-1,4,5-trisphosphate 5-phosphatase 13 [Arabidopsis thaliana] gi|75337868|sp|Q9SYK4.1|IP5PD_ARATH RecName: Full=Type I inositol 1,4,5-trisphosphate 5-phosphatase 13; Short=At5PTase13 gi|4836913|gb|AAD30615.1|AC007153_7 Putative inositol 1,4,5-trisphosphate 5-phosphatase [Arabidopsis thaliana] gi|56405850|gb|AAV87315.1| inositol polyphosphate 5-phosphatase [Arabidopsis thaliana] gi|56405858|gb|AAV87319.1| inositol polyphosphate 5-phosphatase [Arabidopsis thaliana] gi|332189748|gb|AEE27869.1| Type I inositol-1,4,5-trisphosphate 5-phosphatase 13 [Arabidopsis thaliana]	1151	1136	0	98.7	85.9	92.3	Type I inositol-1,4,5-trisphosphate 5-phosphatase 13	gbpln	Arabidopsis thaliana	AT1G05630.2 | Symbols: AT5PTASE13, 5PTASE13 | Endonuclease/exonuclease/phosphatase family protein | chr1:1682483-1687153 FORWARD LENGTH=1136	1151	1136	0	98.7	85.9	92.3
Rsa1.0_00329.1.g11472.t2	gb|EOA39331.1| hypothetical protein CARUB_v10012375mg [Capsella rubella]	138	395	4.00E-61	286.2	81.9	89.1	hypothetical protein CARUB_v10012375mg	gbpln	Capsella rubella	AT1G05650.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:1690264-1692126 REVERSE LENGTH=394	138	394	9.00E-61	285.5	76.8	88.4
Rsa1.0_00329.1.g11473.t1	ref|NP_172059.1| Uridine diphosphate glycosyltransferase 74E2 [Arabidopsis thaliana] gi|75314101|sp|Q9SYK9.1|U74E2_ARATH RecName: Full=UDP-glycosyltransferase 74E2 gi|4836925|gb|AAD30627.1|AC007153_19 Similar to indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana] gi|63003804|gb|AAY25431.1| At1g05680 [Arabidopsis thaliana] gi|115646805|gb|ABJ17124.1| At1g05680 [Arabidopsis thaliana] gi|332189755|gb|AEE27876.1| Uridine diphosphate glycosyltransferase 74E2 [Arabidopsis thaliana]	453	453	0	100.0	88.7	95.8	Uridine diphosphate glycosyltransferase 74E2	gbpln	Arabidopsis thaliana	AT1G05680.1 | Symbols: UGT74E2 | Uridine diphosphate glycosyltransferase 74E2 | chr1:1703196-1704639 REVERSE LENGTH=453	453	453	0	100.0	88.7	95.8
Rsa1.0_00329.1.g11474.t1	ref|XP_002889559.1| hypothetical protein ARALYDRAFT_887760 [Arabidopsis lyrata subsp. lyrata] gi|297335401|gb|EFH65818.1| hypothetical protein ARALYDRAFT_887760 [Arabidopsis lyrata subsp. lyrata]	363	404	1.00E-138	111.3	71.6	81.5	hypothetical protein ARALYDRAFT_887760	gbpln	Arabidopsis lyrata	AT1G05690.1 | Symbols: BT3 | BTB and TAZ domain protein 3 | chr1:1707809-1709132 FORWARD LENGTH=364	363	364	1.00E-131	100.3	67.5	77.1
Rsa1.0_00329.1.g11475.t1	gb|EOA38787.1| hypothetical protein CARUB_v10011047mg [Capsella rubella]	206	854	6.00E-96	414.6	83.0	90.8	hypothetical protein CARUB_v10011047mg	gbpln	Capsella rubella	AT1G05700.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase protein | chr1:1709796-1713245 FORWARD LENGTH=852	206	852	1.00E-97	413.6	83.0	90.3
Rsa1.0_00329.1.g11476.t2	ref|NP_172061.2| Leucine-rich repeat transmembrane protein kinase protein [Arabidopsis thaliana] gi|263430136|sp|C0LGD6.1|Y1570_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g05700; Flags: Precursor gi|224589374|gb|ACN59221.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332189757|gb|AEE27878.1| Leucine-rich repeat transmembrane protein kinase protein [Arabidopsis thaliana]	1442	852	0	59.1	32.1	35.8	Leucine-rich repeat transmembrane protein kinase protein	gbpln	Arabidopsis thaliana	AT1G05700.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase protein | chr1:1709796-1713245 FORWARD LENGTH=852	1442	852	0	59.1	32.1	35.8
Rsa1.0_00329.1.g11477.t1	dbj|BAJ34140.1| unnamed protein product [Thellungiella halophila]	148	149	4.00E-73	100.7	91.2	93.2	unnamed protein product	----	----	AT1G05710.5 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:1716198-1717023 FORWARD LENGTH=149	148	149	4.00E-74	100.7	90.5	92.6
Rsa1.0_00329.1.g11478.t1	dbj|BAF81524.1| putative 15kDa selenoprotein [Brassica rapa]	161	167	1.00E-85	103.7	95.7	99.4	putative 15kDa selenoprotein	gbpln	Brassica rapa	AT1G05720.1 | Symbols: | selenoprotein family protein | chr1:1717677-1718849 REVERSE LENGTH=163	161	163	3.00E-77	101.2	83.9	93.2
Rsa1.0_00329.1.g11479.t1	gb|AEP33756.1| chloroplast biogenesis 19, partial [Raphanus sativus]	501	476	0	95.0	91.8	92.2	chloroplast biogenesis 19, partial	gbpln	Raphanus sativus	AT1G05750.1 | Symbols: PDE247, CLB19 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1721523-1723025 FORWARD LENGTH=500	501	500	0	99.8	84.4	89.8

Rsa1.0_00329.1.g11480.t1	ref|XP_002889565.1| hypothetical protein ARALYDRAFT_311660 [Arabidopsis lyrata subsp. lyrata] gi|297335407|gb|EFH65824.1| hypothetical protein ARALYDRAFT_311660 [Arabidopsis lyrata subsp. lyrata]	758	959	0	126.5	81.9	86.4	hypothetical protein ARALYDRAFT_311660	gbpln	Arabidopsis lyrata	AT1G05790.1 | Symbols: | lipase class 3 family protein | chr1:1733039-1737365 FORWARD LENGTH=687	758	687	0	90.6	77.8	82.8
Rsa1.0_00329.1.g11481.t1	ref|XP_002889569.1| hypothetical protein ARALYDRAFT_887775 [Arabidopsis lyrata subsp. lyrata] gi|297335411|gb|EFH65828.1| hypothetical protein ARALYDRAFT_887775 [Arabidopsis lyrata subsp. lyrata]	540	536	0	99.3	83.5	91.7	hypothetical protein ARALYDRAFT_887775	gbpln	Arabidopsis lyrata	AT1G05820.1 | Symbols: SPPL5, ATSPPL5 | SIGNAL PEPTIDE PEPTIDASE-LIKE 5 | chr1:1749776-1753767 FORWARD LENGTH=536	540	536	0	99.3	83.0	91.7
Rsa1.0_00329.1.g11482.t1	ref|NP_172076.1| chitinase-like protein 1 [Arabidopsis thaliana] gi|75191903|sp|Q9MA41.1|CTL1_ARATH RecName: Full=Chitinase-like protein 1; Short=AtCTL1; AltName: Full=Protein ANION ALTERED ROOT MORPHOLOGY; AltName: Full=Protein ECTOPIC DEPOSITION OF LIGNIN IN PITH 1; AltName: Full=Protein ECTOPIC ROOT HAIR 2; AltName: Full=Protein POM-POM1; AltName: Full=Protein SENSITIVE TO HOT TEMPERATURES 2; Flags: Precursor gi|6850314|gb|AAF29391.1|AC009999_11 Contains similarity to a basic endochitinase from Arabidopsis thaliana gb|AB023448, and contains a Chitinases class I PF|00182 domain. ESTs gb|AI995747, gb|AA728545, gb|Z26222, gb|Z25683, gb|T88386, gb|T14122, gb|T04241, gb|N38122 come from this gene [Arabidopsis thaliana] gi|12083324|gb|AAG48821.1|AF332458_1 putative class I chitinase [Arabidopsis thaliana] gi|17226329|gb|AAL37736.1|AF422178_1 chitinase-like protein 1 [Arabidopsis thaliana] gi|17226331|gb|AAL37737.1|AF422179_1 chitinase-like protein 1 [Arabidopsis thaliana] gi|14334488|gb|AAK59442.1| putative class I chitinase [Arabidopsis thaliana] gi|21280935|gb|AAM44973.1| putative class I chitinase [Arabidopsis	321	321	1.00E-180	100.0	91.9	96.3	chitinase-like protein 1	gbpln	Arabidopsis thaliana	AT1G05850.1 | Symbols: POM1, ERH2, ELP1, CTL1, ELP, HOT2, ATCTL1 | Chitinase family protein | chr1:1766833-1768117 REVERSE LENGTH=321	321	321	0	100.0	91.9	96.3
Rsa1.0_00329.1.g11483.t1	ref|XP_002889573.1| hypothetical protein ARALYDRAFT_470601 [Arabidopsis lyrata subsp. lyrata] gi|297335415|gb|EFH65832.1| hypothetical protein ARALYDRAFT_470601 [Arabidopsis lyrata subsp. lyrata]	878	557	0	63.4	51.4	55.8	hypothetical protein ARALYDRAFT_470601	gbpln	Arabidopsis lyrata	AT2G31510.1 | Symbols: ARI7, ATARI7 | IBR domain-containing protein | chr2:13416991-13421170 REVERSE LENGTH=562	878	562	0	64.0	50.0	55.9
Rsa1.0_00329.1.g11484.t1	gb|EOA36797.1| hypothetical protein CARUB_v10008206mg [Capsella rubella]	945	980	0	103.7	85.0	91.0	hypothetical protein CARUB_v10008206mg	gbpln	Capsella rubella	AT1G05960.1 | Symbols: | ARM repeat superfamily protein | chr1:1808478-1815060 REVERSE LENGTH=982	945	982	0	103.9	84.7	90.6
Rsa1.0_00329.1.g11485.t1	ref|XP_002889579.1| hypothetical protein ARALYDRAFT_887792 [Arabidopsis lyrata subsp. lyrata] gi|297335421|gb|EFH65838.1| hypothetical protein ARALYDRAFT_887792 [Arabidopsis lyrata subsp. lyrata]	151	150	4.00E-68	99.3	92.1	96.0	hypothetical protein ARALYDRAFT_887792	gbpln	Arabidopsis lyrata	AT1G05990.1 | Symbols: RHS1 | EF hand calcium-binding protein family | chr1:1818588-1819040 FORWARD LENGTH=150	151	150	1.00E-70	99.3	92.1	96.7
Rsa1.0_00329.1.g11486.t1	ref|XP_002889580.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335422|gb|EFH65839.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	83	79	1.00E-24	95.2	71.1	79.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G06010.1 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1823347-1823670 FORWARD LENGTH=78	83	78	5.00E-25	94.0	68.7	75.9
Rsa1.0_00329.1.g11487.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1965	1274	0	64.8	33.2	43.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1965	575	2.00E-73	29.3	9.2	14.4
Rsa1.0_00330.1.g11488.t1	gb|EOA23477.1| hypothetical protein CARUB_v10016666mg [Capsella rubella]	919	902	0	98.2	79.3	88.5	hypothetical protein CARUB_v10016666mg	gbpln	Capsella rubella	AT3G45140.1 | Symbols: LOX2, ATLOX2 | lipoxygenase 2 | chr3:16525437-16529233 FORWARD LENGTH=896	919	896	0	97.5	77.0	86.7

Rsa1.0_00330.1.g11489.t1	ref|XP_002878518.1| EMB2221 [Arabidopsis lyrata subsp. lyrata] gi|297324356|gb|EFH54777.1| EMB2221 [Arabidopsis lyrata subsp. lyrata]	1105	1104	0	99.9	86.8	92.2	EMB2221	gbpln	Arabidopsis lyrata	AT3G63460.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:23431009-23437241 REVERSE LENGTH=1104	1105	1104	0	99.9	86.5	92.1
Rsa1.0_00330.1.g11490.t1	gb|AFB74213.1| chloroplast MPBQ/MSBQ methyltransferase [Brassica napus]	341	337	1.00E-169	98.8	91.8	93.5	chloroplast MPBQ/MSBQ methyltransferase	gbpln	Brassica napus	AT3G63410.1 | Symbols: APG1, VTE3, IEP37, E37 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:23415816-23417002 REVERSE LENGTH=338	341	338	1.00E-167	99.1	90.0	93.0
Rsa1.0_00330.1.g11491.t1	gb|EOA25999.1| hypothetical protein CARUB_v10019395mg [Capsella rubella]	488	535	1.00E-45	109.6	20.1	23.2	hypothetical protein CARUB_v10019395mg	gbpln	Capsella rubella	AT3G63130.2 | Symbols: RANGAP1 | RAN GTPase activating protein 1 | chr3:23325108-23326715 FORWARD LENGTH=535	488	535	5.00E-46	109.6	19.1	21.9
Rsa1.0_00330.1.g11492.t1	gb|AAM65910.1| unknown [Arabidopsis thaliana]	404	404	0	100.0	84.2	92.1	unknown	gbpln	Arabidopsis thaliana	AT3G63090.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr3:23313617-23314831 FORWARD LENGTH=404	404	404	0	100.0	83.9	92.1
Rsa1.0_00330.1.g11493.t1	ref|XP_002876707.1| hypothetical protein ARALYDRAFT_907889 [Arabidopsis lyrata subsp. lyrata] gi|297322545|gb|EFH52966.1| hypothetical protein ARALYDRAFT_907889 [Arabidopsis lyrata subsp. lyrata]	45	70	8.00E-12	155.6	82.2	91.1	hypothetical protein ARALYDRAFT_907889	gbpln	Arabidopsis lyrata	AT3G63088.1 | Symbols: RTFL14, DVL14 | ROTUNDIFOLIA like 14 | chr3:23313053-23313199 FORWARD LENGTH=48	45	48	9.00E-14	106.7	80.0	91.1
Rsa1.0_00330.1.g11494.t1	dbj|BAJ34328.1| unnamed protein product [Thellungiella halophila]	161	175	9.00E-84	108.7	91.3	96.9	unnamed protein product	----	----	AT3G63080.1 | Symbols: ATGPX5, MEE42, GPX5 | glutathione peroxidase 5 | chr3:23310161-23311200 FORWARD LENGTH=173	161	173	5.00E-80	107.5	85.1	90.7
Rsa1.0_00330.1.g11495.t10	ref|NP_191866.3| Tudor/PWWP/MBT domain-containing protein [Arabidopsis thaliana] gi|403399430|sp|F4IZM8.1|HUAL2_ARATH RecName: Full=HUA2-like protein 2 gi|332646910|gb|AEE80431.1| Tudor/PWWP/MBT domain-containing protein [Arabidopsis thaliana]	1399	1347	0	96.3	71.4	78.7	Tudor/PWWP/MBT domain-containing protein	gbpln	Arabidopsis thaliana	AT3G63070.1 | Symbols: | Tudor/PWWP/MBT domain-containing protein | chr3:23302667-23309575 FORWARD LENGTH=1347	1399	1347	0	96.3	71.4	78.7
Rsa1.0_00330.1.g11496.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00330.1.g11497.t1	gb|ADT78692.1| gibberellin receptor 1B [Brassica napus]	361	358	0	99.2	90.3	95.6	gibberellin receptor 1B	gbpln	Brassica napus	AT3G63010.1 | Symbols: ATGID1B, GID1B | alpha/beta-Hydrolases superfamily protein | chr3:23289717-23290998 FORWARD LENGTH=358	361	358	0	99.2	88.9	93.4
Rsa1.0_00330.1.g11498.t1	gb|AAZ66952.1| 117M18_33 [Brassica rapa]	494	681	1.00E-134	137.9	54.0	66.8	117M18_33	gbpln	Brassica rapa	AT3G63000.1 | Symbols: NPL41 | NPL4-like protein 1 | chr3:23283836-23285357 FORWARD LENGTH=413	494	413	1.00E-13	83.6	7.5	9.9
Rsa1.0_00330.1.g11499.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00330.1.g11500.t1	ref|NP_567135.1| protein TRANSPORT INHIBITOR RESPONSE 1 [Arabidopsis thaliana] gi|68053009|sp|Q570C0.2|TIR1_ARATH RecName: Full=Protein TRANSPORT INHIBITOR RESPONSE 1; AltName: Full=Weak ethylene-insensitive protein 1 gi|146387658|pdb|2P1M|B Chain B, Tir1-ask1 Complex Structure gi|146387660|pdb|2P1N|B Chain B, Mechanism Of Auxin Perception By The Tir1 Ubiqutin Ligase gi|146387663|pdb|2P1N|E Chain E, Mechanism Of Auxin Perception By The Tir1 Ubiqutin Ligase gi|146387666|pdb|2P1O|B Chain B, Mechanism Of Auxin Perception By The Tir1 Ubiquitin Ligase gi|146387669|pdb|2P1P|B Chain B, Mechanism Of Auxin Perception By The Tir1 Ubiquitin Ligase gi|146387671|pdb|2P1Q|B Chain B, Mechanism Of Auxin Perception By The Tir1 Ubiquitin Ligase gi|185177934|pdb|3C6N|B Chain B, Small Molecule Agonists And Antagonists Of F-Box Protein-Substrate Interactions In Auxin Perception And Signaling gi|185177936|pdb|3C6O|B Chain B, Small Molecule Agonists And Antagonists Of F-Box Protein-Substrate Interactions In Auxin Perception And Signaling	598	594	0	99.3	90.3	95.3	protein TRANSPORT INHIBITOR RESPONSE 1	gbpln	Arabidopsis thaliana	AT3G62980.1 | Symbols: TIR1 | F-box/RNI-like superfamily protein | chr3:23273479-23276181 REVERSE LENGTH=594	598	594	0	99.3	90.3	95.3
Rsa1.0_00330.1.g11501.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00330.1.g11502.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11503.t1	ref|NP_179509.1| senescence-induced receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|30173224|sp|O64483.1|SIRK_ARATH RecName: Full=Senescence-induced receptor-like serine/threonine-protein kinase; AltName: Full=FLG22-induced receptor-like kinase 1; Flags: Precursor gi|19569557|gb|AAL92103.1|AF486619_1 senescence-induced receptor-like serine/threonine kinase [Arabidopsis thaliana] gi|3176723|gb|AAD12037.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|224589513|gb|ACN59290.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|330251762|gb|AEC06856.1| senescence-induced receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	95	876	2.00E-19	922.1	51.6	61.1	senescence-induced receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT2G19190.1 | Symbols: FRK1 | FLG22-induced receptor-like kinase 1 | chr2:8326067-8329893 REVERSE LENGTH=876	95	876	3.00E-22	922.1	51.6	61.1
Rsa1.0_00331.1.g11504.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11505.t1	emb|CAA66376.1| light repressible receptor protein kinase [Arabidopsis thaliana]	862	876	0	101.6	70.8	81.9	light repressible receptor protein kinase	gbpln	Arabidopsis thaliana	AT4G29990.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase protein | chr4:14665802-14669438 REVERSE LENGTH=876	862	876	0	101.6	70.6	81.9
Rsa1.0_00331.1.g11506.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1050	1365	0	130.0	46.0	62.7	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1050	575	5.00E-88	54.8	17.1	28.3
Rsa1.0_00331.1.g11507.t1	gb|AAD49767.1|AC007932_15 ESTs gb|N97074, gb|T13943 and gb|R89965 come from this gene [Arabidopsis thaliana]	355	360	1.00E-125	101.4	78.0	85.1	ESTs gb|N97074, gb|T13943 and gb|R89965 come from this gene	gbpln	Arabidopsis thaliana	AT1G48300.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 96 Blast hits to 87 proteins in 37 species: Archae - 0; Bacteria - 2; Metazoa - 12; Fungi - 2; Plants - 65; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink). | chr1:17847391-17848338 FORWARD LENGTH=285	355	285	1.00E-103	80.3	60.3	64.5
Rsa1.0_00331.1.g11508.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	821	1072	1.00E-138	130.6	34.6	50.5	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	821	746	3.00E-63	90.9	16.3	24.1
Rsa1.0_00331.1.g11509.t3	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1040	1142	1.00E-156	109.8	27.3	35.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1040	575	8.00E-33	55.3	6.8	10.4
Rsa1.0_00331.1.g11510.t1	gb|EOA33218.1| hypothetical protein CARUB_v10020320mg [Capsella rubella]	109	432	7.00E-23	396.3	47.7	54.1	hypothetical protein CARUB_v10020320mg	gbpln	Capsella rubella	AT1G20610.1 | Symbols: CYCB2;3 | Cyclin B2;3 | chr1:7135073-7137273 REVERSE LENGTH=429	109	429	6.00E-24	393.6	44.0	55.0
Rsa1.0_00331.1.g11511.t1	ref|NP_179068.1| pathogenesis-related protein 1 [Arabidopsis thaliana] gi|417527|sp|P33154.1|PR1_ARATH RecName: Full=Pathogenesis-related protein 1; Short=PR-1; Flags: Precursor gi|166861|gb|AAA32863.1| PR-1-like protein [Arabidopsis thaliana] gi|3810599|gb|AAC69381.1| pathogenesis-related PR-1-like protein [Arabidopsis thaliana] gi|17381134|gb|AAL36379.1| putative pathogenesis-related PR-1 protein [Arabidopsis thaliana] gi|21436247|gb|AAM51262.1| putative pathogenesis-related PR-1 protein [Arabidopsis thaliana] gi|91805427|gb|ABE65442.1| pathogenesis-like protein 1 [Arabidopsis thaliana] gi|330251220|gb|AEC06314.1| pathogenesis-related protein 1 [Arabidopsis thaliana]	160	161	1.00E-57	100.6	68.8	76.3	pathogenesis-related protein 1	gbpln	Arabidopsis thaliana	AT2G14610.1 | Symbols: PR1, PR 1, ATPR1 | pathogenesis-related gene 1 | chr2:6241944-6242429 REVERSE LENGTH=161	160	161	4.00E-60	100.6	68.8	76.3
Rsa1.0_00331.1.g11512.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	1206	1239	0	102.7	64.5	77.0	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1206	1262	1.00E-91	104.6	15.3	23.7

Rsa1.0_00331.1.g11513.t1	emb|CAA18194.1| putative protein [Arabidopsis thaliana] gi|7270001|emb|CAB79817.1| putative protein [Arabidopsis thaliana]	134	2895	2.00E−17	2160.4	32.8	36.6	putative protein	gbpln	Arabidopsis thaliana	AT4G30996.1 | Symbols: | Protein of unknown function (DUF1068) | chr4:15101464−15102461 FORWARD LENGTH=172	134	172	2.00E−19	128.4	32.8	36.6
Rsa1.0_00331.1.g11514.t1	gb|AAF79514.1|AC023673_2 F21D18.2 [Arabidopsis thaliana]	480	454	0	94.6	70.4	79.0	F21D18.2	gbpln	Arabidopsis thaliana	AT1G48260.1 | Symbols: CIPK17, SnRK3.21 | CBL−interacting protein kinase 17 | chr1:17814226−17817226 REVERSE LENGTH=432	480	432	1.00E−161	90.0	57.1	63.8
Rsa1.0_00331.1.g11515.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11516.t2	gb|AAD49774.2|AC007932_22 F11A17.20 [Arabidopsis thaliana]	285	285	4.00E−39	100.0	38.2	44.9	F11A17.20	gbpln	Arabidopsis thaliana	AT1G48240.1 | Symbols: ATNPSN12, NPSN12 | novel plant snare 12 | chr1:17809223−17811656 REVERSE LENGTH=265	285	265	8.00E−41	93.0	36.5	42.8
Rsa1.0_00331.1.g11517.t1	ref|NP_175257.1| nodulin MtN21 /EamA−like transporter protein [Arabidopsis thaliana] gi|325530209|sp|Q9LNH5.2|PT148_ARATH RecName: Full=Probable sugar phosphate/phosphate translocator At1g48230 gi|332194146|gb|AEE32267.1| probable sugar phosphate/phosphate translocator [Arabidopsis thaliana]	369	367	0	99.5	94.3	97.3	nodulin MtN21 /EamA−like transporter protein	gbpln	Arabidopsis thaliana	AT1G48230.1 | Symbols: | nodulin MtN21 /EamA−like transporter family protein | chr1:17806264−17808604 FORWARD LENGTH=367	369	367	0	99.5	94.3	97.3
Rsa1.0_00331.1.g11518.t1	emb|CAB78061.1| putative protein [Arabidopsis thaliana]	324	960	7.00E−40	296.3	23.1	30.2	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11519.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11520.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11521.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11522.t2	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11523.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11524.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11525.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00331.1.g11526.t1	gb|EMJ22065.1| hypothetical protein PRUPE_ppa018704mg [Prunus persica]	155	494	7.00E−23	318.7	33.5	36.8	hypothetical protein PRUPE_ppa018704mg	gbpln	Prunus persica	AT5G60120.1 | Symbols: TOE2 | target of early activation tagged (EAT) 2 | chr5:24208153−24211067 FORWARD LENGTH=485	155	485	2.00E−23	312.9	40.0	46.5
Rsa1.0_00331.1.g11527.t4	emb|CAN67863.1| hypothetical protein VITISV_020704 [Vitis vinifera]	969	803	1.00E−120	82.9	29.7	41.6	hypothetical protein VITISV_020704	gbpln	Vitis vinifera	AT5G33406.1 | Symbols: | hAT dimerisation domain−containing protein / transposase−related | chr5:12676126−12678403 REVERSE LENGTH=509	969	509	1.00E−73	52.5	13.2	15.4
Rsa1.0_00332.1.g11528.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1418	1459	0	102.9	58.6	74.4	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1418	1262	1.00E−110	89.0	14.6	21.1
Rsa1.0_00332.1.g11529.t1	ref|NP_191858.2| uncharacterized protein [Arabidopsis thaliana] gi|117168187|gb|ABK32176.1| At3g62990 [Arabidopsis thaliana] gi|332646900|gb|AEE80421.1| uncharacterized protein AT3G62990 [Arabidopsis thaliana]	131	134	4.00E−20	102.3	55.7	69.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G62990.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G47950.1); Has 22 Blast hits to 22 proteins in 5 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 22; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:23282803−23283207 FORWARD LENGTH=134	131	134	8.00E−23	102.3	55.7	69.5

Rsa1.0_00332.1.g11530.t1	ref|NP_567135.1| protein TRANSPORT INHIBITOR RESPONSE 1 [Arabidopsis thaliana] gi|68053009|sp|Q570C0.2|TIR1_ARATH RecName: Full=Protein TRANSPORT INHIBITOR RESPONSE 1; AltName: Full=Weak ethylene-insensitive protein 1 gi|146387658|pdb|2P1M|B Chain B, Tir1-ask1 Complex Structure gi|146387660|pdb|2P1N|B Chain B, Mechanism Of Auxin Perception By The Tir1 Ubiqutin Ligase gi|146387663|pdb|2P1N|E Chain E, Mechanism Of Auxin Perception By The Tir1 Ubiqutin Ligase gi|146387666|pdb|2P1O|B Chain B, Mechanism Of Auxin Perception By The Tir1 Ubiquitin Ligase gi|146387669|pdb|2P1P|B Chain B, Mechanism Of Auxin Perception By The Tir1 Ubiquitin Ligase gi|146387671|pdb|2P1Q|B Chain B, Mechanism Of Auxin Perception By The Tir1 Ubiquitin Ligase gi|185177934|pdb|3C6N|B Chain B, Small Molecule Agonists And Antagonists Of F-Box Protein-Substrate Interactions In Auxin Perception And Signaling gi|185177936|pdb|3C6O|B Chain B, Small Molecule Agonists And Antagonists Of F-Box Protein-Substrate Interactions In Auxin Perception And Signaling	570	594	0	104.2	92.3	95.3	protein TRANSPORT INHIBITOR RESPONSE 1	gbpln	Arabidopsis thaliana	AT3G62980.1 | Symbols: TIR1 | F-box/RNI-like superfamily protein | chr3:23273479-23276181 REVERSE LENGTH=594	570	594	0	104.2	92.3	95.3
Rsa1.0_00332.1.g11531.t1	ref|NP_191856.4| ring finger and CHY zinc finger domain-containing protein 1 [Arabidopsis thaliana] gi|332646897|gb|AEE80418.1| ring finger and CHY zinc finger domain-containing protein 1 [Arabidopsis thaliana]	265	287	1.00E-100	108.3	69.8	77.0	ring finger and CHY zinc finger domain-containing protein 1	gbpln	Arabidopsis thaliana	AT3G62970.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr3:23270636-23272698 FORWARD LENGTH=287	265	287	1.00E-103	108.3	69.8	77.0
Rsa1.0_00332.1.g11532.t1	ref|NP_191855.1| glutaredoxin-C14 [Arabidopsis thaliana] gi|75181054|sp|Q9LYC5.1|GRC14_ARATH RecName: Full=Glutaredoxin-C14; Short=AtGrxC14; AltName: Full=Protein ROXY 8 gi|7573425|emb|CAB87741.1| glutaredoxin-like protein [Arabidopsis thaliana] gi|88900350|gb|ABD57487.1| At3g62960 [Arabidopsis thaliana] gi|226348194|gb|ACO50413.1| glutaredoxin [Arabidopsis thaliana] gi|332646896|gb|AEE80417.1| glutaredoxin-C14 [Arabidopsis thaliana] gi|482560809|gb|EOA25000.1| hypothetical protein CARUB_v10018297mg [Capsella rubella]	102	102	5.00E-52	100.0	97.1	99.0	glutaredoxin-C14	gbpln	Arabidopsis thaliana	AT3G62960.1 | Symbols: | Thioredoxin superfamily protein | chr3:23268780-23269088 FORWARD LENGTH=102	102	102	9.00E-55	100.0	97.1	99.0
Rsa1.0_00332.1.g11533.t1	ref|NP_191854.1| glutaredoxin-C11 [Arabidopsis thaliana] gi|297817626|ref|XP_002876696.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|75264377|sp|Q9LYC6.1|GRC11_ARATH RecName: Full=Glutaredoxin-C11; Short=AtGrxC11; AltName: Full=Protein ROXY 4 gi|7573424|emb|CAB87740.1| glutaredoxin-like protein [Arabidopsis thaliana] gi|50253460|gb|AAT71932.1| At3g62950 [Arabidopsis thaliana] gi|51972084|gb|AAU15146.1| At3g62950 [Arabidopsis thaliana] gi|226348186|gb|ACO50409.1| glutaredoxin [Arabidopsis thaliana] gi|297322534|gb|EFH52955.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|332646895|gb|AEE80416.1| glutaredoxin-C11 [Arabidopsis thaliana]	103	103	3.00E-52	100.0	98.1	98.1	glutaredoxin-C11	gbpln	Arabidopsis lyrata	AT3G62950.1 | Symbols: | Thioredoxin superfamily protein | chr3:23266303-23266614 FORWARD LENGTH=103	103	103	5.00E-55	100.0	98.1	98.1
Rsa1.0_00332.1.g11534.t1	gb|EOA23266.1| hypothetical protein CARUB_v10017631mg [Capsella rubella]	333	327	1.00E-147	98.2	85.3	91.3	hypothetical protein CARUB_v10017631mg	gbpln	Capsella rubella	AT3G62940.3 | Symbols: | Cysteine proteinases superfamily protein | chr3:23263106-23264245 REVERSE LENGTH=332	333	332	1.00E-143	99.7	84.4	90.7

Rsa1.0_00332.1.g11535.t1	gb|EOA23343.1| hypothetical protein CARUB_v10019414mg [Capsella rubella]	80	102	7.00E-38	127.5	96.3	100.0	hypothetical protein CARUB_v10019414mg	gbpln	Capsella rubella	AT3G62930.1 | Symbols: | Thioredoxin superfamily protein | chr3:23261538-23261846 REVERSE LENGTH=102	80	102	1.00E-39	127.5	92.5	97.5
Rsa1.0_00332.1.g11536.t1	ref|NP_191851.1| uncharacterized protein [Arabidopsis thaliana] gi|7573421|emb|CAB87737.1| putative protein [Arabidopsis thaliana] gi|332646890|gb|AEE80411.1| uncharacterized protein AT3G62920 [Arabidopsis thaliana]	80	80	2.00E-32	100.0	82.5	93.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G62920.1 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:23260717-23261171 FORWARD LENGTH=80	80	80	3.00E-35	100.0	82.5	93.8
Rsa1.0_00332.1.g11537.t1	gb|EOA24095.1| hypothetical protein CARUB_v10017325mg [Capsella rubella]	418	422	0	101.0	90.7	95.9	hypothetical protein CARUB_v10017325mg	gbpln	Capsella rubella	AT3G62910.1 | Symbols: APG3 | Peptide chain release factor 1 | chr3:23257661-23260386 REVERSE LENGTH=422	418	422	0	101.0	89.7	95.0
Rsa1.0_00332.1.g11538.t10	ref|XP_002878485.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297324323|gb|EFH54744.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	1460	1387	0	95.0	70.4	77.7	zinc ion binding protein	gbpln	Arabidopsis lyrata	AT3G62900.1 | Symbols: | CW-type Zinc Finger | chr3:23248868-23254810 REVERSE LENGTH=1465	1460	1465	0	100.3	70.0	77.7
Rsa1.0_00332.1.g11539.t1	gb|EOA27436.1| hypothetical protein CARUB_v10023573mg [Capsella rubella]	256	338	1.00E-140	132.0	96.5	97.7	hypothetical protein CARUB_v10023573mg	gbpln	Capsella rubella	AT3G62870.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr3:23242862-23244273 REVERSE LENGTH=256	256	256	1.00E-140	100.0	94.5	97.3
Rsa1.0_00332.1.g11540.t2	ref|XP_002878482.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324320|gb|EFH54741.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	470	348	1.00E-148	74.0	58.3	61.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G62860.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:23239577-23242143 REVERSE LENGTH=348	470	348	1.00E-150	74.0	58.1	61.3
Rsa1.0_00332.1.g11541.t1	ref|NP_191842.1| UDP-glucuronic acid decarboxylase [Arabidopsis thaliana] gi|186511349|ref|NP_001118893.1| UDP-glucuronic acid decarboxylase [Arabidopsis thaliana] gi|75335709|sp|Q9LZI2.1|UXS2_ARATH RecName: Full=UDP-glucuronic acid decarboxylase 2; AltName: Full=UDP-XYL synthase 2; AltName: Full=UDP-glucuronate decarboxylase 2; Short=UGD; Short=UXS-2; AltName: Full=dTDP-glucose 4-6-dehydratase homolog D18 gi|7362763|emb|CAB83133.1| dTDP-glucose 4-6-dehydratase homolog D18 [Arabidopsis thaliana] gi|23505953|gb|AAN28836.1| At3g62830/F26K9_260 [Arabidopsis thaliana] gi|332646877|gb|AEE80398.1| UDP-glucuronic acid decarboxylase [Arabidopsis thaliana] gi|332646878|gb|AEE80399.1| UDP-glucuronic acid decarboxylase [Arabidopsis thaliana]	436	445	0	102.1	95.2	96.6	UDP-glucuronic acid decarboxylase	gbpln	Arabidopsis thaliana	AT3G62830.2 | Symbols: UXS2, ATUXS2 | NAD(P)-binding Rossmann-fold superfamily protein | chr3:23232539-23235353 FORWARD LENGTH=445	436	445	0	102.1	95.2	96.6
Rsa1.0_00332.1.g11542.t1	ref|NP_191841.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|7362762|emb|CAB83132.1| putative protein [Arabidopsis thaliana] gi|21592426|gb|AAM64377.1| putative pectinesterase [Arabidopsis thaliana] gi|51969488|dbj|BAD43436.1| unknown protein [Arabidopsis thaliana] gi|332646876|gb|AEE80397.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	189	194	6.00E-82	102.6	80.4	91.5	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT3G62820.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:23229782-23230366 FORWARD LENGTH=194	189	194	2.00E-84	102.6	80.4	91.5
Rsa1.0_00332.1.g11543.t1	ref|NP_001154686.1| double-stranded-RNA-binding protein 4 [Arabidopsis thaliana] gi|197267565|dbj|BAG69145.1| dsRNA-binding protein [Arabidopsis thaliana] gi|332646874|gb|AEE80395.1| double-stranded-RNA-binding protein 4 [Arabidopsis thaliana]	305	329	1.00E-103	107.9	65.6	80.0	double-stranded-RNA-binding protein 4	gbpln	Arabidopsis thaliana	AT3G62800.3 | Symbols: | double-stranded-RNA-binding protein 4 | chr3:23225749-23227163 REVERSE LENGTH=329	305	329	1.00E-105	107.9	65.6	80.0
Rsa1.0_00332.1.g11544.t1	ref|XP_002878478.1| hypothetical protein ARALYDRAFT_486781 [Arabidopsis lyrata subsp. lyrata] gi|297324316|gb|EFH54737.1| hypothetical protein ARALYDRAFT_486781 [Arabidopsis lyrata subsp. lyrata]	83	83	2.00E-40	100.0	95.2	97.6	hypothetical protein ARALYDRAFT_486781	gbpln	Arabidopsis lyrata	AT3G62790.1 | Symbols: | NADH-ubiquinone oxidoreductase-related | chr3:23223321-23224221 REVERSE LENGTH=83	83	83	6.00E-43	100.0	95.2	97.6

Rsa1.0_00332.1.g11545.t1	ref|NP_567132.4| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|75331631|sp|Q93VB2.1|AT18A_ARATH RecName: Full=Autophagy-related protein 18a; Short=AtATG18a gi|14517420|gb|AAK62600.1| AT3g62770/F26K9_200 [Arabidopsis thaliana] gi|16323362|gb|AAL15394.1| AT3g62770/F26K9_200 [Arabidopsis thaliana] gi|332646868|gb|AEE80389.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	152	425	8.00E-40	279.6	59.2	64.5	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G62770.1 | Symbols: AtATG18a | Transducin/WD40 repeat-like superfamily protein | chr3:23218858-23221110 REVERSE LENGTH=425	152	425	3.00E-42	279.6	59.2	64.5
Rsa1.0_00332.1.g11546.t1	dbj|BAJ34035.1| unnamed protein product [Thellungiella halophila]	539	506	0	93.9	72.7	81.6	unnamed protein product	----	----	AT4G27830.1 | Symbols: BGLU10 | beta glucosidase 10 | chr4:13861794-13864489 REVERSE LENGTH=508	539	508	0	94.2	71.8	80.9
Rsa1.0_00332.1.g11547.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	353	1274	7.00E-45	360.9	34.8	51.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	353	303	1.00E-41	85.8	28.6	43.1
Rsa1.0_00332.1.g11548.t1	ref|XP_002878474.1| hypothetical protein ARALYDRAFT_907848 [Arabidopsis lyrata subsp. lyrata] gi|297324312|gb|EFH54733.1| hypothetical protein ARALYDRAFT_907848 [Arabidopsis lyrata subsp. lyrata]	321	315	1.00E-157	98.1	86.0	90.7	hypothetical protein ARALYDRAFT_907848	gbpln	Arabidopsis lyrata	AT3G62730.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, LP.02 two leaves visible, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G47980.1); Has 172 Blast hits to 172 proteins in 41 species: Archae - 0; Bacteria - 73; Metazoa - 0; Fungi - 0; Plants - 99; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:23208003-23209436 REVERSE LENGTH=317	321	317	1.00E-159	98.8	85.4	89.4
Rsa1.0_00333.1.g11549.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00333.1.g11550.t1	gb|ABD65624.1| hypothetical protein 23.t00036 [Brassica oleracea]	903	842	1.00E-141	93.2	40.3	56.9	hypothetical protein 23.t00036	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	903	673	6.00E-39	74.5	16.2	24.1
Rsa1.0_00333.1.g11551.t24	gb|AAF80658.1|AC012190_14 Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872 [Arabidopsis thaliana]	1260	904	1.00E-143	71.7	19.2	28.5	Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872	gbpln	Arabidopsis thaliana	AT1G26680.1 | Symbols: | transcriptional factor B3 family protein | chr1:9219552-9223193 FORWARD LENGTH=920	1260	920	3.00E-39	73.0	7.6	11.4
Rsa1.0_00333.1.g11552.t1	ref|NP_680296.1| uncharacterized protein [Arabidopsis thaliana] gi|332006517|gb|AED93900.1| uncharacterized protein AT5G33393 [Arabidopsis thaliana]	102	435	7.00E-13	426.5	30.4	42.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G33393.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:12656430-12658588 REVERSE LENGTH=435	102	435	1.00E-15	426.5	30.4	42.2
Rsa1.0_00333.1.g11553.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00333.1.g11554.t1	dbj|BAC42083.1| unknown protein [Arabidopsis thaliana]	384	398	2.33E-156	103.6	81.3	86.2	unknown protein	gbpln	Arabidopsis thaliana	AT2G36400.1 | Symbols: AtGRF3, GRF3 | growth-regulating factor 3 | chr2:15270300-15272617 REVERSE LENGTH=398	384	398	1.00E-143	103.6	80.5	85.7
Rsa1.0_00333.1.g11555.t1	gb|EOA26559.1| hypothetical protein CARUB_v10022617mg, partial [Capsella rubella]	924	870	0	94.2	81.3	85.3	hypothetical protein CARUB_v10022617mg, partial	gbpln	Capsella rubella	AT2G36390.1 | Symbols: SBE2.1, BE3 | starch branching enzyme 2.1 | chr2:15264283-15269940 FORWARD LENGTH=858	924	858	0	92.9	80.2	84.4

Rsa1.0_00333.1.g11556.t2	ref|NP_850263.1| galactose oxidase/kelch repeat-containing protein [Arabidopsis thaliana] gi|79324451|ref|NP_001031493.1| galactose oxidase/kelch repeat-containing protein [Arabidopsis thaliana] gi|20260248|gb|AAM13022.1| unknown protein [Arabidopsis thaliana] gi|22136502|gb|AAM91329.1| unknown protein [Arabidopsis thaliana] gi|222423480|dbj|BAH19710.1| AT2G36360 [Arabidopsis thaliana] gi|330254146|gb|AEC09240.1| galactose oxidase/kelch repeat-containing protein [Arabidopsis thaliana] gi|330254147|gb|AEC09241.1| galactose oxidase/kelch repeat-containing protein [Arabidopsis thaliana]	497	496	0	99.8	91.1	96.0	galactose oxidase/kelch repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G36360.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:15243461-15247523 REVERSE LENGTH=496	497	496	0	99.8	91.1	96.0
Rsa1.0_00333.1.g11557.t1	ref|XP_002879605.1| hypothetical protein ARALYDRAFT_482608 [Arabidopsis lyrata subsp. lyrata] gi|297325444|gb|EFH55864.1| hypothetical protein ARALYDRAFT_482608 [Arabidopsis lyrata subsp. lyrata]	915	949	0	103.7	84.3	90.6	hypothetical protein ARALYDRAFT_482608	gbpln	Arabidopsis lyrata	AT2G36350.1 | Symbols: | Protein kinase superfamily protein | chr2:15238903-15241864 FORWARD LENGTH=949	915	949	0	103.7	84.3	90.3
Rsa1.0_00333.1.g11558.t1	gb|EOA27631.1| hypothetical protein CARUB_v10023779mg [Capsella rubella]	305	287	1.00E-112	94.1	73.8	82.0	hypothetical protein CARUB_v10023779mg	gbpln	Capsella rubella	AT2G36330.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr2:15233620-15235298 FORWARD LENGTH=283	305	283	1.00E-113	92.8	76.1	83.3
Rsa1.0_00333.1.g11559.t1	ref|NP_565844.1| zinc finger A20 and AN1 domain-containing stress-associated protein 4 [Arabidopsis thaliana] gi|73921295|sp|Q9SJM6.1|SAP4_ARATH RecName: Full=Zinc finger A20 and AN1 domain-containing stress-associated protein 4; Short=AtSAP4 gi|4510345|gb|AAD21434.1| expressed protein [Arabidopsis thaliana] gi|21592464|gb|AAM64415.1| zinc finger-like protein [Arabidopsis thaliana] gi|114050557|gb|ABI49428.1| At2g36320 [Arabidopsis thaliana] gi|330254138|gb|AEC09232.1| zinc finger A20 and AN1 domain-containing stress-associated protein 4 [Arabidopsis thaliana]	161	161	9.00E-63	100.0	77.6	82.6	zinc finger A20 and AN1 domain-containing stress-associated protein 4	gbpln	Arabidopsis thaliana	AT2G36320.1 | Symbols: | A20/AN1-like zinc finger family protein | chr2:15229388-15229873 FORWARD LENGTH=161	161	161	3.00E-65	100.0	77.6	82.6
Rsa1.0_00333.1.g11560.t1	gb|EOA27437.1| hypothetical protein CARUB_v10023574mg [Capsella rubella]	339	338	1.00E-177	99.7	89.7	94.4	hypothetical protein CARUB_v10023574mg	gbpln	Capsella rubella	AT2G36310.1 | Symbols: URH1 | uridine-ribohydrolase 1 | chr2:15224692-15226633 REVERSE LENGTH=336	339	336	1.00E-177	99.1	89.4	93.2
Rsa1.0_00333.1.g11561.t2	gb|EOA25012.1| hypothetical protein CARUB_v10018310mg, partial [Capsella rubella]	71	95	1.00E-19	133.8	73.2	90.1	hypothetical protein CARUB_v10018310mg, partial	gbpln	Capsella rubella	AT3G52770.1 | Symbols: ZPR3 | protein binding | chr3:19557891-19558094 REVERSE LENGTH=67	71	67	3.00E-17	94.4	56.3	67.6
Rsa1.0_00333.1.g11562.t1	ref|XP_002881437.1| hypothetical protein ARALYDRAFT_482602 [Arabidopsis lyrata subsp. lyrata] gi|297327276|gb|EFH57696.1| hypothetical protein ARALYDRAFT_482602 [Arabidopsis lyrata subsp. lyrata]	256	255	1.00E-122	99.6	91.4	94.9	hypothetical protein ARALYDRAFT_482602	gbpln	Arabidopsis lyrata	AT2G36300.1 | Symbols: | Integral membrane Yip1 family protein | chr2:15213362-15214129 REVERSE LENGTH=255	256	255	1.00E-122	99.6	90.2	93.8
Rsa1.0_00333.1.g11563.t1	ref|XP_002881436.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297327275|gb|EFH57695.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	394	363	0	92.1	77.9	83.2	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT2G36290.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:15208867-15210768 REVERSE LENGTH=364	394	364	0	92.4	77.7	83.5
Rsa1.0_00333.1.g11564.t1	gb|AFZ45968.1| ABA insensitve 5-like protein [Brassica oleracea var. capitata]	438	425	1.00E-178	97.0	87.9	91.6	ABA insensitve 5-like protein	gbpln	Brassica oleracea	AT2G36270.1 | Symbols: ABI5, GIA1 | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:15204980-15206571 REVERSE LENGTH=442	438	442	1.00E-158	100.9	81.1	87.0
Rsa1.0_00333.1.g11565.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00333.1.g11566.t1	ref|XP_002879598.1| hypothetical protein ARALYDRAFT_902735 [Arabidopsis lyrata subsp. lyrata] gi|297325437|gb|EFH55857.1| hypothetical protein ARALYDRAFT_902735 [Arabidopsis lyrata subsp. lyrata]	527	497	1.00E-121	94.3	41.9	48.8	hypothetical protein ARALYDRAFT_902735	gbpln	Arabidopsis lyrata	AT2G36240.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:15195663-15197156 FORWARD LENGTH=497	527	497	1.00E-123	94.3	40.2	45.5
Rsa1.0_00333.1.g11567.t1	dbj|BAD72794.1| BBMII isomerase [Arabidopsis thaliana]	311	304	1.00E-148	97.7	85.5	91.0	BBMII isomerase	gbpln	Arabidopsis thaliana	AT2G36230.1 | Symbols: APG10, HISN3 | Aldolase-type TIM barrel family protein | chr2:15193878-15195509 REVERSE LENGTH=304	311	304	1.00E-150	97.7	85.2	90.7

Rsa1.0_00333.1.g11568.t1	ref|XP_002879597.1| hypothetical protein ARALYDRAFT_482594 [Arabidopsis lyrata subsp. lyrata] gi|297325436|gb|EFH55856.1| hypothetical protein ARALYDRAFT_482594 [Arabidopsis lyrata subsp. lyrata]	225	263	6.00E-68	116.9	72.9	79.1	hypothetical protein ARALYDRAFT_482594	gbpln	Arabidopsis lyrata	AT2G36220.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G52710.1); Has 74 Blast hits to 74 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15192556-15193347 FORWARD LENGTH=263	225	263	5.00E-68	116.9	71.6	77.3
Rsa1.0_00333.1.g11569.t1	gb|EOA16761.1| hypothetical protein CARUB_v10004974mg [Capsella rubella]	185	398	2.00E-62	215.1	70.8	76.2	hypothetical protein CARUB_v10004974mg	gbpln	Capsella rubella	AT5G40610.1 | Symbols: | NAD-dependent glycerol-3-phosphate dehydrogenase family protein | chr5:16265071-16267258 REVERSE LENGTH=400	185	400	3.00E-63	216.2	70.3	75.1
Rsa1.0_00334.1.g11570.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11571.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11572.t2	dbj|BAB08464.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana]	148	165	9.00E-45	111.5	58.8	64.9	ADP-ribosylation factor-like protein	gbpln	Arabidopsis thaliana	AT3G49870.1 | Symbols: ATARLA1C, ARLA1C | ADP-ribosylation factor-like A1C | chr3:18492674-18494021 REVERSE LENGTH=184	148	184	4.00E-47	124.3	59.5	64.2
Rsa1.0_00334.1.g11573.t1	gb|AAF97281.1|AC010164_3 Hypothetical protein [Arabidopsis thaliana] gi|12324507|gb|AAG52212.1|AC022288_11 putative gag-pol polyprotein; 76173-77576 [Arabidopsis thaliana]	189	467	5.00E-69	247.1	68.3	83.1	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11574.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11575.t1	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	480	578	4.00E-74	120.4	34.8	47.3	hypothetical protein 27.t00126	gbpln	Brassica oleracea	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	480	1399	9.00E-13	291.5	7.1	11.3
Rsa1.0_00334.1.g11576.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	178	672	3.00E-27	377.5	29.2	42.1	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11577.t1	gb|AAF79254.1|AC023279_3 F12K21.6 [Arabidopsis thaliana]	508	755	9.00E-42	148.6	21.3	31.9	F12K21.6	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11578.t1	pir||E84492 probable retroelement pol polyprotein [imported] - Arabidopsis thaliana	554	531	1.00E-109	95.8	37.0	45.1	probable retroelement pol polyprotein	----	----	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11579.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	1430	1239	0	86.6	25.7	32.4	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1430	1262	2.00E-58	88.3	10.1	15.9
Rsa1.0_00334.1.g11580.t1	gb|EOA33021.1| hypothetical protein CARUB_v10016352mg, partial [Capsella rubella]	955	886	5.00E-87	92.8	19.5	28.6	hypothetical protein CARUB_v10016352mg, partial	gbpln	Capsella rubella	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	955	719	2.00E-13	75.3	12.4	23.1
Rsa1.0_00334.1.g11581.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	158	1142	1.00E-12	722.8	22.2	32.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11582.t2	gb|EMJ02968.1| hypothetical protein PRUPE_ppa000155mg [Prunus persica]	190	1600	1.00E-26	842.1	43.7	62.1	hypothetical protein PRUPE_ppa000155mg	gbpln	Prunus persica	AT1G34260.1 | Symbols: FAB1D | FORMS APLOID AND BINUCLEATE CELLS 1A | chr1:12485967-12491799 FORWARD LENGTH=1456	190	1456	2.00E-27	766.3	41.6	61.6
Rsa1.0_00334.1.g11583.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1384	1413	0	102.1	65.2	78.9	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1384	1262	0	91.2	22.7	28.3
Rsa1.0_00334.1.g11584.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1362	1838	0	134.9	54.0	67.2	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11585.t1	gb|AAQ82842.1| At4g20730 [Arabidopsis thaliana] gi|51970840|dbj|BAD44112.1| putative protein [Arabidopsis thaliana]	913	800	2.00E-13	87.6	6.2	9.5	At4g20730	gbpln	Arabidopsis thaliana	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	913	1399	3.00E-15	153.2	6.1	9.6
Rsa1.0_00334.1.g11586.t1	emb|CAN74228.1| hypothetical protein VITISV_000583 [Vitis vinifera]	378	909	1.00E-95	240.5	45.8	52.4	hypothetical protein VITISV_000583	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00334.1.g11587.t1	ref|NP_175361.3| F-box protein [Arabidopsis thaliana] gi|75267565|sp|Q9XIA2.1|FB49_ARATH RecName: Full=F-box protein At1g49360 gi|5430772|gb|AAD43172.1|AC007504_27 Hypothetical Protein [Arabidopsis thaliana] gi|332194301|gb|AEE32422.1| F-box protein [Arabidopsis thaliana]	553	481	1.00E-147	87.0	51.4	62.4	F-box protein	gbpln	Arabidopsis thaliana	AT1G49360.1 | Symbols: | F-box family protein | chr1:18267338-18269423 REVERSE LENGTH=481	553	481	1.00E-149	87.0	51.4	62.4
Rsa1.0_00334.1.g11588.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00335.1.g11589.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	970	1072	0	110.5	55.3	70.3	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	970	289	2.00E-70	29.8	13.5	18.6

Rsa1.0_00335.1_g11590.t1	ref|NP_196021.2| F-box protein [Arabidopsis thaliana] gi|75104736|sp|Q5EAF6.1|FB336_ARATH RecName: Full=Probable F-box protein At5g04010; AltName: Full=Non-specific F-box protein gi|58743286|gb|AAW81721.1| At5g04010 [Arabidopsis thaliana] gi|332003301|gb|AED90684.1| probable F-box protein [Arabidopsis thaliana]	398	287	2.00E-54	72.1	34.2	43.0	F-box protein	gbpln	Arabidopsis thaliana	AT5G04010.1 | Symbols: | F-box family protein | chr5:1080205-1081068 REVERSE LENGTH=287	398	287	6.00E-57	72.1	34.2	43.0
Rsa1.0_00335.1_g11591.t1	gb|AAG50886.1|AC025294_24 hypothetical protein [Arabidopsis thaliana]	200	629	4.00E-26	314.5	33.0	46.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	200	295	6.00E-26	147.5	28.0	41.0
Rsa1.0_00335.1_g11592.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00335.1_g11593.t1	ref|XP_002871067.1| hypothetical protein ARALYDRAFT_487179 [Arabidopsis lyrata subsp. lyrata] gi|297316904|gb|EFH47326.1| hypothetical protein ARALYDRAFT_487179 [Arabidopsis lyrata subsp. lyrata]	293	292	6.00E-92	99.7	71.7	79.5	hypothetical protein ARALYDRAFT_487179	gbpln	Arabidopsis lyrata	AT5G03990.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G51940.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:1075957-1077358 FORWARD LENGTH=302	293	302	3.00E-89	103.1	73.0	80.2
Rsa1.0_00335.1_g11594.t1	gb|EOA19691.1| hypothetical protein CARUB_v10003448mg, partial [Capsella rubella]	322	306	1.00E-66	95.0	51.6	56.5	hypothetical protein CARUB_v10003448mg, partial	gbpln	Capsella rubella	AT5G03980.1 | Symbols: | SGNH hydrolase-type esterase superfamily protein | chr5:1074205-1075289 REVERSE LENGTH=323	322	323	1.00E-67	100.3	52.8	59.0
Rsa1.0_00335.1_g11595.t3	ref|NP_199973.1| microtubule associated protein MAP65-3 [Arabidopsis thaliana] gi|75262488|sp|Q9FHM4.1|MA653_ARATH RecName: Full=65-kDa microtubule-associated protein 3; Short=AtMAP65-3; AltName: Full=Protein PLEIADE gi|9758202|dbj|BAB08676.1| unnamed protein product [Arabidopsis thaliana] gi|332008719|gb|AED96102.1| microtubule associated protein MAP65-3 [Arabidopsis thaliana]	497	707	1.00E-174	142.3	63.0	67.6	microtubule associated protein MAP65-3	gbpln	Arabidopsis thaliana	AT5G51600.1 | Symbols: PLE, ATMAP65-3, MAP65-3 | Microtubule associated protein (MAP65/ASE1) family protein | chr5:20961061-20964080 REVERSE LENGTH=707	497	707	1.00E-177	142.3	63.0	67.6
Rsa1.0_00335.1_g11596.t1	emb|CAB85517.1| putative protein [Arabidopsis thaliana]	405	426	1.00E-170	105.2	69.1	84.2	putative protein	gbpln	Arabidopsis thaliana	AT5G03970.1 | Symbols: | F-box associated ubiquitination effector family protein | chr5:1071721-1072977 REVERSE LENGTH=418	405	418	1.00E-172	103.2	69.1	84.2
Rsa1.0_00335.1_g11597.t1	ref|NP_176732.2| LETM1-like protein [Arabidopsis thaliana] gi|332196272|gb|AEE34393.1| LETM1-like protein [Arabidopsis thaliana]	243	736	1.00E-20	302.9	18.9	19.8	LETM1-like protein	gbpln	Arabidopsis thaliana	AT1G65540.1 | Symbols: | LETM1-like protein | chr1:24362382-24366011 REVERSE LENGTH=736	243	736	3.00E-23	302.9	18.9	19.8
Rsa1.0_00335.1_g11598.t1	ref|NP_196016.1| IQ-domain 12 protein [Arabidopsis thaliana] gi|7406406|emb|CAB85516.1| putative protein [Arabidopsis thaliana] gi|332003293|gb|AED90676.1| IQ-domain 12 protein [Arabidopsis thaliana]	404	403	1.00E-150	99.8	77.7	86.1	IQ-domain 12 protein	gbpln	Arabidopsis thaliana	AT5G03960.1 | Symbols: IQD12 | IQ-domain 12 | chr5:1068333-1069683 REVERSE LENGTH=403	404	403	1.00E-152	99.8	77.7	86.1
Rsa1.0_00335.1_g11599.t1	ref|NP_196014.1| signal recognition particle subunit [Arabidopsis thaliana] gi|586038|sp|P37107.1|SR54C_ARATH RecName: Full=Signal recognition particle 54 kDa protein, chloroplastic; Short=54 chloroplast protein; Short=54CP; Short=SRP54; Short=cpSRP54; AltName: Full=FFC; Flags: Precursor gi|396701|emb|CAA79981.1| 54CP [Arabidopsis thaliana] gi|7406404|emb|CAB85514.1| signal recognition particle 54CP protein precursor [Arabidopsis thaliana] gi|15293131|gb|AAK93676.1| putative signal recognition particle 54CP protein precursor [Arabidopsis thaliana] gi|24030445|gb|AAN41376.1| putative signal recognition particle 54CP protein precursor [Arabidopsis thaliana] gi|332003291|gb|AED90674.1| signal recognition particle subunit [Arabidopsis thaliana]	583	564	0	96.7	89.2	92.3	signal recognition particle subunit	gbpln	Arabidopsis thaliana	AT5G03940.1 | Symbols: FFC, 54CP, CPSRP54, SRP54CP | chloroplast signal recognition particle 54 kDa subunit | chr5:1060265-1063257 REVERSE LENGTH=564	583	564	0	96.7	89.2	92.3

Rsa1.0_00335.1.g11600.t1	ref|XP_002873123.1| hypothetical protein ARALYDRAFT_487170 [Arabidopsis lyrata subsp. lyrata] gi|297318960|gb|EFH49382.1| hypothetical protein ARALYDRAFT_487170 [Arabidopsis lyrata subsp. lyrata]	626	635	0	101.4	82.4	89.0	hypothetical protein ARALYDRAFT_487170	gbpln	Arabidopsis lyrata	AT5G03910.1 | Symbols: ATATH12, ATH12 | ABC2 homolog 12 | chr5:1054313-1057105 REVERSE LENGTH=634	626	634	0	101.3	82.3	88.7
Rsa1.0_00335.1.g11601.t1	gb|EOA22053.1| hypothetical protein CARUB_v10002593mg [Capsella rubella]	163	158	6.00E-68	96.9	84.0	90.2	hypothetical protein CARUB_v10002593mg	gbpln	Capsella rubella	AT5G03905.1 | Symbols: | Iron-sulphur cluster biosynthesis family protein | chr5:1052728-1054041 FORWARD LENGTH=158	163	158	2.00E-62	96.9	74.2	82.8
Rsa1.0_00335.1.g11602.t1	ref|NP_196009.1| uncharacterized protein [Arabidopsis thaliana] gi|7406399|emb|CAB85509.1| putative protein [Arabidopsis thaliana] gi|9758018|dbj|BAB08615.1| unnamed protein product [Arabidopsis thaliana] gi|332003284|gb|AED90667.1| uncharacterized protein AT5G03890 [Arabidopsis thaliana]	173	179	2.00E-58	103.5	78.0	84.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G03890.1 | Symbols: | unknown protein; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G10120.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1047150-1047689 FORWARD LENGTH=179	173	179	1.00E-60	103.5	78.0	84.4
Rsa1.0_00335.1.g11603.t2	ref|XP_002873122.1| hypothetical protein ARALYDRAFT_487166 [Arabidopsis lyrata subsp. lyrata] gi|297318959|gb|EFH49381.1| hypothetical protein ARALYDRAFT_487166 [Arabidopsis lyrata subsp. lyrata]	346	336	1.00E-158	97.1	82.9	87.9	hypothetical protein ARALYDRAFT_487166	gbpln	Arabidopsis lyrata	AT5G03880.1 | Symbols: | Thioredoxin family protein | chr5:1038674-1041453 REVERSE LENGTH=339	346	339	1.00E-153	98.0	81.5	85.8
Rsa1.0_00335.1.g11604.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00335.1.g11605.t1	gb|EOA31777.1| hypothetical protein CARUB_v10014999mg, partial [Capsella rubella]	64	92	1.00E-28	143.8	100.0	100.0	hypothetical protein CARUB_v10014999mg, partial	gbpln	Capsella rubella	AT5G03850.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr5:1028542-1028736 REVERSE LENGTH=64	64	64	7.00E-31	100.0	100.0	100.0
Rsa1.0_00335.1.g11606.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1719	1213	0	70.6	35.4	46.8	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1719	626	2.00E-69	36.4	7.9	13.1
Rsa1.0_00335.1.g11607.t1	dbj|BAA33415.1| BNTFL1-1 [Brassica napus]	178	178	2.00E-93	100.0	94.9	96.6	BNTFL1-1	gbpln	Brassica napus	AT5G03840.1 | Symbols: TFL1, TFL-1 | PEBP (phosphatidylethanolamine-binding protein) family protein | chr5:1024760-1025796 REVERSE LENGTH=177	178	177	2.00E-85	99.4	85.4	92.7
Rsa1.0_00335.1.g11608.t1	ref|NP_001031828.1| putative glycosyltransferase [Arabidopsis thaliana] gi|292630778|sp|Q9FFN2.2|GLYT3_ARATH RecName: Full=Probable glycosyltransferase At5g03795 gi|332003272|gb|AED90655.1| putative glycosyltransferase [Arabidopsis thaliana]	537	518	0	96.5	81.6	86.6	putative glycosyltransferase	gbpln	Arabidopsis thaliana	AT5G03795.1 | Symbols: | Exostosin family protein | chr5:1007554-1010373 REVERSE LENGTH=518	537	518	0	96.5	81.6	86.6
Rsa1.0_00335.1.g11609.t1	ref|XP_002871059.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316896|gb|EFH47318.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	219	215	3.00E-73	98.2	66.7	79.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G03790.1 | Symbols: ATHB51, LMI1, HB51 | homeobox 51 | chr5:1004985-1006373 FORWARD LENGTH=235	219	235	3.00E-73	107.3	63.9	79.5
Rsa1.0_00335.1.g11610.t2	ref|NP_195999.2| homeobox 51 [Arabidopsis thaliana] gi|374095369|sp|Q9LZR0.2|ATB51_ARATH RecName: Full=Putative homeobox-leucine zipper protein ATHB-51; AltName: Full=HD-ZIP protein ATHB-51; AltName: Full=Homeodomain transcription factor ATHB-51 gi|332003271|gb|AED90654.1| homeobox 51 [Arabidopsis thaliana]	230	235	1.00E-106	102.2	81.7	89.6	homeobox 51	gbpln	Arabidopsis thaliana	AT5G03790.1 | Symbols: ATHB51, LMI1, HB51 | homeobox 51 | chr5:1004985-1006373 FORWARD LENGTH=235	230	235	1.00E-108	102.2	81.7	89.6
Rsa1.0_00335.1.g11611.t1	ref|XP_002871057.1| hypothetical protein ARALYDRAFT_325028 [Arabidopsis lyrata subsp. lyrata] gi|297316894|gb|EFH47316.1| hypothetical protein ARALYDRAFT_325028 [Arabidopsis lyrata subsp. lyrata]	464	439	0	94.6	81.9	89.2	hypothetical protein ARALYDRAFT_325028	gbpln	Arabidopsis lyrata	AT5G03770.1 | Symbols: KDTA | KDO transferase A | chr5:995191-997622 FORWARD LENGTH=447	464	447	0	96.3	81.7	88.8
Rsa1.0_00335.1.g11612.t1	emb|CAB39637.1| putative protein [Arabidopsis thaliana] gi|7267665|emb|CAB78093.1| putative protein [Arabidopsis thaliana] gi|91805577|gb|ABE65517.1| hypothetical protein At4g09700 [Arabidopsis thaliana]	752	371	2.00E-71	49.3	19.4	28.1	putative protein	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	752	361	3.00E-22	48.0	8.4	13.0

Rsa1.0_00336.1.g11613.t5	ref|NP_563650.1| transcription factor HFR1 [Arabidopsis thaliana] gi|20532238|sp|Q9FE22.1|HFR1_ARATH RecName: Full=Transcription factor HFR1; AltName: Full=Basic helix-loop-helix protein 26; Short=AtbHLH26; Short=bHLH 26; AltName: Full=Protein LONG HYPOCOTYL IN FAR-RED 1; AltName: Full=Protein REDUCED PHYTOCHROME SIGNALING; AltName: Full=Reduced sensitivity to far-red light; AltName: Full=Transcription factor EN 68; AltName: Full=bHLH transcription factor bHLH026 gi|11870115|gb|AAG40617.1|AF324245_1 bHLH-like protein HFR1 [Arabidopsis thaliana] gi|12025106|gb|AAG45733.1|AF288287_1 reduced phytochrome signaling 1 [Arabidopsis thaliana] gi|13183644|gb|AAK15282.1|AF323182_1 basic helix-loop-helix FBI1 protein [Arabidopsis thaliana] gi|332189297|gb|AEE27418.1| transcription factor HFR1 [Arabidopsis thaliana]	257	292	3.00E-55	113.6	45.5	53.3	transcription factor HFR1	gbpln	Arabidopsis thaliana	AT1G02340.1 | Symbols: HFR1, RSF1, FBI1, REP1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:465933-467685 REVERSE LENGTH=292	257	292	8.00E-58	113.6	45.5	53.3
Rsa1.0_00336.1.g11614.t1	ref|NP_192078.1| protoporphyrinogen oxidase [Arabidopsis thaliana] gi|2495184|sp|P55826.1|PPOC_ARATH RecName: Full=Protoporphyrinogen oxidase, chloroplastic; Short=PPO; Flags: Precursor gi|1877018|dbj|BAA11820.1| protoporphyrinogen oxidase [Arabidopsis thaliana] gi|7268212|emb|CAB77739.1| protoporphyrinogen oxidase [Arabidopsis thaliana] gi|56550711|gb|AAV97809.1| At4g01690 [Arabidopsis thaliana] gi|58331767|gb|AAW70381.1| At4g01690 [Arabidopsis thaliana] gi|332656665|gb|AEE82065.1| protoporphyrinogen oxidase [Arabidopsis thaliana]	539	537	0	99.6	87.0	92.6	protoporphyrinogen oxidase	gbpln	Arabidopsis thaliana	AT4G01690.1 | Symbols: PPOX, HEMG1, PPO1 | Flavin containing amine oxidoreductase family | chr4:729929-732309 FORWARD LENGTH=537	539	537	0	99.6	87.0	92.6
Rsa1.0_00336.1.g11615.t1	ref|XP_002892103.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297337945|gb|EFH68362.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	70	69	4.00E-11	98.6	72.9	80.0	expressed protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00336.1.g11616.t1	dbj|BAJ33936.1| unnamed protein product [Thellungiella halophila]	271	271	1.00E-137	100.0	85.6	88.2	unnamed protein product	----	----	AT1G02360.1 | Symbols: | Chitinase family protein | chr1:472138-473116 REVERSE LENGTH=272	271	272	1.00E-137	100.4	84.5	90.8
Rsa1.0_00336.1.g11617.t1	ref|XP_002889397.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335239|gb|EFH65656.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	513	524	0	102.1	81.9	91.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G02370.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:474516-476383 FORWARD LENGTH=537	513	537	0	104.7	82.1	90.8
Rsa1.0_00336.1.g11618.t1	ref|NP_171740.3| uncharacterized protein [Arabidopsis thaliana] gi|9857534|gb|AAG00889.1|AC064879_7 Hypothetical protein [Arabidopsis thaliana] gi|332189301|gb|AEE27422.1| uncharacterized protein AT1G02380 [Arabidopsis thaliana]	226	231	3.00E-75	102.2	68.6	80.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G02380.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01960.1); Has 66 Blast hits to 66 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 66; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:477814-478850 FORWARD LENGTH=231	226	231	9.00E-78	102.2	68.6	80.1
Rsa1.0_00336.1.g11619.t1	dbj|BAJ33901.1| unnamed protein product [Thellungiella halophila]	527	529	0	100.4	87.1	92.6	unnamed protein product	----	----	AT1G02390.1 | Symbols: ATGPAT2, GPAT2 | glycerol-3-phosphate acyltransferase 2 | chr1:480921-483163 FORWARD LENGTH=530	527	530	0	100.6	82.4	89.8

Rsa1.0_00336.1.g11620.t1	ref|NP_171742.1| gibberellin 2-oxidase 6 [Arabidopsis thaliana] gi|9857536|gb|AAG00891.1|AC064879_9 Unknown protein [Arabidopsis thaliana] gi|48427658|gb|AAT42378.1| At1g02400 [Arabidopsis thaliana] gi|57792118|gb|AAW56770.1| gibberellin 2-oxidase [Arabidopsis thaliana] gi|110737568|dbj|BAF00726.1| hypothetical protein [Arabidopsis thaliana] gi|332189304|gb|AEE27425.1| gibberellin 2-oxidase 6 [Arabidopsis thaliana]	329	329	1.00E-176	100.0	90.3	94.5	gibberellin 2-oxidase 6	gbpln	Arabidopsis thaliana	AT1G02400.1 | Symbols: ATGA2OX4, ATGA2OX6, DTA1, GA2OX6 | gibberellin 2-oxidase 6 | chr1:486964-489391 FORWARD LENGTH=329	329	329	1.00E-178	100.0	90.3	94.5
Rsa1.0_00336.1.g11621.t1	ref|XP_002889401.1| cytochrome c oxidase assembly protein CtaG [Arabidopsis lyrata subsp. lyrata] gi|297335243|gb|EFH65660.1| cytochrome c oxidase assembly protein CtaG [Arabidopsis lyrata subsp. lyrata]	272	287	1.00E-123	105.5	85.3	88.6	cytochrome c oxidase assembly protein CtaG	gbpln	Arabidopsis lyrata	AT1G02410.1 | Symbols: | cytochrome c oxidase assembly protein CtaG / Cox11 family | chr1:491300-492762 FORWARD LENGTH=287	272	287	1.00E-123	105.5	83.1	86.4
Rsa1.0_00336.1.g11622.t1	ref|NP_563653.2| protein NIM1-interacting 1 [Arabidopsis thaliana] gi|75309253|sp|Q9FNZ5.1|NIMI1_ARATH RecName: Full=Protein NIM1-INTERACTING 1; Short=Protein NIMIN-1 gi|12057154|emb|CAC19844.1| NIMIN-1 protein [Arabidopsis thaliana] gi|26453292|dbj|BAC43719.1| unknown protein [Arabidopsis thaliana] gi|28372816|gb|AAO39890.1| At1g02450 [Arabidopsis thaliana] gi|332189310|gb|AEE27431.1| protein NIM1-INTERACTING 1 [Arabidopsis thaliana]	266	142	1.00E-30	53.4	32.0	37.2	protein NIM1-interacting 1	gbpln	Arabidopsis thaliana	AT1G02450.1 | Symbols: NIMIN1, NIMIN-1 | NIM1-interacting 1 | chr1:498052-498480 REVERSE LENGTH=142	266	142	3.00E-33	53.4	32.0	37.2
Rsa1.0_00336.1.g11623.t1	gb|EOA36864.1| hypothetical protein CARUB_v10008847mg, partial [Capsella rubella]	491	523	0	106.5	90.2	94.9	hypothetical protein CARUB_v10008847mg, partial	gbpln	Capsella rubella	AT1G02460.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:504897-507099 REVERSE LENGTH=491	491	491	0	100.0	88.6	94.1
Rsa1.0_00336.1.g11624.t1	ref|XP_002892124.1| hypothetical protein ARALYDRAFT_887420 [Arabidopsis lyrata subsp. lyrata] gi|297337966|gb|EFH68383.1| hypothetical protein ARALYDRAFT_887420 [Arabidopsis lyrata subsp. lyrata]	309	422	1.00E-143	136.6	81.9	87.4	hypothetical protein ARALYDRAFT_887420	gbpln	Arabidopsis lyrata	AT1G02790.1 | Symbols: PGA4 | polygalacturonase 4 | chr1:610681-612225 REVERSE LENGTH=422	309	422	1.00E-144	136.6	81.6	86.7
Rsa1.0_00336.1.g11625.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	330	1274	4.00E-35	386.1	32.4	45.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	330	303	7.00E-23	91.8	19.1	30.3
Rsa1.0_00336.1.g11626.t1	ref|NP_563662.1| pectinesterase 7 [Arabidopsis thaliana] gi|75313808|sp|Q9SRX4.1|PME7_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 7; Includes: RecName: Full=Pectinesterase inhibitor 7; AltName: Full=Pectin methylesterase inhibitor 7; Includes: RecName: Full=Pectinesterase 7; Short=PE 7; AltName: Full=Pectin methylesterase 1; Short=AtPME1; AltName: Full=Pectin methylesterase 7; Flags: Precursor gi|6056422|gb|AAF02886.1|AC009525_20 Similar to pectinesterases [Arabidopsis thaliana] gi|133778888|gb|ABO38784.1| At1g02810 [Arabidopsis thaliana] gi|332189351|gb|AEE27472.1| pectinesterase 7 [Arabidopsis thaliana]	698	579	0	83.0	75.5	78.1	pectinesterase 7	gbpln	Arabidopsis thaliana	AT1G02810.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr1:618284-620333 FORWARD LENGTH=579	698	579	0	83.0	75.5	78.1
Rsa1.0_00336.1.g11627.t1	ref|XP_002892126.1| late embryogenesis abundant 3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297337968|gb|EFH68385.1| late embryogenesis abundant 3 family protein [Arabidopsis lyrata subsp. lyrata]	98	97	1.00E-36	99.0	79.6	86.7	late embryogenesis abundant 3 family protein	gbpln	Arabidopsis lyrata	AT1G02820.1 | Symbols: | Late embryogenesis abundant 3 (LEA3) family protein | chr1:623933-624304 REVERSE LENGTH=91	98	91	4.00E-32	92.9	68.4	75.5
Rsa1.0_00336.1.g11628.t1	dbj|BAJ34418.1| unnamed protein product [Thellungiella halophila]	125	124	1.00E-42	99.2	80.8	88.0	unnamed protein product	----	----	AT3G05560.3 | Symbols: | Ribosomal L22e protein family | chr3:1614641-1615204 FORWARD LENGTH=124	125	124	5.00E-45	99.2	80.0	88.0
Rsa1.0_00336.1.g11629.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00336.1_g11630.t1	ref|NP_849578.5| beta glucosidase 11 [Arabidopsis thaliana] gi|332189361|gb|AEE27482.1| beta glucosidase 11 [Arabidopsis thaliana]	506	497	0	98.2	81.0	89.5	beta glucosidase 11	gbpln	Arabidopsis thaliana	AT1G02850.2 | Symbols: BGLU11 | beta glucosidase 11 | chr1:630569-633085 FORWARD LENGTH=497	506	497	0	98.2	81.0	89.5
Rsa1.0_00336.1_g11631.t1	ref|XP_002889424.1| hypothetical protein ARALYDRAFT_470251 [Arabidopsis lyrata subsp. lyrata] gi|297335266|gb|EFH65683.1| hypothetical protein ARALYDRAFT_470251 [Arabidopsis lyrata subsp. lyrata]	327	334	1.00E-158	102.1	86.5	92.4	hypothetical protein ARALYDRAFT_470251	gbpln	Arabidopsis lyrata	AT1G02860.1 | Symbols: NLA, BAH1 | SPX (SYG1/Pho81/XPR1) domain-containing protein | chr1:635474-637083 FORWARD LENGTH=335	327	335	1.00E-158	102.4	85.6	91.7
Rsa1.0_00336.1_g11632.t1	ref|NP_563668.1| uncharacterized protein [Arabidopsis thaliana] gi|20260268|gb|AAM13032.1| unknown protein [Arabidopsis thaliana] gi|21593889|gb|AAM65856.1| unknown [Arabidopsis thaliana] gi|30102920|gb|AAP21378.1| At1g02870 [Arabidopsis thaliana] gi|332189366|gb|AEE27487.1| uncharacterized protein AT1G02870 [Arabidopsis thaliana]	195	193	1.00E-102	99.0	93.3	96.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G02870.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Ribosome biogenesis protein Nop16 (InterPro:IPR019002); Has 104 Blast hits to 104 proteins in 57 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 63; Plants - 35; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:637401-638603 REVERSE LENGTH=193	195	193	1.00E-104	99.0	93.3	96.4
Rsa1.0_00336.1_g11633.t1	ref|XP_002892131.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337973|gb|EFH68390.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	227	228	3.00E-67	100.4	84.6	89.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G02450.2 | Symbols: | HSP20-like chaperones superfamily protein | chr4:1073987-1075765 REVERSE LENGTH=240	227	240	5.00E-53	105.7	41.0	46.3
Rsa1.0_00336.1_g11634.t1	ref|XP_002892132.1| hypothetical protein ARALYDRAFT_470256 [Arabidopsis lyrata subsp. lyrata] gi|297337974|gb|EFH68391.1| hypothetical protein ARALYDRAFT_470256 [Arabidopsis lyrata subsp. lyrata]	266	266	1.00E-127	100.0	83.1	88.7	hypothetical protein ARALYDRAFT_470256	gbpln	Arabidopsis lyrata	AT1G02880.3 | Symbols: TPK1 | thiamin pyrophosphokinase1 | chr1:643063-644485 REVERSE LENGTH=267	266	267	1.00E-129	100.4	83.1	88.0
Rsa1.0_00336.1_g11635.t1	ref|NP_171788.3| AAA-type ATPase-like protein [Arabidopsis thaliana] gi|332189371|gb|AEE27492.1| AAA-type ATPase-like protein [Arabidopsis thaliana]	1263	1246	0	98.7	80.9	88.8	AAA-type ATPase-like protein	gbpln	Arabidopsis thaliana	AT1G02890.1 | Symbols: | AAA-type ATPase family protein | chr1:645372-651797 REVERSE LENGTH=1246	1263	1246	0	98.7	80.9	88.8
Rsa1.0_00336.1_g11636.t1	gb|EOA37640.1| hypothetical protein CARUB_v10012118mg [Capsella rubella]	122	123	2.00E-49	100.8	82.8	91.8	hypothetical protein CARUB_v10012118mg	gbpln	Capsella rubella	AT1G02900.1 | Symbols: RALFL1, RALF1, ATRALF1 | rapid alkalinization factor 1 | chr1:653976-654338 REVERSE LENGTH=120	122	120	3.00E-51	98.4	80.3	86.1
Rsa1.0_00336.1_g11637.t1	dbj|BAJ34627.1| unnamed protein product [Thellungiella halophila]	182	209	4.00E-87	114.8	89.6	93.4	unnamed protein product	----	----	AT1G02930.2 | Symbols: GSTF6 | glutathione S-transferase 6 | chr1:661363-662191 REVERSE LENGTH=208	182	208	1.00E-81	114.3	83.0	90.1
Rsa1.0_00336.1_g11638.t6	gb|AAD54276.1|AF172097_1 telomerase reverse transcriptase catalytic subunit [Arabidopsis thaliana]	1100	1123	0	102.1	72.0	81.1	telomerase reverse transcriptase catalytic subunit	gbpln	Arabidopsis thaliana	AT5G16850.1 | Symbols: ATTERT, TERT | telomerase reverse transcriptase | chr5:5538323-5543444 REVERSE LENGTH=1123	1100	1123	0	102.1	72.0	81.0
Rsa1.0_00336.1_g11639.t1	ref|XP_002892138.1| hypothetical protein ARALYDRAFT_333621 [Arabidopsis lyrata subsp. lyrata] gi|297337980|gb|EFH68397.1| hypothetical protein ARALYDRAFT_333621 [Arabidopsis lyrata subsp. lyrata]	248	248	4.00E-98	100.0	69.4	79.8	hypothetical protein ARALYDRAFT_333621	gbpln	Arabidopsis lyrata	AT1G02940.1 | Symbols: ATGSTF5, GSTF5 | glutathione S-transferase (class phi) 5 | chr1:663079-664128 REVERSE LENGTH=256	248	256	2.00E-96	103.2	66.5	77.0
Rsa1.0_00336.1_g11640.t1	gb|AAF02872.1|AC009525_6 Similar to glutathione S-transferases [Arabidopsis thaliana]	256	281	1.00E-116	109.8	77.3	85.2	Similar to glutathione S-transferases	gbpln	Arabidopsis thaliana	AT1G02940.1 | Symbols: ATGSTF5, GSTF5 | glutathione S-transferase (class phi) 5 | chr1:663079-664128 REVERSE LENGTH=256	256	256	1.00E-119	100.0	77.3	85.2
Rsa1.0_00336.1_g11641.t1	gb|EOA38451.1| hypothetical protein CARUB_v10010097mg [Capsella rubella]	243	251	1.00E-118	103.3	83.5	90.5	hypothetical protein CARUB_v10010097mg	gbpln	Capsella rubella	AT1G02950.3 | Symbols: ATGSTF4, GST31, GSTF4 | glutathione S-transferase F4 | chr1:665308-666420 REVERSE LENGTH=243	243	243	1.00E-118	100.0	81.9	89.3
Rsa1.0_00336.1_g11642.t1	gb|EOA22672.1| hypothetical protein CARUB_v10003375mg [Capsella rubella]	732	738	0	100.8	66.8	80.1	hypothetical protein CARUB_v10003375mg	gbpln	Capsella rubella	AT4G02570.4 | Symbols: CUL1 | cullin 1 | chr4:1129315-1133435 FORWARD LENGTH=738	732	738	0	100.8	66.3	79.5
Rsa1.0_00336.1_g11643.t1	ref|XP_002892141.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337983|gb|EFH68400.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1438	1287	0	89.5	36.4	41.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G02990.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: CW-type Zinc Finger (TAIR:AT3G62900.1). | chr1:681724-686996 REVERSE LENGTH=1278	1438	1278	0	88.9	35.7	40.5

<table>
<tr><td>Rsa1.0_00336.1.g11644.t1</td><td>ref|NP_171800.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana] gi|75200292|sp|Q9SA69.1|Y1301_ARATH RecName: Full=BTB/POZ domain-containing protein At1g03010 gi|4587577|gb|AAD25808.1|AC006550_16 F10O3.17 [Arabidopsis thaliana] gi|332189393|gb|AEE27514.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana]</td><td>633</td><td>634</td><td>0</td><td>100.2</td><td>90.0</td><td>94.8</td><td>Phototropic-responsive NPH3 family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G03010.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr1:693480-696188 FORWARD LENGTH=634</td><td>633</td><td>634</td><td>0</td><td>100.2</td><td>90.0</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00336.1.g11645.t1</td><td>gb|EOA36418.1| hypothetical protein CARUB_v10010921mg [Capsella rubella]</td><td>102</td><td>102</td><td>2.00E-50</td><td>100.0</td><td>95.1</td><td>98.0</td><td>hypothetical protein CARUB_v10010921mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G03020.1 | Symbols: | Thioredoxin superfamily protein | chr1:698207-698515 REVERSE LENGTH=102</td><td>102</td><td>102</td><td>5.00E-52</td><td>100.0</td><td>93.1</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00336.1.g11646.t1</td><td>gb|EOA38355.1| hypothetical protein CARUB_v10009873mg [Capsella rubella]</td><td>231</td><td>300</td><td>1.00E-124</td><td>129.9</td><td>93.1</td><td>97.0</td><td>hypothetical protein CARUB_v10009873mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G03030.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:701621-703568 FORWARD LENGTH=301</td><td>231</td><td>301</td><td>1.00E-118</td><td>130.3</td><td>92.6</td><td>97.4</td></tr>
<tr><td>Rsa1.0_00336.1.g11647.t1</td><td>dbj|BAJ34239.1| unnamed protein product [Thellungiella halophila]</td><td>308</td><td>308</td><td>1.00E-134</td><td>100.0</td><td>87.3</td><td>90.6</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G03040.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:704279-706457 REVERSE LENGTH=302</td><td>308</td><td>302</td><td>1.00E-129</td><td>98.1</td><td>85.4</td><td>89.6</td></tr>
<tr><td>Rsa1.0_00336.1.g11648.t1</td><td>ref|NP_171804.1| putative clathrin assembly protein [Arabidopsis thaliana] gi|46396022|sp|Q9SA65.1|CAP4_ARATH RecName: Full=Putative clathrin assembly protein At1g03050 gi|4587573|gb|AAD25804.1|AC006550_12 Similar to clathrin assembly protein gb|AF041374 (CALM) from Rattus norvegicus [Arabidopsis thaliana] gi|91805731|gb|ABE65594.1| clathrin assembly protein-like [Arabidopsis thaliana] gi|332189399|gb|AEE27520.1| putative clathrin assembly protein [Arabidopsis thaliana]</td><td>594</td><td>599</td><td>0</td><td>100.8</td><td>88.4</td><td>93.3</td><td>putative clathrin assembly protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G03050.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:707726-709860 FORWARD LENGTH=599</td><td>594</td><td>599</td><td>0</td><td>100.8</td><td>88.4</td><td>93.3</td></tr>
<tr><td>Rsa1.0_00336.1.g11649.t2</td><td>ref|XP_002892146.1| hypothetical protein ARALYDRAFT_311407 [Arabidopsis lyrata subsp. lyrata] gi|297337988|gb|EFH68405.1| hypothetical protein ARALYDRAFT_311407 [Arabidopsis lyrata subsp. lyrata]</td><td>3663</td><td>3606</td><td>0</td><td>98.4</td><td>90.8</td><td>94.0</td><td>hypothetical protein ARALYDRAFT_311407</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G03060.1 | Symbols: SPI | Beige/BEACH domain ;WD domain, G-beta repeat protein | chr1:712971-726891 REVERSE LENGTH=3601</td><td>3663</td><td>3601</td><td>0</td><td>98.3</td><td>90.3</td><td>93.8</td></tr>
<tr><td>Rsa1.0_00336.1.g11650.t1</td><td>ref|XP_002889434.1| glutamate binding protein [Arabidopsis lyrata subsp. lyrata] gi|297335276|gb|EFH65693.1| glutamate binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>245</td><td>246</td><td>1.00E-129</td><td>100.4</td><td>94.3</td><td>98.4</td><td>glutamate binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G03070.2 | Symbols: | Bax inhibitor-1 family protein | chr1:730148-731379 FORWARD LENGTH=247</td><td>245</td><td>247</td><td>1.00E-130</td><td>100.8</td><td>93.5</td><td>98.0</td></tr>
<tr><td>Rsa1.0_00336.1.g11651.t1</td><td>ref|XP_002892147.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] gi|297337989|gb|EFH68406.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]</td><td>2601</td><td>1736</td><td>0</td><td>66.7</td><td>34.1</td><td>37.9</td><td>kinase interacting family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G03080.1 | Symbols: | kinase interacting (KIP1-like) family protein | chr1:731794-737332 REVERSE LENGTH=1733</td><td>2601</td><td>1733</td><td>0</td><td>66.6</td><td>34.0</td><td>38.1</td></tr>
<tr><td>Rsa1.0_00336.1.g11652.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00336.1.g11653.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00336.1.g11654.t1</td><td>ref|XP_002889437.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297335279|gb|EFH65696.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>268</td><td>426</td><td>8.00E-96</td><td>159.0</td><td>71.3</td><td>77.6</td><td>transducin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G03110.1 | Symbols: TRM82, AtTRM82 | Transducin/WD40 repeat-like superfamily protein | chr1:749359-751796 FORWARD LENGTH=427</td><td>268</td><td>427</td><td>4.00E-98</td><td>159.3</td><td>70.1</td><td>77.6</td></tr>
<tr><td>Rsa1.0_00336.1.g11655.t1</td><td>ref|NP_171811.1| responsive to abscisic acid 28 [Arabidopsis thaliana] gi|4587565|gb|AAD25796.1|AC006550_4 Similar to rab28 protein gb|X59138 from Zea mays. EST gb|AA042774 comes from this gene [Arabidopsis thaliana] gi|332189412|gb|AEE27533.1| responsive to abscisic acid 28 [Arabidopsis thaliana]</td><td>169</td><td>182</td><td>2.00E-62</td><td>107.7</td><td>82.2</td><td>87.6</td><td>responsive to abscisic acid 28</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G03120.1 | Symbols: ATRAB28, RAB28 | responsive to abscisic acid 28 | chr1:752271-753140 FORWARD LENGTH=182</td><td>169</td><td>182</td><td>7.00E-65</td><td>107.7</td><td>82.2</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00336.1.g11656.t1</td><td>ref|XP_002888154.1| hypothetical protein ARALYDRAFT_893536 [Arabidopsis lyrata subsp. lyrata] gi|297333995|gb|EFH64413.1| hypothetical protein ARALYDRAFT_893536 [Arabidopsis lyrata subsp. lyrata]</td><td>421</td><td>404</td><td>1.00E-54</td><td>96.0</td><td>37.3</td><td>54.2</td><td>hypothetical protein ARALYDRAFT_893536</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G50870.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:18855147-18856337 FORWARD LENGTH=396</td><td>421</td><td>396</td><td>2.00E-46</td><td>94.1</td><td>32.3</td><td>44.9</td></tr>
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Rsa1.0_00336.1.g11657.t1	ref|NP_563677.1| peptide alpha-N-acetyltransferase [Arabidopsis thaliana] gi|297843116|ref|XP_002889439.1| hypothetical protein ARALYDRAFT_887467 [Arabidopsis lyrata subsp. lyrata] gi|21536510|gb|AAM60842.1| unknown [Arabidopsis thaliana] gi|297335281|gb|EFH65698.1| hypothetical protein ARALYDRAFT_887467 [Arabidopsis lyrata subsp. lyrata] gi|332189415|gb|AEE27536.1| peptide alpha-N-acetyltransferase [Arabidopsis thaliana] gi|482572073|gb|EOA36260.1| hypothetical protein CARUB_v10010452mg [Capsella rubella]	174	174	1.00E-98	100.0	99.4	100.0	peptide alpha-N-acetyltransferase	gbpln	Arabidopsis lyrata	AT1G03150.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr1:756461-758441 FORWARD LENGTH=174	174	174	1.00E-101	100.0	99.4	100.0
Rsa1.0_00336.1.g11658.t1	gb|EOA37699.1| hypothetical protein CARUB_v10012407mg [Capsella rubella]	227	276	6.00E-85	121.6	79.7	86.3	hypothetical protein CARUB_v10012407mg	gbpln	Capsella rubella	AT1G03170.1 | Symbols: | Protein of unknown function (DUF3049) | chr1:769805-770527 FORWARD LENGTH=240	227	240	1.00E-83	105.7	74.0	82.8
Rsa1.0_00336.1.g11659.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00336.1.g11660.t1	ref|XP_002889474.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297335316|gb|EFH65733.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	353	464	1.00E-85	131.4	59.5	68.6	protein binding protein	gbpln	Arabidopsis lyrata	AT1G03770.2 | Symbols: RING1B | RING 1B | chr1:944772-947431 FORWARD LENGTH=468	353	468	1.00E-83	132.6	58.4	68.6
Rsa1.0_00336.1.g11661.t1	ref|XP_002892179.1| hypothetical protein ARALYDRAFT_470351 [Arabidopsis lyrata subsp. lyrata] gi|297338021|gb|EFH68438.1| hypothetical protein ARALYDRAFT_470351 [Arabidopsis lyrata subsp. lyrata]	790	771	0	97.6	82.2	87.6	hypothetical protein ARALYDRAFT_470351	gbpln	Arabidopsis lyrata	AT1G03780.2 | Symbols: TPX2 | targeting protein for XKLP2 | chr1:947785-951696 REVERSE LENGTH=758	790	758	0	95.9	79.5	85.6
Rsa1.0_00337.1.g11662.t1	ref|NP_564379.2| NEDD8-like protein RUB1 [Arabidopsis thaliana] gi|302393813|sp|Q9SHE7.3|RUB1_ARATH RecName: Full=Ubiquitin-NEDD8-like protein RUB1; Contains: RecName: Full=Ubiquitin; Contains: RecName: Full=NEDD8-like protein RUB1; AltName: Full=Ubiquitin-related protein 1; Short=AtRUB1; Flags: Precursor gi|6692129|gb|AAF24594.1|AC007654_10 T19E23.13 [Arabidopsis thaliana] gi|28973676|gb|AAO64156.1| putative ubiquitin (AtRUB1) [Arabidopsis thaliana] gi|29824269|gb|AAP04095.1| putative ubiquitin (AtRUB1) [Arabidopsis thaliana] gi|110737109|dbj|BAF00506.1| putative ubiquitin [Arabidopsis thaliana] gi|312283039|dbj|BAJ34385.1| unnamed protein product [Thellungiella halophila] gi|332193223|gb|AEE31344.1| NEDD8-like protein RUB1 [Arabidopsis thaliana]	156	156	2.00E-82	100.0	100.0	100.0	NEDD8-like protein RUB1	gbpln	Arabidopsis thaliana	AT1G31340.1 | Symbols: RUB1, NEDD8, ATRUB1 | related to ubiquitin 1 | chr1:11218076-11219417 REVERSE LENGTH=156	156	156	6.00E-85	100.0	100.0	100.0
Rsa1.0_00337.1.g11663.t1	ref|NP_564378.1| uncharacterized protein [Arabidopsis thaliana] gi|21536718|gb|AAM61050.1| unknown [Arabidopsis thaliana] gi|94807644|gb|ABF47119.1| At1g31335 [Arabidopsis thaliana] gi|332193222|gb|AEE31343.1| uncharacterized protein AT1G31335 [Arabidopsis thaliana]	72	70	2.00E-20	97.2	81.9	86.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G31335.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; Has 34 Blast hits to 34 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:11217117-11217329 REVERSE LENGTH=70	72	70	3.00E-23	97.2	81.9	86.1
Rsa1.0_00337.1.g11664.t1	emb|CAB52747.1| photosystem I subunit III precursor [Arabidopsis thaliana] gi|21593588|gb|AAM65555.1| photosystem I subunit III precursor, putative [Arabidopsis thaliana]	218	221	1.00E-112	101.4	92.7	96.3	photosystem I subunit III precursor	gbpln	Arabidopsis thaliana	AT1G31330.1 | Symbols: PSAF | photosystem I subunit F | chr1:11215011-11215939 REVERSE LENGTH=221	218	221	1.00E-114	101.4	92.2	95.9
Rsa1.0_00337.1.g11665.t1	ref|XP_002893847.1| LOB domain protein 4 [Arabidopsis lyrata subsp. lyrata] gi|297339689|gb|EFH70106.1| LOB domain protein 4 [Arabidopsis lyrata subsp. lyrata]	172	172	2.00E-95	100.0	98.3	99.4	LOB domain protein 4	gbpln	Arabidopsis lyrata	AT1G31320.1 | Symbols: LBD4 | LOB domain-containing protein 4 | chr1:11213107-11214032 FORWARD LENGTH=172	172	172	3.00E-83	100.0	97.7	98.8

Rsa1.0_00337.1.g11666.t4	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	791	390	4.00E-40	49.3	11.8	15.3	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	791	295	5.00E-36	37.3	11.5	18.1
Rsa1.0_00337.1.g11667.t2	gb|AAC95170.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	705	916	4.00E-33	129.9	17.6	26.0	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11668.t1	emb|CAB75764.1| putative protein [Arabidopsis thaliana]	210	262	2.00E-25	124.8	31.0	36.2	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11669.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11670.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11671.t1	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	596	703	4.00E-51	118.0	19.0	23.2	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11672.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11673.t1	gb|AAD20646.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	113	1040	2.00E-19	920.4	43.4	49.6	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11674.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11675.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11676.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00337.1.g11677.t1	gb|EOA38400.1| hypothetical protein CARUB_v10009967mg [Capsella rubella]	278	278	1.00E-156	100.0	96.0	99.3	hypothetical protein CARUB_v10009967mg	gbpln	Capsella rubella	AT1G31300.2 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr1:11194308-11195955 FORWARD LENGTH=278	278	278	1.00E-158	100.0	95.7	99.3
Rsa1.0_00338.1.g11678.t10	dbj|BAA97354.1| disease resistance protein-like [Arabidopsis thaliana]	643	1152	0	179.2	56.9	74.0	disease resistance protein-like	gbpln	Arabidopsis thaliana	AT5G40060.1 | Symbols: | Disease resistance protein (NBS-LRR class) family | chr5:16035246-16038730 FORWARD LENGTH=968	643	968	1.00E-145	150.5	40.0	51.6
Rsa1.0_00338.1.g11679.t1	gb|ACP30601.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1196	1207	0	100.9	63.9	74.2	disease resistance protein	gbpln	Brassica rapa	AT5G46270.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18764833-18769090 REVERSE LENGTH=1139	1196	1139	0	95.2	52.9	66.7
Rsa1.0_00338.1.g11680.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1440	1501	0	104.2	58.1	73.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1440	1262	1.00E-131	87.6	15.6	21.7
Rsa1.0_00338.1.g11681.t1	ref|XP_002865156.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310991|gb|EFH41415.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	219	287	1.00E-45	131.1	56.2	65.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G46850.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: GPI anchor biosynthetic process; LOCATED IN: endomembrane system, endoplasmic reticulum membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: PIG-X/PBN1 (InterPro:IPR013233). | chr5:19010852-19012010 FORWARD LENGTH=299	219	299	4.00E-48	136.5	52.5	59.8
Rsa1.0_00338.1.g11682.t1	ref|XP_002863386.1| hypothetical protein ARALYDRAFT_494291 [Arabidopsis lyrata subsp. lyrata] gi|297309221|gb|EFH39645.1| hypothetical protein ARALYDRAFT_494291 [Arabidopsis lyrata subsp. lyrata]	271	268	1.00E-131	98.9	87.1	90.0	hypothetical protein ARALYDRAFT_494291	gbpln	Arabidopsis lyrata	AT5G46860.1 | Symbols: VAM3, ATVAM3, SYP22, ATSYP22, SGR3 | Syntaxin/t-SNARE family protein | chr5:19012342-19013795 REVERSE LENGTH=268	271	268	1.00E-133	98.9	86.3	90.0
Rsa1.0_00338.1.g11683.t2	gb|AAF19546.1|AC007190_14 F23N19.13 [Arabidopsis thaliana]	110	633	2.00E-17	575.5	38.2	58.2	F23N19.13	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00338.1.g11684.t1	gb|AAD25557.1|AC005850_14 Hypothetical protein [Arabidopsis thaliana]	244	404	3.00E-80	165.6	61.5	74.6	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G43722.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28730.1); Has 924 Blast hits to 912 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 222; Fungi - 31; Plants - 661; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:16496403-16497377 FORWARD LENGTH=324	244	324	3.00E-42	132.8	34.0	50.0
Rsa1.0_00338.1.g11685.t1	#	#	#	#	#	#	#	-	----	----	AT1G50080.1 | Symbols: | BEST Arabidopsis thaliana protein match is: RNA-directed DNA polymerase (reverse transcriptase)-related family protein (TAIR:AT1G60720.1); Has 42 Blast hits to 42 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18554001-18554276 REVERSE LENGTH=91	113	91	1.00E-12	80.5	24.8	38.9

Rsa1.0_00338.1.g11686.t13	gb|AAK49635.1|AF372919_1 AT5g46920/MQD22_6 [Arabidopsis thaliana] gi|27764956|gb|AAO23599.1| At5g46920/MQD22_6 [Arabidopsis thaliana]	51	282	5.00E-17	552.9	82.4	88.2	AT5g46920/MQD22_6	gbpln	Arabidopsis thaliana	AT5G46920.1 | Symbols: | Intron maturase, type II family protein | chr5:19053668-19055875 FORWARD LENGTH=735	51	735	1.00E-19	1441.2	82.4	88.2
Rsa1.0_00338.1.g11687.t1	gb|EOA14879.1| hypothetical protein CARUB_v10028205mg [Capsella rubella]	170	179	3.00E-60	105.3	68.8	79.4	hypothetical protein CARUB_v10028205mg	gbpln	Capsella rubella	AT5G46970.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19063918-19064412 REVERSE LENGTH=164	170	164	5.00E-54	96.5	60.0	69.4
Rsa1.0_00338.1.g11688.t1	gb|ABD64968.1| hypothetical protein 25.t00005 [Brassica oleracea]	223	299	3.00E-57	134.1	52.0	61.9	hypothetical protein 25.t00005	gbpln	Brassica oleracea	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	223	264	1.00E-49	118.4	46.6	59.6
Rsa1.0_00338.1.g11689.t1	gb|AAP37968.1| seed specific protein Bn15D12A [Brassica napus]	175	157	1.00E-74	89.7	79.4	82.9	seed specific protein Bn15D12A	gbpln	Brassica napus	AT5G46960.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19062220-19062744 REVERSE LENGTH=174	175	174	2.00E-58	99.4	64.6	74.9
Rsa1.0_00338.1.g11690.t1	gb|EOA16073.1| hypothetical protein CARUB_v10004206mg [Capsella rubella]	647	763	0	117.9	55.0	67.7	hypothetical protein CARUB_v10004206mg	gbpln	Capsella rubella	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	647	331	9.00E-56	51.2	17.6	26.4
Rsa1.0_00338.1.g11691.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00338.1.g11692.t1	ref|NP_199510.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|9759441|dbj|BAB10238.1| unnamed protein product [Arabidopsis thaliana] gi|332008072|gb|AED95455.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	179	187	6.00E-48	104.5	58.1	71.5	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT5G46990.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19067692-19068255 REVERSE LENGTH=187	179	187	2.00E-50	104.5	58.1	71.5
Rsa1.0_00339.1.g11693.t1	gb|EOA39511.1| hypothetical protein CARUB_v10008128mg [Capsella rubella] gi|482575325|gb|EOA39512.1| hypothetical protein CARUB_v10008128mg [Capsella rubella] gi|482575326|gb|EOA39513.1| hypothetical protein CARUB_v10008128mg [Capsella rubella]	414	1171	1.00E-118	282.9	56.8	65.2	hypothetical protein CARUB_v10008128mg	gbpln	Capsella rubella	AT1G20920.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:7285342-7288842 FORWARD LENGTH=1166	414	1166	1.00E-119	281.6	56.0	63.5
Rsa1.0_00339.1.g11694.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00339.1.g11695.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00339.1.g11696.t1	dbj|BAC42280.1| putative 60S ribosomal protein [Arabidopsis thaliana]	406	407	0	100.2	91.1	95.1	putative 60S ribosomal protein	gbpln	Arabidopsis thaliana	AT3G09630.1 | Symbols: | Ribosomal protein L4/L1 family | chr3:2953813-2955444 FORWARD LENGTH=406	406	406	0	100.0	93.8	97.0
Rsa1.0_00339.1.g11697.t1	ref|NP_187576.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75204290|sp|Q9SF38.1|PP222_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g09650, chloroplastic; AltName: Full=Protein HIGH CHLOROPHYLL FLUORESCENCE 152; Flags: Precursor gi|6682243|gb|AAF23295.1|AC016661_20 hypothetical protein [Arabidopsis thaliana] gi|332641272|gb|AEE74793.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	778	778	0	100.0	86.6	91.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G09650.1 | Symbols: HCF152, CRM3 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:2958704-2961040 FORWARD LENGTH=778	778	778	0	100.0	86.6	91.1
Rsa1.0_00339.1.g11698.t2	gb|AGC54635.1| minichromosome maintenance 8 [Arabidopsis thaliana]	813	801	0	98.5	86.1	90.7	minichromosome maintenance 8	gbpln	Arabidopsis thaliana	AT3G09660.1 | Symbols: MCM8 | minichromosome maintenance 8 | chr3:2961314-2966166 REVERSE LENGTH=777	813	777	0	95.6	81.3	85.6
Rsa1.0_00339.1.g11699.t1	ref|NP_565338.1| RNA helicase, ATP-dependent, SK12/DOB1 protein [Arabidopsis thaliana] gi|20197305|gb|AAC67203.2| expressed protein [Arabidopsis thaliana] gi|28973761|gb|AAO64196.1| putative DEAD/DEAH box RNA helicase (HUA ENHANCER2) [Arabidopsis thaliana] gi|330250934|gb|AEC06028.1| RNA helicase, ATP-dependent, SK12/DOB1 protein [Arabidopsis thaliana]	1043	995	0	95.4	86.3	90.1	RNA helicase, ATP-dependent, SK12/DOB1 protein	gbpln	Arabidopsis thaliana	AT2G06990.1 | Symbols: HEN2 | RNA helicase, ATP-dependent, SK12/DOB1 protein | chr2:2895135-2900909 FORWARD LENGTH=995	1043	995	0	95.4	86.3	90.1
Rsa1.0_00339.1.g11700.t7	emb|CAO82944.1| putative pre-mRNA-splicing factor cwc-22 [Oryza sativa Indica Group]	209	736	6.00E-73	352.2	61.7	73.2	putative pre-mRNA-splicing factor cwc-22	gbpln	Oryza sativa	AT1G80930.1 | Symbols: | MIF4G domain-containing protein / MA3 domain-containing protein | chr1:30405774-30409499 REVERSE LENGTH=900	209	900	7.00E-74	430.6	59.3	73.2

Rsa1.0_00339.1.g11701.t1	ref|XP_002865608.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297311443|gb|EFH41867.1| binding protein [Arabidopsis lyrata subsp. lyrata]	111	1127	6.00E-11	1015.3	32.4	35.1	binding protein	gbpln	Arabidopsis lyrata	AT5G48120.1 | Symbols: | ARM repeat superfamily protein | chr5:19508210-19514774 REVERSE LENGTH=1134	111	1134	1.00E-12	1021.6	30.6	34.2
Rsa1.0_00339.1.g11702.t1	gb|EOA30702.1| hypothetical protein CARUB_v10013839mg [Capsella rubella]	395	408	0	103.3	84.8	92.7	hypothetical protein CARUB_v10013839mg	gbpln	Capsella rubella	AT3G19760.1 | Symbols: EIF4A-III | eukaryotic initiation factor 4A-III | chr3:6863790-6866242 FORWARD LENGTH=408	395	408	0	103.3	84.1	92.4
Rsa1.0_00339.1.g11703.t17	gb|EOA29622.1| hypothetical protein CARUB_v10014335mg [Capsella rubella]	611	282	9.00E-66	46.2	21.8	22.9	hypothetical protein CARUB_v10014335mg	gbpln	Capsella rubella	AT3G53500.2 | Symbols: RSZ32, RS2Z32, At-RS2Z | RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain | chr3:19834557-19836507 REVERSE LENGTH=284	611	284	1.00E-62	46.5	20.5	22.7
Rsa1.0_00339.1.g11704.t1	gb|EAY82747.1| hypothetical protein OsI_37956 [Oryza sativa Indica Group]	212	556	5.00E-83	262.3	67.9	81.6	hypothetical protein OsI_37956	gbpln	Oryza sativa	AT1G80930.1 | Symbols: | MIF4G domain-containing protein / MA3 domain-containing protein | chr1:30405774-30409499 REVERSE LENGTH=900	212	900	9.00E-84	424.5	66.5	82.1
Rsa1.0_00339.1.g11705.t1	gb|EOA31812.1| hypothetical protein CARUB_v10015035mg [Capsella rubella]	126	73	6.00E-15	57.9	50.0	50.8	hypothetical protein CARUB_v10015035mg	gbpln	Capsella rubella	AT2G37120.1 | Symbols: | S1FA-like DNA-binding protein | chr2:15594250-15594815 REVERSE LENGTH=76	126	76	4.00E-13	60.3	39.7	46.8
Rsa1.0_00339.1.g11706.t1	gb|EOA29627.1| hypothetical protein CARUB_v10014405mg [Capsella rubella]	265	265	1.00E-144	100.0	95.1	98.9	hypothetical protein CARUB_v10014405mg	gbpln	Capsella rubella	AT3G09740.1 | Symbols: SYP71, ATSYP71 | syntaxin of plants 71 | chr3:2989615-2991354 FORWARD LENGTH=266	265	266	1.00E-144	100.4	95.1	98.5
Rsa1.0_00339.1.g11707.t1	ref|NP_566355.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|15809927|gb|AAL06891.1| At3g09760/F8A24.19 [Arabidopsis thaliana] gi|21360565|gb|AAM47479.1| At3g09760/F8A24.19 [Arabidopsis thaliana] gi|66865928|gb|AAY57598.1| RING finger family protein [Arabidopsis thaliana] gi|332641288|gb|AEE74809.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	474	491	0	103.6	77.0	84.2	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G09760.1 | Symbols: | RING/U-box superfamily protein | chr3:2992975-2995451 REVERSE LENGTH=491	474	491	0	103.6	77.0	84.2
Rsa1.0_00339.1.g11708.t1	gb|EOA30448.1| hypothetical protein CARUB_v10013573mg [Capsella rubella]	455	483	1.00E-171	106.2	74.1	80.9	hypothetical protein CARUB_v10013573mg	gbpln	Capsella rubella	AT3G09760.1 | Symbols: | RING/U-box superfamily protein | chr3:2992975-2995451 REVERSE LENGTH=491	455	491	1.00E-166	107.9	71.9	80.9
Rsa1.0_00339.1.g11709.t1	gb|EOA30784.1| hypothetical protein CARUB_v10013928mg [Capsella rubella]	389	384	1.00E-144	98.7	67.6	73.3	hypothetical protein CARUB_v10013928mg	gbpln	Capsella rubella	AT3G09770.1 | Symbols: | RING/U-box superfamily protein | chr3:2996402-2997835 REVERSE LENGTH=388	389	388	1.00E-123	99.7	68.6	73.0
Rsa1.0_00339.1.g11710.t1	ref|NP_187589.1| serine/threonine-protein kinase-like protein CCR1 [Arabidopsis thaliana] gi|75313027|sp|Q9S7D9.1|ACCR1_ARATH RecName: Full=Serine/threonine-protein kinase-like protein CCR1; AltName: Full=Protein CRINKLY 4 RELATED 1; Short=AtCRR1; Flags: Precursor gi|6681340|gb|AAF23257.1|AC015985_15 putative protein kinase [Arabidopsis thaliana] gi|6682254|gb|AAF23306.1|AC016661_31 putative protein kinase [Arabidopsis thaliana] gi|332641291|gb|AEE74812.1| serine/threonine-protein kinase-like protein CCR1 [Arabidopsis thaliana]	774	775	0	100.1	83.2	90.2	serine/threonine-protein kinase-like protein CCR1	gbpln	Arabidopsis thaliana	AT3G09780.1 | Symbols: CCR1, ATCRR1 | CRINKLY4 related 1 | chr3:3000838-3003165 REVERSE LENGTH=775	774	775	0	100.1	83.2	90.2
Rsa1.0_00339.1.g11711.t1	dbj|BAA92778.1| nonclathrin coat protein zeta1-COP [Brassica rapa]	184	184	1.00E-98	100.0	96.2	98.4	nonclathrin coat protein zeta1-COP	gbpln	Brassica rapa	AT3G09800.1 | Symbols: | SNARE-like superfamily protein | chr3:3006731-3007916 REVERSE LENGTH=179	184	179	6.00E-96	97.3	91.8	94.6
Rsa1.0_00339.1.g11712.t1	gb|EOA30648.1| hypothetical protein CARUB_v10013785mg [Capsella rubella]	365	423	0	115.9	94.2	96.4	hypothetical protein CARUB_v10013785mg	gbpln	Capsella rubella	AT3G09810.1 | Symbols: IDH-VI | isocitrate dehydrogenase VI | chr3:3008753-3011070 FORWARD LENGTH=374	365	374	0	102.5	91.5	94.2
Rsa1.0_00339.1.g11713.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00339.1.g11714.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00339.1.g11715.t1	gb|EOA32117.1| hypothetical protein CARUB_v10015367mg [Capsella rubella]	334	371	1.00E-134	111.1	73.1	85.3	hypothetical protein CARUB_v10015367mg	gbpln	Capsella rubella	AT1G68960.1 | Symbols: | Protein of unknown function (DUF295) | chr1:25929943-25931143 FORWARD LENGTH=376	334	376	1.00E-101	112.6	58.4	71.6
Rsa1.0_00339.1.g11716.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00339.1.g11717.t1	gb|EOA30630.1| hypothetical protein CARUB_v10013766mg [Capsella rubella]	424	426	0	100.5	91.7	95.0	hypothetical protein CARUB_v10013766mg	gbpln	Capsella rubella	AT3G09830.2 | Symbols: | Protein kinase superfamily protein | chr3:3017199-3018696 FORWARD LENGTH=418	424	418	0	98.6	89.4	94.8

<table>
<tr><td>Rsa1.0_00339.1.g11718.t1</td><td>ref|NP_187595.1| cell division control protein 48-A [Arabidopsis thaliana] gi|1705677|sp|P54609.1|CD48A_ARATH RecName: Full=Cell division control protein 48 homolog A; Short=AtCDC48a gi|6681343|gb|AAF23260.1|AC015985_18 putative transitional endoplasmic reticulum ATPase [Arabidopsis thaliana] gi|1019904|gb|AAC49120.1| cell division cycle protein [Arabidopsis thaliana] gi|17473551|gb|AAL38252.1| putative transitional endoplasmic reticulum ATPase [Arabidopsis thaliana] gi|20453130|gb|AAM19807.1| AT3g09840/F8A24_11 [Arabidopsis thaliana] gi|110735114|gb|ABG89127.1| CDC48a [synthetic construct] gi|222424942|dbj|BAH20422.1| AT3G09840 [Arabidopsis thaliana] gi|332641299|gb|AEE74820.1| cell division control protein 48-A [Arabidopsis thaliana]</td><td>809</td><td>809</td><td>0</td><td>100.0</td><td>98.9</td><td>99.5</td><td>cell division control protein 48-A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G09840.1 | Symbols: CDC48, ATCDC48, CDC48A | cell division cycle 48 | chr3:3019494-3022832 FORWARD LENGTH=809</td><td>809</td><td>809</td><td>0</td><td>100.0</td><td>98.9</td><td>99.5</td></tr>
<tr><td>Rsa1.0_00339.1.g11719.t1</td><td>ref|NP_566359.1| D111/G-patch domain-containing protein [Arabidopsis thaliana] gi|6681334|gb|AAF23251.1|AC015985_9 hypothetical protein [Arabidopsis thaliana] gi|15982781|gb|AAL09738.1| AT3g09850/F8A24_10 [Arabidopsis thaliana] gi|23308485|gb|AAN18212.1| At3g09850/F8A24_10 [Arabidopsis thaliana] gi|332641300|gb|AEE74821.1| D111/G-patch domain-containing protein [Arabidopsis thaliana]</td><td>754</td><td>781</td><td>0</td><td>103.6</td><td>72.9</td><td>82.9</td><td>D111/G-patch domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G09850.1 | Symbols: | D111/G-patch domain-containing protein | chr3:3023397-3025742 REVERSE LENGTH=781</td><td>754</td><td>781</td><td>0</td><td>103.6</td><td>72.9</td><td>82.9</td></tr>
<tr><td>Rsa1.0_00339.1.g11720.t1</td><td>ref|NP_187601.1| RAB GTPase-like protein E1E [Arabidopsis thaliana] gi|75204351|sp|Q9SF91.1|RAE1E_ARATH RecName: Full=Ras-related protein RABE1e; Short=AtRABE1e; AltName: Full=Ras-related protein Rab8E; Short=AtRab8E gi|6681329|gb|AAF23246.1|AC015985_4 putative Ras-like GTP-binding protein [Arabidopsis thaliana] gi|21536596|gb|AAM60928.1| putative Ras-like GTP-binding protein [Arabidopsis thaliana] gi|90568022|gb|ABD94081.1| At3g09900 [Arabidopsis thaliana] gi|110738463|dbj|BAF01157.1| putative Ras-like GTP-binding protein [Arabidopsis thaliana] gi|332641307|gb|AEE74828.1| RAB GTPase-like protein E1E [Arabidopsis thaliana]</td><td>218</td><td>218</td><td>1.00E-114</td><td>100.0</td><td>96.8</td><td>98.6</td><td>RAB GTPase-like protein E1E</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G09900.1 | Symbols: ATRABE1E, ATRAB8E, RABE1e | RAB GTPase homolog E1E | chr3:3034687-3036379 FORWARD LENGTH=218</td><td>218</td><td>218</td><td>1.00E-116</td><td>100.0</td><td>96.8</td><td>98.6</td></tr>
<tr><td>Rsa1.0_00339.1.g11721.t1</td><td>gb|EOA31469.1| hypothetical protein CARUB_v10014655mg [Capsella rubella]</td><td>204</td><td>205</td><td>9.00E-99</td><td>100.5</td><td>92.2</td><td>96.1</td><td>hypothetical protein CARUB_v10014655mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G09910.3 | Symbols: RABC2b | RAB GTPase homolog C2B | chr3:3036864-3038121 REVERSE LENGTH=205</td><td>204</td><td>205</td><td>1.00E-101</td><td>100.5</td><td>91.7</td><td>95.6</td></tr>
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Rsa1.0_00339.1.g11722.t1	ref|NP_187603.1| phosphatidylinositol-4-phosphate 5-kinase 9 [Arabidopsis thaliana] gi|79313173|ref|NP_001030666.1| phosphatidylinositol-4-phosphate 5-kinase 9 [Arabidopsis thaliana] gi|334185202|ref|NP_001189852.1| phosphatidylinositol-4-phosphate 5-kinase 9 [Arabidopsis thaliana] gi|78099094|sp|Q8L850.2|PI5K9_ARATH RecName: Full=Phosphatidylinositol 4-phosphate 5-kinase 9; Short=AtPIP5K9; AltName: Full=1-phosphatidylinositol 4-phosphate kinase 9; AltName: Full=Diphosphoinositide kinase 9; AltName: Full=PtdIns(4)P-5-kinase 9 gi|6681327|gb|AAF23244.1|AC015985_2 putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana] gi|51490699|emb|CAH18644.1| putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana] gi|110739473|dbj|BAF01646.1| putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana] gi|332641311|gb|AEE74832.1| phosphatidylinositol-4-phosphate 5-kinase 9 [Arabidopsis thaliana] gi|332641312|gb|AEE74833.1| phosphatidylinositol-4-phosphate 5-kinase 9 [Arabidopsis thaliana] gi|332641313|gb|AEE74834.1| phosphatidylinositol-4-phosphate 5-kinase 9 [Arabidopsis thaliana]	814	815	0	100.1	89.9	93.6	phosphatidylinositol-4-phosphate 5-kinase 9	gbpln	Arabidopsis thaliana	AT3G09920.3 | Symbols: PIP5K9 | phosphatidyl inositol monophosphate 5 kinase | chr3:3040426-3043676 REVERSE LENGTH=815	814	815	0	100.1	89.9	93.6
Rsa1.0_00339.1.g11723.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00339.1.g11724.t1	gb|EOA32307.1| hypothetical protein CARUB_v10015569mg [Capsella rubella]	171	171	5.00E-80	100.0	83.0	91.2	hypothetical protein CARUB_v10015569mg	gbpln	Capsella rubella	AT3G09925.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr3:3051868-3052784 REVERSE LENGTH=171	171	171	3.00E-76	100.0	77.8	87.7
Rsa1.0_00339.1.g11725.t1	ref|XP_002882645.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328485|gb|EFH58904.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	354	354	1.00E-156	100.0	77.1	86.7	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT3G09930.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:3053356-3055203 FORWARD LENGTH=354	354	354	1.00E-154	100.0	71.2	81.4
Rsa1.0_00339.1.g11726.t1	ref|XP_002884767.1| hypothetical protein ARALYDRAFT_897165 [Arabidopsis lyrata subsp. lyrata] gi|297330607|gb|EFH61026.1| hypothetical protein ARALYDRAFT_897165 [Arabidopsis lyrata subsp. lyrata]	93	93	2.00E-33	100.0	77.4	84.9	hypothetical protein ARALYDRAFT_897165	gbpln	Arabidopsis lyrata	AT3G09950.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41761.1); Has 128 Blast hits to 128 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 128; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3060354-3060632 REVERSE LENGTH=92	93	92	2.00E-35	98.9	72.0	82.8
Rsa1.0_00339.1.g11727.t1	ref|NP_566363.1| calcineurin-like metallo-phosphoesterase-like protein [Arabidopsis thaliana] gi|21553642|gb|AAM62735.1| unknown [Arabidopsis thaliana] gi|332641320|gb|AEE74841.1| calcineurin-like metallo-phosphoesterase-like protein [Arabidopsis thaliana]	314	311	1.00E-142	99.0	78.0	87.3	calcineurin-like metallo-phosphoesterase-like protein	gbpln	Arabidopsis thaliana	AT3G09960.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr3:3061990-3063455 FORWARD LENGTH=311	314	311	1.00E-144	99.0	78.0	87.3
Rsa1.0_00339.1.g11728.t1	gb|EOA31074.1| hypothetical protein CARUB_v10014233mg [Capsella rubella]	309	309	1.00E-165	100.0	90.0	96.4	hypothetical protein CARUB_v10014233mg	gbpln	Capsella rubella	AT3G09970.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr3:3063813-3065337 FORWARD LENGTH=309	309	309	1.00E-167	100.0	89.6	95.8
Rsa1.0_00339.1.g11729.t2	ref|XP_002882648.1| hypothetical protein ARALYDRAFT_478325 [Arabidopsis lyrata subsp. lyrata] gi|297328488|gb|EFH58907.1| hypothetical protein ARALYDRAFT_478325 [Arabidopsis lyrata subsp. lyrata]	178	178	4.00E-82	100.0	96.1	97.2	hypothetical protein ARALYDRAFT_478325	gbpln	Arabidopsis lyrata	AT3G09980.1 | Symbols: | Family of unknown function (DUF662) | chr3:3069358-3071145 FORWARD LENGTH=178	178	178	3.00E-84	100.0	95.5	97.2

Rsa1.0_00339.1.g11730.t1	ref|NP_566365.1| uncharacterized protein [Arabidopsis thaliana] gi|6143874|gb|AAF04421.1|AC010927_14 unknown protein [Arabidopsis thaliana] gi|15081660|gb|AAK82485.1| AT3g10020/T22K18_16 [Arabidopsis thaliana] gi|15529276|gb|AAK97732.1| AT3g10020/T22K18_16 [Arabidopsis thaliana] gi|15809812|gb|AAL06834.1| AT3g10020/T22K18_16 [Arabidopsis thaliana] gi|20147181|gb|AAM10307.1| AT3g10020/T22K18_16 [Arabidopsis thaliana] gi|21594522|gb|AAM66017.1| unknown [Arabidopsis thaliana] gi|332641328|gb|AEE74849.1| uncharacterized protein AT3G10020 [Arabidopsis thaliana]	153	149	1.00E-64	97.4	81.7	88.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G10020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress, anaerobic respiration; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 47 Blast hits to 47 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3091225-3091674 REVERSE LENGTH=149	153	149	4.00E-67	97.4	81.7	88.9
Rsa1.0_00339.1.g11731.t1	ref|NP_566366.1| aspartate/glutamate/uridylate kinase-like protein [Arabidopsis thaliana] gi|14030681|gb|AAK53015.1|AF375431_1 AT3g10030/T22K18_15 [Arabidopsis thaliana] gi|21464551|gb|AAM52230.1| AT3g10030/T22K18_15 [Arabidopsis thaliana] gi|332641330|gb|AEE74851.1| aspartate/glutamate/uridylate kinase-like protein [Arabidopsis thaliana]	576	542	0	94.1	83.2	88.4	aspartate/glutamate/uridylate kinase-like protein	gbpln	Arabidopsis thaliana	AT3G10030.1 | Symbols: | aspartate/glutamate/uridylate kinase family protein | chr3:3092277-3094831 REVERSE LENGTH=542	576	542	0	94.1	83.2	88.4
Rsa1.0_00339.1.g11732.t1	gb|EOA32794.1| hypothetical protein CARUB_v10016104mg [Capsella rubella]	443	435	1.00E-157	98.2	72.2	81.9	hypothetical protein CARUB_v10016104mg	gbpln	Capsella rubella	AT3G10040.1 | Symbols: | sequence-specific DNA binding transcription factors | chr3:3096580-3097875 REVERSE LENGTH=431	443	431	1.00E-154	97.3	71.6	81.0
Rsa1.0_00340.1.g11733.t1	gb|AAM65223.1| unknown [Arabidopsis thaliana]	342	342	1.00E-135	100.0	79.8	84.2	unknown	gbpln	Arabidopsis thaliana	AT4G24060.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr4:12503970-12505417 FORWARD LENGTH=342	342	342	1.00E-132	100.0	78.7	83.6
Rsa1.0_00340.1.g11734.t8	gb|EOA37750.1| hypothetical protein CARUB_v10012565mg [Capsella rubella]	203	679	7.00E-17	334.5	22.7	32.0	hypothetical protein CARUB_v10012565mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00340.1.g11735.t1	ref|XP_002869744.1| ATTRE1 [Arabidopsis lyrata subsp. lyrata] gi|297315580|gb|EFH46003.1| ATTRE1 [Arabidopsis lyrata subsp. lyrata]	560	628	0	112.1	82.9	88.9	ATTRE1	gbpln	Arabidopsis lyrata	AT4G24040.1 | Symbols: ATTRE1, TRE1 | trehalase 1 | chr4:12488242-12491060 FORWARD LENGTH=626	560	626	0	111.8	81.4	88.4
Rsa1.0_00340.1.g11736.t1	ref|NP_001119037.1| uncharacterized protein [Arabidopsis thaliana] gi|110737703|dbj|BAF00790.1| hypothetical protein [Arabidopsis thaliana] gi|332659443|gb|AEE84843.1| uncharacterized protein AT4G24026 [Arabidopsis thaliana]	84	78	6.00E-20	92.9	71.4	82.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G24026.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10810.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12486415-12486651 FORWARD LENGTH=78	84	78	9.00E-23	92.9	71.4	82.1
Rsa1.0_00340.1.g11737.t1	gb|EOA15435.1| hypothetical protein CARUB_v10004076mg [Capsella rubella]	906	959	0	105.8	86.2	90.1	hypothetical protein CARUB_v10004076mg	gbpln	Capsella rubella	AT4G24020.1 | Symbols: NLP7 | NIN like protein 7 | chr4:12479904-12483822 FORWARD LENGTH=959	906	959	0	105.8	84.3	89.5
Rsa1.0_00340.1.g11738.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00340.1.g11739.t1	gb|ABN79278.1| WRKY53 transcription factor [Noccaea caerulescens]	325	324	1.00E-127	99.7	73.2	83.4	WRKY53 transcription factor	gbpln	Noccaea caerulescens	AT4G23810.1 | Symbols: WRKY53, ATWRKY53 | WRKY family transcription factor | chr4:12392666-12393739 REVERSE LENGTH=324	325	324	1.00E-122	99.7	71.1	83.1
Rsa1.0_00340.1.g11740.t1	ref|XP_002869763.1| hypothetical protein ARALYDRAFT_492489 [Arabidopsis lyrata subsp. lyrata] gi|297315599|gb|EFH46022.1| hypothetical protein ARALYDRAFT_492489 [Arabidopsis lyrata subsp. lyrata]	432	430	0	99.5	85.4	93.1	hypothetical protein ARALYDRAFT_492489	gbpln	Arabidopsis lyrata	AT4G23790.1 | Symbols: TBL24 | TRICHOME BIREFRINGENCE-LIKE 24 | chr4:12387870-12389659 FORWARD LENGTH=430	432	430	0	99.5	83.8	91.9
Rsa1.0_00340.1.g11741.t1	#	#	#	#	#	#	#	-	----	----	AT4G23770.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G23780.1); Has 17 Blast hits to 17 proteins in 6 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:12383514-12384050 REVERSE LENGTH=138	145	138	6.00E-12	95.2	30.3	45.5

<table>
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<tr><td>Rsa1.0_00340.1.g11743.t1</td><td>ref|XP_002891107.1| F12K21.17 [Arabidopsis lyrata subsp. lyrata] gi|297336949|gb|EFH67366.1| F12K21.17 [Arabidopsis lyrata subsp. lyrata]</td><td>331</td><td>333</td><td>6.00E-81</td><td>100.6</td><td>50.2</td><td>64.4</td><td>F12K21.17</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G34520.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr1:12623477-12624487 FORWARD LENGTH=336</td><td>331</td><td>336</td><td>8.00E-83</td><td>101.5</td><td>49.2</td><td>63.4</td></tr>
<tr><td>Rsa1.0_00340.1.g11744.t1</td><td>ref|XP_002869765.1| hypothetical protein ARALYDRAFT_492491 [Arabidopsis lyrata subsp. lyrata] gi|297315601|gb|EFH46024.1| hypothetical protein ARALYDRAFT_492491 [Arabidopsis lyrata subsp. lyrata]</td><td>310</td><td>340</td><td>1.00E-103</td><td>109.7</td><td>69.0</td><td>81.3</td><td>hypothetical protein ARALYDRAFT_492491</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G23750.2 | Symbols: CRF2, TMO3 | cytokinin response factor 2 | chr4:12376751-12377782 FORWARD LENGTH=343</td><td>310</td><td>343</td><td>1.00E-105</td><td>110.6</td><td>69.4</td><td>81.0</td></tr>
<tr><td>Rsa1.0_00340.1.g11745.t1</td><td>gb|EOA16215.1| hypothetical protein CARUB_v10004355mg [Capsella rubella]</td><td>614</td><td>635</td><td>0</td><td>103.4</td><td>80.3</td><td>89.1</td><td>hypothetical protein CARUB_v10004355mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23740.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:12367063-12369159 FORWARD LENGTH=638</td><td>614</td><td>638</td><td>0</td><td>103.9</td><td>80.8</td><td>88.3</td></tr>
<tr><td>Rsa1.0_00340.1.g11746.t1</td><td>ref|XP_002869767.1| aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315603|gb|EFH46026.1| aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>305</td><td>306</td><td>1.00E-159</td><td>100.3</td><td>90.5</td><td>95.4</td><td>aldose 1-epimerase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G23730.1 | Symbols: | Galactose mutarotase-like superfamily protein | chr4:12362955-12364792 FORWARD LENGTH=306</td><td>305</td><td>306</td><td>1.00E-160</td><td>100.3</td><td>88.9</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00340.1.g11747.t1</td><td>gb|ACP30568.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>1013</td><td>1030</td><td>0</td><td>101.7</td><td>87.0</td><td>92.2</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G65850.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:24494734-24498485 FORWARD LENGTH=1036</td><td>1013</td><td>1036</td><td>0</td><td>102.3</td><td>46.8</td><td>64.5</td></tr>
<tr><td>Rsa1.0_00340.1.g11748.t1</td><td>ref|NP_194103.2| uncharacterized protein [Arabidopsis thaliana] gi|55740651|gb|AAV63918.1| hypothetical protein At4g23720 [Arabidopsis thaliana] gi|332659398|gb|AEE84798.1| uncharacterized protein AT4G23720 [Arabidopsis thaliana]</td><td>319</td><td>313</td><td>1.00E-139</td><td>98.1</td><td>77.1</td><td>86.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23720.1 | Symbols: | Protein of unknown function (DUF1191) | chr4:12358707-12359648 FORWARD LENGTH=313</td><td>319</td><td>313</td><td>1.00E-142</td><td>98.1</td><td>77.1</td><td>86.8</td></tr>
<tr><td>Rsa1.0_00340.1.g11749.t1</td><td>ref|NP_194102.1| V-type proton ATPase subunit G2 [Arabidopsis thaliana] gi|12643367|sp|O82629.2|VATG2_ARATH RecName: Full=V-type proton ATPase subunit G2; Short=V-ATPase subunit G2; AltName: Full=Vacuolar H(+)-ATPase subunit G isoform 2; AltName: Full=Vacuolar proton pump subunit G2 gi|4454040|emb|CAA23037.1| V-ATPase subunit G (vag2 gene) [Arabidopsis thaliana] gi|7269220|emb|CAB81289.1| V-ATPase subunit G (vag2 gene) [Arabidopsis thaliana] gi|27808518|gb|AAO24539.1| At4g23710 [Arabidopsis thaliana] gi|110743678|dbj|BAE99676.1| vacuolar-type H+-ATPase (V-ATPase) subunit G2 [Arabidopsis thaliana] gi|332659397|gb|AEE84797.1| V-type proton ATPase subunit G2 [Arabidopsis thaliana]</td><td>231</td><td>106</td><td>8.00E-42</td><td>45.9</td><td>39.0</td><td>41.1</td><td>V-type proton ATPase subunit G2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23710.1 | Symbols: VHA-G2, VAG2, VATG2 | vacuolar ATP synthase subunit G2 | chr4:12350577-12351354 FORWARD LENGTH=106</td><td>231</td><td>106</td><td>3.00E-44</td><td>45.9</td><td>39.0</td><td>41.1</td></tr>
<tr><td>Rsa1.0_00340.1.g11750.t1</td><td>gb|ACC91238.1| putative cation/hydrogen exchanger [Arabidopsis halleri]</td><td>825</td><td>821</td><td>0</td><td>99.5</td><td>86.5</td><td>92.5</td><td>putative cation/hydrogen exchanger</td><td>gbpln</td><td>Arabidopsis halleri</td><td>AT4G23700.1 | Symbols: ATCHX17, CHX17 | cation/H+ exchanger 17 | chr4:12342534-12345616 REVERSE LENGTH=820</td><td>825</td><td>820</td><td>0</td><td>99.4</td><td>87.5</td><td>93.6</td></tr>
<tr><td>Rsa1.0_00340.1.g11751.t1</td><td>gb|ABV89607.1| disease resistance response protein [Brassica rapa]</td><td>187</td><td>187</td><td>5.00E-94</td><td>100.0</td><td>95.2</td><td>98.9</td><td>disease resistance response protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G23690.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr4:12339152-12339715 REVERSE LENGTH=187</td><td>187</td><td>187</td><td>2.00E-94</td><td>100.0</td><td>93.6</td><td>97.3</td></tr>
<tr><td>Rsa1.0_00340.1.g11752.t1</td><td>ref|XP_002876975.1| hypothetical protein ARALYDRAFT_484409 [Arabidopsis lyrata subsp. lyrata] gi|297322813|gb|EFH53234.1| hypothetical protein ARALYDRAFT_484409 [Arabidopsis lyrata subsp. lyrata]</td><td>151</td><td>152</td><td>9.00E-68</td><td>100.7</td><td>80.8</td><td>91.4</td><td>hypothetical protein ARALYDRAFT_484409</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G26450.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr3:9681593-9683299 REVERSE LENGTH=152</td><td>151</td><td>152</td><td>1.00E-68</td><td>100.7</td><td>77.5</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00340.1.g11753.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<tr><td>Rsa1.0_00340.1.g11754.t1</td><td>ref|XP_002867694.1| hypothetical protein ARALYDRAFT_492500 [Arabidopsis lyrata subsp. lyrata] gi|297313530|gb|EFH43953.1| hypothetical protein ARALYDRAFT_492500 [Arabidopsis lyrata subsp. lyrata]</td><td>151</td><td>151</td><td>1.00E-65</td><td>100.0</td><td>78.1</td><td>88.7</td><td>hypothetical protein ARALYDRAFT_492500</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G23680.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:12336416-12337417 REVERSE LENGTH=151</td><td>151</td><td>151</td><td>2.00E-67</td><td>100.0</td><td>76.2</td><td>88.1</td></tr>
<tr><td>Rsa1.0_00340.1.g11755.t1</td><td>gb|EOA16649.1| hypothetical protein CARUB_v10004831mg, partial [Capsella rubella]</td><td>319</td><td>439</td><td>1.00E-149</td><td>137.6</td><td>86.8</td><td>91.5</td><td>hypothetical protein CARUB_v10004831mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23660.2 | Symbols: AtPPT1, PPT1 | polyprenyltransferase 1 | chr4:12328086-12331359 REVERSE LENGTH=407</td><td>319</td><td>407</td><td>1.00E-147</td><td>127.6</td><td>87.5</td><td>91.8</td></tr>
<tr><td>Rsa1.0_00340.1.g11756.t1</td><td>gb|ACC91261.1| putative calcium-dependent protein kinase [Capsella rubella] gi|482552225|gb|EOA16418.1| hypothetical protein CARUB_v10004572mg [Capsella rubella]</td><td>532</td><td>529</td><td>0</td><td>99.4</td><td>91.4</td><td>95.3</td><td>putative calcium-dependent protein kinase</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23650.1 | Symbols: CDPK6, CPK3 | calcium-dependent protein kinase 6 | chr4:12324967-12327415 REVERSE LENGTH=529</td><td>532</td><td>529</td><td>0</td><td>99.4</td><td>90.8</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00340.1.g11757.t1</td><td>dbj|BAJ33905.1| unnamed protein product [Thellungiella halophila]</td><td>182</td><td>275</td><td>1.00E-95</td><td>151.1</td><td>94.0</td><td>98.9</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G23630.1 | Symbols: BTI1, RTNLB1 | VIRB2-interacting protein 1 | chr4:12318070-12319574 FORWARD LENGTH=275</td><td>182</td><td>275</td><td>2.00E-97</td><td>151.1</td><td>94.5</td><td>98.9</td></tr>
<tr><td>Rsa1.0_00340.1.g11758.t4</td><td>gb|EOA18433.1| hypothetical protein CARUB_v10006976mg [Capsella rubella]</td><td>428</td><td>410</td><td>0</td><td>95.8</td><td>73.4</td><td>81.5</td><td>hypothetical protein CARUB_v10006976mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23380.1 | Symbols: | Protein of Unknown Function (DUF239) | chr4:12214667-12216333 REVERSE LENGTH=400</td><td>428</td><td>400</td><td>1.00E-180</td><td>93.5</td><td>71.0</td><td>80.4</td></tr>
<tr><td>Rsa1.0_00340.1.g11759.t1</td><td>ref|NP_199058.1| putative F-box protein [Arabidopsis thaliana] gi|75170830|sp|Q9FIH4.1|FB280_ARATH RecName: Full=Putative F-box protein At5g42430 gi|9759479|dbj|BAB10484.1| unnamed protein product [Arabidopsis thaliana] gi|332007427|gb|AED94810.1| putative F-box protein [Arabidopsis thaliana]</td><td>406</td><td>395</td><td>2.00E-74</td><td>97.3</td><td>47.8</td><td>58.4</td><td>putative F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G42430.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:16971312-16972499 REVERSE LENGTH=395</td><td>406</td><td>395</td><td>6.00E-77</td><td>97.3</td><td>47.8</td><td>58.4</td></tr>
<tr><td>Rsa1.0_00340.1.g11760.t2</td><td>ref|XP_002874691.1| hypothetical protein ARALYDRAFT_489971 [Arabidopsis lyrata subsp. lyrata] gi|297320528|gb|EFH50950.1| hypothetical protein ARALYDRAFT_489971 [Arabidopsis lyrata subsp. lyrata]</td><td>935</td><td>982</td><td>0</td><td>105.0</td><td>64.1</td><td>75.4</td><td>hypothetical protein ARALYDRAFT_489971</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G11420.1 | Symbols: EIF3A, ATEIF3A-1, EIF3A-1, ATTIF3A1, TIF3A1 | eukaryotic translation initiation factor 3A | chr4:6947834-6952053 REVERSE LENGTH=987</td><td>935</td><td>987</td><td>0</td><td>105.6</td><td>59.6</td><td>69.1</td></tr>
<tr><td>Rsa1.0_00340.1.g11761.t1</td><td>ref|NP_001190810.1| uncharacterized protein [Arabidopsis thaliana] gi|332659340|gb|AEE84740.1| uncharacterized protein AT4G23330 [Arabidopsis thaliana]</td><td>144</td><td>147</td><td>2.00E-60</td><td>102.1</td><td>83.3</td><td>90.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23330.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2365 (InterPro:IPR019314). | chr4:12192136-12193383 FORWARD LENGTH=147</td><td>144</td><td>147</td><td>6.00E-63</td><td>102.1</td><td>83.3</td><td>90.3</td></tr>
<tr><td>Rsa1.0_00340.1.g11762.t1</td><td>gb|AAC95354.1| receptor-like protein kinase [Arabidopsis thaliana]</td><td>645</td><td>684</td><td>0</td><td>106.0</td><td>76.1</td><td>85.6</td><td>receptor-like protein kinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23250.1 | Symbols: EMB1290, DUF26-21, RKC1, CRK17 | kinases;protein kinases | chr4:12162004-12167026 REVERSE LENGTH=1035</td><td>645</td><td>1035</td><td>0</td><td>160.5</td><td>75.5</td><td>85.0</td></tr>
<tr><td>Rsa1.0_00340.1.g11763.t1</td><td>sp|Q8L710.2|CRK17_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 17; Short=Cysteine-rich RLK17; AltName: Full=Protein EMBRYO DEFECTIVE 1290; Flags: Precursor</td><td>642</td><td>686</td><td>0</td><td>106.9</td><td>76.2</td><td>86.1</td><td>RecName: Full=Cysteine-rich receptor-like protein kinase 17; Short=Cysteine-rich RLK17; AltName: Full=Protein EMBRYO DEFECTIVE 1290; Flags: Precursor</td><td>----</td><td>----</td><td>AT4G23250.1 | Symbols: EMB1290, DUF26-21, RKC1, CRK17 | kinases;protein kinases | chr4:12162004-12167026 REVERSE LENGTH=1035</td><td>642</td><td>1035</td><td>0</td><td>161.2</td><td>75.4</td><td>85.4</td></tr>
<tr><td>Rsa1.0_00340.1.g11764.t1</td><td>emb|CAA09731.1| receptor-like protein kinase, RLK3 [Arabidopsis thaliana]</td><td>660</td><td>667</td><td>0</td><td>101.1</td><td>60.0</td><td>71.8</td><td>receptor-like protein kinase, RLK3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667</td><td>660</td><td>667</td><td>0</td><td>101.1</td><td>60.0</td><td>71.5</td></tr>
<tr><td>Rsa1.0_00340.1.g11765.t1</td><td>gb|EOA16195.1| hypothetical protein CARUB_v10004335mg [Capsella rubella]</td><td>674</td><td>649</td><td>0</td><td>96.3</td><td>70.6</td><td>80.4</td><td>hypothetical protein CARUB_v10004335mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>674</td><td>1262</td><td>0</td><td>187.2</td><td>68.7</td><td>78.8</td></tr>
<tr><td>Rsa1.0_00340.1.g11766.t1</td><td>ref|XP_002869784.1| hypothetical protein ARALYDRAFT_492546 [Arabidopsis lyrata subsp. lyrata] gi|297315620|gb|EFH46043.1| hypothetical protein ARALYDRAFT_492546 [Arabidopsis lyrata subsp. lyrata]</td><td>658</td><td>662</td><td>0</td><td>100.6</td><td>80.7</td><td>87.8</td><td>hypothetical protein ARALYDRAFT_492546</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G23180.1 | Symbols: CRK10, RLK4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 | chr4:12138171-12140780 FORWARD LENGTH=669</td><td>658</td><td>669</td><td>0</td><td>101.7</td><td>75.4</td><td>84.0</td></tr>
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Rsa1.0_00340.1.g11767.t1	ref|XP_002869787.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315623|gb|EFH46046.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	155	695	2.00E-61	448.4	71.0	83.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G23140.1 | Symbols: CRK6 | cysteine-rich RLK (RECEPTOR-like protein kinase) 6 | chr4:12121397-12124037 FORWARD LENGTH=674	155	674	2.00E-61	434.8	69.0	79.4
Rsa1.0_00341.1.g11768.t1	ref|XP_002869614.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297315450|gb|EFH45873.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	124	418	1.00E-38	337.1	69.4	77.4	F-box family protein	gbpln	Arabidopsis lyrata	AT4G26340.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:13324130-13325559 FORWARD LENGTH=419	124	419	1.00E-39	337.9	65.3	77.4
Rsa1.0_00341.1.g11769.t1	ref|NP_567745.1| antitermination NusB domain-containing protein [Arabidopsis thaliana] gi|15450968|gb|AAK96755.1| putative protein [Arabidopsis thaliana] gi|30984514|gb|AAP42720.1| At4g26370 [Arabidopsis thaliana] gi|332659789|gb|AEE85189.1| antitermination NusB domain-containing protein [Arabidopsis thaliana]	288	301	1.00E-122	104.5	84.7	91.3	antitermination NusB domain-containing protein	gbpln	Arabidopsis thaliana	AT4G26370.1 | Symbols: | antitermination NusB domain-containing protein | chr4:13334099-13336153 REVERSE LENGTH=301	288	301	1.00E-124	104.5	84.7	91.3
Rsa1.0_00341.1.g11770.t1	ref|NP_194370.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|30687206|ref|NP_849554.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|20466682|gb|AAM20658.1| putative protein [Arabidopsis thaliana] gi|23198194|gb|AAN15624.1| putative protein [Arabidopsis thaliana] gi|222424453|dbj|BAH20182.1| AT4G26400 [Arabidopsis thaliana] gi|332659793|gb|AEE85193.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332659794|gb|AEE85194.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	337	356	1.00E-105	105.6	66.5	75.1	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT4G26400.1 | Symbols: | RING/U-box superfamily protein | chr4:13344953-13346023 REVERSE LENGTH=356	337	356	1.00E-107	105.6	66.5	75.1
Rsa1.0_00341.1.g11771.t1	ref|XP_002869612.1| hypothetical protein ARALYDRAFT_913923 [Arabidopsis lyrata subsp. lyrata] gi|297315448|gb|EFH45871.1| hypothetical protein ARALYDRAFT_913923 [Arabidopsis lyrata subsp. lyrata]	299	263	1.00E-123	88.0	77.6	82.3	hypothetical protein ARALYDRAFT_913923	gbpln	Arabidopsis lyrata	AT4G26410.1 | Symbols: | Uncharacterised conserved protein UCP022280 | chr4:13346760-13348791 FORWARD LENGTH=263	299	263	1.00E-117	88.0	75.9	81.3
Rsa1.0_00341.1.g11772.t1	ref|XP_002867565.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313401|gb|EFH43824.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	257	647	1.00E-102	251.8	83.3	90.3	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00341.1.g11773.t1	ref|NP_567746.1| COP9 signalosome complex subunit 6b [Arabidopsis thaliana] gi|55976549|sp|Q8W1P0.2|CSN6B_ARATH RecName: Full=COP9 signalosome complex subunit 6b; Short=AtCSN6b; Short=Signalosome subunit 6b gi|18056667|gb|AAL58107.1|AF395064_1 CSN complex subunit 6B [Arabidopsis thaliana] gi|21593149|gb|AAM65098.1| transcription factor-like [Arabidopsis thaliana] gi|26983852|gb|AAN86178.1| unknown protein [Arabidopsis thaliana] gi|332659798|gb|AEE85198.1| COP9 signalosome complex subunit 6b [Arabidopsis thaliana]	324	317	1.00E-158	97.8	84.0	88.6	COP9 signalosome complex subunit 6b	gbpln	Arabidopsis thaliana	AT4G26430.1 | Symbols: CSN6B | COP9 signalosome subunit 6B | chr4:13355229-13357326 FORWARD LENGTH=317	324	317	1.00E-160	97.8	84.0	88.6
Rsa1.0_00341.1.g11774.t1	ref|XP_002867564.1| microspore-specific promoter 3 [Arabidopsis lyrata subsp. lyrata] gi|297313400|gb|EFH43823.1| microspore-specific promoter 3 [Arabidopsis lyrata subsp. lyrata]	528	568	0	107.6	71.2	79.7	microspore-specific promoter 3	gbpln	Arabidopsis lyrata	AT4G26440.1 | Symbols: WRKY34, ATWRKY34, MSP3 | WRKY DNA-binding protein 34 | chr4:13357596-13359550 REVERSE LENGTH=568	528	568	0	107.6	70.5	78.6
Rsa1.0_00341.1.g11775.t1	gb|EOA16125.1| hypothetical protein CARUB_v10004258mg [Capsella rubella] gi|482551933|gb|EOA16126.1| hypothetical protein CARUB_v10004258mg [Capsella rubella]	697	706	0	101.3	74.9	83.1	hypothetical protein CARUB_v10004258mg	gbpln	Capsella rubella	AT4G26450.1 | Symbols: | unknown protein; Has 614 Blast hits to 492 proteins in 137 species: Archae - 0; Bacteria - 94; Metazoa - 255; Fungi - 76; Plants - 69; Viruses - 0; Other Eukaryotes - 120 (source: NCBI BLink). | chr4:13362556-13364920 FORWARD LENGTH=708	697	708	0	101.6	74.7	82.5

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<tr><td>Rsa1.0_00341.1.g11776.t1</td><td>ref|NP_001119062.1| GPI-anchored protein LORELEI [Arabidopsis thaliana] gi|259495194|sp|B3GS44.1|LRE_ARATH RecName: Full=GPI-anchored protein LORELEI; Flags: Precursor gi|189038616|gb|ACD75469.1| GPI-anchored protein LORELEI [Arabidopsis thaliana] gi|332659802|gb|AEE85202.1| GPI-anchored protein LORELEI [Arabidopsis thaliana]</td><td>156</td><td>165</td><td>2.00E-42</td><td>105.8</td><td>52.6</td><td>65.4</td><td>GPI-anchored protein LORELEI</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26466.1 | Symbols: LRE | lorelei | chr4:13367645-13368629 REVERSE LENGTH=165</td><td>156</td><td>165</td><td>5.00E-45</td><td>105.8</td><td>52.6</td><td>65.4</td></tr>
<tr><td>Rsa1.0_00341.1.g11777.t1</td><td>ref|NP_194377.2| putative calcium-binding protein CML21 [Arabidopsis thaliana] gi|75320017|sp|Q52K82.1|CML21_ARATH RecName: Full=Probable calcium-binding protein CML21; AltName: Full=Calmodulin-like protein 21 gi|62867639|gb|AAY17423.1| At4g26470 [Arabidopsis thaliana] gi|332659804|gb|AEE85204.1| putative calcium-binding protein CML21 [Arabidopsis thaliana]</td><td>231</td><td>231</td><td>1.00E-106</td><td>100.0</td><td>83.1</td><td>87.4</td><td>putative calcium-binding protein CML21</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26470.1 | Symbols: | Calcium-binding EF-hand family protein | chr4:13371377-13372343 FORWARD LENGTH=231</td><td>231</td><td>231</td><td>1.00E-109</td><td>100.0</td><td>83.1</td><td>87.4</td></tr>
<tr><td>Rsa1.0_00341.1.g11778.t1</td><td>gb|EOA17078.1| hypothetical protein CARUB_v10005327mg [Capsella rubella]</td><td>310</td><td>306</td><td>1.00E-148</td><td>98.7</td><td>91.0</td><td>94.5</td><td>hypothetical protein CARUB_v10005327mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G26480.1 | Symbols: | RNA-binding KH domain-containing protein | chr4:13372885-13375793 REVERSE LENGTH=308</td><td>310</td><td>308</td><td>1.00E-150</td><td>99.4</td><td>91.0</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00341.1.g11779.t1</td><td>ref|NP_201502.1| putative ethylene-responsive transcription factor ERF121 [Arabidopsis thaliana] gi|75262435|sp|Q9FGC9.1|EF121_ARATH RecName: Full=Putative ethylene-responsive transcription factor ERF121 gi|9758546|dbj|BAB08940.1| AP2 domain transcription factor-like [Arabidopsis thaliana] gi|332010907|gb|AED98290.1| putative ethylene-responsive transcription factor ERF121 [Arabidopsis thaliana]</td><td>147</td><td>162</td><td>1.00E-47</td><td>110.2</td><td>67.3</td><td>78.9</td><td>putative ethylene-responsive transcription factor ERF121</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G67010.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:26749058-26749616 REVERSE LENGTH=162</td><td>147</td><td>162</td><td>3.00E-50</td><td>110.2</td><td>67.3</td><td>78.9</td></tr>
<tr><td>Rsa1.0_00341.1.g11780.t1</td><td>ref|NP_179625.1| ethylene-responsive transcription factor ERF120 [Arabidopsis thaliana] gi|75265983|sp|Q9SK67.1|EF120_ARATH RecName: Full=Ethylene-responsive transcription factor ERF120 gi|4512700|gb|AAD21753.1| putative AP2 domain transcription factor [Arabidopsis thaliana] gi|48479354|gb|AAT44948.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|88900422|gb|ABD57523.1| At2g20350 [Arabidopsis thaliana] gi|330251902|gb|AEC06996.1| ethylene-responsive transcription factor ERF120 [Arabidopsis thaliana]</td><td>144</td><td>158</td><td>6.00E-44</td><td>109.7</td><td>68.1</td><td>82.6</td><td>ethylene-responsive transcription factor ERF120</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G20350.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr2:8784769-8785396 FORWARD LENGTH=158</td><td>144</td><td>158</td><td>2.00E-46</td><td>109.7</td><td>68.1</td><td>82.6</td></tr>
<tr><td>Rsa1.0_00341.1.g11781.t1</td><td>ref|NP_179625.1| ethylene-responsive transcription factor ERF120 [Arabidopsis thaliana] gi|75265983|sp|Q9SK67.1|EF120_ARATH RecName: Full=Ethylene-responsive transcription factor ERF120 gi|4512700|gb|AAD21753.1| putative AP2 domain transcription factor [Arabidopsis thaliana] gi|48479354|gb|AAT44948.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|88900422|gb|ABD57523.1| At2g20350 [Arabidopsis thaliana] gi|330251902|gb|AEC06996.1| ethylene-responsive transcription factor ERF120 [Arabidopsis thaliana]</td><td>169</td><td>158</td><td>7.00E-47</td><td>93.5</td><td>65.1</td><td>74.0</td><td>ethylene-responsive transcription factor ERF120</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G20350.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr2:8784769-8785396 FORWARD LENGTH=158</td><td>169</td><td>158</td><td>3.00E-49</td><td>93.5</td><td>65.1</td><td>74.0</td></tr>
<tr><td>Rsa1.0_00341.1.g11782.t4</td><td>ref|XP_002867540.1| hypothetical protein ARALYDRAFT_354113 [Arabidopsis lyrata subsp. lyrata] gi|297313376|gb|EFH43799.1| hypothetical protein ARALYDRAFT_354113 [Arabidopsis lyrata subsp. lyrata]</td><td>415</td><td>320</td><td>7.00E-72</td><td>77.1</td><td>33.0</td><td>40.0</td><td>hypothetical protein ARALYDRAFT_354113</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G26820.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr4:13493453-13494181 REVERSE LENGTH=242</td><td>415</td><td>242</td><td>1.00E-71</td><td>58.3</td><td>32.5</td><td>39.5</td></tr>
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Rsa1.0_00341.1.g11783.t1	ref|XP_002867539.1| hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis lyrata subsp. lyrata] gi|297313375|gb|EFH43798.1| hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis lyrata subsp. lyrata]	453	456	0	100.7	82.8	89.4	hydrolase, hydrolyzing O-glycosyl compounds	gbpln	Arabidopsis lyrata	AT4G26830.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr4:13494726-13496487 REVERSE LENGTH=455	453	455	0	100.4	81.7	88.7
Rsa1.0_00341.1.g11784.t1	emb|CAA67923.1| ubiquitin-like protein [Arabidopsis thaliana]	69	104	1.00E-17	150.7	65.2	68.1	ubiquitin-like protein	gbpln	Arabidopsis thaliana	AT5G55160.2 | Symbols: SUM2, SUMO 2, SUMO2, ATSUMO2 | small ubiquitin-like modifier 2 | chr5:22383747-22384772 REVERSE LENGTH=116	69	116	2.00E-19	168.1	62.3	66.7
Rsa1.0_00341.1.g11785.t1	dbj|BAJ34159.1| unnamed protein product [Thellungiella halophila]	437	444	0	101.6	89.9	95.0	unnamed protein product	----	----	AT4G26850.1 | Symbols: VTC2 | mannose-1-phosphate guanylyltransferase (GDP)s;GDP-galactose:mannose-1-phosphate guanylyltransferases;GDP-galactose:glucose-1-phosphate guanylyltransferases;GDP-galactose:myoinositol-1- phosphate guanylyltransferases;glucose-1-phosphate guanylyltransferase | chr4:13499262-13501145 REVERSE LENGTH=442	437	442	0	101.1	86.0	93.6
Rsa1.0_00341.1.g11786.t10	ref|XP_002867534.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313370|gb|EFH43793.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	434	407	0	93.8	84.6	88.2	galactosyltransferase family protein	gbpln	Arabidopsis lyrata	AT4G26940.1 | Symbols: | Galactosyltransferase family protein | chr4:13529911-13532387 REVERSE LENGTH=407	434	407	0	93.8	84.1	88.0
Rsa1.0_00341.1.g11787.t1	ref|NP_194425.1| uncharacterized protein [Arabidopsis thaliana] gi|334186948|ref|NP_001190851.1| uncharacterized protein [Arabidopsis thaliana] gi|4455218|emb|CAB36541.1| putative protein [Arabidopsis thaliana] gi|7269548|emb|CAB79550.1| putative protein [Arabidopsis thaliana] gi|45752618|gb|AAS76207.1| At4g26950 [Arabidopsis thaliana] gi|46359801|gb|AAS88764.1| At4g26950 [Arabidopsis thaliana] gi|332659874|gb|AEE85274.1| uncharacterized protein AT4G26950 [Arabidopsis thaliana] gi|332659875|gb|AEE85275.1| uncharacterized protein AT4G26950 [Arabidopsis thaliana]	152	144	3.00E-47	94.7	70.4	78.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G26950.2 | Symbols: | Protein of unknown function, DUF584 | chr4:13533643-13534077 REVERSE LENGTH=144	152	144	8.00E-50	94.7	70.4	78.3
Rsa1.0_00341.1.g11788.t1	ref|XP_002869584.1| hypothetical protein ARALYDRAFT_492099 [Arabidopsis lyrata subsp. lyrata] gi|297315420|gb|EFH45843.1| hypothetical protein ARALYDRAFT_492099 [Arabidopsis lyrata subsp. lyrata]	994	995	0	100.1	85.7	92.3	hypothetical protein ARALYDRAFT_492099	gbpln	Arabidopsis lyrata	AT4G26970.1 | Symbols: ACO2 | aconitase 2 | chr4:13543077-13548427 FORWARD LENGTH=995	994	995	0	100.1	84.0	89.4
Rsa1.0_00341.1.g11789.t1	ref|XP_002867531.1| hypothetical protein ARALYDRAFT_492098 [Arabidopsis lyrata subsp. lyrata] gi|297313367|gb|EFH43790.1| hypothetical protein ARALYDRAFT_492098 [Arabidopsis lyrata subsp. lyrata]	365	342	1.00E-144	93.7	75.3	83.3	hypothetical protein ARALYDRAFT_492098	gbpln	Arabidopsis lyrata	AT4G26980.1 | Symbols: | RNI-like superfamily protein | chr4:13548813-13550644 REVERSE LENGTH=343	365	343	1.00E-141	94.0	74.5	83.0
Rsa1.0_00341.1.g11790.t1	ref|NP_194429.3| uncharacterized protein [Arabidopsis thaliana] gi|19715628|gb|AAL91635.1| AT4g26990/F10M23_330 [Arabidopsis thaliana] gi|23506167|gb|AAN31095.1| At4g26990/F10M23_330 [Arabidopsis thaliana] gi|332659881|gb|AEE85281.1| uncharacterized protein AT4G26990 [Arabidopsis thaliana]	496	474	1.00E-167	95.6	66.7	78.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G26990.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54920.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13551150-13554253 REVERSE LENGTH=474	496	474	1.00E-170	95.6	66.7	78.4
Rsa1.0_00341.1.g11791.t1	gb|EOA16728.1| hypothetical protein CARUB_v10004931mg [Capsella rubella]	413	413	1.00E-162	100.0	78.0	84.0	hypothetical protein CARUB_v10004931mg	gbpln	Capsella rubella	AT4G27000.1 | Symbols: ATRBP45C | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:13554983-13557763 REVERSE LENGTH=415	413	415	1.00E-162	100.5	77.5	82.8
Rsa1.0_00341.1.g11792.t1	ref|XP_002880468.1| hypothetical protein ARALYDRAFT_481151 [Arabidopsis lyrata subsp. lyrata] gi|297326307|gb|EFH56727.1| hypothetical protein ARALYDRAFT_481151 [Arabidopsis lyrata subsp. lyrata]	264	277	1.00E-114	104.9	75.4	84.5	hypothetical protein ARALYDRAFT_481151	gbpln	Arabidopsis lyrata	AT2G22890.1 | Symbols: | Kua-ubiquitin conjugating enzyme hybrid localisation domain | chr2:9742500-9743339 REVERSE LENGTH=279	264	279	1.00E-116	105.7	74.2	85.2

Rsa1.0_00341.1.g11793.t1	gb|EOA17310.1| hypothetical protein CARUB_v10005583mg [Capsella rubella]	250	250	1.00E-137	100.0	94.8	97.2	hypothetical protein CARUB_v10005583mg	gbpln	Capsella rubella	AT4G27040.4 | Symbols: VPS22 | EAP30/Vps36 family protein | chr4:13573061-13574576 REVERSE LENGTH=250	250	250	1.00E-139	100.0	94.4	97.2
Rsa1.0_00341.1.g11794.t3	ref|NP_194437.1| tryptophan synthase beta chain [Arabidopsis thaliana] gi|1174779|sp|P25269.2|TRBP2_ARATH RecName: Full=Tryptophan synthase beta chain 2, chloroplastic; Flags: Precursor gi|166894|gb|AAA32879.1| tryptophan synthase beta-subunit [Arabidopsis thaliana] gi|4490703|emb|CAB38837.1| tryptophan synthase beta-subunit (TSB2) [Arabidopsis thaliana] gi|7269560|emb|CAB79562.1| tryptophan synthase beta-subunit (TSB2) [Arabidopsis thaliana] gi|21536585|gb|AAM60917.1| tryptophan synthase beta-subunit TSB2 [Arabidopsis thaliana] gi|27808592|gb|AAO24576.1| At4g27070 [Arabidopsis thaliana] gi|110736231|dbj|BAF00086.1| tryptophan synthase beta-subunit [Arabidopsis thaliana] gi|332659896|gb|AEE85296.1| tryptophan synthase beta chain [Arabidopsis thaliana]	473	475	0	100.4	93.7	96.6	tryptophan synthase beta chain	gbpln	Arabidopsis thaliana	AT4G27070.1 | Symbols: TSB2 | tryptophan synthase beta-subunit 2 | chr4:13586564-13588619 FORWARD LENGTH=475	473	475	0	100.4	93.7	96.6
Rsa1.0_00341.1.g11795.t1	gb|EOA17860.1| hypothetical protein CARUB_v10006265mg [Capsella rubella]	506	298	1.00E-123	58.9	53.4	55.9	hypothetical protein CARUB_v10006265mg	gbpln	Capsella rubella	AT4G27120.2 | Symbols: | CONTAINS InterPro DOMAIN/s: DDRGK domain (InterPro:IPR019153); Has 14775 Blast hits to 8764 proteins in 778 species: Archae - 29; Bacteria - 1878; Metazoa - 5164; Fungi - 1447; Plants - 582; Viruses - 164; Other Eukaryotes - 5511 (source: NCBI BLink). | chr4:13602210-13604227 REVERSE LENGTH=298	506	298	1.00E-113	58.9	51.8	53.8
Rsa1.0_00341.1.g11796.t1	ref|NP_200287.1| Translation initiation factor SUI1 family protein [Arabidopsis thaliana] gi|186532111|ref|NP_001119436.1| Translation initiation factor SUI1 family protein [Arabidopsis thaliana] gi|334188393|ref|NP_001190540.1| Translation initiation factor SUI1 family protein [Arabidopsis thaliana] gi|297792937|ref|XP_002864353.1| hypothetical protein ARALYDRAFT_495556 [Arabidopsis lyrata subsp. lyrata] gi|9758256|dbj|BAB08755.1| protein translation factor Sui1 homolog [Arabidopsis thaliana] gi|29028784|gb|AAO64771.1| At5g54760 [Arabidopsis thaliana] gi|297310188|gb|EFH40612.1| hypothetical protein ARALYDRAFT_495556 [Arabidopsis lyrata subsp. lyrata] gi|332009153|gb|AED96536.1| Translation initiation factor SUI1 family protein [Arabidopsis thaliana] gi|332009154|gb|AED96537.1| Translation initiation factor SUI1 family protein [Arabidopsis thaliana] gi|332009155|gb|AED96538.1| Translation initiation factor SUI1 family protein [Arabidopsis thaliana]	113	113	4.00E-59	100.0	98.2	100.0	Translation initiation factor SUI1 family protein	gbpln	Arabidopsis lyrata	AT5G54760.3 | Symbols: | Translation initiation factor SUI1 family protein | chr5:22244732-22245517 FORWARD LENGTH=113	113	113	7.00E-62	100.0	98.2	100.0
Rsa1.0_00341.1.g11797.t1	ref|XP_002869576.1| 2S seed storage protein 3 [Arabidopsis lyrata subsp. lyrata] gi|297315412|gb|EFH45835.1| 2S seed storage protein 3 [Arabidopsis lyrata subsp. lyrata]	153	158	2.00E-52	103.3	69.3	81.0	2S seed storage protein 3	gbpln	Arabidopsis lyrata	AT4G27160.1 | Symbols: AT2S3, SESA3 | seed storage albumin 3 | chr4:13611836-13612330 FORWARD LENGTH=164	153	164	2.00E-54	107.2	68.6	82.4
Rsa1.0_00341.1.g11798.t2	gb|ACP30565.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1130	1009	0	89.3	74.6	79.6	disease resistance protein	gbpln	Brassica rapa	AT4G27190.1 | Symbols: | NB-ARC domain-containing disease resistance protein | chr4:13620977-13623934 REVERSE LENGTH=985	1130	985	0	87.2	48.0	59.1

Rsa1.0_00341.1.g11799.t1	ref|NP_194455.2| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|23296465|gb|AAN13064.1| unknown protein [Arabidopsis thaliana] gi|332659916|gb|AEE85316.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]	408	354	1.00E-169	86.8	70.8	77.2	Rossmann-fold NAD(P)-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT4G27250.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:13642803-13644425 REVERSE LENGTH=354	408	354	1.00E-171	86.8	70.8	77.2
Rsa1.0_00341.1.g11800.t1	gb|ABD65629.1| hypothetical protein 23.t00046 [Brassica oleracea]	156	147	2.00E-30	94.2	41.7	62.2	hypothetical protein 23.t00046	gbpln	Brassica oleracea	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	156	746	1.00E-15	478.2	26.3	36.5
Rsa1.0_00341.1.g11801.t1	gb|EOA16217.1| hypothetical protein CARUB_v10004357mg, partial [Capsella rubella]	623	634	0	101.8	94.7	96.6	hypothetical protein CARUB_v10004357mg, partial	gbpln	Capsella rubella	AT4G27260.1 | Symbols: GH3.5, WES1 | Auxin-responsive GH3 family protein | chr4:13653704-13655892 FORWARD LENGTH=612	623	612	0	98.2	94.4	96.6
Rsa1.0_00341.1.g11802.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00341.1.g11803.t1	gb|EOA18934.1| hypothetical protein CARUB_v10007565mg [Capsella rubella]	555	638	0	115.0	62.0	69.0	hypothetical protein CARUB_v10007565mg	gbpln	Capsella rubella	AT4G27420.1 | Symbols: | ABC-2 type transporter family protein | chr4:13712434-13714797 REVERSE LENGTH=638	555	638	0	115.0	60.9	68.1
Rsa1.0_00341.1.g11804.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00341.1.g11805.t1	ref|NP_567774.1| uncharacterized protein [Arabidopsis thaliana] gi|17981657|gb|AAL51112.1|AF458340_1 At4g27438/At4g27438 [Arabidopsis thaliana] gi|15809978|gb|AAL06916.1| At4g27438 [Arabidopsis thaliana] gi|332659941|gb|AEE85341.1| uncharacterized protein AT4G27435 [Arabidopsis thaliana]	204	173	8.00E-82	84.8	71.6	73.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G27435.1 | Symbols: | Protein of unknown function (DUF1218) | chr4:13723903-13724872 FORWARD LENGTH=173	204	173	3.00E-84	84.8	71.6	73.5
Rsa1.0_00341.1.g11806.t1	ref|XP_002869561.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297315397|gb|EFH45820.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	245	243	6.00E-85	99.2	72.2	77.6	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G27470.1 | Symbols: ATRMA3, RMA3 | RING membrane-anchor 3 | chr4:13735576-13736307 FORWARD LENGTH=243	245	243	3.00E-84	99.2	69.8	75.1
Rsa1.0_00341.1.g11807.t1	ref|NP_194478.3| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|186514118|ref|NP_001119069.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|332659947|gb|AEE85347.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|332659948|gb|AEE85348.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]	426	421	0	98.8	85.2	91.1	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	gbpln	Arabidopsis thaliana	AT4G27480.2 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:13736835-13738317 REVERSE LENGTH=421	426	421	0	98.8	85.2	91.1
Rsa1.0_00341.1.g11808.t1	gb|EOA17279.1| hypothetical protein CARUB_v10005549mg [Capsella rubella]	177	256	1.00E-60	144.6	74.0	81.9	hypothetical protein CARUB_v10005549mg	gbpln	Capsella rubella	AT4G27490.1 | Symbols: | 3'-5'-exoribonuclease family protein | chr4:13739961-13741647 FORWARD LENGTH=256	177	256	2.00E-61	144.6	72.9	80.8
Rsa1.0_00341.1.g11809.t1	ref|NP_194480.2| proton pump interactor 1 [Arabidopsis thaliana] gi|75097739|sp|O23144.2|PPI1_ARATH RecName: Full=Proton pump-interactor 1 gi|13992437|emb|CAA05145.2| proton pump interactor [Arabidopsis thaliana] gi|15215674|gb|AAK91382.1| AT4g27500/F27G19_100 [Arabidopsis thaliana] gi|23505987|gb|AAN28853.1| At4g27500/F27G19_100 [Arabidopsis thaliana] gi|332659950|gb|AEE85350.1| proton pump interactor 1 [Arabidopsis thaliana]	609	612	0	100.5	79.0	85.6	proton pump interactor 1	gbpln	Arabidopsis thaliana	AT4G27500.1 | Symbols: PPI1 | proton pump interactor 1 | chr4:13743614-13745900 FORWARD LENGTH=612	609	612	0	100.5	79.0	85.6

Rsa1.0_00341.1.g11810.t1	ref|NP_194482.1| early nodulin-like protein 2 [Arabidopsis thaliana] gi|34395735|sp|Q9T076.1|ENL2_ARATH RecName: Full=Early nodulin-like protein 2; AltName: Full=Phytocyanin-like protein; Flags: Precursor gi|11762218|gb|AAG40387.1|AF325035_1 AT4g27520 [Arabidopsis thaliana] gi|4469003|emb|CAB38264.1| putative protein [Arabidopsis thaliana] gi|7269606|emb|CAB81402.1| putative protein [Arabidopsis thaliana] gi|23397249|gb|AAN31906.1| unknown protein [Arabidopsis thaliana] gi|24417234|gb|AAN60227.1| unknown [Arabidopsis thaliana] gi|56381997|gb|AAV85717.1| At4g27520 [Arabidopsis thaliana] gi|332659953|gb|AEE85353.1| early nodulin-like protein 2 [Arabidopsis thaliana]	526	349	2.00E-82	66.3	35.9	39.9	early nodulin-like protein 2	gbpln	Arabidopsis thaliana	AT4G27520.1 | Symbols: ENODL2, AtENODL2 | early nodulin-like protein 2 | chr4:13750668-13751819 REVERSE LENGTH=349	526	349	4.00E-85	66.3	35.9	39.9
Rsa1.0_00341.1.g11811.t1	gb|EOA16047.1| hypothetical protein CARUB_v10004177mg [Capsella rubella]	818	786	0	96.1	82.4	89.2	hypothetical protein CARUB_v10004177mg	gbpln	Capsella rubella	AT4G27550.1 | Symbols: ATTPS4, TPS4 | trehalose-6-phosphatase synthase S4 | chr4:13755689-13759740 FORWARD LENGTH=795	818	795	0	97.2	82.3	89.0
Rsa1.0_00341.1.g11812.t1	emb|CAB38270.1| putative protein [Arabidopsis thaliana] gi|7269612|emb|CAB81408.1| putative protein [Arabidopsis thaliana]	101	515	2.00E-30	509.9	80.2	84.2	putative protein	gbpln	Arabidopsis thaliana	AT4G27580.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, cell wall; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13765832-13766306 REVERSE LENGTH=104	101	104	5.00E-32	103.0	80.2	84.2
Rsa1.0_00341.1.g11813.t1	ref|NP_198660.1| self-incompatibility S1 family protein [Arabidopsis thaliana] gi|9758822|dbj|BAB09356.1| unnamed protein product [Arabidopsis thaliana] gi|332006934|gb|AED94317.1| self-incompatibility S1 family protein [Arabidopsis thaliana]	94	133	3.00E-22	141.5	69.1	76.6	self-incompatibility S1 family protein	gbpln	Arabidopsis thaliana	AT5G38440.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:15390223-15390624 FORWARD LENGTH=133	94	133	4.00E-25	141.5	69.1	76.6
Rsa1.0_00341.1.g11814.t1	ref|NP_567780.1| pfkB-like carbohydrate kinase family protein [Arabidopsis thaliana] gi|15450507|gb|AAK96546.1| AT4g27600/T29A15_90 [Arabidopsis thaliana] gi|16974333|gb|AAL31151.1| AT4g27600/T29A15_90 [Arabidopsis thaliana] gi|332659964|gb|AEE85364.1| pfkB-like carbohydrate kinase family protein [Arabidopsis thaliana]	450	471	0	104.7	85.6	90.9	pfkB-like carbohydrate kinase family protein	gbpln	Arabidopsis thaliana	AT4G27600.1 | Symbols: NARA5 | pfkB-like carbohydrate kinase family protein | chr4:13782753-13785005 REVERSE LENGTH=471	450	471	0	104.7	85.6	90.9
Rsa1.0_00341.1.g11815.t1	ref|XP_002867492.1| hypothetical protein ARALYDRAFT_492028 [Arabidopsis lyrata subsp. lyrata] gi|297313328|gb|EFH43751.1| hypothetical protein ARALYDRAFT_492028 [Arabidopsis lyrata subsp. lyrata]	334	337	1.00E-150	100.9	80.5	89.5	hypothetical protein ARALYDRAFT_492028	gbpln	Arabidopsis lyrata	AT4G27610.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27620.2); Has 1304 Blast hits to 1173 proteins in 200 species: Archae - 14; Bacteria - 115; Metazoa - 628; Fungi - 104; Plants - 95; Viruses - 8; Other Eukaryotes - 340 (source: NCBI BLink). | chr4:13785648-13787332 REVERSE LENGTH=334	334	334	1.00E-150	100.0	80.2	88.9
Rsa1.0_00341.1.g11816.t1	ref|NP_194494.2| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|17065302|gb|AAL32805.1| putative protein [Arabidopsis thaliana] gi|38564254|gb|AAR23706.1| At4g27640 [Arabidopsis thaliana] gi|332659973|gb|AEE85373.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	1049	1048	0	99.9	90.8	95.2	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G27640.1 | Symbols: | ARM repeat superfamily protein | chr4:13798013-13802976 REVERSE LENGTH=1048	1049	1048	0	99.9	90.8	95.2
Rsa1.0_00341.1.g11817.t1	gb|EOA16827.1| hypothetical protein CARUB_v10005050mg [Capsella rubella]	378	378	0	100.0	95.0	98.1	hypothetical protein CARUB_v10005050mg	gbpln	Capsella rubella	AT4G27650.1 | Symbols: PEL1 | Eukaryotic release factor 1 (eRF1) family protein | chr4:13803459-13807556 REVERSE LENGTH=378	378	378	0	100.0	92.9	97.6

Rsa1.0_00341.1.g11818.t1	ref|XP_002869552.1| hypothetical protein ARALYDRAFT_492020 [Arabidopsis lyrata subsp. lyrata] gi|297315388|gb|EFH45811.1| hypothetical protein ARALYDRAFT_492020 [Arabidopsis lyrata subsp. lyrata]	68	62	5.00E-20	91.2	77.9	85.3	hypothetical protein ARALYDRAFT_492020	gbpln	Arabidopsis lyrata	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13813124-13813312 FORWARD LENGTH=62	68	62	1.00E-22	91.2	76.5	85.3
Rsa1.0_00341.1.g11819.t1	gb|AAM66967.1| unknown [Arabidopsis thaliana]	62	62	9.00E-20	100.0	75.8	87.1	unknown	gbpln	Arabidopsis thaliana	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13813124-13813312 FORWARD LENGTH=62	62	62	5.00E-20	100.0	71.0	83.9
Rsa1.0_00341.1.g11820.t1	ref|XP_002869553.1| hypothetical protein ARALYDRAFT_913767 [Arabidopsis lyrata subsp. lyrata] gi|297315389|gb|EFH45812.1| hypothetical protein ARALYDRAFT_913767 [Arabidopsis lyrata subsp. lyrata]	62	62	1.00E-24	100.0	87.1	95.2	hypothetical protein ARALYDRAFT_913767	gbpln	Arabidopsis lyrata	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13813124-13813312 FORWARD LENGTH=62	62	62	4.00E-25	100.0	83.9	91.9
Rsa1.0_00341.1.g11821.t1	gb|AAM66967.1| unknown [Arabidopsis thaliana]	62	62	3.00E-21	100.0	82.3	91.9	unknown	gbpln	Arabidopsis thaliana	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13813124-13813312 FORWARD LENGTH=62	62	62	6.00E-24	100.0	83.9	91.9
Rsa1.0_00341.1.g11822.t1	ref|XP_002867486.1| hypothetical protein ARALYDRAFT_492019 [Arabidopsis lyrata subsp. lyrata] gi|297313322|gb|EFH43745.1| hypothetical protein ARALYDRAFT_492019 [Arabidopsis lyrata subsp. lyrata]	174	176	4.00E-55	101.1	69.0	77.0	hypothetical protein ARALYDRAFT_492019	gbpln	Arabidopsis lyrata	AT4G27660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54150.1); Has 115 Blast hits to 109 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 10; Fungi - 0; Plants - 100; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr4:13817249-13818027 REVERSE LENGTH=182	174	182	3.00E-56	104.6	58.6	63.8

Rsa1.0_00341.1.g11823.t1	ref|NP_194498.1| 26S proteasome regulatory particle chain RPT6-like protein [Arabidopsis thaliana] gi|4469019|emb|CAB38280.1| putative protein [Arabidopsis thaliana] gi|7269622|emb|CAB81418.1| putative protein [Arabidopsis thaliana] gi|20260328|gb|AAM13062.1| putative protein [Arabidopsis thaliana] gi|21553404|gb|AAM62497.1| 26S proteasome regulatory particle chain RPT6-like protein [Arabidopsis thaliana] gi|23197836|gb|AAN15445.1| putative protein [Arabidopsis thaliana] gi|110740771|dbj|BAE98483.1| hypothetical protein [Arabidopsis thaliana] gi|332659980|gb|AEE85380.1| P-loop containing nucleoside triphosphate hydrolases superfamily protein [Arabidopsis thaliana]	389	398	0	102.3	91.3	95.6	26S proteasome regulatory particle chain RPT6-like protein	gbpln	Arabidopsis thaliana	AT4G27680.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13821263-13823083 FORWARD LENGTH=398	389	398	0	102.3	91.3	95.6
Rsa1.0_00341.1.g11824.t1	gb|EOA16839.1| hypothetical protein CARUB_v10005060mg [Capsella rubella]	366	376	1.00E-179	102.7	88.3	93.4	hypothetical protein CARUB_v10005060mg	gbpln	Capsella rubella	AT4G27760.1 | Symbols: FEY, FEY3 | NAD(P)-binding Rossmann-fold superfamily protein | chr4:13844151-13846563 FORWARD LENGTH=376	366	376	1.00E-179	102.7	87.2	93.2
Rsa1.0_00341.1.g11825.t1	ref|NP_194507.1| acyl-CoA binding protein 2 [Arabidopsis thaliana] gi|75313883|sp|Q9STP8.1|ACBP2_ARATH RecName: Full=Acyl-CoA-binding domain-containing protein 2; Short=Acyl-CoA binding protein 2 gi|12039032|gb|AAG46056.1|AF178947_1 acyl-CoA binding protein ACBP2 [Arabidopsis thaliana] gi|13661742|gb|AAK38078.1|AF320561_1 putative membrane-bound acyl-CoA binding protein isoform 2 [Arabidopsis thaliana] gi|4972109|emb|CAB43966.1| putative acyl-CoA binding protein [Arabidopsis thaliana] gi|7269631|emb|CAB81427.1| putative acyl-CoA binding protein [Arabidopsis thaliana] gi|19699102|gb|AAL90917.1| AT4g27780/T27E11_20 [Arabidopsis thaliana] gi|21594802|gb|AAM66045.1| putative acyl-CoA binding protein [Arabidopsis thaliana] gi|21689607|gb|AAM67425.1| AT4g27780/T27E11_20 [Arabidopsis thaliana] gi|332659991|gb|AEE85391.1| acyl-CoA binding protein 2 [Arabidopsis thaliana]	254	354	5.00E-98	139.4	80.7	87.0	acyl-CoA binding protein 2	gbpln	Arabidopsis thaliana	AT4G27780.1 | Symbols: ACBP2 | acyl-CoA binding protein 2 | chr4:13847774-13849629 FORWARD LENGTH=354	254	354	1.00E-100	139.4	80.7	87.0
Rsa1.0_00342.1.g11826.t2	ref|XP_002877847.1| starch-excess 4 [Arabidopsis lyrata subsp. lyrata] gi|297323685|gb|EFH54106.1| starch-excess 4 [Arabidopsis lyrata subsp. lyrata]	214	377	1.00E-114	176.2	91.6	95.3	starch-excess 4	gbpln	Arabidopsis lyrata	AT3G52180.1 | Symbols: ATPTPKIS1, DSP4, SEX4, ATSEX4 | dual specificity protein phosphatase (DsPTP1) family protein | chr3:19349884-19353459 REVERSE LENGTH=379	214	379	1.00E-116	177.1	92.1	95.3
Rsa1.0_00342.1.g11827.t17	gb|EOA24621.1| hypothetical protein CARUB_v10017892mg [Capsella rubella]	113	254	3.00E-38	224.8	85.0	88.5	hypothetical protein CARUB_v10017892mg	gbpln	Capsella rubella	AT3G52150.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:19342074-19343090 FORWARD LENGTH=253	113	253	4.00E-40	223.9	82.3	88.5
Rsa1.0_00342.1.g11828.t1	ref|NP_190781.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|4678942|emb|CAB41333.1| 5B protein like protein [Arabidopsis thaliana] gi|44917507|gb|AAS49078.1| At3g52130 [Arabidopsis thaliana] gi|62320556|dbj|BAD95162.1| 5B protein like protein [Arabidopsis thaliana] gi|332645377|gb|AEE78898.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	150	125	9.00E-47	83.3	72.0	73.3	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT3G52130.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:19332081-19332458 REVERSE LENGTH=125	150	125	3.00E-49	83.3	72.0	73.3
Rsa1.0_00342.1.g11829.t1	ref|XP_002876126.1| hypothetical protein ARALYDRAFT_323761 [Arabidopsis lyrata subsp. lyrata] gi|297321964|gb|EFH52385.1| hypothetical protein ARALYDRAFT_323761 [Arabidopsis lyrata subsp. lyrata]	488	1114	0	228.3	76.0	80.7	hypothetical protein ARALYDRAFT_323761	gbpln	Arabidopsis lyrata	AT3G52120.1 | Symbols: | SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein | chr3:19329243-19331738 FORWARD LENGTH=443	488	443	0	90.8	75.6	80.3

Rsa1.0_00342.1.g11830.t1	gb|EOA24248.1| hypothetical protein CARUB_v10017489mg [Capsella rubella]	354	364	1.00E-139	102.8	76.6	84.7	hypothetical protein CARUB_v10017489mg	gbpln	Capsella rubella	AT3G52110.1 | Symbols: | unknown protein; Has 191 Blast hits to 174 proteins in 54 species: Archae - 0; Bacteria - 7; Metazoa - 45; Fungi - 7; Plants - 40; Viruses - 0; Other Eukaryotes - 92 (source: NCBI BLink). | chr3:19323925-19325632 REVERSE LENGTH=362	354	362	1.00E-139	102.3	75.1	84.5
Rsa1.0_00342.1.g11831.t1	emb|CAB41330.1| putative protein [Arabidopsis thaliana]	69	763	7.00E-26	1105.8	81.2	84.1	putative protein	gbpln	Arabidopsis thaliana	AT3G52105.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:19323394-19323606 FORWARD LENGTH=70	69	70	1.00E-25	101.4	78.3	81.2
Rsa1.0_00342.1.g11832.t4	ref|NP_190778.2| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana] gi|332645370|gb|AEE78891.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana]	655	696	0	106.3	79.4	86.3	RING/FYVE/PHD zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT3G52100.1 | Symbols: | RING/FYVE/PHD-type zinc finger family protein | chr3:19319343-19322773 FORWARD LENGTH=696	655	696	0	106.3	79.4	86.3
Rsa1.0_00342.1.g11833.t8	ref|XP_002885456.1| hypothetical protein ARALYDRAFT_898613 [Arabidopsis lyrata subsp. lyrata] gi|297331296|gb|EFH61715.1| hypothetical protein ARALYDRAFT_898613 [Arabidopsis lyrata subsp. lyrata]	976	365	0	37.4	31.5	33.6	hypothetical protein ARALYDRAFT_898613	gbpln	Arabidopsis lyrata	AT3G21640.1 | Symbols: TWD1, UCU2, FKBP42, ATFKBP42 | FKBP-type peptidyl-prolyl cis-trans isomerase family protein | chr3:7619025-7621097 REVERSE LENGTH=365	976	365	0	37.4	31.0	33.4
Rsa1.0_00342.1.g11834.t17	ref|XP_002876121.1| hypothetical protein ARALYDRAFT_485561 [Arabidopsis lyrata subsp. lyrata] gi|297321959|gb|EFH52380.1| hypothetical protein ARALYDRAFT_485561 [Arabidopsis lyrata subsp. lyrata]	389	454	1.00E-157	116.7	76.3	84.3	hypothetical protein ARALYDRAFT_485561	gbpln	Arabidopsis lyrata	AT3G52050.1 | Symbols: | 5'-3' exonuclease family protein | chr3:19305228-19309398 FORWARD LENGTH=425	389	425	1.00E-158	109.3	73.3	79.9
Rsa1.0_00342.1.g11835.t1	gb|EOA25020.1| hypothetical protein CARUB_v10018318mg [Capsella rubella]	91	90	3.00E-38	98.9	83.5	92.3	hypothetical protein CARUB_v10018318mg	gbpln	Capsella rubella	AT3G52040.1 | Symbols: | unknown protein; Has 37 Blast hits to 37 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:19304368-19304802 REVERSE LENGTH=90	91	90	9.00E-40	98.9	81.3	90.1
Rsa1.0_00342.1.g11836.t1	ref|XP_002885549.1| hypothetical protein ARALYDRAFT_342455 [Arabidopsis lyrata subsp. lyrata] gi|297331389|gb|EFH61808.1| hypothetical protein ARALYDRAFT_342455 [Arabidopsis lyrata subsp. lyrata]	416	494	1.00E-90	118.8	49.8	66.1	hypothetical protein ARALYDRAFT_342455	gbpln	Arabidopsis lyrata	AT3G52320.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:19403020-19404192 REVERSE LENGTH=390	416	390	2.00E-76	93.8	38.7	51.0
Rsa1.0_00342.1.g11837.t1	gb|EOA24272.1| hypothetical protein CARUB_v10017513mg [Capsella rubella]	326	358	1.00E-151	109.8	89.3	95.4	hypothetical protein CARUB_v10017513mg	gbpln	Capsella rubella	AT3G51990.1 | Symbols: | Protein kinase superfamily protein | chr3:19287989-19289077 FORWARD LENGTH=362	326	362	1.00E-151	111.0	88.0	94.5
Rsa1.0_00342.1.g11838.t1	ref|XP_002877838.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297323676|gb|EFH54097.1| binding protein [Arabidopsis lyrata subsp. lyrata]	382	382	0	100.0	85.1	91.6	binding protein	gbpln	Arabidopsis lyrata	AT3G51980.1 | Symbols: | ARM repeat superfamily protein | chr3:19285811-19287502 REVERSE LENGTH=382	382	382	0	100.0	84.0	92.1
Rsa1.0_00342.1.g11839.t1	ref|NP_190765.1| acyl-CoA sterol acyl transferase 1 [Arabidopsis thaliana] gi|75209995|sp|Q9SV07.1|ASAT1_ARATH RecName: Full=Acyl-CoA--sterol O-acyltransferase 1; AltName: Full=Sterol O-acyltransferase 1 gi|4678926|emb|CAB41317.1| hypothetical protein [Arabidopsis thaliana] gi|34365695|gb|AAQ65159.1| At3g51970 [Arabidopsis thaliana] gi|51968422|dbj|BAD42903.1| wax synthase-like protein [Arabidopsis thaliana] gi|332645349|gb|AEE78870.1| acyl-CoA sterol acyl transferase 1 [Arabidopsis thaliana]	71	345	8.00E-14	485.9	53.5	59.2	acyl-CoA sterol acyl transferase 1	gbpln	Arabidopsis thaliana	AT3G51970.1 | Symbols: ATSAT1, ASAT1, ATASAT1 | acyl-CoA sterol acyl transferase 1 | chr3:19284420-19285457 FORWARD LENGTH=345	71	345	1.00E-16	485.9	53.5	59.2
Rsa1.0_00342.1.g11840.t1	gb|EOA24836.1| hypothetical protein CARUB_v10018125mg [Capsella rubella]	101	171	4.00E-14	169.3	54.5	62.4	hypothetical protein CARUB_v10018125mg	gbpln	Capsella rubella	AT3G51960.1 | Symbols: ATBZIP24, BZIP24 | basic leucine zipper 24 | chr3:19282828-19284064 REVERSE LENGTH=227	101	227	6.00E-15	224.8	53.5	64.4

Rsa1.0_00342.1.g11841.t2	ref|XP_002877836.1| hypothetical protein ARALYDRAFT_485553 [Arabidopsis lyrata subsp. lyrata] gi|297323674|gb|EFH54095.1| hypothetical protein ARALYDRAFT_485553 [Arabidopsis lyrata subsp. lyrata]	535	539	0	100.7	87.9	92.0	hypothetical protein ARALYDRAFT_485553	gbpln	Arabidopsis lyrata	AT3G51950.2 | Symbols: | Zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein | chr3:19278244-19280407 REVERSE LENGTH=540	535	540	0	100.9	87.7	92.0
Rsa1.0_00342.1.g11842.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	384	1197	1.00E-39	311.7	26.3	41.9	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	384	575	1.00E-19	149.7	21.9	35.7
Rsa1.0_00342.1.g11843.t1	ref|XP_002877834.1| oxidoreductase/ transition metal ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297323672|gb|EFH54093.1| oxidoreductase/ transition metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	407	473	1.00E-124	116.2	65.6	78.1	oxidoreductase/ transition metal ion binding protein	gbpln	Arabidopsis lyrata	AT3G51940.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G03990.1); Has 215 Blast hits to 164 proteins in 38 species: Archae - 0; Bacteria - 35; Metazoa - 16; Fungi - 18; Plants - 121; Viruses - 0; Other Eukaryotes - 25 (source: NCBI BLink). | chr3:19273708-19275157 REVERSE LENGTH=453	407	453	1.00E-119	111.3	64.9	76.7
Rsa1.0_00342.1.g11844.t1	ref|NP_190761.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|4678922|emb|CAB41313.1| putative protein [Arabidopsis thaliana] gi|30725344|gb|AAP37694.1| At3g51930 [Arabidopsis thaliana] gi|110736561|dbj|BAF00246.1| hypothetical protein [Arabidopsis thaliana] gi|332645343|gb|AEE78864.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	427	415	0	97.2	85.5	90.2	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G51930.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:19271672-19272919 FORWARD LENGTH=415	427	415	0	97.2	85.5	90.2
Rsa1.0_00342.1.g11845.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00342.1.g11846.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00343.1.g11847.t1	ref|NP_177927.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] gi|145327725|ref|NP_001077838.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] gi|21592341|gb|AAM64292.1| allergen, putative [Arabidopsis thaliana] gi|28416615|gb|AAO42838.1| At1g78040 [Arabidopsis thaliana] gi|110743227|dbj|BAE99504.1| phosphoglycerate mutase 1 like protein [Arabidopsis thaliana] gi|332197939|gb|AEE36060.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] gi|332197940|gb|AEE36061.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana]	166	171	1.00E-72	103.0	78.9	89.8	pollen Ole e 1 allergen and extensin family protein	gbpln	Arabidopsis thaliana	AT1G78040.2 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr1:29345993-29346840 FORWARD LENGTH=171	166	171	4.00E-75	103.0	78.9	89.8
Rsa1.0_00343.1.g11848.t1	gb|AAF17689.1|AC009243_16 F28K19.26 [Arabidopsis thaliana]	327	677	1.00E-154	207.0	82.6	89.3	F28K19.26	gbpln	Arabidopsis thaliana	AT1G78050.1 | Symbols: PGM | phosphoglycerate/bisphosphoglycerate mutase | chr1:29348095-29349592 FORWARD LENGTH=332	327	332	1.00E-156	101.5	82.6	89.3
Rsa1.0_00343.1.g11849.t1	dbj|BAJ34031.1| unnamed protein product [Thellungiella halophila]	279	356	3.00E-90	127.6	77.4	84.2	unnamed protein product	----	----	AT1G78080.1 | Symbols: RAP2.4 | related to AP2 4 | chr1:29364790-29365794 FORWARD LENGTH=334	279	334	2.00E-88	119.7	74.6	83.2
Rsa1.0_00343.1.g11850.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	393	1142	1.00E-117	290.6	50.1	65.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	393	575	5.00E-50	146.3	26.2	42.2
Rsa1.0_00343.1.g11851.t1	gb|EOA35304.1| hypothetical protein CARUB_v10020479mg [Capsella rubella]	368	376	0	102.2	87.0	93.2	hypothetical protein CARUB_v10020479mg	gbpln	Capsella rubella	AT1G78090.1 | Symbols: ATTPPB, TPPB | trehalose-6-phosphate phosphatase | chr1:29373955-29376295 FORWARD LENGTH=374	368	374	0	101.6	85.9	92.7
Rsa1.0_00343.1.g11852.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00343.1.g11853.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_00343.1.g11854.t1</td><td>ref|NP_565169.1| F-box protein [Arabidopsis thaliana] gi|75262248|sp|Q9C9S2.1|FB91_ARATH RecName: Full=F-box protein At1g78100 gi|12324249|gb|AAG52096.1|AC012680_7 unknown protein; 22671-23675 [Arabidopsis thaliana] gi|15450976|gb|AAK96759.1| Unknown protein [Arabidopsis thaliana] gi|20148731|gb|AAM10256.1| unknown protein [Arabidopsis thaliana] gi|332197946|gb|AEE36067.1| F-box protein [Arabidopsis thaliana]</td><td>201</td><td>334</td><td>2.00E-23</td><td>166.2</td><td>32.8</td><td>36.8</td><td>F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G78100.1 | Symbols: | F-box family protein | chr1:29387907-29388911 FORWARD LENGTH=334</td><td>201</td><td>334</td><td>5.00E-26</td><td>166.2</td><td>32.8</td><td>36.8</td></tr>
<tr><td>Rsa1.0_00343.1.g11855.t1</td><td>gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]</td><td>1742</td><td>1557</td><td>0</td><td>89.4</td><td>42.1</td><td>57.7</td><td>reverse transcriptase, putative; 100033-105622</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1742</td><td>575</td><td>9.00E-75</td><td>33.0</td><td>9.8</td><td>15.0</td></tr>
<tr><td>Rsa1.0_00343.1.g11856.t1</td><td>ref|XP_002887722.1| hypothetical protein ARALYDRAFT_476978 [Arabidopsis lyrata subsp. lyrata] gi|297333563|gb|EFH63981.1| hypothetical protein ARALYDRAFT_476978 [Arabidopsis lyrata subsp. lyrata]</td><td>310</td><td>344</td><td>1.00E-112</td><td>111.0</td><td>73.9</td><td>83.9</td><td>hypothetical protein ARALYDRAFT_476978</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G78110.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22230.1); Has 5452 Blast hits to 3541 proteins in 289 species: Archae - 4; Bacteria - 165; Metazoa - 1756; Fungi - 532; Plants - 205; Viruses - 141; Other Eukaryotes - 2649 (source: NCBI BLink). | chr1:29391879-29392907 FORWARD LENGTH=342</td><td>310</td><td>342</td><td>1.00E-111</td><td>110.3</td><td>73.5</td><td>84.5</td></tr>
<tr><td>Rsa1.0_00343.1.g11857.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00343.1.g11858.t1</td><td>ref|NP_177937.1| putative transporter [Arabidopsis thaliana] gi|12324255|gb|AAG52102.1|AC012680_13 putative transporter; 34935-36578 [Arabidopsis thaliana] gi|28416565|gb|AAO42813.1| At1g78130 [Arabidopsis thaliana] gi|110742895|dbj|BAE99345.1| transporter like protein [Arabidopsis thaliana] gi|332197949|gb|AEE36070.1| putative transporter [Arabidopsis thaliana]</td><td>468</td><td>490</td><td>0</td><td>104.7</td><td>92.1</td><td>96.6</td><td>putative transporter</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G78130.1 | Symbols: UNE2 | Major facilitator superfamily protein | chr1:29400171-29401814 FORWARD LENGTH=490</td><td>468</td><td>490</td><td>0</td><td>104.7</td><td>92.1</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00343.1.g11859.t1</td><td>ref|XP_002889176.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335017|gb|EFH65435.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>350</td><td>352</td><td>1.00E-157</td><td>100.6</td><td>83.7</td><td>89.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G78140.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:29401937-29403878 REVERSE LENGTH=355</td><td>350</td><td>355</td><td>1.00E-159</td><td>101.4</td><td>83.7</td><td>90.0</td></tr>
<tr><td>Rsa1.0_00343.1.g11860.t1</td><td>dbj|BAJ34542.1| unnamed protein product [Thellungiella halophila]</td><td>283</td><td>280</td><td>1.00E-137</td><td>98.9</td><td>88.7</td><td>92.2</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G78150.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G35780.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:29404996-29406341 FORWARD LENGTH=274</td><td>283</td><td>274</td><td>1.00E-122</td><td>96.8</td><td>82.7</td><td>90.1</td></tr>
<tr><td>Rsa1.0_00343.1.g11861.t1</td><td>gb|EOA34555.1| hypothetical protein CARUB_v10022107mg [Capsella rubella]</td><td>546</td><td>665</td><td>0</td><td>121.8</td><td>80.6</td><td>85.7</td><td>hypothetical protein CARUB_v10022107mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G78160.1 | Symbols: APUM7, PUM7 | pumilio 7 | chr1:29407900-29410184 FORWARD LENGTH=650</td><td>546</td><td>650</td><td>0</td><td>119.0</td><td>78.4</td><td>84.6</td></tr>
<tr><td>Rsa1.0_00343.1.g11862.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00343.1.g11863.t1</td><td>gb|EOA35716.1| hypothetical protein CARUB_v10020942mg [Capsella rubella]</td><td>199</td><td>214</td><td>7.00E-60</td><td>107.5</td><td>68.8</td><td>76.9</td><td>hypothetical protein CARUB_v10020942mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G78170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22250.1); Has 66 Blast hits to 66 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 66; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:29414160-29414941 FORWARD LENGTH=221</td><td>199</td><td>221</td><td>8.00E-62</td><td>111.1</td><td>68.3</td><td>76.4</td></tr>
<tr><td>Rsa1.0_00343.1.g11864.t1</td><td>gb|ABV89659.1| dehydration-responsive protein-related [Brassica rapa]</td><td>661</td><td>662</td><td>0</td><td>100.2</td><td>93.3</td><td>96.8</td><td>dehydration-responsive protein-related</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G78240.2 | Symbols: TSD2, QUA2 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:29433173-29435815 REVERSE LENGTH=684</td><td>661</td><td>684</td><td>0</td><td>103.5</td><td>85.0</td><td>92.6</td></tr>
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Rsa1.0_00344.1.g11865.t1	ref|NP_567072.1| Mitogen activated protein kinase kinase kinase-like protein [Arabidopsis thaliana] gi|30694847|ref|NP_850718.1| Mitogen activated protein kinase kinase kinase-like protein [Arabidopsis thaliana] gi|15146176|gb|AAK83572.1| AT3g58640/F14P22_230 [Arabidopsis thaliana] gi|22655030|gb|AAM98106.1| At3g58640/F14P22_230 [Arabidopsis thaliana] gi|110741986|dbj|BAE98932.1| hypothetical protein [Arabidopsis thaliana] gi|332646288|gb|AEE79809.1| Mitogen activated protein kinase kinase kinase-like protein [Arabidopsis thaliana] gi|332646289|gb|AEE79810.1| Mitogen activated protein kinase kinase kinase-like protein [Arabidopsis thaliana]	746	809	0	108.4	92.0	95.4	Mitogen activated protein kinase kinase kinase-like protein	gbpln	Arabidopsis thaliana	AT3G58640.2 | Symbols: | Mitogen activated protein kinase kinase kinase-related | chr3:21687153-21692675 REVERSE LENGTH=809	746	809	0	108.4	92.0	95.4
Rsa1.0_00344.1.g11866.t1	emb|CAB68201.1| putative protein [Arabidopsis thaliana]	293	311	1.00E-112	106.1	77.5	84.6	putative protein	gbpln	Arabidopsis thaliana	AT3G58630.1 | Symbols: | sequence-specific DNA binding transcription factors | chr3:21683928-21685771 REVERSE LENGTH=321	293	321	1.00E-114	109.6	76.5	83.6
Rsa1.0_00344.1.g11867.t1	ref|XP_002878116.1| hypothetical protein ARALYDRAFT_907139 [Arabidopsis lyrata subsp. lyrata] gi|297323954|gb|EFH54375.1| hypothetical protein ARALYDRAFT_907139 [Arabidopsis lyrata subsp. lyrata]	123	343	4.00E-27	278.9	50.4	65.0	hypothetical protein ARALYDRAFT_907139	gbpln	Arabidopsis lyrata	AT3G56890.1 | Symbols: | F-box associated ubiquitination effector family protein | chr3:21062990-21063717 REVERSE LENGTH=219	123	219	8.00E-29	178.0	48.0	58.5
Rsa1.0_00344.1.g11868.t1	gb|ABD65101.1| hypothetical protein 31.t00082 [Brassica oleracea]	248	226	1.00E-39	91.1	39.9	54.8	hypothetical protein 31.t00082	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	248	566	3.00E-22	228.2	25.8	48.4
Rsa1.0_00344.1.g11869.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	520	467	1.00E-143	89.8	49.4	60.0	hypothetical protein 31.t00031	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	520	566	1.00E-85	108.8	34.2	55.0
Rsa1.0_00344.1.g11870.t1	dbj|BAJ34494.1| unnamed protein product [Thellungiella halophila]	428	445	0	104.0	85.5	90.0	unnamed protein product	----	----	AT4G34000.2 | Symbols: ABF3, DPBF5 | abscisic acid responsive elements-binding factor 3 | chr4:16296008-16297971 FORWARD LENGTH=454	428	454	1.00E-175	106.1	80.1	86.2
Rsa1.0_00344.1.g11871.t1	ref|NP_195128.2| class I glutamine amidotransferase domain-containing protein [Arabidopsis thaliana] gi|75161395|sp|Q8VY09.1|DJ1C_ARATH RecName: Full=Protein DJ-1 homolog C; Short=AtDJ1C; Flags: Precursor gi|18377684|gb|AAL66992.1| unknown protein [Arabidopsis thaliana] gi|20465753|gb|AAM20345.1| unknown protein [Arabidopsis thaliana] gi|332660910|gb|AEE86310.1| class I glutamine amidotransferase domain-containing protein [Arabidopsis thaliana]	464	472	0	101.7	80.6	89.2	class I glutamine amidotransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT4G34020.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr4:16298553-16300897 REVERSE LENGTH=472	464	472	0	101.7	80.6	89.2
Rsa1.0_00344.1.g11872.t1	gb|ABE41833.1| caffeoyl-CoA 3-O-methyltransferase [Brassica rapa subsp. pekinensis]	258	258	1.00E-140	100.0	97.7	98.8	caffeoyl-CoA 3-O-methyltransferase	gbpln	Brassica rapa	AT4G34050.1 | Symbols: CCoAOMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:16310844-16311973 FORWARD LENGTH=259	258	259	1.00E-141	100.4	93.0	94.6
Rsa1.0_00344.1.g11873.t2	ref|XP_002869176.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315012|gb|EFH45435.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	1086	1108	0	102.0	91.8	95.2	protein binding protein	gbpln	Arabidopsis lyrata	AT4G34100.2 | Symbols: | RING/U-box superfamily protein | chr4:16330590-16334864 FORWARD LENGTH=1107	1086	1107	0	101.9	91.1	94.8
Rsa1.0_00344.1.g11874.t1	gb|EOA17339.1| hypothetical protein CARUB_v10005622mg [Capsella rubella]	113	239	3.00E-40	211.5	77.0	82.3	hypothetical protein CARUB_v10005622mg	gbpln	Capsella rubella	AT4G34120.1 | Symbols: LEJ1, CDCP1 | Cystathionine beta-synthase (CBS) family protein | chr4:16341194-16342893 FORWARD LENGTH=238	113	238	8.00E-43	210.6	76.1	83.2
Rsa1.0_00344.1.g11875.t1	ref|XP_002867135.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312971|gb|EFH43394.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	484	482	0	99.6	80.0	88.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G34131.1 | Symbols: UGT73B3 | UDP-glucosyl transferase 73B3 | chr4:16343268-16344713 REVERSE LENGTH=481	484	481	0	99.4	79.5	87.8
Rsa1.0_00344.1.g11876.t1	ref|XP_002867135.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312971|gb|EFH43394.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	483	482	0	99.8	82.2	89.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G34131.1 | Symbols: UGT73B3 | UDP-glucosyl transferase 73B3 | chr4:16343268-16344713 REVERSE LENGTH=481	483	481	0	99.6	80.5	88.4

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<tr><td>Rsa1.0_00344.1.g11877.t1</td><td>ref|XP_002867133.1| UDP-glucosyl transferase 73B1 [Arabidopsis lyrata subsp. lyrata] gi|297312969|gb|EFH43392.1| UDP-glucosyl transferase 73B1 [Arabidopsis lyrata subsp. lyrata]</td><td>491</td><td>488</td><td>0</td><td>99.4</td><td>80.2</td><td>90.8</td><td>UDP-glucosyl transferase 73B1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G34138.1 | Symbols: UGT73B1 | UDP-glucosyl transferase 73B1 | chr4:16348267-16349858 REVERSE LENGTH=488</td><td>491</td><td>488</td><td>0</td><td>99.4</td><td>79.8</td><td>90.6</td></tr>
<tr><td>Rsa1.0_00344.1.g11878.t1</td><td>ref|XP_002869171.1| hypothetical protein ARALYDRAFT_912986 [Arabidopsis lyrata subsp. lyrata] gi|297315007|gb|EFH45430.1| hypothetical protein ARALYDRAFT_912986 [Arabidopsis lyrata subsp. lyrata]</td><td>250</td><td>248</td><td>2.00E-86</td><td>99.2</td><td>66.0</td><td>70.4</td><td>hypothetical protein ARALYDRAFT_912986</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G34150.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:16355035-16356955 FORWARD LENGTH=247</td><td>250</td><td>247</td><td>1.00E-85</td><td>98.8</td><td>63.2</td><td>68.8</td></tr>
<tr><td>Rsa1.0_00344.1.g11879.t1</td><td>ref|NP_195142.1| cyclin-D3-1 [Arabidopsis thaliana] gi|59802919|sp|P42753.3|CCD31_ARATH RecName: Full=Cyclin-D3-1; AltName: Full=Cyclin-delta-3; Short=Cyclin-d3; AltName: Full=G1/S-specific cyclin-D3-1; Short=CycD3;1 gi|2911046|emb|CAA17556.1| cyclin delta-3 [Arabidopsis thaliana] gi|7270365|emb|CAB80133.1| cyclin delta-3 [Arabidopsis thaliana] gi|62320771|dbj|BAD95437.1| cyclin delta-3 [Arabidopsis thaliana] gi|332660935|gb|AEE86335.1| cyclin-D3-1 [Arabidopsis thaliana]</td><td>369</td><td>376</td><td>1.00E-161</td><td>101.9</td><td>82.4</td><td>90.5</td><td>cyclin-D3-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G34160.1 | Symbols: CYCD3;1, CYCD3 | CYCLIN D3;1 | chr4:16357903-16359304 FORWARD LENGTH=376</td><td>369</td><td>376</td><td>1.00E-164</td><td>101.9</td><td>82.4</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00344.1.g11880.t1</td><td>gb|EOA32480.1| hypothetical protein CARUB_v10015759mg [Capsella rubella]</td><td>332</td><td>350</td><td>5.00E-90</td><td>105.4</td><td>54.8</td><td>75.6</td><td>hypothetical protein CARUB_v10015759mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G17305.1 | Symbols: | CONTAINS InterPro DOMAIN/s: FBD (InterPro:IPR013596), FBD-like (InterPro:IPR006566); BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT3G62230.1); Has 81 Blast hits to 54 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 81; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:7527676-7528853 FORWARD LENGTH=271</td><td>332</td><td>271</td><td>3.00E-86</td><td>81.6</td><td>47.3</td><td>59.3</td></tr>
<tr><td>Rsa1.0_00344.1.g11881.t4</td><td>gb|EOA16621.1| hypothetical protein CARUB_v10004791mg [Capsella rubella]</td><td>502</td><td>452</td><td>0</td><td>90.0</td><td>81.9</td><td>84.7</td><td>hypothetical protein CARUB_v10004791mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G42050.1 | Symbols: | vacuolar ATP synthase subunit H family protein | chr3:14228846-14232228 REVERSE LENGTH=441</td><td>502</td><td>441</td><td>0</td><td>87.8</td><td>79.7</td><td>83.1</td></tr>
<tr><td>Rsa1.0_00344.1.g11882.t1</td><td>gb|ABV89639.1| stress enhanced protein 1 [Brassica rapa]</td><td>153</td><td>146</td><td>3.00E-60</td><td>95.4</td><td>87.6</td><td>91.5</td><td>stress enhanced protein 1</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G34190.1 | Symbols: SEP1 | stress enhanced protein 1 | chr4:16372606-16373511 REVERSE LENGTH=146</td><td>153</td><td>146</td><td>4.00E-59</td><td>95.4</td><td>81.7</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00344.1.g11883.t1</td><td>ref|XP_002867129.1| hypothetical protein ARALYDRAFT_491252 [Arabidopsis lyrata subsp. lyrata] gi|297312965|gb|EFH43388.1| hypothetical protein ARALYDRAFT_491252 [Arabidopsis lyrata subsp. lyrata]</td><td>598</td><td>603</td><td>0</td><td>100.8</td><td>92.5</td><td>95.5</td><td>hypothetical protein ARALYDRAFT_491252</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G34200.1 | Symbols: EDA9 | D-3-phosphoglycerate dehydrogenase | chr4:16374041-16376561 REVERSE LENGTH=603</td><td>598</td><td>603</td><td>0</td><td>100.8</td><td>92.0</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00344.1.g11884.t1</td><td>gb|AAM65927.1| unknown [Arabidopsis thaliana]</td><td>260</td><td>260</td><td>1.00E-129</td><td>100.0</td><td>88.8</td><td>92.3</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G34215.2 | Symbols: | Domain of unknown function (DUF303) | chr4:16380203-16381192 REVERSE LENGTH=260</td><td>260</td><td>260</td><td>1.00E-130</td><td>100.0</td><td>88.1</td><td>91.5</td></tr>
<tr><td>Rsa1.0_00344.1.g11885.t1</td><td>ref|NP_567961.1| receptor protein kinase-like protein [Arabidopsis thaliana] gi|75165202|sp|Q94C77.1|RPKL_ARATH RecName: Full=Receptor protein kinase-like protein At4g34220; Flags: Precursor gi|14334872|gb|AAK59614.1| putative receptor protein kinase [Arabidopsis thaliana] gi|21281267|gb|AAM44951.1| putative receptor protein kinase [Arabidopsis thaliana] gi|224589647|gb|ACN59356.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332660943|gb|AEE86343.1| receptor protein kinase-like protein [Arabidopsis thaliana]</td><td>758</td><td>757</td><td>0</td><td>99.9</td><td>83.8</td><td>89.4</td><td>receptor protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G34220.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:16381653-16384054 REVERSE LENGTH=757</td><td>758</td><td>757</td><td>0</td><td>99.9</td><td>83.8</td><td>89.4</td></tr>
<tr><td>Rsa1.0_00344.1.g11886.t1</td><td>gb|EOA24678.1| hypothetical protein CARUB_v10017951mg [Capsella rubella]</td><td>241</td><td>239</td><td>1.00E-108</td><td>99.2</td><td>81.3</td><td>93.4</td><td>hypothetical protein CARUB_v10017951mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G57230.1 | Symbols: AGL16 | AGAMOUS-like 16 | chr3:21177710-21180671 FORWARD LENGTH=240</td><td>241</td><td>240</td><td>1.00E-109</td><td>99.6</td><td>80.5</td><td>92.1</td></tr>
</table>

Rsa1.0_00344.1.g11887.t1	ref|NP_195149.1| cinnamyl alcohol dehydrogenase 5 [Arabidopsis thaliana] gi|13626131|sp|O49482.1|CADH5_ARATH RecName: Full=Cinnamyl alcohol dehydrogenase 5; Short=AtCAD5; AltName: Full=Cinnamyl alcohol dehydrogenase D gi|134104089|pdb|2CF5|A Chain A, Crystal Structures Of The Arabidopsis Cinnamyl Alcohol Dehydrogenases, Atcad5 gi|134104090|pdb|2CF6|A Chain A, Crystal Structures Of The Arabidopsis Cinnamyl Alcohol Dehydrogenases Atcad5 gi|2911039|emb|CAA17549.1| cinnamyl alcohol dehydrogenase-like protein [Arabidopsis thaliana] gi|7270373|emb|CAB80140.1| cinnamyl alcohol dehydrogenase-like protein [Arabidopsis thaliana] gi|14334456|gb|AAK59426.1| putative cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|21280925|gb|AAM44967.1| putative cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|31880043|gb|AAP59435.1| cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|332660944|gb|AEE86344.1| cinnamyl alcohol dehydrogenase 5 [Arabidopsis thaliana]	357	357	1.00E-174	100.0	94.1	98.6	cinnamyl alcohol dehydrogenase 5	gbpln	Arabidopsis thaliana	AT4G34230.1 | Symbols: CAD5, ATCAD5, CAD-5 | cinnamyl alcohol dehydrogenase 5 | chr4:16386898-16388666 REVERSE LENGTH=357	357	357	1.00E-176	100.0	94.1	98.6
Rsa1.0_00344.1.g11888.t1	gb|ABC41273.1| putative aldehyde dehydrogenase [Brassica rapa]	551	555	0	100.7	93.1	96.6	putative aldehyde dehydrogenase	gbpln	Brassica rapa	AT4G34240.1 | Symbols: ALDH3I1, ALDH3 | aldehyde dehydrogenase 3I1 | chr4:16389801-16392633 FORWARD LENGTH=550	551	550	0	99.8	85.1	92.2
Rsa1.0_00344.1.g11889.t2	ref|XP_002869162.1| hypothetical protein ARALYDRAFT_491244 [Arabidopsis lyrata subsp. lyrata] gi|297314998|gb|EFH45421.1| hypothetical protein ARALYDRAFT_491244 [Arabidopsis lyrata subsp. lyrata]	476	493	0	103.6	82.4	91.0	hypothetical protein ARALYDRAFT_491244	gbpln	Arabidopsis lyrata	AT4G34250.1 | Symbols: KCS16 | 3-ketoacyl-CoA synthase 16 | chr4:16394749-16396230 FORWARD LENGTH=493	476	493	0	103.6	81.3	90.5
Rsa1.0_00345.1.g11890.t1	ref|XP_002867898.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297313734|gb|EFH44157.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	211	209	3.00E-70	99.1	72.0	79.1	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT4G20000.1 | Symbols: | VQ motif-containing protein | chr4:10838367-10838993 FORWARD LENGTH=208	211	208	6.00E-63	98.6	67.3	76.3
Rsa1.0_00345.1.g11891.t1	gb|AAG03119.1|AC004133_13 F5A9.24 [Arabidopsis thaliana]	1226	1254	0	102.3	34.6	42.3	F5A9.24	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1226	626	2.00E-31	51.1	9.2	14.4
Rsa1.0_00345.1.g11892.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00345.1.g11893.t1	gb|EOA17660.1| hypothetical protein CARUB_v10006027mg [Capsella rubella]	115	125	5.00E-41	108.7	76.5	80.9	hypothetical protein CARUB_v10006027mg	gbpln	Capsella rubella	AT4G19980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: root, pedicel; EXPRESSED DURING: 4 anthesis; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10828153-10828536 REVERSE LENGTH=127	115	127	3.00E-39	110.4	73.0	80.9
Rsa1.0_00345.1.g11894.t1	gb|EOA16028.1| hypothetical protein CARUB_v10004157mg [Capsella rubella]	800	812	0	101.5	90.5	94.4	hypothetical protein CARUB_v10004157mg	gbpln	Capsella rubella	AT4G19960.2 | Symbols: KUP9 | K+ uptake permease 9 | chr4:10813807-10816997 FORWARD LENGTH=807	800	807	0	100.9	90.6	94.6
Rsa1.0_00345.1.g11895.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00345.1.g11896.t1	gb|AAB61111.1| Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb|U12626) [Arabidopsis thaliana]	1364	1315	0	96.4	44.1	52.6	Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb|U12626)	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1364	1262	0	92.5	29.8	34.9
Rsa1.0_00345.1.g11897.t1	ref|XP_002869958.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata] gi|297315794|gb|EFH46217.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata]	410	428	1.00E-125	104.4	58.0	73.2	hypothetical protein ARALYDRAFT_914664	gbpln	Arabidopsis lyrata	AT4G19930.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:10803558-10804853 FORWARD LENGTH=431	410	431	1.00E-121	105.1	58.5	72.2
Rsa1.0_00345.1.g11898.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00345.1.g11899.t2	ref|NP_192163.1| cysteine/histidine−rich C1 domain−containing protein [Arabidopsis thaliana] gi|3892060|gb|AAC78273.1| hypothetical protein [Arabidopsis thaliana] gi|7269014|emb|CAB80747.1| putative protein [Arabidopsis thaliana] gi|110737893|dbj|BAF00884.1| hypothetical protein [Arabidopsis thaliana] gi|332656785|gb|AEE82185.1| cysteine/histidine−rich C1 domain−containing protein [Arabidopsis thaliana]	633	822	0	129.9	57.2	70.1	cysteine/histidine−rich C1 domain−containing protein	gbpln	Arabidopsis thaliana	AT4G02540.1 | Symbols: | Cysteine/Histidine−rich C1 domain family protein | chr4:1117202−1119670 FORWARD LENGTH=822	633	822	0	129.9	57.2	70.1
Rsa1.0_00345.1.g11900.t1	ref|NP_193726.1| F−box/kelch−repeat protein [Arabidopsis thaliana] gi|75219621|sp|O49420.1|FBK86_ARATH RecName: Full=F−box/kelch−repeat protein At4g19930 gi|2827647|emb|CAA16601.1| putative protein [Arabidopsis thaliana] gi|7268787|emb|CAB78993.1| putative protein [Arabidopsis thaliana] gi|332658848|gb|AEE84248.1| F−box/kelch−repeat protein [Arabidopsis thaliana]	167	431	2.00E−30	258.1	42.5	54.5	F−box/kelch−repeat protein	gbpln	Arabidopsis thaliana	AT4G19930.1 | Symbols: | F−box and associated interaction domains−containing protein | chr4:10803558−10804853 FORWARD LENGTH=431	167	431	6.00E−33	258.1	42.5	54.5
Rsa1.0_00345.1.g11901.t8	ref|XP_002867916.1| kelch repeat−containing F−box family protein [Arabidopsis lyrata subsp. lyrata] gi|297313752|gb|EFH44175.1| kelch repeat−containing F−box family protein [Arabidopsis lyrata subsp. lyrata]	396	397	1.00E−100	100.3	54.3	68.4	kelch repeat−containing F−box family protein	gbpln	Arabidopsis lyrata	AT4G19870.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:10783054−10784256 REVERSE LENGTH=400	396	400	1.00E−102	101.0	54.8	67.4
Rsa1.0_00345.1.g11902.t1	ref|XP_002867916.1| kelch repeat−containing F−box family protein [Arabidopsis lyrata subsp. lyrata] gi|297313752|gb|EFH44175.1| kelch repeat−containing F−box family protein [Arabidopsis lyrata subsp. lyrata]	387	397	1.00E−101	102.6	55.8	68.7	kelch repeat−containing F−box family protein	gbpln	Arabidopsis lyrata	AT4G19870.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:10783054−10784256 REVERSE LENGTH=400	387	400	3.00E−97	103.4	52.2	65.6
Rsa1.0_00345.1.g11903.t9	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	3871	1274	0	32.9	13.6	17.9	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G19840.1 | Symbols: ATPP2−A1, ATPP2A−1, PP2−A1 | phloem protein 2−A1 | chr4:10774336−10775701 FORWARD LENGTH=246	3871	246	6.00E−80	6.4	3.8	4.4
Rsa1.0_00345.1.g11904.t1	gb|EOA15606.1| hypothetical protein CARUB_v10005678mg [Capsella rubella]	216	225	3.00E−95	104.2	85.6	89.8	hypothetical protein CARUB_v10005678mg	gbpln	Capsella rubella	AT4G19830.1 | Symbols: | FKBP−like peptidyl−prolyl cis−trans isomerase family protein | chr4:10772579−10773933 REVERSE LENGTH=229	216	229	7.00E−90	106.0	84.3	91.7
Rsa1.0_00345.1.g11905.t3	gb|EOA16822.1| hypothetical protein CARUB_v10005044mg [Capsella rubella]	326	380	1.00E−157	116.6	83.4	90.8	hypothetical protein CARUB_v10005044mg	gbpln	Capsella rubella	AT4G19810.1 | Symbols: | Glycosyl hydrolase family protein with chitinase insertion domain | chr4:10764151−10765753 REVERSE LENGTH=379	326	379	1.00E−157	116.3	83.4	89.6
Rsa1.0_00346.1.g11906.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	302	411	1.00E−79	136.1	58.9	71.2	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT2G38590.1 | Symbols: | F−box and associated interaction domains−containing protein | chr2:16142897−16144171 FORWARD LENGTH=424	302	424	6.00E−68	140.4	54.3	69.5
Rsa1.0_00346.1.g11907.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	964	411	5.00E−91	42.6	19.3	25.0	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT2G38590.1 | Symbols: | F−box and associated interaction domains−containing protein | chr2:16142897−16144171 FORWARD LENGTH=424	964	424	7.00E−84	44.0	18.8	24.7
Rsa1.0_00346.1.g11908.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00346.1.g11909.t1	gb|EOA37442.1| hypothetical protein CARUB_v10011523mg [Capsella rubella]	363	388	1.00E−171	106.9	78.8	88.2	hypothetical protein CARUB_v10011523mg	gbpln	Capsella rubella	AT1G23320.1 | Symbols: TAR1 | tryptophan aminotransferase related 1 | chr1:8273423−8275350 REVERSE LENGTH=388	363	388	1.00E−172	106.9	79.3	87.6
Rsa1.0_00346.1.g11910.t1	gb|ACG60684.1| maize transposon MuDR−like protein [Brassica oleracea var. alboglabra]	198	622	6.00E−59	314.1	57.1	73.2	maize transposon MuDR−like protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00346.1.g11911.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	315	411	6.00E−82	130.5	54.6	69.5	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT3G25090.1 | Symbols: | F−box associated ubiquitination effector family protein | chr3:9140039−9141094 REVERSE LENGTH=325	315	325	6.00E−80	103.2	52.4	65.4
Rsa1.0_00346.1.g11912.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_00346.1.g11913.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	451	411	5.00E−83	91.1	40.8	53.0	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT2G38590.1 | Symbols: | F−box and associated interaction domains−containing protein | chr2:16142897−16144171 FORWARD LENGTH=424	451	424	1.00E−77	94.0	39.2	52.1
Rsa1.0_00346.1.g11914.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	404	411	1.00E−106	101.7	53.5	68.3	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT4G33290.1 | Symbols: | F−box and associated interaction domains−containing protein | chr4:16049573−16050865 FORWARD LENGTH=430	404	430	1.00E−106	106.4	53.2	64.9
Rsa1.0_00346.1.g11915.t1	ref|XP_002870633.1| hypothetical protein ARALYDRAFT_916057 [Arabidopsis lyrata subsp. lyrata] gi|297316469|gb|EFH46892.1| hypothetical protein ARALYDRAFT_916057 [Arabidopsis lyrata subsp. lyrata]	233	351	6.00E−41	150.6	49.4	61.4	hypothetical protein ARALYDRAFT_916057	gbpln	Arabidopsis lyrata	AT4G33290.1 | Symbols: | F−box and associated interaction domains−containing protein | chr4:16049573−16050865 FORWARD LENGTH=430	233	430	8.00E−37	184.5	48.5	63.9
Rsa1.0_00346.1.g11916.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	429	411	1.00E−108	95.8	50.3	67.6	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT4G33290.1 | Symbols: | F−box and associated interaction domains−containing protein | chr4:16049573−16050865 FORWARD LENGTH=430	429	430	1.00E−108	100.2	51.3	66.4
Rsa1.0_00346.1.g11917.t1	ref|XP_002883382.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329222|gb|EFH59641.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	428	403	3.00E−90	94.2	47.7	58.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G33290.1 | Symbols: | F−box and associated interaction domains−containing protein | chr4:16049573−16050865 FORWARD LENGTH=430	428	430	7.00E−86	100.5	45.8	57.9
Rsa1.0_00346.1.g11918.t1	gb|AFU75878.1| lipase [Brassica napus]	473	468	0	98.9	94.7	96.8	lipase	gbpln	Brassica napus	AT1G23330.1 | Symbols: | alpha/beta−Hydrolases superfamily protein | chr1:8279874−8281891 REVERSE LENGTH=471	473	471	0	99.6	89.9	94.9
Rsa1.0_00346.1.g11919.t1	gb|EOA37605.1| hypothetical protein CARUB_v10011971mg [Capsella rubella]	176	166	5.00E−50	94.3	57.4	64.8	hypothetical protein CARUB_v10011971mg	gbpln	Capsella rubella	AT1G23350.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:8293696−8294175 REVERSE LENGTH=159	176	159	4.00E−52	90.3	57.4	65.3
Rsa1.0_00346.1.g11920.t1	ref|XP_002893283.1| hypothetical protein ARALYDRAFT_472599 [Arabidopsis lyrata subsp. lyrata] gi|297339125|gb|EFH69542.1| hypothetical protein ARALYDRAFT_472599 [Arabidopsis lyrata subsp. lyrata]	138	329	2.00E−63	238.4	89.9	94.2	hypothetical protein ARALYDRAFT_472599	gbpln	Arabidopsis lyrata	AT1G23380.1 | Symbols: KNAT6, KNAT6L, KNAT6S | KNOTTED1−like homeobox gene 6 | chr1:8297499−8302492 REVERSE LENGTH=327	138	327	7.00E−66	237.0	87.7	93.5
Rsa1.0_00346.1.g11921.t3	ref|NP_173752.3| homeobox protein knotted−1−like 6 [Arabidopsis thaliana] gi|332192259|gb|AEE30380.1| homeobox protein knotted−1−like 6 [Arabidopsis thaliana]	161	329	2.00E−49	204.3	62.1	64.6	homeobox protein knotted−1−like 6	gbpln	Arabidopsis thaliana	AT1G23380.2 | Symbols: KNAT6, KNAT6L, KNAT6S | KNOTTED1−like homeobox gene 6 | chr1:8297499−8302492 REVERSE LENGTH=329	161	329	8.00E−52	204.3	62.1	64.6
Rsa1.0_00346.1.g11922.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#

Rsa1.0_00346.1.g11923.t1	ref|NP_564193.1| Kelch repeat-containing F-box protein [Arabidopsis thaliana] gi|75173823|sp|Q9LDE3.1|FBK9_ARATH RecName: Full=F-box/kelch-repeat protein At1g23390 gi|8778589|gb|AAF79597.1|AC007945_17 F28C11.3 [Arabidopsis thaliana] gi|9295700|gb|AAF87006.1|AC005292_15 F26F24.26 [Arabidopsis thaliana] gi|21539423|gb|AAM53264.1| putative knotted-like homeobox protein [Arabidopsis thaliana] gi|23197636|gb|AAN15345.1| putative knotted-like homeobox protein [Arabidopsis thaliana] gi|237873580|emb|CAX36488.1| F-box/Kelch repeat-containing F-box family protein [Arabidopsis thaliana] gi|237873584|emb|CAX36490.1| F-box/Kelch repeat-containing F-box family protein [Arabidopsis thaliana] gi|237873588|emb|CAX36492.1| F-box/Kelch repeat-containing F-box family protein [Arabidopsis thaliana] gi|237873596|emb|CAX36496.1| F-box/Kelch repeat-containing F-box family protein [Arabidopsis thaliana] gi|237873598|emb|CAX36497.1| F-box/Kelch repeat-containing F-box family protein [Arabidopsis thaliana] gi|237873604|emb|CAX36500.1| F-box/Kelch repeat-containing F-box family protein [Arabidopsis thaliana]	411	394	1.00E-160	95.9	70.6	76.9	Kelch repeat-containing F-box protein	gbpln	Arabidopsis thaliana	AT1G23390.1 | Symbols: | Kelch repeat-containing F-box family protein | chr1:8309449-8310633 REVERSE LENGTH=394	411	394	1.00E-163	95.9	70.6	76.9
Rsa1.0_00347.1.g11924.t2	gb|EOA29689.1| hypothetical protein CARUB_v10016211mg [Capsella rubella]	116	248	2.00E-38	213.8	71.6	87.1	hypothetical protein CARUB_v10016211mg	gbpln	Capsella rubella	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	116	769	5.00E-36	662.9	65.5	81.9
Rsa1.0_00347.1.g11925.t1	dbj|BAJ34292.1| unnamed protein product [Thellungiella halophila]	461	461	0	100.0	93.1	95.9	unnamed protein product	----	----	AT3G51860.1 | Symbols: CAX3, ATHCX1, CAX1-LIKE, ATCAX3 | cation exchanger 3 | chr3:19239458-19242519 FORWARD LENGTH=459	461	459	0	99.6	88.5	93.7
Rsa1.0_00347.1.g11926.t1	dbj|BAJ34524.1| unnamed protein product [Thellungiella halophila]	657	658	0	100.2	92.2	96.0	unnamed protein product	----	----	AT3G51895.1 | Symbols: SULTR3;1, AST12 | sulfate transporter 3;1 | chr3:19251503-19255677 REVERSE LENGTH=658	657	658	0	100.2	90.4	95.3
Rsa1.0_00347.1.g11927.t1	ref|NP_192687.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|7267644|emb|CAB78072.1| putative proteins [Arabidopsis thaliana] gi|332657356|gb|AEE82756.1| RNase H domain-containing protein [Arabidopsis thaliana]	140	170	3.00E-19	121.4	40.0	57.1	RNase H domain-containing protein	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	140	170	9.00E-22	121.4	40.0	57.1
Rsa1.0_00347.1.g11928.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00347.1.g11929.t1	ref|XP_002876110.1| AT-HSFA7A [Arabidopsis lyrata subsp. lyrata] gi|297321948|gb|EFH52369.1| AT-HSFA7A [Arabidopsis lyrata subsp. lyrata]	268	277	1.00E-115	103.4	83.2	90.7	AT-HSFA7A	gbpln	Arabidopsis lyrata	AT3G51910.1 | Symbols: AT-HSFA7A, HSFA7A | heat shock transcription factor A7A | chr3:19265294-19266619 FORWARD LENGTH=272	268	272	1.00E-115	101.5	80.2	88.4
Rsa1.0_00347.1.g11930.t1	ref|XP_002876110.1| AT-HSFA7A [Arabidopsis lyrata subsp. lyrata] gi|297321948|gb|EFH52369.1| AT-HSFA7A [Arabidopsis lyrata subsp. lyrata]	360	277	1.00E-105	76.9	57.5	64.2	AT-HSFA7A	gbpln	Arabidopsis lyrata	AT3G51910.1 | Symbols: AT-HSFA7A, HSFA7A | heat shock transcription factor A7A | chr3:19265294-19266619 FORWARD LENGTH=272	360	272	1.00E-106	75.6	55.6	62.2
Rsa1.0_00347.1.g11931.t1	gb|EOA25516.1| hypothetical protein CARUB_v10018860mg [Capsella rubella]	939	538	0	57.3	38.6	40.8	hypothetical protein CARUB_v10018860mg	gbpln	Capsella rubella	AT3G51950.2 | Symbols: | Zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein | chr3:19278244-19280407 REVERSE LENGTH=540	939	540	0	57.5	38.8	40.9
Rsa1.0_00347.1.g11932.t1	ref|NP_190768.1| carboxypeptidase D [Arabidopsis thaliana] gi|75337703|sp|Q9SV04.1|SCP36_ARATH RecName: Full=Serine carboxypeptidase-like 36; Flags: Precursor gi|4678929|emb|CAB41320.1| serine-type carboxypeptidase like protein [Arabidopsis thaliana] gi|67633688|gb|AAY78768.1| serine carboxypeptidase S10 family protein [Arabidopsis thaliana] gi|332645352|gb|AEE78873.1| serine carboxypeptidase-like 36 [Arabidopsis thaliana]	465	482	1.00E-161	103.7	61.1	75.9	carboxypeptidase D	gbpln	Arabidopsis thaliana	AT3G52000.1 | Symbols: scpl36 | serine carboxypeptidase-like 36 | chr3:19293071-19294702 FORWARD LENGTH=482	465	482	1.00E-163	103.7	61.1	75.9

Rsa1.0_00347.1.g11933.t1	gb|EOA25727.1| hypothetical protein CARUB_v10019088mg [Capsella rubella]	418	431	0	103.1	85.9	92.1	hypothetical protein CARUB_v10019088mg	gbpln	Capsella rubella	AT3G52030.2 | Symbols: | F-box family protein with WD40/YVTN repeat doamin | chr3:19301872-19304227 FORWARD LENGTH=433	418	433	0	103.6	86.1	92.1
Rsa1.0_00347.1.g11934.t7	ref|NP_190773.2| 5'-3' exonuclease-like protein [Arabidopsis thaliana] gi|145362483|ref|NP_974414.2| 5'-3' exonuclease-like protein [Arabidopsis thaliana] gi|109946597|gb|ABG48477.1| At3g52050 [Arabidopsis thaliana] gi|332645358|gb|AEE78879.1| 5'-3' exonuclease-like protein [Arabidopsis thaliana] gi|332645359|gb|AEE78880.1| 5'-3' exonuclease-like protein [Arabidopsis thaliana]	420	425	1.00E-158	101.2	72.6	78.8	5'-3' exonuclease-like protein	gbpln	Arabidopsis thaliana	AT3G52050.1 | Symbols: | 5'-3' exonuclease family protein | chr3:19305228-19309398 FORWARD LENGTH=425	420	425	1.00E-161	101.2	72.6	78.8
Rsa1.0_00347.1.g11935.t1	ref|XP_002885456.1| hypothetical protein ARALYDRAFT_898613 [Arabidopsis lyrata subsp. lyrata] gi|297331296|gb|EFH61715.1| hypothetical protein ARALYDRAFT_898613 [Arabidopsis lyrata subsp. lyrata]	365	365	1.00E-177	100.0	84.9	90.4	hypothetical protein ARALYDRAFT_898613	gbpln	Arabidopsis lyrata	AT3G21640.1 | Symbols: TWD1, UCU2, FKBP42, ATFKBP42 | FKBP-type peptidyl-prolyl cis-trans isomerase family protein | chr3:7619025-7621097 REVERSE LENGTH=365	365	365	1.00E-178	100.0	84.9	91.2
Rsa1.0_00347.1.g11936.t2	ref|XP_002876124.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297321962|gb|EFH52383.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata]	624	678	0	108.7	77.4	84.8	PHD finger family protein	gbpln	Arabidopsis lyrata	AT3G52100.1 | Symbols: | RING/FYVE/PHD-type zinc finger family protein | chr3:19319343-19322773 FORWARD LENGTH=696	624	696	0	111.5	76.9	85.4
Rsa1.0_00347.1.g11937.t1	emb|CAB41330.1| putative protein [Arabidopsis thaliana]	74	763	1.00E-29	1031.1	79.7	85.1	putative protein	gbpln	Arabidopsis thaliana	AT3G52105.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:19323394-19323606 FORWARD LENGTH=70	74	70	1.00E-28	94.6	79.7	85.1
Rsa1.0_00347.1.g11938.t1	ref|NP_190781.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|4678942|emb|CAB41333.1| 5B protein like protein [Arabidopsis thaliana] gi|44917507|gb|AAS49078.1| At3g52130 [Arabidopsis thaliana] gi|62320556|dbj|BAD95162.1| 5B protein like protein [Arabidopsis thaliana] gi|332645377|gb|AEE78898.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	125	125	7.00E-45	100.0	85.6	89.6	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT3G52130.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:19332081-19332458 REVERSE LENGTH=125	125	125	1.00E-47	100.0	85.6	89.6
Rsa1.0_00347.1.g11939.t1	ref|XP_002876128.1| hypothetical protein ARALYDRAFT_348313 [Arabidopsis lyrata subsp. lyrata] gi|297321966|gb|EFH52387.1| hypothetical protein ARALYDRAFT_348313 [Arabidopsis lyrata subsp. lyrata]	218	467	1.00E-98	214.2	82.1	91.3	hypothetical protein ARALYDRAFT_348313	gbpln	Arabidopsis lyrata	AT3G52155.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:19343740-19344722 FORWARD LENGTH=218	218	218	7.00E-99	100.0	81.2	91.3
Rsa1.0_00347.1.g11940.t1	ref|XP_002877845.1| beta-ketoacyl-CoA synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297323683|gb|EFH54104.1| beta-ketoacyl-CoA synthase family protein [Arabidopsis lyrata subsp. lyrata]	448	452	0	100.9	87.1	93.3	beta-ketoacyl-CoA synthase family protein	gbpln	Arabidopsis lyrata	AT3G52160.1 | Symbols: KCS15 | 3-ketoacyl-CoA synthase 15 | chr3:19345069-19346591 REVERSE LENGTH=451	448	451	0	100.7	86.8	93.3
Rsa1.0_00347.1.g11941.t4	ref|NP_974416.1| RNA pseudourine synthase 5 [Arabidopsis thaliana] gi|229891781|sp|Q5M721.2|PUS5_ARATH RecName: Full=RNA pseudourine synthase 5; AltName: Full=RNA pseudouridylate synthase 5; AltName: Full=RNA-uridine isomerase 5 gi|332645400|gb|AEE78921.1| RNA pseudourine synthase 5 [Arabidopsis thaliana]	682	369	1.00E-158	54.1	41.1	45.3	RNA pseudourine synthase 5	gbpln	Arabidopsis thaliana	AT3G52260.2 | Symbols: | Pseudouridine synthase family protein | chr3:19383452-19386440 REVERSE LENGTH=369	682	369	1.00E-160	54.1	41.1	45.3
Rsa1.0_00347.1.g11942.t1	gb|EOA25462.1| hypothetical protein CARUB_v10018800mg [Capsella rubella]	269	258	2.00E-67	95.9	56.1	62.5	hypothetical protein CARUB_v10018800mg	gbpln	Capsella rubella	AT3G52270.1 | Symbols: | Transcription initiation factor IIF, beta subunit | chr3:19387180-19388902 REVERSE LENGTH=269	269	269	1.00E-63	100.0	53.5	61.7

Rsa1.0_00347.1.g11943.t1	gb|EOA18887.1| hypothetical protein CARUB_v10007517mg, partial [Capsella rubella]	336	533	1.00E-150	158.6	76.5	88.7	hypothetical protein CARUB_v10007517mg, partial	gbpln	Capsella rubella	AT4G38160.2 | Symbols: pde191 | Mitochondrial transcription termination factor family protein | chr4:17902412-17903784 FORWARD LENGTH=363	336	363	1.00E-152	108.0	76.2	88.1
Rsa1.0_00347.1.g11944.t2	gb|EOA25462.1| hypothetical protein CARUB_v10018800mg [Capsella rubella]	110	258	4.00E-15	234.5	48.2	57.3	hypothetical protein CARUB_v10018800mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00347.1.g11945.t1	ref|XP_002877853.1| hypothetical protein ARALYDRAFT_485593 [Arabidopsis lyrata subsp. lyrata] gi|297323691|gb|EFH54112.1| hypothetical protein ARALYDRAFT_485593 [Arabidopsis lyrata subsp. lyrata]	364	371	1.00E-145	101.9	78.8	85.4	hypothetical protein ARALYDRAFT_485593	gbpln	Arabidopsis lyrata	AT3G52280.1 | Symbols: GTE6 | general transcription factor group E6 | chr3:19389103-19391289 REVERSE LENGTH=369	364	369	1.00E-142	101.4	78.6	84.9
Rsa1.0_00347.1.g11946.t1	gb|EOA24848.1| hypothetical protein CARUB_v10018138mg [Capsella rubella]	213	168	2.00E-83	78.9	76.1	77.9	hypothetical protein CARUB_v10018138mg	gbpln	Capsella rubella	AT3G52300.1 | Symbols: ATPQ | ATP synthase D chain, mitochondrial | chr3:19396689-19398119 FORWARD LENGTH=168	213	168	9.00E-84	78.9	74.6	77.0
Rsa1.0_00347.1.g11947.t1	ref|XP_002876141.1| RNA-binding protein cp33 [Arabidopsis lyrata subsp. lyrata] gi|297321979|gb|EFH52400.1| RNA-binding protein cp33 [Arabidopsis lyrata subsp. lyrata]	323	330	1.00E-130	102.2	77.1	81.1	RNA-binding protein cp33	gbpln	Arabidopsis lyrata	AT3G52380.1 | Symbols: CP33, PDE322 | chloroplast RNA-binding protein 33 | chr3:19421619-19422855 FORWARD LENGTH=329	323	329	1.00E-131	101.9	79.9	86.7
Rsa1.0_00348.1.g11948.t1	ref|XP_002879225.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297325064|gb|EFH55484.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	181	373	5.00E-48	206.1	57.5	61.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G29660.1 | Symbols: | zinc finger (C2H2 type) family protein | chr2:12679346-12680467 FORWARD LENGTH=373	181	373	1.00E-42	206.1	54.7	58.6
Rsa1.0_00348.1.g11949.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	85	467	2.00E-12	549.4	38.8	43.5	hypothetical protein 31.t00031	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00348.1.g11950.t1	ref|NP_565685.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana] gi|14030739|gb|AAK53044.1|AF375460_1 At2g29670/T27A16.23 [Arabidopsis thaliana] gi|18377765|gb|AAL67032.1| unknown protein [Arabidopsis thaliana] gi|20197389|gb|AAC35237.2| expressed protein [Arabidopsis thaliana] gi|20465643|gb|AAM20290.1| unknown protein [Arabidopsis thaliana] gi|23308477|gb|AAN18208.1| At2g29670/T27A16.23 [Arabidopsis thaliana] gi|330253196|gb|AEC08290.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	479	536	1.00E-178	111.9	77.9	86.2	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G29670.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:12682309-12684745 REVERSE LENGTH=536	479	536	1.00E-180	111.9	77.9	86.2
Rsa1.0_00348.1.g11951.t3	ref|XP_002879226.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325065|gb|EFH55485.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	634	493	0	77.8	64.5	68.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G29680.2 | Symbols: CDC6, ATCDC6 | cell division control 6 | chr2:12689586-12692854 FORWARD LENGTH=508	634	508	0	80.1	64.8	69.2
Rsa1.0_00348.1.g11952.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00348.1.g11953.t1	ref|XP_002879231.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325070|gb|EFH55490.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	466	475	0	101.9	80.5	90.3	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT2G29730.1 | Symbols: UGT71D1 | UDP-glucosyl transferase 71D1 | chr2:12703652-12705055 FORWARD LENGTH=467	466	467	0	100.2	79.4	89.5
Rsa1.0_00348.1.g11954.t1	ref|XP_002879232.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325071|gb|EFH55491.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	480	474	0	98.8	72.3	83.5	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT2G29740.1 | Symbols: UGT71C2 | UDP-glucosyl transferase 71C2 | chr2:12706747-12708171 FORWARD LENGTH=474	480	474	0	98.8	71.7	83.1

Rsa1.0_00348.1.g11955.t1	ref|NP_180535.1| UDP-glucosyl transferase 71C2 [Arabidopsis thaliana] gi|75279075|sp|O82382.1|U71C2_ARATH RecName: Full=UDP-glycosyltransferase 71C2 gi|3582341|gb|AAC35238.1| putative flavonol 3-O-glucosyltransferase [Arabidopsis thaliana] gi|28393510|gb|AAO42176.1| putative flavonol 3-O-glucosyltransferase [Arabidopsis thaliana] gi|28973169|gb|AAO63909.1| putative flavonol 3-O-glucosyltransferase [Arabidopsis thaliana] gi|330253205|gb|AEC08299.1| UDP-glucosyl transferase 71C2 [Arabidopsis thaliana]	424	474	1.00E-161	111.8	69.3	81.4	UDP-glucosyl transferase 71C2	gbpln	Arabidopsis thaliana	AT2G29740.1 | Symbols: UGT71C2 | UDP-glucosyl transferase 71C2 | chr2:12706747-12708171 FORWARD LENGTH=474	424	474	1.00E-164	111.8	69.3	81.4
Rsa1.0_00348.1.g11956.t1	ref|NP_195670.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75210846|sp|Q9SV98.1|FK103_ARATH RecName: Full=Putative F-box/kelch-repeat protein At4g39600 gi|5042176|emb|CAB44695.1| putative protein [Arabidopsis thaliana] gi|7270944|emb|CAB80623.1| putative protein [Arabidopsis thaliana] gi|332661692|gb|AEE87092.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	386	367	2.00E-88	95.1	47.7	64.2	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT4G39600.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18389436-18390539 REVERSE LENGTH=367	386	367	6.00E-91	95.1	47.7	64.2
Rsa1.0_00348.1.g11957.t1	gb|EOA26647.1| hypothetical protein CARUB_v10022711mg [Capsella rubella]	741	739	0	99.7	90.8	95.5	hypothetical protein CARUB_v10022711mg	gbpln	Capsella rubella	AT2G29760.1 | Symbols: OTP81 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:12712884-12715100 FORWARD LENGTH=738	741	738	0	99.6	90.0	95.1
Rsa1.0_00348.1.g11958.t1	ref|NP_029567.1| villin-1 [Arabidopsis thaliana] gi|147744599|sp|O81643.2|VILI1_ARATH RecName: Full=Villin-1 gi|20198093|gb|AAD23629.2| putative villin [Arabidopsis thaliana] gi|330253221|gb|AEC08315.1| villin-1 [Arabidopsis thaliana]	914	909	0	99.5	81.2	89.6	villin-1	gbpln	Arabidopsis thaliana	AT2G29890.1 | Symbols: VLN1, ATVLN1 | villin-like 1 | chr2:12744597-12749474 FORWARD LENGTH=909	914	909	0	99.5	81.2	89.6
Rsa1.0_00348.1.g11959.t1	ref|XP_002879239.1| presenilin family protein [Arabidopsis lyrata subsp. lyrata] gi|297325078|gb|EFH55498.1| presenilin family protein [Arabidopsis lyrata subsp. lyrata]	396	399	1.00E-170	100.8	82.8	89.6	presenilin family protein	gbpln	Arabidopsis lyrata	AT2G29900.1 | Symbols: PS2 | Presenilin-2 | chr2:12749837-12751030 FORWARD LENGTH=397	396	397	1.00E-164	100.3	82.6	88.6
Rsa1.0_00348.1.g11960.t1	ref|NP_180554.2| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|42570979|ref|NP_973563.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75272176|sp|Q84RK6.1|FBL36_ARATH RecName: Full=F-box/LRR-repeat protein At2g29930 gi|29649041|gb|AAO86840.1| hypothetical protein [Arabidopsis thaliana] gi|55740577|gb|AAV63881.1| hypothetical protein At2g29930 [Arabidopsis thaliana] gi|330253229|gb|AEC08323.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|330253230|gb|AEC08324.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	518	459	1.00E-139	88.6	54.8	65.8	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT2G29930.3 | Symbols: | F-box/RNI-like superfamily protein | chr2:12756457-12758087 REVERSE LENGTH=459	518	459	1.00E-141	88.6	54.8	65.8
Rsa1.0_00348.1.g11961.t1	ref|XP_002881077.1| cyclophilin [Arabidopsis lyrata subsp. lyrata] gi|297326916|gb|EFH57336.1| cyclophilin [Arabidopsis lyrata subsp. lyrata]	201	201	1.00E-105	100.0	93.0	96.0	cyclophilin	gbpln	Arabidopsis lyrata	AT2G29960.1 | Symbols: CYP5, ATCYP5, CYP19-4 | cyclophilin 5 | chr2:12769183-12770528 REVERSE LENGTH=201	201	201	1.00E-106	100.0	92.0	95.5
Rsa1.0_00348.1.g11962.t1	gb|EOA26514.1| hypothetical protein CARUB_v10022567mg [Capsella rubella]	950	1000	0	105.3	79.2	87.5	hypothetical protein CARUB_v10022567mg	gbpln	Capsella rubella	AT2G29970.1 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr2:12776601-12779784 FORWARD LENGTH=1002	950	1002	0	105.5	77.7	85.5
Rsa1.0_00348.1.g11963.t1	gb|ADJ58019.1| fatty acid desaturase 3-N1 [Brassica juncea]	352	383	0	108.8	98.3	99.7	fatty acid desaturase 3-N1	gbpln	Brassica juncea	AT2G29980.1 | Symbols: FAD3 | fatty acid desaturase 3 | chr2:12781787-12784946 REVERSE LENGTH=386	352	386	0	109.7	94.0	96.3
Rsa1.0_00348.1.g11964.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00348.1.g11965.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00349.1.g11966.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00349.1.g11967.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00349.1.g11968.t1	gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]	208	214	1.00E−70	102.9	69.2	76.0	trypsin inhibitor propeptide	gbpln	Brassica oleracea	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410−27548057 REVERSE LENGTH=215	208	215	2.00E−53	103.4	56.3	67.3
Rsa1.0_00349.1.g11969.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00349.1.g11970.t1	ref|XP_002878905.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324744|gb|EFH55164.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	181	480	2.00E−34	265.2	41.4	61.3	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00349.1.g11971.t1	ref|XP_002872320.1| hypothetical protein ARALYDRAFT_351828 [Arabidopsis lyrata subsp. lyrata] gi|297318157|gb|EFH48579.1| hypothetical protein ARALYDRAFT_351828 [Arabidopsis lyrata subsp. lyrata]	303	186	3.00E−21	61.4	16.2	25.1	hypothetical protein ARALYDRAFT_351828	gbpln	Arabidopsis lyrata	AT1G14800.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:5099572−5102558 FORWARD LENGTH=384	303	384	3.00E−16	126.7	17.2	22.8
Rsa1.0_00349.1.g11972.t1	ref|NP_850959.1| stomatal cytokinesis defective / SCD1 protein (SCD1) [Arabidopsis thaliana] gi|19743728|gb|AAL92456.1| stomatal cytokinesis defective [Arabidopsis thaliana] gi|332194264|gb|AEE32385.1| stomatal cytokinesis defective / SCD1 protein (SCD1) [Arabidopsis thaliana]	1187	1187	0	100.0	92.7	96.5	stomatal cytokinesis defective / SCD1 protein (SCD1)	gbpln	Arabidopsis thaliana	AT1G49040.1 | Symbols: SCD1 | stomatal cytokinesis defective / SCD1 protein (SCD1) | chr1:18139419−18148826 REVERSE LENGTH=1187	1187	1187	0	100.0	92.7	96.5
Rsa1.0_00349.1.g11973.t1	gb|AAG52313.1|AC021666_2 Mutator−like transposase; 53847−56139 [Arabidopsis thaliana]	73	583	6.00E−15	798.6	67.1	79.5	Mutator−like transposase; 53847−56139	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00349.1.g11974.t1	ref|NP_175332.1| PLAC8 family protein [Arabidopsis thaliana] gi|75186719|sp|Q9M9A5.1|PCR6_ARATH RecName: Full=Protein PLANT CADMIUM RESISTANCE 6; Short=AtPCR6 gi|7770345|gb|AAF69715.1|AC016041_20 F27J15.18 [Arabidopsis thaliana] gi|38603922|gb|AAR24706.1| At1g49030 [Arabidopsis thaliana] gi|44681424|gb|AAS47652.1| At1g49030 [Arabidopsis thaliana] gi|332194262|gb|AEE32383.1| PLAC8 family protein [Arabidopsis thaliana]	223	224	1.00E−102	100.4	82.5	88.3	PLAC8 family protein	gbpln	Arabidopsis thaliana	AT1G49030.1 | Symbols: | PLAC8 family protein | chr1:18136794−18137846 FORWARD LENGTH=224	223	224	1.00E−105	100.4	82.5	88.3
Rsa1.0_00349.1.g11975.t1	ref|NP_175332.1| PLAC8 family protein [Arabidopsis thaliana] gi|75186719|sp|Q9M9A5.1|PCR6_ARATH RecName: Full=Protein PLANT CADMIUM RESISTANCE 6; Short=AtPCR6 gi|7770345|gb|AAF69715.1|AC016041_20 F27J15.18 [Arabidopsis thaliana] gi|38603922|gb|AAR24706.1| At1g49030 [Arabidopsis thaliana] gi|44681424|gb|AAS47652.1| At1g49030 [Arabidopsis thaliana] gi|332194262|gb|AEE32383.1| PLAC8 family protein [Arabidopsis thaliana]	166	224	3.00E−77	134.9	81.3	85.5	PLAC8 family protein	gbpln	Arabidopsis thaliana	AT1G49030.1 | Symbols: | PLAC8 family protein | chr1:18136794−18137846 FORWARD LENGTH=224	166	224	1.00E−79	134.9	81.3	85.5
Rsa1.0_00349.1.g11976.t1	ref|NP_564537.1| myb/SANT−like DNA−binding domain−containing protein [Arabidopsis thaliana] gi|7770343|gb|AAF69713.1|AC016041_18 F27J15.20 [Arabidopsis thaliana] gi|21555865|gb|AAM63950.1| unknown [Arabidopsis thaliana] gi|41618992|gb|AAS09998.1| MYB transcription factor [Arabidopsis thaliana] gi|89274145|gb|ABD65593.1| At1g49010 [Arabidopsis thaliana] gi|332194260|gb|AEE32381.1| myb/SANT−like DNA−binding domain−containing protein [Arabidopsis thaliana]	296	314	1.00E−123	106.1	84.8	90.5	myb/SANT−like DNA−binding domain−containing protein	gbpln	Arabidopsis thaliana	AT1G49010.1 | Symbols: | Duplicated homeodomain−like superfamily protein | chr1:18132714−18133778 FORWARD LENGTH=314	296	314	1.00E−126	106.1	84.8	90.5
Rsa1.0_00349.1.g11977.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838−20266 [Arabidopsis thaliana]	1596	1142	0	71.6	38.8	48.7	reverse transcriptase, putative; 16838−20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1596	575	1.00E−67	36.0	9.7	14.5
Rsa1.0_00349.1.g11978.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	491	1611	9.00E−33	328.1	18.5	33.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00349.1.g11979.t1</td><td>ref|NP_175330.1| uncharacterized protein [Arabidopsis thaliana] gi|7770334|gb|AAF69704.1|AC016041_9 F27J15.21 [Arabidopsis thaliana] gi|45476547|gb|AAS65939.1| At1g49000 [Arabidopsis thaliana] gi|46359837|gb|AAS88782.1| At1g49000 [Arabidopsis thaliana] gi|332194258|gb|AEE32379.1| uncharacterized protein AT1G49000 [Arabidopsis thaliana]</td><td>144</td><td>156</td><td>2.00E-30</td><td>108.3</td><td>61.1</td><td>67.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G49000.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: stem; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G18560.1); Has 105 Blast hits to 105 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18123559-18124029 REVERSE LENGTH=156</td><td>144</td><td>156</td><td>5.00E-33</td><td>108.3</td><td>61.1</td><td>67.4</td></tr>
<tr><td>Rsa1.0_00349.1.g11980.t1</td><td>ref|XP_002891470.1| hypothetical protein ARALYDRAFT_474043 [Arabidopsis lyrata subsp. lyrata] gi|297337312|gb|EFH67729.1| hypothetical protein ARALYDRAFT_474043 [Arabidopsis lyrata subsp. lyrata]</td><td>161</td><td>168</td><td>2.00E-60</td><td>104.3</td><td>77.6</td><td>85.1</td><td>hypothetical protein ARALYDRAFT_474043</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G48990.1 | Symbols: | Oleosin family protein | chr1:18121470-18121979 FORWARD LENGTH=169</td><td>161</td><td>169</td><td>3.00E-57</td><td>105.0</td><td>79.5</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00349.1.g11981.t1</td><td>ref|XP_002891469.1| hypothetical protein ARALYDRAFT_314327 [Arabidopsis lyrata subsp. lyrata] gi|297337311|gb|EFH67728.1| hypothetical protein ARALYDRAFT_314327 [Arabidopsis lyrata subsp. lyrata]</td><td>306</td><td>335</td><td>1.00E-132</td><td>109.5</td><td>74.8</td><td>86.3</td><td>hypothetical protein ARALYDRAFT_314327</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G48980.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:18118715-18120511 FORWARD LENGTH=331</td><td>306</td><td>331</td><td>1.00E-134</td><td>108.2</td><td>74.8</td><td>85.9</td></tr>
<tr><td>Rsa1.0_00349.1.g11982.t1</td><td>ref|NP_181704.1| uncharacterized protein [Arabidopsis thaliana] gi|2335105|gb|AAC02775.1| hypothetical protein [Arabidopsis thaliana] gi|26450207|dbj|BAC42222.1| unknown protein [Arabidopsis thaliana] gi|30793799|gb|AAP40352.1| unknown protein [Arabidopsis thaliana] gi|330254932|gb|AEC10026.1| uncharacterized protein AT2G41730 [Arabidopsis thaliana]</td><td>130</td><td>119</td><td>2.00E-45</td><td>91.5</td><td>69.2</td><td>78.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G41730.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24640.1); Has 25 Blast hits to 25 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17409488-17409847 FORWARD LENGTH=119</td><td>130</td><td>119</td><td>5.00E-48</td><td>91.5</td><td>69.2</td><td>78.5</td></tr>
<tr><td>Rsa1.0_00349.1.g11983.t2</td><td>ref|XP_002871839.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297317676|gb|EFH48098.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>292</td><td>478</td><td>3.00E-46</td><td>163.7</td><td>35.6</td><td>43.2</td><td>F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G18770.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:6261426-6263172 FORWARD LENGTH=481</td><td>292</td><td>481</td><td>1.00E-43</td><td>164.7</td><td>33.2</td><td>41.4</td></tr>
<tr><td>Rsa1.0_00350.1.g11984.t1</td><td>ref|NP_568597.1| Transmembrane amino acid transporter family protein [Arabidopsis thaliana] gi|75245603|sp|Q8L4X4.1|GAT2_ARATH RecName: Full=Probable GABA transporter 2 gi|20466438|gb|AAM20536.1| amino acid permease-like protein [Arabidopsis thaliana] gi|22136372|gb|AAM91264.1| amino acid permease-like protein [Arabidopsis thaliana] gi|332007347|gb|AED94730.1| Transmembrane amino acid transporter family protein [Arabidopsis thaliana]</td><td>452</td><td>452</td><td>0</td><td>100.0</td><td>94.0</td><td>97.8</td><td>Transmembrane amino acid transporter family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G41800.1 | Symbols: | Transmembrane amino acid transporter family protein | chr5:16733842-16735888 FORWARD LENGTH=452</td><td>452</td><td>452</td><td>0</td><td>100.0</td><td>94.0</td><td>97.8</td></tr>
<tr><td>Rsa1.0_00350.1.g11985.t1</td><td>ref|XP_002868681.1| hypothetical protein ARALYDRAFT_916271 [Arabidopsis lyrata subsp. lyrata] gi|297314517|gb|EFH44940.1| hypothetical protein ARALYDRAFT_916271 [Arabidopsis lyrata subsp. lyrata]</td><td>1181</td><td>1168</td><td>0</td><td>98.9</td><td>88.3</td><td>91.7</td><td>hypothetical protein ARALYDRAFT_916271</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G10320.1 | Symbols: | tRNA synthetase class I (I, L, M and V) family protein | chr4:6397526-6404509 REVERSE LENGTH=1190</td><td>1181</td><td>1190</td><td>0</td><td>100.8</td><td>85.6</td><td>91.4</td></tr>
<tr><td>Rsa1.0_00350.1.g11986.t1</td><td>gb|EOA16625.1| hypothetical protein CARUB_v10004795mg [Capsella rubella]</td><td>456</td><td>450</td><td>0</td><td>98.7</td><td>83.8</td><td>91.0</td><td>hypothetical protein CARUB_v10004795mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G41880.1 | Symbols: POLA3, POLA4 | DNA primases;DNA primases | chr5:16761071-16764074 FORWARD LENGTH=451</td><td>456</td><td>451</td><td>0</td><td>98.9</td><td>84.2</td><td>90.6</td></tr>
<tr><td>Rsa1.0_00350.1.g11987.t4</td><td>gb|AAC97237.1| putative TNP2-like transposon protein [Arabidopsis thaliana]</td><td>926</td><td>889</td><td>0</td><td>96.0</td><td>68.4</td><td>77.8</td><td>putative TNP2-like transposon protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00350.1.g11988.t1</td><td>ref|NP_199005.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] gi|10177374|dbj|BAB10665.1| unnamed protein product [Arabidopsis thaliana] gi|26449651|dbj|BAC41950.1| unknown protein [Arabidopsis thaliana] gi|28951051|gb|AAO63449.1| At5g41900 [Arabidopsis thaliana] gi|332007358|gb|AED94741.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]</td><td>445</td><td>471</td><td>0</td><td>105.8</td><td>83.8</td><td>91.7</td><td>hydrolase, alpha/beta fold family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G41900.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:16769032-16771567 FORWARD LENGTH=471</td><td>445</td><td>471</td><td>0</td><td>105.8</td><td>83.8</td><td>91.7</td></tr>
</table>

Rsa1.0_00350.1.g11989.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	516	390	6.00E-41	75.6	16.7	21.1	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	516	295	2.00E-37	57.2	17.8	29.7
Rsa1.0_00350.1.g11990.t1	dbj|BAJ34468.1| unnamed protein product [Thellungiella halophila]	401	413	0	103.0	83.8	90.3	unnamed protein product	----	----	AT5G41920.1 | Symbols: | GRAS family transcription factor | chr5:16779982-16781199 FORWARD LENGTH=405	401	405	1.00E-178	101.0	79.1	87.3
Rsa1.0_00350.1.g11991.t1	gb|EOA16268.1| hypothetical protein CARUB_v10004413mg, partial [Capsella rubella]	591	603	0	102.0	79.4	84.4	hypothetical protein CARUB_v10004413mg, partial	gbpln	Capsella rubella	AT5G41940.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr5:16782039-16785451 FORWARD LENGTH=549	591	549	0	92.9	78.0	82.9
Rsa1.0_00350.1.g11992.t9	ref|NP_199013.1| uncharacterized protein [Arabidopsis thaliana] gi|9757943|dbj|BAB08431.1| unnamed protein product [Arabidopsis thaliana] gi|28416671|gb|AAO42866.1| At5g41980 [Arabidopsis thaliana] gi|110743283|dbj|BAE99532.1| hypothetical protein [Arabidopsis thaliana] gi|332007366|gb|AED94749.1| uncharacterized protein AT5G41980 [Arabidopsis thaliana]	374	374	1.00E-157	100.0	76.7	81.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G41980.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43722.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:16793765-16794889 FORWARD LENGTH=374	374	374	1.00E-160	100.0	76.7	81.3
Rsa1.0_00350.1.g11993.t1	ref|XP_002868565.1| hypothetical protein ARALYDRAFT_493780 [Arabidopsis lyrata subsp. lyrata] gi|297314401|gb|EFH44824.1| hypothetical protein ARALYDRAFT_493780 [Arabidopsis lyrata subsp. lyrata]	276	279	1.00E-125	101.1	83.7	89.9	hypothetical protein ARALYDRAFT_493780	gbpln	Arabidopsis lyrata	AT5G42030.1 | Symbols: ABIL4 | ABL interactor-like protein 4 | chr5:16811518-16813087 REVERSE LENGTH=279	276	279	1.00E-126	101.1	83.3	88.8
Rsa1.0_00350.1.g11994.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00350.1.g11995.t1	gb|EOA16900.1| hypothetical protein CARUB_v10005124mg [Capsella rubella]	339	357	1.00E-129	105.3	76.1	82.9	hypothetical protein CARUB_v10005124mg	gbpln	Capsella rubella	AT5G42050.1 | Symbols: | DCD (Development and Cell Death) domain protein | chr5:16815630-16816932 FORWARD LENGTH=349	339	349	1.00E-123	102.9	72.6	80.2
Rsa1.0_00350.1.g11996.t3	ref|NP_851120.1| dynamin-related protein 1A [Arabidopsis thaliana] gi|27735181|sp|P42697.3|DRP1A_ARATH RecName: Full=Dynamin-related protein 1A; AltName: Full=Dynamin-like protein 1; AltName: Full=Dynamin-like protein A gi|807577|gb|AAA84446.1| GTP-binding protein [Arabidopsis thaliana] gi|9757953|dbj|BAB08441.1| dynamin-like protein [Arabidopsis thaliana] gi|332007380|gb|AED94763.1| dynamin-related protein 1A [Arabidopsis thaliana]	749	610	0	81.4	79.0	80.6	dynamin-related protein 1A	gbpln	Arabidopsis thaliana	AT5G42080.1 | Symbols: ADL1, ADL1A, AG68, DRP1A, RSW9, DL1 | dynamin-like protein | chr5:16820661-16824536 REVERSE LENGTH=610	749	610	0	81.4	79.0	80.6
Rsa1.0_00350.1.g11997.t1	ref|NP_199026.4| uncharacterized protein [Arabidopsis thaliana] gi|26453100|dbj|BAC43626.1| unknown protein [Arabidopsis thaliana] gi|332007386|gb|AED94769.1| uncharacterized protein AT5G42110 [Arabidopsis thaliana]	63	62	6.00E-17	98.4	79.4	84.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G42110.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; Has 36 Blast hits to 36 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:16831951-16832226 REVERSE LENGTH=62	63	62	9.00E-20	98.4	79.4	84.1
Rsa1.0_00350.1.g11998.t1	ref|NP_187840.7| FKBP-like peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana] gi|380876925|sp|F4J9Q6.1|FKB43_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP43; Short=PPIase FKBP43; AltName: Full=FK506-binding protein 43; Short=AtFKBP43; AltName: Full=Immunophilin FKBP43; AltName: Full=Rotamase gi|332641663|gb|AEE75184.1| FKBP-like peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana]	460	499	1.00E-150	108.5	70.0	84.1	FKBP-like peptidyl-prolyl cis-trans isomerase family protein	gbpln	Arabidopsis thaliana	AT3G12340.1 | Symbols: | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | chr3:3925720-3929346 REVERSE LENGTH=499	460	499	1.00E-152	108.5	70.0	84.1

Rsa1.0_00350.1.g11999.t1	ref|XP_002870534.1| hypothetical protein ARALYDRAFT_493723 [Arabidopsis lyrata subsp. lyrata] gi|297316370|gb|EFH46793.1| hypothetical protein ARALYDRAFT_493723 [Arabidopsis lyrata subsp. lyrata]	250	225	3.00E−77	90.0	70.4	77.2	hypothetical protein ARALYDRAFT_493723	gbpln	Arabidopsis lyrata	AT5G37475.1 | Symbols: | Translation initiation factor eIF3 subunit | chr5:14866328−14867749 REVERSE LENGTH=225	250	225	1.00E−79	90.0	69.6	77.6
Rsa1.0_00350.1.g12000.t1	gb|EOA32182.1| hypothetical protein CARUB_v10015438mg [Capsella rubella]	310	378	4.00E−62	121.9	45.2	63.5	hypothetical protein CARUB_v10015438mg	gbpln	Capsella rubella	AT1G11510.1 | Symbols: | DNA−binding storekeeper protein−related transcriptional regulator | chr1:3871778−3872836 REVERSE LENGTH=352	310	352	5.00E−57	113.5	49.0	67.7
Rsa1.0_00351.1.g12001.t1	gb|AAM19711.1|AF499724_1 aluminum−induced protein−like protein [Eutrema halophilum]	281	251	1.00E−123	89.3	79.0	85.1	aluminum−induced protein−like protein	gbpln	Eutrema halophilum	AT5G43830.1 | Symbols: | Aluminium induced protein with YGL and LRDR motifs | chr5:17622593−17624239 REVERSE LENGTH=251	281	251	1.00E−118	89.3	74.0	81.5
Rsa1.0_00351.1.g12002.t1	gb|ADL70520.1| indole−3−acetic acid inducible 4 [Arabidopsis thaliana]	191	186	3.00E−91	97.4	88.5	91.1	indole−3−acetic acid inducible 4	gbpln	Arabidopsis thaliana	AT5G43700.1 | Symbols: ATAUX2−11, IAA4 | AUX/IAA transcriptional regulator family protein | chr5:17550465−17551206 FORWARD LENGTH=186	191	186	4.00E−92	97.4	86.9	90.6
Rsa1.0_00351.1.g12003.t1	gb|EOA14581.1| hypothetical protein CARUB_v10027822mg [Capsella rubella]	415	524	0	126.3	93.5	97.1	hypothetical protein CARUB_v10027822mg	gbpln	Capsella rubella	AT5G43360.1 | Symbols: PHT3, ATPT4, PHT1;3 | phosphate transporter 1;3 | chr5:17409524−17411214 FORWARD LENGTH=521	415	521	0	125.5	93.5	95.9
Rsa1.0_00351.1.g12004.t1	gb|EOA14581.1| hypothetical protein CARUB_v10027822mg [Capsella rubella]	370	524	0	141.6	91.4	96.2	hypothetical protein CARUB_v10027822mg	gbpln	Capsella rubella	AT5G43360.1 | Symbols: PHT3, ATPT4, PHT1;3 | phosphate transporter 1;3 | chr5:17409524−17411214 FORWARD LENGTH=521	370	521	0	140.8	90.3	94.9
Rsa1.0_00351.1.g12005.t1	ref|NP_199148.1| putative inorganic phosphate transporter 1−6 [Arabidopsis thaliana] gi|75316009|sp|Q9ZWT3.1|PHT16_ARATH RecName: Full=Probable inorganic phosphate transporter 1−6; Short=AtPht1;6; AltName: Full=H(+)/Pi cotransporter gi|3869190|dbj|BAA34390.1| inorganic phosphate transporter [Arabidopsis thaliana] gi|8843887|dbj|BAA97413.1| inorganic phosphate transporter [Arabidopsis thaliana] gi|332007564|gb|AED94947.1| putative inorganic phosphate transporter 1−6 [Arabidopsis thaliana]	510	516	0	101.2	82.9	92.0	putative inorganic phosphate transporter 1−6	gbpln	Arabidopsis thaliana	AT5G43340.1 | Symbols: PHT6, PHT1;6 | phosphate transporter 1;6 | chr5:17393598−17395148 REVERSE LENGTH=516	510	516	0	101.2	82.9	92.0
Rsa1.0_00351.1.g12006.t2	dbj|BAJ34213.1| unnamed protein product [Thellungiella halophila]	367	332	0	90.5	88.6	90.2	unnamed protein product	----	----	AT1G04410.1 | Symbols: | Lactate/malate dehydrogenase family protein | chr1:1189418−1191267 REVERSE LENGTH=332	367	332	0	90.5	87.2	89.6
Rsa1.0_00351.1.g12007.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00351.1.g12008.t1	ref|XP_002863664.1| hypothetical protein ARALYDRAFT_494671 [Arabidopsis lyrata subsp. lyrata] gi|297309499|gb|EFH39923.1| hypothetical protein ARALYDRAFT_494671 [Arabidopsis lyrata subsp. lyrata]	482	480	0	99.6	95.0	97.7	hypothetical protein ARALYDRAFT_494671	gbpln	Arabidopsis lyrata	AT5G43320.1 | Symbols: ckl8 | casein kinase I−like 8 | chr5:17386043−17388941 REVERSE LENGTH=480	482	480	0	99.6	95.2	97.5
Rsa1.0_00351.1.g12009.t1	ref|XP_002863667.1| glycerophosphodiester phosphodiesterase [Arabidopsis lyrata subsp. lyrata] gi|297309502|gb|EFH39926.1| glycerophosphodiester phosphodiesterase [Arabidopsis lyrata subsp. lyrata]	368	372	1.00E−174	101.1	80.7	88.9	glycerophosphodiester phosphodiesterase	gbpln	Arabidopsis lyrata	AT5G43300.1 | Symbols: | PLC−like phosphodiesterases superfamily protein | chr5:17376946−17379070 REVERSE LENGTH=370	368	370	1.00E−173	100.5	78.0	85.6
Rsa1.0_00351.1.g12010.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00351.1.g12011.t1	ref|XP_002862895.1| WRKY DNA−binding protein 49 [Arabidopsis lyrata subsp. lyrata] gi|297308663|gb|EFH39154.1| WRKY DNA−binding protein 49 [Arabidopsis lyrata subsp. lyrata]	329	272	9.00E−96	82.7	55.0	65.0	WRKY DNA−binding protein 49	gbpln	Arabidopsis lyrata	AT5G43290.1 | Symbols: WRKY49, ATWRKY49 | WRKY DNA−binding protein 49 | chr5:17371987−17373083 REVERSE LENGTH=274	329	274	3.00E−95	83.3	55.0	64.7
Rsa1.0_00351.1.g12012.t1	gb|EOA13745.1| hypothetical protein CARUB_v10026833mg, partial [Capsella rubella]	277	307	1.00E−138	110.8	89.9	94.6	hypothetical protein CARUB_v10026833mg, partial	gbpln	Capsella rubella	AT5G43280.1 | Symbols: ATDCI1, DCI1 | delta(3,5),delta(2,4)−dienoyl−CoA isomerase 1 | chr5:17367947−17369113 FORWARD LENGTH=278	277	278	1.00E−136	100.4	86.3	92.4
Rsa1.0_00351.1.g12013.t1	dbj|BAJ34267.1| unnamed protein product [Thellungiella halophila]	356	422	1.00E−152	118.5	81.2	88.8	unnamed protein product	----	----	AT5G43270.1 | Symbols: SPL2 | squamosa promoter binding protein−like 2 | chr5:17360527−17362143 REVERSE LENGTH=419	356	419	1.00E−149	117.7	80.9	88.5

Rsa1.0_00351.1.g12014.t1	gb|EOA14275.1| hypothetical protein CARUB_v10027437mg [Capsella rubella]	98	98	4.00E-42	100.0	83.7	94.9	hypothetical protein CARUB_v10027437mg	gbpln	Capsella rubella	AT5G43260.1 | Symbols: | chaperone protein dnaJ-related | chr5:17357693-17357986 REVERSE LENGTH=97	98	97	7.00E-43	99.0	82.7	93.9
Rsa1.0_00351.1.g12015.t1	ref|NP_199137.2| uncharacterized protein [Arabidopsis thaliana] gi|332007543|gb|AED94926.1| uncharacterized protein AT5G43230 [Arabidopsis thaliana]	843	848	0	100.6	87.8	93.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G43230.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01810.3); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:17349125-17352747 FORWARD LENGTH=848	843	848	0	100.6	87.8	93.1
Rsa1.0_00351.1.g12016.t1	ref|NP_568622.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75170673|sp|Q9FHS6.1|FK119_ARATH RecName: Full=F-box/kelch-repeat protein At5g43190 gi|10177381|dbj|BAB10582.1| unnamed protein product [Arabidopsis thaliana] gi|27765056|gb|AAO23649.1| At5g43190 [Arabidopsis thaliana] gi|110743394|dbj|BAE99583.1| hypothetical protein [Arabidopsis thaliana] gi|332007539|gb|AED94922.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	402	403	1.00E-174	100.2	85.3	92.3	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT5G43190.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:17340300-17341511 REVERSE LENGTH=403	402	403	1.00E-176	100.2	85.3	92.3
Rsa1.0_00351.1.g12017.t1	ref|NP_199125.2| pumilio 14 [Arabidopsis thaliana] gi|75339252|sp|Q4PSD1.1|PUM14_ARATH RecName: Full=Pumilio homolog 14; Short=APUM-14; Short=AtPUM14 gi|67633854|gb|AAY78851.1| pumilio/Puf RNA-binding domain-containing protein [Arabidopsis thaliana] gi|332007528|gb|AED94911.1| pumilio 14 [Arabidopsis thaliana]	462	518	8.00E-92	112.1	45.0	60.8	pumilio 14	gbpln	Arabidopsis thaliana	AT5G43110.1 | Symbols: APUM14, PUM14 | pumilio 14 | chr5:17309842-17311937 FORWARD LENGTH=518	462	518	2.00E-94	112.1	45.0	60.8
Rsa1.0_00351.1.g12018.t1	#	#	#	#	#	#	#	–	----	----	AT5G43066.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:17284583-17284807 FORWARD LENGTH=74	146	74	5.00E-12	50.7	24.7	29.5
Rsa1.0_00351.1.g12019.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00351.1.g12020.t1	gb|AAL60579.1|AF454957_1 senescence-associated cysteine protease [Brassica oleracea]	461	460	0	99.8	93.3	95.4	senescence-associated cysteine protease	gbpln	Brassica oleracea	AT5G43060.1 | Symbols: | Granulin repeat cysteine protease family protein | chr5:17269784-17272117 REVERSE LENGTH=463	461	463	0	100.4	87.0	91.8
Rsa1.0_00351.1.g12021.t1	gb|EOA15078.1| hypothetical protein CARUB_v10028445mg [Capsella rubella]	156	157	7.00E-65	100.6	83.3	89.7	hypothetical protein CARUB_v10028445mg	gbpln	Capsella rubella	AT5G43050.1 | Symbols: NPQ6 | Protein of unknown function (DUF565) | chr5:17268404-17268880 FORWARD LENGTH=158	156	158	1.00E-66	101.3	83.3	90.4
Rsa1.0_00351.1.g12022.t1	emb|CAN83990.1| hypothetical protein VITISV_018454 [Vitis vinifera]	1394	1243	0	89.2	38.1	51.7	hypothetical protein VITISV_018454	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1394	1262	1.00E-171	90.5	20.9	28.2
Rsa1.0_00351.1.g12023.t1	gb|ABR14728.1| ubiquitin conjugating enzyme [Gossypium hirsutum]	148	161	9.00E-72	108.8	87.8	94.6	ubiquitin conjugating enzyme	gbpln	Gossypium hirsutum	AT5G42990.1 | Symbols: UBC18 | ubiquitin-conjugating enzyme 18 | chr5:17244206-17245904 REVERSE LENGTH=161	148	161	8.00E-74	108.8	95.3	98.0
Rsa1.0_00351.1.g12024.t1	sp|O64432.1|TRXH_BRARA RecName: Full=Thioredoxin H-type; Short=Trx-H gi|3062793|dbj|BAA25681.1| Thioredoxin [Brassica rapa]	123	123	4.00E-56	100.0	88.6	95.1	RecName: Full=Thioredoxin H-type; Short=Trx-H gi|3062793|dbj|BAA25681.1| Thioredoxin	gbpln	Brassica rapa	AT5G42980.1 | Symbols: ATTRX3, ATH3, ATTRXH3, TRXH3, TRX3 | thioredoxin 3 | chr5:17242772-17243718 FORWARD LENGTH=118	123	118	1.00E-45	95.9	68.3	79.7
Rsa1.0_00351.1.g12025.t1	gb|EOA12455.1| hypothetical protein CARUB_v10025736mg [Capsella rubella]	1706	1716	0	100.6	75.1	83.8	hypothetical protein CARUB_v10025736mg	gbpln	Capsella rubella	AT5G42950.1 | Symbols: | GYF domain-containing protein | chr5:17224436-17231044 FORWARD LENGTH=1714	1706	1714	0	100.5	75.4	84.2
Rsa1.0_00351.1.g12026.t1	ref|XP_002863715.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297309550|gb|EFH39974.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	423	682	1.00E-121	161.2	58.9	64.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G42940.1 | Symbols: | RING/U-box superfamily protein | chr5:17216649-17219171 REVERSE LENGTH=691	423	691	1.00E-114	163.4	56.0	62.6
Rsa1.0_00351.1.g12027.t1	ref|NP_199107.5| lipase class 3-like protein [Arabidopsis thaliana] gi|332007506|gb|AED94889.1| lipase class 3-like protein [Arabidopsis thaliana]	468	467	0	99.8	80.6	90.4	lipase class 3-like protein	gbpln	Arabidopsis thaliana	AT5G42930.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:17210738-17214152 REVERSE LENGTH=467	468	467	0	99.8	80.6	90.4

Rsa1.0_00351.1.g12028.t1	gb|EOA13922.1| hypothetical protein CARUB_v10027042mg [Capsella rubella]	132	224	2.00E-32	169.7	71.2	80.3	hypothetical protein CARUB_v10027042mg	gbpln	Capsella rubella	AT5G42900.2 | Symbols: | cold regulated gene 27 | chr5:17198366-17199712 REVERSE LENGTH=246	132	246	1.00E-31	186.4	69.7	80.3
Rsa1.0_00351.1.g12029.t1	gb|EOA14063.1| hypothetical protein CARUB_v10027199mg [Capsella rubella]	186	186	1.00E-102	100.0	98.4	99.5	hypothetical protein CARUB_v10027199mg	gbpln	Capsella rubella	AT5G54750.1 | Symbols: | Transport protein particle (TRAPP) component | chr5:22242080-22243477 FORWARD LENGTH=186	186	186	1.00E-104	100.0	97.3	99.5
Rsa1.0_00351.1.g12030.t1	gb|EOA14581.1| hypothetical protein CARUB_v10027822mg [Capsella rubella]	556	524	0	94.2	78.1	83.6	hypothetical protein CARUB_v10027822mg	gbpln	Capsella rubella	AT5G43360.1 | Symbols: PHT3, ATPT4, PHT1;3 | phosphate transporter 1;3 | chr5:17409524-17411214 FORWARD LENGTH=521	556	521	0	93.7	78.2	82.7
Rsa1.0_00351.1.g12031.t1	gb|ABX46557.1| polygalacturonase inhibitor protein 11 [Brassica napus]	332	342	1.00E-157	103.0	84.0	86.1	polygalacturonase inhibitor protein 11	gbpln	Brassica napus	AT5G06860.1 | Symbols: PGIP1, ATPGIP1 | polygalacturonase inhibiting protein 1 | chr5:2132373-2133434 FORWARD LENGTH=330	332	330	1.00E-119	99.4	63.6	74.4
Rsa1.0_00351.1.g12032.t1	ref|NP_174709.1| putative long-chain-alcohol O-fatty-acyltransferase 9 [Arabidopsis thaliana] gi|75339336|sp|Q4PT07.1|WAXS9_ARATH RecName: Full=Probable long-chain-alcohol O-fatty-acyltransferase 9; AltName: Full=Wax synthase 9 gi|67633422|gb|AAY78636.1| membrane bound O-acyl transferase family protein [Arabidopsis thaliana] gi|332193599|gb|AEE31720.1| putative long-chain-alcohol O-fatty-acyltransferase 9 [Arabidopsis thaliana]	338	341	1.00E-144	100.9	78.1	86.4	putative long-chain-alcohol O-fatty-acyltransferase 9	gbpln	Arabidopsis thaliana	AT1G34500.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr1:12611638-12612663 FORWARD LENGTH=341	338	341	2.33E-156	100.9	78.1	86.4
Rsa1.0_00351.1.g12033.t1	ref|XP_002865494.1| hypothetical protein ARALYDRAFT_494763 [Arabidopsis lyrata subsp. lyrata] gi|297311329|gb|EFH41753.1| hypothetical protein ARALYDRAFT_494763 [Arabidopsis lyrata subsp. lyrata]	822	806	0	98.1	69.2	78.8	hypothetical protein ARALYDRAFT_494763	gbpln	Arabidopsis lyrata	AT5G42710.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:17125578-17128696 FORWARD LENGTH=807	822	807	0	98.2	66.9	78.0
Rsa1.0_00351.1.g12034.t1	tpg|DAA55311.1| TPA: histone H3.2 [Zea mays]	136	245	1.00E-72	180.1	100.0	100.0	TPA: histone H3.2	gbenv/gbpln	Zea mays	AT5G65360.1 | Symbols: | Histone superfamily protein | chr5:26120099-26120509 REVERSE LENGTH=136	136	136	5.00E-74	100.0	100.0	100.0
Rsa1.0_00351.1.g12035.t1	ref|NP_175180.1| RNA-binding protein 47C [Arabidopsis thaliana] gi|75337807|sp|Q9SX79.1|RB47C_ARATH RecName: Full=Polyadenylate-binding protein RBP47C; Short=Poly(A)-binding protein RBP47C; AltName: Full=RNA-binding protein 47C; Short=AtRBP47C gi|5668812|gb|AAD46038.1|AC007519_23 Contains 3 PF|00076 RNA recognition motif domains. ESTs gb|R30092, gb|R30093, gb|AA394338, gb|N65719 and gb|AA597577 come from this gene [Arabidopsis thaliana] gi|12744993|gb|AAK06876.1|AF344325_1 putative DNA binding protein [Arabidopsis thaliana] gi|14334552|gb|AAK59684.1| putative DNA binding protein [Arabidopsis thaliana] gi|17065624|gb|AAL33806.1| putative DNA binding protein [Arabidopsis thaliana] gi|332194053|gb|AEE32174.1| RNA-binding protein 47C [Arabidopsis thaliana]	427	432	1.00E-162	101.2	68.1	79.2	RNA-binding protein 47C	gbpln	Arabidopsis thaliana	AT1G47490.1 | Symbols: ATRBP47C, RBP47C | RNA-binding protein 47C | chr1:17424801-17427182 FORWARD LENGTH=432	427	432	1.00E-165	101.2	68.1	79.2
Rsa1.0_00351.1.g12036.t2	ref|XP_002863751.1| hypothetical protein ARALYDRAFT_331132 [Arabidopsis lyrata subsp. lyrata] gi|297309586|gb|EFH40010.1| hypothetical protein ARALYDRAFT_331132 [Arabidopsis lyrata subsp. lyrata]	517	541	0	104.6	75.6	82.6	hypothetical protein ARALYDRAFT_331132	gbpln	Arabidopsis lyrata	AT5G42690.2 | Symbols: | Protein of unknown function, DUF547 | chr5:17116630-17119492 REVERSE LENGTH=540	517	540	0	104.4	75.8	82.6
Rsa1.0_00351.1.g12037.t1	ref|XP_002865496.1| hypothetical protein ARALYDRAFT_494768 [Arabidopsis lyrata subsp. lyrata] gi|297311331|gb|EFH41755.1| hypothetical protein ARALYDRAFT_494768 [Arabidopsis lyrata subsp. lyrata]	238	238	1.00E-127	100.0	91.6	97.5	hypothetical protein ARALYDRAFT_494768	gbpln	Arabidopsis lyrata	AT5G42680.2 | Symbols: | Protein of unknown function, DUF617 | chr5:17114640-17115356 FORWARD LENGTH=238	238	238	1.00E-122	100.0	91.2	97.5
Rsa1.0_00351.1.g12038.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00351.1.g12039.t1	gb|EOA26064.1| hypothetical protein CARUB_v10019482mg [Capsella rubella]	126	624	1.00E-17	495.2	34.1	36.5	hypothetical protein CARUB_v10019482mg	gbpln	Capsella rubella	AT3G60190.1 | Symbols: ADL4, ADLP2, EDR3, DRP1E, ADL1E, DL1E | DYNAMIN-like 1E | chr3:22244367-22247651 REVERSE LENGTH=624	126	624	5.00E-20	495.2	34.1	35.7

Rsa1.0_00352.1.g12040.t1	gb|ABW74585.1| pol polyprotein [Boechera divaricarpa]	217	551	4.00E-34	253.9	47.9	64.1	pol polyprotein	gbpln	Boechera divaricarpa	#	#	#	#	#	#	#
Rsa1.0_00352.1.g12041.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00352.1.g12042.t1	gb|EOA32056.1| hypothetical protein CARUB_v10015301mg [Capsella rubella]	263	263	1.00E-118	100.0	83.3	91.3	hypothetical protein CARUB_v10015301mg	gbpln	Capsella rubella	AT2G17080.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr2:7433326-7434117 REVERSE LENGTH=263	263	263	1.00E-110	100.0	79.1	89.0
Rsa1.0_00352.1.g12043.t1	ref|XP_002884040.1| peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329880|gb|EFH60299.1| peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	364	356	1.00E-147	97.8	73.4	82.4	peptidoglycan-binding LysM domain-containing protein	gbpln	Arabidopsis lyrata	AT2G17120.1 | Symbols: LYM2 | lysm domain GPI-anchored protein 2 precursor | chr2:7459156-7460648 FORWARD LENGTH=350	364	350	1.00E-134	96.2	69.0	78.8
Rsa1.0_00352.1.g12044.t1	gb|EOA30387.1| hypothetical protein CARUB_v10013507mg [Capsella rubella]	738	502	0	68.0	57.2	60.6	hypothetical protein CARUB_v10013507mg	gbpln	Capsella rubella	AT2G13100.1 | Symbols: | Major facilitator superfamily protein | chr2:5390206-5391764 FORWARD LENGTH=493	738	493	0	66.8	56.8	60.3
Rsa1.0_00352.1.g12045.t1	gb|AAO61648.1| NAD-dependent isocitrate dehydrogenase gamma subunit [Brassica napus] gi|28974506|gb|AAO61649.1| NAD-dependent isocitrate dehydrogenase gamma subunit [Brassica napus] gi|28974508|gb|AAO61650.1| NAD-dependent isocitrate dehydrogenase gamma subunit [Brassica napus]	380	368	0	96.8	95.0	95.3	NAD-dependent isocitrate dehydrogenase gamma subunit	gbpln	Brassica napus	AT2G17130.1 | Symbols: IDH2, IDH-II | isocitrate dehydrogenase subunit 2 | chr2:7461062-7462466 REVERSE LENGTH=367	380	367	0	96.6	91.8	92.9
Rsa1.0_00352.1.g12046.t1	ref|XP_002884041.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297329881|gb|EFH60300.1| binding protein [Arabidopsis lyrata subsp. lyrata]	877	874	0	99.7	89.7	94.6	binding protein	gbpln	Arabidopsis lyrata	AT2G17140.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:7462820-7465740 FORWARD LENGTH=874	877	874	0	99.7	89.4	94.4
Rsa1.0_00352.1.g12047.t1	ref|XP_002886100.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331940|gb|EFH62359.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	913	914	0	100.1	80.0	85.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G17150.1 | Symbols: | Plant regulator RWP-RK family protein | chr2:7467049-7470533 REVERSE LENGTH=909	913	909	0	99.6	79.1	84.7
Rsa1.0_00352.1.g12048.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	561	1466	0	261.3	57.9	67.0	copia-like polyprotein	gbpln	Arabidopsis thaliana	AT5G48050.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G34070.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19472661-19473770 REVERSE LENGTH=369	561	369	8.00E-18	65.8	13.9	21.9
Rsa1.0_00352.1.g12049.t1	gb|AAD24567.1|AF120335_1 putative transposase [Arabidopsis thaliana]	428	577	2.00E-80	134.8	36.4	47.4	putative transposase	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	428	696	1.00E-18	162.6	15.2	29.4
Rsa1.0_00352.1.g12050.t1	gb|EOA32781.1| hypothetical protein CARUB_v10016090mg [Capsella rubella]	257	276	5.00E-52	107.4	56.0	67.7	hypothetical protein CARUB_v10016090mg	gbpln	Capsella rubella	AT2G17180.1 | Symbols: | C2H2-like zinc finger protein | chr2:7476835-7477647 REVERSE LENGTH=270	257	270	1.00E-52	105.1	53.3	62.6
Rsa1.0_00352.1.g12051.t2	ref|NP_179311.1| ubiquitin-like protein [Arabidopsis thaliana] gi|4584343|gb|AAD25138.1| putative ubiquitin-like protein [Arabidopsis thaliana] gi|23296306|gb|AAN13037.1| putative ubiquitin protein [Arabidopsis thaliana] gi|110735104|gb|ABG89122.1| Dsk2a [synthetic construct] gi|330251503|gb|AEC06597.1| UBL/UBA protein DSK2b [Arabidopsis thaliana]	569	551	0	96.8	82.2	88.2	ubiquitin-like protein	gbpln	Arabidopsis thaliana	AT2G17200.1 | Symbols: DSK2 | ubiquitin family protein | chr2:7482133-7485090 REVERSE LENGTH=551	569	551	0	96.8	82.2	88.2
Rsa1.0_00352.1.g12052.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	863	1239	1.00E-115	143.6	29.1	36.0	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	863	1262	5.00E-25	146.2	9.0	14.5
Rsa1.0_00352.1.g12053.t2	gb|EOA26181.1| hypothetical protein CARUB_v10019619mg [Capsella rubella]	363	435	1.00E-117	119.8	61.7	76.0	hypothetical protein CARUB_v10019619mg	gbpln	Capsella rubella	AT2G28580.1 | Symbols: | Plant protein of unknown function (DUF247) | chr2:12244885-12248270 FORWARD LENGTH=536	363	536	4.00E-96	147.7	53.2	71.3
Rsa1.0_00352.1.g12054.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00353.1.g12055.t6	gb|EOA39474.1| hypothetical protein CARUB_v10008071mg [Capsella rubella]	219	1950	2.00E-93	890.4	73.5	87.2	hypothetical protein CARUB_v10008071mg	gbpln	Capsella rubella	AT1G56130.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:20994931-21000887 REVERSE LENGTH=1032	219	1032	6.00E-89	471.2	71.2	81.7

<table>
<tr><td>Rsa1.0_00353.1.g12056.t1</td><td>gb|EOA34482.1| hypothetical protein CARUB_v10022023mg [Capsella rubella]</td><td>280</td><td>286</td><td>1.00E−111</td><td>102.1</td><td>79.6</td><td>88.2</td><td>hypothetical protein CARUB_v10022023mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68120.1 | Symbols: BPC3, ATBPC3 | basic pentacysteine 3 | chr1:25526296-25527108 REVERSE LENGTH=270</td><td>280</td><td>270</td><td>1.00E−109</td><td>96.4</td><td>76.1</td><td>85.4</td></tr>
<tr><td>Rsa1.0_00353.1.g12057.t1</td><td>ref|XP_002888638.1| hypothetical protein ARALYDRAFT_894560 [Arabidopsis lyrata subsp. lyrata] gi|297334479|gb|EFH64897.1| hypothetical protein ARALYDRAFT_894560 [Arabidopsis lyrata subsp. lyrata]</td><td>368</td><td>373</td><td>1.00E−156</td><td>101.4</td><td>77.7</td><td>86.4</td><td>hypothetical protein ARALYDRAFT_894560</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68110.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:25524901-25526040 FORWARD LENGTH=379</td><td>368</td><td>379</td><td>1.00E−156</td><td>103.0</td><td>74.7</td><td>86.7</td></tr>
<tr><td>Rsa1.0_00353.1.g12058.t1</td><td>gb|EOA33325.1| hypothetical protein CARUB_v10022100mg [Capsella rubella]</td><td>316</td><td>316</td><td>1.00E−171</td><td>100.0</td><td>91.1</td><td>96.5</td><td>hypothetical protein CARUB_v10022100mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68090.1 | Symbols: ANNAT5, ANN5 | annexin 5 | chr1:25519442-25520774 REVERSE LENGTH=316</td><td>316</td><td>316</td><td>1.00E−173</td><td>100.0</td><td>89.9</td><td>96.2</td></tr>
<tr><td>Rsa1.0_00353.1.g12059.t1</td><td>gb|EOA33379.1| hypothetical protein CARUB_v10020306mg, partial [Capsella rubella]</td><td>133</td><td>442</td><td>5.00E−33</td><td>332.3</td><td>48.1</td><td>52.6</td><td>hypothetical protein CARUB_v10020306mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68080.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(Ⅱ)-dependent oxygenase superfamily protein | chr1:25517530-25519240 FORWARD LENGTH=389</td><td>133</td><td>389</td><td>2.00E−32</td><td>292.5</td><td>44.4</td><td>49.6</td></tr>
<tr><td>Rsa1.0_00353.1.g12060.t1</td><td>ref|XP_002887158.1| hypothetical protein ARALYDRAFT_475916 [Arabidopsis lyrata subsp. lyrata] gi|297332999|gb|EFH63417.1| hypothetical protein ARALYDRAFT_475916 [Arabidopsis lyrata subsp. lyrata]</td><td>335</td><td>344</td><td>1.00E−164</td><td>102.7</td><td>83.6</td><td>90.4</td><td>hypothetical protein ARALYDRAFT_475916</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68070.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr1:25515412-25516767 REVERSE LENGTH=343</td><td>335</td><td>343</td><td>1.00E−166</td><td>102.4</td><td>83.0</td><td>90.4</td></tr>
<tr><td>Rsa1.0_00353.1.g12061.t1</td><td>gb|AAG51872.1|AC079678_2 disease resistance protein, putative; 6346-10057 [Arabidopsis thaliana]</td><td>928</td><td>951</td><td>0</td><td>102.5</td><td>66.4</td><td>79.3</td><td>disease resistance protein, putative; 6346-10057</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G74180.1 | Symbols: AtRLP14, RLP14 | receptor like protein 14 | chr1:27897197-27900908 REVERSE LENGTH=976</td><td>928</td><td>976</td><td>0</td><td>105.2</td><td>66.5</td><td>79.2</td></tr>
<tr><td>Rsa1.0_00353.1.g12062.t1</td><td>gb|EOA35382.1| hypothetical protein CARUB_v10020579mg [Capsella rubella]</td><td>208</td><td>346</td><td>1.00E−32</td><td>166.3</td><td>35.6</td><td>39.4</td><td>hypothetical protein CARUB_v10020579mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68070.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr1:25515412-25516767 REVERSE LENGTH=343</td><td>208</td><td>343</td><td>5.00E−33</td><td>164.9</td><td>33.7</td><td>37.5</td></tr>
<tr><td>Rsa1.0_00353.1.g12063.t1</td><td>ref|XP_002869005.1| hypothetical protein ARALYDRAFT_353131 [Arabidopsis lyrata subsp. lyrata] gi|297314841|gb|EFH45264.1| hypothetical protein ARALYDRAFT_353131 [Arabidopsis lyrata subsp. lyrata]</td><td>73</td><td>281</td><td>3.00E−18</td><td>384.9</td><td>72.6</td><td>82.2</td><td>hypothetical protein ARALYDRAFT_353131</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00353.1.g12064.t2</td><td>gb|AAM77369.1|AF521301_1 phosphatidylinositol synthase [Brassica napus]</td><td>228</td><td>227</td><td>1.00E−127</td><td>99.6</td><td>97.8</td><td>98.7</td><td>phosphatidylinositol synthase</td><td>gbpln</td><td>Brassica napus</td><td>AT1G68000.1 | Symbols: ATPIS1, ATPIS, PIS1 | phosphatidylinositol synthase 1 | chr1:25491346-25492930 FORWARD LENGTH=227</td><td>228</td><td>227</td><td>1.00E−125</td><td>99.6</td><td>93.9</td><td>97.4</td></tr>
<tr><td>Rsa1.0_00353.1.g12065.t1</td><td>ref|NP_191779.1| Putative endonuclease or glycosyl hydrolase [Arabidopsis thaliana] gi|6899930|emb|CAB71880.1| putative protein [Arabidopsis thaliana] gi|332646801|gb|AEE80322.1| Putative endonuclease or glycosyl hydrolase [Arabidopsis thaliana]</td><td>200</td><td>673</td><td>1.00E−21</td><td>336.5</td><td>36.5</td><td>50.0</td><td>Putative endonuclease or glycosyl hydrolase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G62200.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:23023437-23025671 REVERSE LENGTH=673</td><td>200</td><td>673</td><td>4.00E−24</td><td>336.5</td><td>36.5</td><td>50.0</td></tr>
<tr><td>Rsa1.0_00353.1.g12066.t1</td><td>ref|XP_002888647.1| hypothetical protein ARALYDRAFT_475925 [Arabidopsis lyrata subsp. lyrata] gi|297334488|gb|EFH64906.1| hypothetical protein ARALYDRAFT_475925 [Arabidopsis lyrata subsp. lyrata]</td><td>246</td><td>232</td><td>1.00E−106</td><td>94.3</td><td>79.3</td><td>87.0</td><td>hypothetical protein ARALYDRAFT_475925</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G67980.1 | Symbols: CCOAMT | caffeoyl-CoA 3-O-methyltransferase | chr1:25487724-25488934 FORWARD LENGTH=232</td><td>246</td><td>232</td><td>1.00E−107</td><td>94.3</td><td>78.0</td><td>87.0</td></tr>
<tr><td>Rsa1.0_00353.1.g12067.t1</td><td>ref|XP_002888647.1| hypothetical protein ARALYDRAFT_475925 [Arabidopsis lyrata subsp. lyrata] gi|297334488|gb|EFH64906.1| hypothetical protein ARALYDRAFT_475925 [Arabidopsis lyrata subsp. lyrata]</td><td>232</td><td>232</td><td>1.00E−122</td><td>100.0</td><td>92.7</td><td>96.6</td><td>hypothetical protein ARALYDRAFT_475925</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G67980.1 | Symbols: CCOAMT | caffeoyl-CoA 3-O-methyltransferase | chr1:25487724-25488934 FORWARD LENGTH=232</td><td>232</td><td>232</td><td>1.00E−123</td><td>100.0</td><td>90.5</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00353.1.g12068.t1</td><td>ref|XP_002887161.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333002|gb|EFH63420.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>373</td><td>374</td><td>1.00E−149</td><td>100.3</td><td>75.1</td><td>84.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G67970.1 | Symbols: AT-HSFA8, HSFA8 | heat shock transcription factor A8 | chr1:25484844-25486313 REVERSE LENGTH=374</td><td>373</td><td>374</td><td>1.00E−150</td><td>100.3</td><td>77.2</td><td>86.3</td></tr>
</table>

Rsa1.0_00353.1.g12069.t1	ref|NP_173222.1| early nodulin-like protein 22 [Arabidopsis thaliana] gi|9665058|gb|AAF97260.1|AC034106_3 Contains similarity to blue copper-binding protein III from Arabidopsis thaliana gb|U65650 and contains a Plastocyanin-like PF|02298 domain [Arabidopsis thaliana] gi|50897198|gb|AAT85738.1| At1g17800 [Arabidopsis thaliana] gi|51972100|gb|AAU15154.1| At1g17800 [Arabidopsis thaliana] gi|332191517|gb|AEE29638.1| early nodulin-like protein 22 [Arabidopsis thaliana]	138	140	3.00E-52	101.4	70.3	83.3	early nodulin-like protein 22	gbpln	Arabidopsis thaliana	AT1G17800.1 | Symbols: ENODL22, AtENODL22 | early nodulin-like protein 22 | chr1:6128828-6129391 FORWARD LENGTH=140	138	140	7.00E-55	101.4	70.3	83.3
Rsa1.0_00353.1.g12070.t1	dbj|BAJ34019.1| unnamed protein product [Thellungiella halophila]	67	66	1.00E-22	98.5	82.1	85.1	unnamed protein product	----	----	AT1G67920.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24600.1); Has 22 Blast hits to 22 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25473731-25473934 FORWARD LENGTH=67	67	67	7.00E-24	100.0	82.1	88.1
Rsa1.0_00353.1.g12071.t1	ref|XP_002888631.1| hypothetical protein ARALYDRAFT_894547 [Arabidopsis lyrata subsp. lyrata] gi|297334472|gb|EFH64890.1| hypothetical protein ARALYDRAFT_894547 [Arabidopsis lyrata subsp. lyrata]	209	184	3.00E-44	88.0	51.7	58.9	hypothetical protein ARALYDRAFT_894547	gbpln	Arabidopsis lyrata	AT1G67870.1 | Symbols: | glycine-rich protein | chr1:25449593-25450943 REVERSE LENGTH=279	209	279	4.00E-29	133.5	38.8	48.8
Rsa1.0_00354.1.g12072.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	606	1274	1.00E-142	210.2	43.1	61.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	606	575	4.00E-68	94.9	27.6	43.6
Rsa1.0_00354.1.g12073.t1	ref|XP_002879865.1| hypothetical protein ARALYDRAFT_483086 [Arabidopsis lyrata subsp. lyrata] gi|297325704|gb|EFH56124.1| hypothetical protein ARALYDRAFT_483086 [Arabidopsis lyrata subsp. lyrata]	401	425	0	106.0	90.8	94.8	hypothetical protein ARALYDRAFT_483086	gbpln	Arabidopsis lyrata	AT2G40320.1 | Symbols: TBL33 | TRICHOME BIREFRINGENCE-LIKE 33 | chr2:16840330-16842139 FORWARD LENGTH=425	401	425	0	106.0	88.8	91.5
Rsa1.0_00354.1.g12074.t1	gb|EOA23244.1| hypothetical protein CARUB_v10017153mg [Capsella rubella]	477	473	1.00E-125	99.2	53.7	68.3	hypothetical protein CARUB_v10017153mg	gbpln	Capsella rubella	AT3G59000.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21799757-21801536 FORWARD LENGTH=491	477	491	1.00E-119	102.9	52.8	67.1
Rsa1.0_00354.1.g12075.t1	ref|XP_002879864.1| hypothetical protein ARALYDRAFT_903321 [Arabidopsis lyrata subsp. lyrata] gi|297325703|gb|EFH56123.1| hypothetical protein ARALYDRAFT_903321 [Arabidopsis lyrata subsp. lyrata]	317	276	1.00E-115	87.1	65.6	71.0	hypothetical protein ARALYDRAFT_903321	gbpln	Arabidopsis lyrata	AT2G40316.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Autophagy-related protein 27 (InterPro:IPR018939); Has 138 Blast hits to 138 proteins in 57 species: Archae - 0; Bacteria - 0; Metazoa - 32; Fungi - 62; Plants - 33; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr2:16836355-16838688 FORWARD LENGTH=276	317	276	1.00E-114	87.1	62.8	70.3
Rsa1.0_00354.1.g12076.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00354.1.g12077.t1	gb|EOA28841.1| hypothetical protein CARUB_v10025080mg [Capsella rubella]	342	344	1.00E-168	100.6	90.9	96.8	hypothetical protein CARUB_v10025080mg	gbpln	Capsella rubella	AT2G40290.1 | Symbols: | Eukaryotic translation initiation factor 2 subunit 1 | chr2:16829030-16830889 REVERSE LENGTH=344	342	344	1.00E-169	100.6	89.8	96.2
Rsa1.0_00354.1.g12078.t1	gb|EOA28978.1| hypothetical protein CARUB_v10025230mg, partial [Capsella rubella]	225	258	4.00E-68	114.7	64.9	76.4	hypothetical protein CARUB_v10025230mg, partial	gbpln	Capsella rubella	AT5G58530.1 | Symbols: | Glutaredoxin family protein | chr5:23660428-23661249 FORWARD LENGTH=273	225	273	5.00E-43	121.3	37.8	49.8
Rsa1.0_00354.1.g12079.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00354.1.g12080.t2	ref|XP_002881704.1| hypothetical protein ARALYDRAFT_321718 [Arabidopsis lyrata subsp. lyrata] gi|297327543|gb|EFH57963.1| hypothetical protein ARALYDRAFT_321718 [Arabidopsis lyrata subsp. lyrata]	408	411	1.00E-168	100.7	82.4	87.5	hypothetical protein ARALYDRAFT_321718	gbpln	Arabidopsis lyrata	AT2G40260.1 | Symbols: | Homeodomain-like superfamily protein | chr2:16816818-16818473 REVERSE LENGTH=410	408	410	1.00E-165	100.5	80.1	86.5
Rsa1.0_00354.1.g12081.t1	ref|XP_002879857.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325696|gb|EFH56116.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	359	361	1.00E-167	100.6	78.0	86.1	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT2G40250.1 | Symbols: | SGNH hydrolase-type esterase superfamily protein | chr2:16813330-16815251 FORWARD LENGTH=361	359	361	1.00E-169	100.6	79.1	88.9

Rsa1.0_00354.1.g12082.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00354.1.g12083.t1	ref|NP_181552.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|4587997|gb|AAD25938.1|AF085279_11 hypothetical protein [Arabidopsis thaliana] gi|21536614|gb|AAM60946.1| putative anthranilate N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana] gi|330254705|gb|AEC09799.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	430	433	0	100.7	89.1	94.7	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT2G40230.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr2:16803285-16804586 REVERSE LENGTH=433	430	433	0	100.7	89.1	94.7
Rsa1.0_00354.1.g12084.t1	gb|ABK28529.1| unknown [Arabidopsis thaliana]	328	329	1.00E-94	100.3	70.1	81.1	unknown	gbpln	Arabidopsis thaliana	AT2G40220.1 | Symbols: ABI4, SUN6, SIS5, ISI3, GIN6, SAN5, ATABI4 | Integrase-type DNA-binding superfamily protein | chr2:16796599-16797585 REVERSE LENGTH=328	328	328	5.00E-97	100.0	70.1	81.1
Rsa1.0_00354.1.g12085.t1	gb|EOA27018.1| hypothetical protein CARUB_v10023116mg, partial [Capsella rubella]	462	478	0	103.5	89.0	93.9	hypothetical protein CARUB_v10023116mg, partial	gbpln	Capsella rubella	AT2G40190.1 | Symbols: LEW3 | UDP-Glycosyltransferase superfamily protein | chr2:16785232-16787257 FORWARD LENGTH=463	462	463	0	100.2	87.7	93.3
Rsa1.0_00354.1.g12086.t1	ref|XP_002879887.1| hypothetical protein ARALYDRAFT_903365 [Arabidopsis lyrata subsp. lyrata] gi|297325726|gb|EFH56146.1| hypothetical protein ARALYDRAFT_903365 [Arabidopsis lyrata subsp. lyrata]	476	1359	1.00E-123	285.5	52.7	68.5	hypothetical protein ARALYDRAFT_903365	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	476	456	1.00E-115	95.8	49.6	64.3
Rsa1.0_00354.1.g12087.t1	ref|XP_002880609.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata] gi|297326448|gb|EFH56868.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata]	485	464	1.00E-125	95.7	53.6	68.9	hypothetical protein ARALYDRAFT_901029	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	485	456	1.00E-116	94.0	48.9	63.1
Rsa1.0_00354.1.g12088.t1	ref|XP_002880609.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata] gi|297326448|gb|EFH56868.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata]	471	464	1.00E-119	98.5	51.8	66.2	hypothetical protein ARALYDRAFT_901029	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	471	456	1.00E-118	96.8	52.0	66.7
Rsa1.0_00354.1.g12089.t1	ref|XP_002879851.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325690|gb|EFH56110.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	365	392	1.00E-174	107.4	84.1	88.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G40180.1 | Symbols: ATHPP2C5, PP2C5 | phosphatase 2C5 | chr2:16782522-16784014 FORWARD LENGTH=390	365	390	1.00E-170	106.8	83.6	88.2
Rsa1.0_00354.1.g12090.t1	sp|P11573.1|SEEP_RAPSA RecName: Full=Late seed maturation protein P8B6 gi|21122|emb|CAA33479.1| unnamed protein product [Raphanus sativus] gi|169692|gb|AAA33868.1| late maturation protein [Raphanus sativus]	83	83	6.00E-38	100.0	98.8	98.8	RecName: Full=Late seed maturation protein P8B6 gi|21122|emb|CAA33479.1| unnamed protein product	gbpln	Raphanus sativus	AT2G40170.1 | Symbols: ATEM6, GEA6, EM6 | Stress induced protein | chr2:16779792-16780167 REVERSE LENGTH=92	83	92	6.00E-31	110.8	89.2	90.4
Rsa1.0_00354.1.g12091.t1	dbj|BAJ34526.1| unnamed protein product [Thellungiella halophila]	566	600	0	106.0	86.6	92.6	unnamed protein product	----	----	AT2G40140.2 | Symbols: CZF1, ZFAR1, SZF2, ATSZF2 | zinc finger (CCCH-type) family protein | chr2:16772537-16774330 FORWARD LENGTH=597	566	597	0	105.5	84.6	92.8
Rsa1.0_00354.1.g12092.t1	ref|NP_973646.1| heat shock-related protein [Arabidopsis thaliana] gi|330254692|gb|AEC09786.1| heat shock-related protein [Arabidopsis thaliana]	806	910	0	112.9	78.7	87.6	heat shock-related protein	gbpln	Arabidopsis thaliana	AT2G40130.2 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr2:16766030-16769074 FORWARD LENGTH=910	806	910	0	112.9	78.7	87.6
Rsa1.0_00354.1.g12093.t1	gb|EOA28716.1| hypothetical protein CARUB_v10024944mg [Capsella rubella]	482	483	0	100.2	88.0	91.9	hypothetical protein CARUB_v10024944mg	gbpln	Capsella rubella	AT2G39980.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr2:16688437-16689885 REVERSE LENGTH=482	482	482	0	100.0	86.9	91.7
Rsa1.0_00354.1.g12094.t1	gb|EOA27439.1| hypothetical protein CARUB_v10023576mg [Capsella rubella]	336	338	1.00E-162	100.6	89.0	93.2	hypothetical protein CARUB_v10023576mg	gbpln	Capsella rubella	AT2G39970.1 | Symbols: | Mitochondrial substrate carrier family protein | chr2:16684026-16686392 REVERSE LENGTH=331	336	331	1.00E-164	98.5	87.2	91.7

Rsa1.0_00354.1.g12095.t3	ref|NP_181525.2| signal peptidase complex subunit 2 [Arabidopsis thaliana] gi|20140011|sp|P58684.1|SPCS2_ARATH RecName: Full=Probable signal peptidase complex subunit 2; AltName: Full=Microsomal signal peptidase 25 kDa subunit; Short=SPase 25 kDa subunit gi|17528956|gb|AAL38688.1| unknown protein [Arabidopsis thaliana] gi|20465965|gb|AAM20168.1| unknown protein [Arabidopsis thaliana] gi|330254662|gb|AEC09756.1| signal peptidase complex subunit 2 [Arabidopsis thaliana]	454	192	1.00E-70	42.3	30.8	32.6	signal peptidase complex subunit 2	gbpln	Arabidopsis thaliana	AT2G39960.1 | Symbols: | Microsomal signal peptidase 25 kDa subunit (SPC25) | chr2:16681666-16683491 REVERSE LENGTH=192	454	192	3.00E-73	42.3	30.8	32.6
Rsa1.0_00354.1.g12096.t2	ref|NP_181524.1| uncharacterized protein [Arabidopsis thaliana] gi|2088648|gb|AAB95280.1| hypothetical protein [Arabidopsis thaliana] gi|209529767|gb|ACI49778.1| At2g39950 [Arabidopsis thaliana] gi|330254660|gb|AEC09754.1| uncharacterized protein AT2G39950 [Arabidopsis thaliana]	475	636	0	133.9	79.2	87.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G39950.1 | Symbols: | unknown protein; Has 978 Blast hits to 254 proteins in 81 species: Archae - 0; Bacteria - 8; Metazoa - 109; Fungi - 53; Plants - 41; Viruses - 0; Other Eukaryotes - 767 (source: NCBI BLink). | chr2:16676758-16680204 REVERSE LENGTH=636	475	636	0	133.9	79.2	87.2
Rsa1.0_00354.1.g12097.t1	gb|EOA26779.1| hypothetical protein CARUB_v10022866mg [Capsella rubella]	603	594	0	98.5	90.2	94.2	hypothetical protein CARUB_v10022866mg	gbpln	Capsella rubella	AT2G39940.1 | Symbols: COI1 | RNI-like superfamily protein | chr2:16672848-16675486 REVERSE LENGTH=592	603	592	0	98.2	89.9	93.9
Rsa1.0_00354.1.g12098.t2	ref|NP_181522.1| isoamylase 1 [Arabidopsis thaliana] gi|75096955|sp|O04196.1|ISOA1_ARATH RecName: Full=Isoamylase 1, chloroplastic; Short=AtISA1; Flags: Precursor gi|2088646|gb|AAB95278.1| putative isoamylase [Arabidopsis thaliana] gi|23306386|gb|AAN17420.1| putative isoamylase [Arabidopsis thaliana] gi|34098817|gb|AAQ56791.1| At2g39930 [Arabidopsis thaliana] gi|330254658|gb|AEC09752.1| isoamylase 1 [Arabidopsis thaliana]	811	783	0	96.5	87.3	92.0	isoamylase 1	gbpln	Arabidopsis thaliana	AT2G39930.1 | Symbols: ISA1, ATISA1 | isoamylase 1 | chr2:16666078-16672183 FORWARD LENGTH=783	811	783	0	96.5	87.3	92.0
Rsa1.0_00354.1.g12099.t1	ref|NP_001189716.1| acid phosphatase class IIIB protein [Arabidopsis thaliana] gi|330254656|gb|AEC09750.1| acid phosphatase class IIIB protein [Arabidopsis thaliana]	282	282	1.00E-121	100.0	77.3	86.5	acid phosphatase class IIIB protein	gbpln	Arabidopsis thaliana	AT2G39920.2 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr2:16663201-16664305 REVERSE LENGTH=282	282	282	1.00E-124	100.0	77.3	86.5
Rsa1.0_00354.1.g12100.t2	ref|XP_002879830.1| hypothetical protein ARALYDRAFT_483024 [Arabidopsis lyrata subsp. lyrata] gi|297325669|gb|EFH56089.1| hypothetical protein ARALYDRAFT_483024 [Arabidopsis lyrata subsp. lyrata]	685	442	0	64.5	55.3	59.6	hypothetical protein ARALYDRAFT_483024	gbpln	Arabidopsis lyrata	AT2G39890.2 | Symbols: PROT1, ATPROT1 | proline transporter 1 | chr2:16656022-16658202 FORWARD LENGTH=442	685	442	0	64.5	54.7	59.6
Rsa1.0_00354.1.g12101.t1	ref|XP_002879830.1| hypothetical protein ARALYDRAFT_483024 [Arabidopsis lyrata subsp. lyrata] gi|297325669|gb|EFH56089.1| hypothetical protein ARALYDRAFT_483024 [Arabidopsis lyrata subsp. lyrata]	475	442	0	93.1	83.6	88.4	hypothetical protein ARALYDRAFT_483024	gbpln	Arabidopsis lyrata	AT2G39890.2 | Symbols: PROT1, ATPROT1 | proline transporter 1 | chr2:16656022-16658202 FORWARD LENGTH=442	475	442	0	93.1	83.4	88.2
Rsa1.0_00354.1.g12102.t1	ref|XP_002881682.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327521|gb|EFH57941.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	416	382	1.00E-118	91.8	58.4	70.9	predicted protein	gbpln	Arabidopsis lyrata	AT2G39880.1 | Symbols: MYB25, AtMYB25 | myb domain protein 25 | chr2:16647945-16649479 REVERSE LENGTH=367	416	367	1.00E-110	88.2	54.3	64.7
Rsa1.0_00354.1.g12103.t1	ref|XP_002879829.1| hypothetical protein ARALYDRAFT_483023 [Arabidopsis lyrata subsp. lyrata] gi|297325668|gb|EFH56088.1| hypothetical protein ARALYDRAFT_483023 [Arabidopsis lyrata subsp. lyrata]	333	342	1.00E-105	102.7	74.2	83.5	hypothetical protein ARALYDRAFT_483023	gbpln	Arabidopsis lyrata	AT2G39870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G55690.1); Has 73 Blast hits to 71 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 2; Plants - 69; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:16643697-16644950 FORWARD LENGTH=330	333	330	1.00E-100	99.1	71.8	79.6
Rsa1.0_00354.1.g12104.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00354.1_g12105.t2	ref|NP_973642.1| uncharacterized protein [Arabidopsis thaliana] gi|28207122|gb|AAO37201.1| hypothetical protein [Arabidopsis thaliana] gi|330254647|gb|AEC09741.1| uncharacterized protein AT2G39855 [Arabidopsis thaliana]	159	142	5.00E-43	89.3	59.1	65.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G39855.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G55646.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16637845-16638852 FORWARD LENGTH=142	159	142	2.00E-45	89.3	59.1	65.4
Rsa1.0_00354.1_g12106.t1	ref|XP_002879825.1| hypothetical protein ARALYDRAFT_483018 [Arabidopsis lyrata subsp. lyrata] gi|297325664|gb|EFH56084.1| hypothetical protein ARALYDRAFT_483018 [Arabidopsis lyrata subsp. lyrata]	322	319	0	99.1	95.3	98.1	hypothetical protein ARALYDRAFT_483018	gbpln	Arabidopsis lyrata	AT2G39840.1 | Symbols: TOPP4 | type one serine/threonine protein phosphatase 4 | chr2:16627430-16628789 FORWARD LENGTH=321	322	321	0	99.7	93.5	95.3
Rsa1.0_00355.1_g12107.t1	dbj|BAG50513.1| ascorbic acid oxidase [Brassica rapa subsp. chinensis]	571	577	0	101.1	87.4	93.3	ascorbic acid oxidase	gbpln	Brassica rapa	AT5G21105.1 | Symbols: | Plant L-ascorbate oxidase | chr5:7172727-7177409 FORWARD LENGTH=588	571	588	0	103.0	83.9	91.1
Rsa1.0_00355.1_g12108.t1	gb|EOA37492.1| hypothetical protein CARUB_v10011646mg [Capsella rubella]	421	506	1.00E-154	120.2	75.1	79.6	hypothetical protein CARUB_v10011646mg	gbpln	Capsella rubella	AT1G21380.1 | Symbols: | Target of Myb protein 1 | chr1:7485806-7488032 REVERSE LENGTH=506	421	506	1.00E-154	120.2	74.6	79.1
Rsa1.0_00355.1_g12109.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1546	2301	0	148.8	61.6	74.9	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1546	1262	1.00E-110	81.6	12.7	19.7
Rsa1.0_00355.1_g12110.t1	gb|EOA20396.1| hypothetical protein CARUB_v10000708mg [Capsella rubella]	510	524	1.00E-173	102.7	65.9	77.5	hypothetical protein CARUB_v10000708mg	gbpln	Capsella rubella	AT5G21120.1 | Symbols: EIL2 | ETHYLENE-INSENSITIVE3-like 2 | chr5:7182629-7184185 FORWARD LENGTH=518	510	518	1.00E-165	101.6	64.1	73.5
Rsa1.0_00355.1_g12111.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00355.1_g12112.t1	ref|NP_197612.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|29294053|gb|AAO73890.1| hypothetical protein [Arabidopsis thaliana] gi|52354467|gb|AAU44554.1| hypothetical protein AT5G21130 [Arabidopsis thaliana] gi|332005555|gb|AED92938.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	297	281	1.00E-83	94.6	56.6	70.4	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT5G21130.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr5:7185968-7186813 FORWARD LENGTH=281	297	281	3.00E-86	94.6	56.6	70.4
Rsa1.0_00355.1_g12113.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00355.1_g12114.t1	gb|EOA21152.1| hypothetical protein CARUB_v10001499mg [Capsella rubella]	316	315	1.00E-156	99.7	84.2	90.5	hypothetical protein CARUB_v10001499mg	gbpln	Capsella rubella	AT5G21140.1 | Symbols: emb1379 | embryo defective 1379 | chr5:7187416-7189521 REVERSE LENGTH=312	316	312	1.00E-149	98.7	83.2	88.3
Rsa1.0_00355.1_g12115.t1	gb|EOA19916.1| hypothetical protein CARUB_v10000166mg [Capsella rubella]	907	922	0	101.7	80.5	87.9	hypothetical protein CARUB_v10000166mg	gbpln	Capsella rubella	AT5G21150.1 | Symbols: AGO9 | Argonaute family protein | chr5:7193472-7198113 FORWARD LENGTH=896	907	896	0	98.8	80.4	88.9
Rsa1.0_00355.1_g12116.t1	ref|XP_002890258.1| hypothetical protein ARALYDRAFT_312763 [Arabidopsis lyrata subsp. lyrata] gi|297336100|gb|EFH66517.1| hypothetical protein ARALYDRAFT_312763 [Arabidopsis lyrata subsp. lyrata]	320	341	1.00E-37	106.6	24.4	25.3	hypothetical protein ARALYDRAFT_312763	gbpln	Arabidopsis lyrata	AT1G18030.1 | Symbols: | Protein phosphatase 2C family protein | chr1:6204400-6206678 FORWARD LENGTH=351	320	351	2.00E-39	109.7	24.1	25.0
Rsa1.0_00355.1_g12117.t1	gb|ABD65606.1| hypothetical protein 23.t00002 [Brassica oleracea]	108	433	5.00E-12	400.9	34.3	43.5	hypothetical protein 23.t00002	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00355.1_g12118.t1	ref|XP_002874032.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319869|gb|EFH50291.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	818	838	0	102.4	79.1	86.3	La domain-containing protein	gbpln	Arabidopsis lyrata	AT5G21160.1 | Symbols: | LA RNA-binding protein | chr5:7199191-7203879 REVERSE LENGTH=826	818	826	0	101.0	78.1	86.1
Rsa1.0_00355.1_g12119.t1	gb|EOA21286.1| hypothetical protein CARUB_v10001638mg [Capsella rubella]	88	285	5.00E-13	323.9	50.0	56.8	hypothetical protein CARUB_v10001638mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00355.1_g12120.t1	ref|XP_002871972.1| AMP-activated protein kinase [Arabidopsis lyrata subsp. lyrata] gi|297317809|gb|EFH48231.1| AMP-activated protein kinase [Arabidopsis lyrata subsp. lyrata]	223	319	1.00E-111	143.0	86.1	91.0	AMP-activated protein kinase	gbpln	Arabidopsis lyrata	AT5G21170.1 | Symbols: AKINBETA1 | 5'-AMP-activated protein kinase beta-2 subunit protein | chr5:7205718-7208239 FORWARD LENGTH=283	223	283	1.00E-112	126.9	86.1	91.0

Rsa1.0_00355.1.g12121.t1	ref|XP_002871678.1| F−box family protein [Arabidopsis lyrata subsp. lyrata] gi|297317515|gb|EFH47937.1| F−box family protein [Arabidopsis lyrata subsp. lyrata]	470	430	5.00E−44	91.5	28.7	37.0	F−box family protein	gbpln	Arabidopsis lyrata	AT5G15660.1 | Symbols: | F−box and associated interaction domains−containing protein | chr5:5095652−5097041 FORWARD LENGTH=438	470	438	1.00E−43	93.2	30.2	41.1
Rsa1.0_00355.1.g12122.t1	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	566	521	7.00E−71	92.0	26.0	36.0	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	AT2G17920.1 | Symbols: | nucleic acid binding;zinc ion binding | chr2:7782808−7783731 FORWARD LENGTH=307	566	307	2.00E−22	54.2	10.1	16.1
Rsa1.0_00355.1.g12123.t1	ref|XP_004251248.1| PREDICTED: calmodulin−like isoform 1 [Solanum lycopersicum]	149	180	4.00E−80	120.8	100.0	100.0	PREDICTED: calmodulin−like isoform 1	gbpln	Solanum lycopersicum	AT2G27030.3 | Symbols: CAM5 | calmodulin 5 | chr2:11532069−11534176 FORWARD LENGTH=181	149	181	6.00E−82	121.5	98.7	100.0
Rsa1.0_00355.1.g12124.t1	ref|NP_850861.2| CBL−interacting serine/threonine−protein kinase 26 [Arabidopsis thaliana] gi|189082529|sp|Q84VQ3.2|CIPKQ_ARATH RecName: Full=CBL−interacting serine/threonine−protein kinase 26; AltName: Full=SNF1−related kinase 3.26; AltName: Full=SOS2−like protein kinase PKS26 gi|332005565|gb|AED92948.1| CBL−interacting serine/threonine−protein kinase 26 [Arabidopsis thaliana]	447	439	0	98.2	84.1	90.4	CBL−interacting serine/threonine−protein kinase 26	gbpln	Arabidopsis thaliana	AT5G21326.1 | Symbols: | Ca2+regulated serine−threonine protein kinase family protein | chr5:7218081−7221743 FORWARD LENGTH=439	447	439	0	98.2	84.1	90.4
Rsa1.0_00356.1.g12125.t1	gb|AAL37170.1|AF319169_1 CBL−interacting protein kinase [Brassica napus]	440	441	0	100.2	97.0	98.6	CBL−interacting protein kinase	gbpln	Brassica napus	AT4G30960.1 | Symbols: CIPK6, SIP3, SNRK3.14, ATCIPK6 | SOS3−interacting protein 3 | chr4:15067400−15068725 FORWARD LENGTH=441	440	441	0	100.2	94.1	96.1
Rsa1.0_00356.1.g12126.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00356.1.g12127.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00356.1.g12128.t1	emb|CAA18195.1| putative protein [Arabidopsis thaliana] gi|7270000|emb|CAB79816.1| putative protein [Arabidopsis thaliana]	327	367	1.00E−130	112.2	74.6	78.6	putative protein	gbpln	Arabidopsis thaliana	AT4G30980.1 | Symbols: LRL2 | LJRHL1−like 2 | chr4:15079489−15081606 REVERSE LENGTH=310	327	310	1.00E−133	94.8	74.6	78.6
Rsa1.0_00356.1.g12129.t2	gb|AAM65252.1| unknown [Arabidopsis thaliana]	278	285	1.00E−116	102.5	73.4	84.2	unknown	gbpln	Arabidopsis thaliana	AT4G30993.2 | Symbols: | Calcineurin−like metallo−phosphoesterase superfamily protein | chr4:15098201−15099935 FORWARD LENGTH=285	278	285	1.00E−118	102.5	73.0	83.8
Rsa1.0_00356.1.g12130.t1	emb|CAA18194.1| putative protein [Arabidopsis thaliana] gi|7270001|emb|CAB79817.1| putative protein [Arabidopsis thaliana]	172	2895	1.00E−82	1683.1	92.4	97.7	putative protein	gbpln	Arabidopsis thaliana	AT2G24290.1 | Symbols: | Protein of unknown function (DUF1068) | chr2:10338779−10339859 FORWARD LENGTH=173	172	173	9.00E−85	100.6	85.5	94.2
Rsa1.0_00356.1.g12131.t1	ref|NP_194829.2| Calmodulin−binding protein [Arabidopsis thaliana] gi|332660443|gb|AEE85843.1| Calmodulin−binding protein [Arabidopsis thaliana]	553	562	0	101.6	83.2	90.1	Calmodulin−binding protein	gbpln	Arabidopsis thaliana	AT4G31000.1 | Symbols: | Calmodulin−binding protein | chr4:15103402−15105799 FORWARD LENGTH=562	553	562	0	101.6	83.2	90.1
Rsa1.0_00356.1.g12132.t1	ref|XP_002867317.1| hypothetical protein ARALYDRAFT_328615 [Arabidopsis lyrata subsp. lyrata] gi|297313153|gb|EFH43576.1| hypothetical protein ARALYDRAFT_328615 [Arabidopsis lyrata subsp. lyrata]	294	294	1.00E−164	100.0	93.5	98.0	hypothetical protein ARALYDRAFT_328615	gbpln	Arabidopsis lyrata	AT4G31020.1 | Symbols: | alpha/beta−Hydrolases superfamily protein | chr4:15108832−15110079 REVERSE LENGTH=294	294	294	1.00E−166	100.0	93.2	98.0
Rsa1.0_00356.1.g12133.t1	ref|NP_567865.1| CemA−like proton extrusion protein−like protein [Arabidopsis thaliana] gi|19347877|gb|AAL85996.1| unknown protein [Arabidopsis thaliana] gi|29824339|gb|AAP04130.1| unknown protein [Arabidopsis thaliana] gi|51968984|dbj|BAD43184.1| unknown protein [Arabidopsis thaliana] gi|51969232|dbj|BAD43308.1| unknown protein [Arabidopsis thaliana] gi|51971222|dbj|BAD44303.1| unknown protein [Arabidopsis thaliana] gi|51971232|dbj|BAD44308.1| unknown protein [Arabidopsis thaliana] gi|51971855|dbj|BAD44592.1| unknown protein [Arabidopsis thaliana] gi|110741205|dbj|BAF02153.1| hypothetical protein [Arabidopsis thaliana] gi|332660450|gb|AEE85850.1| CemA−like proton extrusion protein−like protein [Arabidopsis thaliana]	441	438	0	99.3	88.2	92.5	CemA−like proton extrusion protein−like protein	gbpln	Arabidopsis thaliana	AT4G31040.1 | Symbols: | CemA−like proton extrusion protein−related | chr4:15111811−15113881 REVERSE LENGTH=438	441	438	0	99.3	88.2	92.5

Rsa1.0_00356.1.g12134.t1	ref|NP_567866.1| Plastidial lipoyltransferase 2 [Arabidopsis thaliana] gi|75164691|sp|Q948J9.1|LIP2P_ARATH RecName: Full=Plastidial lipoyltransferase 2; AltName: Full=Lipoate-protein ligase 2p; AltName: Full=Lipoyl-[acyl-carrier-protein]-protein-N- lipoyltransferase 2p gi|15887052|dbj|BAB69449.1| lipoyltransferase [Arabidopsis thaliana] gi|62320326|dbj|BAD94675.1| putative protein [Arabidopsis thaliana] gi|90186250|gb|ABD91501.1| At4g31050 [Arabidopsis thaliana] gi|332660451|gb|AEE85851.1| Plastidial lipoyltransferase 2 [Arabidopsis thaliana]	519	278	1.00E-133	53.6	44.5	48.4	Plastidial lipoyltransferase 2	gbpln	Arabidopsis thaliana	AT4G31050.1 | Symbols: | Biotin/lipoate A/B protein ligase family | chr4:15114345-15115443 FORWARD LENGTH=278	519	278	1.00E-136	53.6	44.5	48.4
Rsa1.0_00356.1.g12135.t1	gb|EOA15750.1| hypothetical protein CARUB_v10006795mg [Capsella rubella]	699	806	0	115.3	68.1	79.7	hypothetical protein CARUB_v10006795mg	gbpln	Capsella rubella	AT4G31110.1 | Symbols: | Wall-associated kinase family protein | chr4:15127257-15129880 FORWARD LENGTH=793	699	793	0	113.4	67.8	78.8
Rsa1.0_00356.1.g12136.t1	gb|EOA15750.1| hypothetical protein CARUB_v10006795mg [Capsella rubella]	882	806	0	91.4	61.7	68.9	hypothetical protein CARUB_v10006795mg	gbpln	Capsella rubella	AT4G31100.1 | Symbols: | wall-associated kinase, putative | chr4:15123862-15126426 FORWARD LENGTH=786	882	786	0	89.1	60.1	68.0
Rsa1.0_00356.1.g12137.t4	gb|EOA18616.1| hypothetical protein CARUB_v10007189mg [Capsella rubella]	636	642	0	100.9	90.9	94.0	hypothetical protein CARUB_v10007189mg	gbpln	Capsella rubella	AT4G31120.1 | Symbols: SKB1, ATPRMT5 | SHK1 binding protein 1 | chr4:15132185-15136568 REVERSE LENGTH=642	636	642	0	100.9	89.5	93.4
Rsa1.0_00356.1.g12138.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00356.1.g12139.t1	ref|NP_567632.1| Subtilase family protein [Arabidopsis thaliana] gi|4455271|emb|CAB36807.1| serine protease-like protein [Arabidopsis thaliana] gi|7268960|emb|CAB81270.1| serine protease-like protein [Arabidopsis thaliana] gi|332659083|gb|AEE84483.1| Subtilase family protein [Arabidopsis thaliana]	703	772	0	109.8	75.8	84.4	Subtilase family protein	gbpln	Arabidopsis thaliana	AT4G21630.1 | Symbols: | Subtilase family protein | chr4:11492248-11495500 REVERSE LENGTH=772	703	772	0	109.8	75.8	84.4
Rsa1.0_00356.1.g12140.t2	ref|XP_002867835.1| hypothetical protein ARALYDRAFT_914502 [Arabidopsis lyrata subsp. lyrata] gi|297313671|gb|EFH44094.1| hypothetical protein ARALYDRAFT_914502 [Arabidopsis lyrata subsp. lyrata]	516	584	0	113.2	77.5	82.6	hypothetical protein ARALYDRAFT_914502	gbpln	Arabidopsis lyrata	AT4G21660.2 | Symbols: | proline-rich spliceosome-associated (PSP) family protein | chr4:11506259-11509772 REVERSE LENGTH=598	516	598	0	115.9	76.0	83.3
Rsa1.0_00356.1.g12141.t1	ref|XP_002869597.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315433|gb|EFH45856.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	185	538	3.00E-11	290.8	18.4	19.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G26680.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:13454853-13456418 FORWARD LENGTH=521	185	521	2.00E-13	281.6	17.8	20.0
Rsa1.0_00356.1.g12142.t1	gb|EOA21337.1| hypothetical protein CARUB_v10001699mg [Capsella rubella]	283	272	4.00E-14	96.1	23.7	37.8	hypothetical protein CARUB_v10001699mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00356.1.g12143.t1	ref|NP_194085.4| NUC173 domain-containing protein [Arabidopsis thaliana] gi|332659373|gb|AEE84773.1| NUC173 domain-containing protein [Arabidopsis thaliana]	896	1131	0	126.2	57.6	62.2	NUC173 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G23540.1 | Symbols: | ARM repeat superfamily protein | chr4:12280547-12286420 REVERSE LENGTH=1131	896	1131	0	126.2	57.6	62.2
Rsa1.0_00356.1.g12144.t1	ref|XP_002869776.1| hypothetical protein ARALYDRAFT_914244 [Arabidopsis lyrata subsp. lyrata] gi|297315612|gb|EFH46035.1| hypothetical protein ARALYDRAFT_914244 [Arabidopsis lyrata subsp. lyrata]	282	400	1.00E-121	141.8	84.8	92.2	hypothetical protein ARALYDRAFT_914244	gbpln	Arabidopsis lyrata	AT4G23530.1 | Symbols: | Protein of unknown function (DUF793) | chr4:12279171-12280361 FORWARD LENGTH=396	282	396	1.00E-118	140.4	83.7	91.5
Rsa1.0_00357.1.g12145.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00357.1.g12146.t1	gb|EOA40409.1| hypothetical protein CARUB_v10009135mg [Capsella rubella]	431	445	0	103.2	81.9	91.6	hypothetical protein CARUB_v10009135mg	gbpln	Capsella rubella	AT1G31660.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Bystin (InterPro:IPR007955); Has 475 Blast hits to 467 proteins in 210 species: Archae - 0; Bacteria - 9; Metazoa - 155; Fungi - 139; Plants - 55; Viruses - 0; Other Eukaryotes - 117 (source: NCBI BLink). | chr1:11331176-11333440 REVERSE LENGTH=444	431	444	0	103.0	82.6	91.2
Rsa1.0_00357.1.g12147.t14	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	602	1449	3.00E-40	240.7	19.3	27.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	602	746	8.00E-24	123.9	8.1	10.1

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<tr><td>Rsa1.0_00357.1.g12148.t1</td><td>gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]</td><td>165</td><td>1463</td><td>1.00E-19</td><td>886.7</td><td>32.7</td><td>41.2</td><td>F5J5.1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<tr><td>Rsa1.0_00357.1.g12153.t1</td><td>gb|EOA36555.1| hypothetical protein CARUB_v10011695mg [Capsella rubella]</td><td>411</td><td>411</td><td>1.00E-175</td><td>100.0</td><td>73.5</td><td>83.2</td><td>hypothetical protein CARUB_v10011695mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G31790.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:11394744-11395973 REVERSE LENGTH=409</td><td>411</td><td>409</td><td>1.00E-175</td><td>99.5</td><td>75.2</td><td>83.5</td></tr>
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<tr><td>Rsa1.0_00358.1.g12160.t1</td><td>gb|AFI44621.1| putative male sterile protein [Brassica rapa subsp. pekinensis] gi|387913740|gb|AFK10493.1| YABBY1 [Brassica rapa var. parachinensis]</td><td>233</td><td>233</td><td>1.00E-133</td><td>100.0</td><td>98.3</td><td>99.1</td><td>putative male sterile protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT2G45190.1 | Symbols: AFO, FIL, YAB1 | Plant-specific transcription factor YABBY family protein | chr2:18628450-18630552 REVERSE LENGTH=229</td><td>233</td><td>229</td><td>1.00E-109</td><td>98.3</td><td>83.3</td><td>87.1</td></tr>
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<tr><td>Rsa1.0_00358.1.g12162.t1</td><td>ref|XP_002882002.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327841|gb|EFH58261.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>448</td><td>511</td><td>0</td><td>114.1</td><td>88.4</td><td>93.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G45220.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr2:18644281-18646394 REVERSE LENGTH=511</td><td>448</td><td>511</td><td>0</td><td>114.1</td><td>87.5</td><td>92.9</td></tr>
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<tr><td>Rsa1.0_00358.1.g12164.t1</td><td>sp|P17688.1|AROA_BRANA RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Flags: Precursor gi|17815|emb|CAA35839.1| 5-enolpyruvylshikimate-3-phosphate synthase [Brassica napus]</td><td>521</td><td>516</td><td>0</td><td>99.0</td><td>94.0</td><td>95.6</td><td>RecName: Full=3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic; AltName: Full=5-enolpyruvylshikimate-3-phosphate synthase; Short=EPSP synthase; Flags: Precursor gi|17815|emb|CAA35839.1| 5-enolpyruvylshikimate-3-phosphate synthase</td><td>gbpln</td><td>Brassica napus</td><td>AT2G45300.1 | Symbols: | RNA 3'-terminal phosphate cyclase/enolpyruvate transferase, alpha/beta | chr2:18677518-18679868 FORWARD LENGTH=520</td><td>521</td><td>520</td><td>0</td><td>99.8</td><td>91.4</td><td>93.7</td></tr>
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<tr><td>Rsa1.0_00358.1.g12166.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00358.1.g12167.t1</td><td>gb|AFJ66169.1| hypothetical protein 11M19.13 [Arabidopsis halleri]</td><td>610</td><td>1273</td><td>1.00E-144</td><td>208.7</td><td>42.6</td><td>51.8</td><td>hypothetical protein 11M19.13</td><td>gbpln</td><td>Arabidopsis halleri</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>610</td><td>1262</td><td>2.00E-21</td><td>206.9</td><td>8.5</td><td>13.4</td></tr>
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Rsa1.0_00358.1.g12168.t1	gb|EOA26345.1| hypothetical protein CARUB_v10022725mg [Capsella rubella]	695	723	0	104.0	87.2	91.5	hypothetical protein CARUB_v10022725mg	gbpln	Capsella rubella	AT2G45340.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:18691739-18694466 FORWARD LENGTH=691	695	691	0	99.4	87.1	90.8
Rsa1.0_00358.1.g12169.t1	gb|EOA27861.1| hypothetical protein CARUB_v10024019mg [Capsella rubella]	223	221	1.00E-110	99.1	86.1	93.3	hypothetical protein CARUB_v10024019mg	gbpln	Capsella rubella	AT2G45360.1 | Symbols: | Protein of unknown function (DUF1442) | chr2:18698619-18699360 FORWARD LENGTH=215	223	215	1.00E-97	96.4	85.2	89.2
Rsa1.0_00358.1.g12170.t1	ref|XP_002882011.1| dihydroflavonol 4-reductase family [Arabidopsis lyrata subsp. lyrata] gi|297327850|gb|EFH58270.1| dihydroflavonol 4-reductase family [Arabidopsis lyrata subsp. lyrata]	360	360	0	100.0	90.3	93.3	dihydroflavonol 4-reductase family	gbpln	Arabidopsis lyrata	AT2G45400.1 | Symbols: BEN1 | NAD(P)-binding Rossmann-fold superfamily protein | chr2:18703960-18706235 REVERSE LENGTH=364	360	364	1.00E-177	101.1	85.8	89.7
Rsa1.0_00358.1.g12171.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00358.1.g12172.t1	ref|XP_003521945.1| PREDICTED: LOW QUALITY PROTEIN: LOB domain-containing protein 31-like [Glycine max]	104	217	8.00E-27	208.7	52.9	61.5	PREDICTED: LOW QUALITY PROTEIN: LOB domain-containing protein 31-like	gbenv/gbpln	Glycine max	AT2G45410.1 | Symbols: LBD19 | LOB domain-containing protein 19 | chr2:18712449-18713108 REVERSE LENGTH=191	104	191	5.00E-26	183.7	49.0	52.9
Rsa1.0_00358.1.g12173.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00358.1.g12174.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00358.1.g12175.t1	ref|XP_002880178.1| hypothetical protein ARALYDRAFT_483677 [Arabidopsis lyrata subsp. lyrata] gi|297326017|gb|EFH56437.1| hypothetical protein ARALYDRAFT_483677 [Arabidopsis lyrata subsp. lyrata]	253	260	1.00E-99	102.8	85.0	88.5	hypothetical protein ARALYDRAFT_483677	gbpln	Arabidopsis lyrata	AT2G45420.1 | Symbols: LBD18 | LOB domain-containing protein 18 | chr2:18718601-18720445 FORWARD LENGTH=262	253	262	1.00E-95	103.6	83.0	87.0
Rsa1.0_00358.1.g12176.t1	gb|EOA29249.1| hypothetical protein CARUB_v10025523mg [Capsella rubella]	311	316	1.00E-127	101.6	92.9	95.2	hypothetical protein CARUB_v10025523mg	gbpln	Capsella rubella	AT2G45430.1 | Symbols: AHL22 | AT-hook motif nuclear-localized protein 22 | chr2:18727848-18728801 FORWARD LENGTH=317	311	317	1.00E-128	101.9	93.9	95.8
Rsa1.0_00359.1.g12177.t1	gb|EOA29987.1| hypothetical protein CARUB_v10013092mg [Capsella rubella]	680	701	0	103.1	87.5	91.9	hypothetical protein CARUB_v10013092mg	gbpln	Capsella rubella	AT3G19830.2 | Symbols: NTMC2TYPE5.2, NTMC2T5.2 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:6886338-6889974 REVERSE LENGTH=693	680	693	0	101.9	85.6	90.4
Rsa1.0_00359.1.g12178.t1	ref|XP_002883208.1| hypothetical protein ARALYDRAFT_898376 [Arabidopsis lyrata subsp. lyrata] gi|297329048|gb|EFH59467.1| hypothetical protein ARALYDRAFT_898376 [Arabidopsis lyrata subsp. lyrata]	762	835	0	109.6	79.7	86.1	hypothetical protein ARALYDRAFT_898376	gbpln	Arabidopsis lyrata	AT3G19840.1 | Symbols: ATPRP40C, PRP40C | pre-mRNA-processing protein 40C | chr3:6891228-6897227 FORWARD LENGTH=835	762	835	0	109.6	77.2	84.6
Rsa1.0_00359.1.g12179.t1	gb|EOA13622.1| hypothetical protein CARUB_v10026692mg [Capsella rubella]	460	350	0	76.1	68.9	71.1	hypothetical protein CARUB_v10026692mg	gbpln	Capsella rubella	AT5G50960.1 | Symbols: NBP35, ATNBP35 | nucleotide binding protein 35 | chr5:20734267-20735824 FORWARD LENGTH=350	460	350	0	76.1	67.4	71.1
Rsa1.0_00359.1.g12180.t1	ref|XP_002885337.1| hypothetical protein ARALYDRAFT_898378 [Arabidopsis lyrata subsp. lyrata] gi|297331177|gb|EFH61596.1| hypothetical protein ARALYDRAFT_898378 [Arabidopsis lyrata subsp. lyrata]	383	392	1.00E-107	102.3	56.9	72.6	hypothetical protein ARALYDRAFT_898378	gbpln	Arabidopsis lyrata	AT3G20030.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6990254-6991462 FORWARD LENGTH=402	383	402	1.00E-108	105.0	59.5	70.0
Rsa1.0_00359.1.g12181.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00359.1.g12182.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00359.1.g12183.t1	gb|EOA30992.1| hypothetical protein CARUB_v10014137mg [Capsella rubella]	314	335	1.00E-126	106.7	79.0	87.3	hypothetical protein CARUB_v10014137mg	gbpln	Capsella rubella	AT3G19910.1 | Symbols: | RING/U-box superfamily protein | chr3:6926497-6929324 FORWARD LENGTH=340	314	340	1.00E-127	108.3	79.3	87.9
Rsa1.0_00359.1.g12184.t1	gb|EOA30543.1| hypothetical protein CARUB_v10013663mg [Capsella rubella]	438	458	0	104.6	86.8	92.5	hypothetical protein CARUB_v10013663mg	gbpln	Capsella rubella	AT3G19920.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64230.1); Has 217 Blast hits to 217 proteins in 16 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 215; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6929840-6931771 REVERSE LENGTH=416	438	416	0	95.0	83.3	88.1
Rsa1.0_00359.1.g12185.t1	gb|EOA30349.1| hypothetical protein CARUB_v10013472mg [Capsella rubella]	514	514	0	100.0	95.1	98.2	hypothetical protein CARUB_v10013472mg	gbpln	Capsella rubella	AT3G19930.1 | Symbols: STP4, ATSTP4 | sugar transporter 4 | chr3:6935048-6936841 FORWARD LENGTH=514	514	514	0	100.0	94.9	98.2
Rsa1.0_00359.1.g12186.t1	ref|XP_002883213.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297329053|gb|EFH59472.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	276	330	4.00E-84	119.6	71.7	80.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G19950.1 | Symbols: | RING/U-box superfamily protein | chr3:6942853-6943839 FORWARD LENGTH=328	276	328	1.00E-82	118.8	68.5	78.3

Rsa1.0_00359.1_g12187.t13	ref|XP_002883217.1| hypothetical protein ARALYDRAFT_479514 [Arabidopsis lyrata subsp. lyrata] gi|297329057|gb|EFH59476.1| hypothetical protein ARALYDRAFT_479514 [Arabidopsis lyrata subsp. lyrata]	1246	1166	0	93.6	86.2	89.1	hypothetical protein ARALYDRAFT_479514	gbpln	Arabidopsis lyrata	AT3G19960.1 | Symbols: ATM1 | myosin 1 | chr3:6949787-6956736 FORWARD LENGTH=1166	1246	1166	0	93.6	86.0	89.2
Rsa1.0_00359.1_g12188.t1	gb|EOA32491.1| hypothetical protein CARUB_v10015771mg [Capsella rubella]	440	441	0	100.2	88.9	94.1	hypothetical protein CARUB_v10015771mg	gbpln	Capsella rubella	AT3G19970.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:6959644-6961367 FORWARD LENGTH=434	440	434	0	98.6	86.1	92.5
Rsa1.0_00359.1_g12189.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00359.1_g12190.t1	ref|NP_188632.1| phytochrome-associated serine/threonine protein phosphatase 3 [Arabidopsis thaliana] gi|75311171|sp|Q9LHE7.1|FYPP3_ARATH RecName: Full=Phytochrome-associated serine/threonine-protein phosphatase 3; Short=AtFyPP3; AltName: Full=Protein EMBRYO DEFECTIVE 2736 gi|14582206|gb|AAK69404.1|AF275664_1 serine/threonine protein phosphatase [Arabidopsis thaliana] gi|11994773|dbj|BAB03163.1| phosphoprotein phosphatase [Arabidopsis thaliana] gi|17381249|gb|AAL36043.1| AT3g19980/MZE19_3 [Arabidopsis thaliana] gi|20453383|gb|AAM19930.1| AT3g19980/MZE19_3 [Arabidopsis thaliana] gi|332642794|gb|AEE76315.1| phytochrome-associated serine/threonine protein phosphatase 3 [Arabidopsis thaliana]	303	303	1.00E-177	100.0	97.7	99.7	phytochrome-associated serine/threonine protein phosphatase 3	gbpln	Arabidopsis thaliana	AT3G19980.1 | Symbols: ATFYPP3, EMB2736, STPP, FYPP3 | flower-specific, phytochrome-associated protein phosphatase 3 | chr3:6962008-6964761 FORWARD LENGTH=303	303	303	1.00E-180	100.0	97.7	99.7
Rsa1.0_00359.1_g12191.t1	ref|NP_188633.1| uncharacterized protein [Arabidopsis thaliana] gi|63003792|gb|AAY25425.1| At3g19990 [Arabidopsis thaliana] gi|111074436|gb|ABH04591.1| At3g19990 [Arabidopsis thaliana] gi|332642795|gb|AEE76316.1| uncharacterized protein AT3G19990 [Arabidopsis thaliana]	395	425	0	107.6	88.4	93.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G19990.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 118 Blast hits to 118 proteins in 41 species: Archae - 0; Bacteria - 42; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink). | chr3:6965671-6967102 FORWARD LENGTH=425	395	425	0	107.6	88.4	93.9
Rsa1.0_00359.1_g12192.t1	gb|EOA31005.1| hypothetical protein CARUB_v10014148mg [Capsella rubella]	309	308	1.00E-157	99.7	85.4	91.6	hypothetical protein CARUB_v10014148mg	gbpln	Capsella rubella	AT3G20000.1 | Symbols: TOM40 | translocase of the outer mitochondrial membrane 40 | chr3:6967685-6970247 FORWARD LENGTH=309	309	309	1.00E-159	100.0	84.5	90.6
Rsa1.0_00360.1_g12193.t1	ref|XP_002892997.1| hypothetical protein ARALYDRAFT_472054 [Arabidopsis lyrata subsp. lyrata] gi|297338839|gb|EFH69256.1| hypothetical protein ARALYDRAFT_472054 [Arabidopsis lyrata subsp. lyrata]	306	301	1.00E-143	98.4	86.3	91.2	hypothetical protein ARALYDRAFT_472054	gbpln	Arabidopsis lyrata	AT1G18340.1 | Symbols: | basal transcription factor complex subunit-related | chr1:6311612-6313734 REVERSE LENGTH=301	306	301	1.00E-144	98.4	85.0	90.8
Rsa1.0_00360.1_g12194.t1	ref|NP_173273.2| ATP binding microtubule motor family protein [Arabidopsis thaliana] gi|19979627|dbj|BAB88748.1| AtNACK1 kinesin-like protein [Arabidopsis thaliana] gi|332191587|gb|AEE29708.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]	978	974	0	99.6	91.6	94.6	ATP binding microtubule motor family protein	gbpln	Arabidopsis thaliana	AT1G18370.1 | Symbols: HIK, ATNACK1, NACK1 | ATP binding microtubule motor family protein | chr1:6319732-6323820 REVERSE LENGTH=974	978	974	0	99.6	91.6	94.6
Rsa1.0_00360.1_g12195.t1	ref|XP_002890272.1| F15H18.11 [Arabidopsis lyrata subsp. lyrata] gi|297336114|gb|EFH66531.1| F15H18.11 [Arabidopsis lyrata subsp. lyrata]	884	1143	0	129.3	72.2	82.4	F15H18.11	gbpln	Arabidopsis lyrata	AT1G18390.2 | Symbols: | Protein kinase superfamily protein | chr1:6327463-6329935 FORWARD LENGTH=654	884	654	0	74.0	58.1	63.6
Rsa1.0_00360.1_g12196.t1	gb|AAW81732.1| putative bZIPtranscription factor protein [Brassica oleracea]	247	263	1.00E-106	106.5	86.2	91.1	putative bZIPtranscription factor protein	gbpln	Brassica oleracea	AT1G18400.1 | Symbols: BEE1 | BR enhanced expression 1 | chr1:6331464-6333576 FORWARD LENGTH=260	247	260	4.00E-92	105.3	79.4	85.8
Rsa1.0_00360.1_g12197.t2	gb|AAW81733.1| Putative Kinesin motor protein-related [Brassica oleracea]	1224	1116	0	91.2	82.2	85.4	Putative Kinesin motor protein-related	gbpln	Brassica oleracea	AT1G18410.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:6336528-6342460 REVERSE LENGTH=1140	1224	1140	0	93.1	52.4	57.4

Rsa1.0_00360.1.g12198.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2131	1274	0	59.8	33.3	42.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2131	575	9.00E-67	27.0	8.5	12.8
Rsa1.0_00360.1.g12199.t1	gb|AAW81734.1| Putative expressed protein [Brassica oleracea]	602	581	0	96.5	88.4	91.2	Putative expressed protein	gbpln	Brassica oleracea	AT1G18420.1 | Symbols: | Aluminium activated malate transporter family protein | chr1:6343330-6345689 FORWARD LENGTH=581	602	581	0	96.5	76.7	83.4
Rsa1.0_00360.1.g12200.t1	gb|AAF25998.1|AC013354_17 F15H18.8 [Arabidopsis thaliana]	761	777	0	102.1	78.6	82.9	F15H18.8	gbpln	Arabidopsis thaliana	AT1G18450.1 | Symbols: ATARP4, ARP4 | actin-related protein 4 | chr1:6348199-6351766 FORWARD LENGTH=441	761	441	0	58.0	54.5	56.2
Rsa1.0_00360.1.g12201.t1	gb|AAW81737.1| Putative finger family protein [Brassica oleracea]	428	467	0	109.1	94.4	96.3	Putative finger family protein	gbpln	Brassica oleracea	AT1G18470.1 | Symbols: | Transmembrane Fragile-X-F-associated protein | chr1:6356407-6360057 REVERSE LENGTH=467	428	467	0	109.1	90.9	95.1
Rsa1.0_00360.1.g12202.t2	gb|AAF26001.1|AC013354_20 F15H18.4 [Arabidopsis thaliana]	1400	1702	0	121.6	74.5	83.1	F15H18.4	gbpln	Arabidopsis thaliana	AT1G18485.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:6363172-6366084 FORWARD LENGTH=970	1400	970	0	69.3	55.7	62.2
Rsa1.0_00360.1.g12203.t1	ref|XP_002874902.1| hypothetical protein ARALYDRAFT_911948 [Arabidopsis lyrata subsp. lyrata] gi|297320739|gb|EFH51161.1| hypothetical protein ARALYDRAFT_911948 [Arabidopsis lyrata subsp. lyrata]	118	120	9.00E-40	101.7	68.6	83.1	hypothetical protein ARALYDRAFT_911948	gbpln	Arabidopsis lyrata	AT4G02655.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G18486.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:1158876-1159241 FORWARD LENGTH=121	118	121	3.00E-41	102.5	66.1	82.2
Rsa1.0_00360.1.g12204.t1	gb|AAW81740.1| Putative Expressed protein [Brassica oleracea]	277	276	1.00E-154	99.6	94.9	97.5	Putative Expressed protein	gbpln	Brassica oleracea	AT1G18490.1 | Symbols: | Protein of unknown function (DUF1637) | chr1:6367116-6368640 FORWARD LENGTH=282	277	282	1.00E-141	101.8	86.6	92.4
Rsa1.0_00360.1.g12205.t1	gb|AAW81741.1| Putative 2-isopropylmalate synthase [Brassica oleracea]	656	623	0	95.0	89.6	92.1	Putative 2-isopropylmalate synthase	gbpln	Brassica oleracea	AT1G18500.1 | Symbols: MAML-4, IPMS1 | methylthioalkylmalate synthase-like 4 | chr1:6369347-6372861 FORWARD LENGTH=631	656	631	0	96.2	84.6	89.8
Rsa1.0_00360.1.g12206.t1	gb|AAW81742.1| Putative hypothetical protein [Brassica oleracea]	248	248	1.00E-128	100.0	88.7	94.0	Putative hypothetical protein	gbpln	Brassica oleracea	AT1G18510.1 | Symbols: TET16 | tetraspanin 16 | chr1:6373295-6374090 FORWARD LENGTH=238	248	238	1.00E-109	96.0	71.8	83.1
Rsa1.0_00360.1.g12207.t1	ref|XP_002890283.1| hypothetical protein ARALYDRAFT_889272 [Arabidopsis lyrata subsp. lyrata] gi|297336125|gb|EFH66542.1| hypothetical protein ARALYDRAFT_889272 [Arabidopsis lyrata subsp. lyrata]	272	272	1.00E-145	100.0	90.8	96.3	hypothetical protein ARALYDRAFT_889272	gbpln	Arabidopsis lyrata	AT1G18520.1 | Symbols: TET11 | tetraspanin11 | chr1:6375051-6376178 FORWARD LENGTH=271	272	271	1.00E-145	99.6	90.4	95.6
Rsa1.0_00360.1.g12208.t1	gb|EOA33232.1| hypothetical protein CARUB_v10021263mg [Capsella rubella]	234	233	1.00E-106	99.6	87.6	94.0	hypothetical protein CARUB_v10021263mg	gbpln	Capsella rubella	AT1G74050.1 | Symbols: | Ribosomal protein L6 family protein | chr1:27847256-27848680 REVERSE LENGTH=233	234	233	1.00E-109	99.6	90.6	94.4
Rsa1.0_00360.1.g12209.t1	gb|EOA39778.1| hypothetical protein CARUB_v10008434mg [Capsella rubella]	739	724	0	98.0	81.7	88.5	hypothetical protein CARUB_v10008434mg	gbpln	Capsella rubella	AT1G18550.1 | Symbols: | ATP binding microtubule motor family protein | chr1:6381656-6384340 REVERSE LENGTH=725	739	725	0	98.1	81.1	87.3
Rsa1.0_00360.1.g12210.t1	gb|ACR48188.1| MYB domain protein 51-2 [Brassica rapa subsp. pekinensis]	333	333	1.00E-138	100.0	81.7	89.8	MYB domain protein 51-2	gbpln	Brassica rapa	AT1G18570.1 | Symbols: MYB51, AtMYB51, BW51A, BW51B, HIG1 | myb domain protein 51 | chr1:6389765-6391026 FORWARD LENGTH=352	333	352	1.00E-120	105.7	75.7	81.7
Rsa1.0_00361.1.g12211.t1	gb|EOA36377.1| hypothetical protein CARUB_v10010783mg [Capsella rubella]	99	82	4.00E-23	82.8	58.6	63.6	hypothetical protein CARUB_v10010783mg	gbpln	Capsella rubella	AT1G30250.1 | Symbols: | unknown protein; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10647253-10647501 REVERSE LENGTH=82	99	82	2.00E-22	82.8	53.5	59.6
Rsa1.0_00361.1.g12212.t1	ref|NP_001077628.1| uncharacterized protein [Arabidopsis thaliana] gi|110742078|dbj|BAE98970.1| hypothetical protein [Arabidopsis thaliana] gi|332193077|gb|AEE31198.1| uncharacterized protein AT1G30240 [Arabidopsis thaliana]	811	827	0	102.0	79.2	86.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G30240.2 | Symbols: | unknown protein; Has 169 Blast hits to 168 proteins in 75 species: Archae - 0; Bacteria - 0; Metazoa - 49; Fungi - 68; Plants - 46; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:10641241-10645838 REVERSE LENGTH=827	811	827	0	102.0	79.2	86.2

<table>
<tr><td>Rsa1.0_00361.1.g12213.t1</td><td>gb|ABK78691.1| putative elongation factor 1-beta [Brassica rapa]</td><td>271</td><td>230</td><td>1.00E-106</td><td>84.9</td><td>81.2</td><td>83.4</td><td>putative elongation factor 1-beta</td><td>gbpln</td><td>Brassica rapa</td><td>AT2G18110.1 | Symbols: | Translation elongation factor EF1B/ribosomal protein S6 family protein | chr2:7872636-7873713 FORWARD LENGTH=231</td><td>271</td><td>231</td><td>1.00E-106</td><td>85.2</td><td>77.5</td><td>82.7</td></tr>
<tr><td>Rsa1.0_00361.1.g12214.t1</td><td>ref|XP_002893607.1| ATINT2 [Arabidopsis lyrata subsp. lyrata] gi|297339449|gb|EFH69866.1| ATINT2 [Arabidopsis lyrata subsp. lyrata]</td><td>571</td><td>580</td><td>0</td><td>101.6</td><td>90.7</td><td>95.6</td><td>ATINT2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30220.1 | Symbols: ATINT2, INT2 | inositol transporter 2 | chr1:10632957-10635439 REVERSE LENGTH=580</td><td>571</td><td>580</td><td>0</td><td>101.6</td><td>90.4</td><td>95.6</td></tr>
<tr><td>Rsa1.0_00361.1.g12215.t2</td><td>dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]</td><td>271</td><td>329</td><td>2.00E-30</td><td>121.4</td><td>27.7</td><td>34.7</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G50930.1 | Symbols: | Histone superfamily protein | chr5:20722069-20724317 FORWARD LENGTH=242</td><td>271</td><td>242</td><td>2.00E-29</td><td>89.3</td><td>24.4</td><td>28.8</td></tr>
<tr><td>Rsa1.0_00361.1.g12216.t1</td><td>dbj|BAJ34242.1| unnamed protein product [Thellungiella halophila]</td><td>319</td><td>339</td><td>1.00E-111</td><td>106.3</td><td>83.1</td><td>89.3</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G30210.2 | Symbols: TCP24 | TEOSINTE BRANCHED 1, cycloidea, and PCF family 24 | chr1:10628754-10629728 REVERSE LENGTH=324</td><td>319</td><td>324</td><td>1.00E-107</td><td>101.6</td><td>79.3</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00361.1.g12217.t1</td><td>gb|AAG50859.1|AC074176_8 En/Spm-like transposon protein, putative [Arabidopsis thaliana]</td><td>148</td><td>413</td><td>1.00E-11</td><td>279.1</td><td>29.1</td><td>45.9</td><td>En/Spm-like transposon protein, putative</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00361.1.g12218.t1</td><td>ref|XP_002893604.1| hypothetical protein ARALYDRAFT_473236 [Arabidopsis lyrata subsp. lyrata] gi|297339446|gb|EFH69863.1| hypothetical protein ARALYDRAFT_473236 [Arabidopsis lyrata subsp. lyrata]</td><td>717</td><td>366</td><td>1.00E-151</td><td>51.0</td><td>38.5</td><td>43.1</td><td>hypothetical protein ARALYDRAFT_473236</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30170.1 | Symbols: | Protein of unknown function (DUF295) | chr1:10608068-10609529 REVERSE LENGTH=366</td><td>717</td><td>366</td><td>2.33E-156</td><td>51.0</td><td>38.5</td><td>42.7</td></tr>
<tr><td>Rsa1.0_00361.1.g12219.t1</td><td>ref|XP_002890853.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336695|gb|EFH67112.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>129</td><td>131</td><td>4.00E-49</td><td>101.6</td><td>79.8</td><td>89.9</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30135.1 | Symbols: JAZ8, TIFY5A | jasmonate-zim-domain protein 8 | chr1:10596516-10597095 FORWARD LENGTH=131</td><td>129</td><td>131</td><td>1.00E-49</td><td>101.6</td><td>78.3</td><td>88.4</td></tr>
<tr><td>Rsa1.0_00361.1.g12220.t1</td><td>ref|NP_564348.1| uncharacterized protein [Arabidopsis thaliana] gi|42571697|ref|NP_973939.1| uncharacterized protein [Arabidopsis thaliana] gi|12321635|gb|AAG50861.1|AC074176_10 unknown protein [Arabidopsis thaliana] gi|222423586|dbj|BAH19762.1| AT1G30130 [Arabidopsis thaliana] gi|332193061|gb|AEE31182.1| uncharacterized protein AT1G30130 [Arabidopsis thaliana] gi|332193062|gb|AEE31183.1| uncharacterized protein AT1G30130 [Arabidopsis thaliana]</td><td>307</td><td>311</td><td>1.00E-153</td><td>101.3</td><td>85.3</td><td>93.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30130.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1365 (InterPro:IPR010775); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:10587666-10589222 FORWARD LENGTH=311</td><td>307</td><td>311</td><td>1.00E-156</td><td>101.3</td><td>85.3</td><td>93.2</td></tr>
<tr><td>Rsa1.0_00361.1.g12221.t1</td><td>gb|EOA40587.1| hypothetical protein CARUB_v10009315mg [Capsella rubella]</td><td>409</td><td>407</td><td>0</td><td>99.5</td><td>93.2</td><td>95.4</td><td>hypothetical protein CARUB_v10009315mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30120.1 | Symbols: PDH-E1 BETA | pyruvate dehydrogenase E1 beta | chr1:10584350-10586477 REVERSE LENGTH=406</td><td>409</td><td>406</td><td>0</td><td>99.3</td><td>92.4</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00361.1.g12222.t1</td><td>gb|EOA38468.1| hypothetical protein CARUB_v10010189mg [Capsella rubella]</td><td>175</td><td>232</td><td>6.00E-93</td><td>132.6</td><td>92.6</td><td>97.7</td><td>hypothetical protein CARUB_v10010189mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30110.2 | Symbols: NUDX25 | nudix hydrolase homolog 25 | chr1:10582700-10583821 FORWARD LENGTH=175</td><td>175</td><td>175</td><td>1.00E-93</td><td>100.0</td><td>91.4</td><td>97.7</td></tr>
<tr><td>Rsa1.0_00361.1.g12223.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00361.1.g12224.t1</td><td>ref|XP_002893598.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339440|gb|EFH69857.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>382</td><td>376</td><td>0</td><td>98.4</td><td>85.9</td><td>89.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30080.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr1:10551231-10553167 REVERSE LENGTH=408</td><td>382</td><td>408</td><td>0</td><td>106.8</td><td>84.6</td><td>89.0</td></tr>
<tr><td>Rsa1.0_00361.1.g12225.t1</td><td>gb|EOA37925.1| hypothetical protein CARUB_v10009392mg [Capsella rubella]</td><td>379</td><td>390</td><td>1.00E-144</td><td>102.9</td><td>81.3</td><td>86.8</td><td>hypothetical protein CARUB_v10009392mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G01970.1); Has 246 Blast hits to 244 proteins in 61 species: Archae - 0; Bacteria - 8; Metazoa - 78; Fungi - 10; Plants - 117; Viruses - 0; Other Eukaryotes - 33 (source: NCBI BLink). | chr1:10543177-10544418 FORWARD LENGTH=389</td><td>379</td><td>389</td><td>1.00E-140</td><td>102.6</td><td>79.4</td><td>85.2</td></tr>
<tr><td>Rsa1.0_00361.1.g12226.t1</td><td>gb|EOA38156.1| hypothetical protein CARUB_v10009631mg [Capsella rubella]</td><td>335</td><td>343</td><td>0</td><td>102.4</td><td>91.0</td><td>96.4</td><td>hypothetical protein CARUB_v10009631mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30040.1 | Symbols: ATGA2OX2, GA2OX2 | gibberellin 2-oxidase | chr1:10537769-10539570 FORWARD LENGTH=341</td><td>335</td><td>341</td><td>1.00E-180</td><td>101.8</td><td>89.3</td><td>95.2</td></tr>
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<tr><td>Rsa1.0_00362.1.g12227.t1</td><td>ref|NP_199763.1| putative WRKY transcription factor 48 [Arabidopsis thaliana] gi|20978785|sp|Q9FGZ4.1|WRK48_ARATH RecName: Full=Probable WRKY transcription factor 48; AltName: Full=WRKY DNA-binding protein 48 gi|17064166|gb|AAL35290.1|AF442397_1 WRKY transcription factor 48 [Arabidopsis thaliana] gi|10177618|dbj|BAB10765.1| unnamed protein product [Arabidopsis thaliana] gi|17380792|gb|AAL36226.1| unknown protein [Arabidopsis thaliana] gi|20259613|gb|AAM14163.1| unknown protein [Arabidopsis thaliana] gi|332008441|gb|AED95824.1| putative WRKY transcription factor 48 [Arabidopsis thaliana]</td><td>399</td><td>399</td><td>1.00E-136</td><td>100.0</td><td>84.7</td><td>89.0</td><td>putative WRKY transcription factor 48</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G49520.1 | Symbols: WRKY48, ATWRKY48 | WRKY DNA-binding protein 48 | chr5:20090890-20092867 FORWARD LENGTH=399</td><td>399</td><td>399</td><td>1.00E-139</td><td>100.0</td><td>84.7</td><td>89.0</td></tr>
<tr><td>Rsa1.0_00362.1.g12228.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00362.1.g12229.t1</td><td>ref|XP_002863995.1| hypothetical protein ARALYDRAFT_495012 [Arabidopsis lyrata subsp. lyrata] gi|297309830|gb|EFH40254.1| hypothetical protein ARALYDRAFT_495012 [Arabidopsis lyrata subsp. lyrata]</td><td>696</td><td>676</td><td>0</td><td>97.1</td><td>70.8</td><td>79.3</td><td>hypothetical protein ARALYDRAFT_495012</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49530.1 | Symbols: | SIN-like family protein | chr5:20100934-20104242 FORWARD LENGTH=689</td><td>696</td><td>689</td><td>0</td><td>99.0</td><td>71.3</td><td>81.0</td></tr>
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<tr><td>Rsa1.0_00362.1.g12231.t1</td><td>gb|EOA14200.1| hypothetical protein CARUB_v10027352mg, partial [Capsella rubella]</td><td>114</td><td>135</td><td>2.00E-44</td><td>118.4</td><td>82.5</td><td>90.4</td><td>hypothetical protein CARUB_v10027352mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G49550.1 | Symbols: BLOS2 | Putative homolog of mammalian BLOC-1 Subunit 2. Protein - protein interaction with BLOS1. | chr5:20106702-20107156 REVERSE LENGTH=127</td><td>114</td><td>127</td><td>5.00E-47</td><td>111.4</td><td>82.5</td><td>89.5</td></tr>
<tr><td>Rsa1.0_00362.1.g12232.t1</td><td>ref|XP_002865742.1| hypothetical protein ARALYDRAFT_495017 [Arabidopsis lyrata subsp. lyrata] gi|297311577|gb|EFH42001.1| hypothetical protein ARALYDRAFT_495017 [Arabidopsis lyrata subsp. lyrata]</td><td>752</td><td>721</td><td>0</td><td>95.9</td><td>80.9</td><td>88.0</td><td>hypothetical protein ARALYDRAFT_495017</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49570.1 | Symbols: AtPNG1, PNG1 | peptide-N-glycanase 1 | chr5:20112071-20116125 REVERSE LENGTH=721</td><td>752</td><td>721</td><td>0</td><td>95.9</td><td>80.7</td><td>88.0</td></tr>
<tr><td>Rsa1.0_00362.1.g12233.t1</td><td>ref|NP_198678.1| MADS-box protein AGL73 [Arabidopsis thaliana] gi|10176830|dbj|BAB10152.1| MADS-box protein-like [Arabidopsis thaliana] gi|32402438|gb|AAN52801.1| MADS-box protein AGL73 [Arabidopsis thaliana] gi|332006959|gb|AED94342.1| MADS-box protein AGL73 [Arabidopsis thaliana]</td><td>348</td><td>349</td><td>4.00E-50</td><td>100.3</td><td>43.1</td><td>60.1</td><td>MADS-box protein AGL73</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G38620.1 | Symbols: | MADS-box transcription factor family protein | chr5:15463858-15464907 REVERSE LENGTH=349</td><td>348</td><td>349</td><td>1.00E-52</td><td>100.3</td><td>43.1</td><td>60.1</td></tr>
<tr><td>Rsa1.0_00362.1.g12234.t1</td><td>gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>364</td><td>1555</td><td>3.00E-48</td><td>427.2</td><td>32.7</td><td>46.7</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>364</td><td>303</td><td>2.00E-41</td><td>83.2</td><td>31.0</td><td>43.4</td></tr>
<tr><td>Rsa1.0_00362.1.g12235.t1</td><td>ref|XP_002863965.1| hypothetical protein ARALYDRAFT_331330 [Arabidopsis lyrata subsp. lyrata] gi|297309800|gb|EFH40224.1| hypothetical protein ARALYDRAFT_331330 [Arabidopsis lyrata subsp. lyrata]</td><td>1152</td><td>1532</td><td>0</td><td>133.0</td><td>69.7</td><td>80.7</td><td>hypothetical protein ARALYDRAFT_331330</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49160.1 | Symbols: MET1, MET2, METI, DDM2, DMT01, DMT1 | methyltransferase 1 | chr5:19932501-19938186 FORWARD LENGTH=1534</td><td>1152</td><td>1534</td><td>0</td><td>133.2</td><td>69.1</td><td>80.1</td></tr>
<tr><td>Rsa1.0_00362.1.g12236.t1</td><td>ref|NP_199769.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|10177624|dbj|BAB10771.1| unnamed protein product [Arabidopsis thaliana] gi|332008449|gb|AED95832.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]</td><td>678</td><td>695</td><td>0</td><td>102.5</td><td>77.7</td><td>85.5</td><td>chaperone DnaJ-domain containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G49580.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:20123823-20126813 REVERSE LENGTH=695</td><td>678</td><td>695</td><td>0</td><td>102.5</td><td>77.7</td><td>85.5</td></tr>
<tr><td>Rsa1.0_00362.1.g12237.t1</td><td>ref|XP_002864001.1| hypothetical protein ARALYDRAFT_917948 [Arabidopsis lyrata subsp. lyrata] gi|297309836|gb|EFH40260.1| hypothetical protein ARALYDRAFT_917948 [Arabidopsis lyrata subsp. lyrata]</td><td>170</td><td>172</td><td>1.00E-70</td><td>101.2</td><td>82.9</td><td>89.4</td><td>hypothetical protein ARALYDRAFT_917948</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49600.1 | Symbols: | Protein of unknown function, DUF538 | chr5:20130780-20131295 FORWARD LENGTH=171</td><td>170</td><td>171</td><td>9.00E-72</td><td>100.6</td><td>78.2</td><td>87.1</td></tr>
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<tr><td>Rsa1.0_00362.1.g12239.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00362.1.g12240.t1	ref|XP_002865745.1| AtMYB78 [Arabidopsis lyrata subsp. lyrata] gi|297311580|gb|EFH42004.1| AtMYB78 [Arabidopsis lyrata subsp. lyrata]	322	306	1.00E-116	95.0	70.5	80.1	AtMYB78	gbpln	Arabidopsis lyrata	AT5G49620.1 | Symbols: AtMYB78, MYB78 | myb domain protein 78 | chr5:20137491-20139384 REVERSE LENGTH=307	322	307	1.00E-114	95.3	67.7	79.2
Rsa1.0_00362.1.g12241.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00362.1.g12242.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00362.1.g12243.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00362.1.g12244.t1	gb|ACI14408.1| WRKY74-1 transcription factor [Brassica napus]	343	341	1.00E-180	99.4	92.4	97.1	WRKY74-1 transcription factor	gbpln	Brassica napus	AT5G28650.1 | Symbols: WRKY74, ATWRKY74 | WRKY DNA-binding protein 74 | chr5:10677790-10678945 REVERSE LENGTH=330	343	330	1.00E-168	96.2	86.3	91.3
Rsa1.0_00362.1.g12245.t1	ref|NP_001154744.1| TPX2 (targeting protein for Xklp2) family protein [Arabidopsis thaliana] gi|240256363|ref|NP_680247.4| TPX2 (targeting protein for Xklp2) family protein [Arabidopsis thaliana] gi|75149265|sp|Q84ZT9.1|WVD2_ARATH RecName: Full=Protein WAVE-DAMPENED 2; Short=AtWVD2 gi|28453880|gb|AAO43563.1| WAVE-DAMPENED2 [Arabidopsis thaliana] gi|332006439|gb|AED93822.1| TPX2 (targeting protein for Xklp2) family protein [Arabidopsis thaliana] gi|332006440|gb|AED93823.1| protein WAVE-DAMPENED 2 [Arabidopsis thaliana]	231	202	5.00E-78	87.4	71.4	77.9	TPX2 (targeting protein for Xklp2) family protein	gbpln	Arabidopsis thaliana	AT5G28646.2 | Symbols: WVD2 | TPX2 (targeting protein for Xklp2) protein family | chr5:10675192-10676151 FORWARD LENGTH=202	231	202	1.00E-80	87.4	71.4	77.9
Rsa1.0_00362.1.g12246.t1	ref|XP_002884455.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330295|gb|EFH60714.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	163	164	7.00E-47	100.6	65.6	69.9	nucleic acid binding protein	gbpln	Arabidopsis lyrata	AT3G04620.1 | Symbols: | Alba DNA/RNA-binding protein | chr3:1255660-1256739 REVERSE LENGTH=164	163	164	6.00E-49	100.6	65.0	69.9
Rsa1.0_00362.1.g12247.t1	gb|EOA21560.1| hypothetical protein CARUB_v10001969mg [Capsella rubella]	204	208	6.00E-72	102.0	96.6	98.0	hypothetical protein CARUB_v10001969mg	gbpln	Capsella rubella	AT5G28640.1 | Symbols: AN3, GIF, GIF1, ATGIF1 | SSXT family protein | chr5:10647831-10649620 REVERSE LENGTH=210	204	210	1.00E-72	102.9	94.6	96.1
Rsa1.0_00362.1.g12248.t1	gb|EOA30721.1| hypothetical protein CARUB_v10013864mg [Capsella rubella]	396	402	8.00E-93	101.5	57.1	67.4	hypothetical protein CARUB_v10013864mg	gbpln	Capsella rubella	AT3G04590.2 | Symbols: | AT hook motif DNA-binding family protein | chr3:1239245-1241603 REVERSE LENGTH=411	396	411	1.00E-91	103.8	55.8	65.7
Rsa1.0_00362.1.g12249.t1	ref|XP_002872313.1| hypothetical protein ARALYDRAFT_489651 [Arabidopsis lyrata subsp. lyrata] gi|297318150|gb|EFH48572.1| hypothetical protein ARALYDRAFT_489651 [Arabidopsis lyrata subsp. lyrata]	438	435	0	99.3	80.8	90.2	hypothetical protein ARALYDRAFT_489651	gbpln	Arabidopsis lyrata	AT5G28500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G04550.1); Has 109 Blast hits to 109 proteins in 49 species: Archae - 0; Bacteria - 67; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:10477810-10479114 FORWARD LENGTH=434	438	434	0	99.1	81.1	88.4
Rsa1.0_00362.1.g12250.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00362.1.g12251.t1	gb|EOA21624.1| hypothetical protein CARUB_v10002037mg [Capsella rubella]	195	191	2.00E-80	97.9	90.8	91.8	hypothetical protein CARUB_v10002037mg	gbpln	Capsella rubella	AT5G28490.1 | Symbols: LSH1 | Protein of unknown function (DUF640) | chr5:10454541-10455113 REVERSE LENGTH=190	195	190	6.00E-83	97.4	89.2	91.8
Rsa1.0_00362.1.g12252.t1	ref|XP_002872312.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318149|gb|EFH48571.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	569	561	0	98.6	83.7	91.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G28470.1 | Symbols: | Major facilitator superfamily protein | chr5:10429813-10432357 FORWARD LENGTH=559	569	559	0	98.2	81.7	90.0
Rsa1.0_00362.1.g12253.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00362.1.g12254.t1	gb|AAD24567.1|AF120335_1 putative transposase [Arabidopsis thaliana]	288	577	1.00E-108	200.3	63.9	79.2	putative transposase	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	288	696	2.00E-37	241.7	30.9	46.9

<table>
<tr><td>Rsa1.0_00362.1.g12255.t1</td><td>ref|NP_568506.2| putative trihelix DNA-binding protein [Arabidopsis thaliana] gi|75244603|sp|Q8H181.1|GTL2_ARATH RecName: Full=Trihelix transcription factor GTL2; AltName: Full=GT2-LIKE protein 2; Short=AtGTL2; AltName: Full=Trihelix DNA-binding protein GTL2 gi|23306422|gb|AAN17438.1| Unknown protein [Arabidopsis thaliana] gi|30725452|gb|AAP37748.1| At5g28300 [Arabidopsis thaliana] gi|332006404|gb|AED93787.1| trihelix transcription factor GTL2 [Arabidopsis thaliana]</td><td>595</td><td>619</td><td>0</td><td>104.0</td><td>77.6</td><td>85.5</td><td>putative trihelix DNA-binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G28300.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr5:10292789-10295101 REVERSE LENGTH=619</td><td>595</td><td>619</td><td>0</td><td>104.0</td><td>77.6</td><td>85.5</td></tr>
<tr><td>Rsa1.0_00362.1.g12256.t1</td><td>gb|EOA20282.1| hypothetical protein CARUB_v10000590mg [Capsella rubella]</td><td>585</td><td>567</td><td>0</td><td>96.9</td><td>86.2</td><td>90.1</td><td>hypothetical protein CARUB_v10000590mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G28290.1 | Symbols: ATNEK3, NEK3 | NIMA-related kinase 3 | chr5:10278880-10281880 REVERSE LENGTH=568</td><td>585</td><td>568</td><td>0</td><td>97.1</td><td>85.6</td><td>89.9</td></tr>
<tr><td>Rsa1.0_00362.1.g12257.t1</td><td>ref|XP_002872310.1| hypothetical protein ARALYDRAFT_910925 [Arabidopsis lyrata subsp. lyrata] gi|297318147|gb|EFH48569.1| hypothetical protein ARALYDRAFT_910925 [Arabidopsis lyrata subsp. lyrata]</td><td>641</td><td>609</td><td>0</td><td>95.0</td><td>67.4</td><td>78.6</td><td>hypothetical protein ARALYDRAFT_910925</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G28210.1 | Symbols: | mRNA capping enzyme family protein | chr5:10188586-10190463 FORWARD LENGTH=625</td><td>641</td><td>625</td><td>0</td><td>97.5</td><td>66.6</td><td>78.8</td></tr>
<tr><td>Rsa1.0_00362.1.g12258.t1</td><td>ref|XP_002872306.1| hypothetical protein ARALYDRAFT_489643 [Arabidopsis lyrata subsp. lyrata] gi|297318143|gb|EFH48565.1| hypothetical protein ARALYDRAFT_489643 [Arabidopsis lyrata subsp. lyrata]</td><td>294</td><td>288</td><td>1.00E-152</td><td>98.0</td><td>90.8</td><td>95.2</td><td>hypothetical protein ARALYDRAFT_489643</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G28150.1 | Symbols: | Plant protein of unknown function (DUF868) | chr5:10135826-10136695 FORWARD LENGTH=289</td><td>294</td><td>289</td><td>1.00E-147</td><td>98.3</td><td>88.8</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00363.1.g12259.t1</td><td>ref|XP_002882629.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297328469|gb|EFH58888.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]</td><td>321</td><td>297</td><td>1.00E-137</td><td>92.5</td><td>80.1</td><td>85.0</td><td>myb family transcription factor</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G09600.1 | Symbols: | Homeodomain-like superfamily protein | chr3:2946459-2948270 FORWARD LENGTH=298</td><td>321</td><td>298</td><td>1.00E-136</td><td>92.8</td><td>79.4</td><td>84.1</td></tr>
<tr><td>Rsa1.0_00363.1.g12260.t1</td><td>gb|EOA29622.1| hypothetical protein CARUB_v10014335mg [Capsella rubella]</td><td>263</td><td>282</td><td>2.00E-49</td><td>107.2</td><td>57.4</td><td>63.1</td><td>hypothetical protein CARUB_v10014335mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G53500.2 | Symbols: RSZ32, RS2Z32, At-RS2Z | RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain | chr3:19834557-19836507 REVERSE LENGTH=284</td><td>263</td><td>284</td><td>2.00E-32</td><td>108.0</td><td>25.5</td><td>27.0</td></tr>
<tr><td>Rsa1.0_00363.1.g12261.t1</td><td>ref|NP_187569.1| FAD/NAD(P)-binding oxidoreductase domain-containing protein [Arabidopsis thaliana] gi|6682237|gb|AAF23289.1|AC016661_14 putative oxidoreductase [Arabidopsis thaliana] gi|17381088|gb|AAL36356.1| putative oxidoreductase [Arabidopsis thaliana] gi|21436243|gb|AAM51260.1| putative oxidoreductase [Arabidopsis thaliana] gi|332641263|gb|AEE74784.1| FAD/NAD(P)-binding oxidoreductase domain-containing protein [Arabidopsis thaliana]</td><td>478</td><td>477</td><td>0</td><td>99.8</td><td>85.8</td><td>92.1</td><td>FAD/NAD(P)-binding oxidoreductase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G09580.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr3:2942614-2944047 REVERSE LENGTH=477</td><td>478</td><td>477</td><td>0</td><td>99.8</td><td>85.8</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00363.1.g12262.t1</td><td>gb|EOA30589.1| hypothetical protein CARUB_v10013721mg [Capsella rubella]</td><td>442</td><td>440</td><td>0</td><td>99.5</td><td>90.5</td><td>94.6</td><td>hypothetical protein CARUB_v10013721mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G09570.1 | Symbols: | Lung seven transmembrane receptor family protein | chr3:2940524-2941843 FORWARD LENGTH=439</td><td>442</td><td>439</td><td>0</td><td>99.3</td><td>87.8</td><td>92.3</td></tr>
<tr><td>Rsa1.0_00363.1.g12263.t1</td><td>gb|AEA07504.1| putative lipin 1 isoform B [Brassica napus]</td><td>1184</td><td>813</td><td>0</td><td>68.7</td><td>58.8</td><td>61.7</td><td>putative lipin 1 isoform B</td><td>gbpln</td><td>Brassica napus</td><td>AT3G09560.3 | Symbols: | Lipin family protein | chr3:2934953-2938673 REVERSE LENGTH=904</td><td>1184</td><td>904</td><td>0</td><td>76.4</td><td>56.7</td><td>60.6</td></tr>
<tr><td>Rsa1.0_00363.1.g12264.t1</td><td>gb|EOA30087.1| hypothetical protein CARUB_v10013194mg [Capsella rubella]</td><td>626</td><td>636</td><td>0</td><td>101.6</td><td>71.7</td><td>83.9</td><td>hypothetical protein CARUB_v10013194mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G09520.1 | Symbols: ATEXO70H4, EXO70H4 | exocyst subunit exo70 family protein H4 | chr3:2923743-2925629 FORWARD LENGTH=628</td><td>626</td><td>628</td><td>0</td><td>100.3</td><td>71.4</td><td>82.3</td></tr>
<tr><td>Rsa1.0_00363.1.g12265.t1</td><td>gb|EOA31721.1| hypothetical protein CARUB_v10014930mg [Capsella rubella]</td><td>123</td><td>123</td><td>2.00E-58</td><td>100.0</td><td>94.3</td><td>98.4</td><td>hypothetical protein CARUB_v10014930mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G09500.1 | Symbols: | Ribosomal L29 family protein | chr3:2917047-2917895 FORWARD LENGTH=123</td><td>123</td><td>123</td><td>4.00E-61</td><td>100.0</td><td>94.3</td><td>98.4</td></tr>
<tr><td>Rsa1.0_00363.1.g12266.t1</td><td>ref|NP_850546.1| UNC93-like protein [Arabidopsis thaliana] gi|51971813|dbj|BAD44571.1| unnamed protein product [Arabidopsis thaliana] gi|222423196|dbj|BAH19575.1| AT3G09470 [Arabidopsis thaliana] gi|332641250|gb|AEE74771.1| UNC93-like protein [Arabidopsis thaliana]</td><td>436</td><td>437</td><td>0</td><td>100.2</td><td>91.3</td><td>95.6</td><td>UNC93-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G09470.2 | Symbols: | Major facilitator superfamily protein | chr3:2911668-2914410 REVERSE LENGTH=437</td><td>436</td><td>437</td><td>0</td><td>100.2</td><td>91.3</td><td>95.6</td></tr>
</table>

Rsa1.0_00363.1.g12267.t1	ref|XP_002882620.1| hypothetical protein ARALYDRAFT_341087 [Arabidopsis lyrata subsp. lyrata] gi|297328460|gb|EFH58879.1| hypothetical protein ARALYDRAFT_341087 [Arabidopsis lyrata subsp. lyrata]	765	773	0	101.0	80.4	88.4	hypothetical protein ARALYDRAFT_341087	gbpln	Arabidopsis lyrata	AT3G09450.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Fusaric acid resistance protein, conserved region (InterPro:IPR006726); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G28780.1); Has 503 Blast hits to 494 proteins in 215 species: Archae - 0; Bacteria - 423; Metazoa - 0; Fungi - 0; Plants - 65; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink). | chr3:2907548-2910091 FORWARD LENGTH=775	765	775	0	101.3	80.0	87.7
Rsa1.0_00363.1.g12268.t3	ref|XP_002882619.1| hypothetical protein ARALYDRAFT_478263 [Arabidopsis lyrata subsp. lyrata] gi|297328459|gb|EFH58878.1| hypothetical protein ARALYDRAFT_478263 [Arabidopsis lyrata subsp. lyrata]	405	296	1.00E-115	73.1	56.0	61.0	hypothetical protein ARALYDRAFT_478263	gbpln	Arabidopsis lyrata	AT3G09430.1 | Symbols: | unknown protein; Has 17 Blast hits to 17 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2901280-2902893 FORWARD LENGTH=301	405	301	1.00E-115	74.3	54.8	60.0
Rsa1.0_00363.1.g12269.t1	ref|XP_002884736.1| pectinacetylesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330576|gb|EFH60995.1| pectinacetylesterase family protein [Arabidopsis lyrata subsp. lyrata]	423	427	0	100.9	83.0	88.4	pectinacetylesterase family protein	gbpln	Arabidopsis lyrata	AT3G09410.1 | Symbols: | Pectinacetylesterase family protein | chr3:2898243-2900984 REVERSE LENGTH=427	423	427	0	100.9	82.5	88.4
Rsa1.0_00363.1.g12270.t1	gb|EOA30038.1| hypothetical protein CARUB_v10013141mg [Capsella rubella]	627	667	0	106.4	72.7	81.0	hypothetical protein CARUB_v10013141mg	gbpln	Capsella rubella	AT3G09400.1 | Symbols: PLL3 | pol-like 3 | chr3:2891235-2893532 REVERSE LENGTH=650	627	650	0	103.7	72.2	80.4
Rsa1.0_00363.1.g12271.t1	dbj|BAA11391.1| metallothionein-like protein [Brassica rapa]	82	80	1.00E-25	97.6	75.6	76.8	metallothionein-like protein	gbpln	Brassica rapa	AT3G09390.1 | Symbols: MT2A, ATMT-K, ATMT-1 | metallothionein 2A | chr3:2889737-2890188 REVERSE LENGTH=81	82	81	4.00E-22	98.8	63.4	64.6
Rsa1.0_00363.1.g12272.t1	gb|EOA32896.1| hypothetical protein CARUB_v10016220mg [Capsella rubella]	89	150	1.00E-13	168.5	40.4	52.8	hypothetical protein CARUB_v10016220mg	gbpln	Capsella rubella	AT3G09380.1 | Symbols: | Protein of unknown function (DUF59) | chr3:2885265-2886116 REVERSE LENGTH=156	89	156	1.00E-13	175.3	38.2	46.1
Rsa1.0_00363.1.g12273.t1	ref|NP_178208.1| pre-mRNA-splicing factor CWC22 [Arabidopsis thaliana] gi|6503305|gb|AAF14681.1|AC011713_29 Contains similarity to gb|U19615 LET 858 gene from Caenorhabditis elegans. ESTs gb|AI995150, gb|H76674 and gb|R84035 come from this gene [Arabidopsis thaliana] gi|22654971|gb|AAM98078.1| At1g80930/F23A5_23 [Arabidopsis thaliana] gi|28416525|gb|AAO42793.1| At1g80930/F23A5_23 [Arabidopsis thaliana] gi|332198347|gb|AEE36468.1| MIF4G and MA3 domain-containing protein [Arabidopsis thaliana]	504	900	1.00E-180	178.6	61.3	80.4	pre-mRNA-splicing factor CWC22	gbpln	Arabidopsis thaliana	AT1G80930.1 | Symbols: | MIF4G domain-containing protein / MA3 domain-containing protein | chr1:30405774-30409499 REVERSE LENGTH=900	504	900	0	178.6	61.3	80.4
Rsa1.0_00363.1.g12274.t1	ref|NP_565602.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana] gi|18176116|gb|AAL59986.1| unknown protein [Arabidopsis thaliana] gi|20197507|gb|AAD31366.2| expressed protein [Arabidopsis thaliana] gi|20465307|gb|AAM20057.1| unknown protein [Arabidopsis thaliana] gi|21536492|gb|AAM60824.1| unknown [Arabidopsis thaliana] gi|330252636|gb|AEC07730.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana]	345	386	5.00E-61	111.9	45.2	58.8	DNA-binding storekeeper protein-related transcriptional regulator	gbpln	Arabidopsis thaliana	AT2G25650.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr2:10914765-10916006 FORWARD LENGTH=386	345	386	1.00E-63	111.9	45.2	58.8
Rsa1.0_00363.1.g12275.t1	ref|XP_002882616.1| hypothetical protein ARALYDRAFT_317739 [Arabidopsis lyrata subsp. lyrata] gi|297328456|gb|EFH58875.1| hypothetical protein ARALYDRAFT_317739 [Arabidopsis lyrata subsp. lyrata]	504	1245	0	247.0	71.8	77.2	hypothetical protein ARALYDRAFT_317739	gbpln	Arabidopsis lyrata	AT3G09370.1 | Symbols: MYB3R-3, AtMYB3R3 | myb domain protein 3r-3 | chr3:2879534-2882128 FORWARD LENGTH=505	504	505	0	100.2	70.8	77.8
Rsa1.0_00363.1.g12276.t1	ref|XP_002882614.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297328454|gb|EFH58873.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	368	365	0	99.2	92.1	96.5	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT3G09350.1 | Symbols: Fes1A | Fes1A | chr3:2871216-2873109 FORWARD LENGTH=363	368	363	0	98.6	91.3	95.9

Rsa1.0_00363.1.g12277.t1	ref|XP_002884727.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297330567|gb|EFH60986.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	293	286	1.00E−148	97.6	86.3	91.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G09320.1 | Symbols: | DHHC-type zinc finger family protein | chr3:2862142-2864113 REVERSE LENGTH=286	293	286	1.00E−144	97.6	86.3	92.2
Rsa1.0_00363.1.g12278.t1	ref|XP_002882613.1| hypothetical protein ARALYDRAFT_897086 [Arabidopsis lyrata subsp. lyrata] gi|297328453|gb|EFH58872.1| hypothetical protein ARALYDRAFT_897086 [Arabidopsis lyrata subsp. lyrata]	114	116	4.00E−41	101.8	74.6	79.8	hypothetical protein ARALYDRAFT_897086	gbpln	Arabidopsis lyrata	AT5G02120.1 | Symbols: OHP | one helix protein | chr5:419144-419633 FORWARD LENGTH=110	114	110	1.00E−35	96.5	62.3	70.2
Rsa1.0_00363.1.g12279.t1	ref|NP_187542.2| uncharacterized protein [Arabidopsis thaliana] gi|209572699|sp|Q9SR32.2|U161_ARATH RecName: Full=UPF0161 protein At3g09310 gi|89274167|gb|ABD65604.1| At3g09310 [Arabidopsis thaliana] gi|332641228|gb|AEE74749.1| uncharacterized protein AT3G09310 [Arabidopsis thaliana]	169	170	2.00E−63	100.6	70.4	76.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G09310.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF37 (InterPro:IPR002696); Has 5781 Blast hits to 5781 proteins in 1903 species: Archae − 0; Bacteria − 3956; Metazoa − 2; Fungi − 0; Plants − 42; Viruses − 3; Other Eukaryotes − 1778 (source: NCBI BLink). | chr3:2860622-2861297 REVERSE LENGTH=170	169	170	8.00E−66	100.6	70.4	76.3
Rsa1.0_00363.1.g12280.t1	ref|XP_002882612.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297328452|gb|EFH58871.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata]	447	456	0	102.0	95.7	97.3	oxysterol-binding family protein	gbpln	Arabidopsis lyrata	AT3G09300.1 | Symbols: ORP3B | OSBP(oxysterol binding protein)-related protein 3B | chr3:2858068-2860462 FORWARD LENGTH=458	447	458	0	102.5	95.7	97.5
Rsa1.0_00363.1.g12281.t2	dbj|BAJ34410.1| unnamed protein product [Thellungiella halophila]	78	524	4.00E−38	671.8	89.7	96.2	unnamed protein product	----	----	AT3G09260.1 | Symbols: PYK10, PSR3.1, BGLU23, LEB | Glycosyl hydrolase superfamily protein | chr3:2840657-2843730 REVERSE LENGTH=524	78	524	1.00E−32	671.8	87.2	92.3
Rsa1.0_00364.1.g12282.t1	ref|XP_002876123.1| hypothetical protein ARALYDRAFT_485568 [Arabidopsis lyrata subsp. lyrata] gi|297321961|gb|EFH52382.1| hypothetical protein ARALYDRAFT_485568 [Arabidopsis lyrata subsp. lyrata]	802	801	0	99.9	95.0	97.6	hypothetical protein ARALYDRAFT_485568	gbpln	Arabidopsis lyrata	AT3G52080.1 | Symbols: chx28 | cation/hydrogen exchanger 28 | chr3:19315090-19317735 FORWARD LENGTH=801	802	801	0	99.9	92.4	96.9
Rsa1.0_00364.1.g12283.t1	ref|XP_002876122.1| hypothetical protein ARALYDRAFT_906567 [Arabidopsis lyrata subsp. lyrata] gi|297321960|gb|EFH52381.1| hypothetical protein ARALYDRAFT_906567 [Arabidopsis lyrata subsp. lyrata]	108	113	4.00E−40	104.6	78.7	89.8	hypothetical protein ARALYDRAFT_906567	gbpln	Arabidopsis lyrata	AT3G52070.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 23 Blast hits to 23 proteins in 10 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 23; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:19312753-19313097 FORWARD LENGTH=114	108	114	3.00E−42	105.6	79.6	88.0
Rsa1.0_00364.1.g12284.t1	ref|XP_002877841.1| hypothetical protein ARALYDRAFT_485566 [Arabidopsis lyrata subsp. lyrata] gi|297323679|gb|EFH54100.1| hypothetical protein ARALYDRAFT_485566 [Arabidopsis lyrata subsp. lyrata]	342	344	1.00E−151	100.6	84.5	91.8	hypothetical protein ARALYDRAFT_485566	gbpln	Arabidopsis lyrata	AT3G52060.2 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr3:19310987-19312027 REVERSE LENGTH=346	342	346	1.00E−151	101.2	83.3	90.6
Rsa1.0_00364.1.g12285.t1	gb|EOA24836.1| hypothetical protein CARUB_v10018125mg [Capsella rubella]	156	171	7.00E−65	109.6	76.9	82.7	hypothetical protein CARUB_v10018125mg	gbpln	Capsella rubella	AT3G51960.1 | Symbols: ATBZIP24, BZIP24 | basic leucine zipper 24 | chr3:19282828-19284064 REVERSE LENGTH=227	156	227	1.00E−61	145.5	71.8	78.8
Rsa1.0_00364.1.g12286.t1	gb|EOA25516.1| hypothetical protein CARUB_v10018860mg [Capsella rubella]	564	538	0	95.4	83.5	89.5	hypothetical protein CARUB_v10018860mg	gbpln	Capsella rubella	AT3G51950.2 | Symbols: | Zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein | chr3:19278244-19280407 REVERSE LENGTH=540	564	540	0	95.7	84.0	89.2
Rsa1.0_00364.1.g12287.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00364.1.g12288.t3	gb|AAD29774.1|AF074021_6 putative polyprotein [Arabidopsis thaliana] gi|7267218|emb|CAB80825.1| putative polyprotein [Arabidopsis thaliana]	667	922	2.00E−26	138.2	10.9	15.4	putative polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00364.1.g12289.t1	ref|NP_190761.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|4678922|emb|CAB41313.1| putative protein [Arabidopsis thaliana] gi|30725344|gb|AAP37694.1| At3g51930 [Arabidopsis thaliana] gi|110736561|dbj|BAF00246.1| hypothetical protein [Arabidopsis thaliana] gi|332645343|gb|AEE78864.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	424	415	0	97.9	86.6	92.2	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G51930.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:19271672-19272919 FORWARD LENGTH=415	424	415	0	97.9	86.6	92.2

Rsa1.0_00364.1.g12290.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00364.1.g12291.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	642	1239	1.00E–171	193.0	49.5	57.9	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485–12134086 FORWARD LENGTH=1262	642	1262	8.00E–32	196.6	10.3	16.8
Rsa1.0_00364.1.g12292.t1	ref|XP_002877832.1| hypothetical protein ARALYDRAFT_906546 [Arabidopsis lyrata subsp. lyrata] gi|297323670|gb|EFH54091.1| hypothetical protein ARALYDRAFT_906546 [Arabidopsis lyrata subsp. lyrata]	151	151	5.00E–76	100.0	94.0	96.0	hypothetical protein ARALYDRAFT_906546	gbpln	Arabidopsis lyrata	AT3G51920.1 | Symbols: CAM9, CML9, ATCML9 | calmodulin 9 | chr3:19268178–19269314 REVERSE LENGTH=151	151	151	2.00E–78	100.0	94.0	96.0
Rsa1.0_00364.1.g12293.t1	gb|AAG51237.1|AC035249_12 unknown protein; 55998–51558 [Arabidopsis thaliana]	212	593	8.00E–32	279.7	32.5	45.3	unknown protein; 55998–51558	gbpln	Arabidopsis thaliana	AT1G36970.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:14016385–14018356 REVERSE LENGTH=439	212	439	7.00E–28	207.1	28.3	39.6
Rsa1.0_00364.1.g12294.t1	gb|AAC02672.1| polyprotein [Arabidopsis arenosa]	612	1390	1.00E–143	227.1	42.8	52.9	polyprotein	gbpln	Arabidopsis arenosa	AT3G51910.1 | Symbols: AT-HSFA7A, HSFA7A | heat shock transcription factor A7A | chr3:19265294–19266619 FORWARD LENGTH=272	612	272	1.00E–74	44.4	23.7	26.3
Rsa1.0_00365.1.g12295.t1	ref|XP_002875949.1| hypothetical protein ARALYDRAFT_906172 [Arabidopsis lyrata subsp. lyrata] gi|297321787|gb|EFH52208.1| hypothetical protein ARALYDRAFT_906172 [Arabidopsis lyrata subsp. lyrata]	565	967	3.00E–38	171.2	29.9	44.1	hypothetical protein ARALYDRAFT_906172	gbpln	Arabidopsis lyrata	AT5G12280.1 | Symbols: | SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein | chr5:3972014–3973636 REVERSE LENGTH=419	565	419	5.00E–21	74.2	17.3	25.0
Rsa1.0_00365.1.g12296.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00365.1.g12297.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00365.1.g12298.t1	ref|NP_198533.1| putative O-diphenol-O-methyl transferase [Arabidopsis thaliana] gi|332006766|gb|AED94149.1| putative O-diphenol-O-methyl transferase [Arabidopsis thaliana]	269	334	2.00E–41	124.2	37.2	44.2	putative O-diphenol-O-methyl transferase	gbpln	Arabidopsis thaliana	AT5G37170.1 | Symbols: | O-methyltransferase family protein | chr5:14712811–14714303 FORWARD LENGTH=334	269	334	5.00E–44	124.2	37.2	44.2
Rsa1.0_00365.1.g12299.t1	gb|ABB55318.1| conserved hypothetical protein [Asparagus officinalis]	314	324	3.00E–65	103.2	49.4	61.1	conserved hypothetical protein	gbpln	Asparagus officinalis	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae – 0; Bacteria – 0; Metazoa – 28; Fungi – 8; Plants – 388; Viruses – 0; Other Eukaryotes – 27 (source: NCBI BLink). | chr2:5736603–5737847 FORWARD LENGTH=343	314	343	2.00E–62	109.2	42.4	52.5
Rsa1.0_00365.1.g12300.t1	ref|XP_002889151.1| nucleoside-triphosphatase/ nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] gi|297334992|gb|EFH65410.1| nucleoside-triphosphatase/ nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	1168	1154	0	98.8	72.6	80.8	nucleoside-triphosphatase/ nucleotide binding protein	gbpln	Arabidopsis lyrata	AT1G77620.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:29167934–29172867 REVERSE LENGTH=1151	1168	1151	0	98.5	72.1	80.3
Rsa1.0_00365.1.g12301.t1	ref|NP_177876.1| O-methyltransferase family protein [Arabidopsis thaliana] gi|12323395|gb|AAG51676.1|AC010704_20 putative caffeic acid 3-O-methyltransferase; 41078–42528 [Arabidopsis thaliana] gi|332197867|gb|AEE35988.1| O-methyltransferase family protein [Arabidopsis thaliana]	348	381	1.00E–142	109.5	72.7	80.5	O-methyltransferase family protein	gbpln	Arabidopsis thaliana	AT1G77520.1 | Symbols: | O-methyltransferase family protein | chr1:29130557–29132007 FORWARD LENGTH=381	348	381	1.00E–144	109.5	72.7	80.5
Rsa1.0_00365.1.g12302.t1	ref|XP_002862810.1| nucleoside-triphosphatase/ nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] gi|297308545|gb|EFH39068.1| nucleoside-triphosphatase/ nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	304	960	7.00E–52	315.8	38.5	43.1	nucleoside-triphosphatase/ nucleotide binding protein	gbpln	Arabidopsis lyrata	AT1G77620.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:29167934–29172867 REVERSE LENGTH=1151	304	1151	2.00E–44	378.6	36.5	40.8
Rsa1.0_00365.1.g12303.t1	ref|XP_002887693.1| peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297333534|gb|EFH63952.1| peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	426	425	0	99.8	80.3	87.3	peptidoglycan-binding LysM domain-containing protein	gbpln	Arabidopsis lyrata	AT1G77630.1 | Symbols: | Peptidoglycan-binding LysM domain-containing protein | chr1:29173726–29175387 FORWARD LENGTH=423	426	423	0	99.3	78.9	86.2
Rsa1.0_00365.1.g12304.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00365.1.g12305.t1	ref|XP_002883210.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297329050|gb|EFH59469.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	152	337	2.00E–25	221.7	40.8	44.1	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G19910.1 | Symbols: | RING/U-box superfamily protein | chr3:6926497–6929324 FORWARD LENGTH=340	152	340	2.00E–27	223.7	40.1	44.1

Rsa1.0_00365.1.g12306.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00365.1.g12307.t1	ref|NP_177889.1| putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana] gi|12323386|gb|AAG51667.1|AC010704_11 unknown protein; 98021-96594 [Arabidopsis thaliana] gi|110739867|dbj|BAF01839.1| hypothetical protein [Arabidopsis thaliana] gi|332197885|gb|AEE36006.1| putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]	414	421	1.00E-164	101.7	77.8	84.5	putative phosphatidylinositol-4-phosphate 5-kinase	gbpln	Arabidopsis thaliana	AT1G77660.1 | Symbols: | Histone H3 K4-specific methyltransferase SET7/9 family protein | chr1:29186073-29187500 REVERSE LENGTH=421	414	421	1.00E-166	101.7	77.8	84.5
Rsa1.0_00365.1.g12308.t1	ref|XP_002889154.1| ribonuclease II family protein [Arabidopsis lyrata subsp. lyrata] gi|297334995|gb|EFH65413.1| ribonuclease II family protein [Arabidopsis lyrata subsp. lyrata]	1025	1062	0	103.6	78.5	86.3	ribonuclease II family protein	gbpln	Arabidopsis lyrata	AT1G77680.1 | Symbols: | Ribonuclease II/R family protein | chr1:29192188-29195963 REVERSE LENGTH=1055	1025	1055	0	102.9	77.6	86.0
Rsa1.0_00365.1.g12309.t1	gb|EOA33358.1| hypothetical protein CARUB_v10020229mg [Capsella rubella]	472	470	0	99.6	97.7	98.9	hypothetical protein CARUB_v10020229mg	gbpln	Capsella rubella	AT1G77690.1 | Symbols: LAX3 | like AUX1 3 | chr1:29201232-29203317 REVERSE LENGTH=470	472	470	0	99.6	96.8	98.5
Rsa1.0_00365.1.g12310.t1	gb|EOA35553.1| hypothetical protein CARUB_v10020759mg [Capsella rubella]	229	280	1.00E-94	122.3	78.6	86.5	hypothetical protein CARUB_v10020759mg	gbpln	Capsella rubella	AT1G77700.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:29204747-29206217 FORWARD LENGTH=356	229	356	1.00E-83	155.5	66.4	73.4
Rsa1.0_00365.1.g12311.t1	ref|NP_177894.1| ubiquitin-fold modifier 1 [Arabidopsis thaliana] gi|20140765|sp|Q9CA23.1|UFM1_ARATH RecName: Full=Ubiquitin-fold modifier 1; Flags: Precursor gi|12323301|gb|AAG51633.1|AC012193_15 unknown protein; 14107-15252 [Arabidopsis thaliana] gi|20260380|gb|AAM13088.1| unknown protein [Arabidopsis thaliana] gi|23197778|gb|AAN15416.1| unknown protein [Arabidopsis thaliana] gi|332197891|gb|AEE36012.1| ubiquitin-fold modifier 1 [Arabidopsis thaliana]	90	93	8.00E-43	103.3	97.8	97.8	ubiquitin-fold modifier 1	gbpln	Arabidopsis thaliana	AT1G77710.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ubiquitin-like, Ufm1 (InterPro:IPR005375); Has 244 Blast hits to 244 proteins in 106 species: Archae - 0; Bacteria - 0; Metazoa - 149; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink). | chr1:29206750-29207895 FORWARD LENGTH=93	90	93	1.00E-45	103.3	97.8	97.8
Rsa1.0_00365.1.g12312.t1	gb|EOA34054.1| hypothetical protein CARUB_v10021554mg [Capsella rubella]	256	259	1.00E-119	101.2	83.2	90.6	hypothetical protein CARUB_v10021554mg	gbpln	Capsella rubella	AT1G77730.1 | Symbols: | Pleckstrin homology (PH) domain superfamily protein | chr1:29214445-29215564 FORWARD LENGTH=265	256	265	1.00E-121	103.5	82.8	90.6
Rsa1.0_00366.1.g12313.t1	gb|AAM62648.1| dehydration stress-induced protein [Arabidopsis thaliana]	172	182	8.00E-34	105.8	47.1	58.7	dehydration stress-induced protein	gbpln	Arabidopsis thaliana	AT2G22170.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr2:9427010-9427742 REVERSE LENGTH=183	172	183	4.00E-36	106.4	47.1	58.7
Rsa1.0_00366.1.g12314.t1	dbj|BAH97744.1| hypothetical protein [Hypochaeris radicata]	78	78	6.00E-35	100.0	93.6	97.4	hypothetical protein	gbpln	Hypochaeris radicata	AT2G23090.1 | Symbols: | Uncharacterised protein family SERF | chr2:9829657-9830274 REVERSE LENGTH=78	78	78	1.00E-37	100.0	93.6	96.2
Rsa1.0_00366.1.g12315.t1	gb|EOA27027.1| hypothetical protein CARUB_v10023124mg, partial [Capsella rubella]	424	475	0	112.0	81.4	87.7	hypothetical protein CARUB_v10023124mg, partial	gbpln	Capsella rubella	AT2G23093.1 | Symbols: | Major facilitator superfamily protein | chr2:9832193-9834416 FORWARD LENGTH=449	424	449	0	105.9	80.0	87.3
Rsa1.0_00366.1.g12316.t1	ref|XP_002882125.1| UDP-glucuronic acid decarboxylase 2 [Arabidopsis lyrata subsp. lyrata] gi|297327964|gb|EFH58384.1| UDP-glucuronic acid decarboxylase 2 [Arabidopsis lyrata subsp. lyrata]	244	436	2.00E-13	178.7	22.5	26.2	UDP-glucuronic acid decarboxylase 2	gbpln	Arabidopsis lyrata	AT2G47650.2 | Symbols: UXS4 | UDP-xylose synthase 4 | chr2:19538751-19541364 REVERSE LENGTH=449	244	449	1.00E-14	184.0	23.0	27.0
Rsa1.0_00366.1.g12317.t1	ref|NP_182235.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|75278866|sp|O80713.1|SDR3A_ARATH RecName: Full=Short-chain dehydrogenase reductase 3a; Short=AtSDR3a gi|3522935|gb|AAC34217.1| putative alcohol dehydrogenase [Arabidopsis thaliana] gi|34146806|gb|AAQ62411.1| At2g47130 [Arabidopsis thaliana] gi|51968890|dbj|BAD43137.1| putative alcohol dehydrogenase [Arabidopsis thaliana] gi|330255711|gb|AEC10805.1| short-chain dehydrogenase reductase 3a [Arabidopsis thaliana]	258	257	1.00E-129	99.6	88.8	95.0	Rossmann-fold NAD(P)-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT2G47130.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:19349627-19350481 REVERSE LENGTH=257	258	257	1.00E-132	99.6	88.8	95.0

Rsa1.0_00366.1.g12318.t1	ref|XP_002878660.1| hypothetical protein ARALYDRAFT_481185 [Arabidopsis lyrata subsp. lyrata] gi|297324499|gb|EFH54919.1| hypothetical protein ARALYDRAFT_481185 [Arabidopsis lyrata subsp. lyrata]	82	79	4.00E-18	96.3	70.7	80.5	hypothetical protein ARALYDRAFT_481185	gbpln	Arabidopsis lyrata	AT2G23120.1 | Symbols: | Late embryogenesis abundant protein, group 6 | chr2:9842102-9842353 FORWARD LENGTH=83	82	83	6.00E-16	101.2	50.0	61.0
Rsa1.0_00366.1.g12319.t1	ref|XP_002878661.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324500|gb|EFH54920.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	304	180	4.00E-20	59.2	38.2	43.4	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00366.1.g12320.t1	ref|XP_002880484.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297326323|gb|EFH56743.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	817	829	0	101.5	88.4	92.8	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT2G23140.1 | Symbols: | RING/U-box superfamily protein with ARM repeat domain | chr2:9845696-9849105 REVERSE LENGTH=829	817	829	0	101.5	88.2	92.8
Rsa1.0_00366.1.g12321.t1	gb|EOA26902.1| hypothetical protein CARUB_v10022990mg, partial [Capsella rubella]	494	527	0	106.7	75.9	81.4	hypothetical protein CARUB_v10022990mg, partial	gbpln	Capsella rubella	AT2G23150.1 | Symbols: NRAMP3, ATNRAMP3 | natural resistance-associated macrophage protein 3 | chr2:9856422-9858565 REVERSE LENGTH=509	494	509	0	103.0	68.2	71.3
Rsa1.0_00366.1.g12322.t1	gb|EOA26747.1| hypothetical protein CARUB_v10022833mg, partial [Capsella rubella]	596	617	0	103.5	91.3	96.0	hypothetical protein CARUB_v10022833mg, partial	gbpln	Capsella rubella	AT2G23170.1 | Symbols: GH3.3 | Auxin-responsive GH3 family protein | chr2:9864125-9866502 REVERSE LENGTH=595	596	595	0	99.8	91.1	95.3
Rsa1.0_00366.1.g12323.t1	gb|ABD65629.1| hypothetical protein 23.t00046 [Brassica oleracea]	146	147	6.00E-44	100.7	54.8	75.3	hypothetical protein 23.t00046	gbpln	Brassica oleracea	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	146	746	8.00E-16	511.0	28.1	41.8
Rsa1.0_00366.1.g12324.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00366.1.g12325.t1	gb|EOA19915.1| hypothetical protein CARUB_v10000165mg [Capsella rubella]	224	923	7.00E-69	412.1	63.8	67.4	hypothetical protein CARUB_v10000165mg	gbpln	Capsella rubella	AT4G02460.1 | Symbols: PMS1 | DNA mismatch repair protein, putative | chr4:1076306-1080510 REVERSE LENGTH=923	224	923	2.00E-69	412.1	63.8	67.9
Rsa1.0_00366.1.g12326.t1	ref|XP_002878665.1| CYP96A1 [Arabidopsis lyrata subsp. lyrata] gi|297324504|gb|EFH54924.1| CYP96A1 [Arabidopsis lyrata subsp. lyrata]	708	514	0	72.6	58.9	64.1	CYP96A1	gbpln	Arabidopsis lyrata	AT2G23180.1 | Symbols: CYP96A1 | cytochrome P450, family 96, subfamily A, polypeptide 1 | chr2:9874953-9876503 FORWARD LENGTH=516	708	516	0	72.9	58.5	63.1
Rsa1.0_00366.1.g12327.t1	ref|XP_002878666.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324505|gb|EFH54925.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	496	519	0	104.6	85.7	93.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G23190.1 | Symbols: CYP81D7 | cytochrome P450, family 81, subfamily D, polypeptide 7 | chr2:9877058-9879007 FORWARD LENGTH=543	496	543	0	109.5	84.3	92.5
Rsa1.0_00366.1.g12328.t1	ref|NP_179901.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|75317972|sp|O22187.1|Y2232_ARATH RecName: Full=Probable receptor-like protein kinase At2g23200; Flags: Precursor gi|2642445|gb|AAB87113.1| putative protein kinase [Arabidopsis thaliana] gi|330252334|gb|AEC07428.1| putative receptor-like protein kinase [Arabidopsis thaliana]	486	834	1.00E-171	171.6	65.8	78.0	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT2G23200.1 | Symbols: | Protein kinase superfamily protein | chr2:9879351-9881855 FORWARD LENGTH=834	486	834	1.00E-174	171.6	65.8	78.0
Rsa1.0_00367.1.g12329.t1	ref|NP_197887.1| major facilitator protein [Arabidopsis thaliana] gi|75104998|sp|Q5FV41.1|FBT2_ARATH RecName: Full=Probable folate-biopterin transporter 2 gi|58331763|gb|AAW70379.1| At5g25050 [Arabidopsis thaliana] gi|332006011|gb|AED93394.1| probable folate-biopterin transporter 2 [Arabidopsis thaliana]	498	499	0	100.2	89.0	94.8	major facilitator protein	gbpln	Arabidopsis thaliana	AT5G25050.1 | Symbols: | Major facilitator superfamily protein | chr5:8632022-8633828 FORWARD LENGTH=499	498	499	0	100.2	89.0	94.8
Rsa1.0_00367.1.g12330.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00367.1.g12331.t1	gb|AAK68074.1|AF384970_1 somatic embryogenesis receptor-like kinase 3 [Arabidopsis thaliana]	275	615	1.00E-38	223.6	30.2	32.0	somatic embryogenesis receptor-like kinase 3	gbpln	Arabidopsis thaliana	AT4G33430.1 | Symbols: BAK1, RKS10, SERK3, ELG, ATSERK3, ATBAK1 | BRI1-associated receptor kinase | chr4:16086654-16090288 REVERSE LENGTH=615	275	615	4.00E-41	223.6	30.2	32.0
Rsa1.0_00367.1.g12332.t1	ref|XP_002872140.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata] gi|297317977|gb|EFH48399.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata]	496	496	0	100.0	83.1	92.1	CYP71B11	gbpln	Arabidopsis lyrata	AT5G25120.1 | Symbols: CYP71B11 | ytochrome p450, family 71, subfamily B, polypeptide 11 | chr5:8662851-8664432 FORWARD LENGTH=496	496	496	0	100.0	81.7	92.3
Rsa1.0_00367.1.g12333.t1	gb|EOA19571.1| hypothetical protein CARUB_v10002639mg [Capsella rubella]	638	668	0	104.7	89.0	94.4	hypothetical protein CARUB_v10002639mg	gbpln	Capsella rubella	AT5G25150.1 | Symbols: TAF5 | TBP-associated factor 5 | chr5:8677117-8682058 FORWARD LENGTH=669	638	669	0	104.9	90.0	95.5

Rsa1.0_00367.1.g12334.t1	gb|EOA21453.1| hypothetical protein CARUB_v10001837mg [Capsella rubella]	248	241	1.00E-94	97.2	73.4	79.4	hypothetical protein CARUB_v10001837mg	gbpln	Capsella rubella	AT5G25160.1 | Symbols: ZFP3 | zinc finger protein 3 | chr5:8687524-8688231 FORWARD LENGTH=235	248	235	3.00E-91	94.8	74.6	79.4
Rsa1.0_00367.1.g12335.t1	ref|XP_002872143.1| hypothetical protein ARALYDRAFT_910561 [Arabidopsis lyrata subsp. lyrata] gi|297317980|gb|EFH48402.1| hypothetical protein ARALYDRAFT_910561 [Arabidopsis lyrata subsp. lyrata]	194	218	1.00E-92	112.4	85.6	89.2	hypothetical protein ARALYDRAFT_910561	gbpln	Arabidopsis lyrata	AT5G25170.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr5:8693257-8694438 FORWARD LENGTH=218	194	218	3.00E-93	112.4	84.0	88.1
Rsa1.0_00367.1.g12336.t1	ref|NP_197894.1| cytochrome P450 71B11 [Arabidopsis thaliana] gi|13878370|sp|P58049.1|C71BB_ARATH RecName: Full=Cytochrome P450 71B11 gi|51971443|dbj|BAD44386.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|332006020|gb|AED93403.1| cytochrome P450 71B11 [Arabidopsis thaliana]	469	496	0	105.8	81.0	91.7	cytochrome P450 71B11	gbpln	Arabidopsis thaliana	AT5G25120.1 | Symbols: CYP71B11 | ytochrome p450, family 71, subfamily B, polypeptide 11 | chr5:8662851-8664432 FORWARD LENGTH=496	469	496	0	105.8	81.0	91.7
Rsa1.0_00367.1.g12337.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00367.1.g12338.t1	ref|XP_002874244.1| hypothetical protein ARALYDRAFT_489371 [Arabidopsis lyrata subsp. lyrata] gi|297320081|gb|EFH50503.1| hypothetical protein ARALYDRAFT_489371 [Arabidopsis lyrata subsp. lyrata]	185	183	1.00E-76	98.9	83.2	88.6	hypothetical protein ARALYDRAFT_489371	gbpln	Arabidopsis lyrata	AT5G25190.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:8707007-8707655 REVERSE LENGTH=181	185	181	2.00E-76	97.8	81.1	87.6
Rsa1.0_00367.1.g12339.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00367.1.g12340.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	533	490	6.00E-95	91.9	35.6	55.9	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	533	566	1.00E-93	106.2	34.9	57.4
Rsa1.0_00367.1.g12341.t1	gb|AAD15468.1| putative helicase [Arabidopsis thaliana]	1606	1265	0	78.8	44.0	56.1	putative helicase	gbpln	Arabidopsis thaliana	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	1606	344	4.00E-69	21.4	8.7	12.0
Rsa1.0_00367.1.g12342.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00367.1.g12343.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00367.1.g12344.t2	gb|EOA20703.1| hypothetical protein CARUB_v10001020mg [Capsella rubella]	484	427	0	88.2	75.0	77.5	hypothetical protein CARUB_v10001020mg	gbpln	Capsella rubella	AT5G25220.1 | Symbols: KNAT3 | KNOTTED1-like homeobox gene 3 | chr5:8736208-8738115 FORWARD LENGTH=431	484	431	0	89.0	75.4	77.7
Rsa1.0_00367.1.g12345.t1	ref|NP_197906.1| uncharacterized protein [Arabidopsis thaliana] gi|26450052|dbj|BAC42146.1| unknown protein [Arabidopsis thaliana] gi|28827680|gb|AAO50684.1| unknown protein [Arabidopsis thaliana] gi|332006033|gb|AED93416.1| uncharacterized protein AT5G25240 [Arabidopsis thaliana]	125	131	4.00E-44	104.8	78.4	86.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G25240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8746779-8747174 REVERSE LENGTH=131	125	131	7.00E-47	104.8	78.4	86.4
Rsa1.0_00367.1.g12346.t1	ref|NP_197908.1| Flotillin-like protein 2 [Arabidopsis thaliana] gi|75316159|sp|Q4V3D6.1|FLOT2_ARATH RecName: Full=Flotillin-like protein 2; AltName: Full=Nodulin-like protein 2 gi|66792618|gb|AAY56411.1| At5g25260 [Arabidopsis thaliana] gi|332006035|gb|AED93418.1| Flotillin-like protein 2 [Arabidopsis thaliana]	469	463	0	98.7	90.0	94.7	Flotillin-like protein 2	gbpln	Arabidopsis thaliana	AT5G25260.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr5:8752751-8754282 FORWARD LENGTH=463	469	463	0	98.7	90.0	94.7
Rsa1.0_00367.1.g12347.t1	ref|NP_192927.5| S-locus lectin protein kinase-like protein [Arabidopsis thaliana] gi|75266793|sp|Q9T058.1|Y4119_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At4g11900; Flags: Precursor gi|5002525|emb|CAB44328.1| KI domain interacting kinase 1-like protein [Arabidopsis thaliana] gi|7267891|emb|CAB78233.1| KI domain interacting kinase 1-like protein [Arabidopsis thaliana] gi|332657667|gb|AEE83067.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	541	849	1.00E-111	156.9	41.2	47.7	S-locus lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT4G11900.1 | Symbols: | S-locus lectin protein kinase family protein | chr4:7150241-7153542 REVERSE LENGTH=849	541	849	1.00E-113	156.9	41.2	47.7

Rsa1.0_00368.1.g12348.t1	gb|EOA24133.1| hypothetical protein CARUB_v10017366mg, partial [Capsella rubella]	372	407	1.00E−121	109.4	76.1	83.6	hypothetical protein CARUB_v10017366mg, partial	gbpln	Capsella rubella	AT3G52910.1 | Symbols: AtGRF4, GRF4 | growth−regulating factor 4 | chr3:19616177−19618268 REVERSE LENGTH=380	372	380	1.00E−120	102.2	75.0	82.0
Rsa1.0_00368.1.g12349.t1	ref|XP_002882246.1| hypothetical protein ARALYDRAFT_477508 [Arabidopsis lyrata subsp. lyrata] gi|297328086|gb|EFH58505.1| hypothetical protein ARALYDRAFT_477508 [Arabidopsis lyrata subsp. lyrata]	528	537	0	101.7	82.4	89.8	hypothetical protein ARALYDRAFT_477508	gbpln	Arabidopsis lyrata	AT3G02680.1 | Symbols: NBS1, ATNBS1 | nijmegen breakage syndrome 1 | chr3:576378−579226 FORWARD LENGTH=542	528	542	0	102.7	83.1	89.8
Rsa1.0_00368.1.g12350.t1	ref|XP_002877892.1| hypothetical protein ARALYDRAFT_323835 [Arabidopsis lyrata subsp. lyrata] gi|297323730|gb|EFH54151.1| hypothetical protein ARALYDRAFT_323835 [Arabidopsis lyrata subsp. lyrata]	170	542	5.00E−87	318.8	92.9	96.5	hypothetical protein ARALYDRAFT_323835	gbpln	Arabidopsis lyrata	AT3G52905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H−like superfamily protein | chr3:19614142−19615471 REVERSE LENGTH=170	170	170	1.00E−88	100.0	92.9	96.5
Rsa1.0_00368.1.g12351.t1	ref|NP_566973.2| KCBP−interacting protein kinase [Arabidopsis thaliana] gi|30693721|ref|NP_850687.1| KCBP−interacting protein kinase [Arabidopsis thaliana] gi|75263849|sp|Q9LFA2.1|KIPK_ARATH RecName: Full=Serine/threonine−protein kinase KIPK; AltName: Full=KCBP−interacting protein kinase gi|7529713|emb|CAB86893.1| protein kinase−like [Arabidopsis thaliana] gi|21703143|gb|AAM74511.1| AT3g52890/F8J2_60 [Arabidopsis thaliana] gi|25054838|gb|AAN71909.1| putative protein kinase [Arabidopsis thaliana] gi|25090422|gb|AAN72297.1| At3g52890/F8J2_60 [Arabidopsis thaliana] gi|332645484|gb|AEE79005.1| KCBP−interacting protein kinase [Arabidopsis thaliana] gi|332645485|gb|AEE79006.1| KCBP−interacting protein kinase [Arabidopsis thaliana]	826	934	0	113.1	84.3	91.8	KCBP−interacting protein kinase	gbpln	Arabidopsis thaliana	AT3G52890.2 | Symbols: KIPK | KCBP−interacting protein kinase | chr3:19609150−19612032 FORWARD LENGTH=934	826	934	0	113.1	84.3	91.8
Rsa1.0_00368.1.g12352.t1	gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]	362	527	4.00E−34	145.6	29.3	35.1	hypothetical protein CARUB_v10022820mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC−type) family protein | chr4:2728204−2732337 FORWARD LENGTH=735	362	735	1.00E−36	203.0	28.2	36.5
Rsa1.0_00368.1.g12353.t1	gb|AAC69114.1| putative gag−protease polyprotein [Arabidopsis thaliana]	524	627	1.00E−39	119.7	23.5	41.0	putative gag−protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00368.1.g12354.t1	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	568	1274	1.00E−111	224.3	39.6	56.9	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	568	575	4.00E−69	101.2	30.1	49.3
Rsa1.0_00368.1.g12355.t2	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00368.1.g12356.t1	gb|AAG03119.1|AC004133_13 F5A9.24 [Arabidopsis thaliana]	609	1254	0	205.9	55.7	69.8	F5A9.24	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I−like superfamily protein | chr1:16528880−16531065 REVERSE LENGTH=626	609	626	1.00E−30	102.8	17.1	28.2
Rsa1.0_00368.1.g12357.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	296	1231	4.00E−68	415.9	45.9	60.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	296	575	1.00E−37	194.3	27.7	48.3
Rsa1.0_00368.1.g12358.t2	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00368.1.g12359.t1	gb|EOA23972.1| hypothetical protein CARUB_v10017192mg [Capsella rubella]	456	463	0	101.5	86.0	90.4	hypothetical protein CARUB_v10017192mg	gbpln	Capsella rubella	AT3G52870.1 | Symbols: | IQ calmodulin−binding motif family protein | chr3:19593365−19595686 REVERSE LENGTH=456	456	456	0	100.0	84.4	90.4
Rsa1.0_00368.1.g12360.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00369.1.g12361.t1	sp|D7LTJ4.2|CSPLN_ARALL RecName: Full=CASP−like protein ARALYDRAFT_485429	154	154	1.00E−49	100.0	68.2	74.7	RecName: Full=CASP−like protein ARALYDRAFT_485429	−−−−	−−−−	AT3G50810.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr3:18889002−18889868 REVERSE LENGTH=154	154	154	7.00E−52	100.0	68.2	75.3

Rsa1.0_00369.1.g12362.t1	ref|NP_190652.1| cold-regulated 413-plasma membrane 2 [Arabidopsis thaliana] gi|75212080|sp|Q9SVL6.1|CRPM2_ARATH RecName: Full=Cold-regulated 413 plasma membrane protein 2; Short=AtCOR413-PM2 gi|10121843|gb|AAG13394.1|AF283005_1 cold acclimation protein WCOR413-like protein beta form [Arabidopsis thaliana] gi|13430786|gb|AAK26015.1|AF360305_1 putative cold acclimation protein [Arabidopsis thaliana] gi|4835234|emb|CAB42912.1| putative cold acclimation protein [Arabidopsis thaliana] gi|15810635|gb|AAL07242.1| putative cold acclimation protein [Arabidopsis thaliana] gi|332645194|gb|AEE78715.1| cold-regulated 413-plasma membrane 2 [Arabidopsis thaliana]	204	203	1.00E-103	99.5	90.2	96.1	cold-regulated 413-plasma membrane 2	gbpln	Arabidopsis thaliana	AT3G50830.1 | Symbols: COR413-PM2, ATCOR413-PM2 | cold-regulated 413-plasma membrane 2 | chr3:18894109-18895355 REVERSE LENGTH=203	204	203	1.00E-105	99.5	90.2	96.1
Rsa1.0_00369.1.g12363.t1	gb|EOA24850.1| hypothetical protein CARUB_v10018140mg [Capsella rubella]	212	166	3.00E-71	78.3	63.7	64.6	hypothetical protein CARUB_v10018140mg	gbpln	Capsella rubella	AT3G50860.1 | Symbols: | Clathrin adaptor complex small chain family protein | chr3:18902346-18903959 FORWARD LENGTH=166	212	166	1.00E-73	78.3	63.2	64.6
Rsa1.0_00369.1.g12364.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00369.1.g12365.t1	ref|XP_002870704.1| ATMKK3 MITOGEN-ACTIVATED kinase [Arabidopsis lyrata subsp. lyrata] gi|297316540|gb|EFH46963.1| ATMKK3 MITOGEN-ACTIVATED kinase [Arabidopsis lyrata subsp. lyrata]	251	520	9.00E-52	207.2	43.4	49.0	ATMKK3 MITOGEN-ACTIVATED kinase	gbpln	Arabidopsis lyrata	AT5G40440.1 | Symbols: ATMKK3, MKK3 | mitogen-activated protein kinase kinase 3 | chr5:16182149-16184513 FORWARD LENGTH=520	251	520	9.00E-54	207.2	43.0	49.0
Rsa1.0_00369.1.g12366.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1465	1496	0	102.1	59.2	73.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1465	1262	1.00E-139	86.1	16.5	23.7
Rsa1.0_00369.1.g12367.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00369.1.g12368.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00369.1.g12369.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00369.1.g12370.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00369.1.g12371.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00369.1.g12372.t1	gb|EOA23275.1| hypothetical protein CARUB_v10017889mg [Capsella rubella]	255	254	1.00E-128	99.6	91.4	95.3	hypothetical protein CARUB_v10017889mg	gbpln	Capsella rubella	AT3G51090.1 | Symbols: | Protein of unknown function (DUF1640) | chr3:18978192-18979853 REVERSE LENGTH=298	255	298	1.00E-121	116.9	87.5	90.6
Rsa1.0_00369.1.g12373.t1	dbj|BAE99915.1| hypothetical protein [Arabidopsis thaliana]	250	211	1.00E-74	84.4	64.8	72.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G51100.1 | Symbols: | unknown protein; Has 48 Blast hits to 48 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:18980531-18982174 REVERSE LENGTH=211	250	211	3.00E-73	84.4	65.2	72.8
Rsa1.0_00369.1.g12374.t8	#	#	#	#	#	#	#	-	----	----	AT5G35730.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr5:13893941-13896821 FORWARD LENGTH=457	227	457	5.00E-12	201.3	16.3	17.2
Rsa1.0_00369.1.g12375.t1	ref|XP_002877789.1| hypothetical protein ARALYDRAFT_906461 [Arabidopsis lyrata subsp. lyrata] gi|297323627|gb|EFH54048.1| hypothetical protein ARALYDRAFT_906461 [Arabidopsis lyrata subsp. lyrata]	1267	1292	0	102.0	81.5	87.5	hypothetical protein ARALYDRAFT_906461	gbpln	Arabidopsis lyrata	AT3G51120.1 | Symbols: | DNA binding;zinc ion binding;nucleic acid binding;nucleic acid binding | chr3:18986026-18991886 REVERSE LENGTH=1292	1267	1292	0	102.0	80.9	87.0
Rsa1.0_00369.1.g12376.t5	gb|EOA25162.1| hypothetical protein CARUB_v10018473mg [Capsella rubella]	398	410	0	103.0	94.5	97.7	hypothetical protein CARUB_v10018473mg	gbpln	Capsella rubella	AT3G51130.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0183 (InterPro:IPR005373); Has 269 Blast hits to 265 proteins in 123 species: Archae - 0; Bacteria - 0; Metazoa - 131; Fungi - 82; Plants - 37; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink). | chr3:18994219-18997180 FORWARD LENGTH=410	398	410	0	103.0	94.0	96.7

Rsa1.0_00369.1_g12377.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	566	536	2.00E-84	94.7	24.7	32.0	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT5G28823.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: Zinc knuckle (CCHC-type) family protein (TAIR:AT2G07760.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:10837849-10839826 REVERSE LENGTH=568	566	568	3.00E-46	100.4	14.0	17.0
Rsa1.0_00369.1_g12378.t1	ref|NP_001190049.1| ATP binding microtubule motor family protein [Arabidopsis thaliana] gi|332645236|gb|AEE78757.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]	1087	1054	0	97.0	78.8	85.0	ATP binding microtubule motor family protein	gbpln	Arabidopsis thaliana	AT3G51150.2 | Symbols: | ATP binding microtubule motor family protein | chr3:19002006-19006509 FORWARD LENGTH=1054	1087	1054	0	97.0	78.8	85.0
Rsa1.0_00369.1_g12379.t1	gb|EOA25979.1| hypothetical protein CARUB_v10019368mg [Capsella rubella]	365	374	0	102.5	91.2	95.6	hypothetical protein CARUB_v10019368mg	gbpln	Capsella rubella	AT3G51160.1 | Symbols: MUR1, MUR_1, GMD2 | NAD(P)-binding Rossmann-fold superfamily protein | chr3:19007232-19008353 REVERSE LENGTH=373	365	373	0	102.2	91.0	95.1
Rsa1.0_00369.1_g12380.t1	ref|XP_002869043.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata] gi|297314879|gb|EFH45302.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata]	259	258	1.00E-130	99.6	90.0	92.7	60S ribosomal protein L8	gbpln	Arabidopsis lyrata	AT4G36130.1 | Symbols: | Ribosomal protein L2 family | chr4:17097613-17098656 FORWARD LENGTH=258	259	258	1.00E-132	99.6	89.6	92.7
Rsa1.0_00369.1_g12381.t1	ref|XP_002877792.1| hypothetical protein ARALYDRAFT_485473 [Arabidopsis lyrata subsp. lyrata] gi|297323630|gb|EFH54051.1| hypothetical protein ARALYDRAFT_485473 [Arabidopsis lyrata subsp. lyrata]	187	186	9.00E-71	99.5	79.7	85.6	hypothetical protein ARALYDRAFT_485473	gbpln	Arabidopsis lyrata	AT3G51220.1 | Symbols: | Plant protein of unknown function (DUF827) | chr3:19021943-19022612 REVERSE LENGTH=186	187	186	6.00E-73	99.5	78.6	85.6
Rsa1.0_00369.1_g12382.t1	gb|ABB91635.1| flavanone 3-hydroxylase 1 [Brassica napus] gi|82795266|gb|ABB91636.1| flavanone 3-hydroxylase 1 [Brassica napus]	368	358	0	97.3	89.9	93.8	flavanone 3-hydroxylase 1	gbpln	Brassica napus	AT3G51240.1 | Symbols: F3H, TT6, F3'H | flavanone 3-hydroxylase | chr3:19025409-19026658 FORWARD LENGTH=358	368	358	0	97.3	86.7	91.8
Rsa1.0_00369.1_g12383.t1	emb|CAA73622.1| multicatalytic endopeptidase [Arabidopsis thaliana] gi|2511582|emb|CAA73623.1| multicatalytic endopeptidase [Arabidopsis thaliana]	250	235	1.00E-130	94.0	90.0	93.2	multicatalytic endopeptidase	gbpln	Arabidopsis thaliana	AT5G66140.1 | Symbols: PAD2 | proteasome alpha subunit D2 | chr5:26437445-26438677 REVERSE LENGTH=250	250	250	1.00E-131	100.0	95.6	98.8
Rsa1.0_00369.1_g12384.t16	ref|NP_190696.1| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana] gi|6562280|emb|CAB62650.1| MS5-like protein [Arabidopsis thaliana] gi|30102656|gb|AAP21246.1| At3g51280 [Arabidopsis thaliana] gi|110735963|dbj|BAE99956.1| MS5 like protein [Arabidopsis thaliana] gi|332645252|gb|AEE78773.1| tetratricopeptide repeat domain-containing protein [Arabidopsis thaliana]	420	430	0	102.4	88.8	92.9	tetratricopeptide repeat domain-containing protein	gbpln	Arabidopsis thaliana	AT3G51280.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:19037229-19038781 FORWARD LENGTH=430	420	430	0	102.4	88.8	92.9
Rsa1.0_00369.1_g12385.t1	gb|AFK47272.1| unknown [Lotus japonicus]	197	197	1.00E-104	100.0	90.4	97.5	unknown	gbpln	Lotus japonicus	AT4G35950.1 | Symbols: ARAC6, RAC2, ATROP5, ATRAC6, ROP5, RAC6 | RAC-like 6 | chr4:17024051-17025514 REVERSE LENGTH=197	197	197	1.00E-101	100.0	95.9	99.0
Rsa1.0_00369.1_g12386.t2	ref|XP_002877797.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297323635|gb|EFH54056.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	551	530	0	96.2	73.3	81.9	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT3G51330.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:19053480-19056152 REVERSE LENGTH=529	551	529	0	96.0	73.3	81.5
Rsa1.0_00369.1_g12387.t2	gb|AAM19705.1|AF499718_1 protein phosphatase 2c-like protein [Eutrema halophilum]	185	378	2.00E-26	204.3	34.1	37.3	protein phosphatase 2c-like protein	gbpln	Eutrema halophilum	AT3G51370.2 | Symbols: | Protein phosphatase 2C family protein | chr3:19070387-19071975 FORWARD LENGTH=294	185	294	6.00E-27	158.9	32.4	36.2
Rsa1.0_00369.1_g12388.t1	ref|NP_190706.1| protein IQ-domain 20 [Arabidopsis thaliana] gi|6572059|emb|CAB63002.1| putative protein [Arabidopsis thaliana] gi|119360013|gb|ABL66735.1| At3g51380 [Arabidopsis thaliana] gi|332645265|gb|AEE78786.1| protein IQ-domain 20 [Arabidopsis thaliana]	142	103	2.00E-39	72.5	62.0	65.5	protein IQ-domain 20	gbpln	Arabidopsis thaliana	AT3G51380.1 | Symbols: IQD20 | IQ-domain 20 | chr3:19074036-19074426 REVERSE LENGTH=103	142	103	6.00E-42	72.5	62.0	65.5

Rsa1.0_00369.1.g12389.t1	gb|EOA16039.1| hypothetical protein CARUB_v10004167mg [Capsella rubella]	478	799	1.00E-151	167.2	57.5	68.2	hypothetical protein CARUB_v10004167mg	gbpln	Capsella rubella	AT4G13780.1 | Symbols: | methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative | chr4:7993366-7998433 REVERSE LENGTH=797	478	797	1.00E-150	166.7	56.1	66.1
Rsa1.0_00370.1.g12390.t2	gb|ABW81040.1| C-4-methyl-sterase-like protein [Arabidopsis lyrata subsp. lyrata]	331	253	4.00E-97	76.4	55.6	59.2	C-4-methyl-sterase-like protein	gbpln	Arabidopsis lyrata	AT2G29390.3 | Symbols: ATSMO2 | sterol 4-alpha-methyl-oxidase 2-2 | chr2:12610758-12612149 REVERSE LENGTH=253	331	253	2.00E-99	76.4	55.3	58.6
Rsa1.0_00370.1.g12391.t1	ref|XP_002879214.1| hypothetical protein ARALYDRAFT_344701 [Arabidopsis lyrata subsp. lyrata] gi|297325053|gb|EFH55473.1| hypothetical protein ARALYDRAFT_344701 [Arabidopsis lyrata subsp. lyrata]	384	397	1.00E-166	103.4	84.9	92.2	hypothetical protein ARALYDRAFT_344701	gbpln	Arabidopsis lyrata	AT2G29410.1 | Symbols: MTPB1, ATMTPB1 | metal tolerance protein B1 | chr2:12616810-12617937 FORWARD LENGTH=375	384	375	1.00E-159	97.7	79.4	86.5
Rsa1.0_00370.1.g12392.t1	gb|ABW74586.1| glutathione-S-transferase [Boechera divaricarpa]	225	225	1.00E-108	100.0	84.9	91.6	glutathione-S-transferase	gbpln	Boechera divaricarpa	AT2G29420.1 | Symbols: ATGSTU7, GST25, GSTU7 | glutathione S-transferase tau 7 | chr2:12618111-12618871 REVERSE LENGTH=227	225	227	1.00E-107	100.9	84.0	90.7
Rsa1.0_00370.1.g12393.t1	gb|ABW81194.1| glutathione-S-transferase 5 [Arabidopsis cebennensis]	261	224	4.00E-99	85.8	67.4	72.8	glutathione-S-transferase 5	gbpln	Arabidopsis cebennensis	AT2G29460.1 | Symbols: ATGSTU4, GST22, GSTU4 | glutathione S-transferase tau 4 | chr2:12626689-12627600 REVERSE LENGTH=224	261	224	1.00E-100	85.8	67.0	72.4
Rsa1.0_00370.1.g12394.t1	ref|XP_002881051.1| glutathione-s-transferase 2 [Arabidopsis lyrata subsp. lyrata] gi|158828146|gb|ABW81025.1| glutathione-S-transferase 2 [Arabidopsis lyrata subsp. lyrata] gi|297326890|gb|EFH57310.1| glutathione-s-transferase 2 [Arabidopsis lyrata subsp. lyrata]	228	225	1.00E-107	98.7	83.8	90.4	glutathione-s-transferase 2	gbpln	Arabidopsis lyrata	AT2G29470.1 | Symbols: ATGSTU3, GST21, GSTU3 | glutathione S-transferase tau 3 | chr2:12628666-12629490 REVERSE LENGTH=225	228	225	1.00E-109	98.7	83.3	89.0
Rsa1.0_00370.1.g12395.t1	ref|NP_180509.1| glutathione S-transferase [Arabidopsis thaliana] gi|75268092|sp|Q9ZW29.1|GSTU2_ARATH RecName: Full=Glutathione S-transferase U2; Short=AtGSTU2; AltName: Full=GST class-tau member 2; AltName: Full=Glutathione S-transferase 20 gi|11096002|gb|AAG30133.1|AF288184_1 glutathione S-transferase [Arabidopsis thaliana] gi|3980387|gb|AAC95190.1| putative glutathione S-transferase [Arabidopsis thaliana] gi|20453170|gb|AAM19826.1| At2g29480/F16P2.14 [Arabidopsis thaliana] gi|21689633|gb|AAM67438.1| At2g29480/F16P2.14 [Arabidopsis thaliana] gi|330253165|gb|AEC08259.1| glutathione S-transferase U2 [Arabidopsis thaliana]	224	225	1.00E-112	100.4	88.4	93.3	glutathione S-transferase	gbpln	Arabidopsis thaliana	AT2G29480.1 | Symbols: ATGSTU2, GST20, GSTU2 | glutathione S-transferase tau 2 | chr2:12630382-12631232 REVERSE LENGTH=225	224	225	1.00E-114	100.4	88.4	93.3
Rsa1.0_00370.1.g12396.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00370.1.g12397.t1	ref|NP_180511.1| HSP20 family protein [Arabidopsis thaliana] gi|75315964|sp|Q9ZW31.1|HS17B_ARATH RecName: Full=17.6 kDa class I heat shock protein 2; AltName: Full=17.6 kDa heat shock protein 2; Short=AtHsp17.6B gi|3980385|gb|AAC95188.1| putative small heat shock protein [Arabidopsis thaliana] gi|21554599|gb|AAM63628.1| putative small heat shock protein [Arabidopsis thaliana] gi|51968472|dbj|BAD42928.1| putative small heat shock protein [Arabidopsis thaliana] gi|51968688|dbj|BAD43036.1| putative small heat shock protein [Arabidopsis thaliana] gi|51971795|dbj|BAD44562.1| putative small heat shock protein [Arabidopsis thaliana] gi|51971973|dbj|BAD44651.1| putative small heat shock protein [Arabidopsis thaliana] gi|51971989|dbj|BAD44659.1| putative small heat shock protein [Arabidopsis thaliana] gi|62318713|dbj|BAD93726.1| putative small heat shock protein [Arabidopsis thaliana] gi|62320100|dbj|BAD94277.1| putative small heat shock protein [Arabidopsis thaliana] gi|88900410|gb|ABD57517.1| At2g29500 [Arabidopsis thaliana] gi|330253167|gb|AEC08261.1| HSP20 family protein [Arabidopsis thaliana]	154	153	2.00E-65	99.4	91.6	94.2	HSP20 family protein	gbpln	Arabidopsis thaliana	AT2G29500.1 | Symbols: | HSP20-like chaperones superfamily protein | chr2:12633279-12633740 REVERSE LENGTH=153	154	153	5.00E-68	99.4	91.6	94.2
Rsa1.0_00370.1.g12398.t1	ref|XP_002881056.1| hypothetical protein ARALYDRAFT_901916 [Arabidopsis lyrata subsp. lyrata] gi|297326895|gb|EFH57315.1| hypothetical protein ARALYDRAFT_901916 [Arabidopsis lyrata subsp. lyrata]	85	85	2.00E-40	100.0	90.6	96.5	hypothetical protein ARALYDRAFT_901916	gbpln	Arabidopsis lyrata	AT2G29530.2 | Symbols: TIM10 | Tim10/DDP family zinc finger protein | chr2:12641026-12642243 REVERSE LENGTH=83	85	83	1.00E-40	97.6	85.9	90.6
Rsa1.0_00370.1.g12399.t1	ref|NP_180518.1| zinc finger CCCH domain-containing protein 25 [Arabidopsis thaliana] gi|75339110|sp|Q9ZW36.1|C3H25_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 25; Short=AtC3H25 gi|16226863|gb|AAL16284.1|AF428354_1 At2g29580/F16P2.4 [Arabidopsis thaliana] gi|3980378|gb|AAC95181.1| putative RNA-binding protein [Arabidopsis thaliana] gi|27363236|gb|AAO11537.1| At2g29580/F16P2.4 [Arabidopsis thaliana] gi|330253181|gb|AEC08275.1| zinc finger CCCH domain-containing protein 25 [Arabidopsis thaliana]	338	483	4.00E-80	142.9	64.2	72.5	zinc finger CCCH domain-containing protein 25	gbpln	Arabidopsis thaliana	AT2G29580.1 | Symbols: | CCCH-type zinc fingerfamily protein with RNA-binding domain | chr2:12652011-12654158 FORWARD LENGTH=483	338	483	1.00E-82	142.9	64.2	72.5
Rsa1.0_00370.1.g12400.t1	gb|EOA26305.1| hypothetical protein CARUB_v10024771mg [Capsella rubella]	178	313	1.00E-75	175.8	77.0	85.4	hypothetical protein CARUB_v10024771mg	gbpln	Capsella rubella	AT2G29640.1 | Symbols: JOSL | JOSEPHIN-like protein | chr2:12671206-12673300 FORWARD LENGTH=360	178	360	2.00E-75	202.2	74.7	83.7
Rsa1.0_00370.1.g12401.t1	dbj|BAJ34219.1| unnamed protein product [Thellungiella halophila]	366	379	1.00E-136	103.6	77.3	85.5	unnamed protein product	----	----	AT2G29660.1 | Symbols: | zinc finger (C2H2 type) family protein | chr2:12679346-12680467 FORWARD LENGTH=373	366	373	1.00E-126	101.9	80.1	86.9
Rsa1.0_00370.1.g12402.t1	ref|NP_565685.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana] gi|14030739|gb|AAK53044.1|AF375460_1 At2g29670/T27A16.23 [Arabidopsis thaliana] gi|18377765|gb|AAL67032.1| unknown protein [Arabidopsis thaliana] gi|20197389|gb|AAC35237.2| expressed protein [Arabidopsis thaliana] gi|20465643|gb|AAM20290.1| unknown protein [Arabidopsis thaliana] gi|23308477|gb|AAN18208.1| At2g29670/T27A16.23 [Arabidopsis thaliana] gi|330253196|gb|AEC08290.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	514	536	0	104.3	72.6	83.5	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G29670.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:12682309-12684745 REVERSE LENGTH=536	514	536	0	104.3	72.6	83.5
Rsa1.0_00370.1.g12403.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00370.1.g12404.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00370.1.g12405.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00370.1.g12406.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00370.1.g12407.t1	ref|XP_002881067.1| hypothetical protein ARALYDRAFT_901946 [Arabidopsis lyrata subsp. lyrata] gi|297326906|gb|EFH57326.1| hypothetical protein ARALYDRAFT_901946 [Arabidopsis lyrata subsp. lyrata]	114	117	2.00E-41	102.6	67.5	83.3	hypothetical protein ARALYDRAFT_901946	gbpln	Arabidopsis lyrata	AT4G09465.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr4:6001411-6001761 FORWARD LENGTH=116	114	116	2.00E-29	101.8	48.2	67.5
Rsa1.0_00370.1.g12408.t1	ref|NP_973562.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|29649061|gb|AAO86842.1| hypothetical protein [Arabidopsis thaliana] gi|330253228|gb|AEC08322.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	228	339	1.00E-72	148.7	65.8	76.8	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT2G29930.2 | Symbols: | F-box/RNI-like superfamily protein | chr2:12756457-12757727 REVERSE LENGTH=339	228	339	3.00E-75	148.7	65.8	76.8
Rsa1.0_00370.1.g12409.t1	ref|XP_002879240.1| ATPDR3/PDR3 [Arabidopsis lyrata subsp. lyrata] gi|297325079|gb|EFH55499.1| ATPDR3/PDR3 [Arabidopsis lyrata subsp. lyrata]	1428	1428	0	100.0	92.4	96.5	ATPDR3/PDR3	gbpln	Arabidopsis lyrata	AT2G29940.1 | Symbols: PDR3, ATPDR3 | pleiotropic drug resistance 3 | chr2:12760139-12766455 FORWARD LENGTH=1426	1428	1426	0	99.9	91.9	96.4
Rsa1.0_00370.1.g12410.t1	gb|AFJ19037.1| fatty acid desaturase BnaC.FAD3.b [Brassica napus]	380	380	0	100.0	97.6	99.7	fatty acid desaturase BnaC.FAD3.b	gbpln	Brassica napus	AT2G29980.1 | Symbols: FAD3 | fatty acid desaturase 3 | chr2:12781787-12784946 REVERSE LENGTH=386	380	386	0	101.6	91.8	95.8
Rsa1.0_00371.1.g12411.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00371.1.g12412.t1	gb|EOA26942.1| hypothetical protein CARUB_v10023035mg, partial [Capsella rubella]	419	508	1.00E-139	121.2	67.3	77.6	hypothetical protein CARUB_v10023035mg, partial	gbpln	Capsella rubella	AT2G23530.1 | Symbols: | Zinc-finger domain of monoamine-oxidase A repressor R1 | chr2:10020652-10022804 REVERSE LENGTH=552	419	552	1.00E-138	131.7	63.0	70.9
Rsa1.0_00371.1.g12413.t1	gb|EOA28509.1| hypothetical protein CARUB_v10024724mg [Capsella rubella]	876	890	0	101.6	87.8	91.9	hypothetical protein CARUB_v10024724mg	gbpln	Capsella rubella	AT2G23520.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr2:10014256-10016943 REVERSE LENGTH=895	876	895	0	102.2	87.1	91.4
Rsa1.0_00371.1.g12414.t1	ref|XP_002880506.1| hypothetical protein ARALYDRAFT_481217 [Arabidopsis lyrata subsp. lyrata] gi|297326345|gb|EFH56765.1| hypothetical protein ARALYDRAFT_481217 [Arabidopsis lyrata subsp. lyrata]	525	519	0	98.9	82.9	89.0	hypothetical protein ARALYDRAFT_481217	gbpln	Arabidopsis lyrata	AT2G23470.1 | Symbols: RUS4 | Protein of unknown function, DUF647 | chr2:9999105-10001398 REVERSE LENGTH=520	525	520	0	99.0	81.7	88.4
Rsa1.0_00371.1.g12415.t1	gb|EOA26553.1| hypothetical protein CARUB_v10022612mg [Capsella rubella]	859	883	0	102.8	87.0	92.2	hypothetical protein CARUB_v10022612mg	gbpln	Capsella rubella	AT2G23460.1 | Symbols: XLG1, ATXLG1 | extra-large G-protein 1 | chr2:9995699-9998945 FORWARD LENGTH=888	859	888	0	103.4	86.7	92.0
Rsa1.0_00371.1.g12416.t1	ref|NP_565552.1| wall-associated receptor kinase-like 14 [Arabidopsis thaliana] gi|30682087|ref|NP_850041.1| wall-associated receptor kinase-like 14 [Arabidopsis thaliana] gi|116256124|sp|Q8RY67.2|WAKLO_ARATH RecName: Full=Wall-associated receptor kinase-like 14; Flags: Precursor gi|20197000|gb|AAC23760.2| putative protein kinase [Arabidopsis thaliana] gi|330252362|gb|AEC07456.1| wall-associated receptor kinase-like 14 [Arabidopsis thaliana] gi|330252363|gb|AEC07457.1| wall-associated receptor kinase-like 14 [Arabidopsis thaliana]	687	708	0	103.1	79.3	89.2	wall-associated receptor kinase-like 14	gbpln	Arabidopsis thaliana	AT2G23450.1 | Symbols: | Protein kinase superfamily protein | chr2:9988926-9991244 REVERSE LENGTH=708	687	708	0	103.1	79.3	89.2
Rsa1.0_00371.1.g12417.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00371.1.g12418.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00371.1.g12419.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1900	1274	0	67.1	32.9	43.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1900	575	2.00E-66	30.3	9.0	14.2
Rsa1.0_00371.1.g12420.t1	ref|XP_002878685.1| hypothetical protein ARALYDRAFT_900829 [Arabidopsis lyrata subsp. lyrata] gi|297324524|gb|EFH54944.1| hypothetical protein ARALYDRAFT_900829 [Arabidopsis lyrata subsp. lyrata]	83	81	2.00E-25	97.6	72.3	81.9	hypothetical protein ARALYDRAFT_900829	gbpln	Arabidopsis lyrata	AT2G23440.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root; Has 25 Blast hits to 25 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9979482-9979730 FORWARD LENGTH=82	83	82	1.00E-23	98.8	67.5	75.9

Rsa1.0_00371.1.g12421.t1	ref|NP_179919.1| histone-lysine N-methyltransferase CLF [Arabidopsis thaliana] gi|30912630|sp|P93831.2|CLF_ARATH RecName: Full=Histone-lysine N-methyltransferase CLF; AltName: Full=Polycomb group protein CURLY LEAF; AltName: Full=Protein INCURVATA 1; AltName: Full=Protein SET DOMAIN GROUP 1; AltName: Full=Protein photoperiod insensitive flowering gi|3242729|gb|AAC23781.1| curly leaf protein (polycomb-group) [Arabidopsis thaliana] gi|330252355|gb|AEC07449.1| histone-lysine N-methyltransferase CLF [Arabidopsis thaliana]	916	902	0	98.5	84.6	89.0	histone-lysine N-methyltransferase CLF	gbpln	Arabidopsis thaliana	AT2G23380.1 | Symbols: CLF, ICU1, SDG1, SET1 | SET domain-containing protein | chr2:9955570-9960117 FORWARD LENGTH=902	916	902	0	98.5	84.6	89.0
Rsa1.0_00371.1.g12422.t1	ref|NP_179917.2| filament-like plant protein 7 [Arabidopsis thaliana] gi|334302808|sp|Q9SLN1.2|FPP7_ARATH RecName: Full=Filament-like plant protein 7; Short=AtFPP7 gi|330252353|gb|AEC07447.1| filament-like plant protein 7 [Arabidopsis thaliana]	812	898	0	110.6	79.6	89.0	filament-like plant protein 7	gbpln	Arabidopsis thaliana	AT2G23360.1 | Symbols: | Plant protein of unknown function (DUF869) | chr2:9949420-9952727 FORWARD LENGTH=898	812	898	0	110.6	79.6	89.0
Rsa1.0_00371.1.g12423.t1	ref|XP_002878667.1| hypothetical protein ARALYDRAFT_481192 [Arabidopsis lyrata subsp. lyrata] gi|297324506|gb|EFH54926.1| hypothetical protein ARALYDRAFT_481192 [Arabidopsis lyrata subsp. lyrata]	824	828	0	100.5	70.4	82.4	hypothetical protein ARALYDRAFT_481192	gbpln	Arabidopsis lyrata	AT2G23200.1 | Symbols: | Protein kinase superfamily protein | chr2:9879351-9881855 FORWARD LENGTH=834	824	834	0	101.2	69.7	81.9
Rsa1.0_00371.1.g12424.t1	ref|XP_002878667.1| hypothetical protein ARALYDRAFT_481192 [Arabidopsis lyrata subsp. lyrata] gi|297324506|gb|EFH54926.1| hypothetical protein ARALYDRAFT_481192 [Arabidopsis lyrata subsp. lyrata]	85	828	5.00E-11	974.1	50.6	69.4	hypothetical protein ARALYDRAFT_481192	gbpln	Arabidopsis lyrata	AT2G23200.1 | Symbols: | Protein kinase superfamily protein | chr2:9879351-9881855 FORWARD LENGTH=834	85	834	3.00E-12	981.2	48.2	67.1
Rsa1.0_00371.1.g12425.t1	ref|XP_002878680.1| PAB4 binding protein 4 [Arabidopsis lyrata subsp. lyrata] gi|297324519|gb|EFH54939.1| PAB4 binding protein 4 [Arabidopsis lyrata subsp. lyrata]	640	655	0	102.3	87.5	93.9	PAB4 binding protein 4	gbpln	Arabidopsis lyrata	AT2G23350.1 | Symbols: PAB4, PABP4 | poly(A) binding protein 4 | chr2:9943209-9946041 FORWARD LENGTH=662	640	662	0	103.4	86.3	92.5
Rsa1.0_00371.1.g12426.t1	ref|NP_179915.1| ethylene-responsive transcription factor ERF008 [Arabidopsis thaliana] gi|75219088|sp|O22174.1|ERF08_ARATH RecName: Full=Ethylene-responsive transcription factor ERF008 gi|2642430|gb|AAB87098.1| putative AP2 domain transcription factor [Arabidopsis thaliana] gi|26452018|dbj|BAC43099.1| putative AP2 domain transcription factor [Arabidopsis thaliana] gi|28372974|gb|AAO39969.1| At2g23340 [Arabidopsis thaliana] gi|330252350|gb|AEC07444.1| ethylene-responsive transcription factor ERF008 [Arabidopsis thaliana]	167	176	1.00E-66	105.4	82.6	85.6	ethylene-responsive transcription factor ERF008	gbpln	Arabidopsis thaliana	AT2G23340.1 | Symbols: DEAR3 | DREB and EAR motif protein 3 | chr2:9938186-9938716 FORWARD LENGTH=176	167	176	6.00E-69	105.4	82.6	85.6
Rsa1.0_00372.1.g12427.t1	ref|XP_002881852.1| hypothetical protein ARALYDRAFT_321928 [Arabidopsis lyrata subsp. lyrata] gi|297327691|gb|EFH58111.1| hypothetical protein ARALYDRAFT_321928 [Arabidopsis lyrata subsp. lyrata]	381	742	2.00E-63	194.8	46.5	59.3	hypothetical protein ARALYDRAFT_321928	gbpln	Arabidopsis lyrata	AT2G42480.1 | Symbols: | TRAF-like family protein | chr2:17685805-17689851 REVERSE LENGTH=743	381	743	1.00E-59	195.0	44.6	56.7
Rsa1.0_00372.1.g12428.t1	ref|XP_002881852.1| hypothetical protein ARALYDRAFT_321928 [Arabidopsis lyrata subsp. lyrata] gi|297327691|gb|EFH58111.1| hypothetical protein ARALYDRAFT_321928 [Arabidopsis lyrata subsp. lyrata]	453	742	5.00E-79	163.8	42.4	54.7	hypothetical protein ARALYDRAFT_321928	gbpln	Arabidopsis lyrata	AT2G42480.1 | Symbols: | TRAF-like family protein | chr2:17685805-17689851 REVERSE LENGTH=743	453	743	3.00E-72	164.0	38.6	49.2
Rsa1.0_00372.1.g12429.t1	ref|XP_002881854.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327693|gb|EFH58113.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	541	595	4.00E-75	110.0	42.7	59.1	predicted protein	gbpln	Arabidopsis lyrata	AT2G42480.1 | Symbols: | TRAF-like family protein | chr2:17685805-17689851 REVERSE LENGTH=743	541	743	6.00E-76	137.3	35.5	47.9

Rsa1.0_00372.1.g12430.t1	ref|NP_001078216.1| ECA1-like gametogenesis related family protein [Arabidopsis thaliana] gi|332643796|gb|AEE77317.1| ECA1-like gametogenesis related family protein [Arabidopsis thaliana]	104	105	3.00E-20	101.0	51.9	66.3	ECA1-like gametogenesis related family protein	gbpln	Arabidopsis thaliana	AT3G27425.1 | Symbols: | ECA1-like gametogenesis related family protein | chr3:10151058-10151375 FORWARD LENGTH=105	104	105	4.00E-23	101.0	51.9	66.3
Rsa1.0_00372.1.g12431.t1	ref|NP_565974.1| serine/threonine-protein phosphatase PP2A-4 catalytic subunit [Arabidopsis thaliana] gi|297827949|ref|XP_002881857.1| protein phosphatase 2A-4 [Arabidopsis lyrata subsp. lyrata] gi|1352663|sp|Q07100.2|PP2A4_ARATH RecName: Full=Serine/threonine-protein phosphatase PP2A-4 catalytic subunit; AltName: Full=Protein phosphatase 2A isoform 4 gi|466441|gb|AAA64742.1| Ser/Thr protein phosphatase [Arabidopsis thaliana] gi|4567320|gb|AAD23731.1| serine threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] gi|20198072|gb|AAM15383.1| serine/threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] gi|33589738|gb|AAQ22635.1| At2g42500/F14N22.23 [Arabidopsis thaliana] gi|297327696|gb|EFH58116.1| protein phosphatase 2A-4 [Arabidopsis lyrata subsp. lyrata] gi|330255033|gb|AEC10127.1| serine/threonine-protein phosphatase PP2A-4 catalytic subunit [Arabidopsis thaliana] gi|482563348|gb|EOA27538.1| hypothetical protein CARUB_v10023677mg [Capsella rubella]	313	313	0	100.0	98.7	99.7	serine/threonine-protein phosphatase PP2A-4 catalytic subunit	gbpln	Arabidopsis lyrata	AT2G42500.1 | Symbols: PP2A-3 | protein phosphatase 2A-3 | chr2:17698099-17701226 REVERSE LENGTH=313	313	313	0	100.0	98.7	99.7
Rsa1.0_00372.1.g12432.t1	ref|XP_002879989.1| hypothetical protein ARALYDRAFT_483344 [Arabidopsis lyrata subsp. lyrata] gi|297325828|gb|EFH56248.1| hypothetical protein ARALYDRAFT_483344 [Arabidopsis lyrata subsp. lyrata]	381	607	2.00E-63	159.3	47.0	57.7	hypothetical protein ARALYDRAFT_483344	gbpln	Arabidopsis lyrata	AT2G42510.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: spliceosome assembly, nuclear mRNA splicing, via spliceosome; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Survival motor neuron interacting protein 1 (InterPro:IPR007022); BEST Arabidopsis thaliana protein match is: spliceosome protein-related (TAIR:AT1G54380.1); Has 297 Blast hits to 270 proteins in 80 species: Archae - 2; Bacteria - 35; Metazoa - 62; Fungi - 11; Plants - 64; Viruses - 0; Other Eukaryotes - 123 (source: NCBI BLink). | chr2:17701686-17704618 FORWARD LENGTH=653	381	653	2.00E-49	171.4	34.1	39.1
Rsa1.0_00372.1.g12433.t1	ref|XP_002881861.1| hypothetical protein ARALYDRAFT_483351 [Arabidopsis lyrata subsp. lyrata] gi|297327700|gb|EFH58120.1| hypothetical protein ARALYDRAFT_483351 [Arabidopsis lyrata subsp. lyrata]	366	366	0	100.0	86.9	92.6	hypothetical protein ARALYDRAFT_483351	gbpln	Arabidopsis lyrata	AT2G42570.1 | Symbols: TBL39 | TRICHOME BIREFRINGENCE-LIKE 39 | chr2:17717498-17719921 REVERSE LENGTH=367	366	367	0	100.3	86.6	93.2
Rsa1.0_00372.1.g12434.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00372.1.g12435.t1	ref|XP_002879994.1| hypothetical protein ARALYDRAFT_483352 [Arabidopsis lyrata subsp. lyrata] gi|297325833|gb|EFH56253.1| hypothetical protein ARALYDRAFT_483352 [Arabidopsis lyrata subsp. lyrata]	675	688	0	101.9	86.2	92.1	hypothetical protein ARALYDRAFT_483352	gbpln	Arabidopsis lyrata	AT2G42580.1 | Symbols: TTL3, VIT | tetratricopetide-repeat thioredoxin-like 3 | chr2:17728855-17731461 FORWARD LENGTH=691	675	691	0	102.4	85.9	92.3
Rsa1.0_00372.1.g12436.t1	ref|XP_002881863.1| phosphoenolpyruvate carboxylase [Arabidopsis lyrata subsp. lyrata] gi|297327702|gb|EFH58122.1| phosphoenolpyruvate carboxylase [Arabidopsis lyrata subsp. lyrata]	929	963	0	103.7	96.3	98.0	phosphoenolpyruvate carboxylase	gbpln	Arabidopsis lyrata	AT2G42600.1 | Symbols: ATPPC2, PPC2 | phosphoenolpyruvate carboxylase 2 | chr2:17734541-17738679 REVERSE LENGTH=963	929	963	0	103.7	96.0	97.8
Rsa1.0_00372.1.g12437.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00372.1.g12438.t1	gb|EOA29463.1| hypothetical protein CARUB_v100241591mg [Capsella rubella] gi|482565274|gb|EOA29464.1| hypothetical protein CARUB_v100241591mg [Capsella rubella]	178	178	1.00E-85	100.0	88.2	91.0	hypothetical protein CARUB_v100241591mg	gbpln	Capsella rubella	AT2G42610.2 | Symbols: LSH10 | Protein of unknown function (DUF640) | chr2:17748005-17748538 FORWARD LENGTH=177	178	177	9.00E-87	99.4	87.6	89.9

Rsa1.0_00372.1.g12439.t1	ref|XP_002881837.1| hypothetical protein ARALYDRAFT_903588 [Arabidopsis lyrata subsp. lyrata] gi|297327676|gb|EFH58096.1| hypothetical protein ARALYDRAFT_903588 [Arabidopsis lyrata subsp. lyrata]	113	345	1.00E-18	305.3	54.0	64.6	hypothetical protein ARALYDRAFT_903588	gbpln	Arabidopsis lyrata	AT2G42550.1 | Symbols: | Protein kinase superfamily protein | chr2:17713196-17714230 FORWARD LENGTH=344	113	344	8.00E-11	304.4	23.9	28.3
Rsa1.0_00372.1.g12440.t1	dbj|BAJ33992.1| unnamed protein product [Thellungiella halophila]	685	701	0	102.3	88.6	94.0	unnamed protein product	----	----	AT2G42620.1 | Symbols: MAX2, ORE9, PPS | RNI-like superfamily protein | chr2:17756170-17758251 FORWARD LENGTH=693	685	693	0	101.2	85.8	92.0
Rsa1.0_00372.1.g12441.t1	ref|XP_002881866.1| hypothetical protein ARALYDRAFT_903639 [Arabidopsis lyrata subsp. lyrata] gi|297327705|gb|EFH58125.1| hypothetical protein ARALYDRAFT_903639 [Arabidopsis lyrata subsp. lyrata]	239	241	1.00E-124	100.8	90.0	96.2	hypothetical protein ARALYDRAFT_903639	gbpln	Arabidopsis lyrata	AT2G42670.1 | Symbols: | Protein of unknown function (DUF1637) | chr2:17772004-17773700 REVERSE LENGTH=241	239	241	1.00E-126	100.8	89.1	95.4
Rsa1.0_00372.1.g12442.t1	ref|XP_002879999.1| ATMBF1A/MBF1A [Arabidopsis lyrata subsp. lyrata] gi|297325838|gb|EFH56258.1| ATMBF1A/MBF1A [Arabidopsis lyrata subsp. lyrata]	137	142	9.00E-67	103.6	92.0	95.6	ATMBF1A/MBF1A	gbpln	Arabidopsis lyrata	AT3G58680.1 | Symbols: MBF1B, ATMBF1B | multiprotein bridging factor 1B | chr3:21707367-21708625 FORWARD LENGTH=142	137	142	9.00E-68	103.6	89.8	94.2
Rsa1.0_00372.1.g12443.t1	ref|XP_002881868.1| hypothetical protein ARALYDRAFT_903642 [Arabidopsis lyrata subsp. lyrata] gi|297327707|gb|EFH58127.1| hypothetical protein ARALYDRAFT_903642 [Arabidopsis lyrata subsp. lyrata]	392	401	0	102.3	89.5	94.9	hypothetical protein ARALYDRAFT_903642	gbpln	Arabidopsis lyrata	AT2G42690.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:17776356-17777682 REVERSE LENGTH=412	392	412	2.33E-156	105.1	65.1	77.6
Rsa1.0_00372.1.g12444.t1	ref|NP_001189734.1| uncharacterized protein [Arabidopsis thaliana] gi|330255064|gb|AEC10158.1| uncharacterized protein AT2G42700 [Arabidopsis thaliana]	252	867	1.00E-121	344.0	92.5	94.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G42700.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: vesicle-mediated transport, vesicle docking involved in exocytosis; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Sec1-like protein (InterPro:IPR001619). | chr2:17778464-17782034 FORWARD LENGTH=867	252	867	1.00E-124	344.0	92.5	94.4
Rsa1.0_00373.1.g12445.t1	gb|ACP30622.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1414	1459	0	103.2	54.5	66.3	disease resistance protein	gbpln	Brassica rapa	AT5G18350.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6074069-6078569 REVERSE LENGTH=1245	1414	1245	0	88.0	40.9	52.3
Rsa1.0_00373.1.g12446.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1433	1501	0	104.7	57.8	73.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1433	1262	1.00E-127	88.1	16.2	22.8
Rsa1.0_00373.1.g12447.t1	ref|XP_002873884.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319721|gb|EFH50143.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	459	458	1.00E-169	99.8	69.1	80.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G18320.1 | Symbols: | ARM repeat superfamily protein | chr5:6064431-6066186 REVERSE LENGTH=458	459	458	1.00E-167	99.8	68.0	80.0
Rsa1.0_00373.1.g12448.t1	gb|EOA19483.1| hypothetical protein CARUB_v10002130mg [Capsella rubella]	215	166	3.00E-56	77.2	56.7	65.1	hypothetical protein CARUB_v10002130mg	gbpln	Capsella rubella	AT5G18310.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 60 Blast hits to 60 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 0; Plants - 53; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:6061759-6062912 FORWARD LENGTH=167	215	167	3.00E-57	77.7	55.3	62.8
Rsa1.0_00373.1.g12449.t2	ref|NP_197329.4| nucleoside-triphosphatase [Arabidopsis thaliana] gi|332005149|gb|AED92532.1| nucleoside-triphosphatase [Arabidopsis thaliana]	777	578	0	74.4	59.5	62.9	nucleoside-triphosphatase	gbpln	Arabidopsis thaliana	AT5G18280.1 | Symbols: ATAPY2, APY2 | apyrase 2 | chr5:6050799-6054875 REVERSE LENGTH=578	777	578	0	74.4	59.5	62.9
Rsa1.0_00373.1.g12450.t1	ref|XP_002873881.1| ANAC087 [Arabidopsis lyrata subsp. lyrata] gi|297319718|gb|EFH50140.1| ANAC087 [Arabidopsis lyrata subsp. lyrata]	337	334	1.00E-172	99.1	86.9	92.6	ANAC087	gbpln	Arabidopsis lyrata	AT5G18270.1 | Symbols: ANAC087 | Arabidopsis NAC domain containing protein 87 | chr5:6041241-6042743 REVERSE LENGTH=335	337	335	1.00E-174	99.4	87.2	92.3
Rsa1.0_00373.1.g12451.t1	ref|XP_002873880.1| hypothetical protein ARALYDRAFT_909836 [Arabidopsis lyrata subsp. lyrata] gi|297319717|gb|EFH50139.1| hypothetical protein ARALYDRAFT_909836 [Arabidopsis lyrata subsp. lyrata]	376	450	1.00E-124	119.7	66.8	77.4	hypothetical protein ARALYDRAFT_909836	gbpln	Arabidopsis lyrata	AT5G18260.1 | Symbols: | RING/U-box superfamily protein | chr5:6036226-6037295 REVERSE LENGTH=320	376	320	1.00E-102	85.1	56.4	63.8

Rsa1.0_00373.1.g12452.t2	gb|EOA21781.1| hypothetical protein CARUB_v10002242mg [Capsella rubella]	218	133	9.00E-68	61.0	56.9	59.6	hypothetical protein CARUB_v10002242mg	gbpln	Capsella rubella	AT5G18250.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G04040.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:6033797-6035216 FORWARD LENGTH=133	218	133	2.00E-68	61.0	55.0	59.2
Rsa1.0_00373.1.g12453.t1	ref|NP_197325.1| myb-related protein 1 [Arabidopsis thaliana] gi|42573403|ref|NP_974798.1| myb-related protein 1 [Arabidopsis thaliana] gi|9758906|dbj|BAB09482.1| transfactor-like protein [Arabidopsis thaliana] gi|332005140|gb|AED92523.1| myb-related protein 1 [Arabidopsis thaliana] gi|332005141|gb|AED92524.1| myb-related protein 1 [Arabidopsis thaliana]	393	402	0	102.3	90.1	92.9	myb-related protein 1	gbpln	Arabidopsis thaliana	AT5G18240.4 | Symbols: MYR1 | myb-related protein 1 | chr5:6028617-6030573 REVERSE LENGTH=402	393	402	0	102.3	90.1	92.9
Rsa1.0_00373.1.g12454.t1	dbj|BAB09481.1| unnamed protein product [Arabidopsis thaliana]	848	889	0	104.8	90.6	94.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G18230.1 | Symbols: | transcription regulator NOT2/NOT3/NOT5 family protein | chr5:6021610-6027031 REVERSE LENGTH=843	848	843	0	99.4	89.6	93.6
Rsa1.0_00373.1.g12455.t1	ref|XP_002873877.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319714|gb|EFH50136.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	494	490	0	99.2	89.7	94.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G18220.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:6018914-6020453 REVERSE LENGTH=488	494	488	0	98.8	89.7	94.1
Rsa1.0_00373.1.g12456.t1	gb|EOA21381.1| hypothetical protein CARUB_v10001742mg [Capsella rubella]	262	263	1.00E-128	100.4	88.5	93.9	hypothetical protein CARUB_v10001742mg	gbpln	Capsella rubella	AT5G18210.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:6017865-6018919 FORWARD LENGTH=277	262	277	1.00E-118	105.7	79.4	87.4
Rsa1.0_00373.1.g12457.t1	ref|NP_197321.1| galactose-1-phosphate uridylyltransferase [Arabidopsis thaliana] gi|73919619|sp|Q9FK51.1|GALT_ARATH RecName: Full=Probable galactose-1-phosphate uridyltransferase; AltName: Full=Gal-1-P uridylyltransferase; AltName: Full=UDP-glucose--hexose-1-phosphate uridylyltransferase gi|66361361|pdb|1Z84|A Chain A, X-Ray Structure Of Galt-Like Protein From Arabidopsis Thaliana At5g18200 gi|66361362|pdb|1Z84|B Chain B, X-Ray Structure Of Galt-Like Protein From Arabidopsis Thaliana At5g18200 gi|71042524|pdb|1ZWJ|A Chain A, X-Ray Structure Of Galt-Like Protein From Arabidopsis Thaliana At5g18200 gi|71042525|pdb|1ZWJ|B Chain B, X-Ray Structure Of Galt-Like Protein From Arabidopsis Thaliana At5g18200 gi|150261501|pdb|2Q4H|A Chain A, Ensemble Refinement Of The Crystal Structure Of Galt-Like Protein From Arabidopsis Thaliana At5g18200 gi|150261502|pdb|2Q4H|B Chain B, Ensemble Refinement Of The Crystal Structure Of Galt-Like Protein From Arabidopsis Thaliana At5g18200 gi|150261511|pdb|2Q4L|A Chain A, Ensemble Refinement Of The Crystal Structure Of Galt-Like Protein From Arabidopsis Thaliana At5g18200 gi|150261512|pdb|2Q4L|B Chain B	340	351	1.00E-174	103.2	86.5	92.9	galactose-1-phosphate uridylyltransferase	gbpln	Arabidopsis thaliana	AT5G18200.1 | Symbols: | UTP:galactose-1-phosphate uridylyltransferases;ribose-5-phosphate adenylyltransferases | chr5:6015270-6016555 FORWARD LENGTH=351	340	351	1.00E-177	103.2	86.5	92.9
Rsa1.0_00373.1.g12458.t1	gb|EOA20087.1| hypothetical protein CARUB_v10000361mg [Capsella rubella]	706	692	0	98.0	89.8	92.8	hypothetical protein CARUB_v10000361mg	gbpln	Capsella rubella	AT5G18190.1 | Symbols: | Protein kinase family protein | chr5:6010215-6013724 REVERSE LENGTH=691	706	691	0	97.9	88.0	91.5

Rsa1.0_00373.1.g12459.t1	ref|NP_197318.1| glutamate dehydrogenase 1 [Arabidopsis thaliana] gi|12229807|sp|Q43314.1|DHE1_ARATH RecName: Full=Glutamate dehydrogenase 1; Short=GDH 1 gi|1098960|gb|AAA82615.1| glutamate dehydrogenase 1 [Arabidopsis thaliana] gi|1293095|gb|AAB08057.1| glutamate dehydrogenase 1 [Arabidopsis thaliana] gi|9758899|dbj|BAB09475.1| glutamate dehydrogenase (EC 1.4.1.-) 1 [Arabidopsis thaliana] gi|98960991|gb|ABF58979.1| At5g18170 [Arabidopsis thaliana] gi|332005132|gb|AED92515.1| glutamate dehydrogenase 1 [Arabidopsis thaliana]	411	411	0	100.0	95.6	98.5	glutamate dehydrogenase 1	gbpln	Arabidopsis thaliana	AT5G18170.1 | Symbols: GDH1 | glutamate dehydrogenase 1 | chr5:6006172-6008248 FORWARD LENGTH=411	411	411	0	100.0	95.6	98.5
Rsa1.0_00373.1.g12460.t1	gb|EOA19719.1| hypothetical protein CARUB_v10003766mg [Capsella rubella]	83	79	3.00E-33	95.2	88.0	94.0	hypothetical protein CARUB_v10003766mg	gbpln	Capsella rubella	AT5G18150.1 | Symbols: | Methyltransferase-related protein | chr5:6000014-6000331 REVERSE LENGTH=76	83	76	9.00E-31	91.6	78.3	85.5
Rsa1.0_00373.1.g12461.t2	ref|NP_197315.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|9758896|dbj|BAB09472.1| unnamed protein product [Arabidopsis thaliana] gi|20260574|gb|AAM13185.1| unknown protein [Arabidopsis thaliana] gi|28059343|gb|AAO30049.1| unknown protein [Arabidopsis thaliana] gi|332005129|gb|AED92512.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]	319	333	1.00E-117	104.4	76.5	83.1	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT5G18140.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:5998235-5999699 FORWARD LENGTH=333	319	333	1.00E-120	104.4	76.5	83.1
Rsa1.0_00373.1.g12462.t1	ref|XP_002871803.1| hypothetical protein ARALYDRAFT_488679 [Arabidopsis lyrata subsp. lyrata] gi|297317640|gb|EFH48062.1| hypothetical protein ARALYDRAFT_488679 [Arabidopsis lyrata subsp. lyrata]	273	281	1.00E-102	102.9	72.9	82.8	hypothetical protein ARALYDRAFT_488679	gbpln	Arabidopsis lyrata	AT5G18130.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03870.2); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5995634-5997165 FORWARD LENGTH=280	273	280	1.00E-105	102.6	72.5	81.0
Rsa1.0_00373.1.g12463.t1	gb|AAM60945.1| contains similarity to protein disulfide isomerase-related protein [Arabidopsis thaliana]	299	289	1.00E-124	96.7	75.9	85.6	contains similarity to protein disulfide isomerase-related protein	gbpln	Arabidopsis thaliana	AT5G18120.1 | Symbols: ATAPRL7, APRL7 | APR-like 7 | chr5:5991385-5993696 FORWARD LENGTH=289	299	289	1.00E-126	96.7	75.6	85.6
Rsa1.0_00374.1.g12464.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00374.1.g12465.t4	emb|CCH26503.1| calcineurin B-like 10 [Arabidopsis thaliana]	246	256	1.00E-115	104.1	85.0	89.4	calcineurin B-like 10	gbpln	Arabidopsis thaliana	AT4G33000.2 | Symbols: CBL10, SCABP8, ATCBL10 | calcineurin B-like protein 10 | chr4:15924821-15926398 FORWARD LENGTH=246	246	246	1.00E-117	100.0	85.0	88.6
Rsa1.0_00374.1.g12466.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00374.1.g12467.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00374.1.g12468.t11	ref|XP_002867194.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313030|gb|EFH43453.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	773	990	0	128.1	75.0	82.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G33210.1 | Symbols: SLOMO | F-box family protein | chr4:16015971-16020697 REVERSE LENGTH=990	773	990	0	128.1	74.8	82.5
Rsa1.0_00374.1.g12469.t1	gb|EOA16324.1| hypothetical protein CARUB_v10004474mg, partial [Capsella rubella]	504	569	0	112.9	88.5	94.6	hypothetical protein CARUB_v10004474mg, partial	gbpln	Capsella rubella	AT4G33220.1 | Symbols: PME44, ATPME44 | pectin methylesterase 44 | chr4:16022506-16026130 FORWARD LENGTH=525	504	525	0	104.2	88.5	93.8
Rsa1.0_00374.1.g12470.t1	ref|XP_002867191.1| hypothetical protein ARALYDRAFT_913095 [Arabidopsis lyrata subsp. lyrata] gi|297313027|gb|EFH43450.1| hypothetical protein ARALYDRAFT_913095 [Arabidopsis lyrata subsp. lyrata]	224	228	1.00E-121	101.8	92.9	98.2	hypothetical protein ARALYDRAFT_913095	gbpln	Arabidopsis lyrata	AT4G33250.1 | Symbols: EIF3K, TIF3K1, ATTIF3K1 | eukaryotic translation initiation factor 3K | chr4:16039066-16040617 REVERSE LENGTH=226	224	226	1.00E-121	100.9	92.0	96.4
Rsa1.0_00374.1.g12471.t1	emb|CAA11819.1| hypothetical protein [Brassica napus]	452	457	0	101.1	91.4	94.2	hypothetical protein	gbpln	Brassica napus	AT4G33270.1 | Symbols: CDC20.1 | Transducin family protein / WD-40 repeat family protein | chr4:16044545-16046590 REVERSE LENGTH=457	452	457	0	101.1	90.0	93.1
Rsa1.0_00374.1.g12472.t1	gb|ACP30606.1| disease resistance protein [Brassica rapa subsp. pekinensis]	821	836	0	101.8	82.2	91.4	disease resistance protein	gbpln	Brassica rapa	AT4G33300.2 | Symbols: ADR1-L1 | ADR1-like 1 | chr4:16051162-16054005 REVERSE LENGTH=816	821	816	0	99.4	79.0	88.7
Rsa1.0_00374.1.g12473.t1	gb|EOA16266.1| hypothetical protein CARUB_v10004410mg [Capsella rubella]	453	604	0	133.3	88.7	92.7	hypothetical protein CARUB_v10004410mg	gbpln	Capsella rubella	AT4G33330.2 | Symbols: PGSIP3, GUX2 | plant glycogenin-like starch initiation protein 3 | chr4:16059754-16063061 REVERSE LENGTH=626	453	626	0	138.2	87.0	91.4

Rsa1.0_00374.1.g12474.t1	ref|NP_179794.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75206012|sp|Q9SI02.1|FBK33_ARATH RecName: Full=F-box/kelch-repeat protein At2g22030 gi|4587593|gb|AAD25821.1| hypothetical protein [Arabidopsis thaliana] gi|20198005|gb|AAM15347.1| hypothetical protein [Arabidopsis thaliana] gi|330252159|gb|AEC07253.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	431	383	7.00E-86	88.9	44.3	55.9	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT2G22030.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:9372530-9373681 FORWARD LENGTH=383	431	383	2.00E-88	88.9	44.3	55.9
Rsa1.0_00374.1.g12475.t1	ref|NP_179794.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75206012|sp|Q9SI02.1|FBK33_ARATH RecName: Full=F-box/kelch-repeat protein At2g22030 gi|4587593|gb|AAD25821.1| hypothetical protein [Arabidopsis thaliana] gi|20198005|gb|AAM15347.1| hypothetical protein [Arabidopsis thaliana] gi|330252159|gb|AEC07253.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	447	383	2.00E-83	85.7	42.1	52.6	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT2G22030.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:9372530-9373681 FORWARD LENGTH=383	447	383	5.00E-86	85.7	42.1	52.6
Rsa1.0_00374.1.g12476.t1	ref|XP_002869217.1| hypothetical protein ARALYDRAFT_913084 [Arabidopsis lyrata subsp. lyrata] gi|297315053|gb|EFH45476.1| hypothetical protein ARALYDRAFT_913084 [Arabidopsis lyrata subsp. lyrata]	451	328	1.00E-156	72.7	61.9	67.6	hypothetical protein ARALYDRAFT_913084	gbpln	Arabidopsis lyrata	AT4G33380.1 | Symbols: | unknown protein; Has 194 Blast hits to 189 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 184; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr4:16072064-16074605 FORWARD LENGTH=328	451	328	1.00E-156	72.7	60.8	67.2
Rsa1.0_00374.1.g12477.t1	ref|NP_195066.1| Vacuolar import/degradation, Vid27-related protein [Arabidopsis thaliana] gi|4490307|emb|CAB38798.1| Dem-like protein [Arabidopsis thaliana] gi|7270288|emb|CAB80057.1| Dem-like protein [Arabidopsis thaliana] gi|20465423|gb|AAM20135.1| putative Dem protein [Arabidopsis thaliana] gi|28394003|gb|AAO42409.1| putative Dem protein [Arabidopsis thaliana] gi|332660820|gb|AEE86220.1| Vacuolar import/degradation, Vid27-related protein [Arabidopsis thaliana]	638	645	0	101.1	86.7	92.9	Vacuolar import/degradation, Vid27-related protein	gbpln	Arabidopsis thaliana	AT4G33400.1 | Symbols: | Vacuolar import/degradation, Vid27-related protein | chr4:16078189-16080410 REVERSE LENGTH=645	638	645	0	101.1	86.7	92.9
Rsa1.0_00374.1.g12478.t1	ref|XP_002869214.1| hypothetical protein ARALYDRAFT_913079 [Arabidopsis lyrata subsp. lyrata] gi|297315050|gb|EFH45473.1| hypothetical protein ARALYDRAFT_913079 [Arabidopsis lyrata subsp. lyrata]	304	325	1.00E-147	106.9	82.6	89.1	hypothetical protein ARALYDRAFT_913079	gbpln	Arabidopsis lyrata	AT4G33420.1 | Symbols: | Peroxidase superfamily protein | chr4:16084856-16086105 FORWARD LENGTH=325	304	325	1.00E-149	106.9	82.6	89.1
Rsa1.0_00374.1.g12479.t1	gb|AFO67895.1| leucine-rich repeat receptor-like kinase (mitochondrion) [Brassica rapa subsp. oleifera]	611	632	0	103.4	95.7	97.5	leucine-rich repeat receptor-like kinase (mitochondrion)	gbpln	Brassica rapa	AT4G33430.1 | Symbols: BAK1, RKS10, SERK3, ELG, ATSERK3, ATBAK1 | BRI1-associated receptor kinase | chr4:16086654-16090288 REVERSE LENGTH=615	611	615	0	100.7	93.8	96.9
Rsa1.0_00374.1.g12480.t1	ref|XP_002867181.1| AtMYB69 [Arabidopsis lyrata subsp. lyrata] gi|297313017|gb|EFH43440.1| AtMYB69 [Arabidopsis lyrata subsp. lyrata]	249	250	1.00E-116	100.4	81.1	88.8	AtMYB69	gbpln	Arabidopsis lyrata	AT4G33450.1 | Symbols: ATMYB69, MYB69 | myb domain protein 69 | chr4:16095746-16096603 REVERSE LENGTH=250	249	250	1.00E-116	100.4	80.3	87.1
Rsa1.0_00374.1.g12481.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1656	1352	0	81.6	40.6	54.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1656	746	1.00E-116	45.0	12.6	16.4
Rsa1.0_00374.1.g12482.t1	ref|XP_002869211.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315047|gb|EFH45470.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	209	949	2.00E-58	454.1	72.2	76.6	predicted protein	gbpln	Arabidopsis lyrata	AT4G33520.2 | Symbols: PAA1, HMA6 | P-type ATP-ase 1 | chr4:16118993-16125849 FORWARD LENGTH=949	209	949	1.00E-60	454.1	72.7	77.0
Rsa1.0_00374.1.g12483.t1	ref|NP_001078488.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|3549657|emb|CAA20568.1| putative protein [Arabidopsis thaliana] gi|7270303|emb|CAB80072.1| putative protein [Arabidopsis thaliana] gi|332660845|gb|AEE86245.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	114	115	4.00E-48	100.9	82.5	93.9	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT4G33550.2 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:16134538-16134964 FORWARD LENGTH=115	114	115	6.00E-51	100.9	82.5	93.9

Rsa1.0_00374.1.g12484.t1	ref|NP_001078488.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|3549657|emb|CAA20568.1| putative protein [Arabidopsis thaliana] gi|7270303|emb|CAB80072.1| putative protein [Arabidopsis thaliana] gi|332660845|gb|AEE86245.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	116	115	7.00E-51	99.1	87.1	92.2	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT4G33550.2 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:16134538-16134964 FORWARD LENGTH=115	116	115	1.00E-53	99.1	87.1	92.2
Rsa1.0_00374.1.g12485.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00374.1.g12486.t1	ref|XP_002869207.1| hypothetical protein ARALYDRAFT_491329 [Arabidopsis lyrata subsp. lyrata] gi|297315043|gb|EFH45466.1| hypothetical protein ARALYDRAFT_491329 [Arabidopsis lyrata subsp. lyrata]	95	95	1.00E-31	100.0	77.9	82.1	hypothetical protein ARALYDRAFT_491329	gbpln	Arabidopsis lyrata	AT4G33560.1 | Symbols: | Wound-responsive family protein | chr4:16135465-16135752 FORWARD LENGTH=95	95	95	2.00E-25	100.0	68.4	74.7
Rsa1.0_00374.1.g12487.t1	ref|XP_002869206.1| hypothetical protein ARALYDRAFT_328381 [Arabidopsis lyrata subsp. lyrata] gi|297315042|gb|EFH45465.1| hypothetical protein ARALYDRAFT_328381 [Arabidopsis lyrata subsp. lyrata]	308	315	7.00E-92	102.3	67.9	78.9	hypothetical protein ARALYDRAFT_328381	gbpln	Arabidopsis lyrata	AT4G33565.1 | Symbols: | RING/U-box superfamily protein | chr4:16136821-16137924 FORWARD LENGTH=367	308	367	2.00E-88	119.2	68.2	77.3
Rsa1.0_00375.1.g12488.t1	ref|NP_001032052.1| uncharacterized protein [Arabidopsis thaliana] gi|222423776|dbj|BAH19854.1| AT5G51040 [Arabidopsis thaliana] gi|332008642|gb|AED96025.1| uncharacterized protein AT5G51040 [Arabidopsis thaliana]	183	184	8.00E-84	100.5	83.1	90.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G51040.2 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF339 (InterPro:IPR005631); Has 368 Blast hits to 368 proteins in 141 species: Archae - 0; Bacteria - 216; Metazoa - 8; Fungi - 13; Plants - 40; Viruses - 0; Other Eukaryotes - 91 (source: NCBI BLink). | chr5:20750700-20751790 FORWARD LENGTH=184	183	184	3.00E-86	100.5	83.1	90.2
Rsa1.0_00375.1.g12489.t1	gb|EOA23477.1| hypothetical protein CARUB_v10016666mg [Capsella rubella]	780	902	0	115.6	80.8	89.7	hypothetical protein CARUB_v10016666mg	gbpln	Capsella rubella	AT3G45140.1 | Symbols: LOX2, ATLOX2 | lipoxygenase 2 | chr3:16525437-16529233 FORWARD LENGTH=896	780	896	0	114.9	77.1	88.2
Rsa1.0_00375.1.g12490.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00375.1.g12491.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00375.1.g12492.t1	gb|EMJ14584.1| hypothetical protein PRUPE_ppa026473mg [Prunus persica]	79	696	1.00E-14	881.0	51.9	70.9	hypothetical protein PRUPE_ppa026473mg	gbpln	Prunus persica	#	#	#	#	#	#	#
Rsa1.0_00375.1.g12493.t1	gb|AAM61036.1| contains similarity to poly(A)-binding protein II [Arabidopsis thaliana]	228	227	6.00E-98	99.6	86.8	92.5	contains similarity to poly(A)-binding protein II	gbpln	Arabidopsis thaliana	AT5G51120.1 | Symbols: PABN1, ATPABN1 | polyadenylate-binding protein 1 | chr5:20779760-20781241 FORWARD LENGTH=227	228	227	3.00E-96	99.6	82.9	88.2
Rsa1.0_00375.1.g12494.t1	ref|XP_002864098.1| hypothetical protein ARALYDRAFT_495181 [Arabidopsis lyrata subsp. lyrata] gi|297309933|gb|EFH40357.1| hypothetical protein ARALYDRAFT_495181 [Arabidopsis lyrata subsp. lyrata]	318	313	1.00E-128	98.4	72.0	78.3	hypothetical protein ARALYDRAFT_495181	gbpln	Arabidopsis lyrata	AT5G51130.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:20781896-20783901 FORWARD LENGTH=318	318	318	1.00E-128	100.0	71.4	78.6
Rsa1.0_00375.1.g12495.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00375.1.g12496.t1	gb|ACP30595.1| disease resistance protein [Brassica rapa subsp. pekinensis]	394	707	3.00E-88	179.4	42.6	45.9	disease resistance protein	gbpln	Brassica rapa	AT4G16890.1 | Symbols: SNC1, BAL | disease resistance protein (TIR-NBS-LRR class), putative | chr4:9500506-9505455 REVERSE LENGTH=1301	394	1301	5.00E-75	330.2	40.6	52.8
Rsa1.0_00375.1.g12497.t1	ref|XP_002862832.1| hypothetical protein ARALYDRAFT_359344 [Arabidopsis lyrata subsp. lyrata] gi|297308575|gb|EFH39090.1| hypothetical protein ARALYDRAFT_359344 [Arabidopsis lyrata subsp. lyrata]	255	260	1.00E-20	102.0	35.3	49.4	hypothetical protein ARALYDRAFT_359344	gbpln	Arabidopsis lyrata	AT1G73490.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:27633496-27634867 REVERSE LENGTH=260	255	260	6.00E-20	102.0	21.6	34.1
Rsa1.0_00375.1.g12498.t10	gb|AFI23584.1| embryonic flower 2_2 [Brassica oleracea var. italica] gi|384597741|gb|AFI23587.1| embryonic flower 2_2 [Brassica oleracea var. italica]	665	630	0	94.7	89.9	91.7	embryonic flower 2_2	gbpln	Brassica oleracea	AT5G51230.1 | Symbols: EMF2, VEF2, CYR1, AtEMF2 | VEFS-Box of polycomb protein | chr5:20824153-20829344 FORWARD LENGTH=631	665	631	0	94.9	80.2	86.8
Rsa1.0_00375.1.g12499.t1	ref|XP_002865848.1| hypothetical protein ARALYDRAFT_495196 [Arabidopsis lyrata subsp. lyrata] gi|297311683|gb|EFH42107.1| hypothetical protein ARALYDRAFT_495196 [Arabidopsis lyrata subsp. lyrata]	258	257	1.00E-124	99.6	85.7	91.9	hypothetical protein ARALYDRAFT_495196	gbpln	Arabidopsis lyrata	AT5G51260.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr5:20832222-20833466 REVERSE LENGTH=257	258	257	1.00E-126	99.6	84.9	92.2

Rsa1.0_00375.1.g12500.t1	ref|XP_002865850.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311685|gb|EFH42109.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	786	812	0	103.3	76.6	86.6	kinase family protein	gbpln	Arabidopsis lyrata	AT5G51270.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:20835137-20838262 REVERSE LENGTH=819	786	819	0	104.2	73.3	83.0
Rsa1.0_00375.1.g12501.t1	gb|EOA33952.1| hypothetical protein CARUB_v10021447mg [Capsella rubella]	70	813	6.00E-16	1161.4	54.3	54.3	hypothetical protein CARUB_v10021447mg	gbpln	Capsella rubella	AT1G60490.1 | Symbols: ATVPS34, VPS34, PI3K | vacuolar protein sorting 34 | chr1:22285792-22290190 REVERSE LENGTH=814	70	814	1.00E-18	1162.9	54.3	54.3
Rsa1.0_00375.1.g12502.t1	ref|NP_199944.2| gibberellin 20-oxidase-related protein [Arabidopsis thaliana] gi|332008683|gb|AED96066.1| gibberellin 20-oxidase-related protein [Arabidopsis thaliana]	322	325	1.00E-166	100.9	89.1	93.8	gibberellin 20-oxidase-related protein	gbpln	Arabidopsis thaliana	AT5G51310.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:20852854-20854718 REVERSE LENGTH=325	322	325	1.00E-169	100.9	89.1	93.8
Rsa1.0_00376.1.g12503.t1	gb|EOA32351.1| hypothetical protein CARUB_v10015618mg [Capsella rubella]	334	404	1.00E-127	121.0	71.3	75.7	hypothetical protein CARUB_v10015618mg	gbpln	Capsella rubella	AT3G07220.1 | Symbols: | SMAD/FHA domain-containing protein | chr3:2297968-2299407 FORWARD LENGTH=320	334	320	1.00E-124	95.8	71.3	76.6
Rsa1.0_00376.1.g12504.t1	gb|EOA30273.1| hypothetical protein CARUB_v10013394mg [Capsella rubella]	557	546	0	98.0	84.9	89.4	hypothetical protein CARUB_v10013394mg	gbpln	Capsella rubella	AT3G07210.1 | Symbols: | unknown protein; Has 97 Blast hits to 85 proteins in 31 species: Archae - 0; Bacteria - 14; Metazoa - 7; Fungi - 19; Plants - 37; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink). | chr3:2293000-2295119 REVERSE LENGTH=547	557	547	0	98.2	85.8	90.3
Rsa1.0_00376.1.g12505.t1	ref|XP_002882517.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297328357|gb|EFH58776.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	388	181	1.00E-54	46.6	31.7	36.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G07200.2 | Symbols: | RING/U-box superfamily protein | chr3:2291343-2292223 FORWARD LENGTH=182	388	182	4.00E-54	46.9	30.4	35.1
Rsa1.0_00376.1.g12506.t1	ref|XP_002884631.1| hypothetical protein ARALYDRAFT_896875 [Arabidopsis lyrata subsp. lyrata] gi|297330471|gb|EFH60890.1| hypothetical protein ARALYDRAFT_896875 [Arabidopsis lyrata subsp. lyrata]	596	599	0	100.5	87.6	93.8	hypothetical protein ARALYDRAFT_896875	gbpln	Arabidopsis lyrata	AT3G07180.1 | Symbols: | GPI transamidase component PIG-S-related | chr3:2282455-2285475 REVERSE LENGTH=599	596	599	0	100.5	85.7	92.6
Rsa1.0_00376.1.g12507.t1	ref|NP_566300.1| Sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana] gi|6642648|gb|AAF20229.1|AC012395_16 unknown protein [Arabidopsis thaliana] gi|15294218|gb|AAK95286.1|AF410300_1 AT3g07170/T1B9_17 [Arabidopsis thaliana] gi|22655432|gb|AAM98308.1| At3g07170/T1B9_17 [Arabidopsis thaliana] gi|332640986|gb|AEE74507.1| Sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	190	203	8.00E-88	106.8	87.4	92.1	Sterile alpha motif (SAM) domain-containing protein	gbpln	Arabidopsis thaliana	AT3G07170.1 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr3:2280428-2282097 FORWARD LENGTH=203	190	203	3.00E-90	106.8	87.4	92.1
Rsa1.0_00376.1.g12508.t33	ref|NP_187371.1| uncharacterized protein [Arabidopsis thaliana] gi|6642650|gb|AAF20231.1|AC012395_18 hypothetical protein [Arabidopsis thaliana] gi|332640984|gb|AEE74505.1| uncharacterized protein AT3G07150 [Arabidopsis thaliana]	192	199	3.00E-69	103.6	75.0	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G07150.1 | Symbols: | unknown protein; Has 19 Blast hits to 19 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2263806-2264576 REVERSE LENGTH=199	192	199	1.00E-71	103.6	75.0	83.9
Rsa1.0_00376.1.g12509.t1	ref|XP_002882514.1| GPI transamidase component Gpi16 subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297328354|gb|EFH58773.1| GPI transamidase component Gpi16 subunit family protein [Arabidopsis lyrata subsp. lyrata]	639	647	0	101.3	85.3	90.3	GPI transamidase component Gpi16 subunit family protein	gbpln	Arabidopsis lyrata	AT3G07140.2 | Symbols: | GPI transamidase component Gpi16 subunit family protein | chr3:2261278-2263632 FORWARD LENGTH=643	639	643	0	100.6	84.0	89.7
Rsa1.0_00376.1.g12510.t1	gb|EOA30308.1| hypothetical protein CARUB_v10013434mg [Capsella rubella]	545	532	0	97.6	87.0	91.4	hypothetical protein CARUB_v10013434mg	gbpln	Capsella rubella	AT3G07130.1 | Symbols: ATPAP15, PAP15 | purple acid phosphatase 15 | chr3:2255763-2257981 REVERSE LENGTH=532	545	532	0	97.6	86.1	90.8
Rsa1.0_00376.1.g12511.t1	gb|EOA29662.1| hypothetical protein CARUB_v10015595mg [Capsella rubella]	214	365	6.00E-68	170.6	70.1	80.4	hypothetical protein CARUB_v10015595mg	gbpln	Capsella rubella	AT3G07120.1 | Symbols: | RING/U-box superfamily protein | chr3:2254560-2255642 FORWARD LENGTH=360	214	360	3.00E-69	168.2	72.0	81.3

Rsa1.0_00376.1.g12512.t1	ref|NP_187366.2| sec24-like transport protein [Arabidopsis thaliana] gi|78099801|sp|Q9SFU0.2|SC24A_ARATH RecName: Full=Protein transport protein Sec24-like At3g07100 gi|22531076|gb|AAM97042.1| putative Sec24-like COPII protein [Arabidopsis thaliana] gi|23197930|gb|AAN15492.1| putative Sec24-like COPII protein [Arabidopsis thaliana] gi|332640977|gb|AEE74498.1| sec24-like transport protein [Arabidopsis thaliana]	1009	1038	0	102.9	87.6	91.6	sec24-like transport protein	gbpln	Arabidopsis thaliana	AT3G07100.1 | Symbols: ERMO2, SEC24A | Sec23/Sec24 protein transport family protein | chr3:2245689-2250077 REVERSE LENGTH=1038	1009	1038	0	102.9	87.6	91.6
Rsa1.0_00376.1.g12513.t1	ref|XP_002884625.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330465|gb|EFH60884.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	272	265	1.00E-126	97.4	81.3	86.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G07090.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr3:2243153-2244476 REVERSE LENGTH=265	272	265	1.00E-127	97.4	80.1	87.1
Rsa1.0_00376.1.g12514.t1	ref|NP_187364.1| EamA-like transporter [Arabidopsis thaliana] gi|6642657|gb|AAF20238.1|AC012395_25 putative integral membrane protein [Arabidopsis thaliana] gi|30794019|gb|AAP40456.1| putative integral membrane protein [Arabidopsis thaliana] gi|53749190|gb|AAU90080.1| At3g07080 [Arabidopsis thaliana] gi|332640975|gb|AEE74496.1| EamA-like transporter [Arabidopsis thaliana]	232	438	5.00E-46	188.8	56.9	65.1	EamA-like transporter	gbpln	Arabidopsis thaliana	AT3G07080.1 | Symbols: | EamA-like transporter family | chr3:2241360-2242934 FORWARD LENGTH=438	232	438	1.00E-48	188.8	56.9	65.1
Rsa1.0_00376.1.g12515.t4	ref|NP_566298.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|75337179|sp|Q9SFT7.1|Y3707_ARATH RecName: Full=Serine/threonine-protein kinase At3g07070 gi|6642658|gb|AAF20239.1|AC012395_26 putative protein kinase [Arabidopsis thaliana] gi|332640974|gb|AEE74495.1| serine/threonine-protein kinase [Arabidopsis thaliana]	441	414	0	93.9	88.0	90.7	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G07070.1 | Symbols: | Protein kinase superfamily protein | chr3:2238455-2240074 FORWARD LENGTH=414	441	414	0	93.9	88.0	90.7
Rsa1.0_00376.1.g12516.t1	gb|EOA30210.1| hypothetical protein CARUB_v10013329mg [Capsella rubella]	615	574	0	93.3	77.1	82.1	hypothetical protein CARUB_v10013329mg	gbpln	Capsella rubella	AT3G07050.1 | Symbols: | GTP-binding family protein | chr3:2229602-2232279 REVERSE LENGTH=582	615	582	0	94.6	79.5	84.2
Rsa1.0_00376.1.g12517.t1	gb|EOA30082.1| hypothetical protein CARUB_v10013187mg [Capsella rubella]	635	642	0	101.1	89.1	93.7	hypothetical protein CARUB_v10013187mg	gbpln	Capsella rubella	AT3G07020.2 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:2218120-2221590 REVERSE LENGTH=637	635	637	0	100.3	89.3	93.5
Rsa1.0_00376.1.g12518.t1	ref|XP_002882503.1| hypothetical protein ARALYDRAFT_478019 [Arabidopsis lyrata subsp. lyrata] gi|297328343|gb|EFH58762.1| hypothetical protein ARALYDRAFT_478019 [Arabidopsis lyrata subsp. lyrata]	750	782	0	104.3	82.3	89.3	hypothetical protein ARALYDRAFT_478019	gbpln	Arabidopsis lyrata	AT3G06980.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr3:2201531-2204662 FORWARD LENGTH=781	750	781	0	104.1	81.3	88.7
Rsa1.0_00376.1.g12519.t1	ref|XP_002884617.1| hypothetical protein ARALYDRAFT_317559 [Arabidopsis lyrata subsp. lyrata] gi|297330457|gb|EFH60876.1| hypothetical protein ARALYDRAFT_317559 [Arabidopsis lyrata subsp. lyrata]	310	320	2.00E-27	103.2	32.6	44.5	hypothetical protein ARALYDRAFT_317559	gbpln	Arabidopsis lyrata	AT3G06970.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:2199653-2201150 REVERSE LENGTH=317	310	317	2.00E-27	102.3	31.9	44.5
Rsa1.0_00376.1.g12520.t1	gb|EOA18666.1| hypothetical protein CARUB_v10007242mg [Capsella rubella]	377	401	1.00E-104	106.4	56.8	71.1	hypothetical protein CARUB_v10007242mg	gbpln	Capsella rubella	AT4G36840.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:17352166-17352882 FORWARD LENGTH=238	377	238	3.00E-58	63.1	34.0	41.4
Rsa1.0_00377.1.g12521.t1	gb|EOA30334.1| hypothetical protein CARUB_v10013459mg [Capsella rubella]	615	519	0	84.4	72.8	77.6	hypothetical protein CARUB_v10013459mg	gbpln	Capsella rubella	AT3G15180.1 | Symbols: | ARM repeat superfamily protein | chr3:5111952-5115803 FORWARD LENGTH=519	615	519	0	84.4	73.3	77.6
Rsa1.0_00377.1.g12522.t1	gb|EOA29514.1| hypothetical protein CARUB_v10014276mg [Capsella rubella]	308	300	1.00E-123	97.4	79.2	83.8	hypothetical protein CARUB_v10014276mg	gbpln	Capsella rubella	AT3G15170.1 | Symbols: CUC1, ANAC054, ATNAC1 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr3:5109912-5111435 FORWARD LENGTH=310	308	310	1.00E-118	100.6	79.2	85.1
Rsa1.0_00377.1.g12523.t1	ref|XP_002885073.1| hypothetical protein ARALYDRAFT_897788 [Arabidopsis lyrata subsp. lyrata] gi|297330913|gb|EFH61332.1| hypothetical protein ARALYDRAFT_897788 [Arabidopsis lyrata subsp. lyrata]	280	248	1.00E-112	88.6	71.1	80.4	hypothetical protein ARALYDRAFT_897788	gbpln	Arabidopsis lyrata	AT3G15150.1 | Symbols: HPY2, MMS21, ATMMS21 | RING/U-box superfamily protein | chr3:5102210-5104082 REVERSE LENGTH=249	280	249	1.00E-111	88.9	68.9	79.6

Rsa1.0_00377.1.g12524.t2	ref|XP_002885072.1| hypothetical protein ARALYDRAFT_318289 [Arabidopsis lyrata subsp. lyrata] gi|297330912|gb|EFH61331.1| hypothetical protein ARALYDRAFT_318289 [Arabidopsis lyrata subsp. lyrata]	332	1134	1.00E-162	341.6	84.3	89.2	hypothetical protein ARALYDRAFT_318289	gbpln	Arabidopsis lyrata	AT3G15140.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr3:5099712-5101717 REVERSE LENGTH=337	332	337	1.00E-164	101.5	84.6	89.2
Rsa1.0_00377.1.g12525.t1	ref|NP_566501.1| uncharacterized protein [Arabidopsis thaliana] gi|11994501|dbj|BAB02566.1| unnamed protein product [Arabidopsis thaliana] gi|26450163|dbj|BAC42200.1| unknown protein [Arabidopsis thaliana] gi|28827590|gb|AAO50639.1| unknown protein [Arabidopsis thaliana] gi|332642100|gb|AEE75621.1| uncharacterized protein AT3G15115 [Arabidopsis thaliana]	318	339	1.00E-112	106.6	74.2	82.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15115.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53180.1); Has 47 Blast hits to 47 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 13; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr3:5086219-5087352 REVERSE LENGTH=339	318	339	1.00E-114	106.6	74.2	82.7
Rsa1.0_00377.1.g12526.t1	gb|EOA31218.1| hypothetical protein CARUB_v10014384mg [Capsella rubella]	289	271	1.00E-100	93.8	72.0	82.4	hypothetical protein CARUB_v10014384mg	gbpln	Capsella rubella	AT3G15110.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3082 (InterPro:IPR021434); Has 77 Blast hits to 77 proteins in 38 species: Archae - 0; Bacteria - 37; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:5084394-5085823 REVERSE LENGTH=266	289	266	2.00E-98	92.0	69.6	79.9
Rsa1.0_00377.1.g12527.t1	gb|EOA32270.1| hypothetical protein CARUB_v10015530mg [Capsella rubella]	667	682	0	102.2	76.2	82.6	hypothetical protein CARUB_v10015530mg	gbpln	Capsella rubella	AT3G15095.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 9762 Blast hits to 6439 proteins in 764 species: Archae - 77; Bacteria - 1339; Metazoa - 3211; Fungi - 718; Plants - 437; Viruses - 131; Other Eukaryotes - 3849 (source: NCBI BLink). | chr3:5081996-5084050 FORWARD LENGTH=684	667	684	0	102.5	72.9	80.1
Rsa1.0_00377.1.g12528.t1	gb|EOA31192.1| hypothetical protein CARUB_v10014358mg [Capsella rubella]	225	277	1.00E-105	123.1	81.8	85.8	hypothetical protein CARUB_v10014358mg	gbpln	Capsella rubella	AT3G15080.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr3:5074319-5076327 FORWARD LENGTH=275	225	275	1.00E-106	122.2	81.8	84.0
Rsa1.0_00377.1.g12529.t1	ref|XP_002885067.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297330907|gb|EFH61326.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	155	476	1.00E-27	307.1	38.7	44.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G15070.2 | Symbols: | RING/U-box superfamily protein | chr3:5070472-5072344 REVERSE LENGTH=486	155	486	3.00E-28	313.5	36.8	43.2
Rsa1.0_00377.1.g12530.t1	gb|AAM66027.1| unknown [Arabidopsis thaliana]	220	243	3.00E-83	110.5	85.5	93.2	unknown	gbpln	Arabidopsis thaliana	AT3G15040.1 | Symbols: | Protein of unknown function, DUF584 | chr3:5065445-5066176 REVERSE LENGTH=243	220	243	1.00E-81	110.5	84.5	91.8
Rsa1.0_00377.1.g12531.t1	ref|XP_002882910.1| hypothetical protein ARALYDRAFT_897773 [Arabidopsis lyrata subsp. lyrata] gi|297328750|gb|EFH59169.1| hypothetical protein ARALYDRAFT_897773 [Arabidopsis lyrata subsp. lyrata]	405	452	1.00E-157	111.6	80.2	85.4	hypothetical protein ARALYDRAFT_897773	gbpln	Arabidopsis lyrata	AT3G15030.3 | Symbols: TCP4 | TCP family transcription factor 4 | chr3:5062308-5063570 FORWARD LENGTH=420	405	420	1.00E-148	103.7	80.5	84.7
Rsa1.0_00377.1.g12532.t1	ref|XP_002882907.1| hypothetical protein ARALYDRAFT_478926 [Arabidopsis lyrata subsp. lyrata] gi|297328747|gb|EFH59166.1| hypothetical protein ARALYDRAFT_478926 [Arabidopsis lyrata subsp. lyrata]	337	396	1.00E-133	117.5	81.6	84.3	hypothetical protein ARALYDRAFT_478926	gbpln	Arabidopsis lyrata	AT3G15000.1 | Symbols: | cobalt ion binding | chr3:5050321-5052121 FORWARD LENGTH=395	337	395	1.00E-122	117.2	78.6	81.6
Rsa1.0_00377.1.g12533.t1	gb|AAP96742.1| ThiJ-like protein [Brassica rapa subsp. pekinensis]	392	392	0	100.0	96.7	98.0	ThiJ-like protein	gbpln	Brassica rapa	AT3G14990.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr3:5047510-5049621 FORWARD LENGTH=392	392	392	0	100.0	92.3	96.2
Rsa1.0_00377.1.g12534.t1	gb|EOA30576.1| hypothetical protein CARUB_v10013708mg, partial [Capsella rubella]	175	444	5.00E-12	253.7	24.6	24.6	hypothetical protein CARUB_v10013708mg, partial	gbpln	Capsella rubella	AT3G15000.1 | Symbols: | cobalt ion binding | chr3:5050321-5052121 FORWARD LENGTH=395	175	395	3.00E-12	225.7	22.3	22.3
Rsa1.0_00377.1.g12535.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00377.1.g12536.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00377.1.g12537.t1</td><td>ref|NP_188116.1| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain [Arabidopsis thaliana] gi|332642075|gb|AEE75596.1| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain [Arabidopsis thaliana]</td><td>1122</td><td>1189</td><td>0</td><td>106.0</td><td>73.8</td><td>82.4</td><td>Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G14980.1 | Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein | chr3:5039931-5044811 REVERSE LENGTH=1189</td><td>1122</td><td>1189</td><td>0</td><td>106.0</td><td>73.8</td><td>82.4</td></tr>
<tr><td>Rsa1.0_00377.1.g12538.t1</td><td>gb|EOA30944.1| hypothetical protein CARUB_v10014091mg [Capsella rubella]</td><td>401</td><td>347</td><td>1.00E-162</td><td>86.5</td><td>75.6</td><td>79.1</td><td>hypothetical protein CARUB_v10014091mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G53290.1 | Symbols: | Galactosyltransferase family protein | chr1:19871353-19873251 FORWARD LENGTH=345</td><td>401</td><td>345</td><td>1.00E-149</td><td>86.0</td><td>67.8</td><td>75.3</td></tr>
<tr><td>Rsa1.0_00377.1.g12539.t1</td><td>sp|F4IXE4.2|TTL2_ARATH RecName: Full=TPR repeat-containing thioredoxin TTL2; AltName: Full=Tetratricopeptide repeat thioredoxin-like 2</td><td>740</td><td>730</td><td>0</td><td>98.6</td><td>67.8</td><td>77.8</td><td>RecName: Full=TPR repeat-containing thioredoxin TTL2; AltName: Full=Tetratricopeptide repeat thioredoxin-like 2</td><td>----</td><td>----</td><td>AT3G14950.1 | Symbols: TTL2 | tetratricopetide-repeat thioredoxin-like 2 | chr3:5030216-5032892 REVERSE LENGTH=721</td><td>740</td><td>721</td><td>0</td><td>97.4</td><td>67.2</td><td>76.9</td></tr>
<tr><td>Rsa1.0_00377.1.g12540.t1</td><td>dbj|BAJ34436.1| unnamed protein product [Thellungiella halophila]</td><td>957</td><td>968</td><td>0</td><td>101.1</td><td>96.8</td><td>98.6</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G14940.1 | Symbols: ATPPC3, PPC3 | phosphoenolpyruvate carboxylase 3 | chr3:5025584-5029476 FORWARD LENGTH=968</td><td>957</td><td>968</td><td>0</td><td>101.1</td><td>96.3</td><td>98.3</td></tr>
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<tr><td>Rsa1.0_00378.1.g12543.t1</td><td>ref|XP_002875039.1| hypothetical protein ARALYDRAFT_490540 [Arabidopsis lyrata subsp. lyrata] gi|297320876|gb|EFH51298.1| hypothetical protein ARALYDRAFT_490540 [Arabidopsis lyrata subsp. lyrata]</td><td>224</td><td>788</td><td>1.00E-114</td><td>351.8</td><td>85.3</td><td>92.4</td><td>hypothetical protein ARALYDRAFT_490540</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G00300.1 | Symbols: | fringe-related protein | chr4:126509-130126 FORWARD LENGTH=785</td><td>224</td><td>785</td><td>1.00E-116</td><td>350.4</td><td>85.3</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00378.1.g12544.t1</td><td>ref|XP_002875038.1| hypothetical protein ARALYDRAFT_912220 [Arabidopsis lyrata subsp. lyrata] gi|297320875|gb|EFH51297.1| hypothetical protein ARALYDRAFT_912220 [Arabidopsis lyrata subsp. lyrata]</td><td>718</td><td>720</td><td>0</td><td>100.3</td><td>85.1</td><td>92.1</td><td>hypothetical protein ARALYDRAFT_912220</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01580.1 | Symbols: FRO2, FRD1, ATFRO2 | ferric reduction oxidase 2 | chr1:209395-212810 FORWARD LENGTH=725</td><td>718</td><td>725</td><td>0</td><td>101.0</td><td>70.6</td><td>84.4</td></tr>
<tr><td>Rsa1.0_00378.1.g12545.t2</td><td>ref|XP_002875036.1| EDA8/MEE46 [Arabidopsis lyrata subsp. lyrata] gi|297320873|gb|EFH51295.1| EDA8/MEE46 [Arabidopsis lyrata subsp. lyrata]</td><td>316</td><td>302</td><td>1.00E-73</td><td>95.6</td><td>60.8</td><td>70.6</td><td>EDA8/MEE46</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G00310.2 | Symbols: MEE46, EDA8 | Putative membrane lipoprotein | chr4:133857-135235 FORWARD LENGTH=302</td><td>316</td><td>302</td><td>1.00E-71</td><td>95.6</td><td>56.3</td><td>69.3</td></tr>
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<tr><td>Rsa1.0_00378.1.g12547.t1</td><td>ref|XP_002875035.1| ring-H2 finger B1A [Arabidopsis lyrata subsp. lyrata] gi|297320872|gb|EFH51294.1| ring-H2 finger B1A [Arabidopsis lyrata subsp. lyrata]</td><td>196</td><td>190</td><td>2.00E-59</td><td>96.9</td><td>68.4</td><td>75.0</td><td>ring-H2 finger B1A</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G00335.3 | Symbols: RHB1A | RING-H2 finger B1A | chr4:146866-147957 FORWARD LENGTH=189</td><td>196</td><td>189</td><td>1.00E-60</td><td>96.4</td><td>67.9</td><td>75.5</td></tr>
<tr><td>Rsa1.0_00378.1.g12548.t1</td><td>ref|NP_567172.4| receptor-like protein kinase 4 [Arabidopsis thaliana] gi|332656462|gb|AEE81862.1| receptor-like protein kinase 4 [Arabidopsis thaliana]</td><td>827</td><td>818</td><td>0</td><td>98.9</td><td>77.4</td><td>84.8</td><td>receptor-like protein kinase 4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G00340.1 | Symbols: RLK4 | receptor-like protein kinase 4 | chr4:148958-151496 FORWARD LENGTH=818</td><td>827</td><td>818</td><td>0</td><td>98.9</td><td>77.4</td><td>84.8</td></tr>
<tr><td>Rsa1.0_00378.1.g12549.t1</td><td>ref|XP_002875033.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297320870|gb|EFH51292.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]</td><td>544</td><td>542</td><td>0</td><td>99.6</td><td>89.3</td><td>94.9</td><td>mate efflux family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G00350.1 | Symbols: | MATE efflux family protein | chr4:151978-153988 FORWARD LENGTH=542</td><td>544</td><td>542</td><td>0</td><td>99.6</td><td>89.2</td><td>94.7</td></tr>
<tr><td>Rsa1.0_00378.1.g12550.t1</td><td>gb|AAB71442.1| Similar to Arabidopsis hypothetical protein PID:e326839 (gb|Z97337) [Arabidopsis thaliana]</td><td>241</td><td>430</td><td>1.00E-31</td><td>178.4</td><td>29.5</td><td>33.2</td><td>Similar to Arabidopsis hypothetical protein PID:e326839 (gb|Z97337)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G05360.1 | Symbols: | BEST Arabidopsis thaliana protein match is: SNARE associated Golgi protein family (TAIR:AT4G14950.1); Has 332 Blast hits to 326 proteins in 115 species: Archae - 0; Bacteria - 11; Metazoa - 174; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 73 (source: NCBI BLink). | chr1:1564816-1567278 FORWARD LENGTH=416</td><td>241</td><td>416</td><td>3.00E-34</td><td>172.6</td><td>29.5</td><td>33.2</td></tr>
<tr><td>Rsa1.0_00378.1.g12551.t1</td><td>ref|XP_002875027.1| CYP86A2 [Arabidopsis lyrata subsp. lyrata] gi|297320864|gb|EFH51286.1| CYP86A2 [Arabidopsis lyrata subsp. lyrata]</td><td>558</td><td>554</td><td>0</td><td>99.3</td><td>91.2</td><td>94.6</td><td>CYP86A2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G00360.1 | Symbols: CYP86A2, ATT1 | cytochrome P450, family 86, subfamily A, polypeptide 2 | chr4:160951-162778 FORWARD LENGTH=553</td><td>558</td><td>553</td><td>0</td><td>99.1</td><td>91.4</td><td>94.6</td></tr>
</table>

Rsa1.0_00378.1.g12552.t1	ref|NP_567175.2| putative anion transporter 2 [Arabidopsis thaliana] gi|75244391|sp|Q8GX78.1|ANTR2_ARATH RecName: Full=Probable anion transporter 2, chloroplastic; AltName: Full=Phosphate transporter PHT4;4; Flags: Precursor gi|26451814|dbj|BAC43000.1| unknown protein [Arabidopsis thaliana] gi|32306495|gb|AAP78931.1| At4g00370 [Arabidopsis thaliana] gi|332656470|gb|AEE81870.1| putative anion transporter 2 [Arabidopsis thaliana]	531	541	0	101.9	87.2	90.8	putative anion transporter 2	gbpln	Arabidopsis thaliana	AT4G00370.1 | Symbols: ANTR2, PHT4;4 | Major facilitator superfamily protein | chr4:163153-166111 REVERSE LENGTH=541	531	541	0	101.9	87.2	90.8
Rsa1.0_00378.1.g12553.t1	ref|XP_002872955.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297318792|gb|EFH49214.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	499	498	0	99.8	89.0	92.6	phospholipid/glycerol acyltransferase family protein	gbpln	Arabidopsis lyrata	AT4G00400.1 | Symbols: GPAT8, AtGPAT8 | glycerol-3-phosphate acyltransferase 8 | chr4:174312-176734 REVERSE LENGTH=500	499	500	0	100.2	90.4	93.0
Rsa1.0_00378.1.g12554.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00378.1.g12555.t1	gb|ABO71659.2| trans-membrane water channel protein [Brassica juncea]	286	288	1.00E-161	100.7	98.3	99.3	trans-membrane water channel protein	gbpln	Brassica juncea	AT4G00430.1 | Symbols: TMP-C, PIP1;4, PIP1E | plasma membrane intrinsic protein 1;4 | chr4:186143-187531 REVERSE LENGTH=287	286	287	1.00E-162	100.3	97.9	99.3
Rsa1.0_00378.1.g12556.t1	gb|AAG10809.1|AC018460_3 Similar to mutator transposase [Arabidopsis thaliana]	196	884	1.00E-49	451.0	46.9	66.8	Similar to mutator transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00378.1.g12557.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12558.t5	ref|XP_002864242.1| hypothetical protein ARALYDRAFT_918421 [Arabidopsis lyrata subsp. lyrata] gi|297310077|gb|EFH40501.1| hypothetical protein ARALYDRAFT_918421 [Arabidopsis lyrata subsp. lyrata]	1048	1049	0	100.1	82.9	88.0	hypothetical protein ARALYDRAFT_918421	gbpln	Arabidopsis lyrata	AT5G53430.1 | Symbols: SDG29, SET29, ATX5 | SET domain group 29 | chr5:21677623-21683166 FORWARD LENGTH=1043	1048	1043	0	99.5	82.3	87.9
Rsa1.0_00379.1.g12559.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12560.t1	gb|EOA13856.1| hypothetical protein CARUB_v10026959mg [Capsella rubella]	281	266	1.00E-128	94.7	82.9	87.5	hypothetical protein CARUB_v10026959mg	gbpln	Capsella rubella	AT5G53420.1 | Symbols: | CCT motif family protein | chr5:21673683-21675469 FORWARD LENGTH=264	281	264	1.00E-129	94.0	82.9	86.1
Rsa1.0_00379.1.g12561.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12562.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12563.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12564.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12565.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12566.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12567.t1	gb|EOA13779.1| hypothetical protein CARUB_v10026873mg [Capsella rubella]	285	299	1.00E-124	104.9	88.4	94.7	hypothetical protein CARUB_v10026873mg	gbpln	Capsella rubella	AT5G53400.1 | Symbols: BOB1 | HSP20-like chaperones superfamily protein | chr5:21661588-21663383 FORWARD LENGTH=304	285	304	1.00E-124	106.7	83.2	91.2
Rsa1.0_00379.1.g12568.t4	dbj|BAC42871.1| unknown protein [Arabidopsis thaliana]	349	486	1.00E-132	139.3	66.2	70.8	unknown protein	gbpln	Arabidopsis thaliana	AT5G53390.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:21656951-21659207 REVERSE LENGTH=486	349	486	1.00E-134	139.3	66.2	70.8
Rsa1.0_00379.1.g12569.t4	ref|NP_197139.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana] gi|9759117|dbj|BAB09602.1| unnamed protein product [Arabidopsis thaliana] gi|28393404|gb|AAO42125.1| unknown protein [Arabidopsis thaliana] gi|29824351|gb|AAP04136.1| unknown protein [Arabidopsis thaliana] gi|332004899|gb|AED92282.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana]	79	488	2.00E-18	617.7	55.7	59.5	O-acyltransferase (WSD1-like) family protein	gbpln	Arabidopsis thaliana	AT5G16350.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:5352702-5354955 FORWARD LENGTH=488	79	488	3.00E-21	617.7	55.7	59.5
Rsa1.0_00379.1.g12570.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	121	1023	7.00E-23	845.5	47.1	54.5	F27F5.21	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	121	292	9.00E-11	241.3	26.4	38.8
Rsa1.0_00379.1.g12571.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00379.1.g12572.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1412	1501	0	106.3	61.3	74.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1412	1262	1.00E-133	89.4	16.6	23.5

Rsa1.0_00379.1.g12573.t2	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	380	442	2.00E-54	116.3	35.8	44.5	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	380	343	1.00E-23	90.3	18.4	24.7
Rsa1.0_00379.1.g12574.t1	ref|NP_200149.1| Putative pectinesterase/pectinesterase inhibitor 61 [Arabidopsis thaliana] gi|75309150|sp|Q9FK05.1|PME61_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 61; Includes: RecName: Full=Pectinesterase inhibitor 61; AltName: Full=Pectin methylesterase inhibitor 61; Includes: RecName: Full=Pectinesterase 61; Short=PE 61; AltName: Full=AtPMEpcrF; AltName: Full=Pectin methylesterase 61; Short=AtPME61 gi|13507549|gb|AAK28637.1|AF360340_1 putative pectinesterase [Arabidopsis thaliana] gi|9759184|dbj|BAB09799.1| pectinesterase [Arabidopsis thaliana] gi|15293287|gb|AAK93754.1| putative pectinesterase [Arabidopsis thaliana] gi|332008962|gb|AED96345.1| Putative pectinesterase/pectinesterase inhibitor 61 [Arabidopsis thaliana]	746	587	0	78.7	69.0	73.2	Putative pectinesterase/pectinesterase inhibitor 61	gbpln	Arabidopsis thaliana	AT5G53370.1 | Symbols: ATPMEPCRF, PMEPCRF | pectin methylesterase PCR fragment F | chr5:21649683-21651530 REVERSE LENGTH=587	746	587	0	78.7	69.0	73.2
Rsa1.0_00379.1.g12575.t1	ref|NP_568792.1| CLP protease regulatory subunit X [Arabidopsis thaliana] gi|9759182|dbj|BAB09797.1| ATP-dependent Clp protease regulatory subunit CLPX [Arabidopsis thaliana] gi|14334860|gb|AAK59608.1| putative ATP-dependent Clp protease ATP-binding subunit ClpX1 [Arabidopsis thaliana] gi|23296603|gb|AAN13130.1| putative ATP-dependent Clp protease ATP-binding subunit ClpX1 [Arabidopsis thaliana] gi|332008960|gb|AED96343.1| CLP protease regulatory subunit X [Arabidopsis thaliana]	554	579	0	104.5	86.5	89.4	CLP protease regulatory subunit X	gbpln	Arabidopsis thaliana	AT5G53350.1 | Symbols: CLPX | CLP protease regulatory subunit X | chr5:21644060-21647503 FORWARD LENGTH=579	554	579	0	104.5	86.5	89.4
Rsa1.0_00380.1.g12576.t1	gb|AAG50606.1|AC079605_11 unknown protein [Arabidopsis thaliana]	1074	1311	2.00E-75	122.1	16.2	23.8	unknown protein	gbpln	Arabidopsis thaliana	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	1074	673	4.00E-53	62.7	12.8	18.4
Rsa1.0_00380.1.g12577.t1	ref|XP_002890088.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335930|gb|EFH66347.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	93	69	3.00E-32	74.2	72.0	73.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G15120.1 | Symbols: | Ubiquinol-cytochrome C reductase hinge protein | chr1:5203091-5203897 FORWARD LENGTH=69	93	69	5.00E-35	74.2	72.0	73.1
Rsa1.0_00380.1.g12578.t1	ref|NP_683307.2| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|5103811|gb|AAD39641.1|AC007591_6 F9L1.6 [Arabidopsis thaliana] gi|332191148|gb|AEE29269.1| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana]	323	351	1.00E-155	108.7	82.0	91.6	S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G15125.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:5204625-5205912 FORWARD LENGTH=351	323	351	1.00E-158	108.7	82.0	91.6
Rsa1.0_00380.1.g12579.t1	gb|EOA36804.1| hypothetical protein CARUB_v10008299mg [Capsella rubella]	871	845	0	97.0	85.6	89.9	hypothetical protein CARUB_v10008299mg	gbpln	Capsella rubella	AT1G15130.1 | Symbols: | Endosomal targeting BRO1-like domain-containing protein | chr1:5206217-5209848 REVERSE LENGTH=846	871	846	0	97.1	84.8	90.0
Rsa1.0_00380.1.g12580.t1	gb|EOA38363.1| hypothetical protein CARUB_v10009891mg [Capsella rubella]	272	295	1.00E-133	108.5	85.7	92.3	hypothetical protein CARUB_v10009891mg	gbpln	Capsella rubella	AT1G15140.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase | chr1:5210403-5212137 REVERSE LENGTH=295	272	295	1.00E-133	108.5	83.8	91.9
Rsa1.0_00380.1.g12581.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00380.1.g12582.t2	ref|XP_002890091.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297335933|gb|EFH66350.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	479	483	0	100.8	85.6	93.7	mate efflux family protein	gbpln	Arabidopsis lyrata	AT1G15170.1 | Symbols: | MATE efflux family protein | chr1:5220690-5222756 FORWARD LENGTH=481	479	481	0	100.4	84.3	92.7

Rsa1.0_00380.1.g12583.t1	gb|EOA36212.1| hypothetical protein CARUB_v10010136mg [Capsella rubella]	243	243	1.00E-82	100.0	71.6	81.1	hypothetical protein CARUB_v10010136mg	gbpln	Capsella rubella	AT1G15190.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr1:5227275-5228021 FORWARD LENGTH=248	243	248	3.00E-84	102.1	71.2	82.3
Rsa1.0_00380.1.g12584.t1	gb|EOA39023.1| hypothetical protein CARUB_v10011586mg [Capsella rubella]	419	423	1.00E-176	101.0	80.7	87.4	hypothetical protein CARUB_v10011586mg	gbpln	Capsella rubella	AT1G15200.1 | Symbols: | protein-protein interaction regulator family protein | chr1:5228477-5231017 REVERSE LENGTH=423	419	423	1.00E-177	101.0	80.4	86.9
Rsa1.0_00380.1.g12585.t1	ref|XP_002892853.1| ATPDR7/PDR7 [Arabidopsis lyrata subsp. lyrata] gi|297338695|gb|EFH69112.1| ATPDR7/PDR7 [Arabidopsis lyrata subsp. lyrata]	1435	1445	0	100.7	91.2	96.3	ATPDR7/PDR7	gbpln	Arabidopsis lyrata	AT1G15210.1 | Symbols: PDR7, ATPDR7 | pleiotropic drug resistance 7 | chr1:5231552-5236573 REVERSE LENGTH=1442	1435	1442	0	100.5	90.7	96.2
Rsa1.0_00380.1.g12586.t1	ref|NP_849666.2| uncharacterized protein [Arabidopsis thaliana] gi|5103848|gb|AAD39678.1|AC007591_43 F9L1.16 [Arabidopsis thaliana] gi|332191165|gb|AEE29286.1| uncharacterized protein AT1G15215 [Arabidopsis thaliana]	268	258	1.00E-106	96.3	73.1	79.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G15215.2 | Symbols: | BEST Arabidopsis thaliana protein match is: sequence-specific DNA binding transcription factors;sequence-specific DNA binding (TAIR:AT3G18380.1); Has 89 Blast hits to 86 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 89; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5238096-5239770 FORWARD LENGTH=258	268	258	1.00E-108	96.3	73.1	79.9
Rsa1.0_00380.1.g12587.t1	gb|EOA38631.1| hypothetical protein CARUB_v10010517mg [Capsella rubella]	160	159	5.00E-81	99.4	91.3	95.0	hypothetical protein CARUB_v10010517mg	gbpln	Capsella rubella	AT1G15220.2 | Symbols: ATCCMH, CCMH | cytochrome c biogenesis protein family | chr1:5240471-5241117 REVERSE LENGTH=159	160	159	5.00E-81	99.4	89.4	93.8
Rsa1.0_00380.1.g12588.t1	gb|EOA37497.1| hypothetical protein CARUB_v10011666mg [Capsella rubella]	166	155	2.00E-46	93.4	70.5	82.5	hypothetical protein CARUB_v10011666mg	gbpln	Capsella rubella	AT1G15230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 26 Blast hits to 26 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5242729-5243196 REVERSE LENGTH=155	166	155	2.00E-47	93.4	66.9	80.7
Rsa1.0_00380.1.g12589.t3	gb|EOA38912.1| hypothetical protein CARUB_v10011308mg [Capsella rubella]	185	176	4.00E-70	95.1	75.1	85.9	hypothetical protein CARUB_v10011308mg	gbpln	Capsella rubella	AT1G15260.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G16070.1); Has 28 Blast hits to 28 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5249834-5250370 FORWARD LENGTH=178	185	178	8.00E-72	96.2	74.1	86.5
Rsa1.0_00380.1.g12590.t1	ref|NP_563969.1| translation machinery associated protein TMA7 [Arabidopsis thaliana] gi|297849952|ref|XP_002892857.1| hypothetical protein ARALYDRAFT_471721 [Arabidopsis lyrata subsp. lyrata] gi|5103825|gb|AAD39655.1|AC007591_20 ESTs gb|AA650895, gb|AA720043 and gb|R29777 come from this gene [Arabidopsis thaliana] gi|12484215|gb|AAG54006.1|AF336925_1 unknown protein [Arabidopsis thaliana] gi|15028107|gb|AAK76677.1| unknown protein [Arabidopsis thaliana] gi|17065256|gb|AAL32782.1| Unknown protein [Arabidopsis thaliana] gi|20260078|gb|AAM13386.1| unknown protein [Arabidopsis thaliana] gi|21592316|gb|AAM64267.1| unknown [Arabidopsis thaliana] gi|297338699|gb|EFH69116.1| hypothetical protein ARALYDRAFT_471721 [Arabidopsis lyrata subsp. lyrata] gi|332191176|gb|AEE29297.1| translation machinery associated protein TMA7 [Arabidopsis thaliana]	64	64	5.00E-24	100.0	95.3	98.4	translation machinery associated protein TMA7	gbpln	Arabidopsis lyrata	AT1G15270.1 | Symbols: | Translation machinery associated TMA7 | chr1:5250833-5252020 REVERSE LENGTH=64	64	64	9.00E-27	100.0	95.3	98.4
Rsa1.0_00380.1.g12591.t1	ref|XP_002888148.1| EMB1220 [Arabidopsis lyrata subsp. lyrata] gi|297333989|gb|EFH64407.1| EMB1220 [Arabidopsis lyrata subsp. lyrata]	486	480	0	98.8	71.6	82.5	EMB1220	gbpln	Arabidopsis lyrata	AT1G60170.1 | Symbols: emb1220 | pre-mRNA processing ribonucleoprotein binding region-containing protein | chr1:22193008-22195177 FORWARD LENGTH=485	486	485	0	99.8	70.8	81.9

<table>
<tr><td>Rsa1.0_00380.1.g12592.t1</td><td>gb|EOA38784.1| hypothetical protein CARUB_v10011034mg [Capsella rubella]</td><td>596</td><td>584</td><td>0</td><td>98.0</td><td>67.4</td><td>76.8</td><td>hypothetical protein CARUB_v10011034mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G15280.2 | Symbols: | CASC3/Barentsz eIF4AIII binding | chr1:5252538-5256214 FORWARD LENGTH=585</td><td>596</td><td>585</td><td>1.00E-178</td><td>98.2</td><td>68.0</td><td>76.5</td></tr>
<tr><td>Rsa1.0_00380.1.g12593.t1</td><td>ref|XP_002892858.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297338700|gb|EFH69117.1| binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>1577</td><td>1622</td><td>0</td><td>102.9</td><td>78.0</td><td>85.7</td><td>binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G15290.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:5257327-5264814 REVERSE LENGTH=1608</td><td>1577</td><td>1608</td><td>0</td><td>102.0</td><td>77.4</td><td>85.0</td></tr>
<tr><td>Rsa1.0_00380.1.g12594.t1</td><td>gb|AAD39658.1|AC007591_23 Similar to gi|22113 Ac transposase (ORFa) from Zea mays transcript gb|X05424 [Arabidopsis thaliana] gi|20260646|gb|AAM13221.1| similar to Ac transposase [Arabidopsis thaliana] gi|34098823|gb|AAQ56794.1| At1g15300 [Arabidopsis thaliana]</td><td>742</td><td>799</td><td>0</td><td>107.7</td><td>64.2</td><td>75.9</td><td>Similar to gi|22113 Ac transposase (ORFa) from Zea mays transcript gb|X05424</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>742</td><td>696</td><td>1.00E-123</td><td>93.8</td><td>29.9</td><td>43.5</td></tr>
<tr><td>Rsa1.0_00380.1.g12595.t1</td><td>gb|EOA40222.1| hypothetical protein CARUB_v10008947mg [Capsella rubella]</td><td>465</td><td>495</td><td>0</td><td>106.5</td><td>83.2</td><td>90.8</td><td>hypothetical protein CARUB_v10008947mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G48900.1 | Symbols: | Signal recognition particle, SRP54 subunit protein | chr1:18084972-18087743 REVERSE LENGTH=495</td><td>465</td><td>495</td><td>0</td><td>106.5</td><td>82.8</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00380.1.g12596.t1</td><td>ref|XP_002892860.1| F9L1.26 [Arabidopsis lyrata subsp. lyrata] gi|297338702|gb|EFH69119.1| F9L1.26 [Arabidopsis lyrata subsp. lyrata]</td><td>377</td><td>317</td><td>1.00E-132</td><td>84.1</td><td>65.0</td><td>70.6</td><td>F9L1.26</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G15320.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; EXPRESSED DURING: petal differentiation and expansion stage; Has 62 Blast hits to 62 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 62; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5272468-5273699 REVERSE LENGTH=307</td><td>377</td><td>307</td><td>1.00E-130</td><td>81.4</td><td>62.6</td><td>66.6</td></tr>
<tr><td>Rsa1.0_00380.1.g12597.t1</td><td>ref|NP_172985.1| Cystathionine beta-synthase (CBS) protein [Arabidopsis thaliana] gi|75315303|sp|Q9XI37.1|PV42A_ARATH RecName: Full=SNF1-related protein kinase regulatory subunit gamma-like PV42a; Short=AtPV42a; AltName: Full=AKIN subunit gamma-like PV42a; AltName: Full=CBS domain-containing protein CBSCBS4 gi|5103830|gb|AAD39660.1|AC007591_25 Similar to gb|U40713 Pv42p gene from Phaseolus vulgaris and contains PF|00571 CBS (cystathionine beta synthase) domain [Arabidopsis thaliana] gi|66792608|gb|AAY56406.1| At1g15330 [Arabidopsis thaliana] gi|110738205|dbj|BAF01033.1| hypothetical protein [Arabidopsis thaliana] gi|111074494|gb|ABH04620.1| At1g15330 [Arabidopsis thaliana] gi|332191183|gb|AEE29304.1| Cystathionine beta-synthase (CBS) protein [Arabidopsis thaliana]</td><td>355</td><td>352</td><td>1.00E-178</td><td>99.2</td><td>85.6</td><td>93.8</td><td>Cystathionine beta-synthase (CBS) protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G15330.1 | Symbols: | Cystathionine beta-synthase (CBS) protein | chr1:5274368-5275499 FORWARD LENGTH=352</td><td>355</td><td>352</td><td>0</td><td>99.2</td><td>85.6</td><td>93.8</td></tr>
<tr><td>Rsa1.0_00380.1.g12598.t1</td><td>ref|XP_002892861.1| hypothetical protein ARALYDRAFT_312525 [Arabidopsis lyrata subsp. lyrata] gi|297338703|gb|EFH69120.1| hypothetical protein ARALYDRAFT_312525 [Arabidopsis lyrata subsp. lyrata]</td><td>326</td><td>357</td><td>3.00E-84</td><td>109.5</td><td>59.8</td><td>66.3</td><td>hypothetical protein ARALYDRAFT_312525</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G15340.1 | Symbols: MBD10 | methyl-CPG-binding domain 10 | chr1:5275895-5277474 REVERSE LENGTH=384</td><td>326</td><td>384</td><td>2.00E-79</td><td>117.8</td><td>66.0</td><td>74.5</td></tr>
<tr><td>Rsa1.0_00380.1.g12599.t1</td><td>ref|NP_563972.1| uncharacterized protein [Arabidopsis thaliana] gi|30684315|ref|NP_849667.1| uncharacterized protein [Arabidopsis thaliana] gi|21617951|gb|AAM67001.1| unknown [Arabidopsis thaliana] gi|110742955|dbj|BAE99372.1| hypothetical protein [Arabidopsis thaliana] gi|332191186|gb|AEE29307.1| uncharacterized protein AT1G15350 [Arabidopsis thaliana] gi|332191187|gb|AEE29308.1| uncharacterized protein AT1G15350 [Arabidopsis thaliana]</td><td>415</td><td>154</td><td>4.00E-62</td><td>37.1</td><td>28.7</td><td>32.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G15350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G15770.2); Has 148 Blast hits to 148 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 141; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr1:5278481-5279486 REVERSE LENGTH=154</td><td>415</td><td>154</td><td>9.00E-65</td><td>37.1</td><td>28.7</td><td>32.8</td></tr>
</table>

Rsa1.0_00380.1.g12600.t1	ref|NP_172988.1| ethylene−responsive transcription factor WIN1 [Arabidopsis thaliana] gi|75338622|sp|Q9XI33.1|WIN1_ARATH RecName: Full=Ethylene−responsive transcription factor WIN1; AltName: Full=Protein SHINE 1; AltName: Full=Protein WAX INDUCER 1 gi|5103834|gb|AAD39664.1|AC007591_29 Similar to gb|AB008104 ethylene responsive element binding factor 2 from Arabidopsis thaliana and contains an PF|00847 AP2 domain. EST gb|AA728476 comes from this gene [Arabidopsis thaliana] gi|26450944|dbj|BAC42579.1| putative ethylene responsive element [Arabidopsis thaliana] gi|28950721|gb|AAO63284.1| At1g15360 [Arabidopsis thaliana] gi|38426898|gb|AAR20494.1| transcription factor wax inducer 1 [Arabidopsis thaliana] gi|332191189|gb|AEE29310.1| ethylene−responsive transcription factor WIN1 [Arabidopsis thaliana]	191	199	3.00E−83	104.2	89.5	92.1	ethylene−responsive transcription factor WIN1	gbpln	Arabidopsis thaliana	AT1G15360.1 | Symbols: SHN1, WIN1 | Integrase−type DNA−binding superfamily protein | chr1:5283609−5284506 FORWARD LENGTH=199	191	199	1.00E−85	104.2	89.5	92.1
Rsa1.0_00380.1.g12601.t1	gb|EOA38653.1| hypothetical protein CARUB_v10010572mg [Capsella rubella]	147	147	1.00E−75	100.0	94.6	98.0	hypothetical protein CARUB_v10010572mg	gbpln	Capsella rubella	AT1G15370.1 | Symbols: | SNARE−like superfamily protein | chr1:5287135−5288375 FORWARD LENGTH=147	147	147	4.00E−78	100.0	95.2	97.3
Rsa1.0_00381.1.g12602.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00381.1.g12603.t1	ref|XP_002868276.1| cbl−interacting protein kinase 4 [Arabidopsis lyrata subsp. lyrata] gi|297314112|gb|EFH44535.1| cbl−interacting protein kinase 4 [Arabidopsis lyrata subsp. lyrata]	426	423	0	99.3	78.2	88.7	cbl−interacting protein kinase 4	gbpln	Arabidopsis lyrata	AT4G14580.1 | Symbols: CIPK4, SnRK3.3 | CBL−interacting protein kinase 4 | chr4:8367887−8369167 REVERSE LENGTH=426	426	426	0	100.0	75.1	85.4
Rsa1.0_00381.1.g12604.t1	ref|XP_002868276.1| cbl−interacting protein kinase 4 [Arabidopsis lyrata subsp. lyrata] gi|297314112|gb|EFH44535.1| cbl−interacting protein kinase 4 [Arabidopsis lyrata subsp. lyrata]	427	423	1.00E−166	99.1	74.2	84.5	cbl−interacting protein kinase 4	gbpln	Arabidopsis lyrata	AT4G14580.1 | Symbols: CIPK4, SnRK3.3 | CBL−interacting protein kinase 4 | chr4:8367887−8369167 REVERSE LENGTH=426	427	426	1.00E−166	99.8	71.2	81.7
Rsa1.0_00381.1.g12605.t1	ref|XP_002870305.1| hypothetical protein ARALYDRAFT_915409 [Arabidopsis lyrata subsp. lyrata] gi|297316141|gb|EFH46564.1| hypothetical protein ARALYDRAFT_915409 [Arabidopsis lyrata subsp. lyrata]	757	763	0	100.8	80.8	90.6	hypothetical protein ARALYDRAFT_915409	gbpln	Arabidopsis lyrata	AT4G14570.1 | Symbols: | acylaminoacyl−peptidase−related | chr4:8362586−8366525 FORWARD LENGTH=764	757	764	0	100.9	80.8	90.1
Rsa1.0_00381.1.g12606.t1	ref|XP_002868278.1| hypothetical protein ARALYDRAFT_330061 [Arabidopsis lyrata subsp. lyrata] gi|297314114|gb|EFH44537.1| hypothetical protein ARALYDRAFT_330061 [Arabidopsis lyrata subsp. lyrata]	865	919	0	106.2	78.4	85.5	hypothetical protein ARALYDRAFT_330061	gbpln	Arabidopsis lyrata	AT4G14510.1 | Symbols: ATCFM3B, CFM3B | CRM family member 3B | chr4:8337390−8341057 REVERSE LENGTH=907	865	907	0	104.9	77.0	84.2
Rsa1.0_00381.1.g12607.t9	gb|EOA16652.1| hypothetical protein CARUB_v10004845mg [Capsella rubella]	432	434	0	100.5	88.0	91.4	hypothetical protein CARUB_v10004845mg	gbpln	Capsella rubella	AT4G14500.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:8334391−8337022 FORWARD LENGTH=433	432	433	0	100.2	87.7	91.7
Rsa1.0_00381.1.g12608.t2	ref|XP_002877826.1| ATG4/CHLG/G4 [Arabidopsis lyrata subsp. lyrata] gi|297323664|gb|EFH54085.1| ATG4/CHLG/G4 [Arabidopsis lyrata subsp. lyrata]	449	387	0	86.2	76.6	79.1	ATG4/CHLG/G4	gbpln	Arabidopsis lyrata	AT3G51820.1 | Symbols: ATG4, G4, CHLG | UbiA prenyltransferase family protein | chr3:19216301−19218934 REVERSE LENGTH=387	449	387	0	86.2	75.7	78.6
Rsa1.0_00381.1.g12609.t1	gb|ABB55260.1| late embryogenesis−abundant protein [Brassica carinata]	152	152	2.00E−70	100.0	92.8	98.7	late embryogenesis−abundant protein	gbpln	Brassica carinata	AT3G51810.1 | Symbols: ATEM1, GEA1, AT3, EM1 | Stress induced protein | chr3:19214818−19215461 FORWARD LENGTH=152	152	152	3.00E−70	100.0	89.5	96.1
Rsa1.0_00381.1.g12610.t1	ref|NP_001190060.1| metallopeptidase M24 domain−containing protein [Arabidopsis thaliana] gi|332645325|gb|AEE78846.1| metallopeptidase M24 domain−containing protein [Arabidopsis thaliana]	392	385	0	98.2	84.7	91.3	metallopeptidase M24 domain−containing protein	gbpln	Arabidopsis thaliana	AT3G51800.3 | Symbols: ATG2 | metallopeptidase M24 family protein | chr3:19211261−19213568 REVERSE LENGTH=385	392	385	0	98.2	84.7	91.3

Rsa1.0_00381.1.g12611.t1	ref|XP_002877820.1| hypothetical protein ARALYDRAFT_348272 [Arabidopsis lyrata subsp. lyrata] gi|297323658|gb|EFH54079.1| hypothetical protein ARALYDRAFT_348272 [Arabidopsis lyrata subsp. lyrata]	196	113	2.00E-26	57.7	34.7	43.4	hypothetical protein ARALYDRAFT_348272	gbpln	Arabidopsis lyrata	AT3G51750.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 9 growth stages. | chr3:19196706-19197307 REVERSE LENGTH=110	196	110	2.00E-26	56.1	36.2	41.8
Rsa1.0_00381.1.g12612.t1	ref|XP_002876102.1| hypothetical protein ARALYDRAFT_485528 [Arabidopsis lyrata subsp. lyrata] gi|297321940|gb|EFH52361.1| hypothetical protein ARALYDRAFT_485528 [Arabidopsis lyrata subsp. lyrata]	830	832	0	100.2	87.5	92.9	hypothetical protein ARALYDRAFT_485528	gbpln	Arabidopsis lyrata	AT3G51740.1 | Symbols: IMK2 | inflorescence meristem receptor-like kinase 2 | chr3:19189248-19191842 FORWARD LENGTH=836	830	836	0	100.7	86.3	91.4
Rsa1.0_00381.1.g12613.t1	ref|XP_002876095.1| hypothetical protein ARALYDRAFT_485514 [Arabidopsis lyrata subsp. lyrata] gi|297321933|gb|EFH52354.1| hypothetical protein ARALYDRAFT_485514 [Arabidopsis lyrata subsp. lyrata]	807	829	0	102.7	73.7	82.0	hypothetical protein ARALYDRAFT_485514	gbpln	Arabidopsis lyrata	AT3G51620.2 | Symbols: | PAP/OAS1 substrate-binding domain superfamily | chr3:19143859-19147944 FORWARD LENGTH=829	807	829	0	102.7	72.1	81.0
Rsa1.0_00381.1.g12614.t1	ref|XP_002877814.1| hypothetical protein ARALYDRAFT_906509 [Arabidopsis lyrata subsp. lyrata] gi|297323652|gb|EFH54073.1| hypothetical protein ARALYDRAFT_906509 [Arabidopsis lyrata subsp. lyrata]	267	230	1.00E-118	86.1	78.3	81.3	hypothetical protein ARALYDRAFT_906509	gbpln	Arabidopsis lyrata	AT3G51610.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: endomembrane system; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; Has 53 Blast hits to 53 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr3:19139715-19141986 REVERSE LENGTH=230	267	230	1.00E-120	86.1	78.7	80.5
Rsa1.0_00381.1.g12615.t1	gb|AGC11819.1| putative lipid transfer protein 5 [Eutrema halophilum]	116	118	9.00E-55	101.7	92.2	97.4	putative lipid transfer protein 5	gbpln	Eutrema halophilum	AT3G51600.1 | Symbols: LTP5 | lipid transfer protein 5 | chr3:19138661-19139124 REVERSE LENGTH=118	116	118	5.00E-54	101.7	87.1	93.1
Rsa1.0_00381.1.g12616.t1	emb|CAA42870.1| E2 [Brassica napus] gi|384340|prf||1905428A phospholipid transfer protein	185	119	2.00E-57	64.3	59.5	60.0	E2	gbpln	Brassica napus	AT3G51590.1 | Symbols: LTP12 | lipid transfer protein 12 | chr3:19135828-19136654 REVERSE LENGTH=119	185	119	5.00E-48	64.3	48.1	55.1
Rsa1.0_00381.1.g12617.t1	gb|ABT18094.1| FERONIA receptor-like kinase [Brassica oleracea]	897	895	0	99.8	91.8	93.6	FERONIA receptor-like kinase	gbpln	Brassica oleracea	AT3G51550.1 | Symbols: FER | Malectin/receptor-like protein kinase family protein | chr3:19117877-19120564 REVERSE LENGTH=895	897	895	0	99.8	87.1	91.9
Rsa1.0_00381.1.g12618.t1	ref|NP_566952.1| diacylglycerol O-acyltransferase 2 [Arabidopsis thaliana] gi|75167729|sp|Q9ASU1.1|DGAT2_ARATH RecName: Full=Diacylglycerol O-acyltransferase 2 gi|13605702|gb|AAK32844.1|AF361832_1 AT3g51520/F26O13_160 [Arabidopsis thaliana] gi|18700272|gb|AAL77746.1| AT3g51520/F26O13_160 [Arabidopsis thaliana] gi|21593164|gb|AAM65113.1| unknown [Arabidopsis thaliana] gi|332645281|gb|AEE78802.1| diacylglycerol O-acyltransferase 2 [Arabidopsis thaliana]	318	314	1.00E-147	98.7	78.9	88.4	diacylglycerol O-acyltransferase 2	gbpln	Arabidopsis thaliana	AT3G51520.1 | Symbols: | diacylglycerol acyltransferase family | chr3:19110739-19112518 FORWARD LENGTH=314	318	314	1.00E-150	98.7	78.9	88.4
Rsa1.0_00381.1.g12619.t1	ref|NP_190719.1| uncharacterized protein [Arabidopsis thaliana] gi|6572072|emb|CAB63015.1| putative protein [Arabidopsis thaliana] gi|15027917|gb|AAK76489.1| unknown protein [Arabidopsis thaliana] gi|15450643|gb|AAK96593.1| AT3g51510/F26O13_150 [Arabidopsis thaliana] gi|20259289|gb|AAM14380.1| unknown protein [Arabidopsis thaliana] gi|21536487|gb|AAM60819.1| unknown [Arabidopsis thaliana] gi|332645280|gb|AEE78801.1| uncharacterized protein AT3G51510 [Arabidopsis thaliana]	176	181	2.00E-67	102.8	80.7	87.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G51510.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 42 Blast hits to 42 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:19109118-19109842 FORWARD LENGTH=181	176	181	7.00E-70	102.8	80.7	87.5

Rsa1.0_00381.1.g12620.t1	dbj|BAE99300.1| hypothetical protein [Arabidopsis thaliana]	120	116	2.00E-31	96.7	72.5	80.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G51500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 23 Blast hits to 23 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:19108353-19108703 FORWARD LENGTH=116	120	116	5.00E-34	96.7	72.5	80.8
Rsa1.0_00381.1.g12621.t1	ref|NP_190717.1| monosaccharide-sensing protein 3 [Arabidopsis thaliana] gi|75337067|sp|Q9SD00.1|MSSP3_ARATH RecName: Full=Monosaccharide-sensing protein 3; AltName: Full=Sugar transporter MSSP3 gi|6572070|emb|CAB63013.1| sugar transporter-like protein [Arabidopsis thaliana] gi|26800697|emb|CAD58693.1| monosaccharide sensing protein 3 [Arabidopsis thaliana] gi|332645277|gb|AEE78798.1| monosaccharide-sensing protein 3 [Arabidopsis thaliana]	654	729	0	111.5	82.3	89.0	monosaccharide-sensing protein 3	gbpln	Arabidopsis thaliana	AT3G51490.1 | Symbols: TMT3 | tonoplast monosaccharide transporter3 | chr3:19105018-19107562 REVERSE LENGTH=729	654	729	0	111.5	82.3	89.0
Rsa1.0_00381.1.g12622.t1	gb|EOA25689.1| hypothetical protein CARUB_v10019042mg [Capsella rubella]	348	362	1.00E-180	104.0	89.4	95.7	hypothetical protein CARUB_v10019042mg	gbpln	Capsella rubella	AT3G51470.1 | Symbols: | Protein phosphatase 2C family protein | chr3:19097924-19099244 REVERSE LENGTH=361	348	361	0	103.7	88.5	95.7
Rsa1.0_00381.1.g12623.t2	ref|NP_190714.2| phosphatidylinositol-4-phosphate phosphatase RHD4 [Arabidopsis thaliana] gi|75168948|sp|Q9C5G5.1|SAC7_ARATH RecName: Full=Phosphoinositide phosphatase SAC7; Short=AtSAC7; AltName: Full=Protein ROOT HAIR DEFECTIVE 4; AltName: Full=Protein SUPPRESSOR OF ACTIN 1C; Short=AtSAC1c; AltName: Full=Protein SUPPRESSOR OF ACTIN 7; AltName: Full=SAC domain protein 7; AltName: Full=SAC1-like protein AtSAC1c gi|13430710|gb|AAK25977.1|AF360267_1 unknown protein [Arabidopsis thaliana] gi|30840667|gb|AAP41368.1|AF266459_1 SAC1-like protein AtSAC1c [Arabidopsis thaliana] gi|14532908|gb|AAK64136.1| unknown protein [Arabidopsis thaliana] gi|31415731|gb|AAP49840.1| SAC domain protein 7 [Arabidopsis thaliana] gi|332645274|gb|AEE78795.1| phosphatidylinositol-4-phosphate phosphatase RHD4 [Arabidopsis thaliana]	685	597	0	87.2	79.0	83.5	phosphatidylinositol-4-phosphate phosphatase RHD4	gbpln	Arabidopsis thaliana	AT3G51460.1 | Symbols: RHD4 | Phosphoinositide phosphatase family protein | chr3:19093007-19097142 FORWARD LENGTH=597	685	597	0	87.2	79.0	83.5
Rsa1.0_00381.1.g12624.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00382.1.g12625.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00382.1.g12626.t1	ref|NP_001031527.1| Tim17 domain-containing protein [Arabidopsis thaliana] gi|330254993|gb|AEC10087.1| outer envelope pore protein 16-3 [Arabidopsis thaliana]	114	173	4.00E-27	151.8	59.6	64.0	Tim17 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G42210.2 | Symbols: ATOEP16-3, OEP16-3 | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr2:17590600-17591591 FORWARD LENGTH=173	114	173	6.00E-30	151.8	59.6	64.0
Rsa1.0_00382.1.g12627.t1	ref|XP_002893732.1| ATMYC2 [Arabidopsis lyrata subsp. lyrata] gi|297339574|gb|EFH69991.1| ATMYC2 [Arabidopsis lyrata subsp. lyrata]	276	625	1.00E-61	226.4	51.1	64.5	ATMYC2	gbpln	Arabidopsis lyrata	AT1G32640.1 | Symbols: ATMYC2, RD22BP1, JAI1, JIN1, MYC2, ZBF1 | Basic helix-loop-helix (bHLH) DNA-binding family protein | chr1:11799042-11800913 REVERSE LENGTH=623	276	623	1.00E-63	225.7	50.7	64.1
Rsa1.0_00382.1.g12628.t1	ref|NP_190352.1| DNA binding protein [Arabidopsis thaliana] gi|4741185|emb|CAB41851.1| hypothetical protein [Arabidopsis thaliana] gi|189303599|gb|ACD85799.1| At3g47680 [Arabidopsis thaliana] gi|332644797|gb|AEE78318.1| DNA binding protein [Arabidopsis thaliana]	349	302	8.00E-32	86.5	25.2	34.4	DNA binding protein	gbpln	Arabidopsis thaliana	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	349	302	2.00E-34	86.5	25.2	34.4

Rsa1.0_00382.1.g12629.t1	ref|XP_002865157.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310992|gb|EFH41416.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	495	509	0	102.8	81.6	87.7	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT5G46840.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:19005651-19007609 FORWARD LENGTH=501	495	501	0	101.2	78.2	84.6
Rsa1.0_00382.1.g12630.t2	ref|NP_001190481.1| phosphatidylinositol glycan, class X [Arabidopsis thaliana] gi|332008052|gb|AED95435.1| uncharacterized protein AT5G46850 [Arabidopsis thaliana]	379	325	1.00E-108	85.8	55.1	63.9	phosphatidylinositol glycan, class X	gbpln	Arabidopsis thaliana	AT5G46850.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: GPI anchor biosynthetic process; LOCATED IN: endoplasmic reticulum membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: PIG-X/PBN1 (InterPro:IPR013233). | chr5:19010714-19012010 FORWARD LENGTH=325	379	325	1.00E-111	85.8	55.1	63.9
Rsa1.0_00382.1.g12631.t1	gb|EOA13852.1| hypothetical protein CARUB_v10026955mg [Capsella rubella]	270	268	1.00E-129	99.3	84.4	90.4	hypothetical protein CARUB_v10026955mg	gbpln	Capsella rubella	AT5G46860.1 | Symbols: VAM3, ATVAM3, SYP22, ATSYP22, SGR3 | Syntaxin/t-SNARE family protein | chr5:19012342-19013795 REVERSE LENGTH=268	270	268	1.00E-130	99.3	83.7	88.9
Rsa1.0_00382.1.g12632.t1	ref|XP_002865155.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310990|gb|EFH41414.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	318	303	1.00E-126	95.3	80.2	86.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G46870.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:19015486-19016990 FORWARD LENGTH=295	318	295	1.00E-127	92.8	77.7	83.0
Rsa1.0_00382.1.g12633.t1	dbj|BAJ34553.1| unnamed protein product [Thellungiella halophila]	360	389	0	108.1	95.8	97.8	unnamed protein product	----	----	AT1G43170.8 | Symbols: RP1 | ribosomal protein 1 | chr1:16266992-16268631 FORWARD LENGTH=389	360	389	0	108.1	91.7	95.8
Rsa1.0_00382.1.g12634.t4	ref|NP_199499.3| homeobox-leucine zipper protein HDG5 [Arabidopsis thaliana] gi|322510124|sp|Q9FJS2.3|HDG5_ARATH RecName: Full=Homeobox-leucine zipper protein HDG5; AltName: Full=HD-ZIP protein HDG5; AltName: Full=Homeodomain GLABRA 2-like protein 5; AltName: Full=Homeodomain transcription factor HDG5; AltName: Full=Protein HOMEODOMAIN GLABROUS 5 gi|332008060|gb|AED95443.1| homeobox-leucine zipper protein HDG5 [Arabidopsis thaliana]	820	826	0	100.7	84.8	90.7	homeobox-leucine zipper protein HDG5	gbpln	Arabidopsis thaliana	AT5G46880.1 | Symbols: HB-7, HDG5 | homeobox-7 | chr5:19031540-19035388 FORWARD LENGTH=826	820	826	0	100.7	84.8	90.7
Rsa1.0_00382.1.g12635.t1	ref|NP_199503.1| Intron maturase, type II family protein [Arabidopsis thaliana] gi|9759434|dbj|BAB10231.1| unnamed protein product [Arabidopsis thaliana] gi|332008065|gb|AED95448.1| Intron maturase, type II family protein [Arabidopsis thaliana]	731	735	0	100.5	88.5	93.0	Intron maturase, type II family protein	gbpln	Arabidopsis thaliana	AT5G46920.1 | Symbols: | Intron maturase, type II family protein | chr5:19053668-19055875 FORWARD LENGTH=735	731	735	0	100.5	88.5	93.0
Rsa1.0_00382.1.g12636.t1	ref|XP_002863379.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297309214|gb|EFH39638.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	173	179	7.00E-37	103.5	50.3	67.1	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT5G46930.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19056655-19057191 REVERSE LENGTH=178	173	178	2.00E-36	102.9	45.7	65.3
Rsa1.0_00382.1.g12637.t1	gb|ABD64967.1| hypothetical protein 25.t00004 [Brassica oleracea]	143	149	2.00E-43	104.2	61.5	76.9	hypothetical protein 25.t00004	gbpln	Brassica oleracea	AT5G47600.1 | Symbols: | HSP20-like chaperones superfamily protein | chr5:19299945-19300456 REVERSE LENGTH=131	143	131	1.00E-37	91.6	47.6	60.1
Rsa1.0_00382.1.g12638.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00382.1.g12639.t2	ref|NP_199513.2| uncharacterized protein [Arabidopsis thaliana] gi|332008075|gb|AED95458.1| uncharacterized protein AT5G47020 [Arabidopsis thaliana]	1373	1421	0	103.5	90.8	94.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G47020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G11700.2); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19082005-19089800 FORWARD LENGTH=1421	1373	1421	0	103.5	90.8	94.8

Rsa1.0_00382.1.g12640.t1	ref|XP_002868835.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297314671|gb|EFH45094.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	291	301	1.00E-125	103.4	80.4	88.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G38150.2 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:17901211-17902119 REVERSE LENGTH=302	291	302	1.00E-127	103.8	80.1	86.9
Rsa1.0_00382.1.g12641.t1	gb|ABL97963.1| hydrogen-transporting ATP synthase [Brassica rapa]	112	203	2.00E-57	181.3	98.2	100.0	hydrogen-transporting ATP synthase	gbpln	Brassica rapa	AT5G47030.1 | Symbols: | ATPase, F1 complex, delta/epsilon subunit | chr5:19090384-19092034 FORWARD LENGTH=203	112	203	2.00E-56	181.3	92.9	98.2
Rsa1.0_00382.1.g12642.t1	ref|XP_002863374.1| hypothetical protein ARALYDRAFT_494276 [Arabidopsis lyrata subsp. lyrata] gi|297309209|gb|EFH39633.1| hypothetical protein ARALYDRAFT_494276 [Arabidopsis lyrata subsp. lyrata]	878	888	0	101.1	96.7	97.8	hypothetical protein ARALYDRAFT_494276	gbpln	Arabidopsis lyrata	AT5G47040.1 | Symbols: LON2 | lon protease 2 | chr5:19093356-19098678 REVERSE LENGTH=888	878	888	0	101.1	96.5	97.9
Rsa1.0_00382.1.g12643.t1	ref|XP_002865147.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297310982|gb|EFH41406.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	302	303	1.00E-112	100.3	75.2	83.1	ATP binding protein	gbpln	Arabidopsis lyrata	AT5G47050.1 | Symbols: SBP (S-ribonuclease binding protein) family protein | chr5:19106612-19107860 FORWARD LENGTH=300	302	300	1.00E-109	99.3	74.5	83.8
Rsa1.0_00382.1.g12644.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00382.1.g12645.t1	gb|EOA14090.1| hypothetical protein CARUB_v10027227mg [Capsella rubella]	180	177	1.00E-60	98.3	82.2	88.3	hypothetical protein CARUB_v10027227mg	gbpln	Capsella rubella	AT5G47060.1 | Symbols: | Protein of unknown function (DUF581) | chr5:19116843-19117639 FORWARD LENGTH=177	180	177	2.00E-61	98.3	80.0	85.0
Rsa1.0_00382.1.g12646.t1	dbj|BAJ33813.1| unnamed protein product [Thellungiella halophila]	407	412	0	101.2	85.3	92.6	unnamed protein product	----	----	AT5G47070.1 | Symbols: | Protein kinase superfamily protein | chr5:19118683-19120528 REVERSE LENGTH=410	407	410	0	100.7	83.8	92.1
Rsa1.0_00382.1.g12647.t1	gb|ABD65048.1| Casein kinase II beta chain, putative [Brassica oleracea]	269	276	1.00E-141	102.6	92.2	95.2	Casein kinase II beta chain, putative	gbpln	Brassica oleracea	AT5G47080.1 | Symbols: CKB1 | casein kinase II beta chain 1 | chr5:19124969-19126397 REVERSE LENGTH=287	269	287	1.00E-137	106.7	90.7	94.4
Rsa1.0_00382.1.g12648.t1	ref|XP_002863360.1| hypothetical protein ARALYDRAFT_916691 [Arabidopsis lyrata subsp. lyrata] gi|297309195|gb|EFH39619.1| hypothetical protein ARALYDRAFT_916691 [Arabidopsis lyrata subsp. lyrata]	260	264	1.00E-115	101.5	85.0	90.0	hypothetical protein ARALYDRAFT_916691	gbpln	Arabidopsis lyrata	AT5G47110.1 | Symbols: LIL3:2 | Chlorophyll A-B binding family protein | chr5:19134218-19135238 REVERSE LENGTH=258	260	258	1.00E-116	99.2	83.5	89.6
Rsa1.0_00382.1.g12649.t1	gb|AAC25101.1| putative transposase [Arabidopsis thaliana]	761	729	1.00E-111	95.8	24.3	29.4	putative transposase	gbpln	Arabidopsis thaliana	AT3G17450.1 | Symbols: | hAT dimerisation domain-containing protein | chr3:5972793-5975684 REVERSE LENGTH=877	761	877	2.00E-38	115.2	10.8	18.8
Rsa1.0_00382.1.g12650.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	598	1231	1.00E-173	205.9	49.2	66.2	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	598	575	1.00E-91	96.2	27.6	44.6
Rsa1.0_00382.1.g12651.t1	ref|XP_002865139.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310974|gb|EFH41398.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	451	477	1.00E-176	105.8	78.5	87.1	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G47140.1 | Symbols: GATA27 | GATA transcription factor 27 | chr5:19145108-19147303 FORWARD LENGTH=470	451	470	1.00E-170	104.2	77.4	86.7
Rsa1.0_00382.1.g12652.t1	gb|ABD65049.1| histone-lysine N-methyltransferase, putative [Brassica oleracea]	335	392	1.00E-109	117.0	67.2	77.6	histone-lysine N-methyltransferase, putative	gbpln	Brassica oleracea	AT5G47150.1 | Symbols: | YDG/SRA domain-containing protein | chr5:19150807-19151793 FORWARD LENGTH=328	335	328	7.00E-98	97.9	57.9	69.9
Rsa1.0_00382.1.g12653.t1	ref|XP_002865137.1| hypothetical protein ARALYDRAFT_494263 [Arabidopsis lyrata subsp. lyrata] gi|297310972|gb|EFH41396.1| hypothetical protein ARALYDRAFT_494263 [Arabidopsis lyrata subsp. lyrata]	392	332	1.00E-82	84.7	45.9	58.9	hypothetical protein ARALYDRAFT_494263	gbpln	Arabidopsis lyrata	AT5G47160.1 | Symbols: | YDG/SRA domain-containing protein | chr5:19156731-19157978 FORWARD LENGTH=415	392	415	3.00E-81	105.9	48.0	64.3

Rsa1.0_00382.1.g12654.t1	ref|NP_199529.1| VAMP (vesicle-associated membrane protein) family protein [Arabidopsis thaliana] gi|30695123|ref|NP_851144.1| VAMP (vesicle-associated membrane protein) family protein [Arabidopsis thaliana] gi|75180692|sp|Q9LVU1.1|VAP21_ARATH RecName: Full=Vesicle-associated protein 2-1; AltName: Full=Plant VAP homolog 21; Short=AtPVA21; AltName: Full=VAMP-associated protein 2-1 gi|8809600|dbj|BAA97151.1| VAMP (vesicle-associated membrane protein)-associated protein-like [Arabidopsis thaliana] gi|14334974|gb|AAK59664.1| putative VAMP (vesicle-associated membrane protein)-associated protein [Arabidopsis thaliana] gi|17104633|gb|AAL34205.1| putative VAMP-associated protein [Arabidopsis thaliana] gi|21553413|gb|AAM62506.1| VAMP (vesicle-associated membrane protein)-associated protein-like [Arabidopsis thaliana] gi|332008097|gb|AED95480.1| VAMP (vesicle-associated membrane protein) family protein [Arabidopsis thaliana] gi|332008098|gb|AED95481.1| vesicle-associated protein 2-1 [Arabidopsis thaliana]	216	220	1.00E-108	101.9	90.7	95.4	VAMP (vesicle-associated membrane protein) family protein	gbpln	Arabidopsis thaliana	AT5G47180.2 | Symbols: | Plant VAMP (vesicle-associated membrane protein) family protein | chr5:19161384-19163265 REVERSE LENGTH=220	216	220	1.00E-111	101.9	90.7	95.4
Rsa1.0_00382.1.g12655.t1	gb|AAM64533.1| contains similarity to plastid ribosomal protein L19 [Arabidopsis thaliana]	234	229	1.00E-82	97.9	78.6	84.6	contains similarity to plastid ribosomal protein L19	gbpln	Arabidopsis thaliana	AT5G47190.1 | Symbols: | Ribosomal protein L19 family protein | chr5:19164432-19166064 REVERSE LENGTH=229	234	229	7.00E-85	97.9	78.2	84.6
Rsa1.0_00382.1.g12656.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00383.1.g12657.t2	ref|XP_002864736.1| small G protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297310571|gb|EFH40995.1| small G protein family protein [Arabidopsis lyrata subsp. lyrata]	726	376	0	51.8	49.6	50.8	small G protein family protein	gbpln	Arabidopsis lyrata	AT5G61530.1 | Symbols: | small G protein family protein / RhoGAP family protein | chr5:24742630-24744586 FORWARD LENGTH=376	726	376	0	51.8	48.5	50.4
Rsa1.0_00383.1.g12658.t1	gb|EOA14619.1| hypothetical protein CARUB_v10027877mg [Capsella rubella]	846	849	0	100.4	87.4	92.9	hypothetical protein CARUB_v10027877mg	gbpln	Capsella rubella	AT5G61550.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:24748325-24751558 FORWARD LENGTH=845	846	845	0	99.9	84.0	91.7
Rsa1.0_00383.1.g12659.t1	ref|NP_200964.2| U-box domain-containing protein 51 [Arabidopsis thaliana] gi|172045896|sp|Q9FKG5.2|PUB51_ARATH RecName: Full=U-box domain-containing protein 51; AltName: Full=Plant U-box protein 51; Includes: RecName: Full=E3 ubiquitin ligase; Includes: RecName: Full=Serine/threonine-protein kinase gi|332010105|gb|AED97488.1| U-box domain-containing protein 51 [Arabidopsis thaliana]	789	796	0	100.9	86.7	93.2	U-box domain-containing protein 51	gbpln	Arabidopsis thaliana	AT5G61560.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:24753476-24756506 FORWARD LENGTH=796	789	796	0	100.9	86.7	93.2
Rsa1.0_00383.1.g12660.t1	ref|NP_001078779.1| protein kinase-like protein [Arabidopsis thaliana] gi|63003858|gb|AAY25458.1| At5g61570 [Arabidopsis thaliana] gi|332010108|gb|AED97491.1| protein kinase-like protein [Arabidopsis thaliana]	359	358	1.00E-152	99.7	79.9	88.9	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT5G61570.2 | Symbols: | Protein kinase superfamily protein | chr5:24758507-24760201 FORWARD LENGTH=358	359	358	1.00E-154	99.7	79.9	88.9
Rsa1.0_00383.1.g12661.t1	ref|XP_002866443.1| hypothetical protein ARALYDRAFT_919404 [Arabidopsis lyrata subsp. lyrata] gi|297312278|gb|EFH42702.1| hypothetical protein ARALYDRAFT_919404 [Arabidopsis lyrata subsp. lyrata]	753	749	0	99.5	75.4	84.1	hypothetical protein ARALYDRAFT_919404	gbpln	Arabidopsis lyrata	AT3G53360.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:19784502-19786808 FORWARD LENGTH=768	753	768	1.00E-114	102.0	31.3	51.8

<table>
<tr><td>Rsa1.0_00383.1.g12662.t1</td><td>ref|NP_200966.2| 6-phosphofructokinase 4 [Arabidopsis thaliana] gi|75171244|sp|Q9FKG3.1|K6PF4_ARATH RecName: Full=6-phosphofructokinase 4, chloroplastic; Short=Phosphofructokinase 4; AltName: Full=Phosphohexokinase 4; Flags: Precursor gi|9758473|dbj|BAB09002.1| pyrophosphate-fructose-6-phosphate 1-phosphotransferase-like protein [Arabidopsis thaliana] gi|20466456|gb|AAM20545.1| pyrophosphate-dependent phosphofructo-1-kinase-like protein [Arabidopsis thaliana] gi|22136390|gb|AAM91273.1| pyrophosphate-dependent phosphofructo-1-kinase-like protein [Arabidopsis thaliana] gi|332010109|gb|AED97492.1| 6-phosphofructokinase 4 [Arabidopsis thaliana]</td><td>113</td><td>530</td><td>4.00E-34</td><td>469.0</td><td>70.8</td><td>77.0</td><td>6-phosphofructokinase 4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G61580.1 | Symbols: PFK4 | phosphofructokinase 4 | chr5:24761150-24763827 FORWARD LENGTH=530</td><td>113</td><td>530</td><td>7.00E-37</td><td>469.0</td><td>70.8</td><td>77.0</td></tr>
<tr><td>Rsa1.0_00383.1.g12663.t1</td><td>ref|XP_002866451.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312286|gb|EFH42710.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>939</td><td>954</td><td>0</td><td>101.6</td><td>85.7</td><td>91.4</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G61730.1 | Symbols: ATATH11, ATH11 | ABC2 homolog 11 | chr5:24803583-24807898 REVERSE LENGTH=940</td><td>939</td><td>940</td><td>0</td><td>100.1</td><td>83.8</td><td>89.9</td></tr>
<tr><td>Rsa1.0_00383.1.g12664.t2</td><td>sp|Q9FLT4.2|AB10A_ARATH RecName: Full=ABC transporter A family member 10; Short=ABC transporter ABCA.10; Short=AtABCA10; AltName: Full=ABC2 homolog 14</td><td>865</td><td>909</td><td>0</td><td>105.1</td><td>79.5</td><td>87.7</td><td>RecName: Full=ABC transporter A family member 10; Short=ABC transporter ABCA.10; Short=AtABCA10; AltName: Full=ABC2 homolog 14</td><td>----</td><td>----</td><td>AT5G61700.1 | Symbols: ATATH16, ATH16 | ABC2 homolog 16 | chr5:24793864-24797944 FORWARD LENGTH=888</td><td>865</td><td>888</td><td>0</td><td>102.7</td><td>75.0</td><td>85.4</td></tr>
<tr><td>Rsa1.0_00383.1.g12665.t1</td><td>ref|XP_002866452.1| cupin family protein [Arabidopsis lyrata subsp. lyrata] gi|297312287|gb|EFH42711.1| cupin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>330</td><td>210</td><td>2.00E-97</td><td>63.6</td><td>53.3</td><td>55.8</td><td>cupin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G61750.1 | Symbols: | RmlC-like cupins superfamily protein | chr5:24812804-24813436 REVERSE LENGTH=210</td><td>330</td><td>210</td><td>5.00E-97</td><td>63.6</td><td>52.7</td><td>56.1</td></tr>
<tr><td>Rsa1.0_00383.1.g12666.t1</td><td>ref|XP_002875982.1| hypothetical protein ARALYDRAFT_906265 [Arabidopsis lyrata subsp. lyrata] gi|297321820|gb|EFH52241.1| hypothetical protein ARALYDRAFT_906265 [Arabidopsis lyrata subsp. lyrata]</td><td>989</td><td>1001</td><td>0</td><td>101.2</td><td>86.5</td><td>92.0</td><td>hypothetical protein ARALYDRAFT_906265</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G49670.1 | Symbols: BAM2 | Leucine-rich receptor-like protein kinase family protein | chr3:18417741-18420836 FORWARD LENGTH=1002</td><td>989</td><td>1002</td><td>0</td><td>101.3</td><td>85.6</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00383.1.g12667.t1</td><td>gb|EOA26692.1| hypothetical protein CARUB_v10022776mg [Capsella rubella]</td><td>269</td><td>676</td><td>2.00E-18</td><td>251.3</td><td>21.6</td><td>27.1</td><td>hypothetical protein CARUB_v10022776mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G42320.2 | Symbols: | nucleolar protein gar2-related | chr2:17628102-17630657 FORWARD LENGTH=669</td><td>269</td><td>669</td><td>3.00E-19</td><td>248.7</td><td>20.8</td><td>26.4</td></tr>
<tr><td>Rsa1.0_00383.1.g12668.t1</td><td>ref|NP_190539.1| 1-aminocyclopropane-1-carboxylate synthase 9 [Arabidopsis thaliana] gi|50400669|sp|Q9M2Y8.1|1A19_ARATH RecName: Full=1-aminocyclopropane-1-carboxylate synthase 9; Short=ACC synthase 9; AltName: Full=Ethylene-overproduction protein 3; AltName: Full=S-adenosyl-L-methionine methylthioadenosine-lyase 9 gi|12083192|gb|AAG48755.1|AF332391_1 1-aminocyclopropane-1-carboxylate synthase ACS9 [Arabidopsis thaliana] gi|6723415|emb|CAB66908.1| 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana] gi|332645057|gb|AEE78578.1| 1-aminocyclopropane-1-carboxylate synthase 9 [Arabidopsis thaliana]</td><td>470</td><td>470</td><td>0</td><td>100.0</td><td>97.4</td><td>99.1</td><td>1-aminocyclopropane-1-carboxylate synthase 9</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G49700.1 | Symbols: ETO3, ACS9, AtACS9 | 1-aminocyclopropane-1-carboxylate synthase 9 | chr3:18434470-18436141 REVERSE LENGTH=470</td><td>470</td><td>470</td><td>0</td><td>100.0</td><td>97.4</td><td>99.1</td></tr>
<tr><td>Rsa1.0_00383.1.g12669.t1</td><td>ref|XP_002875993.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297321831|gb|EFH52252.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>580</td><td>731</td><td>0</td><td>126.0</td><td>80.7</td><td>90.0</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G49740.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:18447788-18450001 FORWARD LENGTH=737</td><td>580</td><td>737</td><td>0</td><td>127.1</td><td>79.7</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00383.1.g12670.t1</td><td>ref|XP_002875994.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321832|gb|EFH52253.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>95</td><td>147</td><td>3.00E-16</td><td>154.7</td><td>51.6</td><td>65.3</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_00383.1.g12671.t1	ref|NP_190548.1| Carbohydrate-binding protein [Arabidopsis thaliana] gi|6723424|emb|CAB66917.1| putative protein [Arabidopsis thaliana] gi|44681372|gb|AAS47626.1| At3g49790 [Arabidopsis thaliana] gi|46931272|gb|AAT06440.1| At3g49790 [Arabidopsis thaliana] gi|110737624|dbj|BAF00753.1| hypothetical protein [Arabidopsis thaliana] gi|332645069|gb|AEE78590.1| Carbohydrate-binding protein [Arabidopsis thaliana]	357	366	1.00E-150	102.5	81.5	90.5	Carbohydrate-binding protein	gbpln	Arabidopsis thaliana	AT3G49790.1 | Symbols: | Carbohydrate-binding protein | chr3:18468296-18469396 REVERSE LENGTH=366	357	366	1.00E-153	102.5	81.5	90.5
Rsa1.0_00383.1.g12672.t1	ref|XP_002876001.1| hypothetical protein ARALYDRAFT_485345 [Arabidopsis lyrata subsp. lyrata] gi|297321839|gb|EFH52260.1| hypothetical protein ARALYDRAFT_485345 [Arabidopsis lyrata subsp. lyrata]	228	286	1.00E-55	125.4	50.0	59.6	hypothetical protein ARALYDRAFT_485345	gbpln	Arabidopsis lyrata	AT3G49850.1 | Symbols: TRB3, ATTRB3, TBP2 | telomere repeat binding factor 3 | chr3:18489451-18490731 FORWARD LENGTH=295	228	295	1.00E-55	129.4	49.1	59.2
Rsa1.0_00383.1.g12673.t1	gb|EOA24807.1| hypothetical protein CARUB_v10018087mg [Capsella rubella]	184	184	1.00E-101	100.0	98.4	98.4	hypothetical protein CARUB_v10018087mg	gbpln	Capsella rubella	AT3G49870.1 | Symbols: ATARLA1C, ARLA1C | ADP-ribosylation factor-like A1C | chr3:18492674-18494021 REVERSE LENGTH=184	184	184	1.00E-102	100.0	97.8	97.8
Rsa1.0_00383.1.g12674.t1	gb|AAM65029.1| unknown [Arabidopsis thaliana]	224	220	3.00E-84	98.2	71.4	81.3	unknown	gbpln	Arabidopsis thaliana	AT3G49890.1 | Symbols: | unknown protein; Has 27 Blast hits to 27 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:18499296-18500501 FORWARD LENGTH=220	224	220	1.00E-86	98.2	71.9	80.8
Rsa1.0_00383.1.g12675.t1	ref|NP_190560.1| 60S ribosomal protein L26-1 [Arabidopsis thaliana] gi|297816242|ref|XP_002876004.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] gi|27735242|sp|P51414.2|RL261_ARATH RecName: Full=60S ribosomal protein L26-1 gi|13877791|gb|AAK43973.1|AF370158_1 putative 60S ribosomal protein [Arabidopsis thaliana] gi|6723436|emb|CAB66929.1| 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana] gi|16323426|gb|AAL15207.1| putative 60S ribosomal protein [Arabidopsis thaliana] gi|23397084|gb|AAN31827.1| putative 60S ribosomal protein [Arabidopsis thaliana] gi|297321842|gb|EFH52263.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] gi|332645084|gb|AEE78605.1| 60S ribosomal protein L26-1 [Arabidopsis thaliana]	146	146	2.00E-76	100.0	97.3	99.3	60S ribosomal protein L26-1	gbpln	Arabidopsis lyrata	AT3G49910.1 | Symbols: | Translation protein SH3-like family protein | chr3:18504311-18504751 FORWARD LENGTH=146	146	146	6.00E-79	100.0	97.3	99.3
Rsa1.0_00383.1.g12676.t1	ref|XP_002877711.1| hypothetical protein ARALYDRAFT_323570 [Arabidopsis lyrata subsp. lyrata] gi|297323549|gb|EFH53970.1| hypothetical protein ARALYDRAFT_323570 [Arabidopsis lyrata subsp. lyrata]	140	276	6.00E-32	197.1	45.7	50.0	hypothetical protein ARALYDRAFT_323570	gbpln	Arabidopsis lyrata	AT5G67500.1 | Symbols: VDAC2, ATVDAC2 | voltage dependent anion channel 2 | chr5:26935223-26937123 FORWARD LENGTH=276	140	276	1.00E-32	197.1	44.3	47.9
Rsa1.0_00383.1.g12677.t1	gb|AAG50701.1|AC079604_8 hypothetical protein [Arabidopsis thaliana]	391	1453	9.00E-71	371.6	38.9	42.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G58060.1 | Symbols: | RNA helicase family protein | chr1:21489480-21501775 REVERSE LENGTH=1459	391	1459	2.00E-73	373.1	38.9	42.7
Rsa1.0_00383.1.g12678.t3	ref|XP_002877711.1| hypothetical protein ARALYDRAFT_323570 [Arabidopsis lyrata subsp. lyrata] gi|297323549|gb|EFH53970.1| hypothetical protein ARALYDRAFT_323570 [Arabidopsis lyrata subsp. lyrata]	144	276	7.00E-46	191.7	61.1	69.4	hypothetical protein ARALYDRAFT_323570	gbpln	Arabidopsis lyrata	AT5G67500.1 | Symbols: VDAC2, ATVDAC2 | voltage dependent anion channel 2 | chr5:26935223-26937123 FORWARD LENGTH=276	144	276	5.00E-46	191.7	59.0	68.1
Rsa1.0_00383.1.g12679.t1	gb|AAM19784.1| AT5g42080/MJC20_19 [Arabidopsis thaliana] gi|24111387|gb|AAN46817.1| At5g42080/MJC20_19 [Arabidopsis thaliana]	85	610	1.00E-14	717.6	48.2	49.4	AT5g42080/MJC20_19	gbpln	Arabidopsis thaliana	AT5G42080.3 | Symbols: DL1 | dynamin-like protein | chr5:16820661-16824536 REVERSE LENGTH=604	85	604	2.00E-17	710.6	48.2	49.4
Rsa1.0_00383.1.g12680.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00383.1.g12681.t1	gb|EOA24663.1| hypothetical protein CARUB_v10017944mg [Capsella rubella]	238	240	1.00E-102	100.8	81.9	87.8	hypothetical protein CARUB_v10017944mg	gbpln	Capsella rubella	AT3G49940.1 | Symbols: LBD38 | LOB domain-containing protein 38 | chr3:18514465-18515302 FORWARD LENGTH=247	238	247	4.00E-98	103.8	80.7	87.8
Rsa1.0_00383.1.g12682.t1	gb|ABL97967.1| R2R3-MYB transcription factor [Brassica rapa]	345	266	2.00E-87	77.1	54.2	62.0	R2R3-MYB transcription factor	gbpln	Brassica rapa	AT3G50060.1 | Symbols: MYB77 | myb domain protein 77 | chr3:18558146-18559051 REVERSE LENGTH=301	345	301	6.00E-89	87.2	57.1	64.1
Rsa1.0_00383.1.g12683.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00383.1.g12684.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00383.1.g12685.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	432	1486	1.00E-106	344.0	47.2	65.3	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	432	237	2.00E-28	54.9	16.9	27.8
Rsa1.0_00383.1.g12686.t1	ref|NP_190576.1| cyclin-D3-3 [Arabidopsis thaliana] gi|75313638|sp|Q9SN11.1|CCD33_ARATH RecName: Full=Cyclin-D3-3; AltName: Full=G1/S-specific cyclin-D3-3; Short=CycD3;3 gi|6522928|emb|CAB62115.1| cyclin D3-like protein [Arabidopsis thaliana] gi|15450595|gb|AAK96569.1| AT3g50070/F3A4_150 [Arabidopsis thaliana] gi|17380632|gb|AAL36079.1| AT3g50070/F3A4_150 [Arabidopsis thaliana] gi|21593092|gb|AAM65041.1| cyclin D3-like protein [Arabidopsis thaliana] gi|332645102|gb|AEE78623.1| cyclin-D3-3 [Arabidopsis thaliana]	344	361	1.00E-129	104.9	74.1	82.0	cyclin-D3-3	gbpln	Arabidopsis thaliana	AT3G50070.1 | Symbols: CYCD3;3 | CYCLIN D3;3 | chr3:18565322-18566669 REVERSE LENGTH=361	344	361	1.00E-132	104.9	74.1	82.0
Rsa1.0_00383.1.g12687.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	761	1374	0	180.6	54.0	72.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	761	575	1.00E-173	75.6	37.3	52.8
Rsa1.0_00383.1.g12688.t1	ref|XP_002877728.1| hypothetical protein ARALYDRAFT_485369 [Arabidopsis lyrata subsp. lyrata] gi|297323566|gb|EFH53987.1| hypothetical protein ARALYDRAFT_485369 [Arabidopsis lyrata subsp. lyrata]	610	633	0	103.8	84.4	89.2	hypothetical protein ARALYDRAFT_485369	gbpln	Arabidopsis lyrata	AT3G50110.1 | Symbols: ATPEN3, PEN3 | PTEN 3 | chr3:18580777-18583929 REVERSE LENGTH=632	610	632	0	103.6	83.4	88.7
Rsa1.0_00383.1.g12689.t1	gb|EOA25901.1| hypothetical protein CARUB_v10019280mg [Capsella rubella]	59	254	5.00E-19	430.5	78.0	83.1	hypothetical protein CARUB_v10019280mg	gbpln	Capsella rubella	AT3G50410.1 | Symbols: OBP1 | OBF binding protein 1 | chr3:18709872-18710633 FORWARD LENGTH=253	59	253	9.00E-21	428.8	76.3	79.7
Rsa1.0_00383.1.g12690.t1	ref|NP_190611.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75202753|sp|Q9SCT2.1|PP277_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g50420 gi|6561982|emb|CAB62471.1| putative protein [Arabidopsis thaliana] gi|332645144|gb|AEE78665.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	713	794	0	111.4	80.5	87.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G50420.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:18710871-18713649 REVERSE LENGTH=794	713	794	0	111.4	80.5	87.8
Rsa1.0_00383.1.g12691.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00383.1.g12692.t1	gb|EOA24580.1| hypothetical protein CARUB_v10017842mg [Capsella rubella]	262	266	1.00E-128	101.5	82.8	91.6	hypothetical protein CARUB_v10017842mg	gbpln	Capsella rubella	AT3G50440.1 | Symbols: ATMES10, MES10 | methyl esterase 10 | chr3:18717392-18718435 REVERSE LENGTH=288	262	288	1.00E-127	109.9	80.5	88.9
Rsa1.0_00383.1.g12693.t1	ref|NP_001190047.1| serine/threonine-protein kinase SRK2D [Arabidopsis thaliana] gi|332645152|gb|AEE78673.1| serine/threonine-protein kinase SRK2D [Arabidopsis thaliana]	80	369	6.00E-22	461.3	85.0	85.0	serine/threonine-protein kinase SRK2D	gbpln	Arabidopsis thaliana	AT3G50500.2 | Symbols: SNRK2.2 | SNF1-related protein kinase 2.2 | chr3:18741805-18743904 REVERSE LENGTH=369	80	369	1.00E-24	461.3	85.0	85.0
Rsa1.0_00383.1.g12694.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00383.1.g12695.t1	ref|XP_002876034.1| hypothetical protein ARALYDRAFT_485398 [Arabidopsis lyrata subsp. lyrata] gi|37359455|gb|AAP45325.1| HR3 [Arabidopsis lyrata] gi|297321872|gb|EFH52293.1| hypothetical protein ARALYDRAFT_485398 [Arabidopsis lyrata subsp. lyrata]	213	213	2.00E-79	100.0	71.8	80.8	hypothetical protein ARALYDRAFT_485398	gbpln	Arabidopsis lyrata	AT3G50470.1 | Symbols: HR3, MLA10 | homolog of RPW8 3 | chr3:18729146-18730162 FORWARD LENGTH=213	213	213	4.00E-74	100.0	70.9	79.8

Rsa1.0_00383.1.g12696.t1	ref|NP_190616.1| RPW8-like protein 3 [Arabidopsis thaliana] gi|12958164|gb|AAK09268.1|AF273059_3 HR3 [Arabidopsis thaliana] gi|6561987|emb|CAB62476.1| hypothetical protein [Arabidopsis thaliana] gi|51969642|dbj|BAD43513.1| hypothetical protein [Arabidopsis thaliana] gi|332645149|gb|AEE78670.1| RPW8-like protein 3 [Arabidopsis thaliana]	133	213	3.00E-31	160.2	60.2	69.2	RPW8-like protein 3	gbpln	Arabidopsis thaliana	AT3G50470.1 | Symbols: HR3, MLA10 | homolog of RPW8 3 | chr3:18729146-18730162 FORWARD LENGTH=213	133	213	6.00E-34	160.2	60.2	69.2
Rsa1.0_00383.1.g12697.t1	ref|XP_002885880.1| hypothetical protein ARALYDRAFT_899583 [Arabidopsis lyrata subsp. lyrata] gi|297331720|gb|EFH62139.1| hypothetical protein ARALYDRAFT_899583 [Arabidopsis lyrata subsp. lyrata]	203	183	2.00E-17	90.1	28.6	46.8	hypothetical protein ARALYDRAFT_899583	gbpln	Arabidopsis lyrata	AT5G33330.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:12591754-12592896 REVERSE LENGTH=183	203	183	3.00E-18	90.1	26.1	38.9
Rsa1.0_00384.1.g12698.t1	gb|EOA29555.1| hypothetical protein CARUB_v10015898mg [Capsella rubella]	181	163	3.00E-75	90.1	80.7	87.8	hypothetical protein CARUB_v10015898mg	gbpln	Capsella rubella	AT3G11090.1 | Symbols: LBD21 | LOB domain-containing protein 21 | chr3:3475036-3475533 FORWARD LENGTH=165	181	165	1.00E-76	91.2	82.3	87.8
Rsa1.0_00384.1.g12699.t1	ref|NP_187718.1| outer membrane OMP85-like protein [Arabidopsis thaliana] gi|6016688|gb|AAF01515.1|AC009991_11 unknown protein [Arabidopsis thaliana] gi|12321882|gb|AAG50978.1|AC073395_20 unknown protein; 4967-6981 [Arabidopsis thaliana] gi|20466221|gb|AAM20428.1| unknown protein [Arabidopsis thaliana] gi|25084079|gb|AAN72169.1| unknown protein [Arabidopsis thaliana] gi|332641478|gb|AEE74999.1| outer membrane OMP85-like protein [Arabidopsis thaliana]	494	520	0	105.3	78.5	87.9	outer membrane OMP85-like protein	gbpln	Arabidopsis thaliana	AT3G11070.1 | Symbols: | Outer membrane OMP85 family protein | chr3:3467801-3469815 FORWARD LENGTH=520	494	520	0	105.3	78.5	87.9
Rsa1.0_00384.1.g12700.t1	ref|XP_002882712.1| hypothetical protein ARALYDRAFT_317904 [Arabidopsis lyrata subsp. lyrata] gi|297328552|gb|EFH58971.1| hypothetical protein ARALYDRAFT_317904 [Arabidopsis lyrata subsp. lyrata]	120	355	1.00E-35	295.8	64.2	75.0	hypothetical protein ARALYDRAFT_317904	gbpln	Arabidopsis lyrata	AT2G24645.1 | Symbols: | Transcriptional factor B3 family protein | chr2:10480728-10482650 REVERSE LENGTH=490	120	490	1.00E-19	408.3	45.0	60.0
Rsa1.0_00384.1.g12701.t2	ref|XP_002882711.1| ATFER2 [Arabidopsis lyrata subsp. lyrata] gi|297328551|gb|EFH58970.1| ATFER2 [Arabidopsis lyrata subsp. lyrata]	254	250	1.00E-119	98.4	85.0	92.5	ATFER2	gbpln	Arabidopsis lyrata	AT3G11050.1 | Symbols: ATFER2, FER2 | ferritin 2 | chr3:3463651-3465294 FORWARD LENGTH=253	254	253	1.00E-121	99.6	85.8	92.9
Rsa1.0_00384.1.g12702.t1	ref|NP_187714.1| protein trichome birefringence-like 32 [Arabidopsis thaliana] gi|6016691|gb|AAF01518.1|AC009991_14 unknown protein [Arabidopsis thaliana] gi|27754560|gb|AAO22727.1| unknown protein [Arabidopsis thaliana] gi|28394093|gb|AAO42454.1| unknown protein [Arabidopsis thaliana] gi|332641474|gb|AEE74995.1| protein trichome birefringence-like 32 [Arabidopsis thaliana]	443	451	0	101.8	88.5	93.2	protein trichome birefringence-like 32	gbpln	Arabidopsis thaliana	AT3G11030.1 | Symbols: TBL32 | TRICHOME BIREFRINGENCE-LIKE 32 | chr3:3457300-3459300 REVERSE LENGTH=451	443	451	0	101.8	88.5	93.2
Rsa1.0_00384.1.g12703.t1	gb|ABV08790.1| DREB2B [Eutrema halophilum]	309	316	6.00E-96	102.3	66.3	78.3	DREB2B	gbpln	Eutrema halophilum	AT3G11020.1 | Symbols: DREB2B, DREB2 | DRE/CRT-binding protein 2B | chr3:3456009-3457001 FORWARD LENGTH=330	309	330	9.00E-83	106.8	61.8	73.8
Rsa1.0_00384.1.g12704.t1	gb|EOA29651.1| hypothetical protein CARUB_v10015153mg [Capsella rubella]	466	478	1.00E-139	102.6	61.2	71.0	hypothetical protein CARUB_v10015153mg	gbpln	Capsella rubella	AT3G11000.1 | Symbols: | DCD (Development and Cell Death) domain protein | chr3:3448442-3450283 FORWARD LENGTH=488	466	488	1.00E-138	104.7	60.7	71.9
Rsa1.0_00384.1.g12705.t1	gb|EOA32919.1| hypothetical protein CARUB_v10016246mg, partial [Capsella rubella]	201	161	5.00E-73	80.1	67.2	73.1	hypothetical protein CARUB_v10016246mg, partial	gbpln	Capsella rubella	AT3G10985.1 | Symbols: SAG20, WI12, ATWI-12 | senescence associated gene 20 | chr3:3442776-3443108 FORWARD LENGTH=110	201	110	1.00E-40	54.7	43.3	46.8
Rsa1.0_00384.1.g12706.t1	dbj|BAJ34145.1| unnamed protein product [Thellungiella halophila]	537	554	0	103.2	83.6	91.2	unnamed protein product	----	----	AT3G10980.1 | Symbols: | PLAC8 family protein | chr3:3438810-3440501 FORWARD LENGTH=563	537	563	0	104.8	79.3	86.6

Rsa1.0_00384.1.g12707.t1	ref|NP_566385.1| haloacid dehalogenase-like hydrolase [Arabidopsis thaliana] gi|332641462|gb|AEE74983.1| haloacid dehalogenase-like hydrolase [Arabidopsis thaliana]	368	365	0	99.2	90.8	93.8	haloacid dehalogenase-like hydrolase	gbpln	Arabidopsis thaliana	AT3G10970.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr3:3433276-3436077 REVERSE LENGTH=365	368	365	0	99.2	90.8	93.8
Rsa1.0_00384.1.g12708.t1	ref|NP_566384.1| adenine/guanine permease AZG1 [Arabidopsis thaliana] gi|75207346|sp|Q9SRK7.1|AZG1_ARATH RecName: Full=Adenine/guanine permease AZG1; AltName: Full=AzgA-homolog protein; AltName: Full=Protein AZAGUANINE RESISTANT 1; Short=AtAzg1 gi|6016698|gb|AAF01525.1|AC009991_21 hypothetical protein [Arabidopsis thaliana] gi|20260452|gb|AAM13124.1| unknown protein [Arabidopsis thaliana] gi|34365735|gb|AAQ65179.1| At3g10960 [Arabidopsis thaliana] gi|332641461|gb|AEE74982.1| adenine/guanine permease AZG1 [Arabidopsis thaliana]	598	579	0	96.8	88.3	93.0	adenine/guanine permease AZG1	gbpln	Arabidopsis thaliana	AT3G10960.1 | Symbols: ATAZG1, AZG1 | AZA-guanine resistant1 | chr3:3424986-3426725 REVERSE LENGTH=579	598	579	0	96.8	88.3	93.0
Rsa1.0_00384.1.g12709.t1	ref|NP_566383.1| dual-specificity protein-like phosphatase 3 [Arabidopsis thaliana] gi|75266227|sp|Q9SRK5.1|LSF2_ARATH RecName: Full=Phosphoglucan phosphatase LSF2, chloroplastic; AltName: Full=Phosphoglucan phosphatase like sex Four2; AltName: Full=Protein LIKE SEX4 2; Flags: Precursor gi|6016700|gb|AAF01527.1|AC009991_23 unknown protein [Arabidopsis thaliana] gi|87116654|gb|ABD19691.1| At3g10940 [Arabidopsis thaliana] gi|110740568|dbj|BAE98389.1| hypothetical protein [Arabidopsis thaliana] gi|332641459|gb|AEE74980.1| phosphoglucan phosphatase LSF2 [Arabidopsis thaliana]	278	282	1.00E-139	101.4	88.8	92.8	dual-specificity protein-like phosphatase 3	gbpln	Arabidopsis thaliana	AT3G10940.1 | Symbols: | dual specificity protein phosphatase (DsPTP1) family protein | chr3:3422259-3423394 REVERSE LENGTH=282	278	282	1.00E-142	101.4	88.8	92.8
Rsa1.0_00384.1.g12710.t1	gb|AAF01528.1|AC009991_24 hypothetical protein [Arabidopsis thaliana] gi|21618249|gb|AAM67299.1| unknown [Arabidopsis thaliana]	102	97	6.00E-26	95.1	72.5	79.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT5G05300.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 8 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1570102-1570410 REVERSE LENGTH=102	102	102	2.00E-16	100.0	51.0	60.8
Rsa1.0_00384.1.g12711.t1	gb|ABQ81865.1| Mn superoxide dismutase [Eutrema halophilum]	230	231	1.00E-127	100.4	95.7	97.8	Mn superoxide dismutase	gbpln	Eutrema halophilum	AT3G10920.1 | Symbols: MSD1, MEE33, ATMSD1 | manganese superoxide dismutase 1 | chr3:3418015-3419581 FORWARD LENGTH=231	230	231	1.00E-123	100.4	91.7	95.2
Rsa1.0_00384.1.g12712.t1	ref|NP_974275.1| reticulon-like protein B16 [Arabidopsis thaliana] gi|75151434|sp|Q8GYH6.1|RTNLP_ARATH RecName: Full=Reticulon-like protein B16; Short=AtRTNLB16 gi|26450318|dbj|BAC42275.1| unknown protein [Arabidopsis thaliana] gi|28827594|gb|AAO50641.1| unknown protein [Arabidopsis thaliana] gi|332641451|gb|AEE74972.1| reticulon-like protein B16 [Arabidopsis thaliana]	232	226	1.00E-110	97.4	86.2	92.7	reticulon-like protein B16	gbpln	Arabidopsis thaliana	AT3G10915.2 | Symbols: | Reticulon family protein | chr3:3416101-3417497 REVERSE LENGTH=226	232	226	1.00E-112	97.4	86.2	92.7
Rsa1.0_00384.1.g12713.t1	ref|XP_002882702.1| hypothetical protein ARALYDRAFT_341221 [Arabidopsis lyrata subsp. lyrata] gi|297328542|gb|EFH58961.1| hypothetical protein ARALYDRAFT_341221 [Arabidopsis lyrata subsp. lyrata]	346	338	1.00E-75	97.7	52.6	62.1	hypothetical protein ARALYDRAFT_341221	gbpln	Arabidopsis lyrata	AT3G10880.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G05180.1); Has 15699 Blast hits to 11378 proteins in 1134 species: Archae - 391; Bacteria - 2054; Metazoa - 6851; Fungi - 1354; Plants - 1096; Viruses - 119; Other Eukaryotes - 3834 (source: NCBI BLink). | chr3:3406092-3407131 FORWARD LENGTH=319	346	319	3.00E-77	92.2	53.2	62.4
Rsa1.0_00384.1.g12714.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00384.1.g12715.t6	ref|XP_002884817.1| hypothetical protein ARALYDRAFT_478421 [Arabidopsis lyrata subsp. lyrata] gi|297330657|gb|EFH61076.1| hypothetical protein ARALYDRAFT_478421 [Arabidopsis lyrata subsp. lyrata]	299	275	1.00E−127	92.0	75.9	83.6	hypothetical protein ARALYDRAFT_478421	gbpln	Arabidopsis lyrata	AT3G10870.1 | Symbols: MES17, ATMES17 | methyl esterase 17 | chr3:3401228−3402612 REVERSE LENGTH=276	299	276	1.00E−127	92.3	75.3	83.6
Rsa1.0_00384.1.g12716.t2	gb|EOA31272.1| hypothetical protein CARUB_v10014444mg [Capsella rubella]	359	258	1.00E−140	71.9	65.2	69.4	hypothetical protein CARUB_v10014444mg	gbpln	Capsella rubella	AT3G10850.1 | Symbols: GLX2−2, GLY2 | Metallo−hydrolase/oxidoreductase superfamily protein | chr3:3397756−3399522 REVERSE LENGTH=258	359	258	1.00E−142	71.9	65.2	69.4
Rsa1.0_00384.1.g12717.t3	gb|EOA31449.1| hypothetical protein CARUB_v10014632mg [Capsella rubella]	198	209	4.00E−81	105.6	79.3	85.9	hypothetical protein CARUB_v10014632mg	gbpln	Capsella rubella	AT3G10815.1 | Symbols: | RING/U−box superfamily protein | chr3:3385009−3385608 REVERSE LENGTH=199	198	199	5.00E−76	100.5	74.2	82.3
Rsa1.0_00384.1.g12718.t1	ref|XP_002882696.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328536|gb|EFH58955.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	282	227	4.00E−67	80.5	43.3	52.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G10780.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr3:3375161−3376334 FORWARD LENGTH=217	282	217	3.00E−67	77.0	42.2	50.4
Rsa1.0_00385.1.g12719.t1	dbj|BAJ34369.1| unnamed protein product [Thellungiella halophila]	368	384	1.00E−144	104.3	84.2	89.9	unnamed protein product	----	----	AT2G31370.5 | Symbols: | Basic−leucine zipper (bZIP) transcription factor family protein | chr2:13379448−13381037 FORWARD LENGTH=377	368	377	1.00E−145	102.4	74.5	81.0
Rsa1.0_00385.1.g12720.t1	dbj|BAJ34047.1| unnamed protein product [Thellungiella halophila]	243	241	1.00E−119	99.2	89.3	92.2	unnamed protein product	----	----	AT2G31380.1 | Symbols: STH | salt tolerance homologue | chr2:13382150−13383302 FORWARD LENGTH=238	243	238	1.00E−115	97.9	84.8	89.3
Rsa1.0_00385.1.g12721.t1	gb|EOA27492.1| hypothetical protein CARUB_v10023630mg [Capsella rubella]	326	325	1.00E−178	99.7	93.9	96.9	hypothetical protein CARUB_v10023630mg	gbpln	Capsella rubella	AT2G31390.1 | Symbols: | pfkB−like carbohydrate kinase family protein | chr2:13383635−13386116 REVERSE LENGTH=325	326	325	1.00E−178	99.7	92.3	96.6
Rsa1.0_00385.1.g12722.t1	ref|XP_002881173.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327012|gb|EFH57432.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata]	860	917	0	106.6	81.9	88.7	pentatricopeptide repeat−containing protein	gbpln	Arabidopsis lyrata	AT2G31400.1 | Symbols: GUN1 | genomes uncoupled 1 | chr2:13387201−13390550 REVERSE LENGTH=918	860	918	0	106.7	81.0	87.8
Rsa1.0_00385.1.g12723.t1	gb|EOA27918.1| hypothetical protein CARUB_v10024091mg [Capsella rubella]	198	199	4.00E−74	100.5	82.8	90.4	hypothetical protein CARUB_v10024091mg	gbpln	Capsella rubella	AT2G31410.1 | Symbols: | unknown protein; Has 1719 Blast hits to 1091 proteins in 184 species: Archae − 5; Bacteria − 24; Metazoa − 559; Fungi − 169; Plants − 192; Viruses − 1; Other Eukaryotes − 769 (source: NCBI BLink). | chr2:13392220−13392819 REVERSE LENGTH=199	198	199	2.00E−74	100.5	84.3	89.4
Rsa1.0_00385.1.g12724.t1	gb|EOA28709.1| hypothetical protein CARUB_v10024937mg, partial [Capsella rubella]	202	308	3.00E−37	152.5	40.1	59.9	hypothetical protein CARUB_v10024937mg, partial	gbpln	Capsella rubella	AT2G31420.1 | Symbols: | Domain of unknown function (DUF313) | chr2:13393364−13393993 REVERSE LENGTH=209	202	209	3.00E−36	103.5	45.0	59.9
Rsa1.0_00385.1.g12725.t1	ref|NP_180705.1| F−box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F−box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F−box protein DOR [Arabidopsis thaliana]	405	387	2.00E−96	95.6	51.9	63.5	F−box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F−box and associated interaction domains−containing protein | chr2:13407492−13408655 REVERSE LENGTH=387	405	387	5.00E−99	95.6	51.9	63.5
Rsa1.0_00385.1.g12726.t1	ref|XP_002881178.1| hypothetical protein ARALYDRAFT_482077 [Arabidopsis lyrata subsp. lyrata] gi|297327017|gb|EFH57437.1| hypothetical protein ARALYDRAFT_482077 [Arabidopsis lyrata subsp. lyrata]	453	472	1.00E−175	104.2	76.4	85.4	hypothetical protein ARALYDRAFT_482077	gbpln	Arabidopsis lyrata	AT2G31480.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G05894.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr2:13409516−13410934 REVERSE LENGTH=472	453	472	1.00E−176	104.2	77.0	85.7

Rsa1.0_00385.1.g12727.t1	ref|NP_565726.1| uncharacterized protein [Arabidopsis thaliana] gi|297822895|ref|XP_002879330.1| hypothetical protein ARALYDRAFT_902184 [Arabidopsis lyrata subsp. lyrata] gi|4582445|gb|AAD24829.1| expressed protein [Arabidopsis thaliana] gi|20198160|gb|AAM15434.1| expressed protein [Arabidopsis thaliana] gi|26451972|dbj|BAC43077.1| unknown protein [Arabidopsis thaliana] gi|28416745|gb|AAO42903.1| At2g31490 [Arabidopsis thaliana] gi|227204167|dbj|BAH56935.1| AT2G31490 [Arabidopsis thaliana] gi|297325169|gb|EFH55589.1| hypothetical protein ARALYDRAFT_902184 [Arabidopsis lyrata subsp. lyrata] gi|330253460|gb|AEC08554.1| uncharacterized protein AT2G31490 [Arabidopsis thaliana] gi|482564076|gb|EOA28266.1| hypothetical protein CARUB_v10024460mg [Capsella rubella]	152	71	7.00E-26	46.7	36.8	36.8	uncharacterized protein	gbpln	Arabidopsis lyrata	AT2G31490.1 | Symbols: | unknown protein; Has 55 Blast hits to 55 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 55; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:13412060-13413002 FORWARD LENGTH=71	152	71	2.00E-28	46.7	36.8	36.8
Rsa1.0_00385.1.g12728.t1	gb|ABK28519.1| unknown [Arabidopsis thaliana]	606	583	0	96.2	87.5	91.4	unknown	gbpln	Arabidopsis thaliana	AT2G31500.1 | Symbols: CPK24 | calcium-dependent protein kinase 24 | chr2:13414016-13416324 FORWARD LENGTH=582	606	582	0	96.0	87.5	91.4
Rsa1.0_00385.1.g12729.t1	ref|NP_180709.3| putative E3 ubiquitin-protein ligase ARI7 [Arabidopsis thaliana] gi|75328048|sp|Q84RR0.1|ARI7_ARATH RecName: Full=Probable E3 ubiquitin-protein ligase ARI7; AltName: Full=ARIADNE-like protein ARI7; AltName: Full=Protein ariadne homolog 7 gi|29125028|emb|CAD52889.1| ARIADNE-like protein ARI7 [Arabidopsis thaliana] gi|330253462|gb|AEC08556.1| putative E3 ubiquitin-protein ligase ARI7 [Arabidopsis thaliana]	559	562	0	100.5	93.0	95.3	putative E3 ubiquitin-protein ligase ARI7	gbpln	Arabidopsis thaliana	AT2G31510.1 | Symbols: ARI7, ATARI7 | IBR domain-containing protein | chr2:13416991-13421170 REVERSE LENGTH=562	559	562	0	100.5	93.0	95.3
Rsa1.0_00385.1.g12730.t1	ref|XP_002878768.1| carboxylic ester hydrolase [Arabidopsis lyrata subsp. lyrata] gi|297324607|gb|EFH55027.1| carboxylic ester hydrolase [Arabidopsis lyrata subsp. lyrata]	386	359	1.00E-172	93.0	74.6	82.9	carboxylic ester hydrolase	gbpln	Arabidopsis lyrata	AT2G24560.1 | Symbols: | GDSL-like Lipase/Acylhydrolase family protein | chr2:10431537-10432933 FORWARD LENGTH=363	386	363	1.00E-170	94.0	73.1	82.6
Rsa1.0_00385.1.g12731.t1	ref|XP_002870433.1| 40S ribosomal protein S3 [Arabidopsis lyrata subsp. lyrata] gi|297316269|gb|EFH46692.1| 40S ribosomal protein S3 [Arabidopsis lyrata subsp. lyrata]	250	248	1.00E-128	99.2	92.0	94.0	40S ribosomal protein S3	gbpln	Arabidopsis lyrata	AT5G35530.1 | Symbols: | Ribosomal protein S3 family protein | chr5:13710355-13712192 REVERSE LENGTH=248	250	248	1.00E-129	99.2	90.8	93.2
Rsa1.0_00385.1.g12732.t1	ref|NP_850169.1| uncharacterized protein [Arabidopsis thaliana] gi|42571003|ref|NP_973575.1| uncharacterized protein [Arabidopsis thaliana] gi|17528942|gb|AAL38681.1| unknown protein [Arabidopsis thaliana] gi|50897252|gb|AAT85765.1| At2g31560 [Arabidopsis thaliana] gi|222423288|dbj|BAH19620.1| AT2G31560 [Arabidopsis thaliana] gi|222423386|dbj|BAH19665.1| AT2G31560 [Arabidopsis thaliana] gi|330253466|gb|AEC08560.1| uncharacterized protein AT2G31560 [Arabidopsis thaliana] gi|330253467|gb|AEC08561.1| uncharacterized protein AT2G31560 [Arabidopsis thaliana]	192	202	2.00E-70	105.2	75.0	81.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G31560.2 | Symbols: | Protein of unknown function (DUF1685) | chr2:13436611-13437312 FORWARD LENGTH=202	192	202	8.00E-73	105.2	75.0	81.8
Rsa1.0_00385.1.g12733.t1	ref|XP_002879336.1| 40S ribosomal protein S3 [Arabidopsis lyrata subsp. lyrata] gi|297325175|gb|EFH55595.1| 40S ribosomal protein S3 [Arabidopsis lyrata subsp. lyrata]	250	250	1.00E-129	100.0	91.6	94.4	40S ribosomal protein S3	gbpln	Arabidopsis lyrata	AT2G31610.1 | Symbols: | Ribosomal protein S3 family protein | chr2:13450384-13451669 FORWARD LENGTH=250	250	250	1.00E-130	100.0	91.2	94.0

Rsa1.0_00385.1.g12734.t6	ref|XP_002881186.1| hypothetical protein ARALYDRAFT_902198 [Arabidopsis lyrata subsp. lyrata] gi|297327025|gb|EFH57445.1| hypothetical protein ARALYDRAFT_902198 [Arabidopsis lyrata subsp. lyrata]	1072	1066	0	99.4	78.5	84.9	hypothetical protein ARALYDRAFT_902198	gbpln	Arabidopsis lyrata	AT2G31650.1 | Symbols: ATX1, SDG27 | homologue of trithorax | chr2:13455448-13462181 REVERSE LENGTH=1062	1072	1062	0	99.1	77.2	84.5
Rsa1.0_00385.1.g12735.t1	ref|XP_002879337.1| hypothetical protein ARALYDRAFT_482091 [Arabidopsis lyrata subsp. lyrata] gi|297325176|gb|EFH55596.1| hypothetical protein ARALYDRAFT_482091 [Arabidopsis lyrata subsp. lyrata]	1041	1044	0	100.3	90.4	94.9	hypothetical protein ARALYDRAFT_482091	gbpln	Arabidopsis lyrata	AT2G31660.1 | Symbols: SAD2, URM9 | ARM repeat superfamily protein | chr2:13464519-13471353 FORWARD LENGTH=1040	1041	1040	0	99.9	88.9	93.9
Rsa1.0_00385.1.g12736.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00385.1.g12737.t1	#	#	#	#	#	#	#	-	----	----	AT2G31710.1 | Symbols: | Vacuolar ATPase assembly integral membrane protein VMA21-like domain | chr2:13482057-13482895 REVERSE LENGTH=105	76	105	1.00E-11	138.2	39.5	43.4
Rsa1.0_00385.1.g12738.t1	gb|EOA29031.1| hypothetical protein CARUB_v10025285mg [Capsella rubella]	558	514	0	92.1	69.2	77.6	hypothetical protein CARUB_v10025285mg	gbpln	Capsella rubella	AT2G31865.1 | Symbols: PARG2 | poly(ADP-ribose) glycohydrolase 2 | chr2:13546790-13549472 REVERSE LENGTH=522	558	522	0	93.5	66.1	74.9
Rsa1.0_00385.1.g12739.t1	ref|XP_002879346.1| hypothetical protein ARALYDRAFT_902223 [Arabidopsis lyrata subsp. lyrata] gi|297325185|gb|EFH55605.1| hypothetical protein ARALYDRAFT_902223 [Arabidopsis lyrata subsp. lyrata]	407	378	2.00E-28	92.9	27.3	37.1	hypothetical protein ARALYDRAFT_902223	gbpln	Arabidopsis lyrata	AT2G31720.1 | Symbols: | Domain of unknown function (DUF313) | chr2:13485034-13485975 REVERSE LENGTH=313	407	313	3.00E-26	76.9	24.6	34.2
Rsa1.0_00385.1.g12740.t1	ref|NP_565720.1| inhibitor-3 [Arabidopsis thaliana] gi|20197895|gb|AAM15305.1| Expressed protein [Arabidopsis thaliana] gi|21555013|gb|AAM63754.1| unknown [Arabidopsis thaliana] gi|106879151|gb|ABF82605.1| At2g31305 [Arabidopsis thaliana] gi|330253431|gb|AEC08525.1| inhibitor-3 [Arabidopsis thaliana]	107	107	1.00E-33	100.0	81.3	87.9	inhibitor-3	gbpln	Arabidopsis thaliana	AT2G31305.1 | Symbols: INH3 | inhibitor-3 | chr2:13350909-13351232 FORWARD LENGTH=107	107	107	2.00E-36	100.0	81.3	87.9
Rsa1.0_00385.1.g12741.t2	dbj|BAJ34071.1| unnamed protein product [Thellungiella halophila]	716	699	0	97.6	78.2	83.4	unnamed protein product	----	----	AT2G31280.1 | Symbols: CPUORF7 | conserved peptide upstream open reading frame 7 | chr2:13339678-13343424 FORWARD LENGTH=720	716	720	0	100.6	77.0	83.5
Rsa1.0_00385.1.g12742.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00386.1.g12743.t1	ref|NP_191803.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75335717|sp|Q9LZP6.1|FBL70_ARATH RecName: Full=F-box/LRR-repeat protein At3g62440 gi|7340715|emb|CAB82958.1| putative protein [Arabidopsis thaliana] gi|67633712|gb|AAY78780.1| F-box family protein [Arabidopsis thaliana] gi|332646832|gb|AEE80353.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	415	457	7.00E-62	110.1	37.6	51.3	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT3G62440.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:23096104-23097726 REVERSE LENGTH=457	415	457	2.00E-64	110.1	37.6	51.3
Rsa1.0_00386.1.g12744.t1	ref|XP_002873681.1| hypothetical protein ARALYDRAFT_488304 [Arabidopsis lyrata subsp. lyrata] gi|297319518|gb|EFH49940.1| hypothetical protein ARALYDRAFT_488304 [Arabidopsis lyrata subsp. lyrata]	580	629	0	108.4	72.6	83.3	hypothetical protein ARALYDRAFT_488304	gbpln	Arabidopsis lyrata	AT5G14620.1 | Symbols: DRM2, DMT7 | domains rearranged methyltransferase 2 | chr5:4715429-4718578 REVERSE LENGTH=626	580	626	0	107.9	70.0	80.5
Rsa1.0_00386.1.g12745.t1	ref|NP_001190309.1| DEAD-box ATP-dependent RNA helicase 46 [Arabidopsis thaliana] gi|114153757|sp|Q9LYJ9.2|RH46_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 46 gi|332004672|gb|AED92055.1| DEAD-box ATP-dependent RNA helicase 46 [Arabidopsis thaliana]	686	645	0	94.0	81.3	85.7	DEAD-box ATP-dependent RNA helicase 46	gbpln	Arabidopsis thaliana	AT5G14610.2 | Symbols: | DEAD box RNA helicase family protein | chr5:4711271-4714713 FORWARD LENGTH=645	686	645	0	94.0	81.3	85.7

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<tr><td>Rsa1.0_00386.1.g12746.t1</td><td>gb|EOA19719.1| hypothetical protein CARUB_v10003766mg [Capsella rubella]</td><td>80</td><td>79</td><td>4.00E-28</td><td>98.8</td><td>77.5</td><td>86.3</td><td>hypothetical protein CARUB_v10003766mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G14602.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: Methyltransferase-related protein (TAIR:AT5G18150.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4709436-4709678 FORWARD LENGTH=80</td><td>80</td><td>80</td><td>1.00E-27</td><td>100.0</td><td>72.5</td><td>83.8</td></tr>
<tr><td>Rsa1.0_00386.1.g12747.t1</td><td>ref|XP_002873677.1| ATNRT2.7 [Arabidopsis lyrata subsp. lyrata] gi|297319514|gb|EFH49936.1| ATNRT2.7 [Arabidopsis lyrata subsp. lyrata]</td><td>482</td><td>490</td><td>0</td><td>101.7</td><td>83.2</td><td>90.2</td><td>ATNRT2.7</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G14570.1 | Symbols: ATNRT2.7, NRT2.7 | high affinity nitrate transporter 2.7 | chr5:4695331-4696890 REVERSE LENGTH=493</td><td>482</td><td>493</td><td>0</td><td>102.3</td><td>84.0</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00386.1.g12748.t1</td><td>gb|EOA22128.1| hypothetical protein CARUB_v10002686mg [Capsella rubella]</td><td>538</td><td>541</td><td>0</td><td>100.6</td><td>75.7</td><td>81.8</td><td>hypothetical protein CARUB_v10002686mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G01560.1 | Symbols: | Protein of unknown function (DUF1421) | chr3:219884-221707 FORWARD LENGTH=511</td><td>538</td><td>511</td><td>1.00E-121</td><td>95.0</td><td>58.7</td><td>66.5</td></tr>
<tr><td>Rsa1.0_00386.1.g12749.t1</td><td>gb|EOA22220.1| hypothetical protein CARUB_v10002807mg [Capsella rubella]</td><td>332</td><td>334</td><td>0</td><td>100.6</td><td>97.0</td><td>97.9</td><td>hypothetical protein CARUB_v10002807mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G14530.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:4684782-4686865 REVERSE LENGTH=330</td><td>332</td><td>330</td><td>0</td><td>99.4</td><td>95.2</td><td>97.0</td></tr>
<tr><td>Rsa1.0_00386.1.g12750.t1</td><td>gb|EOA20817.1| hypothetical protein CARUB_v10001154mg [Capsella rubella]</td><td>382</td><td>387</td><td>0</td><td>101.3</td><td>88.7</td><td>95.5</td><td>hypothetical protein CARUB_v10001154mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G14480.1 | Symbols: | beta-1,4-N-acetylglucosaminyltransferase family protein | chr5:4667984-4669693 FORWARD LENGTH=387</td><td>382</td><td>387</td><td>0</td><td>101.3</td><td>89.0</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00386.1.g12751.t1</td><td>gb|EOA21250.1| hypothetical protein CARUB_v10001600mg [Capsella rubella]</td><td>282</td><td>295</td><td>3.00E-88</td><td>104.6</td><td>73.4</td><td>84.4</td><td>hypothetical protein CARUB_v10001600mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G14440.2 | Symbols: | Surfeit locus protein 2 (SURF2) | chr5:4656065-4657807 REVERSE LENGTH=291</td><td>282</td><td>291</td><td>3.00E-89</td><td>103.2</td><td>67.7</td><td>76.6</td></tr>
<tr><td>Rsa1.0_00386.1.g12752.t1</td><td>gb|EOA20582.1| hypothetical protein CARUB_v10000894mg [Capsella rubella]</td><td>460</td><td>466</td><td>0</td><td>101.3</td><td>87.0</td><td>90.9</td><td>hypothetical protein CARUB_v10000894mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G14420.2 | Symbols: RGLG2 | RING domain ligase2 | chr5:4648355-4650563 REVERSE LENGTH=468</td><td>460</td><td>468</td><td>0</td><td>101.7</td><td>86.3</td><td>90.7</td></tr>
<tr><td>Rsa1.0_00386.1.g12753.t1</td><td>ref|XP_002871617.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317454|gb|EFH47876.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>435</td><td>381</td><td>0</td><td>87.6</td><td>79.5</td><td>83.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G14400.1 | Symbols: CYP724A1 | cytochrome P450, family 724, subfamily A, polypeptide 1 | chr5:4644128-4646382 FORWARD LENGTH=367</td><td>435</td><td>367</td><td>0</td><td>84.4</td><td>74.9</td><td>79.1</td></tr>
<tr><td>Rsa1.0_00386.1.g12754.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00386.1.g12755.t1</td><td>ref|XP_002873663.1| hypothetical protein ARALYDRAFT_488279 [Arabidopsis lyrata subsp. lyrata] gi|297319500|gb|EFH49922.1| hypothetical protein ARALYDRAFT_488279 [Arabidopsis lyrata subsp. lyrata]</td><td>334</td><td>369</td><td>1.00E-174</td><td>110.5</td><td>91.9</td><td>95.8</td><td>hypothetical protein ARALYDRAFT_488279</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G14390.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:4637551-4639575 REVERSE LENGTH=369</td><td>334</td><td>369</td><td>1.00E-176</td><td>110.5</td><td>91.0</td><td>95.5</td></tr>
<tr><td>Rsa1.0_00386.1.g12756.t1</td><td>ref|XP_002873661.1| hypothetical protein ARALYDRAFT_488277 [Arabidopsis lyrata subsp. lyrata] gi|297319498|gb|EFH49920.1| hypothetical protein ARALYDRAFT_488277 [Arabidopsis lyrata subsp. lyrata]</td><td>333</td><td>335</td><td>1.00E-127</td><td>100.6</td><td>78.4</td><td>85.6</td><td>hypothetical protein ARALYDRAFT_488277</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G14370.1 | Symbols: | CCT motif family protein | chr5:4632147-4633651 REVERSE LENGTH=339</td><td>333</td><td>339</td><td>1.00E-121</td><td>101.8</td><td>76.0</td><td>84.1</td></tr>
<tr><td>Rsa1.0_00386.1.g12757.t1</td><td>ref|NP_196940.1| ubiquitin family protein [Arabidopsis thaliana] gi|7573461|emb|CAB87775.1| putative protein [Arabidopsis thaliana] gi|45752638|gb|AAS76217.1| At5g14360 [Arabidopsis thaliana] gi|46359805|gb|AAS88766.1| At5g14360 [Arabidopsis thaliana] gi|332004639|gb|AED92022.1| ubiquitin family protein [Arabidopsis thaliana]</td><td>161</td><td>163</td><td>1.00E-72</td><td>101.2</td><td>90.7</td><td>95.7</td><td>ubiquitin family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14360.1 | Symbols: | Ubiquitin-like superfamily protein | chr5:4631038-4631641 FORWARD LENGTH=163</td><td>161</td><td>163</td><td>4.00E-75</td><td>101.2</td><td>90.7</td><td>95.7</td></tr>
<tr><td>Rsa1.0_00386.1.g12758.t1</td><td>ref|NP_001078582.1| early nodulin-like protein 21 [Arabidopsis thaliana] gi|332004637|gb|AED92020.1| early nodulin-like protein 21 [Arabidopsis thaliana]</td><td>145</td><td>145</td><td>7.00E-63</td><td>100.0</td><td>80.7</td><td>86.2</td><td>early nodulin-like protein 21</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14345.1 | Symbols: ENODL21, AtENODL21 | early nodulin-like protein 21 | chr5:4626175-4626722 REVERSE LENGTH=145</td><td>145</td><td>145</td><td>2.00E-65</td><td>100.0</td><td>80.7</td><td>86.2</td></tr>
<tr><td>Rsa1.0_00386.1.g12759.t1</td><td>ref|NP_196937.1| uncharacterized protein [Arabidopsis thaliana] gi|7573458|emb|CAB87772.1| putative protein [Arabidopsis thaliana] gi|332004635|gb|AED92018.1| uncharacterized protein AT5G14330 [Arabidopsis thaliana]</td><td>77</td><td>128</td><td>2.00E-15</td><td>166.2</td><td>76.6</td><td>80.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14330.1 | Symbols: | unknown protein; Has 8 Blast hits to 8 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:4619947-4620551 REVERSE LENGTH=128</td><td>77</td><td>128</td><td>4.00E-18</td><td>166.2</td><td>76.6</td><td>80.5</td></tr>
<tr><td>Rsa1.0_00386.1.g12760.t1</td><td>dbj|BAJ34069.1| unnamed protein product [Thellungiella halophila]</td><td>680</td><td>429</td><td>0</td><td>63.1</td><td>52.4</td><td>57.6</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G14250.1 | Symbols: COP13, CSN3, FUS11 | Proteasome component (PCI) domain protein | chr5:4597970-4600561 FORWARD LENGTH=429</td><td>680</td><td>429</td><td>0</td><td>63.1</td><td>49.3</td><td>55.4</td></tr>
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Rsa1.0_00386.1.g12761.t1	gb|EOA19327.1| hypothetical protein CARUB_v10003397mg [Capsella rubella]	408	408	0	100.0	90.7	94.4	hypothetical protein CARUB_v10003397mg	gbpln	Capsella rubella	AT5G14200.1 | Symbols: ATIMD1, IMD1 | isopropylmalate dehydrogenase 1 | chr5:4576220-4578111 FORWARD LENGTH=409	408	409	0	100.2	90.9	94.6
Rsa1.0_00386.1.g12762.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00386.1.g12763.t2	gb|EOA21047.1| hypothetical protein CARUB_v10001386mg [Capsella rubella]	400	335	1.00E-135	83.8	59.0	65.0	hypothetical protein CARUB_v10001386mg	gbpln	Capsella rubella	AT5G14130.1 | Symbols: | Peroxidase superfamily protein | chr5:4558862-4560028 REVERSE LENGTH=330	400	330	1.00E-134	82.5	57.8	64.8
Rsa1.0_00386.1.g12764.t1	ref|XP_002528055.1| conserved hypothetical protein [Ricinus communis] gi|223532516|gb|EEF34305.1| conserved hypothetical protein [Ricinus communis]	75	76	6.00E-25	101.3	70.7	86.7	conserved hypothetical protein	gbpln	Ricinus communis	AT5G14105.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4552169-4552901 REVERSE LENGTH=76	75	76	1.00E-25	101.3	86.7	96.0
Rsa1.0_00386.1.g12765.t1	gb|EOA21767.1| hypothetical protein CARUB_v10002222mg [Capsella rubella]	138	140	6.00E-65	101.4	89.1	95.7	hypothetical protein CARUB_v10002222mg	gbpln	Capsella rubella	AT5G14070.1 | Symbols: ROXY2 | Thioredoxin superfamily protein | chr5:4541915-4542337 FORWARD LENGTH=140	138	140	3.00E-67	101.4	89.9	94.9
Rsa1.0_00387.1.g12766.t1	ref|XP_002877087.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297322925|gb|EFH53346.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	209	252	3.00E-88	120.6	85.6	91.9	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT3G28007.1 | Symbols: SWEET4, AtSWEET4 | Nodulin MtN3 family protein | chr3:10408243-10409633 REVERSE LENGTH=251	209	251	1.00E-84	120.1	87.6	91.9
Rsa1.0_00387.1.g12767.t1	ref|XP_002875418.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321256|gb|EFH51677.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1545	1463	0	94.7	71.3	79.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G28030.1 | Symbols: UVH3, UVR1 | 5'-3' exonuclease family protein | chr3:10424321-10431178 FORWARD LENGTH=1479	1545	1479	0	95.7	70.1	78.1
Rsa1.0_00387.1.g12768.t1	ref|NP_189443.2| probably inactive leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|75335370|sp|Q9LRT1.1|Y3804_ARATH RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040; Flags: Precursor gi|11994124|dbj|BAB01126.1| receptor protein kinase [Arabidopsis thaliana] gi|224589581|gb|ACN59324.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332643873|gb|AEE77394.1| probably inactive leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	1014	1016	0	100.2	87.6	93.4	probably inactive leucine-rich repeat receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT3G28040.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr3:10435139-10438268 FORWARD LENGTH=1016	1014	1016	0	100.2	87.6	93.4
Rsa1.0_00387.1.g12769.t1	ref|XP_002875422.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321260|gb|EFH51681.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	363	363	0	100.0	92.3	95.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G40210.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:16073725-16076088 REVERSE LENGTH=339	363	339	1.00E-115	93.4	55.9	72.7
Rsa1.0_00387.1.g12770.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	346	1534	2.00E-99	443.4	56.4	70.2	F17L21.7	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00387.1.g12771.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1789	1270	0	71.0	35.6	47.7	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1789	575	6.00E-94	32.1	10.1	17.2
Rsa1.0_00387.1.g12772.t1	gb|EOA23588.1| hypothetical protein CARUB_v10016783mg [Capsella rubella]	675	673	0	99.7	94.5	97.3	hypothetical protein CARUB_v10016783mg	gbpln	Capsella rubella	AT3G28180.1 | Symbols: ATCSLC04, CSLC04, ATCSLC4, CSLC4 | Cellulose-synthase-like C4 | chr3:10506110-10509067 FORWARD LENGTH=673	675	673	0	99.7	93.5	97.0
Rsa1.0_00387.1.g12773.t1	gb|EOA24756.1| hypothetical protein CARUB_v10018042mg [Capsella rubella]	188	204	5.00E-88	108.5	81.9	86.7	hypothetical protein CARUB_v10018042mg	gbpln	Capsella rubella	AT3G28210.1 | Symbols: PMZ, SAP12 | zinc finger (AN1-like) family protein | chr3:10520585-10521223 FORWARD LENGTH=186	188	186	8.00E-86	98.9	77.7	84.6
Rsa1.0_00387.1.g12774.t1	ref|XP_002877098.1| hypothetical protein ARALYDRAFT_905093 [Arabidopsis lyrata subsp. lyrata] gi|297322936|gb|EFH53357.1| hypothetical protein ARALYDRAFT_905093 [Arabidopsis lyrata subsp. lyrata]	363	364	0	100.3	88.4	93.7	hypothetical protein ARALYDRAFT_905093	gbpln	Arabidopsis lyrata	AT3G28340.1 | Symbols: GATL10 | galacturonosyltransferase-like 10 | chr3:10589396-10590493 REVERSE LENGTH=365	363	365	0	100.6	87.1	92.3
Rsa1.0_00387.1.g12775.t1	gb|EOA13153.1| hypothetical protein CARUB_v10026171mg [Capsella rubella]	128	560	6.00E-46	437.5	78.9	83.6	hypothetical protein CARUB_v10026171mg	gbpln	Capsella rubella	AT5G62560.1 | Symbols: | RING/U-box superfamily protein with ARM repeat domain | chr5:25110073-25111752 FORWARD LENGTH=559	128	559	9.00E-47	436.7	79.7	85.2
Rsa1.0_00387.1.g12776.t1	gb|EOA23410.1| hypothetical protein CARUB_v10016590mg [Capsella rubella]	1244	1245	0	100.1	92.5	96.7	hypothetical protein CARUB_v10016590mg	gbpln	Capsella rubella	AT3G28345.1 | Symbols: | ABC transporter family protein | chr3:10593921-10598775 REVERSE LENGTH=1240	1244	1240	0	99.7	91.6	96.7

Rsa1.0_00387.1.g12777.t2	ref|XP_002875450.1| hypothetical protein ARALYDRAFT_484614 [Arabidopsis lyrata subsp. lyrata] gi|297321288|gb|EFH51709.1| hypothetical protein ARALYDRAFT_484614 [Arabidopsis lyrata subsp. lyrata]	300	269	6.00E-98	89.7	62.7	68.7	hypothetical protein ARALYDRAFT_484614	gbpln	Arabidopsis lyrata	AT3G28370.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G51430.1); Has 6174 Blast hits to 4953 proteins in 685 species: Archae - 195; Bacteria - 792; Metazoa - 2688; Fungi - 653; Plants - 470; Viruses - 15; Other Eukaryotes - 1361 (source: NCBI BLink). | chr3:10620627-10623259 FORWARD LENGTH=292	300	292	1.00E-97	97.3	61.7	68.0
Rsa1.0_00387.1.g12778.t1	dbj|BAB02858.1| multidrug resistance p-glycoprotein; ABC transporter-like protein [Arabidopsis thaliana]	1268	1262	0	99.5	76.7	86.2	multidrug resistance p-glycoprotein; ABC transporter-like protein	gbpln	Arabidopsis thaliana	AT3G28390.1 | Symbols: PGP18 | P-glycoprotein 18 | chr3:10629425-10633967 REVERSE LENGTH=1225	1268	1225	0	96.6	76.4	85.9
Rsa1.0_00387.1.g12779.t1	sp|P17333.1|2SS4_BRANA RecName: Full=Napin; AltName: Full=1.7S seed storage protein; Contains: RecName: Full=Napin small chain; Contains: RecName: Full=Napin large chain; Flags: Precursor gi|17833|emb|CAA35580.1| unnamed protein product [Brassica napus] gi|468022|gb|AAA81909.1| napin [Brassica napus]	174	180	3.00E-78	103.4	89.7	94.8	RecName: Full=Napin; AltName: Full=1.7S seed storage protein; Contains: RecName: Full=Napin small chain; Contains: RecName: Full=Napin large chain; Flags: Precursor gi|17833|emb|CAA35580.1| unnamed protein product	gbpln	Brassica napus	AT4G27170.1 | Symbols: SESA4, AT2S4 | seed storage albumin 4 | chr4:13613637-13614137 FORWARD LENGTH=166	174	166	2.00E-50	95.4	60.3	71.8
Rsa1.0_00387.1.g12780.t1	ref|NP_189483.1| Putative membrane lipoprotein [Arabidopsis thaliana] gi|9294578|dbj|BAB02859.1| unnamed protein product [Arabidopsis thaliana] gi|38454112|gb|AAR20750.1| At3g28420 [Arabidopsis thaliana] gi|332643922|gb|AEE77443.1| Putative membrane lipoprotein [Arabidopsis thaliana]	388	216	8.00E-79	55.7	43.0	46.4	Putative membrane lipoprotein	gbpln	Arabidopsis thaliana	AT3G28420.1 | Symbols: | Putative membrane lipoprotein | chr3:10654674-10655324 REVERSE LENGTH=216	388	216	2.00E-81	55.7	43.0	46.4
Rsa1.0_00387.1.g12781.t1	ref|XP_002877106.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322944|gb|EFH53365.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	803	548	6.00E-72	68.2	26.7	32.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G19010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74860.1); Has 337 Blast hits to 320 proteins in 97 species: Archae - 0; Bacteria - 14; Metazoa - 153; Fungi - 26; Plants - 76; Viruses - 0; Other Eukaryotes - 68 (source: NCBI BLink). | chr1:6565616-6567354 FORWARD LENGTH=319	803	319	1.00E-24	39.7	7.1	9.8
Rsa1.0_00387.1.g12782.t1	ref|NP_189486.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|9294580|dbj|BAB02861.1| receptor-like protein kinase-like protein [Arabidopsis thaliana] gi|26449808|dbj|BAC42027.1| putative receptor kinase [Arabidopsis thaliana] gi|224589583|gb|ACN59325.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332643925|gb|AEE77446.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]	597	605	0	101.3	80.4	89.3	leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT3G28450.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:10667359-10669176 FORWARD LENGTH=605	597	605	0	101.3	80.4	89.3
Rsa1.0_00387.1.g12783.t1	gb|EOA25615.1| hypothetical protein CARUB_v10018963mg [Capsella rubella]	81	81	1.00E-19	100.0	64.2	70.4	hypothetical protein CARUB_v10018963mg	gbpln	Capsella rubella	AT3G28455.1 | Symbols: CLE25 | CLAVATA3/ESR-RELATED 25 | chr3:10670220-10670931 REVERSE LENGTH=81	81	81	3.00E-21	100.0	63.0	69.1
Rsa1.0_00387.1.g12784.t22	ref|XP_002877109.1| hypothetical protein ARALYDRAFT_905108 [Arabidopsis lyrata subsp. lyrata] gi|297322947|gb|EFH53368.1| hypothetical protein ARALYDRAFT_905108 [Arabidopsis lyrata subsp. lyrata]	277	312	1.00E-124	112.6	84.1	88.4	hypothetical protein ARALYDRAFT_905108	gbpln	Arabidopsis lyrata	AT3G28460.1 | Symbols: | methyltransferases | chr3:10672673-10674297 REVERSE LENGTH=314	277	314	1.00E-123	113.4	83.0	86.6
Rsa1.0_00387.1.g12785.t1	gb|EOA24401.1| hypothetical protein CARUB_v10017650mg [Capsella rubella]	324	322	1.00E-141	99.4	86.1	91.0	hypothetical protein CARUB_v10017650mg	gbpln	Capsella rubella	AT3G28470.1 | Symbols: ATMYB35, TDF1 | Duplicated homeodomain-like superfamily protein | chr3:10674579-10675724 REVERSE LENGTH=317	324	317	1.00E-137	97.8	83.6	88.6
Rsa1.0_00387.1.g12786.t1	ref|XP_002877111.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297322949|gb|EFH53370.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	317	316	1.00E-160	99.7	84.9	89.3	oxidoreductase	gbpln	Arabidopsis lyrata	AT3G28480.1 | Symbols: | Oxoglutarate/iron-dependent oxygenase | chr3:10676266-10678262 REVERSE LENGTH=316	317	316	1.00E-161	99.7	84.5	89.3

Rsa1.0_00387.1.g12787.t1	ref|NP_974372.1| basic helix-loop-helix (bHLH) DNA-binding family protein [Arabidopsis thaliana] gi|9294226|dbj|BAB02128.1| DNA-binding protein-like [Arabidopsis thaliana] gi|88900306|gb|ABD57465.1| At3g28857 [Arabidopsis thaliana] gi|332643976|gb|AEE77497.1| basic helix-loop-helix (bHLH) DNA-binding family protein [Arabidopsis thaliana]	92	92	5.00E-38	100.0	90.2	95.7	basic helix-loop-helix (bHLH) DNA-binding family protein	gbpln	Arabidopsis thaliana	AT3G28857.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding family protein | chr3:10855781-10856313 REVERSE LENGTH=92	92	92	8.00E-41	100.0	90.2	95.7
Rsa1.0_00387.1.g12788.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00387.1.g12789.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00387.1.g12790.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1477	1496	0	101.3	59.5	73.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1477	1262	1.00E-143	85.4	16.8	23.6
Rsa1.0_00387.1.g12791.t1	ref|NP_189528.1| ABC transporter B family member 19 [Arabidopsis thaliana] gi|75335092|sp|Q9LJX0.1|AB19B_ARATH RecName: Full=ABC transporter B family member 19; Short=ABC transporter ABCB.19; Short=AtABCB19; AltName: Full=Multidrug resistance protein 11; AltName: Full=P-glycoprotein 19 gi|9294227|dbj|BAB02129.1| P-glycoprotein; multi-drug resistance related; ABC transporter-like protein [Arabidopsis thaliana] gi|332643977|gb|AEE77498.1| ABC transporter B family member 19 [Arabidopsis thaliana]	1252	1252	0	100.0	97.0	99.0	ABC transporter B family member 19	gbpln	Arabidopsis thaliana	AT3G28860.1 | Symbols: ATMDR1, ATMDR11, PGP19, MDR11, MDR1, ATPGP19, ABCB19, ATABCB19 | ATP binding cassette subfamily B19 | chr3:10870287-10877286 REVERSE LENGTH=1252	1252	1252	0	100.0	97.0	99.0
Rsa1.0_00387.1.g12792.t1	gb|EOA39186.1| hypothetical protein CARUB_v10012153mg [Capsella rubella]	184	508	3.00E-29	276.1	42.4	50.5	hypothetical protein CARUB_v10012153mg	gbpln	Capsella rubella	AT1G21060.1 | Symbols: | Protein of unknown function, DUF547 | chr1:7371799-7374085 FORWARD LENGTH=505	184	505	7.00E-28	274.5	39.1	48.9
Rsa1.0_00387.1.g12793.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00387.1.g12794.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00387.1.g12795.t1	dbj|BAJ34042.1| unnamed protein product [Thellungiella halophila]	337	337	1.00E-154	100.0	90.8	92.6	unnamed protein product	----	----	AT3G28910.1 | Symbols: ATMYB30, MYB30 | myb domain protein 30 | chr3:10911443-10912856 FORWARD LENGTH=323	337	323	2.33E-156	95.8	86.9	87.8
Rsa1.0_00387.1.g12796.t1	ref|NP_001147103.1| zinc finger homeodomain protein 1 [Zea mays] gi|195607236|gb|ACG25448.1| zinc finger homeodomain protein 1 [Zea mays]	100	100	5.00E-40	100.0	97.0	97.0	zinc finger homeodomain protein 1	gbenv/gbpln	Zea mays	AT3G28917.1 | Symbols: MIF2 | mini zinc finger 2 | chr3:10925014-10925316 FORWARD LENGTH=100	100	100	6.00E-41	100.0	94.0	95.0
Rsa1.0_00387.1.g12797.t1	ref|NP_189534.1| homeobox protein 34 [Arabidopsis thaliana] gi|9294358|dbj|BAB02255.1| unnamed protein product [Arabidopsis thaliana] gi|20260544|gb|AAM13170.1| unknown protein [Arabidopsis thaliana] gi|22136284|gb|AAM91220.1| unknown protein [Arabidopsis thaliana] gi|332643987|gb|AEE77508.1| homeobox protein 34 [Arabidopsis thaliana]	346	312	1.00E-93	90.2	69.4	75.1	homeobox protein 34	gbpln	Arabidopsis thaliana	AT3G28920.1 | Symbols: AtHB34, HB34, ZHD9 | homeobox protein 34 | chr3:10940598-10941536 REVERSE LENGTH=312	346	312	3.00E-96	90.2	69.4	75.1
Rsa1.0_00387.1.g12798.t1	ref|NP_001190492.1| structural maintenance of chromosomes protein 4 [Arabidopsis thaliana] gi|332008312|gb|AED95695.1| structural maintenance of chromosomes protein 4 [Arabidopsis thaliana]	1221	1244	0	101.9	91.3	95.8	structural maintenance of chromosomes protein 4	gbpln	Arabidopsis thaliana	AT5G48600.2 | Symbols: SMC3 | structural maintenance of chromosome 3 | chr5:19701908-19709091 FORWARD LENGTH=1244	1221	1244	0	101.9	91.3	95.8
Rsa1.0_00387.1.g12799.t1	dbj|BAJ34156.1| unnamed protein product [Thellungiella halophila]	168	168	6.00E-83	100.0	85.7	93.5	unnamed protein product	----	----	AT3G28930.1 | Symbols: AIG2 | AIG2-like (avirulence induced gene) family protein | chr3:10959890-10960728 REVERSE LENGTH=170	168	170	6.00E-83	101.2	83.3	93.5
Rsa1.0_00387.1.g12800.t1	gb|EOA24839.1| hypothetical protein CARUB_v10018128mg [Capsella rubella]	169	170	5.00E-82	100.6	82.8	93.5	hypothetical protein CARUB_v10018128mg	gbpln	Capsella rubella	AT3G28940.1 | Symbols: | AIG2-like (avirulence induced gene) family protein | chr3:10968324-10969311 REVERSE LENGTH=169	169	169	1.00E-79	100.0	76.9	93.5
Rsa1.0_00387.1.g12801.t1	dbj|BAJ34156.1| unnamed protein product [Thellungiella halophila]	168	168	7.00E-86	100.0	90.5	95.2	unnamed protein product	----	----	AT3G28940.1 | Symbols: | AIG2-like (avirulence induced gene) family protein | chr3:10968324-10969311 REVERSE LENGTH=169	168	169	1.00E-79	100.6	79.2	91.1
Rsa1.0_00387.1.g12802.t3	gb|EOA24101.1| hypothetical protein CARUB_v10017331mg, partial [Capsella rubella]	405	418	0	103.2	90.1	95.3	hypothetical protein CARUB_v10017331mg, partial	gbpln	Capsella rubella	AT3G28960.1 | Symbols: | Transmembrane amino acid transporter family protein | chr3:10984245-10985767 REVERSE LENGTH=405	405	405	0	100.0	88.9	94.8

Rsa1.0_00387.1.g12803.t3	ref|XP_002877147.1| hypothetical protein ARALYDRAFT_347271 [Arabidopsis lyrata subsp. lyrata] gi|297322985|gb|EFH53406.1| hypothetical protein ARALYDRAFT_347271 [Arabidopsis lyrata subsp. lyrata]	313	279	2.00E-91	89.1	54.6	62.0	hypothetical protein ARALYDRAFT_347271	gbpln	Arabidopsis lyrata	AT3G28970.1 | Symbols: AAR3 | Domain of unknown function (DUF298) | chr3:10987970-10989782 REVERSE LENGTH=295	313	295	3.00E-93	94.2	55.0	62.3
Rsa1.0_00387.1.g12804.t1	ref|XP_002875484.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297321322|gb|EFH51743.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	184	178	2.00E-57	96.7	69.6	77.2	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT5G39670.1 | Symbols: | Calcium-binding EF-hand family protein | chr5:15883270-15883884 FORWARD LENGTH=204	184	204	1.00E-56	110.9	64.1	77.7
Rsa1.0_00387.1.g12805.t1	ref|XP_002875485.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321323|gb|EFH51744.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	263	262	1.00E-135	99.6	85.9	96.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G29010.1 | Symbols: | Biotin/lipoate A/B protein ligase family | chr3:11006945-11007977 FORWARD LENGTH=262	263	262	1.00E-138	99.6	86.7	95.4
Rsa1.0_00387.1.g12806.t2	gb|EOA25741.1| hypothetical protein CARUB_v10019103mg [Capsella rubella]	138	309	1.00E-48	223.9	67.4	73.9	hypothetical protein CARUB_v10019103mg	gbpln	Capsella rubella	AT3G29020.2 | Symbols: MYB110 | myb domain protein 110 | chr3:11008233-11009419 REVERSE LENGTH=305	138	305	1.00E-49	221.0	65.9	73.2
Rsa1.0_00387.1.g12807.t2	ref|NP_189545.1| expansin A5 [Arabidopsis thaliana] gi|20138196|sp|Q38864.1|EXPA5_ARATH RecName: Full=Expansin-A5; Short=AtEXPA5; AltName: Full=Alpha-expansin-5; Short=At-EXP5; Short=AtEx5; AltName: Full=Ath-ExpAlpha-1.4; Flags: Precursor gi|1041704|gb|AAB38071.1| expansin At-EXPA5 [Arabidopsis thaliana] gi|7939553|dbj|BAA95756.1| expansin-like protein [Arabidopsis thaliana] gi|106879169|gb|ABF82614.1| At3g29030 [Arabidopsis thaliana] gi|332644002|gb|AEE77523.1| expansin A5 [Arabidopsis thaliana]	216	255	8.00E-99	118.1	92.1	95.8	expansin A5	gbpln	Arabidopsis thaliana	AT3G29030.1 | Symbols: ATEXPA5, ATEXP5, ATHEXP ALPHA 1.4, EXP5, EXPA5 | expansin A5 | chr3:11011538-11013068 REVERSE LENGTH=255	216	255	1.00E-101	118.1	92.1	95.8
Rsa1.0_00387.1.g12808.t1	ref|NP_850646.1| uncharacterized protein [Arabidopsis thaliana] gi|26451841|dbj|BAC43013.1| unknown protein [Arabidopsis thaliana] gi|28416777|gb|AAO42919.1| At3g29034 [Arabidopsis thaliana] gi|332644005|gb|AEE77526.1| uncharacterized protein AT3G29034 [Arabidopsis thaliana]	87	86	8.00E-32	98.9	83.9	93.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G29034.1 | Symbols: | unknown protein; Has 7 Blast hits to 7 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:11030343-11030603 REVERSE LENGTH=86	87	86	1.00E-34	98.9	83.9	93.1
Rsa1.0_00387.1.g12809.t1	ref|XP_002875486.1| ANAC059/ATNAC3 [Arabidopsis lyrata subsp. lyrata] gi|297321324|gb|EFH51745.1| ANAC059/ATNAC3 [Arabidopsis lyrata subsp. lyrata]	316	322	1.00E-123	101.9	73.4	81.6	ANAC059/ATNAC3	gbpln	Arabidopsis lyrata	AT3G29035.1 | Symbols: ATNAC3, ANAC059, NAC3 | NAC domain containing protein 3 | chr3:11033839-11035006 FORWARD LENGTH=318	316	318	1.00E-121	100.6	69.9	79.7
Rsa1.0_00387.1.g12810.t1	gb|AAS76703.1| At3g29075 [Arabidopsis thaliana] gi|46402446|gb|AAS92325.1| At3g29075 [Arabidopsis thaliana]	277	236	3.00E-47	85.2	48.4	54.2	At3g29075	gbpln	Arabidopsis thaliana	AT3G29075.1 | Symbols: | glycine-rich protein | chr3:11051645-11052629 REVERSE LENGTH=294	277	294	2.00E-49	106.1	46.6	51.6
Rsa1.0_00387.1.g12811.t1	ref|XP_002875491.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321329|gb|EFH51750.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	317	317	0	100.0	94.6	98.4	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT3G29090.1 | Symbols: PME31, ATPME31 | pectin methylesterase 31 | chr3:11073804-11075335 FORWARD LENGTH=317	317	317	0	100.0	94.3	98.4
Rsa1.0_00387.1.g12812.t1	ref|XP_002877157.1| hypothetical protein ARALYDRAFT_905203 [Arabidopsis lyrata subsp. lyrata] gi|297322995|gb|EFH53416.1| hypothetical protein ARALYDRAFT_905203 [Arabidopsis lyrata subsp. lyrata]	121	119	1.00E-56	98.3	89.3	95.0	hypothetical protein ARALYDRAFT_905203	gbpln	Arabidopsis lyrata	AT3G29130.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Domain of unknown function KxDL (InterPro:IPR019371). | chr3:11102546-11103847 REVERSE LENGTH=168	121	168	2.00E-58	138.8	87.6	93.4
Rsa1.0_00387.1.g12813.t1	gb|EOA23756.1| hypothetical protein CARUB_v10016968mg, partial [Capsella rubella]	508	543	0	106.9	91.9	95.3	hypothetical protein CARUB_v10016968mg, partial	gbpln	Capsella rubella	AT3G29160.2 | Symbols: AKIN11, KIN11 | SNF1 kinase homolog 11 | chr3:11128893-11131510 REVERSE LENGTH=512	508	512	0	100.8	91.3	94.9
Rsa1.0_00387.1.g12814.t1	gb|EOA23180.1| hypothetical protein CARUB_v10018086mg, partial [Capsella rubella]	116	184	5.00E-44	158.6	88.8	94.0	hypothetical protein CARUB_v10018086mg, partial	gbpln	Capsella rubella	AT3G29170.1 | Symbols: | Eukaryotic protein of unknown function (DUF872) | chr3:11136240-11137542 REVERSE LENGTH=121	116	121	1.00E-42	104.3	89.7	94.8
Rsa1.0_00387.1.g12815.t1	gb|EOA23831.1| hypothetical protein CARUB_v10017046mg [Capsella rubella]	511	512	0	100.2	89.0	95.1	hypothetical protein CARUB_v10017046mg	gbpln	Capsella rubella	AT3G29180.2 | Symbols: | Protein of unknown function (DUF1336) | chr3:11149073-11151322 FORWARD LENGTH=513	511	513	0	100.4	90.2	94.7

Rsa1.0_00387.1.g12816.t1	gb|EOA24077.1| hypothetical protein CARUB_v10017314mg [Capsella rubella]	400	394	0	98.5	86.0	91.5	hypothetical protein CARUB_v10017314mg	gbpln	Capsella rubella	AT3G29185.1 | Symbols: | Domain of unknown function (DUF3598) | chr3:11155092-11157207 REVERSE LENGTH=396	400	396	0	99.0	84.0	90.0
Rsa1.0_00387.1.g12817.t1	ref|NP_566846.1| chorismate mutase 1 [Arabidopsis thaliana] gi|334302922|sp|P42738.3|CM1_ARATH RecName: Full=Chorismate mutase 1, chloroplastic; Short=AtCM1; AltName: Full=CM-1; Flags: Precursor gi|89000961|gb|ABD59070.1| At3g29200 [Arabidopsis thaliana] gi|332644031|gb|AEE77552.1| chorismate mutase 1 [Arabidopsis thaliana]	336	340	1.00E-161	101.2	88.1	90.5	chorismate mutase 1	gbpln	Arabidopsis thaliana	AT3G29200.1 | Symbols: CM1, ATCM1 | chorismate mutase 1 | chr3:11164582-11166258 REVERSE LENGTH=340	336	340	1.00E-163	101.2	88.1	90.5
Rsa1.0_00387.1.g12818.t1	ref|NP_189568.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75273910|sp|Q9LS72.1|PP261_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g29230 gi|9293916|dbj|BAB01819.1| unnamed protein product [Arabidopsis thaliana] gi|332644032|gb|AEE77553.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	597	600	0	100.5	85.3	93.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G29230.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:11188803-11190605 FORWARD LENGTH=600	597	600	0	100.5	85.3	93.6
Rsa1.0_00387.1.g12819.t1	ref|NP_566847.1| uncharacterized protein [Arabidopsis thaliana] gi|30689543|ref|NP_850648.1| uncharacterized protein [Arabidopsis thaliana] gi|9293917|dbj|BAB01820.1| unnamed protein product [Arabidopsis thaliana] gi|19310484|gb|AAL84976.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|21537141|gb|AAM61482.1| unknown [Arabidopsis thaliana] gi|22654969|gb|AAM98077.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|28416521|gb|AAO42791.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|332644033|gb|AEE77554.1| uncharacterized protein AT3G29240 [Arabidopsis thaliana] gi|332644034|gb|AEE77555.1| uncharacterized protein AT3G29240 [Arabidopsis thaliana]	311	317	1.00E-164	101.9	92.3	96.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G29240.2 | Symbols: | Protein of unknown function (DUF179) | chr3:11191780-11192868 FORWARD LENGTH=317	311	317	1.00E-167	101.9	92.3	96.1
Rsa1.0_00387.1.g12820.t1	gb|EOA24175.1| hypothetical protein CARUB_v10017408mg [Capsella rubella]	387	393	1.00E-178	101.6	86.8	93.3	hypothetical protein CARUB_v10017408mg	gbpln	Capsella rubella	AT3G29770.1 | Symbols: ATMES11, MES11 | methyl esterase 11 | chr3:11648471-11650565 FORWARD LENGTH=390	387	390	1.00E-168	100.8	86.0	92.2
Rsa1.0_00387.1.g12821.t1	ref|XP_002875545.1| hypothetical protein ARALYDRAFT_905307 [Arabidopsis lyrata subsp. lyrata] gi|297321383|gb|EFH51804.1| hypothetical protein ARALYDRAFT_905307 [Arabidopsis lyrata subsp. lyrata]	101	116	4.00E-25	114.9	62.4	74.3	hypothetical protein ARALYDRAFT_905307	gbpln	Arabidopsis lyrata	AT3G29780.1 | Symbols: RALFL27 | ralf-like 27 | chr3:11671741-11672094 FORWARD LENGTH=117	101	117	1.00E-18	115.8	55.4	64.4
Rsa1.0_00387.1.g12822.t1	ref|XP_002875546.1| hypothetical protein ARALYDRAFT_484733 [Arabidopsis lyrata subsp. lyrata] gi|297321384|gb|EFH51805.1| hypothetical protein ARALYDRAFT_484733 [Arabidopsis lyrata subsp. lyrata]	437	439	0	100.5	87.6	93.1	hypothetical protein ARALYDRAFT_484733	gbpln	Arabidopsis lyrata	AT3G29810.1 | Symbols: COBL2 | COBRA-like protein 2 precursor | chr3:11728212-11730158 FORWARD LENGTH=441	437	441	0	100.9	86.3	93.1
Rsa1.0_00387.1.g12823.t1	ref|XP_002875526.1| hypothetical protein ARALYDRAFT_323026 [Arabidopsis lyrata subsp. lyrata] gi|297321364|gb|EFH51785.1| hypothetical protein ARALYDRAFT_323026 [Arabidopsis lyrata subsp. lyrata]	87	87	5.00E-42	100.0	94.3	97.7	hypothetical protein ARALYDRAFT_323026	gbpln	Arabidopsis lyrata	AT3G29970.1 | Symbols: | B12D protein | chr3:11745299-11746481 FORWARD LENGTH=87	87	87	3.00E-44	100.0	93.1	96.6
Rsa1.0_00387.1.g12824.t2	ref|XP_002877204.1| hypothetical protein ARALYDRAFT_323027 [Arabidopsis lyrata subsp. lyrata] gi|297323042|gb|EFH53463.1| hypothetical protein ARALYDRAFT_323027 [Arabidopsis lyrata subsp. lyrata]	1081	977	0	90.4	51.2	61.6	hypothetical protein ARALYDRAFT_323027	gbpln	Arabidopsis lyrata	AT2G10440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15780.1); Has 8319 Blast hits to 5104 proteins in 317 species: Archae - 0; Bacteria - 285; Metazoa - 1706; Fungi - 535; Plants - 320; Viruses - 18; Other Eukaryotes - 5455 (source: NCBI BLink). | chr2:4013752-4018046 REVERSE LENGTH=935	1081	935	1.00E-174	86.5	39.1	47.9
Rsa1.0_00387.1.g12825.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00387.1.g12826.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00388.1.g12827.t1	gb|EOA14349.1| hypothetical protein CARUB_v10027529mg [Capsella rubella]	165	222	4.00E-49	134.5	66.1	86.1	hypothetical protein CARUB_v10027529mg	gbpln	Capsella rubella	AT5G51860.2 | Symbols: | K-box region and MADS-box transcription factor family protein | chr5:21081844-21084126 REVERSE LENGTH=202	165	202	4.00E-30	122.4	47.9	58.8
Rsa1.0_00388.1.g12828.t1	ref|NP_194273.2| uncharacterized protein [Arabidopsis thaliana] gi|332659656|gb|AEE85056.1| uncharacterized protein AT4G25430 [Arabidopsis thaliana]	446	459	2.00E-96	102.9	57.0	69.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G25430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G51850.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12998571-13000211 FORWARD LENGTH=459	446	459	6.00E-99	102.9	57.0	69.5
Rsa1.0_00388.1.g12829.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00388.1.g12830.t1	ref|XP_002869672.1| basix helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297315508|gb|EFH45931.1| basix helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	219	222	2.00E-81	101.4	76.3	87.2	basix helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT4G25410.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:12985772-12987149 FORWARD LENGTH=230	219	230	7.00E-82	105.0	73.5	84.9
Rsa1.0_00388.1.g12831.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00388.1.g12832.t1	ref|NP_194265.2| phosphate transporter PHO1-4 [Arabidopsis thaliana] gi|75127840|sp|Q6R8G6.1|PHO14_ARATH RecName: Full=Phosphate transporter PHO1 homolog 4; AltName: Full=Protein PHO1 homolog 4; Short=AtPHO1;H4 gi|41079263|gb|AAR99486.1| PHO1-like protein [Arabidopsis thaliana] gi|332659645|gb|AEE85045.1| phosphate transporter PHO1-4 [Arabidopsis thaliana]	727	745	0	102.5	82.4	89.7	phosphate transporter PHO1-4	gbpln	Arabidopsis thaliana	AT4G25350.1 | Symbols: SHB1 | EXS (ERD1/XPR1/SYG1) family protein | chr4:12963382-12966448 REVERSE LENGTH=745	727	745	0	102.5	82.4	89.7
Rsa1.0_00388.1.g12833.t1	ref|XP_002869680.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297315516|gb|EFH45939.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	358	356	1.00E-172	99.4	79.3	91.1	oxidoreductase	gbpln	Arabidopsis lyrata	AT4G25300.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:12945263-12946642 FORWARD LENGTH=356	358	356	1.00E-171	99.4	77.7	89.9
Rsa1.0_00388.1.g12834.t2	ref|NP_194253.2| E3 ubiquitin protein ligase RIN2 [Arabidopsis thaliana] gi|30686808|ref|NP_849552.1| E3 ubiquitin protein ligase RIN2 [Arabidopsis thaliana] gi|75304438|sp|Q8VYC8.1|RIN2_ARATH RecName: Full=E3 ubiquitin protein ligase RIN2; AltName: Full=AMF receptor-like protein 1A; AltName: Full=RPM1-interacting protein 2 gi|18176187|gb|AAL60000.1| unknown protein [Arabidopsis thaliana] gi|332659628|gb|AEE85028.1| E3 ubiquitin protein ligase RIN2 [Arabidopsis thaliana] gi|332659629|gb|AEE85029.1| E3 ubiquitin protein ligase RIN2 [Arabidopsis thaliana]	986	578	0	58.6	54.9	56.3	E3 ubiquitin protein ligase RIN2	gbpln	Arabidopsis thaliana	AT4G25230.2 | Symbols: RIN2 | RPM1 interacting protein 2 | chr4:12924446-12928671 FORWARD LENGTH=578	986	578	0	58.6	54.9	56.3
Rsa1.0_00388.1.g12835.t1	sp|P29110.1|OLEO3_BRANA RecName: Full=Oleosin Bn-III; Short=BnIII gi|17839|emb|CAA43941.1| oleosin BN-III [Brassica napus] gi|196122088|gb|ACG69519.1| oleosin S3-7 [Brassica napus] gi|742387|prf||2009397A oleosin	188	195	6.00E-80	103.7	87.2	91.5	RecName: Full=Oleosin Bn-III; Short=BnIII gi|17839|emb|CAA43941.1| oleosin BN-III	gbpln	Brassica napus	AT4G25140.1 | Symbols: OLEO1, OLE1 | oleosin 1 | chr4:12900498-12901259 FORWARD LENGTH=173	188	173	6.00E-74	92.0	83.0	86.7
Rsa1.0_00388.1.g12836.t1	ref|NP_001190831.1| acyl carrier protein 4 [Arabidopsis thaliana] gi|332659597|gb|AEE84997.1| acyl carrier protein 4 [Arabidopsis thaliana]	42	149	4.00E-12	354.8	85.7	92.9	acyl carrier protein 4	gbpln	Arabidopsis thaliana	AT4G25050.2 | Symbols: ACP4 | acyl carrier protein 4 | chr4:12870178-12871024 FORWARD LENGTH=149	42	149	7.00E-15	354.8	85.7	92.9
Rsa1.0_00388.1.g12837.t1	ref|NP_194234.1| uncharacterized protein [Arabidopsis thaliana] gi|75181563|sp|Q9M0L3.1|CSPLR_ARATH RecName: Full=CASP-like protein At4g25040 gi|7269354|emb|CAB79413.1| putative protein [Arabidopsis thaliana] gi|332659595|gb|AEE84995.1| CASP-like protein [Arabidopsis thaliana]	168	170	2.00E-65	101.2	79.2	87.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G25040.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:12868320-12869319 FORWARD LENGTH=170	168	170	8.00E-68	101.2	79.2	87.5
Rsa1.0_00388.1.g12838.t1	ref|XP_002867630.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297313466|gb|EFH43889.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	272	280	1.00E-137	102.9	90.1	95.6	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT4G25010.1 | Symbols: SWEET14, AtSWEET14 | Nodulin MtN3 family protein | chr4:12854630-12856351 REVERSE LENGTH=281	272	281	1.00E-137	103.3	89.0	93.8

Rsa1.0_00388.1.g12839.t1	ref|XP_002867632.1| hypothetical protein ARALYDRAFT_492339 [Arabidopsis lyrata subsp. lyrata] gi|297313468|gb|EFH43891.1| hypothetical protein ARALYDRAFT_492339 [Arabidopsis lyrata subsp. lyrata] gi|482553486|gb|EOA17679.1| hypothetical protein CARUB_v10006048mg [Capsella rubella]	118	118	7.00E-59	100.0	94.1	97.5	hypothetical protein ARALYDRAFT_492339	gbpln	Arabidopsis lyrata	AT4G24990.1 | Symbols: ATGP4 | Ubiquitin family protein | chr4:12849973-12851249 REVERSE LENGTH=118	118	118	7.00E-61	100.0	92.4	97.5
Rsa1.0_00388.1.g12840.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00388.1.g12841.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00388.1.g12842.t1	ref|XP_002869699.1| sumo-activating enzyme 1A [Arabidopsis lyrata subsp. lyrata] gi|297315535|gb|EFH45958.1| sumo-activating enzyme 1A [Arabidopsis lyrata subsp. lyrata]	105	322	5.00E-42	306.7	80.0	87.6	sumo-activating enzyme 1A	gbpln	Arabidopsis lyrata	AT4G24940.1 | Symbols: SAE1A, AT-SAE1-1, ATSAE1A | SUMO-activating enzyme 1A | chr4:12823651-12825971 FORWARD LENGTH=322	105	322	5.00E-44	306.7	78.1	86.7
Rsa1.0_00388.1.g12843.t1	ref|NP_195361.1| peroxidase 49 [Arabidopsis thaliana] gi|26397550|sp|O23237.2|PER49_ARATH RecName: Full=Peroxidase 49; Short=Atperox P49; AltName: Full=ATP31; Flags: Precursor gi|17530562|gb|AAL40848.1|AF452384_1 class III peroxidase ATP31 [Arabidopsis thaliana] gi|4006918|emb|CAB16848.1| peroxidase like protein [Arabidopsis thaliana] gi|6822093|emb|CAB71009.1| peroxidase [Arabidopsis thaliana] gi|7270591|emb|CAB80309.1| peroxidase like protein [Arabidopsis thaliana] gi|18377686|gb|AAL66993.1| putative peroxidase [Arabidopsis thaliana] gi|21436133|gb|AAM51313.1| putative peroxidase [Arabidopsis thaliana] gi|332661255|gb|AEE86655.1| peroxidase 49 [Arabidopsis thaliana]	315	331	1.00E-116	105.1	65.1	74.3	peroxidase 49	gbpln	Arabidopsis thaliana	AT4G36430.1 | Symbols: | Peroxidase superfamily protein | chr4:17204648-17205917 REVERSE LENGTH=331	315	331	1.00E-119	105.1	65.1	74.3
Rsa1.0_00388.1.g12844.t1	gb|EOA30030.1| hypothetical protein CARUB_v10013133mg [Capsella rubella]	110	671	3.00E-14	610.0	35.5	39.1	hypothetical protein CARUB_v10013133mg	gbpln	Capsella rubella	AT3G13460.4 | Symbols: ECT2 | evolutionarily conserved C-terminal region 2 | chr3:4385274-4388220 REVERSE LENGTH=666	110	666	6.00E-17	605.5	35.5	39.1
Rsa1.0_00388.1.g12845.t1	gb|EOA17016.1| hypothetical protein CARUB_v10005251mg [Capsella rubella]	331	322	1.00E-155	97.3	81.9	88.8	hypothetical protein CARUB_v10005251mg	gbpln	Capsella rubella	AT4G24940.1 | Symbols: SAE1A, AT-SAE1-1, ATSAE1A | SUMO-activating enzyme 1A | chr4:12823651-12825971 FORWARD LENGTH=322	331	322	1.00E-154	97.3	81.0	87.3
Rsa1.0_00389.1.g12846.t2	ref|NP_186970.2| NAC domain containing protein 45 [Arabidopsis thaliana] gi|145651780|gb|ABP88115.1| At3g03200 [Arabidopsis thaliana] gi|332640391|gb|AEE73912.1| NAC domain containing protein 45 [Arabidopsis thaliana]	483	479	0	99.2	67.9	74.3	NAC domain containing protein 45	gbpln	Arabidopsis thaliana	AT3G03200.1 | Symbols: anac045, NAC045 | NAC domain containing protein 45 | chr3:736141-738527 REVERSE LENGTH=479	483	479	0	99.2	67.9	74.3
Rsa1.0_00389.1.g12847.t1	gb|EOA12297.1| hypothetical protein CARUB_v10007977mg [Capsella rubella]	437	417	2.00E-74	95.4	33.9	53.1	hypothetical protein CARUB_v10007977mg	gbpln	Capsella rubella	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	437	575	2.00E-50	131.6	27.5	46.5
Rsa1.0_00389.1.g12848.t1	gb|EOA30849.1| hypothetical protein CARUB_v10013992mg [Capsella rubella]	359	368	1.00E-178	102.5	89.1	95.5	hypothetical protein CARUB_v10013992mg	gbpln	Capsella rubella	AT3G03210.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 59 Blast hits to 59 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:740987-742093 FORWARD LENGTH=368	359	368	1.00E-180	102.5	89.1	95.0
Rsa1.0_00389.1.g12849.t1	ref|XP_002884363.1| ATEXPA13 [Arabidopsis lyrata subsp. lyrata] gi|297330203|gb|EFH60622.1| ATEXPA13 [Arabidopsis lyrata subsp. lyrata]	264	266	1.00E-130	100.8	81.8	86.0	ATEXPA13	gbpln	Arabidopsis lyrata	AT3G03220.1 | Symbols: ATEXPA13, EXP13, ATEXP13, ATHEXP ALPHA 1.22, EXPA13 | expansin A13 | chr3:742655-743975 REVERSE LENGTH=266	264	266	1.00E-132	100.8	82.2	86.0
Rsa1.0_00389.1.g12850.t1	ref|XP_002884365.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330205|gb|EFH60624.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	333	333	1.00E-168	100.0	86.8	92.8	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G03240.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:746781-748291 REVERSE LENGTH=333	333	333	1.00E-166	100.0	85.0	92.2
Rsa1.0_00389.1.g12851.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00389.1.g12852.t1	ref|XP_002884365.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330205|gb|EFH60624.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	306	333	1.00E-143	108.8	85.3	90.5	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G03240.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:746781-748291 REVERSE LENGTH=333	306	333	1.00E-143	108.8	83.3	90.2
Rsa1.0_00389.1.g12853.t1	gb|EOA30501.1| hypothetical protein CARUB_v10013624mg [Capsella rubella]	469	469	0	100.0	95.7	98.5	hypothetical protein CARUB_v10013624mg	gbpln	Capsella rubella	AT3G03250.1 | Symbols: UGP, UGP1, AtUGP1 | UDP-GLUCOSE PYROPHOSPHORYLASE 1 | chr3:749761-754014 REVERSE LENGTH=469	469	469	0	100.0	94.9	98.1
Rsa1.0_00389.1.g12854.t1	gb|EOA32484.1| hypothetical protein CARUB_v10015764mg [Capsella rubella]	696	687	0	98.7	60.8	75.0	hypothetical protein CARUB_v10015764mg	gbpln	Capsella rubella	AT3G03260.1 | Symbols: HDG8 | homeodomain GLABROUS 8 | chr3:755356-759234 REVERSE LENGTH=699	696	699	0	100.4	59.6	73.6
Rsa1.0_00389.1.g12855.t1	gb|ABV89642.1| universal stress protein family protein [Brassica rapa]	135	159	9.00E-66	117.8	97.0	99.3	universal stress protein family protein	gbpln	Brassica rapa	AT3G03270.2 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:762136-763075 REVERSE LENGTH=159	135	159	4.00E-64	117.8	92.6	95.6
Rsa1.0_00389.1.g12856.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00389.1.g12857.t1	ref|XP_002882281.1| hypothetical protein ARALYDRAFT_896322 [Arabidopsis lyrata subsp. lyrata] gi|297328121|gb|EFH58540.1| hypothetical protein ARALYDRAFT_896322 [Arabidopsis lyrata subsp. lyrata]	173	166	3.00E-69	96.0	77.5	86.1	hypothetical protein ARALYDRAFT_896322	gbpln	Arabidopsis lyrata	AT3G03280.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G17350.1); Has 137 Blast hits to 137 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 137; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:765559-766059 FORWARD LENGTH=166	173	166	8.00E-71	96.0	75.1	86.1
Rsa1.0_00389.1.g12858.t1	ref|XP_002882282.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328122|gb|EFH58541.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	477	494	1.00E-165	103.6	62.7	76.1	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00389.1.g12859.t1	ref|NP_186979.1| Adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana] gi|6714411|gb|AAF26099.1|AC012328_2 hypothetical protein [Arabidopsis thaliana] gi|67633618|gb|AAY78733.1| universal stress protein family protein [Arabidopsis thaliana] gi|332640402|gb|AEE73923.1| Adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana]	288	274	1.00E-112	95.1	80.2	84.7	Adenine nucleotide alpha hydrolases-like protein	gbpln	Arabidopsis thaliana	AT3G03290.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:766745-767742 FORWARD LENGTH=274	288	274	1.00E-114	95.1	80.2	84.7
Rsa1.0_00389.1.g12860.t4	gb|ACE60552.1| dicer-like protein 2 [Brassica rapa]	1416	1392	0	98.3	89.8	93.7	dicer-like protein 2	gbpln	Brassica rapa	AT3G03300.3 | Symbols: DCL2 | dicer-like 2 | chr3:768020-774833 REVERSE LENGTH=1388	1416	1388	0	98.0	79.5	87.3
Rsa1.0_00389.1.g12861.t1	ref|XP_002884369.1| hypothetical protein ARALYDRAFT_317213 [Arabidopsis lyrata subsp. lyrata] gi|297330209|gb|EFH60628.1| hypothetical protein ARALYDRAFT_317213 [Arabidopsis lyrata subsp. lyrata]	750	2033	0	271.1	79.3	88.5	hypothetical protein ARALYDRAFT_317213	gbpln	Arabidopsis lyrata	AT3G03305.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr3:775504-778271 REVERSE LENGTH=743	750	743	0	99.1	81.9	90.1
Rsa1.0_00389.1.g12862.t1	gb|EOA30564.1| hypothetical protein CARUB_v10013690mg [Capsella rubella]	450	448	0	99.6	88.0	93.8	hypothetical protein CARUB_v10013690mg	gbpln	Capsella rubella	AT3G03310.1 | Symbols: ATLCAT3, LCAT3 | lecithin:cholesterol acyltransferase 3 | chr3:778767-781488 REVERSE LENGTH=447	450	447	0	99.3	89.8	95.3
Rsa1.0_00389.1.g12863.t5	ref|XP_002882284.1| hypothetical protein ARALYDRAFT_477581 [Arabidopsis lyrata subsp. lyrata] gi|297328124|gb|EFH58543.1| hypothetical protein ARALYDRAFT_477581 [Arabidopsis lyrata subsp. lyrata]	314	240	1.00E-101	76.4	60.5	63.4	hypothetical protein ARALYDRAFT_477581	gbpln	Arabidopsis lyrata	AT3G03320.1 | Symbols: | RNA-binding ASCH domain protein | chr3:781872-783289 FORWARD LENGTH=244	314	244	1.00E-100	77.7	58.9	63.7
Rsa1.0_00389.1.g12864.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00389.1.g12865.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00389.1.g12866.t3	ref|XP_002882284.1| hypothetical protein ARALYDRAFT_477581 [Arabidopsis lyrata subsp. lyrata] gi|297328124|gb|EFH58543.1| hypothetical protein ARALYDRAFT_477581 [Arabidopsis lyrata subsp. lyrata]	245	240	2.00E-91	98.0	75.1	79.6	hypothetical protein ARALYDRAFT_477581	gbpln	Arabidopsis lyrata	AT3G03320.1 | Symbols: | RNA-binding ASCH domain protein | chr3:781872-783289 FORWARD LENGTH=244	245	244	5.00E-90	99.6	72.7	80.0

Rsa1.0_00389.1.g12867.t1	ref|XP_002884371.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330211|gb|EFH60630.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	410	327	1.00E-135	79.8	59.5	64.4	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G03330.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:783572-786148 REVERSE LENGTH=328	410	328	1.00E-134	80.0	59.5	64.4
Rsa1.0_00389.1.g12868.t1	ref|XP_002884371.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330211|gb|EFH60630.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	399	327	1.00E-125	82.0	58.4	62.9	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G03330.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:783572-786148 REVERSE LENGTH=328	399	328	1.00E-123	82.2	58.4	62.7
Rsa1.0_00389.1.g12869.t1	ref|XP_002884371.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330211|gb|EFH60630.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	328	327	1.00E-172	99.7	91.8	94.5	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G03330.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:783572-786148 REVERSE LENGTH=328	328	328	1.00E-170	100.0	91.8	94.5
Rsa1.0_00390.1.g12870.t1	ref|XP_002862843.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308590|gb|EFH39101.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	379	550	1.00E-13	145.1	15.6	28.5	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00390.1.g12871.t1	ref|XP_002865450.1| hypothetical protein ARALYDRAFT_917371 [Arabidopsis lyrata subsp. lyrata] gi|297311285|gb|EFH41709.1| hypothetical protein ARALYDRAFT_917371 [Arabidopsis lyrata subsp. lyrata]	92	91	5.00E-36	98.9	80.4	87.0	hypothetical protein ARALYDRAFT_917371	gbpln	Arabidopsis lyrata	AT5G43150.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:17325076-17325689 FORWARD LENGTH=91	92	91	1.00E-36	98.9	78.3	85.9
Rsa1.0_00390.1.g12872.t1	ref|XP_002865451.1| hypothetical protein ARALYDRAFT_917372 [Arabidopsis lyrata subsp. lyrata] gi|297311286|gb|EFH41710.1| hypothetical protein ARALYDRAFT_917372 [Arabidopsis lyrata subsp. lyrata]	250	253	1.00E-118	101.2	86.4	90.8	hypothetical protein ARALYDRAFT_917372	gbpln	Arabidopsis lyrata	AT5G43140.1 | Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr5:17321570-17323224 FORWARD LENGTH=254	250	254	1.00E-120	101.6	85.2	91.6
Rsa1.0_00390.1.g12873.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00390.1.g12874.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	116	149	1.00E-23	128.4	41.4	62.9	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	116	292	5.00E-11	251.7	29.3	48.3
Rsa1.0_00390.1.g12875.t1	gb|EOA39894.1| hypothetical protein CARUB_v10008573mg [Capsella rubella]	1022	630	3.00E-77	61.6	16.3	23.0	hypothetical protein CARUB_v10008573mg	gbpln	Capsella rubella	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	1022	673	5.00E-56	65.9	14.3	22.3
Rsa1.0_00390.1.g12876.t2	gb|AAF78267.1|AC020576_11 Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene [Arabidopsis thaliana]	956	1206	1.00E-171	126.2	33.5	45.6	Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	956	719	7.00E-35	75.2	14.0	23.4
Rsa1.0_00390.1.g12877.t1	ref|NP_199127.3| TBP-associated factor 4 [Arabidopsis thaliana] gi|38490053|gb|AAR21620.1| TATA-binding protein associated factor 4b [Arabidopsis thaliana] gi|110738778|dbj|BAF01312.1| hypothetical protein [Arabidopsis thaliana] gi|332007530|gb|AED94913.1| TBP-associated factor 4 [Arabidopsis thaliana]	783	823	0	105.1	86.8	91.7	TBP-associated factor 4	gbpln	Arabidopsis thaliana	AT5G43130.1 | Symbols: TAF4, TAF4B | TBP-associated factor 4 | chr5:17315608-17321144 REVERSE LENGTH=823	783	823	0	105.1	86.8	91.7
Rsa1.0_00390.1.g12878.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1518	1499	0	98.7	64.8	77.8	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1518	158	2.00E-29	10.4	4.2	5.3

Rsa1.0_00390.1.g12879.t4	gb|AAC26674.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1722	970	0	56.3	28.5	36.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337-69884 REVERSE LENGTH=515	1722	515	1.00E-132	29.9	14.5	18.6
Rsa1.0_00390.1.g12880.t1	ref|NP_171890.1| HXXXD-type acyl-transferase family protein [Arabidopsis thaliana] gi|75217119|sp|Q9ZWB4.1|3AT1_ARATH RecName: Full=Coumaroyl-CoA:anthocyanidin 3-O-glucoside-6''-O-coumaroyltransferase 1 gi|4204295|gb|AAD10676.1| Hypothetical protein [Arabidopsis thaliana] gi|332189515|gb|AEE27636.1| coumaroyl-CoA:anthocyanidin 3-O-glucoside-6'-O-coumaroyltransferase 1 [Arabidopsis thaliana]	467	469	0	100.4	81.2	88.4	HXXXD-type acyl-transferase family protein	gbpln	Arabidopsis thaliana	AT1G03940.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:1009542-1010951 REVERSE LENGTH=469	467	469	0	100.4	81.2	88.4
Rsa1.0_00390.1.g12881.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00390.1.g12882.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	545	1356	1.00E-115	248.8	37.6	48.8	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT1G03905.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:993478-995594 FORWARD LENGTH=290	545	290	4.00E-81	53.2	28.6	30.8
Rsa1.0_00390.1.g12883.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00390.1.g12884.t3	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	866	1142	1.00E-79	131.9	18.7	28.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	866	575	3.00E-39	66.4	12.7	21.9
Rsa1.0_00390.1.g12885.t1	ref|XP_002877500.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323338|gb|EFH53759.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	135	136	2.00E-28	100.7	42.2	63.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G05095.1 | Symbols: | BEST Arabidopsis thaliana protein match is: RNA-directed DNA polymerase (reverse transcriptase)-related family protein (TAIR:AT4G04650.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:2613798-2614214 REVERSE LENGTH=138	135	138	1.00E-13	102.2	33.3	49.6
Rsa1.0_00390.1.g12886.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	116	1123	2.00E-31	968.1	55.2	63.8	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00391.1.g12887.t1	ref|NP_565402.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|13877877|gb|AAK44016.1|AF370201_1 unknown protein [Arabidopsis thaliana] gi|21280879|gb|AAM44931.1| unknown protein [Arabidopsis thaliana] gi|330251481|gb|AEC06575.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	514	504	0	98.1	72.4	79.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G17033.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:7401205-7403207 FORWARD LENGTH=504	514	504	0	98.1	72.4	79.8
Rsa1.0_00391.1.g12888.t2	ref|NP_565401.1| F-box protein SKIP23 [Arabidopsis thaliana] gi|122215148|sp|Q3EBZ2.1|SKI23_ARATH RecName: Full=F-box protein SKIP23; AltName: Full=SKP1-interacting partner 23 gi|119935952|gb|ABM06043.1| At2g17030 [Arabidopsis thaliana] gi|330251480|gb|AEC06574.1| F-box protein SKIP23 [Arabidopsis thaliana]	445	407	0	91.5	74.8	82.5	F-box protein SKIP23	gbpln	Arabidopsis thaliana	AT2G17030.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr2:7399108-7400650 FORWARD LENGTH=407	445	407	0	91.5	74.8	82.5
Rsa1.0_00391.1.g12889.t1	sp|F4IME2.2|MSL8_ARATH RecName: Full=Mechanosensitive ion channel protein 8; AltName: Full=Mechanosensitive channel of small conductance-like 8; AltName: Full=MscS-Like protein 8	859	908	0	105.7	81.1	88.6	RecName: Full=Mechanosensitive ion channel protein 8; AltName: Full=Mechanosensitive channel of small conductance-like 8; AltName: Full=MscS-Like protein 8	----	----	AT2G17000.1 | Symbols: | Mechanosensitive ion channel family protein | chr2:7388893-7392105 REVERSE LENGTH=849	859	849	0	98.8	60.8	74.6
Rsa1.0_00391.1.g12890.t1	ref|XP_002886089.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297331929|gb|EFH62348.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	856	851	0	99.4	84.6	90.9	mechanosensitive ion channel domain-containing protein	gbpln	Arabidopsis lyrata	AT2G17000.1 | Symbols: | Mechanosensitive ion channel family protein | chr2:7388893-7392105 REVERSE LENGTH=849	856	849	0	99.2	83.6	90.2
Rsa1.0_00391.1.g12891.t1	ref|NP_179291.2| major facilitator protein [Arabidopsis thaliana] gi|79322376|ref|NP_001031360.1| major facilitator protein [Arabidopsis thaliana] gi|330251475|gb|AEC06569.1| major facilitator protein [Arabidopsis thaliana] gi|330251476|gb|AEC06570.1| major facilitator protein [Arabidopsis thaliana]	266	456	1.00E-119	171.4	85.0	91.4	major facilitator protein	gbpln	Arabidopsis thaliana	AT2G16990.2 | Symbols: | Major facilitator superfamily protein | chr2:7383194-7387783 FORWARD LENGTH=456	266	456	1.00E-122	171.4	85.0	91.4

Rsa1.0_00391.1.g12892.t1	gb|EOA30555.1| hypothetical protein CARUB_v10013679mg [Capsella rubella]	87	455	1.00E−34	523.0	83.9	89.7	hypothetical protein CARUB_v10013679mg	gbpln	Capsella rubella	AT2G16990.2 | Symbols: | Major facilitator superfamily protein | chr2:7383194−7387783 FORWARD LENGTH=456	87	456	9.00E−37	524.1	83.9	88.5
Rsa1.0_00391.1.g12893.t1	ref|NP_188314.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana] gi|75274022|sp|Q9LSQ2.1|PP239_ARATH RecName: Full=Putative pentatricopeptide repeat−containing protein At3g16890, mitochondrial; AltName: Full=Protein PENTATRICOPEPTIDE REPEAT 40; Flags: Precursor gi|7670019|dbj|BAA94973.1| salt−inducible protein−like [Arabidopsis thaliana] gi|332642359|gb|AEE75880.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana]	644	659	0	102.3	74.8	84.0	pentatricopeptide repeat−containing protein	gbpln	Arabidopsis thaliana	AT3G16890.1 | Symbols: PPR40 | pentatricopeptide (PPR) domain protein 40 | chr3:5768401−5770380 REVERSE LENGTH=659	644	659	0	102.3	74.8	84.0
Rsa1.0_00391.1.g12894.t1	gb|EOA31984.1| hypothetical protein CARUB_v10015224mg [Capsella rubella]	896	891	0	99.4	90.1	93.3	hypothetical protein CARUB_v10015224mg	gbpln	Capsella rubella	AT2G16950.2 | Symbols: TRN1, ATTRN1 | transportin 1 | chr2:7353939−7360637 FORWARD LENGTH=891	896	891	0	99.4	89.2	92.5
Rsa1.0_00391.1.g12895.t1	gb|EOA29763.1| hypothetical protein CARUB_v10012853mg [Capsella rubella]	1103	1127	0	102.2	79.5	88.3	hypothetical protein CARUB_v10012853mg	gbpln	Capsella rubella	AT2G16920.1 | Symbols: UBC23, PFU2 | ubiquitin−conjugating enzyme 23 | chr2:7334559−7338827 REVERSE LENGTH=1102	1103	1102	0	99.9	79.2	87.0
Rsa1.0_00391.1.g12896.t1	emb|CAD54298.1| bHLH transcription factor [Brassica napus]	560	564	0	100.7	93.2	95.7	bHLH transcription factor	gbpln	Brassica napus	AT2G16910.1 | Symbols: AMS | basic helix−loop−helix (bHLH) DNA−binding superfamily protein | chr2:7331721−7334077 FORWARD LENGTH=571	560	571	0	102.0	85.5	90.9
Rsa1.0_00391.1.g12897.t1	ref|XP_002884020.1| hypothetical protein ARALYDRAFT_480568 [Arabidopsis lyrata subsp. lyrata] gi|297329860|gb|EFH60279.1| hypothetical protein ARALYDRAFT_480568 [Arabidopsis lyrata subsp. lyrata]	475	479	0	100.8	83.2	91.8	hypothetical protein ARALYDRAFT_480568	gbpln	Arabidopsis lyrata	AT2G16890.2 | Symbols: | UDP−Glycosyltransferase superfamily protein | chr2:7316938−7319022 FORWARD LENGTH=478	475	478	0	100.6	80.6	90.1
Rsa1.0_00391.1.g12898.t1	gb|AAB88009.1| heat shock cognate protein HSC70 [Brassica napus]	587	645	0	109.9	95.4	98.1	heat shock cognate protein HSC70	gbpln	Brassica napus	AT5G02500.1 | Symbols: HSC70−1, HSP70−1, AT−HSC70−1, HSC70 | heat shock cognate protein 70−1 | chr5:554055−556334 REVERSE LENGTH=651	587	651	0	110.9	95.4	98.1
Rsa1.0_00391.1.g12899.t1	gb|EOA16600.1| hypothetical protein CARUB_v10004773mg, partial [Capsella rubella]	66	458	5.00E−18	693.9	74.2	81.8	hypothetical protein CARUB_v10004773mg, partial	gbpln	Capsella rubella	AT4G35050.1 | Symbols: MSI3, NFC3 | Transducin family protein / WD−40 repeat family protein | chr4:16682752−16684751 REVERSE LENGTH=424	66	424	1.00E−20	642.4	74.2	81.8
Rsa1.0_00391.1.g12900.t1	gb|EOA31263.1| hypothetical protein CARUB_v10014436mg [Capsella rubella] gi|482567075|gb|EOA31264.1| hypothetical protein CARUB_v10014436mg [Capsella rubella]	249	258	1.00E−106	103.6	82.3	89.6	hypothetical protein CARUB_v10014436mg	gbpln	Capsella rubella	AT2G16770.1 | Symbols: bZIP23 | Basic−leucine zipper (bZIP) transcription factor family protein | chr2:7279859−7280817 FORWARD LENGTH=249	249	249	1.00E−106	100.0	80.7	86.3
Rsa1.0_00391.1.g12901.t22	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	929	1274	0	137.1	46.1	60.4	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	929	575	1.00E−64	61.9	18.5	29.4
Rsa1.0_00391.1.g12902.t1	ref|XP_002886073.1| beta−galactosidase 13 [Arabidopsis lyrata subsp. lyrata] gi|297331913|gb|EFH62332.1| beta−galactosidase 13 [Arabidopsis lyrata subsp. lyrata]	844	848	0	100.5	88.6	94.1	beta−galactosidase 13	gbpln	Arabidopsis lyrata	AT2G16730.1 | Symbols: BGAL13 | glycosyl hydrolase family 35 protein | chr2:7261986−7266105 REVERSE LENGTH=848	844	848	0	100.5	87.8	94.2
Rsa1.0_00391.1.g12903.t4	ref|XP_002886070.1| hypothetical protein ARALYDRAFT_899989 [Arabidopsis lyrata subsp. lyrata] gi|297331910|gb|EFH62329.1| hypothetical protein ARALYDRAFT_899989 [Arabidopsis lyrata subsp. lyrata]	338	292	1.00E−140	86.4	80.5	83.4	hypothetical protein ARALYDRAFT_899989	gbpln	Arabidopsis lyrata	AT4G35000.1 | Symbols: APX3 | ascorbate peroxidase 3 | chr4:16665007−16667541 REVERSE LENGTH=287	338	287	1.00E−126	84.9	72.2	77.2
Rsa1.0_00392.1.g12904.t1	dbj|BAC42653.1| putative glycine−rich protein [Arabidopsis thaliana] gi|28416867|gb|AAO42964.1| At4g29030 [Arabidopsis thaliana]	109	115	3.00E−13	105.5	36.7	40.4	putative glycine−rich protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00392.1.g12905.t1	ref|NP_194631.1| glycine−rich protein [Arabidopsis thaliana] gi|4972048|emb|CAB43916.1| glycine−rich protein like [Arabidopsis thaliana] gi|7269800|emb|CAB79660.1| glycine−rich protein like [Arabidopsis thaliana] gi|15292933|gb|AAK93577.1| putative glycine−rich protein [Arabidopsis thaliana] gi|20465685|gb|AAM20311.1| putative glycine−rich protein 5 [Arabidopsis thaliana] gi|21592872|gb|AAM64822.1| glycine−rich protein like [Arabidopsis thaliana] gi|332660173|gb|AEE85573.1| glycine−rich protein [Arabidopsis thaliana]	145	158	2.00E−15	109.0	26.2	28.3	glycine−rich protein	gbpln	Arabidopsis thaliana	AT4G29020.2 | Symbols: | glycine−rich protein | chr4:14305032−14305508 FORWARD LENGTH=113	145	113	6.00E−18	77.9	26.2	28.3
Rsa1.0_00392.1.g12906.t1	#	#	#	#	#	#	#	–	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00392.1.g12907.t2	ref|XP_002867428.1| hypothetical protein ARALYDRAFT_491857 [Arabidopsis lyrata subsp. lyrata] gi|297313264|gb|EFH43687.1| hypothetical protein ARALYDRAFT_491857 [Arabidopsis lyrata subsp. lyrata]	728	721	0	99.0	88.0	94.0	hypothetical protein ARALYDRAFT_491857	gbpln	Arabidopsis lyrata	AT4G29010.1 | Symbols: AIM1 | Enoyl−CoA hydratase/isomerase family | chr4:14297312−14302016 REVERSE LENGTH=721	728	721	0	99.0	87.5	93.7
Rsa1.0_00392.1.g12908.t1	ref|XP_002869459.1| hypothetical protein ARALYDRAFT_491858 [Arabidopsis lyrata subsp. lyrata] gi|297315295|gb|EFH45718.1| hypothetical protein ARALYDRAFT_491858 [Arabidopsis lyrata subsp. lyrata]	496	601	0	121.2	73.0	80.8	hypothetical protein ARALYDRAFT_491858	gbpln	Arabidopsis lyrata	AT4G29000.1 | Symbols: | Tesmin/TSO1−like CXC domain−containing protein | chr4:14293957−14296602 FORWARD LENGTH=603	496	603	0	121.6	75.2	82.5
Rsa1.0_00392.1.g12909.t1	ref|XP_002867435.1| ring−H2 finger protein ATL4J precursor [Arabidopsis lyrata subsp. lyrata] gi|297313271|gb|EFH43694.1| ring−H2 finger protein ATL4J precursor [Arabidopsis lyrata subsp. lyrata]	486	435	1.00E−171	89.5	69.3	75.3	ring−H2 finger protein ATL4J precursor	gbpln	Arabidopsis lyrata	AT4G28890.1 | Symbols: | RING/U−box superfamily protein | chr4:14256437−14257735 REVERSE LENGTH=432	486	432	1.00E−170	88.9	67.1	72.6
Rsa1.0_00392.1.g12910.t1	ref|XP_002867438.1| hypothetical protein ARALYDRAFT_491882 [Arabidopsis lyrata subsp. lyrata] gi|297313274|gb|EFH43697.1| hypothetical protein ARALYDRAFT_491882 [Arabidopsis lyrata subsp. lyrata]	143	143	1.00E−48	100.0	81.8	91.6	hypothetical protein ARALYDRAFT_491882	gbpln	Arabidopsis lyrata	AT2G20260.1 | Symbols: PSAE−2 | photosystem I subunit E−2 | chr2:8736780−8737644 FORWARD LENGTH=145	143	145	2.00E−42	101.4	71.3	81.1
Rsa1.0_00392.1.g12911.t1	gb|EOA15635.1| hypothetical protein CARUB_v10005878mg [Capsella rubella]	94	173	4.00E−13	184.0	41.5	47.9	hypothetical protein CARUB_v10005878mg	gbpln	Capsella rubella	AT4G28730.1 | Symbols: | Glutaredoxin family protein | chr4:14199174−14200712 FORWARD LENGTH=174	94	174	5.00E−15	185.1	38.3	48.9
Rsa1.0_00392.1.g12912.t1	gb|EOA18198.1| hypothetical protein CARUB_v10006681mg [Capsella rubella]	425	426	0	100.2	90.6	94.8	hypothetical protein CARUB_v10006681mg	gbpln	Capsella rubella	AT4G28720.1 | Symbols: YUC8 | Flavin−binding monooxygenase family protein | chr4:14192688−14193968 FORWARD LENGTH=426	425	426	0	100.2	89.9	95.1
Rsa1.0_00392.1.g12913.t1	#	#	#	#	#	#	#	–	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00392.1.g12914.t1	dbj|BAJ34056.1| unnamed protein product [Thellungiella halophila]	408	415	1.00E−177	101.7	85.5	90.0	unnamed protein product	−−−−	−−−−	AT4G28610.1 | Symbols: PHR1, AtPHR1 | phosphate starvation response 1 | chr4:14133164−14134951 REVERSE LENGTH=409	408	409	1.00E−173	100.2	79.7	87.7
Rsa1.0_00392.1.g12915.t1	ref|XP_002869490.1| hypothetical protein ARALYDRAFT_328837 [Arabidopsis lyrata subsp. lyrata] gi|297315326|gb|EFH45749.1| hypothetical protein ARALYDRAFT_328837 [Arabidopsis lyrata subsp. lyrata]	658	739	0	112.3	82.2	90.1	hypothetical protein ARALYDRAFT_328837	gbpln	Arabidopsis lyrata	AT4G28600.1 | Symbols: NPGR2 | no pollen germination related 2 | chr4:14130046−14132599 FORWARD LENGTH=739	658	739	0	112.3	81.8	90.0
Rsa1.0_00392.1.g12916.t1	ref|NP_194588.2| uncharacterized protein [Arabidopsis thaliana] gi|332660110|gb|AEE85510.1| uncharacterized protein AT4G28590 [Arabidopsis thaliana]	326	331	1.00E−138	101.5	81.0	86.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G28590.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: Thioredoxin superfamily protein (TAIR:AT2G31840.1); Has 114 Blast hits to 112 proteins in 39 species: Archae − 2; Bacteria − 0; Metazoa − 17; Fungi − 6; Plants − 67; Viruses − 0; Other Eukaryotes − 22 (source: NCBI BLink). | chr4:14125367−14126828 REVERSE LENGTH=331	326	331	1.00E−141	101.5	81.0	86.8

<table>
<tr><td>Rsa1.0_00392.1.g12917.t1</td><td>ref|NP_194584.3| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|119935837|gb|ABM06008.1| At4g28550 [Arabidopsis thaliana] gi|332660104|gb|AEE85504.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana]</td><td>421</td><td>424</td><td>0</td><td>100.7</td><td>91.4</td><td>96.0</td><td>RabGAP/TBC domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G28550.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr4:14111204-14113468 FORWARD LENGTH=424</td><td>421</td><td>424</td><td>0</td><td>100.7</td><td>91.4</td><td>96.0</td></tr>
<tr><td>Rsa1.0_00392.1.g12918.t1</td><td>ref|NP_567812.1| casein kinase I-like 6 [Arabidopsis thaliana] gi|20466498|gb|AAM20566.1| protein kinase ADK1-like protein [Arabidopsis thaliana] gi|23198156|gb|AAN15605.1| protein kinase ADK1-like protein [Arabidopsis thaliana] gi|62996982|gb|AAY24535.1| casein kinase 1-like protein 6 [Arabidopsis thaliana] gi|332660103|gb|AEE85503.1| casein kinase I-like 6 [Arabidopsis thaliana]</td><td>487</td><td>479</td><td>0</td><td>98.4</td><td>88.9</td><td>93.0</td><td>casein kinase I-like 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G28540.1 | Symbols: CKL6, PAPK1 | casein kinase I-like 6 | chr4:14107284-14110511 FORWARD LENGTH=479</td><td>487</td><td>479</td><td>0</td><td>98.4</td><td>88.9</td><td>93.0</td></tr>
<tr><td>Rsa1.0_00392.1.g12919.t1</td><td>ref|NP_188381.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75274267|sp|Q9LUP4.1|FBK60_ARATH RecName: Full=Putative F-box/kelch-repeat protein At3g17540 gi|9294141|dbj|BAB02043.1| unnamed protein product [Arabidopsis thaliana] gi|332642445|gb|AEE75966.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]</td><td>379</td><td>396</td><td>3.00E-96</td><td>104.5</td><td>52.8</td><td>69.7</td><td>putative F-box/kelch-repeat protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G17540.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6002783-6003973 FORWARD LENGTH=396</td><td>379</td><td>396</td><td>7.00E-99</td><td>104.5</td><td>52.8</td><td>69.7</td></tr>
<tr><td>Rsa1.0_00393.1.g12920.t1</td><td>ref|NP_187361.1| putative GTP-binding protein [Arabidopsis thaliana] gi|6729012|gb|AAF27009.1|AC016827_20 putative GTPase [Arabidopsis thaliana] gi|332640972|gb|AEE74493.1| putative GTP-binding protein [Arabidopsis thaliana] gi|414420744|gb|AFW99797.1| nucleostemin-like 1 protein [Arabidopsis thaliana]</td><td>722</td><td>582</td><td>2.00E-39</td><td>80.6</td><td>12.7</td><td>14.4</td><td>putative GTP-binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G07050.1 | Symbols: | GTP-binding family protein | chr3:2229602-2232279 REVERSE LENGTH=582</td><td>722</td><td>582</td><td>4.00E-42</td><td>80.6</td><td>12.7</td><td>14.4</td></tr>
<tr><td>Rsa1.0_00393.1.g12921.t1</td><td>ref|NP_198906.2| Nucleotide-diphospho-sugar transferase family protein [Arabidopsis thaliana] gi|332007231|gb|AED94614.1| Nucleotide-diphospho-sugar transferase family protein [Arabidopsis thaliana]</td><td>303</td><td>322</td><td>1.00E-123</td><td>106.3</td><td>76.2</td><td>86.5</td><td>Nucleotide-diphospho-sugar transferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G40900.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr5:16391847-16393375 FORWARD LENGTH=322</td><td>303</td><td>322</td><td>1.00E-125</td><td>106.3</td><td>76.2</td><td>86.5</td></tr>
<tr><td>Rsa1.0_00393.1.g12922.t2</td><td>ref|XP_002875828.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321666|gb|EFH52087.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>291</td><td>486</td><td>5.00E-54</td><td>167.0</td><td>36.1</td><td>48.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361</td><td>291</td><td>361</td><td>3.00E-21</td><td>124.1</td><td>19.9</td><td>30.2</td></tr>
<tr><td>Rsa1.0_00393.1.g12923.t1</td><td>gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]</td><td>1371</td><td>1463</td><td>0</td><td>106.7</td><td>46.4</td><td>61.3</td><td>F5J5.1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1371</td><td>1262</td><td>3.00E-54</td><td>92.0</td><td>8.7</td><td>13.0</td></tr>
<tr><td>Rsa1.0_00393.1.g12924.t1</td><td>gb|AAF18631.1|AC006228_2 F5J5.2 [Arabidopsis thaliana]</td><td>411</td><td>463</td><td>3.00E-34</td><td>112.7</td><td>23.6</td><td>38.9</td><td>F5J5.2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00393.1.g12925.t1</td><td>gb|ADD09860.1| chloride channel A [Eutrema halophilum]</td><td>770</td><td>776</td><td>0</td><td>100.8</td><td>96.8</td><td>98.6</td><td>chloride channel A</td><td>gbpln</td><td>Eutrema halophilum</td><td>AT5G40890.1 | Symbols: ATCLC-A, CLC-A, CLCA, ATCLCA | chloride channel A | chr5:16381645-16384999 REVERSE LENGTH=775</td><td>770</td><td>775</td><td>0</td><td>100.6</td><td>94.9</td><td>96.8</td></tr>
<tr><td>Rsa1.0_00393.1.g12926.t1</td><td>gb|AAF79253.1|AC023279_2 F12K21.4 [Arabidopsis thaliana]</td><td>591</td><td>857</td><td>1.00E-108</td><td>145.0</td><td>40.6</td><td>58.0</td><td>F12K21.4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785</td><td>591</td><td>785</td><td>7.00E-14</td><td>132.8</td><td>10.8</td><td>19.0</td></tr>
<tr><td>Rsa1.0_00393.1.g12927.t1</td><td>ref|XP_002868626.1| hypothetical protein ARALYDRAFT_493894 [Arabidopsis lyrata subsp. lyrata] gi|297314462|gb|EFH44885.1| hypothetical protein ARALYDRAFT_493894 [Arabidopsis lyrata subsp. lyrata]</td><td>706</td><td>805</td><td>1.00E-149</td><td>114.0</td><td>42.2</td><td>51.3</td><td>hypothetical protein ARALYDRAFT_493894</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G40840.1 | Symbols: SYN2, AtRAD21.1 | Rad21/Rec8-like family protein | chr5:16359611-16363722 REVERSE LENGTH=809</td><td>706</td><td>809</td><td>1.00E-149</td><td>114.6</td><td>41.9</td><td>50.7</td></tr>
<tr><td>Rsa1.0_00393.1.g12928.t1</td><td>gb|EOA17181.1| hypothetical protein CARUB_v10005452mg [Capsella rubella]</td><td>266</td><td>277</td><td>7.00E-50</td><td>104.1</td><td>45.1</td><td>59.0</td><td>hypothetical protein CARUB_v10005452mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G36340.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr2:15235858-15237489 FORWARD LENGTH=414</td><td>266</td><td>414</td><td>3.00E-24</td><td>155.6</td><td>21.1</td><td>27.4</td></tr>
<tr><td>Rsa1.0_00393.1.g12929.t3</td><td>gb|ABD65056.1| hypothetical protein 27.t00122 [Brassica oleracea]</td><td>474</td><td>239</td><td>5.00E-23</td><td>50.4</td><td>15.0</td><td>21.7</td><td>hypothetical protein 27.t00122</td><td>gbpln</td><td>Brassica oleracea</td><td>ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154</td><td>474</td><td>154</td><td>2.00E-15</td><td>32.5</td><td>10.8</td><td>13.9</td></tr>
</table>

Rsa1.0_00393.1.g12930.t1	ref|NP_198894.2| Lysine histidine transporter 1 [Arabidopsis thaliana] gi|332007211|gb|AED94594.1| Lysine histidine transporter 1 [Arabidopsis thaliana]	443	445	0	100.5	94.6	98.2	Lysine histidine transporter 1	gbpln	Arabidopsis thaliana	AT5G40780.2 | Symbols: | lysine histidine transporter 1 | chr5:16323823-16327082 FORWARD LENGTH=445	443	445	0	100.5	94.6	98.2
Rsa1.0_00394.1.g12931.t1	ref|XP_002884781.1| hypothetical protein ARALYDRAFT_478343 [Arabidopsis lyrata subsp. lyrata] gi|297330621|gb|EFH61040.1| hypothetical protein ARALYDRAFT_478343 [Arabidopsis lyrata subsp. lyrata]	121	1377	3.00E-63	1138.0	95.9	99.2	hypothetical protein ARALYDRAFT_478343	gbpln	Arabidopsis lyrata	AT3G10180.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:3146393-3154644 REVERSE LENGTH=1273	121	1273	2.00E-65	1052.1	95.0	98.3
Rsa1.0_00394.1.g12932.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1525	1307	0	85.7	55.0	67.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1525	1262	1.00E-103	82.8	12.9	20.3
Rsa1.0_00394.1.g12933.t1	ref|XP_002882566.1| hypothetical protein ARALYDRAFT_478142 [Arabidopsis lyrata subsp. lyrata] gi|297328406|gb|EFH58825.1| hypothetical protein ARALYDRAFT_478142 [Arabidopsis lyrata subsp. lyrata]	373	374	0	100.3	91.7	95.7	hypothetical protein ARALYDRAFT_478142	gbpln	Arabidopsis lyrata	AT3G08010.1 | Symbols: ATAB2 | RNA binding | chr3:2556046-2557426 FORWARD LENGTH=374	373	374	0	100.3	90.6	95.2
Rsa1.0_00394.1.g12934.t1	emb|CAB54520.1| MAP3K epsilon 1 protein kinase [Brassica napus]	1143	1299	0	113.6	88.8	90.1	MAP3K epsilon 1 protein kinase	gbpln	Brassica napus	AT3G13530.1 | Symbols: MAPKKK7, MAP3KE1 | mitogen-activated protein kinase kinase kinase 7 | chr3:4411934-4419320 REVERSE LENGTH=1368	1143	1368	0	119.7	81.5	85.9
Rsa1.0_00394.1.g12935.t1	ref|NP_187454.2| Polygalacturonase QRT2 [Arabidopsis thaliana] gi|226736750|sp|Q9SFB7.2|QRT2_ARATH RecName: Full=Polygalacturonase QRT2; Short=AtQRT2; Short=PG QRT2; AltName: Full=Pectinase QRT2; AltName: Full=Protein QUARTET 2; Flags: Precursor gi|332641105|gb|AEE74626.1| Polygalacturonase QRT2 [Arabidopsis thaliana]	441	439	0	99.5	78.5	87.5	Polygalacturonase QRT2	gbpln	Arabidopsis thaliana	AT3G07970.1 | Symbols: QRT2 | Pectin lyase-like superfamily protein | chr3:2541006-2543370 FORWARD LENGTH=439	441	439	0	99.5	78.5	87.5
Rsa1.0_00394.1.g12936.t1	ref|XP_002882563.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328403|gb|EFH58822.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata]	743	715	0	96.2	91.8	94.2	phosphatidylinositol-4-phosphate 5-kinase family protein	gbpln	Arabidopsis lyrata	AT3G07960.1 | Symbols: | Phosphatidylinositol-4-phosphate 5-kinase family protein | chr3:2535274-2538090 FORWARD LENGTH=715	743	715	0	96.2	90.4	93.7
Rsa1.0_00394.1.g12937.t1	ref|XP_002882559.1| hypothetical protein ARALYDRAFT_478135 [Arabidopsis lyrata subsp. lyrata] gi|297328399|gb|EFH58818.1| hypothetical protein ARALYDRAFT_478135 [Arabidopsis lyrata subsp. lyrata]	398	383	0	96.2	84.4	88.9	hypothetical protein ARALYDRAFT_478135	gbpln	Arabidopsis lyrata	AT3G07940.1 | Symbols: | Calcium-dependent ARF-type GTPase activating protein family | chr3:2529542-2531368 FORWARD LENGTH=385	398	385	0	96.7	83.7	89.2
Rsa1.0_00394.1.g12938.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00394.1.g12939.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00394.1.g12940.t1	ref|NP_566323.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|145332002|ref|NP_001078123.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|98960973|gb|ABF58970.1| At3g07890 [Arabidopsis thaliana] gi|110737642|dbj|BAF00761.1| putative GTPase activator protein [Arabidopsis thaliana] gi|332641094|gb|AEE74615.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|332641095|gb|AEE74616.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	401	400	0	99.8	95.0	98.0	RabGAP/TBC domain-containing protein	gbpln	Arabidopsis thaliana	AT3G07890.2 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr3:2516639-2518784 REVERSE LENGTH=400	401	400	0	99.8	95.0	98.0
Rsa1.0_00394.1.g12941.t1	gb|EOA31341.1| hypothetical protein CARUB_v10014515mg [Capsella rubella]	241	238	1.00E-117	98.8	87.6	92.5	hypothetical protein CARUB_v10014515mg	gbpln	Capsella rubella	AT3G07880.1 | Symbols: SCN1 | Immunoglobulin E-set superfamily protein | chr3:2514175-2515544 FORWARD LENGTH=240	241	240	1.00E-114	99.6	85.9	90.0
Rsa1.0_00394.1.g12942.t1	ref|XP_002882554.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297328394|gb|EFH58813.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	410	415	0	101.2	90.5	94.9	F-box family protein	gbpln	Arabidopsis lyrata	AT3G07870.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:2510871-2512124 FORWARD LENGTH=417	410	417	0	101.7	89.5	94.4

Rsa1.0_00394.1.g12943.t1	gb|EOA31581.1| hypothetical protein CARUB_v10014777mg [Capsella rubella] gi|482567393|gb|EOA31582.1| hypothetical protein CARUB_v10014777mg [Capsella rubella]	170	172	9.00E-81	101.2	87.6	93.5	hypothetical protein CARUB_v10014777mg	gbpln	Capsella rubella	AT3G07860.1 | Symbols: | Ubiquitin-like superfamily protein | chr3:2507895-2508656 FORWARD LENGTH=165	170	165	3.00E-78	97.1	87.1	91.8
Rsa1.0_00394.1.g12944.t1	ref|XP_002884670.1| exopolygalacturonase [Arabidopsis lyrata subsp. lyrata] gi|297330510|gb|EFH60929.1| exopolygalacturonase [Arabidopsis lyrata subsp. lyrata]	431	449	1.00E-166	104.2	70.1	81.9	exopolygalacturonase	gbpln	Arabidopsis lyrata	AT3G14040.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:4648607-4650226 REVERSE LENGTH=445	431	445	1.00E-159	103.2	69.6	81.2
Rsa1.0_00394.1.g12945.t1	ref|XP_002869665.1| ShTK domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315501|gb|EFH45924.1| ShTK domain-containing protein [Arabidopsis lyrata subsp. lyrata]	168	290	8.00E-44	172.6	57.7	66.1	ShTK domain-containing protein	gbpln	Arabidopsis lyrata	AT4G25600.1 | Symbols: | Oxoglutarate/iron-dependent oxygenase | chr4:13060712-13062359 FORWARD LENGTH=291	168	291	9.00E-46	173.2	55.4	63.1
Rsa1.0_00394.1.g12946.t1	gb|ABN13878.1| polygalacturonase [Brassica rapa subsp. oleifera]	395	395	0	100.0	93.9	98.2	polygalacturonase	gbpln	Brassica rapa	AT3G07820.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:2496597-2498028 REVERSE LENGTH=391	395	391	0	99.0	85.1	92.7
Rsa1.0_00394.1.g12947.t1	ref|NP_566321.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|16930693|gb|AAL32012.1|AF436830_1 AT3g07810/F17A17_15 [Arabidopsis thaliana] gi|23297627|gb|AAN12995.1| putative RNA-binding protein [Arabidopsis thaliana] gi|332641085|gb|AEE74606.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	496	494	0	99.6	83.9	88.7	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT3G07810.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:2492875-2495052 FORWARD LENGTH=494	496	494	0	99.6	83.9	88.7
Rsa1.0_00394.1.g12948.t1	gb|EOA31343.1| hypothetical protein CARUB_v10014517mg [Capsella rubella]	158	238	4.00E-71	150.6	79.7	83.5	hypothetical protein CARUB_v10014517mg	gbpln	Capsella rubella	AT3G07800.1 | Symbols: | Thymidine kinase | chr3:2489944-2490935 REVERSE LENGTH=238	158	238	1.00E-71	150.6	78.5	81.6
Rsa1.0_00394.1.g12949.t1	gb|AAF13094.1|AC009176_21 unknown protein [Arabidopsis thaliana] gi|6648188|gb|AAF21186.1|AC013483_10 unknown protein [Arabidopsis thaliana]	126	196	3.00E-62	155.6	91.3	96.0	unknown protein	gbpln	Arabidopsis thaliana	AT3G07760.2 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr3:2476723-2477947 FORWARD LENGTH=125	126	125	6.00E-64	99.2	91.3	96.0
Rsa1.0_00394.1.g12950.t1	ref|XP_002882543.1| hypothetical protein ARALYDRAFT_478100 [Arabidopsis lyrata subsp. lyrata] gi|297328383|gb|EFH58802.1| hypothetical protein ARALYDRAFT_478100 [Arabidopsis lyrata subsp. lyrata]	208	208	1.00E-117	100.0	97.6	99.5	hypothetical protein ARALYDRAFT_478100	gbpln	Arabidopsis lyrata	AT3G07680.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr3:2455627-2456652 FORWARD LENGTH=208	208	208	1.00E-119	100.0	97.1	98.6
Rsa1.0_00394.1.g12951.t1	ref|NP_187422.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|42572309|ref|NP_974250.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|79313159|ref|NP_001030659.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|186509893|ref|NP_001118599.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|17433084|sp|Q9SSE5.1|COL9_ARATH RecName: Full=Zinc finger protein CONSTANS-LIKE 9 gi|6466948|gb|AAF13083.1|AC009176_10 unknown protein [Arabidopsis thaliana] gi|119360037|gb|ABL66747.1| At3g07650 [Arabidopsis thaliana] gi|222423327|dbj|BAH19639.1| AT3G07650 [Arabidopsis thaliana] gi|332641059|gb|AEE74580.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641060|gb|AEE74581.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641061|gb|AEE74582.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana] gi|332641062|gb|AEE74583.1| zinc finger protein CONSTANS-LIKE 9 [Arabidopsis thaliana]	358	372	1.00E-167	103.9	84.6	90.2	zinc finger protein CONSTANS-LIKE 9	gbpln	Arabidopsis thaliana	AT3G07650.4 | Symbols: COL9 | CONSTANS-like 9 | chr3:2442494-2443901 FORWARD LENGTH=372	358	372	1.00E-169	103.9	84.6	90.2

Rsa1.0_00394.1.g12952.t1	ref|XP_002882540.1| hypothetical protein ARALYDRAFT_478093 [Arabidopsis lyrata subsp. lyrata] gi|297328380|gb|EFH58799.1| hypothetical protein ARALYDRAFT_478093 [Arabidopsis lyrata subsp. lyrata]	237	241	1.00E-106	101.7	81.0	90.3	hypothetical protein ARALYDRAFT_478093	gbpln	Arabidopsis lyrata	AT3G07640.1 | Symbols: | unknown protein; Has 27 Blast hits to 27 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2438171-2439661 FORWARD LENGTH=241	237	241	1.00E-106	101.7	78.9	89.5
Rsa1.0_00394.1.g12953.t1	gb|AAM61395.1| putative P-protein: chorismate mutase, prephenate dehydratase [Arabidopsis thaliana]	367	381	1.00E-174	103.8	86.6	93.2	putative P-protein: chorismate mutase, prephenate dehydratase	gbpln	Arabidopsis thaliana	AT3G07630.2 | Symbols: ADT2 | arogenate dehydratase 2 | chr3:2435457-2437530 FORWARD LENGTH=381	367	381	1.00E-176	103.8	86.4	92.9
Rsa1.0_00394.1.g12954.t1	gb|AAD09508.1| ATFP4, partial [Arabidopsis thaliana]	139	179	5.00E-47	128.8	73.4	81.3	ATFP4, partial	gbpln	Arabidopsis thaliana	AT3G07600.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:2424300-2424954 REVERSE LENGTH=157	139	157	1.00E-48	112.9	72.7	80.6
Rsa1.0_00394.1.g12955.t1	ref|XP_002882536.1| hypothetical protein ARALYDRAFT_478080 [Arabidopsis lyrata subsp. lyrata] gi|297328376|gb|EFH58795.1| hypothetical protein ARALYDRAFT_478080 [Arabidopsis lyrata subsp. lyrata]	254	251	1.00E-124	98.8	85.8	91.7	hypothetical protein ARALYDRAFT_478080	gbpln	Arabidopsis lyrata	AT3G07565.1 | Symbols: | Protein of unknown function (DUF3755) | chr3:2413823-2415872 FORWARD LENGTH=258	254	258	1.00E-126	101.6	88.2	93.7
Rsa1.0_00394.1.g12956.t1	gb|EOA31112.1| hypothetical protein CARUB_v10014265mg [Capsella rubella]	315	302	8.00E-96	95.9	76.2	78.7	hypothetical protein CARUB_v10014265mg	gbpln	Capsella rubella	AT3G07560.1 | Symbols: APM2, PEX13 | peroxin 13 | chr3:2411616-2413310 REVERSE LENGTH=304	315	304	3.00E-65	96.5	37.8	38.4
Rsa1.0_00394.1.g12957.t1	gb|EOA29856.1| hypothetical protein CARUB_v10012950mg, partial [Capsella rubella]	288	883	5.00E-92	306.6	66.3	80.6	hypothetical protein CARUB_v10012950mg, partial	gbpln	Capsella rubella	AT3G07540.1 | Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr3:2404763-2407464 REVERSE LENGTH=841	288	841	4.00E-93	292.0	65.3	78.5
Rsa1.0_00394.1.g12958.t1	ref|NP_566310.1| uncharacterized protein [Arabidopsis thaliana] gi|145331996|ref|NP_001078120.1| uncharacterized protein [Arabidopsis thaliana] gi|13877549|gb|AAK43852.1|AF370475_1 Unknown protein [Arabidopsis thaliana] gi|20148735|gb|AAM10258.1| unknown protein [Arabidopsis thaliana] gi|332641030|gb|AEE74551.1| uncharacterized protein AT3G07510 [Arabidopsis thaliana] gi|332641031|gb|AEE74552.1| uncharacterized protein AT3G07510 [Arabidopsis thaliana]	305	189	1.00E-61	62.0	44.3	46.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G07510.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G01580.1); Has 133 Blast hits to 133 proteins in 14 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 129; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2393895-2394464 REVERSE LENGTH=189	305	189	3.00E-64	62.0	44.3	46.2
Rsa1.0_00395.1.g12959.t1	gb|AEX07593.1| cyclin-dependent kinase B2_2, partial [Brassica juncea]	314	307	1.00E-176	97.8	95.9	95.9	cyclin-dependent kinase B2_2, partial	gbpln	Brassica juncea	AT1G20930.1 | Symbols: CDKB2;2 | cyclin-dependent kinase B2;2 | chr1:7292752-7294664 REVERSE LENGTH=315	314	315	1.00E-176	100.3	94.3	96.5
Rsa1.0_00395.1.g12960.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00395.1.g12961.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00395.1.g12962.t1	ref|NP_173523.1| DC1 domain-containing protein [Arabidopsis thaliana] gi|332191930|gb|AEE30051.1| DC1 domain-containing protein [Arabidopsis thaliana]	176	319	3.00E-62	181.3	85.2	92.0	DC1 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G20990.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:7330524-7331946 REVERSE LENGTH=319	176	319	1.00E-64	181.3	85.2	92.0
Rsa1.0_00395.1.g12963.t1	ref|XP_002893147.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338989|gb|EFH69406.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	161	322	2.00E-58	200.0	71.4	78.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G20990.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:7330524-7331946 REVERSE LENGTH=319	161	319	2.00E-59	198.1	68.3	78.3
Rsa1.0_00395.1.g12964.t1	gb|EOA36953.1| hypothetical protein CARUB_v10009886mg [Capsella rubella]	199	296	7.00E-79	148.7	82.9	89.4	hypothetical protein CARUB_v10009886mg	gbpln	Capsella rubella	AT1G21010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76600.1); Has 206 Blast hits to 206 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 206; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7346239-7346871 FORWARD LENGTH=210	199	210	6.00E-79	105.5	82.9	88.9
Rsa1.0_00395.1.g12965.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00395.1.g12966.t1	ref|NP_177787.1| uncharacterized protein [Arabidopsis thaliana] gi|12323988|gb|AAG51959.1|AC015450_20 hypothetical protein; 87351-88031 [Arabidopsis thaliana] gi|55740535|gb|AAV63860.1| hypothetical protein At1g76610 [Arabidopsis thaliana] gi|332197743|gb|AEE35864.1| uncharacterized protein AT1G76610 [Arabidopsis thaliana]	201	226	1.00E-50	112.4	61.2	75.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G76610.1 | Symbols: | Protein of unknown function, DUF617 | chr1:28751049-28751729 FORWARD LENGTH=226	201	226	4.00E-53	112.4	61.2	75.1
Rsa1.0_00395.1.g12967.t1	gb|ABW74585.1| pol polyprotein [Boechera divaricarpa]	367	551	3.00E-82	150.1	46.6	57.8	pol polyprotein	gbpln	Boechera divaricarpa	#	#	#	#	#	#	#
Rsa1.0_00395.1.g12968.t1	gb|AFJ66169.1| hypothetical protein 11M19.13 [Arabidopsis halleri]	98	1273	7.00E-19	1299.0	42.9	62.2	hypothetical protein 11M19.13	gbpln	Arabidopsis halleri	#	#	#	#	#	#	#
Rsa1.0_00395.1.g12969.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00395.1.g12970.t1	ref|NP_564135.1| cupredoxin-like protein [Arabidopsis thaliana] gi|111074298|gb|ABH04522.1| At1g21090 [Arabidopsis thaliana] gi|332191942|gb|AEE30063.1| cupredoxin-like protein [Arabidopsis thaliana]	244	242	1.00E-110	99.2	82.4	89.8	cupredoxin-like protein	gbpln	Arabidopsis thaliana	AT1G21090.1 | Symbols: | Cupredoxin superfamily protein | chr1:7384854-7386199 FORWARD LENGTH=242	244	242	1.00E-113	99.2	82.4	89.8
Rsa1.0_00395.1.g12971.t1	ref|NP_173534.1| O-methyltransferase-like protein [Arabidopsis thaliana] gi|8886991|gb|AAF80651.1|AC012190_7 Contains similarity to O-Methyltransferase 1 from Arabidopsis thaliana gb|U70424. It is a member of O-methyltransferase family. ESTs gb|AI994826, gb|N65066 and gb|N38589 come from this gene [Arabidopsis thaliana] gi|12744975|gb|AAK06867.1|AF344316_1 putative O-methyltransferase [Arabidopsis thaliana] gi|15982844|gb|AAL09769.1| At1g21100/T22I11_7 [Arabidopsis thaliana] gi|23506107|gb|AAN28913.1| At1g21100/T22I11_7 [Arabidopsis thaliana] gi|332191943|gb|AEE30064.1| O-methyltransferase-like protein [Arabidopsis thaliana]	376	373	0	99.2	89.4	94.1	O-methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT1G21100.1 | Symbols: | O-methyltransferase family protein | chr1:7386991-7388318 REVERSE LENGTH=373	376	373	0	99.2	89.4	94.1
Rsa1.0_00395.1.g12972.t1	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	687	521	4.00E-44	75.8	16.0	22.4	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	687	336	2.00E-15	48.9	7.1	11.9
Rsa1.0_00395.1.g12973.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	787	1142	0	145.1	45.7	57.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	787	626	5.00E-40	79.5	16.0	25.2
Rsa1.0_00395.1.g12974.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00395.1.g12975.t1	gb|EOA36591.1| hypothetical protein CARUB_v10011787mg [Capsella rubella]	756	732	0	96.8	73.0	83.1	hypothetical protein CARUB_v10011787mg	gbpln	Capsella rubella	AT1G21210.1 | Symbols: WAK4 | wall associated kinase 4 | chr1:7424653-7427041 FORWARD LENGTH=738	756	738	0	97.6	70.2	81.1
Rsa1.0_00395.1.g12976.t1	gb|EOA39743.1| hypothetical protein CARUB_v10008400mg [Capsella rubella]	628	740	0	117.8	73.6	81.1	hypothetical protein CARUB_v10008400mg	gbpln	Capsella rubella	AT1G21270.1 | Symbols: WAK2 | wall-associated kinase 2 | chr1:7444997-7447345 FORWARD LENGTH=732	628	732	0	116.6	68.5	77.1

Rsa1.0_00395.1.g12977.t1	ref|NP_173553.1| extensin 3 [Arabidopsis thaliana] gi|334302912|sp|Q9FS16.3|EXTN3_ARATH RecName: Full=Extensin-3; Short=AtExt3; Short=AtExt5; Flags: Precursor gi|8920638|gb|AAF81360.1|AC036104_9 Contains similarity to Extensin (atExt1) from Arabidopsis thaliana gb|U43627 and contains 12 concatamers of 28 amino acids rich in proline. ESTs gb|AA597816, gb|AA712635, gb|N65860, gb|AA598180, gb|H77085, gb|AA394416, gb|AA394413, gb|AA650774, gb|AA650748, gb|Z25975, gb|AA597958, gb|AA597955 come from this gene [Arabidopsis thaliana] gi|332191962|gb|AEE30083.1| extensin 3 [Arabidopsis thaliana]	352	431	5.00E-81	122.4	98.0	98.0	extensin 3	gbpln	Arabidopsis thaliana	AT1G21310.1 | Symbols: ATEXT3, RSH, EXT3 | extensin 3 | chr1:7453693-7454988 REVERSE LENGTH=431	352	431	1.00E-83	122.4	98.0	98.0
Rsa1.0_00396.1.g12978.t1	ref|NP_189147.1| fatA acyl-ACP thioesterase [Arabidopsis thaliana] gi|75275267|sp|Q42561.1|FATA1_ARATH RecName: Full=Oleoyl-acyl carrier protein thioesterase 1, chloroplastic; AltName: Full=18:0-acyl-carrier protein thioesterase; Short=18:0-ACP thioesterase; AltName: Full=Acyl-[acyl-carrier-protein] hydrolase; Flags: Precursor gi|804946|emb|CAA85389.1| acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana] gi|9294167|dbj|BAB02069.1| acyl carrier protein thioesterase [Arabidopsis thaliana] gi|51970352|dbj|BAD43868.1| acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana] gi|332643459|gb|AEE76980.1| fatA acyl-ACP thioesterase [Arabidopsis thaliana]	151	362	1.00E-16	239.7	27.2	29.1	fatA acyl-ACP thioesterase	gbpln	Arabidopsis thaliana	AT3G25110.1 | Symbols: AtFaTA, FaTA | fatA acyl-ACP thioesterase | chr3:9146589-9148273 REVERSE LENGTH=362	151	362	4.00E-19	239.7	27.2	29.1
Rsa1.0_00396.1.g12979.t1	gb|AAM66136.1| polyneuridine aldehyde esterase, putative [Arabidopsis thaliana]	347	347	0	100.0	93.9	96.5	polyneuridine aldehyde esterase, putative	gbpln	Arabidopsis thaliana	AT1G33990.1 | Symbols: ATMES14, MES14 | methyl esterase 14 | chr1:12355909-12357894 FORWARD LENGTH=348	347	348	0	100.3	92.8	95.4
Rsa1.0_00396.1.g12980.t1	dbj|BAJ33748.1| unnamed protein product [Thellungiella halophila]	172	177	8.00E-69	102.9	87.8	94.2	unnamed protein product	----	----	AT1G34000.1 | Symbols: OHP2 | one-helix protein 2 | chr1:12358151-12358902 REVERSE LENGTH=172	172	172	9.00E-71	100.0	88.4	92.4
Rsa1.0_00396.1.g12981.t1	ref|XP_002893799.1| hypothetical protein ARALYDRAFT_313917 [Arabidopsis lyrata subsp. lyrata] gi|297339641|gb|EFH70058.1| hypothetical protein ARALYDRAFT_313917 [Arabidopsis lyrata subsp. lyrata]	214	187	5.00E-70	87.4	64.0	71.5	hypothetical protein ARALYDRAFT_313917	gbpln	Arabidopsis lyrata	AT1G34010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22790.2); Has 74 Blast hits to 74 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12359821-12360838 REVERSE LENGTH=182	214	182	1.00E-69	85.0	65.0	72.0
Rsa1.0_00396.1.g12982.t1	emb|CAN82943.1| hypothetical protein VITISV_001812 [Vitis vinifera]	405	817	1.00E-127	201.7	58.8	70.9	hypothetical protein VITISV_001812	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	405	1262	1.00E-24	311.6	23.5	34.8
Rsa1.0_00396.1.g12983.t1	emb|CAN60947.1| hypothetical protein VITISV_015758 [Vitis vinifera]	200	1306	1.00E-28	653.0	31.5	34.5	hypothetical protein VITISV_015758	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00396.1.g12984.t1	ref|XP_002891071.1| hypothetical protein ARALYDRAFT_473556 [Arabidopsis lyrata subsp. lyrata] gi|297336913|gb|EFH67330.1| hypothetical protein ARALYDRAFT_473556 [Arabidopsis lyrata subsp. lyrata]	337	335	1.00E-179	99.4	90.2	92.9	hypothetical protein ARALYDRAFT_473556	gbpln	Arabidopsis lyrata	AT1G34020.1 | Symbols: | Nucleotide-sugar transporter family protein | chr1:12367359-12368965 FORWARD LENGTH=335	337	335	0	99.4	89.9	92.9
Rsa1.0_00396.1.g12985.t1	gb|EOA21645.1| hypothetical protein CARUB_v10002063mg, partial [Capsella rubella]	152	183	7.00E-83	120.4	98.0	99.3	hypothetical protein CARUB_v10002063mg, partial	gbpln	Capsella rubella	AT4G09800.1 | Symbols: RPS18C | S18 ribosomal protein | chr4:6173818-6174963 FORWARD LENGTH=152	152	152	2.00E-85	100.0	98.7	100.0
Rsa1.0_00396.1.g12986.t1	emb|CAN79264.1| hypothetical protein VITISV_034881 [Vitis vinifera]	138	1360	5.00E-55	985.5	71.0	85.5	hypothetical protein VITISV_034881	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	138	1262	2.00E-14	914.5	29.0	40.6
Rsa1.0_00396.1.g12987.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00396.1.g12988.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00396.1.g12989.t2	gb|EOA21997.1| hypothetical protein CARUB_v10002508mg, partial [Capsella rubella]	474	448	2.00E-99	94.5	47.0	60.1	hypothetical protein CARUB_v10002508mg, partial	gbpln	Capsella rubella	AT4G02760.3 | Symbols: | RNI-like superfamily protein | chr4:1224336-1227857 REVERSE LENGTH=551	474	551	1.00E-102	116.2	47.5	61.0
Rsa1.0_00396.1.g12990.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00396.1.g12991.t1	gb|AAC02672.1| polyprotein [Arabidopsis arenosa]	136	1390	2.00E-38	1022.1	57.4	75.0	polyprotein	gbpln	Arabidopsis arenosa	#	#	#	#	#	#	#
Rsa1.0_00396.1.g12992.t1	ref|NP_177373.1| trypsin inhibitor (Kunitz) domain-containing protein [Arabidopsis thaliana] gi|12323668|gb|AAG51801.1|AC067754_17 drought induced protein, putative; 79797-80444 [Arabidopsis thaliana] gi|21536624|gb|AAM60956.1| drought induced protein, putative [Arabidopsis thaliana] gi|94442485|gb|ABF19030.1| At1g72290 [Arabidopsis thaliana] gi|332197178|gb|AEE35299.1| trypsin inhibitor (Kunitz) domain-containing protein [Arabidopsis thaliana]	178	215	1.00E-45	120.8	55.6	64.0	trypsin inhibitor (Kunitz) domain-containing protein	gbpln	Arabidopsis thaliana	AT1G72290.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27215852-27216499 FORWARD LENGTH=215	178	215	5.00E-48	120.8	55.6	64.0
Rsa1.0_00396.1.g12993.t1	ref|XP_002888867.1| hypothetical protein ARALYDRAFT_476358 [Arabidopsis lyrata subsp. lyrata] gi|297334708|gb|EFH65126.1| hypothetical protein ARALYDRAFT_476358 [Arabidopsis lyrata subsp. lyrata]	1084	1096	0	101.1	80.0	88.6	hypothetical protein ARALYDRAFT_476358	gbpln	Arabidopsis lyrata	AT1G72300.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr1:27217679-27220966 REVERSE LENGTH=1095	1084	1095	0	101.0	79.2	88.7
Rsa1.0_00396.1.g12994.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00396.1.g12995.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00396.1.g12996.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1495	1529	0	102.3	43.1	61.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1495	746	9.00E-93	49.9	12.2	15.3
Rsa1.0_00396.1.g12997.t1	ref|XP_002887428.1| hypothetical protein ARALYDRAFT_476359 [Arabidopsis lyrata subsp. lyrata] gi|297333269|gb|EFH63687.1| hypothetical protein ARALYDRAFT_476359 [Arabidopsis lyrata subsp. lyrata]	303	324	1.00E-116	106.9	80.9	88.1	hypothetical protein ARALYDRAFT_476359	gbpln	Arabidopsis lyrata	AT1G72310.1 | Symbols: ATL3 | RING/U-box superfamily protein | chr1:27226405-27227379 FORWARD LENGTH=324	303	324	1.00E-116	106.9	76.6	83.5
Rsa1.0_00396.1.g12998.t1	ref|XP_002887429.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333270|gb|EFH63688.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	76	101	3.00E-15	132.9	76.3	80.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G17285.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17300.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:5920895-5921287 FORWARD LENGTH=95	76	95	2.00E-14	125.0	52.6	65.8
Rsa1.0_00397.1.g12999.t1	ref|NP_188337.1| uncharacterized protein [Arabidopsis thaliana] gi|42572461|ref|NP_974326.1| uncharacterized protein [Arabidopsis thaliana] gi|18087521|gb|AAL58895.1|AF462799_1 AT3g17120/K14A17_24 [Arabidopsis thaliana] gi|7670036|dbj|BAA94990.1| unnamed protein product [Arabidopsis thaliana] gi|332642385|gb|AEE75906.1| uncharacterized protein AT3G17120 [Arabidopsis thaliana] gi|332642386|gb|AEE75907.1| uncharacterized protein AT3G17120 [Arabidopsis thaliana]	200	219	1.00E-76	109.5	84.5	88.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G17120.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02380.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:5842410-5843246 FORWARD LENGTH=219	200	219	4.00E-79	109.5	84.5	88.5
Rsa1.0_00397.1.g13000.t1	gb|EOA31631.1| hypothetical protein CARUB_v10014831mg [Capsella rubella]	174	153	2.00E-22	87.9	45.4	58.6	hypothetical protein CARUB_v10014831mg	gbpln	Capsella rubella	AT3G16660.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr3:5676904-5677788 FORWARD LENGTH=180	174	180	2.00E-24	103.4	48.9	65.5
Rsa1.0_00397.1.g13001.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	509	1501	1.00E-133	294.9	43.4	53.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	509	1262	8.00E-80	247.9	25.3	39.1
Rsa1.0_00397.1.g13002.t1	dbj|BAJ34012.1| unnamed protein product [Thellungiella halophila]	207	227	2.00E-62	109.7	74.9	83.6	unnamed protein product	----	----	AT3G17100.2 | Symbols: | sequence-specific DNA binding transcription factors | chr3:5831552-5832244 FORWARD LENGTH=230	207	230	2.00E-61	111.1	71.5	80.7
Rsa1.0_00397.1.g13003.t1	gb|AAM61747.1| protein phosphatase-2c, putative [Arabidopsis thaliana]	380	384	0	101.1	90.5	95.3	protein phosphatase-2c, putative	gbpln	Arabidopsis thaliana	AT3G17090.1 | Symbols: | Protein phosphatase 2C family protein | chr3:5826984-5829327 FORWARD LENGTH=384	380	384	0	101.1	89.7	94.5

Rsa1.0_00397.1.g13004.t2	ref|XP_002885186.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331026|gb|EFH61445.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	151	344	1.00E-67	227.8	89.4	93.4	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT3G17060.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:5816953-5818458 REVERSE LENGTH=344	151	344	5.00E-69	227.8	88.7	92.7
Rsa1.0_00397.1.g13005.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00397.1.g13006.t1	ref|NP_188328.5| nucleic acid-binding-like protein [Arabidopsis thaliana] gi|332642375|gb|AEE75896.1| nucleic acid-binding-like protein [Arabidopsis thaliana]	665	668	0	100.5	84.7	91.9	nucleic acid-binding-like protein	gbpln	Arabidopsis thaliana	AT3G17030.1 | Symbols: | Nucleic acid-binding proteins superfamily | chr3:5804509-5808462 REVERSE LENGTH=668	665	668	0	100.5	84.7	91.9
Rsa1.0_00397.1.g13007.t1	gb|ABL97971.1| unknown [Brassica rapa]	163	163	1.00E-88	100.0	96.9	98.2	unknown	gbpln	Brassica rapa	AT3G17020.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:5802728-5804063 REVERSE LENGTH=163	163	163	3.00E-82	100.0	86.5	94.5
Rsa1.0_00397.1.g13008.t1	dbj|BAB09171.1| serine/threonine-protein kinase Mak (male germ cell-associated kinase)-like protein [Arabidopsis thaliana]	251	530	1.00E-44	211.2	36.3	39.0	serine/threonine-protein kinase Mak (male germ cell-associated kinase)-like protein	gbpln	Arabidopsis thaliana	AT5G45430.1 | Symbols: | Protein kinase superfamily protein | chr5:18409200-18411711 FORWARD LENGTH=499	251	499	6.00E-47	198.8	36.3	39.0
Rsa1.0_00397.1.g13009.t1	#	#	#	#	#	#	#	-	----	----	AT3G49560.1 | Symbols: | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr3:18370644-18371821 FORWARD LENGTH=261	144	261	1.00E-12	181.3	36.1	53.5
Rsa1.0_00397.1.g13010.t1	gb|EOA18266.1| hypothetical protein CARUB_v10006759mg [Capsella rubella]	137	128	2.00E-12	93.4	31.4	45.3	hypothetical protein CARUB_v10006759mg	gbpln	Capsella rubella	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	137	384	9.00E-14	280.3	30.7	46.0
Rsa1.0_00397.1.g13011.t1	ref|XP_002883037.1| ubiquitin-conjugating enzyme 31 [Arabidopsis lyrata subsp. lyrata] gi|297328877|gb|EFH59296.1| ubiquitin-conjugating enzyme 31 [Arabidopsis lyrata subsp. lyrata]	301	308	1.00E-152	102.3	87.0	92.0	ubiquitin-conjugating enzyme 31	gbpln	Arabidopsis lyrata	AT3G17000.1 | Symbols: UBC32 | ubiquitin-conjugating enzyme 32 | chr3:5797296-5799467 FORWARD LENGTH=309	301	309	1.00E-151	102.7	85.4	89.4
Rsa1.0_00397.1.g13012.t1	gb|EOA32502.1| hypothetical protein CARUB_v10015783mg [Capsella rubella]	366	398	1.00E-125	108.7	65.6	78.1	hypothetical protein CARUB_v10015783mg	gbpln	Capsella rubella	AT3G16740.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:5699476-5700651 FORWARD LENGTH=391	366	391	1.00E-113	106.8	60.7	75.4
Rsa1.0_00397.1.g13013.t1	ref|XP_002885181.1| hypothetical protein ARALYDRAFT_318461 [Arabidopsis lyrata subsp. lyrata] gi|297331021|gb|EFH61440.1| hypothetical protein ARALYDRAFT_318461 [Arabidopsis lyrata subsp. lyrata]	146	143	6.00E-50	97.9	64.4	73.3	hypothetical protein ARALYDRAFT_318461	gbpln	Arabidopsis lyrata	AT3G16970.1 | Symbols: | Plant self-incompatibility protein S1 family | chr3:5793668-5794090 REVERSE LENGTH=140	146	140	4.00E-51	95.9	63.0	73.3
Rsa1.0_00397.1.g13014.t1	gb|EOA31883.1| hypothetical protein CARUB_v10015111mg [Capsella rubella]	186	186	5.00E-94	100.0	89.2	95.7	hypothetical protein CARUB_v10015111mg	gbpln	Capsella rubella	AT3G16900.1 | Symbols: | Protein of unknown function (DUF567) | chr3:5772106-5772849 FORWARD LENGTH=185	186	185	5.00E-91	99.5	84.4	93.5
Rsa1.0_00397.1.g13015.t3	gb|EOA30062.1| hypothetical protein CARUB_v10013169mg [Capsella rubella]	419	654	1.00E-105	156.1	50.4	58.2	hypothetical protein CARUB_v10013169mg	gbpln	Capsella rubella	AT3G16890.1 | Symbols: PPR40 | pentatricopeptide (PPR) domain protein 40 | chr3:5768401-5770380 REVERSE LENGTH=659	419	659	1.00E-107	157.3	51.6	58.7
Rsa1.0_00397.1.g13016.t1	ref|XP_002885174.1| hypothetical protein ARALYDRAFT_479155 [Arabidopsis lyrata subsp. lyrata] gi|297331014|gb|EFH61433.1| hypothetical protein ARALYDRAFT_479155 [Arabidopsis lyrata subsp. lyrata]	131	175	3.00E-16	133.6	54.2	65.6	hypothetical protein ARALYDRAFT_479155	gbpln	Arabidopsis lyrata	AT3G16870.1 | Symbols: GATA17 | GATA transcription factor 17 | chr3:5763752-5764576 REVERSE LENGTH=190	131	190	3.00E-12	145.0	56.5	68.7
Rsa1.0_00398.1.g13017.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00398.1.g13018.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00398.1.g13019.t1	ref|XP_002889113.1| hypothetical protein ARALYDRAFT_316612 [Arabidopsis lyrata subsp. lyrata] gi|297334954|gb|EFH65372.1| hypothetical protein ARALYDRAFT_316612 [Arabidopsis lyrata subsp. lyrata]	240	195	8.00E-14	81.3	23.3	29.6	hypothetical protein ARALYDRAFT_316612	gbpln	Arabidopsis lyrata	AT1G76965.1 | Symbols: | Encodes a Protease inhibitor/seed storage/LTP family protein | chr1:28921729-28922292 REVERSE LENGTH=187	240	187	1.00E-15	77.9	20.0	25.8
Rsa1.0_00398.1.g13020.t2	gb|EOA34253.1| hypothetical protein CARUB_v10021765mg [Capsella rubella]	496	471	0	95.0	75.0	81.0	hypothetical protein CARUB_v10021765mg	gbpln	Capsella rubella	AT1G76970.1 | Symbols: | Target of Myb protein 1 | chr1:28922841-28924854 REVERSE LENGTH=446	496	446	1.00E-171	89.9	68.3	76.4

Rsa1.0_00398.1.g13021.t1	ref|XP_002862501.1| hypothetical protein ARALYDRAFT_497423 [Arabidopsis lyrata subsp. lyrata] gi|297842467|ref|XP_002889115.1| hypothetical protein ARALYDRAFT_476857 [Arabidopsis lyrata subsp. lyrata] gi|297308058|gb|EFH38759.1| hypothetical protein ARALYDRAFT_497423 [Arabidopsis lyrata subsp. lyrata] gi|297334956|gb|EFH65374.1| hypothetical protein ARALYDRAFT_476857 [Arabidopsis lyrata subsp. lyrata]	219	246	3.00E-71	112.3	68.5	74.9	hypothetical protein ARALYDRAFT_497423	gbpln	Arabidopsis lyrata	AT1G76980.1 | Symbols: | BEST Arabidopsis thaliana protein match is: embryo defective 2170 (TAIR:AT1G21390.1); Has 65 Blast hits to 65 proteins in 23 species: Archae - 0; Bacteria - 8; Metazoa - 1; Fungi - 8; Plants - 40; Viruses - 3; Other Eukaryotes - 5 (source: NCBI BLink). | chr1:28926466-28927242 REVERSE LENGTH=258	219	258	5.00E-65	117.8	66.7	73.5
Rsa1.0_00398.1.g13022.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00398.1.g13023.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	942	1223	1.00E-171	129.8	36.8	53.9	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	942	746	3.00E-55	79.2	14.9	22.1
Rsa1.0_00398.1.g13024.t1	ref|NP_565146.1| ACT domain-containing protein 3 [Arabidopsis thaliana] gi|30699222|ref|NP_849896.1| ACT domain-containing protein 3 [Arabidopsis thaliana] gi|30699224|ref|NP_849897.1| ACT domain-containing protein 3 [Arabidopsis thaliana] gi|79321337|ref|NP_001031289.1| ACT domain-containing protein 3 [Arabidopsis thaliana] gi|186495930|ref|NP_001117608.1| ACT domain-containing protein 3 [Arabidopsis thaliana] gi|13430820|gb|AAK26032.1|AF360322_1 unknown protein [Arabidopsis thaliana] gi|2829923|gb|AAC00631.1| Similar to uridylyl transferases [Arabidopsis thaliana] gi|21280959|gb|AAM44939.1| unknown protein [Arabidopsis thaliana] gi|22138096|gb|AAM93428.1| ACR3 [Arabidopsis thaliana] gi|222424164|dbj|BAH20041.1| AT1G76990 [Arabidopsis thaliana] gi|332197796|gb|AEE35917.1| ACT domain-containing protein 3 [Arabidopsis thaliana] gi|332197797|gb|AEE35918.1| ACT domain-containing protein 3 [Arabidopsis thaliana] gi|332197798|gb|AEE35919.1| ACT domain-containing protein 3 [Arabidopsis thaliana] gi|332197799|gb|AEE35920.1| ACT	449	453	0	100.9	92.7	96.7	ACT domain-containing protein 3	gbpln	Arabidopsis thaliana	AT1G76990.5 | Symbols: ACR3 | ACT domain repeat 3 | chr1:28933387-28935179 FORWARD LENGTH=453	449	453	0	100.9	92.7	96.7
Rsa1.0_00398.1.g13025.t1	dbj|BAJ33955.1| unnamed protein product [Thellungiella halophila]	358	367	0	102.5	92.5	96.6	unnamed protein product	----	----	AT1G77000.2 | Symbols: SKP2B | RNI-like superfamily protein | chr1:28940888-28942401 FORWARD LENGTH=360	358	360	0	100.6	88.3	94.4
Rsa1.0_00398.1.g13026.t1	ref|NP_177828.2| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] gi|332197805|gb|AEE35926.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	356	379	0	106.5	93.3	96.3	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT1G77020.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr1:28945056-28946867 REVERSE LENGTH=379	356	379	0	106.5	93.3	96.3
Rsa1.0_00398.1.g13027.t1	gb|AAL61930.1| putative carboxyphosphonoenolpyruvate mutase [Arabidopsis thaliana] gi|21386949|gb|AAM47878.1| putative carboxyphosphonoenolpyruvate mutase [Arabidopsis thaliana]	344	337	0	98.0	90.4	93.9	putative carboxyphosphonoenolpyruvate mutase	gbpln	Arabidopsis thaliana	AT1G77060.1 | Symbols: | Phosphoenolpyruvate carboxylase family protein | chr1:28951804-28953449 REVERSE LENGTH=339	344	339	0	98.5	90.4	93.9
Rsa1.0_00398.1.g13028.t1	ref|XP_002889122.1| thylakoid lumenal 29.8 kDa protein [Arabidopsis lyrata subsp. lyrata] gi|297334963|gb|EFH65381.1| thylakoid lumenal 29.8 kDa protein [Arabidopsis lyrata subsp. lyrata]	248	256	1.00E-111	103.2	83.9	89.9	thylakoid lumenal 29.8 kDa protein	gbpln	Arabidopsis lyrata	AT1G77090.1 | Symbols: | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | chr1:28960576-28961875 REVERSE LENGTH=260	248	260	1.00E-112	104.8	84.3	91.5
Rsa1.0_00398.1.g13029.t1	sp|O49293.2|PER13_ARATH RecName: Full=Peroxidase 13; Short=Atperox P13; Flags: Precursor	319	319	1.00E-152	100.0	80.6	90.0	RecName: Full=Peroxidase 13; Short=Atperox P13; Flags: Precursor	----	----	AT1G77100.1 | Symbols: | Peroxidase superfamily protein | chr1:28965772-28967066 REVERSE LENGTH=336	319	336	1.00E-154	105.3	80.6	90.0

Rsa1.0_00398.1.g13030.t1	gb|EOA34971.1| hypothetical protein CARUB_v10020056mg [Capsella rubella]	549	570	0	103.8	89.6	94.2	hypothetical protein CARUB_v10020056mg	gbpln	Capsella rubella	AT1G77110.1 | Symbols: PIN6 | Auxin efflux carrier family protein | chr1:28970855-28974408 FORWARD LENGTH=570	549	570	0	103.8	87.6	92.9
Rsa1.0_00398.1.g13031.t1	gb|AEC13713.1| alcohol dehydrogenase 1 [Brassica rapa]	379	379	0	100.0	97.4	99.5	alcohol dehydrogenase 1	gbpln	Brassica rapa	AT1G77120.1 | Symbols: ADH1, ADH, ATADH, ATADH1 | alcohol dehydrogenase 1 | chr1:28975509-28977216 FORWARD LENGTH=379	379	379	0	100.0	94.7	98.4
Rsa1.0_00398.1.g13032.t1	ref|XP_002887161.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333002|gb|EFH63420.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	388	374	1.00E-153	96.4	76.3	83.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G67970.1 | Symbols: AT-HSFA8, HSFA8 | heat shock transcription factor A8 | chr1:25484844-25486313 REVERSE LENGTH=374	388	374	1.00E-154	96.4	76.5	82.7
Rsa1.0_00398.1.g13033.t1	ref|NP_176961.1| ABC transporter I family member 17 [Arabidopsis thaliana] gi|75333593|sp|Q9C9W0.1|AB17I_ARATH RecName: Full=ABC transporter I family member 17; Short=ABC transporter ABCI.17; Short=AtABCI17; AltName: Full=MRP-related protein 1; AltName: Full=Non-intrinsic ABC protein 3 gi|12324076|gb|AAG52004.1|AC012563_14 putative ABC transporter; 66585-65723 [Arabidopsis thaliana] gi|21554406|gb|AAM63511.1| putative ABC transporter [Arabidopsis thaliana] gi|26450485|dbj|BAC42356.1| putative ABC transporter [Arabidopsis thaliana] gi|28827588|gb|AAO50638.1| putative ABC transporter protein [Arabidopsis thaliana] gi|298286464|dbj|BAJ09459.1| sensitive to aluminum rhizotoxicity 1 [Arabidopsis thaliana] gi|332196603|gb|AEE34724.1| ABC transporter I family member 17 [Arabidopsis thaliana]	264	263	1.00E-130	99.6	87.9	95.1	ABC transporter I family member 17	gbpln	Arabidopsis thaliana	AT1G67940.1 | Symbols: ATNAP3, AtSTAR1, NAP3 | non-intrinsic ABC protein 3 | chr1:25477805-25478667 FORWARD LENGTH=263	264	263	1.00E-132	99.6	87.9	95.1
Rsa1.0_00398.1.g13034.t6	gb|EOA35564.1| hypothetical protein CARUB_v10020770mg [Capsella rubella]	288	278	1.00E-128	96.5	81.6	88.5	hypothetical protein CARUB_v10020770mg	gbpln	Capsella rubella	AT1G67950.3 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:25478884-25480420 REVERSE LENGTH=279	288	279	1.00E-130	96.9	80.6	87.8
Rsa1.0_00398.1.g13035.t1	ref|XP_002888635.1| hypothetical protein ARALYDRAFT_475901 [Arabidopsis lyrata subsp. lyrata] gi|297334476|gb|EFH64894.1| hypothetical protein ARALYDRAFT_475901 [Arabidopsis lyrata subsp. lyrata]	827	832	0	100.6	90.2	95.2	hypothetical protein ARALYDRAFT_475901	gbpln	Arabidopsis lyrata	AT1G67930.1 | Symbols: | Golgi transport complex protein-related | chr1:25474218-25477332 REVERSE LENGTH=832	827	832	0	100.6	87.2	92.5
Rsa1.0_00398.1.g13036.t1	ref|NP_564914.1| uncharacterized protein [Arabidopsis thaliana] gi|12324082|gb|AAG52010.1|AC012563_20 unknown protein; 70659-70456 [Arabidopsis thaliana] gi|21537331|gb|AAM61672.1| unknown [Arabidopsis thaliana] gi|89111818|gb|ABD60681.1| At1g67920 [Arabidopsis thaliana] gi|332196601|gb|AEE34722.1| uncharacterized protein AT1G67920 [Arabidopsis thaliana]	80	67	1.00E-18	83.8	67.5	70.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G67920.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24600.1); Has 22 Blast hits to 22 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25473731-25473934 FORWARD LENGTH=67	80	67	2.00E-21	83.8	67.5	70.0
Rsa1.0_00398.1.g13037.t1	gb|EOA35521.1| hypothetical protein CARUB_v10020730mg [Capsella rubella]	235	295	2.00E-55	125.5	63.0	74.9	hypothetical protein CARUB_v10020730mg	gbpln	Capsella rubella	AT1G67870.1 | Symbols: | glycine-rich protein | chr1:25449593-25450943 REVERSE LENGTH=279	235	279	4.00E-37	118.7	51.9	63.0
Rsa1.0_00399.1.g13038.t1	ref|NP_198361.1| uncharacterized protein [Arabidopsis thaliana] gi|10176810|dbj|BAB10018.1| unnamed protein product [Arabidopsis thaliana] gi|332006549|gb|AED93932.1| uncharacterized protein AT5G35110 [Arabidopsis thaliana]	114	112	2.00E-23	98.2	65.8	75.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G35110.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G46490.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:13363937-13364275 REVERSE LENGTH=112	114	112	3.00E-26	98.2	65.8	75.4
Rsa1.0_00399.1.g13039.t1	gb|EOA17182.1| hypothetical protein CARUB_v10005453mg [Capsella rubella]	287	277	1.00E-123	96.5	81.9	86.8	hypothetical protein CARUB_v10005453mg	gbpln	Capsella rubella	AT5G35100.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr5:13360459-13361377 REVERSE LENGTH=281	287	281	1.00E-124	97.9	82.9	89.2

Rsa1.0_00399.1.g13040.t1	ref|XP_002868405.1| hypothetical protein ARALYDRAFT_493584 [Arabidopsis lyrata subsp. lyrata] gi|297314241|gb|EFH44664.1| hypothetical protein ARALYDRAFT_493584 [Arabidopsis lyrata subsp. lyrata]	144	161	5.00E-43	111.8	70.8	79.9	hypothetical protein ARALYDRAFT_493584	gbpln	Arabidopsis lyrata	AT5G35090.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:13358536-13359015 FORWARD LENGTH=159	144	159	2.00E-44	110.4	68.8	79.2
Rsa1.0_00399.1.g13041.t1	ref|XP_002870409.1| glycosyl hydrolase family 79 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297316245|gb|EFH46668.1| glycosyl hydrolase family 79 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	536	536	0	100.0	80.0	87.1	glycosyl hydrolase family 79 N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT5G34940.2 | Symbols: AtGUS3, GUS3 | glucuronidase 3 | chr5:13235912-13238718 REVERSE LENGTH=536	536	536	0	100.0	77.1	84.7
Rsa1.0_00399.1.g13042.t1	ref|XP_002870409.1| glycosyl hydrolase family 79 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297316245|gb|EFH46668.1| glycosyl hydrolase family 79 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	532	536	0	100.8	84.2	91.9	glycosyl hydrolase family 79 N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT5G34940.2 | Symbols: AtGUS3, GUS3 | glucuronidase 3 | chr5:13235912-13238718 REVERSE LENGTH=536	532	536	0	100.8	82.1	90.2
Rsa1.0_00399.1.g13043.t1	ref|NP_198334.1| purple acid phosphatase 26 [Arabidopsis thaliana] gi|75249765|sp|Q949Y3.1|PPA26_ARATH RecName: Full=Bifunctional purple acid phosphatase 26; Includes: RecName: Full=Acid phosphatase; Includes: RecName: Full=Peroxidase; Flags: Precursor gi|15292757|gb|AAK92747.1| putative acid phosphatase [Arabidopsis thaliana] gi|20259673|gb|AAM14354.1| putative acid phosphatase [Arabidopsis thaliana] gi|332006529|gb|AED93912.1| purple acid phosphatase 26 [Arabidopsis thaliana]	474	475	0	100.2	89.0	94.9	purple acid phosphatase 26	gbpln	Arabidopsis thaliana	AT5G34850.1 | Symbols: ATPAP26, PAP26 | purple acid phosphatase 26 | chr5:13108475-13111217 REVERSE LENGTH=475	474	475	0	100.2	89.0	94.9
Rsa1.0_00399.1.g13044.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00399.1.g13045.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00399.1.g13046.t1	gb|EOA15445.1| hypothetical protein CARUB_v10004088mg [Capsella rubella]	909	933	0	102.6	85.8	92.6	hypothetical protein CARUB_v10004088mg	gbpln	Capsella rubella	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	909	785	1.00E-28	86.4	13.9	25.7
Rsa1.0_00399.1.g13047.t1	ref|NP_198313.2| putative chloride channel-like protein CLC-g [Arabidopsis thaliana] gi|363548399|sp|P60300.2|CLCG_ARATH RecName: Full=Putative chloride channel-like protein CLC-g; AltName: Full=CBS domain-containing protein CBSCLC6 gi|332006508|gb|AED93891.1| putative chloride channel-like protein CLC-g [Arabidopsis thaliana]	764	765	0	100.1	91.0	95.8	putative chloride channel-like protein CLC-g	gbpln	Arabidopsis thaliana	AT5G33280.1 | Symbols: | Voltage-gated chloride channel family protein | chr5:12549280-12552305 FORWARD LENGTH=765	764	765	0	100.1	91.0	95.8
Rsa1.0_00399.1.g13048.t1	ref|NP_198314.2| xylogalacturonan beta-1,3-xylosyltransferase [Arabidopsis thaliana] gi|292630939|sp|Q94AA9.2|XGD1_ARATH RecName: Full=Xylogalacturonan beta-1,3-xylosyltransferase; AltName: Full=Protein XYLOGALACTURONAN DEFICIENT 1 gi|332006509|gb|AED93892.1| xylogalacturonan beta-1,3-xylosyltransferase [Arabidopsis thaliana]	448	500	0	111.6	85.9	91.5	xylogalacturonan beta-1,3-xylosyltransferase	gbpln	Arabidopsis thaliana	AT5G33290.1 | Symbols: XGD1 | xylogalacturonan deficient 1 | chr5:12558439-12561840 FORWARD LENGTH=500	448	500	0	111.6	85.9	91.5
Rsa1.0_00399.1.g13049.t3	ref|XP_002868397.1| hypothetical protein ARALYDRAFT_915622 [Arabidopsis lyrata subsp. lyrata] gi|297314233|gb|EFH44656.1| hypothetical protein ARALYDRAFT_915622 [Arabidopsis lyrata subsp. lyrata]	468	444	1.00E-161	94.9	70.9	79.1	hypothetical protein ARALYDRAFT_915622	gbpln	Arabidopsis lyrata	AT5G33300.1 | Symbols: | chromosome-associated kinesin-related | chr5:12562649-12565675 REVERSE LENGTH=439	468	439	1.00E-163	93.8	71.8	79.3
Rsa1.0_00399.1.g13050.t1	gb|EOA16196.1| hypothetical protein CARUB_v10004336mg, partial [Capsella rubella]	600	648	0	108.0	84.2	90.8	hypothetical protein CARUB_v10004336mg, partial	gbpln	Capsella rubella	AT5G32470.1 | Symbols: | Haem oxygenase-like, multi-helical | chr5:12085328-12088569 REVERSE LENGTH=617	600	617	0	102.8	86.7	93.3
Rsa1.0_00399.1.g13051.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00399.1.g13052.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00399.1.g13053.t1	ref|NP_197291.2| protein DA1-related 4 [Arabidopsis thaliana] gi|302595926|sp|Q9FKN7.2|DAR4_ARATH RecName: Full=Protein DA1-related 4 gi|332005099|gb|AED92482.1| protein DA1-related 4 [Arabidopsis thaliana]	377	1613	1.00E-116	427.9	61.5	74.0	protein DA1-related 4	gbpln	Arabidopsis thaliana	AT5G17890.1 | Symbols: CHS3, DAR4 | DA1-related protein 4 | chr5:5917015-5923160 FORWARD LENGTH=1613	377	1613	1.00E-119	427.9	61.5	74.0
Rsa1.0_00399.1.g13054.t1	ref|XP_002870515.1| transporter [Arabidopsis lyrata subsp. lyrata] gi|297316351|gb|EFH46774.1| transporter [Arabidopsis lyrata subsp. lyrata]	605	593	0	98.0	91.7	95.5	transporter	gbpln	Arabidopsis lyrata	AT5G37310.1 | Symbols: | Endomembrane protein 70 protein family | chr5:14772836-14776093 REVERSE LENGTH=593	605	593	0	98.0	91.4	95.4
Rsa1.0_00399.1.g13055.t1	ref|XP_002870516.1| zinc finger (ZPR1-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297316352|gb|EFH46775.1| zinc finger (ZPR1-type) family protein [Arabidopsis lyrata subsp. lyrata]	484	493	0	101.9	87.6	92.4	zinc finger (ZPR1-type) family protein	gbpln	Arabidopsis lyrata	AT5G37340.3 | Symbols: | ZPR1 zinc-finger domain protein | chr5:14787488-14792373 REVERSE LENGTH=493	484	493	0	101.9	88.0	92.8
Rsa1.0_00399.1.g13056.t1	ref|NP_198554.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|30693076|ref|NP_851102.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|145334655|ref|NP_001078673.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|186527150|ref|NP_001119323.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|186527153|ref|NP_001119324.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|9758724|dbj|BAB09110.1| unnamed protein product [Arabidopsis thaliana] gi|15450367|gb|AAK96477.1| AT5g37380/MNJ8_170 [Arabidopsis thaliana] gi|27363370|gb|AAO11604.1| At5g37380/MNJ8_170 [Arabidopsis thaliana] gi|332006794|gb|AED94177.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|332006795|gb|AED94178.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|332006796|gb|AED94179.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|332006797|gb|AED94180.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|332006798|gb|AED94181.1| chaperone DnaJ-domain containing protein	392	431	1.00E-143	109.9	68.9	82.4	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT5G37380.5 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:14817035-14818330 REVERSE LENGTH=431	392	431	1.00E-145	109.9	68.9	82.4
Rsa1.0_00399.1.g13057.t1	ref|XP_002874348.1| hypothetical protein ARALYDRAFT_489554 [Arabidopsis lyrata subsp. lyrata] gi|297320185|gb|EFH50607.1| hypothetical protein ARALYDRAFT_489554 [Arabidopsis lyrata subsp. lyrata]	282	457	8.00E-46	162.1	39.4	48.9	hypothetical protein ARALYDRAFT_489554	gbpln	Arabidopsis lyrata	AT1G13780.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:4724681-4726314 FORWARD LENGTH=456	282	456	1.00E-47	161.7	39.0	48.9
Rsa1.0_00399.1.g13058.t1	ref|NP_193135.2| Exostosin family protein [Arabidopsis thaliana] gi|29824391|gb|AAP04155.1| unknown protein [Arabidopsis thaliana] gi|332657957|gb|AEE83357.1| Exostosin family protein [Arabidopsis thaliana]	520	521	0	100.2	81.9	89.6	Exostosin family protein	gbpln	Arabidopsis thaliana	AT4G13990.1 | Symbols: | Exostosin family protein | chr4:8084395-8085960 FORWARD LENGTH=521	520	521	0	100.2	81.9	89.6
Rsa1.0_00399.1.g13059.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00400.1.g13060.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00400.1.g13061.t1	ref|NP_197207.1| Flavonoid 3-O-glucosyltransferase [Arabidopsis thaliana] gi|75311137|sp|Q9LFJ8.1|U78D2_ARATH RecName: Full=UDP-glycosyltransferase 78D2; AltName: Full=Anthocyanin 3-O-glucosyltransferase; AltName: Full=Flavonol 3-O-glucosyltransferase.; AltName: Full=UDP glucose:flavonoid 3-O-glucosyltransferase gi|9755706|emb|CAC01718.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|18252199|gb|AAL61932.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|22136122|gb|AAM91139.1| UDP glucose:flavonoid 3-o-glucosyltransferase-like protein [Arabidopsis thaliana] gi|332004994|gb|AED92377.1| Flavonoid 3-O-glucosyltransferase [Arabidopsis thaliana]	459	460	0	100.2	73.2	84.5	Flavonoid 3-O-glucosyltransferase	gbpln	Arabidopsis thaliana	AT5G17050.1 | Symbols: UGT78D2 | UDP-glucosyl transferase 78D2 | chr5:5607828-5609392 REVERSE LENGTH=460	459	460	0	100.2	73.2	84.5
Rsa1.0_00400.1.g13062.t1	gb|EOA18272.1| hypothetical protein CARUB_v10006771mg [Capsella rubella]	571	447	2.00E-35	78.3	17.2	27.5	hypothetical protein CARUB_v10006771mg	gbpln	Capsella rubella	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	571	452	7.00E-32	79.2	16.5	24.7
Rsa1.0_00400.1.g13063.t1	emb|CAB80843.1| hypothetical protein [Arabidopsis thaliana]	149	381	3.00E-20	255.7	31.5	44.3	hypothetical protein	gbpln	Arabidopsis thaliana	AT5G15690.1 | Symbols: | zinc ion binding | chr5:5113823-5114402 REVERSE LENGTH=169	149	169	1.00E-22	113.4	32.2	45.6
Rsa1.0_00400.1.g13064.t1	emb|CAB51200.1| putative protein [Arabidopsis thaliana]	705	739	1.00E-117	104.8	35.3	56.6	putative protein	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	705	785	1.00E-28	111.3	17.9	32.3
Rsa1.0_00400.1.g13065.t1	gb|EOA22387.1| hypothetical protein CARUB_v10003022mg [Capsella rubella]	211	259	2.00E-38	122.7	40.8	42.2	hypothetical protein CARUB_v10003022mg	gbpln	Capsella rubella	AT5G17070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein phosphatase 4 core regulatory subunit R2 (InterPro:IPR015267); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5613514-5616088 REVERSE LENGTH=277	211	277	1.00E-39	131.3	40.8	44.1
Rsa1.0_00400.1.g13066.t1	gb|AAC14510.1| En/Spm-like transposon protein [Arabidopsis thaliana]	142	292	4.00E-36	205.6	52.8	57.7	En/Spm-like transposon protein	gbpln	Arabidopsis thaliana	AT4G10890.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2439 (InterPro:IPR018838); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43722.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:6688833-6692937 FORWARD LENGTH=527	142	527	9.00E-20	371.1	31.0	38.0
Rsa1.0_00400.1.g13067.t1	emb|CAA22150.1| hypothetical protein [Arabidopsis thaliana] gi|7269091|emb|CAB79200.1| hypothetical protein [Arabidopsis thaliana]	459	457	3.00E-28	99.6	15.3	20.0	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00400.1.g13068.t1	gb|AAC23763.1| hypothetical protein [Arabidopsis thaliana]	606	705	2.00E-82	116.3	28.4	37.6	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	606	249	4.00E-46	41.1	16.3	21.8
Rsa1.0_00400.1.g13069.t1	gb|AAC23765.1| Mutator-like transposase [Arabidopsis thaliana]	432	784	6.00E-53	181.5	22.5	32.2	Mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00400.1.g13070.t1	gb|EOA22387.1| hypothetical protein CARUB_v10003022mg [Capsella rubella]	56	259	5.00E-13	462.5	75.0	80.4	hypothetical protein CARUB_v10003022mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00400.1.g13071.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00400.1.g13072.t1	ref|XP_002865515.1| hypothetical protein ARALYDRAFT_917509 [Arabidopsis lyrata subsp. lyrata] gi|297311350|gb|EFH41774.1| hypothetical protein ARALYDRAFT_917509 [Arabidopsis lyrata subsp. lyrata]	376	380	0	101.1	86.4	92.3	hypothetical protein ARALYDRAFT_917509	gbpln	Arabidopsis lyrata	AT5G42470.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Brain/reproductive organ-expressed protein (InterPro:IPR010358); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:16982365-16984738 FORWARD LENGTH=382	376	382	0	101.6	84.8	92.0
Rsa1.0_00400.1.g13073.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00400.1.g13074.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00400.1.g13075.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00400.1.g13076.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00400.1.g13077.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00401.1.g13078.t1	gb|EOA28996.1| hypothetical protein CARUB_v10025249mg [Capsella rubella]	317	314	1.00E-154	99.1	84.2	91.8	hypothetical protein CARUB_v10025249mg	gbpln	Capsella rubella	AT2G22500.1 | Symbols: UCP5, ATPUMP5, DIC1 | uncoupling protein 5 | chr2:9563531-9564472 REVERSE LENGTH=313	317	313	1.00E-154	98.7	84.5	94.0
Rsa1.0_00401.1.g13079.t1	ref|XP_002880446.1| CYCD2_1 [Arabidopsis lyrata subsp. lyrata] gi|297326285|gb|EFH56705.1| CYCD2_1 [Arabidopsis lyrata subsp. lyrata]	349	358	1.00E-139	102.6	76.2	85.1	CYCD2_1	gbpln	Arabidopsis lyrata	AT2G22490.1 | Symbols: CYCD2;1, ATCYCD2;1 | Cyclin D2;1 | chr2:9554157-9555873 REVERSE LENGTH=361	349	361	1.00E-135	103.4	75.4	86.0
Rsa1.0_00401.1.g13080.t1	ref|NP_565538.1| GLABRA2 expression modulator [Arabidopsis thaliana] gi|75160436|sp|Q8S8F8.1|GEM_ARATH RecName: Full=GLABRA2 expression modulator gi|20197888|gb|AAM15301.1| Expressed protein [Arabidopsis thaliana] gi|145076288|gb|ABP35534.1| GL2 expression modulator [Arabidopsis thaliana] gi|330252217|gb|AEC07311.1| GLABRA2 expression modulator [Arabidopsis thaliana]	283	299	1.00E-126	105.7	83.4	89.0	GLABRA2 expression modulator	gbpln	Arabidopsis thaliana	AT2G22475.1 | Symbols: GEM | GRAM domain family protein | chr2:9541523-9544778 FORWARD LENGTH=299	283	299	1.00E-129	105.7	83.4	89.0
Rsa1.0_00401.1.g13081.t1	ref|NP_565537.1| arabinogalactan protein 2 [Arabidopsis thaliana] gi|75206344|sp|Q9SJY7.1|AGP2_ARATH RecName: Full=Classical arabinogalactan protein 2; Flags: Precursor gi|4544458|gb|AAD22366.1| expressed protein [Arabidopsis thaliana] gi|17065300|gb|AAL32804.1| Unknown protein [Arabidopsis thaliana] gi|20260016|gb|AAM13355.1| unknown protein [Arabidopsis thaliana] gi|330252215|gb|AEC07309.1| arabinogalactan protein 2 [Arabidopsis thaliana]	132	131	2.00E-22	99.2	74.2	84.1	arabinogalactan protein 2	gbpln	Arabidopsis thaliana	AT2G22470.1 | Symbols: AGP2, ATAGP2 | arabinogalactan protein 2 | chr2:9538400-9538795 REVERSE LENGTH=131	132	131	4.00E-25	99.2	74.2	84.1
Rsa1.0_00401.1.g13082.t1	ref|XP_002880444.1| hypothetical protein ARALYDRAFT_481106 [Arabidopsis lyrata subsp. lyrata] gi|297326283|gb|EFH56703.1| hypothetical protein ARALYDRAFT_481106 [Arabidopsis lyrata subsp. lyrata]	245	245	1.00E-112	100.0	86.5	93.5	hypothetical protein ARALYDRAFT_481106	gbpln	Arabidopsis lyrata	AT2G22460.1 | Symbols: | Protein of unknown function, DUF617 | chr2:9533354-9534091 REVERSE LENGTH=245	245	245	1.00E-106	100.0	85.7	92.2
Rsa1.0_00401.1.g13083.t1	ref|XP_002893409.1| hypothetical protein ARALYDRAFT_890118 [Arabidopsis lyrata subsp. lyrata] gi|297339251|gb|EFH69668.1| hypothetical protein ARALYDRAFT_890118 [Arabidopsis lyrata subsp. lyrata]	71	191	4.00E-12	269.0	53.5	64.8	hypothetical protein ARALYDRAFT_890118	gbpln	Arabidopsis lyrata	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	71	384	7.00E-14	540.8	45.1	53.5
Rsa1.0_00401.1.g13084.t1	ref|NP_179819.1| uncharacterized protein [Arabidopsis thaliana] gi|4567195|gb|AAD23611.1| hypothetical protein [Arabidopsis thaliana] gi|330252199|gb|AEC07293.1| uncharacterized protein AT2G22320 [Arabidopsis thaliana]	113	111	2.00E-28	98.2	66.4	77.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G22320.1 | Symbols: | unknown protein; Has 7 Blast hits to 7 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9480105-9480440 FORWARD LENGTH=111	113	111	3.00E-31	98.2	66.4	77.9
Rsa1.0_00401.1.g13085.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00401.1.g13086.t1	gb|EOA28523.1| hypothetical protein CARUB_v10024738mg [Capsella rubella]	1031	1032	0	100.1	86.4	92.6	hypothetical protein CARUB_v10024738mg	gbpln	Capsella rubella	AT2G22300.2 | Symbols: CAMTA3, SR1 | signal responsive 1 | chr2:9471599-9476472 FORWARD LENGTH=1032	1031	1032	0	100.1	87.0	92.5

Rsa1.0_00401.1.g13087.t1	gb|EOA27602.1| hypothetical protein CARUB_v10023742mg [Capsella rubella]	268	298	7.00E-92	111.2	72.0	80.2	hypothetical protein CARUB_v10023742mg	gbpln	Capsella rubella	AT2G22270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G39860.2); Has 247 Blast hits to 231 proteins in 42 species: Archae - 0; Bacteria - 17; Metazoa - 14; Fungi - 5; Plants - 145; Viruses - 0; Other Eukaryotes - 66 (source: NCBI BLink). | chr2:9463765-9465282 FORWARD LENGTH=328	268	328	2.00E-89	122.4	72.8	81.7
Rsa1.0_00401.1.g13088.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00401.1.g13089.t4	gb|EOA18064.1| hypothetical protein CARUB_v10006510mg, partial [Capsella rubella]	256	555	7.00E-22	216.8	24.2	37.1	hypothetical protein CARUB_v10006510mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	256	566	5.00E-18	221.1	21.9	35.2
Rsa1.0_00401.1.g13090.t1	ref|NP_196021.2| F-box protein [Arabidopsis thaliana] gi|75104736|sp|Q5EAF6.1|FB336_ARATH RecName: Full=Probable F-box protein At5g04010; AltName: Full=Non-specific F-box protein gi|58743286|gb|AAW81721.1| At5g04010 [Arabidopsis thaliana] gi|332003301|gb|AED90684.1| probable F-box protein [Arabidopsis thaliana]	286	287	1.00E-72	100.3	51.7	70.3	F-box protein	gbpln	Arabidopsis thaliana	AT5G04010.1 | Symbols: | F-box family protein | chr5:1080205-1081068 REVERSE LENGTH=287	286	287	3.00E-75	100.3	51.7	70.3
Rsa1.0_00401.1.g13091.t1	ref|NP_565529.1| aspartate aminotransferase [Arabidopsis thaliana] gi|79322722|ref|NP_001031394.1| aspartate aminotransferase [Arabidopsis thaliana] gi|75206088|sp|Q9SIE1.2|PAT_ARATH RecName: Full=Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase; Short=AtAAT; Short=AtPPA-AT; AltName: Full=Protein MATERNAL EFFECT EMBRYO ARREST 17; Flags: Precursor gi|17381280|gb|AAL36058.1| At2g22250/T26C19.9 [Arabidopsis thaliana] gi|20198151|gb|AAD23617.2| putative aspartate aminotransferase [Arabidopsis thaliana] gi|21700793|gb|AAM70520.1| At2g22250/T26C19.9 [Arabidopsis thaliana] gi|305855255|gb|ADM67558.1| prephenate aminotransferase [Arabidopsis thaliana] gi|330252190|gb|AEC07284.1| aspartate aminotransferase [Arabidopsis thaliana] gi|330252191|gb|AEC07285.1| aspartate aminotransferase [Arabidopsis thaliana]	475	475	0	100.0	90.3	95.6	aspartate aminotransferase	gbpln	Arabidopsis thaliana	AT2G22250.3 | Symbols: ATAAT, AAT, MEE17 | aspartate aminotransferase | chr2:9458011-9460297 REVERSE LENGTH=475	475	475	0	100.0	90.3	95.6
Rsa1.0_00401.1.g13092.t1	dbj|BAB02902.1| disease resistance protein-like [Arabidopsis thaliana]	885	883	0	99.8	67.1	76.4	disease resistance protein-like	gbpln	Arabidopsis thaliana	AT3G24982.1 | Symbols: ATRLP40, RLP40 | receptor like protein 40 | chr3:9106157-9108937 REVERSE LENGTH=915	885	915	0	103.4	67.1	76.4
Rsa1.0_00401.1.g13093.t1	gb|AAF40460.1|AC004809_18 Strong similarity to the synaptobrevin homolog F25I18.14 gi|2924792 from A. thaliana on BAC gb|AC002334 [Arabidopsis thaliana]	213	229	1.00E-32	107.5	32.4	35.2	Strong similarity to the synaptobrevin homolog F25I18.14 gi|2924792 from A. thaliana on BAC gb|AC002334	gbpln	Arabidopsis thaliana	AT2G32670.1 | Symbols: ATVAMP725, VAMP725 | vesicle-associated membrane protein 725 | chr2:13857941-13859346 FORWARD LENGTH=285	213	285	1.00E-34	133.8	31.9	34.7
Rsa1.0_00401.1.g13094.t1	gb|AAC04914.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana]	191	800	7.00E-78	418.8	75.9	87.4	putative leucine-rich repeat disease resistance protein	gbpln	Arabidopsis thaliana	AT2G33060.1 | Symbols: AtRLP27, RLP27 | receptor like protein 27 | chr2:14025661-14028087 FORWARD LENGTH=808	191	808	3.00E-80	423.0	75.9	87.4
Rsa1.0_00401.1.g13095.t1	ref|NP_180867.1| receptor like protein 28 [Arabidopsis thaliana] gi|2924783|gb|AAC04912.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|330253689|gb|AEC08783.1| receptor like protein 28 [Arabidopsis thaliana]	423	740	1.00E-124	174.9	60.3	72.1	receptor like protein 28	gbpln	Arabidopsis thaliana	AT2G33080.1 | Symbols: AtRLP28, RLP28 | receptor like protein 28 | chr2:14032015-14034237 FORWARD LENGTH=740	423	740	1.00E-126	174.9	60.3	72.1
Rsa1.0_00401.1.g13096.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1455	1459	0	100.3	57.2	72.8	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1455	1262	1.00E-113	86.7	13.6	19.6
Rsa1.0_00401.1.g13097.t1	gb|EOA39215.1| hypothetical protein CARUB_v10012187mg [Capsella rubella]	253	220	1.00E-64	87.0	47.0	52.2	hypothetical protein CARUB_v10012187mg	gbpln	Capsella rubella	AT1G04760.1 | Symbols: ATVAMP726, VAMP726 | vesicle-associated membrane protein 726 | chr1:1334760-1336070 FORWARD LENGTH=220	253	220	3.00E-59	87.0	46.6	51.8

Rsa1.0_00401.1.g13098.t1	ref|NP_180861.1| receptor like protein 24 [Arabidopsis thaliana] gi|2924789|gb|AAC04918.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|20196994|gb|AAM14862.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|330253681|gb|AEC08775.1| receptor like protein 24 [Arabidopsis thaliana]	338	864	1.00E-125	255.6	70.4	80.2	receptor like protein 24	gbpln	Arabidopsis thaliana	AT2G33020.1 | Symbols: AtRLP24, RLP24 | receptor like protein 24 | chr2:14013874-14016516 REVERSE LENGTH=864	338	864	1.00E-128	255.6	70.4	80.2
Rsa1.0_00401.1.g13099.t1	gb|EOA30595.1| hypothetical protein CARUB_v10013726mg [Capsella rubella]	206	439	1.00E-52	213.1	54.4	61.2	hypothetical protein CARUB_v10013726mg	gbpln	Capsella rubella	AT3G19130.1 | Symbols: ATRBP47B, RBP47B | RNA-binding protein 47B | chr3:6611398-6613823 REVERSE LENGTH=435	206	435	2.00E-53	211.2	50.5	56.3
Rsa1.0_00401.1.g13100.t1	sp|Q9S7U0.1|INO1_WHEAT RecName: Full=Inositol-3-phosphate synthase; Short=MIP synthase; AltName: Full=Myo-inositol 1-phosphate synthase; Short=IPS; Short=MI-1-P synthase gi|4589062|gb|AAD26330.1|AF120146_1 myo-inositol 1-phosphate synthase [Triticum aestivum] gi|4589064|gb|AAD26331.1|AF120147_1 myo-inositol 1-phosphate synthase [Triticum aestivum] gi|4589066|gb|AAD26332.1|AF120148_1 myo-inositol 1-phosphate synthase [Triticum aestivum]	510	510	0	100.0	97.3	98.6	RecName: Full=Inositol-3-phosphate synthase; Short=MIP synthase; AltName: Full=Myo-inositol 1-phosphate synthase; Short=IPS; Short=MI-1-P synthase gi|4589062|gb|AAD26330.1|AF120146_1 myo-inositol 1-phosphate synthase	gbpln	Triticum aestivum	AT2G22240.1 | Symbols: ATMIPS2, MIPS2, ATIPS2 | myo-inositol-1-phosphate synthase 2 | chr2:9451901-9453938 REVERSE LENGTH=510	510	510	0	100.0	95.9	99.0
Rsa1.0_00401.1.g13101.t1	ref|XP_002878603.1| hypothetical protein ARALYDRAFT_481086 [Arabidopsis lyrata subsp. lyrata] gi|297324442|gb|EFH54862.1| hypothetical protein ARALYDRAFT_481086 [Arabidopsis lyrata subsp. lyrata]	83	224	5.00E-32	269.9	83.1	92.8	hypothetical protein ARALYDRAFT_481086	gbpln	Arabidopsis lyrata	AT2G22230.1 | Symbols: | Thioesterase superfamily protein | chr2:9450042-9451427 FORWARD LENGTH=220	83	220	1.00E-34	265.1	83.1	92.8
Rsa1.0_00402.1.g13102.t1	gb|AAM15154.1| unknown protein [Arabidopsis thaliana] gi|20198162|gb|AAM15435.1| unknown protein [Arabidopsis thaliana]	288	1308	2.00E-47	454.2	36.8	45.8	unknown protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00402.1.g13103.t1	ref|NP_198138.2| uncharacterized protein [Arabidopsis thaliana] gi|238481400|ref|NP_001154743.1| uncharacterized protein [Arabidopsis thaliana] gi|332006354|gb|AED93737.1| uncharacterized protein AT5G27860 [Arabidopsis thaliana] gi|332006355|gb|AED93738.1| uncharacterized protein AT5G27860 [Arabidopsis thaliana]	178	177	1.00E-33	99.4	49.4	53.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G27860.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: pollen tube; Has 23049 Blast hits to 11981 proteins in 648 species: Archae - 2; Bacteria - 589; Metazoa - 13464; Fungi - 1977; Plants - 1635; Viruses - 89; Other Eukaryotes - 5293 (source: NCBI BLink). | chr5:9875068-9876442 REVERSE LENGTH=177	178	177	5.00E-36	99.4	49.4	53.4
Rsa1.0_00402.1.g13104.t1	dbj|BAC42193.1| putative FUSCA protein FUS6 [Arabidopsis thaliana]	176	441	1.00E-23	250.6	31.3	37.5	putative FUSCA protein FUS6	gbpln	Arabidopsis thaliana	AT3G61140.1 | Symbols: FUS6, ATFUS6, CSN1, COP11, EMB78, ATSK31, SK31 | 26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain | chr3:22626335-22628895 FORWARD LENGTH=441	176	441	4.00E-26	250.6	31.3	37.5
Rsa1.0_00402.1.g13105.t1	ref|NP_567410.1| nucleoside-triphosphate pyrophosphatase [Arabidopsis thaliana] gi|75301199|sp|Q8L968.1|ITPA_ARATH RecName: Full=Inosine triphosphate pyrophosphatase; Short=ITPase; Short=Inosine triphosphatase; AltName: Full=Non-canonical purine NTP pyrophosphatase; AltName: Full=Non-standard purine NTP pyrophosphatase; AltName: Full=Nucleoside-triphosphate diphosphatase; AltName: Full=Nucleoside-triphosphate pyrophosphatase; Short=NTPase gi|21617884|gb|AAM66934.1| putative HAM1 protein [Arabidopsis thaliana] gi|62319786|dbj|BAD93787.1| hypothetical protein [Arabidopsis thaliana] gi|90962982|gb|ABE02415.1| At4g13720 [Arabidopsis thaliana] gi|332657917|gb|AEE83317.1| Inosine triphosphate pyrophosphatase [Arabidopsis thaliana]	205	206	1.00E-107	100.5	92.2	93.7	nucleoside-triphosphate pyrophosphatase	gbpln	Arabidopsis thaliana	AT4G13720.1 | Symbols: | Inosine triphosphate pyrophosphatase family protein | chr4:7967166-7968894 REVERSE LENGTH=206	205	206	1.00E-109	100.5	92.2	93.7

Rsa1.0_00402.1.g13106.t1	ref|XP_002870357.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata] gi|297316193|gb|EFH46616.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata]	451	484	0	107.3	89.8	93.1	pectate lyase family protein	gbpln	Arabidopsis lyrata	AT4G13710.2 | Symbols: | Pectin lyase-like superfamily protein | chr4:7962550-7966012 FORWARD LENGTH=451	451	451	0	100.0	89.6	92.7
Rsa1.0_00402.1.g13107.t1	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	224	1752	2.00E-66	782.1	51.8	68.3	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00402.1.g13108.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00402.1.g13109.t1	ref|XP_002868345.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297314181|gb|EFH44604.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	1058	1047	0	99.0	86.5	92.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G13650.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:7939611-7942898 REVERSE LENGTH=1064	1058	1064	0	100.6	86.1	91.7
Rsa1.0_00402.1.g13110.t1	gb|EOA16725.1| hypothetical protein CARUB_v10004928mg [Capsella rubella]	382	414	1.00E-152	108.4	75.9	86.6	hypothetical protein CARUB_v10004928mg	gbpln	Capsella rubella	AT4G13670.1 | Symbols: PTAC5 | plastid transcriptionally active 5 | chr4:7948644-7950779 FORWARD LENGTH=387	382	387	1.00E-154	101.3	74.9	85.6
Rsa1.0_00402.1.g13111.t1	ref|XP_002870359.1| hypothetical protein ARALYDRAFT_355445 [Arabidopsis lyrata subsp. lyrata] gi|297316195|gb|EFH46618.1| hypothetical protein ARALYDRAFT_355445 [Arabidopsis lyrata subsp. lyrata]	254	254	6.00E-83	100.0	68.1	79.5	hypothetical protein ARALYDRAFT_355445	gbpln	Arabidopsis lyrata	AT4G13690.1 | Symbols: | unknown protein; Has 37 Blast hits to 37 proteins in 16 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr4:7953662-7955380 REVERSE LENGTH=249	254	249	3.00E-81	98.0	63.8	75.2
Rsa1.0_00402.1.g13112.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00402.1.g13113.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00402.1.g13114.t1	ref|NP_193099.2| uncharacterized protein [Arabidopsis thaliana] gi|334186497|ref|NP_001190719.1| uncharacterized protein [Arabidopsis thaliana] gi|332657905|gb|AEE83305.1| uncharacterized protein AT4G13630 [Arabidopsis thaliana] gi|332657906|gb|AEE83306.1| uncharacterized protein AT4G13630 [Arabidopsis thaliana]	490	569	1.00E-157	116.1	71.4	81.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G13630.2 | Symbols: | Protein of unknown function, DUF593 | chr4:7934093-7936029 REVERSE LENGTH=569	490	569	1.00E-159	116.1	71.4	81.0
Rsa1.0_00402.1.g13115.t1	ref|NP_193098.1| ethylene-responsive transcription factor ERF062 [Arabidopsis thaliana] gi|75337746|sp|Q9SVQ0.1|ERF62_ARATH RecName: Full=Ethylene-responsive transcription factor ERF062 gi|5748494|emb|CAB36826.2| putative protein [Arabidopsis thaliana] gi|7268066|emb|CAB78404.1| putative protein [Arabidopsis thaliana] gi|119935810|gb|ABM05999.1| At4g13620 [Arabidopsis thaliana] gi|332657904|gb|AEE83304.1| ethylene-responsive transcription factor ERF062 [Arabidopsis thaliana]	345	388	1.00E-149	112.5	81.7	89.0	ethylene-responsive transcription factor ERF062	gbpln	Arabidopsis thaliana	AT4G13620.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:7932138-7933304 FORWARD LENGTH=388	345	388	1.00E-152	112.5	81.7	89.0
Rsa1.0_00402.1.g13116.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00402.1.g13117.t10	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1300	1475	0	113.5	60.8	75.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1300	1262	1.00E-158	97.1	21.8	28.6
Rsa1.0_00402.1.g13118.t1	ref|NP_193096.5| carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana] gi|332657901|gb|AEE83301.1| carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana]	189	231	5.00E-75	122.2	82.5	88.4	carbohydrate-binding X8 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G13600.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr4:7911179-7912892 REVERSE LENGTH=231	189	231	2.00E-77	122.2	82.5	88.4
Rsa1.0_00402.1.g13119.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	448	490	5.00E-75	109.4	36.6	57.6	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	448	566	3.00E-71	126.3	33.9	58.0
Rsa1.0_00402.1.g13120.t1	ref|NP_197911.1| F-box protein [Arabidopsis thaliana] gi|75339263|sp|Q4PSE7.1|FB262_ARATH RecName: Full=F-box protein At5g25290 gi|67633822|gb|AAY78835.1| F-box family protein [Arabidopsis thaliana] gi|332006040|gb|AED93423.1| F-box protein [Arabidopsis thaliana]	409	397	1.00E-112	97.1	57.0	68.9	F-box protein	gbpln	Arabidopsis thaliana	AT5G25290.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr5:8778592-8779785 FORWARD LENGTH=397	409	397	1.00E-114	97.1	57.0	68.9

<table>
<tr><td>Rsa1.0_00402.1.g13121.t1</td><td>gb|EOA30761.1| hypothetical protein CARUB_v10013903mg [Capsella rubella]</td><td>364</td><td>392</td><td>4.00E-58</td><td>107.7</td><td>46.2</td><td>63.7</td><td>hypothetical protein CARUB_v10013903mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G61730.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:22793447-22794577 REVERSE LENGTH=376</td><td>364</td><td>376</td><td>1.00E-58</td><td>103.3</td><td>38.2</td><td>47.5</td></tr>
<tr><td>Rsa1.0_00402.1.g13122.t1</td><td>emb|CAB77996.1| putative protein [Arabidopsis thaliana] gi|7321060|emb|CAB82107.1| putative protein [Arabidopsis thaliana]</td><td>578</td><td>715</td><td>3.00E-85</td><td>123.7</td><td>29.1</td><td>40.8</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249</td><td>578</td><td>249</td><td>4.00E-57</td><td>43.1</td><td>18.5</td><td>24.2</td></tr>
<tr><td>Rsa1.0_00402.1.g13123.t1</td><td>gb|ABL97981.1| unknown [Brassica rapa]</td><td>109</td><td>109</td><td>2.00E-51</td><td>100.0</td><td>95.4</td><td>95.4</td><td>unknown</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G13560.1 | Symbols: UNE15 | Late embryogenesis abundant protein (LEA) family protein | chr4:7879764-7880311 REVERSE LENGTH=109</td><td>109</td><td>109</td><td>1.00E-43</td><td>100.0</td><td>79.8</td><td>82.6</td></tr>
<tr><td>Rsa1.0_00402.1.g13124.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00402.1.g13125.t1</td><td>gb|EOA15979.1| hypothetical protein CARUB_v10004094mg [Capsella rubella]</td><td>847</td><td>915</td><td>0</td><td>108.0</td><td>77.0</td><td>85.4</td><td>hypothetical protein CARUB_v10004094mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G13550.1 | Symbols: | triglyceride lipases;triglyceride lipases | chr4:7871251-7876160 REVERSE LENGTH=715</td><td>847</td><td>715</td><td>0</td><td>84.4</td><td>62.3</td><td>69.2</td></tr>
<tr><td>Rsa1.0_00402.1.g13126.t1</td><td>gb|EOA17915.1| hypothetical protein CARUB_v10006324mg [Capsella rubella]</td><td>204</td><td>210</td><td>2.00E-77</td><td>102.9</td><td>76.5</td><td>84.8</td><td>hypothetical protein CARUB_v10006324mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G13540.1 | Symbols: | unknown protein; INVOLVED IN: N-terminal protein myristoylation; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23930.1); Has 4658 Blast hits to 3455 proteins in 431 species: Archae - 39; Bacteria - 387; Metazoa - 1842; Fungi - 436; Plants - 133; Viruses - 38; Other Eukaryotes - 1783 (source: NCBI BLink). | chr4:7869896-7870604 FORWARD LENGTH=210</td><td>204</td><td>210</td><td>2.00E-73</td><td>102.9</td><td>77.0</td><td>84.3</td></tr>
<tr><td>Rsa1.0_00402.1.g13127.t1</td><td>gb|EOA16151.1| hypothetical protein CARUB_v10004289mg [Capsella rubella]</td><td>617</td><td>677</td><td>0</td><td>109.7</td><td>72.6</td><td>80.6</td><td>hypothetical protein CARUB_v10004289mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667</td><td>617</td><td>667</td><td>0</td><td>108.1</td><td>54.0</td><td>66.6</td></tr>
<tr><td>Rsa1.0_00402.1.g13128.t1</td><td>dbj|BAJ33699.1| unnamed protein product [Thellungiella halophila]</td><td>476</td><td>504</td><td>0</td><td>105.9</td><td>95.0</td><td>97.7</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G13250.1 | Symbols: NYC1 | NAD(P)-binding Rossmann-fold superfamily protein | chr4:7684417-7686691 REVERSE LENGTH=496</td><td>476</td><td>496</td><td>0</td><td>104.2</td><td>92.0</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00402.1.g13129.t3</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1250</td><td>1307</td><td>0</td><td>104.6</td><td>57.2</td><td>72.5</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1250</td><td>1262</td><td>6.00E-99</td><td>101.0</td><td>14.6</td><td>24.1</td></tr>
<tr><td>Rsa1.0_00402.1.g13130.t1</td><td>gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]</td><td>287</td><td>1486</td><td>1.00E-56</td><td>517.8</td><td>40.1</td><td>46.7</td><td>Putative retroelement polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>287</td><td>1262</td><td>3.00E-31</td><td>439.7</td><td>28.9</td><td>40.8</td></tr>
<tr><td>Rsa1.0_00402.1.g13131.t1</td><td>gb|AAD36942.1|AF069441_2 hypothetical protein [Arabidopsis thaliana] gi|7267196|emb|CAB77907.1| hypothetical protein [Arabidopsis thaliana]</td><td>212</td><td>963</td><td>9.00E-31</td><td>454.2</td><td>36.3</td><td>50.5</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874</td><td>212</td><td>874</td><td>5.00E-29</td><td>412.3</td><td>31.1</td><td>47.6</td></tr>
<tr><td>Rsa1.0_00402.1.g13132.t1</td><td>gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]</td><td>331</td><td>1023</td><td>4.00E-34</td><td>309.1</td><td>27.8</td><td>39.0</td><td>F27F5.21</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00402.1.g13133.t1</td><td>gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]</td><td>410</td><td>940</td><td>2.00E-64</td><td>229.3</td><td>33.2</td><td>47.6</td><td>contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00402.1.g13134.t4</td><td>gb|AAD17349.1| similar to Antirrhinum majus (garden snapdragon) TNP2 protein (GB:X57297) [Arabidopsis thaliana] gi|7267145|emb|CAB80813.1| putative transposon protein [Arabidopsis thaliana]</td><td>453</td><td>817</td><td>1.00E-51</td><td>180.4</td><td>33.3</td><td>45.9</td><td>similar to Antirrhinum majus (garden snapdragon) TNP2 protein (GB:X57297)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00402.1.g13135.t8</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1459</td><td>1529</td><td>0</td><td>104.8</td><td>44.6</td><td>62.1</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>1459</td><td>746</td><td>1.00E-107</td><td>51.1</td><td>13.8</td><td>17.8</td></tr>
</table>

Rsa1.0_00403.1.g13136.t1	ref|NP_195457.1| cytochrome P450, family 81, subfamily F, polypeptide 4 [Arabidopsis thaliana] gi|4468807|emb|CAB38208.1| cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana] gi|7270723|emb|CAB80406.1| cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana] gi|21536532|gb|AAM60864.1| cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana] gi|116325950|gb|ABJ98576.1| At4g37410 [Arabidopsis thaliana] gi|332661390|gb|AEE86790.1| cytochrome P450, family 81, subfamily F, polypeptide 4 [Arabidopsis thaliana]	501	501	0	100.0	78.8	90.2	cytochrome P450, family 81, subfamily F, polypeptide 4	gbpln	Arabidopsis thaliana	AT4G37410.1 | Symbols: CYP81F4 | cytochrome P450, family 81, subfamily F, polypeptide 4 | chr4:17590848-17592780 FORWARD LENGTH=501	501	501	0	100.0	78.8	90.2
Rsa1.0_00403.1.g13137.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00403.1.g13138.t2	ref|XP_002868986.1| hypothetical protein ARALYDRAFT_490875 [Arabidopsis lyrata subsp. lyrata] gi|297314822|gb|EFH45245.1| hypothetical protein ARALYDRAFT_490875 [Arabidopsis lyrata subsp. lyrata]	540	447	1.00E-148	82.8	54.1	65.0	hypothetical protein ARALYDRAFT_490875	gbpln	Arabidopsis lyrata	AT4G37440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G50040.1); Has 220 Blast hits to 205 proteins in 55 species: Archae - 0; Bacteria - 15; Metazoa - 50; Fungi - 11; Plants - 76; Viruses - 3; Other Eukaryotes - 65 (source: NCBI BLink). | chr4:17601647-17603846 FORWARD LENGTH=471	540	471	1.00E-145	87.2	54.6	64.6
Rsa1.0_00403.1.g13139.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	103	442	9.00E-31	429.1	62.1	70.9	hypothetical protein 24.t00017	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00403.1.g13140.t1	gb|ABD65634.1| hypothetical protein 23.t00051 [Brassica oleracea]	165	133	2.00E-30	80.6	38.8	46.7	hypothetical protein 23.t00051	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00403.1.g13141.t1	gb|EOA18971.1| hypothetical protein CARUB_v10007609mg [Capsella rubella]	497	496	0	99.8	85.9	92.6	hypothetical protein CARUB_v10007609mg	gbpln	Capsella rubella	AT4G37400.1 | Symbols: CYP81F3 | cytochrome P450, family 81, subfamily F, polypeptide 3 | chr4:17584096-17586197 FORWARD LENGTH=501	497	501	0	100.8	85.7	92.8
Rsa1.0_00403.1.g13142.t1	gb|EOA17212.1| hypothetical protein CARUB_v10005485mg [Capsella rubella]	271	271	1.00E-148	100.0	93.4	97.0	hypothetical protein CARUB_v10005485mg	gbpln	Capsella rubella	AT4G37470.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:17617045-17618363 REVERSE LENGTH=270	271	270	1.00E-149	99.6	92.3	97.8
Rsa1.0_00403.1.g13143.t2	ref|NP_195464.2| chaperone DnaJ-domain-containing protein [Arabidopsis thaliana] gi|332661399|gb|AEE86799.1| chaperone DnaJ-domain-containing protein [Arabidopsis thaliana]	530	531	0	100.2	83.0	88.1	chaperone DnaJ-domain-containing protein	gbpln	Arabidopsis thaliana	AT4G37480.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:17619261-17621596 FORWARD LENGTH=531	530	531	0	100.2	83.0	88.1
Rsa1.0_00403.1.g13144.t1	gb|EOA16747.1| hypothetical protein CARUB_v10004955mg [Capsella rubella]	403	404	0	100.2	90.1	96.0	hypothetical protein CARUB_v10004955mg	gbpln	Capsella rubella	AT4G37580.1 | Symbols: HLS1, COP3, UNS2 | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr4:17658932-17660564 FORWARD LENGTH=403	403	403	0	100.0	91.1	96.3
Rsa1.0_00403.1.g13145.t1	dbj|BAF02155.1| hypothetical protein [Arabidopsis thaliana]	574	580	0	101.0	86.8	93.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G37590.1 | Symbols: NPY5 | Phototropic-responsive NPH3 family protein | chr4:17663080-17665299 REVERSE LENGTH=580	574	580	0	101.0	86.8	93.7
Rsa1.0_00403.1.g13146.t1	gb|EOA17745.1| hypothetical protein CARUB_v10006133mg [Capsella rubella]	96	88	2.00E-22	91.7	62.5	74.0	hypothetical protein CARUB_v10006133mg	gbpln	Capsella rubella	AT4G37608.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 22 Blast hits to 22 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17669825-17670429 FORWARD LENGTH=87	96	87	2.00E-22	90.6	58.3	68.8

Rsa1.0_00403.1.g13147.t1	ref|NP_195479.1| Ca2+-transporting ATPase [Arabidopsis thaliana] gi|12229639|sp|O81108.1|ACA2_ARATH RecName: Full=Calcium-transporting ATPase 2, plasma membrane-type; AltName: Full=Ca(2+)-ATPase isoform 2 gi|3335060|gb|AAC26997.1| plasma membrane-type calcium ATPase [Arabidopsis thaliana] gi|4468989|emb|CAB38303.1| plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana] gi|7270746|emb|CAB80429.1| plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana] gi|17064816|gb|AAL32562.1| plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana] gi|37201998|gb|AAQ89614.1| At4g37640 [Arabidopsis thaliana] gi|332661419|gb|AEE86819.1| calcium-transporting ATPase 2 [Arabidopsis thaliana]	155	1014	6.00E-77	654.2	89.0	94.2	Ca2+-transporting ATPase	gbpln	Arabidopsis thaliana	AT4G37640.1 | Symbols: ACA2 | calcium ATPase 2 | chr4:17683225-17686808 REVERSE LENGTH=1014	155	1014	2.00E-79	654.2	89.0	94.2
Rsa1.0_00403.1.g13148.t1	gb|EOA16409.1| hypothetical protein CARUB_v10004568mg [Capsella rubella]	264	531	1.00E-104	201.1	86.4	90.2	hypothetical protein CARUB_v10004568mg	gbpln	Capsella rubella	AT4G37650.1 | Symbols: SHR, SGR7 | GRAS family transcription factor | chr4:17691871-17693466 FORWARD LENGTH=531	264	531	1.00E-106	201.1	87.5	91.3
Rsa1.0_00404.1.g13149.t2	ref|XP_002892447.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297338289|gb|EFH68706.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	365	493	1.00E-142	135.1	69.6	72.3	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT1G08210.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:2577119-2580581 REVERSE LENGTH=492	365	492	1.00E-144	134.8	69.6	72.3
Rsa1.0_00404.1.g13150.t1	ref|NP_175926.1| TBP-associated factor 7 [Arabidopsis thaliana] gi|12323163|gb|AAG51559.1|AC027034_5 Serine/arginine-rich protein, putative; 48931-50251 [Arabidopsis thaliana] gi|38638688|gb|AAR25638.1| At1g55300 [Arabidopsis thaliana] gi|39545922|gb|AAR28024.1| TAF7 [Arabidopsis thaliana] gi|50253538|gb|AAT71971.1| At1g55300 [Arabidopsis thaliana] gi|222423319|dbj|BAH19635.1| AT1G55300 [Arabidopsis thaliana] gi|332195099|gb|AEE33220.1| TBP-associated factor 7 [Arabidopsis thaliana]	85	203	2.00E-11	238.8	51.8	56.5	TBP-associated factor 7	gbpln	Arabidopsis thaliana	AT1G55300.1 | Symbols: TAF7 | TBP-associated factor 7 | chr1:20628170-20629490 REVERSE LENGTH=203	85	203	3.00E-14	238.8	51.8	56.5
Rsa1.0_00404.1.g13151.t1	ref|NP_563809.1| arogenate dehydratase 6 [Arabidopsis thaliana] gi|75204832|sp|Q9SGD6.1|AROD6_ARATH RecName: Full=Arogenate dehydratase/prephenate dehydratase 6, chloroplastic; Short=AtADT6; Short=AtPDT6; Flags: Precursor gi|6579207|gb|AAF18250.1|AC011438_12 T23G18.10 [Arabidopsis thaliana] gi|15810503|gb|AAL07139.1| unknown protein [Arabidopsis thaliana] gi|20259555|gb|AAM14120.1| unknown protein [Arabidopsis thaliana] gi|89340490|gb|ABD67754.1| arogenate dehydratase isoform 5 [Arabidopsis thaliana] gi|332190144|gb|AEE28265.1| arogenate dehydratase 6 [Arabidopsis thaliana]	339	413	1.00E-167	121.8	88.5	92.3	arogenate dehydratase 6	gbpln	Arabidopsis thaliana	AT1G08250.1 | Symbols: ADT6 | arogenate dehydratase 6 | chr1:2588994-2590235 REVERSE LENGTH=413	339	413	1.00E-169	121.8	88.5	92.3
Rsa1.0_00404.1.g13152.t1	gb|AAF18253.1|AC011438_15 T23G18.7 [Arabidopsis thaliana]	58	566	8.00E-20	975.9	86.2	89.7	T23G18.7	gbpln	Arabidopsis thaliana	AT1G08210.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:2577119-2580581 REVERSE LENGTH=492	58	492	4.00E-15	848.3	58.6	58.6
Rsa1.0_00404.1.g13153.t1	ref|NP_563807.1| UDP-apiose/xylose synthase [Arabidopsis thaliana] gi|6579211|gb|AAF18254.1|AC011438_16 T23G18.6 [Arabidopsis thaliana] gi|24899785|gb|AAN65107.1| similar to dihydroflavonol reductase [Arabidopsis thaliana] gi|332190139|gb|AEE28260.1| UDP-apiose/xylose synthase [Arabidopsis thaliana]	389	389	0	100.0	97.2	98.7	UDP-apiose/xylose synthase	gbpln	Arabidopsis thaliana	AT1G08200.1 | Symbols: AXS2 | UDP-D-apiose/UDP-D-xylose synthase 2 | chr1:2574259-2576609 REVERSE LENGTH=389	389	389	0	100.0	97.2	98.7
Rsa1.0_00404.1.g13154.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00404.1.g13155.t1	gb|EOA37085.1| hypothetical protein CARUB_v10010243mg [Capsella rubella]	207	222	1.00E-89	107.2	88.9	95.2	hypothetical protein CARUB_v10010243mg	gbpln	Capsella rubella	AT1G08160.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr1:2559672-2560337 REVERSE LENGTH=221	207	221	4.00E-90	106.8	86.0	92.8
Rsa1.0_00404.1.g13156.t1	gb|EOA37645.1| hypothetical protein CARUB_v10012128mg [Capsella rubella]	809	810	0	100.1	75.8	88.3	hypothetical protein CARUB_v10012128mg	gbpln	Capsella rubella	AT1G08150.1 | Symbols: ATCHX5, CHX5 | Cation/hydrogen exchanger family protein | chr1:2556343-2559074 REVERSE LENGTH=815	809	815	0	100.7	73.8	86.4
Rsa1.0_00404.1.g13157.t7	gb|EOA39250.1| hypothetical protein CARUB_v10012247mg [Capsella rubella]	952	818	0	85.9	63.1	72.9	hypothetical protein CARUB_v10012247mg	gbpln	Capsella rubella	AT1G08140.1 | Symbols: ATCHX6A, CHX6A | cation/H+ exchanger 6A | chr1:2552206-2555074 REVERSE LENGTH=818	952	818	0	85.9	59.3	71.1
Rsa1.0_00404.1.g13158.t1	#	#	#	#	#	#	#	–	----	----	AT5G46740.1 | Symbols: UBP21 | ubiquitin-specific protease 21 | chr5:18965410-18968492 REVERSE LENGTH=732	113	732	3.00E-12	647.8	28.3	34.5
Rsa1.0_00404.1.g13159.t1	gb|EOA37659.1| hypothetical protein CARUB_v10012226mg [Capsella rubella]	794	793	0	99.9	72.9	85.6	hypothetical protein CARUB_v10012226mg	gbpln	Capsella rubella	AT1G08135.1 | Symbols: ATCHX6B, CHX6B | cation/H+ exchanger 6B | chr1:2548819-2551473 REVERSE LENGTH=796	794	796	0	100.3	71.0	84.5
Rsa1.0_00404.1.g13160.t1	gb|AAG50652.1|AC073433_4 transposase, putative [Arabidopsis thaliana]	208	659	5.00E-23	316.8	27.9	35.1	transposase, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00404.1.g13161.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00404.1.g13162.t4	dbj|BAB09501.1| unnamed protein product [Arabidopsis thaliana]	190	312	7.00E-18	164.2	27.9	41.6	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00404.1.g13163.t1	gb|AFK65609.1| high-affinity nitrate transporter [Brassica rapa subsp. chinensis]	502	530	0	105.6	88.0	92.8	high-affinity nitrate transporter	gbpln	Brassica rapa	AT1G08090.1 | Symbols: ATNRT2:1, NRT2, NRT2;1AT, ACH1, LIN1, ATNRT2.1, NRT2.1, NRT2:1 | nitrate transporter 2:1 | chr1:2524139-2525920 FORWARD LENGTH=530	502	530	0	105.6	86.9	91.8
Rsa1.0_00404.1.g13164.t1	gb|AFK65609.1| high-affinity nitrate transporter [Brassica rapa subsp. chinensis]	529	530	0	100.2	97.4	98.1	high-affinity nitrate transporter	gbpln	Brassica rapa	AT1G08090.1 | Symbols: ATNRT2:1, NRT2, NRT2;1AT, ACH1, LIN1, ATNRT2.1, NRT2.1, NRT2:1 | nitrate transporter 2:1 | chr1:2524139-2525920 FORWARD LENGTH=530	529	530	0	100.2	94.3	97.5
Rsa1.0_00404.1.g13165.t3	gb|AAF73380.1| MOM [Arabidopsis thaliana]	1932	2001	0	103.6	46.4	54.5	MOM	gbpln	Arabidopsis thaliana	AT1G08060.2 | Symbols: MOM, MOM1 | ATP-dependent helicase family protein | chr1:2501981-2510488 REVERSE LENGTH=2001	1932	2001	0	103.6	46.3	54.3
Rsa1.0_00404.1.g13166.t1	gb|EOA36949.1| hypothetical protein CARUB_v10009871mg [Capsella rubella] gi|482572763|gb|EOA36950.1| hypothetical protein CARUB_v10009871mg [Capsella rubella]	271	300	1.00E-95	110.7	72.0	80.1	hypothetical protein CARUB_v10009871mg	gbpln	Capsella rubella	AT1G08010.2 | Symbols: GATA11 | GATA transcription factor 11 | chr1:2486202-2487402 REVERSE LENGTH=303	271	303	1.00E-95	111.8	70.5	80.1
Rsa1.0_00404.1.g13167.t1	ref|XP_002889676.1| hypothetical protein ARALYDRAFT_470850 [Arabidopsis lyrata subsp. lyrata] gi|297335518|gb|EFH65935.1| hypothetical protein ARALYDRAFT_470850 [Arabidopsis lyrata subsp. lyrata]	217	144	1.00E-31	66.4	47.0	50.2	hypothetical protein ARALYDRAFT_470850	gbpln	Arabidopsis lyrata	AT1G07985.1 | Symbols: | Expressed protein | chr1:2475508-2475942 FORWARD LENGTH=144	217	144	1.00E-32	66.4	46.5	49.3
Rsa1.0_00404.1.g13168.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00404.1.g13169.t1	dbj|BAF00898.1| hypothetical protein [Arabidopsis thaliana] gi|110738408|dbj|BAF01130.1| hypothetical protein [Arabidopsis thaliana]	183	206	1.00E-56	112.6	73.2	79.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G07980.1 | Symbols: NF-YC10 | nuclear factor Y, subunit C10 | chr1:2473523-2474910 REVERSE LENGTH=206	183	206	1.00E-53	112.6	52.5	55.2
Rsa1.0_00405.1.g13170.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00405.1.g13171.t1	gb|EOA23251.1| hypothetical protein CARUB_v10017299mg [Capsella rubella]	426	431	2.00E-29	101.2	19.7	32.4	hypothetical protein CARUB_v10017299mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00405.1.g13172.t1	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	1484	1643	0	110.7	47.6	62.5	gag/pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1484	1262	2.00E-79	85.0	11.4	17.0
Rsa1.0_00405.1.g13173.t3	gb|EOA20465.1| hypothetical protein CARUB_v10000778mg [Capsella rubella]	100	503	1.00E-32	503.0	75.0	81.0	hypothetical protein CARUB_v10000778mg	gbpln	Capsella rubella	AT5G11780.1 | Symbols: | unknown protein; Has 37 Blast hits to 37 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 3; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:3793928-3795983 FORWARD LENGTH=504	100	504	8.00E-30	504.0	71.0	77.0
Rsa1.0_00405.1.g13174.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00405.1.g13175.t1	gb|EOA35189.1| hypothetical protein CARUB_v10020338mg [Capsella rubella]	424	425	0	100.2	87.3	92.7	hypothetical protein CARUB_v10020338mg	gbpln	Capsella rubella	AT1G61600.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:22729816-22731182 FORWARD LENGTH=421	424	421	0	99.3	86.8	92.0

Rsa1.0_00405.1.g13176.t2	gb|ABD65633.1| hypothetical protein 23.t00050 [Brassica oleracea]	240	260	4.00E-14	108.3	17.1	22.9	hypothetical protein 23.t00050	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00405.1.g13177.t1	ref|NP_176355.1| S-locus lectin protein kinase-like protein [Arabidopsis thaliana] gi|75213389|sp|Q9SY89.1|Y1661_ARATH RecName: Full=Putative G-type lectin S-receptor-like serine/threonine-protein kinase At1g61610; Flags: Precursor gi|4585876|gb|AAD25549.1|AC005850_6 Putative serine/threonine kinase [Arabidopsis thaliana] gi|332195741|gb|AEE33862.1| putative G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	843	842	0	99.9	79.6	88.4	S-locus lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G61610.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:22733472-22736509 FORWARD LENGTH=842	843	842	0	99.9	79.6	88.4
Rsa1.0_00405.1.g13178.t1	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1055	910	0	86.3	32.2	42.7	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1055	626	6.00E-82	59.3	13.4	19.4
Rsa1.0_00405.1.g13179.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	187	1142	9.00E-20	610.7	37.4	55.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	187	256	4.00E-11	136.9	21.9	31.6
Rsa1.0_00405.1.g13180.t1	ref|XP_002888079.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297333920|gb|EFH64338.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	629	310	9.00E-30	49.3	9.5	10.5	protein binding protein	gbpln	Arabidopsis lyrata	AT1G61620.1 | Symbols: | phosphoinositide binding | chr1:22737653-22739209 FORWARD LENGTH=310	629	310	3.00E-32	49.3	9.4	10.5
Rsa1.0_00405.1.g13181.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00405.1.g13182.t1	gb|AAM63037.1| unknown [Arabidopsis thaliana]	157	157	1.00E-74	100.0	92.4	96.2	unknown	gbpln	Arabidopsis thaliana	AT1G61667.1 | Symbols: | Protein of unknown function, DUF538 | chr1:22767674-22768269 FORWARD LENGTH=156	157	156	1.00E-76	99.4	86.6	89.8
Rsa1.0_00405.1.g13183.t1	emb|CAB43904.1| putative protein [Arabidopsis thaliana] gi|7269745|emb|CAB81478.1| putative protein [Arabidopsis thaliana]	317	1415	5.00E-71	446.4	43.5	53.9	putative protein	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	317	240	4.00E-32	75.7	22.1	27.8
Rsa1.0_00405.1.g13184.t3	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	2029	1643	0	81.0	39.5	52.6	gag/pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	2029	1262	2.00E-96	62.2	9.2	14.1
Rsa1.0_00405.1.g13185.t1	gb|ACY30424.1| A.BANb [Brassica napus]	316	342	1.00E-149	108.2	85.8	89.2	A.BANb	gbpln	Brassica napus	AT1G61720.1 | Symbols: BAN | NAD(P)-binding Rossmann-fold superfamily protein | chr1:22791326-22792757 REVERSE LENGTH=340	316	340	1.00E-133	107.6	74.4	84.8
Rsa1.0_00405.1.g13186.t1	ref|NP_564784.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana] gi|4508074|gb|AAD21418.1| Unknown protein [Arabidopsis thaliana] gi|222424594|dbj|BAH20252.1| AT1G61730 [Arabidopsis thaliana] gi|332195759|gb|AEE33880.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana]	219	376	1.00E-18	171.7	21.5	25.1	DNA-binding storekeeper protein-related transcriptional regulator	gbpln	Arabidopsis thaliana	AT1G61730.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:22793447-22794577 REVERSE LENGTH=376	219	376	4.00E-21	171.7	21.5	25.1
Rsa1.0_00405.1.g13187.t1	gb|ABB97041.1| unknown [Brassica rapa]	346	346	1.00E-173	100.0	85.5	88.7	unknown	gbpln	Brassica rapa	AT1G61790.1 | Symbols: | Oligosaccharyltransferase complex/magnesium transporter family protein | chr1:22814390-22815430 FORWARD LENGTH=346	346	346	1.00E-170	100.0	86.1	93.1
Rsa1.0_00405.1.g13188.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1602	1529	0	95.4	39.2	54.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1602	746	5.00E-81	46.6	10.2	14.2
Rsa1.0_00405.1.g13189.t1	ref|XP_003635668.1| PREDICTED: uncharacterized protein LOC100854178, partial [Vitis vinifera]	380	478	4.00E-46	125.8	32.9	45.0	PREDICTED: uncharacterized protein LOC100854178, partial	gbpln	Vitis vinifera	#	#	#	#	#	#	#

Rsa1.0_00405.1.g13190.t1	ref|XP_002886504.1| hypothetical protein ARALYDRAFT_475144 [Arabidopsis lyrata subsp. lyrata] gi|297332345|gb|EFH62763.1| hypothetical protein ARALYDRAFT_475144 [Arabidopsis lyrata subsp. lyrata]	392	388	0	99.0	91.1	93.9	hypothetical protein ARALYDRAFT_475144	gbpln	Arabidopsis lyrata	AT1G61860.1 | Symbols: | Protein kinase superfamily protein | chr1:22863079-22864619 REVERSE LENGTH=389	392	389	0	99.2	90.1	92.9
Rsa1.0_00405.1.g13191.t1	gb|EOA35229.1| hypothetical protein CARUB_v10020389mg [Capsella rubella]	68	408	9.00E-24	600.0	79.4	89.7	hypothetical protein CARUB_v10020389mg	gbpln	Capsella rubella	AT1G61870.1 | Symbols: PPR336 | pentatricopeptide repeat 336 | chr1:22865326-22866552 REVERSE LENGTH=408	68	408	1.00E-20	600.0	77.9	91.2
Rsa1.0_00405.1.g13192.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	872	1024	1.00E-54	117.4	13.8	17.7	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00405.1.g13193.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00406.1.g13194.t1	gb|AAF67372.1| Hypothetical protein T15F17.d [Arabidopsis thaliana]	775	677	3.00E-13	87.4	5.5	7.7	Hypothetical protein T15F17.d	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00406.1.g13195.t2	ref|NP_178819.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|3327395|gb|AAC26677.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana] gi|330251037|gb|AEC06131.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	294	530	1.00E-12	180.3	11.9	14.6	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	294	530	4.00E-15	180.3	11.9	14.6
Rsa1.0_00406.1.g13196.t1	gb|EOA11934.1| hypothetical protein CARUB_v10016549mg, partial [Capsella rubella]	894	499	2.00E-15	55.8	5.9	8.5	hypothetical protein CARUB_v10016549mg, partial	gbpln	Capsella rubella	AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957	894	957	8.00E-17	107.0	5.9	9.5
Rsa1.0_00406.1.g13197.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	617	1838	0	297.9	57.1	74.2	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00406.1.g13198.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	735	1838	3.00E-36	250.1	16.7	25.7	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00406.1.g13199.t1	ref|XP_002893700.1| hypothetical protein ARALYDRAFT_473393 [Arabidopsis lyrata subsp. lyrata] gi|297339542|gb|EFH69959.1| hypothetical protein ARALYDRAFT_473393 [Arabidopsis lyrata subsp. lyrata]	377	317	1.00E-161	84.1	72.9	76.1	hypothetical protein ARALYDRAFT_473393	gbpln	Arabidopsis lyrata	AT1G32100.1 | Symbols: ATPRR1, PRR1 | pinoresinol reductase 1 | chr1:11546472-11547953 REVERSE LENGTH=317	377	317	1.00E-163	84.1	72.9	75.9
Rsa1.0_00406.1.g13200.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00406.1.g13201.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00406.1.g13202.t1	ref|XP_002893700.1| hypothetical protein ARALYDRAFT_473393 [Arabidopsis lyrata subsp. lyrata] gi|297339542|gb|EFH69959.1| hypothetical protein ARALYDRAFT_473393 [Arabidopsis lyrata subsp. lyrata]	317	317	1.00E-168	100.0	89.0	94.6	hypothetical protein ARALYDRAFT_473393	gbpln	Arabidopsis lyrata	AT1G32100.1 | Symbols: ATPRR1, PRR1 | pinoresinol reductase 1 | chr1:11546472-11547953 REVERSE LENGTH=317	317	317	1.00E-170	100.0	89.3	94.3
Rsa1.0_00406.1.g13203.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00406.1.g13204.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	553	1274	1.00E-139	230.4	47.2	65.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	553	575	3.00E-77	104.0	33.6	51.4
Rsa1.0_00406.1.g13205.t1	emb|CAB86926.1| putative protein [Arabidopsis thaliana]	443	977	1.00E-151	220.5	63.2	77.0	putative protein	gbpln	Arabidopsis thaliana	AT3G58980.1 | Symbols: | F-box family protein | chr3:21794445-21797006 REVERSE LENGTH=594	443	594	1.00E-153	134.1	63.2	77.0
Rsa1.0_00406.1.g13206.t1	ref|NP_564389.1| uncharacterized protein [Arabidopsis thaliana] gi|10801369|gb|AAG23441.1|AC084165_7 unknown protein [Arabidopsis thaliana] gi|14335034|gb|AAK59781.1| At1g32160/F3C3_6 [Arabidopsis thaliana] gi|21593480|gb|AAM65447.1| unknown [Arabidopsis thaliana] gi|27363354|gb|AAO11596.1| At1g32160/F3C3_6 [Arabidopsis thaliana] gi|332193321|gb|AEE31442.1| uncharacterized protein AT1G32160 [Arabidopsis thaliana]	396	406	0	102.5	86.1	92.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G32160.1 | Symbols: | Protein of unknown function (DUF760) | chr1:11568701-11570241 FORWARD LENGTH=406	396	406	0	102.5	86.1	92.9
Rsa1.0_00407.1.g13207.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	382	368	4.00E-87	96.3	48.4	63.1	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	382	370	2.00E-78	96.9	42.9	61.5

Rsa1.0_00407.1.g13208.t1	ref|XP_002879295.1| hypothetical protein ARALYDRAFT_482020 [Arabidopsis lyrata subsp. lyrata] gi|297325134|gb|EFH55554.1| hypothetical protein ARALYDRAFT_482020 [Arabidopsis lyrata subsp. lyrata]	431	430	0	99.8	89.3	93.5	hypothetical protein ARALYDRAFT_482020	gbpln	Arabidopsis lyrata	AT2G30970.2 | Symbols: ASP1 | aspartate aminotransferase 1 | chr2:13179012-13181686 FORWARD LENGTH=430	431	430	0	99.8	88.6	93.3
Rsa1.0_00407.1.g13209.t2	ref|XP_002881139.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326978|gb|EFH57398.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	179	232	1.00E-53	129.6	73.7	76.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G30933.2 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr2:13165235-13166517 REVERSE LENGTH=159	179	159	8.00E-55	88.8	72.6	76.0
Rsa1.0_00407.1.g13210.t1	gb|EOA28009.1| hypothetical protein CARUB_v10024186mg [Capsella rubella]	161	170	1.00E-36	105.6	60.9	72.0	hypothetical protein CARUB_v10024186mg	gbpln	Capsella rubella	AT2G30930.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, plasma membrane, membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06540.1); Has 194 Blast hits to 176 proteins in 78 species: Archae - 0; Bacteria - 101; Metazoa - 15; Fungi - 25; Plants - 12; Viruses - 4; Other Eukaryotes - 37 (source: NCBI BLink). | chr2:13162458-13163156 FORWARD LENGTH=164	161	164	5.00E-37	101.9	58.4	69.6
Rsa1.0_00407.1.g13211.t1	gb|EOA28009.1| hypothetical protein CARUB_v10024186mg [Capsella rubella]	173	170	1.00E-59	98.3	72.3	83.2	hypothetical protein CARUB_v10024186mg	gbpln	Capsella rubella	AT2G30930.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, plasma membrane, membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06540.1); Has 194 Blast hits to 176 proteins in 78 species: Archae - 0; Bacteria - 101; Metazoa - 15; Fungi - 25; Plants - 12; Viruses - 4; Other Eukaryotes - 37 (source: NCBI BLink). | chr2:13162458-13163156 FORWARD LENGTH=164	173	164	9.00E-59	94.8	69.4	79.8
Rsa1.0_00407.1.g13212.t1	ref|XP_002881138.1| ATCOQ3 [Arabidopsis lyrata subsp. lyrata] gi|297326977|gb|EFH57397.1| ATCOQ3 [Arabidopsis lyrata subsp. lyrata]	312	323	1.00E-149	103.5	84.0	93.3	ATCOQ3	gbpln	Arabidopsis lyrata	AT2G30920.1 | Symbols: ATCOQ3, EMB3002, COQ3 | coenzyme Q 3 | chr2:13157409-13159824 REVERSE LENGTH=322	312	322	1.00E-147	103.2	81.7	92.3
Rsa1.0_00407.1.g13213.t1	ref|XP_002873095.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318932|gb|EFH49354.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	284	227	4.00E-19	79.9	22.9	34.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321	284	321	5.00E-19	113.0	22.9	35.9
Rsa1.0_00407.1.g13214.t1	ref|NP_001031338.1| glycine-rich protein 3 [Arabidopsis thaliana] gi|330250855|gb|AEC05949.1| glycine-rich protein 3 [Arabidopsis thaliana]	115	111	3.00E-20	96.5	65.2	69.6	glycine-rich protein 3	gbpln	Arabidopsis thaliana	AT2G05520.5 | Symbols: GRP-3, ATGRP-3 | glycine-rich protein 3 | chr2:2026217-2026882 FORWARD LENGTH=111	115	111	5.00E-23	96.5	65.2	69.6
Rsa1.0_00407.1.g13215.t1	ref|NP_850155.1| Pleckstrin homology (PH) domain-containing protein [Arabidopsis thaliana] gi|17979458|gb|AAL50066.1| At2g30880/F7F1.9 [Arabidopsis thaliana] gi|23506089|gb|AAN28904.1| At2g30880/F7F1.9 [Arabidopsis thaliana] gi|330253357|gb|AEC08451.1| Pleckstrin homology (PH) domain-containing protein [Arabidopsis thaliana]	514	504	0	98.1	87.4	93.4	Pleckstrin homology (PH) domain-containing protein	gbpln	Arabidopsis thaliana	AT2G30880.1 | Symbols: | Pleckstrin homology (PH) domain-containing protein | chr2:13142926-13145718 REVERSE LENGTH=504	514	504	0	98.1	87.4	93.4

Rsa1.0_00407.1.g13216.t1	ref|NP_180643.1| glutathione S-transferase [Arabidopsis thaliana] gi|297822799|ref|XP_002879282.1| hypothetical protein ARALYDRAFT_482003 [Arabidopsis lyrata subsp. lyrata] gi|75318706|sp|O80852.1|GSTF9_ARATH RecName: Full=Glutathione S-transferase F9; Short=AtGSTF9; AltName: Full=AtGSTF7; AltName: Full=GST class-phi member 9 gi|13926310|gb|AAK49621.1|AF372905_1 At2g30860/F7F1.7 [Arabidopsis thaliana] gi|3201613|gb|AAC20720.1| glutathione S-transferase [Arabidopsis thaliana] gi|27363352|gb|AAO11595.1| At2g30860/F7F1.7 [Arabidopsis thaliana] gi|297325121|gb|EFH55541.1| hypothetical protein ARALYDRAFT_482003 [Arabidopsis lyrata subsp. lyrata] gi|330253354|gb|AEC08448.1| glutathione S-transferase [Arabidopsis thaliana]	215	215	1.00E-118	100.0	97.2	98.1	glutathione S-transferase	gbpln	Arabidopsis lyrata	AT2G30860.1 | Symbols: ATGSTF9, GLUTTR, ATGSTF7, GSTF9 | glutathione S-transferase PHI 9 | chr2:13139132-13140057 FORWARD LENGTH=215	215	215	1.00E-120	100.0	97.2	98.1
Rsa1.0_00407.1.g13217.t1	gb|EOA27250.1| hypothetical protein CARUB_v10023369mg, partial [Capsella rubella]	361	396	0	109.7	85.0	90.6	hypothetical protein CARUB_v10023369mg, partial	gbpln	Capsella rubella	AT2G30840.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr2:13135581-13136833 REVERSE LENGTH=362	361	362	1.00E-175	100.3	81.4	88.9
Rsa1.0_00407.1.g13218.t1	ref|NP_180641.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|3201632|gb|AAC20718.1| putative dioxygenase [Arabidopsis thaliana] gi|330253352|gb|AEC08446.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	353	358	1.00E-176	101.4	86.1	92.9	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT2G30830.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr2:13132707-13134284 REVERSE LENGTH=358	353	358	1.00E-179	101.4	86.1	92.9
Rsa1.0_00407.1.g13219.t3	ref|XP_002879280.1| hypothetical protein ARALYDRAFT_481999 [Arabidopsis lyrata subsp. lyrata] gi|297325119|gb|EFH55539.1| hypothetical protein ARALYDRAFT_481999 [Arabidopsis lyrata subsp. lyrata]	426	437	1.00E-124	102.6	63.4	73.9	hypothetical protein ARALYDRAFT_481999	gbpln	Arabidopsis lyrata	AT2G30820.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06660.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:13129800-13132391 FORWARD LENGTH=421	426	421	1.00E-116	98.8	60.3	70.0
Rsa1.0_00407.1.g13220.t1	ref|XP_002881133.1| hypothetical protein ARALYDRAFT_902078 [Arabidopsis lyrata subsp. lyrata] gi|297326972|gb|EFH57392.1| hypothetical protein ARALYDRAFT_902078 [Arabidopsis lyrata subsp. lyrata]	1312	1299	0	99.0	87.1	92.7	hypothetical protein ARALYDRAFT_902078	gbpln	Arabidopsis lyrata	AT2G30800.1 | Symbols: HVT1, ATVT-1 | helicase in vascular tissue and tapetum | chr2:13120585-13126635 REVERSE LENGTH=1299	1312	1299	0	99.0	86.7	92.4
Rsa1.0_00407.1.g13221.t1	ref|XP_002879279.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325118|gb|EFH55538.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	471	452	0	96.0	78.8	87.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT2G30780.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:13116547-13118059 FORWARD LENGTH=452	471	452	0	96.0	78.6	87.0
Rsa1.0_00407.1.g13222.t2	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	303	1515	2.00E-13	500.0	20.8	27.4	retrotransposon like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00407.1.g13223.t1	gb|EOA27372.1| hypothetical protein CARUB_v10023490mg [Capsella rubella] gi|482563183|gb|EOA27373.1| hypothetical protein CARUB_v10023490mg [Capsella rubella]	909	364	1.00E-167	40.0	33.6	34.8	hypothetical protein CARUB_v10023490mg	gbpln	Capsella rubella	AT2G30740.1 | Symbols: | Protein kinase superfamily protein | chr2:13096399-13098285 FORWARD LENGTH=366	909	366	1.00E-169	40.3	33.4	34.5
Rsa1.0_00407.1.g13224.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00407.1.g13225.t1	ref|NP_180621.1| nucleoside/nucleotide kinase-like protein [Arabidopsis thaliana] gi|2880041|gb|AAC02735.1| unknown protein [Arabidopsis thaliana] gi|20198326|gb|AAM15524.1| unknown protein [Arabidopsis thaliana] gi|55740579|gb|AAV63882.1| hypothetical protein At2g30630 [Arabidopsis thaliana] gi|330253328|gb|AEC08422.1| nucleoside/nucleotide kinase-like protein [Arabidopsis thaliana]	530	531	0	100.2	92.6	95.5	nucleoside/nucleotide kinase-like protein	gbpln	Arabidopsis thaliana	AT2G30630.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:13046883-13049106 REVERSE LENGTH=531	530	531	0	100.2	92.6	95.5
Rsa1.0_00407.1.g13226.t1	ref|NP_180620.1| histone H1.2 [Arabidopsis thaliana] gi|121907|sp|P26569.1|H12_ARATH RecName: Full=Histone H1.2 gi|13430598|gb|AAK25921.1|AF360211_1 putative histone H1 protein [Arabidopsis thaliana] gi|16320|emb|CAA44316.1| Histone H1-2 [Arabidopsis thaliana] gi|14532870|gb|AAK64117.1| putative histone H1 protein [Arabidopsis thaliana] gi|20198329|gb|AAM15525.1| histone H1 [Arabidopsis thaliana] gi|21553923|gb|AAM63006.1| histone H1 [Arabidopsis thaliana] gi|330253325|gb|AEC08419.1| histone H1.2 [Arabidopsis thaliana]	265	273	1.00E-53	103.0	68.7	75.5	histone H1.2	gbpln	Arabidopsis thaliana	AT2G30620.1 | Symbols: | winged-helix DNA-binding transcription factor family protein | chr2:13045360-13046267 FORWARD LENGTH=273	265	273	3.00E-56	103.0	68.7	75.5
Rsa1.0_00407.1.g13227.t1	ref|XP_002879271.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325110|gb|EFH55530.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	815	809	0	99.3	88.3	92.3	BTB/POZ domain-containing protein	gbpln	Arabidopsis lyrata	AT2G30600.4 | Symbols: | BTB/POZ domain-containing protein | chr2:13037410-13041475 FORWARD LENGTH=809	815	809	0	99.3	86.6	91.5
Rsa1.0_00407.1.g13228.t1	ref|XP_002879270.1| WRKY DNA-binding protein 21 [Arabidopsis lyrata subsp. lyrata] gi|297325109|gb|EFH55529.1| WRKY DNA-binding protein 21 [Arabidopsis lyrata subsp. lyrata]	343	370	1.00E-133	107.9	84.3	89.8	WRKY DNA-binding protein 21	gbpln	Arabidopsis lyrata	AT2G30590.1 | Symbols: WRKY21 | WRKY DNA-binding protein 21 | chr2:13033891-13035303 FORWARD LENGTH=380	343	380	1.00E-133	110.8	82.2	88.0
Rsa1.0_00407.1.g13229.t1	ref|XP_002879269.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297325108|gb|EFH55528.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	290	420	1.00E-116	144.8	81.7	86.6	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G30580.1 | Symbols: DRIP2 | DREB2A-interacting protein 2 | chr2:13026444-13030363 FORWARD LENGTH=420	290	420	1.00E-117	144.8	82.1	85.9
Rsa1.0_00407.1.g13230.t4	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	2193	2301	0	104.9	39.8	48.6	disease resistance protein	gbpln	Brassica rapa	AT2G30575.1 | Symbols: GAUT5, LGT5 | los glycosyltransferase 5 | chr2:13020564-13023906 REVERSE LENGTH=610	2193	610	0	27.8	21.2	24.2
Rsa1.0_00407.1.g13231.t1	ref|XP_002879268.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325107|gb|EFH55527.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	89	89	2.00E-13	100.0	40.4	41.6	predicted protein	gbpln	Arabidopsis lyrata	AT2G30560.1 | Symbols: | glycine-rich protein | chr2:13017347-13018857 FORWARD LENGTH=171	89	171	1.00E-10	192.1	31.5	31.5
Rsa1.0_00407.1.g13232.t1	gb|EOA26886.1| hypothetical protein CARUB_v10022980mg [Capsella rubella]	526	530	0	100.8	85.0	91.3	hypothetical protein CARUB_v10022980mg	gbpln	Capsella rubella	AT2G30550.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:13014885-13017005 FORWARD LENGTH=529	526	529	0	100.6	84.2	90.7
Rsa1.0_00408.1.g13233.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1879	1274	0	67.8	32.4	44.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1879	575	5.00E-64	30.6	8.9	14.3
Rsa1.0_00408.1.g13234.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00408.1.g13235.t1	gb|EOA23861.1| hypothetical protein CARUB_v10017078mg, partial [Capsella rubella]	465	496	0	106.7	90.5	95.7	hypothetical protein CARUB_v10017078mg, partial	gbpln	Capsella rubella	AT3G30180.1 | Symbols: CYP85A2, BR6OX2 | brassinosteroid-6-oxidase 2 | chr3:11810867-11813509 FORWARD LENGTH=465	465	465	0	100.0	89.0	95.3
Rsa1.0_00408.1.g13236.t1	ref|XP_002875529.1| MYB121 [Arabidopsis lyrata subsp. lyrata] gi|297321367|gb|EFH51788.1| MYB121 [Arabidopsis lyrata subsp. lyrata]	263	271	1.00E-109	103.0	79.5	86.3	MYB121	gbpln	Arabidopsis lyrata	AT3G30210.1 | Symbols: ATMYB121, MYB121 | myb domain protein 121 | chr3:11838567-11840313 FORWARD LENGTH=276	263	276	1.00E-108	104.9	76.4	86.3
Rsa1.0_00408.1.g13237.t1	gb|EOA12330.1| hypothetical protein CARUB_v10007925mg, partial [Capsella rubella]	312	539	5.00E-47	172.8	28.8	36.9	hypothetical protein CARUB_v10007925mg, partial	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	312	696	5.00E-15	223.1	14.7	25.0

Rsa1.0_00408.1.g13238.t1	gb|AAF70842.1|AC003113_9 F24O1.21 [Arabidopsis thaliana]	231	361	6.00E-77	156.3	63.2	76.6	F24O1.21	gbpln	Arabidopsis thaliana	AT5G48050.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G34070.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19472661-19473770 REVERSE LENGTH=369	231	369	5.00E-14	159.7	19.9	34.6
Rsa1.0_00408.1.g13239.t3	ref|NP_189645.2| protein agamous-like 79 [Arabidopsis thaliana] gi|32402440|gb|AAN52802.1| MADS-box protein AGL79 [Arabidopsis thaliana] gi|332644107|gb|AEE77628.1| protein agamous-like 79 [Arabidopsis thaliana]	187	249	7.00E-62	133.2	76.5	85.0	protein agamous-like 79	gbpln	Arabidopsis thaliana	AT3G30260.1 | Symbols: AGL79 | AGAMOUS-like 79 | chr3:11909119-11912880 FORWARD LENGTH=249	187	249	3.00E-64	133.2	76.5	85.0
Rsa1.0_00408.1.g13240.t1	ref|XP_003531882.1| PREDICTED: uncharacterized protein LOC100788724 [Glycine max]	876	787	0	89.8	61.5	72.3	PREDICTED: uncharacterized protein LOC100788724	gbenv/gbpln	Glycine max	AT5G38880.1 | Symbols: | unknown protein; Has 474 Blast hits to 433 proteins in 138 species: Archae - 6; Bacteria - 80; Metazoa - 195; Fungi - 44; Plants - 59; Viruses - 0; Other Eukaryotes - 90 (source: NCBI BLink). | chr5:15563621-15568804 REVERSE LENGTH=796	876	796	0	90.9	55.9	62.8
Rsa1.0_00408.1.g13241.t1	ref|XP_002877209.1| hypothetical protein ARALYDRAFT_484728 [Arabidopsis lyrata subsp. lyrata] gi|297323047|gb|EFH53468.1| hypothetical protein ARALYDRAFT_484728 [Arabidopsis lyrata subsp. lyrata]	681	677	0	99.4	91.6	94.7	hypothetical protein ARALYDRAFT_484728	gbpln	Arabidopsis lyrata	AT3G30300.1 | Symbols: | O-fucosyltransferase family protein | chr3:11921390-11924254 REVERSE LENGTH=677	681	677	0	99.4	91.3	94.7
Rsa1.0_00408.1.g13242.t2	gb|EOA24256.1| hypothetical protein CARUB_v10017497mg [Capsella rubella]	359	364	1.00E-167	101.4	82.7	89.1	hypothetical protein CARUB_v10017497mg	gbpln	Capsella rubella	AT3G30340.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:11956626-11958969 FORWARD LENGTH=364	359	364	1.00E-169	101.4	81.6	89.7
Rsa1.0_00408.1.g13243.t1	dbj|BAB02236.1| unnamed protein product [Arabidopsis thaliana]	152	180	8.00E-37	118.4	50.7	59.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G30350.2 | Symbols: RGF4 | Encodes a root meristem growth factor (RGF). Belongs to a family of functionally redundant homologous peptides that are secreted, tyrosine-sulfated, and expressed mainly in the stem cell area and the innermost layer of central columella cells. RGFs are required for maintenance of the root stem cell niche and transit amplifying cell proliferation. Members of this family include: At5g60810 (RGF1), At1g13620 (RGF2), At2g04025 (RGF3), At3g30350 (RGF4), At5g51451 (RGF5), At4g16515 (RGF6), At3g02240 (RGF7), At2g03830 (RGF8) and At5g64770 (RGF9). | chr3:11960552-11961764 REVERSE LENGTH=182	152	182	5.00E-33	119.7	44.1	53.3
Rsa1.0_00408.1.g13244.t1	gb|EOA26153.1| hypothetical protein CARUB_v10019591mg [Capsella rubella]	384	377	0	98.2	89.8	93.2	hypothetical protein CARUB_v10019591mg	gbpln	Capsella rubella	AT3G30380.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:11974424-11976571 FORWARD LENGTH=377	384	377	0	98.2	89.1	93.0
Rsa1.0_00408.1.g13245.t1	gb|EOA25673.1| hypothetical protein CARUB_v10019025mg [Capsella rubella]	453	458	0	101.1	91.4	96.2	hypothetical protein CARUB_v10019025mg	gbpln	Capsella rubella	AT3G30390.2 | Symbols: | Transmembrane amino acid transporter family protein | chr3:11977112-11978827 REVERSE LENGTH=460	453	460	0	101.5	90.1	95.4
Rsa1.0_00408.1.g13246.t1	ref|XP_002875553.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297321391|gb|EFH51812.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	194	146	9.00E-52	75.3	53.6	58.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G30460.1 | Symbols: | RING/U-box superfamily protein | chr3:12104433-12104876 FORWARD LENGTH=147	194	147	2.00E-52	75.8	53.1	57.7
Rsa1.0_00408.1.g13247.t1	gb|ABE65398.1| hypothetical protein At1g43570 [Arabidopsis thaliana]	413	348	1.00E-77	84.3	34.6	45.3	hypothetical protein At1g43570	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	413	746	1.00E-63	180.6	30.0	38.3
Rsa1.0_00408.1.g13248.t1	ref|XP_002875554.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297321392|gb|EFH51813.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	172	172	1.00E-82	100.0	90.1	92.4	bZIP transcription factor family protein	gbpln	Arabidopsis lyrata	AT3G30530.1 | Symbols: ATBZIP42, bZIP42 | basic leucine-zipper 42 | chr3:12139512-12140033 FORWARD LENGTH=173	172	173	4.00E-84	100.6	90.1	93.6

Rsa1.0_00408.1.g13249.t1	gb|EOA12358.1| hypothetical protein CARUB_v10016510mg [Capsella rubella]	132	134	7.00E-46	101.5	81.8	84.1	hypothetical protein CARUB_v10016510mg	gbpln	Capsella rubella	AT3G30580.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G38790.1); Has 75 Blast hits to 75 proteins in 16 species: Archae - 2; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 63; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr3:12167767-12168153 REVERSE LENGTH=128	132	128	1.00E-40	97.0	82.6	86.4
Rsa1.0_00408.1.g13250.t1	ref|NP_850650.1| glutamine dumper 6 [Arabidopsis thaliana] gi|122214817|sp|Q3EAV6.1|GDU6_ARATH RecName: Full=Protein GLUTAMINE DUMPER 6 gi|332644133|gb|AEE77654.1| glutamine dumper 6 [Arabidopsis thaliana]	112	111	2.00E-22	99.1	66.1	81.3	glutamine dumper 6	gbpln	Arabidopsis thaliana	AT3G30725.1 | Symbols: AtGDU6, GDU6 | glutamine dumper 6 | chr3:12352509-12352844 FORWARD LENGTH=111	112	111	4.00E-25	99.1	66.1	81.3
Rsa1.0_00408.1.g13251.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00409.1.g13252.t1	gb|EOA29639.1| hypothetical protein CARUB_v10014964mg [Capsella rubella]	113	113	2.00E-38	100.0	74.3	88.5	hypothetical protein CARUB_v10014964mg	gbpln	Capsella rubella	AT3G08770.1 | Symbols: LTP6 | lipid transfer protein 6 | chr3:2664349-2664784 REVERSE LENGTH=113	113	113	1.00E-38	100.0	71.7	81.4
Rsa1.0_00409.1.g13253.t1	ref|XP_002884696.1| hypothetical protein ARALYDRAFT_478180 [Arabidopsis lyrata subsp. lyrata] gi|297330536|gb|EFH60955.1| hypothetical protein ARALYDRAFT_478180 [Arabidopsis lyrata subsp. lyrata]	380	312	1.00E-129	82.1	63.7	70.8	hypothetical protein ARALYDRAFT_478180	gbpln	Arabidopsis lyrata	AT3G08780.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, cultured cell; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:2666514-2667452 REVERSE LENGTH=312	380	312	1.00E-130	82.1	63.4	70.8
Rsa1.0_00409.1.g13254.t1	ref|NP_187491.1| ENTH/VHS/GAT family protein [Arabidopsis thaliana] gi|12322744|gb|AAG51368.1|AC012562_29 hypothetical protein; 78804-81924 [Arabidopsis thaliana] gi|332641159|gb|AEE74680.1| ENTH/VHS/GAT family protein [Arabidopsis thaliana]	151	607	2.00E-28	402.0	59.6	66.2	ENTH/VHS/GAT family protein	gbpln	Arabidopsis thaliana	AT3G08790.1 | Symbols: | ENTH/VHS/GAT family protein | chr3:2667881-2671001 FORWARD LENGTH=607	151	607	5.00E-31	402.0	59.6	66.2
Rsa1.0_00409.1.g13255.t1	ref|XP_002882584.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297328424|gb|EFH58843.1| binding protein [Arabidopsis lyrata subsp. lyrata]	932	932	0	100.0	81.2	88.3	binding protein	gbpln	Arabidopsis lyrata	AT3G08800.1 | Symbols: | ARM repeat superfamily protein | chr3:2671148-2674910 FORWARD LENGTH=936	932	936	0	100.4	80.2	88.1
Rsa1.0_00409.1.g13256.t1	ref|XP_002884698.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330538|gb|EFH60957.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	691	685	0	99.1	82.2	90.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G08820.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:2677122-2679179 REVERSE LENGTH=685	691	685	0	99.1	81.6	89.9
Rsa1.0_00409.1.g13257.t1	ref|XP_002885026.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330866|gb|EFH61285.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	328	303	1.00E-109	92.4	59.8	70.1	protein binding protein	gbpln	Arabidopsis lyrata	AT3G14250.1 | Symbols: | RING/U-box superfamily protein | chr3:4745963-4746958 REVERSE LENGTH=303	328	303	1.00E-104	92.4	57.3	68.9
Rsa1.0_00409.1.g13258.t1	ref|NP_566335.1| regulatory associated protein of mTOR [Arabidopsis thaliana] gi|75331762|sp|Q93YQ1.1|RTOR1_ARATH RecName: Full=Regulatory-associated protein of TOR 1; AltName: Full=Protein RAPTOR 1; AltName: Full=Protein RAPTOR 1B; Short=AtRaptor1b gi|16648937|gb|AAL24320.1| Unknown protein [Arabidopsis thaliana] gi|31711792|gb|AAP68252.1| At3g08850 [Arabidopsis thaliana] gi|56266687|gb|AAV84960.1| raptor1B [Arabidopsis thaliana] gi|332641166|gb|AEE74687.1| regulatory associated protein of mTOR [Arabidopsis thaliana]	1335	1344	0	100.7	91.2	94.7	regulatory associated protein of mTOR	gbpln	Arabidopsis thaliana	AT3G08850.1 | Symbols: RAPTOR1B, ATRAPTOR1B, RAPTOR1 | HEAT repeat ;WD domain, G-beta repeat protein protein | chr3:2686978-2694911 REVERSE LENGTH=1344	1335	1344	0	100.7	91.2	94.7

Rsa1.0_00409.1.g13259.t1	ref|NP_566336.1| uncharacterized protein [Arabidopsis thaliana] gi|30680674|ref|NP_850544.1| uncharacterized protein [Arabidopsis thaliana] gi|6403495|gb|AAF07835.1|AC010871_11 unknown protein [Arabidopsis thaliana] gi|21554089|gb|AAM63170.1| unknown [Arabidopsis thaliana] gi|98960915|gb|ABF58941.1| At3g08890 [Arabidopsis thaliana] gi|110743674|dbj|BAE99674.1| hypothetical protein [Arabidopsis thaliana] gi|332641170|gb|AEE74691.1| uncharacterized protein AT3G08890 [Arabidopsis thaliana] gi|332641171|gb|AEE74692.1| uncharacterized protein AT3G08890 [Arabidopsis thaliana]	121	170	2.00E-63	140.5	95.9	100.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G08890.2 | Symbols: | Protein of unknown function, DUF538 | chr3:2706701-2707775 FORWARD LENGTH=170	121	170	3.00E-66	140.5	95.9	100.0
Rsa1.0_00409.1.g13260.t1	ref|XP_002884703.1| hypothetical protein ARALYDRAFT_317692 [Arabidopsis lyrata subsp. lyrata] gi|297330543|gb|EFH60962.1| hypothetical protein ARALYDRAFT_317692 [Arabidopsis lyrata subsp. lyrata]	368	374	0	101.6	91.0	95.1	hypothetical protein ARALYDRAFT_317692	gbpln	Arabidopsis lyrata	AT3G08900.1 | Symbols: RGP3, RGP | reversibly glycosylated polypeptide 3 | chr3:2708347-2709714 REVERSE LENGTH=362	368	362	0	98.4	88.9	92.1
Rsa1.0_00409.1.g13261.t1	ref|NP_187503.1| DnaJ domain-containing protein [Arabidopsis thaliana] gi|6403504|gb|AAF07844.1|AC010871_20 putative heat shock protein [Arabidopsis thaliana] gi|208879540|gb|ACI31315.1| At3g08910 [Arabidopsis thaliana] gi|332641173|gb|AEE74694.1| DnaJ domain-containing protein [Arabidopsis thaliana]	91	323	2.00E-23	354.9	67.0	76.9	DnaJ domain-containing protein	gbpln	Arabidopsis thaliana	AT3G08910.1 | Symbols: | DNAJ heat shock family protein | chr3:2710402-2711811 REVERSE LENGTH=323	91	323	3.00E-26	354.9	67.0	76.9
Rsa1.0_00409.1.g13262.t1	ref|NP_187506.1| chlorophyll a-b binding protein CP29.2 [Arabidopsis thaliana] gi|38503262|sp|Q9XF88.1|CB4B_ARATH RecName: Full=Chlorophyll a-b binding protein CP29.2, chloroplastic; AltName: Full=LHCB4.2; AltName: Full=LHCII protein 4.2; Flags: Precursor gi|4741954|gb|AAD28774.1|AF134127_1 Lhcb4.2 protein [Arabidopsis thaliana] gi|6403491|gb|AAF07831.1|AC010871_7 putative chlorophyll a/b-binding protein [Arabidopsis thaliana] gi|17473745|gb|AAL38316.1| putative chlorophyll a/b-binding protein [Arabidopsis thaliana] gi|20148559|gb|AAM10170.1| putative chlorophyll a/b-binding protein [Arabidopsis thaliana] gi|332641177|gb|AEE74698.1| chlorophyll a-b binding protein CP29.2 [Arabidopsis thaliana]	288	287	1.00E-151	99.7	95.1	97.6	chlorophyll a-b binding protein CP29.2	gbpln	Arabidopsis thaliana	AT3G08940.2 | Symbols: LHCB4.2 | light harvesting complex photosystem II | chr3:2717717-2718665 FORWARD LENGTH=287	288	287	1.00E-153	99.7	95.1	97.6
Rsa1.0_00409.1.g13263.t1	ref|NP_001154598.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332641179|gb|AEE74700.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	872	873	0	100.1	87.5	93.2	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G08947.1 | Symbols: | ARM repeat superfamily protein | chr3:2724007-2726722 FORWARD LENGTH=873	872	873	0	100.1	87.5	93.2
Rsa1.0_00409.1.g13264.t2	ref|XP_002882593.1| electron transport SCO1/SenC family protein [Arabidopsis lyrata subsp. lyrata] gi|297328433|gb|EFH58852.1| electron transport SCO1/SenC family protein [Arabidopsis lyrata subsp. lyrata]	358	334	1.00E-160	93.3	82.1	86.9	electron transport SCO1/SenC family protein	gbpln	Arabidopsis lyrata	AT3G08950.1 | Symbols: HCC1 | electron transport SCO1/SenC family protein | chr3:2727285-2729289 FORWARD LENGTH=334	358	334	1.00E-161	93.3	82.1	86.0
Rsa1.0_00409.1.g13265.t1	ref|XP_002884706.1| hypothetical protein ARALYDRAFT_317700 [Arabidopsis lyrata subsp. lyrata] gi|297330546|gb|EFH60965.1| hypothetical protein ARALYDRAFT_317700 [Arabidopsis lyrata subsp. lyrata]	1002	1010	0	100.8	92.0	96.1	hypothetical protein ARALYDRAFT_317700	gbpln	Arabidopsis lyrata	AT3G08960.1 | Symbols: | ARM repeat superfamily protein | chr3:2730405-2736762 REVERSE LENGTH=1010	1002	1010	0	100.8	91.4	95.5

Rsa1.0_00409.1_g13266.t1	ref|XP_002882594.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297328434|gb|EFH58853.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	588	575	0	97.8	83.2	87.9	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT3G08970.1 | Symbols: ATERDJ3A, TMS1 | DNAJ heat shock N-terminal domain-containing protein | chr3:2737589-2740265 FORWARD LENGTH=572	588	572	0	97.3	81.5	87.1
Rsa1.0_00409.1_g13267.t1	ref|XP_002882596.1| yippee family protein [Arabidopsis lyrata subsp. lyrata] gi|297328436|gb|EFH58855.1| yippee family protein [Arabidopsis lyrata subsp. lyrata]	127	127	5.00E-61	100.0	87.4	93.7	yippee family protein	gbpln	Arabidopsis lyrata	AT3G08990.2 | Symbols: | Yippee family putative zinc-binding protein | chr3:2743590-2744709 FORWARD LENGTH=128	127	128	2.00E-61	100.8	83.5	93.7
Rsa1.0_00409.1_g13268.t1	gb|EOA31912.1| hypothetical protein CARUB_v10015141mg [Capsella rubella]	653	523	0	80.1	66.3	70.8	hypothetical protein CARUB_v10015141mg	gbpln	Capsella rubella	AT3G09000.1 | Symbols: | proline-rich family protein | chr3:2746014-2748326 FORWARD LENGTH=541	653	541	0	82.8	66.9	72.0
Rsa1.0_00409.1_g13269.t1	ref|XP_002882599.1| hypothetical protein ARALYDRAFT_478210 [Arabidopsis lyrata subsp. lyrata] gi|297328439|gb|EFH58858.1| hypothetical protein ARALYDRAFT_478210 [Arabidopsis lyrata subsp. lyrata]	406	412	0	101.5	84.0	92.9	hypothetical protein ARALYDRAFT_478210	gbpln	Arabidopsis lyrata	AT3G09020.1 | Symbols: | alpha 1,4-glycosyltransferase family protein | chr3:2753307-2754542 FORWARD LENGTH=411	406	411	0	101.2	81.8	90.9
Rsa1.0_00409.1_g13270.t1	ref|XP_002882600.1| potassium channel tetramerization domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297328440|gb|EFH58859.1| potassium channel tetramerization domain-containing protein [Arabidopsis lyrata subsp. lyrata]	385	454	1.00E-165	117.9	74.5	79.2	potassium channel tetramerization domain-containing protein	gbpln	Arabidopsis lyrata	AT3G09030.1 | Symbols: | BTB/POZ domain-containing protein | chr3:2754841-2756223 FORWARD LENGTH=460	385	460	1.00E-168	119.5	74.5	79.7
Rsa1.0_00409.1_g13271.t1	gb|EOA31664.1| hypothetical protein CARUB_v10014868mg [Capsella rubella]	137	142	1.00E-37	103.6	73.0	83.2	hypothetical protein CARUB_v10014868mg	gbpln	Capsella rubella	AT3G09032.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G01225.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:2757605-2758045 REVERSE LENGTH=146	137	146	5.00E-39	106.6	62.8	75.2
Rsa1.0_00409.1_g13272.t1	ref|NP_001154599.1| putative lectin [Arabidopsis thaliana] gi|332641214|gb|AEE74735.1| putative lectin [Arabidopsis thaliana]	354	345	1.00E-132	97.5	70.1	79.4	putative lectin	gbpln	Arabidopsis thaliana	AT3G09190.1 | Symbols: | Concanavalin A-like lectin family protein | chr3:2821650-2822687 REVERSE LENGTH=345	354	345	1.00E-135	97.5	70.1	79.4
Rsa1.0_00409.1_g13273.t1	ref|XP_002882608.1| hypothetical protein ARALYDRAFT_897068 [Arabidopsis lyrata subsp. lyrata] gi|297328448|gb|EFH58867.1| hypothetical protein ARALYDRAFT_897068 [Arabidopsis lyrata subsp. lyrata]	397	402	0	101.3	89.9	95.0	hypothetical protein ARALYDRAFT_897068	gbpln	Arabidopsis lyrata	AT3G09180.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Mediator complex subunit Med27 (InterPro:IPR021627); Has 112 Blast hits to 112 proteins in 38 species: Archae - 0; Bacteria - 0; Metazoa - 79; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr3:2819278-2821096 FORWARD LENGTH=402	397	402	0	101.3	89.7	95.2
Rsa1.0_00409.1_g13274.t1	ref|NP_187517.1| uncharacterized protein [Arabidopsis thaliana] gi|5923670|gb|AAD56321.1|AC009326_8 unknown protein [Arabidopsis thaliana] gi|44681474|gb|AAS47677.1| At3g09050 [Arabidopsis thaliana] gi|62320254|dbj|BAD94528.1| hypothetical protein [Arabidopsis thaliana] gi|332641193|gb|AEE74714.1| uncharacterized protein AT3G09050 [Arabidopsis thaliana]	258	258	1.00E-119	100.0	88.8	93.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G09050.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 120 Blast hits to 120 proteins in 47 species: Archae - 4; Bacteria - 10; Metazoa - 33; Fungi - 2; Plants - 44; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr3:2764860-2765907 FORWARD LENGTH=258	258	258	1.00E-122	100.0	88.8	93.8
Rsa1.0_00409.1_g13275.t1	gb|EOA29845.1| hypothetical protein CARUB_v10012938mg [Capsella rubella]	941	896	0	95.2	83.0	87.0	hypothetical protein CARUB_v10012938mg	gbpln	Capsella rubella	AT3G09090.1 | Symbols: DEX1 | defective in exine formation protein (DEX1) | chr3:2782912-2787552 REVERSE LENGTH=896	941	896	0	95.2	83.3	87.2
Rsa1.0_00409.1_g13276.t1	ref|XP_002884713.1| mRNA capping enzyme family protein [Arabidopsis lyrata subsp. lyrata] gi|297330553|gb|EFH60972.1| mRNA capping enzyme family protein [Arabidopsis lyrata subsp. lyrata]	200	668	4.00E-99	334.0	90.5	95.5	mRNA capping enzyme family protein	gbpln	Arabidopsis lyrata	AT3G09100.2 | Symbols: | mRNA capping enzyme family protein | chr3:2788435-2792913 REVERSE LENGTH=672	200	672	1.00E-101	336.0	90.0	95.5
Rsa1.0_00409.1_g13277.t1	ref|XP_002884714.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330554|gb|EFH60973.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	474	492	1.00E-109	103.8	50.0	66.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G01150.1 | Symbols: | Protein of unknown function (DUF674) | chr5:51988-53649 FORWARD LENGTH=501	474	501	9.00E-93	105.7	44.7	61.6

Rsa1.0_00409.1.g13278.t1	ref|XP_002882607.1| hypothetical protein ARALYDRAFT_478229 [Arabidopsis lyrata subsp. lyrata] gi|297328447|gb|EFH58866.1| hypothetical protein ARALYDRAFT_478229 [Arabidopsis lyrata subsp. lyrata]	340	329	2.00E-58	96.8	34.1	37.1	hypothetical protein ARALYDRAFT_478229	gbpln	Arabidopsis lyrata	AT3G09150.1 | Symbols: HY2, GUN3, ATHY2 | phytochromobilin:ferredoxin oxidoreductase, chloroplast / phytochromobilin synthase (HY2) | chr3:2803665-2805333 FORWARD LENGTH=327	340	327	8.00E-60	96.2	31.5	33.5
Rsa1.0_00409.1.g13279.t1	gb|AAD56334.1|AC009326_21 putative lectin [Arabidopsis thaliana]	246	313	6.00E-88	127.2	65.0	80.1	putative lectin	gbpln	Arabidopsis thaliana	AT3G09190.1 | Symbols: | Concanavalin A-like lectin family protein | chr3:2821650-2822687 REVERSE LENGTH=345	246	345	8.00E-90	140.2	64.6	80.1
Rsa1.0_00410.1.g13280.t1	gb|EOA16607.1| hypothetical protein CARUB_v10004780mg [Capsella rubella]	449	454	0	101.1	80.6	88.4	hypothetical protein CARUB_v10004780mg	gbpln	Capsella rubella	AT4G29700.1 | Symbols: | Alkaline-phosphatase-like family protein | chr4:14543739-14545124 REVERSE LENGTH=461	449	461	0	102.7	79.3	87.8
Rsa1.0_00410.1.g13281.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00410.1.g13282.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00410.1.g13283.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00410.1.g13284.t1	ref|NP_194697.1| alkaline-phosphatase-like protein [Arabidopsis thaliana] gi|5123562|emb|CAB45328.1| nucleotide pyrophosphatase-like protein [Arabidopsis thaliana] gi|7269867|emb|CAB79726.1| nucleotide pyrophosphatase-like protein [Arabidopsis thaliana] gi|225898829|dbj|BAH30545.1| hypothetical protein [Arabidopsis thaliana] gi|332660261|gb|AEE85661.1| alkaline-phosphatase-like protein [Arabidopsis thaliana]	443	496	0	112.0	78.6	85.8	alkaline-phosphatase-like protein	gbpln	Arabidopsis thaliana	AT4G29680.1 | Symbols: | Alkaline-phosphatase-like family protein | chr4:14538067-14539557 REVERSE LENGTH=496	443	496	0	112.0	78.6	85.8
Rsa1.0_00410.1.g13285.t1	ref|XP_002867402.1| hypothetical protein ARALYDRAFT_491802 [Arabidopsis lyrata subsp. lyrata] gi|297313238|gb|EFH43661.1| hypothetical protein ARALYDRAFT_491802 [Arabidopsis lyrata subsp. lyrata]	501	493	0	98.4	76.8	86.8	hypothetical protein ARALYDRAFT_491802	gbpln	Arabidopsis lyrata	AT4G29560.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Fanconi Anaemia group E protein, C-terminal (InterPro:IPR021025); Has 41 Blast hits to 41 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 10; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:14504421-14505999 REVERSE LENGTH=493	501	493	0	98.4	76.2	85.2
Rsa1.0_00410.1.g13286.t1	ref|XP_002869427.1| acyl--UDP-N-acetylglucosamine O-acyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297315263|gb|EFH45686.1| acyl--UDP-N-acetylglucosamine O-acyltransferase [Arabidopsis lyrata subsp. lyrata]	335	336	1.00E-165	100.3	88.4	92.2	acyl--UDP-N-acetylglucosamine O-acyltransferase	gbpln	Arabidopsis lyrata	AT4G29540.2 | Symbols: | bacterial transferase hexapeptide repeat-containing protein | chr4:14497775-14499765 FORWARD LENGTH=336	335	336	1.00E-165	100.3	86.3	91.0
Rsa1.0_00410.1.g13287.t1	gb|EOA17071.1| hypothetical protein CARUB_v10005319mg [Capsella rubella]	354	307	1.00E-114	86.7	65.8	72.3	hypothetical protein CARUB_v10005319mg	gbpln	Capsella rubella	AT4G29520.1 | Symbols: | LOCATED IN: endoplasmic reticulum, plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Saposin B (InterPro:IPR008139); Has 137 Blast hits to 137 proteins in 50 species: Archae - 2; Bacteria - 0; Metazoa - 41; Fungi - 10; Plants - 36; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink). | chr4:14494056-14495657 REVERSE LENGTH=306	354	306	1.00E-112	86.4	62.1	66.9
Rsa1.0_00410.1.g13288.t1	ref|NP_174578.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana] gi|378405165|sp|Q9MAP1.2|FB33_ARATH RecName: Full=Putative F-box protein At1g33020 gi|332193429|gb|AEE31550.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana]	380	548	4.00E-68	144.2	43.9	56.1	F-box and associated interaction domain-containing protein	gbpln	Arabidopsis thaliana	AT1G33020.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11962746-11964832 FORWARD LENGTH=548	380	548	1.00E-70	144.2	43.9	56.1

Rsa1.0_00410.1.g13289.t1	ref|NP_194675.1| Phospholipase A2 family protein [Arabidopsis thaliana] gi|75264514|sp|Q9M0D7.1|PLA2C_ARATH RecName: Full=Phospholipase A2-gamma; AltName: Full=Secretory phospholipase A2-gamma; Short=AtsPLA2-gamma; Flags: Precursor gi|7269845|emb|CAB79704.1| phospholipase A2-like protein [Arabidopsis thaliana] gi|26006457|gb|AAN63044.1| phospholipase A2 gamma [Arabidopsis thaliana] gi|332660234|gb|AEE85634.1| phospholipase A2-gamma [Arabidopsis thaliana]	186	187	4.00E-80	100.5	75.8	87.1	Phospholipase A2 family protein	gbpln	Arabidopsis thaliana	AT4G29460.1 | Symbols: | Phospholipase A2 family protein | chr4:14483066-14483930 REVERSE LENGTH=187	186	187	2.00E-82	100.5	75.8	87.1
Rsa1.0_00410.1.g13290.t1	ref|XP_002867410.1| 60S ribosomal protein L28 [Arabidopsis lyrata subsp. lyrata] gi|297313246|gb|EFH43669.1| 60S ribosomal protein L28 [Arabidopsis lyrata subsp. lyrata]	143	143	4.00E-72	100.0	93.0	96.5	60S ribosomal protein L28	gbpln	Arabidopsis lyrata	AT4G29410.2 | Symbols: | Ribosomal L28e protein family | chr4:14468439-14469964 REVERSE LENGTH=143	143	143	1.00E-72	100.0	90.9	95.1
Rsa1.0_00410.1.g13291.t1	gb|EOA18586.1| hypothetical protein CARUB_v10007158mg [Capsella rubella]	596	538	0	90.3	76.3	81.0	hypothetical protein CARUB_v10007158mg	gbpln	Capsella rubella	AT4G29360.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr4:14451562-14453687 REVERSE LENGTH=534	596	534	0	89.6	77.2	81.4
Rsa1.0_00410.1.g13292.t1	sp|Q9FUB8.1|PROF_BRANA RecName: Full=Profilin gi|11229030|gb|AAG33237.1|AF315326_1 profilin [Brassica napus]	134	134	3.00E-72	100.0	97.8	99.3	RecName: Full=Profilin gi|11229030|gb|AAG33237.1|AF315326_1 profilin	gbpln	Brassica napus	AT4G29340.1 | Symbols: PRF4 | profilin 4 | chr4:14447718-14448467 FORWARD LENGTH=134	134	134	3.00E-72	100.0	93.3	98.5
Rsa1.0_00410.1.g13293.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00410.1.g13294.t1	ref|XP_002867418.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313254|gb|EFH43677.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	260	256	1.00E-103	98.5	70.8	80.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G29270.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr4:14423797-14424848 REVERSE LENGTH=256	260	256	1.00E-101	98.5	67.7	78.5
Rsa1.0_00410.1.g13295.t1	dbj|BAJ33902.1| unnamed protein product [Thellungiella halophila]	351	365	1.00E-162	104.0	82.3	89.2	unnamed protein product	----	----	AT4G29190.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr4:14392233-14393303 REVERSE LENGTH=356	351	356	1.00E-150	101.4	78.3	84.0
Rsa1.0_00410.1.g13296.t1	ref|XP_002869450.1| hypothetical protein ARALYDRAFT_913597 [Arabidopsis lyrata subsp. lyrata] gi|297315286|gb|EFH45709.1| hypothetical protein ARALYDRAFT_913597 [Arabidopsis lyrata subsp. lyrata]	526	533	0	101.3	85.6	92.8	hypothetical protein ARALYDRAFT_913597	gbpln	Arabidopsis lyrata	AT4G29140.1 | Symbols: | MATE efflux family protein | chr4:14369148-14370746 FORWARD LENGTH=532	526	532	0	101.1	84.8	91.8
Rsa1.0_00410.1.g13297.t5	ref|XP_002869950.1| hypothetical protein ARALYDRAFT_914645 [Arabidopsis lyrata subsp. lyrata] gi|297315786|gb|EFH46209.1| hypothetical protein ARALYDRAFT_914645 [Arabidopsis lyrata subsp. lyrata]	290	529	3.00E-36	182.4	31.4	37.6	hypothetical protein ARALYDRAFT_914645	gbpln	Arabidopsis lyrata	AT4G20070.1 | Symbols: ATAAH, AAH | allantoate amidohydrolase | chr4:10861548-10864529 FORWARD LENGTH=525	290	525	3.00E-38	181.0	31.0	37.2
Rsa1.0_00410.1.g13298.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00410.1.g13299.t1	ref|NP_194639.1| transcription factor bHLH68 [Arabidopsis thaliana] gi|75159400|sp|Q8S3D1.2|BH068_ARATH RecName: Full=Transcription factor bHLH68; AltName: Full=Basic helix-loop-helix protein 68; Short=AtbHLH68; Short=bHLH 68; AltName: Full=Transcription factor EN 60; AltName: Full=bHLH transcription factor bHLH068 gi|22711852|gb|AAM10966.2|AF488634_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|4972056|emb|CAB43924.1| putative protein [Arabidopsis thaliana] gi|7269808|emb|CAB79668.1| putative protein [Arabidopsis thaliana] gi|19698939|gb|AAL91205.1| putative protein [Arabidopsis thaliana] gi|23197826|gb|AAN15440.1| putative protein [Arabidopsis thaliana] gi|332660186|gb|AEE85586.1| transcription factor bHLH68 [Arabidopsis thaliana]	408	407	1.00E-173	99.8	85.5	90.2	transcription factor bHLH68	gbpln	Arabidopsis thaliana	AT4G29100.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:14341140-14344575 FORWARD LENGTH=407	408	407	1.00E-175	99.8	85.5	90.2
Rsa1.0_00411.1.g13300.t1	gb|EOA12485.1| hypothetical protein CARUB_v10026032mg [Capsella rubella]	670	668	0	99.7	66.9	75.4	hypothetical protein CARUB_v10026032mg	gbpln	Capsella rubella	AT5G62190.1 | Symbols: PRH75 | DEAD box RNA helicase (PRH75) | chr5:24980542-24983879 REVERSE LENGTH=671	670	671	0	100.1	66.4	75.1

Rsa1.0_00411.1.g13301.t1	gb|EOA39029.1| hypothetical protein CARUB_v10011599mg [Capsella rubella]	289	329	5.00E-89	113.8	60.2	73.7	hypothetical protein CARUB_v10011599mg	gbpln	Capsella rubella	AT5G62180.1 | Symbols: AtCXE20, CXE20 | carboxyesterase 20 | chr5:24978866-24979849 REVERSE LENGTH=327	289	327	2.00E-84	113.1	56.1	71.3
Rsa1.0_00411.1.g13302.t1	gb|EOA39029.1| hypothetical protein CARUB_v10011599mg [Capsella rubella]	249	329	3.00E-94	132.1	71.9	83.9	hypothetical protein CARUB_v10011599mg	gbpln	Capsella rubella	AT5G62180.1 | Symbols: AtCXE20, CXE20 | carboxyesterase 20 | chr5:24978866-24979849 REVERSE LENGTH=327	249	327	6.00E-91	131.3	67.1	81.9
Rsa1.0_00411.1.g13303.t1	gb|EOA39029.1| hypothetical protein CARUB_v10011599mg [Capsella rubella]	327	329	1.00E-137	100.6	73.4	83.8	hypothetical protein CARUB_v10011599mg	gbpln	Capsella rubella	AT5G62180.1 | Symbols: AtCXE20, CXE20 | carboxyesterase 20 | chr5:24978866-24979849 REVERSE LENGTH=327	327	327	1.00E-132	100.0	69.4	83.5
Rsa1.0_00411.1.g13304.t1	gb|EOA39029.1| hypothetical protein CARUB_v10011599mg [Capsella rubella]	342	329	1.00E-120	96.2	64.3	76.3	hypothetical protein CARUB_v10011599mg	gbpln	Capsella rubella	AT5G62180.1 | Symbols: AtCXE20, CXE20 | carboxyesterase 20 | chr5:24978866-24979849 REVERSE LENGTH=327	342	327	1.00E-116	95.6	59.6	76.0
Rsa1.0_00411.1.g13305.t1	ref|NP_568952.1| protein agamous-like 42 [Arabidopsis thaliana] gi|30697641|ref|NP_851247.1| protein agamous-like 42 [Arabidopsis thaliana] gi|79331885|ref|NP_001032123.1| protein agamous-like 42 [Arabidopsis thaliana] gi|10176935|dbj|BAB10179.1| MADS box protein-like [Arabidopsis thaliana] gi|15809905|gb|AAL06880.1| At2g45660/F17K2.19 [Arabidopsis thaliana] gi|17528944|gb|AAL38682.1| unknown protein [Arabidopsis thaliana] gi|17978861|gb|AAL47402.1| At2g45660/F17K2.19 [Arabidopsis thaliana] gi|20465947|gb|AAM20159.1| unknown protein [Arabidopsis thaliana] gi|32402390|gb|AAN52777.1| MADS-box protein AGL42 [Arabidopsis thaliana] gi|332010189|gb|AED97572.1| protein agamous-like 42 [Arabidopsis thaliana] gi|332010190|gb|AED97573.1| protein agamous-like 42 [Arabidopsis thaliana] gi|332010191|gb|AED97574.1| protein agamous-like 42 [Arabidopsis thaliana	209	210	1.00E-100	100.5	85.6	94.7	protein agamous-like 42	gbpln	Arabidopsis thaliana	AT5G62165.3 | Symbols: AGL42 | AGAMOUS-like 42 | chr5:24965075-24968437 FORWARD LENGTH=210	209	210	1.00E-102	100.5	85.6	94.7
Rsa1.0_00411.1.g13306.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00411.1.g13307.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00411.1.g13308.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00411.1.g13309.t1	ref|XP_002864774.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310609|gb|EFH41033.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	409	356	1.00E-161	87.0	70.2	75.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G62160.1 | Symbols: AtZIP12, ZIP12 | zinc transporter 12 precursor | chr5:24960107-24961263 FORWARD LENGTH=355	409	355	1.00E-155	86.8	68.9	74.6
Rsa1.0_00411.1.g13310.t1	ref|XP_002866474.1| hypothetical protein ARALYDRAFT_496390 [Arabidopsis lyrata subsp. lyrata] gi|297312309|gb|EFH42733.1| hypothetical protein ARALYDRAFT_496390 [Arabidopsis lyrata subsp. lyrata]	241	238	1.00E-104	98.8	79.3	87.6	hypothetical protein ARALYDRAFT_496390	gbpln	Arabidopsis lyrata	AT5G62140.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; Has 60 Blast hits to 60 proteins in 24 species: Archae - 0; Bacteria - 14; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:24954563-24955376 REVERSE LENGTH=241	241	241	1.00E-106	100.0	79.3	88.4
Rsa1.0_00411.1.g13311.t1	ref|NP_568951.1| Per1-like family protein [Arabidopsis thaliana] gi|15294204|gb|AAK95279.1|AF410293_1 AT5g62130/mtg10_150 [Arabidopsis thaliana] gi|20147283|gb|AAM10355.1| AT5g62130/mtg10_150 [Arabidopsis thaliana] gi|332010184|gb|AED97567.1| Per1-like family protein [Arabidopsis thaliana]	346	343	1.00E-174	99.1	84.1	92.8	Per1-like family protein	gbpln	Arabidopsis thaliana	AT5G62130.1 | Symbols: | Per1-like family protein | chr5:24950685-24952918 REVERSE LENGTH=343	346	343	1.00E-177	99.1	84.1	92.8
Rsa1.0_00411.1.g13312.t2	ref|XP_002866471.1| hypothetical protein ARALYDRAFT_332444 [Arabidopsis lyrata subsp. lyrata] gi|297312306|gb|EFH42730.1| hypothetical protein ARALYDRAFT_332444 [Arabidopsis lyrata subsp. lyrata]	611	639	1.00E-54	104.6	33.2	43.9	hypothetical protein ARALYDRAFT_332444	gbpln	Arabidopsis lyrata	AT5G07210.1 | Symbols: ARR21, RR21 | response regulator 21 | chr5:2252237-2256018 FORWARD LENGTH=621	611	621	2.00E-22	101.6	16.9	24.1

Rsa1.0_00411.1.g13313.t1	ref|NP_568950.2| BCL-2-associated athanogene 2 [Arabidopsis thaliana] gi|378548292|sp|Q0WPX7.1|BAG2_ARATH RecName: Full=BAG family molecular chaperone regulator 2; AltName: Full=Bcl-2-associated athanogene 2 gi|110737767|dbj|BAF00822.1| hypothetical protein [Arabidopsis thaliana] gi|332010180|gb|AED97563.1| BCL-2-associated athanogene 2 [Arabidopsis thaliana]	297	285	1.00E-117	96.0	71.7	82.2	BCL-2-associated athanogene 2	gbpln	Arabidopsis thaliana	AT5G62100.2 | Symbols: ATBAG2, BAG2 | BCL-2-associated athanogene 2 | chr5:24940477-24941775 FORWARD LENGTH=285	297	285	1.00E-120	96.0	71.7	82.2
Rsa1.0_00411.1.g13314.t1	ref|XP_002866470.1| hypothetical protein ARALYDRAFT_919461 [Arabidopsis lyrata subsp. lyrata] gi|297312305|gb|EFH42729.1| hypothetical protein ARALYDRAFT_919461 [Arabidopsis lyrata subsp. lyrata]	773	815	0	105.4	56.3	59.6	hypothetical protein ARALYDRAFT_919461	gbpln	Arabidopsis lyrata	AT5G62090.2 | Symbols: SLK2 | SEUSS-like 2 | chr5:24935221-24938540 REVERSE LENGTH=816	773	816	0	105.6	56.8	59.5
Rsa1.0_00411.1.g13315.t3	gb|EOA13663.1| hypothetical protein CARUB_v10026734mg, partial [Capsella rubella]	325	339	3.00E-87	104.3	56.3	63.1	hypothetical protein CARUB_v10026734mg, partial	gbpln	Capsella rubella	AT5G62020.1 | Symbols: AT-HSFB2A, HSFB2A | heat shock transcription factor B2A | chr5:24916212-24917194 FORWARD LENGTH=299	325	299	2.00E-88	92.0	56.9	63.1
Rsa1.0_00411.1.g13316.t10	gb|EOA12910.1| hypothetical protein CARUB_v10025886mg [Capsella rubella]	819	831	0	101.5	93.3	95.6	hypothetical protein CARUB_v10025886mg	gbpln	Capsella rubella	AT5G61980.1 | Symbols: AGD1 | ARF-GAP domain 1 | chr5:24894472-24899178 FORWARD LENGTH=828	819	828	0	101.1	92.3	95.0
Rsa1.0_00412.1.g13317.t1	ref|NP_197666.1| glucomannan 4-beta-mannosyltransferase 2 [Arabidopsis thaliana] gi|75171864|sp|Q9FNI7.1|CSLA2_ARATH RecName: Full=Glucomannan 4-beta-mannosyltransferase 2; AltName: Full=Cellulose synthase-like protein A2; Short=AtCslA2; AltName: Full=Glucomannan synthase; AltName: Full=Mannan synthase 2 gi|10178248|dbj|BAB11680.1| glucosyltransferase-like protein [Arabidopsis thaliana] gi|16648764|gb|AAL25573.1| AT5g22740/MDJ22_16 [Arabidopsis thaliana] gi|16648965|gb|AAL24334.1| glucosyltransferase-like protein [Arabidopsis thaliana] gi|20259890|gb|AAM13292.1| glucosyltransferase-like protein [Arabidopsis thaliana] gi|332005686|gb|AED93069.1| glucomannan 4-beta-mannosyltransferase 2 [Arabidopsis thaliana]	264	534	1.00E-148	202.3	96.2	98.5	glucomannan 4-beta-mannosyltransferase 2	gbpln	Arabidopsis thaliana	AT5G22740.1 | Symbols: ATCSLA02, CSLA02, ATCSLA2, CSLA2 | cellulose synthase-like A02 | chr5:7555379-7559866 REVERSE LENGTH=534	264	534	1.00E-151	202.3	96.2	98.5
Rsa1.0_00412.1.g13318.t1	ref|NP_197667.1| DNA/RNA helicase protein RAD5 [Arabidopsis thaliana] gi|60390961|sp|Q9FNI6.1|SM3L2_ARATH RecName: Full=Putative SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 3-like 2; Short=SMARCA3-like protein 2 gi|10178249|dbj|BAB11681.1| DNA repair protein RAD5 protein [Arabidopsis thaliana] gi|110737306|dbj|BAF00599.1| hypothetical protein [Arabidopsis thaliana] gi|332005687|gb|AED93070.1| DNA/RNA helicase protein RAD5 [Arabidopsis thaliana]	1021	1029	0	100.8	86.9	91.5	DNA/RNA helicase protein RAD5	gbpln	Arabidopsis thaliana	AT5G22750.1 | Symbols: RAD5 | DNA/RNA helicase protein | chr5:7565374-7570871 REVERSE LENGTH=1029	1021	1029	0	100.8	86.9	91.5
Rsa1.0_00412.1.g13319.t1	gb|EOA22590.1| hypothetical protein CARUB_v10003253mg [Capsella rubella]	1533	1591	0	103.8	79.4	87.7	hypothetical protein CARUB_v10003253mg	gbpln	Capsella rubella	AT5G22760.1 | Symbols: | PHD finger family protein | chr5:7571635-7577662 FORWARD LENGTH=1566	1533	1566	0	102.2	79.1	87.1
Rsa1.0_00412.1.g13320.t1	ref|XP_002882729.1| hypothetical protein ARALYDRAFT_478477 [Arabidopsis lyrata subsp. lyrata] gi|297328569|gb|EFH58988.1| hypothetical protein ARALYDRAFT_478477 [Arabidopsis lyrata subsp. lyrata]	149	154	2.00E-43	103.4	62.4	77.9	hypothetical protein ARALYDRAFT_478477	gbpln	Arabidopsis lyrata	AT3G11405.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G55570.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:3580895-3581359 FORWARD LENGTH=154	149	154	2.00E-40	103.4	60.4	77.2
Rsa1.0_00412.1.g13321.t1	gb|EOA20677.1| hypothetical protein CARUB_v10000989mg [Capsella rubella]	925	436	1.00E-165	47.1	34.7	37.3	hypothetical protein CARUB_v10000989mg	gbpln	Capsella rubella	AT5G22790.1 | Symbols: RER1 | reticulata-related 1 | chr5:7599395-7601573 REVERSE LENGTH=433	925	433	1.00E-165	46.8	34.5	37.3

Rsa1.0_00412.1.g13322.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	176	1197	9.00E-17	680.1	29.5	46.0	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	176	170	5.00E-13	96.6	20.5	32.4
Rsa1.0_00412.1.g13323.t1	ref|XP_003606631.1| Histone H2B [Medicago truncatula] gi|355507686|gb|AES88828.1| Histone H2B [Medicago truncatula]	141	147	6.00E-62	104.3	92.2	95.0	Histone H2B	gbpln	Medicago truncatula	AT3G45980.1 | Symbols: H2B, HTB9 | Histone superfamily protein | chr3:16897492-16897944 REVERSE LENGTH=150	141	150	6.00E-61	106.4	92.9	94.3
Rsa1.0_00412.1.g13324.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2271	1274	0	56.1	30.4	39.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT5G22910.1 | Symbols: ATCHX9, CHX9 | cation/H+ exchanger 9 | chr5:7660927-7663829 REVERSE LENGTH=800	2271	800	0	35.2	14.0	15.9
Rsa1.0_00412.1.g13325.t1	ref|NP_197683.1| ring finger and CHY zinc finger domain-containing protein 1 [Arabidopsis thaliana] gi|10177239|dbj|BAB10613.1| PGPD14 protein [Arabidopsis thaliana] gi|15450521|gb|AAK96553.1| AT5g22920/MRN17_15 [Arabidopsis thaliana] gi|27363264|gb|AAO11551.1| At5g22920/MRN17_15 [Arabidopsis thaliana] gi|66865966|gb|AAY57617.1| RING finger family protein [Arabidopsis thaliana] gi|332005714|gb|AED93097.1| ring finger and CHY zinc finger domain-containing protein 1 [Arabidopsis thaliana]	292	291	1.00E-156	99.7	90.4	96.2	ring finger and CHY zinc finger domain-containing protein 1	gbpln	Arabidopsis thaliana	AT5G22920.1 | Symbols: | CHY-type/CTCHY-type/RING-type Zinc finger protein | chr5:7665143-7667031 FORWARD LENGTH=291	292	291	1.00E-159	99.7	90.4	96.2
Rsa1.0_00412.1.g13326.t1	ref|XP_002874104.1| hypothetical protein ARALYDRAFT_351315 [Arabidopsis lyrata subsp. lyrata] gi|297319941|gb|EFH50363.1| hypothetical protein ARALYDRAFT_351315 [Arabidopsis lyrata subsp. lyrata]	239	238	1.00E-110	99.6	82.8	90.4	hypothetical protein ARALYDRAFT_351315	gbpln	Arabidopsis lyrata	AT5G22930.1 | Symbols: | Protein of unknown function (DUF1635) | chr5:7668229-7669315 REVERSE LENGTH=238	239	238	1.00E-111	99.6	81.2	89.1
Rsa1.0_00412.1.g13327.t1	ref|XP_002872025.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297317862|gb|EFH48284.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	461	465	0	100.9	82.9	88.1	exostosin family protein	gbpln	Arabidopsis lyrata	AT5G22940.1 | Symbols: F8H | FRA8 homolog | chr5:7677197-7678892 FORWARD LENGTH=469	461	469	0	101.7	81.1	87.6
Rsa1.0_00412.1.g13328.t1	ref|XP_002872026.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|297317863|gb|EFH48285.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	229	229	1.00E-113	100.0	96.1	99.1	SNF7 family protein	gbpln	Arabidopsis lyrata	AT5G22950.1 | Symbols: VPS24.1 | SNF7 family protein | chr5:7681380-7682720 FORWARD LENGTH=229	229	229	1.00E-114	100.0	95.6	98.7
Rsa1.0_00412.1.g13329.t1	ref|XP_002872027.1| hypothetical protein ARALYDRAFT_489152 [Arabidopsis lyrata subsp. lyrata] gi|297317864|gb|EFH48286.1| hypothetical protein ARALYDRAFT_489152 [Arabidopsis lyrata subsp. lyrata]	419	508	1.00E-170	121.2	67.8	79.0	hypothetical protein ARALYDRAFT_489152	gbpln	Arabidopsis lyrata	AT5G22980.1 | Symbols: scpl47 | serine carboxypeptidase-like 47 | chr5:7688084-7690481 FORWARD LENGTH=505	419	505	1.00E-169	120.5	68.0	79.0
Rsa1.0_00412.1.g13330.t1	ref|NP_200808.1| uncharacterized protein [Arabidopsis thaliana] gi|9757921|dbj|BAB08368.1| unnamed protein product [Arabidopsis thaliana] gi|61742769|gb|AAX55205.1| hypothetical protein At5g60000 [Arabidopsis thaliana] gi|332009882|gb|AED97265.1| uncharacterized protein AT5G60000 [Arabidopsis thaliana]	169	149	2.00E-29	88.2	45.6	59.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G60000.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22970.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:24159331-24159780 REVERSE LENGTH=149	169	149	8.00E-32	88.2	45.6	59.8
Rsa1.0_00412.1.g13331.t1	ref|NP_200808.1| uncharacterized protein [Arabidopsis thaliana] gi|9757921|dbj|BAB08368.1| unnamed protein product [Arabidopsis thaliana] gi|61742769|gb|AAX55205.1| hypothetical protein At5g60000 [Arabidopsis thaliana] gi|332009882|gb|AED97265.1| uncharacterized protein AT5G60000 [Arabidopsis thaliana]	155	149	5.00E-29	96.1	47.1	63.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G60000.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22970.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:24159331-24159780 REVERSE LENGTH=149	155	149	2.00E-31	96.1	47.1	63.9

Rsa1.0_00412.1.g13332.t1	gb|EOA13802.1| hypothetical protein CARUB_v10026897mg [Capsella rubella]	276	290	2.00E-60	105.1	59.8	72.8	hypothetical protein CARUB_v10026897mg	gbpln	Capsella rubella	AT5G60800.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:24461116-24462464 REVERSE LENGTH=283	276	283	7.00E-59	102.5	58.7	70.3
Rsa1.0_00413.1.g13333.t1	gb|EOA22581.1| hypothetical protein CARUB_v10003247mg [Capsella rubella]	260	445	1.00E-147	171.2	96.9	97.3	hypothetical protein CARUB_v10003247mg	gbpln	Capsella rubella	AT5G09550.1 | Symbols: | GDP dissociation inhibitor family protein / Rab GTPase activator family protein | chr5:2963850-2966465 FORWARD LENGTH=445	260	445	1.00E-149	171.2	96.5	97.7
Rsa1.0_00413.1.g13334.t1	dbj|BAJ34398.1| unnamed protein product [Thellungiella halophila]	682	683	0	100.1	95.0	97.7	unnamed protein product	----	----	AT5G09590.1 | Symbols: MTHSC70-2, HSC70-5 | mitochondrial HSO70 2 | chr5:2975721-2978508 FORWARD LENGTH=682	682	682	0	100.0	93.3	97.1
Rsa1.0_00413.1.g13335.t1	ref|XP_002873412.1| hypothetical protein ARALYDRAFT_908914 [Arabidopsis lyrata subsp. lyrata] gi|297319249|gb|EFH49671.1| hypothetical protein ARALYDRAFT_908914 [Arabidopsis lyrata subsp. lyrata]	383	384	1.00E-108	100.3	53.5	71.0	hypothetical protein ARALYDRAFT_908914	gbpln	Arabidopsis lyrata	AT5G09630.1 | Symbols: | LisH/CRA/RING-U-box domains-containing protein | chr5:2986016-2987176 REVERSE LENGTH=386	383	386	1.00E-109	100.8	53.5	70.0
Rsa1.0_00413.1.g13336.t1	ref|XP_002873413.1| inorganic pyrophosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319250|gb|EFH49672.1| inorganic pyrophosphatase family protein [Arabidopsis lyrata subsp. lyrata]	297	299	1.00E-154	100.7	91.9	97.6	inorganic pyrophosphatase family protein	gbpln	Arabidopsis lyrata	AT5G09650.1 | Symbols: AtPPa6, PPa6 | pyrophosphorylase 6 | chr5:2991331-2993117 REVERSE LENGTH=300	297	300	1.00E-155	101.0	91.9	97.0
Rsa1.0_00413.1.g13337.t1	ref|NP_001031010.1| uncharacterized protein [Arabidopsis thaliana] gi|3249106|gb|AAC24089.1| T12M4.16 [Arabidopsis thaliana] gi|98961961|gb|ABF59310.1| unknown protein [Arabidopsis thaliana] gi|332190283|gb|AEE28404.1| uncharacterized protein AT1G09157 [Arabidopsis thaliana]	242	243	1.00E-104	100.4	88.0	93.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G09157.1 | Symbols: | Protein of unknown function (DUF679) | chr1:2951665-2952396 REVERSE LENGTH=243	242	243	1.00E-107	100.4	88.0	93.4
Rsa1.0_00413.1.g13338.t1	gb|AGK89951.1| Hpp1 protein [Eutrema halophilum]	83	300	2.00E-22	361.4	74.7	79.5	Hpp1 protein	gbpln	Eutrema halophilum	AT5G09650.1 | Symbols: AtPPa6, PPa6 | pyrophosphorylase 6 | chr5:2991331-2993117 REVERSE LENGTH=300	83	300	3.00E-24	361.4	72.3	77.1
Rsa1.0_00413.1.g13339.t1	ref|NP_196538.1| Putative pectinesterase/pectinesterase inhibitor 51 [Arabidopsis thaliana] gi|75180831|sp|Q9LXD9.1|PME51_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 51; Includes: RecName: Full=Pectinesterase inhibitor 51; AltName: Full=Pectin methylesterase inhibitor 51; Includes: RecName: Full=Pectinesterase 51; Short=PE 51; AltName: Full=Pectin methylesterase 51; Short=AtPME51; Flags: Precursor gi|7671413|emb|CAB89354.1| pectin methylesterase-like protein [Arabidopsis thaliana] gi|17979183|gb|AAL49830.1| putative pectin methylesterase [Arabidopsis thaliana] gi|29824167|gb|AAP04044.1| putative pectin methylesterase [Arabidopsis thaliana] gi|332004060|gb|AED91443.1| Putative pectinesterase/pectinesterase inhibitor 51 [Arabidopsis thaliana]	549	551	0	100.4	82.1	88.3	Putative pectinesterase/pectinesterase inhibitor 51	gbpln	Arabidopsis thaliana	AT5G09760.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:3032446-3034364 FORWARD LENGTH=551	549	551	0	100.4	82.1	88.3

Rsa1.0_00413.1.g13340.t1	ref|NP_196538.1| Putative pectinesterase/pectinesterase inhibitor 51 [Arabidopsis thaliana] gi|75180831|sp|Q9LXD9.1|PME51_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 51; Includes: RecName: Full=Pectinesterase inhibitor 51; AltName: Full=Pectin methylesterase inhibitor 51; Includes: RecName: Full=Pectinesterase 51; Short=PE 51; AltName: Full=Pectin methylesterase 51; Short=AtPME51; Flags: Precursor gi|7671413|emb|CAB89354.1| pectin methylesterase-like protein [Arabidopsis thaliana] gi|17979183|gb|AAL49830.1| putative pectin methylesterase [Arabidopsis thaliana] gi|29824167|gb|AAP04044.1| putative pectin methylesterase [Arabidopsis thaliana] gi|332004060|gb|AED91443.1| Putative pectinesterase/pectinesterase inhibitor 51 [Arabidopsis thaliana]	546	551	0	100.9	78.4	86.6	Putative pectinesterase/pectinesterase inhibitor 51	gbpln	Arabidopsis thaliana	AT5G09760.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:3032446-3034364 FORWARD LENGTH=551	546	551	0	100.9	78.4	86.6
Rsa1.0_00413.1.g13341.t1	ref|XP_002873421.1| ribosomal protein L17 family protein [Arabidopsis lyrata subsp. lyrata] gi|297319258|gb|EFH49680.1| ribosomal protein L17 family protein [Arabidopsis lyrata subsp. lyrata]	160	160	2.00E-79	100.0	89.4	95.0	ribosomal protein L17 family protein	gbpln	Arabidopsis lyrata	AT5G09770.1 | Symbols: | Ribosomal protein L17 family protein | chr5:3035267-3036518 REVERSE LENGTH=160	160	160	1.00E-81	100.0	90.0	95.0
Rsa1.0_00413.1.g13342.t1	gb|EOA20292.1| hypothetical protein CARUB_v10000600mg [Capsella rubella]	122	561	8.00E-20	459.8	39.3	41.0	hypothetical protein CARUB_v10000600mg	gbpln	Capsella rubella	AT5G24470.1 | Symbols: APRR5, PRR5 | pseudo-response regulator 5 | chr5:8356204-8358873 REVERSE LENGTH=667	122	667	2.00E-22	546.7	39.3	41.0
Rsa1.0_00413.1.g13343.t1	ref|XP_002871385.1| hypothetical protein ARALYDRAFT_908929 [Arabidopsis lyrata subsp. lyrata] gi|297317222|gb|EFH47644.1| hypothetical protein ARALYDRAFT_908929 [Arabidopsis lyrata subsp. lyrata]	105	103	4.00E-29	98.1	74.3	83.8	hypothetical protein ARALYDRAFT_908929	gbpln	Arabidopsis lyrata	AT5G09805.1 | Symbols: IDL3 | inflorescence deficient in abscission (IDA)-like 3 | chr5:3047218-3047517 FORWARD LENGTH=99	105	99	3.00E-30	94.3	69.5	78.1
Rsa1.0_00413.1.g13344.t1	gb|AEN25580.1| actin 7 [Brassica rapa subsp. pekinensis]	377	377	0	100.0	99.7	100.0	actin 7	gbpln	Brassica rapa	AT5G09810.1 | Symbols: ACT7 | actin 7 | chr5:3052809-3054220 FORWARD LENGTH=377	377	377	0	100.0	99.2	99.7
Rsa1.0_00413.1.g13345.t1	ref|NP_001031862.1| putative plastid-lipid-associated protein 7 [Arabidopsis thaliana] gi|75102996|sp|Q5M755.1|PAP7_ARATH RecName: Full=Probable plastid-lipid-associated protein 7, chloroplastic; AltName: Full=Fibrillin-7; Flags: Precursor gi|56461766|gb|AAV91339.1| At5g09820 [Arabidopsis thaliana] gi|110737316|dbj|BAF00604.1| hypothetical protein [Arabidopsis thaliana] gi|332004069|gb|AED91452.1| putative plastid-lipid-associated protein 7 [Arabidopsis thaliana]	271	273	1.00E-124	100.7	86.7	91.9	putative plastid-lipid-associated protein 7	gbpln	Arabidopsis thaliana	AT5G09820.2 | Symbols: | Plastid-lipid associated protein PAP / fibrillin family protein | chr5:3056090-3057380 REVERSE LENGTH=273	271	273	1.00E-126	100.7	86.7	91.9
Rsa1.0_00413.1.g13346.t1	ref|NP_568218.1| Transcription elongation factor (TFIIS) family protein [Arabidopsis thaliana] gi|395406779|sp|F4KFC7.1|MD26C_ARATH RecName: Full=Probable mediator of RNA polymerase II transcription subunit 26c gi|332004072|gb|AED91455.1| Transcription elongation factor (TFIIS) family protein [Arabidopsis thaliana]	348	353	1.00E-158	101.4	84.5	90.5	Transcription elongation factor (TFIIS) family protein	gbpln	Arabidopsis thaliana	AT5G09850.1 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr5:3063488-3065221 REVERSE LENGTH=353	348	353	1.00E-160	101.4	84.5	90.5
Rsa1.0_00413.1.g13347.t1	ref|NP_196549.1| cellulose synthase A catalytic subunit 5 [UDP-forming] [Arabidopsis thaliana] gi|73917713|sp|Q8L778.2|CESA5_ARATH RecName: Full=Cellulose synthase A catalytic subunit 5 [UDP-forming]; Short=AtCesA5 gi|9758965|dbj|BAB09408.1| cellulose synthase catalytic subunit [Arabidopsis thaliana] gi|332004075|gb|AED91458.1| cellulose synthase A catalytic subunit 5 [UDP-forming] [Arabidopsis thaliana]	1069	1069	0	100.0	92.7	95.4	cellulose synthase A catalytic subunit 5	gbpln	Arabidopsis thaliana	AT5G09870.1 | Symbols: CESA5 | cellulose synthase 5 | chr5:3073356-3077974 FORWARD LENGTH=1069	1069	1069	0	100.0	92.7	95.4

Rsa1.0_00413.1.g13348.t1	ref|XP_002871390.1| hypothetical protein ARALYDRAFT_908937 [Arabidopsis lyrata subsp. lyrata] gi|297317227|gb|EFH47649.1| hypothetical protein ARALYDRAFT_908937 [Arabidopsis lyrata subsp. lyrata]	83	103	9.00E-13	124.1	66.3	75.9	hypothetical protein ARALYDRAFT_908937	gbpln	Arabidopsis lyrata	AT5G09876.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:3079987-3080304 FORWARD LENGTH=105	83	105	2.00E-15	126.5	61.4	74.7
Rsa1.0_00413.1.g13349.t1	gb|EOA19397.1| hypothetical protein CARUB_v10000967mg [Capsella rubella]	538	442	0	82.2	78.8	80.3	hypothetical protein CARUB_v10000967mg	gbpln	Capsella rubella	AT5G09900.1 | Symbols: EMB2107, RPN5A, MSA | 26S proteasome regulatory subunit, putative (RPN5) | chr5:3089462-3092434 REVERSE LENGTH=442	538	442	0	82.2	77.5	80.5
Rsa1.0_00413.1.g13350.t1	ref|NP_196554.1| DNA-directed RNA polymerase II subunit D [Arabidopsis thaliana] gi|2760362|gb|AAB95261.1| 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana] gi|9758970|dbj|BAB09413.1| 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana] gi|21554212|gb|AAM63291.1| 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana] gi|98960869|gb|ABF58918.1| At5g09920 [Arabidopsis thaliana] gi|222423668|dbj|BAH19801.1| AT5G09920 [Arabidopsis thaliana] gi|332004084|gb|AED91467.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana]	90	138	1.00E-12	153.3	38.9	41.1	DNA-directed RNA polymerase II subunit D	gbpln	Arabidopsis thaliana	AT5G09920.1 | Symbols: RPB15.9, ATRPB15.9, RPB15.9.9, NRPB4 | RNA polymerase II, Rpb4, core protein | chr5:3096276-3097370 FORWARD LENGTH=138	90	138	2.00E-15	153.3	38.9	41.1
Rsa1.0_00413.1.g13351.t1	gb|AAZ66921.1| 117M18_2 [Brassica rapa]	193	329	9.00E-86	170.5	81.3	88.6	117M18_2	gbpln	Brassica rapa	AT5G09940.1 | Symbols: | Protein of unknown function (DUF1635) | chr5:3101192-3101833 FORWARD LENGTH=213	193	213	5.00E-40	110.4	54.9	67.9
Rsa1.0_00413.1.g13352.t1	gb|AAZ66922.1| 117M18_3 [Brassica rapa]	82	87	1.00E-18	106.1	80.5	82.9	117M18_3	gbpln	Brassica rapa	AT5G09980.1 | Symbols: PROPEP4 | elicitor peptide 4 precursor | chr5:3122790-3123728 FORWARD LENGTH=81	82	81	4.00E-11	98.8	62.2	72.0
Rsa1.0_00413.1.g13353.t1	gb|AAZ66923.1| 117M18_4 [Brassica rapa]	407	424	0	104.2	86.7	89.7	117M18_4	gbpln	Brassica rapa	AT5G10010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64910.1); Has 33260 Blast hits to 16857 proteins in 1270 species: Archae - 88; Bacteria - 3040; Metazoa - 11915; Fungi - 3137; Plants - 1371; Viruses - 424; Other Eukaryotes - 13285 (source: NCBI BLink). | chr5:3128098-3131452 FORWARD LENGTH=434	407	434	2.33E-156	106.6	72.7	81.8
Rsa1.0_00413.1.g13354.t1	gb|AAZ66924.1| 117M18_5 [Brassica rapa]	947	1037	0	109.5	78.9	82.9	117M18_5	gbpln	Brassica rapa	AT5G10020.2 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr5:3133514-3136949 FORWARD LENGTH=1000	947	1000	0	105.6	79.3	85.7
Rsa1.0_00413.1.g13355.t2	gb|AAZ66925.1| 117M18_6 [Brassica rapa]	296	280	1.00E-154	94.6	91.2	93.2	117M18_6	gbpln	Brassica rapa	AT5G10050.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:3144254-3145643 FORWARD LENGTH=279	296	279	1.00E-151	94.3	87.8	91.6
Rsa1.0_00413.1.g13356.t1	gb|AAZ66926.1| 117M18_7 [Brassica rapa]	474	468	0	98.7	91.1	93.9	117M18_7	gbpln	Brassica rapa	AT5G10060.1 | Symbols: | ENTH/VHS family protein | chr5:3145994-3148049 REVERSE LENGTH=469	474	469	0	98.9	84.4	90.3
Rsa1.0_00413.1.g13357.t1	gb|AAZ66927.1| 117M18_8 [Brassica rapa]	589	582	0	98.8	89.1	93.5	117M18_8	gbpln	Brassica rapa	AT5G10090.1 | Symbols: TPR13 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:3153722-3155745 REVERSE LENGTH=594	589	594	0	100.8	78.3	84.9
Rsa1.0_00413.1.g13358.t1	ref|NP_178356.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|3184287|gb|AAC18934.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana] gi|330250497|gb|AEC05591.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	129	211	6.00E-23	163.6	36.4	47.3	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT2G02520.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr2:676771-678145 REVERSE LENGTH=211	129	211	1.00E-25	163.6	36.4	47.3

Rsa1.0_00414.1.g13359.t1	gb|EOA15138.1| hypothetical protein CARUB_v10028513mg [Capsella rubella]	128	129	5.00E−48	100.8	78.1	88.3	hypothetical protein CARUB_v10028513mg	gbpln	Capsella rubella	AT5G46890.1 | Symbols: | Bifunctional inhibitor/lipid−transfer protein/seed storage 2S albumin superfamily protein | chr5:19036437−19036820 REVERSE LENGTH=127	128	127	2.00E−43	99.2	77.3	88.3
Rsa1.0_00414.1.g13360.t1	ref|NP_199502.2| transcription factor jumonji and C5HC2 type zinc finger domain−containing protein [Arabidopsis thaliana] gi|332008063|gb|AED95446.1| transcription factor jumonji and C5HC2 type zinc finger domain−containing protein [Arabidopsis thaliana]	764	787	0	103.0	85.1	91.2	transcription factor jumonji and C5HC2 type zinc finger domain−containing protein	gbpln	Arabidopsis thaliana	AT5G46910.1 | Symbols: | Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein | chr5:19046888−19050880 FORWARD LENGTH=787	764	787	0	103.0	85.1	91.2
Rsa1.0_00414.1.g13361.t1	gb|EOA14414.1| hypothetical protein CARUB_v10027615mg [Capsella rubella]	181	177	8.00E−33	97.8	45.3	61.3	hypothetical protein CARUB_v10027615mg	gbpln	Capsella rubella	AT5G46930.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19056655−19057191 REVERSE LENGTH=178	181	178	1.00E−32	98.3	43.6	59.7
Rsa1.0_00414.1.g13362.t1	gb|ACT35474.1| peroxidase 65 [Brassica rapa]	326	330	1.00E−178	101.2	94.2	97.2	peroxidase 65	gbpln	Brassica rapa	AT5G47000.1 | Symbols: | Peroxidase superfamily protein | chr5:19069171−19070175 REVERSE LENGTH=334	326	334	1.00E−177	102.5	91.4	94.5
Rsa1.0_00414.1.g13363.t1	dbj|BAG69285.1| cathepsin B−like cysteine protease [Raphanus sativus]	98	343	6.00E−14	350.0	38.8	40.8	cathepsin B−like cysteine protease	gbpln	Raphanus sativus	AT4G01610.1 | Symbols: | Cysteine proteinases superfamily protein | chr4:694857−696937 FORWARD LENGTH=359	98	359	9.00E−15	366.3	34.7	38.8
Rsa1.0_00414.1.g13364.t1	ref|NP_199513.2| uncharacterized protein [Arabidopsis thaliana] gi|332008075|gb|AED95458.1| uncharacterized protein AT5G47020 [Arabidopsis thaliana]	1393	1421	0	102.0	87.2	92.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G47020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G11700.2); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:19082005−19089800 FORWARD LENGTH=1421	1393	1421	0	102.0	87.2	92.7
Rsa1.0_00414.1.g13365.t1	gb|ABL97963.1| hydrogen−transporting ATP synthase [Brassica rapa]	154	203	1.00E−41	131.8	64.9	76.6	hydrogen−transporting ATP synthase	gbpln	Brassica rapa	AT5G47030.1 | Symbols: | ATPase, F1 complex, delta/epsilon subunit | chr5:19090384−19092034 FORWARD LENGTH=203	154	203	2.00E−39	131.8	51.3	55.8
Rsa1.0_00414.1.g13366.t1	gb|ABL97963.1| hydrogen−transporting ATP synthase [Brassica rapa]	112	203	9.00E−57	181.3	97.3	99.1	hydrogen−transporting ATP synthase	gbpln	Brassica rapa	AT5G47030.1 | Symbols: | ATPase, F1 complex, delta/epsilon subunit | chr5:19090384−19092034 FORWARD LENGTH=203	112	203	4.00E−56	181.3	92.0	97.3
Rsa1.0_00414.1.g13367.t1	ref|XP_002865147.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297310982|gb|EFH41406.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	307	303	1.00E−110	98.7	74.6	81.8	ATP binding protein	gbpln	Arabidopsis lyrata	AT5G47050.1 | Symbols: | SBP (S−ribonuclease binding protein) family protein | chr5:19106612−19107860 FORWARD LENGTH=300	307	300	1.00E−107	97.7	74.3	81.1
Rsa1.0_00414.1.g13368.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00414.1.g13369.t1	gb|EOA14090.1| hypothetical protein CARUB_v10027227mg [Capsella rubella]	175	177	1.00E−54	101.1	78.3	86.3	hypothetical protein CARUB_v10027227mg	gbpln	Capsella rubella	AT5G47060.1 | Symbols: | Protein of unknown function (DUF581) | chr5:19116843−19117639 FORWARD LENGTH=177	175	177	1.00E−52	101.1	76.6	84.6
Rsa1.0_00414.1.g13370.t1	dbj|BAJ33813.1| unnamed protein product [Thellungiella halophila]	410	412	0	100.5	86.6	92.2	unnamed protein product	----	----	AT5G47070.1 | Symbols: | Protein kinase superfamily protein | chr5:19118683−19120528 REVERSE LENGTH=410	410	410	0	100.0	82.7	89.8
Rsa1.0_00414.1.g13371.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00414.1.g13372.t1	gb|ABD64921.1| calcineurin B−like protein, putative [Brassica oleracea]	213	213	1.00E−119	100.0	99.1	99.1	calcineurin B−like protein, putative	gbpln	Brassica oleracea	AT5G47100.1 | Symbols: CBL9, ATCBL9 | calcineurin B−like protein 9 | chr5:19129896−19131727 REVERSE LENGTH=213	213	213	1.00E−118	100.0	96.2	98.1
Rsa1.0_00414.1.g13373.t1	gb|ABD64937.1| hypothetical protein 24.t00015 [Brassica oleracea]	401	1327	0	330.9	93.0	95.5	hypothetical protein 24.t00015	gbpln	Brassica oleracea	AT5G47480.1 | Symbols: | RGPR−related | chr5:19257420−19263132 FORWARD LENGTH=1350	401	1350	0	336.7	80.3	86.0
Rsa1.0_00414.1.g13374.t1	gb|ABD64975.1| Ras family GTP−binding protein [Brassica oleracea]	206	221	7.00E−43	107.3	40.8	41.3	Ras family GTP−binding protein	gbpln	Brassica oleracea	AT5G47520.1 | Symbols: AtRABA5a, RABA5a | RAB GTPase homolog A5A | chr5:19277596−19278366 REVERSE LENGTH=221	206	221	2.00E−44	107.3	40.3	41.3
Rsa1.0_00414.1.g13375.t1	gb|ABD64933.1| hypothetical protein 24.t00011 [Brassica oleracea]	235	241	1.00E−103	102.6	82.6	88.1	hypothetical protein 24.t00011	gbpln	Brassica oleracea	AT5G47530.1 | Symbols: | Auxin−responsive family protein | chr5:19281471−19282870 FORWARD LENGTH=395	235	395	2.00E−85	168.1	64.7	71.9
Rsa1.0_00414.1.g13376.t1	ref|XP_002863336.1| ATSDAT [Arabidopsis lyrata subsp. lyrata] gi|297309171|gb|EFH39595.1| ATSDAT [Arabidopsis lyrata subsp. lyrata]	1082	540	0	49.9	44.3	46.9	ATSDAT	gbpln	Arabidopsis lyrata	AT5G47560.1 | Symbols: ATTDT, ATSDAT, TDT | tonoplast dicarboxylate transporter | chr5:19287895−19290347 REVERSE LENGTH=540	1082	540	0	49.9	43.7	46.8

Rsa1.0_00414.1.g13377.t1	gb|EOA14220.1| hypothetical protein CARUB_v10027375mg [Capsella rubella]	122	125	1.00E−58	102.5	95.1	96.7	hypothetical protein CARUB_v10027375mg	gbpln	Capsella rubella	AT5G47570.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:19292869−19294666 REVERSE LENGTH=125	122	125	1.00E−53	102.5	94.3	95.1
Rsa1.0_00414.1.g13378.t1	gb|AAM63044.1| RNA−binding protein−like [Arabidopsis thaliana]	439	431	0	98.2	82.2	89.5	RNA−binding protein−like	gbpln	Arabidopsis thaliana	AT5G47620.2 | Symbols: | RNA−binding (RRM/RBD/RNP motifs) family protein | chr5:19302548−19304278 REVERSE LENGTH=431	439	431	0	98.2	82.9	90.4
Rsa1.0_00414.1.g13379.t1	gb|EOA14124.1| hypothetical protein CARUB_v10027269mg [Capsella rubella]	164	162	3.00E−63	98.8	72.6	82.9	hypothetical protein CARUB_v10027269mg	gbpln	Capsella rubella	AT5G47635.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:19307281−19307849 REVERSE LENGTH=164	164	164	6.00E−64	100.0	75.0	82.3
Rsa1.0_00414.1.g13380.t1	gb|ABD64993.1| transcription factor Hap3b, putative [Brassica oleracea]	197	185	2.00E−67	93.9	64.0	65.0	transcription factor Hap3b, putative	gbpln	Brassica oleracea	AT5G47640.1 | Symbols: NF−YB2 | nuclear factor Y, subunit B2 | chr5:19309414−19309986 FORWARD LENGTH=190	197	190	7.00E−68	96.4	68.0	68.0
Rsa1.0_00414.1.g13381.t1	ref|NP_568687.1| nudix hydrolase 2 [Arabidopsis thaliana] gi|68565924|sp|Q94B74.1|NUDT2_ARATH RecName: Full=Nudix hydrolase 2; Short=AtNUDT2; AltName: Full=ADP−ribose pyrophosphatase; AltName: Full=NADH pyrophosphatase gi|14596037|gb|AAK68746.1| MutT domain protein−like [Arabidopsis thaliana] gi|17978727|gb|AAL47357.1| MutT domain protein−like [Arabidopsis thaliana] gi|332008163|gb|AED95546.1| nudix hydrolase 2 [Arabidopsis thaliana]	336	278	1.00E−138	82.7	70.2	76.2	nudix hydrolase 2	gbpln	Arabidopsis thaliana	AT5G47650.1 | Symbols: ATNUDT2, ATNUDX2, NUDT2 | nudix hydrolase homolog 2 | chr5:19310391−19312084 REVERSE LENGTH=278	336	278	1.00E−141	82.7	70.2	76.2
Rsa1.0_00414.1.g13382.t1	ref|NP_001078727.1| nuclear transcription factor Y subunit B−6 [Arabidopsis thaliana] gi|9758795|dbj|BAB09093.1| unnamed protein product [Arabidopsis thaliana] gi|332008166|gb|AED95549.1| nuclear transcription factor Y subunit B−6 [Arabidopsis thaliana]	196	205	1.00E−81	104.6	84.2	89.8	nuclear transcription factor Y subunit B−6	gbpln	Arabidopsis thaliana	AT5G47670.2 | Symbols: NF−YB6, L1L | nuclear factor Y, subunit B6 | chr5:19315358−19315975 FORWARD LENGTH=205	196	205	5.00E−84	104.6	84.2	89.8
Rsa1.0_00414.1.g13383.t1	gb|EOA15250.1| hypothetical protein CARUB_v10028649mg [Capsella rubella]	405	347	1.00E−125	85.7	68.9	75.6	hypothetical protein CARUB_v10028649mg	gbpln	Capsella rubella	AT5G47680.1 | Symbols: TRM10, AtTRM | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: tRNA (guanine−N1−)−methyltransferase (InterPro:IPR016009), tRNA (guanine−N(1)−)−methyltransferase, metazoa (InterPro:IPR016653), tRNA (guanine−N1−)−methyltransferase, eukaryotic (InterPro:IPR007356); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:19316329−19317467 REVERSE LENGTH=344	405	344	1.00E−100	84.9	42.5	46.4
Rsa1.0_00415.1.g13384.t1	ref|NP_001238519.1| uncharacterized protein LOC100499953 [Glycine max] gi|255627951|gb|ACU14320.1| unknown [Glycine max]	186	139	6.00E−70	74.7	66.1	72.0	uncharacterized protein LOC100499953	gbenv/gbpln	Glycine max	AT3G46010.2 | Symbols: ADF1, atadf, ATADF1 | actin depolymerizing factor 1 | chr3:16909679−16910678 REVERSE LENGTH=150	186	150	2.00E−71	80.6	65.6	74.2
Rsa1.0_00415.1.g13385.t1	gb|EOA14190.1| hypothetical protein CARUB_v10027342mg [Capsella rubella]	132	139	4.00E−70	105.3	97.0	99.2	hypothetical protein CARUB_v10027342mg	gbpln	Capsella rubella	AT3G46010.2 | Symbols: ADF1, atadf, ATADF1 | actin depolymerizing factor 1 | chr3:16909679−16910678 REVERSE LENGTH=150	132	150	4.00E−72	113.6	95.5	98.5

Rsa1.0_00415.1.g13386.t1	ref|NP_190184.1| histone H2B [Arabidopsis thaliana] gi|297819124|ref|XP_002877445.1| hypothetical protein ARALYDRAFT_484977 [Arabidopsis lyrata subsp. lyrata] gi|75097936|sp|O23629.3|H2B6_ARATH RecName: Full=Histone H2B.6; AltName: Full=H2BAt; AltName: Full=HTB9 gi|2407802|emb|CAA73156.1| histone H2B [Arabidopsis thaliana] gi|7339499|emb|CAB82822.1| histone H2B [Arabidopsis thaliana] gi|21592825|gb|AAM64775.1| histone H2B [Arabidopsis thaliana] gi|30102580|gb|AAP21208.1| At3g45980 [Arabidopsis thaliana] gi|110743640|dbj|BAE99657.1| histone H2B [Arabidopsis thaliana] gi|297323283|gb|EFH53704.1| hypothetical protein ARALYDRAFT_484977 [Arabidopsis lyrata subsp. lyrata] gi|332644576|gb|AEE78097.1| histone H2B [Arabidopsis thaliana]	146	150	2.00E−65	102.7	96.6	98.6	histone H2B	gbpln	Arabidopsis lyrata	AT3G45980.1 | Symbols: H2B, HTB9 | Histone superfamily protein | chr3:16897492−16897944 REVERSE LENGTH=150	146	150	5.00E−68	102.7	96.6	98.6
Rsa1.0_00415.1.g13387.t1	ref|NP_001154789.1| ribonuclease P subunit Rpp30 [Arabidopsis thaliana] gi|332009879|gb|AED97262.1| ribonuclease P subunit Rpp30 [Arabidopsis thaliana]	663	705	0	106.3	70.3	80.1	ribonuclease P subunit Rpp30	gbpln	Arabidopsis thaliana	AT5G59980.2 | Symbols: | Polymerase/histidinol phosphatase−like | chr5:24147207−24149783 FORWARD LENGTH=705	663	705	0	106.3	70.3	80.1
Rsa1.0_00415.1.g13388.t1	ref|XP_002866360.1| hypothetical protein ARALYDRAFT_919236 [Arabidopsis lyrata subsp. lyrata] gi|297312195|gb|EFH42619.1| hypothetical protein ARALYDRAFT_919236 [Arabidopsis lyrata subsp. lyrata]	239	241	7.00E−96	100.8	82.0	87.9	hypothetical protein ARALYDRAFT_919236	gbpln	Arabidopsis lyrata	AT5G59990.1 | Symbols: | CCT motif family protein | chr5:24151206−24153084 REVERSE LENGTH=241	239	241	3.00E−92	100.8	82.8	88.7
Rsa1.0_00415.1.g13389.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00415.1.g13390.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00415.1.g13391.t1	dbj|BAB21595.1| Tat binding protein like protein [Brassica rapa]	239	424	2.00E−21	177.4	29.3	31.8	Tat binding protein like protein	gbpln	Brassica rapa	AT3G05530.1 | Symbols: RPT5A, ATS6A.2 | regulatory particle triple−A ATPase 5A | chr3:1603540−1605993 FORWARD LENGTH=424	239	424	7.00E−24	177.4	29.3	31.8
Rsa1.0_00415.1.g13392.t5	gb|EOA14805.1| hypothetical protein CARUB_v10028111mg [Capsella rubella]	859	885	0	103.0	87.4	92.7	hypothetical protein CARUB_v10028111mg	gbpln	Capsella rubella	AT5G60010.1 | Symbols: | ferric reductase−like transmembrane component family protein | chr5:24160456−24164755 FORWARD LENGTH=886	859	886	0	103.1	87.0	93.0
Rsa1.0_00415.1.g13393.t1	ref|NP_200810.1| laccase 17 [Arabidopsis thaliana] gi|75333948|sp|Q9FJD5.1|LAC17_ARATH RecName: Full=Laccase−17; AltName: Full=Benzenediol:oxygen oxidoreductase 17; AltName: Full=Diphenol oxidase 17; AltName: Full=Urishiol oxidase 17; Flags: Precursor gi|9757923|dbj|BAB08370.1| laccase (diphenol oxidase) [Arabidopsis thaliana] gi|51536488|gb|AAU05482.1| At5g60020 [Arabidopsis thaliana] gi|53850499|gb|AAU95426.1| At5g60020 [Arabidopsis thaliana] gi|332009884|gb|AED97267.1| laccase 17 [Arabidopsis thaliana]	572	577	0	100.9	92.3	96.0	laccase 17	gbpln	Arabidopsis thaliana	AT5G60020.1 | Symbols: LAC17, ATLAC17 | laccase 17 | chr5:24168072−24170223 FORWARD LENGTH=577	572	577	0	100.9	92.3	96.0
Rsa1.0_00415.1.g13394.t1	ref|NP_200811.1| uncharacterized protein [Arabidopsis thaliana] gi|8777342|dbj|BAA96932.1| unnamed protein product [Arabidopsis thaliana] gi|332009885|gb|AED97268.1| uncharacterized protein AT5G60030 [Arabidopsis thaliana]	206	292	1.00E−24	141.7	39.3	46.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G60030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G75335.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:24172082−24172960 REVERSE LENGTH=292	206	292	5.00E−27	141.7	39.3	46.6
Rsa1.0_00415.1.g13395.t1	gb|EOA12363.1| hypothetical protein CARUB_v10025743mg [Capsella rubella]	1376	1376	0	100.0	86.3	92.6	hypothetical protein CARUB_v10025743mg	gbpln	Capsella rubella	AT5G60040.1 | Symbols: NRPC1 | nuclear RNA polymerase C1 | chr5:24173590−24183269 FORWARD LENGTH=1376	1376	1376	0	100.0	86.1	91.5
Rsa1.0_00415.1.g13396.t1	gb|EOA14531.1| hypothetical protein CARUB_v10027763mg [Capsella rubella]	501	500	0	99.8	89.4	94.0	hypothetical protein CARUB_v10027763mg	gbpln	Capsella rubella	AT5G60050.1 | Symbols: | BTB/POZ domain−containing protein | chr5:24183680−24185264 REVERSE LENGTH=499	501	499	0	99.6	87.8	93.0
Rsa1.0_00416.1.g13397.t1	#	#	#	#	#	#	#	−	----	----	AT3G10360.1 | Symbols: APUM4, PUM4 | pumilio 4 | chr3:3211276−3215144 REVERSE LENGTH=1003	157	1003	2.00E−12	638.9	19.1	19.7

Rsa1.0_00416.1.g13398.t1	ref|XP_002882663.1| anion-transporting ATPase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328503|gb|EFH58922.1| anion-transporting ATPase family protein [Arabidopsis lyrata subsp. lyrata]	331	410	1.00E-178	123.9	96.4	99.1	anion-transporting ATPase family protein	gbpln	Arabidopsis lyrata	AT3G10350.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:3208310-3210678 FORWARD LENGTH=411	331	411	1.00E-180	124.2	95.8	98.5
Rsa1.0_00416.1.g13399.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00416.1.g13400.t1	ref|NP_187645.1| phenylalanine ammonia-lyase 4 [Arabidopsis thaliana] gi|14195018|sp|Q9SS45.1|PAL4_ARATH RecName: Full=Phenylalanine ammonia-lyase 4 gi|6056192|gb|AAF02809.1|AC009400_5 putative phenylalanine ammonia-lyase [Arabidopsis thaliana] gi|20466382|gb|AAM20508.1| putative phenylalanine ammonia-lyase [Arabidopsis thaliana] gi|23198088|gb|AAN15571.1| putative phenylalanine ammonia-lyase [Arabidopsis thaliana] gi|32140425|gb|AAP59440.1| phenylalanine ammonia lyase [Arabidopsis thaliana] gi|332641372|gb|AEE74893.1| phenylalanine ammonia-lyase 4 [Arabidopsis thaliana]	702	707	0	100.7	91.0	94.4	phenylalanine ammonia-lyase 4	gbpln	Arabidopsis thaliana	AT3G10340.1 | Symbols: PAL4 | phenylalanine ammonia-lyase 4 | chr3:3204260-3207809 FORWARD LENGTH=707	702	707	0	100.7	91.0	94.4
Rsa1.0_00416.1.g13401.t1	gb|EOA29558.1| hypothetical protein CARUB_v10015940mg [Capsella rubella]	488	492	0	100.8	80.3	88.3	hypothetical protein CARUB_v10015940mg	gbpln	Capsella rubella	AT3G10320.1 | Symbols: | Glycosyltransferase family 61 protein | chr3:3195441-3197111 REVERSE LENGTH=494	488	494	0	101.2	80.1	87.5
Rsa1.0_00416.1.g13402.t1	gb|EOA29791.1| hypothetical protein CARUB_v10012886mg, partial [Capsella rubella]	980	1011	0	103.2	83.9	90.2	hypothetical protein CARUB_v10012886mg, partial	gbpln	Capsella rubella	AT3G10310.1 | Symbols: | P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain | chr3:3190208-3195005 FORWARD LENGTH=922	980	922	0	94.1	80.7	86.6
Rsa1.0_00416.1.g13403.t18	gb|EOA30978.1| hypothetical protein CARUB_v10014124mg, partial [Capsella rubella]	326	337	1.00E-171	103.4	92.6	97.2	hypothetical protein CARUB_v10014124mg, partial	gbpln	Capsella rubella	AT3G10290.1 | Symbols: | Nucleotide-sugar transporter family protein | chr3:3183511-3185324 REVERSE LENGTH=355	326	355	1.00E-173	108.9	92.6	97.5
Rsa1.0_00416.1.g13404.t1	ref|NP_566371.1| reticulon-like protein B8 [Arabidopsis thaliana] gi|30681222|ref|NP_850551.1| reticulon-like protein B8 [Arabidopsis thaliana] gi|75207442|sp|Q9SS37.1|RTNLH_ARATH RecName: Full=Reticulon-like protein B8; Short=AtRTNLB8 gi|6056199|gb|AAF02816.1|AC009400_12 unknown protein [Arabidopsis thaliana] gi|15027947|gb|AAK76504.1| unknown protein [Arabidopsis thaliana] gi|20259183|gb|AAM14307.1| unknown protein [Arabidopsis thaliana] gi|21553569|gb|AAM62662.1| unknown [Arabidopsis thaliana] gi|332641358|gb|AEE74879.1| reticulon-like protein B8 [Arabidopsis thaliana] gi|332641359|gb|AEE74880.1| reticulon-like protein B8 [Arabidopsis thaliana]	239	247	1.00E-119	103.3	85.4	95.0	reticulon-like protein B8	gbpln	Arabidopsis thaliana	AT3G10260.2 | Symbols: | Reticulon family protein | chr3:3171413-3172508 REVERSE LENGTH=247	239	247	1.00E-122	103.3	85.4	95.0
Rsa1.0_00416.1.g13405.t1	ref|NP_566370.1| uncharacterized protein [Arabidopsis thaliana] gi|42572351|ref|NP_974271.1| uncharacterized protein [Arabidopsis thaliana] gi|15809982|gb|AAL06918.1| AT3g10250/F14P13_15 [Arabidopsis thaliana] gi|18958054|gb|AAL79600.1| AT3g10250/F14P13_15 [Arabidopsis thaliana] gi|21536630|gb|AAM60962.1| unknown [Arabidopsis thaliana] gi|222423631|dbj|BAH19784.1| AT3G10250 [Arabidopsis thaliana] gi|332641356|gb|AEE74877.1| uncharacterized protein AT3G10250 [Arabidopsis thaliana] gi|332641357|gb|AEE74878.1| uncharacterized protein AT3G10250 [Arabidopsis thaliana]	339	324	1.00E-158	95.6	85.3	90.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G10250.2 | Symbols: | Plant protein 1589 of unknown function | chr3:3168371-3170418 REVERSE LENGTH=324	339	324	1.00E-160	95.6	85.3	90.6
Rsa1.0_00416.1.g13406.t1	gb|ADT89710.1| chloroplast lycopene beta-cyclase [Brassica napus]	494	493	0	99.8	95.5	97.2	chloroplast lycopene beta-cyclase	gbpln	Brassica napus	AT3G10230.1 | Symbols: LYC | lycopene cyclase | chr3:3164340-3165845 REVERSE LENGTH=501	494	501	0	101.4	91.9	96.4
Rsa1.0_00416.1.g13407.t1	gb|EOA31328.1| hypothetical protein CARUB_v10014499mg [Capsella rubella]	294	243	1.00E-124	82.7	71.4	76.9	hypothetical protein CARUB_v10014499mg	gbpln	Capsella rubella	AT3G10220.1 | Symbols: | tubulin folding cofactor B | chr3:3161977-3164037 FORWARD LENGTH=243	294	243	1.00E-125	82.7	70.4	76.2

Rsa1.0_00416.1.g13408.t1	ref|XP_002884783.1| hypothetical protein ARALYDRAFT_897197 [Arabidopsis lyrata subsp. lyrata] gi|297330623|gb|EFH61042.1| hypothetical protein ARALYDRAFT_897197 [Arabidopsis lyrata subsp. lyrata]	242	237	1.00E-119	97.9	91.3	95.0	hypothetical protein ARALYDRAFT_897197	gbpln	Arabidopsis lyrata	AT3G10210.1 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr3:3160416-3161579 REVERSE LENGTH=237	242	237	1.00E-120	97.9	89.7	95.0
Rsa1.0_00416.1.g13409.t1	ref|NP_187631.2| putative methyltransferase PMT6 [Arabidopsis thaliana] gi|75243292|sp|Q84TJ0.1|PMT6_ARATH RecName: Full=Probable methyltransferase PMT6 gi|28973663|gb|AAO64151.1| unknown protein [Arabidopsis thaliana] gi|110737121|dbj|BAF00512.1| hypothetical protein [Arabidopsis thaliana] gi|332641350|gb|AEE74871.1| putative methyltransferase PMT6 [Arabidopsis thaliana]	580	591	0	101.9	82.6	90.5	putative methyltransferase PMT6	gbpln	Arabidopsis thaliana	AT3G10200.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:3157618-3160016 FORWARD LENGTH=591	580	591	0	101.9	82.6	90.5
Rsa1.0_00416.1.g13410.t2	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	321	390	3.00E-33	121.5	22.1	31.2	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	321	295	3.00E-32	91.9	25.2	40.2
Rsa1.0_00416.1.g13411.t1	ref|NP_187630.1| putative calcium-binding protein CML36 [Arabidopsis thaliana] gi|75337581|sp|Q9SS31.1|CML36_ARATH RecName: Full=Probable calcium-binding protein CML36; AltName: Full=Calmodulin-like protein 36 gi|6056210|gb|AAF02827.1|AC009400_23 calmodulin-like protein [Arabidopsis thaliana] gi|27808532|gb|AAO24546.1| At3g10190 [Arabidopsis thaliana] gi|110736233|dbj|BAF00087.1| calmodulin like protein [Arabidopsis thaliana] gi|332641348|gb|AEE74869.1| putative calcium-binding protein CML36 [Arabidopsis thaliana]	218	209	6.00E-72	95.9	72.5	80.3	putative calcium-binding protein CML36	gbpln	Arabidopsis thaliana	AT3G10190.1 | Symbols: | Calcium-binding EF-hand family protein | chr3:3155309-3155938 FORWARD LENGTH=209	218	209	2.00E-74	95.9	72.5	80.3
Rsa1.0_00416.1.g13412.t1	ref|NP_001078130.1| Gibberellin-regulated family protein [Arabidopsis thaliana] gi|357580452|sp|A8MR46.1|GASAD_ARATH RecName: Full=Gibberellin-regulated protein 13; AltName: Full=GAST1 protein homolog 13; Flags: Precursor gi|332641346|gb|AEE74867.1| Gibberellin-regulated family protein [Arabidopsis thaliana]	84	103	4.00E-12	122.6	56.0	66.7	Gibberellin-regulated family protein	gbpln	Arabidopsis thaliana	AT3G10185.1 | Symbols: | Gibberellin-regulated family protein | chr3:3145579-3146199 FORWARD LENGTH=103	84	103	6.00E-15	122.6	56.0	66.7
Rsa1.0_00416.1.g13413.t1	ref|NP_187626.1| putative inactive purple acid phosphatase 16 [Arabidopsis thaliana] gi|75266220|sp|Q9SR79.1|PPA16_ARATH RecName: Full=Probable inactive purple acid phosphatase 16; Flags: Precursor gi|6143862|gb|AAF04409.1|AC010927_2 hypothetical protein [Arabidopsis thaliana] gi|332641344|gb|AEE74865.1| putative inactive purple acid phosphatase 16 [Arabidopsis thaliana]	371	367	1.00E-167	98.9	78.7	83.3	putative inactive purple acid phosphatase 16	gbpln	Arabidopsis thaliana	AT3G10150.1 | Symbols: ATPAP16, PAP16 | purple acid phosphatase 16 | chr3:3137502-3139056 REVERSE LENGTH=367	371	367	1.00E-170	98.9	78.7	83.3
Rsa1.0_00416.1.g13414.t1	gb|EOA12562.1| hypothetical protein CARUB_v10026829mg [Capsella rubella]	294	308	1.00E-138	104.8	82.3	88.8	hypothetical protein CARUB_v10026829mg	gbpln	Capsella rubella	AT3G10130.1 | Symbols: | SOUL heme-binding family protein | chr3:3131122-3133158 REVERSE LENGTH=309	294	309	1.00E-126	105.1	79.6	86.1
Rsa1.0_00416.1.g13415.t1	ref|NP_187623.2| uncharacterized protein [Arabidopsis thaliana] gi|26450718|dbj|BAC42468.1| unknown protein [Arabidopsis thaliana] gi|28372890|gb|AAO39927.1| At3g10120 [Arabidopsis thaliana] gi|332641341|gb|AEE74862.1| uncharacterized protein AT3G10120 [Arabidopsis thaliana]	169	173	4.00E-65	102.4	78.1	87.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G10120.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G03890.1); Has 57 Blast hits to 57 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3130155-3130676 FORWARD LENGTH=173	169	173	2.00E-67	102.4	78.1	87.0
Rsa1.0_00416.1.g13416.t1	ref|XP_002884775.1| tata-associated factor II 58 [Arabidopsis lyrata subsp. lyrata] gi|297330615|gb|EFH61034.1| tata-associated factor II 58 [Arabidopsis lyrata subsp. lyrata]	531	541	0	101.9	78.3	83.2	tata-associated factor II 58	gbpln	Arabidopsis lyrata	AT3G10070.1 | Symbols: TAF12, TAFII58 | TBP-associated factor 12 | chr3:3104195-3106798 REVERSE LENGTH=539	531	539	0	101.5	75.9	81.5

Rsa1.0_00416.1.g13417.t1	gb|EOA31367.1| hypothetical protein CARUB_v10014538mg [Capsella rubella]	231	232	1.00E-114	100.4	90.9	95.7	hypothetical protein CARUB_v10014538mg	gbpln	Capsella rubella	AT3G10060.1 | Symbols: | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | chr3:3102291-3103801 FORWARD LENGTH=230	231	230	1.00E-116	99.6	89.6	94.4
Rsa1.0_00416.1.g13418.t1	ref|XP_002884774.1| L-O-methylthreonine resistant 1 [Arabidopsis lyrata subsp. lyrata] gi|297330614|gb|EFH61033.1| L-O-methylthreonine resistant 1 [Arabidopsis lyrata subsp. lyrata]	607	591	0	97.4	82.5	89.3	L-O-methylthreonine resistant 1	gbpln	Arabidopsis lyrata	AT3G10050.1 | Symbols: OMR1 | L-O-methylthreonine resistant 1 | chr3:3099164-3101741 REVERSE LENGTH=592	607	592	0	97.5	81.1	89.1
Rsa1.0_00417.1.g13419.t2	ref|NP_567241.1| xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] gi|46576207|sp|O22775.1|GT2_ARATH RecName: Full=Putative glycosyltransferase 2; Short=AtGT2 gi|3193287|gb|AAC19271.1| T14P8.23 [Arabidopsis thaliana] gi|9716844|emb|CAC01674.1| putative golgi glycosyltransferase [Arabidopsis thaliana] gi|16209669|gb|AAL14393.1| AT4g02500/T10P11_20 [Arabidopsis thaliana] gi|22655160|gb|AAM98170.1| putative glycosyltransferase [Arabidopsis thaliana] gi|30387559|gb|AAP31945.1| At4g02500 [Arabidopsis thaliana] gi|332656781|gb|AEE82181.1| putative glycosyltransferase 2 [Arabidopsis thaliana]	167	461	1.00E-19	276.0	33.5	34.1	xyloglucan 6-xylosyltransferase	gbpln	Arabidopsis thaliana	AT4G02500.1 | Symbols: ATXT2, XXT2, XT2 | UDP-xylosyltransferase 2 | chr4:1101638-1103345 FORWARD LENGTH=461	167	461	5.00E-22	276.0	33.5	34.1
Rsa1.0_00417.1.g13420.t1	ref|NP_567242.2| translocase of chloroplast 159 [Arabidopsis thaliana] gi|75100143|sp|O81283.1|TC159_ARATH RecName: Full=Translocase of chloroplast 159, chloroplastic; Short=AtToc159; AltName: Full=159 kDa chloroplast outer envelope protein; AltName: Full=Plastid protein import 2; AltName: Full=Translocase of chloroplast 160, chloroplastic; Short=AtToc160; AltName: Full=Translocase of chloroplast 86, chloroplastic; Short=AtToc86 gi|3193301|gb|AAC19285.1| T14P8.24 [Arabidopsis thaliana] gi|332656782|gb|AEE82182.1| translocase of chloroplast 159 [Arabidopsis thaliana]	1561	1503	0	96.3	56.2	58.7	translocase of chloroplast 159	gbpln	Arabidopsis thaliana	AT4G02510.1 | Symbols: TOC159, TOC86, PPI2, TOC160, ATTOC159 | translocon at the outer envelope membrane of chloroplasts 159 | chr4:1104766-1109360 FORWARD LENGTH=1503	1561	1503	0	96.3	56.2	58.7
Rsa1.0_00417.1.g13421.t1	gb|AFP86475.1| glutathione-S-transferase, partial [Brassica rapa subsp. chinensis]	213	213	1.00E-117	100.0	95.8	98.6	glutathione-S-transferase, partial	gbpln	Brassica rapa	AT2G02930.1 | Symbols: ATGSTF3, GST16, GSTF3 | glutathione S-transferase F3 | chr2:851348-852106 REVERSE LENGTH=212	213	212	1.00E-111	99.5	89.2	95.3
Rsa1.0_00417.1.g13422.t1	gb|AAP58393.1| glutathione S-transferase 3 [Brassica juncea]	213	213	1.00E-117	100.0	97.7	98.6	glutathione S-transferase 3	gbpln	Brassica juncea	AT2G02930.1 | Symbols: ATGSTF3, GST16, GSTF3 | glutathione S-transferase F3 | chr2:851348-852106 REVERSE LENGTH=212	213	212	1.00E-111	99.5	90.6	95.3
Rsa1.0_00417.1.g13423.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00417.1.g13424.t1	gb|EOA24064.1| hypothetical protein CARUB_v10017284mg [Capsella rubella]	240	435	3.00E-25	181.3	27.1	33.8	hypothetical protein CARUB_v10017284mg	gbpln	Capsella rubella	AT3G46650.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:17185561-17187812 REVERSE LENGTH=435	240	435	2.00E-25	181.3	25.0	32.5
Rsa1.0_00417.1.g13425.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00417.1.g13426.t2	gb|AAC67205.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	716	1413	2.00E-26	197.3	12.6	19.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	716	1262	2.00E-12	176.3	6.6	11.2
Rsa1.0_00417.1.g13427.t1	gb|AAF97297.1|AC010164_19 Hypothetical protein [Arabidopsis thaliana]	300	308	6.00E-45	102.7	35.0	46.0	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00417.1.g13428.t1	ref|XP_002874894.1| hypothetical protein ARALYDRAFT_911920 [Arabidopsis lyrata subsp. lyrata] gi|297320731|gb|EFH51153.1| hypothetical protein ARALYDRAFT_911920 [Arabidopsis lyrata subsp. lyrata]	250	260	6.00E-88	104.0	69.2	80.4	hypothetical protein ARALYDRAFT_911920	gbpln	Arabidopsis lyrata	AT4G02810.1 | Symbols: | Protein of unknown function (DUF3049) | chr4:1256253-1257068 FORWARD LENGTH=271	250	271	6.00E-74	108.4	65.6	76.8

Rsa1.0_00417.1.g13429.t1	ref|NP_192192.1| uncharacterized protein [Arabidopsis thaliana] gi|4263528|gb|AAD15354.1| predicted protein of unknown function [Arabidopsis thaliana] gi|7269768|emb|CAB77768.1| predicted protein of unknown function [Arabidopsis thaliana] gi|332656834|gb|AEE82234.1| uncharacterized protein AT4G02830 [Arabidopsis thaliana]	124	184	4.00E-35	148.4	68.5	76.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G02830.1 | Symbols: | unknown protein; Has 74 Blast hits to 74 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:1262447-1263932 FORWARD LENGTH=184	124	184	7.00E-38	148.4	68.5	76.6
Rsa1.0_00417.1.g13430.t1	ref|XP_002874881.1| hypothetical protein ARALYDRAFT_490253 [Arabidopsis lyrata subsp. lyrata] gi|297320718|gb|EFH51140.1| hypothetical protein ARALYDRAFT_490253 [Arabidopsis lyrata subsp. lyrata]	424	423	0	99.8	79.7	83.3	hypothetical protein ARALYDRAFT_490253	gbpln	Arabidopsis lyrata	AT4G03100.1 | Symbols: | Rho GTPase activating protein with PAK-box/P21-Rho-binding domain | chr4:1374361-1375913 FORWARD LENGTH=430	424	430	0	101.4	83.3	88.0
Rsa1.0_00417.1.g13431.t1	gb|EOA20635.1| hypothetical protein CARUB_v10000954mg [Capsella rubella]	427	446	0	104.4	83.1	88.3	hypothetical protein CARUB_v10000954mg	gbpln	Capsella rubella	AT4G03110.1 | Symbols: AtRBP-DR1, RBP-DR1 | RNA-binding protein-defense related 1 | chr4:1376612-1379275 REVERSE LENGTH=441	427	441	0	103.3	82.2	87.6
Rsa1.0_00417.1.g13432.t1	ref|NP_680566.5| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|332656874|gb|AEE82274.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana]	333	314	1.00E-157	94.3	83.8	88.3	Mitochondrial substrate carrier family protein	gbpln	Arabidopsis thaliana	AT4G03115.1 | Symbols: | Mitochondrial substrate carrier family protein | chr4:1383366-1385485 REVERSE LENGTH=314	333	314	1.00E-159	94.3	83.8	88.3
Rsa1.0_00417.1.g13433.t1	ref|XP_002874880.1| hypothetical protein ARALYDRAFT_911890 [Arabidopsis lyrata subsp. lyrata] gi|297320717|gb|EFH51139.1| hypothetical protein ARALYDRAFT_911890 [Arabidopsis lyrata subsp. lyrata]	188	194	2.00E-59	103.2	87.2	89.9	hypothetical protein ARALYDRAFT_911890	gbpln	Arabidopsis lyrata	AT4G03120.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr4:1385747-1387331 FORWARD LENGTH=207	188	207	1.00E-58	110.1	87.8	89.9
Rsa1.0_00417.1.g13434.t1	ref|XP_002872794.1| hypothetical protein ARALYDRAFT_490249 [Arabidopsis lyrata subsp. lyrata] gi|297318631|gb|EFH49053.1| hypothetical protein ARALYDRAFT_490249 [Arabidopsis lyrata subsp. lyrata]	717	762	0	106.3	70.3	79.8	hypothetical protein ARALYDRAFT_490249	gbpln	Arabidopsis lyrata	AT4G03130.1 | Symbols: | BRCT domain-containing DNA repair protein | chr4:1387781-1390646 REVERSE LENGTH=766	717	766	0	106.8	68.5	78.8
Rsa1.0_00417.1.g13435.t1	ref|NP_567251.2| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|332656878|gb|AEE82278.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]	271	343	1.00E-143	126.6	91.1	94.5	Rossmann-fold NAD(P)-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT4G03140.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:1392191-1393662 FORWARD LENGTH=343	271	343	1.00E-145	126.6	91.1	94.5
Rsa1.0_00417.1.g13436.t1	ref|XP_002872793.1| hypothetical protein ARALYDRAFT_911887 [Arabidopsis lyrata subsp. lyrata] gi|297318630|gb|EFH49052.1| hypothetical protein ARALYDRAFT_911887 [Arabidopsis lyrata subsp. lyrata]	174	174	1.00E-67	100.0	77.6	83.3	hypothetical protein ARALYDRAFT_911887	gbpln	Arabidopsis lyrata	AT4G03150.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:1393731-1394529 REVERSE LENGTH=185	174	185	3.00E-67	106.3	75.9	83.3
Rsa1.0_00417.1.g13437.t1	dbj|BAJ33601.1| unnamed protein product [Thellungiella halophila]	585	585	0	100.0	88.9	93.8	unnamed protein product	----	----	AT4G03190.1 | Symbols: GRH1, ATGRH1, AFB1 | GRR1-like protein 1 | chr4:1405108-1407057 REVERSE LENGTH=585	585	585	0	100.0	84.4	92.0
Rsa1.0_00417.1.g13438.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00417.1.g13439.t1	gb|EOA19687.1| hypothetical protein CARUB_v10003357mg [Capsella rubella]	811	816	0	100.6	90.8	94.9	hypothetical protein CARUB_v10003357mg	gbpln	Capsella rubella	AT4G03200.1 | Symbols: | catalytics | chr4:1408296-1412566 FORWARD LENGTH=818	811	818	0	100.9	90.9	94.9
Rsa1.0_00417.1.g13440.t1	gb|AAV92081.1| xyloglucan endotransglycosylase/hydrolase [Brassica rapa subsp. oleifera]	291	281	1.00E-163	96.6	93.1	96.2	xyloglucan endotransglycosylase/hydrolase	gbpln	Brassica rapa	AT4G03210.1 | Symbols: XTH9 | xyloglucan endotransglucosylase/hydrolase 9 | chr4:1416019-1417197 FORWARD LENGTH=290	291	290	1.00E-162	99.7	91.4	96.2
Rsa1.0_00417.1.g13441.t1	gb|EOA21150.1| hypothetical protein CARUB_v10001497mg [Capsella rubella]	316	315	2.00E-95	99.7	57.9	67.1	hypothetical protein CARUB_v10001497mg	gbpln	Capsella rubella	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	316	302	1.00E-85	95.6	57.0	66.1

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<tr><td>Rsa1.0_00417.1.g13443.t1</td><td>ref|XP_002874843.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata] gi|297320680|gb|EFH51102.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata]</td><td>290</td><td>610</td><td>2.00E-83</td><td>210.3</td><td>58.6</td><td>68.6</td><td>hypothetical protein ARALYDRAFT_911810</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302</td><td>290</td><td>302</td><td>2.00E-83</td><td>104.1</td><td>59.7</td><td>71.4</td></tr>
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<tr><td>Rsa1.0_00417.1.g13446.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00417.1.g13447.t1</td><td>gb|EOA21150.1| hypothetical protein CARUB_v10001497mg [Capsella rubella]</td><td>303</td><td>315</td><td>1.00E-92</td><td>104.0</td><td>59.7</td><td>70.3</td><td>hypothetical protein CARUB_v10001497mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302</td><td>303</td><td>302</td><td>5.00E-87</td><td>99.7</td><td>57.4</td><td>68.6</td></tr>
<tr><td>Rsa1.0_00417.1.g13448.t1</td><td>ref|NP_192232.5| S-locus lectin protein kinase-like protein [Arabidopsis thaliana] gi|332656895|gb|AEE82295.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]</td><td>1157</td><td>1010</td><td>0</td><td>87.3</td><td>73.8</td><td>79.8</td><td>S-locus lectin protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G03230.1 | Symbols: | S-locus lectin protein kinase family protein | chr4:1419278-1422828 REVERSE LENGTH=1010</td><td>1157</td><td>1010</td><td>0</td><td>87.3</td><td>73.8</td><td>79.8</td></tr>
<tr><td>Rsa1.0_00417.1.g13449.t1</td><td>ref|NP_192234.2| homeobox-leucine zipper family protein [Arabidopsis thaliana] gi|332656897|gb|AEE82297.1| homeobox-leucine zipper family protein [Arabidopsis thaliana]</td><td>475</td><td>507</td><td>1.00E-179</td><td>106.7</td><td>73.5</td><td>82.9</td><td>homeobox-leucine zipper family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G03250.1 | Symbols: | Homeodomain-like superfamily protein | chr4:1425050-1427744 FORWARD LENGTH=507</td><td>475</td><td>507</td><td>0</td><td>106.7</td><td>73.5</td><td>82.9</td></tr>
<tr><td>Rsa1.0_00417.1.g13450.t1</td><td>ref|XP_002874872.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297320709|gb|EFH51131.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]</td><td>637</td><td>680</td><td>0</td><td>106.8</td><td>79.0</td><td>86.0</td><td>leucine-rich repeat family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G03260.2 | Symbols: | Outer arm dynein light chain 1 protein | chr4:1429092-1431431 FORWARD LENGTH=677</td><td>637</td><td>677</td><td>0</td><td>106.3</td><td>77.9</td><td>85.9</td></tr>
<tr><td>Rsa1.0_00417.1.g13451.t1</td><td>ref|XP_002872788.1| CYCD6_1 [Arabidopsis lyrata subsp. lyrata] gi|297318625|gb|EFH49047.1| CYCD6_1 [Arabidopsis lyrata subsp. lyrata]</td><td>303</td><td>300</td><td>1.00E-130</td><td>99.0</td><td>80.2</td><td>88.1</td><td>CYCD6_1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G03270.1 | Symbols: CYCD6;1 | Cyclin D6;1 | chr4:1432375-1433691 REVERSE LENGTH=302</td><td>303</td><td>302</td><td>1.00E-130</td><td>99.7</td><td>80.5</td><td>86.8</td></tr>
<tr><td>Rsa1.0_00417.1.g13452.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00417.1.g13453.t1</td><td>ref|XP_002874864.1| hypothetical protein ARALYDRAFT_911855 [Arabidopsis lyrata subsp. lyrata] gi|297320701|gb|EFH51123.1| hypothetical protein ARALYDRAFT_911855 [Arabidopsis lyrata subsp. lyrata]</td><td>307</td><td>314</td><td>1.00E-140</td><td>102.3</td><td>87.6</td><td>90.6</td><td>hypothetical protein ARALYDRAFT_911855</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G03420.1 | Symbols: | Protein of unknown function (DUF789) | chr4:1512226-1513594 FORWARD LENGTH=310</td><td>307</td><td>310</td><td>1.00E-139</td><td>101.0</td><td>86.3</td><td>89.3</td></tr>
<tr><td>Rsa1.0_00417.1.g13454.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00417.1.g13455.t1</td><td>gb|EOA12837.1| hypothetical protein CARUB_v10025803mg [Capsella rubella]</td><td>1014</td><td>1021</td><td>0</td><td>100.7</td><td>89.6</td><td>94.9</td><td>hypothetical protein CARUB_v10025803mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G03430.1 | Symbols: STA1, EMB2770 | pre-mRNA splicing factor-related | chr4:1517411-1520500 REVERSE LENGTH=1029</td><td>1014</td><td>1029</td><td>0</td><td>101.5</td><td>89.5</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00417.1.g13456.t1</td><td>ref|NP_192259.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|4206204|gb|AAD11592.1| hypothetical protein [Arabidopsis thaliana] gi|7270673|emb|CAB77835.1| hypothetical protein [Arabidopsis thaliana] gi|332656929|gb|AEE82329.1| ankyrin repeat-containing protein [Arabidopsis thaliana]</td><td>303</td><td>652</td><td>1.00E-110</td><td>215.2</td><td>67.7</td><td>78.5</td><td>ankyrin repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G03500.1 | Symbols: | Ankyrin repeat family protein | chr4:1553453-1556571 FORWARD LENGTH=652</td><td>303</td><td>652</td><td>1.00E-112</td><td>215.2</td><td>67.7</td><td>78.5</td></tr>
<tr><td>Rsa1.0_00417.1.g13457.t3</td><td>ref|NP_192258.5| Ankyrin repeat family protein [Arabidopsis thaliana] gi|332656927|gb|AEE82327.1| Ankyrin repeat family protein [Arabidopsis thaliana]</td><td>958</td><td>662</td><td>0</td><td>69.1</td><td>46.2</td><td>51.8</td><td>Ankyrin repeat family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G03490.1 | Symbols: | Ankyrin repeat family protein | chr4:1549345-1552784 REVERSE LENGTH=662</td><td>958</td><td>662</td><td>0</td><td>69.1</td><td>46.2</td><td>51.8</td></tr>
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Rsa1.0_00417.1.g13458.t1	ref|NP_192260.1| E3 ubiquitin-protein ligase RMA1 [Arabidopsis thaliana] gi|42572819|ref|NP_974506.1| E3 ubiquitin-protein ligase RMA1 [Arabidopsis thaliana] gi|75318457|sp|O64425.1|RMA1_ARATH RecName: Full=E3 ubiquitin-protein ligase RMA1; AltName: Full=Protein RING membrane-anchor 1 gi|3164222|dbj|BAA28598.1| RMA1 [Arabidopsis thaliana] gi|4206205|gb|AAD11593.1| RMA1 RING zinc finger protein [Arabidopsis thaliana] gi|7270674|emb|CAB77836.1| RMA1 RING zinc finger protein [Arabidopsis thaliana] gi|28392896|gb|AAO41884.1| putative E3 ubiquitin ligase, RMA1 [Arabidopsis thaliana] gi|28827754|gb|AAO50721.1| putative E3 ubiquitin ligase, RMA1 [Arabidopsis thaliana] gi|332656931|gb|AEE82331.1| E3 ubiquitin-protein ligase RMA1 [Arabidopsis thaliana] gi|332656932|gb|AEE82332.1| E3 ubiquitin-protein ligase RMA1 [Arabidopsis thaliana	240	249	5.00E-97	103.8	77.1	87.1	E3 ubiquitin-protein ligase RMA1	gbpln	Arabidopsis thaliana	AT4G03510.2 | Symbols: RMA1, ATRMA1 | RING membrane-anchor 1 | chr4:1557905-1558654 REVERSE LENGTH=249	240	249	2.00E-99	103.8	77.1	87.1
Rsa1.0_00417.1.g13459.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00418.1.g13460.t1	ref|NP_565495.1| synaptotagmin A [Arabidopsis thaliana] gi|75313542|sp|Q9SKR2.2|SYT1_ARATH RecName: Full=Synaptotagmin-1; AltName: Full=NTMC2T1.1; AltName: Full=Synaptotagmin A gi|15027959|gb|AAK76510.1| unknown protein [Arabidopsis thaliana] gi|20197686|gb|AAM15203.1| expressed protein [Arabidopsis thaliana] gi|20197724|gb|AAD29817.2| expressed protein [Arabidopsis thaliana] gi|21593508|gb|AAM65475.1| unknown [Arabidopsis thaliana] gi|28393915|gb|AAO42365.1| unknown protein [Arabidopsis thaliana] gi|31071599|dbj|BAC76812.1| synaptotagmin A [Arabidopsis thaliana] gi|39918793|emb|CAE85115.1| synaptotagmin [Arabidopsis thaliana] gi|330252015|gb|AEC07109.1| synaptotagmin A [Arabidopsis thaliana]	541	541	0	100.0	91.7	96.3	synaptotagmin A	gbpln	Arabidopsis thaliana	AT2G20990.1 | Symbols: SYTA, NTMC2TYPE1.1, ATSYTA, NTMC2T1.1, SYT1 | synaptotagmin A | chr2:9014827-9017829 FORWARD LENGTH=541	541	541	0	100.0	91.7	96.3
Rsa1.0_00418.1.g13461.t1	gb|EOA27008.1| hypothetical protein CARUB_v10023108mg [Capsella rubella]	287	483	1.00E-155	168.3	96.2	97.9	hypothetical protein CARUB_v10023108mg	gbpln	Capsella rubella	AT2G21050.1 | Symbols: LAX2 | like AUXIN RESISTANT 2 | chr2:9034289-9036439 FORWARD LENGTH=483	287	483	1.00E-157	168.3	96.9	98.3
Rsa1.0_00418.1.g13462.t1	ref|NP_179702.1| glycine-rich protein 2B [Arabidopsis thaliana] gi|17366505|sp|Q38896.1|CSP4_ARATH RecName: Full=Cold shock domain-containing protein 4; Short=AtCSP4; AltName: Full=Glycine-rich protein 2b; Short=AtGRP2b gi|1063684|gb|AAA91165.1| AtGRP2b [Arabidopsis thaliana] gi|4803937|gb|AAD29810.1| glycine-rich protein (AtGRP2) [Arabidopsis thaliana] gi|16323178|gb|AAL15323.1| At2g21060/F26H11.18 [Arabidopsis thaliana] gi|60543359|gb|AAX22277.1| At2g21060 [Arabidopsis thaliana] gi|330252023|gb|AEC07117.1| glycine-rich protein 2B [Arabidopsis thaliana]	184	201	5.00E-20	109.2	54.3	56.5	glycine-rich protein 2B	gbpln	Arabidopsis thaliana	AT2G21060.1 | Symbols: ATGRP2B, ATCSP4, GRP2B | glycine-rich protein 2B | chr2:9036983-9037588 REVERSE LENGTH=201	184	201	2.00E-22	109.2	54.3	56.5
Rsa1.0_00418.1.g13463.t1	gb|EOA29035.1| hypothetical protein CARUB_v10025289mg [Capsella rubella]	559	597	0	106.8	82.8	91.8	hypothetical protein CARUB_v10025289mg	gbpln	Capsella rubella	AT2G21090.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr2:9045695-9047488 REVERSE LENGTH=597	559	597	0	106.8	80.1	90.9
Rsa1.0_00418.1.g13464.t1	gb|EOA27954.1| hypothetical protein CARUB_v10024124mg [Capsella rubella]	188	189	9.00E-97	100.5	89.4	96.3	hypothetical protein CARUB_v10024124mg	gbpln	Capsella rubella	AT2G21100.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr2:9048687-9049336 REVERSE LENGTH=187	188	187	3.00E-97	99.5	86.7	95.2
Rsa1.0_00418.1.g13465.t1	gb|EOA28830.1| hypothetical protein CARUB_v10025069mg [Capsella rubella]	188	184	7.00E-82	97.9	79.8	88.3	hypothetical protein CARUB_v10025069mg	gbpln	Capsella rubella	AT2G21110.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr2:9050290-9050850 REVERSE LENGTH=186	188	186	4.00E-84	98.9	79.3	88.3

Rsa1.0_00418.1.g13466.t1	ref|NP_179708.2| uncharacterized protein [Arabidopsis thaliana] gi|26452186|dbj|BAC43181.1| unknown protein [Arabidopsis thaliana] gi|109946593|gb|ABG48475.1| At2g21120 [Arabidopsis thaliana] gi|330252031|gb|AEC07125.1| uncharacterized protein AT2G21120 [Arabidopsis thaliana]	339	328	1.00E-179	96.8	92.3	95.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G21120.1 | Symbols: | Protein of unknown function (DUF803) | chr2:9052103-9054266 REVERSE LENGTH=328	339	328	0	96.8	92.3	95.6
Rsa1.0_00418.1.g13467.t1	gb|EOA29108.1| hypothetical protein CARUB_v10025375mg [Capsella rubella]	361	337	1.00E-160	93.4	87.5	90.3	hypothetical protein CARUB_v10025375mg	gbpln	Capsella rubella	AT2G21150.1 | Symbols: XCT | XAP5 family protein | chr2:9065397-9067921 FORWARD LENGTH=337	361	337	1.00E-162	93.4	87.3	90.6
Rsa1.0_00418.1.g13468.t1	gb|EOA27737.1| hypothetical protein CARUB_v10023890mg [Capsella rubella]	257	258	1.00E-110	100.4	84.4	89.1	hypothetical protein CARUB_v10023890mg	gbpln	Capsella rubella	AT2G21160.1 | Symbols: | Translocon-associated protein (TRAP), alpha subunit | chr2:9068428-9070207 FORWARD LENGTH=258	257	258	1.00E-107	100.4	81.3	87.2
Rsa1.0_00418.1.g13469.t1	gb|EOA27531.1| hypothetical protein CARUB_v10023671mg [Capsella rubella]	315	315	1.00E-149	100.0	88.6	91.7	hypothetical protein CARUB_v10023671mg	gbpln	Capsella rubella	AT2G21170.1 | Symbols: TIM, PDTPI | triosephosphate isomerase | chr2:9071047-9073106 REVERSE LENGTH=315	315	315	1.00E-150	100.0	89.2	91.7
Rsa1.0_00418.1.g13470.t1	ref|XP_002880362.1| hypothetical protein ARALYDRAFT_900527 [Arabidopsis lyrata subsp. lyrata] gi|297326201|gb|EFH56621.1| hypothetical protein ARALYDRAFT_900527 [Arabidopsis lyrata subsp. lyrata]	132	130	1.00E-44	98.5	84.8	90.2	hypothetical protein ARALYDRAFT_900527	gbpln	Arabidopsis lyrata	AT2G21180.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19875.1); Has 124 Blast hits to 124 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 124; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9074956-9075351 REVERSE LENGTH=131	132	131	2.00E-39	99.2	81.1	87.1
Rsa1.0_00418.1.g13471.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00418.1.g13472.t1	gb|EOA17208.1| hypothetical protein CARUB_v10005480mg [Capsella rubella]	272	273	1.00E-139	100.4	88.6	94.1	hypothetical protein CARUB_v10005480mg	gbpln	Capsella rubella	AT4G38790.1 | Symbols: | ER lumen protein retaining receptor family protein | chr4:18111426-18112977 FORWARD LENGTH=273	272	273	1.00E-141	100.4	87.9	93.4
Rsa1.0_00418.1.g13473.t1	gb|EOA28190.1| hypothetical protein CARUB_v10024381mg [Capsella rubella]	91	104	9.00E-46	114.3	96.7	96.7	hypothetical protein CARUB_v10024381mg	gbpln	Capsella rubella	AT2G21220.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:9089380-9089694 FORWARD LENGTH=104	91	104	2.00E-47	114.3	95.6	95.6
Rsa1.0_00418.1.g13474.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00418.1.g13475.t1	ref|XP_002880366.1| hypothetical protein ARALYDRAFT_480978 [Arabidopsis lyrata subsp. lyrata] gi|297326205|gb|EFH56625.1| hypothetical protein ARALYDRAFT_480978 [Arabidopsis lyrata subsp. lyrata]	801	518	2.00E-90	64.7	29.6	33.6	hypothetical protein ARALYDRAFT_480978	gbpln	Arabidopsis lyrata	AT2G21230.1 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:9093920-9096059 REVERSE LENGTH=519	801	519	1.00E-85	64.8	28.5	32.2
Rsa1.0_00418.1.g13476.t2	ref|XP_002880370.1| hypothetical protein ARALYDRAFT_480985 [Arabidopsis lyrata subsp. lyrata] gi|297326209|gb|EFH56629.1| hypothetical protein ARALYDRAFT_480985 [Arabidopsis lyrata subsp. lyrata]	295	309	1.00E-141	104.7	82.4	86.1	hypothetical protein ARALYDRAFT_480985	gbpln	Arabidopsis lyrata	AT2G21250.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr2:9103408-9105116 REVERSE LENGTH=309	295	309	1.00E-142	104.7	81.4	85.8
Rsa1.0_00418.1.g13477.t2	ref|XP_002878541.1| hypothetical protein ARALYDRAFT_480987 [Arabidopsis lyrata subsp. lyrata] gi|297324380|gb|EFH54800.1| hypothetical protein ARALYDRAFT_480987 [Arabidopsis lyrata subsp. lyrata]	131	319	4.00E-72	243.5	96.9	99.2	hypothetical protein ARALYDRAFT_480987	gbpln	Arabidopsis lyrata	AT2G21270.2 | Symbols: UFD1 | ubiquitin fusion degradation 1 | chr2:9108126-9110012 FORWARD LENGTH=319	131	319	1.00E-74	243.5	96.9	99.2
Rsa1.0_00418.1.g13478.t1	ref|XP_002878564.1| hypothetical protein ARALYDRAFT_481032 [Arabidopsis lyrata subsp. lyrata] gi|297324403|gb|EFH54823.1| hypothetical protein ARALYDRAFT_481032 [Arabidopsis lyrata subsp. lyrata]	100	96	2.00E-41	96.0	80.0	90.0	hypothetical protein ARALYDRAFT_481032	gbpln	Arabidopsis lyrata	AT2G21650.1 | Symbols: MEE3, ATRL2, RSM1 | Homeodomain-like superfamily protein | chr2:9259654-9260419 FORWARD LENGTH=101	100	101	1.00E-40	101.0	86.0	94.0
Rsa1.0_00418.1.g13479.t1	gb|AFL91694.1| glycine-rich RNA binding protein [Raphanus sativus var. raphanistroides]	169	153	5.00E-44	90.5	50.3	50.9	glycine-rich RNA binding protein	gbpln	Raphanus sativus	AT2G21660.2 | Symbols: ATGRP7, CCR2 | cold, circadian rhythm, and rna binding 2 | chr2:9265477-9266316 REVERSE LENGTH=159	169	159	2.00E-42	94.1	46.2	49.1
Rsa1.0_00418.1.g13480.t1	ref|NP_173379.1| Kelch repeat-containing protein [Arabidopsis thaliana] gi|125991225|sp|P0C2F7.1|Y1947_ARATH RecName: Full=Kelch repeat-containing protein At1g19470 gi|332191734|gb|AEE29855.1| Kelch repeat-containing protein [Arabidopsis thaliana]	347	412	8.00E-56	118.7	43.5	63.4	Kelch repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G19470.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:6741296-6742534 FORWARD LENGTH=412	347	412	2.00E-58	118.7	43.5	63.4

<table>
<tr><td>Rsa1.0_00418.1.g13481.t1</td><td>gb|AAF79430.1|AC025808_12 F18O14.24 [Arabidopsis thaliana]</td><td>397</td><td>840</td><td>5.00E-75</td><td>211.6</td><td>43.3</td><td>62.5</td><td>F18O14.24</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G19470.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:6741296-6742534 FORWARD LENGTH=412</td><td>397</td><td>412</td><td>1.00E-77</td><td>103.8</td><td>43.3</td><td>62.5</td></tr>
<tr><td>Rsa1.0_00418.1.g13482.t1</td><td>sp|P49311.1|GRP2_SINAL RecName: Full=Glycine-rich RNA-binding protein GRP2A gi|496237|gb|AAA59213.1| homology with RNA-binding proteins in meristematic tissue [Sinapis alba]</td><td>239</td><td>169</td><td>2.00E-22</td><td>70.7</td><td>20.9</td><td>27.6</td><td>RecName: Full=Glycine-rich RNA-binding protein GRP2A gi|496237|gb|AAA59213.1| homology with RNA-binding proteins in meristematic tissue</td><td>gbpln</td><td>Sinapis alba</td><td>AT2G21660.2 | Symbols: ATGRP7, CCR2 | cold, circadian rhythm, and rna binding 2 | chr2:9265477-9266316 REVERSE LENGTH=159</td><td>239</td><td>159</td><td>3.00E-23</td><td>66.5</td><td>20.1</td><td>26.4</td></tr>
<tr><td>Rsa1.0_00418.1.g13483.t1</td><td>ref|XP_002878567.1| EMB2219 [Arabidopsis lyrata subsp. lyrata] gi|297324406|gb|EFH54826.1| EMB2219 [Arabidopsis lyrata subsp. lyrata]</td><td>364</td><td>613</td><td>1.00E-143</td><td>168.4</td><td>76.1</td><td>81.6</td><td>EMB2219</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G21710.1 | Symbols: EMB2219 | Mitochondrial transcription termination factor family protein | chr2:9270886-9273307 FORWARD LENGTH=641</td><td>364</td><td>641</td><td>1.00E-140</td><td>176.1</td><td>74.2</td><td>81.3</td></tr>
<tr><td>Rsa1.0_00419.1.g13484.t1</td><td>gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]</td><td>1468</td><td>1485</td><td>0</td><td>101.2</td><td>45.2</td><td>61.1</td><td>hypothetical protein PRUPE_ppa017790mg</td><td>gbpln</td><td>Prunus persica</td><td>ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158</td><td>1468</td><td>158</td><td>2.00E-29</td><td>10.8</td><td>3.8</td><td>5.7</td></tr>
<tr><td>Rsa1.0_00419.1.g13485.t1</td><td>gb|EOA40353.1| hypothetical protein CARUB_v10009081mg [Capsella rubella]</td><td>185</td><td>461</td><td>3.00E-93</td><td>249.2</td><td>91.4</td><td>94.6</td><td>hypothetical protein CARUB_v10009081mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G12860.1 | Symbols: SCRM2, ICE2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:4384758-4386392 FORWARD LENGTH=450</td><td>185</td><td>450</td><td>2.00E-95</td><td>243.2</td><td>91.4</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00419.1.g13486.t1</td><td>gb|AAF78493.1|AC012187_13 Contains similarity to AP2/EREBP-like transcription factor from Arabidopsis thaliana gb|AF216581 and contains Bacterial mutT protein PF|00293 and AP2 PF|00847 domains [Arabidopsis thaliana]</td><td>166</td><td>411</td><td>2.00E-73</td><td>247.6</td><td>83.1</td><td>90.4</td><td>Contains similarity to AP2/EREBP-like transcription factor from Arabidopsis thaliana gb|AF216581 and contains Bacterial mutT protein PF|00293 and AP2 PF|00847 domains</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G12880.1 | Symbols: atnudt12, NUDT12 | nudix hydrolase homolog 12 | chr1:4390036-4391046 FORWARD LENGTH=203</td><td>166</td><td>203</td><td>8.00E-75</td><td>122.3</td><td>83.1</td><td>90.4</td></tr>
<tr><td>Rsa1.0_00419.1.g13487.t1</td><td>ref|XP_002889975.1| hypothetical protein ARALYDRAFT_471441 [Arabidopsis lyrata subsp. lyrata] gi|297335817|gb|EFH66234.1| hypothetical protein ARALYDRAFT_471441 [Arabidopsis lyrata subsp. lyrata]</td><td>206</td><td>203</td><td>4.00E-93</td><td>98.5</td><td>83.5</td><td>90.8</td><td>hypothetical protein ARALYDRAFT_471441</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G12880.1 | Symbols: atnudt12, NUDT12 | nudix hydrolase homolog 12 | chr1:4390036-4391046 FORWARD LENGTH=203</td><td>206</td><td>203</td><td>1.00E-93</td><td>98.5</td><td>81.1</td><td>89.8</td></tr>
<tr><td>Rsa1.0_00419.1.g13488.t1</td><td>dbj|BAJ10475.1| glyceraldehyde-3-phosphate dehydrogenase [Brassica rapa subsp. chinensis]</td><td>399</td><td>399</td><td>0</td><td>100.0</td><td>98.2</td><td>98.5</td><td>glyceraldehyde-3-phosphate dehydrogenase</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G12900.1 | Symbols: GAPA-2 | glyceraldehyde 3-phosphate dehydrogenase A subunit 2 | chr1:4392634-4394283 REVERSE LENGTH=399</td><td>399</td><td>399</td><td>0</td><td>100.0</td><td>97.2</td><td>99.2</td></tr>
<tr><td>Rsa1.0_00419.1.g13489.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00419.1.g13490.t13</td><td>ref|XP_002892722.1| hypothetical protein ARALYDRAFT_471447 [Arabidopsis lyrata subsp. lyrata] gi|297338564|gb|EFH68981.1| hypothetical protein ARALYDRAFT_471447 [Arabidopsis lyrata subsp. lyrata]</td><td>310</td><td>1007</td><td>2.00E-62</td><td>324.8</td><td>50.6</td><td>53.9</td><td>hypothetical protein ARALYDRAFT_471447</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G12930.1 | Symbols: | ARM repeat superfamily protein | chr1:4398588-4405495 REVERSE LENGTH=1005</td><td>310</td><td>1005</td><td>3.00E-64</td><td>324.2</td><td>50.0</td><td>53.9</td></tr>
<tr><td>Rsa1.0_00419.1.g13491.t1</td><td>gb|EOA37327.1| hypothetical protein CARUB_v10011023mg [Capsella rubella]</td><td>303</td><td>331</td><td>1.00E-83</td><td>109.2</td><td>64.7</td><td>71.3</td><td>hypothetical protein CARUB_v10011023mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G12980.1 | Symbols: ESR1, DRN | Integrase-type DNA-binding superfamily protein | chr1:4429791-4430777 FORWARD LENGTH=328</td><td>303</td><td>328</td><td>3.00E-76</td><td>108.3</td><td>61.7</td><td>71.9</td></tr>
<tr><td>Rsa1.0_00419.1.g13492.t1</td><td>ref|NP_172759.2| beta-1,4-mannosyl-glycoprotein [Arabidopsis thaliana] gi|332190836|gb|AEE28957.1| beta-1,4-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]</td><td>392</td><td>392</td><td>0</td><td>100.0</td><td>92.9</td><td>96.9</td><td>beta-1,4-mannosyl-glycoprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G12990.1 | Symbols: | beta-1,4-N-acetylglucosaminyltransferase family protein | chr1:4433973-4435552 FORWARD LENGTH=392</td><td>392</td><td>392</td><td>0</td><td>100.0</td><td>92.9</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00419.1.g13493.t1</td><td>gb|EOA36479.1| hypothetical protein CARUB_v10011103mg [Capsella rubella]</td><td>419</td><td>401</td><td>0</td><td>95.7</td><td>84.7</td><td>91.4</td><td>hypothetical protein CARUB_v10011103mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G13000.2 | Symbols: | Protein of unknown function (DUF707) | chr1:4436402-4438693 REVERSE LENGTH=401</td><td>419</td><td>401</td><td>0</td><td>95.7</td><td>85.0</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00419.1.g13494.t1</td><td>gb|EOA36832.1| hypothetical protein CARUB_v10008617mg [Capsella rubella]</td><td>606</td><td>608</td><td>0</td><td>100.3</td><td>75.9</td><td>84.0</td><td>hypothetical protein CARUB_v10008617mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G13030.1 | Symbols: | sphere organelles protein-related | chr1:4444284-4447278 REVERSE LENGTH=608</td><td>606</td><td>608</td><td>0</td><td>100.3</td><td>74.9</td><td>82.0</td></tr>
<tr><td>Rsa1.0_00419.1.g13495.t1</td><td>ref|XP_002889980.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335822|gb|EFH66239.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>507</td><td>517</td><td>0</td><td>102.0</td><td>89.0</td><td>95.1</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G13040.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:4447647-4449200 FORWARD LENGTH=517</td><td>507</td><td>517</td><td>0</td><td>102.0</td><td>89.0</td><td>95.1</td></tr>
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<tr><td>Rsa1.0_00419.1.g13496.t1</td><td>gb|EOA36472.1| hypothetical protein CARUB_v10011087mg [Capsella rubella]</td><td>320</td><td>317</td><td>1.00E-131</td><td>99.1</td><td>78.1</td><td>86.3</td><td>hypothetical protein CARUB_v10011087mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G13050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G26350.1); Has 538 Blast hits to 510 proteins in 88 species: Archae - 0; Bacteria - 23; Metazoa - 81; Fungi - 36; Plants - 361; Viruses - 8; Other Eukaryotes - 29 (source: NCBI BLink). | chr1:4450568-4451521 FORWARD LENGTH=317</td><td>320</td><td>317</td><td>1.00E-127</td><td>99.1</td><td>81.3</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00419.1.g13497.t1</td><td>ref|NP_189265.1| proteasome subunit beta type-5-B [Arabidopsis thaliana] gi|75273433|sp|Q9LIP2.1|PSB5B_ARATH RecName: Full=Proteasome subunit beta type-5-B; AltName: Full=20S proteasome beta subunit E-2; AltName: Full=Proteasome epsilon-2 chain; Flags: Precursor gi|16612308|gb|AAL27514.1|AF439846_1 AT3g26340/F20C19_6 [Arabidopsis thaliana] gi|9294292|dbj|BAB02194.1| proteasome epsilon chain precursor [Arabidopsis thaliana] gi|21553804|gb|AAM62897.1| 26S proteasome beta subunit, putative [Arabidopsis thaliana] gi|21928101|gb|AAM78079.1| AT3g26340/F20C19_6 [Arabidopsis thaliana] gi|332643626|gb|AEE77147.1| proteasome subunit beta type-5-B [Arabidopsis thaliana]</td><td>281</td><td>273</td><td>1.00E-143</td><td>97.2</td><td>89.7</td><td>92.2</td><td>proteasome subunit beta type-5-B</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G26340.1 | Symbols: | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:9650600-9652572 REVERSE LENGTH=273</td><td>281</td><td>273</td><td>2.33E-156</td><td>97.2</td><td>89.7</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00419.1.g13498.t1</td><td>ref|NP_172770.1| cytochrome P450 71B7 [Arabidopsis thaliana] gi|5915830|sp|Q96514.1|C71B7_ARATH RecName: Full=Cytochrome P450 71B7 gi|4850394|gb|AAD31064.1|AC007357_13 Identical to gb|X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF|00067 Cytochrome P450 family. ESTs gb|T44875, gb|T04814, gb|R65111, gb|T44310 and gb|T04541 come from this gene [Arabidopsis thaliana] gi|18087623|gb|AAL58941.1|AF462855_1 At1g13110/F3F19_13 [Arabidopsis thaliana] gi|1523796|emb|CAA66458.1| cytochrome P450 [Arabidopsis thaliana] gi|29028730|gb|AAO64744.1| At1g13110/F3F19_13 [Arabidopsis thaliana] gi|332190850|gb|AEE28971.1| cytochrome P450 71B7 [Arabidopsis thaliana]</td><td>501</td><td>504</td><td>0</td><td>100.6</td><td>77.0</td><td>90.2</td><td>cytochrome P450 71B7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G13110.1 | Symbols: CYP71B7 | cytochrome P450, family 71 subfamily B, polypeptide 7 | chr1:4467272-4468857 FORWARD LENGTH=504</td><td>501</td><td>504</td><td>0</td><td>100.6</td><td>77.0</td><td>90.2</td></tr>
<tr><td>Rsa1.0_00419.1.g13499.t1</td><td>ref|NP_172770.1| cytochrome P450 71B7 [Arabidopsis thaliana] gi|5915830|sp|Q96514.1|C71B7_ARATH RecName: Full=Cytochrome P450 71B7 gi|4850394|gb|AAD31064.1|AC007357_13 Identical to gb|X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF|00067 Cytochrome P450 family. ESTs gb|T44875, gb|T04814, gb|R65111, gb|T44310 and gb|T04541 come from this gene [Arabidopsis thaliana] gi|18087623|gb|AAL58941.1|AF462855_1 At1g13110/F3F19_13 [Arabidopsis thaliana] gi|1523796|emb|CAA66458.1| cytochrome P450 [Arabidopsis thaliana] gi|29028730|gb|AAO64744.1| At1g13110/F3F19_13 [Arabidopsis thaliana] gi|332190850|gb|AEE28971.1| cytochrome P450 71B7 [Arabidopsis thaliana]</td><td>507</td><td>504</td><td>0</td><td>99.4</td><td>80.1</td><td>90.9</td><td>cytochrome P450 71B7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G13110.1 | Symbols: CYP71B7 | cytochrome P450, family 71 subfamily B, polypeptide 7 | chr1:4467272-4468857 FORWARD LENGTH=504</td><td>507</td><td>504</td><td>0</td><td>99.4</td><td>80.1</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00419.1.g13500.t1</td><td>ref|XP_002889989.1| glycosyl hydrolase family 5 protein [Arabidopsis lyrata subsp. lyrata] gi|297335831|gb|EFH66248.1| glycosyl hydrolase family 5 protein [Arabidopsis lyrata subsp. lyrata]</td><td>550</td><td>552</td><td>0</td><td>100.4</td><td>82.7</td><td>88.9</td><td>glycosyl hydrolase family 5 protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G13130.1 | Symbols: | Cellulase (glycosyl hydrolase family 5) protein | chr1:4474726-4477820 FORWARD LENGTH=552</td><td>550</td><td>552</td><td>0</td><td>100.4</td><td>82.5</td><td>88.5</td></tr>
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Rsa1.0_00419.1.g13501.t1	ref|NP_172773.4| cytochrome P450, family 86, subfamily C, polypeptide 3 [Arabidopsis thaliana] gi|63147398|gb|AAY34172.1| At1g13140 [Arabidopsis thaliana] gi|332190853|gb|AEE28974.1| cytochrome P450, family 86, subfamily C, polypeptide 3 [Arabidopsis thaliana]	526	534	0	101.5	87.5	93.3	cytochrome P450, family 86, subfamily C, polypeptide 3	gbpln	Arabidopsis thaliana	AT1G13140.1 | Symbols: CYP86C3 | cytochrome P450, family 86, subfamily C, polypeptide 3 | chr1:4478667-4480271 REVERSE LENGTH=534	526	534	0	101.5	87.5	93.3
Rsa1.0_00419.1.g13502.t1	ref|NP_172776.1| oxysterol binding protein-related protein 1D [Arabidopsis thaliana] gi|75200684|sp|Q9SAF0.1|ORP1D_ARATH RecName: Full=Oxysterol-binding protein-related protein 1D; AltName: Full=OSBP-related protein 1D gi|4850400|gb|AAD31070.1|AC007357_19 Similar to gb|M86917 oxysterol-binding protein from Homo sapiens [Arabidopsis thaliana] gi|18087546|gb|AAL58905.1|AF462814_1 At1g13170/F3F19_19 [Arabidopsis thaliana] gi|332190857|gb|AEE28978.1| oxysterol binding protein-related protein 1D [Arabidopsis thaliana]	797	816	0	102.4	91.3	94.1	oxysterol binding protein-related protein 1D	gbpln	Arabidopsis thaliana	AT1G13170.1 | Symbols: ORP1D | OSBP(oxysterol binding protein)-related protein 1D | chr1:4488826-4492278 REVERSE LENGTH=816	797	816	0	102.4	91.3	94.1
Rsa1.0_00419.1.g13503.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00419.1.g13504.t1	ref|NP_172777.1| actin-related protein 3 [Arabidopsis thaliana] gi|75313139|sp|Q9SAF1.1|ARP3_ARATH RecName: Full=Actin-related protein 3; AltName: Full=Protein DISTORTED TRICHOMES 1 gi|4850401|gb|AAD31071.1|AC007357_20 Strong similarity to gb|U29610 Actin-like protein (Arp3) from Acanthamoeba castellanii and is a member of the PF|00022 Actin family [Arabidopsis thaliana] gi|21427461|gb|AAM53243.1|AF507911_1 actin-related protein 3 [Arabidopsis thaliana] gi|20260500|gb|AAM13148.1| similar to actin-like protein [Arabidopsis thaliana] gi|21489929|tpg|DAA00033.1| TPA_exp: actin-related protein 3; AtARP3 [Arabidopsis thaliana] gi|30387525|gb|AAP31928.1| At1g13180 [Arabidopsis thaliana] gi|332190859|gb|AEE28980.1| actin-related protein 3 [Arabidopsis thaliana]	428	427	0	99.8	94.4	97.7	actin-related protein 3	gbpln	Arabidopsis thaliana	AT1G13180.1 | Symbols: DIS1, ARP3, ATARP3 | Actin-like ATPase superfamily protein | chr1:4495394-4498204 FORWARD LENGTH=427	428	427	0	99.8	94.4	97.7
Rsa1.0_00419.1.g13505.t1	ref|NP_180115.1| putative 2-oxoacid dependent dioxygenase [Arabidopsis thaliana] gi|75313535|sp|Q9SKK4.1|GSL_ARATH RecName: Full=Probable 2-oxoacid dependent dioxygenase gi|4432856|gb|AAD20704.1| putative dioxygenase [Arabidopsis thaliana] gi|15292707|gb|AAK92722.1| putative dioxygenase [Arabidopsis thaliana] gi|21280917|gb|AAM45103.1| putative dioxygenase [Arabidopsis thaliana] gi|330252609|gb|AEC07703.1| putative 2-oxoacid dependent dioxygenase [Arabidopsis thaliana]	299	359	1.00E-116	120.1	65.9	78.3	putative 2-oxoacid dependent dioxygenase	gbpln	Arabidopsis thaliana	AT2G25450.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr2:10830286-10831563 REVERSE LENGTH=359	299	359	1.00E-118	120.1	65.9	78.3
Rsa1.0_00420.1.g13506.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00420.1.g13507.t1	ref|XP_002882437.1| hypothetical protein ARALYDRAFT_340760 [Arabidopsis lyrata subsp. lyrata] gi|297328277|gb|EFH58696.1| hypothetical protein ARALYDRAFT_340760 [Arabidopsis lyrata subsp. lyrata]	329	350	1.00E-155	106.4	86.0	93.0	hypothetical protein ARALYDRAFT_340760	gbpln	Arabidopsis lyrata	AT3G05830.1 | Symbols: | Encodes alpha-helical IF (intermediate filament)-like protein. | chr3:1736796-1738565 FORWARD LENGTH=336	329	336	1.00E-151	102.1	85.4	91.2
Rsa1.0_00420.1.g13508.t1	gb|EOA32504.1| hypothetical protein CARUB_v10015785mg [Capsella rubella]	410	409	0	99.8	96.6	98.0	hypothetical protein CARUB_v10015785mg	gbpln	Capsella rubella	AT3G05840.1 | Symbols: ATSK12 | Protein kinase superfamily protein | chr3:1740793-1742927 FORWARD LENGTH=409	410	409	0	99.8	96.6	97.8
Rsa1.0_00420.1.g13509.t1	gb|AAF26087.1|AC012393_13 unknown protein [Arabidopsis thaliana] gi|30793999|gb|AAP40449.1| unknown protein [Arabidopsis thaliana]	788	777	0	98.6	87.1	92.3	unknown protein	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	788	719	8.00E-35	91.2	21.2	39.5
Rsa1.0_00420.1.g13510.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00420.1.g13511.t1	ref|NP_001118584.1| uncharacterized protein [Arabidopsis thaliana] gi|98962065|gb|ABF59362.1| unknown protein [Arabidopsis thaliana] gi|332640784|gb|AEE74305.1| uncharacterized protein AT3G05858 [Arabidopsis thaliana]	80	90	2.00E-30	112.5	83.8	87.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G05858.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26620.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:1749464-1749736 FORWARD LENGTH=90	80	90	3.00E-33	112.5	83.8	87.5
Rsa1.0_00420.1.g13512.t1	ref|NP_187237.2| MADS-box domain-containing protein [Arabidopsis thaliana] gi|332640785|gb|AEE74306.1| MADS-box domain-containing protein [Arabidopsis thaliana]	300	260	7.00E-71	86.7	50.7	64.0	MADS-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G05860.1 | Symbols: | MADS-box transcription factor family protein | chr3:1751406-1752355 REVERSE LENGTH=260	300	260	2.00E-73	86.7	50.7	64.0
Rsa1.0_00420.1.g13513.t1	gb|EOA31081.1| hypothetical protein CARUB_v10014232mg [Capsella rubella]	326	310	2.00E-51	95.1	42.3	53.7	hypothetical protein CARUB_v10014232mg	gbpln	Capsella rubella	AT5G48670.1 | Symbols: FEM111, AGL80 | AGAMOUS-like 80 | chr5:19738825-19739790 REVERSE LENGTH=321	326	321	2.00E-52	98.5	40.8	53.4
Rsa1.0_00420.1.g13514.t1	gb|AFC41201.1| PM-YC3.6-Lti6b [Binary expression vector PM-YC3.6-LTI6b]	54	726	2.00E-20	1344.4	77.8	94.4	PM-YC3.6-Lti6b	----	----	AT3G05880.1 | Symbols: RCI2A | Low temperature and salt responsive protein family | chr3:1756195-1756494 REVERSE LENGTH=54	54	54	3.00E-21	100.0	85.2	98.1
Rsa1.0_00420.1.g13515.t1	ref|NP_187241.2| neurofilament protein-related protein [Arabidopsis thaliana] gi|332640792|gb|AEE74313.1| neurofilament protein-related protein [Arabidopsis thaliana]	542	673	3.00E-48	124.2	37.3	47.2	neurofilament protein-related protein	gbpln	Arabidopsis thaliana	AT3G05900.1 | Symbols: | neurofilament protein-related | chr3:1761408-1763854 REVERSE LENGTH=673	542	673	8.00E-51	124.2	37.3	47.2
Rsa1.0_00420.1.g13516.t1	ref|NP_566263.1| Pectin lyase-like protein [Arabidopsis thaliana] gi|6671966|gb|AAF23225.1|AC013454_12 putative pectinacetylesterase [Arabidopsis thaliana] gi|16226325|gb|AAL16135.1|AF428303_1 AT3g05910/F2O10_3 [Arabidopsis thaliana] gi|15292827|gb|AAK92782.1| putative pectinacetylesterase [Arabidopsis thaliana] gi|20465793|gb|AAM20385.1| putative pectinacetylesterase [Arabidopsis thaliana] gi|332640793|gb|AEE74314.1| Pectin lyase-like protein [Arabidopsis thaliana]	414	415	0	100.2	92.8	96.6	Pectin lyase-like protein	gbpln	Arabidopsis thaliana	AT3G05910.1 | Symbols: | Pectinacetylesterase family protein | chr3:1764509-1767240 REVERSE LENGTH=415	414	415	0	100.2	92.8	96.6
Rsa1.0_00420.1.g13517.t1	gb|AAM61454.1| unknown [Arabidopsis thaliana]	145	126	2.00E-37	86.9	73.8	78.6	unknown	gbpln	Arabidopsis thaliana	AT3G05920.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1768991-1769522 REVERSE LENGTH=126	145	126	5.00E-40	86.9	74.5	79.3
Rsa1.0_00420.1.g13518.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1651	1213	0	73.5	26.3	38.9	unknown protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	1651	295	2.00E-83	17.9	9.5	12.6
Rsa1.0_00420.1.g13519.t1	ref|XP_002882441.1| hypothetical protein ARALYDRAFT_896692 [Arabidopsis lyrata subsp. lyrata] gi|297328281|gb|EFH58700.1| hypothetical protein ARALYDRAFT_896692 [Arabidopsis lyrata subsp. lyrata]	218	219	4.00E-95	100.5	79.8	87.2	hypothetical protein ARALYDRAFT_896692	gbpln	Arabidopsis lyrata	AT3G05930.1 | Symbols: GLP8 | germin-like protein 8 | chr3:1770377-1771183 FORWARD LENGTH=219	218	219	4.00E-96	100.5	78.9	87.2
Rsa1.0_00420.1.g13520.t2	ref|XP_002884544.1| hypothetical protein ARALYDRAFT_896695 [Arabidopsis lyrata subsp. lyrata] gi|297330384|gb|EFH60803.1| hypothetical protein ARALYDRAFT_896695 [Arabidopsis lyrata subsp. lyrata]	109	101	7.00E-25	92.7	78.0	82.6	hypothetical protein ARALYDRAFT_896695	gbpln	Arabidopsis lyrata	AT5G26731.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:9295676-9295975 FORWARD LENGTH=99	109	99	2.00E-12	90.8	37.6	45.0
Rsa1.0_00420.1.g13521.t1	ref|XP_002884547.1| hypothetical protein ARALYDRAFT_317457 [Arabidopsis lyrata subsp. lyrata] gi|297330387|gb|EFH60806.1| hypothetical protein ARALYDRAFT_317457 [Arabidopsis lyrata subsp. lyrata]	504	507	0	100.6	94.6	97.4	hypothetical protein ARALYDRAFT_317457	gbpln	Arabidopsis lyrata	AT3G05960.1 | Symbols: ATSTP6, STP6 | sugar transporter 6 | chr3:1783587-1785334 REVERSE LENGTH=507	504	507	0	100.6	94.2	97.4
Rsa1.0_00420.1.g13522.t1	ref|XP_002884548.1| long-chain acyl-CoA synthetase [Arabidopsis lyrata subsp. lyrata] gi|297330388|gb|EFH60807.1| long-chain acyl-CoA synthetase [Arabidopsis lyrata subsp. lyrata]	620	695	0	112.1	83.9	89.4	long-chain acyl-CoA synthetase	gbpln	Arabidopsis lyrata	AT3G05970.1 | Symbols: LACS6, ATLACS6 | long-chain acyl-CoA synthetase 6 | chr3:1786510-1791746 REVERSE LENGTH=701	620	701	0	113.1	83.5	89.5

Rsa1.0_00420.1.g13523.t1	ref|XP_002884549.1| hypothetical protein ARALYDRAFT_896701 [Arabidopsis lyrata subsp. lyrata] gi|297330389|gb|EFH60808.1| hypothetical protein ARALYDRAFT_896701 [Arabidopsis lyrata subsp. lyrata]	122	189	2.00E-51	154.9	78.7	89.3	hypothetical protein ARALYDRAFT_896701	gbpln	Arabidopsis lyrata	AT3G05975.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:1792145-1792714 REVERSE LENGTH=189	122	189	7.00E-51	154.9	76.2	86.1
Rsa1.0_00420.1.g13524.t1	ref|XP_002882443.1| hypothetical protein ARALYDRAFT_896702 [Arabidopsis lyrata subsp. lyrata] gi|297328283|gb|EFH58702.1| hypothetical protein ARALYDRAFT_896702 [Arabidopsis lyrata subsp. lyrata]	238	248	1.00E-85	104.2	89.9	93.7	hypothetical protein ARALYDRAFT_896702	gbpln	Arabidopsis lyrata	AT3G05980.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19340.1); Has 202 Blast hits to 202 proteins in 28 species: Archae - 0; Bacteria - 0; Metazoa - 39; Fungi - 4; Plants - 148; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr3:1795514-1796251 FORWARD LENGTH=245	238	245	2.00E-81	102.9	85.3	90.8
Rsa1.0_00420.1.g13525.t1	ref|NP_187250.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|6671958|gb|AAF23217.1|AC013454_4 hypothetical protein [Arabidopsis thaliana] gi|30102730|gb|AAP21283.1| At3g05990 [Arabidopsis thaliana] gi|110743247|dbj|BAE99514.1| hypothetical protein [Arabidopsis thaliana] gi|332640806|gb|AEE74327.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	525	517	0	98.5	77.1	86.1	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G05990.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:1797116-1799732 REVERSE LENGTH=517	525	517	0	98.5	77.1	86.1
Rsa1.0_00421.1.g13526.t1	ref|NP_198140.1| C2H2 and C2HC zinc finger-containing protein [Arabidopsis thaliana] gi|332006357|gb|AED93740.1| C2H2 and C2HC zinc finger-containing protein [Arabidopsis thaliana]	275	278	4.00E-88	101.1	64.7	74.2	C2H2 and C2HC zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT5G27880.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:9885908-9886744 FORWARD LENGTH=278	275	278	1.00E-90	101.1	64.7	74.2
Rsa1.0_00421.1.g13527.t1	gb|AAQ81585.1| putative tubulin alpha-2/alpha-4 chain [Brassica napus]	474	450	0	94.9	92.4	93.2	putative tubulin alpha-2/alpha-4 chain	gbpln	Brassica napus	AT4G14960.2 | Symbols: TUA6 | Tubulin/FtsZ family protein | chr4:8548769-8550319 REVERSE LENGTH=450	474	450	0	94.9	90.1	90.7
Rsa1.0_00421.1.g13528.t1	ref|NP_187210.1| 60S ribosomal protein L18-2 [Arabidopsis thaliana] gi|21431838|sp|P42791.2|RL182_ARATH RecName: Full=60S ribosomal protein L18-2 gi|6714451|gb|AAF26138.1|AC011620_14 putative 60S ribosomal protein L18 [Arabidopsis thaliana] gi|14335090|gb|AAK59824.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gi|16974509|gb|AAL31164.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gi|332640742|gb|AEE74263.1| 60S ribosomal protein L18-2 [Arabidopsis thaliana]	187	187	4.00E-96	100.0	94.7	96.8	60S ribosomal protein L18-2	gbpln	Arabidopsis thaliana	AT3G05590.1 | Symbols: RPL18 | ribosomal protein L18 | chr3:1621511-1622775 FORWARD LENGTH=187	187	187	1.00E-98	100.0	94.7	96.8
Rsa1.0_00421.1.g13529.t1	ref|NP_568501.3| serine/threonine-protein phosphatase PP1 isozyme 8 [Arabidopsis thaliana] gi|38503411|sp|O82734.3|PP18_ARATH RecName: Full=Serine/threonine-protein phosphatase PP1 isozyme 8 gi|332006352|gb|AED93735.1| serine/threonine-protein phosphatase PP1 isozyme 8 [Arabidopsis thaliana]	360	324	1.00E-170	90.0	81.1	84.4	serine/threonine-protein phosphatase PP1 isozyme 8	gbpln	Arabidopsis thaliana	AT5G27840.2 | Symbols: TOPP8 | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:9863465-9864828 REVERSE LENGTH=324	360	324	1.00E-173	90.0	81.1	84.4
Rsa1.0_00421.1.g13530.t1	gb|EOA19497.1| hypothetical protein CARUB_v10002200mg, partial [Capsella rubella]	114	149	1.00E-57	130.7	93.9	98.2	hypothetical protein CARUB_v10002200mg, partial	gbpln	Capsella rubella	AT5G27820.1 | Symbols: | Ribosomal L18p/L5e family protein | chr5:9860584-9860928 FORWARD LENGTH=114	114	114	2.00E-59	100.0	93.9	97.4
Rsa1.0_00421.1.g13531.t1	ref|XP_002882425.1| 60S ribosomal protein L22-2 [Arabidopsis lyrata subsp. lyrata] gi|297328265|gb|EFH58684.1| 60S ribosomal protein L22-2 [Arabidopsis lyrata subsp. lyrata]	83	124	9.00E-20	149.4	69.9	75.9	60S ribosomal protein L22-2	gbpln	Arabidopsis lyrata	AT3G05560.3 | Symbols: | Ribosomal L22e protein family | chr3:1614641-1615204 FORWARD LENGTH=124	83	124	3.00E-22	149.4	68.7	75.9
Rsa1.0_00421.1.g13532.t10	ref|XP_002874347.1| hypoxia-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297320184|gb|EFH50606.1| hypoxia-responsive family protein [Arabidopsis lyrata subsp. lyrata]	96	96	2.00E-37	100.0	94.8	96.9	hypoxia-responsive family protein	gbpln	Arabidopsis lyrata	AT5G27760.1 | Symbols: | Hypoxia-responsive family protein | chr5:9830396-9831559 FORWARD LENGTH=96	96	96	1.00E-38	100.0	92.7	94.8
Rsa1.0_00421.1.g13533.t1	gb|EOA21887.1| hypothetical protein CARUB_v10002364mg [Capsella rubella]	82	82	2.00E-39	100.0	91.5	97.6	hypothetical protein CARUB_v10002364mg	gbpln	Capsella rubella	AT5G27700.1 | Symbols: | Ribosomal protein S21e | chr5:9807541-9808048 REVERSE LENGTH=82	82	82	5.00E-42	100.0	91.5	97.6

Rsa1.0_00421.1.g13534.t1	ref|XP_002874359.1| hypothetical protein ARALYDRAFT_489559 [Arabidopsis lyrata subsp. lyrata] gi|297320196|gb|EFH50618.1| hypothetical protein ARALYDRAFT_489559 [Arabidopsis lyrata subsp. lyrata]	364	345	1.00E-101	94.8	70.6	78.3	hypothetical protein ARALYDRAFT_489559	gbpln	Arabidopsis lyrata	AT5G27690.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:9803796-9805036 FORWARD LENGTH=352	364	352	1.00E-103	96.7	72.3	80.2
Rsa1.0_00421.1.g13535.t1	ref|NP_198119.1| histone H2A 7 [Arabidopsis thaliana] gi|75306451|sp|Q94F49.1|H2A5_ARATH RecName: Full=Probable histone H2A.5; AltName: Full=HTA7 gi|14326516|gb|AAK60303.1|AF385711_1 AT5g27670/F15A18_130 [Arabidopsis thaliana] gi|18700220|gb|AAL77720.1| AT5g27670/F15A18_130 [Arabidopsis thaliana] gi|332006330|gb|AED93713.1| histone H2A 7 [Arabidopsis thaliana]	158	150	5.00E-65	94.9	82.3	87.3	histone H2A 7	gbpln	Arabidopsis thaliana	AT5G27670.1 | Symbols: HTA7 | histone H2A 7 | chr5:9792807-9793365 REVERSE LENGTH=150	158	150	2.00E-67	94.9	82.3	87.3
Rsa1.0_00421.1.g13536.t1	gb|EOA22209.1| hypothetical protein CARUB_v10002793mg [Capsella rubella]	674	668	0	99.1	81.6	89.2	hypothetical protein CARUB_v10002793mg	gbpln	Capsella rubella	AT5G27630.1 | Symbols: ACBP5 | acyl-CoA binding protein 5 | chr5:9776101-9780780 FORWARD LENGTH=648	674	648	0	96.1	80.4	88.0
Rsa1.0_00421.1.g13537.t6	ref|NP_198113.2| protein ALWAYS EARLY 1 [Arabidopsis thaliana] gi|296439606|sp|Q6A331.2|ALY1_ARATH RecName: Full=Protein ALWAYS EARLY 1; Short=AtALY1 gi|225898943|dbj|BAH30602.1| hypothetical protein [Arabidopsis thaliana] gi|332006323|gb|AED93706.1| protein ALWAYS EARLY 1 [Arabidopsis thaliana]	1244	971	0	78.1	48.1	56.8	protein ALWAYS EARLY 1	gbpln	Arabidopsis thaliana	AT5G27610.1 | Symbols: ATALY1, ALY1 | DIRP ;Myb-like DNA-binding domain | chr5:9764852-9769706 FORWARD LENGTH=971	1244	971	0	78.1	48.1	56.8
Rsa1.0_00421.1.g13538.t1	gb|EOA19994.1| hypothetical protein CARUB_v10000259mg [Capsella rubella]	778	793	0	101.9	84.8	91.1	hypothetical protein CARUB_v10000259mg	gbpln	Capsella rubella	AT5G27550.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:9727634-9731323 REVERSE LENGTH=765	778	765	0	98.3	84.1	90.5
Rsa1.0_00421.1.g13539.t1	gb|EOA20124.1| hypothetical protein CARUB_v10000404mg, partial [Capsella rubella]	644	664	0	103.1	91.1	96.0	hypothetical protein CARUB_v10000404mg, partial	gbpln	Capsella rubella	AT5G27540.2 | Symbols: MIRO1 | MIRO-related GTP-ase 1 | chr5:9722816-9727112 FORWARD LENGTH=648	644	648	0	100.6	90.8	96.1
Rsa1.0_00421.1.g13540.t1	ref|NP_198099.1| seryl-tRNA synthetase [Arabidopsis thaliana] gi|2501056|sp|Q39230.1|SYS_ARATH RecName: Full=Serine--tRNA ligase; AltName: Full=Seryl-tRNA synthetase; Short=SerRS; AltName: Full=Seryl-tRNA(Ser/Sec) synthetase gi|13507571|gb|AAK28648.1|AF360352_1 putative seryl-tRNA synthetase [Arabidopsis thaliana] gi|1359497|emb|CAA94388.1| seryl-tRNA Synthetase [Arabidopsis thaliana] gi|15293241|gb|AAK93731.1| putative seryl-tRNA synthetase [Arabidopsis thaliana] gi|332006309|gb|AED93692.1| seryl-tRNA synthetase [Arabidopsis thaliana]	451	451	0	100.0	92.0	95.8	seryl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT5G27470.1 | Symbols: | seryl-tRNA synthetase / serine--tRNA ligase | chr5:9695087-9697154 FORWARD LENGTH=451	451	451	0	100.0	92.0	95.8
Rsa1.0_00421.1.g13541.t1	ref|XP_002874371.1| hypothetical protein ARALYDRAFT_489582 [Arabidopsis lyrata subsp. lyrata] gi|297320208|gb|EFH50630.1| hypothetical protein ARALYDRAFT_489582 [Arabidopsis lyrata subsp. lyrata]	386	378	0	97.9	84.2	91.5	hypothetical protein ARALYDRAFT_489582	gbpln	Arabidopsis lyrata	AT5G27450.3 | Symbols: MK | mevalonate kinase | chr5:9691051-9692975 FORWARD LENGTH=378	386	378	0	97.9	84.2	91.2
Rsa1.0_00421.1.g13542.t1	ref|NP_198095.1| Signal peptidase complex subunit 3B [Arabidopsis thaliana] gi|75270222|sp|Q53YF3.1|SPC3B_ARATH RecName: Full=Signal peptidase complex subunit 3B; AltName: Full=Microsomal signal peptidase 22 kDa subunit; Short=SPC22; Short=SPase 22 kDa subunit gi|3044218|gb|AAC13316.1| signal peptidase [Arabidopsis thaliana] gi|28393474|gb|AAO42158.1| putative signal peptidase [Arabidopsis thaliana] gi|28973603|gb|AAO64126.1| putative signal peptidase [Arabidopsis thaliana] gi|332006303|gb|AED93686.1| Signal peptidase complex subunit 3B [Arabidopsis thaliana]	90	167	3.00E-44	185.6	93.3	96.7	Signal peptidase complex subunit 3B	gbpln	Arabidopsis thaliana	AT5G27430.1 | Symbols: | Signal peptidase subunit | chr5:9687470-9689185 FORWARD LENGTH=167	90	167	5.00E-47	185.6	93.3	96.7

Rsa1.0_00422.1.g13543.t1	ref|XP_002878123.1| OBP3-responsive gene 3 [Arabidopsis lyrata subsp. lyrata] gi|297323961|gb|EFH54382.1| OBP3-responsive gene 3 [Arabidopsis lyrata subsp. lyrata]	85	258	2.00E-29	303.5	78.8	88.2	OBP3-responsive gene 3	gbpln	Arabidopsis lyrata	AT3G56980.1 | Symbols: BHLH039, ORG3 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:21086612-21087494 REVERSE LENGTH=258	85	258	6.00E-32	303.5	80.0	88.2
Rsa1.0_00422.1.g13544.t1	ref|NP_191256.1| transcription factor ORG2 [Arabidopsis thaliana] gi|75311784|sp|Q9M1K1.1|ORG2_ARATH RecName: Full=Transcription factor ORG2; AltName: Full=Basic helix-loop-helix protein 38; Short=AtbHLH38; Short=bHLH 38; AltName: Full=OBP3-responsive gene 2; AltName: Full=Transcription factor EN 8; AltName: Full=bHLH transcription factor bHLH038 gi|20127034|gb|AAM10940.1|AF488576_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|6911867|emb|CAB72167.1| putative protein [Arabidopsis thaliana] gi|62320432|dbj|BAD94899.1| putative bHLH transcription factor [Arabidopsis thaliana] gi|111074306|gb|ABH04526.1| At3g56970 [Arabidopsis thaliana] gi|332646073|gb|AEE79594.1| transcription factor ORG2 [Arabidopsis thaliana]	183	253	4.00E-60	138.3	63.9	72.1	transcription factor ORG2	gbpln	Arabidopsis thaliana	AT3G56970.1 | Symbols: BHLH038, ORG2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:21084204-21085094 REVERSE LENGTH=253	183	253	1.00E-62	138.3	63.9	72.1
Rsa1.0_00422.1.g13545.t1	gb|EOA23522.1| hypothetical protein CARUB_v10016715mg [Capsella rubella]	773	778	0	100.6	92.2	97.0	hypothetical protein CARUB_v10016715mg	gbpln	Capsella rubella	AT3G56960.1 | Symbols: PIP5K4 | phosphatidyl inositol monophosphate 5 kinase 4 | chr3:21080957-21083885 FORWARD LENGTH=779	773	779	0	100.8	91.7	96.2
Rsa1.0_00422.1.g13546.t1	ref|XP_002878121.1| SIP2_1 [Arabidopsis lyrata subsp. lyrata] gi|297323959|gb|EFH54380.1| SIP2_1 [Arabidopsis lyrata subsp. lyrata]	101	237	1.00E-40	234.7	82.2	89.1	SIP2_1	gbpln	Arabidopsis lyrata	AT3G56950.1 | Symbols: SIP2;1, SIP2 | small and basic intrinsic protein 2;1 | chr3:21078586-21079644 REVERSE LENGTH=237	101	237	6.00E-42	234.7	79.2	88.1
Rsa1.0_00422.1.g13547.t1	ref|NP_001190113.1| putative aquaporin SIP2-1 [Arabidopsis thaliana] gi|332646071|gb|AEE79592.1| putative aquaporin SIP2-1 [Arabidopsis thaliana]	98	260	4.00E-47	265.3	88.8	98.0	putative aquaporin SIP2-1	gbpln	Arabidopsis thaliana	AT3G56950.2 | Symbols: SIP2;1 | small and basic intrinsic protein 2;1 | chr3:21078411-21079644 REVERSE LENGTH=260	98	260	7.00E-50	265.3	88.8	98.0
Rsa1.0_00422.1.g13548.t1	gb|EOA24121.1| hypothetical protein CARUB_v10017355mg [Capsella rubella]	57	409	6.00E-15	717.5	73.7	75.4	hypothetical protein CARUB_v10017355mg	gbpln	Capsella rubella	AT3G56940.1 | Symbols: CRD1, CHL27, ACSF | dicarboxylate diiron protein, putative (Crd1) | chr3:21076594-21078269 FORWARD LENGTH=409	57	409	9.00E-16	717.5	66.7	71.9
Rsa1.0_00422.1.g13549.t1	gb|EOA24894.1| hypothetical protein CARUB_v10018185mg [Capsella rubella]	139	151	2.00E-23	108.6	80.6	88.5	hypothetical protein CARUB_v10018185mg	gbpln	Capsella rubella	AT3G56910.1 | Symbols: PSRP5 | plastid-specific 50S ribosomal protein 5 | chr3:21069558-21070257 REVERSE LENGTH=148	139	148	5.00E-25	106.5	78.4	84.2
Rsa1.0_00422.1.g13550.t1	ref|XP_002876384.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322222|gb|EFH52643.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	233	242	2.00E-75	103.9	75.1	83.7	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT3G56880.1 | Symbols: | VQ motif-containing protein | chr3:21060044-21060781 FORWARD LENGTH=245	233	245	6.00E-77	105.2	73.4	81.5
Rsa1.0_00422.1.g13551.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	237	478	4.00E-68	201.7	47.3	70.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	237	746	1.00E-55	314.8	40.9	58.6
Rsa1.0_00422.1.g13552.t1	dbj|BAJ33737.1| unnamed protein product [Thellungiella halophila]	433	479	1.00E-142	110.6	63.0	68.8	unnamed protein product	----	----	AT3G56860.5 | Symbols: UBA2A | UBP1-associated protein 2A | chr3:21050708-21052144 REVERSE LENGTH=478	433	478	1.00E-138	110.4	60.0	66.3
Rsa1.0_00422.1.g13553.t1	ref|XP_002878113.1| aba-responsive element binding protein 3 [Arabidopsis lyrata subsp. lyrata] gi|297323951|gb|EFH54372.1| aba-responsive element binding protein 3 [Arabidopsis lyrata subsp. lyrata]	284	299	1.00E-107	105.3	81.7	85.2	aba-responsive element binding protein 3	gbpln	Arabidopsis lyrata	AT3G56850.1 | Symbols: AREB3, DPBF3 | ABA-responsive element binding protein 3 | chr3:21046554-21047894 REVERSE LENGTH=297	284	297	1.00E-109	104.6	79.2	83.1
Rsa1.0_00422.1.g13554.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00422.1.g13555.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00422.1.g13556.t1	gb|EOA24368.1| hypothetical protein CARUB_v10017605mg [Capsella rubella]	326	333	1.00E-127	102.1	77.3	86.5	hypothetical protein CARUB_v10017605mg	gbpln	Capsella rubella	AT3G56810.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 14 Blast hits to 14 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:21036927-21038927 REVERSE LENGTH=332	326	332	1.00E-129	101.8	75.5	85.3
Rsa1.0_00422.1.g13557.t1	gb|EOA27855.1| hypothetical protein CARUB_v10024013mg [Capsella rubella]	149	224	2.00E-80	150.3	100.0	100.0	hypothetical protein CARUB_v10024013mg	gbpln	Capsella rubella	AT2G27030.3 | Symbols: CAM5 | calmodulin 5 | chr2:11532069-11534176 FORWARD LENGTH=181	149	181	9.00E-83	121.5	100.0	100.0
Rsa1.0_00422.1.g13558.t1	ref|XP_002878108.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297323946|gb|EFH54367.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	231	232	1.00E-85	100.4	73.6	87.0	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT3G56770.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:21029202-21030618 REVERSE LENGTH=230	231	230	9.00E-82	99.6	71.9	84.8
Rsa1.0_00422.1.g13559.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00422.1.g13560.t1	ref|NP_191235.1| protein kinase-domain containing protein [Arabidopsis thaliana] gi|75334901|sp|Q9LET1.1|CAMK7_ARATH RecName: Full=CDPK-related kinase 7; Short=AtCRK7; AltName: Full=Calcium/calmodulin-dependent protein kinase CRK7 gi|9662995|emb|CAC00739.1| calcium-dependent protein kinase-like [Arabidopsis thaliana] gi|332646041|gb|AEE79562.1| CDPK-related kinase 7 [Arabidopsis thaliana]	574	577	0	100.5	89.4	93.4	protein kinase-domain containing protein	gbpln	Arabidopsis thaliana	AT3G56760.1 | Symbols: | Protein kinase superfamily protein | chr3:21020661-21023756 REVERSE LENGTH=577	574	577	0	100.5	89.4	93.4
Rsa1.0_00422.1.g13561.t1	ref|XP_002878104.1| hypothetical protein ARALYDRAFT_486111 [Arabidopsis lyrata subsp. lyrata] gi|297323942|gb|EFH54363.1| hypothetical protein ARALYDRAFT_486111 [Arabidopsis lyrata subsp. lyrata]	155	155	2.00E-41	100.0	62.6	71.0	hypothetical protein ARALYDRAFT_486111	gbpln	Arabidopsis lyrata	AT3G56710.1 | Symbols: SIB1 | sigma factor binding protein 1 | chr3:21007053-21007508 REVERSE LENGTH=151	155	151	9.00E-44	97.4	60.0	67.1
Rsa1.0_00422.1.g13562.t1	ref|XP_002878104.1| hypothetical protein ARALYDRAFT_486111 [Arabidopsis lyrata subsp. lyrata] gi|297323942|gb|EFH54363.1| hypothetical protein ARALYDRAFT_486111 [Arabidopsis lyrata subsp. lyrata]	151	155	2.00E-46	102.6	68.2	74.8	hypothetical protein ARALYDRAFT_486111	gbpln	Arabidopsis lyrata	AT3G56710.1 | Symbols: SIB1 | sigma factor binding protein 1 | chr3:21007053-21007508 REVERSE LENGTH=151	151	151	2.00E-47	100.0	64.9	74.2
Rsa1.0_00422.1.g13563.t1	ref|XP_002878101.1| CIP111 [Arabidopsis lyrata subsp. lyrata] gi|297323939|gb|EFH54360.1| CIP111 [Arabidopsis lyrata subsp. lyrata]	245	1025	6.00E-89	418.4	72.2	81.2	CIP111	gbpln	Arabidopsis lyrata	AT3G56690.1 | Symbols: CIP111 | Cam interacting protein 111 | chr3:20993869-20998531 REVERSE LENGTH=1022	245	1022	7.00E-91	417.1	71.4	81.6
Rsa1.0_00422.1.g13564.t1	ref|XP_002876378.1| hypothetical protein ARALYDRAFT_486108 [Arabidopsis lyrata subsp. lyrata] gi|297322216|gb|EFH52637.1| hypothetical protein ARALYDRAFT_486108 [Arabidopsis lyrata subsp. lyrata]	350	354	1.00E-133	101.1	73.4	82.0	hypothetical protein ARALYDRAFT_486108	gbpln	Arabidopsis lyrata	AT3G56680.1 | Symbols: | Single-stranded nucleic acid binding R3H protein | chr3:20991537-20993446 FORWARD LENGTH=353	350	353	1.00E-135	100.9	72.3	80.6
Rsa1.0_00423.1.g13565.t1	ref|NP_187901.1| trypsin-like protein [Arabidopsis thaliana] gi|15795124|dbj|BAB02502.1| unnamed protein product [Arabidopsis thaliana] gi|45773814|gb|AAS76711.1| At3g12950 [Arabidopsis thaliana] gi|52627109|gb|AAU84681.1| At3g12950 [Arabidopsis thaliana] gi|332641744|gb|AEE75265.1| trypsin-like protein [Arabidopsis thaliana]	529	558	0	105.5	94.3	96.6	trypsin-like protein	gbpln	Arabidopsis thaliana	AT3G12950.1 | Symbols: | Trypsin family protein | chr3:4132798-4134818 REVERSE LENGTH=558	529	558	0	105.5	94.3	96.6
Rsa1.0_00423.1.g13566.t1	ref|NP_566440.1| SAUR-like auxin-responsive family protein [Arabidopsis thaliana] gi|15795125|dbj|BAB02503.1| unnamed protein product [Arabidopsis thaliana] gi|89111858|gb|ABD60701.1| At3g12955 [Arabidopsis thaliana] gi|332641745|gb|AEE75266.1| SAUR-like auxin-responsive family protein [Arabidopsis thaliana]	140	139	7.00E-69	99.3	90.7	96.4	SAUR-like auxin-responsive family protein	gbpln	Arabidopsis thaliana	AT3G12955.1 | Symbols: | SAUR-like auxin-responsive protein family | chr3:4135659-4136078 REVERSE LENGTH=139	140	139	2.00E-71	99.3	90.7	96.4

Rsa1.0_00423.1.g13567.t1	ref|NP_187902.1| uncharacterized protein [Arabidopsis thaliana] gi|15795126|dbj|BAB02504.1| unnamed protein product [Arabidopsis thaliana] gi|48596999|gb|AAT46040.1| At3g12960 [Arabidopsis thaliana] gi|52627125|gb|AAU84689.1| At3g12960 [Arabidopsis thaliana] gi|332641746|gb|AEE75267.1| uncharacterized protein AT3G12960 [Arabidopsis thaliana]	89	86	1.00E−29	96.6	77.5	87.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G12960.1 | Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 14 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 44; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:4136546−4136806 FORWARD LENGTH=86	89	86	2.00E−32	96.6	77.5	87.6
Rsa1.0_00423.1.g13568.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00423.1.g13569.t1	ref|XP_002882800.1| histone acetyltransferase 5 [Arabidopsis lyrata subsp. lyrata] gi|297328640|gb|EFH59059.1| histone acetyltransferase 5 [Arabidopsis lyrata subsp. lyrata]	1646	1657	0	100.7	79.8	86.8	histone acetyltransferase 5	gbpln	Arabidopsis lyrata	AT3G12980.1 | Symbols: HAC5, ATHPCAT4 | histone acetyltransferase of the CBP family 5 | chr3:4146919−4154495 FORWARD LENGTH=1670	1646	1670	0	101.5	79.5	87.2
Rsa1.0_00423.1.g13570.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00423.1.g13571.t1	ref|NP_187908.1| hAT dimerization domain−containing protein [Arabidopsis thaliana] gi|15795134|dbj|BAB02512.1| transposase−like protein [Arabidopsis thaliana] gi|332641756|gb|AEE75277.1| hAT dimerization domain−containing protein [Arabidopsis thaliana]	529	605	1.00E−174	114.4	63.5	77.5	hAT dimerization domain−containing protein	gbpln	Arabidopsis thaliana	AT3G13020.1 | Symbols: | hAT transposon superfamily protein | chr3:4166995−4168917 REVERSE LENGTH=605	529	605	1.00E−176	114.4	63.5	77.5
Rsa1.0_00423.1.g13572.t1	ref|NP_181350.2| lactosylceramide 4−alpha−galactosyltransferase [Arabidopsis thaliana] gi|330254401|gb|AEC09495.1| alpha 1,4−glycosyltransferase family protein [Arabidopsis thaliana]	402	405	0	100.7	79.9	88.6	lactosylceramide 4−alpha−galactosyltransferase	gbpln	Arabidopsis thaliana	AT2G38150.1 | Symbols: | alpha 1,4−glycosyltransferase family protein | chr2:15981700−15982917 REVERSE LENGTH=405	402	405	0	100.7	79.9	88.6
Rsa1.0_00423.1.g13573.t1	ref|NP_187908.1| hAT dimerization domain−containing protein [Arabidopsis thaliana] gi|15795134|dbj|BAB02512.1| transposase−like protein [Arabidopsis thaliana] gi|332641756|gb|AEE75277.1| hAT dimerization domain−containing protein [Arabidopsis thaliana]	623	605	0	97.1	60.2	75.3	hAT dimerization domain−containing protein	gbpln	Arabidopsis thaliana	AT3G13020.1 | Symbols: | hAT transposon superfamily protein | chr3:4166995−4168917 REVERSE LENGTH=605	623	605	0	97.1	60.2	75.3
Rsa1.0_00423.1.g13574.t1	dbj|BAB02514.1| transfactor−like protein [Arabidopsis thaliana]	446	554	0	124.2	78.7	85.9	transfactor−like protein	gbpln	Arabidopsis thaliana	AT3G13040.2 | Symbols: | myb−like HTH transcriptional regulator family protein | chr3:4172415−4174456 REVERSE LENGTH=449	446	449	0	100.7	79.6	86.3
Rsa1.0_00423.1.g13575.t1	gb|EOA32797.1| hypothetical protein CARUB_v10016107mg [Capsella rubella]	504	500	0	99.2	82.7	90.1	hypothetical protein CARUB_v10016107mg	gbpln	Capsella rubella	AT3G13050.1 | Symbols: | Major facilitator superfamily protein | chr3:4176866−4178868 FORWARD LENGTH=500	504	500	0	99.2	81.0	88.5
Rsa1.0_00423.1.g13576.t1	ref|XP_002882804.1| hypothetical protein ARALYDRAFT_478675 [Arabidopsis lyrata subsp. lyrata] gi|297328644|gb|EFH59063.1| hypothetical protein ARALYDRAFT_478675 [Arabidopsis lyrata subsp. lyrata]	620	635	0	102.4	87.6	91.8	hypothetical protein ARALYDRAFT_478675	gbpln	Arabidopsis lyrata	AT3G13060.2 | Symbols: ECT5 | evolutionarily conserved C−terminal region 5 | chr3:4180625−4183632 FORWARD LENGTH=634	620	634	0	102.3	87.4	91.9
Rsa1.0_00423.1.g13577.t8	ref|NP_850574.1| lipid−binding START domain−containing protein [Arabidopsis thaliana] gi|332641765|gb|AEE75286.1| lipid−binding START domain−containing protein [Arabidopsis thaliana]	109	411	3.00E−29	377.1	69.7	77.1	lipid−binding START domain−containing protein	gbpln	Arabidopsis thaliana	AT3G13062.3 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr3:4184777−4186795 FORWARD LENGTH=411	109	411	5.00E−32	377.1	69.7	77.1
Rsa1.0_00423.1.g13578.t1	dbj|BAD11207.1| multidrug resistance−associated protein [Thlaspi caerulescens]	1486	1514	0	101.9	86.1	92.3	multidrug resistance−associated protein	gbpln	Thlaspi caerulescens	AT3G13080.1 | Symbols: ATMRP3, MRP3, ABCC3 | multidrug resistance−associated protein 3 | chr3:4196019−4201250 REVERSE LENGTH=1514	1486	1514	0	101.9	84.3	91.9
Rsa1.0_00423.1.g13579.t1	ref|XP_002884942.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330782|gb|EFH61201.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1459	1463	0	100.3	84.3	92.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G13090.1 | Symbols: ATMRP8, ABCC6, MRP8 | multidrug resistance−associated protein 8 | chr3:4203013−4208171 REVERSE LENGTH=1466	1459	1466	0	100.5	83.3	92.1
Rsa1.0_00423.1.g13580.t1	gb|AAL14776.1| ATP−binding cassette transporter MRP6 [Arabidopsis thaliana]	1574	1466	0	93.1	77.4	84.5	ATP−binding cassette transporter MRP6	gbpln	Arabidopsis thaliana	AT3G13090.1 | Symbols: ATMRP8, ABCC6, MRP8 | multidrug resistance−associated protein 8 | chr3:4203013−4208171 REVERSE LENGTH=1466	1574	1466	0	93.1	77.4	84.6
Rsa1.0_00423.1.g13581.t1	gb|ABL97980.1| 30S ribosomal protein S10−like [Brassica rapa]	192	193	4.00E−83	100.5	88.0	91.7	30S ribosomal protein S10−like	gbpln	Brassica rapa	AT3G13120.2 | Symbols: | Ribosomal protein S10p/S20e family protein | chr3:4220310−4221526 REVERSE LENGTH=191	192	191	3.00E−74	99.5	81.3	84.9

Rsa1.0_00423.1.g13582.t1	ref|NP_187921.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|10172601|dbj|BAB01405.1| unnamed protein product [Arabidopsis thaliana] gi|67633630|gb|AAY78739.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|332641780|gb|AEE75301.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	188	183	1.00E-25	97.3	42.0	55.3	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT3G13140.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr3:4226654-4227377 REVERSE LENGTH=183	188	183	4.00E-28	97.3	42.0	55.3
Rsa1.0_00423.1.g13583.t1	ref|NP_187922.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75311241|sp|Q9LK58.1|PP225_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g13150 gi|10172602|dbj|BAB01406.1| unnamed protein product [Arabidopsis thaliana] gi|66792658|gb|AAY56431.1| At3g13150 [Arabidopsis thaliana] gi|332641781|gb|AEE75302.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	426	551	0	129.3	77.2	87.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G13150.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:4227975-4229630 REVERSE LENGTH=551	426	551	0	129.3	77.2	87.8
Rsa1.0_00423.1.g13584.t1	gb|EOA31905.1| hypothetical protein CARUB_v10015134mg [Capsella rubella]	391	394	0	100.8	82.6	92.1	hypothetical protein CARUB_v10015134mg	gbpln	Capsella rubella	AT3G13160.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:4229994-4231178 REVERSE LENGTH=394	391	394	0	100.8	81.3	90.3
Rsa1.0_00423.1.g13585.t1	ref|XP_002884949.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330789|gb|EFH61208.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	377	362	0	96.0	83.3	87.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G13170.1 | Symbols: ATSPO11-1 | Spo11/DNA topoisomerase VI, subunit A protein | chr3:4231560-4234192 REVERSE LENGTH=362	377	362	0	96.0	82.5	87.8
Rsa1.0_00424.1.g13586.t1	ref|NP_191330.1| protein kinase family protein [Arabidopsis thaliana] gi|4678276|emb|CAB41184.1| putative protein [Arabidopsis thaliana] gi|21537362|gb|AAM61703.1| protein kinase-like protein [Arabidopsis thaliana] gi|51968400|dbj|BAD42892.1| protein kinase - like protein [Arabidopsis thaliana] gi|51969234|dbj|BAD43309.1| protein kinase - like protein [Arabidopsis thaliana] gi|51969278|dbj|BAD43331.1| protein kinase - like protein [Arabidopsis thaliana] gi|332646167|gb|AEE79688.1| protein kinase family protein [Arabidopsis thaliana]	316	351	7.00E-83	111.1	55.1	71.5	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G57710.1 | Symbols: | Protein kinase superfamily protein | chr3:21386233-21387288 REVERSE LENGTH=351	316	351	2.00E-85	111.1	55.1	71.5
Rsa1.0_00424.1.g13587.t1	ref|NP_191330.1| protein kinase family protein [Arabidopsis thaliana] gi|4678276|emb|CAB41184.1| putative protein [Arabidopsis thaliana] gi|21537362|gb|AAM61703.1| protein kinase-like protein [Arabidopsis thaliana] gi|51968400|dbj|BAD42892.1| protein kinase - like protein [Arabidopsis thaliana] gi|51969234|dbj|BAD43309.1| protein kinase - like protein [Arabidopsis thaliana] gi|51969278|dbj|BAD43331.1| protein kinase - like protein [Arabidopsis thaliana] gi|332646167|gb|AEE79688.1| protein kinase family protein [Arabidopsis thaliana]	204	351	1.00E-45	172.1	54.9	73.5	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G57710.1 | Symbols: | Protein kinase superfamily protein | chr3:21386233-21387288 REVERSE LENGTH=351	204	351	4.00E-48	172.1	54.9	73.5
Rsa1.0_00424.1.g13588.t1	gb|EOA25819.1| hypothetical protein CARUB_v10019188mg [Capsella rubella]	355	349	6.00E-94	98.3	51.0	64.2	hypothetical protein CARUB_v10019188mg	gbpln	Capsella rubella	AT3G57710.1 | Symbols: | Protein kinase superfamily protein | chr3:21386233-21387288 REVERSE LENGTH=351	355	351	9.00E-95	98.9	50.4	65.6
Rsa1.0_00424.1.g13589.t1	ref|NP_191329.1| putative protein kinase [Arabidopsis thaliana] gi|4678277|emb|CAB41185.1| protein kinase-like protein [Arabidopsis thaliana] gi|332646168|gb|AEE79689.1| putative protein kinase [Arabidopsis thaliana]	341	340	1.00E-157	99.7	80.9	90.9	putative protein kinase	gbpln	Arabidopsis thaliana	AT3G57700.1 | Symbols: | Protein kinase superfamily protein | chr3:21384917-21385939 FORWARD LENGTH=340	341	340	1.00E-160	99.7	80.9	90.9

Rsa1.0_00424.1.g13590.t1	gb|EOA28140.1| hypothetical protein CARUB_v10024329mg [Capsella rubella]	61	123	3.00E-17	201.6	80.3	93.4	hypothetical protein CARUB_v10024329mg	gbpln	Capsella rubella	AT2G41905.1 | Symbols: | BEST Arabidopsis thaliana protein match is: arabinogalactan protein 23 (TAIR:AT3G57690.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17495766-17495951 FORWARD LENGTH=61	61	61	1.00E-19	100.0	83.6	93.4
Rsa1.0_00424.1.g13591.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00424.1.g13592.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1336	1213	0	90.8	40.3	49.7	unknown protein	gbpln	Arabidopsis thaliana	AT3G57670.1 | Symbols: NTT, WIP2 | C2H2-type zinc finger family protein | chr3:21370936-21373121 FORWARD LENGTH=383	1336	383	1.00E-155	28.7	23.6	24.5
Rsa1.0_00424.1.g13593.t1	gb|ADC97478.1| lysophosphatidic acid acyltransferase [Brassica napus] gi|289472613|gb|ADC97480.1| lysophosphatidic acid acyltransferase [Brassica napus]	403	390	0	96.8	81.4	85.9	lysophosphatidic acid acyltransferase	gbpln	Brassica napus	AT3G57650.1 | Symbols: LPAT2 | lysophosphatidyl acyltransferase 2 | chr3:21349751-21352839 FORWARD LENGTH=389	403	389	0	96.5	80.4	84.6
Rsa1.0_00424.1.g13594.t2	ref|NP_191320.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|2500026|sp|Q96529.1|PURA_ARATH RecName: Full=Adenylosuccinate synthetase, chloroplastic; Short=AMPSase; Short=AdSS; AltName: Full=IMP--aspartate ligase; Flags: Precursor gi|1616657|gb|AAB16828.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|4678286|emb|CAB41194.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|15451052|gb|AAK96797.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|20148265|gb|AAM10023.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|332646157|gb|AEE79678.1| adenylosuccinate synthetase [Arabidopsis thaliana]	550	490	0	89.1	82.2	85.5	adenylosuccinate synthetase	gbpln	Arabidopsis thaliana	AT3G57610.1 | Symbols: ADSS | adenylosuccinate synthase | chr3:21334519-21336603 REVERSE LENGTH=490	550	490	0	89.1	82.2	85.5
Rsa1.0_00424.1.g13595.t1	gb|EOA24542.1| hypothetical protein CARUB_v10017800mg [Capsella rubella]	249	278	1.00E-101	111.6	77.1	86.3	hypothetical protein CARUB_v10017800mg	gbpln	Capsella rubella	AT3G57600.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:21332841-21333674 FORWARD LENGTH=277	249	277	1.00E-101	111.2	75.5	85.9
Rsa1.0_00424.1.g13596.t1	ref|XP_002876425.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297322263|gb|EFH52684.1| binding protein [Arabidopsis lyrata subsp. lyrata]	145	1082	2.00E-24	746.2	45.5	58.6	binding protein	gbpln	Arabidopsis lyrata	AT3G57570.2 | Symbols: | ARM repeat superfamily protein | chr3:21312598-21320105 FORWARD LENGTH=1096	145	1096	1.00E-26	755.9	45.5	57.9
Rsa1.0_00424.1.g13597.t1	ref|XP_002878162.1| aspartate/glutamate/uridylate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297324000|gb|EFH54421.1| aspartate/glutamate/uridylate kinase family protein [Arabidopsis lyrata subsp. lyrata]	339	346	1.00E-167	102.1	92.9	95.3	aspartate/glutamate/uridylate kinase family protein	gbpln	Arabidopsis lyrata	AT3G57560.1 | Symbols: NAGK | N-acetyl-l-glutamate kinase | chr3:21311164-21312207 REVERSE LENGTH=347	339	347	1.00E-166	102.4	91.4	94.7
Rsa1.0_00424.1.g13598.t1	gb|EOA24182.1| hypothetical protein CARUB_v10017419mg [Capsella rubella]	378	389	0	102.9	91.3	96.0	hypothetical protein CARUB_v10017419mg	gbpln	Capsella rubella	AT3G57550.1 | Symbols: AGK2, GK-2 | guanylate kinase | chr3:21307269-21309193 FORWARD LENGTH=389	378	389	0	102.9	89.9	95.8
Rsa1.0_00424.1.g13599.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1256	1307	0	104.1	60.3	72.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1256	1262	8.00E-70	100.5	12.6	19.8
Rsa1.0_00424.1.g13600.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00425.1.g13601.t1	ref|XP_002892072.1| hypothetical protein ARALYDRAFT_470143 [Arabidopsis lyrata subsp. lyrata] gi|297337914|gb|EFH68331.1| hypothetical protein ARALYDRAFT_470143 [Arabidopsis lyrata subsp. lyrata]	239	241	3.00E-93	100.8	73.6	81.6	hypothetical protein ARALYDRAFT_470143	gbpln	Arabidopsis lyrata	AT1G01310.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr1:120221-120946 FORWARD LENGTH=241	239	241	2.00E-92	100.8	70.7	80.3
Rsa1.0_00425.1.g13602.t3	ref|NP_001184884.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332189151|gb|AEE27272.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	1780	1787	0	100.4	88.6	93.3	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G01320.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:121582-130099 REVERSE LENGTH=1787	1780	1787	0	100.4	88.6	93.3

<table>
<tr><td>Rsa1.0_00425.1.g13603.t2</td><td>gb|EOA38162.1| hypothetical protein CARUB_v10009639mg [Capsella rubella]</td><td>403</td><td>342</td><td>1.00E-167</td><td>84.9</td><td>74.9</td><td>79.2</td><td>hypothetical protein CARUB_v10009639mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G01350.1 | Symbols: | Zinc finger (CCCH-type/C3HC4-type RING finger) family protein | chr1:136732-137970 FORWARD LENGTH=343</td><td>403</td><td>343</td><td>1.00E-161</td><td>85.1</td><td>74.2</td><td>78.9</td></tr>
<tr><td>Rsa1.0_00425.1.g13604.t1</td><td>dbj|BAF63139.1| hypothetical protein [Arabidopsis suecica]</td><td>198</td><td>189</td><td>2.00E-93</td><td>95.5</td><td>82.8</td><td>87.4</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis suecica</td><td>AT1G01360.1 | Symbols: RCAR1, PYL9 | regulatory component of ABA receptor 1 | chr1:142138-142914 FORWARD LENGTH=187</td><td>198</td><td>187</td><td>3.00E-95</td><td>94.4</td><td>82.3</td><td>87.9</td></tr>
<tr><td>Rsa1.0_00425.1.g13605.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00425.1.g13606.t1</td><td>dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]</td><td>107</td><td>329</td><td>2.00E-17</td><td>307.5</td><td>41.1</td><td>57.0</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00425.1.g13607.t1</td><td>ref|XP_002889367.1| hypothetical protein ARALYDRAFT_887310 [Arabidopsis lyrata subsp. lyrata] gi|297335209|gb|EFH65626.1| hypothetical protein ARALYDRAFT_887310 [Arabidopsis lyrata subsp. lyrata]</td><td>549</td><td>663</td><td>1.00E-170</td><td>120.8</td><td>68.9</td><td>78.1</td><td>hypothetical protein ARALYDRAFT_887310</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01440.1 | Symbols: | Protein of unknown function (DUF3133) | chr1:159935-162219 REVERSE LENGTH=664</td><td>549</td><td>664</td><td>1.00E-170</td><td>120.9</td><td>68.5</td><td>78.3</td></tr>
<tr><td>Rsa1.0_00425.1.g13608.t1</td><td>ref|XP_002889366.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335208|gb|EFH65625.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>292</td><td>970</td><td>1.00E-108</td><td>332.2</td><td>71.9</td><td>78.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01453.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01110.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:166853-167798 REVERSE LENGTH=267</td><td>292</td><td>267</td><td>1.00E-105</td><td>91.4</td><td>70.9</td><td>79.1</td></tr>
<tr><td>Rsa1.0_00425.1.g13609.t2</td><td>ref|XP_002892064.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297337906|gb|EFH68323.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>419</td><td>426</td><td>0</td><td>101.7</td><td>89.5</td><td>95.0</td><td>phosphatidylinositol-4-phosphate 5-kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01460.1 | Symbols: ATPIPK11, PIPK11 | Phosphatidylinositol-4-phosphate 5-kinase, core | chr1:169115-171154 FORWARD LENGTH=427</td><td>419</td><td>427</td><td>0</td><td>101.9</td><td>90.2</td><td>94.7</td></tr>
<tr><td>Rsa1.0_00425.1.g13610.t1</td><td>ref|XP_002892062.1| 1-amino-cyclopropane-1-carboxylate synthase 2 [Arabidopsis lyrata subsp. lyrata] gi|297337904|gb|EFH68321.1| 1-amino-cyclopropane-1-carboxylate synthase 2 [Arabidopsis lyrata subsp. lyrata]</td><td>499</td><td>496</td><td>0</td><td>99.4</td><td>86.6</td><td>92.2</td><td>1-amino-cyclopropane-1-carboxylate synthase 2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01480.1 | Symbols: ACS2, AT-ACC2 | 1-amino-cyclopropane-1-carboxylate synthase 2 | chr1:175862-178051 FORWARD LENGTH=496</td><td>499</td><td>496</td><td>0</td><td>99.4</td><td>85.2</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00425.1.g13611.t1</td><td>ref|XP_002889363.1| hypothetical protein ARALYDRAFT_887301 [Arabidopsis lyrata subsp. lyrata] gi|297335205|gb|EFH65622.1| hypothetical protein ARALYDRAFT_887301 [Arabidopsis lyrata subsp. lyrata]</td><td>177</td><td>177</td><td>2.00E-53</td><td>100.0</td><td>97.2</td><td>98.3</td><td>hypothetical protein ARALYDRAFT_887301</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01490.2 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:180401-182066 REVERSE LENGTH=177</td><td>177</td><td>177</td><td>1.00E-55</td><td>100.0</td><td>95.5</td><td>97.7</td></tr>
<tr><td>Rsa1.0_00425.1.g13612.t1</td><td>gb|EOA25182.1| hypothetical protein CARUB_v10018494mg [Capsella rubella]</td><td>259</td><td>282</td><td>3.00E-31</td><td>108.9</td><td>34.4</td><td>52.9</td><td>hypothetical protein CARUB_v10018494mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>259</td><td>303</td><td>5.00E-32</td><td>117.0</td><td>33.2</td><td>49.0</td></tr>
<tr><td>Rsa1.0_00425.1.g13613.t2</td><td>ref|NP_563629.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|75274951|sp|O23702.1|CTBP_ARATH RecName: Full=C-terminal binding protein AN; Short=CtBP; AltName: Full=Protein ANGUSTIFOLIA gi|2505877|emb|CAA73306.1| dehydrogenase [Arabidopsis thaliana] gi|332189177|gb|AEE27298.1| C-terminal binding protein AN [Arabidopsis thaliana]</td><td>630</td><td>636</td><td>0</td><td>101.0</td><td>91.3</td><td>96.0</td><td>Rossmann-fold NAD(P)-binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G01510.1 | Symbols: AN | NAD(P)-binding Rossmann-fold superfamily protein | chr1:187235-189836 FORWARD LENGTH=636</td><td>630</td><td>636</td><td>0</td><td>101.0</td><td>91.3</td><td>96.0</td></tr>
<tr><td>Rsa1.0_00425.1.g13614.t1</td><td>gb|EOA39056.1| hypothetical protein CARUB_v10011679mg [Capsella rubella]</td><td>275</td><td>273</td><td>1.00E-113</td><td>99.3</td><td>77.1</td><td>85.1</td><td>hypothetical protein CARUB_v10011679mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G01520.1 | Symbols: | Homeodomain-like superfamily protein | chr1:190596-192139 FORWARD LENGTH=287</td><td>275</td><td>287</td><td>1.00E-110</td><td>104.4</td><td>75.6</td><td>84.7</td></tr>
<tr><td>Rsa1.0_00425.1.g13615.t1</td><td>ref|XP_002892058.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297337900|gb|EFH68317.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>458</td><td>472</td><td>0</td><td>103.1</td><td>94.5</td><td>97.2</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G01540.2 | Symbols: | Protein kinase superfamily protein | chr1:195980-198383 FORWARD LENGTH=472</td><td>458</td><td>472</td><td>0</td><td>103.1</td><td>94.3</td><td>96.9</td></tr>
</table>

Rsa1.0_00425.1.g13616.t1	ref|NP_563630.1| protein BPS1 [Arabidopsis thaliana] gi|79316260|ref|NP_001030929.1| protein BPS1 [Arabidopsis thaliana] gi|75174796|sp|Q9LMM6.1|BPS1_ARATH RecName: Full=Protein BPS1, chloroplastic; AltName: Full=Protein BYPASS 1; Flags: Precursor gi|8920591|gb|AAF81313.1|AC061957_9 Contains similarity to an unknown protein T3F17.27 gi|3702339 from Arabidopsis thaliana BAC T3F17 gb|AC005397. ESTs gb|T43647, gb|H36161, gb|T22185, gb|Z37624, gb|AI100650 come from this gene [Arabidopsis thaliana] gi|13194834|gb|AAK15579.1|AF349532_1 unknown protein [Arabidopsis thaliana] gi|16648871|gb|AAL24287.1| Unknown protein [Arabidopsis thaliana] gi|17380900|gb|AAL36262.1| unknown protein [Arabidopsis thaliana] gi|20259587|gb|AAM14136.1| unknown protein [Arabidopsis thaliana] gi|23197666|gb|AAN15360.1| Unknown protein [Arabidopsis thaliana] gi|24417250|gb|AAN60235.1| unknown [Arabidopsis thaliana] gi|332189182|gb|AEE27303.1| protein BPS1 [Arabidopsis thaliana] gi|332189183|gb|AEE27304.1| protein BPS1 [Arabidopsis thaliana]	350	349	1.00E-178	99.7	88.3	94.6	protein BPS1	gbpln	Arabidopsis thaliana	AT1G01550.2 | Symbols: BPS1 | Protein of unknown function (DUF793) | chr1:200526-201575 FORWARD LENGTH=349	350	349	0	99.7	88.3	94.6
Rsa1.0_00425.1.g13617.t1	gb|EOA36874.1| hypothetical protein CARUB_v10008901mg [Capsella rubella]	517	507	0	98.1	78.5	86.8	hypothetical protein CARUB_v10008901mg	gbpln	Capsella rubella	AT1G01570.1 | Symbols: | Protein of unknown function (DUF604) | chr1:205176-207435 FORWARD LENGTH=478	517	478	0	92.5	72.7	81.6
Rsa1.0_00425.1.g13618.t1	gb|EOA39785.1| hypothetical protein CARUB_v10008441mg [Capsella rubella]	702	723	0	103.0	83.5	91.3	hypothetical protein CARUB_v10008441mg	gbpln	Capsella rubella	AT1G01580.1 | Symbols: FRO2, FRD1, ATFRO2 | ferric reduction oxidase 2 | chr1:209395-212810 FORWARD LENGTH=725	702	725	0	103.3	81.5	90.5
Rsa1.0_00425.1.g13619.t1	ref|XP_002892051.1| CYP86A4 [Arabidopsis lyrata subsp. lyrata] gi|297337893|gb|EFH68310.1| CYP86A4 [Arabidopsis lyrata subsp. lyrata]	551	554	0	100.5	91.1	95.8	CYP86A4	gbpln	Arabidopsis lyrata	AT1G01600.1 | Symbols: CYP86A4 | cytochrome P450, family 86, subfamily A, polypeptide 4 | chr1:219200-220994 FORWARD LENGTH=554	551	554	0	100.5	90.4	95.5
Rsa1.0_00425.1.g13620.t1	gb|AFH02722.1| sn-glycerol-3-phosphate acyltransferase 4 isoform C2 [Brassica napus] gi|383289235|gb|AFH02725.1| sn-glycerol-3-phosphate acyltransferase 4 isoform C2 [Brassica napus]	503	503	0	100.0	98.4	99.4	sn-glycerol-3-phosphate acyltransferase 4 isoform C2	gbpln	Brassica napus	AT1G01610.1 | Symbols: ATGPAT4, GPAT4 | glycerol-3-phosphate acyltransferase 4 | chr1:221950-224255 REVERSE LENGTH=503	503	503	0	100.0	95.0	98.0
Rsa1.0_00425.1.g13621.t1	ref|XP_003604065.1| DEAD-box ATP-dependent RNA helicase [Medicago truncatula] gi|355493113|gb|AES74316.1| DEAD-box ATP-dependent RNA helicase [Medicago truncatula]	213	568	1.00E-13	266.7	23.9	30.0	DEAD-box ATP-dependent RNA helicase	gbpln	Medicago truncatula	AT3G06980.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr3:2201531-2204662 FORWARD LENGTH=781	213	781	2.00E-15	366.7	16.4	16.9
Rsa1.0_00425.1.g13622.t1	dbj|BAJ34288.1| unnamed protein product [Thellungiella halophila]	286	286	1.00E-162	100.0	97.9	100.0	unnamed protein product	----	----	AT4G00430.1 | Symbols: TMP-C, PIP1;4, PIP1E | plasma membrane intrinsic protein 1;4 | chr4:186143-187531 REVERSE LENGTH=287	286	287	1.00E-162	100.3	97.9	99.7
Rsa1.0_00425.1.g13623.t1	ref|XP_002892050.1| hypothetical protein ARALYDRAFT_470113 [Arabidopsis lyrata subsp. lyrata] gi|297337892|gb|EFH68309.1| hypothetical protein ARALYDRAFT_470113 [Arabidopsis lyrata subsp. lyrata]	258	256	1.00E-131	99.2	86.8	92.2	hypothetical protein ARALYDRAFT_470113	gbpln	Arabidopsis lyrata	AT1G01630.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:229206-230675 FORWARD LENGTH=255	258	255	1.00E-132	98.8	85.3	91.5

Rsa1.0_00425.1.g13624.t1	ref|NP_171670.1| BTB/POZ domain-containing protein [Arabidopsis thaliana] gi|30678163|ref|NP_849574.1| BTB/POZ domain-containing protein [Arabidopsis thaliana] gi|75311457|sp|Q9LQ95.1|Y1164_ARATH RecName: Full=BTB/POZ domain-containing protein At1g01640 gi|8671833|gb|AAF78396.1|AC009273_2 Contains similarity to the speckle-type POZ protein from Homo sapiens gb|AJ000644. It contains a BTB/POZ domain PF|00651 [Arabidopsis thaliana] gi|332189194|gb|AEE27315.1| BTB/POZ domain-containing protein [Arabidopsis thaliana] gi|332189195|gb|AEE27316.1| BTB/POZ domain-containing protein [Arabidopsis thaliana]	216	207	4.00E-89	95.8	75.5	81.5	BTB/POZ domain-containing protein	gbpln	Arabidopsis thaliana	AT1G01640.2 | Symbols: | BTB/POZ domain-containing protein | chr1:231164-231915 REVERSE LENGTH=207	216	207	1.00E-91	95.8	75.5	81.5
Rsa1.0_00425.1.g13625.t2	ref|NP_171671.2| signal peptide peptidase-like 4 [Arabidopsis thaliana] gi|403377882|sp|Q0WMJ8.1|SIPL4_ARATH RecName: Full=Signal peptide peptidase-like 4; Short=AtSPPL4; Flags: Precursor gi|110739487|dbj|BAF01653.1| hypothetical protein [Arabidopsis thaliana] gi|332189196|gb|AEE27317.1| signal peptide peptidase-like 4 [Arabidopsis thaliana]	538	540	0	100.4	89.8	93.3	signal peptide peptidase-like 4	gbpln	Arabidopsis thaliana	AT1G01650.1 | Symbols: SPPL4, ATSPPL4 | SIGNAL PEPTIDE PEPTIDASE-LIKE 4 | chr1:233188-237647 REVERSE LENGTH=540	538	540	0	100.4	89.8	93.3
Rsa1.0_00425.1.g13626.t1	gb|AAF78397.1|AC009273_3 Contains similarity to a putative protein T2J13.100 gi|6522560 from Arabidopsis thaliana BAC T2J13 gb|AL132967 [Arabidopsis thaliana]	569	952	0	167.3	92.4	97.2	Contains similarity to a putative protein T2J13.100 gi|6522560 from Arabidopsis thaliana BAC T2J13 gb|AL132967	gbpln	Arabidopsis thaliana	AT1G01660.1 | Symbols: | RING/U-box superfamily protein | chr1:240057-242608 REVERSE LENGTH=568	569	568	0	99.8	92.1	96.8
Rsa1.0_00425.1.g13627.t1	gb|EOA40469.1| hypothetical protein CARUB_v10009194mg [Capsella rubella]	434	431	1.00E-150	99.3	68.4	78.6	hypothetical protein CARUB_v10009194mg	gbpln	Capsella rubella	AT1G01670.1 | Symbols: | RING/U-box superfamily protein | chr1:242943-245163 REVERSE LENGTH=365	434	365	1.00E-139	84.1	62.0	69.4
Rsa1.0_00425.1.g13628.t1	ref|XP_002889356.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335198|gb|EFH65615.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	309	309	1.00E-107	100.0	67.0	78.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G01680.1 | Symbols: ATPUB54, PUB54 | plant U-box 54 | chr1:246411-248329 REVERSE LENGTH=308	309	308	1.00E-108	99.7	65.7	77.3
Rsa1.0_00425.1.g13629.t2	dbj|BAJ33966.1| unnamed protein product [Thellungiella halophila]	276	431	1.00E-126	156.2	79.3	82.6	unnamed protein product	----	----	AT1G01710.1 | Symbols: | Acyl-CoA thioesterase family protein | chr1:262950-266029 FORWARD LENGTH=427	276	427	1.00E-122	154.7	74.6	80.4
Rsa1.0_00426.1.g13630.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1743	1214	0	69.7	39.0	49.4	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1743	626	8.00E-84	35.9	9.5	14.5
Rsa1.0_00426.1.g13631.t1	gb|EOA15756.1| hypothetical protein CARUB_v10006834mg [Capsella rubella]	315	332	1.00E-133	105.4	81.0	89.2	hypothetical protein CARUB_v10006834mg	gbpln	Capsella rubella	AT4G37850.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:17796362-17797647 REVERSE LENGTH=328	315	328	1.00E-131	104.1	74.9	84.1
Rsa1.0_00426.1.g13632.t1	ref|XP_002866928.1| hypothetical protein ARALYDRAFT_353053 [Arabidopsis lyrata subsp. lyrata] gi|297312764|gb|EFH43187.1| hypothetical protein ARALYDRAFT_353053 [Arabidopsis lyrata subsp. lyrata]	379	344	2.00E-77	90.8	50.4	63.9	hypothetical protein ARALYDRAFT_353053	gbpln	Arabidopsis lyrata	AT4G37860.1 | Symbols: | SPT2 chromatin protein | chr4:17800589-17801907 REVERSE LENGTH=354	379	354	3.00E-77	93.4	47.2	61.7

Rsa1.0_00426.1.g13633.t1	ref|NP_195500.1| phosphoenolpyruvate carboxykinase [ATP] [Arabidopsis thaliana] gi|12230482|sp|Q9T074.1|PEPCK_ARATH RecName: Full=Phosphoenolpyruvate carboxykinase [ATP]; Short=PEP carboxykinase; Short=PEPCK; AltName: Full=Phosphoenolpyruvate carboxylase gi|13937137|gb|AAK50062.1|AF372922_1 AT4g37870/T28I19_150 [Arabidopsis thaliana] gi|4490732|emb|CAB38935.1| phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana] gi|7270770|emb|CAB80452.1| phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana] gi|18700252|gb|AAL77736.1| AT4g37870/T28I19_150 [Arabidopsis thaliana] gi|110740763|dbj|BAE98480.1| phosphoenolpyruvate carboxykinase (ATP) -like protein [Arabidopsis thaliana] gi|332661447|gb|AEE86847.1| phosphoenolpyruvate carboxykinase [ATP] [Arabidopsis thaliana]	666	671	0	100.8	96.8	98.2	phosphoenolpyruvate carboxykinase	gbpln	Arabidopsis thaliana	AT4G37870.1 | Symbols: PCK1, PEPCK | phosphoenolpyruvate carboxykinase 1 | chr4:17802974-17806332 REVERSE LENGTH=671	666	671	0	100.8	96.8	98.2
Rsa1.0_00426.1.g13634.t1	ref|XP_002866923.1| hypothetical protein ARALYDRAFT_327981 [Arabidopsis lyrata subsp. lyrata] gi|297312759|gb|EFH43182.1| hypothetical protein ARALYDRAFT_327981 [Arabidopsis lyrata subsp. lyrata]	432	643	0	148.8	87.5	93.1	hypothetical protein ARALYDRAFT_327981	gbpln	Arabidopsis lyrata	AT4G37920.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast, chloroplast envelope; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G36320.1); Has 123 Blast hits to 120 proteins in 40 species: Archae - 2; Bacteria - 11; Metazoa - 8; Fungi - 0; Plants - 85; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr4:17828538-17830317 REVERSE LENGTH=427	432	427	0	98.8	87.0	92.1
Rsa1.0_00426.1.g13635.t1	gb|EOA16298.1| hypothetical protein CARUB_v10004441mg, partial [Capsella rubella]	517	583	0	112.8	97.3	99.4	hypothetical protein CARUB_v10004441mg, partial	gbpln	Capsella rubella	AT4G37930.1 | Symbols: SHM1, STM, SHMT1 | serine transhydroxymethyltransferase 1 | chr4:17831891-17834742 REVERSE LENGTH=517	517	517	0	100.0	97.5	99.2
Rsa1.0_00426.1.g13636.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	254	1555	3.00E-48	612.2	40.6	56.7	disease resistance protein	gbpln	Brassica rapa	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	254	303	3.00E-24	119.3	29.1	45.3
Rsa1.0_00426.1.g13637.t1	ref|XP_002868956.1| hypothetical protein ARALYDRAFT_490819 [Arabidopsis lyrata subsp. lyrata] gi|297314792|gb|EFH45215.1| hypothetical protein ARALYDRAFT_490819 [Arabidopsis lyrata subsp. lyrata]	362	363	0	100.3	89.0	94.8	hypothetical protein ARALYDRAFT_490819	gbpln	Arabidopsis lyrata	AT4G37970.1 | Symbols: ATCAD6, CAD6 | cinnamyl alcohol dehydrogenase 6 | chr4:17849672-17852145 FORWARD LENGTH=363	362	363	0	100.3	88.1	94.8
Rsa1.0_00426.1.g13638.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00426.1.g13639.t1	dbj|BAJ33843.1| unnamed protein product [Thellungiella halophila]	363	358	1.00E-173	98.6	86.8	92.8	unnamed protein product	----	----	AT4G37980.1 | Symbols: ELI3-1, ELI3, ATCAD7, CAD7 | elicitor-activated gene 3-1 | chr4:17852670-17854302 FORWARD LENGTH=357	363	357	1.00E-169	98.3	82.4	90.1
Rsa1.0_00426.1.g13640.t1	ref|XP_002868951.1| tRNA/rRNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314787|gb|EFH45210.1| tRNA/rRNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	587	355	1.00E-159	60.5	48.6	54.0	tRNA/rRNA methyltransferase family protein	gbpln	Arabidopsis lyrata	AT4G38020.1 | Symbols: | tRNA/rRNA methyltransferase (SpoU) family protein | chr4:17861568-17863010 FORWARD LENGTH=352	587	352	1.00E-159	60.0	47.5	52.5
Rsa1.0_00426.1.g13641.t1	gb|EOA16170.1| hypothetical protein CARUB_v10004306mg [Capsella rubella]	656	668	0	101.8	80.5	88.7	hypothetical protein CARUB_v10004306mg	gbpln	Capsella rubella	AT4G38030.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr4:17863206-17866730 REVERSE LENGTH=667	656	667	0	101.7	80.5	87.3
Rsa1.0_00426.1.g13642.t1	gb|EOA16680.1| hypothetical protein CARUB_v10004872mg [Capsella rubella]	410	426	0	103.9	91.7	96.8	hypothetical protein CARUB_v10004872mg	gbpln	Capsella rubella	AT4G38040.1 | Symbols: | Exostosin family protein | chr4:17867501-17869131 FORWARD LENGTH=425	410	425	0	103.7	90.7	96.8
Rsa1.0_00426.1.g13643.t1	gb|EOA16123.1| hypothetical protein CARUB_v10004255mg [Capsella rubella]	714	710	0	99.4	81.8	88.1	hypothetical protein CARUB_v10004255mg	gbpln	Capsella rubella	AT4G38050.1 | Symbols: | Xanthine/uracil permease family protein | chr4:17869529-17872461 REVERSE LENGTH=709	714	709	0	99.3	79.8	86.8

Rsa1.0_00426.1.g13644.t1	ref|XP_002866917.1| hypothetical protein ARALYDRAFT_490808 [Arabidopsis lyrata subsp. lyrata] gi|297312753|gb|EFH43176.1| hypothetical protein ARALYDRAFT_490808 [Arabidopsis lyrata subsp. lyrata]	124	126	8.00E-31	101.6	66.1	75.0	hypothetical protein ARALYDRAFT_490808	gbpln	Arabidopsis lyrata	AT4G38060.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65480.1); Has 63 Blast hits to 63 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17874002-17874379 REVERSE LENGTH=125	124	125	3.00E-32	100.8	66.1	76.6
Rsa1.0_00426.1.g13645.t1	gb|EOA18943.1| hypothetical protein CARUB_v10007575mg [Capsella rubella]	143	138	1.00E-28	96.5	73.4	81.8	hypothetical protein CARUB_v10007575mg	gbpln	Capsella rubella	AT4G40090.1 | Symbols: AGP3 | arabinogalactan protein 3 | chr4:18581085-18581504 REVERSE LENGTH=139	143	139	3.00E-28	97.2	74.8	83.2
Rsa1.0_00426.1.g13646.t1	ref|NP_195718.1| putative clathrin assembly protein [Arabidopsis thaliana] gi|46395895|sp|Q8L936.2|CAP16_ARATH RecName: Full=Putative clathrin assembly protein At4g40080 gi|5918311|emb|CAB56391.1| putative protein [Arabidopsis thaliana] gi|7271063|emb|CAB80671.1| putative protein [Arabidopsis thaliana] gi|119360027|gb|ABL66742.1| At4g40080 [Arabidopsis thaliana] gi|332661765|gb|AEE87165.1| putative clathrin assembly protein [Arabidopsis thaliana]	365	365	1.00E-177	100.0	83.3	90.1	putative clathrin assembly protein	gbpln	Arabidopsis thaliana	AT4G40080.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr4:18579371-18580542 FORWARD LENGTH=365	365	365	1.00E-180	100.0	83.3	90.1
Rsa1.0_00427.1.g13647.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	1371	1239	0	90.4	59.7	73.0	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1371	1262	4.00E-97	92.0	13.9	21.4
Rsa1.0_00427.1.g13648.t1	gb|EOA27737.1| hypothetical protein CARUB_v10023890mg [Capsella rubella]	258	258	1.00E-100	100.0	79.1	85.7	hypothetical protein CARUB_v10023890mg	gbpln	Capsella rubella	AT2G21160.1 | Symbols: | Translocon-associated protein (TRAP), alpha subunit | chr2:9068428-9070207 FORWARD LENGTH=258	258	258	4.00E-99	100.0	76.0	85.3
Rsa1.0_00427.1.g13649.t2	gb|EOA27531.1| hypothetical protein CARUB_v10023671mg [Capsella rubella]	320	315	1.00E-150	98.4	88.1	91.3	hypothetical protein CARUB_v10023671mg	gbpln	Capsella rubella	AT2G21170.1 | Symbols: TIM, PDTPI | triosephosphate isomerase | chr2:9071047-9073106 REVERSE LENGTH=315	320	315	1.00E-150	98.4	88.8	90.6
Rsa1.0_00427.1.g13650.t1	ref|XP_002878538.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324377|gb|EFH54797.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	101	93	2.00E-36	92.1	72.3	74.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G21195.1 | Symbols: | unknown protein; Has 28 Blast hits to 28 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9083191-9083687 FORWARD LENGTH=93	101	93	7.00E-39	92.1	71.3	74.3
Rsa1.0_00427.1.g13651.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00427.1.g13652.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00427.1.g13653.t1	gb|EOA26967.1| hypothetical protein CARUB_v10023063mg [Capsella rubella] gi|482562778|gb|EOA26968.1| hypothetical protein CARUB_v10023063mg [Capsella rubella]	472	500	1.00E-165	105.9	75.2	81.4	hypothetical protein CARUB_v10023063mg	gbpln	Capsella rubella	AT2G21230.1 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:9093920-9096059 REVERSE LENGTH=519	472	519	1.00E-162	110.0	75.8	81.1
Rsa1.0_00427.1.g13654.t1	gb|AAL87314.1| unknown protein [Arabidopsis thaliana]	405	547	1.00E-26	135.1	24.0	33.3	unknown protein	gbpln	Arabidopsis thaliana	AT4G38900.3 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:18139564-18141520 REVERSE LENGTH=547	405	547	3.00E-29	135.1	24.0	33.3
Rsa1.0_00427.1.g13655.t1	ref|XP_002880369.1| ATBPC4/BBR/BPC4/BPC4 [Arabidopsis lyrata subsp. lyrata] gi|297326208|gb|EFH56628.1| ATBPC4/BBR/BPC4/BPC4 [Arabidopsis lyrata subsp. lyrata]	443	296	1.00E-127	66.8	52.6	55.8	ATBPC4/BBR/BPC4/BPC4	gbpln	Arabidopsis lyrata	AT2G21240.2 | Symbols: BPC4, BBR, ATBPC4 | basic pentacysteine 4 | chr2:9101515-9102489 REVERSE LENGTH=296	443	296	1.00E-125	66.8	49.9	53.7
Rsa1.0_00427.1.g13656.t1	gb|EOA29062.1| hypothetical protein CARUB_v10025318mg [Capsella rubella]	335	320	1.00E-161	95.5	86.3	89.6	hypothetical protein CARUB_v10025318mg	gbpln	Capsella rubella	AT2G21270.3 | Symbols: UFD1 | ubiquitin fusion degradation 1 | chr2:9107841-9110012 FORWARD LENGTH=340	335	340	1.00E-160	101.5	86.0	88.4
Rsa1.0_00427.1.g13657.t1	ref|XP_002880372.1| hypothetical protein ARALYDRAFT_900542 [Arabidopsis lyrata subsp. lyrata] gi|297326211|gb|EFH56631.1| hypothetical protein ARALYDRAFT_900542 [Arabidopsis lyrata subsp. lyrata]	350	350	1.00E-179	100.0	86.0	91.1	hypothetical protein ARALYDRAFT_900542	gbpln	Arabidopsis lyrata	AT2G21280.1 | Symbols: GC1, ATSULA, SULA | NAD(P)-binding Rossmann-fold superfamily protein | chr2:9110502-9112679 REVERSE LENGTH=347	350	347	0	99.1	90.9	95.1

Rsa1.0_00427.1.g13658.t1	ref|XP_002513001.1| 30S ribosomal protein S31, mitochondrial precursor, putative [Ricinus communis] gi|223548012|gb|EEF49504.1| 30S ribosomal protein S31, mitochondrial precursor, putative [Ricinus communis]	86	87	1.00E-27	101.2	75.6	87.2	30S ribosomal protein S31, mitochondrial precursor, putative	gbpln	Ricinus communis	AT2G21290.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 63 Blast hits to 63 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9112888-9113184 FORWARD LENGTH=98	86	98	1.00E-29	114.0	84.9	88.4
Rsa1.0_00427.1.g13659.t1	ref|XP_002880373.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] gi|297326212|gb|EFH56632.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	840	862	0	102.6	89.0	93.5	kinesin motor family protein	gbpln	Arabidopsis lyrata	AT2G21300.2 | Symbols: | ATP binding microtubule motor family protein | chr2:9114396-9118292 REVERSE LENGTH=862	840	862	0	102.6	88.8	93.1
Rsa1.0_00427.1.g13660.t1	dbj|BAJ33780.1| unnamed protein product [Thellungiella halophila]	394	399	0	101.3	95.7	97.7	unnamed protein product	----	----	AT2G21330.1 | Symbols: FBA1 | fructose-bisphosphate aldolase 1 | chr2:9128416-9130152 REVERSE LENGTH=399	394	399	0	101.3	93.7	96.7
Rsa1.0_00427.1.g13661.t1	ref|NP_179731.4| RNA-binding CRS1 / YhbY (CRM) domain protein [Arabidopsis thaliana] gi|330252071|gb|AEC07165.1| RNA-binding CRS1 / YhbY (CRM) domain protein [Arabidopsis thaliana]	229	222	4.00E-55	96.9	58.1	68.1	RNA-binding CRS1 / YhbY (CRM) domain protein	gbpln	Arabidopsis thaliana	AT2G21350.1 | Symbols: | RNA-binding CRS1 / YhbY (CRM) domain protein | chr2:9136451-9137267 REVERSE LENGTH=222	229	222	1.00E-57	96.9	58.1	68.1
Rsa1.0_00427.1.g13662.t1	ref|NP_179735.1| SHI-related sequence protein [Arabidopsis thaliana] gi|4567272|gb|AAD23685.1| hypothetical protein [Arabidopsis thaliana] gi|330252080|gb|AEC07174.1| SHI-related sequence protein [Arabidopsis thaliana]	237	174	1.00E-65	73.4	55.7	62.4	SHI-related sequence protein	gbpln	Arabidopsis thaliana	AT2G21400.1 | Symbols: SRS3 | SHI-related sequence3 | chr2:9158390-9159541 FORWARD LENGTH=174	237	174	3.00E-68	73.4	55.7	62.4
Rsa1.0_00427.1.g13663.t1	ref|NP_179742.2| SUMO-activating enzyme subunit 2 [Arabidopsis thaliana] gi|26450535|dbj|BAC42380.1| putative ubiquitin activating enzyme [Arabidopsis thaliana] gi|208879522|gb|ACI31306.1| At2g21470 [Arabidopsis thaliana] gi|330252087|gb|AEC07181.1| SUMO-activating enzyme subunit 2 [Arabidopsis thaliana]	634	625	0	98.6	89.7	93.4	SUMO-activating enzyme subunit 2	gbpln	Arabidopsis thaliana	AT2G21470.1 | Symbols: SAE2, ATSAE2, EMB2764 | SUMO-activating enzyme 2 | chr2:9198752-9202136 FORWARD LENGTH=625	634	625	0	98.6	89.7	93.4
Rsa1.0_00427.1.g13664.t1	ref|NP_179743.1| Malectin/receptor-like protein kinase [Arabidopsis thaliana] gi|75337322|sp|Q9SJT0.1|Y2214_ARATH RecName: Full=Probable receptor-like protein kinase At2g21480; Flags: Precursor gi|4567279|gb|AAD23692.1| putative protein kinase [Arabidopsis thaliana] gi|330252090|gb|AEC07184.1| Malectin/receptor-like protein kinase [Arabidopsis thaliana]	851	871	0	102.4	85.1	90.5	Malectin/receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT2G21480.1 | Symbols: | Malectin/receptor-like protein kinase family protein | chr2:9202753-9205368 REVERSE LENGTH=871	851	871	0	102.4	85.1	90.5
Rsa1.0_00427.1.g13665.t1	gb|EOA29328.1| hypothetical protein CARUB_v10025610mg [Capsella rubella]	336	635	1.00E-169	189.0	86.3	91.1	hypothetical protein CARUB_v10025610mg	gbpln	Capsella rubella	AT2G21520.2 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr2:9215956-9218953 FORWARD LENGTH=637	336	637	1.00E-171	189.6	85.1	91.4
Rsa1.0_00427.1.g13666.t1	ref|NP_001189571.1| SEC14-like 3 protein [Arabidopsis thaliana] gi|330252100|gb|AEC07194.1| SEC14-like 3 protein [Arabidopsis thaliana]	544	542	0	99.6	87.3	93.8	SEC14-like 3 protein	gbpln	Arabidopsis thaliana	AT2G21540.3 | Symbols: SFH3 | SEC14-like 3 | chr2:9220831-9223737 REVERSE LENGTH=542	544	542	0	99.6	87.3	93.8
Rsa1.0_00427.1.g13667.t1	ref|XP_002880390.1| hypothetical protein ARALYDRAFT_481023 [Arabidopsis lyrata subsp. lyrata] gi|297326229|gb|EFH56649.1| hypothetical protein ARALYDRAFT_481023 [Arabidopsis lyrata subsp. lyrata]	218	265	6.00E-86	121.6	80.3	86.7	hypothetical protein ARALYDRAFT_481023	gbpln	Arabidopsis lyrata	AT2G21560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G39190.1); Has 3685 Blast hits to 2305 proteins in 270 species: Archae - 0; Bacteria - 156; Metazoa - 1145; Fungi - 322; Plants - 177; Viruses - 6; Other Eukaryotes - 1879 (source: NCBI BLink). | chr2:9230473-9231297 REVERSE LENGTH=274	218	274	7.00E-84	125.7	77.1	84.9
Rsa1.0_00427.1.g13668.t1	gb|EOA37750.1| hypothetical protein CARUB_v10012565mg [Capsella rubella]	221	679	2.00E-32	307.2	35.3	50.2	hypothetical protein CARUB_v10012565mg	gbpln	Capsella rubella	AT1G18560.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr1:6385614-6388005 FORWARD LENGTH=690	221	690	3.00E-14	312.2	19.0	29.4
Rsa1.0_00427.1.g13669.t1	#	#	#	#	#	#	#	–	----	----	AT5G59790.1 | Symbols: | Domain of unknown function (DUF966) | chr5:24090950-24092804 FORWARD LENGTH=423	40	423	4.00E-12	1057.5	80.0	80.0
Rsa1.0_00427.1.g13670.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00427.1.g13671.t1	ref|NP_195631.1| 40S ribosomal protein S25-4 [Arabidopsis thaliana] gi|30580493|sp|Q9T029.1|RS254_ARATH RecName: Full=40S ribosomal protein S25-4 gi|4914432|emb|CAB43635.1| ribosomal protein S25 [Arabidopsis thaliana] gi|7270903|emb|CAB80583.1| ribosomal protein S25 [Arabidopsis thaliana] gi|14335026|gb|AAK59777.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gi|16323232|gb|AAL15350.1| AT4g39200/T22F8_100 [Arabidopsis thaliana] gi|21553704|gb|AAM62797.1| ribosomal protein S25 [Arabidopsis thaliana] gi|332661636|gb|AEE87036.1| 40S ribosomal protein S25-4 [Arabidopsis thaliana] gi|482553510|gb|EOA17703.1| hypothetical protein CARUB_v10006075mg [Capsella rubella]	108	108	3.00E-55	100.0	99.1	100.0	40S ribosomal protein S25-4	gbpln	Arabidopsis thaliana	AT4G39200.1 | Symbols: | Ribosomal protein S25 family protein | chr4:18257464-18258464 FORWARD LENGTH=108	108	108	5.00E-58	100.0	99.1	100.0
Rsa1.0_00427.1.g13672.t1	gb|EOA26914.1| hypothetical protein CARUB_v10023004mg [Capsella rubella]	659	523	0	79.4	72.4	75.4	hypothetical protein CARUB_v10023004mg	gbpln	Capsella rubella	AT2G21590.2 | Symbols: APL4 | Glucose-1-phosphate adenylyltransferase family protein | chr2:9239362-9242150 FORWARD LENGTH=523	659	523	0	79.4	71.3	74.4
Rsa1.0_00427.1.g13673.t1	ref|NP_179755.1| pectinesterase 11 [Arabidopsis thaliana] gi|75206124|sp|Q9SIJ9.1|PME11_ARATH RecName: Full=Putative pectinesterase 11; Short=PE 11; AltName: Full=Pectin methylesterase 11; Short=AtPME11 gi|4567229|gb|AAD23644.1| putative pectinesterase [Arabidopsis thaliana] gi|330252108|gb|AEC07202.1| pectinesterase 11 [Arabidopsis thaliana]	316	352	1.00E-155	111.4	80.7	88.9	pectinesterase 11	gbpln	Arabidopsis thaliana	AT2G21610.1 | Symbols: PE11, ATPE11 | pectinesterase 11 | chr2:9245161-9247025 REVERSE LENGTH=352	316	352	1.00E-157	111.4	80.7	88.9
Rsa1.0_00427.1.g13674.t1	gb|EOA33402.1| hypothetical protein CARUB_v10020424mg [Capsella rubella]	462	394	0	85.3	71.4	76.2	hypothetical protein CARUB_v10020424mg	gbpln	Capsella rubella	AT1G80360.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr1:30208736-30210643 REVERSE LENGTH=394	462	394	0	85.3	70.6	75.5
Rsa1.0_00427.1.g13675.t2	ref|XP_002870488.1| AMP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297316324|gb|EFH46747.1| AMP binding protein [Arabidopsis lyrata subsp. lyrata]	747	743	0	99.5	92.6	95.6	AMP binding protein	gbpln	Arabidopsis lyrata	AT5G36880.2 | Symbols: ACS | acetyl-CoA synthetase | chr5:14534961-14540296 REVERSE LENGTH=743	747	743	0	99.5	91.8	95.2
Rsa1.0_00427.1.g13676.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00428.1.g13677.t1	emb|CAN68931.1| hypothetical protein VITISV_006966 [Vitis vinifera]	914	1021	0	111.7	64.8	78.9	hypothetical protein VITISV_006966	gbpln	Vitis vinifera	AT5G53890.1 | Symbols: PSKR2, AtPSKR2 | phytosylfokine-alpha receptor 2 | chr5:21877235-21880345 FORWARD LENGTH=1036	914	1036	0	113.3	55.8	61.3
Rsa1.0_00428.1.g13678.t2	ref|NP_200201.3| Serine/threonine-protein kinase-like protein [Arabidopsis thaliana] gi|10177252|dbj|BAB10720.1| unnamed protein product [Arabidopsis thaliana] gi|332009043|gb|AED96426.1| Serine/threonine-protein kinase-like protein [Arabidopsis thaliana]	376	377	0	100.3	92.0	94.9	Serine/threonine-protein kinase-like protein	gbpln	Arabidopsis thaliana	AT5G53900.2 | Symbols: | Serine/threonine-protein kinase WNK (With No Lysine)-related | chr5:21881375-21883133 REVERSE LENGTH=377	376	377	0	100.3	92.0	94.9
Rsa1.0_00428.1.g13679.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1664	1352	1.00E-173	81.3	20.6	29.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1664	746	9.00E-41	44.8	6.0	9.3
Rsa1.0_00428.1.g13680.t1	gb|EOA17344.1| hypothetical protein CARUB_v10005627mg [Capsella rubella]	216	238	1.00E-63	110.2	60.6	75.0	hypothetical protein CARUB_v10005627mg	gbpln	Capsella rubella	AT4G27540.1 | Symbols: PRA1.H | prenylated RAB acceptor 1.H | chr4:13753449-13754660 REVERSE LENGTH=241	216	241	2.00E-63	111.6	57.9	75.0
Rsa1.0_00428.1.g13681.t1	ref|XP_002864292.1| hypothetical protein ARALYDRAFT_495472 [Arabidopsis lyrata subsp. lyrata] gi|297310127|gb|EFH40551.1| hypothetical protein ARALYDRAFT_495472 [Arabidopsis lyrata subsp. lyrata]	349	368	1.00E-161	105.4	87.7	92.0	hypothetical protein ARALYDRAFT_495472	gbpln	Arabidopsis lyrata	AT5G53920.1 | Symbols: | ribosomal protein L11 methyltransferase-related | chr5:21892124-21894087 FORWARD LENGTH=371	349	371	1.00E-157	106.3	88.3	92.6

Rsa1.0_00428.1.g13682.t1	ref|NP_200204.1| uncharacterized protein [Arabidopsis thaliana] gi|10177255|dbj|BAB10723.1| unnamed protein product [Arabidopsis thaliana] gi|26453018|dbj|BAC43585.1| unknown protein [Arabidopsis thaliana] gi|28973163|gb|AAO63906.1| unknown protein [Arabidopsis thaliana] gi|332009047|gb|AED96430.1| uncharacterized protein AT5G53930 [Arabidopsis thaliana]	495	529	2.00E-99	106.9	48.5	56.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G53930.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:21894387-21896283 REVERSE LENGTH=529	495	529	1.00E-102	106.9	48.5	56.2
Rsa1.0_00428.1.g13683.t1	gb|EOA14167.1| hypothetical protein CARUB_v10027317mg, partial [Capsella rubella]	125	148	5.00E-59	118.4	91.2	95.2	hypothetical protein CARUB_v10027317mg, partial	gbpln	Capsella rubella	AT5G53940.1 | Symbols: | Yippee family putative zinc-binding protein | chr5:21897164-21898589 REVERSE LENGTH=129	125	129	2.00E-61	103.2	90.4	95.2
Rsa1.0_00428.1.g13684.t1	ref|XP_002866009.1| cup-shaped cotyledon2 [Arabidopsis lyrata subsp. lyrata] gi|297311844|gb|EFH42268.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	367	369	1.00E-168	100.5	86.4	92.9	cup-shaped cotyledon2	gbpln	Arabidopsis lyrata	AT5G53950.1 | Symbols: CUC2, ANAC098, ATCUC2 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr5:21901966-21903795 REVERSE LENGTH=375	367	375	1.00E-170	102.2	86.4	92.6
Rsa1.0_00428.1.g13685.t1	ref|NP_200208.1| tyrosine aminotransferase [Arabidopsis thaliana] gi|75171781|sp|Q9FN30.1|TAT2_ARATH RecName: Full=Probable aminotransferase TAT2; AltName: Full=Tyrosine aminotransferase 2 gi|10177259|dbj|BAB10727.1| tyrosine aminotransferase [Arabidopsis thaliana] gi|25054842|gb|AAN71911.1| putative tyrosine aminotransferase [Arabidopsis thaliana] gi|332009051|gb|AED96434.1| tyrosine aminotransferase [Arabidopsis thaliana]	417	414	0	99.3	93.3	95.4	tyrosine aminotransferase	gbpln	Arabidopsis thaliana	AT5G53970.1 | Symbols: | Tyrosine transaminase family protein | chr5:21910676-21912594 FORWARD LENGTH=414	417	414	0	99.3	93.3	95.4
Rsa1.0_00428.1.g13686.t1	ref|NP_850699.1| uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|332645635|gb|AEE79156.1| uracil phosphoribosyltransferase [Arabidopsis thaliana]	261	231	3.00E-12	88.5	14.9	17.2	uracil phosphoribosyltransferase	gbpln	Arabidopsis thaliana	AT3G53900.1 | Symbols: UPP, PYRR | uracil phosphoribosyltransferase | chr3:19956914-19958699 REVERSE LENGTH=231	261	231	7.00E-15	88.5	14.9	17.2
Rsa1.0_00428.1.g13687.t1	ref|XP_002864296.1| ATHB52 [Arabidopsis lyrata subsp. lyrata] gi|297310131|gb|EFH40555.1| ATHB52 [Arabidopsis lyrata subsp. lyrata]	154	156	2.00E-72	101.3	87.7	95.5	ATHB52	gbpln	Arabidopsis lyrata	AT5G53980.1 | Symbols: ATHB52, HB52 | homeobox protein 52 | chr5:21914087-21914557 FORWARD LENGTH=156	154	156	8.00E-73	101.3	86.4	93.5
Rsa1.0_00428.1.g13688.t1	ref|XP_002888294.1| glycosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334135|gb|EFH64553.1| glycosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	442	447	0	101.1	83.7	91.9	glycosyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G64910.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:24115324-24116667 REVERSE LENGTH=447	442	447	0	101.1	81.7	92.1
Rsa1.0_00428.1.g13689.t1	ref|NP_200210.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75171780|sp|Q9FN28.1|U79B9_ARATH RecName: Full=UDP-glycosyltransferase 79B9 gi|10177261|dbj|BAB10729.1| flavonol 3-O-glucosyltransferase-like protein [Arabidopsis thaliana] gi|17529306|gb|AAL38880.1| putative flavonol 3-O-glucosyltransferase [Arabidopsis thaliana] gi|20465447|gb|AAM20183.1| putative flavonol 3-O-glucosyltransferase [Arabidopsis thaliana] gi|332009053|gb|AED96436.1| UDP-glycosyltransferase 79B9 [Arabidopsis thaliana]	447	447	0	100.0	81.2	90.8	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G53990.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:21915707-21917050 REVERSE LENGTH=447	447	447	0	100.0	81.2	90.8
Rsa1.0_00428.1.g13690.t1	ref|XP_002870717.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297316553|gb|EFH46976.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	228	240	2.00E-27	105.3	36.4	57.5	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT5G40260.1 | Symbols: SWEET8, AtSWEET8 | Nodulin MtN3 family protein | chr5:16089842-16091527 FORWARD LENGTH=239	228	239	6.00E-29	104.8	36.8	54.8
Rsa1.0_00429.1.g13691.t1	emb|CAN69340.1| hypothetical protein VITISV_032634 [Vitis vinifera]	1123	1298	0	115.6	62.7	75.7	hypothetical protein VITISV_032634	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1123	1262	4.00E-67	112.4	13.6	19.9
Rsa1.0_00429.1.g13692.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00429.1.g13693.t1	gb|EOA36147.1| hypothetical protein CARUB_v10009836mg [Capsella rubella]	328	307	8.00E-82	93.6	63.4	72.6	hypothetical protein CARUB_v10009836mg	gbpln	Capsella rubella	AT1G49950.1 | Symbols: TRB1, ATTRB1 | telomere repeat binding factor 1 | chr1:18494439-18496713 REVERSE LENGTH=300	328	300	3.00E-81	91.5	63.1	70.7

Rsa1.0_00429.1.g13694.t1	ref|XP_002894225.1| hypothetical protein ARALYDRAFT_891918 [Arabidopsis lyrata subsp. lyrata] gi|297340067|gb|EFH70484.1| hypothetical protein ARALYDRAFT_891918 [Arabidopsis lyrata subsp. lyrata]	390	387	0	99.2	94.4	96.7	hypothetical protein ARALYDRAFT_891918	gbpln	Arabidopsis lyrata	AT1G49970.1 | Symbols: CLPR1, NCLPP5, SVR2 | CLP protease proteolytic subunit 1 | chr1:18501936-18504462 REVERSE LENGTH=387	390	387	0	99.2	93.3	96.2
Rsa1.0_00429.1.g13695.t1	ref|XP_002891550.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata] gi|297337392|gb|EFH67809.1| hypothetical protein ARALYDRAFT_474131 [Arabidopsis lyrata subsp. lyrata]	386	422	1.00E-75	109.3	46.1	58.3	hypothetical protein ARALYDRAFT_474131	gbpln	Arabidopsis lyrata	AT1G49990.1 | Symbols: | F-box family protein | chr1:18513696-18514988 FORWARD LENGTH=430	386	430	5.00E-72	111.4	44.0	57.0
Rsa1.0_00429.1.g13696.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00429.1.g13697.t1	ref|NP_171974.1| tubulin alpha-2/alpha-4 chain [Arabidopsis thaliana] gi|15222856|ref|NP_175423.1| tubulin alpha-2/alpha-4 chain [Arabidopsis thaliana] gi|297791421|ref|XP_002863595.1| tubulin alpha-2/alpha-4 chain [Arabidopsis lyrata subsp. lyrata] gi|297847340|ref|XP_002891551.1| tubulin alpha-2/alpha-4 chain [Arabidopsis lyrata subsp. lyrata] gi|408387609|sp|B9DGT7.2|TBA2_ARATH RecName: Full=Tubulin alpha-2 chain gi|408407917|sp|Q0WV25.2|TBA4_ARATH RecName: Full=Tubulin alpha-4 chain gi|7211983|gb|AAF40454.1|AC004809_12 Identical to the alpha-4 tubulin (TUA4) gene from A. thaliana gb|M84697. ESTs gb|T46564. gb|T04381, gb|T76028, gb|T21602, gb|H37154 gb|H37663 and gb|T21719 come from this gene [Arabidopsis thaliana] gi|8569104|gb|AAF76449.1|AC015445_16 Identical to Tubulin Alpha-6 Chain from Arabidopsis thaliana gi|267070 and contains a Tubulin PF|00091 domain. ESTs gb|N37387, gb|N37805, gb|R90497, gb|T44684, gb|H36144, gb|N38686, gb|AI994844, gb|R90689, gb|T04725, gb|H36928, gb|N96479, gb|H36922, gb|R90670, gb|Z17980, gb|T4428, gb|H36248, gb|N65408, gb|T46222 come from this gene [Arabidopsis thaliana] gi|15294278|gb|AAK95316.1|AF410330_1	450	450	0	100.0	99.8	100.0	tubulin alpha-2/alpha-4 chain	gbpln	Arabidopsis lyrata	AT1G50010.1 | Symbols: TUA2 | tubulin alpha-2 chain | chr1:18517737-18519729 FORWARD LENGTH=450	450	450	0	100.0	99.8	100.0
Rsa1.0_00429.1.g13698.t19	gb|AEH16576.1| target of rapamycin [Eutrema halophilum] gi|334855093|gb|AEH16577.1| target of rapamycin [Eutrema halophilum]	2519	2479	0	98.4	94.9	96.4	target of rapamycin	gbpln	Eutrema halophilum	AT1G50030.1 | Symbols: TOR | target of rapamycin | chr1:18522626-18539619 REVERSE LENGTH=2481	2519	2481	0	98.5	93.8	96.0
Rsa1.0_00429.1.g13699.t4	gb|EOA38839.1| hypothetical protein CARUB_v10011180mg [Capsella rubella]	856	1003	0	117.2	88.2	94.2	hypothetical protein CARUB_v10011180mg	gbpln	Capsella rubella	AT1G50200.1 | Symbols: ALATS, ACD | Alanyl-tRNA synthetase | chr1:18591429-18598311 REVERSE LENGTH=1003	856	1003	0	117.2	87.7	94.0
Rsa1.0_00429.1.g13700.t1	ref|XP_002891565.1| monosaccharide transporter [Arabidopsis lyrata subsp. lyrata] gi|297337407|gb|EFH67824.1| monosaccharide transporter [Arabidopsis lyrata subsp. lyrata]	516	517	0	100.2	92.2	96.1	monosaccharide transporter	gbpln	Arabidopsis lyrata	AT1G50310.1 | Symbols: ATSTP9, STP9 | sugar transporter 9 | chr1:18635984-18638110 FORWARD LENGTH=517	516	517	0	100.2	91.5	96.1
Rsa1.0_00429.1.g13701.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00429.1.g13702.t1	ref|XP_002891568.1| hypothetical protein ARALYDRAFT_474163 [Arabidopsis lyrata subsp. lyrata] gi|297337410|gb|EFH67827.1| hypothetical protein ARALYDRAFT_474163 [Arabidopsis lyrata subsp. lyrata]	1143	1153	0	100.9	86.4	92.3	hypothetical protein ARALYDRAFT_474163	gbpln	Arabidopsis lyrata	AT1G50360.1 | Symbols: VIIIA, ATVIIIA | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:18650688-18657106 FORWARD LENGTH=1153	1143	1153	0	100.9	85.8	92.0
Rsa1.0_00429.1.g13703.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1625	1529	0	94.1	28.4	45.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	1625	295	1.00E-39	18.2	5.7	9.1
Rsa1.0_00429.1.g13704.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00430.1.g13705.t19	ref|XP_002879161.1| VHA-A1 [Arabidopsis lyrata subsp. lyrata] gi|297325000|gb|EFH55420.1| VHA-A1 [Arabidopsis lyrata subsp. lyrata]	773	822	0	106.3	89.8	93.0	VHA-A1	gbpln	Arabidopsis lyrata	AT2G28520.1 | Symbols: VHA-A1 | vacuolar proton ATPase A1 | chr2:12210026-12215532 FORWARD LENGTH=817	773	817	0	105.7	87.8	91.5
Rsa1.0_00430.1.g13706.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00430.1.g13707.t1	gb|EOA27347.1| hypothetical protein CARUB_v10023462mg [Capsella rubella]	372	371	1.00E-160	99.7	82.5	90.1	hypothetical protein CARUB_v10023462mg	gbpln	Capsella rubella	AT2G28480.1 | Symbols: | RNA-binding CRS1 / YhbY (CRM) domain protein | chr2:12176642-12178031 REVERSE LENGTH=372	372	372	1.00E-151	100.0	76.6	81.2
Rsa1.0_00430.1.g13708.t1	dbj|BAD20774.2| beta-galactosidase [Raphanus sativus]	844	851	0	100.8	90.9	95.4	beta-galactosidase	gbpln	Raphanus sativus	AT2G28470.1 | Symbols: BGAL8 | beta-galactosidase 8 | chr2:12169047-12173164 REVERSE LENGTH=852	844	852	0	100.9	88.5	94.2
Rsa1.0_00430.1.g13709.t1	gb|AAB36545.1| ubiquitin-like protein [Phaseolus vulgaris]	229	407	1.00E-126	177.7	99.6	99.6	ubiquitin-like protein	gbpln	Phaseolus vulgaris	AT4G05320.4 | Symbols: UBQ10 | polyubiquitin 10 | chr4:2718559-2719932 FORWARD LENGTH=457	229	457	1.00E-128	199.6	99.6	99.6
Rsa1.0_00430.1.g13710.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00430.1.g13711.t1	ref|XP_002879099.1| sand family protein [Arabidopsis lyrata subsp. lyrata] gi|297324938|gb|EFH55358.1| sand family protein [Arabidopsis lyrata subsp. lyrata]	610	618	0	101.3	85.1	88.7	sand family protein	gbpln	Arabidopsis lyrata	AT2G28390.1 | Symbols: | SAND family protein | chr2:12139836-12143375 REVERSE LENGTH=607	610	607	0	99.5	84.1	88.4
Rsa1.0_00430.1.g13712.t2	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1852	1838	0	99.2	33.3	42.8	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00430.1.g13713.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00430.1.g13714.t1	gb|AAD17351.1| contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana] gi|7267432|emb|CAB77944.1| putative polyprotein [Arabidopsis thaliana]	536	1138	7.00E-92	212.3	30.8	37.3	contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00430.1.g13715.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00430.1.g13716.t1	ref|NP_565665.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|20197467|gb|AAM15087.1| Expressed protein [Arabidopsis thaliana] gi|91806281|gb|ABE65868.1| auxin-responsive family protein [Arabidopsis thaliana] gi|330252983|gb|AEC08077.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	124	124	5.00E-60	100.0	90.3	92.7	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT2G28085.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:11968182-11968556 REVERSE LENGTH=124	124	124	9.00E-63	100.0	90.3	92.7
Rsa1.0_00430.1.g13717.t1	gb|AAC13582.1| similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana] gi|8843876|dbj|BAA97402.1| mutator-like transposase [Arabidopsis thaliana]	130	806	3.00E-17	620.0	32.3	43.8	similar to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00430.1.g13718.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13719.t1	ref|XP_002894585.1| rubredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297340427|gb|EFH70844.1| rubredoxin family protein [Arabidopsis lyrata subsp. lyrata]	182	195	2.00E-63	107.1	81.3	87.4	rubredoxin family protein	gbpln	Arabidopsis lyrata	AT1G54500.1 | Symbols: | Rubredoxin-like superfamily protein | chr1:20357084-20357671 REVERSE LENGTH=195	182	195	1.00E-65	107.1	81.9	86.3
Rsa1.0_00431.1.g13720.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13721.t1	gb|AAP96742.1| ThiJ-like protein [Brassica rapa subsp. pekinensis]	572	392	0	68.5	61.0	64.2	ThiJ-like protein	gbpln	Brassica rapa	AT3G14990.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr3:5047510-5049621 FORWARD LENGTH=392	572	392	0	68.5	61.5	64.7
Rsa1.0_00431.1.g13722.t1	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	673	521	8.00E-32	77.4	10.8	15.8	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	AT3G42140.1 | Symbols: | zinc ion binding;nucleic acid binding | chr3:14302060-14303018 REVERSE LENGTH=273	673	273	1.00E-11	40.6	4.9	7.9
Rsa1.0_00431.1.g13723.t2	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	799	1225	1.00E-63	153.3	15.0	21.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	799	154	3.00E-20	19.3	5.8	8.4
Rsa1.0_00431.1.g13724.t1	gb|AAL87314.1| unknown protein [Arabidopsis thaliana]	139	547	8.00E-53	393.5	82.7	89.9	unknown protein	gbpln	Arabidopsis thaliana	AT4G38900.3 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:18139564-18141520 REVERSE LENGTH=547	139	547	2.00E-55	393.5	82.7	89.9
Rsa1.0_00431.1.g13725.t1	emb|CAB77974.1| putative athila-like protein [Arabidopsis thaliana]	148	587	1.00E-11	396.6	24.3	32.4	putative athila-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13726.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	210	1024	9.00E-27	487.6	29.0	37.1	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13727.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13728.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13729.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	969	1838	1.00E-171	189.7	32.0	39.8	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13730.t1	gb|EOA18727.1| hypothetical protein CARUB_v10007306mg [Capsella rubella]	263	284	1.00E-119	108.0	89.0	94.7	hypothetical protein CARUB_v10007306mg	gbpln	Capsella rubella	AT4G14465.1 | Symbols: AHL20 | AT-hook motif nuclear-localized protein 20 | chr4:8320972-8321817 FORWARD LENGTH=281	263	281	1.00E-120	106.8	90.5	95.1

Rsa1.0_00431.1.g13731.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13732.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13733.t1	gb|AAF97298.1|AC007843_1 Hypothetical protein [Arabidopsis thaliana]	235	362	4.00E-56	154.0	52.3	66.0	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13734.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	185	1142	2.00E-40	617.3	42.2	53.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13735.t1	gb|EOA18445.1| hypothetical protein CARUB_v10006988mg [Capsella rubella]	546	683	1.00E-142	125.1	51.1	67.6	hypothetical protein CARUB_v10006988mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	546	696	3.00E-19	127.5	20.7	37.4
Rsa1.0_00431.1.g13736.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00431.1.g13737.t1	ref|XP_002870312.1| hypothetical protein ARALYDRAFT_915420 [Arabidopsis lyrata subsp. lyrata] gi|297316148|gb|EFH46571.1| hypothetical protein ARALYDRAFT_915420 [Arabidopsis lyrata subsp. lyrata]	106	105	9.00E-29	99.1	63.2	75.5	hypothetical protein ARALYDRAFT_915420	gbpln	Arabidopsis lyrata	AT4G14450.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23170.1); Has 74 Blast hits to 74 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:8309519-8309896 FORWARD LENGTH=125	106	125	1.00E-30	117.9	66.0	73.6
Rsa1.0_00432.1.g13738.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13739.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13740.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13741.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13742.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13743.t6	gb|AAD30632.1|AC006085_5 Hypothetical protein [Arabidopsis thaliana]	1010	1295	1.00E-97	128.2	24.5	34.8	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13744.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13745.t1	dbj|BAB88750.1| gag protein [Silene latifolia]	313	196	5.00E-20	62.6	14.7	25.2	gag protein	gbpln	Silene latifolia	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13746.t1	ref|XP_002885617.1| hypothetical protein ARALYDRAFT_898967 [Arabidopsis lyrata subsp. lyrata] gi|297331457|gb|EFH61876.1| hypothetical protein ARALYDRAFT_898967 [Arabidopsis lyrata subsp. lyrata]	502	488	8.00E-27	97.2	21.9	38.2	hypothetical protein ARALYDRAFT_898967	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13747.t1	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	2016	1864	0	92.5	17.2	20.4	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	ATMG00750.1 | Symbols: ORF119 | GAG/POL/ENV polyprotein | chrM:220830-221189 FORWARD LENGTH=119	2016	119	1.00E-17	5.9	2.0	2.2
Rsa1.0_00432.1.g13748.t15	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	220	940	3.00E-30	427.3	31.8	40.9	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13749.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13750.t1	gb|AAF79348.1|AC007887_7 F15O4.13 [Arabidopsis thaliana]	1313	1887	0	143.7	54.6	67.8	F15O4.13	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1313	158	3.00E-22	12.0	3.9	5.6
Rsa1.0_00432.1.g13751.t15	gb|AAM15254.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	275	930	2.00E-41	338.2	34.9	50.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13752.t6	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00432.1.g13753.t12	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	799	695	1.00E-164	87.0	43.7	54.4	hypothetical protein 26.t00052	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00433.1.g13754.t1	gb|EOA34242.1| hypothetical protein CARUB_v10021762mg [Capsella rubella]	162	163	4.00E-64	100.6	72.8	88.3	hypothetical protein CARUB_v10021762mg	gbpln	Capsella rubella	AT1G22590.2 | Symbols: AGL87 | AGAMOUS-like 87 | chr1:7983511-7984002 FORWARD LENGTH=163	162	163	2.00E-66	100.6	73.5	86.4
Rsa1.0_00433.1.g13755.t1	gb|EOA39123.1| hypothetical protein CARUB_v10011935mg [Capsella rubella]	170	560	3.00E-60	329.4	67.1	72.4	hypothetical protein CARUB_v10011935mg	gbpln	Capsella rubella	AT1G22550.1 | Symbols: | Major facilitator superfamily protein | chr1:7966608-7968552 REVERSE LENGTH=564	170	564	2.00E-62	331.8	67.1	72.9
Rsa1.0_00433.1.g13756.t1	ref|XP_002890519.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297336361|gb|EFH66778.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	561	561	0	100.0	90.4	94.5	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G22540.1 | Symbols: | Major facilitator superfamily protein | chr1:7964202-7966222 FORWARD LENGTH=557	561	557	0	99.3	88.6	93.6

Rsa1.0_00433.1.g13757.t1	ref|XP_002893236.1| hypothetical protein ARALYDRAFT_472493 [Arabidopsis lyrata subsp. lyrata] gi|297339078|gb|EFH69495.1| hypothetical protein ARALYDRAFT_472493 [Arabidopsis lyrata subsp. lyrata]	732	676	0	92.3	75.3	80.9	hypothetical protein ARALYDRAFT_472493	gbpln	Arabidopsis lyrata	AT1G22530.1 | Symbols: PATL2 | PATELLIN 2 | chr1:7955773-7958326 REVERSE LENGTH=683	732	683	0	93.3	72.5	79.1
Rsa1.0_00433.1.g13758.t1	gb|EOA36747.1| hypothetical protein CARUB_v10012585mg [Capsella rubella]	375	382	1.00E-166	101.9	78.7	85.6	hypothetical protein CARUB_v10012585mg	gbpln	Capsella rubella	AT1G22500.1 | Symbols: | RING/U-box superfamily protein | chr1:7949581-7950726 FORWARD LENGTH=381	375	381	1.00E-164	101.6	77.6	85.1
Rsa1.0_00433.1.g13759.t1	ref|NP_200608.3| reticulon-like protein B21 [Arabidopsis thaliana] gi|332278149|sp|Q56X72.2|RTNLS_ARATH RecName: Full=Reticulon-like protein B21; Short=AtRTNLB21 gi|332009600|gb|AED96983.1| reticulon-like protein B21 [Arabidopsis thaliana]	124	487	1.00E-25	392.7	49.2	52.4	reticulon-like protein B21	gbpln	Arabidopsis thaliana	AT5G58000.1 | Symbols: | Reticulon family protein | chr5:23477416-23479496 FORWARD LENGTH=487	124	487	2.00E-28	392.7	49.2	52.4
Rsa1.0_00433.1.g13760.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00433.1.g13761.t1	ref|NP_564171.1| transcription factor bHLH94 [Arabidopsis thaliana] gi|218563531|sp|Q9SK91.2|BH094_ARATH RecName: Full=Transcription factor bHLH94; AltName: Full=Basic helix-loop-helix protein 94; Short=AtbHLH94; Short=bHLH 94; AltName: Full=Transcription factor EN 16; AltName: Full=bHLH transcription factor bHLH094 gi|332192126|gb|AEE30247.1| transcription factor bHLH94 [Arabidopsis thaliana]	295	304	1.00E-116	103.1	79.0	87.1	transcription factor bHLH94	gbpln	Arabidopsis thaliana	AT1G22490.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:7938448-7940489 REVERSE LENGTH=304	295	304	1.00E-118	103.1	79.0	87.1
Rsa1.0_00433.1.g13762.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00433.1.g13763.t1	gb|EOA37135.1| hypothetical protein CARUB_v10010418mg [Capsella rubella]	172	180	2.00E-52	104.7	73.3	80.2	hypothetical protein CARUB_v10010418mg	gbpln	Capsella rubella	AT1G22480.1 | Symbols: | Cupredoxin superfamily protein | chr1:7934232-7935054 REVERSE LENGTH=174	172	174	9.00E-54	101.2	72.1	79.1
Rsa1.0_00433.1.g13764.t1	ref|XP_002893230.1| hypothetical protein ARALYDRAFT_472486 [Arabidopsis lyrata subsp. lyrata] gi|297339072|gb|EFH69489.1| hypothetical protein ARALYDRAFT_472486 [Arabidopsis lyrata subsp. lyrata]	564	566	0	100.4	84.9	90.2	hypothetical protein ARALYDRAFT_472486	gbpln	Arabidopsis lyrata	AT1G22460.1 | Symbols: | O-fucosyltransferase family protein | chr1:7927530-7930351 REVERSE LENGTH=565	564	565	0	100.2	84.9	90.4
Rsa1.0_00433.1.g13765.t1	ref|XP_002890515.1| hypothetical protein ARALYDRAFT_889753 [Arabidopsis lyrata subsp. lyrata] gi|297336357|gb|EFH66774.1| hypothetical protein ARALYDRAFT_889753 [Arabidopsis lyrata subsp. lyrata]	150	192	1.00E-58	128.0	88.7	93.3	hypothetical protein ARALYDRAFT_889753	gbpln	Arabidopsis lyrata	AT1G22450.1 | Symbols: COX6B, ATCOX6B2 | cytochrome C oxidase 6B | chr1:7925447-7926918 FORWARD LENGTH=191	150	191	5.00E-60	127.3	89.3	94.7
Rsa1.0_00433.1.g13766.t1	ref|XP_002890513.1| hypothetical protein ARALYDRAFT_472482 [Arabidopsis lyrata subsp. lyrata] gi|297336355|gb|EFH66772.1| hypothetical protein ARALYDRAFT_472482 [Arabidopsis lyrata subsp. lyrata]	389	388	0	99.7	86.9	94.9	hypothetical protein ARALYDRAFT_472482	gbpln	Arabidopsis lyrata	AT1G22430.2 | Symbols: | GroES-like zinc-binding dehydrogenase family protein | chr1:7919235-7921594 FORWARD LENGTH=388	389	388	0	99.7	86.1	94.6
Rsa1.0_00433.1.g13767.t1	ref|XP_002890510.1| hypothetical protein ARALYDRAFT_472481 [Arabidopsis lyrata subsp. lyrata] gi|297336352|gb|EFH66769.1| hypothetical protein ARALYDRAFT_472481 [Arabidopsis lyrata subsp. lyrata]	518	527	0	101.7	93.8	96.5	hypothetical protein ARALYDRAFT_472481	gbpln	Arabidopsis lyrata	AT1G22410.1 | Symbols: | Class-II DAHP synthetase family protein | chr1:7912120-7914742 FORWARD LENGTH=527	518	527	0	101.7	93.6	96.7
Rsa1.0_00433.1.g13768.t1	gb|EOA40264.1| hypothetical protein CARUB_v10008992mg [Capsella rubella]	491	484	0	98.6	74.1	85.3	hypothetical protein CARUB_v10008992mg	gbpln	Capsella rubella	AT1G22360.1 | Symbols: AtUGT85A2, UGT85A2 | UDP-glucosyl transferase 85A2 | chr1:7895068-7897527 REVERSE LENGTH=481	491	481	0	98.0	73.3	84.7
Rsa1.0_00434.1.g13769.t1	ref|XP_002887617.1| hypothetical protein ARALYDRAFT_316513 [Arabidopsis lyrata subsp. lyrata] gi|297333458|gb|EFH63876.1| hypothetical protein ARALYDRAFT_316513 [Arabidopsis lyrata subsp. lyrata]	165	163	8.00E-42	98.8	55.2	69.1	hypothetical protein ARALYDRAFT_316513	gbpln	Arabidopsis lyrata	AT1G75870.1 | Symbols: | unknown protein; Has 10 Blast hits to 10 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:28486532-28487114 FORWARD LENGTH=165	165	165	2.00E-43	100.0	50.3	66.1

Rsa1.0_00434.1.g13770.t1	ref|XP_002889047.1| hypothetical protein ARALYDRAFT_895460 [Arabidopsis lyrata subsp. lyrata] gi|297334888|gb|EFH65306.1| hypothetical protein ARALYDRAFT_895460 [Arabidopsis lyrata subsp. lyrata]	795	791	0	99.5	93.8	96.4	hypothetical protein ARALYDRAFT_895460	gbpln	Arabidopsis lyrata	AT1G75850.1 | Symbols: VPS35B | VPS35 homolog B | chr1:28478053-28483874 REVERSE LENGTH=790	795	790	0	99.4	93.5	96.2
Rsa1.0_00434.1.g13771.t1	gb|EOA38545.1| hypothetical protein CARUB_v10010350mg [Capsella rubella]	196	196	1.00E-110	100.0	99.0	99.0	hypothetical protein CARUB_v10010350mg	gbpln	Capsella rubella	AT1G20090.1 | Symbols: ARAC4, ROP2, ATROP2, ATRAC4 | RHO-related protein from plants 2 | chr1:6967223-6968603 FORWARD LENGTH=195	196	195	1.00E-111	99.5	98.0	98.0
Rsa1.0_00434.1.g13772.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00434.1.g13773.t1	sp|P69241.1|DEF1_RAPSA RecName: Full=Defensin-like protein 1; AltName: Full=Cysteine-rich antifungal protein 1; Short=AFP1; Flags: Precursor gi|609322|gb|AAA69541.1| antifungal protein 1 preprotein [Raphanus sativus] gi|115529964|gb|ABJ09663.1| antifungal rafp1 [Raphanus sativus]	80	80	2.00E-39	100.0	100.0	100.0	RecName: Full=Defensin-like protein 1; AltName: Full=Cysteine-rich antifungal protein 1; Short=AFP1; Flags: Precursor gi|609322|gb|AAA69541.1| antifungal protein 1 preprotein	gbpln	Raphanus sativus	AT5G44420.1 | Symbols: PDF1.2, PDF1.2A, LCR77 | plant defensin 1.2 | chr5:17907216-17907550 REVERSE LENGTH=80	80	80	6.00E-38	100.0	88.8	95.0
Rsa1.0_00434.1.g13774.t1	gb|AAY27736.1| putative plant defensin PDF1.1 [Arabidopsis halleri] gi|410066989|emb|CCN97877.1| defensin [Arabidopsis halleri subsp. halleri]	80	80	4.00E-29	100.0	75.0	83.8	putative plant defensin PDF1.1	gbpln	Arabidopsis halleri	AT5G44420.1 | Symbols: PDF1.2, PDF1.2A, LCR77 | plant defensin 1.2 | chr5:17907216-17907550 REVERSE LENGTH=80	80	80	3.00E-30	100.0	71.3	81.3
Rsa1.0_00434.1.g13775.t1	gb|ABV89616.1| pathogenesis-related thaumatin family protein [Brassica rapa] gi|157849670|gb|ABV89618.1| pathogenesis-related thaumatin family protein [Brassica rapa]	492	321	1.00E-165	65.2	60.6	62.0	pathogenesis-related thaumatin family protein	gbpln	Brassica rapa	AT1G75800.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:28458889-28460447 FORWARD LENGTH=330	492	330	1.00E-159	67.1	56.3	59.8
Rsa1.0_00434.1.g13776.t1	ref|XP_002889045.1| hypothetical protein ARALYDRAFT_476726 [Arabidopsis lyrata subsp. lyrata] gi|297334886|gb|EFH65304.1| hypothetical protein ARALYDRAFT_476726 [Arabidopsis lyrata subsp. lyrata]	554	545	0	98.4	78.3	87.2	hypothetical protein ARALYDRAFT_476726	gbpln	Arabidopsis lyrata	AT1G75790.1 | Symbols: sks18 | SKU5 similar 18 | chr1:28454980-28457388 REVERSE LENGTH=545	554	545	0	98.4	76.4	85.4
Rsa1.0_00434.1.g13777.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00434.1.g13778.t1	gb|ACV70139.1| gast1-like protein [Jatropha curcas]	109	103	1.00E-18	94.5	46.8	57.8	gast1-like protein	gbpln	Jatropha curcas	AT1G75750.1 | Symbols: GASA1 | GAST1 protein homolog 1 | chr1:28441813-28442284 REVERSE LENGTH=98	109	98	9.00E-19	89.9	54.1	57.8
Rsa1.0_00434.1.g13779.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00434.1.g13780.t1	ref|NP_177702.2| uncharacterized protein [Arabidopsis thaliana] gi|334183931|ref|NP_001185406.1| uncharacterized protein [Arabidopsis thaliana] gi|133778892|gb|ABO38786.1| At1g75730 [Arabidopsis thaliana] gi|332197631|gb|AEE35752.1| uncharacterized protein AT1G75730 [Arabidopsis thaliana] gi|332197632|gb|AEE35753.1| uncharacterized protein AT1G75730 [Arabidopsis thaliana]	568	589	1.00E-165	103.7	66.4	77.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G75730.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages. | chr1:28435991-28438983 REVERSE LENGTH=589	568	589	1.00E-168	103.7	66.4	77.3
Rsa1.0_00434.1.g13781.t1	gb|EOA33227.1| hypothetical protein CARUB_v10020976mg [Capsella rubella]	187	198	1.00E-55	105.9	72.2	80.2	hypothetical protein CARUB_v10020976mg	gbpln	Capsella rubella	AT1G75720.2 | Symbols: | Plant protein of unknown function (DUF827) | chr1:28434648-28435321 REVERSE LENGTH=193	187	193	1.00E-55	103.2	71.1	80.7
Rsa1.0_00434.1.g13782.t1	ref|XP_002887608.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297333449|gb|EFH63867.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	443	461	0	104.1	86.7	89.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G75710.1 | Symbols: | C2H2-like zinc finger protein | chr1:28428806-28431128 FORWARD LENGTH=462	443	462	0	104.3	85.8	90.1
Rsa1.0_00434.1.g13783.t2	gb|EOA35847.1| hypothetical protein CARUB_v10021088mg [Capsella rubella]	153	155	2.00E-71	101.3	87.6	93.5	hypothetical protein CARUB_v10021088mg	gbpln	Capsella rubella	AT1G75690.1 | Symbols: | DnaJ/Hsp40 cysteine-rich domain superfamily protein | chr1:28422273-28423170 REVERSE LENGTH=154	153	154	2.00E-72	100.7	88.9	92.8

Rsa1.0_00434.1.g13784.t1	ref|XP_002510517.1| conserved hypothetical protein [Ricinus communis] gi|223551218|gb|EEF52704.1| conserved hypothetical protein [Ricinus communis]	297	311	5.00E-78	104.7	52.9	66.7	conserved hypothetical protein	gbpln	Ricinus communis	AT5G05800.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11290.1); Has 881 Blast hits to 512 proteins in 30 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 38; Plants - 833; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr5:1743234-1744751 REVERSE LENGTH=449	297	449	4.00E-17	151.2	26.6	41.8
Rsa1.0_00434.1.g13785.t1	gb|AAM63477.1| endo-beta-1,4-glucanase, putative [Arabidopsis thaliana]	524	525	0	100.2	88.0	94.1	endo-beta-1,4-glucanase, putative	gbpln	Arabidopsis thaliana	AT1G75680.1 | Symbols: AtGH9B7, GH9B7 | glycosyl hydrolase 9B7 | chr1:28417215-28419231 REVERSE LENGTH=525	524	525	0	100.2	86.6	93.1
Rsa1.0_00434.1.g13786.t1	ref|XP_002868503.1| hypothetical protein ARALYDRAFT_493700 [Arabidopsis lyrata subsp. lyrata] gi|297314339|gb|EFH44762.1| hypothetical protein ARALYDRAFT_493700 [Arabidopsis lyrata subsp. lyrata]	235	632	9.00E-48	268.9	42.1	48.5	hypothetical protein ARALYDRAFT_493700	gbpln	Arabidopsis lyrata	AT5G37010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G65710.1); Has 6746 Blast hits to 5259 proteins in 486 species: Archae - 7; Bacteria - 485; Metazoa - 3508; Fungi - 577; Plants - 378; Viruses - 50; Other Eukaryotes - 1741 (source: NCBI BLink). | chr5:14620853-14622879 REVERSE LENGTH=637	235	637	1.00E-49	271.1	43.0	48.9
Rsa1.0_00434.1.g13787.t1	ref|XP_002889036.1| hypothetical protein ARALYDRAFT_316494 [Arabidopsis lyrata subsp. lyrata] gi|297334877|gb|EFH65295.1| hypothetical protein ARALYDRAFT_316494 [Arabidopsis lyrata subsp. lyrata]	201	196	2.00E-77	97.5	72.1	80.1	hypothetical protein ARALYDRAFT_316494	gbpln	Arabidopsis lyrata	AT1G75670.2 | Symbols: | DNA-directed RNA polymerases | chr1:28415378-28416505 REVERSE LENGTH=196	201	196	3.00E-77	97.5	69.7	79.1
Rsa1.0_00434.1.g13788.t1	gb|EOA33199.1| hypothetical protein CARUB_v10019710mg [Capsella rubella]	1051	1024	0	97.4	84.4	89.2	hypothetical protein CARUB_v10019710mg	gbpln	Capsella rubella	AT1G75660.1 | Symbols: XRN3, AtXRN3 | 5'-3' exoribonuclease 3 | chr1:28408289-28414825 FORWARD LENGTH=1020	1051	1020	0	97.1	83.3	88.6
Rsa1.0_00434.1.g13789.t1	gb|EOA33194.1| hypothetical protein CARUB_v10021300mg [Capsella rubella]	217	547	2.00E-90	252.1	75.1	85.7	hypothetical protein CARUB_v10021300mg	gbpln	Capsella rubella	AT1G75620.1 | Symbols: | glyoxal oxidase-related protein | chr1:28394951-28396594 REVERSE LENGTH=547	217	547	9.00E-89	252.1	73.3	81.6
Rsa1.0_00435.1.g13790.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00435.1.g13791.t1	dbj|BAJ34187.1| unnamed protein product [Thellungiella halophila]	313	316	1.00E-141	101.0	88.5	93.0	unnamed protein product	----	----	AT4G01460.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:621334-622697 FORWARD LENGTH=315	313	315	1.00E-130	100.6	81.2	89.1
Rsa1.0_00435.1.g13792.t1	gb|AAF18643.1|AC006228_14 F5J5.14 [Arabidopsis thaliana]	548	743	7.00E-79	135.6	31.9	44.5	F5J5.14	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00435.1.g13793.t1	ref|XP_002874982.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297320819|gb|EFH51241.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	363	363	0	100.0	88.4	93.7	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT4G01440.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:596531-598512 FORWARD LENGTH=365	363	365	0	100.6	88.7	93.9
Rsa1.0_00435.1.g13794.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00435.1.g13795.t1	ref|NP_192050.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|7267638|emb|CAB80950.1| putative hypoersensitive response protein [Arabidopsis thaliana] gi|21555824|gb|AAM63942.1| putative hypoersensitive response protein [Arabidopsis thaliana] gi|26451865|dbj|BAC43025.1| putative hypoersensitive response protein [Arabidopsis thaliana] gi|30017263|gb|AAP12865.1| At4g01410 [Arabidopsis thaliana] gi|332656622|gb|AEE82022.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	230	227	2.00E-98	98.7	87.8	93.0	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT4G01410.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr4:578308-578991 FORWARD LENGTH=227	230	227	1.00E-101	98.7	87.8	93.0
Rsa1.0_00435.1.g13796.t1	gb|ABD65000.1| hypothetical protein 26.t00020 [Brassica oleracea]	372	302	2.00E-83	81.2	46.0	56.5	hypothetical protein 26.t00020	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	372	302	3.00E-55	81.2	37.1	50.5

Rsa1.0_00435.1.g13797.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	405	442	1.00E-176	109.1	77.3	87.2	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	405	343	8.00E-52	84.7	30.6	40.2
Rsa1.0_00435.1.g13798.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00435.1.g13799.t1	ref|XP_002875014.1| hypothetical protein ARALYDRAFT_490488 [Arabidopsis lyrata subsp. lyrata] gi|297320851|gb|EFH51273.1| hypothetical protein ARALYDRAFT_490488 [Arabidopsis lyrata subsp. lyrata]	287	298	1.00E-108	103.8	67.9	77.7	hypothetical protein ARALYDRAFT_490488	gbpln	Arabidopsis lyrata	AT4G00780.1 | Symbols: | TRAF-like family protein | chr4:334779-336120 FORWARD LENGTH=299	287	299	1.00E-108	104.2	67.6	76.7
Rsa1.0_00435.1.g13800.t1	ref|NP_567189.6| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] gi|332656536|gb|AEE81936.1| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	1892	1913	0	101.1	82.4	88.3	transducin family protein / WD-40 repeat family protein	gbpln	Arabidopsis thaliana	AT4G00800.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr4:337114-345581 REVERSE LENGTH=1913	1892	1913	0	101.1	82.4	88.3
Rsa1.0_00435.1.g13801.t1	ref|NP_567190.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|30678744|ref|NP_849278.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|41019478|sp|O23095.2|RLA12_ARATH RecName: Full=60S acidic ribosomal protein P1-2 gi|13605597|gb|AAK32792.1|AF361624_1 AT4g00810/A_TM018A10_9 [Arabidopsis thaliana] gi|15777871|gb|AAL05896.1| AT4g00810/A_TM018A10_9 [Arabidopsis thaliana] gi|21554797|gb|AAM63694.1| acidic ribosomal protein p1 [Arabidopsis thaliana] gi|222423235|dbj|BAH19594.1| AT4G00810 [Arabidopsis thaliana] gi|332656537|gb|AEE81937.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|332656538|gb|AEE81938.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana]	113	113	5.00E-55	100.0	99.1	99.1	60S acidic ribosomal protein P1-2	gbpln	Arabidopsis thaliana	AT4G00810.2 | Symbols: | 60S acidic ribosomal protein family | chr4:346179-346957 REVERSE LENGTH=113	113	113	8.00E-58	100.0	99.1	99.1
Rsa1.0_00435.1.g13802.t1	ref|NP_567192.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|79324963|ref|NP_001031566.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|13605916|gb|AAK32943.1|AF367357_1 AT4g00830/A_TM018A10_14 [Arabidopsis thaliana] gi|21360555|gb|AAM47474.1| AT4g00830/A_TM018A10_14 [Arabidopsis thaliana] gi|110743368|dbj|BAE99571.1| hypothetical protein [Arabidopsis thaliana] gi|332656540|gb|AEE81940.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|332656541|gb|AEE81941.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	510	495	0	97.1	87.1	91.8	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT4G00830.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:352782-354965 FORWARD LENGTH=495	510	495	0	97.1	87.1	91.8

Rsa1.0_00435.1.g13803.t1	ref|NP_567193.2| putative S-acyltransferase [Arabidopsis thaliana] gi|75222970|sp|Q5M757.1|ZDH15_ARATH RecName: Full=Probable S-acyltransferase At4g00840; AltName: Full=Probable palmitoyltransferase At4g00840; AltName: Full=Zinc finger DHHC domain-containing protein At4g00840 gi|56461762|gb|AAV91337.1| At4g00840 [Arabidopsis thaliana] gi|57222210|gb|AAW39012.1| At4g00840 [Arabidopsis thaliana] gi|110738461|dbj|BAF01156.1| hypothetical protein [Arabidopsis thaliana] gi|332656544|gb|AEE81944.1| putative S-acyltransferase [Arabidopsis thaliana]	287	291	1.00E-141	101.4	89.5	94.8	putative S-acyltransferase	gbpln	Arabidopsis thaliana	AT4G00840.1 | Symbols: | DHHC-type zinc finger family protein | chr4:355483-357105 REVERSE LENGTH=291	287	291	1.00E-144	101.4	89.5	94.8
Rsa1.0_00435.1.g13804.t1	ref|XP_002871206.1| EMB2735 [Arabidopsis lyrata subsp. lyrata] gi|297317043|gb|EFH47465.1| EMB2735 [Arabidopsis lyrata subsp. lyrata]	166	162	5.00E-38	97.6	50.0	54.8	EMB2735	gbpln	Arabidopsis lyrata	AT5G06240.1 | Symbols: emb2735 | embryo defective 2735 | chr5:1888380-1889512 FORWARD LENGTH=162	166	162	4.00E-39	97.6	48.2	53.6
Rsa1.0_00435.1.g13805.t1	ref|NP_192535.1| DNA-directed RNA polymerase, subunit M [Arabidopsis thaliana] gi|4309697|gb|AAD15481.1| putative DNA-directed RNA polymerase subunit [Arabidopsis thaliana] gi|7267434|emb|CAB77946.1| putative DNA-directed RNA polymerase subunit [Arabidopsis thaliana] gi|18253033|gb|AAL62443.1| putative DNA-directed RNA polymerase subunit [Arabidopsis thaliana] gi|23198220|gb|AAN15637.1| putative DNA-directed RNA polymerase subunit [Arabidopsis thaliana] gi|332657185|gb|AEE82585.1| DNA-directed RNA polymerase, subunit M [Arabidopsis thaliana]	103	106	1.00E-45	102.9	87.4	94.2	DNA-directed RNA polymerase, subunit M	gbpln	Arabidopsis thaliana	AT4G07950.1 | Symbols: | DNA-directed RNA polymerase, subunit M, archaeal | chr4:4798910-4799510 FORWARD LENGTH=106	103	106	2.00E-48	102.9	87.4	94.2
Rsa1.0_00435.1.g13806.t1	ref|NP_567196.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|2252854|gb|AAB62852.1| similar to auxin-induced protein [Arabidopsis thaliana] gi|7267427|emb|CAB80897.1| AT4g00880 [Arabidopsis thaliana] gi|17380988|gb|AAL36306.1| unknown protein [Arabidopsis thaliana] gi|20466031|gb|AAM20350.1| unknown protein [Arabidopsis thaliana] gi|332656549|gb|AEE81949.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	133	122	2.00E-49	91.7	82.0	88.7	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT4G00880.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:366692-367060 REVERSE LENGTH=122	133	122	5.00E-52	91.7	82.0	88.7
Rsa1.0_00435.1.g13807.t1	ref|NP_567204.3| cysteine-rich receptor-like protein kinase 41 [Arabidopsis thaliana] gi|152013451|sp|O23081.2|CRK41_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 41; Short=Cysteine-rich RLK41; Flags: Precursor gi|332656562|gb|AEE81962.1| cysteine-rich receptor-like protein kinase 41 [Arabidopsis thaliana]	250	665	1.00E-117	266.0	84.4	91.6	cysteine-rich receptor-like protein kinase 41	gbpln	Arabidopsis thaliana	AT4G00970.1 | Symbols: CRK41 | cysteine-rich RLK (RECEPTOR-like protein kinase) 41 | chr4:418437-421694 FORWARD LENGTH=665	250	665	1.00E-120	266.0	84.4	91.6
Rsa1.0_00435.1.g13808.t1	ref|NP_567205.2| zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|26451026|dbj|BAC42619.1| unknown protein [Arabidopsis thaliana] gi|29028884|gb|AAO64821.1| At4g00980 [Arabidopsis thaliana] gi|332656563|gb|AEE81963.1| zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	508	488	0	96.1	68.1	75.2	zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT4G00980.1 | Symbols: | zinc knuckle (CCHC-type) family protein | chr4:422732-424580 REVERSE LENGTH=488	508	488	0	96.1	68.1	75.2
Rsa1.0_00435.1.g13809.t1	gb|EOA19940.1| hypothetical protein CARUB_v10000192mg [Capsella rubella]	888	876	0	98.6	62.0	71.5	hypothetical protein CARUB_v10000192mg	gbpln	Capsella rubella	AT4G00990.1 | Symbols: | Transcription factor jumonji (jmjC) domain-containing protein | chr4:427035-431535 FORWARD LENGTH=840	888	840	0	94.6	47.9	56.4
Rsa1.0_00435.1.g13810.t2	gb|EOA19940.1| hypothetical protein CARUB_v10000192mg [Capsella rubella]	894	876	0	98.0	63.2	72.6	hypothetical protein CARUB_v10000192mg	gbpln	Capsella rubella	AT4G00990.1 | Symbols: | Transcription factor jumonji (jmjC) domain-containing protein | chr4:427035-431535 FORWARD LENGTH=840	894	840	0	94.0	61.7	72.6
Rsa1.0_00435.1.g13811.t1	# #	#	#	#	#	#	-	----	----	# #	#	#	#	#	#	#	

<table>
<tr><td>Rsa1.0_00435.1.g13812.t1</td><td>ref|XP_002874992.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297320829|gb|EFH51251.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>523</td><td>502</td><td>0</td><td>96.0</td><td>71.7</td><td>81.1</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G01270.1 | Symbols: | RING/U-box superfamily protein | chr4:532351-534891 FORWARD LENGTH=506</td><td>523</td><td>506</td><td>0</td><td>96.7</td><td>70.6</td><td>79.9</td></tr>
<tr><td>Rsa1.0_00435.1.g13813.t1</td><td>gb|EOA29347.1| hypothetical protein CARUB_v10025632mg [Capsella rubella]</td><td>368</td><td>366</td><td>1.00E-97</td><td>99.5</td><td>51.1</td><td>62.5</td><td>hypothetical protein CARUB_v10025632mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44700.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:18431015-18432121 FORWARD LENGTH=368</td><td>368</td><td>368</td><td>7.00E-93</td><td>100.0</td><td>50.5</td><td>63.9</td></tr>
<tr><td>Rsa1.0_00436.1.g13814.t1</td><td>emb|CAA55893.1| putative imbibition protein [Brassica oleracea]</td><td>766</td><td>765</td><td>0</td><td>99.9</td><td>95.8</td><td>97.5</td><td>putative imbibition protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G57520.1 | Symbols: AtSIP2, SIP2 | seed imbibition 2 | chr3:21288982-21292694 REVERSE LENGTH=773</td><td>766</td><td>773</td><td>0</td><td>100.9</td><td>92.2</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00436.1.g13815.t1</td><td>gb|AAZ30035.1| putative calcium-dependent protein kinase [Isatis tinctoria] gi|94958384|gb|ABF47341.1| calcium-dependent protein kinase [Isatis tinctoria] gi|95020533|gb|ABF50790.1| calcium-dependent protein kinase [Isatis tinctoria]</td><td>424</td><td>537</td><td>0</td><td>126.7</td><td>95.3</td><td>97.9</td><td>putative calcium-dependent protein kinase</td><td>gbpln</td><td>Isatis tinctoria</td><td>AT3G57530.1 | Symbols: CPK32, ATCPK32, CDPK32 | calcium-dependent protein kinase 32 | chr3:21296898-21299351 REVERSE LENGTH=538</td><td>424</td><td>538</td><td>0</td><td>126.9</td><td>94.8</td><td>97.4</td></tr>
<tr><td>Rsa1.0_00436.1.g13816.t1</td><td>ref|XP_002875407.1| hypothetical protein ARALYDRAFT_484576 [Arabidopsis lyrata subsp. lyrata] gi|297321245|gb|EFH51666.1| hypothetical protein ARALYDRAFT_484576 [Arabidopsis lyrata subsp. lyrata]</td><td>1139</td><td>661</td><td>6.00E-39</td><td>58.0</td><td>9.7</td><td>13.6</td><td>hypothetical protein ARALYDRAFT_484576</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G27860.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr3:10326128-10328086 FORWARD LENGTH=652</td><td>1139</td><td>652</td><td>3.00E-36</td><td>57.2</td><td>10.6</td><td>14.2</td></tr>
<tr><td>Rsa1.0_00436.1.g13817.t1</td><td>ref|XP_002878161.1| hypothetical protein ARALYDRAFT_486202 [Arabidopsis lyrata subsp. lyrata] gi|297323999|gb|EFH54420.1| hypothetical protein ARALYDRAFT_486202 [Arabidopsis lyrata subsp. lyrata]</td><td>299</td><td>296</td><td>1.00E-124</td><td>99.0</td><td>81.9</td><td>88.3</td><td>hypothetical protein ARALYDRAFT_486202</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G57540.1 | Symbols: | Remorin family protein | chr3:21301623-21302924 REVERSE LENGTH=296</td><td>299</td><td>296</td><td>1.00E-126</td><td>99.0</td><td>79.6</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00436.1.g13818.t1</td><td>gb|EOA24182.1| hypothetical protein CARUB_v10017419mg [Capsella rubella]</td><td>413</td><td>389</td><td>0</td><td>94.2</td><td>87.2</td><td>91.3</td><td>hypothetical protein CARUB_v10017419mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G57550.1 | Symbols: AGK2, GK-2 | guanylate kinase | chr3:21307269-21309193 FORWARD LENGTH=389</td><td>413</td><td>389</td><td>0</td><td>94.2</td><td>86.4</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00436.1.g13819.t17</td><td>gb|EOA25774.1| hypothetical protein CARUB_v10019137mg [Capsella rubella]</td><td>996</td><td>347</td><td>4.00E-78</td><td>34.8</td><td>16.1</td><td>16.5</td><td>hypothetical protein CARUB_v10019137mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G57560.1 | Symbols: NAGK | N-acetyl-l-glutamate kinase | chr3:21311164-21312207 REVERSE LENGTH=347</td><td>996</td><td>347</td><td>7.00E-80</td><td>34.8</td><td>15.9</td><td>16.5</td></tr>
<tr><td>Rsa1.0_00436.1.g13820.t19</td><td>dbj|BAB01845.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]</td><td>1304</td><td>893</td><td>7.00E-83</td><td>68.5</td><td>17.3</td><td>25.8</td><td>non-LTR retroelement reverse transcriptase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1304</td><td>626</td><td>6.00E-44</td><td>48.0</td><td>10.0</td><td>16.7</td></tr>
<tr><td>Rsa1.0_00436.1.g13821.t1</td><td>emb|CAB10321.1| UFD1 like protein [Arabidopsis thaliana] gi|7268289|emb|CAB78584.1| UFD1 like protein [Arabidopsis thaliana]</td><td>156</td><td>778</td><td>5.00E-14</td><td>498.7</td><td>25.6</td><td>32.7</td><td>UFD1 like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15420.1 | Symbols: | Ubiquitin fusion degradation UFD1 family protein | chr4:8823822-8825949 FORWARD LENGTH=561</td><td>156</td><td>561</td><td>2.00E-16</td><td>359.6</td><td>26.9</td><td>36.5</td></tr>
<tr><td>Rsa1.0_00436.1.g13822.t25</td><td>ref|NP_191316.5| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332646152|gb|AEE79673.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]</td><td>1108</td><td>1092</td><td>0</td><td>98.6</td><td>81.4</td><td>87.3</td><td>armadillo/beta-catenin-like repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G57570.1 | Symbols: | ARM repeat superfamily protein | chr3:21312598-21320105 FORWARD LENGTH=1092</td><td>1108</td><td>1092</td><td>0</td><td>98.6</td><td>81.4</td><td>87.3</td></tr>
<tr><td>Rsa1.0_00436.1.g13823.t1</td><td>ref|XP_002876426.1| hypothetical protein ARALYDRAFT_486209 [Arabidopsis lyrata subsp. lyrata] gi|297322264|gb|EFH52685.1| hypothetical protein ARALYDRAFT_486209 [Arabidopsis lyrata subsp. lyrata]</td><td>275</td><td>277</td><td>1.00E-106</td><td>100.7</td><td>72.7</td><td>83.6</td><td>hypothetical protein ARALYDRAFT_486209</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G57600.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:21332841-21333674 FORWARD LENGTH=277</td><td>275</td><td>277</td><td>1.00E-107</td><td>100.7</td><td>71.6</td><td>83.6</td></tr>
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Rsa1.0_00436.1.g13824.t1	ref|NP_191320.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|2500026|sp|Q96529.1|PURA_ARATH RecName: Full=Adenylosuccinate synthetase, chloroplastic; Short=AMPSase; Short=AdSS; AltName: Full=IMP--aspartate ligase; Flags: Precursor gi|1616657|gb|AAB16828.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|4678286|emb|CAB41194.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|15451052|gb|AAK96797.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|20148265|gb|AAM10023.1| adenylosuccinate synthetase [Arabidopsis thaliana] gi|332646157|gb|AEE79678.1| adenylosuccinate synthetase [Arabidopsis thaliana]	491	490	0	99.8	89.6	93.9	adenylosuccinate synthetase	gbpln	Arabidopsis thaliana	AT3G57610.1 | Symbols: ADSS | adenylosuccinate synthase | chr3:21334519-21336603 REVERSE LENGTH=490	491	490	0	99.8	89.6	93.9
Rsa1.0_00436.1.g13825.t1	ref|XP_002878165.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297324003|gb|EFH54424.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	503	792	0	157.5	76.1	82.1	exostosin family protein	gbpln	Arabidopsis lyrata	AT3G57630.1 | Symbols: | exostosin family protein | chr3:21339543-21343080 REVERSE LENGTH=793	503	793	0	157.7	74.6	81.3
Rsa1.0_00437.1.g13826.t2	gb|EOA39644.1| hypothetical protein CARUB_v10008281mg [Capsella rubella] gi|482575458|gb|EOA39645.1| hypothetical protein CARUB_v10008281mg [Capsella rubella]	923	867	0	93.9	84.5	88.4	hypothetical protein CARUB_v10008281mg	gbpln	Capsella rubella	AT1G23870.1 | Symbols: ATTPS9, TPS9 | trehalose-phosphatase/synthase 9 | chr1:8432695-8435506 FORWARD LENGTH=867	923	867	0	93.9	83.7	87.8
Rsa1.0_00437.1.g13827.t1	ref|XP_002890597.1| hypothetical protein ARALYDRAFT_889925 [Arabidopsis lyrata subsp. lyrata] gi|297336439|gb|EFH66856.1| hypothetical protein ARALYDRAFT_889925 [Arabidopsis lyrata subsp. lyrata]	319	378	1.00E-161	118.5	90.6	94.0	hypothetical protein ARALYDRAFT_889925	gbpln	Arabidopsis lyrata	AT1G23820.1 | Symbols: SPDS1 | spermidine synthase 1 | chr1:8420278-8422724 FORWARD LENGTH=378	319	378	1.00E-163	118.5	90.3	93.4
Rsa1.0_00437.1.g13828.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	731	723	0	98.9	57.7	73.1	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	731	696	2.00E-52	95.2	24.1	45.1
Rsa1.0_00437.1.g13829.t1	ref|XP_002893307.1| hypothetical protein ARALYDRAFT_472641 [Arabidopsis lyrata subsp. lyrata] gi|297339149|gb|EFH69566.1| hypothetical protein ARALYDRAFT_472641 [Arabidopsis lyrata subsp. lyrata]	533	534	0	100.2	90.4	95.3	hypothetical protein ARALYDRAFT_472641	gbpln	Arabidopsis lyrata	AT1G23800.1 | Symbols: ALDH2B7, ALDH2B | aldehyde dehydrogenase 2B7 | chr1:8412238-8414804 REVERSE LENGTH=534	533	534	0	100.2	91.0	95.5
Rsa1.0_00437.1.g13830.t1	gb|EOA40104.1| hypothetical protein CARUB_v10008797mg [Capsella rubella]	538	538	0	100.0	84.6	90.5	hypothetical protein CARUB_v10008797mg	gbpln	Capsella rubella	AT1G23790.1 | Symbols: | Plant protein of unknown function (DUF936) | chr1:8410099-8411917 FORWARD LENGTH=518	538	518	0	96.3	81.6	87.2
Rsa1.0_00437.1.g13831.t1	gb|EOA37583.1| hypothetical protein CARUB_v10011933mg [Capsella rubella]	293	481	5.00E-57	164.2	52.2	62.8	hypothetical protein CARUB_v10011933mg	gbpln	Capsella rubella	AT1G23770.1 | Symbols: | F-box family protein | chr1:8405214-8406266 REVERSE LENGTH=350	293	350	1.00E-48	119.5	44.0	50.5
Rsa1.0_00437.1.g13832.t1	#	#	#	#	#	#	#	–	----	----	AT1G70430.1 | Symbols: | Protein kinase superfamily protein | chr1:26545589-26548756 FORWARD LENGTH=594	143	594	9.00E-11	415.4	26.6	40.6
Rsa1.0_00437.1.g13833.t1	gb|EOA34992.1| hypothetical protein CARUB_v10020084mg [Capsella rubella]	141	556	2.00E-11	394.3	35.5	53.9	hypothetical protein CARUB_v10020084mg	gbpln	Capsella rubella	AT1G70430.1 | Symbols: | Protein kinase superfamily protein | chr1:26545589-26548756 FORWARD LENGTH=594	141	594	1.00E-12	421.3	31.9	42.6
Rsa1.0_00437.1.g13834.t1	gb|AAD14492.1| Hypothetical protein [Arabidopsis thaliana]	155	240	7.00E-27	154.8	43.9	51.0	Hypothetical protein	gbpln	Arabidopsis thaliana	AT3G32050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14780.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:13067626-13068582 REVERSE LENGTH=175	155	175	2.00E-11	112.9	18.1	21.9

Rsa1.0_00437.1.g13835.t1	ref|NP_173771.1| uncharacterized protein [Arabidopsis thaliana] gi|4056441|gb|AAC98014.1| Similar to OBP32pep protein gb|U37698 from Arabidopsis thaliana [Arabidopsis thaliana] gi|45476571|gb|AAS65951.1| At1g23580 [Arabidopsis thaliana] gi|46402436|gb|AAS92320.1| At1g23580 [Arabidopsis thaliana] gi|332192286|gb|AEE30407.1| uncharacterized protein AT1G23580 [Arabidopsis thaliana]	288	285	2.00E-84	99.0	57.6	72.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23580.1 | Symbols: | Domain of unknown function DUF220 | chr1:8357491-8358706 REVERSE LENGTH=285	288	285	4.00E-87	99.0	57.6	72.9
Rsa1.0_00437.1.g13836.t2	ref|NP_173771.1| uncharacterized protein [Arabidopsis thaliana] gi|4056441|gb|AAC98014.1| Similar to OBP32pep protein gb|U37698 from Arabidopsis thaliana [Arabidopsis thaliana] gi|45476571|gb|AAS65951.1| At1g23580 [Arabidopsis thaliana] gi|46402436|gb|AAS92320.1| At1g23580 [Arabidopsis thaliana] gi|332192286|gb|AEE30407.1| uncharacterized protein AT1G23580 [Arabidopsis thaliana]	278	285	4.00E-81	102.5	55.0	72.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23580.1 | Symbols: | Domain of unknown function DUF220 | chr1:8357491-8358706 REVERSE LENGTH=285	278	285	1.00E-83	102.5	55.0	72.7
Rsa1.0_00437.1.g13837.t1	ref|NP_173767.1| uncharacterized protein [Arabidopsis thaliana] gi|8778581|gb|AAF79589.1|AC007945_9 F28C11.16 [Arabidopsis thaliana] gi|4056436|gb|AAC98009.1| EST gb|AA650912 comes from this gene [Arabidopsis thaliana] gi|34365603|gb|AAQ65113.1| At1g23530 [Arabidopsis thaliana] gi|51969024|dbj|BAD43204.1| unknown protein [Arabidopsis thaliana] gi|332192279|gb|AEE30400.1| uncharacterized protein AT1G23530 [Arabidopsis thaliana]	172	189	1.00E-63	109.9	80.8	87.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G70470.1); Has 38 Blast hits to 38 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:8345861-8346430 FORWARD LENGTH=189	172	189	4.00E-66	109.9	80.8	87.2
Rsa1.0_00437.1.g13838.t1	ref|NP_173766.1| uncharacterized protein [Arabidopsis thaliana] gi|8778585|gb|AAF79593.1|AC007945_13 F28C11.15 [Arabidopsis thaliana] gi|4056435|gb|AAC98008.1| Similar to OBP32pep protein gb|U37698 from Arabidopsis thaliana [Arabidopsis thaliana] gi|332192277|gb|AEE30398.1| uncharacterized protein AT1G23520 [Arabidopsis thaliana]	256	263	5.00E-67	102.7	55.9	71.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23520.1 | Symbols: | Domain of unknown function (DUF220) | chr1:8343571-8344675 REVERSE LENGTH=263	256	263	1.00E-69	102.7	55.9	71.9
Rsa1.0_00437.1.g13839.t1	gb|ACD37536.1| putative ADP-ribosylation factor [Brassica napus]	181	181	1.00E-102	100.0	99.4	100.0	putative ADP-ribosylation factor	gbpln	Brassica napus	AT3G62290.3 | Symbols: ARFA1E | ADP-ribosylation factor A1E | chr3:23052287-23053545 FORWARD LENGTH=181	181	181	1.00E-104	100.0	99.4	99.4
Rsa1.0_00437.1.g13840.t1	gb|EOA38890.1| hypothetical protein CARUB_v10011268mg [Capsella rubella]	470	1077	0	229.1	83.2	89.4	hypothetical protein CARUB_v10011268mg	gbpln	Capsella rubella	AT1G23460.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:8327382-8329622 FORWARD LENGTH=460	470	460	0	97.9	84.3	88.9
Rsa1.0_00437.1.g13841.t1	gb|AAC98003.1| This gene may be continued from BAC T23E23 [Arabidopsis thaliana]	72	278	5.00E-15	386.1	65.3	69.4	This gene may be continued from BAC T23E23	gbpln	Arabidopsis thaliana	AT1G23450.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:8324698-8326697 FORWARD LENGTH=666	72	666	1.00E-17	925.0	65.3	69.4
Rsa1.0_00437.1.g13842.t1	ref|XP_002890583.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336425|gb|EFH66842.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	218	217	1.00E-109	99.5	87.2	95.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G23440.1 | Symbols: | Peptidase C15, pyroglutamyl peptidase I-like | chr1:8321940-8324019 FORWARD LENGTH=217	218	217	1.00E-111	99.5	87.2	94.0
Rsa1.0_00438.1.g13843.t3	gb|EOA31608.1| hypothetical protein CARUB_v10014805mg, partial [Capsella rubella]	204	161	6.00E-58	78.9	59.3	59.8	hypothetical protein CARUB_v10014805mg, partial	gbpln	Capsella rubella	AT3G04400.1 | Symbols: emb2171 | Ribosomal protein L14p/L23e family protein | chr3:1167339-1168308 FORWARD LENGTH=140	204	140	5.00E-60	68.6	59.3	59.8
Rsa1.0_00438.1.g13844.t1	gb|EOA39245.1| hypothetical protein CARUB_v10012233mg [Capsella rubella]	1029	1032	0	100.3	91.5	94.6	hypothetical protein CARUB_v10012233mg	gbpln	Capsella rubella	AT1G04470.1 | Symbols: | Protein of unknown function (DUF810) | chr1:1211177-1214591 REVERSE LENGTH=1035	1029	1035	0	100.6	89.3	93.1
Rsa1.0_00438.1.g13845.t1	ref|XP_002889506.1| hypothetical protein ARALYDRAFT_470423 [Arabidopsis lyrata subsp. lyrata] gi|297335348|gb|EFH65765.1| hypothetical protein ARALYDRAFT_470423 [Arabidopsis lyrata subsp. lyrata]	164	154	2.00E-33	93.9	51.2	61.6	hypothetical protein ARALYDRAFT_470423	gbpln	Arabidopsis lyrata	AT1G04445.1 | Symbols: | C2H2-like zinc finger protein | chr1:1207344-1207862 FORWARD LENGTH=172	164	172	2.00E-28	104.9	51.8	62.8
Rsa1.0_00438.1.g13846.t1	gb|EOA36675.1| hypothetical protein CARUB_v10012017mg [Capsella rubella]	461	468	0	101.5	88.3	93.9	hypothetical protein CARUB_v10012017mg	gbpln	Capsella rubella	AT1G04440.1 | Symbols: CKL13 | casein kinase like 13 | chr1:1202815-1205664 FORWARD LENGTH=468	461	468	0	101.5	87.4	93.7
Rsa1.0_00438.1.g13847.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00438.1.g13848.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00438.1.g13849.t1	gb|EOA38791.1| hypothetical protein CARUB_v10011057mg [Capsella rubella]	133	130	3.00E-47	97.7	87.2	89.5	hypothetical protein CARUB_v10011057mg	gbpln	Capsella rubella	AT1G04370.1 | Symbols: ATERF14, ERF14 | Ethylene-responsive element binding factor 14 | chr1:1175177-1175578 FORWARD LENGTH=133	133	133	3.00E-47	100.0	81.2	85.7
Rsa1.0_00438.1.g13850.t1	dbj|BAB10876.1| polyprotein [Arabidopsis thaliana]	213	1429	6.00E-50	670.9	45.1	50.2	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	213	1262	2.00E-15	592.5	19.7	30.5
Rsa1.0_00438.1.g13851.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1714	1307	0	76.3	45.8	58.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1714	1262	1.00E-103	73.6	11.7	18.3
Rsa1.0_00438.1.g13852.t2	ref|XP_002876745.1| hypothetical protein ARALYDRAFT_904327 [Arabidopsis lyrata subsp. lyrata] gi|297322583|gb|EFH53004.1| hypothetical protein ARALYDRAFT_904327 [Arabidopsis lyrata subsp. lyrata]	499	589	1.00E-51	118.0	29.3	43.3	hypothetical protein ARALYDRAFT_904327	gbpln	Arabidopsis lyrata	AT1G01355.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr1:138513-139568 FORWARD LENGTH=228	499	228	3.00E-42	45.7	19.8	25.9
Rsa1.0_00438.1.g13853.t1	gb|EOA23062.1| hypothetical protein CARUB_v10003832mg [Capsella rubella]	218	588	5.00E-37	269.7	40.8	43.6	hypothetical protein CARUB_v10003832mg	gbpln	Capsella rubella	AT5G11670.1 | Symbols: ATNADP-ME2, NADP-ME2 | NADP-malic enzyme 2 | chr5:3754456-3758040 FORWARD LENGTH=588	218	588	2.00E-39	269.7	40.8	43.6
Rsa1.0_00438.1.g13854.t1	#	#	#	#	#	#	#	-	----	----	AT3G60940.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:22521615-22523029 REVERSE LENGTH=257	164	257	8.00E-13	156.7	22.0	40.2
Rsa1.0_00438.1.g13855.t1	gb|EOA39428.1| hypothetical protein CARUB_v10012550mg [Capsella rubella]	534	538	0	100.7	86.1	91.4	hypothetical protein CARUB_v10012550mg	gbpln	Capsella rubella	AT1G04280.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:1143643-1146541 REVERSE LENGTH=534	534	534	0	100.0	83.0	87.8
Rsa1.0_00438.1.g13856.t1	gb|EOA36082.1| hypothetical protein CARUB_v10010394mg, partial [Capsella rubella]	153	186	3.00E-80	121.6	98.0	99.3	hypothetical protein CARUB_v10010394mg, partial	gbpln	Capsella rubella	AT1G04270.1 | Symbols: RPS15 | cytosolic ribosomal protein S15 | chr1:1141852-1142960 REVERSE LENGTH=152	153	152	3.00E-75	99.3	98.7	98.7
Rsa1.0_00438.1.g13857.t1	gb|EOA36534.1| hypothetical protein CARUB_v10011583mg [Capsella rubella]	139	182	2.00E-32	130.9	60.4	76.3	hypothetical protein CARUB_v10011583mg	gbpln	Capsella rubella	AT1G04260.1 | Symbols: MPI7, MPIP7, PRA1.D | CAMV movement protein interacting protein 7 | chr1:1140749-1141297 REVERSE LENGTH=182	139	182	8.00E-34	130.9	58.3	75.5
Rsa1.0_00438.1.g13858.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	726	1142	1.00E-112	157.3	27.1	34.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	726	295	1.00E-65	40.6	16.7	23.4
Rsa1.0_00439.1.g13859.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00439.1.g13860.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	1634	1557	0	95.3	37.6	52.0	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1634	575	7.00E-78	35.2	9.3	14.4
Rsa1.0_00439.1.g13861.t1	ref|NP_179390.1| uncharacterized protein [Arabidopsis thaliana] gi|4406819|gb|AAD20127.1| unknown protein [Arabidopsis thaliana] gi|50198801|gb|AAT70434.1| At2g17990 [Arabidopsis thaliana] gi|56121928|gb|AAV74245.1| At2g17990 [Arabidopsis thaliana] gi|330251618|gb|AEC06712.1| uncharacterized protein AT2G17990 [Arabidopsis thaliana]	302	338	1.00E-128	111.9	85.1	93.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G17990.1 | Symbols: | BEST Arabidopsis thaliana protein match is: kinectin-related (TAIR:AT5G66250.3); Has 7578 Blast hits to 6129 proteins in 783 species: Archae - 220; Bacteria - 1045; Metazoa - 3605; Fungi - 575; Plants - 442; Viruses - 38; Other Eukaryotes - 1653 (source: NCBI BLink). | chr2:7827480-7828596 FORWARD LENGTH=338	302	338	1.00E-131	111.9	85.1	93.0
Rsa1.0_00439.1.g13862.t1	ref|NP_001189547.1| TBP-associated factor 14 [Arabidopsis thaliana] gi|330251620|gb|AEC06714.1| TBP-associated factor 14 [Arabidopsis thaliana]	258	268	1.00E-103	103.9	73.3	85.3	TBP-associated factor 14	gbpln	Arabidopsis thaliana	AT2G18000.2 | Symbols: TAF14 | TBP-associated factor 14 | chr2:7829035-7830580 FORWARD LENGTH=268	258	268	1.00E-106	103.9	73.3	85.3
Rsa1.0_00439.1.g13863.t2	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	846	1123	0	132.7	43.7	49.8	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	846	1262	2.00E-59	149.2	17.1	26.1
Rsa1.0_00439.1.g13864.t1	ref|NP_179392.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|4406817|gb|AAD20125.1| putative auxin-regulated protein [Arabidopsis thaliana] gi|330251621|gb|AEC06715.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	107	112	2.00E-47	104.7	85.0	92.5	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT2G18010.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:7833902-7834240 FORWARD LENGTH=112	107	112	4.00E-50	104.7	85.0	92.5

Rsa1.0_00439.1.g13865.t1	ref|XP_002869043.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata] gi|297314879|gb|EFH45302.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata]	258	258	1.00E-143	100.0	96.1	98.8	60S ribosomal protein L8	gbpln	Arabidopsis lyrata	AT4G36130.1 | Symbols: | Ribosomal protein L2 family | chr4:17097613-17098656 FORWARD LENGTH=258	258	258	1.00E-144	100.0	95.3	98.8
Rsa1.0_00439.1.g13866.t1	dbj|BAJ34365.1| unnamed protein product [Thellungiella halophila]	129	119	9.00E-60	92.2	90.7	92.2	unnamed protein product	----	----	AT2G18040.1 | Symbols: PIN1AT | peptidylprolyl cis/trans isomerase, NIMA-interacting 1 | chr2:7842346-7843537 FORWARD LENGTH=119	129	119	1.00E-60	92.2	88.4	91.5
Rsa1.0_00439.1.g13867.t1	gb|EOA17220.1| hypothetical protein CARUB_v10005495mg [Capsella rubella]	264	268	1.00E-116	101.5	83.0	89.8	hypothetical protein CARUB_v10005495mg	gbpln	Capsella rubella	AT5G32450.1 | Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr5:12079707-12081317 FORWARD LENGTH=267	264	267	1.00E-116	101.1	81.4	89.8
Rsa1.0_00439.1.g13868.t1	ref|XP_002886145.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331985|gb|EFH62404.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	361	365	1.00E-168	101.1	79.5	87.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G18060.1 | Symbols: VND1, ANAC037 | vascular related NAC-domain protein 1 | chr2:7848399-7850303 REVERSE LENGTH=365	361	365	1.00E-169	101.1	78.9	87.5
Rsa1.0_00439.1.g13869.t1	emb|CAN66432.1| hypothetical protein VITISV_027451 [Vitis vinifera]	568	576	4.00E-72	101.4	35.2	51.8	hypothetical protein VITISV_027451	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	568	1262	3.00E-21	222.2	8.1	13.7
Rsa1.0_00439.1.g13870.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00439.1.g13871.t1	gb|AAF99785.1|AC012463_2 T2E6.4 [Arabidopsis thaliana]	435	740	1.00E-125	170.1	50.8	66.7	T2E6.4	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	435	746	2.00E-97	171.5	37.5	48.7
Rsa1.0_00439.1.g13872.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00439.1.g13873.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00439.1.g13874.t1	gb|EOA29875.1| hypothetical protein CARUB_v10012971mg [Capsella rubella]	738	840	0	113.8	79.9	87.7	hypothetical protein CARUB_v10012971mg	gbpln	Capsella rubella	AT2G18090.1 | Symbols: | PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein | chr2:7864501-7867317 FORWARD LENGTH=824	738	824	0	111.7	79.4	86.4
Rsa1.0_00439.1.g13875.t1	ref|XP_002886148.1| hypothetical protein ARALYDRAFT_319764 [Arabidopsis lyrata subsp. lyrata] gi|297331988|gb|EFH62407.1| hypothetical protein ARALYDRAFT_319764 [Arabidopsis lyrata subsp. lyrata]	221	208	1.00E-86	94.1	72.9	81.0	hypothetical protein ARALYDRAFT_319764	gbpln	Arabidopsis lyrata	AT2G18120.1 | Symbols: SRS4 | SHI-related sequence 4 | chr2:7876722-7877681 REVERSE LENGTH=222	221	222	3.00E-87	100.5	74.7	84.6
Rsa1.0_00439.1.g13876.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	984	1365	0	138.7	45.5	62.9	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	984	575	1.00E-80	58.4	18.1	28.6
Rsa1.0_00439.1.g13877.t1	gb|ABK28184.1| unknown [Arabidopsis thaliana]	451	488	1.00E-36	108.2	22.2	37.3	unknown	gbpln	Arabidopsis thaliana	AT3G47920.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41590.1); Has 154 Blast hits to 152 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 154; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:17682952-17683854 FORWARD LENGTH=300	451	300	4.00E-15	66.5	10.0	18.2
Rsa1.0_00439.1.g13878.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00440.1.g13879.t1	gb|EOA39250.1| hypothetical protein CARUB_v10012247mg [Capsella rubella]	815	818	0	100.4	72.5	85.3	hypothetical protein CARUB_v10012247mg	gbpln	Capsella rubella	AT1G08140.1 | Symbols: ATCHX6A, CHX6A | cation/H+ exchanger 6A | chr1:2552206-2555074 REVERSE LENGTH=818	815	818	0	100.4	70.7	83.6
Rsa1.0_00440.1.g13880.t1	gb|EOA37659.1| hypothetical protein CARUB_v10012226mg [Capsella rubella]	796	793	0	99.6	72.2	84.2	hypothetical protein CARUB_v10012226mg	gbpln	Capsella rubella	AT1G08135.1 | Symbols: ATCHX6B, CHX6B | cation/H+ exchanger 6B | chr1:2548819-2551473 REVERSE LENGTH=796	796	796	0	100.0	71.4	84.4
Rsa1.0_00440.1.g13881.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1960	1274	0	65.0	31.2	43.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1960	575	8.00E-74	29.3	9.3	14.8
Rsa1.0_00440.1.g13882.t2	ref|XP_002892438.1| ATLIG1 [Arabidopsis lyrata subsp. lyrata] gi|297338280|gb|EFH68697.1| ATLIG1 [Arabidopsis lyrata subsp. lyrata]	1101	793	0	72.0	60.7	63.6	ATLIG1	gbpln	Arabidopsis lyrata	AT1G08130.1 | Symbols: ATLIG1, LIG1 | DNA ligase 1 | chr1:2542913-2547815 REVERSE LENGTH=790	1101	790	0	71.8	59.9	63.1

Rsa1.0_00440.1.g13883.t1	ref|XP_002889680.1| calmodulin binding protein [Arabidopsis lyrata subsp. lyrata] gi|297335522|gb|EFH65939.1| calmodulin binding protein [Arabidopsis lyrata subsp. lyrata]	232	235	1.00E-120	101.3	90.1	94.0	calmodulin binding protein	gbpln	Arabidopsis lyrata	AT1G08110.4 | Symbols: | lactoylglutathione lyase family protein / glyoxalase I family protein | chr1:2535463-2537630 FORWARD LENGTH=235	232	235	1.00E-108	101.3	84.5	88.8
Rsa1.0_00440.1.g13884.t1	gb|AFK65609.1| high-affinity nitrate transporter [Brassica rapa subsp. chinensis]	530	530	0	100.0	97.4	98.9	high-affinity nitrate transporter	gbpln	Brassica rapa	AT1G08090.1 | Symbols: ATNRT2:1, NRT2, NRT2;1AT, ACH1, LIN1, ATNRT2.1, NRT2.1, NRT2:1 | nitrate transporter 2:1 | chr1:2524139-2525920 FORWARD LENGTH=530	530	530	0	100.0	94.0	97.2
Rsa1.0_00440.1.g13885.t1	gb|AFK65609.1| high-affinity nitrate transporter [Brassica rapa subsp. chinensis]	530	530	0	100.0	97.2	98.9	high-affinity nitrate transporter	gbpln	Brassica rapa	AT1G08090.1 | Symbols: ATNRT2:1, NRT2, NRT2;1AT, ACH1, LIN1, ATNRT2.1, NRT2.1, NRT2:1 | nitrate transporter 2:1 | chr1:2524139-2525920 FORWARD LENGTH=530	530	530	0	100.0	95.3	97.9
Rsa1.0_00440.1.g13886.t1	gb|EOA36129.1| hypothetical protein CARUB_v10012300mg [Capsella rubella]	273	276	1.00E-133	101.1	82.8	91.9	hypothetical protein CARUB_v10012300mg	gbpln	Capsella rubella	AT1G08080.1 | Symbols: ATACA7, ACA7 | alpha carbonic anhydrase 7 | chr1:2517022-2518546 REVERSE LENGTH=275	273	275	1.00E-131	100.7	82.8	92.7
Rsa1.0_00440.1.g13887.t1	gb|AEP33770.1| organelle transcript processing 82, partial [Raphanus sativus]	750	675	0	90.0	87.9	89.2	organelle transcript processing 82, partial	gbpln	Raphanus sativus	AT1G08070.1 | Symbols: OTP82 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:2514374-2516599 REVERSE LENGTH=741	750	741	0	98.8	81.5	89.3
Rsa1.0_00440.1.g13888.t1	ref|NP_172285.2| carbonic anhydrase [Arabidopsis thaliana] gi|332190117|gb|AEE28238.1| alpha carbonic anhydrase 5 [Arabidopsis thaliana]	274	277	1.00E-126	101.1	77.4	85.8	carbonic anhydrase	gbpln	Arabidopsis thaliana	AT1G08065.1 | Symbols: ATACA5, ACA5 | alpha carbonic anhydrase 5 | chr1:2511788-2513341 REVERSE LENGTH=277	274	277	1.00E-128	101.1	77.4	85.8
Rsa1.0_00440.1.g13889.t1	gb|AAF79839.1|AC026875_19 T6D22.14 [Arabidopsis thaliana]	2260	2254	0	99.7	50.4	58.8	T6D22.14	gbpln	Arabidopsis thaliana	AT1G08060.2 | Symbols: MOM, MOM1 | ATP-dependent helicase family protein | chr1:2501981-2510488 REVERSE LENGTH=2001	2260	2001	0	88.5	49.4	58.4
Rsa1.0_00440.1.g13890.t1	ref|NP_172283.1| C3HC4-type RING finger-containing protein [Arabidopsis thaliana] gi|8778841|gb|AAF79840.1|AC026875_20 T6D22.13 [Arabidopsis thaliana] gi|332190114|gb|AEE28235.1| C3HC4-type RING finger-containing protein [Arabidopsis thaliana]	625	641	0	102.6	71.0	80.2	C3HC4-type RING finger-containing protein	gbpln	Arabidopsis thaliana	AT1G08050.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr1:2499088-2501311 REVERSE LENGTH=641	625	641	0	102.6	71.0	80.2
Rsa1.0_00440.1.g13891.t1	ref|XP_002892430.1| hypothetical protein ARALYDRAFT_888027 [Arabidopsis lyrata subsp. lyrata] gi|297338272|gb|EFH68689.1| hypothetical protein ARALYDRAFT_888027 [Arabidopsis lyrata subsp. lyrata]	398	382	0	96.0	87.7	91.5	hypothetical protein ARALYDRAFT_888027	gbpln	Arabidopsis lyrata	AT1G08040.2 | Symbols: | Protein of unknown function (DUF707) | chr1:2495507-2497973 REVERSE LENGTH=382	398	382	0	96.0	87.7	91.7
Rsa1.0_00440.1.g13892.t1	ref|NP_172283.1| C3HC4-type RING finger-containing protein [Arabidopsis thaliana] gi|8778841|gb|AAF79840.1|AC026875_20 T6D22.13 [Arabidopsis thaliana] gi|332190114|gb|AEE28235.1| C3HC4-type RING finger-containing protein [Arabidopsis thaliana]	758	641	0	84.6	55.0	64.8	C3HC4-type RING finger-containing protein	gbpln	Arabidopsis thaliana	AT1G08050.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr1:2499088-2501311 REVERSE LENGTH=641	758	641	0	84.6	55.0	64.8
Rsa1.0_00440.1.g13893.t1	gb|EOA22612.1| hypothetical protein CARUB_v10003280mg [Capsella rubella]	1246	762	0	61.2	48.6	53.5	hypothetical protein CARUB_v10003280mg	gbpln	Capsella rubella	AT5G04500.1 | Symbols: | glycosyltransferase family protein 47 | chr5:1283604-1286155 FORWARD LENGTH=765	1246	765	0	61.4	47.9	53.0
Rsa1.0_00441.1.g13894.t1	ref|NP_194075.1| TIR-NBS class of disease resistance protein [Arabidopsis thaliana] gi|3451069|emb|CAA20465.1| hypothetical protein [Arabidopsis thaliana] gi|7269192|emb|CAB79299.1| hypothetical protein [Arabidopsis thaliana] gi|332659357|gb|AEE84757.1| TIR-NBS class of disease resistance protein [Arabidopsis thaliana]	900	964	0	107.1	82.6	89.7	TIR-NBS class of disease resistance protein	gbpln	Arabidopsis thaliana	AT4G23440.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr4:12237765-12240659 FORWARD LENGTH=964	900	964	0	107.1	82.6	89.7
Rsa1.0_00441.1.g13895.t1	gb|EOA15733.1| hypothetical protein CARUB_v10006703mg [Capsella rubella]	162	155	8.00E-45	95.7	67.3	77.8	hypothetical protein CARUB_v10006703mg	gbpln	Capsella rubella	AT4G23450.3 | Symbols: AIRP1, AtAIRP1 | RING/U-box superfamily protein | chr4:12241113-12242190 REVERSE LENGTH=208	162	208	1.00E-44	128.4	59.9	72.8
Rsa1.0_00441.1.g13896.t1	dbj|BAB02625.1| unnamed protein product [Arabidopsis thaliana]	412	420	4.00E-82	101.9	47.1	60.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G28330.1 | Symbols: | F-box family protein-related | chr3:10586566-10587712 REVERSE LENGTH=349	412	349	5.00E-66	84.7	37.9	49.3

Rsa1.0_00441.1.g13897.t1	ref|NP_194077.1| beta-adaptin-like protein C [Arabidopsis thaliana] gi|306531056|sp|O81742.2|APBLC_ARATH RecName: Full=Beta-adaptin-like protein C; Short=At-bC-Ad; Short=At-betaC-Ad; AltName: Full=AP complex subunit beta-C; AltName: Full=Adaptor protein complex AP subunit beta-C; AltName: Full=Beta-adaptin C; AltName: Full=Clathrin assembly protein complex beta large chain C gi|332659361|gb|AEE84761.1| beta-adaptin-like protein C [Arabidopsis thaliana]	880	893	0	101.5	94.7	97.3	beta-adaptin-like protein C	gbpln	Arabidopsis thaliana	AT4G23460.1 | Symbols: | Adaptin family protein | chr4:12243899-12248898 REVERSE LENGTH=893	880	893	0	101.5	94.7	97.3
Rsa1.0_00441.1.g13898.t1	gb|EOA17284.1| hypothetical protein CARUB_v10005554mg [Capsella rubella]	240	255	1.00E-118	106.3	87.1	90.8	hypothetical protein CARUB_v10005554mg	gbpln	Capsella rubella	AT4G23470.1 | Symbols: | PLAC8 family protein | chr4:12249289-12251079 FORWARD LENGTH=255	240	255	1.00E-114	106.3	82.5	88.3
Rsa1.0_00441.1.g13899.t1	gb|ACC91275.1| fringe-related protein [Capsella rubella] gi|482552213|gb|EOA16406.1| hypothetical protein CARUB_v10004561mg [Capsella rubella]	494	534	0	108.1	85.2	89.9	fringe-related protein	gbpln	Capsella rubella	AT4G23490.1 | Symbols: | Protein of unknown function (DUF604) | chr4:12251580-12253973 REVERSE LENGTH=526	494	526	0	106.5	84.2	89.1
Rsa1.0_00441.1.g13900.t1	ref|XP_002869777.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297315613|gb|EFH46036.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	493	494	0	100.2	93.9	96.6	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT4G23500.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:12264640-12267074 FORWARD LENGTH=495	493	495	0	100.4	93.5	96.6
Rsa1.0_00441.1.g13901.t1	ref|XP_002867703.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313539|gb|EFH43962.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	371	879	3.00E-32	236.9	18.1	20.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G23515.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr4:12271382-12272842 REVERSE LENGTH=331	371	331	3.00E-33	89.2	19.7	24.8
Rsa1.0_00441.1.g13902.t1	ref|XP_002867703.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313539|gb|EFH43962.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	476	879	2.00E-39	184.7	23.1	30.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G23515.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr4:12271382-12272842 REVERSE LENGTH=331	476	331	9.00E-38	69.5	20.6	26.9
Rsa1.0_00441.1.g13903.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00441.1.g13904.t1	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	1377	1453	0	105.5	68.6	80.1	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1377	1262	1.00E-103	91.6	14.2	21.6
Rsa1.0_00441.1.g13905.t1	gb|EOA18423.1| hypothetical protein CARUB_v10006966mg [Capsella rubella]	156	312	2.00E-33	200.0	44.9	56.4	hypothetical protein CARUB_v10006966mg	gbpln	Capsella rubella	AT4G23515.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr4:12271382-12272842 REVERSE LENGTH=331	156	331	2.00E-32	212.2	42.3	52.6
Rsa1.0_00441.1.g13906.t1	ref|XP_002869776.1| hypothetical protein ARALYDRAFT_914244 [Arabidopsis lyrata subsp. lyrata] gi|297315612|gb|EFH46035.1| hypothetical protein ARALYDRAFT_914244 [Arabidopsis lyrata subsp. lyrata]	373	400	1.00E-133	107.2	76.7	85.0	hypothetical protein ARALYDRAFT_914244	gbpln	Arabidopsis lyrata	AT4G23530.1 | Symbols: | Protein of unknown function (DUF793) | chr4:12279171-12280361 FORWARD LENGTH=396	373	396	1.00E-132	106.2	76.1	85.0
Rsa1.0_00441.1.g13907.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00441.1.g13908.t1	gb|EOA16931.1| hypothetical protein CARUB_v10005155mg [Capsella rubella]	299	351	1.00E-143	117.4	87.3	93.0	hypothetical protein CARUB_v10005155mg	gbpln	Capsella rubella	AT4G23550.1 | Symbols: WRKY29, ATWRKY29 | WRKY family transcription factor | chr4:12291831-12293088 FORWARD LENGTH=304	299	304	1.00E-142	101.7	83.9	91.0
Rsa1.0_00441.1.g13909.t1	ref|XP_002874585.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata] gi|297320422|gb|EFH50844.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata]	480	483	0	100.6	83.3	89.6	glycosyl hydrolase family 9 protein	gbpln	Arabidopsis lyrata	AT4G23560.1 | Symbols: AtGH9B15, GH9B15 | glycosyl hydrolase 9B15 | chr4:12293633-12295788 REVERSE LENGTH=479	480	479	0	99.8	82.3	89.4
Rsa1.0_00441.1.g13910.t1	gb|ACC91268.1| phosphatase-related protein [Capsella rubella] gi|482552711|gb|EOA16904.1| hypothetical protein CARUB_v10005128mg [Capsella rubella]	344	356	1.00E-171	103.5	87.5	95.6	phosphatase-related protein	gbpln	Capsella rubella	AT4G23570.2 | Symbols: SGT1A | phosphatase-related | chr4:12300015-12302493 FORWARD LENGTH=350	344	350	1.00E-163	101.7	87.2	93.6
Rsa1.0_00441.1.g13911.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00441.1.g13912.t1	ref|NP_194090.2| tyrosine transaminase-like protein [Arabidopsis thaliana] gi|75161515|sp|Q8VYP2.1|TAT4_ARATH RecName: Full=Probable aminotransferase TAT4; AltName: Full=Tyrosine aminotransferase 4 gi|17979319|gb|AAL49885.1| putative tyrosine transaminase [Arabidopsis thaliana] gi|21689827|gb|AAM67557.1| putative tyrosine transaminase [Arabidopsis thaliana] gi|332659380|gb|AEE84780.1| probable aminotransferase TAT4 [Arabidopsis thaliana]	418	424	0	101.4	74.6	85.2	tyrosine transaminase-like protein	gbpln	Arabidopsis thaliana	AT4G23590.1 | Symbols: | Tyrosine transaminase family protein | chr4:12307195-12309445 FORWARD LENGTH=424	418	424	0	101.4	74.6	85.2
Rsa1.0_00442.1.g13913.t1	ref|XP_002892335.1| agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338177|gb|EFH68594.1| agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata]	147	139	8.00E-34	94.6	49.0	57.1	agenet domain-containing protein	gbpln	Arabidopsis lyrata	AT1G06340.1 | Symbols: | Plant Tudor-like protein | chr1:1933583-1933987 REVERSE LENGTH=134	147	134	7.00E-28	91.2	39.5	51.0
Rsa1.0_00442.1.g13914.t1	ref|XP_002892334.1| copper-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297338176|gb|EFH68593.1| copper-binding family protein [Arabidopsis lyrata subsp. lyrata]	132	145	4.00E-59	109.8	84.8	89.4	copper-binding family protein	gbpln	Arabidopsis lyrata	AT1G06330.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:1931671-1932266 REVERSE LENGTH=159	132	159	3.00E-61	120.5	84.1	87.9
Rsa1.0_00442.1.g13915.t1	ref|NP_171719.2| metacaspase 1 [Arabidopsis thaliana] gi|75232683|sp|Q7XJE6.1|MCA1_ARATH RecName: Full=Metacaspase-1; Short=AtMC1; AltName: Full=Metacaspase 1b; Short=AtMCP1b; AltName: Full=Protein LSD ONE LIKE 3 gi|32482812|gb|AAP84706.1| metacaspase 1 [Arabidopsis thaliana] gi|37788545|gb|AAP44514.1| metacaspase 1 [Arabidopsis thaliana] gi|332189275|gb|AEE27396.1| metacaspase 1 [Arabidopsis thaliana]	366	367	1.00E-180	100.3	90.4	93.7	metacaspase 1	gbpln	Arabidopsis thaliana	AT1G02170.1 | Symbols: LOL3, ATMCPB1, MCP1B, ATMC1, MC1 | metacaspase 1 | chr1:411883-413426 FORWARD LENGTH=367	366	367	0	100.3	90.4	93.7
Rsa1.0_00442.1.g13916.t1	ref|XP_002892332.1| hypothetical protein ARALYDRAFT_887830 [Arabidopsis lyrata subsp. lyrata] gi|297338174|gb|EFH68591.1| hypothetical protein ARALYDRAFT_887830 [Arabidopsis lyrata subsp. lyrata]	204	205	5.00E-86	100.5	77.9	83.8	hypothetical protein ARALYDRAFT_887830	gbpln	Arabidopsis lyrata	AT1G06280.1 | Symbols: LBD2 | LOB domain-containing protein 2 | chr1:1920327-1920947 REVERSE LENGTH=206	204	206	4.00E-84	101.0	78.4	83.8
Rsa1.0_00442.1.g13917.t1	ref|XP_002889594.1| DNA-binding bromodomain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335436|gb|EFH65853.1| DNA-binding bromodomain-containing protein [Arabidopsis lyrata subsp. lyrata]	808	767	0	94.9	69.1	74.3	DNA-binding bromodomain-containing protein	gbpln	Arabidopsis lyrata	AT1G06230.3 | Symbols: GTE4 | global transcription factor group E4 | chr1:1907626-1910183 FORWARD LENGTH=766	808	766	0	94.8	68.4	74.0
Rsa1.0_00442.1.g13918.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00442.1.g13919.t1	ref|XP_002889592.1| hypothetical protein ARALYDRAFT_470642 [Arabidopsis lyrata subsp. lyrata] gi|297335434|gb|EFH65851.1| hypothetical protein ARALYDRAFT_470642 [Arabidopsis lyrata subsp. lyrata]	990	987	0	99.7	94.7	97.7	hypothetical protein ARALYDRAFT_470642	gbpln	Arabidopsis lyrata	AT1G06220.1 | Symbols: MEE5, CLO, GFA1 | Ribosomal protein S5/Elongation factor G/III/V family protein | chr1:1900524-1904583 FORWARD LENGTH=987	990	987	0	99.7	94.6	97.7
Rsa1.0_00442.1.g13920.t1	ref|XP_002889588.1| hypothetical protein ARALYDRAFT_470633 [Arabidopsis lyrata subsp. lyrata] gi|297335430|gb|EFH65847.1| hypothetical protein ARALYDRAFT_470633 [Arabidopsis lyrata subsp. lyrata]	227	237	1.00E-70	104.4	72.7	75.8	hypothetical protein ARALYDRAFT_470633	gbpln	Arabidopsis lyrata	AT1G06160.1 | Symbols: ORA59 | octadecanoid-responsive Arabidopsis AP2/ERF 59 | chr1:1883046-1883780 FORWARD LENGTH=244	227	244	7.00E-67	107.5	77.5	84.6
Rsa1.0_00442.1.g13921.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	100	1529	6.00E-13	1529.0	31.0	56.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00442.1.g13922.t3	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1993	1142	0	57.3	22.4	28.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1993	626	4.00E-37	31.4	5.4	9.2
Rsa1.0_00442.1.g13923.t1	ref|XP_002892322.1| hypothetical protein ARALYDRAFT_311694 [Arabidopsis lyrata subsp. lyrata] gi|297338164|gb|EFH68581.1| hypothetical protein ARALYDRAFT_311694 [Arabidopsis lyrata subsp. lyrata]	569	1329	0	233.6	81.2	89.1	hypothetical protein ARALYDRAFT_311694	gbpln	Arabidopsis lyrata	AT1G06150.1 | Symbols: EMB1444 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:1867129-1873194 REVERSE LENGTH=1322	569	1322	0	232.3	80.1	88.4

Rsa1.0_00442.1.g13924.t1	ref|XP_002892321.1| hypothetical protein ARALYDRAFT_311691 [Arabidopsis lyrata subsp. lyrata] gi|297338163|gb|EFH68580.1| hypothetical protein ARALYDRAFT_311691 [Arabidopsis lyrata subsp. lyrata]	70	485	9.00E-15	692.9	70.0	77.1	hypothetical protein ARALYDRAFT_311691	gbpln	Arabidopsis lyrata	AT1G06137.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06135.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:1863544-1863750 REVERSE LENGTH=68	70	68	3.00E-15	97.1	67.1	72.9
Rsa1.0_00442.1.g13925.t1	gb|AAF80136.1|AC024174_18 Contains similarity to glyoxalase II isozyme from Arabidopsis thaliana gb|U90927 and is a member of the Metallo-beta-lactamase seperfamily PF|00753. ESTs gb|AV519053, gb|AV535897, gb|AV535667, gb|AV556046, gb|BE039169, gb|AV525509 come from this gene [Arabidopsis thaliana]	139	512	2.00E-47	368.3	65.5	70.5	Contains similarity to glyoxalase II isozyme from Arabidopsis thaliana gb|U90927 and is a member of the Metallo-beta-lactamase seperfamily PF|00753. ESTs gb|AV519053, gb|AV535897, gb|AV535667, gb|AV556046, gb|BE039169, gb|AV525509 come from this gene	gbpln	Arabidopsis thaliana	AT1G06130.2 | Symbols: GLX2-4 | glyoxalase 2-4 | chr1:1858034-1860640 REVERSE LENGTH=330	139	330	4.00E-49	237.4	65.5	70.5
Rsa1.0_00442.1.g13926.t1	ref|XP_002879320.1| hypothetical protein ARALYDRAFT_902163 [Arabidopsis lyrata subsp. lyrata] gi|297325159|gb|EFH55579.1| hypothetical protein ARALYDRAFT_902163 [Arabidopsis lyrata subsp. lyrata]	70	69	1.00E-15	98.6	60.0	72.9	hypothetical protein ARALYDRAFT_902163	gbpln	Arabidopsis lyrata	AT1G06137.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06135.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:1863544-1863750 REVERSE LENGTH=68	70	68	1.00E-15	97.1	70.0	75.7
Rsa1.0_00442.1.g13927.t1	ref|NP_563760.1| putative hydroxyacylglutathione hydrolase 2, chloroplast [Arabidopsis thaliana] gi|75246000|sp|Q8LDW8.1|GLO2D_ARATH RecName: Full=Probable hydroxyacylglutathione hydrolase 2, chloroplast; AltName: Full=Glyoxalase 2-4; AltName: Full=Glyoxalase II; Short=Glx II; Flags: Precursor gi|21553879|gb|AAM62972.1| glyoxalase II isozyme, putative [Arabidopsis thaliana] gi|110742461|dbj|BAE99149.1| glyoxalase II isozyme like protein [Arabidopsis thaliana] gi|332189821|gb|AEE27942.1| putative hydroxyacylglutathione hydrolase 2, chloroplast [Arabidopsis thaliana]	289	331	1.00E-152	114.5	87.9	94.5	putative hydroxyacylglutathione hydrolase 2, chloroplast	gbpln	Arabidopsis thaliana	AT1G06130.1 | Symbols: GLX2-4 | glyoxalase 2-4 | chr1:1858034-1860640 REVERSE LENGTH=331	289	331	1.00E-155	114.5	87.9	94.5
Rsa1.0_00442.1.g13928.t1	ref|NP_172099.1| delta-9 desaturase-like 1 protein [Arabidopsis thaliana] gi|62510518|sp|Q9LND9.1|ADSL1_ARATH RecName: Full=Delta-9 desaturase-like 1 protein gi|8810471|gb|AAF80132.1|AC024174_14 Contains similarity to delta 9 desaturase mRNA from Arabidopsis thaliana gb|D88536 and contains a fatty acid desaturase PF|01069 domain. ESTs gb|AV546954, gb|AI993202, gb|AV554343, gb|T46147 come from this gene [Arabidopsis thaliana] gi|332189817|gb|AEE27938.1| delta-9 desaturase-like 1 protein [Arabidopsis thaliana]	300	299	1.00E-157	99.7	89.0	93.7	delta-9 desaturase-like 1 protein	gbpln	Arabidopsis thaliana	AT1G06090.1 | Symbols: | Fatty acid desaturase family protein | chr1:1847921-1849500 FORWARD LENGTH=299	300	299	1.00E-160	99.7	89.0	93.7
Rsa1.0_00442.1.g13929.t1	ref|XP_002889584.1| hypothetical protein ARALYDRAFT_887802 [Arabidopsis lyrata subsp. lyrata] gi|297335426|gb|EFH65843.1| hypothetical protein ARALYDRAFT_887802 [Arabidopsis lyrata subsp. lyrata]	303	305	1.00E-169	100.7	93.4	97.4	hypothetical protein ARALYDRAFT_887802	gbpln	Arabidopsis lyrata	AT1G06080.1 | Symbols: ADS1 | delta 9 desaturase 1 | chr1:1843661-1846093 FORWARD LENGTH=305	303	305	1.00E-170	100.7	92.4	97.0
Rsa1.0_00443.1.g13930.t1	emb|CAN84035.1| hypothetical protein VITISV_016995 [Vitis vinifera]	1318	965	0	73.2	31.3	41.7	hypothetical protein VITISV_016995	gbpln	Vitis vinifera	#	#	#	#	#	#	#

Rsa1.0_00443.1.g13931.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13932.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13933.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13934.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13935.t2	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1753	1838	0	104.8	37.5	47.2	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13936.t1	ref|XP_003631962.1| PREDICTED: uncharacterized protein LOC100855226 [Vitis vinifera]	1101	1011	5.00E-99	91.8	17.3	22.2	PREDICTED: uncharacterized protein LOC100855226	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1101	1262	1.00E-43	114.6	7.5	10.6
Rsa1.0_00443.1.g13937.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13938.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13939.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13940.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13941.t5	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	815	1611	3.00E-30	197.7	9.7	13.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13942.t1	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	422	777	2.00E-21	184.1	12.8	18.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00443.1.g13943.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13944.t2	ref|XP_001537841.1| predicted protein [Ajellomyces capsulatus NAm1] gi|150415449|gb|EDN10802.1| predicted protein [Ajellomyces capsulatus NAm1]	864	801	6.00E-17	92.7	12.0	17.9	predicted protein	gbenv/gbpln	Ajellomyces capsulatus	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13945.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13946.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	460	672	1.00E-58	146.1	32.4	51.5	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13947.t1	gb|ABD65091.1| hypothetical protein 31.t00049 [Brassica oleracea]	299	530	1.00E-47	177.3	40.1	55.5	hypothetical protein 31.t00049	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13948.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13949.t2	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	646	723	0	111.9	51.7	68.4	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	646	696	3.00E-41	107.7	20.6	39.5
Rsa1.0_00444.1.g13950.t1	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	596	190	9.00E-18	31.9	11.1	12.8	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13951.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	763	1529	0	200.4	48.6	62.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	763	746	2.00E-62	97.8	15.7	19.9
Rsa1.0_00444.1.g13952.t2	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1582	940	1.00E-65	59.4	10.1	14.4	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13953.t1	gb|EMJ12193.1| hypothetical protein PRUPE_ppa021032mg [Prunus persica]	517	781	6.00E-41	151.1	24.4	40.0	hypothetical protein PRUPE_ppa021032mg	gbpln	Prunus persica	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	517	484	4.00E-16	93.6	7.4	12.2
Rsa1.0_00444.1.g13954.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13955.t1	gb|AAF79348.1|AC007887_7 F15O4.13 [Arabidopsis thaliana]	147	1887	1.00E-18	1283.7	38.1	52.4	F15O4.13	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13956.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13957.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13958.t1	ref|XP_002865504.1| hypothetical protein ARALYDRAFT_917484 [Arabidopsis lyrata subsp. lyrata] gi|297311339|gb|EFH41763.1| hypothetical protein ARALYDRAFT_917484 [Arabidopsis lyrata subsp. lyrata]	282	293	1.00E-121	103.9	78.0	85.8	hypothetical protein ARALYDRAFT_917484	gbpln	Arabidopsis lyrata	AT5G42610.1 | Symbols: | Protein of unknown function (DUF607) | chr5:17062507-17063934 FORWARD LENGTH=293	282	293	1.00E-123	103.9	78.0	85.1
Rsa1.0_00444.1.g13959.t1	gb|AAL59842.1| cysteine protease inhibitor CPI-1 [Brassica oleracea]	104	207	1.00E-15	199.0	47.1	50.0	cysteine protease inhibitor CPI-1	gbpln	Brassica oleracea	AT3G12490.2 | Symbols: ATCYSB, ATCYS6, CYSB | cystatin B | chr3:3960523-3961876 REVERSE LENGTH=234	104	234	5.00E-16	225.0	43.3	48.1
Rsa1.0_00444.1.g13960.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	348	1024	2.00E-36	294.3	21.8	29.3	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00444.1.g13961.t1	gb|AAD19762.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	254	616	1.00E-15	242.5	24.4	32.3	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00445.1.g13962.t1	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1259	1449	0	115.1	35.9	53.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1259	746	2.00E-78	59.3	11.8	16.0

Rsa1.0_00445.1.g13963.t1	gb|EOA25808.1| hypothetical protein CARUB_v10019176mg [Capsella rubella]	147	204	9.00E-43	138.8	57.8	72.1	hypothetical protein CARUB_v10019176mg	gbpln	Capsella rubella	AT4G04090.1 | Symbols: | BTB/POZ domain-containing protein | chr4:1964980-1965650 FORWARD LENGTH=192	147	192	2.00E-41	130.6	57.8	71.4
Rsa1.0_00445.1.g13964.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00445.1.g13965.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	729	1142	0	156.7	52.3	63.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	729	575	4.00E-27	78.9	9.6	16.7
Rsa1.0_00445.1.g13966.t1	gb|EOA22943.1| hypothetical protein CARUB_v10003680mg, partial [Capsella rubella]	555	669	1.00E-136	120.5	49.0	65.6	hypothetical protein CARUB_v10003680mg, partial	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	555	696	1.00E-31	125.4	24.9	42.0
Rsa1.0_00445.1.g13967.t1	ref|XP_004292625.1| PREDICTED: uncharacterized protein LOC101299743 [Fragaria vesca subsp. vesca]	479	746	1.00E-141	155.7	54.3	69.9	PREDICTED: uncharacterized protein LOC101299743	gbpln	Fragaria vesca	AT5G31412.1 | Symbols: | hAT transposon superfamily protein | chr5:11541463-11543768 REVERSE LENGTH=433	479	433	8.00E-83	90.4	37.8	50.1
Rsa1.0_00445.1.g13968.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00445.1.g13969.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	209	657	1.00E-64	314.4	54.5	68.9	T14P8.10	gbpln	Arabidopsis thaliana	AT5G16486.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:5383597-5384226 REVERSE LENGTH=209	209	209	9.00E-61	100.0	52.2	67.9
Rsa1.0_00445.1.g13970.t1	ref|NP_176277.1| AP-1 complex subunit mu [Arabidopsis thaliana] gi|2462748|gb|AAB71967.1| putative Clathrin Coat Assembly protein [Arabidopsis thaliana] gi|20466372|gb|AAM20503.1| clathrin adaptor medium chain protein MU1B, putative [Arabidopsis thaliana] gi|25084014|gb|AAN72155.1| clathrin adaptor medium chain protein MU1B, putative [Arabidopsis thaliana] gi|332195610|gb|AEE33731.1| protein HAPLESS 13 [Arabidopsis thaliana]	300	428	1.00E-167	142.7	93.7	97.0	AP-1 complex subunit mu	gbpln	Arabidopsis thaliana	AT1G60780.1 | Symbols: HAP13 | Clathrin adaptor complexes medium subunit family protein | chr1:22369289-22371885 REVERSE LENGTH=428	300	428	1.00E-170	142.7	93.7	97.0
Rsa1.0_00445.1.g13971.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1421	1499	0	105.5	55.0	66.3	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1421	158	1.00E-31	11.1	4.5	6.2
Rsa1.0_00445.1.g13972.t1	gb|ABD65091.1| hypothetical protein 31.t00049 [Brassica oleracea]	320	530	2.00E-71	165.6	47.8	64.1	hypothetical protein 31.t00049	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00445.1.g13973.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	762	672	3.00E-96	88.2	27.4	42.1	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00445.1.g13974.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1866	940	5.00E-94	50.4	12.5	19.3	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	1866	921	5.00E-16	49.4	2.3	3.6
Rsa1.0_00445.1.g13975.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00445.1.g13976.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	78	341	3.00E-12	437.2	44.9	65.4	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00446.1.g13977.t2	ref|NP_199384.2| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332007905|gb|AED95288.1| AAA-type ATPase family protein [Arabidopsis thaliana]	583	966	0	165.7	63.5	71.7	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT5G45720.1 | Symbols: | AAA-type ATPase family protein | chr5:18543338-18546629 REVERSE LENGTH=966	583	966	0	165.7	63.5	71.7
Rsa1.0_00446.1.g13978.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00446.1.g13979.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00446.1.g13980.t5	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	795	1231	0	154.8	46.5	61.6	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	795	575	3.00E-77	72.3	20.1	32.1
Rsa1.0_00446.1.g13981.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00446.1.g13982.t1	emb|CAB77974.1| putative athila-like protein [Arabidopsis thaliana]	580	587	2.00E-16	101.2	8.6	13.8	putative athila-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00446.1.g13983.t1	ref|NP_567562.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] gi|44681468|gb|AAS47674.1| At4g18596 [Arabidopsis thaliana] gi|62320348|dbj|BAD94719.1| pollen-specific protein - like [Arabidopsis thaliana] gi|332658666|gb|AEE84066.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana]	174	172	6.00E-84	98.9	89.1	93.1	pollen Ole e 1 allergen and extensin family protein	gbpln	Arabidopsis thaliana	AT4G18596.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr4:10239114-10239728 FORWARD LENGTH=172	174	172	3.00E-86	98.9	89.1	93.1
Rsa1.0_00446.1.g13984.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00446.1.g13985.t4	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	400	1529	2.00E-46	382.3	27.8	38.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	400	746	7.00E-30	186.5	23.0	31.0

Rsa1.0_00446.1.g13986.t1	gb|AAD53012.1|AF089849_1 senescence-specific cysteine protease [Brassica napus]	402	344	1.00E-159	85.6	69.9	72.9	senescence-specific cysteine protease	gbpln	Brassica napus	AT5G45890.1 | Symbols: SAG12 | senescence-associated gene 12 | chr5:18613300-18614759 FORWARD LENGTH=346	402	346	1.00E-140	86.1	58.5	65.9
Rsa1.0_00446.1.g13987.t1	ref|XP_002863434.1| hypothetical protein ARALYDRAFT_494379 [Arabidopsis lyrata subsp. lyrata] gi|297309269|gb|EFH39693.1| hypothetical protein ARALYDRAFT_494379 [Arabidopsis lyrata subsp. lyrata]	164	164	2.00E-55	100.0	93.3	97.6	hypothetical protein ARALYDRAFT_494379	gbpln	Arabidopsis lyrata	AT5G46020.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Casein kinase substrate, phosphoprotein PP28 (InterPro:IPR019380); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:18663075-18664629 REVERSE LENGTH=164	164	164	5.00E-57	100.0	93.3	97.6
Rsa1.0_00446.1.g13988.t1	gb|EOA14228.1| hypothetical protein CARUB_v10027385mg [Capsella rubella]	127	120	1.00E-42	94.5	79.5	85.0	hypothetical protein CARUB_v10027385mg	gbpln	Capsella rubella	AT5G46030.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF701, zinc-binding putative (InterPro:IPR007808); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:18670531-18671138 FORWARD LENGTH=120	127	120	6.00E-40	94.5	78.0	84.3
Rsa1.0_00446.1.g13989.t1	ref|NP_199419.2| Guanylate-binding protein [Arabidopsis thaliana] gi|332007951|gb|AED95334.1| Guanylate-binding protein [Arabidopsis thaliana]	1081	1082	0	100.1	88.5	93.5	Guanylate-binding protein	gbpln	Arabidopsis thaliana	AT5G46070.1 | Symbols: | Guanylate-binding family protein | chr5:18683468-18688397 FORWARD LENGTH=1082	1081	1082	0	100.1	88.5	93.5
Rsa1.0_00446.1.g13990.t1	ref|NP_199420.1| protein kinase family protein [Arabidopsis thaliana] gi|9757728|dbj|BAB08253.1| serine/threonine protein kinase-like protein [Arabidopsis thaliana] gi|332007952|gb|AED95335.1| protein kinase family protein [Arabidopsis thaliana]	333	332	1.00E-147	99.7	82.6	89.8	protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G46080.1 | Symbols: | Protein kinase superfamily protein | chr5:18689723-18690721 REVERSE LENGTH=332	333	332	1.00E-150	99.7	82.6	89.8
Rsa1.0_00446.1.g13991.t1	gb|EOA14650.1| hypothetical protein CARUB_v10027911mg [Capsella rubella]	222	224	1.00E-104	100.9	82.9	90.5	hypothetical protein CARUB_v10027911mg	gbpln	Capsella rubella	AT5G46090.1 | Symbols: | Protein of unknown function (DUF679) | chr5:18693485-18694129 FORWARD LENGTH=214	222	214	8.00E-92	96.4	73.0	82.4
Rsa1.0_00446.1.g13992.t1	gb|EOA14650.1| hypothetical protein CARUB_v10027911mg [Capsella rubella]	210	224	1.00E-90	106.7	77.1	84.8	hypothetical protein CARUB_v10027911mg	gbpln	Capsella rubella	AT5G46090.1 | Symbols: | Protein of unknown function (DUF679) | chr5:18693485-18694129 FORWARD LENGTH=214	210	214	7.00E-91	101.9	74.3	85.2
Rsa1.0_00446.1.g13993.t1	ref|XP_002863429.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297309264|gb|EFH39688.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	473	472	0	99.8	90.7	96.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G46100.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:18694316-18695734 REVERSE LENGTH=472	473	472	0	99.8	89.6	96.2
Rsa1.0_00446.1.g13994.t1	sp|P52177.1|TPT1_BRAOB RecName: Full=Triose phosphate/phosphate translocator, chloroplastic; Short=cTPT; Flags: Precursor gi|1143709|gb|AAA84890.1| chloroplast phosphate/triose-phosphate translocator precursor [Brassica oleracea var. botrytis]	430	407	0	94.7	90.5	91.9	RecName: Full=Triose phosphate/phosphate translocator, chloroplastic; Short=cTPT; Flags: Precursor gi|1143709|gb|AAA84890.1| chloroplast phosphate/triose-phosphate translocator precursor	gbpln	Brassica oleracea	AT5G46110.4 | Symbols: APE2, TPT | Glucose-6-phosphate/phosphate translocator-related | chr5:18697606-18700223 FORWARD LENGTH=415	430	415	0	96.5	86.0	90.7
Rsa1.0_00446.1.g13995.t1	ref|XP_002863425.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297309260|gb|EFH39684.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	79	79	4.00E-31	100.0	83.5	87.3	expressed protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#

Rsa1.0_00446.1.g13996.t1	ref|NP_196114.1| nicotianamine synthase 1 [Arabidopsis thaliana] gi|27151631|sp|Q9FF79.1|NAS1_ARATH RecName: Full=Nicotianamine synthase 1; AltName: Full=S-adenosyl-L-methionine:S-adenosyl-L-methionine:S- adenosyl-methionine 3-amino-3-carboxypropyltransferase 1; Short=AtNAS1 gi|10178034|dbj|BAB11517.1| nicotianamine synthase [Arabidopsis thaliana] gi|18252859|gb|AAL62356.1| nicotianamine synthase [Arabidopsis thaliana] gi|23198368|gb|AAN15711.1| nicotianamine synthase [Arabidopsis thaliana] gi|332003425|gb|AED90808.1| nicotianamine synthase 1 [Arabidopsis thaliana]	280	320	1.00E-106	114.3	69.3	83.6	nicotianamine synthase 1	gbpln	Arabidopsis thaliana	AT5G04950.1 | Symbols: NAS1, ATNAS1 | nicotianamine synthase 1 | chr5:1457876-1458838 REVERSE LENGTH=320	280	320	1.00E-109	114.3	69.3	83.6
Rsa1.0_00447.1.g13997.t4	ref|NP_567013.1| tonneau 1b (TON1b) [Arabidopsis thaliana] gi|75262840|sp|Q9FQ24.1|TON1B_ARATH RecName: Full=Protein TONNEAU 1b gi|11494365|gb|AAG35780.1|AF280058_2 tonneau 1b [Arabidopsis thaliana] gi|18700182|gb|AAL77702.1| AT3g55000/F28P10_20 [Arabidopsis thaliana] gi|332645805|gb|AEE79326.1| tonneau 1b (TON1b) [Arabidopsis thaliana]	391	257	1.00E-96	65.7	48.1	52.2	tonneau 1b (TON1b)	gbpln	Arabidopsis thaliana	AT3G55005.1 | Symbols: TON1B | tonneau 1b (TON1b) | chr3:20384131-20386193 FORWARD LENGTH=257	391	257	3.00E-99	65.7	48.1	52.2
Rsa1.0_00447.1.g13998.t1	gb|EOA25829.1| hypothetical protein CARUB_v10019201mg [Capsella rubella]	384	383	0	99.7	86.5	93.2	hypothetical protein CARUB_v10019201mg	gbpln	Capsella rubella	AT3G55010.2 | Symbols: ATPURM, PUR5 | phosphoribosylformylglycinamidine cyclo-ligase, chloroplast / phosphoribosyl-aminoimidazole synthetase / AIR synthase (PUR5) | chr3:20386818-20388549 FORWARD LENGTH=389	384	389	1.00E-179	101.3	86.2	92.7
Rsa1.0_00447.1.g13999.t1	ref|XP_002878011.1| hypothetical protein ARALYDRAFT_324032 [Arabidopsis lyrata subsp. lyrata] gi|297323849|gb|EFH54270.1| hypothetical protein ARALYDRAFT_324032 [Arabidopsis lyrata subsp. lyrata]	812	825	0	101.6	87.4	92.2	hypothetical protein ARALYDRAFT_324032	gbpln	Arabidopsis lyrata	AT3G55020.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr3:20389278-20394713 REVERSE LENGTH=777	812	777	0	95.7	80.7	85.3
Rsa1.0_00447.1.g14000.t1	gb|EOA25129.1| hypothetical protein CARUB_v10018438mg [Capsella rubella]	210	235	1.00E-102	111.9	93.3	96.7	hypothetical protein CARUB_v10018438mg	gbpln	Capsella rubella	AT3G55030.1 | Symbols: PGPS2 | phosphatidylglycerolphosphate synthase 2 | chr3:20396860-20398224 FORWARD LENGTH=233	210	233	1.00E-104	111.0	92.9	96.2
Rsa1.0_00447.1.g14001.t1	ref|XP_002878012.1| hypothetical protein ARALYDRAFT_906920 [Arabidopsis lyrata subsp. lyrata] gi|297323850|gb|EFH54271.1| hypothetical protein ARALYDRAFT_906920 [Arabidopsis lyrata subsp. lyrata]	296	294	1.00E-133	99.3	78.4	87.5	hypothetical protein ARALYDRAFT_906920	gbpln	Arabidopsis lyrata	AT3G55040.1 | Symbols: GSTL2 | glutathione transferase lambda 2 | chr3:20398718-20400305 REVERSE LENGTH=292	296	292	1.00E-124	98.6	77.4	86.1
Rsa1.0_00447.1.g14002.t1	ref|NP_191065.2| putative protein phosphatase 2C 48 [Arabidopsis thaliana] gi|42572685|ref|NP_974438.1| putative protein phosphatase 2C 48 [Arabidopsis thaliana] gi|75249980|sp|Q94CL8.1|P2C48_ARATH RecName: Full=Probable protein phosphatase 2C 48; Short=AtPP2C48; AltName: Full=Protein phosphatase 2C 6 gi|15020818|emb|CAC44619.1| Ser/Thr protein phosphatase 2C [Arabidopsis thaliana] gi|48525333|gb|AAT44968.1| At3g55050 [Arabidopsis thaliana] gi|61656143|gb|AAX49374.1| At3g55050 [Arabidopsis thaliana] gi|110738459|dbj|BAF01155.1| protein phosphatase 2C like protein [Arabidopsis thaliana] gi|332645811|gb|AEE79332.1| putative protein phosphatase 2C 48 [Arabidopsis thaliana] gi|332645812|gb|AEE79333.1| putative protein phosphatase 2C 48 [Arabidopsis thaliana]	390	384	0	98.5	87.7	94.6	putative protein phosphatase 2C 48	gbpln	Arabidopsis thaliana	AT3G55050.2 | Symbols: | Protein phosphatase 2C family protein | chr3:20400669-20401922 REVERSE LENGTH=384	390	384	0	98.5	87.7	94.6

Rsa1.0_00447.1.g14003.t1	ref|XP_002876284.1| hypothetical protein ARALYDRAFT_485927 [Arabidopsis lyrata subsp. lyrata] gi|297322122|gb|EFH52543.1| hypothetical protein ARALYDRAFT_485927 [Arabidopsis lyrata subsp. lyrata]	413	418	0	101.2	86.4	92.3	hypothetical protein ARALYDRAFT_485927	gbpln	Arabidopsis lyrata	AT3G55070.1 | Symbols: | LisH/CRA/RING-U-box domains-containing protein | chr3:20408377-20410887 FORWARD LENGTH=418	413	418	0	101.2	84.7	90.8
Rsa1.0_00447.1.g14004.t1	ref|XP_002878015.1| SET domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297323853|gb|EFH54274.1| SET domain-containing protein [Arabidopsis lyrata subsp. lyrata]	473	473	0	100.0	79.1	87.5	SET domain-containing protein	gbpln	Arabidopsis lyrata	AT3G55080.1 | Symbols: | SET domain-containing protein | chr3:20411476-20415830 REVERSE LENGTH=463	473	463	0	97.9	76.3	84.8
Rsa1.0_00447.1.g14005.t1	gb|ABB97036.1| ABC transporter-like protein [Brassica rapa]	709	708	0	99.9	94.5	97.3	ABC transporter-like protein	gbpln	Brassica rapa	AT3G55110.1 | Symbols: | ABC-2 type transporter family protein | chr3:20424766-20426892 REVERSE LENGTH=708	709	708	0	99.9	83.6	91.8
Rsa1.0_00447.1.g14006.t1	sp|O22651.1|CFI_RAPSA RecName: Full=Chalcone--flavonone isomerase; Short=Chalcone isomerase gi|2642604|gb|AAB87071.1| chalcone isomerase [Raphanus sativus]	247	247	1.00E-133	100.0	97.6	98.4	RecName: Full=Chalcone--flavonone isomerase; Short=Chalcone isomerase gi|2642604|gb|AAB87071.1| chalcone isomerase	gbpln	Raphanus sativus	AT3G55120.1 | Symbols: TT5, A11, CFI | Chalcone-flavanone isomerase family protein | chr3:20430248-20431415 REVERSE LENGTH=246	247	246	1.00E-110	99.6	81.8	89.1
Rsa1.0_00447.1.g14007.t1	ref|XP_002886490.1| hypothetical protein ARALYDRAFT_315177 [Arabidopsis lyrata subsp. lyrata] gi|297332331|gb|EFH62749.1| hypothetical protein ARALYDRAFT_315177 [Arabidopsis lyrata subsp. lyrata]	178	812	1.00E-33	456.2	45.5	54.5	hypothetical protein ARALYDRAFT_315177	gbpln	Arabidopsis lyrata	AT1G62120.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:22960326-22961639 REVERSE LENGTH=437	178	437	1.00E-33	245.5	44.9	52.2
Rsa1.0_00447.1.g14008.t1	ref|NP_191075.2| exocyst complex component 7 [Arabidopsis thaliana] gi|18377618|gb|AAL66959.1| unknown protein [Arabidopsis thaliana] gi|20465379|gb|AAM20093.1| unknown protein [Arabidopsis thaliana] gi|332645825|gb|AEE79346.1| exocyst subunit exo70 family protein H1 [Arabidopsis thaliana]	635	636	0	100.2	84.7	92.3	exocyst complex component 7	gbpln	Arabidopsis thaliana	AT3G55150.1 | Symbols: ATEXO70H1, EXO70H1 | exocyst subunit exo70 family protein H1 | chr3:20440655-20442565 REVERSE LENGTH=636	635	636	0	100.2	84.7	92.3
Rsa1.0_00447.1.g14009.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00447.1.g14010.t1	ref|NP_191078.1| esterase/lipase/thioesterase family protein [Arabidopsis thaliana] gi|7019651|emb|CAB75752.1| lipase-like protein [Arabidopsis thaliana] gi|332645829|gb|AEE79350.1| esterase/lipase/thioesterase family protein [Arabidopsis thaliana]	304	312	1.00E-158	102.6	86.8	92.8	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis thaliana	AT3G55180.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:20454903-20456682 FORWARD LENGTH=312	304	312	1.00E-160	102.6	86.8	92.8
Rsa1.0_00448.1.g14011.t1	dbj|BAJ33859.1| unnamed protein product [Thellungiella halophila]	334	343	1.00E-147	102.7	85.6	92.2	unnamed protein product	----	----	AT3G52400.1 | Symbols: SYP122, ATSYP122 | syntaxin of plants 122 | chr3:19425835-19427032 REVERSE LENGTH=341	334	341	1.00E-136	102.1	79.6	90.4
Rsa1.0_00448.1.g14012.t1	gb|EOA24991.1| hypothetical protein CARUB_v10018288mg, partial [Capsella rubella]	66	106	2.00E-19	160.6	77.3	83.3	hypothetical protein CARUB_v10018288mg, partial	gbpln	Capsella rubella	AT3G52420.1 | Symbols: OEP7, ATOEP7 | outer envelope membrane protein 7 | chr3:19429775-19429969 FORWARD LENGTH=64	66	64	6.00E-21	97.0	71.2	74.2
Rsa1.0_00448.1.g14013.t1	gb|ABR46042.1| phytoalexin deficient 4 [Arabidopsis thaliana]	547	541	0	98.9	65.1	76.8	phytoalexin deficient 4	gbpln	Arabidopsis thaliana	AT3G52430.1 | Symbols: PAD4, ATPAD4 | alpha/beta-Hydrolases superfamily protein | chr3:19431566-19434292 FORWARD LENGTH=541	547	541	0	98.9	64.5	75.9
Rsa1.0_00448.1.g14014.t1	dbj|BAH30484.1| hypothetical protein [Arabidopsis thaliana]	236	266	1.00E-111	112.7	85.6	91.1	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G52440.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr3:19435447-19436190 FORWARD LENGTH=247	236	247	1.00E-113	104.7	85.6	91.1
Rsa1.0_00448.1.g14015.t1	dbj|BAJ34414.1| unnamed protein product [Thellungiella halophila]	423	435	0	102.8	92.7	94.8	unnamed protein product	----	----	AT3G52450.1 | Symbols: PUB22 | plant U-box 22 | chr3:19440943-19442250 REVERSE LENGTH=435	423	435	0	102.8	89.6	93.4
Rsa1.0_00448.1.g14016.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00448.1.g14017.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00448.1.g14018.t1	ref|XP_002876145.1| hypothetical protein ARALYDRAFT_906612 [Arabidopsis lyrata subsp. lyrata] gi|297321983|gb|EFH52404.1| hypothetical protein ARALYDRAFT_906612 [Arabidopsis lyrata subsp. lyrata]	302	295	1.00E-110	97.7	72.2	79.1	hypothetical protein ARALYDRAFT_906612	gbpln	Arabidopsis lyrata	AT3G52460.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr3:19446970-19447872 FORWARD LENGTH=300	302	300	1.00E-107	99.3	74.5	83.1

Rsa1.0_00448.1.g14019.t1	gb|EOA33837.1| hypothetical protein CARUB_v10021318mg, partial [Capsella rubella]	110	290	2.00E-23	263.6	49.1	61.8	hypothetical protein CARUB_v10021318mg, partial	gbpln	Capsella rubella	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	110	332	1.00E-23	301.8	44.5	58.2
Rsa1.0_00448.1.g14020.t1	dbj|BAJ34290.1| unnamed protein product [Thellungiella halophila]	208	208	1.00E-114	100.0	95.2	98.6	unnamed protein product	----	----	AT3G52470.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:19450750-19451376 FORWARD LENGTH=208	208	208	1.00E-109	100.0	88.9	94.7
Rsa1.0_00448.1.g14021.t1	ref|NP_190817.1| heat shock protein-like protein [Arabidopsis thaliana] gi|4886278|emb|CAB43425.1| putative protein [Arabidopsis thaliana] gi|44917467|gb|AAS49058.1| At3g52490 [Arabidopsis thaliana] gi|332645430|gb|AEE78951.1| heat shock protein-like protein [Arabidopsis thaliana]	786	815	0	103.7	83.2	90.3	heat shock protein-like protein	gbpln	Arabidopsis thaliana	AT3G52490.1 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr3:19455850-19458721 REVERSE LENGTH=815	786	815	0	103.7	83.2	90.3
Rsa1.0_00448.1.g14022.t1	ref|NP_192687.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|7267644|emb|CAB78072.1| putative proteins [Arabidopsis thaliana] gi|332657356|gb|AEE82756.1| RNase H domain-containing protein [Arabidopsis thaliana]	94	170	2.00E-11	180.9	39.4	57.4	RNase H domain-containing protein	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	94	170	3.00E-14	180.9	39.4	57.4
Rsa1.0_00448.1.g14023.t1	ref|XP_002877867.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297323705|gb|EFH54126.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	471	469	0	99.6	79.2	88.1	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT3G52500.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:19465644-19467053 REVERSE LENGTH=469	471	469	0	99.6	78.1	88.1
Rsa1.0_00448.1.g14024.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00448.1.g14025.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00448.1.g14026.t1	ref|XP_002870253.1| hypothetical protein ARALYDRAFT_355259 [Arabidopsis lyrata subsp. lyrata] gi|297316089|gb|EFH46512.1| hypothetical protein ARALYDRAFT_355259 [Arabidopsis lyrata subsp. lyrata]	1377	1390	0	100.9	82.4	92.4	hypothetical protein ARALYDRAFT_355259	gbpln	Arabidopsis lyrata	AT4G15236.1 | Symbols: | ABC-2 and Plant PDR ABC-type transporter family protein | chr4:8696683-8702727 FORWARD LENGTH=1388	1377	1388	0	100.8	81.7	91.0
Rsa1.0_00448.1.g14027.t2	ref|XP_002870253.1| hypothetical protein ARALYDRAFT_355259 [Arabidopsis lyrata subsp. lyrata] gi|297316089|gb|EFH46512.1| hypothetical protein ARALYDRAFT_355259 [Arabidopsis lyrata subsp. lyrata]	1240	1390	0	112.1	80.4	89.9	hypothetical protein ARALYDRAFT_355259	gbpln	Arabidopsis lyrata	AT4G15236.1 | Symbols: | ABC-2 and Plant PDR ABC-type transporter family protein | chr4:8696683-8702727 FORWARD LENGTH=1388	1240	1388	0	111.9	79.5	88.7
Rsa1.0_00448.1.g14028.t1	ref|XP_002868218.1| hypothetical protein ARALYDRAFT_493365 [Arabidopsis lyrata subsp. lyrata] gi|297314054|gb|EFH44477.1| hypothetical protein ARALYDRAFT_493365 [Arabidopsis lyrata subsp. lyrata]	450	488	1.00E-155	108.4	56.9	60.4	hypothetical protein ARALYDRAFT_493365	gbpln	Arabidopsis lyrata	AT4G15240.1 | Symbols: | Protein of unknown function (DUF604) | chr4:8703518-8705378 REVERSE LENGTH=488	450	488	1.00E-155	108.4	56.2	60.0
Rsa1.0_00448.1.g14029.t1	ref|XP_002870248.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297316084|gb|EFH46507.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	471	466	0	98.9	69.4	83.7	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT4G15280.1 | Symbols: UGT71B5 | UDP-glucosyl transferase 71B5 | chr4:8719182-8720618 FORWARD LENGTH=478	471	478	0	101.5	69.4	83.7
Rsa1.0_00449.1.g14030.t1	gb|EOA17853.1| hypothetical protein CARUB_v10006257mg [Capsella rubella]	503	518	0	103.0	92.8	94.8	hypothetical protein CARUB_v10006257mg	gbpln	Capsella rubella	AT4G35230.1 | Symbols: BSK1 | BR-signaling kinase 1 | chr4:16755325-16758041 REVERSE LENGTH=512	503	512	0	101.8	92.4	95.0
Rsa1.0_00449.1.g14031.t1	gb|EOA18585.1| hypothetical protein CARUB_v10007157mg [Capsella rubella]	251	251	1.00E-116	100.0	84.5	94.8	hypothetical protein CARUB_v10007157mg	gbpln	Capsella rubella	AT4G35210.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16751428-16752180 FORWARD LENGTH=250	251	250	1.00E-117	99.6	83.7	94.0
Rsa1.0_00449.1.g14032.t1	gb|EOA18908.1| hypothetical protein CARUB_v10007538mg [Capsella rubella]	254	253	1.00E-109	99.6	81.1	90.6	hypothetical protein CARUB_v10007538mg	gbpln	Capsella rubella	AT4G35200.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16749142-16749903 REVERSE LENGTH=253	254	253	1.00E-109	99.6	79.5	89.4
Rsa1.0_00449.1.g14033.t1	gb|EOA18585.1| hypothetical protein CARUB_v10007157mg [Capsella rubella]	232	251	6.00E-98	108.2	78.4	91.4	hypothetical protein CARUB_v10007157mg	gbpln	Capsella rubella	AT4G35210.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16751428-16752180 FORWARD LENGTH=250	232	250	1.00E-100	107.8	78.0	91.8

Rsa1.0_00449.1.g14034.t1	ref|NP_567977.2| LYS/HIS transporter 7 [Arabidopsis thaliana] gi|334302829|sp|Q84WE9.2|LHTL7_ARATH RecName: Full=Lysine histidine transporter-like 7 gi|332661077|gb|AEE86477.1| LYS/HIS transporter 7 [Arabidopsis thaliana]	597	478	0	80.1	57.1	65.5	LYS/HIS transporter 7	gbpln	Arabidopsis thaliana	AT4G35180.1 | Symbols: LHT7 | LYS/HIS transporter 7 | chr4:16738517-16740385 REVERSE LENGTH=478	597	478	0	80.1	57.1	65.5
Rsa1.0_00449.1.g14035.t2	sp|P14874.1|ILVB2_BRANA RecName: Full=Acetolactate synthase 2, chloroplastic; AltName: Full=ALS II; AltName: Full=Acetohydroxy-acid synthase II; AltName: Full=Acetolactate synthase II; Flags: Precursor gi|17774|emb|CAA77614.1| acetohydroxyacid synthase II [Brassica napus] gi|17778|emb|CAA34680.1| unnamed protein product [Brassica napus]	338	637	8.00E-97	188.5	55.3	60.4	RecName: Full=Acetolactate synthase 2, chloroplastic; AltName: Full=ALS II; AltName: Full=Acetohydroxy-acid synthase II; AltName: Full=Acetolactate synthase II; Flags: Precursor gi|17774|emb|CAA77614.1| acetohydroxyacid synthase II	gbpln	Brassica napus	AT3G48560.1 | Symbols: CSR1, ALS, AHAS, TZP5, IMR1 | chlorsulfuron/imidazolinone resistant 1 | chr3:18001530-18003542 REVERSE LENGTH=670	338	670	1.00E-87	198.2	49.7	55.0
Rsa1.0_00449.1.g14036.t2	ref|XP_002869102.1| hypothetical protein ARALYDRAFT_912862 [Arabidopsis lyrata subsp. lyrata] gi|297314938|gb|EFH45361.1| hypothetical protein ARALYDRAFT_912862 [Arabidopsis lyrata subsp. lyrata]	236	225	1.00E-120	95.3	87.7	92.4	hypothetical protein ARALYDRAFT_912862	gbpln	Arabidopsis lyrata	AT4G35190.1 | Symbols: | Putative lysine decarboxylase family protein | chr4:16746724-16748090 FORWARD LENGTH=228	236	228	1.00E-116	96.6	87.3	92.4
Rsa1.0_00449.1.g14037.t1	ref|XP_002867087.1| O-methyltransferase family 2 protein [Arabidopsis lyrata subsp. lyrata] gi|297312923|gb|EFH43346.1| O-methyltransferase family 2 protein [Arabidopsis lyrata subsp. lyrata]	368	368	0	100.0	86.4	91.0	O-methyltransferase family 2 protein	gbpln	Arabidopsis lyrata	AT4G35160.1 | Symbols: | O-methyltransferase family protein | chr4:16730989-16732808 REVERSE LENGTH=382	368	382	0	103.8	86.4	92.1
Rsa1.0_00449.1.g14038.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00449.1.g14039.t1	ref|XP_002867091.1| hypothetical protein ARALYDRAFT_353319 [Arabidopsis lyrata subsp. lyrata] gi|297312927|gb|EFH43350.1| hypothetical protein ARALYDRAFT_353319 [Arabidopsis lyrata subsp. lyrata]	368	386	1.00E-151	104.9	78.0	86.1	hypothetical protein ARALYDRAFT_353319	gbpln	Arabidopsis lyrata	AT4G35110.2 | Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) family | chr4:16712660-16713987 REVERSE LENGTH=386	368	386	1.00E-151	104.9	78.3	85.3
Rsa1.0_00449.1.g14040.t1	gb|AAG30607.1|AF314656_1 aquaporin [Brassica oleracea]	281	281	1.00E-159	100.0	97.9	100.0	aquaporin	gbpln	Brassica oleracea	AT4G35100.2 | Symbols: PIP3 | plasma membrane intrinsic protein 3 | chr4:16708672-16709958 FORWARD LENGTH=280	281	280	1.00E-155	99.6	95.0	97.5
Rsa1.0_00449.1.g14041.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00449.1.g14042.t1	gb|AAD17935.1| catalase [Brassica juncea]	492	492	0	100.0	99.6	100.0	catalase	gbpln	Brassica juncea	AT4G35090.1 | Symbols: CAT2 | catalase 2 | chr4:16700937-16703215 REVERSE LENGTH=492	492	492	0	100.0	97.8	99.8
Rsa1.0_00449.1.g14043.t1	ref|XP_002869109.1| hypothetical protein ARALYDRAFT_912877 [Arabidopsis lyrata subsp. lyrata] gi|297314945|gb|EFH45368.1| hypothetical protein ARALYDRAFT_912877 [Arabidopsis lyrata subsp. lyrata]	359	365	1.00E-149	101.7	85.8	91.6	hypothetical protein ARALYDRAFT_912877	gbpln	Arabidopsis lyrata	AT4G35080.1 | Symbols: | high-affinity nickel-transport family protein | chr4:16698384-16700012 FORWARD LENGTH=365	359	365	1.00E-145	101.7	83.6	89.7
Rsa1.0_00449.1.g14044.t1	ref|XP_002869110.1| hypothetical protein ARALYDRAFT_491149 [Arabidopsis lyrata subsp. lyrata] gi|297314946|gb|EFH45369.1| hypothetical protein ARALYDRAFT_491149 [Arabidopsis lyrata subsp. lyrata]	252	265	2.00E-97	105.2	79.0	86.1	hypothetical protein ARALYDRAFT_491149	gbpln	Arabidopsis lyrata	AT4G35070.1 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr4:16694488-16695387 FORWARD LENGTH=265	252	265	2.00E-99	105.2	75.8	86.5
Rsa1.0_00450.1.g14045.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	201	1231	1.00E-21	612.4	24.9	35.8	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14046.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14047.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14048.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14049.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14050.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14051.t1	gb|AFJ94635.1| P1B-ATPase 4 [Brassica juncea]	1237	1272	0	102.8	89.6	91.8	P1B-ATPase 4	gbpln	Brassica juncea	AT2G19110.1 | Symbols: HMA4, ATHMA4 | heavy metal atpase 4 | chr2:8279478-8286255 FORWARD LENGTH=1172	1237	1172	0	94.7	68.8	74.9

Rsa1.0_00450.1.g14052.t1	gb|ACC68157.1| unknown [Arabidopsis halleri subsp. halleri]	378	393	0	104.0	81.2	90.5	unknown	gbpln	Arabidopsis halleri	AT2G19160.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr2:8310921-8313595 FORWARD LENGTH=394	378	394	0	104.2	81.5	90.5
Rsa1.0_00450.1.g14053.t2	gb|ACC68158.1| putative subtilase family protein [Arabidopsis halleri subsp. halleri]	797	815	0	102.3	94.9	97.5	putative subtilase family protein	gbpln	Arabidopsis halleri	AT2G19170.1 | Symbols: SLP3 | subtilisin-like serine protease 3 | chr2:8314154-8317620 REVERSE LENGTH=815	797	815	0	102.3	94.5	97.2
Rsa1.0_00450.1.g14054.t1	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	747	1643	1.00E-131	219.9	41.8	62.8	gag/pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14055.t2	ref|NP_565448.1| uncharacterized protein [Arabidopsis thaliana] gi|3176718|gb|AAD12033.1| expressed protein [Arabidopsis thaliana] gi|21593481|gb|AAM65448.1| unknown [Arabidopsis thaliana] gi|21805656|gb|AAM76745.1| hypothetical protein [Arabidopsis thaliana] gi|61742592|gb|AAX55117.1| hypothetical protein At2g19180 [Arabidopsis thaliana] gi|330251761|gb|AEC06855.1| uncharacterized protein AT2G19180 [Arabidopsis thaliana]	211	179	2.00E-36	84.8	40.8	48.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G19180.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16840.1); Has 64 Blast hits to 64 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:8324742-8325575 FORWARD LENGTH=179	211	179	5.00E-39	84.8	40.8	48.8
Rsa1.0_00450.1.g14056.t1	gb|ABK28562.1| unknown [Arabidopsis thaliana]	318	381	5.00E-81	119.8	53.5	65.4	unknown	gbpln	Arabidopsis thaliana	AT3G18720.1 | Symbols: | F-box family protein | chr3:6444433-6445751 REVERSE LENGTH=380	318	380	1.00E-83	119.5	53.5	65.4
Rsa1.0_00450.1.g14057.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14058.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00450.1.g14059.t1	ref|NP_179516.2| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana] gi|330251767|gb|AEC06861.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana]	633	631	0	99.7	67.1	76.9	RING/FYVE/PHD zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT2G19260.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:8357331-8359931 FORWARD LENGTH=631	633	631	0	99.7	67.1	76.9
Rsa1.0_00450.1.g14060.t1	ref|XP_002883998.1| hypothetical protein ARALYDRAFT_319616 [Arabidopsis lyrata subsp. lyrata] gi|297329838|gb|EFH60257.1| hypothetical protein ARALYDRAFT_319616 [Arabidopsis lyrata subsp. lyrata]	370	360	1.00E-110	97.3	72.2	78.6	hypothetical protein ARALYDRAFT_319616	gbpln	Arabidopsis lyrata	AT2G19270.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Mitotic checkpoint protein PRCC, C-terminal (InterPro:IPR018800); Has 930 Blast hits to 533 proteins in 146 species: Archae - 0; Bacteria - 18; Metazoa - 327; Fungi - 143; Plants - 61; Viruses - 0; Other Eukaryotes - 381 (source: NCBI BLink). | chr2:8360349-8361907 REVERSE LENGTH=359	370	359	1.00E-105	97.0	69.2	77.3
Rsa1.0_00450.1.g14061.t3	ref|NP_179518.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|334184304|ref|NP_001189552.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546774|sp|Q6NKW7.2|PP164_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g19280 gi|3135258|gb|AAC16458.1| putative salt-inducible protein [Arabidopsis thaliana] gi|330251769|gb|AEC06863.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|330251770|gb|AEC06864.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	1393	693	0	49.7	38.3	42.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G19280.2 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:8362672-8364753 FORWARD LENGTH=693	1393	693	0	49.7	38.3	42.7
Rsa1.0_00451.1.g14062.t1	dbj|BAB01972.1| copia-like retrotransposable element [Arabidopsis thaliana]	214	1499	1.00E-75	700.5	65.4	73.4	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT3G21000.1 | Symbols: | Gag-Pol-related retrotransposon family protein | chr3:7363921-7365138 FORWARD LENGTH=405	214	405	5.00E-12	189.3	22.9	43.5
Rsa1.0_00451.1.g14063.t1	gb|EOA15533.1| hypothetical protein CARUB_v10004950mg [Capsella rubella]	409	406	0	99.3	80.4	86.6	hypothetical protein CARUB_v10004950mg	gbpln	Capsella rubella	AT4G24630.1 | Symbols: | DHHC-type zinc finger family protein | chr4:12714919-12717111 FORWARD LENGTH=407	409	407	0	99.5	79.2	87.0
Rsa1.0_00451.1.g14064.t1	ref|XP_002869710.1| hypothetical protein ARALYDRAFT_492383 [Arabidopsis lyrata subsp. lyrata] gi|297315546|gb|EFH45969.1| hypothetical protein ARALYDRAFT_492383 [Arabidopsis lyrata subsp. lyrata]	230	241	1.00E-81	104.8	74.8	83.0	hypothetical protein ARALYDRAFT_492383	gbpln	Arabidopsis lyrata	AT4G24590.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G49710.3); Has 105 Blast hits to 105 proteins in 26 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 3; Plants - 85; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr4:12696651-12698036 FORWARD LENGTH=241	230	241	4.00E-84	104.8	73.5	81.3

Rsa1.0_00451.1.g14065.t1	ref|NP_194189.6| Rho GTPase activation protein (RhoGAP) with PH domain [Arabidopsis thaliana] gi|332659528|gb|AEE84928.1| Rho GTPase activation protein (RhoGAP) with PH domain [Arabidopsis thaliana]	897	933	0	104.0	76.5	83.9	Rho GTPase activation protein (RhoGAP) with PH domain	gbpln	Arabidopsis thaliana	AT4G24580.1 | Symbols: REN1 | Rho GTPase activation protein (RhoGAP) with PH domain | chr4:12687879-12694248 REVERSE LENGTH=933	897	933	0	104.0	76.5	83.9
Rsa1.0_00451.1.g14066.t2	gb|EOA16624.1| hypothetical protein CARUB_v10004794mg [Capsella rubella]	426	451	0	105.9	96.0	98.8	hypothetical protein CARUB_v10004794mg	gbpln	Capsella rubella	AT4G24550.2 | Symbols: | Clathrin adaptor complexes medium subunit family protein | chr4:12675873-12678903 FORWARD LENGTH=451	426	451	0	105.9	95.5	98.6
Rsa1.0_00451.1.g14067.t1	ref|NP_563794.1| thioredoxin-like 4 [Arabidopsis thaliana] gi|75168930|sp|Q9C5C5.1|TRL4_ARATH RecName: Full=Thioredoxin-like 4, chloroplastic; AltName: Full=Lilium-type thioredoxin 3; Flags: Precursor gi|13507559|gb|AAK28642.1|AF360345_1 unknown protein [Arabidopsis thaliana] gi|15293297|gb|AAK93759.1| unknown protein [Arabidopsis thaliana] gi|110739213|dbj|BAF01521.1| hypothetical protein [Arabidopsis thaliana] gi|332190043|gb|AEE28164.1| thioredoxin-like 4 [Arabidopsis thaliana]	121	204	7.00E-34	168.6	65.3	75.2	thioredoxin-like 4	gbpln	Arabidopsis thaliana	AT1G07700.1 | Symbols: | Thioredoxin superfamily protein | chr1:2380214-2381127 FORWARD LENGTH=204	121	204	1.00E-36	168.6	65.3	75.2
Rsa1.0_00451.1.g14068.t1	ref|NP_194175.1| transcription initiation factor IIA subunit 2 [Arabidopsis thaliana] gi|30686529|ref|NP_849434.1| transcription initiation factor IIA subunit 2 [Arabidopsis thaliana] gi|297803670|ref|XP_002869719.1| transcription initiation factor IIA gamma chain [Arabidopsis lyrata subsp. lyrata] gi|20141796|sp|Q39236.2|T2AG_ARATH RecName: Full=Transcription initiation factor IIA subunit 2; AltName: Full=General transcription factor IIA subunit 2; AltName: Full=Transcription initiation factor IIA gamma chain; Short=TFIIA-gamma gi|2826882|emb|CAA11524.1| transcription factor IIA small subunit [Arabidopsis thaliana] gi|5051786|emb|CAB45079.1| transcription factor IIA small subunit [Arabidopsis thaliana] gi|7269294|emb|CAB79354.1| transcription factor IIA small subunit [Arabidopsis thaliana] gi|18176271|gb|AAL60014.1| putative transcription factor IIA small subunit [Arabidopsis thaliana] gi|20465319|gb|AAM20063.1| putative transcription factor IIA small subunit [Arabidopsis thaliana] gi|21553865|gb|AAM62958.1| transcription factor IIA small subunit [Arabidopsis thaliana] gi|39545876|gb|AAP28001.1| TFIIA-S	106	106	5.00E-55	100.0	99.1	99.1	transcription initiation factor IIA subunit 2	gbpln	Arabidopsis lyrata	AT4G24440.2 | Symbols: | transcription initiation factor IIA gamma chain / TFIIA-gamma (TFIIA-S) | chr4:12633460-12634553 FORWARD LENGTH=106	106	106	7.00E-58	100.0	99.1	99.1
Rsa1.0_00451.1.g14069.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1759	1270	0	72.2	35.0	46.3	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1759	575	1.00E-94	32.7	10.7	17.2
Rsa1.0_00451.1.g14070.t1	dbj|BAJ33821.1| unnamed protein product [Thellungiella halophila]	235	233	1.00E-112	99.1	83.8	93.2	unnamed protein product	----	----	AT4G24380.1 | Symbols: | INVOLVED IN: 10-formyltetrahydrofolate biosynthetic process, folic acid and derivative biosynthetic process; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Serine hydrolase (InterPro:IPR005645); BEST Arabidopsis thaliana protein match is: alpha/beta-Hydrolases superfamily protein (TAIR:AT5G65400.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12612554-12613586 FORWARD LENGTH=234	235	234	1.00E-113	99.6	81.7	91.1

Rsa1.0_00451.1.g14071.t1	ref|XP_002869724.1| hypothetical protein ARALYDRAFT_492419 [Arabidopsis lyrata subsp. lyrata] gi|297315560|gb|EFH45983.1| hypothetical protein ARALYDRAFT_492419 [Arabidopsis lyrata subsp. lyrata]	220	213	1.00E-100	96.8	83.6	87.7	hypothetical protein ARALYDRAFT_492419	gbpln	Arabidopsis lyrata	AT4G24310.1 | Symbols: | Protein of unknown function (DUF679) | chr4:12600900-12601541 FORWARD LENGTH=213	220	213	7.00E-96	96.8	82.3	87.7
Rsa1.0_00451.1.g14072.t1	gb|EOA16263.1| hypothetical protein CARUB_v10004407mg [Capsella rubella]	609	606	0	99.5	91.3	95.2	hypothetical protein CARUB_v10004407mg	gbpln	Capsella rubella	AT4G24290.2 | Symbols: | MAC/Perforin domain-containing protein | chr4:12594856-12597815 FORWARD LENGTH=606	609	606	0	99.5	91.0	94.7
Rsa1.0_00451.1.g14073.t1	ref|XP_002869727.1| cphsc70-1 [Arabidopsis lyrata subsp. lyrata] gi|297315563|gb|EFH45986.1| cphsc70-1 [Arabidopsis lyrata subsp. lyrata]	181	718	1.00E-53	396.7	65.7	70.7	cphsc70-1	gbpln	Arabidopsis lyrata	AT4G24280.1 | Symbols: cpHsc70-1 | chloroplast heat shock protein 70-1 | chr4:12590094-12593437 FORWARD LENGTH=718	181	718	4.00E-56	396.7	65.7	70.7
Rsa1.0_00451.1.g14074.t1	ref|XP_002863119.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308943|gb|EFH39378.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1936	1121	0	57.9	29.4	37.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189	1936	1189	0	61.4	26.6	33.6
Rsa1.0_00451.1.g14075.t1	ref|NP_199802.1| heat shock protein 70-2 [Arabidopsis thaliana] gi|75311568|sp|Q9LTX9.1|HSP7G_ARATH RecName: Full=Heat shock 70 kDa protein 7, chloroplastic; AltName: Full=Chloroplast heat shock protein 70-2; Short=cpHsc70-2; AltName: Full=Heat shock protein 70-7; Short=AtHsp70-7; Flags: Precursor gi|8777422|dbj|BAA97012.1| heat shock protein 70 [Arabidopsis thaliana] gi|24030296|gb|AAN41319.1| putative heat shock protein 70 [Arabidopsis thaliana] gi|332008487|gb|AED95870.1| heat shock protein 70-2 [Arabidopsis thaliana]	240	718	1.00E-112	299.2	90.8	94.2	heat shock protein 70-2	gbpln	Arabidopsis thaliana	AT5G49910.1 | Symbols: CPHSC70-2EAT SHOCK PROTEIN 70-2, HSC70-7, cpHsc70-2 | chloroplast heat shock protein 70-2 | chr5:20303470-20306295 FORWARD LENGTH=718	240	718	1.00E-114	299.2	90.8	94.2
Rsa1.0_00451.1.g14076.t3	ref|XP_002867042.1| hypothetical protein ARALYDRAFT_912762 [Arabidopsis lyrata subsp. lyrata] gi|297312878|gb|EFH43301.1| hypothetical protein ARALYDRAFT_912762 [Arabidopsis lyrata subsp. lyrata]	411	302	1.00E-138	73.5	65.2	67.9	hypothetical protein ARALYDRAFT_912762	gbpln	Arabidopsis lyrata	AT4G36010.2 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr4:17039472-17040976 REVERSE LENGTH=301	411	301	1.00E-138	73.2	63.3	66.4
Rsa1.0_00451.1.g14077.t1	ref|XP_002869051.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314887|gb|EFH45310.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	275	282	1.00E-105	102.5	78.9	84.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G35900.1 | Symbols: FD, FD-1, atbzip14 | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:17004746-17005952 FORWARD LENGTH=285	275	285	1.00E-103	103.6	76.4	82.9
Rsa1.0_00451.1.g14078.t1	ref|NP_001031892.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|98962153|gb|ABF59406.1| unknown protein [Arabidopsis thaliana] gi|332004916|gb|AED92299.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	200	209	2.00E-20	104.5	28.5	41.5	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT5G16486.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:5383597-5384226 REVERSE LENGTH=209	200	209	7.00E-23	104.5	28.5	41.5
Rsa1.0_00451.1.g14079.t1	ref|XP_002869052.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297314888|gb|EFH45311.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	497	526	1.00E-117	105.8	51.3	57.3	La domain-containing protein	gbpln	Arabidopsis lyrata	AT4G35890.1 | Symbols: | winged-helix DNA-binding transcription factor family protein | chr4:16997433-17000410 FORWARD LENGTH=523	497	523	1.00E-116	105.2	49.3	55.9
Rsa1.0_00451.1.g14080.t1	ref|NP_195312.1| early-responsive to dehydration stress protein (ERD4) [Arabidopsis thaliana] gi|3805853|emb|CAA21473.1| putative protein [Arabidopsis thaliana] gi|7270539|emb|CAB81496.1| putative protein [Arabidopsis thaliana] gi|19699093|gb|AAL90913.1| AT4g35870/F4B14_140 [Arabidopsis thaliana] gi|332661183|gb|AEE86583.1| early-responsive to dehydration stress protein (ERD4) [Arabidopsis thaliana]	810	817	0	100.9	92.2	97.0	early-responsive to dehydration stress protein (ERD4)	gbpln	Arabidopsis thaliana	AT4G35870.1 | Symbols: | early-responsive to dehydration stress protein (ERD4) | chr4:16990332-16992785 FORWARD LENGTH=817	810	817	0	100.9	92.2	97.0
Rsa1.0_00451.1.g14081.t1	gb|EOA17424.1| hypothetical protein CARUB_v10005728mg [Capsella rubella]	163	211	1.00E-69	129.4	89.0	92.0	hypothetical protein CARUB_v10005728mg	gbpln	Capsella rubella	AT4G35860.1 | Symbols: ATRABB1B, ATGB2, ATRAB2C, GB2 | GTP-binding 2 | chr4:16987118-16988839 REVERSE LENGTH=211	163	211	2.00E-70	129.4	86.5	91.4

Rsa1.0_00451.1.g14082.t1	ref|NP_195308.1| aconitate hydratase 1 [Arabidopsis thaliana] gi|13124706|sp|Q42560.2|ACO1_ARATH RecName: Full=Aconitate hydratase 1; Short=Aconitase 1; AltName: Full=Citrate hydro-lyase 1 gi|3805849|emb|CAA21469.1| cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana] gi|7270535|emb|CAB81492.1| cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana] gi|17065392|gb|AAL32850.1| Unknown protein [Arabidopsis thaliana] gi|332661176|gb|AEE86576.1| aconitate hydratase 1 [Arabidopsis thaliana]	898	898	0	100.0	97.9	99.4	aconitate hydratase 1	gbpln	Arabidopsis thaliana	AT4G35830.1 | Symbols: ACO1 | aconitase 1 | chr4:16973007-16977949 REVERSE LENGTH=898	898	898	0	100.0	97.9	99.4
Rsa1.0_00451.1.g14083.t1	ref|XP_002869059.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297314895|gb|EFH45318.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	332	290	1.00E-141	87.3	73.2	81.0	oxidoreductase	gbpln	Arabidopsis lyrata	AT4G35810.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:16968921-16970358 FORWARD LENGTH=290	332	290	1.00E-131	87.3	70.5	79.5
Rsa1.0_00451.1.g14084.t1	ref|NP_173161.1| glutathione S-transferase TAU 25 [Arabidopsis thaliana] gi|75337230|sp|Q9SHH7.1|GSTUP_ARATH RecName: Full=Glutathione S-transferase U25; Short=AtGSTU25; AltName: Full=GST class-tau member 25 gi|5734750|gb|AAD50015.1|AC007651_10 Putative glutathione transferase [Arabidopsis thaliana] gi|26452821|dbj|BAC43490.1| putative glutathione transferase [Arabidopsis thaliana] gi|28973477|gb|AAO64063.1| putative glutathione transferase [Arabidopsis thaliana] gi|332191434|gb|AEE29555.1| glutathione S-transferase TAU 25 [Arabidopsis thaliana]	182	221	3.00E-71	121.4	75.8	88.5	glutathione S-transferase TAU 25	gbpln	Arabidopsis thaliana	AT1G17180.1 | Symbols: ATGSTU25, GSTU25 | glutathione S-transferase TAU 25 | chr1:5872208-5872958 FORWARD LENGTH=221	182	221	1.00E-73	121.4	75.8	88.5
Rsa1.0_00451.1.g14085.t1	ref|XP_002869067.1| hypothetical protein ARALYDRAFT_491077 [Arabidopsis lyrata subsp. lyrata] gi|297314903|gb|EFH45326.1| hypothetical protein ARALYDRAFT_491077 [Arabidopsis lyrata subsp. lyrata]	206	280	3.00E-72	135.9	71.4	80.1	hypothetical protein ARALYDRAFT_491077	gbpln	Arabidopsis lyrata	AT4G35690.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16921886-16922740 FORWARD LENGTH=284	206	284	3.00E-67	137.9	68.9	77.2
Rsa1.0_00451.1.g14086.t1	gb|EOA17852.1| hypothetical protein CARUB_v10006256mg [Capsella rubella]	368	368	0	100.0	94.0	97.3	hypothetical protein CARUB_v10006256mg	gbpln	Capsella rubella	AT4G35650.1 | Symbols: IDH-III | isocitrate dehydrogenase III | chr4:16908584-16909973 FORWARD LENGTH=368	368	368	0	100.0	93.2	97.3
Rsa1.0_00451.1.g14087.t1	ref|XP_002869075.1| phosphoserine aminotransferase [Arabidopsis lyrata subsp. lyrata] gi|297314911|gb|EFH45334.1| phosphoserine aminotransferase [Arabidopsis lyrata subsp. lyrata]	433	431	0	99.5	88.5	93.5	phosphoserine aminotransferase	gbpln	Arabidopsis lyrata	AT4G35630.1 | Symbols: PSAT | phosphoserine aminotransferase | chr4:16904205-16905497 FORWARD LENGTH=430	433	430	0	99.3	87.3	92.8
Rsa1.0_00451.1.g14088.t1	ref|NP_195285.3| putative serine/threonine-protein kinase Cx32 [Arabidopsis thaliana] gi|49066036|sp|P27450.2|CX32_ARATH RecName: Full=Probable serine/threonine-protein kinase Cx32, chloroplastic; Flags: Precursor gi|17529234|gb|AAL38844.1| putative protein kinase [Arabidopsis thaliana] gi|20465931|gb|AAM20151.1| putative protein kinase [Arabidopsis thaliana] gi|332661138|gb|AEE86538.1| putative serine/threonine-protein kinase Cx32 [Arabidopsis thaliana]	367	419	1.00E-143	114.2	69.8	82.0	putative serine/threonine-protein kinase Cx32	gbpln	Arabidopsis thaliana	AT4G35600.1 | Symbols: CONNEXIN 32 | Protein kinase superfamily protein | chr4:16896448-16898714 FORWARD LENGTH=419	367	419	1.00E-145	114.2	69.8	82.0
Rsa1.0_00451.1.g14089.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	645	536	5.00E-91	83.1	25.1	33.6	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	645	530	3.00E-52	82.2	15.0	20.2

Rsa1.0_00451.1.g14090.t1	ref|NP_195285.3| putative serine/threonine-protein kinase Cx32 [Arabidopsis thaliana] gi|49066036|sp|P27450.2|CX32_ARATH RecName: Full=Probable serine/threonine-protein kinase Cx32, chloroplastic; Flags: Precursor gi|17529234|gb|AAL38844.1| putative protein kinase [Arabidopsis thaliana] gi|20465931|gb|AAM20151.1| putative protein kinase [Arabidopsis thaliana] gi|332661138|gb|AEE86538.1| putative serine/threonine-protein kinase Cx32 [Arabidopsis thaliana]	423	419	0	99.1	79.4	87.5	putative serine/threonine-protein kinase Cx32	gbpln	Arabidopsis thaliana	AT4G35600.1 | Symbols: CONNEXIN 32 | Protein kinase superfamily protein | chr4:16896448-16898714 FORWARD LENGTH=419	423	419	0	99.1	79.4	87.5
Rsa1.0_00451.1.g14091.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00451.1.g14092.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00451.1.g14093.t2	gb|EOA16985.1| hypothetical protein CARUB_v10005217mg [Capsella rubella]	249	332	1.00E-101	133.3	82.3	89.6	hypothetical protein CARUB_v10005217mg	gbpln	Capsella rubella	AT4G35550.1 | Symbols: HB-4, WOX13, ATWOX13 | WUSCHEL related homeobox 13 | chr4:16875814-16877167 REVERSE LENGTH=268	249	268	1.00E-100	107.6	82.7	90.0
Rsa1.0_00451.1.g14094.t1	ref|XP_002867072.1| ring-H2 finger A3B [Arabidopsis lyrata subsp. lyrata] gi|297312908|gb|EFH43331.1| ring-H2 finger A3B [Arabidopsis lyrata subsp. lyrata]	197	200	8.00E-86	101.5	82.7	90.9	ring-H2 finger A3B	gbpln	Arabidopsis lyrata	AT4G35480.1 | Symbols: RHA3B | RING-H2 finger A3B | chr4:16852233-16852835 REVERSE LENGTH=200	197	200	3.00E-87	101.5	82.2	89.8
Rsa1.0_00451.1.g14095.t2	ref|XP_002869086.1| NADPH-dependent thioredoxin reductase 1 [Arabidopsis lyrata subsp. lyrata] gi|297314922|gb|EFH45345.1| NADPH-dependent thioredoxin reductase 1 [Arabidopsis lyrata subsp. lyrata]	311	375	1.00E-162	120.6	93.2	96.8	NADPH-dependent thioredoxin reductase 1	gbpln	Arabidopsis lyrata	AT4G35460.1 | Symbols: ATNTRB, NTRB, NTR1 | NADPH-dependent thioredoxin reductase B | chr4:16842218-16843740 FORWARD LENGTH=375	311	375	1.00E-163	120.6	92.6	96.5
Rsa1.0_00451.1.g14096.t1	dbj|BAJ33771.1| unnamed protein product [Thellungiella halophila]	355	342	1.00E-163	96.3	86.5	90.7	unnamed protein product	----	----	AT4G35450.1 | Symbols: AKR2, AFT, AKR2A | ankyrin repeat-containing protein 2 | chr4:16839862-16841759 FORWARD LENGTH=342	355	342	1.00E-161	96.3	83.9	89.6
Rsa1.0_00451.1.g14097.t1	dbj|BAJ34269.1| unnamed protein product [Thellungiella halophila]	444	472	1.00E-164	106.3	75.2	84.2	unnamed protein product	----	----	AT1G14580.2 | Symbols: | C2H2-like zinc finger protein | chr1:4990070-4992442 FORWARD LENGTH=467	444	467	1.00E-153	105.2	68.9	80.0
Rsa1.0_00451.1.g14098.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	422	657	1.00E-105	155.7	42.4	56.9	T14P8.10	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	422	332	3.00E-79	78.7	31.5	44.8
Rsa1.0_00451.1.g14099.t1	ref|NP_195268.2| dihydroflavonol 4-reductase-like1 [Arabidopsis thaliana] gi|75276293|sp|Q500U8.1|TKPR1_ARATH RecName: Full=Tetraketide alpha-pyrone reductase 1; AltName: Full=Protein DIHYDROFLAVONOL 4-REDUCTASE-LIKE 1 gi|63147414|gb|AAY34180.1| At4g35420 [Arabidopsis thaliana] gi|105830365|gb|ABF74722.1| At4g35420 [Arabidopsis thaliana] gi|332661109|gb|AEE86509.1| dihydroflavonol 4-reductase-like1 [Arabidopsis thaliana]	317	326	1.00E-170	102.8	92.4	96.2	dihydroflavonol 4-reductase-like1	gbpln	Arabidopsis thaliana	AT4G35420.1 | Symbols: DRL1 | dihydroflavonol 4-reductase-like1 | chr4:16834091-16835611 REVERSE LENGTH=326	317	326	1.00E-173	102.8	92.4	96.2
Rsa1.0_00451.1.g14100.t2	gb|EOA19090.1| hypothetical protein CARUB_v10007758mg [Capsella rubella]	387	352	0	91.0	86.8	89.9	hypothetical protein CARUB_v10007758mg	gbpln	Capsella rubella	AT4G35335.1 | Symbols: | Nucleotide-sugar transporter family protein | chr4:16807286-16810015 FORWARD LENGTH=352	387	352	0	91.0	86.8	89.7
Rsa1.0_00451.1.g14101.t1	gb|ACC91264.1| 50S ribosomal protein [Capsella rubella] gi|482553078|gb|EOA17271.1| hypothetical protein CARUB_v10005544mg [Capsella rubella]	272	257	1.00E-132	94.5	86.8	91.2	50S ribosomal protein	gbpln	Capsella rubella	AT4G23620.1 | Symbols: | Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain | chr4:12315016-12316659 REVERSE LENGTH=264	272	264	1.00E-131	97.1	84.9	90.4
Rsa1.0_00451.1.g14102.t1	dbj|BAJ33905.1| unnamed protein product [Thellungiella halophila]	275	275	1.00E-127	100.0	89.8	94.9	unnamed protein product	----	----	AT4G23630.1 | Symbols: BTI1, RTNLB1 | VIRB2-interacting protein 1 | chr4:12318070-12319574 FORWARD LENGTH=275	275	275	1.00E-124	100.0	89.5	94.5
Rsa1.0_00451.1.g14103.t1	ref|XP_002867696.1| ATPPT1 [Arabidopsis lyrata subsp. lyrata] gi|297313532|gb|EFH43955.1| ATPPT1 [Arabidopsis lyrata subsp. lyrata]	383	405	1.00E-167	105.7	85.6	90.1	ATPPT1	gbpln	Arabidopsis lyrata	AT4G23660.2 | Symbols: AtPPT1, PPT1 | polyprenyltransferase 1 | chr4:12328086-12331359 REVERSE LENGTH=407	383	407	1.00E-168	106.3	83.0	89.0
Rsa1.0_00451.1.g14104.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00451.1.g14105.t1	ref|XP_002875076.1| hypothetical protein ARALYDRAFT_904347 [Arabidopsis lyrata subsp. lyrata] gi|297320914|gb|EFH51335.1| hypothetical protein ARALYDRAFT_904347 [Arabidopsis lyrata subsp. lyrata]	151	151	4.00E-72	100.0	84.1	89.4	hypothetical protein ARALYDRAFT_904347	gbpln	Arabidopsis lyrata	AT2G01520.1 | Symbols: MLP328 | MLP-like protein 328 | chr2:235992-236881 FORWARD LENGTH=151	151	151	3.00E-74	100.0	84.1	88.7
Rsa1.0_00451.1.g14106.t1	gb|ACC91257.1| disease resistance-responsive family protein [Capsella rubella] gi|482553287|gb|EOA17480.1| hypothetical protein CARUB_v10005816mg [Capsella rubella]	186	187	1.00E-91	100.5	93.0	96.8	disease resistance-responsive family protein	gbpln	Capsella rubella	AT4G23690.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr4:12339152-12339715 REVERSE LENGTH=187	186	187	2.00E-92	100.5	91.4	96.2
Rsa1.0_00452.1.g14107.t1	ref|XP_002878881.1| ATP-dependent protease La domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324720|gb|EFH55140.1| ATP-dependent protease La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	577	542	0	93.9	74.9	80.1	ATP-dependent protease La domain-containing protein	gbpln	Arabidopsis lyrata	AT2G25740.1 | Symbols: | ATP-dependent protease La (LON) domain protein | chr2:10980175-10983632 FORWARD LENGTH=547	577	547	0	94.8	74.5	79.9
Rsa1.0_00452.1.g14108.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	475	490	5.00E-62	103.2	34.9	52.4	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	475	566	5.00E-63	119.2	33.7	53.7
Rsa1.0_00452.1.g14109.t2	dbj|BAB02793.1| helicase-like protein [Arabidopsis thaliana]	1193	1428	0	119.7	36.0	46.4	helicase-like protein	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1193	331	4.00E-42	27.7	6.6	9.4
Rsa1.0_00452.1.g14110.t1	ref|NP_187198.1| formin-like protein 11 [Arabidopsis thaliana] gi|75191978|sp|Q9MA60.1|FH11_ARATH RecName: Full=Formin-like protein 11; Short=AtFH11; Flags: Precursor gi|7596775|gb|AAF64546.1| unknown protein [Arabidopsis thaliana] gi|332640723|gb|AEE74244.1| formin-like protein 11 [Arabidopsis thaliana]	180	884	4.00E-15	491.1	26.7	30.6	formin-like protein 11	gbpln	Arabidopsis thaliana	AT3G05470.1 | Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr3:1579667-1582547 REVERSE LENGTH=884	180	884	2.00E-17	491.1	26.7	30.6
Rsa1.0_00452.1.g14111.t3	dbj|BAB03186.1| En/Spm transposon protein-like [Arabidopsis thaliana]	609	1516	3.00E-35	248.9	16.1	23.0	En/Spm transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00452.1.g14112.t2	gb|EOA18445.1| hypothetical protein CARUB_v10006988mg [Capsella rubella]	592	683	3.00E-47	115.4	26.0	37.3	hypothetical protein CARUB_v10006988mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00452.1.g14113.t1	ref|NP_199370.1| Ulp1 protease family protein [Arabidopsis thaliana] gi|10177930|dbj|BAB11195.1| unnamed protein product [Arabidopsis thaliana] gi|332007886|gb|AED95269.1| Ulp1 protease family protein [Arabidopsis thaliana]	649	921	1.00E-96	141.9	31.0	45.1	Ulp1 protease family protein	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	649	921	3.00E-99	141.9	31.0	45.1
Rsa1.0_00452.1.g14114.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00452.1.g14115.t1	ref|XP_002880703.1| hypothetical protein ARALYDRAFT_901230 [Arabidopsis lyrata subsp. lyrata] gi|297326542|gb|EFH56962.1| hypothetical protein ARALYDRAFT_901230 [Arabidopsis lyrata subsp. lyrata]	121	117	7.00E-43	96.7	84.3	87.6	hypothetical protein ARALYDRAFT_901230	gbpln	Arabidopsis lyrata	AT2G25735.1 | Symbols: | unknown protein; Has 31 Blast hits to 31 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:10975345-10975704 REVERSE LENGTH=119	121	119	1.00E-41	98.3	80.2	84.3
Rsa1.0_00452.1.g14116.t6	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00452.1.g14117.t14	ref|NP_001189602.1| uncharacterized protein [Arabidopsis thaliana] gi|330252650|gb|AEC07744.1| uncharacterized protein AT2G25730 [Arabidopsis thaliana]	2545	2487	0	97.7	86.0	90.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G25730.2 | Symbols: | unknown protein; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages. | chr2:10956751-10972729 REVERSE LENGTH=2487	2545	2487	0	97.7	86.0	90.7

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<tr><td>Rsa1.0_00453.1.g14118.t1</td><td>ref|NP_563952.1| NADH dehydrogenase (ubiquinone) [Arabidopsis thaliana] gi|297849852|ref|XP_002892807.1| hypothetical protein ARALYDRAFT_471620 [Arabidopsis lyrata subsp. lyrata] gi|75191411|sp|Q9M9R9.1|NDB3B_ARATH RecName: Full=NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-B gi|7262687|gb|AAF43945.1|AC012188_22 Contains similarity to an unknown protein from Arabidopsis thaliana gb|AC004136.2. ESTs gb|Z47683, gb|Z47682, gb|AA597850, gb|Z29736, gb|Z29735, gb|AA042623 come from this gene [Arabidopsis thaliana] gi|12083314|gb|AAG48816.1|AF332453_1 unknown protein [Arabidopsis thaliana] gi|21592691|gb|AAM64640.1| unknown [Arabidopsis thaliana] gi|30725334|gb|AAP37689.1| At1g14450 [Arabidopsis thaliana] gi|110736426|dbj|BAF00181.1| hypothetical protein [Arabidopsis thaliana] gi|297338649|gb|EFH69066.1| hypothetical protein ARALYDRAFT_471620 [Arabidopsis lyrata subsp. lyrata] gi|332191044|gb|AEE29165.1| NADH dehydrogenase (ubiquinone) [Arabidopsis thaliana]</td><td>74</td><td>73</td><td>3.00E-32</td><td>98.6</td><td>91.9</td><td>97.3</td><td>NADH dehydrogenase (ubiquinone)</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G14450.1 | Symbols: | NADH dehydrogenase (ubiquinone)s | chr1:4947337-4947558 REVERSE LENGTH=73</td><td>74</td><td>73</td><td>5.00E-35</td><td>98.6</td><td>91.9</td><td>97.3</td></tr>
<tr><td>Rsa1.0_00453.1.g14119.t1</td><td>gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]</td><td>179</td><td>441</td><td>6.00E-36</td><td>246.4</td><td>37.4</td><td>50.8</td><td>tn7 reverse transcriptase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>179</td><td>746</td><td>2.00E-25</td><td>416.8</td><td>31.3</td><td>38.5</td></tr>
<tr><td>Rsa1.0_00453.1.g14120.t1</td><td>ref|XP_002892806.1| ATHB31 [Arabidopsis lyrata subsp. lyrata] gi|297338648|gb|EFH69065.1| ATHB31 [Arabidopsis lyrata subsp. lyrata]</td><td>304</td><td>311</td><td>1.00E-134</td><td>102.3</td><td>82.6</td><td>87.8</td><td>ATHB31</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G14440.2 | Symbols: AtHB31, HB31, ZHD4 | homeobox protein 31 | chr1:4939076-4940014 REVERSE LENGTH=312</td><td>304</td><td>312</td><td>1.00E-133</td><td>102.6</td><td>82.2</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00453.1.g14121.t1</td><td>ref|XP_002890054.1| hypothetical protein ARALYDRAFT_888820 [Arabidopsis lyrata subsp. lyrata] gi|297335896|gb|EFH66313.1| hypothetical protein ARALYDRAFT_888820 [Arabidopsis lyrata subsp. lyrata]</td><td>560</td><td>564</td><td>0</td><td>100.7</td><td>90.9</td><td>96.3</td><td>hypothetical protein ARALYDRAFT_888820</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G14430.1 | Symbols: | glyoxal oxidase-related protein | chr1:4934359-4936053 FORWARD LENGTH=564</td><td>560</td><td>564</td><td>0</td><td>100.7</td><td>89.1</td><td>95.5</td></tr>
<tr><td>Rsa1.0_00453.1.g14122.t1</td><td>ref|XP_002892805.1| hypothetical protein ARALYDRAFT_471616 [Arabidopsis lyrata subsp. lyrata] gi|297338647|gb|EFH69064.1| hypothetical protein ARALYDRAFT_471616 [Arabidopsis lyrata subsp. lyrata]</td><td>458</td><td>459</td><td>0</td><td>100.2</td><td>82.3</td><td>91.3</td><td>hypothetical protein ARALYDRAFT_471616</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G14420.1 | Symbols: AT59 | Pectate lyase family protein | chr1:4931844-4933405 REVERSE LENGTH=459</td><td>458</td><td>459</td><td>0</td><td>100.2</td><td>81.7</td><td>90.0</td></tr>
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Rsa1.0_00453.1.g14123.t2	ref|NP_563951.1| ubiquitin-conjugating enzyme E2 1 [Arabidopsis thaliana] gi|42571469|ref|NP_973825.1| ubiquitin-conjugating enzyme E2 1 [Arabidopsis thaliana] gi|297849844|ref|XP_002892803.1| hypothetical protein ARALYDRAFT_471614 [Arabidopsis lyrata subsp. lyrata] gi|136636|sp|P25865.1|UBC1_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 1; AltName: Full=Ubiquitin carrier protein 1; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 1; AltName: Full=Ubiquitin-protein ligase 1 gi|157834522|pdb|2AAK|A Chain A, Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana gi|7262682|gb|AAF43940.1|AC012188_17 Strong similarity to a Ubiquitin-conjugating Enzyme (E2-17 KD 1) from Arabidopsis thaliana gi|136636 and contains a Ubiqutin-conjugating Enzyme PF|00179 domain. ESTs gb|AA728508, gb|H36735, gb|AI100736 come from this gene [Arabidopsis thaliana] gi|12083310|gb|AAG48814.1|AF332451_1 putative E2, ubiquitin-conjugating enzyme 1 [Arabidopsis thaliana] gi|166924|gb|AAA32903.1| ubiquitin carrier protein [Arabidopsis thaliana] gi|431260|gb|AAA32897.1| ubiquitin conjugating enzyme [Arabidopsis	158	152	6.00E-82	96.2	94.9	96.2	ubiquitin-conjugating enzyme E2 1	gbpln	Arabidopsis lyrata	AT1G14400.2 | Symbols: UBC1, ATUBC1 | ubiquitin carrier protein 1 | chr1:4927294-4928136 REVERSE LENGTH=152	158	152	2.00E-84	96.2	94.9	96.2
Rsa1.0_00453.1.g14124.t1	gb|EOA39444.1| hypothetical protein CARUB_v10012614mg [Capsella rubella]	732	750	0	102.5	86.6	90.7	hypothetical protein CARUB_v10012614mg	gbpln	Capsella rubella	AT1G14390.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:4924277-4926794 FORWARD LENGTH=747	732	747	0	102.0	86.2	91.0
Rsa1.0_00453.1.g14125.t2	ref|XP_002892802.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338644|gb|EFH69061.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	628	661	0	105.3	66.6	77.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G14380.3 | Symbols: IQD28 | IQ-domain 28 | chr1:4918279-4920761 REVERSE LENGTH=664	628	664	0	105.7	64.8	75.8
Rsa1.0_00453.1.g14126.t1	ref|XP_002890052.1| hypothetical protein ARALYDRAFT_471608 [Arabidopsis lyrata subsp. lyrata] gi|297335894|gb|EFH66311.1| hypothetical protein ARALYDRAFT_471608 [Arabidopsis lyrata subsp. lyrata]	426	426	0	100.0	84.3	92.0	hypothetical protein ARALYDRAFT_471608	gbpln	Arabidopsis lyrata	AT1G14370.1 | Symbols: APK2A, PBL2 | protein kinase 2A | chr1:4915859-4917959 FORWARD LENGTH=426	426	426	0	100.0	84.3	91.3
Rsa1.0_00453.1.g14127.t1	ref|XP_002890052.1| hypothetical protein ARALYDRAFT_471608 [Arabidopsis lyrata subsp. lyrata] gi|297335894|gb|EFH66311.1| hypothetical protein ARALYDRAFT_471608 [Arabidopsis lyrata subsp. lyrata]	366	426	1.00E-145	116.4	73.2	86.1	hypothetical protein ARALYDRAFT_471608	gbpln	Arabidopsis lyrata	AT1G14370.1 | Symbols: APK2A, PBL2 | protein kinase 2A | chr1:4915859-4917959 FORWARD LENGTH=426	366	426	2.33E-156	116.4	72.1	85.0
Rsa1.0_00453.1.g14128.t1	ref|XP_002892801.1| UDP-galactose transporter 3 [Arabidopsis lyrata subsp. lyrata] gi|297338643|gb|EFH69060.1| UDP-galactose transporter 3 [Arabidopsis lyrata subsp. lyrata]	331	331	0	100.0	98.5	99.7	UDP-galactose transporter 3	gbpln	Arabidopsis lyrata	AT1G14360.1 | Symbols: ATUTR3, UTR3 | UDP-galactose transporter 3 | chr1:4911362-4913029 REVERSE LENGTH=331	331	331	0	100.0	97.6	99.4
Rsa1.0_00453.1.g14129.t1	ref|NP_563948.1| FOUR LIPS transcription factor R2R3-MYB [Arabidopsis thaliana] gi|145323890|ref|NP_001077534.1| FOUR LIPS transcription factor R2R3-MYB [Arabidopsis thaliana] gi|15375305|gb|AAK54745.2|AF371982_1 putative transcription factor MYB124 [Arabidopsis thaliana] gi|109946607|gb|ABG48482.1| At1g14350 [Arabidopsis thaliana] gi|332191029|gb|AEE29150.1| FOUR LIPS transcription factor R2R3-MYB [Arabidopsis thaliana] gi|332191030|gb|AEE29151.1| FOUR LIPS transcription factor R2R3-MYB [Arabidopsis thaliana]	437	436	0	99.8	87.4	92.7	FOUR LIPS transcription factor R2R3-MYB	gbpln	Arabidopsis thaliana	AT1G14350.2 | Symbols: FLP, MYB124 | Duplicated homeodomain-like superfamily protein | chr1:4908427-4910647 FORWARD LENGTH=436	437	436	0	99.8	87.4	92.7

Rsa1.0_00453.1.g14130.t1	gb|AAF43934.1|AC012188_11 Contains similarity to Vip1 protein from Schizosaccharomyces pombe gb|Y13635.1 and contains a RNA recognition motif PF|00076. EST gb|AI996906 comes from this gene [Arabidopsis thaliana]	197	431	1.00E-92	218.8	88.3	94.9	Contains similarity to Vip1 protein from Schizosaccharomyces pombe gb|Y13635.1 and contains a RNA recognition motif PF|00076. EST gb|AI996906 comes from this gene	gbpln	Arabidopsis thaliana	AT1G14345.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr1:4899176-4899766 FORWARD LENGTH=196	197	196	1.00E-93	99.5	88.3	94.4
Rsa1.0_00453.1.g14131.t1	ref|XP_002892800.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297338642|gb|EFH69059.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	428	436	0	101.9	84.8	91.4	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT1G14330.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:4890375-4891700 REVERSE LENGTH=441	428	441	0	103.0	85.3	91.4
Rsa1.0_00453.1.g14132.t1	ref|NP_563945.2| 60S ribosomal protein L10-1 [Arabidopsis thaliana] gi|297844336|ref|XP_002890049.1| hypothetical protein ARALYDRAFT_888807 [Arabidopsis lyrata subsp. lyrata] gi|75305724|sp|Q93VT9.1|RL101_ARATH RecName: Full=60S ribosomal protein L10-1 gi|7262674|gb|AAF43932.1|AC012188_9 Strong similarity, practically identical, to a 60S Ribosomal Protein L10 (Wilm's Tumor Suppressor Protein Homolog) from Arabidopsis thaliana gi|1172806, and contains a Ribosomal L10 PF|00826 domain. ESTs gb|Z18472, gb|T76209, gb|N65098, gb|T43013, gb|T46279, gb|AA394948, gb|AA713166, gb|T44895, gb|AA042691 come from this gene [Arabidopsis thaliana] gi|16226263|gb|AAL16118.1|AF428286_1 At1g14320/F14L17_28 [Arabidopsis thaliana] gi|16226713|gb|AAL16239.1|AF428470_1 At1g14320/F14L17_28 [Arabidopsis thaliana] gi|15028019|gb|AAK76540.1| putative tumor suppressor protein [Arabidopsis thaliana] gi|21281241|gb|AAM45037.1| putative tumor suppressor protein [Arabidopsis thaliana] gi|23397080|gb|AAN31825.1| putative tumor suppressor [Arabidopsis thaliana] gi|297335891|gb|EFH66308.1| hypothetical protein	220	220	1.00E-124	100.0	99.1	99.1	60S ribosomal protein L10-1	gbpln	Arabidopsis lyrata	AT1G14320.1 | Symbols: SAC52, RPL10, RPL10A | Ribosomal protein L16p/L10e family protein | chr1:4888270-4889408 FORWARD LENGTH=220	220	220	1.00E-127	100.0	99.1	99.1
Rsa1.0_00453.1.g14133.t1	ref|XP_002892799.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297338641|gb|EFH69058.1| binding protein [Arabidopsis lyrata subsp. lyrata]	340	339	0	99.7	93.8	96.8	binding protein	gbpln	Arabidopsis lyrata	AT1G14300.1 | Symbols: | ARM repeat superfamily protein | chr1:4882654-4884686 REVERSE LENGTH=339	340	339	0	99.7	92.1	96.2
Rsa1.0_00453.1.g14134.t1	ref|XP_002892798.1| hypothetical protein ARALYDRAFT_888804 [Arabidopsis lyrata subsp. lyrata] gi|297338640|gb|EFH69057.1| hypothetical protein ARALYDRAFT_888804 [Arabidopsis lyrata subsp. lyrata]	283	259	1.00E-140	91.5	86.2	90.1	hypothetical protein ARALYDRAFT_888804	gbpln	Arabidopsis lyrata	AT1G14290.1 | Symbols: SBH2 | sphingoid base hydroxylase 2 | chr1:4880307-4881784 REVERSE LENGTH=259	283	259	1.00E-142	91.5	86.2	90.1
Rsa1.0_00453.1.g14135.t1	ref|XP_002890047.1| hypothetical protein ARALYDRAFT_888803 [Arabidopsis lyrata subsp. lyrata] gi|297335889|gb|EFH66306.1| hypothetical protein ARALYDRAFT_888803 [Arabidopsis lyrata subsp. lyrata]	441	446	1.00E-169	101.1	77.3	87.1	hypothetical protein ARALYDRAFT_888803	gbpln	Arabidopsis lyrata	AT1G14280.1 | Symbols: PKS2 | phytochrome kinase substrate 2 | chr1:4877657-4878985 FORWARD LENGTH=442	441	442	1.00E-165	100.2	78.0	87.3
Rsa1.0_00453.1.g14136.t1	ref|XP_002892797.1| hypothetical protein ARALYDRAFT_471595 [Arabidopsis lyrata subsp. lyrata] gi|297338639|gb|EFH69056.1| hypothetical protein ARALYDRAFT_471595 [Arabidopsis lyrata subsp. lyrata]	340	338	1.00E-161	99.4	85.6	91.5	hypothetical protein ARALYDRAFT_471595	gbpln	Arabidopsis lyrata	AT1G14270.1 | Symbols: | CAAX amino terminal protease family protein | chr1:4875099-4877195 REVERSE LENGTH=353	340	353	1.00E-157	103.8	85.9	91.5
Rsa1.0_00453.1.g14137.t1	gb|EOA39225.1| hypothetical protein CARUB_v10012202mg [Capsella rubella]	179	261	9.00E-38	145.8	52.5	57.5	hypothetical protein CARUB_v10012202mg	gbpln	Capsella rubella	AT1G14260.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:4873200-4874430 FORWARD LENGTH=265	179	265	7.00E-31	148.0	53.6	57.5

Rsa1.0_00454.1.g14138.t1	gb|ABD64975.1| Ras family GTP-binding protein [Brassica oleracea]	179	221	5.00E-33	123.5	38.5	41.9	Ras family GTP-binding protein	gbpln	Brassica oleracea	AT5G47520.1 | Symbols: AtRABA5a, RABA5a | RAB GTPase homolog A5A | chr5:19277596-19278366 REVERSE LENGTH=221	179	221	1.00E-34	123.5	37.4	41.3
Rsa1.0_00454.1.g14139.t2	gb|AAX77014.1| MLO1 [Brassica rapa]	576	574	0	99.7	96.0	97.9	MLO1	gbpln	Brassica rapa	AT1G11310.1 | Symbols: MLO2, ATMLO2, PMR2 | Seven transmembrane MLO family protein | chr1:3800899-3803870 REVERSE LENGTH=573	576	573	0	99.5	88.2	93.1
Rsa1.0_00454.1.g14140.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1502	1496	0	99.6	58.9	73.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1502	1262	1.00E-141	84.0	15.6	22.2
Rsa1.0_00454.1.g14141.t1	gb|EOA37991.1| hypothetical protein CARUB_v10009460mg [Capsella rubella]	379	377	1.00E-122	99.5	58.6	71.5	hypothetical protein CARUB_v10009460mg	gbpln	Capsella rubella	AT1G11270.2 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3785715-3786653 REVERSE LENGTH=312	379	312	1.00E-93	82.3	48.0	59.1
Rsa1.0_00454.1.g14142.t1	ref|XP_002890588.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336430|gb|EFH66847.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	221	317	3.00E-29	143.4	30.3	34.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G23550.1 | Symbols: SRO2 | similar to RCD one 2 | chr1:8350912-8352232 FORWARD LENGTH=323	221	323	3.00E-30	146.2	29.9	33.5
Rsa1.0_00454.1.g14143.t1	gb|EOA37991.1| hypothetical protein CARUB_v10009460mg [Capsella rubella]	369	377	1.00E-125	102.2	64.0	76.4	hypothetical protein CARUB_v10009460mg	gbpln	Capsella rubella	AT1G11270.2 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3785715-3786653 REVERSE LENGTH=312	369	312	3.00E-95	84.6	48.8	57.7
Rsa1.0_00454.1.g14144.t1	ref|XP_002892604.1| TIF3H1 [Arabidopsis lyrata subsp. lyrata] gi|297338446|gb|EFH68863.1| TIF3H1 [Arabidopsis lyrata subsp. lyrata]	460	337	0	73.3	70.9	72.0	TIF3H1	gbpln	Arabidopsis lyrata	AT1G10840.1 | Symbols: TIF3H1 | translation initiation factor 3 subunit H1 | chr1:3607885-3610299 REVERSE LENGTH=337	460	337	0	73.3	70.7	72.0
Rsa1.0_00454.1.g14145.t1	ref|NP_973807.1| uncharacterized protein [Arabidopsis thaliana] gi|332190529|gb|AEE28650.1| uncharacterized protein AT1G10820 [Arabidopsis thaliana]	244	258	1.00E-106	105.7	81.1	89.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G10820.2 | Symbols: | Protein of unknown function (DUF3755) | chr1:3601437-3604650 REVERSE LENGTH=258	244	258	1.00E-108	105.7	81.1	89.3
Rsa1.0_00454.1.g14146.t1	ref|NP_172551.1| NAD(P)-linked oxidoreductase-like protein [Arabidopsis thaliana] gi|75268154|sp|Q9C5B9.1|AKR1_ARATH RecName: Full=Probable aldo-keto reductase 1 gi|13448928|gb|AAK27238.1|AF361098_1 putative auxin-induced protein [Arabidopsis thaliana] gi|332190527|gb|AEE28648.1| probable aldo-keto reductase 1 [Arabidopsis thaliana]	337	344	1.00E-173	102.1	88.4	93.5	NAD(P)-linked oxidoreductase-like protein	gbpln	Arabidopsis thaliana	AT1G10810.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr1:3599369-3600757 FORWARD LENGTH=344	337	344	1.00E-176	102.1	88.4	93.5
Rsa1.0_00454.1.g14147.t1	ref|NP_172548.2| F-box/RNI-like protein [Arabidopsis thaliana] gi|75265517|sp|Q9SAC4.1|FB2_ARATH RecName: Full=F-box protein At1g10780 gi|4874270|gb|AAD31335.1|AC007354_8 T16B5.8 [Arabidopsis thaliana] gi|50253496|gb|AAT71950.1| At1g10780 [Arabidopsis thaliana] gi|53850513|gb|AAU95433.1| At1g10780 [Arabidopsis thaliana] gi|332190524|gb|AEE28645.1| F-box/RNI-like protein [Arabidopsis thaliana]	418	418	0	100.0	82.8	91.1	F-box/RNI-like protein	gbpln	Arabidopsis thaliana	AT1G10780.1 | Symbols: | F-box/RNI-like superfamily protein | chr1:3592875-3594310 REVERSE LENGTH=418	418	418	0	100.0	82.8	91.1
Rsa1.0_00454.1.g14148.t1	gb|AAZ20131.1| pectin methylesterase inhibitor [Brassica oleracea var. botrytis]	167	168	3.00E-82	100.6	94.0	98.8	pectin methylesterase inhibitor	gbpln	Brassica oleracea	AT1G10770.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:3591859-3592362 REVERSE LENGTH=167	167	167	4.00E-69	100.0	75.4	88.6
Rsa1.0_00454.1.g14149.t1	ref|NP_563877.1| alpha-glucan water dikinase 1 [Arabidopsis thaliana] gi|57012990|sp|Q9SAC6.2|GWD1_ARATH RecName: Full=Alpha-glucan water dikinase 1, chloroplastic; AltName: Full=Protein starch excess 1; AltName: Full=Protein starch-related R1; Flags: Precursor gi|12044358|gb|AAG47821.1|AF312027_1 SEX1 [Arabidopsis thaliana] gi|332190522|gb|AEE28643.1| alpha-glucan water dikinase 1 [Arabidopsis thaliana]	1399	1399	0	100.0	89.0	94.6	alpha-glucan water dikinase 1	gbpln	Arabidopsis thaliana	AT1G10760.1 | Symbols: SEX1, SOP1, SOP, GWD1, GWD | Pyruvate phosphate dikinase, PEP/pyruvate binding domain | chr1:3581210-3590043 REVERSE LENGTH=1399	1399	1399	0	100.0	89.0	94.6

<table>
<tr><td>Rsa1.0_00454.1.g14150.t1</td><td>ref|XP_002892596.1| hypothetical protein ARALYDRAFT_888367 [Arabidopsis lyrata subsp. lyrata] gi|297338438|gb|EFH68855.1| hypothetical protein ARALYDRAFT_888367 [Arabidopsis lyrata subsp. lyrata]</td><td>471</td><td>468</td><td>0</td><td>99.4</td><td>88.1</td><td>91.3</td><td>hypothetical protein ARALYDRAFT_888367</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10750.1 | Symbols: | Protein of Unknown Function (DUF239) | chr1:3574986-3578310 REVERSE LENGTH=467</td><td>471</td><td>467</td><td>0</td><td>99.2</td><td>87.9</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00454.1.g14151.t1</td><td>ref|NP_172544.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|334182439|ref|NP_001184955.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|334182441|ref|NP_001184956.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|4874274|gb|AAD31339.1|AC007354_12 Similar to gb|X02844 lipase precursor from Staphylococcus hyicus. ESTs gb|AI239406 and gb|T76725 come from this gene [Arabidopsis thaliana] gi|13448930|gb|AAK27239.1|AF361099_1 putative lipase [Arabidopsis thaliana] gi|21539509|gb|AAM53307.1| putative lipase [Arabidopsis thaliana] gi|30387585|gb|AAP31958.1| At1g10740 [Arabidopsis thaliana] gi|332190515|gb|AEE28636.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|332190517|gb|AEE28638.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|332190518|gb|AEE28639.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana]</td><td>467</td><td>473</td><td>0</td><td>101.3</td><td>89.1</td><td>94.4</td><td>alpha/beta-hydrolase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10740.4 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:3568343-3570466 REVERSE LENGTH=473</td><td>467</td><td>473</td><td>0</td><td>101.3</td><td>89.1</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00454.1.g14152.t1</td><td>ref|XP_002889832.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297335674|gb|EFH66091.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata]</td><td>428</td><td>428</td><td>0</td><td>100.0</td><td>99.1</td><td>99.5</td><td>clathrin adaptor complexes medium subunit family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G60780.1 | Symbols: HAP13 | Clathrin adaptor complexes medium subunit family protein | chr1:22369289-22371885 REVERSE LENGTH=428</td><td>428</td><td>428</td><td>0</td><td>100.0</td><td>97.2</td><td>99.5</td></tr>
<tr><td>Rsa1.0_00454.1.g14153.t1</td><td>gb|AAF17660.1|AC009398_9 F20B24.15 [Arabidopsis thaliana]</td><td>466</td><td>452</td><td>1.00E-152</td><td>97.0</td><td>73.0</td><td>78.1</td><td>F20B24.15</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10720.1 | Symbols: | BSD domain-containing protein | chr1:3562964-3564446 FORWARD LENGTH=429</td><td>466</td><td>429</td><td>1.00E-150</td><td>92.1</td><td>73.2</td><td>78.1</td></tr>
<tr><td>Rsa1.0_00454.1.g14154.t1</td><td>ref|XP_002889827.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335669|gb|EFH66086.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>356</td><td>412</td><td>1.00E-103</td><td>115.7</td><td>59.3</td><td>67.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10710.2 | Symbols: PHS1 | poor homologous synapsis 1 | chr1:3558423-3560407 FORWARD LENGTH=349</td><td>356</td><td>349</td><td>1.00E-102</td><td>98.0</td><td>58.4</td><td>67.7</td></tr>
<tr><td>Rsa1.0_00454.1.g14155.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00454.1.g14156.t12</td><td>gb|AAF78272.1|AC020576_16 Contains similarity to a putative protein T32A11_100 gi|7413627 from Arabidopsis thaliana BAC T32A11 gb|AL138653 [Arabidopsis thaliana]</td><td>1099</td><td>1075</td><td>1.00E-68</td><td>97.8</td><td>18.8</td><td>26.8</td><td>Contains similarity to a putative protein T32A11_100 gi|7413627 from Arabidopsis thaliana BAC T32A11 gb|AL138653</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673</td><td>1099</td><td>673</td><td>5.00E-49</td><td>61.2</td><td>11.0</td><td>16.7</td></tr>
<tr><td>Rsa1.0_00454.1.g14157.t1</td><td>gb|AAF78267.1|AC020576_11 Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene [Arabidopsis thaliana]</td><td>1025</td><td>1206</td><td>0</td><td>117.7</td><td>35.0</td><td>46.2</td><td>Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719</td><td>1025</td><td>719</td><td>1.00E-31</td><td>70.1</td><td>12.9</td><td>22.0</td></tr>
<tr><td>Rsa1.0_00454.1.g14158.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_00454.1.g14159.t1	ref|NP_199321.1| protein PHLOEM protein 2-LIKE A6 [Arabidopsis thaliana] gi|75170595|sp|Q9FHE8.1|P2A06_ARATH RecName: Full=Protein PHLOEM PROTEIN 2-LIKE A6; Short=AtPP2-A6 gi|9758981|dbj|BAB09491.1| unnamed protein product [Arabidopsis thaliana] gi|332007815|gb|AED95198.1| protein PHLOEM protein 2-LIKE A6 [Arabidopsis thaliana]	358	392	7.00E-90	109.5	52.2	66.5	protein PHLOEM protein 2-LIKE A6	gbpln	Arabidopsis thaliana	AT5G45080.1 | Symbols: AtPP2-A6, PP2-A6 | phloem protein 2-A6 | chr5:18191575-18193207 REVERSE LENGTH=392	358	392	2.00E-92	109.5	52.2	66.5
Rsa1.0_00455.1.g14160.t2	gb|EOA36037.1| hypothetical protein CARUB_v10008116mg [Capsella rubella]	779	1204	0	154.6	85.6	89.2	hypothetical protein CARUB_v10008116mg	gbpln	Capsella rubella	AT1G13210.1 | Symbols: ACA.l | autoinhibited Ca2+/ATPase II | chr1:4509252-4513774 REVERSE LENGTH=1203	779	1203	0	154.4	84.7	88.6
Rsa1.0_00455.1.g14161.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00455.1.g14162.t1	sp|P04796.2|G3PC_SINAL RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product [Sinapis alba]	133	338	3.00E-62	254.1	85.7	88.0	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product	gbpln	Sinapis alba	AT3G04120.1 | Symbols: GAPC, GAPC-1, GAPC1 | glyceraldehyde-3-phosphate dehydrogenase C subunit 1 | chr3:1081077-1083131 FORWARD LENGTH=338	133	338	4.00E-63	254.1	82.0	87.2
Rsa1.0_00455.1.g14163.t2	gb|ABV89646.1| DNA binding protein GT-1 [Brassica rapa]	425	399	0	93.9	84.2	88.0	DNA binding protein GT-1	gbpln	Brassica rapa	AT1G13450.1 | Symbols: GT-1 | Homeodomain-like superfamily protein | chr1:4612999-4615115 REVERSE LENGTH=406	425	406	0	95.5	81.6	88.0
Rsa1.0_00455.1.g14164.t1	ref|NP_172804.2| uncharacterized protein [Arabidopsis thaliana] gi|332190902|gb|AEE29023.1| uncharacterized protein AT1G13470 [Arabidopsis thaliana]	384	379	1.00E-154	98.7	71.6	83.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G13470.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4620322-4621542 REVERSE LENGTH=379	384	379	1.00E-157	98.7	71.6	83.1
Rsa1.0_00455.1.g14165.t1	gb|ABD65164.1| hypothetical protein 40.t00049 [Brassica oleracea]	436	297	7.00E-55	68.1	23.2	24.1	hypothetical protein 40.t00049	gbpln	Brassica oleracea	AT4G17760.2 | Symbols: | damaged DNA binding;exodeoxyribonuclease IIIs | chr4:9871921-9873257 FORWARD LENGTH=250	436	250	2.00E-54	57.3	22.0	22.9
Rsa1.0_00455.1.g14166.t1	ref|NP_187210.1| 60S ribosomal protein L18-2 [Arabidopsis thaliana] gi|21431838|sp|P42791.2|RL182_ARATH RecName: Full=60S ribosomal protein L18-2 gi|6714451|gb|AAF26138.1|AC011620_14 putative 60S ribosomal protein L18 [Arabidopsis thaliana] gi|14335090|gb|AAK59824.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gi|16974509|gb|AAL31164.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gi|332640742|gb|AEE74263.1| 60S ribosomal protein L18-2 [Arabidopsis thaliana]	178	187	8.00E-46	105.1	53.4	56.2	60S ribosomal protein L18-2	gbpln	Arabidopsis thaliana	AT3G05590.1 | Symbols: RPL18 | ribosomal protein L18 | chr3:1621511-1622775 FORWARD LENGTH=187	178	187	3.00E-48	105.1	53.4	56.2
Rsa1.0_00455.1.g14167.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00455.1.g14168.t1	ref|NP_172804.2| uncharacterized protein [Arabidopsis thaliana] gi|332190902|gb|AEE29023.1| uncharacterized protein AT1G13470 [Arabidopsis thaliana]	379	379	1.00E-160	100.0	75.7	85.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G13470.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4620322-4621542 REVERSE LENGTH=379	379	379	1.00E-162	100.0	75.7	85.8
Rsa1.0_00455.1.g14169.t1	ref|XP_002892756.1| hypothetical protein ARALYDRAFT_312360 [Arabidopsis lyrata subsp. lyrata] gi|297338598|gb|EFH69015.1| hypothetical protein ARALYDRAFT_312360 [Arabidopsis lyrata subsp. lyrata]	380	772	1.00E-153	203.2	72.9	83.7	hypothetical protein ARALYDRAFT_312360	gbpln	Arabidopsis lyrata	AT1G13520.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4631857-4633223 REVERSE LENGTH=387	380	387	1.00E-152	101.8	73.9	82.6
Rsa1.0_00455.1.g14170.t1	ref|NP_172812.2| uncharacterized protein [Arabidopsis thaliana] gi|91805779|gb|ABE65618.1| unknown [Arabidopsis thaliana] gi|332190911|gb|AEE29032.1| uncharacterized protein AT1G13550 [Arabidopsis thaliana]	389	388	0	99.7	85.3	91.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G13550.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4637072-4638315 REVERSE LENGTH=388	389	388	0	99.7	85.3	91.0
Rsa1.0_00455.1.g14171.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00455.1.g14172.t1	gb|AAL46934.3|AF446089_1 aminoalcoholphosphotransferase [Brassica rapa subsp. pekinensis]	269	392	1.00E-127	145.7	84.8	87.4	aminoalcoholphosphotransferase	gbpln	Brassica rapa	AT1G13560.2 | Symbols: AAPT1, ATAAPT1 | aminoalcoholphosphotransferase 1 | chr1:4638834-4641563 REVERSE LENGTH=346	269	346	1.00E-125	128.6	80.7	85.1

Rsa1.0_00455.1.g14173.t1	ref|XP_002892760.1| hypothetical protein ARALYDRAFT_471517 [Arabidopsis lyrata subsp. lyrata] gi|297338602|gb|EFH69019.1| hypothetical protein ARALYDRAFT_471517 [Arabidopsis lyrata subsp. lyrata]	188	308	1.00E-91	163.8	85.6	89.4	hypothetical protein ARALYDRAFT_471517	gbpln	Arabidopsis lyrata	AT1G13580.1 | Symbols: LAG13 | LAG1 longevity assurance homolog 3 | chr1:4645380-4646765 REVERSE LENGTH=239	188	239	1.00E-93	127.1	85.1	89.9
Rsa1.0_00455.1.g14174.t1	ref|NP_172816.2| phytosulfokine-beta [Arabidopsis thaliana] gi|41019236|sp|Q9LMY9.3|PSK1_ARATH RecName: Full=Phytosulfokines 1; Short=AtPSK1; Contains: RecName: Full=Phytosulfokine-alpha; Short=PSK-alpha; Short=Phytosulfokine-a; Contains: RecName: Full=Phytosulfokine-beta; Short=PSK-beta; Short=Phytosulfokine-b; Flags: Precursor gi|23466369|tpg|DAA00275.1| TPA_exp: putative phytosulfokine peptide precursor [Arabidopsis thaliana] gi|27529964|dbj|BAB72176.2| phytosulfokine precursor 1 [Arabidopsis thaliana] gi|51970324|dbj|BAD43854.1| hypothetical protein [Arabidopsis thaliana] gi|332190918|gb|AEE29039.1| phytosulfokine-beta [Arabidopsis thaliana]	90	87	7.00E-31	96.7	76.7	84.4	phytosulfokine-beta	gbpln	Arabidopsis thaliana	AT1G13590.1 | Symbols: ATPSK1, PSK1 | phytosulfokine 1 precursor | chr1:4647979-4648612 FORWARD LENGTH=87	90	87	1.00E-33	96.7	76.7	84.4
Rsa1.0_00455.1.g14175.t1	ref|NP_172817.2| basic leucine-zipper 58 [Arabidopsis thaliana] gi|8920564|gb|AAF81286.1|AC027656_3 Contains similarity to bZIP DNA-binding protein HBF-1 - soybean from Glycine max gb|Y10685. It contains a bZIP transcription factor PF|00170. EST gb|N37717 comes from this gene [Arabidopsis thaliana] gi|9802757|gb|AAF99826.1|AC027134_8 Hypothetical protein [Arabidopsis thaliana] gi|12083268|gb|AAG48793.1|AF332430_1 putative bZIP transcription factor [Arabidopsis thaliana] gi|225897922|dbj|BAH30293.1| hypothetical protein [Arabidopsis thaliana] gi|332190919|gb|AEE29040.1| basic leucine-zipper 58 [Arabidopsis thaliana]	195	196	3.00E-82	100.5	84.6	90.8	basic leucine-zipper 58	gbpln	Arabidopsis thaliana	AT1G13600.1 | Symbols: AtbZIP58, bZIP58 | basic leucine-zipper 58 | chr1:4650787-4651377 REVERSE LENGTH=196	195	196	1.00E-84	100.5	84.6	90.8
Rsa1.0_00455.1.g14176.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00455.1.g14177.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00455.1.g14178.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00456.1.g14179.t1	gb|ACA61613.1| hypothetical protein AP2_E11.1 [Arabidopsis lyrata subsp. petraea]	138	471	9.00E-17	341.3	35.5	47.1	hypothetical protein AP2_E11.1	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00456.1.g14180.t2	gb|EOA27002.1| hypothetical protein CARUB_v10023097mg [Capsella rubella] gi|482562813|gb|EOA27003.1| hypothetical protein CARUB_v10023097mg [Capsella rubella]	465	486	0	104.5	82.6	87.7	hypothetical protein CARUB_v10023097mg	gbpln	Capsella rubella	AT2G37440.1 | Symbols: | DNAse I-like superfamily protein | chr2:15719230-15721885 FORWARD LENGTH=479	465	479	0	103.0	82.6	87.7
Rsa1.0_00456.1.g14181.t1	ref|NP_181282.1| nodulin MtN21 /EamA-like transporter-like protein [Arabidopsis thaliana] gi|75216840|sp|Q9ZUS1.1|WTR13_ARATH RecName: Full=WAT1-related protein At2g37460 gi|4056506|gb|AAC98072.1| nodulin-like protein [Arabidopsis thaliana] gi|14334858|gb|AAK59607.1| putative nodulin protein [Arabidopsis thaliana] gi|14994253|gb|AAK73261.1| nodulin-like protein [Arabidopsis thaliana] gi|17104641|gb|AAL34209.1| putative nodulin protein [Arabidopsis thaliana] gi|330254309|gb|AEC09403.1| WAT1-related protein [Arabidopsis thaliana]	362	380	0	105.0	89.2	94.2	nodulin MtN21 /EamA-like transporter-like protein	gbpln	Arabidopsis thaliana	AT2G37460.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr2:15726667-15729010 REVERSE LENGTH=380	362	380	0	105.0	89.2	94.2

Rsa1.0_00456.1.g14182.t1	ref|NP_973623.1| uncharacterized protein [Arabidopsis thaliana] gi|110741336|dbj|BAF02218.1| hypothetical protein [Arabidopsis thaliana] gi|330254313|gb|AEC09407.1| uncharacterized protein AT2G37480 [Arabidopsis thaliana]	185	193	1.00E-64	104.3	72.4	84.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G37480.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G53670.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:15738645-15739579 FORWARD LENGTH=193	185	193	4.00E-67	104.3	72.4	84.3
Rsa1.0_00456.1.g14183.t1	ref|NP_181289.2| uncharacterized protein [Arabidopsis thaliana] gi|330254318|gb|AEC09412.1| uncharacterized protein AT2G37530 [Arabidopsis thaliana]	125	122	2.00E-49	97.6	79.2	89.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G37530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G07795.1); Has 39 Blast hits to 39 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15751060-15751428 FORWARD LENGTH=122	125	122	3.00E-52	97.6	79.2	89.6
Rsa1.0_00456.1.g14184.t2	ref|XP_003542460.1| PREDICTED: ADP-ribosylation factor GTPase-activating protein AGD7-like [Glycine max]	441	481	1.00E-120	109.1	59.2	72.3	PREDICTED: ADP-ribosylation factor GTPase-activating protein AGD7-like	gbenv/gbpln	Glycine max	AT2G37550.2 | Symbols: ASP1, AGD7 | ARF-GAP domain 7 | chr2:15755544-15757456 REVERSE LENGTH=456	441	456	6.00E-86	103.4	44.7	46.0
Rsa1.0_00456.1.g14185.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_00456.1.g14186.t1	emb|CAB46045.1| retrotransposon like protein [Arabidopsis thaliana] gi|7268441|emb|CAB80961.1| retrotransposon like protein [Arabidopsis thaliana]	462	687	9.00E-22	148.7	10.6	15.6	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT5G20300.2 | Symbols: | Avirulence induced gene (AIG1) family protein | chr5:6853544-6856332 REVERSE LENGTH=793	462	793	2.00E-17	171.6	16.0	22.1
Rsa1.0_00456.1.g14187.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	792	1475	0	186.2	66.8	81.6	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	792	1262	0	159.3	40.4	52.9
Rsa1.0_00456.1.g14188.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00456.1.g14189.t1	emb|CAB72476.1| putative protein [Arabidopsis thaliana]	469	661	8.00E-91	140.9	47.8	65.5	putative protein	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	469	696	2.00E-13	148.4	11.3	18.1
Rsa1.0_00456.1.g14190.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00456.1.g14191.t1	gb|EOA27799.1| hypothetical protein CARUB_v10023951mg [Capsella rubella]	213	241	1.00E-57	113.1	72.3	79.3	hypothetical protein CARUB_v10023951mg	gbpln	Capsella rubella	AT2G37580.1 | Symbols: | RING/U-box superfamily protein | chr2:15764745-15765452 FORWARD LENGTH=235	213	235	2.00E-51	110.3	65.7	74.6
Rsa1.0_00456.1.g14192.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00456.1.g14193.t1	ref|XP_002879686.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325525|gb|EFH55945.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	301	326	1.00E-120	108.3	83.7	87.0	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT2G37590.1 | Symbols: ATDOF2.4, DOF2.4 | DNA binding with one finger 2.4 | chr2:15769292-15770497 FORWARD LENGTH=330	301	330	1.00E-114	109.6	82.4	85.4
Rsa1.0_00456.1.g14194.t1	gb|EOA28156.1| hypothetical protein CARUB_v10024358mg [Capsella rubella]	136	112	7.00E-51	82.4	77.2	77.2	hypothetical protein CARUB_v10024358mg	gbpln	Capsella rubella	AT3G53740.4 | Symbols: | Ribosomal protein L36e family protein | chr3:19913921-19914813 REVERSE LENGTH=112	136	112	9.00E-53	82.4	75.7	77.9
Rsa1.0_00456.1.g14195.t1	gb|ABK28208.1| unknown [Arabidopsis thaliana]	122	122	6.00E-26	100.0	58.2	66.4	unknown	gbpln	Arabidopsis thaliana	AT2G37610.1 | Symbols: | unknown protein; Has 21 Blast hits to 21 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15776869-15777673 REVERSE LENGTH=161	122	161	1.00E-28	132.0	58.2	66.4

Rsa1.0_00456.1.g14196.t1	ref|NP_566988.1| actin 3 [Arabidopsis thaliana] gi|30687201|ref|NP_850284.1| actin 1 [Arabidopsis thaliana] gi|79324605|ref|NP_001031504.1| actin 1 [Arabidopsis thaliana] gi|460415910|ref|XP_004253296.1| PREDICTED: actin-1-like [Solanum lycopersicum] gi|317374840|sp|P0CJ46.1|ACT1_ARATH RecName: Full=Actin-1 gi|317374841|sp|P0CJ47.1|ACT3_ARATH RecName: Full=Actin-3 gi|1145695|gb|AAA98562.1| actin 3 [Arabidopsis thaliana] gi|15146304|gb|AAK83635.1| AT3g53750/F5K20_50 [Arabidopsis thaliana] gi|18650648|gb|AAL75893.1| At2g37620/F13M22.12 [Arabidopsis thaliana] gi|20147381|gb|AAM10400.1| At2g37620/F13M22.12 [Arabidopsis thaliana] gi|21554576|gb|AAM63620.1| actin (ACT3) [Arabidopsis thaliana] gi|25090278|gb|AAN72268.1| At3g53750/F5K20_50 [Arabidopsis thaliana] gi|330254332|gb|AEC09426.1| actin 1 [Arabidopsis thaliana] gi|330254333|gb|AEC09427.1| actin 1 [Arabidopsis thaliana] gi|332645617|gb|AEE79138.1| actin 3 [Arabidopsis thaliana]	375	377	0	100.5	97.9	98.7	actin 3	gbpln	Arabidopsis thaliana	AT3G53750.1 | Symbols: ACT3 | actin 3 | chr3:19915924-19917371 FORWARD LENGTH=377	375	377	0	100.5	97.9	98.7
Rsa1.0_00456.1.g14197.t1	ref|NP_181299.1| transcription factor AS1 [Arabidopsis thaliana] gi|29427581|sp|O80931.1|AS1_ARATH RecName: Full=Transcription factor AS1; AltName: Full=Myb-related protein 91; Short=AtMYB91; AltName: Full=Protein ASYMMETRIC LEAVES 1; AltName: Full=Protein PHANTASTICA; Short=AtPHAN gi|5823325|gb|AAD53101.1|AF175996_1 putative transcription factor [Arabidopsis thaliana] gi|3236245|gb|AAC23633.1| putative MYB family transcription factor [Arabidopsis thaliana] gi|41619204|gb|AAS10048.1| MYB transcription factor [Arabidopsis thaliana] gi|109946409|gb|ABG48383.1| At2g37630 [Arabidopsis thaliana] gi|330254334|gb|AEC09428.1| transcription factor AS1 [Arabidopsis thaliana]	368	367	1.00E-174	99.7	89.7	92.7	transcription factor AS1	gbpln	Arabidopsis thaliana	AT2G37630.1 | Symbols: ATPHAN, AS1, ATMYB91, MYB91 | myb-like HTH transcriptional regulator family protein | chr2:15781798-15782901 REVERSE LENGTH=367	368	367	1.00E-176	99.7	89.7	92.7
Rsa1.0_00457.1.g14198.t1	ref|XP_002889391.1| hypothetical protein ARALYDRAFT_470181 [Arabidopsis lyrata subsp. lyrata] gi|297335233|gb|EFH65650.1| hypothetical protein ARALYDRAFT_470181 [Arabidopsis lyrata subsp. lyrata]	201	245	7.00E-89	121.9	80.6	88.1	hypothetical protein ARALYDRAFT_470181	gbpln	Arabidopsis lyrata	AT1G01020.1 | Symbols: ARV1 | Arv1-like protein | chr1:6915-8666 REVERSE LENGTH=245	201	245	5.00E-86	121.9	77.1	87.1
Rsa1.0_00457.1.g14199.t1	ref|XP_002892089.1| ANAC001 [Arabidopsis lyrata subsp. lyrata] gi|297337931|gb|EFH68348.1| ANAC001 [Arabidopsis lyrata subsp. lyrata]	428	465	1.00E-131	108.6	64.3	74.5	ANAC001	gbpln	Arabidopsis lyrata	AT1G01010.1 | Symbols: ANAC001, NAC001 | NAC domain containing protein 1 | chr1:3760-5630 FORWARD LENGTH=429	428	429	1.00E-130	100.2	61.2	72.0
Rsa1.0_00457.1.g14200.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00457.1.g14201.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	198	441	1.00E-42	222.7	42.4	57.6	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	198	746	7.00E-25	376.8	28.8	39.4
Rsa1.0_00457.1.g14202.t1	ref|NP_563655.1| SRPBCC ligand-binding domain-containing protein [Arabidopsis thaliana] gi|332189312|gb|AEE27433.1| SRPBCC ligand-binding domain-containing protein [Arabidopsis thaliana]	204	220	1.00E-56	107.8	67.6	75.5	SRPBCC ligand-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G02470.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:511916-513573 REVERSE LENGTH=220	204	220	4.00E-59	107.8	67.6	75.5
Rsa1.0_00457.1.g14203.t1	gb|EOA36427.1| hypothetical protein CARUB_v10010960mg [Capsella rubella]	227	219	2.00E-90	96.5	81.5	85.9	hypothetical protein CARUB_v10010960mg	gbpln	Capsella rubella	AT1G02475.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:514110-515331 REVERSE LENGTH=219	227	219	1.00E-89	96.5	78.9	85.5
Rsa1.0_00457.1.g14204.t2	gb|EOA36035.1| hypothetical protein CARUB_v10008098mg, partial [Capsella rubella]	1330	1325	0	99.6	89.7	93.7	hypothetical protein CARUB_v10008098mg, partial	gbpln	Capsella rubella	AT1G02520.1 | Symbols: PGP11 | P-glycoprotein 11 | chr1:524134-528745 FORWARD LENGTH=1278	1330	1278	0	96.1	89.2	92.4

Rsa1.0_00457.1.g14205.t1	ref|XP_002889406.1| hypothetical protein ARALYDRAFT_887394 [Arabidopsis lyrata subsp. lyrata] gi|297335248|gb|EFH65665.1| hypothetical protein ARALYDRAFT_887394 [Arabidopsis lyrata subsp. lyrata]	299	298	1.00E-168	99.7	96.3	98.0	hypothetical protein ARALYDRAFT_887394	gbpln	Arabidopsis lyrata	AT1G02560.1 | Symbols: CLPP5, NCLPP5, NCLPP1 | nuclear encoded CLP protease 5 | chr1:538000-539805 FORWARD LENGTH=298	299	298	1.00E-169	99.7	95.7	97.3
Rsa1.0_00457.1.g14206.t1	gb|EOA38398.1| hypothetical protein CARUB_v10009964mg [Capsella rubella]	270	279	1.00E-104	103.3	78.9	87.0	hypothetical protein CARUB_v10009964mg	gbpln	Capsella rubella	AT1G02570.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02575.1); Has 108 Blast hits to 55 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 108; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:541380-542216 FORWARD LENGTH=278	270	278	1.00E-105	103.0	80.4	86.7
Rsa1.0_00457.1.g14207.t6	ref|XP_002889408.1| hypothetical protein ARALYDRAFT_470218 [Arabidopsis lyrata subsp. lyrata] gi|297335250|gb|EFH65667.1| hypothetical protein ARALYDRAFT_470218 [Arabidopsis lyrata subsp. lyrata]	659	672	0	102.0	55.4	70.0	hypothetical protein ARALYDRAFT_470218	gbpln	Arabidopsis lyrata	AT1G02580.1 | Symbols: MEA, EMB173, FIS1, SDG5 | SET domain-containing protein | chr1:544796-548994 FORWARD LENGTH=689	659	689	0	104.6	54.6	70.3
Rsa1.0_00457.1.g14208.t1	gb|EOA22812.1| hypothetical protein CARUB_v10003530mg [Capsella rubella]	406	288	7.00E-90	70.9	42.9	51.0	hypothetical protein CARUB_v10003530mg	gbpln	Capsella rubella	AT1G45063.2 | Symbols: | copper ion binding;electron carriers | chr1:17034068-17034886 REVERSE LENGTH=272	406	272	7.00E-82	67.0	39.4	47.3
Rsa1.0_00457.1.g14209.t1	ref|XP_002892113.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337955|gb|EFH68372.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	217	220	4.00E-87	101.4	80.6	87.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G02610.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:553181-555854 REVERSE LENGTH=221	217	221	1.00E-86	101.8	77.9	85.3
Rsa1.0_00457.1.g14210.t1	ref|XP_002892115.1| hypothetical protein ARALYDRAFT_470221 [Arabidopsis lyrata subsp. lyrata] gi|297337957|gb|EFH68374.1| hypothetical protein ARALYDRAFT_470221 [Arabidopsis lyrata subsp. lyrata]	102	389	5.00E-24	381.4	73.5	78.4	hypothetical protein ARALYDRAFT_470221	gbpln	Arabidopsis lyrata	AT1G02630.1 | Symbols: | Nucleoside transporter family protein | chr1:561007-562382 REVERSE LENGTH=389	102	389	1.00E-26	381.4	71.6	79.4
Rsa1.0_00457.1.g14211.t1	ref|NP_563659.1| beta-glucosidase [Arabidopsis thaliana] gi|75250279|sp|Q94KD8.1|BXL2_ARATH RecName: Full=Probable beta-D-xylosidase 2; Short=AtBXL2; Flags: Precursor gi|14194121|gb|AAK56255.1|AF367266_1 At1g02640/T14P4_11 [Arabidopsis thaliana] gi|23506063|gb|AAN28891.1| At1g02640/T14P4_11 [Arabidopsis thaliana] gi|332189332|gb|AEE27453.1| probable beta-D-xylosidase 2 [Arabidopsis thaliana]	767	768	0	100.1	92.0	95.3	beta-glucosidase	gbpln	Arabidopsis thaliana	AT1G02640.1 | Symbols: BXL2, ATBXL2 | beta-xylosidase 2 | chr1:564293-567580 FORWARD LENGTH=768	767	768	0	100.1	92.0	95.3
Rsa1.0_00457.1.g14212.t1	gb|EOA36263.1| hypothetical protein CARUB_v10010486mg, partial [Capsella rubella]	127	167	8.00E-54	131.5	88.2	91.3	hypothetical protein CARUB_v10010486mg, partial	gbpln	Capsella rubella	AT1G02680.1 | Symbols: TAF13 | TBP-associated factor 13 | chr1:581084-581919 FORWARD LENGTH=126	127	126	3.00E-55	99.2	85.0	89.0
Rsa1.0_00457.1.g14213.t1	gb|EOA38580.1| hypothetical protein CARUB_v10010400mg [Capsella rubella]	187	183	1.00E-82	97.9	83.4	91.4	hypothetical protein CARUB_v10010400mg	gbpln	Capsella rubella	AT5G38700.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.04 four leaves visible, LP.10 ten leaves visible, petal differentiation and expansion stage, LP.08 eight leaves visible, LP.12 twelve leaves visible; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02170.1); Has 64 Blast hits to 64 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:15489690-15490238 FORWARD LENGTH=182	187	182	4.00E-82	97.3	79.1	86.6
Rsa1.0_00457.1.g14214.t1	ref|XP_002874719.1| hypothetical protein ARALYDRAFT_911537 [Arabidopsis lyrata subsp. lyrata] gi|297320556|gb|EFH50978.1| hypothetical protein ARALYDRAFT_911537 [Arabidopsis lyrata subsp. lyrata]	374	456	2.00E-90	121.9	51.1	61.2	hypothetical protein ARALYDRAFT_911537	gbpln	Arabidopsis lyrata	AT4G36840.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:17352166-17352882 FORWARD LENGTH=238	374	238	5.00E-32	63.6	27.8	37.2

Rsa1.0_00457.1.g14215.t1	gb|EOA38865.1| hypothetical protein CARUB_v10011230mg [Capsella rubella]	207	221	2.00E−52	106.8	72.0	82.1	hypothetical protein CARUB_v10011230mg	gbpln	Capsella rubella	AT5G61710.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02160.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:24800045−24800512 FORWARD LENGTH=155	207	155	2.00E−47	74.9	56.5	61.4
Rsa1.0_00457.1.g14216.t1	ref|XP_002889414.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335256|gb|EFH65673.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	197	217	2.00E−66	110.2	70.1	76.1	predicted protein	gbpln	Arabidopsis lyrata	AT2G36110.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H−like superfamily protein | chr2:15161877−15162596 FORWARD LENGTH=239	197	239	4.00E−11	121.3	27.4	44.2
Rsa1.0_00457.1.g14217.t1	ref|NP_171769.1| importin alpha isoform 6 [Arabidopsis thaliana] gi|9972381|gb|AAG10631.1|AC022521_9 Putative importin alpha subunit [Arabidopsis thaliana] gi|17979135|gb|AAL49825.1| putative importin alpha protein [Arabidopsis thaliana] gi|20465347|gb|AAM20077.1| putative importin alpha protein [Arabidopsis thaliana] gi|332189337|gb|AEE27458.1| importin alpha isoform 6 [Arabidopsis thaliana]	527	538	0	102.1	75.7	85.0	importin alpha isoform 6	gbpln	Arabidopsis thaliana	AT1G02690.1 | Symbols: IMPA−6 | importin alpha isoform 6 | chr1:584397−587036 FORWARD LENGTH=538	527	538	0	102.1	75.7	85.0
Rsa1.0_00457.1.g14218.t1	ref|NP_563661.1| uncharacterized protein [Arabidopsis thaliana] gi|9972373|gb|AAG10623.1|AC022521_1 Unknown protein [Arabidopsis thaliana] gi|15810579|gb|AAL07177.1| unknown protein [Arabidopsis thaliana] gi|20259577|gb|AAM14131.1| unknown protein [Arabidopsis thaliana] gi|332189339|gb|AEE27460.1| uncharacterized protein AT1G02700 [Arabidopsis thaliana]	226	247	1.00E−108	109.3	87.2	94.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G02700.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02140.1); Has 49 Blast hits to 49 proteins in 21 species: Archae − 0; Bacteria − 0; Metazoa − 10; Fungi − 6; Plants − 29; Viruses − 0; Other Eukaryotes − 4 (source: NCBI BLink). | chr1:588367−589232 FORWARD LENGTH=247	226	247	1.00E−111	109.3	87.2	94.7
Rsa1.0_00457.1.g14219.t1	ref|XP_002892121.1| hypothetical protein ARALYDRAFT_887416 [Arabidopsis lyrata subsp. lyrata] gi|297337963|gb|EFH68380.1| hypothetical protein ARALYDRAFT_887416 [Arabidopsis lyrata subsp. lyrata]	1181	1184	0	100.3	93.2	96.4	hypothetical protein ARALYDRAFT_887416	gbpln	Arabidopsis lyrata	AT1G02730.1 | Symbols: ATCSLD5, CSLD5, SOS6 | cellulose synthase−like D5 | chr1:594697−598473 REVERSE LENGTH=1181	1181	1181	0	100.0	92.9	95.9
Rsa1.0_00457.1.g14220.t1	dbj|BAJ33794.1| unnamed protein product [Thellungiella halophila] gi|312281899|dbj|BAJ33815.1| unnamed protein product [Thellungiella halophila]	189	220	9.00E−52	116.4	70.4	80.4	unnamed protein product	----	----	AT1G02750.2 | Symbols: | Drought−responsive family protein | chr1:602673−604134 FORWARD LENGTH=205	189	205	1.00E−50	108.5	65.1	75.1
Rsa1.0_00457.1.g14221.t1	gb|EOA31438.1| hypothetical protein CARUB_v10014622mg [Capsella rubella]	216	210	4.00E−96	97.2	84.3	88.0	hypothetical protein CARUB_v10014622mg	gbpln	Capsella rubella	AT3G16780.1 | Symbols: | Ribosomal protein L19e family protein | chr3:5708982−5710249 FORWARD LENGTH=209	216	209	4.00E−97	96.8	82.9	87.0
Rsa1.0_00457.1.g14222.t1	dbj|BAB09923.1| copia−like retrotransposable element [Arabidopsis thaliana]	1418	1342	0	94.6	50.2	66.7	copia−like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1418	1262	2.00E−87	89.0	13.8	20.9
Rsa1.0_00457.1.g14223.t1	gb|EOA38368.1| hypothetical protein CARUB_v10009900mg [Capsella rubella]	300	292	1.00E−127	97.3	75.3	85.7	hypothetical protein CARUB_v10009900mg	gbpln	Capsella rubella	AT1G03210.1 | Symbols: | Phenazine biosynthesis PhzC/PhzF protein | chr1:782948−784240 FORWARD LENGTH=286	300	286	1.00E−128	95.3	75.7	85.0
Rsa1.0_00457.1.g14224.t1	ref|NP_001184897.1| uncharacterized protein [Arabidopsis thaliana] gi|332189429|gb|AEE27550.1| uncharacterized protein AT1G03250 [Arabidopsis thaliana]	257	251	1.00E−121	97.7	86.0	91.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G03250.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages. | chr1:793576−795159 REVERSE LENGTH=251	257	251	1.00E−124	97.7	86.0	91.1
Rsa1.0_00457.1.g14225.t1	gb|EOA40220.1| hypothetical protein CARUB_v10008943mg [Capsella rubella]	502	496	0	98.8	87.3	91.8	hypothetical protein CARUB_v10008943mg	gbpln	Capsella rubella	AT1G03270.1 | Symbols: | CBS domain−containing protein with a domain of unknown function (DUF21) | chr1:799191−802436 FORWARD LENGTH=499	502	499	0	99.4	87.6	90.6

Rsa1.0_00457.1.g14226.t2	ref|XP_002889451.1| hypothetical protein ARALYDRAFT_470307 [Arabidopsis lyrata subsp. lyrata] gi|297335293|gb|EFH65710.1| hypothetical protein ARALYDRAFT_470307 [Arabidopsis lyrata subsp. lyrata]	577	573	1.00E-157	99.3	61.9	71.6	hypothetical protein ARALYDRAFT_470307	gbpln	Arabidopsis lyrata	AT1G03290.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02880.2). | chr1:807970-810680 FORWARD LENGTH=571	577	571	1.00E-157	99.0	60.0	71.4
Rsa1.0_00457.1.g14227.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00457.1.g14228.t1	ref|XP_002889452.1| ATISA2/BE2/DBE1/ISA2 [Arabidopsis lyrata subsp. lyrata] gi|297335294|gb|EFH65711.1| ATISA2/BE2/DBE1/ISA2 [Arabidopsis lyrata subsp. lyrata]	885	872	0	98.5	81.6	88.7	ATISA2/BE2/DBE1/ISA2	gbpln	Arabidopsis lyrata	AT1G03310.1 | Symbols: ATISA2, ISA2, DBE1, BE2 | debranching enzyme 1 | chr1:813975-816623 FORWARD LENGTH=882	885	882	0	99.7	82.5	90.1
Rsa1.0_00457.1.g14229.t1	gb|EOA39128.1| hypothetical protein CARUB_v10012047mg [Capsella rubella]	221	207	3.00E-16	93.7	41.6	52.9	hypothetical protein CARUB_v10012047mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00457.1.g14230.t1	ref|XP_002875353.1| hypothetical protein ARALYDRAFT_347067 [Arabidopsis lyrata subsp. lyrata] gi|297321191|gb|EFH51612.1| hypothetical protein ARALYDRAFT_347067 [Arabidopsis lyrata subsp. lyrata]	284	296	1.00E-70	104.2	59.5	73.2	hypothetical protein ARALYDRAFT_347067	gbpln	Arabidopsis lyrata	AT3G27025.1 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9969735-9971084 FORWARD LENGTH=289	284	289	2.00E-66	101.8	56.0	70.1
Rsa1.0_00457.1.g14231.t1	gb|EOA38703.1| hypothetical protein CARUB_v10010754mg [Capsella rubella]	93	93	3.00E-47	100.0	100.0	100.0	hypothetical protein CARUB_v10010754mg	gbpln	Capsella rubella	AT1G03330.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:818161-819297 REVERSE LENGTH=93	93	93	4.00E-49	100.0	98.9	98.9
Rsa1.0_00457.1.g14232.t1	ref|NP_171833.1| uncharacterized protein [Arabidopsis thaliana] gi|3850570|gb|AAC72110.1| F15K9.6 [Arabidopsis thaliana] gi|332189440|gb|AEE27561.1| uncharacterized protein AT1G03340 [Arabidopsis thaliana]	360	385	1.00E-100	106.9	64.7	77.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G03340.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02920.1); Has 44 Blast hits to 41 proteins in 13 species: Archae - 0; Bacteria - 1; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:819712-821227 FORWARD LENGTH=385	360	385	1.00E-103	106.9	64.7	77.2
Rsa1.0_00457.1.g14233.t1	gb|EOA40387.1| hypothetical protein CARUB_v10009113mg [Capsella rubella]	456	451	1.00E-162	98.9	71.9	81.1	hypothetical protein CARUB_v10009113mg	gbpln	Capsella rubella	AT1G03350.1 | Symbols: | BSD domain-containing protein | chr1:822834-824246 REVERSE LENGTH=470	456	470	1.00E-161	103.1	71.3	81.1
Rsa1.0_00457.1.g14234.t1	ref|NP_171835.1| exosome complex component RRP4 [Arabidopsis thaliana] gi|3850568|gb|AAC72108.1| Similar to hypothetical protein SPAC2F7.14c gi|1052797 from Schizosaccharomyces pombe cosmid gb|Z50142 [Arabidopsis thaliana] gi|34365689|gb|AAQ65156.1| At1g03360 [Arabidopsis thaliana] gi|51970606|dbj|BAD43995.1| hypothetical protein [Arabidopsis thaliana] gi|332189442|gb|AEE27563.1| ribosomal RNA processing protein 4 [Arabidopsis thaliana]	320	322	1.00E-169	100.6	89.7	96.6	exosome complex component RRP4	gbpln	Arabidopsis thaliana	AT1G03360.1 | Symbols: ATRRP4, RRP4 | ribosomal RNA processing 4 | chr1:824653-826179 FORWARD LENGTH=322	320	322	1.00E-172	100.6	89.7	96.6
Rsa1.0_00457.1.g14235.t1	ref|XP_002889457.1| hypothetical protein ARALYDRAFT_333664 [Arabidopsis lyrata subsp. lyrata] gi|297335299|gb|EFH65716.1| hypothetical protein ARALYDRAFT_333664 [Arabidopsis lyrata subsp. lyrata]	961	958	0	99.7	85.4	90.9	hypothetical protein ARALYDRAFT_333664	gbpln	Arabidopsis lyrata	AT1G03380.1 | Symbols: ATATG18G, ATG18G | homolog of yeast autophagy 18 (ATG18) G | chr1:836155-840362 FORWARD LENGTH=959	961	959	0	99.8	84.6	90.8
Rsa1.0_00457.1.g14236.t1	ref|XP_002892159.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338001|gb|EFH68418.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	462	462	0	100.0	88.5	93.9	transferase family protein	gbpln	Arabidopsis lyrata	AT1G03390.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:841033-842418 REVERSE LENGTH=461	462	461	0	99.8	87.2	93.3
Rsa1.0_00457.1.g14237.t1	ref|NP_171840.2| putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana] gi|332310331|sp|Q43383.2|ACCH5_ARATH RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 5 gi|332189448|gb|AEE27569.1| 1-aminocyclopropane-1-carboxylate oxidase homolog 5 [Arabidopsis thaliana]	372	398	1.00E-134	107.0	59.4	74.7	putative 1-aminocyclopropane-1-carboxylate oxidase	gbpln	Arabidopsis thaliana	AT1G03410.1 | Symbols: 2A6 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:844782-846574 REVERSE LENGTH=398	372	398	1.00E-136	107.0	59.4	74.7

<table>
<tr><td>Rsa1.0_00458.1.g14238.t2</td><td>gb|AAZ41811.1| 01P13–1 [Brassica rapa subsp. pekinensis]</td><td>549</td><td>1545</td><td>1.00E–117</td><td>281.4</td><td>47.2</td><td>55.7</td><td>01P13–1</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine–rich RLK (RECEPTOR–like protein kinase) 8 | chr4:12129485–12134086 FORWARD LENGTH=1262</td><td>549</td><td>1262</td><td>6.00E–12</td><td>229.9</td><td>7.5</td><td>11.8</td></tr>
<tr><td>Rsa1.0_00458.1.g14239.t1</td><td>dbj|BAJ33719.1| unnamed protein product [Thellungiella halophila]</td><td>360</td><td>392</td><td>2.33E–156</td><td>108.9</td><td>85.0</td><td>90.8</td><td>unnamed protein product</td><td>––––</td><td>––––</td><td>AT5G44190.1 | Symbols: GLK2, ATGLK2, GPRI2 | GOLDEN2–like 2 | chr5:17798435–17800647 FORWARD LENGTH=386</td><td>360</td><td>386</td><td>1.00E–139</td><td>107.2</td><td>79.7</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00458.1.g14240.t1</td><td>ref|XP_002866574.1| IBR domain–containing protein [Arabidopsis lyrata subsp. lyrata] gi|297312409|gb|EFH42833.1| IBR domain–containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>593</td><td>518</td><td>1.00E–34</td><td>87.4</td><td>17.7</td><td>23.6</td><td>IBR domain–containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63750.1 | Symbols: ATARI13, ARI13 | RING/U–box superfamily protein | chr5:25513038–25514729 REVERSE LENGTH=536</td><td>593</td><td>536</td><td>1.00E–36</td><td>90.4</td><td>17.9</td><td>22.9</td></tr>
<tr><td>Rsa1.0_00458.1.g14241.t1</td><td>gb|AEW23125.1| phytochelatin synthase [Amaranthus tricolor]</td><td>428</td><td>485</td><td>0</td><td>113.3</td><td>90.0</td><td>94.9</td><td>phytochelatin synthase</td><td>gbpln</td><td>Amaranthus tricolor</td><td>AT5G44070.1 | Symbols: CAD1, ARA8, ATPCS1, PCS1 | phytochelatin synthase 1 (PCS1) | chr5:17734876–17737672 FORWARD LENGTH=485</td><td>428</td><td>485</td><td>0</td><td>113.3</td><td>88.8</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00458.1.g14242.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00458.1.g14243.t1</td><td>ref|XP_002865388.1| hypothetical protein ARALYDRAFT_917224 [Arabidopsis lyrata subsp. lyrata] gi|297311223|gb|EFH41647.1| hypothetical protein ARALYDRAFT_917224 [Arabidopsis lyrata subsp. lyrata]</td><td>256</td><td>272</td><td>1.00E–132</td><td>106.3</td><td>89.1</td><td>94.9</td><td>hypothetical protein ARALYDRAFT_917224</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G44020.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr5:17712433–17714046 FORWARD LENGTH=272</td><td>256</td><td>272</td><td>1.00E–132</td><td>106.3</td><td>87.9</td><td>94.5</td></tr>
<tr><td>Rsa1.0_00458.1.g14244.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1321</td><td>1307</td><td>0</td><td>98.9</td><td>57.1</td><td>71.5</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine–rich RLK (RECEPTOR–like protein kinase) 8 | chr4:12129485–12134086 FORWARD LENGTH=1262</td><td>1321</td><td>1262</td><td>2.00E–83</td><td>95.5</td><td>13.2</td><td>20.5</td></tr>
<tr><td>Rsa1.0_00458.1.g14245.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838–20266 [Arabidopsis thaliana]</td><td>1020</td><td>1142</td><td>0</td><td>112.0</td><td>44.2</td><td>59.7</td><td>reverse transcriptase, putative; 16838–20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H–like superfamily protein | chr4:14333528–14335255 FORWARD LENGTH=575</td><td>1020</td><td>575</td><td>1.00E–80</td><td>56.4</td><td>17.2</td><td>28.0</td></tr>
<tr><td>Rsa1.0_00458.1.g14246.t1</td><td>pir||S65812 RNA–directed DNA polymerase (EC 2.7.7.49) (clone DW15) – Arabidopsis thaliana retrotransposon Ta11–1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]</td><td>114</td><td>1333</td><td>2.00E–11</td><td>1169.3</td><td>32.5</td><td>50.9</td><td>RNA–directed DNA polymerase (EC 2.7.7.49) (clone DW15) – Arabidopsis thaliana retrotransposon Ta11–1 gi|976278|gb|AAA75254.1| reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00458.1.g14247.t1</td><td>ref|XP_002865389.1| SET domain protein SUVR2 [Arabidopsis lyrata subsp. lyrata] gi|297311224|gb|EFH41648.1| SET domain protein SUVR2 [Arabidopsis lyrata subsp. lyrata]</td><td>631</td><td>712</td><td>0</td><td>112.8</td><td>71.8</td><td>82.7</td><td>SET domain protein SUVR2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G43990.5 | Symbols: SUVR2 | SET–domain containing protein lysine methyltransferase family protein | chr5:17698523–17701733 FORWARD LENGTH=697</td><td>631</td><td>697</td><td>0</td><td>110.5</td><td>70.2</td><td>81.9</td></tr>
<tr><td>Rsa1.0_00458.1.g14248.t1</td><td>gb|AAD17398.1| putative non–LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>602</td><td>1225</td><td>1.00E–127</td><td>203.5</td><td>40.2</td><td>56.5</td><td>putative non–LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H–like superfamily protein | chr4:14333528–14335255 FORWARD LENGTH=575</td><td>602</td><td>575</td><td>2.00E–81</td><td>95.5</td><td>29.6</td><td>45.7</td></tr>
<tr><td>Rsa1.0_00458.1.g14249.t1</td><td>gb|EOA14888.1| hypothetical protein CARUB_v10028217mg [Capsella rubella]</td><td>99</td><td>99</td><td>5.00E–40</td><td>100.0</td><td>85.9</td><td>93.9</td><td>hypothetical protein CARUB_v10028217mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G43970.1 | Symbols: TOM22–V, TOM9–2, ATTOM22–V | translocase of outer membrane 22–V | chr5:17692888–17693187 FORWARD LENGTH=99</td><td>99</td><td>99</td><td>1.00E–42</td><td>100.0</td><td>87.9</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00458.1.g14250.t1</td><td>gb|EOA14513.1| hypothetical protein CARUB_v10027740mg [Capsella rubella]</td><td>571</td><td>565</td><td>0</td><td>98.9</td><td>82.1</td><td>89.5</td><td>hypothetical protein CARUB_v10027740mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G43950.1 | Symbols: | Plant protein of unknown function (DUF946) | chr5:17686707–17688623 REVERSE LENGTH=566</td><td>571</td><td>566</td><td>0</td><td>99.1</td><td>79.5</td><td>90.0</td></tr>
<tr><td>Rsa1.0_00459.1.g14251.t1</td><td>gb|EOA39562.1| hypothetical protein CARUB_v10008180mg [Capsella rubella]</td><td>58</td><td>1021</td><td>4.00E–11</td><td>1760.3</td><td>77.6</td><td>87.9</td><td>hypothetical protein CARUB_v10008180mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G31280.1 | Symbols: AGO2 | Argonaute family protein | chr1:11181777–11185112 FORWARD LENGTH=1014</td><td>58</td><td>1014</td><td>1.00E–12</td><td>1748.3</td><td>74.1</td><td>86.2</td></tr>
<tr><td>Rsa1.0_00459.1.g14252.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838–20266 [Arabidopsis thaliana]</td><td>198</td><td>1142</td><td>1.00E–30</td><td>576.8</td><td>41.9</td><td>59.1</td><td>reverse transcriptase, putative; 16838–20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00459.1.g14253.t1</td><td>gb|EOA38400.1| hypothetical protein CARUB_v10009967mg [Capsella rubella]</td><td>278</td><td>278</td><td>1.00E–155</td><td>100.0</td><td>95.3</td><td>98.9</td><td>hypothetical protein CARUB_v10009967mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G31300.2 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid–sensing domain containing protein | chr1:11194308–11195955 FORWARD LENGTH=278</td><td>278</td><td>278</td><td>1.00E–157</td><td>100.0</td><td>95.0</td><td>98.9</td></tr>
<tr><td>Rsa1.0_00459.1.g14254.t1</td><td>gb|EOA39311.1| hypothetical protein CARUB_v10012336mg [Capsella rubella]</td><td>387</td><td>403</td><td>1.00E–125</td><td>104.1</td><td>72.4</td><td>80.4</td><td>hypothetical protein CARUB_v10012336mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G31310.1 | Symbols: | hydroxyproline–rich glycoprotein family protein | chr1:11198565–11200025 REVERSE LENGTH=383</td><td>387</td><td>383</td><td>1.00E–124</td><td>99.0</td><td>73.1</td><td>79.6</td></tr>
<tr><td>Rsa1.0_00459.1.g14255.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00459.1.g14256.t1</td><td>emb|CAB52747.1| photosystem I subunit III precursor [Arabidopsis thaliana] gi|21593588|gb|AAM65555.1| photosystem I subunit III precursor, putative [Arabidopsis thaliana]</td><td>221</td><td>221</td><td>1.00E–117</td><td>100.0</td><td>92.8</td><td>96.8</td><td>photosystem I subunit III precursor</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31330.1 | Symbols: PSAF | photosystem I subunit F | chr1:11215011–11215939 REVERSE LENGTH=221</td><td>221</td><td>221</td><td>1.00E–119</td><td>100.0</td><td>92.3</td><td>96.4</td></tr>
</table>

Rsa1.0_00459.1.g14257.t1	gb|EOA37259.1| hypothetical protein CARUB_v10010814mg [Capsella rubella]	72	70	5.00E-21	97.2	83.3	84.7	hypothetical protein CARUB_v10010814mg	gbpln	Capsella rubella	AT1G31335.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; Has 34 Blast hits to 34 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:11217117-11217329 REVERSE LENGTH=70	72	70	2.00E-23	97.2	84.7	86.1
Rsa1.0_00459.1.g14258.t1	ref|NP_564379.2| NEDD8-like protein RUB1 [Arabidopsis thaliana] gi|302393813|sp|Q9SHE7.3|RUB1_ARATH RecName: Full=Ubiquitin-NEDD8-like protein RUB1; Contains: RecName: Full=Ubiquitin; Contains: RecName: Full=NEDD8-like protein RUB1; AltName: Full=Ubiquitin-related protein 1; Short=AtRUB1; Flags: Precursor gi|6692129|gb|AAF24594.1|AC007654_10 T19E23.13 [Arabidopsis thaliana] gi|28973676|gb|AAO64156.1| putative ubiquitin (AtRUB1) [Arabidopsis thaliana] gi|29824269|gb|AAP04095.1| putative ubiquitin (AtRUB1) [Arabidopsis thaliana] gi|110737109|dbj|BAF00506.1| putative ubiquitin [Arabidopsis thaliana] gi|312283039|dbj|BAJ34385.1| unnamed protein product [Thellungiella halophila] gi|332193223|gb|AEE31344.1| NEDD8-like protein RUB1 [Arabidopsis thaliana]	172	156	1.00E-77	90.7	90.1	90.7	NEDD8-like protein RUB1	gbpln	Arabidopsis thaliana	AT1G31340.1 | Symbols: RUB1, NEDD8, ATRUB1 | related to ubiquitin 1 | chr1:11218076-11219417 REVERSE LENGTH=156	172	156	4.00E-80	90.7	90.1	90.7
Rsa1.0_00459.1.g14259.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00459.1.g14260.t1	ref|XP_002891150.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297336992|gb|EFH67409.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	384	385	1.00E-163	100.3	76.8	87.8	F-box family protein	gbpln	Arabidopsis lyrata	AT1G31350.1 | Symbols: KUF1 | KAR-UP F-box 1 | chr1:11221519-11222706 REVERSE LENGTH=395	384	395	1.00E-159	102.9	76.3	87.5
Rsa1.0_00459.1.g14261.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00460.1.g14262.t1	ref|XP_002867362.1| hypothetical protein ARALYDRAFT_491730 [Arabidopsis lyrata subsp. lyrata] gi|297313198|gb|EFH43621.1| hypothetical protein ARALYDRAFT_491730 [Arabidopsis lyrata subsp. lyrata]	358	718	1.00E-144	200.6	76.5	83.8	hypothetical protein ARALYDRAFT_491730	gbpln	Arabidopsis lyrata	AT4G30200.3 | Symbols: VEL1, VIL2 | vernalization5/VIN3-like | chr4:14786852-14790070 REVERSE LENGTH=702	358	702	1.00E-144	196.1	75.7	83.2
Rsa1.0_00460.1.g14263.t1	ref|NP_194751.1| small nuclear ribonucleoprotein F [Arabidopsis thaliana] gi|297798954|ref|XP_002867361.1| hypothetical protein ARALYDRAFT_913456 [Arabidopsis lyrata subsp. lyrata] gi|297836060|ref|XP_002885912.1| hypothetical protein ARALYDRAFT_899645 [Arabidopsis lyrata subsp. lyrata] gi|10720264|sp|Q9SUM2.1|RUXF_ARATH RecName: Full=Probable small nuclear ribonucleoprotein F; Short=snRNP-F; AltName: Full=Sm protein F; Short=Sm-F; Short=SmF gi|5730132|emb|CAB52466.1| snRNP Sm protein F-like [Arabidopsis thaliana] gi|7269922|emb|CAB81015.1| snRNP Sm protein F-like [Arabidopsis thaliana] gi|21593208|gb|AAM65157.1| snRNP Sm protein F-like [Arabidopsis thaliana] gi|30102544|gb|AAP21190.1| At4g30220 [Arabidopsis thaliana] gi|110743810|dbj|BAE99740.1| snRNP Sm protein F - like [Arabidopsis thaliana] gi|297313197|gb|EFH43620.1| hypothetical protein ARALYDRAFT_913456 [Arabidopsis lyrata subsp. lyrata] gi|297331752|gb|EFH62171.1| hypothetical protein ARALYDRAFT_899645 [Arabidopsis lyrata subsp. lyrata]	88	88	2.00E-42	100.0	97.7	98.9	small nuclear ribonucleoprotein F	gbpln	Arabidopsis lyrata	AT4G30220.1 | Symbols: RUXF | small nuclear ribonucleoprotein F | chr4:14803100-14804259 REVERSE LENGTH=88	88	88	3.00E-45	100.0	97.7	98.9
Rsa1.0_00460.1.g14264.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00460.1.g14265.t1	gb|EOA17247.1| hypothetical protein CARUB_v10005521mg [Capsella rubella]	260	263	2.00E-82	101.2	68.1	80.8	hypothetical protein CARUB_v10005521mg	gbpln	Capsella rubella	AT4G30230.1 | Symbols: | unknown protein; Has 42 Blast hits to 42 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14806376-14807158 FORWARD LENGTH=260	260	260	9.00E-83	100.0	69.2	80.0
Rsa1.0_00460.1.g14266.t1	ref|XP_002867359.1| integral membrane Yip1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297313195|gb|EFH43618.1| integral membrane Yip1 family protein [Arabidopsis lyrata subsp. lyrata]	190	283	3.00E-28	148.9	33.7	35.3	integral membrane Yip1 family protein	gbpln	Arabidopsis lyrata	AT4G30260.1 | Symbols: | Integral membrane Yip1 family protein | chr4:14816890-14818722 REVERSE LENGTH=280	190	280	2.00E-30	147.4	33.2	35.3
Rsa1.0_00460.1.g14267.t1	ref|XP_002867358.1| meristem-5 [Arabidopsis lyrata subsp. lyrata] gi|297313194|gb|EFH43617.1| meristem-5 [Arabidopsis lyrata subsp. lyrata]	279	269	1.00E-147	96.4	90.7	93.5	meristem-5	gbpln	Arabidopsis lyrata	AT4G30270.1 | Symbols: MERI5B, MERI-5, XTH24, SEN4 | xyloglucan endotransglucosylase/hydrolase 24 | chr4:14819445-14820448 REVERSE LENGTH=269	279	269	1.00E-147	96.4	88.5	92.8
Rsa1.0_00460.1.g14268.t1	ref|XP_002867357.1| ATXTH18/XTH18 [Arabidopsis lyrata subsp. lyrata] gi|297313193|gb|EFH43616.1| ATXTH18/XTH18 [Arabidopsis lyrata subsp. lyrata]	282	282	1.00E-145	100.0	89.7	94.7	ATXTH18/XTH18	gbpln	Arabidopsis lyrata	AT4G30280.1 | Symbols: ATXTH18, XTH18 | xyloglucan endotransglucosylase/hydrolase 18 | chr4:14825958-14826998 REVERSE LENGTH=282	282	282	1.00E-147	100.0	89.4	94.3
Rsa1.0_00460.1.g14269.t1	ref|NP_199618.1| xyloglucan endotransglucosylase/hydrolase protein 20 [Arabidopsis thaliana] gi|38605469|sp|Q9FI31.1|XTH20_ARATH RecName: Full=Xyloglucan endotransglucosylase/hydrolase protein 20; Short=At-XTH20; Short=XTH-20; Flags: Precursor gi|10177758|dbj|BAB11071.1| xyloglucan endo-1,4-beta-D-glucanase [Arabidopsis thaliana] gi|45825157|gb|AAS77486.1| At5g48070 [Arabidopsis thaliana] gi|62320256|dbj|BAD94531.1| xyloglucan endo-1,4-beta-D-glucanase [Arabidopsis thaliana] gi|332008233|gb|AED95616.1| xyloglucan endotransglucosylase/hydrolase protein 20 [Arabidopsis thaliana]	283	282	1.00E-142	99.6	84.8	90.8	xyloglucan endotransglucosylase/hydrolase protein 20	gbpln	Arabidopsis thaliana	AT5G48070.1 | Symbols: ATXTH20, XTH20 | xyloglucan endotransglucosylase/hydrolase 20 | chr5:19482158-19483231 FORWARD LENGTH=282	283	282	1.00E-144	99.6	84.8	90.8
Rsa1.0_00460.1.g14270.t1	ref|NP_194760.2| FGGY family of carbohydrate kinase [Arabidopsis thaliana] gi|332660351|gb|AEE85751.1| FGGY family of carbohydrate kinase [Arabidopsis thaliana]	573	579	0	101.0	92.5	97.0	FGGY family of carbohydrate kinase	gbpln	Arabidopsis thaliana	AT4G30310.2 | Symbols: | FGGY family of carbohydrate kinase | chr4:14831913-14835092 FORWARD LENGTH=579	573	579	0	101.0	92.5	97.0
Rsa1.0_00460.1.g14271.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00460.1.g14272.t1	gb|EOA18929.1| hypothetical protein CARUB_v10007576mg [Capsella rubella]	167	164	1.00E-74	98.2	82.6	88.0	hypothetical protein CARUB_v10007576mg	gbpln	Capsella rubella	AT4G30320.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:14835833-14836318 FORWARD LENGTH=161	167	161	3.00E-75	96.4	79.6	85.0
Rsa1.0_00460.1.g14273.t1	ref|NP_194764.1| heat shock-related protein [Arabidopsis thaliana] gi|7269935|emb|CAB81028.1| putative protein [Arabidopsis thaliana] gi|332660355|gb|AEE85755.1| heat shock-related protein [Arabidopsis thaliana]	857	924	0	107.8	82.6	89.4	heat shock-related protein	gbpln	Arabidopsis thaliana	AT4G30350.1 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr4:14848031-14850973 FORWARD LENGTH=924	857	924	0	107.8	82.6	89.4
Rsa1.0_00460.1.g14274.t1	gb|EOA19101.1| hypothetical protein CARUB_v10007769mg [Capsella rubella]	663	724	0	109.2	86.0	93.5	hypothetical protein CARUB_v10007769mg	gbpln	Capsella rubella	AT4G30360.1 | Symbols: ATCNGC17, CNGC17 | cyclic nucleotide-gated channel 17 | chr4:14855060-14857779 REVERSE LENGTH=720	663	720	0	108.6	86.0	92.5
Rsa1.0_00460.1.g14275.t1	ref|XP_002867351.1| hypothetical protein ARALYDRAFT_491714 [Arabidopsis lyrata subsp. lyrata] gi|297313187|gb|EFH43610.1| hypothetical protein ARALYDRAFT_491714 [Arabidopsis lyrata subsp. lyrata]	96	95	2.00E-35	99.0	80.2	90.6	hypothetical protein ARALYDRAFT_491714	gbpln	Arabidopsis lyrata	AT4G30390.1 | Symbols: | unknown protein; Has 22 Blast hits to 22 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14862224-14862906 REVERSE LENGTH=95	96	95	9.00E-38	99.0	77.1	88.5
Rsa1.0_00460.1.g14276.t1	ref|NP_567846.1| RING-H2 finger protein ATL13 [Arabidopsis thaliana] gi|68565248|sp|Q940Q4.2|ATL13_ARATH RecName: Full=RING-H2 finger protein ATL13 gi|332660360|gb|AEE85760.1| RING-H2 finger protein ATL13 [Arabidopsis thaliana]	447	472	1.00E-177	105.6	85.2	89.5	RING-H2 finger protein ATL13	gbpln	Arabidopsis thaliana	AT4G30400.1 | Symbols: | RING/U-box superfamily protein | chr4:14867068-14868486 FORWARD LENGTH=472	447	472	1.00E-179	105.6	85.2	89.5

Rsa1.0_00460.1.g14277.t1	ref|NP_194771.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75181441|sp|Q9M0B8.1|WTR37_ARATH RecName: Full=WAT1-related protein At4g30420 gi|7269943|emb|CAB79760.1| nodulin-like protein [Arabidopsis thaliana] gi|332660363|gb|AEE85763.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]	368	373	1.00E-150	101.4	70.7	83.7	nodulin MtN21 /EamA-like transporter family protein	gbpln	Arabidopsis thaliana	AT4G30420.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:14877069-14878914 FORWARD LENGTH=373	368	373	1.00E-153	101.4	70.7	83.7
Rsa1.0_00460.1.g14278.t1	gb|EOA35038.1| hypothetical protein CARUB_v10020144mg, partial [Capsella rubella]	676	521	1.00E-170	77.1	49.9	55.9	hypothetical protein CARUB_v10020144mg, partial	gbpln	Capsella rubella	AT1G66980.1 | Symbols: SNC4 | suppressor of npr1-1 constitutive 4 | chr1:24997491-25001961 REVERSE LENGTH=1118	676	1118	1.00E-137	165.4	35.5	40.7
Rsa1.0_00460.1.g14279.t1	ref|NP_567849.1| putative F-box/LRR-repeat protein 19 [Arabidopsis thaliana] gi|75335738|sp|Q9M096.1|FBL19_ARATH RecName: Full=Putative F-box/LRR-repeat protein 19 gi|7269965|emb|CAB79782.1| putative protein [Arabidopsis thaliana] gi|332660389|gb|AEE85789.1| putative F-box/LRR-repeat protein 19 [Arabidopsis thaliana]	278	301	1.00E-87	108.3	58.3	73.4	putative F-box/LRR-repeat protein 19	gbpln	Arabidopsis thaliana	AT4G30640.1 | Symbols: | RNI-like superfamily protein | chr4:14952670-14953682 FORWARD LENGTH=301	278	301	3.00E-90	108.3	58.3	73.4
Rsa1.0_00460.1.g14280.t1	ref|XP_002869365.1| hypothetical protein ARALYDRAFT_913409 [Arabidopsis lyrata subsp. lyrata] gi|297315201|gb|EFH45624.1| hypothetical protein ARALYDRAFT_913409 [Arabidopsis lyrata subsp. lyrata]	75	74	2.00E-29	98.7	86.7	94.7	hypothetical protein ARALYDRAFT_913409	gbpln	Arabidopsis lyrata	AT4G30660.2 | Symbols: | Low temperature and salt responsive protein family | chr4:14955470-14955944 FORWARD LENGTH=74	75	74	5.00E-31	98.7	82.7	92.0
Rsa1.0_00460.1.g14281.t1	ref|NP_567850.1| Putative membrane lipoprotein [Arabidopsis thaliana] gi|21536573|gb|AAM60905.1| unknown [Arabidopsis thaliana] gi|26449845|dbj|BAC42045.1| unknown protein [Arabidopsis thaliana] gi|51970566|dbj|BAD43975.1| putative protein [Arabidopsis thaliana] gi|89111838|gb|ABD60691.1| At4g30670 [Arabidopsis thaliana] gi|332660394|gb|AEE85794.1| Putative membrane lipoprotein [Arabidopsis thaliana]	104	102	3.00E-15	98.1	69.2	78.8	Putative membrane lipoprotein	gbpln	Arabidopsis thaliana	AT4G30670.1 | Symbols: | Putative membrane lipoprotein | chr4:14957597-14957905 REVERSE LENGTH=102	104	102	4.00E-18	98.1	69.2	78.8
Rsa1.0_00460.1.g14282.t1	gb|EOA16004.1| hypothetical protein CARUB_v10004122mg [Capsella rubella]	169	841	6.00E-71	497.6	80.5	88.8	hypothetical protein CARUB_v10004122mg	gbpln	Capsella rubella	AT4G30680.1 | Symbols: | Initiation factor eIF-4 gamma, MA3 | chr4:14958687-14960012 REVERSE LENGTH=263	169	263	5.00E-71	155.6	76.9	87.0
Rsa1.0_00460.1.g14283.t1	ref|XP_002867334.1| hypothetical protein ARALYDRAFT_353746 [Arabidopsis lyrata subsp. lyrata] gi|297313170|gb|EFH43593.1| hypothetical protein ARALYDRAFT_353746 [Arabidopsis lyrata subsp. lyrata]	748	745	0	99.6	80.6	87.2	hypothetical protein ARALYDRAFT_353746	gbpln	Arabidopsis lyrata	AT2G24050.1 | Symbols: eIFiso4G2 | MIF4G domain-containing protein / MA3 domain-containing protein | chr2:10225500-10228456 REVERSE LENGTH=747	748	747	0	99.9	69.5	80.6
Rsa1.0_00460.1.g14284.t1	ref|NP_567851.1| translation initiation factor IF-3 [Arabidopsis thaliana] gi|14596121|gb|AAK68788.1| putative protein [Arabidopsis thaliana] gi|18377498|gb|AAL66915.1| putative protein [Arabidopsis thaliana] gi|332660396|gb|AEE85796.1| translation initiation factor IF-3 [Arabidopsis thaliana]	284	281	1.00E-118	98.9	87.3	91.2	translation initiation factor IF-3	gbpln	Arabidopsis thaliana	AT4G30690.1 | Symbols: | Translation initiation factor 3 protein | chr4:14960742-14962328 FORWARD LENGTH=281	284	281	1.00E-121	98.9	87.3	91.2
Rsa1.0_00460.1.g14285.t1	gb|EOA18812.1| hypothetical protein CARUB_v10007425mg [Capsella rubella]	633	644	0	101.7	82.0	88.3	hypothetical protein CARUB_v10007425mg	gbpln	Capsella rubella	AT4G30710.1 | Symbols: QWRF8 | Family of unknown function (DUF566) | chr4:14965538-14967881 REVERSE LENGTH=644	633	644	0	101.7	85.2	90.2
Rsa1.0_00461.1.g14286.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00461.1.g14287.t1	gb|ABA42147.1| aintegumenta 2 [Brassica napus]	546	562	0	102.9	88.6	94.0	aintegumenta 2	gbpln	Brassica napus	AT4G37750.1 | Symbols: ANT, DRG, CKC, CKC1 | Integrase-type DNA-binding superfamily protein | chr4:17739782-17742189 FORWARD LENGTH=555	546	555	0	101.6	86.6	91.9
Rsa1.0_00461.1.g14288.t1	ref|XP_002868966.1| hypothetical protein ARALYDRAFT_490840 [Arabidopsis lyrata subsp. lyrata] gi|297314802|gb|EFH45225.1| hypothetical protein ARALYDRAFT_490840 [Arabidopsis lyrata subsp. lyrata]	517	521	0	100.8	91.9	95.6	hypothetical protein ARALYDRAFT_490840	gbpln	Arabidopsis lyrata	AT4G37760.1 | Symbols: SQE3 | squalene epoxidase 3 | chr4:17744085-17746426 FORWARD LENGTH=525	517	525	0	101.5	90.9	94.6

Rsa1.0_00461.1.g14289.t1	ref|XP_002868965.1| 1-amino-cyclopropane-1-carboxylate synthase 8 [Arabidopsis lyrata subsp. lyrata] gi|297314801|gb|EFH45224.1| 1-amino-cyclopropane-1-carboxylate synthase 8 [Arabidopsis lyrata subsp. lyrata]	469	469	0	100.0	93.0	96.6	1-amino-cyclopropane-1-carboxylate synthase 8	gbpln	Arabidopsis lyrata	AT4G37770.1 | Symbols: ACS8 | 1-amino-cyclopropane-1-carboxylate synthase 8 | chr4:17752222-17753925 FORWARD LENGTH=469	469	469	0	100.0	91.9	95.9
Rsa1.0_00461.1.g14290.t1	ref|NP_195492.2| myb domain protein 87 [Arabidopsis thaliana] gi|332661437|gb|AEE86837.1| myb domain protein 87 [Arabidopsis thaliana]	310	305	1.00E-121	98.4	72.9	83.9	myb domain protein 87	gbpln	Arabidopsis thaliana	AT4G37780.1 | Symbols: MYB87, ATMYB87 | myb domain protein 87 | chr4:17758404-17759526 REVERSE LENGTH=305	310	305	1.00E-124	98.4	72.9	83.9
Rsa1.0_00461.1.g14291.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00461.1.g14292.t1	ref|XP_002868963.1| homeobox-leucine zipper protein 22 [Arabidopsis lyrata subsp. lyrata] gi|297314799|gb|EFH45222.1| homeobox-leucine zipper protein 22 [Arabidopsis lyrata subsp. lyrata]	282	283	1.00E-124	100.4	90.1	92.9	homeobox-leucine zipper protein 22	gbpln	Arabidopsis lyrata	AT4G37790.1 | Symbols: HAT22 | Homeobox-leucine zipper protein family | chr4:17768241-17769272 FORWARD LENGTH=278	282	278	1.00E-126	98.6	88.7	91.5
Rsa1.0_00461.1.g14293.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00461.1.g14294.t1	dbj|BAD22536.1| gamma-glutamyl transferase [Raphanus sativus]	90	635	5.00E-20	705.6	53.3	63.3	gamma-glutamyl transferase	gbpln	Raphanus sativus	AT4G29210.1 | Symbols: GGT3, GGT4 | gamma-glutamyl transpeptidase 4 | chr4:14400990-14403319 FORWARD LENGTH=637	90	637	6.00E-16	707.8	48.9	57.8
Rsa1.0_00461.1.g14295.t1	gb|EOA17720.1| hypothetical protein CARUB_v10006101mg [Capsella rubella]	102	102	2.00E-44	100.0	85.3	90.2	hypothetical protein CARUB_v10006101mg	gbpln	Capsella rubella	AT4G37830.1 | Symbols: | cytochrome c oxidase-related | chr4:17787672-17788762 REVERSE LENGTH=102	102	102	2.00E-44	100.0	80.4	86.3
Rsa1.0_00461.1.g14296.t1	ref|NP_194638.1| Ribonuclease H-like protein [Arabidopsis thaliana] gi|4972055|emb|CAB43923.1| putative protein [Arabidopsis thaliana] gi|7269807|emb|CAB79667.1| putative protein [Arabidopsis thaliana] gi|67633766|gb|AAY78807.1| putative reverse transcriptase/RNA-dependent DNA polymerase [Arabidopsis thaliana] gi|332660185|gb|AEE85585.1| Ribonuclease H-like protein [Arabidopsis thaliana]	136	575	6.00E-23	422.8	39.7	59.6	Ribonuclease H-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	136	575	2.00E-25	422.8	39.7	59.6
Rsa1.0_00461.1.g14297.t1	ref|NP_195497.1| hexokinase [Arabidopsis thaliana] gi|11386888|sp|Q9T071.1|HXKL2_ARATH RecName: Full=Probable hexokinase-like 2 protein gi|4490729|emb|CAB38932.1| hexokinase-like protein [Arabidopsis thaliana] gi|7270767|emb|CAB80449.1| hexokinase-like protein [Arabidopsis thaliana] gi|332661444|gb|AEE86844.1| hexokinase-like 3 [Arabidopsis thaliana]	490	493	0	100.6	82.7	88.4	hexokinase	gbpln	Arabidopsis thaliana	AT4G37840.1 | Symbols: HKL3 | hexokinase-like 3 | chr4:17790147-17792198 REVERSE LENGTH=493	490	493	0	100.6	82.7	88.4
Rsa1.0_00462.1.g14298.t1	gb|EOA38356.1| hypothetical protein CARUB_v10009876mg [Capsella rubella]	296	299	1.00E-152	101.0	90.5	94.6	hypothetical protein CARUB_v10009876mg	gbpln	Capsella rubella	AT1G33800.1 | Symbols: | Protein of unknown function (DUF579) | chr1:12261480-12262456 FORWARD LENGTH=297	296	297	1.00E-147	100.3	88.2	93.2
Rsa1.0_00462.1.g14299.t5	gb|AAD14459.1| hypothetical protein [Arabidopsis thaliana] gi|7270201|emb|CAB77816.1| hypothetical protein [Arabidopsis thaliana]	312	562	2.00E-43	180.1	33.3	44.6	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00462.1.g14300.t2	gb|ABD65089.1| zinc knuckle containing protein [Brassica oleracea]	198	333	4.00E-15	168.2	20.7	23.7	zinc knuckle containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00462.1.g14301.t1	gb|ABD65089.1| zinc knuckle containing protein [Brassica oleracea]	301	333	4.00E-33	110.6	30.6	31.9	zinc knuckle containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00462.1.g14302.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00462.1.g14303.t1	ref|XP_002891064.1| hypothetical protein ARALYDRAFT_336448 [Arabidopsis lyrata subsp. lyrata] gi|297336906|gb|EFH67323.1| hypothetical protein ARALYDRAFT_336448 [Arabidopsis lyrata subsp. lyrata]	136	139	5.00E-63	102.2	93.4	96.3	hypothetical protein ARALYDRAFT_336448	gbpln	Arabidopsis lyrata	AT1G33810.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast, chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 39 Blast hits to 39 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12265084-12266655 FORWARD LENGTH=138	136	138	2.00E-65	101.5	92.6	97.1

<table>
<tr><td>Rsa1.0_00462.1.g14304.t3</td><td>dbj|BAJ34639.1| unnamed protein product [Thellungiella halophila]</td><td>338</td><td>343</td><td>1.00E-172</td><td>101.5</td><td>92.0</td><td>96.7</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G33970.5 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:12349614-12350960 REVERSE LENGTH=342</td><td>338</td><td>342</td><td>1.00E-155</td><td>101.2</td><td>82.5</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00462.1.g14305.t1</td><td>gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>1514</td><td>2726</td><td>0</td><td>180.1</td><td>51.5</td><td>68.6</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158</td><td>1514</td><td>158</td><td>4.00E-34</td><td>10.4</td><td>4.4</td><td>5.8</td></tr>
<tr><td>Rsa1.0_00462.1.g14306.t5</td><td>ref|XP_002891069.1| ATUPF3/UPF3 [Arabidopsis lyrata subsp. lyrata] gi|297336911|gb|EFH67328.1| ATUPF3/UPF3 [Arabidopsis lyrata subsp. lyrata]</td><td>532</td><td>486</td><td>0</td><td>91.4</td><td>67.7</td><td>75.0</td><td>ATUPF3/UPF3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G33980.1 | Symbols: ATUPF3, UPF3 | Smg-4/UPF3 family protein | chr1:12351719-12354401 FORWARD LENGTH=482</td><td>532</td><td>482</td><td>0</td><td>90.6</td><td>66.9</td><td>74.8</td></tr>
<tr><td>Rsa1.0_00462.1.g14307.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00463.1.g14308.t1</td><td>gb|EOA15630.1| hypothetical protein CARUB_v10005867mg [Capsella rubella]</td><td>175</td><td>176</td><td>2.00E-64</td><td>100.6</td><td>82.3</td><td>87.4</td><td>hypothetical protein CARUB_v10005867mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G16750.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:9421121-9421660 REVERSE LENGTH=179</td><td>175</td><td>179</td><td>9.00E-65</td><td>102.3</td><td>80.0</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00463.1.g14309.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00463.1.g14310.t1</td><td>ref|XP_002890956.1| GHMP kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336798|gb|EFH67215.1| GHMP kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>494</td><td>505</td><td>0</td><td>102.2</td><td>87.9</td><td>91.5</td><td>GHMP kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G31910.1 | Symbols: | GHMP kinase family protein | chr1:11459050-11461649 FORWARD LENGTH=505</td><td>494</td><td>505</td><td>0</td><td>102.2</td><td>87.7</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00463.1.g14311.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00463.1.g14312.t3</td><td>ref|NP_198442.2| AMP-dependent synthetase and ligase family protein [Arabidopsis thaliana] gi|378548266|sp|F4K1G2.1|AEE19_ARATH RecName: Full=Putative acyl-activating enzyme 19 gi|332006646|gb|AED94029.1| putative acyl-activating enzyme 19 [Arabidopsis thaliana]</td><td>989</td><td>1040</td><td>0</td><td>105.2</td><td>80.6</td><td>86.9</td><td>AMP-dependent synthetase and ligase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G35930.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr5:14067197-14074404 REVERSE LENGTH=1040</td><td>989</td><td>1040</td><td>0</td><td>105.2</td><td>80.6</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00463.1.g14313.t1</td><td>ref|XP_002870449.1| glucose-6-phosphate dehydrogenase 1 [Arabidopsis lyrata subsp. lyrata] gi|297316285|gb|EFH46708.1| glucose-6-phosphate dehydrogenase 1 [Arabidopsis lyrata subsp. lyrata]</td><td>576</td><td>578</td><td>0</td><td>100.3</td><td>91.3</td><td>95.0</td><td>glucose-6-phosphate dehydrogenase 1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G35790.1 | Symbols: G6PD1 | glucose-6-phosphate dehydrogenase 1 | chr5:13956879-13959686 REVERSE LENGTH=576</td><td>576</td><td>576</td><td>0</td><td>100.0</td><td>90.5</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00463.1.g14314.t7</td><td>gb|ABD65073.1| hypothetical protein 27.t00059 [Brassica oleracea]</td><td>175</td><td>341</td><td>6.00E-22</td><td>194.9</td><td>40.0</td><td>54.3</td><td>hypothetical protein 27.t00059</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00463.1.g14315.t2</td><td>ref|NP_198420.1| fimbrin-like protein 2 [Arabidopsis thaliana] gi|59797968|sp|Q9FKI0.1|FIMB2_ARATH RecName: Full=Fimbrin-like protein 2 gi|9758643|dbj|BAB09267.1| fimbrin [Arabidopsis thaliana] gi|15027847|gb|AAK76454.1| putative fimbrin protein [Arabidopsis thaliana] gi|23296651|gb|AAN13139.1| putative fimbrin protein [Arabidopsis thaliana] gi|332006624|gb|AED94007.1| fimbrin-like protein 2 [Arabidopsis thaliana]</td><td>199</td><td>687</td><td>2.00E-88</td><td>345.2</td><td>84.9</td><td>89.4</td><td>fimbrin-like protein 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G35700.1 | Symbols: FIM2, FIM5 | fimbrin-like protein 2 | chr5:13872833-13876432 REVERSE LENGTH=687</td><td>199</td><td>687</td><td>6.00E-91</td><td>345.2</td><td>84.9</td><td>89.4</td></tr>
<tr><td>Rsa1.0_00463.1.g14316.t1</td><td>ref|XP_002868430.1| hypothetical protein ARALYDRAFT_493625 [Arabidopsis lyrata subsp. lyrata] gi|297314266|gb|EFH44689.1| hypothetical protein ARALYDRAFT_493625 [Arabidopsis lyrata subsp. lyrata]</td><td>416</td><td>445</td><td>1.00E-163</td><td>107.0</td><td>77.4</td><td>87.5</td><td>hypothetical protein ARALYDRAFT_493625</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G35670.1 | Symbols: iqd33 | IQ-domain 33 | chr5:13856170-13857910 FORWARD LENGTH=442</td><td>416</td><td>442</td><td>1.00E-155</td><td>106.3</td><td>75.2</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00463.1.g14317.t1</td><td>gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1435</td><td>1496</td><td>0</td><td>104.3</td><td>58.6</td><td>72.1</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1435</td><td>1262</td><td>1.00E-136</td><td>87.9</td><td>18.0</td><td>25.9</td></tr>
<tr><td>Rsa1.0_00463.1.g14318.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT5G35660.1 | Symbols: | Glycine-rich protein family | chr5:13852609-13853717 REVERSE LENGTH=343</td><td>266</td><td>343</td><td>1.00E-12</td><td>128.9</td><td>16.9</td><td>20.3</td></tr>
<tr><td>Rsa1.0_00463.1.g14319.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00463.1.g14320.t5</td><td>gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>559</td><td>1225</td><td>1.00E-101</td><td>219.1</td><td>34.2</td><td>49.9</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>559</td><td>575</td><td>7.00E-33</td><td>102.9</td><td>18.1</td><td>30.1</td></tr>
<tr><td>Rsa1.0_00463.1.g14321.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00463.1.g14322.t1</td><td>gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>605</td><td>1225</td><td>1.00E-15</td><td>202.5</td><td>10.7</td><td>15.4</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00463.1.g14323.t1	sp|Q42624.1|GLNAC_BRANA RecName: Full=Glutamine synthetase, chloroplastic; AltName: Full=GS2; AltName: Full=Glutamate--ammonia ligase; Flags: Precursor gi|296223|emb|CAA51280.1| glutamate--ammonia ligase precursor [Brassica napus]	465	428	0	92.0	90.1	91.4	RecName: Full=Glutamine synthetase, chloroplastic; AltName: Full=GS2; AltName: Full=Glutamate--ammonia ligase; Flags: Precursor gi|296223|emb|CAA51280.1| glutamate--ammonia ligase precursor	gbpln	Brassica napus	AT5G35630.3 | Symbols: GS2, GLN2, ATGSL1 | glutamine synthetase 2 | chr5:13831220-13833239 FORWARD LENGTH=430	465	430	0	92.5	84.7	89.7
Rsa1.0_00463.1.g14324.t1	gb|AAF79675.1|AC022314_16 F9C16.30 [Arabidopsis thaliana]	180	1001	7.00E-69	556.1	69.4	79.4	F9C16.30	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00463.1.g14325.t1	gb|ADK94611.1| translation initiation factor eIF(iso)4E.c [Brassica rapa]	180	200	3.00E-88	111.1	90.0	92.2	translation initiation factor eIF(iso)4E.c	gbpln	Brassica rapa	AT5G35620.2 | Symbols: LSP1, EIF(ISO)4E, LSP, EIF4E2, eIFiso4E | Eukaryotic initiation factor 4E protein | chr5:13825570-13826331 REVERSE LENGTH=167	180	167	3.00E-74	92.8	76.7	84.4
Rsa1.0_00463.1.g14326.t6	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00463.1.g14327.t1	gb|ABI13034.1| transparent testa 2 family isoform 1 [Brassica napus] gi|112142579|gb|ABI13038.1| transparent testa 2 family isoform 1 [Brassica napus]	258	260	1.00E-132	100.8	89.5	93.8	transparent testa 2 family isoform 1	gbpln	Brassica napus	AT5G35550.1 | Symbols: TT2, ATMYB123, MYB123, ATTT2 | Duplicated homeodomain-like superfamily protein | chr5:13726807-13727729 FORWARD LENGTH=258	258	258	1.00E-98	100.0	73.6	82.6
Rsa1.0_00464.1.g14328.t1	gb|EOA17264.1| hypothetical protein CARUB_v10005538mg [Capsella rubella]	256	258	1.00E-101	100.8	79.7	87.1	hypothetical protein CARUB_v10005538mg	gbpln	Capsella rubella	AT4G35040.1 | Symbols: bZIP19 | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:16680821-16681805 FORWARD LENGTH=261	256	261	1.00E-100	102.0	76.2	84.8
Rsa1.0_00464.1.g14329.t1	ref|NP_001190918.1| protein kinase-like protein [Arabidopsis thaliana] gi|332661053|gb|AEE86453.1| protein kinase-like protein [Arabidopsis thaliana]	489	448	0	91.6	77.1	83.6	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT4G35030.3 | Symbols: | Protein kinase superfamily protein | chr4:16676234-16677962 FORWARD LENGTH=448	489	448	0	91.6	77.1	83.6
Rsa1.0_00464.1.g14330.t2	ref|NP_195228.1| Rac-like GTP-binding protein ARAC3 [Arabidopsis thaliana] gi|334187165|ref|NP_001190916.1| Rac-like GTP-binding protein ARAC3 [Arabidopsis thaliana] gi|334187167|ref|NP_001190917.1| Rac-like GTP-binding protein ARAC3 [Arabidopsis thaliana] gi|297802458|ref|XP_002869113.1| hypothetical protein ARALYDRAFT_491155 [Arabidopsis lyrata subsp. lyrata] gi|2500192|sp|Q38912.1|RAC3_ARATH RecName: Full=Rac-like GTP-binding protein ARAC3; AltName: Full=GTPase protein ROP6; Flags: Precursor gi|7211200|gb|AAF40242.1|AF115470_1 Arac3 [Arabidopsis thaliana] gi|1304413|gb|AAC49853.1| Rac-like protein [Arabidopsis thaliana] gi|2645643|gb|AAC78241.1| Rho-like GTP binding protein [Arabidopsis thaliana] gi|2924513|emb|CAA17767.1| Rho1Ps homolog/ Rac-like protein [Arabidopsis thaliana] gi|7270453|emb|CAB80219.1| Rho1Ps homolog/ Rac-like protein [Arabidopsis thaliana] gi|56381909|gb|AAV85673.1| At4g35020 [Arabidopsis thaliana] gi|58652102|gb|AAW80876.1| At4g35020 [Arabidopsis thaliana] gi|297314949|gb|EFH45372.1| hypothetical protein ARALYDRAFT_491155 [Arabidopsis	212	198	1.00E-78	93.4	81.6	82.1	Rac-like GTP-binding protein ARAC3	gbpln	Arabidopsis lyrata	AT4G35020.3 | Symbols: RAC3 | RAC-like 3 | chr4:16673176-16674540 FORWARD LENGTH=198	212	198	3.00E-81	93.4	81.6	82.1
Rsa1.0_00464.1.g14331.t1	ref|NP_567973.1| beta-galactosidase 11 [Arabidopsis thaliana] gi|75202765|sp|Q9SCV1.1|BGL11_ARATH RecName: Full=Beta-galactosidase 11; Short=Lactase 11; Flags: Precursor gi|6686894|emb|CAB64747.1| putative beta-galactosidase [Arabidopsis thaliana] gi|332661046|gb|AEE86446.1| beta-galactosidase 11 [Arabidopsis thaliana]	845	845	0	100.0	89.7	94.8	beta-galactosidase 11	gbpln	Arabidopsis thaliana	AT4G35010.1 | Symbols: BGAL11 | beta-galactosidase 11 | chr4:16668075-16671974 REVERSE LENGTH=845	845	845	0	100.0	89.7	94.8
Rsa1.0_00464.1.g14332.t1	ref|XP_002867097.1| AtMYB32 [Arabidopsis lyrata subsp. lyrata] gi|297312933|gb|EFH43356.1| AtMYB32 [Arabidopsis lyrata subsp. lyrata]	285	278	1.00E-117	97.5	79.6	84.9	AtMYB32	gbpln	Arabidopsis lyrata	AT4G34990.1 | Symbols: AtMYB32, MYB32 | myb domain protein 32 | chr4:16661370-16662289 REVERSE LENGTH=274	285	274	1.00E-117	96.1	78.9	84.6

Rsa1.0_00464.1.g14333.t1	ref|XP_002327946.1| predicted protein [Populus trichocarpa] gi|118487306|gb|ABK95481.1| unknown [Populus trichocarpa] gi|222837355|gb|EEE75734.1| predicted protein [Populus trichocarpa]	89	363	3.00E−34	407.9	80.9	85.4	predicted protein	gbpln	Populus trichocarpa	AT1G48210.2 | Symbols: | Protein kinase superfamily protein | chr1:17799551−17801798 FORWARD LENGTH=363	89	363	2.00E−32	407.9	73.0	82.0
Rsa1.0_00464.1.g14334.t3	ref|XP_002869114.1| actin binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314950|gb|EFH45373.1| actin binding protein [Arabidopsis lyrata subsp. lyrata]	142	141	9.00E−71	99.3	89.4	96.5	actin binding protein	gbpln	Arabidopsis lyrata	AT4G34970.1 | Symbols: ADF9 | actin depolymerizing factor 9 | chr4:16653784−16654593 FORWARD LENGTH=141	142	141	5.00E−73	99.3	88.7	96.5
Rsa1.0_00464.1.g14335.t1	ref|NP_195222.1| Cyclophilin−like peptidyl−prolyl cis−trans isomerase family protein [Arabidopsis thaliana] gi|2924507|emb|CAA17761.1| cyclophilin−like protein [Arabidopsis thaliana] gi|7270447|emb|CAB80213.1| cyclophilin−like protein [Arabidopsis thaliana] gi|26450419|dbj|BAC42324.1| putative cyclophilin like protein ROC14 [Arabidopsis thaliana] gi|28827322|gb|AAO50505.1| putative cyclophilin [Arabidopsis thaliana] gi|45680864|gb|AAS75301.1| single domain cyclophilin type peptidyl−prolyl cis−trans isomerase [Arabidopsis thaliana] gi|332661041|gb|AEE86441.1| Cyclophilin−like peptidyl−prolyl cis−trans isomerase family protein [Arabidopsis thaliana]	224	224	1.00E−113	100.0	95.1	98.7	Cyclophilin−like peptidyl−prolyl cis−trans isomerase family protein	gbpln	Arabidopsis thaliana	AT4G34960.1 | Symbols: | Cyclophilin−like peptidyl−prolyl cis−trans isomerase family protein | chr4:16648865−16650646 FORWARD LENGTH=224	224	224	1.00E−116	100.0	95.1	98.7
Rsa1.0_00464.1.g14336.t1	ref|XP_002867099.1| nodulin family protein [Arabidopsis lyrata subsp. lyrata] gi|297312935|gb|EFH43358.1| nodulin family protein [Arabidopsis lyrata subsp. lyrata]	585	567	0	96.9	70.8	77.1	nodulin family protein	gbpln	Arabidopsis lyrata	AT4G34950.1 | Symbols: | Major facilitator superfamily protein | chr4:16642544−16644759 REVERSE LENGTH=567	585	567	0	96.9	70.4	76.8
Rsa1.0_00464.1.g14337.t1	gb|EOA19138.1| hypothetical protein CARUB_v10007809mg [Capsella rubella]	659	668	0	101.4	93.5	97.1	hypothetical protein CARUB_v10007809mg	gbpln	Capsella rubella	AT4G34940.1 | Symbols: ARO1 | armadillo repeat only 1 | chr4:16639760−16641754 FORWARD LENGTH=664	659	664	0	100.8	93.5	96.8
Rsa1.0_00464.1.g14338.t1	gb|EOA16221.1| hypothetical protein CARUB_v10004361mg [Capsella rubella]	626	633	0	101.1	84.5	90.7	hypothetical protein CARUB_v10004361mg	gbpln	Capsella rubella	AT4G34910.1 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:16631661−16634834 FORWARD LENGTH=626	626	626	0	100.0	83.1	89.3
Rsa1.0_00464.1.g14339.t1	ref|XP_002869119.1| ATXDH1 [Arabidopsis lyrata subsp. lyrata] gi|297314955|gb|EFH45378.1| ATXDH1 [Arabidopsis lyrata subsp. lyrata]	1358	1361	0	100.2	92.4	96.8	ATXDH1	gbpln	Arabidopsis lyrata	AT4G34890.1 | Symbols: ATXDH1, XDH1 | xanthine dehydrogenase 1 | chr4:16618736−16624983 REVERSE LENGTH=1361	1358	1361	0	100.2	92.3	96.8
Rsa1.0_00464.1.g14340.t1	gb|EOA16479.1| hypothetical protein CARUB_v10004638mg [Capsella rubella]	470	500	0	106.4	73.8	82.1	hypothetical protein CARUB_v10004638mg	gbpln	Capsella rubella	AT4G34880.1 | Symbols: | Amidase family protein | chr4:16615549−16617424 FORWARD LENGTH=466	470	466	1.00E−161	99.1	64.3	74.3
Rsa1.0_00464.1.g14341.t1	gb|EOA18997.1| hypothetical protein CARUB_v10007642mg [Capsella rubella]	172	172	2.00E−84	100.0	85.5	93.6	hypothetical protein CARUB_v10007642mg	gbpln	Capsella rubella	AT4G34870.1 | Symbols: ROC5, ATCYP1 | rotamase cyclophilin 5 | chr4:16614451−16614969 FORWARD LENGTH=172	172	172	5.00E−84	100.0	83.1	92.4
Rsa1.0_00464.1.g14342.t1	gb|EOA16316.1| hypothetical protein CARUB_v10004468mg [Capsella rubella]	570	571	0	100.2	94.9	98.4	hypothetical protein CARUB_v10004468mg	gbpln	Capsella rubella	AT4G34860.2 | Symbols: | Plant neutral invertase family protein | chr4:16609955−16612019 REVERSE LENGTH=571	570	571	0	100.2	95.3	97.5
Rsa1.0_00464.1.g14343.t1	gb|ADF43047.1| chalcone synthase 6 protein [Brassica rapa subsp. rapa]	235	392	1.00E−67	166.8	52.8	54.0	chalcone synthase 6 protein	gbpln	Brassica rapa	AT4G34850.1 | Symbols: LAP5 | Chalcone and stilbene synthase family protein | chr4:16608349−16609720 FORWARD LENGTH=392	235	392	1.00E−69	166.8	51.9	54.5
Rsa1.0_00464.1.g14344.t1	gb|EOA19012.1| hypothetical protein CARUB_v10007663mg [Capsella rubella]	1106	1122	0	101.4	82.4	88.7	hypothetical protein CARUB_v10007663mg	gbpln	Capsella rubella	AT4G34830.1 | Symbols: MRL1 | Pentatricopeptide repeat (PPR) superfamily protein | chr4:16599976−16605994 REVERSE LENGTH=1089	1106	1089	0	98.5	81.7	89.0
Rsa1.0_00464.1.g14345.t1	ref|NP_195207.1| SAUR−like auxin−responsive protein [Arabidopsis thaliana] gi|5123698|emb|CAB45442.1| putative protein [Arabidopsis thaliana] gi|7270432|emb|CAB80198.1| putative protein [Arabidopsis thaliana] gi|332661025|gb|AEE86425.1| SAUR−like auxin−responsive protein [Arabidopsis thaliana]	107	105	5.00E−46	98.1	89.7	95.3	SAUR−like auxin−responsive protein	gbpln	Arabidopsis thaliana	AT4G34810.1 | Symbols: | SAUR−like auxin−responsive protein family | chr4:16599104−16599421 FORWARD LENGTH=105	107	105	8.00E−49	98.1	89.7	95.3
Rsa1.0_00464.1.g14346.t1	ref|XP_002869125.1| auxin−responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297314961|gb|EFH45384.1| auxin−responsive family protein [Arabidopsis lyrata subsp. lyrata]	94	94	1.00E−46	100.0	97.9	97.9	auxin−responsive family protein	gbpln	Arabidopsis lyrata	AT4G34800.1 | Symbols: | SAUR−like auxin−responsive protein family | chr4:16596860−16597144 FORWARD LENGTH=94	94	94	7.00E−49	100.0	96.8	97.9

Rsa1.0_00464.1.g14347.t1	ref|XP_002869126.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297314962|gb|EFH45385.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	105	106	1.00E-42	101.0	86.7	92.4	auxin-responsive family protein	gbpln	Arabidopsis lyrata	AT4G34790.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:16594539-16594865 FORWARD LENGTH=108	105	108	1.00E-44	102.9	84.8	91.4
Rsa1.0_00465.1.g14348.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1927	1274	0	66.1	34.8	45.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1927	575	1.00E-78	29.8	9.6	15.1
Rsa1.0_00465.1.g14349.t1	ref|NP_196049.1| kow domain-containing transcription factor 1 [Arabidopsis thaliana] gi|332003341|gb|AED90724.1| kow domain-containing transcription factor 1 [Arabidopsis thaliana]	1594	1493	0	93.7	64.2	72.3	kow domain-containing transcription factor 1	gbpln	Arabidopsis thaliana	AT5G04290.1 | Symbols: KTF1, SPT5L | kow domain-containing transcription factor 1 | chr5:1196069-1202653 FORWARD LENGTH=1493	1594	1493	0	93.7	64.2	72.3
Rsa1.0_00465.1.g14350.t1	ref|NP_196051.2| pectate lyase family protein [Arabidopsis thaliana] gi|332003342|gb|AED90725.1| pectate lyase family protein [Arabidopsis thaliana]	504	518	0	102.8	87.3	92.3	pectate lyase family protein	gbpln	Arabidopsis thaliana	AT5G04310.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:1203356-1207352 REVERSE LENGTH=518	504	518	0	102.8	87.3	92.3
Rsa1.0_00465.1.g14351.t13	ref|XP_002871086.1| hypothetical protein ARALYDRAFT_487213 [Arabidopsis lyrata subsp. lyrata] gi|297316923|gb|EFH47345.1| hypothetical protein ARALYDRAFT_487213 [Arabidopsis lyrata subsp. lyrata]	745	413	2.00E-85	55.4	25.4	29.7	hypothetical protein ARALYDRAFT_487213	gbpln	Arabidopsis lyrata	AT5G04320.2 | Symbols: | Shugoshin C terminus | chr5:1209613-1212376 FORWARD LENGTH=470	745	470	3.00E-87	63.1	28.1	34.0
Rsa1.0_00465.1.g14352.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00465.1.g14353.t1	ref|NP_196053.2| ferulate-5-hydroxylase [Arabidopsis thaliana] gi|332003345|gb|AED90728.1| cytochrome P450 84A4 [Arabidopsis thaliana]	513	512	0	99.8	86.0	92.2	ferulate-5-hydroxylase	gbpln	Arabidopsis thaliana	AT5G04330.1 | Symbols: | Cytochrome P450 superfamily protein | chr5:1212695-1214310 REVERSE LENGTH=512	513	512	0	99.8	86.0	92.2
Rsa1.0_00465.1.g14354.t1	gb|ABI74691.1| C2H2 zinc finger protein [Brassica carinata]	242	239	5.00E-96	98.8	87.2	90.1	C2H2 zinc finger protein	gbpln	Brassica carinata	AT5G04340.1 | Symbols: C2H2, CZF2, ZAT6 | zinc finger of Arabidopsis thaliana 6 | chr5:1216321-1217037 REVERSE LENGTH=238	242	238	6.00E-83	98.3	80.6	86.4
Rsa1.0_00465.1.g14355.t1	ref|NP_196055.1| self-incompatibility S1 family protein [Arabidopsis thaliana] gi|332003348|gb|AED90731.1| self-incompatibility S1 family protein [Arabidopsis thaliana]	124	146	7.00E-38	117.7	64.5	80.6	self-incompatibility S1 family protein	gbpln	Arabidopsis thaliana	AT5G04350.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:1220829-1221269 FORWARD LENGTH=146	124	146	1.00E-40	117.7	64.5	80.6
Rsa1.0_00465.1.g14356.t1	gb|EOA22765.1| hypothetical protein CARUB_v10003478mg [Capsella rubella]	111	144	4.00E-21	129.7	47.7	64.0	hypothetical protein CARUB_v10003478mg	gbpln	Capsella rubella	AT5G04350.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:1220829-1221269 FORWARD LENGTH=146	111	146	3.00E-23	131.5	48.6	68.5
Rsa1.0_00465.1.g14357.t1	ref|XP_002871089.1| hypothetical protein ARALYDRAFT_487216 [Arabidopsis lyrata subsp. lyrata] gi|297316926|gb|EFH47348.1| hypothetical protein ARALYDRAFT_487216 [Arabidopsis lyrata subsp. lyrata]	1030	964	0	93.6	80.4	86.0	hypothetical protein ARALYDRAFT_487216	gbpln	Arabidopsis lyrata	AT5G04360.1 | Symbols: ATPU1, ATLDA, PU1, LDA | limit dextrinase | chr5:1221566-1228399 FORWARD LENGTH=965	1030	965	0	93.7	80.0	85.3
Rsa1.0_00465.1.g14358.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00465.1.g14359.t1	ref|NP_196058.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|332003352|gb|AED90735.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	389	385	1.00E-168	99.0	75.3	83.5	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G04380.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:1234883-1236317 FORWARD LENGTH=385	389	385	1.00E-170	99.0	75.3	83.5
Rsa1.0_00465.1.g14360.t1	ref|NP_196058.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|332003352|gb|AED90735.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	319	385	2.33E-156	120.7	79.0	88.1	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G04380.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:1234883-1236317 FORWARD LENGTH=385	319	385	1.00E-149	120.7	79.0	88.1
Rsa1.0_00466.1.g14361.t1	gb|EOA16761.1| hypothetical protein CARUB_v10004974mg [Capsella rubella]	89	398	5.00E-32	447.2	75.3	77.5	hypothetical protein CARUB_v10004974mg	gbpln	Capsella rubella	AT5G40610.1 | Symbols: | NAD-dependent glycerol-3-phosphate dehydrogenase family protein | chr5:16265071-16267258 REVERSE LENGTH=400	89	400	5.00E-34	449.4	74.2	76.4

Rsa1.0_00466.1.g14362.t1	ref|XP_002882916.1| cup-shaped cotyledon1 [Arabidopsis lyrata subsp. lyrata] gi|297328756|gb|EFH59175.1| cup-shaped cotyledon1 [Arabidopsis lyrata subsp. lyrata]	315	310	1.00E-124	98.4	82.2	87.0	cup-shaped cotyledon1	gbpln	Arabidopsis lyrata	AT3G15170.1 | Symbols: CUC1, ANAC054, ATNAC1 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr3:5109912-5111435 FORWARD LENGTH=310	315	310	1.00E-119	98.4	80.3	85.7
Rsa1.0_00466.1.g14363.t10	ref|NP_188134.2| uncharacterized protein [Arabidopsis thaliana] gi|23297454|gb|AAN12973.1| unknown protein [Arabidopsis thaliana] gi|332642105|gb|AEE75626.1| uncharacterized protein AT3G15160 [Arabidopsis thaliana]	386	562	1.00E-46	145.6	30.1	32.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15160.1 | Symbols: | unknown protein; Has 266 Blast hits to 264 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 58; Fungi - 0; Plants - 199; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr3:5104582-5108279 FORWARD LENGTH=562	386	562	2.00E-49	145.6	30.1	32.9
Rsa1.0_00466.1.g14364.t1	ref|XP_002885069.1| hypothetical protein ARALYDRAFT_478943 [Arabidopsis lyrata subsp. lyrata] gi|297330909|gb|EFH61328.1| hypothetical protein ARALYDRAFT_478943 [Arabidopsis lyrata subsp. lyrata]	393	334	1.00E-113	85.0	61.8	66.4	hypothetical protein ARALYDRAFT_478943	gbpln	Arabidopsis lyrata	AT3G15115.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53180.1); Has 47 Blast hits to 47 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 13; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr3:5086219-5087352 REVERSE LENGTH=339	393	339	1.00E-114	86.3	59.0	64.9
Rsa1.0_00466.1.g14365.t1	gb|EOA32270.1| hypothetical protein CARUB_v10015530mg [Capsella rubella]	531	682	1.00E-179	128.4	74.6	81.5	hypothetical protein CARUB_v10015530mg	gbpln	Capsella rubella	AT3G15095.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 9762 Blast hits to 6439 proteins in 764 species: Archae - 77; Bacteria - 1339; Metazoa - 3211; Fungi - 718; Plants - 437; Viruses - 131; Other Eukaryotes - 3849 (source: NCBI BLink). | chr3:5081996-5084050 FORWARD LENGTH=684	531	684	1.00E-152	128.8	68.9	77.8
Rsa1.0_00466.1.g14366.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00466.1.g14367.t1	gb|EOA30402.1| hypothetical protein CARUB_v10013526mg [Capsella rubella]	140	497	9.00E-20	355.0	51.4	59.3	hypothetical protein CARUB_v10013526mg	gbpln	Capsella rubella	AT3G15070.2 | Symbols: | RING/U-box superfamily protein | chr3:5070472-5072344 REVERSE LENGTH=486	140	486	1.00E-20	347.1	41.4	47.1
Rsa1.0_00466.1.g14368.t1	ref|NP_188124.1| RAB GTPase-like protein A1G [Arabidopsis thaliana] gi|75273740|sp|Q9LK99.1|RAA1G_ARATH RecName: Full=Ras-related protein RABA1g; Short=AtRABA1g gi|8777489|dbj|BAA97069.1| GTP-binding protein-like [Arabidopsis thaliana] gi|26452472|dbj|BAC43321.1| putative ras-related GTP-binding protein [Arabidopsis thaliana] gi|28973321|gb|AAO63985.1| putative Ras family GTP-binding protein [Arabidopsis thaliana] gi|332642090|gb|AEE75611.1| RAB GTPase-like protein A1G [Arabidopsis thaliana]	61	217	1.00E-16	355.7	78.7	90.2	RAB GTPase-like protein A1G	gbpln	Arabidopsis thaliana	AT3G15060.1 | Symbols: AtRABA1g, RABA1g | RAB GTPase homolog A1G | chr3:5069239-5070025 FORWARD LENGTH=217	61	217	2.00E-19	355.7	78.7	90.2
Rsa1.0_00466.1.g14369.t1	ref|NP_179179.1| Plastocyanin-like domain-containing protein [Arabidopsis thaliana] gi|5306254|gb|AAD41987.1| hypothetical protein [Arabidopsis thaliana] gi|20145855|emb|CAD29618.1| auxin response factor 30 [Arabidopsis thaliana] gi|330251342|gb|AEC06436.1| Plastocyanin-like domain-containing protein [Arabidopsis thaliana]	307	301	2.00E-25	98.0	18.9	25.7	Plastocyanin-like domain-containing protein	gbpln	Arabidopsis thaliana	AT2G15770.1 | Symbols: | Cupredoxin superfamily protein | chr2:6871257-6872245 REVERSE LENGTH=301	307	301	4.00E-28	98.0	18.9	25.7
Rsa1.0_00466.1.g14370.t1	gb|EOA31422.1| hypothetical protein CARUB_v10014602mg [Capsella rubella]	221	217	1.00E-112	98.2	90.0	95.0	hypothetical protein CARUB_v10014602mg	gbpln	Capsella rubella	AT3G15060.1 | Symbols: AtRABA1g, RABA1g | RAB GTPase homolog A1G | chr3:5069239-5070025 FORWARD LENGTH=217	221	217	1.00E-114	98.2	89.6	95.0
Rsa1.0_00466.1.g14371.t2	ref|XP_002885066.1| IQ-domain 10 [Arabidopsis lyrata subsp. lyrata] gi|297330906|gb|EFH61325.1| IQ-domain 10 [Arabidopsis lyrata subsp. lyrata]	265	259	1.00E-121	97.7	81.9	88.7	IQ-domain 10	gbpln	Arabidopsis lyrata	AT3G15050.1 | Symbols: IQD10 | IQ-domain 10 | chr3:5066879-5067892 REVERSE LENGTH=259	265	259	1.00E-122	97.7	81.1	88.3
Rsa1.0_00466.1.g14372.t1	gb|EOA31321.1| hypothetical protein CARUB_v10014502mg [Capsella rubella] gi|482567133|gb|EOA31322.1| hypothetical protein CARUB_v10014502mg [Capsella rubella]	234	242	7.00E-77	103.4	81.6	88.0	hypothetical protein CARUB_v10014502mg	gbpln	Capsella rubella	AT3G15040.1 | Symbols: | Protein of unknown function, DUF584 | chr3:5065445-5066176 REVERSE LENGTH=243	234	243	5.00E-72	103.8	77.4	84.6
Rsa1.0_00466.1.g14373.t1	gb|EOA30715.1| hypothetical protein CARUB_v10013851mg [Capsella rubella]	362	406	1.00E-127	112.2	77.9	84.5	hypothetical protein CARUB_v10013851mg	gbpln	Capsella rubella	AT3G15030.3 | Symbols: TCP4 | TCP family transcription factor 4 | chr3:5062308-5063570 FORWARD LENGTH=420	362	420	1.00E-122	116.0	76.2	82.6

Rsa1.0_00466.1.g14374.t2	ref|XP_002869260.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315096|gb|EFH45519.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	172	1550	4.00E-29	901.2	41.3	45.3	nucleic acid binding protein	gbpln	Arabidopsis lyrata	AT4G32620.2 | Symbols: | Enhancer of polycomb-like transcription factor protein | chr4:15731968-15737222 FORWARD LENGTH=1540	172	1540	7.00E-31	895.3	40.1	45.9
Rsa1.0_00466.1.g14375.t1	ref|XP_003518855.1| PREDICTED: uncharacterized protein LOC100803580 [Glycine max]	312	177	6.00E-21	56.7	17.0	24.4	PREDICTED: uncharacterized protein LOC100803580	gbenv/gbpln	Glycine max	AT2G15780.1 | Symbols: | Cupredoxin superfamily protein | chr2:6873666-6874701 REVERSE LENGTH=257	312	257	1.00E-21	82.4	15.7	23.1
Rsa1.0_00466.1.g14376.t1	ref|XP_002882907.1| hypothetical protein ARALYDRAFT_478926 [Arabidopsis lyrata subsp. lyrata] gi|297328747|gb|EFH59166.1| hypothetical protein ARALYDRAFT_478926 [Arabidopsis lyrata subsp. lyrata]	375	396	1.00E-119	105.6	72.0	76.3	hypothetical protein ARALYDRAFT_478926	gbpln	Arabidopsis lyrata	AT3G15000.1 | Symbols: | cobalt ion binding | chr3:5050321-5052121 FORWARD LENGTH=395	375	395	1.00E-109	105.3	68.5	72.8
Rsa1.0_00466.1.g14377.t2	sp|F4IXE4.2|TTL2_ARATH RecName: Full=TPR repeat-containing thioredoxin TTL2; AltName: Full=Tetratricopeptide repeat thioredoxin-like 2	785	730	0	93.0	60.4	70.3	RecName: Full=TPR repeat-containing thioredoxin TTL2; AltName: Full=Tetratricopeptide repeat thioredoxin-like 2	----	----	AT3G14950.1 | Symbols: TTL2 | tetratricopetide-repeat thioredoxin-like 2 | chr3:5030216-5032892 REVERSE LENGTH=721	785	721	0	91.8	59.6	69.4
Rsa1.0_00466.1.g14378.t1	gb|EOA29805.1| hypothetical protein CARUB_v10012899mg [Capsella rubella]	196	968	2.00E-74	493.9	77.0	81.1	hypothetical protein CARUB_v10012899mg	gbpln	Capsella rubella	AT3G14940.1 | Symbols: ATPPC3, PPC3 | phosphoenolpyruvate carboxylase 3 | chr3:5025584-5029476 FORWARD LENGTH=968	196	968	9.00E-77	493.9	77.0	80.6
Rsa1.0_00466.1.g14379.t1	ref|NP_188110.1| Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein [Arabidopsis thaliana] gi|8777475|dbj|BAA97055.1| unnamed protein product [Arabidopsis thaliana] gi|332642067|gb|AEE75588.1| Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein [Arabidopsis thaliana]	604	609	0	100.8	80.0	87.4	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein	gbpln	Arabidopsis thaliana	AT3G14920.1 | Symbols: | Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein | chr3:5018275-5020104 FORWARD LENGTH=609	604	609	0	100.8	80.0	87.4
Rsa1.0_00466.1.g14380.t1	ref|XP_004244285.1| PREDICTED: uncharacterized protein LOC101246450 [Solanum lycopersicum]	86	479	9.00E-11	557.0	33.7	44.2	PREDICTED: uncharacterized protein LOC101246450	gbpln	Solanum lycopersicum	AT3G14860.2 | Symbols: | NHL domain-containing protein | chr3:4998591-5000894 REVERSE LENGTH=493	86	493	8.00E-13	573.3	34.9	38.4
Rsa1.0_00466.1.g14381.t1	ref|XP_002882897.1| hypothetical protein ARALYDRAFT_478900 [Arabidopsis lyrata subsp. lyrata] gi|297328737|gb|EFH59156.1| hypothetical protein ARALYDRAFT_478900 [Arabidopsis lyrata subsp. lyrata]	351	350	1.00E-178	99.7	87.5	92.3	hypothetical protein ARALYDRAFT_478900	gbpln	Arabidopsis lyrata	AT3G14850.2 | Symbols: TBL41 | TRICHOME BIREFRINGENCE-LIKE 41 | chr3:4995615-4997611 FORWARD LENGTH=356	351	356	1.00E-171	101.4	84.0	91.7
Rsa1.0_00466.1.g14382.t1	ref|NP_188102.5| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|313471762|sp|C0LGN2.1|Y3148_ARATH RecName: Full=Probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840; Flags: Precursor gi|224589567|gb|ACN59317.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332642053|gb|AEE75574.1| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana]	1021	1020	0	99.9	77.5	87.3	Leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT3G14840.2 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr3:4988271-4993891 FORWARD LENGTH=1020	1021	1020	0	99.9	77.5	87.3
Rsa1.0_00466.1.g14383.t1	ref|XP_002882894.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328734|gb|EFH59153.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	311	311	1.00E-150	100.0	81.4	90.4	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT3G14820.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:4978726-4980241 FORWARD LENGTH=351	311	351	1.00E-151	112.9	79.1	90.7
Rsa1.0_00466.1.g14384.t1	gb|EOA30039.1| hypothetical protein CARUB_v10013145mg [Capsella rubella] gi|482565851|gb|EOA30040.1| hypothetical protein CARUB_v10013145mg [Capsella rubella]	673	667	0	99.1	87.1	92.0	hypothetical protein CARUB_v10013145mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	673	696	1.00E-107	103.4	33.0	51.4
Rsa1.0_00467.1.g14385.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00467.1.g14386.t3	gb|AAL66955.1| putative UV-damaged DNA binding factor [Arabidopsis thaliana]	385	270	3.00E-89	70.1	46.0	48.6	putative UV-damaged DNA binding factor	gbpln	Arabidopsis thaliana	AT4G05420.2 | Symbols: DDB1A | damaged DNA binding protein 1A | chr4:2746288-2752663 FORWARD LENGTH=1067	385	1067	9.00E-91	277.1	46.0	48.6
Rsa1.0_00467.1.g14387.t5	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	698	1529	1.00E-122	219.1	38.5	54.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	698	626	1.00E-43	89.7	18.1	27.9

Rsa1.0_00467.1.g14388.t1	gb|AAV92081.1| xyloglucan endotransglycosylase/hydrolase [Brassica rapa subsp. oleifera]	290	281	1.00E-163	96.9	93.8	96.2	xyloglucan endotransglycosylase/ hydrolase	gbpln	Brassica rapa	AT4G03210.1 | Symbols: XTH9 | xyloglucan endotransglucosylase/hydrolase 9 | chr4:1416019-1417197 FORWARD LENGTH=290	290	290	1.00E-160	100.0	90.3	96.6
Rsa1.0_00467.1.g14389.t1	ref|NP_192233.2| frataxin [Arabidopsis thaliana] gi|83302740|sp|Q9ZR07.2|FRDA_ARATH RecName: Full=Frataxin, mitochondrial; Short=Fxn; Flags: Precursor gi|48958525|gb|AAT47815.1| At4g03240 [Arabidopsis thaliana] gi|51860727|gb|AAU11485.1| mitochondrial frataxin-like [Arabidopsis thaliana] gi|51971038|dbj|BAD44211.1| putative frataxin-like protein [Arabidopsis thaliana] gi|51971859|dbj|BAD44594.1| putative frataxin-like protein [Arabidopsis thaliana] gi|332656896|gb|AEE82296.1| frataxin [Arabidopsis thaliana]	187	187	1.00E-70	100.0	80.7	87.2	frataxin	gbpln	Arabidopsis thaliana	AT4G03240.1 | Symbols: ATFH, FH | frataxin homolog | chr4:1423685-1424758 REVERSE LENGTH=187	187	187	4.00E-73	100.0	80.7	87.2
Rsa1.0_00467.1.g14390.t1	ref|XP_002874872.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297320709|gb|EFH51131.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	619	680	0	109.9	81.7	89.7	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT4G03260.2 | Symbols: | Outer arm dynein light chain 1 protein | chr4:1429092-1431431 FORWARD LENGTH=677	619	677	0	109.4	81.1	88.7
Rsa1.0_00467.1.g14391.t3	dbj|BAJ34429.1| unnamed protein product [Thellungiella halophila]	213	271	1.00E-28	127.2	31.5	32.4	unnamed protein product	----	----	AT1G74840.1 | Symbols: | Homeodomain-like superfamily protein | chr1:28116201-28117317 REVERSE LENGTH=265	213	265	4.00E-25	124.4	27.7	31.0
Rsa1.0_00467.1.g14392.t1	ref|NP_850841.1| AAA-type ATPase family protein [Arabidopsis thaliana] gi|9759053|dbj|BAB09575.1| AAA-type ATPase-like protein [Arabidopsis thaliana] gi|332005081|gb|AED92464.1| AAA-type ATPase family protein [Arabidopsis thaliana]	182	505	2.00E-29	277.5	40.1	56.6	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT5G17760.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:5860591-5862301 REVERSE LENGTH=505	182	505	8.00E-32	277.5	40.1	56.6
Rsa1.0_00467.1.g14393.t1	dbj|BAJ34370.1| unnamed protein product [Thellungiella halophila]	233	229	1.00E-115	98.3	91.8	95.3	unnamed protein product	----	----	AT4G03280.1 | Symbols: PETC, PGR1 | photosynthetic electron transfer C | chr4:1440314-1441717 FORWARD LENGTH=229	233	229	1.00E-109	98.3	89.3	95.3
Rsa1.0_00467.1.g14394.t1	gb|EOA19331.1| hypothetical protein CARUB_v10003659mg [Capsella rubella]	150	154	1.00E-71	102.7	91.3	96.0	hypothetical protein CARUB_v10003659mg	gbpln	Capsella rubella	AT4G03290.1 | Symbols: | EF hand calcium-binding protein family | chr4:1442813-1443277 FORWARD LENGTH=154	150	154	9.00E-67	102.7	90.7	95.3
Rsa1.0_00467.1.g14395.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00467.1.g14396.t7	ref|NP_192243.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|4262162|gb|AAD14462.1| putative glycosylation enzyme [Arabidopsis thaliana] gi|7270204|emb|CAB77819.1| putative glycosylation enzyme [Arabidopsis thaliana] gi|110741957|dbj|BAE98919.1| putative glycosylation enzyme [Arabidopsis thaliana] gi|332656908|gb|AEE82308.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]	810	448	0	55.3	46.8	49.1	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	gbpln	Arabidopsis thaliana	AT4G03340.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:1467865-1469465 REVERSE LENGTH=448	810	448	0	55.3	46.8	49.1
Rsa1.0_00467.1.g14397.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00467.1.g14398.t1	ref|NP_188381.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75274267|sp|Q9LUP4.1|FBK60_ARATH RecName: Full=Putative F-box/kelch-repeat protein At3g17540 gi|9294141|dbj|BAB02043.1| unnamed protein product [Arabidopsis thaliana] gi|332642445|gb|AEE75966.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	375	396	1.00E-103	105.6	56.0	70.9	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G17540.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6002783-6003973 FORWARD LENGTH=396	375	396	1.00E-106	105.6	56.0	70.9
Rsa1.0_00467.1.g14399.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00467.1.g14400.t2	gb|ADM21174.1| SRF3 [Arabidopsis thaliana]	802	776	0	96.8	76.9	84.2	SRF3	gbpln	Arabidopsis thaliana	AT4G03390.1 | Symbols: SRF3 | STRUBBELIG-receptor family 3 | chr4:1490912-1494553 REVERSE LENGTH=776	802	776	0	96.8	76.9	83.9

Rsa1.0_00467.1.g14401.t1	ref|XP_002874865.1| hypothetical protein ARALYDRAFT_490222 [Arabidopsis lyrata subsp. lyrata] gi|297320702|gb|EFH51124.1| hypothetical protein ARALYDRAFT_490222 [Arabidopsis lyrata subsp. lyrata]	316	341	1.00E-150	107.9	81.3	89.6	hypothetical protein ARALYDRAFT_490222	gbpln	Arabidopsis lyrata	AT4G03410.2 | Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr4:1501907-1503503 FORWARD LENGTH=361	316	361	1.00E-152	114.2	81.6	88.3
Rsa1.0_00467.1.g14402.t1	gb|EOA21158.1| hypothetical protein CARUB_v10001504mg [Capsella rubella]	313	314	1.00E-164	100.3	93.9	97.8	hypothetical protein CARUB_v10001504mg	gbpln	Capsella rubella	AT4G03420.1 | Symbols: | Protein of unknown function (DUF789) | chr4:1512226-1513594 FORWARD LENGTH=310	313	310	1.00E-163	99.0	93.0	96.2
Rsa1.0_00467.1.g14403.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	220	1231	7.00E-47	559.5	43.6	60.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	220	292	9.00E-20	132.7	26.4	43.6
Rsa1.0_00467.1.g14404.t1	gb|EOA12837.1| hypothetical protein CARUB_v10025803mg [Capsella rubella]	388	1021	0	263.1	80.4	89.4	hypothetical protein CARUB_v10025803mg	gbpln	Capsella rubella	AT4G03430.1 | Symbols: STA1, EMB2770 | pre-mRNA splicing factor-related | chr4:1517411-1520500 REVERSE LENGTH=1029	388	1029	0	265.2	79.4	89.4
Rsa1.0_00468.1.g14405.t1	gb|EOA30546.1| hypothetical protein CARUB_v10013666mg [Capsella rubella]	455	457	0	100.4	91.9	95.4	hypothetical protein CARUB_v10013666mg	gbpln	Capsella rubella	AT3G22990.1 | Symbols: LFR | ARM repeat superfamily protein | chr3:8164015-8166145 FORWARD LENGTH=460	455	460	0	101.1	92.1	96.0
Rsa1.0_00468.1.g14406.t1	gb|EOA29789.1| hypothetical protein CARUB_v10012884mg [Capsella rubella]	1011	1015	0	100.4	91.7	96.9	hypothetical protein CARUB_v10012884mg	gbpln	Capsella rubella	AT3G22980.1 | Symbols: | Ribosomal protein S5/Elongation factor G/III/V family protein | chr3:8160269-8163316 REVERSE LENGTH=1015	1011	1015	0	100.4	92.0	96.5
Rsa1.0_00468.1.g14407.t1	ref|NP_190938.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75174107|sp|Q9LFF1.1|PP281_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g53700, chloroplastic; AltName: Full=Protein MATERNAL EFFECT EMBRYO ARREST 40; Flags: Precursor gi|6729521|emb|CAB67677.1| putative protein [Arabidopsis thaliana] gi|15982931|gb|AAL09812.1| AT3g53700/F4P12_400 [Arabidopsis thaliana] gi|332645608|gb|AEE79129.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	167	754	7.00E-40	451.5	53.3	58.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G53700.1 | Symbols: MEE40 | Pentatricopeptide repeat (PPR) superfamily protein | chr3:19900303-19902567 FORWARD LENGTH=754	167	754	3.00E-42	451.5	53.3	58.7
Rsa1.0_00468.1.g14408.t1	ref|XP_002879135.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297324974|gb|EFH55394.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	175	223	4.00E-26	127.4	41.7	44.6	nucleic acid binding protein	gbpln	Arabidopsis lyrata	AT2G27790.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:11847335-11849285 REVERSE LENGTH=240	175	240	2.00E-24	137.1	38.3	42.9
Rsa1.0_00468.1.g14409.t1	gb|EOA32294.1| hypothetical protein CARUB_v10015556mg [Capsella rubella]	252	182	2.00E-13	72.2	20.2	29.8	hypothetical protein CARUB_v10015556mg	gbpln	Capsella rubella	AT3G22961.1 | Symbols: | Paired amphipathic helix (PAH2) superfamily protein | chr3:8142138-8142809 FORWARD LENGTH=223	252	223	2.00E-12	88.5	25.4	34.5
Rsa1.0_00468.1.g14410.t1	dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	139	1098	1.00E-28	789.9	44.6	54.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00468.1.g14411.t1	ref|NP_001118679.1| uncharacterized protein [Arabidopsis thaliana] gi|11994728|dbj|BAB03044.1| unnamed protein product [Arabidopsis thaliana] gi|332643177|gb|AEE76698.1| uncharacterized protein AT3G22961 [Arabidopsis thaliana]	338	223	7.00E-33	66.0	29.0	39.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G22961.1 | Symbols: | Paired amphipathic helix (PAH2) superfamily protein | chr3:8142138-8142809 FORWARD LENGTH=223	338	223	2.00E-35	66.0	29.0	39.1
Rsa1.0_00468.1.g14412.t1	ref|XP_002279593.1| PREDICTED: putative calcium-transporting ATPase 13, plasma membrane-type-like [Vitis vinifera]	111	1011	9.00E-47	910.8	75.7	88.3	PREDICTED: putative calcium-transporting ATPase 13, plasma membrane-type-like	gbpln	Vitis vinifera	AT3G22910.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr3:8116335-8119388 REVERSE LENGTH=1017	111	1017	1.00E-46	916.2	86.5	93.7
Rsa1.0_00468.1.g14413.t1	gb|ABY59052.1| chloroplast ATP sulfurylase 1 precursor [Brassica oleracea]	466	459	0	98.5	95.9	97.4	chloroplast ATP sulfurylase 1 precursor	gbpln	Brassica oleracea	AT3G22890.1 | Symbols: APS1 | ATP sulfurylase 1 | chr3:8112837-8114734 FORWARD LENGTH=463	466	463	0	99.4	91.4	95.3
Rsa1.0_00468.1.g14414.t1	ref|XP_002885060.1| hypothetical protein ARALYDRAFT_478918 [Arabidopsis lyrata subsp. lyrata] gi|297330900|gb|EFH61319.1| hypothetical protein ARALYDRAFT_478918 [Arabidopsis lyrata subsp. lyrata]	238	715	4.00E-19	300.4	22.7	26.1	hypothetical protein ARALYDRAFT_478918	gbpln	Arabidopsis lyrata	AT3G14950.1 | Symbols: TTL2 | tetratricopetide-repeat thioredoxin-like 2 | chr3:5030216-5032892 REVERSE LENGTH=721	238	721	6.00E-20	302.9	21.4	25.2
Rsa1.0_00468.1.g14415.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	288	1274	1.00E-66	442.4	49.7	62.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	288	303	9.00E-45	105.2	40.3	55.2

Rsa1.0_00468.1.g14416.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00468.1.g14417.t1	ref|NP_001185158.1| F-box associated ubiquitination effector family protein [Arabidopsis thaliana] gi|332194011|gb|AEE32132.1| F-box associated ubiquitination effector family protein [Arabidopsis thaliana]		198	220	2.00E-23	111.1	33.3	46.0	F-box associated ubiquitination effector family protein	gbpln	Arabidopsis thaliana	AT1G46912.2 | Symbols: | F-box associated ubiquitination effector family protein | chr1:17272521-17273629 FORWARD LENGTH=220	198	220	6.00E-26	111.1	33.3	46.0
Rsa1.0_00468.1.g14418.t1	ref|NP_188924.3| emp24/gp25L/p24 family/GOLD domain-containing protein [Arabidopsis thaliana] gi|75273406|sp|Q9LIL4.1|P24B3_ARATH RecName: Full=Transmembrane emp24 domain-containing protein p24beta3; AltName: Full=p24 family protein beta2; Short=p24beta2; AltName: Full=p24 family protein beta3; Short=p24beta3; Flags: Precursor gi|11994713|dbj|BAB03029.1| coated vesicle membrane protein-like [Arabidopsis thaliana] gi|17979492|gb|AAL50082.1| AT3g22845/MWI23_22 [Arabidopsis thaliana] gi|20147305|gb|AAM10366.1| AT3g22845/MWI23_22 [Arabidopsis thaliana] gi|332643162|gb|AEE76683.1| emp24/gp25L/p24 family/GOLD domain-containing protein [Arabidopsis thaliana]		219	214	1.00E-117	97.7	93.6	96.3	emp24/gp25L/p24 family/GOLD domain-containing protein	gbpln	Arabidopsis thaliana	AT3G22845.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr3:8087373-8088550 FORWARD LENGTH=214	219	214	1.00E-119	97.7	93.6	96.3
Rsa1.0_00469.1.g14419.t1	gb|EOA27506.1| hypothetical protein CARUB_v10023644mg [Capsella rubella]		307	322	1.00E-119	104.9	75.9	83.4	hypothetical protein CARUB_v10023644mg	gbpln	Capsella rubella	AT2G42380.2 | Symbols: ATBZIP34, BZIP34 | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:17647205-17648660 REVERSE LENGTH=321	307	321	1.00E-116	104.6	74.9	82.7
Rsa1.0_00469.1.g14420.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00469.1.g14421.t1	gb|EOA27998.1| hypothetical protein CARUB_v10024176mg [Capsella rubella]		181	173	8.00E-58	95.6	66.3	77.9	hypothetical protein CARUB_v10024176mg	gbpln	Capsella rubella	AT3G58100.1 | Symbols: PDCB5 | plasmodesmata callose-binding protein 5 | chr3:21515397-21516329 REVERSE LENGTH=180	181	180	4.00E-45	99.4	51.9	62.4
Rsa1.0_00469.1.g14422.t1	ref|XP_002879982.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297325821|gb|EFH56241.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]		237	236	2.00E-96	99.6	75.5	82.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G42360.1 | Symbols: | RING/U-box superfamily protein | chr2:17640907-17641617 FORWARD LENGTH=236	237	236	1.00E-97	99.6	75.5	83.1
Rsa1.0_00469.1.g14423.t1	ref|XP_002879981.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297325820|gb|EFH56240.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]		216	217	7.00E-87	100.5	75.0	85.2	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G42350.1 | Symbols: | RING/U-box superfamily protein | chr2:17639245-17639898 FORWARD LENGTH=217	216	217	3.00E-79	100.5	73.6	83.8
Rsa1.0_00469.1.g14424.t1	ref|XP_002881837.1| hypothetical protein ARALYDRAFT_903588 [Arabidopsis lyrata subsp. lyrata] gi|297327676|gb|EFH58096.1| hypothetical protein ARALYDRAFT_903588 [Arabidopsis lyrata subsp. lyrata]		356	345	1.00E-140	96.9	72.2	81.7	hypothetical protein ARALYDRAFT_903588	gbpln	Arabidopsis lyrata	AT2G42550.1 | Symbols: | Protein kinase superfamily protein | chr2:17713196-17714230 FORWARD LENGTH=344	356	344	1.00E-100	96.6	55.9	68.8
Rsa1.0_00469.1.g14425.t1	gb|EOA35866.1| hypothetical protein CARUB_v10021107mg [Capsella rubella]		147	148	2.00E-61	100.7	78.9	83.0	hypothetical protein CARUB_v10021107mg	gbpln	Capsella rubella	AT1G75350.1 | Symbols: emb2184 | Ribosomal protein L31 | chr1:28272163-28272687 FORWARD LENGTH=144	147	144	4.00E-61	98.0	74.1	82.3
Rsa1.0_00469.1.g14426.t1	ref|XP_002879979.1| hypothetical protein ARALYDRAFT_483324 [Arabidopsis lyrata subsp. lyrata] gi|297325818|gb|EFH56238.1| hypothetical protein ARALYDRAFT_483324 [Arabidopsis lyrata subsp. lyrata]		601	662	0	110.1	80.2	88.4	hypothetical protein ARALYDRAFT_483324	gbpln	Arabidopsis lyrata	AT2G42320.2 | Symbols: | nucleolar protein gar2-related | chr2:17628102-17630657 FORWARD LENGTH=669	601	669	0	111.3	80.2	88.7

Rsa1.0_00469.1.g14427.t1	ref|NP_181760.1| uncharacterized protein [Arabidopsis thaliana] gi|297824191|ref|XP_002879978.1| hypothetical protein ARALYDRAFT_903579 [Arabidopsis lyrata subsp. lyrata] gi|4567303|gb|AAD23714.1| unknown protein [Arabidopsis thaliana] gi|18176258|gb|AAL60012.1| unknown protein [Arabidopsis thaliana] gi|20465315|gb|AAM20061.1| unknown protein [Arabidopsis thaliana] gi|297325817|gb|EFH56237.1| hypothetical protein ARALYDRAFT_903579 [Arabidopsis lyrata subsp. lyrata] gi|330255010|gb|AEC10104.1| uncharacterized protein AT2G42310 [Arabidopsis thaliana]	117	114	8.00E-54	97.4	91.5	93.2	uncharacterized protein	gbpln	Arabidopsis lyrata	AT2G42310.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G57785.1); Has 115 Blast hits to 115 proteins in 48 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 44; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17625251-17625595 FORWARD LENGTH=114	117	114	1.00E-56	97.4	91.5	93.2
Rsa1.0_00469.1.g14428.t3	ref|XP_002881830.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297327669|gb|EFH58089.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	326	359	1.00E-121	110.1	81.3	85.9	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT2G42280.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:17611428-17613163 REVERSE LENGTH=359	326	359	1.00E-122	110.1	80.4	85.6
Rsa1.0_00469.1.g14429.t1	ref|NP_181755.1| uv-b-insensitive 4 [Arabidopsis thaliana] gi|2673916|gb|AAB88650.1| hypothetical protein [Arabidopsis thaliana] gi|28950705|gb|AAO63276.1| At2g42260 [Arabidopsis thaliana] gi|110735686|dbj|BAE99823.1| hypothetical protein [Arabidopsis thaliana] gi|330255003|gb|AEC10097.1| uv-b-insensitive 4 [Arabidopsis thaliana]	235	259	5.00E-88	110.2	81.3	89.4	uv-b-insensitive 4	gbpln	Arabidopsis thaliana	AT2G42260.1 | Symbols: UVI4, PYM | uv-b-insensitive 4 | chr2:17602240-17603283 REVERSE LENGTH=259	235	259	1.00E-90	110.2	81.3	89.4
Rsa1.0_00469.1.g14430.t1	ref|NP_973669.1| C-CAP/cofactor C-like domain-containing protein [Arabidopsis thaliana] gi|51536484|gb|AAU05480.1| At2g42230 [Arabidopsis thaliana] gi|53850497|gb|AAU95425.1| At2g42230 [Arabidopsis thaliana] gi|110740775|dbj|BAE98485.1| hypothetical protein [Arabidopsis thaliana] gi|330254997|gb|AEC10091.1| C-CAP/cofactor C-like domain-containing protein [Arabidopsis thaliana]	638	568	0	89.0	74.9	80.6	C-CAP/cofactor C-like domain-containing protein	gbpln	Arabidopsis thaliana	AT2G42230.2 | Symbols: | C-CAP/cofactor C-like domain-containing protein | chr2:17593705-17596563 REVERSE LENGTH=568	638	568	0	89.0	74.9	80.6
Rsa1.0_00469.1.g14431.t1	ref|NP_001031527.1| Tim17 domain-containing protein [Arabidopsis thaliana] gi|330254993|gb|AEC10087.1| outer envelope pore protein 16-3 [Arabidopsis thaliana]	160	173	8.00E-80	108.1	91.9	97.5	Tim17 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G42210.2 | Symbols: ATOEP16-3, OEP16-3 | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr2:17590600-17591591 FORWARD LENGTH=173	160	173	3.00E-82	108.1	91.9	97.5
Rsa1.0_00469.1.g14432.t1	dbj|BAJ34624.1| unnamed protein product [Thellungiella halophila]	368	372	1.00E-168	101.1	88.0	93.2	unnamed protein product	----	----	AT2G42200.1 | Symbols: SPL9, AtSPL9 | squamosa promoter binding protein-like 9 | chr2:17587601-17589451 FORWARD LENGTH=375	368	375	1.00E-159	101.9	87.5	92.1
Rsa1.0_00469.1.g14433.t1	gb|EOA28102.1| hypothetical protein CARUB_v10024288mg [Capsella rubella] gi|482563913|gb|EOA28103.1| hypothetical protein CARUB_v10024288mg [Capsella rubella]	141	138	4.00E-39	97.9	74.5	85.8	hypothetical protein CARUB_v10024288mg	gbpln	Capsella rubella	AT2G42190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G57930.2); Has 1381 Blast hits to 1230 proteins in 175 species: Archae - 3; Bacteria - 25; Metazoa - 672; Fungi - 135; Plants - 127; Viruses - 30; Other Eukaryotes - 389 (source: NCBI BLink). | chr2:17583625-17584050 FORWARD LENGTH=141	141	141	4.00E-38	100.0	75.9	86.5
Rsa1.0_00469.1.g14434.t1	ref|XP_002881826.1| hypothetical protein ARALYDRAFT_483306 [Arabidopsis lyrata subsp. lyrata] gi|297327665|gb|EFH58085.1| hypothetical protein ARALYDRAFT_483306 [Arabidopsis lyrata subsp. lyrata]	159	161	2.00E-55	101.3	74.8	84.9	hypothetical protein ARALYDRAFT_483306	gbpln	Arabidopsis lyrata	AT2G42180.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G57950.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17581133-17581633 REVERSE LENGTH=166	159	166	5.00E-54	104.4	72.3	83.0

Rsa1.0_00469.1.g14435.t1	ref|NP_973667.2| putative plastid-lipid-associated protein 13 [Arabidopsis thaliana] gi|147719766|sp|Q8S9M1.2|PAP13_ARATH RecName: Full=Probable plastid-lipid-associated protein 13, chloroplastic; AltName: Full=Fibrillin-13; Short=AtPGL30; Flags: Precursor gi|20196973|gb|AAB88638.2| unknown protein [Arabidopsis thaliana] gi|330254981|gb|AEC10075.1| putative plastid-lipid-associated protein 13 [Arabidopsis thaliana]	306	299	1.00E-133	97.7	81.0	88.9	putative plastid-lipid-associated protein 13	gbpln	Arabidopsis thaliana	AT2G42130.4 | Symbols: | Plastid-lipid associated protein PAP / fibrillin family protein | chr2:17566242-17567916 FORWARD LENGTH=299	306	299	1.00E-136	97.7	81.0	88.9
Rsa1.0_00469.1.g14436.t1	gb|EOA27133.1| hypothetical protein CARUB_v10023232mg [Capsella rubella]	83	439	6.00E-28	528.9	92.8	95.2	hypothetical protein CARUB_v10023232mg	gbpln	Capsella rubella	AT2G42120.1 | Symbols: POLD2 | DNA polymerase delta small subunit | chr2:17563282-17565965 REVERSE LENGTH=441	83	441	5.00E-29	531.3	90.4	92.8
Rsa1.0_00469.1.g14437.t1	ref|NP_181741.1| uncharacterized protein [Arabidopsis thaliana] gi|2673903|gb|AAB88637.1| hypothetical protein [Arabidopsis thaliana] gi|20198320|gb|AAM15521.1| hypothetical protein [Arabidopsis thaliana] gi|149944371|gb|ABR46228.1| At2g42110 [Arabidopsis thaliana] gi|330254977|gb|AEC10071.1| uncharacterized protein AT2G42110 [Arabidopsis thaliana]	87	137	1.00E-22	157.5	73.6	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G42110.1 | Symbols: | unknown protein; Has 27 Blast hits to 27 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:17562234-17562732 REVERSE LENGTH=137	87	137	2.00E-25	157.5	73.6	83.9
Rsa1.0_00469.1.g14438.t1	ref|NP_565965.1| nudix hydrolase 23 [Arabidopsis thaliana] gi|68565870|sp|P93740.2|NUD23_ARATH RecName: Full=Nudix hydrolase 23, chloroplastic; Short=AtNUDT23; AltName: Full=ADP-ribose pyrophosphatase; AltName: Full=FAD diphosphatase; Flags: Precursor gi|20198322|gb|AAB63537.2| expressed protein [Arabidopsis thaliana] gi|62320524|dbj|BAD95098.1| hypothetical protein [Arabidopsis thaliana] gi|107738412|gb|ABF83693.1| At2g42070 [Arabidopsis thaliana] gi|330254973|gb|AEC10067.1| nudix hydrolase 23 [Arabidopsis thaliana]	562	280	1.00E-136	49.8	44.1	45.2	nudix hydrolase 23	gbpln	Arabidopsis thaliana	AT2G42070.1 | Symbols: ATNUDT23, ATNUDX23, NUDX23 | nudix hydrolase homolog 23 | chr2:17549669-17551066 REVERSE LENGTH=280	562	280	1.00E-139	49.8	44.1	45.2
Rsa1.0_00469.1.g14439.t1	gb|EOA27725.1| hypothetical protein CARUB_v10023878mg [Capsella rubella]	275	260	1.00E-83	94.5	70.5	76.4	hypothetical protein CARUB_v10023878mg	gbpln	Capsella rubella	AT2G42040.1 | Symbols: | CONTAINS InterPro DOMAIN/s: WRC (InterPro:IPR014977); Has 219 Blast hits to 219 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 215; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:17543282-17545063 FORWARD LENGTH=269	275	269	7.00E-80	97.8	73.1	78.9
Rsa1.0_00469.1.g14440.t1	ref|XP_002881818.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297327657|gb|EFH58077.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	425	413	1.00E-141	97.2	69.4	77.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G42030.1 | Symbols: | RING/U-box superfamily protein | chr2:17539069-17540346 REVERSE LENGTH=425	425	425	1.00E-132	100.0	64.2	74.1
Rsa1.0_00469.1.g14441.t1	ref|NP_181728.1| putative protein kinase [Arabidopsis thaliana] gi|75319137|sp|P93749.1|Y2197_ARATH RecName: Full=Probable protein kinase At2g41970 gi|1871186|gb|AAB63546.1| putative protein kinase [Arabidopsis thaliana] gi|38603828|gb|AAR24659.1| At2g41970 [Arabidopsis thaliana] gi|51968610|dbj|BAD42997.1| putative protein kinase [Arabidopsis thaliana] gi|51968682|dbj|BAD43033.1| putative protein kinase [Arabidopsis thaliana] gi|51971150|dbj|BAD44267.1| putative protein kinase [Arabidopsis thaliana] gi|51971369|dbj|BAD44349.1| putative protein kinase [Arabidopsis thaliana] gi|51971789|dbj|BAD44559.1| putative protein kinase [Arabidopsis thaliana] gi|62318717|dbj|BAD93732.1| putative protein kinase [Arabidopsis thaliana] gi|330254963|gb|AEC10057.1| putative protein kinase [Arabidopsis thaliana]	366	365	0	99.7	94.3	97.8	putative protein kinase	gbpln	Arabidopsis thaliana	AT2G41970.1 | Symbols: | Protein kinase superfamily protein | chr2:17520517-17522304 REVERSE LENGTH=365	366	365	0	99.7	94.3	97.8
Rsa1.0_00470.1.g14442.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00470.1.g14443.t2	gb|EOA38463.1| hypothetical protein CARUB_v10010159mg, partial [Capsella rubella]	169	238	4.00E-38	140.8	59.2	71.6	hypothetical protein CARUB_v10010159mg, partial	gbpln	Capsella rubella	AT1G09580.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:3104657-3106092 FORWARD LENGTH=217	169	217	2.00E-39	128.4	58.6	70.4
Rsa1.0_00470.1.g14444.t8	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1683	1529	0	90.8	40.5	54.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1683	746	5.00E-95	44.3	10.6	14.0
Rsa1.0_00470.1.g14445.t1	gb|EOA35819.1| hypothetical protein CARUB_v10021057mg [Capsella rubella] gi|482571634|gb|EOA35822.1| hypothetical protein CARUB_v10021062mg [Capsella rubella]	79	164	8.00E-30	207.6	81.0	84.8	hypothetical protein CARUB_v10021057mg	gbpln	Capsella rubella	AT1G09690.1 | Symbols: | Translation protein SH3-like family protein | chr1:3136407-3137430 REVERSE LENGTH=164	79	164	2.00E-32	207.6	81.0	83.5
Rsa1.0_00470.1.g14446.t1	ref|XP_002872611.1| hypothetical protein ARALYDRAFT_911524 [Arabidopsis lyrata subsp. lyrata] gi|297318448|gb|EFH48870.1| hypothetical protein ARALYDRAFT_911524 [Arabidopsis lyrata subsp. lyrata]	237	405	2.00E-86	170.9	66.2	80.2	hypothetical protein ARALYDRAFT_911524	gbpln	Arabidopsis lyrata	AT4G15050.1 | Symbols: | Protein of Unknown Function (DUF239) | chr4:8588548-8590345 REVERSE LENGTH=396	237	396	6.00E-24	167.1	32.9	48.5
Rsa1.0_00470.1.g14447.t1	ref|XP_002889760.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata] gi|297335602|gb|EFH66019.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata]	164	164	6.00E-88	100.0	97.0	98.8	60S ribosomal protein L21	gbpln	Arabidopsis lyrata	AT1G09690.1 | Symbols: | Translation protein SH3-like family protein | chr1:3136407-3137430 REVERSE LENGTH=164	164	164	6.00E-90	100.0	96.3	98.2
Rsa1.0_00470.1.g14448.t1	emb|CAA48890.1| U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana]	237	249	1.00E-110	105.1	88.6	93.7	U2 small nuclear ribonucleoprotein A'	gbpln	Arabidopsis thaliana	AT1G09760.1 | Symbols: U2A' | U2 small nuclear ribonucleoprotein A | chr1:3159476-3161603 REVERSE LENGTH=249	237	249	1.00E-113	105.1	88.6	93.7
Rsa1.0_00470.1.g14449.t1	ref|XP_002869101.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314937|gb|EFH45360.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	141	248	3.00E-17	175.9	38.3	52.5	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00470.1.g14450.t1	dbj|BAD44444.1| unnamed protein product [Arabidopsis thaliana] gi|51971573|dbj|BAD44451.1| unnamed protein product [Arabidopsis thaliana]	319	368	1.00E-147	115.4	83.4	87.1	unnamed protein product	gbpln	Arabidopsis thaliana	AT1G09800.1 | Symbols: | Pseudouridine synthase family protein | chr1:3177121-3180336 REVERSE LENGTH=372	319	372	1.00E-149	116.6	83.4	87.1
Rsa1.0_00470.1.g14451.t1	ref|XP_002889774.1| histidine acid phosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335616|gb|EFH66033.1| histidine acid phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	479	487	0	101.7	89.8	95.8	histidine acid phosphatase family protein	gbpln	Arabidopsis lyrata	AT1G09870.1 | Symbols: | histidine acid phosphatase family protein | chr1:3205817-3208444 FORWARD LENGTH=487	479	487	0	101.7	89.6	95.4
Rsa1.0_00470.1.g14452.t1	ref|NP_563857.1| TRAF-type zinc finger-related protein [Arabidopsis thaliana] gi|22531082|gb|AAM97045.1| expressed protein [Arabidopsis thaliana] gi|23197978|gb|AAN15516.1| expressed protein [Arabidopsis thaliana] gi|332190393|gb|AEE28514.1| TRAF-type zinc finger-related protein [Arabidopsis thaliana]	113	192	4.00E-22	169.9	42.5	46.9	TRAF-type zinc finger-related protein	gbpln	Arabidopsis thaliana	AT1G09920.1 | Symbols: | TRAF-type zinc finger-related | chr1:3224863-3226860 REVERSE LENGTH=192	113	192	7.00E-25	169.9	42.5	46.9
Rsa1.0_00470.1.g14453.t1	gb|EOA40255.1| hypothetical protein CARUB_v10008976mg [Capsella rubella]	94	487	3.00E-27	518.1	69.1	73.4	hypothetical protein CARUB_v10008976mg	gbpln	Capsella rubella	AT1G09870.1 | Symbols: | histidine acid phosphatase family protein | chr1:3205817-3208444 FORWARD LENGTH=487	94	487	1.00E-29	518.1	76.6	85.1
Rsa1.0_00470.1.g14454.t1	ref|NP_563857.1| TRAF-type zinc finger-related protein [Arabidopsis thaliana] gi|22531082|gb|AAM97045.1| expressed protein [Arabidopsis thaliana] gi|23197978|gb|AAN15516.1| expressed protein [Arabidopsis thaliana] gi|332190393|gb|AEE28514.1| TRAF-type zinc finger-related protein [Arabidopsis thaliana]	192	192	2.00E-86	100.0	79.7	89.1	TRAF-type zinc finger-related protein	gbpln	Arabidopsis thaliana	AT1G09920.1 | Symbols: | TRAF-type zinc finger-related | chr1:3224863-3226860 REVERSE LENGTH=192	192	192	7.00E-89	100.0	79.7	89.1
Rsa1.0_00470.1.g14455.t1	ref|XP_002892535.1| ATOPT2 [Arabidopsis lyrata subsp. lyrata] gi|297338377|gb|EFH68794.1| ATOPT2 [Arabidopsis lyrata subsp. lyrata]	733	734	0	100.1	92.9	96.9	ATOPT2	gbpln	Arabidopsis lyrata	AT1G09930.1 | Symbols: ATOPT2, OPT2 | oligopeptide transporter 2 | chr1:3227490-3230043 REVERSE LENGTH=734	733	734	0	100.1	92.6	96.9
Rsa1.0_00470.1.g14456.t1	ref|NP_194164.1| uncharacterized protein [Arabidopsis thaliana] gi|5051775|emb|CAB45068.1| putative protein [Arabidopsis thaliana] gi|7269283|emb|CAB79343.1| putative protein [Arabidopsis thaliana] gi|58652054|gb|AAW80852.1| At4g24330 [Arabidopsis thaliana] gi|332659490|gb|AEE84890.1| uncharacterized protein AT4G24330 [Arabidopsis thaliana]	319	478	3.00E-97	149.8	54.9	58.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G24330.1 | Symbols: | Protein of unknown function (DUF1682) | chr4:12603848-12606229 REVERSE LENGTH=478	319	478	1.00E-100	149.8	54.9	58.6

Rsa1.0_00470.1.g14457.t1	gb|EOA15579.1| hypothetical protein CARUB_v10005317mg [Capsella rubella]	126	307	2.00E−13	243.7	38.1	44.4	hypothetical protein CARUB_v10005317mg	gbpln	Capsella rubella	AT4G22320.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G55210.1). | chr4:11793129−11794596 REVERSE LENGTH=237	126	237	1.00E−13	188.1	34.9	38.9
Rsa1.0_00470.1.g14458.t1	ref|NP_683294.2| phosphoglycerate mutase−like protein [Arabidopsis thaliana] gi|332190397|gb|AEE28518.1| phosphoglycerate mutase−like protein [Arabidopsis thaliana]	216	231	1.00E−110	106.9	91.7	95.8	phosphoglycerate mutase−like protein	gbpln	Arabidopsis thaliana	AT1G09935.1 | Symbols: | Phosphoglycerate mutase family protein | chr1:3234060−3235530 REVERSE LENGTH=231	216	231	1.00E−113	106.9	91.7	95.8
Rsa1.0_00470.1.g14459.t1	pir||S65812 RNA−directed DNA polymerase (EC 2.7.7.49) (clone DW15) − Arabidopsis thaliana retrotransposon Ta11−1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	1003	1333	0	132.9	35.8	46.7	RNA−directed DNA polymerase (EC 2.7.7.49) (clone DW15) − Arabidopsis thaliana retrotransposon Ta11−1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1003	575	8.00E−46	57.3	10.2	16.3
Rsa1.0_00470.1.g14460.t1	dbj|BAB01217.1| Ta11 non−LTR retroelement protein−like [Arabidopsis thaliana] gi|67633664|gb|AAY78756.1| putative zinc finger protein [Arabidopsis thaliana]	507	487	2.00E−94	96.1	41.2	59.0	Ta11 non−LTR retroelement protein−like	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691−14272776 FORWARD LENGTH=361	507	361	4.00E−24	71.2	10.8	21.1
Rsa1.0_00470.1.g14461.t1	ref|XP_002892538.1| glutamyl−tRNA reductase [Arabidopsis lyrata subsp. lyrata] gi|297338380|gb|EFH68797.1| glutamyl−tRNA reductase [Arabidopsis lyrata subsp. lyrata]	526	526	0	100.0	81.6	89.9	glutamyl−tRNA reductase	gbpln	Arabidopsis lyrata	AT1G09940.1 | Symbols: HEMA2 | Glutamyl−tRNA reductase family protein | chr1:3237224−3239262 REVERSE LENGTH=530	526	530	0	100.8	82.5	91.1
Rsa1.0_00471.1.g14462.t1	ref|XP_002876613.1| beta−substituted ala synthase 3_1 [Arabidopsis lyrata subsp. lyrata] gi|297322451|gb|EFH52872.1| beta−substituted ala synthase 3_1 [Arabidopsis lyrata subsp. lyrata]	352	368	1.00E−169	104.5	86.1	93.5	beta−substituted ala synthase 3_1	gbpln	Arabidopsis lyrata	AT3G61440.1 | Symbols: ATCYSC1, ARATH;BSAS3;1, CYSC1 | cysteine synthase C1 | chr3:22735885−22737792 FORWARD LENGTH=368	352	368	1.00E−172	104.5	86.1	93.5
Rsa1.0_00471.1.g14463.t1	dbj|BAA32777.1| plasma membrane aquaporin (PAQ1) [Raphanus sativus]	286	286	1.00E−164	100.0	100.0	100.0	plasma membrane aquaporin (PAQ1)	gbpln	Raphanus sativus	AT3G61430.2 | Symbols: PIP1A, ATPIP1, PIP1, PIP1;1 | plasma membrane intrinsic protein 1A | chr3:22733657−22735113 FORWARD LENGTH=286	286	286	1.00E−164	100.0	98.3	99.0
Rsa1.0_00471.1.g14464.t1	ref|XP_002878380.1| hypothetical protein ARALYDRAFT_486615 [Arabidopsis lyrata subsp. lyrata] gi|297324218|gb|EFH54639.1| hypothetical protein ARALYDRAFT_486615 [Arabidopsis lyrata subsp. lyrata]	345	346	1.00E−162	100.3	86.7	91.6	hypothetical protein ARALYDRAFT_486615	gbpln	Arabidopsis lyrata	AT3G61415.1 | Symbols: ASK21, SK21 | SKP1−like 21 | chr3:22722962−22725577 REVERSE LENGTH=351	345	351	1.00E−164	101.7	85.8	91.9
Rsa1.0_00471.1.g14465.t1	ref|XP_002876611.1| hypothetical protein ARALYDRAFT_486614 [Arabidopsis lyrata subsp. lyrata] gi|297322449|gb|EFH52870.1| hypothetical protein ARALYDRAFT_486614 [Arabidopsis lyrata subsp. lyrata]	301	295	1.00E−113	98.0	74.8	83.4	hypothetical protein ARALYDRAFT_486614	gbpln	Arabidopsis lyrata	AT3G61410.1 | Symbols: | BEST Arabidopsis thaliana protein match is: U−box domain−containing protein kinase family protein (TAIR:AT2G45910.1); Has 232 Blast hits to 229 proteins in 13 species: Archae − 0; Bacteria − 0; Metazoa − 13; Fungi − 0; Plants − 218; Viruses − 0; Other Eukaryotes − 1 (source: NCBI BLink). | chr3:22721112−22722452 FORWARD LENGTH=294	301	294	1.00E−116	97.7	73.8	82.7
Rsa1.0_00471.1.g14466.t1	gb|EOA24031.1| hypothetical protein CARUB_v10017247mg [Capsella rubella]	434	447	1.00E−165	103.0	68.7	80.2	hypothetical protein CARUB_v10017247mg	gbpln	Capsella rubella	AT3G61390.2 | Symbols: | RING/U−box superfamily protein | chr3:22716418−22718270 FORWARD LENGTH=435	434	435	1.00E−160	100.2	67.7	77.9
Rsa1.0_00471.1.g14467.t1	ref|XP_002878378.1| hypothetical protein ARALYDRAFT_486612 [Arabidopsis lyrata subsp. lyrata] gi|297324216|gb|EFH54637.1| hypothetical protein ARALYDRAFT_486612 [Arabidopsis lyrata subsp. lyrata]	678	714	0	105.3	74.0	84.5	hypothetical protein ARALYDRAFT_486612	gbpln	Arabidopsis lyrata	AT3G61380.1 | Symbols: | Phosphatidylinositol N−acetyglucosaminlytransferase subunit P−related | chr3:22708769−22711279 REVERSE LENGTH=718	678	718	0	105.9	73.0	83.9
Rsa1.0_00471.1.g14468.t2	ref|XP_002876607.1| hypothetical protein ARALYDRAFT_486610 [Arabidopsis lyrata subsp. lyrata] gi|297322445|gb|EFH52866.1| hypothetical protein ARALYDRAFT_486610 [Arabidopsis lyrata subsp. lyrata]	128	127	1.00E−47	99.2	78.1	85.2	hypothetical protein ARALYDRAFT_486610	gbpln	Arabidopsis lyrata	AT3G61370.1 | Symbols: | Protein of unknown function (DUF3245) | chr3:22707796−22708380 FORWARD LENGTH=127	128	127	4.00E−42	99.2	75.0	82.8
Rsa1.0_00471.1.g14469.t1	gb|EOA23307.1| hypothetical protein CARUB_v10019081mg [Capsella rubella]	488	495	0	101.4	82.6	91.2	hypothetical protein CARUB_v10019081mg	gbpln	Capsella rubella	AT3G61360.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr3:22704630−22706126 REVERSE LENGTH=498	488	498	0	102.0	83.2	91.4

Rsa1.0_00471.1.g14470.t1	ref|NP_191691.2| Bestrophin-like protein [Arabidopsis thaliana] gi|20141056|sp|Q9M2D2.2|YU88_ARATH RecName: Full=UPF0187 protein At3g61320, chloroplastic; Flags: Precursor gi|16604549|gb|AAL24280.1| AT3g61320/T20K12_220 [Arabidopsis thaliana] gi|23296291|gb|AAN12915.1| At3g61320/T20K12_220 [Arabidopsis thaliana] gi|332646666|gb|AEE80187.1| Bestrophin-like protein [Arabidopsis thaliana]	360	410	1.00E-171	113.9	85.6	90.6	Bestrophin-like protein	gbpln	Arabidopsis thaliana	AT3G61320.1 | Symbols: | Bestrophin-like protein | chr3:22694002-22695474 FORWARD LENGTH=410	360	410	1.00E-173	113.9	85.6	90.6
Rsa1.0_00471.1.g14471.t1	gb|EOA24312.1| hypothetical protein CARUB_v10017552mg [Capsella rubella]	346	350	1.00E-137	101.2	80.9	87.3	hypothetical protein CARUB_v10017552mg	gbpln	Capsella rubella	AT3G61310.1 | Symbols: | AT hook motif DNA-binding family protein | chr3:22690799-22692445 REVERSE LENGTH=354	346	354	1.00E-125	102.3	80.1	88.4
Rsa1.0_00471.1.g14472.t1	ref|NP_191689.1| C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein [Arabidopsis thaliana] gi|6850897|emb|CAB71060.1| anthranilate phosphoribosyltransferase-like protein [Arabidopsis thaliana] gi|28392941|gb|AAO41906.1| putative anthranilate phosphoribosyltransferase [Arabidopsis thaliana] gi|28973565|gb|AAO64107.1| putative anthranilate phosphoribosyltransferase [Arabidopsis thaliana] gi|332646664|gb|AEE80185.1| C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein [Arabidopsis thaliana]	1010	972	0	96.2	77.2	86.4	C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT3G61300.1 | Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr3:22687662-22690580 FORWARD LENGTH=972	1010	972	0	96.2	77.2	86.4
Rsa1.0_00471.1.g14473.t1	gb|EOA23775.1| hypothetical protein CARUB_v10016988mg [Capsella rubella]	499	535	0	107.2	81.0	88.8	hypothetical protein CARUB_v10016988mg	gbpln	Capsella rubella	AT3G61280.1 | Symbols: | Arabidopsis thaliana protein of unknown function (DUF821) | chr3:22681145-22683589 FORWARD LENGTH=536	499	536	0	107.4	81.6	89.8
Rsa1.0_00471.1.g14474.t1	ref|NP_191687.2| uncharacterized protein [Arabidopsis thaliana] gi|55978809|gb|AAV68866.1| hypothetical protein AT3G61280 [Arabidopsis thaliana] gi|61742723|gb|AAX55182.1| hypothetical protein At3g61280 [Arabidopsis thaliana] gi|110739424|dbj|BAF01622.1| hypothetical protein [Arabidopsis thaliana] gi|332646661|gb|AEE80182.1| uncharacterized protein AT3G61280 [Arabidopsis thaliana]	524	536	0	102.3	84.5	91.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G61280.1 | Symbols: | Arabidopsis thaliana protein of unknown function (DUF821) | chr3:22681145-22683589 FORWARD LENGTH=536	524	536	0	102.3	84.5	91.8
Rsa1.0_00471.1.g14475.t1	ref|XP_002876559.1| hypothetical protein ARALYDRAFT_349109 [Arabidopsis lyrata subsp. lyrata] gi|297322397|gb|EFH52818.1| hypothetical protein ARALYDRAFT_349109 [Arabidopsis lyrata subsp. lyrata]	134	443	1.00E-19	330.6	49.3	61.9	hypothetical protein ARALYDRAFT_349109	gbpln	Arabidopsis lyrata	AT2G44930.1 | Symbols: | Plant protein of unknown function (DUF247) | chr2:18529700-18531671 REVERSE LENGTH=515	134	515	1.00E-19	384.3	47.8	60.4
Rsa1.0_00471.1.g14476.t4	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	401	442	1.00E-174	110.2	77.1	86.3	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	401	343	3.00E-52	85.5	32.4	43.9
Rsa1.0_00471.1.g14477.t15	gb|ABD65000.1| hypothetical protein 26.t00020 [Brassica oleracea]	297	302	2.00E-84	101.7	56.2	71.0	hypothetical protein 26.t00020	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	297	302	4.00E-59	101.7	45.5	62.0
Rsa1.0_00471.1.g14478.t1	gb|EOA24748.1| hypothetical protein CARUB_v10018025mg [Capsella rubella]	191	208	4.00E-67	108.9	75.9	85.9	hypothetical protein CARUB_v10018025mg	gbpln	Capsella rubella	AT3G61260.1 | Symbols: | Remorin family protein | chr3:22675403-22676701 REVERSE LENGTH=212	191	212	1.00E-66	111.0	74.3	83.8

Rsa1.0_00471.1.g14479.t1	ref|NP_191684.1| myb domain protein 17 [Arabidopsis thaliana] gi|6850892|emb|CAB71055.1| putative transcription factor (MYB17) [Arabidopsis thaliana] gi|41619302|gb|AAS10071.1| MYB transcription factor [Arabidopsis thaliana] gi|193885153|gb|ACF28390.1| At3g61250 [Arabidopsis thaliana] gi|332646658|gb|AEE80179.1| myb domain protein 17 [Arabidopsis thaliana]	291	299	1.00E-136	102.7	83.5	89.3	myb domain protein 17	gbpln	Arabidopsis thaliana	AT3G61250.1 | Symbols: AtMYB17, MYB17 | myb domain protein 17 | chr3:22671306-22672551 FORWARD LENGTH=299	291	299	1.00E-138	102.7	83.5	89.3
Rsa1.0_00471.1.g14480.t1	ref|XP_002876600.1| hypothetical protein ARALYDRAFT_486601 [Arabidopsis lyrata subsp. lyrata] gi|297322438|gb|EFH52859.1| hypothetical protein ARALYDRAFT_486601 [Arabidopsis lyrata subsp. lyrata]	143	494	7.00E-44	345.5	62.2	62.9	hypothetical protein ARALYDRAFT_486601	gbpln	Arabidopsis lyrata	AT3G61240.2 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr3:22666590-22669154 FORWARD LENGTH=498	143	498	2.00E-46	348.3	62.2	62.9
Rsa1.0_00471.1.g14481.t1	ref|XP_002878372.1| LIM domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324210|gb|EFH54631.1| LIM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	214	214	1.00E-104	100.0	88.3	92.5	LIM domain-containing protein	gbpln	Arabidopsis lyrata	AT3G61230.1 | Symbols: | GATA type zinc finger transcription factor family protein | chr3:22664601-22665503 REVERSE LENGTH=213	214	213	1.00E-104	99.5	85.5	91.1
Rsa1.0_00471.1.g14482.t1	ref|NP_191681.1| (+)-neomenthol dehydrogenase [Arabidopsis thaliana] gi|75311801|sp|Q9M2E2.1|SDR1_ARATH RecName: Full=(+)-neomenthol dehydrogenase; AltName: Full=Menthone:neomenthol reductase; AltName: Full=Short-chain dehydrogenase/reductase 1; Short=AtSDR1 gi|6850889|emb|CAB71052.1| putative protein [Arabidopsis thaliana] gi|15028055|gb|AAK76558.1| unknown protein [Arabidopsis thaliana] gi|20259057|gb|AAM14244.1| unknown protein [Arabidopsis thaliana] gi|332646653|gb|AEE80174.1| (+)-neomenthol dehydrogenase [Arabidopsis thaliana]	296	296	1.00E-144	100.0	81.1	89.9	(+)-neomenthol dehydrogenase	gbpln	Arabidopsis thaliana	AT3G61220.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:22663025-22664316 FORWARD LENGTH=296	296	296	1.00E-147	100.0	81.1	89.9
Rsa1.0_00471.1.g14483.t1	ref|NP_191680.1| S-adenosylmethionine-dependent methyltransferasedomain-containing protein [Arabidopsis thaliana] gi|6850888|emb|CAB71051.1| putative protein [Arabidopsis thaliana] gi|26452065|dbj|BAC43122.1| unknown protein [Arabidopsis thaliana] gi|332646652|gb|AEE80173.1| S-adenosylmethionine-dependent methyltransferasedomain-containing protein [Arabidopsis thaliana]	261	261	1.00E-126	100.0	81.6	90.0	S-adenosylmethionine-dependent methyltransferasedomain-containing protein	gbpln	Arabidopsis thaliana	AT3G61210.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:22658881-22659815 REVERSE LENGTH=261	261	261	1.00E-129	100.0	81.6	90.0
Rsa1.0_00472.1.g14484.t1	dbj|BAJ33985.1| unnamed protein product [Thellungiella halophila]	454	478	0	105.3	91.2	95.8	unnamed protein product	----	----	AT2G38400.1 | Symbols: AGT3 | alanine:glyoxylate aminotransferase 3 | chr2:16083779-16085974 FORWARD LENGTH=477	454	477	0	105.1	89.6	94.9
Rsa1.0_00472.1.g14485.t1	ref|NP_181375.1| VHS and GAT domain-containing protein [Arabidopsis thaliana] gi|3395431|gb|AAC28763.1| unknown protein [Arabidopsis thaliana] gi|209529799|gb|ACI49794.1| At2g38410 [Arabidopsis thaliana] gi|330254440|gb|AEC09534.1| VHS and GAT domain-containing protein [Arabidopsis thaliana]	700	671	0	95.9	56.1	59.1	VHS and GAT domain-containing protein	gbpln	Arabidopsis thaliana	AT2G38410.1 | Symbols: | ENTH/VHS/GAT family protein | chr2:16086912-16090047 REVERSE LENGTH=671	700	671	0	95.9	56.1	59.1
Rsa1.0_00472.1.g14486.t1	ref|NP_181376.3| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546769|sp|Q8L6Y7.2|PP193_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g38420, mitochondrial; Flags: Precursor gi|3395430|gb|AAC28762.1| hypothetical protein [Arabidopsis thaliana] gi|330254441|gb|AEC09535.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	454	453	0	99.8	77.3	88.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G38420.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:16091093-16092454 FORWARD LENGTH=453	454	453	0	99.8	77.3	88.5

Rsa1.0_00472.1.g14487.t2	ref|XP_002881597.1| hypothetical protein ARALYDRAFT_345626 [Arabidopsis lyrata subsp. lyrata] gi|297327436|gb|EFH57856.1| hypothetical protein ARALYDRAFT_345626 [Arabidopsis lyrata subsp. lyrata]	332	366	1.00E-78	110.2	52.7	66.3	hypothetical protein ARALYDRAFT_345626	gbpln	Arabidopsis lyrata	AT2G38430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54310.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16092950-16094810 REVERSE LENGTH=393	332	393	4.00E-74	118.4	46.1	59.9
Rsa1.0_00472.1.g14488.t1	ref|XP_002881597.1| hypothetical protein ARALYDRAFT_345626 [Arabidopsis lyrata subsp. lyrata] gi|297327436|gb|EFH57856.1| hypothetical protein ARALYDRAFT_345626 [Arabidopsis lyrata subsp. lyrata]	124	366	3.00E-37	295.2	67.7	80.6	hypothetical protein ARALYDRAFT_345626	gbpln	Arabidopsis lyrata	AT2G38430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54310.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16092950-16094810 REVERSE LENGTH=393	124	393	2.00E-36	316.9	60.5	73.4
Rsa1.0_00472.1.g14489.t2	ref|NP_568490.3| lon protease 1 [Arabidopsis thaliana] gi|27735209|sp|P93655.2|LONM1_ARATH RecName: Full=Lon protease homolog 1, mitochondrial; Flags: Precursor gi|20259500|gb|AAM13870.1| putative Lon protease homolog 2 precursor [Arabidopsis thaliana] gi|21436459|gb|AAM51430.1| putative Lon protease homolog 2 precursor [Arabidopsis thaliana] gi|332006234|gb|AED93617.1| lon protease 1 [Arabidopsis thaliana]	353	940	3.00E-53	266.3	28.9	31.7	lon protease 1	gbpln	Arabidopsis thaliana	AT5G26860.1 | Symbols: LON_ARA_ARA, LON1 | lon protease 1 | chr5:9451183-9456631 FORWARD LENGTH=940	353	940	8.00E-56	266.3	28.9	31.7
Rsa1.0_00472.1.g14490.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00472.1.g14491.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	399	1197	4.00E-69	300.0	38.6	56.4	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	399	303	2.00E-46	75.9	29.6	38.8
Rsa1.0_00472.1.g14492.t2	ref|NP_568470.1| uncharacterized protein [Arabidopsis thaliana] gi|15529244|gb|AAK97716.1| AT5g25410/F18G18_150 [Arabidopsis thaliana] gi|16974397|gb|AAL31124.1| AT5g25410/F18G18_150 [Arabidopsis thaliana] gi|332006054|gb|AED93437.1| uncharacterized protein AT5G25410 [Arabidopsis thaliana]	344	369	1.00E-122	107.3	62.5	75.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G25410.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:8831692-8833437 FORWARD LENGTH=369	344	369	1.00E-125	107.3	62.5	75.3
Rsa1.0_00472.1.g14493.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00472.1.g14494.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	1382	1356	0	98.1	50.1	67.9	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1382	1262	5.00E-78	91.3	11.9	19.2
Rsa1.0_00472.1.g14495.t1	ref|NP_181385.1| MATE efflux family protein [Arabidopsis thaliana] gi|3786021|gb|AAC67367.1| hypothetical protein [Arabidopsis thaliana] gi|67633596|gb|AAY78722.1| MATE efflux protein-related [Arabidopsis thaliana] gi|330254451|gb|AEC09545.1| MATE efflux family protein [Arabidopsis thaliana]	452	486	0	107.5	90.9	97.1	MATE efflux family protein	gbpln	Arabidopsis thaliana	AT2G38510.1 | Symbols: | MATE efflux family protein | chr2:16123985-16125445 FORWARD LENGTH=486	452	486	0	107.5	90.9	97.1
Rsa1.0_00472.1.g14496.t1	gb|ABM69132.1| lipid transfer protein precursor [Brassica rapa subsp. pekinensis]	118	118	3.00E-52	100.0	89.8	94.9	lipid transfer protein precursor	gbpln	Brassica rapa	AT2G38540.1 | Symbols: LP1, LTP1, ATLTP1 | lipid transfer protein 1 | chr2:16130418-16130893 FORWARD LENGTH=118	118	118	2.00E-44	100.0	75.4	87.3
Rsa1.0_00472.1.g14497.t3	gb|AAA84891.1| non-green plastid inner envelope membrane protein precursor [Brassica oleracea var. botrytis]	373	336	1.00E-162	90.1	81.5	83.4	non-green plastid inner envelope membrane protein precursor	gbpln	Brassica oleracea	AT2G38550.1 | Symbols: | Transmembrane proteins 14C | chr2:16132178-16134229 FORWARD LENGTH=335	373	335	1.00E-125	89.8	64.6	73.5
Rsa1.0_00472.1.g14498.t1	gb|EOA23646.1| hypothetical protein CARUB_v10016844mg [Capsella rubella]	654	626	0	95.7	76.8	85.5	hypothetical protein CARUB_v10016844mg	gbpln	Capsella rubella	AT3G52850.1 | Symbols: VSR1, BP-80, ATELP, BP80, BP80B, ATELP1, ATVSR1, GFS1, VSR1;1, BP80-1;1 | vacuolar sorting receptor homolog 1 | chr3:19587999-19591690 FORWARD LENGTH=623	654	623	0	95.3	77.2	86.1
Rsa1.0_00472.1.g14499.t1	dbj|BAJ34462.1| unnamed protein product [Thellungiella halophila]	334	381	1.00E-154	114.1	84.7	93.7	unnamed protein product	----	----	AT2G38560.1 | Symbols: TFIIS | transcript elongation factor IIS | chr2:16134802-16136319 FORWARD LENGTH=378	334	378	1.00E-145	113.2	81.7	90.7
Rsa1.0_00472.1.g14500.t1	ref|XP_002879756.1| acid phosphatase class B family protein [Arabidopsis lyrata subsp. lyrata] gi|297325595|gb|EFH56015.1| acid phosphatase class B family protein [Arabidopsis lyrata subsp. lyrata]	251	251	1.00E-126	100.0	83.3	92.8	acid phosphatase class B family protein	gbpln	Arabidopsis lyrata	AT2G38600.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr2:16145907-16146857 FORWARD LENGTH=251	251	251	1.00E-127	100.0	82.9	92.0

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<tr><td>Rsa1.0_00472.1.g14504.t1</td><td>ref|XP_002879775.1| transcription factor jumonji family protein [Arabidopsis lyrata subsp. lyrata] gi|297325614|gb|EFH56034.1| transcription factor jumonji family protein [Arabidopsis lyrata subsp. lyrata]</td><td>713</td><td>710</td><td>0</td><td>99.6</td><td>67.7</td><td>79.8</td><td>transcription factor jumonji family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G38950.1 | Symbols: | Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein | chr2:16261599-16265044 FORWARD LENGTH=708</td><td>713</td><td>708</td><td>0</td><td>99.3</td><td>65.9</td><td>78.0</td></tr>
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<tr><td>Rsa1.0_00472.1.g14507.t1</td><td>gb|AAL77698.1| At2g38970/T7F6.14 [Arabidopsis thaliana]</td><td>72</td><td>692</td><td>7.00E-28</td><td>961.1</td><td>83.3</td><td>90.3</td><td>At2g38970/T7F6.14</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G38970.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr2:16274135-16276651 FORWARD LENGTH=692</td><td>72</td><td>692</td><td>1.00E-30</td><td>961.1</td><td>83.3</td><td>90.3</td></tr>
<tr><td>Rsa1.0_00472.1.g14508.t1</td><td>gb|AAC79610.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>600</td><td>689</td><td>0</td><td>114.8</td><td>88.0</td><td>92.7</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G38970.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr2:16274135-16276651 FORWARD LENGTH=692</td><td>600</td><td>692</td><td>0</td><td>115.3</td><td>88.0</td><td>92.7</td></tr>
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Rsa1.0_00472.1.g14509.t2	ref|XP_002879777.1| hypothetical protein ARALYDRAFT_321593 [Arabidopsis lyrata subsp. lyrata] gi|297325616|gb|EFH56036.1| hypothetical protein ARALYDRAFT_321593 [Arabidopsis lyrata subsp. lyrata]	443	474	0	107.0	72.2	85.3	hypothetical protein ARALYDRAFT_321593	gbpln	Arabidopsis lyrata	AT2G38995.2 | Symbols: | O−acyltransferase (WSD1−like) family protein | chr2:16282139−16284700 FORWARD LENGTH=487	443	487	0	109.9	74.0	86.0
Rsa1.0_00472.1.g14510.t9	ref|XP_002881629.1| hypothetical protein ARALYDRAFT_903150 [Arabidopsis lyrata subsp. lyrata] gi|297327468|gb|EFH57888.1| hypothetical protein ARALYDRAFT_903150 [Arabidopsis lyrata subsp. lyrata]	339	344	1.00E−161	101.5	84.4	89.7	hypothetical protein ARALYDRAFT_903150	gbpln	Arabidopsis lyrata	AT2G39080.1 | Symbols: | NAD(P)−binding Rossmann−fold superfamily protein | chr2:16309981−16312475 REVERSE LENGTH=351	339	351	1.00E−158	103.5	82.0	88.5
Rsa1.0_00472.1.g14511.t2	ref|XP_002862908.1| hypothetical protein ARALYDRAFT_921086 [Arabidopsis lyrata subsp. lyrata] gi|297308678|gb|EFH39167.1| hypothetical protein ARALYDRAFT_921086 [Arabidopsis lyrata subsp. lyrata]	431	434	0	100.7	89.6	94.7	hypothetical protein ARALYDRAFT_921086	gbpln	Arabidopsis lyrata	AT2G39110.1 | Symbols: | Protein kinase superfamily protein | chr2:16319770−16321568 FORWARD LENGTH=435	431	435	0	100.9	89.6	94.9
Rsa1.0_00472.1.g14512.t2	ref|NP_850312.1| transmembrane amino acid transporter−like protein [Arabidopsis thaliana] gi|330254544|gb|AEC09638.1| transmembrane amino acid transporter−like protein [Arabidopsis thaliana]	559	550	0	98.4	89.8	93.6	transmembrane amino acid transporter−like protein	gbpln	Arabidopsis thaliana	AT2G39130.1 | Symbols: | Transmembrane amino acid transporter family protein | chr2:16323171−16326744 REVERSE LENGTH=550	559	550	0	98.4	89.8	93.6
Rsa1.0_00472.1.g14513.t1	gb|EOA27086.1| hypothetical protein CARUB_v10023183mg, partial [Capsella rubella]	468	456	1.00E−174	97.4	69.7	75.2	hypothetical protein CARUB_v10023183mg, partial	gbpln	Capsella rubella	AT2G39140.1 | Symbols: SVR1 | pseudouridine synthase family protein | chr2:16330238−16333153 FORWARD LENGTH=410	468	410	1.00E−167	87.6	66.2	71.4
Rsa1.0_00472.1.g14514.t1	ref|NP_181454.1| major facilitator protein [Arabidopsis thaliana] gi|16930479|gb|AAL31925.1|AF419593_1 At2g39210/T16B24.15 [Arabidopsis thaliana] gi|3402684|gb|AAC28987.1| nodulin−like protein [Arabidopsis thaliana] gi|330254552|gb|AEC09646.1| major facilitator protein [Arabidopsis thaliana]	584	601	0	102.9	84.1	90.9	major facilitator protein	gbpln	Arabidopsis thaliana	AT2G39210.1 | Symbols: | Major facilitator superfamily protein | chr2:16366287−16368231 REVERSE LENGTH=601	584	601	0	102.9	84.1	90.9
Rsa1.0_00472.1.g14515.t1	gb|EOA26975.1| hypothetical protein CARUB_v10023072mg [Capsella rubella] gi|482562786|gb|EOA26976.1| hypothetical protein CARUB_v10023072mg [Capsella rubella]	489	497	0	101.6	85.3	89.8	hypothetical protein CARUB_v10023072mg	gbpln	Capsella rubella	AT2G39220.1 | Symbols: PLP6, PLA IIB | PATATIN−like protein 6 | chr2:16375055−16376663 REVERSE LENGTH=499	489	499	0	102.0	84.9	90.0
Rsa1.0_00473.1.g14516.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00473.1.g14517.t15	ref|XP_002867740.1| hypothetical protein ARALYDRAFT_492569 [Arabidopsis lyrata subsp. lyrata] gi|297313576|gb|EFH43999.1| hypothetical protein ARALYDRAFT_492569 [Arabidopsis lyrata subsp. lyrata]	2220	2186	0	98.5	77.8	86.4	hypothetical protein ARALYDRAFT_492569	gbpln	Arabidopsis lyrata	AT4G22970.1 | Symbols: RSW4, AESP, ESP | homolog of separase | chr4:12033703−12043572 REVERSE LENGTH=2180	2220	2180	0	98.2	77.0	85.5
Rsa1.0_00473.1.g14518.t1	gb|EOA20085.1| hypothetical protein CARUB_v10000359mg [Capsella rubella]	554	693	1.00E−115	125.1	48.9	64.4	hypothetical protein CARUB_v10000359mg	gbpln	Capsella rubella	AT4G11860.1 | Symbols: | Protein of unknown function (DUF544) | chr4:7134237−7138361 REVERSE LENGTH=682	554	682	1.00E−116	123.1	50.2	66.8
Rsa1.0_00473.1.g14519.t1	ref|XP_002887270.1| hypothetical protein ARALYDRAFT_894796 [Arabidopsis lyrata subsp. lyrata] gi|297333111|gb|EFH63529.1| hypothetical protein ARALYDRAFT_894796 [Arabidopsis lyrata subsp. lyrata]	123	177	2.00E−22	143.9	47.2	55.3	hypothetical protein ARALYDRAFT_894796	gbpln	Arabidopsis lyrata	AT1G70040.1 | Symbols: | Protein of unknown function (DUF1163) | chr1:26381233−26381908 FORWARD LENGTH=193	123	193	6.00E−22	156.9	43.9	53.7

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<tr><td>Rsa1.0_00473.1.g14522.t18</td><td>gb|EOA16740.1| hypothetical protein CARUB_v10004941mg, partial [Capsella rubella]</td><td>485</td><td>409</td><td>0</td><td>84.3</td><td>71.1</td><td>73.8</td><td>hypothetical protein CARUB_v10004941mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G22930.1 | Symbols: PYR4, DHOASE | pyrimidin 4 | chr4:12019315-12021200 FORWARD LENGTH=377</td><td>485</td><td>377</td><td>0</td><td>77.7</td><td>69.7</td><td>73.2</td></tr>
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<tr><td>Rsa1.0_00473.1.g14524.t1</td><td>emb|CAA09731.1| receptor-like protein kinase, RLK3 [Arabidopsis thaliana]</td><td>650</td><td>667</td><td>0</td><td>102.6</td><td>70.2</td><td>79.2</td><td>receptor-like protein kinase, RLK3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667</td><td>650</td><td>667</td><td>0</td><td>102.6</td><td>69.5</td><td>78.3</td></tr>
<tr><td>Rsa1.0_00473.1.g14525.t1</td><td>gb|EOA16337.1| hypothetical protein CARUB_v10004487mg [Capsella rubella]</td><td>653</td><td>560</td><td>0</td><td>85.8</td><td>68.1</td><td>76.6</td><td>hypothetical protein CARUB_v10004487mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667</td><td>653</td><td>667</td><td>1.00E-166</td><td>102.1</td><td>47.2</td><td>64.9</td></tr>
<tr><td>Rsa1.0_00473.1.g14526.t1</td><td>gb|EOA17219.1| hypothetical protein CARUB_v10005494mg [Capsella rubella]</td><td>271</td><td>268</td><td>1.00E-133</td><td>98.9</td><td>85.6</td><td>94.1</td><td>hypothetical protein CARUB_v10005494mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G22920.1 | Symbols: ATNYE1, NYE1 | non-yellowing 1 | chr4:12016776-12017969 REVERSE LENGTH=268</td><td>271</td><td>268</td><td>1.00E-130</td><td>98.9</td><td>84.5</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00473.1.g14527.t1</td><td>ref|XP_002869798.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297315634|gb|EFH46057.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]</td><td>478</td><td>476</td><td>0</td><td>99.6</td><td>92.1</td><td>94.6</td><td>WD-40 repeat family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22910.1 | Symbols: FZR2, CCS52A1 | FIZZY-related 2 | chr4:12012743-12015663 FORWARD LENGTH=483</td><td>478</td><td>483</td><td>0</td><td>101.0</td><td>92.7</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00473.1.g14528.t1</td><td>gb|EOA16965.1| hypothetical protein CARUB_v10005193mg [Capsella rubella]</td><td>118</td><td>339</td><td>1.00E-29</td><td>287.3</td><td>60.2</td><td>72.0</td><td>hypothetical protein CARUB_v10005193mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G22900.1 | Symbols: | Protein of unknown function (DUF1191) | chr4:12010221-12011252 FORWARD LENGTH=343</td><td>118</td><td>343</td><td>7.00E-30</td><td>290.7</td><td>61.9</td><td>71.2</td></tr>
<tr><td>Rsa1.0_00473.1.g14529.t1</td><td>ref|XP_002869800.1| hypothetical protein ARALYDRAFT_492575 [Arabidopsis lyrata subsp. lyrata] gi|297315636|gb|EFH46059.1| hypothetical protein ARALYDRAFT_492575 [Arabidopsis lyrata subsp. lyrata]</td><td>317</td><td>320</td><td>1.00E-161</td><td>100.9</td><td>88.3</td><td>95.0</td><td>hypothetical protein ARALYDRAFT_492575</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22890.2 | Symbols: PGR5-LIKE A | PGR5-LIKE A | chr4:12007157-12009175 FORWARD LENGTH=324</td><td>317</td><td>324</td><td>1.00E-162</td><td>102.2</td><td>88.0</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00473.1.g14530.t1</td><td>gb|ABY89681.1| anthocyanidin synthase 1 protein [Brassica rapa subsp. oleifera] gi|166798273|gb|ABY89682.1| anthocyanidin synthase 2 protein [Brassica rapa subsp. oleifera] gi|288551983|gb|ADC53481.1| anthoncyanidin synthase [Brassica rapa var. purpuraria]</td><td>363</td><td>358</td><td>0</td><td>98.6</td><td>93.7</td><td>97.0</td><td>anthocyanidin synthase 1 protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G22880.2 | Symbols: LDOX, TDS4, TT18, ANS | leucoanthocyanidin dioxygenase | chr4:12004905-12006059 REVERSE LENGTH=356</td><td>363</td><td>356</td><td>0</td><td>98.1</td><td>88.7</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00473.1.g14531.t1</td><td>gb|EOA17107.1| hypothetical protein CARUB_v10005366mg [Capsella rubella]</td><td>301</td><td>298</td><td>1.00E-132</td><td>99.0</td><td>79.4</td><td>87.7</td><td>hypothetical protein CARUB_v10005366mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G22850.1 | Symbols: | SNARE associated Golgi protein family | chr4:11994194-11995941 FORWARD LENGTH=296</td><td>301</td><td>296</td><td>1.00E-126</td><td>98.3</td><td>78.4</td><td>87.0</td></tr>
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Rsa1.0_00473.1.g14532.t1	ref|XP_002867747.1| hypothetical protein ARALYDRAFT_914324 [Arabidopsis lyrata subsp. lyrata] gi|297313583|gb|EFH44006.1| hypothetical protein ARALYDRAFT_914324 [Arabidopsis lyrata subsp. lyrata]	191	190	9.00E-82	99.5	78.5	87.4	hypothetical protein ARALYDRAFT_914324	gbpln	Arabidopsis lyrata	AT4G22830.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2499 (InterPro:IPR019634); Has 319 Blast hits to 317 proteins in 103 species: Archae - 0; Bacteria - 147; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 108 (source: NCBI BLink). | chr4:11990296-11991325 REVERSE LENGTH=193	191	193	5.00E-79	101.0	76.4	86.9
Rsa1.0_00473.1.g14533.t1	ref|XP_002867758.1| hypothetical protein ARALYDRAFT_914352 [Arabidopsis lyrata subsp. lyrata] gi|297313594|gb|EFH44017.1| hypothetical protein ARALYDRAFT_914352 [Arabidopsis lyrata subsp. lyrata]	276	272	1.00E-128	98.6	87.0	92.0	hypothetical protein ARALYDRAFT_914352	gbpln	Arabidopsis lyrata	AT4G22600.1 | Symbols: | unknown protein; Has 26 Blast hits to 26 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11900211-11901032 REVERSE LENGTH=273	276	273	1.00E-129	98.9	85.9	91.7
Rsa1.0_00473.1.g14534.t1	ref|NP_193990.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|75209575|sp|Q9SUW0.1|TPPG_ARATH RecName: Full=Probable trehalose-phosphate phosphatase G; Short=AtTPPG; AltName: Full=Trehalose 6-phosphate phosphatase; AltName: Full=Trehalose-phosphate phosphatase 6 gi|3892714|emb|CAA22164.1| trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana] gi|7269105|emb|CAB79214.1| trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana] gi|62321206|dbj|BAD94370.1| trehalose-6-phosphate phosphatase - like protein [Arabidopsis thaliana] gi|222422885|dbj|BAH19429.1| AT4G22590 [Arabidopsis thaliana] gi|332659227|gb|AEE84627.1| probable trehalose-phosphate phosphatase G [Arabidopsis thaliana]	371	377	0	101.6	89.2	95.4	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT4G22590.1 | Symbols: TPPG | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr4:11893707-11895371 REVERSE LENGTH=377	371	377	0	101.6	89.2	95.4
Rsa1.0_00473.1.g14535.t1	ref|XP_002867760.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297313596|gb|EFH44019.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	440	435	0	98.9	90.7	93.4	exostosin family protein	gbpln	Arabidopsis lyrata	AT4G22580.1 | Symbols: | Exostosin family protein | chr4:11889382-11890689 REVERSE LENGTH=435	440	435	0	98.9	90.0	92.5
Rsa1.0_00473.1.g14536.t1	sp|Q3ECR3.3|FB305_ARATH RecName: Full=Putative F-box protein At1g53360	395	384	3.00E-77	97.2	44.6	59.7	RecName: Full=Putative F-box protein At1g53360	----	----	AT1G53360.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:19907517-19908548 FORWARD LENGTH=343	395	343	4.00E-77	86.8	43.0	57.2
Rsa1.0_00473.1.g14537.t1	#	#	#	#	#	#	#	-	----	----	AT4G12590.1 | Symbols: | Protein of unknown function DUF106, transmembrane | chr4:7451291-7452976 REVERSE LENGTH=246	119	246	4.00E-12	206.7	38.7	46.2
Rsa1.0_00473.1.g14538.t2	ref|NP_193986.1| Phosphatidic acid phosphatase (PAP2) family protein [Arabidopsis thaliana] gi|3892710|emb|CAA22160.1| putative protein [Arabidopsis thaliana] gi|7269101|emb|CAB79210.1| putative protein [Arabidopsis thaliana] gi|28973659|gb|AAO64149.1| unknown protein [Arabidopsis thaliana] gi|29824231|gb|AAP04076.1| unknown protein [Arabidopsis thaliana] gi|110737243|dbj|BAF00569.1| hypothetical protein [Arabidopsis thaliana] gi|332659223|gb|AEE84623.1| Phosphatidic acid phosphatase (PAP2) family protein [Arabidopsis thaliana]	246	213	1.00E-76	86.6	68.3	74.0	Phosphatidic acid phosphatase (PAP2) family protein	gbpln	Arabidopsis thaliana	AT4G22550.1 | Symbols: | Phosphatidic acid phosphatase (PAP2) family protein | chr4:11878255-11878896 REVERSE LENGTH=213	246	213	3.00E-79	86.6	68.3	74.0
Rsa1.0_00474.1.g14539.t1	gb|EOA27104.1| hypothetical protein CARUB_v10023202mg [Capsella rubella]	142	449	2.00E-54	316.2	70.4	78.2	hypothetical protein CARUB_v10023202mg	gbpln	Capsella rubella	AT2G43820.1 | Symbols: GT, UGT74F2, ATSAGT1, SGT1, SAGT1 | UDP-glucosyltransferase 74F2 | chr2:18152279-18153715 FORWARD LENGTH=449	142	449	1.00E-52	316.2	66.2	75.4

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<tr><td>Rsa1.0_00474.1.g14540.t1</td><td>ref|NP_181908.1| formin-like protein 2 [Arabidopsis thaliana] gi|75097595|sp|O22824.1|FH2_ARATH RecName: Full=Formin-like protein 2; Short=AtFH2; Short=AtFORMIN-2; Flags: Precursor gi|2281090|gb|AAB64026.1| unknown protein [Arabidopsis thaliana] gi|330255234|gb|AEC10328.1| formin-like protein 2 [Arabidopsis thaliana]</td><td>867</td><td>894</td><td>0</td><td>103.1</td><td>73.9</td><td>81.5</td><td>formin-like protein 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G43800.1 | Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr2:18145721-18148721 FORWARD LENGTH=894</td><td>867</td><td>894</td><td>0</td><td>103.1</td><td>73.9</td><td>81.5</td></tr>
<tr><td>Rsa1.0_00474.1.g14541.t1</td><td>gb|AAC63844.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1751</td><td>1231</td><td>0</td><td>70.3</td><td>38.0</td><td>48.4</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337-69884 REVERSE LENGTH=515</td><td>1751</td><td>515</td><td>1.00E-117</td><td>29.4</td><td>12.7</td><td>16.2</td></tr>
<tr><td>Rsa1.0_00474.1.g14542.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00474.1.g14543.t1</td><td>gb|ADM89008.1| MPK6 protein [Brassica napus]</td><td>391</td><td>394</td><td>0</td><td>100.8</td><td>95.7</td><td>98.2</td><td>MPK6 protein</td><td>gbpln</td><td>Brassica napus</td><td>AT2G43790.1 | Symbols: ATMPK6, MPK6, MAPK6, ATMAPK6 | MAP kinase 6 | chr2:18138477-18140693 FORWARD LENGTH=395</td><td>391</td><td>395</td><td>0</td><td>101.0</td><td>95.4</td><td>97.7</td></tr>
<tr><td>Rsa1.0_00474.1.g14544.t4</td><td>ref|XP_002881928.1| hypothetical protein ARALYDRAFT_346189 [Arabidopsis lyrata subsp. lyrata] gi|297327767|gb|EFH58187.1| hypothetical protein ARALYDRAFT_346189 [Arabidopsis lyrata subsp. lyrata]</td><td>219</td><td>179</td><td>8.00E-35</td><td>81.7</td><td>40.2</td><td>50.2</td><td>hypothetical protein ARALYDRAFT_346189</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G43730.1 | Symbols: | Mannose-binding lectin superfamily protein | chr2:18124821-18125669 REVERSE LENGTH=224</td><td>219</td><td>224</td><td>2.00E-26</td><td>102.3</td><td>28.8</td><td>38.4</td></tr>
<tr><td>Rsa1.0_00474.1.g14545.t1</td><td>ref|XP_002881925.1| hypothetical protein ARALYDRAFT_903775 [Arabidopsis lyrata subsp. lyrata] gi|297327764|gb|EFH58184.1| hypothetical protein ARALYDRAFT_903775 [Arabidopsis lyrata subsp. lyrata]</td><td>166</td><td>170</td><td>7.00E-50</td><td>102.4</td><td>69.3</td><td>78.3</td><td>hypothetical protein ARALYDRAFT_903775</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G43730.1 | Symbols: | Mannose-binding lectin superfamily protein | chr2:18124821-18125669 REVERSE LENGTH=224</td><td>166</td><td>224</td><td>3.00E-25</td><td>134.9</td><td>44.6</td><td>56.6</td></tr>
<tr><td>Rsa1.0_00474.1.g14546.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00474.1.g14547.t5</td><td>gb|EOA30377.1| hypothetical protein CARUB_v10013516mg [Capsella rubella]</td><td>448</td><td>499</td><td>0</td><td>111.4</td><td>74.6</td><td>83.7</td><td>hypothetical protein CARUB_v10013516mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G62750.1 | Symbols: BGLU8 | beta glucosidase 8 | chr3:23214375-23216900 FORWARD LENGTH=497</td><td>448</td><td>497</td><td>1.00E-161</td><td>110.9</td><td>62.5</td><td>76.6</td></tr>
<tr><td>Rsa1.0_00474.1.g14548.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00474.1.g14549.t1</td><td>gb|AAD19773.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1272</td><td>1335</td><td>0</td><td>105.0</td><td>54.3</td><td>68.7</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1272</td><td>1262</td><td>7.00E-53</td><td>99.2</td><td>11.9</td><td>18.6</td></tr>
<tr><td>Rsa1.0_00474.1.g14550.t1</td><td>gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]</td><td>786</td><td>657</td><td>0</td><td>83.6</td><td>50.6</td><td>64.1</td><td>T14P8.10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332</td><td>786</td><td>332</td><td>3.00E-85</td><td>42.2</td><td>18.3</td><td>24.9</td></tr>
<tr><td>Rsa1.0_00474.1.g14551.t1</td><td>gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]</td><td>571</td><td>1161</td><td>6.00E-92</td><td>203.3</td><td>32.6</td><td>45.2</td><td>F14N23.4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>571</td><td>626</td><td>4.00E-75</td><td>109.6</td><td>25.7</td><td>38.4</td></tr>
<tr><td>Rsa1.0_00474.1.g14552.t1</td><td>gb|EOA30377.1| hypothetical protein CARUB_v10013516mg [Capsella rubella]</td><td>339</td><td>499</td><td>1.00E-103</td><td>147.2</td><td>52.5</td><td>59.3</td><td>hypothetical protein CARUB_v10013516mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G62750.1 | Symbols: BGLU8 | beta glucosidase 8 | chr3:23214375-23216900 FORWARD LENGTH=497</td><td>339</td><td>497</td><td>7.00E-75</td><td>146.6</td><td>41.0</td><td>52.2</td></tr>
<tr><td>Rsa1.0_00475.1.g14553.t2</td><td>ref|NP_199242.1| protein kinase-like protein [Arabidopsis thaliana] gi|79329869|ref|NP_001032009.1| protein kinase-like protein [Arabidopsis thaliana] gi|79329882|ref|NP_001032010.1| protein kinase-like protein [Arabidopsis thaliana] gi|145334725|ref|NP_001078708.1| protein kinase-like protein [Arabidopsis thaliana] gi|10176884|dbj|BAB10114.1| cyclin-dependent protein kinase-like protein [Arabidopsis thaliana] gi|222424232|dbj|BAH20074.1| AT5G44290 [Arabidopsis thaliana] gi|332007704|gb|AED95087.1| protein kinase-like protein [Arabidopsis thaliana] gi|332007705|gb|AED95088.1| protein kinase-like protein [Arabidopsis thaliana] gi|332007706|gb|AED95089.1| protein kinase-like protein [Arabidopsis thaliana] gi|332007707|gb|AED95090.1| protein kinase-like protein [Arabidopsis thaliana]</td><td>621</td><td>644</td><td>0</td><td>103.7</td><td>85.8</td><td>91.3</td><td>protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G44290.4 | Symbols: | Protein kinase superfamily protein | chr5:17840750-17843190 REVERSE LENGTH=644</td><td>621</td><td>644</td><td>0</td><td>103.7</td><td>85.8</td><td>91.3</td></tr>
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Rsa1.0_00475.1.g14554.t1	ref|NP_179144.1| myosin heavy chain-related protein [Arabidopsis thaliana] gi|4544371|gb|AAD22282.1| hypothetical protein [Arabidopsis thaliana] gi|330251305|gb|AEC06399.1| myosin heavy chain-related protein [Arabidopsis thaliana]	293	957	1.00E-16	326.6	13.3	19.8	myosin heavy chain-related protein	gbpln	Arabidopsis thaliana	AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957	293	957	3.00E-19	326.6	13.3	19.8
Rsa1.0_00475.1.g14555.t1	ref|XP_002885378.1| tetraacyldisaccharide 4'-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331218|gb|EFH61637.1| tetraacyldisaccharide 4'-kinase family protein [Arabidopsis lyrata subsp. lyrata]	393	395	1.00E-180	100.5	79.4	86.5	tetraacyldisaccharide 4'-kinase family protein	gbpln	Arabidopsis lyrata	AT3G20480.1 | Symbols: | tetraacyldisaccharide 4'-kinase family protein | chr3:7151497-7153369 REVERSE LENGTH=395	393	395	1.00E-179	100.5	77.4	86.8
Rsa1.0_00475.1.g14556.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00475.1.g14557.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00475.1.g14558.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	822	1161	2.00E-88	141.2	31.0	48.2	F14N23.4	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	822	626	2.00E-35	76.2	11.4	18.6
Rsa1.0_00475.1.g14559.t1	gb|EOA14899.1| hypothetical protein CARUB_v10028228mg, partial [Capsella rubella]	56	370	7.00E-12	660.7	64.3	71.4	hypothetical protein CARUB_v10028228mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00475.1.g14560.t1	ref|XP_002863598.1| dormancy/auxin associated family protein [Arabidopsis lyrata subsp. lyrata] gi|297309433|gb|EFH39857.1| dormancy/auxin associated family protein [Arabidopsis lyrata subsp. lyrata]	120	114	1.00E-42	95.0	75.8	79.2	dormancy/auxin associated family protein	gbpln	Arabidopsis lyrata	AT5G44300.1 | Symbols: | Dormancy/auxin associated family protein | chr5:17845371-17846179 REVERSE LENGTH=114	120	114	1.00E-44	95.0	75.0	78.3
Rsa1.0_00475.1.g14561.t1	gb|AAS49101.1| At5g44310 [Arabidopsis thaliana] gi|51970006|dbj|BAD43695.1| late embryogenesis abundant protein-like [Arabidopsis thaliana] gi|51971018|dbj|BAD44201.1| late embryogenesis abundant protein-like [Arabidopsis thaliana]	248	342	5.00E-85	137.9	78.6	88.3	At5g44310	gbpln	Arabidopsis thaliana	AT5G44310.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr5:17847998-17848885 REVERSE LENGTH=295	248	295	9.00E-85	119.0	76.2	85.5
Rsa1.0_00475.1.g14562.t1	ref|NP_563864.1| S-phase kinase-associated protein 1 [Arabidopsis thaliana] gi|4914325|gb|AAD32873.1|AC005489_11 F14N23.11 [Arabidopsis thaliana] gi|27754385|gb|AAO22641.1| putative E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At18) [Arabidopsis thaliana] gi|28394095|gb|AAO42455.1| putative E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At18) [Arabidopsis thaliana] gi|332190436|gb|AEE28557.1| SKP1-like protein 18 [Arabidopsis thaliana]	174	183	2.00E-46	105.2	61.5	71.8	S-phase kinase-associated protein 1	gbpln	Arabidopsis thaliana	AT1G10230.1 | Symbols: ASK18, SK18 | SKP1-like 18 | chr1:3355600-3356151 FORWARD LENGTH=183	174	183	9.00E-49	105.2	61.5	71.8
Rsa1.0_00475.1.g14563.t1	ref|XP_002863588.1| tubulin beta-4 chain [Arabidopsis lyrata subsp. lyrata] gi|297309423|gb|EFH39847.1| tubulin beta-4 chain [Arabidopsis lyrata subsp. lyrata] gi|482550217|gb|EOA14411.1| hypothetical protein CARUB_v10027611mg [Capsella rubella]	452	444	0	98.2	94.5	94.7	tubulin beta-4 chain	gbpln	Arabidopsis lyrata	AT5G44340.1 | Symbols: TUB4 | tubulin beta chain 4 | chr5:17859442-17860994 REVERSE LENGTH=444	452	444	0	98.2	94.5	94.7
Rsa1.0_00475.1.g14564.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00475.1.g14565.t1	ref|XP_002865368.1| hypothetical protein ARALYDRAFT_494551 [Arabidopsis lyrata subsp. lyrata] gi|297311203|gb|EFH41627.1| hypothetical protein ARALYDRAFT_494551 [Arabidopsis lyrata subsp. lyrata]	342	333	6.00E-85	97.4	60.8	70.8	hypothetical protein ARALYDRAFT_494551	gbpln	Arabidopsis lyrata	AT5G44350.1 | Symbols: | ethylene-responsive nuclear protein -related | chr5:17864628-17865632 FORWARD LENGTH=334	342	334	8.00E-76	97.7	57.0	69.6
Rsa1.0_00475.1.g14566.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	150	1715	4.00E-12	1143.3	23.3	37.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	150	256	3.00E-11	170.7	20.7	32.7
Rsa1.0_00475.1.g14567.t1	gb|EOA32467.1| hypothetical protein CARUB_v10015744mg [Capsella rubella]	80	633	3.00E-13	791.3	50.0	57.5	hypothetical protein CARUB_v10015744mg	gbpln	Capsella rubella	AT3G01085.1 | Symbols: | Protein kinase superfamily protein | chr3:28060-30556 FORWARD LENGTH=629	80	629	2.00E-15	786.3	52.5	60.0

Rsa1.0_00475.1.g14568.t1	ref|XP_002863581.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297309416|gb|EFH39840.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	481	540	0	112.3	75.9	87.1	FAD-binding domain-containing protein	gbpln	Arabidopsis lyrata	AT5G44400.1 | Symbols: | FAD-binding Berberine family protein | chr5:17886365-17888071 REVERSE LENGTH=537	481	537	0	111.6	76.1	86.7
Rsa1.0_00475.1.g14569.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00475.1.g14570.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00475.1.g14571.t1	ref|NP_199253.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana] gi|10176895|dbj|BAB10125.1| berberine bridge enzyme [Arabidopsis thaliana] gi|18176302|gb|AAL60019.1| putative berberine bridge enzyme [Arabidopsis thaliana] gi|332007722|gb|AED95105.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana]	509	537	0	105.5	79.6	89.8	FAD-binding and BBE domain-containing protein	gbpln	Arabidopsis thaliana	AT5G44400.1 | Symbols: | FAD-binding Berberine family protein | chr5:17886365-17888071 REVERSE LENGTH=537	509	537	0	105.5	79.6	89.8
Rsa1.0_00476.1.g14572.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00476.1.g14573.t1	sp|Q02498.1|CRU1_RAPSA RecName: Full=Cruciferin PGCRURSE5; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin PGCRURSE5 alpha chain; Contains: RecName: Full=Cruciferin PGCRURSE5 beta chain; Flags: Precursor gi|21118|emb|CAA42478.1| cruciferin precursor [Raphanus sativus]	491	479	0	97.6	96.7	97.1	RecName: Full=Cruciferin PGCRURSE5; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin PGCRURSE5 alpha chain; Contains: RecName: Full=Cruciferin PGCRURSE5 beta chain; Flags: Precursor gi|21118|emb|CAA42478.1| cruciferin precursor	gbpln	Raphanus sativus	AT5G44120.3 | Symbols: CRA1, ATCRA1, CRU1 | RmlC-like cupins superfamily protein | chr5:17756460-17758246 REVERSE LENGTH=472	491	472	1.00E-153	96.1	55.8	71.5
Rsa1.0_00476.1.g14574.t1	gb|AAK07610.1|AF319771_2 prohibitin 1-like protein [Brassica napus]	290	290	1.00E-166	100.0	99.3	100.0	prohibitin 1-like protein	gbpln	Brassica napus	AT4G28510.1 | Symbols: ATPHB1, PHB1 | prohibitin 1 | chr4:14084970-14086372 REVERSE LENGTH=288	290	288	1.00E-145	99.3	93.1	97.2
Rsa1.0_00476.1.g14575.t1	ref|NP_194579.1| NAC domain containing protein 73 [Arabidopsis thaliana] gi|2842493|emb|CAA16890.1| predicted protein [Arabidopsis thaliana] gi|7269704|emb|CAB79652.1| predicted protein [Arabidopsis thaliana] gi|67633762|gb|AAY78805.1| no apical meristem family protein [Arabidopsis thaliana] gi|332660095|gb|AEE85495.1| NAC domain containing protein 73 [Arabidopsis thaliana]	306	305	2.33E-156	99.7	87.3	91.5	NAC domain containing protein 73	gbpln	Arabidopsis thaliana	AT4G28500.1 | Symbols: ANAC073, SND2, NAC073 | NAC domain containing protein 73 | chr4:14083014-14084266 FORWARD LENGTH=305	306	305	1.00E-148	99.7	87.3	91.5
Rsa1.0_00476.1.g14576.t1	ref|XP_002869498.1| hypothetical protein ARALYDRAFT_491919 [Arabidopsis lyrata subsp. lyrata] gi|297315334|gb|EFH45757.1| hypothetical protein ARALYDRAFT_491919 [Arabidopsis lyrata subsp. lyrata]	979	996	0	101.7	82.6	89.7	hypothetical protein ARALYDRAFT_491919	gbpln	Arabidopsis lyrata	AT4G28490.1 | Symbols: RLK5, HAE | Leucine-rich receptor-like protein kinase family protein | chr4:14077894-14080965 FORWARD LENGTH=999	979	999	0	102.0	81.8	89.4
Rsa1.0_00476.1.g14577.t1	ref|XP_002867447.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313283|gb|EFH43706.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	200	200	1.00E-92	100.0	81.0	89.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G46090.1 | Symbols: | Protein of unknown function (DUF679) | chr5:18693485-18694129 FORWARD LENGTH=214	200	214	5.00E-51	107.0	49.5	68.0
Rsa1.0_00476.1.g14578.t1	ref|XP_002869499.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata] gi|297315335|gb|EFH45758.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata]	363	344	1.00E-160	94.8	86.0	89.0	DNAJ heat shock family protein	gbpln	Arabidopsis lyrata	AT4G28480.1 | Symbols: | DNAJ heat shock family protein | chr4:14073310-14075091 FORWARD LENGTH=348	363	348	1.00E-160	95.9	84.8	87.9
Rsa1.0_00476.1.g14579.t1	ref|XP_002867448.1| 26S proteasome subunit RPN1b [Arabidopsis lyrata subsp. lyrata] gi|297313284|gb|EFH43707.1| 26S proteasome subunit RPN1b [Arabidopsis lyrata subsp. lyrata]	894	891	0	99.7	91.5	95.6	26S proteasome subunit RPN1b	gbpln	Arabidopsis lyrata	AT4G28470.1 | Symbols: RPN1B, ATRPN1B | 26S proteasome regulatory subunit S2 1B | chr4:14067082-14072357 REVERSE LENGTH=891	894	891	0	99.7	90.7	95.6

Rsa1.0_00476.1.g14580.t1	gb|ABK28261.1| unknown [Arabidopsis thaliana]	73	73	2.00E−24	100.0	82.2	87.7	unknown	gbpln	Arabidopsis thaliana	AT4G28460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; Has 8 Blast hits to 8 proteins in 3 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 8; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr4:14066083−14066301 FORWARD LENGTH=72	73	72	3.00E−27	98.6	82.2	87.7
Rsa1.0_00476.1.g14581.t1	gb|EOA17584.1| hypothetical protein CARUB_v10005945mg [Capsella rubella]	145	152	2.00E−68	104.8	86.2	90.3	hypothetical protein CARUB_v10005945mg	gbpln	Capsella rubella	AT4G28440.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr4:14060054−14060970 FORWARD LENGTH=153	145	153	1.00E−68	105.5	84.1	87.6
Rsa1.0_00476.1.g14582.t1	ref|XP_002869503.1| hypothetical protein ARALYDRAFT_491927 [Arabidopsis lyrata subsp. lyrata] gi|297315339|gb|EFH45762.1| hypothetical protein ARALYDRAFT_491927 [Arabidopsis lyrata subsp. lyrata]	461	463	1.00E−162	100.4	77.0	86.1	hypothetical protein ARALYDRAFT_491927	gbpln	Arabidopsis lyrata	AT4G28430.1 | Symbols: | Reticulon family protein | chr4:14057846−14059772 FORWARD LENGTH=457	461	457	1.00E−161	99.1	73.5	83.9
Rsa1.0_00476.1.g14583.t1	ref|XP_002869504.1| transaminase [Arabidopsis lyrata subsp. lyrata] gi|297315340|gb|EFH45763.1| transaminase [Arabidopsis lyrata subsp. lyrata]	448	449	0	100.2	83.3	92.9	transaminase	gbpln	Arabidopsis lyrata	AT4G28420.2 | Symbols: | Tyrosine transaminase family protein | chr4:14055687−14057409 FORWARD LENGTH=449	448	449	0	100.2	83.0	92.9
Rsa1.0_00476.1.g14584.t1	ref|XP_002869504.1| transaminase [Arabidopsis lyrata subsp. lyrata] gi|297315340|gb|EFH45763.1| transaminase [Arabidopsis lyrata subsp. lyrata]	431	449	0	104.2	80.5	89.1	transaminase	gbpln	Arabidopsis lyrata	AT4G28420.2 | Symbols: | Tyrosine transaminase family protein | chr4:14055687−14057409 FORWARD LENGTH=449	431	449	0	104.2	80.3	89.1
Rsa1.0_00476.1.g14585.t1	ref|NP_683422.3| bifunctional inhibitor/lipid−transfer protein/seed storage 2S albumin−like protein [Arabidopsis thaliana] gi|332194683|gb|AEE32804.1| bifunctional inhibitor/lipid−transfer protein/seed storage 2S albumin−like protein [Arabidopsis thaliana]	123	116	2.00E−47	94.3	71.5	82.9	bifunctional inhibitor/lipid−transfer protein/seed storage 2S albumin−like protein	gbpln	Arabidopsis thaliana	AT1G52415.1 | Symbols: | Bifunctional inhibitor/lipid−transfer protein/seed storage 2S albumin superfamily protein | chr1:19526166−19526686 FORWARD LENGTH=116	123	116	3.00E−50	94.3	71.5	82.9
Rsa1.0_00476.1.g14586.t1	ref|NP_567808.1| putative protein phosphatase 2C 58 [Arabidopsis thaliana] gi|75163673|sp|Q93YW5.1|P2C58_ARATH RecName: Full=Probable protein phosphatase 2C 58; Short=AtPP2C58 gi|16604585|gb|AAL24149.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|20258991|gb|AAM14211.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|332660081|gb|AEE85481.1| putative protein phosphatase 2C 58 [Arabidopsis thaliana]	316	283	1.00E−141	89.6	78.2	82.9	putative protein phosphatase 2C 58	gbpln	Arabidopsis thaliana	AT4G28400.1 | Symbols: | Protein phosphatase 2C family protein | chr4:14048499−14050118 FORWARD LENGTH=283	316	283	1.00E−144	89.6	78.2	82.9
Rsa1.0_00476.1.g14587.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	117	1486	2.00E−34	1270.1	55.6	73.5	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00476.1.g14588.t1	ref|XP_002867465.1| AtMYB41 [Arabidopsis lyrata subsp. lyrata] gi|297313301|gb|EFH43724.1| AtMYB41 [Arabidopsis lyrata subsp. lyrata]	289	283	1.00E−123	97.9	82.0	87.2	AtMYB41	gbpln	Arabidopsis lyrata	AT4G28110.1 | Symbols: AtMYB41, MYB41 | myb domain protein 41 | chr4:13968166−13969384 REVERSE LENGTH=282	289	282	1.00E−119	97.6	82.0	87.5
Rsa1.0_00476.1.g14589.t1	ref|XP_002867466.1| hypothetical protein ARALYDRAFT_491965 [Arabidopsis lyrata subsp. lyrata] gi|297313302|gb|EFH43725.1| hypothetical protein ARALYDRAFT_491965 [Arabidopsis lyrata subsp. lyrata]	264	304	1.00E−120	115.2	83.0	87.9	hypothetical protein ARALYDRAFT_491965	gbpln	Arabidopsis lyrata	AT4G28100.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: anchored to plasma membrane, anchored to membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G18050.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:13965300−13966697 REVERSE LENGTH=304	264	304	1.00E−121	115.2	82.6	88.6

Rsa1.0_00476.1.g14590.t1	gb|AAF37283.1|AF225704_1 RSH3 [Arabidopsis thaliana]	186	712	1.00E-11	382.8	18.8	20.4	RSH3	gbpln	Arabidopsis thaliana	AT1G54130.1 | Symbols: RSH3, AT-RSH3, ATRSH3 | RELA/SPOT homolog 3 | chr1:20211177-20213761 FORWARD LENGTH=715	186	715	4.00E-14	384.4	18.8	20.4
Rsa1.0_00476.1.g14591.t1	ref|NP_974629.1| Low temperature and salt responsive protein [Arabidopsis thaliana] gi|297799168|ref|XP_002867468.1| hypothetical protein ARALYDRAFT_328884 [Arabidopsis lyrata subsp. lyrata] gi|297313304|gb|EFH43727.1| hypothetical protein ARALYDRAFT_328884 [Arabidopsis lyrata subsp. lyrata] gi|332660039|gb|AEE85439.1| Low temperature and salt responsive protein [Arabidopsis thaliana] gi|482553953|gb|EOA18146.1| hypothetical protein CARUB_v10006610mg [Capsella rubella]	77	77	1.00E-35	100.0	96.1	100.0	Low temperature and salt responsive protein	gbpln	Arabidopsis lyrata	AT4G28088.1 | Symbols: | Low temperature and salt responsive protein family | chr4:13961244-13961560 REVERSE LENGTH=77	77	77	2.00E-38	100.0	96.1	100.0
Rsa1.0_00476.1.g14592.t1	ref|XP_002869520.1| hypothetical protein ARALYDRAFT_491969 [Arabidopsis lyrata subsp. lyrata] gi|297315356|gb|EFH45779.1| hypothetical protein ARALYDRAFT_491969 [Arabidopsis lyrata subsp. lyrata]	80	82	2.00E-20	102.5	63.8	71.3	hypothetical protein ARALYDRAFT_491969	gbpln	Arabidopsis lyrata	AT4G28085.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:13960054-13960308 FORWARD LENGTH=84	80	84	2.00E-21	105.0	61.3	70.0
Rsa1.0_00476.1.g14593.t1	ref|XP_002869520.1| hypothetical protein ARALYDRAFT_491969 [Arabidopsis lyrata subsp. lyrata] gi|297315356|gb|EFH45779.1| hypothetical protein ARALYDRAFT_491969 [Arabidopsis lyrata subsp. lyrata]	82	82	3.00E-20	100.0	62.2	74.4	hypothetical protein ARALYDRAFT_491969	gbpln	Arabidopsis lyrata	AT4G28085.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:13960054-13960308 FORWARD LENGTH=84	82	84	1.00E-22	102.4	61.0	73.2
Rsa1.0_00476.1.g14594.t2	ref|NP_001031737.1| AFG1-like protein [Arabidopsis thaliana] gi|53850477|gb|AAU95415.1| At4g28070 [Arabidopsis thaliana] gi|56790192|gb|AAW30013.1| At4g28070 [Arabidopsis thaliana] gi|332660035|gb|AEE85435.1| AFG1-like protein [Arabidopsis thaliana]	502	473	0	94.2	83.5	86.5	AFG1-like protein	gbpln	Arabidopsis thaliana	AT4G28070.2 | Symbols: | AFG1-like ATPase family protein | chr4:13946009-13948462 FORWARD LENGTH=473	502	473	0	94.2	83.5	86.5
Rsa1.0_00476.1.g14595.t1	gb|EOA17644.1| hypothetical protein CARUB_v10006010mg [Capsella rubella]	78	133	2.00E-40	170.5	100.0	100.0	hypothetical protein CARUB_v10006010mg	gbpln	Capsella rubella	AT4G28060.1 | Symbols: | Cytochrome c oxidase, subunit Vib family protein | chr4:13944018-13945602 REVERSE LENGTH=78	78	78	1.00E-41	100.0	98.7	100.0
Rsa1.0_00476.1.g14596.t1	ref|XP_002869522.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297315358|gb|EFH45781.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	573	359	1.00E-178	62.7	53.4	58.3	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT4G28040.5 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:13940881-13942201 FORWARD LENGTH=359	573	359	1.00E-179	62.7	53.2	57.9
Rsa1.0_00476.1.g14597.t1	ref|NP_001190856.1| uncharacterized protein [Arabidopsis thaliana] gi|332660023|gb|AEE85423.1| uncharacterized protein AT4G28025 [Arabidopsis thaliana]	131	148	2.00E-49	113.0	79.4	83.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G28025.2 | Symbols: | unknown protein. | chr4:13935836-13937367 REVERSE LENGTH=148	131	148	4.00E-52	113.0	79.4	83.2
Rsa1.0_00476.1.g14598.t1	ref|NP_194529.4| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332660018|gb|AEE85418.1| AAA-type ATPase family protein [Arabidopsis thaliana]	811	830	0	102.3	92.7	96.4	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT4G28000.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13925456-13929280 FORWARD LENGTH=830	811	830	0	102.3	92.7	96.4
Rsa1.0_00476.1.g14599.t1	ref|NP_567792.1| SLAC1 homologue 2 [Arabidopsis thaliana] gi|75167715|sp|Q9ASQ7.1|SLAH2_ARATH RecName: Full=S-type anion channel SLAH2; AltName: Full=SLAC1-homolog protein 2 gi|13605877|gb|AAK32924.1|AF367337_1 AT4g27970/T13J8_80 [Arabidopsis thaliana] gi|25090193|gb|AAN72249.1| At4g27970/T13J8_80 [Arabidopsis thaliana] gi|332660015|gb|AEE85415.1| SLAC1 homologue 2 [Arabidopsis thaliana]	513	519	0	101.2	83.6	91.6	SLAC1 homologue 2	gbpln	Arabidopsis thaliana	AT4G27970.1 | Symbols: SLAH2 | SLAC1 homologue 2 | chr4:13918290-13920122 REVERSE LENGTH=519	513	519	0	101.2	83.6	91.6
Rsa1.0_00476.1.g14600.t1	dbj|BAH57245.1| AT4G27860 [Arabidopsis thaliana]	448	352	2.00E-32	78.6	19.2	26.1	AT4G27860	gbpln	Arabidopsis thaliana	AT4G27860.1 | Symbols: | vacuolar iron transporter (VIT) family protein | chr4:13873808-13876240 FORWARD LENGTH=611	448	611	5.00E-35	136.4	18.5	25.4

Rsa1.0_00476.1.g14601.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	651	1274	0	195.7	55.0	71.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	651	575	8.00E-58	88.3	20.6	31.3
Rsa1.0_00476.1.g14602.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00476.1.g14603.t1	ref|XP_002867481.1| hypothetical protein ARALYDRAFT_492001 [Arabidopsis lyrata subsp. lyrata] gi|297313317|gb|EFH43740.1| hypothetical protein ARALYDRAFT_492001 [Arabidopsis lyrata subsp. lyrata]	109	195	3.00E-35	178.9	68.8	71.6	hypothetical protein ARALYDRAFT_492001	gbpln	Arabidopsis lyrata	AT4G27810.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF688 (InterPro:IPR007789); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G53030.1); Has 73 Blast hits to 66 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:13854641-13855671 REVERSE LENGTH=196	109	196	3.00E-32	179.8	67.9	71.6
Rsa1.0_00476.1.g14604.t1	gb|EOA18032.1| hypothetical protein CARUB_v10006475mg [Capsella rubella]	346	346	1.00E-174	100.0	86.7	93.1	hypothetical protein CARUB_v10006475mg	gbpln	Capsella rubella	AT4G27790.1 | Symbols: | Calcium-binding EF hand family protein | chr4:13850066-13851488 FORWARD LENGTH=345	346	345	1.00E-176	99.7	86.7	92.2
Rsa1.0_00476.1.g14605.t1	ref|NP_194507.1| acyl-CoA binding protein 2 [Arabidopsis thaliana] gi|75313883|sp|Q9STP8.1|ACBP2_ARATH RecName: Full=Acyl-CoA-binding domain-containing protein 2; Short=Acyl-CoA binding protein 2 gi|12039032|gb|AAG46056.1|AF178947_1 acyl-CoA binding protein ACBP2 [Arabidopsis thaliana] gi|13661742|gb|AAK38078.1|AF320561_1 putative membrane-bound acyl-CoA binding protein isoform 2 [Arabidopsis thaliana] gi|4972109|emb|CAB43966.1| putative acyl-CoA binding protein [Arabidopsis thaliana] gi|7269631|emb|CAB81427.1| putative acyl-CoA binding protein [Arabidopsis thaliana] gi|19699102|gb|AAL90917.1| AT4g27780/T27E11_20 [Arabidopsis thaliana] gi|21594802|gb|AAM66045.1| putative acyl-CoA binding protein [Arabidopsis thaliana] gi|21689607|gb|AAM67425.1| AT4g27780/T27E11_20 [Arabidopsis thaliana] gi|332659991|gb|AEE85391.1| acyl-CoA binding protein 2 [Arabidopsis thaliana]	358	354	1.00E-168	98.9	86.0	91.3	acyl-CoA binding protein 2	gbpln	Arabidopsis thaliana	AT4G27780.1 | Symbols: ACBP2 | acyl-CoA binding protein 2 | chr4:13847774-13849629 FORWARD LENGTH=354	358	354	1.00E-170	98.9	86.0	91.3
Rsa1.0_00476.1.g14606.t1	ref|XP_002869542.1| forever young oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297315378|gb|EFH45801.1| forever young oxidoreductase [Arabidopsis lyrata subsp. lyrata]	374	374	0	100.0	91.4	97.1	forever young oxidoreductase	gbpln	Arabidopsis lyrata	AT4G27760.1 | Symbols: FEY, FEY3 | NAD(P)-binding Rossmann-fold superfamily protein | chr4:13844151-13846563 FORWARD LENGTH=376	374	376	0	100.5	90.9	97.3
Rsa1.0_00476.1.g14607.t1	ref|NP_194505.2| impaired sucrose induction 1 protein [Arabidopsis thaliana] gi|28393094|gb|AAO41981.1| unknown protein [Arabidopsis thaliana] gi|28827484|gb|AAO50586.1| unknown protein [Arabidopsis thaliana] gi|55956219|emb|CAG26905.1| impaired sucrose induction 1 [Arabidopsis thaliana] gi|332659989|gb|AEE85389.1| impaired sucrose induction 1 protein [Arabidopsis thaliana]	305	305	1.00E-167	100.0	94.8	98.0	impaired sucrose induction 1 protein	gbpln	Arabidopsis thaliana	AT4G27750.1 | Symbols: ISI1 | binding | chr4:13841708-13843501 FORWARD LENGTH=305	305	305	1.00E-170	100.0	94.8	98.0
Rsa1.0_00476.1.g14608.t1	ref|XP_002869544.1| hypothetical protein ARALYDRAFT_328916 [Arabidopsis lyrata subsp. lyrata] gi|297315380|gb|EFH45803.1| hypothetical protein ARALYDRAFT_328916 [Arabidopsis lyrata subsp. lyrata]	107	148	2.00E-55	138.3	96.3	98.1	hypothetical protein ARALYDRAFT_328916	gbpln	Arabidopsis lyrata	AT4G27745.1 | Symbols: | Yippee family putative zinc-binding protein | chr4:13840530-13841279 FORWARD LENGTH=106	107	106	5.00E-57	99.1	94.4	98.1
Rsa1.0_00476.1.g14609.t1	ref|NP_194504.2| yippee-like protein [Arabidopsis thaliana] gi|122209321|sp|Q2V3E2.1|YIPL5_ARATH RecName: Full=Protein yippee-like At4g27740 gi|110738581|dbj|BAF01216.1| hypothetical protein [Arabidopsis thaliana] gi|332659987|gb|AEE85387.1| yippee-like protein [Arabidopsis thaliana]	105	105	3.00E-49	100.0	89.5	92.4	yippee-like protein	gbpln	Arabidopsis thaliana	AT4G27740.1 | Symbols: | Yippee family putative zinc-binding protein | chr4:13839148-13839616 FORWARD LENGTH=105	105	105	4.00E-52	100.0	89.5	92.4

Rsa1.0_00476.1.g14610.t1	ref|XP_002867483.1| ATOPT6 [Arabidopsis lyrata subsp. lyrata] gi|297313319|gb|EFH43742.1| ATOPT6 [Arabidopsis lyrata subsp. lyrata]	735	735	0	100.0	95.8	97.8	ATOPT6	gbpln	Arabidopsis lyrata	AT4G27730.1 | Symbols: ATOPT6, OPT6 | oligopeptide transporter 1 | chr4:13834024-13836468 REVERSE LENGTH=736	735	736	0	100.1	95.5	97.8
Rsa1.0_00476.1.g14611.t1	ref|NP_567786.1| major facilitator protein [Arabidopsis thaliana] gi|13272473|gb|AAK17175.1|AF325107_1 putative protein [Arabidopsis thaliana] gi|16930439|gb|AAL31905.1|AF419573_1 AT4g27720/T29A15_210 [Arabidopsis thaliana] gi|15912261|gb|AAL08264.1| AT4g27720/T29A15_210 [Arabidopsis thaliana] gi|21536852|gb|AAM61184.1| putative transporter [Arabidopsis thaliana] gi|27764934|gb|AAO23588.1| At4g27720/T29A15_210 [Arabidopsis thaliana] gi|332659985|gb|AEE85385.1| major facilitator protein [Arabidopsis thaliana]	460	460	0	100.0	92.6	97.2	major facilitator protein	gbpln	Arabidopsis thaliana	AT4G27720.1 | Symbols: | Major facilitator superfamily protein | chr4:13831203-13833521 FORWARD LENGTH=460	460	460	0	100.0	92.6	97.2
Rsa1.0_00476.1.g14612.t1	ref|XP_002869545.1| hypothetical protein ARALYDRAFT_913755 [Arabidopsis lyrata subsp. lyrata] gi|297315381|gb|EFH45804.1| hypothetical protein ARALYDRAFT_913755 [Arabidopsis lyrata subsp. lyrata]	460	460	0	100.0	94.1	98.0	hypothetical protein ARALYDRAFT_913755	gbpln	Arabidopsis lyrata	AT4G27720.1 | Symbols: | Major facilitator superfamily protein | chr4:13831203-13833521 FORWARD LENGTH=460	460	460	0	100.0	93.9	97.8
Rsa1.0_00476.1.g14613.t1	gb|EOA17385.1| hypothetical protein CARUB_v10005676mg [Capsella rubella]	230	226	1.00E-111	98.3	87.4	90.9	hypothetical protein CARUB_v10005676mg	gbpln	Capsella rubella	AT4G27700.1 | Symbols: | Rhodanese/Cell cycle control phosphatase superfamily protein | chr4:13826541-13827673 REVERSE LENGTH=224	230	224	1.00E-111	97.4	86.5	90.4
Rsa1.0_00476.1.g14614.t1	ref|XP_002869547.1| hypothetical protein ARALYDRAFT_913758 [Arabidopsis lyrata subsp. lyrata] gi|297315383|gb|EFH45806.1| hypothetical protein ARALYDRAFT_913758 [Arabidopsis lyrata subsp. lyrata]	304	303	1.00E-170	99.7	95.4	98.0	hypothetical protein ARALYDRAFT_913758	gbpln	Arabidopsis lyrata	AT4G27690.1 | Symbols: VPS26B | vacuolar protein sorting 26B | chr4:13824019-13826235 FORWARD LENGTH=303	304	303	1.00E-172	99.7	95.1	97.7
Rsa1.0_00476.1.g14615.t1	gb|EOA15537.1| hypothetical protein CARUB_v10004969mg [Capsella rubella]	383	398	0	103.9	91.1	93.7	hypothetical protein CARUB_v10004969mg	gbpln	Capsella rubella	AT4G27680.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13821263-13823083 FORWARD LENGTH=398	383	398	0	103.9	90.6	94.8
Rsa1.0_00476.1.g14616.t1	ref|XP_002867485.1| chloroplast small heat shock protein [Arabidopsis lyrata subsp. lyrata] gi|297313321|gb|EFH43744.1| chloroplast small heat shock protein [Arabidopsis lyrata subsp. lyrata]	229	226	6.00E-99	98.7	83.4	90.0	chloroplast small heat shock protein	gbpln	Arabidopsis lyrata	AT4G27670.1 | Symbols: HSP21 | heat shock protein 21 | chr4:13819048-13819895 REVERSE LENGTH=227	229	227	3.00E-94	99.1	82.1	87.8
Rsa1.0_00476.1.g14617.t1	ref|XP_002869549.1| hypothetical protein ARALYDRAFT_354029 [Arabidopsis lyrata subsp. lyrata] gi|297315385|gb|EFH45808.1| hypothetical protein ARALYDRAFT_354029 [Arabidopsis lyrata subsp. lyrata]	345	369	0	107.0	91.3	94.5	hypothetical protein ARALYDRAFT_354029	gbpln	Arabidopsis lyrata	AT5G54160.1 | Symbols: ATOMT1, OMT1 | O-methyltransferase 1 | chr5:21982075-21984167 FORWARD LENGTH=363	345	363	1.00E-148	105.2	71.3	83.8
Rsa1.0_00476.1.g14618.t1	ref|XP_002869540.1| hypothetical protein ARALYDRAFT_913747 [Arabidopsis lyrata subsp. lyrata] gi|297315376|gb|EFH45799.1| hypothetical protein ARALYDRAFT_913747 [Arabidopsis lyrata subsp. lyrata]	367	367	0	100.0	91.0	95.6	hypothetical protein ARALYDRAFT_913747	gbpln	Arabidopsis lyrata	AT5G54160.1 | Symbols: ATOMT1, OMT1 | O-methyltransferase 1 | chr5:21982075-21984167 FORWARD LENGTH=363	367	363	1.00E-167	98.9	73.6	88.3
Rsa1.0_00476.1.g14619.t1	ref|XP_002867486.1| hypothetical protein ARALYDRAFT_492019 [Arabidopsis lyrata subsp. lyrata] gi|297313322|gb|EFH43745.1| hypothetical protein ARALYDRAFT_492019 [Arabidopsis lyrata subsp. lyrata]	174	176	5.00E-53	101.1	62.1	71.8	hypothetical protein ARALYDRAFT_492019	gbpln	Arabidopsis lyrata	AT4G27660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54150.1); Has 115 Blast hits to 109 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 10; Fungi - 0; Plants - 100; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr4:13817249-13818027 REVERSE LENGTH=182	174	182	3.00E-55	104.6	54.0	62.1

Rsa1.0_00476.1.g14620.t1	ref|NP_567784.1| uncharacterized protein [Arabidopsis thaliana] gi|21537308|gb|AAM61649.1| unknown [Arabidopsis thaliana] gi|109134199|gb|ABG25097.1| At4g27657 [Arabidopsis thaliana] gi|332659977|gb|AEE85377.1| uncharacterized protein AT4G27657 [Arabidopsis thaliana]	63	62	2.00E-11	98.4	66.7	76.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13813124-13813312 FORWARD LENGTH=62	63	62	4.00E-14	98.4	66.7	76.2
Rsa1.0_00476.1.g14621.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00476.1.g14622.t1	ref|NP_567784.1| uncharacterized protein [Arabidopsis thaliana] gi|21537308|gb|AAM61649.1| unknown [Arabidopsis thaliana] gi|109134199|gb|ABG25097.1| At4g27657 [Arabidopsis thaliana] gi|332659977|gb|AEE85377.1| uncharacterized protein AT4G27657 [Arabidopsis thaliana]	62	62	2.00E-21	100.0	83.9	91.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13813124-13813312 FORWARD LENGTH=62	62	62	4.00E-24	100.0	83.9	91.9
Rsa1.0_00476.1.g14623.t1	ref|XP_002869553.1| hypothetical protein ARALYDRAFT_913767 [Arabidopsis lyrata subsp. lyrata] gi|297315389|gb|EFH45812.1| hypothetical protein ARALYDRAFT_913767 [Arabidopsis lyrata subsp. lyrata]	62	62	2.00E-23	100.0	80.6	93.5	hypothetical protein ARALYDRAFT_913767	gbpln	Arabidopsis lyrata	AT4G27657.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13813124-13813312 FORWARD LENGTH=62	62	62	5.00E-25	100.0	83.9	90.3
Rsa1.0_00476.1.g14624.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00476.1.g14625.t1	ref|XP_002867488.1| hypothetical protein ARALYDRAFT_492022 [Arabidopsis lyrata subsp. lyrata] gi|297313324|gb|EFH43747.1| hypothetical protein ARALYDRAFT_492022 [Arabidopsis lyrata subsp. lyrata]	223	378	1.00E-115	169.5	91.0	93.3	hypothetical protein ARALYDRAFT_492022	gbpln	Arabidopsis lyrata	AT4G27650.1 | Symbols: PEL1 | Eukaryotic release factor 1 (eRF1) family protein | chr4:13803459-13807556 REVERSE LENGTH=378	223	378	1.00E-118	169.5	90.6	93.3
Rsa1.0_00477.1.g14626.t1	gb|ABD64930.1| hypothetical protein 24.t00076 [Brassica oleracea]	523	407	3.00E-13	77.8	15.5	21.8	hypothetical protein 24.t00076	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00477.1.g14627.t1	gb|EOA28212.1| hypothetical protein CARUB_v10024401mg [Capsella rubella]	98	97	1.00E-22	99.0	70.4	78.6	hypothetical protein CARUB_v10024401mg	gbpln	Capsella rubella	AT2G27775.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: Tetratricopeptide repeat (TPR)-like superfamily protein (TAIR:AT2G27800.1); Has 21 Blast hits to 21 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:11842618-11843254 REVERSE LENGTH=100	98	100	3.00E-22	102.0	66.3	76.5
Rsa1.0_00477.1.g14628.t2	ref|XP_002880968.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata] gi|297326807|gb|EFH57227.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata]	666	715	0	107.4	89.0	92.5	xanthine/uracil permease family protein	gbpln	Arabidopsis lyrata	AT2G27810.1 | Symbols: ATNAT12, NAT12 | nucleobase-ascorbate transporter 12 | chr2:11852338-11855988 FORWARD LENGTH=709	666	709	0	106.5	87.7	92.0
Rsa1.0_00477.1.g14629.t1	ref|XP_002880966.1| hypothetical protein ARALYDRAFT_481721 [Arabidopsis lyrata subsp. lyrata] gi|297326805|gb|EFH57225.1| hypothetical protein ARALYDRAFT_481721 [Arabidopsis lyrata subsp. lyrata]	424	406	0	95.8	86.1	90.1	hypothetical protein ARALYDRAFT_481721	gbpln	Arabidopsis lyrata	AT2G27820.1 | Symbols: PD1, ADT3 | prephenate dehydratase 1 | chr2:11856808-11858082 FORWARD LENGTH=424	424	424	0	100.0	84.2	88.0

Rsa1.0_00477.1.g14630.t1	ref|NP_565661.2| histone deacetylase HDT4 [Arabidopsis thaliana] gi|73919944|sp|Q9M4T3.1|HDT4_ARATH RecName: Full=Histone deacetylase HDT4; AltName: Full=HD-tuins protein 4; AltName: Full=Histone deacetylase 2d gi|7804965|gb|AAF70198.1|AF255713_1 putative histone deacetylase HD2d [Arabidopsis thaliana] gi|29824372|gb|AAP04146.1| unknown protein [Arabidopsis thaliana] gi|30793819|gb|AAP40362.1| unknown protein [Arabidopsis thaliana] gi|110739095|dbj|BAF01464.1| putative histone deacetylase HD2d [Arabidopsis thaliana] gi|330252958|gb|AEC08052.1| histone deacetylase HDT4 [Arabidopsis thaliana]	204	203	8.00E-27	99.5	39.7	56.4	histone deacetylase HDT4	gbpln	Arabidopsis thaliana	AT2G27840.1 | Symbols: HDT4, HDA13, HDT04 | histone deacetylase-related / HD-related | chr2:11862085-11863707 FORWARD LENGTH=203	204	203	3.00E-29	99.5	39.7	56.4
Rsa1.0_00477.1.g14631.t1	ref|XP_002879132.1| UDP-D-apiose/UDP-D-xylose synthase 1 [Arabidopsis lyrata subsp. lyrata] gi|297324971|gb|EFH55391.1| UDP-D-apiose/UDP-D-xylose synthase 1 [Arabidopsis lyrata subsp. lyrata]	389	389	0	100.0	96.9	98.7	UDP-D-apiose/UDP-D-xylose synthase 1	gbpln	Arabidopsis lyrata	AT2G27860.1 | Symbols: AXS1 | UDP-D-apiose/UDP-D-xylose synthase 1 | chr2:11864684-11866843 REVERSE LENGTH=389	389	389	0	100.0	96.7	98.5
Rsa1.0_00477.1.g14632.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00477.1.g14633.t9	gb|EMJ06153.1| hypothetical protein PRUPE_ppa000504mg [Prunus persica]	1187	1124	0	94.7	61.0	72.5	hypothetical protein PRUPE_ppa000504mg	gbpln	Prunus persica	AT2G27900.2 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2451, C-terminal (InterPro:IPR019514), Vacuolar protein sorting-associated protein 54 (InterPro:IPR019515); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:11877654-11885238 FORWARD LENGTH=1124	1187	1124	0	94.7	50.0	53.2
Rsa1.0_00477.1.g14634.t1	ref|NP_565663.1| serine carboxypeptidase-like 51 [Arabidopsis thaliana] gi|125987784|sp|Q67Y83.2|SCP51_ARATH RecName: Full=Serine carboxypeptidase-like 51; Flags: Precursor gi|15724218|gb|AAL06502.1|AF412049_1 At2g27920/T1E2.16 [Arabidopsis thaliana] gi|20197951|gb|AAD21510.2| putative carboxypeptidase [Arabidopsis thaliana] gi|27764970|gb|AAO23606.1| At2g27920/T1E2.16 [Arabidopsis thaliana] gi|330252965|gb|AEC08059.1| serine carboxypeptidase-like 51 [Arabidopsis thaliana]	458	461	0	100.7	84.1	92.8	serine carboxypeptidase-like 51	gbpln	Arabidopsis thaliana	AT2G27920.1 | Symbols: SCPL51 | serine carboxypeptidase-like 51 | chr2:11885777-11889043 REVERSE LENGTH=461	458	461	0	100.7	84.1	92.8
Rsa1.0_00477.1.g14635.t1	ref|NP_180360.4| PLATZ transcription factor family protein [Arabidopsis thaliana] gi|330252967|gb|AEC08061.1| PLATZ transcription factor family protein [Arabidopsis thaliana]	224	189	3.00E-71	84.4	55.4	58.9	PLATZ transcription factor family protein	gbpln	Arabidopsis thaliana	AT2G27930.1 | Symbols: | PLATZ transcription factor family protein | chr2:11892369-11893488 FORWARD LENGTH=189	224	189	9.00E-74	84.4	55.4	58.9
Rsa1.0_00477.1.g14636.t1	ref|NP_180364.1| cyclin-dependent kinases regulatory subunit 2 [Arabidopsis thaliana] gi|297822483|ref|XP_002879124.1| cdk-subunit 2 [Arabidopsis lyrata subsp. lyrata] gi|75206284|sp|Q9SJJ5.1|CKS2_ARATH RecName: Full=Cyclin-dependent kinases regulatory subunit 2 gi|4510419|gb|AAD21505.1| putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana] gi|38566522|gb|AAR24151.1| At2g27970 [Arabidopsis thaliana] gi|40823612|gb|AAR92293.1| At2g27970 [Arabidopsis thaliana] gi|297324963|gb|EFH55383.1| cdk-subunit 2 [Arabidopsis lyrata subsp. lyrata] gi|330252971|gb|AEC08065.1| cyclin-dependent kinases regulatory subunit 2 [Arabidopsis thaliana]	84	83	1.00E-34	98.8	84.5	88.1	cyclin-dependent kinases regulatory subunit 2	gbpln	Arabidopsis lyrata	AT2G27970.1 | Symbols: CKS2 | CDK-subunit 2 | chr2:11912460-11913112 REVERSE LENGTH=83	84	83	2.00E-37	98.8	84.5	88.1

Rsa1.0_00477.1.g14637.t1	ref|NP_180365.6| acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein [Arabidopsis thaliana] gi|330252972|gb|AEC08066.1| acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein [Arabidopsis thaliana]	1104	1072	0	97.1	64.7	74.4	acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT2G27980.1 | Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain | chr2:11913950-11919741 REVERSE LENGTH=1072	1104	1072	0	97.1	64.7	74.4
Rsa1.0_00477.1.g14638.t2	gb|EOA39500.1| hypothetical protein CARUB_v10008106mg [Capsella rubella]	1258	1260	0	100.2	90.5	95.9	hypothetical protein CARUB_v10008106mg	gbpln	Capsella rubella	AT1G42470.1 | Symbols: | Patched family protein | chr1:15926987-15935128 FORWARD LENGTH=1272	1258	1272	0	101.1	83.5	87.8
Rsa1.0_00477.1.g14639.t1	sp|P21239.2|RUB1_BRANA RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor gi|289365|gb|AAA32979.1| 60-kDa chaperonin-60 alpha-polypeptide precursor, partial [Brassica napus]	185	546	3.00E-65	295.1	69.2	70.3	RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor gi|289365|gb|AAA32979.1| 60-kDa chaperonin-60 alpha-polypeptide precursor, partial	gbpln	Brassica napus	AT2G28000.1 | Symbols: CPN60A, CH-CPN60A, SLP | chaperonin-60alpha | chr2:11926603-11929184 FORWARD LENGTH=586	185	586	2.00E-56	316.8	58.9	62.2
Rsa1.0_00477.1.g14640.t1	gb|EOA28199.1| hypothetical protein CARUB_v10024391mg [Capsella rubella]	118	99	3.00E-18	83.9	38.1	44.9	hypothetical protein CARUB_v10024391mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00478.1.g14641.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00478.1.g14642.t1	ref|NP_683599.1| ABC transporter B family member 22 [Arabidopsis thaliana] gi|332643921|gb|AEE77442.1| ABC transporter B family member 22 [Arabidopsis thaliana]	1186	1221	0	103.0	80.8	90.1	ABC transporter B family member 22	gbpln	Arabidopsis thaliana	AT3G28415.1 | Symbols: | ABC transporter family protein | chr3:10647123-10651540 REVERSE LENGTH=1221	1186	1221	0	103.0	80.8	90.1
Rsa1.0_00478.1.g14643.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	416	1501	1.00E-123	360.8	49.3	62.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	416	1262	5.00E-72	303.4	31.7	47.4
Rsa1.0_00478.1.g14644.t1	dbj|BAB02858.1| multidrug resistance p-glycoprotein; ABC transporter-like protein [Arabidopsis thaliana]	1233	1262	0	102.4	81.4	90.6	multidrug resistance p-glycoprotein; ABC transporter-like protein	gbpln	Arabidopsis thaliana	AT3G28415.1 | Symbols: | ABC transporter family protein | chr3:10647123-10651540 REVERSE LENGTH=1221	1233	1221	0	99.0	80.8	89.9
Rsa1.0_00478.1.g14645.t1	gb|EOA14179.1| hypothetical protein CARUB_v10027329mg [Capsella rubella]	144	144	6.00E-65	100.0	93.8	97.2	hypothetical protein CARUB_v10027329mg	gbpln	Capsella rubella	AT5G51940.1 | Symbols: NRPB6A, NRPD6A, NRPE6A | RNA polymerase Rpb6 | chr5:21104679-21105796 FORWARD LENGTH=144	144	144	7.00E-67	100.0	93.8	96.5
Rsa1.0_00478.1.g14646.t1	ref|XP_002877098.1| hypothetical protein ARALYDRAFT_905093 [Arabidopsis lyrata subsp. lyrata] gi|297322936|gb|EFH53357.1| hypothetical protein ARALYDRAFT_905093 [Arabidopsis lyrata subsp. lyrata]	353	364	0	103.1	89.8	94.3	hypothetical protein ARALYDRAFT_905093	gbpln	Arabidopsis lyrata	AT3G28340.1 | Symbols: GATL10 | galacturonosyltransferase-like 10 | chr3:10589396-10590493 REVERSE LENGTH=365	353	365	0	103.4	89.5	94.6
Rsa1.0_00478.1.g14647.t1	dbj|BAJ34116.1| unnamed protein product [Thellungiella halophila]	323	323	1.00E-162	100.0	88.2	93.8	unnamed protein product	----	----	AT3G28200.1 | Symbols: | Peroxidase superfamily protein | chr3:10518082-10519032 FORWARD LENGTH=316	323	316	1.00E-160	97.8	81.4	88.5
Rsa1.0_00478.1.g14648.t1	gb|EOA23588.1| hypothetical protein CARUB_v10016783mg [Capsella rubella]	631	673	0	106.7	94.3	97.6	hypothetical protein CARUB_v10016783mg	gbpln	Capsella rubella	AT3G28180.1 | Symbols: ATCSLC04, CSLC04, ATCSLC4, CSLC4 | Cellulose-synthase-like C4 | chr3:10506110-10509067 FORWARD LENGTH=673	631	673	0	106.7	93.2	97.3
Rsa1.0_00478.1.g14649.t1	ref|NP_566831.1| EamA domain-containing protein [Arabidopsis thaliana] gi|75166353|sp|Q94JU2.1|WTR18_ARATH RecName: Full=WAT1-related protein At3g28050 gi|13937165|gb|AAK50076.1|AF372936_1 AT3g28050/MMG15_6 [Arabidopsis thaliana] gi|22137010|gb|AAM91350.1| At3g28050/MMG15_6 [Arabidopsis thaliana] gi|332643874|gb|AEE77395.1| nodulin MtN21-like transporter UMAMIT41 [Arabidopsis thaliana]	368	367	0	99.7	91.3	95.9	EamA domain-containing protein	gbpln	Arabidopsis thaliana	AT3G28050.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:10442984-10445216 FORWARD LENGTH=367	368	367	0	99.7	91.3	95.9
Rsa1.0_00478.1.g14650.t1	gb|AFW72878.1| hypothetical protein ZEAMMB73_112131 [Zea mays]	276	282	5.00E-17	102.2	22.1	24.3	hypothetical protein ZEAMMB73_112131	gbenv/gbpln	Zea mays	AT5G46630.1 | Symbols: | Clathrin adaptor complexes medium subunit family protein | chr5:18920580-18923252 FORWARD LENGTH=438	276	438	2.00E-19	158.7	22.1	24.6

Rsa1.0_00478.1.g14651.t1	ref|NP_189443.2| probably inactive leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|75335370|sp|Q9LRT1.1|Y3804_ARATH RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040; Flags: Precursor gi|11994124|dbj|BAB01126.1| receptor protein kinase [Arabidopsis thaliana] gi|224589581|gb|ACN59324.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332643873|gb|AEE77394.1| probably inactive leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	1102	1016	0	92.2	75.9	81.5	probably inactive leucine-rich repeat receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT3G28040.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr3:10435139-10438268 FORWARD LENGTH=1016	1102	1016	0	92.2	75.9	81.5
Rsa1.0_00478.1.g14652.t1	ref|NP_189436.2| exonuclease-like protein [Arabidopsis thaliana] gi|193211503|gb|ACF16171.1| At3g27970 [Arabidopsis thaliana] gi|225898687|dbj|BAH30474.1| hypothetical protein [Arabidopsis thaliana] gi|332643867|gb|AEE77388.1| exonuclease-like protein [Arabidopsis thaliana]	357	357	0	100.0	93.8	96.9	exonuclease-like protein	gbpln	Arabidopsis thaliana	AT3G27970.1 | Symbols: | Exonuclease family protein | chr3:10389609-10391544 FORWARD LENGTH=357	357	357	0	100.0	93.8	96.9
Rsa1.0_00479.1.g14653.t1	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1683	910	0	54.1	27.7	36.6	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1683	626	1.00E-109	37.2	11.9	17.6
Rsa1.0_00479.1.g14654.t1	ref|XP_002879560.1| hypothetical protein ARALYDRAFT_902668 [Arabidopsis lyrata subsp. lyrata] gi|297325399|gb|EFH55819.1| hypothetical protein ARALYDRAFT_902668 [Arabidopsis lyrata subsp. lyrata]	154	417	6.00E-31	270.8	54.5	63.6	hypothetical protein ARALYDRAFT_902668	gbpln	Arabidopsis lyrata	AT1G31650.1 | Symbols: ATROPGEF14, ROPGEF14 | RHO guanyl-nucleotide exchange factor 14 | chr1:11326474-11329767 REVERSE LENGTH=576	154	576	3.00E-29	374.0	48.7	59.1
Rsa1.0_00479.1.g14655.t1	ref|XP_002879561.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297325400|gb|EFH55820.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	200	447	8.00E-90	223.5	83.0	90.0	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT2G35615.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:14959391-14960734 FORWARD LENGTH=447	200	447	1.00E-91	223.5	82.5	89.5
Rsa1.0_00479.1.g14656.t1	ref|NP_181105.2| LRR receptor-like serine/threonine-protein kinase FEI 2 [Arabidopsis thaliana] gi|334184705|ref|NP_001189684.1| LRR receptor-like serine/threonine-protein kinase FEI 2 [Arabidopsis thaliana] gi|263419018|sp|C0LGL9.1|FEI2_ARATH RecName: Full=LRR receptor-like serine/threonine-protein kinase FEI 2; Flags: Precursor gi|224589541|gb|ACN59304.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|330254037|gb|AEC09131.1| LRR receptor-like serine/threonine-protein kinase FEI 2 [Arabidopsis thaliana] gi|330254038|gb|AEC09132.1| LRR receptor-like serine/threonine-protein kinase FEI 2 [Arabidopsis thaliana]	595	589	0	99.0	86.2	91.3	LRR receptor-like serine/threonine-protein kinase FEI 2	gbpln	Arabidopsis thaliana	AT2G35620.2 | Symbols: FEI2 | Leucine-rich repeat protein kinase family protein | chr2:14961187-14964640 REVERSE LENGTH=589	595	589	0	99.0	86.2	91.3
Rsa1.0_00479.1.g14657.t1	gb|EOA29247.1| hypothetical protein CARUB_v10025521mg [Capsella rubella]	1472	1981	0	134.6	92.3	95.9	hypothetical protein CARUB_v10025521mg	gbpln	Capsella rubella	AT2G35630.1 | Symbols: MOR1, GEM1 | ARM repeat superfamily protein | chr2:14966828-14980361 FORWARD LENGTH=1978	1472	1978	0	134.4	92.1	95.9
Rsa1.0_00479.1.g14658.t1	gb|EOA28062.1| hypothetical protein CARUB_v10024242mg [Capsella rubella]	155	154	3.00E-80	99.4	98.1	98.1	hypothetical protein CARUB_v10024242mg	gbpln	Capsella rubella	AT1G31340.1 | Symbols: RUB1, NEDD8, ATRUB1 | related to ubiquitin 1 | chr1:11218076-11219417 REVERSE LENGTH=156	155	156	1.00E-82	100.6	98.1	98.1
Rsa1.0_00479.1.g14659.t1	ref|XP_002862622.1| hypothetical protein ARALYDRAFT_333274 [Arabidopsis lyrata subsp. lyrata] gi|297308259|gb|EFH38880.1| hypothetical protein ARALYDRAFT_333274 [Arabidopsis lyrata subsp. lyrata]	364	366	1.00E-179	100.5	82.1	90.4	hypothetical protein ARALYDRAFT_333274	gbpln	Arabidopsis lyrata	AT2G30900.1 | Symbols: TBL43 | TRICHOME BIREFRINGENCE-LIKE 43 | chr2:13150481-13152417 FORWARD LENGTH=368	364	368	1.00E-179	101.1	81.9	89.8
Rsa1.0_00479.1.g14660.t1	gb|AFI23585.1| vernalization 2 [Brassica oleracea var. italica] gi|384597743|gb|AFI23588.1| vernalization 2 [Brassica oleracea var. italica]	476	425	1.00E-59	89.3	30.9	47.5	vernalization 2	gbpln	Brassica oleracea	AT4G16845.1 | Symbols: VRN2 | VEFS-Box of polycomb protein | chr4:9476708-9479725 FORWARD LENGTH=440	476	440	3.00E-54	92.4	29.0	43.3

Rsa1.0_00479.1.g14661.t1	gb|EOA27449.1| hypothetical protein CARUB_v10023586mg [Capsella rubella]	102	335	8.00E-14	328.4	61.8	64.7	hypothetical protein CARUB_v10023586mg	gbpln	Capsella rubella	AT2G35680.1 | Symbols: | Phosphotyrosine protein phosphatases superfamily protein | chr2:14997004-14998590 REVERSE LENGTH=337	102	337	2.00E-12	330.4	39.2	42.2
Rsa1.0_00479.1.g14662.t1	gb|AAW28084.1| transcription factor DREBIII-1 [Brassica napus]	205	204	5.00E-84	99.5	88.8	92.7	transcription factor DREBIII-1	gbpln	Brassica napus	AT2G35700.1 | Symbols: ATERF38, ERF38 | ERF family protein 38 | chr2:15005205-15005789 FORWARD LENGTH=194	205	194	4.00E-70	94.6	70.7	77.6
Rsa1.0_00479.1.g14663.t1	gb|EOA26908.1| hypothetical protein CARUB_v10022998mg [Capsella rubella]	494	524	0	106.1	92.7	95.3	hypothetical protein CARUB_v10022998mg	gbpln	Capsella rubella	AT2G35710.1 | Symbols: | Nucleotide-diphospho-sugar transferases superfamily protein | chr2:15010925-15014070 REVERSE LENGTH=497	494	497	0	100.6	91.3	94.3
Rsa1.0_00479.1.g14664.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00479.1.g14665.t1	gb|EOA26688.1| hypothetical protein CARUB_v10022772mg [Capsella rubella]	661	679	0	102.7	85.9	91.4	hypothetical protein CARUB_v10022772mg	gbpln	Capsella rubella	AT2G35940.3 | Symbols: BLH1 | BEL1-like homeodomain 1 | chr2:15089171-15091699 REVERSE LENGTH=680	661	680	0	102.9	85.5	90.9
Rsa1.0_00480.1.g14666.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00480.1.g14667.t1	gb|AAK38472.1| putative oleosin [Brassica oleracea] gi|38196017|gb|AAR13697.1| pollen coat oleosin-glycine rich protein [Brassica oleracea]	295	353	4.00E-82	119.7	76.3	79.7	putative oleosin	gbpln	Brassica oleracea	AT5G07540.1 | Symbols: GRP16, ATGRP16, ATGRP-6 | glycine-rich protein 16 | chr5:2386212-2387206 REVERSE LENGTH=244	295	244	2.00E-29	82.7	26.4	31.2
Rsa1.0_00480.1.g14668.t1	sp|Q42626.1|OLNB3_BRANA RecName: Full=Oleosin-B3; Contains: RecName: Full=Pollen coat protein B3 gi|904228|gb|AAA70400.1| STA 41-2 [Brassica napus]	375	424	2.00E-82	113.1	67.5	71.2	RecName: Full=Oleosin-B3; Contains: RecName: Full=Pollen coat protein B3 gi|904228|gb|AAA70400.1| STA 41-2	gbpln	Brassica napus	AT5G07530.2 | Symbols: GRP17, ATGRP17, ATGRP-7 | glycine rich protein 17 | chr5:2382629-2384495 REVERSE LENGTH=512	375	512	1.00E-23	136.5	12.5	16.5
Rsa1.0_00480.1.g14669.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	251	390	2.00E-39	155.4	32.7	42.6	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	251	289	5.00E-29	115.1	30.3	47.8
Rsa1.0_00480.1.g14670.t1	gb|AAK38474.1| putative oleosin [Brassica oleracea] gi|38196015|gb|AAR13695.1| pollen coat oleosin-glycine rich protein [Brassica oleracea]	192	186	2.00E-50	96.9	72.4	76.6	putative oleosin	gbpln	Brassica oleracea	AT5G07530.2 | Symbols: GRP17, ATGRP17, ATGRP-7 | glycine rich protein 17 | chr5:2382629-2384495 REVERSE LENGTH=512	192	512	2.00E-25	266.7	30.2	37.0
Rsa1.0_00480.1.g14671.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	770	1274	0	165.5	50.6	67.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	770	575	4.00E-76	74.7	23.1	37.0
Rsa1.0_00480.1.g14672.t1	gb|AAK38475.1| putative oleosin [Brassica oleracea] gi|38196014|gb|AAR13694.1| pollen coat oleosin-glycine rich protein [Brassica oleracea]	179	171	1.00E-45	95.5	72.1	76.5	putative oleosin	gbpln	Brassica oleracea	AT5G07520.1 | Symbols: GRP18, ATGRP18, ATGRP-8 | glycine-rich protein 18 | chr5:2380208-2381230 REVERSE LENGTH=228	179	228	8.00E-26	127.4	44.7	55.3
Rsa1.0_00480.1.g14673.t1	gb|AAR13693.1| zinc finger transcription factor [Brassica oleracea]	246	246	1.00E-140	100.0	96.3	98.4	zinc finger transcription factor	gbpln	Brassica oleracea	AT5G07500.1 | Symbols: PEI1 | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr5:2372716-2373453 FORWARD LENGTH=245	246	245	1.00E-124	99.6	85.0	91.1
Rsa1.0_00480.1.g14674.t1	gb|AAR13691.1| Cu2+ plastocyanin-like protein [Brassica oleracea]	196	195	5.00E-90	99.5	84.7	90.3	Cu2+ plastocyanin-like protein	gbpln	Brassica oleracea	AT5G07475.1 | Symbols: | Cupredoxin superfamily protein | chr5:2364827-2365536 REVERSE LENGTH=192	196	192	2.00E-79	98.0	73.5	81.1
Rsa1.0_00480.1.g14675.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	660	1274	1.00E-145	193.0	42.6	58.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	660	575	2.00E-63	87.1	24.2	40.3
Rsa1.0_00480.1.g14676.t1	gb|AAR13690.1| peptide methionine sulfoxide reductase [Brassica oleracea]	202	202	1.00E-110	100.0	93.6	96.5	peptide methionine sulfoxide reductase	gbpln	Brassica oleracea	AT5G07470.1 | Symbols: PMSR3, ATMSRA3 | peptidemethionine sulfoxide reductase 3 | chr5:2362760-2364286 REVERSE LENGTH=202	202	202	1.00E-104	100.0	86.6	91.1
Rsa1.0_00480.1.g14677.t1	gb|AAR13689.1| peptide methionine sulfoxide reductase [Brassica oleracea]	204	204	1.00E-113	100.0	95.6	97.1	peptide methionine sulfoxide reductase	gbpln	Brassica oleracea	AT5G07460.1 | Symbols: PMSR2, ATMSRA2 | peptidemethionine sulfoxide reductase 2 | chr5:2360844-2361885 REVERSE LENGTH=218	204	218	1.00E-102	106.9	84.8	89.7
Rsa1.0_00480.1.g14678.t1	ref|XP_002873308.1| CYCP4_3 [Arabidopsis lyrata subsp. lyrata] gi|297319145|gb|EFH49567.1| CYCP4_3 [Arabidopsis lyrata subsp. lyrata]	216	220	1.00E-102	101.9	83.3	90.7	CYCP4_3	gbpln	Arabidopsis lyrata	AT5G07450.1 | Symbols: CYCP4;3 | cyclin p4;3 | chr5:2358418-2359253 REVERSE LENGTH=216	216	216	1.00E-101	100.0	81.0	89.8

Rsa1.0_00480.1.g14679.t1	ref|NP_196361.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|186521018|ref|NP_001119183.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|297806777|ref|XP_002871272.1| hypothetical protein ARALYDRAFT_487575 [Arabidopsis lyrata subsp. lyrata] gi|12229806|sp|Q38946.1|DHE2_ARATH RecName: Full=Glutamate dehydrogenase 2; Short=GDH 2 gi|1336084|gb|AAB01222.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|7576182|emb|CAB87933.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|297317109|gb|EFH47531.1| hypothetical protein ARALYDRAFT_487575 [Arabidopsis lyrata subsp. lyrata] gi|332003774|gb|AED91157.1| glutamate dehydrogenase 2 [Arabidopsis thaliana] gi|332003775|gb|AED91158.1| glutamate dehydrogenase 2 [Arabidopsis thaliana]	411	411	0	100.0	97.1	99.5	glutamate dehydrogenase 2	gbpln	Arabidopsis lyrata	AT5G07440.2 | Symbols: GDH2 | glutamate dehydrogenase 2 | chr5:2356153-2358012 FORWARD LENGTH=411	411	411	0	100.0	97.1	99.5
Rsa1.0_00480.1.g14680.t1	gb|EOA19726.1| hypothetical protein CARUB_v10003776mg [Capsella rubella]	354	362	1.00E-180	102.3	83.1	91.8	hypothetical protein CARUB_v10003776mg	gbpln	Capsella rubella	AT5G07420.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:2349547-2351366 FORWARD LENGTH=361	354	361	1.00E-177	102.0	80.5	89.3
Rsa1.0_00480.1.g14681.t1	gb|EOA22708.1| hypothetical protein CARUB_v10003415mg [Capsella rubella]	247	361	1.00E-127	146.2	86.2	91.5	hypothetical protein CARUB_v10003415mg	gbpln	Capsella rubella	AT1G69940.1 | Symbols: ATPPME1, PPME1 | Pectin lyase-like superfamily protein | chr1:26343549-26344971 REVERSE LENGTH=361	247	361	1.00E-128	146.2	86.2	91.1
Rsa1.0_00480.1.g14682.t1	gb|AAC39475.1| respiratory burst oxidase protein A [Arabidopsis thaliana]	906	902	0	99.6	81.9	88.7	respiratory burst oxidase protein A	gbpln	Arabidopsis thaliana	AT5G07390.1 | Symbols: ATRBOHA, RBOHA | respiratory burst oxidase homolog A | chr5:2336063-2339728 REVERSE LENGTH=902	906	902	0	99.6	82.0	88.7
Rsa1.0_00480.1.g14683.t3	ref|NP_001031848.1| uncharacterized protein [Arabidopsis thaliana] gi|79508236|ref|NP_196355.2| uncharacterized protein [Arabidopsis thaliana] gi|55978831|gb|AAV68877.1| hypothetical protein AT5G07380 [Arabidopsis thaliana] gi|55978833|gb|AAV68878.1| hypothetical protein AT5G07380 [Arabidopsis thaliana] gi|61742743|gb|AAX55192.1| hypothetical protein At5g07380 [Arabidopsis thaliana] gi|332003765|gb|AED91148.1| uncharacterized protein AT5G07380 [Arabidopsis thaliana] gi|332003766|gb|AED91149.1| uncharacterized protein AT5G07380 [Arabidopsis thaliana]	637	641	0	100.6	76.3	85.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G07380.2 | Symbols: | unknown protein; Has 84 Blast hits to 81 proteins in 31 species: Archae - 0; Bacteria - 0; Metazoa - 42; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:2332527-2335736 FORWARD LENGTH=641	637	641	0	100.6	76.3	85.1
Rsa1.0_00480.1.g14684.t1	gb|AAM64773.1| putative inositol hexaphosphate kinase [Arabidopsis thaliana]	284	286	1.00E-143	100.7	86.3	91.9	putative inositol hexaphosphate kinase	gbpln	Arabidopsis thaliana	AT5G07370.4 | Symbols: IPK2a, ATIPK2A | inositol polyphosphate kinase 2 alpha | chr5:2331251-2332111 FORWARD LENGTH=286	284	286	2.33E-156	100.7	85.9	91.9
Rsa1.0_00480.1.g14685.t7	ref|XP_002873306.1| amidase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319143|gb|EFH49565.1| amidase family protein [Arabidopsis lyrata subsp. lyrata]	723	622	0	86.0	73.6	77.3	amidase family protein	gbpln	Arabidopsis lyrata	AT5G07360.1 | Symbols: | Amidase family protein | chr5:2326925-2330011 REVERSE LENGTH=659	723	659	0	91.1	74.0	77.3
Rsa1.0_00480.1.g14686.t1	ref|NP_196350.1| uncharacterized protein [Arabidopsis thaliana] gi|7576171|emb|CAB87922.1| putative protein [Arabidopsis thaliana] gi|26452141|dbj|BAC43159.1| unknown protein [Arabidopsis thaliana] gi|34098921|gb|AAQ56843.1| At5g07330 [Arabidopsis thaliana] gi|332003754|gb|AED91137.1| uncharacterized protein AT5G07330 [Arabidopsis thaliana]	167	165	6.00E-71	98.8	83.2	89.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G07330.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G63060.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:2316064-2316641 FORWARD LENGTH=165	167	165	2.00E-73	98.8	83.2	89.2
Rsa1.0_00480.1.g14687.t1	gb|EOA20534.1| hypothetical protein CARUB_v10000847mg [Capsella rubella]	475	481	0	101.3	93.9	96.0	hypothetical protein CARUB_v10000847mg	gbpln	Capsella rubella	AT5G07320.1 | Symbols: | Mitochondrial substrate carrier family protein | chr5:2310248-2312082 FORWARD LENGTH=479	475	479	0	100.8	92.0	95.4
Rsa1.0_00481.1.g14688.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00481.1.g14689.t2	ref|XP_002865011.1| hypothetical protein ARALYDRAFT_496871 [Arabidopsis lyrata subsp. lyrata] gi|297310846|gb|EFH41270.1| hypothetical protein ARALYDRAFT_496871 [Arabidopsis lyrata subsp. lyrata]	300	403	5.00E-68	134.3	40.3	43.3	hypothetical protein ARALYDRAFT_496871	gbpln	Arabidopsis lyrata	AT5G67290.1 | Symbols: | FAD-dependent oxidoreductase family protein | chr5:26848419-26849755 REVERSE LENGTH=406	300	406	8.00E-70	135.3	40.3	43.0
Rsa1.0_00481.1.g14690.t1	ref|XP_002866710.1| AtMYB44/AtMYBr1 [Arabidopsis lyrata subsp. lyrata] gi|297312545|gb|EFH42969.1| AtMYB44/AtMYBr1 [Arabidopsis lyrata subsp. lyrata]	298	305	1.00E-141	102.3	86.9	89.3	AtMYB44/AtMYBr1	gbpln	Arabidopsis lyrata	AT5G67300.1 | Symbols: ATMYBR1, ATMYB44, MYBR1, MYB44 | myb domain protein r1 | chr5:26854109-26855026 FORWARD LENGTH=305	298	305	1.00E-138	102.3	87.2	89.6
Rsa1.0_00481.1.g14691.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00481.1.g14692.t1	ref|NP_569048.1| subtilisin-like protease [Arabidopsis thaliana] gi|75099392|sp|O65351.1|SUBL_ARATH RecName: Full=Subtilisin-like protease; AltName: Full=Cucumisin-like serine protease; Flags: Precursor gi|13430746|gb|AAK25995.1|AF360285_1 putative subtilisin serine protease ARA12 [Arabidopsis thaliana] gi|3176874|gb|AAC18851.1| cucumisin-like serine protease [Arabidopsis thaliana] gi|9758435|dbj|BAB09021.1| cucumisin-like serine protease [Arabidopsis thaliana] gi|23296832|gb|AAN13181.1| putative subtilisin serine protease ARA12 [Arabidopsis thaliana] gi|332010949|gb|AED98332.1| subtilisin-like protease [Arabidopsis thaliana]	754	757	0	100.4	87.4	92.7	subtilisin-like protease	gbpln	Arabidopsis thaliana	AT5G67360.1 | Symbols: ARA12 | Subtilase family protein | chr5:26872192-26874465 REVERSE LENGTH=757	754	757	0	100.4	87.4	92.7
Rsa1.0_00481.1.g14693.t1	ref|XP_002865007.1| hypothetical protein ARALYDRAFT_496863 [Arabidopsis lyrata subsp. lyrata] gi|297310842|gb|EFH41266.1| hypothetical protein ARALYDRAFT_496863 [Arabidopsis lyrata subsp. lyrata]	322	326	1.00E-152	101.2	88.5	95.0	hypothetical protein ARALYDRAFT_496863	gbpln	Arabidopsis lyrata	AT5G67370.1 | Symbols: | Protein of unknown function (DUF1230) | chr5:26877667-26879465 REVERSE LENGTH=327	322	327	1.00E-154	101.6	87.9	95.3
Rsa1.0_00481.1.g14694.t1	gb|EOA15160.1| hypothetical protein CARUB_v10028548mg [Capsella rubella]	411	411	0	100.0	83.0	87.8	hypothetical protein CARUB_v10028548mg	gbpln	Capsella rubella	AT5G67380.1 | Symbols: CKA1, ATCKA1 | casein kinase alpha 1 | chr5:26881156-26883383 REVERSE LENGTH=409	411	409	0	99.5	82.0	85.6
Rsa1.0_00481.1.g14695.t1	dbj|BAJ34215.1| unnamed protein product [Thellungiella halophila]	600	603	0	100.5	90.5	94.2	unnamed protein product	----	----	AT5G67385.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr5:26884754-26887083 FORWARD LENGTH=604	600	604	0	100.7	90.2	94.0
Rsa1.0_00481.1.g14696.t1	ref|XP_002865005.1| hypothetical protein ARALYDRAFT_358820 [Arabidopsis lyrata subsp. lyrata] gi|297310840|gb|EFH41264.1| hypothetical protein ARALYDRAFT_358820 [Arabidopsis lyrata subsp. lyrata]	175	174	1.00E-55	99.4	82.3	90.3	hypothetical protein ARALYDRAFT_358820	gbpln	Arabidopsis lyrata	AT5G67390.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: Plant protein of unknown function (DUF863) (TAIR:AT1G69360.1); Has 186 Blast hits to 186 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 170; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink). | chr5:26887883-26888512 REVERSE LENGTH=176	175	176	1.00E-57	100.6	80.6	90.3
Rsa1.0_00481.1.g14697.t1	ref|XP_002876006.1| LOB domain protein 38 [Arabidopsis lyrata subsp. lyrata] gi|297321844|gb|EFH52265.1| LOB domain protein 38 [Arabidopsis lyrata subsp. lyrata]	239	236	3.00E-94	98.7	78.7	84.9	LOB domain protein 38	gbpln	Arabidopsis lyrata	AT5G67420.1 | Symbols: LBD37, ASL39 | LOB domain-containing protein 37 | chr5:26904576-26905415 REVERSE LENGTH=250	239	250	6.00E-96	104.6	83.7	90.4
Rsa1.0_00481.1.g14698.t1	gb|AAD25622.1|AC005287_24 Hypothetical protein [Arabidopsis thaliana]	264	224	7.00E-17	84.8	20.8	34.1	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	264	384	1.00E-15	145.5	17.4	29.2
Rsa1.0_00481.1.g14699.t1	gb|AAB53260.1| zinc-finger protein-1 [Brassica rapa subsp. oleifera]	239	235	4.00E-95	98.3	84.9	88.7	zinc-finger protein-1	gbpln	Brassica rapa	AT5G67450.1 | Symbols: AZF1, ZF1 | zinc-finger protein 1 | chr5:26919142-26919879 REVERSE LENGTH=245	239	245	2.00E-83	102.5	76.2	82.8
Rsa1.0_00481.1.g14700.t1	ref|XP_002865000.1| glycosyl hydrolase family protein 17 [Arabidopsis lyrata subsp. lyrata] gi|297310835|gb|EFH41259.1| glycosyl hydrolase family protein 17 [Arabidopsis lyrata subsp. lyrata]	415	382	1.00E-163	92.0	75.2	80.7	glycosyl hydrolase family protein 17	gbpln	Arabidopsis lyrata	AT5G67460.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:26921984-26923274 REVERSE LENGTH=380	415	380	1.00E-160	91.6	72.5	78.6
Rsa1.0_00481.1.g14701.t1	gb|EOA12871.1| hypothetical protein CARUB_v10025843mg [Capsella rubella]	950	922	0	97.1	73.7	78.6	hypothetical protein CARUB_v10025843mg	gbpln	Capsella rubella	AT5G67470.1 | Symbols: ATFH6, FH6 | formin homolog 6 | chr5:26926835-26930212 FORWARD LENGTH=899	950	899	0	94.6	71.9	76.8

Rsa1.0_00481.1.g14702.t1	gb|EOA17180.1| hypothetical protein CARUB_v10005451mg [Capsella rubella]	293	278	3.00E-73	94.9	50.2	65.2	hypothetical protein CARUB_v10005451mg	gbpln	Capsella rubella	AT4G17700.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17990.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9854322-9855227 FORWARD LENGTH=164	293	164	1.00E-42	56.0	29.0	36.5
Rsa1.0_00481.1.g14703.t1	ref|NP_201556.2| uncharacterized protein [Arabidopsis thaliana] gi|91807108|gb|ABE66281.1| unknown [Arabidopsis thaliana] gi|332010976|gb|AED98359.1| uncharacterized protein AT5G67550 [Arabidopsis thaliana]	575	509	0	88.5	59.5	67.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G67550.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; EXPRESSED DURING: 4 anthesis; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G71110.1); Has 161 Blast hits to 154 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 161; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:26946908-26949112 REVERSE LENGTH=509	575	509	0	88.5	59.5	67.0
Rsa1.0_00482.1.g14704.t1	ref|NP_974731.1| 8-amino-7-oxononanoate synthase [Arabidopsis thaliana] gi|67847131|gb|AAY82238.1| 7-keto-8-amino pelargonic acid synthase [Arabidopsis thaliana] gi|332003382|gb|AED90765.1| 8-amino-7-oxononanoate synthase [Arabidopsis thaliana]	472	476	0	100.8	89.4	94.9	8-amino-7-oxononanoate synthase	gbpln	Arabidopsis thaliana	AT5G04620.2 | Symbols: ATBIOF, BIOF | biotin F | chr5:1327292-1329934 FORWARD LENGTH=476	472	476	0	100.8	89.4	94.9
Rsa1.0_00482.1.g14705.t1	ref|XP_002873158.1| hypothetical protein ARALYDRAFT_487242 [Arabidopsis lyrata subsp. lyrata] gi|297318995|gb|EFH49417.1| hypothetical protein ARALYDRAFT_487242 [Arabidopsis lyrata subsp. lyrata]	417	435	1.00E-166	104.3	75.5	84.9	hypothetical protein ARALYDRAFT_487242	gbpln	Arabidopsis lyrata	AT5G04610.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:1325612-1326916 REVERSE LENGTH=434	417	434	1.00E-164	104.1	74.1	83.9
Rsa1.0_00482.1.g14706.t1	gb|EOA21520.1| hypothetical protein CARUB_v10001924mg [Capsella rubella]	244	220	1.00E-103	90.2	82.4	87.3	hypothetical protein CARUB_v10001924mg	gbpln	Capsella rubella	AT5G04600.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:1323700-1325486 FORWARD LENGTH=222	244	222	3.00E-99	91.0	71.3	79.9
Rsa1.0_00482.1.g14707.t1	ref|XP_002871103.1| hypothetical protein ARALYDRAFT_908346 [Arabidopsis lyrata subsp. lyrata] gi|297316940|gb|EFH47362.1| hypothetical protein ARALYDRAFT_908346 [Arabidopsis lyrata subsp. lyrata]	645	642	0	99.5	95.0	96.9	hypothetical protein ARALYDRAFT_908346	gbpln	Arabidopsis lyrata	AT5G04590.1 | Symbols: SIR | sulfite reductase | chr5:1319404-1322298 FORWARD LENGTH=642	645	642	0	99.5	94.7	96.6
Rsa1.0_00482.1.g14708.t1	ref|NP_196074.2| Myotubularin-like phosphatases II-like protein [Arabidopsis thaliana] gi|332003375|gb|AED90758.1| Myotubularin-like phosphatases II-like protein [Arabidopsis thaliana]	840	833	0	99.2	76.9	85.1	Myotubularin-like phosphatases II-like protein	gbpln	Arabidopsis thaliana	AT5G04540.1 | Symbols: | Myotubularin-like phosphatases II superfamily | chr5:1296826-1302299 REVERSE LENGTH=833	840	833	0	99.2	76.9	85.1
Rsa1.0_00482.1.g14709.t1	ref|XP_002873154.1| beta-ketoacyl-CoA synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297318991|gb|EFH49413.1| beta-ketoacyl-CoA synthase family protein [Arabidopsis lyrata subsp. lyrata]	463	464	0	100.2	87.5	92.4	beta-ketoacyl-CoA synthase family protein	gbpln	Arabidopsis lyrata	AT5G04530.1 | Symbols: KCS19 | 3-ketoacyl-CoA synthase 19 | chr5:1292222-1293616 REVERSE LENGTH=464	463	464	0	100.2	86.8	92.2
Rsa1.0_00482.1.g14710.t1	gb|EOA20487.1| hypothetical protein CARUB_v10000799mg [Capsella rubella]	485	495	0	102.1	94.4	96.7	hypothetical protein CARUB_v10000799mg	gbpln	Capsella rubella	AT5G04510.1 | Symbols: PDK1, ATPDK1 | 3'-phosphoinositide-dependent protein kinase 1 | chr5:1287235-1289681 FORWARD LENGTH=491	485	491	0	101.2	93.6	96.7
Rsa1.0_00482.1.g14711.t1	gb|AFB74217.1| phytol kinase [Brassica napus]	299	307	1.00E-140	102.7	83.6	91.6	phytol kinase	gbpln	Brassica napus	AT5G04490.1 | Symbols: VTE5 | vitamin E pathway gene 5 | chr5:1279867-1281587 FORWARD LENGTH=304	299	304	1.00E-133	101.7	79.3	88.3
Rsa1.0_00482.1.g14712.t1	ref|NP_568137.1| UDP-glycosyltransferase family protein [Arabidopsis thaliana] gi|15450503|gb|AAK96544.1| AT5g04480/T32M21_80 [Arabidopsis thaliana] gi|24111433|gb|AAN46867.1| At5g04480/T32M21_80 [Arabidopsis thaliana] gi|332003367|gb|AED90750.1| UDP-glycosyltransferase family protein [Arabidopsis thaliana]	1035	1050	0	101.4	89.5	95.2	UDP-glycosyltransferase family protein	gbpln	Arabidopsis thaliana	AT5G04480.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1271886-1277793 REVERSE LENGTH=1050	1035	1050	0	101.4	89.5	95.2

Rsa1.0_00482.1.g14713.t1	ref|NP_196067.1| cyclin-dependent protein kinase inhibitor [Arabidopsis thaliana] gi|75181205|sp|Q9LZ78.1|SIM_ARATH RecName: Full=Cyclin-dependent protein kinase inhibitor SIM; AltName: Full=Protein SIAMESE gi|7406451|emb|CAB85553.1| putative protein [Arabidopsis thaliana] gi|21537413|gb|AAM61754.1| unknown [Arabidopsis thaliana] gi|32815859|gb|AAP88332.1| At5g04470 [Arabidopsis thaliana] gi|332003366|gb|AED90749.1| cyclin-dependent protein kinase inhibitor SIM [Arabidopsis thaliana]	134	127	2.00E-29	94.8	71.6	77.6	cyclin-dependent protein kinase inhibitor	gbpln	Arabidopsis thaliana	AT5G04470.1 | Symbols: SIM | cyclin-dependent protein kinase inhibitors | chr5:1266893-1267276 REVERSE LENGTH=127	134	127	4.00E-32	94.8	71.6	77.6
Rsa1.0_00482.1.g14714.t1	ref|XP_002871095.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297316932|gb|EFH47354.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	786	860	0	109.4	80.5	87.4	protein binding protein	gbpln	Arabidopsis lyrata	AT5G04460.3 | Symbols: | RING/U-box superfamily protein | chr5:1260009-1263695 FORWARD LENGTH=863	786	863	0	109.8	80.5	87.8
Rsa1.0_00482.1.g14715.t1	ref|XP_002871094.1| hypothetical protein ARALYDRAFT_487226 [Arabidopsis lyrata subsp. lyrata] gi|297316931|gb|EFH47353.1| hypothetical protein ARALYDRAFT_487226 [Arabidopsis lyrata subsp. lyrata]	253	252	1.00E-124	99.6	91.7	95.3	hypothetical protein ARALYDRAFT_487226	gbpln	Arabidopsis lyrata	AT5G04440.1 | Symbols: | Protein of unknown function (DUF1997) | chr5:1254957-1256624 FORWARD LENGTH=255	253	255	1.00E-121	100.8	89.7	94.1
Rsa1.0_00482.1.g14716.t1	ref|NP_850764.1| binding to TOMV RNA 1L (long form) protein [Arabidopsis thaliana] gi|332003360|gb|AED90743.1| binding to TOMV RNA 1L (long form) protein [Arabidopsis thaliana]	339	334	1.00E-176	98.5	90.9	94.1	binding to TOMV RNA 1L (long form) protein	gbpln	Arabidopsis thaliana	AT5G04430.2 | Symbols: BTR1, BTR1L | binding to TOMV RNA 1L (long form) | chr5:1250602-1253523 REVERSE LENGTH=334	339	334	1.00E-179	98.5	90.9	94.1
Rsa1.0_00482.1.g14717.t1	ref|XP_002871092.1| hypothetical protein ARALYDRAFT_908325 [Arabidopsis lyrata subsp. lyrata] gi|297316929|gb|EFH47351.1| hypothetical protein ARALYDRAFT_908325 [Arabidopsis lyrata subsp. lyrata]	568	568	0	100.0	83.6	90.0	hypothetical protein ARALYDRAFT_908325	gbpln	Arabidopsis lyrata	AT5G04410.1 | Symbols: NAC2, anac078 | NAC domain containing protein 2 | chr5:1243980-1246416 FORWARD LENGTH=567	568	567	0	99.8	81.9	88.7
Rsa1.0_00482.1.g14718.t1	ref|NP_196059.1| C2H2-type zinc finger protein [Arabidopsis thaliana] gi|28392998|gb|AAO41934.1| putative zinc finger transcription factor [Arabidopsis thaliana] gi|28827440|gb|AAO50564.1| putative zinc finger transcription factor [Arabidopsis thaliana] gi|332003354|gb|AED90737.1| C2H2-type zinc finger protein [Arabidopsis thaliana]	349	362	1.00E-147	103.7	80.2	86.8	C2H2-type zinc finger protein	gbpln	Arabidopsis thaliana	AT5G04390.1 | Symbols: | C2H2-type zinc finger family protein | chr5:1239166-1240254 FORWARD LENGTH=362	349	362	1.00E-149	103.7	80.2	86.8
Rsa1.0_00482.1.g14719.t1	ref|NP_196058.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|332003352|gb|AED90735.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	393	385	1.00E-174	98.0	76.3	84.2	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G04380.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:1234883-1236317 FORWARD LENGTH=385	393	385	1.00E-177	98.0	76.3	84.2
Rsa1.0_00483.1.g14720.t2	ref|XP_002871957.1| hypothetical protein ARALYDRAFT_488986 [Arabidopsis lyrata subsp. lyrata] gi|297317794|gb|EFH48216.1| hypothetical protein ARALYDRAFT_488986 [Arabidopsis lyrata subsp. lyrata]	205	165	5.00E-77	80.5	69.8	72.7	hypothetical protein ARALYDRAFT_488986	gbpln	Arabidopsis lyrata	AT5G20810.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:7044791-7045555 FORWARD LENGTH=165	205	165	5.00E-77	80.5	67.8	71.7
Rsa1.0_00483.1.g14721.t1	ref|NP_197582.1| SAUR-like auxin-responsive protein family [Arabidopsis thaliana] gi|89111850|gb|ABD60697.1| At5g20820 [Arabidopsis thaliana] gi|332005510|gb|AED92893.1| SAUR-like auxin-responsive protein family [Arabidopsis thaliana]	127	127	9.00E-61	100.0	89.0	93.7	SAUR-like auxin-responsive protein family	gbpln	Arabidopsis thaliana	AT5G20820.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:7046911-7047294 REVERSE LENGTH=127	127	127	2.00E-63	100.0	89.0	93.7
Rsa1.0_00483.1.g14722.t1	ref|XP_002874016.1| hypothetical protein ARALYDRAFT_910122 [Arabidopsis lyrata subsp. lyrata] gi|297319853|gb|EFH50275.1| hypothetical protein ARALYDRAFT_910122 [Arabidopsis lyrata subsp. lyrata]	805	808	0	100.4	94.0	97.1	hypothetical protein ARALYDRAFT_910122	gbpln	Arabidopsis lyrata	AT5G20830.2 | Symbols: SUS1, ASUS1, atsus1 | sucrose synthase 1 | chr5:7050599-7054032 REVERSE LENGTH=808	805	808	0	100.4	93.4	97.1
Rsa1.0_00483.1.g14723.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00483.1.g14724.t1</td><td>gb|EOA22650.1| hypothetical protein CARUB_v10003342mg [Capsella rubella]</td><td>837</td><td>828</td><td>0</td><td>98.9</td><td>84.3</td><td>91.0</td><td>hypothetical protein CARUB_v10003342mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G20840.1 | Symbols: | Phosphoinositide phosphatase family protein | chr5:7061638-7068572 REVERSE LENGTH=831</td><td>837</td><td>831</td><td>0</td><td>99.3</td><td>83.8</td><td>89.7</td></tr>
<tr><td>Rsa1.0_00483.1.g14725.t1</td><td>gb|ACQ44224.1| unknown [Arabis alpina]</td><td>145</td><td>291</td><td>2.00E-33</td><td>200.7</td><td>50.3</td><td>66.2</td><td>unknown</td><td>gbpln</td><td>Arabis alpina</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00483.1.g14726.t1</td><td>gb|EOA21011.1| hypothetical protein CARUB_v10001345mg [Capsella rubella]</td><td>388</td><td>342</td><td>0</td><td>88.1</td><td>85.6</td><td>87.1</td><td>hypothetical protein CARUB_v10001345mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G20850.1 | Symbols: ATRAD51, RAD51 | RAS associated with diabetes protein 51 | chr5:7070758-7072860 REVERSE LENGTH=342</td><td>388</td><td>342</td><td>0</td><td>88.1</td><td>85.3</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00483.1.g14727.t1</td><td>ref|NP_001146854.1| RING zinc finger protein-like [Zea mays] gi|195604260|gb|ACG23960.1| RING zinc finger protein-like [Zea mays]</td><td>172</td><td>173</td><td>6.00E-82</td><td>100.6</td><td>95.3</td><td>96.5</td><td>RING zinc finger protein-like</td><td>gbenv/gbpln</td><td>Zea mays</td><td>AT5G20885.1 | Symbols: | RING/U-box superfamily protein | chr5:7084133-7084663 REVERSE LENGTH=176</td><td>172</td><td>176</td><td>3.00E-80</td><td>102.3</td><td>87.2</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00483.1.g14728.t1</td><td>gb|EOA20386.1| hypothetical protein CARUB_v10000699mg [Capsella rubella]</td><td>527</td><td>527</td><td>0</td><td>100.0</td><td>96.2</td><td>98.9</td><td>hypothetical protein CARUB_v10000699mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G20890.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr5:7087020-7089906 REVERSE LENGTH=527</td><td>527</td><td>527</td><td>0</td><td>100.0</td><td>95.8</td><td>98.7</td></tr>
<tr><td>Rsa1.0_00483.1.g14729.t1</td><td>dbj|BAJ34102.1| unnamed protein product [Thellungiella halophila]</td><td>199</td><td>214</td><td>6.00E-75</td><td>107.5</td><td>79.4</td><td>83.4</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G20900.1 | Symbols: JAZ12, TIFY3B | jasmonate-zim-domain protein 12 | chr5:7090883-7092201 FORWARD LENGTH=187</td><td>199</td><td>187</td><td>1.00E-66</td><td>94.0</td><td>66.8</td><td>75.9</td></tr>
<tr><td>Rsa1.0_00483.1.g14730.t1</td><td>gb|EOA21161.1| hypothetical protein CARUB_v10001508mg, partial [Capsella rubella]</td><td>275</td><td>314</td><td>1.00E-126</td><td>114.2</td><td>86.9</td><td>91.6</td><td>hypothetical protein CARUB_v10001508mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G20920.2 | Symbols: EIF2 BETA | eukaryotic translation initiation factor 2 beta subunit | chr5:7094994-7096661 REVERSE LENGTH=267</td><td>275</td><td>267</td><td>1.00E-126</td><td>97.1</td><td>85.1</td><td>90.2</td></tr>
<tr><td>Rsa1.0_00483.1.g14731.t1</td><td>gb|EOA25553.1| hypothetical protein CARUB_v10018898mg [Capsella rubella]</td><td>329</td><td>316</td><td>1.00E-108</td><td>96.0</td><td>65.3</td><td>75.7</td><td>hypothetical protein CARUB_v10018898mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G25290.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr5:8778592-8779785 FORWARD LENGTH=397</td><td>329</td><td>397</td><td>4.00E-65</td><td>120.7</td><td>45.3</td><td>64.1</td></tr>
<tr><td>Rsa1.0_00483.1.g14732.t4</td><td>ref|XP_002889622.1| hypothetical protein ARALYDRAFT_470709 [Arabidopsis lyrata subsp. lyrata] gi|297335464|gb|EFH65881.1| hypothetical protein ARALYDRAFT_470709 [Arabidopsis lyrata subsp. lyrata]</td><td>153</td><td>365</td><td>9.00E-32</td><td>238.6</td><td>47.7</td><td>51.0</td><td>hypothetical protein ARALYDRAFT_470709</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06870.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr1:2108832-2110642 FORWARD LENGTH=367</td><td>153</td><td>367</td><td>4.00E-33</td><td>239.9</td><td>46.4</td><td>50.3</td></tr>
<tr><td>Rsa1.0_00483.1.g14733.t1</td><td>gb|ABK28572.1| unknown [Arabidopsis thaliana]</td><td>410</td><td>415</td><td>1.00E-102</td><td>101.2</td><td>52.2</td><td>67.3</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G26010.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:9511901-9513145 FORWARD LENGTH=414</td><td>410</td><td>414</td><td>1.00E-105</td><td>101.0</td><td>52.2</td><td>67.3</td></tr>
<tr><td>Rsa1.0_00483.1.g14734.t1</td><td>ref|NP_176872.1| uncharacterized protein [Arabidopsis thaliana] gi|9755450|gb|AAF98211.1|AC007152_7 Hypothetical protein [Arabidopsis thaliana] gi|332196462|gb|AEE34583.1| uncharacterized protein AT1G67020 [Arabidopsis thaliana]</td><td>851</td><td>659</td><td>3.00E-12</td><td>77.4</td><td>6.1</td><td>8.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G67020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf; Has 72 Blast hits to 72 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 72; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25011008-25012987 REVERSE LENGTH=659</td><td>851</td><td>659</td><td>6.00E-15</td><td>77.4</td><td>6.1</td><td>8.8</td></tr>
<tr><td>Rsa1.0_00483.1.g14735.t2</td><td>gb|EOA20091.1| hypothetical protein CARUB_v10000368mg [Capsella rubella]</td><td>693</td><td>688</td><td>0</td><td>99.3</td><td>84.1</td><td>89.8</td><td>hypothetical protein CARUB_v10000368mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G20930.1 | Symbols: TSL | Protein kinase superfamily protein | chr5:7098213-7102970 FORWARD LENGTH=688</td><td>693</td><td>688</td><td>0</td><td>99.3</td><td>84.4</td><td>89.5</td></tr>
<tr><td>Rsa1.0_00483.1.g14736.t2</td><td>gb|EOA19371.1| hypothetical protein CARUB_v10000466mg [Capsella rubella]</td><td>630</td><td>624</td><td>0</td><td>99.0</td><td>89.4</td><td>93.5</td><td>hypothetical protein CARUB_v10000466mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G20950.2 | Symbols: | Glycosyl hydrolase family protein | chr5:7107609-7110775 REVERSE LENGTH=624</td><td>630</td><td>624</td><td>0</td><td>99.0</td><td>89.5</td><td>93.7</td></tr>
<tr><td>Rsa1.0_00484.1.g14737.t1</td><td>gb|EOA40302.1| hypothetical protein CARUB_v10009029mg [Capsella rubella]</td><td>491</td><td>475</td><td>3.00E-41</td><td>96.7</td><td>32.8</td><td>44.0</td><td>hypothetical protein CARUB_v10009029mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G18035.1 | Symbols: HON4 | winged-helix DNA-binding transcription factor family protein | chr3:6169384-6171558 REVERSE LENGTH=480</td><td>491</td><td>480</td><td>2.00E-39</td><td>97.8</td><td>34.2</td><td>44.2</td></tr>
<tr><td>Rsa1.0_00484.1.g14738.t1</td><td>gb|EOA40302.1| hypothetical protein CARUB_v10009029mg [Capsella rubella]</td><td>512</td><td>475</td><td>4.00E-47</td><td>92.8</td><td>31.4</td><td>43.2</td><td>hypothetical protein CARUB_v10009029mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G18035.1 | Symbols: HON4 | winged-helix DNA-binding transcription factor family protein | chr3:6169384-6171558 REVERSE LENGTH=480</td><td>512</td><td>480</td><td>1.00E-43</td><td>93.8</td><td>37.9</td><td>48.6</td></tr>
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Rsa1.0_00484.1.g14739.t1	ref|NP_188430.1| phosphopantothenoylcysteine decarboxylase [Arabidopsis thaliana] gi|13124313|sp|Q9SWE5.1|HAL3A_ARATH RecName: Full=Phosphopantothenoylcysteine decarboxylase; Short=PPCDC; AltName: Full=Halotolerance protein Hal3a; Short=AtCoaC; Short=AtHal3a gi|10835869|pdb|1E20|A Chain A, The Fmn Binding Protein Athal3 gi|5802225|gb|AAD51616.1|AF166262_1 HAL3A protein [Arabidopsis thaliana] gi|11994209|dbj|BAB01331.1| HAL3A protein [Arabidopsis thaliana] gi|48310154|gb|AAT41764.1| At3g18030 [Arabidopsis thaliana] gi|52218792|gb|AAU29466.1| At3g18030 [Arabidopsis thaliana] gi|110737049|dbj|BAF00478.1| HAL3A protein [Arabidopsis thaliana] gi|332642515|gb|AEE76036.1| phosphopantothenoylcysteine decarboxylase [Arabidopsis thaliana]	210	209	1.00E-114	99.5	94.3	98.1	phosphopantothenoylcysteine decarboxylase	gbpln	Arabidopsis thaliana	AT3G18030.1 | Symbols: ATHAL3A, HAL3A, HAL3, ATHAL3 | HAL3-like protein A | chr3:6167883-6168629 REVERSE LENGTH=209	210	209	1.00E-116	99.5	94.3	98.1
Rsa1.0_00484.1.g14740.t1	gb|EOA32381.1| hypothetical protein CARUB_v10015648mg [Capsella rubella]	688	687	0	99.9	79.8	89.1	hypothetical protein CARUB_v10015648mg	gbpln	Capsella rubella	AT3G18020.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:6165449-6167515 FORWARD LENGTH=688	688	688	0	100.0	79.5	88.2
Rsa1.0_00484.1.g14741.t1	ref|XP_002862807.1| WOX1 protein [Arabidopsis lyrata subsp. lyrata] gi|297308541|gb|EFH39065.1| WOX1 protein [Arabidopsis lyrata subsp. lyrata]	346	348	1.00E-145	100.6	77.7	84.1	WOX1 protein	gbpln	Arabidopsis lyrata	AT3G18010.1 | Symbols: WOX1 | WUSCHEL related homeobox 1 | chr3:6161155-6163183 REVERSE LENGTH=350	346	350	1.00E-143	101.2	76.9	83.8
Rsa1.0_00484.1.g14742.t1	gb|AAP83582.1| phosphoethanolamine N-methyltransferase [Brassica napus]	492	491	0	99.8	97.6	99.0	phosphoethanolamine N-methyltransferase	gbpln	Brassica napus	AT3G18000.1 | Symbols: NMT1, XPL1, PEAMT | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:6154578-6157331 FORWARD LENGTH=491	492	491	0	99.8	93.3	97.6
Rsa1.0_00484.1.g14743.t1	gb|EOA31949.1| hypothetical protein CARUB_v10015190mg [Capsella rubella]	177	177	1.00E-90	100.0	91.5	96.0	hypothetical protein CARUB_v10015190mg	gbpln	Capsella rubella	AT3G17980.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:6152417-6153115 FORWARD LENGTH=177	177	177	9.00E-93	100.0	92.1	96.6
Rsa1.0_00484.1.g14744.t5	ref|NP_188424.2| translocon at the outer membrane of chloroplasts 64-III [Arabidopsis thaliana] gi|75335547|sp|Q9LVH5.1|OE64C_ARATH RecName: Full=Outer envelope protein 64, chloroplastic; AltName: Full=Translocon at the outer membrane of chloroplasts 64-III gi|9294499|dbj|BAB02718.1| unnamed protein product [Arabidopsis thaliana] gi|332642509|gb|AEE76030.1| translocon at the outer membrane of chloroplasts 64-III [Arabidopsis thaliana]	612	589	0	96.2	83.7	89.2	translocon at the outer membrane of chloroplasts 64-III	gbpln	Arabidopsis thaliana	AT3G17970.1 | Symbols: atToc64-III, TOC64-III | translocon at the outer membrane of chloroplasts 64-III | chr3:6148030-6151794 FORWARD LENGTH=589	612	589	0	96.2	83.7	89.2
Rsa1.0_00484.1.g14745.t1	ref|XP_002885235.1| aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331075|gb|EFH61494.1| aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata]	343	341	0	99.4	88.9	95.3	aldose 1-epimerase family protein	gbpln	Arabidopsis lyrata	AT3G17940.1 | Symbols: | Galactose mutarotase-like superfamily protein | chr3:6143707-6145244 REVERSE LENGTH=341	343	341	0	99.4	88.9	94.5
Rsa1.0_00484.1.g14746.t1	ref|XP_002874264.1| hypothetical protein ARALYDRAFT_489405 [Arabidopsis lyrata subsp. lyrata] gi|297320101|gb|EFH50523.1| hypothetical protein ARALYDRAFT_489405 [Arabidopsis lyrata subsp. lyrata]	268	280	8.00E-75	104.5	54.5	68.3	hypothetical protein ARALYDRAFT_489405	gbpln	Arabidopsis lyrata	AT5G25475.3 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:8867920-8869492 REVERSE LENGTH=282	268	282	5.00E-74	105.2	55.2	69.0

Rsa1.0_00484.1.g14747.t1	ref|XP_002885234.1| hypothetical protein ARALYDRAFT_898147 [Arabidopsis lyrata subsp. lyrata] gi|297331074|gb|EFH61493.1| hypothetical protein ARALYDRAFT_898147 [Arabidopsis lyrata subsp. lyrata]	188	190	8.00E-80	101.1	83.0	89.9	hypothetical protein ARALYDRAFT_898147	gbpln	Arabidopsis lyrata	AT3G17930.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3007 (InterPro:IPR021562); Has 236 Blast hits to 236 proteins in 83 species: Archae - 0; Bacteria - 117; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 80 (source: NCBI BLink). | chr3:6142307-6143246 REVERSE LENGTH=190	188	190	1.00E-80	101.1	82.4	89.9
Rsa1.0_00484.1.g14748.t2	gb|EOA32684.1| hypothetical protein CARUB_v10015982mg [Capsella rubella]	1020	1020	0	100.0	81.9	88.4	hypothetical protein CARUB_v10015982mg	gbpln	Capsella rubella	AT3G17920.1 | Symbols: | Outer arm dynein light chain 1 protein | chr3:6137255-6142023 FORWARD LENGTH=1010	1020	1010	0	99.0	81.2	87.4
Rsa1.0_00484.1.g14749.t1	gb|AAD17360.1| contains similarity to transposase [Arabidopsis thaliana]	273	428	3.00E-26	156.8	22.7	30.8	contains similarity to transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00484.1.g14750.t1	dbj|BAA04994.1| glutamine synthetase [Raphanus sativus]	354	354	0	100.0	100.0	100.0	glutamine synthetase	gbpln	Raphanus sativus	AT3G17820.1 | Symbols: ATGSKB6, GLN1.3, GLN1;3 | glutamine synthetase 1.3 | chr3:6097503-6099408 FORWARD LENGTH=354	354	354	0	100.0	93.2	97.2
Rsa1.0_00484.1.g14751.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00484.1.g14752.t1	ref|NP_188408.1| pyrimidine 1 [Arabidopsis thaliana] gi|9294485|dbj|BAB02704.1| senescencs-related protein; dihydroorotate dehydrogenase-like protein [Arabidopsis thaliana] gi|14334712|gb|AAK59534.1| putative dehydrogenase [Arabidopsis thaliana] gi|16323430|gb|AAL15209.1| putative dehydrogenase [Arabidopsis thaliana] gi|24850451|gb|AAN64919.1| putative dehydrogenase [Arabidopsis thaliana] gi|332642489|gb|AEE76010.1| pyrimidine 1 [Arabidopsis thaliana]	427	426	0	99.8	92.3	97.0	pyrimidine 1	gbpln	Arabidopsis thaliana	AT3G17810.1 | Symbols: PYD1 | pyrimidine 1 | chr3:6094279-6096289 FORWARD LENGTH=426	427	426	0	99.8	92.3	97.0
Rsa1.0_00484.1.g14753.t1	dbj|BAJ34170.1| unnamed protein product [Thellungiella halophila]	393	419	0	106.6	85.8	92.4	unnamed protein product	----	----	AT3G17800.1 | Symbols: | Protein of unknown function (DUF760) | chr3:6091248-6092873 REVERSE LENGTH=421	393	421	1.00E-177	107.1	84.2	91.6
Rsa1.0_00484.1.g14754.t1	gb|ADG45868.1| purple acid phosphatase 17 isoform 1 [Brassica oleracea var. viridis] gi|295854831|gb|ADG45872.1| purple acid phosphatase 17 isoform 1 [Brassica oleracea var. viridis]	334	337	0	100.9	95.5	97.6	purple acid phosphatase 17 isoform 1	gbpln	Brassica oleracea	AT3G17790.1 | Symbols: ATACP5, ATPAP17, PAP17 | purple acid phosphatase 17 | chr3:6089779-6090988 FORWARD LENGTH=338	334	338	1.00E-170	101.2	85.3	92.8
Rsa1.0_00484.1.g14755.t1	ref|XP_002891431.1| hypothetical protein ARALYDRAFT_473983 [Arabidopsis lyrata subsp. lyrata] gi|297337273|gb|EFH67690.1| hypothetical protein ARALYDRAFT_473983 [Arabidopsis lyrata subsp. lyrata]	129	129	3.00E-59	100.0	86.0	92.2	hypothetical protein ARALYDRAFT_473983	gbpln	Arabidopsis lyrata	AT1G48440.1 | Symbols: | B-cell receptor-associated 31-like | chr1:17907075-17908327 FORWARD LENGTH=129	129	129	3.00E-61	100.0	85.3	91.5
Rsa1.0_00484.1.g14756.t3	ref|XP_002885229.1| dihydroxyacetone kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331069|gb|EFH61488.1| dihydroxyacetone kinase family protein [Arabidopsis lyrata subsp. lyrata]	618	595	0	96.3	88.5	91.6	dihydroxyacetone kinase family protein	gbpln	Arabidopsis lyrata	AT3G17770.1 | Symbols: | Dihydroxyacetone kinase | chr3:6081973-6085957 REVERSE LENGTH=595	618	595	0	96.3	88.7	91.4
Rsa1.0_00484.1.g14757.t1	gb|EOA32282.1| hypothetical protein CARUB_v10015543mg [Capsella rubella]	490	492	0	100.4	96.7	98.4	hypothetical protein CARUB_v10015543mg	gbpln	Capsella rubella	AT3G17760.2 | Symbols: GAD5 | glutamate decarboxylase 5 | chr3:6078893-6080838 REVERSE LENGTH=494	490	494	0	100.8	95.1	98.0
Rsa1.0_00484.1.g14758.t1	ref|XP_002883085.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328925|gb|EFH59344.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	1039	1138	0	109.5	82.5	88.5	kinase family protein	gbpln	Arabidopsis lyrata	AT3G17750.1 | Symbols: | Protein kinase superfamily protein | chr3:6074228-6078428 FORWARD LENGTH=1138	1039	1138	0	109.5	82.2	88.0

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<tr><td>Rsa1.0_00484.1.g14760.t1</td><td>ref|XP_002887058.1| hypothetical protein ARALYDRAFT_315690 [Arabidopsis lyrata subsp. lyrata] gi|297332899|gb|EFH63317.1| hypothetical protein ARALYDRAFT_315690 [Arabidopsis lyrata subsp. lyrata]</td><td>209</td><td>353</td><td>1.00E-25</td><td>168.9</td><td>30.1</td><td>35.4</td><td>hypothetical protein ARALYDRAFT_315690</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G17710.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6055597-6056703 FORWARD LENGTH=368</td><td>209</td><td>368</td><td>5.00E-27</td><td>176.1</td><td>32.1</td><td>35.4</td></tr>
<tr><td>Rsa1.0_00484.1.g14761.t1</td><td>ref|NP_188400.1| NAC domain containing protein 57 [Arabidopsis thaliana] gi|9294586|dbj|BAB02867.1| unnamed protein product [Arabidopsis thaliana] gi|67633638|gb|AAY78743.1| no apical meristem family protein [Arabidopsis thaliana] gi|332642479|gb|AEE76000.1| NAC domain containing protein 57 [Arabidopsis thaliana]</td><td>244</td><td>246</td><td>1.00E-131</td><td>100.8</td><td>94.7</td><td>98.0</td><td>NAC domain containing protein 57</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G17730.1 | Symbols: anac057, NAC057 | NAC domain containing protein 57 | chr3:6064379-6065813 FORWARD LENGTH=246</td><td>244</td><td>246</td><td>1.00E-133</td><td>100.8</td><td>94.7</td><td>98.0</td></tr>
<tr><td>Rsa1.0_00484.1.g14762.t1</td><td>ref|NP_566585.1| cyclic nucleotide gated channel [Arabidopsis thaliana] gi|38503198|sp|Q9LD37.1|CNG20_ARATH RecName: Full=Probable cyclic nucleotide-gated ion channel 20, chloroplastic; AltName: Full=Cyclic nucleotide-binding transporter 1; Flags: Precursor gi|8131898|gb|AAF73128.1|AF148541_1 cyclic nucleotide-binding transporter 1 [Arabidopsis thaliana] gi|8131901|gb|AAF73130.1|AF148542_2 cyclic nucleotide-binding transporter 1 [Arabidopsis thaliana] gi|9294160|dbj|BAB02062.1| unnamed protein product [Arabidopsis thaliana] gi|332642473|gb|AEE75994.1| cyclic nucleotide-binding transporter 1 [Arabidopsis thaliana]</td><td>720</td><td>764</td><td>0</td><td>106.1</td><td>85.6</td><td>91.9</td><td>cyclic nucleotide gated channel</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G17700.1 | Symbols: CNBT1, CNGC20, ATCNGC20 | cyclic nucleotide-binding transporter 1 | chr3:6049074-6052449 FORWARD LENGTH=764</td><td>720</td><td>764</td><td>0</td><td>106.1</td><td>85.6</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00484.1.g14763.t1</td><td>ref|XP_002892763.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338605|gb|EFH69022.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>377</td><td>804</td><td>4.00E-80</td><td>213.3</td><td>42.7</td><td>49.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G13630.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4669784-4672826 REVERSE LENGTH=806</td><td>377</td><td>806</td><td>5.00E-81</td><td>213.8</td><td>41.6</td><td>49.1</td></tr>
<tr><td>Rsa1.0_00484.1.g14764.t1</td><td>gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1923</td><td>1496</td><td>0</td><td>77.8</td><td>34.9</td><td>43.8</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G17690.1 | Symbols: ATCNGC19, CNGC19 | cyclic nucleotide gated channel 19 | chr3:6045382-6048339 FORWARD LENGTH=729</td><td>1923</td><td>729</td><td>0</td><td>37.9</td><td>24.4</td><td>27.8</td></tr>
<tr><td>Rsa1.0_00484.1.g14765.t1</td><td>ref|XP_002883079.1| ATCNGC19 [Arabidopsis lyrata subsp. lyrata] gi|297328919|gb|EFH59338.1| ATCNGC19 [Arabidopsis lyrata subsp. lyrata]</td><td>788</td><td>753</td><td>0</td><td>95.6</td><td>78.3</td><td>85.7</td><td>ATCNGC19</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G17690.1 | Symbols: ATCNGC19, CNGC19 | cyclic nucleotide gated channel 19 | chr3:6045382-6048339 FORWARD LENGTH=729</td><td>788</td><td>729</td><td>0</td><td>92.5</td><td>74.5</td><td>81.5</td></tr>
<tr><td>Rsa1.0_00485.1.g14766.t1</td><td>gb|AAM61483.1| unknown [Arabidopsis thaliana]</td><td>533</td><td>532</td><td>0</td><td>99.8</td><td>91.7</td><td>96.2</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G01680.1 | Symbols: | Ankyrin repeat family protein | chr2:306597-308427 FORWARD LENGTH=532</td><td>533</td><td>532</td><td>0</td><td>99.8</td><td>91.6</td><td>96.1</td></tr>
<tr><td>Rsa1.0_00485.1.g14767.t1</td><td>ref|NP_565275.1| uncharacterized protein [Arabidopsis thaliana] gi|75268025|sp|Q9ZU97.2|VAC14_ARATH RecName: Full=Protein VAC14 homolog gi|20197546|gb|AAD12702.2| expressed protein [Arabidopsis thaliana] gi|330250391|gb|AEC05485.1| uncharacterized protein AT2G01690 [Arabidopsis thaliana]</td><td>730</td><td>743</td><td>0</td><td>101.8</td><td>86.3</td><td>92.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G01690.1 | Symbols: | ARM repeat superfamily protein | chr2:309144-313499 REVERSE LENGTH=743</td><td>730</td><td>743</td><td>0</td><td>101.8</td><td>86.3</td><td>92.3</td></tr>
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Rsa1.0_00485.1.g14768.t2	ref|XP_002876772.1| ribophorin I family protein [Arabidopsis lyrata subsp. lyrata] gi|297322610|gb|EFH53031.1| ribophorin I family protein [Arabidopsis lyrata subsp. lyrata]	538	464	0	86.2	78.6	83.3	ribophorin I family protein	gbpln	Arabidopsis lyrata	AT2G01720.1 | Symbols: | Ribophorin I | chr2:317193-320016 REVERSE LENGTH=464	538	464	0	86.2	78.1	82.7
Rsa1.0_00485.1.g14769.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00485.1.g14770.t1	ref|NP_849924.1| E3 ubiquitin protein ligase RIE1 [Arabidopsis thaliana] gi|75299491|sp|Q8GUU2.1|RIE1_ARATH RecName: Full=E3 ubiquitin protein ligase RIE1; AltName: Full=Protein RING-FINGER FOR EMBRYOGENESIS 1 gi|27372067|gb|AAN87884.1| RES protein [Arabidopsis thaliana] gi|330250396|gb|AEC05490.1| E3 ubiquitin protein ligase RIE1 [Arabidopsis thaliana]	399	359	1.00E-167	90.0	76.4	81.2	E3 ubiquitin protein ligase RIE1	gbpln	Arabidopsis thaliana	AT2G01735.1 | Symbols: RIE1 | RING-finger protein for embryogenesis | chr2:324499-325895 FORWARD LENGTH=359	399	359	1.00E-169	90.0	76.4	81.2
Rsa1.0_00485.1.g14771.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00485.1.g14772.t1	gb|EOA25655.1| hypothetical protein CARUB_v10019005mg [Capsella rubella]	652	628	0	96.3	86.3	91.3	hypothetical protein CARUB_v10019005mg	gbpln	Capsella rubella	AT2G01750.1 | Symbols: ATMAP70-3, MAP70-3 | microtubule-associated proteins 70-3 | chr2:328351-331848 FORWARD LENGTH=629	652	629	0	96.5	85.4	90.2
Rsa1.0_00485.1.g14773.t1	ref|XP_002876776.1| hypothetical protein ARALYDRAFT_484093 [Arabidopsis lyrata subsp. lyrata] gi|297322614|gb|EFH53035.1| hypothetical protein ARALYDRAFT_484093 [Arabidopsis lyrata subsp. lyrata]	170	166	5.00E-54	97.6	71.2	78.8	hypothetical protein ARALYDRAFT_484093	gbpln	Arabidopsis lyrata	AT2G01755.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 120 Blast hits to 120 proteins in 52 species: Archae - 0; Bacteria - 80; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink). | chr2:332249-332770 REVERSE LENGTH=173	170	173	1.00E-53	101.8	68.8	77.1
Rsa1.0_00485.1.g14774.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00485.1.g14775.t1	ref|XP_004238758.1| PREDICTED: eukaryotic translation initiation factor 5A-3-like [Solanum lycopersicum]	183	159	6.00E-17	86.9	31.7	48.6	PREDICTED: eukaryotic translation initiation factor 5A-3-like	gbpln	Solanum lycopersicum	AT1G69410.1 | Symbols: ATELF5A-3, ELF5A-3 | eukaryotic elongation factor 5A-3 | chr1:26089301-26090194 FORWARD LENGTH=158	183	158	2.00E-17	86.3	30.6	47.0
Rsa1.0_00485.1.g14776.t1	ref|XP_002876777.1| hypothetical protein ARALYDRAFT_484095 [Arabidopsis lyrata subsp. lyrata] gi|297322615|gb|EFH53036.1| hypothetical protein ARALYDRAFT_484095 [Arabidopsis lyrata subsp. lyrata]	250	250	1.00E-125	100.0	88.4	93.6	hypothetical protein ARALYDRAFT_484095	gbpln	Arabidopsis lyrata	AT2G01770.1 | Symbols: VIT1, ATVIT1 | vacuolar iron transporter 1 | chr2:334775-336425 REVERSE LENGTH=250	250	250	1.00E-127	100.0	88.0	93.2
Rsa1.0_00485.1.g14777.t1	ref|NP_178290.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana] gi|75268028|sp|Q9ZUA9.1|Y2181_ARATH RecName: Full=PHD finger protein At2g01810 gi|4220491|gb|AAD12714.1| hypothetical protein [Arabidopsis thaliana] gi|330250408|gb|AEC05502.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana]	703	697	0	99.1	67.4	80.2	RING/FYVE/PHD zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT2G01810.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:347537-349952 FORWARD LENGTH=697	703	697	0	99.1	67.4	80.2
Rsa1.0_00485.1.g14778.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00485.1.g14779.t1	gb|EOA23460.1| hypothetical protein CARUB_v10016649mg [Capsella rubella]	954	947	0	99.3	81.3	89.6	hypothetical protein CARUB_v10016649mg	gbpln	Capsella rubella	AT2G01820.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:357664-360681 REVERSE LENGTH=943	954	943	0	98.8	80.4	88.7
Rsa1.0_00485.1.g14780.t1	dbj|BAH47482.1| phytochrome E [Cardamine resedifolia]	262	1116	2.00E-67	426.0	58.8	69.8	phytochrome E	gbpln	Cardamine resedifolia	AT4G18130.1 | Symbols: PHYE | phytochrome E | chr4:10042312-10045948 REVERSE LENGTH=1112	262	1112	1.00E-69	424.4	51.9	56.5
Rsa1.0_00485.1.g14781.t1	gb|EOA23460.1| hypothetical protein CARUB_v10016649mg [Capsella rubella]	114	947	5.00E-39	830.7	67.5	80.7	hypothetical protein CARUB_v10016649mg	gbpln	Capsella rubella	AT2G01820.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:357664-360681 REVERSE LENGTH=943	114	943	2.00E-39	827.2	64.9	78.9

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<tr><td>Rsa1.0_00486.1.g14782.t1</td><td>ref|NP_177024.1| putative nitrite transporter [Arabidopsis thaliana] gi|75266596|sp|Q9SX20.1|PTR18_ARATH RecName: Full=Probable nitrite transporter At1g68570 gi|5734721|gb|AAD49986.1|AC008075_19 Similar to gb|AF023472 peptide transporter from Hordeum vulgare and is a member of the PF|00854 Peptide transporter family. ESTs gb|T41927 and gb|AA395024 come from this gene [Arabidopsis thaliana] gi|20147231|gb|AAM10330.1| At1g68570/F24J5_7 [Arabidopsis thaliana] gi|25090385|gb|AAN72289.1| At1g68570/F24J5_7 [Arabidopsis thaliana] gi|110742209|dbj|BAE99031.1| peptide transporter like [Arabidopsis thaliana] gi|332196691|gb|AEE34812.1| probable nitrite transporter [Arabidopsis thaliana]</td><td>595</td><td>596</td><td>0</td><td>100.2</td><td>88.9</td><td>93.9</td><td>putative nitrite transporter</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68570.1 | Symbols: | Major facilitator superfamily protein | chr1:25746811-25750110 FORWARD LENGTH=596</td><td>595</td><td>596</td><td>0</td><td>100.2</td><td>88.9</td><td>93.9</td></tr>
<tr><td>Rsa1.0_00486.1.g14783.t1</td><td>ref|XP_002887191.1| hypothetical protein ARALYDRAFT_475982 [Arabidopsis lyrata subsp. lyrata] gi|297333032|gb|EFH63450.1| hypothetical protein ARALYDRAFT_475982 [Arabidopsis lyrata subsp. lyrata]</td><td>669</td><td>649</td><td>0</td><td>97.0</td><td>70.9</td><td>79.5</td><td>hypothetical protein ARALYDRAFT_475982</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68580.2 | Symbols: | agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein | chr1:25752869-25755631 FORWARD LENGTH=648</td><td>669</td><td>648</td><td>0</td><td>96.9</td><td>68.3</td><td>77.3</td></tr>
<tr><td>Rsa1.0_00486.1.g14784.t1</td><td>gb|EOA33969.1| hypothetical protein CARUB_v10021464mg [Capsella rubella]</td><td>68</td><td>115</td><td>6.00E-21</td><td>169.1</td><td>80.9</td><td>88.2</td><td>hypothetical protein CARUB_v10021464mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68585.1 | Symbols: | unknown protein; Has 23 Blast hits to 23 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25756911-25757426 FORWARD LENGTH=116</td><td>68</td><td>116</td><td>9.00E-23</td><td>170.6</td><td>77.9</td><td>88.2</td></tr>
<tr><td>Rsa1.0_00486.1.g14785.t1</td><td>gb|AAM63350.1| plastid-specific ribosomal protein 3 precursor [Arabidopsis thaliana]</td><td>161</td><td>166</td><td>9.00E-68</td><td>103.1</td><td>85.1</td><td>88.8</td><td>plastid-specific ribosomal protein 3 precursor</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68590.1 | Symbols: | Ribosomal protein PSRP-3/Ycf65 | chr1:25757593-25758169 REVERSE LENGTH=166</td><td>161</td><td>166</td><td>6.00E-70</td><td>103.1</td><td>85.1</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00486.1.g14786.t1</td><td>ref|XP_002887194.1| hypothetical protein ARALYDRAFT_475988 [Arabidopsis lyrata subsp. lyrata] gi|297333035|gb|EFH63453.1| hypothetical protein ARALYDRAFT_475988 [Arabidopsis lyrata subsp. lyrata]</td><td>329</td><td>336</td><td>1.00E-154</td><td>102.1</td><td>82.1</td><td>87.8</td><td>hypothetical protein ARALYDRAFT_475988</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68620.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:25766018-25767028 FORWARD LENGTH=336</td><td>329</td><td>336</td><td>1.00E-152</td><td>102.1</td><td>78.7</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00486.1.g14787.t1</td><td>emb|CAN65188.1| hypothetical protein VITISV_004365 [Vitis vinifera]</td><td>1342</td><td>1265</td><td>0</td><td>94.3</td><td>53.6</td><td>66.7</td><td>hypothetical protein VITISV_004365</td><td>gbpln</td><td>Vitis vinifera</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1342</td><td>1262</td><td>1.00E-103</td><td>94.0</td><td>14.2</td><td>22.7</td></tr>
<tr><td>Rsa1.0_00486.1.g14788.t1</td><td>gb|EOA33841.1| hypothetical protein CARUB_v10021324mg [Capsella rubella]</td><td>113</td><td>161</td><td>3.00E-55</td><td>142.5</td><td>90.3</td><td>95.6</td><td>hypothetical protein CARUB_v10021324mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68630.1 | Symbols: | PLAC8 family protein | chr1:25768653-25769458 FORWARD LENGTH=161</td><td>113</td><td>161</td><td>4.00E-57</td><td>142.5</td><td>91.2</td><td>94.7</td></tr>
<tr><td>Rsa1.0_00486.1.g14789.t1</td><td>gb|EOA35838.1| hypothetical protein CARUB_v10021079mg [Capsella rubella]</td><td>164</td><td>159</td><td>3.00E-67</td><td>97.0</td><td>76.8</td><td>79.9</td><td>hypothetical protein CARUB_v10021079mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68660.1 | Symbols: | Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein | chr1:25778058-25779083 REVERSE LENGTH=159</td><td>164</td><td>159</td><td>2.00E-68</td><td>97.0</td><td>76.2</td><td>78.7</td></tr>
<tr><td>Rsa1.0_00486.1.g14790.t1</td><td>ref|XP_002887198.1| hypothetical protein ARALYDRAFT_315886 [Arabidopsis lyrata subsp. lyrata] gi|297333039|gb|EFH63457.1| hypothetical protein ARALYDRAFT_315886 [Arabidopsis lyrata subsp. lyrata]</td><td>94</td><td>75</td><td>7.00E-26</td><td>79.8</td><td>62.8</td><td>67.0</td><td>hypothetical protein ARALYDRAFT_315886</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68680.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 16 growth stages; Has 20 Blast hits to 20 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25785627-25786622 FORWARD LENGTH=75</td><td>94</td><td>75</td><td>7.00E-28</td><td>79.8</td><td>61.7</td><td>66.0</td></tr>
</table>

Rsa1.0_00486.1.g14791.t1	ref|NP_177036.1| protein kinase-like protein [Arabidopsis thaliana] gi|75337798|sp|Q9SX31.1|PERK9_ARATH RecName: Full=Proline-rich receptor-like protein kinase PERK9; AltName: Full=Proline-rich extensin-like receptor kinase 9; Short=AtPERK9 gi|5734709|gb|AAD49974.1|AC008075_7 Contains PF|00069 Eukaryotic protein kinase domain [Arabidopsis thaliana] gi|14334806|gb|AAK59581.1| putative protein kinase [Arabidopsis thaliana] gi|21280865|gb|AAM44925.1| putative protein kinase [Arabidopsis thaliana] gi|332196707|gb|AEE34828.1| proline-rich receptor-like protein kinase PERK9 [Arabidopsis thaliana]	745	708	0	95.0	48.5	52.5	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G68690.1 | Symbols: | Protein kinase superfamily protein | chr1:25789192-25791886 FORWARD LENGTH=708	745	708	0	95.0	48.5	52.5
Rsa1.0_00486.1.g14792.t1	ref|NP_177038.1| phospholipid-translocating ATPase [Arabidopsis thaliana] gi|12229673|sp|Q9SX33.1|ALA9_ARATH RecName: Full=Putative phospholipid-transporting ATPase 9; Short=AtALA9; AltName: Full=Aminophospholipid flippase 9 gi|5734708|gb|AAD49973.1|AC008075_6 Similar to gb|AF067820 ATPase II from Homo sapiens and is a member of PF|00122 E1-E2 ATPases family [Arabidopsis thaliana] gi|332196709|gb|AEE34830.1| putative phospholipid-transporting ATPase 9 [Arabidopsis thaliana]	1202	1200	0	99.8	92.7	96.3	phospholipid-translocating ATPase	gbpln	Arabidopsis thaliana	AT1G68710.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:25793498-25797975 REVERSE LENGTH=1200	1202	1200	0	99.8	92.7	96.3
Rsa1.0_00486.1.g14793.t1	#	#	#	#	#	#	#	-	----	----	AT2G21640.1 | Symbols: | Encodes a protein of unknown function that is a marker for oxidative stress response. | chr2:9254985-9255453 FORWARD LENGTH=104	82	104	8.00E-11	126.8	32.9	41.5
Rsa1.0_00486.1.g14794.t1	ref|XP_002280608.2| PREDICTED: phosphate transporter PHO1 homolog 1 isoform 1 [Vitis vinifera]	720	780	0	108.3	71.5	83.6	PREDICTED: phosphate transporter PHO1 homolog 1 isoform 1	gbpln	Vitis vinifera	AT1G68740.1 | Symbols: PHO1;H1 | EXS (ERD1/XPR1/SYG1) family protein | chr1:25812735-25816574 REVERSE LENGTH=784	720	784	0	108.9	47.9	51.9
Rsa1.0_00487.1.g14795.t1	ref|XP_002867018.1| radical SAM domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297312854|gb|EFH43277.1| radical SAM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	631	636	0	100.8	89.2	94.5	radical SAM domain-containing protein	gbpln	Arabidopsis lyrata	AT4G36390.1 | Symbols: | Methylthiotransferase | chr4:17194746-17197054 REVERSE LENGTH=640	631	640	0	101.4	87.5	92.2
Rsa1.0_00487.1.g14796.t1	ref|NP_568004.1| putative ubiquitin-conjugating enzyme E2 17 [Arabidopsis thaliana] gi|75318090|sp|O23239.1|UBC17_ARATH RecName: Full=Probable ubiquitin-conjugating enzyme E2 17; AltName: Full=Ubiquitin carrier protein 17 gi|2464941|emb|CAB16814.1| ubiquitin-conjugating enzyme [Arabidopsis thaliana] gi|2801446|gb|AAC39326.1| ubiquitin-conjugating enzyme 17 [Arabidopsis thaliana] gi|7270589|emb|CAB80307.1| ubiquitin-conjugating enzyme [Arabidopsis thaliana] gi|21593655|gb|AAM65622.1| E2, ubiquitin-conjugating enzyme 17 (UBC17) [Arabidopsis thaliana] gi|66354444|gb|AAY44857.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|332661253|gb|AEE86653.1| putative ubiquitin-conjugating enzyme E2 17 [Arabidopsis thaliana] gi|482553365|gb|EOA17558.1| hypothetical protein CARUB_v10005917mg [Capsella rubella]	161	161	1.00E-82	100.0	96.9	98.8	putative ubiquitin-conjugating enzyme E2 17	gbpln	Arabidopsis thaliana	AT4G36410.1 | Symbols: UBC17 | ubiquitin-conjugating enzyme 17 | chr4:17201969-17202890 FORWARD LENGTH=161	161	161	4.00E-85	100.0	96.9	98.8
Rsa1.0_00487.1.g14797.t1	emb|CCJ34843.1| horseradish peroxidase isoenzyme HRP_08562.1 [Armoracia rusticana]	331	331	1.00E-175	100.0	92.4	97.0	horseradish peroxidase isoenzyme HRP_08562.1	gbpln	Armoracia rusticana	AT4G36430.1 | Symbols: | Peroxidase superfamily protein | chr4:17204648-17205917 REVERSE LENGTH=331	331	331	1.00E-176	100.0	90.3	96.7

Rsa1.0_00487.1.g14798.t1	gb|AAM20633.1| putative protein [Arabidopsis thaliana] gi|22136408|gb|AAM91282.1| putative protein [Arabidopsis thaliana]	456	406	0	89.0	81.1	83.8	putative protein	gbpln	Arabidopsis thaliana	AT4G36440.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 41 Blast hits to 41 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17207213-17209873 REVERSE LENGTH=394	456	394	0	86.4	78.9	81.4
Rsa1.0_00487.1.g14799.t1	gb|ACH61906.1| serine palmitoyltransferase long chain base subunit [Brassica rapa subsp. chinensis] gi|197311352|gb|ACH61907.1| serine palmitoyltransferase long chain base subunit [Brassica rapa subsp. chinensis]	170	482	2.00E-37	283.5	47.6	48.8	serine palmitoyltransferase long chain base subunit	gbpln	Brassica rapa	AT4G36480.2 | Symbols: ATLCB1, LCB1, EMB2779, FBR11 | long-chain base1 | chr4:17218598-17221124 FORWARD LENGTH=482	170	482	5.00E-37	283.5	44.7	49.4
Rsa1.0_00487.1.g14800.t1	ref|NP_195365.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|4006915|emb|CAB16845.1| hypothetical protein [Arabidopsis thaliana] gi|7270595|emb|CAB80313.1| hypothetical protein [Arabidopsis thaliana] gi|48427662|gb|AAT42380.1| At4g36470 [Arabidopsis thaliana] gi|110741629|dbj|BAE98762.1| hypothetical protein [Arabidopsis thaliana] gi|332661259|gb|AEE86659.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	359	371	1.00E-177	103.3	83.3	91.9	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT4G36470.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:17215128-17216475 REVERSE LENGTH=371	359	371	1.00E-180	103.3	83.3	91.9
Rsa1.0_00487.1.g14801.t1	ref|NP_195368.1| uncharacterized protein [Arabidopsis thaliana] gi|2464932|emb|CAB16811.1| putative protein [Arabidopsis thaliana] gi|7270598|emb|CAB80316.1| putative protein [Arabidopsis thaliana] gi|28393196|gb|AAO42028.1| unknown protein [Arabidopsis thaliana] gi|28827518|gb|AAO50603.1| unknown protein [Arabidopsis thaliana] gi|332661263|gb|AEE86663.1| uncharacterized protein AT4G36500 [Arabidopsis thaliana]	123	122	1.00E-51	99.2	90.2	93.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G36500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G18210.1); Has 50 Blast hits to 50 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17226139-17226507 REVERSE LENGTH=122	123	122	2.00E-54	99.2	90.2	93.5
Rsa1.0_00487.1.g14802.t1	ref|NP_195368.1| uncharacterized protein [Arabidopsis thaliana] gi|2464932|emb|CAB16811.1| putative protein [Arabidopsis thaliana] gi|7270598|emb|CAB80316.1| putative protein [Arabidopsis thaliana] gi|28393196|gb|AAO42028.1| unknown protein [Arabidopsis thaliana] gi|28827518|gb|AAO50603.1| unknown protein [Arabidopsis thaliana] gi|332661263|gb|AEE86663.1| uncharacterized protein AT4G36500 [Arabidopsis thaliana]	124	122	2.00E-52	98.4	91.1	91.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G36500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G18210.1); Has 50 Blast hits to 50 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17226139-17226507 REVERSE LENGTH=122	124	122	3.00E-55	98.4	91.1	91.9
Rsa1.0_00487.1.g14803.t1	ref|NP_195370.5| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|332661266|gb|AEE86666.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]	1311	1422	0	108.5	73.3	81.3	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT4G36520.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:17230589-17235435 REVERSE LENGTH=1422	1311	1422	0	108.5	73.3	81.3
Rsa1.0_00487.1.g14804.t1	ref|XP_002867009.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297312845|gb|EFH43268.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	354	376	1.00E-177	106.2	88.7	93.2	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT4G36530.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:17240120-17241770 REVERSE LENGTH=378	354	378	1.00E-174	106.8	88.1	93.2
Rsa1.0_00487.1.g14805.t1	ref|XP_002867008.1| U-box domain-containing protein 5 [Arabidopsis lyrata subsp. lyrata] gi|297312844|gb|EFH43267.1| U-box domain-containing protein 5 [Arabidopsis lyrata subsp. lyrata]	717	751	0	104.7	73.2	83.8	U-box domain-containing protein 5	gbpln	Arabidopsis lyrata	AT4G36550.1 | Symbols: | ARM repeat superfamily protein | chr4:17245400-17247926 REVERSE LENGTH=718	717	718	0	100.1	72.0	82.1

Rsa1.0_00487.1.g14806.t1	gb|EOA15655.1| hypothetical protein CARUB_v10006084mg, partial [Capsella rubella]	79	105	3.00E-33	132.9	86.1	91.1	hypothetical protein CARUB_v10006084mg, partial	gbpln	Capsella rubella	AT1G75250.2 | Symbols: ATRL6, RSM3, RL6 | RAD-like 6 | chr1:28244463-28245453 REVERSE LENGTH=97	79	97	8.00E-26	122.8	62.0	79.7
Rsa1.0_00487.1.g14807.t1	ref|NP_195376.2| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332661274|gb|AEE86674.1| AAA-type ATPase family protein [Arabidopsis thaliana]	601	632	0	105.2	86.0	90.3	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT4G36580.1 | Symbols: | AAA-type ATPase family protein | chr4:17257958-17260661 FORWARD LENGTH=632	601	632	0	105.2	86.0	90.3
Rsa1.0_00487.1.g14808.t1	gb|EOA32387.1| hypothetical protein CARUB_v10015657mg [Capsella rubella]	250	313	4.00E-82	125.2	62.4	79.6	hypothetical protein CARUB_v10015657mg	gbpln	Capsella rubella	AT4G36610.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:17265545-17267274 REVERSE LENGTH=317	250	317	9.00E-83	126.8	60.4	78.4
Rsa1.0_00487.1.g14809.t1	ref|XP_002867006.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312842|gb|EFH43265.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	315	315	1.00E-155	100.0	88.6	93.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G36610.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:17265545-17267274 REVERSE LENGTH=317	315	317	1.00E-156	100.6	87.6	92.4
Rsa1.0_00487.1.g14810.t1	gb|EOA18681.1| hypothetical protein CARUB_v10007257mg [Capsella rubella]	293	293	1.00E-152	100.0	85.7	93.9	hypothetical protein CARUB_v10007257mg	gbpln	Capsella rubella	AT4G36640.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr4:17277187-17278447 REVERSE LENGTH=294	293	294	1.00E-149	100.3	83.3	92.2
Rsa1.0_00487.1.g14811.t1	gb|EOA16387.1| hypothetical protein CARUB_v10004541mg, partial [Capsella rubella]	510	540	0	105.9	86.9	91.4	hypothetical protein CARUB_v10004541mg, partial	gbpln	Capsella rubella	AT4G36650.1 | Symbols: ATPBRP, PBRP | plant-specific TFIIB-related protein | chr4:17283283-17285527 REVERSE LENGTH=503	510	503	0	98.6	85.5	91.0
Rsa1.0_00487.1.g14812.t1	gb|EOA18172.1| hypothetical protein CARUB_v10006648mg [Capsella rubella]	697	493	0	70.7	65.6	68.1	hypothetical protein CARUB_v10006648mg	gbpln	Capsella rubella	AT4G36670.1 | Symbols: | Major facilitator superfamily protein | chr4:17287680-17289483 REVERSE LENGTH=493	697	493	0	70.7	64.7	67.6
Rsa1.0_00488.1.g14813.t1	ref|NP_174496.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|38605150|sp|Q38908.2|XTH30_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 30; Short=At-XTH30; Short=XTH-30; Flags: Precursor gi|10801367|gb|AAG23439.1|AC084165_5 endoxyloglucan transferase, putative [Arabidopsis thaliana] gi|17065244|gb|AAL32776.1| endoxyloglucan transferase, putative [Arabidopsis thaliana] gi|332193322|gb|AEE31443.1| probable xyloglucan endotransglucosylase/hydrolase protein 30 [Arabidopsis thaliana]	345	343	1.00E-178	99.4	92.5	96.2	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT1G32170.1 | Symbols: XTR4, XTH30 | xyloglucan endotransglucosylase/hydrolase 30 | chr1:11575434-11577776 FORWARD LENGTH=343	345	343	1.00E-180	99.4	92.5	96.2
Rsa1.0_00488.1.g14814.t1	ref|NP_175150.1| F-box protein [Arabidopsis thaliana] gi|75268184|sp|Q9C627.1|FB36_ARATH RecName: Full=Putative F-box protein At1g46984 gi|12321006|gb|AAG50624.1|AC083835_9 hypothetical protein [Arabidopsis thaliana] gi|332194012|gb|AEE32133.1| F-box protein [Arabidopsis thaliana]	398	370	4.00E-98	93.0	51.8	64.6	F-box protein	gbpln	Arabidopsis thaliana	AT1G46984.1 | Symbols: | F-box family protein | chr1:17274722-17275834 FORWARD LENGTH=370	398	370	1.00E-100	93.0	51.8	64.6
Rsa1.0_00488.1.g14815.t1	ref|XP_002893707.1| hypothetical protein ARALYDRAFT_473399 [Arabidopsis lyrata subsp. lyrata] gi|297339549|gb|EFH69966.1| hypothetical protein ARALYDRAFT_473399 [Arabidopsis lyrata subsp. lyrata]	969	974	0	100.5	83.4	89.7	hypothetical protein ARALYDRAFT_473399	gbpln	Arabidopsis lyrata	AT1G32180.1 | Symbols: ATCSLD6, CSLD6 | cellulose synthase-like D6 | chr1:11586516-11589651 REVERSE LENGTH=979	969	979	0	101.0	83.3	89.9
Rsa1.0_00488.1.g14816.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1225	1142	0	93.2	39.2	49.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1225	575	2.00E-79	46.9	14.9	24.1
Rsa1.0_00488.1.g14817.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00488.1.g14818.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	136	1213	3.00E-12	891.9	29.4	52.2	unknown protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00488.1.g14819.t2	ref|XP_002893708.1| hypothetical protein ARALYDRAFT_473401 [Arabidopsis lyrata subsp. lyrata] gi|297339550|gb|EFH69967.1| hypothetical protein ARALYDRAFT_473401 [Arabidopsis lyrata subsp. lyrata]	438	429	0	97.9	83.8	86.3	hypothetical protein ARALYDRAFT_473401	gbpln	Arabidopsis lyrata	AT1G32190.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:11593059-11595731 REVERSE LENGTH=422	438	422	0	96.3	82.0	85.4
Rsa1.0_00488.1.g14820.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00488.1.g14821.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	714	1223	0	171.3	48.0	66.2	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	714	746	3.00E-71	104.5	21.7	29.3
Rsa1.0_00488.1.g14822.t1	gb|AGC55014.1| glycerin-3-phosphate acylase 2 [Brassica oleracea var. viridis]	453	451	0	99.6	94.0	96.5	glycerin-3-phosphate acylase 2	gbpln	Brassica oleracea	AT1G32200.2 | Symbols: ATS1, ACT1 | phospholipid/glycerol acyltransferase family protein | chr1:11602223-11605001 REVERSE LENGTH=459	453	459	0	101.3	87.9	93.8
Rsa1.0_00489.1.g14823.t2	gb|ADL70730.1| indole-3-acetic acid inducible 20 [Arabidopsis thaliana]	208	171	9.00E-36	82.2	44.7	47.1	indole-3-acetic acid inducible 20	gbpln	Arabidopsis thaliana	AT2G46990.1 | Symbols: IAA20 | indole-3-acetic acid inducible 20 | chr2:19307861-19308869 FORWARD LENGTH=175	208	175	1.00E-37	84.1	44.2	46.6
Rsa1.0_00489.1.g14824.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00489.1.g14825.t1	ref|XP_002868583.1| ATCHX18 [Arabidopsis lyrata subsp. lyrata] gi|297314419|gb|EFH44842.1| ATCHX18 [Arabidopsis lyrata subsp. lyrata]	800	810	0	101.3	89.9	95.5	ATCHX18	gbpln	Arabidopsis lyrata	AT5G41610.1 | Symbols: ATCHX18, CHX18 | cation/H+ exchanger 18 | chr5:16638554-16641146 REVERSE LENGTH=810	800	810	0	101.3	88.6	94.3
Rsa1.0_00489.1.g14826.t1	gb|EOA17391.1| hypothetical protein CARUB_v10005685mg [Capsella rubella]	163	224	2.00E-72	137.4	81.6	87.7	hypothetical protein CARUB_v10005685mg	gbpln	Capsella rubella	AT5G41590.1 | Symbols: | Protein of unknown function (DUF567) | chr5:16632221-16633896 REVERSE LENGTH=221	163	221	6.00E-73	135.6	79.1	85.3
Rsa1.0_00489.1.g14827.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	2161	1307	0	60.5	36.6	46.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT5G39020.1 | Symbols: | Malectin/receptor-like protein kinase family protein | chr5:15616917-15619358 FORWARD LENGTH=813	2161	813	1.00E-175	37.6	14.1	16.3
Rsa1.0_00489.1.g14828.t3	dbj|BAB11464.1| transcription factor-like protein [Arabidopsis thaliana]	643	719	1.00E-169	111.8	56.5	70.0	transcription factor-like protein	gbpln	Arabidopsis thaliana	AT5G41580.1 | Symbols: | RING/U-box superfamily protein | chr5:16626563-16630659 REVERSE LENGTH=760	643	760	1.00E-153	118.2	46.0	53.8
Rsa1.0_00489.1.g14829.t1	gb|ACN89258.1| WRKY transcription factor 24 [Brassica napus]	176	150	8.00E-80	85.2	80.1	82.4	WRKY transcription factor 24	gbpln	Brassica napus	AT5G41570.1 | Symbols: WRKY24, ATWRKY24 | WRKY DNA-binding protein 24 | chr5:16624220-16625689 FORWARD LENGTH=179	176	179	1.00E-76	101.7	81.8	88.6
Rsa1.0_00489.1.g14830.t1	gb|EOA17721.1| hypothetical protein CARUB_v10006102mg [Capsella rubella]	100	102	4.00E-45	102.0	90.0	95.0	hypothetical protein CARUB_v10006102mg	gbpln	Capsella rubella	AT5G41560.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin ligase, Det1/DDB1-complexing (InterPro:IPR018276); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:16621427-16622619 REVERSE LENGTH=101	100	101	6.00E-47	101.0	89.0	94.0
Rsa1.0_00489.1.g14831.t1	ref|XP_002868591.1| hypothetical protein ARALYDRAFT_493833 [Arabidopsis lyrata subsp. lyrata] gi|297314427|gb|EFH44850.1| hypothetical protein ARALYDRAFT_493833 [Arabidopsis lyrata subsp. lyrata]	179	183	8.00E-72	102.2	77.1	81.0	hypothetical protein ARALYDRAFT_493833	gbpln	Arabidopsis lyrata	AT5G41520.1 | Symbols: | RNA binding Plectin/S10 domain-containing protein | chr5:16609377-16610583 REVERSE LENGTH=180	179	180	7.00E-66	100.6	75.4	78.2
Rsa1.0_00489.1.g14832.t1	gb|EOA40394.1| hypothetical protein CARUB_v10009120mg [Capsella rubella]	436	449	2.00E-87	103.0	47.9	62.8	hypothetical protein CARUB_v10009120mg	gbpln	Capsella rubella	AT1G16930.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:5789987-5791534 FORWARD LENGTH=449	436	449	1.00E-88	103.0	47.5	62.8
Rsa1.0_00489.1.g14833.t1	ref|NP_198970.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|10178009|dbj|BAB11461.1| disease resistance protein-like [Arabidopsis thaliana] gi|332007308|gb|AED94691.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1491	1085	0	72.8	43.2	52.8	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G41550.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16617232-16620785 REVERSE LENGTH=1085	1491	1085	0	72.8	43.2	52.8
Rsa1.0_00489.1.g14834.t1	ref|NP_198970.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|10178009|dbj|BAB11461.1| disease resistance protein-like [Arabidopsis thaliana] gi|332007308|gb|AED94691.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1083	1085	0	100.2	47.7	56.8	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G41550.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16617232-16620785 REVERSE LENGTH=1085	1083	1085	0	100.2	47.7	56.8
Rsa1.0_00489.1.g14835.t1	ref|XP_002870622.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316458|gb|EFH46881.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	162	1127	9.00E-69	695.7	79.6	87.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G41550.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16617232-16620785 REVERSE LENGTH=1085	162	1085	9.00E-70	669.8	76.5	84.6

Rsa1.0_00490.1.g14836.t1	gb|EOA26337.1| hypothetical protein CARUB_v10022511mg [Capsella rubella]	1337	1347	0	100.7	93.8	96.9	hypothetical protein CARUB_v10022511mg	gbpln	Capsella rubella	AT2G36910.1 | Symbols: ATPGP1, PGP1, ABCB1 | ATP binding cassette subfamily B1 | chr2:15502162-15507050 FORWARD LENGTH=1286	1337	1286	0	96.2	91.5	94.3
Rsa1.0_00490.1.g14837.t1	ref|NP_850272.1| uncharacterized protein [Arabidopsis thaliana] gi|22531199|gb|AAM97103.1| unknown protein [Arabidopsis thaliana] gi|23198030|gb|AAN15542.1| unknown protein [Arabidopsis thaliana] gi|110741110|dbj|BAE98649.1| hypothetical protein [Arabidopsis thaliana] gi|330254222|gb|AEC09316.1| uncharacterized protein AT2G36895 [Arabidopsis thaliana]	226	232	3.00E-99	102.7	82.7	88.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G36895.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 32 Blast hits to 32 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15489176-15490296 REVERSE LENGTH=232	226	232	1.00E-101	102.7	82.7	88.1
Rsa1.0_00490.1.g14838.t1	ref|XP_002881476.1| hypothetical protein ARALYDRAFT_902809 [Arabidopsis lyrata subsp. lyrata] gi|297327315|gb|EFH57735.1| hypothetical protein ARALYDRAFT_902809 [Arabidopsis lyrata subsp. lyrata] gi|482563079|gb|EOA27269.1| hypothetical protein CARUB_v10023389mg [Capsella rubella] gi|482563080|gb|EOA27270.1| hypothetical protein CARUB_v10023389mg [Capsella rubella]	390	390	0	100.0	98.5	99.5	hypothetical protein ARALYDRAFT_902809	gbpln	Arabidopsis lyrata	AT2G36880.2 | Symbols: MAT3 | methionine adenosyltransferase 3 | chr2:15479721-15480893 REVERSE LENGTH=390	390	390	0	100.0	97.9	99.5
Rsa1.0_00490.1.g14839.t1	ref|NP_181224.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|38605514|sp|Q9SJL9.1|XTH32_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 32; Short=At-XTH32; Short=XTH-32; Flags: Precursor gi|4883603|gb|AAD31572.1| xyloglucan endotransglycosylase, putative [Arabidopsis thaliana] gi|15027967|gb|AAK76514.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|21595304|gb|AAM66089.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|22136872|gb|AAM91780.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|330254214|gb|AEC09308.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana]	299	299	1.00E-163	100.0	91.6	97.0	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT2G36870.1 | Symbols: XTH32 | xyloglucan endotransglucosylase/hydrolase 32 | chr2:15472869-15474630 REVERSE LENGTH=299	299	299	1.00E-166	100.0	91.6	97.0
Rsa1.0_00490.1.g14840.t1	ref|XP_002881473.1| hypothetical protein ARALYDRAFT_482665 [Arabidopsis lyrata subsp. lyrata] gi|297327312|gb|EFH57732.1| hypothetical protein ARALYDRAFT_482665 [Arabidopsis lyrata subsp. lyrata]	416	411	0	98.8	88.9	92.8	hypothetical protein ARALYDRAFT_482665	gbpln	Arabidopsis lyrata	AT2G36840.1 | Symbols: | ACT-like superfamily protein | chr2:15451834-15453550 REVERSE LENGTH=410	416	410	0	98.6	88.7	92.8
Rsa1.0_00490.1.g14841.t3	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1692	910	0	53.8	26.7	35.0	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1692	626	1.00E-101	37.0	11.8	16.6
Rsa1.0_00490.1.g14842.t1	gb|AAB51393.2| tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]	251	251	1.00E-134	100.0	98.4	99.2	tonoplast intrinsic protein bobTIP26-1	gbpln	Brassica oleracea	AT2G36830.1 | Symbols: GAMMA-TIP, TIP1;1, GAMMA-TIP1 | gamma tonoplast intrinsic protein | chr2:15445490-15446336 FORWARD LENGTH=251	251	251	1.00E-133	100.0	94.4	98.4
Rsa1.0_00490.1.g14843.t13	gb|EOA29221.1| hypothetical protein CARUB_v10025495mg [Capsella rubella]	1692	1708	0	100.9	90.8	94.9	hypothetical protein CARUB_v10025495mg	gbpln	Capsella rubella	AT2G36810.1 | Symbols: | ARM repeat superfamily protein | chr2:15425739-15439462 REVERSE LENGTH=1716	1692	1716	0	101.4	91.0	94.6

Rsa1.0_00490.1.g14844.t1	ref|NP_181213.1| cytokinin-O-glucosyltransferase 1 [Arabidopsis thaliana] gi|66774040|sp|Q9ZQ99.1|U73C1_ARATH RecName: Full=UDP-glycosyltransferase 73C1; AltName: Full=Cytokinin-O-glucosyltransferase 1; AltName: Full=Zeatin O-glucosyltransferase 1; Short=AtZOG1 gi|4415920|gb|AAD20151.1| putative glucosyl transferase [Arabidopsis thaliana] gi|46318041|gb|AAS87590.1| zeatin O-glucosyltransferase 1 [Arabidopsis thaliana] gi|111074234|gb|ABH04490.1| At2g36750 [Arabidopsis thaliana] gi|330254200|gb|AEC09294.1| cytokinin-O-glucosyltransferase 1 [Arabidopsis thaliana]	496	491	0	99.0	82.7	89.5	cytokinin-O-glucosyltransferase 1	gbpln	Arabidopsis thaliana	AT2G36750.1 | Symbols: UGT73C1 | UDP-glucosyl transferase 73C1 | chr2:15410531-15412006 REVERSE LENGTH=491	496	491	0	99.0	82.7	89.5
Rsa1.0_00490.1.g14845.t1	ref|NP_181214.1| UDP-glucosyl transferase 73C [Arabidopsis thaliana] gi|75315659|sp|Q9ZQ98.1|U73C2_ARATH RecName: Full=UDP-glycosyltransferase 73C2 gi|4415921|gb|AAD20152.1| putative glucosyl transferase [Arabidopsis thaliana] gi|330254201|gb|AEC09295.1| UDP-glucosyl transferase 73C2 [Arabidopsis thaliana]	496	496	0	100.0	83.1	90.3	UDP-glucosyl transferase 73C	gbpln	Arabidopsis thaliana	AT2G36760.1 | Symbols: UGT73C2 | UDP-glucosyl transferase 73C2 | chr2:15413042-15414532 REVERSE LENGTH=496	496	496	0	100.0	83.1	90.3
Rsa1.0_00490.1.g14846.t1	gb|EOA28908.1| hypothetical protein CARUB_v10025154mg [Capsella rubella]	394	263	4.00E-59	66.8	34.0	40.9	hypothetical protein CARUB_v10025154mg	gbpln	Capsella rubella	AT2G36540.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:15325237-15326449 FORWARD LENGTH=249	394	249	1.00E-55	63.2	31.0	36.3
Rsa1.0_00490.1.g14847.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00490.1.g14848.t1	gb|EOA28908.1| hypothetical protein CARUB_v10025154mg [Capsella rubella]	262	263	3.00E-94	100.4	70.2	83.6	hypothetical protein CARUB_v10025154mg	gbpln	Capsella rubella	AT2G36540.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:15325237-15326449 FORWARD LENGTH=249	262	249	4.00E-83	95.0	64.9	76.7
Rsa1.0_00490.1.g14849.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00490.1.g14850.t1	gb|EOA27123.1| hypothetical protein CARUB_v10023223mg [Capsella rubella]	452	444	0	98.2	91.4	92.7	hypothetical protein CARUB_v10023223mg	gbpln	Capsella rubella	AT2G36530.1 | Symbols: LOS2, ENO2 | Enolase | chr2:15321081-15323786 REVERSE LENGTH=444	452	444	0	98.2	90.9	92.7
Rsa1.0_00490.1.g14851.t1	gb|EOA26873.1| hypothetical protein CARUB_v10022966mg [Capsella rubella]	554	536	0	96.8	74.4	83.2	hypothetical protein CARUB_v10022966mg	gbpln	Capsella rubella	AT2G36500.1 | Symbols: | CBS / octicosapeptide/Phox/Bemp1 (PB1) domains-containing protein | chr2:15318473-15320083 FORWARD LENGTH=536	554	536	0	96.8	75.1	83.8
Rsa1.0_00490.1.g14852.t2	ref|NP_181187.1| fructose-bisphosphate aldolase, class I [Arabidopsis thaliana] gi|4581146|gb|AAD24630.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|14334412|gb|AAK59404.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|17104659|gb|AAL34218.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|21537327|gb|AAM61668.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|110741992|dbj|BAE98935.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|330254162|gb|AEC09256.1| fructose-bisphosphate aldolase, class I [Arabidopsis thaliana]	359	358	0	99.7	91.6	96.4	fructose-bisphosphate aldolase, class I	gbpln	Arabidopsis thaliana	AT2G36460.1 | Symbols: | Aldolase superfamily protein | chr2:15296929-15298387 REVERSE LENGTH=358	359	358	0	99.7	91.6	96.4

<table>
<tr><td>Rsa1.0_00490.1.g14853.t1</td><td>ref|NP_181187.1| fructose-bisphosphate aldolase, class I [Arabidopsis thaliana] gi|4581146|gb|AAD24630.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|14334412|gb|AAK59404.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|17104659|gb|AAL34218.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|21537327|gb|AAM61668.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|110741992|dbj|BAE98935.1| putative fructose bisphosphate aldolase [Arabidopsis thaliana] gi|330254162|gb|AEC09256.1| fructose-bisphosphate aldolase, class I [Arabidopsis thaliana]</td><td>169</td><td>358</td><td>4.00E-75</td><td>211.8</td><td>85.8</td><td>88.8</td><td>fructose-bisphosphate aldolase, class I</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G36460.1 | Symbols: | Aldolase superfamily protein | chr2:15296929-15298387 REVERSE LENGTH=358</td><td>169</td><td>358</td><td>1.00E-77</td><td>211.8</td><td>85.8</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00490.1.g14854.t1</td><td>gb|EOA25343.1| hypothetical protein CARUB_v10018664mg [Capsella rubella]</td><td>161</td><td>181</td><td>8.00E-24</td><td>112.4</td><td>42.9</td><td>54.7</td><td>hypothetical protein CARUB_v10018664mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170</td><td>161</td><td>170</td><td>4.00E-19</td><td>105.6</td><td>32.3</td><td>43.5</td></tr>
<tr><td>Rsa1.0_00490.1.g14855.t1</td><td>ref|XP_002881444.1| AP2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327283|gb|EFH57703.1| AP2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>182</td><td>184</td><td>2.00E-71</td><td>101.1</td><td>79.7</td><td>87.4</td><td>AP2 domain-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G36450.1 | Symbols: HRD | Integrase-type DNA-binding superfamily protein | chr2:15294303-15294857 REVERSE LENGTH=184</td><td>182</td><td>184</td><td>1.00E-69</td><td>101.1</td><td>79.7</td><td>86.8</td></tr>
<tr><td>Rsa1.0_00490.1.g14856.t1</td><td>gb|EOA27098.1| hypothetical protein CARUB_v10023196mg [Capsella rubella]</td><td>449</td><td>451</td><td>0</td><td>100.4</td><td>73.1</td><td>84.2</td><td>hypothetical protein CARUB_v10023196mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G36430.1 | Symbols: | Plant protein of unknown function (DUF247) | chr2:15290211-15291557 FORWARD LENGTH=448</td><td>449</td><td>448</td><td>0</td><td>99.8</td><td>74.4</td><td>85.5</td></tr>
<tr><td>Rsa1.0_00490.1.g14857.t1</td><td>ref|XP_002879611.1| hypothetical protein ARALYDRAFT_482620 [Arabidopsis lyrata subsp. lyrata] gi|297325450|gb|EFH55870.1| hypothetical protein ARALYDRAFT_482620 [Arabidopsis lyrata subsp. lyrata]</td><td>422</td><td>442</td><td>1.00E-157</td><td>104.7</td><td>78.9</td><td>87.0</td><td>hypothetical protein ARALYDRAFT_482620</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G36420.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G03670.1); Has 10588 Blast hits to 6606 proteins in 440 species: Archae - 8; Bacteria - 365; Metazoa - 4146; Fungi - 1198; Plants - 483; Viruses - 212; Other Eukaryotes - 4176 (source: NCBI BLink). | chr2:15286498-15288990 FORWARD LENGTH=439</td><td>422</td><td>439</td><td>1.00E-158</td><td>104.0</td><td>77.5</td><td>85.5</td></tr>
<tr><td>Rsa1.0_00491.1.g14858.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>1329</td><td>1142</td><td>0</td><td>85.9</td><td>25.3</td><td>33.9</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1329</td><td>575</td><td>1.00E-96</td><td>43.3</td><td>15.2</td><td>23.6</td></tr>
<tr><td>Rsa1.0_00491.1.g14859.t1</td><td>dbj|BAA95777.1| unnamed protein product [Arabidopsis thaliana]</td><td>1140</td><td>1161</td><td>0</td><td>101.8</td><td>90.4</td><td>94.7</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G16830.1 | Symbols: TPR2 | TOPLESS-related 2 | chr3:5731709-5737531 FORWARD LENGTH=1131</td><td>1140</td><td>1131</td><td>0</td><td>99.2</td><td>90.4</td><td>94.7</td></tr>
<tr><td>Rsa1.0_00491.1.g14860.t1</td><td>gb|AFP47629.1| nitrile-specifier protein [Schouwia purpurea]</td><td>511</td><td>467</td><td>0</td><td>91.4</td><td>71.0</td><td>81.0</td><td>nitrile-specifier protein</td><td>gbpln</td><td>Schouwia purpurea</td><td>AT3G16400.2 | Symbols: ATMLP-470 | nitrile specifier protein 1 | chr3:5566516-5568330 FORWARD LENGTH=470</td><td>511</td><td>470</td><td>0</td><td>92.0</td><td>68.5</td><td>78.5</td></tr>
<tr><td>Rsa1.0_00491.1.g14861.t1</td><td>ref|NP_566559.1| protein pumilio 24 [Arabidopsis thaliana] gi|75273869|sp|Q9LRZ3.1|PUM24_ARATH RecName: Full=Pumilio homolog 24; Short=APUM-24; Short=AtPUM24 gi|7939573|dbj|BAA95774.1| unnamed protein product [Arabidopsis thaliana] gi|15010674|gb|AAK73996.1| AT3g16810/K20I9_3 [Arabidopsis thaliana] gi|332642348|gb|AEE75869.1| protein pumilio 24 [Arabidopsis thaliana]</td><td>630</td><td>641</td><td>0</td><td>101.7</td><td>78.7</td><td>87.5</td><td>protein pumilio 24</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G16810.1 | Symbols: APUM24, PUM24 | pumilio 24 | chr3:5723436-5727539 REVERSE LENGTH=641</td><td>630</td><td>641</td><td>0</td><td>101.7</td><td>78.7</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00491.1.g14862.t8</td><td>ref|XP_002883023.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297328863|gb|EFH59282.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>528</td><td>389</td><td>1.00E-101</td><td>73.7</td><td>40.5</td><td>49.1</td><td>F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G16740.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:5699476-5700651 FORWARD LENGTH=391</td><td>528</td><td>391</td><td>1.00E-101</td><td>74.1</td><td>39.2</td><td>48.7</td></tr>
<tr><td>Rsa1.0_00491.1.g14863.t15</td><td>gb|EOA31942.1| hypothetical protein CARUB_v10015182mg [Capsella rubella]</td><td>1211</td><td>1096</td><td>0</td><td>90.5</td><td>86.2</td><td>87.9</td><td>hypothetical protein CARUB_v10015182mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G16785.1 | Symbols: PLDP1, PLDZ1, PLDZETA1, PLD ZETA 1 | phospholipase D P1 | chr3:5711329-5718696 FORWARD LENGTH=1096</td><td>1211</td><td>1096</td><td>0</td><td>90.5</td><td>85.5</td><td>87.7</td></tr>
<tr><td>Rsa1.0_00491.1.g14864.t1</td><td>ref|XP_002883026.1| 60S ribosomal protein L19 [Arabidopsis lyrata subsp. lyrata] gi|297328866|gb|EFH59285.1| 60S ribosomal protein L19 [Arabidopsis lyrata subsp. lyrata]</td><td>186</td><td>209</td><td>8.00E-57</td><td>112.4</td><td>63.4</td><td>67.2</td><td>60S ribosomal protein L19</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G16780.1 | Symbols: | Ribosomal protein L19e family protein | chr3:5708982-5710249 FORWARD LENGTH=209</td><td>186</td><td>209</td><td>8.00E-59</td><td>112.4</td><td>62.9</td><td>67.2</td></tr>
</table>

Rsa1.0_00491.1.g14865.t1	ref|NP_188299.1| ethylene-responsive transcription factor RAP2-3 [Arabidopsis thaliana] gi|27735162|sp|P42736.2|RAP23_ARATH RecName: Full=Ethylene-responsive transcription factor RAP2-3; AltName: Full=Cadmium-induced protein AS30; AltName: Full=Ethylene response factor 72; Short=ERF72; AltName: Full=Ethylene-responsive element binding protein; Short=AtEBP; AltName: Full=Protein RELATED TO APETALA2 3; Short=Related to AP2 3 gi|2281631|gb|AAC49769.1| AP2 domain containing protein RAP2.3 [Arabidopsis thaliana] gi|11994632|dbj|BAB02769.1| AP2 domain transcription factor RAP2.3 [Arabidopsis thaliana] gi|14334854|gb|AAK59605.1| putative AP2 domain containing protein RAP2.3 [Arabidopsis thaliana] gi|16649095|gb|AAL24399.1| AP2 domain transcription factor RAP2.3 [Arabidopsis thaliana] gi|21593082|gb|AAM65031.1| AP2 domain containing protein RAP2.3 [Arabidopsis thaliana] gi|23296611|gb|AAN13131.1| putative AP2 domain containing protein RAP2.3 [Arabidopsis thaliana] gi|332642342|gb|AEE75863.1| ethylene-responsive transcription factor RAP2-3 [Arabidopsis thaliana]	237	248	3.00E-92	104.6	75.1	84.4	ethylene-responsive transcription factor RAP2-3	gbpln	Arabidopsis thaliana	AT3G16770.1 | Symbols: RAP2.3, ATEBP, ERF72, EBP | ethylene-responsive element binding protein | chr3:5705784-5706768 FORWARD LENGTH=248	237	248	8.00E-95	104.6	75.1	84.4
Rsa1.0_00491.1.g14866.t1	ref|XP_002885164.1| hypothetical protein ARALYDRAFT_897993 [Arabidopsis lyrata subsp. lyrata] gi|297331004|gb|EFH61423.1| hypothetical protein ARALYDRAFT_897993 [Arabidopsis lyrata subsp. lyrata]	663	683	0	103.0	83.0	88.4	hypothetical protein ARALYDRAFT_897993	gbpln	Arabidopsis lyrata	AT3G16730.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Non-SMC condensin II complex, subunit H2-like (InterPro:IPR009378); Has 249 Blast hits to 211 proteins in 82 species: Archae - 0; Bacteria - 0; Metazoa - 145; Fungi - 8; Plants - 30; Viruses - 0; Other Eukaryotes - 66 (source: NCBI BLink). | chr3:5695633-5698863 REVERSE LENGTH=683	663	683	0	103.0	82.5	88.1
Rsa1.0_00491.1.g14867.t1	ref|XP_002883022.1| hypothetical protein ARALYDRAFT_479140 [Arabidopsis lyrata subsp. lyrata] gi|297328862|gb|EFH59281.1| hypothetical protein ARALYDRAFT_479140 [Arabidopsis lyrata subsp. lyrata]	295	304	1.00E-103	103.1	76.9	83.4	hypothetical protein ARALYDRAFT_479140	gbpln	Arabidopsis lyrata	AT3G16720.1 | Symbols: ATL2, TL2 | TOXICOS EN LEVADURA 2 | chr3:5692880-5693794 FORWARD LENGTH=304	295	304	1.00E-102	103.1	75.9	82.7
Rsa1.0_00491.1.g14868.t1	ref|XP_002889141.1| CYCA1_2 [Arabidopsis lyrata subsp. lyrata] gi|297334982|gb|EFH65400.1| CYCA1_2 [Arabidopsis lyrata subsp. lyrata]	357	443	1.00E-112	124.1	65.3	77.0	CYCA1_2	gbpln	Arabidopsis lyrata	AT1G77390.1 | Symbols: TAM, CYCA1;2, DYP, CYCA1 | CYCLIN A1;2 | chr1:29081904-29084137 REVERSE LENGTH=442	357	442	1.00E-111	123.8	64.1	74.2
Rsa1.0_00491.1.g14869.t1	gb|AAM66134.1| translationally controlled tumor protein-like protein [Arabidopsis thaliana]	168	168	2.00E-88	100.0	94.6	98.2	translationally controlled tumor protein-like protein	gbpln	Arabidopsis thaliana	AT3G16640.1 | Symbols: TCTP | translationally controlled tumor protein | chr3:5669709-5670729 REVERSE LENGTH=168	168	168	2.00E-90	100.0	94.0	97.6
Rsa1.0_00491.1.g14870.t1	ref|NP_188285.1| kinesin family member 2/24 [Arabidopsis thaliana] gi|30684173|ref|NP_850598.1| kinesin family member 2/24 [Arabidopsis thaliana] gi|15810129|gb|AAL07208.1| putative kinesin protein [Arabidopsis thaliana] gi|110741480|dbj|BAE98696.1| kinesin like protein [Arabidopsis thaliana] gi|332642324|gb|AEE75845.1| kinesin 13A [Arabidopsis thaliana] gi|332642325|gb|AEE75846.1| kinesin family member 2/24 [Arabidopsis thaliana]	847	794	0	93.7	77.6	82.4	kinesin family member 2/24	gbpln	Arabidopsis thaliana	AT3G16630.2 | Symbols: ATKINESIN-13A, KINESIN-13A | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:5662660-5667261 REVERSE LENGTH=794	847	794	0	93.7	77.6	82.4
Rsa1.0_00491.1.g14871.t1	ref|XP_002885158.1| hypothetical protein ARALYDRAFT_479127 [Arabidopsis lyrata subsp. lyrata] gi|297330998|gb|EFH61417.1| hypothetical protein ARALYDRAFT_479127 [Arabidopsis lyrata subsp. lyrata]	715	1071	0	149.8	57.1	62.0	hypothetical protein ARALYDRAFT_479127	gbpln	Arabidopsis lyrata	AT3G16620.1 | Symbols: ATTOC120, TOC120 | translocon outer complex protein 120 | chr3:5658469-5661738 REVERSE LENGTH=1089	715	1089	0	152.3	56.8	63.2
Rsa1.0_00492.1.g14872.t1	gb|AAR15430.1| autophagocytosis protein [Sisymbrium irio]	310	312	1.00E-168	100.6	92.9	95.5	autophagocytosis protein	gbpln	Sisymbrium irio	AT5G61500.1 | Symbols: ATATG3, ATG3 | autophagy 3 (APG3) | chr5:24734216-24736711 REVERSE LENGTH=313	310	313	1.00E-165	101.0	90.6	95.5

<table>
<tr><td>Rsa1.0_00492.1.g14873.t29</td><td>gb|AAR15439.1| nuclear division RFT1-like protein [Sisymbrium irio]</td><td>597</td><td>481</td><td>0</td><td>80.6</td><td>68.8</td><td>72.2</td><td>nuclear division RFT1-like protein</td><td>gbpln</td><td>Sisymbrium irio</td><td>AT5G07630.1 | Symbols: | lipid transporters | chr5:2410703-2414523 FORWARD LENGTH=611</td><td>597</td><td>611</td><td>0</td><td>102.3</td><td>67.3</td><td>74.0</td></tr>
<tr><td>Rsa1.0_00492.1.g14874.t1</td><td>ref|NP_196383.1| structural maintenance of chromosomes 6A [Arabidopsis thaliana] gi|9759587|dbj|BAB11444.1| SMC-like protein [Arabidopsis thaliana] gi|332003807|gb|AED91190.1| structural maintenance of chromosomes 6A [Arabidopsis thaliana]</td><td>1085</td><td>1058</td><td>0</td><td>97.5</td><td>77.9</td><td>86.6</td><td>structural maintenance of chromosomes 6A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07660.1 | Symbols: SMC6A | structural maintenance of chromosomes 6A | chr5:2422839-2429912 FORWARD LENGTH=1058</td><td>1085</td><td>1058</td><td>0</td><td>97.5</td><td>77.9</td><td>86.6</td></tr>
<tr><td>Rsa1.0_00492.1.g14875.t1</td><td>ref|NP_196384.2| F-box protein [Arabidopsis thaliana] gi|75248498|sp|Q8VYT5.1|FB254_ARATH RecName: Full=F-box protein At5g07670 gi|17979057|gb|AAL49796.1| unknown protein [Arabidopsis thaliana] gi|20465475|gb|AAM20197.1| unknown protein [Arabidopsis thaliana] gi|222423582|dbj|BAH19760.1| AT5G07670 [Arabidopsis thaliana] gi|332003808|gb|AED91191.1| F-box protein [Arabidopsis thaliana]</td><td>462</td><td>476</td><td>0</td><td>103.0</td><td>75.8</td><td>84.0</td><td>F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07670.1 | Symbols: | RNI-like superfamily protein | chr5:2430421-2432065 FORWARD LENGTH=476</td><td>462</td><td>476</td><td>0</td><td>103.0</td><td>75.8</td><td>84.0</td></tr>
<tr><td>Rsa1.0_00492.1.g14876.t1</td><td>ref|NP_568182.2| NAC domain containing protein 80 [Arabidopsis thaliana] gi|9759589|dbj|BAB11446.1| NAM (no apical meristem)-like protein [Arabidopsis thaliana] gi|30102618|gb|AAP21227.1| At5g07680 [Arabidopsis thaliana] gi|110736032|dbj|BAE99988.1| no apical meristem (NAM) -like protein [Arabidopsis thaliana] gi|332003809|gb|AED91192.1| NAC domain containing protein 80 [Arabidopsis thaliana]</td><td>320</td><td>329</td><td>1.00E-161</td><td>102.8</td><td>89.4</td><td>94.1</td><td>NAC domain containing protein 80</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07680.1 | Symbols: ANAC080, ANAC079, ATNAC4, NAC080 | NAC domain containing protein 80 | chr5:2436092-2437322 FORWARD LENGTH=329</td><td>320</td><td>329</td><td>1.00E-164</td><td>102.8</td><td>89.4</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00492.1.g14877.t1</td><td>sp|Q9FLQ7.3|FH20_ARATH RecName: Full=Formin-like protein 20; Short=AtFH20 gi|332003816|gb|AED91199.1| actin binding protein [Arabidopsis thaliana]</td><td>1712</td><td>1649</td><td>0</td><td>96.3</td><td>42.9</td><td>46.6</td><td>RecName: Full=Formin-like protein 20; Short=AtFH20 gi|332003816|gb|AED91199.1| actin binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07740.1 | Symbols: | actin binding | chr5:2459076-2466580 REVERSE LENGTH=1649</td><td>1712</td><td>1649</td><td>0</td><td>96.3</td><td>42.9</td><td>46.6</td></tr>
<tr><td>Rsa1.0_00492.1.g14878.t1</td><td>ref|XP_002873324.1| flavin-containing monooxygenase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319161|gb|EFH49583.1| flavin-containing monooxygenase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>460</td><td>460</td><td>0</td><td>100.0</td><td>90.7</td><td>95.9</td><td>flavin-containing monooxygenase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G07800.1 | Symbols: | Flavin-binding monooxygenase family protein | chr5:2486717-2489241 REVERSE LENGTH=460</td><td>460</td><td>460</td><td>0</td><td>100.0</td><td>90.2</td><td>95.7</td></tr>
<tr><td>Rsa1.0_00492.1.g14879.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00492.1.g14880.t4</td><td>gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]</td><td>442</td><td>442</td><td>1.00E-134</td><td>100.0</td><td>54.8</td><td>62.2</td><td>hypothetical protein 24.t00017</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343</td><td>442</td><td>343</td><td>2.00E-41</td><td>77.6</td><td>25.3</td><td>34.8</td></tr>
<tr><td>Rsa1.0_00492.1.g14881.t1</td><td>gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]</td><td>287</td><td>255</td><td>2.00E-65</td><td>88.9</td><td>48.4</td><td>59.9</td><td>hypothetical protein 40.t00057</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302</td><td>287</td><td>302</td><td>1.00E-43</td><td>105.2</td><td>39.7</td><td>56.8</td></tr>
<tr><td>Rsa1.0_00492.1.g14882.t1</td><td>ref|NP_565423.1| uncharacterized protein [Arabidopsis thaliana] gi|17933281|gb|AAL48224.1|AF446349_1 At2g17710/T17A5.17 [Arabidopsis thaliana] gi|20453391|gb|AAM19934.1| At2g17710/T17A5.17 [Arabidopsis thaliana] gi|110736849|dbj|BAF00382.1| hypothetical protein [Arabidopsis thaliana] gi|330251578|gb|AEC06672.1| uncharacterized protein AT2G17710 [Arabidopsis thaliana]</td><td>287</td><td>152</td><td>3.00E-63</td><td>53.0</td><td>45.6</td><td>48.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17710.1 | Symbols: | unknown protein; Has 39 Blast hits to 39 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:7693856-7694554 FORWARD LENGTH=152</td><td>287</td><td>152</td><td>8.00E-66</td><td>53.0</td><td>45.6</td><td>48.4</td></tr>
</table>

Rsa1.0_00492.1.g14883.t1	ref|NP_179363.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|25411813|pir||F84555 similar to prolyl 4-hydroxylase alpha subunit [imported] - Arabidopsis thaliana gi|89274129|gb|ABD65585.1| At2g17720 [Arabidopsis thaliana] gi|110738861|dbj|BAF01353.1| similar to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana] gi|330251579|gb|AEC06673.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	308	291	1.00E-144	94.5	88.0	91.9	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT2G17720.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr2:7697513-7699174 FORWARD LENGTH=291	308	291	2.33E-156	94.5	88.0	91.9
Rsa1.0_00492.1.g14884.t1	dbj|BAB01350.1| Mutator-like transposase [Arabidopsis thaliana]	206	811	4.00E-37	393.7	40.8	49.5	Mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00493.1.g14885.t1	gb|AAZ66942.1| 117M18_23 [Brassica rapa]	471	518	0	110.0	81.1	91.1	117M18_23	gbpln	Brassica rapa	AT5G44050.1 | Symbols: | MATE efflux family protein | chr5:17722484-17726209 FORWARD LENGTH=491	471	491	0	104.2	78.3	88.1
Rsa1.0_00493.1.g14886.t1	tpg|DAA55311.1| TPA: histone H3.2 [Zea mays]	136	245	1.00E-72	180.1	100.0	100.0	TPA: histone H3.2	gbenv/gbpln	Zea mays	AT5G65360.1 | Symbols: | Histone superfamily protein | chr5:26120099-26120509 REVERSE LENGTH=136	136	136	5.00E-74	100.0	100.0	100.0
Rsa1.0_00493.1.g14887.t1	gb|AAZ66937.1| 117M18_18 [Brassica rapa]	249	249	1.00E-138	100.0	98.8	99.6	117M18_18	gbpln	Brassica rapa	AT5G10360.1 | Symbols: EMB3010, RPS6B | Ribosomal protein S6e | chr5:3258734-3260142 REVERSE LENGTH=249	249	249	1.00E-136	100.0	96.0	97.6
Rsa1.0_00493.1.g14888.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00493.1.g14889.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00493.1.g14890.t1	ref|XP_002873449.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297319286|gb|EFH49708.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	612	613	0	100.2	94.4	97.2	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT5G10290.1 | Symbols: | leucine-rich repeat transmembrane protein kinase family protein | chr5:3235462-3238171 REVERSE LENGTH=613	612	613	0	100.2	94.1	97.4
Rsa1.0_00493.1.g14891.t1	ref|NP_196590.1| myb domain protein 92 [Arabidopsis thaliana] gi|3941524|gb|AAC83638.1| putative transcription factor [Arabidopsis thaliana] gi|8953409|emb|CAB96684.1| putative transcription factor MYB92 [Arabidopsis thaliana] gi|27754493|gb|AAO22694.1| putative myb family transcription factor [Arabidopsis thaliana] gi|28393977|gb|AAO42396.1| putative myb family transcription factor [Arabidopsis thaliana] gi|41619378|gb|AAS10089.1| MYB transcription factor [Arabidopsis thaliana] gi|332004133|gb|AED91516.1| myb domain protein 92 [Arabidopsis thaliana]	338	334	1.00E-157	98.8	84.3	90.5	myb domain protein 92	gbpln	Arabidopsis thaliana	AT5G10280.1 | Symbols: MYB92, ATMYB92, ATMYB64 | myb domain protein 92 | chr5:3232776-3233956 FORWARD LENGTH=334	338	334	1.00E-160	98.8	84.3	90.5
Rsa1.0_00493.1.g14892.t1	ref|NP_196581.1| major facilitator protein [Arabidopsis thaliana] gi|13430500|gb|AAK25872.1|AF360162_1 unknown protein [Arabidopsis thaliana] gi|21281225|gb|AAM44941.1| unknown protein [Arabidopsis thaliana] gi|332004123|gb|AED91506.1| major facilitator protein [Arabidopsis thaliana]	575	488	0	84.9	76.7	80.9	major facilitator protein	gbpln	Arabidopsis thaliana	AT5G10190.1 | Symbols: | Major facilitator superfamily protein | chr5:3199205-3201140 FORWARD LENGTH=488	575	488	0	84.9	76.7	80.9
Rsa1.0_00493.1.g14893.t1	gb|ACO25294.1| low affinity sulfate transporter Bnst2-1 [Brassica napus]	650	677	0	104.2	96.3	98.0	low affinity sulfate transporter Bnst2-1	gbpln	Brassica napus	AT5G10180.1 | Symbols: AST68, SULTR2;1 | slufate transporter 2;1 | chr5:3193225-3196818 FORWARD LENGTH=677	650	677	0	104.2	90.6	96.6
Rsa1.0_00493.1.g14894.t1	gb|ACQ44221.1| putative inositol-3-phosphate synthase isozyme 3 [Arabis alpina]	510	510	0	100.0	96.3	98.6	putative inositol-3-phosphate synthase isozyme 3	gbpln	Arabis alpina	AT5G10170.1 | Symbols: ATMIPS3, MIPS3 | myo-inositol-1-phosphate synthase 3 | chr5:3187538-3190161 REVERSE LENGTH=510	510	510	0	100.0	95.3	98.0
Rsa1.0_00493.1.g14895.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00493.1.g14896.t1	ref|XP_002873442.1| hypothetical protein ARALYDRAFT_350224 [Arabidopsis lyrata subsp. lyrata] gi|297319279|gb|EFH49701.1| hypothetical protein ARALYDRAFT_350224 [Arabidopsis lyrata subsp. lyrata]	411	412	1.00E-169	100.2	78.8	84.7	hypothetical protein ARALYDRAFT_350224	gbpln	Arabidopsis lyrata	AT5G10150.1 | Symbols: | Domain of unknown function (DUF966) | chr5:3182176-3183834 REVERSE LENGTH=414	411	414	1.00E-169	100.7	80.3	86.4
Rsa1.0_00493.1.g14897.t4	gb|EOA21702.1| hypothetical protein CARUB_v10002136mg [Capsella rubella]	166	164	8.00E-78	98.8	83.7	91.6	hypothetical protein CARUB_v10002136mg	gbpln	Capsella rubella	AT5G10130.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:3171551-3172428 REVERSE LENGTH=164	166	164	4.00E-79	98.8	84.9	91.0

Rsa1.0_00493.1.g14898.t1	gb|ACQ44230.1| putative ethylene insensitive 3 protein [Arabis alpina]	539	460	0	85.3	63.1	66.8	putative ethylene insensitive 3 protein	gbpln	Arabis alpina	AT5G10120.1 | Symbols: | Ethylene insensitive 3 family protein | chr5:3169732-3171147 FORWARD LENGTH=471	539	471	0	87.4	62.5	66.4
Rsa1.0_00493.1.g14899.t1	gb|AAZ67592.1| 80A08_7 [Brassica rapa subsp. pekinensis]	575	560	0	97.4	82.1	87.1	80A08_7	gbpln	Brassica rapa	AT5G10090.1 | Symbols: TPR13 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:3153722-3155745 REVERSE LENGTH=594	575	594	0	103.3	82.3	90.3
Rsa1.0_00493.1.g14900.t1	ref|XP_002873435.1| hypothetical protein ARALYDRAFT_487831 [Arabidopsis lyrata subsp. lyrata] gi|297319272|gb|EFH49694.1| hypothetical protein ARALYDRAFT_487831 [Arabidopsis lyrata subsp. lyrata]	485	470	0	96.9	84.1	88.5	hypothetical protein ARALYDRAFT_487831	gbpln	Arabidopsis lyrata	AT5G10060.1 | Symbols: | ENTH/VHS family protein | chr5:3145994-3148049 REVERSE LENGTH=469	485	469	0	96.7	83.5	88.0
Rsa1.0_00493.1.g14901.t1	gb|AAZ66925.1| 117M18_6 [Brassica rapa]	317	280	1.00E-138	88.3	73.2	81.4	117M18_6	gbpln	Brassica rapa	AT5G10050.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:3144254-3145643 FORWARD LENGTH=279	317	279	1.00E-137	88.0	71.3	79.5
Rsa1.0_00494.1.g14902.t1	ref|XP_002877550.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323388|gb|EFH53809.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	448	467	2.33E-156	104.2	61.6	76.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G47170.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:17368672-17370494 REVERSE LENGTH=468	448	468	1.00E-147	104.5	60.5	75.0
Rsa1.0_00494.1.g14903.t1	ref|XP_003606631.1| Histone H2B [Medicago truncatula] gi|355507686|gb|AES88828.1| Histone H2B [Medicago truncatula]	153	147	6.00E-63	96.1	86.3	90.2	Histone H2B	gbpln	Medicago truncatula	AT2G28720.1 | Symbols: | Histone superfamily protein | chr2:12327043-12327498 FORWARD LENGTH=151	153	151	8.00E-64	98.7	86.9	90.2
Rsa1.0_00494.1.g14904.t1	gb|AAD29058.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	707	1229	0	173.8	48.7	67.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	707	626	5.00E-27	88.5	11.3	16.7
Rsa1.0_00494.1.g14905.t1	gb|EOA25343.1| hypothetical protein CARUB_v10018664mg [Capsella rubella]	161	181	6.00E-13	112.4	29.2	40.4	hypothetical protein CARUB_v10018664mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00494.1.g14906.t1	gb|EOA28002.1| hypothetical protein CARUB_v10024179mg, partial [Capsella rubella]	148	171	8.00E-65	115.5	90.5	95.9	hypothetical protein CARUB_v10024179mg, partial	gbpln	Capsella rubella	AT2G28710.1 | Symbols: | C2H2-type zinc finger family protein | chr2:12322974-12323444 FORWARD LENGTH=156	148	156	2.00E-65	105.4	89.2	93.9
Rsa1.0_00494.1.g14907.t1	gb|EOA27317.1| hypothetical protein CARUB_v10023441mg, partial [Capsella rubella]	356	377	0	105.9	94.9	97.5	hypothetical protein CARUB_v10023441mg, partial	gbpln	Capsella rubella	AT2G28680.1 | Symbols: | RmlC-like cupins superfamily protein | chr2:12303118-12304747 REVERSE LENGTH=356	356	356	0	100.0	94.9	97.5
Rsa1.0_00494.1.g14908.t1	ref|NP_973782.1| disease resistance-responsive, dirigent domain-containing protein [Arabidopsis thaliana] gi|8439894|gb|AAF75080.1|AC007583_16 Contains similarity to disease resistance response protein from Pisum sativum gb|M18250. EST gb|F13940 comes from this gene [Arabidopsis thaliana] gi|332190051|gb|AEE28172.1| disease resistance-responsive, dirigent domain-containing protein [Arabidopsis thaliana]	418	389	1.00E-127	93.1	70.1	78.7	disease resistance-responsive, dirigent domain-containing protein	gbpln	Arabidopsis thaliana	AT1G07730.2 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr1:2397527-2398696 REVERSE LENGTH=389	418	389	1.00E-130	93.1	70.1	78.7
Rsa1.0_00494.1.g14909.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00494.1.g14910.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00494.1.g14911.t1	ref|XP_002879179.1| copper-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297325018|gb|EFH55438.1| copper-binding family protein [Arabidopsis lyrata subsp. lyrata]	265	258	7.00E-97	97.4	77.4	86.8	copper-binding family protein	gbpln	Arabidopsis lyrata	AT2G28660.1 | Symbols: | Chloroplast-targeted copper chaperone protein | chr2:12295419-12296944 FORWARD LENGTH=265	265	265	3.00E-82	100.0	72.8	82.3
Rsa1.0_00494.1.g14912.t1	gb|EOA26326.1| hypothetical protein CARUB_v10025404mg [Capsella rubella]	569	609	0	107.0	77.9	87.2	hypothetical protein CARUB_v10025404mg	gbpln	Capsella rubella	AT2G28640.1 | Symbols: ATEXO70H5, EXO70H5 | exocyst subunit exo70 family protein H5 | chr2:12284625-12286645 REVERSE LENGTH=605	569	605	0	106.3	76.8	86.6
Rsa1.0_00494.1.g14913.t1	gb|EOA27024.1| hypothetical protein CARUB_v10023121mg [Capsella rubella]	476	476	0	100.0	91.2	96.8	hypothetical protein CARUB_v10023121mg	gbpln	Capsella rubella	AT2G28630.1 | Symbols: KCS12 | 3-ketoacyl-CoA synthase 12 | chr2:12275719-12277149 REVERSE LENGTH=476	476	476	0	100.0	89.1	93.9
Rsa1.0_00494.1.g14914.t1	gb|EOA28833.1| hypothetical protein CARUB_v10025072mg [Capsella rubella]	80	100	7.00E-16	125.0	63.8	73.8	hypothetical protein CARUB_v10025072mg	gbpln	Capsella rubella	AT2G28625.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:12272381-12272756 FORWARD LENGTH=98	80	98	1.00E-16	122.5	65.0	70.0

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<tr><td>Rsa1.0_00494.1.g14915.t1</td><td>ref|NP_195377.1| MADS-box transcription factor family protein [Arabidopsis thaliana] gi|4006904|emb|CAB16834.1| putative MADS-box protein [Arabidopsis thaliana] gi|7270607|emb|CAB80325.1| putative MADS-box protein [Arabidopsis thaliana] gi|21592306|gb|AAM64257.1| putative MADS-box protein [Arabidopsis thaliana] gi|32402432|gb|AAN52798.1| MADS-box protein AGL40 [Arabidopsis thaliana] gi|91806780|gb|ABE66117.1| MADS-box protein [Arabidopsis thaliana] gi|332661275|gb|AEE86675.1| MADS-box transcription factor family protein [Arabidopsis thaliana]</td><td>174</td><td>248</td><td>1.00E-19</td><td>142.5</td><td>47.1</td><td>62.1</td><td>MADS-box transcription factor family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G36590.1 | Symbols: | MADS-box transcription factor family protein | chr4:17261146-17262189 REVERSE LENGTH=248</td><td>174</td><td>248</td><td>5.00E-22</td><td>142.5</td><td>47.1</td><td>62.1</td></tr>
<tr><td>Rsa1.0_00494.1.g14916.t1</td><td>ref|XP_002880998.1| hypothetical protein ARALYDRAFT_481773 [Arabidopsis lyrata subsp. lyrata] gi|297326837|gb|EFH57257.1| hypothetical protein ARALYDRAFT_481773 [Arabidopsis lyrata subsp. lyrata]</td><td>1049</td><td>1042</td><td>0</td><td>99.3</td><td>92.2</td><td>95.5</td><td>hypothetical protein ARALYDRAFT_481773</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G28620.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:12265167-12270020 REVERSE LENGTH=1042</td><td>1049</td><td>1042</td><td>0</td><td>99.3</td><td>91.9</td><td>95.9</td></tr>
<tr><td>Rsa1.0_00494.1.g14917.t2</td><td>ref|XP_002879170.1| hypothetical protein ARALYDRAFT_481772 [Arabidopsis lyrata subsp. lyrata] gi|297325009|gb|EFH55429.1| hypothetical protein ARALYDRAFT_481772 [Arabidopsis lyrata subsp. lyrata]</td><td>238</td><td>242</td><td>2.00E-82</td><td>101.7</td><td>82.4</td><td>90.3</td><td>hypothetical protein ARALYDRAFT_481772</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G28610.1 | Symbols: PRS, WOX3, PRS1 | Homeodomain-like superfamily protein | chr2:12262115-12263286 FORWARD LENGTH=244</td><td>238</td><td>244</td><td>4.00E-83</td><td>102.5</td><td>81.5</td><td>89.1</td></tr>
<tr><td>Rsa1.0_00495.1.g14918.t1</td><td>gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]</td><td>259</td><td>1463</td><td>4.00E-84</td><td>564.9</td><td>59.5</td><td>71.0</td><td>F5J5.1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>259</td><td>1262</td><td>5.00E-37</td><td>487.3</td><td>30.9</td><td>44.4</td></tr>
<tr><td>Rsa1.0_00495.1.g14919.t10</td><td>gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]</td><td>734</td><td>1643</td><td>1.00E-160</td><td>223.8</td><td>47.0</td><td>62.3</td><td>gag/pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>ATMG00820.1 | Symbols: ORF170 | Reverse transcriptase (RNA-dependent DNA polymerase) | chrM:228573-229085 REVERSE LENGTH=170</td><td>734</td><td>170</td><td>2.00E-13</td><td>23.2</td><td>4.9</td><td>6.7</td></tr>
<tr><td>Rsa1.0_00495.1.g14920.t1</td><td>gb|ACI96072.1| protein phosphatase 2a 55 kda regulatory subunit b [Brassica rapa subsp. pekinensis]</td><td>487</td><td>494</td><td>0</td><td>101.4</td><td>89.1</td><td>93.8</td><td>protein phosphatase 2a 55 kda regulatory subunit b</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G51690.3 | Symbols: B ALPHA | protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform | chr1:19164124-19169974 FORWARD LENGTH=603</td><td>487</td><td>603</td><td>0</td><td>123.8</td><td>87.3</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00495.1.g14921.t1</td><td>gb|EOA31629.1| hypothetical protein CARUB_v10014828mg [Capsella rubella]</td><td>140</td><td>154</td><td>8.00E-16</td><td>110.0</td><td>39.3</td><td>59.3</td><td>hypothetical protein CARUB_v10014828mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G20625.1 | Symbols: | Protein of unknown function (DUF626) | chr2:8896154-8897218 REVERSE LENGTH=179</td><td>140</td><td>179</td><td>1.00E-14</td><td>127.9</td><td>25.0</td><td>38.6</td></tr>
<tr><td>Rsa1.0_00495.1.g14922.t1</td><td>gb|EOA40270.1| hypothetical protein CARUB_v10008998mg [Capsella rubella]</td><td>533</td><td>482</td><td>0</td><td>90.4</td><td>80.3</td><td>83.9</td><td>hypothetical protein CARUB_v10008998mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G51710.1 | Symbols: UBP6, ATUBP6 | ubiquitin-specific protease 6 | chr1:19175805-19179894 REVERSE LENGTH=482</td><td>533</td><td>482</td><td>0</td><td>90.4</td><td>79.2</td><td>83.1</td></tr>
<tr><td>Rsa1.0_00495.1.g14923.t1</td><td>gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1222</td><td>1225</td><td>0</td><td>100.2</td><td>34.2</td><td>48.5</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1222</td><td>575</td><td>4.00E-65</td><td>47.1</td><td>13.7</td><td>22.5</td></tr>
<tr><td>Rsa1.0_00495.1.g14924.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>919</td><td>1142</td><td>0</td><td>124.3</td><td>52.1</td><td>68.2</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>919</td><td>575</td><td>1.00E-71</td><td>62.6</td><td>18.4</td><td>29.2</td></tr>
<tr><td>Rsa1.0_00495.1.g14925.t1</td><td>ref|XP_002864149.1| hypothetical protein ARALYDRAFT_495276 [Arabidopsis lyrata subsp. lyrata] gi|297309984|gb|EFH40408.1| hypothetical protein ARALYDRAFT_495276 [Arabidopsis lyrata subsp. lyrata]</td><td>310</td><td>500</td><td>2.00E-92</td><td>161.3</td><td>57.4</td><td>65.8</td><td>hypothetical protein ARALYDRAFT_495276</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G52050.1 | Symbols: | MATE efflux family protein | chr5:21138933-21140450 FORWARD LENGTH=505</td><td>310</td><td>505</td><td>5.00E-93</td><td>162.9</td><td>56.1</td><td>65.5</td></tr>
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Rsa1.0_00495.1.g14927.t6	gb|ABD96944.1| hypothetical protein [Cleome spinosa]	129	826	9.00E-11	640.3	26.4	40.3	hypothetical protein	gbpln	Cleome spinosa	#	#	#	#	#	#	#
Rsa1.0_00495.1.g14928.t3	ref|XP_002891654.1| hypothetical protein ARALYDRAFT_474290 [Arabidopsis lyrata subsp. lyrata] gi|297337496|gb|EFH67913.1| hypothetical protein ARALYDRAFT_474290 [Arabidopsis lyrata subsp. lyrata]	464	624	0	134.5	85.8	89.9	hypothetical protein ARALYDRAFT_474290	gbpln	Arabidopsis lyrata	AT1G51720.1 | Symbols: | Amino acid dehydrogenase family protein | chr1:19181741-19186297 FORWARD LENGTH=637	464	637	0	137.3	85.3	89.9
Rsa1.0_00496.1.g14929.t1	ref|NP_850164.1| protein autophagy 9 [Arabidopsis thaliana] gi|19715618|gb|AAL91630.1| At2g31260/F16D14.10 [Arabidopsis thaliana] gi|19912149|dbj|BAB88386.1| autophagy 9 [Arabidopsis thaliana] gi|20466356|gb|AAM20495.1| unknown protein [Arabidopsis thaliana] gi|23198070|gb|AAN15562.1| unknown protein [Arabidopsis thaliana] gi|23463043|gb|AAN33191.1| At2g31260/F16D14.10 [Arabidopsis thaliana] gi|330253421|gb|AEC08515.1| protein autophagy 9 [Arabidopsis thaliana]	877	866	0	98.7	84.7	89.1	protein autophagy 9	gbpln	Arabidopsis thaliana	AT2G31260.1 | Symbols: APG9, ATAPG9 | autophagy 9 (APG9) | chr2:13322291-13326293 REVERSE LENGTH=866	877	866	0	98.7	84.7	89.1
Rsa1.0_00496.1.g14930.t1	gb|EOA26748.1| hypothetical protein CARUB_v10022834mg [Capsella rubella]	630	617	0	97.9	81.3	88.7	hypothetical protein CARUB_v10022834mg	gbpln	Capsella rubella	AT2G31240.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:13317570-13319518 REVERSE LENGTH=617	630	617	0	97.9	80.3	87.8
Rsa1.0_00496.1.g14931.t1	gb|AAD20668.1| ethylene reponse factor-like AP2 domain transcription factor [Arabidopsis thaliana]	254	236	3.00E-96	92.9	81.1	87.0	ethylene reponse factor-like AP2 domain transcription factor	gbpln	Arabidopsis thaliana	AT2G31230.1 | Symbols: ATERF15, ERF15 | ethylene-responsive element binding factor 15 | chr2:13306676-13307407 REVERSE LENGTH=243	254	243	2.00E-98	95.7	75.6	81.5
Rsa1.0_00496.1.g14932.t2	ref|NP_180680.2| transcription factor bHLH10 [Arabidopsis thaliana] gi|75298101|sp|Q84TK1.1|BH010_ARATH RecName: Full=Transcription factor bHLH10; AltName: Full=Basic helix-loop-helix protein 10; Short=AtbHLH10; Short=bHLH 10; AltName: Full=Transcription factor EN 23; AltName: Full=bHLH transcription factor bHLH010 gi|28973613|gb|AAO64131.1| putative bHLH protein [Arabidopsis thaliana] gi|30793963|gb|AAP40433.1| putative bHLH protein [Arabidopsis thaliana] gi|110737111|dbj|BAF00507.1| putative transcription factor BHLH10 [Arabidopsis thaliana] gi|330253417|gb|AEC08511.1| transcription factor bHLH10 [Arabidopsis thaliana]	287	458	5.00E-81	159.6	55.4	60.3	transcription factor bHLH10	gbpln	Arabidopsis thaliana	AT2G31220.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:13303014-13304661 FORWARD LENGTH=458	287	458	1.00E-83	159.6	55.4	60.3
Rsa1.0_00496.1.g14933.t1	ref|XP_002879311.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297325150|gb|EFH55570.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	443	430	0	97.1	77.4	85.6	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT2G31210.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:13296655-13298139 FORWARD LENGTH=428	443	428	0	96.6	77.7	86.2

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<tr><td>Rsa1.0_00496.1.g14934.t1</td><td>ref|NP_565718.1| uncharacterized protein [Arabidopsis thaliana] gi|20197897|gb|AAD20664.2| expressed protein [Arabidopsis thaliana] gi|21553562|gb|AAM62655.1| unknown [Arabidopsis thaliana] gi|109134157|gb|ABG25076.1| At2g31190 [Arabidopsis thaliana] gi|330253411|gb|AEC08505.1| uncharacterized protein AT2G31190 [Arabidopsis thaliana]</td><td>426</td><td>433</td><td>0</td><td>101.6</td><td>89.4</td><td>94.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G31190.1 | Symbols: RUS2, WXR1 | Protein of unknown function, DUF647 | chr2:13291458-13293681 REVERSE LENGTH=433</td><td>426</td><td>433</td><td>0</td><td>101.6</td><td>89.4</td><td>94.6</td></tr>
<tr><td>Rsa1.0_00496.1.g14935.t1</td><td>ref|NP_180676.1| myb domain protein 14 [Arabidopsis thaliana] gi|4432813|gb|AAD20663.1| myb family transcription factor [Arabidopsis thaliana] gi|20197333|gb|AAM15030.1| myb DNA-binding protein [Arabidopsis thaliana] gi|41619192|gb|AAS10045.1| MYB transcription factor [Arabidopsis thaliana] gi|89111928|gb|ABD60736.1| At2g31180 [Arabidopsis thaliana] gi|330253410|gb|AEC08504.1| myb domain protein 14 [Arabidopsis thaliana]</td><td>250</td><td>249</td><td>1.00E-123</td><td>99.6</td><td>84.8</td><td>92.8</td><td>myb domain protein 14</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G31180.1 | Symbols: ATMYB14, MYB14AT, MYB14 | myb domain protein 14 | chr2:13286806-13288175 REVERSE LENGTH=249</td><td>250</td><td>249</td><td>1.00E-126</td><td>99.6</td><td>84.8</td><td>92.8</td></tr>
<tr><td>Rsa1.0_00496.1.g14936.t1</td><td>ref|NP_565716.1| uncharacterized protein [Arabidopsis thaliana] gi|3746060|gb|AAC63835.1| expressed protein [Arabidopsis thaliana] gi|15912211|gb|AAL08239.1| At2g31160/T16B12.3 [Arabidopsis thaliana] gi|19547989|gb|AAL87358.1| At2g31160/T16B12.3 [Arabidopsis thaliana] gi|330253407|gb|AEC08501.1| uncharacterized protein AT2G31160 [Arabidopsis thaliana]</td><td>219</td><td>219</td><td>1.00E-89</td><td>100.0</td><td>88.1</td><td>90.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G31160.1 | Symbols: LSH3 | Protein of unknown function (DUF640) | chr2:13277903-13278562 FORWARD LENGTH=219</td><td>219</td><td>219</td><td>3.00E-92</td><td>100.0</td><td>88.1</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00496.1.g14937.t1</td><td>ref|XP_002862788.1| hypothetical protein ARALYDRAFT_920271 [Arabidopsis lyrata subsp. lyrata] gi|297308512|gb|EFH39046.1| hypothetical protein ARALYDRAFT_920271 [Arabidopsis lyrata subsp. lyrata]</td><td>187</td><td>417</td><td>5.00E-14</td><td>223.0</td><td>29.4</td><td>38.5</td><td>hypothetical protein ARALYDRAFT_920271</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06190.1 | Symbols: | Rho termination factor | chr1:1892467-1894078 REVERSE LENGTH=401</td><td>187</td><td>401</td><td>3.00E-13</td><td>214.4</td><td>23.0</td><td>30.5</td></tr>
<tr><td>Rsa1.0_00496.1.g14938.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00496.1.g14939.t1</td><td>ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]</td><td>402</td><td>387</td><td>1.00E-103</td><td>96.3</td><td>53.2</td><td>66.2</td><td>F-box protein DOR</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387</td><td>402</td><td>387</td><td>1.00E-106</td><td>96.3</td><td>53.2</td><td>66.2</td></tr>
<tr><td>Rsa1.0_00496.1.g14940.t1</td><td>gb|EOA33274.1| hypothetical protein CARUB_v10019647mg [Capsella rubella]</td><td>2360</td><td>2361</td><td>0</td><td>100.0</td><td>98.4</td><td>99.2</td><td>hypothetical protein CARUB_v10019647mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G80070.1 | Symbols: SUS2, EMB33, EMB177, EMB14 | Pre-mRNA-processing-splicing factor | chr1:30118052-30127574 FORWARD LENGTH=2359</td><td>2360</td><td>2359</td><td>0</td><td>100.0</td><td>97.9</td><td>99.0</td></tr>
<tr><td>Rsa1.0_00496.1.g14941.t1</td><td>gb|EOA28821.1| hypothetical protein CARUB_v10025060mg [Capsella rubella]</td><td>96</td><td>191</td><td>1.00E-13</td><td>199.0</td><td>37.5</td><td>47.9</td><td>hypothetical protein CARUB_v10025060mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G31050.1 | Symbols: | Cupredoxin superfamily protein | chr2:13212150-13212752 FORWARD LENGTH=200</td><td>96</td><td>200</td><td>2.00E-14</td><td>208.3</td><td>39.6</td><td>47.9</td></tr>
<tr><td>Rsa1.0_00496.1.g14942.t1</td><td>gb|EOA27142.1| hypothetical protein CARUB_v10023243mg, partial [Capsella rubella]</td><td>256</td><td>436</td><td>5.00E-39</td><td>170.3</td><td>37.9</td><td>43.0</td><td>hypothetical protein CARUB_v10023243mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G31130.1 | Symbols: | unknown protein; Has 116 Blast hits to 113 proteins in 44 species: Archae - 0; Bacteria - 3; Metazoa - 21; Fungi - 2; Plants - 40; Viruses - 0; Other Eukaryotes - 50 (source: NCBI BLink). | chr2:13263829-13265534 REVERSE LENGTH=419</td><td>256</td><td>419</td><td>2.00E-40</td><td>163.7</td><td>35.9</td><td>39.1</td></tr>
<tr><td>Rsa1.0_00497.1.g14943.t1</td><td>gb|EOA36944.1| hypothetical protein CARUB_v10009854mg [Capsella rubella]</td><td>259</td><td>304</td><td>3.00E-55</td><td>117.4</td><td>47.1</td><td>63.7</td><td>hypothetical protein CARUB_v10009854mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G63900.1 | Symbols: DAL1 | E3 Ubiquitin ligase family protein | chr1:23717056-23719086 FORWARD LENGTH=343</td><td>259</td><td>343</td><td>4.00E-20</td><td>132.4</td><td>31.3</td><td>48.3</td></tr>
</table>

Rsa1.0_00497.1.g14944.t1	gb|ABC25625.1| GAGA-binding transcriptional activator [Capsella rubella] gi|83616242|gb|ABC25626.1| GAGA-binding transcriptional activator [Capsella rubella] gi|482574222|gb|EOA38409.1| hypothetical protein CARUB_v10009978mg [Capsella rubella] gi|482574223|gb|EOA38410.1| hypothetical protein CARUB_v10009978mg [Capsella rubella]	279	277	1.00E-134	99.3	86.7	91.0	GAGA-binding transcriptional activator	gbpln	Capsella rubella	AT1G14685.1 | Symbols: BPC2, BBR/BPC2, ATBPC2 | basic pentacysteine 2 | chr1:5043086-5043925 FORWARD LENGTH=279	279	279	1.00E-131	100.0	83.9	88.2
Rsa1.0_00497.1.g14945.t1	gb|AAF63169.1|AC010657_5 T5E21.13 [Arabidopsis thaliana]	786	1776	0	226.0	86.0	91.1	T5E21.13	gbpln	Arabidopsis thaliana	AT1G14650.2 | Symbols: | SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin family protein | chr1:5028077-5030520 FORWARD LENGTH=785	786	785	0	99.9	86.0	91.1
Rsa1.0_00497.1.g14946.t1	emb|CAC05441.1| putative protein [Arabidopsis thaliana]	847	706	0	83.4	51.4	62.5	putative protein	gbpln	Arabidopsis thaliana	AT5G13130.1 | Symbols: | Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein | chr5:4166755-4170324 FORWARD LENGTH=708	847	708	0	83.6	53.6	64.9
Rsa1.0_00497.1.g14947.t2	ref|NP_172913.1| Valyl-tRNA synthetase [Arabidopsis thaliana] gi|21542452|sp|P93736.2|SYV_ARATH RecName: Full=Valine--tRNA ligase; AltName: Full=Valyl-tRNA synthetase; Short=ValRS gi|332191069|gb|AEE29190.1| Valyl-tRNA synthetase [Arabidopsis thaliana]	1030	1108	0	107.6	82.9	91.2	Valyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT1G14610.1 | Symbols: TWN2, VALRS | valyl-tRNA synthetase / valine--tRNA ligase (VALRS) | chr1:5008502-5014486 REVERSE LENGTH=1108	1030	1108	0	107.6	82.9	91.2
Rsa1.0_00497.1.g14948.t1	dbj|BAJ34269.1| unnamed protein product [Thellungiella halophila]	470	472	0	100.4	89.6	94.0	unnamed protein product	----	----	AT1G14580.2 | Symbols: | C2H2-like zinc finger protein | chr1:4990070-4992442 FORWARD LENGTH=467	470	467	0	99.4	82.1	89.1
Rsa1.0_00497.1.g14949.t1	ref|XP_002890064.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335906|gb|EFH66323.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	464	472	0	101.7	78.7	87.9	UBX domain-containing protein	gbpln	Arabidopsis lyrata	AT1G14570.1 | Symbols: | UBX domain-containing protein | chr1:4983770-4987192 FORWARD LENGTH=468	464	468	0	100.9	77.6	86.2
Rsa1.0_00497.1.g14950.t1	ref|NP_172908.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|332191060|gb|AEE29181.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana]	335	331	1.00E-176	98.8	93.7	96.7	Mitochondrial substrate carrier family protein	gbpln	Arabidopsis thaliana	AT1G14560.1 | Symbols: | Mitochondrial substrate carrier family protein | chr1:4981300-4983082 FORWARD LENGTH=331	335	331	1.00E-178	98.8	93.7	96.7
Rsa1.0_00497.1.g14951.t1	ref|NP_172903.1| protein alfin-like 7 [Arabidopsis thaliana] gi|75245845|sp|Q8LA16.1|ALFL7_ARATH RecName: Full=PHD finger protein ALFIN-LIKE 7; Short=Protein AL7 gi|21593666|gb|AAM65633.1| nucleic acid binding protein (alfin-1), putative [Arabidopsis thaliana] gi|30017229|gb|AAP12848.1| At1g14510 [Arabidopsis thaliana] gi|110736110|dbj|BAF00027.1| hypothetical protein [Arabidopsis thaliana] gi|332191052|gb|AEE29173.1| protein alfin-like 7 [Arabidopsis thaliana]	251	252	1.00E-108	100.4	87.6	96.8	protein alfin-like 7	gbpln	Arabidopsis thaliana	AT1G14510.1 | Symbols: AL7 | alfin-like 7 | chr1:4962171-4964154 REVERSE LENGTH=252	251	252	1.00E-111	100.4	87.6	96.8

Rsa1.0_00497.1.g14952.t1	ref|NP_563952.1| NADH dehydrogenase (ubiquinone) [Arabidopsis thaliana] gi|297849852|ref|XP_002892807.1| hypothetical protein ARALYDRAFT_471620 [Arabidopsis lyrata subsp. lyrata] gi|75191411|sp|Q9M9R9.1|NDB3B_ARATH RecName: Full=NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-B gi|7262687|gb|AAF43945.1|AC012188_22 Contains similarity to an unknown protein from Arabidopsis thaliana gb|AC004136.2. ESTs gb|Z47683, gb|Z47682, gb|AA597850, gb|Z29736, gb|Z29735, gb|AA042623 come from this gene [Arabidopsis thaliana] gi|12083314|gb|AAG48816.1|AF332453_1 unknown protein [Arabidopsis thaliana] gi|21592691|gb|AAM64640.1| unknown [Arabidopsis thaliana] gi|30725334|gb|AAP37689.1| At1g14450 [Arabidopsis thaliana] gi|110736426|dbj|BAF00181.1| hypothetical protein [Arabidopsis thaliana] gi|297338649|gb|EFH69066.1| hypothetical protein ARALYDRAFT_471620 [Arabidopsis lyrata subsp. lyrata] gi|332191044|gb|AEE29165.1| NADH dehydrogenase (ubiquinone) [Arabidopsis thaliana]	73	73	1.00E-33	100.0	94.5	95.9	NADH dehydrogenase (ubiquinone)	gbpln	Arabidopsis lyrata	AT1G14450.1 | Symbols: | NADH dehydrogenase (ubiquinone)s | chr1:4947337-4947558 REVERSE LENGTH=73	73	73	2.00E-36	100.0	94.5	95.9
Rsa1.0_00497.1.g14953.t1	ref|XP_002892805.1| hypothetical protein ARALYDRAFT_471616 [Arabidopsis lyrata subsp. lyrata] gi|297338647|gb|EFH69064.1| hypothetical protein ARALYDRAFT_471616 [Arabidopsis lyrata subsp. lyrata]	459	459	0	100.0	82.1	90.6	hypothetical protein ARALYDRAFT_471616	gbpln	Arabidopsis lyrata	AT1G14420.1 | Symbols: AT59 | Pectate lyase family protein | chr1:4931844-4933405 REVERSE LENGTH=459	459	459	0	100.0	81.7	89.5
Rsa1.0_00497.1.g14954.t1	ref|XP_002889764.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297335606|gb|EFH66023.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	367	374	4.00E-93	101.9	56.7	69.2	F-box family protein	gbpln	Arabidopsis lyrata	AT1G09650.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3125978-3127126 FORWARD LENGTH=382	367	382	3.00E-94	104.1	56.9	68.4
Rsa1.0_00497.1.g14955.t1	ref|NP_172893.1| ssDNA-binding transcriptional regulator [Arabidopsis thaliana] gi|75191428|sp|Q9M9S3.1|WHY1_ARATH RecName: Full=Single-stranded DNA-binding protein WHY1, chloroplastic; AltName: Full=Protein PLASTID TRANSCRIPTIONALLY ACTIVE 1; AltName: Full=Protein WHIRLY 1; Short=AtWHY1; Flags: Precursor gi|7262683|gb|AAF43941.1|AC012188_18 Contains similarity to a hypothetical protein from Arabidopsis thaliana gb|AC002521.2. EST gb|AI995686 comes from this gene [Arabidopsis thaliana] gi|12083312|gb|AAG48815.1|AF332452_1 putative DNA-binding protein p24 [Arabidopsis thaliana] gi|13877787|gb|AAK43971.1|AF370156_1 putative DNA-binding protein p24 [Arabidopsis thaliana] gi|16323418|gb|AAL15203.1| putative DNA-binding protein p24 [Arabidopsis thaliana] gi|332191039|gb|AEE29160.1| ssDNA-binding transcriptional regulator [Arabidopsis thaliana]	269	263	1.00E-127	97.8	85.5	89.6	ssDNA-binding transcriptional regulator	gbpln	Arabidopsis thaliana	AT1G14410.1 | Symbols: ATWHY1, PTAC1, WHY1 | ssDNA-binding transcriptional regulator | chr1:4929352-4930810 REVERSE LENGTH=263	269	263	1.00E-129	97.8	85.5	89.6

Rsa1.0_00497.1.g14956.t1	ref|NP_563951.1| ubiquitin-conjugating enzyme E2 1 [Arabidopsis thaliana] gi|42571469|ref|NP_973825.1| ubiquitin-conjugating enzyme E2 1 [Arabidopsis thaliana] gi|297849844|ref|XP_002892803.1| hypothetical protein ARALYDRAFT_471614 [Arabidopsis lyrata subsp. lyrata] gi|136636|sp|P25865.1|UBC1_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 1; AltName: Full=Ubiquitin carrier protein 1; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 1; AltName: Full=Ubiquitin-protein ligase 1 gi|157834522|pdb|2AAK|A Chain A, Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana gi|7262682|gb|AAF43940.1|AC012188_17 Strong similarity to a Ubiquitin-conjugating Enzyme (E2-17 KD 1) from Arabidopsis thaliana gi|136636 and contains a Ubiqutin-conjugating Enzyme PF|00179 domain. ESTs gb|AA728508, gb|H36735, gb|AI100736 come from this gene [Arabidopsis thaliana] gi|12083310|gb|AAG48814.1|AF332451_1 putative E2, ubiquitin-conjugating enzyme 1 [Arabidopsis thaliana] gi|166924|gb|AAA32903.1| ubiquitin carrier protein [Arabidopsis thaliana] gi|431260|gb|AAA32897.1| ubiquitin	152	152	1.00E-84	100.0	100.0	100.0	ubiquitin-conjugating enzyme E2 1	gbpln	Arabidopsis lyrata	AT1G14400.2 | Symbols: UBC1, ATUBC1 | ubiquitin carrier protein 1 | chr1:4927294-4928136 REVERSE LENGTH=152	152	152	4.00E-87	100.0	100.0	100.0
Rsa1.0_00497.1.g14957.t2	ref|NP_563951.1| ubiquitin-conjugating enzyme E2 1 [Arabidopsis thaliana] gi|42571469|ref|NP_973825.1| ubiquitin-conjugating enzyme E2 1 [Arabidopsis thaliana] gi|297849844|ref|XP_002892803.1| hypothetical protein ARALYDRAFT_471614 [Arabidopsis lyrata subsp. lyrata] gi|136636|sp|P25865.1|UBC1_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 1; AltName: Full=Ubiquitin carrier protein 1; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 1; AltName: Full=Ubiquitin-protein ligase 1 gi|157834522|pdb|2AAK|A Chain A, Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana gi|7262682|gb|AAF43940.1|AC012188_17 Strong similarity to a Ubiquitin-conjugating Enzyme (E2-17 KD 1) from Arabidopsis thaliana gi|136636 and contains a Ubiqutin-conjugating Enzyme PF|00179 domain. ESTs gb|AA728508, gb|H36735, gb|AI100736 come from this gene [Arabidopsis thaliana] gi|12083310|gb|AAG48814.1|AF332451_1 putative E2, ubiquitin-conjugating enzyme 1 [Arabidopsis thaliana] gi|166924|gb|AAA32903.1| ubiquitin carrier protein [Arabidopsis thaliana] gi|431260|gb|AAA32897.1| ubiquitin	168	152	6.00E-69	90.5	78.0	83.3	ubiquitin-conjugating enzyme E2 1	gbpln	Arabidopsis lyrata	AT1G14400.2 | Symbols: UBC1, ATUBC1 | ubiquitin carrier protein 1 | chr1:4927294-4928136 REVERSE LENGTH=152	168	152	2.00E-71	90.5	78.0	83.3

Rsa1.0_00497.1.g14958.t1	ref|NP_563951.1| ubiquitin-conjugating enzyme E2 1 [Arabidopsis thaliana] gi|42571469|ref|NP_973825.1| ubiquitin-conjugating enzyme E2 1 [Arabidopsis thaliana] gi|297849844|ref|XP_002892803.1| hypothetical protein ARALYDRAFT_471614 [Arabidopsis lyrata subsp. lyrata] gi|136636|sp|P25865.1|UBC1_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 1; AltName: Full=Ubiquitin carrier protein 1; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 1; AltName: Full=Ubiquitin-protein ligase 1 gi|157834522|pdb|2AAK|A Chain A, Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana gi|7262682|gb|AAF43940.1|AC012188_17 Strong similarity to a Ubiquitin-conjugating Enzyme (E2-17 KD 1) from Arabidopsis thaliana gi|136636 and contains a Ubiqutin-conjugating Enzyme PF|00179 domain. ESTs gb|AA728508, gb|H36735, gb|AI100736 come from this gene [Arabidopsis thaliana] gi|12083310|gb|AAG48814.1|AF332451_1 putative E2, ubiquitin-conjugating enzyme 1 [Arabidopsis thaliana] gi|166924|gb|AAA32903.1| ubiquitin carrier protein [Arabidopsis thaliana] gi|431260|gb|AAA32897.1| ubiquitin conjugating enzyme [Arabidopsis	144	152	4.00E-68	105.6	86.8	92.4	ubiquitin-conjugating enzyme E2 1	gbpln	Arabidopsis lyrata	AT1G14400.2 | Symbols: UBC1, ATUBC1 | ubiquitin carrier protein 1 | chr1:4927294-4928136 REVERSE LENGTH=152		144	152	1.00E-70	105.6	86.8	92.4
Rsa1.0_00497.1.g14959.t1	gb|AAM67095.1| unknown [Arabidopsis thaliana]		244	244	1.00E-114	100.0	87.3	93.0	unknown	gbpln	Arabidopsis thaliana	AT1G14340.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:4897709-4898776 FORWARD LENGTH=244		244	244	1.00E-115	100.0	86.9	92.6
Rsa1.0_00497.1.g14960.t1	ref|NP_563945.2| 60S ribosomal protein L10-1 [Arabidopsis thaliana] gi|297844336|ref|XP_002890049.1| hypothetical protein ARALYDRAFT_888807 [Arabidopsis lyrata subsp. lyrata] gi|75305724|sp|Q93VT9.1|RL101_ARATH RecName: Full=60S ribosomal protein L10-1 gi|7262674|gb|AAF43932.1|AC012188_9 Strong similarity, practically identical, to a 60S Ribosomal Protein L10 (Wilm's Tumor Suppressor Protein Homolog) from Arabidopsis thaliana gi|1172806, and contains a Ribosomal L10 PF|00826 domain. ESTs gb|Z18472, gb|T76209, gb|N65098, gb|T43013, gb|T46279, gb|AA394948, gb|AA713166, gb|T44895, gb|AA042691 come from this gene [Arabidopsis thaliana] gi|16226263|gb|AAL16118.1|AF428286_1 At1g14320/F14L17_28 [Arabidopsis thaliana] gi|16226713|gb|AAL16239.1|AF428470_1 At1g14320/F14L17_28 [Arabidopsis thaliana] gi|15028019|gb|AAK76540.1| putative tumor suppressor protein [Arabidopsis thaliana] gi|21281241|gb|AAM45037.1| putative tumor suppressor protein [Arabidopsis thaliana] gi|23397080|gb|AAN31825.1| putative tumor suppressor [Arabidopsis thaliana] gi|297335891|gb|EFH66308.1| hypothetical protein		220	220	1.00E-124	100.0	99.1	99.1	60S ribosomal protein L10-1	gbpln	Arabidopsis lyrata	AT1G14320.1 | Symbols: SAC52, RPL10, RPL10A | Ribosomal protein L16p/L10e family protein | chr1:4888270-4889408 FORWARD LENGTH=220		220	220	1.00E-127	100.0	99.1	99.1
Rsa1.0_00497.1.g14961.t3	ref|XP_002892796.1| ribonuclease T2 family protein [Arabidopsis lyrata subsp. lyrata] gi|297338638|gb|EFH69055.1| ribonuclease T2 family protein [Arabidopsis lyrata subsp. lyrata]		228	226	1.00E-114	99.1	85.1	92.5	ribonuclease T2 family protein	gbpln	Arabidopsis lyrata	AT1G14220.1 | Symbols: | Ribonuclease T2 family protein | chr1:4858642-4859601 REVERSE LENGTH=228		228	228	1.00E-109	100.0	80.3	89.5
Rsa1.0_00497.1.g14962.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	

Rsa1.0_00497.1.g14963.t1	ref|NP_172865.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|5080789|gb|AAD39299.1|AC007576_22 Very similar to adventitious rooting related oxygenase [Arabidopsis thaliana] gi|26451604|dbj|BAC42899.1| putative dioxygenase [Arabidopsis thaliana] gi|28973391|gb|AAO64020.1| putative dioxygenase [Arabidopsis thaliana] gi|332190988|gb|AEE29109.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	305	308	1.00E-159	101.0	87.9	94.4	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT1G14130.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:4836041-4837040 REVERSE LENGTH=308	305	308	1.00E-162	101.0	87.9	94.4
Rsa1.0_00497.1.g14964.t1	ref|NP_172864.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|5080788|gb|AAD39298.1|AC007576_21 Very similar to adventitious rooting related oxygenase [Arabidopsis thaliana] gi|21553384|gb|AAM62477.1| dioxygenase-like protein [Arabidopsis thaliana] gi|24030341|gb|AAN41336.1| putative dioxygenase [Arabidopsis thaliana] gi|332190987|gb|AEE29108.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	311	312	1.00E-127	100.3	68.5	81.4	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT1G14120.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:4833648-4834833 REVERSE LENGTH=312	311	312	1.00E-130	100.3	68.5	81.4
Rsa1.0_00497.1.g14965.t1	sp|Q9XI80.1|FUT6_ARATH RecName: Full=Fucosyltransferase 6; Short=AtFUT6 gi|5080783|gb|AAD39293.1|AC007576_16 Hypothetical protein [Arabidopsis thaliana]	535	537	0	100.4	66.9	79.8	RecName: Full=Fucosyltransferase 6; Short=AtFUT6 gi|5080783|gb|AAD39293.1|AC007576_16 Hypothetical protein	gbpln	Arabidopsis thaliana	AT2G15390.2 | Symbols: FUT4, atfut4 | fucosyltransferase 4 | chr2:6709345-6711044 REVERSE LENGTH=535	535	535	0	100.0	64.9	78.3
Rsa1.0_00498.1.g14966.t1	ref|NP_187980.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75273359|sp|Q9LID1.1|FBK54_ARATH RecName: Full=F-box/kelch-repeat protein At3g13680 gi|9294013|dbj|BAB01916.1| unnamed protein product [Arabidopsis thaliana] gi|332641875|gb|AEE75396.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	371	395	3.00E-96	106.5	56.1	70.4	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	371	395	8.00E-99	106.5	56.1	70.4
Rsa1.0_00498.1.g14967.t1	ref|NP_187980.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75273359|sp|Q9LID1.1|FBK54_ARATH RecName: Full=F-box/kelch-repeat protein At3g13680 gi|9294013|dbj|BAB01916.1| unnamed protein product [Arabidopsis thaliana] gi|332641875|gb|AEE75396.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	371	395	5.00E-97	106.5	55.8	72.0	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	371	395	1.00E-99	106.5	55.8	72.0
Rsa1.0_00498.1.g14968.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00498.1.g14969.t1	ref|XP_002884981.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297330821|gb|EFH61240.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	333	400	3.00E-85	120.1	57.7	70.9	F-box family protein	gbpln	Arabidopsis lyrata	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	333	395	1.00E-85	118.6	57.1	69.4
Rsa1.0_00498.1.g14970.t1	ref|XP_002884981.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297330821|gb|EFH61240.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	386	400	3.00E-91	103.6	52.6	68.4	F-box family protein	gbpln	Arabidopsis lyrata	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	386	395	9.00E-92	102.3	50.3	67.1
Rsa1.0_00498.1.g14971.t1	ref|NP_187980.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75273359|sp|Q9LID1.1|FBK54_ARATH RecName: Full=F-box/kelch-repeat protein At3g13680 gi|9294013|dbj|BAB01916.1| unnamed protein product [Arabidopsis thaliana] gi|332641875|gb|AEE75396.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	296	395	3.00E-70	133.4	53.7	66.6	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	296	395	8.00E-73	133.4	53.7	66.6

Rsa1.0_00498.1.g14972.t1	ref|XP_002868615.1| hypothetical protein ARALYDRAFT_916104 [Arabidopsis lyrata subsp. lyrata] gi|297314451|gb|EFH44874.1| hypothetical protein ARALYDRAFT_916104 [Arabidopsis lyrata subsp. lyrata]	163	254	4.00E-16	155.8	30.7	41.7	hypothetical protein ARALYDRAFT_916104	gbpln	Arabidopsis lyrata	AT5G41530.1 | Symbols: | BEST Arabidopsis thaliana protein match is: DNA-binding storekeeper protein-related (TAIR:AT5G14280.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:16611660-16612088 FORWARD LENGTH=142	163	142	4.00E-15	87.1	23.9	28.8
Rsa1.0_00498.1.g14973.t9	ref|NP_181175.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana] gi|4510343|gb|AAD21432.1| hypothetical protein [Arabidopsis thaliana] gi|55740599|gb|AAV63892.1| hypothetical protein At2g36340 [Arabidopsis thaliana] gi|225898571|dbj|BAH30416.1| hypothetical protein [Arabidopsis thaliana] gi|330254141|gb|AEC09235.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana]	463	414	4.00E-66	89.4	40.8	54.0	DNA-binding storekeeper protein-related transcriptional regulator	gbpln	Arabidopsis thaliana	AT2G36340.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr2:15235858-15237489 FORWARD LENGTH=414	463	414	9.00E-69	89.4	40.8	54.0
Rsa1.0_00498.1.g14974.t1	ref|XP_002879607.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325446|gb|EFH55866.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	924	941	0	101.8	76.1	83.4	predicted protein	gbpln	Arabidopsis lyrata	AT2G36370.1 | Symbols: | ubiquitin-protein ligases | chr2:15247894-15252800 FORWARD LENGTH=898	924	898	0	97.2	72.3	80.1
Rsa1.0_00498.1.g14975.t1	dbj|BAM77406.1| clubroot disease resistance protein [Brassica rapa]	1087	1224	0	112.6	57.9	71.6	clubroot disease resistance protein	gbpln	Brassica rapa	AT3G44480.1 | Symbols: RPP1, cog1 | Disease resistance protein (TIR-NBS-LRR class) family | chr3:16090878-16096041 REVERSE LENGTH=1194	1087	1194	0	109.8	51.7	67.8
Rsa1.0_00498.1.g14976.t1	ref|XP_002879608.1| ATPDR6/PDR6 [Arabidopsis lyrata subsp. lyrata] gi|297325447|gb|EFH55867.1| ATPDR6/PDR6 [Arabidopsis lyrata subsp. lyrata]	1451	1452	0	100.1	91.2	96.2	ATPDR6/PDR6	gbpln	Arabidopsis lyrata	AT2G36380.1 | Symbols: PDR6, ATPDR6 | pleiotropic drug resistance 6 | chr2:15257583-15263627 FORWARD LENGTH=1453	1451	1453	0	100.1	90.2	95.5
Rsa1.0_00498.1.g14977.t1	dbj|BAC42083.1| unknown protein [Arabidopsis thaliana]	390	398	1.00E-148	102.1	83.3	87.7	unknown protein	gbpln	Arabidopsis thaliana	AT2G36400.1 | Symbols: AtGRF3, GRF3 | growth-regulating factor 3 | chr2:15270300-15272617 REVERSE LENGTH=398	390	398	1.00E-144	102.1	82.6	87.2
Rsa1.0_00498.1.g14978.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00498.1.g14979.t1	gb|EOA39854.1| hypothetical protein CARUB_v10008528mg [Capsella rubella]	91	659	2.00E-20	724.2	61.5	64.8	hypothetical protein CARUB_v10008528mg	gbpln	Capsella rubella	AT1G49890.1 | Symbols: QWRF2 | Family of unknown function (DUF566) | chr1:18470282-18473463 FORWARD LENGTH=659	91	659	2.00E-21	724.2	59.3	62.6
Rsa1.0_00498.1.g14980.t1	gb|EOA28004.1| hypothetical protein CARUB_v10024181mg [Capsella rubella]	174	170	1.00E-74	97.7	83.3	88.5	hypothetical protein CARUB_v10024181mg	gbpln	Capsella rubella	AT2G36410.2 | Symbols: | Family of unknown function (DUF662) | chr2:15279041-15280270 FORWARD LENGTH=192	174	192	3.00E-64	110.3	73.0	83.9
Rsa1.0_00498.1.g14981.t1	ref|XP_002879610.1| hypothetical protein ARALYDRAFT_482617 [Arabidopsis lyrata subsp. lyrata] gi|297325449|gb|EFH55869.1| hypothetical protein ARALYDRAFT_482617 [Arabidopsis lyrata subsp. lyrata]	186	191	9.00E-82	102.7	88.7	91.4	hypothetical protein ARALYDRAFT_482617	gbpln	Arabidopsis lyrata	AT2G36410.1 | Symbols: | Family of unknown function (DUF662) | chr2:15279041-15280270 FORWARD LENGTH=195	186	195	1.00E-83	104.8	88.2	90.9
Rsa1.0_00498.1.g14982.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00499.1.g14983.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	809	1838	0	227.2	43.3	55.7	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00499.1.g14984.t2	gb|AAC28207.1| T24H24.13 gene product [Arabidopsis thaliana] gi|7267161|emb|CAB77873.1| putative transposon protein [Arabidopsis thaliana]	418	681	1.00E-14	162.9	12.4	17.7	T24H24.13 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00499.1.g14985.t3	gb|EOA37510.1| hypothetical protein CARUB_v10011684mg, partial [Capsella rubella]	722	273	1.00E-26	37.8	7.9	13.2	hypothetical protein CARUB_v10011684mg, partial	gbpln	Capsella rubella	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	722	361	1.00E-15	50.0	6.5	10.9
Rsa1.0_00499.1.g14986.t1	gb|ELR54187.1| hypothetical protein M91_18163 [Bos grunniens mutus]	564	753	4.00E-19	133.5	8.9	14.7	hypothetical protein M91_18163	gbmam	Bos grunniens	#	#	#	#	#	#	#
Rsa1.0_00499.1.g14987.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	1093	1023	0	93.6	33.4	43.8	F27F5.21	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1093	626	2.00E-25	57.3	6.0	9.3
Rsa1.0_00499.1.g14988.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00499.1.g14989.t2	ref|XP_002872056.1| hypothetical protein ARALYDRAFT_910353 [Arabidopsis lyrata subsp. lyrata] gi|297317893|gb|EFH48315.1| hypothetical protein ARALYDRAFT_910353 [Arabidopsis lyrata subsp. lyrata]		168	588	4.00E-16	350.0	21.4	22.6	hypothetical protein ARALYDRAFT_910353	gbpln	Arabidopsis lyrata	AT5G23400.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:7880603-7882372 FORWARD LENGTH=589		168	589	2.00E-18	350.6	21.4	22.6
Rsa1.0_00499.1.g14990.t1	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]		578	578	1.00E-144	100.0	47.1	63.3	hypothetical protein 27.t00126	gbpln	Brassica oleracea	AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957		578	957	4.00E-15	165.6	6.9	10.6
Rsa1.0_00499.1.g14991.t1	gb|AAD30632.1|AC006085_5 Hypothetical protein [Arabidopsis thaliana]		743	1295	6.00E-60	174.3	22.3	33.6	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#	
Rsa1.0_00499.1.g14992.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]		800	1274	0	159.3	48.1	63.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575		800	575	1.00E-55	71.9	19.1	32.3
Rsa1.0_00499.1.g14993.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00499.1.g14994.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]		897	1485	1.00E-148	165.6	34.2	47.4	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	AT1G47350.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:17358447-17360722 REVERSE LENGTH=528		897	528	3.00E-30	58.9	7.6	10.0
Rsa1.0_00500.1.g14995.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00500.1.g14996.t1	ref|XP_002880160.1| hypothetical protein ARALYDRAFT_483647 [Arabidopsis lyrata subsp. lyrata] gi|297325999|gb|EFH56419.1| hypothetical protein ARALYDRAFT_483647 [Arabidopsis lyrata subsp. lyrata]		227	239	2.00E-72	105.3	62.6	70.9	hypothetical protein ARALYDRAFT_483647	gbpln	Arabidopsis lyrata	AT2G45140.1 | Symbols: PVA12 | plant VAP homolog 12 | chr2:18611029-18612971 FORWARD LENGTH=239		227	239	3.00E-73	105.3	61.2	70.9
Rsa1.0_00500.1.g14997.t1	ref|XP_002880157.1| hypothetical protein ARALYDRAFT_483645 [Arabidopsis lyrata subsp. lyrata] gi|297325996|gb|EFH56416.1| hypothetical protein ARALYDRAFT_483645 [Arabidopsis lyrata subsp. lyrata]		303	325	1.00E-111	107.3	78.9	86.1	hypothetical protein ARALYDRAFT_483645	gbpln	Arabidopsis lyrata	AT2G45120.1 | Symbols: | C2H2-like zinc finger protein | chr2:18603680-18604624 FORWARD LENGTH=314		303	314	1.00E-100	103.6	72.9	81.2
Rsa1.0_00500.1.g14998.t1	ref|XP_002881717.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297327556|gb|EFH57976.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]		712	757	0	106.3	79.2	86.5	transducin family protein	gbpln	Arabidopsis lyrata	AT2G40360.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:16853123-16856635 REVERSE LENGTH=753		712	753	0	105.8	77.7	85.7
Rsa1.0_00500.1.g14999.t2	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]		675	940	5.00E-41	139.3	15.4	21.9	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#	
Rsa1.0_00500.1.g15000.t1	ref|XP_002886254.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297332094|gb|EFH62513.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]		106	392	1.00E-28	369.8	55.7	58.5	kinase family protein	gbpln	Arabidopsis lyrata	AT2G18890.1 | Symbols: | Protein kinase superfamily protein | chr2:8184027-8186685 FORWARD LENGTH=392		106	392	2.00E-30	369.8	53.8	57.5
Rsa1.0_00500.1.g15001.t1	ref|XP_002880155.1| CYCP3_1 [Arabidopsis lyrata subsp. lyrata] gi|297325994|gb|EFH56414.1| CYCP3_1 [Arabidopsis lyrata subsp. lyrata]		224	222	1.00E-117	99.1	92.4	94.6	CYCP3_1	gbpln	Arabidopsis lyrata	AT2G45080.1 | Symbols: cycp3;1 | cyclin p3;1 | chr2:18591688-18592443 FORWARD LENGTH=222		224	222	1.00E-119	99.1	91.5	94.6
Rsa1.0_00500.1.g15002.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00500.1.g15003.t1	gb|EOA27694.1| hypothetical protein CARUB_v10023846mg [Capsella rubella]		147	271	5.00E-29	184.4	42.2	44.2	hypothetical protein CARUB_v10023846mg	gbpln	Capsella rubella	AT2G45060.1 | Symbols: | Uncharacterised conserved protein UCP022280 | chr2:18584674-18586688 REVERSE LENGTH=272		147	272	1.00E-30	185.0	40.8	43.5
Rsa1.0_00500.1.g15004.t1	ref|XP_002880148.1| hypothetical protein ARALYDRAFT_483623 [Arabidopsis lyrata subsp. lyrata] gi|297325987|gb|EFH56407.1| hypothetical protein ARALYDRAFT_483623 [Arabidopsis lyrata subsp. lyrata]		277	290	7.00E-99	104.7	74.4	82.7	hypothetical protein ARALYDRAFT_483623	gbpln	Arabidopsis lyrata	AT2G44940.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr2:18537294-18538181 FORWARD LENGTH=295		277	295	3.00E-92	106.5	69.7	80.1
Rsa1.0_00500.1.g15005.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00500.1.g15006.t1	gb|AAC33961.1| contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]		1299	1662	1.00E-88	127.9	15.2	23.8	contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57)	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626		1299	626	3.00E-35	48.2	8.6	14.0
Rsa1.0_00500.1.g15007.t1	gb|EOA26609.1| hypothetical protein CARUB_v10022668mg [Capsella rubella]		838	791	0	94.4	79.5	84.8	hypothetical protein CARUB_v10022668mg	gbpln	Capsella rubella	AT3G60320.1 | Symbols: | Protein of unknown function (DUF630 and DUF632) | chr3:22292073-22295228 REVERSE LENGTH=796		838	796	0	95.0	72.7	81.6

Rsa1.0_00500.1.g15008.t1	gb|EOA26625.1| hypothetical protein CARUB_v10022689mg [Capsella rubella] gi|482562436|gb|EOA26626.1| hypothetical protein CARUB_v10022689mg [Capsella rubella]	63	767	6.00E-15	1217.5	66.7	74.6	hypothetical protein CARUB_v10022689mg	gbpln	Capsella rubella	AT2G44830.1 | Symbols: | Protein kinase superfamily protein | chr2:18490398-18492779 FORWARD LENGTH=765	63	765	1.00E-17	1214.3	66.7	74.6
Rsa1.0_00500.1.g15009.t1	gb|AAL65634.1| transaldolase-like protein [Arabidopsis thaliana] gi|22497334|gb|AAL65636.1| transaldolase-like protein [Arabidopsis thaliana]	69	375	6.00E-12	543.5	68.1	76.8	transaldolase-like protein	gbpln	Arabidopsis thaliana	AT1G12230.1 | Symbols: | Aldolase superfamily protein | chr1:4148050-4150708 FORWARD LENGTH=405	69	405	4.00E-14	587.0	66.7	76.8
Rsa1.0_00500.1.g15010.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1860	1374	0	73.9	41.1	55.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1860	575	1.00E-172	30.9	14.6	21.4
Rsa1.0_00500.1.g15011.t2	gb|EOA27938.1| hypothetical protein CARUB_v10024107mg [Capsella rubella]	216	195	1.00E-56	90.3	71.8	79.6	hypothetical protein CARUB_v10024107mg	gbpln	Capsella rubella	AT2G44790.1 | Symbols: UCC2 | uclacyanin 2 | chr2:18462182-18463232 REVERSE LENGTH=202	216	202	1.00E-43	93.5	60.2	69.9
Rsa1.0_00500.1.g15012.t1	ref|NP_566027.1| ELMO/CED-12 domain-containing protein [Arabidopsis thaliana] gi|20197031|gb|AAC27479.2| expressed protein [Arabidopsis thaliana] gi|21593197|gb|AAM65146.1| unknown [Arabidopsis thaliana] gi|330255372|gb|AEC10466.1| ELMO/CED-12 domain-containing protein [Arabidopsis thaliana]	282	266	1.00E-141	94.3	86.9	92.2	ELMO/CED-12 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G44770.1 | Symbols: | ELMO/CED-12 family protein | chr2:18457817-18459886 FORWARD LENGTH=266	282	266	1.00E-143	94.3	86.9	92.2
Rsa1.0_00500.1.g15013.t1	ref|NP_181961.1| C3HC4-type RING finger-containing protein [Arabidopsis thaliana] gi|3128178|gb|AAC16082.1| hypothetical protein [Arabidopsis thaliana] gi|18491237|gb|AAL69443.1| At2g44330/F4I1.14 [Arabidopsis thaliana] gi|70905065|gb|AAZ14058.1| At2g44330 [Arabidopsis thaliana] gi|330255314|gb|AEC10408.1| C3HC4-type RING finger-containing protein [Arabidopsis thaliana]	175	180	2.00E-54	102.9	68.6	80.0	C3HC4-type RING finger-containing protein	gbpln	Arabidopsis thaliana	AT2G44330.1 | Symbols: | RING/U-box superfamily protein | chr2:18310621-18311163 FORWARD LENGTH=180	175	180	8.00E-57	102.9	68.6	80.0
Rsa1.0_00500.1.g15014.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00501.1.g15015.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	578	1374	1.00E-143	237.7	44.3	64.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	578	626	7.00E-36	108.3	17.3	26.6
Rsa1.0_00501.1.g15016.t1	ref|XP_002886713.1| CYP79C2 [Arabidopsis lyrata subsp. lyrata] gi|297332554|gb|EFH62972.1| CYP79C2 [Arabidopsis lyrata subsp. lyrata]	646	528	0	81.7	63.2	70.9	CYP79C2	gbpln	Arabidopsis lyrata	AT1G58260.1 | Symbols: CYP79C2, CYP79C3P | cytochrome p450 79c2 | chr1:21605752-21607995 FORWARD LENGTH=530	646	530	0	82.0	62.4	70.6
Rsa1.0_00501.1.g15017.t1	gb|AAD17414.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	1286	1166	0	90.7	51.6	65.1	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1286	1262	2.00E-86	98.1	14.1	22.2
Rsa1.0_00501.1.g15018.t2	ref|XP_002875315.1| glycosyl hydrolase family protein 27 [Arabidopsis lyrata subsp. lyrata] gi|297321153|gb|EFH51574.1| glycosyl hydrolase family protein 27 [Arabidopsis lyrata subsp. lyrata]	641	651	0	101.6	86.9	93.0	glycosyl hydrolase family protein 27	gbpln	Arabidopsis lyrata	AT3G26380.1 | Symbols: | Melibiase family protein | chr3:9660140-9663145 FORWARD LENGTH=647	641	647	0	100.9	84.9	91.4
Rsa1.0_00501.1.g15019.t1	ref|NP_566792.1| methyltransferase / nucleic acid binding protein [Arabidopsis thaliana] gi|13430750|gb|AAK25997.1|AF360287_1 unknown protein [Arabidopsis thaliana] gi|9294300|dbj|BAB02202.1| unnamed protein product [Arabidopsis thaliana] gi|15293219|gb|AAK93720.1| unknown protein [Arabidopsis thaliana] gi|332643633|gb|AEE77154.1| methyltransferase / nucleic acid binding protein [Arabidopsis thaliana]	474	477	0	100.6	92.4	96.6	methyltransferase / nucleic acid binding protein	gbpln	Arabidopsis thaliana	AT3G26410.1 | Symbols: TRM11, AtTRM11 | methyltransferases;nucleic acid binding | chr3:9669508-9671273 REVERSE LENGTH=477	474	477	0	100.6	92.4	96.6

Rsa1.0_00501.1.g15020.t1	ref|NP_189273.1| RNA recognition motif and CCHC-type zinc finger domain-containing protein [Arabidopsis thaliana] gi|15983477|gb|AAL11606.1|AF424613_1 AT3g26420/F20C19_14 [Arabidopsis thaliana] gi|9294301|dbj|BAB02203.1| unnamed protein product [Arabidopsis thaliana] gi|15451066|gb|AAK96804.1| Unknown protein [Arabidopsis thaliana] gi|18377412|gb|AAL66872.1| unknown protein [Arabidopsis thaliana] gi|62320797|dbj|BAD93728.1| RNA-binding protein [Arabidopsis thaliana] gi|110742443|dbj|BAE99140.1| putative RNA-binding protein [Arabidopsis thaliana] gi|332643635|gb|AEE77156.1| RNA recognition motif and CCHC-type zinc finger domain-containing protein [Arabidopsis thaliana]	230	245	7.00E-86	106.5	83.9	88.3	RNA recognition motif and CCHC-type zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT3G26420.1 | Symbols: ATRZ-1A | RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain | chr3:9671953-9673055 FORWARD LENGTH=245	230	245	2.00E-88	106.5	83.9	88.3
Rsa1.0_00501.1.g15021.t1	ref|NP_001168670.1| uncharacterized protein LOC100382458 [Zea mays] gi|223944871|gb|ACN26519.1| unknown [Zea mays] gi|223950089|gb|ACN29128.1| unknown [Zea mays] gi|224030281|gb|ACN34216.1| unknown [Zea mays] gi|413924555|gb|AFW64487.1| hypothetical protein ZEAMMB73_909642 [Zea mays] gi|413924556|gb|AFW64488.1| hypothetical protein ZEAMMB73_909642 [Zea mays] gi|413924557|gb|AFW64489.1| hypothetical protein ZEAMMB73_909642 [Zea mays] gi|413924558|gb|AFW64490.1| hypothetical protein ZEAMMB73 909642 [Zea mays]	326	423	9.00E-37	129.8	30.4	45.4	uncharacterized protein LOC100382458	gbenv/gbpln	Zea mays	AT2G02870.3 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:838378-839781 FORWARD LENGTH=467	326	467	1.00E-36	143.3	27.3	42.9
Rsa1.0_00501.1.g15022.t1	ref|NP_001049113.1| Os03g0171600 [Oryza sativa Japonica Group] gi|108706423|gb|ABF94218.1| kelch repeat-containing F-box family protein, putative, expressed [Oryza sativa Japonica Group] gi|108706424|gb|ABF94219.1| kelch repeat-containing F-box family protein, putative, expressed [Oryza sativa Japonica Group] gi|108706425|gb|ABF94220.1| kelch repeat-containing F-box family protein, putative, expressed [Oryza sativa Japonica Group] gi|113547584|dbj|BAF11027.1| Os03g0171600 [Oryza sativa Japonica Group] gi|125585086|gb|EAZ25750.1| hypothetical protein OsJ_09589 [Oryza sativa Japonica Group] gi|215692448|dbj|BAG87868.1| unnamed protein product [Oryza sativa Japonica Group] gi|215704271|dbj|BAG93111.1| unnamed protein product [Oryza sativa Japonica Group]	366	431	2.00E-31	117.8	25.1	37.7	Os03g0171600	gbpln	Oryza sativa	AT2G02870.3 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:838378-839781 FORWARD LENGTH=467	366	467	2.00E-32	127.6	23.8	36.9
Rsa1.0_00501.1.g15023.t1	ref|NP_189281.2| plant intracellular ras group-related LRR 2 [Arabidopsis thaliana] gi|9293927|dbj|BAB01830.1| leucine-rich-repeat protein-like [Arabidopsis thaliana] gi|26453000|dbj|BAC43576.1| unknown protein [Arabidopsis thaliana] gi|29824149|gb|AAP04035.1| unknown protein [Arabidopsis thaliana] gi|57868146|gb|AAW57411.1| plant intracellular Ras-group-related LRR protein 2 [Arabidopsis thaliana] gi|332643646|gb|AEE77167.1| plant intracellular ras group-related LRR 2 [Arabidopsis thaliana]	473	471	0	99.6	82.0	90.7	plant intracellular ras group-related LRR 2	gbpln	Arabidopsis thaliana	AT3G26500.1 | Symbols: PIRL2 | plant intracellular ras group-related LRR 2 | chr3:9708195-9709944 REVERSE LENGTH=471	473	471	0	99.6	82.0	90.7
Rsa1.0_00501.1.g15024.t1	gb|EOA25649.1| hypothetical protein CARUB_v10018998mg [Capsella rubella]	188	194	1.00E-68	103.2	81.9	89.4	hypothetical protein CARUB_v10018998mg	gbpln	Capsella rubella	AT3G26510.4 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr3:9711886-9712588 REVERSE LENGTH=196	188	196	5.00E-70	104.3	86.2	93.1

Rsa1.0_00501.1.g15025.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	611	1214	0	198.7	73.6	83.5	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	611	746	3.00E-57	122.1	23.1	30.6
Rsa1.0_00501.1.g15026.t1	gb|AAD39372.1|AF118381_1 tonoplast intrinsic protein [Brassica napus]	253	253	1.00E-129	100.0	93.7	97.2	tonoplast intrinsic protein	gbpln	Brassica napus	AT3G26520.1 | Symbols: TIP2, SITIP, GAMMA-TIP2, TIP1;2 | tonoplast intrinsic protein 2 | chr3:9722770-9723703 REVERSE LENGTH=253	253	253	1.00E-129	100.0	91.3	95.7
Rsa1.0_00501.1.g15027.t4	dbj|BAJ34149.1| unnamed protein product [Thellungiella halophila]	402	400	0	99.5	96.8	98.0	unnamed protein product	----	----	AT3G26650.1 | Symbols: GAPA, GAPA-1 | glyceraldehyde 3-phosphate dehydrogenase A subunit | chr3:9795226-9796848 FORWARD LENGTH=396	402	396	0	98.5	94.0	96.5
Rsa1.0_00501.1.g15028.t1	ref|XP_002876987.1| hypothetical protein ARALYDRAFT_904865 [Arabidopsis lyrata subsp. lyrata] gi|297322825|gb|EFH53246.1| hypothetical protein ARALYDRAFT_904865 [Arabidopsis lyrata subsp. lyrata]	199	202	5.00E-92	101.5	84.9	91.0	hypothetical protein ARALYDRAFT_904865	gbpln	Arabidopsis lyrata	AT3G26690.2 | Symbols: ATNUDT13, ATNUDX13, NUDX13 | nudix hydrolase homolog 13 | chr3:9804418-9805398 REVERSE LENGTH=202	199	202	3.00E-94	101.5	84.9	90.5
Rsa1.0_00501.1.g15029.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	262	1374	3.00E-41	524.4	41.2	60.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	262	575	2.00E-35	219.5	24.0	34.7
Rsa1.0_00502.1.g15030.t1	ref|XP_002871867.1| hypothetical protein ARALYDRAFT_326316 [Arabidopsis lyrata subsp. lyrata] gi|297317704|gb|EFH48126.1| hypothetical protein ARALYDRAFT_326316 [Arabidopsis lyrata subsp. lyrata]	161	390	9.00E-18	242.2	32.3	43.5	hypothetical protein ARALYDRAFT_326316	gbpln	Arabidopsis lyrata	AT5G19170.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:6445245-6447305 FORWARD LENGTH=391	161	391	2.00E-18	242.9	31.7	42.2
Rsa1.0_00502.1.g15031.t1	dbj|BAJ34425.1| unnamed protein product [Thellungiella halophila]	313	311	1.00E-142	99.4	78.3	89.5	unnamed protein product	----	----	AT1G75300.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr1:28255552-28256927 FORWARD LENGTH=322	313	322	1.00E-137	102.9	76.4	87.5
Rsa1.0_00502.1.g15032.t1	dbj|BAJ34425.1| unnamed protein product [Thellungiella halophila]	311	311	1.00E-167	100.0	92.3	97.4	unnamed protein product	----	----	AT1G75280.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr1:28252030-28253355 FORWARD LENGTH=310	311	310	1.00E-155	99.7	84.2	92.0
Rsa1.0_00502.1.g15033.t1	dbj|BAJ34425.1| unnamed protein product [Thellungiella halophila]	312	311	1.00E-136	99.7	73.4	90.1	unnamed protein product	----	----	AT1G75280.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr1:28252030-28253355 FORWARD LENGTH=310	312	310	1.00E-129	99.4	70.5	85.6
Rsa1.0_00502.1.g15034.t1	gb|EOA35043.1| hypothetical protein CARUB_v10020148mg [Capsella rubella]	563	518	1.00E-122	92.0	54.9	66.6	hypothetical protein CARUB_v10020148mg	gbpln	Capsella rubella	AT1G75260.1 | Symbols: | oxidoreductases, acting on NADH or NADPH | chr1:28247854-28249395 FORWARD LENGTH=513	563	513	1.00E-123	91.1	56.7	68.6
Rsa1.0_00502.1.g15035.t1	ref|NP_177661.1| RAD-like 6 protein [Arabidopsis thaliana] gi|10092271|gb|AAG12684.1|AC025814_8 myb-related protein; 20671-21051 [Arabidopsis thaliana] gi|41618978|gb|AAS09995.1| MYB transcription factor [Arabidopsis thaliana] gi|109946537|gb|ABG48447.1| At1g75250 [Arabidopsis thaliana] gi|332197572|gb|AEE35693.1| RAD-like 6 protein [Arabidopsis thaliana]	92	126	7.00E-39	137.0	88.0	90.2	RAD-like 6 protein	gbpln	Arabidopsis thaliana	AT1G75250.1 | Symbols: ATRL6, RSM3, RL6 | RAD-like 6 | chr1:28245073-28245453 REVERSE LENGTH=126	92	126	1.00E-41	137.0	88.0	90.2
Rsa1.0_00502.1.g15036.t1	gb|EOA35498.1| hypothetical protein CARUB_v10020705mg [Capsella rubella]	310	306	1.00E-115	98.7	84.2	89.4	hypothetical protein CARUB_v10020705mg	gbpln	Capsella rubella	AT1G75240.1 | Symbols: AtHB33, HB33, ZHD5 | homeobox protein 33 | chr1:28241576-28242505 FORWARD LENGTH=309	310	309	1.00E-103	99.7	83.2	88.7
Rsa1.0_00502.1.g15037.t1	gb|EOA35085.1| hypothetical protein CARUB_v10020200mg [Capsella rubella]	485	487	0	100.4	96.5	97.9	hypothetical protein CARUB_v10020200mg	gbpln	Capsella rubella	AT1G75220.1 | Symbols: | Major facilitator superfamily protein | chr1:28229412-28232606 REVERSE LENGTH=487	485	487	0	100.4	95.9	97.5
Rsa1.0_00502.1.g15038.t2	ref|XP_002887578.1| hypothetical protein ARALYDRAFT_895388 [Arabidopsis lyrata subsp. lyrata] gi|297333419|gb|EFH63837.1| hypothetical protein ARALYDRAFT_895388 [Arabidopsis lyrata subsp. lyrata]	562	642	0	114.2	85.6	91.1	hypothetical protein ARALYDRAFT_895388	gbpln	Arabidopsis lyrata	AT1G75210.1 | Symbols: | HAD-superfamily hydrolase, subfamily IG, 5'-nucleotidase | chr1:28223990-28228751 FORWARD LENGTH=642	562	642	0	114.2	84.5	91.3
Rsa1.0_00502.1.g15039.t1	gb|EOA33528.1| hypothetical protein CARUB_v10019936mg [Capsella rubella]	648	647	0	99.8	87.7	93.7	hypothetical protein CARUB_v10019936mg	gbpln	Capsella rubella	AT1G75200.1 | Symbols: | flavodoxin family protein / radical SAM domain-containing protein | chr1:28220849-28223597 REVERSE LENGTH=647	648	647	0	99.8	86.7	93.2

Rsa1.0_00502.1.g15040.t1	gb|AAM62539.1| unknown [Arabidopsis thaliana] gi|24417366|gb|AAN60293.1| unknown [Arabidopsis thaliana]	129	131	2.00E-11	101.6	65.9	74.4	unknown	gbpln	Arabidopsis thaliana	AT1G75190.1 | Symbols: | unknown protein; Has 7306 Blast hits to 3858 proteins in 279 species: Archae - 15; Bacteria - 134; Metazoa - 3314; Fungi - 546; Plants - 228; Viruses - 207; Other Eukaryotes - 2862 (source: NCBI BLink). | chr1:28219598-28219993 FORWARD LENGTH=131	129	131	1.00E-13	101.6	65.1	74.4
Rsa1.0_00502.1.g15041.t1	gb|EOA35457.1| hypothetical protein CARUB_v10020666mg [Capsella rubella] gi|482571270|gb|EOA35458.1| hypothetical protein CARUB_v10020666mg [Capsella rubella]	310	318	1.00E-130	102.6	82.6	88.4	hypothetical protein CARUB_v10020666mg	gbpln	Capsella rubella	AT1G75180.3 | Symbols: | Erythronate-4-phosphate dehydrogenase family protein | chr1:28216150-28217911 REVERSE LENGTH=315	310	315	1.00E-129	101.6	79.7	84.2
Rsa1.0_00502.1.g15042.t1	gb|EOA33881.1| hypothetical protein CARUB_v10021373mg [Capsella rubella]	301	296	1.00E-155	98.3	88.7	93.4	hypothetical protein CARUB_v10021373mg	gbpln	Capsella rubella	AT1G75170.2 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:28214405-28215686 FORWARD LENGTH=296	301	296	1.00E-156	98.3	88.0	93.4
Rsa1.0_00502.1.g15043.t1	gb|EOA35962.1| hypothetical protein CARUB_v10021223mg [Capsella rubella]	86	86	1.00E-24	100.0	80.2	83.7	hypothetical protein CARUB_v10021223mg	gbpln	Capsella rubella	AT1G61570.1 | Symbols: TIM13 | translocase of the inner mitochondrial membrane 13 | chr1:22718897-22719473 REVERSE LENGTH=87	86	87	2.00E-24	101.2	70.9	80.2
Rsa1.0_00502.1.g15044.t3	ref|XP_002889011.1| CYP721A1 [Arabidopsis lyrata subsp. lyrata] gi|297334852|gb|EFH65270.1| CYP721A1 [Arabidopsis lyrata subsp. lyrata]	2005	505	0	25.2	20.2	21.8	CYP721A1	gbpln	Arabidopsis lyrata	AT1G75130.1 | Symbols: CYP721A1 | cytochrome P450, family 721, subfamily A, polypeptide 1 | chr1:28200073-28201911 REVERSE LENGTH=505	2005	505	0	25.2	20.0	22.0
Rsa1.0_00502.1.g15045.t1	ref|XP_002888991.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334832|gb|EFH65250.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	662	670	0	101.2	91.5	95.6	galactosyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G74800.1 | Symbols: | Galactosyltransferase family protein | chr1:28102221-28104993 REVERSE LENGTH=672	662	672	0	101.5	90.8	95.6
Rsa1.0_00502.1.g15046.t1	gb|EOA33703.1| hypothetical protein CARUB_v10019888mg [Capsella rubella]	687	694	0	101.0	87.9	93.9	hypothetical protein CARUB_v10019888mg	gbpln	Capsella rubella	AT1G74790.1 | Symbols: | catalytics | chr1:28098912-28101673 FORWARD LENGTH=695	687	695	0	101.2	86.9	92.6
Rsa1.0_00502.1.g15047.t1	ref|XP_002888990.1| hypothetical protein ARALYDRAFT_476613 [Arabidopsis lyrata subsp. lyrata] gi|297334831|gb|EFH65249.1| hypothetical protein ARALYDRAFT_476613 [Arabidopsis lyrata subsp. lyrata]	1255	1263	0	100.6	80.4	88.5	hypothetical protein ARALYDRAFT_476613	gbpln	Arabidopsis lyrata	AT1G74770.1 | Symbols: | zinc ion binding | chr1:28089695-28094834 REVERSE LENGTH=1259	1255	1259	0	100.3	80.3	88.0
Rsa1.0_00502.1.g15048.t1	ref|XP_002887557.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297333398|gb|EFH63816.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	750	845	0	112.7	84.1	90.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G74750.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:28086800-28089367 FORWARD LENGTH=855	750	855	0	114.0	84.1	90.0
Rsa1.0_00502.1.g15049.t1	dbj|BAJ33607.1| unnamed protein product [Thellungiella halophila]	553	546	0	98.7	94.0	96.4	unnamed protein product	----	----	AT1G74740.1 | Symbols: CPK30, CDPK1A, ATCPK30 | calcium-dependent protein kinase 30 | chr1:28080199-28082476 REVERSE LENGTH=541	553	541	0	97.8	90.2	94.2
Rsa1.0_00502.1.g15050.t1	dbj|BAJ33994.1| unnamed protein product [Thellungiella halophila]	747	567	0	75.9	64.1	66.5	unnamed protein product	----	----	AT1G74710.1 | Symbols: EDS16, ICS1, SID2, ATICS1 | ADC synthase superfamily protein | chr1:28070391-28073898 FORWARD LENGTH=569	747	569	0	76.2	63.5	66.5
Rsa1.0_00502.1.g15051.t1	gb|EOA35942.1| hypothetical protein CARUB_v10021199mg [Capsella rubella]	97	101	1.00E-34	104.1	90.7	95.9	hypothetical protein CARUB_v10021199mg	gbpln	Capsella rubella	AT1G74660.1 | Symbols: MIF1 | mini zinc finger 1 | chr1:28047742-28048050 REVERSE LENGTH=102	97	102	2.00E-37	105.2	90.7	95.9
Rsa1.0_00502.1.g15052.t1	gb|EOA35418.1| hypothetical protein CARUB_v10020618mg [Capsella rubella]	333	336	1.00E-136	100.9	78.4	85.3	hypothetical protein CARUB_v10020618mg	gbpln	Capsella rubella	AT1G74650.1 | Symbols: ATY13, ATMYB31, MYB31 | myb domain protein 31 | chr1:28041493-28042773 FORWARD LENGTH=330	333	330	1.00E-136	99.1	78.7	84.1
Rsa1.0_00503.1.g15053.t1	ref|XP_002876745.1| hypothetical protein ARALYDRAFT_904327 [Arabidopsis lyrata subsp. lyrata] gi|297322583|gb|EFH53004.1| hypothetical protein ARALYDRAFT_904327 [Arabidopsis lyrata subsp. lyrata]	201	589	3.00E-12	293.0	26.9	37.8	hypothetical protein ARALYDRAFT_904327	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00503.1.g15054.t1	ref|NP_188947.2| CRM family member 3A [Arabidopsis thaliana] gi|332643191|gb|AEE76712.1| CRM family member 3A [Arabidopsis thaliana]	390	881	3.00E-66	225.9	33.6	40.3	CRM family member 3A	gbpln	Arabidopsis thaliana	AT3G23070.1 | Symbols: ATCFM3A, CFM3A | CRM family member 3A | chr3:8203548-8207243 FORWARD LENGTH=881	390	881	8.00E-69	225.9	33.6	40.3

Rsa1.0_00503.1.g15055.t1	ref|XP_002882759.1| hypothetical protein ARALYDRAFT_478549 [Arabidopsis lyrata subsp. lyrata] gi|297328599|gb|EFH59018.1| hypothetical protein ARALYDRAFT_478549 [Arabidopsis lyrata subsp. lyrata]	134	616	2.00E-33	459.7	62.7	69.4	hypothetical protein ARALYDRAFT_478549	gbpln	Arabidopsis lyrata	AT3G11980.1 | Symbols: MS2, FAR2 | Jojoba acyl CoA reductase-related male sterility protein | chr3:3814484-3816927 FORWARD LENGTH=616	134	616	1.00E-31	459.7	61.2	68.7
Rsa1.0_00503.1.g15056.t2	dbj|BAD94568.1| putative acyl-CoA synthetase [Arabidopsis thaliana]	175	228	3.00E-50	130.3	60.6	67.4	putative acyl-CoA synthetase	gbpln	Arabidopsis thaliana	AT2G47240.2 | Symbols: LACS1 | AMP-dependent synthetase and ligase family protein | chr2:19393835-19397616 FORWARD LENGTH=660	175	660	2.00E-52	377.1	60.6	67.4
Rsa1.0_00503.1.g15057.t1	emb|CBK20932.2| unnamed protein product [Blastocystis hominis] gi|300175649|emb|CBK20960.2| unnamed protein product [Blastocystis hominis]	259	150	1.00E-19	57.9	25.5	35.1	unnamed protein product	gbpln	Blastocystis hominis	AT4G05320.6 | Symbols: UBQ10 | polyubiquitin 10 | chr4:2718559-2719932 FORWARD LENGTH=381	259	381	1.00E-20	147.1	19.7	23.9
Rsa1.0_00503.1.g15058.t1	ref|NP_001154580.1| uncharacterized protein [Arabidopsis thaliana] gi|330255381|gb|AEC10475.1| uncharacterized protein AT2G44850 [Arabidopsis thaliana]	302	319	1.00E-120	105.6	77.8	86.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G44850.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: M germinated pollen stage, LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0565 (InterPro:IPR018881); Has 106 Blast hits to 106 proteins in 50 species: Archae - 0; Bacteria - 0; Metazoa - 73; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:18499770-18500823 FORWARD LENGTH=319	302	319	1.00E-123	105.6	77.8	86.8
Rsa1.0_00503.1.g15059.t1	ref|NP_182011.1| ethylene-responsive transcription factor 13 [Arabidopsis thaliana] gi|57012834|sp|Q8L9K1.2|ERF99_ARATH RecName: Full=Ethylene-responsive transcription factor 13; Short=AtERF13; AltName: Full=Ethylene-responsive element-binding factor 13; Short=EREBP-13 gi|13272437|gb|AAK17157.1|AF325089_1 putative ethylene response element binding protein (EREBP) [Arabidopsis thaliana] gi|13899091|gb|AAK48967.1|AF370540_1 putative ethylene response element binding protein; EREBP [Arabidopsis thaliana] gi|2344900|gb|AAC31840.1| putative ethylene response element binding protein (EREBP) [Arabidopsis thaliana] gi|18377440|gb|AAL66886.1| putative ethylene response element binding protein (EREBP) [Arabidopsis thaliana] gi|330255379|gb|AEC10473.1| ethylene-responsive transcription factor 13 [Arabidopsis thaliana]	226	226	7.00E-95	100.0	76.5	83.6	ethylene-responsive transcription factor 13	gbpln	Arabidopsis thaliana	AT2G44840.1 | Symbols: ATERF13, EREBP, ERF13 | ethylene-responsive element binding factor 13 | chr2:18495440-18496120 FORWARD LENGTH=226	226	226	2.00E-97	100.0	76.5	83.6
Rsa1.0_00503.1.g15060.t1	ref|NP_850426.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|330255378|gb|AEC10472.1| protein kinase domain-containing protein [Arabidopsis thaliana]	678	765	0	112.8	86.1	91.4	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G44830.1 | Symbols: | Protein kinase superfamily protein | chr2:18490398-18492779 FORWARD LENGTH=765	678	765	0	112.8	86.1	91.4
Rsa1.0_00503.1.g15061.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00503.1.g15062.t2	ref|XP_002867613.1| hypothetical protein ARALYDRAFT_914041 [Arabidopsis lyrata subsp. lyrata] gi|297313449|gb|EFH43872.1| hypothetical protein ARALYDRAFT_914041 [Arabidopsis lyrata subsp. lyrata]	302	344	2.00E-43	113.9	44.0	55.0	hypothetical protein ARALYDRAFT_914041	gbpln	Arabidopsis lyrata	AT1G05080.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:1459091-1460579 FORWARD LENGTH=439	302	439	6.00E-24	145.4	35.1	46.4
Rsa1.0_00503.1.g15063.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00503.1.g15064.t1	ref|NP_182007.2| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|330255374|gb|AEC10468.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	356	357	0	100.3	88.2	93.8	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT2G44800.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr2:18467004-18468551 FORWARD LENGTH=357	356	357	0	100.3	88.2	93.8
Rsa1.0_00503.1.g15065.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_00503.1.g15066.t1</td><td>ref|NP_566027.1| ELMO/CED-12 domain-containing protein [Arabidopsis thaliana] gi|20197031|gb|AAC27479.2| expressed protein [Arabidopsis thaliana] gi|21593197|gb|AAM65146.1| unknown [Arabidopsis thaliana] gi|330255372|gb|AEC10466.1| ELMO/CED-12 domain-containing protein [Arabidopsis thaliana]</td><td>266</td><td>266</td><td>1.00E-150</td><td>100.0</td><td>96.6</td><td>98.9</td><td>ELMO/CED-12 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G44770.1 | Symbols: | ELMO/CED-12 family protein | chr2:18457817-18459886 FORWARD LENGTH=266</td><td>266</td><td>266</td><td>1.00E-153</td><td>100.0</td><td>96.6</td><td>98.9</td></tr>
<tr><td>Rsa1.0_00503.1.g15067.t1</td><td>ref|NP_189038.1| putative F-box protein [Arabidopsis thaliana] gi|75273446|sp|Q9LIR1.1|FB182_ARATH RecName: Full=Putative F-box protein At3g23960 gi|9294665|dbj|BAB03014.1| unnamed protein product [Arabidopsis thaliana] gi|332643318|gb|AEE76839.1| putative F-box protein [Arabidopsis thaliana]</td><td>400</td><td>402</td><td>1.00E-57</td><td>100.5</td><td>36.0</td><td>48.0</td><td>putative F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G23960.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8657736-8658944 FORWARD LENGTH=402</td><td>400</td><td>402</td><td>3.00E-60</td><td>100.5</td><td>36.0</td><td>48.0</td></tr>
<tr><td>Rsa1.0_00503.1.g15068.t1</td><td>ref|XP_002881979.1| WRKY family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297327818|gb|EFH58238.1| WRKY family transcription factor [Arabidopsis lyrata subsp. lyrata]</td><td>219</td><td>218</td><td>1.00E-100</td><td>99.5</td><td>88.1</td><td>90.9</td><td>WRKY family transcription factor</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G44745.1 | Symbols: | WRKY family transcription factor | chr2:18447482-18449004 REVERSE LENGTH=218</td><td>219</td><td>218</td><td>1.00E-101</td><td>99.5</td><td>88.1</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00503.1.g15069.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00503.1.g15070.t1</td><td>gb|EOA27921.1| hypothetical protein CARUB_v10024094mg [Capsella rubella]</td><td>201</td><td>199</td><td>5.00E-99</td><td>99.0</td><td>89.1</td><td>92.0</td><td>hypothetical protein CARUB_v10024094mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44740.1 | Symbols: CYCP4;1 | cyclin p4;1 | chr2:18442287-18443304 REVERSE LENGTH=202</td><td>201</td><td>202</td><td>7.00E-98</td><td>100.5</td><td>90.0</td><td>93.5</td></tr>
<tr><td>Rsa1.0_00503.1.g15071.t1</td><td>ref|NP_566023.1| uncharacterized protein [Arabidopsis thaliana] gi|13272435|gb|AAK17156.1|AF325088_1 unknown protein [Arabidopsis thaliana] gi|3341687|gb|AAC27469.1| expressed protein [Arabidopsis thaliana] gi|15081775|gb|AAK82542.1| At2g44670/F16B22.16 [Arabidopsis thaliana] gi|21593625|gb|AAM65592.1| unknown [Arabidopsis thaliana] gi|24797042|gb|AAN64533.1| At2g44670/F16B22.16 [Arabidopsis thaliana] gi|110736091|dbj|BAF00018.1| hypothetical protein [Arabidopsis thaliana] gi|330255359|gb|AEC10453.1| uncharacterized protein AT2G44670 [Arabidopsis thaliana]</td><td>95</td><td>93</td><td>4.00E-35</td><td>97.9</td><td>80.0</td><td>86.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G44670.1 | Symbols: | Protein of unknown function (DUF581) | chr2:18425279-18425673 FORWARD LENGTH=93</td><td>95</td><td>93</td><td>7.00E-38</td><td>97.9</td><td>80.0</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00503.1.g15072.t1</td><td>gb|ABL97949.1| CHL-CPN10 [Brassica rapa]</td><td>138</td><td>139</td><td>4.00E-68</td><td>100.7</td><td>92.8</td><td>95.7</td><td>CHL-CPN10</td><td>gbpln</td><td>Brassica rapa</td><td>AT2G44650.1 | Symbols: CHL-CPN10, CPN10 | chloroplast chaperonin 10 | chr2:18419521-18420510 REVERSE LENGTH=139</td><td>138</td><td>139</td><td>3.00E-65</td><td>100.7</td><td>86.2</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00503.1.g15073.t1</td><td>ref|NP_181989.1| Ras-related protein RABH1B [Arabidopsis thaliana] gi|297828175|ref|XP_002881970.1| hypothetical protein ARALYDRAFT_903887 [Arabidopsis lyrata subsp. lyrata] gi|75318653|sp|O80501.1|RAH1B_ARATH RecName: Full=Ras-related protein RABH1b; Short=AtRABH1b; AltName: Full=Ras-related protein Rab6A; Short=AtRab6A gi|3341681|gb|AAC27463.1| putative small GTP-binding protein [Arabidopsis thaliana] gi|21593488|gb|AAM65455.1| putative small GTP-binding protein [Arabidopsis thaliana] gi|107738267|gb|ABF83670.1| At2g44610 [Arabidopsis thaliana] gi|110742258|dbj|BAE99055.1| putative small GTP-binding protein [Arabidopsis thaliana] gi|297327809|gb|EFH58229.1| hypothetical protein ARALYDRAFT_903887 [Arabidopsis lyrata subsp. lyrata] gi|330255353|gb|AEC10447.1| Ras-related protein RABH1B [Arabidopsis thaliana] gi|741994|prf||2008312A GTP-binding protein</td><td>208</td><td>208</td><td>1.00E-116</td><td>100.0</td><td>99.0</td><td>99.0</td><td>Ras-related protein RABH1B</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G44610.1 | Symbols: RAB6, ATRABH1B, ATRAB6A, RAB6A | Ras-related small GTP-binding family protein | chr2:18411778-18413883 REVERSE LENGTH=208</td><td>208</td><td>208</td><td>1.00E-119</td><td>100.0</td><td>99.0</td><td>99.0</td></tr>
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Rsa1.0_00503.1.g15074.t1	dbj|BAF01125.1| hypothetical protein [Arabidopsis thaliana]	270	313	6.00E-85	115.9	71.1	81.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G44600.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G60200.1); Has 56 Blast hits to 55 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 52; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:18408845-18409786 FORWARD LENGTH=313	270	313	1.00E-86	115.9	71.1	81.9
Rsa1.0_00503.1.g15075.t1	ref|XP_002881969.1| hypothetical protein ARALYDRAFT_483589 [Arabidopsis lyrata subsp. lyrata] gi|297327808|gb|EFH58228.1| hypothetical protein ARALYDRAFT_483589 [Arabidopsis lyrata subsp. lyrata]	618	614	0	99.4	85.6	93.9	hypothetical protein ARALYDRAFT_483589	gbpln	Arabidopsis lyrata	AT2G44590.3 | Symbols: ADL1D, DL1D | DYNAMIN-like 1D | chr2:18403856-18406961 REVERSE LENGTH=612	618	612	0	99.0	85.1	93.5
Rsa1.0_00503.1.g15076.t1	gb|AAC27460.1| putative RING zinc finger protein [Arabidopsis thaliana]	134	624	1.00E-51	465.7	70.9	85.1	putative RING zinc finger protein	gbpln	Arabidopsis thaliana	AT2G44581.1 | Symbols: | RING/U-box superfamily protein | chr2:18397996-18398433 REVERSE LENGTH=145	134	145	1.00E-53	108.2	70.9	85.1
Rsa1.0_00504.1.g15077.t1	gb|EOA39486.1| hypothetical protein CARUB_v10008094mg [Capsella rubella] gi|482575300|gb|EOA39487.1| hypothetical protein CARUB_v10008094mg [Capsella rubella]	998	1371	0	137.4	70.2	82.2	hypothetical protein CARUB_v10008094mg	gbpln	Capsella rubella	AT1G27170.1 | Symbols: | transmembrane receptors;ATP binding | chr1:9434718-9439219 FORWARD LENGTH=1384	998	1384	0	138.7	69.1	82.0
Rsa1.0_00504.1.g15078.t1	ref|NP_174062.1| kelch repeat-containing F-box protein [Arabidopsis thaliana] gi|374095396|sp|Q9FZJ3.2|FBK16_ARATH RecName: Full=Putative F-box/kelch-repeat protein At1g27420 gi|332192706|gb|AEE30827.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	345	346	1.00E-101	100.3	58.8	71.9	kelch repeat-containing F-box protein	gbpln	Arabidopsis thaliana	AT1G27420.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9519108-9520520 FORWARD LENGTH=346	345	346	1.00E-104	100.3	58.8	71.9
Rsa1.0_00504.1.g15079.t1	ref|NP_174062.1| kelch repeat-containing F-box protein [Arabidopsis thaliana] gi|374095396|sp|Q9FZJ3.2|FBK16_ARATH RecName: Full=Putative F-box/kelch-repeat protein At1g27420 gi|332192706|gb|AEE30827.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	321	346	2.00E-90	107.8	57.9	71.3	kelch repeat-containing F-box protein	gbpln	Arabidopsis thaliana	AT1G27420.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9519108-9520520 FORWARD LENGTH=346	321	346	5.00E-93	107.8	57.9	71.3
Rsa1.0_00504.1.g15080.t1	ref|XP_002893356.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297339198|gb|EFH69615.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	652	672	0	103.1	86.0	92.2	galactosyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G27120.1 | Symbols: | Galactosyltransferase family protein | chr1:9421389-9423910 FORWARD LENGTH=673	652	673	0	103.2	85.6	91.7
Rsa1.0_00504.1.g15081.t1	ref|NP_174031.2| StaR-like protein domain-containing protein [Arabidopsis thaliana] gi|60547597|gb|AAX23762.1| hypothetical protein At1g27110 [Arabidopsis thaliana] gi|332192659|gb|AEE30780.1| StaR-like protein domain-containing protein [Arabidopsis thaliana]	508	483	0	95.1	73.4	82.9	StaR-like protein domain-containing protein	gbpln	Arabidopsis thaliana	AT1G27110.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:9413018-9417392 REVERSE LENGTH=483	508	483	0	95.1	73.4	82.9
Rsa1.0_00504.1.g15082.t1	ref|NP_174030.2| Actin cross-linking protein [Arabidopsis thaliana] gi|110737362|dbj|BAF00626.1| hypothetical protein [Arabidopsis thaliana] gi|190016000|gb|ACE62888.1| At1g27100 [Arabidopsis thaliana] gi|332192658|gb|AEE30779.1| Actin cross-linking protein [Arabidopsis thaliana]	265	519	1.00E-113	195.8	83.0	91.7	Actin cross-linking protein	gbpln	Arabidopsis thaliana	AT1G27100.1 | Symbols: | Actin cross-linking protein | chr1:9407557-9411074 REVERSE LENGTH=519	265	519	1.00E-116	195.8	83.0	91.7
Rsa1.0_00504.1.g15083.t1	ref|NP_174029.1| uncharacterized glycine-rich protein [Arabidopsis thaliana] gi|8778876|gb|AAF79875.1|AC000348_28 T7N9.15 [Arabidopsis thaliana] gi|18389240|gb|AAL67063.1| unknown protein [Arabidopsis thaliana] gi|20259227|gb|AAM14329.1| unknown protein [Arabidopsis thaliana] gi|332192657|gb|AEE30778.1| uncharacterized glycine-rich protein [Arabidopsis thaliana]	456	420	1.00E-120	92.1	62.7	73.2	uncharacterized glycine-rich protein	gbpln	Arabidopsis thaliana	AT1G27090.1 | Symbols: | glycine-rich protein | chr1:9404041-9406098 REVERSE LENGTH=420	456	420	1.00E-122	92.1	62.7	73.2

Rsa1.0_00504.1.g15084.t1	ref|XP_002893358.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] gi|297339200|gb|EFH69617.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	392	388	0	99.0	82.7	89.5	regulator of chromosome condensation family protein	gbpln	Arabidopsis lyrata	AT1G27060.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr1:9395023-9396673 FORWARD LENGTH=386	392	386	1.00E-180	98.5	80.1	88.3
Rsa1.0_00504.1.g15085.t1	ref|XP_002893361.1| hypothetical protein ARALYDRAFT_890014 [Arabidopsis lyrata subsp. lyrata] gi|297339203|gb|EFH69620.1| hypothetical protein ARALYDRAFT_890014 [Arabidopsis lyrata subsp. lyrata]	310	310	1.00E-154	100.0	84.5	91.6	hypothetical protein ARALYDRAFT_890014	gbpln	Arabidopsis lyrata	AT1G27030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27020.1); Has 504 Blast hits to 502 proteins in 169 species: Archae - 0; Bacteria - 299; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 138 (source: NCBI BLink). | chr1:9381842-9383712 FORWARD LENGTH=310	310	310	1.00E-154	100.0	82.6	90.6
Rsa1.0_00504.1.g15086.t1	ref|NP_174062.1| kelch repeat-containing F-box protein [Arabidopsis thaliana] gi|374095396|sp|Q9FZJ3.2|FBK16_ARATH RecName: Full=Putative F-box/kelch-repeat protein At1g27420 gi|332192706|gb|AEE30827.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	326	346	1.00E-112	106.1	69.0	78.2	kelch repeat-containing F-box protein	gbpln	Arabidopsis thaliana	AT1G27420.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9519108-9520520 FORWARD LENGTH=346	326	346	1.00E-115	106.1	69.0	78.2
Rsa1.0_00504.1.g15087.t1	gb|AAF79851.1|AC000348_4 T7N9.6 [Arabidopsis thaliana]	314	334	1.00E-142	106.4	83.1	91.7	T7N9.6	gbpln	Arabidopsis thaliana	AT1G27000.1 | Symbols: | Protein of unknown function (DUF1664) | chr1:9374068-9376422 FORWARD LENGTH=304	314	304	1.00E-140	96.8	78.7	86.9
Rsa1.0_00504.1.g15088.t1	ref|NP_174019.2| protein kinase domain-containing protein [Arabidopsis thaliana] gi|56236066|gb|AAV84489.1| At1g26970 [Arabidopsis thaliana] gi|56790206|gb|AAW30020.1| At1g26970 [Arabidopsis thaliana] gi|332192644|gb|AEE30765.1| protein kinase domain-containing protein [Arabidopsis thaliana]	410	412	0	100.5	82.9	89.8	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G26970.1 | Symbols: | Protein kinase superfamily protein | chr1:9359826-9361666 FORWARD LENGTH=412	410	412	0	100.5	82.9	89.8
Rsa1.0_00504.1.g15089.t1	gb|EOA37024.1| hypothetical protein CARUB_v10010076mg [Capsella rubella]	255	254	1.00E-121	99.6	87.1	93.3	hypothetical protein CARUB_v10010076mg	gbpln	Capsella rubella	AT1G26960.1 | Symbols: AtHB23, HB23 | homeobox protein 23 | chr1:9356126-9357239 FORWARD LENGTH=255	255	255	1.00E-121	100.0	86.3	92.5
Rsa1.0_00504.1.g15090.t1	ref|NP_001031615.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|98962109|gb|ABF59384.1| unknown protein [Arabidopsis thaliana] gi|332657509|gb|AEE82909.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	213	146	4.00E-18	68.5	23.9	32.9	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT4G10613.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:6561039-6561479 FORWARD LENGTH=146	213	146	1.00E-20	68.5	23.9	32.9
Rsa1.0_00504.1.g15091.t1	gb|EOA36365.1| hypothetical protein CARUB_v10010751mg [Capsella rubella]	94	94	9.00E-34	100.0	78.7	80.9	hypothetical protein CARUB_v10010751mg	gbpln	Capsella rubella	AT1G26945.1 | Symbols: KDR | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:9351571-9352474 FORWARD LENGTH=94	94	94	4.00E-36	100.0	77.7	80.9
Rsa1.0_00504.1.g15092.t1	gb|EOA37078.1| hypothetical protein CARUB_v10010228mg [Capsella rubella]	234	226	1.00E-105	96.6	82.9	88.5	hypothetical protein CARUB_v10010228mg	gbpln	Capsella rubella	AT1G26940.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr1:9343193-9344962 FORWARD LENGTH=226	234	226	1.00E-106	96.6	80.8	86.8
Rsa1.0_00504.1.g15093.t1	gb|EOA40529.1| hypothetical protein CARUB_v10009257mg [Capsella rubella]	427	419	0	98.1	88.1	92.7	hypothetical protein CARUB_v10009257mg	gbpln	Capsella rubella	AT1G26930.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9336211-9337476 REVERSE LENGTH=421	427	421	0	98.6	86.2	92.0
Rsa1.0_00504.1.g15094.t1	ref|NP_564266.1| uncharacterized protein [Arabidopsis thaliana] gi|13877719|gb|AAK43937.1|AF370618_1 Unknown protein [Arabidopsis thaliana] gi|4262181|gb|AAD14498.1| Unknown protein [Arabidopsis thaliana] gi|17065576|gb|AAL32942.1| Unknown protein [Arabidopsis thaliana] gi|20148583|gb|AAM10182.1| unknown protein [Arabidopsis thaliana] gi|21592517|gb|AAM64467.1| unknown [Arabidopsis thaliana] gi|332192638|gb|AEE30759.1| uncharacterized protein AT1G26920 [Arabidopsis thaliana]	174	173	2.00E-61	99.4	72.4	86.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G26920.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G69760.1); Has 47 Blast hits to 47 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 7; Plants - 34; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:9329584-9330105 FORWARD LENGTH=173	174	173	8.00E-64	99.4	72.4	86.8

Rsa1.0_00505.1.g15095.t2	ref|XP_002873168.1| hypothetical protein ARALYDRAFT_908364 [Arabidopsis lyrata subsp. lyrata] gi|297319005|gb|EFH49427.1| hypothetical protein ARALYDRAFT_908364 [Arabidopsis lyrata subsp. lyrata]	190	213	8.00E-85	112.1	83.7	90.0	hypothetical protein ARALYDRAFT_908364	gbpln	Arabidopsis lyrata	AT5G04760.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr5:1373752-1374529 REVERSE LENGTH=215	190	215	1.00E-77	113.2	80.0	87.9
Rsa1.0_00505.1.g15096.t1	ref|NP_196094.1| ACT domain-containing protein [Arabidopsis thaliana] gi|7413536|emb|CAB86016.1| putative protein [Arabidopsis thaliana] gi|9758449|dbj|BAB08978.1| unnamed protein product [Arabidopsis thaliana] gi|18252933|gb|AAL62393.1| putative protein [Arabidopsis thaliana] gi|21389645|gb|AAM48021.1| putative protein [Arabidopsis thaliana] gi|332003394|gb|AED90777.1| ACT domain-containing protein [Arabidopsis thaliana] gi|347949480|gb|AEP31953.1| ACT domain-containing protein [Arabidopsis thaliana]	298	301	1.00E-136	101.0	83.2	90.3	ACT domain-containing protein	gbpln	Arabidopsis thaliana	AT5G04740.1 | Symbols: | ACT domain-containing protein | chr5:1368713-1371391 REVERSE LENGTH=301	298	301	1.00E-138	101.0	83.2	90.3
Rsa1.0_00505.1.g15097.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00505.1.g15098.t1	dbj|BAJ34016.1| unnamed protein product [Thellungiella halophila]	298	522	5.00E-46	175.2	35.6	41.3	unnamed protein product	----	----	AT5G04720.1 | Symbols: ADR1-L2 | ADR1-like 2 | chr5:1360748-1363665 FORWARD LENGTH=811	298	811	7.00E-46	272.1	33.2	37.9
Rsa1.0_00505.1.g15099.t1	ref|NP_564870.1| homolog of anti-oxidant 1 [Arabidopsis thaliana] gi|14532548|gb|AAK64002.1| At1g66240/T6J19_6 [Arabidopsis thaliana] gi|18655401|gb|AAL76156.1| At1g66240/T6J19_6 [Arabidopsis thaliana] gi|332196360|gb|AEE34481.1| homolog of anti-oxidant 1 [Arabidopsis thaliana]	77	106	4.00E-29	137.7	85.7	94.8	homolog of anti-oxidant 1	gbpln	Arabidopsis thaliana	AT1G66240.1 | Symbols: ATX1, ATATX1 | homolog of anti-oxidant 1 | chr1:24686445-24687327 REVERSE LENGTH=106	77	106	6.00E-32	137.7	85.7	94.8
Rsa1.0_00505.1.g15100.t1	gb|EOA20007.1| hypothetical protein CARUB_v10000280mg [Capsella rubella]	229	769	3.00E-76	335.8	69.4	79.5	hypothetical protein CARUB_v10000280mg	gbpln	Capsella rubella	AT5G04670.1 | Symbols: | Enhancer of polycomb-like transcription factor protein | chr5:1337998-1340884 REVERSE LENGTH=766	229	766	3.00E-72	334.5	64.6	75.5
Rsa1.0_00505.1.g15101.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00505.1.g15102.t1	gb|EOA21520.1| hypothetical protein CARUB_v10001924mg [Capsella rubella]	222	220	1.00E-104	99.1	89.6	94.1	hypothetical protein CARUB_v10001924mg	gbpln	Capsella rubella	AT5G04600.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:1323700-1325486 FORWARD LENGTH=222	222	222	1.00E-99	100.0	76.6	86.5
Rsa1.0_00505.1.g15103.t1	ref|XP_002873156.1| hypothetical protein ARALYDRAFT_908343 [Arabidopsis lyrata subsp. lyrata] gi|297318993|gb|EFH49415.1| hypothetical protein ARALYDRAFT_908343 [Arabidopsis lyrata subsp. lyrata]	599	599	0	100.0	86.6	93.2	hypothetical protein ARALYDRAFT_908343	gbpln	Arabidopsis lyrata	AT5G04550.1 | Symbols: | Protein of unknown function (DUF668) | chr5:1303757-1305556 REVERSE LENGTH=599	599	599	0	100.0	86.3	93.2
Rsa1.0_00505.1.g15104.t1	ref|NP_196074.2| Myotubularin-like phosphatases II-like protein [Arabidopsis thaliana] gi|332003375|gb|AED90758.1| Myotubularin-like phosphatases II-like protein [Arabidopsis thaliana]	830	833	0	100.4	84.0	91.2	Myotubularin-like phosphatases II-like protein	gbpln	Arabidopsis thaliana	AT5G04540.1 | Symbols: | Myotubularin-like phosphatases II superfamily | chr5:1296826-1302299 REVERSE LENGTH=833	830	833	0	100.4	84.0	91.2
Rsa1.0_00505.1.g15105.t1	ref|XP_002873154.1| beta-ketoacyl-CoA synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297318991|gb|EFH49413.1| beta-ketoacyl-CoA synthase family protein [Arabidopsis lyrata subsp. lyrata]	462	464	0	100.4	89.2	93.1	beta-ketoacyl-CoA synthase family protein	gbpln	Arabidopsis lyrata	AT5G04530.1 | Symbols: KCS19 | 3-ketoacyl-CoA synthase 19 | chr5:1292222-1293616 REVERSE LENGTH=464	462	464	0	100.4	88.3	93.7
Rsa1.0_00505.1.g15106.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00505.1.g15107.t1	gb|EOA22612.1| hypothetical protein CARUB_v10003280mg [Capsella rubella]	725	762	0	105.1	81.2	90.1	hypothetical protein CARUB_v10003280mg	gbpln	Capsella rubella	AT5G04500.1 | Symbols: | glycosyltransferase family protein 47 | chr5:1283604-1286155 FORWARD LENGTH=765	725	765	0	105.5	80.6	88.8
Rsa1.0_00505.1.g15108.t1	gb|EOA19863.1| hypothetical protein CARUB_v10000114mg [Capsella rubella]	209	1048	9.00E-32	501.4	31.1	36.4	hypothetical protein CARUB_v10000114mg	gbpln	Capsella rubella	AT5G04480.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1271886-1277793 REVERSE LENGTH=1050	209	1050	3.00E-33	502.4	31.1	35.9
Rsa1.0_00505.1.g15109.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	112	1555	3.00E-17	1388.4	42.0	58.9	disease resistance protein	gbpln	Brassica rapa	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	112	170	6.00E-12	151.8	32.1	47.3

<table>
<tr><td>Rsa1.0_00505.1.g15110.t1</td><td>ref|NP_196067.1| cyclin-dependent protein kinase inhibitor [Arabidopsis thaliana] gi|75181205|sp|Q9LZ78.1|SIM_ARATH RecName: Full=Cyclin-dependent protein kinase inhibitor SIM; AltName: Full=Protein SIAMESE gi|7406451|emb|CAB85553.1| putative protein [Arabidopsis thaliana] gi|21537413|gb|AAM61754.1| unknown [Arabidopsis thaliana] gi|32815859|gb|AAP88332.1| At5g04470 [Arabidopsis thaliana] gi|332003366|gb|AED90749.1| cyclin-dependent protein kinase inhibitor SIM [Arabidopsis thaliana]</td><td>130</td><td>127</td><td>7.00E-29</td><td>97.7</td><td>57.7</td><td>65.4</td><td>cyclin-dependent protein kinase inhibitor</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G04470.1 | Symbols: SIM | cyclin-dependent protein kinase inhibitors | chr5:1266893-1267276 REVERSE LENGTH=127</td><td>130</td><td>127</td><td>1.00E-31</td><td>97.7</td><td>57.7</td><td>65.4</td></tr>
<tr><td>Rsa1.0_00505.1.g15111.t1</td><td>gb|EOA21054.1| hypothetical protein CARUB_v10001394mg [Capsella rubella]</td><td>330</td><td>334</td><td>1.00E-173</td><td>101.2</td><td>92.4</td><td>96.1</td><td>hypothetical protein CARUB_v10001394mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G04430.2 | Symbols: BTR1, BTR1L | binding to TOMV RNA 1L (long form) | chr5:1250602-1253523 REVERSE LENGTH=334</td><td>330</td><td>334</td><td>1.00E-175</td><td>101.2</td><td>91.5</td><td>95.5</td></tr>
<tr><td>Rsa1.0_00505.1.g15112.t1</td><td>ref|XP_002871092.1| hypothetical protein ARALYDRAFT_908325 [Arabidopsis lyrata subsp. lyrata] gi|297316929|gb|EFH47351.1| hypothetical protein ARALYDRAFT_908325 [Arabidopsis lyrata subsp. lyrata]</td><td>547</td><td>568</td><td>0</td><td>103.8</td><td>80.8</td><td>88.8</td><td>hypothetical protein ARALYDRAFT_908325</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G04410.1 | Symbols: NAC2, anac078 | NAC domain containing protein 2 | chr5:1243980-1246416 FORWARD LENGTH=567</td><td>547</td><td>567</td><td>0</td><td>103.7</td><td>79.7</td><td>88.5</td></tr>
<tr><td>Rsa1.0_00506.1.g15113.t1</td><td>ref|NP_189058.1| putative type 1 membrane protein [Arabidopsis thaliana] gi|4206765|gb|AAD11797.1| putative type 1 membrane protein [Arabidopsis thaliana] gi|11994235|dbj|BAB01357.1| unnamed protein product [Arabidopsis thaliana] gi|15450743|gb|AAK96643.1| AT3g24160/MUJ8_16 [Arabidopsis thaliana] gi|21537239|gb|AAM61580.1| type 1 membrane protein, putative [Arabidopsis thaliana] gi|22137144|gb|AAM91417.1| AT3g24160/MUJ8_16 [Arabidopsis thaliana] gi|332643343|gb|AEE76864.1| putative type 1 membrane protein [Arabidopsis thaliana]</td><td>365</td><td>364</td><td>1.00E-161</td><td>99.7</td><td>82.5</td><td>90.1</td><td>putative type 1 membrane protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24160.1 | Symbols: PMP | putative type 1 membrane protein | chr3:8726241-8729023 FORWARD LENGTH=364</td><td>365</td><td>364</td><td>1.00E-164</td><td>99.7</td><td>82.5</td><td>90.1</td></tr>
<tr><td>Rsa1.0_00506.1.g15114.t2</td><td>sp|O04955.2|GSHRC_BRARP RecName: Full=Glutathione reductase, cytosolic; Short=GR; Short=GRase gi|7689373|gb|AAF67753.1|AF255651_1 cytosolic glutathione reductase [Brassica rapa subsp. pekinensis] gi|7547136|gb|AAC49980.2| glutathione reductase [Brassica rapa]</td><td>485</td><td>502</td><td>0</td><td>103.5</td><td>96.5</td><td>97.5</td><td>RecName: Full=Glutathione reductase, cytosolic; Short=GR; Short=GRase gi|7689373|gb|AAF67753.1|AF255651_1 cytosolic glutathione reductase</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G24170.3 | Symbols: ATGR1, GR1 | glutathione-disulfide reductase | chr3:8729762-8734115 REVERSE LENGTH=499</td><td>485</td><td>499</td><td>0</td><td>102.9</td><td>93.8</td><td>97.7</td></tr>
<tr><td>Rsa1.0_00506.1.g15115.t1</td><td>gb|EOA29913.1| hypothetical protein CARUB_v10013006mg [Capsella rubella]</td><td>832</td><td>799</td><td>0</td><td>96.0</td><td>88.0</td><td>91.2</td><td>hypothetical protein CARUB_v10013006mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G24190.1 | Symbols: | Protein kinase superfamily protein | chr3:8743319-8747703 FORWARD LENGTH=793</td><td>832</td><td>793</td><td>0</td><td>95.3</td><td>88.9</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00506.1.g15116.t1</td><td>ref|XP_002883477.1| monooxygenase [Arabidopsis lyrata subsp. lyrata] gi|297329317|gb|EFH59736.1| monooxygenase [Arabidopsis lyrata subsp. lyrata]</td><td>507</td><td>505</td><td>0</td><td>99.6</td><td>90.3</td><td>94.1</td><td>monooxygenase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G24200.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr3:8748095-8751575 REVERSE LENGTH=505</td><td>507</td><td>505</td><td>0</td><td>99.6</td><td>90.5</td><td>93.7</td></tr>
<tr><td>Rsa1.0_00506.1.g15117.t1</td><td>gb|EOA30105.1| hypothetical protein CARUB_v10013216mg [Capsella rubella]</td><td>606</td><td>626</td><td>0</td><td>103.3</td><td>78.4</td><td>86.1</td><td>hypothetical protein CARUB_v10013216mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G24210.1 | Symbols: | Ankyrin repeat family protein | chr3:8753712-8755627 REVERSE LENGTH=607</td><td>606</td><td>607</td><td>0</td><td>100.2</td><td>80.2</td><td>87.1</td></tr>
<tr><td>Rsa1.0_00506.1.g15118.t1</td><td>ref|XP_002885610.1| nine-cis-epoxycarotenoid dioxygenase 6 [Arabidopsis lyrata subsp. lyrata] gi|297331450|gb|EFH61869.1| nine-cis-epoxycarotenoid dioxygenase 6 [Arabidopsis lyrata subsp. lyrata]</td><td>585</td><td>577</td><td>0</td><td>98.6</td><td>84.6</td><td>90.8</td><td>nine-cis-epoxycarotenoid dioxygenase 6</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G24220.1 | Symbols: NCED6, ATNCED6 | nine-cis-epoxycarotenoid dioxygenase 6 | chr3:8761439-8763172 FORWARD LENGTH=577</td><td>585</td><td>577</td><td>0</td><td>98.6</td><td>83.2</td><td>90.8</td></tr>
<tr><td>Rsa1.0_00506.1.g15119.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00506.1.g15120.t1</td><td>ref|XP_002886768.1| hypothetical protein ARALYDRAFT_475482 [Arabidopsis lyrata subsp. lyrata] gi|297332609|gb|EFH63027.1| hypothetical protein ARALYDRAFT_475482 [Arabidopsis lyrata subsp. lyrata]</td><td>428</td><td>435</td><td>0</td><td>101.6</td><td>85.3</td><td>93.0</td><td>hypothetical protein ARALYDRAFT_475482</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G64810.2 | Symbols: APO1 | Arabidopsis thaliana protein of unknown function (DUF794) | chr1:24086810-24088276 FORWARD LENGTH=460</td><td>428</td><td>460</td><td>0</td><td>107.5</td><td>84.6</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00506.1.g15121.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00506.1.g15122.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	219	1274	8.00E-11	581.7	19.2	27.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	219	303	1.00E-11	138.4	20.1	33.3
Rsa1.0_00506.1.g15123.t1	ref|NP_189065.2| putative pectate lyase 9 [Arabidopsis thaliana] gi|32129847|sp|Q9LRM5.1|PEL9_ARATH RecName: Full=Probable pectate lyase 9; Flags: Precursor gi|11994243|dbj|BAB01365.1| pectate lyase [Arabidopsis thaliana] gi|332643356|gb|AEE76877.1| putative pectate lyase 9 [Arabidopsis thaliana]	56	452	2.00E-11	807.1	66.1	78.6	putative pectate lyase 9	gbpln	Arabidopsis thaliana	AT3G24230.1 | Symbols: | Pectate lyase family protein | chr3:8774637-8777306 FORWARD LENGTH=452	56	452	3.00E-14	807.1	66.1	78.6
Rsa1.0_00507.1.g15124.t1	ref|XP_002884574.1| hypothetical protein ARALYDRAFT_896752 [Arabidopsis lyrata subsp. lyrata] gi|297330414|gb|EFH60833.1| hypothetical protein ARALYDRAFT_896752 [Arabidopsis lyrata subsp. lyrata]	559	554	0	99.1	89.1	93.0	hypothetical protein ARALYDRAFT_896752	gbpln	Arabidopsis lyrata	AT3G06370.1 | Symbols: NHX4, ATNHX4 | sodium hydrogen exchanger 4 | chr3:1930899-1933515 REVERSE LENGTH=503	559	503	0	90.0	80.1	83.9
Rsa1.0_00507.1.g15125.t1	ref|XP_002884572.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330412|gb|EFH60831.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	648	671	0	103.5	61.6	75.3	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT3G06340.3 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr3:1920607-1922628 REVERSE LENGTH=673	648	673	0	103.9	61.0	76.1
Rsa1.0_00507.1.g15126.t1	gb|EOA30590.1| hypothetical protein CARUB_v10013722mg [Capsella rubella]	465	440	0	94.6	77.2	82.4	hypothetical protein CARUB_v10013722mg	gbpln	Capsella rubella	AT3G06330.1 | Symbols: | RING/U-box superfamily protein | chr3:1917334-1919709 FORWARD LENGTH=426	465	426	1.00E-174	91.6	73.1	79.4
Rsa1.0_00507.1.g15127.t2	ref|XP_002882461.1| hypothetical protein ARALYDRAFT_896742 [Arabidopsis lyrata subsp. lyrata] gi|297328301|gb|EFH58720.1| hypothetical protein ARALYDRAFT_896742 [Arabidopsis lyrata subsp. lyrata]	416	409	1.00E-141	98.3	61.3	73.3	hypothetical protein ARALYDRAFT_896742	gbpln	Arabidopsis lyrata	AT1G03710.2 | Symbols: | Cystatin/monellin superfamily protein | chr1:923492-924287 FORWARD LENGTH=202	416	202	7.00E-25	48.6	18.8	27.6
Rsa1.0_00507.1.g15128.t1	ref|XP_002882461.1| hypothetical protein ARALYDRAFT_896742 [Arabidopsis lyrata subsp. lyrata] gi|297328301|gb|EFH58720.1| hypothetical protein ARALYDRAFT_896742 [Arabidopsis lyrata subsp. lyrata]	399	409	1.00E-140	102.5	64.2	78.4	hypothetical protein ARALYDRAFT_896742	gbpln	Arabidopsis lyrata	AT1G03710.2 | Symbols: | Cystatin/monellin superfamily protein | chr1:923492-924287 FORWARD LENGTH=202	399	202	3.00E-24	50.6	16.0	23.1
Rsa1.0_00507.1.g15129.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00507.1.g15130.t2	ref|XP_002884569.1| hypothetical protein ARALYDRAFT_896743 [Arabidopsis lyrata subsp. lyrata] gi|297330409|gb|EFH60828.1| hypothetical protein ARALYDRAFT_896743 [Arabidopsis lyrata subsp. lyrata]	297	280	2.00E-70	94.3	48.1	61.3	hypothetical protein ARALYDRAFT_896743	gbpln	Arabidopsis lyrata	AT5G17080.1 | Symbols: | Cysteine proteinases superfamily protein | chr5:5619594-5620949 FORWARD LENGTH=298	297	298	2.00E-29	100.3	27.6	45.1
Rsa1.0_00507.1.g15131.t3	gb|EOA31003.1| hypothetical protein CARUB_v10014146mg [Capsella rubella]	316	334	1.00E-155	105.7	89.6	91.8	hypothetical protein CARUB_v10014146mg	gbpln	Capsella rubella	AT3G06300.1 | Symbols: AT-P4H-2 | P4H isoform 2 | chr3:1907744-1909675 FORWARD LENGTH=299	316	299	1.00E-153	94.6	87.3	90.2
Rsa1.0_00507.1.g15132.t1	ref|XP_002884568.1| hypothetical protein ARALYDRAFT_477928 [Arabidopsis lyrata subsp. lyrata] gi|297330408|gb|EFH60827.1| hypothetical protein ARALYDRAFT_477928 [Arabidopsis lyrata subsp. lyrata]	1472	1703	0	115.7	78.3	85.6	hypothetical protein ARALYDRAFT_477928	gbpln	Arabidopsis lyrata	AT3G06290.1 | Symbols: | SAC3/GANP/Nin1/mts3/eIF-3 p25 family | chr3:1899123-1907297 REVERSE LENGTH=1697	1472	1697	0	115.3	76.5	84.3
Rsa1.0_00507.1.g15133.t1	gb|EOA29649.1| hypothetical protein CARUB_v10015151mg [Capsella rubella]	349	351	0	100.6	94.6	96.8	hypothetical protein CARUB_v10015151mg	gbpln	Capsella rubella	AT3G06260.1 | Symbols: GATL4 | galacturonosyltransferase-like 4 | chr3:1893804-1894859 REVERSE LENGTH=351	349	351	0	100.6	94.6	97.4
Rsa1.0_00507.1.g15134.t1	gb|EOA32170.1| hypothetical protein CARUB_v10015426mg [Capsella rubella]	419	440	1.00E-144	105.0	65.2	79.5	hypothetical protein CARUB_v10015426mg	gbpln	Capsella rubella	AT3G06240.1 | Symbols: | F-box family protein | chr3:1887336-1888619 FORWARD LENGTH=427	419	427	1.00E-143	101.9	64.0	77.6
Rsa1.0_00507.1.g15135.t1	gb|EOA30696.1| hypothetical protein CARUB_v10013833mg [Capsella rubella]	423	410	0	96.9	90.8	93.6	hypothetical protein CARUB_v10013833mg	gbpln	Capsella rubella	AT3G06170.1 | Symbols: | Serinc-domain containing serine and sphingolipid biosynthesis protein | chr3:1867520-1869738 FORWARD LENGTH=409	423	409	0	96.7	89.4	92.4
Rsa1.0_00507.1.g15136.t2	gb|EOA30708.1| hypothetical protein CARUB_v10013845mg [Capsella rubella]	361	407	0	112.7	89.8	93.9	hypothetical protein CARUB_v10013845mg	gbpln	Capsella rubella	AT3G06190.1 | Symbols: ATBPM2, BPM2 | BTB-POZ and MATH domain 2 | chr3:1874577-1876575 REVERSE LENGTH=406	361	406	0	112.5	88.1	93.1

Rsa1.0_00507.1.g15137.t1	ref|NP_566276.1| guanylate kinase [Arabidopsis thaliana] gi|14190399|gb|AAK55680.1|AF378877_1 AT3g06200/F28L1_14 [Arabidopsis thaliana] gi|17386098|gb|AAL38595.1|AF446862_1 AT3g06200/F28L1_14 [Arabidopsis thaliana] gi|332640839|gb|AEE74360.1| P-loop containing nucleoside triphosphate hydrolases superfamily protein [Arabidopsis thaliana]	281	282	1.00E-116	100.4	77.2	86.1	guanylate kinase	gbpln	Arabidopsis thaliana	AT3G06200.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:1877678-1878526 FORWARD LENGTH=282	281	282	1.00E-119	100.4	77.2	86.1
Rsa1.0_00507.1.g15138.t1	ref|NP_001118347.1| F-box protein [Arabidopsis thaliana] gi|330251811|gb|AEC06905.1| F-box protein [Arabidopsis thaliana]	171	218	9.00E-22	127.5	41.5	55.6	F-box protein	gbpln	Arabidopsis thaliana	AT2G19630.2 | Symbols: | F-box and associated interaction domains-containing protein | chr2:8490217-8491110 REVERSE LENGTH=218	171	218	4.00E-24	127.5	41.5	55.6
Rsa1.0_00507.1.g15139.t1	ref|NP_187272.3| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|6862925|gb|AAF30314.1|AC018907_14 hypothetical protein [Arabidopsis thaliana] gi|332640840|gb|AEE74361.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	866	840	0	97.0	81.3	87.4	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G06210.1 | Symbols: | ARM repeat superfamily protein | chr3:1880093-1883317 FORWARD LENGTH=840	866	840	0	97.0	81.3	87.4
Rsa1.0_00507.1.g15140.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00507.1.g15141.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00507.1.g15142.t1	ref|NP_187266.1| uncharacterized protein [Arabidopsis thaliana] gi|6862919|gb|AAF30308.1|AC018907_8 unknown protein [Arabidopsis thaliana] gi|332640832|gb|AEE74353.1| uncharacterized protein AT3G06150 [Arabidopsis thaliana]	596	594	0	99.7	84.9	90.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G06150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19060.1); Has 61 Blast hits to 59 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:1861971-1863755 REVERSE LENGTH=594	596	594	0	99.7	84.9	90.8
Rsa1.0_00508.1.g15143.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00508.1.g15144.t1	ref|NP_565380.1| Plastocyanin-like domain-containing protein [Arabidopsis thaliana] gi|15294186|gb|AAK95270.1|AF410284_1 At2g15780/F19G14.22 [Arabidopsis thaliana] gi|5306253|gb|AAD41986.1| expressed protein [Arabidopsis thaliana] gi|20147265|gb|AAM10346.1| At2g15780/F19G14.22 [Arabidopsis thaliana] gi|330251343|gb|AEC06437.1| Plastocyanin-like domain-containing protein [Arabidopsis thaliana]	258	257	5.00E-78	99.6	76.4	83.3	Plastocyanin-like domain-containing protein	gbpln	Arabidopsis thaliana	AT2G15780.1 | Symbols: | Cupredoxin superfamily protein | chr2:6873666-6874701 REVERSE LENGTH=257	258	257	1.00E-80	99.6	76.4	83.3
Rsa1.0_00508.1.g15145.t1	gb|EOA18064.1| hypothetical protein CARUB_v10006510mg, partial [Capsella rubella]	165	555	9.00E-14	336.4	24.2	37.6	hypothetical protein CARUB_v10006510mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	165	566	2.00E-12	343.0	21.8	35.2
Rsa1.0_00508.1.g15146.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00508.1.g15147.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00508.1.g15148.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	380	1142	3.00E-39	300.5	23.7	35.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	380	256	1.00E-24	67.4	21.6	33.4
Rsa1.0_00508.1.g15149.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1192	1365	0	114.5	34.3	47.1	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	1192	154	8.00E-29	12.9	4.7	6.2
Rsa1.0_00508.1.g15150.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00508.1.g15151.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00508.1.g15152.t1	ref|NP_565380.1| Plastocyanin-like domain-containing protein [Arabidopsis thaliana] gi|15294186|gb|AAK95270.1|AF410284_1 At2g15780/F19G14.22 [Arabidopsis thaliana] gi|5306253|gb|AAD41986.1| expressed protein [Arabidopsis thaliana] gi|20147265|gb|AAM10346.1| At2g15780/F19G14.22 [Arabidopsis thaliana] gi|330251343|gb|AEC06437.1| Plastocyanin-like domain-containing protein [Arabidopsis thaliana]	275	257	1.00E-77	93.5	68.4	74.2	Plastocyanin-like domain-containing protein	gbpln	Arabidopsis thaliana	AT2G15780.1 | Symbols: | Cupredoxin superfamily protein | chr2:6873666-6874701 REVERSE LENGTH=257	275	257	3.00E-80	93.5	68.4	74.2
Rsa1.0_00508.1.g15153.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00508.1.g15154.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1328	2726	0	205.3	50.5	69.5	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1328	158	4.00E-36	11.9	5.5	6.9
Rsa1.0_00508.1.g15155.t1	gb|AAD17399.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana]	543	589	2.00E-27	108.5	11.6	16.2	putative Ta11-like non-LTR retroelement protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00508.1.g15156.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1191	1142	0	95.9	41.4	56.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1191	575	4.00E-77	48.3	12.1	19.4
Rsa1.0_00508.1.g15157.t1	ref|NP_565376.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|20197705|gb|AAD17402.2| putative RING-H2 zinc finger protein [Arabidopsis thaliana] gi|21594677|gb|AAM66032.1| putative RING-H2 zinc finger protein [Arabidopsis thaliana] gi|66865916|gb|AAY57592.1| RING finger family protein [Arabidopsis thaliana] gi|149944335|gb|ABR46210.1| At2g15580 [Arabidopsis thaliana] gi|222423846|dbj|BAH19888.1| AT2G15580 [Arabidopsis thaliana] gi|330251325|gb|AEC06419.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	195	196	1.00E-92	100.5	85.1	90.8	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT2G15580.1 | Symbols: | RING/U-box superfamily protein | chr2:6797687-6798815 FORWARD LENGTH=196	195	196	4.00E-95	100.5	85.1	90.8
Rsa1.0_00509.1.g15158.t2	ref|NP_001190294.1| uncharacterized protein [Arabidopsis thaliana] gi|34365673|gb|AAQ65148.1| At5g12240 [Arabidopsis thaliana] gi|51969328|dbj|BAD43356.1| unnamed protein product [Arabidopsis thaliana] gi|332004399|gb|AED91782.1| uncharacterized protein AT5G12240 [Arabidopsis thaliana]	138	114	5.00E-39	82.6	67.4	74.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G12240.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages. | chr5:3959120-3960777 REVERSE LENGTH=114	138	114	1.00E-41	82.6	67.4	74.6
Rsa1.0_00509.1.g15159.t1	dbj|BAJ34332.1| unnamed protein product [Thellungiella halophila]	448	450	0	100.4	98.7	99.3	unnamed protein product	----	----	AT5G12250.1 | Symbols: TUB6 | beta-6 tubulin | chr5:3961317-3962971 REVERSE LENGTH=449	448	449	0	100.2	97.5	98.7
Rsa1.0_00509.1.g15160.t2	ref|XP_002871521.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317358|gb|EFH47780.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	656	631	0	96.2	71.8	80.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G12260.1 | Symbols: | BEST Arabidopsis thaliana protein match is: glycosyltransferase family protein 2 (TAIR:AT5G60700.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3966417-3968684 FORWARD LENGTH=624	656	624	0	95.1	71.3	80.0
Rsa1.0_00509.1.g15161.t1	dbj|BAC43370.1| unknown protein [Arabidopsis thaliana]	529	602	0	113.8	86.4	93.2	unknown protein	gbpln	Arabidopsis thaliana	AT5G12290.1 | Symbols: DGS1 | dgd1 suppressor 1 | chr5:3974374-3978066 REVERSE LENGTH=602	529	602	0	113.8	82.0	90.0
Rsa1.0_00509.1.g15162.t1	ref|NP_193937.2| F-box protein [Arabidopsis thaliana] gi|374095389|sp|O65454.2|FB334_ARATH RecName: Full=Probable F-box protein At4g22060 gi|332659145|gb|AEE84545.1| probable F-box protein [Arabidopsis thaliana]	394	399	1.00E-109	101.3	58.6	72.8	F-box protein	gbpln	Arabidopsis thaliana	AT4G22060.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr4:11687620-11688819 FORWARD LENGTH=399	394	399	1.00E-112	101.3	58.6	72.8
Rsa1.0_00509.1.g15163.t1	ref|NP_193936.2| aspartyl protease family protein [Arabidopsis thaliana] gi|332659144|gb|AEE84544.1| aspartyl protease family protein [Arabidopsis thaliana]	357	354	8.00E-82	99.2	46.8	62.2	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT4G22050.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr4:11683865-11685506 FORWARD LENGTH=354	357	354	2.00E-84	99.2	46.8	62.2
Rsa1.0_00509.1.g15164.t4	dbj|BAJ34639.1| unnamed protein product [Thellungiella halophila]	993	343	2.00E-82	34.5	16.3	19.1	unnamed protein product	----	----	AT1G33970.5 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:12349614-12350960 REVERSE LENGTH=342	993	342	7.00E-80	34.4	15.8	18.6

Rsa1.0_00509.1.g15165.t1	gb|EOA22673.1| hypothetical protein CARUB_v10003376mg [Capsella rubella]	827	825	0	99.8	92.0	95.6	hypothetical protein CARUB_v10003376mg	gbpln	Capsella rubella	AT5G12370.2 | Symbols: SEC10 | exocyst complex component sec10 | chr5:4003002-4008445 REVERSE LENGTH=825	827	825	0	99.8	91.9	95.4
Rsa1.0_00509.1.g15166.t1	ref|NP_568273.2| PHD-finger and DNA binding domain-containing protein [Arabidopsis thaliana] gi|332004422|gb|AED91805.1| PHD-finger and DNA binding domain-containing protein [Arabidopsis thaliana]	1509	1602	0	106.2	75.3	85.8	PHD-finger and DNA binding domain-containing protein	gbpln	Arabidopsis thaliana	AT5G12400.1 | Symbols: | DNA binding;zinc ion binding;DNA binding | chr5:4013813-4021018 FORWARD LENGTH=1602	1509	1602	0	106.2	75.3	85.8
Rsa1.0_00509.1.g15167.t1	ref|XP_002873570.1| hypothetical protein ARALYDRAFT_488089 [Arabidopsis lyrata subsp. lyrata] gi|297319407|gb|EFH49829.1| hypothetical protein ARALYDRAFT_488089 [Arabidopsis lyrata subsp. lyrata]	849	480	0	56.5	42.0	47.9	hypothetical protein ARALYDRAFT_488089	gbpln	Arabidopsis lyrata	AT5G12420.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:4024568-4026715 REVERSE LENGTH=480	849	480	0	56.5	41.9	47.6
Rsa1.0_00509.1.g15168.t1	ref|NP_568275.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana] gi|14586372|emb|CAC42903.1| putative protein [Arabidopsis thaliana] gi|19424037|gb|AAL87279.1| unknown protein [Arabidopsis thaliana] gi|21280907|gb|AAM45124.1| unknown protein [Arabidopsis thaliana] gi|26450061|dbj|BAC42150.1| unknown protein [Arabidopsis thaliana] gi|332004424|gb|AED91807.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana]	80	480	1.00E-20	600.0	61.3	70.0	O-acyltransferase (WSD1-like) family protein	gbpln	Arabidopsis thaliana	AT5G12420.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:4024568-4026715 REVERSE LENGTH=480	80	480	2.00E-23	600.0	61.3	70.0
Rsa1.0_00509.1.g15169.t1	ref|XP_002873573.1| hypothetical protein ARALYDRAFT_325766 [Arabidopsis lyrata subsp. lyrata] gi|297319410|gb|EFH49832.1| hypothetical protein ARALYDRAFT_325766 [Arabidopsis lyrata subsp. lyrata]	517	651	0	125.9	78.3	85.1	hypothetical protein ARALYDRAFT_325766	gbpln	Arabidopsis lyrata	AT5G12440.3 | Symbols: | CCCH-type zinc fingerfamily protein with RNA-binding domain | chr5:4035891-4038604 REVERSE LENGTH=650	517	650	0	125.7	77.4	84.5
Rsa1.0_00509.1.g15170.t1	ref|XP_002873579.1| hypothetical protein ARALYDRAFT_909228 [Arabidopsis lyrata subsp. lyrata] gi|297319416|gb|EFH49838.1| hypothetical protein ARALYDRAFT_909228 [Arabidopsis lyrata subsp. lyrata]	387	385	1.00E-174	99.5	82.7	89.1	hypothetical protein ARALYDRAFT_909228	gbpln	Arabidopsis lyrata	AT5G12470.1 | Symbols: | Protein of unknown function (DUF3411) | chr5:4044950-4047290 REVERSE LENGTH=386	387	386	1.00E-175	99.7	82.2	89.1
Rsa1.0_00509.1.g15171.t2	ref|NP_568282.1| nuclear transcription factor Y subunit A-1 [Arabidopsis thaliana] gi|42573353|ref|NP_974773.1| nuclear transcription factor Y subunit A-1 [Arabidopsis thaliana] gi|75180950|sp|Q9LXV5.1|NFYA1_ARATH RecName: Full=Nuclear transcription factor Y subunit A-1; Short=AtNF-YA-1; AltName: Full=Protein EMBRYO DEFECTIVE 2220; AltName: Full=Transcriptional activator HAP2A gi|7630040|emb|CAB88248.1| CCAAT box binding factor/ transcription factor Hap2a [Arabidopsis thaliana] gi|107738403|gb|ABF83691.1| At5g12840 [Arabidopsis thaliana] gi|332004434|gb|AED91817.1| nuclear transcription factor Y subunit A-1 [Arabidopsis thaliana] gi|332004437|gb|AED91820.1| nuclear transcription factor Y subunit A-1 [Arabidopsis thaliana]	256	272	4.00E-89	106.3	70.7	78.9	nuclear transcription factor Y subunit A-1	gbpln	Arabidopsis thaliana	AT5G12840.3 | Symbols: HAP2A, ATHAP2A, NF-YA1 | nuclear factor Y, subunit A1 | chr5:4051147-4052961 REVERSE LENGTH=272	256	272	1.00E-91	106.3	70.7	78.9
Rsa1.0_00510.1.g15172.t1	gb|AAZ66952.1| 117M18_33 [Brassica rapa]	1110	681	0	61.4	30.9	39.7	117M18_33	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1110	1262	8.00E-45	113.7	8.5	13.9
Rsa1.0_00510.1.g15173.t1	gb|ACT67493.1| expansin A1 [Raphanus sativus]	258	258	1.00E-145	100.0	96.9	98.8	expansin A1	gbpln	Raphanus sativus	AT2G39700.1 | Symbols: ATEXPA4, ATEXP4, ATHEXP ALPHA 1.6, EXPA4 | expansin A4 | chr2:16544246-16545434 REVERSE LENGTH=257	258	257	2.33E-156	99.6	95.7	97.7
Rsa1.0_00510.1.g15174.t1	ref|XP_002879808.1| botrytis-induced kinase1 [Arabidopsis lyrata subsp. lyrata] gi|297325647|gb|EFH56067.1| botrytis-induced kinase1 [Arabidopsis lyrata subsp. lyrata]	393	394	0	100.3	89.8	94.1	botrytis-induced kinase1	gbpln	Arabidopsis lyrata	AT2G39660.1 | Symbols: BIK1 | botrytis-induced kinase1 | chr2:16531943-16533601 FORWARD LENGTH=395	393	395	0	100.5	89.3	93.9

Rsa1.0_00510.1.g15175.t1	gb|EOA27564.1| hypothetical protein CARUB_v10023703mg [Capsella rubella]	298	306	1.00E-138	102.7	84.6	91.3	hypothetical protein CARUB_v10023703mg	gbpln	Capsella rubella	AT2G39650.1 | Symbols: | Protein of unknown function (DUF506) | chr2:16528094-16529274 REVERSE LENGTH=291	298	291	1.00E-139	97.7	83.9	87.6
Rsa1.0_00510.1.g15176.t1	gb|EOA26396.1| hypothetical protein CARUB_v10023563mg [Capsella rubella]	337	342	1.00E-176	101.5	88.7	94.4	hypothetical protein CARUB_v10023563mg	gbpln	Capsella rubella	AT2G39630.1 | Symbols: | Nucleotide-diphospho-sugar transferases superfamily protein | chr2:16522008-16524561 REVERSE LENGTH=336	337	336	1.00E-176	99.7	87.2	93.8
Rsa1.0_00510.1.g15177.t1	ref|XP_002881665.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327504|gb|EFH57924.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	836	836	0	100.0	78.7	88.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT2G39620.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:16518968-16521478 REVERSE LENGTH=836	836	836	0	100.0	76.0	86.1
Rsa1.0_00510.1.g15178.t1	gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]	140	214	9.00E-48	152.9	70.7	78.6	trypsin inhibitor propeptide	gbpln	Brassica oleracea	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410-27548057 REVERSE LENGTH=215	140	215	4.00E-26	153.6	48.6	62.1
Rsa1.0_00510.1.g15179.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00510.1.g15180.t1	gb|AAM19777.1| At2g39480/F12L6.14 [Arabidopsis thaliana]	1402	1407	0	100.4	93.8	96.7	At2g39480/F12L6.14	gbpln	Arabidopsis thaliana	AT2G39480.1 | Symbols: PGP6 | P-glycoprotein 6 | chr2:16478249-16484827 REVERSE LENGTH=1407	1402	1407	0	100.4	93.8	96.8
Rsa1.0_00510.1.g15181.t1	dbj|BAJ33853.1| unnamed protein product [Thellungiella halophila]	154	154	4.00E-79	100.0	99.4	100.0	unnamed protein product	----	----	AT2G39460.2 | Symbols: ATRPL23A, RPL23A, RPL23AA | ribosomal protein L23AA | chr2:16475049-16475904 FORWARD LENGTH=154	154	154	3.00E-59	100.0	96.8	97.4
Rsa1.0_00510.1.g15182.t1	ref|XP_002881655.1| hypothetical protein ARALYDRAFT_321630 [Arabidopsis lyrata subsp. lyrata] gi|297327494|gb|EFH57914.1| hypothetical protein ARALYDRAFT_321630 [Arabidopsis lyrata subsp. lyrata]	458	719	1.00E-132	157.0	63.1	75.3	hypothetical protein ARALYDRAFT_321630	gbpln	Arabidopsis lyrata	AT2G39435.1 | Symbols: | Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-related | chr2:16464806-16466492 REVERSE LENGTH=464	458	464	1.00E-135	101.3	62.0	75.1
Rsa1.0_00510.1.g15183.t1	gb|EOA29283.1| hypothetical protein CARUB_v10025558mg [Capsella rubella]	313	325	1.00E-147	103.8	90.7	93.9	hypothetical protein CARUB_v10025558mg	gbpln	Capsella rubella	AT2G39430.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr2:16463422-16464390 FORWARD LENGTH=322	313	322	1.00E-149	102.9	92.7	94.2
Rsa1.0_00510.1.g15184.t1	ref|XP_002879795.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325634|gb|EFH56054.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	337	317	1.00E-169	94.1	85.5	90.2	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT2G39420.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:16460442-16462872 FORWARD LENGTH=317	337	317	1.00E-170	94.1	84.0	89.9
Rsa1.0_00510.1.g15185.t1	gb|EOA28139.1| hypothetical protein CARUB_v10024328mg [Capsella rubella]	123	123	3.00E-59	100.0	95.9	98.4	hypothetical protein CARUB_v10024328mg	gbpln	Capsella rubella	AT2G39390.1 | Symbols: | Ribosomal L29 family protein | chr2:16450803-16451762 REVERSE LENGTH=123	123	123	2.00E-61	100.0	95.1	97.6
Rsa1.0_00510.1.g15186.t1	gb|EOA18680.1| hypothetical protein CARUB_v10007256mg [Capsella rubella]	773	793	0	102.6	86.0	91.5	hypothetical protein CARUB_v10007256mg	gbpln	Capsella rubella	AT4G38180.1 | Symbols: FRS5 | FAR1-related sequence 5 | chr4:17906702-17909404 REVERSE LENGTH=788	773	788	0	101.9	85.5	90.3
Rsa1.0_00511.1.g15187.t1	gb|AEQ02413.1| phospholipase D [Brassica napus]	281	637	1.00E-101	226.7	62.6	64.8	phospholipase D	gbpln	Brassica napus	AT4G11850.1 | Symbols: PLDGAMMA1, MEE54 | phospholipase D gamma 1 | chr4:7129352-7132937 REVERSE LENGTH=858	281	858	2.00E-81	305.3	51.2	59.4
Rsa1.0_00511.1.g15188.t1	gb|ACB98704.1| phospholipase D gamma 1 [Brassica oleracea var. capitata]	306	859	2.33E-156	280.7	80.7	90.5	phospholipase D gamma 1	gbpln	Brassica oleracea	AT4G11830.1 | Symbols: PLDGAMMA2 | phospholipase D gamma 2 | chr4:7115985-7119683 REVERSE LENGTH=824	306	824	1.00E-147	269.3	81.0	90.5
Rsa1.0_00511.1.g15189.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00511.1.g15190.t1	gb|AAF67379.1| Hypothetical protein T15F17.k [Arabidopsis thaliana]	155	341	9.00E-23	220.0	45.2	58.7	Hypothetical protein T15F17.k	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00511.1.g15191.t1	gb|ABK28372.1| unknown [Arabidopsis thaliana]	379	389	1.00E-108	102.6	53.6	66.8	unknown	gbpln	Arabidopsis thaliana	AT4G00893.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12370.1); Has 220 Blast hits to 215 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 220; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:379971-381396 REVERSE LENGTH=388	379	388	1.00E-111	102.4	53.6	66.8
Rsa1.0_00511.1.g15192.t1	gb|ABK28372.1| unknown [Arabidopsis thaliana]	268	389	8.00E-28	145.1	26.5	33.6	unknown	gbpln	Arabidopsis thaliana	AT4G00893.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12370.1); Has 220 Blast hits to 215 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 220; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:379971-381396 REVERSE LENGTH=388	268	388	2.00E-30	144.8	26.5	33.6

Rsa1.0_00511.1.g15193.t1	ref|NP_192903.1| heat stress transcription factor B-2b [Arabidopsis thaliana] gi|12643858|sp|Q9T0D3.1|HFB2B_ARATH RecName: Full=Heat stress transcription factor B-2b; Short=AtHsfB2b; AltName: Full=AtHsf-11; AltName: Full=Heat shock factor protein 7; Short=HSF 7; AltName: Full=Heat shock transcription factor 7; Short=HSTF 7 gi|4539457|emb|CAB39937.1| heat shock transcription factor-like protein [Arabidopsis thaliana] gi|7267866|emb|CAB78209.1| heat shock transcription factor-like protein [Arabidopsis thaliana] gi|20260614|gb|AAM13205.1| heat shock transcription factor-like protein [Arabidopsis thaliana] gi|30725616|gb|AAP37830.1| At4g11660 [Arabidopsis thaliana] gi|332657636|gb|AEE83036.1| heat stress transcription factor B-2b [Arabidopsis thaliana]	310	377	1.00E-109	121.6	72.9	81.9	heat stress transcription factor B-2b	gbpln	Arabidopsis thaliana	AT4G11660.1 | Symbols: AT-HSFB2B, HSFB2B | winged-helix DNA-binding transcription factor family protein | chr4:7043006-7044227 FORWARD LENGTH=377	310	377	1.00E-112	121.6	72.9	81.9
Rsa1.0_00511.1.g15194.t1	dbj|BAJ34101.1| unnamed protein product [Thellungiella halophila]	221	222	1.00E-117	100.5	91.4	95.0	unnamed protein product	----	----	AT4G11650.1 | Symbols: ATOSM34, OSM34 | osmotin 34 | chr4:7025127-7026113 REVERSE LENGTH=244	221	244	1.00E-114	110.4	89.1	92.8
Rsa1.0_00511.1.g15195.t1	ref|NP_171648.1| pumilio 22 [Arabidopsis thaliana] gi|75264077|sp|Q9LNI2.1|PUM22_ARATH RecName: Full=Putative pumilio homolog 22; Short=APUM-22; Short=AtPUM22 gi|9665150|gb|AAF97334.1|AC023628_15 Hypothetical protein [Arabidopsis thaliana] gi|332189162|gb|AEE27283.1| pumilio 22 [Arabidopsis thaliana]	228	361	2.00E-47	158.3	43.4	52.6	pumilio 22	gbpln	Arabidopsis thaliana	AT1G01410.1 | Symbols: APUM22, PUM22 | pumilio 22 | chr1:153113-154198 FORWARD LENGTH=361	228	361	6.00E-50	158.3	43.4	52.6
Rsa1.0_00511.1.g15196.t1	ref|NP_171649.1| hydroquinone glucosyltransferase [Arabidopsis thaliana] gi|75311399|sp|Q9LNI1.1|U72B3_ARATH RecName: Full=UDP-glycosyltransferase 72B3 gi|9665137|gb|AAF97321.1|AC023628_2 Similar to UTP-glucose glucosyltransferases [Arabidopsis thaliana] gi|145651796|gb|ABP88123.1| At1g01420 [Arabidopsis thaliana] gi|332189163|gb|AEE27284.1| UDP-glucosyltransferase 72B3 [Arabidopsis thaliana]	478	481	0	100.6	77.4	86.6	hydroquinone glucosyltransferase	gbpln	Arabidopsis thaliana	AT1G01420.1 | Symbols: UGT72B3 | UDP-glucosyl transferase 72B3 | chr1:154566-156011 REVERSE LENGTH=481	478	481	0	100.6	77.4	86.6
Rsa1.0_00511.1.g15197.t2	gb|EOA20251.1| hypothetical protein CARUB_v10000551mg [Capsella rubella]	566	584	0	103.2	76.3	85.5	hypothetical protein CARUB_v10000551mg	gbpln	Capsella rubella	AT4G11560.1 | Symbols: | bromo-adjacent homology (BAH) domain-containing protein | chr4:7000095-7003445 REVERSE LENGTH=587	566	587	0	103.7	76.7	85.0
Rsa1.0_00512.1.g15198.t1	gb|EOA22563.1| hypothetical protein CARUB_v10003224mg [Capsella rubella]	296	486	1.00E-85	164.2	63.2	72.6	hypothetical protein CARUB_v10003224mg	gbpln	Capsella rubella	AT5G18950.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:6328519-6329970 REVERSE LENGTH=483	296	483	1.00E-83	163.2	60.8	73.0
Rsa1.0_00512.1.g15199.t1	gb|EOA19261.1| hypothetical protein CARUB_v10000255mg [Capsella rubella]	805	787	0	97.8	84.7	90.3	hypothetical protein CARUB_v10000255mg	gbpln	Capsella rubella	AT5G18960.1 | Symbols: FRS12 | FAR1-related sequence 12 | chr5:6330556-6333071 FORWARD LENGTH=788	805	788	0	97.9	85.1	90.1
Rsa1.0_00512.1.g15200.t1	gb|EOA21686.1| hypothetical protein CARUB_v10002111mg [Capsella rubella]	170	170	8.00E-88	100.0	94.7	98.2	hypothetical protein CARUB_v10002111mg	gbpln	Capsella rubella	AT5G18970.1 | Symbols: | AWPM-19-like family protein | chr5:6333714-6334539 REVERSE LENGTH=171	170	171	5.00E-88	100.6	94.1	97.6
Rsa1.0_00512.1.g15201.t1	ref|NP_197401.2| BTB-POZ and math domain-containing protein [Arabidopsis thaliana] gi|75301130|sp|Q8L765.1|BPM1_ARATH RecName: Full=BTB/POZ and MATH domain-containing protein 1; AltName: Full=Protein BTB-POZ AND MATH DOMAIN 1; Short=AtBPM1 gi|22531225|gb|AAM97116.1| putative protein [Arabidopsis thaliana] gi|27311975|gb|AAO00953.1| putative protein [Arabidopsis thaliana] gi|332005254|gb|AED92637.1| BTB-POZ and math domain-containing protein [Arabidopsis thaliana]	222	407	3.00E-72	183.3	59.5	63.1	BTB-POZ and math domain-containing protein	gbpln	Arabidopsis thaliana	AT5G19000.1 | Symbols: ATBPM1, BPM1 | BTB-POZ and MATH domain 1 | chr5:6342563-6344641 FORWARD LENGTH=407	222	407	1.00E-74	183.3	59.5	63.1
Rsa1.0_00512.1.g15202.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00512.1.g15203.t2	ref|NP_197406.1| esterase/lipase domain-containing protein [Arabidopsis thaliana] gi|14250874|emb|CAC39243.1| hypothetical protein [Arabidopsis thaliana] gi|18377688|gb|AAL66994.1| unknown protein [Arabidopsis thaliana] gi|23296801|gb|AAN13173.1| unknown protein [Arabidopsis thaliana] gi|332005263|gb|AED92646.1| esterase/lipase domain-containing protein [Arabidopsis thaliana]	385	361	1.00E-170	93.8	79.2	80.8	esterase/lipase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G19050.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:6369307-6371726 FORWARD LENGTH=361	385	361	1.00E-172	93.8	79.2	80.8
Rsa1.0_00512.1.g15204.t1	ref|XP_002871857.1| hypothetical protein ARALYDRAFT_488790 [Arabidopsis lyrata subsp. lyrata] gi|297317694|gb|EFH48116.1| hypothetical protein ARALYDRAFT_488790 [Arabidopsis lyrata subsp. lyrata]	265	280	1.00E-106	105.7	79.6	83.8	hypothetical protein ARALYDRAFT_488790	gbpln	Arabidopsis lyrata	AT5G19070.1 | Symbols: | SNARE associated Golgi protein family | chr5:6375569-6377470 FORWARD LENGTH=280	265	280	1.00E-108	105.7	79.2	83.8
Rsa1.0_00512.1.g15205.t1	ref|NP_197413.1| aspartyl protease family protein [Arabidopsis thaliana] gi|15010798|gb|AAK74058.1| AT5g19120/T24G5_20 [Arabidopsis thaliana] gi|15810069|gb|AAL06960.1| AT5g19120/T24G5_20 [Arabidopsis thaliana] gi|332005272|gb|AED92655.1| aspartyl protease family protein [Arabidopsis thaliana]	392	386	1.00E-164	98.5	75.0	86.0	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT5G19120.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:6414585-6415745 FORWARD LENGTH=386	392	386	1.00E-167	98.5	75.0	86.0
Rsa1.0_00512.1.g15206.t1	ref|NP_173247.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|79318119|ref|NP_001031063.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|21539549|gb|AAM53327.1| putative guanine nucleotide regulatory protein [Arabidopsis thaliana] gi|31711944|gb|AAP68328.1| At1g18070 [Arabidopsis thaliana] gi|332191549|gb|AEE29670.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|332191550|gb|AEE29671.1| Translation elongation factor EF1A/initiation factor IF2gamma family protein [Arabidopsis thaliana]	469	532	1.00E-80	113.4	39.7	57.1	G1 to S phase transition protein	gbpln	Arabidopsis thaliana	AT1G18070.2 | Symbols: | Translation elongation factor EF1A/initiation factor IF2gamma family protein | chr1:6214236-6218211 REVERSE LENGTH=532	469	532	3.00E-83	113.4	39.7	57.1
Rsa1.0_00512.1.g15207.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	138	1231	1.00E-20	892.0	34.8	47.1	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00512.1.g15208.t1	gb|AFO66531.1| putative NADH-ubiquinone oxidoreductase 20 kDa subunit [Brassica napus]	146	248	4.00E-64	169.9	87.7	91.1	putative NADH-ubiquinone oxidoreductase 20 kDa subunit	gbpln	Brassica napus	AT5G11770.1 | Symbols: | NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial | chr5:3791148-3792929 REVERSE LENGTH=218	146	218	3.00E-58	149.3	84.9	89.0
Rsa1.0_00512.1.g15209.t1	ref|XP_002877525.1| hypothetical protein ARALYDRAFT_905911 [Arabidopsis lyrata subsp. lyrata] gi|297323363|gb|EFH53784.1| hypothetical protein ARALYDRAFT_905911 [Arabidopsis lyrata subsp. lyrata]	266	158	9.00E-17	59.4	22.2	30.5	hypothetical protein ARALYDRAFT_905911	gbpln	Arabidopsis lyrata	AT3G02070.1 | Symbols: | Cysteine proteinases superfamily protein | chr3:361368-363132 FORWARD LENGTH=219	266	219	2.00E-14	82.3	19.9	28.2
Rsa1.0_00512.1.g15210.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00512.1.g15211.t1	ref|NP_180542.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75100652|sp|O82375.1|FBK39_ARATH RecName: Full=Putative F-box/kelch-repeat protein At2g29810 gi|3582323|gb|AAC35220.1| hypothetical protein [Arabidopsis thaliana] gi|330253213|gb|AEC08307.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	364	383	5.00E-80	105.2	48.1	64.8	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT2G29810.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:12726102-12727253 REVERSE LENGTH=383	364	383	1.00E-82	105.2	48.1	64.8
Rsa1.0_00512.1.g15212.t1	ref|XP_002890292.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297336134|gb|EFH66551.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	224	476	4.00E-46	212.5	39.3	42.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G18660.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:6421433-6425565 FORWARD LENGTH=486	224	486	4.00E-48	217.0	38.8	42.4
Rsa1.0_00512.1.g15213.t2	ref|NP_001154709.2| uncharacterized protein [Arabidopsis thaliana] gi|332004329|gb|AED91712.1| uncharacterized protein AT5G11700 [Arabidopsis thaliana]	1102	1476	0	133.9	39.3	42.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G11700.2 | Symbols: | BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT4G32920.3); Has 8203 Blast hits to 3102 proteins in 389 species: Archae - 3; Bacteria - 5624; Metazoa - 852; Fungi - 139; Plants - 704; Viruses - 77; Other Eukaryotes - 804 (source: NCBI BLink). | chr5:3762961-3771123 REVERSE LENGTH=1476	1102	1476	0	133.9	39.3	42.3

Rsa1.0_00512.1.g15214.t1	ref|XP_002893723.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339565|gb|EFH69982.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	603	385	1.00E−102	63.8	33.2	43.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G16580.1 | Symbols: | F−box and associated interaction domains−containing protein | chr3:5647577−5648725 REVERSE LENGTH=382	603	382	2.00E−99	63.3	33.0	41.8
Rsa1.0_00512.1.g15215.t1	gb|ABV89631.1| aluminum−induced protein [Brassica rapa]	220	236	1.00E−109	107.3	86.4	88.6	aluminum−induced protein	gbpln	Brassica rapa	AT5G19140.1 | Symbols: ATAILP1, AILP1 | Aluminium induced protein with YGL and LRDR motifs | chr5:6423398−6425785 FORWARD LENGTH=234	220	234	1.00E−108	106.4	85.0	87.3
Rsa1.0_00512.1.g15216.t1	ref|XP_002873934.1| carbohydrate kinase family [Arabidopsis lyrata subsp. lyrata] gi|297319771|gb|EFH50193.1| carbohydrate kinase family [Arabidopsis lyrata subsp. lyrata]	357	370	0	103.6	92.7	96.6	carbohydrate kinase family	gbpln	Arabidopsis lyrata	AT5G19150.2 | Symbols: | pfkB−like carbohydrate kinase family protein | chr5:6426280−6428402 REVERSE LENGTH=365	357	365	0	102.2	89.6	93.0
Rsa1.0_00512.1.g15217.t1	ref|XP_002871869.1| hypothetical protein ARALYDRAFT_909950 [Arabidopsis lyrata subsp. lyrata] gi|297317706|gb|EFH48128.1| hypothetical protein ARALYDRAFT_909950 [Arabidopsis lyrata subsp. lyrata]	201	453	1.00E−86	225.4	77.6	84.6	hypothetical protein ARALYDRAFT_909950	gbpln	Arabidopsis lyrata	AT5G19180.1 | Symbols: ECR1 | E1 C−terminal related 1 | chr5:6453375−6455750 FORWARD LENGTH=454	201	454	1.00E−85	225.9	75.6	83.1
Rsa1.0_00512.1.g15218.t1	ref|NP_197420.1| uncharacterized protein [Arabidopsis thaliana] gi|26449943|dbj|BAC42092.1| unknown protein [Arabidopsis thaliana] gi|28972989|gb|AAO63819.1| unknown protein [Arabidopsis thaliana] gi|332005285|gb|AED92668.1| uncharacterized protein AT5G19190 [Arabidopsis thaliana]	106	154	6.00E−29	145.3	72.6	84.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G19190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06070.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:6457349−6457918 FORWARD LENGTH=154	106	154	9.00E−32	145.3	72.6	84.9
Rsa1.0_00512.1.g15219.t1	gb|EOA19562.1| hypothetical protein CARUB_v10002583mg [Capsella rubella]	113	450	7.00E−60	398.2	96.5	96.5	hypothetical protein CARUB_v10002583mg	gbpln	Capsella rubella	AT5G19780.1 | Symbols: TUA5 | tubulin alpha−5 | chr5:6687212−6688926 FORWARD LENGTH=450	113	450	2.00E−62	398.2	96.5	96.5
Rsa1.0_00512.1.g15220.t3	gb|EOA19838.1| hypothetical protein CARUB_v10000085mg [Capsella rubella]	353	1116	0	316.1	96.0	97.7	hypothetical protein CARUB_v10000085mg	gbpln	Capsella rubella	AT5G19820.1 | Symbols: emb2734 | ARM repeat superfamily protein | chr5:6695731−6701247 REVERSE LENGTH=1116	353	1116	0	316.1	95.5	98.0
Rsa1.0_00513.1.g15221.t1	gb|ABD65089.1| zinc knuckle containing protein [Brassica oleracea]	165	333	2.00E−74	201.8	83.0	93.3	zinc knuckle containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00513.1.g15222.t5	gb|EOA26133.1| hypothetical protein CARUB_v10019559mg [Capsella rubella]	380	969	2.00E−66	255.0	33.9	36.1	hypothetical protein CARUB_v10019559mg	gbpln	Capsella rubella	AT3G42850.1 | Symbols: | Mevalonate/galactokinase family protein | chr3:14940114−14945291 REVERSE LENGTH=964	380	964	2.00E−67	253.7	33.2	35.3
Rsa1.0_00513.1.g15223.t1	ref|XP_002874976.1| hypothetical protein ARALYDRAFT_912083 [Arabidopsis lyrata subsp. lyrata] gi|297320813|gb|EFH51235.1| hypothetical protein ARALYDRAFT_912083 [Arabidopsis lyrata subsp. lyrata]	337	332	1.00E−125	98.5	72.4	81.0	hypothetical protein ARALYDRAFT_912083	gbpln	Arabidopsis lyrata	AT4G01500.1 | Symbols: NGA4 | AP2/B3−like transcriptional factor family protein | chr4:639791−640792 FORWARD LENGTH=333	337	333	1.00E−126	98.8	71.5	79.5
Rsa1.0_00513.1.g15224.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	485	1838	1.00E−158	379.0	59.2	75.7	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00513.1.g15225.t3	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00513.1.g15226.t1	gb|AAD17351.1| contains similarity to retrovirus−related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana] gi|7267432|emb|CAB77944.1| putative polyprotein [Arabidopsis thaliana]	494	1138	5.00E−74	230.4	30.2	46.4	contains similarity to retrovirus−related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00513.1.g15227.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00513.1.g15228.t1	gb|EGV96854.1| Keratin−associated protein 4−3 [Cricetulus griseus]	416	224	1.00E−13	53.8	13.9	16.1	Keratin−associated protein 4−3	gbrod	Cricetulus griseus	#	#	#	#	#	#	#
Rsa1.0_00513.1.g15229.t1	ref|NP_192064.1| NAC domain−containing protein 69 [Arabidopsis thaliana] gi|75181714|sp|Q9M126.1|NAC69_ARATH RecName: Full=NAC domain−containing protein 69; Short=ANAC069; AltName: Full=Protein NAC WITH TRANSMEMBRANE MOTIF 2 gi|7268198|emb|CAB77725.1| putative NAM−like protein [Arabidopsis thaliana] gi|110738499|dbj|BAF01175.1| putative NAM−like protein [Arabidopsis thaliana] gi|332656640|gb|AEE82040.1| NAC domain−containing protein 69 [Arabidopsis thaliana]	424	457	1.00E−140	107.8	65.1	77.4	NAC domain−containing protein 69	gbpln	Arabidopsis thaliana	AT4G01550.1 | Symbols: anac069, NAC069 | NAC domain containing protein 69 | chr4:674025−676225 REVERSE LENGTH=457	424	457	1.00E−143	107.8	65.1	77.4

Rsa1.0_00513.1.g15230.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1392	1413	0	101.5	65.2	78.1	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1392	1262	0	90.7	22.4	28.4
Rsa1.0_00513.1.g15231.t1	gb|ACA61620.1| hypothetical protein AP6_E08.1 [Arabidopsis lyrata subsp. petraea]	217	220	1.00E-55	101.4	49.8	59.4	hypothetical protein AP6_E08.1	gbpln	Arabidopsis lyrata	AT4G01590.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: Arabidopsis protein of unknown function (DUF241) (TAIR:AT4G35680.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:689077-690192 REVERSE LENGTH=199	217	199	5.00E-52	91.7	46.5	58.1
Rsa1.0_00513.1.g15232.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00513.1.g15233.t1	gb|EOA19391.1| hypothetical protein CARUB_v10000764mg [Capsella rubella]	192	507	9.00E-90	264.1	90.1	94.3	hypothetical protein CARUB_v10000764mg	gbpln	Capsella rubella	AT4G01730.1 | Symbols: | DHHC-type zinc finger family protein | chr4:749574-752034 FORWARD LENGTH=508	192	508	2.00E-82	264.6	89.6	93.8
Rsa1.0_00513.1.g15234.t1	gb|EOA19391.1| hypothetical protein CARUB_v10000764mg [Capsella rubella]	299	507	1.00E-130	169.6	83.6	89.6	hypothetical protein CARUB_v10000764mg	gbpln	Capsella rubella	AT4G01730.1 | Symbols: | DHHC-type zinc finger family protein | chr4:749574-752034 FORWARD LENGTH=508	299	508	1.00E-127	169.9	85.6	92.0
Rsa1.0_00513.1.g15235.t1	ref|XP_002863331.1| hypothetical protein ARALYDRAFT_916628 [Arabidopsis lyrata subsp. lyrata] gi|297309166|gb|EFH39590.1| hypothetical protein ARALYDRAFT_916628 [Arabidopsis lyrata subsp. lyrata]	106	243	1.00E-11	229.2	48.1	67.9	hypothetical protein ARALYDRAFT_916628	gbpln	Arabidopsis lyrata	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	106	264	1.00E-10	249.1	40.6	63.2
Rsa1.0_00513.1.g15236.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00513.1.g15237.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00514.1.g15238.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00514.1.g15239.t1	ref|XP_002892845.1| quiescin-sulfhydryl oxidase 1 [Arabidopsis lyrata subsp. lyrata] gi|297338687|gb|EFH69104.1| quiescin-sulfhydryl oxidase 1 [Arabidopsis lyrata subsp. lyrata]	141	528	2.00E-36	374.5	69.5	78.7	quiescin-sulfhydryl oxidase 1	gbpln	Arabidopsis lyrata	AT1G15020.2 | Symbols: ATQSOX1, QSO2, QSOX1 | quiescin-sulfhydryl oxidase 1 | chr1:5173341-5176105 REVERSE LENGTH=528	141	528	2.00E-33	374.5	58.9	68.1
Rsa1.0_00514.1.g15240.t1	ref|XP_002883045.1| hypothetical protein ARALYDRAFT_479182 [Arabidopsis lyrata subsp. lyrata] gi|297328885|gb|EFH59304.1| hypothetical protein ARALYDRAFT_479182 [Arabidopsis lyrata subsp. lyrata]	217	219	5.00E-83	100.9	79.3	87.1	hypothetical protein ARALYDRAFT_479182	gbpln	Arabidopsis lyrata	AT3G17120.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02380.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:5842410-5843246 FORWARD LENGTH=219	217	219	4.00E-84	100.9	77.9	86.2
Rsa1.0_00514.1.g15241.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	688	1274	1.00E-118	185.2	34.9	45.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT3G17130.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:5844495-5845046 REVERSE LENGTH=183	688	183	1.00E-65	26.6	17.6	20.1
Rsa1.0_00514.1.g15242.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00514.1.g15243.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	283	478	2.00E-65	168.9	43.1	61.1	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	283	746	3.00E-53	263.6	36.0	49.5
Rsa1.0_00514.1.g15244.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00514.1.g15245.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00514.1.g15246.t1	gb|AAC02666.1| polyprotein [Arabidopsis thaliana]	1363	1451	0	106.5	59.5	73.1	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1363	1262	9.00E-83	92.6	12.0	18.4
Rsa1.0_00514.1.g15247.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00514.1.g15248.t1	gb|EOA30281.1| hypothetical protein CARUB_v10013409mg [Capsella rubella]	537	538	0	100.2	77.1	84.0	hypothetical protein CARUB_v10013409mg	gbpln	Capsella rubella	AT3G21320.1 | Symbols: | BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT2G25930.1); Has 63 Blast hits to 58 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:7499408-7501312 REVERSE LENGTH=540	537	540	0	100.6	73.6	82.3
Rsa1.0_00514.1.g15249.t1	gb|EOA32015.1| hypothetical protein CARUB_v10015258mg [Capsella rubella]	381	384	0	100.8	80.8	87.1	hypothetical protein CARUB_v10015258mg	gbpln	Capsella rubella	AT3G21310.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr3:7497774-7499011 FORWARD LENGTH=383	381	383	1.00E-180	100.5	80.8	88.7

Rsa1.0_00514.1.g15250.t1	gb|EOA30225.1| hypothetical protein CARUB_v10013347mg, partial [Capsella rubella]	554	567	0	102.3	87.4	93.0	hypothetical protein CARUB_v10013347mg, partial	gbpln	Capsella rubella	AT3G21300.1 | Symbols: | RNA methyltransferase family protein | chr3:7493654-7496257 REVERSE LENGTH=554	554	554	0	100.0	87.5	93.1
Rsa1.0_00514.1.g15251.t1	gb|EOA31808.1| hypothetical protein CARUB_v10015031mg [Capsella rubella]	74	75	5.00E-22	101.4	78.4	86.5	hypothetical protein CARUB_v10015031mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00514.1.g15252.t1	ref|NP_001078195.1| uncharacterized protein [Arabidopsis thaliana] gi|332642968|gb|AEE76489.1| uncharacterized protein AT3G21295 [Arabidopsis thaliana]	581	645	1.00E-180	111.0	70.9	79.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G21295.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr3:7489635-7492296 FORWARD LENGTH=645	581	645	0	111.0	70.9	79.7
Rsa1.0_00514.1.g15253.t1	ref|NP_566681.1| dentin sialophosphoprotein-like protein [Arabidopsis thaliana] gi|332642967|gb|AEE76488.1| dentin sialophosphoprotein-like protein [Arabidopsis thaliana]	1145	1192	0	104.1	75.4	82.6	dentin sialophosphoprotein-like protein	gbpln	Arabidopsis thaliana	AT3G21290.1 | Symbols: | dentin sialophosphoprotein-related | chr3:7482318-7488676 FORWARD LENGTH=1192	1145	1192	0	104.1	75.4	82.6
Rsa1.0_00515.1.g15254.t2	ref|NP_191470.1| protein kinase family protein [Arabidopsis thaliana] gi|7529754|emb|CAB86939.1| receptor-like protein kinase [Arabidopsis thaliana] gi|332646358|gb|AEE79879.1| protein kinase family protein [Arabidopsis thaliana]	482	512	0	106.2	84.9	90.0	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G59110.1 | Symbols: | Protein kinase superfamily protein | chr3:21855673-21857847 FORWARD LENGTH=512	482	512	0	106.2	84.9	90.0
Rsa1.0_00515.1.g15255.t16	ref|NP_195508.2| Rhamnogalacturonate lyase family protein [Arabidopsis thaliana] gi|28393444|gb|AAO42144.1| unknown protein [Arabidopsis thaliana] gi|110736900|dbj|BAF00407.1| hypothetical protein [Arabidopsis thaliana] gi|332661457|gb|AEE86857.1| Rhamnogalacturonate lyase family protein [Arabidopsis thaliana]	1613	678	0	42.0	24.6	27.1	Rhamnogalacturonate lyase family protein	gbpln	Arabidopsis thaliana	AT4G37950.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr4:17844792-17849156 FORWARD LENGTH=678	1613	678	0	42.0	24.6	27.1
Rsa1.0_00515.1.g15256.t1	ref|NP_191480.2| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|334186120|ref|NP_001190132.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|334186122|ref|NP_001190133.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|334186124|ref|NP_001190134.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75244355|sp|Q8GW80.1|FBL65_ARATH RecName: Full=F-box/LRR-repeat protein At3g59210 gi|26453044|dbj|BAC43598.1| unknown protein [Arabidopsis thaliana] gi|332646368|gb|AEE79889.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|332646369|gb|AEE79890.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|332646370|gb|AEE79891.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|332646371|gb|AEE79892.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	301	484	1.00E-138	160.8	82.4	87.7	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT3G59210.4 | Symbols: | F-box/RNI-like superfamily protein | chr3:21889942-21891553 FORWARD LENGTH=484	301	484	1.00E-141	160.8	82.4	87.7
Rsa1.0_00515.1.g15257.t1	gb|EOA23973.1| hypothetical protein CARUB_v10017193mg [Capsella rubella]	741	463	1.00E-158	62.5	38.7	46.3	hypothetical protein CARUB_v10017193mg	gbpln	Capsella rubella	AT3G59250.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21901726-21903284 REVERSE LENGTH=425	741	425	1.00E-156	57.4	39.1	46.0
Rsa1.0_00515.1.g15258.t1	gb|AAF80658.1|AC012190_14 Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872 [Arabidopsis thaliana]	887	904	1.00E-157	101.9	36.9	55.4	Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	887	719	2.00E-29	81.1	12.6	23.8
Rsa1.0_00515.1.g15259.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	912	871	2.00E-83	95.5	29.5	44.5	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	912	874	2.00E-25	95.8	7.7	11.6

Rsa1.0_00515.1.g15260.t1	ref|XP_002876494.1| hypothetical protein ARALYDRAFT_324401 [Arabidopsis lyrata subsp. lyrata] gi|297322332|gb|EFH52753.1| hypothetical protein ARALYDRAFT_324401 [Arabidopsis lyrata subsp. lyrata]	285	285	1.00E-131	100.0	79.6	89.1	hypothetical protein ARALYDRAFT_324401	gbpln	Arabidopsis lyrata	AT3G59260.1 | Symbols: | pirin, putative | chr3:21903839-21905188 FORWARD LENGTH=271	285	271	1.00E-119	95.1	71.2	80.7
Rsa1.0_00515.1.g15261.t1	gb|EOA26103.1| hypothetical protein CARUB_v10019525mg, partial [Capsella rubella]	374	383	1.00E-154	102.4	73.0	84.2	hypothetical protein CARUB_v10019525mg, partial	gbpln	Capsella rubella	AT3G59270.1 | Symbols: | FBD-like domain family protein | chr3:21906593-21907872 REVERSE LENGTH=335	374	335	1.00E-128	89.6	65.5	73.3
Rsa1.0_00515.1.g15262.t1	gb|EOA24964.1| hypothetical protein CARUB_v10018261mg [Capsella rubella]	101	116	6.00E-47	114.9	93.1	96.0	hypothetical protein CARUB_v10018261mg	gbpln	Capsella rubella	AT3G59280.1 | Symbols: TXR1 | Protein Transporter, Pam16 | chr3:21909266-21910519 REVERSE LENGTH=116	101	116	8.00E-47	114.9	87.1	94.1
Rsa1.0_00515.1.g15263.t1	gb|EOA26121.1| hypothetical protein CARUB_v10019547mg [Capsella rubella]	339	594	1.00E-140	175.2	79.9	87.9	hypothetical protein CARUB_v10019547mg	gbpln	Capsella rubella	AT3G59320.1 | Symbols: | Eukaryotic protein of unknown function (DUF914) | chr3:21924705-21926840 REVERSE LENGTH=339	339	339	1.00E-139	100.0	76.4	86.7
Rsa1.0_00515.1.g15264.t1	gb|EOA23981.1| hypothetical protein CARUB_v10017200mg [Capsella rubella]	408	460	0	112.7	90.2	93.4	hypothetical protein CARUB_v10017200mg	gbpln	Capsella rubella	AT3G59350.3 | Symbols: | Protein kinase superfamily protein | chr3:21932930-21934883 FORWARD LENGTH=408	408	408	0	100.0	89.2	93.1
Rsa1.0_00515.1.g15265.t1	ref|XP_002876501.1| hypothetical protein ARALYDRAFT_486406 [Arabidopsis lyrata subsp. lyrata] gi|297322339|gb|EFH52760.1| hypothetical protein ARALYDRAFT_486406 [Arabidopsis lyrata subsp. lyrata]	272	272	1.00E-136	100.0	89.7	94.9	hypothetical protein ARALYDRAFT_486406	gbpln	Arabidopsis lyrata	AT3G59390.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2054 (InterPro:IPR019352); Has 184 Blast hits to 184 proteins in 72 species: Archae - 0; Bacteria - 0; Metazoa - 116; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 25 (source: NCBI BLink). | chr3:21946160-21948166 FORWARD LENGTH=273	272	273	1.00E-133	100.4	87.9	94.1
Rsa1.0_00515.1.g15266.t3	gb|AFX68809.1| tetrapyrrole-binding protein [Brassica oleracea]	258	256	1.00E-107	99.2	84.5	88.8	tetrapyrrole-binding protein	gbpln	Brassica oleracea	AT3G59400.1 | Symbols: GUN4 | enzyme binding;tetrapyrrole binding | chr3:21948881-21949678 REVERSE LENGTH=265	258	265	2.00E-97	102.7	78.3	84.5
Rsa1.0_00515.1.g15267.t1	gb|AAM19705.1|AF499718_1 protein phosphatase 2c-like protein [Eutrema halophilum]	288	378	2.00E-20	131.3	20.8	25.3	protein phosphatase 2c-like protein	gbpln	Eutrema halophilum	AT2G02040.1 | Symbols: ATPTR2-B, NTR1, PTR2-B, PTR2, ATPTR2 | peptide transporter 2 | chr2:487542-489707 FORWARD LENGTH=585	288	585	4.00E-22	203.1	16.7	18.1
Rsa1.0_00515.1.g15268.t1	gb|EOA24726.1| hypothetical protein CARUB_v10018003mg, partial [Capsella rubella]	204	216	4.00E-94	105.9	83.3	89.2	hypothetical protein CARUB_v10018003mg, partial	gbpln	Capsella rubella	AT3G59440.1 | Symbols: | Calcium-binding EF-hand family protein | chr3:21970423-21971010 FORWARD LENGTH=195	204	195	2.00E-94	95.6	83.8	87.7
Rsa1.0_00515.1.g15269.t1	gb|EOA24572.1| hypothetical protein CARUB_v10017836mg [Capsella rubella]	397	269	1.00E-123	67.8	56.9	60.2	hypothetical protein CARUB_v10017836mg	gbpln	Capsella rubella	AT3G59470.2 | Symbols: | Far-red impaired responsive (FAR1) family protein | chr3:21979099-21980097 REVERSE LENGTH=251	397	251	1.00E-124	63.2	54.9	57.2
Rsa1.0_00515.1.g15270.t1	gb|AAM64445.1| fructokinase-like protein [Arabidopsis thaliana]	237	326	1.00E-115	137.6	89.0	92.0	fructokinase-like protein	gbpln	Arabidopsis thaliana	AT3G59480.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr3:21983103-21984440 FORWARD LENGTH=326	237	326	1.00E-117	137.6	89.0	91.6
Rsa1.0_00516.1.g15271.t1	ref|XP_002868672.1| hypothetical protein ARALYDRAFT_916251 [Arabidopsis lyrata subsp. lyrata] gi|297314508|gb|EFH44931.1| hypothetical protein ARALYDRAFT_916251 [Arabidopsis lyrata subsp. lyrata]	323	328	1.00E-155	101.5	84.5	90.7	hypothetical protein ARALYDRAFT_916251	gbpln	Arabidopsis lyrata	AT5G40150.1 | Symbols: | Peroxidase superfamily protein | chr5:16059750-16060736 REVERSE LENGTH=328	323	328	1.00E-156	101.5	83.3	89.2
Rsa1.0_00516.1.g15272.t1	ref|XP_002873025.1| hypothetical protein ARALYDRAFT_486965 [Arabidopsis lyrata subsp. lyrata] gi|297318862|gb|EFH49284.1| hypothetical protein ARALYDRAFT_486965 [Arabidopsis lyrata subsp. lyrata]	458	503	1.00E-140	109.8	60.0	74.9	hypothetical protein ARALYDRAFT_486965	gbpln	Arabidopsis lyrata	AT5G01150.1 | Symbols: | Protein of unknown function (DUF674) | chr5:51988-53649 FORWARD LENGTH=501	458	501	1.00E-142	109.4	59.2	74.7

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<tr><td>Rsa1.0_00516.1.g15273.t1</td><td>ref|NP_198832.1| ankyrin repeat domain-containing protein EMB506 [Arabidopsis thaliana] gi|75313777|sp|Q9SQK3.1|EM506_ARATH RecName: Full=Ankyrin repeat domain-containing protein EMB506, chloroplastic; AltName: Full=Protein EMBRYO DEFECTIVE 506; Flags: Precursor gi|5911312|gb|AAD55746.1|AF026167_1 ankyrin repeat protein EMB506 [Arabidopsis thaliana] gi|10177503|dbj|BAB10897.1| ankyrin repeat protein EMB506 [Arabidopsis thaliana] gi|17380824|gb|AAL36099.1| putative ankyrin repeat protein EMB506 [Arabidopsis thaliana] gi|21436371|gb|AAM51355.1| putative ankyrin repeat protein EMB506 [Arabidopsis thaliana] gi|332007132|gb|AED94515.1| ankyrin repeat domain-containing protein EMB506 [Arabidopsis thaliana]</td><td>324</td><td>315</td><td>1.00E-138</td><td>97.2</td><td>79.3</td><td>87.0</td><td>ankyrin repeat domain-containing protein EMB506</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G40160.1 | Symbols: EMB139, EMB506 | Ankyrin repeat family protein | chr5:16062726-16064301 REVERSE LENGTH=315</td><td>324</td><td>315</td><td>1.00E-141</td><td>97.2</td><td>79.3</td><td>87.0</td></tr>
<tr><td>Rsa1.0_00516.1.g15274.t1</td><td>ref|NP_001031402.1| serine carboxypeptidase-like 13 [Arabidopsis thaliana] gi|330252292|gb|AEC07386.1| serine carboxypeptidase-like 13 [Arabidopsis thaliana]</td><td>391</td><td>411</td><td>1.00E-174</td><td>105.1</td><td>75.7</td><td>85.4</td><td>serine carboxypeptidase-like 13</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G22980.2 | Symbols: SCPL13 | serine carboxypeptidase-like 13 | chr2:9779029-9782915 FORWARD LENGTH=411</td><td>391</td><td>411</td><td>1.00E-176</td><td>105.1</td><td>75.7</td><td>85.4</td></tr>
<tr><td>Rsa1.0_00516.1.g15275.t1</td><td>gb|EOA16285.1| hypothetical protein CARUB_v10004432mg [Capsella rubella]</td><td>580</td><td>590</td><td>0</td><td>101.7</td><td>92.6</td><td>95.3</td><td>hypothetical protein CARUB_v10004432mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G40200.1 | Symbols: DegP9 | DegP protease 9 | chr5:16070402-16073101 FORWARD LENGTH=592</td><td>580</td><td>592</td><td>0</td><td>102.1</td><td>91.6</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00516.1.g15276.t5</td><td>ref|XP_002868667.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297314503|gb|EFH44926.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>254</td><td>336</td><td>2.00E-54</td><td>132.3</td><td>42.9</td><td>44.5</td><td>nodulin MtN21 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G40210.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:16073725-16076088 REVERSE LENGTH=339</td><td>254</td><td>339</td><td>4.00E-56</td><td>133.5</td><td>42.1</td><td>44.1</td></tr>
<tr><td>Rsa1.0_00516.1.g15277.t1</td><td>gb|EOA19024.1| hypothetical protein CARUB_v10007676mg [Capsella rubella]</td><td>368</td><td>365</td><td>1.00E-159</td><td>99.2</td><td>76.1</td><td>87.5</td><td>hypothetical protein CARUB_v10007676mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G40230.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:16079814-16081735 REVERSE LENGTH=370</td><td>368</td><td>370</td><td>1.00E-158</td><td>100.5</td><td>75.8</td><td>87.0</td></tr>
<tr><td>Rsa1.0_00516.1.g15278.t2</td><td>ref|NP_195557.2| uncharacterized protein [Arabidopsis thaliana] gi|26449867|dbj|BAC42056.1| unknown protein [Arabidopsis thaliana] gi|28973069|gb|AAO63859.1| unknown protein [Arabidopsis thaliana] gi|332661529|gb|AEE86929.1| uncharacterized protein AT4G38440 [Arabidopsis thaliana]</td><td>1417</td><td>1465</td><td>0</td><td>103.4</td><td>67.6</td><td>75.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G38440.1 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: RNA polymerase II-associated protein 1, C-terminal (InterPro:IPR013929), RNA polymerase II-associated protein 1, N-terminal (InterPro:IPR013930); Has 276 Blast hits to 220 proteins in 102 species: Archae - 0; Bacteria - 2; Metazoa - 151; Fungi - 65; Plants - 41; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr4:17989115-17994549 FORWARD LENGTH=1465</td><td>1417</td><td>1465</td><td>0</td><td>103.4</td><td>67.6</td><td>75.3</td></tr>
<tr><td>Rsa1.0_00516.1.g15279.t1</td><td>ref|NP_198840.2| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75171374|sp|Q9FL08.1|WTR42_ARATH RecName: Full=WAT1-related protein At5g40240 gi|10177511|dbj|BAB10905.1| nodulin-like protein [Arabidopsis thaliana] gi|30725298|gb|AAP37671.1| At5g40240 [Arabidopsis thaliana] gi|110743630|dbj|BAE99652.1| hypothetical protein [Arabidopsis thaliana] gi|332007140|gb|AED94523.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]</td><td>403</td><td>368</td><td>1.00E-151</td><td>91.3</td><td>66.5</td><td>74.2</td><td>nodulin MtN21 /EamA-like transporter family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G40240.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:16082325-16084466 REVERSE LENGTH=368</td><td>403</td><td>368</td><td>1.00E-154</td><td>91.3</td><td>66.5</td><td>74.2</td></tr>
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Rsa1.0_00516.1.g15280.t1	ref|NP_198840.2| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75171374|sp|Q9FL08.1|WTR42_ARATH RecName: Full=WAT1-related protein At5g40240 gi|10177511|dbj|BAB10905.1| nodulin-like protein [Arabidopsis thaliana] gi|30725298|gb|AAP37671.1| At5g40240 [Arabidopsis thaliana] gi|110743630|dbj|BAE99652.1| hypothetical protein [Arabidopsis thaliana] gi|332007140|gb|AED94523.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]	293	368	2.00E-77	125.6	50.5	55.3	nodulin MtN21 /EamA-like transporter family protein	gbpln	Arabidopsis thaliana	AT5G40240.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:16082325-16084466 REVERSE LENGTH=368	293	368	5.00E-80	125.6	50.5	55.3
Rsa1.0_00516.1.g15281.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1344	1307	0	97.2	58.0	73.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1344	1262	3.00E-99	93.9	13.9	23.0
Rsa1.0_00516.1.g15282.t1	gb|EOA16864.1| hypothetical protein CARUB_v10005089mg [Capsella rubella]	94	368	5.00E-37	391.5	78.7	89.4	hypothetical protein CARUB_v10005089mg	gbpln	Capsella rubella	AT5G40240.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:16082325-16084466 REVERSE LENGTH=368	94	368	2.00E-38	391.5	76.6	88.3
Rsa1.0_00516.1.g15283.t1	ref|NP_177880.2| Winged helix-turn-helix transcription repressor DNA-binding protein [Arabidopsis thaliana] gi|51971819|dbj|BAD44574.1| putative DNA-binding protein [Arabidopsis thaliana] gi|332197872|gb|AEE35993.1| Winged helix-turn-helix transcription repressor DNA-binding protein [Arabidopsis thaliana]	143	147	2.00E-18	102.8	42.0	57.3	Winged helix-turn-helix transcription repressor DNA-binding protein	gbpln	Arabidopsis thaliana	AT1G77570.1 | Symbols: | Winged helix-turn-helix transcription repressor DNA-binding | chr1:29143350-29143793 FORWARD LENGTH=147	143	147	6.00E-21	102.8	42.0	57.3
Rsa1.0_00516.1.g15284.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1363	1459	0	107.0	60.2	73.8	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1363	1262	1.00E-112	92.6	14.2	21.6
Rsa1.0_00516.1.g15285.t1	ref|XP_002868698.1| hypothetical protein ARALYDRAFT_916318 [Arabidopsis lyrata subsp. lyrata] gi|297314534|gb|EFH44957.1| hypothetical protein ARALYDRAFT_916318 [Arabidopsis lyrata subsp. lyrata]	111	336	2.00E-14	302.7	53.2	64.0	hypothetical protein ARALYDRAFT_916318	gbpln	Arabidopsis lyrata	AT5G41200.1 | Symbols: AGL75 | AGAMOUS-like 75 | chr5:16490544-16491536 FORWARD LENGTH=330	111	330	2.00E-12	297.3	52.3	63.1
Rsa1.0_00516.1.g15286.t1	ref|XP_002868698.1| hypothetical protein ARALYDRAFT_916318 [Arabidopsis lyrata subsp. lyrata] gi|297314534|gb|EFH44957.1| hypothetical protein ARALYDRAFT_916318 [Arabidopsis lyrata subsp. lyrata]	290	336	3.00E-53	115.9	47.2	57.6	hypothetical protein ARALYDRAFT_916318	gbpln	Arabidopsis lyrata	AT5G41200.1 | Symbols: AGL75 | AGAMOUS-like 75 | chr5:16490544-16491536 FORWARD LENGTH=330	290	330	7.00E-52	113.8	46.2	56.2
Rsa1.0_00516.1.g15287.t1	gb|EOA19027.1| hypothetical protein CARUB_v10007680mg [Capsella rubella]	363	376	1.00E-165	103.6	86.0	92.3	hypothetical protein CARUB_v10007680mg	gbpln	Capsella rubella	AT5G40250.1 | Symbols: | RING/U-box superfamily protein | chr5:16086056-16087186 FORWARD LENGTH=376	363	376	1.00E-167	103.6	86.5	91.5
Rsa1.0_00517.1.g15288.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00517.1.g15289.t1	gb|EMS54598.1| Transposon Ty3-G Gag-Pol polyprotein [Triticum urartu]	180	1704	8.00E-16	946.7	21.1	28.9	Transposon Ty3-G Gag-Pol polyprotein	gbpln	Triticum urartu	#	#	#	#	#	#	#
Rsa1.0_00517.1.g15290.t1	gb|EOA25703.1| hypothetical protein CARUB_v10019056mg [Capsella rubella]	230	232	3.00E-87	100.9	85.7	90.9	hypothetical protein CARUB_v10019056mg	gbpln	Capsella rubella	AT3G50330.1 | Symbols: HEC2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:18657423-18658118 REVERSE LENGTH=231	230	231	2.00E-89	100.4	84.8	88.7
Rsa1.0_00517.1.g15291.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	302	341	2.00E-69	112.9	41.4	55.6	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00517.1.g15292.t5	gb|EOA24845.1| hypothetical protein CARUB_v10018135mg [Capsella rubella]	169	169	6.00E-81	100.0	88.8	92.9	hypothetical protein CARUB_v10018135mg	gbpln	Capsella rubella	AT3G50360.1 | Symbols: ATCEN2, CEN1, CEN2 | centrin2 | chr3:18674421-18675502 FORWARD LENGTH=169	169	169	3.00E-83	100.0	88.8	93.5
Rsa1.0_00517.1.g15293.t1	ref|XP_002877743.1| hypothetical protein ARALYDRAFT_485389 [Arabidopsis lyrata subsp. lyrata] gi|297323581|gb|EFH54002.1| hypothetical protein ARALYDRAFT_485389 [Arabidopsis lyrata subsp. lyrata]	114	117	1.00E-35	102.6	64.9	80.7	hypothetical protein ARALYDRAFT_485389	gbpln	Arabidopsis lyrata	AT5G51360.1 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr5:20871918-20872277 FORWARD LENGTH=119	114	119	8.00E-32	104.4	60.5	80.7
Rsa1.0_00517.1.g15294.t16	ref|XP_002877744.1| hypothetical protein ARALYDRAFT_485391 [Arabidopsis lyrata subsp. lyrata] gi|297323582|gb|EFH54003.1| hypothetical protein ARALYDRAFT_485391 [Arabidopsis lyrata subsp. lyrata]	3174	3074	0	96.8	80.6	87.7	hypothetical protein ARALYDRAFT_485391	gbpln	Arabidopsis lyrata	AT3G50380.1 | Symbols: | Protein of unknown function (DUF1162) | chr3:18686527-18700533 REVERSE LENGTH=3072	3174	3072	0	96.8	80.4	87.3

Rsa1.0_00517.1.g15295.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	260	530	4.00E-29	203.8	24.2	30.0	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00517.1.g15296.t1	ref|XP_002876029.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321867|gb|EFH52288.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	371	374	0	100.8	91.1	94.9	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT3G50400.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:18704797-18706437 FORWARD LENGTH=374	371	374	0	100.8	89.8	94.6
Rsa1.0_00517.1.g15297.t1	emb|CAB62472.1| hypothetical protein [Arabidopsis thaliana]	698	730	0	104.6	65.8	76.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G50430.1 | Symbols: | unknown protein; Has 54 Blast hits to 54 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 29; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:18713718-18716759 FORWARD LENGTH=642	698	642	0	92.0	61.2	70.2
Rsa1.0_00517.1.g15298.t1	ref|XP_004288064.1| PREDICTED: LOB domain-containing protein 36-like [Fragaria vesca subsp. vesca]	117	306	8.00E-23	261.5	44.4	59.0	PREDICTED: LOB domain-containing protein 36-like	gbpln	Fragaria vesca	AT5G66870.1 | Symbols: ASL1, LBD36 | ASYMMETRIC LEAVES 2-like 1 | chr5:26706621-26707562 FORWARD LENGTH=313	117	313	6.00E-24	267.5	41.0	56.4
Rsa1.0_00517.1.g15299.t1	ref|NP_190620.1| LOB domain-containing protein 28 [Arabidopsis thaliana] gi|29428036|sp|Q9SCS4.1|LBD28_ARATH RecName: Full=LOB domain-containing protein 28; AltName: Full=ASYMMETRIC LEAVES 2-like protein 25; Short=AS2-like protein 25 gi|6561991|emb|CAB62480.1| putative protein [Arabidopsis thaliana] gi|219807126|dbj|BAH10569.1| ASYMMETRIC LEAVES2-like 25 protein [Arabidopsis thaliana] gi|332645153|gb|AEE78674.1| LOB domain-containing protein 28 [Arabidopsis thaliana]	224	198	3.00E-36	88.4	42.4	57.1	LOB domain-containing protein 28	gbpln	Arabidopsis thaliana	AT3G50510.1 | Symbols: LBD28 | LOB domain-containing protein 28 | chr3:18745002-18745598 REVERSE LENGTH=198	224	198	8.00E-39	88.4	42.4	57.1
Rsa1.0_00517.1.g15300.t1	ref|NP_190621.1| phosphoglycerate mutase [Arabidopsis thaliana] gi|6561992|emb|CAB62481.1| putative protein [Arabidopsis thaliana] gi|14334856|gb|AAK59606.1| unknown protein [Arabidopsis thaliana] gi|17104695|gb|AAL34236.1| unknown protein [Arabidopsis thaliana] gi|332645154|gb|AEE78675.1| phosphoglycerate mutase [Arabidopsis thaliana]	229	230	1.00E-118	100.4	89.1	93.9	phosphoglycerate mutase	gbpln	Arabidopsis thaliana	AT3G50520.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:18748058-18749418 FORWARD LENGTH=230	229	230	1.00E-120	100.4	89.1	93.9
Rsa1.0_00517.1.g15301.t1	gb|ACA61613.1| hypothetical protein AP2_E11.1 [Arabidopsis lyrata subsp. petraea]	737	471	0	63.9	43.6	51.6	hypothetical protein AP2_E11.1	gbpln	Arabidopsis lyrata	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	737	1262	5.00E-98	171.2	25.4	38.9
Rsa1.0_00517.1.g15302.t1	ref|XP_002876036.1| hypothetical protein ARALYDRAFT_485401 [Arabidopsis lyrata subsp. lyrata] gi|297321874|gb|EFH52295.1| hypothetical protein ARALYDRAFT_485401 [Arabidopsis lyrata subsp. lyrata]	595	597	0	100.3	86.2	89.9	hypothetical protein ARALYDRAFT_485401	gbpln	Arabidopsis lyrata	AT3G50530.1 | Symbols: CRK | CDPK-related kinase | chr3:18753833-18756487 FORWARD LENGTH=601	595	601	0	101.0	86.1	89.9
Rsa1.0_00517.1.g15303.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00517.1.g15304.t2	gb|EOA24556.1| hypothetical protein CARUB_v10017814mg [Capsella rubella]	277	275	1.00E-132	99.3	88.1	91.3	hypothetical protein CARUB_v10017814mg	gbpln	Capsella rubella	AT3G50560.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:18761247-18763835 REVERSE LENGTH=272	277	272	1.00E-134	98.2	87.7	90.3
Rsa1.0_00518.1.g15305.t1	ref|NP_178819.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|3327395|gb|AAC26677.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana] gi|330251037|gb|AEC06131.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	284	530	1.00E-22	186.6	17.6	21.8	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	284	530	3.00E-25	186.6	17.6	21.8
Rsa1.0_00518.1.g15306.t1	ref|XP_002894457.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340299|gb|EFH70716.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	92	769	2.00E-14	835.9	44.6	56.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G53645.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:20026434-20028587 REVERSE LENGTH=523	92	523	3.00E-16	568.5	44.6	55.4

<table>
<tr><td>Rsa1.0_00518.1.g15307.t1</td><td>gb|EOA40131.1| hypothetical protein CARUB_v10008838mg [Capsella rubella]</td><td>562</td><td>525</td><td>1.00E-166</td><td>93.4</td><td>64.8</td><td>70.6</td><td>hypothetical protein CARUB_v10008838mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G53645.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:20026434-20028587 REVERSE LENGTH=523</td><td>562</td><td>523</td><td>1.00E-152</td><td>93.1</td><td>63.7</td><td>69.9</td></tr>
<tr><td>Rsa1.0_00518.1.g15308.t1</td><td>ref|NP_001031182.1| CTC-interacting domain 8 protein [Arabidopsis thaliana] gi|332194856|gb|AEE32977.1| CTC-interacting domain 8 protein [Arabidopsis thaliana]</td><td>309</td><td>308</td><td>1.00E-128</td><td>99.7</td><td>79.0</td><td>86.4</td><td>CTC-interacting domain 8 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G53650.2 | Symbols: CID8 | CTC-interacting domain 8 | chr1:20029262-20031243 REVERSE LENGTH=308</td><td>309</td><td>308</td><td>1.00E-131</td><td>99.7</td><td>79.0</td><td>86.4</td></tr>
<tr><td>Rsa1.0_00518.1.g15309.t1</td><td>ref|NP_564640.2| peptide methionine sulfoxide reductase B1 [Arabidopsis thaliana] gi|75169541|sp|Q9C8M2.1|MSRB1_ARATH RecName: Full=Peptide methionine sulfoxide reductase B1, chloroplastic; Short=AtMSRB1; AltName: Full=Peptide-methionine (R)-S-oxide reductase; Flags: Precursor gi|12324015|gb|AAG51964.1|AC024260_2 transcriptional regulator, putative; 35498-34111 [Arabidopsis thaliana] gi|332194858|gb|AEE32979.1| peptide methionine sulfoxide reductase B1 [Arabidopsis thaliana]</td><td>221</td><td>202</td><td>9.00E-86</td><td>91.4</td><td>76.0</td><td>83.7</td><td>peptide methionine sulfoxide reductase B1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G53670.1 | Symbols: MSRB1, ATMSRB1 | methionine sulfoxide reductase B 1 | chr1:20036687-20038074 FORWARD LENGTH=202</td><td>221</td><td>202</td><td>3.00E-88</td><td>91.4</td><td>76.0</td><td>83.7</td></tr>
<tr><td>Rsa1.0_00518.1.g15310.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1359</td><td>1307</td><td>0</td><td>96.2</td><td>59.0</td><td>73.5</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1359</td><td>1262</td><td>1.00E-103</td><td>92.9</td><td>14.6</td><td>22.7</td></tr>
<tr><td>Rsa1.0_00518.1.g15311.t1</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>961</td><td>1529</td><td>0</td><td>159.1</td><td>53.6</td><td>69.2</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>961</td><td>746</td><td>1.00E-121</td><td>77.6</td><td>20.9</td><td>27.2</td></tr>
<tr><td>Rsa1.0_00518.1.g15312.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00518.1.g15313.t1</td><td>ref|NP_197885.1| uncharacterized protein [Arabidopsis thaliana] gi|332006007|gb|AED93390.1| uncharacterized protein AT5G25030 [Arabidopsis thaliana]</td><td>204</td><td>193</td><td>1.00E-49</td><td>94.6</td><td>49.5</td><td>58.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G25030.1 | Symbols: | Domain of unknown function (DUF2431) | chr5:8620083-8620991 REVERSE LENGTH=193</td><td>204</td><td>193</td><td>5.00E-52</td><td>94.6</td><td>49.5</td><td>58.8</td></tr>
<tr><td>Rsa1.0_00518.1.g15314.t1</td><td>gb|EOA26640.1| hypothetical protein CARUB_v10022704mg [Capsella rubella]</td><td>81</td><td>745</td><td>7.00E-17</td><td>919.8</td><td>46.9</td><td>49.4</td><td>hypothetical protein CARUB_v10022704mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G27460.1 | Symbols: | sec23/sec24 transport family protein | chr2:11740670-11744867 FORWARD LENGTH=745</td><td>81</td><td>745</td><td>5.00E-19</td><td>919.8</td><td>45.7</td><td>49.4</td></tr>
<tr><td>Rsa1.0_00518.1.g15315.t1</td><td>gb|ABB20817.1| putative leucine-rich repeat transmembrane protein kinase [Isatis tinctoria] gi|95020537|gb|ABF50792.1| leucine-rich repeat transmembrane protein kinase [Isatis tinctoria]</td><td>732</td><td>719</td><td>0</td><td>98.2</td><td>87.4</td><td>91.7</td><td>putative leucine-rich repeat transmembrane protein kinase</td><td>gbpln</td><td>Isatis tinctoria</td><td>AT1G53730.1 | Symbols: SRF6 | STRUBBELIG-receptor family 6 | chr1:20061771-20065475 FORWARD LENGTH=719</td><td>732</td><td>719</td><td>0</td><td>98.2</td><td>84.4</td><td>90.0</td></tr>
<tr><td>Rsa1.0_00518.1.g15316.t1</td><td>ref|NP_175778.1| regulatory particle triple-A 1A [Arabidopsis thaliana] gi|297853156|ref|XP_002894459.1| regulatory particle triple-a 1A [Arabidopsis lyrata subsp. lyrata] gi|28558169|sp|Q9SSB5.1|PRS7A_ARATH RecName: Full=26S protease regulatory subunit 7 homolog A; AltName: Full=26S proteasome AAA-ATPase subunit RPT1a; AltName: Full=26S proteasome subunit 7 homolog A; AltName: Full=Regulatory particle triple-A ATPase subunit 1a gi|6056388|gb|AAF02852.1|AC009324_1 26S proteasome ATPase subunit [Arabidopsis thaliana] gi|12324021|gb|AAG51970.1|AC024260_8 26S proteasome ATPase subunit; 3861-6264 [Arabidopsis thaliana] gi|17065568|gb|AAL32938.1| 26S proteasome ATPase subunit [Arabidopsis thaliana] gi|23197722|gb|AAN15388.1| 26S proteasome ATPase subunit [Arabidopsis thaliana] gi|297340301|gb|EFH70718.1| regulatory particle triple-a 1A [Arabidopsis lyrata subsp. lyrata] gi|332194871|gb|AEE32992.1| regulatory particle triple-A 1A [Arabidopsis thaliana]</td><td>426</td><td>426</td><td>0</td><td>100.0</td><td>99.3</td><td>99.8</td><td>regulatory particle triple-A 1A</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G53750.1 | Symbols: RPT1A | regulatory particle triple-A 1A | chr1:20065921-20068324 REVERSE LENGTH=426</td><td>426</td><td>426</td><td>0</td><td>100.0</td><td>99.3</td><td>99.8</td></tr>
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Rsa1.0_00518.1.g15317.t1	ref|XP_002891519.1| hypothetical protein ARALYDRAFT_337099 [Arabidopsis lyrata subsp. lyrata] gi|297337361|gb|EFH67778.1| hypothetical protein ARALYDRAFT_337099 [Arabidopsis lyrata subsp. lyrata]	135	1163	1.00E-26	861.5	46.7	63.0	hypothetical protein ARALYDRAFT_337099	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00518.1.g15318.t1	ref|NP_175779.1| uncharacterized protein [Arabidopsis thaliana] gi|12324017|gb|AAG51966.1|AC024260_4 hypothetical protein; 1267-3026 [Arabidopsis thaliana] gi|62321744|dbj|BAD95368.1| hypothetical protein [Arabidopsis thaliana] gi|110739374|dbj|BAF01599.1| hypothetical protein [Arabidopsis thaliana] gi|110741179|dbj|BAF02140.1| hypothetical protein [Arabidopsis thaliana] gi|110741288|dbj|BAF02194.1| hypothetical protein [Arabidopsis thaliana] gi|332194872|gb|AEE32993.1| uncharacterized protein AT1G53760 [Arabidopsis thaliana]	266	272	1.00E-131	102.3	87.2	94.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G53760.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, plasma membrane, plastid, membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2343 (InterPro:IPR018786); Has 171 Blast hits to 171 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 127; Plants - 41; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr1:20069159-20070918 REVERSE LENGTH=272	266	272	1.00E-134	102.3	87.2	94.0
Rsa1.0_00518.1.g15319.t1	ref|NP_175780.1| peptide-O-fucosyltransferase [Arabidopsis thaliana] gi|63003828|gb|AAY25443.1| At1g53770 [Arabidopsis thaliana] gi|332194874|gb|AEE32995.1| peptide-O-fucosyltransferase [Arabidopsis thaliana]	549	563	0	102.6	79.6	88.0	peptide-O-fucosyltransferase	gbpln	Arabidopsis thaliana	AT1G53770.1 | Symbols: | O-fucosyltransferase family protein | chr1:20071460-20073708 REVERSE LENGTH=563	549	563	0	102.6	79.6	88.0
Rsa1.0_00518.1.g15320.t1	gb|EOA39987.1| hypothetical protein CARUB_v10008677mg [Capsella rubella]	769	583	0	75.8	56.8	63.1	hypothetical protein CARUB_v10008677mg	gbpln	Capsella rubella	AT1G53800.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53250.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:20081888-20084320 FORWARD LENGTH=572	769	572	0	74.4	55.4	61.5
Rsa1.0_00519.1.g15321.t2	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1763	1213	0	68.8	24.8	37.3	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1763	746	2.00E-53	42.3	7.4	11.2
Rsa1.0_00519.1.g15322.t1	gb|EOA39265.1| hypothetical protein CARUB_v10012271mg [Capsella rubella]	488	484	0	99.2	90.2	94.1	hypothetical protein CARUB_v10012271mg	gbpln	Capsella rubella	AT1G30270.1 | Symbols: CIPK23, SnRK3.23, ATCIPK23, LKS1 | CBL-interacting protein kinase 23 | chr1:10655270-10658524 FORWARD LENGTH=482	488	482	0	98.8	88.1	91.2
Rsa1.0_00519.1.g15323.t1	ref|XP_002893610.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297339452|gb|EFH69869.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	439	455	1.00E-167	103.6	80.2	87.2	heat shock protein binding protein	gbpln	Arabidopsis lyrata	AT1G30280.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:10662851-10664570 REVERSE LENGTH=455	439	455	1.00E-168	103.6	79.7	86.8
Rsa1.0_00519.1.g15324.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00519.1.g15325.t1	ref|NP_174320.2| PPR repeat domain-containing protein [Arabidopsis thaliana] gi|332193082|gb|AEE31203.1| PPR repeat domain-containing protein [Arabidopsis thaliana]	791	806	0	101.9	82.0	88.9	PPR repeat domain-containing protein	gbpln	Arabidopsis thaliana	AT1G30290.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:10670320-10672740 REVERSE LENGTH=806	791	806	0	101.9	82.0	88.9
Rsa1.0_00519.1.g15326.t1	gb|AAG50569.1|AC073506_11 hypothetical protein [Arabidopsis thaliana]	194	323	1.00E-103	166.5	92.3	95.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G30300.1 | Symbols: | Metallo-hydrolase/oxidoreductase superfamily protein | chr1:10673084-10675061 FORWARD LENGTH=324	194	324	1.00E-105	167.0	92.3	95.9
Rsa1.0_00519.1.g15327.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00519.1.g15328.t1	gb|EOA39268.1| hypothetical protein CARUB_v10012274mg [Capsella rubella]	73	516	1.00E-19	706.8	69.9	80.8	hypothetical protein CARUB_v10012274mg	gbpln	Capsella rubella	AT1G30320.1 | Symbols: | Remorin family protein | chr1:10680348-10682852 FORWARD LENGTH=509	73	509	8.00E-18	697.3	61.6	72.6
Rsa1.0_00519.1.g15329.t4	gb|EOA39268.1| hypothetical protein CARUB_v10012274mg [Capsella rubella]	355	516	1.00E-162	145.4	81.4	87.9	hypothetical protein CARUB_v10012274mg	gbpln	Capsella rubella	AT1G30320.1 | Symbols: | Remorin family protein | chr1:10680348-10682852 FORWARD LENGTH=509	355	509	1.00E-155	143.4	79.7	86.8
Rsa1.0_00519.1.g15330.t1	gb|AAD20434.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	356	507	2.00E-42	142.4	27.0	33.1	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00519.1.g15331.t1	ref|NP_001031115.1| auxin response factor 6 [Arabidopsis thaliana] gi|238054274|sp|Q9ZTX8.2|ARFF_ARATH RecName: Full=Auxin response factor 6 gi|49616351|gb|AAT67072.1| ARF6 [Arabidopsis thaliana] gi|332193086|gb|AEE31207.1| auxin response factor 6 [Arabidopsis thaliana]	901	935	0	103.8	93.3	95.1	auxin response factor 6	gbpln	Arabidopsis thaliana	AT1G30330.2 | Symbols: ARF6 | auxin response factor 6 | chr1:10686125-10690036 REVERSE LENGTH=935	901	935	0	103.8	93.3	95.1
Rsa1.0_00519.1.g15332.t1	ref|XP_002890867.1| hypothetical protein ARALYDRAFT_473263 [Arabidopsis lyrata subsp. lyrata] gi|297336709|gb|EFH67126.1| hypothetical protein ARALYDRAFT_473263 [Arabidopsis lyrata subsp. lyrata]	1623	1622	0	99.9	93.8	97.0	hypothetical protein ARALYDRAFT_473263	gbpln	Arabidopsis lyrata	AT1G30400.2 | Symbols: ATMRP1, EST1, ABCC1 | multidrug resistance-associated protein 1 | chr1:10728139-10737697 FORWARD LENGTH=1622	1623	1622	0	99.9	93.8	96.9
Rsa1.0_00519.1.g15333.t1	ref|XP_002890868.1| ATMRP13 [Arabidopsis lyrata subsp. lyrata] gi|297336710|gb|EFH67127.1| ATMRP13 [Arabidopsis lyrata subsp. lyrata]	1489	1495	0	100.4	85.4	92.7	ATMRP13	gbpln	Arabidopsis lyrata	AT1G30420.1 | Symbols: ATMRP12, MRP12, ABCC11 | multidrug resistance-associated protein 12 | chr1:10748816-10756316 FORWARD LENGTH=1495	1489	1495	0	100.4	83.8	91.5
Rsa1.0_00519.1.g15334.t1	gb|ABU90830.1| pollen-expressed protein MF10 [Brassica rapa subsp. oleifera]	288	434	5.00E-93	150.7	66.7	68.4	pollen-expressed protein MF10	gbpln	Brassica rapa	AT3G28980.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10993403-10994925 REVERSE LENGTH=445	288	445	1.00E-78	154.5	54.5	67.0
Rsa1.0_00520.1.g15335.t1	ref|NP_568551.1| aspartyl protease family protein [Arabidopsis thaliana] gi|10177438|dbj|BAB10671.1| unnamed protein product [Arabidopsis thaliana] gi|15809850|gb|AAL06853.1| AT5g37540/mpa22_p_70 [Arabidopsis thaliana] gi|20260182|gb|AAM12989.1| unknown protein [Arabidopsis thaliana] gi|23197748|gb|AAN15401.1| unknown protein [Arabidopsis thaliana] gi|332006821|gb|AED94204.1| aspartyl protease family protein [Arabidopsis thaliana]	438	442	0	100.9	84.9	90.0	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT5G37540.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:14912862-14914190 FORWARD LENGTH=442	438	442	0	100.9	84.9	90.0
Rsa1.0_00520.1.g15336.t1	ref|XP_002893831.1| phosphoribosylglycinamide formyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297339673|gb|EFH70090.1| phosphoribosylglycinamide formyltransferase [Arabidopsis lyrata subsp. lyrata]	65	292	1.00E-20	449.2	72.3	75.4	phosphoribosylglycinamide formyltransferase	gbpln	Arabidopsis lyrata	AT1G31220.1 | Symbols: | Formyl transferase | chr1:11157064-11158408 FORWARD LENGTH=292	65	292	1.00E-22	449.2	69.2	73.8
Rsa1.0_00520.1.g15337.t1	gb|EOA16522.1| hypothetical protein CARUB_v10004681mg [Capsella rubella]	458	488	0	106.6	90.8	95.2	hypothetical protein CARUB_v10004681mg	gbpln	Capsella rubella	AT5G37530.2 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:14906505-14909020 FORWARD LENGTH=456	458	456	0	99.6	90.0	94.3
Rsa1.0_00520.1.g15338.t1	ref|NP_851103.1| NADH-ubiquinone oxidoreductase subunit [Arabidopsis thaliana] gi|10177435|dbj|BAB10668.1| NADH-ubiquinone reductase 75kd subnit [Arabidopsis thaliana] gi|222423198|dbj|BAH19576.1| AT5G37510 [Arabidopsis thaliana] gi|332006816|gb|AED94199.1| NADH-ubiquinone oxidoreductase subunit [Arabidopsis thaliana]	747	745	0	99.7	95.6	97.9	NADH-ubiquinone oxidoreductase subunit	gbpln	Arabidopsis thaliana	AT5G37510.1 | Symbols: EMB1467, CI76 | NADH-ubiquinone dehydrogenase, mitochondrial, putative | chr5:14897490-14900352 FORWARD LENGTH=745	747	745	0	99.7	95.6	97.9
Rsa1.0_00520.1.g15339.t1	gb|AAD36942.1|AF069441_2 hypothetical protein [Arabidopsis thaliana] gi|7267196|emb|CAB77907.1| hypothetical protein [Arabidopsis thaliana]	846	963	4.00E-66	113.8	18.7	28.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	846	673	8.00E-30	79.6	9.9	16.1
Rsa1.0_00520.1.g15340.t1	gb|AAF80658.1|AC012190_14 Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872 [Arabidopsis thaliana]	815	904	1.00E-136	110.9	38.5	56.3	Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	815	719	4.00E-30	88.2	12.3	20.5
Rsa1.0_00520.1.g15341.t1	ref|XP_002868612.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314448|gb|EFH44871.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	183	326	2.00E-13	178.1	39.9	55.7	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#

Rsa1.0_00520.1.g15342.t1	ref|XP_002870538.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316374|gb|EFH46797.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	171	172	4.00E-57	100.6	71.9	84.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G37480.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:14884477-14885517 REVERSE LENGTH=156	171	156	3.00E-57	91.2	69.0	76.6
Rsa1.0_00520.1.g15343.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00520.1.g15344.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00520.1.g15345.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00520.1.g15346.t1	ref|NP_974857.5| TPX2 (targeting protein for Xklp2) family protein [Arabidopsis thaliana] gi|332006812|gb|AED94195.1| TPX2 (targeting protein for Xklp2) family protein [Arabidopsis thaliana]	144	178	1.00E-71	123.6	89.6	95.1	TPX2 (targeting protein for Xklp2) family protein	gbpln	Arabidopsis thaliana	AT5G37478.1 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr5:14881560-14883799 FORWARD LENGTH=178	144	178	3.00E-74	123.6	89.6	95.1
Rsa1.0_00520.1.g15347.t8	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1594	1225	1.00E-172	76.9	22.0	31.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1594	575	5.00E-33	36.1	4.3	6.1
Rsa1.0_00521.1.g15348.t1	emb|CAA57284.1| ACC oxidase [Brassica oleracea] gi|14148977|emb|CAC39108.1| ACC oxidase [Brassica rapa subsp. rapa]	320	320	0	100.0	98.4	99.4	ACC oxidase	gbpln	Brassica oleracea	AT1G62380.1 | Symbols: ACO2, ATACO2 | ACC oxidase 2 | chr1:23082340-23084068 FORWARD LENGTH=320	320	320	1.00E-177	100.0	91.9	96.3
Rsa1.0_00521.1.g15349.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00521.1.g15350.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00521.1.g15351.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00521.1.g15352.t1	ref|NP_178819.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|3327395|gb|AAC26677.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana] gi|330251037|gb|AEC06131.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	413	530	6.00E-13	128.3	9.9	14.8	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	413	530	2.00E-15	128.3	9.9	14.8
Rsa1.0_00521.1.g15353.t1	gb|ACG60687.1| transposon related predicted protein [Brassica oleracea var. alboglabra]	120	183	3.00E-17	152.5	35.0	36.7	transposon related predicted protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00521.1.g15354.t1	gb|ADD64787.1| SHOOT MERISTEMLESS [Brassica napus]	382	382	0	100.0	96.9	97.6	SHOOT MERISTEMLESS	gbpln	Brassica napus	AT1G62360.1 | Symbols: STM, BUM1, SHL, WAM1, BUM, WAM | KNOX/ELK homeobox transcription factor | chr1:23058796-23061722 REVERSE LENGTH=382	382	382	1.00E-158	100.0	89.5	92.4
Rsa1.0_00521.1.g15355.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00521.1.g15356.t1	gb|EOA33213.1| hypothetical protein CARUB_v10019899mg, partial [Capsella rubella]	671	682	0	101.6	88.8	91.8	hypothetical protein CARUB_v10019899mg, partial	gbpln	Capsella rubella	AT1G62330.1 | Symbols: | O-fucosyltransferase family protein | chr1:23046965-23050053 FORWARD LENGTH=652	671	652	0	97.2	89.1	91.8
Rsa1.0_00521.1.g15357.t2	dbj|BAA77394.1| SAE1-S9-protein [Brassica rapa]	550	255	1.00E-45	46.4	15.6	21.6	SAE1-S9-protein	gbpln	Brassica rapa	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	550	295	4.00E-44	53.6	14.2	19.6
Rsa1.0_00522.1.g15358.t1	ref|XP_002892653.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297338495|gb|EFH68912.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	316	503	1.00E-161	159.2	86.7	94.9	mate efflux family protein	gbpln	Arabidopsis lyrata	AT1G11670.1 | Symbols: | MATE efflux family protein | chr1:3928520-3931482 REVERSE LENGTH=503	316	503	1.00E-163	159.2	86.4	94.9
Rsa1.0_00522.1.g15359.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00522.1.g15360.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00522.1.g15361.t1	ref|XP_002889887.1| CYP51G1 [Arabidopsis lyrata subsp. lyrata] gi|297335729|gb|EFH66146.1| CYP51G1 [Arabidopsis lyrata subsp. lyrata]	491	488	0	99.4	92.1	95.9	CYP51G1	gbpln	Arabidopsis lyrata	AT1G11680.1 | Symbols: CYP51G1, EMB1738, CYP51A2, CYP51 | CYTOCHROME P450 51G1 | chr1:3938925-3940585 FORWARD LENGTH=488	491	488	0	99.4	91.2	96.1
Rsa1.0_00522.1.g15362.t1	ref|XP_002889888.1| hypothetical protein ARALYDRAFT_888481 [Arabidopsis lyrata subsp. lyrata] gi|297335730|gb|EFH66147.1| hypothetical protein ARALYDRAFT_888481 [Arabidopsis lyrata subsp. lyrata]	304	247	2.00E-87	81.3	57.6	66.8	hypothetical protein ARALYDRAFT_888481	gbpln	Arabidopsis lyrata	AT1G11690.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G20350.1); Has 5959 Blast hits to 4807 proteins in 476 species: Archae - 156; Bacteria - 436; Metazoa - 2789; Fungi - 309; Plants - 336; Viruses - 9; Other Eukaryotes - 1924 (source: NCBI BLink). | chr1:3941469-3942212 FORWARD LENGTH=247	304	247	2.00E-88	81.3	56.6	66.4
Rsa1.0_00522.1.g15363.t1	gb|EOA37371.1| hypothetical protein CARUB_v10011175mg [Capsella rubella]	1054	1093	0	103.7	88.7	93.9	hypothetical protein CARUB_v10011175mg	gbpln	Capsella rubella	AT1G11720.2 | Symbols: SS3 | starch synthase 3 | chr1:3951597-3956840 FORWARD LENGTH=1094	1054	1094	0	103.8	88.2	93.5

Rsa1.0_00522.1.g15364.t1	ref|XP_002892654.1| ankyrin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297338496|gb|EFH68913.1| ankyrin repeat family protein [Arabidopsis lyrata subsp. lyrata]	517	628	0	121.5	70.4	80.1	ankyrin repeat family protein	gbpln	Arabidopsis lyrata	AT1G11740.1 | Symbols: | ankyrin repeat family protein | chr1:3963317-3966824 REVERSE LENGTH=644	517	644	0	124.6	70.2	79.7
Rsa1.0_00522.1.g15365.t2	ref|XP_002889893.1| hypothetical protein ARALYDRAFT_471314 [Arabidopsis lyrata subsp. lyrata] gi|297335735|gb|EFH66152.1| hypothetical protein ARALYDRAFT_471314 [Arabidopsis lyrata subsp. lyrata]	288	271	1.00E-136	94.1	87.5	88.9	hypothetical protein ARALYDRAFT_471314	gbpln	Arabidopsis lyrata	AT1G11750.1 | Symbols: CLPP6, NCLPP1, NCLPP6 | CLP protease proteolytic subunit 6 | chr1:3967609-3969535 FORWARD LENGTH=271	288	271	1.00E-138	94.1	86.8	88.5
Rsa1.0_00522.1.g15366.t2	ref|XP_002892655.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338497|gb|EFH68914.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	238	414	6.00E-96	173.9	76.5	86.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G11755.1 | Symbols: LEW1 | Undecaprenyl pyrophosphate synthetase family protein | chr1:3969987-3971488 REVERSE LENGTH=254	238	254	3.00E-97	106.7	75.2	87.4
Rsa1.0_00522.1.g15367.t1	ref|NP_172641.2| uncharacterized protein [Arabidopsis thaliana] gi|75148615|sp|Q84VW5.1|MED32_ARATH RecName: Full=Mediator of RNA polymerase II transcription subunit 32; AltName: Full=Mediator of RNA polymerase II transcription subunit 2 gi|28466841|gb|AAO44029.1| At1g11760 [Arabidopsis thaliana] gi|110736112|dbj|BAF00028.1| hypothetical protein [Arabidopsis thaliana] gi|332190660|gb|AEE28781.1| mediator of RNA polymerase II transcription subunit 32 [Arabidopsis thaliana]	157	151	2.00E-64	96.2	85.4	86.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11760.1 | Symbols: MED32 | MED32; Has 41 Blast hits to 40 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:3972356-3972811 REVERSE LENGTH=151	157	151	5.00E-67	96.2	85.4	86.6
Rsa1.0_00522.1.g15368.t1	ref|XP_002889896.1| prephenate dehydratase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335738|gb|EFH66155.1| prephenate dehydratase family protein [Arabidopsis lyrata subsp. lyrata]	385	392	0	101.8	89.1	93.0	prephenate dehydratase family protein	gbpln	Arabidopsis lyrata	AT1G11790.1 | Symbols: ADT1 | arogenate dehydratase 1 | chr1:3981476-3984962 FORWARD LENGTH=392	385	392	0	101.8	88.8	92.5
Rsa1.0_00522.1.g15369.t1	ref|NP_001184967.1| O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana] gi|357529541|sp|O65399.3|E131_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 1; AltName: Full=(1-3)-beta-glucan endohydrolase 1; Short=(1-3)-beta-glucanase 1; AltName: Full=Beta-1,3-endoglucanase 1; Short=Beta-1,3-glucanase 1; Flags: Precursor gi|332190670|gb|AEE28791.1| O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana]	517	511	0	98.8	84.5	90.5	O-Glycosyl hydrolases family 17 protein	gbpln	Arabidopsis thaliana	AT1G11820.2 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr1:3991144-3993327 REVERSE LENGTH=511	517	511	0	98.8	84.5	90.5
Rsa1.0_00522.1.g15370.t3	gb|EOA40508.1| hypothetical protein CARUB_v10009236mg, partial [Capsella rubella]	409	423	0	103.4	96.1	98.5	hypothetical protein CARUB_v10009236mg, partial	gbpln	Capsella rubella	AT1G11860.3 | Symbols: | Glycine cleavage T-protein family | chr1:4001801-4003245 FORWARD LENGTH=408	409	408	0	99.8	95.6	98.0
Rsa1.0_00522.1.g15371.t1	ref|NP_200105.1| uncharacterized protein [Arabidopsis thaliana] gi|10177107|dbj|BAB10441.1| unnamed protein product [Arabidopsis thaliana] gi|60547939|gb|AAX23933.1| hypothetical protein At5g52930 [Arabidopsis thaliana] gi|71905609|gb|AAZ52782.1| expressed protein [Arabidopsis thaliana] gi|332008896|gb|AED96279.1| uncharacterized protein AT5G52930 [Arabidopsis thaliana]	348	359	4.00E-78	103.2	42.8	56.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G52930.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21470370-21471449 FORWARD LENGTH=359	348	359	9.00E-81	103.2	42.8	56.0
Rsa1.0_00522.1.g15372.t1	ref|NP_172652.2| phosphatidylinositol glycan, class V [Arabidopsis thaliana] gi|46931244|gb|AAT06426.1| At1g11880 [Arabidopsis thaliana] gi|50897228|gb|AAT85753.1| At1g11880 [Arabidopsis thaliana] gi|332190687|gb|AEE28808.1| transferases, transferring hexosyl groups [Arabidopsis thaliana]	478	489	0	102.3	78.7	87.0	phosphatidylinositol glycan, class V	gbpln	Arabidopsis thaliana	AT1G11880.1 | Symbols: | transferases, transferring hexosyl groups | chr1:4007909-4010327 REVERSE LENGTH=489	478	489	0	102.3	78.7	87.0
Rsa1.0_00522.1.g15373.t1	gb|EOA38494.1| hypothetical protein CARUB_v10010262mg [Capsella rubella]	301	218	1.00E-121	72.4	71.1	71.8	hypothetical protein CARUB_v10010262mg	gbpln	Capsella rubella	AT1G11890.1 | Symbols: SEC22, ATSEC22 | Synaptobrevin family protein | chr1:4011509-4012835 FORWARD LENGTH=218	301	218	1.00E-123	72.4	70.8	71.8

Rsa1.0_00522.1.g15374.t2	dbj|BAJ34217.1| unnamed protein product [Thellungiella halophila]	512	506	0	98.8	91.8	95.5	unnamed protein product	----	----	AT1G11910.1 | Symbols: APA1, ATAPA1 | aspartic proteinase A1 | chr1:4017119-4019874 REVERSE LENGTH=506	512	506	0	98.8	92.2	94.3
Rsa1.0_00522.1.g15375.t2	ref|XP_002889903.1| hypothetical protein ARALYDRAFT_471341 [Arabidopsis lyrata subsp. lyrata] gi|297335745|gb|EFH66162.1| hypothetical protein ARALYDRAFT_471341 [Arabidopsis lyrata subsp. lyrata]	330	329	1.00E-153	99.7	87.6	94.5	hypothetical protein ARALYDRAFT_471341	gbpln	Arabidopsis lyrata	AT1G11915.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G17350.1); Has 261 Blast hits to 261 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 261; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4021830-4023084 FORWARD LENGTH=329	330	329	1.00E-155	99.7	87.0	94.5
Rsa1.0_00522.1.g15376.t1	ref|NP_849649.1| putative pyridoxal phosphate-dependent enzyme, YBL036C type [Arabidopsis thaliana] gi|3157934|gb|AAC17617.1| Similar to hypothetical protein F09E5.8 gb|U37429 from C. elegans. ESTs gb|T42019 and gb|N97000 come from this gene [Arabidopsis thaliana] gi|332190697|gb|AEE28818.1| putative pyridoxal phosphate-dependent enzyme, YBL036C type [Arabidopsis thaliana]	265	255	1.00E-133	96.2	88.7	92.5	putative pyridoxal phosphate-dependent enzyme, YBL036C type	gbpln	Arabidopsis thaliana	AT1G11930.2 | Symbols: | Predicted pyridoxal phosphate-dependent enzyme, YBL036C type | chr1:4028783-4030298 FORWARD LENGTH=255	265	255	1.00E-135	96.2	88.7	92.5
Rsa1.0_00522.1.g15377.t3	ref|XP_002892665.1| hypothetical protein ARALYDRAFT_312224 [Arabidopsis lyrata subsp. lyrata] gi|297338507|gb|EFH68924.1| hypothetical protein ARALYDRAFT_312224 [Arabidopsis lyrata subsp. lyrata]	381	383	0	100.5	82.4	89.2	hypothetical protein ARALYDRAFT_312224	gbpln	Arabidopsis lyrata	AT1G11940.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:4031768-4033946 REVERSE LENGTH=383	381	383	0	100.5	81.1	89.2
Rsa1.0_00523.1.g15378.t2	ref|NP_194037.2| protein IQ-domain 22 [Arabidopsis thaliana] gi|56693675|gb|AAW22634.1| calmodulin binding protein IQD22 [Arabidopsis thaliana] gi|332659301|gb|AEE84701.1| protein IQ-domain 22 [Arabidopsis thaliana]	461	484	1.00E-174	105.0	74.4	83.5	protein IQ-domain 22	gbpln	Arabidopsis thaliana	AT4G23060.1 | Symbols: IQD22 | IQ-domain 22 | chr4:12087283-12090408 FORWARD LENGTH=484	461	484	1.00E-176	105.0	74.4	83.5
Rsa1.0_00523.1.g15379.t2	emb|CAK24967.1| gamma-glutamylcysteine synthetase [Brassica napus]	408	514	3.00E-82	126.0	40.7	43.1	gamma-glutamylcysteine synthetase	gbpln	Brassica napus	AT4G23100.3 | Symbols: GSH1 | glutamate-cysteine ligase | chr4:12103458-12106751 REVERSE LENGTH=522	408	522	3.00E-82	127.9	40.7	44.6
Rsa1.0_00523.1.g15380.t3	gb|EOA18852.1| hypothetical protein CARUB_v10007481mg [Capsella rubella]	622	653	0	105.0	74.4	84.6	hypothetical protein CARUB_v10007481mg	gbpln	Capsella rubella	AT4G23220.1 | Symbols: CRK14 | cysteine-rich RLK (RECEPTOR-like protein kinase) 14 | chr4:12154091-12157091 REVERSE LENGTH=728	622	728	0	117.0	61.6	75.9
Rsa1.0_00523.1.g15381.t2	gb|EOA16184.1| hypothetical protein CARUB_v10004325mg [Capsella rubella]	659	654	0	99.2	68.4	78.5	hypothetical protein CARUB_v10004325mg	gbpln	Capsella rubella	AT4G23180.1 | Symbols: CRK10, RLK4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 | chr4:12138171-12140780 FORWARD LENGTH=669	659	669	0	101.5	64.5	75.4
Rsa1.0_00523.1.g15382.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15383.t1	ref|XP_002867728.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313564|gb|EFH43987.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	660	671	0	101.7	78.5	85.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G23130.2 | Symbols: CRK5, RLK6 | cysteine-rich RLK (RECEPTOR-like protein kinase) 5 | chr4:12117688-12120134 REVERSE LENGTH=663	660	663	0	100.5	81.1	87.9
Rsa1.0_00523.1.g15384.t1	gb|AAC95354.1| receptor-like protein kinase [Arabidopsis thaliana]	649	684	0	105.4	72.6	81.7	receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT4G23250.1 | Symbols: EMB1290, DUF26-21, RKC1, CRK17 | kinases;protein kinases | chr4:12162004-12167026 REVERSE LENGTH=1035	649	1035	0	159.5	71.5	80.6
Rsa1.0_00523.1.g15385.t1	ref|XP_002867715.1| hypothetical protein ARALYDRAFT_492542 [Arabidopsis lyrata subsp. lyrata] gi|297313551|gb|EFH43974.1| hypothetical protein ARALYDRAFT_492542 [Arabidopsis lyrata subsp. lyrata]	677	659	0	97.3	72.5	81.7	hypothetical protein ARALYDRAFT_492542	gbpln	Arabidopsis lyrata	AT4G23260.1 | Symbols: CRK18 | cysteine-rich RLK (RECEPTOR-like protein kinase) 18 | chr4:12167528-12170055 REVERSE LENGTH=659	677	659	0	97.3	73.0	81.7
Rsa1.0_00523.1.g15386.t1	gb|ACC91270.1| short-chain dehydrogenase/reductase family protein [Capsella rubella] gi|482552824|gb|EOA17017.1| hypothetical protein CARUB_v10005252mg [Capsella rubella]	322	322	1.00E-163	100.0	86.3	93.2	short-chain dehydrogenase/reductase family protein	gbpln	Capsella rubella	AT4G23420.2 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:12226288-12228562 FORWARD LENGTH=316	322	316	1.00E-164	98.1	83.9	91.6

Rsa1.0_00523.1.g15387.t1	ref|XP_002867705.1| hypothetical protein ARALYDRAFT_492522 [Arabidopsis lyrata subsp. lyrata] gi|297313541|gb|EFH43964.1| hypothetical protein ARALYDRAFT_492522 [Arabidopsis lyrata subsp. lyrata]	86	86	1.00E-30	100.0	79.1	88.4	hypothetical protein ARALYDRAFT_492522	gbpln	Arabidopsis lyrata	AT4G23493.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12256327-12256693 REVERSE LENGTH=87	86	87	1.00E-31	101.2	77.9	88.4
Rsa1.0_00523.1.g15388.t1	ref|XP_002867704.1| hypothetical protein ARALYDRAFT_492521 [Arabidopsis lyrata subsp. lyrata] gi|297313540|gb|EFH43963.1| hypothetical protein ARALYDRAFT_492521 [Arabidopsis lyrata subsp. lyrata]	97	97	2.00E-25	100.0	70.1	76.3	hypothetical protein ARALYDRAFT_492521	gbpln	Arabidopsis lyrata	AT4G23496.1 | Symbols: SP1L5 | SPIRAL1-like5 | chr4:12257914-12258297 REVERSE LENGTH=99	97	99	3.00E-27	102.1	63.9	69.1
Rsa1.0_00523.1.g15389.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15390.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15391.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15392.t1	gb|ACC91282.1| unknown [Capsella rubella] gi|482552567|gb|EOA16760.1| hypothetical protein CARUB_v10004973mg [Capsella rubella]	371	398	1.00E-135	107.3	73.3	83.3	unknown	gbpln	Capsella rubella	AT4G23530.1 | Symbols: | Protein of unknown function (DUF793) | chr4:12279171-12280361 FORWARD LENGTH=396	371	396	1.00E-136	106.7	75.7	86.3
Rsa1.0_00523.1.g15393.t1	gb|AAF99785.1|AC012463_2 T2E6.4 [Arabidopsis thaliana]	149	740	2.00E-27	496.6	40.3	49.0	T2E6.4	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15394.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	383	536	2.00E-63	139.9	29.8	38.6	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	383	530	7.00E-36	138.4	17.5	21.7
Rsa1.0_00523.1.g15395.t1	gb|ACI14394.1| WRKY29-1 transcription factor [Brassica napus]	308	302	1.00E-157	98.1	89.9	93.2	WRKY29-1 transcription factor	gbpln	Brassica napus	AT4G23550.1 | Symbols: WRKY29, ATWRKY29 | WRKY family transcription factor | chr4:12291831-12293088 FORWARD LENGTH=304	308	304	1.00E-143	98.7	81.8	88.0
Rsa1.0_00523.1.g15396.t1	gb|AAD15372.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	135	469	2.00E-14	347.4	36.3	50.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15397.t1	ref|NP_194090.2| tyrosine transaminase-like protein [Arabidopsis thaliana] gi|75161515|sp|Q8VYP2.1|TAT4_ARATH RecName: Full=Probable aminotransferase TAT4; AltName: Full=Tyrosine aminotransferase 4 gi|17979319|gb|AAL49885.1| putative tyrosine transaminase [Arabidopsis thaliana] gi|21689827|gb|AAM67557.1| putative tyrosine transaminase [Arabidopsis thaliana] gi|332659380|gb|AEE84780.1| probable aminotransferase TAT4 [Arabidopsis thaliana]	409	424	0	103.7	82.4	90.5	tyrosine transaminase-like protein	gbpln	Arabidopsis thaliana	AT4G23590.1 | Symbols: | Tyrosine transaminase family protein | chr4:12307195-12309445 FORWARD LENGTH=424	409	424	0	103.7	82.4	90.5
Rsa1.0_00523.1.g15398.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15399.t1	dbj|BAJ34129.1| unnamed protein product [Thellungiella halophila]	438	423	0	96.6	72.8	83.3	unnamed protein product	----	----	AT4G23590.1 | Symbols: | Tyrosine transaminase family protein | chr4:12307195-12309445 FORWARD LENGTH=424	438	424	0	96.8	71.2	82.9
Rsa1.0_00523.1.g15400.t1	dbj|BAJ34129.1| unnamed protein product [Thellungiella halophila]	400	423	1.00E-174	105.8	75.5	86.0	unnamed protein product	----	----	AT4G23590.1 | Symbols: | Tyrosine transaminase family protein | chr4:12307195-12309445 FORWARD LENGTH=424	400	424	1.00E-172	106.0	73.8	84.0
Rsa1.0_00523.1.g15401.t1	dbj|BAJ34129.1| unnamed protein product [Thellungiella halophila]	434	423	0	97.5	75.1	85.5	unnamed protein product	----	----	AT4G23590.1 | Symbols: | Tyrosine transaminase family protein | chr4:12307195-12309445 FORWARD LENGTH=424	434	424	0	97.7	73.0	83.9
Rsa1.0_00523.1.g15402.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	219	1197	5.00E-18	546.6	23.7	29.2	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15403.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00523.1.g15404.t1	dbj|BAJ34129.1| unnamed protein product [Thellungiella halophila]	423	423	0	100.0	79.2	88.9	unnamed protein product	----	----	AT4G23590.1 | Symbols: | Tyrosine transaminase family protein | chr4:12307195-12309445 FORWARD LENGTH=424	423	424	0	100.2	76.1	87.5

Rsa1.0_00524.1.g15405.t1	ref|NP_193408.1| ethylene-responsive transcription factor ERF039 [Arabidopsis thaliana] gi|75337675|sp|Q9SUK8.1|ERF39_ARATH RecName: Full=Ethylene-responsive transcription factor ERF039 gi|5302798|emb|CAB46040.1| apetala2 domain TINY like protein [Arabidopsis thaliana] gi|7268425|emb|CAB78717.1| apetala2 domain TINY like protein [Arabidopsis thaliana] gi|44021914|gb|AAS46629.1| At4g16750 [Arabidopsis thaliana] gi|48479340|gb|AAT44941.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|58652080|gb|AAW80865.1| At4g16750 [Arabidopsis thaliana] gi|332658397|gb|AEE83797.1| ethylene-responsive transcription factor ERF039 [Arabidopsis thaliana]	181	179	1.00E-70	98.9	85.1	87.8	ethylene-responsive transcription factor ERF039	gbpln	Arabidopsis thaliana	AT4G16750.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:9421121-9421660 REVERSE LENGTH=179	181	179	4.00E-73	98.9	85.1	87.8
Rsa1.0_00524.1.g15406.t1	emb|CAB88075.1| hypothetical protein [Arabidopsis thaliana]	383	305	3.00E-87	79.6	39.2	43.1	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G16765.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:9429974-9431791 REVERSE LENGTH=247	383	247	1.00E-89	64.5	39.2	43.1
Rsa1.0_00524.1.g15407.t1	ref|NP_567515.1| lipase class 3 family protein [Arabidopsis thaliana] gi|374095438|sp|O23522.2|PLA14_ARATH RecName: Full=Phospholipase A1-Ibeta2, chloroplastic; Flags: Precursor gi|332658408|gb|AEE83808.1| phospholipase A1-Ibeta2 [Arabidopsis thaliana]	508	517	0	101.8	90.2	94.1	lipase class 3 family protein	gbpln	Arabidopsis thaliana	AT4G16820.1 | Symbols: PLA-I{beta]2 | alpha/beta-Hydrolases superfamily protein | chr4:9467563-9469116 FORWARD LENGTH=517	508	517	0	101.8	90.2	94.1
Rsa1.0_00524.1.g15408.t7	gb|ACP30552.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1461	1346	0	92.1	73.4	76.6	disease resistance protein	gbpln	Brassica rapa	AT5G51630.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:20970069-20974666 FORWARD LENGTH=1229	1461	1229	0	84.1	39.5	48.6
Rsa1.0_00524.1.g15409.t1	gb|EOA16302.1| hypothetical protein CARUB_v10004452mg [Capsella rubella]	581	580	0	99.8	91.4	94.5	hypothetical protein CARUB_v10004452mg	gbpln	Capsella rubella	AT5G04770.1 | Symbols: ATCAT6, CAT6 | cationic amino acid transporter 6 | chr5:1379118-1382304 FORWARD LENGTH=583	581	583	1.00E-156	100.3	50.1	67.8
Rsa1.0_00524.1.g15410.t1	ref|XP_002868125.1| hypothetical protein ARALYDRAFT_915089 [Arabidopsis lyrata subsp. lyrata] gi|297313961|gb|EFH44384.1| hypothetical protein ARALYDRAFT_915089 [Arabidopsis lyrata subsp. lyrata]	406	429	1.00E-154	105.7	66.5	80.3	hypothetical protein ARALYDRAFT_915089	gbpln	Arabidopsis lyrata	AT1G10270.1 | Symbols: GRP23 | glutamine-rich protein 23 | chr1:3363535-3366276 FORWARD LENGTH=913	406	913	1.00E-66	224.9	38.4	59.6
Rsa1.0_00524.1.g15411.t1	ref|XP_002868122.1| hypothetical protein ARALYDRAFT_915086 [Arabidopsis lyrata subsp. lyrata] gi|297804534|ref|XP_002870151.1| hypothetical protein ARALYDRAFT_915085 [Arabidopsis lyrata subsp. lyrata] gi|297313958|gb|EFH44381.1| hypothetical protein ARALYDRAFT_915086 [Arabidopsis lyrata subsp. lyrata] gi|297315987|gb|EFH46410.1| hypothetical protein ARALYDRAFT_915085 [Arabidopsis lyrata subsp. lyrata]	329	283	7.00E-46	86.0	32.8	46.8	hypothetical protein ARALYDRAFT_915086	gbpln	Arabidopsis lyrata	AT5G15300.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:4968384-4970030 REVERSE LENGTH=548	329	548	5.00E-11	166.6	11.9	19.5
Rsa1.0_00524.1.g15412.t3	ref|NP_192838.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|4539374|emb|CAB40068.1| putative protein [Arabidopsis thaliana] gi|7267798|emb|CAB81201.1| putative protein [Arabidopsis thaliana] gi|332657560|gb|AEE82960.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	354	406	3.00E-64	114.7	47.7	57.9	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G11000.1 | Symbols: | Ankyrin repeat family protein | chr4:6731020-6732464 FORWARD LENGTH=406	354	406	8.00E-67	114.7	47.7	57.9
Rsa1.0_00524.1.g15413.t1	ref|XP_002864196.1| hypothetical protein ARALYDRAFT_918330 [Arabidopsis lyrata subsp. lyrata] gi|297310031|gb|EFH40455.1| hypothetical protein ARALYDRAFT_918330 [Arabidopsis lyrata subsp. lyrata]	441	472	1.00E-179	107.0	69.4	83.0	hypothetical protein ARALYDRAFT_918330	gbpln	Arabidopsis lyrata	AT5G52820.1 | Symbols: | WD-40 repeat family protein / notchless protein, putative | chr5:21401423-21404203 FORWARD LENGTH=473	441	473	0	107.3	68.9	82.8

<table>
<tr><td>Rsa1.0_00524.1.g15414.t1</td><td>ref|XP_002870122.1| hypothetical protein ARALYDRAFT_329817 [Arabidopsis lyrata subsp. lyrata] gi|297315958|gb|EFH46381.1| hypothetical protein ARALYDRAFT_329817 [Arabidopsis lyrata subsp. lyrata]</td><td>58</td><td>57</td><td>4.00E-21</td><td>98.3</td><td>86.2</td><td>91.4</td><td>hypothetical protein ARALYDRAFT_329817</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G17085.1 | Symbols: | Putative membrane lipoprotein | chr4:9604527-9604804 FORWARD LENGTH=57</td><td>58</td><td>57</td><td>2.00E-23</td><td>98.3</td><td>86.2</td><td>89.7</td></tr>
<tr><td>Rsa1.0_00524.1.g15415.t1</td><td>gb|EOA18043.1| hypothetical protein CARUB_v10006488mg [Capsella rubella]</td><td>547</td><td>548</td><td>0</td><td>100.2</td><td>95.8</td><td>98.5</td><td>hypothetical protein CARUB_v10006488mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G17090.1 | Symbols: CT-BMY, BAM3, BMY8 | chloroplast beta-amylase | chr4:9605266-9607250 REVERSE LENGTH=548</td><td>547</td><td>548</td><td>0</td><td>100.2</td><td>95.1</td><td>97.8</td></tr>
<tr><td>Rsa1.0_00524.1.g15416.t1</td><td>ref|XP_002868084.1| hypothetical protein ARALYDRAFT_915009 [Arabidopsis lyrata subsp. lyrata] gi|297313920|gb|EFH44343.1| hypothetical protein ARALYDRAFT_915009 [Arabidopsis lyrata subsp. lyrata]</td><td>425</td><td>447</td><td>0</td><td>105.2</td><td>88.9</td><td>95.3</td><td>hypothetical protein ARALYDRAFT_915009</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G17100.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Endoribonuclease XendoU (InterPro:IPR018998); Has 943 Blast hits to 770 proteins in 162 species: Archae - 0; Bacteria - 61; Metazoa - 472; Fungi - 40; Plants - 78; Viruses - 35; Other Eukaryotes - 257 (source: NCBI BLink). | chr4:9610164-9612513 REVERSE LENGTH=434</td><td>425</td><td>434</td><td>0</td><td>102.1</td><td>88.2</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00524.1.g15417.t1</td><td>ref|NP_193450.1| RAB GTPase homolog B1C [Arabidopsis thaliana] gi|297800394|ref|XP_002868081.1| hypothetical protein ARALYDRAFT_493160 [Arabidopsis lyrata subsp. lyrata] gi|75279776|sp|P92963.1|RAB1C_ARATH RecName: Full=Ras-related protein RABB1c; Short=AtRABB1c; AltName: Full=Ras-related protein Rab2A; Short=AtRab2A gi|1765896|emb|CAA70498.1| Rab2-like protein [Arabidopsis thaliana] gi|5281023|emb|CAB45962.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|7268468|emb|CAB80988.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|27311815|gb|AAO00873.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] gi|30023652|gb|AAP13359.1| At4g17170 [Arabidopsis thaliana] gi|297313917|gb|EFH44340.1| hypothetical protein ARALYDRAFT_493160 [Arabidopsis lyrata subsp. lyrata] gi|332658457|gb|AEE83857.1| RAB GTPase homolog B1C [Arabidopsis thaliana] gi|482553233|gb|EOA17426.1| hypothetical protein CARUB_v10005730mg [Capsella rubella]</td><td>211</td><td>211</td><td>1.00E-119</td><td>100.0</td><td>97.6</td><td>99.1</td><td>RAB GTPase homolog B1C</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G17170.1 | Symbols: AT-RAB2, ATRABB1C, ATRAB2A, RAB2A, RABB1C, ATRAB-B1B, RAB-B1B | RAB GTPase homolog B1C | chr4:9644908-9646220 REVERSE LENGTH=211</td><td>211</td><td>211</td><td>1.00E-121</td><td>100.0</td><td>97.6</td><td>99.1</td></tr>
<tr><td>Rsa1.0_00524.1.g15418.t1</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>95</td><td>1529</td><td>9.00E-15</td><td>1609.5</td><td>36.8</td><td>53.7</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00524.1.g15419.t1</td><td>gb|ABD65130.1| hypothetical protein 40.t00005 [Brassica oleracea]</td><td>529</td><td>530</td><td>0</td><td>100.2</td><td>94.0</td><td>97.2</td><td>hypothetical protein 40.t00005</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17210.1 | Symbols: | Plant protein of unknown function (DUF827) | chr4:9652585-9654257 REVERSE LENGTH=527</td><td>529</td><td>527</td><td>0</td><td>99.6</td><td>77.1</td><td>87.3</td></tr>
<tr><td>Rsa1.0_00524.1.g15420.t1</td><td>gb|ABD65131.1| hypothetical protein 40.t00006 [Brassica oleracea]</td><td>151</td><td>148</td><td>2.00E-73</td><td>98.0</td><td>95.4</td><td>97.4</td><td>hypothetical protein 40.t00006</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17215.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr4:9655884-9656425 FORWARD LENGTH=150</td><td>151</td><td>150</td><td>2.00E-52</td><td>99.3</td><td>75.5</td><td>82.1</td></tr>
<tr><td>Rsa1.0_00524.1.g15421.t1</td><td>gb|ABD65109.1| Myosin II heavy chain-like domain containing protein [Brassica oleracea]</td><td>489</td><td>508</td><td>0</td><td>103.9</td><td>89.2</td><td>93.3</td><td>Myosin II heavy chain-like domain containing protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17220.1 | Symbols: ATMAP70-5, MAP70-5 | microtubule-associated proteins 70-5 | chr4:9657008-9659405 REVERSE LENGTH=513</td><td>489</td><td>513</td><td>0</td><td>104.9</td><td>87.7</td><td>93.7</td></tr>
<tr><td>Rsa1.0_00524.1.g15422.t1</td><td>gb|ABD65133.1| hypothetical protein 40.t00008 [Brassica oleracea]</td><td>733</td><td>742</td><td>0</td><td>101.2</td><td>85.3</td><td>89.5</td><td>hypothetical protein 40.t00008</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G47580.1); Has 31 Blast hits to 31 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:9671104-9673329 FORWARD LENGTH=741</td><td>733</td><td>741</td><td>0</td><td>101.1</td><td>80.2</td><td>87.3</td></tr>
<tr><td>Rsa1.0_00524.1.g15423.t1</td><td>gb|ABD65134.1| L-lactate dehydrogenase, putative [Brassica oleracea]</td><td>350</td><td>350</td><td>0</td><td>100.0</td><td>97.1</td><td>98.9</td><td>L-lactate dehydrogenase, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G17260.1 | Symbols: | Lactate/malate dehydrogenase family protein | chr4:9674057-9675309 FORWARD LENGTH=353</td><td>350</td><td>353</td><td>0</td><td>100.9</td><td>93.4</td><td>96.3</td></tr>
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Rsa1.0_00524.1.g15424.t1	ref|NP_193460.1| putative MO25-like protein [Arabidopsis thaliana] gi|15214078|sp|Q9M0M4.1|MO25M_ARATH RecName: Full=Putative MO25-like protein At4g17270 gi|14190519|gb|AAK55740.1|AF380659_1 AT4g17270/dl4670w [Arabidopsis thaliana] gi|7268479|emb|CAB78730.1| putative protein [Arabidopsis thaliana] gi|15810067|gb|AAL06959.1| AT4g17270/dl4670w [Arabidopsis thaliana] gi|332658472|gb|AEE83872.1| putative MO25-like protein [Arabidopsis thaliana]	339	343	1.00E-180	101.2	91.4	96.2	putative MO25-like protein	gbpln	Arabidopsis thaliana	AT4G17270.1 | Symbols: | Mo25 family protein | chr4:9676406-9678568 FORWARD LENGTH=343	339	343	0	101.2	91.4	96.2
Rsa1.0_00524.1.g15425.t2	gb|ABD65136.1| oxidoreductase family protein [Brassica oleracea]	367	397	0	108.2	94.3	97.3	oxidoreductase family protein	gbpln	Brassica oleracea	AT4G17370.1 | Symbols: | Oxidoreductase family protein | chr4:9706188-9708142 FORWARD LENGTH=368	367	368	0	100.3	88.8	93.2
Rsa1.0_00524.1.g15426.t1	ref|NP_193405.1| 60S ribosomal protein L15-1 [Arabidopsis thaliana] gi|297800374|ref|XP_002868071.1| 60S ribosomal protein L15 [Arabidopsis lyrata subsp. lyrata] gi|3122673|sp|O23515.1|RL151_ARATH RecName: Full=60S ribosomal protein L15-1 gi|13878179|gb|AAK44167.1|AF370352_1 putative ribosomal protein [Arabidopsis thaliana] gi|2245027|emb|CAB10447.1| ribosomal protein [Arabidopsis thaliana] gi|7268422|emb|CAB78714.1| ribosomal protein [Arabidopsis thaliana] gi|16604446|gb|AAL24229.1| AT4g16720/dl4385c [Arabidopsis thaliana] gi|19715591|gb|AAL91619.1| AT4g16720/dl4385c [Arabidopsis thaliana] gi|21592436|gb|AAM64387.1| ribosomal protein [Arabidopsis thaliana] gi|22136774|gb|AAM91731.1| putative ribosomal protein [Arabidopsis thaliana] gi|23505795|gb|AAN28757.1| At4g16720/dl4385c [Arabidopsis thaliana] gi|297313907|gb|EFH44330.1| 60S ribosomal protein L15 [Arabidopsis lyrata subsp. lyrata] gi|332658391|gb|AEE83791.1| 60S ribosomal protein L15-1 [Arabidopsis thaliana]	204	204	1.00E-113	100.0	99.5	100.0	60S ribosomal protein L15-1	gbpln	Arabidopsis lyrata	AT4G16720.1 | Symbols: | Ribosomal protein L23/L15e family protein | chr4:9400156-9401315 REVERSE LENGTH=204	204	204	1.00E-115	100.0	99.5	100.0
Rsa1.0_00524.1.g15427.t1	gb|ABD65094.1| myb family transcription factor [Brassica oleracea]	172	359	7.00E-76	208.7	87.2	91.3	myb family transcription factor	gbpln	Brassica oleracea	AT5G47390.1 | Symbols: | myb-like transcription factor family protein | chr5:19227001-19228546 FORWARD LENGTH=365	172	365	3.00E-46	212.2	65.1	77.9
Rsa1.0_00524.1.g15428.t1	gb|ABD65094.1| myb family transcription factor [Brassica oleracea]	340	359	1.00E-158	105.6	85.6	90.6	myb family transcription factor	gbpln	Brassica oleracea	AT5G47390.1 | Symbols: | myb-like transcription factor family protein | chr5:19227001-19228546 FORWARD LENGTH=365	340	365	1.00E-126	107.4	71.5	80.6
Rsa1.0_00525.1.g15429.t1	ref|XP_002887812.1| zinc-finger protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297333653|gb|EFH64071.1| zinc-finger protein 1 [Arabidopsis lyrata subsp. lyrata]	209	220	2.00E-81	105.3	80.9	88.5	zinc-finger protein 1	gbpln	Arabidopsis lyrata	AT1G80730.1 | Symbols: ZFP1, ATZFP1 | zinc-finger protein 1 | chr1:30339493-30340179 REVERSE LENGTH=228	209	228	3.00E-82	109.1	80.9	88.0
Rsa1.0_00525.1.g15430.t1	ref|XP_002889277.1| hypothetical protein ARALYDRAFT_340150 [Arabidopsis lyrata subsp. lyrata] gi|297335118|gb|EFH65536.1| hypothetical protein ARALYDRAFT_340150 [Arabidopsis lyrata subsp. lyrata]	244	242	1.00E-117	99.2	84.4	91.4	hypothetical protein ARALYDRAFT_340150	gbpln	Arabidopsis lyrata	AT1G80720.1 | Symbols: | Mitochondrial glycoprotein family protein | chr1:30336289-30337347 FORWARD LENGTH=190	244	190	2.00E-94	77.9	65.2	72.1
Rsa1.0_00525.1.g15431.t1	ref|XP_002887814.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297333655|gb|EFH64073.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	973	520	1.00E-171	53.4	33.6	39.3	transducin family protein	gbpln	Arabidopsis lyrata	AT1G80710.1 | Symbols: DRS1 | DROUGHT SENSITIVE 1 | chr1:30333499-30335796 REVERSE LENGTH=516	973	516	1.00E-169	53.0	33.1	38.5

Rsa1.0_00525.1.g15432.t1	ref|XP_002889278.1| hypothetical protein ARALYDRAFT_477177 [Arabidopsis lyrata subsp. lyrata] gi|297335119|gb|EFH65537.1| hypothetical protein ARALYDRAFT_477177 [Arabidopsis lyrata subsp. lyrata]	222	217	2.00E-80	97.7	79.3	84.7	hypothetical protein ARALYDRAFT_477177	gbpln	Arabidopsis lyrata	AT1G80980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80700.1); Has 477 Blast hits to 341 proteins in 85 species: Archae - 2; Bacteria - 44; Metazoa - 78; Fungi - 37; Plants - 42; Viruses - 0; Other Eukaryotes - 274 (source: NCBI BLink). | chr1:30422184-30423440 REVERSE LENGTH=214	222	214	3.00E-79	96.4	76.6	83.3
Rsa1.0_00525.1.g15433.t1	gb|EOA35675.1| hypothetical protein CARUB_v10020909mg [Capsella rubella]	234	224	1.00E-107	95.7	86.8	91.5	hypothetical protein CARUB_v10020909mg	gbpln	Capsella rubella	AT1G80690.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr1:30329283-30330524 REVERSE LENGTH=227	234	227	1.00E-104	97.0	88.0	92.7
Rsa1.0_00525.1.g15434.t1	gb|AAF79835.1|AC026875_15 T6D22.19 [Arabidopsis thaliana]	370	745	1.00E-104	201.4	48.1	65.4	T6D22.19	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	370	696	1.00E-40	188.1	25.1	39.5
Rsa1.0_00525.1.g15435.t2	gb|EOA31083.1| hypothetical protein CARUB_v10014234mg, partial [Capsella rubella]	356	309	3.00E-25	86.8	26.4	43.8	hypothetical protein CARUB_v10014234mg, partial	gbpln	Capsella rubella	AT3G01280.1 | Symbols: VDAC1, ATVDAC1 | voltage dependent anion channel 1 | chr3:85754-87612 FORWARD LENGTH=276	356	276	1.00E-26	77.5	24.2	41.6
Rsa1.0_00525.1.g15436.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00525.1.g15437.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00525.1.g15438.t1	ref|NP_178182.1| Rae1-like protein [Arabidopsis thaliana] gi|83305440|sp|Q38942.2|RAE1L_ARATH RecName: Full=Rae1-like protein At1g80670 gi|6503279|gb|AAF14655.1|AC011713_3 F23A5.2(form2) [Arabidopsis thaliana] gi|21593271|gb|AAM65220.1| mRNA export protein, putative [Arabidopsis thaliana] gi|94442413|gb|ABF18994.1| At1g80670 [Arabidopsis thaliana] gi|332198314|gb|AEE36435.1| Rae1-like protein [Arabidopsis thaliana]	345	349	0	101.2	93.6	97.7	Rae1-like protein	gbpln	Arabidopsis thaliana	AT1G80670.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:30320809-30323543 REVERSE LENGTH=349	345	349	0	101.2	93.6	97.7
Rsa1.0_00525.1.g15439.t1	gb|EOA33270.1| hypothetical protein CARUB_v10022427mg [Capsella rubella]	937	955	0	101.9	96.9	98.8	hypothetical protein CARUB_v10022427mg	gbpln	Capsella rubella	AT1G80660.1 | Symbols: AHA9, HA9 | H(+)-ATPase 9 | chr1:30316227-30319948 REVERSE LENGTH=954	937	954	0	101.8	95.9	98.4
Rsa1.0_00525.1.g15440.t1	ref|XP_002889280.1| hypothetical protein ARALYDRAFT_316895 [Arabidopsis lyrata subsp. lyrata] gi|297335121|gb|EFH65539.1| hypothetical protein ARALYDRAFT_316895 [Arabidopsis lyrata subsp. lyrata]	132	190	9.00E-32	143.9	58.3	64.4	hypothetical protein ARALYDRAFT_316895	gbpln	Arabidopsis lyrata	AT1G80650.1 | Symbols: RTL1 | RNAse THREE-like protein 1 | chr1:30314609-30315600 FORWARD LENGTH=198	132	198	9.00E-32	150.0	55.3	62.1
Rsa1.0_00525.1.g15441.t1	gb|EOA35187.1| hypothetical protein CARUB_v10020332mg [Capsella rubella]	419	428	0	102.1	82.1	88.1	hypothetical protein CARUB_v10020332mg	gbpln	Capsella rubella	AT1G80640.1 | Symbols: | Protein kinase superfamily protein | chr1:30311979-30314238 FORWARD LENGTH=427	419	427	0	101.9	81.9	89.0
Rsa1.0_00525.1.g15442.t1	ref|XP_002887817.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297333658|gb|EFH64076.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	559	577	0	103.2	70.8	81.6	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G80630.1 | Symbols: | RNI-like superfamily protein | chr1:30308879-30310615 REVERSE LENGTH=578	559	578	0	103.4	69.1	80.7
Rsa1.0_00525.1.g15443.t1	gb|EOA35169.1| hypothetical protein CARUB_v10020315mg [Capsella rubella]	403	435	1.00E-145	107.9	74.4	81.9	hypothetical protein CARUB_v10020315mg	gbpln	Capsella rubella	AT1G80620.1 | Symbols: | S15/NS1, RNA-binding protein | chr1:30305404-30307182 FORWARD LENGTH=414	403	414	2.33E-156	102.7	73.0	81.9
Rsa1.0_00525.1.g15444.t1	gb|EOA35732.1| hypothetical protein CARUB_v10020966mg [Capsella rubella]	197	203	2.00E-75	103.0	79.2	86.3	hypothetical protein CARUB_v10020966mg	gbpln	Capsella rubella	AT1G80610.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15800.1); Has 73 Blast hits to 69 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 2; Plants - 55; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink). | chr1:30301204-30303960 REVERSE LENGTH=211	197	211	3.00E-73	107.1	77.7	86.8
Rsa1.0_00525.1.g15445.t1	sp|P29102.1|LEU3_BRANA RecName: Full=3-isopropylmalate dehydrogenase, chloroplastic; Short=3-IPM-DH; Short=IMDH; AltName: Full=Beta-IPM dehydrogenase; Flags: Precursor gi|17827|emb|CAA42596.1| 3-isopropylmalate dehydrogenase [Brassica napus]	401	406	0	101.2	91.0	93.8	RecName: Full=3-isopropylmalate dehydrogenase, chloroplastic; Short=3-IPM-DH; Short=IMDH; AltName: Full=Beta-IPM dehydrogenase; Flags: Precursor gi|17827|emb|CAA42596.1| 3-isopropylmalate dehydrogenase	gbpln	Brassica napus	AT1G80560.1 | Symbols: ATIMD2, IMD2 | isopropylmalate dehydrogenase 2 | chr1:30287833-30290126 FORWARD LENGTH=405	401	405	0	101.0	88.5	91.8

Rsa1.0_00525.1.g15446.t1	gb|EOA35156.1| hypothetical protein CARUB_v10020295mg [Capsella rubella]	448	447	0	99.8	82.1	91.1	hypothetical protein CARUB_v10020295mg	gbpln	Capsella rubella	AT1G80550.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:30285358−30286704 REVERSE LENGTH=448	448	448	0	100.0	81.3	90.8
Rsa1.0_00525.1.g15447.t3	gb|EOA35018.1| hypothetical protein CARUB_v10020121mg [Capsella rubella]	655	535	0	81.7	52.8	55.6	hypothetical protein CARUB_v10020121mg	gbpln	Capsella rubella	AT1G80540.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G12400.1); Has 175 Blast hits to 171 proteins in 20 species: Archae − 0; Bacteria − 0; Metazoa − 2; Fungi − 0; Plants − 171; Viruses − 0; Other Eukaryotes − 2 (source: NCBI BLink). | chr1:30281638−30284258 REVERSE LENGTH=538	655	538	0	82.1	51.8	55.0
Rsa1.0_00525.1.g15448.t1	ref|XP_002887824.1| hypothetical protein ARALYDRAFT_895939 [Arabidopsis lyrata subsp. lyrata] gi|297333665|gb|EFH64083.1| hypothetical protein ARALYDRAFT_895939 [Arabidopsis lyrata subsp. lyrata]	559	563	0	100.7	81.4	92.3	hypothetical protein ARALYDRAFT_895939	gbpln	Arabidopsis lyrata	AT1G80530.1 | Symbols: | Major facilitator superfamily protein | chr1:30278224−30280247 REVERSE LENGTH=561	559	561	0	100.4	80.5	91.4
Rsa1.0_00525.1.g15449.t1	gb|EOA36532.1| hypothetical protein CARUB_v10011581mg [Capsella rubella]	419	425	1.00E−100	101.4	54.2	67.5	hypothetical protein CARUB_v10011581mg	gbpln	Capsella rubella	AT1G25150.1 | Symbols: | F−box family protein | chr1:8821027−8822328 FORWARD LENGTH=433	419	433	1.00E−101	103.3	52.5	65.4
Rsa1.0_00525.1.g15450.t1	ref|NP_178167.1| Sterile alpha motif (SAM) domain−containing protein [Arabidopsis thaliana] gi|6730731|gb|AAF27121.1|AC018849_9 hypothetical protein; 42149−41571 [Arabidopsis thaliana] gi|332198294|gb|AEE36415.1| Sterile alpha motif (SAM) domain−containing protein [Arabidopsis thaliana]	183	192	1.00E−60	104.9	74.9	82.0	Sterile alpha motif (SAM) domain−containing protein	gbpln	Arabidopsis thaliana	AT1G80520.1 | Symbols: | Sterile alpha motif (SAM) domain−containing protein | chr1:30276481−30277059 FORWARD LENGTH=192	183	192	5.00E−63	104.9	74.9	82.0
Rsa1.0_00526.1.g15451.t1	gb|EOA12787.1| hypothetical protein CARUB_v10025731mg [Capsella rubella]	184	2732	4.00E−69	1484.8	77.2	84.8	hypothetical protein CARUB_v10025731mg	gbpln	Capsella rubella	AT4G36150.1 | Symbols: | Disease resistance protein (TIR−NBS−LRR class) family | chr4:17104776−17108711 FORWARD LENGTH=1179	184	1179	2.00E−43	640.8	53.8	70.1
Rsa1.0_00526.1.g15452.t1	ref|XP_002891891.1| hypothetical protein ARALYDRAFT_337726 [Arabidopsis lyrata subsp. lyrata] gi|297337733|gb|EFH68150.1| hypothetical protein ARALYDRAFT_337726 [Arabidopsis lyrata subsp. lyrata]	183	183	1.00E−63	100.0	72.7	82.0	hypothetical protein ARALYDRAFT_337726	gbpln	Arabidopsis lyrata	AT1G54400.1 | Symbols: | HSP20−like chaperones superfamily protein | chr1:20307667−20308768 FORWARD LENGTH=183	183	183	1.00E−61	100.0	71.0	80.9
Rsa1.0_00526.1.g15453.t1	ref|NP_199342.2| RING/U−box domain−containing protein [Arabidopsis thaliana] gi|58652066|gb|AAW80858.1| At5g45290 [Arabidopsis thaliana] gi|58652090|gb|AAW80870.1| At5g45290 [Arabidopsis thaliana] gi|332007844|gb|AED95227.1| RING/U−box domain−containing protein [Arabidopsis thaliana]	509	545	0	107.1	79.6	86.4	RING/U−box domain−containing protein	gbpln	Arabidopsis thaliana	AT5G45290.1 | Symbols: | RING/U−box superfamily protein | chr5:18350011−18352092 REVERSE LENGTH=545	509	545	0	107.1	79.6	86.4
Rsa1.0_00526.1.g15454.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	129	871	3.00E−33	675.2	57.4	71.3	Ulp1 protease family protein	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097−11122412 FORWARD LENGTH=673	129	673	3.00E−17	521.7	36.4	55.8
Rsa1.0_00526.1.g15455.t1	gb|EOA14484.1| hypothetical protein CARUB_v10027699mg [Capsella rubella]	276	198	2.00E−75	71.7	49.3	55.1	hypothetical protein CARUB_v10027699mg	gbpln	Capsella rubella	AT5G45320.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: inflorescence meristem, root, flower; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Late embryogenesis abundant protein, group 2 (InterPro:IPR004864); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G26350.1); Has 253 Blast hits to 253 proteins in 16 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 253; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr5:18362354−18363053 REVERSE LENGTH=198	276	198	3.00E−71	71.7	45.3	51.1
Rsa1.0_00526.1.g15456.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00526.1.g15457.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_00526.1.g15458.t1	ref|XP_002865545.1| hypothetical protein ARALYDRAFT_494804 [Arabidopsis lyrata subsp. lyrata] gi|297311380|gb|EFH41804.1| hypothetical protein ARALYDRAFT_494804 [Arabidopsis lyrata subsp. lyrata]	389	390	0	100.3	91.5	96.1	hypothetical protein ARALYDRAFT_494804	gbpln	Arabidopsis lyrata	AT5G42250.1 | Symbols: | Zinc-binding alcohol dehydrogenase family protein | chr5:16894087-16897450 FORWARD LENGTH=390	389	390	0	100.3	91.5	95.9
Rsa1.0_00526.1.g15459.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00526.1.g15460.t1	ref|XP_002863486.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297309321|gb|EFH39745.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	315	317	1.00E-136	100.6	79.4	88.3	F-box family protein	gbpln	Arabidopsis lyrata	AT5G45360.1 | Symbols: | F-box family protein | chr5:18384783-18386670 REVERSE LENGTH=316	315	316	1.00E-136	100.3	76.8	87.6
Rsa1.0_00526.1.g15461.t1	ref|XP_002874096.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297319933|gb|EFH50355.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	189	493	4.00E-23	260.8	32.8	40.7	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT5G22850.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:7633717-7636298 REVERSE LENGTH=493	189	493	3.00E-25	260.8	32.3	40.7
Rsa1.0_00526.1.g15462.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00526.1.g15463.t1	dbj|BAA82068.1| nClpP4 [Arabidopsis thaliana]	293	299	1.00E-145	102.0	87.7	88.4	nClpP4	gbpln	Arabidopsis thaliana	AT5G45390.1 | Symbols: CLPP4, NCLPP4 | CLP protease P4 | chr5:18396351-18397586 FORWARD LENGTH=292	293	292	1.00E-147	99.7	87.7	88.4
Rsa1.0_00526.1.g15464.t2	gb|EOA13618.1| hypothetical protein CARUB_v10026685mg [Capsella rubella] gi|482549425|gb|EOA13619.1| hypothetical protein CARUB_v10026685mg [Capsella rubella]	204	353	9.00E-43	173.0	59.3	65.2	hypothetical protein CARUB_v10026685mg	gbpln	Capsella rubella	AT5G45410.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25030.2); Has 124 Blast hits to 124 proteins in 34 species: Archae - 2; Bacteria - 31; Metazoa - 0; Fungi - 0; Plants - 91; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:18402071-18403282 REVERSE LENGTH=342	204	342	3.00E-37	167.6	52.0	59.8
Rsa1.0_00526.1.g15465.t1	dbj|BAJ34628.1| unnamed protein product [Thellungiella halophila]	299	314	1.00E-135	105.0	83.9	91.3	unnamed protein product	----	----	AT5G45420.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr5:18405668-18406597 REVERSE LENGTH=309	299	309	1.00E-110	103.3	77.9	87.0
Rsa1.0_00526.1.g15466.t1	gb|EOA14350.1| hypothetical protein CARUB_v10027531mg [Capsella rubella]	217	493	1.00E-116	227.2	91.2	94.9	hypothetical protein CARUB_v10027531mg	gbpln	Capsella rubella	AT5G45430.1 | Symbols: | Protein kinase superfamily protein | chr5:18409200-18411711 FORWARD LENGTH=499	217	499	1.00E-118	230.0	91.2	94.5
Rsa1.0_00527.1.g15467.t1	ref|XP_002869016.1| hypothetical protein ARALYDRAFT_328081 [Arabidopsis lyrata subsp. lyrata] gi|297314852|gb|EFH45275.1| hypothetical protein ARALYDRAFT_328081 [Arabidopsis lyrata subsp. lyrata]	668	726	0	108.7	79.8	85.6	hypothetical protein ARALYDRAFT_328081	gbpln	Arabidopsis lyrata	AT4G36870.2 | Symbols: BLH2, SAW1 | BEL1-like homeodomain 2 | chr4:17369423-17373723 FORWARD LENGTH=739	668	739	0	110.6	79.5	85.3
Rsa1.0_00527.1.g15468.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00527.1.g15469.t1	gb|EOA15637.1| hypothetical protein CARUB_v10005881mg [Capsella rubella]	150	173	3.00E-59	115.3	84.0	86.7	hypothetical protein CARUB_v10005881mg	gbpln	Capsella rubella	AT4G37240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G23690.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17524546-17525052 FORWARD LENGTH=168	150	168	7.00E-55	112.0	80.0	85.3
Rsa1.0_00527.1.g15470.t1	gb|ABY86895.1| stress responsive protein [Eutrema halophilum]	203	203	1.00E-100	100.0	86.7	93.1	stress responsive protein	gbpln	Eutrema halophilum	AT4G37220.1 | Symbols: | Cold acclimation protein WCOR413 family | chr4:17515106-17515969 FORWARD LENGTH=202	203	202	1.00E-92	99.5	81.3	89.7
Rsa1.0_00527.1.g15471.t2	ref|XP_002866981.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297312817|gb|EFH43240.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	485	498	0	102.7	79.4	86.0	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G37210.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:17512376-17514421 FORWARD LENGTH=492	485	492	0	101.4	77.7	83.7
Rsa1.0_00527.1.g15472.t1	gb|EOA16738.1| hypothetical protein CARUB_v10004940mg, partial [Capsella rubella]	326	409	1.00E-121	125.5	78.2	85.9	hypothetical protein CARUB_v10004940mg, partial	gbpln	Capsella rubella	AT4G37180.1 | Symbols: | Homeodomain-like superfamily protein | chr4:17504648-17506107 FORWARD LENGTH=356	326	356	1.00E-119	109.2	77.3	84.4

Rsa1.0_00527.1.g15473.t1	ref|NP_195430.2| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|20260346|gb|AAM13071.1| unknown protein [Arabidopsis thaliana] gi|31711924|gb|AAP68318.1| At4g37130 [Arabidopsis thaliana] gi|332661357|gb|AEE86757.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	472	513	1.00E-152	108.7	66.5	75.0	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT4G37130.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:17489567-17491773 FORWARD LENGTH=513	472	513	1.00E-155	108.7	66.5	75.0
Rsa1.0_00527.1.g15474.t1	ref|XP_002866975.1| hypothetical protein ARALYDRAFT_912652 [Arabidopsis lyrata subsp. lyrata] gi|297312811|gb|EFH43234.1| hypothetical protein ARALYDRAFT_912652 [Arabidopsis lyrata subsp. lyrata]	190	188	4.00E-65	98.9	76.3	86.3	hypothetical protein ARALYDRAFT_912652	gbpln	Arabidopsis lyrata	AT4G37090.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17477338-17478559 FORWARD LENGTH=186	190	186	1.00E-58	97.9	73.2	82.1
Rsa1.0_00527.1.g15475.t1	ref|NP_974698.1| uncharacterized protein [Arabidopsis thaliana] gi|334187237|ref|NP_001190943.1| uncharacterized protein [Arabidopsis thaliana] gi|332661348|gb|AEE86748.1| uncharacterized protein AT4G37080 [Arabidopsis thaliana] gi|332661350|gb|AEE86750.1| uncharacterized protein AT4G37080 [Arabidopsis thaliana]	565	610	0	108.0	89.0	93.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G37080.3 | Symbols: | Protein of unknown function, DUF547 | chr4:17473719-17476716 FORWARD LENGTH=610	565	610	0	108.0	89.0	93.8
Rsa1.0_00527.1.g15476.t3	ref|NP_568014.1| methionine aminopeptidase 1D [Arabidopsis thaliana] gi|75172582|sp|Q9FV50.1|AMP1D_ARATH RecName: Full=Methionine aminopeptidase 1D, chloroplastic/mitochondrial; Short=MAP 1D; Short=MetAP 1D; AltName: Full=Peptidase M 1D; Flags: Precursor gi|11320960|gb|AAG33977.1|AF250963_1 methionine aminopeptidase-like protein [Arabidopsis thaliana] gi|21553973|gb|AAM63054.1| methionyl aminopeptidase-like protein [Arabidopsis thaliana] gi|26451668|dbj|BAC42930.1| putative ap2 methionine aminopeptidase [Arabidopsis thaliana] gi|28973551|gb|AAO64100.1| putative methionyl aminopeptidase [Arabidopsis thaliana] gi|332661340|gb|AEE86740.1| methionine aminopeptidase 1D [Arabidopsis thaliana]	148	350	3.00E-37	236.5	55.4	64.9	methionine aminopeptidase 1D	gbpln	Arabidopsis thaliana	AT4G37040.1 | Symbols: MAP1D | methionine aminopeptidase 1D | chr4:17455175-17457085 FORWARD LENGTH=350	148	350	7.00E-40	236.5	55.4	64.9
Rsa1.0_00527.1.g15477.t1	ref|NP_179024.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|330251184|gb|AEC06278.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1091	1215	0	111.4	55.3	69.2	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT2G14080.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr2:5925225-5929600 FORWARD LENGTH=1215	1091	1215	0	111.4	55.3	69.2
Rsa1.0_00527.1.g15478.t1	ref|NP_195420.2| uncharacterized protein [Arabidopsis thaliana] gi|61742737|gb|AAX55189.1| hypothetical protein At4g37030 [Arabidopsis thaliana] gi|332661339|gb|AEE86739.1| uncharacterized protein AT4G37030 [Arabidopsis thaliana]	780	569	0	72.9	65.8	68.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G37030.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12680.1); Has 101 Blast hits to 99 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17452150-17454629 FORWARD LENGTH=569	780	569	0	72.9	65.8	68.7
Rsa1.0_00527.1.g15479.t1	ref|NP_568013.1| uncharacterized protein [Arabidopsis thaliana] gi|11762152|gb|AAG40354.1|AF325002_1 AT4g37020 [Arabidopsis thaliana] gi|110736928|dbj|BAF00421.1| hypothetical protein [Arabidopsis thaliana] gi|332661336|gb|AEE86736.1| uncharacterized protein AT4G37020 [Arabidopsis thaliana]	217	212	4.00E-95	97.7	87.1	93.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G37020.1 | Symbols: | BEST Arabidopsis thaliana protein match is: eukaryotic initiation factor 4A-III (TAIR:AT3G19760.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17445778-17447135 FORWARD LENGTH=212	217	212	1.00E-97	97.7	87.1	93.1

Rsa1.0_00527.1.g15480.t1	ref|XP_002863115.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308939|gb|EFH39374.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	940	1222	0	130.0	44.9	54.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G38340.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:15320507-15324061 FORWARD LENGTH=1059	940	1059	1.00E-159	112.7	30.1	36.9
Rsa1.0_00527.1.g15481.t1	ref|XP_002874357.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320194|gb|EFH50616.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	156	155	5.00E-15	99.4	37.8	46.8	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00527.1.g15482.t1	ref|XP_002863119.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308943|gb|EFH39378.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1004	1121	0	111.7	55.4	69.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G65850.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:24494734-24498485 FORWARD LENGTH=1036	1004	1036	0	103.2	53.1	68.3
Rsa1.0_00527.1.g15483.t2	ref|XP_002866973.1| hypothetical protein ARALYDRAFT_912645 [Arabidopsis lyrata subsp. lyrata] gi|297312809|gb|EFH43232.1| hypothetical protein ARALYDRAFT_912645 [Arabidopsis lyrata subsp. lyrata]	45	350	9.00E-11	777.8	77.8	82.2	hypothetical protein ARALYDRAFT_912645	gbpln	Arabidopsis lyrata	AT4G37040.1 | Symbols: MAP1D | methionine aminopeptidase 1D | chr4:17455175-17457085 FORWARD LENGTH=350	45	350	1.00E-13	777.8	77.8	82.2
Rsa1.0_00527.1.g15484.t3	ref|XP_002863116.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308940|gb|EFH39375.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	763	1090	1.00E-137	142.9	41.7	55.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189	763	1189	3.00E-93	155.8	32.6	43.3
Rsa1.0_00528.1.g15485.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	232	1239	1.00E-123	534.1	89.7	95.7	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	232	1262	3.00E-34	544.0	31.9	46.6
Rsa1.0_00528.1.g15486.t1	ref|XP_002877131.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297322969|gb|EFH53390.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	267	671	2.00E-72	251.3	46.4	58.1	expressed protein	gbpln	Arabidopsis lyrata	AT3G28780.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10806131-10808369 REVERSE LENGTH=674	267	674	3.00E-74	252.4	46.4	56.9
Rsa1.0_00528.1.g15487.t1	ref|XP_002877469.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323307|gb|EFH53728.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	199	328	5.00E-34	164.8	37.2	53.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	199	295	6.00E-23	148.2	36.7	47.2
Rsa1.0_00528.1.g15488.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	130	149	6.00E-17	114.6	35.4	47.7	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00528.1.g15489.t1	ref|NP_189521.1| uncharacterized protein [Arabidopsis thaliana] gi|11994787|dbj|BAB03177.1| unnamed protein product [Arabidopsis thaliana] gi|28973701|gb|AAO64167.1| unknown protein [Arabidopsis thaliana] gi|110737047|dbj|BAF00477.1| hypothetical protein [Arabidopsis thaliana] gi|332643970|gb|AEE77491.1| uncharacterized protein AT3G28790 [Arabidopsis thaliana]	779	608	2.00E-56	78.0	13.9	18.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G28790.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10813577-10815588 REVERSE LENGTH=608	779	608	4.00E-59	78.0	13.9	18.4
Rsa1.0_00528.1.g15490.t1	ref|XP_002876780.1| hypothetical protein ARALYDRAFT_484098 [Arabidopsis lyrata subsp. lyrata] gi|297322618|gb|EFH53039.1| hypothetical protein ARALYDRAFT_484098 [Arabidopsis lyrata subsp. lyrata]	163	946	4.00E-21	580.4	33.1	44.2	hypothetical protein ARALYDRAFT_484098	gbpln	Arabidopsis lyrata	AT2G01820.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:357664-360681 REVERSE LENGTH=943	163	943	7.00E-22	578.5	33.1	43.6
Rsa1.0_00528.1.g15491.t1	ref|XP_002875472.1| hypothetical protein ARALYDRAFT_484653 [Arabidopsis lyrata subsp. lyrata] gi|297321310|gb|EFH51731.1| hypothetical protein ARALYDRAFT_484653 [Arabidopsis lyrata subsp. lyrata]	263	518	9.00E-53	197.0	43.3	58.9	hypothetical protein ARALYDRAFT_484653	gbpln	Arabidopsis lyrata	AT3G28790.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10813577-10815588 REVERSE LENGTH=608	263	608	6.00E-54	231.2	39.5	52.1

Rsa1.0_00528.1.g15492.t1	ref|NP_680368.1| glutaredoxin-like protein [Arabidopsis thaliana] gi|75171457|sp|Q9FLE8.1|Y5986_ARATH RecName: Full=Uncharacterized protein At5g39865 gi|10176979|dbj|BAB10211.1| unnamed protein product [Arabidopsis thaliana] gi|19347749|gb|AAL86299.1| unknown protein [Arabidopsis thaliana] gi|22136720|gb|AAM91679.1| unknown protein [Arabidopsis thaliana] gi|332007102|gb|AED94485.1| glutaredoxin-like protein [Arabidopsis thaliana]	333	390	1.00E-109	117.1	66.7	79.6	glutaredoxin-like protein	gbpln	Arabidopsis thaliana	AT5G39865.1 | Symbols: | Glutaredoxin family protein | chr5:15965560-15966732 REVERSE LENGTH=390	333	390	1.00E-112	117.1	66.7	79.6
Rsa1.0_00528.1.g15493.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	136	478	6.00E-27	351.5	44.1	62.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	136	746	1.00E-12	548.5	27.2	35.3
Rsa1.0_00528.1.g15494.t1	gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]	600	527	3.00E-55	87.8	30.0	43.5	hypothetical protein CARUB_v10022820mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	600	735	7.00E-52	122.5	22.2	30.0
Rsa1.0_00528.1.g15495.t1	ref|NP_974372.1| basic helix-loop-helix (bHLH) DNA-binding family protein [Arabidopsis thaliana] gi|9294226|dbj|BAB02128.1| DNA-binding protein-like [Arabidopsis thaliana] gi|88900306|gb|ABD57465.1| At3g28857 [Arabidopsis thaliana] gi|332643976|gb|AEE77497.1| basic helix-loop-helix (bHLH) DNA-binding family protein [Arabidopsis thaliana]	92	92	2.00E-35	100.0	87.0	94.6	basic helix-loop-helix (bHLH) DNA-binding family protein	gbpln	Arabidopsis thaliana	AT3G28857.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding family protein | chr3:10855781-10856313 REVERSE LENGTH=92	92	92	3.00E-38	100.0	87.0	94.6
Rsa1.0_00528.1.g15496.t1	ref|XP_002875477.1| hypothetical protein ARALYDRAFT_484658 [Arabidopsis lyrata subsp. lyrata] gi|297321315|gb|EFH51736.1| hypothetical protein ARALYDRAFT_484658 [Arabidopsis lyrata subsp. lyrata]	797	780	0	97.9	62.5	72.9	hypothetical protein ARALYDRAFT_484658	gbpln	Arabidopsis lyrata	AT3G28880.1 | Symbols: | Ankyrin repeat family protein | chr3:10892435-10895895 FORWARD LENGTH=772	797	772	0	96.9	60.0	70.6
Rsa1.0_00528.1.g15497.t1	gb|EOA24881.1| hypothetical protein CARUB_v10018171mg, partial [Capsella rubella]	72	156	3.00E-17	216.7	69.4	75.0	hypothetical protein CARUB_v10018171mg, partial	gbpln	Capsella rubella	AT3G28900.1 | Symbols: | Ribosomal protein L34e superfamily protein | chr3:10902864-10904415 REVERSE LENGTH=120	72	120	1.00E-19	166.7	68.1	75.0
Rsa1.0_00528.1.g15498.t1	dbj|BAJ34042.1| unnamed protein product [Thellungiella halophila]	332	337	1.00E-144	101.5	86.1	89.8	unnamed protein product	----	----	AT3G28910.1 | Symbols: ATMYB30, MYB30 | myb domain protein 30 | chr3:10911443-10912856 FORWARD LENGTH=323	332	323	1.00E-142	97.3	80.7	86.1
Rsa1.0_00528.1.g15499.t2	gb|ABD65039.1| GTP-binding protein, putative [Brassica oleracea]	285	189	1.00E-36	66.3	26.7	27.4	GTP-binding protein, putative	gbpln	Brassica oleracea	AT5G47200.1 | Symbols: ATRABD2B, ATRAB1A, RAB1A | RAB GTPase homolog 1A | chr5:19167029-19168718 FORWARD LENGTH=202	285	202	1.00E-37	70.9	26.0	27.0
Rsa1.0_00528.1.g15500.t2	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1348	1515	0	112.4	58.1	72.8	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1348	1262	2.00E-90	93.6	12.8	18.9
Rsa1.0_00528.1.g15501.t1	gb|EOA24839.1| hypothetical protein CARUB_v10018128mg [Capsella rubella]	168	170	8.00E-84	101.2	86.9	92.3	hypothetical protein CARUB_v10018128mg	gbpln	Capsella rubella	AT3G28940.1 | Symbols: | AIG2-like (avirulence induced gene) family protein | chr3:10968324-10969311 REVERSE LENGTH=169	168	169	5.00E-83	100.6	84.5	92.9
Rsa1.0_00528.1.g15502.t1	dbj|BAJ34156.1| unnamed protein product [Thellungiella halophila]	167	168	1.00E-85	100.6	91.0	94.6	unnamed protein product	----	----	AT3G28930.1 | Symbols: AIG2 | AIG2-like (avirulence induced gene) family protein | chr3:10959890-10960728 REVERSE LENGTH=170	167	170	3.00E-77	101.8	77.2	87.4
Rsa1.0_00528.1.g15503.t1	ref|NP_001050981.1| Os03g0698500 [Oryza sativa Japonica Group] gi|28273361|gb|AAO38447.1| putative zinc binding protein [Oryza sativa Japonica Group] gi|108710575|gb|ABF98370.1| Yippee, putative, expressed [Oryza sativa Japonica Group] gi|113549452|dbj|BAF12895.1| Os03g0698500 [Oryza sativa Japonica Group] gi|215766470|dbj|BAG98778.1| unnamed protein product [Oryza sativa Japonica Group] gi|218193579|gb|EEC76006.1| hypothetical protein OsI_13146 [Oryza sativa Indica Group] gi|222625619|gb|EEE59751.1| hypothetical protein OsJ_12219 [Oryza sativa Japonica Group]	101	129	4.00E-12	127.7	43.6	61.4	Os03g0698500	gbpln	Oryza sativa	AT3G08990.2 | Symbols: | Yippee family putative zinc-binding protein | chr3:2743590-2744709 FORWARD LENGTH=128	101	128	4.00E-12	126.7	41.6	57.4
Rsa1.0_00528.1.g15504.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00529.1.g15505.t2	ref|XP_002867141.1| hypothetical protein ARALYDRAFT_491275 [Arabidopsis lyrata subsp. lyrata] gi|297312977|gb|EFH43400.1| hypothetical protein ARALYDRAFT_491275 [Arabidopsis lyrata subsp. lyrata]	277	217	2.00E-30	78.3	35.0	40.8	hypothetical protein ARALYDRAFT_491275	gbpln	Arabidopsis lyrata	AT4G33980.1 | Symbols: | BEST Arabidopsis thaliana protein match is: cold regulated gene 27 (TAIR:AT5G42900.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16283047-16284946 REVERSE LENGTH=218	277	218	2.00E-30	78.7	33.2	37.9
Rsa1.0_00529.1.g15506.t1	ref|NP_195123.1| Pollen-specific leucine-rich repeat extensin-like protein 4 [Arabidopsis thaliana] gi|75318791|sp|O81765.1|PLRX4_ARATH RecName: Full=Pollen-specific leucine-rich repeat extensin-like protein 4; Short=AtPEX4; Short=Pollen-specific LRR/EXTENSIN4; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor gi|3297821|emb|CAA19879.1| extensin-like protein [Arabidopsis thaliana] gi|7270346|emb|CAB80114.1| extensin-like protein [Arabidopsis thaliana] gi|332660902|gb|AEE86302.1| Pollen-specific leucine-rich repeat extensin-like protein 4 [Arabidopsis thaliana]	693	699	0	100.9	54.7	58.7	Pollen-specific leucine-rich repeat extensin-like protein 4	gbpln	Arabidopsis thaliana	AT4G33970.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:16279795-16281894 REVERSE LENGTH=699	693	699	0	100.9	54.7	58.7
Rsa1.0_00529.1.g15507.t1	ref|NP_195122.1| uncharacterized protein [Arabidopsis thaliana] gi|3297820|emb|CAA19878.1| putative protein [Arabidopsis thaliana] gi|7270345|emb|CAB80113.1| putative protein [Arabidopsis thaliana] gi|38566498|gb|AAR24139.1| At4g33960 [Arabidopsis thaliana] gi|40823521|gb|AAR92287.1| At4g33960 [Arabidopsis thaliana] gi|332660901|gb|AEE86301.1| uncharacterized protein AT4G33960 [Arabidopsis thaliana]	65	67	3.00E-12	103.1	73.8	86.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G33960.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G15830.1); Has 32 Blast hits to 32 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:16277392-16277595 FORWARD LENGTH=67	65	67	6.00E-15	103.1	73.8	86.2
Rsa1.0_00529.1.g15508.t1	ref|XP_002869183.1| hypothetical protein ARALYDRAFT_491280 [Arabidopsis lyrata subsp. lyrata] gi|297315019|gb|EFH45442.1| hypothetical protein ARALYDRAFT_491280 [Arabidopsis lyrata subsp. lyrata]	331	362	1.00E-176	109.4	97.6	100.0	hypothetical protein ARALYDRAFT_491280	gbpln	Arabidopsis lyrata	AT4G33950.1 | Symbols: OST1, SNRK2-6, SRK2E, SNRK2.6, P44, ATOST1 | Protein kinase superfamily protein | chr4:16272364-16274657 FORWARD LENGTH=362	331	362	1.00E-179	109.4	97.3	99.7
Rsa1.0_00529.1.g15509.t2	gb|EOA17941.1| hypothetical protein CARUB_v10006351mg [Capsella rubella]	463	464	0	100.2	87.9	93.1	hypothetical protein CARUB_v10006351mg	gbpln	Capsella rubella	AT4G33945.1 | Symbols: | ARM repeat superfamily protein | chr4:16268119-16270514 FORWARD LENGTH=464	463	464	0	100.2	87.9	92.4
Rsa1.0_00529.1.g15510.t1	gb|AAM62531.1| unknown [Arabidopsis thaliana]	238	262	1.00E-105	110.1	78.2	87.4	unknown	gbpln	Arabidopsis thaliana	AT4G33940.1 | Symbols: | RING/U-box superfamily protein | chr4:16266085-16267612 FORWARD LENGTH=262	238	262	1.00E-107	110.1	78.6	87.4
Rsa1.0_00529.1.g15511.t1	gb|EOA17648.1| hypothetical protein CARUB_v10006015mg [Capsella rubella]	151	132	9.00E-61	87.4	79.5	82.8	hypothetical protein CARUB_v10006015mg	gbpln	Capsella rubella	AT4G33925.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16263292-16264064 FORWARD LENGTH=132	151	132	3.00E-63	87.4	78.8	82.8
Rsa1.0_00529.1.g15512.t1	gb|EEC76251.1| hypothetical protein OsI_13694 [Oryza sativa Indica Group]	56	828	5.00E-23	1478.6	80.4	85.7	hypothetical protein OsI_13694	gbpln	Oryza sativa	AT4G33865.1 | Symbols: | Ribosomal protein S14p/S29e family protein | chr4:16233395-16234114 REVERSE LENGTH=56	56	56	4.00E-25	100.0	91.1	94.6
Rsa1.0_00529.1.g15513.t1	gb|EOA15721.1| hypothetical protein CARUB_v10006623mg [Capsella rubella]	348	353	1.00E-162	101.4	84.5	90.2	hypothetical protein CARUB_v10006623mg	gbpln	Capsella rubella	AT4G33880.1 | Symbols: RSL2 | ROOT HAIR DEFECTIVE 6-LIKE 2 | chr4:16239566-16241052 REVERSE LENGTH=352	348	352	1.00E-160	101.1	82.2	88.5
Rsa1.0_00529.1.g15514.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00529.1.g15515.t1	gb|EOA18079.1| hypothetical protein CARUB_v10006531mg [Capsella rubella]	401	414	1.00E-162	103.2	73.8	83.8	hypothetical protein CARUB_v10006531mg	gbpln	Capsella rubella	AT4G33870.1 | Symbols: | Peroxidase superfamily protein | chr4:16234670-16236492 REVERSE LENGTH=401	401	401	1.00E-155	100.0	69.3	80.0
Rsa1.0_00529.1.g15516.t1	ref|NP_567937.1| uncharacterized protein [Arabidopsis thaliana] gi|21594003|gb|AAM65921.1| unknown [Arabidopsis thaliana] gi|107738065|gb|ABF83626.1| At4g33800 [Arabidopsis thaliana] gi|332660879|gb|AEE86279.1| uncharacterized protein AT4G33800 [Arabidopsis thaliana]	175	170	3.00E-60	97.1	74.3	77.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G33800.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16210404-16211307 REVERSE LENGTH=170	175	170	1.00E-62	97.1	74.3	77.1

Rsa1.0_00529.1.g15517.t9	ref|XP_002867157.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312993|gb|EFH43416.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	526	493	0	93.7	69.6	77.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G33790.1 | Symbols: CER4, G7, FAR3 | Jojoba acyl CoA reductase-related male sterility protein | chr4:16204325-16207891 REVERSE LENGTH=493	526	493	0	93.7	68.6	78.1
Rsa1.0_00529.1.g15518.t1	gb|EOA16776.1| hypothetical protein CARUB_v10004995mg [Capsella rubella]	389	392	1.00E-174	100.8	83.8	90.5	hypothetical protein CARUB_v10004995mg	gbpln	Capsella rubella	AT4G33770.1 | Symbols: | Inositol 1,3,4-trisphosphate 5/6-kinase family protein | chr4:16193589-16196242 REVERSE LENGTH=391	389	391	1.00E-172	100.5	83.8	91.3
Rsa1.0_00529.1.g15519.t1	ref|NP_195102.2| aspartyl-tRNA synthetase [Arabidopsis thaliana] gi|332660874|gb|AEE86274.1| tRNA synthetase class II (D, K and N) family protein [Arabidopsis thaliana]	661	664	0	100.5	87.9	91.5	aspartyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT4G33760.1 | Symbols: | tRNA synthetase class II (D, K and N) family protein | chr4:16189285-16193260 REVERSE LENGTH=664	661	664	0	100.5	87.9	91.5
Rsa1.0_00529.1.g15520.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00530.1.g15521.t1	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	317	1089	6.00E-53	343.5	38.2	52.1	transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00530.1.g15522.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	354	704	1.00E-136	198.9	68.4	79.9	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00530.1.g15523.t1	ref|NP_174766.1| RING-H2 finger protein ATL34 [Arabidopsis thaliana] gi|68565270|sp|Q9C7I1.1|ATL34_ARATH RecName: Full=RING-H2 finger protein ATL34; Flags: Precursor gi|12322941|gb|AAG51457.1|AC069160_3 RING zinc finger protein, putative [Arabidopsis thaliana] gi|332193658|gb|AEE31779.1| RING-H2 finger protein ATL34 [Arabidopsis thaliana]	359	327	1.00E-132	91.1	68.2	75.5	RING-H2 finger protein ATL34	gbpln	Arabidopsis thaliana	AT1G35330.1 | Symbols: | RING/U-box superfamily protein | chr1:12965046-12966113 FORWARD LENGTH=327	359	327	1.00E-135	91.1	68.2	75.5
Rsa1.0_00530.1.g15524.t1	gb|EOA36180.1| hypothetical protein CARUB_v10010050mg [Capsella rubella]	250	260	1.00E-106	104.0	80.0	88.4	hypothetical protein CARUB_v10010050mg	gbpln	Capsella rubella	AT1G35460.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:13040092-13041907 FORWARD LENGTH=259	250	259	1.00E-106	103.6	84.8	91.6
Rsa1.0_00530.1.g15525.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00530.1.g15526.t11	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	787	414	2.00E-71	52.6	24.5	28.6	hypothetical protein 23.t00055	gbpln	Brassica oleracea	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	787	256	1.00E-16	32.5	7.1	10.8
Rsa1.0_00530.1.g15527.t1	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	1025	1089	0	106.2	51.3	67.3	transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00530.1.g15528.t1	gb|AAD15525.1| Mutator-like transposase [Arabidopsis thaliana]	393	550	2.00E-63	139.9	42.7	61.3	Mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00530.1.g15529.t2	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1688	1611	0	95.4	46.6	59.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1688	158	9.00E-24	9.4	3.3	4.7
Rsa1.0_00530.1.g15530.t10	#	#	#	#	#	#	#	-	----	----	AT5G15690.1 | Symbols: | zinc ion binding | chr5:5113823-5114402 REVERSE LENGTH=169	136	169	3.00E-12	124.3	23.5	31.6
Rsa1.0_00530.1.g15531.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00531.1.g15532.t2	sp|H3K2Y6.1|MED12_ARATH RecName: Full=Mediator of RNA polymerase II transcription subunit 12; AltName: Full=Protein CENTER CITY; AltName: Full=Protein CRYPTIC PRECOCIOUS gi|374428817|dbj|BAL49816.1| cryptic precocious [Arabidopsis thaliana] gi|374428819|dbj|BAL49817.1| cryptic precocious splicing variant [Arabidopsis thaliana] gi|374428821|dbj|BAL49818.1| cryptic precocious [Arabidopsis thaliana]	2239	2235	0	99.8	85.4	91.2	RecName: Full=Mediator of RNA polymerase II transcription subunit 12; AltName: Full=Protein CENTER CITY; AltName: Full=Protein CRYPTIC PRECOCIOUS gi|374428817|dbj|BAL49816.1| cryptic precocious	gbpln	Arabidopsis thaliana	AT4G00450.1 | Symbols: CRP, CCT | RNA polymerase II transcription mediators | chr4:202425-210666 FORWARD LENGTH=2253	2239	2253	0	100.6	80.8	87.4
Rsa1.0_00531.1.g15533.t1	gb|EOA19675.1| hypothetical protein CARUB_v10003327mg [Capsella rubella]	476	479	0	100.6	92.6	95.6	hypothetical protein CARUB_v10003327mg	gbpln	Capsella rubella	AT4G00460.2 | Symbols: ATROPGEF3, ROPGEF3 | RHO guanyl-nucleotide exchange factor 3 | chr4:211146-213094 REVERSE LENGTH=473	476	473	0	99.4	91.0	94.5
Rsa1.0_00531.1.g15534.t2	gb|EOA20272.1| hypothetical protein CARUB_v10000576mg [Capsella rubella]	530	573	0	108.1	73.6	82.3	hypothetical protein CARUB_v10000576mg	gbpln	Capsella rubella	AT4G00480.1 | Symbols: ATMYC1, myc1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:217106-219684 REVERSE LENGTH=526	530	526	0	99.2	75.1	83.8

Rsa1.0_00531.1.g15535.t1	ref|XP_002875024.1| beta-amylase 9 [Arabidopsis lyrata subsp. lyrata] gi|297320861|gb|EFH51283.1| beta-amylase 9 [Arabidopsis lyrata subsp. lyrata]	549	542	0	98.7	86.9	90.5	beta-amylase 9	gbpln	Arabidopsis lyrata	AT4G00490.1 | Symbols: BAM2, BMY9 | beta-amylase 2 | chr4:222422-224862 FORWARD LENGTH=542	549	542	0	98.7	86.3	89.4
Rsa1.0_00531.1.g15536.t1	ref|XP_002875022.1| hypothetical protein ARALYDRAFT_490514 [Arabidopsis lyrata subsp. lyrata] gi|297320859|gb|EFH51281.1| hypothetical protein ARALYDRAFT_490514 [Arabidopsis lyrata subsp. lyrata]	124	140	3.00E-22	112.9	60.5	75.0	hypothetical protein ARALYDRAFT_490514	gbpln	Arabidopsis lyrata	AT4G00525.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:231862-232769 FORWARD LENGTH=140	124	140	6.00E-23	112.9	58.1	73.4
Rsa1.0_00531.1.g15537.t1	ref|XP_002872946.1| hypothetical protein ARALYDRAFT_912190 [Arabidopsis lyrata subsp. lyrata] gi|297318783|gb|EFH49205.1| hypothetical protein ARALYDRAFT_912190 [Arabidopsis lyrata subsp. lyrata]	189	153	1.00E-46	81.0	54.5	64.0	hypothetical protein ARALYDRAFT_912190	gbpln	Arabidopsis lyrata	AT2G45760.1 | Symbols: BAP2, BAL | BON association protein 2 | chr2:18847125-18847748 REVERSE LENGTH=207	189	207	5.00E-26	109.5	33.3	44.4
Rsa1.0_00531.1.g15538.t1	dbj|BAD94208.1| digalactosyldiacylglycerol synthase [Arabidopsis thaliana]	100	149	1.00E-28	149.0	71.0	80.0	digalactosyldiacylglycerol synthase	gbpln	Arabidopsis thaliana	AT4G00550.1 | Symbols: DGD2 | digalactosyl diacylglycerol deficient 2 | chr4:238154-240019 REVERSE LENGTH=473	100	473	3.00E-31	473.0	71.0	80.0
Rsa1.0_00531.1.g15539.t1	gb|EOA18986.1| hypothetical protein CARUB_v10007631mg [Capsella rubella]	293	347	1.00E-151	118.4	92.2	96.9	hypothetical protein CARUB_v10007631mg	gbpln	Capsella rubella	AT2G22190.1 | Symbols: TPPE | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:9433897-9436482 REVERSE LENGTH=354	293	354	1.00E-129	120.8	81.6	87.7
Rsa1.0_00531.1.g15540.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1059	1274	0	120.3	49.4	65.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1059	575	3.00E-75	54.3	16.4	25.9
Rsa1.0_00531.1.g15541.t1	ref|XP_003537506.1| PREDICTED: uncharacterized protein LOC100816245 [Glycine max]	218	705	3.00E-24	323.4	35.3	44.0	PREDICTED: uncharacterized protein LOC100816245	gbenv/gbpln	Glycine max	AT4G39680.2 | Symbols: | SAP domain-containing protein | chr4:18414604-18416938 REVERSE LENGTH=633	218	633	6.00E-16	290.4	18.3	20.6
Rsa1.0_00531.1.g15542.t1	ref|XP_002866875.1| hypothetical protein ARALYDRAFT_912448 [Arabidopsis lyrata subsp. lyrata] gi|297312711|gb|EFH43134.1| hypothetical protein ARALYDRAFT_912448 [Arabidopsis lyrata subsp. lyrata]	240	232	1.00E-103	96.7	77.9	83.3	hypothetical protein ARALYDRAFT_912448	gbpln	Arabidopsis lyrata	AT4G39670.1 | Symbols: | Glycolipid transfer protein (GLTP) family protein | chr4:18410172-18410861 FORWARD LENGTH=229	240	229	1.00E-103	95.4	75.0	80.8
Rsa1.0_00531.1.g15543.t1	ref|XP_002866873.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312709|gb|EFH43132.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	567	578	0	101.9	82.2	90.5	predicted protein	gbpln	Arabidopsis lyrata	AT4G39640.2 | Symbols: GGT1 | gamma-glutamyl transpeptidase 1 | chr4:18400608-18402861 FORWARD LENGTH=572	567	572	0	100.9	82.4	90.7
Rsa1.0_00531.1.g15544.t2	gb|AAF82236.1|AC069143_12 Contains similarity to a transposable element Tip100 protein for transposase from Ipomoea purpurea gb|4063769 and is a member of the transmembrane 4 family PF|00335 [Arabidopsis thaliana]	1227	811	0	66.1	36.1	43.9	Contains similarity to a transposable element Tip100 protein for transposase from Ipomoea purpurea gb|4063769 and is a member of the transmembrane 4 family PF|00335	gbpln	Arabidopsis thaliana	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	1227	769	0	62.7	36.1	43.9
Rsa1.0_00531.1.g15545.t1	gb|EOA16490.1| hypothetical protein CARUB_v10004648mg [Capsella rubella]	97	497	1.00E-34	512.4	78.4	82.5	hypothetical protein CARUB_v10004648mg	gbpln	Capsella rubella	AT4G39620.1 | Symbols: EMB2453, ATPPR5 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:18395294-18397578 FORWARD LENGTH=563	97	563	5.00E-36	580.4	74.2	78.4
Rsa1.0_00532.1.g15546.t2	ref|XP_002883265.1| hypothetical protein ARALYDRAFT_318821 [Arabidopsis lyrata subsp. lyrata] gi|297329105|gb|EFH59524.1| hypothetical protein ARALYDRAFT_318821 [Arabidopsis lyrata subsp. lyrata]	1242	1199	0	96.5	87.2	91.8	hypothetical protein ARALYDRAFT_318821	gbpln	Arabidopsis lyrata	AT3G20720.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages. | chr3:7240098-7246754 FORWARD LENGTH=1199	1242	1199	0	96.5	87.4	91.5
Rsa1.0_00532.1.g15547.t1	sp|Q9LT48.1|PP244_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g20730 gi|9294399|dbj|BAB02480.1| unnamed protein product [Arabidopsis thaliana] gi|51971823|dbj|BAD44576.1| unknown protein [Arabidopsis thaliana]	234	565	6.00E-94	241.5	75.6	86.8	RecName: Full=Pentatricopeptide repeat-containing protein At3g20730 gi|9294399|dbj|BAB02480.1| unnamed protein product	gbpln	Arabidopsis thaliana	AT3G20730.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:7247095-7248878 FORWARD LENGTH=564	234	564	2.00E-96	241.0	75.6	86.8

Rsa1.0_00532.1.g15548.t1	ref|NP_188710.1| polycomb group protein FERTILIZATION-INDEPENDENT ENDOSPERM [Arabidopsis thaliana] gi|30913043|sp|Q9LT47.2|FIE_ARATH RecName: Full=Polycomb group protein FERTILIZATION-INDEPENDENT ENDOSPERM; AltName: Full=Protein FERTILIZATION-INDEPENDENT SEED 3 gi|4567095|gb|AAD23584.1| fertilization-independent endosperm protein [Arabidopsis thaliana] gi|26449331|dbj|BAC41793.1| putative fertilization-independent endosperm protein [Arabidopsis thaliana] gi|28950933|gb|AAO63390.1| At3g20730 [Arabidopsis thaliana] gi|332642897|gb|AEE76418.1| polycomb group protein FERTILIZATION-INDEPENDENT ENDOSPERM [Arabidopsis thaliana]	369	369	0	100.0	91.6	96.5	polycomb group protein FERTILIZATION-INDEPENDENT ENDOSPERM	gbpln	Arabidopsis thaliana	AT3G20740.1 | Symbols: FIE, FIS3, FIE1 | Transducin/WD40 repeat-like superfamily protein | chr3:7249064-7252254 REVERSE LENGTH=369	369	369	0	100.0	91.6	96.5
Rsa1.0_00532.1.g15549.t1	gb|EOA33107.1| hypothetical protein CARUB_v10016445mg [Capsella rubella]	201	230	9.00E-30	114.4	48.3	63.2	hypothetical protein CARUB_v10016445mg	gbpln	Capsella rubella	AT3G20750.1 | Symbols: GATA29 | GATA transcription factor 29 | chr3:7255016-7256140 FORWARD LENGTH=208	201	208	3.00E-27	103.5	52.7	64.7
Rsa1.0_00532.1.g15550.t1	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	144	326	7.00E-15	226.4	28.5	46.5	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00532.1.g15551.t1	gb|AAD36942.1|AF069441_2 hypothetical protein [Arabidopsis thaliana] gi|7267196|emb|CAB77907.1| hypothetical protein [Arabidopsis thaliana]	632	963	6.00E-51	152.4	21.7	33.1	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	632	874	1.00E-28	138.3	11.6	17.2
Rsa1.0_00532.1.g15552.t1	ref|XP_002885442.1| hypothetical protein ARALYDRAFT_898595 [Arabidopsis lyrata subsp. lyrata] gi|297331282|gb|EFH61701.1| hypothetical protein ARALYDRAFT_898595 [Arabidopsis lyrata subsp. lyrata]	219	238	1.00E-55	108.7	57.1	69.9	hypothetical protein ARALYDRAFT_898595	gbpln	Arabidopsis lyrata	AT2G16600.1 | Symbols: ROC3 | rotamase CYP 3 | chr2:7200862-7201383 FORWARD LENGTH=173	219	173	3.00E-53	79.0	49.8	58.4
Rsa1.0_00532.1.g15553.t1	gb|EOA30103.1| hypothetical protein CARUB_v10013213mg [Capsella rubella]	546	627	0	114.8	78.2	85.5	hypothetical protein CARUB_v10013213mg	gbpln	Capsella rubella	AT3G20770.1 | Symbols: EIN3, AtEIN3 | Ethylene insensitive 3 family protein | chr3:7260702-7262588 REVERSE LENGTH=628	546	628	0	115.0	77.5	83.5
Rsa1.0_00532.1.g15554.t1	gb|EOA30908.1| hypothetical protein CARUB_v10014055mg, partial [Capsella rubella]	338	356	1.00E-163	105.3	85.8	85.8	hypothetical protein CARUB_v10014055mg, partial	gbpln	Capsella rubella	AT3G20800.1 | Symbols: | Cell differentiation, Rcd1-like protein | chr3:7271412-7273897 REVERSE LENGTH=316	338	316	1.00E-164	93.5	84.9	85.2
Rsa1.0_00532.1.g15555.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00532.1.g15556.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00532.1.g15557.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00532.1.g15558.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	545	1475	3.00E-88	270.6	28.3	34.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	545	237	2.00E-20	43.5	10.5	19.4
Rsa1.0_00532.1.g15559.t1	gb|AAD23705.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	432	333	2.00E-19	77.1	18.8	24.5	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00533.1.g15560.t1	gb|EOA38827.1| hypothetical protein CARUB_v10011150mg [Capsella rubella]	184	196	2.00E-68	106.5	78.3	85.3	hypothetical protein CARUB_v10011150mg	gbpln	Capsella rubella	AT1G17700.1 | Symbols: PRA1.F1 | prenylated RAB acceptor 1.F1 | chr1:6089588-6090130 FORWARD LENGTH=180	184	180	2.00E-68	97.8	75.5	84.8
Rsa1.0_00533.1.g15561.t1	ref|XP_002892964.1| phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata] gi|297338806|gb|EFH69223.1| phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata]	283	284	1.00E-142	100.4	86.9	93.6	phosphoric monoester hydrolase	gbpln	Arabidopsis lyrata	AT1G17710.1 | Symbols: | Pyridoxal phosphate phosphatase-related protein | chr1:6090763-6091975 REVERSE LENGTH=279	283	279	1.00E-139	98.6	84.8	90.8
Rsa1.0_00533.1.g15562.t8	gb|EOA40186.1| hypothetical protein CARUB_v10008904mg [Capsella rubella]	501	506	0	101.0	87.4	91.2	hypothetical protein CARUB_v10008904mg	gbpln	Capsella rubella	AT1G17720.2 | Symbols: ATB BETA | Protein phosphatase 2A, regulatory subunit PR55 | chr1:6093949-6098065 REVERSE LENGTH=500	501	500	0	99.8	86.8	90.8
Rsa1.0_00533.1.g15563.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00533.1.g15564.t1	ref|NP_173217.1| PEP1 receptor 2 [Arabidopsis thaliana] gi|75334548|sp|Q9FZ59.1|PEPR2_ARATH RecName: Full=Leucine-rich repeat receptor-like protein kinase PEPR2; AltName: Full=Elicitor peptide 1 receptor 2; Short=PEP1 receptor 2; Flags: Precursor gi|9802748|gb|AAF99817.1|AC034257_9 Unknown protein [Arabidopsis thaliana] gi|224589394|gb|ACN59231.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332191511|gb|AEE29632.1| PEP1 receptor 2 [Arabidopsis thaliana]	1112	1088	0	97.8	74.8	83.5	PEP1 receptor 2	gbpln	Arabidopsis thaliana	AT1G17750.1 | Symbols: PEPR2, AtPEPR2 | PEP1 receptor 2 | chr1:6106656-6110008 FORWARD LENGTH=1088	1112	1088	0	97.8	74.8	83.5
Rsa1.0_00533.1.g15565.t1	ref|XP_002890248.1| hypothetical protein ARALYDRAFT_312743 [Arabidopsis lyrata subsp. lyrata] gi|297336090|gb|EFH66507.1| hypothetical protein ARALYDRAFT_312743 [Arabidopsis lyrata subsp. lyrata]	754	978	0	129.7	49.2	61.0	hypothetical protein ARALYDRAFT_312743	gbpln	Arabidopsis lyrata	AT1G17770.1 | Symbols: SUVH7, SDG17 | SU(VAR)3-9 homolog 7 | chr1:6120741-6122822 FORWARD LENGTH=693	754	693	0	91.9	48.3	60.7
Rsa1.0_00533.1.g15566.t1	gb|EOA39163.1| hypothetical protein CARUB_v10012112mg [Capsella rubella]	117	273	8.00E-22	233.3	53.8	65.0	hypothetical protein CARUB_v10012112mg	gbpln	Capsella rubella	AT2G16575.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17780.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:7184652-7185245 FORWARD LENGTH=170	117	170	7.00E-24	145.3	52.1	65.0
Rsa1.0_00533.1.g15567.t1	ref|XP_002892967.1| hypothetical protein ARALYDRAFT_312744 [Arabidopsis lyrata subsp. lyrata] gi|297338809|gb|EFH69226.1| hypothetical protein ARALYDRAFT_312744 [Arabidopsis lyrata subsp. lyrata]	474	482	1.00E-143	101.7	62.9	71.1	hypothetical protein ARALYDRAFT_312744	gbpln	Arabidopsis lyrata	AT1G17790.1 | Symbols: | DNA-binding bromodomain-containing protein | chr1:6125532-6127276 REVERSE LENGTH=487	474	487	1.00E-138	102.7	59.7	68.4
Rsa1.0_00533.1.g15568.t1	ref|NP_173223.1| putative aquaporin TIP3-2 [Arabidopsis thaliana] gi|32363213|sp|O22588.1|TIP32_ARATH RecName: Full=Probable aquaporin TIP3-2; AltName: Full=Beta-tonoplast intrinsic protein; Short=Beta-TIP; AltName: Full=Tonoplast intrinsic protein 3-2; Short=AtTIP3;2 gi|9665059|gb|AAF97261.1|AC034106_4 Identical to beta-tonoplast intrinsic protein (beta-TIP) from Arabidopsis thaliana gb|AF026275 and contains a MIP (major intrinsic protein) PF|00230 domain. ESTs gb|R64952, gb|AI999191 come from this gene [Arabidopsis thaliana] gi|2605714|gb|AAB84183.1| beta-tonoplast intrinsic protein [Arabidopsis thaliana] gi|110737967|dbj|BAF00920.1| hypothetical protein [Arabidopsis thaliana] gi|332191518|gb|AEE29639.1| putative aquaporin TIP3-2 [Arabidopsis thaliana]	268	267	1.00E-127	99.6	90.3	95.9	putative aquaporin TIP3-2	gbpln	Arabidopsis thaliana	AT1G17810.1 | Symbols: BETA-TIP | beta-tonoplast intrinsic protein | chr1:6130209-6131442 FORWARD LENGTH=267	268	267	1.00E-129	99.6	90.3	95.9
Rsa1.0_00533.1.g15569.t1	ref|XP_002892968.1| hypothetical protein ARALYDRAFT_889192 [Arabidopsis lyrata subsp. lyrata] gi|297338810|gb|EFH69227.1| hypothetical protein ARALYDRAFT_889192 [Arabidopsis lyrata subsp. lyrata]	780	797	0	102.2	81.8	89.5	hypothetical protein ARALYDRAFT_889192	gbpln	Arabidopsis lyrata	AT1G17820.1 | Symbols: | Putative integral membrane protein conserved region (DUF2404) | chr1:6131751-6135115 REVERSE LENGTH=803	780	803	0	102.9	80.6	88.3
Rsa1.0_00533.1.g15570.t1	ref|XP_002892969.1| hypothetical protein ARALYDRAFT_471996 [Arabidopsis lyrata subsp. lyrata] gi|297338811|gb|EFH69228.1| hypothetical protein ARALYDRAFT_471996 [Arabidopsis lyrata subsp. lyrata]	329	337	1.00E-148	102.4	83.3	90.3	hypothetical protein ARALYDRAFT_471996	gbpln	Arabidopsis lyrata	AT1G17830.1 | Symbols: | Protein of unknown function (DUF789) | chr1:6136118-6138172 REVERSE LENGTH=337	329	337	1.00E-149	102.4	81.5	90.0
Rsa1.0_00533.1.g15571.t1	gb|AGC11818.1| putative ABC transporter G family member 11 [Eutrema halophilum]	678	703	0	103.7	97.6	98.7	putative ABC transporter G family member 11	gbpln	Eutrema halophilum	AT1G17840.1 | Symbols: WBC11, ABCG11, DSO, COF1, ATWBC11 | white-brown complex homolog protein 11 | chr1:6142870-6145894 FORWARD LENGTH=703	678	703	0	103.7	97.1	98.4

<table>
<tr><td>Rsa1.0_00533.1.g15572.t1</td><td>ref|NP_001185025.1| rhodanese homology domain-containing protein [Arabidopsis thaliana] gi|384950757|sp|F4I933.1|STR8_ARATH RecName: Full=Rhodanese-like domain-containing protein 8, chloroplastic; AltName: Full=Sulfurtransferase 8; Short=AtStr8; Flags: Precursor gi|332191523|gb|AEE29644.1| rhodanese homology domain-containing protein [Arabidopsis thaliana]</td><td>450</td><td>448</td><td>0</td><td>99.6</td><td>80.0</td><td>85.1</td><td>rhodanese homology domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G17850.2 | Symbols: | Rhodanese/Cell cycle control phosphatase superfamily protein | chr1:6146470-6148820 REVERSE LENGTH=448</td><td>450</td><td>448</td><td>0</td><td>99.6</td><td>80.0</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00533.1.g15573.t1</td><td>ref|NP_173228.1| kunitz type trypsin and protease inhibitor domain-containing protein [Arabidopsis thaliana] gi|9665064|gb|AAF97266.1|AC034106_9 Contains similarity to a tumor-related protein from Nicotiana tabacum gb|U66263 and contains a trypsin and protease inhibitor PF|00197 domain. ESTs gb|AV561824, gb|T44961, gb|H36186, gb|T45060, gb|N38006, gb|F19847 come from this gene [Arabidopsis thaliana] gi|12083240|gb|AAG48779.1|AF332416_1 putative lemir (miraculin) protein [Arabidopsis thaliana] gi|13899081|gb|AAK48962.1|AF370535_1 Unknown protein [Arabidopsis thaliana] gi|15294166|gb|AAK95260.1|AF410274_1 At1g17860/F2H15_8 [Arabidopsis thaliana] gi|20148401|gb|AAM10091.1| unknown protein [Arabidopsis thaliana] gi|20453293|gb|AAM19885.1| At1g17860/F2H15_8 [Arabidopsis thaliana] gi|332191524|gb|AEE29645.1| kunitz type trypsin and protease inhibitor domain-containing protein [Arabidopsis thaliana]</td><td>197</td><td>196</td><td>3.00E-80</td><td>99.5</td><td>74.1</td><td>83.2</td><td>kunitz type trypsin and protease inhibitor domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G17860.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:6149343-6149933 FORWARD LENGTH=196</td><td>197</td><td>196</td><td>1.00E-82</td><td>99.5</td><td>74.1</td><td>83.2</td></tr>
<tr><td>Rsa1.0_00533.1.g15574.t1</td><td>ref|XP_002892971.1| hypothetical protein ARALYDRAFT_889199 [Arabidopsis lyrata subsp. lyrata] gi|297338813|gb|EFH69230.1| hypothetical protein ARALYDRAFT_889199 [Arabidopsis lyrata subsp. lyrata]</td><td>575</td><td>573</td><td>0</td><td>99.7</td><td>89.4</td><td>94.1</td><td>hypothetical protein ARALYDRAFT_889199</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G17870.1 | Symbols: ATEGY3, EGY3 | ethylene-dependent gravitropism-deficient and yellow-green-like 3 | chr1:6150036-6152185 REVERSE LENGTH=573</td><td>575</td><td>573</td><td>0</td><td>99.7</td><td>89.4</td><td>93.4</td></tr>
<tr><td>Rsa1.0_00533.1.g15575.t1</td><td>gb|EOA37168.1| hypothetical protein CARUB_v10010502mg [Capsella rubella]</td><td>173</td><td>163</td><td>4.00E-76</td><td>94.2</td><td>83.2</td><td>87.3</td><td>hypothetical protein CARUB_v10010502mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G17880.1 | Symbols: BTF3, ATBTF3 | basic transcription factor 3 | chr1:6152572-6153425 REVERSE LENGTH=165</td><td>173</td><td>165</td><td>5.00E-71</td><td>95.4</td><td>75.1</td><td>78.6</td></tr>
<tr><td>Rsa1.0_00533.1.g15576.t1</td><td>ref|NP_564040.1| GDP-L-fucose synthase [Arabidopsis thaliana] gi|75174832|sp|Q9LMU0.1|FCL2_ARATH RecName: Full=Putative GDP-L-fucose synthase 2; AltName: Full=GDP-4-keto-6-deoxy-D-mannose-3, 5-epimerase-4-reductase 2; Short=AtGER2 gi|9665067|gb|AAF97269.1|AC034106_12 Strong similarity to GER1 from Arabidopsis thaliana gb|AF045286. ESTs gb|AI996642, gb|AV533951 come from this gene [Arabidopsis thaliana] gi|17380848|gb|AAL36236.1| putative GDP-L-fucose synthetase [Arabidopsis thaliana] gi|20465283|gb|AAM20005.1| putative GDP-L-fucose synthetase [Arabidopsis thaliana] gi|332191529|gb|AEE29650.1| putative GDP-L-fucose synthase 2 [Arabidopsis thaliana]</td><td>326</td><td>328</td><td>1.00E-180</td><td>100.6</td><td>92.6</td><td>96.9</td><td>GDP-L-fucose synthase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G17890.1 | Symbols: GER2 | NAD(P)-binding Rossmann-fold superfamily protein | chr1:6154478-6155596 REVERSE LENGTH=328</td><td>326</td><td>328</td><td>0</td><td>100.6</td><td>92.6</td><td>96.9</td></tr>
</table>

Rsa1.0_00533.1.g15577.t1	ref|NP_564041.2| homeobox-leucine zipper protein HDG12 [Arabidopsis thaliana] gi|75264044|sp|Q9LMT8.1|HDG12_ARATH RecName: Full=Homeobox-leucine zipper protein HDG12; AltName: Full=HD-ZIP protein HDG12; AltName: Full=Homeodomain GLABRA 2-like protein 12; AltName: Full=Homeodomain transcription factor HDG12; AltName: Full=Protein HOMEODOMAIN GLABROUS 12 gi|9665069|gb|AAF97271.1|AC034106_14 Strong similarity to meristem L1 layer homeobox protein (ATML1) from Arabidopsis thaliana gb|U37589 and contains Transposase PF|01527, Homeobox PF|00046, and START PF|01852 domains. EST gb|AI995645 comes from this gene [Arabidopsis thaliana] gi|225897942|dbj|BAH30303.1| hypothetical protein [Arabidopsis thaliana] gi|332191531|gb|AEE29652.1| homeobox-leucine zipper protein HDG12 [Arabidopsis thaliana]	686	687	0	100.1	83.2	90.2	homeobox-leucine zipper protein HDG12	gbpln	Arabidopsis thaliana	AT1G17920.1 | Symbols: HDG12 | homeodomain GLABROUS 12 | chr1:6162214-6165033 REVERSE LENGTH=687	686	687	0	100.1	83.2	90.2
Rsa1.0_00533.1.g15578.t1	gb|AAM62582.1| unknown [Arabidopsis thaliana]	477	478	0	100.2	91.8	96.0	unknown	gbpln	Arabidopsis thaliana	AT1G17930.1 | Symbols: | Aminotransferase-like, plant mobile domain family protein | chr1:6166638-6168432 REVERSE LENGTH=478	477	478	0	100.2	91.6	95.8
Rsa1.0_00533.1.g15579.t1	gb|EOA35199.1| hypothetical protein CARUB_v10020350mg [Capsella rubella] gi|482571012|gb|EOA35200.1| hypothetical protein CARUB_v10020350mg [Capsella rubella]	405	424	0	104.7	93.1	97.0	hypothetical protein CARUB_v10020350mg	gbpln	Capsella rubella	AT1G17940.1 | Symbols: | Endosomal targeting BRO1-like domain-containing protein | chr1:6169621-6172035 REVERSE LENGTH=405	405	405	0	100.0	94.1	97.0
Rsa1.0_00534.1.g15580.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	300	341	1.00E-37	113.7	39.7	54.7	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00534.1.g15581.t1	ref|XP_004136969.1| PREDICTED: polyadenylate-binding protein 2-like [Cucumis sativus] gi|449495630|ref|XP_004159899.1| PREDICTED: polyadenylate-binding protein 2-like [Cucumis sativus]	205	649	2.00E-25	316.6	31.2	38.0	PREDICTED: polyadenylate-binding protein 2-like	gbpln	Cucumis sativus	AT1G49760.2 | Symbols: PAB8 | poly(A) binding protein 8 | chr1:18416740-18419753 FORWARD LENGTH=671	205	671	1.00E-26	327.3	30.2	35.6
Rsa1.0_00534.1.g15582.t1	ref|XP_002891531.1| PAB8 binding protein 8 [Arabidopsis lyrata subsp. lyrata] gi|297337373|gb|EFH67790.1| PAB8 binding protein 8 [Arabidopsis lyrata subsp. lyrata]	121	669	1.00E-32	552.9	58.7	76.0	PAB8 binding protein 8	gbpln	Arabidopsis lyrata	AT1G49760.2 | Symbols: PAB8 | poly(A) binding protein 8 | chr1:18416740-18419753 FORWARD LENGTH=671	121	671	6.00E-35	554.5	58.7	75.2
Rsa1.0_00534.1.g15583.t1	ref|XP_002885307.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297331147|gb|EFH61566.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	459	494	0	107.6	83.7	88.9	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT3G19320.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:6696395-6698073 REVERSE LENGTH=493	459	493	0	107.4	72.5	75.6
Rsa1.0_00534.1.g15584.t1	ref|XP_002883171.1| phospholipase C [Arabidopsis lyrata subsp. lyrata] gi|297329011|gb|EFH59430.1| phospholipase C [Arabidopsis lyrata subsp. lyrata]	406	412	0	101.5	85.5	93.3	phospholipase C	gbpln	Arabidopsis lyrata	AT3G19310.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr3:6694260-6696193 FORWARD LENGTH=413	406	413	0	101.7	84.0	93.6
Rsa1.0_00534.1.g15585.t1	ref|XP_002885306.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331146|gb|EFH61565.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	657	663	0	100.9	81.1	85.8	kinase family protein	gbpln	Arabidopsis lyrata	AT3G19300.1 | Symbols: | Protein kinase superfamily protein | chr3:6690242-6693210 REVERSE LENGTH=663	657	663	0	100.9	81.0	86.5
Rsa1.0_00534.1.g15586.t2	ref|XP_002883170.1| hypothetical protein ARALYDRAFT_479444 [Arabidopsis lyrata subsp. lyrata] gi|297329010|gb|EFH59429.1| hypothetical protein ARALYDRAFT_479444 [Arabidopsis lyrata subsp. lyrata]	371	432	1.00E-133	116.4	82.7	87.1	hypothetical protein ARALYDRAFT_479444	gbpln	Arabidopsis lyrata	AT3G19290.1 | Symbols: ABF4, AREB2 | ABRE binding factor 4 | chr3:6687956-6689784 FORWARD LENGTH=431	371	431	1.00E-128	116.2	81.1	84.9
Rsa1.0_00534.1.g15587.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00534.1.g15588.t1	ref|NP_188559.1| glycoprotein 3-alpha-L-fucosyltransferase A [Arabidopsis thaliana] gi|17376382|sp|Q9LJK1.1|FUT11_ARATH RecName: Full=Glycoprotein 3-alpha-L-fucosyltransferase A; AltName: Full=Core alpha-(1,3)-fucosyltransferase; AltName: Full=Fuc-T C3; AltName: Full=FucT1; AltName: Full=FucTA; AltName: Full=Fucosyltransferase 11; Short=AtFUT11 gi|9294630|dbj|BAB02969.1| fucosyltransferase 3 (Fuct c3 protein) [Arabidopsis thaliana] gi|13992483|emb|CAC38048.1| alpha1,3-fucosyltransferase [Arabidopsis thaliana] gi|15722480|emb|CAC78979.1| core-alpha1,3fucosyltransferase 1 [Arabidopsis thaliana] gi|332642696|gb|AEE76217.1| glycoprotein 3-alpha-L-fucosyltransferase A [Arabidopsis thaliana]	496	501	0	101.0	80.2	88.7	glycoprotein 3-alpha-L-fucosyltransferase A	gbpln	Arabidopsis thaliana	AT3G19280.1 | Symbols: FUT11, ATFUT11, FUCT1, FUCTA | fucosyltransferase 11 | chr3:6681409-6683801 REVERSE LENGTH=501	496	501	0	101.0	80.2	88.7
Rsa1.0_00534.1.g15589.t1	ref|XP_002885304.1| CYP707A4 [Arabidopsis lyrata subsp. lyrata] gi|297331144|gb|EFH61563.1| CYP707A4 [Arabidopsis lyrata subsp. lyrata]	473	468	0	98.9	89.2	94.5	CYP707A4	gbpln	Arabidopsis lyrata	AT3G19270.1 | Symbols: CYP707A4 | cytochrome P450, family 707, subfamily A, polypeptide 4 | chr3:6673885-6676400 REVERSE LENGTH=468	473	468	0	98.9	87.9	93.9
Rsa1.0_00534.1.g15590.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15591.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15592.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15593.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15594.t4	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	914	190	4.00E-22	20.8	9.3	11.1	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15595.t1	gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]	150	198	4.00E-37	132.0	56.7	70.0	hypothetical protein 27.t00041	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15596.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	495	467	1.00E-103	94.3	39.2	53.1	hypothetical protein 31.t00031	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	495	566	3.00E-50	114.3	26.5	48.3
Rsa1.0_00535.1.g15597.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	490	467	3.00E-89	95.3	38.6	50.4	hypothetical protein 31.t00031	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	490	566	2.00E-57	115.5	31.8	52.4
Rsa1.0_00535.1.g15598.t2	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	1082	1231	0	113.8	48.2	63.7	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1082	575	1.00E-76	53.1	15.9	24.9
Rsa1.0_00535.1.g15599.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	266	1715	5.00E-20	644.7	23.7	35.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15600.t1	gb|AAF79797.1|AC020646_20 T32E20.30 [Arabidopsis thaliana]	148	1397	7.00E-18	943.9	29.1	37.8	T32E20.30	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15601.t16	dbj|BAB03186.1| En/Spm transposon protein-like [Arabidopsis thaliana]	671	1516	3.00E-72	225.9	24.4	35.3	En/Spm transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15602.t1	dbj|BAB03186.1| En/Spm transposon protein-like [Arabidopsis thaliana]	309	1516	1.00E-103	490.6	59.9	73.1	En/Spm transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15603.t7	gb|AAD23705.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	962	333	1.00E-17	34.6	6.5	10.1	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15604.t1	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	849	777	5.00E-69	91.5	21.8	33.6	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00535.1.g15605.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00536.1.g15606.t3	ref|XP_002894190.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340032|gb|EFH70449.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	241	193	4.00E-28	80.1	32.8	42.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G11362.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:3824630-3825184 REVERSE LENGTH=184	241	184	2.00E-28	76.3	27.4	41.1

Rsa1.0_00536.1.g15607.t1	ref|NP_564513.1| PPPDE putative thiol peptidase family protein [Arabidopsis thaliana] gi|42571793|ref|NP_973987.1| PPPDE putative thiol peptidase family protein [Arabidopsis thaliana] gi|19424079|gb|AAL87252.1| unknown protein [Arabidopsis thaliana] gi|21280795|gb|AAM45073.1| unknown protein [Arabidopsis thaliana] gi|110742177|dbj|BAE99016.1| hypothetical protein [Arabidopsis thaliana] gi|332194085|gb|AEE32206.1| PPPDE putative thiol peptidase family protein [Arabidopsis thaliana] gi|332194086|gb|AEE32207.1| PPPDE putative thiol peptidase family protein [Arabidopsis thaliana]	282	279	1.00E-135	98.9	86.5	91.1	PPPDE putative thiol peptidase family protein	gbpln	Arabidopsis thaliana	AT1G47740.2 | Symbols: | PPPDE putative thiol peptidase family protein | chr1:17567903-17569035 FORWARD LENGTH=279	282	279	1.00E-137	98.9	86.5	91.1
Rsa1.0_00536.1.g15608.t1	gb|AAM60843.1| unknown [Arabidopsis thaliana] gi|56368451|emb|CAD58677.1| putative PEX11-3 protein [Arabidopsis thaliana]	246	248	1.00E-101	100.8	75.6	91.5	unknown	gbpln	Arabidopsis thaliana	AT1G47750.1 | Symbols: PEX11A | peroxin 11A | chr1:17569388-17570134 REVERSE LENGTH=248	246	248	1.00E-104	100.8	75.6	91.5
Rsa1.0_00536.1.g15609.t1	gb|EOA30753.1| hypothetical protein CARUB_v10013896mg [Capsella rubella]	388	393	1.00E-112	101.3	58.8	70.9	hypothetical protein CARUB_v10013896mg	gbpln	Capsella rubella	AT1G47790.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:17600004-17601173 REVERSE LENGTH=389	388	389	1.00E-112	100.3	54.9	69.3
Rsa1.0_00536.1.g15610.t1	gb|EOA20860.1| hypothetical protein CARUB_v10001197mg [Capsella rubella]	377	375	1.00E-177	99.5	81.2	88.9	hypothetical protein CARUB_v10001197mg	gbpln	Capsella rubella	AT5G22100.1 | Symbols: | RNA cyclase family protein | chr5:7329015-7330718 FORWARD LENGTH=375	377	375	1.00E-172	99.5	78.8	89.1
Rsa1.0_00536.1.g15611.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00536.1.g15612.t2	ref|XP_003745280.1| PREDICTED: DNA topoisomerase 2-alpha-like [Metaseiulus occidentalis]	292	1411	3.00E-47	483.2	34.9	57.2	PREDICTED: DNA topoisomerase 2-alpha-like	gbinv	Metaseiulus occidentalis	AT3G23890.1 | Symbols: TOPII, ATTOPII | topoisomerase II | chr3:8624931-8631106 FORWARD LENGTH=1473	292	1473	3.00E-43	504.5	34.9	54.8
Rsa1.0_00536.1.g15613.t1	gb|AAF99784.1|AC012463_1 T2E6.3 [Arabidopsis thaliana] gi|110737661|dbj|BAF00770.1| hypothetical protein [Arabidopsis thaliana]	416	419	0	100.7	87.3	92.3	T2E6.3	gbpln	Arabidopsis thaliana	AT1G75710.1 | Symbols: | C2H2-like zinc finger protein | chr1:28428806-28431128 FORWARD LENGTH=462	416	462	1.00E-130	111.1	63.9	76.0
Rsa1.0_00537.1.g15614.t1	ref|NP_180137.3| embryo defective 2410 protein [Arabidopsis thaliana] gi|330252637|gb|AEC07731.1| embryo defective 2410 protein [Arabidopsis thaliana]	2118	2166	0	102.3	89.4	94.5	embryo defective 2410 protein	gbpln	Arabidopsis thaliana	AT2G25660.1 | Symbols: emb2410 | embryo defective 2410 | chr2:10916456-10927390 REVERSE LENGTH=2166	2118	2166	0	102.3	89.4	94.5
Rsa1.0_00537.1.g15615.t1	ref|XP_002878404.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324242|gb|EFH54663.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	802	791	0	98.6	65.3	75.6	C2 domain-containing protein	gbpln	Arabidopsis lyrata	AT3G61720.1 | Symbols: | Ca2+dependent plant phosphoribosyltransferase family protein | chr3:22843011-22845398 REVERSE LENGTH=795	802	795	0	99.1	62.7	75.2
Rsa1.0_00537.1.g15616.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	230	258	4.00E-70	112.2	59.1	72.2	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT5G41220.1 | Symbols: ATGSTT3, GST10C, GSTT3 | glutathione S-transferase THETA 3 | chr5:16494560-16496969 REVERSE LENGTH=590	230	590	8.00E-41	256.5	33.5	43.5
Rsa1.0_00537.1.g15617.t1	gb|ABD65112.1| hypothetical protein 31.t00014 [Brassica oleracea]	137	122	3.00E-30	89.1	52.6	66.4	hypothetical protein 31.t00014	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00537.1.g15618.t3	dbj|BAJ34331.1| unnamed protein product [Thellungiella halophila]	519	585	0	112.7	80.9	86.1	unnamed protein product	----	----	AT1G73730.1 | Symbols: EIL3, SLIM1, ATSLIM, AtEIL3 | ETHYLENE-INSENSITIVE3-like 3 | chr1:27730434-27732363 REVERSE LENGTH=567	519	567	0	109.2	75.1	81.3
Rsa1.0_00537.1.g15619.t1	ref|XP_002453601.1| hypothetical protein SORBIDRAFT_04g008820 [Sorghum bicolor] gi|241933432|gb|EES06577.1| hypothetical protein SORBIDRAFT_04g008820 [Sorghum bicolor]	247	266	1.00E-38	107.7	37.7	48.2	hypothetical protein SORBIDRAFT_04g008820	gbpln	Sorghum bicolor	AT5G31412.1 | Symbols: | hAT transposon superfamily protein | chr5:11541463-11543768 REVERSE LENGTH=433	247	433	1.00E-19	175.3	16.2	21.5
Rsa1.0_00537.1.g15620.t1	ref|XP_002868325.1| hypothetical protein ARALYDRAFT_915512 [Arabidopsis lyrata subsp. lyrata] gi|297314161|gb|EFH44584.1| hypothetical protein ARALYDRAFT_915512 [Arabidopsis lyrata subsp. lyrata]	475	366	1.00E-106	77.1	46.7	55.4	hypothetical protein ARALYDRAFT_915512	gbpln	Arabidopsis lyrata	AT4G36840.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:17352166-17352882 FORWARD LENGTH=238	475	238	2.00E-47	50.1	24.2	29.7
Rsa1.0_00537.1.g15621.t1	dbj|BAJ33800.1| unnamed protein product [Thellungiella halophila]	127	631	9.00E-57	496.9	84.3	90.6	unnamed protein product	----	----	AT1G73680.1 | Symbols: ALPHA DOX2 | alpha dioxygenase | chr1:27704221-27707417 REVERSE LENGTH=631	127	631	4.00E-59	496.9	82.7	89.8

Rsa1.0_00537.1.g15622.t1	ref|XP_002889006.1| hypothetical protein ARALYDRAFT_476644 [Arabidopsis lyrata subsp. lyrata] gi|297334847|gb|EFH65265.1| hypothetical protein ARALYDRAFT_476644 [Arabidopsis lyrata subsp. lyrata]	169	244	1.00E-57	144.4	67.5	79.3	hypothetical protein ARALYDRAFT_476644	gbpln	Arabidopsis lyrata	AT1G75060.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G19330.2); Has 104 Blast hits to 104 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:28181481-28183285 REVERSE LENGTH=241	169	241	4.00E-57	142.6	65.1	75.1
Rsa1.0_00537.1.g15623.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00537.1.g15624.t1	ref|NP_180117.4| receptor like protein 21 [Arabidopsis thaliana] gi|330252611|gb|AEC07705.1| receptor like protein 21 [Arabidopsis thaliana]	714	935	0	131.0	61.9	72.7	receptor like protein 21	gbpln	Arabidopsis thaliana	AT2G25470.1 | Symbols: AtRLP21, RLP21 | receptor like protein 21 | chr2:10838420-10841881 FORWARD LENGTH=935	714	935	0	131.0	61.9	72.7
Rsa1.0_00537.1.g15625.t1	gb|EOA26736.1| hypothetical protein CARUB_v10022822mg [Capsella rubella]	646	628	0	97.2	80.7	89.0	hypothetical protein CARUB_v10022822mg	gbpln	Capsella rubella	AT2G25490.1 | Symbols: EBF1, FBL6 | EIN3-binding F box protein 1 | chr2:10848018-10850275 REVERSE LENGTH=628	646	628	0	97.2	80.0	89.0
Rsa1.0_00537.1.g15626.t1	gb|EOA26520.1| hypothetical protein CARUB_v10022573mg [Capsella rubella]	916	974	0	106.3	62.9	75.4	hypothetical protein CARUB_v10022573mg	gbpln	Capsella rubella	AT2G25470.1 | Symbols: AtRLP21, RLP21 | receptor like protein 21 | chr2:10838420-10841881 FORWARD LENGTH=935	916	935	0	102.1	60.9	73.9
Rsa1.0_00537.1.g15627.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00537.1.g15628.t1	gb|ACB59217.1| ENTH [Brassica oleracea]	637	646	0	101.4	93.7	94.5	ENTH	gbpln	Brassica oleracea	AT2G25430.1 | Symbols: | epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related | chr2:10822716-10824677 FORWARD LENGTH=653	637	653	0	102.5	92.0	94.2
Rsa1.0_00537.1.g15629.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00538.1.g15630.t1	gb|EOA19925.1| hypothetical protein CARUB_v10000175mg [Capsella rubella]	553	896	0	162.0	82.8	89.3	hypothetical protein CARUB_v10000175mg	gbpln	Capsella rubella	AT5G06220.2 | Symbols: | LETM1-like protein | chr5:1880049-1885366 FORWARD LENGTH=909	553	909	0	164.4	79.7	87.9
Rsa1.0_00538.1.g15631.t3	ref|XP_002871200.1| sucrose-proton symporter 6 [Arabidopsis lyrata subsp. lyrata] gi|297317037|gb|EFH47459.1| sucrose-proton symporter 6 [Arabidopsis lyrata subsp. lyrata]	494	492	0	99.6	80.6	90.9	sucrose-proton symporter 6	gbpln	Arabidopsis lyrata	AT1G66570.1 | Symbols: ATSUC7, SUC7 | sucrose-proton symporter 7 | chr1:24835309-24837242 REVERSE LENGTH=491	494	491	0	99.4	79.1	90.5
Rsa1.0_00538.1.g15632.t1	gb|AAA50234.1| nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707, partial [Arabidopsis thaliana]	128	382	1.00E-10	298.4	32.0	36.7	nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707, partial	gbpln	Arabidopsis thaliana	AT4G26110.1 | Symbols: NAP1;1, ATNAP1;1 | nucleosome assembly protein1;1 | chr4:13232712-13235502 FORWARD LENGTH=372	128	372	3.00E-13	290.6	32.0	36.7
Rsa1.0_00538.1.g15633.t3	gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	86	150	9.00E-43	174.4	98.8	98.8	cytoplasmic ribosomal protein S14	gbpln	Brassica napus	AT3G11510.1 | Symbols: | Ribosomal protein S11 family protein | chr3:3623757-3624866 REVERSE LENGTH=150	86	150	3.00E-43	174.4	93.0	97.7
Rsa1.0_00538.1.g15634.t1	gb|EOA36691.1| hypothetical protein CARUB_v10012096mg [Capsella rubella]	329	327	1.00E-160	99.4	80.5	88.4	hypothetical protein CARUB_v10012096mg	gbpln	Capsella rubella	AT5G43690.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273-17547268 FORWARD LENGTH=331	329	331	1.00E-155	100.6	78.4	86.6
Rsa1.0_00538.1.g15635.t1	gb|EOA36691.1| hypothetical protein CARUB_v10012096mg [Capsella rubella]	331	327	1.00E-128	98.8	66.5	80.1	hypothetical protein CARUB_v10012096mg	gbpln	Capsella rubella	AT5G43690.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273-17547268 FORWARD LENGTH=331	331	331	1.00E-125	100.0	64.4	78.5
Rsa1.0_00538.1.g15636.t2	ref|NP_001190236.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|334187454|ref|NP_001190237.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332003588|gb|AED90971.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332003589|gb|AED90972.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	1074	1052	0	98.0	85.1	89.3	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G06120.2 | Symbols: | ARM repeat superfamily protein | chr5:1845309-1852601 FORWARD LENGTH=1052	1074	1052	0	98.0	85.1	89.3
Rsa1.0_00538.1.g15637.t1	ref|NP_196227.1| glycerol-3-phosphate acyltransferase 7 [Arabidopsis thaliana] gi|83288236|sp|Q9LHS7.1|GPAT7_ARATH RecName: Full=Glycerol-3-phosphate acyltransferase 7; Short=AtGPAT7 gi|8978345|dbj|BAA98198.1| unnamed protein product [Arabidopsis thaliana] gi|332003580|gb|AED90963.1| glycerol-3-phosphate acyltransferase 7 [Arabidopsis thaliana]	614	500	0	81.4	71.5	75.6	glycerol-3-phosphate acyltransferase 7	gbpln	Arabidopsis thaliana	AT5G06090.1 | Symbols: ATGPAT7, GPAT7 | glycerol-3-phosphate acyltransferase 7 | chr5:1835106-1836722 FORWARD LENGTH=500	614	500	0	81.4	71.5	75.6

<table>
<tr><td>Rsa1.0_00538.1.g15638.t1</td><td>ref|XP_002873236.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319073|gb|EFH49495.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>185</td><td>182</td><td>4.00E-82</td><td>98.4</td><td>79.5</td><td>87.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G06080.1 | Symbols: LBD33 | LOB domain-containing protein 33 | chr5:1830796-1831427 REVERSE LENGTH=177</td><td>185</td><td>177</td><td>6.00E-79</td><td>95.7</td><td>75.1</td><td>82.2</td></tr>
<tr><td>Rsa1.0_00538.1.g15639.t1</td><td>ref|NP_568161.1| putative transcriptional regulator RABBIT EARS [Arabidopsis thaliana] gi|41688606|sp|Q9LHS9.2|RBE_ARATH RecName: Full=Probable transcriptional regulator RABBIT EARS gi|37514920|dbj|BAC98433.1| one finger-type zinc finger protein for RABBIT EARS [Arabidopsis thaliana] gi|94442519|gb|ABF19047.1| At5g06070 [Arabidopsis thaliana] gi|332003578|gb|AED90961.1| putative transcriptional regulator RABBIT EARS [Arabidopsis thaliana]</td><td>239</td><td>226</td><td>9.00E-93</td><td>94.6</td><td>72.4</td><td>80.8</td><td>putative transcriptional regulator RABBIT EARS</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06070.1 | Symbols: RBE, RAB | C2H2 and C2HC zinc fingers superfamily protein | chr5:1828426-1829106 REVERSE LENGTH=226</td><td>239</td><td>226</td><td>3.00E-95</td><td>94.6</td><td>72.4</td><td>80.8</td></tr>
<tr><td>Rsa1.0_00538.1.g15640.t1</td><td>ref|XP_002873234.1| hypothetical protein ARALYDRAFT_487407 [Arabidopsis lyrata subsp. lyrata] gi|297319071|gb|EFH49493.1| hypothetical protein ARALYDRAFT_487407 [Arabidopsis lyrata subsp. lyrata]</td><td>262</td><td>262</td><td>1.00E-127</td><td>100.0</td><td>83.6</td><td>92.0</td><td>hypothetical protein ARALYDRAFT_487407</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G06060.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:1824066-1825833 REVERSE LENGTH=264</td><td>262</td><td>264</td><td>1.00E-130</td><td>100.8</td><td>83.2</td><td>92.4</td></tr>
<tr><td>Rsa1.0_00538.1.g15641.t1</td><td>ref|NP_196224.1| putative methyltransferase PMT12 [Arabidopsis thaliana] gi|75262411|sp|Q9FG39.1|PMTC_ARATH RecName: Full=Probable methyltransferase PMT12 gi|10257485|dbj|BAB10206.1| ankyrin-like protein [Arabidopsis thaliana] gi|51536506|gb|AAU05491.1| At5g06050 [Arabidopsis thaliana] gi|58652086|gb|AAW80868.1| At5g06050 [Arabidopsis thaliana] gi|110740549|dbj|BAE98380.1| ankyrin like protein [Arabidopsis thaliana] gi|332003576|gb|AED90959.1| putative methyltransferase PMT12 [Arabidopsis thaliana]</td><td>476</td><td>682</td><td>0</td><td>143.3</td><td>79.2</td><td>81.9</td><td>putative methyltransferase PMT12</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06050.1 | Symbols: | Putative methyltransferase family protein | chr5:1820196-1823572 FORWARD LENGTH=682</td><td>476</td><td>682</td><td>0</td><td>143.3</td><td>79.2</td><td>81.9</td></tr>
<tr><td>Rsa1.0_00538.1.g15642.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00538.1.g15643.t1</td><td>ref|NP_196224.1| putative methyltransferase PMT12 [Arabidopsis thaliana] gi|75262411|sp|Q9FG39.1|PMTC_ARATH RecName: Full=Probable methyltransferase PMT12 gi|10257485|dbj|BAB10206.1| ankyrin-like protein [Arabidopsis thaliana] gi|51536506|gb|AAU05491.1| At5g06050 [Arabidopsis thaliana] gi|58652086|gb|AAW80868.1| At5g06050 [Arabidopsis thaliana] gi|110740549|dbj|BAE98380.1| ankyrin like protein [Arabidopsis thaliana] gi|332003576|gb|AED90959.1| putative methyltransferase PMT12 [Arabidopsis thaliana]</td><td>307</td><td>682</td><td>4.00E-99</td><td>222.1</td><td>62.2</td><td>70.4</td><td>putative methyltransferase PMT12</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06050.1 | Symbols: | Putative methyltransferase family protein | chr5:1820196-1823572 FORWARD LENGTH=682</td><td>307</td><td>682</td><td>1.00E-102</td><td>222.1</td><td>62.2</td><td>70.4</td></tr>
<tr><td>Rsa1.0_00538.1.g15644.t1</td><td>ref|XP_002873233.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297319070|gb|EFH49492.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]</td><td>262</td><td>259</td><td>1.00E-107</td><td>98.9</td><td>78.6</td><td>88.2</td><td>mitochondrial glycoprotein family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05990.1 | Symbols: | Mitochondrial glycoprotein family protein | chr5:1806911-1807895 REVERSE LENGTH=259</td><td>262</td><td>259</td><td>1.00E-107</td><td>98.9</td><td>77.9</td><td>87.0</td></tr>
<tr><td>Rsa1.0_00538.1.g15645.t10</td><td>gb|EOA20243.1| hypothetical protein CARUB_v10000544mg [Capsella rubella]</td><td>583</td><td>587</td><td>0</td><td>100.7</td><td>88.2</td><td>92.1</td><td>hypothetical protein CARUB_v10000544mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G05980.1 | Symbols: ATDFB, DFB, FPGS1 | DHFS-FPGS homolog B | chr5:1799738-1804441 REVERSE LENGTH=571</td><td>583</td><td>571</td><td>0</td><td>97.9</td><td>86.6</td><td>89.9</td></tr>
<tr><td>Rsa1.0_00538.1.g15646.t1</td><td>ref|XP_002871192.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297317029|gb|EFH47451.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>750</td><td>780</td><td>0</td><td>104.0</td><td>81.9</td><td>89.2</td><td>transducin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05970.2 | Symbols: NEDD1 | Transducin/WD40 repeat-like superfamily protein | chr5:1795464-1799313 FORWARD LENGTH=782</td><td>750</td><td>782</td><td>0</td><td>104.3</td><td>80.7</td><td>88.1</td></tr>
<tr><td>Rsa1.0_00539.1.g15647.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00539.1.g15648.t1</td><td>dbj|BAJ34392.1| unnamed protein product [Thellungiella halophila]</td><td>350</td><td>350</td><td>1.00E-166</td><td>100.0</td><td>83.4</td><td>89.7</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT2G38380.1 | Symbols: | Peroxidase superfamily protein | chr2:16076443-16078314 FORWARD LENGTH=349</td><td>350</td><td>349</td><td>1.00E-167</td><td>99.7</td><td>81.7</td><td>88.6</td></tr>
</table>

Rsa1.0_00539.1.g15649.t1	dbj|BAJ34392.1| unnamed protein product [Thellungiella halophila]	348	350	1.00E-157	100.6	80.7	88.2	unnamed protein product	----	----	AT2G38380.1 | Symbols: | Peroxidase superfamily protein | chr2:16076443-16078314 FORWARD LENGTH=349	348	349	1.00E-155	100.3	78.2	85.1
Rsa1.0_00539.1.g15650.t1	dbj|BAJ33985.1| unnamed protein product [Thellungiella halophila]	645	478	0	74.1	69.9	72.4	unnamed protein product	----	----	AT2G38400.1 | Symbols: AGT3 | alanine:glyoxylate aminotransferase 3 | chr2:16083779-16085974 FORWARD LENGTH=477	645	477	0	74.0	67.9	71.0
Rsa1.0_00539.1.g15651.t1	ref|XP_002881597.1| hypothetical protein ARALYDRAFT_345626 [Arabidopsis lyrata subsp. lyrata] gi|297327436|gb|EFH57856.1| hypothetical protein ARALYDRAFT_345626 [Arabidopsis lyrata subsp. lyrata]	373	366	2.33E-156	98.1	71.6	81.0	hypothetical protein ARALYDRAFT_345626	gbpln	Arabidopsis lyrata	AT2G38430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54310.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16092950-16094810 REVERSE LENGTH=393	373	393	1.00E-148	105.4	71.6	82.3
Rsa1.0_00539.1.g15652.t1	emb|CAC08339.1| katanin p80 subunit-like protein [Arabidopsis thaliana]	235	823	5.00E-20	350.2	23.4	26.0	katanin p80 subunit-like protein	gbpln	Arabidopsis thaliana	AT5G08390.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:2701448-2706910 FORWARD LENGTH=839	235	839	2.00E-22	357.0	23.4	26.0
Rsa1.0_00539.1.g15653.t1	gb|AAC28761.1| hypothetical protein [Arabidopsis thaliana]	361	399	1.00E-116	110.5	62.9	78.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G38430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54310.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16092950-16094810 REVERSE LENGTH=393	361	393	1.00E-116	108.9	61.8	77.3
Rsa1.0_00539.1.g15654.t1	gb|AAC28761.1| hypothetical protein [Arabidopsis thaliana]	401	399	1.00E-133	99.5	61.3	74.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G38430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54310.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16092950-16094810 REVERSE LENGTH=393	401	393	1.00E-133	98.0	60.1	73.8
Rsa1.0_00539.1.g15655.t1	gb|EOA28106.1| hypothetical protein CARUB_v10024290mg [Capsella rubella]	141	137	1.00E-53	97.2	77.3	86.5	hypothetical protein CARUB_v10024290mg	gbpln	Capsella rubella	AT2G38450.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Sel1-like (InterPro:IPR006597); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G05360.1); Has 88 Blast hits to 88 proteins in 25 species: Archae - 0; Bacteria - 16; Metazoa - 0; Fungi - 0; Plants - 70; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:16102016-16102683 FORWARD LENGTH=138	141	138	3.00E-50	97.9	75.2	85.8
Rsa1.0_00539.1.g15656.t1	gb|ACI14397.1| WRKY33-1 transcription factor [Brassica napus]	505	490	0	97.0	88.5	90.9	WRKY33-1 transcription factor	gbpln	Brassica napus	AT2G38470.1 | Symbols: WRKY33, ATWRKY33 | WRKY DNA-binding protein 33 | chr2:16108476-16110539 FORWARD LENGTH=519	505	519	0	102.8	81.8	88.9
Rsa1.0_00539.1.g15657.t1	ref|XP_002881599.1| hypothetical protein ARALYDRAFT_321547 [Arabidopsis lyrata subsp. lyrata] gi|391358735|sp|D7LBN4.1|CSPLH_ARALL RecName: Full=CASP-like protein ARALYDRAFT_321547 gi|297327438|gb|EFH57858.1| hypothetical protein ARALYDRAFT_321547 [Arabidopsis lyrata subsp. lyrata]	187	188	1.00E-79	100.5	80.2	88.2	hypothetical protein ARALYDRAFT_321547	gbpln	Arabidopsis lyrata	AT2G38480.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr2:16110960-16111694 REVERSE LENGTH=188	187	188	4.00E-80	100.5	78.1	88.2
Rsa1.0_00539.1.g15658.t1	gb|EOA27166.1| hypothetical protein CARUB_v10023265mg [Capsella rubella]	430	428	0	99.5	86.5	92.3	hypothetical protein CARUB_v10023265mg	gbpln	Capsella rubella	AT2G38490.1 | Symbols: CIPK22, SnRK3.19 | CBL-interacting protein kinase 22 | chr2:16113909-16115276 REVERSE LENGTH=455	430	455	0	105.8	87.2	94.0
Rsa1.0_00539.1.g15659.t1	gb|EOA27392.1| hypothetical protein CARUB_v10023522mg [Capsella rubella]	403	353	1.00E-164	87.6	78.2	82.1	hypothetical protein CARUB_v10023522mg	gbpln	Capsella rubella	AT2G38500.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr2:16117610-16119041 REVERSE LENGTH=356	403	356	1.00E-164	88.3	77.7	80.9
Rsa1.0_00539.1.g15660.t1	dbj|BAJ34462.1| unnamed protein product [Thellungiella halophila]	390	381	1.00E-176	97.7	80.8	87.9	unnamed protein product	----	----	AT2G38560.1 | Symbols: TFIIS | transcript elongation factor IIS | chr2:16134802-16136319 FORWARD LENGTH=378	390	378	1.00E-167	96.9	78.2	86.4
Rsa1.0_00539.1.g15661.t1	gb|EOA27387.1| hypothetical protein CARUB_v10023517mg [Capsella rubella]	341	354	1.00E-104	103.8	69.8	80.1	hypothetical protein CARUB_v10023517mg	gbpln	Capsella rubella	AT2G38570.1 | Symbols: | CONTAINS InterPro DOMAIN/s: PRC-barrel-like (InterPro:IPR011033); Has 300 Blast hits to 300 proteins in 81 species: Archae - 0; Bacteria - 135; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 128 (source: NCBI BLink). | chr2:16136854-16138417 REVERSE LENGTH=328	341	328	1.00E-101	96.2	66.3	76.2

Rsa1.0_00539.1.g15662.t1	gb|EOA29214.1| hypothetical protein CARUB_v10025488mg [Capsella rubella]	509	772	0	151.7	69.4	79.0	hypothetical protein CARUB_v10025488mg	gbpln	Capsella rubella	AT2G38580.1 | Symbols: | Mitochondrial ATP synthase D chain−related protein | chr2:16138838−16142371 FORWARD LENGTH=482	509	482	1.00E−170	94.7	65.4	74.5
Rsa1.0_00540.1.g15663.t1	ref|NP_189436.2| exonuclease−like protein [Arabidopsis thaliana] gi|193211503|gb|ACF16171.1| At3g27970 [Arabidopsis thaliana] gi|225898687|dbj|BAH30474.1| hypothetical protein [Arabidopsis thaliana] gi|332643867|gb|AEE77388.1| exonuclease−like protein [Arabidopsis thaliana]	351	357	0	101.7	92.0	96.3	exonuclease−like protein	gbpln	Arabidopsis thaliana	AT3G27970.1 | Symbols: | Exonuclease family protein | chr3:10389609−10391544 FORWARD LENGTH=357	351	357	0	101.7	92.0	96.3
Rsa1.0_00540.1.g15664.t1	gb|AAG50751.1|AC079733_19 polyprotein, putative [Arabidopsis thaliana]	1478	1468	0	99.3	57.6	72.0	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1478	1262	1.00E−141	85.4	16.4	24.2
Rsa1.0_00540.1.g15665.t1	dbj|BAA97287.1| retroelement pol polyprotein−like [Arabidopsis thaliana]	1261	1491	0	118.2	63.1	77.2	retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1261	1262	1.00E−106	100.1	16.7	24.1
Rsa1.0_00540.1.g15666.t1	ref|XP_002877087.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297322925|gb|EFH53346.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	213	252	1.00E−100	118.3	86.4	93.9	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT3G28007.1 | Symbols: SWEET4, AtSWEET4 | Nodulin MtN3 family protein | chr3:10408243−10409633 REVERSE LENGTH=251	213	251	1.00E−100	117.8	85.4	91.5
Rsa1.0_00540.1.g15667.t1	ref|NP_566831.1| EamA domain−containing protein [Arabidopsis thaliana] gi|75166353|sp|Q94JU2.1|WTR18_ARATH RecName: Full=WAT1−related protein At3g28050 gi|13937165|gb|AAK50076.1|AF372936_1 AT3g28050/MMG15_6 [Arabidopsis thaliana] gi|22137010|gb|AAM91350.1| At3g28050/MMG15_6 [Arabidopsis thaliana] gi|332643874|gb|AEE77395.1| nodulin MtN21−like transporter UMAMIT41 [Arabidopsis thaliana]	367	367	0	100.0	92.6	96.7	EamA domain−containing protein	gbpln	Arabidopsis thaliana	AT3G28050.1 | Symbols: | nodulin MtN21 /EamA−like transporter family protein | chr3:10442984−10445216 FORWARD LENGTH=367	367	367	0	100.0	92.6	96.7
Rsa1.0_00540.1.g15668.t1	ref|XP_002875424.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321262|gb|EFH51683.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	358	357	1.00E−171	99.7	84.6	92.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G28100.1 | Symbols: | nodulin MtN21 /EamA−like transporter family protein | chr3:10456151−10460813 FORWARD LENGTH=353	358	353	1.00E−158	98.6	83.2	91.3
Rsa1.0_00540.1.g15669.t1	gb|EOA23588.1| hypothetical protein CARUB_v10016783mg [Capsella rubella]	675	673	0	99.7	93.9	97.3	hypothetical protein CARUB_v10016783mg	gbpln	Capsella rubella	AT3G28180.1 | Symbols: ATCSLC04, CSLC04, ATCSLC4, CSLC4 | Cellulose−synthase−like C4 | chr3:10506110−10509067 FORWARD LENGTH=673	675	673	0	99.7	93.2	97.0
Rsa1.0_00540.1.g15670.t1	dbj|BAJ34116.1| unnamed protein product [Thellungiella halophila]	322	323	1.00E−156	100.3	82.6	87.9	unnamed protein product	−−−−	−−−−	AT3G28200.1 | Symbols: | Peroxidase superfamily protein | chr3:10518082−10519032 FORWARD LENGTH=316	322	316	1.00E−157	98.1	79.8	87.9
Rsa1.0_00540.1.g15671.t1	ref|NP_001118726.2| F−box family protein [Arabidopsis thaliana] gi|332643898|gb|AEE77419.1| F−box family protein [Arabidopsis thaliana]	395	391	9.00E−80	99.0	43.8	60.3	F−box family protein	gbpln	Arabidopsis thaliana	AT3G28223.1 | Symbols: | F−box family protein | chr3:10527669−10528921 REVERSE LENGTH=391	395	391	2.00E−82	99.0	43.8	60.3
Rsa1.0_00540.1.g15672.t1	dbj|BAB02625.1| unnamed protein product [Arabidopsis thaliana]	415	420	1.00E−139	101.2	61.0	73.5	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G28330.1 | Symbols: | F−box family protein−related | chr3:10586566−10587712 REVERSE LENGTH=349	415	349	1.00E−117	84.1	50.8	61.0
Rsa1.0_00540.1.g15673.t1	ref|NP_189483.1| Putative membrane lipoprotein [Arabidopsis thaliana] gi|9294578|dbj|BAB02859.1| unnamed protein product [Arabidopsis thaliana] gi|38454112|gb|AAR20750.1| At3g28420 [Arabidopsis thaliana] gi|332643922|gb|AEE77443.1| Putative membrane lipoprotein [Arabidopsis thaliana]	200	216	5.00E−73	108.0	83.0	88.0	Putative membrane lipoprotein	gbpln	Arabidopsis thaliana	AT3G28420.1 | Symbols: | Putative membrane lipoprotein | chr3:10654674−10655324 REVERSE LENGTH=216	200	216	2.00E−75	108.0	83.0	88.0
Rsa1.0_00540.1.g15674.t1	ref|NP_189486.1| leucine−rich repeat protein kinase−like protein [Arabidopsis thaliana] gi|9294580|dbj|BAB02861.1| receptor−like protein kinase−like protein [Arabidopsis thaliana] gi|26449808|dbj|BAC42027.1| putative receptor kinase [Arabidopsis thaliana] gi|224589583|gb|ACN59325.1| leucine−rich repeat receptor−like protein kinase [Arabidopsis thaliana] gi|332643925|gb|AEE77446.1| leucine−rich repeat protein kinase−like protein [Arabidopsis thaliana]	614	605	0	98.5	80.1	88.6	leucine−rich repeat protein kinase−like protein	gbpln	Arabidopsis thaliana	AT3G28450.1 | Symbols: | Leucine−rich repeat protein kinase family protein | chr3:10667359−10669176 FORWARD LENGTH=605	614	605	0	98.5	80.1	88.6

Rsa1.0_00540.1.g15675.t1	gb|EOA25615.1| hypothetical protein CARUB_v10018963mg [Capsella rubella]	217	81	3.00E-30	37.3	31.3	33.6	hypothetical protein CARUB_v10018963mg	gbpln	Capsella rubella	AT3G28455.1 | Symbols: CLE25 | CLAVATA3/ESR-RELATED 25 | chr3:10670220-10670931 REVERSE LENGTH=81	217	81	2.00E-32	37.3	30.9	33.2
Rsa1.0_00540.1.g15676.t1	ref|XP_002862551.1| hypothetical protein ARALYDRAFT_497404 [Arabidopsis lyrata subsp. lyrata] gi|297815144|ref|XP_002875455.1| hypothetical protein ARALYDRAFT_484625 [Arabidopsis lyrata subsp. lyrata] gi|297308140|gb|EFH38809.1| hypothetical protein ARALYDRAFT_497404 [Arabidopsis lyrata subsp. lyrata] gi|297321293|gb|EFH51714.1| hypothetical protein ARALYDRAFT_484625 [Arabidopsis lyrata subsp. lyrata]	114	116	4.00E-29	101.8	70.2	77.2	hypothetical protein ARALYDRAFT_497404	gbpln	Arabidopsis lyrata	AT3G28500.1 | Symbols: | 60S acidic ribosomal protein family | chr3:10682204-10682551 FORWARD LENGTH=115	114	115	5.00E-31	100.9	71.1	77.2
Rsa1.0_00541.1.g15677.t1	ref|NP_187937.2| varicose-related protein [Arabidopsis thaliana] gi|75335477|sp|Q9LTT9.1|VCR_ARATH RecName: Full=Varicose-related protein gi|9294535|dbj|BAB02798.1| unnamed protein product [Arabidopsis thaliana] gi|332641808|gb|AEE75329.1| varicose-related protein [Arabidopsis thaliana]	331	1340	1.00E-141	404.8	78.2	86.4	varicose-related protein	gbpln	Arabidopsis thaliana	AT3G13290.1 | Symbols: VCR | varicose-related | chr3:4297529-4303113 FORWARD LENGTH=1340	331	1340	1.00E-144	404.8	78.2	86.4
Rsa1.0_00541.1.g15678.t1	gb|EOA31822.1| hypothetical protein CARUB_v10015044mg [Capsella rubella]	69	68	2.00E-23	98.6	81.2	87.0	hypothetical protein CARUB_v10015044mg	gbpln	Capsella rubella	AT3G13275.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 29 Blast hits to 29 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4289425-4289634 REVERSE LENGTH=69	69	69	2.00E-19	100.0	84.1	89.9
Rsa1.0_00541.1.g15679.t1	gb|EOA32619.1| hypothetical protein CARUB_v10015913mg [Capsella rubella]	112	112	1.00E-31	100.0	73.2	79.5	hypothetical protein CARUB_v10015913mg	gbpln	Capsella rubella	AT3G13227.1 | Symbols: | serine-rich protein-related | chr3:4258028-4258363 FORWARD LENGTH=111	112	111	2.00E-30	99.1	71.4	77.7
Rsa1.0_00541.1.g15680.t1	ref|XP_004294923.1| PREDICTED: ABC transporter G family member 26-like [Fragaria vesca subsp. vesca]	194	688	3.00E-26	354.6	33.5	47.4	PREDICTED: ABC transporter G family member 26-like	gbpln	Fragaria vesca	AT3G13220.1 | Symbols: WBC27, ABCG26 | ABC-2 type transporter family protein | chr3:4247968-4250703 REVERSE LENGTH=685	194	685	1.00E-28	353.1	40.7	47.9
Rsa1.0_00541.1.g15681.t1	gb|EOA29633.1| hypothetical protein CARUB_v10014543mg [Capsella rubella]	232	230	1.00E-107	99.1	95.3	98.7	hypothetical protein CARUB_v10014543mg	gbpln	Capsella rubella	AT3G13200.1 | Symbols: EMB2769 | Cwf15 / Cwc15 cell cycle control family protein | chr3:4242239-4243976 FORWARD LENGTH=230	232	230	1.00E-99	99.1	94.4	97.8
Rsa1.0_00541.1.g15682.t1	ref|NP_187925.1| uncharacterized protein [Arabidopsis thaliana] gi|42572411|ref|NP_974301.1| uncharacterized protein [Arabidopsis thaliana] gi|145332373|ref|NP_001078143.1| uncharacterized protein [Arabidopsis thaliana] gi|75273724|sp|Q9LK53.1|Y3319_ARATH RecName: Full=WEB family protein At3g13190 gi|10172607|dbj|BAB01411.1| unnamed protein product [Arabidopsis thaliana] gi|22531008|gb|AAM97008.1| unknown protein [Arabidopsis thaliana] gi|23197916|gb|AAN15485.1| unknown protein [Arabidopsis thaliana] gi|62320648|dbj|BAD95315.1| hypothetical protein [Arabidopsis thaliana] gi|332641786|gb|AEE75307.1| uncharacterized protein AT3G13190 [Arabidopsis thaliana] gi|332641787|gb|AEE75308.1| uncharacterized protein AT3G13190 [Arabidopsis thaliana] gi|332641788|gb|AEE75309.1| uncharacterized protein AT3G13190 [Arabidopsis thaliana]	326	316	2.00E-90	96.9	66.0	76.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G13190.3 | Symbols: | Plant protein of unknown function (DUF827) | chr3:4240751-4241804 FORWARD LENGTH=316	326	316	5.00E-93	96.9	66.0	76.7

Rsa1.0_00541.1.g15683.t1	ref|XP_002884950.1| hypothetical protein ARALYDRAFT_478694 [Arabidopsis lyrata subsp. lyrata] gi|297330790|gb|EFH61209.1| hypothetical protein ARALYDRAFT_478694 [Arabidopsis lyrata subsp. lyrata]	105	106	4.00E-44	101.0	88.6	94.3	hypothetical protein ARALYDRAFT_478694	gbpln	Arabidopsis lyrata	AT3G13175.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G16400.1); Has 29 Blast hits to 29 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4235260-4235580 REVERSE LENGTH=106	105	106	3.00E-45	101.0	86.7	91.4
Rsa1.0_00541.1.g15684.t1	ref|NP_566445.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75273726|sp|Q9LK57.1|PP226_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g13160, mitochondrial; Flags: Precursor gi|10172603|dbj|BAB01407.1| unnamed protein product [Arabidopsis thaliana] gi|22531265|gb|AAM97136.1| expressed protein [Arabidopsis thaliana] gi|27311983|gb|AAO00957.1| expressed protein [Arabidopsis thaliana] gi|332641782|gb|AEE75303.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	235	394	1.00E-50	167.7	45.1	55.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G13160.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:4229994-4231178 REVERSE LENGTH=394	235	394	4.00E-53	167.7	45.1	55.3
Rsa1.0_00541.1.g15685.t1	emb|CAB75932.1| putative protein [Arabidopsis thaliana]	1354	1339	0	98.9	52.4	70.8	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1354	1262	1.00E-108	93.2	14.9	23.0
Rsa1.0_00541.1.g15686.t1	ref|NP_187921.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|10172601|dbj|BAB01405.1| unnamed protein product [Arabidopsis thaliana] gi|67633630|gb|AAY78739.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|332641780|gb|AEE75301.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	183	183	1.00E-31	100.0	44.3	59.6	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT3G13140.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr3:4226654-4227377 REVERSE LENGTH=183	183	183	5.00E-34	100.0	44.3	59.6
Rsa1.0_00541.1.g15687.t1	ref|NP_187920.1| uncharacterized protein [Arabidopsis thaliana] gi|10172600|dbj|BAB01404.1| unnamed protein product [Arabidopsis thaliana] gi|332641779|gb|AEE75300.1| uncharacterized protein AT3G13130 [Arabidopsis thaliana]	192	201	2.00E-60	104.7	67.7	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G13130.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: male gametophyte; Has 140 Blast hits to 132 proteins in 41 species: Archae - 2; Bacteria - 4; Metazoa - 29; Fungi - 20; Plants - 51; Viruses - 0; Other Eukaryotes - 34 (source: NCBI BLink). | chr3:4223008-4223613 FORWARD LENGTH=201	192	201	6.00E-63	104.7	67.7	83.9
Rsa1.0_00541.1.g15688.t1	gb|ABL97980.1| 30S ribosomal protein S10-like [Brassica rapa]	198	193	1.00E-93	97.5	90.9	93.9	30S ribosomal protein S10-like	gbpln	Brassica rapa	AT3G13120.2 | Symbols: | Ribosomal protein S10p/S20e family protein | chr3:4220310-4221526 REVERSE LENGTH=191	198	191	4.00E-88	96.5	86.9	90.4
Rsa1.0_00541.1.g15689.t1	gb|AAT38561.1| mitochondrial serine acetyltransferase [Thlaspi goesingense]	389	395	0	101.5	88.2	93.1	mitochondrial serine acetyltransferase	gbpln	Thlaspi goesingense	AT3G13110.1 | Symbols: ATSERAT2;2, SAT-1, SAT-A, SAT3, SAT-M, SERAT2;2 | serine acetyltransferase 2;2 | chr3:4214939-4216114 REVERSE LENGTH=391	389	391	0	100.5	85.3	89.7
Rsa1.0_00541.1.g15690.t1	ref|XP_002884943.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330783|gb|EFH61202.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1484	1486	0	100.1	88.3	93.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G13100.1 | Symbols: ATMRP7, MRP7, ABCC7 | multidrug resistance-associated protein 7 | chr3:4208859-4214173 REVERSE LENGTH=1493	1484	1493	0	100.6	87.5	92.5
Rsa1.0_00541.1.g15691.t1	ref|NP_179351.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|4914381|gb|AAD32917.1| unknown protein [Arabidopsis thaliana] gi|330251563|gb|AEC06657.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	550	580	2.33E-156	105.5	52.5	66.2	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G17600.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:7654477-7656219 REVERSE LENGTH=580	550	580	1.00E-149	105.5	52.5	66.2
Rsa1.0_00541.1.g15692.t1	ref|XP_002884940.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330780|gb|EFH61199.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	664	660	0	99.4	91.1	95.3	CBS domain-containing protein	gbpln	Arabidopsis lyrata	AT3G13070.1 | Symbols: | CBS domain-containing protein / transporter associated domain-containing protein | chr3:4191511-4195112 REVERSE LENGTH=661	664	661	0	99.5	91.7	94.9

Rsa1.0_00541.1.g15693.t1	gb|EOA33017.1| hypothetical protein CARUB_v10016348mg [Capsella rubella]	689	688	0	99.9	87.8	93.6	hypothetical protein CARUB_v10016348mg	gbpln	Capsella rubella	AT3G13065.1 | Symbols: SRF4 | STRUBBELIG-receptor family 4 | chr3:4187510-4190863 FORWARD LENGTH=687	689	687	0	99.7	85.5	93.5
Rsa1.0_00541.1.g15694.t1	ref|XP_002882804.1| hypothetical protein ARALYDRAFT_478675 [Arabidopsis lyrata subsp. lyrata] gi|297328644|gb|EFH59063.1| hypothetical protein ARALYDRAFT_478675 [Arabidopsis lyrata subsp. lyrata]	628	635	0	101.1	83.4	88.5	hypothetical protein ARALYDRAFT_478675	gbpln	Arabidopsis lyrata	AT3G13060.2 | Symbols: ECT5 | evolutionarily conserved C-terminal region 5 | chr3:4180625-4183632 FORWARD LENGTH=634	628	634	0	101.0	82.8	87.9
Rsa1.0_00541.1.g15695.t1	ref|NP_187908.1| hAT dimerization domain-containing protein [Arabidopsis thaliana] gi|15795134|dbj|BAB02512.1| transposase-like protein [Arabidopsis thaliana] gi|332641756|gb|AEE75277.1| hAT dimerization domain-containing protein [Arabidopsis thaliana]	742	605	0	81.5	51.3	62.9	hAT dimerization domain-containing protein	gbpln	Arabidopsis thaliana	AT3G13020.1 | Symbols: | hAT transposon superfamily protein | chr3:4166995-4168917 REVERSE LENGTH=605	742	605	0	81.5	51.3	62.9
Rsa1.0_00541.1.g15696.t1	dbj|BAJ33667.1| unnamed protein product [Thellungiella halophila]	562	590	0	105.0	89.5	94.7	unnamed protein product	----	----	AT3G13000.2 | Symbols: | Protein of unknown function, DUF547 | chr3:4158214-4160989 REVERSE LENGTH=582	562	582	0	103.6	85.9	93.2
Rsa1.0_00541.1.g15697.t1	ref|XP_002882800.1| histone acetyltransferase 5 [Arabidopsis lyrata subsp. lyrata] gi|297328640|gb|EFH59059.1| histone acetyltransferase 5 [Arabidopsis lyrata subsp. lyrata]	181	1657	2.00E-63	915.5	66.9	74.6	histone acetyltransferase 5	gbpln	Arabidopsis lyrata	AT3G12980.1 | Symbols: HAC5, ATHPCAT4 | histone acetyltransferase of the CBP family 5 | chr3:4146919-4154495 FORWARD LENGTH=1670	181	1670	1.00E-64	922.7	64.6	74.0
Rsa1.0_00541.1.g15698.t1	ref|NP_001030683.2| no apical meristem-domain containing transcriptional regulator [Arabidopsis thaliana] gi|15795128|dbj|BAB02506.1| NAM (no apical meristem) protein-like [Arabidopsis thaliana] gi|332641748|gb|AEE75269.1| no apical meristem-domain containing transcriptional regulator [Arabidopsis thaliana]	101	279	1.00E-26	276.2	69.3	76.2	no apical meristem-domain containing transcriptional regulator	gbpln	Arabidopsis thaliana	AT3G12977.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr3:4143832-4145860 FORWARD LENGTH=279	101	279	2.00E-29	276.2	69.3	76.2
Rsa1.0_00542.1.g15699.t1	gb|EOA29854.1| hypothetical protein CARUB_v10012947mg [Capsella rubella]	764	885	0	115.8	86.1	91.8	hypothetical protein CARUB_v10012947mg	gbpln	Capsella rubella	AT3G06920.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:2181717-2184449 FORWARD LENGTH=871	764	871	0	114.0	84.8	90.4
Rsa1.0_00542.1.g15700.t1	gb|EOA29943.1| hypothetical protein CARUB_v10013043mg [Capsella rubella] gi|482565755|gb|EOA29944.1| hypothetical protein CARUB_v10013043mg [Capsella rubella]	832	748	0	89.9	71.4	77.0	hypothetical protein CARUB_v10013043mg	gbpln	Capsella rubella	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	832	785	4.00E-19	94.4	9.3	16.9
Rsa1.0_00542.1.g15701.t1	ref|XP_002882501.1| tRNA pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328341|gb|EFH58760.1| tRNA pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	322	323	1.00E-163	100.3	86.3	91.3	tRNA pseudouridine synthase family protein	gbpln	Arabidopsis lyrata	AT3G06950.1 | Symbols: | Pseudouridine synthase family protein | chr3:2192869-2194254 FORWARD LENGTH=323	322	323	1.00E-165	100.3	86.3	91.0
Rsa1.0_00542.1.g15702.t1	ref|NP_187353.2| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|91806393|gb|ABE65924.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|332640961|gb|AEE74482.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	391	317	1.00E-46	81.1	35.3	49.6	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT3G06970.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:2199653-2201150 REVERSE LENGTH=317	391	317	3.00E-49	81.1	35.3	49.6
Rsa1.0_00542.1.g15703.t1	ref|XP_002884620.1| UDP-glucose:sterol glucosyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297330460|gb|EFH60879.1| UDP-glucose:sterol glucosyltransferase [Arabidopsis lyrata subsp. lyrata]	640	635	0	99.2	88.1	91.6	UDP-glucose:sterol glucosyltransferase	gbpln	Arabidopsis lyrata	AT3G07020.2 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:2218120-2221590 REVERSE LENGTH=637	640	637	0	99.5	87.5	91.4
Rsa1.0_00542.1.g15704.t1	gb|EOA30714.1| hypothetical protein CARUB_v10013850mg [Capsella rubella]	361	406	1.00E-83	112.5	56.5	61.2	hypothetical protein CARUB_v10013850mg	gbpln	Capsella rubella	AT3G07030.1 | Symbols: | Alba DNA/RNA-binding protein | chr3:2223001-2225254 REVERSE LENGTH=405	361	405	9.00E-67	112.2	34.9	39.6
Rsa1.0_00542.1.g15705.t2	gb|EOA31372.1| hypothetical protein CARUB_v10014546mg [Capsella rubella]	253	229	6.00E-71	90.5	61.7	68.4	hypothetical protein CARUB_v10014546mg	gbpln	Capsella rubella	AT4G33690.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: pollen tube; Has 543 Blast hits to 512 proteins in 106 species: Archae - 0; Bacteria - 0; Metazoa - 281; Fungi - 54; Plants - 72; Viruses - 0; Other Eukaryotes - 136 (source: NCBI BLink). | chr4:16175198-16176137 FORWARD LENGTH=246	253	246	7.00E-50	97.2	48.6	57.7

Rsa1.0_00542.1.g15706.t1	ref|NP_187361.1| putative GTP-binding protein [Arabidopsis thaliana] gi|6729012|gb|AAF27009.1|AC016827_20 putative GTPase [Arabidopsis thaliana] gi|332640972|gb|AEE74493.1| putative GTP-binding protein [Arabidopsis thaliana] gi|414420744|gb|AFW99797.1| nucleostemin-like 1 protein [Arabidopsis thaliana]	584	582	0	99.7	85.6	89.2	putative GTP-binding protein	gbpln	Arabidopsis thaliana	AT3G07050.1 | Symbols: | GTP-binding family protein | chr3:2229602-2232279 REVERSE LENGTH=582	584	582	0	99.7	85.6	89.2
Rsa1.0_00542.1.g15707.t1	gb|EOA30591.1| hypothetical protein CARUB_v10013723mg [Capsella rubella]	462	440	1.00E-125	95.2	52.6	56.9	hypothetical protein CARUB_v10013723mg	gbpln	Capsella rubella	AT3G07080.1 | Symbols: | EamA-like transporter family | chr3:2241360-2242934 FORWARD LENGTH=438	462	438	1.00E-124	94.8	51.9	55.6
Rsa1.0_00542.1.g15708.t3	ref|NP_187366.2| sec24-like transport protein [Arabidopsis thaliana] gi|78099801|sp|Q9SFU0.2|SC24A_ARATH RecName: Full=Protein transport protein Sec24-like At3g07100 gi|22531076|gb|AAM97042.1| putative Sec24-like COPII protein [Arabidopsis thaliana] gi|23197930|gb|AAN15492.1| putative Sec24-like COPII protein [Arabidopsis thaliana] gi|332640977|gb|AEE74498.1| sec24-like transport protein [Arabidopsis thaliana]	1006	1038	0	103.2	88.0	91.8	sec24-like transport protein	gbpln	Arabidopsis thaliana	AT3G07100.1 | Symbols: ERMO2, SEC24A | Sec23/Sec24 protein transport family protein | chr3:2245689-2250077 REVERSE LENGTH=1038	1006	1038	0	103.2	88.0	91.8
Rsa1.0_00542.1.g15709.t1	ref|NP_187368.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|6642653|gb|AAF20234.1|AC012395_21 putative RING zinc finger protein [Arabidopsis thaliana] gi|56381891|gb|AAV85664.1| At3g07120 [Arabidopsis thaliana] gi|58531344|gb|AAW78594.1| At3g07120 [Arabidopsis thaliana] gi|332640980|gb|AEE74501.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	349	360	1.00E-119	103.2	75.6	84.8	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G07120.1 | Symbols: | RING/U-box superfamily protein | chr3:2254560-2255642 FORWARD LENGTH=360	349	360	1.00E-122	103.2	75.6	84.8
Rsa1.0_00542.1.g15710.t1	gb|EOA20112.1| hypothetical protein CARUB_v10000391mg [Capsella rubella]	460	672	1.00E-161	146.1	62.6	73.5	hypothetical protein CARUB_v10000391mg	gbpln	Capsella rubella	AT2G47250.1 | Symbols: | RNA helicase family protein | chr2:19399923-19402981 REVERSE LENGTH=729	460	729	1.00E-162	158.5	62.2	76.3
Rsa1.0_00542.1.g15711.t15	ref|NP_187372.5| callose synthase [Arabidopsis thaliana] gi|378405154|sp|Q9SFU6.2|CALS9_ARATH RecName: Full=Callose synthase 9; AltName: Full=1,3-beta-glucan synthase; AltName: Full=Protein GLUCAN SYNTHASE-LIKE 10 gi|332640985|gb|AEE74506.1| callose synthase 10 [Arabidopsis thaliana]	1961	1890	0	96.4	84.8	90.1	callose synthase	gbpln	Arabidopsis thaliana	AT3G07160.1 | Symbols: ATGSL10, gsl10, CALS9 | glucan synthase-like 10 | chr3:2265142-2279383 REVERSE LENGTH=1890	1961	1890	0	96.4	84.8	90.1
Rsa1.0_00542.1.g15712.t2	ref|XP_002882515.1| sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297328355|gb|EFH58774.1| sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata]	201	203	7.00E-82	101.0	80.1	85.1	sterile alpha motif domain-containing protein	gbpln	Arabidopsis lyrata	AT3G07170.1 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr3:2280428-2282097 FORWARD LENGTH=203	201	203	5.00E-84	101.0	79.6	85.1
Rsa1.0_00542.1.g15713.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1483	1496	0	100.9	56.4	71.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1483	1262	1.00E-133	85.1	15.6	22.9
Rsa1.0_00542.1.g15714.t1	ref|XP_002882516.1| hypothetical protein ARALYDRAFT_896877 [Arabidopsis lyrata subsp. lyrata] gi|297328356|gb|EFH58775.1| hypothetical protein ARALYDRAFT_896877 [Arabidopsis lyrata subsp. lyrata]	233	225	1.00E-42	96.6	57.5	63.9	hypothetical protein ARALYDRAFT_896877	gbpln	Arabidopsis lyrata	AT3G07195.1 | Symbols: | RPM1-interacting protein 4 (RIN4) family protein | chr3:2288959-2290309 FORWARD LENGTH=225	233	225	6.00E-43	96.6	53.6	60.9
Rsa1.0_00542.1.g15715.t1	ref|XP_002884637.1| hypothetical protein ARALYDRAFT_340917 [Arabidopsis lyrata subsp. lyrata] gi|297330477|gb|EFH60896.1| hypothetical protein ARALYDRAFT_340917 [Arabidopsis lyrata subsp. lyrata]	277	286	3.00E-91	103.2	71.8	79.8	hypothetical protein ARALYDRAFT_340917	gbpln	Arabidopsis lyrata	AT3G07250.1 | Symbols: | nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein | chr3:2300579-2308305 REVERSE LENGTH=1294	277	1294	6.00E-78	467.1	63.9	72.2

Rsa1.0_00543.1.g15716.t1	ref|NP_849679.1| SAUR-like auxin-responsive protein family [Arabidopsis thaliana] gi|9665126|gb|AAF97310.1|AC007843_13 Hypothetical protein [Arabidopsis thaliana] gi|26452787|dbj|BAC43474.1| unknown protein [Arabidopsis thaliana] gi|109946549|gb|ABG48453.1| At1g17345 [Arabidopsis thaliana] gi|332191454|gb|AEE29575.1| SAUR-like auxin-responsive protein family [Arabidopsis thaliana]	135	131	9.00E-51	97.0	74.8	83.7	SAUR-like auxin-responsive protein family	gbpln	Arabidopsis thaliana	AT1G17345.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:5940525-5940920 FORWARD LENGTH=131	135	131	2.00E-53	97.0	74.8	83.7
Rsa1.0_00543.1.g15717.t2	ref|NP_173178.3| putative complex I intermediate-associated protein 30 [Arabidopsis thaliana] gi|209572597|sp|Q9LQI7.2|CIA30_ARATH RecName: Full=Probable complex I intermediate-associated protein 30 gi|117168231|gb|ABK32198.1| At1g17350 [Arabidopsis thaliana] gi|332191455|gb|AEE29576.1| putative complex I intermediate-associated protein 30 [Arabidopsis thaliana]	224	227	1.00E-109	101.3	86.6	91.1	putative complex I intermediate-associated protein 30	gbpln	Arabidopsis thaliana	AT1G17350.1 | Symbols: | NADH:ubiquinone oxidoreductase intermediate-associated protein 30 | chr1:5942391-5944272 FORWARD LENGTH=227	224	227	1.00E-111	101.3	86.6	91.1
Rsa1.0_00543.1.g15718.t1	ref|NP_173179.4| uncharacterized protein [Arabidopsis thaliana] gi|9665120|gb|AAF97304.1|AC007843_7 Hypothetical protein [Arabidopsis thaliana] gi|332191457|gb|AEE29578.1| uncharacterized protein AT1G17360 [Arabidopsis thaliana]	1034	1061	0	102.6	75.2	83.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G17360.1 | Symbols: | BEST Arabidopsis thaliana protein match is: COP1-interacting protein-related (TAIR:AT1G72410.1); Has 9949 Blast hits to 7480 proteins in 576 species: Archae - 12; Bacteria - 1007; Metazoa - 3636; Fungi - 982; Plants - 444; Viruses - 50; Other Eukaryotes - 3818 (source: NCBI BLink). | chr1:5947441-5951399 FORWARD LENGTH=1061	1034	1061	0	102.6	75.2	83.5
Rsa1.0_00543.1.g15719.t1	ref|NP_564019.1| protein TIFY 11A [Arabidopsis thaliana] gi|75173855|sp|Q9LDU5.1|TI11A_ARATH RecName: Full=Protein TIFY 11A; AltName: Full=Jasmonate ZIM domain-containing protein 5 gi|8778483|gb|AAF79491.1|AC022492_35 F1L3.3 [Arabidopsis thaliana] gi|9665119|gb|AAF97303.1|AC007843_6 Hypothetical protein [Arabidopsis thaliana] gi|23306360|gb|AAN17407.1| expressed protein [Arabidopsis thaliana] gi|27311875|gb|AAO00903.1| expressed protein [Arabidopsis thaliana] gi|332191460|gb|AEE29581.1| protein TIFY 11A [Arabidopsis thaliana]	351	274	2.00E-89	78.1	51.9	60.7	protein TIFY 11A	gbpln	Arabidopsis thaliana	AT1G17380.1 | Symbols: JAZ5, TIFY11A | jasmonate-zim-domain protein 5 | chr1:5955654-5957070 REVERSE LENGTH=274	351	274	5.00E-92	78.1	51.9	60.7
Rsa1.0_00543.1.g15720.t1	ref|XP_002892949.1| hypothetical protein ARALYDRAFT_471945 [Arabidopsis lyrata subsp. lyrata] gi|297338791|gb|EFH69208.1| hypothetical protein ARALYDRAFT_471945 [Arabidopsis lyrata subsp. lyrata]	501	296	1.00E-119	59.1	50.3	54.9	hypothetical protein ARALYDRAFT_471945	gbpln	Arabidopsis lyrata	AT1G17400.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G72490.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:5960920-5962245 REVERSE LENGTH=295	501	295	1.00E-120	58.9	50.1	54.5
Rsa1.0_00543.1.g15721.t1	ref|XP_002892951.1| hypothetical protein ARALYDRAFT_471949 [Arabidopsis lyrata subsp. lyrata] gi|297338793|gb|EFH69210.1| hypothetical protein ARALYDRAFT_471949 [Arabidopsis lyrata subsp. lyrata]	656	670	0	102.1	76.2	81.7	hypothetical protein ARALYDRAFT_471949	gbpln	Arabidopsis lyrata	AT1G17440.2 | Symbols: EER4, TAF12B | Transcription initiation factor TFIID subunit A | chr1:5984407-5987663 REVERSE LENGTH=683	656	683	0	104.1	66.3	70.3
Rsa1.0_00543.1.g15722.t1	ref|NP_564024.1| protein ELF4-like 4 [Arabidopsis thaliana] gi|238478519|ref|NP_001154348.1| protein ELF4-like 4 [Arabidopsis thaliana] gi|75218652|sp|Q570U6.1|EF4L4_ARATH RecName: Full=Protein ELF4-LIKE 4 gi|62318582|dbj|BAD94981.1| hypothetical protein [Arabidopsis thaliana] gi|98961045|gb|ABF59006.1| At1g17455 [Arabidopsis thaliana] gi|332191470|gb|AEE29591.1| protein ELF4-like 4 [Arabidopsis thaliana] gi|332191471|gb|AEE29592.1| protein ELF4-like 4 [Arabidopsis thaliana]	115	114	5.00E-55	99.1	95.7	98.3	protein ELF4-like 4	gbpln	Arabidopsis thaliana	AT1G17455.2 | Symbols: ELF4-L4 | ELF4-like 4 | chr1:5997932-5998276 FORWARD LENGTH=114	115	114	8.00E-58	99.1	95.7	98.3
Rsa1.0_00543.1.g15723.t1	gb|EOA37706.1| hypothetical protein CARUB_v10012426mg [Capsella rubella]	666	599	0	89.9	60.8	70.1	hypothetical protein CARUB_v10012426mg	gbpln	Capsella rubella	AT1G17460.2 | Symbols: TRFL3 | TRF-like 3 | chr1:5999519-6002546 FORWARD LENGTH=624	666	624	0	93.7	59.0	68.6

Rsa1.0_00543.1.g15724.t1	gb|EOA40609.1| hypothetical protein CARUB_v10009345mg [Capsella rubella]	392	399	0	101.8	99.2	99.7	hypothetical protein CARUB_v10009345mg	gbpln	Capsella rubella	AT1G17470.2 | Symbols: ATDRG1, ATDRG, DRG1 | developmentally regulated G-protein 1 | chr1:6003442-6006155 FORWARD LENGTH=399	392	399	0	101.8	99.0	99.5
Rsa1.0_00543.1.g15725.t1	ref|XP_002892953.1| IQ-domain 7 [Arabidopsis lyrata subsp. lyrata] gi|297338795|gb|EFH69212.1| IQ-domain 7 [Arabidopsis lyrata subsp. lyrata]	375	376	1.00E-150	100.3	78.4	83.5	IQ-domain 7	gbpln	Arabidopsis lyrata	AT1G17480.1 | Symbols: IQD7 | IQ-domain 7 | chr1:6006675-6008132 REVERSE LENGTH=371	375	371	2.33E-156	98.9	76.5	82.4
Rsa1.0_00543.1.g15726.t1	ref|NP_564026.1| uncharacterized protein [Arabidopsis thaliana] gi|8778458|gb|AAF79466.1|AC022492_10 F1L3.19 [Arabidopsis thaliana] gi|15450369|gb|AAK96478.1| At1g17490/F1L3_4 [Arabidopsis thaliana] gi|16974479|gb|AAL31243.1| At1g17490/F1L3_4 [Arabidopsis thaliana] gi|21537369|gb|AAM61710.1| unknown [Arabidopsis thaliana] gi|332191477|gb|AEE29598.1| uncharacterized protein AT1G17490 [Arabidopsis thaliana]	82	77	4.00E-20	93.9	68.3	75.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G17490.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G72690.1); Has 57 Blast hits to 45 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6008669-6009165 FORWARD LENGTH=77	82	77	7.00E-23	93.9	68.3	75.6
Rsa1.0_00543.1.g15727.t1	ref|XP_002892954.1| hypothetical protein ARALYDRAFT_471958 [Arabidopsis lyrata subsp. lyrata] gi|297338796|gb|EFH69213.1| hypothetical protein ARALYDRAFT_471958 [Arabidopsis lyrata subsp. lyrata]	127	117	2.00E-26	92.1	57.5	66.9	hypothetical protein ARALYDRAFT_471958	gbpln	Arabidopsis lyrata	AT1G17510.1 | Symbols: | unknown protein; Has 11 Blast hits to 11 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6023704-6024211 REVERSE LENGTH=122	127	122	4.00E-24	96.1	51.2	62.2
Rsa1.0_00543.1.g15728.t1	ref|NP_173195.2| Homeodomain-like/winged-helix DNA-binding protein [Arabidopsis thaliana] gi|332191480|gb|AEE29601.1| telomere repeat-binding factor 4 [Arabidopsis thaliana]	300	296	1.00E-90	98.7	67.0	79.7	Homeodomain-like/winged-helix DNA-binding protein	gbpln	Arabidopsis thaliana	AT1G17520.1 | Symbols: | Homeodomain-like/winged-helix DNA-binding family protein | chr1:6024959-6027224 REVERSE LENGTH=296	300	296	3.00E-93	98.7	67.0	79.7
Rsa1.0_00543.1.g15729.t1	ref|NP_564028.1| translocase of inner mitochondrial membrane 23 [Arabidopsis thaliana] gi|75175255|sp|Q9LNQ1.1|TI231_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM23-1 gi|8778460|gb|AAF79468.1|AC022492_12 F1L3.24 [Arabidopsis thaliana] gi|15010570|gb|AAK73944.1| At1g17530/F11A6.4 [Arabidopsis thaliana] gi|20147387|gb|AAM10403.1| At1g17530/F11A6.4 [Arabidopsis thaliana] gi|38678776|gb|AAR26373.1| mitochondrial inner membrane translocase TM23-1 [Arabidopsis thaliana] gi|332191481|gb|AEE29602.1| translocase of inner mitochondrial membrane 23 [Arabidopsis thaliana]	186	187	6.00E-66	100.5	74.2	82.3	translocase of inner mitochondrial membrane 23	gbpln	Arabidopsis thaliana	AT1G17530.1 | Symbols: ATTIM23-1, TIM23-1 | translocase of inner mitochondrial membrane 23 | chr1:6027723-6028286 FORWARD LENGTH=187	186	187	2.00E-68	100.5	74.2	82.3
Rsa1.0_00543.1.g15730.t3	ref|NP_173197.2| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana] gi|51969566|dbj|BAD43475.1| putative protein kinase [Arabidopsis thaliana] gi|332191482|gb|AEE29603.1| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana]	721	728	0	101.0	80.2	86.4	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	gbpln	Arabidopsis thaliana	AT1G17540.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:6029551-6032641 REVERSE LENGTH=728	721	728	0	101.0	80.2	86.4
Rsa1.0_00543.1.g15731.t1	ref|XP_002890234.1| hypothetical protein ARALYDRAFT_889163 [Arabidopsis lyrata subsp. lyrata] gi|297336076|gb|EFH66493.1| hypothetical protein ARALYDRAFT_889163 [Arabidopsis lyrata subsp. lyrata]	515	514	0	99.8	88.5	93.2	hypothetical protein ARALYDRAFT_889163	gbpln	Arabidopsis lyrata	AT1G17550.1 | Symbols: HAB2 | homology to ABI2 | chr1:6034917-6036939 FORWARD LENGTH=511	515	511	0	99.2	87.4	92.4
Rsa1.0_00543.1.g15732.t1	ref|NP_173200.1| large subunit ribosomal protein L14 [Arabidopsis thaliana] gi|28393761|gb|AAO42290.1| putative ribosomal protein [Arabidopsis thaliana] gi|28973235|gb|AAO63942.1| putative ribosomal protein [Arabidopsis thaliana] gi|332191485|gb|AEE29606.1| large subunit ribosomal protein L14 [Arabidopsis thaliana]	202	196	6.00E-65	97.0	70.8	79.2	large subunit ribosomal protein L14	gbpln	Arabidopsis thaliana	AT1G17560.1 | Symbols: HLL | Ribosomal protein L14p/L23e family protein | chr1:6037635-6038574 REVERSE LENGTH=196	202	196	2.00E-67	97.0	70.8	79.2

Rsa1.0_00543.1.g15733.t1	ref|XP_002890238.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336080|gb|EFH66497.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	379	380	0	100.3	82.1	88.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G17615.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:6059441-6060667 FORWARD LENGTH=380	379	380	1.00E-178	100.3	79.7	87.1
Rsa1.0_00543.1.g15734.t1	gb|EOA37010.1| hypothetical protein CARUB_v10010038mg [Capsella rubella]	258	263	1.00E-105	101.9	82.2	92.6	hypothetical protein CARUB_v10010038mg	gbpln	Capsella rubella	AT1G17620.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr1:6062313-6063107 FORWARD LENGTH=264	258	264	5.00E-97	102.3	81.8	90.7
Rsa1.0_00544.1.g15735.t1	sp|Q941Q2.1|HBL2_BRANA RecName: Full=Non-symbiotic hemoglobin 2; AltName: Full=BRAna GLB2; AltName: Full=Hb2 gi|15809392|gb|AAK07741.1| class 2 non-symbiotic hemoglobin [Brassica napus]	94	161	2.00E-39	171.3	85.1	88.3	RecName: Full=Non-symbiotic hemoglobin 2; AltName: Full=BRAna GLB2; AltName: Full=Hb2 gi|15809392|gb|AAK07741.1| class 2 non-symbiotic hemoglobin	gbpln	Brassica napus	AT3G10520.1 | Symbols: AHB2, GLB2, ARATH GLB2, NSHB2, ATGLB2, HB2 | haemoglobin 2 | chr3:3276516-3277765 REVERSE LENGTH=158	94	158	1.00E-40	168.1	80.9	88.3
Rsa1.0_00544.1.g15736.t1	ref|XP_002871095.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297316932|gb|EFH47354.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	793	860	0	108.4	65.7	76.3	protein binding protein	gbpln	Arabidopsis lyrata	AT5G04460.3 | Symbols: | RING/U-box superfamily protein | chr5:1260009-1263695 FORWARD LENGTH=863	793	863	0	108.8	65.6	76.4
Rsa1.0_00544.1.g15737.t5	ref|NP_850764.1| binding to TOMV RNA 1L (long form) protein [Arabidopsis thaliana] gi|332003360|gb|AED90743.1| binding to TOMV RNA 1L (long form) protein [Arabidopsis thaliana]	351	334	1.00E-92	95.2	56.4	70.4	binding to TOMV RNA 1L (long form) protein	gbpln	Arabidopsis thaliana	AT5G04430.2 | Symbols: BTR1, BTR1L | binding to TOMV RNA 1L (long form) | chr5:1250602-1253523 REVERSE LENGTH=334	351	334	3.00E-95	95.2	56.4	70.4
Rsa1.0_00544.1.g15738.t1	gb|EOA30567.1| hypothetical protein CARUB_v10013694mg [Capsella rubella]	485	447	0	92.2	78.1	83.9	hypothetical protein CARUB_v10013694mg	gbpln	Capsella rubella	AT3G10490.2 | Symbols: ANAC052, NAC052 | NAC domain containing protein 52 | chr3:3268075-3270608 FORWARD LENGTH=451	485	451	0	93.0	79.0	84.3
Rsa1.0_00544.1.g15739.t1	gb|EOA32729.1| hypothetical protein CARUB_v10016033mg [Capsella rubella]	395	395	1.00E-141	100.0	74.2	80.8	hypothetical protein CARUB_v10016033mg	gbpln	Capsella rubella	AT3G10470.1 | Symbols: | C2H2-type zinc finger family protein | chr3:3260424-3261620 FORWARD LENGTH=398	395	398	1.00E-142	100.8	75.4	81.5
Rsa1.0_00544.1.g15740.t5	ref|NP_177471.1| serine carboxypeptidase-like 3 [Arabidopsis thaliana] gi|75169954|sp|Q9CAU1.1|SCP3_ARATH RecName: Full=Serine carboxypeptidase-like 3; Flags: Precursor gi|12324329|gb|AAG52138.1|AC010556_20 putative serine carboxypeptidase; 12385-14737 [Arabidopsis thaliana] gi|332197316|gb|AEE35437.1| serine carboxypeptidase-like 3 [Arabidopsis thaliana]	409	441	1.00E-179	107.8	74.6	83.6	serine carboxypeptidase-like 3	gbpln	Arabidopsis thaliana	AT1G73280.1 | Symbols: scpl3 | serine carboxypeptidase-like 3 | chr1:27552970-27555322 REVERSE LENGTH=441	409	441	0	107.8	74.6	83.6
Rsa1.0_00544.1.g15741.t1	gb|EOA30606.1| hypothetical protein CARUB_v10013737mg [Capsella rubella]	418	437	0	104.5	77.5	85.2	hypothetical protein CARUB_v10013737mg	gbpln	Capsella rubella	AT3G10450.1 | Symbols: SCPL7 | serine carboxypeptidase-like 7 | chr3:3249544-3252320 FORWARD LENGTH=437	418	437	0	104.5	76.8	84.9
Rsa1.0_00544.1.g15742.t1	gb|EOA30599.1| hypothetical protein CARUB_v10013730mg [Capsella rubella]	49	438	1.00E-16	893.9	77.6	83.7	hypothetical protein CARUB_v10013730mg	gbpln	Capsella rubella	AT1G73280.1 | Symbols: scpl3 | serine carboxypeptidase-like 3 | chr1:27552970-27555322 REVERSE LENGTH=441	49	441	5.00E-19	900.0	75.5	79.6
Rsa1.0_00544.1.g15743.t1	emb|CAN80919.1| hypothetical protein VITISV_002640 [Vitis vinifera]	1438	1450	0	100.8	48.8	65.3	hypothetical protein VITISV_002640	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1438	1262	1.00E-136	87.8	16.9	23.9
Rsa1.0_00544.1.g15744.t1	gb|EOA32148.1| hypothetical protein CARUB_v10015399mg, partial [Capsella rubella]	445	419	5.00E-81	94.2	45.6	58.0	hypothetical protein CARUB_v10015399mg, partial	gbpln	Capsella rubella	AT1G22000.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr1:7744189-7747123 FORWARD LENGTH=717	445	717	3.00E-70	161.1	43.6	56.0
Rsa1.0_00545.1.g15745.t1	ref|NP_001078161.1| cytochrome c oxidase subunit Vb [Arabidopsis thaliana] gi|332642186|gb|AEE75707.1| cytochrome c oxidase subunit Vb [Arabidopsis thaliana]	41	175	5.00E-17	426.8	100.0	100.0	cytochrome c oxidase subunit Vb	gbpln	Arabidopsis thaliana	AT3G15640.2 | Symbols: | Rubredoxin-like superfamily protein | chr3:5299273-5301371 FORWARD LENGTH=175	41	175	8.00E-20	426.8	100.0	100.0
Rsa1.0_00545.1.g15746.t1	ref|XP_002882955.1| hypothetical protein ARALYDRAFT_479016 [Arabidopsis lyrata subsp. lyrata] gi|297328795|gb|EFH59214.1| hypothetical protein ARALYDRAFT_479016 [Arabidopsis lyrata subsp. lyrata]	179	177	7.00E-70	98.9	89.4	91.1	hypothetical protein ARALYDRAFT_479016	gbpln	Arabidopsis lyrata	AT3G15640.1 | Symbols: | Rubredoxin-like superfamily protein | chr3:5299273-5301371 FORWARD LENGTH=176	179	176	1.00E-70	98.3	89.4	90.5
Rsa1.0_00545.1.g15747.t1	ref|NP_001189903.1| phospholipase/carboxylesterase family protein [Arabidopsis thaliana] gi|332642188|gb|AEE75709.1| phospholipase/carboxylesterase family protein [Arabidopsis thaliana]	255	274	1.00E-135	107.5	93.7	97.6	phospholipase/carboxylesterase family protein	gbpln	Arabidopsis thaliana	AT3G15650.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:5306006-5307764 FORWARD LENGTH=274	255	274	1.00E-138	107.5	93.7	97.6

Rsa1.0_00545.1.g15748.t1	dbj|BAB88878.1| late embryogenesis-abundant protein [Brassica rapa]	204	226	2.00E-83	110.8	87.3	92.6	late embryogenesis-abundant protein	gbpln	Brassica rapa	AT3G15670.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr3:5310141-5310901 REVERSE LENGTH=225	204	225	7.00E-81	110.3	86.3	91.7
Rsa1.0_00545.1.g15749.t1	gb|ADK63398.1| Ran-binding zinc finger protein [Brassica rapa]	163	163	2.00E-79	100.0	97.5	99.4	Ran-binding zinc finger protein	gbpln	Brassica rapa	AT3G15680.1 | Symbols: | Ran BP2/NZF zinc finger-like superfamily protein | chr3:5315437-5316048 FORWARD LENGTH=164	163	164	1.00E-72	100.6	87.7	92.6
Rsa1.0_00545.1.g15750.t1	ref|XP_002885106.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297330946|gb|EFH61365.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	414	454	0	109.7	79.0	84.5	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT3G15720.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:5325329-5327457 REVERSE LENGTH=456	414	456	0	110.1	77.3	84.8
Rsa1.0_00545.1.g15751.t1	ref|XP_002885109.1| hypothetical protein ARALYDRAFT_897880 [Arabidopsis lyrata subsp. lyrata] gi|297330949|gb|EFH61368.1| hypothetical protein ARALYDRAFT_897880 [Arabidopsis lyrata subsp. lyrata]	214	220	1.00E-107	102.8	91.6	95.3	hypothetical protein ARALYDRAFT_897880	gbpln	Arabidopsis lyrata	AT3G15810.1 | Symbols: | Protein of unknown function (DUF567) | chr3:5348054-5349178 REVERSE LENGTH=220	214	220	1.00E-108	102.8	91.1	94.4
Rsa1.0_00545.1.g15752.t1	ref|XP_002882965.1| hypothetical protein ARALYDRAFT_897881 [Arabidopsis lyrata subsp. lyrata] gi|297328805|gb|EFH59224.1| hypothetical protein ARALYDRAFT_897881 [Arabidopsis lyrata subsp. lyrata]	280	301	1.00E-130	107.5	86.8	92.5	hypothetical protein ARALYDRAFT_897881	gbpln	Arabidopsis lyrata	AT3G15820.1 | Symbols: ROD1 | phosphatidic acid phosphatase-related / PAP2-related | chr3:5351217-5353573 FORWARD LENGTH=301	280	301	1.00E-130	107.5	85.4	91.4
Rsa1.0_00545.1.g15753.t1	ref|NP_566528.1| post-illumination chlorophyll fluorescence increase protein [Arabidopsis thaliana] gi|11994356|dbj|BAB02315.1| unnamed protein product [Arabidopsis thaliana] gi|14334704|gb|AAK59530.1| unknown protein [Arabidopsis thaliana] gi|22136938|gb|AAM91813.1| unknown protein [Arabidopsis thaliana] gi|332642211|gb|AEE75732.1| post-illumination chlorophyll fluorescence increase protein [Arabidopsis thaliana]	268	268	2.33E-156	100.0	92.5	95.1	post-illumination chlorophyll fluorescence increase protein	gbpln	Arabidopsis thaliana	AT3G15840.1 | Symbols: PIFI | post-illumination chlorophyll fluorescence increase | chr3:5356782-5358418 REVERSE LENGTH=268	268	268	1.00E-149	100.0	92.5	95.1
Rsa1.0_00545.1.g15754.t1	dbj|BAJ33684.1| unnamed protein product [Thellungiella halophila]	371	375	0	101.1	88.4	93.3	unnamed protein product	----	----	AT3G15850.1 | Symbols: FAD5, FADB, JB67, ADS3 | fatty acid desaturase 5 | chr3:5359087-5360998 FORWARD LENGTH=371	371	371	1.00E-179	100.0	86.0	90.3
Rsa1.0_00545.1.g15755.t1	gb|ABS86965.1| delta-9 fatty acid desaturase [Descurainia sophia]	329	377	1.00E-122	114.6	69.9	80.9	delta-9 fatty acid desaturase	gbpln	Descurainia sophia	AT3G15870.1 | Symbols: | Fatty acid desaturase family protein | chr3:5362911-5364425 FORWARD LENGTH=361	329	361	1.00E-119	109.7	66.3	76.3
Rsa1.0_00545.1.g15756.t1	ref|NP_851003.2| Topless-related protein 4 [Arabidopsis thaliana] gi|298352695|sp|Q27GK7.2|TPR4_ARATH RecName: Full=Topless-related protein 4; AltName: Full=WUS-interacting protein 2 gi|332642219|gb|AEE75740.1| Topless-related protein 4 [Arabidopsis thaliana]	1105	1135	0	102.7	94.3	97.5	Topless-related protein 4	gbpln	Arabidopsis thaliana	AT3G15880.1 | Symbols: WSIP2, TPR4 | WUS-interacting protein 2 | chr3:5364792-5371869 REVERSE LENGTH=1135	1105	1135	0	102.7	94.3	97.5
Rsa1.0_00545.1.g15757.t1	ref|XP_002882968.1| hypothetical protein ARALYDRAFT_479045 [Arabidopsis lyrata subsp. lyrata] gi|297328808|gb|EFH59227.1| hypothetical protein ARALYDRAFT_479045 [Arabidopsis lyrata subsp. lyrata]	348	359	1.00E-153	103.2	80.5	88.5	hypothetical protein ARALYDRAFT_479045	gbpln	Arabidopsis lyrata	AT3G15890.1 | Symbols: | Protein kinase superfamily protein | chr3:5374389-5376114 FORWARD LENGTH=361	348	361	1.00E-154	103.7	79.0	88.2
Rsa1.0_00545.1.g15758.t1	emb|CAN64334.1| hypothetical protein VITISV_039730 [Vitis vinifera]	188	1098	6.00E-68	584.0	71.3	78.2	hypothetical protein VITISV_039730	gbpln	Vitis vinifera	AT4G14540.1 | Symbols: NF-YB3 | nuclear factor Y, subunit B3 | chr4:8344663-8345148 FORWARD LENGTH=161	188	161	9.00E-69	85.6	72.9	77.1
Rsa1.0_00545.1.g15759.t4	ref|NP_188217.4| mismatched DNA binding / ATP binding protein [Arabidopsis thaliana] gi|332642232|gb|AEE75753.1| mismatched DNA binding / ATP binding protein [Arabidopsis thaliana]	523	490	1.00E-128	93.7	55.1	67.7	mismatched DNA binding / ATP binding protein	gbpln	Arabidopsis thaliana	AT3G15960.1 | Symbols: | mismatched DNA binding;ATP binding | chr3:5404000-5406461 REVERSE LENGTH=490	523	490	1.00E-131	93.7	55.1	67.7
Rsa1.0_00545.1.g15760.t1	ref|XP_002885120.1| Ran-binding protein 1 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330960|gb|EFH61379.1| Ran-binding protein 1 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	379	470	9.00E-83	124.0	60.9	73.4	Ran-binding protein 1 domain-containing protein	gbpln	Arabidopsis lyrata	AT3G15970.1 | Symbols: | NUP50 (Nucleoporin 50 kDa) protein | chr3:5408982-5410379 REVERSE LENGTH=465	379	465	7.00E-83	122.7	59.4	70.4

Rsa1.0_00545.1.g15761.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1451	1459	0	100.6	61.0	75.3	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1451	1262	1.00E-105	87.0	13.2	18.7
Rsa1.0_00545.1.g15762.t1	ref|XP_002885142.1| IQ-domain 26 [Arabidopsis lyrata subsp. lyrata] gi|297330982|gb|EFH61401.1| IQ-domain 26 [Arabidopsis lyrata subsp. lyrata]	377	390	1.00E-167	103.4	86.5	91.2	IQ-domain 26	gbpln	Arabidopsis lyrata	AT3G16490.1 | Symbols: IQD26 | IQ-domain 26 | chr3:5603962-5605489 REVERSE LENGTH=389	377	389	1.00E-165	103.2	85.7	89.9
Rsa1.0_00546.1.g15763.t1	ref|NP_001078180.1| protein IDA-LIKE 4 [Arabidopsis thaliana] gi|75120853|sp|Q6DUW6.1|IDL4_ARATH RecName: Full=Protein IDA-LIKE 4; Flags: Precursor gi|49425320|gb|AAT66018.1| ida like-protein 4 [Arabidopsis thaliana] gi|332642614|gb|AEE76135.1| protein IDA-LIKE 4 [Arabidopsis thaliana]	94	93	8.00E-24	98.9	71.3	75.5	protein IDA-LIKE 4	gbpln	Arabidopsis thaliana	AT3G18715.1 | Symbols: IDL4 | inflorescence deficient in abscission (IDA)-like 4 | chr3:6441067-6441348 FORWARD LENGTH=93	94	93	1.00E-26	98.9	71.3	75.5
Rsa1.0_00546.1.g15764.t1	gb|EOA32379.1| hypothetical protein CARUB_v10015646mg [Capsella rubella]	1327	1322	0	99.6	81.8	89.7	hypothetical protein CARUB_v10015646mg	gbpln	Capsella rubella	AT3G18730.1 | Symbols: TSK, MGO3, BRU1 | tetratricopeptide repeat (TPR)-containing protein | chr3:6446062-6453045 REVERSE LENGTH=1311	1327	1311	0	98.8	81.6	89.9
Rsa1.0_00546.1.g15765.t1	ref|XP_002883147.1| 60S ribosomal protein L30 [Arabidopsis lyrata subsp. lyrata] gi|297846666|ref|XP_002891214.1| 60S ribosomal protein L30 [Arabidopsis lyrata subsp. lyrata] gi|297328987|gb|EFH59406.1| 60S ribosomal protein L30 [Arabidopsis lyrata subsp. lyrata] gi|297337056|gb|EFH67473.1| 60S ribosomal protein L30 [Arabidopsis lyrata subsp. lyrata]	112	112	1.00E-57	100.0	99.1	100.0	60S ribosomal protein L30	gbpln	Arabidopsis lyrata	AT1G36240.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr1:13614890-13616233 FORWARD LENGTH=112	112	112	1.00E-59	100.0	99.1	99.1
Rsa1.0_00546.1.g15766.t2	ref|NP_566618.1| small subunit ribosomal protein S6 [Arabidopsis thaliana] gi|9293899|dbj|BAB01802.1| unnamed protein product [Arabidopsis thaliana] gi|21617981|gb|AAM67031.1| unknown [Arabidopsis thaliana] gi|26451219|dbj|BAC42712.1| unknown protein [Arabidopsis thaliana] gi|28827770|gb|AAO50729.1| unknown protein [Arabidopsis thaliana] gi|332642621|gb|AEE76142.1| small subunit ribosomal protein S6 [Arabidopsis thaliana]	138	139	2.00E-61	100.7	85.5	92.8	small subunit ribosomal protein S6	gbpln	Arabidopsis thaliana	AT3G18760.1 | Symbols: | Translation elongation factor EF1B/ribosomal protein S6 family protein | chr3:6457930-6459558 REVERSE LENGTH=139	138	139	6.00E-64	100.7	85.5	92.8
Rsa1.0_00546.1.g15767.t1	dbj|BAJ33918.1| unnamed protein product [Thellungiella halophila]	213	225	5.00E-96	105.6	86.4	91.1	unnamed protein product	----	----	AT3G18773.1 | Symbols: | RING/U-box superfamily protein | chr3:6466304-6466966 FORWARD LENGTH=220	213	220	1.00E-93	103.3	78.4	87.8
Rsa1.0_00546.1.g15768.t1	dbj|BAB01805.1| unnamed protein product [Arabidopsis thaliana]	218	222	2.00E-97	101.8	81.7	87.6	unnamed protein product	gbpln	Arabidopsis thaliana	AT1G49230.1 | Symbols: | RING/U-box superfamily protein | chr1:18209320-18209979 FORWARD LENGTH=219	218	219	8.00E-78	100.5	68.3	75.7
Rsa1.0_00546.1.g15769.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1275	1515	0	118.8	54.0	69.6	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1275	1262	2.00E-84	99.0	12.9	20.3

Rsa1.0_00546.1.g15770.t1	ref|NP_188508.1| actin 2 [Arabidopsis thaliana] gi|297830536|ref|XP_002883150.1| hypothetical protein ARALYDRAFT_342019 [Arabidopsis lyrata subsp. lyrata] gi|297847210|ref|XP_002891486.1| hypothetical protein ARALYDRAFT_474065 [Arabidopsis lyrata subsp. lyrata] gi|25452790|sp|Q96292.1|ACT2_ARATH RecName: Full=Actin-2 gi|16226780|gb|AAL16260.1|AF428330_1 AT3g18780/MVE11_16 [Arabidopsis thaliana] gi|1669387|gb|AAB37098.1| actin 2 [Arabidopsis thaliana] gi|9293903|dbj|BAB01806.1| actin 2 [Arabidopsis thaliana] gi|17381174|gb|AAL36399.1| putative actin 2 protein [Arabidopsis thaliana] gi|20465835|gb|AAM20022.1| putative actin 2 protein [Arabidopsis thaliana] gi|21593338|gb|AAM65287.1| actin 2 [Arabidopsis thaliana] gi|110740435|dbj|BAF02112.1| actin 2 [Arabidopsis thaliana] gi|222424040|dbj|BAH19981.1| AT3G18780 [Arabidopsis thaliana] gi|241740080|gb|ACS68188.1| actin2.2 [Brassica napus] gi|297328990|gb|EFH59409.1| hypothetical protein ARALYDRAFT_342019 [Arabidopsis lyrata subsp. lyrata]	377	377	0	100.0	100.0	100.0	actin 2	gbpln	Arabidopsis lyrata	AT3G18780.2 | Symbols: ACT2, DER1, LSR2, ENL2 | actin 2 | chr3:6475535-6476832 FORWARD LENGTH=377	377	377	0	100.0	100.0	100.0
Rsa1.0_00546.1.g15771.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00546.1.g15772.t1	gb|EOA31115.1| hypothetical protein CARUB_v10014275mg [Capsella rubella] gi|482566927|gb|EOA31116.1| hypothetical protein CARUB_v10014275mg [Capsella rubella]	301	300	1.00E-130	99.7	84.1	91.7	hypothetical protein CARUB_v10014275mg	gbpln	Capsella rubella	AT3G18790.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Isy1-like splicing (InterPro:IPR009360); Has 1147 Blast hits to 965 proteins in 236 species: Archae - 12; Bacteria - 13; Metazoa - 351; Fungi - 230; Plants - 49; Viruses - 9; Other Eukaryotes - 483 (source: NCBI BLink). | chr3:6477853-6478755 FORWARD LENGTH=300	301	300	1.00E-125	99.7	81.7	89.0
Rsa1.0_00546.1.g15773.t1	ref|NP_566619.1| uncharacterized protein [Arabidopsis thaliana] gi|9293905|dbj|BAB01808.1| unnamed protein product [Arabidopsis thaliana] gi|21555103|gb|AAM63777.1| unknown [Arabidopsis thaliana] gi|89001037|gb|ABD59108.1| At3g18800 [Arabidopsis thaliana] gi|332642629|gb|AEE76150.1| uncharacterized protein AT3G18800 [Arabidopsis thaliana]	200	197	2.00E-98	98.5	93.5	96.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G18800.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 12 growth stages; Has 58 Blast hits to 58 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6479746-6480339 FORWARD LENGTH=197	200	197	1.00E-101	98.5	93.5	96.0
Rsa1.0_00546.1.g15774.t1	ref|XP_002885280.1| hypothetical protein ARALYDRAFT_898257 [Arabidopsis lyrata subsp. lyrata] gi|297331120|gb|EFH61539.1| hypothetical protein ARALYDRAFT_898257 [Arabidopsis lyrata subsp. lyrata]	667	696	0	104.3	67.6	71.5	hypothetical protein ARALYDRAFT_898257	gbpln	Arabidopsis lyrata	AT3G18810.1 | Symbols: | Protein kinase superfamily protein | chr3:6480701-6483593 REVERSE LENGTH=700	667	700	0	104.9	66.9	71.5
Rsa1.0_00546.1.g15775.t1	ref|XP_002883153.1| hypothetical protein ARALYDRAFT_898258 [Arabidopsis lyrata subsp. lyrata] gi|297328993|gb|EFH59412.1| hypothetical protein ARALYDRAFT_898258 [Arabidopsis lyrata subsp. lyrata]	215	206	1.00E-115	95.8	95.8	95.8	hypothetical protein ARALYDRAFT_898258	gbpln	Arabidopsis lyrata	AT3G18820.1 | Symbols: ATRABG3F, ATRAB7B, RAB71, RABG3F, RAB7B | RAB GTPase homolog G3F | chr3:6484266-6486005 FORWARD LENGTH=206	215	206	1.00E-116	95.8	94.4	94.9
Rsa1.0_00546.1.g15776.t1	ref|XP_002880609.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata] gi|297326448|gb|EFH56868.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata]	520	464	3.00E-77	89.2	34.6	44.8	hypothetical protein ARALYDRAFT_901029	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	520	456	2.00E-74	87.7	32.1	41.9

Rsa1.0_00546.1.g15777.t1	gb|EOA30023.1| hypothetical protein CARUB_v10013125mg [Capsella rubella]	663	678	0	102.3	80.5	90.0	hypothetical protein CARUB_v10013125mg	gbpln	Capsella rubella	AT3G18840.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:6496198-6498234 FORWARD LENGTH=678	663	678	0	102.3	77.7	88.1
Rsa1.0_00546.1.g15778.t1	gb|EOA32324.1| hypothetical protein CARUB_v10015587mg [Capsella rubella]	101	102	1.00E-34	101.0	75.2	84.2	hypothetical protein CARUB_v10015587mg	gbpln	Capsella rubella	AT5G48485.1 | Symbols: DIR1 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:19646317-19646625 REVERSE LENGTH=102	101	102	5.00E-14	101.0	40.6	53.5
Rsa1.0_00546.1.g15779.t1	ref|XP_002885282.1| hypothetical protein ARALYDRAFT_318646 [Arabidopsis lyrata subsp. lyrata] gi|297331122|gb|EFH61541.1| hypothetical protein ARALYDRAFT_318646 [Arabidopsis lyrata subsp. lyrata]	343	375	0	109.3	87.5	94.8	hypothetical protein ARALYDRAFT_318646	gbpln	Arabidopsis lyrata	AT3G18850.4 | Symbols: LPAT5 | lysophosphatidyl acyltransferase 5 | chr3:6499529-6500840 REVERSE LENGTH=375	343	375	0	109.3	86.6	93.9
Rsa1.0_00546.1.g15780.t4	ref|NP_566620.1| phospholipase A-2-activating protein [Arabidopsis thaliana] gi|15294240|gb|AAK95297.1|AF410311_1 AT3g18860/MCB22_3 [Arabidopsis thaliana] gi|9294695|dbj|BAB03095.1| unnamed protein product [Arabidopsis thaliana] gi|332642639|gb|AEE76160.1| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	791	760	0	96.1	86.2	91.3	phospholipase A-2-activating protein	gbpln	Arabidopsis thaliana	AT3G18860.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:6501774-6508352 FORWARD LENGTH=760	791	760	0	96.1	86.2	91.3
Rsa1.0_00546.1.g15781.t1	gb|EOA32273.1| hypothetical protein CARUB_v10015534mg [Capsella rubella]	283	277	1.00E-130	97.9	85.2	90.5	hypothetical protein CARUB_v10015534mg	gbpln	Capsella rubella	AT3G18870.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr3:6508515-6509339 REVERSE LENGTH=274	283	274	1.00E-131	96.8	78.4	81.6
Rsa1.0_00546.1.g15782.t1	ref|NP_188518.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|9294697|dbj|BAB03097.1| 40S ribosomal protein S17-like [Arabidopsis thaliana] gi|26451825|dbj|BAC43005.1| putative ribosomal protein [Arabidopsis thaliana] gi|28416831|gb|AAO42946.1| At3g18880 [Arabidopsis thaliana] gi|332642642|gb|AEE76163.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	108	105	7.00E-42	97.2	82.4	88.0	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT3G18880.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr3:6509588-6510069 FORWARD LENGTH=105	108	105	1.00E-44	97.2	82.4	88.0
Rsa1.0_00546.1.g15783.t1	gb|ABV89636.1| catalytic/coenzyme binding protein [Brassica rapa]	650	624	0	96.0	85.1	89.2	catalytic/coenzyme binding protein	gbpln	Brassica rapa	AT3G18890.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:6511169-6514729 FORWARD LENGTH=641	650	641	0	98.6	76.9	82.2
Rsa1.0_00546.1.g15784.t1	ref|NP_188523.1| RING-H2 finger protein ATL65 [Arabidopsis thaliana] gi|42572481|ref|NP_974336.1| RING-H2 finger protein ATL65 [Arabidopsis thaliana] gi|68565164|sp|Q67YI6.2|ATL65_ARATH RecName: Full=RING-H2 finger protein ATL65 gi|9280310|dbj|BAB01689.1| unnamed protein product [Arabidopsis thaliana] gi|20258806|gb|AAM13984.1| unknown protein [Arabidopsis thaliana] gi|21689663|gb|AAM67453.1| unknown protein [Arabidopsis thaliana] gi|22531227|gb|AAM97117.1| unknown protein [Arabidopsis thaliana] gi|30725686|gb|AAP37865.1| At3g18930 [Arabidopsis thaliana] gi|51969336|dbj|BAD43360.1| unknown protein [Arabidopsis thaliana] gi|332642648|gb|AEE76169.1| RING-H2 finger protein ATL65 [Arabidopsis thaliana] gi|332642649|gb|AEE76170.1| RING-H2 finger protein ATL65 [Arabidopsis thaliana]	281	411	1.00E-108	146.3	79.0	84.0	RING-H2 finger protein ATL65	gbpln	Arabidopsis thaliana	AT3G18930.2 | Symbols: | RING/U-box superfamily protein | chr3:6524110-6525345 REVERSE LENGTH=411	281	411	1.00E-110	146.3	79.0	84.0
Rsa1.0_00547.1.g15785.t1	gb|AAB63623.1| cellulose synthase isolog [Arabidopsis thaliana]	298	730	1.00E-126	245.0	73.2	82.9	cellulose synthase isolog	gbpln	Arabidopsis thaliana	AT4G24000.1 | Symbols: ATCSLG2, CSLG2 | cellulose synthase like G2 | chr4:12462142-12465471 FORWARD LENGTH=722	298	722	1.00E-129	242.3	73.2	82.9
Rsa1.0_00547.1.g15786.t1	ref|XP_002867682.1| hypothetical protein ARALYDRAFT_492461 [Arabidopsis lyrata subsp. lyrata] gi|297313518|gb|EFH43941.1| hypothetical protein ARALYDRAFT_492461 [Arabidopsis lyrata subsp. lyrata]	173	174	2.00E-75	100.6	90.2	93.6	hypothetical protein ARALYDRAFT_492461	gbpln	Arabidopsis lyrata	AT4G24015.1 | Symbols: | RING/U-box superfamily protein | chr4:12469887-12471197 REVERSE LENGTH=174	173	174	7.00E-78	100.6	90.2	93.6

Rsa1.0_00547.1.g15787.t1	ref|NP_194133.1| NIN like protein 7 [Arabidopsis thaliana] gi|313471382|sp|Q84TH9.2|NLP7_ARATH RecName: Full=Protein NLP7; Short=AtNLP7; AltName: Full=NIN-like protein 7; AltName: Full=Nodule inception protein-like protein 7 gi|2262113|gb|AAB63621.1| unknown protein [Arabidopsis thaliana] gi|5668630|emb|CAB51645.1| putative protein [Arabidopsis thaliana] gi|7269251|emb|CAB81320.1| putative protein [Arabidopsis thaliana] gi|332659441|gb|AEE84841.1| NIN like protein 7 [Arabidopsis thaliana]	970	959	0	98.9	91.8	94.5	NIN like protein 7	gbpln	Arabidopsis thaliana	AT4G24020.1 | Symbols: NLP7 | NIN like protein 7 | chr4:12479904-12483822 FORWARD LENGTH=959	970	959	0	98.9	91.8	94.5
Rsa1.0_00547.1.g15788.t1	#	#	#	#	#	#	#	-	----	----	AT4G24030.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 4 Blast hits to 4 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:12486247-12486633 REVERSE LENGTH=128	93	128	1.00E-12	137.6	50.5	55.9
Rsa1.0_00547.1.g15789.t1	ref|XP_002869744.1| ATTRE1 [Arabidopsis lyrata subsp. lyrata] gi|297315580|gb|EFH46003.1| ATTRE1 [Arabidopsis lyrata subsp. lyrata]	562	628	0	111.7	84.9	91.8	ATTRE1	gbpln	Arabidopsis lyrata	AT4G24040.1 | Symbols: ATTRE1, TRE1 | trehalase 1 | chr4:12488242-12491060 FORWARD LENGTH=626	562	626	0	111.4	82.7	90.6
Rsa1.0_00547.1.g15790.t1	ref|XP_002869743.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315579|gb|EFH46002.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	332	332	0	100.0	92.5	97.9	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT4G24050.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:12497287-12499661 FORWARD LENGTH=332	332	332	0	100.0	91.9	98.2
Rsa1.0_00547.1.g15791.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	1265	1356	0	107.2	56.8	74.9	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1265	1262	1.00E-76	99.8	13.8	21.8
Rsa1.0_00547.1.g15792.t1	gb|AAM65223.1| unknown [Arabidopsis thaliana]	337	342	1.00E-137	101.5	79.8	85.2	unknown	gbpln	Arabidopsis thaliana	AT4G24060.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr4:12503970-12505417 FORWARD LENGTH=342	337	342	1.00E-134	101.5	80.1	84.9
Rsa1.0_00547.1.g15793.t1	ref|NP_194138.1| carbon-carbon lyase [Arabidopsis thaliana] gi|2262109|gb|AAB63617.1| hypothetical protein [Arabidopsis thaliana] gi|5668635|emb|CAB51650.1| putative protein [Arabidopsis thaliana] gi|7269256|emb|CAB81325.1| putative protein [Arabidopsis thaliana] gi|332659447|gb|AEE84847.1| carbon-carbon lyase [Arabidopsis thaliana]	77	66	1.00E-13	85.7	45.5	57.1	carbon-carbon lyase	gbpln	Arabidopsis thaliana	AT4G24070.1 | Symbols: | carbon-carbon lyases | chr4:12508895-12509095 FORWARD LENGTH=66	77	66	2.00E-16	85.7	45.5	57.1
Rsa1.0_00547.1.g15794.t1	gb|EOA18904.1| hypothetical protein CARUB_v10007534mg [Capsella rubella]	439	283	1.00E-115	64.5	46.0	51.5	hypothetical protein CARUB_v10007534mg	gbpln	Capsella rubella	AT4G24080.1 | Symbols: ALL1 | aldolase like | chr4:12511384-12512290 FORWARD LENGTH=231	439	231	1.00E-98	52.6	41.2	45.1
Rsa1.0_00547.1.g15795.t9	ref|NP_194141.2| protein kinase family protein [Arabidopsis thaliana] gi|20268686|gb|AAM14047.1| unknown protein [Arabidopsis thaliana] gi|22136716|gb|AAM91677.1| unknown protein [Arabidopsis thaliana] gi|332659450|gb|AEE84850.1| protein kinase family protein [Arabidopsis thaliana]	1096	709	0	64.7	54.0	57.6	protein kinase family protein	gbpln	Arabidopsis thaliana	AT4G24100.1 | Symbols: | Protein kinase superfamily protein | chr4:12515223-12519336 FORWARD LENGTH=709	1096	709	0	64.7	54.0	57.6
Rsa1.0_00547.1.g15796.t1	gb|EOA17299.1| hypothetical protein CARUB_v10005571mg [Capsella rubella]	249	252	5.00E-94	101.2	84.3	90.0	hypothetical protein CARUB_v10005571mg	gbpln	Capsella rubella	AT4G24110.1 | Symbols: | unknown protein; Has 76 Blast hits to 76 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 75; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:12520010-12520762 REVERSE LENGTH=250	249	250	3.00E-87	100.4	84.7	89.2

<table>
<tr><td>Rsa1.0_00547.1.g15797.t1</td><td>ref|NP_567694.2| metal-nicotianamine transporter YSL1 [Arabidopsis thaliana] gi|160359043|sp|Q6R3L0.2|YSL1_ARATH RecName: Full=Metal-nicotianamine transporter YSL1; AltName: Full=Protein YELLOW STRIPE LIKE 1; Short=AtYSL1 gi|332659452|gb|AEE84852.1| metal-nicotianamine transporter YSL1 [Arabidopsis thaliana]</td><td>674</td><td>673</td><td>0</td><td>99.9</td><td>92.7</td><td>96.6</td><td>metal-nicotianamine transporter YSL1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G24120.1 | Symbols: YSL1, ATYSL1 | YELLOW STRIPE like 1 | chr4:12524581-12527023 FORWARD LENGTH=673</td><td>674</td><td>673</td><td>0</td><td>99.9</td><td>92.7</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00547.1.g15798.t1</td><td>ref|XP_002869736.1| hypothetical protein ARALYDRAFT_492450 [Arabidopsis lyrata subsp. lyrata] gi|297315572|gb|EFH45995.1| hypothetical protein ARALYDRAFT_492450 [Arabidopsis lyrata subsp. lyrata]</td><td>157</td><td>157</td><td>9.00E-79</td><td>100.0</td><td>91.1</td><td>94.9</td><td>hypothetical protein ARALYDRAFT_492450</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G24130.1 | Symbols: | Protein of unknown function, DUF538 | chr4:12527861-12528423 FORWARD LENGTH=157</td><td>157</td><td>157</td><td>2.00E-80</td><td>100.0</td><td>89.8</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00548.1.g15799.t2</td><td>emb|CAB39609.1| pumilio-like protein [Arabidopsis thaliana] gi|7269439|emb|CAB79443.1| pumilio-like protein [Arabidopsis thaliana]</td><td>232</td><td>849</td><td>1.00E-16</td><td>365.9</td><td>22.8</td><td>26.7</td><td>pumilio-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G25880.1 | Symbols: APUM6, PUM6 | pumilio 6 | chr4:13155518-13159078 FORWARD LENGTH=861</td><td>232</td><td>861</td><td>4.00E-19</td><td>371.1</td><td>22.8</td><td>26.7</td></tr>
<tr><td>Rsa1.0_00548.1.g15800.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT1G10180.1 | Symbols: | BEST Arabidopsis thaliana protein match is: exocyst complex component 84B (TAIR:AT5G49830.1); Has 132 Blast hits to 132 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 0; Plants - 117; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr1:3338381-3341494 REVERSE LENGTH=769</td><td>131</td><td>769</td><td>2.00E-12</td><td>587.0</td><td>22.9</td><td>25.2</td></tr>
<tr><td>Rsa1.0_00548.1.g15801.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT1G61730.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:22793447-22794577 REVERSE LENGTH=376</td><td>153</td><td>376</td><td>1.00E-10</td><td>245.8</td><td>21.6</td><td>30.1</td></tr>
<tr><td>Rsa1.0_00548.1.g15802.t1</td><td>ref|NP_176815.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana] gi|12322267|gb|AAG51162.1|AC074025_12 hypothetical protein [Arabidopsis thaliana] gi|12324403|gb|AAG52170.1|AC020665_15 hypothetical protein; 78831-79679 [Arabidopsis thaliana] gi|225898052|dbj|BAH30358.1| hypothetical protein [Arabidopsis thaliana] gi|332196386|gb|AEE34507.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana]</td><td>311</td><td>282</td><td>3.00E-29</td><td>90.7</td><td>34.7</td><td>49.5</td><td>DNA-binding storekeeper protein-related transcriptional regulator</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G66420.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:24777184-24778032 FORWARD LENGTH=282</td><td>311</td><td>282</td><td>9.00E-32</td><td>90.7</td><td>34.7</td><td>49.5</td></tr>
<tr><td>Rsa1.0_00548.1.g15803.t1</td><td>ref|XP_002868503.1| hypothetical protein ARALYDRAFT_493700 [Arabidopsis lyrata subsp. lyrata] gi|297314339|gb|EFH44762.1| hypothetical protein ARALYDRAFT_493700 [Arabidopsis lyrata subsp. lyrata]</td><td>605</td><td>632</td><td>0</td><td>104.5</td><td>74.5</td><td>82.5</td><td>hypothetical protein ARALYDRAFT_493700</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G37010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G65710.1); Has 6746 Blast hits to 5259 proteins in 486 species: Archae - 7; Bacteria - 485; Metazoa - 3508; Fungi - 577; Plants - 378; Viruses - 50; Other Eukaryotes - 1741 (source: NCBI BLink). | chr5:14620853-14622879 REVERSE LENGTH=637</td><td>605</td><td>637</td><td>0</td><td>105.3</td><td>73.9</td><td>83.0</td></tr>
<tr><td>Rsa1.0_00548.1.g15804.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT3G26115.1 | Symbols: | Pyridoxal-5'-phosphate-dependent enzyme family protein | chr3:9542301-9544246 FORWARD LENGTH=427</td><td>73</td><td>427</td><td>6.00E-12</td><td>584.9</td><td>41.1</td><td>46.6</td></tr>
<tr><td>Rsa1.0_00548.1.g15805.t1</td><td>gb|AFD01306.1| auxin response factor 8-2 [Brassica rapa subsp. pekinensis]</td><td>820</td><td>844</td><td>0</td><td>102.9</td><td>96.2</td><td>97.1</td><td>auxin response factor 8-2</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G37020.1 | Symbols: ARF8, ATARF8 | auxin response factor 8 | chr5:14630151-14634106 FORWARD LENGTH=811</td><td>820</td><td>811</td><td>0</td><td>98.9</td><td>91.3</td><td>93.4</td></tr>
<tr><td>Rsa1.0_00548.1.g15806.t1</td><td>dbj|BAB11372.1| unnamed protein product [Arabidopsis thaliana]</td><td>854</td><td>880</td><td>0</td><td>103.0</td><td>75.3</td><td>83.8</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G37150.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:14701330-14704562 FORWARD LENGTH=839</td><td>854</td><td>839</td><td>0</td><td>98.2</td><td>73.1</td><td>82.1</td></tr>
<tr><td>Rsa1.0_00548.1.g15807.t1</td><td>emb|CAB75481.1| copia-like polyprotein [Arabidopsis thaliana]</td><td>761</td><td>1363</td><td>1.00E-130</td><td>179.1</td><td>36.7</td><td>52.6</td><td>copia-like polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145</td><td>761</td><td>145</td><td>1.00E-20</td><td>19.1</td><td>5.9</td><td>9.1</td></tr>
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Rsa1.0_00548.1.g15808.t1	dbj|BAB11372.1| unnamed protein product [Arabidopsis thaliana]	841	880	0	104.6	71.3	83.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G37150.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:14701330-14704562 FORWARD LENGTH=839	841	839	0	99.8	70.0	81.9
Rsa1.0_00548.1.g15809.t1	gb|EOA33463.1| hypothetical protein CARUB_v10021117mg [Capsella rubella]	145	145	6.00E-65	100.0	78.6	88.3	hypothetical protein CARUB_v10021117mg	gbpln	Capsella rubella	AT1G65820.1 | Symbols: | microsomal glutathione s-transferase, putative | chr1:24485213-24486682 FORWARD LENGTH=146	145	146	4.00E-67	100.7	79.3	86.9
Rsa1.0_00548.1.g15810.t1	ref|XP_002870519.1| hypothetical protein ARALYDRAFT_493710 [Arabidopsis lyrata subsp. lyrata] gi|297316355|gb|EFH46778.1| hypothetical protein ARALYDRAFT_493710 [Arabidopsis lyrata subsp. lyrata]	307	307	1.00E-130	100.0	75.9	83.1	hypothetical protein ARALYDRAFT_493710	gbpln	Arabidopsis lyrata	AT5G37360.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:14805437-14808113 REVERSE LENGTH=309	307	309	1.00E-125	100.7	78.2	85.7
Rsa1.0_00548.1.g15811.t1	ref|XP_002870522.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297316358|gb|EFH46781.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	97	419	6.00E-18	432.0	66.0	75.3	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT5G37380.5 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:14817035-14818330 REVERSE LENGTH=431	97	431	1.00E-19	444.3	67.0	77.3
Rsa1.0_00548.1.g15812.t1	gb|EOA15471.1| hypothetical protein CARUB_v10004388mg [Capsella rubella]	605	618	0	102.1	55.0	71.9	hypothetical protein CARUB_v10004388mg	gbpln	Capsella rubella	AT5G37460.1 | Symbols: | Family of unknown function (DUF577) | chr5:14858494-14860362 REVERSE LENGTH=622	605	622	1.00E-179	102.8	55.9	71.4
Rsa1.0_00548.1.g15813.t1	gb|AAF97298.1|AC007843_1 Hypothetical protein [Arabidopsis thaliana]	342	362	2.00E-61	105.8	38.0	48.2	Hypothetical protein	gbpln	Arabidopsis thaliana	AT5G37410.1 | Symbols: | Family of unknown function (DUF577) | chr5:14836661-14838508 FORWARD LENGTH=615	342	615	7.00E-18	179.8	13.2	17.5
Rsa1.0_00549.1.g15814.t1	gb|ABQ15204.1| rop [Musa acuminata]	62	196	1.00E-29	316.1	100.0	100.0	rop	gbpln	Musa acuminata	AT1G75840.1 | Symbols: ARAC5, ATGP3, ROP4, ATROP4 | RAC-like GTP binding protein 5 | chr1:28475964-28477377 FORWARD LENGTH=196	62	196	3.00E-31	316.1	100.0	100.0
Rsa1.0_00549.1.g15815.t1	ref|XP_002890369.1| plant synaptotagmin [Arabidopsis lyrata subsp. lyrata] gi|297336211|gb|EFH66628.1| plant synaptotagmin [Arabidopsis lyrata subsp. lyrata]	537	537	0	100.0	93.3	95.9	plant synaptotagmin	gbpln	Arabidopsis lyrata	AT1G20080.1 | Symbols: SYTB, ATSYTB, NTMC2TYPE1.2, NTMC2T1.2, SYT2 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:6962236-6964912 FORWARD LENGTH=537	537	537	0	100.0	92.4	95.5
Rsa1.0_00549.1.g15816.t1	gb|EOA38550.1| hypothetical protein CARUB_v10010355mg [Capsella rubella]	172	195	5.00E-41	113.4	76.2	81.4	hypothetical protein CARUB_v10010355mg	gbpln	Capsella rubella	AT1G20070.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 11 growth stages; Has 26 Blast hits to 26 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6958244-6958825 REVERSE LENGTH=193	172	193	2.00E-40	112.2	69.2	79.7
Rsa1.0_00549.1.g15817.t1	gb|AAF79911.1|AC022472_20 Contains similarity to ferredoxin-NADP+ reductase from Arabidopsis thaliana gb|AJ243705 and contains an oxidoreductase FAD/NAD-binding PF|00175 domain. ESTs gb|AI997056, gb|AV520008, gb|AV520028, gb|AV536019, gb|AI099538, gb|T22815, gb|R83951, gb|AV526060, gb|AV526098, gb|AV527136, gb|T76914, gb|H37111 come from this gene [Arabidopsis thaliana]	321	348	1.00E-161	108.4	90.3	93.8	Contains similarity to ferredoxin-NADP+ reductase from Arabidopsis thaliana gb|AJ243705 and contains an oxidoreductase FAD/NAD-binding PF|00175 domain. ESTs gb|AI997056, gb|AV520008, gb|AV520028, gb|AV536019, gb|AI099538, gb|T22815, gb|R83951, gb|AV526060, gb|AV526098, gb|AV527136, gb|T76914, gb|H37111 come from this gene	gbpln	Arabidopsis thaliana	AT1G20020.1 | Symbols: ATLFNR2, FNR2 | ferredoxin-NADP(+)-oxidoreductase 2 | chr1:6942851-6944868 FORWARD LENGTH=369	321	369	1.00E-161	115.0	90.3	93.8

Rsa1.0_00549.1.g15818.t1	ref|NP_173427.1| cytomatrix protein-like protein [Arabidopsis thaliana] gi|28392994|gb|AAO41932.1| unknown protein [Arabidopsis thaliana] gi|28827278|gb|AAO50483.1| unknown protein [Arabidopsis thaliana] gi|332191798|gb|AEE29919.1| cytomatrix protein-like protein [Arabidopsis thaliana]	336	342	1.00E-123	101.8	70.2	84.5	cytomatrix protein-like protein	gbpln	Arabidopsis thaliana	AT1G19980.1 | Symbols: | cytomatrix protein-related | chr1:6933162-6934643 FORWARD LENGTH=342	336	342	1.00E-126	101.8	70.2	84.5
Rsa1.0_00549.1.g15819.t1	gb|EOA36994.1| hypothetical protein CARUB_v10010001mg [Capsella rubella]	272	272	1.00E-144	100.0	91.5	95.2	hypothetical protein CARUB_v10010001mg	gbpln	Capsella rubella	AT1G19970.1 | Symbols: | ER lumen protein retaining receptor family protein | chr1:6931194-6932597 REVERSE LENGTH=272	272	272	1.00E-147	100.0	90.4	95.6
Rsa1.0_00549.1.g15820.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00549.1.g15821.t2	ref|XP_002890359.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata] gi|297336201|gb|EFH66618.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata]	309	309	1.00E-125	100.0	79.6	85.4	abscisic acid-responsive HVA22 family protein	gbpln	Arabidopsis lyrata	AT1G19950.1 | Symbols: HVA22H | HVA22-like protein H (ATHVA22H) | chr1:6925043-6926527 FORWARD LENGTH=315	309	315	1.00E-119	101.9	78.0	84.5
Rsa1.0_00549.1.g15822.t1	gb|AAB67995.1| ATP-sulfurylase precursor [Brassica oleracea]	431	483	0	112.1	94.4	97.2	ATP-sulfurylase precursor	gbpln	Brassica oleracea	AT1G19920.1 | Symbols: APS2, ASA1 | Pseudouridine synthase/archaeosine transglycosylase-like family protein | chr1:6914835-6916657 REVERSE LENGTH=476	431	476	0	110.4	89.6	95.4
Rsa1.0_00549.1.g15823.t1	ref|XP_002513751.1| vacuolar ATP synthase proteolipid subunit 1, 2, 3, putative [Ricinus communis] gi|223546837|gb|EEF48334.1| vacuolar ATP synthase proteolipid subunit 1, 2, 3, putative [Ricinus communis]	165	169	2.00E-84	102.4	99.4	100.0	vacuolar ATP synthase proteolipid subunit 1, 2, 3, putative	gbpln	Ricinus communis	AT1G19910.1 | Symbols: AVA-P2, AVA-2PE, ATVHA-C2 | ATPase, F0/V0 complex, subunit C protein | chr1:6913317-6914322 FORWARD LENGTH=165	165	165	1.00E-86	100.0	99.4	99.4
Rsa1.0_00549.1.g15824.t1	ref|NP_564097.1| protein IQ-domain 32 [Arabidopsis thaliana] gi|332278202|sp|Q9FXI5.3|IQD32_ARATH RecName: Full=Protein IQ-DOMAIN 32 gi|332191787|gb|AEE29908.1| protein IQ-domain 32 [Arabidopsis thaliana]	731	794	0	108.6	75.8	84.3	protein IQ-domain 32	gbpln	Arabidopsis thaliana	AT1G19870.1 | Symbols: iqd32 | IQ-domain 32 | chr1:6895400-6898539 REVERSE LENGTH=794	731	794	0	108.6	75.8	84.3
Rsa1.0_00549.1.g15825.t1	ref|XP_002893076.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297338918|gb|EFH69335.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	412	411	0	99.8	82.0	87.9	zinc finger (CCCH-type) family protein	gbpln	Arabidopsis lyrata	AT1G19860.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:6891654-6894400 REVERSE LENGTH=413	412	413	1.00E-177	100.2	79.4	86.7
Rsa1.0_00549.1.g15826.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00549.1.g15827.t1	gb|AFD01300.1| auxin response factor 5-2 [Brassica rapa subsp. pekinensis]	629	836	0	132.9	88.7	91.1	auxin response factor 5-2	gbpln	Brassica rapa	AT1G19850.1 | Symbols: MP, ARF5, IAA24 | Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related | chr1:6887353-6891182 FORWARD LENGTH=902	629	902	0	143.4	86.5	90.8
Rsa1.0_00549.1.g15828.t1	gb|AFD01299.1| auxin response factor 5-1 [Brassica rapa subsp. pekinensis]	202	867	8.00E-96	429.2	85.1	88.1	auxin response factor 5-1	gbpln	Brassica rapa	AT1G19850.1 | Symbols: MP, ARF5, IAA24 | Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related | chr1:6887353-6891182 FORWARD LENGTH=902	202	902	2.00E-95	446.5	84.2	88.1
Rsa1.0_00549.1.g15829.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00549.1.g15830.t1	gb|AAF79835.1|AC026875_15 T6D22.19 [Arabidopsis thaliana]	842	745	1.00E-178	88.5	37.1	50.8	T6D22.19	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	842	696	2.00E-73	82.7	20.5	35.7
Rsa1.0_00549.1.g15831.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00549.1.g15832.t1	ref|XP_002893072.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297338914|gb|EFH69331.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	147	153	8.00E-63	104.1	87.1	91.2	auxin-responsive family protein	gbpln	Arabidopsis lyrata	AT1G19840.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:6872794-6873255 REVERSE LENGTH=153	147	153	3.00E-65	104.1	86.4	91.2
Rsa1.0_00550.1.g15833.t1	ref|XP_002873897.1| hypothetical protein ARALYDRAFT_488728 [Arabidopsis lyrata subsp. lyrata] gi|297319734|gb|EFH50156.1| hypothetical protein ARALYDRAFT_488728 [Arabidopsis lyrata subsp. lyrata]	537	538	0	100.2	85.8	90.9	hypothetical protein ARALYDRAFT_488728	gbpln	Arabidopsis lyrata	AT5G18480.1 | Symbols: PGSIP6 | plant glycogenin-like starch initiation protein 6 | chr5:6131307-6133787 REVERSE LENGTH=537	537	537	0	100.0	85.7	90.9

Rsa1.0_00550.1.g15834.t1	ref|NP_197351.1| protein kinase family protein [Arabidopsis thaliana] gi|79328036|ref|NP_001031898.1| protein kinase family protein [Arabidopsis thaliana] gi|75330007|sp|Q8LEB6.1|Y5185_ARATH RecName: Full=Probable receptor-like protein kinase At5g18500 gi|21553648|gb|AAM62741.1| Ser Thr specific protein kinase-like protein [Arabidopsis thaliana] gi|115646738|gb|ABJ17100.1| At5g18500 [Arabidopsis thaliana] gi|332005188|gb|AED92571.1| protein kinase family protein [Arabidopsis thaliana] gi|332005189|gb|AED92572.1| probable receptor-like protein kinase [Arabidopsis thaliana]	305	484	1.00E-158	158.7	92.8	95.4	protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G18500.2 | Symbols: | Protein kinase superfamily protein | chr5:6139263-6141283 FORWARD LENGTH=484	305	484	1.00E-161	158.7	92.8	95.4
Rsa1.0_00550.1.g15835.t1	ref|NP_189068.2| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana] gi|332643359|gb|AEE76880.1| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana]	235	746	2.00E-38	317.4	31.1	42.1	RNA-directed DNA polymerase (reverse transcriptase)-related protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	235	746	5.00E-41	317.4	31.1	42.1
Rsa1.0_00550.1.g15836.t1	gb|EOA20522.1| hypothetical protein CARUB_v10000836mg [Capsella rubella]	162	485	2.00E-66	299.4	78.4	84.0	hypothetical protein CARUB_v10000836mg	gbpln	Capsella rubella	AT5G18500.2 | Symbols: | Protein kinase superfamily protein | chr5:6139263-6141283 FORWARD LENGTH=484	162	484	5.00E-68	298.8	77.8	84.0
Rsa1.0_00550.1.g15837.t1	ref|NP_175400.1| U-box domain-containing protein 26 [Arabidopsis thaliana] gi|75173046|sp|Q9FXA4.1|PUB26_ARATH RecName: Full=U-box domain-containing protein 26; AltName: Full=Plant U-box protein 26 gi|10120432|gb|AAG13057.1|AC011807_16 Hypothetical protein [Arabidopsis thaliana] gi|115311483|gb|ABI93922.1| At1g49780 [Arabidopsis thaliana] gi|332194354|gb|AEE32475.1| U-box domain-containing protein 26 [Arabidopsis thaliana]	94	421	1.00E-30	447.9	72.3	75.5	U-box domain-containing protein 26	gbpln	Arabidopsis thaliana	AT1G49780.1 | Symbols: PUB26 | plant U-box 26 | chr1:18429024-18430289 REVERSE LENGTH=421	94	421	2.00E-33	447.9	72.3	75.5
Rsa1.0_00550.1.g15838.t1	ref|NP_198605.2| E3 ubiquitin-protein ligase SINA-like 7 [Arabidopsis thaliana] gi|75171229|sp|Q9FKD7.1|SINL7_ARATH RecName: Full=E3 ubiquitin-protein ligase SINA-like 7; AltName: Full=Seven in absentia-like protein 7 gi|9758489|dbj|BAB09035.1| unnamed protein product [Arabidopsis thaliana] gi|18253003|gb|AAL62428.1| putative protein [Arabidopsis thaliana] gi|21389685|gb|AAM48041.1| putative protein [Arabidopsis thaliana] gi|332006861|gb|AED94244.1| E3 ubiquitin-protein ligase SINA-like 7 [Arabidopsis thaliana]	256	286	2.00E-70	111.7	50.4	66.0	E3 ubiquitin-protein ligase SINA-like 7	gbpln	Arabidopsis thaliana	AT5G37890.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr5:15090512-15091822 REVERSE LENGTH=286	256	286	6.00E-73	111.7	50.4	66.0
Rsa1.0_00550.1.g15839.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00550.1.g15840.t1	ref|XP_002871820.1| hypothetical protein ARALYDRAFT_488733 [Arabidopsis lyrata subsp. lyrata] gi|297317657|gb|EFH48079.1| hypothetical protein ARALYDRAFT_488733 [Arabidopsis lyrata subsp. lyrata]	442	440	0	99.5	93.2	96.6	hypothetical protein ARALYDRAFT_488733	gbpln	Arabidopsis lyrata	AT5G18520.1 | Symbols: | Lung seven transmembrane receptor family protein | chr5:6145027-6146349 FORWARD LENGTH=440	442	440	0	99.5	92.8	95.7
Rsa1.0_00550.1.g15841.t2	ref|NP_197355.2| uncharacterized protein [Arabidopsis thaliana] gi|48958465|gb|AAT47785.1| At5g18540 [Arabidopsis thaliana] gi|51972056|gb|AAU15132.1| At5g18540 [Arabidopsis thaliana] gi|332005193|gb|AED92576.1| uncharacterized protein AT5G18540 [Arabidopsis thaliana]	167	168	6.00E-58	100.6	92.8	97.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G18540.1 | Symbols: | unknown protein; Has 2026 Blast hits to 792 proteins in 129 species: Archae - 2; Bacteria - 12; Metazoa - 1126; Fungi - 267; Plants - 292; Viruses - 0; Other Eukaryotes - 327 (source: NCBI BLink). | chr5:6153924-6155877 FORWARD LENGTH=168	167	168	2.00E-60	100.6	92.8	97.6
Rsa1.0_00550.1.g15842.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	334	255	3.00E-45	76.3	33.8	41.9	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	334	302	2.00E-45	90.4	32.0	44.3
Rsa1.0_00550.1.g15843.t1	gb|EOA20563.1| hypothetical protein CARUB_v10000876mg [Capsella rubella]	454	473	0	104.2	78.9	86.3	hypothetical protein CARUB_v10000876mg	gbpln	Capsella rubella	AT5G18550.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr5:6160515-6162729 FORWARD LENGTH=465	454	465	0	102.4	79.7	85.7

Rsa1.0_00550.1.g15844.t1	ref|NP_197357.2| ethylene response factor PUCHI [Arabidopsis thaliana] gi|334302788|sp|Q6J9Q2.2|ERF86_ARATH RecName: Full=Ethylene-responsive transcription factor ERF086 gi|332005196|gb|AED92579.1| ethylene response factor PUCHI [Arabidopsis thaliana]	316	348	2.33E-156	110.1	88.3	92.7	ethylene response factor PUCHI	gbpln	Arabidopsis thaliana	AT5G18560.1 | Symbols: PUCHI | Integrase-type DNA-binding superfamily protein | chr5:6164859-6165905 REVERSE LENGTH=348	316	348	1.00E-149	110.1	88.3	92.7
Rsa1.0_00550.1.g15845.t1	ref|NP_197358.2| GTP1/OBG family protein [Arabidopsis thaliana] gi|22136032|gb|AAM91598.1| GTP-binding protein obg-like [Arabidopsis thaliana] gi|30725516|gb|AAP37780.1| At5g18570 [Arabidopsis thaliana] gi|332005197|gb|AED92580.1| GTP1/OBG family protein [Arabidopsis thaliana]	677	681	0	100.6	88.9	93.5	GTP1/OBG family protein	gbpln	Arabidopsis thaliana	AT5G18570.1 | Symbols: EMB269, ATOBGC, CPSAR1 | GTP1/OBG family protein | chr5:6171839-6174823 REVERSE LENGTH=681	677	681	0	100.6	88.9	93.5
Rsa1.0_00550.1.g15846.t2	ref|XP_002871823.1| hypothetical protein ARALYDRAFT_909871 [Arabidopsis lyrata subsp. lyrata] gi|297317660|gb|EFH48082.1| hypothetical protein ARALYDRAFT_909871 [Arabidopsis lyrata subsp. lyrata]	480	480	0	100.0	94.4	95.0	hypothetical protein ARALYDRAFT_909871	gbpln	Arabidopsis lyrata	AT5G18580.1 | Symbols: FASS, TON2, EMB40, FS1, GDO, FASS 2 | tonneau 2 (TON2) | chr5:6175154-6178214 FORWARD LENGTH=480	480	480	0	100.0	93.5	94.6
Rsa1.0_00550.1.g15847.t1	ref|XP_002873906.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297319743|gb|EFH50165.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	102	102	1.00E-49	100.0	92.2	100.0	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT5G18600.1 | Symbols: | Thioredoxin superfamily protein | chr5:6183466-6183774 REVERSE LENGTH=102	102	102	4.00E-52	100.0	92.2	98.0
Rsa1.0_00550.1.g15848.t4	gb|AAB84340.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1083	1094	0	101.0	29.0	38.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18610.2 | Symbols: | Protein kinase superfamily protein | chr5:6192736-6195371 FORWARD LENGTH=513	1083	513	7.00E-41	47.4	8.0	8.7
Rsa1.0_00550.1.g15849.t1	gb|EOA19325.1| hypothetical protein CARUB_v10003350mg [Capsella rubella]	899	886	0	98.6	76.3	85.4	hypothetical protein CARUB_v10003350mg	gbpln	Capsella rubella	AT5G18860.1 | Symbols: | inosine-uridine preferring nucleoside hydrolase family protein | chr5:6291023-6295581 FORWARD LENGTH=890	899	890	0	99.0	74.0	82.2
Rsa1.0_00550.1.g15850.t1	gb|EOA21225.1| hypothetical protein CARUB_v10001574mg [Capsella rubella]	295	300	1.00E-150	101.7	87.5	92.2	hypothetical protein CARUB_v10001574mg	gbpln	Capsella rubella	AT5G18900.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:6304409-6306166 REVERSE LENGTH=298	295	298	1.00E-152	101.0	84.7	88.1
Rsa1.0_00550.1.g15851.t1	ref|NP_565032.2| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|63003832|gb|AAY25445.1| At1g72040 [Arabidopsis thaliana] gi|110737520|dbj|BAF00702.1| hypothetical protein [Arabidopsis thaliana] gi|332197145|gb|AEE35266.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana]	233	580	2.00E-34	248.9	28.3	30.5	P-loop containing nucleoside triphosphate hydrolase-like protein	gbpln	Arabidopsis thaliana	AT1G72040.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:27112159-27114248 REVERSE LENGTH=580	233	580	5.00E-37	248.9	28.3	30.5
Rsa1.0_00550.1.g15852.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00550.1.g15853.t1	gb|EOA22691.1| hypothetical protein CARUB_v10003395mg [Capsella rubella]	526	520	0	98.9	76.6	82.7	hypothetical protein CARUB_v10003395mg	gbpln	Capsella rubella	AT5G18910.1 | Symbols: | Protein kinase superfamily protein | chr5:6306994-6309396 REVERSE LENGTH=511	526	511	0	97.1	75.5	81.6
Rsa1.0_00550.1.g15854.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00550.1.g15855.t1	ref|NP_001190334.1| BTB-POZ and math domain-containing protein [Arabidopsis thaliana] gi|332005255|gb|AED92638.1| BTB-POZ and math domain-containing protein [Arabidopsis thaliana]	422	442	0	104.7	82.5	88.4	BTB-POZ and math domain-containing protein	gbpln	Arabidopsis thaliana	AT5G19000.2 | Symbols: BPM1 | BTB-POZ and MATH domain 1 | chr5:6342563-6344641 FORWARD LENGTH=442	422	442	0	104.7	82.5	88.4
Rsa1.0_00550.1.g15856.t1	dbj|BAE43828.1| isopentenyltransferase [Brassica rapa subsp. pekinensis]	334	331	1.00E-179	99.1	91.6	94.0	isopentenyltransferase	gbpln	Brassica rapa	AT5G19040.1 | Symbols: ATIPT5, IPT5 | isopentenyltransferase 5 | chr5:6362389-6363381 REVERSE LENGTH=330	334	330	1.00E-167	98.8	84.4	91.6
Rsa1.0_00550.1.g15857.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00550.1.g15858.t1	emb|CAN75440.1| hypothetical protein VITISV_007304 [Vitis vinifera]	142	1362	2.00E-43	959.2	62.0	78.9	hypothetical protein VITISV_007304	gbpln	Vitis vinifera	#	#	#	#	#	#	#

Rsa1.0_00551.1.g15859.t1	ref|NP_175998.1| uncharacterized protein [Arabidopsis thaliana] gi|6056382|gb|AAF02846.1|AC009894_17 Unknown protein [Arabidopsis thaliana] gi|8778317|gb|AAF79326.1|AC002304_19 F14J16.33 [Arabidopsis thaliana] gi|44681358|gb|AAS47619.1| At1g56020 [Arabidopsis thaliana] gi|45773898|gb|AAS76753.1| At1g56020 [Arabidopsis thaliana] gi|332195211|gb|AEE33332.1| uncharacterized protein AT1G56020 [Arabidopsis thaliana]	334	398	3.00E−92	119.2	68.3	76.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G56020.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12970.1); Has 3011 Blast hits to 958 proteins in 192 species: Archae − 0; Bacteria − 193; Metazoa − 479; Fungi − 286; Plants − 158; Viruses − 8; Other Eukaryotes − 1887 (source: NCBI BLink). | chr1:20952216−20953412 FORWARD LENGTH=398	334	398	8.00E−95	119.2	68.3	76.3
Rsa1.0_00551.1.g15860.t1	ref|XP_002884938.1| hypothetical protein ARALYDRAFT_478672 [Arabidopsis lyrata subsp. lyrata] gi|297330778|gb|EFH61197.1| hypothetical protein ARALYDRAFT_478672 [Arabidopsis lyrata subsp. lyrata]	282	445	1.00E−57	157.8	48.6	57.1	hypothetical protein ARALYDRAFT_478672	gbpln	Arabidopsis lyrata	AT3G13040.2 | Symbols: | myb−like HTH transcriptional regulator family protein | chr3:4172415−4174456 REVERSE LENGTH=449	282	449	1.00E−58	159.2	53.5	64.5
Rsa1.0_00551.1.g15861.t1	gb|EOA37940.1| hypothetical protein CARUB_v10009408mg [Capsella rubella]	371	387	1.00E−125	104.3	66.3	75.2	hypothetical protein CARUB_v10009408mg	gbpln	Capsella rubella	AT1G55960.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:20927962−20929825 REVERSE LENGTH=403	371	403	1.00E−119	108.6	64.4	74.1
Rsa1.0_00551.1.g15862.t1	gb|AAT38562.1| chloroplast serine acetyltransferase [Thlaspi goesingense]	318	319	1.00E−141	100.3	81.8	88.1	chloroplast serine acetyltransferase	gbpln	Thlaspi goesingense	AT1G55920.1 | Symbols: ATSERAT2;1, SAT5, SAT1, SERAT2;1 | serine acetyltransferase 2;1 | chr1:20912378−20913322 FORWARD LENGTH=314	318	314	1.00E−141	98.7	78.6	87.1
Rsa1.0_00551.1.g15863.t1	gb|EOA40594.1| hypothetical protein CARUB_v10009325mg, partial [Capsella rubella]	224	403	6.00E−68	179.9	54.0	58.5	hypothetical protein CARUB_v10009325mg, partial	gbpln	Capsella rubella	AT1G55900.1 | Symbols: TIM50, emb1860 | Haloacid dehalogenase−like hydrolase (HAD) superfamily protein | chr1:20903163−20905420 FORWARD LENGTH=376	224	376	3.00E−70	167.9	53.1	58.5
Rsa1.0_00551.1.g15864.t1	emb|CAB10381.1| retrotransposon like protein [Arabidopsis thaliana] gi|7268351|emb|CAB78644.1| retrotransposon like protein [Arabidopsis thaliana]	224	326	6.00E−39	145.5	34.8	41.5	retrotransposon like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00551.1.g15865.t1	ref|NP_175984.1| cysteine synthase A [Arabidopsis thaliana] gi|46518441|gb|AAS99702.1| At1g55880 [Arabidopsis thaliana] gi|110741637|dbj|BAE98765.1| hypothetical protein [Arabidopsis thaliana] gi|332195192|gb|AEE33313.1| pyridoxal−5'−phosphate−dependent enzyme family protein [Arabidopsis thaliana]	417	421	0	101.0	88.0	93.8	cysteine synthase A	gbpln	Arabidopsis thaliana	AT1G55880.1 | Symbols: | Pyridoxal−5'−phosphate−dependent enzyme family protein | chr1:20899292−20901140 REVERSE LENGTH=421	417	421	0	101.0	88.0	93.8
Rsa1.0_00551.1.g15866.t1	ref|XP_002891857.1| Poly(A)−specific ribonuclease [Arabidopsis lyrata subsp. lyrata] gi|297337699|gb|EFH68116.1| Poly(A)−specific ribonuclease [Arabidopsis lyrata subsp. lyrata]	687	689	0	100.3	82.5	88.8	Poly(A)−specific ribonuclease	gbpln	Arabidopsis lyrata	AT1G55870.1 | Symbols: ATPARN, AHG2 | Polynucleotidyl transferase, ribonuclease H−like superfamily protein | chr1:20895663−20898359 FORWARD LENGTH=689	687	689	0	100.3	80.9	88.2
Rsa1.0_00551.1.g15867.t1	gb|EOA39047.1| hypothetical protein CARUB_v10011657mg [Capsella rubella]	3620	3915	0	108.1	84.3	90.0	hypothetical protein CARUB_v10011657mg	gbpln	Capsella rubella	AT1G55860.2 | Symbols: UPL1 | ubiquitin−protein ligase 1 | chr1:20879900−20892910 REVERSE LENGTH=3681	3620	3681	0	101.7	84.6	90.0
Rsa1.0_00551.1.g15868.t2	ref|NP_175980.1| sec.4−like phosphatidylinositol transfer protein [Arabidopsis thaliana] gi|16930447|gb|AAL31909.1|AF419577_1 At1g55840/F14J16_2 [Arabidopsis thaliana] gi|19310517|gb|AAL84992.1| At1g55840/F14J16_2 [Arabidopsis thaliana] gi|332195185|gb|AEE33306.1| sec.4−like phosphatidylinositol transfer protein [Arabidopsis thaliana]	329	325	1.00E−172	98.8	89.1	93.9	sec.4−like phosphatidylinositol transfer protein	gbpln	Arabidopsis thaliana	AT1G55840.1 | Symbols: | Sec14p−like phosphatidylinositol transfer family protein | chr1:20873891−20876018 FORWARD LENGTH=325	329	325	1.00E−175	98.8	89.1	93.9
Rsa1.0_00551.1.g15869.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00551.1.g15870.t1	ref|NP_001185244.1| uncharacterized protein [Arabidopsis thaliana] gi|332195184|gb|AEE33305.1| uncharacterized protein AT1G55830 [Arabidopsis thaliana]	491	493	0	100.4	74.1	85.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G55830.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF812 (InterPro:IPR008530). | chr1:20867918−20870205 REVERSE LENGTH=493	491	493	0	100.4	74.1	85.3
Rsa1.0_00551.1.g15871.t1	gb|EOA23321.1| hypothetical protein CARUB_v10019219mg [Capsella rubella]	392	444	1.00E−140	113.3	65.8	76.0	hypothetical protein CARUB_v10019219mg	gbpln	Capsella rubella	AT2G40920.1 | Symbols: | F−box and associated interaction domains−containing protein | chr2:17072586−17074012 REVERSE LENGTH=436	392	436	3.00E−82	111.2	46.9	61.5

Rsa1.0_00551.1.g15872.t1	ref|NP_001185244.1| uncharacterized protein [Arabidopsis thaliana] gi|332195184|gb|AEE33305.1| uncharacterized protein AT1G55830 [Arabidopsis thaliana]	105	493	3.00E-25	469.5	55.2	59.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G55830.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF812 (InterPro:IPR008530). | chr1:20867918-20870205 REVERSE LENGTH=493	105	493	4.00E-28	469.5	55.2	59.0
Rsa1.0_00551.1.g15873.t1	gb|EOA40054.1| hypothetical protein CARUB_v10008748mg [Capsella rubella]	663	554	1.00E-166	83.6	56.1	64.9	hypothetical protein CARUB_v10008748mg	gbpln	Capsella rubella	AT1G55820.1 | Symbols: | Kinase-related protein of unknown function (DUF1296) | chr1:20864397-20867418 FORWARD LENGTH=575	663	575	1.00E-162	86.7	54.9	64.6
Rsa1.0_00551.1.g15874.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00551.1.g15875.t2	ref|XP_002894530.1| hypothetical protein ARALYDRAFT_892585 [Arabidopsis lyrata subsp. lyrata] gi|297340372|gb|EFH70789.1| hypothetical protein ARALYDRAFT_892585 [Arabidopsis lyrata subsp. lyrata]	454	480	1.00E-125	105.7	61.7	69.8	hypothetical protein ARALYDRAFT_892585	gbpln	Arabidopsis lyrata	AT1G55790.1 | Symbols: | Domain of unknown function (DUF2431) | chr1:20852685-20856069 REVERSE LENGTH=515	454	515	1.00E-107	113.4	43.6	48.5
Rsa1.0_00551.1.g15876.t1	ref|XP_002894528.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297340370|gb|EFH70787.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	175	175	3.00E-68	100.0	84.0	91.4	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT1G55770.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:20851039-20851566 REVERSE LENGTH=175	175	175	5.00E-67	100.0	80.6	89.7
Rsa1.0_00552.1.g15877.t1	gb|AAF24568.1|AC007764_10 F22C12.22 [Arabidopsis thaliana]	75	651	7.00E-20	868.0	70.7	78.7	F22C12.22	gbpln	Arabidopsis thaliana	AT1G64010.1 | Symbols: | Serine protease inhibitor (SERPIN) family protein | chr1:23750884-23751441 REVERSE LENGTH=185	75	185	2.00E-22	246.7	70.7	78.7
Rsa1.0_00552.1.g15878.t1	gb|EOA13968.1| hypothetical protein CARUB_v10027093mg [Capsella rubella]	268	220	7.00E-81	82.1	62.3	73.1	hypothetical protein CARUB_v10027093mg	gbpln	Capsella rubella	AT5G51870.3 | Symbols: AGL71 | AGAMOUS-like 71 | chr5:21085635-21087923 REVERSE LENGTH=219	268	219	6.00E-80	81.7	60.8	70.1
Rsa1.0_00552.1.g15879.t1	gb|EOA12032.1| hypothetical protein CARUB_v10008034mg [Capsella rubella]	383	435	1.00E-110	113.6	61.4	71.3	hypothetical protein CARUB_v10008034mg	gbpln	Capsella rubella	AT1G62170.1 | Symbols: | Serine protease inhibitor (SERPIN) family protein | chr1:22973876-22975463 FORWARD LENGTH=433	383	433	1.00E-112	113.1	61.6	72.6
Rsa1.0_00552.1.g15880.t1	ref|NP_568766.1| uncharacterized protein [Arabidopsis thaliana] gi|87116564|gb|ABD19646.1| At5g51840 [Arabidopsis thaliana] gi|332008750|gb|AED96133.1| uncharacterized protein AT5G51840 [Arabidopsis thaliana]	263	245	1.00E-113	93.2	80.6	85.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G51840.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21072143-21074131 FORWARD LENGTH=245	263	245	1.00E-116	93.2	80.6	85.9
Rsa1.0_00552.1.g15881.t2	ref|NP_199996.1| fructokinase [Arabidopsis thaliana] gi|13878053|gb|AAK44104.1|AF370289_1 putative fructokinase 1 [Arabidopsis thaliana] gi|10177882|dbj|BAB11252.1| fructokinase 1 [Arabidopsis thaliana] gi|17104645|gb|AAL34211.1| putative fructokinase 1 [Arabidopsis thaliana] gi|332008749|gb|AED96132.1| pfkB-like carbohydrate kinase family protein [Arabidopsis thaliana]	350	343	1.00E-172	98.0	87.1	90.6	fructokinase	gbpln	Arabidopsis thaliana	AT5G51830.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr5:21069709-21071450 FORWARD LENGTH=343	350	343	1.00E-174	98.0	87.1	90.6
Rsa1.0_00552.1.g15882.t1	ref|NP_199990.1| protein kinase family protein [Arabidopsis thaliana] gi|10177876|dbj|BAB11246.1| unnamed protein product [Arabidopsis thaliana] gi|332008741|gb|AED96124.1| protein kinase family protein [Arabidopsis thaliana]	608	654	0	107.6	71.1	78.5	protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G51770.1 | Symbols: | Protein kinase superfamily protein | chr5:21031030-21032994 FORWARD LENGTH=654	608	654	0	107.6	71.1	78.5
Rsa1.0_00552.1.g15883.t1	ref|NP_199989.1| protein phosphatase [Arabidopsis thaliana] gi|75309185|sp|Q9FLI3.1|P2C75_ARATH RecName: Full=Probable protein phosphatase 2C 75; Short=AtPP2C75; AltName: Full=Protein ABA-HYPERSENSITIVE GERMINATION 1; AltName: Full=Protein phosphatase 2C AHG1; Short=PP2C AHG1 gi|10177875|dbj|BAB11245.1| protein phosphatase-2C; PP2C-like protein [Arabidopsis thaliana] gi|332008740|gb|AED96123.1| probable protein phosphatase AHG1 [Arabidopsis thaliana]	423	416	1.00E-178	98.3	79.9	87.9	protein phosphatase	gbpln	Arabidopsis thaliana	AT5G51760.1 | Symbols: AHG1 | Protein phosphatase 2C family protein | chr5:21026916-21028912 FORWARD LENGTH=416	423	416	0	98.3	79.9	87.9

Rsa1.0_00552.1.g15884.t1	ref|XP_002883761.1| hypothetical protein ARALYDRAFT_480234 [Arabidopsis lyrata subsp. lyrata] gi|297329601|gb|EFH60020.1| hypothetical protein ARALYDRAFT_480234 [Arabidopsis lyrata subsp. lyrata]	128	128	8.00E-58	100.0	86.7	94.5	hypothetical protein ARALYDRAFT_480234	gbpln	Arabidopsis lyrata	AT2G07340.1 | Symbols: PFD1 | PREFOLDIN 1 | chr2:3045644-3046606 FORWARD LENGTH=128	128	128	2.00E-60	100.0	85.9	95.3
Rsa1.0_00552.1.g15885.t1	ref|XP_002865872.1| 1-amino-cyclopropane-1-carboxylate synthase 12 [Arabidopsis lyrata subsp. lyrata] gi|297311707|gb|EFH42131.1| 1-amino-cyclopropane-1-carboxylate synthase 12 [Arabidopsis lyrata subsp. lyrata]	489	495	0	101.2	81.0	89.8	1-amino-cyclopropane-1-carboxylate synthase 12	gbpln	Arabidopsis lyrata	AT5G51690.1 | Symbols: ACS12 | 1-amino-cyclopropane-1-carboxylate synthase 12 | chr5:20999015-21000957 REVERSE LENGTH=495	489	495	0	101.2	80.4	89.6
Rsa1.0_00552.1.g15886.t1	ref|NP_001189515.1| SH3 domain-containing protein [Arabidopsis thaliana] gi|330250956|gb|AEC06050.1| SH3 domain-containing protein [Arabidopsis thaliana]	1192	1198	0	100.5	93.6	97.5	SH3 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G07360.2 | Symbols: | SH3 domain-containing protein | chr2:3047623-3057099 REVERSE LENGTH=1198	1192	1198	0	100.5	93.6	97.5
Rsa1.0_00552.1.g15887.t1	gb|EOA13428.1| hypothetical protein CARUB_v10026469mg [Capsella rubella]	431	423	1.00E-135	98.1	73.1	80.3	hypothetical protein CARUB_v10026469mg	gbpln	Capsella rubella	AT5G51590.1 | Symbols: | AT hook motif DNA-binding family protein | chr5:20956863-20958929 REVERSE LENGTH=419	431	419	1.00E-127	97.2	71.5	78.9
Rsa1.0_00552.1.g15888.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00552.1.g15889.t3	gb|EOA12557.1| hypothetical protein CARUB_v10026824mg, partial [Capsella rubella]	325	309	1.00E-157	95.1	84.3	88.0	hypothetical protein CARUB_v10026824mg, partial	gbpln	Capsella rubella	AT5G51570.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr5:20949511-20951234 FORWARD LENGTH=292	325	292	1.00E-157	89.8	83.7	87.7
Rsa1.0_00552.1.g15890.t1	ref|XP_002866483.1| 40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata] gi|297312318|gb|EFH42742.1| 40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata]	123	124	3.00E-59	100.8	93.5	93.5	40S ribosomal protein S20	gbpln	Arabidopsis lyrata	AT5G62300.2 | Symbols: | Ribosomal protein S10p/S20e family protein | chr5:25021388-25022235 REVERSE LENGTH=124	123	124	2.00E-61	100.8	94.3	94.3
Rsa1.0_00552.1.g15891.t1	ref|XP_002866483.1| 40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata] gi|297312318|gb|EFH42742.1| 40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata]	207	124	6.00E-55	59.9	51.7	51.7	40S ribosomal protein S20	gbpln	Arabidopsis lyrata	AT5G62300.2 | Symbols: | Ribosomal protein S10p/S20e family protein | chr5:25021388-25022235 REVERSE LENGTH=124	207	124	5.00E-57	59.9	52.2	52.2
Rsa1.0_00552.1.g15892.t1	ref|XP_002864118.1| hypothetical protein ARALYDRAFT_495227 [Arabidopsis lyrata subsp. lyrata] gi|297309953|gb|EFH40377.1| hypothetical protein ARALYDRAFT_495227 [Arabidopsis lyrata subsp. lyrata]	178	184	2.00E-66	103.4	78.1	87.6	hypothetical protein ARALYDRAFT_495227	gbpln	Arabidopsis lyrata	AT5G51545.1 | Symbols: LPA2 | low psii accumulation2 | chr5:20936434-20937243 FORWARD LENGTH=185	178	185	5.00E-65	103.9	77.0	87.1
Rsa1.0_00552.1.g15893.t1	gb|AFJ66229.1| hypothetical protein 34G24.15 [Capsella rubella] gi|482548516|gb|EOA12710.1| hypothetical protein CARUB_v10028013mg [Capsella rubella]	427	435	0	101.9	84.5	91.8	hypothetical protein 34G24.15	gbpln	Capsella rubella	AT5G51160.1 | Symbols: | Ankyrin repeat family protein | chr5:20792280-20793681 FORWARD LENGTH=442	427	442	0	103.5	83.8	89.5
Rsa1.0_00552.1.g15894.t1	gb|EOA13190.1| hypothetical protein CARUB_v10026216mg [Capsella rubella]	525	531	0	101.1	90.5	94.1	hypothetical protein CARUB_v10026216mg	gbpln	Capsella rubella	AT5G51150.1 | Symbols: | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr5:20789034-20791495 FORWARD LENGTH=531	525	531	0	101.1	85.3	89.1
Rsa1.0_00552.1.g15895.t1	ref|XP_002865844.1| pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311679|gb|EFH42103.1| pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	393	392	0	99.7	88.5	93.9	pseudouridine synthase family protein	gbpln	Arabidopsis lyrata	AT5G51140.1 | Symbols: | Pseudouridine synthase family protein | chr5:20784277-20786793 REVERSE LENGTH=395	393	395	0	100.5	89.3	93.4
Rsa1.0_00552.1.g15896.t1	ref|XP_002864098.1| hypothetical protein ARALYDRAFT_495181 [Arabidopsis lyrata subsp. lyrata] gi|297309933|gb|EFH40357.1| hypothetical protein ARALYDRAFT_495181 [Arabidopsis lyrata subsp. lyrata]	326	313	1.00E-130	96.0	75.8	83.4	hypothetical protein ARALYDRAFT_495181	gbpln	Arabidopsis lyrata	AT5G51130.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:20781896-20783901 FORWARD LENGTH=318	326	318	1.00E-128	97.5	74.5	81.9
Rsa1.0_00552.1.g15897.t1	gb|ADK63417.1| C2H2 type zinc finger protein [Brassica rapa]	381	349	1.00E-153	91.6	71.9	77.2	C2H2 type zinc finger protein	gbpln	Brassica rapa	AT4G06634.1 | Symbols: | zinc finger (C2H2 type) family protein | chr4:3764499-3766439 REVERSE LENGTH=387	381	387	1.00E-142	101.6	73.2	79.8
Rsa1.0_00552.1.g15898.t4	gb|AAM61036.1| contains similarity to poly(A)-binding protein II [Arabidopsis thaliana]	254	227	6.00E-87	89.4	73.2	76.8	contains similarity to poly(A)-binding protein II	gbpln	Arabidopsis thaliana	AT5G51120.2 | Symbols: PABN1 | polyadenylate-binding protein 1 | chr5:20779760-20781241 FORWARD LENGTH=265	254	265	1.00E-86	104.3	71.3	77.2
Rsa1.0_00552.1.g15899.t1	gb|EOA13876.1| hypothetical protein CARUB_v10026978mg [Capsella rubella]	215	257	2.00E-99	119.5	86.0	90.7	hypothetical protein CARUB_v10026978mg	gbpln	Capsella rubella	AT5G51110.1 | Symbols: | Transcriptional coactivator/pterin dehydratase | chr5:20778316-20779380 REVERSE LENGTH=220	215	220	2.00E-99	102.3	84.7	89.3

Rsa1.0_00552.1.g15900.t1	gb|EOA22066.1| hypothetical protein CARUB_v10002606mg [Capsella rubella]	130	123	1.00E-36	94.6	63.8	75.4	hypothetical protein CARUB_v10002606mg	gbpln	Capsella rubella	AT5G51105.1 | Symbols: | Protein of unknown function (DUF1278) | chr5:20777632-20778003 FORWARD LENGTH=123	130	123	4.00E-34	94.6	60.0	72.3
Rsa1.0_00552.1.g15901.t1	gb|EOA22066.1| hypothetical protein CARUB_v10002606mg [Capsella rubella]	132	123	4.00E-40	93.2	65.9	79.5	hypothetical protein CARUB_v10002606mg	gbpln	Capsella rubella	AT4G09545.1 | Symbols: | ECA1 gametogenesis related family protein | chr4:6037569-6037937 FORWARD LENGTH=122	132	122	4.00E-39	92.4	62.9	72.0
Rsa1.0_00553.1.g15902.t1	gb|EOA21499.1| hypothetical protein CARUB_v10001894mg [Capsella rubella]	251	227	1.00E-36	90.4	36.7	50.2	hypothetical protein CARUB_v10001894mg	gbpln	Capsella rubella	AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321	251	321	1.00E-25	127.9	29.5	42.2
Rsa1.0_00553.1.g15903.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00553.1.g15904.t1	ref|XP_002873209.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319046|gb|EFH49468.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	230	170	2.00E-28	73.9	33.5	44.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G09160.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:2806262-2806912 REVERSE LENGTH=132	230	132	2.00E-27	57.4	25.7	33.9
Rsa1.0_00553.1.g15905.t5	dbj|BAJ34172.1| unnamed protein product [Thellungiella halophila]	1177	1115	0	94.7	89.7	91.4	unnamed protein product	––––	––––	AT5G06600.1 | Symbols: UBP12 | ubiquitin-specific protease 12 | chr5:2019545-2027834 REVERSE LENGTH=1116	1177	1116	0	94.8	89.0	90.9
Rsa1.0_00553.1.g15906.t1	ref|XP_002871222.1| hypothetical protein ARALYDRAFT_487469 [Arabidopsis lyrata subsp. lyrata] gi|297317059|gb|EFH47481.1| hypothetical protein ARALYDRAFT_487469 [Arabidopsis lyrata subsp. lyrata]	308	315	1.00E-123	102.3	76.0	86.4	hypothetical protein ARALYDRAFT_487469	gbpln	Arabidopsis lyrata	AT5G06590.1 | Symbols: | unknown protein; Has 38 Blast hits to 38 proteins in 14 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:2016713-2018744 FORWARD LENGTH=314	308	314	1.00E-126	101.9	76.0	85.7
Rsa1.0_00553.1.g15907.t1	ref|XP_002873268.1| FAD linked oxidase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319105|gb|EFH49527.1| FAD linked oxidase family protein [Arabidopsis lyrata subsp. lyrata]	556	566	0	101.8	83.1	88.5	FAD linked oxidase family protein	gbpln	Arabidopsis lyrata	AT5G06580.1 | Symbols: | FAD-linked oxidases family protein | chr5:2011486-2016473 REVERSE LENGTH=567	556	567	0	102.0	82.6	87.2
Rsa1.0_00553.1.g15908.t1	ref|NP_196275.1| alpha/beta hydrolase fold-containing protein [Arabidopsis thaliana] gi|30681513|ref|NP_850782.1| alpha/beta hydrolase fold-containing protein [Arabidopsis thaliana] gi|75333783|sp|Q9FG13.1|CXE15_ARATH RecName: Full=Probable carboxylesterase 15; AltName: Full=AtCXE15 gi|10178113|dbj|BAB11406.1| unnamed protein product [Arabidopsis thaliana] gi|26452184|dbj|BAC43180.1| unknown protein [Arabidopsis thaliana] gi|30725374|gb|AAP37709.1| At5g06570 [Arabidopsis thaliana] gi|332003652|gb|AED91035.1| probable carboxylesterase 15 [Arabidopsis thaliana] gi|332003653|gb|AED91036.1| alpha/beta hydrolase fold-containing protein [Arabidopsis thaliana]	330	329	1.00E-152	99.7	83.0	91.8	alpha/beta hydrolase fold-containing protein	gbpln	Arabidopsis thaliana	AT5G06570.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:2008075-2011013 REVERSE LENGTH=329	330	329	1.00E-155	99.7	83.0	91.8
Rsa1.0_00553.1.g15909.t2	gb|EOA20411.1| hypothetical protein CARUB_v10000722mg [Capsella rubella] gi|482556220|gb|EOA20412.1| hypothetical protein CARUB_v10000722mg [Capsella rubella]	480	520	1.00E-153	108.3	64.2	73.8	hypothetical protein CARUB_v10000722mg	gbpln	Capsella rubella	AT5G06560.1 | Symbols: | Protein of unknown function, DUF593 | chr5:2003678-2005543 REVERSE LENGTH=518	480	518	1.00E-155	107.9	64.8	74.8
Rsa1.0_00553.1.g15910.t1	gb|EOA22732.1| hypothetical protein CARUB_v10003439mg [Capsella rubella]	508	497	0	97.8	78.3	84.8	hypothetical protein CARUB_v10003439mg	gbpln	Capsella rubella	AT5G06550.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Transcription factor jumonji/aspartyl beta-hydroxylase (InterPro:IPR003347), F-box domain, Skp2-like (InterPro:IPR022364), Transcription factor jumonji (InterPro:IPR013129); BEST Arabidopsis thaliana protein match is: transferases, transferring glycosyl groups (TAIR:AT1G78280.1); Has 1762 Blast hits to 1747 proteins in 292 species: Archae - 0; Bacteria - 297; Metazoa - 877; Fungi - 168; Plants - 221; Viruses - 0; Other Eukaryotes - 199 (source: NCBI BLink). | chr5:2001246-2003068 REVERSE LENGTH=502	508	502	0	98.8	76.0	81.9
Rsa1.0_00553.1.g15911.t1	ref|XP_002873264.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319101|gb|EFH49523.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	617	624	0	101.1	85.7	91.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G06540.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:1999181-2001049 REVERSE LENGTH=622	617	622	0	100.8	84.1	91.7

Rsa1.0_00553.1.g15912.t1	gb|EOA20021.1| hypothetical protein CARUB_v10000295mg [Capsella rubella]	805	752	0	93.4	87.3	90.4	hypothetical protein CARUB_v10000295mg	gbpln	Capsella rubella	AT5G06530.1 | Symbols: | ABC-2 type transporter family protein | chr5:1990060-1994605 REVERSE LENGTH=751	805	751	0	93.3	87.5	89.9
Rsa1.0_00553.1.g15913.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00553.1.g15914.t1	gb|EOA13237.1| hypothetical protein CARUB_v10026265mg, partial [Capsella rubella]	487	504	0	103.5	73.5	81.5	hypothetical protein CARUB_v10026265mg, partial	gbpln	Capsella rubella	AT5G52820.1 | Symbols: | WD-40 repeat family protein / notchless protein, putative | chr5:21401423-21404203 FORWARD LENGTH=473	487	473	0	97.1	73.1	81.3
Rsa1.0_00553.1.g15915.t1	ref|XP_002871220.1| CCAAT-binding transcription factor (CBF-B/NF-YA) family protein [Arabidopsis lyrata subsp. lyrata] gi|297317057|gb|EFH47479.1| CCAAT-binding transcription factor (CBF-B/NF-YA) family protein [Arabidopsis lyrata subsp. lyrata]	268	269	1.00E-97	100.4	74.6	79.1	CCAAT-binding transcription factor (CBF-B/NF-YA) family protein	gbpln	Arabidopsis lyrata	AT5G06510.2 | Symbols: NF-YA10 | nuclear factor Y, subunit A10 | chr5:1985439-1986591 FORWARD LENGTH=269	268	269	1.00E-95	100.4	72.0	77.2
Rsa1.0_00553.1.g15916.t2	ref|NP_196268.1| protein agamous-like 96 [Arabidopsis thaliana] gi|10178106|dbj|BAB11399.1| unnamed protein product [Arabidopsis thaliana] gi|67633788|gb|AAY78818.1| MADS-box family protein [Arabidopsis thaliana] gi|332003641|gb|AED91024.1| protein agamous-like 96 [Arabidopsis thaliana]	224	242	1.00E-34	108.0	42.9	59.4	protein agamous-like 96	gbpln	Arabidopsis thaliana	AT5G06500.1 | Symbols: AGL96 | AGAMOUS-like 96 | chr5:1982444-1983172 FORWARD LENGTH=242	224	242	4.00E-37	108.0	42.9	59.4
Rsa1.0_00553.1.g15917.t1	ref|XP_002873260.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297319097|gb|EFH49519.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	189	197	3.00E-67	104.2	69.8	79.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G06490.1 | Symbols: | RING/U-box superfamily protein | chr5:1977996-1978589 REVERSE LENGTH=197	189	197	1.00E-68	104.2	69.3	77.8
Rsa1.0_00553.1.g15918.t1	gb|EOA21743.1| hypothetical protein CARUB_v10002191mg [Capsella rubella]	150	152	2.00E-60	101.3	79.3	89.3	hypothetical protein CARUB_v10002191mg	gbpln	Capsella rubella	AT5G06480.1 | Symbols: | Immunoglobulin E-set superfamily protein | chr5:1976219-1977231 REVERSE LENGTH=153	150	153	1.00E-61	102.0	72.0	78.7
Rsa1.0_00553.1.g15919.t1	ref|XP_002873258.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297319095|gb|EFH49517.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	241	239	1.00E-105	99.2	80.9	88.0	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT5G06470.1 | Symbols: | Glutaredoxin family protein | chr5:1974659-1975378 REVERSE LENGTH=239	241	239	1.00E-107	99.2	80.9	88.8
Rsa1.0_00553.1.g15920.t1	gb|EOA19837.1| hypothetical protein CARUB_v10000084mg [Capsella rubella]	1079	1122	0	104.0	90.1	95.0	hypothetical protein CARUB_v10000084mg	gbpln	Capsella rubella	AT5G06460.1 | Symbols: ATUBA2, UBA 2 | ubiquitin activating enzyme 2 | chr5:1970239-1974382 FORWARD LENGTH=1077	1079	1077	0	99.8	89.6	94.4
Rsa1.0_00554.1.g15921.t1	emb|CAN66323.1| hypothetical protein VITISV_007384 [Vitis vinifera]	94	1317	2.00E-20	1401.1	50.0	56.4	hypothetical protein VITISV_007384	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	94	1262	8.00E-12	1342.6	26.6	44.7
Rsa1.0_00554.1.g15922.t1	gb|ABK28609.1| unknown [Arabidopsis thaliana]	260	249	1.00E-129	95.8	87.7	92.3	unknown	gbpln	Arabidopsis thaliana	AT3G58780.1 | Symbols: SHP1, AGL1 | K-box region and MADS-box transcription factor family protein | chr3:21739150-21741766 FORWARD LENGTH=248	260	248	1.00E-132	95.4	87.7	92.3
Rsa1.0_00554.1.g15923.t1	gb|EOA23218.1| hypothetical protein CARUB_v10019589mg [Capsella rubella]	116	119	9.00E-38	102.6	79.3	87.9	hypothetical protein CARUB_v10019589mg	gbpln	Capsella rubella	AT3G58850.1 | Symbols: PAR2, HLH2 | phy rapidly regulated 2 | chr3:21759562-21759918 REVERSE LENGTH=118	116	118	1.00E-35	101.7	79.3	84.5
Rsa1.0_00554.1.g15924.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1811	1274	0	70.3	34.0	45.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1811	575	2.00E-71	31.8	10.0	15.5
Rsa1.0_00554.1.g15925.t1	ref|NP_191445.1| putative F-box protein [Arabidopsis thaliana] gi|75264355|sp|Q9LXR6.1|FB207_ARATH RecName: Full=Putative F-box protein At3g58860 gi|7630081|emb|CAB88303.1| putative protein [Arabidopsis thaliana] gi|332646320|gb|AEE79841.1| putative F-box protein [Arabidopsis thaliana]	448	457	0	102.0	73.0	84.8	putative F-box protein	gbpln	Arabidopsis thaliana	AT3G58860.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21763742-21765306 REVERSE LENGTH=457	448	457	0	102.0	73.0	84.8
Rsa1.0_00554.1.g15926.t2	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1630	910	0	55.8	30.9	40.6	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1630	626	1.00E-134	38.4	13.8	20.4

Rsa1.0_00554.1.g15927.t1	ref|NP_191460.1| pectinesterase 35 [Arabidopsis thaliana] gi|75311708|sp|Q9LYT5.1|PME35_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 35; Includes: RecName: Full=Pectinesterase inhibitor 35; AltName: Full=Pectin methylesterase inhibitor 35; Includes: RecName: Full=Pectinesterase 35; Short=PE 35; AltName: Full=Pectin methylesterase 35; Short=AtPME35; Flags: Precursor gi|7529744|emb|CAB86929.1| pectinesterase precursor-like protein [Arabidopsis thaliana] gi|16974625|gb|AAL31215.1| AT3g59010/F17J16_60 [Arabidopsis thaliana] gi|24111417|gb|AAN46858.1| At3g59010/F17J16_60 [Arabidopsis thaliana] gi|332646339|gb|AEE79860.1| pectinesterase 35 [Arabidopsis thaliana]	525	529	0	100.8	84.8	90.1	pectinesterase 35	gbpln	Arabidopsis thaliana	AT3G59010.1 | Symbols: PME61 | pectin methylesterase 61 | chr3:21803015-21805098 REVERSE LENGTH=529	525	529	0	100.8	84.8	90.1
Rsa1.0_00554.1.g15928.t1	gb|AAD17414.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	151	1166	1.00E-11	772.2	28.5	41.7	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00554.1.g15929.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	586	1239	0	211.4	61.4	73.5	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	586	1262	4.00E-69	215.4	25.6	38.4
Rsa1.0_00554.1.g15930.t1	ref|NP_191535.2| cysteine synthase [Arabidopsis thaliana] gi|41019511|sp|Q43725.3|CYSKM_ARATH RecName: Full=Cysteine synthase, mitochondrial; AltName: Full=CSase C; Short=AtCS-C; Short=CS-C; AltName: Full=O-acetylserine (thiol)-lyase; AltName: Full=O-acetylserine sulfhydrylase; AltName: Full=OAS-TL C; Flags: Precursor gi|377656559|pdb|4AEC|A Chain A, Crystal Structure Of The Arabidopsis Thaliana O-Acetyl- Serine-(Thiol)-Lyase C gi|377656560|pdb|4AEC|B Chain B, Crystal Structure Of The Arabidopsis Thaliana O-Acetyl- Serine-(Thiol)-Lyase C gi|20466510|gb|AAM20572.1| cysteine synthase [Arabidopsis thaliana] gi|22136414|gb|AAM91285.1| cysteine synthase [Arabidopsis thaliana] gi|110740682|dbj|BAE98443.1| cysteine synthase [Arabidopsis thaliana] gi|332646442|gb|AEE79963.1| cysteine synthase [Arabidopsis thaliana]	420	430	0	102.4	89.8	94.8	cysteine synthase	gbpln	Arabidopsis thaliana	AT3G59760.3 | Symbols: OASC, ATCS-C | O-acetylserine (thiol) lyase isoform C | chr3:22072668-22075345 REVERSE LENGTH=430	420	430	0	102.4	89.8	94.8
Rsa1.0_00554.1.g15931.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00554.1.g15932.t1	ref|XP_002881930.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297327769|gb|EFH58189.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	259	343	4.00E-20	132.4	23.6	27.4	transducin family protein	gbpln	Arabidopsis lyrata	AT2G43770.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:18134272-18135303 REVERSE LENGTH=343	259	343	1.00E-22	132.4	23.6	27.4
Rsa1.0_00554.1.g15933.t1	sp|Q40532.1|NTF4_TOBAC RecName: Full=Mitogen-activated protein kinase homolog NTF4; AltName: Full=P45 gi|634070|emb|CAA58761.1| p45Ntf4 serine/threonine protein kinase [Nicotiana tabacum]	358	393	1.00E-136	109.8	67.3	78.8	RecName: Full=Mitogen-activated protein kinase homolog NTF4; AltName: Full=P45 gi|634070|emb|CAA58761.1| p45Ntf4 serine/threonine protein kinase	gbpln	Nicotiana tabacum	AT2G43790.1 | Symbols: ATMPK6, MPK6, MAPK6, ATMAPK6 | MAP kinase 6 | chr2:18138477-18140693 FORWARD LENGTH=395	358	395	1.00E-131	110.3	66.2	76.8
Rsa1.0_00554.1.g15934.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00554.1.g15935.t1	ref|XP_004287160.1| PREDICTED: U6 snRNA-associated Sm-like protein LSm6-like [Fragaria vesca subsp. vesca]	93	92	7.00E-39	98.9	88.2	91.4	PREDICTED: U6 snRNA-associated Sm-like protein LSm6-like	gbpln	Fragaria vesca	AT3G59810.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr3:22096841-22097666 FORWARD LENGTH=91	93	91	6.00E-41	97.8	89.2	91.4
Rsa1.0_00554.1.g15936.t1	ref|XP_002878295.1| hypothetical protein ARALYDRAFT_486447 [Arabidopsis lyrata subsp. lyrata] gi|297324133|gb|EFH54554.1| hypothetical protein ARALYDRAFT_486447 [Arabidopsis lyrata subsp. lyrata]	746	755	0	101.2	89.8	94.2	hypothetical protein ARALYDRAFT_486447	gbpln	Arabidopsis lyrata	AT3G59820.1 | Symbols: | LETM1-like protein | chr3:22098306-22101759 REVERSE LENGTH=755	746	755	0	101.2	89.1	94.0

Rsa1.0_00554.1.g15937.t1	gb|EOA23944.1| hypothetical protein CARUB_v10017160mg [Capsella rubella]	421	473	1.00E-135	112.4	61.0	73.6	hypothetical protein CARUB_v10017160mg	gbpln	Capsella rubella	AT1G06630.2 | Symbols: | F-box/RNI-like superfamily protein | chr1:2028071-2029442 FORWARD LENGTH=403	421	403	1.00E-90	95.7	45.8	61.0
Rsa1.0_00555.1.g15938.t1	gb|EOA37440.1| hypothetical protein CARUB_v10011510mg [Capsella rubella]	159	158	4.00E-70	99.4	89.9	94.3	hypothetical protein CARUB_v10011510mg	gbpln	Capsella rubella	AT1G29520.1 | Symbols: | AWPM-19-like family protein | chr1:10323735-10324525 FORWARD LENGTH=158	159	158	2.00E-71	99.4	88.7	93.7
Rsa1.0_00555.1.g15939.t1	gb|EOA36216.1| hypothetical protein CARUB_v10010140mg [Capsella rubella]	241	242	1.00E-41	100.4	53.5	63.1	hypothetical protein CARUB_v10010140mg	gbpln	Capsella rubella	AT1G29530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34310.3); Has 84 Blast hits to 78 proteins in 24 species: Archae - 2; Bacteria - 4; Metazoa - 9; Fungi - 8; Plants - 55; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:10325553-10326651 REVERSE LENGTH=236	241	236	1.00E-41	97.9	54.4	61.4
Rsa1.0_00555.1.g15940.t1	gb|EOA36198.1| hypothetical protein CARUB_v10010112mg [Capsella rubella]	248	247	1.00E-104	99.6	74.6	86.7	hypothetical protein CARUB_v10010112mg	gbpln	Capsella rubella	AT1G29550.1 | Symbols: | Eukaryotic initiation factor 4E protein | chr1:10330514-10332094 FORWARD LENGTH=240	248	240	1.00E-102	96.8	73.4	83.1
Rsa1.0_00555.1.g15941.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00555.1.g15942.t11	ref|NP_193173.4| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332658031|gb|AEE83431.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1084	1008	0	93.0	60.1	70.1	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT4G14370.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:8279946-8283263 REVERSE LENGTH=1008	1084	1008	0	93.0	60.1	70.1
Rsa1.0_00555.1.g15943.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00555.1.g15944.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	1338	1466	0	109.6	68.4	81.4	copia-like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1338	1262	2.00E-85	94.3	13.5	20.2
Rsa1.0_00555.1.g15945.t1	gb|EOA24554.1| hypothetical protein CARUB_v10017811mg [Capsella rubella]	89	275	2.00E-12	309.0	52.8	57.3	hypothetical protein CARUB_v10017811mg	gbpln	Capsella rubella	AT3G57360.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02370.2); Has 122 Blast hits to 122 proteins in 54 species: Archae - 0; Bacteria - 0; Metazoa - 74; Fungi - 4; Plants - 41; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:21225571-21226621 FORWARD LENGTH=254	89	254	1.00E-13	285.4	51.7	56.2
Rsa1.0_00555.1.g15946.t2	ref|NP_174257.1| uncharacterized protein [Arabidopsis thaliana] gi|12323541|gb|AAG51753.1|AC068667_32 hypothetical protein; 98808-98386 [Arabidopsis thaliana] gi|28466825|gb|AAO44021.1| At1g29640 [Arabidopsis thaliana] gi|110743019|dbj|BAE99402.1| hypothetical protein [Arabidopsis thaliana] gi|332192993|gb|AEE31114.1| uncharacterized protein AT1G29640 [Arabidopsis thaliana]	300	140	2.00E-41	46.7	33.3	35.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G29640.1 | Symbols: | Protein of unknown function, DUF584 | chr1:10355959-10356381 REVERSE LENGTH=140	300	140	4.00E-44	46.7	33.3	35.3
Rsa1.0_00555.1.g15947.t1	gb|EOA33828.1| hypothetical protein CARUB_v10021307mg [Capsella rubella]	607	515	3.00E-63	84.8	19.1	23.7	hypothetical protein CARUB_v10021307mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	607	530	4.00E-40	87.3	13.7	18.1
Rsa1.0_00555.1.g15948.t1	gb|EOA38724.1| hypothetical protein CARUB_v10010854mg [Capsella rubella]	237	237	1.00E-126	100.0	88.2	94.9	hypothetical protein CARUB_v10010854mg	gbpln	Capsella rubella	AT1G29680.1 | Symbols: | Protein of unknown function (DUF1264) | chr1:10377900-10378931 REVERSE LENGTH=237	237	237	1.00E-124	100.0	87.3	92.4
Rsa1.0_00555.1.g15949.t15	gb|EOA39560.1| hypothetical protein CARUB_v10008178mg [Capsella rubella]	1013	1022	0	100.9	72.7	83.5	hypothetical protein CARUB_v10008178mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	1013	1019	0	100.6	73.8	83.5
Rsa1.0_00556.1.g15950.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00556.1.g15951.t1	ref|NP_563684.1| histidine-containing phosphotransfer protein 5 [Arabidopsis thaliana] gi|56749792|sp|Q8L9T7.2|AHP5_ARATH RecName: Full=Histidine-containing phosphotransfer protein 5 gi|7630189|dbj|BAA94764.1| HPt phosphotransmitter [Arabidopsis thaliana] gi|51970654|dbj|BAD44019.1| HPt phosphotransmitter (AHP5) [Arabidopsis thaliana] gi|51971731|dbj|BAD44530.1| HPt phosphotransmitter (AHP5) [Arabidopsis thaliana] gi|149944283|gb|ABR46184.1| At1g03430 [Arabidopsis thaliana] gi|332189449|gb|AEE27570.1| histidine-containing phosphotransfer protein 5 [Arabidopsis thaliana]	190	157	8.00E-75	82.6	76.3	78.9	histidine-containing phosphotransfer protein 5	gbpln	Arabidopsis thaliana	AT1G03430.1 | Symbols: AHP5 | histidine-containing phosphotransfer factor 5 | chr1:848159-849235 FORWARD LENGTH=157	190	157	3.00E-77	82.6	76.3	78.9
Rsa1.0_00556.1.g15952.t1	ref|XP_002889459.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297335301|gb|EFH65718.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	395	396	0	100.3	93.7	96.5	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G03440.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr1:852681-853874 FORWARD LENGTH=397	395	397	0	100.5	92.2	96.5
Rsa1.0_00556.1.g15953.t1	ref|XP_002892161.1| hypothetical protein ARALYDRAFT_470321 [Arabidopsis lyrata subsp. lyrata] gi|297338003|gb|EFH68420.1| hypothetical protein ARALYDRAFT_470321 [Arabidopsis lyrata subsp. lyrata]	425	435	0	102.4	81.4	87.8	hypothetical protein ARALYDRAFT_470321	gbpln	Arabidopsis lyrata	AT1G03457.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:861109-864019 REVERSE LENGTH=429	425	429	0	100.9	79.8	86.8
Rsa1.0_00556.1.g15954.t1	ref|XP_002892163.1| coproporphyrinogen III oxidase [Arabidopsis lyrata subsp. lyrata] gi|297338005|gb|EFH68422.1| coproporphyrinogen III oxidase [Arabidopsis lyrata subsp. lyrata]	388	387	0	99.7	91.8	96.1	coproporphyrinogen III oxidase	gbpln	Arabidopsis lyrata	AT1G03475.1 | Symbols: LIN2, HEMF1, ATCPO-I | Coproporphyrinogen III oxidase | chr1:869302-871175 REVERSE LENGTH=386	388	386	0	99.5	91.8	95.9
Rsa1.0_00556.1.g15955.t2	gb|EOA39229.1| hypothetical protein CARUB_v10012206mg, partial [Capsella rubella]	546	447	2.00E-31	81.9	16.3	21.1	hypothetical protein CARUB_v10012206mg, partial	gbpln	Capsella rubella	AT1G03490.1 | Symbols: ANAC006, NAC006 | NAC domain containing protein 6 | chr1:871874-872906 FORWARD LENGTH=281	546	281	5.00E-25	51.5	10.6	12.8
Rsa1.0_00556.1.g15956.t1	ref|NP_171850.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75180302|sp|Q9LR72.1|PPR7_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At1g03510 gi|9280666|gb|AAF86535.1|AC002560_28 F21B7.13 [Arabidopsis thaliana] gi|332189459|gb|AEE27580.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	154	429	5.00E-47	278.6	64.9	71.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G03510.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:876258-877547 REVERSE LENGTH=429	154	429	2.00E-49	278.6	64.9	71.4
Rsa1.0_00556.1.g15957.t1	ref|NP_171851.1| core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase-like protein [Arabidopsis thaliana] gi|9280665|gb|AAF86534.1|AC002560_27 F21B7.14 [Arabidopsis thaliana] gi|15292807|gb|AAK92772.1| putative glycosylation enzyme [Arabidopsis thaliana] gi|20465791|gb|AAM20384.1| putative glycosylation enzyme [Arabidopsis thaliana] gi|332189460|gb|AEE27581.1| core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase-like protein [Arabidopsis thaliana]	450	447	0	99.3	85.6	91.6	core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase-like protein	gbpln	Arabidopsis thaliana	AT1G03520.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:877948-879553 REVERSE LENGTH=447	450	447	0	99.3	85.6	91.6
Rsa1.0_00556.1.g15958.t1	ref|XP_002892167.1| hypothetical protein ARALYDRAFT_311450 [Arabidopsis lyrata subsp. lyrata] gi|297338009|gb|EFH68426.1| hypothetical protein ARALYDRAFT_311450 [Arabidopsis lyrata subsp. lyrata]	722	804	0	111.4	64.5	73.4	hypothetical protein ARALYDRAFT_311450	gbpln	Arabidopsis lyrata	AT1G03530.1 | Symbols: ATNAF1, NAF1 | nuclear assembly factor 1 | chr1:880638-883338 REVERSE LENGTH=801	722	801	0	110.9	64.4	73.3
Rsa1.0_00556.1.g15959.t1	gb|EOA39421.1| hypothetical protein CARUB_v10012530mg [Capsella rubella]	283	283	1.00E-151	100.0	90.1	95.1	hypothetical protein CARUB_v10012530mg	gbpln	Capsella rubella	AT1G03550.1 | Symbols: | Secretory carrier membrane protein (SCAMP) family protein | chr1:885851-887778 REVERSE LENGTH=283	283	283	1.00E-144	100.0	88.7	94.0

Rsa1.0_00556.1.g15960.t1	ref|XP_002892169.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338011|gb|EFH68428.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	666	662	0	99.4	84.1	90.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G03560.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:890428-892410 REVERSE LENGTH=660	666	660	0	99.1	83.5	90.4
Rsa1.0_00556.1.g15961.t1	gb|EOA40336.1| hypothetical protein CARUB_v10009068mg [Capsella rubella] gi|482576150|gb|EOA40337.1| hypothetical protein CARUB_v10009068mg [Capsella rubella]	460	462	0	100.4	83.7	91.1	hypothetical protein CARUB_v10009068mg	gbpln	Capsella rubella	AT1G03590.1 | Symbols: | Protein phosphatase 2C family protein | chr1:894480-896257 REVERSE LENGTH=462	460	462	0	100.4	83.3	91.7
Rsa1.0_00556.1.g15962.t1	ref|XP_002870997.1| ubiquitin-protein ligase 4 [Arabidopsis lyrata subsp. lyrata] gi|297316834|gb|EFH47256.1| ubiquitin-protein ligase 4 [Arabidopsis lyrata subsp. lyrata]	149	1509	3.00E-27	1012.8	57.7	67.8	ubiquitin-protein ligase 4	gbpln	Arabidopsis lyrata	AT5G02880.1 | Symbols: UPL4 | ubiquitin-protein ligase 4 | chr5:662643-668847 FORWARD LENGTH=1502	149	1502	1.00E-26	1008.1	53.7	59.7
Rsa1.0_00556.1.g15963.t1	gb|EOA39350.1| hypothetical protein CARUB_v10012401mg [Capsella rubella]	305	312	1.00E-156	102.3	90.5	93.8	hypothetical protein CARUB_v10012401mg	gbpln	Capsella rubella	AT1G03610.1 | Symbols: | Protein of unknown function (DUF789) | chr1:901304-902672 FORWARD LENGTH=308	305	308	1.00E-158	101.0	89.2	93.4
Rsa1.0_00556.1.g15964.t1	ref|NP_171859.1| ELMO/CED-12 family protein [Arabidopsis thaliana] gi|124300970|gb|ABN04737.1| At1g03620 [Arabidopsis thaliana] gi|332189469|gb|AEE27590.1| ELMO/CED-12 family protein [Arabidopsis thaliana]	265	265	1.00E-144	100.0	90.9	96.2	ELMO/CED-12 family protein	gbpln	Arabidopsis thaliana	AT1G03620.1 | Symbols: | ELMO/CED-12 family protein | chr1:904319-906013 REVERSE LENGTH=265	265	265	2.33E-156	100.0	90.9	96.2
Rsa1.0_00556.1.g15965.t1	ref|XP_002889465.1| por C [Arabidopsis lyrata subsp. lyrata] gi|297335307|gb|EFH65724.1| por C [Arabidopsis lyrata subsp. lyrata]	401	401	0	100.0	94.8	98.5	por C	gbpln	Arabidopsis lyrata	AT1G03630.1 | Symbols: POR C, PORC | protochlorophyllide oxidoreductase C | chr1:907699-909245 FORWARD LENGTH=401	401	401	0	100.0	93.8	98.3
Rsa1.0_00556.1.g15966.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00556.1.g15967.t1	ref|NP_563689.1| UPF0497 membrane protein [Arabidopsis thaliana] gi|297843172|ref|XP_002889467.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|75180289|sp|Q9LR57.1|CSPL1_ARATH RecName: Full=CASP-like protein At1g03700 gi|341958561|sp|D7KCH2.1|CSPLE_ARALL RecName: Full=CASP-like protein ARALYDRAFT_470341 gi|9280651|gb|AAF86520.1|AC002560_13 F21B7.30 [Arabidopsis thaliana] gi|297335309|gb|EFH65726.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|332189478|gb|AEE27599.1| UPF0497 membrane protein [Arabidopsis thaliana]	164	164	1.00E-83	100.0	95.7	98.8	UPF0497 membrane protein	gbpln	Arabidopsis lyrata	AT1G03700.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr1:921038-921844 FORWARD LENGTH=164	164	164	3.00E-86	100.0	95.7	98.8
Rsa1.0_00556.1.g15968.t1	ref|XP_002889471.1| hypothetical protein ARALYDRAFT_470343 [Arabidopsis lyrata subsp. lyrata] gi|297335313|gb|EFH65730.1| hypothetical protein ARALYDRAFT_470343 [Arabidopsis lyrata subsp. lyrata]	188	219	2.00E-47	116.5	63.3	75.5	hypothetical protein ARALYDRAFT_470343	gbpln	Arabidopsis lyrata	AT1G03710.2 | Symbols: | Cystatin/monellin superfamily protein | chr1:923492-924287 FORWARD LENGTH=202	188	202	5.00E-40	107.4	58.5	70.2
Rsa1.0_00556.1.g15969.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	403	1274	2.00E-50	316.1	31.5	50.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	403	303	9.00E-49	75.2	28.5	40.4
Rsa1.0_00556.1.g15970.t1	ref|XP_002889471.1| hypothetical protein ARALYDRAFT_470343 [Arabidopsis lyrata subsp. lyrata] gi|297335313|gb|EFH65730.1| hypothetical protein ARALYDRAFT_470343 [Arabidopsis lyrata subsp. lyrata]	229	219	1.00E-53	95.6	56.3	67.2	hypothetical protein ARALYDRAFT_470343	gbpln	Arabidopsis lyrata	AT1G03710.2 | Symbols: | Cystatin/monellin superfamily protein | chr1:923492-924287 FORWARD LENGTH=202	229	202	1.00E-50	88.2	52.8	65.1
Rsa1.0_00556.1.g15971.t1	dbj|BAJ34139.1| unnamed protein product [Thellungiella halophila]	156	158	8.00E-50	101.3	79.5	84.6	unnamed protein product	----	----	AT1G03850.2 | Symbols: | Glutaredoxin family protein | chr1:977233-977685 REVERSE LENGTH=150	156	150	3.00E-52	96.2	70.5	78.8
Rsa1.0_00556.1.g15972.t1	gb|EOA38381.1| hypothetical protein CARUB_v10009925mg [Capsella rubella]	288	286	1.00E-162	99.3	96.9	98.3	hypothetical protein CARUB_v10009925mg	gbpln	Capsella rubella	AT1G03860.3 | Symbols: ATPHB2, PHB2 | prohibitin 2 | chr1:979611-981157 REVERSE LENGTH=286	288	286	1.00E-156	99.3	95.8	98.3

Rsa1.0_00556.1.g15973.t1	gb|ABK78690.1| unknown [Brassica rapa]	248	250	1.00E-122	100.8	93.1	96.4	unknown	gbpln	Brassica rapa	AT1G03870.1 | Symbols: FLA9 | FASCICLIN-like arabinoogalactan 9 | chr1:982625-983368 REVERSE LENGTH=247	248	247	1.00E-103	99.6	70.6	79.4
Rsa1.0_00556.1.g15974.t1	gb|AFQ32288.1| 12S seed storage protein [Camelina sativa]	463	456	0	98.5	85.1	93.5	12S seed storage protein	gbpln	Camelina sativa	AT1G03880.1 | Symbols: CRU2, CRB | cruciferin 2 | chr1:985786-987916 FORWARD LENGTH=455	463	455	0	98.3	84.4	92.4
Rsa1.0_00556.1.g15975.t1	gb|EOA35015.1| hypothetical protein CARUB_v10020118mg [Capsella rubella]	536	535	0	99.8	93.7	98.1	hypothetical protein CARUB_v10020118mg	gbpln	Capsella rubella	AT1G65660.1 | Symbols: SMP1 | Pre-mRNA splicing Prp18-interacting factor | chr1:24418295-24421231 REVERSE LENGTH=535	536	535	0	99.8	92.9	97.8
Rsa1.0_00556.1.g15976.t1	gb|EOA38251.1| hypothetical protein CARUB_v10009732mg [Capsella rubella]	278	326	1.00E-118	117.3	85.6	88.1	hypothetical protein CARUB_v10009732mg	gbpln	Capsella rubella	AT1G03900.1 | Symbols: ATNAP4, NAP4 | non-intrinsic ABC protein 4 | chr1:991252-992852 FORWARD LENGTH=272	278	272	1.00E-117	97.8	84.9	87.4
Rsa1.0_00556.1.g15977.t1	ref|XP_002889482.1| hypothetical protein ARALYDRAFT_333714 [Arabidopsis lyrata subsp. lyrata] gi|297335324|gb|EFH65741.1| hypothetical protein ARALYDRAFT_333714 [Arabidopsis lyrata subsp. lyrata]	664	671	0	101.1	89.5	93.5	hypothetical protein ARALYDRAFT_333714	gbpln	Arabidopsis lyrata	AT1G03910.1 | Symbols: | EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Cactin protein, cactus-binding domain, C-terminal (InterPro:IPR019134), Cactin, central region (InterPro:IPR018816); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G36815.2); Has 11711 Blast hits to 7382 proteins in 452 species: Archae - 31; Bacteria - 352; Metazoa - 6006; Fungi - 1138; Plants - 599; Viruses - 33; Other Eukaryotes - 3552 (source: NCBI BLink). | chr1:996432-1000231 FORWARD LENGTH=672	664	672	0	101.2	88.4	92.3
Rsa1.0_00556.1.g15978.t1	gb|EOA36843.1| hypothetical protein CARUB_v10008713mg [Capsella rubella]	567	569	0	100.4	89.4	94.2	hypothetical protein CARUB_v10008713mg	gbpln	Capsella rubella	AT1G03920.1 | Symbols: | Protein kinase family protein | chr1:1001473-1004240 FORWARD LENGTH=569	567	569	0	100.4	86.2	92.9
Rsa1.0_00556.1.g15979.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00556.1.g15980.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00556.1.g15981.t1	ref|XP_002892189.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|297338031|gb|EFH68448.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	211	210	1.00E-109	99.5	93.8	97.6	SNF7 family protein	gbpln	Arabidopsis lyrata	AT1G03950.1 | Symbols: VPS2.3 | vacuolar protein sorting-associated protein 2.3 | chr1:1011388-1013212 REVERSE LENGTH=210	211	210	1.00E-111	99.5	93.8	96.7
Rsa1.0_00556.1.g15982.t1	ref|NP_171893.1| G-box binding factor 4 [Arabidopsis thaliana] gi|1169863|sp|P42777.1|GBF4_ARATH RecName: Full=G-box-binding factor 4; AltName: Full=bZIP transcription factor 40; Short=AtbZIP40 gi|403418|gb|AAA18414.1| GBF4 [Arabidopsis thaliana] gi|4204292|gb|AAD10673.1| GBF4 [Arabidopsis thaliana] gi|21593196|gb|AAM65145.1| G-box binding factor, GBF4 [Arabidopsis thaliana] gi|87116624|gb|ABD19676.1| At1g03970 [Arabidopsis thaliana] gi|332189519|gb|AEE27640.1| G-box binding factor 4 [Arabidopsis thaliana]	286	270	2.00E-81	94.4	70.3	77.6	G-box binding factor 4	gbpln	Arabidopsis thaliana	AT1G03970.1 | Symbols: GBF4 | G-box binding factor 4 | chr1:1018237-1019049 FORWARD LENGTH=270	286	270	7.00E-84	94.4	70.3	77.6
Rsa1.0_00556.1.g15983.t1	ref|XP_002892191.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338033|gb|EFH68450.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	186	170	2.00E-47	91.4	60.2	64.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G03982.1 | Symbols: | PAK-box/P21-Rho-binding family protein | chr1:1022424-1023136 REVERSE LENGTH=177	186	177	9.00E-42	95.2	48.9	52.2
Rsa1.0_00556.1.g15984.t1	gb|EOA39375.1| hypothetical protein CARUB_v10012453mg [Capsella rubella]	756	752	0	99.5	80.7	91.0	hypothetical protein CARUB_v10012453mg	gbpln	Capsella rubella	AT1G03990.1 | Symbols: | Long-chain fatty alcohol dehydrogenase family protein | chr1:1024847-1027616 FORWARD LENGTH=758	756	758	0	100.3	80.3	91.5
Rsa1.0_00556.1.g15985.t1	ref|XP_002892192.1| hypothetical protein ARALYDRAFT_470377 [Arabidopsis lyrata subsp. lyrata] gi|297338034|gb|EFH68451.1| hypothetical protein ARALYDRAFT_470377 [Arabidopsis lyrata subsp. lyrata]	154	154	1.00E-50	100.0	72.1	81.2	hypothetical protein ARALYDRAFT_470377	gbpln	Arabidopsis lyrata	AT1G04000.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G44060.1); Has 62 Blast hits to 62 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 62; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1028415-1028873 REVERSE LENGTH=152	154	152	9.00E-50	98.7	69.5	77.3

Rsa1.0_00556.1.g15986.t2	ref|NP_171897.2| phospholipid sterol acyl transferase 1 [Arabidopsis thaliana] gi|308191549|sp|Q4VCM1.2|LCAT2_ARATH RecName: Full=Phospholipid--sterol O-acyltransferase; AltName: Full=Lecithin-cholesterol acyltransferase-like 2 gi|332189524|gb|AEE27645.1| phospholipid sterol acyl transferase 1 [Arabidopsis thaliana]	645	633	0	98.1	92.2	95.0	phospholipid sterol acyl transferase 1	gbpln	Arabidopsis thaliana	AT1G04010.1 | Symbols: PSAT1, ATPSAT1 | phospholipid sterol acyl transferase 1 | chr1:1031703-1036128 REVERSE LENGTH=633	645	633	0	98.1	92.2	95.0
Rsa1.0_00556.1.g15987.t1	ref|NP_563699.1| mitochondrial import receptor subunit TOM22-1 [Arabidopsis thaliana] gi|75099064|sp|O64497.1|TOM91_ARATH RecName: Full=Mitochondrial import receptor subunit TOM9-1; AltName: Full=Mitochondrial import receptor subunit TOM22 homolog 1; AltName: Full=Translocase of outer membrane 22 kDa subunit homolog 1; AltName: Full=Translocase of outer membrane 9 kDa subunit TOM9-1 gi|3142296|gb|AAC16747.1| Contains similarity to hypothetical mitochondrial import receptor subunit gb|Z98597 from S. pombe. ESTs gb|T45575 and gb|Z26435 and gb|AA394576 come from this gene [Arabidopsis thaliana] gi|21592382|gb|AAM64333.1| unknown [Arabidopsis thaliana] gi|51969224|dbj|BAD43304.1| unknown protein [Arabidopsis thaliana] gi|98961009|gb|ABF58988.1| At1g04070 [Arabidopsis thaliana] gi|332189530|gb|AEE27651.1| mitochondrial import receptor subunit TOM22-1 [Arabidopsis thaliana]	97	94	8.00E-30	96.9	67.0	83.5	mitochondrial import receptor subunit TOM22-1	gbpln	Arabidopsis thaliana	AT1G04070.1 | Symbols: TOM22-I, ATTOM22-I | translocase of outer membrane 22-I | chr1:1050832-1051116 REVERSE LENGTH=94	97	94	1.00E-32	96.9	67.0	83.5
Rsa1.0_00556.1.g15988.t1	ref|XP_002889490.1| hypothetical protein ARALYDRAFT_333729 [Arabidopsis lyrata subsp. lyrata] gi|297335332|gb|EFH65749.1| hypothetical protein ARALYDRAFT_333729 [Arabidopsis lyrata subsp. lyrata]	749	1328	0	177.3	79.6	87.2	hypothetical protein ARALYDRAFT_333729	gbpln	Arabidopsis lyrata	AT1G04080.1 | Symbols: PRP39 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1051803-1056550 FORWARD LENGTH=768	749	768	0	102.5	82.8	89.5
Rsa1.0_00556.1.g15989.t1	ref|XP_002889490.1| hypothetical protein ARALYDRAFT_333729 [Arabidopsis lyrata subsp. lyrata] gi|297335332|gb|EFH65749.1| hypothetical protein ARALYDRAFT_333729 [Arabidopsis lyrata subsp. lyrata]	767	1328	0	173.1	57.9	62.6	hypothetical protein ARALYDRAFT_333729	gbpln	Arabidopsis lyrata	AT1G04090.1 | Symbols: | Plant protein of unknown function (DUF946) | chr1:1057225-1059247 FORWARD LENGTH=572	767	572	0	74.6	56.8	61.8
Rsa1.0_00556.1.g15990.t1	gb|ABD64827.1| putative subtilisin serine protease of stomatal density and distribution [Isatis tinctoria]	757	778	0	102.8	87.6	93.5	putative subtilisin serine protease of stomatal density and distribution	gbpln	Isatis tinctoria	AT1G04110.1 | Symbols: SDD1 | Subtilase family protein | chr1:1061457-1063784 REVERSE LENGTH=775	757	775	0	102.4	86.7	93.5
Rsa1.0_00556.1.g15991.t1	gb|EOA39482.1| hypothetical protein CARUB_v10008087mg [Capsella rubella]	1486	1514	0	101.9	91.7	95.6	hypothetical protein CARUB_v10008087mg	gbpln	Capsella rubella	AT1G04120.1 | Symbols: ATMRP5, MRP5, ATABCC5, ABCC5 | multidrug resistance-associated protein 5 | chr1:1064848-1070396 REVERSE LENGTH=1514	1486	1514	0	101.9	91.4	95.6
Rsa1.0_00557.1.g15992.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00557.1.g15993.t1	ref|XP_002887872.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333713|gb|EFH64131.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	333	334	1.00E-153	100.3	87.1	91.9	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT1G64590.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:23993592-23995200 FORWARD LENGTH=334	333	334	1.00E-153	100.3	85.9	91.3
Rsa1.0_00557.1.g15994.t1	gb|EOA33754.1| hypothetical protein CARUB_v10019949mg [Capsella rubella]	646	636	0	98.5	86.8	91.6	hypothetical protein CARUB_v10019949mg	gbpln	Capsella rubella	AT1G58030.1 | Symbols: CAT2 | cationic amino acid transporter 2 | chr1:21464185-21468141 REVERSE LENGTH=635	646	635	0	98.3	85.4	90.7

Rsa1.0_00557.1.g15995.t1	ref|NP_176642.1| WD40 domain-containing protein [Arabidopsis thaliana] gi|42571997|ref|NP_974089.1| WD40 domain-containing protein [Arabidopsis thaliana] gi|17381206|gb|AAL36415.1| unknown protein [Arabidopsis thaliana] gi|20465811|gb|AAM20010.1| unknown protein [Arabidopsis thaliana] gi|332196139|gb|AEE34260.1| WD40 domain-containing protein [Arabidopsis thaliana] gi|332196140|gb|AEE34261.1| WD40 domain-containing protein [Arabidopsis thaliana]	649	647	0	99.7	69.5	79.7	WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G64610.2 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:23998920-24001297 REVERSE LENGTH=647	649	647	0	99.7	69.5	79.7
Rsa1.0_00557.1.g15996.t1	gb|EOA35019.1| hypothetical protein CARUB_v10020122mg [Capsella rubella]	380	534	2.00E-95	140.5	51.8	56.8	hypothetical protein CARUB_v10020122mg	gbpln	Capsella rubella	AT1G64625.3 | Symbols: | Serine/threonine-protein kinase WNK (With No Lysine)-related | chr1:24016878-24019181 FORWARD LENGTH=503	380	503	1.00E-96	132.4	48.9	55.8
Rsa1.0_00557.1.g15997.t1	gb|AAF19684.1|AC009519_18 F1N19.24 [Arabidopsis thaliana]	457	637	0	139.4	91.9	95.8	F1N19.24	gbpln	Arabidopsis thaliana	AT1G64670.1 | Symbols: BDG1 | alpha/beta-Hydrolases superfamily protein | chr1:24030990-24033474 REVERSE LENGTH=469	457	469	0	102.6	91.9	95.8
Rsa1.0_00557.1.g15998.t1	ref|NP_176647.1| methionine gamma-lyase [Arabidopsis thaliana] gi|75205145|sp|Q9SGU9.1|MGL_ARATH RecName: Full=Methionine gamma-lyase; Short=AtMGL; AltName: Full=L-methioninase gi|6633821|gb|AAF19680.1|AC009519_14 F1N19.23 [Arabidopsis thaliana] gi|16226491|gb|AAL16181.1|AF428413_1 At1g64660/F1N19_22 [Arabidopsis thaliana] gi|15450932|gb|AAK96737.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana] gi|30387533|gb|AAP31932.1| At1g64660 [Arabidopsis thaliana] gi|110740851|dbj|BAE98522.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana] gi|332196150|gb|AEE34271.1| methionine gamma-lyase [Arabidopsis thaliana]	441	441	0	100.0	88.4	93.2	methionine gamma-lyase	gbpln	Arabidopsis thaliana	AT1G64660.1 | Symbols: ATMGL, MGL | methionine gamma-lyase | chr1:24028977-24030537 FORWARD LENGTH=441	441	441	0	100.0	88.4	93.2
Rsa1.0_00557.1.g15999.t1	ref|XP_002886333.1| hypothetical protein ARALYDRAFT_474878 [Arabidopsis lyrata subsp. lyrata] gi|297332174|gb|EFH62592.1| hypothetical protein ARALYDRAFT_474878 [Arabidopsis lyrata subsp. lyrata]	183	190	1.00E-79	103.8	85.2	92.3	hypothetical protein ARALYDRAFT_474878	gbpln	Arabidopsis lyrata	AT1G64640.1 | Symbols: ENODL8, AtENODL8 | early nodulin-like protein 8 | chr1:24022482-24023151 REVERSE LENGTH=191	183	191	2.00E-77	104.4	85.2	90.2
Rsa1.0_00557.1.g16000.t1	ref|NP_199015.1| ORMDL domain-containing protein [Arabidopsis thaliana] gi|9757945|dbj|BAB08433.1| unnamed protein product [Arabidopsis thaliana] gi|44681462|gb|AAS47671.1| At5g42000 [Arabidopsis thaliana] gi|62320266|dbj|BAD94546.1| putative protein [Arabidopsis thaliana] gi|332007369|gb|AED94752.1| ORMDL domain-containing protein [Arabidopsis thaliana]	110	154	2.00E-55	140.0	93.6	97.3	ORMDL domain-containing protein	gbpln	Arabidopsis thaliana	AT5G42000.1 | Symbols: | ORMDL family protein | chr5:16799455-16800681 FORWARD LENGTH=154	110	154	4.00E-58	140.0	93.6	97.3
Rsa1.0_00558.1.g16001.t2	gb|EOA18305.1| hypothetical protein CARUB_v10006813mg [Capsella rubella]	175	769	2.00E-33	439.4	39.4	44.0	hypothetical protein CARUB_v10006813mg	gbpln	Capsella rubella	AT4G13820.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:8008535-8010694 REVERSE LENGTH=719	175	719	1.00E-33	410.9	38.9	46.3

Table S4-2 Genes of 80,521 predicted by Augustus. (continued)

	vs NR (Non Redundant Database: http://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins)										vs TAIR10 of A. thaliana						
Query	NR	Length (query)	Length (subject)	E-value	Length%	Identity%	Positive%	Product	Genbank	Species	Subject	Query	Subject	E-value	Length%	Identity%	Positve%
Rsa1.0_00558.1.g16002.t1	gb|EOA15770.1| hypothetical protein CARUB_v10006927mg [Capsella rubella]	723	852	0	117.8	65.6	76.6	hypothetical protein CARUB_v10006927mg	gbpln	Capsella rubella	AT4G13810.2 | Symbols: RLP47 | receptor like protein 47 | chr4:8005062-8007464 REVERSE LENGTH=706	723	706	0	97.6	58.6	70.5
Rsa1.0_00558.1.g16003.t1	ref|XP_002868327.1| hypothetical protein ARALYDRAFT_915517 [Arabidopsis lyrata subsp. lyrata] gi|297314163|gb|EFH44586.1| hypothetical protein ARALYDRAFT_915517 [Arabidopsis lyrata subsp. lyrata]	471	471	0	100.0	94.1	97.9	hypothetical protein ARALYDRAFT_915517	gbpln	Arabidopsis lyrata	AT4G13930.1 | Symbols: SHM4 | serine hydroxymethyltransferase 4 | chr4:8048013-8050021 REVERSE LENGTH=471	471	471	0	100.0	93.6	97.5
Rsa1.0_00558.1.g16004.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00558.1.g16005.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	103	1486	2.00E-25	1442.7	53.4	65.0	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00558.1.g16006.t1	gb|AAP92453.1| S-adenosyl-L-homocystein hydrolase [Arabidopsis thaliana]	233	485	1.00E-133	208.2	98.3	98.7	S-adenosyl-L-homocystein hydrolase	gbpln	Arabidopsis thaliana	AT3G23810.1 | Symbols: SAHH2, ATSAHH2 | S-adenosyl-l-homocysteine (SAH) hydrolase 2 | chr3:8588013-8589671 REVERSE LENGTH=485	233	485	1.00E-133	208.2	96.1	98.3
Rsa1.0_00558.1.g16007.t1	gb|AAC26241.1| F9D12.15 gene product [Arabidopsis thaliana]	438	850	1.00E-14	194.1	10.3	17.6	F9D12.15 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00558.1.g16008.t1	ref|XP_002868326.1| hypothetical protein ARALYDRAFT_493518 [Arabidopsis lyrata subsp. lyrata] gi|297314162|gb|EFH44585.1| hypothetical protein ARALYDRAFT_493518 [Arabidopsis lyrata subsp. lyrata]	110	112	1.00E-43	101.8	78.2	86.4	hypothetical protein ARALYDRAFT_493518	gbpln	Arabidopsis lyrata	AT4G13950.1 | Symbols: RALFL31 | ralf-like 31 | chr4:8058268-8058609 REVERSE LENGTH=113	110	113	2.00E-44	102.7	74.5	85.5
Rsa1.0_00558.1.g16009.t4	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	222	1142	2.00E-18	514.4	21.2	29.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT3G23810.1 | Symbols: SAHH2, ATSAHH2 | S-adenosyl-l-homocysteine (SAH) hydrolase 2 | chr3:8588013-8589671 REVERSE LENGTH=485	222	485	9.00E-15	218.5	15.3	16.7
Rsa1.0_00558.1.g16010.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	393	414	3.00E-51	105.3	33.8	44.0	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00558.1.g16011.t17	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	807	704	1.00E-176	87.2	42.8	45.4	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00558.1.g16012.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	989	1529	1.00E-100	154.6	18.3	24.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	989	746	4.00E-85	75.4	16.7	21.3
Rsa1.0_00559.1.g16013.t1	ref|NP_190242.1| methyl-CPG-binding domain protein 5 [Arabidopsis thaliana] gi|75206905|sp|Q9SNC0.1|MBD5_ARATH RecName: Full=Methyl-CpG-binding domain-containing protein 5; Short=AtMBD5; Short=MBD05; AltName: Full=Methyl-CpG-binding protein MBD5 gi|6523061|emb|CAB62328.1| putative protein [Arabidopsis thaliana] gi|17380750|gb|AAL36205.1| unknown protein [Arabidopsis thaliana] gi|23296870|gb|AAN13191.1| unknown protein [Arabidopsis thaliana] gi|332644653|gb|AEE78174.1| methyl-CPG-binding domain protein 5 [Arabidopsis thaliana]	184	182	8.00E-62	98.9	65.8	75.0	methyl-CPG-binding domain protein 5	gbpln	Arabidopsis thaliana	AT3G46580.1 | Symbols: MBD05, MBD5, ATMBD5 | methyl-CPG-binding domain protein 5 | chr3:17148397-17149328 FORWARD LENGTH=182	184	182	3.00E-64	98.9	65.8	75.0
Rsa1.0_00559.1.g16014.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	778	1142	0	146.8	49.6	66.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	778	575	7.00E-76	73.9	21.9	34.7
Rsa1.0_00559.1.g16015.t1	gb|EOA14339.1| hypothetical protein CARUB_v10027520mg [Capsella rubella]	310	495	1.00E-55	159.7	41.9	51.3	hypothetical protein CARUB_v10027520mg	gbpln	Capsella rubella	AT3G62120.2 | Symbols: | Class II aaRS and biotin synthetases superfamily protein | chr3:23001227-23003849 REVERSE LENGTH=530	310	530	8.00E-54	171.0	38.4	48.1
Rsa1.0_00559.1.g16016.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16017.t3	gb|AAU90169.1| putative polyprotein [Oryza sativa Japonica Group]	1160	1154	1.00E-175	99.5	30.9	41.7	putative polyprotein	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16018.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16019.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16020.t1	gb|AAM15062.1| putative retroelement integrase [Arabidopsis thaliana]	163	1215	4.00E-28	745.4	48.5	66.3	putative retroelement integrase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16021.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16022.t1	gb|AAF79254.1|AC023279_3 F12K21.6 [Arabidopsis thaliana]	506	755	7.00E-42	149.2	22.9	36.8	F12K21.6	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00559.1.g16023.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	120	672	6.00E-11	560.0	25.0	33.3	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16024.t1	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	706	578	9.00E-93	81.9	27.2	36.5	hypothetical protein 27.t00126	gbpln	Brassica oleracea	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	706	1399	3.00E-13	198.2	7.8	10.9
Rsa1.0_00559.1.g16025.t1	gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]	121	863	2.00E-36	713.2	66.9	78.5	Ulp1 protease family protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16026.t1	gb|EEE68470.1| hypothetical protein OsJ_26870 [Oryza sativa Japonica Group]	362	709	6.00E-62	195.9	37.3	53.0	hypothetical protein OsJ_26870	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16027.t2	ref|XP_002283871.1| PREDICTED: UDP-glucuronic acid decarboxylase 1 [Vitis vinifera] gi|147766093|emb|CAN65700.1| hypothetical protein VITISV_010481 [Vitis vinifera] gi|296086255|emb|CBI31696.3| unnamed protein product [Vitis vinifera]	146	345	3.00E-56	236.3	76.0	81.5	PREDICTED: UDP-glucuronic acid decarboxylase 1	gbpln	Vitis vinifera	AT3G46440.2 | Symbols: UXS5 | UDP-XYL synthase 5 | chr3:17089268-17091611 REVERSE LENGTH=341	146	341	4.00E-55	233.6	81.5	84.9
Rsa1.0_00559.1.g16028.t1	ref|NP_190214.1| receptor-like protein kinase HERK 1 [Arabidopsis thaliana] gi|75335601|sp|Q9LX66.1|HERK_ARATH RecName: Full=Receptor-like protein kinase HERK 1; AltName: Full=Protein HERCULES RECEPTOR KINASE 1; Flags: Precursor gi|7799017|emb|CAB90956.1| receptor protein kinase-like [Arabidopsis thaliana] gi|332644622|gb|AEE78143.1| receptor-like protein kinase HERK 1 [Arabidopsis thaliana]	834	830	0	99.5	84.3	92.1	receptor-like protein kinase HERK 1	gbpln	Arabidopsis thaliana	AT3G46290.1 | Symbols: HERK1 | hercules receptor kinase 1 | chr3:17013009-17015501 FORWARD LENGTH=830	834	830	0	99.5	84.3	92.1
Rsa1.0_00559.1.g16029.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00559.1.g16030.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00560.1.g16031.t1	ref|XP_002875529.1| MYB121 [Arabidopsis lyrata subsp. lyrata] gi|297321367|gb|EFH51788.1| MYB121 [Arabidopsis lyrata subsp. lyrata]	114	271	9.00E-23	237.7	59.6	68.4	MYB121	gbpln	Arabidopsis lyrata	AT3G30210.1 | Symbols: ATMYB121, MYB121 | myb domain protein 121 | chr3:11838567-11840313 FORWARD LENGTH=276	114	276	5.00E-25	242.1	61.4	74.6
Rsa1.0_00560.1.g16032.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00560.1.g16033.t1	gb|EOA23861.1| hypothetical protein CARUB_v10017078mg, partial [Capsella rubella]	464	496	0	106.9	93.8	98.1	hypothetical protein CARUB_v10017078mg, partial	gbpln	Capsella rubella	AT3G30180.1 | Symbols: CYP85A2, BR6OX2 | brassinosteroid-6-oxidase 2 | chr3:11810867-11813509 FORWARD LENGTH=465	464	465	0	100.2	92.0	97.2
Rsa1.0_00560.1.g16034.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00560.1.g16035.t1	ref|XP_002877204.1| hypothetical protein ARALYDRAFT_323027 [Arabidopsis lyrata subsp. lyrata] gi|297323042|gb|EFH53463.1| hypothetical protein ARALYDRAFT_323027 [Arabidopsis lyrata subsp. lyrata]	913	977	1.00E-139	107.0	40.4	51.4	hypothetical protein ARALYDRAFT_323027	gbpln	Arabidopsis lyrata	AT2G10440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15780.1); Has 8319 Blast hits to 5104 proteins in 317 species: Archae - 0; Bacteria - 285; Metazoa - 1706; Fungi - 535; Plants - 320; Viruses - 18; Other Eukaryotes - 5455 (source: NCBI BLink). | chr2:4013752-4018046 REVERSE LENGTH=935	913	935	1.00E-123	102.4	35.8	45.1
Rsa1.0_00560.1.g16036.t1	ref|XP_002877204.1| hypothetical protein ARALYDRAFT_323027 [Arabidopsis lyrata subsp. lyrata] gi|297323042|gb|EFH53463.1| hypothetical protein ARALYDRAFT_323027 [Arabidopsis lyrata subsp. lyrata]	709	977	5.00E-79	137.8	24.3	30.2	hypothetical protein ARALYDRAFT_323027	gbpln	Arabidopsis lyrata	AT2G10440.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15780.1); Has 1628 Blast hits to 1350 proteins in 149 species: Archae - 0; Bacteria - 39; Metazoa - 480; Fungi - 159; Plants - 187; Viruses - 2; Other Eukaryotes - 761 (source: NCBI BLink). | chr2:4013752-4018046 REVERSE LENGTH=845	709	845	1.00E-77	119.2	25.2	30.2
Rsa1.0_00560.1.g16037.t1	ref|XP_002877216.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323054|gb|EFH53475.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	316	379	1.00E-110	119.9	71.5	81.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G29760.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr3:11590064-11591833 REVERSE LENGTH=465	316	465	5.00E-67	147.2	34.8	38.6
Rsa1.0_00560.1.g16038.t1	ref|XP_002877196.1| hypothetical protein ARALYDRAFT_905267 [Arabidopsis lyrata subsp. lyrata] gi|297323034|gb|EFH53455.1| hypothetical protein ARALYDRAFT_905267 [Arabidopsis lyrata subsp. lyrata]	462	466	0	100.9	71.4	84.0	hypothetical protein ARALYDRAFT_905267	gbpln	Arabidopsis lyrata	AT3G29635.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:11465851-11467227 REVERSE LENGTH=458	462	458	1.00E-155	99.1	58.7	76.2

Rsa1.0_00560.1.g16039.t1	ref|XP_002877196.1| hypothetical protein ARALYDRAFT_905267 [Arabidopsis lyrata subsp. lyrata] gi|297323034|gb|EFH53455.1| hypothetical protein ARALYDRAFT_905267 [Arabidopsis lyrata subsp. lyrata]	555	466	0	84.0	56.9	65.4	hypothetical protein ARALYDRAFT_905267	gbpln	Arabidopsis lyrata	AT3G29635.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:11465851-11467227 REVERSE LENGTH=458	555	458	1.00E-143	82.5	47.6	58.7
Rsa1.0_00560.1.g16040.t1	ref|NP_189600.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|75273519|sp|Q9LJB4.1|5MAT_ARATH RecName: Full=Malonyl-CoA:anthocyanidin 5-O-glucoside-6''-O-malonyltransferase; AltName: Full=Anthocyanin 5-aromatic acyltransferase-like protein; Short=At5MAT gi|11994162|dbj|BAB01191.1| anthocyanin 5-aromatic acyltransferase-like protein [Arabidopsis thaliana] gi|332644071|gb|AEE77592.1| malonyl-CoA:anthocyanidin 5-O-glucoside-6'-O-malonyltransferase [Arabidopsis thaliana]	453	449	0	99.1	83.9	92.3	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT3G29590.1 | Symbols: AT5MAT | HXXXD-type acyl-transferase family protein | chr3:11398917-11400266 REVERSE LENGTH=449	453	449	0	99.1	83.9	92.3
Rsa1.0_00560.1.g16041.t1	gb|EOA24648.1| hypothetical protein CARUB_v10017919mg, partial [Capsella rubella]	257	246	1.00E-81	95.7	71.2	79.4	hypothetical protein CARUB_v10017919mg, partial	gbpln	Capsella rubella	AT3G29575.4 | Symbols: AFP3 | ABI five binding protein 3 | chr3:11382416-11383657 REVERSE LENGTH=231	257	231	6.00E-81	89.9	71.6	79.0
Rsa1.0_00560.1.g16042.t3	gb|AAC23765.1| Mutator-like transposase [Arabidopsis thaliana]	651	784	6.00E-75	120.4	25.3	33.2	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT3G29390.1 | Symbols: RIK | RS2-interacting KH protein | chr3:11289675-11294524 FORWARD LENGTH=578	651	578	2.00E-49	88.8	16.6	20.0
Rsa1.0_00561.1.g16043.t1	gb|AAD24601.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	327	1319	6.00E-86	403.4	49.5	67.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G20520.1 | Symbols: | RNA binding;RNA-directed DNA polymerases | chr4:11045912-11047716 FORWARD LENGTH=376	327	376	2.00E-13	115.0	9.5	15.6
Rsa1.0_00561.1.g16044.t1	ref|XP_002864232.1| hypothetical protein ARALYDRAFT_495401 [Arabidopsis lyrata subsp. lyrata] gi|297310067|gb|EFH40491.1| hypothetical protein ARALYDRAFT_495401 [Arabidopsis lyrata subsp. lyrata]	270	269	3.00E-88	99.6	67.8	77.8	hypothetical protein ARALYDRAFT_495401	gbpln	Arabidopsis lyrata	AT5G53280.1 | Symbols: PDV1 | plastid division1 | chr5:21607586-21609080 FORWARD LENGTH=272	270	272	3.00E-84	100.7	64.1	74.8
Rsa1.0_00561.1.g16045.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	546	530	1.00E-59	97.1	25.5	30.2	predicted protein	gbpln	Arabidopsis lyrata	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	546	530	3.00E-14	97.1	7.5	13.0
Rsa1.0_00561.1.g16046.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1254	1213	0	96.7	34.2	49.8	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1254	626	7.00E-67	49.9	11.6	17.2
Rsa1.0_00561.1.g16047.t1	ref|XP_002864231.1| AGP22/ATAGP22 [Arabidopsis lyrata subsp. lyrata] gi|297310066|gb|EFH40490.1| AGP22/ATAGP22 [Arabidopsis lyrata subsp. lyrata]	63	63	5.00E-25	100.0	95.2	98.4	AGP22/ATAGP22	gbpln	Arabidopsis lyrata	AT5G53250.1 | Symbols: AGP22, ATAGP22 | arabinogalactan protein 22 | chr5:21603715-21604007 FORWARD LENGTH=63	63	63	5.00E-26	100.0	90.5	95.2
Rsa1.0_00561.1.g16048.t1	gb|EOA39094.1| hypothetical protein CARUB_v10011830mg [Capsella rubella]	366	363	4.00E-97	99.2	51.1	63.9	hypothetical protein CARUB_v10011830mg	gbpln	Capsella rubella	AT4G13680.1 | Symbols: | Protein of unknown function (DUF295) | chr4:7951716-7952780 REVERSE LENGTH=354	366	354	6.00E-95	96.7	51.1	62.8
Rsa1.0_00561.1.g16049.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	103	1274	2.00E-20	1236.9	44.7	53.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00561.1.g16050.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00561.1.g16051.t4	dbj|BAJ34295.1| unnamed protein product [Thellungiella halophila]	677	368	1.00E-153	54.4	46.1	48.4	unnamed protein product	----	----	AT5G53210.1 | Symbols: SPCH | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:21586606-21588941 REVERSE LENGTH=364	677	364	1.00E-136	53.8	46.1	48.3
Rsa1.0_00562.1.g16052.t1	gb|EOA23741.1| hypothetical protein CARUB_v10016954mg [Capsella rubella]	572	554	1.00E-120	96.9	55.1	67.0	hypothetical protein CARUB_v10016954mg	gbpln	Capsella rubella	AT3G26050.1 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr3:9521907-9524241 FORWARD LENGTH=533	572	533	1.00E-106	93.2	49.5	62.2
Rsa1.0_00562.1.g16053.t1	gb|EOA23303.1| hypothetical protein CARUB_v10018772mg [Capsella rubella]	473	476	0	100.6	86.7	92.2	hypothetical protein CARUB_v10018772mg	gbpln	Capsella rubella	AT3G26030.1 | Symbols: ATB' DELTA | serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B prime delta | chr3:9517741-9519260 FORWARD LENGTH=477	473	477	0	100.8	86.3	91.5

Rsa1.0_00562.1.g16054.t1	ref|NP_189231.1| protein phosphatase 2A regulatory subunit B' eta [Arabidopsis thaliana] gi|79313549|ref|NP_001030770.1| protein phosphatase 2A regulatory subunit B' eta [Arabidopsis thaliana] gi|75274192|sp|Q9LU89.1|2A5N_ARATH RecName: Full=Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' eta isoform; Short=AtB' eta; Short=PP2A, B' subunit, eta isoform gi|14194123|gb|AAK56256.1|AF367267_1 AT3g26020/MPE11_17 [Arabidopsis thaliana] gi|9279607|dbj|BAB01065.1| protein phosphatase 2A regulatory subunit B' [Arabidopsis thaliana] gi|16323340|gb|AAL15383.1| AT3g26020/MPE11_17 [Arabidopsis thaliana] gi|222424130|dbj|BAH20024.1| AT3G26020 [Arabidopsis thaliana] gi|332643581|gb|AEE77102.1| protein phosphatase 2A regulatory subunit B' eta [Arabidopsis thaliana] gi|332643582|gb|AEE77103.1| protein phosphatase 2A regulatory subunit B' eta [Arabidopsis thaliana]	512	510	0	99.6	89.6	92.4	protein phosphatase 2A regulatory subunit B' eta	gbpln	Arabidopsis thaliana	AT3G26020.2 | Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr3:9514363-9516585 FORWARD LENGTH=510	512	510	0	99.6	89.6	92.4
Rsa1.0_00562.1.g16055.t1	ref|XP_002876943.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297322781|gb|EFH53202.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	484	451	1.00E-141	93.2	56.2	63.4	F-box family protein	gbpln	Arabidopsis lyrata	AT3G26000.1 | Symbols: | Ribonuclease inhibitor | chr3:9507042-9508542 REVERSE LENGTH=453	484	453	1.00E-136	93.6	53.7	62.0
Rsa1.0_00562.1.g16056.t1	gb|EOA24178.1| hypothetical protein CARUB_v10017413mg, partial [Capsella rubella]	400	391	1.00E-159	97.8	74.5	82.5	hypothetical protein CARUB_v10017413mg, partial	gbpln	Capsella rubella	AT3G25990.1 | Symbols: | Homeodomain-like superfamily protein | chr3:9504846-9506703 REVERSE LENGTH=372	400	372	1.00E-155	93.0	71.3	79.5
Rsa1.0_00562.1.g16057.t1	ref|XP_002876941.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322779|gb|EFH53200.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	629	652	0	103.7	81.6	89.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G25970.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:9500116-9502221 REVERSE LENGTH=701	629	701	0	111.4	80.3	89.7
Rsa1.0_00562.1.g16058.t1	ref|XP_002876940.1| universal stress protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297322778|gb|EFH53199.1| universal stress protein family protein [Arabidopsis lyrata subsp. lyrata]	161	156	1.00E-51	96.9	62.1	72.7	universal stress protein family protein	gbpln	Arabidopsis lyrata	AT3G25930.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:9493032-9493871 REVERSE LENGTH=154	161	154	8.00E-53	95.7	60.9	70.2
Rsa1.0_00562.1.g16059.t1	gb|EOA25813.1| hypothetical protein CARUB_v10019181mg [Capsella rubella]	333	358	1.00E-124	107.5	78.4	83.8	hypothetical protein CARUB_v10019181mg	gbpln	Capsella rubella	AT3G25910.1 | Symbols: | Protein of unknown function (DUF1644) | chr3:9489836-9490954 FORWARD LENGTH=372	333	372	1.00E-110	111.7	70.3	78.1
Rsa1.0_00562.1.g16060.t1	gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]	181	198	2.00E-31	109.4	40.3	57.5	hypothetical protein 27.t00041	gbpln	Brassica oleracea	AT2G35280.1 | Symbols: | F-box family protein | chr2:14859709-14860200 REVERSE LENGTH=163	181	163	1.00E-10	90.1	17.1	29.3
Rsa1.0_00562.1.g16061.t1	ref|NP_566783.1| protein CLAVATA3/ESR-related 27 [Arabidopsis thaliana] gi|75274199|sp|Q9LUA1.1|CLE27_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 27; Contains: RecName: Full=CLE27p; Flags: Precursor gi|9279595|dbj|BAB01053.1| unnamed protein product [Arabidopsis thaliana] gi|114050673|gb|ABI49486.1| At3g25905 [Arabidopsis thaliana] gi|254803081|gb|ACT82820.1| At3g25905 [Arabidopsis thaliana] gi|332643568|gb|AEE77089.1| protein CLAVATA3/ESR-related 27 [Arabidopsis thaliana]	81	91	4.00E-21	112.3	61.7	74.1	protein CLAVATA3/ESR-related 27	gbpln	Arabidopsis thaliana	AT3G25905.1 | Symbols: CLE27 | CLAVATA3/ESR-RELATED 27 | chr3:9486348-9486623 REVERSE LENGTH=91	81	91	6.00E-24	112.3	61.7	74.1
Rsa1.0_00562.1.g16062.t7	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1532	1365	0	89.1	33.9	47.5	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1532	575	1.00E-49	37.5	9.5	14.4
Rsa1.0_00562.1.g16063.t1	dbj|BAJ34405.1| unnamed protein product [Thellungiella halophila]	281	341	1.00E-102	121.4	78.3	85.8	unnamed protein product	----	----	AT3G25890.2 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:9476052-9477050 FORWARD LENGTH=332	281	332	1.00E-84	118.1	72.2	81.5
Rsa1.0_00562.1.g16064.t5	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1533	1213	1.00E-180	79.1	26.2	38.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1533	626	3.00E-53	40.8	8.7	14.8

Rsa1.0_00562.1.g16065.t1	ref|NP_683594.1| NIM1-interacting 2 protein [Arabidopsis thaliana] gi|75274201|sp|Q9LUA3.1|NIMI2_ARATH RecName: Full=Protein NIM1-INTERACTING 2; Short=Protein NIMIN-2 gi|9279592|dbj|BAB01050.1| unnamed protein product [Arabidopsis thaliana] gi|12057156|emb|CAC19845.1| NIMIN-2 protein [Arabidopsis thaliana] gi|109946525|gb|ABG48441.1| At3g25882 [Arabidopsis thaliana] gi|332643562|gb|AEE77083.1| protein NIM1-INTERACTING 2 [Arabidopsis thaliana]	117	122	1.00E-40	104.3	78.6	85.5	NIM1-interacting 2 protein	gbpln	Arabidopsis thaliana	AT3G25882.1 | Symbols: NIMIN-2 | NIM1-interacting 2 | chr3:9470521-9470889 REVERSE LENGTH=122	117	122	2.00E-43	104.3	78.6	85.5
Rsa1.0_00563.1.g16066.t3	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	150	484	4.00E-12	322.7	36.0	57.3	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00563.1.g16067.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00563.1.g16068.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1851	2301	0	124.3	54.3	65.1	disease resistance protein	gbpln	Brassica rapa	AT4G09060.1 | Symbols: | unknown protein; LOCATED IN: membrane; EXPRESSED IN: leaf; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G14680.1); Has 8168 Blast hits to 6036 proteins in 601 species: Archae - 151; Bacteria - 570; Metazoa - 4684; Fungi - 544; Plants - 345; Viruses - 91; Other Eukaryotes - 1783 (source: NCBI BLink). | chr4:5797781-5800253 REVERSE LENGTH=341	1851	341	1.00E-138	18.4	14.0	15.8
Rsa1.0_00563.1.g16069.t1	ref|XP_002891255.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297337097|gb|EFH67514.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	112	210	8.00E-24	187.5	50.0	60.7	NLI interacting factor family protein	gbpln	Arabidopsis lyrata	AT1G43610.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:16424578-16425345 FORWARD LENGTH=255	112	255	6.00E-25	227.7	50.0	58.0
Rsa1.0_00563.1.g16070.t1	ref|NP_192642.1| arabinogalactan protein 10 [Arabidopsis thaliana] gi|75181652|sp|Q9M0S4.1|AGP10_ARATH RecName: Full=Classical arabinogalactan protein 10; Flags: Precursor gi|10880497|gb|AAG24278.1|AF195891_1 arabinogalactan protein [Arabidopsis thaliana] gi|7267545|emb|CAB78027.1| arabinogalactan-protein homolog [Arabidopsis thaliana] gi|110738133|dbj|BAF00998.1| arabinogalactan-protein AGP10 [Arabidopsis thaliana] gi|332657314|gb|AEE82714.1| arabinogalactan protein 10 [Arabidopsis thaliana]	132	127	1.00E-20	96.2	68.9	77.3	arabinogalactan protein 10	gbpln	Arabidopsis thaliana	AT4G09030.1 | Symbols: AGP10, ATAGP10 | arabinogalactan protein 10 | chr4:5792249-5792632 FORWARD LENGTH=127	132	127	3.00E-23	96.2	68.9	77.3
Rsa1.0_00563.1.g16071.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00563.1.g16072.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	299	368	7.00E-63	123.1	47.2	58.5	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	299	370	9.00E-50	123.7	38.8	54.5
Rsa1.0_00563.1.g16073.t1	#	#	#	#	#	#	#	-	----	----	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	116	370	5.00E-12	319.0	33.6	43.1
Rsa1.0_00563.1.g16074.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00563.1.g16075.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	322	368	9.00E-57	114.3	44.4	61.2	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	322	370	4.00E-49	114.9	40.1	56.2
Rsa1.0_00563.1.g16076.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	367	368	2.00E-68	100.3	45.5	60.2	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	367	370	3.00E-68	100.8	43.1	57.5
Rsa1.0_00563.1.g16077.t2	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	1476	1356	0	91.9	45.1	61.0	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1476	1262	4.00E-78	85.5	11.6	18.0
Rsa1.0_00563.1.g16078.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	310	368	1.00E-56	118.7	46.1	57.7	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	310	370	2.00E-47	119.4	39.4	55.5

Rsa1.0_00563.1.g16079.t1	ref|NP_192641.2| isoamylase 3 [Arabidopsis thaliana] gi|251764781|sp|Q9M0S5.2|ISOA3_ARATH RecName: Full=Isoamylase 3, chloroplastic; Short=AtISA3; Flags: Precursor gi|20259518|gb|AAM13879.1| putative isoamylase [Arabidopsis thaliana] gi|22136708|gb|AAM91673.1| putative isoamylase [Arabidopsis thaliana] gi|110742373|dbj|BAE99109.1| isoamylase-like protein [Arabidopsis thaliana] gi|332657313|gb|AEE82713.1| isoamylase 3 [Arabidopsis thaliana]	735	764	0	103.9	86.7	91.6	isoamylase 3	gbpln	Arabidopsis thaliana	AT4G09020.1 | Symbols: ATISA3, ISA3 | isoamylase 3 | chr4:5784099-5788839 FORWARD LENGTH=764	735	764	0	103.9	86.7	91.6
Rsa1.0_00564.1.g16080.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00564.1.g16081.t1	ref|XP_002875545.1| hypothetical protein ARALYDRAFT_905307 [Arabidopsis lyrata subsp. lyrata] gi|297321383|gb|EFH51804.1| hypothetical protein ARALYDRAFT_905307 [Arabidopsis lyrata subsp. lyrata]	113	116	2.00E-21	102.7	51.3	59.3	hypothetical protein ARALYDRAFT_905307	gbpln	Arabidopsis lyrata	AT3G29780.1 | Symbols: RALFL27 | ralf-like 27 | chr3:11671741-11672094 FORWARD LENGTH=117	113	117	6.00E-14	103.5	38.9	46.0
Rsa1.0_00564.1.g16082.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00564.1.g16083.t1	ref|XP_002875545.1| hypothetical protein ARALYDRAFT_905307 [Arabidopsis lyrata subsp. lyrata] gi|297321383|gb|EFH51804.1| hypothetical protein ARALYDRAFT_905307 [Arabidopsis lyrata subsp. lyrata]	114	116	9.00E-31	101.8	61.4	69.3	hypothetical protein ARALYDRAFT_905307	gbpln	Arabidopsis lyrata	AT3G29780.1 | Symbols: RALFL27 | ralf-like 27 | chr3:11671741-11672094 FORWARD LENGTH=117	114	117	1.00E-23	102.6	50.9	56.1
Rsa1.0_00564.1.g16084.t1	gb|EOA24175.1| hypothetical protein CARUB_v10017408mg [Capsella rubella]	375	393	1.00E-170	104.8	87.7	92.5	hypothetical protein CARUB_v10017408mg	gbpln	Capsella rubella	AT3G29770.1 | Symbols: ATMES11, MES11 | methyl esterase 11 | chr3:11648471-11650565 FORWARD LENGTH=390	375	390	1.00E-163	104.0	87.2	92.0
Rsa1.0_00564.1.g16085.t1	ref|NP_001077832.1| LYR family of Fe/S cluster biogenesis protein [Arabidopsis thaliana] gi|8778812|gb|AAF79817.1|AC007396_17 T4O12.27 [Arabidopsis thaliana] gi|62321766|dbj|BAD95391.1| hypothetical protein [Arabidopsis thaliana] gi|98961727|gb|ABF59193.1| unknown protein [Arabidopsis thaliana] gi|332197671|gb|AEE35792.1| LYR family of Fe/S cluster biogenesis protein [Arabidopsis thaliana]	81	80	2.00E-31	98.8	84.0	87.7	LYR family of Fe/S cluster biogenesis protein	gbpln	Arabidopsis thaliana	AT1G76065.1 | Symbols: | LYR family of Fe/S cluster biogenesis protein | chr1:28544899-28545306 REVERSE LENGTH=80	81	80	3.00E-34	98.8	84.0	87.7
Rsa1.0_00564.1.g16086.t1	ref|NP_189605.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|11994174|dbj|BAB01203.1| anthocyanin acyltransferase-like protein [Arabidopsis thaliana] gi|332644074|gb|AEE77595.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	405	458	1.00E-153	113.1	73.1	83.7	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT3G29635.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:11465851-11467227 REVERSE LENGTH=458	405	458	1.00E-155	113.1	73.1	83.7
Rsa1.0_00564.1.g16087.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00564.1.g16088.t1	gb|EOA24648.1| hypothetical protein CARUB_v10017919mg, partial [Capsella rubella]	253	246	2.00E-82	97.2	70.4	76.7	hypothetical protein CARUB_v10017919mg, partial	gbpln	Capsella rubella	AT3G29575.4 | Symbols: AFP3 | ABI five binding protein 3 | chr3:11382416-11383657 REVERSE LENGTH=231	253	231	7.00E-85	91.3	72.3	77.1
Rsa1.0_00564.1.g16089.t1	ref|NP_189586.1| exocyst complex component 7 [Arabidopsis thaliana] gi|11994523|dbj|BAB02587.1| unnamed protein product [Arabidopsis thaliana] gi|30794118|gb|AAP40501.1| unknown protein [Arabidopsis thaliana] gi|332644060|gb|AEE77581.1| exocyst subunit exo70 family protein E1 [Arabidopsis thaliana]	644	658	0	102.2	85.1	91.8	exocyst complex component 7	gbpln	Arabidopsis thaliana	AT3G29400.1 | Symbols: ATEXO70E1, EXO70E1 | exocyst subunit exo70 family protein E1 | chr3:11297339-11299315 REVERSE LENGTH=658	644	658	0	102.2	85.1	91.8
Rsa1.0_00564.1.g16090.t1	ref|XP_002875519.1| hypothetical protein ARALYDRAFT_905257 [Arabidopsis lyrata subsp. lyrata] gi|297321357|gb|EFH51778.1| hypothetical protein ARALYDRAFT_905257 [Arabidopsis lyrata subsp. lyrata]	553	592	0	107.1	77.9	85.4	hypothetical protein ARALYDRAFT_905257	gbpln	Arabidopsis lyrata	AT3G29390.1 | Symbols: RIK | RS2-interacting KH protein | chr3:11289675-11294524 FORWARD LENGTH=578	553	578	0	104.5	75.4	82.6
Rsa1.0_00564.1.g16091.t1	ref|XP_002877179.1| transcription factor IIB family protein [Arabidopsis lyrata subsp. lyrata] gi|297323017|gb|EFH53438.1| transcription factor IIB family protein [Arabidopsis lyrata subsp. lyrata]	335	336	1.00E-112	100.3	63.9	75.5	transcription factor IIB family protein	gbpln	Arabidopsis lyrata	AT3G29380.1 | Symbols: | Cyclin-like family protein | chr3:11282407-11283524 REVERSE LENGTH=336	335	336	1.00E-110	100.3	62.7	75.5

Rsa1.0_00564.1.g16092.t1	ref|XP_002875515.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321353|gb|EFH51774.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	247	257	1.00E-117	104.0	82.2	90.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G39300.1 | Symbols: ATEXPA25, EXP25, ATEXP25, ATHEXP ALPHA 1.18, EXPA25 | expansin A25 | chr5:15737427-15738387 REVERSE LENGTH=260	247	260	8.00E-88	105.3	59.9	72.9
Rsa1.0_00564.1.g16093.t1	ref|NP_189578.1| glycosyl transferase, family 35 protein [Arabidopsis thaliana] gi|75335028|sp|Q9LIB2.1|PHS1_ARATH RecName: Full=Alpha-glucan phosphorylase 1; Short=AtPHS1; AltName: Full=Alpha-glucan phosphorylase, L isozyme; AltName: Full=Starch phosphorylase L; Flags: Precursor gi|11994512|dbj|BAB02576.1| glycogen phosphorylase B; starch phosphorylase [Arabidopsis thaliana] gi|15146189|gb|AAK83578.1| AT3g29320/MUO10_2 [Arabidopsis thaliana] gi|27764918|gb|AAO23580.1| At3g29320/MUO10_2 [Arabidopsis thaliana] gi|332644046|gb|AEE77567.1| alpha-glucan phosphorylase 1 [Arabidopsis thaliana]	945	962	0	101.8	88.9	93.8	glycosyl transferase, family 35 protein	gbpln	Arabidopsis thaliana	AT3G29320.1 | Symbols: | Glycosyl transferase, family 35 | chr3:11252871-11257587 FORWARD LENGTH=962	945	962	0	101.8	88.9	93.8
Rsa1.0_00564.1.g16094.t1	ref|NP_189577.2| calmodulin-binding protein-like protein [Arabidopsis thaliana] gi|75273349|sp|Q9LIB3.1|BAG8_ARATH RecName: Full=BAG family molecular chaperone regulator 8, chloroplastic; AltName: Full=Bcl-2-associated athanogene 8; Flags: Precursor gi|11994511|dbj|BAB02575.1| unnamed protein product [Arabidopsis thaliana] gi|19310462|gb|AAL84966.1| AT3g29310/MUO10_1 [Arabidopsis thaliana] gi|23506159|gb|AAN31091.1| At3g29310/MUO10_1 [Arabidopsis thaliana] gi|332644045|gb|AEE77566.1| calmodulin-binding protein-like protein [Arabidopsis thaliana]	484	551	1.00E-118	113.8	60.1	71.9	calmodulin-binding protein-like protein	gbpln	Arabidopsis thaliana	AT3G29310.1 | Symbols: | calmodulin-binding protein-related | chr3:11249712-11251452 FORWARD LENGTH=551	484	551	1.00E-120	113.8	60.1	71.9
Rsa1.0_00564.1.g16095.t1	gb|EOA25900.1| hypothetical protein CARUB_v10019279mg [Capsella rubella]	519	560	0	107.9	77.3	87.7	hypothetical protein CARUB_v10019279mg	gbpln	Capsella rubella	AT3G29290.1 | Symbols: emb2076 | Pentatricopeptide repeat (PPR) superfamily protein | chr3:11238421-11240125 FORWARD LENGTH=540	519	540	0	104.0	76.9	86.5
Rsa1.0_00564.1.g16096.t1	gb|EOA24783.1| hypothetical protein CARUB_v10018062mg, partial [Capsella rubella]	172	193	3.00E-83	112.2	90.7	95.3	hypothetical protein CARUB_v10018062mg, partial	gbpln	Capsella rubella	AT3G29280.1 | Symbols: | unknown protein; Has 24 Blast hits to 24 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:11236705-11237947 REVERSE LENGTH=178	172	178	6.00E-81	103.5	83.1	86.0
Rsa1.0_00564.1.g16097.t2	ref|XP_002882791.1| hypothetical protein ARALYDRAFT_478647 [Arabidopsis lyrata subsp. lyrata] gi|297328631|gb|EFH59050.1| hypothetical protein ARALYDRAFT_478647 [Arabidopsis lyrata subsp. lyrata]	477	499	0	104.6	65.4	76.9	hypothetical protein ARALYDRAFT_478647	gbpln	Arabidopsis lyrata	AT3G12860.1 | Symbols: | NOP56-like pre RNA processing ribonucleoprotein | chr3:4091678-4093921 FORWARD LENGTH=499	477	499	0	104.6	65.2	76.5
Rsa1.0_00564.1.g16098.t1	gb|EOA15049.1| hypothetical protein CARUB_v10028408mg [Capsella rubella]	108	122	1.00E-41	113.0	79.6	90.7	hypothetical protein CARUB_v10028408mg	gbpln	Capsella rubella	AT2G14378.1 | Symbols: | Protein of unknown function (DUF1278) | chr2:6104869-6105231 REVERSE LENGTH=120	108	120	2.00E-44	111.1	74.1	85.2
Rsa1.0_00564.1.g16099.t1	ref|NP_566847.1| uncharacterized protein [Arabidopsis thaliana] gi|30689543|ref|NP_850648.1| uncharacterized protein [Arabidopsis thaliana] gi|9293917|dbj|BAB01820.1| unnamed protein product [Arabidopsis thaliana] gi|19310484|gb|AAL84976.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|21537141|gb|AAM61482.1| unknown [Arabidopsis thaliana] gi|22654969|gb|AAM98077.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|28416521|gb|AAO42791.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|332644033|gb|AEE77554.1| uncharacterized protein AT3G29240 [Arabidopsis thaliana] gi|332644034|gb|AEE77555.1| uncharacterized protein AT3G29240 [Arabidopsis thaliana]	309	317	1.00E-150	102.6	83.5	92.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G29240.2 | Symbols: | Protein of unknown function (DUF179) | chr3:11191780-11192868 FORWARD LENGTH=317	309	317	1.00E-153	102.6	83.5	92.2

Rsa1.0_00565.1.g16100.t1	ref|NP_199482.1| Tetraspanin family protein [Arabidopsis thaliana] gi|75262522|sp|Q9FIQ5.1|TRN2_ARATH RecName: Full=Protein TORNADO 2; AltName: Full=Protein EKEKO; AltName: Full=TETRASPANIN-1 gi|9758506|dbj|BAB08914.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] gi|56381915|gb|AAV85676.1| At5g46700 [Arabidopsis thaliana] gi|110740669|dbj|BAE98437.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] gi|332008032|gb|AED95415.1| Tetraspanin family protein [Arabidopsis thaliana]	262	269	1.00E-106	102.7	77.5	89.3	Tetraspanin family protein	gbpln	Arabidopsis thaliana	AT5G46700.1 | Symbols: TET1, TRN2 | Tetraspanin family protein | chr5:18951035-18952439 FORWARD LENGTH=269	262	269	1.00E-108	102.7	77.5	89.3
Rsa1.0_00565.1.g16101.t1	gb|EOA18064.1| hypothetical protein CARUB_v10006510mg, partial [Capsella rubella]	90	555	4.00E-12	616.7	32.2	58.9	hypothetical protein CARUB_v10006510mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	90	566	1.00E-13	628.9	32.2	51.1
Rsa1.0_00565.1.g16102.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1789	1142	0	63.8	27.9	37.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1789	575	5.00E-63	32.1	9.2	14.9
Rsa1.0_00565.1.g16103.t1	ref|NP_199482.1| Tetraspanin family protein [Arabidopsis thaliana] gi|75262522|sp|Q9FIQ5.1|TRN2_ARATH RecName: Full=Protein TORNADO 2; AltName: Full=Protein EKEKO; AltName: Full=TETRASPANIN-1 gi|9758506|dbj|BAB08914.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] gi|56381915|gb|AAV85676.1| At5g46700 [Arabidopsis thaliana] gi|110740669|dbj|BAE98437.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] gi|332008032|gb|AED95415.1| Tetraspanin family protein [Arabidopsis thaliana]	271	269	1.00E-123	99.3	85.6	93.7	Tetraspanin family protein	gbpln	Arabidopsis thaliana	AT5G46700.1 | Symbols: TET1, TRN2 | Tetraspanin family protein | chr5:18951035-18952439 FORWARD LENGTH=269	271	269	1.00E-126	99.3	85.6	93.7
Rsa1.0_00565.1.g16104.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00565.1.g16105.t1	dbj|BAJ34641.1| unnamed protein product [Thellungiella halophila]	323	324	1.00E-150	100.3	91.0	95.4	unnamed protein product	----	----	AT5G46690.1 | Symbols: bHLH071 | beta HLH protein 71 | chr5:18945639-18947434 FORWARD LENGTH=327	323	327	1.00E-139	101.2	85.1	91.6
Rsa1.0_00565.1.g16106.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00565.1.g16107.t1	ref|NP_199477.1| RING-H2 finger protein ATL30 [Arabidopsis thaliana] gi|68565288|sp|Q9FIR0.1|ATL30_ARATH RecName: Full=RING-H2 finger protein ATL30 gi|9758501|dbj|BAB08909.1| unnamed protein product [Arabidopsis thaliana] gi|332008027|gb|AED95410.1| RING-H2 finger protein ATL30 [Arabidopsis thaliana]	287	289	1.00E-131	100.7	81.9	89.2	RING-H2 finger protein ATL30	gbpln	Arabidopsis thaliana	AT5G46650.1 | Symbols: | RING/U-box superfamily protein | chr5:18930443-18931312 FORWARD LENGTH=289	287	289	1.00E-133	100.7	81.9	89.2
Rsa1.0_00565.1.g16108.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00565.1.g16109.t1	ref|XP_002863395.1| hypothetical protein ARALYDRAFT_494317 [Arabidopsis lyrata subsp. lyrata] gi|297309230|gb|EFH39654.1| hypothetical protein ARALYDRAFT_494317 [Arabidopsis lyrata subsp. lyrata]	580	551	0	95.0	80.5	86.6	hypothetical protein ARALYDRAFT_494317	gbpln	Arabidopsis lyrata	AT5G46610.1 | Symbols: | Aluminium activated malate transporter family protein | chr5:18913115-18915736 REVERSE LENGTH=543	580	543	0	93.6	80.0	86.4
Rsa1.0_00565.1.g16110.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	714	1413	1.00E-168	197.9	41.6	48.9	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	714	1262	1.00E-140	176.8	33.3	41.3
Rsa1.0_00565.1.g16111.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	158	1123	8.00E-48	710.8	55.7	65.8	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00566.1.g16112.t1	gb|AAL32631.1| putative elongation factor 1-a [Arabidopsis thaliana] gi|21387133|gb|AAM47970.1| putative elongation factor 1-a [Arabidopsis thaliana]	187	449	1.00E-107	240.1	100.0	100.0	putative elongation factor 1-a	gbpln	Arabidopsis thaliana	AT5G60390.3 | Symbols: | GTP binding Elongation factor Tu family protein | chr5:24289226-24290675 FORWARD LENGTH=449	187	449	1.00E-110	240.1	100.0	100.0
Rsa1.0_00566.1.g16113.t9	ref|XP_002889671.1| LOB domain protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297335513|gb|EFH65930.1| LOB domain protein 1 [Arabidopsis lyrata subsp. lyrata]	207	190	1.00E-72	91.8	71.0	78.3	LOB domain protein 1	gbpln	Arabidopsis lyrata	AT1G07900.1 | Symbols: LBD1 | LOB domain-containing protein 1 | chr1:2442624-2443631 FORWARD LENGTH=190	207	190	2.00E-74	91.8	70.5	78.3

Rsa1.0_00566.1.g16114.t1	gb|AAN60795.1| ascorbate peroxidase [Brassica juncea]	250	250	1.00E-142	100.0	97.6	99.2	ascorbate peroxidase	gbpln	Brassica juncea	AT1G07890.8 | Symbols: APX1, MEE6, CS1, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250	250	250	1.00E-141	100.0	94.4	98.0
Rsa1.0_00566.1.g16115.t2	ref|XP_002892423.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338265|gb|EFH68682.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	360	363	0	100.8	92.2	96.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G07880.2 | Symbols: ATMPK13 | Protein kinase superfamily protein | chr1:2434193-2435712 REVERSE LENGTH=363	360	363	0	100.8	90.3	96.4
Rsa1.0_00566.1.g16116.t1	ref|XP_002889667.1| ribosomal protein L29 family protein [Arabidopsis lyrata subsp. lyrata] gi|297335509|gb|EFH65926.1| ribosomal protein L29 family protein [Arabidopsis lyrata subsp. lyrata]	147	143	3.00E-65	97.3	89.8	91.2	ribosomal protein L29 family protein	gbpln	Arabidopsis lyrata	AT1G07830.1 | Symbols: | ribosomal protein L29 family protein | chr1:2422549-2423392 FORWARD LENGTH=144	147	144	2.00E-65	98.0	89.8	90.5
Rsa1.0_00566.1.g16117.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_00566.1.g16118.t1	ref|NP_172246.3| Ca2+-transporting ATPase [Arabidopsis thaliana] gi|12643934|sp|Q9XES1.2|ECA4_ARATH RecName: Full=Calcium-transporting ATPase 4, endoplasmic reticulum-type gi|8439902|gb|AAF75088.1|AC007583_24 Strong similarity to ER-type calcium pump protein from Arabidopsis thaliana gb|U93845. It is a member of Na+/K+ ATPase C-terminus PF|00690 and a member of E1-E2 ATPase PF|00122 [Arabidopsis thaliana] gi|332190039|gb|AEE28160.1| calcium-transporting ATPase 4 [Arabidopsis thaliana]	1060	1061	0	100.1	94.2	97.4	Ca2+-transporting ATPase	gbpln	Arabidopsis thaliana	AT1G07670.1 | Symbols: ATECA4, ECA4 | endomembrane-type CA-ATPase 4 | chr1:2370305-2374196 REVERSE LENGTH=1061	1060	1061	0	100.1	94.2	97.4
Rsa1.0_00566.1.g16119.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00566.1.g16120.t1	ref|XP_002892418.1| hypothetical protein ARALYDRAFT_470808 [Arabidopsis lyrata subsp. lyrata] gi|297338260|gb|EFH68677.1| hypothetical protein ARALYDRAFT_470808 [Arabidopsis lyrata subsp. lyrata]	356	356	0	100.0	90.4	94.9	hypothetical protein ARALYDRAFT_470808	gbpln	Arabidopsis lyrata	AT2G28680.1 | Symbols: | RmlC-like cupins superfamily protein | chr2:12303118-12304747 REVERSE LENGTH=356	356	356	0	100.0	88.8	94.9
Rsa1.0_00566.1.g16121.t1	ref|NP_172256.1| 40S ribosomal protein S15a-1 [Arabidopsis thaliana] gi|15238544|ref|NP_200793.1| 40S ribosomal protein S15a-1 [Arabidopsis thaliana] gi|42571385|ref|NP_973783.1| 40S ribosomal protein S15a-1 [Arabidopsis thaliana] gi|297796939|ref|XP_002866354.1| RPS15A [Arabidopsis lyrata subsp. lyrata] gi|297815756|ref|XP_002875761.1| RPS15A [Arabidopsis lyrata subsp. lyrata] gi|297849076|ref|XP_002892419.1| RPS15A [Arabidopsis lyrata subsp. lyrata] gi|1173218|sp|P42798.2|R15A1_ARATH RecName: Full=40S ribosomal protein S15a-1 gi|8439890|gb|AAF75076.1|AC007583_12 Strong similarity to 40S ribosomal protein S15A from Arabidopsis thaliana gb|L27461. EST gb|R30315 comes from this gene [Arabidopsis thaliana] gi|12083302|gb|AAG48810.1|AF332447_1 putative ribosomal protein S15 [Arabidopsis thaliana] gi|13430744|gb|AAK25994.1|AF360284_1 putative ribosomal protein S15 [Arabidopsis thaliana] gi|14423370|gb|AAK62367.1|AF386922_1 40S ribosomal protein S15A [Arabidopsis thaliana] gi|440824|gb|AAA61608.1| ribosomal	130	130	1.00E-69	100.0	100.0	100.0	40S ribosomal protein S15a-1	gbpln	Arabidopsis lyrata	AT5G59850.1 | Symbols: | Ribosomal protein S8 family protein | chr5:24112499-24113084 REVERSE LENGTH=130	130	130	3.00E-72	100.0	100.0	100.0
Rsa1.0_00566.1.g16122.t1	gb|EOA39283.1| hypothetical protein CARUB_v10012292mg [Capsella rubella]	317	137	2.00E-71	43.2	40.7	42.0	hypothetical protein CARUB_v10012292mg	gbpln	Capsella rubella	AT1G07645.1 | Symbols: ATDSI-1VOC, DSI-1VOC | dessication-induced 1VOC superfamily protein | chr1:2367612-2368349 REVERSE LENGTH=137	317	137	9.00E-73	43.2	40.1	41.6

Rsa1.0_00566.1.g16123.t1	gb|ACR48175.1| OBF binding protein 2 Dof1.1-1 [Brassica rapa subsp. pekinensis]	324	317	1.00E-125	97.8	77.8	81.8	OBF binding protein 2 Dof1.1-1	gbpln	Brassica rapa	AT1G07640.3 | Symbols: OBP2 | Dof-type zinc finger DNA-binding family protein | chr1:2354707-2356012 REVERSE LENGTH=339	324	339	1.00E-103	104.6	69.8	78.1
Rsa1.0_00566.1.g16124.t1	gb|EOA40249.1| hypothetical protein CARUB_v10008970mg [Capsella rubella]	495	490	0	99.0	81.4	89.9	hypothetical protein CARUB_v10008970mg	gbpln	Capsella rubella	AT1G07615.1 | Symbols: | GTP-binding protein Obg/CgtA | chr1:2342277-2344200 REVERSE LENGTH=493	495	493	0	99.6	80.6	88.9
Rsa1.0_00566.1.g16125.t1	gb|ABO71662.1| metallothionein protein [Brassica juncea]	45	45	4.00E-13	100.0	100.0	100.0	metallothionein protein	gbpln	Brassica juncea	AT1G07610.1 | Symbols: MT1C | metallothionein 1C | chr1:2341603-2341865 FORWARD LENGTH=45	45	45	1.00E-13	100.0	91.1	93.3
Rsa1.0_00566.1.g16126.t1	gb|EOA40109.1| hypothetical protein CARUB_v10008810mg [Capsella rubella]	534	534	0	100.0	88.2	94.4	hypothetical protein CARUB_v10008810mg	gbpln	Capsella rubella	AT1G07590.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:2336649-2338481 REVERSE LENGTH=534	534	534	0	100.0	88.8	94.6
Rsa1.0_00566.1.g16127.t1	gb|EOA40572.1| hypothetical protein CARUB_v10009302mg [Capsella rubella] gi|482576386|gb|EOA40573.1| hypothetical protein CARUB_v10009302mg [Capsella rubella]	406	410	0	101.0	93.6	97.0	hypothetical protein CARUB_v10009302mg	gbpln	Capsella rubella	AT1G07570.1 | Symbols: APK1A, APK1 | Protein kinase superfamily protein | chr1:2331369-2333210 REVERSE LENGTH=410	406	410	0	101.0	93.3	96.8
Rsa1.0_00566.1.g16128.t1	gb|EOA37445.1| hypothetical protein CARUB_v10011533mg [Capsella rubella]	812	871	0	107.3	81.7	90.1	hypothetical protein CARUB_v10011533mg	gbpln	Capsella rubella	AT1G07560.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:2327320-2331096 FORWARD LENGTH=871	812	871	0	107.3	76.0	85.8
Rsa1.0_00566.1.g16129.t1	gb|EOA21150.1| hypothetical protein CARUB_v10001497mg [Capsella rubella]	269	315	8.00E-97	117.1	69.1	78.1	hypothetical protein CARUB_v10001497mg	gbpln	Capsella rubella	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	269	302	5.00E-92	112.3	66.2	76.2
Rsa1.0_00567.1.g16130.t1	emb|CAC19877.1| long chain acyl-CoA synthetase [Brassica napus]	82	693	5.00E-34	845.1	84.1	90.2	long chain acyl-CoA synthetase	gbpln	Brassica napus	AT1G77590.1 | Symbols: LACS9 | long chain acyl-CoA synthetase 9 | chr1:29148501-29151776 REVERSE LENGTH=691	82	691	8.00E-28	842.7	67.1	78.0
Rsa1.0_00567.1.g16131.t1	ref|XP_002886918.1| hypothetical protein ARALYDRAFT_315582 [Arabidopsis lyrata subsp. lyrata] gi|297332759|gb|EFH63177.1| hypothetical protein ARALYDRAFT_315582 [Arabidopsis lyrata subsp. lyrata]	452	450	0	99.6	86.9	92.7	hypothetical protein ARALYDRAFT_315582	gbpln	Arabidopsis lyrata	AT1G65450.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:24315875-24318895 FORWARD LENGTH=450	452	450	0	99.6	85.0	91.8
Rsa1.0_00567.1.g16132.t1	ref|NP_851232.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|79331627|ref|NP_001032112.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332009965|gb|AED97348.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332009967|gb|AED97350.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	116	494	7.00E-11	425.9	31.9	33.6	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G60580.4 | Symbols: | RING/U-box superfamily protein | chr5:24354298-24356706 FORWARD LENGTH=494	116	494	1.00E-13	425.9	31.9	33.6
Rsa1.0_00567.1.g16133.t1	gb|EOA21404.1| hypothetical protein CARUB_v10001777mg [Capsella rubella]	259	255	8.00E-35	98.5	29.0	31.3	hypothetical protein CARUB_v10001777mg	gbpln	Capsella rubella	AT5G13830.1 | Symbols: | FtsJ-like methyltransferase family protein | chr5:4467363-4468487 FORWARD LENGTH=224	259	224	3.00E-37	86.5	29.0	30.9
Rsa1.0_00567.1.g16134.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00567.1.g16135.t1	ref|NP_001077775.1| transcription elongation factor SPT6 [Arabidopsis thaliana] gi|332196253|gb|AEE34374.1| transcription elongation factor SPT6-like protein [Arabidopsis thaliana]	1595	1642	0	102.9	81.6	87.6	transcription elongation factor SPT6	gbpln	Arabidopsis thaliana	AT1G65440.2 | Symbols: GTB1 | global transcription factor group B1 | chr1:24306908-24314327 REVERSE LENGTH=1642	1595	1642	0	102.9	81.6	87.6
Rsa1.0_00567.1.g16136.t1	gb|EOA34978.1| hypothetical protein CARUB_v10020067mg [Capsella rubella]	563	566	0	100.5	88.8	94.1	hypothetical protein CARUB_v10020067mg	gbpln	Capsella rubella	AT1G65430.1 | Symbols: ARI8, ATARI8 | IBR domain-containing protein | chr1:24301165-24306159 REVERSE LENGTH=567	563	567	0	100.7	87.9	93.1
Rsa1.0_00567.1.g16137.t1	ref|NP_564851.1| Ycf20-like protein [Arabidopsis thaliana] gi|209572697|sp|O80813.2|YC20L_ARATH RecName: Full=Ycf20-like protein gi|107738233|gb|ABF83666.1| At1g65420 [Arabidopsis thaliana] gi|332196250|gb|AEE34371.1| Ycf20-like protein [Arabidopsis thaliana]	200	197	3.00E-72	98.5	77.5	84.0	Ycf20-like protein	gbpln	Arabidopsis thaliana	AT1G65420.1 | Symbols: NPQ7 | Protein of unknown function (DUF565) | chr1:24297669-24298374 REVERSE LENGTH=197	200	197	1.00E-74	98.5	77.5	84.0
Rsa1.0_00567.1.g16138.t1	gb|AAC27147.1| Contains similarity to ABC transporter gb|1651790 from Synechocystis sp. gb|D90900 [Arabidopsis thaliana]	364	364	1.00E-154	100.0	78.8	83.2	Contains similarity to ABC transporter gb|1651790 from Synechocystis sp. gb|D90900	gbpln	Arabidopsis thaliana	AT1G65410.1 | Symbols: ATNAP11, TGD3, NAP11 | non-intrinsic ABC protein 11 | chr1:24295362-24297332 FORWARD LENGTH=345	364	345	1.00E-154	94.8	77.5	81.6

Rsa1.0_00567.1.g16139.t1	ref|XP_002868913.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297314749|gb|EFH45172.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	403	389	1.00E-132	96.5	62.0	71.5	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G39550.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18380681-18381859 REVERSE LENGTH=392	403	392	1.00E-133	97.3	64.8	74.7
Rsa1.0_00568.1.g16140.t1	ref|NP_189581.1| histidine-containing phosphotransfer protein 2 [Arabidopsis thaliana] gi|51702212|sp|Q9ZNV8.1|AHP2_ARATH RecName: Full=Histidine-containing phosphotransfer protein 2 gi|4107101|dbj|BAA36336.1| AHP2 [Arabidopsis thaliana] gi|4156241|dbj|BAA37110.1| ATHP1 [Arabidopsis thaliana] gi|11994516|dbj|BAB02580.1| histidine-containing phosphotransfer protein-like [Arabidopsis thaliana] gi|17381272|gb|AAL36054.1| AT3g29350/MUO10_5 [Arabidopsis thaliana] gi|20453361|gb|AAM19919.1| AT3g29350/MUO10_5 [Arabidopsis thaliana] gi|332644050|gb|AEE77571.1| histidine-containing phosphotransfer protein 2 [Arabidopsis thaliana]	156	156	4.00E-75	100.0	87.2	93.6	histidine-containing phosphotransfer protein 2	gbpln	Arabidopsis thaliana	AT3G29350.1 | Symbols: AHP2 | histidine-containing phosphotransmitter 2 | chr3:11264379-11265408 REVERSE LENGTH=156	156	156	1.00E-77	100.0	87.2	93.6
Rsa1.0_00568.1.g16141.t1	ref|NP_566847.1| uncharacterized protein [Arabidopsis thaliana] gi|30689543|ref|NP_850648.1| uncharacterized protein [Arabidopsis thaliana] gi|9293917|dbj|BAB01820.1| unnamed protein product [Arabidopsis thaliana] gi|19310484|gb|AAL84976.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|21537141|gb|AAM61482.1| unknown [Arabidopsis thaliana] gi|22654969|gb|AAM98077.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|28416521|gb|AAO42791.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] gi|332644033|gb|AEE77554.1| uncharacterized protein AT3G29240 [Arabidopsis thaliana] gi|332644034|gb|AEE77555.1| uncharacterized protein AT3G29240 [Arabidopsis thaliana]	308	317	1.00E-143	102.9	88.0	92.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G29240.2 | Symbols: | Protein of unknown function (DUF179) | chr3:11191780-11192868 FORWARD LENGTH=317	308	317	2.33E-156	102.9	88.0	92.2
Rsa1.0_00568.1.g16142.t1	ref|NP_566846.1| chorismate mutase 1 [Arabidopsis thaliana] gi|334302922|sp|P42738.3|CM1_ARATH RecName: Full=Chorismate mutase 1, chloroplastic; Short=AtCM1; AltName: Full=CM-1; Flags: Precursor gi|89000961|gb|ABD59070.1| At3g29200 [Arabidopsis thaliana] gi|332644031|gb|AEE77552.1| chorismate mutase 1 [Arabidopsis thaliana]	330	340	1.00E-154	103.0	86.4	90.9	chorismate mutase 1	gbpln	Arabidopsis thaliana	AT3G29200.1 | Symbols: CM1, ATCM1 | chorismate mutase 1 | chr3:11164582-11166258 REVERSE LENGTH=340	330	340	1.00E-157	103.0	86.4	90.9
Rsa1.0_00568.1.g16143.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00568.1.g16144.t1	ref|XP_002875491.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321329|gb|EFH51750.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	317	317	1.00E-157	100.0	83.3	90.5	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT3G29090.1 | Symbols: PME31, ATPME31 | pectin methylesterase 31 | chr3:11073804-11075335 FORWARD LENGTH=317	317	317	1.00E-159	100.0	82.0	90.5
Rsa1.0_00568.1.g16145.t1	gb|AAS76703.1| At3g29075 [Arabidopsis thaliana] gi|46402446|gb|AAS92325.1| At3g29075 [Arabidopsis thaliana]	317	236	1.00E-34	74.4	25.6	29.0	At3g29075	gbpln	Arabidopsis thaliana	AT3G29075.1 | Symbols: | glycine-rich protein | chr3:11051645-11052629 REVERSE LENGTH=294	317	294	3.00E-37	92.7	25.6	29.0
Rsa1.0_00568.1.g16146.t1	ref|XP_002875490.1| protein carrier [Arabidopsis lyrata subsp. lyrata] gi|297321328|gb|EFH51749.1| protein carrier [Arabidopsis lyrata subsp. lyrata]	220	222	1.00E-100	100.9	79.5	89.1	protein carrier	gbpln	Arabidopsis lyrata	AT3G29070.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr3:11050193-11051153 FORWARD LENGTH=225	220	225	2.00E-99	102.3	80.5	87.7

<table>
<tr><td>Rsa1.0_00568.1.g16147.t1</td><td>ref|NP_189549.2| phosphate transporter PHO1-9 [Arabidopsis thaliana] gi|75273666|sp|Q9LJW0.1|PHO19_ARATH RecName: Full=Phosphate transporter PHO1 homolog 9; AltName: Full=Protein PHO1 homolog 9; Short=AtPHO1;H9 gi|11994710|dbj|BAB02948.1| unnamed protein product [Arabidopsis thaliana] gi|332644009|gb|AEE77530.1| phosphate transporter PHO1-9 [Arabidopsis thaliana]</td><td>793</td><td>800</td><td>0</td><td>100.9</td><td>82.2</td><td>91.0</td><td>phosphate transporter PHO1-9</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G29060.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr3:11044990-11048465 REVERSE LENGTH=800</td><td>793</td><td>800</td><td>0</td><td>100.9</td><td>82.2</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00568.1.g16148.t1</td><td>ref|XP_002875486.1| ANAC059/ATNAC3 [Arabidopsis lyrata subsp. lyrata] gi|297321324|gb|EFH51745.1| ANAC059/ATNAC3 [Arabidopsis lyrata subsp. lyrata]</td><td>326</td><td>322</td><td>1.00E-136</td><td>98.8</td><td>75.5</td><td>84.7</td><td>ANAC059/ATNAC3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G29035.1 | Symbols: ATNAC3, ANAC059, NAC3 | NAC domain containing protein 3 | chr3:11033839-11035006 FORWARD LENGTH=318</td><td>326</td><td>318</td><td>1.00E-133</td><td>97.5</td><td>72.7</td><td>82.5</td></tr>
<tr><td>Rsa1.0_00568.1.g16149.t1</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>552</td><td>1529</td><td>1.00E-175</td><td>277.0</td><td>52.0</td><td>70.3</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>552</td><td>746</td><td>1.00E-124</td><td>135.1</td><td>39.9</td><td>49.6</td></tr>
<tr><td>Rsa1.0_00568.1.g16150.t1</td><td>ref|NP_189545.1| expansin A5 [Arabidopsis thaliana] gi|20138196|sp|Q38864.1|EXPA5_ARATH RecName: Full=Expansin-A5; Short=AtEXPA5; AltName: Full=Alpha-expansin-5; Short=At-EXP5; Short=AtEx5; AltName: Full=Ath-ExpAlpha-1.4; Flags: Precursor gi|1041704|gb|AAB38071.1| expansin At-EXPA5 [Arabidopsis thaliana] gi|7939553|dbj|BAA95756.1| expansin-like protein [Arabidopsis thaliana] gi|106879169|gb|ABF82614.1| At3g29030 [Arabidopsis thaliana] gi|332644002|gb|AEE77523.1| expansin A5 [Arabidopsis thaliana]</td><td>255</td><td>255</td><td>1.00E-130</td><td>100.0</td><td>93.3</td><td>96.9</td><td>expansin A5</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G29030.1 | Symbols: ATEXPA5, ATEXP5, ATHEXP ALPHA 1.4, EXP5, EXPA5 | expansin A5 | chr3:11011538-11013068 REVERSE LENGTH=255</td><td>255</td><td>255</td><td>1.00E-132</td><td>100.0</td><td>93.3</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00568.1.g16151.t1</td><td>ref|XP_002877150.1| MYB110 [Arabidopsis lyrata subsp. lyrata] gi|297322988|gb|EFH53409.1| MYB110 [Arabidopsis lyrata subsp. lyrata]</td><td>282</td><td>304</td><td>1.00E-114</td><td>107.8</td><td>78.4</td><td>84.8</td><td>MYB110</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G29020.2 | Symbols: MYB110 | myb domain protein 110 | chr3:11008233-11009419 REVERSE LENGTH=305</td><td>282</td><td>305</td><td>1.00E-110</td><td>108.2</td><td>73.8</td><td>82.3</td></tr>
<tr><td>Rsa1.0_00568.1.g16152.t1</td><td>ref|XP_002875484.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297321322|gb|EFH51743.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]</td><td>120</td><td>178</td><td>9.00E-28</td><td>148.3</td><td>62.5</td><td>70.0</td><td>calcium-binding EF hand family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G39670.1 | Symbols: | Calcium-binding EF-hand family protein | chr5:15883270-15883884 FORWARD LENGTH=204</td><td>120</td><td>204</td><td>3.00E-29</td><td>170.0</td><td>52.5</td><td>67.5</td></tr>
<tr><td>Rsa1.0_00568.1.g16153.t1</td><td>ref|XP_002534013.1| transcription factor, putative [Ricinus communis] gi|223525986|gb|EEF28371.1| transcription factor, putative [Ricinus communis]</td><td>151</td><td>98</td><td>6.00E-33</td><td>64.9</td><td>47.7</td><td>49.7</td><td>transcription factor, putative</td><td>gbpln</td><td>Ricinus communis</td><td>AT3G28917.1 | Symbols: MIF2 | mini zinc finger 2 | chr3:10925014-10925316 FORWARD LENGTH=100</td><td>151</td><td>100</td><td>1.00E-30</td><td>66.2</td><td>52.3</td><td>52.3</td></tr>
<tr><td>Rsa1.0_00568.1.g16154.t1</td><td>dbj|BAJ34042.1| unnamed protein product [Thellungiella halophila]</td><td>330</td><td>337</td><td>2.33E-156</td><td>102.1</td><td>88.8</td><td>92.1</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G28910.1 | Symbols: ATMYB30, MYB30 | myb domain protein 30 | chr3:10911443-10912856 FORWARD LENGTH=323</td><td>330</td><td>323</td><td>1.00E-143</td><td>97.9</td><td>87.0</td><td>89.7</td></tr>
<tr><td>Rsa1.0_00568.1.g16155.t1</td><td>gb|EOA35904.1| hypothetical protein CARUB_v10021161mg [Capsella rubella]</td><td>120</td><td>120</td><td>3.00E-58</td><td>100.0</td><td>94.2</td><td>97.5</td><td>hypothetical protein CARUB_v10021161mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G28900.1 | Symbols: | Ribosomal protein L34e superfamily protein | chr3:10902864-10904415 REVERSE LENGTH=120</td><td>120</td><td>120</td><td>8.00E-61</td><td>100.0</td><td>93.3</td><td>97.5</td></tr>
<tr><td>Rsa1.0_00568.1.g16156.t1</td><td>dbj|BAC41846.1| putative P-glycoprotein [Arabidopsis thaliana]</td><td>229</td><td>1252</td><td>1.00E-121</td><td>546.7</td><td>93.9</td><td>96.9</td><td>putative P-glycoprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G28860.1 | Symbols: ATMDR1, ATMDR11, PGP19, MDR11, MDR1, ATPGP19, ABCB19, ATABCB19 | ATP binding cassette subfamily B19 | chr3:10870287-10877286 REVERSE LENGTH=1252</td><td>229</td><td>1252</td><td>1.00E-123</td><td>546.7</td><td>93.9</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00569.1.g16157.t1</td><td>emb|CAN74139.1| hypothetical protein VITISV_038754 [Vitis vinifera]</td><td>780</td><td>1387</td><td>4.00E-63</td><td>177.8</td><td>24.6</td><td>37.6</td><td>hypothetical protein VITISV_038754</td><td>gbpln</td><td>Vitis vinifera</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00569.1.g16158.t1</td><td>gb|AAG52211.1|AC022288_10 hypothetical protein; 74056-75837 [Arabidopsis thaliana]</td><td>260</td><td>503</td><td>9.00E-34</td><td>193.5</td><td>30.8</td><td>36.2</td><td>hypothetical protein; 74056-75837</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00569.1.g16159.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00569.1.g16160.t1</td><td>gb|AAF79318.1|AC002304_11 F14J16.17 [Arabidopsis thaliana]</td><td>132</td><td>450</td><td>2.00E-38</td><td>340.9</td><td>63.6</td><td>67.4</td><td>F14J16.17</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G55915.1 | Symbols: | zinc ion binding | chr1:20907663-20909429 FORWARD LENGTH=404</td><td>132</td><td>404</td><td>5.00E-41</td><td>306.1</td><td>63.6</td><td>67.4</td></tr>
<tr><td>Rsa1.0_00569.1.g16161.t2</td><td>ref|NP_001185167.1| filament-like plant protein 6 [Arabidopsis thaliana] gi|332194106|gb|AEE32227.1| filament-like plant protein 6 [Arabidopsis thaliana]</td><td>1096</td><td>1052</td><td>0</td><td>96.0</td><td>65.1</td><td>72.2</td><td>filament-like plant protein 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G47900.2 | Symbols: | Plant protein of unknown function (DUF869) | chr1:17647340-17651035 REVERSE LENGTH=1052</td><td>1096</td><td>1052</td><td>0</td><td>96.0</td><td>65.1</td><td>72.2</td></tr>
</table>

Rsa1.0_00569.1.g16162.t2	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1229	2726	0	221.8	62.1	77.8	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1229	158	1.00E-35	12.9	5.9	7.1
Rsa1.0_00569.1.g16163.t1	ref|NP_194641.1| 3-hydroxyisobutyrate dehydrogenase [Arabidopsis thaliana] gi|75266757|sp|Q9SZE1.1|3HID1_ARATH RecName: Full=Probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial; Short=HIBADH-like; Flags: Precursor gi|13877869|gb|AAK44012.1|AF370197_1 unknown protein [Arabidopsis thaliana] gi|4972058|emb|CAB43926.1| putative protein [Arabidopsis thaliana] gi|7269810|emb|CAB79670.1| putative protein [Arabidopsis thaliana] gi|17065608|gb|AAL33784.1| unknown protein [Arabidopsis thaliana] gi|332660189|gb|AEE85589.1| probable 3-hydroxyisobutyrate dehydrogenase-like 1 [Arabidopsis thaliana]	335	334	1.00E-170	99.7	88.1	94.0	3-hydroxyisobutyrate dehydrogenase	gbpln	Arabidopsis thaliana	AT4G29120.1 | Symbols: | 6-phosphogluconate dehydrogenase family protein | chr4:14350861-14351865 FORWARD LENGTH=334	335	334	1.00E-172	99.7	88.1	94.0
Rsa1.0_00569.1.g16164.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00569.1.g16165.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00569.1.g16166.t1	ref|XP_002894085.1| hypothetical protein ARALYDRAFT_891603 [Arabidopsis lyrata subsp. lyrata] gi|297339927|gb|EFH70344.1| hypothetical protein ARALYDRAFT_891603 [Arabidopsis lyrata subsp. lyrata]	161	152	2.00E-75	94.4	87.0	90.7	hypothetical protein ARALYDRAFT_891603	gbpln	Arabidopsis lyrata	AT1G47960.1 | Symbols: C/VIF1, ATC/VIF1 | cell wall / vacuolar inhibitor of fructosidase 1 | chr1:17681954-17683516 REVERSE LENGTH=205	161	205	4.00E-71	127.3	79.5	83.2
Rsa1.0_00569.1.g16167.t1	ref|XP_002891402.1| hypothetical protein ARALYDRAFT_473932 [Arabidopsis lyrata subsp. lyrata] gi|297337244|gb|EFH67661.1| hypothetical protein ARALYDRAFT_473932 [Arabidopsis lyrata subsp. lyrata]	195	196	6.00E-25	100.5	80.5	89.2	hypothetical protein ARALYDRAFT_473932	gbpln	Arabidopsis lyrata	AT1G47970.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; Has 93717 Blast hits to 40765 proteins in 1891 species: Archae - 1046; Bacteria - 16276; Metazoa - 26677; Fungi - 16127; Plants - 6028; Viruses - 1519; Other Eukaryotes - 26044 (source: NCBI BLink). | chr1:17687342-17688562 FORWARD LENGTH=198	195	198	4.00E-25	101.5	75.9	86.2
Rsa1.0_00569.1.g16168.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	433	1342	2.00E-86	309.9	50.1	69.1	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	433	1262	2.00E-30	291.5	18.7	31.6
Rsa1.0_00569.1.g16169.t1	gb|AAM65140.1| dessication-related protein, putative [Arabidopsis thaliana]	309	315	1.00E-156	101.9	88.7	91.9	dessication-related protein, putative	gbpln	Arabidopsis thaliana	AT1G47980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G62730.1); Has 169 Blast hits to 169 proteins in 41 species: Archae - 0; Bacteria - 68; Metazoa - 0; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:17691985-17693818 REVERSE LENGTH=315	309	315	1.00E-158	101.9	88.3	91.6
Rsa1.0_00570.1.g16170.t1	gb|AAD12368.1| arginine-tRNA-protein transferase 1 [Arabidopsis thaliana]	634	629	0	99.2	76.0	83.3	arginine-tRNA-protein transferase 1	gbpln	Arabidopsis thaliana	AT5G05700.1 | Symbols: ATE1, DLS1, ATATE1 | arginine-tRNA protein transferase 1 | chr5:1712950-1715639 REVERSE LENGTH=632	634	632	0	99.7	76.2	83.3
Rsa1.0_00570.1.g16171.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	370	387	4.00E-74	104.6	47.3	61.1	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	370	387	1.00E-76	104.6	47.3	61.1

<table>
<tr><td>Rsa1.0_00570.1.g16172.t1</td><td>ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]</td><td>410</td><td>387</td><td>1.00E-102</td><td>94.4</td><td>49.5</td><td>63.2</td><td>F-box protein DOR</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387</td><td>410</td><td>387</td><td>1.00E-104</td><td>94.4</td><td>49.5</td><td>63.2</td></tr>
<tr><td>Rsa1.0_00570.1.g16173.t1</td><td>ref|XP_002526888.1| anthranilate synthase component I, putative [Ricinus communis] gi|223533787|gb|EEF35519.1| anthranilate synthase component I, putative [Ricinus communis]</td><td>71</td><td>574</td><td>5.00E-15</td><td>808.5</td><td>50.7</td><td>60.6</td><td>anthranilate synthase component I, putative</td><td>gbpln</td><td>Ricinus communis</td><td>AT5G05730.1 | Symbols: ASA1, TRP5, AMT1, WEI2, JDL1 | anthranilate synthase alpha subunit 1 | chr5:1719740-1722811 REVERSE LENGTH=595</td><td>71</td><td>595</td><td>2.00E-17</td><td>838.0</td><td>56.3</td><td>64.8</td></tr>
<tr><td>Rsa1.0_00570.1.g16174.t1</td><td>ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]</td><td>399</td><td>387</td><td>1.00E-105</td><td>97.0</td><td>55.1</td><td>65.9</td><td>F-box protein DOR</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387</td><td>399</td><td>387</td><td>1.00E-108</td><td>97.0</td><td>55.1</td><td>65.9</td></tr>
<tr><td>Rsa1.0_00570.1.g16175.t1</td><td>ref|NP_196192.1| anthranilate synthase component I-1 [Arabidopsis thaliana] gi|418133|sp|P32068.1|TRPE_ARATH RecName: Full=Anthranilate synthase component I-1, chloroplastic; Flags: Precursor gi|166604|gb|AAA32738.1| anthranilate synthase alpha subunit [Arabidopsis thaliana] gi|9759098|dbj|BAB09667.1| anthranilate synthase component I-1 precursor [Arabidopsis thaliana] gi|332003532|gb|AED90915.1| anthranilate synthase component I-1 [Arabidopsis thaliana]</td><td>595</td><td>595</td><td>0</td><td>100.0</td><td>93.1</td><td>95.8</td><td>anthranilate synthase component I-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G05730.1 | Symbols: ASA1, TRP5, AMT1, WEI2, JDL1 | anthranilate synthase alpha subunit 1 | chr5:1719740-1722811 REVERSE LENGTH=595</td><td>595</td><td>595</td><td>0</td><td>100.0</td><td>93.1</td><td>95.8</td></tr>
<tr><td>Rsa1.0_00570.1.g16176.t1</td><td>gb|EOA22037.1| hypothetical protein CARUB_v10002562mg [Capsella rubella]</td><td>357</td><td>358</td><td>1.00E-163</td><td>100.3</td><td>85.2</td><td>89.9</td><td>hypothetical protein CARUB_v10002562mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G57340.2 | Symbols: | Heat shock protein DnaJ, N-terminal with domain of unknown function (DUF1977) | chr3:21219175-21220278 FORWARD LENGTH=367</td><td>357</td><td>367</td><td>1.00E-137</td><td>102.8</td><td>72.0</td><td>84.6</td></tr>
<tr><td>Rsa1.0_00570.1.g16177.t1</td><td>ref|XP_002871179.1| hypothetical protein ARALYDRAFT_349845 [Arabidopsis lyrata subsp. lyrata] gi|297317016|gb|EFH47438.1| hypothetical protein ARALYDRAFT_349845 [Arabidopsis lyrata subsp. lyrata]</td><td>192</td><td>193</td><td>2.00E-78</td><td>100.5</td><td>79.7</td><td>84.9</td><td>hypothetical protein ARALYDRAFT_349845</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G11260.1 | Symbols: WOX5 | WUSCHEL related homeobox 5 | chr3:3527606-3528263 FORWARD LENGTH=182</td><td>192</td><td>182</td><td>1.00E-60</td><td>94.8</td><td>64.6</td><td>73.4</td></tr>
<tr><td>Rsa1.0_00570.1.g16178.t1</td><td>ref|XP_002871180.1| ATHMOV34 [Arabidopsis lyrata subsp. lyrata] gi|297317017|gb|EFH47439.1| ATHMOV34 [Arabidopsis lyrata subsp. lyrata]</td><td>308</td><td>308</td><td>1.00E-175</td><td>100.0</td><td>99.0</td><td>99.7</td><td>ATHMOV34</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05780.1 | Symbols: RPN8A, AE3, ATHMOV34 | RP non-ATPase subunit 8A | chr5:1735862-1738176 FORWARD LENGTH=308</td><td>308</td><td>308</td><td>1.00E-177</td><td>100.0</td><td>99.0</td><td>99.4</td></tr>
<tr><td>Rsa1.0_00570.1.g16179.t1</td><td>ref|NP_196198.1| duplicated SANT DNA-binding domain-containing protein [Arabidopsis thaliana] gi|9759104|dbj|BAB09673.1| unnamed protein product [Arabidopsis thaliana] gi|41619004|gb|AAS10001.1| MYB transcription factor [Arabidopsis thaliana] gi|109946463|gb|ABG48410.1| At5g05790 [Arabidopsis thaliana] gi|332003542|gb|AED90925.1| duplicated SANT DNA-binding domain-containing protein [Arabidopsis thaliana]</td><td>271</td><td>277</td><td>1.00E-132</td><td>102.2</td><td>85.2</td><td>90.8</td><td>duplicated SANT DNA-binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G05790.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr5:1740724-1741671 REVERSE LENGTH=277</td><td>271</td><td>277</td><td>1.00E-135</td><td>102.2</td><td>85.2</td><td>90.8</td></tr>
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Rsa1.0_00570.1.g16180.t1	gb|EOA20628.1| hypothetical protein CARUB_v10000941mg [Capsella rubella] gi|482556437|gb|EOA20629.1| hypothetical protein CARUB_v10000941mg [Capsella rubella]	428	450	0	105.1	79.9	88.6	hypothetical protein CARUB_v10000941mg	gbpln	Capsella rubella	AT5G05800.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11290.1); Has 881 Blast hits to 512 proteins in 30 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 38; Plants - 833; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr5:1743234-1744751 REVERSE LENGTH=449	428	449	0	104.9	78.0	87.4
Rsa1.0_00570.1.g16181.t1	gb|EOA20765.1| hypothetical protein CARUB_v10001094mg [Capsella rubella]	412	407	1.00E-158	98.8	77.7	83.5	hypothetical protein CARUB_v10001094mg	gbpln	Capsella rubella	AT5G05810.1 | Symbols: ATL43 | RING/U-box superfamily protein | chr5:1746938-1747999 FORWARD LENGTH=353	412	353	1.00E-153	85.7	71.4	75.2
Rsa1.0_00570.1.g16182.t1	gb|EOA21192.1| hypothetical protein CARUB_v10001537mg [Capsella rubella]	308	308	1.00E-169	100.0	96.1	98.7	hypothetical protein CARUB_v10001537mg	gbpln	Capsella rubella	AT3G11320.1 | Symbols: | Nucleotide-sugar transporter family protein | chr3:3547017-3548539 REVERSE LENGTH=308	308	308	1.00E-171	100.0	95.1	99.0
Rsa1.0_00570.1.g16183.t1	gb|ABK56014.1| zinc finger protein [Brassica rapa]	203	199	6.00E-95	98.0	87.7	92.1	zinc finger protein	gbpln	Brassica rapa	AT5G05830.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:1755910-1756825 FORWARD LENGTH=204	203	204	3.00E-76	100.5	72.4	80.3
Rsa1.0_00570.1.g16184.t1	ref|XP_002873227.1| hypothetical protein ARALYDRAFT_487384 [Arabidopsis lyrata subsp. lyrata] gi|297319064|gb|EFH49486.1| hypothetical protein ARALYDRAFT_487384 [Arabidopsis lyrata subsp. lyrata]	446	432	0	96.9	90.8	94.6	hypothetical protein ARALYDRAFT_487384	gbpln	Arabidopsis lyrata	AT5G05840.1 | Symbols: | Protein of unknown function (DUF620) | chr5:1757268-1760458 REVERSE LENGTH=439	446	439	0	98.4	90.6	93.5
Rsa1.0_00570.1.g16185.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00570.1.g16186.t1	ref|XP_002873228.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297319065|gb|EFH49487.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	502	506	0	100.8	91.0	94.0	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT5G05850.1 | Symbols: PIRL1 | plant intracellular ras group-related LRR 1 | chr5:1762691-1764609 REVERSE LENGTH=506	502	506	0	100.8	91.6	94.8
Rsa1.0_00570.1.g16187.t1	gb|ACP30611.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1062	1050	0	98.9	89.0	93.2	disease resistance protein	gbpln	Brassica rapa	AT5G22690.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:7541369-7544888 FORWARD LENGTH=1008	1062	1008	0	94.9	44.9	55.6
Rsa1.0_00570.1.g16188.t1	gb|EOA20617.1| hypothetical protein CARUB_v10000929mg [Capsella rubella]	483	456	0	94.4	76.0	86.1	hypothetical protein CARUB_v10000929mg	gbpln	Capsella rubella	AT5G05860.1 | Symbols: UGT76C2 | UDP-glucosyl transferase 76C2 | chr5:1765545-1767348 FORWARD LENGTH=450	483	450	0	93.2	77.4	85.7
Rsa1.0_00570.1.g16189.t1	ref|NP_196209.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] gi|75262507|sp|Q9FI96.1|U76C3_ARATH RecName: Full=UDP-glycosyltransferase 76C3 gi|10177563|dbj|BAB10795.1| glucuronosyl transferase-like protein [Arabidopsis thaliana] gi|332003554|gb|AED90937.1| UDP-glycosyltransferase 76C3 [Arabidopsis thaliana]	302	450	1.00E-138	149.0	80.8	89.1	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis thaliana	AT5G05900.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1774513-1776381 FORWARD LENGTH=450	302	450	1.00E-141	149.0	80.8	89.1
Rsa1.0_00571.1.g16190.t1	gb|EOA30301.1| hypothetical protein CARUB_v10013425mg [Capsella rubella]	528	535	0	101.3	79.7	90.0	hypothetical protein CARUB_v10013425mg	gbpln	Capsella rubella	AT2G17440.1 | Symbols: PIRL5 | plant intracellular ras group-related LRR 5 | chr2:7571331-7573406 FORWARD LENGTH=526	528	526	0	99.6	79.7	88.1
Rsa1.0_00571.1.g16191.t3	ref|NP_179337.1| RING-H2 finger protein ATL44 [Arabidopsis thaliana] gi|51316192|sp|O22755.1|ATL44_ARATH RecName: Full=RING-H2 finger protein ATL44; AltName: Full=RING-H2 zinc finger protein RHA3a gi|13877953|gb|AAK44054.1|AF370239_1 putative RING zinc finger protein [Arabidopsis thaliana] gi|3790573|gb|AAC68673.1| RING-H2 finger protein RHA3a [Arabidopsis thaliana] gi|4914367|gb|AAD32903.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|17065626|gb|AAL33807.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|330251537|gb|AEC06631.1| RING-H2 finger protein ATL44 [Arabidopsis thaliana]	190	185	2.00E-78	97.4	78.9	86.8	RING-H2 finger protein ATL44	gbpln	Arabidopsis thaliana	AT2G17450.1 | Symbols: RHA3A | RING-H2 finger A3A | chr2:7576640-7577197 REVERSE LENGTH=185	190	185	9.00E-81	97.4	78.9	86.8
Rsa1.0_00571.1.g16192.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00571.1.g16193.t1	ref|NP_565419.1| endoribonuclease/protein kinase IRE1-like protein [Arabidopsis thaliana] gi|75168985|sp|Q9C5S2.1|IRE1A_ARATH RecName: Full=Serine/threonine-protein kinase/endoribonuclease IRE1a; AltName: Full=Endoplasmic reticulum-to-nucleus signaling 1-2; AltName: Full=Inositol-requiring protein 1-2; Short=AtIRE1-2; AltName: Full=Serine/threonine-protein kinase/endoribonuclease IRE1-2; Includes: RecName: Full=Serine/threonine-protein kinase; Includes: RecName: Full=Endoribonuclease; Flags: Precursor gi|13194578|gb|AAK15470.1|AF308596_1 endoribonuclease/protein kinase IRE1-like protein [Arabidopsis thaliana] gi|15277139|dbj|BAB63367.1| Ire1 homolog-2 [Arabidopsis thaliana] gi|20198262|gb|AAD32909.2| putative protein kinase/endoribonuclease [Arabidopsis thaliana] gi|330251546|gb|AEC06640.1| endoribonuclease/protein kinase IRE1-like protein [Arabidopsis thaliana]	904	841	0	93.0	62.9	71.8	endoribonuclease/protein kinase IRE1-like protein	gbpln	Arabidopsis thaliana	AT2G17520.1 | Symbols: IRE1A, ATIRE1-2, IRE1-2 | Endoribonuclease/protein kinase IRE1-like | chr2:7617504-7620929 FORWARD LENGTH=841	904	841	0	93.0	62.9	71.8
Rsa1.0_00571.1.g16194.t1	gb|EOA31017.1| hypothetical protein CARUB_v10014165mg [Capsella rubella] gi|482566829|gb|EOA31018.1| hypothetical protein CARUB_v10014165mg [Capsella rubella]	276	329	4.00E-78	119.2	71.0	79.7	hypothetical protein CARUB_v10014165mg	gbpln	Capsella rubella	AT2G17540.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G35510.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:7630662-7631489 REVERSE LENGTH=275	276	275	6.00E-57	99.6	60.9	69.6
Rsa1.0_00571.1.g16195.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00571.1.g16196.t1	ref|XP_002884069.1| polynucleotide adenylyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329909|gb|EFH60328.1| polynucleotide adenylyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	751	761	0	101.3	73.8	84.2	polynucleotide adenylyltransferase family protein	gbpln	Arabidopsis lyrata	AT2G17580.1 | Symbols: | Polynucleotide adenylyltransferase family protein | chr2:7646507-7650066 FORWARD LENGTH=757	751	757	0	100.8	73.4	83.5
Rsa1.0_00571.1.g16197.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00571.1.g16198.t8	emb|CAA83275.1| cyclin 2a protein [Arabidopsis thaliana]	429	429	1.00E-155	100.0	72.7	77.2	cyclin 2a protein	gbpln	Arabidopsis thaliana	AT2G17620.1 | Symbols: CYCB2;1 | Cyclin B2;1 | chr2:7664164-7666261 FORWARD LENGTH=429	429	429	1.00E-158	100.0	72.7	77.2
Rsa1.0_00571.1.g16199.t1	ref|XP_002886123.1| AtSerat3_1 [Arabidopsis lyrata subsp. lyrata] gi|297331963|gb|EFH62382.1| AtSerat3_1 [Arabidopsis lyrata subsp. lyrata]	320	323	1.00E-162	100.9	89.1	93.8	AtSerat3_1	gbpln	Arabidopsis lyrata	AT2G17640.1 | Symbols: ATSERAT3;1, SAT-106 | Trimeric LpxA-like enzymes superfamily protein | chr2:7668238-7670226 REVERSE LENGTH=323	320	323	1.00E-158	100.9	89.7	94.1
Rsa1.0_00571.1.g16200.t1	ref|NP_179357.1| RPM1-interacting protein 4-like protein [Arabidopsis thaliana] gi|11762120|gb|AAG40338.1|AF324986_1 At2g17660 [Arabidopsis thaliana] gi|115646839|gb|ABJ17136.1| At2g17660 [Arabidopsis thaliana] gi|330251568|gb|AEC06662.1| RPM1-interacting protein 4-like protein [Arabidopsis thaliana]	69	69	4.00E-30	100.0	92.8	98.6	RPM1-interacting protein 4-like protein	gbpln	Arabidopsis thaliana	AT2G17660.1 | Symbols: | RPM1-interacting protein 4 (RIN4) family protein | chr2:7673359-7673568 FORWARD LENGTH=69	69	69	7.00E-33	100.0	92.8	98.6
Rsa1.0_00571.1.g16201.t16	gb|EOA31407.1| hypothetical protein CARUB_v10014585mg, partial [Capsella rubella]	210	220	1.00E-106	104.8	85.2	93.8	hypothetical protein CARUB_v10014585mg, partial	gbpln	Capsella rubella	AT2G17695.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; CONTAINS InterPro DOMAIN/s: Domain of unknown function DUF1990 (InterPro:IPR018960). | chr2:7684214-7685009 REVERSE LENGTH=205	210	205	1.00E-108	97.6	84.3	93.8

Rsa1.0_00571.1.g16202.t1	ref|NP_179389.1| SEC1 family transport protein SLY1 [Arabidopsis thaliana] gi|28201895|sp|Q9SL48.1|SLY1_ARATH RecName: Full=SEC1 family transport protein SLY1; Short=AtSLY1 gi|4406820|gb|AAD20128.1| putative SEC1 family transport protein [Arabidopsis thaliana] gi|15215770|gb|AAK91430.1| At2g17980/T27K22.15 [Arabidopsis thaliana] gi|16974335|gb|AAL31152.1| At2g17980/T27K22.15 [Arabidopsis thaliana] gi|330251617|gb|AEC06711.1| SEC1 family transport protein SLY1 [Arabidopsis thaliana]	628	627	0	99.8	87.7	92.0	SEC1 family transport protein SLY1	gbpln	Arabidopsis thaliana	AT2G17980.1 | Symbols: ATSLY1 | Sec1/munc18-like (SM) proteins superfamily | chr2:7824352-7826404 FORWARD LENGTH=627	628	627	0	99.8	87.7	92.0
Rsa1.0_00571.1.g16203.t1	ref|XP_002884094.1| hypothetical protein ARALYDRAFT_480699 [Arabidopsis lyrata subsp. lyrata] gi|297329934|gb|EFH60353.1| hypothetical protein ARALYDRAFT_480699 [Arabidopsis lyrata subsp. lyrata]	309	337	1.00E-138	109.1	87.7	94.5	hypothetical protein ARALYDRAFT_480699	gbpln	Arabidopsis lyrata	AT2G17990.1 | Symbols: | BEST Arabidopsis thaliana protein match is: kinectin-related (TAIR:AT5G66250.3); Has 7578 Blast hits to 6129 proteins in 783 species: Archae - 220; Bacteria - 1045; Metazoa - 3605; Fungi - 575; Plants - 442; Viruses - 38; Other Eukaryotes - 1653 (source: NCBI BLink). | chr2:7827480-7828596 FORWARD LENGTH=338	309	338	1.00E-137	109.4	85.8	93.5
Rsa1.0_00571.1.g16204.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	1839	1333	0	72.5	37.1	48.5	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1839	575	1.00E-101	31.3	10.5	16.8
Rsa1.0_00571.1.g16205.t1	gb|EOA31137.1| hypothetical protein CARUB_v10014300mg [Capsella rubella]	258	290	1.00E-145	112.4	98.1	99.6	hypothetical protein CARUB_v10014300mg	gbpln	Capsella rubella	AT4G36130.1 | Symbols: | Ribosomal protein L2 family | chr4:17097613-17098656 FORWARD LENGTH=258	258	258	1.00E-144	100.0	95.7	98.8
Rsa1.0_00571.1.g16206.t1	dbj|BAJ34365.1| unnamed protein product [Thellungiella halophila]	119	119	2.00E-61	100.0	97.5	100.0	unnamed protein product	----	----	AT2G18040.1 | Symbols: PIN1AT | peptidylprolyl cis/trans isomerase, NIMA-interacting 1 | chr2:7842346-7843537 FORWARD LENGTH=119	119	119	2.00E-62	100.0	95.0	99.2
Rsa1.0_00571.1.g16207.t1	ref|XP_002886147.1| hypothetical protein ARALYDRAFT_319761 [Arabidopsis lyrata subsp. lyrata] gi|297331987|gb|EFH62406.1| hypothetical protein ARALYDRAFT_319761 [Arabidopsis lyrata subsp. lyrata]	491	503	0	102.4	91.0	95.3	hypothetical protein ARALYDRAFT_319761	gbpln	Arabidopsis lyrata	AT4G36220.1 | Symbols: FAH1, CYP84A1 | ferulic acid 5-hydroxylase 1 | chr4:17137584-17139619 REVERSE LENGTH=520	491	520	0	105.9	75.2	88.4
Rsa1.0_00571.1.g16208.t1	gb|EOA23342.1| hypothetical protein CARUB_v10019413mg [Capsella rubella]	364	381	4.00E-69	104.7	41.5	63.2	hypothetical protein CARUB_v10019413mg	gbpln	Capsella rubella	AT3G28270.1 | Symbols: | Protein of unknown function (DUF677) | chr3:10538725-10539849 FORWARD LENGTH=374	364	374	9.00E-68	102.7	41.8	62.4
Rsa1.0_00571.1.g16209.t1	gb|AAM15144.1| hypothetical protein [Arabidopsis thaliana] gi|20198201|gb|AAM15455.1| hypothetical protein [Arabidopsis thaliana]	348	296	1.00E-24	85.1	25.0	29.0	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00571.1.g16210.t1	dbj|BAJ34571.1| unnamed protein product [Thellungiella halophila]	171	172	2.00E-73	100.6	88.3	93.6	unnamed protein product	----	----	AT2G18160.1 | Symbols: ATBZIP2, GBF5, bZIP2 | basic leucine-zipper 2 | chr2:7898288-7898803 REVERSE LENGTH=171	171	171	4.00E-67	100.0	84.8	90.6
Rsa1.0_00571.1.g16211.t1	gb|AAD31347.1| putative AAA-type ATPase [Arabidopsis thaliana]	535	996	0	186.2	74.8	80.2	putative AAA-type ATPase	gbpln	Arabidopsis thaliana	AT2G18193.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:7917621-7919184 REVERSE LENGTH=495	535	495	0	92.5	74.8	80.2
Rsa1.0_00571.1.g16212.t1	ref|NP_179418.2| syntaxin-112 [Arabidopsis thaliana] gi|148887439|sp|Q9ZPV9.2|SY112_ARATH RecName: Full=Syntaxin-112; Short=AtSYP112 gi|91806192|gb|ABE65824.1| syntaxin-like protein [Arabidopsis thaliana] gi|330251653|gb|AEC06747.1| syntaxin-112 [Arabidopsis thaliana]	280	305	1.00E-125	108.9	82.5	90.4	syntaxin-112	gbpln	Arabidopsis thaliana	AT2G18260.1 | Symbols: SYP112, ATSYP112 | syntaxin of plants 112 | chr2:7942275-7943192 FORWARD LENGTH=305	280	305	1.00E-128	108.9	82.5	90.4

Rsa1.0_00571.1.g16213.t2	ref|NP_565433.1| anaphase-promoting complex subunit 10 [Arabidopsis thaliana] gi|34395513|sp|Q9ZPW2.2|APC10_ARATH RecName: Full=Anaphase-promoting complex subunit 10; Short=APC10; AltName: Full=Cyclosome subunit 10 gi|20197809|gb|AAD15507.2| expressed protein [Arabidopsis thaliana] gi|90567996|gb|ABD94068.1| At2g18290 [Arabidopsis thaliana] gi|110738941|dbj|BAF01391.1| hypothetical protein [Arabidopsis thaliana] gi|330251657|gb|AEC06751.1| anaphase-promoting complex subunit 10 [Arabidopsis thaliana]	164	192	3.00E-34	117.1	51.8	56.1	anaphase-promoting complex subunit 10	gbpln	Arabidopsis thaliana	AT2G18290.1 | Symbols: APC10 | anaphase promoting complex 10 | chr2:7948522-7950096 REVERSE LENGTH=192	164	192	1.00E-36	117.1	51.8	56.1
Rsa1.0_00571.1.g16214.t1	gb|EOA31794.1| hypothetical protein CARUB_v10015016mg [Capsella rubella]	82	82	1.00E-28	100.0	86.6	91.5	hypothetical protein CARUB_v10015016mg	gbpln	Capsella rubella	AT2G18328.1 | Symbols: ATRL4, RL4 | RAD-like 4 | chr2:7964478-7964711 FORWARD LENGTH=77	82	77	4.00E-28	93.9	65.9	72.0
Rsa1.0_00571.1.g16215.t1	gb|EOA30093.1| hypothetical protein CARUB_v10013202mg [Capsella rubella]	634	631	0	99.5	87.9	92.6	hypothetical protein CARUB_v10013202mg	gbpln	Capsella rubella	AT2G18330.1 | Symbols: | AAA-type ATPase family protein | chr2:7965829-7968915 FORWARD LENGTH=636	634	636	0	100.3	88.0	93.1
Rsa1.0_00571.1.g16216.t1	gb|EOA32387.1| hypothetical protein CARUB_v10015657mg [Capsella rubella]	374	313	1.00E-143	83.7	65.5	71.4	hypothetical protein CARUB_v10015657mg	gbpln	Capsella rubella	AT2G18360.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:7976848-7979221 REVERSE LENGTH=313	374	313	1.00E-145	83.7	65.0	71.9
Rsa1.0_00571.1.g16217.t1	ref|NP_179430.1| ADP-ribosylation factor-like 2 [Arabidopsis thaliana] gi|11131460|sp|Q9ZPX1.1|ARF5_ARATH RecName: Full=Probable ADP-ribosylation factor At2g18390 gi|20514265|gb|AAM22961.1|AF486852_1 ARL2 G-protein [Arabidopsis thaliana] gi|4309728|gb|AAD15498.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gi|14334672|gb|AAK59514.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gi|17104667|gb|AAL34222.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gi|21593903|gb|AAM65870.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gi|330251670|gb|AEC06764.1| probable ADP-ribosylation factor [Arabidopsis thaliana]	185	185	1.00E-100	100.0	98.9	100.0	ADP-ribosylation factor-like 2	gbpln	Arabidopsis thaliana	AT2G18390.1 | Symbols: TTN5, HAL, ARL2, ATARLC1 | ADP-ribosylation factor family protein | chr2:7988335-7989374 FORWARD LENGTH=185	185	185	1.00E-103	100.0	98.9	100.0
Rsa1.0_00571.1.g16218.t1	ref|XP_004143514.1| PREDICTED: 60S ribosomal protein L6, mitochondrial-like [Cucumis sativus] gi|449496483|ref|XP_004160146.1| PREDICTED: 60S ribosomal protein L6, mitochondrial-like [Cucumis sativus]	102	102	1.00E-47	100.0	91.2	94.1	PREDICTED: 60S ribosomal protein L6, mitochondrial-like	gbpln	Cucumis sativus	AT2G18400.1 | Symbols: | ribosomal protein L6 family protein | chr2:7989665-7989973 REVERSE LENGTH=102	102	102	6.00E-48	100.0	88.2	88.2
Rsa1.0_00571.1.g16219.t2	dbj|BAJ33909.1| unnamed protein product [Thellungiella halophila]	537	534	0	99.4	81.9	86.4	unnamed protein product	----	----	AT1G44446.1 | Symbols: CH1, ATCAO, CAO | Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain | chr1:16848664-16851152 REVERSE LENGTH=536	537	536	0	99.8	79.5	84.7
Rsa1.0_00571.1.g16220.t1	ref|NP_176586.1| serpin-Z1 [Arabidopsis thaliana] gi|189029934|sp|Q9SH52.2|SPZ1_ARATH RecName: Full=Serpin-Z1; AltName: Full=ArathZ1 gi|332196061|gb|AEE34182.1| serpin-Z1 [Arabidopsis thaliana]	308	385	1.00E-115	125.0	74.7	83.8	serpin-Z1	gbpln	Arabidopsis thaliana	AT1G64030.1 | Symbols: ATSRP3, SRP3 | serpin 3 | chr1:23752873-23754348 REVERSE LENGTH=385	308	385	1.00E-117	125.0	74.7	83.8
Rsa1.0_00572.1.g16221.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00572.1.g16222.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00572.1.g16223.t2	gb|AAF24584.1|AC007764_26 F22C12.1 [Arabidopsis thaliana]	171	3290	2.00E-30	1924.0	42.7	48.0	F22C12.1	gbpln	Arabidopsis thaliana	AT1G64255.1 | Symbols: | MuDR family transposase | chr1:23844954-23847206 FORWARD LENGTH=750	171	750	9.00E-33	438.6	42.7	48.0
Rsa1.0_00572.1.g16224.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1490	1501	0	100.7	57.8	73.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1490	1262	1.00E-142	84.7	16.2	22.8
Rsa1.0_00572.1.g16225.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	385	627	2.00E-41	162.9	24.9	36.4	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00572.1.g16226.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	727	1223	0	168.2	47.3	65.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	727	746	2.00E-71	102.6	20.1	27.5

Rsa1.0_00572.1.g16227.t1	gb|EOA39981.1| hypothetical protein CARUB_v10008669mg [Capsella rubella]	584	586	0	100.3	91.8	96.4	hypothetical protein CARUB_v10008669mg	gbpln	Capsella rubella	AT1G17120.1 | Symbols: CAT8 | cationic amino acid transporter 8 | chr1:5851964-5853736 FORWARD LENGTH=590	584	590	0	101.0	92.1	96.9
Rsa1.0_00572.1.g16228.t1	gb|ABD65000.1| hypothetical protein 26.t00020 [Brassica oleracea]	281	302	3.00E-78	107.5	55.9	69.4	hypothetical protein 26.t00020	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	281	302	5.00E-52	107.5	41.6	57.3
Rsa1.0_00572.1.g16229.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00572.1.g16230.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	196	149	7.00E-17	76.0	21.9	28.1	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00572.1.g16231.t1	gb|EOA36632.1| hypothetical protein CARUB_v10011872mg [Capsella rubella]	2233	2254	0	100.9	94.7	97.9	hypothetical protein CARUB_v10011872mg	gbpln	Capsella rubella	AT1G36160.2 | Symbols: ACC1 | acetyl-CoA carboxylase 1 | chr1:13534196-13543773 FORWARD LENGTH=2254	2233	2254	0	100.9	94.4	97.4
Rsa1.0_00573.1.g16232.t1	gb|AAC95212.1| Mutator-like transposase [Arabidopsis thaliana]	1014	915	1.00E-165	90.2	27.4	39.3	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	1014	719	5.00E-39	70.9	13.0	23.3
Rsa1.0_00573.1.g16233.t2	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	904	871	1.00E-155	96.3	40.5	57.6	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	904	874	3.00E-36	96.7	9.6	15.7
Rsa1.0_00573.1.g16234.t2	gb|EOA25699.1| hypothetical protein CARUB_v10019052mg [Capsella rubella]	692	1016	0	146.8	57.8	65.9	hypothetical protein CARUB_v10019052mg	gbpln	Capsella rubella	AT2G02220.1 | Symbols: ATPSKR1, PSKR1 | phytosulfokin receptor 1 | chr2:584098-587124 REVERSE LENGTH=1008	692	1008	1.00E-165	145.7	47.7	53.9
Rsa1.0_00573.1.g16235.t1	ref|NP_172188.1| 60S ribosomal protein L35a-1 [Arabidopsis thaliana] gi|297843500|ref|XP_002889631.1| 60S ribosomal protein L35a [Arabidopsis lyrata subsp. lyrata] gi|75174783|sp|Q9LMK0.1|R35A1_ARATH RecName: Full=60S ribosomal protein L35a-1 gi|8954039|gb|AAF82213.1|AC067971_21 Strong similarity to a ribosomal protein from Arabidopsis thaliana gb|AL161667. It contains a ribosomal protein L35Ae domain PF|01247 [Arabidopsis thaliana] gi|21555376|gb|AAM63844.1| ribosomal protein, putative [Arabidopsis thaliana] gi|26453120|dbj|BAC43636.1| unknown protein [Arabidopsis thaliana] gi|28416859|gb|AAO42960.1| At1g07070 [Arabidopsis thaliana] gi|297335473|gb|EFH65890.1| 60S ribosomal protein L35a [Arabidopsis lyrata subsp. lyrata] gi|332189953|gb|AEE28074.1| 60S ribosomal protein L35a-1 [Arabidopsis thaliana]	96	112	1.00E-44	116.7	96.9	99.0	60S ribosomal protein L35a-1	gbpln	Arabidopsis lyrata	AT1G07070.1 | Symbols: | Ribosomal protein L35Ae family protein | chr1:2168652-2169703 FORWARD LENGTH=112	96	112	2.00E-47	116.7	96.9	99.0
Rsa1.0_00573.1.g16236.t1	ref|XP_002888971.1| ATHSP101 [Arabidopsis lyrata subsp. lyrata] gi|297334812|gb|EFH65230.1| ATHSP101 [Arabidopsis lyrata subsp. lyrata]	916	911	0	99.5	93.9	97.2	ATHSP101	gbpln	Arabidopsis lyrata	AT1G74310.1 | Symbols: ATHSP101, HSP101, HOT1 | heat shock protein 101 | chr1:27936715-27939862 REVERSE LENGTH=911	916	911	0	99.5	92.0	95.5
Rsa1.0_00573.1.g16237.t1	ref|XP_002888973.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297334814|gb|EFH65232.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	225	259	2.00E-93	115.1	78.2	86.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G74370.1 | Symbols: | RING/U-box superfamily protein | chr1:27958200-27958985 REVERSE LENGTH=261	225	261	4.00E-94	116.0	77.8	86.7
Rsa1.0_00573.1.g16238.t1	ref|XP_002887538.1| galactosyl transferase GMA12/MNN10 family protein [Arabidopsis lyrata subsp. lyrata] gi|297333379|gb|EFH63797.1| galactosyl transferase GMA12/MNN10 family protein [Arabidopsis lyrata subsp. lyrata]	459	457	0	99.6	93.5	95.2	galactosyl transferase GMA12/MNN10 family protein	gbpln	Arabidopsis lyrata	AT1G74380.1 | Symbols: XXT5 | xyloglucan xylosyltransferase 5 | chr1:27959848-27961221 FORWARD LENGTH=457	459	457	0	99.6	92.8	95.0
Rsa1.0_00573.1.g16239.t1	ref|XP_002887539.1| hypothetical protein ARALYDRAFT_339633 [Arabidopsis lyrata subsp. lyrata] gi|297333380|gb|EFH63798.1| hypothetical protein ARALYDRAFT_339633 [Arabidopsis lyrata subsp. lyrata]	471	665	0	141.2	77.7	88.1	hypothetical protein ARALYDRAFT_339633	gbpln	Arabidopsis lyrata	AT1G74400.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:27963953-27965341 FORWARD LENGTH=462	471	462	0	98.1	74.5	84.1
Rsa1.0_00573.1.g16240.t1	ref|NP_974142.1| fucosyltransferase 3 [Arabidopsis thaliana] gi|332197469|gb|AEE35590.1| fucosyltransferase 3 [Arabidopsis thaliana]	503	525	0	104.4	77.1	87.5	fucosyltransferase 3	gbpln	Arabidopsis thaliana	AT1G74420.2 | Symbols: FUT3, ATFUT3 | fucosyltransferase 3 | chr1:27968021-27969799 REVERSE LENGTH=525	503	525	0	104.4	77.1	87.5

Rsa1.0_00573.1.g16241.t1	ref|NP_177583.1| myb domain protein 95 [Arabidopsis thaliana] gi|6715434|gb|AAF26414.1|AF217205_1 putative transcription factor [Arabidopsis thaliana] gi|12324794|gb|AAG52356.1|AC011765_8 putative MYB family transcription factor; 31729-33438 [Arabidopsis thaliana] gi|26451798|dbj|BAC42993.1| putative transcription factor MYB95 [Arabidopsis thaliana] gi|28950825|gb|AAO63336.1| At1g74430 [Arabidopsis thaliana] gi|41619172|gb|AAS10040.1| MYB transcription factor [Arabidopsis thaliana] gi|332197470|gb|AEE35591.1| myb domain protein 95 [Arabidopsis thaliana]	277	271	2.00E-85	97.8	63.2	73.6	myb domain protein 95	gbpln	Arabidopsis thaliana	AT1G74430.1 | Symbols: MYB95, ATMYB95, ATMYBCP66 | myb domain protein 95 | chr1:27975409-27977118 FORWARD LENGTH=271	277	271	4.00E-88	97.8	63.2	73.6
Rsa1.0_00573.1.g16242.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00573.1.g16243.t1	ref|NP_177583.1| myb domain protein 95 [Arabidopsis thaliana] gi|6715434|gb|AAF26414.1|AF217205_1 putative transcription factor [Arabidopsis thaliana] gi|12324794|gb|AAG52356.1|AC011765_8 putative MYB family transcription factor; 31729-33438 [Arabidopsis thaliana] gi|26451798|dbj|BAC42993.1| putative transcription factor MYB95 [Arabidopsis thaliana] gi|28950825|gb|AAO63336.1| At1g74430 [Arabidopsis thaliana] gi|41619172|gb|AAS10040.1| MYB transcription factor [Arabidopsis thaliana] gi|332197470|gb|AEE35591.1| myb domain protein 95 [Arabidopsis thaliana]	273	271	2.00E-90	99.3	66.7	79.5	myb domain protein 95	gbpln	Arabidopsis thaliana	AT1G74430.1 | Symbols: MYB95, ATMYB95, ATMYBCP66 | myb domain protein 95 | chr1:27975409-27977118 FORWARD LENGTH=271	273	271	6.00E-93	99.3	66.7	79.5
Rsa1.0_00573.1.g16244.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00574.1.g16245.t1	gb|ACN65499.1| chloroplast carboxyltransferase alpha subunit isoform 1 [Brassica rapa]	775	770	0	99.4	94.2	96.6	chloroplast carboxyltransferase alpha subunit isoform 1	gbpln	Brassica rapa	AT2G38040.2 | Symbols: CAC3 | acetyl Co-enzyme a carboxylase carboxyltransferase alpha subunit | chr2:15917612-15920749 FORWARD LENGTH=769	775	769	0	99.2	81.0	88.0
Rsa1.0_00574.1.g16246.t1	ref|XP_002865572.1| eukaryotic release factor 1-1 [Arabidopsis lyrata subsp. lyrata] gi|297311407|gb|EFH41831.1| eukaryotic release factor 1-1 [Arabidopsis lyrata subsp. lyrata]	283	436	1.00E-104	154.1	67.1	79.9	eukaryotic release factor 1-1	gbpln	Arabidopsis lyrata	AT5G47880.2 | Symbols: ERF1-1 | eukaryotic release factor 1-1 | chr5:19386555-19387865 REVERSE LENGTH=436	283	436	1.00E-106	154.1	66.4	79.5
Rsa1.0_00574.1.g16247.t1	dbj|BAK41511.1| polyprotein [Arabidopsis thaliana]	223	1466	4.00E-23	657.4	37.7	48.9	polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00574.1.g16248.t1	gb|EOA27596.1| hypothetical protein CARUB_v10023736mg [Capsella rubella]	297	299	1.00E-160	100.7	91.2	94.9	hypothetical protein CARUB_v10023736mg	gbpln	Capsella rubella	AT2G38090.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr2:15945278-15946775 FORWARD LENGTH=298	297	298	1.00E-158	100.3	92.3	96.0
Rsa1.0_00574.1.g16249.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00574.1.g16250.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	253	1023	5.00E-32	404.3	31.6	41.9	F27F5.21	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	253	292	4.00E-13	115.4	18.2	27.3
Rsa1.0_00574.1.g16251.t1	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	265	1250	6.00E-19	471.7	16.2	22.3	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00574.1.g16252.t1	gb|ACZ67478.1| auxin resistant 1 protein [Brassica rapa subsp. oleifera]	493	493	0	100.0	95.1	97.0	auxin resistant 1 protein	gbpln	Brassica rapa	AT2G38120.1 | Symbols: AUX1, WAV5, PIR1, MAP1 | Transmembrane amino acid transporter family protein | chr2:15973493-15976792 FORWARD LENGTH=485	493	485	0	98.4	93.7	95.7
Rsa1.0_00574.1.g16253.t1	ref|XP_002879730.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325569|gb|EFH55989.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	265	294	1.00E-120	110.9	78.5	86.8	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT2G38180.1 | Symbols: | SGNH hydrolase-type esterase superfamily protein | chr2:15997187-15998751 FORWARD LENGTH=312	265	312	1.00E-122	117.7	78.5	86.0

<table>
<tr><td>Rsa1.0_00575.1.g16254.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT4G29735.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0197 (InterPro:IPR007915); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:14562962-14564277 REVERSE LENGTH=76</td><td>35</td><td>76</td><td>6.00E-11</td><td>217.1</td><td>88.6</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00575.1.g16255.t1</td><td>gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]</td><td>152</td><td>214</td><td>1.00E-34</td><td>140.8</td><td>53.9</td><td>67.8</td><td>trypsin inhibitor propeptide</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410-27548057 REVERSE LENGTH=215</td><td>152</td><td>215</td><td>7.00E-26</td><td>141.4</td><td>42.8</td><td>55.9</td></tr>
<tr><td>Rsa1.0_00575.1.g16256.t1</td><td>gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]</td><td>207</td><td>214</td><td>5.00E-56</td><td>103.4</td><td>58.5</td><td>71.5</td><td>trypsin inhibitor propeptide</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410-27548057 REVERSE LENGTH=215</td><td>207</td><td>215</td><td>5.00E-40</td><td>103.9</td><td>46.9</td><td>59.4</td></tr>
<tr><td>Rsa1.0_00575.1.g16257.t1</td><td>gb|EOA40469.1| hypothetical protein CARUB_v10009194mg [Capsella rubella]</td><td>380</td><td>431</td><td>1.00E-116</td><td>113.4</td><td>65.8</td><td>76.3</td><td>hypothetical protein CARUB_v10009194mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G01670.1 | Symbols: | RING/U-box superfamily protein | chr1:242943-245163 REVERSE LENGTH=365</td><td>380</td><td>365</td><td>1.00E-104</td><td>96.1</td><td>55.5</td><td>64.7</td></tr>
<tr><td>Rsa1.0_00575.1.g16258.t1</td><td>gb|EOA27427.1| hypothetical protein CARUB_v10023560mg, partial [Capsella rubella]</td><td>321</td><td>343</td><td>1.00E-177</td><td>106.9</td><td>95.6</td><td>98.4</td><td>hypothetical protein CARUB_v10023560mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G29830.1 | Symbols: VIP3 | Transducin/WD40 repeat-like superfamily protein | chr4:14597728-14599157 FORWARD LENGTH=321</td><td>321</td><td>321</td><td>1.00E-180</td><td>100.0</td><td>95.6</td><td>99.1</td></tr>
<tr><td>Rsa1.0_00575.1.g16259.t1</td><td>ref|NP_194713.1| threonine synthase 1 [Arabidopsis thaliana] gi|20140904|sp|Q9S7B5.1|THRC1_ARATH RecName: Full=Threonine synthase 1, chloroplastic; AltName: Full=Protein METHIONINE OVER-ACCUMULATOR 2; Flags: Precursor gi|4850369|dbj|BAA77707.1| threonine synthase [Arabidopsis thaliana] gi|4914408|emb|CAB43659.1| threonine synthase [Arabidopsis thaliana] gi|7269883|emb|CAB79742.1| threonine synthase [Arabidopsis thaliana] gi|332660284|gb|AEE85684.1| threonine synthase 1 [Arabidopsis thaliana]</td><td>526</td><td>526</td><td>0</td><td>100.0</td><td>91.4</td><td>94.7</td><td>threonine synthase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29840.1 | Symbols: MTO2, TS | Pyridoxal-5'-phosphate-dependent enzyme family protein | chr4:14599434-14601014 REVERSE LENGTH=526</td><td>526</td><td>526</td><td>0</td><td>100.0</td><td>91.4</td><td>94.7</td></tr>
<tr><td>Rsa1.0_00575.1.g16260.t1</td><td>ref|XP_002880694.1| hypothetical protein ARALYDRAFT_901214 [Arabidopsis lyrata subsp. lyrata] gi|297326533|gb|EFH56953.1| hypothetical protein ARALYDRAFT_901214 [Arabidopsis lyrata subsp. lyrata]</td><td>294</td><td>422</td><td>1.00E-63</td><td>143.5</td><td>47.6</td><td>55.8</td><td>hypothetical protein ARALYDRAFT_901214</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63820.1 | Symbols: | Protein of unknown function (DUF626) | chr5:25541576-25542893 FORWARD LENGTH=225</td><td>294</td><td>225</td><td>9.00E-34</td><td>76.5</td><td>31.3</td><td>40.5</td></tr>
<tr><td>Rsa1.0_00575.1.g16261.t1</td><td>ref|XP_002880694.1| hypothetical protein ARALYDRAFT_901214 [Arabidopsis lyrata subsp. lyrata] gi|297326533|gb|EFH56953.1| hypothetical protein ARALYDRAFT_901214 [Arabidopsis lyrata subsp. lyrata]</td><td>339</td><td>422</td><td>7.00E-68</td><td>124.5</td><td>42.2</td><td>50.1</td><td>hypothetical protein ARALYDRAFT_901214</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G29550.1 | Symbols: | Protein of unknown function (DUF626) | chr4:14502433-14503763 FORWARD LENGTH=358</td><td>339</td><td>358</td><td>2.00E-39</td><td>105.6</td><td>29.5</td><td>44.8</td></tr>
<tr><td>Rsa1.0_00575.1.g16262.t1</td><td>gb|EOA15953.1| hypothetical protein CARUB_v10004050mg [Capsella rubella]</td><td>1012</td><td>1034</td><td>0</td><td>102.2</td><td>87.2</td><td>93.0</td><td>hypothetical protein CARUB_v10004050mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G29920.1 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr4:14632653-14635885 REVERSE LENGTH=1017</td><td>1012</td><td>1017</td><td>0</td><td>100.5</td><td>86.8</td><td>92.3</td></tr>
<tr><td>Rsa1.0_00575.1.g16263.t1</td><td>ref|NP_001078471.1| transcription factor bHLH27 [Arabidopsis thaliana] gi|75294403|sp|Q700E3.1|BH027_ARATH RecName: Full=Transcription factor bHLH27; AltName: Full=Basic helix-loop-helix protein 27; Short=AtbHLH27; Short=bHLH 27; AltName: Full=Transcription factor EN 42; AltName: Full=bHLH transcription factor bHLH027 gi|45935019|gb|AAS79544.1| At4g29930 [Arabidopsis thaliana] gi|46367458|emb|CAG25855.1| hypothetical protein [Arabidopsis thaliana] gi|332660296|gb|AEE85696.1| transcription factor bHLH27 [Arabidopsis thaliana]</td><td>240</td><td>263</td><td>1.00E-103</td><td>109.6</td><td>79.6</td><td>86.3</td><td>transcription factor bHLH27</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29930.3 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:14644108-14645505 FORWARD LENGTH=263</td><td>240</td><td>263</td><td>1.00E-105</td><td>109.6</td><td>79.6</td><td>86.3</td></tr>
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Rsa1.0_00575.1.g16264.t2	ref|NP_194723.1| Pathogenesis-related homeodomain protein [Arabidopsis thaliana] gi|1346790|sp|P48785.1|PRH_ARATH RecName: Full=Pathogenesis-related homeodomain protein; Short=PRHA gi|507220|gb|AAA32843.1| homeodomain protein [Arabidopsis thaliana] gi|2501810|gb|AAC49836.1| PRHA [Arabidopsis thaliana] gi|4914418|emb|CAB43669.1| pathogenesis related homeodomain protein (PRHA) [Arabidopsis thaliana] gi|7269893|emb|CAB79752.1| pathogenesis related homeodomain protein (PRHA) [Arabidopsis thaliana] gi|332660298|gb|AEE85698.1| Pathogenesis-related homeodomain protein [Arabidopsis thaliana]	844	796	0	94.3	63.0	73.5	Pathogenesis-related homeodomain protein	gbpln	Arabidopsis thaliana	AT4G29940.1 | Symbols: PRHA | pathogenesis related homeodomain protein A | chr4:14648346-14652710 REVERSE LENGTH=796	844	796	0	94.3	63.0	73.5
Rsa1.0_00575.1.g16265.t3	gb|EOA17148.1| hypothetical protein CARUB_v10005416mg [Capsella rubella]	175	287	1.00E-36	164.0	44.6	47.4	hypothetical protein CARUB_v10005416mg	gbpln	Capsella rubella	AT4G29960.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:14660753-14662274 REVERSE LENGTH=291	175	291	5.00E-39	166.3	44.6	46.9
Rsa1.0_00575.1.g16266.t1	gb|EOA15663.1| hypothetical protein CARUB_v10006130mg [Capsella rubella]	90	90	3.00E-42	100.0	88.9	95.6	hypothetical protein CARUB_v10006130mg	gbpln	Capsella rubella	AT4G30010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, plastid; EXPRESSED IN: 26 plant structures; EXPRESSED DURING: 15 growth stages; Has 39 Blast hits to 39 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14672947-14673219 FORWARD LENGTH=90	90	90	2.00E-44	100.0	87.8	96.7
Rsa1.0_00575.1.g16267.t2	ref|XP_002878873.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324712|gb|EFH55132.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	253	220	8.00E-49	87.0	43.9	55.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G63820.1 | Symbols: | Protein of unknown function (DUF626) | chr5:25541576-25542893 FORWARD LENGTH=225	253	225	4.00E-23	88.9	29.6	40.3
Rsa1.0_00575.1.g16268.t1	gb|EOA18758.1| hypothetical protein CARUB_v10007364mg [Capsella rubella]	412	400	0	97.1	88.1	91.5	hypothetical protein CARUB_v10007364mg	gbpln	Capsella rubella	AT4G30060.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:14689420-14691519 REVERSE LENGTH=401	412	401	0	97.3	87.1	92.2
Rsa1.0_00576.1.g16269.t1	gb|EOA14082.1| hypothetical protein CARUB_v10027219mg, partial [Capsella rubella]	143	180	4.00E-77	125.9	97.9	99.3	hypothetical protein CARUB_v10027219mg, partial	gbpln	Capsella rubella	AT5G61170.1 | Symbols: | Ribosomal protein S19e family protein | chr5:24611158-24612202 FORWARD LENGTH=143	143	143	1.00E-79	100.0	99.3	99.3
Rsa1.0_00576.1.g16270.t1	gb|EOA14034.1| hypothetical protein CARUB_v10027167mg [Capsella rubella]	197	198	2.00E-74	100.5	76.1	83.2	hypothetical protein CARUB_v10027167mg	gbpln	Capsella rubella	AT5G61130.1 | Symbols: PDCB1 | plasmodesmata callose-binding protein 1 | chr5:24587438-24589369 REVERSE LENGTH=201	197	201	1.00E-67	102.0	75.1	80.2
Rsa1.0_00576.1.g16271.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00576.1.g16272.t1	ref|XP_002866417.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297312252|gb|EFH42676.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	372	437	1.00E-144	117.5	70.7	80.1	zinc ion binding protein	gbpln	Arabidopsis lyrata	AT5G61120.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Polynucleotidyl transferase, ribonuclease H-like superfamily protein (TAIR:AT5G61090.1); Has 125 Blast hits to 115 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 22; Fungi - 0; Plants - 102; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:24582486-24585030 REVERSE LENGTH=426	372	426	1.00E-142	114.5	69.4	79.6
Rsa1.0_00576.1.g16273.t1	gb|EOA14652.1| hypothetical protein CARUB_v10027913mg [Capsella rubella]	299	228	3.00E-12	76.3	15.1	19.4	hypothetical protein CARUB_v10027913mg	gbpln	Capsella rubella	AT5G61100.1 | Symbols: | BEST Arabidopsis thaliana protein match is: zinc ion binding (TAIR:AT5G61110.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:24579170-24580327 REVERSE LENGTH=227	299	227	1.00E-13	75.9	14.0	18.1

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<tr><td>Rsa1.0_00576.1.g16275.t1</td><td>ref|NP_200912.1| uncharacterized protein [Arabidopsis thaliana] gi|9759451|dbj|BAB10367.1| unnamed protein product [Arabidopsis thaliana] gi|332010032|gb|AED97415.1| uncharacterized protein AT5G61040 [Arabidopsis thaliana]</td><td>548</td><td>590</td><td>0</td><td>107.7</td><td>78.6</td><td>86.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G61040.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G08010.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:24562431-24564395 REVERSE LENGTH=590</td><td>548</td><td>590</td><td>0</td><td>107.7</td><td>78.6</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00576.1.g16276.t1</td><td>ref|NP_200909.1| exocyst complex component 7 [Arabidopsis thaliana] gi|79331752|ref|NP_001032116.1| exocyst complex component 7 [Arabidopsis thaliana] gi|9759448|dbj|BAB10364.1| leucine zipper protein-like [Arabidopsis thaliana] gi|15215764|gb|AAK91427.1| AT5g61010/maf19_10 [Arabidopsis thaliana] gi|16974329|gb|AAL31149.1| AT5g61010/maf19_10 [Arabidopsis thaliana] gi|222424078|dbj|BAH19999.1| AT5G61010 [Arabidopsis thaliana] gi|332010027|gb|AED97410.1| exocyst complex component 7 [Arabidopsis thaliana] gi|332010028|gb|AED97411.1| exocyst subunit exo70 family protein E2 [Arabidopsis thaliana]</td><td>966</td><td>639</td><td>0</td><td>66.1</td><td>48.2</td><td>54.1</td><td>exocyst complex component 7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G61010.2 | Symbols: ATEXO70E2, EXO70E2 | exocyst subunit exo70 family protein E2 | chr5:24554612-24556531 FORWARD LENGTH=639</td><td>966</td><td>639</td><td>0</td><td>66.1</td><td>48.2</td><td>54.1</td></tr>
<tr><td>Rsa1.0_00576.1.g16277.t1</td><td>ref|NP_200908.1| Replication factor-A protein 1-like protein [Arabidopsis thaliana] gi|10177323|dbj|BAB10649.1| replication protein A1 [Arabidopsis thaliana] gi|28393124|gb|AAO41995.1| putative RNA helicase [Arabidopsis thaliana] gi|332010026|gb|AED97409.1| Replication factor-A protein 1-like protein [Arabidopsis thaliana]</td><td>626</td><td>629</td><td>0</td><td>100.5</td><td>88.7</td><td>94.4</td><td>Replication factor-A protein 1-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G61000.1 | Symbols: RPA70D, ATRPA70D | Replication factor-A protein 1-related | chr5:24549682-24552641 REVERSE LENGTH=629</td><td>626</td><td>629</td><td>0</td><td>100.5</td><td>88.7</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00576.1.g16278.t1</td><td>gb|EOA13353.1| hypothetical protein CARUB_v10026387mg [Capsella rubella]</td><td>452</td><td>451</td><td>0</td><td>99.8</td><td>91.4</td><td>95.6</td><td>hypothetical protein CARUB_v10026387mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G60990.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr5:24546601-24549148 REVERSE LENGTH=456</td><td>452</td><td>456</td><td>0</td><td>100.9</td><td>91.6</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00576.1.g16279.t1</td><td>ref|NP_200906.2| nuclear transport factor 2 and RNA recognition motif domain-containing protein [Arabidopsis thaliana] gi|10177321|dbj|BAB10647.1| unnamed protein product [Arabidopsis thaliana] gi|17063173|gb|AAL32982.1| AT5g60980/MSL3_100 [Arabidopsis thaliana] gi|27764908|gb|AAO23575.1| At5g60980/MSL3_100 [Arabidopsis thaliana] gi|332010024|gb|AED97407.1| nuclear transport factor 2 and RNA recognition motif domain-containing protein [Arabidopsis thaliana]</td><td>459</td><td>460</td><td>0</td><td>100.2</td><td>83.0</td><td>86.3</td><td>nuclear transport factor 2 and RNA recognition motif domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G60980.2 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr5:24543988-24546027 FORWARD LENGTH=460</td><td>459</td><td>460</td><td>0</td><td>100.2</td><td>83.0</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00576.1.g16280.t1</td><td>gb|EOA13591.1| hypothetical protein CARUB_v10026656mg [Capsella rubella]</td><td>494</td><td>359</td><td>1.00E-162</td><td>72.7</td><td>63.4</td><td>67.8</td><td>hypothetical protein CARUB_v10026656mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G60970.1 | Symbols: TCP5 | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 5 | chr5:24535570-24536652 REVERSE LENGTH=360</td><td>494</td><td>360</td><td>1.00E-153</td><td>72.9</td><td>61.3</td><td>66.8</td></tr>
<tr><td>Rsa1.0_00576.1.g16281.t1</td><td>ref|XP_002876993.1| hypothetical protein ARALYDRAFT_347050 [Arabidopsis lyrata subsp. lyrata] gi|297322831|gb|EFH53252.1| hypothetical protein ARALYDRAFT_347050 [Arabidopsis lyrata subsp. lyrata]</td><td>483</td><td>266</td><td>1.00E-104</td><td>55.1</td><td>41.6</td><td>47.2</td><td>hypothetical protein ARALYDRAFT_347050</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G26850.2 | Symbols: | histone-lysine N-methyltransferases | chr3:9896541-9897415 REVERSE LENGTH=265</td><td>483</td><td>265</td><td>1.00E-106</td><td>54.9</td><td>41.2</td><td>47.2</td></tr>
<tr><td>Rsa1.0_00576.1.g16282.t1</td><td>gb|EOA14973.1| hypothetical protein CARUB_v10028321mg [Capsella rubella]</td><td>484</td><td>522</td><td>0</td><td>107.9</td><td>82.6</td><td>89.3</td><td>hypothetical protein CARUB_v10028321mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G60960.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:24528423-24529988 REVERSE LENGTH=521</td><td>484</td><td>521</td><td>0</td><td>107.6</td><td>81.6</td><td>89.5</td></tr>
</table>

Rsa1.0_00576.1.g16283.t1	ref|NP_200903.1| COBRA-like protein 5 [Arabidopsis thaliana] gi|34222630|sp|Q9FME5.1|COBL5_ARATH RecName: Full=COBRA-like protein 5; Flags: Precursor gi|10177318|dbj|BAB10644.1| unnamed protein product [Arabidopsis thaliana] gi|38566616|gb|AAR24198.1| At5g60950 [Arabidopsis thaliana] gi|40824050|gb|AAR92332.1| At5g60950 [Arabidopsis thaliana] gi|332010019|gb|AED97402.1| COBRA-like protein 5 [Arabidopsis thaliana]	206	204	5.00E-93	99.0	79.6	88.3	COBRA-like protein 5	gbpln	Arabidopsis thaliana	AT5G60950.1 | Symbols: COBL5 | COBRA-like protein 5 precursor | chr5:24527157-24528005 REVERSE LENGTH=204	206	204	2.00E-95	99.0	79.6	88.3
Rsa1.0_00576.1.g16284.t1	ref|XP_002864711.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297310546|gb|EFH40970.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	476	429	0	90.1	80.9	85.3	transducin family protein	gbpln	Arabidopsis lyrata	AT5G60940.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:24523092-24525655 FORWARD LENGTH=429	476	429	0	90.1	80.9	85.5
Rsa1.0_00576.1.g16285.t1	gb|EOA12365.1| hypothetical protein CARUB_v10025749mg [Capsella rubella]	1281	1298	0	101.3	87.0	92.3	hypothetical protein CARUB_v10025749mg	gbpln	Capsella rubella	AT5G60930.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:24515398-24522511 REVERSE LENGTH=1294	1281	1294	0	101.0	84.4	89.6
Rsa1.0_00576.1.g16286.t1	sp|Q39202.2|RLK1_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase RLK1; AltName: Full=Receptor-like protein kinase 1; Flags: Precursor	839	832	0	99.2	68.2	78.3	RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase RLK1; AltName: Full=Receptor-like protein kinase 1; Flags: Precursor	----	----	AT5G60900.1 | Symbols: RLK1 | receptor-like protein kinase 1 | chr5:24498467-24501494 REVERSE LENGTH=748	839	748	0	89.2	63.5	73.2
Rsa1.0_00576.1.g16287.t1	gb|EOA15342.1| hypothetical protein CARUB_v10004135mg [Capsella rubella]	870	825	0	94.8	63.4	72.5	hypothetical protein CARUB_v10004135mg	gbpln	Capsella rubella	AT5G60900.1 | Symbols: RLK1 | receptor-like protein kinase 1 | chr5:24498467-24501494 REVERSE LENGTH=748	870	748	0	86.0	61.6	68.5
Rsa1.0_00576.1.g16288.t1	gb|ACR48185.1| MYB domain protein 34-2 [Brassica rapa subsp. pekinensis]	315	316	1.00E-158	100.3	86.0	92.4	MYB domain protein 34-2	gbpln	Brassica rapa	AT5G60890.1 | Symbols: ATMYB34, ATR1, MYB34 | myb domain protein 34 | chr5:24495029-24496220 FORWARD LENGTH=295	315	295	1.00E-129	93.7	75.6	83.2
Rsa1.0_00576.1.g16289.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00576.1.g16290.t1	gb|EOA32065.1| hypothetical protein CARUB_v10015308mg [Capsella rubella]	112	1366	7.00E-24	1219.6	53.6	60.7	hypothetical protein CARUB_v10015308mg	gbpln	Capsella rubella	AT3G01320.1 | Symbols: SNL1 | SIN3-like 1 | chr3:106730-113197 FORWARD LENGTH=1372	112	1372	7.00E-21	1225.0	50.0	54.5
Rsa1.0_00576.1.g16291.t1	ref|XP_002887681.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297333522|gb|EFH63940.1| binding protein [Arabidopsis lyrata subsp. lyrata]	277	459	1.00E-128	165.7	83.0	89.9	binding protein	gbpln	Arabidopsis lyrata	AT1G77405.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:29087145-29088521 FORWARD LENGTH=458	277	458	1.00E-129	165.3	82.3	88.4
Rsa1.0_00576.1.g16292.t1	ref|XP_002866400.1| hypothetical protein ARALYDRAFT_919327 [Arabidopsis lyrata subsp. lyrata] gi|297312235|gb|EFH42659.1| hypothetical protein ARALYDRAFT_919327 [Arabidopsis lyrata subsp. lyrata]	260	264	2.00E-93	101.5	80.0	88.5	hypothetical protein ARALYDRAFT_919327	gbpln	Arabidopsis lyrata	AT5G60880.1 | Symbols: BASL | breaking of asymmetry in the stomatal lineage | chr5:24488553-24489703 REVERSE LENGTH=262	260	262	9.00E-95	100.8	77.7	85.8
Rsa1.0_00576.1.g16293.t1	ref|XP_002525153.1| protein with unknown function [Ricinus communis] gi|223535612|gb|EEF37280.1| protein with unknown function [Ricinus communis]	180	216	6.00E-95	120.0	94.4	97.2	protein with unknown function	gbpln	Ricinus communis	AT5G60860.1 | Symbols: AtRABA1f, RABA1f | RAB GTPase homolog A1F | chr5:24484750-24485565 FORWARD LENGTH=217	180	217	3.00E-96	120.6	93.3	97.2
Rsa1.0_00576.1.g16294.t1	dbj|BAJ34224.1| unnamed protein product [Thellungiella halophila]	302	300	1.00E-110	99.3	81.8	85.8	unnamed protein product	----	----	AT5G60850.1 | Symbols: OBP4 | OBF binding protein 4 | chr5:24480578-24481501 FORWARD LENGTH=307	302	307	1.00E-108	101.7	75.2	80.8
Rsa1.0_00577.1.g16295.t1	gb|EOA33062.1| hypothetical protein CARUB_v10016395mg [Capsella rubella]	182	188	3.00E-78	103.3	78.6	86.8	hypothetical protein CARUB_v10016395mg	gbpln	Capsella rubella	AT3G13720.1 | Symbols: PRA1.F3, PRA8 | PRA1 (Prenylated rab acceptor) family protein | chr3:4495202-4495768 REVERSE LENGTH=188	182	188	2.00E-71	103.3	75.8	85.2
Rsa1.0_00577.1.g16296.t1	ref|NP_566461.1| PRA1 family protein F3 [Arabidopsis thaliana] gi|75273356|sp|Q9LIC6.1|PR1F3_ARATH RecName: Full=PRA1 family protein F3; Short=AtPRA1.F3 gi|9294018|dbj|BAB01921.1| unnamed protein product [Arabidopsis thaliana] gi|28393547|gb|AAO42194.1| unknown protein [Arabidopsis thaliana] gi|28827282|gb|AAO50485.1| unknown protein [Arabidopsis thaliana] gi|332641882|gb|AEE75403.1| PRA1 family protein F3 [Arabidopsis thaliana]	210	188	4.00E-44	89.5	51.9	63.8	PRA1 family protein F3	gbpln	Arabidopsis thaliana	AT3G13720.1 | Symbols: PRA1.F3, PRA8 | PRA1 (Prenylated rab acceptor) family protein | chr3:4495202-4495768 REVERSE LENGTH=188	210	188	1.00E-46	89.5	51.9	63.8

Rsa1.0_00577.1.g16297.t1	gb|EOA33062.1| hypothetical protein CARUB_v10016395mg [Capsella rubella]	213	188	5.00E−39	88.3	48.8	59.6	hypothetical protein CARUB_v10016395mg	gbpln	Capsella rubella	AT3G13720.1 | Symbols: PRA1.F3, PRA8 | PRA1 (Prenylated rab acceptor) family protein | chr3:4495202−4495768 REVERSE LENGTH=188	213	188	9.00E−40	88.3	51.2	60.1
Rsa1.0_00577.1.g16298.t2	ref|NP_187982.1| protein kinase protein with adenine nucleotide alpha hydrolases−like domain−containing protein [Arabidopsis thaliana] gi|9294015|dbj|BAB01918.1| unnamed protein product [Arabidopsis thaliana] gi|332641878|gb|AEE75399.1| protein kinase protein with adenine nucleotide alpha hydrolases−like domain−containing protein [Arabidopsis thaliana]	763	753	0	98.7	89.8	93.3	protein kinase protein with adenine nucleotide alpha hydrolases−like domain−containing protein	gbpln	Arabidopsis thaliana	AT3G13690.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases−like domain | chr3:4486920−4490011 FORWARD LENGTH=753	763	753	0	98.7	89.8	93.3
Rsa1.0_00577.1.g16299.t1	gb|EOA29951.1| hypothetical protein CARUB_v10013055mg [Capsella rubella]	735	735	0	100.0	85.2	91.3	hypothetical protein CARUB_v10013055mg	gbpln	Capsella rubella	AT3G13682.1 | Symbols: LDL2 | LSD1−like2 | chr3:4479193−4481509 REVERSE LENGTH=746	735	746	0	101.5	85.0	91.7
Rsa1.0_00577.1.g16300.t1	gb|EOA31550.1| hypothetical protein CARUB_v10014742mg [Capsella rubella]	185	184	6.00E−75	99.5	74.6	84.3	hypothetical protein CARUB_v10014742mg	gbpln	Capsella rubella	AT5G49040.1 | Symbols: | Disease resistance−responsive (dirigent−like protein) family protein | chr5:19882676−19883251 REVERSE LENGTH=191	185	191	2.00E−69	103.2	69.7	81.6
Rsa1.0_00577.1.g16301.t1	ref|NP_199715.1| disease resistance−responsive, dirigent domain−containing protein [Arabidopsis thaliana] gi|10177194|dbj|BAB10328.1| unnamed protein product [Arabidopsis thaliana] gi|332008382|gb|AED95765.1| disease resistance−responsive, dirigent domain−containing protein [Arabidopsis thaliana]	169	191	3.00E−60	113.0	75.7	83.4	disease resistance−responsive, dirigent domain−containing protein	gbpln	Arabidopsis thaliana	AT5G49040.1 | Symbols: | Disease resistance−responsive (dirigent−like protein) family protein | chr5:19882676−19883251 REVERSE LENGTH=191	169	191	1.00E−62	113.0	75.7	83.4
Rsa1.0_00577.1.g16302.t1	ref|NP_187969.1| calmodulin−binding protein−like protein [Arabidopsis thaliana] gi|11994562|dbj|BAB02602.1| unnamed protein product [Arabidopsis thaliana] gi|332641860|gb|AEE75381.1| calmodulin−binding protein−like protein [Arabidopsis thaliana]	111	605	4.00E−26	545.0	51.4	51.4	calmodulin−binding protein−like protein	gbpln	Arabidopsis thaliana	AT3G13600.1 | Symbols: | calmodulin−binding family protein | chr3:4445102−4447383 FORWARD LENGTH=605	111	605	7.00E−29	545.0	51.4	51.4
Rsa1.0_00577.1.g16303.t1	ref|XP_002885061.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297330901|gb|EFH61320.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	184	361	4.00E−99	196.2	94.6	99.5	oxidoreductase	gbpln	Arabidopsis lyrata	AT3G13610.1 | Symbols: | 2−oxoglutarate (2OG) and Fe(II)−dependent oxygenase superfamily protein | chr3:4449448−4450616 FORWARD LENGTH=361	184	361	2.00E−98	196.2	91.3	97.8
Rsa1.0_00577.1.g16304.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00577.1.g16305.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00577.1.g16306.t1	ref|NP_001142677.1| uncharacterized protein LOC100274972 [Zea mays] gi|195608106|gb|ACG25883.1| hypothetical protein [Zea mays]	251	249	1.00E−115	99.2	82.5	90.0	uncharacterized protein LOC100274972	gbenv/gbpln	Zea mays	AT3G13440.1 | Symbols: | S−adenosyl−L−methionine−dependent methyltransferases superfamily protein | chr3:4378338−4379347 FORWARD LENGTH=278	251	278	1.00E−110	110.8	76.9	88.4
Rsa1.0_00577.1.g16307.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00577.1.g16308.t1	ref|NP_187110.1| tryptophanyl−tRNA synthetase [Arabidopsis thaliana] gi|145331754|ref|NP_001078104.1| tryptophanyl−tRNA synthetase [Arabidopsis thaliana] gi|6175164|gb|AAF04890.1|AC011437_5 putative tryptophanyl−tRNA synthetase [Arabidopsis thaliana] gi|19310593|gb|AAL85027.1| putative tryptophanyl−tRNA synthetase [Arabidopsis thaliana] gi|21436361|gb|AAM51350.1| putative tryptophanyl−tRNA synthetase [Arabidopsis thaliana] gi|110740619|dbj|BAE98413.1| putative tryptophanyl−tRNA synthetase [Arabidopsis thaliana] gi|332640582|gb|AEE74103.1| tryptophanyl−tRNA synthetase [Arabidopsis thaliana] gi|332640584|gb|AEE74105.1| tryptophanyl−tRNA synthetase−like protein [Arabidopsis thaliana]	450	402	1.00E−164	89.3	62.2	72.7	tryptophanyl−tRNA synthetase	gbpln	Arabidopsis thaliana	AT3G04600.3 | Symbols: | Nucleotidylyl transferase superfamily protein | chr3:1243152−1245958 FORWARD LENGTH=402	450	402	1.00E−166	89.3	62.2	72.7

Rsa1.0_00577.1.g16309.t1	gb|AAN60225.1| unknown [Arabidopsis thaliana]	309	321	1.00E-147	103.9	87.7	91.9	unknown	gbpln	Arabidopsis thaliana	AT3G13410.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G55546.1); Has 49 Blast hits to 49 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:4362149-4364032 REVERSE LENGTH=321	309	321	1.00E-148	103.9	87.4	91.3
Rsa1.0_00577.1.g16310.t1	ref|XP_002882820.1| hypothetical protein ARALYDRAFT_478721 [Arabidopsis lyrata subsp. lyrata] gi|297328660|gb|EFH59079.1| hypothetical protein ARALYDRAFT_478721 [Arabidopsis lyrata subsp. lyrata]	551	551	0	100.0	94.6	98.0	hypothetical protein ARALYDRAFT_478721	gbpln	Arabidopsis lyrata	AT3G13400.1 | Symbols: sks13 | SKU5 similar 13 | chr3:4355257-4357305 FORWARD LENGTH=551	551	551	0	100.0	94.4	98.0
Rsa1.0_00577.1.g16311.t1	emb|CAA47176.1| Bplo [Brassica napus]	555	554	0	99.8	95.3	98.0	Bplo	gbpln	Brassica napus	AT1G55570.1 | Symbols: sks12 | SKU5 similar 12 | chr1:20757882-20759771 FORWARD LENGTH=555	555	555	0	100.0	87.6	94.2
Rsa1.0_00577.1.g16312.t1	dbj|BAB02805.1| unnamed protein product [Arabidopsis thaliana]	399	538	1.00E-121	134.8	69.2	76.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G13360.1 | Symbols: WIP3 | WPP domain interacting protein 3 | chr3:4338472-4339982 REVERSE LENGTH=459	399	459	1.00E-124	115.0	69.2	76.9
Rsa1.0_00577.1.g16313.t3	gb|EOA30587.1| hypothetical protein CARUB_v10013719mg [Capsella rubella]	477	441	0	92.5	83.2	86.8	hypothetical protein CARUB_v10013719mg	gbpln	Capsella rubella	AT3G13320.1 | Symbols: CAX2, atcax2 | cation exchanger 2 | chr3:4315418-4317997 FORWARD LENGTH=441	477	441	0	92.5	82.2	86.6
Rsa1.0_00577.1.g16314.t1	ref|XP_002884960.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330800|gb|EFH61219.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	160	157	8.00E-58	98.1	76.9	83.1	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT3G13310.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr3:4310827-4311300 REVERSE LENGTH=157	160	157	2.00E-59	98.1	75.6	83.1
Rsa1.0_00577.1.g16315.t12	ref|NP_001189876.1| DNA damage-inducible protein 1 [Arabidopsis thaliana] gi|332641803|gb|AEE75324.1| DNA damage-inducible protein 1 [Arabidopsis thaliana]	803	413	0	51.4	45.1	47.4	DNA damage-inducible protein 1	gbpln	Arabidopsis thaliana	AT3G13235.3 | Symbols: | ubiquitin family protein | chr3:4271492-4274348 REVERSE LENGTH=413	803	413	0	51.4	45.1	47.4
Rsa1.0_00577.1.g16316.t1	gb|EOA29852.1| hypothetical protein CARUB_v10012949mg [Capsella rubella]	890	883	0	99.2	72.4	82.4	hypothetical protein CARUB_v10012949mg	gbpln	Capsella rubella	AT3G13225.2 | Symbols: | WW domain-containing protein | chr3:4258928-4262853 REVERSE LENGTH=892	890	892	0	100.2	73.6	83.7
Rsa1.0_00577.1.g16317.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00577.1.g16318.t1	ref|NP_683559.2| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|11994764|dbj|BAB03120.1| unnamed protein product [Arabidopsis thaliana] gi|19347908|gb|AAL85976.1| unknown protein [Arabidopsis thaliana] gi|21689785|gb|AAM67536.1| unknown protein [Arabidopsis thaliana] gi|62320244|dbj|BAD94504.1| hypothetical protein [Arabidopsis thaliana] gi|332641794|gb|AEE75315.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	368	358	1.00E-129	97.3	84.5	86.7	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT3G13224.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:4254848-4256621 FORWARD LENGTH=358	368	358	1.00E-132	97.3	84.5	86.7
Rsa1.0_00577.1.g16319.t2	gb|EOA31950.1| hypothetical protein CARUB_v10015191mg [Capsella rubella]	558	572	1.00E-179	102.5	66.7	75.3	hypothetical protein CARUB_v10015191mg	gbpln	Capsella rubella	AT3G13222.1 | Symbols: GIP1 | GBF-interacting protein 1 | chr3:4251287-4254206 REVERSE LENGTH=567	558	567	1.00E-169	101.6	65.6	76.2
Rsa1.0_00577.1.g16320.t1	ref|XP_002884953.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297330793|gb|EFH61212.1| abc transporter family protein [Arabidopsis lyrata subsp. lyrata]	681	685	0	100.6	93.5	97.4	abc transporter family protein	gbpln	Arabidopsis lyrata	AT3G13220.1 | Symbols: WBC27, ABCG26 | ABC-2 type transporter family protein | chr3:4247968-4250703 REVERSE LENGTH=685	681	685	0	100.6	93.1	96.9
Rsa1.0_00577.1.g16321.t1	gb|EOA29633.1| hypothetical protein CARUB_v10014543mg [Capsella rubella]	254	230	1.00E-100	90.6	83.1	88.2	hypothetical protein CARUB_v10014543mg	gbpln	Capsella rubella	AT3G13200.1 | Symbols: EMB2769 | Cwf15 / Cwc15 cell cycle control family protein | chr3:4242239-4243976 FORWARD LENGTH=230	254	230	5.00E-94	90.6	82.3	85.8

Rsa1.0_00577.1.g16322.t1	ref|NP_187924.2| ribosomal RNA small subunit methyltransferase B [Arabidopsis thaliana] gi|18176252|gb|AAL60011.1| putative sun protein fmu [Arabidopsis thaliana] gi|21436219|gb|AAM51397.1| putative sun protein fmu [Arabidopsis thaliana] gi|110740623|dbj|BAE98415.1| putative sun (fmu) protein [Arabidopsis thaliana] gi|332641785|gb|AEE75306.1| NOL1/NOP2/sun family protein / antitermination NusB domain-containing protein [Arabidopsis thaliana]	680	523	0	76.9	70.9	72.8	ribosomal RNA small subunit methyltransferase B	gbpln	Arabidopsis thaliana	AT3G13180.1 | Symbols: | NOL1/NOP2/sun family protein / antitermination NusB domain-containing protein | chr3:4236326-4239966 REVERSE LENGTH=523	680	523	0	76.9	70.9	72.8
Rsa1.0_00578.1.g16323.t1	ref|XP_002881353.1| hypothetical protein ARALYDRAFT_902559 [Arabidopsis lyrata subsp. lyrata] gi|297327192|gb|EFH57612.1| hypothetical protein ARALYDRAFT_902559 [Arabidopsis lyrata subsp. lyrata]	850	859	0	101.1	94.4	96.9	hypothetical protein ARALYDRAFT_902559	gbpln	Arabidopsis lyrata	AT2G34710.1 | Symbols: PHB, ATHB14, ATHB-14, PHB-1D | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr2:14639548-14643993 REVERSE LENGTH=852	850	852	0	100.2	94.7	97.3
Rsa1.0_00578.1.g16324.t1	gb|AAB54117.1| putative serine/threonine protein kinase [Brassica rapa]	431	439	0	101.9	94.9	97.2	putative serine/threonine protein kinase	gbpln	Brassica rapa	AT2G34650.1 | Symbols: PID, ABR | Protein kinase superfamily protein | chr2:14589934-14591557 REVERSE LENGTH=438	431	438	0	101.6	91.2	94.9
Rsa1.0_00578.1.g16325.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	902	1142	0	126.6	45.1	59.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	902	575	4.00E-53	63.7	14.9	24.2
Rsa1.0_00578.1.g16326.t1	ref|NP_850233.1| uncharacterized protein [Arabidopsis thaliana] gi|17979357|gb|AAL49904.1| unknown protein [Arabidopsis thaliana] gi|21689695|gb|AAM67469.1| unknown protein [Arabidopsis thaliana] gi|330253904|gb|AEC08998.1| uncharacterized protein AT2G34610 [Arabidopsis thaliana]	407	290	2.00E-76	71.3	40.0	47.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G34610.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G30190.1); Has 342 Blast hits to 279 proteins in 74 species: Archae - 0; Bacteria - 7; Metazoa - 76; Fungi - 18; Plants - 51; Viruses - 0; Other Eukaryotes - 190 (source: NCBI BLink). | chr2:14575467-14576339 FORWARD LENGTH=290	407	290	4.00E-79	71.3	40.0	47.2
Rsa1.0_00578.1.g16327.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00578.1.g16328.t1	ref|NP_181007.1| protein TIFY 5B [Arabidopsis thaliana] gi|75099146|sp|O64687.1|TIF5B_ARATH RecName: Full=Protein TIFY 5B; AltName: Full=Jasmonate ZIM domain-containing protein 7 gi|3128215|gb|AAC26695.1| hypothetical protein [Arabidopsis thaliana] gi|38454058|gb|AAR20723.1| At2g34600 [Arabidopsis thaliana] gi|38603996|gb|AAR24741.1| At2g34600 [Arabidopsis thaliana] gi|330253903|gb|AEC08997.1| protein TIFY 5B [Arabidopsis thaliana]	122	148	1.00E-43	121.3	75.4	86.9	protein TIFY 5B	gbpln	Arabidopsis thaliana	AT2G34600.1 | Symbols: JAZ7, TIFY5B | jasmonate-zim-domain protein 7 | chr2:14573172-14573718 FORWARD LENGTH=148	122	148	2.00E-46	121.3	75.4	86.9
Rsa1.0_00578.1.g16329.t1	ref|XP_002881345.1| hypothetical protein ARALYDRAFT_902544 [Arabidopsis lyrata subsp. lyrata] gi|297327184|gb|EFH57604.1| hypothetical protein ARALYDRAFT_902544 [Arabidopsis lyrata subsp. lyrata]	86	81	6.00E-20	94.2	79.1	83.7	hypothetical protein ARALYDRAFT_902544	gbpln	Arabidopsis lyrata	AT2G34585.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 43 Blast hits to 43 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:14568227-14568472 REVERSE LENGTH=81	86	81	1.00E-22	94.2	74.4	81.4
Rsa1.0_00578.1.g16330.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	914	2726	2.00E-40	298.2	10.6	16.1	disease resistance protein	gbpln	Brassica rapa	AT1G67020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf; Has 72 Blast hits to 72 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 72; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25011008-25012987 REVERSE LENGTH=659	914	659	6.00E-20	72.1	6.2	9.8
Rsa1.0_00578.1.g16331.t1	gb|EOA28410.1| hypothetical protein CARUB_v10024616mg [Capsella rubella]	326	336	1.00E-149	103.1	79.8	89.0	hypothetical protein CARUB_v10024616mg	gbpln	Capsella rubella	AT2G34555.1 | Symbols: ATGA2OX3, GA2OX3 | gibberellin 2-oxidase 3 | chr2:14557102-14558682 FORWARD LENGTH=335	326	335	1.00E-151	102.8	78.8	88.3

Rsa1.0_00578.1.g16332.t1	ref|XP_002877469.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323307|gb|EFH53728.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	240	328	1.00E-24	136.7	28.8	40.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	240	289	3.00E-24	120.4	24.2	36.7
Rsa1.0_00579.1.g16333.t1	gb|AAZ67609.1| 80A08_24 [Brassica rapa subsp. pekinensis]	440	475	9.00E-26	108.0	33.6	46.6	80A08_24	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00579.1.g16334.t1	gb|AAO85536.1| terpene synthase [Arabidopsis thaliana]	602	603	0	100.2	70.6	84.4	terpene synthase	gbpln	Arabidopsis thaliana	AT3G29410.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr3:11302574-11305060 REVERSE LENGTH=603	602	603	0	100.2	71.1	83.7
Rsa1.0_00579.1.g16335.t2	gb|EOA19267.1| hypothetical protein CARUB_v10000372mg [Capsella rubella]	239	686	3.00E-13	287.0	14.2	16.3	hypothetical protein CARUB_v10000372mg	gbpln	Capsella rubella	AT4G04960.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr4:2533096-2535156 FORWARD LENGTH=686	239	686	9.00E-16	287.0	14.2	16.3
Rsa1.0_00579.1.g16336.t1	gb|EOA31011.1| hypothetical protein CARUB_v10014154mg [Capsella rubella]	334	331	1.00E-155	99.1	83.5	88.0	hypothetical protein CARUB_v10014154mg	gbpln	Capsella rubella	AT3G14450.1 | Symbols: CID9 | CTC-interacting domain 9 | chr3:4849788-4851601 FORWARD LENGTH=327	334	327	1.00E-151	97.9	80.8	85.6
Rsa1.0_00579.1.g16337.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00579.1.g16338.t2	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	893	1213	0	135.8	39.2	52.4	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	893	626	1.00E-74	70.1	16.6	24.9
Rsa1.0_00579.1.g16339.t1	gb|AEN94304.1| 9-cis-epoxycarotenoid dioxygenase [Brassica napus]	591	592	0	100.2	90.4	94.2	9-cis-epoxycarotenoid dioxygenase	gbpln	Brassica napus	AT3G14440.1 | Symbols: NCED3, ATNCED3, STO1, SIS7 | nine-cis-epoxycarotenoid dioxygenase 3 | chr3:4831678-4833477 REVERSE LENGTH=599	591	599	0	101.4	89.0	94.6
Rsa1.0_00579.1.g16340.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00579.1.g16341.t1	gb|EOA29697.1| hypothetical protein CARUB_v10016402mg [Capsella rubella]	76	76	2.00E-31	100.0	88.2	93.4	hypothetical protein CARUB_v10016402mg	gbpln	Capsella rubella	AT3G14430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 16 Blast hits to 16 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4824399-4824732 REVERSE LENGTH=76	76	76	5.00E-34	100.0	88.2	93.4
Rsa1.0_00579.1.g16342.t1	ref|NP_188060.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|30683149|ref|NP_850584.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|297829994|ref|XP_002882879.1| hypothetical protein ARALYDRAFT_478862 [Arabidopsis lyrata subsp. lyrata] gi|13124262|sp|Q9LRR9.1|GLO1_ARATH RecName: Full=Peroxisomal (S)-2-hydroxy-acid oxidase GLO1; AltName: Full=Glycolate oxidase 1; Short=AtGLO1; Short=GOX 1; AltName: Full=Short chain alpha-hydroxy acid oxidase GLO1 gi|16226423|gb|AAL16164.1|AF428396_1 AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|11994212|dbj|BAB01334.1| glycolate oxidase [Arabidopsis thaliana] gi|15450741|gb|AAK96642.1| AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|18491119|gb|AAL69528.1| AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|297328719|gb|EFH59138.1| hypothetical protein ARALYDRAFT_478862 [Arabidopsis lyrata subsp. lyrata] gi|332641997|gb|AEE75518.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|332641999|gb|AEE75520.1| putative peroxisomal (S)-2-hydroxy-acid	372	367	0	98.7	95.2	97.6	putative peroxisomal (S)-2-hydroxy-acid oxidase 2	gbpln	Arabidopsis lyrata	AT3G14420.2 | Symbols: | Aldolase-type TIM barrel family protein | chr3:4821804-4823899 FORWARD LENGTH=367	372	367	0	98.7	95.2	97.6
Rsa1.0_00579.1.g16343.t1	gb|AAV28535.1| glycolate oxidase [Brassica napus]	367	367	0	100.0	99.5	99.7	glycolate oxidase	gbpln	Brassica napus	AT3G14415.3 | Symbols: | Aldolase-type TIM barrel family protein | chr3:4818667-4820748 FORWARD LENGTH=367	367	367	0	100.0	96.2	98.9
Rsa1.0_00579.1.g16344.t1	gb|EOA30970.1| hypothetical protein CARUB_v10014116mg [Capsella rubella]	366	339	1.00E-171	92.6	85.5	89.6	hypothetical protein CARUB_v10014116mg	gbpln	Capsella rubella	AT3G14410.1 | Symbols: | Nucleotide/sugar transporter family protein | chr3:4815982-4817852 REVERSE LENGTH=340	366	340	1.00E-173	92.9	85.0	89.1

Rsa1.0_00579.1.g16345.t1	gb|EOA32869.1| hypothetical protein CARUB_v10016184mg [Capsella rubella]	293	576	1.00E-100	196.6	63.1	75.8	hypothetical protein CARUB_v10016184mg	gbpln	Capsella rubella	AT4G02320.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr4:1022725-1026118 REVERSE LENGTH=518	293	518	2.00E-69	176.8	44.4	65.5
Rsa1.0_00579.1.g16346.t1	ref|NP_188043.2| LURP-one-related 11 protein [Arabidopsis thaliana] gi|75335508|sp|Q9LUM1.1|LOR11_ARATH RecName: Full=Protein LURP-one-related 11 gi|9279574|dbj|BAB01032.1| unnamed protein product [Arabidopsis thaliana] gi|49660157|gb|AAT68369.1| hypothetical protein At3g14260 [Arabidopsis thaliana] gi|67633632|gb|AAY78740.1| hypothetical protein At3g14260 [Arabidopsis thaliana] gi|332641974|gb|AEE75495.1| LURP-one-related 11 protein [Arabidopsis thaliana]	208	230	1.00E-102	110.6	85.1	92.3	LURP-one-related 11 protein	gbpln	Arabidopsis thaliana	AT3G14260.1 | Symbols: | Protein of unknown function (DUF567) | chr3:4747986-4748779 REVERSE LENGTH=230	208	230	1.00E-105	110.6	85.1	92.3
Rsa1.0_00580.1.g16347.t1	ref|NP_200279.1| transcription factor ILR3 [Arabidopsis thaliana] gi|297792933|ref|XP_002864351.1| hypothetical protein ARALYDRAFT_495549 [Arabidopsis lyrata subsp. lyrata] gi|75309075|sp|Q9FH37.1|ILR3_ARATH RecName: Full=Transcription factor ILR3; AltName: Full=Basic helix-loop-helix protein 105; Short=AtbHLH105; Short=bHLH 105; AltName: Full=Protein IAA-LEUCINE RESISTANT 3; AltName: Full=Transcription factor EN 133; AltName: Full=bHLH transcription factor bHLH105 gi|20127111|gb|AAM10964.1|AF488629_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|10176795|dbj|BAB09934.1| unnamed protein product [Arabidopsis thaliana] gi|15451010|gb|AAK96776.1| Unknown protein [Arabidopsis thaliana] gi|25084222|gb|AAN72200.1| Unknown protein [Arabidopsis thaliana] gi|297310186|gb|EFH40610.1| hypothetical protein ARALYDRAFT_495549 [Arabidopsis lyrata subsp. lyrata] gi|332009143|gb|AED96526.1| transcription factor ILR3 [Arabidopsis thaliana]	117	234	2.00E-51	200.0	88.9	91.5	transcription factor ILR3	gbpln	Arabidopsis lyrata	AT5G54680.1 | Symbols: ILR3, bHLH105 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:22217270-22218993 FORWARD LENGTH=234	117	234	3.00E-54	200.0	88.9	91.5
Rsa1.0_00580.1.g16348.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00580.1.g16349.t1	gb|EOA12956.1| hypothetical protein CARUB_v10025939mg [Capsella rubella] gi|482548763|gb|EOA12957.1| hypothetical protein CARUB_v10025939mg [Capsella rubella]	754	754	0	100.0	92.8	96.3	hypothetical protein CARUB_v10025939mg	gbpln	Capsella rubella	AT5G54670.1 | Symbols: ATK3, KATC | kinesin 3 | chr5:22209912-22213843 FORWARD LENGTH=754	754	754	0	100.0	92.4	96.0
Rsa1.0_00580.1.g16350.t1	ref|NP_568810.1| nuclear-enriched phloem companion cell 8 protein [Arabidopsis thaliana] gi|75262527|sp|Q9FIT9.1|HS217_ARATH RecName: Full=21.7 kDa class VI heat shock protein; AltName: Full=21.7 kDa heat shock protein; Short=AtHsp21.7 gi|9758958|dbj|BAB09345.1| unnamed protein product [Arabidopsis thaliana] gi|119360049|gb|ABL66753.1| At5g54660 [Arabidopsis thaliana] gi|332009141|gb|AED96524.1| class VI heat shock protein 21.7 [Arabidopsis thaliana]	184	192	2.00E-88	104.3	88.0	93.5	nuclear-enriched phloem companion cell 8 protein	gbpln	Arabidopsis thaliana	AT5G54660.1 | Symbols: | HSP20-like chaperones superfamily protein | chr5:22203950-22204986 FORWARD LENGTH=192	184	192	6.00E-91	104.3	88.0	93.5
Rsa1.0_00580.1.g16351.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00580.1.g16352.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00580.1.g16353.t1	ref|XP_003634699.1| PREDICTED: histone H2A.6 isoform 2 [Vitis vinifera]	73	159	3.00E-16	217.8	71.2	74.0	PREDICTED: histone H2A.6 isoform 2	gbpln	Vitis vinifera	AT1G51060.1 | Symbols: HTA10 | histone H2A 10 | chr1:18926948-18927443 FORWARD LENGTH=132	73	132	1.00E-18	180.8	64.4	65.8
Rsa1.0_00580.1.g16354.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00580.1.g16355.t1	dbj|BAJ33911.1| unnamed protein product [Thellungiella halophila]	309	487	1.00E-150	157.6	88.7	92.9	unnamed protein product	----	----	AT5G54630.1 | Symbols: | zinc finger protein-related | chr5:22192607-22194260 REVERSE LENGTH=472	309	472	1.00E-151	152.8	88.3	91.9

Rsa1.0_00580.1.g16356.t1	ref|XP_002864348.1| 50S ribosomal protein L24, chloroplast [Arabidopsis lyrata subsp. lyrata] gi|297310183|gb|EFH40607.1| 50S ribosomal protein L24, chloroplast [Arabidopsis lyrata subsp. lyrata]	198	198	1.00E-91	100.0	90.9	96.0	50S ribosomal protein L24, chloroplast	gbpln	Arabidopsis lyrata	AT5G54600.1 | Symbols: | Translation protein SH3-like family protein | chr5:22183046-22184403 FORWARD LENGTH=198	198	198	2.00E-92	100.0	89.4	94.4
Rsa1.0_00580.1.g16357.t1	gb|EOA14610.1| hypothetical protein CARUB_v10027862mg [Capsella rubella]	377	369	1.00E-111	97.9	57.3	72.1	hypothetical protein CARUB_v10027862mg	gbpln	Capsella rubella	AT5G55270.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22419218-22420303 FORWARD LENGTH=361	377	361	1.00E-108	95.8	57.3	70.3
Rsa1.0_00580.1.g16358.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00580.1.g16359.t1	dbj|BAJ34286.1| unnamed protein product [Thellungiella halophila]	310	358	6.00E-56	115.5	33.5	35.2	unnamed protein product	----	----	AT5G60360.2 | Symbols: AALP, ALP | aleurain-like protease | chr5:24280044-24282152 FORWARD LENGTH=357	310	357	4.00E-56	115.2	32.6	34.8
Rsa1.0_00580.1.g16360.t1	gb|AAA81907.1| napin [Brassica napus] gi|468020|gb|AAA81908.1| napin [Brassica napus] gi|45593278|gb|AAS68187.1| napin [Brassica napus var. napus]	175	180	2.00E-76	102.9	84.6	92.6	napin	gbpln	Brassica napus	AT4G27170.1 | Symbols: SESA4, AT2S4 | seed storage albumin 4 | chr4:13613637-13614137 FORWARD LENGTH=166	175	166	9.00E-53	94.9	59.4	73.7
Rsa1.0_00580.1.g16361.t1	ref|NP_200267.1| uncharacterized protein [Arabidopsis thaliana] gi|9758948|dbj|BAB09335.1| unnamed protein product [Arabidopsis thaliana] gi|91805707|gb|ABE65582.1| hypothetical protein At5g54560 [Arabidopsis thaliana] gi|332009127|gb|AED96510.1| uncharacterized protein AT5G54560 [Arabidopsis thaliana]	375	360	2.00E-99	96.0	56.0	68.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54560.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22161134-22162216 FORWARD LENGTH=360	375	360	1.00E-102	96.0	56.0	68.5
Rsa1.0_00580.1.g16362.t2	gb|EOA37834.1| hypothetical protein CARUB_v10011422mg [Capsella rubella]	366	373	1.00E-102	101.9	51.9	65.8	hypothetical protein CARUB_v10011422mg	gbpln	Capsella rubella	AT5G52940.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21472301-21473389 FORWARD LENGTH=362	366	362	1.00E-102	98.9	52.2	63.7
Rsa1.0_00580.1.g16363.t1	ref|XP_002864339.1| hypothetical protein ARALYDRAFT_495534 [Arabidopsis lyrata subsp. lyrata] gi|297310174|gb|EFH40598.1| hypothetical protein ARALYDRAFT_495534 [Arabidopsis lyrata subsp. lyrata]	288	297	1.00E-101	103.1	72.6	83.3	hypothetical protein ARALYDRAFT_495534	gbpln	Arabidopsis lyrata	AT5G54540.1 | Symbols: | Uncharacterised conserved protein (UCP012943) | chr5:22156604-22157857 FORWARD LENGTH=297	288	297	4.00E-97	103.1	71.2	81.9
Rsa1.0_00580.1.g16364.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00581.1.g16365.t2	gb|AAC97237.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	978	889	1.00E-164	90.9	28.0	32.0	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	AT2G31750.1 | Symbols: UGT74D1 | UDP-glucosyl transferase 74D1 | chr2:13497312-13499870 FORWARD LENGTH=456	978	456	1.00E-126	46.6	22.0	23.4
Rsa1.0_00581.1.g16366.t1	ref|XP_002879339.1| hypothetical protein ARALYDRAFT_482098 [Arabidopsis lyrata subsp. lyrata] gi|297325178|gb|EFH55598.1| hypothetical protein ARALYDRAFT_482098 [Arabidopsis lyrata subsp. lyrata]	968	456	0	47.1	42.5	45.2	hypothetical protein ARALYDRAFT_482098	gbpln	Arabidopsis lyrata	AT2G31750.1 | Symbols: UGT74D1 | UDP-glucosyl transferase 74D1 | chr2:13497312-13499870 FORWARD LENGTH=456	968	456	0	47.1	42.3	45.1
Rsa1.0_00581.1.g16367.t1	ref|XP_002879340.1| hypothetical protein ARALYDRAFT_320921 [Arabidopsis lyrata subsp. lyrata] gi|297325179|gb|EFH55599.1| hypothetical protein ARALYDRAFT_320921 [Arabidopsis lyrata subsp. lyrata]	397	528	1.00E-141	133.0	65.0	74.1	hypothetical protein ARALYDRAFT_320921	gbpln	Arabidopsis lyrata	AT2G31770.1 | Symbols: ARI9, ATARI9 | RING/U-box superfamily protein | chr2:13511579-13513550 FORWARD LENGTH=543	397	543	1.00E-138	136.8	64.7	74.1
Rsa1.0_00581.1.g16368.t1	gb|ACR10263.1| UDP-glucosyl transferase 74c1 [Brassica rapa subsp. pekinensis]	547	456	0	83.4	77.9	80.8	UDP-glucosyl transferase 74c1	gbpln	Brassica rapa	AT2G31790.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:13518269-13520167 FORWARD LENGTH=457	547	457	0	83.5	67.8	74.4
Rsa1.0_00581.1.g16369.t1	gb|AAT94403.1| ankyrin protein kinase [Brassica napus]	411	476	0	115.8	87.8	92.2	ankyrin protein kinase	gbpln	Brassica napus	AT2G31800.1 | Symbols: | Integrin-linked protein kinase family | chr2:13520605-13523646 REVERSE LENGTH=476	411	476	0	115.8	88.1	93.7
Rsa1.0_00581.1.g16370.t1	ref|XP_002879344.1| hypothetical protein ARALYDRAFT_482103 [Arabidopsis lyrata subsp. lyrata] gi|297325183|gb|EFH55603.1| hypothetical protein ARALYDRAFT_482103 [Arabidopsis lyrata subsp. lyrata]	524	492	0	93.9	76.5	81.9	hypothetical protein ARALYDRAFT_482103	gbpln	Arabidopsis lyrata	AT2G31810.1 | Symbols: | ACT domain-containing small subunit of acetolactate synthase protein | chr2:13524271-13528246 FORWARD LENGTH=491	524	491	0	93.7	76.0	82.1
Rsa1.0_00581.1.g16371.t8	gb|EOA28988.1| hypothetical protein CARUB_v10025247mg [Capsella rubella]	1223	876	0	71.6	39.2	47.6	hypothetical protein CARUB_v10025247mg	gbpln	Capsella rubella	AT3G25020.1 | Symbols: AtRLP42, RLP42 | receptor like protein 42 | chr3:9116868-9119540 REVERSE LENGTH=890	1223	890	0	72.8	41.3	48.6
Rsa1.0_00581.1.g16372.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00581.1.g16373.t1	ref|NP_180827.1| receptor like protein 23 [Arabidopsis thaliana] gi|2914705|gb|AAC04495.1| putative disease resistance protein [Arabidopsis thaliana] gi|330253621|gb|AEC08715.1| receptor like protein 23 [Arabidopsis thaliana]	886	890	0	100.5	65.1	77.5	receptor like protein 23	gbpln	Arabidopsis thaliana	AT2G32680.1 | Symbols: AtRLP23, RLP23 | receptor like protein 23 | chr2:13859942-13862614 REVERSE LENGTH=890	886	890	0	100.5	65.1	77.5
Rsa1.0_00581.1.g16374.t2	gb|AAD17409.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	672	1347	0	200.4	74.7	83.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	672	1262	1.00E-99	187.8	26.9	41.8
Rsa1.0_00581.1.g16375.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00581.1.g16376.t1	gb|ACB59218.1| leucine-rich repeat family protein [Brassica oleracea]	250	724	4.00E-94	289.6	80.8	85.6	leucine-rich repeat family protein	gbpln	Brassica oleracea	AT3G24900.1 | Symbols: AtRLP39, RLP39 | receptor like protein 39 | chr3:9099183-9101837 REVERSE LENGTH=884	250	884	8.00E-77	353.6	65.6	75.2
Rsa1.0_00581.1.g16377.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	331	1501	2.00E-97	453.5	54.1	67.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	331	1262	2.00E-58	381.3	34.7	46.2
Rsa1.0_00581.1.g16378.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	763	1459	0	191.2	59.9	74.4	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	763	1262	1.00E-102	165.4	25.8	39.1
Rsa1.0_00581.1.g16379.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00581.1.g16380.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00581.1.g16381.t1	ref|NP_850179.1| uncharacterized protein [Arabidopsis thaliana] gi|26452388|dbj|BAC43279.1| unknown protein [Arabidopsis thaliana] gi|28950805|gb|AAO63326.1| At2g31985 [Arabidopsis thaliana] gi|330253524|gb|AEC08618.1| uncharacterized protein AT2G31985 [Arabidopsis thaliana]	241	241	1.00E-129	100.0	90.9	94.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G31985.1 | Symbols: | Protein of unknown function (DUF1264) | chr2:13614086-13615619 REVERSE LENGTH=241	241	241	1.00E-132	100.0	90.9	94.6
Rsa1.0_00581.1.g16382.t1	gb|EOA26764.1| hypothetical protein CARUB_v10022849mg [Capsella rubella]	586	598	0	102.0	91.6	95.2	hypothetical protein CARUB_v10022849mg	gbpln	Capsella rubella	AT2G32010.2 | Symbols: CVL1 | CVP2 like 1 | chr2:13625344-13628081 FORWARD LENGTH=594	586	594	0	101.4	90.3	94.2
Rsa1.0_00582.1.g16383.t1	gb|ABV89649.1| universal stress protein family protein [Brassica rapa]	175	172	5.00E-92	98.3	96.0	97.1	universal stress protein family protein	gbpln	Brassica rapa	AT3G01520.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:208506-209921 FORWARD LENGTH=175	175	175	2.00E-88	100.0	87.4	92.6
Rsa1.0_00582.1.g16384.t1	gb|EOA32918.1| hypothetical protein CARUB_v10016245mg [Capsella rubella]	208	203	1.00E-85	97.6	76.9	86.1	hypothetical protein CARUB_v10016245mg	gbpln	Capsella rubella	AT3G01530.1 | Symbols: ATMYB57, MYB57 | myb domain protein 57 | chr3:210352-211151 REVERSE LENGTH=206	208	206	3.00E-86	99.0	76.9	82.2
Rsa1.0_00582.1.g16385.t1	ref|XP_002882170.1| glycosyl transferase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297328010|gb|EFH58429.1| glycosyl transferase family 17 protein [Arabidopsis lyrata subsp. lyrata]	381	388	0	101.8	84.3	91.3	glycosyl transferase family 17 protein	gbpln	Arabidopsis lyrata	AT3G01620.1 | Symbols: | beta-1,4-N-acetylglucosaminyltransferase family protein | chr3:235327-236729 REVERSE LENGTH=388	381	388	0	101.8	85.6	91.6
Rsa1.0_00582.1.g16386.t9	ref|NP_186815.1| S-adenosylmethionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|6016723|gb|AAF01549.1|AC009325_19 hypothetical protein [Arabidopsis thaliana] gi|38454124|gb|AAR20756.1| At3g01660 [Arabidopsis thaliana] gi|46402482|gb|AAS92343.1| At3g01660 [Arabidopsis thaliana] gi|332640179|gb|AEE73700.1| S-adenosylmethionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana]	280	273	1.00E-135	97.5	83.9	89.6	S-adenosylmethionine-dependent methyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G01660.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:245532-246432 FORWARD LENGTH=273	280	273	1.00E-137	97.5	83.9	89.6
Rsa1.0_00582.1.g16387.t1	gb|AAF01550.1|AC009325_20 unknown protein [Arabidopsis thaliana]	824	846	0	102.7	87.9	94.4	unknown protein	gbpln	Arabidopsis thaliana	AT3G01670.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01680.1); Has 121 Blast hits to 111 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 121; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:247288-250261 FORWARD LENGTH=822	824	822	0	99.8	87.9	94.4

Rsa1.0_00582.1.g16388.t1	ref|NP_186817.1| uncharacterized protein [Arabidopsis thaliana] gi|6016725|gb|AAF01551.1|AC009325_21 unknown protein [Arabidopsis thaliana] gi|30725324|gb|AAP37684.1| At3g01680 [Arabidopsis thaliana] gi|110736167|dbj|BAF00055.1| hypothetical protein [Arabidopsis thaliana] gi|307101698|gb|ADN32814.1| sieve element occlusion b [Arabidopsis thaliana] gi|332640181|gb|AEE73702.1| uncharacterized protein AT3G01680 [Arabidopsis thaliana]	739	740	0	100.1	90.9	95.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01680.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Mediator complex subunit Med28 (InterPro:IPR021640); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01670.1); Has 122 Blast hits to 112 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 122; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:252033-255246 FORWARD LENGTH=740	739	740	0	100.1	90.9	95.8
Rsa1.0_00582.1.g16389.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00582.1.g16390.t1	emb|CAB42531.1| AGP6 protein [Arabidopsis thaliana]	138	150	1.00E-33	108.7	71.0	81.9	AGP6 protein	gbpln	Arabidopsis thaliana	AT5G14380.1 | Symbols: AGP6 | arabinogalactan protein 6 | chr5:4636088-4636540 REVERSE LENGTH=150	138	150	4.00E-35	108.7	69.6	80.4
Rsa1.0_00582.1.g16391.t1	ref|XP_002884262.1| hypothetical protein ARALYDRAFT_896070 [Arabidopsis lyrata subsp. lyrata] gi|297330102|gb|EFH60521.1| hypothetical protein ARALYDRAFT_896070 [Arabidopsis lyrata subsp. lyrata]	129	125	6.00E-35	96.9	71.3	75.2	hypothetical protein ARALYDRAFT_896070	gbpln	Arabidopsis lyrata	AT3G01740.1 | Symbols: | Mitochondrial ribosomal protein L37 | chr3:268118-268498 FORWARD LENGTH=126	129	126	6.00E-36	97.7	69.8	73.6
Rsa1.0_00582.1.g16392.t1	ref|XP_002884261.1| hypothetical protein ARALYDRAFT_896068 [Arabidopsis lyrata subsp. lyrata] gi|297330101|gb|EFH60520.1| hypothetical protein ARALYDRAFT_896068 [Arabidopsis lyrata subsp. lyrata]	371	449	0	121.0	82.7	88.1	hypothetical protein ARALYDRAFT_896068	gbpln	Arabidopsis lyrata	AT1G61270.1 | Symbols: | Transmembrane amino acid transporter family protein | chr1:22599665-22602140 REVERSE LENGTH=451	371	451	0	121.6	81.7	88.9
Rsa1.0_00582.1.g16393.t2	ref|NP_186833.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|75337203|sp|Q9SGI7.1|LYK2_ARATH RecName: Full=Protein LYK2; AltName: Full=LysM domain receptor-like kinase 2; AltName: Full=LysM-containing receptor-like kinase 2; Flags: Precursor gi|6091745|gb|AAF03457.1|AC010797_33 putative protein kinase [Arabidopsis thaliana] gi|332640202|gb|AEE73723.1| protein LYK2 [Arabidopsis thaliana]	866	654	0	75.5	51.4	57.4	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G01840.1 | Symbols: | Protein kinase superfamily protein | chr3:296582-298634 REVERSE LENGTH=654	866	654	0	75.5	51.4	57.4
Rsa1.0_00582.1.g16394.t1	ref|XP_002884255.1| hypothetical protein ARALYDRAFT_896056 [Arabidopsis lyrata subsp. lyrata] gi|297330095|gb|EFH60514.1| hypothetical protein ARALYDRAFT_896056 [Arabidopsis lyrata subsp. lyrata]	591	583	0	98.6	74.3	85.1	hypothetical protein ARALYDRAFT_896056	gbpln	Arabidopsis lyrata	AT3G01870.1 | Symbols: | Plant protein of unknown function (DUF946) | chr3:305276-307027 FORWARD LENGTH=583	591	583	0	98.6	73.1	83.6
Rsa1.0_00582.1.g16395.t1	ref|NP_566155.1| cytochrome P450, family 94, subfamily B, polypeptide 2 [Arabidopsis thaliana] gi|6091730|gb|AAF03442.1|AC010797_18 putative cytochrome P450 [Arabidopsis thaliana] gi|6513941|gb|AAF14845.1|AC011664_27 putative cytochrome P450 [Arabidopsis thaliana] gi|332640210|gb|AEE73731.1| cytochrome P450, family 94, subfamily B, polypeptide 2 [Arabidopsis thaliana]	500	496	0	99.2	81.8	89.0	cytochrome P450, family 94, subfamily B, polypeptide 2	gbpln	Arabidopsis thaliana	AT3G01900.1 | Symbols: CYP94B2 | cytochrome P450, family 94, subfamily B, polypeptide 2 | chr3:312359-313849 REVERSE LENGTH=496	500	496	0	99.2	81.8	89.0
Rsa1.0_00582.1.g16396.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00582.1.g16397.t1	ref|NP_186844.1| uncharacterized protein [Arabidopsis thaliana] gi|6091734|gb|AAF03446.1|AC010797_22 hypothetical protein [Arabidopsis thaliana] gi|6513936|gb|AAF14840.1|AC011664_22 hypothetical protein [Arabidopsis thaliana] gi|26453294|dbj|BAC43720.1| GPI-anchored protein [Arabidopsis thaliana] gi|28416747|gb|AAO42904.1| At3g01950 [Arabidopsis thaliana] gi|332640218|gb|AEE73739.1| uncharacterized protein AT3G01950 [Arabidopsis thaliana]	70	70	1.00E-28	100.0	94.3	98.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01950.1 | Symbols: | Protein of unknown function (DUF 3339) | chr3:324026-324238 FORWARD LENGTH=70	70	70	2.00E-31	100.0	94.3	98.6

Rsa1.0_00582.1.g16398.t2	ref|XP_002886105.1| hypothetical protein ARALYDRAFT_480605 [Arabidopsis lyrata subsp. lyrata] gi|297331945|gb|EFH62364.1| hypothetical protein ARALYDRAFT_480605 [Arabidopsis lyrata subsp. lyrata]	168	414	3.00E-27	246.4	34.5	36.3	hypothetical protein ARALYDRAFT_480605	gbpln	Arabidopsis lyrata	AT2G17220.2 | Symbols: | Protein kinase superfamily protein | chr2:7487866-7489768 REVERSE LENGTH=413	168	413	7.00E-29	245.8	33.9	35.7
Rsa1.0_00582.1.g16399.t1	ref|XP_002882155.1| hypothetical protein ARALYDRAFT_316997 [Arabidopsis lyrata subsp. lyrata] gi|297327995|gb|EFH58414.1| hypothetical protein ARALYDRAFT_316997 [Arabidopsis lyrata subsp. lyrata]	139	138	1.00E-53	99.3	75.5	85.6	hypothetical protein ARALYDRAFT_316997	gbpln	Arabidopsis lyrata	AT3G01960.1 | Symbols: | unknown protein; Has 13 Blast hits to 13 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:324581-325087 REVERSE LENGTH=138	139	138	4.00E-55	99.3	77.0	87.1
Rsa1.0_00582.1.g16400.t1	gb|ACH99806.1| WRKY45 transcription factor [Brassica napus]	228	144	1.00E-71	63.2	61.0	62.3	WRKY45 transcription factor	gbpln	Brassica napus	AT3G01970.1 | Symbols: WRKY45, ATWRKY45 | WRKY DNA-binding protein 45 | chr3:326614-327159 REVERSE LENGTH=147	228	147	3.00E-55	64.5	50.9	53.9
Rsa1.0_00582.1.g16401.t1	ref|NP_188565.1| uncharacterized protein [Arabidopsis thaliana] gi|20260588|gb|AAM13192.1| unknown protein [Arabidopsis thaliana] gi|332642706|gb|AEE76227.1| uncharacterized protein AT3G19340 [Arabidopsis thaliana]	487	487	0	100.0	90.1	95.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G19340.1 | Symbols: | Protein of unknown function (DUF3754) | chr3:6701387-6704071 REVERSE LENGTH=487	487	487	0	100.0	90.1	95.7
Rsa1.0_00582.1.g16402.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	127	329	3.00E-15	259.1	40.9	48.0	unnamed protein product	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	127	256	6.00E-15	201.6	36.2	48.0
Rsa1.0_00582.1.g16403.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00583.1.g16404.t1	gb|EOA36870.1| hypothetical protein CARUB_v10008862mg [Capsella rubella]	520	519	0	99.8	90.6	94.0	hypothetical protein CARUB_v10008862mg	gbpln	Capsella rubella	AT1G27680.1 | Symbols: APL2 | ADPGLC-PPase large subunit | chr1:9631630-9634450 FORWARD LENGTH=518	520	518	0	99.6	89.6	93.7
Rsa1.0_00583.1.g16405.t2	gb|EOA36870.1| hypothetical protein CARUB_v10008862mg [Capsella rubella]	122	519	8.00E-37	425.4	63.1	68.0	hypothetical protein CARUB_v10008862mg	gbpln	Capsella rubella	AT1G27680.1 | Symbols: APL2 | ADPGLC-PPase large subunit | chr1:9631630-9634450 FORWARD LENGTH=518	122	518	2.00E-37	424.6	61.5	66.4
Rsa1.0_00583.1.g16406.t1	ref|XP_002893484.1| hypothetical protein ARALYDRAFT_890303 [Arabidopsis lyrata subsp. lyrata] gi|297339326|gb|EFH69743.1| hypothetical protein ARALYDRAFT_890303 [Arabidopsis lyrata subsp. lyrata]	262	256	7.00E-95	97.7	69.5	79.4	hypothetical protein ARALYDRAFT_890303	gbpln	Arabidopsis lyrata	AT1G27670.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G75360.1); Has 35 Blast hits to 35 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:9627715-9628413 REVERSE LENGTH=232	262	232	8.00E-82	88.5	64.5	73.7
Rsa1.0_00583.1.g16407.t1	ref|XP_002893783.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339625|gb|EFH70042.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	256	276	2.00E-31	107.8	33.6	45.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G03495.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:873804-875025 REVERSE LENGTH=226	256	226	3.00E-23	88.3	28.9	40.2
Rsa1.0_00583.1.g16408.t1	ref|XP_002893783.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339625|gb|EFH70042.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	170	276	1.00E-12	162.4	24.1	32.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321	170	321	5.00E-12	188.8	21.2	36.5
Rsa1.0_00583.1.g16409.t1	ref|NP_568874.2| phototropin 2 [Arabidopsis thaliana] gi|332009618|gb|AED97001.1| phototropin 2 [Arabidopsis thaliana]	193	689	2.00E-17	357.0	29.0	34.2	phototropin 2	gbpln	Arabidopsis thaliana	AT5G58140.4 | Symbols: PHOT2, NPL1 | phototropin 2 | chr5:23524771-23528541 FORWARD LENGTH=689	193	689	8.00E-20	357.0	29.0	34.2
Rsa1.0_00583.1.g16410.t21	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00583.1.g16411.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00583.1.g16412.t1	ref|XP_004230758.1| PREDICTED: polyadenylate-binding protein 2-like [Solanum lycopersicum]	104	643	1.00E-15	618.3	44.2	60.6	PREDICTED: polyadenylate-binding protein 2-like	gbpln	Solanum lycopersicum	AT2G23350.1 | Symbols: PAB4, PABP4 | poly(A) binding protein 4 | chr2:9943209-9946041 FORWARD LENGTH=662	104	662	5.00E-17	636.5	38.5	51.9
Rsa1.0_00583.1.g16413.t1	gb|EOA37527.1| hypothetical protein CARUB_v10011729mg [Capsella rubella]	166	174	6.00E-83	104.8	92.8	95.2	hypothetical protein CARUB_v10011729mg	gbpln	Capsella rubella	AT1G27530.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ubiquitin-conjugating enzyme/RWD-like (InterPro:IPR016135), Ubiquitin-fold modifier-conjugating enzyme 1 (InterPro:IPR014806); Has 269 Blast hits to 269 proteins in 110 species: Archae - 0; Bacteria - 0; Metazoa - 175; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink). | chr1:9562761-9563887 REVERSE LENGTH=174	166	174	3.00E-84	104.8	91.6	94.6

Rsa1.0_00583.1.g16414.t1	ref|XP_002885580.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331420|gb|EFH61839.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	93	252	6.00E-13	271.0	43.0	59.1	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00583.1.g16415.t1	gb|EOA37527.1| hypothetical protein CARUB_v10011729mg [Capsella rubella]	162	174	2.00E-77	107.4	88.9	92.0	hypothetical protein CARUB_v10011729mg	gbpln	Capsella rubella	AT1G27530.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ubiquitin-conjugating enzyme/RWD-like (InterPro:IPR016135), Ubiquitin-fold modifier-conjugating enzyme 1 (InterPro:IPR014806); Has 269 Blast hits to 269 proteins in 110 species: Archae - 0; Bacteria - 0; Metazoa - 175; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink). | chr1:9562761-9563887 REVERSE LENGTH=174	162	174	1.00E-78	107.4	87.7	91.4
Rsa1.0_00583.1.g16416.t1	ref|XP_002890731.1| glycoside hydrolase family 47 protein [Arabidopsis lyrata subsp. lyrata] gi|297336573|gb|EFH66990.1| glycoside hydrolase family 47 protein [Arabidopsis lyrata subsp. lyrata]	585	574	0	98.1	86.0	91.5	glycoside hydrolase family 47 protein	gbpln	Arabidopsis lyrata	AT1G27520.1 | Symbols: | Glycosyl hydrolase family 47 protein | chr1:9558752-9562091 FORWARD LENGTH=574	585	574	0	98.1	85.1	90.6
Rsa1.0_00583.1.g16417.t1	ref|XP_002893471.1| hypothetical protein ARALYDRAFT_472955 [Arabidopsis lyrata subsp. lyrata] gi|297339313|gb|EFH69730.1| hypothetical protein ARALYDRAFT_472955 [Arabidopsis lyrata subsp. lyrata]	663	645	0	97.3	83.0	89.1	hypothetical protein ARALYDRAFT_472955	gbpln	Arabidopsis lyrata	AT1G27500.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:9551629-9553654 REVERSE LENGTH=650	663	650	0	98.0	81.7	89.4
Rsa1.0_00583.1.g16418.t4	ref|NP_174067.2| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] gi|17979117|gb|AAL49816.1| unknown protein [Arabidopsis thaliana] gi|23297582|gb|AAN12900.1| unknown protein [Arabidopsis thaliana] gi|332192715|gb|AEE30836.1| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	863	810	0	93.9	77.6	84.1	transducin family protein / WD-40 repeat family protein	gbpln	Arabidopsis thaliana	AT1G27470.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr1:9540368-9544218 REVERSE LENGTH=810	863	810	0	93.9	77.6	84.1
Rsa1.0_00583.1.g16419.t1	ref|NP_001117365.1| uncharacterized protein [Arabidopsis thaliana] gi|98961611|gb|ABF59135.1| unknown protein [Arabidopsis thaliana] gi|332192714|gb|AEE30835.1| uncharacterized protein AT1G27461 [Arabidopsis thaliana]	363	354	1.00E-148	97.5	77.4	86.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G27461.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:9537948-9539012 REVERSE LENGTH=354	363	354	1.00E-150	97.5	77.4	86.5
Rsa1.0_00583.1.g16420.t6	gb|AAP85303.1| adenine phosphoribosyltransferase [Brassica napus]	292	204	1.00E-85	69.9	57.5	58.2	adenine phosphoribosyltransferase	gbpln	Brassica napus	AT1G27450.1 | Symbols: APT1, ATAPT1 | adenine phosphoribosyl transferase 1 | chr1:9532042-9533807 FORWARD LENGTH=243	292	243	2.00E-86	83.2	55.5	57.2
Rsa1.0_00583.1.g16421.t1	#	#	#	#	#	#	#	-	----	----	AT5G61840.1 | Symbols: GUT1 | Exostosin family protein | chr5:24839365-24841703 REVERSE LENGTH=415	56	415	3.00E-11	741.1	51.8	55.4
Rsa1.0_00583.1.g16422.t1	ref|NP_174060.1| 60S ribosomal protein L17-1 [Arabidopsis thaliana] gi|27734446|sp|Q93VI3.1|RL171_ARATH RecName: Full=60S ribosomal protein L17-1 gi|16226209|gb|AAL16103.1|AF428271_1 At1g27400/F17L21_20 [Arabidopsis thaliana] gi|16226630|gb|AAL16218.1|AF428449_1 At1g27400/F17L21_20 [Arabidopsis thaliana] gi|14335140|gb|AAK59850.1| At1g27400/F17L21_20 [Arabidopsis thaliana] gi|18655347|gb|AAL76129.1| At1g27400/F17L21_20 [Arabidopsis thaliana] gi|21594923|gb|AAM66056.1| putative 60S ribosomal protein L17 [Arabidopsis thaliana] gi|332192704|gb|AEE30825.1| 60S ribosomal protein L17-1 [Arabidopsis thaliana]	176	176	1.00E-98	100.0	98.3	99.4	60S ribosomal protein L17-1	gbpln	Arabidopsis thaliana	AT1G27400.1 | Symbols: | Ribosomal protein L22p/L17e family protein | chr1:9515230-9516725 FORWARD LENGTH=176	176	176	1.00E-101	100.0	98.3	99.4
Rsa1.0_00584.1.g16423.t1	gb|EOA19024.1| hypothetical protein CARUB_v10007676mg [Capsella rubella]	412	365	1.00E-137	88.6	62.9	73.5	hypothetical protein CARUB_v10007676mg	gbpln	Capsella rubella	AT5G40230.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:16079814-16081735 REVERSE LENGTH=370	412	370	1.00E-138	89.8	62.9	73.5

Rsa1.0_00584.1.g16424.t1	ref|XP_002865424.1| hypothetical protein ARALYDRAFT_494656 [Arabidopsis lyrata subsp. lyrata] gi|297311259|gb|EFH41683.1| hypothetical protein ARALYDRAFT_494656 [Arabidopsis lyrata subsp. lyrata]	380	379	1.00E-133	99.7	77.4	85.0	hypothetical protein ARALYDRAFT_494656	gbpln	Arabidopsis lyrata	AT5G43420.1 | Symbols: | RING/U-box superfamily protein | chr5:17451790-17452917 FORWARD LENGTH=375	380	375	1.00E-136	98.7	77.1	84.7
Rsa1.0_00584.1.g16425.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1476	1515	0	102.6	59.1	72.7	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1476	1262	1.00E-107	85.5	13.3	19.6
Rsa1.0_00584.1.g16426.t1	gb|EOA13618.1| hypothetical protein CARUB_v10026685mg [Capsella rubella] gi|482549425|gb|EOA13619.1| hypothetical protein CARUB_v10026685mg [Capsella rubella]	132	353	2.00E-11	267.4	26.5	30.3	hypothetical protein CARUB_v10026685mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00584.1.g16427.t4	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1357	2726	0	200.9	54.5	70.6	disease resistance protein	gbpln	Brassica rapa	AT3G29750.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:11579125-11580600 REVERSE LENGTH=421	1357	421	5.00E-14	31.0	3.5	5.6
Rsa1.0_00584.1.g16428.t2	ref|XP_002863658.1| hypothetical protein ARALYDRAFT_917317 [Arabidopsis lyrata subsp. lyrata] gi|297309493|gb|EFH39917.1| hypothetical protein ARALYDRAFT_917317 [Arabidopsis lyrata subsp. lyrata]	650	657	0	101.1	78.5	87.8	hypothetical protein ARALYDRAFT_917317	gbpln	Arabidopsis lyrata	AT5G43400.1 | Symbols: | Uncharacterised conserved protein UCP015417, vWA | chr5:17426182-17428149 REVERSE LENGTH=655	650	655	0	100.8	77.7	87.5
Rsa1.0_00584.1.g16429.t2	ref|XP_003635668.1| PREDICTED: uncharacterized protein LOC100854178, partial [Vitis vinifera]	235	478	7.00E-33	203.4	35.3	50.6	PREDICTED: uncharacterized protein LOC100854178, partial	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00584.1.g16430.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00584.1.g16431.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00584.1.g16432.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	290	1142	1.00E-62	393.8	43.1	58.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	290	575	3.00E-30	198.3	27.2	47.2
Rsa1.0_00584.1.g16433.t1	ref|XP_002886661.1| hypothetical protein ARALYDRAFT_893587 [Arabidopsis lyrata subsp. lyrata] gi|297332502|gb|EFH62920.1| hypothetical protein ARALYDRAFT_893587 [Arabidopsis lyrata subsp. lyrata]	289	988	6.00E-12	341.9	12.1	15.2	hypothetical protein ARALYDRAFT_893587	gbpln	Arabidopsis lyrata	AT1G59760.1 | Symbols: | RNA helicase, ATP-dependent, SK12/DOB1 protein | chr1:21984571-21990110 REVERSE LENGTH=988	289	988	5.00E-14	341.9	11.8	15.2
Rsa1.0_00585.1.g16434.t1	gb|AAM62487.1| unknown [Arabidopsis thaliana]	70	70	2.00E-21	100.0	85.7	87.1	unknown	gbpln	Arabidopsis thaliana	AT5G24570.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:8405814-8406026 REVERSE LENGTH=70	70	70	1.00E-23	100.0	84.3	85.7
Rsa1.0_00585.1.g16435.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00585.1.g16436.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00585.1.g16437.t1	ref|NP_568449.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|10177858|dbj|BAB11210.1| unnamed protein product [Arabidopsis thaliana] gi|18175601|gb|AAL59894.1| unknown protein [Arabidopsis thaliana] gi|22136850|gb|AAM91769.1| unknown protein [Arabidopsis thaliana] gi|332005944|gb|AED93327.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana]	314	319	1.00E-106	101.6	81.2	86.0	heavy metal transport/detoxification domain-containing protein	gbpln	Arabidopsis thaliana	AT5G24580.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:8410394-8412087 REVERSE LENGTH=319	314	319	1.00E-109	101.6	81.2	86.0
Rsa1.0_00585.1.g16438.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1244	1142	0	91.8	53.0	67.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1244	575	4.00E-80	46.2	14.7	23.3

Rsa1.0_00585.1.g16439.t1	ref|NP_197848.1| uncharacterized protein [Arabidopsis thaliana] gi|10177860|dbj|BAB11212.1| unnamed protein product [Arabidopsis thaliana] gi|48310199|gb|AAT41773.1| At5g24600 [Arabidopsis thaliana] gi|50198891|gb|AAT70465.1| At5g24600 [Arabidopsis thaliana] gi|332005949|gb|AED93332.1| uncharacterized protein AT5G24600 [Arabidopsis thaliana]	245	248	1.00E-124	101.2	90.6	93.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G24600.1 | Symbols: | Protein of unknown function, DUF599 | chr5:8421790-8423342 REVERSE LENGTH=248	245	248	1.00E-126	101.2	90.6	93.9
Rsa1.0_00585.1.g16440.t1	ref|NP_197850.2| pathogenesis-related thaumatin-like protein [Arabidopsis thaliana] gi|193788746|gb|ACF20472.1| At5g24620 [Arabidopsis thaliana] gi|332005952|gb|AED93335.1| pathogenesis-related thaumatin-like protein [Arabidopsis thaliana]	441	420	0	95.2	78.9	84.4	pathogenesis-related thaumatin-like protein	gbpln	Arabidopsis thaliana	AT5G24620.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr5:8430918-8432289 FORWARD LENGTH=420	441	420	0	95.2	78.9	84.4
Rsa1.0_00585.1.g16441.t1	ref|NP_197854.1| response to low sulfur 2 [Arabidopsis thaliana] gi|9759206|dbj|BAB09648.1| unnamed protein product [Arabidopsis thaliana] gi|21555007|gb|AAM63752.1| unknown [Arabidopsis thaliana] gi|26452227|dbj|BAC43201.1| unknown protein [Arabidopsis thaliana] gi|28416793|gb|AAO42927.1| At5g24660 [Arabidopsis thaliana] gi|332005963|gb|AED93346.1| response to low sulfur 2 [Arabidopsis thaliana]	100	94	9.00E-40	94.0	82.0	88.0	response to low sulfur 2	gbpln	Arabidopsis thaliana	AT5G24660.1 | Symbols: LSU2 | response to low sulfur 2 | chr5:8443472-8443756 REVERSE LENGTH=94	100	94	1.00E-42	94.0	82.0	88.0
Rsa1.0_00585.1.g16442.t1	ref|NP_568452.2| sterol glucosyltransferase-like protein [Arabidopsis thaliana] gi|332005971|gb|AED93354.1| sterol glucosyltransferase-like protein [Arabidopsis thaliana]	899	520	0	57.8	45.9	50.5	sterol glucosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G24750.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:8490821-8494536 REVERSE LENGTH=520	899	520	0	57.8	45.9	50.5
Rsa1.0_00585.1.g16443.t1	gb|EOA21357.1| hypothetical protein CARUB_v10001720mg [Capsella rubella]	264	268	9.00E-99	101.5	67.4	79.9	hypothetical protein CARUB_v10001720mg	gbpln	Capsella rubella	AT5G24770.1 | Symbols: VSP2, ATVSP2 | vegetative storage protein 2 | chr5:8500713-8501844 REVERSE LENGTH=265	264	265	9.00E-97	100.4	69.7	82.2
Rsa1.0_00585.1.g16444.t1	gb|EOA21129.1| hypothetical protein CARUB_v10001471mg [Capsella rubella]	291	320	1.00E-125	110.0	85.2	89.7	hypothetical protein CARUB_v10001471mg	gbpln	Capsella rubella	AT5G24800.1 | Symbols: ATBZIP9, BZO2H2, BZIP9 | basic leucine zipper 9 | chr5:8515259-8516541 FORWARD LENGTH=277	291	277	1.00E-127	95.2	81.1	85.6
Rsa1.0_00585.1.g16445.t1	gb|EOA19667.1| hypothetical protein CARUB_v10003319mg [Capsella rubella]	968	1011	0	104.4	88.3	94.2	hypothetical protein CARUB_v10003319mg	gbpln	Capsella rubella	AT5G24810.1 | Symbols: | ABC1 family protein | chr5:8516902-8522616 REVERSE LENGTH=1009	968	1009	0	104.2	86.5	93.6
Rsa1.0_00585.1.g16446.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00586.1.g16447.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00586.1.g16448.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	1651	1072	0	64.9	30.4	40.0	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	1651	289	4.00E-73	17.5	8.2	11.3
Rsa1.0_00586.1.g16449.t1	gb|EOA35811.1| hypothetical protein CARUB_v10021047mg [Capsella rubella]	143	168	3.00E-56	117.5	76.9	85.3	hypothetical protein CARUB_v10021047mg	gbpln	Capsella rubella	AT1G71000.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:26769336-26770111 REVERSE LENGTH=165	143	165	5.00E-57	115.4	76.9	83.2
Rsa1.0_00586.1.g16450.t1	ref|NP_565006.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|21536546|gb|AAM60878.1| unknown [Arabidopsis thaliana] gi|332197026|gb|AEE35147.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	148	135	1.00E-41	91.2	72.3	77.7	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT1G70985.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:26764774-26765181 REVERSE LENGTH=135	148	135	3.00E-44	91.2	72.3	77.7
Rsa1.0_00586.1.g16451.t1	emb|CAN79684.1| hypothetical protein VITISV_003855 [Vitis vinifera]	320	406	7.00E-73	126.9	50.6	62.5	hypothetical protein VITISV_003855	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00586.1.g16452.t1	ref|NP_001077806.1| MLP-like protein 28 [Arabidopsis thaliana] gi|332197002|gb|AEE35123.1| MLP-like protein 28 [Arabidopsis thaliana]	225	201	5.00E-81	89.3	67.1	69.8	MLP-like protein 28	gbpln	Arabidopsis thaliana	AT1G70830.3 | Symbols: MLP28 | MLP-like protein 28 | chr1:26710203-26711395 REVERSE LENGTH=201	225	201	1.00E-83	89.3	67.1	69.8
Rsa1.0_00586.1.g16453.t1	gb|ACG60680.1| unknown protein [Brassica oleracea var. alboglabra]	122	128	1.00E-11	104.9	35.2	55.7	unknown protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00586.1.g16454.t5	gb|EOA33919.1| hypothetical protein CARUB_v10021412mg [Capsella rubella]	326	615	4.00E-28	188.7	25.2	31.0	hypothetical protein CARUB_v10021412mg	gbpln	Capsella rubella	AT1G70820.1 | Symbols: | phosphoglucomutase, putative / glucose phosphomutase, putative | chr1:26705594-26708034 FORWARD LENGTH=615	326	615	1.00E-29	188.7	25.8	31.3
Rsa1.0_00586.1.g16455.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00586.1.g16456.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]		1807	1274	0	70.5	38.7	48.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575		1807	575	5.00E-64	31.8	9.9	14.9
Rsa1.0_00586.1.g16457.t1	dbj|BAJ34604.1| unnamed protein product [Thellungiella halophila]		132	141	4.00E-58	106.8	84.8	91.7	unnamed protein product	----	----	AT1G70780.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23150.1); Has 143 Blast hits to 143 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 143; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26695462-26695975 REVERSE LENGTH=140		132	140	1.00E-58	106.1	82.6	91.7
Rsa1.0_00586.1.g16458.t1	ref|XP_002888794.1| hypothetical protein ARALYDRAFT_476207 [Arabidopsis lyrata subsp. lyrata] gi|297334635|gb|EFH65053.1| hypothetical protein ARALYDRAFT_476207 [Arabidopsis lyrata subsp. lyrata]		602	616	0	102.3	84.9	90.0	hypothetical protein ARALYDRAFT_476207	gbpln	Arabidopsis lyrata	AT1G70770.2 | Symbols: | Protein of unknown function DUF2359, transmembrane | chr1:26688622-26691185 REVERSE LENGTH=610		602	610	0	101.3	83.6	89.5
Rsa1.0_00586.1.g16459.t1	gb|ACG25170.1| hypothetical protein [Zea mays]		193	192	1.00E-98	99.5	91.7	93.3	hypothetical protein	gbenv/gbpln	Zea mays	AT1G70760.1 | Symbols: CRR23 | inorganic carbon transport protein-related | chr1:26687267-26688201 FORWARD LENGTH=191		193	191	3.00E-89	99.0	82.9	87.0
Rsa1.0_00586.1.g16460.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00586.1.g16461.t1	gb|EOA33298.1| hypothetical protein CARUB_v10019836mg [Capsella rubella]		427	776	1.00E-113	181.7	54.6	60.4	hypothetical protein CARUB_v10019836mg	gbpln	Capsella rubella	AT1G70750.1 | Symbols: | Protein of unknown function, DUF593 | chr1:26680728-26683147 REVERSE LENGTH=749		427	749	1.00E-113	175.4	54.8	61.4
Rsa1.0_00587.1.g16462.t2	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]		714	777	5.00E-49	108.8	15.8	23.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#	
Rsa1.0_00587.1.g16463.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00587.1.g16464.t1	gb|EOA19086.1| hypothetical protein CARUB_v10007753mg [Capsella rubella]		170	172	1.00E-67	101.2	73.5	82.4	hypothetical protein CARUB_v10007753mg	gbpln	Capsella rubella	AT5G39720.1 | Symbols: AIG2L | avirulence induced gene 2 like protein | chr5:15899673-15900517 FORWARD LENGTH=165		170	165	6.00E-69	97.1	72.9	81.2
Rsa1.0_00587.1.g16465.t1	ref|XP_002868704.1| EMB2744 [Arabidopsis lyrata subsp. lyrata] gi|297314540|gb|EFH44963.1| EMB2744 [Arabidopsis lyrata subsp. lyrata]		680	710	0	104.4	76.2	87.4	EMB2744	gbpln	Arabidopsis lyrata	AT5G39680.1 | Symbols: EMB2744 | Pentatricopeptide repeat (PPR) superfamily protein | chr5:15884236-15886368 REVERSE LENGTH=710		680	710	0	104.4	75.4	87.2
Rsa1.0_00587.1.g16466.t1	ref|NP_568568.1| putative calcium-binding protein CML45 [Arabidopsis thaliana] gi|75331780|sp|Q93Z27.1|CML45_ARATH RecName: Full=Probable calcium-binding protein CML45; AltName: Full=Calmodulin-like protein 45 gi|16648830|gb|AAL25605.1| AT5g39670/MIJ24_140 [Arabidopsis thaliana] gi|20466131|gb|AAM19987.1| AT5g39670/MIJ24_140 [Arabidopsis thaliana] gi|332007079|gb|AED94462.1| putative calcium-binding protein CML45 [Arabidopsis thaliana]		188	204	2.00E-80	108.5	81.4	89.9	putative calcium-binding protein CML45	gbpln	Arabidopsis thaliana	AT5G39670.1 | Symbols: | Calcium-binding EF-hand family protein | chr5:15883270-15883884 FORWARD LENGTH=204		188	204	7.00E-83	108.5	81.4	89.9
Rsa1.0_00587.1.g16467.t3	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00587.1.g16468.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00587.1.g16469.t1	gb|AAL10495.1| AT5g39660/MIJ24_130 [Arabidopsis thaliana]		413	457	1.00E-126	110.7	69.7	77.5	AT5g39660/MIJ24_130	gbpln	Arabidopsis thaliana	AT5G39660.2 | Symbols: CDF2 | cycling DOF factor 2 | chr5:15878920-15880712 FORWARD LENGTH=457		413	457	1.00E-128	110.7	69.7	77.5
Rsa1.0_00587.1.g16470.t1	gb|AAD29789.1|AF147259_12 contains similarity to a family of Arabidopsis thaliana hypothetical proteins, which have similarity to retrotransposon Athila gi|7267359|emb|CAB81132.1| putative athila transposon protein [Arabidopsis thaliana]		277	683	4.00E-15	246.6	18.8	25.3	contains similarity to a family of Arabidopsis thaliana hypothetical proteins, which have similarity to retrotransposon Athila gi|7267359|emb|CAB81132.1| putative athila transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#	
Rsa1.0_00587.1.g16471.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00587.1.g16472.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00587.1.g16473.t1	dbj|BAA97083.1| unnamed protein product [Arabidopsis thaliana]		257	583	6.00E-11	226.8	14.4	18.7	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#	
Rsa1.0_00587.1.g16474.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	

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<tr><td>Rsa1.0_00587.1.g16476.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00587.1.g16477.t1</td><td>gb|EOA19050.1| hypothetical protein CARUB_v10007711mg [Capsella rubella]</td><td>318</td><td>319</td><td>1.00E-159</td><td>100.3</td><td>86.5</td><td>92.8</td><td>hypothetical protein CARUB_v10007711mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G39580.1 | Symbols: | Peroxidase superfamily protein | chr5:15847281-15849027 REVERSE LENGTH=319</td><td>318</td><td>319</td><td>1.00E-160</td><td>100.3</td><td>85.8</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00588.1.g16478.t2</td><td>gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>361</td><td>1225</td><td>1.00E-54</td><td>339.3</td><td>28.8</td><td>42.7</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G23160.1 | Symbols: | Auxin-responsive GH3 family protein | chr1:8209232-8211325 FORWARD LENGTH=578</td><td>361</td><td>578</td><td>3.00E-34</td><td>160.1</td><td>22.4</td><td>29.6</td></tr>
<tr><td>Rsa1.0_00588.1.g16479.t1</td><td>gb|EOA14421.1| hypothetical protein CARUB_v10027623mg [Capsella rubella]</td><td>669</td><td>672</td><td>0</td><td>100.4</td><td>89.2</td><td>95.5</td><td>hypothetical protein CARUB_v10027623mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G53550.2 | Symbols: YSL3 | YELLOW STRIPE like 3 | chr5:21756081-21758776 FORWARD LENGTH=675</td><td>669</td><td>675</td><td>0</td><td>100.9</td><td>87.6</td><td>93.6</td></tr>
<tr><td>Rsa1.0_00588.1.g16480.t1</td><td>ref|NP_200165.1| vacuolar protein sorting 26A [Arabidopsis thaliana] gi|75171014|sp|Q9FJD0.1|VP26A_ARATH RecName: Full=Vacuolar protein sorting-associated protein 26A; AltName: Full=Vesicle protein sorting 26A gi|9759192|dbj|BAB09729.1| vacuolar sorting protein-like; embryogenesis protein H beta 58-like protein [Arabidopsis thaliana] gi|110735821|dbj|BAE99887.1| vacuolar sorting protein-like [Arabidopsis thaliana] gi|332008990|gb|AED96373.1| vacuolar protein sorting 26A [Arabidopsis thaliana]</td><td>302</td><td>302</td><td>1.00E-168</td><td>100.0</td><td>95.0</td><td>98.0</td><td>vacuolar protein sorting 26A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G53530.1 | Symbols: VPS26A | vacuolar protein sorting 26A | chr5:21746275-21748156 REVERSE LENGTH=302</td><td>302</td><td>302</td><td>1.00E-170</td><td>100.0</td><td>95.0</td><td>98.0</td></tr>
<tr><td>Rsa1.0_00588.1.g16481.t1</td><td>ref|XP_002864248.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310083|gb|EFH40507.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>739</td><td>739</td><td>0</td><td>100.0</td><td>89.4</td><td>96.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G53520.1 | Symbols: ATOPT8, OPT8 | oligopeptide transporter 8 | chr5:21743450-21745981 FORWARD LENGTH=733</td><td>739</td><td>733</td><td>0</td><td>99.2</td><td>88.8</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00588.1.g16482.t1</td><td>gb|EOA14879.1| hypothetical protein CARUB_v10028205mg [Capsella rubella]</td><td>110</td><td>179</td><td>2.00E-17</td><td>162.7</td><td>44.5</td><td>62.7</td><td>hypothetical protein CARUB_v10028205mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G46940.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19058230-19058760 REVERSE LENGTH=176</td><td>110</td><td>176</td><td>2.00E-18</td><td>160.0</td><td>40.0</td><td>57.3</td></tr>
<tr><td>Rsa1.0_00588.1.g16483.t1</td><td>gb|EOA14879.1| hypothetical protein CARUB_v10028205mg [Capsella rubella]</td><td>176</td><td>179</td><td>3.00E-37</td><td>101.7</td><td>47.7</td><td>64.8</td><td>hypothetical protein CARUB_v10028205mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G46950.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19059565-19060089 REVERSE LENGTH=174</td><td>176</td><td>174</td><td>3.00E-38</td><td>98.9</td><td>48.3</td><td>64.8</td></tr>
<tr><td>Rsa1.0_00588.1.g16484.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00588.1.g16485.t1</td><td>ref|NP_200162.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|9759189|dbj|BAB09726.1| unnamed protein product [Arabidopsis thaliana] gi|20268729|gb|AAM14068.1| unknown protein [Arabidopsis thaliana] gi|23296399|gb|AAN13109.1| unknown protein [Arabidopsis thaliana] gi|332008987|gb|AED96370.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]</td><td>737</td><td>654</td><td>0</td><td>88.7</td><td>68.4</td><td>74.6</td><td>transducin/WD40 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G53500.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:21726167-21728524 REVERSE LENGTH=654</td><td>737</td><td>654</td><td>0</td><td>88.7</td><td>68.4</td><td>74.6</td></tr>
<tr><td>Rsa1.0_00588.1.g16486.t1</td><td>gb|AAB94051.1| PAP-specific phosphatase [Arabidopsis thaliana]</td><td>127</td><td>373</td><td>1.00E-25</td><td>293.7</td><td>44.1</td><td>48.0</td><td>PAP-specific phosphatase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G54390.1 | Symbols: AHL, ATAHL, HL | HAL2-like | chr5:22086133-22087586 FORWARD LENGTH=373</td><td>127</td><td>373</td><td>3.00E-28</td><td>293.7</td><td>44.1</td><td>48.0</td></tr>
<tr><td>Rsa1.0_00588.1.g16487.t1</td><td>ref|NP_200159.1| acyl-CoA binding protein 1 [Arabidopsis thaliana] gi|75266075|sp|Q9SM23.2|ACBP1_ARATH RecName: Full=Acyl-CoA-binding domain-containing protein 1; Short=Acyl-CoA binding protein 1 gi|8843776|dbj|BAA97324.1| unnamed protein product [Arabidopsis thaliana] gi|16649023|gb|AAL24363.1| Unknown protein [Arabidopsis thaliana] gi|20260070|gb|AAM13382.1| unknown protein [Arabidopsis thaliana] gi|21284374|gb|AAF08323.2| acyl-CoA binding protein [Arabidopsis thaliana] gi|332008978|gb|AED96361.1| acyl-CoA binding protein 1 [Arabidopsis thaliana]</td><td>341</td><td>338</td><td>1.00E-152</td><td>99.1</td><td>86.8</td><td>92.1</td><td>acyl-CoA binding protein 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G53470.1 | Symbols: ACBP1, ACBP | acyl-CoA binding protein 1 | chr5:21710497-21712391 FORWARD LENGTH=338</td><td>341</td><td>338</td><td>1.00E-155</td><td>99.1</td><td>86.8</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00588.1.g16488.t1</td><td>gb|EOA14610.1| hypothetical protein CARUB_v10027862mg [Capsella rubella]</td><td>282</td><td>369</td><td>1.00E-65</td><td>130.9</td><td>48.9</td><td>57.8</td><td>hypothetical protein CARUB_v10027862mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G54550.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22158401-22159480 FORWARD LENGTH=359</td><td>282</td><td>359</td><td>9.00E-67</td><td>127.3</td><td>46.1</td><td>55.0</td></tr>
<tr><td>Rsa1.0_00588.1.g16489.t1</td><td>gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>487</td><td>1352</td><td>1.00E-117</td><td>277.6</td><td>46.8</td><td>64.7</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>487</td><td>746</td><td>2.00E-58</td><td>153.2</td><td>27.3</td><td>38.0</td></tr>
<tr><td>Rsa1.0_00588.1.g16490.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00588.1.g16491.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00589.1.g16492.t1	gb|EOA13893.1| hypothetical protein CARUB_v10027002mg [Capsella rubella]	147	247	7.00E-17	168.0	34.0	44.2	hypothetical protein CARUB_v10027002mg	gbpln	Capsella rubella	AT1G73490.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:27633496-27634867 REVERSE LENGTH=259	147	259	3.00E-16	176.2	38.8	57.1
Rsa1.0_00589.1.g16493.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00589.1.g16494.t1	gb|EOA29053.1| hypothetical protein CARUB_v10025307mg [Capsella rubella]	207	207	1.00E-103	100.0	93.2	96.6	hypothetical protein CARUB_v10025307mg	gbpln	Capsella rubella	AT2G38310.1 | Symbols: PYL4, RCAR10 | PYR1-like 4 | chr2:16050251-16050874 FORWARD LENGTH=207	207	207	1.00E-106	100.0	92.8	96.6
Rsa1.0_00589.1.g16495.t1	ref|NP_198523.1| uncharacterized protein [Arabidopsis thaliana] gi|10177986|dbj|BAB11359.1| unnamed protein product [Arabidopsis thaliana] gi|34365659|gb|AAQ65141.1| At5g37070 [Arabidopsis thaliana] gi|51970366|dbj|BAD43875.1| putative protein [Arabidopsis thaliana] gi|51971132|dbj|BAD44258.1| putative protein [Arabidopsis thaliana] gi|332006761|gb|AED94144.1| uncharacterized protein AT5G37070 [Arabidopsis thaliana]	121	170	2.00E-61	140.5	95.9	97.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G37070.1 | Symbols: | Protein of unknown function, DUF538 | chr5:14651091-14652147 FORWARD LENGTH=170	121	170	4.00E-64	140.5	95.9	97.5
Rsa1.0_00589.1.g16496.t1	dbj|BAB11167.1| 40S ribosomal protein S4 [Arabidopsis thaliana]	270	263	1.00E-149	97.4	94.4	97.0	40S ribosomal protein S4	gbpln	Arabidopsis thaliana	AT2G17360.1 | Symbols: | Ribosomal protein S4 (RPS4A) family protein | chr2:7546598-7548138 FORWARD LENGTH=261	270	261	1.00E-150	96.7	94.1	95.9
Rsa1.0_00589.1.g16497.t1	gb|EOA33218.1| hypothetical protein CARUB_v10020320mg [Capsella rubella]	80	432	2.00E-23	540.0	67.5	72.5	hypothetical protein CARUB_v10020320mg	gbpln	Capsella rubella	AT1G20610.1 | Symbols: CYCB2;3 | Cyclin B2;3 | chr1:7135073-7137273 REVERSE LENGTH=429	80	429	1.00E-24	536.3	61.3	75.0
Rsa1.0_00589.1.g16498.t1	dbj|BAJ34198.1| unnamed protein product [Thellungiella halophila]	179	958	4.00E-85	535.2	83.8	92.7	unnamed protein product	----	----	AT3G51770.2 | Symbols: ETO1 | tetratricopeptide repeat (TPR)-containing protein | chr3:19200328-19203998 REVERSE LENGTH=959	179	959	1.00E-85	535.8	82.1	91.6
Rsa1.0_00589.1.g16499.t1	gb|ABD64955.1| hypothetical protein 25.t00048 [Brassica oleracea]	239	339	1.00E-108	141.8	79.9	85.4	hypothetical protein 25.t00048	gbpln	Brassica oleracea	AT2G38255.1 | Symbols: | Protein of Unknown Function (DUF239) | chr2:16021750-16024825 REVERSE LENGTH=333	239	333	6.00E-80	139.3	61.1	74.9
Rsa1.0_00589.1.g16500.t1	ref|NP_001030839.5| tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana] gi|332645320|gb|AEE78841.1| tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	885	959	0	108.4	83.5	91.1	tetratricopeptide repeat (TPR)-containing protein	gbpln	Arabidopsis thaliana	AT3G51770.2 | Symbols: ETO1 | tetratricopeptide repeat (TPR)-containing protein | chr3:19200328-19203998 REVERSE LENGTH=959	885	959	0	108.4	83.5	91.1
Rsa1.0_00589.1.g16501.t1	ref|NP_181364.2| myb-like HTH transcriptional regulator-like protein [Arabidopsis thaliana] gi|26450454|dbj|BAC42341.1| unknown protein [Arabidopsis thaliana] gi|28827324|gb|AAO50506.1| unknown protein [Arabidopsis thaliana] gi|330254426|gb|AEC09520.1| myb-like HTH transcriptional regulator-like protein [Arabidopsis thaliana]	342	340	1.00E-138	99.4	81.6	88.0	myb-like HTH transcriptional regulator-like protein	gbpln	Arabidopsis thaliana	AT2G38300.1 | Symbols: | myb-like HTH transcriptional regulator family protein | chr2:16044175-16045679 REVERSE LENGTH=340	342	340	1.00E-140	99.4	81.6	88.0
Rsa1.0_00589.1.g16502.t1	dbj|BAJ33778.1| unnamed protein product [Thellungiella halophila]	489	490	0	100.2	92.4	95.5	unnamed protein product	----	----	AT2G38290.1 | Symbols: ATAMT2, AMT2;1, AMT2 | ammonium transporter 2 | chr2:16039672-16042291 REVERSE LENGTH=475	489	475	0	97.1	89.2	93.7
Rsa1.0_00589.1.g16503.t1	ref|NP_565886.1| AMP deaminase [Arabidopsis thaliana] gi|30687456|ref|NP_850294.1| AMP deaminase [Arabidopsis thaliana] gi|75223196|sp|O80452.2|AMPD_ARATH RecName: Full=AMP deaminase; Short=AtAMPD; AltName: Full=Protein EMBRYONIC FACTOR 1 gi|15810525|gb|AAL07150.1| putative AMP deaminase [Arabidopsis thaliana] gi|20196986|gb|AAC27176.2| putative AMP deaminase [Arabidopsis thaliana] gi|22136884|gb|AAM91786.1| putative AMP deaminase [Arabidopsis thaliana] gi|330254422|gb|AEC09516.1| AMP deaminase [Arabidopsis thaliana] gi|330254423|gb|AEC09517.1| AMP deaminase [Arabidopsis thaliana]	865	839	0	97.0	91.7	93.8	AMP deaminase	gbpln	Arabidopsis thaliana	AT2G38280.2 | Symbols: FAC1, ATAMPD | AMP deaminase, putative / myoadenylate deaminase, putative | chr2:16033767-16038793 REVERSE LENGTH=839	865	839	0	97.0	91.7	93.8
Rsa1.0_00589.1.g16504.t1	ref|XP_002879733.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325572|gb|EFH55992.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	294	291	1.00E-104	99.0	81.3	87.1	predicted protein	gbpln	Arabidopsis lyrata	AT2G38250.1 | Symbols: | Homeodomain-like superfamily protein | chr2:16018384-16019500 FORWARD LENGTH=289	294	289	3.00E-98	98.3	81.6	87.4

Rsa1.0_00589.1.g16505.t2	ref|NP_565884.2| RING-finger domain-containing protein [Arabidopsis thaliana] gi|42571115|ref|NP_973631.1| RING-finger domain-containing protein [Arabidopsis thaliana] gi|110736245|dbj|BAF00093.1| hypothetical protein [Arabidopsis thaliana] gi|330254409|gb|AEC09503.1| RING-finger domain-containing protein [Arabidopsis thaliana] gi|330254410|gb|AEC09504.1| RING-finger domain-containing protein [Arabidopsis thaliana]	315	441	9.00E-85	140.0	54.9	70.2	RING-finger domain-containing protein	gbpln	Arabidopsis thaliana	AT2G38185.2 | Symbols: | RING/U-box superfamily protein | chr2:16000155-16002699 FORWARD LENGTH=441	315	441	2.00E-87	140.0	54.9	70.2
Rsa1.0_00589.1.g16506.t5	ref|NP_565877.1| Yos1-like protein [Arabidopsis thaliana] gi|297827347|ref|XP_002881556.1| hypothetical protein ARALYDRAFT_902987 [Arabidopsis lyrata subsp. lyrata] gi|21536714|gb|AAM61046.1| unknown [Arabidopsis thaliana] gi|62319249|dbj|BAD94470.1| hypothetical protein [Arabidopsis thaliana] gi|88010893|gb|ABD38869.1| At2g37975 [Arabidopsis thaliana] gi|297327395|gb|EFH57815.1| hypothetical protein ARALYDRAFT_902987 [Arabidopsis lyrata subsp. lyrata] gi|330254379|gb|AEC09473.1| Yos1-like protein [Arabidopsis thaliana]	78	78	2.00E-36	100.0	96.2	98.7	Yos1-like protein	gbpln	Arabidopsis lyrata	AT2G37975.1 | Symbols: | Yos1-like protein | chr2:15891900-15892136 REVERSE LENGTH=78	78	78	4.00E-39	100.0	96.2	98.7
Rsa1.0_00589.1.g16507.t1	gb|AAK43920.1|AF370601_1 Unknown protein [Arabidopsis thaliana] gi|15451064|gb|AAK96803.1| Unknown protein [Arabidopsis thaliana] gi|20148421|gb|AAM10101.1| unknown protein [Arabidopsis thaliana]	202	215	1.00E-91	106.4	85.1	92.1	Unknown protein	gbpln	Arabidopsis thaliana	AT2G37970.1 | Symbols: SOUL-1 | SOUL heme-binding family protein | chr2:15891027-15891704 FORWARD LENGTH=225	202	225	4.00E-94	111.4	85.1	92.1
Rsa1.0_00589.1.g16508.t1	ref|XP_002881555.1| hypothetical protein ARALYDRAFT_902985 [Arabidopsis lyrata subsp. lyrata] gi|297327394|gb|EFH57814.1| hypothetical protein ARALYDRAFT_902985 [Arabidopsis lyrata subsp. lyrata]	409	483	1.00E-141	118.1	67.7	78.0	hypothetical protein ARALYDRAFT_902985	gbpln	Arabidopsis lyrata	AT2G37960.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54060.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:15886962-15889180 REVERSE LENGTH=480	409	480	1.00E-138	117.4	65.5	77.5
Rsa1.0_00589.1.g16509.t1	ref|XP_002881554.1| hypothetical protein ARALYDRAFT_482801 [Arabidopsis lyrata subsp. lyrata] gi|297327393|gb|EFH57813.1| hypothetical protein ARALYDRAFT_482801 [Arabidopsis lyrata subsp. lyrata]	212	207	5.00E-89	97.6	77.8	87.7	hypothetical protein ARALYDRAFT_482801	gbpln	Arabidopsis lyrata	AT2G37950.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:15882536-15883665 REVERSE LENGTH=207	212	207	2.00E-88	97.6	78.8	86.8
Rsa1.0_00589.1.g16510.t1	ref|XP_002879716.1| hypothetical protein ARALYDRAFT_482800 [Arabidopsis lyrata subsp. lyrata] gi|297325555|gb|EFH55975.1| hypothetical protein ARALYDRAFT_482800 [Arabidopsis lyrata subsp. lyrata]	305	305	1.00E-170	100.0	94.4	96.7	hypothetical protein ARALYDRAFT_482800	gbpln	Arabidopsis lyrata	AT2G37940.1 | Symbols: AtIPCS2 | Arabidopsis Inositol phosphorylceramide synthase 2 | chr2:15877169-15879411 FORWARD LENGTH=305	305	305	1.00E-172	100.0	94.1	96.7
Rsa1.0_00589.1.g16511.t1	ref|XP_002879715.1| hypothetical protein ARALYDRAFT_345557 [Arabidopsis lyrata subsp. lyrata] gi|297325554|gb|EFH55974.1| hypothetical protein ARALYDRAFT_345557 [Arabidopsis lyrata subsp. lyrata]	290	574	1.00E-109	197.9	72.1	84.1	hypothetical protein ARALYDRAFT_345557	gbpln	Arabidopsis lyrata	AT2G37930.1 | Symbols: | Protein of unknown function (DUF3527) | chr2:15873284-15874770 FORWARD LENGTH=467	290	467	1.00E-110	161.0	70.3	82.1
Rsa1.0_00589.1.g16512.t1	gb|EOA28075.1| hypothetical protein CARUB_v10024256mg [Capsella rubella]	150	149	3.00E-60	99.3	82.7	87.3	hypothetical protein CARUB_v10024256mg	gbpln	Capsella rubella	AT2G37925.1 | Symbols: COPT4 | copper transporter 4 | chr2:15870258-15870695 REVERSE LENGTH=145	150	145	7.00E-56	96.7	76.7	81.3
Rsa1.0_00589.1.g16513.t1	gb|EOA26793.1| hypothetical protein CARUB_v10022888mg [Capsella rubella]	583	583	0	100.0	79.8	88.5	hypothetical protein CARUB_v10022888mg	gbpln	Capsella rubella	AT2G37900.1 | Symbols: | Major facilitator superfamily protein | chr2:15864396-15866408 REVERSE LENGTH=575	583	575	0	98.6	78.7	87.7

<table>
<tr><td>Rsa1.0_00589.1.g16514.t1</td><td>ref|NP_565872.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] gi|15451110|gb|AAK96826.1| Unknown protein [Arabidopsis thaliana] gi|18377476|gb|AAL66904.1| unknown protein [Arabidopsis thaliana] gi|330254366|gb|AEC09460.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]</td><td>176</td><td>115</td><td>1.00E-45</td><td>65.3</td><td>52.8</td><td>55.1</td><td>protease inhibitor/seed storage/lipid transfer protein (LTP) family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G37870.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr2:15859280-15859723 FORWARD LENGTH=115</td><td>176</td><td>115</td><td>5.00E-48</td><td>65.3</td><td>52.8</td><td>55.1</td></tr>
<tr><td>Rsa1.0_00589.1.g16515.t1</td><td>ref|XP_002879711.1| hypothetical protein ARALYDRAFT_482793 [Arabidopsis lyrata subsp. lyrata] gi|297325550|gb|EFH55970.1| hypothetical protein ARALYDRAFT_482793 [Arabidopsis lyrata subsp. lyrata]</td><td>457</td><td>431</td><td>1.00E-178</td><td>94.3</td><td>75.5</td><td>81.8</td><td>hypothetical protein ARALYDRAFT_482793</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G37860.3 | Symbols: LCD1 | Protein of unknown function (DUF3411) | chr2:15856952-15858793 FORWARD LENGTH=432</td><td>457</td><td>432</td><td>1.00E-177</td><td>94.5</td><td>74.6</td><td>80.7</td></tr>
<tr><td>Rsa1.0_00589.1.g16516.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00589.1.g16517.t1</td><td>gb|EOA28788.1| hypothetical protein CARUB_v10025020mg [Capsella rubella]</td><td>302</td><td>286</td><td>1.00E-131</td><td>94.7</td><td>79.8</td><td>86.4</td><td>hypothetical protein CARUB_v10025020mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G37820.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:15847541-15848413 FORWARD LENGTH=290</td><td>302</td><td>290</td><td>1.00E-131</td><td>96.0</td><td>77.2</td><td>85.4</td></tr>
<tr><td>Rsa1.0_00589.1.g16518.t1</td><td>ref|NP_181315.2| NAD(P)-linked oxidoreductase-like protein [Arabidopsis thaliana] gi|75243290|sp|Q84TF0.1|AKRCA_ARATH RecName: Full=Aldo-keto reductase family 4 member C10 gi|29028836|gb|AAO64797.1| At2g37790 [Arabidopsis thaliana] gi|110742937|dbj|BAE99364.1| putative alcohol dehydrogenase [Arabidopsis thaliana] gi|111182167|gb|ABH07516.1| aldo-keto reductase [Arabidopsis thaliana] gi|330254357|gb|AEC09451.1| aldo-keto reductase family 4 member C10 [Arabidopsis thaliana]</td><td>314</td><td>314</td><td>1.00E-173</td><td>100.0</td><td>93.9</td><td>97.1</td><td>NAD(P)-linked oxidoreductase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G37790.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr2:15838838-15840752 FORWARD LENGTH=314</td><td>314</td><td>314</td><td>1.00E-176</td><td>100.0</td><td>93.9</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00589.1.g16519.t1</td><td>gb|EOA29194.1| hypothetical protein CARUB_v10025466mg [Capsella rubella]</td><td>226</td><td>182</td><td>4.00E-63</td><td>80.5</td><td>54.9</td><td>61.5</td><td>hypothetical protein CARUB_v10025466mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G37780.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:15837442-15838302 REVERSE LENGTH=286</td><td>226</td><td>286</td><td>2.00E-58</td><td>126.5</td><td>49.6</td><td>59.7</td></tr>
<tr><td>Rsa1.0_00589.1.g16520.t1</td><td>dbj|BAJ33839.1| unnamed protein product [Thellungiella halophila]</td><td>313</td><td>315</td><td>1.00E-157</td><td>100.6</td><td>85.3</td><td>92.0</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT2G37770.2 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr2:15834888-15836659 FORWARD LENGTH=315</td><td>313</td><td>315</td><td>1.00E-159</td><td>100.6</td><td>84.0</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00589.1.g16521.t1</td><td>dbj|BAJ33839.1| unnamed protein product [Thellungiella halophila]</td><td>315</td><td>315</td><td>1.00E-172</td><td>100.0</td><td>93.0</td><td>96.5</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT2G37770.2 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr2:15834888-15836659 FORWARD LENGTH=315</td><td>315</td><td>315</td><td>1.00E-170</td><td>100.0</td><td>89.8</td><td>95.6</td></tr>
<tr><td>Rsa1.0_00589.1.g16522.t1</td><td>ref|XP_002879706.1| hypothetical protein ARALYDRAFT_482777 [Arabidopsis lyrata subsp. lyrata] gi|297325545|gb|EFH55965.1| hypothetical protein ARALYDRAFT_482777 [Arabidopsis lyrata subsp. lyrata]</td><td>80</td><td>81</td><td>6.00E-17</td><td>101.3</td><td>70.0</td><td>82.5</td><td>hypothetical protein ARALYDRAFT_482777</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G37750.1 | Symbols: | unknown protein; Has 21 Blast hits to 21 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15831017-15831265 FORWARD LENGTH=82</td><td>80</td><td>82</td><td>2.00E-18</td><td>102.5</td><td>66.3</td><td>81.3</td></tr>
<tr><td>Rsa1.0_00589.1.g16523.t1</td><td>ref|NP_181310.1| zinc-finger protein 10 [Arabidopsis thaliana] gi|3236256|gb|AAC23644.1| putative C2H2-type zinc finger protein [Arabidopsis thaliana] gi|330254347|gb|AEC09441.1| zinc-finger protein 10 [Arabidopsis thaliana]</td><td>291</td><td>304</td><td>1.00E-102</td><td>104.5</td><td>72.9</td><td>79.7</td><td>zinc-finger protein 10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G37740.1 | Symbols: ATZFP10, ZFP10 | zinc-finger protein 10 | chr2:15827706-15828620 REVERSE LENGTH=304</td><td>291</td><td>304</td><td>1.00E-105</td><td>104.5</td><td>72.9</td><td>79.7</td></tr>
<tr><td>Rsa1.0_00590.1.g16524.t1</td><td>gb|EOA36913.1| hypothetical protein CARUB_v10011480mg [Capsella rubella]</td><td>104</td><td>527</td><td>8.00E-43</td><td>506.7</td><td>76.0</td><td>90.4</td><td>hypothetical protein CARUB_v10011480mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30720.1 | Symbols: | FAD-binding Berberine family protein | chr1:10898197-10899780 FORWARD LENGTH=527</td><td>104</td><td>527</td><td>2.00E-45</td><td>506.7</td><td>77.9</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00590.1.g16525.t1</td><td>ref|NP_174363.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana] gi|16323167|gb|AAL15318.1| At1g30760/T5I8_22 [Arabidopsis thaliana] gi|28416457|gb|AAO42759.1| At1g30760/T5I8_22 [Arabidopsis thaliana] gi|332193149|gb|AEE31270.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana]</td><td>635</td><td>534</td><td>0</td><td>84.1</td><td>74.8</td><td>79.1</td><td>FAD-binding and BBE domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30760.1 | Symbols: | FAD-binding Berberine family protein | chr1:10918321-10920441 FORWARD LENGTH=534</td><td>635</td><td>534</td><td>0</td><td>84.1</td><td>74.8</td><td>79.1</td></tr>
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Rsa1.0_00590.1.g16526.t2	ref|XP_002893649.1| hypothetical protein ARALYDRAFT_473316 [Arabidopsis lyrata subsp. lyrata] gi|297339491|gb|EFH69908.1| hypothetical protein ARALYDRAFT_473316 [Arabidopsis lyrata subsp. lyrata]	602	600	0	99.7	92.4	95.7	hypothetical protein ARALYDRAFT_473316	gbpln	Arabidopsis lyrata	AT1G30820.1 | Symbols: | CTP synthase family protein | chr1:10945251-10948825 REVERSE LENGTH=600	602	600	0	99.7	90.7	94.5
Rsa1.0_00590.1.g16527.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	813	1529	0	188.1	45.4	63.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	813	746	2.00E-68	91.8	17.5	23.7
Rsa1.0_00590.1.g16528.t1	gb|AAC63678.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	714	1216	1.00E-173	170.3	45.1	64.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	714	746	4.00E-78	104.5	22.5	31.7
Rsa1.0_00590.1.g16529.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00590.1.g16530.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00591.1.g16531.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00591.1.g16532.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00591.1.g16533.t1	emb|CAD48302.1| MADS-box protein AGL3-a [Brassica oleracea var. botrytis]	263	256	1.00E-132	97.3	86.3	92.8	MADS-box protein AGL3-a	gbpln	Brassica oleracea	AT2G03710.2 | Symbols: SEP4, AGL3 | K-box region and MADS-box transcription factor family protein | chr2:1129622-1131628 FORWARD LENGTH=257	263	257	1.00E-128	97.7	87.5	92.8
Rsa1.0_00591.1.g16534.t1	ref|NP_178465.1| ubiquinone biosynthesis protein COQ4-like protein [Arabidopsis thaliana] gi|24211606|sp|Q9ZPR0.1|COQ4_ARATH RecName: Full=Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial; AltName: Full=Coenzyme Q biosynthesis protein 4 homolog; Flags: Precursor gi|4406761|gb|AAD20072.1| putative ubiquinone biosynthesis protein [Arabidopsis thaliana] gi|17473563|gb|AAL38257.1| putative ubiquinone biosynthesis protein [Arabidopsis thaliana] gi|21386913|gb|AAM47860.1| putative ubiquinone biosynthesis protein [Arabidopsis thaliana] gi|21553964|gb|AAM63045.1| putative ubiquinone biosynthesis protein [Arabidopsis thaliana] gi|330250643|gb|AEC05737.1| ubiquinone biosynthesis protein COQ4-like protein [Arabidopsis thaliana]	226	226	1.00E-125	100.0	95.1	97.8	ubiquinone biosynthesis protein COQ4-like protein	gbpln	Arabidopsis thaliana	AT2G03690.1 | Symbols: | coenzyme Q biosynthesis Coq4 family protein / ubiquinone biosynthesis Coq4 family protein | chr2:1122122-1123011 REVERSE LENGTH=226	226	226	1.00E-128	100.0	95.1	97.8
Rsa1.0_00591.1.g16535.t1	gb|EOA24844.1| hypothetical protein CARUB_v10018134mg, partial [Capsella rubella]	110	169	2.00E-34	153.6	82.7	86.4	hypothetical protein CARUB_v10018134mg, partial	gbpln	Capsella rubella	AT2G03680.2 | Symbols: SPR1, SKU6 | spiral1 | chr2:1121398-1121850 FORWARD LENGTH=119	110	119	2.00E-36	108.2	80.0	82.7
Rsa1.0_00591.1.g16536.t1	ref|XP_002867135.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312971|gb|EFH43394.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	480	482	0	100.4	83.5	90.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G34131.1 | Symbols: UGT73B3 | UDP-glucosyl transferase 73B3 | chr4:16343268-16344713 REVERSE LENGTH=481	480	481	0	100.2	81.7	88.5
Rsa1.0_00591.1.g16537.t1	ref|XP_002867135.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312971|gb|EFH43394.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	480	482	0	100.4	82.9	90.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G34131.1 | Symbols: UGT73B3 | UDP-glucosyl transferase 73B3 | chr4:16343268-16344713 REVERSE LENGTH=481	480	481	0	100.2	80.4	87.7
Rsa1.0_00591.1.g16538.t1	ref|NP_565303.1| ureide permease 1 [Arabidopsis thaliana] gi|68566149|sp|Q9ZPR7.1|UPS1_ARATH RecName: Full=Ureide permease 1; Short=AtUPS1 gi|4406756|gb|AAD20067.1| expressed protein [Arabidopsis thaliana] gi|21554091|gb|AAM63172.1| putative integral membrane protein [Arabidopsis thaliana] gi|115646808|gb|ABJ17125.1| At2g03590 [Arabidopsis thaliana] gi|330250624|gb|AEC05718.1| ureide permease 1 [Arabidopsis thaliana]	390	390	0	100.0	93.8	97.2	ureide permease 1	gbpln	Arabidopsis thaliana	AT2G03590.1 | Symbols: ATUPS1, UPS1 | ureide permease 1 | chr2:1095129-1096711 FORWARD LENGTH=390	390	390	0	100.0	93.8	97.2
Rsa1.0_00591.1.g16539.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1708	1307	0	76.5	44.3	56.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT2G03510.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr2:1066717-1068934 FORWARD LENGTH=356	1708	356	0	20.8	17.7	18.9

Rsa1.0_00591.1.g16540.t1	ref|XP_002875207.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297321045|gb|EFH51466.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	423	432	0	102.1	86.3	90.3	myb family transcription factor	gbpln	Arabidopsis lyrata	AT2G03500.1 | Symbols: | Homeodomain-like superfamily protein | chr2:1059926-1062259 FORWARD LENGTH=432	423	432	0	102.1	86.5	89.8
Rsa1.0_00592.1.g16541.t1	gb|ACJ11252.1| epithiospecifier protein [Brassica rapa subsp. pekinensis]	135	343	7.00E-23	254.1	40.7	44.4	epithiospecifier protein	gbpln	Brassica rapa	AT5G44450.1 | Symbols: | methyltransferases | chr5:17914360-17916017 REVERSE LENGTH=334	135	334	4.00E-18	247.4	29.6	31.1
Rsa1.0_00592.1.g16542.t1	ref|XP_002865365.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311200|gb|EFH41624.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	379	412	0	108.7	94.7	97.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G44480.1 | Symbols: DUR | NAD(P)-binding Rossmann-fold superfamily protein | chr5:17921515-17923643 FORWARD LENGTH=436	379	436	0	115.0	94.5	97.1
Rsa1.0_00592.1.g16543.t1	gb|EOA13806.1| hypothetical protein CARUB_v10026901mg [Capsella rubella]	289	289	1.00E-140	100.0	84.8	93.4	hypothetical protein CARUB_v10026901mg	gbpln	Capsella rubella	AT5G44520.1 | Symbols: | NagB/RpiA/CoA transferase-like superfamily protein | chr5:17934610-17936441 REVERSE LENGTH=296	289	296	1.00E-130	102.4	79.6	88.6
Rsa1.0_00592.1.g16544.t1	gb|EOA14555.1| hypothetical protein CARUB_v10027793mg [Capsella rubella]	862	845	0	98.0	84.1	91.9	hypothetical protein CARUB_v10027793mg	gbpln	Capsella rubella	AT5G44530.1 | Symbols: | Subtilase family protein | chr5:17937931-17941193 FORWARD LENGTH=840	862	840	0	97.4	83.3	90.5
Rsa1.0_00592.1.g16545.t1	emb|CAA50331.1| SaTAP 44 [Sinapis alba]	116	115	2.00E-49	99.1	86.2	91.4	SaTAP 44	gbpln	Sinapis alba	AT5G44540.1 | Symbols: | Tapetum specific protein TAP35/TAP44 | chr5:17941287-17941646 REVERSE LENGTH=119	116	119	3.00E-34	102.6	75.9	82.8
Rsa1.0_00592.1.g16546.t1	ref|NP_199268.1| uncharacterized protein [Arabidopsis thaliana] gi|75170734|sp|Q9FI10.1|CSPLW_ARATH RecName: Full=CASP-like protein At5g44550 gi|9758708|dbj|BAB09162.1| unnamed protein product [Arabidopsis thaliana] gi|17473557|gb|AAL38255.1| unknown protein [Arabidopsis thaliana] gi|21386917|gb|AAM47862.1| unknown protein [Arabidopsis thaliana] gi|332007739|gb|AED95122.1| uncharacterized protein AT5G44550 [Arabidopsis thaliana]	199	197	2.00E-90	99.0	88.9	93.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G44550.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr5:17942100-17943174 REVERSE LENGTH=197	199	197	8.00E-93	99.0	88.9	93.5
Rsa1.0_00592.1.g16547.t1	gb|ADK63407.1| zinc finger protein [Brassica rapa]	162	191	8.00E-57	117.9	77.2	83.3	zinc finger protein	gbpln	Brassica rapa	AT4G20380.7 | Symbols: LSD1 | LSD1 zinc finger family protein | chr4:11005012-11006438 FORWARD LENGTH=189	162	189	8.00E-53	116.7	72.2	79.6
Rsa1.0_00592.1.g16548.t1	ref|XP_002872140.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata] gi|297317977|gb|EFH48399.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata]	496	496	0	100.0	79.0	89.9	CYP71B11	gbpln	Arabidopsis lyrata	AT5G25120.1 | Symbols: CYP71B11 | ytochrome p450, family 71, subfamily B, polypeptide 11 | chr5:8662851-8664432 FORWARD LENGTH=496	496	496	0	100.0	78.8	90.7
Rsa1.0_00592.1.g16549.t1	ref|XP_002862972.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308761|gb|EFH39231.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	207	223	4.00E-99	107.7	96.6	99.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G44560.1 | Symbols: VPS2.2 | SNF7 family protein | chr5:17946081-17948222 FORWARD LENGTH=222	207	222	1.00E-100	107.2	92.8	95.2
Rsa1.0_00592.1.g16550.t1	gb|AAD25557.1|AC005850_14 Hypothetical protein [Arabidopsis thaliana]	192	404	3.00E-53	210.4	53.6	66.7	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G43722.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28730.1); Has 924 Blast hits to 912 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 222; Fungi - 31; Plants - 661; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:16496403-16497377 FORWARD LENGTH=324	192	324	1.00E-25	168.8	31.3	49.0
Rsa1.0_00592.1.g16551.t1	ref|XP_002863624.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297309459|gb|EFH39883.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	365	365	0	100.0	85.8	91.8	pfkB-type carbohydrate kinase family protein	gbpln	Arabidopsis lyrata	AT5G43910.2 | Symbols: | pfkB-like carbohydrate kinase family protein | chr5:17667537-17670085 REVERSE LENGTH=365	365	365	1.00E-179	100.0	84.7	91.2
Rsa1.0_00592.1.g16552.t1	gb|EOA18090.1| hypothetical protein CARUB_v10006542mg [Capsella rubella]	470	480	0	102.1	90.2	93.8	hypothetical protein CARUB_v10006542mg	gbpln	Capsella rubella	AT4G20360.1 | Symbols: ATRAB8D, ATRABE1B, RABE1b | RAB GTPase homolog E1B | chr4:10990036-10991466 FORWARD LENGTH=476	470	476	0	101.3	89.8	93.2
Rsa1.0_00592.1.g16553.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	1562	1356	0	86.8	45.3	59.7	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1562	1262	4.00E-79	80.8	10.4	17.2
Rsa1.0_00593.1.g16554.t1	ref|XP_002869540.1| hypothetical protein ARALYDRAFT_913747 [Arabidopsis lyrata subsp. lyrata] gi|297315376|gb|EFH45799.1| hypothetical protein ARALYDRAFT_913747 [Arabidopsis lyrata subsp. lyrata]	369	367	0	99.5	88.6	92.4	hypothetical protein ARALYDRAFT_913747	gbpln	Arabidopsis lyrata	AT5G54160.1 | Symbols: ATOMT1, OMT1 | O-methyltransferase 1 | chr5:21982075-21984167 FORWARD LENGTH=363	369	363	1.00E-164	98.4	73.2	86.4

Rsa1.0_00593.1.g16555.t1	dbj|BAJ34030.1| unnamed protein product [Thellungiella halophila]	393	390	0	99.2	88.8	94.9	unnamed protein product	----	----	AT4G27800.1 | Symbols: TAP38, PPH1 | thylakoid-associated phosphatase 38 | chr4:13852013-13854091 REVERSE LENGTH=388	393	388	0	98.7	86.0	93.6
Rsa1.0_00593.1.g16556.t1	ref|XP_002867481.1| hypothetical protein ARALYDRAFT_492001 [Arabidopsis lyrata subsp. lyrata] gi|297313317|gb|EFH43740.1| hypothetical protein ARALYDRAFT_492001 [Arabidopsis lyrata subsp. lyrata]	192	195	3.00E-62	101.6	69.3	73.4	hypothetical protein ARALYDRAFT_492001	gbpln	Arabidopsis lyrata	AT4G27810.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF688 (InterPro:IPR007789); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G53030.1); Has 73 Blast hits to 66 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:13854641-13855671 REVERSE LENGTH=196	192	196	1.00E-63	102.1	67.2	72.4
Rsa1.0_00593.1.g16557.t1	ref|XP_002893415.1| hypothetical protein ARALYDRAFT_890136 [Arabidopsis lyrata subsp. lyrata] gi|297339257|gb|EFH69674.1| hypothetical protein ARALYDRAFT_890136 [Arabidopsis lyrata subsp. lyrata]	364	400	9.00E-30	109.9	26.9	34.1	hypothetical protein ARALYDRAFT_890136	gbpln	Arabidopsis lyrata	AT3G19890.1 | Symbols: | F-box family protein | chr3:6914910-6916142 REVERSE LENGTH=410	364	410	2.00E-29	112.6	23.1	32.4
Rsa1.0_00593.1.g16558.t1	ref|NP_194513.1| SNARE-like family protein [Arabidopsis thaliana] gi|4972115|emb|CAB43972.1| putative protein [Arabidopsis thaliana] gi|7269637|emb|CAB81433.1| putative protein [Arabidopsis thaliana] gi|17978989|gb|AAL47455.1| AT4g27840/T27E11_80 [Arabidopsis thaliana] gi|22655346|gb|AAM98265.1| At4g27840/T27E11_80 [Arabidopsis thaliana] gi|332659999|gb|AEE85399.1| SNARE-like family protein [Arabidopsis thaliana]	252	260	5.00E-95	103.2	75.0	85.3	SNARE-like family protein	gbpln	Arabidopsis thaliana	AT4G27840.1 | Symbols: | SNARE-like superfamily protein | chr4:13865268-13866050 REVERSE LENGTH=260	252	260	2.00E-97	103.2	75.0	85.3
Rsa1.0_00593.1.g16559.t1	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	330	1044	7.00E-99	316.4	53.6	72.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	330	626	5.00E-19	189.7	14.8	23.0
Rsa1.0_00593.1.g16560.t11	emb|CAB43975.1| putative protein [Arabidopsis thaliana] gi|7269640|emb|CAB81436.1| putative protein [Arabidopsis thaliana]	694	770	1.00E-127	111.0	51.0	63.8	putative protein	gbpln	Arabidopsis thaliana	AT4G27870.1 | Symbols: | Vacuolar iron transporter (VIT) family protein | chr4:13878983-13882679 FORWARD LENGTH=761	694	761	1.00E-117	109.7	49.0	61.7
Rsa1.0_00593.1.g16561.t1	ref|XP_002869536.1| hypothetical protein ARALYDRAFT_328905 [Arabidopsis lyrata subsp. lyrata] gi|297315372|gb|EFH45795.1| hypothetical protein ARALYDRAFT_328905 [Arabidopsis lyrata subsp. lyrata]	321	777	1.00E-99	242.1	66.4	77.9	hypothetical protein ARALYDRAFT_328905	gbpln	Arabidopsis lyrata	AT4G27870.1 | Symbols: | Vacuolar iron transporter (VIT) family protein | chr4:13878983-13882679 FORWARD LENGTH=761	321	761	2.00E-94	237.1	67.3	79.4
Rsa1.0_00593.1.g16562.t1	gb|EOA18541.1| hypothetical protein CARUB_v10007095mg [Capsella rubella]	276	301	2.00E-73	109.1	58.0	71.4	hypothetical protein CARUB_v10007095mg	gbpln	Capsella rubella	AT4G27890.1 | Symbols: | HSP20-like chaperones superfamily protein | chr4:13886033-13887220 FORWARD LENGTH=293	276	293	4.00E-73	106.2	55.4	71.7
Rsa1.0_00593.1.g16563.t1	ref|NP_194524.2| ethylene-responsive transcription factor CRF4 [Arabidopsis thaliana] gi|334302779|sp|Q9SUE3.2|CRF4_ARATH RecName: Full=Ethylene-responsive transcription factor CRF4; AltName: Full=Protein CYTOKININ RESPONSE FACTOR 4 gi|192571732|gb|ACF04811.1| At4g27950 [Arabidopsis thaliana] gi|332660012|gb|AEE85412.1| ethylene-responsive transcription factor CRF4 [Arabidopsis thaliana]	329	335	1.00E-118	101.8	73.9	83.0	ethylene-responsive transcription factor CRF4	gbpln	Arabidopsis thaliana	AT4G27950.1 | Symbols: CRF4 | cytokinin response factor 4 | chr4:13909732-13910739 REVERSE LENGTH=335	329	335	1.00E-121	101.8	73.9	83.0
Rsa1.0_00593.1.g16564.t2	ref|NP_567792.1| SLAC1 homologue 2 [Arabidopsis thaliana] gi|75167715|sp|Q9ASQ7.1|SLAH2_ARATH RecName: Full=S-type anion channel SLAH2; AltName: Full=SLAC1-homolog protein 2 gi|13605877|gb|AAK32924.1|AF367337_1 AT4g27970/T13J8_80 [Arabidopsis thaliana] gi|25090193|gb|AAN72249.1| At4g27970/T13J8_80 [Arabidopsis thaliana] gi|332660015|gb|AEE85415.1| SLAC1 homologue 2 [Arabidopsis thaliana]	533	519	0	97.4	80.5	86.5	SLAC1 homologue 2	gbpln	Arabidopsis thaliana	AT4G27970.1 | Symbols: SLAH2 | SLAC1 homologue 2 | chr4:13918290-13920122 REVERSE LENGTH=519	533	519	0	97.4	80.5	86.5

Rsa1.0_00593.1.g16565.t1	ref|XP_002869528.1| hypothetical protein ARALYDRAFT_491985 [Arabidopsis lyrata subsp. lyrata] gi|297315364|gb|EFH45787.1| hypothetical protein ARALYDRAFT_491985 [Arabidopsis lyrata subsp. lyrata]	497	566	1.00E-149	113.9	65.0	78.1	hypothetical protein ARALYDRAFT_491985	gbpln	Arabidopsis lyrata	AT4G27980.1 | Symbols: | Domain of unknown function (DUF3444) | chr4:13921677-13923374 FORWARD LENGTH=565	497	565	1.00E-150	113.7	63.6	77.5
Rsa1.0_00593.1.g16566.t1	ref|NP_194529.4| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332660018|gb|AEE85418.1| AAA-type ATPase family protein [Arabidopsis thaliana]	815	830	0	101.8	91.4	95.7	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT4G28000.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13925456-13929280 FORWARD LENGTH=830	815	830	0	101.8	91.4	95.7
Rsa1.0_00593.1.g16567.t1	ref|XP_002867473.1| hypothetical protein ARALYDRAFT_491980 [Arabidopsis lyrata subsp. lyrata] gi|297313309|gb|EFH43732.1| hypothetical protein ARALYDRAFT_491980 [Arabidopsis lyrata subsp. lyrata]	216	156	3.00E-54	72.2	57.9	62.5	hypothetical protein ARALYDRAFT_491980	gbpln	Arabidopsis lyrata	AT4G28025.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13935836-13937367 REVERSE LENGTH=157	216	157	1.00E-52	72.7	59.3	62.5
Rsa1.0_00593.1.g16568.t1	ref|NP_567795.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] gi|15081771|gb|AAK82540.1| AT4g28030/T13J8_140 [Arabidopsis thaliana] gi|22137098|gb|AAM91394.1| At4g28030/T13J8_140 [Arabidopsis thaliana] gi|332660024|gb|AEE85424.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana]	265	274	1.00E-123	103.4	84.5	90.9	GCN5-related N-acetyltransferase (GNAT) family protein	gbpln	Arabidopsis thaliana	AT4G28030.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr4:13937748-13939131 REVERSE LENGTH=274	265	274	1.00E-126	103.4	84.5	90.9
Rsa1.0_00593.1.g16569.t1	gb|EOA18435.1| hypothetical protein CARUB_v10006978mg [Capsella rubella]	270	264	1.00E-116	97.8	75.6	83.3	hypothetical protein CARUB_v10006978mg	gbpln	Capsella rubella	AT4G28050.1 | Symbols: TET7 | tetraspanin7 | chr4:13942566-13943621 REVERSE LENGTH=263	270	263	1.00E-116	97.4	74.4	82.6
Rsa1.0_00593.1.g16570.t1	gb|EOA17644.1| hypothetical protein CARUB_v10006010mg [Capsella rubella]	135	133	2.00E-48	98.5	77.0	82.2	hypothetical protein CARUB_v10006010mg	gbpln	Capsella rubella	AT5G57815.1 | Symbols: | Cytochrome c oxidase, subunit Vib family protein | chr5:23426753-23427637 FORWARD LENGTH=78	135	78	1.00E-41	57.8	55.6	57.8
Rsa1.0_00593.1.g16571.t1	ref|NP_194537.7| tetratricopeptide repeat domain protein [Arabidopsis thaliana] gi|332660036|gb|AEE85436.1| tetratricopeptide repeat domain protein [Arabidopsis thaliana]	1767	1819	0	102.9	85.0	90.8	tetratricopeptide repeat domain protein	gbpln	Arabidopsis thaliana	AT4G28080.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:13948993-13957840 REVERSE LENGTH=1819	1767	1819	0	102.9	85.0	90.8
Rsa1.0_00593.1.g16572.t1	ref|XP_002867465.1| AtMYB41 [Arabidopsis lyrata subsp. lyrata] gi|297313301|gb|EFH43724.1| AtMYB41 [Arabidopsis lyrata subsp. lyrata]	282	283	1.00E-124	100.4	82.6	89.7	AtMYB41	gbpln	Arabidopsis lyrata	AT4G28110.1 | Symbols: AtMYB41, MYB41 | myb domain protein 41 | chr4:13968166-13969384 REVERSE LENGTH=282	282	282	1.00E-117	100.0	80.9	89.4
Rsa1.0_00593.1.g16573.t2	ref|NP_194542.2| diacylglycerol kinase 6 [Arabidopsis thaliana] gi|487523707|sp|F4JKI3.1|DGK6_ARATH RecName: Full=Diacylglycerol kinase 6; Short=AtDGK6; Short=DAG kinase 6; AltName: Full=Diglyceride kinase 6; Short=DGK 6 gi|332660043|gb|AEE85443.1| diacylglycerol kinase 6 [Arabidopsis thaliana]	535	466	0	87.1	67.5	75.9	diacylglycerol kinase 6	gbpln	Arabidopsis thaliana	AT4G28130.1 | Symbols: DGK6, ATDGK6 | diacylglycerol kinase 6 | chr4:13971552-13974323 FORWARD LENGTH=466	535	466	0	87.1	67.5	75.9
Rsa1.0_00593.1.g16574.t1	ref|XP_002867464.1| hypothetical protein ARALYDRAFT_491962 [Arabidopsis lyrata subsp. lyrata] gi|297313300|gb|EFH43723.1| hypothetical protein ARALYDRAFT_491962 [Arabidopsis lyrata subsp. lyrata]	282	278	1.00E-103	98.6	74.5	83.0	hypothetical protein ARALYDRAFT_491962	gbpln	Arabidopsis lyrata	AT4G28140.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:13974905-13975783 REVERSE LENGTH=292	282	292	1.00E-103	103.5	73.0	82.6
Rsa1.0_00593.1.g16575.t1	ref|XP_002867463.1| hypothetical protein ARALYDRAFT_491960 [Arabidopsis lyrata subsp. lyrata] gi|297313299|gb|EFH43722.1| hypothetical protein ARALYDRAFT_491960 [Arabidopsis lyrata subsp. lyrata]	284	284	1.00E-147	100.0	88.0	95.1	hypothetical protein ARALYDRAFT_491960	gbpln	Arabidopsis lyrata	AT4G28150.1 | Symbols: | Protein of unknown function (DUF789) | chr4:13977642-13978912 REVERSE LENGTH=285	284	285	1.00E-141	100.4	83.8	89.8

Rsa1.0_00593.1.g16576.t1	ref|XP_002869518.1| hypothetical protein ARALYDRAFT_491959 [Arabidopsis lyrata subsp. lyrata] gi|297315354|gb|EFH45777.1| hypothetical protein ARALYDRAFT_491959 [Arabidopsis lyrata subsp. lyrata]	124	113	7.00E-29	91.1	56.5	67.7	hypothetical protein ARALYDRAFT_491959	gbpln	Arabidopsis lyrata	AT4G28160.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:13980390-13980725 FORWARD LENGTH=111	124	111	9.00E-31	89.5	55.6	65.3
Rsa1.0_00593.1.g16577.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00594.1.g16578.t1	emb|CAD92450.1| amino acid permease 6 [Brassica napus]	470	481	0	102.3	98.5	99.6	amino acid permease 6	gbpln	Brassica napus	AT5G49630.1 | Symbols: AAP6 | amino acid permease 6 | chr5:20142681-20146441 REVERSE LENGTH=481	470	481	0	102.3	91.5	96.0
Rsa1.0_00594.1.g16579.t1	gb|EOA35503.1| hypothetical protein CARUB_v10020710mg, partial [Capsella rubella]	243	304	1.00E-102	125.1	78.6	86.4	hypothetical protein CARUB_v10020710mg, partial	gbpln	Capsella rubella	AT1G65690.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr1:24431642-24432898 REVERSE LENGTH=252	243	252	1.00E-102	103.7	79.0	86.8
Rsa1.0_00594.1.g16580.t1	ref|NP_176747.1| U6 snRNA-associated Sm-like protein LSm8 [Arabidopsis thaliana] gi|79320777|ref|NP_001031238.1| U6 snRNA-associated Sm-like protein LSm8 [Arabidopsis thaliana] gi|17979539|gb|AAL50104.1| At1g65700/F1E22_3 [Arabidopsis thaliana] gi|20334918|gb|AAM16215.1| At1g65700/F1E22_3 [Arabidopsis thaliana] gi|21592627|gb|AAM64576.1| small nuclear ribonucleoprotein, putative [Arabidopsis thaliana] gi|332196292|gb|AEE34413.1| U6 snRNA-associated Sm-like protein LSm8 [Arabidopsis thaliana] gi|332196293|gb|AEE34414.1| U6 snRNA-associated Sm-like protein LSm8 [Arabidopsis thaliana]	98	98	2.00E-45	100.0	94.9	96.9	U6 snRNA-associated Sm-like protein LSm8	gbpln	Arabidopsis thaliana	AT1G65700.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:24434463-24435870 REVERSE LENGTH=98	98	98	4.00E-48	100.0	94.9	96.9
Rsa1.0_00594.1.g16581.t1	gb|EOA34542.1| hypothetical protein CARUB_v10022088mg [Capsella rubella]	187	186	2.00E-50	99.5	64.7	74.3	hypothetical protein CARUB_v10022088mg	gbpln	Capsella rubella	AT1G65720.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 44 Blast hits to 44 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:24440471-24441013 REVERSE LENGTH=180	187	180	4.00E-45	96.3	65.8	74.3
Rsa1.0_00594.1.g16582.t2	ref|NP_176758.1| glutathione S-transferase [Arabidopsis thaliana] gi|25991925|gb|AAN76990.1|AF461148_1 MAPEG-like protein [Arabidopsis thaliana] gi|14517464|gb|AAK62622.1| At1g65820/F1E22_4 [Arabidopsis thaliana] gi|17978909|gb|AAL47424.1| At1g65820/F1E22_4 [Arabidopsis thaliana] gi|21617891|gb|AAM66941.1| glutathione-s-transferase, putative [Arabidopsis thaliana] gi|332196306|gb|AEE34427.1| glutathione S-transferase [Arabidopsis thaliana]	153	146	4.00E-70	95.4	85.0	89.5	glutathione S-transferase	gbpln	Arabidopsis thaliana	AT1G65820.1 | Symbols: | microsomal glutathione s-transferase, putative | chr1:24485213-24486682 FORWARD LENGTH=146	153	146	1.00E-72	95.4	85.0	89.5
Rsa1.0_00594.1.g16583.t1	ref|NP_176759.1| putative polyamine oxidase 4 [Arabidopsis thaliana] gi|75151901|sp|Q8H191.1|PAO4_ARATH RecName: Full=Probable polyamine oxidase 4; Short=AtPAO4; AltName: Full=Amine oxidase 2 gi|29468126|gb|AAO85405.1|AF364953_1 putative amine oxidase 2 [Arabidopsis thaliana] gi|23198290|gb|AAN15672.1| putative protein kinase gb|AAD22129 [Arabidopsis thaliana] gi|332196309|gb|AEE34430.1| putative polyamine oxidase 4 [Arabidopsis thaliana]	495	497	0	100.4	91.9	96.8	putative polyamine oxidase 4	gbpln	Arabidopsis thaliana	AT1G65840.1 | Symbols: ATPAO4, PAO4 | polyamine oxidase 4 | chr1:24490173-24492728 FORWARD LENGTH=497	495	497	0	100.4	91.9	96.8
Rsa1.0_00594.1.g16584.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00594.1.g16585.t1	gb|AAP03024.1| acyl-activating enzyme 11 [Arabidopsis thaliana]	579	572	0	98.8	79.1	86.7	acyl-activating enzyme 11	gbpln	Arabidopsis thaliana	AT1G66120.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr1:24612640-24614690 FORWARD LENGTH=572	579	572	0	98.8	78.6	86.4

Rsa1.0_00594.1.g16586.t2	dbj|BAB02146.1| copia retroelement pol polyprotein-like [Arabidopsis thaliana]	475	526	8.00E-60	110.7	25.7	34.1	copia retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00594.1.g16587.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1420	2726	0	192.0	48.9	67.9	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1420	158	6.00E-37	11.1	5.0	6.3
Rsa1.0_00594.1.g16588.t1	ref|XP_002894230.1| aminotransferase class IV family protein [Arabidopsis lyrata subsp. lyrata] gi|297340072|gb|EFH70489.1| aminotransferase class IV family protein [Arabidopsis lyrata subsp. lyrata]	232	355	1.00E-114	153.0	84.9	93.5	aminotransferase class IV family protein	gbpln	Arabidopsis lyrata	AT1G50090.1 | Symbols: | D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein | chr1:18554641-18556794 REVERSE LENGTH=367	232	367	1.00E-115	158.2	83.2	92.7
Rsa1.0_00595.1.g16589.t1	ref|XP_002888066.1| glucose-6-phosphate/phosphate translocator 2 [Arabidopsis lyrata subsp. lyrata] gi|297333907|gb|EFH64325.1| glucose-6-phosphate/phosphate translocator 2 [Arabidopsis lyrata subsp. lyrata]	412	388	0	94.2	84.0	89.6	glucose-6-phosphate/phosphate translocator 2	gbpln	Arabidopsis lyrata	AT1G61800.1 | Symbols: GPT2, ATGPT2 | glucose-6-phosphate/phosphate translocator 2 | chr1:22824527-22826459 FORWARD LENGTH=388	412	388	0	94.2	81.1	86.4
Rsa1.0_00595.1.g16590.t28	ref|NP_187680.2| DNA gyrase subunit A [Arabidopsis thaliana] gi|110808536|sp|Q9CAF6.2|GYRA_ARATH RecName: Full=Probable DNA gyrase subunit A, chloroplastic/mitochondrial; Flags: Precursor gi|332641422|gb|AEE74943.1| DNA gyrase subunit A [Arabidopsis thaliana]	91	950	5.00E-23	1044.0	62.6	65.9	DNA gyrase subunit A	gbpln	Arabidopsis thaliana	AT3G10690.1 | Symbols: GYRA | DNA GYRASE A | chr3:3339612-3346243 REVERSE LENGTH=950	91	950	8.00E-26	1044.0	62.6	65.9
Rsa1.0_00595.1.g16591.t1	ref|XP_002886504.1| hypothetical protein ARALYDRAFT_475144 [Arabidopsis lyrata subsp. lyrata] gi|297332345|gb|EFH62763.1| hypothetical protein ARALYDRAFT_475144 [Arabidopsis lyrata subsp. lyrata]	395	388	0	98.2	90.4	92.9	hypothetical protein ARALYDRAFT_475144	gbpln	Arabidopsis lyrata	AT1G61860.1 | Symbols: | Protein kinase superfamily protein | chr1:22863079-22864619 REVERSE LENGTH=389	395	389	0	98.5	89.4	91.9
Rsa1.0_00595.1.g16592.t1	gb|EOA35229.1| hypothetical protein CARUB_v10020389mg [Capsella rubella]	410	408	0	99.5	84.4	92.7	hypothetical protein CARUB_v10020389mg	gbpln	Capsella rubella	AT1G61870.1 | Symbols: PPR336 | pentatricopeptide repeat 336 | chr1:22865326-22866552 REVERSE LENGTH=408	410	408	0	99.5	85.4	92.9
Rsa1.0_00595.1.g16593.t1	ref|XP_002878376.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324214|gb|EFH54635.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	144	498	6.00E-19	345.8	28.5	32.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G61360.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:22704630-22706126 REVERSE LENGTH=498	144	498	3.00E-20	345.8	29.2	31.9
Rsa1.0_00595.1.g16594.t1	dbj|BAJ34317.1| unnamed protein product [Thellungiella halophila]	501	501	0	100.0	93.2	96.8	unnamed protein product	----	----	AT1G61890.1 | Symbols: | MATE efflux family protein | chr1:22868103-22871163 REVERSE LENGTH=501	501	501	0	100.0	91.8	96.8
Rsa1.0_00595.1.g16595.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00595.1.g16596.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00595.1.g16597.t1	gb|EOA34147.1| hypothetical protein CARUB_v10021649mg [Capsella rubella]	409	430	0	105.1	80.2	90.2	hypothetical protein CARUB_v10021649mg	gbpln	Capsella rubella	AT1G61900.3 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30700.1). | chr1:22882508-22884722 REVERSE LENGTH=429	409	429	0	104.9	80.2	89.5
Rsa1.0_00595.1.g16598.t2	gb|EOA32429.1| hypothetical protein CARUB_v10015703mg [Capsella rubella]	631	697	0	110.5	60.1	65.5	hypothetical protein CARUB_v10015703mg	gbpln	Capsella rubella	AT3G24550.1 | Symbols: ATPERK1, PERK1 | proline extensin-like receptor kinase 1 | chr3:8960411-8963303 FORWARD LENGTH=652	631	652	0	103.3	59.6	66.6
Rsa1.0_00595.1.g16599.t1	ref|NP_189078.2| syntaxin-32 [Arabidopsis thaliana] gi|28380163|sp|Q9LK09.1|SYP32_ARATH RecName: Full=Syntaxin-32; Short=AtSYP32 gi|11994697|dbj|BAB02935.1| probable t-SNARE (soluble NSF attachment protein receptor) SED5; ER to Golgi transport [Arabidopsis thaliana] gi|28393777|gb|AAO42298.1| putative syntaxin SYP32 [Arabidopsis thaliana] gi|30793955|gb|AAP40429.1| putative syntaxin SYP32 [Arabidopsis thaliana] gi|332643371|gb|AEE76892.1| syntaxin-32 [Arabidopsis thaliana]	346	347	1.00E-136	100.3	79.2	86.7	syntaxin-32	gbpln	Arabidopsis thaliana	AT3G24350.1 | Symbols: SYP32, ATSYP32 | syntaxin of plants 32 | chr3:8837733-8839402 FORWARD LENGTH=347	346	347	1.00E-139	100.3	79.2	86.7
Rsa1.0_00595.1.g16600.t1	gb|AAD23706.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	324	733	7.00E-25	226.2	28.1	48.8	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00595.1.g16601.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00595.1.g16602.t1	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	223	695	8.00E-36	311.7	36.3	41.3	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00595.1.g16603.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00595.1.g16604.t1	ref|XP_002885636.1| hypothetical protein ARALYDRAFT_479944 [Arabidopsis lyrata subsp. lyrata] gi|297331476|gb|EFH61895.1| hypothetical protein ARALYDRAFT_479944 [Arabidopsis lyrata subsp. lyrata]	274	274	1.00E-105	100.0	82.5	86.9	hypothetical protein ARALYDRAFT_479944	gbpln	Arabidopsis lyrata	AT3G24310.1 | Symbols: MYB305, ATMYB71 | myb domain protein 305 | chr3:8811336-8812330 REVERSE LENGTH=269	274	269	1.00E-106	98.2	83.2	89.1
Rsa1.0_00595.1.g16605.t1	gb|EOA29700.1| hypothetical protein CARUB_v10016472mg [Capsella rubella]	491	498	0	101.4	91.0	95.1	hypothetical protein CARUB_v10016472mg	gbpln	Capsella rubella	AT3G24300.1 | Symbols: AMT1;3, ATAMT1;3 | ammonium transporter 1;3 | chr3:8805858-8807354 REVERSE LENGTH=498	491	498	0	101.4	90.0	93.9
Rsa1.0_00595.1.g16606.t1	gb|EOA30145.1| hypothetical protein CARUB_v10013252mg [Capsella rubella]	613	609	0	99.3	94.0	95.8	hypothetical protein CARUB_v10013252mg	gbpln	Capsella rubella	AT3G23940.1 | Symbols: | dehydratase family | chr3:8648780-8652323 FORWARD LENGTH=608	613	608	0	99.2	93.3	95.3
Rsa1.0_00595.1.g16607.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00595.1.g16608.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00595.1.g16609.t1	gb|EOA33053.1| hypothetical protein CARUB_v10016386mg [Capsella rubella]	246	243	1.00E-130	98.8	95.9	97.6	hypothetical protein CARUB_v10016386mg	gbpln	Capsella rubella	AT3G24020.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr3:8678827-8679558 FORWARD LENGTH=243	246	243	1.00E-131	98.8	95.1	96.3
Rsa1.0_00595.1.g16610.t1	ref|XP_002883496.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata] gi|297329336|gb|EFH59755.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata]	404	416	0	103.0	83.2	88.6	glycosyltransferase family 14 protein	gbpln	Arabidopsis lyrata	AT3G24040.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr3:8681118-8683211 REVERSE LENGTH=417	404	417	0	103.2	81.2	87.9
Rsa1.0_00595.1.g16611.t1	ref|NP_189048.1| self-incompatibility S1 family protein [Arabidopsis thaliana] gi|9294675|dbj|BAB03024.1| unnamed protein product [Arabidopsis thaliana] gi|332643328|gb|AEE76849.1| self-incompatibility S1 family protein [Arabidopsis thaliana]	126	147	9.00E-60	116.7	86.5	93.7	self-incompatibility S1 family protein	gbpln	Arabidopsis thaliana	AT3G24060.1 | Symbols: | Plant self-incompatibility protein S1 family | chr3:8689589-8690032 REVERSE LENGTH=147	126	147	2.00E-62	116.7	86.5	93.7
Rsa1.0_00595.1.g16612.t1	gb|ABD65088.1| hypothetical protein 27.t00109 [Brassica oleracea]	289	1176	1.00E-82	406.9	47.8	70.9	hypothetical protein 27.t00109	gbpln	Brassica oleracea	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	289	452	2.00E-42	156.4	29.4	40.5
Rsa1.0_00595.1.g16613.t3	ref|XP_002868499.1| ATCHX24 [Arabidopsis lyrata subsp. lyrata] gi|297314335|gb|EFH44758.1| ATCHX24 [Arabidopsis lyrata subsp. lyrata]	803	861	0	107.2	72.0	85.3	ATCHX24	gbpln	Arabidopsis lyrata	AT5G37060.1 | Symbols: ATCHX24, CHX24 | cation/H+ exchanger 24 | chr5:14642741-14645414 REVERSE LENGTH=859	803	859	0	107.0	71.1	84.3
Rsa1.0_00596.1.g16614.t1	ref|NP_850951.2| homeobox protein knotted-1-like 6 [Arabidopsis thaliana] gi|75146711|sp|Q84JS6.1|KNAT6_ARATH RecName: Full=Homeobox protein knotted-1-like 6; AltName: Full=Protein KNAT6 gi|27754596|gb|AAO22744.1| putative homeodomain transcription factor KNAT6 [Arabidopsis thaliana] gi|28393913|gb|AAO42364.1| putative homeodomain transcription factor KNAT6 [Arabidopsis thaliana] gi|332192260|gb|AEE30381.1| homeobox protein knotted-1-like 6 [Arabidopsis thaliana]	230	327	2.00E-85	142.2	70.4	75.7	homeobox protein knotted-1-like 6	gbpln	Arabidopsis thaliana	AT1G23380.1 | Symbols: KNAT6, KNAT6L, KNAT6S | KNOTTED1-like homeobox gene 6 | chr1:8297499-8302492 REVERSE LENGTH=327	230	327	6.00E-88	142.2	70.4	75.7
Rsa1.0_00596.1.g16615.t1	ref|XP_002893283.1| hypothetical protein ARALYDRAFT_472599 [Arabidopsis lyrata subsp. lyrata] gi|297339125|gb|EFH69542.1| hypothetical protein ARALYDRAFT_472599 [Arabidopsis lyrata subsp. lyrata]	126	329	2.00E-53	261.1	86.5	91.3	hypothetical protein ARALYDRAFT_472599	gbpln	Arabidopsis lyrata	AT1G23380.2 | Symbols: KNAT6, KNAT6L, KNAT6S | KNOTTED1-like homeobox gene 6 | chr1:8297499-8302492 REVERSE LENGTH=329	126	329	2.00E-55	261.1	84.1	90.5

<table>
<tr><td>Rsa1.0_00596.1.g16616.t1</td><td>ref|NP_173750.3| S-adenosylmethionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|122215535|sp|Q3ED65.2|MENG_ARATH RecName: Full=2-phytyl-1,4-beta-naphthoquinone methyltransferase, chloroplastic; AltName: Full=Demethylphylloquinone methyltransferase; AltName: Full=Menaquinone biosynthesis methyltransferase ubiE-like protein; Flags: Precursor gi|222423878|dbj|BAH19903.1| AT1G23360 [Arabidopsis thaliana] gi|332192256|gb|AEE30377.1| 2-phytyl-1,4-beta-naphthoquinone methyltransferase [Arabidopsis thaliana]</td><td>273</td><td>261</td><td>1.00E-121</td><td>95.6</td><td>80.2</td><td>86.1</td><td>S-adenosylmethionine-dependent methyltransferase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G23360.1 | Symbols: MENG | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:8295421-8296893 REVERSE LENGTH=261</td><td>273</td><td>261</td><td>1.00E-123</td><td>95.6</td><td>80.2</td><td>86.1</td></tr>
<tr><td>Rsa1.0_00596.1.g16617.t1</td><td>gb|EOA37605.1| hypothetical protein CARUB_v10011971mg [Capsella rubella]</td><td>166</td><td>166</td><td>3.00E-63</td><td>100.0</td><td>76.5</td><td>85.5</td><td>hypothetical protein CARUB_v10011971mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G23350.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:8293696-8294175 REVERSE LENGTH=159</td><td>166</td><td>159</td><td>8.00E-63</td><td>95.8</td><td>75.3</td><td>83.7</td></tr>
<tr><td>Rsa1.0_00596.1.g16618.t1</td><td>gb|AFU75878.1| lipase [Brassica napus]</td><td>464</td><td>468</td><td>0</td><td>100.9</td><td>86.2</td><td>92.9</td><td>lipase</td><td>gbpln</td><td>Brassica napus</td><td>AT1G23330.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:8279874-8281891 REVERSE LENGTH=471</td><td>464</td><td>471</td><td>0</td><td>101.5</td><td>83.4</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00596.1.g16619.t1</td><td>gb|EOA40275.1| hypothetical protein CARUB_v10009003mg [Capsella rubella]</td><td>478</td><td>481</td><td>0</td><td>100.6</td><td>96.7</td><td>98.7</td><td>hypothetical protein CARUB_v10009003mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G23310.1 | Symbols: GGT1, AOAT1, GGAT1 | glutamate:glyoxylate aminotransferase | chr1:8268720-8271329 REVERSE LENGTH=481</td><td>478</td><td>481</td><td>0</td><td>100.6</td><td>96.0</td><td>99.0</td></tr>
<tr><td>Rsa1.0_00596.1.g16620.t1</td><td>ref|NP_173743.1| 60S ribosomal protein L27a-2 [Arabidopsis thaliana] gi|297845396|ref|XP_002890579.1| RPL27A [Arabidopsis lyrata subsp. lyrata] gi|20143883|sp|Q9LR33.1|R27A2_ARATH RecName: Full=60S ribosomal protein L27a-2 gi|9295692|gb|AAF86998.1|AC005292_7 F26F24.13 [Arabidopsis thaliana] gi|11692928|gb|AAG40067.1|AF324716_1 At1g23290 [Arabidopsis thaliana] gi|13194820|gb|AAK15572.1|AF349525_1 putative 60s ribosomal protein l27a [Arabidopsis thaliana] gi|15294178|gb|AAK95266.1|AF410280_1 At1g23290/F26F24_23 [Arabidopsis thaliana] gi|23308283|gb|AAN18111.1| At1g23290/F26F24_23 [Arabidopsis thaliana] gi|297336421|gb|EFH66838.1| RPL27A [Arabidopsis lyrata subsp. lyrata] gi|332192247|gb|AEE30368.1| 60S ribosomal protein L27a-2 [Arabidopsis thaliana]</td><td>146</td><td>146</td><td>5.00E-74</td><td>100.0</td><td>93.8</td><td>97.9</td><td>60S ribosomal protein L27a-2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G23290.1 | Symbols: RPL27A, RPL27AB | Ribosomal protein L18e/L15 superfamily protein | chr1:8263007-8263447 FORWARD LENGTH=146</td><td>146</td><td>146</td><td>1.00E-76</td><td>100.0</td><td>93.8</td><td>97.9</td></tr>
<tr><td>Rsa1.0_00596.1.g16621.t1</td><td>ref|NP_564191.1| ubiquitin-conjugating enzyme E2 variant 1A [Arabidopsis thaliana] gi|75305892|sp|Q93YP0.1|UEV1A_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 variant 1A; Short=Ubc enzyme variant 1A; AltName: Full=Protein MMS ZWEI HOMOLOG 1 gi|16649053|gb|AAL24378.1| similar to DNA binding protein [Arabidopsis thaliana] gi|20259984|gb|AAM13339.1| similar to DNA binding protein [Arabidopsis thaliana] gi|332192244|gb|AEE30365.1| ubiquitin-conjugating enzyme E2 variant 1A [Arabidopsis thaliana]</td><td>158</td><td>158</td><td>4.00E-86</td><td>100.0</td><td>96.2</td><td>98.1</td><td>ubiquitin-conjugating enzyme E2 variant 1A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G23260.1 | Symbols: MMZ1, UEV1A | MMS ZWEI homologue 1 | chr1:8257209-8258573 REVERSE LENGTH=158</td><td>158</td><td>158</td><td>1.00E-88</td><td>100.0</td><td>96.2</td><td>98.1</td></tr>
<tr><td>Rsa1.0_00596.1.g16622.t1</td><td>gb|EOA36326.1| hypothetical protein CARUB_v10010634mg [Capsella rubella]</td><td>107</td><td>129</td><td>2.00E-31</td><td>120.6</td><td>66.4</td><td>71.0</td><td>hypothetical protein CARUB_v10010634mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G23220.1 | Symbols: | Dynein light chain type 1 family protein | chr1:8242614-8244136 FORWARD LENGTH=129</td><td>107</td><td>129</td><td>9.00E-34</td><td>120.6</td><td>66.4</td><td>70.1</td></tr>
<tr><td>Rsa1.0_00596.1.g16623.t1</td><td>dbj|BAJ34519.1| unnamed protein product [Thellungiella halophila]</td><td>583</td><td>582</td><td>0</td><td>99.8</td><td>96.9</td><td>99.1</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G23190.1 | Symbols: PGM3 | Phosphoglucomutase/phosphomannomutase family protein | chr1:8219946-8224186 FORWARD LENGTH=583</td><td>583</td><td>583</td><td>0</td><td>100.0</td><td>96.7</td><td>98.1</td></tr>
</table>

Rsa1.0_00596.1.g16624.t1	ref|NP_173731.2| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|25083231|gb|AAN72053.1| unknown protein [Arabidopsis thaliana] gi|31711764|gb|AAP68238.1| At1g23180 [Arabidopsis thaliana] gi|110742235|dbj|BAE99044.1| hypothetical protein [Arabidopsis thaliana] gi|332192231|gb|AEE30352.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	838	834	0	99.5	82.2	89.6	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G23180.1 | Symbols: | ARM repeat superfamily protein | chr1:8216125-8219515 FORWARD LENGTH=834	838	834	0	99.5	82.2	89.6
Rsa1.0_00596.1.g16625.t1	gb|EOA36585.1| hypothetical protein CARUB_v10011772mg [Capsella rubella]	290	148	3.00E-63	51.0	39.7	43.8	hypothetical protein CARUB_v10011772mg	gbpln	Capsella rubella	AT1G23120.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:8198788-8199359 FORWARD LENGTH=148	290	148	3.00E-65	51.0	39.7	43.4
Rsa1.0_00596.1.g16626.t1	gb|EOA36585.1| hypothetical protein CARUB_v10011772mg [Capsella rubella]	307	148	2.00E-68	48.2	40.7	43.3	hypothetical protein CARUB_v10011772mg	gbpln	Capsella rubella	AT1G23120.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:8198788-8199359 FORWARD LENGTH=148	307	148	1.00E-70	48.2	41.0	43.3
Rsa1.0_00596.1.g16627.t1	ref|NP_198153.1| SRPBCC ligand-binding domain-containing protein [Arabidopsis thaliana] gi|332006375|gb|AED93758.1| SRPBCC ligand-binding domain-containing protein [Arabidopsis thaliana]	157	166	9.00E-74	105.7	82.8	92.4	SRPBCC ligand-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT5G28010.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr5:10024813-10025382 FORWARD LENGTH=166	157	166	3.00E-76	105.7	82.8	92.4
Rsa1.0_00596.1.g16628.t1	ref|NP_849700.1| auxin efflux carrier component 7 [Arabidopsis thaliana] gi|42558877|sp|Q940Y5.2|PIN7_ARATH RecName: Full=Auxin efflux carrier component 7; Short=AtPIN7 gi|5817305|gb|AAD52697.1|AF087820_1 auxin transport protein [Arabidopsis thaliana] gi|332192211|gb|AEE30332.1| auxin efflux carrier component 7 [Arabidopsis thaliana]	615	619	0	100.7	78.9	84.4	auxin efflux carrier component 7	gbpln	Arabidopsis thaliana	AT1G23080.1 | Symbols: PIN7, ATPIN7 | Auxin efflux carrier family protein | chr1:8180768-8183406 REVERSE LENGTH=619	615	619	0	100.7	78.9	84.4
Rsa1.0_00596.1.g16629.t1	ref|NP_565012.1| ethylene-responsive transcription factor ERF070 [Arabidopsis thaliana] gi|75333560|sp|Q9C995.1|ERF70_ARATH RecName: Full=Ethylene-responsive transcription factor ERF070 gi|12323426|gb|AAG51689.1|AC016972_8 hypothetical protein; 47633-48118 [Arabidopsis thaliana] gi|51969298|dbj|BAD43341.1| unknown protein [Arabidopsis thaliana] gi|51969508|dbj|BAD43446.1| unknown protein [Arabidopsis thaliana] gi|51969622|dbj|BAD43503.1| unknown protein [Arabidopsis thaliana] gi|51969690|dbj|BAD43537.1| unknown protein [Arabidopsis thaliana] gi|51970004|dbj|BAD43694.1| unknown protein [Arabidopsis thaliana] gi|51970228|dbj|BAD43806.1| unknown protein [Arabidopsis thaliana] gi|51970430|dbj|BAD43907.1| unknown protein [Arabidopsis thaliana] gi|51970702|dbj|BAD44043.1| unknown protein [Arabidopsis thaliana] gi|98961105|gb|ABF59036.1| At1g71130 [Arabidopsis thaliana] gi|332197043|gb|AEE35164.1| ethylene-responsive transcription factor ERF070 [Arabidopsis thaliana]	119	161	3.00E-27	135.3	61.3	70.6	ethylene-responsive transcription factor ERF070	gbpln	Arabidopsis thaliana	AT1G71130.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:26822877-26823362 FORWARD LENGTH=161	119	161	5.00E-30	135.3	61.3	70.6
Rsa1.0_00596.1.g16630.t1	ref|XP_002893253.1| hypothetical protein ARALYDRAFT_313173 [Arabidopsis lyrata subsp. lyrata] gi|297339095|gb|EFH69512.1| hypothetical protein ARALYDRAFT_313173 [Arabidopsis lyrata subsp. lyrata]	47	1147	2.00E-12	2440.4	74.5	80.9	hypothetical protein ARALYDRAFT_313173	gbpln	Arabidopsis lyrata	AT1G22960.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:8128086-8130242 REVERSE LENGTH=718	47	718	4.00E-13	1527.7	70.2	78.7
Rsa1.0_00596.1.g16631.t1	ref|NP_173708.3| uncharacterized PKHD-type hydroxylase [Arabidopsis thaliana] gi|193806639|sp|Q3ED68.2|Y1295_ARATH RecName: Full=Uncharacterized PKHD-type hydroxylase At1g22950 gi|332192193|gb|AEE30314.1| uncharacterized PKHD-type hydroxylase [Arabidopsis thaliana]	401	397	1.00E-160	99.0	68.8	80.3	uncharacterized PKHD-type hydroxylase	gbpln	Arabidopsis thaliana	AT1G22950.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:8125291-8127168 REVERSE LENGTH=397	401	397	1.00E-163	99.0	68.8	80.3

Rsa1.0_00597.1.g16632.t1	gb|EOA37644.1| hypothetical protein CARUB_v10012122mg [Capsella rubella]	171	171	1.00E-87	100.0	91.2	94.7	hypothetical protein CARUB_v10012122mg	gbpln	Capsella rubella	AT1G29140.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr1:10179029-10179811 FORWARD LENGTH=171	171	171	3.00E-87	100.0	87.7	93.0
Rsa1.0_00597.1.g16633.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00597.1.g16634.t1	ref|NP_174210.1| 26S proteasome regulatory subunit N6 [Arabidopsis thaliana] gi|75264101|sp|Q9LP45.1|PSD11_ARATH RecName: Full=26S proteasome non-ATPase regulatory subunit 11; AltName: Full=19S proteosome subunit 9; AltName: Full=26S proteasome regulatory subunit N6; AltName: Full=26S proteasome regulatory subunit RPN6a; AltName: Full=26S proteasome regulatory subunit S9; Short=AtS9 gi|9502423|gb|AAF88122.1|AC021043_15 Similar to 26S proteasome subunits [Arabidopsis thaliana] gi|13877881|gb|AAK44018.1|AF370203_1 putative 19S proteosome subunit 9 [Arabidopsis thaliana] gi|15810545|gb|AAL07160.1| putative 19S proteosome subunit 9 [Arabidopsis thaliana] gi|32700024|gb|AAP86662.1| 26S proteasome subunit RPN6a [Arabidopsis thaliana] gi|32700026|gb|AAP86663.1| 26S proteasome subunit RPN6a [Arabidopsis thaliana] gi|332192929|gb|AEE31050.1| 26S proteasome non-ATPase regulatory subunit 11 [Arabidopsis thaliana]	419	419	0	100.0	96.4	99.0	26S proteasome regulatory subunit N6	gbpln	Arabidopsis thaliana	AT1G29150.1 | Symbols: ATS9, RPN6 | non-ATPase subunit 9 | chr1:10181240-10182499 FORWARD LENGTH=419	419	419	0	100.0	96.4	99.0
Rsa1.0_00597.1.g16635.t1	ref|XP_002893549.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297339391|gb|EFH69808.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	176	173	5.00E-79	98.3	86.9	90.9	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT1G29160.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr1:10183797-10184324 REVERSE LENGTH=175	176	175	5.00E-81	99.4	84.7	88.1
Rsa1.0_00597.1.g16636.t1	gb|EOA12097.1| hypothetical protein CARUB_v10016515mg [Capsella rubella]	656	409	1.00E-60	62.3	18.8	27.4	hypothetical protein CARUB_v10016515mg	gbpln	Capsella rubella	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	656	249	8.00E-30	38.0	11.7	16.5
Rsa1.0_00597.1.g16637.t3	dbj|BAB01350.1| Mutator-like transposase [Arabidopsis thaliana]	653	811	1.00E-80	124.2	31.2	45.0	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64255.1 | Symbols: | MuDR family transposase | chr1:23844954-23847206 FORWARD LENGTH=750	653	750	1.00E-11	114.9	10.4	17.5
Rsa1.0_00597.1.g16638.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1410	1270	1.00E-108	90.1	15.8	22.1	F21J9.30	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	1410	154	1.00E-35	10.9	4.9	6.5
Rsa1.0_00597.1.g16639.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00597.1.g16640.t1	gb|EMS58970.1| Protein FIZZY-RELATED 3 [Triticum urartu]	116	389	9.00E-11	335.3	26.7	35.3	Protein FIZZY-RELATED 3	gbpln	Triticum urartu	AT4G22910.1 | Symbols: FZR2, CCS52A1 | FIZZY-related 2 | chr4:12012743-12015663 FORWARD LENGTH=483	116	483	4.00E-13	416.4	26.7	32.8
Rsa1.0_00597.1.g16641.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00597.1.g16642.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1067	1213	0	113.7	53.0	69.8	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1067	626	4.00E-66	58.7	12.7	20.7
Rsa1.0_00597.1.g16643.t1	gb|ACB59223.1| glutathione S-transferase [Brassica oleracea]	237	523	7.00E-50	220.7	51.5	62.9	glutathione S-transferase	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00597.1.g16644.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00597.1.g16645.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00597.1.g16646.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00597.1.g16647.t1	gb|EOA37296.1| hypothetical protein CARUB_v10010917mg [Capsella rubella]	176	184	4.00E-69	104.5	80.1	86.9	hypothetical protein CARUB_v10010917mg	gbpln	Capsella rubella	AT1G29195.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, 4 leaf senescence stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30230.1); Has 180 Blast hits to 180 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 180; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10202673-10203254 REVERSE LENGTH=193	176	193	1.00E-70	109.7	81.3	91.5
Rsa1.0_00597.1.g16648.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	134	1142	2.00E-21	852.2	43.3	60.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	134	575	8.00E-11	429.1	32.1	49.3
Rsa1.0_00598.1.g16649.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	473	695	1.00E-120	146.9	54.5	68.3	hypothetical protein 26.t00052	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00598.1.g16650.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	1729	1103	0	63.8	29.2	36.9	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00598.1.g16651.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00598.1.g16652.t1	gb|EOA20431.1| hypothetical protein CARUB_v10000741mg [Capsella rubella]	514	514	0	100.0	92.4	96.7	hypothetical protein CARUB_v10000741mg	gbpln	Capsella rubella	AT4G02290.1 | Symbols: AtGH9B13, GH9B13 | glycosyl hydrolase 9B13 | chr4:1002654-1005125 REVERSE LENGTH=516	514	516	0	100.4	91.1	95.3
Rsa1.0_00598.1.g16653.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00598.1.g16654.t1	ref|XP_002872848.1| pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata] gi|297318685|gb|EFH49107.1| pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata]	165	165	3.00E-84	100.0	92.1	95.8	pollen ole e 1 allergen and extensin family protein	gbpln	Arabidopsis lyrata	AT4G02270.1 | Symbols: RHS13 | root hair specific 13 | chr4:992383-992996 REVERSE LENGTH=165	165	165	6.00E-82	100.0	85.5	92.7
Rsa1.0_00598.1.g16655.t1	ref|XP_002874925.1| hypothetical protein ARALYDRAFT_490346 [Arabidopsis lyrata subsp. lyrata] gi|297320762|gb|EFH51184.1| hypothetical protein ARALYDRAFT_490346 [Arabidopsis lyrata subsp. lyrata]	866	883	0	102.0	91.6	95.2	hypothetical protein ARALYDRAFT_490346	gbpln	Arabidopsis lyrata	AT4G02260.2 | Symbols: RSH1, AT-RSH1 | RELA/SPOT homolog 1 | chr4:985451-991178 FORWARD LENGTH=883	866	883	0	102.0	91.0	94.9
Rsa1.0_00598.1.g16656.t3	gb|AAC95212.1| Mutator-like transposase [Arabidopsis thaliana]	808	915	1.00E-126	113.2	28.2	39.5	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	808	719	1.00E-29	89.0	12.0	22.6
Rsa1.0_00598.1.g16657.t1	gb|EOA29684.1| hypothetical protein CARUB_v10016007mg [Capsella rubella]	128	134	4.00E-15	104.7	32.0	46.1	hypothetical protein CARUB_v10016007mg	gbpln	Capsella rubella	AT2G07505.1 | Symbols: | zinc ion binding | chr2:3125671-3126173 FORWARD LENGTH=143	128	143	6.00E-14	111.7	26.6	31.3
Rsa1.0_00598.1.g16658.t3	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	827	871	0	105.3	51.0	62.4	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	827	874	3.00E-41	105.7	11.7	18.1
Rsa1.0_00598.1.g16659.t4	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1632	1274	0	78.1	33.6	45.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1632	575	6.00E-56	35.2	9.9	16.4
Rsa1.0_00598.1.g16660.t1	gb|AAT41847.1| At4g02250 [Arabidopsis thaliana]	184	184	1.00E-88	100.0	87.0	94.0	At4g02250	gbpln	Arabidopsis thaliana	AT4G02250.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:983970-984523 FORWARD LENGTH=160	184	160	2.00E-72	87.0	74.5	81.5
Rsa1.0_00598.1.g16661.t1	ref|XP_002893409.1| hypothetical protein ARALYDRAFT_890118 [Arabidopsis lyrata subsp. lyrata] gi|297339251|gb|EFH69668.1| hypothetical protein ARALYDRAFT_890118 [Arabidopsis lyrata subsp. lyrata]	123	191	4.00E-15	155.3	33.3	54.5	hypothetical protein ARALYDRAFT_890118	gbpln	Arabidopsis lyrata	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	123	384	2.00E-16	312.2	34.1	59.3

Rsa1.0_00598.1.g16662.t3	gb|AAK38380.1|AC079028_3 hypothetical protein [Arabidopsis thaliana]	354	609	3.00E-15	172.0	13.8	20.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	354	681	8.00E-11	192.4	8.2	14.1
Rsa1.0_00599.1.g16663.t1	gb|AAG52211.1|AC022288_10 hypothetical protein; 74056-75837 [Arabidopsis thaliana]	83	503	8.00E-22	606.0	68.7	79.5	hypothetical protein; 74056-75837	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00599.1.g16664.t1	ref|NP_179250.2| Translocon-associated protein (TRAP), alpha subunit [Arabidopsis thaliana] gi|50897256|gb|AAT85767.1| At2g16595 [Arabidopsis thaliana] gi|330251422|gb|AEC06516.1| Translocon-associated protein (TRAP), alpha subunit [Arabidopsis thaliana]	120	251	2.00E-42	209.2	74.2	78.3	Translocon-associated protein (TRAP), alpha subunit	gbpln	Arabidopsis thaliana	AT2G16595.1 | Symbols: | Translocon-associated protein (TRAP), alpha subunit | chr2:7198363-7200086 FORWARD LENGTH=251	120	251	4.00E-45	209.2	74.2	78.3
Rsa1.0_00599.1.g16665.t1	gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]	615	527	4.00E-82	85.7	33.8	47.3	hypothetical protein CARUB_v10022820mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	615	735	9.00E-77	119.5	27.6	38.9
Rsa1.0_00599.1.g16666.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	229	149	2.00E-19	65.1	24.0	33.6	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	229	292	2.00E-12	127.5	17.5	30.6
Rsa1.0_00599.1.g16667.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00599.1.g16668.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00599.1.g16669.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	194	258	1.00E-23	133.0	30.9	42.8	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT5G41220.1 | Symbols: ATGSTT3, GST10C, GSTT3 | glutathione S-transferase THETA 3 | chr5:16494560-16496969 REVERSE LENGTH=590	194	590	4.00E-22	304.1	25.8	37.6
Rsa1.0_00599.1.g16670.t1	ref|XP_002883908.1| hypothetical protein ARALYDRAFT_899780 [Arabidopsis lyrata subsp. lyrata] gi|297329748|gb|EFH60167.1| hypothetical protein ARALYDRAFT_899780 [Arabidopsis lyrata subsp. lyrata]	293	378	1.00E-19	129.0	21.2	30.7	hypothetical protein ARALYDRAFT_899780	gbpln	Arabidopsis lyrata	AT2G05350.1 | Symbols: | unknown protein; Has 22 Blast hits to 16 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:1950455-1954740 FORWARD LENGTH=453	293	453	3.00E-13	154.6	13.0	17.7
Rsa1.0_00599.1.g16671.t1	ref|XP_002883909.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329749|gb|EFH60168.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	184	528	2.00E-13	287.0	35.3	52.2	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00599.1.g16672.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00599.1.g16673.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00599.1.g16674.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00599.1.g16675.t1	ref|XP_002886057.1| amidophosphoribosyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297331897|gb|EFH62316.1| amidophosphoribosyltransferase [Arabidopsis lyrata subsp. lyrata]	566	563	0	99.5	90.3	92.6	amidophosphoribosyltransferase	gbpln	Arabidopsis lyrata	AT2G16570.1 | Symbols: ATASE, ATASE1, ASE1 | GLN phosphoribosyl pyrophosphate amidotransferase 1 | chr2:7180424-7182124 REVERSE LENGTH=566	566	566	0	100.0	89.4	92.0
Rsa1.0_00599.1.g16676.t1	#	#	#	#	#	#	#	-	----	----	AT1G27600.2 | Symbols: IRX9-L, I9H | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:9604083-9605881 REVERSE LENGTH=394	99	394	2.00E-11	398.0	26.3	29.3
Rsa1.0_00599.1.g16677.t2	ref|XP_002872763.1| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein [Arabidopsis lyrata subsp. lyrata] gi|297318600|gb|EFH49022.1| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein [Arabidopsis lyrata subsp. lyrata]	357	342	1.00E-150	95.8	75.9	82.9	3-oxo-5-alpha-steroid 4-dehydrogenase family protein	gbpln	Arabidopsis lyrata	AT2G16530.1 | Symbols: | 3-oxo-5-alpha-steroid 4-dehydrogenase family protein | chr2:7163276-7165064 REVERSE LENGTH=343	357	343	1.00E-151	96.1	75.4	82.9

Rsa1.0_00599.1.g16678.t1	sp|O82475.1|SPE1_BRAJU RecName: Full=Arginine decarboxylase; Short=ADC; Short=ARGDC gi|3342902|gb|AAC62017.1| arginine decarboxylase [Brassica juncea]	705	702	0	99.6	93.3	95.7	RecName: Full=Arginine decarboxylase; Short=ADC; Short=ARGDC gi|3342902|gb|AAC62017.1| arginine decarboxylase	gbpln	Brassica juncea	AT2G16500.1 | Symbols: ADC1, ARGDC1, ARGDC, SPE1 | arginine decarboxylase 1 | chr2:7150796-7152904 REVERSE LENGTH=702	705	702	0	99.6	84.8	90.2
Rsa1.0_00599.1.g16679.t1	gb|ABD64965.1| hypothetical protein 25.t00002 [Brassica oleracea]	204	445	3.00E-19	218.1	30.4	35.3	hypothetical protein 25.t00002	gbpln	Brassica oleracea	AT5G47620.4 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:19302548-19304278 REVERSE LENGTH=453	204	453	8.00E-19	222.1	30.4	32.4
Rsa1.0_00599.1.g16680.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00599.1.g16681.t1	gb|AAC13599.1| similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]	674	928	2.00E-90	137.7	23.7	32.0	similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31)	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	674	746	4.00E-52	110.7	17.7	24.5
Rsa1.0_00599.1.g16682.t1	ref|XP_002884156.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329996|gb|EFH60415.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	109	511	9.00E-50	468.8	91.7	94.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G16120.1 | Symbols: PMT1, ATPMT1 | polyol/monosaccharide transporter 1 | chr2:6996727-6998441 REVERSE LENGTH=511	109	511	2.00E-52	468.8	89.9	95.4
Rsa1.0_00600.1.g16683.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00600.1.g16684.t1	gb|EOA37768.1| hypothetical protein CARUB_v10012626mg [Capsella rubella]	104	90	5.00E-33	86.5	65.4	73.1	hypothetical protein CARUB_v10012626mg	gbpln	Capsella rubella	AT1G27220.1 | Symbols: | paired amphipathic helix repeat-containing protein | chr1:9463806-9465444 FORWARD LENGTH=184	104	184	3.00E-34	176.9	62.5	67.3
Rsa1.0_00600.1.g16685.t1	ref|XP_002893336.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339178|gb|EFH69595.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	347	810	3.00E-26	233.4	31.4	42.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G24220.1 | Symbols: | paired amphipathic helix repeat-containing protein | chr1:8578658-8582413 REVERSE LENGTH=744	347	744	1.00E-17	214.4	26.5	38.0
Rsa1.0_00600.1.g16686.t1	gb|EOA40424.1| hypothetical protein CARUB_v10009149mg [Capsella rubella]	237	442	3.00E-77	186.5	68.4	77.2	hypothetical protein CARUB_v10009149mg	gbpln	Capsella rubella	AT1G24180.1 | Symbols: IAR4 | Thiamin diphosphate-binding fold (THDP-binding) superfamily protein | chr1:8560777-8563382 REVERSE LENGTH=393	237	393	5.00E-79	165.8	69.2	76.8
Rsa1.0_00600.1.g16687.t1	gb|EOA37428.1| hypothetical protein CARUB_v10011392mg [Capsella rubella]	386	390	0	101.0	86.3	90.4	hypothetical protein CARUB_v10011392mg	gbpln	Capsella rubella	AT1G24170.1 | Symbols: GATL8, LGT9 | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:8557451-8558632 REVERSE LENGTH=393	386	393	0	101.8	84.7	88.6
Rsa1.0_00600.1.g16688.t1	ref|XP_002893328.1| hypothetical protein ARALYDRAFT_472677 [Arabidopsis lyrata subsp. lyrata] gi|297339170|gb|EFH69587.1| hypothetical protein ARALYDRAFT_472677 [Arabidopsis lyrata subsp. lyrata]	534	539	0	100.9	70.0	78.7	hypothetical protein ARALYDRAFT_472677	gbpln	Arabidopsis lyrata	AT1G24160.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: guard cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G70100.3). | chr1:8553669-8555830 REVERSE LENGTH=540	534	540	1.00E-173	101.1	68.7	77.9
Rsa1.0_00600.1.g16689.t1	ref|NP_180861.1| receptor like protein 24 [Arabidopsis thaliana] gi|2924789|gb|AAC04918.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|20196994|gb|AAM14862.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|330253681|gb|AEC08775.1| receptor like protein 24 [Arabidopsis thaliana]	877	864	0	98.5	66.8	77.5	receptor like protein 24	gbpln	Arabidopsis thaliana	AT2G33020.1 | Symbols: AtRLP24, RLP24 | receptor like protein 24 | chr2:14013874-14016516 REVERSE LENGTH=864	877	864	0	98.5	66.8	77.5
Rsa1.0_00600.1.g16690.t1	gb|ACB59209.1| group I formin [Brassica oleracea]	747	719	0	96.3	84.1	87.0	group I formin	gbpln	Brassica oleracea	AT1G70140.1 | Symbols: ATFH8, FH8 | formin 8 | chr1:26412688-26415048 REVERSE LENGTH=760	747	760	0	101.7	70.7	82.1
Rsa1.0_00600.1.g16691.t1	gb|ACB59207.1| matrixin family protein [Brassica oleracea]	535	383	0	71.6	63.9	66.0	matrixin family protein	gbpln	Brassica oleracea	AT1G24140.1 | Symbols: | Matrixin family protein | chr1:8536131-8537285 REVERSE LENGTH=384	535	384	1.00E-170	71.8	54.0	58.7
Rsa1.0_00600.1.g16692.t1	gb|ACB59206.1| transducin family protein [Brassica oleracea]	409	410	0	100.2	91.7	94.9	transducin family protein	gbpln	Brassica oleracea	AT1G24130.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:8534183-8535430 REVERSE LENGTH=415	409	415	1.00E-176	101.5	82.6	90.5
Rsa1.0_00600.1.g16693.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	364	1274	3.00E-37	350.0	28.6	40.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	364	303	3.00E-29	83.2	25.3	37.6

Rsa1.0_00600.1.g16694.t1	ref|NP_173822.2| chaperone protein dnaJ 16 [Arabidopsis thaliana] gi|67462409|sp|Q8VXV4.1|DNJ16_ARATH RecName: Full=Chaperone protein dnaJ 16; Short=AtDjB16; Short=AtJ16; AltName: Full=Protein ARG1-LIKE 1; Short=AtARL1 gi|18377835|gb|AAL67104.1| At1g24120/F3I6_4 [Arabidopsis thaliana] gi|34583419|gb|AAP49704.1| ARG1-like protein 1 [Arabidopsis thaliana] gi|109134177|gb|ABG25086.1| At1g24120 [Arabidopsis thaliana] gi|332192359|gb|AEE30480.1| chaperone protein dnaJ 16 [Arabidopsis thaliana]	439	436	0	99.3	91.8	97.3	chaperone protein dnaJ 16	gbpln	Arabidopsis thaliana	AT1G24120.1 | Symbols: ARL1 | ARG1-like 1 | chr1:8529283-8531946 REVERSE LENGTH=436	439	436	0	99.3	91.8	97.3
Rsa1.0_00600.1.g16695.t1	gb|ACB59205.1| peroxidase [Brassica oleracea]	300	331	1.00E-164	110.3	96.0	97.7	peroxidase	gbpln	Brassica oleracea	AT1G24110.1 | Symbols: | Peroxidase superfamily protein | chr1:8527838-8528818 FORWARD LENGTH=326	300	326	1.00E-140	108.7	81.0	90.7
Rsa1.0_00600.1.g16696.t1	ref|NP_180632.1| protein kinase-like protein [Arabidopsis thaliana] gi|75318362|sp|O49339.1|PTI12_ARATH RecName: Full=PTI1-like tyrosine-protein kinase 2; Short=PTI1-2 gi|2880051|gb|AAC02745.1| putative protein kinase [Arabidopsis thaliana] gi|13374083|emb|CAC34450.1| putative PTI1-like protein tyrosine kinase [Arabidopsis thaliana] gi|90093302|gb|ABD85164.1| At2g30740 [Arabidopsis thaliana] gi|110740423|dbj|BAF02106.1| putative protein kinase [Arabidopsis thaliana] gi|330253340|gb|AEC08434.1| PTI1-like tyrosine-protein kinase 2 [Arabidopsis thaliana]	270	366	2.00E-96	135.6	63.7	65.9	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT2G30740.1 | Symbols: | Protein kinase superfamily protein | chr2:13096399-13098285 FORWARD LENGTH=366	270	366	5.00E-99	135.6	63.7	65.9
Rsa1.0_00601.1.g16697.t1	ref|XP_002893522.1| hypothetical protein ARALYDRAFT_473042 [Arabidopsis lyrata subsp. lyrata] gi|297339364|gb|EFH69781.1| hypothetical protein ARALYDRAFT_473042 [Arabidopsis lyrata subsp. lyrata]	299	321	1.00E-112	107.4	81.3	88.6	hypothetical protein ARALYDRAFT_473042	gbpln	Arabidopsis lyrata	AT1G28310.2 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr1:9912534-9913685 REVERSE LENGTH=325	299	325	1.00E-112	108.7	80.6	87.0
Rsa1.0_00601.1.g16698.t1	gb|EOA38805.1| hypothetical protein CARUB_v10011114mg [Capsella rubella]	854	709	0	83.0	65.9	72.1	hypothetical protein CARUB_v10011114mg	gbpln	Capsella rubella	AT1G28320.1 | Symbols: DEG15 | protease-related | chr1:9920673-9924347 REVERSE LENGTH=709	854	709	0	83.0	65.5	71.7
Rsa1.0_00601.1.g16699.t2	gb|ACQ90305.1| dormancy-associated protein 1 [Brassica rapa subsp. pekinensis]	193	128	1.00E-55	66.3	60.6	61.1	dormancy-associated protein 1	gbpln	Brassica rapa	AT1G28330.5 | Symbols: DYL1 | dormancy-associated protein-like 1 | chr1:9934252-9935216 REVERSE LENGTH=159	193	159	9.00E-51	82.4	57.0	58.5
Rsa1.0_00601.1.g16700.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	490	1231	3.00E-81	251.2	37.1	51.4	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	490	575	1.00E-43	117.3	26.3	42.4
Rsa1.0_00601.1.g16701.t1	gb|EOA39898.1| hypothetical protein CARUB_v10008578mg [Capsella rubella]	629	626	0	99.5	89.5	94.9	hypothetical protein CARUB_v10008578mg	gbpln	Capsella rubella	AT1G28340.1 | Symbols: AtRLP4, RLP4 | receptor like protein 4 | chr1:9940175-9943252 FORWARD LENGTH=626	629	626	0	99.5	89.7	95.5
Rsa1.0_00601.1.g16702.t1	ref|XP_002890772.1| ATERF12/ERF12 [Arabidopsis lyrata subsp. lyrata] gi|297336614|gb|EFH67031.1| ATERF12/ERF12 [Arabidopsis lyrata subsp. lyrata]	182	183	1.00E-66	100.5	79.1	86.8	ATERF12/ERF12	gbpln	Arabidopsis lyrata	AT1G28360.1 | Symbols: ERF12, ATERF12 | ERF domain protein 12 | chr1:9951934-9952503 FORWARD LENGTH=189	182	189	7.00E-67	103.8	78.0	85.7
Rsa1.0_00601.1.g16703.t1	gb|EOA37505.1| hypothetical protein CARUB_v10011676mg [Capsella rubella]	161	168	4.00E-40	104.3	63.4	73.9	hypothetical protein CARUB_v10011676mg	gbpln	Capsella rubella	AT1G28370.1 | Symbols: ERF11, ATERF11 | ERF domain protein 11 | chr1:9956351-9956851 REVERSE LENGTH=166	161	166	9.00E-40	103.1	61.5	70.2
Rsa1.0_00601.1.g16704.t1	dbj|BAJ34587.1| unnamed protein product [Thellungiella halophila]	607	612	0	100.8	85.0	91.9	unnamed protein product	----	----	AT1G28380.1 | Symbols: NSL1 | MAC/Perforin domain-containing protein | chr1:9963696-9966060 FORWARD LENGTH=612	607	612	0	100.8	79.2	88.8
Rsa1.0_00601.1.g16705.t1	gb|EOA36323.1| hypothetical protein CARUB_v10010643mg [Capsella rubella] gi|482572138|gb|EOA36325.1| hypothetical protein CARUB_v10010643mg [Capsella rubella]	132	127	3.00E-25	96.2	41.7	43.9	hypothetical protein CARUB_v10010643mg	gbpln	Capsella rubella	AT1G28395.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G33847.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:9970134-9971433 REVERSE LENGTH=95	132	95	5.00E-27	72.0	40.2	43.2

Rsa1.0_00601.1.g16706.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00601.1.g16707.t1	gb|EOA38190.1| hypothetical protein CARUB_v10009667mg [Capsella rubella]	318	337	1.00E-124	106.0	80.2	87.1	hypothetical protein CARUB_v10009667mg	gbpln	Capsella rubella	AT1G28400.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G33850.1); Has 45374 Blast hits to 18870 proteins in 668 species: Archae - 72; Bacteria - 1460; Metazoa - 1191; Fungi - 1038; Plants - 174; Viruses - 64; Other Eukaryotes - 41375 (source: NCBI BLink). | chr1:9972732-9973739 REVERSE LENGTH=335	318	335	1.00E-122	105.3	80.8	87.7
Rsa1.0_00601.1.g16708.t1	ref|NP_174163.2| uncharacterized protein [Arabidopsis thaliana] gi|332192853|gb|AEE30974.1| uncharacterized protein AT1G28410 [Arabidopsis thaliana]	256	277	1.00E-96	108.2	75.0	87.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G28410.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT4G31340.2); Has 425 Blast hits to 402 proteins in 77 species: Archae - 4; Bacteria - 22; Metazoa - 249; Fungi - 4; Plants - 98; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink). | chr1:9976596-9979080 REVERSE LENGTH=277	256	277	3.00E-99	108.2	75.0	87.5
Rsa1.0_00601.1.g16709.t1	ref|XP_002890775.1| HB-1 [Arabidopsis lyrata subsp. lyrata] gi|297336617|gb|EFH67034.1| HB-1 [Arabidopsis lyrata subsp. lyrata]	1720	1705	0	99.1	77.7	85.4	HB-1	gbpln	Arabidopsis lyrata	AT1G28420.1 | Symbols: HB-1 | homeobox-1 | chr1:9979936-9987460 FORWARD LENGTH=1705	1720	1705	0	99.1	76.6	84.5
Rsa1.0_00601.1.g16710.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00601.1.g16711.t1	ref|XP_002890776.1| hypothetical protein ARALYDRAFT_473063 [Arabidopsis lyrata subsp. lyrata] gi|297336618|gb|EFH67035.1| hypothetical protein ARALYDRAFT_473063 [Arabidopsis lyrata subsp. lyrata]	996	996	0	100.0	84.0	90.9	hypothetical protein ARALYDRAFT_473063	gbpln	Arabidopsis lyrata	AT1G28440.1 | Symbols: HSL1 | HAESA-like 1 | chr1:9996914-10000171 FORWARD LENGTH=996	996	996	0	100.0	83.8	90.6
Rsa1.0_00601.1.g16712.t1	ref|NP_564309.1| NAC domain containing protein 10 [Arabidopsis thaliana] gi|332192859|gb|AEE30980.1| NAC domain containing protein 10 [Arabidopsis thaliana]	314	314	1.00E-174	100.0	94.3	95.9	NAC domain containing protein 10	gbpln	Arabidopsis thaliana	AT1G28470.1 | Symbols: ANAC010, SND3, NAC010 | NAC domain containing protein 10 | chr1:10010259-10011867 FORWARD LENGTH=314	314	314	1.00E-176	100.0	94.3	95.9
Rsa1.0_00602.1.g16713.t1	gb|EOA31555.1| hypothetical protein CARUB_v10014747mg [Capsella rubella]	112	182	2.00E-49	162.5	86.6	88.4	hypothetical protein CARUB_v10014747mg	gbpln	Capsella rubella	AT3G13550.1 | Symbols: FUS9, EMB144, COP10, CIN4 | Ubiquitin-conjugating enzyme family protein | chr3:4423569-4424797 REVERSE LENGTH=182	112	182	4.00E-52	162.5	85.7	88.4
Rsa1.0_00602.1.g16714.t1	ref|XP_002884972.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297330812|gb|EFH61231.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	503	501	0	99.6	84.5	90.5	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT3G13560.2 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr3:4425484-4427284 REVERSE LENGTH=505	503	505	0	100.4	84.9	91.1
Rsa1.0_00602.1.g16715.t1	ref|NP_187968.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|332641858|gb|AEE75379.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	560	513	6.00E-47	91.6	19.8	25.5	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G13590.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:4435316-4437334 REVERSE LENGTH=513	560	513	1.00E-49	91.6	19.8	25.5
Rsa1.0_00602.1.g16716.t1	gb|EOA30149.1| hypothetical protein CARUB_v10013255mg [Capsella rubella]	582	608	0	104.5	87.6	92.3	hypothetical protein CARUB_v10013255mg	gbpln	Capsella rubella	AT3G13600.1 | Symbols: | calmodulin-binding family protein | chr3:4445102-4447383 FORWARD LENGTH=605	582	605	0	104.0	85.7	91.6
Rsa1.0_00602.1.g16717.t1	ref|XP_002885061.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297330901|gb|EFH61320.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	361	361	0	100.0	92.0	97.8	oxidoreductase	gbpln	Arabidopsis lyrata	AT3G13610.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:4449448-4450616 FORWARD LENGTH=361	361	361	0	100.0	89.2	96.1
Rsa1.0_00602.1.g16718.t1	gb|EOA30472.1| hypothetical protein CARUB_v10013597mg [Capsella rubella]	472	478	0	101.3	91.1	97.0	hypothetical protein CARUB_v10013597mg	gbpln	Capsella rubella	AT3G13620.1 | Symbols: | Amino acid permease family protein | chr3:4450904-4452556 REVERSE LENGTH=478	472	478	0	101.3	90.3	96.4

Rsa1.0_00602.1.g16719.t1	ref|NP_187974.1| disease resistance-responsive, dirigent domain-containing protein [Arabidopsis thaliana] gi|9294009|dbj|BAB01912.1| disease resistance response protein-like [Arabidopsis thaliana] gi|26451116|dbj|BAC42662.1| putative dirigent protein [Arabidopsis thaliana] gi|37201988|gb|AAQ89609.1| At3g13650 [Arabidopsis thaliana] gi|332641866|gb|AEE75387.1| disease resistance-responsive, dirigent domain-containing protein [Arabidopsis thaliana]	186	186	4.00E-86	100.0	81.2	90.9	disease resistance-responsive, dirigent domain-containing protein	gbpln	Arabidopsis thaliana	AT3G13650.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr3:4463056-4463616 FORWARD LENGTH=186	186	186	1.00E-88	100.0	81.2	90.9
Rsa1.0_00602.1.g16720.t1	ref|XP_002882838.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328678|gb|EFH59097.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	679	703	0	103.5	95.4	97.3	kinase family protein	gbpln	Arabidopsis lyrata	AT3G13670.1 | Symbols: | Protein kinase family protein | chr3:4469434-4473234 FORWARD LENGTH=703	679	703	0	103.5	93.8	96.3
Rsa1.0_00602.1.g16721.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00602.1.g16722.t1	ref|XP_002882838.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328678|gb|EFH59097.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	695	703	0	101.2	93.5	96.1	kinase family protein	gbpln	Arabidopsis lyrata	AT3G13670.1 | Symbols: | Protein kinase family protein | chr3:4469434-4473234 FORWARD LENGTH=703	695	703	0	101.2	92.7	95.7
Rsa1.0_00602.1.g16723.t3	gb|EOA29951.1| hypothetical protein CARUB_v10013055mg [Capsella rubella]	276	735	3.00E-36	266.3	39.1	45.7	hypothetical protein CARUB_v10013055mg	gbpln	Capsella rubella	AT3G13682.1 | Symbols: LDL2 | LSD1-like2 | chr3:4479193-4481509 REVERSE LENGTH=746	276	746	1.00E-37	270.3	38.0	45.3
Rsa1.0_00602.1.g16724.t2	ref|NP_187982.1| protein kinase protein with adenine nucleotide alpha hydrolases-like domain-containing protein [Arabidopsis thaliana] gi|9294015|dbj|BAB01918.1| unnamed protein product [Arabidopsis thaliana] gi|332641878|gb|AEE75399.1| protein kinase protein with adenine nucleotide alpha hydrolases-like domain-containing protein [Arabidopsis thaliana]	756	753	0	99.6	92.5	95.5	protein kinase protein with adenine nucleotide alpha hydrolases-like domain-containing protein	gbpln	Arabidopsis thaliana	AT3G13690.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr3:4486920-4490011 FORWARD LENGTH=753	756	753	0	99.6	92.5	95.5
Rsa1.0_00602.1.g16725.t1	ref|NP_001118622.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|26449895|dbj|BAC42069.1| unknown protein [Arabidopsis thaliana] gi|332641880|gb|AEE75401.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	270	287	1.00E-126	106.3	86.3	90.4	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT3G13700.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:4490859-4492632 REVERSE LENGTH=287	270	287	1.00E-129	106.3	86.3	90.4
Rsa1.0_00602.1.g16726.t1	gb|EOA33062.1| hypothetical protein CARUB_v10016395mg [Capsella rubella]	182	188	6.00E-75	103.3	77.5	85.2	hypothetical protein CARUB_v10016395mg	gbpln	Capsella rubella	AT3G13720.1 | Symbols: PRA1.F3, PRA8 | PRA1 (Prenylated rab acceptor) family protein | chr3:4495202-4495768 REVERSE LENGTH=188	182	188	1.00E-70	103.3	76.9	85.2
Rsa1.0_00602.1.g16727.t1	dbj|BAB01922.1| cytochrome P450-like protein [Arabidopsis thaliana]	463	464	0	100.2	86.6	90.9	cytochrome P450-like protein	gbpln	Arabidopsis thaliana	AT3G13730.1 | Symbols: CYP90D1 | cytochrome P450, family 90, subfamily D, polypeptide 1 | chr3:4498330-4500836 REVERSE LENGTH=491	463	491	0	106.0	86.6	90.9
Rsa1.0_00603.1.g16728.t1	gb|EOA20111.1| hypothetical protein CARUB_v10000390mg [Capsella rubella]	672	673	0	100.1	69.8	83.3	hypothetical protein CARUB_v10000390mg	gbpln	Capsella rubella	AT4G02420.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr4:1064363-1066372 REVERSE LENGTH=669	672	669	0	99.6	70.2	81.5
Rsa1.0_00603.1.g16729.t1	gb|EOA20111.1| hypothetical protein CARUB_v10000390mg [Capsella rubella]	676	673	0	99.6	67.5	81.2	hypothetical protein CARUB_v10000390mg	gbpln	Capsella rubella	AT4G02420.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr4:1064363-1066372 REVERSE LENGTH=669	676	669	0	99.0	67.9	80.0
Rsa1.0_00603.1.g16730.t1	ref|NP_567234.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana] gi|75318755|sp|O81291.1|LRK44_ARATH RecName: Full=L-type lectin-domain containing receptor kinase IV.4; Short=LecRK-IV.4; Flags: Precursor gi|3193290|gb|AAC19274.1| T14P8.4 [Arabidopsis thaliana] gi|7269002|emb|CAB80735.1| AT4g02420 [Arabidopsis thaliana] gi|332656768|gb|AEE82168.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana]	667	669	0	100.3	72.6	84.0	concanavalin A-like lectin kinase-like protein	gbpln	Arabidopsis thaliana	AT4G02420.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr4:1064363-1066372 REVERSE LENGTH=669	667	669	0	100.3	72.6	84.0

Rsa1.0_00603.1.g16731.t1	ref|XP_002872842.1| hypothetical protein ARALYDRAFT_911979 [Arabidopsis lyrata subsp. lyrata] gi|297318679|gb|EFH49101.1| hypothetical protein ARALYDRAFT_911979 [Arabidopsis lyrata subsp. lyrata]	326	335	1.00E-143	102.8	77.3	84.4	hypothetical protein ARALYDRAFT_911979	gbpln	Arabidopsis lyrata	AT4G02405.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:1057999-1059671 REVERSE LENGTH=333	326	333	1.00E-141	102.1	76.4	84.0
Rsa1.0_00603.1.g16732.t1	ref|XP_002874918.1| poly(ADP-ribose) polymerase [Arabidopsis lyrata subsp. lyrata] gi|297320755|gb|EFH51177.1| poly(ADP-ribose) polymerase [Arabidopsis lyrata subsp. lyrata]	636	636	0	100.0	88.5	92.6	poly(ADP-ribose) polymerase	gbpln	Arabidopsis lyrata	AT4G02390.1 | Symbols: APP, PARP1, ATPARP1, PP | poly(ADP-ribose) polymerase | chr4:1050104-1053960 FORWARD LENGTH=637	636	637	0	100.2	86.0	91.7
Rsa1.0_00603.1.g16733.t1	gb|EOA14700.1| hypothetical protein CARUB_v10027975mg [Capsella rubella]	731	766	0	104.8	69.6	83.0	hypothetical protein CARUB_v10027975mg	gbpln	Capsella rubella	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	731	769	0	105.2	69.1	82.4
Rsa1.0_00603.1.g16734.t1	ref|XP_002872843.1| hypothetical protein ARALYDRAFT_327563 [Arabidopsis lyrata subsp. lyrata] gi|297318680|gb|EFH49102.1| hypothetical protein ARALYDRAFT_327563 [Arabidopsis lyrata subsp. lyrata]	94	180	3.00E-38	191.5	84.0	89.4	hypothetical protein ARALYDRAFT_327563	gbpln	Arabidopsis lyrata	AT4G02380.1 | Symbols: SAG21, AtLEA5 | senescence-associated gene 21 | chr4:1046414-1046807 REVERSE LENGTH=97	94	97	8.00E-38	103.2	85.1	90.4
Rsa1.0_00603.1.g16735.t1	gb|ABD65624.1| hypothetical protein 23.t00036 [Brassica oleracea]	794	842	7.00E-50	106.0	23.2	34.4	hypothetical protein 23.t00036	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	794	874	2.00E-28	110.1	10.2	17.6
Rsa1.0_00603.1.g16736.t1	gb|AAM63118.1| unknown [Arabidopsis thaliana]	162	167	2.00E-72	103.1	84.6	91.4	unknown	gbpln	Arabidopsis thaliana	AT4G02370.1 | Symbols: | Protein of unknown function, DUF538 | chr4:1042458-1042961 FORWARD LENGTH=167	162	167	2.00E-74	103.1	84.0	90.7
Rsa1.0_00603.1.g16737.t1	dbj|BAF01687.1| hypothetical protein [Arabidopsis thaliana]	1269	1072	0	84.5	45.5	59.2	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G02270.1 | Symbols: RHS13 | root hair specific 13 | chr4:992383-992996 REVERSE LENGTH=165	1269	165	7.00E-72	13.0	9.6	11.0
Rsa1.0_00603.1.g16738.t1	gb|AAT41847.1| At4g02250 [Arabidopsis thaliana]	184	184	7.00E-90	100.0	87.5	95.1	At4g02250	gbpln	Arabidopsis thaliana	AT4G02250.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:983970-984523 FORWARD LENGTH=160	184	160	4.00E-74	87.0	75.5	83.2
Rsa1.0_00603.1.g16739.t1	ref|NP_175139.1| receptor like protein 6 [Arabidopsis thaliana] gi|12321005|gb|AAG50623.1|AC083835_8 disease resistance protein, putative [Arabidopsis thaliana] gi|332193999|gb|AEE32120.1| receptor like protein 6 [Arabidopsis thaliana]	994	994	0	100.0	65.1	75.8	receptor like protein 6	gbpln	Arabidopsis thaliana	AT1G45616.1 | Symbols: AtRLP6, RLP6 | receptor like protein 6 | chr1:17183550-17186534 REVERSE LENGTH=994	994	994	0	100.0	65.1	75.8
Rsa1.0_00603.1.g16740.t12	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1356	1213	0	89.5	43.1	55.2	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1356	746	9.00E-67	55.0	10.8	14.7
Rsa1.0_00604.1.g16741.t1	gb|EOA29965.1| hypothetical protein CARUB_v10013068mg [Capsella rubella]	423	722	4.00E-23	170.7	13.9	17.0	hypothetical protein CARUB_v10013068mg	gbpln	Capsella rubella	AT3G16000.1 | Symbols: MFP1 | MAR binding filament-like protein 1 | chr3:5431041-5433613 REVERSE LENGTH=726	423	726	4.00E-24	171.6	13.7	16.3
Rsa1.0_00604.1.g16742.t2	gb|AFO11038.1| S domain subfamily receptor-like kinase [Arabidopsis thaliana]	875	852	0	97.4	75.7	83.7	S domain subfamily receptor-like kinase	gbpln	Arabidopsis thaliana	AT3G16030.1 | Symbols: CES101 | lectin protein kinase family protein | chr3:5439609-5442802 FORWARD LENGTH=850	875	850	0	97.1	75.5	83.1
Rsa1.0_00604.1.g16743.t1	ref|XP_002862267.1| hypothetical protein ARALYDRAFT_497537 [Arabidopsis lyrata subsp. lyrata] gi|297307590|gb|EFH38525.1| hypothetical protein ARALYDRAFT_497537 [Arabidopsis lyrata subsp. lyrata]	308	314	1.00E-154	101.9	85.7	93.2	hypothetical protein ARALYDRAFT_497537	gbpln	Arabidopsis lyrata	AT3G16050.1 | Symbols: A37, ATPDX1.2, PDX1.2 | pyridoxine biosynthesis 1.2 | chr3:5444121-5445065 REVERSE LENGTH=314	308	314	1.00E-156	101.9	85.4	93.2
Rsa1.0_00604.1.g16744.t2	gb|EOA30013.1| hypothetical protein CARUB_v10013116mg [Capsella rubella]	793	687	0	86.6	81.1	83.6	hypothetical protein CARUB_v10013116mg	gbpln	Capsella rubella	AT3G16060.1 | Symbols: | ATP binding microtubule motor family protein | chr3:5447503-5451196 FORWARD LENGTH=684	793	684	0	86.3	80.1	82.8
Rsa1.0_00604.1.g16745.t1	ref|XP_002882977.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297328817|gb|EFH59236.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	502	502	0	100.0	85.3	91.2	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G16090.1 | Symbols: | RING/U-box superfamily protein | chr3:5456513-5458694 FORWARD LENGTH=492	502	492	0	98.0	83.1	89.0
Rsa1.0_00604.1.g16746.t1	ref|XP_002882990.1| hypothetical protein ARALYDRAFT_897930 [Arabidopsis lyrata subsp. lyrata] gi|297328830|gb|EFH59249.1| hypothetical protein ARALYDRAFT_897930 [Arabidopsis lyrata subsp. lyrata]	212	309	3.00E-30	145.8	35.8	46.7	hypothetical protein ARALYDRAFT_897930	gbpln	Arabidopsis lyrata	AT3G02470.4 | Symbols: | S-adenosylmethionine decarboxylase | chr3:510223-511323 FORWARD LENGTH=366	212	366	5.00E-26	172.6	30.7	43.9
Rsa1.0_00604.1.g16747.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00604.1.g16748.t1	ref|XP_002882981.1| hypothetical protein ARALYDRAFT_479067 [Arabidopsis lyrata subsp. lyrata] gi|297328821|gb|EFH59240.1| hypothetical protein ARALYDRAFT_479067 [Arabidopsis lyrata subsp. lyrata]	552	577	0	104.5	78.3	88.6	hypothetical protein ARALYDRAFT_479067	gbpln	Arabidopsis lyrata	AT3G16130.1 | Symbols: ATROPGEF13, ROPGEF13, PIRF2 | RHO guanyl-nucleotide exchange factor 13 | chr3:5466246-5468512 FORWARD LENGTH=576	552	576	0	104.3	76.4	87.0
Rsa1.0_00604.1.g16749.t1	ref|NP_188235.1| photosystem I reaction center subunit VI-1 [Arabidopsis thaliana] gi|20143886|sp|Q9SUI7.1|PSAH1_ARATH RecName: Full=Photosystem I reaction center subunit VI-1, chloroplastic; AltName: Full=PSI-H1; Flags: Precursor gi|5734522|emb|CAB52749.1| photosystem I subunit VI precursor [Arabidopsis thaliana] gi|9294461|dbj|BAB02680.1| photosystem I subunit VI (PSI-H) precursor-like protein [Arabidopsis thaliana] gi|21618081|gb|AAM67131.1| photosystem I subunit VI precursor [Arabidopsis thaliana] gi|110740595|dbj|BAE98402.1| PSI-H protein [Arabidopsis thaliana] gi|114050607|gb|ABI49453.1| At3g16140 [Arabidopsis thaliana] gi|332642255|gb|AEE75776.1| photosystem I reaction center subunit VI-1 [Arabidopsis thaliana]	132	145	2.00E-43	109.8	72.7	75.8	photosystem I reaction center subunit VI-1	gbpln	Arabidopsis thaliana	AT3G16140.1 | Symbols: PSAH-1 | photosystem I subunit H-1 | chr3:5468670-5469415 REVERSE LENGTH=145	132	145	4.00E-46	109.8	72.7	75.8
Rsa1.0_00604.1.g16750.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00604.1.g16751.t1	gb|EOA31031.1| hypothetical protein CARUB_v10014177mg [Capsella rubella]	323	325	1.00E-176	100.6	94.1	96.9	hypothetical protein CARUB_v10014177mg	gbpln	Capsella rubella	AT3G16150.1 | Symbols: | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:5471794-5473033 FORWARD LENGTH=325	323	325	1.00E-177	100.6	93.2	96.6
Rsa1.0_00604.1.g16752.t1	dbj|BAB02797.1| unnamed protein product [Arabidopsis thaliana]	80	345	4.00E-16	431.3	61.3	72.5	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G13280.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:4295327-4297000 REVERSE LENGTH=383	80	383	3.00E-15	478.8	55.0	65.0
Rsa1.0_00604.1.g16753.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	211	442	5.00E-87	209.5	72.0	78.7	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	211	343	1.00E-25	162.6	25.6	32.2
Rsa1.0_00604.1.g16754.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	246	258	2.00E-39	104.9	44.7	60.6	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	246	302	2.00E-33	122.8	40.2	58.1
Rsa1.0_00604.1.g16755.t1	gb|ABD65168.1| hypothetical protein 40.t00055 [Brassica oleracea]	121	154	6.00E-34	127.3	53.7	71.9	hypothetical protein 40.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00604.1.g16756.t1	ref|XP_002882983.1| hypothetical protein ARALYDRAFT_318392 [Arabidopsis lyrata subsp. lyrata] gi|297328823|gb|EFH59242.1| hypothetical protein ARALYDRAFT_318392 [Arabidopsis lyrata subsp. lyrata]	593	608	0	102.5	87.0	94.1	hypothetical protein ARALYDRAFT_318392	gbpln	Arabidopsis lyrata	AT3G16170.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr3:5476490-5480128 FORWARD LENGTH=544	593	544	0	91.7	81.5	87.4
Rsa1.0_00604.1.g16757.t1	gb|EOA31619.1| hypothetical protein CARUB_v10014816mg [Capsella rubella]	158	158	1.00E-59	100.0	73.4	83.5	hypothetical protein CARUB_v10014816mg	gbpln	Capsella rubella	AT3G16175.1 | Symbols: | Thioesterase superfamily protein | chr3:5480497-5481208 FORWARD LENGTH=157	158	157	2.00E-60	99.4	70.9	83.5
Rsa1.0_00604.1.g16758.t1	ref|NP_188239.1| major facilitator protein [Arabidopsis thaliana] gi|310947330|sp|Q8LPL2.2|PTR32_ARATH RecName: Full=Probable peptide/nitrate transporter At3g16180 gi|332642260|gb|AEE75781.1| probable peptide/nitrate transporter [Arabidopsis thaliana]	594	591	0	99.5	86.4	91.2	major facilitator protein	gbpln	Arabidopsis thaliana	AT3G16180.1 | Symbols: | Major facilitator superfamily protein | chr3:5481477-5484943 REVERSE LENGTH=591	594	591	0	99.5	86.4	91.2
Rsa1.0_00604.1.g16759.t1	ref|XP_002885129.1| hypothetical protein ARALYDRAFT_479073 [Arabidopsis lyrata subsp. lyrata] gi|297330969|gb|EFH61388.1| hypothetical protein ARALYDRAFT_479073 [Arabidopsis lyrata subsp. lyrata]	477	456	0	95.6	84.7	89.1	hypothetical protein ARALYDRAFT_479073	gbpln	Arabidopsis lyrata	AT3G16200.1 | Symbols: | unknown protein; Has 97 Blast hits to 97 proteins in 15 species: Archae - 0; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink). | chr3:5491619-5493605 REVERSE LENGTH=456	477	456	0	95.6	84.5	89.1

Rsa1.0_00604.1.g16760.t1	gb|EOA31266.1| hypothetical protein CARUB_v10014438mg [Capsella rubella]	278	258	6.00E-93	92.8	62.9	72.3	hypothetical protein CARUB_v10014438mg	gbpln	Capsella rubella	AT3G16220.1 | Symbols: | Predicted eukaryotic LigT | chr3:5497713-5499068 FORWARD LENGTH=257	278	257	1.00E-91	92.4	59.7	70.5
Rsa1.0_00604.1.g16761.t1	gb|EOA31266.1| hypothetical protein CARUB_v10014438mg [Capsella rubella]	249	258	1.00E-77	103.6	59.4	71.9	hypothetical protein CARUB_v10014438mg	gbpln	Capsella rubella	AT3G16220.1 | Symbols: | Predicted eukaryotic LigT | chr3:5497713-5499068 FORWARD LENGTH=257	249	257	1.00E-78	103.2	59.4	70.7
Rsa1.0_00604.1.g16762.t1	ref|NP_188245.1| aquaporin TIP2-1 [Arabidopsis thaliana] gi|32363275|sp|Q41951.2|TIP21_ARATH RecName: Full=Aquaporin TIP2-1; AltName: Full=Delta-tonoplast intrinsic protein; Short=Delta-TIP; AltName: Full=Tonoplast intrinsic protein 2-1; Short=AtTIP2;1 gi|1145697|gb|AAC49281.1| delta tonoplast integral protein [Arabidopsis thaliana] gi|9279707|dbj|BAB01264.1| delta tonoplast intrinsic protein [Arabidopsis thaliana] gi|21554052|gb|AAM63133.1| delta tonoplast integral protein delta-TIP [Arabidopsis thaliana] gi|110739746|dbj|BAF01780.1| delta tonoplast integral protein [Arabidopsis thaliana] gi|332642268|gb|AEE75789.1| aquaporin TIP2-1 [Arabidopsis thaliana]	249	250	1.00E-128	100.4	95.6	98.4	aquaporin TIP2-1	gbpln	Arabidopsis thaliana	AT3G16240.1 | Symbols: DELTA-TIP, TIP2;1, DELTA-TIP1, AQP1, ATTIP2;1 | delta tonoplast integral protein | chr3:5505534-5506788 FORWARD LENGTH=250	249	250	1.00E-130	100.4	95.6	98.4
Rsa1.0_00604.1.g16763.t1	gb|EOA31467.1| hypothetical protein CARUB_v10014651mg [Capsella rubella]	204	205	1.00E-105	100.5	92.6	94.6	hypothetical protein CARUB_v10014651mg	gbpln	Capsella rubella	AT3G16250.1 | Symbols: NDF4 | NDH-dependent cyclic electron flow 1 | chr3:5507091-5508320 REVERSE LENGTH=204	204	204	1.00E-102	100.0	89.2	91.7
Rsa1.0_00604.1.g16764.t1	gb|EOA31439.1| hypothetical protein CARUB_v10014623mg [Capsella rubella]	204	210	2.00E-94	102.9	84.3	92.2	hypothetical protein CARUB_v10014623mg	gbpln	Capsella rubella	AT3G16330.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52140.1); Has 109 Blast hits to 109 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 109; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5535263-5535880 FORWARD LENGTH=205	204	205	4.00E-93	100.5	80.9	88.7
Rsa1.0_00604.1.g16765.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00604.1.g16766.t1	ref|NP_001189911.1| ABC transporter G family member 29 [Arabidopsis thaliana] gi|332642279|gb|AEE75800.1| ABC transporter G family member 29 [Arabidopsis thaliana]	333	1411	1.00E-122	423.7	74.5	80.8	ABC transporter G family member 29	gbpln	Arabidopsis thaliana	AT3G16340.2 | Symbols: PDR1 | pleiotropic drug resistance 1 | chr3:5539897-5546263 FORWARD LENGTH=1411	333	1411	1.00E-125	423.7	74.5	80.8
Rsa1.0_00604.1.g16767.t1	gb|AFP47629.1| nitrile-specifier protein [Schouwia purpurea]	467	467	0	100.0	93.8	97.2	nitrile-specifier protein	gbpln	Schouwia purpurea	AT3G16400.2 | Symbols: ATMLP-470 | nitrile specifier protein 1 | chr3:5566516-5568330 FORWARD LENGTH=470	467	470	0	100.6	80.5	88.0
Rsa1.0_00604.1.g16768.t1	gb|AAB63636.1| jasmonate inducible protein isolog [Arabidopsis thaliana] gi|9279640|dbj|BAB01140.1| jasmonate inducible protein; myrosinase binding protein-like [Arabidopsis thaliana]	463	429	1.00E-173	92.7	71.3	78.8	jasmonate inducible protein isolog	gbpln	Arabidopsis thaliana	AT1G52030.1 | Symbols: MBP2, MBP1.2, F-ATMBP | myrosinase-binding protein 2 | chr1:19346090-19348282 REVERSE LENGTH=642	463	642	1.00E-116	138.7	52.5	68.0
Rsa1.0_00604.1.g16769.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00605.1.g16770.t1	ref|XP_002892571.1| protein phosphatase 2a-2 [Arabidopsis lyrata subsp. lyrata] gi|297338413|gb|EFH68830.1| protein phosphatase 2a-2 [Arabidopsis lyrata subsp. lyrata]	306	306	1.00E-177	100.0	97.1	98.4	protein phosphatase 2a-2	gbpln	Arabidopsis lyrata	AT1G10430.1 | Symbols: PP2A-2 | protein phosphatase 2A-2 | chr1:3428705-3430437 REVERSE LENGTH=306	306	306	1.00E-179	100.0	96.7	98.4
Rsa1.0_00605.1.g16771.t1	ref|XP_002886670.1| hypothetical protein ARALYDRAFT_893615 [Arabidopsis lyrata subsp. lyrata] gi|297332511|gb|EFH62929.1| hypothetical protein ARALYDRAFT_893615 [Arabidopsis lyrata subsp. lyrata]	266	264	4.00E-95	99.2	71.1	81.6	hypothetical protein ARALYDRAFT_893615	gbpln	Arabidopsis lyrata	AT1G59640.1 | Symbols: ZCW32, BPE, BPEub | BIG PETAL P | chr1:21909464-21911030 REVERSE LENGTH=264	266	264	1.00E-96	99.2	71.8	81.6
Rsa1.0_00605.1.g16772.t5	gb|EOA40541.1| hypothetical protein CARUB_v10009270mg, partial [Capsella rubella] gi|482576355|gb|EOA40542.1| hypothetical protein CARUB_v10009270mg, partial [Capsella rubella]	380	417	1.00E-127	109.7	68.2	75.5	hypothetical protein CARUB_v10009270mg, partial	gbpln	Capsella rubella	AT1G10417.1 | Symbols: | Encodes protein with unknown function whose expression is repressed by inoculation with Agrobacterium tumerifaciens. | chr1:3424616-3427457 REVERSE LENGTH=431	380	431	1.00E-85	113.4	53.7	64.5
Rsa1.0_00605.1.g16773.t1	ref|XP_002892568.1| hypothetical protein ARALYDRAFT_471155 [Arabidopsis lyrata subsp. lyrata] gi|297338410|gb|EFH68827.1| hypothetical protein ARALYDRAFT_471155 [Arabidopsis lyrata subsp. lyrata]	504	485	0	96.2	82.7	88.9	hypothetical protein ARALYDRAFT_471155	gbpln	Arabidopsis lyrata	AT1G10410.1 | Symbols: | Protein of unknown function (DUF1336) | chr1:3416842-3419264 REVERSE LENGTH=485	504	485	0	96.2	83.3	89.3

<table>
<tr><td>Rsa1.0_00605.1.g16774.t1</td><td>ref|NP_172510.2| Nucleoporin autopeptidase [Arabidopsis thaliana] gi|79317517|ref|NP_001031018.1| Nucleoporin autopeptidase [Arabidopsis thaliana] gi|19310423|gb|AAL84948.1| At1g10390/F14N23_29 [Arabidopsis thaliana] gi|27764948|gb|AAO23595.1| At1g10390/F14N23_29 [Arabidopsis thaliana] gi|110742211|dbj|BAE99032.1| hypothetical protein [Arabidopsis thaliana] gi|332190453|gb|AEE28574.1| Nucleoporin autopeptidase [Arabidopsis thaliana] gi|332190454|gb|AEE28575.1| Nucleoporin autopeptidase [Arabidopsis thaliana]</td><td>1055</td><td>1041</td><td>0</td><td>98.7</td><td>84.6</td><td>90.2</td><td>Nucleoporin autopeptidase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10390.2 | Symbols: | Nucleoporin autopeptidase | chr1:3407265-3412045 REVERSE LENGTH=1041</td><td>1055</td><td>1041</td><td>0</td><td>98.7</td><td>84.6</td><td>90.2</td></tr>
<tr><td>Rsa1.0_00605.1.g16775.t1</td><td>ref|XP_002889802.1| hypothetical protein ARALYDRAFT_888300 [Arabidopsis lyrata subsp. lyrata] gi|297335644|gb|EFH66061.1| hypothetical protein ARALYDRAFT_888300 [Arabidopsis lyrata subsp. lyrata]</td><td>294</td><td>306</td><td>1.00E-135</td><td>104.1</td><td>83.3</td><td>84.7</td><td>hypothetical protein ARALYDRAFT_888300</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10380.1 | Symbols: | Putative membrane lipoprotein | chr1:3400706-3402110 FORWARD LENGTH=305</td><td>294</td><td>305</td><td>1.00E-134</td><td>103.7</td><td>81.3</td><td>83.3</td></tr>
<tr><td>Rsa1.0_00605.1.g16776.t1</td><td>dbj|BAJ33933.1| unnamed protein product [Thellungiella halophila]</td><td>227</td><td>228</td><td>1.00E-115</td><td>100.4</td><td>87.7</td><td>95.2</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G10370.1 | Symbols: GST30, ATGSTU17, GST30B, ERD9 | Glutathione S-transferase family protein | chr1:3397274-3398273 REVERSE LENGTH=227</td><td>227</td><td>227</td><td>1.00E-112</td><td>100.0</td><td>83.7</td><td>92.5</td></tr>
<tr><td>Rsa1.0_00605.1.g16777.t1</td><td>gb|EOA37379.1| hypothetical protein CARUB_v10011208mg [Capsella rubella]</td><td>458</td><td>467</td><td>0</td><td>102.0</td><td>77.9</td><td>88.0</td><td>hypothetical protein CARUB_v10011208mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G10330.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:3388747-3390150 FORWARD LENGTH=467</td><td>458</td><td>467</td><td>0</td><td>102.0</td><td>76.4</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00605.1.g16778.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT3G04830.2 | Symbols: | Protein prenylyltransferase superfamily protein | chr3:1326289-1329132 FORWARD LENGTH=299</td><td>117</td><td>299</td><td>1.00E-10</td><td>255.6</td><td>25.6</td><td>29.1</td></tr>
<tr><td>Rsa1.0_00605.1.g16779.t1</td><td>ref|XP_002889800.1| hypothetical protein ARALYDRAFT_888292 [Arabidopsis lyrata subsp. lyrata] gi|297335642|gb|EFH66059.1| hypothetical protein ARALYDRAFT_888292 [Arabidopsis lyrata subsp. lyrata]</td><td>650</td><td>668</td><td>0</td><td>102.8</td><td>78.5</td><td>89.7</td><td>hypothetical protein ARALYDRAFT_888292</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G50920.1 | Symbols: | Nucleolar GTP-binding protein | chr1:18870555-18872570 FORWARD LENGTH=671</td><td>650</td><td>671</td><td>0</td><td>103.2</td><td>74.8</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00605.1.g16780.t1</td><td>ref|XP_002887691.1| nucleotide-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297333532|gb|EFH63950.1| nucleotide-binding family protein [Arabidopsis lyrata subsp. lyrata]</td><td>362</td><td>355</td><td>1.00E-150</td><td>98.1</td><td>74.3</td><td>85.4</td><td>nucleotide-binding family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G50960.1 | Symbols: NBP35, ATNBP35 | nucleotide binding protein 35 | chr5:20734267-20735824 FORWARD LENGTH=350</td><td>362</td><td>350</td><td>1.00E-151</td><td>96.7</td><td>73.8</td><td>83.7</td></tr>
<tr><td>Rsa1.0_00605.1.g16781.t3</td><td>gb|EOA39624.1| hypothetical protein CARUB_v10008252mg [Capsella rubella]</td><td>942</td><td>911</td><td>0</td><td>96.7</td><td>88.6</td><td>91.8</td><td>hypothetical protein CARUB_v10008252mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G59610.1 | Symbols: ADL3, CF1, DRP2B, DL3 | dynamin-like 3 | chr1:21893413-21900780 FORWARD LENGTH=920</td><td>942</td><td>920</td><td>0</td><td>97.7</td><td>86.5</td><td>90.6</td></tr>
<tr><td>Rsa1.0_00605.1.g16782.t1</td><td>ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]</td><td>270</td><td>390</td><td>5.00E-38</td><td>144.4</td><td>27.0</td><td>42.6</td><td>hypothetical protein ARALYDRAFT_917455</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332</td><td>270</td><td>332</td><td>5.00E-32</td><td>123.0</td><td>25.9</td><td>44.8</td></tr>
<tr><td>Rsa1.0_00605.1.g16783.t1</td><td>ref|NP_172499.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|4914330|gb|AAD32878.1|AC005489_16 F14N23.16 [Arabidopsis thaliana] gi|117168053|gb|ABK32109.1| At1g10280 [Arabidopsis thaliana] gi|332190440|gb|AEE28561.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]</td><td>416</td><td>412</td><td>0</td><td>99.0</td><td>88.2</td><td>93.8</td><td>Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10280.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:3366795-3368739 REVERSE LENGTH=412</td><td>416</td><td>412</td><td>0</td><td>99.0</td><td>88.2</td><td>93.8</td></tr>
<tr><td>Rsa1.0_00605.1.g16784.t1</td><td>gb|EOA37763.1| hypothetical protein CARUB_v10012602mg [Capsella rubella]</td><td>821</td><td>888</td><td>0</td><td>108.2</td><td>77.6</td><td>84.5</td><td>hypothetical protein CARUB_v10012602mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G10270.1 | Symbols: GRP23 | glutamine-rich protein 23 | chr1:3363535-3366276 FORWARD LENGTH=913</td><td>821</td><td>913</td><td>0</td><td>111.2</td><td>75.9</td><td>83.8</td></tr>
<tr><td>Rsa1.0_00605.1.g16785.t1</td><td>gb|EOA37760.1| hypothetical protein CARUB_v10012599mg [Capsella rubella]</td><td>679</td><td>679</td><td>0</td><td>100.0</td><td>94.7</td><td>98.4</td><td>hypothetical protein CARUB_v10012599mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G10240.1 | Symbols: FRS11 | FAR1-related sequence 11 | chr1:3356835-3359271 REVERSE LENGTH=680</td><td>679</td><td>680</td><td>0</td><td>100.1</td><td>93.7</td><td>98.1</td></tr>
<tr><td>Rsa1.0_00605.1.g16786.t1</td><td>gb|ADI79334.1| chloroplast biotin carboxylase [Brassica napus]</td><td>535</td><td>536</td><td>0</td><td>100.2</td><td>97.8</td><td>99.4</td><td>chloroplast biotin carboxylase</td><td>gbpln</td><td>Brassica napus</td><td>AT5G35360.1 | Symbols: CAC2 | acetyl Co-enzyme a carboxylase biotin carboxylase subunit | chr5:13584300-13588268 FORWARD LENGTH=537</td><td>535</td><td>537</td><td>0</td><td>100.4</td><td>90.5</td><td>93.6</td></tr>
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Rsa1.0_00606.1.g16787.t1	ref|XP_002872610.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318447|gb|EFH48869.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	107	575	4.00E-42	537.4	79.4	87.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G11690.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr4:7056254-7057954 FORWARD LENGTH=566	107	566	5.00E-40	529.0	72.0	81.3
Rsa1.0_00606.1.g16788.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00606.1.g16789.t1	gb|EOA37583.1| hypothetical protein CARUB_v10011933mg [Capsella rubella]	303	481	3.00E-54	158.7	39.9	48.8	hypothetical protein CARUB_v10011933mg	gbpln	Capsella rubella	AT1G23770.1 | Symbols: | F-box family protein | chr1:8405214-8406266 REVERSE LENGTH=350	303	350	3.00E-49	115.5	40.9	50.8
Rsa1.0_00606.1.g16790.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00606.1.g16791.t1	gb|EOA20188.1| hypothetical protein CARUB_v10000484mg, partial [Capsella rubella]	553	617	0	111.6	82.5	89.5	hypothetical protein CARUB_v10000484mg, partial	gbpln	Capsella rubella	AT4G11740.1 | Symbols: SAY1 | Ubiquitin-like superfamily protein | chr4:7071955-7075256 FORWARD LENGTH=564	553	564	0	102.0	81.2	88.4
Rsa1.0_00606.1.g16792.t1	ref|XP_002872624.1| hypothetical protein ARALYDRAFT_489994 [Arabidopsis lyrata subsp. lyrata] gi|297318461|gb|EFH48883.1| hypothetical protein ARALYDRAFT_489994 [Arabidopsis lyrata subsp. lyrata]	480	477	1.00E-164	99.4	71.9	81.0	hypothetical protein ARALYDRAFT_489994	gbpln	Arabidopsis lyrata	AT4G11780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G23020.2); Has 550 Blast hits to 387 proteins in 92 species: Archae - 0; Bacteria - 32; Metazoa - 132; Fungi - 122; Plants - 80; Viruses - 0; Other Eukaryotes - 184 (source: NCBI BLink). | chr4:7085970-7088212 FORWARD LENGTH=473	480	473	1.00E-166	98.5	71.5	79.4
Rsa1.0_00606.1.g16793.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00606.1.g16794.t1	ref|XP_002883909.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329749|gb|EFH60168.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	202	528	8.00E-19	261.4	33.2	49.5	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00606.1.g16795.t1	gb|EOA18216.1| hypothetical protein CARUB_v10006701mg, partial [Capsella rubella]	123	279	4.00E-11	226.8	29.3	32.5	hypothetical protein CARUB_v10006701mg, partial	gbpln	Capsella rubella	AT5G37890.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr5:15090512-15091822 REVERSE LENGTH=286	123	286	1.00E-12	232.5	27.6	30.1
Rsa1.0_00606.1.g16796.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00606.1.g16797.t1	ref|XP_002872625.1| hypothetical protein ARALYDRAFT_489995 [Arabidopsis lyrata subsp. lyrata] gi|297318462|gb|EFH48884.1| hypothetical protein ARALYDRAFT_489995 [Arabidopsis lyrata subsp. lyrata]	359	425	1.00E-123	118.4	76.3	82.5	hypothetical protein ARALYDRAFT_489995	gbpln	Arabidopsis lyrata	AT4G11790.1 | Symbols: | Pleckstrin homology (PH) domain superfamily protein | chr4:7090456-7093208 FORWARD LENGTH=443	359	443	1.00E-115	123.4	74.1	80.2
Rsa1.0_00606.1.g16798.t1	gb|EOA19882.1| hypothetical protein CARUB_v10000128mg [Capsella rubella]	986	1013	0	102.7	89.4	94.4	hypothetical protein CARUB_v10000128mg	gbpln	Capsella rubella	AT4G11800.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr4:7093666-7098519 REVERSE LENGTH=1013	986	1013	0	102.7	88.7	94.1
Rsa1.0_00607.1.g16799.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00607.1.g16800.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00607.1.g16801.t1	ref|XP_002872519.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297318356|gb|EFH48778.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	261	350	1.00E-136	134.1	88.1	94.3	oxidoreductase	gbpln	Arabidopsis lyrata	AT4G10500.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:6491089-6492342 FORWARD LENGTH=349	261	349	1.00E-136	133.7	85.4	93.5
Rsa1.0_00607.1.g16802.t1	ref|NP_175207.1| protein agamous-like 102 [Arabidopsis thaliana] gi|9802597|gb|AAF99799.1|AC012463_16 T2E6.17 [Arabidopsis thaliana] gi|32402446|gb|AAN52805.1| MADS-box protein AGL102 [Arabidopsis thaliana] gi|332194088|gb|AEE32209.1| protein agamous-like 102 [Arabidopsis thaliana]	145	184	5.00E-15	126.9	35.9	59.3	protein agamous-like 102	gbpln	Arabidopsis thaliana	AT1G47760.1 | Symbols: AGL102 | AGAMOUS-like 102 | chr1:17572451-17573159 FORWARD LENGTH=184	145	184	1.00E-17	126.9	35.9	59.3
Rsa1.0_00607.1.g16803.t1	gb|ABK28054.1| unknown [Arabidopsis thaliana]	75	73	3.00E-11	97.3	57.3	69.3	unknown	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00607.1.g16804.t1	gb|AAC35520.1| contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]	92	466	4.00E-16	506.5	48.9	59.8	contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89)	gbpln	Arabidopsis thaliana	AT4G10790.1 | Symbols: | UBX domain-containing protein | chr4:6640752-6643035 REVERSE LENGTH=480	92	480	6.00E-19	521.7	48.9	59.8
Rsa1.0_00607.1.g16805.t1	ref|XP_002874637.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320474|gb|EFH50896.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	907	913	0	100.7	87.0	93.9	ubiquitin carboxyl-terminal hydrolase family protein	gbpln	Arabidopsis lyrata	AT4G10570.1 | Symbols: UBP9 | ubiquitin-specific protease 9 | chr4:6523657-6528058 REVERSE LENGTH=923	907	923	0	101.8	86.4	93.5
Rsa1.0_00607.1.g16806.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00607.1.g16807.t1</td><td>ref|XP_002874638.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297320475|gb|EFH50897.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>207</td><td>230</td><td>1.00E-60</td><td>111.1</td><td>62.3</td><td>71.0</td><td>PHD finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G10600.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr4:6547934-6548647 REVERSE LENGTH=237</td><td>207</td><td>237</td><td>8.00E-59</td><td>114.5</td><td>64.3</td><td>71.0</td></tr>
<tr><td>Rsa1.0_00607.1.g16808.t1</td><td>ref|XP_002872527.1| RNA-binding protein 37 [Arabidopsis lyrata subsp. lyrata] gi|297318364|gb|EFH48786.1| RNA-binding protein 37 [Arabidopsis lyrata subsp. lyrata]</td><td>339</td><td>336</td><td>1.00E-151</td><td>99.1</td><td>83.5</td><td>88.5</td><td>RNA-binding protein 37</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G10610.1 | Symbols: RBP37, ATRBP37, CID12 | CTC-interacting domain 12 | chr4:6557336-6559143 FORWARD LENGTH=336</td><td>339</td><td>336</td><td>1.00E-153</td><td>99.1</td><td>82.6</td><td>87.9</td></tr>
<tr><td>Rsa1.0_00608.1.g16809.t1</td><td>ref|XP_002879272.1| hypothetical protein ARALYDRAFT_481979 [Arabidopsis lyrata subsp. lyrata] gi|297325111|gb|EFH55531.1| hypothetical protein ARALYDRAFT_481979 [Arabidopsis lyrata subsp. lyrata]</td><td>274</td><td>264</td><td>2.00E-63</td><td>96.4</td><td>69.3</td><td>73.0</td><td>hypothetical protein ARALYDRAFT_481979</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G30620.1 | Symbols: | winged-helix DNA-binding transcription factor family protein | chr2:13045360-13046267 FORWARD LENGTH=273</td><td>274</td><td>273</td><td>3.00E-61</td><td>99.6</td><td>70.4</td><td>74.8</td></tr>
<tr><td>Rsa1.0_00608.1.g16810.t1</td><td>ref|NP_973567.1| nucleoside/nucleotide kinase-like protein [Arabidopsis thaliana] gi|330253327|gb|AEC08421.1| nucleoside/nucleotide kinase-like protein [Arabidopsis thaliana]</td><td>317</td><td>552</td><td>1.00E-125</td><td>174.1</td><td>71.9</td><td>73.5</td><td>nucleoside/nucleotide kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G30630.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:13046883-13049106 REVERSE LENGTH=552</td><td>317</td><td>552</td><td>1.00E-128</td><td>174.1</td><td>71.9</td><td>73.5</td></tr>
<tr><td>Rsa1.0_00608.1.g16811.t1</td><td>gb|AAC02734.1| putative Mutator-like transposase [Arabidopsis thaliana] gi|20198324|gb|AAM15523.1| putative Mutator-like transposase [Arabidopsis thaliana]</td><td>763</td><td>754</td><td>0</td><td>98.8</td><td>70.8</td><td>81.4</td><td>putative Mutator-like transposase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719</td><td>763</td><td>719</td><td>8.00E-44</td><td>94.2</td><td>18.0</td><td>30.5</td></tr>
<tr><td>Rsa1.0_00608.1.g16812.t5</td><td>ref|NP_001184913.1| callose synthase 1 [Arabidopsis thaliana] gi|332189735|gb|AEE27856.1| callose synthase 1 [Arabidopsis thaliana]</td><td>275</td><td>1909</td><td>1.00E-22</td><td>694.2</td><td>27.6</td><td>43.3</td><td>callose synthase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G05570.2 | Symbols: CALS1 | callose synthase 1 | chr1:1647880-1658677 REVERSE LENGTH=1909</td><td>275</td><td>1909</td><td>4.00E-25</td><td>694.2</td><td>27.6</td><td>43.3</td></tr>
<tr><td>Rsa1.0_00608.1.g16813.t1</td><td>ref|XP_002879276.1| hypothetical protein ARALYDRAFT_344831 [Arabidopsis lyrata subsp. lyrata] gi|297325115|gb|EFH55535.1| hypothetical protein ARALYDRAFT_344831 [Arabidopsis lyrata subsp. lyrata]</td><td>722</td><td>761</td><td>0</td><td>105.4</td><td>67.7</td><td>76.3</td><td>hypothetical protein ARALYDRAFT_344831</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G30690.1 | Symbols: | Protein of unknown function, DUF593 | chr2:13076229-13078595 FORWARD LENGTH=760</td><td>722</td><td>760</td><td>0</td><td>105.3</td><td>68.0</td><td>76.6</td></tr>
<tr><td>Rsa1.0_00608.1.g16814.t1</td><td>gb|EOA28009.1| hypothetical protein CARUB_v10024186mg [Capsella rubella]</td><td>66</td><td>170</td><td>7.00E-16</td><td>257.6</td><td>65.2</td><td>74.2</td><td>hypothetical protein CARUB_v10024186mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G30930.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, plasma membrane, membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06540.1); Has 194 Blast hits to 176 proteins in 78 species: Archae - 0; Bacteria - 101; Metazoa - 15; Fungi - 25; Plants - 12; Viruses - 4; Other Eukaryotes - 37 (source: NCBI BLink). | chr2:13162458-13163156 FORWARD LENGTH=164</td><td>66</td><td>164</td><td>2.00E-17</td><td>248.5</td><td>62.1</td><td>71.2</td></tr>
<tr><td>Rsa1.0_00608.1.g16815.t1</td><td>ref|NP_195605.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75212071|sp|Q9SVJ9.1|FBK95_ARATH RecName: Full=F-box/kelch-repeat protein At4g38940 gi|4539313|emb|CAB38814.1| putative protein [Arabidopsis thaliana] gi|7270877|emb|CAB80557.1| putative protein [Arabidopsis thaliana] gi|21593554|gb|AAM65521.1| unknown [Arabidopsis thaliana] gi|51968770|dbj|BAD43077.1| unknown protein [Arabidopsis thaliana] gi|51969398|dbj|BAD43391.1| unknown protein [Arabidopsis thaliana] gi|332661596|gb|AEE86996.1| F-box/kelch-repeat protein [Arabidopsis thaliana]</td><td>389</td><td>370</td><td>6.00E-67</td><td>95.1</td><td>38.6</td><td>55.5</td><td>F-box/kelch-repeat protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370</td><td>389</td><td>370</td><td>1.00E-69</td><td>95.1</td><td>38.6</td><td>55.5</td></tr>
<tr><td>Rsa1.0_00608.1.g16816.t1</td><td>gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]</td><td>348</td><td>368</td><td>1.00E-75</td><td>105.7</td><td>48.6</td><td>64.4</td><td>hypothetical protein CARUB_v10027748mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370</td><td>348</td><td>370</td><td>6.00E-75</td><td>106.3</td><td>44.3</td><td>64.7</td></tr>
<tr><td>Rsa1.0_00608.1.g16817.t3</td><td>gb|EOA28434.1| hypothetical protein CARUB_v10024642mg [Capsella rubella]</td><td>438</td><td>426</td><td>0</td><td>97.3</td><td>78.3</td><td>85.8</td><td>hypothetical protein CARUB_v10024642mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G30940.1 | Symbols: | Protein kinase superfamily protein | chr2:13168533-13170285 FORWARD LENGTH=451</td><td>438</td><td>451</td><td>0</td><td>103.0</td><td>76.9</td><td>84.9</td></tr>
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Rsa1.0_00608.1.g16818.t1	ref|XP_002879294.1| hypothetical protein ARALYDRAFT_482018 [Arabidopsis lyrata subsp. lyrata] gi|297325133|gb|EFH55553.1| hypothetical protein ARALYDRAFT_482018 [Arabidopsis lyrata subsp. lyrata]	695	695	0	100.0	92.5	96.1	hypothetical protein ARALYDRAFT_482018	gbpln	Arabidopsis lyrata	AT2G30950.1 | Symbols: VAR2, FTSH2 | FtsH extracellular protease family | chr2:13174692-13177064 FORWARD LENGTH=695	695	695	0	100.0	90.6	94.0
Rsa1.0_00608.1.g16819.t1	gb|EOA29296.1| hypothetical protein CARUB_v10025574mg [Capsella rubella]	242	268	1.00E-26	110.7	50.0	64.9	hypothetical protein CARUB_v10025574mg	gbpln	Capsella rubella	AT2G30960.1 | Symbols: | unknown protein; Has 4906 Blast hits to 2903 proteins in 334 species: Archae - 5; Bacteria - 381; Metazoa - 1639; Fungi - 509; Plants - 244; Viruses - 5; Other Eukaryotes - 2123 (source: NCBI BLink). | chr2:13177541-13178323 REVERSE LENGTH=260	242	260	4.00E-22	107.4	44.2	60.3
Rsa1.0_00608.1.g16820.t1	ref|XP_002879295.1| hypothetical protein ARALYDRAFT_482020 [Arabidopsis lyrata subsp. lyrata] gi|297325134|gb|EFH55554.1| hypothetical protein ARALYDRAFT_482020 [Arabidopsis lyrata subsp. lyrata]	429	430	0	100.2	92.1	95.6	hypothetical protein ARALYDRAFT_482020	gbpln	Arabidopsis lyrata	AT2G30970.2 | Symbols: ASP1 | aspartate aminotransferase 1 | chr2:13179012-13181686 FORWARD LENGTH=430	429	430	0	100.2	91.6	95.6
Rsa1.0_00608.1.g16821.t4	ref|XP_002881148.1| hypothetical protein ARALYDRAFT_482023 [Arabidopsis lyrata subsp. lyrata] gi|297326987|gb|EFH57407.1| hypothetical protein ARALYDRAFT_482023 [Arabidopsis lyrata subsp. lyrata]	561	591	1.00E-129	105.3	58.8	65.8	hypothetical protein ARALYDRAFT_482023	gbpln	Arabidopsis lyrata	AT2G30990.2 | Symbols: | Protein of unknown function (DUF688) | chr2:13187776-13189761 REVERSE LENGTH=593	561	593	1.00E-128	105.7	56.5	65.8
Rsa1.0_00608.1.g16822.t1	ref|NP_001078598.1| rubredoxin family protein [Arabidopsis thaliana] gi|332005009|gb|AED92392.1| rubredoxin family protein [Arabidopsis thaliana]	187	224	4.00E-47	119.8	59.9	64.7	rubredoxin family protein	gbpln	Arabidopsis thaliana	AT5G17170.2 | Symbols: ENH1 | rubredoxin family protein | chr5:5649335-5650835 FORWARD LENGTH=224	187	224	1.00E-49	119.8	59.9	64.7
Rsa1.0_00608.1.g16823.t1	gb|EOA29196.1| hypothetical protein CARUB_v10025469mg [Capsella rubella]	200	194	3.00E-68	97.0	71.0	79.0	hypothetical protein CARUB_v10025469mg	gbpln	Capsella rubella	AT2G31050.1 | Symbols: | Cupredoxin superfamily protein | chr2:13212150-13212752 FORWARD LENGTH=200	200	200	7.00E-70	100.0	67.5	77.0
Rsa1.0_00608.1.g16824.t1	dbj|BAJ34111.1| unnamed protein product [Thellungiella halophila]	347	349	1.00E-141	100.6	83.3	87.0	unnamed protein product	----	----	AT2G31070.1 | Symbols: TCP10 | TCP domain protein 10 | chr2:13220984-13222069 REVERSE LENGTH=361	347	361	1.00E-116	104.0	78.1	83.0
Rsa1.0_00608.1.g16825.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00608.1.g16826.t1	gb|EOA29350.1| hypothetical protein CARUB_v10025636mg [Capsella rubella]	82	81	7.00E-29	98.8	78.0	85.4	hypothetical protein CARUB_v10025636mg	gbpln	Capsella rubella	AT2G31085.1 | Symbols: CLE6 | CLAVATA3/ESR-RELATED 6 | chr2:13254263-13254508 FORWARD LENGTH=81	82	81	2.00E-29	98.8	72.0	82.9
Rsa1.0_00608.1.g16827.t1	sp|O82274.2|PLA19_ARATH RecName: Full=Phospholipase A1-IIbeta	414	414	0	100.0	78.0	85.5	RecName: Full=Phospholipase A1-IIbeta	----	----	AT2G31100.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:13256738-13258174 REVERSE LENGTH=414	414	414	0	100.0	78.0	85.5
Rsa1.0_00608.1.g16828.t1	gb|EOA29166.1| hypothetical protein CARUB_v10025433mg [Capsella rubella]	259	349	5.00E-76	134.7	60.6	74.5	hypothetical protein CARUB_v10025433mg	gbpln	Capsella rubella	AT2G41930.1 | Symbols: | Protein kinase superfamily protein | chr2:17501629-17502684 FORWARD LENGTH=351	259	351	5.00E-75	135.5	57.5	76.1
Rsa1.0_00609.1.g16829.t1	gb|EOA33134.1| hypothetical protein CARUB_v10016476mg [Capsella rubella]	346	354	1.00E-166	102.3	86.7	91.6	hypothetical protein CARUB_v10016476mg	gbpln	Capsella rubella	AT3G01400.1 | Symbols: | ARM repeat superfamily protein | chr3:151920-152987 FORWARD LENGTH=355	346	355	1.00E-166	102.6	85.8	90.5
Rsa1.0_00609.1.g16830.t1	gb|EOA31134.1| hypothetical protein CARUB_v10014297mg [Capsella rubella]	302	292	1.00E-112	96.7	70.9	80.8	hypothetical protein CARUB_v10014297mg	gbpln	Capsella rubella	AT3G01410.2 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr3:153650-155439 REVERSE LENGTH=294	302	294	1.00E-111	97.4	70.5	80.1
Rsa1.0_00609.1.g16831.t1	emb|CAC01808.1| putative protein [Arabidopsis thaliana]	153	733	2.00E-51	479.1	67.3	74.5	putative protein	gbpln	Arabidopsis thaliana	AT5G14890.1 | Symbols: | NHL domain-containing protein | chr5:4818056-4821534 FORWARD LENGTH=754	153	754	8.00E-54	492.8	67.3	74.5
Rsa1.0_00609.1.g16832.t1	ref|NP_974205.1| uncharacterized protein [Arabidopsis thaliana] gi|75123851|sp|Q6ID77.1|MED11_ARATH RecName: Full=Mediator of RNA polymerase II transcription subunit 11 gi|48310228|gb|AAT41779.1| At3g01435 [Arabidopsis thaliana] gi|52218796|gb|AAU29468.1| At3g01435 [Arabidopsis thaliana] gi|110738543|dbj|BAF01197.1| hypothetical protein [Arabidopsis thaliana] gi|332640145|gb|AEE73666.1| uncharacterized protein AT3G01435 [Arabidopsis thaliana]	115	115	2.00E-53	100.0	86.1	93.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01435.1 | Symbols: | Expressed protein | chr3:166853-167984 REVERSE LENGTH=115	115	115	3.00E-56	100.0	86.1	93.9

Rsa1.0_00609.1.g16833.t2	ref|XP_002884279.1| methyl-CpG-binding domain 9 [Arabidopsis lyrata subsp. lyrata] gi|297330119|gb|EFH60538.1| methyl-CpG-binding domain 9 [Arabidopsis lyrata subsp. lyrata]	2140	2183	0	102.0	81.6	88.5	methyl-CpG-binding domain 9	gbpln	Arabidopsis lyrata	AT3G01460.1 | Symbols: MBD9, ATMBD9 | methyl-CPG-binding domain 9 | chr3:173316-182038 FORWARD LENGTH=2176	2140	2176	0	101.7	80.8	87.9
Rsa1.0_00609.1.g16834.t1	dbj|BAJ33940.1| unnamed protein product [Thellungiella halophila] gi|312283511|dbj|BAJ34621.1| unnamed protein product [Thellungiella halophila]	271	274	1.00E-107	101.1	76.8	84.9	unnamed protein product	----	----	AT3G01470.1 | Symbols: ATHB-1, ATHB1, HD-ZIP-1, HAT5, HB-1 | homeobox 1 | chr3:182648-184034 REVERSE LENGTH=272	271	272	4.00E-99	100.4	76.0	81.5
Rsa1.0_00609.1.g16835.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00609.1.g16836.t1	gb|ADI52861.1| chloroplast beta-carbonic anhydrase [Brassica napus]	332	331	1.00E-176	99.7	94.6	97.3	chloroplast beta-carbonic anhydrase	gbpln	Brassica napus	AT3G01500.2 | Symbols: CA1 | carbonic anhydrase 1 | chr3:194853-197873 REVERSE LENGTH=347	332	347	1.00E-170	104.5	93.7	96.7
Rsa1.0_00609.1.g16837.t1	ref|XP_002882192.1| hypothetical protein ARALYDRAFT_896138 [Arabidopsis lyrata subsp. lyrata] gi|297328032|gb|EFH58451.1| hypothetical protein ARALYDRAFT_896138 [Arabidopsis lyrata subsp. lyrata]	174	126	6.00E-27	72.4	44.8	57.5	hypothetical protein ARALYDRAFT_896138	gbpln	Arabidopsis lyrata	AT3G01230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01240.1); Has 11 Blast hits to 11 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:76937-77317 REVERSE LENGTH=126	174	126	8.00E-29	72.4	44.3	58.0
Rsa1.0_00609.1.g16838.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	591	1274	1.00E-107	215.6	32.1	43.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	591	575	1.00E-38	97.3	15.2	24.0
Rsa1.0_00609.1.g16839.t1	ref|XP_002884288.1| ATHB20 [Arabidopsis lyrata subsp. lyrata] gi|297330128|gb|EFH60547.1| ATHB20 [Arabidopsis lyrata subsp. lyrata]	263	283	1.00E-130	107.6	87.5	94.3	ATHB20	gbpln	Arabidopsis lyrata	AT3G01220.1 | Symbols: ATHB20, HB20 | homeobox protein 20 | chr3:73599-75295 FORWARD LENGTH=286	263	286	1.00E-128	108.7	84.0	90.5
Rsa1.0_00609.1.g16840.t1	ref|XP_002882193.1| hypothetical protein ARALYDRAFT_477409 [Arabidopsis lyrata subsp. lyrata] gi|297328033|gb|EFH58452.1| hypothetical protein ARALYDRAFT_477409 [Arabidopsis lyrata subsp. lyrata]	370	378	1.00E-177	102.2	84.9	89.7	hypothetical protein ARALYDRAFT_477409	gbpln	Arabidopsis lyrata	AT3G01200.1 | Symbols: AtRP2, RP2 | PPDK regulatory protein 2 | chr3:69826-71348 REVERSE LENGTH=377	370	377	1.00E-179	101.9	83.8	90.3
Rsa1.0_00609.1.g16841.t1	gb|EOA32852.1| hypothetical protein CARUB_v10016167mg, partial [Capsella rubella]	319	318	1.00E-167	99.7	88.7	94.0	hypothetical protein CARUB_v10016167mg, partial	gbpln	Capsella rubella	AT3G01190.1 | Symbols: | Peroxidase superfamily protein | chr3:67236-68477 REVERSE LENGTH=321	319	321	1.00E-168	100.6	89.0	93.4
Rsa1.0_00609.1.g16842.t1	gb|EOA29906.1| hypothetical protein CARUB_v10013000mg [Capsella rubella]	104	804	3.00E-16	773.1	51.0	57.7	hypothetical protein CARUB_v10013000mg	gbpln	Capsella rubella	AT3G01180.1 | Symbols: AtSS2, SS2 | starch synthase 2 | chr3:62456-65678 REVERSE LENGTH=792	104	792	5.00E-17	761.5	49.0	55.8
Rsa1.0_00609.1.g16843.t1	ref|NP_186767.1| starch synthase 2 [Arabidopsis thaliana] gi|75264912|sp|Q9MAC8.1|SSY2_ARATH RecName: Full=Starch synthase 2, chloroplastic/amyloplastic; Short=AtSS2; AltName: Full=Soluble starch synthase II; Flags: Precursor gi|6714470|gb|AAF26156.1|AC008261_13 putative glycogen synthase [Arabidopsis thaliana] gi|15450775|gb|AAK96659.1| putative glycogen synthase [Arabidopsis thaliana] gi|27311899|gb|AAO00915.1| putative glycogen synthase [Arabidopsis thaliana] gi|332640100|gb|AEE73621.1| starch synthase 2 [Arabidopsis thaliana]	197	792	1.00E-103	402.0	92.9	94.9	starch synthase 2	gbpln	Arabidopsis thaliana	AT3G01180.1 | Symbols: AtSS2, SS2 | starch synthase 2 | chr3:62456-65678 REVERSE LENGTH=792	197	792	1.00E-105	402.0	92.9	94.9
Rsa1.0_00609.1.g16844.t1	gb|EOA30212.1| hypothetical protein CARUB_v10013334mg [Capsella rubella]	576	572	0	99.3	66.1	78.3	hypothetical protein CARUB_v10013334mg	gbpln	Capsella rubella	AT3G01175.1 | Symbols: | Protein of unknown function (DUF1666) | chr3:59484-60845 FORWARD LENGTH=401	576	401	1.00E-140	69.6	47.0	56.1
Rsa1.0_00609.1.g16845.t2	ref|XP_002884293.1| polypyrimidine tract-binding [Arabidopsis lyrata subsp. lyrata] gi|297330133|gb|EFH60552.1| polypyrimidine tract-binding [Arabidopsis lyrata subsp. lyrata]	396	398	0	100.5	90.7	95.5	polypyrimidine tract-binding	gbpln	Arabidopsis lyrata	AT3G01150.1 | Symbols: PTB, ATPTB1, PTB1 | polypyrimidine tract-binding protein 1 | chr3:51732-54344 FORWARD LENGTH=399	396	399	0	100.8	89.1	93.9
Rsa1.0_00609.1.g16846.t1	ref|XP_002882197.1| hypothetical protein ARALYDRAFT_477416 [Arabidopsis lyrata subsp. lyrata] gi|297328037|gb|EFH58456.1| hypothetical protein ARALYDRAFT_477416 [Arabidopsis lyrata subsp. lyrata]	330	390	1.00E-153	118.2	84.5	90.0	hypothetical protein ARALYDRAFT_477416	gbpln	Arabidopsis lyrata	AT3G01140.1 | Symbols: MYB106, NOK, AtMYB106 | myb domain protein 106 | chr3:46619-48143 REVERSE LENGTH=388	330	388	2.33E-156	117.6	82.4	87.0

Rsa1.0_00609.1.g16847.t1	gb|ABA96411.1| retrotransposon protein, putative, unclassified [Oryza sativa Japonica Group]	171	256	2.00E-72	149.7	74.3	87.1	retrotransposon protein, putative, unclassified	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	171	1262	5.00E-33	738.0	33.3	49.7
Rsa1.0_00610.1.g16848.t1	ref|XP_002864628.1| hypothetical protein ARALYDRAFT_496062 [Arabidopsis lyrata subsp. lyrata] gi|297310463|gb|EFH40887.1| hypothetical protein ARALYDRAFT_496062 [Arabidopsis lyrata subsp. lyrata]	396	284	1.00E-73	71.7	47.7	53.3	hypothetical protein ARALYDRAFT_496062	gbpln	Arabidopsis lyrata	AT5G59350.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:23941132-23941995 FORWARD LENGTH=287	396	287	2.00E-74	72.5	47.0	53.3
Rsa1.0_00610.1.g16849.t1	ref|XP_002866327.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312162|gb|EFH42586.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	241	261	5.00E-93	108.3	75.1	83.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G59340.1 | Symbols: WOX2 | WUSCHEL related homeobox 2 | chr5:23933408-23934627 REVERSE LENGTH=260	241	260	3.00E-92	107.9	73.4	83.4
Rsa1.0_00610.1.g16850.t1	gb|EOA23128.1| hypothetical protein CARUB_v100024710mg, partial [Capsella rubella]	646	488	1.00E-136	75.5	35.8	48.0	hypothetical protein CARUB_v100024710mg , partial	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	646	696	5.00E-30	107.7	22.4	38.2
Rsa1.0_00610.1.g16851.t2	gb|EOA14120.1| hypothetical protein CARUB_v10027262mg [Capsella rubella]	154	166	3.00E-85	107.8	97.4	99.4	hypothetical protein CARUB_v10027262mg	gbpln	Capsella rubella	AT5G59300.1 | Symbols: UBC7, ATUBC7 | ubiquitin carrier protein 7 | chr5:23919868-23921304 REVERSE LENGTH=203	154	203	2.00E-87	131.8	96.1	98.7
Rsa1.0_00610.1.g16852.t1	gb|EOA15174.1| hypothetical protein CARUB_v10028557mg [Capsella rubella]	358	329	3.00E-97	91.9	52.2	69.6	hypothetical protein CARUB_v10028557mg	gbpln	Capsella rubella	AT5G60110.1 | Symbols: APUM18, PUM18 | pumilio 18 | chr5:24201954-24202937 FORWARD LENGTH=327	358	327	3.00E-92	91.3	53.4	68.2
Rsa1.0_00610.1.g16853.t1	gb|EOA23492.1| hypothetical protein CARUB_v10016683mg, partial [Capsella rubella]	797	845	0	106.0	71.6	82.4	hypothetical protein CARUB_v10016683mg, partial	gbpln	Capsella rubella	AT3G46740.1 | Symbols: TOC75-III, MAR1 | translocon at the outer envelope membrane of chloroplasts 75-III | chr3:17216104-17219296 REVERSE LENGTH=818	797	818	0	102.6	71.0	81.4
Rsa1.0_00610.1.g16854.t1	ref|NP_200711.1| copper transporter 1 [Arabidopsis thaliana] gi|12230995|sp|Q39065.2|COPT1_ARATH RecName: Full=Copper transporter 1; Short=AtCOPT1 gi|18496858|gb|AAL74265.1|AF466373_1 copper transporter COPT1 [Arabidopsis thaliana] gi|10177631|dbj|BAB10779.1| copper transporter-like protein [Arabidopsis thaliana] gi|20258855|gb|AAM13909.1| putative copper transport protein [Arabidopsis thaliana] gi|21689855|gb|AAM67571.1| putative copper transport protein [Arabidopsis thaliana] gi|110741978|dbj|BAE98928.1| copper transport protein [Arabidopsis thaliana] gi|332009749|gb|AED97132.1| copper transporter 1 [Arabidopsis thaliana]	161	170	3.00E-59	105.6	81.4	87.6	copper transporter 1	gbpln	Arabidopsis thaliana	AT5G59030.1 | Symbols: COPT1 | copper transporter 1 | chr5:23833945-23834457 REVERSE LENGTH=170	161	170	1.00E-61	105.6	81.4	87.6
Rsa1.0_00610.1.g16855.t1	ref|NP_200713.2| uncharacterized protein [Arabidopsis thaliana] gi|332009751|gb|AED97134.1| uncharacterized protein AT5G59050 [Arabidopsis thaliana]	299	312	1.00E-113	104.3	81.3	88.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G59050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54000.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:23839494-23842519 REVERSE LENGTH=312	299	312	1.00E-115	104.3	81.3	88.0
Rsa1.0_00610.1.g16856.t1	ref|XP_002864620.1| hypothetical protein ARALYDRAFT_496048 [Arabidopsis lyrata subsp. lyrata] gi|297310455|gb|EFH40879.1| hypothetical protein ARALYDRAFT_496048 [Arabidopsis lyrata subsp. lyrata]	133	135	1.00E-50	101.5	84.2	88.0	hypothetical protein ARALYDRAFT_496048	gbpln	Arabidopsis lyrata	AT5G59080.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: chloroplast; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G46880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:23847691-23848403 REVERSE LENGTH=135	133	135	2.00E-51	101.5	82.0	88.0

Rsa1.0_00610.1.g16857.t1	ref|NP_568898.2| subtilase 4.13 [Arabidopsis thaliana] gi|9759234|dbj|BAB09758.1| serine protease-like protein [Arabidopsis thaliana] gi|20260320|gb|AAM13058.1| unknown protein [Arabidopsis thaliana] gi|34098789|gb|AAQ56777.1| At5g59120 [Arabidopsis thaliana] gi|332009762|gb|AED97145.1| subtilase 4.13 [Arabidopsis thaliana]	736	732	0	99.5	81.1	87.6	subtilase 4.13	gbpln	Arabidopsis thaliana	AT5G59120.1 | Symbols: ATSBT4.13, SBT4.13 | subtilase 4.13 | chr5:23864897-23868020 REVERSE LENGTH=732	736	732	0	99.5	81.1	87.6
Rsa1.0_00611.1.g16858.t1	ref|NP_195321.1| L-ascorbate peroxidase [Arabidopsis thaliana] gi|118572829|sp|Q7XZP5.2|APX5_ARATH RecName: Full=L-ascorbate peroxidase 5, peroxisomal; Short=AtAPx04; Flags: Precursor gi|3036801|emb|CAA18491.1| putative ascorbate peroxidase [Arabidopsis thaliana] gi|3805863|emb|CAA21483.1| putative ascorbate peroxidase [Arabidopsis thaliana] gi|7270549|emb|CAB81506.1| putative ascorbate peroxidase [Arabidopsis thaliana] gi|26453046|dbj|BAC43599.1| putative ascorbate peroxidase [Arabidopsis thaliana] gi|29824155|gb|AAP04038.1| putative ascorbate peroxidase [Arabidopsis thaliana] gi|332661196|gb|AEE86596.1| L-ascorbate peroxidase [Arabidopsis thaliana]	280	279	1.00E-137	99.6	84.3	91.8	L-ascorbate peroxidase	gbpln	Arabidopsis thaliana	AT4G35970.1 | Symbols: APX5 | ascorbate peroxidase 5 | chr4:17028651-17030205 FORWARD LENGTH=279	280	279	1.00E-140	99.6	84.3	91.8
Rsa1.0_00611.1.g16859.t1	ref|XP_002867044.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312880|gb|EFH43303.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	96	540	3.00E-39	562.5	81.3	84.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G35980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17030816-17031586 REVERSE LENGTH=87	96	87	2.00E-37	90.6	76.0	83.3
Rsa1.0_00611.1.g16860.t1	ref|NP_680769.4| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|332661199|gb|AEE86599.1| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana]	307	304	1.00E-148	99.0	81.8	90.6	S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT4G35987.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:17035121-17036823 FORWARD LENGTH=304	307	304	1.00E-150	99.0	81.8	90.6
Rsa1.0_00611.1.g16861.t1	gb|EOA17099.1| hypothetical protein CARUB_v10005355mg [Capsella rubella]	301	301	1.00E-138	100.0	89.0	94.0	hypothetical protein CARUB_v10005355mg	gbpln	Capsella rubella	AT4G36010.2 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr4:17039472-17040976 REVERSE LENGTH=301	301	301	1.00E-137	100.0	87.4	92.4
Rsa1.0_00611.1.g16862.t1	ref|NP_195326.1| cellular nucleic acid-binding protein [Arabidopsis thaliana] gi|75318587|sp|O65639.1|CSP1_ARATH RecName: Full=Cold shock protein 1; Short=AtCSP1; AltName: Full=Cold shock domain-containing protein 1 gi|3036806|emb|CAA18496.1| glycine-rich protein [Arabidopsis thaliana] gi|7270554|emb|CAB81511.1| glycine-rich protein [Arabidopsis thaliana] gi|110741941|dbj|BAE98911.1| glycine-rich protein [Arabidopsis thaliana] gi|332661203|gb|AEE86603.1| cold shock protein 1 [Arabidopsis thaliana]	282	299	7.00E-77	106.0	63.5	70.6	cellular nucleic acid-binding protein	gbpln	Arabidopsis thaliana	AT4G36020.1 | Symbols: CSDP1 | cold shock domain protein 1 | chr4:17043443-17044342 REVERSE LENGTH=299	282	299	2.00E-79	106.0	63.5	70.6
Rsa1.0_00611.1.g16863.t1	dbj|BAJ34233.1| unnamed protein product [Thellungiella halophila]	167	162	8.00E-67	97.0	87.4	91.6	unnamed protein product	----	----	AT4G36040.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:17049708-17050193 REVERSE LENGTH=161	167	161	3.00E-68	96.4	86.8	91.6
Rsa1.0_00611.1.g16864.t1	ref|XP_002867038.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297312874|gb|EFH43297.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	594	616	0	103.7	80.1	85.7	endonuclease/exonuclease/phosphatase family protein	gbpln	Arabidopsis lyrata	AT4G36050.2 | Symbols: | endonuclease/exonuclease/phosphatase family protein | chr4:17052323-17055044 REVERSE LENGTH=610	594	610	0	102.7	81.3	86.4

Rsa1.0_00611.1.g16865.t5	ref|NP_680770.2| transformation/transcription domain-associated protein [Arabidopsis thaliana] gi|332661212|gb|AEE86612.1| transformation/transcription domain-associated protein [Arabidopsis thaliana]	4007	3834	0	95.7	81.9	87.0	transformation/transcription domain-associated protein	gbpln	Arabidopsis thaliana	AT4G36080.1 | Symbols: | phosphotransferases, alcohol group as acceptor;binding;inositol or phosphatidylinositol kinases | chr4:17059996-17077628 REVERSE LENGTH=3834	4007	3834	0	95.7	81.9	87.0
Rsa1.0_00611.1.g16866.t1	ref|XP_002867035.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297312871|gb|EFH43294.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	476	490	1.00E-180	102.9	71.8	81.3	oxidoreductase	gbpln	Arabidopsis lyrata	AT4G36090.3 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr4:17078376-17080670 REVERSE LENGTH=520	476	520	1.00E-180	109.2	72.7	81.7
Rsa1.0_00611.1.g16867.t1	gb|EOA17042.1| hypothetical protein CARUB_v10005277mg [Capsella rubella]	336	318	6.00E-90	94.6	62.5	70.5	hypothetical protein CARUB_v10005277mg	gbpln	Capsella rubella	AT2G17990.1 | Symbols: | BEST Arabidopsis thaliana protein match is: kinectin-related (TAIR:AT5G66250.3); Has 7578 Blast hits to 6129 proteins in 783 species: Archae - 220; Bacteria - 1045; Metazoa - 3605; Fungi - 575; Plants - 442; Viruses - 38; Other Eukaryotes - 1653 (source: NCBI BLink). | chr2:7827480-7828596 FORWARD LENGTH=338	336	338	1.00E-74	100.6	50.6	61.3
Rsa1.0_00611.1.g16868.t1	ref|XP_002869044.1| hypothetical protein ARALYDRAFT_491020 [Arabidopsis lyrata subsp. lyrata] gi|297314880|gb|EFH45303.1| hypothetical protein ARALYDRAFT_491020 [Arabidopsis lyrata subsp. lyrata]	104	104	3.00E-48	100.0	84.6	95.2	hypothetical protein ARALYDRAFT_491020	gbpln	Arabidopsis lyrata	AT4G36110.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:17090031-17090345 FORWARD LENGTH=104	104	104	3.00E-50	100.0	84.6	94.2
Rsa1.0_00611.1.g16869.t1	ref|XP_002867034.1| hypothetical protein ARALYDRAFT_491019 [Arabidopsis lyrata subsp. lyrata] gi|297312870|gb|EFH43293.1| hypothetical protein ARALYDRAFT_491019 [Arabidopsis lyrata subsp. lyrata]	813	975	0	119.9	54.5	59.5	hypothetical protein ARALYDRAFT_491019	gbpln	Arabidopsis lyrata	AT4G36120.1 | Symbols: | Plant protein of unknown function (DUF869) | chr4:17093213-17096573 REVERSE LENGTH=996	813	996	0	122.5	53.0	58.1
Rsa1.0_00611.1.g16870.t1	ref|XP_002869043.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata] gi|297314879|gb|EFH45302.1| 60S ribosomal protein L8 [Arabidopsis lyrata subsp. lyrata]	258	258	1.00E-144	100.0	97.3	99.2	60S ribosomal protein L8	gbpln	Arabidopsis lyrata	AT4G36130.1 | Symbols: | Ribosomal protein L2 family | chr4:17097613-17098656 FORWARD LENGTH=258	258	258	2.33E-156	100.0	96.5	99.2
Rsa1.0_00611.1.g16871.t1	gb|EOA15884.1| hypothetical protein CARUB_v10003971mg [Capsella rubella]	1456	1946	0	133.7	67.6	78.6	hypothetical protein CARUB_v10003971mg	gbpln	Capsella rubella	AT4G36140.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr4:17098956-17104479 REVERSE LENGTH=1607	1456	1607	0	110.4	56.8	63.9
Rsa1.0_00611.1.g16872.t2	gb|ACP30607.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1004	1128	0	112.4	83.1	86.5	disease resistance protein	gbpln	Brassica rapa	AT4G36150.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:17104776-17108711 FORWARD LENGTH=1179	1004	1179	0	117.4	73.6	81.7
Rsa1.0_00612.1.g16873.t1	ref|NP_849612.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|75161568|sp|Q8VZ13.1|Y1816_ARATH RecName: Full=Uncharacterized protein At1g08160 gi|17529202|gb|AAL38827.1| unknown protein [Arabidopsis thaliana] gi|20259001|gb|AAM14216.1| unknown protein [Arabidopsis thaliana] gi|332190134|gb|AEE28255.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	207	221	9.00E-87	106.8	87.0	92.8	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT1G08160.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr1:2559672-2560337 REVERSE LENGTH=221	207	221	3.00E-89	106.8	87.0	92.8
Rsa1.0_00612.1.g16874.t1	ref|NP_172295.1| histone H2B [Arabidopsis thaliana] gi|75337200|sp|Q9SGE3.1|H2B2_ARATH RecName: Full=Histone H2B.2; AltName: Full=HTB8 gi|6579213|gb|AAF18256.1|AC011438_18 T23G18.3 [Arabidopsis thaliana] gi|8778831|gb|AAF79830.1|AC026875_10 T6D22.26 [Arabidopsis thaliana] gi|67633360|gb|AAY78605.1| histone H2B family protein [Arabidopsis thaliana] gi|332190136|gb|AEE28257.1| histone H2B [Arabidopsis thaliana]	257	243	2.00E-64	94.6	58.4	68.9	histone H2B	gbpln	Arabidopsis thaliana	AT1G08170.1 | Symbols: | Histone superfamily protein | chr1:2562941-2563672 REVERSE LENGTH=243	257	243	6.00E-67	94.6	58.4	68.9
Rsa1.0_00612.1.g16875.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00612.1.g16876.t1	ref|XP_002892445.1| hypothetical protein ARALYDRAFT_888049 [Arabidopsis lyrata subsp. lyrata] gi|297338287|gb|EFH68704.1| hypothetical protein ARALYDRAFT_888049 [Arabidopsis lyrata subsp. lyrata]	354	111	1.00E-30	31.4	24.3	26.3	hypothetical protein ARALYDRAFT_888049	gbpln	Arabidopsis lyrata	AT1G08180.1 | Symbols: | unknown protein; Has 53 Blast hits to 53 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 52; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2564741-2565076 REVERSE LENGTH=111	354	111	2.00E-32	31.4	24.0	26.0
Rsa1.0_00612.1.g16877.t1	gb|EOA36603.1| hypothetical protein CARUB_v10011806mg [Capsella rubella]	961	971	0	101.0	91.8	95.5	hypothetical protein CARUB_v10011806mg	gbpln	Capsella rubella	AT1G08190.1 | Symbols: ATVPS41, ZIP2, VPS41, ATVAM2, VAM2 | vacuolar protein sorting 41 | chr1:2567652-2573142 FORWARD LENGTH=980	961	980	0	102.0	91.5	95.9
Rsa1.0_00612.1.g16878.t1	gb|EOA37933.1| hypothetical protein CARUB_v10009400mg [Capsella rubella]	368	389	0	105.7	97.8	98.6	hypothetical protein CARUB_v10009400mg	gbpln	Capsella rubella	AT1G08200.1 | Symbols: AXS2 | UDP-D-apiose/UDP-D-xylose synthase 2 | chr1:2574259-2576609 REVERSE LENGTH=389	368	389	0	105.7	97.0	98.6
Rsa1.0_00612.1.g16879.t1	gb|EOA25534.1| hypothetical protein CARUB_v10018879mg [Capsella rubella]	158	159	2.00E-68	100.6	84.8	93.0	hypothetical protein CARUB_v10018879mg	gbpln	Capsella rubella	AT3G50685.1 | Symbols: | unknown protein; Has 52 Blast hits to 46 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr3:18834272-18834748 REVERSE LENGTH=158	158	158	3.00E-70	100.0	84.2	90.5
Rsa1.0_00612.1.g16880.t5	ref|NP_172303.5| DNA polymerase epsilon subunit 1 [Arabidopsis thaliana] gi|426019656|sp|F4HW04.1|DPOE1_ARATH RecName: Full=DNA polymerase epsilon catalytic subunit A; AltName: Full=DNA polymerase 2 a; Short=AtPOL2a; AltName: Full=DNA polymerase II subunit a; AltName: Full=Protein ABA OVERLY SENSITIVE a; AltName: Full=Protein EARLY IN SHORT DAYS 7; AltName: Full=Protein EMBRYO DEFECTIVE 142; AltName: Full=Protein EMBRYO DEFECTIVE 2284; AltName: Full=Protein EMBRYO DEFECTIVE 529; AltName: Full=Protein TILTED 1 gi|332190145|gb|AEE28266.1| DNA polymerase epsilon catalytic subunit A [Arabidopsis thaliana]	2203	2161	0	98.1	86.7	91.7	DNA polymerase epsilon subunit 1	gbpln	Arabidopsis thaliana	AT1G08260.1 | Symbols: EMB142, EMB2284, POL2A, TIL1, EMB529, ABO4, ESD7 | DNA polymerase epsilon catalytic subunit | chr1:2590944-2606892 FORWARD LENGTH=2161	2203	2161	0	98.1	86.7	91.7
Rsa1.0_00612.1.g16881.t1	gb|EOA27146.1| hypothetical protein CARUB_v10023246mg [Capsella rubella]	436	435	0	99.8	92.7	95.4	hypothetical protein CARUB_v10023246mg	gbpln	Capsella rubella	AT2G27600.1 | Symbols: SKD1, VPS4, ATSKD1 | AAA-type ATPase family protein | chr2:11781226-11783730 FORWARD LENGTH=435	436	435	0	99.8	92.4	95.4
Rsa1.0_00612.1.g16882.t1	gb|EOA37894.1| hypothetical protein CARUB_v10009362mg [Capsella rubella]	401	396	0	98.8	80.8	88.0	hypothetical protein CARUB_v10009362mg	gbpln	Capsella rubella	AT1G08280.1 | Symbols: | Glycosyltransferase family 29 (sialyltransferase) family protein | chr1:2608408-2609604 FORWARD LENGTH=398	401	398	0	99.3	80.8	88.5
Rsa1.0_00612.1.g16883.t1	gb|EOA38145.1| hypothetical protein CARUB_v10009617mg [Capsella rubella]	141	346	7.00E-78	245.4	96.5	97.9	hypothetical protein CARUB_v10009617mg	gbpln	Capsella rubella	AT1G08290.1 | Symbols: WIP3 | WIP domain protein 3 | chr1:2610680-2613180 REVERSE LENGTH=337	141	337	2.00E-79	239.0	95.0	96.5
Rsa1.0_00612.1.g16884.t1	ref|NP_172306.1| WIP domain protein 3 [Arabidopsis thaliana] gi|6579204|gb|AAF18247.1|AC011438_9 T23G18.15 [Arabidopsis thaliana] gi|18027014|gb|AAL55723.1|AF254448_1 WIP3 protein [Arabidopsis thaliana] gi|20258782|gb|AAM13913.1| unknown protein [Arabidopsis thaliana] gi|26452714|dbj|BAC43439.1| unknown protein [Arabidopsis thaliana] gi|332190149|gb|AEE28270.1| WIP domain protein 3 [Arabidopsis thaliana]	210	337	8.00E-76	160.5	71.9	80.0	WIP domain protein 3	gbpln	Arabidopsis thaliana	AT1G08290.1 | Symbols: WIP3 | WIP domain protein 3 | chr1:2610680-2613180 REVERSE LENGTH=337	210	337	3.00E-78	160.5	71.9	80.0
Rsa1.0_00612.1.g16885.t1	ref|XP_002889684.1| hypothetical protein ARALYDRAFT_470891 [Arabidopsis lyrata subsp. lyrata] gi|297335526|gb|EFH65943.1| hypothetical protein ARALYDRAFT_470891 [Arabidopsis lyrata subsp. lyrata]	916	456	1.00E-168	49.8	33.2	36.9	hypothetical protein ARALYDRAFT_470891	gbpln	Arabidopsis lyrata	AT4G13750.1 | Symbols: NOV | Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein | chr4:7975191-7987558 FORWARD LENGTH=2729	916	2729	1.00E-165	297.9	32.5	38.1
Rsa1.0_00612.1.g16886.t1	ref|XP_002890492.1| hypothetical protein ARALYDRAFT_889708 [Arabidopsis lyrata subsp. lyrata] gi|297336334|gb|EFH66751.1| hypothetical protein ARALYDRAFT_889708 [Arabidopsis lyrata subsp. lyrata]	341	326	8.00E-50	95.6	38.7	53.4	hypothetical protein ARALYDRAFT_889708	gbpln	Arabidopsis lyrata	AT1G22090.1 | Symbols: emb2204 | Protein of unknown function (DUF626) | chr1:7795721-7797252 FORWARD LENGTH=329	341	329	7.00E-50	96.5	38.7	53.7

Rsa1.0_00612.1.g16887.t1	gb|AAF18244.1|AC011438_6 T23G18.18 [Arabidopsis thaliana]	296	382	1.00E-144	129.1	81.8	89.2	T23G18.18	gbpln	Arabidopsis thaliana	AT1G08310.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:2619134-2620338 FORWARD LENGTH=315	296	315	1.00E-141	106.4	82.8	90.2
Rsa1.0_00612.1.g16888.t1	gb|EOA37335.1| hypothetical protein CARUB_v10011052mg [Capsella rubella]	321	322	1.00E-158	100.3	88.2	94.7	hypothetical protein CARUB_v10011052mg	gbpln	Capsella rubella	AT1G08315.1 | Symbols: | ARM repeat superfamily protein | chr1:2620500-2621477 REVERSE LENGTH=325	321	325	1.00E-155	101.2	87.9	94.1
Rsa1.0_00612.1.g16889.t8	ref|NP_563810.2| bZIP transcription factor-like protein [Arabidopsis thaliana] gi|79317351|ref|NP_001030999.1| bZIP transcription factor-like protein [Arabidopsis thaliana] gi|14272369|emb|CAC40022.1| bZIP transcription factor [Arabidopsis thaliana] gi|309952053|gb|ADO95300.1| bZIP21 [Arabidopsis thaliana] gi|332190154|gb|AEE28275.1| bZIP transcription factor-like protein [Arabidopsis thaliana] gi|332190156|gb|AEE28277.1| bZIP transcription factor-like protein [Arabidopsis thaliana]	524	481	0	91.8	73.7	75.4	bZIP transcription factor-like protein	gbpln	Arabidopsis thaliana	AT1G08320.3 | Symbols: TGA9, bZIP21 | bZIP transcription factor family protein | chr1:2622113-2627451 REVERSE LENGTH=481	524	481	0	91.8	73.7	75.4
Rsa1.0_00613.1.g16890.t1	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	754	1250	0	165.8	56.6	71.4	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	754	1262	2.00E-68	167.4	19.4	28.9
Rsa1.0_00613.1.g16891.t1	ref|XP_003529636.1| PREDICTED: 5'-adenylylsulfate reductase 3, chloroplastic-like [Glycine max]	372	466	9.00E-20	125.3	15.6	16.1	PREDICTED: 5'-adenylylsulfate reductase 3, chloroplastic-like	gbenv/gbpln	Glycine max	AT4G21990.1 | Symbols: APR3, PRH-26, PRH26, ATAPR3 | APS reductase 3 | chr4:11657284-11658973 REVERSE LENGTH=458	372	458	2.00E-21	123.1	15.1	15.9
Rsa1.0_00613.1.g16892.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00613.1.g16893.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00613.1.g16894.t1	gb|EOA22450.1| hypothetical protein CARUB_v10003097mg [Capsella rubella]	207	91	1.00E-34	44.0	34.8	36.2	hypothetical protein CARUB_v10003097mg	gbpln	Capsella rubella	AT4G04580.1 | Symbols: | Homeodomain-like superfamily protein | chr4:2293761-2294906 REVERSE LENGTH=166	207	166	2.00E-28	80.2	35.3	47.3
Rsa1.0_00613.1.g16895.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00613.1.g16896.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1445	1491	0	103.2	57.2	74.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1445	1262	1.00E-135	87.3	16.5	24.1
Rsa1.0_00613.1.g16897.t1	ref|XP_002872697.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318534|gb|EFH48956.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	656	659	0	100.5	78.7	86.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G04540.1 | Symbols: CRK39 | cysteine-rich RLK (RECEPTOR-like protein kinase) 39 | chr4:2259580-2262138 FORWARD LENGTH=659	656	659	0	100.5	78.5	86.6
Rsa1.0_00613.1.g16898.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00613.1.g16899.t2	ref|NP_192363.1| putative cysteine-rich receptor-like protein kinase 39 [Arabidopsis thaliana] gi|75337882|sp|Q9SYS7.1|CRK39_ARATH RecName: Full=Putative cysteine-rich receptor-like protein kinase 39; Short=Cysteine-rich RLK39; Flags: Precursor gi|4773893|gb|AAD29766.1|AF076243_13 putative receptor-like protein kinase [Arabidopsis thaliana] gi|7267211|emb|CAB77922.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|332656997|gb|AEE82397.1| putative cysteine-rich receptor-like protein kinase 39 [Arabidopsis thaliana]	583	659	0	113.0	74.4	85.8	putative cysteine-rich receptor-like protein kinase 39	gbpln	Arabidopsis thaliana	AT4G04540.1 | Symbols: CRK39 | cysteine-rich RLK (RECEPTOR-like protein kinase) 39 | chr4:2259580-2262138 FORWARD LENGTH=659	583	659	0	113.0	74.4	85.8
Rsa1.0_00613.1.g16900.t1	ref|XP_002886226.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332066|gb|EFH62485.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	416	475	7.00E-29	114.2	16.3	17.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G16430.2 | Symbols: PAP10, ATPAP10 | purple acid phosphatase 10 | chr2:7120502-7122772 REVERSE LENGTH=468	416	468	2.00E-31	112.5	16.3	17.8
Rsa1.0_00613.1.g16901.t10	gb|AAF80658.1|AC012190_14 Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872 [Arabidopsis thaliana]	680	904	1.00E-84	132.9	27.8	40.4	Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	680	719	1.00E-12	105.7	10.0	18.5

Rsa1.0_00613.1.g16902.t1	gb|AAG10812.1|AC018460_6 Putative retroelement polyprotein [Arabidopsis thaliana]		208	1404	2.00E-47	675.0	56.3	70.2	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00613.1.g16903.t1	ref|NP_001031620.1| putative stress-inducible protein [Arabidopsis thaliana] gi|5281051|emb|CAB45987.1| stress-induced protein sti1-like protein [Arabidopsis thaliana] gi|7267942|emb|CAB78283.1| stress-induced protein sti1-like protein [Arabidopsis thaliana] gi|332657726|gb|AEE83126.1| putative stress-inducible protein [Arabidopsis thaliana]		568	558	0	98.2	85.4	91.2	putative stress-inducible protein	gbpln	Arabidopsis thaliana	AT4G12400.2 | Symbols: Hop3 | stress-inducible protein, putative | chr4:7338866-7341239 REVERSE LENGTH=558	568	558	0	98.2	85.4	91.2
Rsa1.0_00613.1.g16904.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#
Rsa1.0_00613.1.g16905.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]		516	414	4.00E-39	80.2	22.9	28.7	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00613.1.g16906.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#
Rsa1.0_00614.1.g16907.t1	ref|NP_179853.1| C3HC4-type RING finger domain-containing protein [Arabidopsis thaliana] gi|4314365|gb|AAD15576.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana] gi|20268717|gb|AAM14062.1| putative copia-like retroelement pol polyprotein [Arabidopsis thaliana] gi|23296688|gb|AAN13147.1| putative copia-like retroelement pol polyprotein [Arabidopsis thaliana] gi|70905061|gb|AAZ14056.1| At2g22680 [Arabidopsis thaliana] gi|330252246|gb|AEC07340.1| C3HC4-type RING finger domain-containing protein [Arabidopsis thaliana]		675	683	0	101.2	77.3	86.7	C3HC4-type RING finger domain-containing protein	gbpln	Arabidopsis thaliana	AT2G22680.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr2:9645433-9647484 FORWARD LENGTH=683	675	683	0	101.2	77.3	86.7
Rsa1.0_00614.1.g16908.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#
Rsa1.0_00614.1.g16909.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#
Rsa1.0_00614.1.g16910.t1	gb|EOA27465.1| hypothetical protein CARUB_v10023602mg [Capsella rubella]		271	323	1.00E-127	119.2	87.8	93.0	hypothetical protein CARUB_v10023602mg	gbpln	Capsella rubella	AT2G22670.4 | Symbols: IAA8 | indoleacetic acid-induced protein 8 | chr2:9636877-9638459 FORWARD LENGTH=338	271	338	1.00E-129	124.7	87.5	92.6
Rsa1.0_00614.1.g16911.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#
Rsa1.0_00614.1.g16912.t1	ref|XP_002878627.1| hypothetical protein ARALYDRAFT_343817 [Arabidopsis lyrata subsp. lyrata] gi|297324466|gb|EFH54886.1| hypothetical protein ARALYDRAFT_343817 [Arabidopsis lyrata subsp. lyrata]		865	920	0	106.4	77.6	84.4	hypothetical protein ARALYDRAFT_343817	gbpln	Arabidopsis lyrata	AT2G22660.2 | Symbols: | Protein of unknown function (duplicated DUF1399) | chr2:9627737-9630840 FORWARD LENGTH=819	865	819	0	94.7	74.1	81.3
Rsa1.0_00614.1.g16913.t1	ref|NP_179849.2| protein BRICK 1 [Arabidopsis thaliana] gi|75166375|sp|Q94JY4.1|BRK1_ARATH RecName: Full=Protein BRICK 1; Short=AtBRK1 gi|13899071|gb|AAK48957.1|AF370530_1 Unknown protein [Arabidopsis thaliana] gi|21553772|gb|AAM62865.1| unknown [Arabidopsis thaliana] gi|23197618|gb|AAN15336.1| Unknown protein [Arabidopsis thaliana] gi|330252238|gb|AEC07332.1| protein BRICK 1 [Arabidopsis thaliana] gi|482564046|gb|EOA28236.1| hypothetical protein CARUB_v10024428mg [Capsella rubella]		85	85	4.00E-41	100.0	100.0	100.0	protein BRICK 1	gbpln	Arabidopsis thaliana	AT2G22640.1 | Symbols: HSPC300, BRK1, ATBRK1 | BRICK1, putative | chr2:9623283-9623938 FORWARD LENGTH=85	85	85	7.00E-44	100.0	100.0	100.0
Rsa1.0_00614.1.g16914.t1	gb|EOA27841.1| hypothetical protein CARUB_v10023996mg [Capsella rubella]		112	228	1.00E-53	203.6	90.2	93.8	hypothetical protein CARUB_v10023996mg	gbpln	Capsella rubella	AT4G37940.1 | Symbols: AGL21 | AGAMOUS-like 21 | chr4:17835695-17838621 REVERSE LENGTH=228	112	228	6.00E-54	203.6	86.6	93.8
Rsa1.0_00615.1.g16915.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]		295	1161	7.00E-60	393.6	40.0	55.9	F14N23.4	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	295	332	2.00E-61	112.5	40.7	57.6
Rsa1.0_00615.1.g16916.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#
Rsa1.0_00615.1.g16917.t1	gb|AAL58072.1| sucrose transporter SUC2 [Brassica oleracea]		468	508	0	108.5	94.7	96.4	sucrose transporter SUC2	gbpln	Brassica oleracea	AT1G22710.1 | Symbols: SUC2, SUT1, ATSUC2 | sucrose-proton symporter 2 | chr1:8030911-8032970 REVERSE LENGTH=512	468	512	0	109.4	90.8	94.9

Rsa1.0_00615.1.g16918.t1	ref|XP_002893245.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297339087|gb|EFH69504.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	291	291	1.00E-140	100.0	90.7	93.8	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G22700.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:8028323-8029878 REVERSE LENGTH=296	291	296	1.00E-142	101.7	90.7	93.1
Rsa1.0_00615.1.g16919.t1	gb|EOA37204.1| hypothetical protein CARUB_v10010675mg [Capsella rubella]	139	120	3.00E-14	86.3	30.2	33.8	hypothetical protein CARUB_v10010675mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00615.1.g16920.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00615.1.g16921.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00615.1.g16922.t1	ref|XP_002893243.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339085|gb|EFH69502.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	312	426	4.00E-75	136.5	54.5	67.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G22670.1 | Symbols: | Protease-associated (PA) RING/U-box zinc finger family protein | chr1:8021854-8023516 REVERSE LENGTH=422	312	422	3.00E-73	135.3	52.6	64.4
Rsa1.0_00615.1.g16923.t1	ref|NP_564177.1| putative neutral invertase [Arabidopsis thaliana] gi|332192143|gb|AEE30264.1| putative neutral invertase [Arabidopsis thaliana]	540	534	0	98.9	93.3	96.5	putative neutral invertase	gbpln	Arabidopsis thaliana	AT1G22650.1 | Symbols: | Plant neutral invertase family protein | chr1:8013529-8015647 REVERSE LENGTH=534	540	534	0	98.9	93.3	96.5
Rsa1.0_00615.1.g16924.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00615.1.g16925.t1	dbj|BAJ34375.1| unnamed protein product [Thellungiella halophila]	266	273	1.00E-120	102.6	85.0	88.0	unnamed protein product	----	----	AT1G22640.1 | Symbols: ATMYB3, MYB3 | myb domain protein 3 | chr1:8006289-8007219 FORWARD LENGTH=257	266	257	1.00E-102	96.6	76.3	81.6
Rsa1.0_00615.1.g16926.t1	ref|XP_002890521.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297336363|gb|EFH66780.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1021	1025	0	100.4	90.0	94.1	C2 domain-containing protein	gbpln	Arabidopsis lyrata	AT1G22610.1 | Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr1:7994478-7997567 FORWARD LENGTH=1029	1021	1029	0	100.8	89.3	93.8
Rsa1.0_00615.1.g16927.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00615.1.g16928.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	203	149	8.00E-26	73.4	29.6	38.4	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	203	292	2.00E-14	143.8	19.7	30.0
Rsa1.0_00616.1.g16929.t7	gb|EMJ24402.1| hypothetical protein PRUPE_ppa009332mg [Prunus persica]	80	297	1.00E-10	371.3	47.5	52.5	hypothetical protein PRUPE_ppa009332mg	gbpln	Prunus persica	AT2G31610.1 | Symbols: | Ribosomal protein S3 family protein | chr2:13450384-13451669 FORWARD LENGTH=250	80	250	4.00E-13	312.5	42.5	47.5
Rsa1.0_00616.1.g16930.t1	gb|EOA26346.1| hypothetical protein CARUB_v10022726mg [Capsella rubella]	179	723	8.00E-63	403.9	64.2	65.9	hypothetical protein CARUB_v10022726mg	gbpln	Capsella rubella	AT2G32950.1 | Symbols: COP1, ATCOP1, DET340, FUS1, EMB168 | Transducin/WD40 repeat-like superfamily protein | chr2:13978000-13983282 FORWARD LENGTH=675	179	675	5.00E-65	377.1	64.2	65.9
Rsa1.0_00616.1.g16931.t1	ref|XP_002881253.1| hypothetical protein ARALYDRAFT_345050 [Arabidopsis lyrata subsp. lyrata] gi|297327092|gb|EFH57512.1| hypothetical protein ARALYDRAFT_345050 [Arabidopsis lyrata subsp. lyrata]	418	460	1.00E-155	110.0	69.6	81.1	hypothetical protein ARALYDRAFT_345050	gbpln	Arabidopsis lyrata	AT2G32930.1 | Symbols: ZFN2 | zinc finger nuclease 2 | chr2:13965990-13968419 REVERSE LENGTH=453	418	453	1.00E-151	108.4	66.0	78.5
Rsa1.0_00616.1.g16932.t1	ref|NP_180848.1| protein ralf-like 17 [Arabidopsis thaliana] gi|75098498|sp|O48776.1|RLF17_ARATH RecName: Full=Protein RALF-like 17; Flags: Precursor gi|2702275|gb|AAB91978.1| hypothetical protein [Arabidopsis thaliana] gi|330253664|gb|AEC08758.1| protein ralf-like 17 [Arabidopsis thaliana]	76	77	3.00E-16	101.3	86.8	93.4	protein ralf-like 17	gbpln	Arabidopsis thaliana	AT2G32890.1 | Symbols: RALFL17 | RALF-like 17 | chr2:13953058-13953291 REVERSE LENGTH=77	76	77	5.00E-19	101.3	86.8	93.4
Rsa1.0_00616.1.g16933.t1	ref|XP_002879420.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297325259|gb|EFH55679.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata]	597	614	0	102.8	78.1	88.8	glycosyl hydrolase family 1 protein	gbpln	Arabidopsis lyrata	AT2G32860.1 | Symbols: BGLU33 | beta glucosidase 33 | chr2:13940233-13943596 FORWARD LENGTH=613	597	613	0	102.7	76.5	87.8
Rsa1.0_00616.1.g16934.t1	ref|XP_002881245.1| hypothetical protein ARALYDRAFT_902346 [Arabidopsis lyrata subsp. lyrata] gi|297327084|gb|EFH57504.1| hypothetical protein ARALYDRAFT_902346 [Arabidopsis lyrata subsp. lyrata]	896	887	0	99.0	89.0	94.6	hypothetical protein ARALYDRAFT_902346	gbpln	Arabidopsis lyrata	AT2G32810.1 | Symbols: BGAL9 | beta galactosidase 9 | chr2:13919410-13925325 REVERSE LENGTH=887	896	887	0	99.0	89.1	94.5
Rsa1.0_00616.1.g16935.t1	ref|XP_002881642.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327481|gb|EFH57901.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	374	405	7.00E-83	108.3	50.3	63.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G49790.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:18436137-18437068 REVERSE LENGTH=283	374	283	1.00E-65	75.7	38.2	47.3

Rsa1.0_00616.1.g16936.t1	ref|NP_850197.1| uncharacterized protein [Arabidopsis thaliana] gi|18700113|gb|AAL77668.1| At2g32760/F24L7.10 [Arabidopsis thaliana] gi|62320642|dbj|BAD95308.1| hypothetical protein [Arabidopsis thaliana] gi|94442409|gb|ABF18992.1| At2g32760 [Arabidopsis thaliana] gi|330253639|gb|AEC08733.1| uncharacterized protein AT2G32760 [Arabidopsis thaliana]	371	352	1.00E-174	94.9	80.1	84.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G32760.1 | Symbols: | unknown protein; Has 229 Blast hits to 229 proteins in 104 species: Archae - 0; Bacteria - 2; Metazoa - 79; Fungi - 90; Plants - 49; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr2:13892140-13894295 FORWARD LENGTH=352	371	352	1.00E-177	94.9	80.1	84.9
Rsa1.0_00616.1.g16937.t1	ref|XP_002879410.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297325249|gb|EFH55669.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	475	469	0	98.7	79.4	88.2	exostosin family protein	gbpln	Arabidopsis lyrata	AT2G32740.1 | Symbols: ATGT13, GT13 | galactosyltransferase 13 | chr2:13886826-13888232 FORWARD LENGTH=468	475	468	0	98.5	78.9	88.0
Rsa1.0_00616.1.g16938.t1	ref|XP_002879409.1| hypothetical protein ARALYDRAFT_482209 [Arabidopsis lyrata subsp. lyrata] gi|297325248|gb|EFH55668.1| hypothetical protein ARALYDRAFT_482209 [Arabidopsis lyrata subsp. lyrata]	1038	1002	0	96.5	92.4	93.8	hypothetical protein ARALYDRAFT_482209	gbpln	Arabidopsis lyrata	AT2G32730.1 | Symbols: | 26S proteasome regulatory complex, non-ATPase subcomplex, Rpn2/Psmd1 subunit | chr2:13880189-13885464 FORWARD LENGTH=1004	1038	1004	0	96.7	92.0	93.4
Rsa1.0_00616.1.g16939.t1	ref|XP_002881239.1| B5 #4 [Arabidopsis lyrata subsp. lyrata] gi|297327078|gb|EFH57498.1| B5 #4 [Arabidopsis lyrata subsp. lyrata]	135	134	4.00E-69	99.3	94.8	96.3	B5 #4	gbpln	Arabidopsis lyrata	AT2G32720.1 | Symbols: B5 #4, ATCB5-B, CB5-B | cytochrome B5 isoform B | chr2:13877013-13878447 REVERSE LENGTH=134	135	134	4.00E-71	99.3	93.3	96.3
Rsa1.0_00616.1.g16940.t1	gb|EOA27561.1| hypothetical protein CARUB_v10023701mg, partial [Capsella rubella]	234	306	4.00E-67	130.8	70.1	80.8	hypothetical protein CARUB_v10023701mg, partial	gbpln	Capsella rubella	AT2G32710.2 | Symbols: KRP4, ACK2, ICK7 | Cyclin-dependent kinase inhibitor family protein | chr2:13873496-13875350 FORWARD LENGTH=286	234	286	6.00E-63	122.2	71.4	80.8
Rsa1.0_00616.1.g16941.t1	#	#	#	#	#	#	#	-	----	----	AT2G32700.2 | Symbols: LUH | LEUNIG_homolog | chr2:13867235-13871844 FORWARD LENGTH=787	130	787	6.00E-12	605.4	36.9	40.8
Rsa1.0_00616.1.g16942.t1	ref|XP_002881238.1| hypothetical protein ARALYDRAFT_482197 [Arabidopsis lyrata subsp. lyrata] gi|297327077|gb|EFH57497.1| hypothetical protein ARALYDRAFT_482197 [Arabidopsis lyrata subsp. lyrata]	203	163	4.00E-24	80.3	24.1	26.6	hypothetical protein ARALYDRAFT_482197	gbpln	Arabidopsis lyrata	AT2G32690.4 | Symbols: ATGRP23, GRP23 | glycine-rich protein 23 | chr2:13863934-13864539 REVERSE LENGTH=172	203	172	6.00E-26	84.7	23.6	26.6
Rsa1.0_00617.1.g16943.t1	ref|XP_002879242.1| hypothetical protein ARALYDRAFT_901974 [Arabidopsis lyrata subsp. lyrata] gi|297325081|gb|EFH55501.1| hypothetical protein ARALYDRAFT_901974 [Arabidopsis lyrata subsp. lyrata]	129	129	6.00E-46	100.0	68.2	83.7	hypothetical protein ARALYDRAFT_901974	gbpln	Arabidopsis lyrata	AT4G12617.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G05630.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:7459180-7459563 FORWARD LENGTH=127	129	127	4.00E-25	98.4	42.6	62.8
Rsa1.0_00617.1.g16944.t1	gb|EOA14790.1| hypothetical protein CARUB_v10028090mg [Capsella rubella]	427	419	1.00E-120	98.1	57.8	71.7	hypothetical protein CARUB_v10028090mg	gbpln	Capsella rubella	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	427	422	1.00E-122	98.8	56.7	70.0
Rsa1.0_00617.1.g16945.t1	gb|EOA18720.1| hypothetical protein CARUB_v10007298mg [Capsella rubella]	131	465	4.00E-15	355.0	38.9	49.6	hypothetical protein CARUB_v10007298mg	gbpln	Capsella rubella	AT4G24150.1 | Symbols: AtGRF8, GRF8 | growth-regulating factor 8 | chr4:12535972-12539387 FORWARD LENGTH=493	131	493	4.00E-11	376.3	34.4	41.2
Rsa1.0_00617.1.g16946.t2	gb|EOA37082.1| hypothetical protein CARUB_v10010237mg [Capsella rubella]	196	223	1.00E-72	113.8	77.6	88.3	hypothetical protein CARUB_v10010237mg	gbpln	Capsella rubella	AT1G05190.1 | Symbols: emb2394 | Ribosomal protein L6 family | chr1:1502515-1503738 REVERSE LENGTH=223	196	223	4.00E-74	113.8	76.5	87.8
Rsa1.0_00617.1.g16947.t1	ref|XP_002866147.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311982|gb|EFH42406.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	394	423	3.00E-97	107.4	52.8	69.8	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56420.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22850863-22852334 REVERSE LENGTH=422	394	422	2.00E-97	107.1	51.5	69.5
Rsa1.0_00617.1.g16948.t1	ref|XP_002866147.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311982|gb|EFH42406.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	539	423	1.00E-105	78.5	38.4	52.3	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56420.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22850863-22852334 REVERSE LENGTH=422	539	422	1.00E-105	78.3	38.0	52.1
Rsa1.0_00617.1.g16949.t1	ref|XP_002866147.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311982|gb|EFH42406.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	425	423	0	99.5	80.0	89.9	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56420.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22850863-22852334 REVERSE LENGTH=422	425	422	0	99.3	78.8	89.6

Rsa1.0_00617.1.g16950.t1	gb|EOA12750.1| hypothetical protein CARUB_v10028431mg [Capsella rubella]	237	423	1.00E-35	178.5	38.0	49.4	hypothetical protein CARUB_v10028431mg	gbpln	Capsella rubella	AT5G56440.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22855742-22857117 REVERSE LENGTH=430	237	430	3.00E-35	181.4	37.6	43.9
Rsa1.0_00617.1.g16951.t1	ref|NP_200455.1| FBD-associated F-box protein [Arabidopsis thaliana] gi|75262697|sp|Q9FM87.1|FBD26_ARATH RecName: Full=Putative FBD-associated F-box protein At5g56440 gi|10177843|dbj|BAB11272.1| unnamed protein product [Arabidopsis thaliana] gi|332009382|gb|AED96765.1| FBD-associated F-box protein [Arabidopsis thaliana]	420	430	1.00E-116	102.4	56.4	68.8	FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT5G56440.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22855742-22857117 REVERSE LENGTH=430	420	430	1.00E-119	102.4	56.4	68.8
Rsa1.0_00617.1.g16952.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00617.1.g16953.t1	ref|XP_002864456.1| hypothetical protein ARALYDRAFT_331952 [Arabidopsis lyrata subsp. lyrata] gi|297310291|gb|EFH40715.1| hypothetical protein ARALYDRAFT_331952 [Arabidopsis lyrata subsp. lyrata]	414	419	0	101.2	93.2	95.9	hypothetical protein ARALYDRAFT_331952	gbpln	Arabidopsis lyrata	AT5G56460.1 | Symbols: | Protein kinase superfamily protein | chr5:22865509-22867866 FORWARD LENGTH=408	414	408	0	98.6	91.3	94.7
Rsa1.0_00617.1.g16954.t1	ref|XP_002864457.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310292|gb|EFH40716.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	736	578	0	78.5	64.5	70.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G32300.1 | Symbols: | D-arabinono-1,4-lactone oxidase family protein | chr1:11651342-11653365 FORWARD LENGTH=595	736	595	0	80.8	63.5	69.3
Rsa1.0_00617.1.g16955.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00618.1.g16956.t1	gb|EOA29697.1| hypothetical protein CARUB_v10016402mg [Capsella rubella]	73	76	2.00E-28	104.1	89.0	93.2	hypothetical protein CARUB_v10016402mg	gbpln	Capsella rubella	AT3G14430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 16 Blast hits to 16 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4824399-4824732 REVERSE LENGTH=76	73	76	5.00E-31	104.1	89.0	93.2
Rsa1.0_00618.1.g16957.t1	ref|NP_188060.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|30683149|ref|NP_850584.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|297829994|ref|XP_002882879.1| hypothetical protein ARALYDRAFT_478862 [Arabidopsis lyrata subsp. lyrata] gi|13124262|sp|Q9LRR9.1|GLO1_ARATH RecName: Full=Peroxisomal (S)-2-hydroxy-acid oxidase GLO1; AltName: Full=Glycolate oxidase 1; Short=AtGLO1; Short=GOX 1; AltName: Full=Short chain alpha-hydroxy acid oxidase GLO1 gi|16226423|gb|AAL16164.1|AF428396_1 AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|11994212|dbj|BAB01334.1| glycolate oxidase [Arabidopsis thaliana] gi|15450741|gb|AAK96642.1| AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|18491119|gb|AAL69528.1| AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|297328719|gb|EFH59138.1| hypothetical protein ARALYDRAFT_478862 [Arabidopsis lyrata subsp. lyrata] gi|332641997|gb|AEE75518.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|332641999|gb|AEE75520.1| putative peroxisomal (S)-2-hydroxy-acid	367	367	0	100.0	97.8	100.0	putative peroxisomal (S)-2-hydroxy-acid oxidase 2	gbpln	Arabidopsis lyrata	AT3G14420.2 | Symbols: | Aldolase-type TIM barrel family protein | chr3:4821804-4823899 FORWARD LENGTH=367	367	367	0	100.0	97.8	100.0
Rsa1.0_00618.1.g16958.t5	gb|AAV28535.1| glycolate oxidase [Brassica napus]	393	367	1.00E-176	93.4	83.0	87.0	glycolate oxidase	gbpln	Brassica napus	AT3G14415.3 | Symbols: | Aldolase-type TIM barrel family protein | chr3:4818667-4820748 FORWARD LENGTH=367	393	367	1.00E-177	93.4	82.2	86.0

Rsa1.0_00618.1.g16959.t1	ref|XP_002885043.1| hypothetical protein ARALYDRAFT_897714 [Arabidopsis lyrata subsp. lyrata] gi|297330883|gb|EFH61302.1| hypothetical protein ARALYDRAFT_897714 [Arabidopsis lyrata subsp. lyrata]	347	339	1.00E-179	97.7	93.1	95.4	hypothetical protein ARALYDRAFT_897714	gbpln	Arabidopsis lyrata	AT3G14410.1 | Symbols: | Nucleotide/sugar transporter family protein | chr3:4815982-4817852 REVERSE LENGTH=340	347	340	1.00E-179	98.0	93.1	95.7
Rsa1.0_00618.1.g16960.t1	ref|XP_002885042.1| ubiquitin-specific protease 25 [Arabidopsis lyrata subsp. lyrata] gi|297330882|gb|EFH61301.1| ubiquitin-specific protease 25 [Arabidopsis lyrata subsp. lyrata]	684	662	0	96.8	75.7	83.5	ubiquitin-specific protease 25	gbpln	Arabidopsis lyrata	AT3G14400.1 | Symbols: UBP25 | ubiquitin-specific protease 25 | chr3:4811953-4815210 REVERSE LENGTH=661	684	661	0	96.6	75.7	83.3
Rsa1.0_00618.1.g16961.t1	ref|XP_002882878.1| hypothetical protein ARALYDRAFT_478858 [Arabidopsis lyrata subsp. lyrata] gi|297328718|gb|EFH59137.1| hypothetical protein ARALYDRAFT_478858 [Arabidopsis lyrata subsp. lyrata]	76	75	2.00E-18	98.7	77.6	86.8	hypothetical protein ARALYDRAFT_478858	gbpln	Arabidopsis lyrata	AT3G14395.1 | Symbols: | unknown protein; Has 4 Blast hits to 4 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4811044-4811271 FORWARD LENGTH=75	76	75	7.00E-21	98.7	77.6	85.5
Rsa1.0_00618.1.g16962.t1	ref|XP_002885041.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|341958542|sp|D7L342.1|CSPL8_ARALL RecName: Full=CASP-like protein ARALYDRAFT_478855 gi|297330881|gb|EFH61300.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata]	230	178	4.00E-44	77.4	50.9	59.1	integral membrane family protein	gbpln	Arabidopsis lyrata	AT3G14380.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr3:4803175-4803799 REVERSE LENGTH=178	230	178	1.00E-43	77.4	48.3	58.3
Rsa1.0_00618.1.g16963.t1	ref|NP_188054.1| protein kinase WAG2 [Arabidopsis thaliana] gi|9279584|dbj|BAB01042.1| protein kinase [Arabidopsis thaliana] gi|21618089|gb|AAM67139.1| putative protein kinase [Arabidopsis thaliana] gi|116325946|gb|ABJ98574.1| At3g14370 [Arabidopsis thaliana] gi|332641988|gb|AEE75509.1| protein kinase WAG2 [Arabidopsis thaliana]	480	480	0	100.0	93.3	96.3	protein kinase WAG2	gbpln	Arabidopsis thaliana	AT3G14370.1 | Symbols: WAG2 | Protein kinase superfamily protein | chr3:4798026-4799468 REVERSE LENGTH=480	480	480	0	100.0	93.3	96.3
Rsa1.0_00618.1.g16964.t1	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	964	915	1.00E-139	94.9	26.9	38.4	F22O13.21	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	964	719	3.00E-27	74.6	12.3	22.3
Rsa1.0_00618.1.g16965.t1	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	203	326	4.00E-25	160.6	31.0	47.3	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00618.1.g16966.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	944	871	2.00E-86	92.3	29.7	44.8	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	944	874	4.00E-34	92.6	10.1	16.0
Rsa1.0_00618.1.g16967.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00618.1.g16968.t1	ref|XP_002882876.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297328716|gb|EFH59135.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	520	521	0	100.2	81.2	88.8	lipase class 3 family protein	gbpln	Arabidopsis lyrata	AT3G14360.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:4791596-4793534 FORWARD LENGTH=518	520	518	0	99.6	79.6	87.9
Rsa1.0_00618.1.g16969.t1	gb|AFQ91933.1| leucine-rich repeat receptor-like kinase [Brassica rapa subsp. oleifera]	830	707	0	85.2	79.8	81.6	leucine-rich repeat receptor-like kinase	gbpln	Brassica rapa	AT3G14350.1 | Symbols: SRF7 | STRUBBELIG-receptor family 7 | chr3:4783115-4786999 REVERSE LENGTH=717	830	717	0	86.4	77.3	81.9
Rsa1.0_00618.1.g16970.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00619.1.g16971.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00619.1.g16972.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00619.1.g16973.t1	ref|XP_002881476.1| hypothetical protein ARALYDRAFT_902809 [Arabidopsis lyrata subsp. lyrata] gi|297327315|gb|EFH57735.1| hypothetical protein ARALYDRAFT_902809 [Arabidopsis lyrata subsp. lyrata] gi|482563079|gb|EOA27269.1| hypothetical protein CARUB_v10023389mg [Capsella rubella] gi|482563080|gb|EOA27270.1| hypothetical protein CARUB_v10023389mg [Capsella rubella]	390	390	0	100.0	99.2	100.0	hypothetical protein ARALYDRAFT_902809	gbpln	Arabidopsis lyrata	AT2G36880.2 | Symbols: MAT3 | methionine adenosyltransferase 3 | chr2:15479721-15480893 REVERSE LENGTH=390	390	390	0	100.0	98.7	100.0

Rsa1.0_00619.1.g16974.t1	gb|EOA27604.1| hypothetical protein CARUB_v10023744mg [Capsella rubella]	288	297	1.00E-113	103.1	81.3	86.5	hypothetical protein CARUB_v10023744mg	gbpln	Capsella rubella	AT2G36890.1 | Symbols: RAX2, MYB38, ATMYB38, BIT1 | Duplicated homeodomain-like superfamily protein | chr2:15485821-15487245 FORWARD LENGTH=298	288	298	1.00E-108	103.5	80.6	87.5
Rsa1.0_00619.1.g16975.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00619.1.g16976.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00619.1.g16977.t1	gb|EOA26337.1| hypothetical protein CARUB_v10022511mg [Capsella rubella]	301	1347	1.00E-133	447.5	83.7	87.7	hypothetical protein CARUB_v10022511mg	gbpln	Capsella rubella	AT2G36910.1 | Symbols: ATPGP1, PGP1, ABCB1 | ATP binding cassette subfamily B1 | chr2:15502162-15507050 FORWARD LENGTH=1286	301	1286	1.00E-127	427.2	72.1	73.8
Rsa1.0_00619.1.g16978.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1366	1307	0	95.7	59.5	74.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1366	1262	1.00E-103	92.4	14.8	22.5
Rsa1.0_00619.1.g16979.t1	gb|ABB97035.1| ABC transporter-like protein [Brassica rapa]	1014	1300	0	128.2	98.7	99.5	ABC transporter-like protein	gbpln	Brassica rapa	AT2G36910.1 | Symbols: ATPGP1, PGP1, ABCB1 | ATP binding cassette subfamily B1 | chr2:15502162-15507050 FORWARD LENGTH=1286	1014	1286	0	126.8	96.6	98.9
Rsa1.0_00619.1.g16980.t2	ref|NP_565854.1| C2H2-type zinc finger-containing protein [Arabidopsis thaliana] gi|15027949|gb|AAK76505.1| unknown protein [Arabidopsis thaliana] gi|20197946|gb|AAD31578.2| expressed protein [Arabidopsis thaliana] gi|20259185|gb|AAM14308.1| unknown protein [Arabidopsis thaliana] gi|330254229|gb|AEC09323.1| C2H2-type zinc finger-containing protein [Arabidopsis thaliana]	109	198	9.00E-48	181.7	87.2	90.8	C2H2-type zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT2G36930.1 | Symbols: | zinc finger (C2H2 type) family protein | chr2:15510002-15511347 REVERSE LENGTH=198	109	198	1.00E-50	181.7	87.2	90.8
Rsa1.0_00620.1.g16981.t2	ref|XP_002873770.1| hypothetical protein ARALYDRAFT_488488 [Arabidopsis lyrata subsp. lyrata] gi|297319607|gb|EFH50029.1| hypothetical protein ARALYDRAFT_488488 [Arabidopsis lyrata subsp. lyrata]	314	282	9.00E-74	89.8	48.1	55.7	hypothetical protein ARALYDRAFT_488488	gbpln	Arabidopsis lyrata	AT5G16360.1 | Symbols: | NC domain-containing protein-related | chr5:5355236-5356195 REVERSE LENGTH=283	314	283	3.00E-75	90.1	47.1	54.8
Rsa1.0_00620.1.g16982.t1	ref|NP_197136.1| protein FRIGIDA like 1 [Arabidopsis thaliana] gi|9759114|dbj|BAB09599.1| unnamed protein product [Arabidopsis thaliana] gi|18700117|gb|AAL77670.1| AT5g16320/MQK4_4 [Arabidopsis thaliana] gi|20856075|gb|AAM26646.1| AT5g16320/MQK4_4 [Arabidopsis thaliana] gi|46810269|tpg|DAA05285.1| TPA_exp: flowering time protein [Arabidopsis thaliana] gi|332004896|gb|AED92279.1| protein FRIGIDA like 1 [Arabidopsis thaliana]	466	470	1.00E-156	100.9	66.3	79.8	protein FRIGIDA like 1	gbpln	Arabidopsis thaliana	AT5G16320.1 | Symbols: FRL1 | FRIGIDA like 1 | chr5:5344507-5345919 FORWARD LENGTH=470	466	470	1.00E-158	100.9	66.3	79.8
Rsa1.0_00620.1.g16983.t1	ref|XP_002871714.1| hypothetical protein ARALYDRAFT_488483 [Arabidopsis lyrata subsp. lyrata] gi|297317551|gb|EFH47973.1| hypothetical protein ARALYDRAFT_488483 [Arabidopsis lyrata subsp. lyrata]	1133	1067	0	94.2	83.4	88.6	hypothetical protein ARALYDRAFT_488483	gbpln	Arabidopsis lyrata	AT5G16300.1 | Symbols: | Vps51/Vps67 family (components of vesicular transport) protein | chr5:5338119-5342186 FORWARD LENGTH=1068	1133	1068	0	94.3	83.1	88.5
Rsa1.0_00620.1.g16984.t2	ref|NP_197132.2| uncharacterized protein [Arabidopsis thaliana] gi|332004885|gb|AED92268.1| uncharacterized protein AT5G16280 [Arabidopsis thaliana]	1275	1272	0	99.8	87.6	93.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G16280.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:5323377-5331345 REVERSE LENGTH=1272	1275	1272	0	99.8	87.6	93.1
Rsa1.0_00620.1.g16985.t1	gb|EOA23068.1| hypothetical protein CARUB_v10003848mg [Capsella rubella]	342	341	5.00E-29	99.7	24.6	33.6	hypothetical protein CARUB_v10003848mg	gbpln	Capsella rubella	AT4G11340.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:6894208-6899130 REVERSE LENGTH=495	342	495	4.00E-31	144.7	23.4	30.4
Rsa1.0_00620.1.g16986.t1	ref|NP_192873.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|5596480|emb|CAB51418.1| putative protein [Arabidopsis thaliana] gi|7267833|emb|CAB81235.1| putative protein [Arabidopsis thaliana] gi|332657598|gb|AEE82998.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	393	495	8.00E-30	126.0	20.9	25.4	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT4G11340.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:6894208-6899130 REVERSE LENGTH=495	393	495	2.00E-32	126.0	20.9	25.4
Rsa1.0_00620.1.g16987.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00620.1.g16988.t4</td><td>ref|XP_002871712.1| hypothetical protein ARALYDRAFT_909607 [Arabidopsis lyrata subsp. lyrata] gi|297317549|gb|EFH47971.1| hypothetical protein ARALYDRAFT_909607 [Arabidopsis lyrata subsp. lyrata]</td><td>1037</td><td>1030</td><td>0</td><td>99.3</td><td>78.9</td><td>86.6</td><td>hypothetical protein ARALYDRAFT_909607</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G16270.1 | Symbols: ATRAD21.3, SYN4 | sister chromatid cohesion 1 protein 4 | chr5:5316783-5322330 FORWARD LENGTH=1031</td><td>1037</td><td>1031</td><td>0</td><td>99.4</td><td>77.0</td><td>84.7</td></tr>
<tr><td>Rsa1.0_00620.1.g16989.t1</td><td>ref|NP_197130.1| HIV Tat-specific factor 1 [Arabidopsis thaliana] gi|9755836|emb|CAC01867.1| putative protein [Arabidopsis thaliana] gi|63003814|gb|AAY25436.1| At5g16260 [Arabidopsis thaliana] gi|110738266|dbj|BAF01062.1| hypothetical protein [Arabidopsis thaliana] gi|332004883|gb|AED92266.1| RNA binding protein ELF9 [Arabidopsis thaliana]</td><td>534</td><td>519</td><td>0</td><td>97.2</td><td>79.0</td><td>86.5</td><td>HIV Tat-specific factor 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G16260.1 | Symbols: ELF9 | RNA binding (RRM/RBD/RNP motifs) family protein | chr5:5311363-5315496 FORWARD LENGTH=519</td><td>534</td><td>519</td><td>0</td><td>97.2</td><td>79.0</td><td>86.5</td></tr>
<tr><td>Rsa1.0_00620.1.g16990.t1</td><td>gb|AAM63009.1| unknown [Arabidopsis thaliana]</td><td>185</td><td>183</td><td>1.00E-84</td><td>98.9</td><td>89.7</td><td>95.7</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G16250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02640.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5310264-5310815 REVERSE LENGTH=183</td><td>185</td><td>183</td><td>1.00E-86</td><td>98.9</td><td>89.2</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00620.1.g16991.t1</td><td>gb|EOA18445.1| hypothetical protein CARUB_v10006988mg [Capsella rubella]</td><td>217</td><td>683</td><td>4.00E-53</td><td>314.7</td><td>49.8</td><td>65.9</td><td>hypothetical protein CARUB_v10006988mg</td><td>gbpln</td><td>Capsella rubella</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00620.1.g16992.t1</td><td>gb|EOA20786.1| hypothetical protein CARUB_v10001122mg [Capsella rubella]</td><td>420</td><td>399</td><td>0</td><td>95.0</td><td>82.1</td><td>88.1</td><td>hypothetical protein CARUB_v10001122mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G02630.1 | Symbols: | Plant stearoyl-acyl-carrier-protein desaturase family protein | chr3:562164-564524 FORWARD LENGTH=396</td><td>420</td><td>396</td><td>0</td><td>94.3</td><td>79.5</td><td>86.4</td></tr>
<tr><td>Rsa1.0_00620.1.g16993.t1</td><td>ref|NP_197127.1| acyl-[acyl-carrier-protein] desaturase [Arabidopsis thaliana] gi|334302876|sp|Q9LF05.3|STAD3_ARATH RecName: Full=Acyl-[acyl-carrier-protein] desaturase 3, chloroplastic; AltName: Full=Stearoyl-ACP desaturase 3; Flags: Precursor gi|9755833|emb|CAC01864.1| stearoyl-acyl carrier protein desaturase [Arabidopsis thaliana] gi|117168051|gb|ABK32108.1| At5g16230 [Arabidopsis thaliana] gi|332004880|gb|AED92263.1| acyl-[acyl-carrier-protein] desaturase [Arabidopsis thaliana]</td><td>430</td><td>401</td><td>0</td><td>93.3</td><td>83.7</td><td>87.9</td><td>acyl-</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G16230.1 | Symbols: | Plant stearoyl-acyl-carrier-protein desaturase family protein | chr5:5303394-5305944 FORWARD LENGTH=401</td><td>430</td><td>401</td><td>0</td><td>93.3</td><td>83.7</td><td>87.9</td></tr>
<tr><td>Rsa1.0_00620.1.g16994.t2</td><td>gb|EOA20509.1| hypothetical protein CARUB_v10000823mg [Capsella rubella]</td><td>493</td><td>490</td><td>1.00E-172</td><td>99.4</td><td>72.2</td><td>79.1</td><td>hypothetical protein CARUB_v10000823mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G16220.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr5:5298604-5300579 REVERSE LENGTH=476</td><td>493</td><td>476</td><td>1.00E-167</td><td>96.6</td><td>69.0</td><td>76.1</td></tr>
<tr><td>Rsa1.0_00621.1.g16995.t1</td><td>gb|EOA18862.1| hypothetical protein CARUB_v10007485mg [Capsella rubella]</td><td>85</td><td>86</td><td>3.00E-27</td><td>101.2</td><td>74.1</td><td>83.5</td><td>hypothetical protein CARUB_v10007485mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G37290.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; LOCATED IN: endomembrane system; EXPRESSED IN: cotyledon, hypocotyl, leaf; EXPRESSED DURING: LP.04 four leaves visible; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G23270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17549929-17550183 REVERSE LENGTH=84</td><td>85</td><td>84</td><td>7.00E-27</td><td>98.8</td><td>71.8</td><td>80.0</td></tr>
<tr><td>Rsa1.0_00621.1.g16996.t1</td><td>gb|AAC49776.1| AP2 domain containing protein RAP2.10 [Arabidopsis thaliana] gi|2632063|emb|CAA05630.1| TINY-like protein [Arabidopsis thaliana]</td><td>186</td><td>259</td><td>1.00E-67</td><td>139.2</td><td>84.4</td><td>86.6</td><td>AP2 domain containing protein RAP2.10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G36900.1 | Symbols: RAP2.10, DEAR4 | related to AP2 10 | chr4:17389015-17389605 FORWARD LENGTH=196</td><td>186</td><td>196</td><td>2.00E-69</td><td>105.4</td><td>84.4</td><td>86.6</td></tr>
<tr><td>Rsa1.0_00621.1.g16997.t1</td><td>gb|EOA17171.1| hypothetical protein CARUB_v10005437mg, partial [Capsella rubella]</td><td>233</td><td>282</td><td>1.00E-99</td><td>121.0</td><td>83.3</td><td>88.4</td><td>hypothetical protein CARUB_v10005437mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G36910.1 | Symbols: LEJ2, CDCP2 | Cystathionine beta-synthase (CBS) family protein | chr4:17391016-17393218 REVERSE LENGTH=236</td><td>233</td><td>236</td><td>7.00E-99</td><td>101.3</td><td>82.8</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00621.1.g16998.t1</td><td>gb|ADU04499.1| APETALA2 [Brassica napus]</td><td>433</td><td>432</td><td>0</td><td>99.8</td><td>93.1</td><td>95.8</td><td>APETALA2</td><td>gbpln</td><td>Brassica napus</td><td>AT4G36920.2 | Symbols: AP2 | Integrase-type DNA-binding superfamily protein | chr4:17400998-17403140 FORWARD LENGTH=432</td><td>433</td><td>432</td><td>0</td><td>99.8</td><td>86.8</td><td>91.0</td></tr>
</table>

Rsa1.0_00621.1.g16999.t1	ref|NP_195412.3| nicotinate phosphoribosyltransferase 1 [Arabidopsis thaliana] gi|20260210|gb|AAM13003.1| unknown protein [Arabidopsis thaliana] gi|332661321|gb|AEE86721.1| nicotinate phosphoribosyltransferase 1 [Arabidopsis thaliana]	568	559	0	98.4	90.3	93.7	nicotinate phosphoribosyltransferase 1	gbpln	Arabidopsis thaliana	AT4G36940.1 | Symbols: NAPRT1 | nicotinate phosphoribosyltransferase 1 | chr4:17416938-17419883 FORWARD LENGTH=559	568	559	0	98.4	90.3	93.7
Rsa1.0_00621.1.g17000.t1	ref|NP_001078503.4| phospholipase C/ phosphoric diester hydrolase [Arabidopsis thaliana] gi|332661322|gb|AEE86722.1| phospholipase C/ phosphoric diester hydrolase [Arabidopsis thaliana]	413	408	0	98.8	80.6	88.6	phospholipase C/ phosphoric diester hydrolase	gbpln	Arabidopsis thaliana	AT4G36945.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr4:17420098-17422047 REVERSE LENGTH=408	413	408	0	98.8	80.6	88.6
Rsa1.0_00621.1.g17001.t1	ref|XP_002869001.1| hypothetical protein ARALYDRAFT_328051 [Arabidopsis lyrata subsp. lyrata] gi|297314837|gb|EFH45260.1| hypothetical protein ARALYDRAFT_328051 [Arabidopsis lyrata subsp. lyrata]	346	787	1.00E-150	227.5	78.0	86.7	hypothetical protein ARALYDRAFT_328051	gbpln	Arabidopsis lyrata	AT4G36950.1 | Symbols: MAPKKK21 | mitogen-activated protein kinase kinase kinase 21 | chr4:17422834-17423844 REVERSE LENGTH=336	346	336	1.00E-149	97.1	77.5	85.0
Rsa1.0_00621.1.g17002.t1	ref|XP_002866967.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297312803|gb|EFH43226.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	384	380	0	99.0	90.6	94.3	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT4G36960.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:17427349-17429589 FORWARD LENGTH=379	384	379	0	98.7	88.0	92.4
Rsa1.0_00621.1.g17003.t1	ref|XP_002869002.1| hypothetical protein ARALYDRAFT_912636 [Arabidopsis lyrata subsp. lyrata] gi|297314838|gb|EFH45261.1| hypothetical protein ARALYDRAFT_912636 [Arabidopsis lyrata subsp. lyrata]	423	433	1.00E-134	102.4	75.7	81.1	hypothetical protein ARALYDRAFT_912636	gbpln	Arabidopsis lyrata	AT4G36970.1 | Symbols: | Remorin family protein | chr4:17429826-17431459 REVERSE LENGTH=427	423	427	1.00E-136	100.9	73.8	81.1
Rsa1.0_00621.1.g17004.t1	gb|ABV89640.1| heat shock factor 4 [Brassica rapa]	271	285	1.00E-125	105.2	88.6	93.0	heat shock factor 4	gbpln	Brassica rapa	AT4G36990.1 | Symbols: HSF4, HSFB1, AT-HSFB1, ATHSF4 | heat shock factor 4 | chr4:17440660-17441706 FORWARD LENGTH=284	271	284	1.00E-110	104.8	79.7	86.3
Rsa1.0_00621.1.g17005.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00621.1.g17006.t1	gb|AAB81881.1| putative MuDR-A-like transposon protein [Arabidopsis thaliana] gi|7267510|emb|CAB77993.1| putative MuDR-A-like transposon protein [Arabidopsis thaliana]	338	761	1.00E-95	225.1	47.0	58.6	putative MuDR-A-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00621.1.g17007.t3	ref|XP_002869006.1| hypothetical protein ARALYDRAFT_490916 [Arabidopsis lyrata subsp. lyrata] gi|297314842|gb|EFH45265.1| hypothetical protein ARALYDRAFT_490916 [Arabidopsis lyrata subsp. lyrata]	469	412	0	87.8	69.9	78.7	hypothetical protein ARALYDRAFT_490916	gbpln	Arabidopsis lyrata	AT4G37050.1 | Symbols: PLP4, PLA V, AtPLAIVC | PATATIN-like protein 4 | chr4:17457261-17459642 REVERSE LENGTH=428	469	428	0	91.3	69.5	78.7
Rsa1.0_00621.1.g17008.t1	gb|EOA18418.1| hypothetical protein CARUB_v10006962mg [Capsella rubella]	408	414	0	101.5	85.3	93.4	hypothetical protein CARUB_v10006962mg	gbpln	Capsella rubella	AT4G37070.2 | Symbols: PLP1, PLA IVA, AtPLAIVA | Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein | chr4:17464916-17467058 REVERSE LENGTH=414	408	414	0	101.5	84.3	93.1
Rsa1.0_00622.1.g17009.t4	ref|XP_002893514.1| hypothetical protein ARALYDRAFT_473032 [Arabidopsis lyrata subsp. lyrata] gi|297339356|gb|EFH69773.1| hypothetical protein ARALYDRAFT_473032 [Arabidopsis lyrata subsp. lyrata]	895	578	0	64.6	50.8	54.3	hypothetical protein ARALYDRAFT_473032	gbpln	Arabidopsis lyrata	AT1G28240.1 | Symbols: | Protein of unknown function (DUF616) | chr1:9868521-9871798 REVERSE LENGTH=581	895	581	0	64.9	51.4	54.6
Rsa1.0_00622.1.g17010.t1	ref|NP_173137.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana] gi|75263252|sp|Q9FZ52.1|FDL3_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g16930 gi|9802769|gb|AAF99838.1|AC051629_5 Hypothetical protein [Arabidopsis thaliana] gi|332191402|gb|AEE29523.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana]	267	449	1.00E-37	168.2	39.0	44.9	F-box/RNI-like/FBD-like domains-containing protein	gbpln	Arabidopsis thaliana	AT1G16930.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:5789987-5791534 FORWARD LENGTH=449	267	449	4.00E-40	168.2	39.0	44.9

Rsa1.0_00622.1.g17011.t1	gb|EOA38694.1| hypothetical protein CARUB_v10010709mg [Capsella rubella]	159	106	1.00E-34	66.7	54.7	61.6	hypothetical protein CARUB_v10010709mg	gbpln	Capsella rubella	AT1G28250.1 | Symbols: | unknown protein; Has 22 Blast hits to 22 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:9874296-9875175 FORWARD LENGTH=102	159	102	2.00E-35	64.2	53.5	58.5
Rsa1.0_00622.1.g17012.t1	gb|EOA37416.1| hypothetical protein CARUB_v10011353mg [Capsella rubella]	860	914	0	106.3	78.8	85.9	hypothetical protein CARUB_v10011353mg	gbpln	Capsella rubella	AT1G28260.2 | Symbols: | Telomerase activating protein Est1 | chr1:9875776-9878782 REVERSE LENGTH=880	860	880	0	102.3	79.1	86.2
Rsa1.0_00622.1.g17013.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00622.1.g17014.t1	ref|NP_174148.1| protein ralf-like 4 [Arabidopsis thaliana] gi|297845772|ref|XP_002890767.1| hypothetical protein ARALYDRAFT_473036 [Arabidopsis lyrata subsp. lyrata] gi|75173390|sp|Q9FZA0.1|RLF4_ARATH RecName: Full=Protein RALF-like 4; Flags: Precursor gi|9795610|gb|AAF98428.1|AC021044_7 Hypothetical protein [Arabidopsis thaliana] gi|28973673|gb|AAO64155.1| unknown protein [Arabidopsis thaliana] gi|110737076|dbj|BAF00491.1| hypothetical protein [Arabidopsis thaliana] gi|297336609|gb|EFH67026.1| hypothetical protein ARALYDRAFT_473036 [Arabidopsis lyrata subsp. lyrata] gi|332192818|gb|AEE30939.1| protein ralf-like 4 [Arabidopsis thaliana]	95	110	2.00E-46	115.8	95.8	98.9	protein ralf-like 4	gbpln	Arabidopsis lyrata	AT1G28270.1 | Symbols: RALFL4 | ralf-like 4 | chr1:9883165-9883497 FORWARD LENGTH=110	95	110	3.00E-49	115.8	95.8	98.9
Rsa1.0_00622.1.g17015.t1	ref|NP_001117368.1| VQ motif-containing protein [Arabidopsis thaliana] gi|332192820|gb|AEE30941.1| VQ motif-containing protein [Arabidopsis thaliana]	230	243	2.00E-89	105.7	82.2	88.3	VQ motif-containing protein	gbpln	Arabidopsis thaliana	AT1G28280.2 | Symbols: | VQ motif-containing protein | chr1:9886297-9887395 REVERSE LENGTH=243	230	243	7.00E-92	105.7	82.2	88.3
Rsa1.0_00622.1.g17016.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00622.1.g17017.t1	dbj|BAF01102.1| putative proline-rich protein [Arabidopsis thaliana]	359	315	2.00E-79	87.7	72.1	78.6	putative proline-rich protein	gbpln	Arabidopsis thaliana	AT1G28290.1 | Symbols: AGP31 | arabinogalactan protein 31 | chr1:9889331-9890843 REVERSE LENGTH=359	359	359	2.00E-65	100.0	30.4	35.4
Rsa1.0_00622.1.g17018.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00622.1.g17019.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	880	1142	1.00E-154	129.8	32.2	42.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	880	575	2.00E-74	65.3	19.2	30.8
Rsa1.0_00622.1.g17020.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00622.1.g17021.t1	gb|ADO16343.1| leafy cotyledon 2 [Brassica napus]	356	349	1.00E-133	98.0	73.3	81.7	leafy cotyledon 2	gbpln	Brassica napus	AT1G28300.1 | Symbols: LEC2 | AP2/B3-like transcriptional factor family protein | chr1:9897054-9899838 REVERSE LENGTH=363	356	363	1.00E-122	102.0	68.0	80.3
Rsa1.0_00623.1.g17022.t1	dbj|BAB69682.1| receptor kinase 3 [Brassica rapa]	522	847	0	162.3	78.9	87.4	receptor kinase 3	gbpln	Brassica rapa	AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850	522	850	0	162.8	65.9	78.9
Rsa1.0_00623.1.g17023.t1	ref|XP_003553761.1| PREDICTED: ankyrin repeat domain-containing protein 13C-B-like [Glycine max]	490	629	1.00E-120	128.4	56.9	66.5	PREDICTED: ankyrin repeat domain-containing protein 13C-B-like	gbenv/gbpln	Glycine max	AT3G04470.1 | Symbols: | Ankyrin repeat family protein | chr3:1189841-1191853 REVERSE LENGTH=640	490	640	6.00E-91	130.6	46.3	53.3
Rsa1.0_00623.1.g17024.t3	ref|XP_002872330.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297318167|gb|EFH48589.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	584	536	0	91.8	83.0	87.2	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT5G28900.1 | Symbols: | Calcium-binding EF-hand family protein | chr5:10925852-10929892 FORWARD LENGTH=536	584	536	0	91.8	82.7	86.8
Rsa1.0_00623.1.g17025.t1	gb|AAD20714.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	409	1750	7.00E-32	427.9	18.6	29.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	409	626	1.00E-14	153.1	12.2	19.8
Rsa1.0_00623.1.g17026.t1	gb|AET14213.1| GDP-D-mannose-3,5-epimerase [Brassica rapa subsp. chinensis]	379	379	0	100.0	98.9	99.5	GDP-D-mannose-3,5-epimerase	gbpln	Brassica rapa	AT5G28840.2 | Symbols: GME | GDP-D-mannose 3',5'-epimerase | chr5:10862472-10864024 REVERSE LENGTH=377	379	377	0	99.5	96.8	97.9
Rsa1.0_00623.1.g17027.t1	gb|AAC63678.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	98	1216	3.00E-12	1240.8	38.8	57.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00623.1.g17028.t1	ref|XP_002872303.1| cysteine synthase [Arabidopsis lyrata subsp. lyrata] gi|297318140|gb|EFH48562.1| cysteine synthase [Arabidopsis lyrata subsp. lyrata]	323	324	1.00E-158	100.3	86.4	93.5	cysteine synthase	gbpln	Arabidopsis lyrata	AT5G28020.6 | Symbols: CYSD2, ATCYSD2 | cysteine synthase D2 | chr5:10026395-10028166 REVERSE LENGTH=323	323	323	1.00E-159	100.0	89.5	95.4
Rsa1.0_00623.1.g17029.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00623.1.g17030.t1	ref|NP_198150.1| Seed maturation protein [Arabidopsis thaliana] gi|26452310|dbj|BAC43241.1| putative embryonic abundant protein [Arabidopsis thaliana] gi|332006372|gb|AED93755.1| Seed maturation protein [Arabidopsis thaliana]	191	192	9.00E-78	100.5	85.3	90.1	Seed maturation protein	gbpln	Arabidopsis thaliana	AT5G27980.1 | Symbols: | Seed maturation protein | chr5:10015883-10016676 REVERSE LENGTH=192	191	192	3.00E-80	100.5	85.3	90.1
Rsa1.0_00623.1.g17031.t8	ref|NP_198149.2| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332006370|gb|AED93753.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	1620	1630	0	100.6	92.4	95.9	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G27970.1 | Symbols: | ARM repeat superfamily protein | chr5:10004720-10015429 FORWARD LENGTH=1630	1620	1630	0	100.6	92.4	95.9
Rsa1.0_00623.1.g17032.t1	ref|XP_002882393.1| hypothetical protein ARALYDRAFT_317378 [Arabidopsis lyrata subsp. lyrata] gi|297328233|gb|EFH58652.1| hypothetical protein ARALYDRAFT_317378 [Arabidopsis lyrata subsp. lyrata]	313	341	2.33E-156	108.9	81.2	92.3	hypothetical protein ARALYDRAFT_317378	gbpln	Arabidopsis lyrata	AT3G05100.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:1424155-1425667 FORWARD LENGTH=336	313	336	1.00E-147	107.3	81.8	92.3
Rsa1.0_00623.1.g17033.t1	gb|EOA19672.1| hypothetical protein CARUB_v10003325mg [Capsella rubella]	634	636	0	100.3	86.1	91.3	hypothetical protein CARUB_v10003325mg	gbpln	Capsella rubella	AT5G27950.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:9984774-9987493 FORWARD LENGTH=625	634	625	0	98.6	84.4	89.9
Rsa1.0_00623.1.g17034.t1	ref|XP_002872288.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318125|gb|EFH48547.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	688	690	0	100.3	81.3	91.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G27110.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:9538572-9540647 REVERSE LENGTH=691	688	691	0	100.4	80.2	90.4
Rsa1.0_00623.1.g17035.t1	ref|NP_198064.1| putative nucleolar protein 5-1 [Arabidopsis thaliana] gi|147744575|sp|O04658.2|NOP5A_ARATH RecName: Full=Probable nucleolar protein 5-1; AltName: Full=MAR-binding NOP56/58 homolog 1; AltName: Full=NOP58-like protein F108; AltName: Full=Nucleolar protein 58-1 gi|11878185|gb|AAG40836.1|AF302490_1 NOP58-like protein F108 [Arabidopsis thaliana] gi|18377656|gb|AAL66978.1| putative SAR DNA-binding protein [Arabidopsis thaliana] gi|20465699|gb|AAM20318.1| putative SAR DNA-binding protein [Arabidopsis thaliana] gi|332006269|gb|AED93652.1| putative nucleolar protein 5-1 [Arabidopsis thaliana]	535	533	0	99.6	77.0	81.5	putative nucleolar protein 5-1	gbpln	Arabidopsis thaliana	AT5G27120.1 | Symbols: | NOP56-like pre RNA processing ribonucleoprotein | chr5:9541287-9543684 FORWARD LENGTH=533	535	533	0	99.6	77.0	81.5
Rsa1.0_00623.1.g17036.t1	gb|EOA19817.1| hypothetical protein CARUB_v10000063mg [Capsella rubella]	1259	1207	0	95.9	82.9	88.0	hypothetical protein CARUB_v10000063mg	gbpln	Capsella rubella	AT3G05040.1 | Symbols: HST, HST1 | ARM repeat superfamily protein | chr3:1401479-1408095 REVERSE LENGTH=1202	1259	1202	0	95.5	74.7	83.2
Rsa1.0_00623.1.g17037.t1	ref|XP_002874393.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320230|gb|EFH50652.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1257	1191	0	94.7	53.5	68.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G27220.1 | Symbols: | Frigida-like protein | chr5:9578757-9582752 FORWARD LENGTH=1181	1257	1181	0	94.0	51.3	64.6
Rsa1.0_00623.1.g17038.t1	gb|EOA19886.1| hypothetical protein CARUB_v10000134mg [Capsella rubella]	1036	1000	0	96.5	56.3	68.8	hypothetical protein CARUB_v10000134mg	gbpln	Capsella rubella	AT5G27230.1 | Symbols: | Frigida-like protein | chr5:9584255-9587838 FORWARD LENGTH=948	1036	948	0	91.5	51.4	61.4
Rsa1.0_00623.1.g17039.t1	gb|AAB61072.1| contains similarity to a DNAJ-like domain [Arabidopsis thaliana]	659	1609	1.00E-110	244.2	35.5	42.8	contains similarity to a DNAJ-like domain	gbpln	Arabidopsis thaliana	AT5G27240.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:9597552-9600866 FORWARD LENGTH=1104	659	1104	1.00E-112	167.5	35.5	42.8
Rsa1.0_00623.1.g17040.t1	gb|EOA19865.1| hypothetical protein CARUB_v10000116mg [Capsella rubella]	1405	1039	0	74.0	56.6	63.3	hypothetical protein CARUB_v10000116mg	gbpln	Capsella rubella	AT5G27270.1 | Symbols: EMB976 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:9605650-9609625 FORWARD LENGTH=1038	1405	1038	0	73.9	51.6	56.7
Rsa1.0_00623.1.g17041.t1	ref|XP_002886121.1| hypothetical protein ARALYDRAFT_480649 [Arabidopsis lyrata subsp. lyrata] gi|297331961|gb|EFH62380.1| hypothetical protein ARALYDRAFT_480649 [Arabidopsis lyrata subsp. lyrata]	133	143	3.00E-31	107.5	54.9	63.2	hypothetical protein ARALYDRAFT_480649	gbpln	Arabidopsis lyrata	AT2G17560.2 | Symbols: HMGB4, NFD4, NFD04 | high mobility group B4 | chr2:7642486-7643468 REVERSE LENGTH=138	133	138	2.00E-33	103.8	51.9	60.9
Rsa1.0_00624.1.g17042.t2	gb|EOA38874.1| hypothetical protein CARUB_v10011239mg [Capsella rubella]	165	216	5.00E-61	130.9	69.1	73.9	hypothetical protein CARUB_v10011239mg	gbpln	Capsella rubella	AT1G49230.1 | Symbols: | RING/U-box superfamily protein | chr1:18209320-18209979 FORWARD LENGTH=219	165	219	4.00E-62	132.7	67.3	72.1

Rsa1.0_00624.1.g17043.t1	gb|EOA38711.1| hypothetical protein CARUB_v10010802mg [Capsella rubella]	76	76	6.00E-19	100.0	69.7	80.3	hypothetical protein CARUB_v10010802mg	gbpln	Capsella rubella	AT1G49245.1 | Symbols: | Prefoldin chaperone subunit family protein | chr1:18218861-18219085 FORWARD LENGTH=74	76	74	3.00E-16	97.4	64.5	78.9
Rsa1.0_00624.1.g17044.t1	ref|XP_002891480.1| hypothetical protein ARALYDRAFT_474061 [Arabidopsis lyrata subsp. lyrata] gi|297337322|gb|EFH67739.1| hypothetical protein ARALYDRAFT_474061 [Arabidopsis lyrata subsp. lyrata]	434	530	2.00E-96	122.1	53.2	70.0	hypothetical protein ARALYDRAFT_474061	gbpln	Arabidopsis lyrata	AT1G49190.1 | Symbols: ARR19, RR19 | response regulator 19 | chr1:18191342-18193598 FORWARD LENGTH=608	434	608	5.00E-57	140.1	27.6	36.2
Rsa1.0_00624.1.g17045.t1	emb|CAB75484.1| putative protein [Arabidopsis thaliana]	144	851	5.00E-13	591.0	28.5	41.0	putative protein	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	144	484	2.00E-12	336.1	25.7	36.1
Rsa1.0_00624.1.g17046.t1	gb|EOA36184.1| hypothetical protein CARUB_v10010068mg [Capsella rubella]	206	256	1.00E-113	124.3	96.1	97.6	hypothetical protein CARUB_v10010068mg	gbpln	Capsella rubella	AT1G49300.2 | Symbols: ATRAB7, ATRABG3E, RABG3E | RAB GTPase homolog G3E | chr1:18234842-18236968 FORWARD LENGTH=206	206	206	1.00E-116	100.0	95.6	97.1
Rsa1.0_00624.1.g17047.t1	ref|XP_002894168.1| hypothetical protein ARALYDRAFT_314350 [Arabidopsis lyrata subsp. lyrata] gi|297340010|gb|EFH70427.1| hypothetical protein ARALYDRAFT_314350 [Arabidopsis lyrata subsp. lyrata]	81	81	2.00E-26	100.0	76.5	85.2	hypothetical protein ARALYDRAFT_314350	gbpln	Arabidopsis lyrata	AT1G49310.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: LP.04 four leaves visible, petal differentiation and expansion stage; Has 11 Blast hits to 11 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18237997-18238325 REVERSE LENGTH=82	81	82	4.00E-29	101.2	75.3	82.7
Rsa1.0_00624.1.g17048.t1	gb|EOA30781.1| hypothetical protein CARUB_v10013925mg [Capsella rubella]	123	385	4.00E-26	313.0	54.5	66.7	hypothetical protein CARUB_v10013925mg	gbpln	Capsella rubella	AT1G53910.3 | Symbols: RAP2.12 | related to AP2 12 | chr1:20135242-20136581 FORWARD LENGTH=356	123	356	1.00E-17	289.4	43.9	48.8
Rsa1.0_00624.1.g17049.t1	gb|ACO54862.1| BURP domain protein [Brassica napus] gi|226427147|gb|ACO54863.1| BURP domain protein [Brassica napus]	281	281	1.00E-150	100.0	91.1	94.0	BURP domain protein	gbpln	Brassica napus	AT1G49320.1 | Symbols: ATUSPL1, USPL1 | unknown seed protein like 1 | chr1:18246441-18247817 FORWARD LENGTH=280	281	280	1.00E-127	99.6	74.4	86.8
Rsa1.0_00624.1.g17050.t1	ref|NP_175355.1| RAB GTPase homolog G3E [Arabidopsis thaliana] gi|79319588|ref|NP_001031161.1| RAB GTPase homolog G3E [Arabidopsis thaliana] gi|75215673|sp|Q9XI98.1|RAG3E_ARATH RecName: Full=Ras-related protein RABG3e; Short=AtRABG3e; AltName: Full=Ras-related protein Rab74; Short=AtRab74 gi|5430767|gb|AAD43167.1|AC007504_22 Putative RAB7 GTP-binding Protein [Arabidopsis thaliana] gi|15718414|dbj|BAB68374.1| AtRab74 [Arabidopsis thaliana] gi|28416619|gb|AAO42840.1| At1g49300 [Arabidopsis thaliana] gi|110743311|dbj|BAE99544.1| hypothetical protein [Arabidopsis thaliana] gi|332194293|gb|AEE32414.1| RAB GTPase homolog G3E [Arabidopsis thaliana] gi|332194294|gb|AEE32415.1| RAB GTPase homolog G3E [Arabidopsis thaliana]	88	206	4.00E-30	234.1	70.5	72.7	RAB GTPase homolog G3E	gbpln	Arabidopsis thaliana	AT1G49300.2 | Symbols: ATRAB7, ATRABG3E, RABG3E | RAB GTPase homolog G3E | chr1:18234842-18236968 FORWARD LENGTH=206	88	206	6.00E-33	234.1	70.5	72.7
Rsa1.0_00624.1.g17051.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00624.1.g17052.t1	ref|XP_002894168.1| hypothetical protein ARALYDRAFT_314350 [Arabidopsis lyrata subsp. lyrata] gi|297340010|gb|EFH70427.1| hypothetical protein ARALYDRAFT_314350 [Arabidopsis lyrata subsp. lyrata]	81	81	7.00E-28	100.0	77.8	88.9	hypothetical protein ARALYDRAFT_314350	gbpln	Arabidopsis lyrata	AT1G49310.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: LP.04 four leaves visible, petal differentiation and expansion stage; Has 11 Blast hits to 11 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18237997-18238325 REVERSE LENGTH=82	81	82	1.00E-30	101.2	76.5	86.4
Rsa1.0_00624.1.g17053.t1	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	680	1089	0	160.1	64.6	77.1	transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00624.1.g17054.t4	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2111	1274	0	60.4	28.6	39.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2111	575	3.00E-64	27.2	8.5	12.6
Rsa1.0_00624.1.g17055.t14	ref|XP_002891491.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297337333|gb|EFH67750.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	351	294	7.00E-85	83.8	49.0	56.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G49330.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:18250043-18251038 FORWARD LENGTH=331	351	331	3.00E-83	94.3	49.9	59.0
Rsa1.0_00625.1.g17056.t1	gb|AAD14492.1| Hypothetical protein [Arabidopsis thaliana]	112	240	2.00E-18	214.3	47.3	60.7	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	112	303	4.00E-11	270.5	31.3	48.2
Rsa1.0_00625.1.g17057.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00625.1.g17058.t1	gb|ACI14391.1| WRKY26-1 transcription factor [Brassica napus]	321	344	1.00E-159	107.2	88.8	94.1	WRKY26-1 transcription factor	gbpln	Brassica napus	AT5G07100.1 | Symbols: WRKY26 | WRKY DNA-binding protein 26 | chr5:2204313-2205647 FORWARD LENGTH=309	321	309	1.00E-115	96.3	68.8	79.1
Rsa1.0_00625.1.g17059.t1	gb|EOA31247.1| hypothetical protein CARUB_v10014418mg [Capsella rubella]	283	262	1.00E-145	92.6	88.7	90.8	hypothetical protein CARUB_v10014418mg	gbpln	Capsella rubella	AT2G17360.1 | Symbols: | Ribosomal protein S4 (RPS4A) family protein | chr2:7546598-7548138 FORWARD LENGTH=261	283	261	2.33E-156	92.2	88.0	90.5
Rsa1.0_00625.1.g17060.t1	gb|EOA22250.1| hypothetical protein CARUB_v10002839mg [Capsella rubella]	442	455	0	102.9	76.5	88.0	hypothetical protein CARUB_v10002839mg	gbpln	Capsella rubella	AT5G07070.1 | Symbols: CIPK2, SnRK3.2 | CBL-interacting protein kinase 2 | chr5:2196743-2198113 REVERSE LENGTH=456	442	456	0	103.2	74.9	87.6
Rsa1.0_00625.1.g17061.t1	gb|AAM62950.1| unknown [Arabidopsis thaliana]	153	235	3.00E-50	153.6	78.4	81.0	unknown	gbpln	Arabidopsis thaliana	AT5G07020.1 | Symbols: | proline-rich family protein | chr5:2180669-2182284 REVERSE LENGTH=235	153	235	3.00E-51	153.6	73.9	77.1
Rsa1.0_00625.1.g17062.t1	ref|NP_568177.1| sulfotransferase 2A [Arabidopsis thaliana] gi|75153823|sp|Q8L5A7.1|SOT15_ARATH RecName: Full=Cytosolic sulfotransferase 15; Short=AtSOT15; AltName: Full=Sulfotransferase 2a; Short=AtST2a gi|20466686|gb|AAM20660.1| steroid sulfotransferase-like protein [Arabidopsis thaliana] gi|21537216|gb|AAM61557.1| steroid sulfotransferase-like protein [Arabidopsis thaliana] gi|31711860|gb|AAP68286.1| At5g07010 [Arabidopsis thaliana] gi|332003715|gb|AED91098.1| sulfotransferase 2A [Arabidopsis thaliana]	364	359	1.00E-177	98.6	83.5	92.3	sulfotransferase 2A	gbpln	Arabidopsis thaliana	AT5G07010.1 | Symbols: ATST2A, ST2A | sulfotransferase 2A | chr5:2174960-2176039 REVERSE LENGTH=359	364	359	1.00E-179	98.6	83.5	92.3
Rsa1.0_00625.1.g17063.t1	gb|EOA22608.1| hypothetical protein CARUB_v10003275mg [Capsella rubella]	258	258	1.00E-124	100.0	91.1	93.8	hypothetical protein CARUB_v10003275mg	gbpln	Capsella rubella	AT5G06990.1 | Symbols: | Protein of unknown function, DUF617 | chr5:2169699-2170484 FORWARD LENGTH=261	258	261	1.00E-124	101.2	90.7	94.2
Rsa1.0_00625.1.g17064.t2	gb|EOA21076.1| hypothetical protein CARUB_v10001413mg [Capsella rubella]	337	330	1.00E-134	97.9	78.6	85.8	hypothetical protein CARUB_v10001413mg	gbpln	Capsella rubella	AT5G06960.2 | Symbols: OBF5, TGA5 | OCS-element binding factor 5 | chr5:2155742-2157400 FORWARD LENGTH=330	337	330	1.00E-135	97.9	77.7	85.8
Rsa1.0_00625.1.g17065.t1	ref|XP_002873284.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319121|gb|EFH49543.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	475	525	0	110.5	89.5	94.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G06905.1 | Symbols: CYP712A2 | cytochrome P450, family 712, subfamily A, polypeptide 2 | chr5:2138438-2140078 REVERSE LENGTH=521	475	521	0	109.7	89.7	94.7
Rsa1.0_00625.1.g17066.t1	ref|XP_002873283.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319120|gb|EFH49542.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	794	508	0	64.0	55.3	59.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G06900.1 | Symbols: CYP93D1 | cytochrome P450, family 93, subfamily D, polypeptide 1 | chr5:2136160-2137925 REVERSE LENGTH=507	794	507	0	63.9	54.8	60.2
Rsa1.0_00625.1.g17067.t1	ref|XP_002871231.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317068|gb|EFH47490.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	573	1144	0	199.7	68.6	80.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G06810.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr5:2108493-2112256 FORWARD LENGTH=1141	573	1141	0	199.1	68.1	80.6
Rsa1.0_00625.1.g17068.t1	ref|XP_002871230.1| hypothetical protein ARALYDRAFT_487493 [Arabidopsis lyrata subsp. lyrata] gi|297317067|gb|EFH47489.1| hypothetical protein ARALYDRAFT_487493 [Arabidopsis lyrata subsp. lyrata]	372	365	1.00E-163	98.1	79.6	87.4	hypothetical protein ARALYDRAFT_487493	gbpln	Arabidopsis lyrata	AT5G06800.1 | Symbols: | myb-like HTH transcriptional regulator family protein | chr5:2103374-2105680 FORWARD LENGTH=375	372	375	1.00E-161	100.8	80.6	87.6

<table>
<tr><td>Rsa1.0_00625.1.g17069.t2</td><td>ref|XP_002884884.1| KH domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330724|gb|EFH61143.1| KH domain-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>182</td><td>245</td><td>1.00E-23</td><td>134.6</td><td>31.9</td><td>37.4</td><td>KH domain-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G06770.1 | Symbols: | KH domain-containing protein / zinc finger (CCCH type) family protein | chr5:2090937-2092787 REVERSE LENGTH=240</td><td>182</td><td>240</td><td>2.00E-23</td><td>131.9</td><td>31.3</td><td>36.3</td></tr>
<tr><td>Rsa1.0_00625.1.g17070.t1</td><td>dbj|BAB09809.1| protein phosphatase 2C-like [Arabidopsis thaliana]</td><td>307</td><td>386</td><td>1.00E-156</td><td>125.7</td><td>90.2</td><td>94.5</td><td>protein phosphatase 2C-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06750.3 | Symbols: | Protein phosphatase 2C family protein | chr5:2086403-2088245 REVERSE LENGTH=393</td><td>307</td><td>393</td><td>1.00E-158</td><td>128.0</td><td>90.2</td><td>94.5</td></tr>
<tr><td>Rsa1.0_00626.1.g17071.t1</td><td>emb|CAA09986.1| WUSCHEL protein [Arabidopsis thaliana]</td><td>294</td><td>291</td><td>1.00E-115</td><td>99.0</td><td>75.5</td><td>85.7</td><td>WUSCHEL protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17950.1 | Symbols: WUS, PGA6, WUS1 | Homeodomain-like superfamily protein | chr2:7809100-7810671 REVERSE LENGTH=292</td><td>294</td><td>292</td><td>1.00E-111</td><td>99.3</td><td>74.8</td><td>85.0</td></tr>
<tr><td>Rsa1.0_00626.1.g17072.t1</td><td>ref|NP_179383.3| transformation/transcription domain-associated protein [Arabidopsis thaliana] gi|330251608|gb|AEC06702.1| phosphatidylinositol 3- and 4-kinase family protein with FAT domain [Arabidopsis thaliana]</td><td>3871</td><td>3858</td><td>0</td><td>99.7</td><td>95.0</td><td>97.1</td><td>transformation/transcription domain-associated protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17930.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase family protein with FAT domain | chr2:7784455-7802230 REVERSE LENGTH=3858</td><td>3871</td><td>3858</td><td>0</td><td>99.7</td><td>95.0</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00626.1.g17073.t3</td><td>ref|NP_179379.1| calcium-dependent protein kinase 16 [Arabidopsis thaliana] gi|75327228|sp|Q7XJR9.1|CDPKG_ARATH RecName: Full=Calcium-dependent protein kinase 16 gi|330251605|gb|AEC06699.1| calcium-dependent protein kinase 16 [Arabidopsis thaliana]</td><td>895</td><td>571</td><td>0</td><td>63.8</td><td>58.3</td><td>59.9</td><td>calcium-dependent protein kinase 16</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17890.1 | Symbols: CPK16 | calcium-dependent protein kinase 16 | chr2:7769885-7772627 REVERSE LENGTH=571</td><td>895</td><td>571</td><td>0</td><td>63.8</td><td>58.3</td><td>59.9</td></tr>
<tr><td>Rsa1.0_00626.1.g17074.t1</td><td>ref|NP_176527.4| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|332195971|gb|AEE34092.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]</td><td>278</td><td>282</td><td>1.00E-125</td><td>101.4</td><td>77.0</td><td>88.1</td><td>Rossmann-fold NAD(P)-binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G63380.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:23505582-23506504 FORWARD LENGTH=282</td><td>278</td><td>282</td><td>1.00E-127</td><td>101.4</td><td>77.0</td><td>88.1</td></tr>
<tr><td>Rsa1.0_00626.1.g17075.t1</td><td>ref|XP_002886134.1| hypothetical protein ARALYDRAFT_480688 [Arabidopsis lyrata subsp. lyrata] gi|297331974|gb|EFH62393.1| hypothetical protein ARALYDRAFT_480688 [Arabidopsis lyrata subsp. lyrata]</td><td>157</td><td>158</td><td>7.00E-49</td><td>100.6</td><td>73.9</td><td>81.5</td><td>hypothetical protein ARALYDRAFT_480688</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G17880.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr2:7767176-7767658 REVERSE LENGTH=160</td><td>157</td><td>160</td><td>3.00E-51</td><td>101.9</td><td>70.1</td><td>79.0</td></tr>
<tr><td>Rsa1.0_00626.1.g17076.t1</td><td>ref|XP_002876294.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322132|gb|EFH52553.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>278</td><td>280</td><td>1.00E-133</td><td>100.7</td><td>85.6</td><td>94.6</td><td>short-chain dehydrogenase/reductase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G55290.2 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:20502653-20503730 FORWARD LENGTH=279</td><td>278</td><td>279</td><td>1.00E-134</td><td>100.4</td><td>84.2</td><td>93.9</td></tr>
<tr><td>Rsa1.0_00626.1.g17077.t1</td><td>ref|XP_002886130.1| early-responsive to dehydration 7 [Arabidopsis lyrata subsp. lyrata] gi|297331970|gb|EFH62389.1| early-responsive to dehydration 7 [Arabidopsis lyrata subsp. lyrata]</td><td>462</td><td>450</td><td>0</td><td>97.4</td><td>82.9</td><td>89.8</td><td>early-responsive to dehydration 7</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G17840.1 | Symbols: ERD7 | Senescence/dehydration-associated protein-related | chr2:7755923-7757798 REVERSE LENGTH=452</td><td>462</td><td>452</td><td>0</td><td>97.8</td><td>82.9</td><td>90.0</td></tr>
<tr><td>Rsa1.0_00626.1.g17078.t1</td><td>ref|XP_004233565.1| PREDICTED: rac-like GTP-binding protein ARAC1-like [Solanum lycopersicum]</td><td>175</td><td>197</td><td>2.00E-86</td><td>112.6</td><td>94.9</td><td>97.7</td><td>PREDICTED: rac-like GTP-binding protein ARAC1-like</td><td>gbpln</td><td>Solanum lycopersicum</td><td>AT4G35950.1 | Symbols: ARAC6, RAC2, ATROP5, ATRAC6, ROP5, RAC6 | RAC-like 6 | chr4:17024051-17025514 REVERSE LENGTH=197</td><td>175</td><td>197</td><td>5.00E-85</td><td>112.6</td><td>97.7</td><td>99.4</td></tr>
<tr><td>Rsa1.0_00626.1.g17079.t1</td><td>ref|XP_002882336.1| hypothetical protein ARALYDRAFT_896441 [Arabidopsis lyrata subsp. lyrata] gi|297328176|gb|EFH58595.1| hypothetical protein ARALYDRAFT_896441 [Arabidopsis lyrata subsp. lyrata]</td><td>146</td><td>319</td><td>1.00E-14</td><td>218.5</td><td>41.1</td><td>56.2</td><td>hypothetical protein ARALYDRAFT_896441</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00626.1.g17080.t1</td><td>gb|EOA32800.1| hypothetical protein CARUB_v10016111mg [Capsella rubella]</td><td>514</td><td>513</td><td>0</td><td>99.8</td><td>84.8</td><td>90.9</td><td>hypothetical protein CARUB_v10016111mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G17760.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:7713488-7716269 FORWARD LENGTH=513</td><td>514</td><td>513</td><td>0</td><td>99.8</td><td>86.8</td><td>92.4</td></tr>
<tr><td>Rsa1.0_00626.1.g17081.t1</td><td>gb|EOA23612.1| hypothetical protein CARUB_v10016812mg [Capsella rubella]</td><td>597</td><td>651</td><td>1.00E-165</td><td>109.0</td><td>54.9</td><td>71.7</td><td>hypothetical protein CARUB_v10016812mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G58940.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21781002-21783213 REVERSE LENGTH=618</td><td>597</td><td>618</td><td>1.00E-158</td><td>103.5</td><td>54.1</td><td>68.3</td></tr>
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Rsa1.0_00626.1.g17082.t1	ref|NP_179364.2| NEP1-interacting protein 2 [Arabidopsis thaliana] gi|68565195|sp|Q8GT74.1|NIP2_ARATH RecName: Full=NEP1-interacting protein 2; AltName: Full=RING-H2 finger protein ATL25 gi|27524904|emb|CAC81898.1| NEP1-interacting protein 2 [Arabidopsis thaliana] gi|330251581|gb|AEC06675.1| NEP1-interacting protein 2 [Arabidopsis thaliana]	190	241	3.00E-54	126.8	62.6	72.1	NEP1-interacting protein 2	gbpln	Arabidopsis thaliana	AT2G17730.1 | Symbols: NIP2 | NEP-interacting protein 2 | chr2:7704142-7705312 FORWARD LENGTH=241	190	241	1.00E-56	126.8	62.6	72.1
Rsa1.0_00626.1.g17083.t1	ref|NP_191453.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75264349|sp|Q9LXQ8.1|FBL60_ARATH RecName: Full=F-box/LRR-repeat protein At3g58940 gi|7630089|emb|CAB88311.1| putative protein [Arabidopsis thaliana] gi|332646331|gb|AEE79852.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	264	618	2.00E-78	234.1	59.5	73.1	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT3G58940.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21781002-21783213 REVERSE LENGTH=618	264	618	6.00E-81	234.1	59.5	73.1
Rsa1.0_00627.1.g17084.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	444	2301	1.00E-148	518.2	59.7	70.5	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	444	1262	2.00E-43	284.2	19.4	28.4
Rsa1.0_00627.1.g17085.t2	gb|AAD05576.1| Cu/Zn superoxide dismutase [Raphanus sativus]	147	152	7.00E-76	103.4	98.6	99.3	Cu/Zn superoxide dismutase	gbpln	Raphanus sativus	AT1G08830.2 | Symbols: CSD1 | copper/zinc superoxide dismutase 1 | chr1:2827700-2829053 FORWARD LENGTH=152	147	152	1.00E-74	103.4	94.6	95.9
Rsa1.0_00627.1.g17086.t1	ref|XP_002894041.1| hypothetical protein ARALYDRAFT_473884 [Arabidopsis lyrata subsp. lyrata] gi|297339883|gb|EFH70300.1| hypothetical protein ARALYDRAFT_473884 [Arabidopsis lyrata subsp. lyrata]	458	480	1.00E-126	104.8	54.8	64.4	hypothetical protein ARALYDRAFT_473884	gbpln	Arabidopsis lyrata	AT1G47340.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:17354123-17356494 REVERSE LENGTH=459	458	459	1.00E-126	100.2	54.6	65.5
Rsa1.0_00627.1.g17087.t12	ref|NP_172361.1| DNA replication ATP-dependent helicase Dna2 [Arabidopsis thaliana] gi|332190235|gb|AEE28356.1| DNA replication ATP-dependent helicase Dna2 [Arabidopsis thaliana]	1267	1296	0	102.3	85.2	90.2	DNA replication ATP-dependent helicase Dna2	gbpln	Arabidopsis thaliana	AT1G08840.1 | Symbols: emb2411 | DNA replication helicase, putative | chr1:2829579-2838369 REVERSE LENGTH=1296	1267	1296	0	102.3	85.2	90.2
Rsa1.0_00627.1.g17088.t1	ref|NP_001154322.1| Ribosomal L.8/L5e family protein [Arabidopsis thaliana] gi|332190238|gb|AEE28359.1| Ribosomal L.8/L5e family protein [Arabidopsis thaliana]	188	234	1.00E-101	124.5	95.7	97.3	Ribosomal L.8/L5e family protein	gbpln	Arabidopsis thaliana	AT1G08845.2 | Symbols: | Ribosomal L18p/L5e family protein | chr1:2838789-2840955 FORWARD LENGTH=234	188	234	1.00E-104	124.5	95.7	97.3
Rsa1.0_00627.1.g17089.t1	ref|NP_172362.3| protein BONZAI 3 [Arabidopsis thaliana] gi|75287888|sp|Q5XQC7.1|BON3_ARATH RecName: Full=Protein BONZAI 3 gi|53636240|gb|AAU89273.1| BON3 [Arabidopsis thaliana] gi|332190239|gb|AEE28360.1| protein BONZAI 3 [Arabidopsis thaliana]	586	584	0	99.7	86.7	93.2	protein BONZAI 3	gbpln	Arabidopsis thaliana	AT1G08860.1 | Symbols: BON3 | Calcium-dependent phospholipid-binding Copine family protein | chr1:2842153-2846138 FORWARD LENGTH=584	586	584	0	99.7	86.7	93.2
Rsa1.0_00627.1.g17090.t1	ref|XP_002867835.1| hypothetical protein ARALYDRAFT_914502 [Arabidopsis lyrata subsp. lyrata] gi|297313671|gb|EFH44094.1| hypothetical protein ARALYDRAFT_914502 [Arabidopsis lyrata subsp. lyrata]	511	584	1.00E-175	114.3	74.4	84.0	hypothetical protein ARALYDRAFT_914502	gbpln	Arabidopsis lyrata	AT4G21660.1 | Symbols: | proline-rich spliceosome-associated (PSP) family protein | chr4:11506259-11509772 REVERSE LENGTH=584	511	584	1.00E-178	114.3	74.4	83.4
Rsa1.0_00627.1.g17091.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00627.1.g17092.t1	ref|XP_002889721.1| EMB3001 [Arabidopsis lyrata subsp. lyrata] gi|297335563|gb|EFH65980.1| EMB3001 [Arabidopsis lyrata subsp. lyrata]	757	836	0	110.4	50.2	57.6	EMB3001	gbpln	Arabidopsis lyrata	AT1G08910.1 | Symbols: EMB3001 | zinc ion binding;zinc ion binding | chr1:2856227-2860816 FORWARD LENGTH=829	757	829	0	109.5	48.5	57.1
Rsa1.0_00627.1.g17093.t1	ref|NP_563829.1| sugar transporter ERD6-like 3 [Arabidopsis thaliana] gi|75332302|sp|Q94KE0.1|ERDL3_ARATH RecName: Full=Sugar transporter ERD6-like 3; AltName: Full=Sugar transporter-like protein 2 gi|14194109|gb|AAK56249.1|AF367260_1 At1g08920/F7G19_20 [Arabidopsis thaliana] gi|22137064|gb|AAM91377.1| At1g08920/F7G19_20 [Arabidopsis thaliana] gi|169403716|emb|CAQ16329.1| hexose transporter-like protein [Arabidopsis thaliana] gi|332190246|gb|AEE28367.1| sugar transporter ERD6-like 3 [Arabidopsis thaliana]	470	470	0	100.0	85.5	93.2	sugar transporter ERD6-like 3	gbpln	Arabidopsis thaliana	AT1G08920.1 | Symbols: ESL1 | ERD (early response to dehydration) six-like 1 | chr1:2867446-2870360 FORWARD LENGTH=470	470	470	0	100.0	85.5	93.2

Rsa1.0_00627.1.g17094.t1	ref|NP_563830.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|79317421|ref|NP_001031006.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|117940144|sp|O04036.3|ERD6_ARATH RecName: Full=Sugar transporter ERD6; AltName: Full=Early-responsive to dehydration protein 6; AltName: Full=Sugar transporter-like protein 1 gi|3123712|dbj|BAA25989.1| ERD6 protein [Arabidopsis thaliana] gi|6686825|emb|CAB64732.1| putative sugar transporter [Arabidopsis thaliana] gi|30794056|gb|AAP40473.1| putative zinc finger protein ATZF1 [Arabidopsis thaliana] gi|332190249|gb|AEE28370.1| sugar transporter ERD6 [Arabidopsis thaliana] gi|332190250|gb|AEE28371.1| sugar transporter ERD6 [Arabidopsis thaliana]	497	496	0	99.8	91.5	96.8	sugar transporter ERD6	gbpln	Arabidopsis thaliana	AT1G08930.2 | Symbols: ERD6 | Major facilitator superfamily protein | chr1:2873604-2876979 FORWARD LENGTH=496	497	496	0	99.8	91.5	96.8
Rsa1.0_00627.1.g17095.t1	ref|NP_172370.3| cation exchanger 11 [Arabidopsis thaliana] gi|75096914|sp|O04034.1|CCX5_ARATH RecName: Full=Cation/calcium exchanger 5; AltName: Full=Protein CATION EXCHANGER 11 gi|1922938|gb|AAB70411.1| Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb|Z29094) [Arabidopsis thaliana] gi|45773954|gb|AAS76781.1| At1g08960 [Arabidopsis thaliana] gi|62320618|dbj|BAD95271.1| hypothetical protein [Arabidopsis thaliana] gi|332190252|gb|AEE28373.1| cation exchanger 11 [Arabidopsis thaliana]	529	546	0	103.2	86.0	91.3	cation exchanger 11	gbpln	Arabidopsis thaliana	AT1G08960.1 | Symbols: CAX11, ATCAX11 | cation exchanger 11 | chr1:2879698-2881877 FORWARD LENGTH=546	529	546	0	103.2	86.0	91.3
Rsa1.0_00627.1.g17096.t1	dbj|BAJ33993.1| unnamed protein product [Thellungiella halophila]	231	234	1.00E-115	101.3	96.1	97.4	unnamed protein product	----	----	AT1G08970.2 | Symbols: HAP5C, NF-YC9 | nuclear factor Y, subunit C9 | chr1:2883144-2883839 FORWARD LENGTH=231	231	231	1.00E-110	100.0	90.0	91.3
Rsa1.0_00627.1.g17097.t5	ref|XP_002889727.1| hypothetical protein ARALYDRAFT_888131 [Arabidopsis lyrata subsp. lyrata] gi|297335569|gb|EFH65986.1| hypothetical protein ARALYDRAFT_888131 [Arabidopsis lyrata subsp. lyrata]	495	425	0	85.9	71.1	77.6	hypothetical protein ARALYDRAFT_888131	gbpln	Arabidopsis lyrata	AT1G08980.1 | Symbols: ATAMI1, AMI1, ATTOC64-I, TOC64-I | amidase 1 | chr1:2884455-2886430 FORWARD LENGTH=425	495	425	0	85.9	71.9	77.8
Rsa1.0_00627.1.g17098.t1	ref|NP_172373.3| plant glycogenin-like starch initiation protein 5 [Arabidopsis thaliana] gi|385178635|sp|F4HZC3.1|GUX5_ARATH RecName: Full=Putative UDP-glucuronate:xylan alpha-glucuronosyltransferase 5; Short=UDP-GlcA:xylan glucuronyltransferase 5; AltName: Full=Glycogenin-like protein 5; AltName: Full=Plant glycogenin-like starch initiation protein 5; AltName: Full=Protein GLUCURONIC ACID SUBSTITUTION OF XYLAN 5; Short=AtGUX5 gi|332190259|gb|AEE28380.1| plant glycogenin-like starch initiation protein 5 [Arabidopsis thaliana]	529	566	0	107.0	80.9	88.3	plant glycogenin-like starch initiation protein 5	gbpln	Arabidopsis thaliana	AT1G08990.1 | Symbols: PGSIP5 | plant glycogenin-like starch initiation protein 5 | chr1:2888753-2890753 FORWARD LENGTH=566	529	566	0	107.0	80.9	88.3
Rsa1.0_00628.1.g17099.t1	emb|CAG28416.1| plasma membrane sulphate transporter [Brassica oleracea var. viridis]	656	656	0	100.0	95.6	97.1	plasma membrane sulphate transporter	gbpln	Brassica oleracea	AT3G15990.1 | Symbols: SULTR3;4 | sulfate transporter 3;4 | chr3:5427081-5430679 FORWARD LENGTH=653	656	653	0	99.5	91.3	95.4
Rsa1.0_00628.1.g17100.t1	ref|NP_188221.2| MAR-binding filament-like protein 1 [Arabidopsis thaliana] gi|83304464|sp|Q9LW85.2|MFP1_ARATH RecName: Full=MAR-binding filament-like protein 1 gi|30794108|gb|AAP40496.1| putative myosin heavy chain [Arabidopsis thaliana] gi|332642240|gb|AEE75761.1| MAR-binding filament-like protein 1 [Arabidopsis thaliana]	724	726	0	100.3	75.6	87.6	MAR-binding filament-like protein 1	gbpln	Arabidopsis thaliana	AT3G16000.1 | Symbols: MFP1 | MAR binding filament-like protein 1 | chr3:5431041-5433613 REVERSE LENGTH=726	724	726	0	100.3	75.6	87.6
Rsa1.0_00628.1.g17101.t2	gb|AFO11038.1| S domain subfamily receptor-like kinase [Arabidopsis thaliana]	965	852	0	88.3	71.0	76.7	S domain subfamily receptor-like kinase	gbpln	Arabidopsis thaliana	AT3G16030.1 | Symbols: CES101 | lectin protein kinase family protein | chr3:5439609-5442802 FORWARD LENGTH=850	965	850	0	88.1	66.0	71.8

Rsa1.0_00628.1.g17102.t2	gb|EOA30013.1| hypothetical protein CARUB_v10013116mg [Capsella rubella]	716	687	0	95.9	86.3	88.8	hypothetical protein CARUB_v10013116mg	gbpln	Capsella rubella	AT3G16060.1 | Symbols: | ATP binding microtubule motor family protein | chr3:5447503-5451196 FORWARD LENGTH=684	716	684	0	95.5	84.8	87.7
Rsa1.0_00628.1.g17103.t1	ref|NP_188228.1| uncharacterized protein [Arabidopsis thaliana] gi|9294453|dbj|BAB02672.1| unnamed protein product [Arabidopsis thaliana] gi|332642247|gb|AEE75768.1| uncharacterized protein AT3G16070 [Arabidopsis thaliana]	151	150	4.00E-65	99.3	80.1	86.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G16070.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15260.1); Has 26 Blast hits to 26 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5451864-5452316 REVERSE LENGTH=150	151	150	1.00E-67	99.3	80.1	86.1
Rsa1.0_00628.1.g17104.t1	ref|NP_175640.1| 60S ribosomal protein L37-2 [Arabidopsis thaliana] gi|20143906|sp|Q43292.2|RL372_ARATH RecName: Full=60S ribosomal protein L37-2 gi|12323122|gb|AAG51542.1|AC037424_7 60S ribosomal protein L37, putative; 56921-57860 [Arabidopsis thaliana] gi|13877907|gb|AAK44031.1|AF370216_1 putative 60S ribosomal protein L37 [Arabidopsis thaliana] gi|21280805|gb|AAM44969.1| putative 60S ribosomal protein L37 [Arabidopsis thaliana] gi|222423584|dbj|BAH19761.1| AT1G52300 [Arabidopsis thaliana] gi|332194658|gb|AEE32779.1| 60S ribosomal protein L37-2 [Arabidopsis thaliana]	96	95	5.00E-43	99.0	90.6	95.8	60S ribosomal protein L37-2	gbpln	Arabidopsis thaliana	AT1G52300.1 | Symbols: | Zinc-binding ribosomal protein family protein | chr1:19475213-19476152 REVERSE LENGTH=95	96	95	8.00E-46	99.0	90.6	95.8
Rsa1.0_00628.1.g17105.t1	gb|EOA31101.1| hypothetical protein CARUB_v10014254mg [Capsella rubella]	385	304	1.00E-111	79.0	51.4	59.0	hypothetical protein CARUB_v10014254mg	gbpln	Capsella rubella	AT3G24600.1 | Symbols: | Late embryogenesis abundant protein, group 2 | chr3:8972195-8974867 REVERSE LENGTH=506	385	506	1.00E-37	131.4	19.2	31.4
Rsa1.0_00628.1.g17106.t1	gb|EOA33145.1| hypothetical protein CARUB_v10016487mg [Capsella rubella] gi|482568957|gb|EOA33146.1| hypothetical protein CARUB_v10016487mg [Capsella rubella]	93	93	1.00E-43	100.0	91.4	95.7	hypothetical protein CARUB_v10016487mg	gbpln	Capsella rubella	AT3G16120.1 | Symbols: | Dynein light chain type 1 family protein | chr3:5465035-5465395 FORWARD LENGTH=93	93	93	4.00E-45	100.0	90.3	94.6
Rsa1.0_00628.1.g17107.t1	ref|XP_002882981.1| hypothetical protein ARALYDRAFT_479067 [Arabidopsis lyrata subsp. lyrata] gi|297328821|gb|EFH59240.1| hypothetical protein ARALYDRAFT_479067 [Arabidopsis lyrata subsp. lyrata]	544	577	0	106.1	76.1	87.1	hypothetical protein ARALYDRAFT_479067	gbpln	Arabidopsis lyrata	AT3G16130.1 | Symbols: ATROPGEF13, ROPGEF13, PIRF2 | RHO guanyl-nucleotide exchange factor 13 | chr3:5466246-5468512 FORWARD LENGTH=576	544	576	0	105.9	74.3	85.8
Rsa1.0_00628.1.g17108.t1	gb|EOA31654.1| hypothetical protein CARUB_v10014856mg [Capsella rubella]	145	145	8.00E-70	100.0	93.1	95.9	hypothetical protein CARUB_v10014856mg	gbpln	Capsella rubella	AT3G16140.1 | Symbols: PSAH-1 | photosystem I subunit H-1 | chr3:5468670-5469415 REVERSE LENGTH=145	145	145	9.00E-72	100.0	91.7	95.9
Rsa1.0_00628.1.g17109.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	164	1142	6.00E-19	696.3	32.9	43.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00628.1.g17110.t1	gb|EOA31031.1| hypothetical protein CARUB_v10014177mg [Capsella rubella]	324	325	1.00E-176	100.3	94.4	97.2	hypothetical protein CARUB_v10014177mg	gbpln	Capsella rubella	AT3G16150.1 | Symbols: | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:5471794-5473033 FORWARD LENGTH=325	324	325	1.00E-178	100.3	94.1	96.9
Rsa1.0_00628.1.g17111.t1	ref|XP_002882983.1| hypothetical protein ARALYDRAFT_318392 [Arabidopsis lyrata subsp. lyrata] gi|297328823|gb|EFH59242.1| hypothetical protein ARALYDRAFT_318392 [Arabidopsis lyrata subsp. lyrata]	588	608	0	103.4	86.7	93.4	hypothetical protein ARALYDRAFT_318392	gbpln	Arabidopsis lyrata	AT3G16170.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr3:5476490-5480128 FORWARD LENGTH=544	588	544	0	92.5	81.0	86.9
Rsa1.0_00628.1.g17112.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00628.1.g17113.t1	ref|NP_188239.1| major facilitator protein [Arabidopsis thaliana] gi|310947330|sp|Q8LPL2.2|PTR32_ARATH RecName: Full=Probable peptide/nitrate transporter At3g16180 gi|332642260|gb|AEE75781.1| probable peptide/nitrate transporter [Arabidopsis thaliana]	593	591	0	99.7	89.7	94.3	major facilitator protein	gbpln	Arabidopsis thaliana	AT3G16180.1 | Symbols: | Major facilitator superfamily protein | chr3:5481477-5484943 REVERSE LENGTH=591	593	591	0	99.7	89.7	94.3
Rsa1.0_00628.1.g17114.t1	gb|AAD17395.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	264	1138	5.00E-49	431.1	37.9	59.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	264	575	5.00E-26	217.8	28.4	44.3

Rsa1.0_00628.1.g17115.t1	dbj|BAJ33727.1| unnamed protein product [Thellungiella halophila]	210	196	2.00E-98	93.3	86.2	89.5	unnamed protein product	----	----	AT3G16190.1 | Symbols: | Isochorismatase family protein | chr3:5489883-5491195 REVERSE LENGTH=196	210	196	2.00E-95	93.3	81.4	86.7
Rsa1.0_00628.1.g17116.t1	ref|XP_002885129.1| hypothetical protein ARALYDRAFT_479073 [Arabidopsis lyrata subsp. lyrata] gi|297330969|gb|EFH61388.1| hypothetical protein ARALYDRAFT_479073 [Arabidopsis lyrata subsp. lyrata]	463	456	0	98.5	90.9	96.1	hypothetical protein ARALYDRAFT_479073	gbpln	Arabidopsis lyrata	AT3G16200.1 | Symbols: | unknown protein; Has 97 Blast hits to 97 proteins in 15 species: Archae - 0; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink). | chr3:5491619-5493605 REVERSE LENGTH=456	463	456	0	98.5	90.7	96.1
Rsa1.0_00628.1.g17117.t1	ref|XP_002885130.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297330970|gb|EFH61389.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	280	362	1.00E-116	129.3	71.4	84.3	F-box family protein	gbpln	Arabidopsis lyrata	AT3G16210.1 | Symbols: | F-box family protein | chr3:5494533-5495615 REVERSE LENGTH=360	280	360	1.00E-118	128.6	71.4	83.9
Rsa1.0_00628.1.g17118.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	356	258	2.00E-42	72.5	29.5	37.9	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	356	302	2.00E-30	84.8	24.7	32.9
Rsa1.0_00628.1.g17119.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	317	442	1.00E-118	139.4	65.9	72.9	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	317	343	4.00E-57	108.2	40.4	50.2
Rsa1.0_00628.1.g17120.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	346	1142	2.00E-66	330.1	39.9	57.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	346	575	3.00E-40	166.2	29.2	48.8
Rsa1.0_00628.1.g17121.t1	dbj|BAB01275.1| histidine-containing phosphotransfer protein-like [Arabidopsis thaliana]	133	133	1.00E-66	100.0	91.0	95.5	histidine-containing phosphotransfer protein-like	gbpln	Arabidopsis thaliana	AT3G16360.2 | Symbols: AHP4 | HPT phosphotransmitter 4 | chr3:5554351-5555518 FORWARD LENGTH=145	133	145	6.00E-68	109.0	88.7	93.2
Rsa1.0_00628.1.g17122.t2	dbj|BAJ33787.1| unnamed protein product [Thellungiella halophila]	354	358	0	101.1	94.1	96.6	unnamed protein product	----	----	AT3G16370.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:5556928-5558351 FORWARD LENGTH=353	354	353	0	99.7	87.0	91.2
Rsa1.0_00628.1.g17123.t1	gb|EOA30118.1| hypothetical protein CARUB_v10013228mg [Capsella rubella]	573	622	0	108.6	67.9	77.3	hypothetical protein CARUB_v10013228mg	gbpln	Capsella rubella	AT3G16380.1 | Symbols: PAB6 | poly(A) binding protein 6 | chr3:5558676-5560993 REVERSE LENGTH=537	573	537	0	93.7	63.7	72.6
Rsa1.0_00628.1.g17124.t1	gb|AAM64705.1| outward rectifying potassium channel KCO [Arabidopsis thaliana]	100	363	3.00E-14	363.0	47.0	57.0	outward rectifying potassium channel KCO	gbpln	Arabidopsis thaliana	AT5G55630.2 | Symbols: KCO1, TPK1 | Outward rectifying potassium channel protein | chr5:22531718-22532893 FORWARD LENGTH=363	100	363	5.00E-17	363.0	47.0	57.0
Rsa1.0_00628.1.g17125.t1	emb|CAA72271.1| jasmonate inducible protein [Brassica napus]	674	680	0	100.9	55.3	59.5	jasmonate inducible protein	gbpln	Brassica napus	AT1G52040.1 | Symbols: MBP1, ATMBP | myrosinase-binding protein 1 | chr1:19350595-19352578 REVERSE LENGTH=462	674	462	1.00E-131	68.5	36.9	47.3
Rsa1.0_00628.1.g17126.t1	ref|XP_002885141.1| hypothetical protein ARALYDRAFT_479107 [Arabidopsis lyrata subsp. lyrata] gi|297330981|gb|EFH61400.1| hypothetical protein ARALYDRAFT_479107 [Arabidopsis lyrata subsp. lyrata]	450	451	0	100.2	82.2	90.0	hypothetical protein ARALYDRAFT_479107	gbpln	Arabidopsis lyrata	AT3G16470.2 | Symbols: JR1 | Mannose-binding lectin superfamily protein | chr3:5596096-5597709 REVERSE LENGTH=451	450	451	0	100.2	82.0	90.0
Rsa1.0_00628.1.g17127.t7	gb|AAS21632.1| voltage-dependent anion-selective channel protein [Brassica rapa]	281	276	4.00E-41	98.2	35.6	43.4	voltage-dependent anion-selective channel protein	gbpln	Brassica rapa	AT5G15090.2 | Symbols: VDAC3 | voltage dependent anion channel 3 | chr5:4889641-4891389 REVERSE LENGTH=274	281	274	9.00E-35	97.5	31.3	40.2
Rsa1.0_00629.1.g17128.t5	ref|XP_002883053.1| hypothetical protein ARALYDRAFT_479191 [Arabidopsis lyrata subsp. lyrata] gi|297328893|gb|EFH59312.1| hypothetical protein ARALYDRAFT_479191 [Arabidopsis lyrata subsp. lyrata]	1099	1029	0	93.6	85.2	89.4	hypothetical protein ARALYDRAFT_479191	gbpln	Arabidopsis lyrata	AT3G17205.3 | Symbols: UPL6 | ubiquitin protein ligase 6 | chr3:5873528-5881132 FORWARD LENGTH=1029	1099	1029	0	93.6	84.3	89.2
Rsa1.0_00629.1.g17129.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	910	1447	9.00E-95	159.0	24.7	38.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	910	746	7.00E-43	82.0	12.7	19.0
Rsa1.0_00629.1.g17130.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	881	1274	0	144.6	56.9	69.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	881	626	3.00E-37	71.1	13.1	21.5

Rsa1.0_00629.1.g17131.t1	ref|XP_002883298.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297329138|gb|EFH59557.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	337	374	1.00E-161	111.0	89.6	93.2	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT3G21330.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:7507720-7508841 FORWARD LENGTH=373	337	373	1.00E-158	110.7	90.2	93.5
Rsa1.0_00629.1.g17132.t1	gb|EOA32824.1| hypothetical protein CARUB_v10016135mg [Capsella rubella]	890	897	0	100.8	76.2	86.0	hypothetical protein CARUB_v10016135mg	gbpln	Capsella rubella	AT3G21340.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:7511848-7515937 REVERSE LENGTH=899	890	899	0	101.0	76.7	86.5
Rsa1.0_00629.1.g17133.t1	ref|XP_002883299.1| hypothetical protein ARALYDRAFT_479655 [Arabidopsis lyrata subsp. lyrata] gi|297329139|gb|EFH59558.1| hypothetical protein ARALYDRAFT_479655 [Arabidopsis lyrata subsp. lyrata]	259	257	1.00E-120	99.2	85.7	92.3	hypothetical protein ARALYDRAFT_479655	gbpln	Arabidopsis lyrata	AT3G21350.1 | Symbols: MED6 | RNA polymerase transcriptional regulation mediator-related | chr3:7517106-7518587 FORWARD LENGTH=257	259	257	1.00E-122	99.2	84.6	92.3
Rsa1.0_00629.1.g17134.t1	ref|NP_001078196.1| uncharacterized protein [Arabidopsis thaliana] gi|98961873|gb|ABF59266.1| unknown protein [Arabidopsis thaliana] gi|332642978|gb|AEE76499.1| uncharacterized protein AT3G21352 [Arabidopsis thaliana]	74	74	1.00E-21	100.0	74.3	82.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G21352.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G21351.1); Has 26 Blast hits to 26 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7520033-7520360 FORWARD LENGTH=74	74	74	2.00E-24	100.0	74.3	82.4
Rsa1.0_00629.1.g17135.t1	ref|NP_188773.1| clavaminate synthase-like protein [Arabidopsis thaliana] gi|73921104|sp|Q9LIG0.1|Y3136_ARATH RecName: Full=Clavaminate synthase-like protein At3g21360 gi|56967335|pdb|1Y0Z|A Chain A, X-Ray Structure Of Gene Product From Arabidopsis Thaliana At3g21360 gi|56967336|pdb|1Y0Z|B Chain B, X-Ray Structure Of Gene Product From Arabidopsis Thaliana At3g21360 gi|150261485|pdb|2Q4A|A Chain A, Ensemble Refinement Of The Protein Crystal Structure Of Gene Product From Arabidopsis Thaliana At3g21360 gi|150261486|pdb|2Q4A|B Chain B, Ensemble Refinement Of The Protein Crystal Structure Of Gene Product From Arabidopsis Thaliana At3g21360 gi|9294683|dbj|BAB03049.1| syringomycin biosynthesis enzyme-like protein [Arabidopsis thaliana] gi|26450615|dbj|BAC42419.1| unknown protein [Arabidopsis thaliana] gi|182623791|gb|ACB88834.1| At3g21360 [Arabidopsis thaliana] gi|332642979|gb|AEE76500.1| clavaminate synthase-like protein [Arabidopsis thaliana]	328	330	1.00E-172	100.6	90.5	94.8	clavaminate synthase-like protein	gbpln	Arabidopsis thaliana	AT3G21360.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:7522865-7524036 FORWARD LENGTH=330	328	330	1.00E-175	100.6	90.5	94.8
Rsa1.0_00629.1.g17136.t1	ref|NP_188777.1| uncharacterized protein [Arabidopsis thaliana] gi|9294687|dbj|BAB03053.1| unnamed protein product [Arabidopsis thaliana] gi|26453072|dbj|BAC43612.1| unknown protein [Arabidopsis thaliana] gi|28973457|gb|AAO64053.1| unknown protein [Arabidopsis thaliana] gi|332642984|gb|AEE76505.1| uncharacterized protein AT3G21400 [Arabidopsis thaliana]	188	188	5.00E-83	100.0	83.5	89.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G21400.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 29 Blast hits to 29 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7534824-7536293 REVERSE LENGTH=188	188	188	2.00E-85	100.0	83.5	89.9
Rsa1.0_00629.1.g17137.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00629.1.g17138.t1	gb|EOA30874.1| hypothetical protein CARUB_v10014020mg [Capsella rubella]	363	364	0	100.3	92.0	95.6	hypothetical protein CARUB_v10014020mg	gbpln	Capsella rubella	AT3G21420.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:7541579-7543221 FORWARD LENGTH=364	363	364	0	100.3	91.7	95.3

Rsa1.0_00630.1.g17139.t1	ref|XP_002867492.1| hypothetical protein ARALYDRAFT_492028 [Arabidopsis lyrata subsp. lyrata] gi|297313328|gb|EFH43751.1| hypothetical protein ARALYDRAFT_492028 [Arabidopsis lyrata subsp. lyrata]	341	337	1.00E-161	98.8	83.0	89.1	hypothetical protein ARALYDRAFT_492028	gbpln	Arabidopsis lyrata	AT4G27610.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27620.2); Has 1304 Blast hits to 1173 proteins in 200 species: Archae - 14; Bacteria - 115; Metazoa - 628; Fungi - 104; Plants - 95; Viruses - 8; Other Eukaryotes - 340 (source: NCBI BLink). | chr4:13785648-13787332 REVERSE LENGTH=334	341	334	1.00E-152	97.9	80.6	87.4
Rsa1.0_00630.1.g17140.t1	ref|NP_567780.1| pfkB-like carbohydrate kinase family protein [Arabidopsis thaliana] gi|15450507|gb|AAK96546.1| AT4g27600/T29A15_90 [Arabidopsis thaliana] gi|16974333|gb|AAL31151.1| AT4g27600/T29A15_90 [Arabidopsis thaliana] gi|332659964|gb|AEE85364.1| pfkB-like carbohydrate kinase family protein [Arabidopsis thaliana]	404	471	0	116.6	89.9	93.6	pfkB-like carbohydrate kinase family protein	gbpln	Arabidopsis thaliana	AT4G27600.1 | Symbols: NARA5 | pfkB-like carbohydrate kinase family protein | chr4:13782753-13785005 REVERSE LENGTH=471	404	471	0	116.6	89.9	93.6
Rsa1.0_00630.1.g17141.t1	gb|EOA15913.1| hypothetical protein CARUB_v10004004mg [Capsella rubella]	1274	1255	0	98.5	72.4	82.4	hypothetical protein CARUB_v10004004mg	gbpln	Capsella rubella	AT4G27595.1 | Symbols: | Plant protein of unknown function (DUF827) | chr4:13772819-13777128 REVERSE LENGTH=1221	1274	1221	0	95.8	73.3	81.6
Rsa1.0_00630.1.g17142.t1	ref|XP_002869556.1| hypothetical protein ARALYDRAFT_913778 [Arabidopsis lyrata subsp. lyrata] gi|297315392|gb|EFH45815.1| hypothetical protein ARALYDRAFT_913778 [Arabidopsis lyrata subsp. lyrata]	156	161	2.00E-66	103.2	83.3	90.4	hypothetical protein ARALYDRAFT_913778	gbpln	Arabidopsis lyrata	AT4G27590.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr4:13771224-13771790 FORWARD LENGTH=156	156	156	3.00E-64	100.0	80.8	89.1
Rsa1.0_00630.1.g17143.t1	gb|EOA16742.1| hypothetical protein CARUB_v10004943mg [Capsella rubella]	402	408	0	101.5	89.6	93.3	hypothetical protein CARUB_v10004943mg	gbpln	Capsella rubella	AT4G27585.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr4:13766984-13769832 REVERSE LENGTH=411	402	411	0	102.2	88.3	94.0
Rsa1.0_00630.1.g17144.t1	emb|CAB38270.1| putative protein [Arabidopsis thaliana] gi|7269612|emb|CAB81408.1| putative protein [Arabidopsis thaliana]	101	515	3.00E-29	509.9	78.2	83.2	putative protein	gbpln	Arabidopsis thaliana	AT4G27580.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, cell wall; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13765832-13766306 REVERSE LENGTH=104	101	104	2.00E-31	103.0	78.2	83.2
Rsa1.0_00630.1.g17145.t1	gb|EOA17344.1| hypothetical protein CARUB_v10005627mg [Capsella rubella]	245	238	1.00E-114	97.1	88.6	93.5	hypothetical protein CARUB_v10005627mg	gbpln	Capsella rubella	AT4G27540.1 | Symbols: PRA1.H | prenylated RAB acceptor 1.H | chr4:13753449-13754660 REVERSE LENGTH=241	245	241	1.00E-116	98.4	89.8	94.3
Rsa1.0_00630.1.g17146.t1	ref|NP_194482.1| early nodulin-like protein 2 [Arabidopsis thaliana] gi|34395735|sp|Q9T076.1|ENL2_ARATH RecName: Full=Early nodulin-like protein 2; AltName: Full=Phytocyanin-like protein; Flags: Precursor gi|11762218|gb|AAG40387.1|AF325035_1 AT4g27520 [Arabidopsis thaliana] gi|4469003|emb|CAB38264.1| putative protein [Arabidopsis thaliana] gi|7269606|emb|CAB81402.1| putative protein [Arabidopsis thaliana] gi|23397249|gb|AAN31906.1| unknown protein [Arabidopsis thaliana] gi|24417234|gb|AAN60227.1| unknown [Arabidopsis thaliana] gi|56381997|gb|AAV85717.1| At4g27520 [Arabidopsis thaliana] gi|332659953|gb|AEE85353.1| early nodulin-like protein 2 [Arabidopsis thaliana]	316	349	5.00E-93	110.4	69.9	77.2	early nodulin-like protein 2	gbpln	Arabidopsis thaliana	AT4G27520.1 | Symbols: ENODL2, AtENODL2 | early nodulin-like protein 2 | chr4:13750668-13751819 REVERSE LENGTH=349	316	349	1.00E-95	110.4	69.9	77.2
Rsa1.0_00630.1.g17147.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00630.1.g17148.t1	ref|XP_002867500.1| hypothetical protein ARALYDRAFT_492043 [Arabidopsis lyrata subsp. lyrata] gi|297313336|gb|EFH43759.1| hypothetical protein ARALYDRAFT_492043 [Arabidopsis lyrata subsp. lyrata]	707	733	0	103.7	69.9	82.3	hypothetical protein ARALYDRAFT_492043	gbpln	Arabidopsis lyrata	AT4G27510.1 | Symbols: | unknown protein; Has 25 Blast hits to 23 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:13746284-13748996 REVERSE LENGTH=728	707	728	0	103.0	68.5	81.8

Rsa1.0_00630.1.g17149.t2	ref|XP_002869559.1| hypothetical protein ARALYDRAFT_328945 [Arabidopsis lyrata subsp. lyrata] gi|297315395|gb|EFH45818.1| hypothetical protein ARALYDRAFT_328945 [Arabidopsis lyrata subsp. lyrata]	579	617	0	106.6	77.0	85.5	hypothetical protein ARALYDRAFT_328945	gbpln	Arabidopsis lyrata	AT4G27500.1 | Symbols: PPI1 | proton pump interactor 1 | chr4:13743614-13745900 FORWARD LENGTH=612	579	612	0	105.7	73.6	81.5
Rsa1.0_00630.1.g17150.t1	ref|NP_194479.2| 3'-5'-exoribonuclease family protein [Arabidopsis thaliana] gi|124300968|gb|ABN04736.1| At4g27490 [Arabidopsis thaliana] gi|124301080|gb|ABN04792.1| At4g27490 [Arabidopsis thaliana] gi|332659949|gb|AEE85349.1| 3'-5'-exoribonuclease family protein [Arabidopsis thaliana]	257	256	1.00E-135	99.6	92.2	94.9	3'-5'-exoribonuclease family protein	gbpln	Arabidopsis thaliana	AT4G27490.1 | Symbols: | 3'-5'-exoribonuclease family protein | chr4:13739961-13741647 FORWARD LENGTH=256	257	256	1.00E-138	99.6	92.2	94.9
Rsa1.0_00630.1.g17151.t2	ref|NP_194478.3| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|186514118|ref|NP_001119069.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|332659947|gb|AEE85347.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|332659948|gb|AEE85348.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]	350	421	1.00E-141	120.3	75.1	83.4	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	gbpln	Arabidopsis thaliana	AT4G27480.2 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:13736835-13738317 REVERSE LENGTH=421	350	421	1.00E-144	120.3	75.1	83.4
Rsa1.0_00630.1.g17152.t1	ref|XP_002869561.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297315397|gb|EFH45820.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	248	243	1.00E-106	98.0	79.4	83.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G27470.1 | Symbols: ATRMA3, RMA3 | RING membrane-anchor 3 | chr4:13735576-13736307 FORWARD LENGTH=243	248	243	1.00E-108	98.0	79.0	83.5
Rsa1.0_00630.1.g17153.t1	ref|XP_002869562.1| hypothetical protein ARALYDRAFT_328949 [Arabidopsis lyrata subsp. lyrata] gi|297315398|gb|EFH45821.1| hypothetical protein ARALYDRAFT_328949 [Arabidopsis lyrata subsp. lyrata]	386	394	1.00E-165	102.1	79.5	88.3	hypothetical protein ARALYDRAFT_328949	gbpln	Arabidopsis lyrata	AT4G27460.1 | Symbols: | Cystathionine beta-synthase (CBS) family protein | chr4:13732939-13734263 FORWARD LENGTH=391	386	391	1.00E-160	101.3	77.7	87.8
Rsa1.0_00630.1.g17154.t1	gb|EOA14968.1| hypothetical protein CARUB_v10028315mg [Capsella rubella]	143	536	1.00E-27	374.8	44.1	51.0	hypothetical protein CARUB_v10028315mg	gbpln	Capsella rubella	AT5G49950.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:20319871-20323552 REVERSE LENGTH=537	143	537	3.00E-23	375.5	46.9	51.0
Rsa1.0_00630.1.g17155.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	715	723	0	101.1	55.4	73.0	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	715	696	3.00E-50	97.3	23.4	42.5
Rsa1.0_00630.1.g17156.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1013	1274	0	125.8	48.5	64.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1013	575	4.00E-67	56.8	16.4	26.0
Rsa1.0_00630.1.g17157.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00630.1.g17158.t1	ref|NP_567775.1| aluminum induced protein with YGL and LRDR motifs [Arabidopsis thaliana] gi|297799238|ref|XP_002867503.1| hypothetical protein ARALYDRAFT_913794 [Arabidopsis lyrata subsp. lyrata] gi|14030723|gb|AAK53036.1|AF375452_1 AT4g27450/F27G19_50 [Arabidopsis thaliana] gi|15028057|gb|AAK76559.1| unknown protein [Arabidopsis thaliana] gi|20259059|gb|AAM14245.1| unknown protein [Arabidopsis thaliana] gi|21593019|gb|AAM64968.1| unknown [Arabidopsis thaliana] gi|297313339|gb|EFH43762.1| hypothetical protein ARALYDRAFT_913794 [Arabidopsis lyrata subsp. lyrata] gi|332659944|gb|AEE85344.1| aluminum induced protein with YGL and LRDR motifs [Arabidopsis thaliana]	250	250	1.00E-142	100.0	96.8	98.4	aluminum induced protein with YGL and LRDR motifs	gbpln	Arabidopsis lyrata	AT4G27450.1 | Symbols: | Aluminium induced protein with YGL and LRDR motifs | chr4:13727665-13728683 REVERSE LENGTH=250	250	250	1.00E-144	100.0	96.8	98.4

Rsa1.0_00630.1.g17159.t1	ref|XP_002869563.1| hypothetical protein ARALYDRAFT_492051 [Arabidopsis lyrata subsp. lyrata] gi|297315399|gb|EFH45822.1| hypothetical protein ARALYDRAFT_492051 [Arabidopsis lyrata subsp. lyrata]	398	401	0	100.8	95.2	98.0	hypothetical protein ARALYDRAFT_492051	gbpln	Arabidopsis lyrata	AT4G27440.2 | Symbols: PORB | protochlorophyllide oxidoreductase B | chr4:13725648-13727107 FORWARD LENGTH=401	398	401	0	100.8	94.7	97.2
Rsa1.0_00630.1.g17160.t1	gb|EOA17531.1| hypothetical protein CARUB_v10005876mg [Capsella rubella]	173	173	2.00E-92	100.0	96.5	98.3	hypothetical protein CARUB_v10005876mg	gbpln	Capsella rubella	AT4G27435.1 | Symbols: | Protein of unknown function (DUF1218) | chr4:13723903-13724872 FORWARD LENGTH=173	173	173	1.00E-94	100.0	95.4	98.8
Rsa1.0_00630.1.g17161.t1	ref|NP_194473.1| COP1-interacting protein 7 [Arabidopsis thaliana] gi|186514102|ref|NP_001119068.1| COP1-interacting protein 7 [Arabidopsis thaliana] gi|3327868|dbj|BAA31738.1| COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana] gi|4972068|emb|CAB43875.1| COP1-interacting protein 7 (CIP7) [Arabidopsis thaliana] gi|7269597|emb|CAB81393.1| COP1-interacting protein 7 (CIP7) [Arabidopsis thaliana] gi|332659939|gb|AEE85339.1| COP1-interacting protein 7 [Arabidopsis thaliana] gi|332659940|gb|AEE85340.1| COP1-interacting protein 7 [Arabidopsis thaliana]	1052	1058	0	100.6	76.0	83.9	COP1-interacting protein 7	gbpln	Arabidopsis thaliana	AT4G27430.2 | Symbols: CIP7 | COP1-interacting protein 7 | chr4:13718817-13722736 FORWARD LENGTH=1058	1052	1058	0	100.6	76.0	83.9
Rsa1.0_00631.1.g17162.t1	ref|XP_002881104.1| hypothetical protein ARALYDRAFT_481948 [Arabidopsis lyrata subsp. lyrata] gi|297326943|gb|EFH57363.1| hypothetical protein ARALYDRAFT_481948 [Arabidopsis lyrata subsp. lyrata]	425	434	0	102.1	85.2	91.1	hypothetical protein ARALYDRAFT_481948	gbpln	Arabidopsis lyrata	AT2G30360.1 | Symbols: CIPK11, PKS5, SIP4, SNRK3.22 | SOS3-interacting protein 4 | chr2:12937265-12938572 REVERSE LENGTH=435	425	435	0	102.4	84.2	90.8
Rsa1.0_00631.1.g17163.t5	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2451	1274	0	52.0	23.4	32.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	2451	696	2.00E-65	28.4	7.5	12.8
Rsa1.0_00631.1.g17164.t1	gb|EOA28561.1| hypothetical protein CARUB_v10024779mg [Capsella rubella]	135	160	2.00E-44	118.5	73.3	79.3	hypothetical protein CARUB_v10024779mg	gbpln	Capsella rubella	AT2G30370.2 | Symbols: CHAL, EPFL6 | allergen-related | chr2:12940577-12942167 REVERSE LENGTH=156	135	156	9.00E-47	115.6	76.3	84.4
Rsa1.0_00631.1.g17165.t1	ref|XP_002879262.1| hypothetical protein ARALYDRAFT_902024 [Arabidopsis lyrata subsp. lyrata] gi|297325101|gb|EFH55521.1| hypothetical protein ARALYDRAFT_902024 [Arabidopsis lyrata subsp. lyrata]	69	420	2.00E-18	608.7	76.8	82.6	hypothetical protein ARALYDRAFT_902024	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00631.1.g17166.t1	gb|EOA27511.1| hypothetical protein CARUB_v10023651mg [Capsella rubella]	316	320	1.00E-102	101.3	71.2	81.0	hypothetical protein CARUB_v10023651mg	gbpln	Capsella rubella	AT2G30400.1 | Symbols: ATOFP2, OFP2 | ovate family protein 2 | chr2:12956592-12957554 FORWARD LENGTH=320	316	320	5.00E-97	101.3	70.3	80.7
Rsa1.0_00631.1.g17167.t1	ref|NP_181887.1| chitinase-like protein [Arabidopsis thaliana] gi|2281111|gb|AAB64047.1| putative endochitinase [Arabidopsis thaliana] gi|20196867|gb|AAM14810.1| putative endochitinase [Arabidopsis thaliana] gi|32815951|gb|AAP88360.1| At2g43590 [Arabidopsis thaliana] gi|110736333|dbj|BAF00136.1| putative endochitinase [Arabidopsis thaliana] gi|330255199|gb|AEC10293.1| chitinase-like protein [Arabidopsis thaliana]	272	264	1.00E-125	97.1	81.3	84.9	chitinase-like protein	gbpln	Arabidopsis thaliana	AT2G43590.1 | Symbols: | Chitinase family protein | chr2:18081592-18082749 REVERSE LENGTH=264	272	264	1.00E-127	97.1	81.3	84.9
Rsa1.0_00631.1.g17168.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1622	2726	0	168.1	52.8	69.5	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1622	158	4.00E-36	9.7	4.4	5.3
Rsa1.0_00631.1.g17169.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	321	1555	2.00E-23	484.4	19.0	25.5	disease resistance protein	gbpln	Brassica rapa	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	321	170	1.00E-17	53.0	15.3	23.7
Rsa1.0_00631.1.g17170.t1	gb|EOA27407.1| hypothetical protein CARUB_v10023541mg [Capsella rubella]	91	349	9.00E-22	383.5	61.5	72.5	hypothetical protein CARUB_v10023541mg	gbpln	Capsella rubella	AT2G30440.1 | Symbols: TPP | thylakoid processing peptide | chr2:12973244-12975027 FORWARD LENGTH=340	91	340	7.00E-24	373.6	61.5	71.4

<table>
<tr><td>Rsa1.0_00632.1.g17171.t1</td><td>ref|XP_002864881.1| hypothetical protein ARALYDRAFT_496593 [Arabidopsis lyrata subsp. lyrata] gi|297310716|gb|EFH41140.1| hypothetical protein ARALYDRAFT_496593 [Arabidopsis lyrata subsp. lyrata]</td><td>218</td><td>357</td><td>1.00E-105</td><td>163.8</td><td>90.8</td><td>95.0</td><td>hypothetical protein ARALYDRAFT_496593</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63990.1 | Symbols: | Inositol monophosphatase family protein | chr5:25613387-25615736 FORWARD LENGTH=357</td><td>218</td><td>357</td><td>1.00E-106</td><td>163.8</td><td>90.4</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00632.1.g17172.t1</td><td>ref|NP_201205.1| SAL2 phosphatase [Arabidopsis thaliana] gi|34395614|sp|O49623.1|DPNP2_ARATH RecName: Full=SAL2 phosphatase; AltName: Full=3'(2'),5'-bisphosphate nucleotidase 2; AltName: Full=3'(2'),5'-bisphosphonucleoside 3'(2')-phosphohydrolase 2; AltName: Full=DPNPase 2; AltName: Full=Inositol polyphosphate 1-phosphatase 2; Short=IPPase 2; AltName: Full=Inositol-1,4-bisphosphate 1-phosphatase 2 gi|2765667|emb|CAB05889.1| 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana] gi|8777313|dbj|BAA96903.1| 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana] gi|17979307|gb|AAL49879.1| putative 3(2),5-bisphosphate nucleotidase [Arabidopsis thaliana] gi|20466007|gb|AAM20225.1| putative 3(2),5-bisphosphate nucleotidase [Arabidopsis thaliana] gi|332010445|gb|AED97828.1| SAL2 phosphatase [Arabidopsis thaliana]</td><td>355</td><td>347</td><td>1.00E-167</td><td>97.7</td><td>82.8</td><td>89.6</td><td>SAL2 phosphatase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G64000.1 | Symbols: SAL2, ATSAL2 | Inositol monophosphatase family protein | chr5:25616664-25618478 FORWARD LENGTH=347</td><td>355</td><td>347</td><td>1.00E-169</td><td>97.7</td><td>82.8</td><td>89.6</td></tr>
<tr><td>Rsa1.0_00632.1.g17173.t1</td><td>ref|XP_002866586.1| hypothetical protein ARALYDRAFT_496595 [Arabidopsis lyrata subsp. lyrata] gi|297312421|gb|EFH42845.1| hypothetical protein ARALYDRAFT_496595 [Arabidopsis lyrata subsp. lyrata]</td><td>233</td><td>236</td><td>1.00E-101</td><td>101.3</td><td>81.1</td><td>89.3</td><td>hypothetical protein ARALYDRAFT_496595</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G64010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 34 Blast hits to 34 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:25618810-25620179 REVERSE LENGTH=236</td><td>233</td><td>236</td><td>1.00E-100</td><td>101.3</td><td>79.4</td><td>87.1</td></tr>
<tr><td>Rsa1.0_00632.1.g17174.t1</td><td>gb|EOA14829.1| hypothetical protein CARUB_v10028139mg [Capsella rubella]</td><td>976</td><td>817</td><td>0</td><td>83.7</td><td>65.6</td><td>70.3</td><td>hypothetical protein CARUB_v10028139mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G64030.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:25624965-25628257 FORWARD LENGTH=829</td><td>976</td><td>829</td><td>0</td><td>84.9</td><td>63.8</td><td>68.2</td></tr>
<tr><td>Rsa1.0_00632.1.g17175.t1</td><td>ref|XP_002866588.1| photosystem I reaction center subunit psi-N [Arabidopsis lyrata subsp. lyrata] gi|297312423|gb|EFH42847.1| photosystem I reaction center subunit psi-N [Arabidopsis lyrata subsp. lyrata]</td><td>167</td><td>171</td><td>6.00E-83</td><td>102.4</td><td>92.8</td><td>96.4</td><td>photosystem I reaction center subunit psi-N</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G64040.1 | Symbols: PSAN | photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN) | chr5:25628724-25629409 REVERSE LENGTH=171</td><td>167</td><td>171</td><td>5.00E-85</td><td>102.4</td><td>92.2</td><td>95.8</td></tr>
<tr><td>Rsa1.0_00632.1.g17176.t3</td><td>gb|EOA14683.1| hypothetical protein CARUB_v10027955mg [Capsella rubella]</td><td>542</td><td>570</td><td>0</td><td>105.2</td><td>93.9</td><td>96.7</td><td>hypothetical protein CARUB_v10027955mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G64050.1 | Symbols: ATERS, OVA3, ERS | glutamate tRNA synthetase | chr5:25630196-25633099 REVERSE LENGTH=570</td><td>542</td><td>570</td><td>0</td><td>105.2</td><td>93.0</td><td>95.9</td></tr>
<tr><td>Rsa1.0_00632.1.g17177.t1</td><td>gb|EOA13578.1| hypothetical protein CARUB_v10026643mg [Capsella rubella]</td><td>170</td><td>364</td><td>6.00E-38</td><td>214.1</td><td>43.5</td><td>45.3</td><td>hypothetical protein CARUB_v10026643mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G64060.1 | Symbols: anac103, NAC103 | NAC domain containing protein 103 | chr5:25633818-25635152 REVERSE LENGTH=356</td><td>170</td><td>356</td><td>3.00E-39</td><td>209.4</td><td>42.4</td><td>45.3</td></tr>
<tr><td>Rsa1.0_00632.1.g17178.t2</td><td>ref|XP_002866591.1| phosphatidylinositol 4-kinase [Arabidopsis lyrata subsp. lyrata] gi|297312426|gb|EFH42850.1| phosphatidylinositol 4-kinase [Arabidopsis lyrata subsp. lyrata]</td><td>1153</td><td>1123</td><td>0</td><td>97.4</td><td>89.2</td><td>91.9</td><td>phosphatidylinositol 4-kinase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G64070.1 | Symbols: PI-4KBETA1, PI4KBETA1 | phosphatidylinositol 4-OH kinase beta1 | chr5:25637492-25643902 REVERSE LENGTH=1121</td><td>1153</td><td>1121</td><td>0</td><td>97.2</td><td>88.7</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00632.1.g17179.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_00632.1.g17180.t1	ref|NP_568984.1| Non-specific lipid-transfer protein-like protein [Arabidopsis thaliana] gi|75161488|sp|Q8VYI9.1|NLTL5_ARATH RecName: Full=Non-specific lipid-transfer protein-like protein At5g64080; Flags: Precursor gi|17979494|gb|AAL50083.1| AT5g64080/MHJ24_6 [Arabidopsis thaliana] gi|20147301|gb|AAM10364.1| AT5g64080/MHJ24_6 [Arabidopsis thaliana] gi|332010454|gb|AED97837.1| Non-specific lipid-transfer protein-like protein [Arabidopsis thaliana]	183	182	2.00E-56	99.5	70.5	80.3	Non-specific lipid-transfer protein-like protein	gbpln	Arabidopsis thaliana	AT5G64080.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:25645475-25646638 REVERSE LENGTH=182	183	182	7.00E-59	99.5	70.5	80.3
Rsa1.0_00632.1.g17181.t1	dbj|BAJ34593.1| unnamed protein product [Thellungiella halophila]	334	333	1.00E-169	99.7	89.5	93.7	unnamed protein product	----	----	AT5G64100.1 | Symbols: | Peroxidase superfamily protein | chr5:25650824-25652062 REVERSE LENGTH=331	334	331	1.00E-156	99.1	85.9	91.0
Rsa1.0_00632.1.g17182.t1	gb|EOA14660.1| hypothetical protein CARUB_v10027924mg [Capsella rubella]	333	332	1.00E-159	99.7	82.3	88.9	hypothetical protein CARUB_v10027924mg	gbpln	Capsella rubella	AT5G64110.1 | Symbols: | Peroxidase superfamily protein | chr5:25654575-25655946 REVERSE LENGTH=330	333	330	1.00E-156	99.1	81.4	86.2
Rsa1.0_00632.1.g17183.t1	gb|EOA13703.1| hypothetical protein CARUB_v10026774mg [Capsella rubella]	329	328	1.00E-166	99.7	87.5	92.7	hypothetical protein CARUB_v10026774mg	gbpln	Capsella rubella	AT5G64120.1 | Symbols: | Peroxidase superfamily protein | chr5:25659551-25660946 REVERSE LENGTH=328	329	328	1.00E-165	99.7	85.4	91.8
Rsa1.0_00632.1.g17184.t1	gb|ABD64964.1| hypothetical protein 25.t00001 [Brassica oleracea]	998	1103	3.00E-32	110.5	7.0	9.3	hypothetical protein 25.t00001	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00632.1.g17185.t1	ref|NP_568985.1| cAMP-regulated phosphoprotein 19-related protein [Arabidopsis thaliana] gi|16648718|gb|AAL25551.1| AT5g64130/MHJ24_11 [Arabidopsis thaliana] gi|20453353|gb|AAM19915.1| AT5g64130/MHJ24_11 [Arabidopsis thaliana] gi|21618212|gb|AAM67262.1| unknown [Arabidopsis thaliana] gi|332010460|gb|AED97843.1| cAMP-regulated phosphoprotein 19-related protein [Arabidopsis thaliana]	73	115	6.00E-27	157.5	79.5	82.2	cAMP-regulated phosphoprotein 19-related protein	gbpln	Arabidopsis thaliana	AT5G64130.1 | Symbols: | cAMP-regulated phosphoprotein 19-related protein | chr5:25664547-25665339 REVERSE LENGTH=115	73	115	1.00E-29	157.5	79.5	82.2
Rsa1.0_00632.1.g17186.t1	ref|XP_002881853.1| hypothetical protein ARALYDRAFT_903615 [Arabidopsis lyrata subsp. lyrata] gi|297327692|gb|EFH58112.1| hypothetical protein ARALYDRAFT_903615 [Arabidopsis lyrata subsp. lyrata]	372	370	2.00E-94	99.5	54.8	70.7	hypothetical protein ARALYDRAFT_903615	gbpln	Arabidopsis lyrata	AT2G42480.1 | Symbols: | TRAF-like family protein | chr2:17685805-17689851 REVERSE LENGTH=743	372	743	1.00E-74	199.7	50.5	65.1
Rsa1.0_00632.1.g17187.t2	ref|NP_201220.1| RNA methyltransferase family protein [Arabidopsis thaliana] gi|10176963|dbj|BAB10283.1| unnamed protein product [Arabidopsis thaliana] gi|15451004|gb|AAK96773.1| Unknown protein [Arabidopsis thaliana] gi|30725624|gb|AAP37834.1| At5g64156 [Arabidopsis thaliana] gi|332010464|gb|AED97847.1| RNA methyltransferase family protein [Arabidopsis thaliana]	421	377	1.00E-154	89.5	70.3	76.7	RNA methyltransferase family protein	gbpln	Arabidopsis thaliana	AT5G64150.1 | Symbols: | RNA methyltransferase family protein | chr5:25668997-25670731 REVERSE LENGTH=377	421	377	1.00E-157	89.5	70.3	76.7
Rsa1.0_00632.1.g17188.t1	dbj|BAB09864.1| non-phototropic hypocotyl 3 [Arabidopsis thaliana]	729	745	0	102.2	91.2	94.1	non-phototropic hypocotyl 3	gbpln	Arabidopsis thaliana	AT5G64330.1 | Symbols: NPH3, RPT3, JK218 | Phototropic-responsive NPH3 family protein | chr5:25727568-25730225 FORWARD LENGTH=746	729	746	0	102.3	90.9	93.8
Rsa1.0_00632.1.g17189.t1	gb|EOA12685.1| hypothetical protein CARUB_v10027906mg [Capsella rubella]	374	339	6.00E-95	90.6	58.0	63.4	hypothetical protein CARUB_v10027906mg	gbpln	Capsella rubella	AT5G64340.1 | Symbols: SAC51 | sequence-specific DNA binding transcription factors;transcription regulators | chr5:25730890-25731936 REVERSE LENGTH=348	374	348	5.00E-95	93.0	58.0	63.9
Rsa1.0_00632.1.g17190.t1	ref|XP_002866611.1| FK506-binding protein 12 kD [Arabidopsis lyrata subsp. lyrata] gi|297312446|gb|EFH42870.1| FK506-binding protein 12 kD [Arabidopsis lyrata subsp. lyrata]	112	112	1.00E-54	100.0	94.6	97.3	FK506-binding protein 12 kD	gbpln	Arabidopsis lyrata	AT5G64350.1 | Symbols: FKBP12, ATFKBP12 | FK506-binding protein 12 | chr5:25734810-25735990 REVERSE LENGTH=112	112	112	5.00E-56	100.0	92.9	94.6
Rsa1.0_00632.1.g17191.t1	ref|XP_002869205.1| carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315041|gb|EFH45464.1| carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata]	316	301	7.00E-95	95.3	56.0	72.8	carbonic anhydrase family protein	gbpln	Arabidopsis lyrata	AT4G33580.1 | Symbols: ATBCA5, BCA5 | beta carbonic anhydrase 5 | chr4:16139406-16141363 FORWARD LENGTH=301	316	301	1.00E-95	95.3	56.6	71.5

Rsa1.0_00632.1.g17192.t1	gb|EOA12386.1| hypothetical protein CARUB_v10026348mg [Capsella rubella] gi|482548193|gb|EOA12387.1| hypothetical protein CARUB_v10026348mg [Capsella rubella]	464	469	1.00E-177	101.1	73.3	81.0	hypothetical protein CARUB_v10026348mg	gbpln	Capsella rubella	AT5G64360.4 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:25737208-25738602 REVERSE LENGTH=464	464	464	1.00E-165	100.0	71.1	78.9
Rsa1.0_00632.1.g17193.t1	ref|NP_201242.2| beta-ureidopropionase [Arabidopsis thaliana] gi|28193999|gb|AAO33358.1|AF465754_1 N-carbamyl-beta-alanine amidohydrolase [Arabidopsis thaliana] gi|23306402|gb|AAN17428.1| beta-ureidopropionase [Arabidopsis thaliana] gi|30725680|gb|AAP37862.1| At5g64370 [Arabidopsis thaliana] gi|332010498|gb|AED97881.1| beta-ureidopropionase [Arabidopsis thaliana]	408	408	0	100.0	92.2	96.8	beta-ureidopropionase	gbpln	Arabidopsis thaliana	AT5G64370.1 | Symbols: BETA-UP, PYD3 | beta-ureidopropionase | chr5:25739264-25741031 FORWARD LENGTH=408	408	408	0	100.0	92.2	96.8
Rsa1.0_00632.1.g17194.t1	ref|XP_002864897.1| fructose-1,6-bisphosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310732|gb|EFH41156.1| fructose-1,6-bisphosphatase family protein [Arabidopsis lyrata subsp. lyrata]	412	403	0	97.8	89.6	92.5	fructose-1,6-bisphosphatase family protein	gbpln	Arabidopsis lyrata	AT5G64380.1 | Symbols: | Inositol monophosphatase family protein | chr5:25741342-25743024 FORWARD LENGTH=404	412	404	0	98.1	88.8	92.2
Rsa1.0_00632.1.g17195.t1	ref|XP_002864897.1| fructose-1,6-bisphosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310732|gb|EFH41156.1| fructose-1,6-bisphosphatase family protein [Arabidopsis lyrata subsp. lyrata]	75	403	7.00E-35	537.3	96.0	98.7	fructose-1,6-bisphosphatase family protein	gbpln	Arabidopsis lyrata	AT5G64380.1 | Symbols: | Inositol monophosphatase family protein | chr5:25741342-25743024 FORWARD LENGTH=404	75	404	5.00E-37	538.7	94.7	97.3
Rsa1.0_00632.1.g17196.t2	ref|XP_002864898.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310733|gb|EFH41157.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	868	865	0	99.7	77.3	85.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G64390.1 | Symbols: HEN4 | RNA-binding KH domain-containing protein | chr5:25743442-25747380 FORWARD LENGTH=857	868	857	0	98.7	75.9	83.8
Rsa1.0_00632.1.g17197.t1	ref|NP_196519.1| Cox19-like CHCH family protein [Arabidopsis thaliana] gi|7671432|emb|CAB89373.1| putative protein [Arabidopsis thaliana] gi|26452406|dbj|BAC43288.1| unknown protein [Arabidopsis thaliana] gi|28372814|gb|AAO39889.1| At5g09570 [Arabidopsis thaliana] gi|332004028|gb|AED91411.1| Cox19-like CHCH family protein [Arabidopsis thaliana]	143	139	6.00E-45	97.2	65.0	78.3	Cox19-like CHCH family protein	gbpln	Arabidopsis thaliana	AT5G09570.1 | Symbols: | Cox19-like CHCH family protein | chr5:2970733-2971970 FORWARD LENGTH=139	143	139	2.00E-47	97.2	65.0	78.3
Rsa1.0_00632.1.g17198.t1	ref|XP_002864901.1| DNA polymerase V family [Arabidopsis lyrata subsp. lyrata] gi|297310736|gb|EFH41160.1| DNA polymerase V family [Arabidopsis lyrata subsp. lyrata]	1311	1301	0	99.2	81.3	89.2	DNA polymerase V family	gbpln	Arabidopsis lyrata	AT5G64420.1 | Symbols: | DNA polymerase V family | chr5:25756416-25761122 FORWARD LENGTH=1306	1311	1306	0	99.6	80.1	87.9
Rsa1.0_00632.1.g17199.t1	gb|EOA12745.1| hypothetical protein CARUB_v10028367mg [Capsella rubella]	494	503	0	101.8	76.5	81.0	hypothetical protein CARUB_v10028367mg	gbpln	Capsella rubella	AT5G64430.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr5:25762540-25764081 REVERSE LENGTH=513	494	513	1.00E-167	103.8	76.3	81.0
Rsa1.0_00632.1.g17200.t1	ref|NP_201249.2| fatty acid amide hydrolase [Arabidopsis thaliana] gi|75142814|sp|Q7XJJ7.1|FAAH_ARATH RecName: Full=Fatty acid amide hydrolase; AltName: Full=N-acylethanolamine amidohydrolase gi|32454719|gb|AAP83139.1| N-acylethanolamine amidohydrolase [Arabidopsis thaliana] gi|332010510|gb|AED97893.1| fatty acid amide hydrolase [Arabidopsis thaliana]	436	607	0	139.2	70.4	75.2	fatty acid amide hydrolase	gbpln	Arabidopsis thaliana	AT5G64440.1 | Symbols: AtFAAH, FAAH | fatty acid amide hydrolase | chr5:25766229-25770260 FORWARD LENGTH=607	436	607	0	139.2	70.4	75.2
Rsa1.0_00633.1.g17201.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17202.t1	ref|XP_002875017.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297320854|gb|EFH51276.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	624	633	0	101.4	91.2	95.8	dehydration-responsive family protein	gbpln	Arabidopsis lyrata	AT4G00750.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:314405-317507 FORWARD LENGTH=633	624	633	0	101.4	89.6	94.9
Rsa1.0_00633.1.g17203.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17204.t2	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	732	954	2.00E-33	130.3	20.5	31.4	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17205.t5	gb|EOA32134.1| hypothetical protein CARUB_v10015385mg, partial [Capsella rubella]	370	581	6.00E-14	157.0	12.2	15.4	hypothetical protein CARUB_v10015385mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#

Rsa1.0_00633.1.g17206.t2	ref|XP_004301998.1| PREDICTED: uncharacterized protein LOC101300066 [Fragaria vesca subsp. vesca]	525	583	2.00E−78	111.0	34.9	48.2	PREDICTED: uncharacterized protein LOC101300066	gbpln	Fragaria vesca	AT5G31412.1 | Symbols: | hAT transposon superfamily protein | chr5:11541463-11543768 REVERSE LENGTH=433	525	433	3.00E−59	82.5	27.4	35.2
Rsa1.0_00633.1.g17207.t1	ref|XP_002875016.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297320853|gb|EFH51275.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	368	380	1.00E−151	103.3	75.3	85.6	F-box family protein	gbpln	Arabidopsis lyrata	AT4G00755.2 | Symbols: | F-box family protein | chr4:325294-326787 FORWARD LENGTH=377	368	377	1.00E−150	102.4	72.0	84.2
Rsa1.0_00633.1.g17208.t7	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	694	1024	2.00E−13	147.6	6.6	8.6	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17209.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	204	1103	2.00E−49	540.7	50.5	60.3	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17210.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	803	1103	0	137.4	56.0	69.2	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17211.t1	gb|AAC26241.1| F9D12.15 gene product [Arabidopsis thaliana]	543	850	5.00E−42	156.5	21.4	31.5	F9D12.15 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17212.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17213.t1	gb|ABD65060.1| hypothetical protein 27.t00039 [Brassica oleracea]	181	1367	6.00E−39	755.2	44.8	58.6	hypothetical protein 27.t00039	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00633.1.g17214.t2	gb|EOA34846.1| hypothetical protein CARUB_v10022425mg, partial [Capsella rubella]	595	719	3.00E−99	120.8	35.3	44.7	hypothetical protein CARUB_v10022425mg, partial	gbpln	Capsella rubella	AT5G33406.1 | Symbols: | hAT dimerisation domain-containing protein / transposase-related | chr5:12676126-12678403 REVERSE LENGTH=509	595	509	1.00E−66	85.5	25.7	33.3
Rsa1.0_00633.1.g17215.t1	gb|ABE65508.1| hypothetical protein At4g01240 [Arabidopsis thaliana]	474	478	0	100.8	92.4	95.4	hypothetical protein At4g01240	gbpln	Arabidopsis thaliana	AT4G01240.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:517795-521972 REVERSE LENGTH=659	474	659	0	139.0	88.0	91.4
Rsa1.0_00634.1.g17216.t1	ref|XP_002883854.1| hypothetical protein ARALYDRAFT_899691 [Arabidopsis lyrata subsp. lyrata] gi|297329694|gb|EFH60113.1| hypothetical protein ARALYDRAFT_899691 [Arabidopsis lyrata subsp. lyrata]	624	627	0	100.5	93.8	95.8	hypothetical protein ARALYDRAFT_899691	gbpln	Arabidopsis lyrata	AT2G14740.2 | Symbols: ATVSR3, VSR3, VSR2;2, BP80-2;2 | vaculolar sorting receptor 3 | chr2:6308895-6312303 FORWARD LENGTH=628	624	628	0	100.6	93.6	95.7
Rsa1.0_00634.1.g17217.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	532	1529	4.00E−67	287.4	25.4	32.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	532	746	2.00E−54	140.2	20.3	27.8
Rsa1.0_00634.1.g17218.t1	ref|XP_002885939.1| basic helix-loop-helix protein [Arabidopsis lyrata subsp. lyrata] gi|297331779|gb|EFH62198.1| basic helix-loop-helix protein [Arabidopsis lyrata subsp. lyrata]	305	328	1.00E−121	107.5	74.4	83.0	basic helix-loop-helix protein	gbpln	Arabidopsis lyrata	AT2G14760.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:6321840-6323312 REVERSE LENGTH=328	305	328	1.00E−118	107.5	74.4	81.3
Rsa1.0_00634.1.g17219.t1	gb|EOA30095.1| hypothetical protein CARUB_v10013204mg [Capsella rubella]	635	631	0	99.4	86.8	93.9	hypothetical protein CARUB_v10013204mg	gbpln	Capsella rubella	AT2G14820.1 | Symbols: NPY2 | Phototropic-responsive NPH3 family protein | chr2:6358864-6361300 FORWARD LENGTH=634	635	634	0	99.8	85.4	92.9
Rsa1.0_00634.1.g17220.t1	gb|EOA31658.1| hypothetical protein CARUB_v10014863mg [Capsella rubella]	271	144	1.00E−39	53.1	28.8	31.4	hypothetical protein CARUB_v10014863mg	gbpln	Capsella rubella	AT2G14830.2 | Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr2:6362524-6363893 FORWARD LENGTH=146	271	146	4.00E−42	53.9	28.8	31.0
Rsa1.0_00634.1.g17221.t1	gb|EOA30958.1| hypothetical protein CARUB_v10014104mg [Capsella rubella]	343	343	0	100.0	91.3	95.6	hypothetical protein CARUB_v10014104mg	gbpln	Capsella rubella	AT2G14835.2 | Symbols: | RING/U-box superfamily protein | chr2:6367238-6370610 FORWARD LENGTH=343	343	343	0	100.0	90.1	95.3
Rsa1.0_00634.1.g17222.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00634.1.g17223.t4	gb|ABS30827.1| myrosinase [Brassica oleracea]	545	546	0	100.2	88.1	93.0	myrosinase	gbpln	Brassica oleracea	AT5G26000.1 | Symbols: TGG1, BGLU38 | thioglucoside glucohydrolase 1 | chr5:9079678-9082347 REVERSE LENGTH=541	545	541	0	99.3	71.4	81.8
Rsa1.0_00634.1.g17224.t1	ref|NP_179091.1| uncharacterized protein [Arabidopsis thaliana] gi|3650027|gb|AAC61282.1| hypothetical protein [Arabidopsis thaliana] gi|17529282|gb|AAL38868.1| unknown protein [Arabidopsis thaliana] gi|20197261|gb|AAM14999.1| hypothetical protein [Arabidopsis thaliana] gi|20465829|gb|AAM20019.1| unknown protein [Arabidopsis thaliana] gi|330251248|gb|AEC06342.1| uncharacterized protein AT2G14850 [Arabidopsis thaliana]	270	291	1.00E−94	107.8	69.3	81.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G14850.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G33890.2); Has 140 Blast hits to 132 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 2; Plants - 133; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr2:6386400-6387275 FORWARD LENGTH=291	270	291	3.00E−97	107.8	69.3	81.9
Rsa1.0_00634.1.g17225.t1	gb|EOA32458.1| hypothetical protein CARUB_v10015735mg [Capsella rubella]	249	256	2.00E−96	102.8	74.3	81.9	hypothetical protein CARUB_v10015735mg	gbpln	Capsella rubella	AT2G14860.1 | Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr2:6387820-6389563 REVERSE LENGTH=252	249	252	1.00E−97	101.2	74.3	80.3
Rsa1.0_00635.1.g17226.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00635.1.g17227.t1	gb|EOA19787.1| hypothetical protein CARUB_v10000034mg [Capsella rubella]	669	1498	1.00E-167	223.9	52.8	58.1	hypothetical protein CARUB_v10000034mg	gbpln	Capsella rubella	AT5G17910.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29620.1). | chr5:5927906-5932292 FORWARD LENGTH=1342	669	1342	1.00E-166	200.6	53.1	60.5
Rsa1.0_00635.1.g17228.t1	gb|EOA15185.1| hypothetical protein CARUB_v10028571mg [Capsella rubella]	214	209	3.00E-87	97.7	81.8	85.0	hypothetical protein CARUB_v10028571mg	gbpln	Capsella rubella	AT5G58250.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: thylakoid, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2488 (InterPro:IPR019616); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:23559558-23560372 FORWARD LENGTH=211	214	211	1.00E-84	98.6	77.6	80.8
Rsa1.0_00635.1.g17229.t1	gb|AAO24535.1| At5g58240 [Arabidopsis thaliana] gi|110736300|dbj|BAF00120.1| bis(5'-adenosyl)-triphosphatase-like [Arabidopsis thaliana]	159	180	3.00E-85	113.2	93.1	98.1	At5g58240	gbpln	Arabidopsis thaliana	AT5G58240.1 | Symbols: FHIT | FRAGILE HISTIDINE TRIAD | chr5:23558349-23559313 REVERSE LENGTH=180	159	180	4.00E-87	113.2	92.5	97.5
Rsa1.0_00635.1.g17230.t1	ref|XP_002864557.1| hypothetical protein ARALYDRAFT_495932 [Arabidopsis lyrata subsp. lyrata] gi|297310392|gb|EFH40816.1| hypothetical protein ARALYDRAFT_495932 [Arabidopsis lyrata subsp. lyrata]	428	426	0	99.5	83.6	92.8	hypothetical protein ARALYDRAFT_495932	gbpln	Arabidopsis lyrata	AT5G58230.1 | Symbols: MSI1, MEE70, ATMSI1 | Transducin/WD40 repeat-like superfamily protein | chr5:23556112-23557994 FORWARD LENGTH=424	428	424	0	99.1	83.4	92.5
Rsa1.0_00635.1.g17231.t1	gb|EOA12800.1| hypothetical protein CARUB_v10025755mg [Capsella rubella]	1276	1252	0	98.1	75.6	81.8	hypothetical protein CARUB_v10025755mg	gbpln	Capsella rubella	AT5G58160.1 | Symbols: | actin binding | chr5:23533724-23539465 FORWARD LENGTH=1324	1276	1324	0	103.8	75.5	81.7
Rsa1.0_00635.1.g17232.t1	ref|NP_851210.1| phototropin 2 [Arabidopsis thaliana] gi|30697010|ref|NP_851211.1| phototropin 2 [Arabidopsis thaliana] gi|82593023|sp|P93025.2|PHOT2_ARATH RecName: Full=Phototropin-2; AltName: Full=Defective in chloroplast avoidance protein 1; AltName: Full=Non-phototropic hypocotyl 1-like protein 1; Short=AtKin7; Short=NPH1-like protein 1 gi|5391442|gb|AAC27293.2| non phototropic hypocotyl 1-like [Arabidopsis thaliana] gi|10176790|dbj|BAB09904.1| unnamed protein product [Arabidopsis thaliana] gi|332009619|gb|AED97002.1| phototropin 2 [Arabidopsis thaliana] gi|332009621|gb|AED97004.1| phototropin 2 [Arabidopsis thaliana]	118	915	2.00E-58	775.4	94.1	94.9	phototropin 2	gbpln	Arabidopsis thaliana	AT5G58140.1 | Symbols: PHOT2, NPL1 | phototropin 2 | chr5:23524771-23529993 FORWARD LENGTH=915	118	915	4.00E-61	775.4	94.1	94.9
Rsa1.0_00635.1.g17233.t1	dbj|BAB08861.1| unnamed protein product [Arabidopsis thaliana]	164	166	4.00E-54	101.2	73.8	86.0	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G57910.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G30630.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:23451259-23452463 REVERSE LENGTH=207	164	207	3.00E-56	126.2	73.8	86.0

Rsa1.0_00635.1.g17234.t1	ref|NP_568870.1| F-box protein SKIP1 [Arabidopsis thaliana] gi|75333679|sp|Q9FDX1.1|SKIP1_ARATH RecName: Full=F-box protein SKIP1; AltName: Full=SKP1-interacting partner 1 gi|9758359|dbj|BAB08860.1| unnamed protein product [Arabidopsis thaliana] gi|10716947|gb|AAG21976.1| SKP1 interacting partner 1 [Arabidopsis thaliana] gi|109946489|gb|ABG48423.1| At5g57900 [Arabidopsis thaliana] gi|110738798|dbj|BAF01322.1| hypothetical protein [Arabidopsis thaliana] gi|332009586|gb|AED96969.1| F-box protein SKIP1 [Arabidopsis thaliana]	303	300	1.00E-147	99.0	85.5	90.1	F-box protein SKIP1	gbpln	Arabidopsis thaliana	AT5G57900.1 | Symbols: SKIP1 | SKP1 interacting partner 1 | chr5:23449916-23450915 REVERSE LENGTH=300	303	300	1.00E-150	99.0	85.5	90.1
Rsa1.0_00635.1.g17235.t1	ref|XP_002864534.1| hypothetical protein ARALYDRAFT_918971 [Arabidopsis lyrata subsp. lyrata] gi|297310369|gb|EFH40793.1| hypothetical protein ARALYDRAFT_918971 [Arabidopsis lyrata subsp. lyrata]	436	388	1.00E-140	89.0	62.8	67.7	hypothetical protein ARALYDRAFT_918971	gbpln	Arabidopsis lyrata	AT5G57880.1 | Symbols: MPS1, ATPRD2, PRD2 | multipolar spindle 1 | chr5:23443977-23446439 FORWARD LENGTH=385	436	385	1.00E-143	88.3	65.4	69.5
Rsa1.0_00635.1.g17236.t1	ref|NP_200591.2| uncharacterized protein [Arabidopsis thaliana] gi|332009574|gb|AED96957.1| uncharacterized protein AT5G57830 [Arabidopsis thaliana]	370	387	1.00E-150	104.6	81.9	90.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G57830.1 | Symbols: | Protein of unknown function, DUF593 | chr5:23429406-23430860 REVERSE LENGTH=387	370	387	1.00E-153	104.6	81.9	90.0
Rsa1.0_00635.1.g17237.t1	gb|EOA15016.1| hypothetical protein CARUB_v10028373mg [Capsella rubella]	148	154	4.00E-38	104.1	60.1	72.3	hypothetical protein CARUB_v10028373mg	gbpln	Capsella rubella	AT5G57820.1 | Symbols: | zinc ion binding | chr5:23428601-23429165 FORWARD LENGTH=161	148	161	1.00E-37	108.8	56.1	73.0
Rsa1.0_00635.1.g17238.t1	ref|NP_568866.1| tetraspanin15 [Arabidopsis thaliana] gi|122180030|sp|Q1PDI1.1|TET15_ARATH RecName: Full=Tetraspanin-15 gi|91807060|gb|ABE66257.1| senescence-associated protein-like protein [Arabidopsis thaliana] gi|332009571|gb|AED96954.1| tetraspanin15 [Arabidopsis thaliana]	316	317	1.00E-138	100.3	83.9	91.1	tetraspanin15	gbpln	Arabidopsis thaliana	AT5G57810.1 | Symbols: TET15 | tetraspanin15 | chr5:23424466-23425589 REVERSE LENGTH=317	316	317	1.00E-140	100.3	83.9	91.1
Rsa1.0_00635.1.g17239.t1	dbj|BAJ33654.1| unnamed protein product [Thellungiella halophila]	647	631	0	97.5	86.6	91.7	unnamed protein product	----	----	AT5G57800.1 | Symbols: FLP1, YRE, CER3, WAX2 | Fatty acid hydroxylase superfamily | chr5:23420589-23423832 FORWARD LENGTH=632	647	632	0	97.7	85.3	91.0
Rsa1.0_00635.1.g17240.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	639	1501	0	234.9	52.6	62.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	639	1262	1.00E-138	197.5	34.7	49.1
Rsa1.0_00635.1.g17241.t2	gb|EOA20295.1| hypothetical protein CARUB_v10000603mg [Capsella rubella]	132	559	7.00E-21	423.5	37.1	37.9	hypothetical protein CARUB_v10000603mg	gbpln	Capsella rubella	AT5G08680.1 | Symbols: | ATP synthase alpha/beta family protein | chr5:2821992-2824683 FORWARD LENGTH=559	132	559	6.00E-23	423.5	36.4	37.9
Rsa1.0_00635.1.g17242.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00635.1.g17243.t1	gb|AAD26953.1| putative non-LTR retrolelement reverse transcriptase [Arabidopsis thaliana]	350	323	7.00E-71	92.3	39.7	53.7	putative non-LTR retrolelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	350	332	4.00E-66	94.9	35.7	49.4
Rsa1.0_00635.1.g17244.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00635.1.g17245.t1	ref|XP_002866229.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312064|gb|EFH42488.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	164	173	4.00E-67	105.5	76.8	87.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G57780.1 | Symbols: | EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: sequence-specific DNA binding transcription factors (TAIR:AT4G30410.1); Has 123 Blast hits to 123 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 123; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:23405505-23406008 REVERSE LENGTH=167	164	167	1.00E-68	101.8	75.6	86.6

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<tr><td>Rsa1.0_00636.1.g17247.t1</td><td>ref|NP_683519.2| protein kinase domain-containing protein [Arabidopsis thaliana] gi|195546964|gb|ACG49252.1| At3g01085 [Arabidopsis thaliana] gi|332640085|gb|AEE73606.1| protein kinase domain-containing protein [Arabidopsis thaliana]</td><td>631</td><td>629</td><td>0</td><td>99.7</td><td>89.2</td><td>92.7</td><td>protein kinase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G01085.1 | Symbols: | Protein kinase superfamily protein | chr3:28060-30556 FORWARD LENGTH=629</td><td>631</td><td>629</td><td>0</td><td>99.7</td><td>89.2</td><td>92.7</td></tr>
<tr><td>Rsa1.0_00636.1.g17248.t1</td><td>ref|NP_186756.1| early nodulin-like protein 16 [Arabidopsis thaliana] gi|6714481|gb|AAF26167.1|AC008261_24 putative lamin [Arabidopsis thaliana] gi|62319463|dbj|BAD94832.1| lamin -like predicted GPI-anchored protein [Arabidopsis thaliana] gi|194708794|gb|ACF88481.1| At3g01070 [Arabidopsis thaliana] gi|332640083|gb|AEE73604.1| early nodulin-like protein 16 [Arabidopsis thaliana]</td><td>176</td><td>167</td><td>4.00E-61</td><td>94.9</td><td>77.3</td><td>83.5</td><td>early nodulin-like protein 16</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G01070.1 | Symbols: ENODL16, AtENODL16 | early nodulin-like protein 16 | chr3:19659-20444 FORWARD LENGTH=167</td><td>176</td><td>167</td><td>2.00E-63</td><td>94.9</td><td>77.3</td><td>83.5</td></tr>
<tr><td>Rsa1.0_00636.1.g17249.t1</td><td>gb|ABC41272.1| unknown [Brassica rapa]</td><td>444</td><td>453</td><td>0</td><td>102.0</td><td>96.4</td><td>98.9</td><td>unknown</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G01060.1 | Symbols: | unknown protein; Has 640 Blast hits to 638 proteins in 201 species: Archae - 0; Bacteria - 293; Metazoa - 0; Fungi - 71; Plants - 72; Viruses - 0; Other Eukaryotes - 204 (source: NCBI BLink). | chr3:16831-18782 REVERSE LENGTH=455</td><td>444</td><td>455</td><td>0</td><td>102.5</td><td>90.5</td><td>95.7</td></tr>
<tr><td>Rsa1.0_00636.1.g17250.t1</td><td>ref|NP_186857.1| 40S ribosomal protein S19-1 [Arabidopsis thaliana] gi|27923843|sp|Q9SGA6.1|RS191_ARATH RecName: Full=40S ribosomal protein S19-1 gi|6513924|gb|AAF14828.1|AC011664_10 putative 40S ribosomal protein S19 [Arabidopsis thaliana] gi|13878029|gb|AAK44092.1|AF370277_1 putative 40S ribosomal protein S19 [Arabidopsis thaliana] gi|17104595|gb|AAL34186.1| putative 40S ribosomal protein S19 [Arabidopsis thaliana] gi|21593712|gb|AAM65679.1| putative 40S ribosomal protein S19 [Arabidopsis thaliana] gi|332640239|gb|AEE73760.1| 40S ribosomal protein S19-1 [Arabidopsis thaliana] gi|482567473|gb|EOA31662.1| hypothetical protein CARUB_v10014866mg [Capsella rubella]</td><td>143</td><td>143</td><td>7.00E-77</td><td>100.0</td><td>97.9</td><td>99.3</td><td>40S ribosomal protein S19-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G02080.1 | Symbols: | Ribosomal protein S19e family protein | chr3:364138-365161 REVERSE LENGTH=143</td><td>143</td><td>143</td><td>2.00E-79</td><td>100.0</td><td>97.9</td><td>99.3</td></tr>
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<tr><td>Rsa1.0_00636.1.g17251.t1</td><td>ref|NP_186858.1| mitochondrial processing peptidase [Arabidopsis thaliana] gi|85700445|sp|Q42290.2|MPPB_ARATH RecName: Full=Probable mitochondrial-processing peptidase subunit beta; AltName: Full=Beta-MPP; Flags: Precursor gi|6513923|gb|AAF14827.1|AC011664_9 putative mitochondrial processing peptidase [Arabidopsis thaliana] gi|22022518|gb|AAM83217.1| AT3g02090/F1C9_12 [Arabidopsis thaliana] gi|23397047|gb|AAN31809.1| putative mitochondrial processing peptidase [Arabidopsis thaliana] gi|23463071|gb|AAN33205.1| At3g02090/F1C9_12 [Arabidopsis thaliana] gi|25054848|gb|AAN71914.1| putative mitochondrial processing peptidase [Arabidopsis thaliana] gi|332640240|gb|AEE73761.1| probable mitochondrial-processing peptidase subunit beta [Arabidopsis thaliana]</td><td>527</td><td>531</td><td>0</td><td>100.8</td><td>92.4</td><td>96.4</td><td>mitochondrial processing peptidase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G02090.1 | Symbols: MPPBETA | Insulinase (Peptidase family M16) protein | chr3:365624-368526 FORWARD LENGTH=531</td><td>527</td><td>531</td><td>0</td><td>100.8</td><td>92.4</td><td>96.4</td></tr>
<tr><td>Rsa1.0_00636.1.g17252.t1</td><td>gb|AAM64731.1| nitrilase associated protein-like [Arabidopsis thaliana]</td><td>103</td><td>127</td><td>1.00E-10</td><td>123.3</td><td>68.9</td><td>76.7</td><td>nitrilase associated protein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G15600.1 | Symbols: SP1L4 | SPIRAL1-like4 | chr5:5078405-5078863 FORWARD LENGTH=127</td><td>103</td><td>127</td><td>4.00E-13</td><td>123.3</td><td>68.9</td><td>76.7</td></tr>
<tr><td>Rsa1.0_00636.1.g17253.t1</td><td>gb|EOA29756.1| hypothetical protein CARUB_v10012845mg [Capsella rubella]</td><td>1519</td><td>1155</td><td>0</td><td>76.0</td><td>66.6</td><td>70.2</td><td>hypothetical protein CARUB_v10012845mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G02130.1 | Symbols: RPK2, TOAD2, CLI1 | receptor-like protein kinase 2 | chr3:380726-384181 FORWARD LENGTH=1151</td><td>1519</td><td>1151</td><td>0</td><td>75.8</td><td>66.2</td><td>70.4</td></tr>
<tr><td>Rsa1.0_00636.1.g17254.t1</td><td>ref|XP_002884309.1| hypothetical protein ARALYDRAFT_477457 [Arabidopsis lyrata subsp. lyrata] gi|297330149|gb|EFH60568.1| hypothetical protein ARALYDRAFT_477457 [Arabidopsis lyrata subsp. lyrata]</td><td>129</td><td>227</td><td>3.00E-32</td><td>176.0</td><td>55.0</td><td>61.2</td><td>hypothetical protein ARALYDRAFT_477457</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G02220.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2039 (InterPro:IPR019351); Has 215 Blast hits to 215 proteins in 94 species: Archae - 2; Bacteria - 2; Metazoa - 125; Fungi - 4; Plants - 38; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink). | chr3:412210-413536 REVERSE LENGTH=227</td><td>129</td><td>227</td><td>3.00E-31</td><td>176.0</td><td>51.9</td><td>58.9</td></tr>
<tr><td>Rsa1.0_00636.1.g17255.t2</td><td>ref|XP_002316078.1| predicted protein [Populus trichocarpa] gi|222865118|gb|EEF02249.1| predicted protein [Populus trichocarpa]</td><td>416</td><td>358</td><td>1.00E-171</td><td>86.1</td><td>71.6</td><td>77.2</td><td>predicted protein</td><td>gbpln</td><td>Populus trichocarpa</td><td>AT3G02230.1 | Symbols: RGP1, ATRGP1 | reversibly glycosylated polypeptide 1 | chr3:415463-417304 FORWARD LENGTH=357</td><td>416</td><td>357</td><td>1.00E-171</td><td>85.8</td><td>74.3</td><td>77.4</td></tr>
<tr><td>Rsa1.0_00636.1.g17256.t1</td><td>ref|XP_002884311.1| hypothetical protein ARALYDRAFT_896190 [Arabidopsis lyrata subsp. lyrata] gi|297330151|gb|EFH60570.1| hypothetical protein ARALYDRAFT_896190 [Arabidopsis lyrata subsp. lyrata]</td><td>523</td><td>513</td><td>0</td><td>98.1</td><td>91.2</td><td>96.4</td><td>hypothetical protein ARALYDRAFT_896190</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G02250.1 | Symbols: | O-fucosyltransferase family protein | chr3:424185-426376 REVERSE LENGTH=512</td><td>523</td><td>512</td><td>0</td><td>97.9</td><td>91.0</td><td>95.4</td></tr>
<tr><td>Rsa1.0_00636.1.g17257.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00636.1.g17258.t8</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00636.1.g17259.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00636.1.g17260.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT3G02300.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:461551-463929 FORWARD LENGTH=471</td><td>84</td><td>471</td><td>1.00E-11</td><td>560.7</td><td>34.5</td><td>44.0</td></tr>
<tr><td>Rsa1.0_00636.1.g17261.t1</td><td>ref|XP_002884314.1| SEPALLATA2 [Arabidopsis lyrata subsp. lyrata] gi|297330154|gb|EFH60573.1| SEPALLATA2 [Arabidopsis lyrata subsp. lyrata]</td><td>253</td><td>250</td><td>1.00E-133</td><td>98.8</td><td>94.1</td><td>96.4</td><td>SEPALLATA2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G02310.1 | Symbols: SEP2, AGL4 | K-box region and MADS-box transcription factor family protein | chr3:464554-466687 REVERSE LENGTH=250</td><td>253</td><td>250</td><td>1.00E-134</td><td>98.8</td><td>92.5</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00636.1.g17262.t1</td><td>ref|XP_002882222.1| RNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297328062|gb|EFH58481.1| RNA binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>573</td><td>589</td><td>0</td><td>102.8</td><td>90.6</td><td>95.3</td><td>RNA binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G02320.1 | Symbols: | N2,N2-dimethylguanosine tRNA methyltransferase | chr3:470097-473492 FORWARD LENGTH=589</td><td>573</td><td>589</td><td>0</td><td>102.8</td><td>89.5</td><td>94.6</td></tr>
<tr><td>Rsa1.0_00636.1.g17263.t1</td><td>ref|NP_186882.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546764|sp|Q9FWA6.2|PP207_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g02330 gi|332640272|gb|AEE73793.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]</td><td>892</td><td>903</td><td>0</td><td>101.2</td><td>87.7</td><td>93.7</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G02330.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:473881-476592 REVERSE LENGTH=903</td><td>892</td><td>903</td><td>0</td><td>101.2</td><td>87.7</td><td>93.7</td></tr>
</table>

Rsa1.0_00636.1.g17264.t1	ref|XP_002882223.1| hypothetical protein ARALYDRAFT_477467 [Arabidopsis lyrata subsp. lyrata] gi|297328063|gb|EFH58482.1| hypothetical protein ARALYDRAFT_477467 [Arabidopsis lyrata subsp. lyrata]	191	406	2.00E-38	212.6	62.8	72.3	hypothetical protein ARALYDRAFT_477467	gbpln	Arabidopsis lyrata	AT3G02340.1 | Symbols: | RING/U-box superfamily protein | chr3:477032-478261 FORWARD LENGTH=409	191	409	6.00E-30	214.1	59.7	69.1
Rsa1.0_00637.1.g17265.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00637.1.g17266.t1	gb|EOA26378.1| hypothetical protein CARUB_v10023356mg [Capsella rubella]	427	401	0	93.9	87.8	91.6	hypothetical protein CARUB_v10023356mg	gbpln	Capsella rubella	AT2G43710.1 | Symbols: SSI2, FAB2 | Plant stearoyl-acyl-carrier-protein desaturase family protein | chr2:18120107-18122495 FORWARD LENGTH=401	427	401	0	93.9	87.6	90.9
Rsa1.0_00637.1.g17267.t1	ref|NP_181898.1| concanavalin A-like lectin protein kinase-like protein [Arabidopsis thaliana] gi|75318036|sp|O22833.1|LRK54_ARATH RecName: Full=L-type lectin-domain containing receptor kinase V.4; Short=Arabidopsis thaliana lectin-receptor kinase c1; Short=AthlecRK-c1; Short=LecRK-V.4; Flags: Precursor gi|2281100|gb|AAB64036.1| putative receptor protein kinase [Arabidopsis thaliana] gi|18491245|gb|AAL69447.1| At2g43700/F18O19.19 [Arabidopsis thaliana] gi|330255215|gb|AEC10309.1| concanavalin A-like lectin protein kinase-like protein [Arabidopsis thaliana]	652	658	0	100.9	77.6	85.9	concanavalin A-like lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT2G43700.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr2:18116523-18118499 FORWARD LENGTH=658	652	658	0	100.9	77.6	85.9
Rsa1.0_00637.1.g17268.t1	ref|XP_002880061.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325900|gb|EFH56320.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	433	631	1.00E-154	145.7	66.3	76.9	predicted protein	gbpln	Arabidopsis lyrata	AT2G43690.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr2:18112589-18114583 FORWARD LENGTH=664	433	664	1.00E-147	153.3	64.7	76.9
Rsa1.0_00637.1.g17269.t2	ref|XP_002880059.1| hypothetical protein ARALYDRAFT_903766 [Arabidopsis lyrata subsp. lyrata] gi|297325898|gb|EFH56318.1| hypothetical protein ARALYDRAFT_903766 [Arabidopsis lyrata subsp. lyrata]	603	682	0	113.1	73.3	79.9	hypothetical protein ARALYDRAFT_903766	gbpln	Arabidopsis lyrata	AT2G43680.3 | Symbols: IQD14 | IQ-domain 14 | chr2:18109302-18111587 FORWARD LENGTH=668	603	668	0	110.8	72.6	79.4
Rsa1.0_00637.1.g17270.t1	ref|XP_002880057.1| Sas10/U3 ribonucleoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297325896|gb|EFH56316.1| Sas10/U3 ribonucleoprotein family protein [Arabidopsis lyrata subsp. lyrata]	650	662	0	101.8	76.0	84.6	Sas10/U3 ribonucleoprotein family protein	gbpln	Arabidopsis lyrata	AT2G43650.1 | Symbols: EMB2777 | Sas10/U3 ribonucleoprotein (Utp) family protein | chr2:18099430-18103147 FORWARD LENGTH=654	650	654	0	100.6	72.8	82.0
Rsa1.0_00637.1.g17271.t1	ref|XP_002881922.1| signal recognition particle 14 kDa family protein [Arabidopsis lyrata subsp. lyrata] gi|297327761|gb|EFH58181.1| signal recognition particle 14 kDa family protein [Arabidopsis lyrata subsp. lyrata]	126	118	1.00E-49	93.7	86.5	89.7	signal recognition particle 14 kDa family protein	gbpln	Arabidopsis lyrata	AT2G43640.2 | Symbols: | Signal recognition particle, SRP9/SRP14 subunit | chr2:18097614-18098619 REVERSE LENGTH=121	126	121	6.00E-51	96.0	84.9	88.1
Rsa1.0_00637.1.g17272.t1	dbj|BAK48742.1| endochitinase [Brassica rapa subsp. chinensis]	275	278	1.00E-153	101.1	97.5	98.5	endochitinase	gbpln	Brassica rapa	AT2G43620.1 | Symbols: | Chitinase family protein | chr2:18093954-18095025 REVERSE LENGTH=283	275	283	1.00E-141	102.9	86.2	91.3
Rsa1.0_00637.1.g17273.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00637.1.g17274.t2	ref|XP_002881920.1| glycoside hydrolase family 19 protein [Arabidopsis lyrata subsp. lyrata] gi|297327759|gb|EFH58179.1| glycoside hydrolase family 19 protein [Arabidopsis lyrata subsp. lyrata]	269	281	1.00E-148	104.5	95.2	96.7	glycoside hydrolase family 19 protein	gbpln	Arabidopsis lyrata	AT2G43610.1 | Symbols: | Chitinase family protein | chr2:18088058-18089184 REVERSE LENGTH=281	269	281	1.00E-149	104.5	94.1	96.3
Rsa1.0_00637.1.g17275.t1	gb|AAD26943.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1448	1454	0	100.4	67.5	82.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1448	1262	1.00E-172	87.2	20.6	26.6
Rsa1.0_00637.1.g17276.t1	ref|XP_002881919.1| glycoside hydrolase family 19 protein [Arabidopsis lyrata subsp. lyrata] gi|297327758|gb|EFH58178.1| glycoside hydrolase family 19 protein [Arabidopsis lyrata subsp. lyrata]	183	269	2.00E-93	147.0	89.1	92.9	glycoside hydrolase family 19 protein	gbpln	Arabidopsis lyrata	AT2G43600.1 | Symbols: | Chitinase family protein | chr2:18086049-18087018 REVERSE LENGTH=273	183	273	6.00E-93	149.2	89.6	93.4
Rsa1.0_00637.1.g17277.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00637.1.g17278.t1	gb|EOA26434.1| hypothetical protein CARUB_v10025330mg [Capsella rubella]	280	280	1.00E-110	100.0	66.4	80.4	hypothetical protein CARUB_v10025330mg	gbpln	Capsella rubella	AT2G43600.1 | Symbols: | Chitinase family protein | chr2:18086049-18087018 REVERSE LENGTH=273	280	273	1.00E-109	97.5	65.4	78.9
Rsa1.0_00638.1.g17279.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00638.1.g17280.t1	ref|XP_002876582.1| hypothetical protein ARALYDRAFT_486551 [Arabidopsis lyrata subsp. lyrata] gi|297322420|gb|EFH52841.1| hypothetical protein ARALYDRAFT_486551 [Arabidopsis lyrata subsp. lyrata]	463	494	1.00E-103	106.7	46.7	60.9	hypothetical protein ARALYDRAFT_486551	gbpln	Arabidopsis lyrata	AT3G60790.1 | Symbols: | F-box family protein | chr3:22464623-22466948 FORWARD LENGTH=488	463	488	4.00E-95	105.4	44.3	57.7
Rsa1.0_00638.1.g17281.t1	gb|EOA24450.1| hypothetical protein CARUB_v10017708mg [Capsella rubella]	304	306	1.00E-157	100.7	92.4	96.7	hypothetical protein CARUB_v10017708mg	gbpln	Capsella rubella	AT3G60800.1 | Symbols: | DHHC-type zinc finger family protein | chr3:22467486-22469273 REVERSE LENGTH=307	304	307	1.00E-156	101.0	91.1	94.7
Rsa1.0_00638.1.g17282.t1	emb|CAA47753.1| proteosome subunit [Arabidopsis thaliana]	223	230	1.00E-123	103.1	94.6	97.3	proteosome subunit	gbpln	Arabidopsis thaliana	AT3G60820.3 | Symbols: PBF1 | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:22472038-22473809 REVERSE LENGTH=223	223	223	1.00E-125	100.0	94.6	97.3
Rsa1.0_00638.1.g17283.t1	emb|CAB82687.1| actin-like protein [Arabidopsis thaliana]	198	368	1.00E-98	185.9	87.9	92.9	actin-like protein	gbpln	Arabidopsis thaliana	AT3G60830.1 | Symbols: ATARP7, ARP7 | actin-related protein 7 | chr3:22474298-22476000 FORWARD LENGTH=363	198	363	4.00E-96	183.3	86.9	90.4
Rsa1.0_00638.1.g17284.t1	sp|Q9LZY0.2|MA654_ARATH RecName: Full=65-kDa microtubule-associated protein 4; Short=AtMAP65-4	681	677	0	99.4	83.6	90.7	RecName: Full=65-kDa microtubule-associated protein 4; Short=AtMAP65-4	----	----	AT3G60840.1 | Symbols: MAP65-4 | microtubule-associated protein 65-4 | chr3:22477573-22480463 REVERSE LENGTH=648	681	648	0	95.2	79.6	86.5
Rsa1.0_00638.1.g17285.t1	gb|EOA22050.1| hypothetical protein CARUB_v10002590mg, partial [Capsella rubella]	223	254	2.00E-39	113.9	33.6	49.3	hypothetical protein CARUB_v10002590mg, partial	gbpln	Capsella rubella	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	223	575	3.00E-39	257.8	33.6	48.0
Rsa1.0_00638.1.g17286.t3	ref|XP_002874898.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297320735|gb|EFH51157.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	224	327	1.00E-44	146.0	39.7	43.3	transducin family protein	gbpln	Arabidopsis lyrata	AT4G02730.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:1207759-1209066 FORWARD LENGTH=333	224	333	2.00E-46	148.7	38.8	43.3
Rsa1.0_00638.1.g17287.t3	ref|XP_002876588.1| dihydrodipicolinate synthase 1 [Arabidopsis lyrata subsp. lyrata] gi|297322426|gb|EFH52847.1| dihydrodipicolinate synthase 1 [Arabidopsis lyrata subsp. lyrata]	365	365	0	100.0	90.4	95.9	dihydrodipicolinate synthase 1	gbpln	Arabidopsis lyrata	AT3G60880.2 | Symbols: DHDPS, DHDPS1 | dihydrodipicolinate synthase 1 | chr3:22495086-22496542 FORWARD LENGTH=365	365	365	0	100.0	89.9	95.9
Rsa1.0_00638.1.g17288.t1	ref|NP_001118868.1| protein little zipper 2 [Arabidopsis thaliana] gi|332646602|gb|AEE80123.1| protein little zipper 2 [Arabidopsis thaliana]	93	106	6.00E-31	114.0	79.6	87.1	protein little zipper 2	gbpln	Arabidopsis thaliana	AT3G60890.2 | Symbols: ZPR2 | protein binding | chr3:22497024-22497442 REVERSE LENGTH=106	93	106	1.00E-33	114.0	79.6	87.1
Rsa1.0_00638.1.g17289.t1	ref|XP_002878354.1| hypothetical protein ARALYDRAFT_324535 [Arabidopsis lyrata subsp. lyrata] gi|297324192|gb|EFH54613.1| hypothetical protein ARALYDRAFT_324535 [Arabidopsis lyrata subsp. lyrata]	2620	2860	0	109.2	82.2	88.4	hypothetical protein ARALYDRAFT_324535	gbpln	Arabidopsis lyrata	AT2G45540.1 | Symbols: | WD-40 repeat family protein / beige-related | chr2:18757881-18772229 REVERSE LENGTH=2946	2620	2946	0	112.4	76.7	85.3
Rsa1.0_00638.1.g17290.t1	ref|XP_002882021.1| CYP76C2 [Arabidopsis lyrata subsp. lyrata] gi|297327860|gb|EFH58280.1| CYP76C2 [Arabidopsis lyrata subsp. lyrata]	365	512	1.00E-140	140.3	66.8	81.6	CYP76C2	gbpln	Arabidopsis lyrata	AT2G45570.1 | Symbols: CYP76C2 | cytochrome P450, family 76, subfamily C, polypeptide 2 | chr2:18779935-18781922 REVERSE LENGTH=512	365	512	1.00E-138	140.3	64.4	80.5
Rsa1.0_00638.1.g17291.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00639.1.g17292.t1	ref|NP_181002.1| gibberellin 2-beta-dioxygenase 3 [Arabidopsis thaliana] gi|49035761|sp|O64692.1|G2OX3_ARATH RecName: Full=Gibberellin 2-beta-dioxygenase 3; AltName: Full=GA 2-oxidase 3; AltName: Full=Gibberellin 2-beta-hydroxylase 3; AltName: Full=Gibberellin 2-oxidase 3 gi|4678370|emb|CAB41009.1| GA 2-oxidase [Arabidopsis thaliana] gi|20197080|gb|AAM14908.1| putative gibberellin 2-oxidase [Arabidopsis thaliana] gi|330253895|gb|AEC08989.1| gibberellin 2-beta-dioxygenase 3 [Arabidopsis thaliana]	326	335	1.00E-150	102.8	78.8	87.4	gibberellin 2-beta-dioxygenase 3	gbpln	Arabidopsis thaliana	AT2G34555.1 | Symbols: ATGA2OX3, GA2OX3 | gibberellin 2-oxidase 3 | chr2:14557102-14558682 FORWARD LENGTH=335	326	335	1.00E-153	102.8	78.8	87.4
Rsa1.0_00639.1.g17293.t1	ref|XP_002879501.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297325340|gb|EFH55760.1| binding protein [Arabidopsis lyrata subsp. lyrata]	286	290	1.00E-136	101.4	87.4	93.7	binding protein	gbpln	Arabidopsis lyrata	AT2G34540.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34530.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:14550699-14552037 FORWARD LENGTH=288	286	288	1.00E-134	100.7	82.2	91.6

Rsa1.0_00639.1.g17294.t1	gb|AAC26706.1| hypothetical protein [Arabidopsis thaliana]	261	266	1.00E-110	101.9	76.6	85.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G34530.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34540.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:14549141-14550217 REVERSE LENGTH=282	261	282	1.00E-103	108.0	73.6	82.0
Rsa1.0_00639.1.g17295.t1	ref|XP_002881341.1| hypothetical protein ARALYDRAFT_482413 [Arabidopsis lyrata subsp. lyrata] gi|297327180|gb|EFH57600.1| hypothetical protein ARALYDRAFT_482413 [Arabidopsis lyrata subsp. lyrata]	159	164	2.00E-63	103.1	80.5	86.8	hypothetical protein ARALYDRAFT_482413	gbpln	Arabidopsis lyrata	AT2G34520.1 | Symbols: RPS14 | mitochondrial ribosomal protein S14 | chr2:14548218-14548712 REVERSE LENGTH=164	159	164	3.00E-63	103.1	77.4	85.5
Rsa1.0_00639.1.g17296.t1	ref|NP_180998.1| uncharacterized protein [Arabidopsis thaliana] gi|13272421|gb|AAK17149.1|AF325081_1 unknown protein [Arabidopsis thaliana] gi|3128209|gb|AAC26689.1| unknown protein [Arabidopsis thaliana] gi|330253889|gb|AEC08983.1| uncharacterized protein AT2G34510 [Arabidopsis thaliana]	422	401	0	95.0	85.1	91.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G34510.1 | Symbols: | Protein of unknown function, DUF642 | chr2:14544114-14546732 REVERSE LENGTH=401	422	401	0	95.0	85.1	91.2
Rsa1.0_00639.1.g17297.t1	ref|NP_180997.1| cytochrome P450, family 710, subfamily A [Arabidopsis thaliana] gi|75278303|sp|O64697.1|C7101_ARATH RecName: Full=Cytochrome P450 710A1; AltName: Full=C-22 sterol desaturase gi|3128210|gb|AAC26690.1| putative cytochrome P450 [Arabidopsis thaliana] gi|20197156|gb|AAM14944.1| putative cytochrome P450 [Arabidopsis thaliana] gi|25083451|gb|AAN72080.1| putative cytochrome P450 [Arabidopsis thaliana] gi|34365731|gb|AAQ65177.1| At2g34500 [Arabidopsis thaliana] gi|84468537|dbj|BAE71351.1| CYP710 [Arabidopsis thaliana] gi|330253888|gb|AEC08982.1| cytochrome P450 710A1 [Arabidopsis thaliana]	501	495	0	98.8	85.4	92.2	cytochrome P450, family 710, subfamily A	gbpln	Arabidopsis thaliana	AT2G34500.1 | Symbols: CYP710A1 | cytochrome P450, family 710, subfamily A, polypeptide 1 | chr2:14539712-14541199 REVERSE LENGTH=495	501	495	0	98.8	85.4	92.2
Rsa1.0_00639.1.g17298.t1	ref|NP_180995.1| 60S ribosomal protein L18a-2 [Arabidopsis thaliana] gi|297826909|ref|XP_002881337.1| 60S ribosomal protein L18A [Arabidopsis lyrata subsp. lyrata] gi|21431842|sp|P51418.2|R18A2_ARATH RecName: Full=60S ribosomal protein L18a-2 gi|3128228|gb|AAC26708.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|14596031|gb|AAK68743.1| Unknown protein [Arabidopsis thaliana] gi|20197170|gb|AAM14956.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|21539567|gb|AAM53336.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|23197736|gb|AAN15395.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|30102898|gb|AAP21367.1| At2g34480 [Arabidopsis thaliana] gi|297327176|gb|EFH57596.1| 60S ribosomal protein L18A [Arabidopsis lyrata subsp. lyrata] gi|330253886|gb|AEC08980.1| 60S ribosomal protein L18a-2 [Arabidopsis thaliana]	178	178	1.00E-100	100.0	98.3	100.0	60S ribosomal protein L18a-2	gbpln	Arabidopsis lyrata	AT2G34480.1 | Symbols: | Ribosomal protein L18ae/LX family protein | chr2:14532916-14534161 REVERSE LENGTH=178	178	178	1.00E-102	100.0	98.3	100.0

Rsa1.0_00639.1.g17299.t1	ref|XP_002279938.1| PREDICTED: eukaryotic translation initiation factor 1A-like [Vitis vinifera] gi|225459517|ref|XP_002285844.1| PREDICTED: eukaryotic translation initiation factor 1A [Vitis vinifera] gi|147807310|emb|CAN73005.1| hypothetical protein VITISV_021007 [Vitis vinifera] gi|147821636|emb|CAN70425.1| hypothetical protein VITISV_033730 [Vitis vinifera]	148	145	3.00E-51	98.0	70.9	81.8	PREDICTED: eukaryotic translation initiation factor 1A-like	gbpln	Vitis vinifera	AT2G04520.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr2:1574802-1575239 REVERSE LENGTH=145	148	145	7.00E-49	98.0	68.9	79.7
Rsa1.0_00639.1.g17300.t1	sp|P13851.1|CB21_SINAL RecName: Full=Chlorophyll a-b binding protein 1, chloroplastic; AltName: Full=LHCII type I CAB-1; Short=LHCP; Flags: Precursor gi|21138|emb|CAA34459.1| unnamed protein product [Sinapis alba] gi|21140|emb|CAA33903.1| chlorophyll a/b-binding polypeptide [Sinapis alba]	232	266	1.00E-131	114.7	99.1	100.0	RecName: Full=Chlorophyll a-b binding protein 1, chloroplastic; AltName: Full=LHCII type I CAB-1; Short=LHCP; Flags: Precursor gi|21138|emb|CAA34459.1| unnamed protein product	gbpln	Sinapis alba	AT2G34430.1 | Symbols: LHB1B1, LHCB1.4 | light-harvesting chlorophyll-protein complex II subunit B1 | chr2:14524818-14525618 FORWARD LENGTH=266	232	266	1.00E-131	114.7	97.0	99.1
Rsa1.0_00639.1.g17301.t1	sp|P13851.1|CB21_SINAL RecName: Full=Chlorophyll a-b binding protein 1, chloroplastic; AltName: Full=LHCII type I CAB-1; Short=LHCP; Flags: Precursor gi|21138|emb|CAA34459.1| unnamed protein product [Sinapis alba] gi|21140|emb|CAA33903.1| chlorophyll a/b-binding polypeptide [Sinapis alba]	266	266	1.00E-151	100.0	99.6	99.6	RecName: Full=Chlorophyll a-b binding protein 1, chloroplastic; AltName: Full=LHCII type I CAB-1; Short=LHCP; Flags: Precursor gi|21138|emb|CAA34459.1| unnamed protein product	gbpln	Sinapis alba	AT2G34430.1 | Symbols: LHB1B1, LHCB1.4 | light-harvesting chlorophyll-protein complex II subunit B1 | chr2:14524818-14525618 FORWARD LENGTH=266	266	266	1.00E-149	100.0	96.6	98.1
Rsa1.0_00639.1.g17302.t6	ref|XP_002879496.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325335|gb|EFH55755.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	880	617	0	70.1	55.6	61.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT2G34400.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr2:14516226-14518186 FORWARD LENGTH=621	880	621	0	70.6	54.8	61.7
Rsa1.0_00639.1.g17303.t1	gb|ACD75049.1| aquaporin [Arabidopsis thaliana]	282	282	1.00E-157	100.0	98.2	99.3	aquaporin	gbpln	Arabidopsis thaliana	AT2G34390.1 | Symbols: NIP2;1, NLM4 | NOD26-like intrinsic protein 2;1 | chr2:14514617-14515793 REVERSE LENGTH=288	282	288	1.00E-144	102.1	88.3	95.7
Rsa1.0_00639.1.g17304.t13	ref|NP_174267.4| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|332193002|gb|AEE31123.1| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana]	923	1078	0	116.8	73.3	85.7	Leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT1G29740.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10407379-10412997 REVERSE LENGTH=1078	923	1078	0	116.8	73.3	85.7
Rsa1.0_00639.1.g17305.t1	ref|XP_002879493.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297325332|gb|EFH55752.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	483	473	0	97.9	82.6	90.3	mate efflux family protein	gbpln	Arabidopsis lyrata	AT2G34360.1 | Symbols: | MATE efflux family protein | chr2:14507294-14510231 FORWARD LENGTH=480	483	480	0	99.4	83.9	91.5
Rsa1.0_00639.1.g17306.t2	gb|EOA26471.1| hypothetical protein CARUB_v10022520mg [Capsella rubella]	1402	1281	0	91.4	76.3	82.5	hypothetical protein CARUB_v10022520mg	gbpln	Capsella rubella	AT2G34357.1 | Symbols: | ARM repeat superfamily protein | chr2:14499236-14505555 FORWARD LENGTH=1280	1402	1280	0	91.3	76.9	82.5
Rsa1.0_00639.1.g17307.t1	ref|XP_002881332.1| hypothetical protein ARALYDRAFT_482377 [Arabidopsis lyrata subsp. lyrata] gi|297327171|gb|EFH57591.1| hypothetical protein ARALYDRAFT_482377 [Arabidopsis lyrata subsp. lyrata]	134	134	5.00E-41	100.0	68.7	82.1	hypothetical protein ARALYDRAFT_482377	gbpln	Arabidopsis lyrata	AT2G34340.1 | Symbols: | Protein of unknown function, DUF584 | chr2:14489032-14489442 REVERSE LENGTH=136	134	136	3.00E-38	101.5	67.2	78.4
Rsa1.0_00640.1.g17308.t1	gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]	165	543	3.00E-20	329.1	28.5	41.8	hypothetical protein CARUB_v10015730mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	165	566	5.00E-15	343.0	20.6	40.0
Rsa1.0_00640.1.g17309.t1	gb|EOA16073.1| hypothetical protein CARUB_v10004206mg [Capsella rubella]	728	763	0	104.8	44.6	51.6	hypothetical protein CARUB_v10004206mg	gbpln	Capsella rubella	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	728	331	4.00E-75	45.5	19.4	26.5
Rsa1.0_00640.1.g17310.t1	ref|XP_003617633.1| hypothetical protein MTR_5g093740 [Medicago truncatula] gi|355518968|gb|AET00592.1| hypothetical protein MTR_5g093740 [Medicago truncatula]	414	525	8.00E-86	126.8	41.8	58.5	hypothetical protein MTR_5g093740	gbpln	Medicago truncatula	AT5G56060.1 | Symbols: | Domain of unknown function (DUF2431) | chr5:22704008-22704892 FORWARD LENGTH=220	414	220	2.00E-62	53.1	28.3	34.1
Rsa1.0_00640.1.g17311.t1	gb|AFH08366.1| nicotianamine synthase 2 [Arabidopsis halleri subsp. halleri]	320	320	1.00E-174	100.0	91.3	97.2	nicotianamine synthase 2	gbpln	Arabidopsis halleri	AT5G56080.1 | Symbols: ATNAS2, NAS2 | nicotianamine synthase 2 | chr5:22711402-22712364 REVERSE LENGTH=320	320	320	1.00E-175	100.0	90.3	96.9

Rsa1.0_00640.1.g17312.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00640.1.g17313.t1	ref|XP_002864430.1| hypothetical protein ARALYDRAFT_918751 [Arabidopsis lyrata subsp. lyrata] gi|297310265|gb|EFH40689.1| hypothetical protein ARALYDRAFT_918751 [Arabidopsis lyrata subsp. lyrata]	145	143	4.00E-43	98.6	70.3	75.9	hypothetical protein ARALYDRAFT_918751	gbpln	Arabidopsis lyrata	AT5G56100.1 | Symbols: | glycine-rich protein / oleosin | chr5:22717121-22717573 FORWARD LENGTH=150	145	150	1.00E-44	103.4	70.3	77.2
Rsa1.0_00640.1.g17314.t1	ref|NP_200422.1| myb domain protein 103 [Arabidopsis thaliana] gi|5163509|gb|AAD40692.1|AF048839_1 Atmyb103 [Arabidopsis thaliana] gi|9758631|dbj|BAB09293.1| Atmyb103 [Arabidopsis thaliana] gi|41619468|gb|AAS10109.1| MYB transcription factor [Arabidopsis thaliana] gi|225879122|dbj|BAH30631.1| hypothetical protein [Arabidopsis thaliana] gi|332009339|gb|AED96722.1| myb domain protein 103 [Arabidopsis thaliana]	326	320	1.00E-147	98.2	90.8	95.1	myb domain protein 103	gbpln	Arabidopsis thaliana	AT5G56110.1 | Symbols: AtMYB103, ATMYB80, MYB103, MS188 | myb domain protein 103 | chr5:22719191-22720664 FORWARD LENGTH=320	326	320	1.00E-149	98.2	90.8	95.1
Rsa1.0_00640.1.g17315.t1	ref|XP_002274367.1| PREDICTED: ubiquitin-conjugating enzyme E2-17 kDa isoform 2 [Vitis vinifera] gi|225462033|ref|XP_002274335.1| PREDICTED: ubiquitin-conjugating enzyme E2-17 kDa isoform 1 [Vitis vinifera] gi|359494225|ref|XP_003634740.1| PREDICTED: ubiquitin-conjugating enzyme E2-17 kDa [Vitis vinifera] gi|147771931|emb|CAN77946.1| hypothetical protein VITISV_029275 [Vitis vinifera] gi|296089984|emb|CBI39803.3| unnamed protein product [Vitis vinifera]	331	148	3.00E-73	44.7	39.6	41.7	PREDICTED: ubiquitin-conjugating enzyme E2-17 kDa isoform 2	gbpln	Vitis vinifera	AT5G56150.2 | Symbols: UBC30 | ubiquitin-conjugating enzyme 30 | chr5:22729756-22730964 FORWARD LENGTH=148	331	148	1.00E-73	44.7	38.1	40.8
Rsa1.0_00640.1.g17316.t1	ref|NP_200428.1| LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 [Arabidopsis thaliana] gi|9758637|dbj|BAB09299.1| unnamed protein product [Arabidopsis thaliana] gi|23306374|gb|AAN17414.1| putative protein [Arabidopsis thaliana] gi|24899659|gb|AAN65044.1| putative protein [Arabidopsis thaliana] gi|332009346|gb|AED96729.1| LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 [Arabidopsis thaliana]	111	168	3.00E-42	151.4	71.2	91.0	LORELEI-LIKE-GPI-ANCHORED PROTEIN 1	gbpln	Arabidopsis thaliana	AT5G56170.1 | Symbols: LLG1 | LORELEI-LIKE-GPI-ANCHORED PROTEIN 1 | chr5:22736072-22737108 FORWARD LENGTH=168	111	168	5.00E-45	151.4	71.2	91.0
Rsa1.0_00640.1.g17317.t1	gb|EOA12511.1| hypothetical protein CARUB_v10026334mg [Capsella rubella]	469	473	0	100.9	88.9	94.9	hypothetical protein CARUB_v10026334mg	gbpln	Capsella rubella	AT5G56180.1 | Symbols: ATARP8, ARP8 | actin-related protein 8 | chr5:22737539-22740986 REVERSE LENGTH=471	469	471	0	100.4	89.6	95.1
Rsa1.0_00640.1.g17318.t1	gb|EOA13366.1| hypothetical protein CARUB_v10026403mg [Capsella rubella]	644	444	0	68.9	62.3	64.4	hypothetical protein CARUB_v10026403mg	gbpln	Capsella rubella	AT5G56190.2 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:22742654-22744909 FORWARD LENGTH=447	644	447	0	69.4	61.0	64.1
Rsa1.0_00640.1.g17319.t1	ref|NP_200431.1| C2H2 type zinc finger transcription factor-like protein [Arabidopsis thaliana] gi|9758747|dbj|BAB09111.1| unnamed protein product [Arabidopsis thaliana] gi|225879124|dbj|BAH30632.1| hypothetical protein [Arabidopsis thaliana] gi|332009351|gb|AED96734.1| C2H2 type zinc finger transcription factor-like protein [Arabidopsis thaliana]	464	493	1.00E-117	106.3	66.4	74.8	C2H2 type zinc finger transcription factor-like protein	gbpln	Arabidopsis thaliana	AT5G56200.1 | Symbols: | C2H2 type zinc finger transcription factor family | chr5:22747768-22749249 FORWARD LENGTH=493	464	493	1.00E-120	106.3	66.4	74.8
Rsa1.0_00640.1.g17320.t1	ref|XP_002866132.1| hypothetical protein ARALYDRAFT_495713 [Arabidopsis lyrata subsp. lyrata] gi|297311967|gb|EFH42391.1| hypothetical protein ARALYDRAFT_495713 [Arabidopsis lyrata subsp. lyrata]	896	993	0	110.8	67.7	76.0	hypothetical protein ARALYDRAFT_495713	gbpln	Arabidopsis lyrata	AT5G56240.2 | Symbols: | INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hapless 8 (TAIR:AT5G56250.1). | chr5:22760088-22763539 REVERSE LENGTH=987	896	987	0	110.2	67.0	76.1
Rsa1.0_00640.1.g17321.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00641.1.g17322.t1	ref|XP_002885750.1| hypothetical protein ARALYDRAFT_342773 [Arabidopsis lyrata subsp. lyrata] gi|297331590|gb|EFH62009.1| hypothetical protein ARALYDRAFT_342773 [Arabidopsis lyrata subsp. lyrata]	449	453	0	100.9	94.2	96.7	hypothetical protein ARALYDRAFT_342773	gbpln	Arabidopsis lyrata	AT2G04305.1 | Symbols: | Magnesium transporter CorA-like family protein | chr2:1501679-1503448 REVERSE LENGTH=434	449	434	0	96.7	88.2	91.8

<table>
<tr><td>Rsa1.0_00641.1.g17323.t2</td><td>gb|AAF79797.1|AC020646_20 T32E20.30 [Arabidopsis thaliana]</td><td>718</td><td>1397</td><td>2.00E-40</td><td>194.6</td><td>14.5</td><td>20.5</td><td>T32E20.30</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00641.1.g17324.t1</td><td>ref|XP_002877500.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323338|gb|EFH53759.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>187</td><td>136</td><td>3.00E-31</td><td>72.7</td><td>34.2</td><td>46.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295</td><td>187</td><td>295</td><td>5.00E-19</td><td>157.8</td><td>36.4</td><td>52.9</td></tr>
<tr><td>Rsa1.0_00641.1.g17325.t1</td><td>sp|Q9M462.1|GLGS_BRANA RecName: Full=Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose synthase; AltName: Full=AGPase B; AltName: Full=Alpha-D-glucose-1-phosphate adenyl transferase; Flags: Precursor gi|7688095|emb|CAB89863.1| ADP-glucose pyrophosphorylase small subunit [Brassica napus]</td><td>519</td><td>520</td><td>0</td><td>100.2</td><td>98.5</td><td>98.5</td><td>RecName: Full=Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose synthase; AltName: Full=AGPase B; AltName: Full=Alpha-D-glucose-1-phosphate adenyl transferase; Flags: Precursor gi|7688095|emb|CAB89863.1| ADP-glucose pyrophosphorylase small subunit</td><td>gbpln</td><td>Brassica napus</td><td>AT5G48300.1 | Symbols: ADG1, APS1 | ADP glucose pyrophosphorylase 1 | chr5:19570326-19572557 FORWARD LENGTH=520</td><td>519</td><td>520</td><td>0</td><td>100.2</td><td>87.5</td><td>93.8</td></tr>
<tr><td>Rsa1.0_00641.1.g17326.t1</td><td>gb|ACG60669.1| copia-type polyprotein-like protein [Brassica oleracea var. alboglabra]</td><td>118</td><td>196</td><td>5.00E-36</td><td>166.1</td><td>64.4</td><td>69.5</td><td>copia-type polyprotein-like protein</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00641.1.g17327.t1</td><td>ref|XP_002883731.1| hypothetical protein ARALYDRAFT_899405 [Arabidopsis lyrata subsp. lyrata] gi|297329571|gb|EFH59990.1| hypothetical protein ARALYDRAFT_899405 [Arabidopsis lyrata subsp. lyrata]</td><td>375</td><td>393</td><td>2.00E-55</td><td>104.8</td><td>39.5</td><td>50.7</td><td>hypothetical protein ARALYDRAFT_899405</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G06020.1 | Symbols: | Homeodomain-like superfamily protein | chr2:2342535-2346207 FORWARD LENGTH=301</td><td>375</td><td>301</td><td>2.00E-34</td><td>80.3</td><td>23.2</td><td>25.9</td></tr>
<tr><td>Rsa1.0_00641.1.g17328.t1</td><td>ref|XP_002885736.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297331576|gb|EFH61995.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]</td><td>483</td><td>483</td><td>0</td><td>100.0</td><td>84.5</td><td>91.1</td><td>mate efflux family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G04100.1 | Symbols: | MATE efflux family protein | chr2:1377020-1379051 REVERSE LENGTH=483</td><td>483</td><td>483</td><td>0</td><td>100.0</td><td>83.9</td><td>90.7</td></tr>
<tr><td>Rsa1.0_00641.1.g17329.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00641.1.g17330.t2</td><td>gb|EOA30054.1| hypothetical protein CARUB_v10013160mg [Capsella rubella]</td><td>181</td><td>660</td><td>4.00E-15</td><td>364.6</td><td>22.1</td><td>23.2</td><td>hypothetical protein CARUB_v10013160mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G14400.1 | Symbols: UBP25 | ubiquitin-specific protease 25 | chr3:4811953-4815210 REVERSE LENGTH=661</td><td>181</td><td>661</td><td>3.00E-17</td><td>365.2</td><td>22.1</td><td>23.2</td></tr>
<tr><td>Rsa1.0_00641.1.g17331.t1</td><td>gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]</td><td>316</td><td>527</td><td>4.00E-43</td><td>166.8</td><td>37.7</td><td>45.6</td><td>hypothetical protein CARUB_v10022820mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735</td><td>316</td><td>735</td><td>3.00E-12</td><td>232.6</td><td>10.4</td><td>13.0</td></tr>
<tr><td>Rsa1.0_00641.1.g17332.t3</td><td>pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)</td><td>1170</td><td>1365</td><td>0</td><td>116.7</td><td>43.4</td><td>60.3</td><td>RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)</td><td>----</td><td>----</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1170</td><td>575</td><td>8.00E-68</td><td>49.1</td><td>13.6</td><td>22.8</td></tr>
<tr><td>Rsa1.0_00641.1.g17333.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00641.1.g17334.t1</td><td>ref|XP_002885733.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297331573|gb|EFH61992.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]</td><td>246</td><td>476</td><td>1.00E-111</td><td>193.5</td><td>81.7</td><td>86.2</td><td>mate efflux family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G04040.1 | Symbols: ATDTX1, TX1 | MATE efflux family protein | chr2:1334614-1336480 REVERSE LENGTH=476</td><td>246</td><td>476</td><td>1.00E-113</td><td>193.5</td><td>79.7</td><td>87.8</td></tr>
<tr><td>Rsa1.0_00642.1.g17335.t1</td><td>gb|EOA29836.1| hypothetical protein CARUB_v10012933mg [Capsella rubella]</td><td>735</td><td>907</td><td>0</td><td>123.4</td><td>85.4</td><td>92.2</td><td>hypothetical protein CARUB_v10012933mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G14810.1 | Symbols: MSL5 | mechanosensitive channel of small conductance-like 5 | chr3:4971223-4974216 REVERSE LENGTH=881</td><td>735</td><td>881</td><td>0</td><td>119.9</td><td>83.9</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00642.1.g17336.t2</td><td>ref|XP_002882888.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata] gi|297328728|gb|EFH59147.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata]</td><td>1104</td><td>512</td><td>0</td><td>46.4</td><td>36.1</td><td>39.9</td><td>CYP72A15</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G14690.1 | Symbols: CYP72A15 | cytochrome P450, family 72, subfamily A, polypeptide 15 | chr3:4937410-4939310 FORWARD LENGTH=512</td><td>1104</td><td>512</td><td>0</td><td>46.4</td><td>36.0</td><td>39.9</td></tr>
<tr><td>Rsa1.0_00642.1.g17337.t1</td><td>ref|XP_002882888.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata] gi|297328728|gb|EFH59147.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata]</td><td>560</td><td>512</td><td>0</td><td>91.4</td><td>74.8</td><td>82.0</td><td>CYP72A15</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G14690.1 | Symbols: CYP72A15 | cytochrome P450, family 72, subfamily A, polypeptide 15 | chr3:4937410-4939310 FORWARD LENGTH=512</td><td>560</td><td>512</td><td>0</td><td>91.4</td><td>74.1</td><td>82.0</td></tr>
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Rsa1.0_00642.1.g17338.t1	ref|NP_188081.1| cytochrome P450, family 72, subfamily A, polypeptide 9 [Arabidopsis thaliana] gi|332642028|gb|AEE75549.1| cytochrome P450, family 72, subfamily A, polypeptide 9 [Arabidopsis thaliana]	508	508	0	100.0	81.7	90.6	cytochrome P450, family 72, subfamily A, polypeptide 9	gbpln	Arabidopsis thaliana	AT3G14630.1 | Symbols: CYP72A9 | cytochrome P450, family 72, subfamily A, polypeptide 9 | chr3:4917498-4919409 FORWARD LENGTH=508	508	508	0	100.0	81.7	90.6
Rsa1.0_00642.1.g17339.t1	ref|NP_180995.1| 60S ribosomal protein L18a-2 [Arabidopsis thaliana] gi|297826909|ref|XP_002881337.1| 60S ribosomal protein L18A [Arabidopsis lyrata subsp. lyrata] gi|21431842|sp|P51418.2|R18A2_ARATH RecName: Full=60S ribosomal protein L18a-2 gi|3128228|gb|AAC26708.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|14596031|gb|AAK68743.1| Unknown protein [Arabidopsis thaliana] gi|20197170|gb|AAM14956.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|21539567|gb|AAM53336.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|23197736|gb|AAN15395.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|30102898|gb|AAP21367.1| At2g34480 [Arabidopsis thaliana] gi|297327176|gb|EFH57596.1| 60S ribosomal protein L18A [Arabidopsis lyrata subsp. lyrata] gi|330253886|gb|AEC08980.1| 60S ribosomal protein L18a-2 [Arabidopsis thaliana]	201	178	9.00E-94	88.6	82.1	84.6	60S ribosomal protein L18a-2	gbpln	Arabidopsis lyrata	AT2G34480.1 | Symbols: | Ribosomal protein L18ae/LX family protein | chr2:14532916-14534161 REVERSE LENGTH=178	201	178	3.00E-96	88.6	82.1	84.6
Rsa1.0_00642.1.g17340.t1	ref|NP_188067.1| terpene cyclase, C1 domain-containing protein [Arabidopsis thaliana] gi|317412204|sp|Q9LRR2.2|TPS17_ARATH RecName: Full=Terpenoid synthase 17; Short=AtTPS17 gi|332642011|gb|AEE75532.1| terpenoid synthase 17 [Arabidopsis thaliana]	589	601	0	102.0	80.5	89.0	terpene cyclase, C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G14490.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr3:4863631-4865949 REVERSE LENGTH=601	589	601	0	102.0	80.5	89.0
Rsa1.0_00642.1.g17341.t1	ref|NP_188063.1| CTC-interacting domain 9 protein [Arabidopsis thaliana] gi|11994215|dbj|BAB01337.1| unnamed protein product [Arabidopsis thaliana] gi|332642006|gb|AEE75527.1| CTC-interacting domain 9 protein [Arabidopsis thaliana]	326	327	1.00E-158	100.3	86.5	90.2	CTC-interacting domain 9 protein	gbpln	Arabidopsis thaliana	AT3G14450.1 | Symbols: CID9 | CTC-interacting domain 9 | chr3:4849788-4851601 FORWARD LENGTH=327	326	327	1.00E-161	100.3	86.5	90.2
Rsa1.0_00642.1.g17342.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00642.1.g17343.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	695	1529	0	220.0	59.6	75.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	695	746	6.00E-78	107.3	22.2	26.6
Rsa1.0_00642.1.g17344.t1	gb|AEN94304.1| 9-cis-epoxycarotenoid dioxygenase [Brassica napus]	592	592	0	100.0	95.3	98.0	9-cis-epoxycarotenoid dioxygenase	gbpln	Brassica napus	AT3G14440.1 | Symbols: NCED3, ATNCED3, STO1, SIS7 | nine-cis-epoxycarotenoid dioxygenase 3 | chr3:4831678-4833477 REVERSE LENGTH=599	592	599	0	101.2	91.7	96.3

Rsa1.0_00642.1.g17345.t1	ref|NP_188060.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|30683149|ref|NP_850584.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|297829994|ref|XP_002882879.1| hypothetical protein ARALYDRAFT_478862 [Arabidopsis lyrata subsp. lyrata] gi|13124262|sp|Q9LRR9.1|GLO1_ARATH RecName: Full=Peroxisomal (S)-2-hydroxy-acid oxidase GLO1; AltName: Full=Glycolate oxidase 1; Short=AtGLO1; Short=GOX 1; AltName: Full=Short chain alpha-hydroxy acid oxidase GLO1 gi|16226423|gb|AAL16164.1|AF428396_1 AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|11994212|dbj|BAB01334.1| glycolate oxidase [Arabidopsis thaliana] gi|15450741|gb|AAK96642.1| AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|18491119|gb|AAL69528.1| AT3g14420/MOA2_2 [Arabidopsis thaliana] gi|297328719|gb|EFH59138.1| hypothetical protein ARALYDRAFT_478862 [Arabidopsis lyrata subsp. lyrata] gi|332641997|gb|AEE75518.1| putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana] gi|332641999|gb|AEE75520.1| putative peroxisomal (S)-2-hydroxy-acid	109	367	9.00E-28	336.7	56.0	56.9	putative peroxisomal (S)-2-hydroxy-acid oxidase 2	gbpln	Arabidopsis lyrata	AT3G14420.2 | Symbols: | Aldolase-type TIM barrel family protein | chr3:4821804-4823899 FORWARD LENGTH=367	109	367	2.00E-30	336.7	56.0	56.9
Rsa1.0_00642.1.g17346.t1	gb|AAV28535.1| glycolate oxidase [Brassica napus]	367	367	0	100.0	99.5	99.7	glycolate oxidase	gbpln	Brassica napus	AT3G14415.3 | Symbols: | Aldolase-type TIM barrel family protein | chr3:4818667-4820748 FORWARD LENGTH=367	367	367	0	100.0	96.2	98.9
Rsa1.0_00642.1.g17347.t1	ref|XP_002885042.1| ubiquitin-specific protease 25 [Arabidopsis lyrata subsp. lyrata] gi|297330882|gb|EFH61301.1| ubiquitin-specific protease 25 [Arabidopsis lyrata subsp. lyrata]	673	662	0	98.4	77.1	86.2	ubiquitin-specific protease 25	gbpln	Arabidopsis lyrata	AT3G14400.1 | Symbols: UBP25 | ubiquitin-specific protease 25 | chr3:4811953-4815210 REVERSE LENGTH=661	673	661	0	98.2	76.8	86.0
Rsa1.0_00642.1.g17348.t1	ref|XP_002885025.1| hypothetical protein ARALYDRAFT_478841 [Arabidopsis lyrata subsp. lyrata] gi|297330865|gb|EFH61284.1| hypothetical protein ARALYDRAFT_478841 [Arabidopsis lyrata subsp. lyrata]	407	776	0	190.7	93.6	97.5	hypothetical protein ARALYDRAFT_478841	gbpln	Arabidopsis lyrata	AT3G14240.1 | Symbols: | Subtilase family protein | chr3:4741637-4743964 REVERSE LENGTH=775	407	775	0	190.4	93.6	97.1
Rsa1.0_00642.1.g17349.t1	gb|EOA30781.1| hypothetical protein CARUB_v10013925mg [Capsella rubella]	350	385	1.00E-131	110.0	78.3	86.6	hypothetical protein CARUB_v10013925mg	gbpln	Capsella rubella	AT3G14230.2 | Symbols: RAP2.2 | related to AP2 2 | chr3:4737616-4739000 REVERSE LENGTH=375	350	375	1.00E-123	107.1	77.4	86.0
Rsa1.0_00642.1.g17350.t1	ref|NP_188036.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|9294648|dbj|BAB02987.1| unnamed protein product [Arabidopsis thaliana] gi|20268707|gb|AAM14057.1| unknown protein [Arabidopsis thaliana] gi|21689885|gb|AAM67503.1| unknown protein [Arabidopsis thaliana] gi|110743929|dbj|BAE99798.1| hypothetical protein [Arabidopsis thaliana] gi|332641964|gb|AEE75485.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]	227	230	2.00E-94	101.3	81.1	88.1	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT3G14200.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr3:4712881-4714361 REVERSE LENGTH=230	227	230	6.00E-97	101.3	81.1	88.1
Rsa1.0_00642.1.g17351.t1	ref|XP_002882871.1| At3g14190 [Arabidopsis lyrata subsp. lyrata] gi|297328711|gb|EFH59130.1| At3g14190 [Arabidopsis lyrata subsp. lyrata]	199	193	7.00E-82	97.0	77.4	86.4	At3g14190	gbpln	Arabidopsis lyrata	AT3G14190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12360.1); Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4710907-4711790 FORWARD LENGTH=193	199	193	2.00E-80	97.0	76.4	84.9

Rsa1.0_00642.1.g17352.t1	ref|NP_188034.1| sequence-specific DNA binding transcription factor [Arabidopsis thaliana] gi|9294645|dbj|BAB02984.1| unnamed protein product [Arabidopsis thaliana] gi|18176240|gb|AAL60009.1| unknown protein [Arabidopsis thaliana] gi|21281263|gb|AAM44901.1| unknown protein [Arabidopsis thaliana] gi|332641962|gb|AEE75483.1| sequence-specific DNA binding transcription factor [Arabidopsis thaliana]	449	443	0	98.7	78.0	83.5	sequence-specific DNA binding transcription factor	gbpln	Arabidopsis thaliana	AT3G14180.1 | Symbols: | sequence-specific DNA binding transcription factors | chr3:4707290-4708621 REVERSE LENGTH=443	449	443	0	98.7	78.0	83.5
Rsa1.0_00642.1.g17353.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00642.1.g17354.t1	ref|XP_002885016.1| hypothetical protein ARALYDRAFT_478831 [Arabidopsis lyrata subsp. lyrata] gi|297330856|gb|EFH61275.1| hypothetical protein ARALYDRAFT_478831 [Arabidopsis lyrata subsp. lyrata]	1161	1256	0	108.2	79.6	86.7	hypothetical protein ARALYDRAFT_478831	gbpln	Arabidopsis lyrata	AT3G14172.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: COP1-interacting protein-related (TAIR:AT1G72410.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:4698860-4704773 REVERSE LENGTH=1270	1161	1270	0	109.4	80.2	87.2
Rsa1.0_00642.1.g17355.t1	gb|EOA25626.1| hypothetical protein CARUB_v10018979mg [Capsella rubella]	114	121	1.00E-53	106.1	90.4	93.0	hypothetical protein CARUB_v10018979mg	gbpln	Capsella rubella	AT3G26620.1 | Symbols: LBD23 | LOB domain-containing protein 23 | chr3:9790628-9791112 FORWARD LENGTH=121	114	121	3.00E-55	106.1	87.7	92.1
Rsa1.0_00642.1.g17356.t1	ref|NP_188031.1| Aldolase-type TIM barrel family protein [Arabidopsis thaliana] gi|145332391|ref|NP_001078152.1| Aldolase-type TIM barrel family protein [Arabidopsis thaliana] gi|122195548|sp|Q24JJ8.1|GLO3_ARATH RecName: Full=Peroxisomal (S)-2-hydroxy-acid oxidase GLO3; AltName: Full=Glycolate oxidase 3; Short=AtGLO3; Short=GOX 3; AltName: Full=Short chain alpha-hydroxy acid oxidase GLO3 gi|90093298|gb|ABD85162.1| At3g14150 [Arabidopsis thaliana] gi|332641956|gb|AEE75477.1| Aldolase-type TIM barrel family protein [Arabidopsis thaliana] gi|332641957|gb|AEE75478.1| Aldolase-type TIM barrel family protein [Arabidopsis thaliana]	363	363	0	100.0	86.8	95.3	Aldolase-type TIM barrel family protein	gbpln	Arabidopsis thaliana	AT3G14150.2 | Symbols: | Aldolase-type TIM barrel family protein | chr3:4690667-4692679 REVERSE LENGTH=363	363	363	0	100.0	86.8	95.3
Rsa1.0_00642.1.g17357.t1	ref|NP_566478.1| flourescent in blue light protein [Arabidopsis thaliana] gi|75331838|sp|Q940U6.1|FLU_ARATH RecName: Full=Protein FLUORESCENT IN BLUE LIGHT, chloroplastic; Flags: Precursor gi|17386154|gb|AAL38623.1|AF446890_1 AT3g14110/MAG2_6 [Arabidopsis thaliana] gi|15450619|gb|AAK96581.1| AT3g14110/MAG2_6 [Arabidopsis thaliana] gi|21593122|gb|AAM65071.1| unknown [Arabidopsis thaliana] gi|332641949|gb|AEE75470.1| flourescent in blue light protein [Arabidopsis thaliana]	469	316	1.00E-127	67.4	51.8	57.4	flourescent in blue light protein	gbpln	Arabidopsis thaliana	AT3G14110.1 | Symbols: FLU | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:4676222-4677602 REVERSE LENGTH=316	469	316	1.00E-130	67.4	51.8	57.4
Rsa1.0_00642.1.g17358.t3	ref|XP_002882865.1| hypothetical protein ARALYDRAFT_897659 [Arabidopsis lyrata subsp. lyrata] gi|297328705|gb|EFH59124.1| hypothetical protein ARALYDRAFT_897659 [Arabidopsis lyrata subsp. lyrata]	652	597	1.00E-120	91.6	43.1	50.2	hypothetical protein ARALYDRAFT_897659	gbpln	Arabidopsis lyrata	AT3G14010.4 | Symbols: CID4 | CTC-interacting domain 4 | chr3:4637164-4640324 FORWARD LENGTH=549	652	549	1.00E-121	84.2	42.9	49.2
Rsa1.0_00642.1.g17359.t1	gb|AEK86528.1| growth-regulating factor 5 [Brassica rapa subsp. pekinensis]	363	363	1.00E-153	100.0	83.2	87.3	growth-regulating factor 5	gbpln	Brassica rapa	AT3G13960.1 | Symbols: AtGRF5, GRF5 | growth-regulating factor 5 | chr3:4608526-4610160 FORWARD LENGTH=397	363	397	1.00E-123	109.4	76.6	84.8
Rsa1.0_00642.1.g17360.t1	gb|EOA32882.1| hypothetical protein CARUB_v10016198mg [Capsella rubella]	510	541	0	106.1	87.5	92.5	hypothetical protein CARUB_v10016198mg	gbpln	Capsella rubella	AT3G13930.1 | Symbols: | Dihydrolipoamide acetyltransferase, long form protein | chr3:4596240-4600143 FORWARD LENGTH=539	510	539	0	105.7	86.9	91.6
Rsa1.0_00643.1.g17361.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00643.1.g17362.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00643.1.g17363.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00643.1.g17364.t4	gb|AFJ66186.1| hypothetical protein 11M19.5 [Arabidopsis halleri]	634	1557	6.00E-33	245.6	15.1	22.9	hypothetical protein 11M19.5	gbpln	Arabidopsis halleri	#	#	#	#	#	#	#
Rsa1.0_00643.1.g17365.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00643.1.g17366.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00643.1.g17367.t5	gb|AFJ66186.1| hypothetical protein 11M19.5 [Arabidopsis halleri]	689	1557	0	226.0	52.0	60.5	hypothetical protein 11M19.5	gbpln	Arabidopsis halleri	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	689	158	3.00E-23	22.9	7.5	9.4
Rsa1.0_00643.1.g17368.t1	dbj|BAB10837.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	716	1462	0	204.2	52.1	67.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	716	1262	5.00E-93	176.3	23.2	35.8
Rsa1.0_00643.1.g17369.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	490	1486	1.00E-127	303.3	51.0	69.4	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	490	237	2.00E-13	48.4	10.0	18.6
Rsa1.0_00643.1.g17370.t1	ref|NP_176329.1| F-box protein [Arabidopsis thaliana] gi|75244390|sp|Q8GX77.1|FB316_ARATH RecName: Full=F-box protein At1g61340 gi|26451816|dbj|BAC43001.1| unknown protein [Arabidopsis thaliana] gi|332195701|gb|AEE33822.1| F-box protein [Arabidopsis thaliana]	177	185	1.00E-59	104.5	74.0	79.1	F-box protein	gbpln	Arabidopsis thaliana	AT1G61340.1 | Symbols: | F-box family protein | chr1:22628526-22629741 FORWARD LENGTH=185	177	185	6.00E-62	104.5	74.0	79.1
Rsa1.0_00643.1.g17371.t14	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00643.1.g17372.t1	gb|ABD65088.1| hypothetical protein 27.t00109 [Brassica oleracea]	403	1176	1.00E-41	291.8	27.5	42.2	hypothetical protein 27.t00109	gbpln	Brassica oleracea	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	403	452	2.00E-24	112.2	19.9	30.3
Rsa1.0_00643.1.g17373.t1	ref|NP_564773.1| uncharacterized protein [Arabidopsis thaliana] gi|2443885|gb|AAB71478.1| Unknown protein [Arabidopsis thaliana] gi|30017227|gb|AAP12847.1| At1g61170 [Arabidopsis thaliana] gi|110735914|dbj|BAE99932.1| hypothetical protein [Arabidopsis thaliana] gi|332195677|gb|AEE33798.1| uncharacterized protein AT1G61170 [Arabidopsis thaliana]	491	251	4.00E-69	51.1	33.6	37.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G61170.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G11125.1); Has 54 Blast hits to 54 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 17; Fungi - 0; Plants - 34; Viruses - 1; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:22549718-22550473 FORWARD LENGTH=251	491	251	9.00E-72	51.1	33.6	37.9
Rsa1.0_00643.1.g17374.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00643.1.g17375.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00644.1.g17376.t8	gb|AAC02669.1| polyprotein [Arabidopsis thaliana]	519	1451	3.00E-43	279.6	21.0	28.1	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	519	1262	2.00E-20	243.2	10.4	17.1
Rsa1.0_00644.1.g17377.t2	emb|CAE46442.1| sulphate transporter [Brassica napus]	658	658	0	100.0	96.4	98.6	sulphate transporter	gbpln	Brassica napus	AT3G51895.1 | Symbols: SULTR3;1, AST12 | sulfate transporter 3;1 | chr3:19251503-19255677 REVERSE LENGTH=658	658	658	0	100.0	91.5	96.2
Rsa1.0_00644.1.g17378.t1	ref|NP_974413.1| high mobility group protein B1 [Arabidopsis thaliana] gi|222423104|dbj|BAH19531.1| AT3G51880 [Arabidopsis thaliana] gi|332645335|gb|AEE78856.1| high mobility group protein B1 [Arabidopsis thaliana]	201	185	1.00E-68	92.0	70.1	73.6	high mobility group protein B1	gbpln	Arabidopsis thaliana	AT3G51880.2 | Symbols: HMGB1, NFD1 | high mobility group B1 | chr3:19247241-19248491 REVERSE LENGTH=185	201	185	5.00E-71	92.0	70.1	73.6
Rsa1.0_00644.1.g17379.t1	gb|ACA61613.1| hypothetical protein AP2_E11.1 [Arabidopsis lyrata subsp. petraea]	1155	471	1.00E-145	40.8	22.1	27.0	hypothetical protein AP2_E11.1	gbpln	Arabidopsis lyrata	AT1G34070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48050.1); Has 648 Blast hits to 647 proteins in 29 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 25; Plants - 607; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12402283-12403209 FORWARD LENGTH=308	1155	308	1.00E-80	26.7	13.4	17.2

Rsa1.0_00644.1.g17380.t1	ref|NP_190752.1| acyl-coenzyme A oxidase 4 [Arabidopsis thaliana] gi|62286630|sp|Q96329.1|ACOX4_ARATH RecName: Full=Acyl-coenzyme A oxidase 4, peroxisomal; Short=AOX 4; AltName: Full=G6p; AltName: Full=Short-chain acyl-CoA oxidase; Short=AtCX4; Short=AtG6; Short=SAOX gi|114794822|pdb|2IX5|A Chain A, Short Chain Specific Acyl-Coa Oxidase From Arabidopsis Thaliana, Acx4 In Complex With Acetoacetyl-Coa gi|114794823|pdb|2IX5|B Chain B, Short Chain Specific Acyl-Coa Oxidase From Arabidopsis Thaliana, Acx4 In Complex With Acetoacetyl-Coa gi|114794824|pdb|2IX5|C Chain C, Short Chain Specific Acyl-Coa Oxidase From Arabidopsis Thaliana, Acx4 In Complex With Acetoacetyl-Coa gi|114794825|pdb|2IX5|D Chain D, Short Chain Specific Acyl-Coa Oxidase From Arabidopsis Thaliana, Acx4 In Complex With Acetoacetyl-Coa gi|1657621|gb|AAB18129.1| G6p [Arabidopsis thaliana] gi|3068711|gb|AAC14411.1| putative acyl-coA dehydrogenase [Arabidopsis thaliana] gi|5478795|dbj|BAA82478.1| Short-chain acyl CoA oxidase [Arabidopsis thaliana] gi|20453143|gb|AAM19813.1| At3g51840/AtG6 [Arabidopsis thaliana] gi|21593380|gb|AAM65329.1| acyl-coA	438	436	0	99.5	89.3	93.6	acyl-coenzyme A oxidase 4	gbpln	Arabidopsis thaliana	AT3G51840.1 | Symbols: ACX4, ATSCX, ATG6 | acyl-CoA oxidase 4 | chr3:19225653-19229008 REVERSE LENGTH=436	438	436	0	99.5	89.3	93.6
Rsa1.0_00644.1.g17381.t1	ref|XP_002877826.1| ATG4/CHLG/G4 [Arabidopsis lyrata subsp. lyrata] gi|297323664|gb|EFH54085.1| ATG4/CHLG/G4 [Arabidopsis lyrata subsp. lyrata]	411	387	0	94.2	83.5	85.9	ATG4/CHLG/G4	gbpln	Arabidopsis lyrata	AT3G51820.1 | Symbols: ATG4, G4, CHLG | UbiA prenyltransferase family protein | chr3:19216301-19218934 REVERSE LENGTH=387	411	387	0	94.2	82.7	85.6
Rsa1.0_00644.1.g17382.t1	ref|NP_001190060.1| metallopeptidase M24 domain-containing protein [Arabidopsis thaliana] gi|332645325|gb|AEE78846.1| metallopeptidase M24 domain-containing protein [Arabidopsis thaliana]	391	385	0	98.5	86.2	92.1	metallopeptidase M24 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G51800.3 | Symbols: ATG2 | metallopeptidase M24 family protein | chr3:19211261-19213568 REVERSE LENGTH=385	391	385	0	98.5	86.2	92.1
Rsa1.0_00644.1.g17383.t1	ref|XP_002877824.1| hypothetical protein ARALYDRAFT_485534 [Arabidopsis lyrata subsp. lyrata] gi|297323662|gb|EFH54083.1| hypothetical protein ARALYDRAFT_485534 [Arabidopsis lyrata subsp. lyrata]	251	257	1.00E-114	102.4	82.5	86.1	hypothetical protein ARALYDRAFT_485534	gbpln	Arabidopsis lyrata	AT3G51790.1 | Symbols: ATG1, TG1 | transmembrane protein G1P-related 1 | chr3:19209893-19210663 REVERSE LENGTH=256	251	256	1.00E-116	102.0	82.5	85.7
Rsa1.0_00644.1.g17384.t1	ref|NP_190746.2| BCL-2-associated athanogene 4 [Arabidopsis thaliana] gi|75158813|sp|Q8RX71.1|BAG4_ARATH RecName: Full=BAG family molecular chaperone regulator 4; AltName: Full=Bcl-2-associated athanogene 4 gi|19699283|gb|AAL91253.1| At3g51780/ORF3 [Arabidopsis thaliana] gi|23505833|gb|AAN28776.1| At3g51780/ORF3 [Arabidopsis thaliana] gi|332645321|gb|AEE78842.1| BCL-2-associated athanogene 4 [Arabidopsis thaliana]	278	269	1.00E-111	96.8	79.5	88.8	BCL-2-associated athanogene 4	gbpln	Arabidopsis thaliana	AT3G51780.1 | Symbols: ATBAG4, BAG4 | BCL-2-associated athanogene 4 | chr3:19207029-19208178 REVERSE LENGTH=269	278	269	1.00E-114	96.8	79.5	88.8
Rsa1.0_00644.1.g17385.t1	dbj|BAJ34198.1| unnamed protein product [Thellungiella halophila]	953	958	0	100.5	90.1	93.3	unnamed protein product	----	----	AT3G51770.2 | Symbols: ETO1 | tetratricopeptide repeat (TPR)-containing protein | chr3:19200328-19203998 REVERSE LENGTH=959	953	959	0	100.6	87.5	91.5
Rsa1.0_00644.1.g17386.t1	ref|XP_002877821.1| hypothetical protein ARALYDRAFT_906526 [Arabidopsis lyrata subsp. lyrata] gi|297323659|gb|EFH54080.1| hypothetical protein ARALYDRAFT_906526 [Arabidopsis lyrata subsp. lyrata]	249	257	1.00E-113	103.2	84.3	92.8	hypothetical protein ARALYDRAFT_906526	gbpln	Arabidopsis lyrata	AT3G51760.2 | Symbols: | Protein of unknown function (DUF688) | chr3:19198541-19199405 REVERSE LENGTH=259	249	259	1.00E-113	104.0	83.5	91.2
Rsa1.0_00644.1.g17387.t1	dbj|BAJ33968.1| unnamed protein product [Thellungiella halophila]	216	213	2.00E-89	98.6	81.5	88.9	unnamed protein product	----	----	AT3G51730.1 | Symbols: | saposin B domain-containing protein | chr3:19186970-19188436 FORWARD LENGTH=213	216	213	2.00E-88	98.6	76.4	87.0

Rsa1.0_00644.1.g17388.t1	gb|EOA29438.1| hypothetical protein CARUB_v100225660mg, partial [Capsella rubella]	275	382	1.00E-109	138.9	68.0	73.1	hypothetical protein CARUB_v100225660mg, partial	gbpln	Capsella rubella	AT3G47090.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17341512-17344645 REVERSE LENGTH=1009	275	1009	1.00E-108	366.9	66.2	73.1
Rsa1.0_00645.1.g17389.t1	gb|AAF97297.1|AC010164_19 Hypothetical protein [Arabidopsis thaliana]	76	308	2.00E-26	405.3	75.0	88.2	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00645.1.g17390.t1	ref|NP_191481.1| pirin [Arabidopsis thaliana] gi|14195011|sp|Q9LX49.1|PRN1_ARATH RecName: Full=Pirin-1; AltName: Full=AtPirin1 gi|19070663|gb|AAL83949.1|AF353716_1 pirin [Arabidopsis thaliana] gi|7801672|emb|CAB91592.1| pirin-like protein [Arabidopsis thaliana] gi|109946467|gb|ABG48412.1| At3g59220 [Arabidopsis thaliana] gi|332646372|gb|AEE79893.1| pirin [Arabidopsis thaliana]	289	287	1.00E-137	99.3	81.0	89.3	pirin	gbpln	Arabidopsis thaliana	AT3G59220.1 | Symbols: PRN, PRN1, ATPIRIN1 | pirin | chr3:21894205-21895501 FORWARD LENGTH=287	289	287	1.00E-140	99.3	81.0	89.3
Rsa1.0_00645.1.g17391.t1	ref|NP_567081.1| uncharacterized protein [Arabidopsis thaliana] gi|16416387|dbj|BAB70614.1| anthocyanin-related membrane protein 3 [Arabidopsis thaliana] gi|332646386|gb|AEE79907.1| uncharacterized protein AT3G59340 [Arabidopsis thaliana]	434	333	1.00E-147	76.7	59.9	67.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G59340.1 | Symbols: | Eukaryotic protein of unknown function (DUF914) | chr3:21928971-21931030 REVERSE LENGTH=333	434	333	1.00E-149	76.7	59.9	67.1
Rsa1.0_00645.1.g17392.t1	ref|NP_567081.1| uncharacterized protein [Arabidopsis thaliana] gi|16416387|dbj|BAB70614.1| anthocyanin-related membrane protein 3 [Arabidopsis thaliana] gi|332646386|gb|AEE79907.1| uncharacterized protein AT3G59340 [Arabidopsis thaliana]	337	333	1.00E-144	98.8	77.2	87.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G59340.1 | Symbols: | Eukaryotic protein of unknown function (DUF914) | chr3:21928971-21931030 REVERSE LENGTH=333	337	333	2.33E-156	98.8	77.2	87.8
Rsa1.0_00645.1.g17393.t1	ref|NP_567082.2| protein kinase family protein [Arabidopsis thaliana] gi|79315708|ref|NP_001030893.1| protein kinase family protein [Arabidopsis thaliana] gi|317411799|sp|B9DFG5.1|PTI13_ARATH RecName: Full=PTI1-like tyrosine-protein kinase 3; Short=PTI1-3 gi|222422997|dbj|BAH19482.1| AT3G59350 [Arabidopsis thaliana] gi|332646387|gb|AEE79908.1| protein kinase family protein [Arabidopsis thaliana] gi|332646389|gb|AEE79910.1| PTI1-like tyrosine-protein kinase 3 [Arabidopsis thaliana]	407	408	0	100.2	92.4	94.8	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G59350.3 | Symbols: | Protein kinase superfamily protein | chr3:21932930-21934883 FORWARD LENGTH=408	407	408	0	100.2	92.4	94.8
Rsa1.0_00645.1.g17394.t1	gb|AAM64445.1| fructokinase-like protein [Arabidopsis thaliana]	326	326	1.00E-180	100.0	94.2	97.9	fructokinase-like protein	gbpln	Arabidopsis thaliana	AT3G59480.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr3:21983103-21984440 FORWARD LENGTH=326	326	326	0	100.0	93.9	97.2
Rsa1.0_00645.1.g17395.t1	gb|EOA26152.1| hypothetical protein CARUB_v10019590mg [Capsella rubella]	236	289	1.00E-104	122.5	80.9	88.1	hypothetical protein CARUB_v10019590mg	gbpln	Capsella rubella	AT3G59490.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:21984660-21986262 REVERSE LENGTH=293	236	293	1.00E-106	124.2	80.9	88.1
Rsa1.0_00645.1.g17396.t1	gb|EOA24578.1| hypothetical protein CARUB_v10017840mg [Capsella rubella]	273	269	2.33E-156	98.5	91.9	96.3	hypothetical protein CARUB_v10017840mg	gbpln	Capsella rubella	AT3G59500.1 | Symbols: | Integral membrane HRF1 family protein | chr3:21987110-21988169 FORWARD LENGTH=269	273	269	1.00E-147	98.5	91.9	96.0
Rsa1.0_00645.1.g17397.t1	ref|XP_002878275.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297324113|gb|EFH54534.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	410	416	0	101.5	87.1	93.2	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT3G59510.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:21988453-21989712 REVERSE LENGTH=419	410	419	0	102.2	85.4	92.2
Rsa1.0_00645.1.g17398.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00645.1.g17399.t1	gb|EOA33287.1| hypothetical protein CARUB_v10019720mg [Capsella rubella]	1244	984	0	79.1	58.0	66.2	hypothetical protein CARUB_v10019720mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	1244	696	1.00E-142	55.9	20.7	28.4

Rsa1.0_00645.1.g17400.t1	gb|AAX38236.1| strictosidine synthase family protein [Brassica napus]	414	414	0	100.0	93.7	97.6	strictosidine synthase family protein	gbpln	Brassica napus	AT3G59530.2 | Symbols: LAP3 | Calcium-dependent phosphotriesterase superfamily protein | chr3:21993710-21995164 FORWARD LENGTH=403	414	403	0	97.3	88.6	93.2
Rsa1.0_00645.1.g17401.t1	gb|EOA25003.1| hypothetical protein CARUB_v10018301mg, partial [Capsella rubella]	64	100	2.00E-28	156.3	98.4	98.4	hypothetical protein CARUB_v10018301mg, partial	gbpln	Capsella rubella	AT3G59540.1 | Symbols: | Ribosomal L38e protein family | chr3:21995897-21996742 REVERSE LENGTH=69	64	69	8.00E-31	107.8	98.4	98.4
Rsa1.0_00645.1.g17402.t7	gb|AAG44843.1|AF281155_1 cohesion family protein SYN3 [Arabidopsis thaliana]	367	692	1.00E-107	188.6	62.7	72.2	cohesion family protein SYN3	gbpln	Arabidopsis thaliana	AT3G59550.1 | Symbols: SYN3, ATRAD21.2, ATSYN3 | Rad21/Rec8-like family protein | chr3:21997262-22000496 FORWARD LENGTH=693	367	693	1.00E-104	188.8	62.9	72.8
Rsa1.0_00645.1.g17403.t1	gb|ACR10272.1| sulfotransferase 5b [Brassica rapa subsp. pekinensis]	306	342	1.00E-119	111.8	73.5	81.7	sulfotransferase 5b	gbpln	Brassica rapa	AT1G74090.1 | Symbols: SOT18, ATSOT18, ATST5B | desulfo-glucosinolate sulfotransferase 18 | chr1:27863003-27864055 FORWARD LENGTH=350	306	350	1.00E-108	114.4	69.0	77.8
Rsa1.0_00645.1.g17404.t1	ref|NP_191520.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75264553|sp|Q9M1A7.1|FBK75_ARATH RecName: Full=F-box/kelch-repeat protein At3g59610 gi|6996297|emb|CAB75458.1| putative protein [Arabidopsis thaliana] gi|332646424|gb|AEE79945.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	508	521	1.00E-142	102.6	55.5	69.9	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G59610.1 | Symbols: | F-box family protein / jacalin lectin family protein | chr3:22019553-22021199 FORWARD LENGTH=521	508	521	1.00E-145	102.6	55.5	69.9
Rsa1.0_00645.1.g17405.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00645.1.g17406.t1	gb|EOA23604.1| hypothetical protein CARUB_v10016803mg [Capsella rubella]	660	657	0	99.5	83.3	91.1	hypothetical protein CARUB_v10016803mg	gbpln	Capsella rubella	AT3G59700.1 | Symbols: ATHLECRK, LECRK1, HLECRK | lectin-receptor kinase | chr3:22052146-22054131 FORWARD LENGTH=661	660	661	0	100.2	83.5	90.5
Rsa1.0_00645.1.g17407.t1	gb|AFE83591.1| putative coat protein [Raphanus sativas chrysovirus 1]	541	1101	1.00E-134	203.5	47.9	62.5	putative coat protein	gbvrl	Raphanus sativas	#	#	#	#	#	#	#
Rsa1.0_00645.1.g17408.t2	gb|EOA23944.1| hypothetical protein CARUB_v10017160mg [Capsella rubella]	553	473	1.00E-101	85.5	36.0	42.7	hypothetical protein CARUB_v10017160mg	gbpln	Capsella rubella	AT3G60040.1 | Symbols: | F-box family protein | chr3:22175937-22179728 REVERSE LENGTH=838	553	838	2.00E-72	151.5	28.2	36.7
Rsa1.0_00645.1.g17409.t1	gb|EOA23880.1| hypothetical protein CARUB_v10017095mg, partial [Capsella rubella]	440	491	1.00E-156	111.6	67.0	81.1	hypothetical protein CARUB_v10017095mg, partial	gbpln	Capsella rubella	AT3G60040.1 | Symbols: | F-box family protein | chr3:22175937-22179728 REVERSE LENGTH=838	440	838	1.00E-116	190.5	55.2	69.3
Rsa1.0_00645.1.g17410.t1	gb|EOA24035.1| hypothetical protein CARUB_v10017252mg [Capsella rubella]	444	444	0	100.0	95.5	98.2	hypothetical protein CARUB_v10017252mg	gbpln	Capsella rubella	AT3G59920.1 | Symbols: ATGDI2, GDI2 | RAB GDP dissociation inhibitor 2 | chr3:22135157-22138221 FORWARD LENGTH=444	444	444	0	100.0	95.5	97.7
Rsa1.0_00645.1.g17411.t2	ref|XP_002878306.1| autophagy 4b [Arabidopsis lyrata subsp. lyrata] gi|297324144|gb|EFH54565.1| autophagy 4b [Arabidopsis lyrata subsp. lyrata]	425	476	0	112.0	88.5	92.7	autophagy 4b	gbpln	Arabidopsis lyrata	AT3G59950.1 | Symbols: | Peptidase family C54 protein | chr3:22144468-22146887 REVERSE LENGTH=477	425	477	0	112.2	87.5	93.2
Rsa1.0_00645.1.g17412.t1	gb|EOA27380.1| hypothetical protein CARUB_v10023499mg [Capsella rubella]	220	361	2.00E-69	164.1	63.2	75.9	hypothetical protein CARUB_v10023499mg	gbpln	Capsella rubella	AT3G59960.1 | Symbols: ASHH4, SDG24 | histone-lysine N-methyltransferase ASHH4 | chr3:22148334-22150386 FORWARD LENGTH=352	220	352	2.00E-71	160.0	60.5	65.5

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<tr><td>Rsa1.0_00645.1.g17413.t1</td><td>ref|NP_567089.1| methionine aminopeptidase 2B [Arabidopsis thaliana] gi|30695106|ref|NP_850725.1| methionine aminopeptidase 2B [Arabidopsis thaliana] gi|79315754|ref|NP_001030898.1| methionine aminopeptidase 2B [Arabidopsis thaliana] gi|334186141|ref|NP_001190139.1| methionine aminopeptidase 2B [Arabidopsis thaliana] gi|85700451|sp|Q56Y85.2|AMP2B_ARATH RecName: Full=Methionine aminopeptidase 2B; Short=MAP 2B; Short=MetAP 2B; AltName: Full=Peptidase M 2B gi|11344922|gb|AAG34551.1|AF300880_1 putative methionine aminopeptidase 2 [Arabidopsis thaliana] gi|21536943|gb|AAM61284.1| putative methionine aminopeptidase [Arabidopsis thaliana] gi|332646475|gb|AEE79996.1| methionine aminopeptidase 2B [Arabidopsis thaliana] gi|332646476|gb|AEE79997.1| methionine aminopeptidase 2B [Arabidopsis thaliana] gi|332646477|gb|AEE79998.1| methionine aminopeptidase 2B [Arabidopsis thaliana] gi|332646478|gb|AEE79999.1| methionine aminopeptidase 2B [Arabidopsis thaliana]</td><td>442</td><td>439</td><td>0</td><td>99.3</td><td>88.9</td><td>92.5</td><td>methionine aminopeptidase 2B</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G59990.4 | Symbols: MAP2B | methionine aminopeptidase 2B | chr3:22155921-22158551 REVERSE LENGTH=439</td><td>442</td><td>439</td><td>0</td><td>99.3</td><td>88.9</td><td>92.5</td></tr>
<tr><td>Rsa1.0_00645.1.g17414.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00645.1.g17415.t1</td><td>gb|EMJ20595.1| hypothetical protein PRUPE_ppa020403mg [Prunus persica]</td><td>158</td><td>156</td><td>3.00E-50</td><td>98.7</td><td>62.7</td><td>75.3</td><td>hypothetical protein PRUPE_ppa020403mg</td><td>gbpln</td><td>Prunus persica</td><td>AT1G75950.1 | Symbols: SKP1, ASK1, ATSKP1, SKP1A, UIP1 | S phase kinase-associated protein 1 | chr1:28516715-28517454 FORWARD LENGTH=160</td><td>158</td><td>160</td><td>2.00E-49</td><td>101.3</td><td>62.0</td><td>79.7</td></tr>
<tr><td>Rsa1.0_00645.1.g17416.t1</td><td>ref|XP_002269499.1| PREDICTED: uncharacterized protein LOC100247715 [Vitis vinifera] gi|296080944|emb|CBI18666.3| unnamed protein product [Vitis vinifera]</td><td>376</td><td>409</td><td>1.00E-91</td><td>108.8</td><td>46.3</td><td>66.0</td><td>PREDICTED: uncharacterized protein LOC100247715</td><td>gbpln</td><td>Vitis vinifera</td><td>AT5G56530.2 | Symbols: | Protein of Unknown Function (DUF239) | chr5:22889382-22891439 FORWARD LENGTH=420</td><td>376</td><td>420</td><td>4.00E-90</td><td>111.7</td><td>45.5</td><td>61.4</td></tr>
<tr><td>Rsa1.0_00645.1.g17417.t1</td><td>ref|XP_002269499.1| PREDICTED: uncharacterized protein LOC100247715 [Vitis vinifera] gi|296080944|emb|CBI18666.3| unnamed protein product [Vitis vinifera]</td><td>378</td><td>409</td><td>4.00E-90</td><td>108.2</td><td>45.5</td><td>66.9</td><td>PREDICTED: uncharacterized protein LOC100247715</td><td>gbpln</td><td>Vitis vinifera</td><td>AT5G56530.2 | Symbols: | Protein of Unknown Function (DUF239) | chr5:22889382-22891439 FORWARD LENGTH=420</td><td>378</td><td>420</td><td>6.00E-89</td><td>111.1</td><td>45.5</td><td>62.2</td></tr>
<tr><td>Rsa1.0_00645.1.g17418.t1</td><td>ref|XP_002269499.1| PREDICTED: uncharacterized protein LOC100247715 [Vitis vinifera] gi|296080944|emb|CBI18666.3| unnamed protein product [Vitis vinifera]</td><td>425</td><td>409</td><td>1.00E-109</td><td>96.2</td><td>44.9</td><td>64.5</td><td>PREDICTED: uncharacterized protein LOC100247715</td><td>gbpln</td><td>Vitis vinifera</td><td>AT5G56530.2 | Symbols: | Protein of Unknown Function (DUF239) | chr5:22889382-22891439 FORWARD LENGTH=420</td><td>425</td><td>420</td><td>1.00E-111</td><td>98.8</td><td>44.5</td><td>62.8</td></tr>
<tr><td>Rsa1.0_00645.1.g17419.t1</td><td>ref|XP_002878314.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324152|gb|EFH54573.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>477</td><td>475</td><td>0</td><td>99.6</td><td>83.4</td><td>89.3</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G60050.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:22180231-22181652 REVERSE LENGTH=473</td><td>477</td><td>473</td><td>0</td><td>99.2</td><td>82.8</td><td>89.3</td></tr>
<tr><td>Rsa1.0_00645.1.g17420.t1</td><td>ref|NP_191566.5| major facilitator protein [Arabidopsis thaliana] gi|21703097|gb|AAM74491.1| AT3g60070/T2O9_50 [Arabidopsis thaliana] gi|332646487|gb|AEE80008.1| major facilitator protein [Arabidopsis thaliana]</td><td>459</td><td>458</td><td>0</td><td>99.8</td><td>93.7</td><td>96.9</td><td>major facilitator protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G60070.1 | Symbols: | Major facilitator superfamily protein | chr3:22183572-22185941 REVERSE LENGTH=458</td><td>459</td><td>458</td><td>0</td><td>99.8</td><td>93.7</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00646.1.g17421.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00646.1.g17422.t1</td><td>gb|EOA27783.1| hypothetical protein CARUB_v10023935mg, partial [Capsella rubella]</td><td>212</td><td>244</td><td>1.00E-105</td><td>115.1</td><td>90.6</td><td>95.3</td><td>hypothetical protein CARUB_v10023935mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44065.2 | Symbols: | Ribosomal protein L2 family | chr2:18228860-18230368 FORWARD LENGTH=214</td><td>212</td><td>214</td><td>1.00E-107</td><td>100.9</td><td>89.6</td><td>94.8</td></tr>
<tr><td>Rsa1.0_00646.1.g17423.t1</td><td>gb|EOA27458.1| hypothetical protein CARUB_v10023596mg [Capsella rubella]</td><td>326</td><td>332</td><td>1.00E-155</td><td>101.8</td><td>87.7</td><td>93.9</td><td>hypothetical protein CARUB_v10023596mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44060.2 | Symbols: | Late embryogenesis abundant protein, group 2 | chr2:18226922-18227988 FORWARD LENGTH=325</td><td>326</td><td>325</td><td>1.00E-155</td><td>99.7</td><td>84.0</td><td>90.8</td></tr>
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Rsa1.0_00646.1.g17424.t1	ref|NP_181933.1| 6,7-dimethyl-8-ribityllumazine synthase [Arabidopsis thaliana] gi|20139375|sp|O80575.1|RISB_ARATH RecName: Full=6,7-dimethyl-8-ribityllumazine synthase, chloroplastic; Short=DMRL synthase; Short=LS; Short=Lumazine synthase; Flags: Precursor gi|5532610|gb|AAD44810.1|AF148649_1 6,7-dimethyl-8-ribityllumazine synthase precursor [Arabidopsis thaliana] gi|3212862|gb|AAC23413.1| 6,7-dimethyl-8-ribityllumazine synthase precursor [Arabidopsis thaliana] gi|15292959|gb|AAK93590.1| putative 6,7-dimethyl-8-ribityllumazine synthase precursor [Arabidopsis thaliana] gi|20259133|gb|AAM14282.1| putative 6,7-dimethyl-8-ribityllumazine synthase precursor [Arabidopsis thaliana] gi|330255271|gb|AEC10365.1| 6,7-dimethyl-8-ribityllumazine synthase [Arabidopsis thaliana]	231	227	1.00E-103	98.3	86.1	89.2	6,7-dimethyl-8-ribityllumazine synthase	gbpln	Arabidopsis thaliana	AT2G44050.1 | Symbols: COS1 | 6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase | chr2:18224304-18225917 FORWARD LENGTH=227	231	227	1.00E-106	98.3	86.1	89.2
Rsa1.0_00646.1.g17425.t1	gb|EOA27404.1| hypothetical protein CARUB_v10023537mg [Capsella rubella]	349	350	1.00E-175	100.3	87.1	92.3	hypothetical protein CARUB_v10023537mg	gbpln	Capsella rubella	AT2G44040.1 | Symbols: | Dihydrodipicolinate reductase, bacterial/plant | chr2:18221985-18223998 REVERSE LENGTH=347	349	347	1.00E-176	99.4	87.4	90.8
Rsa1.0_00646.1.g17426.t1	gb|EOA28560.1| hypothetical protein CARUB_v10024778mg [Capsella rubella]	98	100	1.00E-32	102.0	77.6	85.7	hypothetical protein CARUB_v10024778mg	gbpln	Capsella rubella	AT2G44010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G59880.1); Has 18 Blast hits to 18 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18216879-18217184 FORWARD LENGTH=101	98	101	9.00E-33	103.1	75.5	83.7
Rsa1.0_00646.1.g17427.t1	ref|XP_002880077.1| hypothetical protein ARALYDRAFT_483519 [Arabidopsis lyrata subsp. lyrata] gi|297325916|gb|EFH56336.1| hypothetical protein ARALYDRAFT_483519 [Arabidopsis lyrata subsp. lyrata]	208	209	1.00E-77	100.5	73.6	83.7	hypothetical protein ARALYDRAFT_483519	gbpln	Arabidopsis lyrata	AT2G44000.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:18214627-18215256 FORWARD LENGTH=209	208	209	2.00E-74	100.5	70.2	82.2
Rsa1.0_00646.1.g17428.t1	ref|XP_002868402.1| arogenate dehydrogenase [Arabidopsis lyrata subsp. lyrata] gi|297314238|gb|EFH44661.1| arogenate dehydrogenase [Arabidopsis lyrata subsp. lyrata]	621	618	0	99.5	77.3	84.2	arogenate dehydrogenase	gbpln	Arabidopsis lyrata	AT5G34930.1 | Symbols: | arogenate dehydrogenase | chr5:13233391-13235522 FORWARD LENGTH=640	621	640	0	103.1	76.0	83.1
Rsa1.0_00646.1.g17429.t1	gb|EOA27254.1| hypothetical protein CARUB_v10023373mg, partial [Capsella rubella]	534	395	1.00E-151	74.0	51.9	56.9	hypothetical protein CARUB_v10023373mg, partial	gbpln	Capsella rubella	AT2G43950.1 | Symbols: OEP37, ATOEP37 | chloroplast outer envelope protein 37 | chr2:18200553-18202644 REVERSE LENGTH=343	534	343	1.00E-153	64.2	51.5	56.2
Rsa1.0_00646.1.g17430.t1	gb|EOA29354.1| hypothetical protein CARUB_v10025640mg [Capsella rubella]	1295	1294	0	99.9	87.0	92.6	hypothetical protein CARUB_v10025640mg	gbpln	Capsella rubella	AT2G43900.1 | Symbols: | Endonuclease/exonuclease/phosphatase family protein | chr2:18178801-18183823 REVERSE LENGTH=1316	1295	1316	0	101.6	78.5	82.7
Rsa1.0_00646.1.g17431.t1	ref|XP_002881935.1| hypothetical protein ARALYDRAFT_483504 [Arabidopsis lyrata subsp. lyrata] gi|297327774|gb|EFH58194.1| hypothetical protein ARALYDRAFT_483504 [Arabidopsis lyrata subsp. lyrata]	386	384	0	99.5	93.5	96.1	hypothetical protein ARALYDRAFT_483504	gbpln	Arabidopsis lyrata	AT2G43870.1 | Symbols: | Pectin lyase-like superfamily protein | chr2:18166615-18168264 REVERSE LENGTH=384	386	384	0	99.5	93.3	96.4
Rsa1.0_00646.1.g17432.t1	ref|XP_002881934.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327773|gb|EFH58193.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	409	405	0	99.0	80.9	88.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G43860.1 | Symbols: | Pectin lyase-like superfamily protein | chr2:18162945-18164428 REVERSE LENGTH=405	409	405	0	99.0	80.2	89.2
Rsa1.0_00646.1.g17433.t1	gb|EOA27104.1| hypothetical protein CARUB_v10023202mg [Capsella rubella]	334	449	1.00E-144	134.4	73.1	77.5	hypothetical protein CARUB_v10023202mg	gbpln	Capsella rubella	AT2G43820.1 | Symbols: GT, UGT74F2, ATSAGT1, SGT1, SAGT1 | UDP-glucosyltransferase 74F2 | chr2:18152279-18153715 FORWARD LENGTH=449	334	449	1.00E-140	134.4	70.4	76.3
Rsa1.0_00646.1.g17434.t1	gb|EOA27104.1| hypothetical protein CARUB_v10023202mg [Capsella rubella]	296	449	1.00E-131	151.7	75.3	80.1	hypothetical protein CARUB_v10023202mg	gbpln	Capsella rubella	AT2G43820.1 | Symbols: GT, UGT74F2, ATSAGT1, SGT1, SAGT1 | UDP-glucosyltransferase 74F2 | chr2:18152279-18153715 FORWARD LENGTH=449	296	449	1.00E-127	151.7	72.0	78.4

Rsa1.0_00646.1.g17435.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	242	1447	4.00E-30	597.9	38.8	58.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	242	295	1.00E-22	121.9	30.2	45.5
Rsa1.0_00647.1.g17436.t1	ref|XP_002881863.1| phosphoenolpyruvate carboxylase [Arabidopsis lyrata subsp. lyrata] gi|297327702|gb|EFH58122.1| phosphoenolpyruvate carboxylase [Arabidopsis lyrata subsp. lyrata]	964	963	0	99.9	97.5	98.9	phosphoenolpyruvate carboxylase	gbpln	Arabidopsis lyrata	AT2G42600.1 | Symbols: ATPPC2, PPC2 | phosphoenolpyruvate carboxylase 2 | chr2:17734541-17738679 REVERSE LENGTH=963	964	963	0	99.9	97.2	98.8
Rsa1.0_00647.1.g17437.t1	gb|EOA29463.1| hypothetical protein CARUB_v100241591mg [Capsella rubella] gi|482565274|gb|EOA29464.1| hypothetical protein CARUB_v100241591mg [Capsella rubella]	169	178	2.00E-79	105.3	89.3	90.5	hypothetical protein CARUB_v100241591mg	gbpln	Capsella rubella	AT2G42610.2 | Symbols: LSH10 | Protein of unknown function (DUF640) | chr2:17748005-17748538 FORWARD LENGTH=177	169	177	8.00E-80	104.7	87.6	89.3
Rsa1.0_00647.1.g17438.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	723	723	0	100.0	56.4	72.8	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	723	696	3.00E-54	96.3	23.2	41.9
Rsa1.0_00647.1.g17439.t1	dbj|BAJ33992.1| unnamed protein product [Thellungiella halophila]	689	701	0	101.7	87.7	93.6	unnamed protein product	----	----	AT2G42620.1 | Symbols: MAX2, ORE9, PPS | RNI-like superfamily protein | chr2:17756170-17758251 FORWARD LENGTH=693	689	693	0	100.6	86.2	92.7
Rsa1.0_00647.1.g17440.t7	ref|XP_002881864.1| hypothetical protein ARALYDRAFT_903636 [Arabidopsis lyrata subsp. lyrata] gi|297327703|gb|EFH58123.1| hypothetical protein ARALYDRAFT_903636 [Arabidopsis lyrata subsp. lyrata]	642	740	1.00E-166	115.3	54.4	68.8	hypothetical protein ARALYDRAFT_903636	gbpln	Arabidopsis lyrata	AT3G58640.2 | Symbols: | Mitogen activated protein kinase kinase kinase-related | chr3:21687153-21692675 REVERSE LENGTH=809	642	809	1.00E-119	126.0	30.5	37.4
Rsa1.0_00647.1.g17441.t1	ref|NP_181797.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|75265946|sp|Q9SJI7.1|PLA20_ARATH RecName: Full=Phospholipase A1-IIdelta gi|4512683|gb|AAD21737.1| putative lipase [Arabidopsis thaliana] gi|15293129|gb|AAK93675.1| putative lipase [Arabidopsis thaliana] gi|19310713|gb|AAL85087.1| putative lipase [Arabidopsis thaliana] gi|20198071|gb|AAM15382.1| putative lipase [Arabidopsis thaliana] gi|330255062|gb|AEC10156.1| phospholipase A1-IIdelta [Arabidopsis thaliana]	414	412	0	99.5	88.9	94.0	alpha/beta-hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G42690.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:17776356-17777682 REVERSE LENGTH=412	414	412	0	99.5	88.9	94.0
Rsa1.0_00647.1.g17442.t1	gb|EOA27699.1| hypothetical protein CARUB_v10023852mg [Capsella rubella]	251	267	5.00E-67	106.4	66.1	78.9	hypothetical protein CARUB_v10023852mg	gbpln	Capsella rubella	AT2G42760.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1685 (InterPro:IPR012881); Has 170 Blast hits to 164 proteins in 34 species: Archae - 0; Bacteria - 1; Metazoa - 26; Fungi - 10; Plants - 107; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink). | chr2:17796382-17797185 REVERSE LENGTH=267	251	267	4.00E-69	106.4	65.7	77.7
Rsa1.0_00647.1.g17443.t1	emb|CAN61307.1| hypothetical protein VITISV_035681 [Vitis vinifera]	167	249	3.00E-17	149.1	32.3	49.1	hypothetical protein VITISV_035681	gbpln	Vitis vinifera	AT1G05920.1 | Symbols: | Domain of unknown function (DUF313) | chr1:1797044-1797991 FORWARD LENGTH=315	167	315	4.00E-16	188.6	25.7	43.1
Rsa1.0_00647.1.g17444.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00647.1.g17445.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00647.1.g17446.t1	emb|CAA18463.1| putative protein [Arabidopsis thaliana] gi|7269163|emb|CAB79271.1| putative protein [Arabidopsis thaliana]	170	1240	6.00E-38	729.4	51.2	61.2	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	170	1262	3.00E-40	742.4	51.2	61.2
Rsa1.0_00647.1.g17447.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00647.1.g17448.t1	gb|EOA26283.1| hypothetical protein CARUB_v10023965mg, partial [Capsella rubella]	236	237	1.00E-108	100.4	88.1	92.8	hypothetical protein CARUB_v10023965mg, partial	gbpln	Capsella rubella	AT2G42770.1 | Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr2:17798635-17799927 REVERSE LENGTH=232	236	232	1.00E-102	98.3	89.8	94.1
Rsa1.0_00647.1.g17449.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2009	1274	0	63.4	29.5	39.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2009	575	1.00E-62	28.6	7.9	13.7
Rsa1.0_00647.1.g17450.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00648.1.g17451.t1	gb|EOA15832.1| hypothetical protein CARUB_v10007453mg [Capsella rubella]	187	187	1.00E-100	100.0	94.7	97.3	hypothetical protein CARUB_v10007453mg	gbpln	Capsella rubella	AT4G15770.1 | Symbols: | RNA binding | chr4:8978060-8978623 FORWARD LENGTH=187	187	187	1.00E-101	100.0	93.0	96.3
Rsa1.0_00648.1.g17452.t1	gb|ABD65089.1| zinc knuckle containing protein [Brassica oleracea]	244	333	5.00E-31	136.5	30.7	33.6	zinc knuckle containing protein	gbpln	Brassica oleracea	AT4G15780.1 | Symbols: ATVAMP724, VAMP724 | vesicle-associated membrane protein 724 | chr4:8980081-8981697 REVERSE LENGTH=222	244	222	1.00E-17	91.0	18.0	18.9
Rsa1.0_00648.1.g17453.t1	emb|CAB75484.1| putative protein [Arabidopsis thaliana]	675	851	1.00E-100	126.1	28.7	40.6	putative protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	675	575	6.00E-62	85.2	18.2	27.3
Rsa1.0_00648.1.g17454.t2	ref|XP_002868179.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314015|gb|EFH44438.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	82	90	1.00E-24	109.8	75.6	80.5	predicted protein	gbpln	Arabidopsis lyrata	AT4G15802.1 | Symbols: HSBP, AtHSBP | heat shock factor binding protein | chr4:8986864-8988339 REVERSE LENGTH=86	82	86	8.00E-27	104.9	72.0	78.0
Rsa1.0_00648.1.g17455.t1	gb|AAM65484.1| unknown [Arabidopsis thaliana]	303	296	1.00E-136	97.7	83.8	91.1	unknown	gbpln	Arabidopsis thaliana	AT4G15830.1 | Symbols: | ARM repeat superfamily protein | chr4:8995285-8996548 REVERSE LENGTH=296	303	296	1.00E-138	97.7	83.2	91.1
Rsa1.0_00648.1.g17456.t1	ref|XP_002870203.1| hypothetical protein ARALYDRAFT_493298 [Arabidopsis lyrata subsp. lyrata] gi|297316039|gb|EFH46462.1| hypothetical protein ARALYDRAFT_493298 [Arabidopsis lyrata subsp. lyrata]	458	499	0	109.0	74.9	85.2	hypothetical protein ARALYDRAFT_493298	gbpln	Arabidopsis lyrata	AT4G15880.1 | Symbols: ESD4, ATESD4 | Cysteine proteinases superfamily protein | chr4:9012769-9015797 FORWARD LENGTH=489	458	489	0	106.8	74.0	83.6
Rsa1.0_00648.1.g17457.t1	ref|NP_193328.4| dynein light chain LC8-type [Arabidopsis thaliana] gi|28466885|gb|AAO44051.1| At4g15930 [Arabidopsis thaliana] gi|332658267|gb|AEE83667.1| dynein light chain LC8-type [Arabidopsis thaliana]	104	123	6.00E-38	118.3	77.9	84.6	dynein light chain LC8-type	gbpln	Arabidopsis thaliana	AT4G15930.1 | Symbols: | Dynein light chain type 1 family protein | chr4:9036344-9037825 FORWARD LENGTH=123	104	123	1.00E-40	118.3	77.9	84.6
Rsa1.0_00648.1.g17458.t1	gb|AAL14388.1| AT4g15940/dl4011w [Arabidopsis thaliana] gi|21593651|gb|AAM65618.1| isomerase like protein [Arabidopsis thaliana] gi|58331823|gb|AAW70409.1| At4g15940 [Arabidopsis thaliana]	223	223	1.00E-121	100.0	95.1	98.2	AT4g15940/dl4011w	gbpln	Arabidopsis thaliana	AT4G15940.1 | Symbols: | Fumarylacetoacetate (FAA) hydrolase family | chr4:9038361-9040163 FORWARD LENGTH=222	223	222	1.00E-122	99.6	94.6	97.8
Rsa1.0_00648.1.g17459.t1	gb|AAM62604.1| growth factor like protein [Arabidopsis thaliana]	279	282	1.00E-135	101.1	80.3	92.8	growth factor like protein	gbpln	Arabidopsis thaliana	AT4G12720.3 | Symbols: AtNUDT7, GFG1, ATNUDX7 | MutT/nudix family protein | chr4:7487716-7489557 FORWARD LENGTH=282	279	282	1.00E-137	101.1	79.6	91.4
Rsa1.0_00648.1.g17460.t1	gb|EOA16118.1| hypothetical protein CARUB_v10004250mg, partial [Capsella rubella]	322	715	1.00E-152	222.0	82.9	88.5	hypothetical protein CARUB_v10004250mg, partial	gbpln	Capsella rubella	AT4G15960.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:9045763-9047199 REVERSE LENGTH=375	322	375	1.00E-151	116.5	81.1	87.0
Rsa1.0_00648.1.g17461.t1	ref|XP_002870193.1| hypothetical protein ARALYDRAFT_329916 [Arabidopsis lyrata subsp. lyrata] gi|297316029|gb|EFH46452.1| hypothetical protein ARALYDRAFT_329916 [Arabidopsis lyrata subsp. lyrata]	274	242	3.00E-72	88.3	57.7	66.1	hypothetical protein ARALYDRAFT_329916	gbpln	Arabidopsis lyrata	AT3G16720.1 | Symbols: ATL2, TL2 | TOXICOS EN LEVADURA 2 | chr3:5692880-5693794 FORWARD LENGTH=304	274	304	6.00E-65	110.9	58.8	72.6
Rsa1.0_00648.1.g17462.t1	ref|XP_002868170.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314006|gb|EFH44429.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	736	713	0	96.9	71.9	82.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G15980.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr4:9057466-9059983 REVERSE LENGTH=701	736	701	0	95.2	71.6	81.4
Rsa1.0_00648.1.g17463.t1	gb|ABD64994.1| hypothetical protein 26.t00013 [Brassica oleracea]	126	103	1.00E-11	81.7	34.9	46.0	hypothetical protein 26.t00013	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00648.1.g17464.t5	gb|AAC63844.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1653	1231	0	74.5	43.0	53.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17201414-17202323 REVERSE LENGTH=258	1653	258	3.00E-80	15.6	8.8	11.2
Rsa1.0_00648.1.g17465.t1	gb|EOA25923.1| hypothetical protein CARUB_v10019305mg, partial [Capsella rubella]	225	361	3.00E-76	160.4	57.3	72.9	hypothetical protein CARUB_v10019305mg, partial	gbpln	Capsella rubella	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337-69884 REVERSE LENGTH=515	225	515	2.00E-74	228.9	55.6	69.8
Rsa1.0_00648.1.g17466.t1	ref|NP_193340.2| Aminotransferase-like, plant mobile domain family protein [Arabidopsis thaliana] gi|19699015|gb|AAL91243.1| unknown protein [Arabidopsis thaliana] gi|22136336|gb|AAM91246.1| unknown protein [Arabidopsis thaliana] gi|332658286|gb|AEE83686.1| Aminotransferase-like, plant mobile domain family protein [Arabidopsis thaliana]	731	666	0	91.1	55.3	67.2	Aminotransferase-like, plant mobile domain family protein	gbpln	Arabidopsis thaliana	AT4G16050.1 | Symbols: | Aminotransferase-like, plant mobile domain family protein | chr4:9092243-9094243 FORWARD LENGTH=666	731	666	0	91.1	55.3	67.2

Rsa1.0_00648.1.g17467.t1	dbj|BAF01893.1| galactokinase like protein [Arabidopsis thaliana]	220	587	1.00E−11	266.8	24.1	27.7	galactokinase like protein	gbpln	Arabidopsis thaliana	AT4G16130.1 | Symbols: ARA1, ISA1, ATISA1 | arabinose kinase | chr4:9120875−9127656 FORWARD LENGTH=1039	220	1039	6.00E−14	472.3	24.1	27.7
Rsa1.0_00649.1.g17468.t1	ref|XP_002884185.1| hypothetical protein ARALYDRAFT_343571 [Arabidopsis lyrata subsp. lyrata] gi|297330025|gb|EFH60444.1| hypothetical protein ARALYDRAFT_343571 [Arabidopsis lyrata subsp. lyrata]	614	607	0	98.9	88.6	93.0	hypothetical protein ARALYDRAFT_343571	gbpln	Arabidopsis lyrata	AT2G18915.2 | Symbols: LKP2, ADO2 | LOV KELCH protein 2 | chr2:8194792−8197255 REVERSE LENGTH=611	614	611	0	99.5	88.6	92.7
Rsa1.0_00649.1.g17469.t1	ref|NP_849983.1| LOV KELCH protein 2 [Arabidopsis thaliana] gi|75162385|sp|Q8W420.1|ADO2_ARATH RecName: Full=Adagio protein 2; AltName: Full=F−box only protein 2c; Short=FBX2c; AltName: Full=Flavin−binding kelch repeat F−box protein 1−like protein 1; Short=FKF1−like protein 1; AltName: Full=LOV kelch protein 2 gi|18146958|dbj|BAB83169.1| LOV kelch protein 2 [Arabidopsis thaliana] gi|20466486|gb|AAM20560.1| unknown protein [Arabidopsis thaliana] gi|209414528|gb|ACI46504.1| At2g18915 [Arabidopsis thaliana] gi|330251732|gb|AEC06826.1| LOV KELCH protein 2 [Arabidopsis thaliana]	78	611	8.00E−33	783.3	91.0	92.3	LOV KELCH protein 2	gbpln	Arabidopsis thaliana	AT2G18915.2 | Symbols: LKP2, ADO2 | LOV KELCH protein 2 | chr2:8194792−8197255 REVERSE LENGTH=611	78	611	1.00E−35	783.3	91.0	92.3
Rsa1.0_00649.1.g17470.t1	ref|NP_565444.2| LOV KELCH protein 2 [Arabidopsis thaliana] gi|330251731|gb|AEC06825.1| LOV KELCH protein 2 [Arabidopsis thaliana]	515	601	0	116.7	90.3	93.6	LOV KELCH protein 2	gbpln	Arabidopsis thaliana	AT2G18915.1 | Symbols: LKP2, ADO2 | LOV KELCH protein 2 | chr2:8194792−8197255 REVERSE LENGTH=601	515	601	0	116.7	90.3	93.6
Rsa1.0_00649.1.g17471.t1	gb|EOA30141.1| hypothetical protein CARUB_v10013248mg [Capsella rubella]	569	612	0	107.6	86.3	91.6	hypothetical protein CARUB_v10013248mg	gbpln	Capsella rubella	AT2G18915.2 | Symbols: LKP2, ADO2 | LOV KELCH protein 2 | chr2:8194792−8197255 REVERSE LENGTH=611	569	611	0	107.4	85.4	91.2
Rsa1.0_00649.1.g17472.t1	gb|AFB74211.1| homogentisate phytyltransferase [Brassica napus]	481	394	0	81.9	73.6	74.8	homogentisate phytyltransferase	gbpln	Brassica napus	AT2G18950.1 | Symbols: HPT1, TPT1, ATHPT, VTE2 | homogentisate phytyltransferase 1 | chr2:8207491−8210047 FORWARD LENGTH=393	481	393	0	81.7	69.9	72.3
Rsa1.0_00649.1.g17473.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00649.1.g17474.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00649.1.g17475.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00649.1.g17476.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1420	1496	0	105.4	56.5	71.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1420	1262	1.00E−123	88.9	15.5	21.9
Rsa1.0_00649.1.g17477.t1	gb|EOA29818.1| hypothetical protein CARUB_v10012913mg [Capsella rubella]	949	949	0	100.0	98.4	99.4	hypothetical protein CARUB_v10012913mg	gbpln	Capsella rubella	AT2G18960.1 | Symbols: AHA1, PMA, OST2, HA1 | H(+)−ATPase 1 | chr2:8221858−8227268 FORWARD LENGTH=949	949	949	0	100.0	97.7	99.1
Rsa1.0_00649.1.g17478.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1505	2726	0	181.1	51.8	69.2	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916−236392 FORWARD LENGTH=158	1505	158	4.00E−37	10.5	5.0	5.8
Rsa1.0_00650.1.g17479.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	222	149	6.00E−23	67.1	21.6	32.4	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00650.1.g17480.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00650.1.g17481.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00650.1.g17482.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00650.1.g17483.t1	ref|XP_002865381.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297311216|gb|EFH41640.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	461	464	0	100.7	85.5	90.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G44160.1 | Symbols: NUC | C2H2−like zinc finger protein | chr5:17773091−17775513 FORWARD LENGTH=466	461	466	0	101.1	86.1	90.7
Rsa1.0_00650.1.g17484.t1	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	167	1463	1.00E−42	876.0	55.7	73.1	F5J5.1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00650.1.g17485.t3	ref|NP_199231.1| Homeodomain−like transcriptional regulator [Arabidopsis thaliana] gi|9759519|dbj|BAB10985.1| unnamed protein product [Arabidopsis thaliana] gi|332007687|gb|AED95070.1| Homeodomain−like transcriptional regulator [Arabidopsis thaliana]	1633	1694	0	103.7	80.8	87.2	Homeodomain−like transcriptional regulator	gbpln	Arabidopsis thaliana	AT5G44180.1 | Symbols: | Homeodomain−like transcriptional regulator | chr5:17783172−17789872 FORWARD LENGTH=1694	1633	1694	0	103.7	80.8	87.2

Rsa1.0_00650.1.g17486.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	448	442	5.00E-94	98.7	36.4	39.5	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	448	343	2.00E-24	76.6	10.9	12.9
Rsa1.0_00650.1.g17487.t1	ref|NP_199232.1| protein GOLDEN2-like 2 [Arabidopsis thaliana] gi|75333752|sp|Q9FFH0.1|GLK2_ARATH RecName: Full=Transcription activator GLK2; AltName: Full=GBF'S PRO-RICH REGION-INTERACTING factor 2; AltName: Full=Golden2-like protein 2; Short=AtGLK2 gi|9759520|dbj|BAB10986.1| unnamed protein product [Arabidopsis thaliana] gi|13311005|gb|AAK16744.1| golden2-like transcription factor [Arabidopsis thaliana] gi|13432090|gb|AAK20121.1| golden2-like protein 2 [Arabidopsis thaliana] gi|17221601|dbj|BAB78467.1| GPRI2 [Arabidopsis thaliana] gi|332007689|gb|AED95072.1| transcription activator GLK2 [Arabidopsis thaliana]	377	386	1.00E-150	102.4	81.4	87.5	protein GOLDEN2-like 2	gbpln	Arabidopsis thaliana	AT5G44190.1 | Symbols: GLK2, ATGLK2, GPRI2 | GOLDEN2-like 2 | chr5:17798435-17800647 FORWARD LENGTH=386	377	386	1.00E-153	102.4	81.4	87.5
Rsa1.0_00651.1.g17488.t1	ref|XP_002877484.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323322|gb|EFH53743.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	489	494	0	101.0	84.3	89.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G46450.1 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr3:17093297-17095319 REVERSE LENGTH=486	489	486	0	99.4	82.4	87.5
Rsa1.0_00651.1.g17489.t1	gb|EOA28162.1| hypothetical protein CARUB_v10024350mg [Capsella rubella]	112	114	7.00E-28	101.8	86.6	90.2	hypothetical protein CARUB_v10024350mg	gbpln	Capsella rubella	AT2G27710.4 | Symbols: | 60S acidic ribosomal protein family | chr2:11816929-11817670 FORWARD LENGTH=98	112	98	2.00E-28	87.5	56.3	58.0
Rsa1.0_00651.1.g17490.t10	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00651.1.g17491.t1	ref|NP_190194.1| C2H2-type zinc finger protein [Arabidopsis thaliana] gi|75335605|sp|Q9LX85.1|ZAT8_ARATH RecName: Full=Zinc finger protein ZAT8 gi|7798996|emb|CAB90935.1| zinc finger-like protein [Arabidopsis thaliana] gi|225898695|dbj|BAH30478.1| hypothetical protein [Arabidopsis thaliana] gi|332644589|gb|AEE78110.1| zinc finger protein ZAT8 [Arabidopsis thaliana]	162	164	5.00E-48	101.2	67.3	75.9	C2H2-type zinc finger protein	gbpln	Arabidopsis thaliana	AT3G46080.1 | Symbols: | C2H2-type zinc finger family protein | chr3:16922753-16923247 REVERSE LENGTH=164	162	164	2.00E-50	101.2	67.3	75.9
Rsa1.0_00651.1.g17492.t1	ref|XP_002864652.1| hypothetical protein ARALYDRAFT_919218 [Arabidopsis lyrata subsp. lyrata] gi|297310487|gb|EFH40911.1| hypothetical protein ARALYDRAFT_919218 [Arabidopsis lyrata subsp. lyrata]	171	162	1.00E-43	94.7	60.8	72.5	hypothetical protein ARALYDRAFT_919218	gbpln	Arabidopsis lyrata	AT3G46080.1 | Symbols: | C2H2-type zinc finger family protein | chr3:16922753-16923247 REVERSE LENGTH=164	171	164	1.00E-45	95.9	60.8	70.2

Rsa1.0_00651.1.g17493.t5	ref|NP_190192.1| Ras-related protein ARA-3 [Arabidopsis thaliana] gi|145332765|ref|NP_001078248.1| Ras-related protein ARA-3 [Arabidopsis thaliana] gi|186510716|ref|NP_001118780.1| Ras-related protein ARA-3 [Arabidopsis thaliana] gi|297815758|ref|XP_002875762.1| hypothetical protein ARALYDRAFT_484985 [Arabidopsis lyrata subsp. lyrata] gi|114088|sp|P28186.1|RAE1C_ARATH RecName: Full=Ras-related protein RABE1c; Short=AtRABE1c; AltName: Full=Ras-related protein Ara-3; AltName: Full=Ras-related protein Rab8A; Short=AtRab8A gi|217837|dbj|BAA00830.1| small GTP-binding protein [Arabidopsis thaliana] gi|7798994|emb|CAB90933.1| GTP-binding protein ara-3 [Arabidopsis thaliana] gi|14334918|gb|AAK59637.1| putative GTP-binding protein ara-3 [Arabidopsis thaliana] gi|14596015|gb|AAK68735.1| GTP-binding protein ara-3 [Arabidopsis thaliana] gi|25054949|gb|AAN71951.1| putative GTP-binding protein ara-3 [Arabidopsis thaliana] gi|25084212|gb|AAN72197.1| GTP-binding protein ara-3 [Arabidopsis thaliana] gi|297321600|gb|EFH52021.1| hypothetical protein	216	216	1.00E-123	100.0	100.0	100.0	Ras-related protein ARA-3	gbpln	Arabidopsis lyrata	AT3G46060.3 | Symbols: ARA3 | RAB GTPase homolog 8A | chr3:16917908-16919740 FORWARD LENGTH=216	216	216	1.00E-125	100.0	100.0	100.0
Rsa1.0_00651.1.g17494.t1	ref|XP_002877404.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297323242|gb|EFH53663.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	673	670	0	99.6	75.5	84.5	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT3G45440.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:16664875-16666884 REVERSE LENGTH=669	673	669	0	99.4	74.3	84.1
Rsa1.0_00651.1.g17495.t1	ref|NP_190058.1| arogenate dehydratase 4 [Arabidopsis thaliana] gi|75097389|sp|O22241.1|AROD4_ARATH RecName: Full=Arogenate dehydratase 4, chloroplastic; Short=AtADT4; Flags: Precursor gi|2392772|gb|AAB70035.1| putative chloroplast prephenate dehydratase [Arabidopsis thaliana] gi|17065232|gb|AAL32770.1| putative chloroplast prephenate dehydratase [Arabidopsis thaliana] gi|31711890|gb|AAP68301.1| At3g44720 [Arabidopsis thaliana] gi|89340488|gb|ABD67753.1| arogenate dehydratase isoform 4 [Arabidopsis thaliana] gi|332644418|gb|AEE77939.1| arogenate dehydratase 4 [Arabidopsis thaliana]	422	424	0	100.5	88.9	93.6	arogenate dehydratase 4	gbpln	Arabidopsis thaliana	AT3G44720.1 | Symbols: ADT4 | arogenate dehydratase 4 | chr3:16271759-16273033 FORWARD LENGTH=424	422	424	0	100.5	88.9	93.6
Rsa1.0_00651.1.g17496.t1	emb|CCD74534.1| myrosinase-binding protein-like protein [Arabidopsis halleri subsp. halleri]	465	463	0	99.6	73.5	82.6	myrosinase-binding protein-like protein	gbpln	Arabidopsis halleri	AT2G25980.1 | Symbols: | Mannose-binding lectin superfamily protein | chr2:11077718-11079642 REVERSE LENGTH=449	465	449	0	96.6	72.0	81.5
Rsa1.0_00651.1.g17497.t1	emb|CAC03543.1| putative protein [Arabidopsis thaliana]	809	731	0	90.4	67.1	78.1	putative protein	gbpln	Arabidopsis thaliana	AT3G44930.1 | Symbols: ATCHX10, CHX10 | cation/H+ exchanger 10 | chr3:16402058-16404672 REVERSE LENGTH=783	809	783	0	96.8	67.1	78.1
Rsa1.0_00651.1.g17498.t3	ref|NP_190082.1| uncharacterized protein [Arabidopsis thaliana] gi|7671397|emb|CAB89311.1| putative protein [Arabidopsis thaliana] gi|332644452|gb|AEE77973.1| uncharacterized protein AT3G44960 [Arabidopsis thaliana]	229	207	2.00E-48	90.4	56.8	68.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G44960.1 | Symbols: | unknown protein; Has 34 Blast hits to 34 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:16427795-16429151 FORWARD LENGTH=207	229	207	7.00E-51	90.4	56.8	68.6
Rsa1.0_00651.1.g17499.t1	ref|XP_004251248.1| PREDICTED: calmodulin-like isoform 1 [Solanum lycopersicum]	149	180	6.00E-80	120.8	99.3	100.0	PREDICTED: calmodulin-like isoform 1	gbpln	Solanum lycopersicum	AT2G27030.3 | Symbols: CAM5 | calmodulin 5 | chr2:11532069-11534176 FORWARD LENGTH=181	149	181	1.00E-81	121.5	98.0	100.0
Rsa1.0_00651.1.g17500.t1	ref|NP_178872.2| MAK10-like protein [Arabidopsis thaliana] gi|330251069|gb|AEC06163.1| MAK10-like protein [Arabidopsis thaliana]	743	728	0	98.0	82.2	89.0	MAK10-like protein	gbpln	Arabidopsis thaliana	AT2G11000.1 | Symbols: ATMAK10, MAK10 | MAK10 homologue | chr2:4341328-4347768 REVERSE LENGTH=728	743	728	0	98.0	82.2	89.0

<table>
<tr><td>Rsa1.0_00651.1.g17501.t1</td><td>ref|XP_002866765.1| hypothetical protein ARALYDRAFT_920105 [Arabidopsis lyrata subsp. lyrata] gi|297312600|gb|EFH43024.1| hypothetical protein ARALYDRAFT_920105 [Arabidopsis lyrata subsp. lyrata]</td><td>102</td><td>100</td><td>1.00E-26</td><td>98.0</td><td>62.7</td><td>70.6</td><td>hypothetical protein ARALYDRAFT_920105</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00651.1.g17502.t1</td><td>ref|XP_002877284.1| tubulin family protein [Arabidopsis lyrata subsp. lyrata] gi|297323122|gb|EFH53543.1| tubulin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>1200</td><td>1211</td><td>0</td><td>100.9</td><td>83.3</td><td>88.5</td><td>tubulin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G43610.1 | Symbols: | Spc97 / Spc98 family of spindle pole body (SBP) component | chr3:15517772-15523927 REVERSE LENGTH=1207</td><td>1200</td><td>1207</td><td>0</td><td>100.6</td><td>81.3</td><td>87.9</td></tr>
<tr><td>Rsa1.0_00651.1.g17503.t1</td><td>ref|XP_002877283.1| hypothetical protein ARALYDRAFT_323092 [Arabidopsis lyrata subsp. lyrata] gi|297323121|gb|EFH53542.1| hypothetical protein ARALYDRAFT_323092 [Arabidopsis lyrata subsp. lyrata]</td><td>1282</td><td>1318</td><td>0</td><td>102.8</td><td>81.1</td><td>89.5</td><td>hypothetical protein ARALYDRAFT_323092</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G43600.1 | Symbols: AAO2, AO3, atAO-2, AOgamma, AtAO3 | aldehyde oxidase 2 | chr3:15512778-15517375 REVERSE LENGTH=1321</td><td>1282</td><td>1321</td><td>0</td><td>103.0</td><td>80.7</td><td>89.5</td></tr>
<tr><td>Rsa1.0_00651.1.g17504.t1</td><td>ref|XP_002875609.1| hypothetical protein ARALYDRAFT_484801 [Arabidopsis lyrata subsp. lyrata] gi|297321447|gb|EFH51868.1| hypothetical protein ARALYDRAFT_484801 [Arabidopsis lyrata subsp. lyrata]</td><td>226</td><td>241</td><td>1.00E-66</td><td>106.6</td><td>76.1</td><td>83.2</td><td>hypothetical protein ARALYDRAFT_484801</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G43520.1 | Symbols: | Transmembrane proteins 14C | chr3:15406088-15407699 FORWARD LENGTH=240</td><td>226</td><td>240</td><td>3.00E-68</td><td>106.2</td><td>70.4</td><td>78.3</td></tr>
<tr><td>Rsa1.0_00651.1.g17505.t2</td><td>sp|F4IXW2.2|BIG5_ARATH RecName: Full=Brefeldin A-inhibited guanine nucleotide-exchange protein 5; Short=BIG5; AltName: Full=ARF guanine-nucleotide exchange factor BIG5; AltName: Full=Protein BFA-VISUALIZED ENDOCYTIC TRAFFICKING DEFECTIVE 1; Short=Protein BEN1; AltName: Full=Protein HOPM INTERACTOR 7</td><td>1734</td><td>1739</td><td>0</td><td>100.3</td><td>91.5</td><td>94.6</td><td>RecName: Full=Brefeldin A-inhibited guanine nucleotide-exchange protein 5; Short=BIG5; AltName: Full=ARF guanine-nucleotide exchange factor BIG5; AltName: Full=Protein BFA-VISUALIZED ENDOCYTIC TRAFFICKING DEFECTIVE 1; Short=Protein BEN1; AltName: Full=Protein HOPM INTERACTOR 7</td><td>----</td><td>----</td><td>AT3G43300.1 | Symbols: ATMIN7, BEN1 | HOPM interactor 7 | chr3:15234235-15245034 REVERSE LENGTH=1758</td><td>1734</td><td>1758</td><td>0</td><td>101.4</td><td>91.5</td><td>94.6</td></tr>
<tr><td>Rsa1.0_00651.1.g17506.t1</td><td>dbj|BAJ33808.1| unnamed protein product [Thellungiella halophila]</td><td>483</td><td>479</td><td>0</td><td>99.2</td><td>76.2</td><td>83.2</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G43230.1 | Symbols: | RING/FYVE/PHD-type zinc finger family protein | chr3:15207776-15209599 FORWARD LENGTH=485</td><td>483</td><td>485</td><td>0</td><td>100.4</td><td>71.8</td><td>79.1</td></tr>
<tr><td>Rsa1.0_00651.1.g17507.t1</td><td>gb|EOA23461.1| hypothetical protein CARUB_v10016650mg [Capsella rubella]</td><td>909</td><td>941</td><td>0</td><td>103.5</td><td>87.2</td><td>92.7</td><td>hypothetical protein CARUB_v10016650mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G43210.1 | Symbols: TES, ATNACK2, NACK2 | ATP binding microtubule motor family protein | chr3:15191429-15196021 FORWARD LENGTH=938</td><td>909</td><td>938</td><td>0</td><td>103.2</td><td>87.5</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00651.1.g17508.t1</td><td>ref|XP_004306259.1| PREDICTED: SKP1-like protein 4-like [Fragaria vesca subsp. vesca]</td><td>161</td><td>172</td><td>2.00E-36</td><td>106.8</td><td>54.0</td><td>72.0</td><td>PREDICTED: SKP1-like protein 4-like</td><td>gbpln</td><td>Fragaria vesca</td><td>AT1G20140.1 | Symbols: ASK4, SK4 | SKP1-like 4 | chr1:6986430-6987079 FORWARD LENGTH=163</td><td>161</td><td>163</td><td>1.00E-38</td><td>101.2</td><td>52.2</td><td>70.2</td></tr>
<tr><td>Rsa1.0_00651.1.g17509.t1</td><td>gb|EOA24721.1| hypothetical protein CARUB_v10017999mg [Capsella rubella]</td><td>220</td><td>216</td><td>1.00E-100</td><td>98.2</td><td>85.5</td><td>89.1</td><td>hypothetical protein CARUB_v10017999mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G26060.1 | Symbols: ATPRX Q | Thioredoxin superfamily protein | chr3:9524807-9526123 FORWARD LENGTH=216</td><td>220</td><td>216</td><td>5.00E-98</td><td>98.2</td><td>83.2</td><td>86.4</td></tr>
<tr><td>Rsa1.0_00651.1.g17510.t1</td><td>ref|NP_189874.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|7529259|emb|CAB86675.1| receptor protein kinase-like protein [Arabidopsis thaliana] gi|91806516|gb|ABE65985.1| leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|224589585|gb|ACN59326.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332644237|gb|AEE77758.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]</td><td>636</td><td>633</td><td>0</td><td>99.5</td><td>81.6</td><td>90.9</td><td>leucine-rich repeat protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42880.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:14954587-14956577 FORWARD LENGTH=633</td><td>636</td><td>633</td><td>0</td><td>99.5</td><td>81.6</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00651.1.g17511.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>1216</td><td>1274</td><td>0</td><td>104.8</td><td>41.5</td><td>55.0</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1216</td><td>626</td><td>3.00E-35</td><td>51.5</td><td>9.0</td><td>16.1</td></tr>
</table>

Rsa1.0_00651.1.g17512.t1	gb|EOA23959.1| hypothetical protein CARUB_v10017176mg [Capsella rubella]	464	469	0	101.1	83.6	89.9	hypothetical protein CARUB_v10017176mg	gbpln	Capsella rubella	AT3G52610.1 | Symbols: | unknown protein; Has 68 Blast hits to 67 proteins in 21 species: Archae - 0; Bacteria - 11; Metazoa - 0; Fungi - 0; Plants - 55; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:19510513-19512547 FORWARD LENGTH=475	464	475	0	102.4	82.3	89.2
Rsa1.0_00651.1.g17513.t1	ref|XP_002876160.1| hypothetical protein ARALYDRAFT_485631 [Arabidopsis lyrata subsp. lyrata] gi|297321998|gb|EFH52419.1| hypothetical protein ARALYDRAFT_485631 [Arabidopsis lyrata subsp. lyrata]	90	87	8.00E-25	96.7	81.1	90.0	hypothetical protein ARALYDRAFT_485631	gbpln	Arabidopsis lyrata	AT3G52620.1 | Symbols: | unknown protein; Has 11 Blast hits to 11 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:19513113-19513556 FORWARD LENGTH=87	90	87	3.00E-22	96.7	75.6	86.7
Rsa1.0_00652.1.g17514.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	500	1352	2.00E-72	270.4	34.2	49.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	500	746	2.00E-55	149.2	27.0	38.0
Rsa1.0_00652.1.g17515.t1	gb|EOA25343.1| hypothetical protein CARUB_v10018664mg [Capsella rubella]	172	181	1.00E-22	105.2	39.0	55.2	hypothetical protein CARUB_v10018664mg	gbpln	Capsella rubella	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	172	170	3.00E-19	98.8	31.4	45.3
Rsa1.0_00652.1.g17516.t1	ref|NP_175139.1| receptor like protein 6 [Arabidopsis thaliana] gi|12321005|gb|AAG50623.1|AC083835_8 disease resistance protein, putative [Arabidopsis thaliana] gi|332193999|gb|AEE32120.1| receptor like protein 6 [Arabidopsis thaliana]	937	994	0	106.1	66.4	77.3	receptor like protein 6	gbpln	Arabidopsis thaliana	AT1G45616.1 | Symbols: AtRLP6, RLP6 | receptor like protein 6 | chr1:17183550-17186534 REVERSE LENGTH=994	937	994	0	106.1	66.4	77.3
Rsa1.0_00652.1.g17517.t1	ref|NP_192110.2| protein kinase family protein [Arabidopsis thaliana] gi|21928159|gb|AAM78107.1| AT4g02010/T10M13_2 [Arabidopsis thaliana] gi|32815839|gb|AAP88328.1| At4g02010/T10M13_2 [Arabidopsis thaliana] gi|332656711|gb|AEE82111.1| protein kinase family protein [Arabidopsis thaliana]	714	725	0	101.5	90.1	92.9	protein kinase family protein	gbpln	Arabidopsis thaliana	AT4G02010.1 | Symbols: | Protein kinase superfamily protein | chr4:881457-885222 FORWARD LENGTH=725	714	725	0	101.5	90.1	92.9
Rsa1.0_00652.1.g17518.t1	ref|NP_680560.1| uncharacterized protein [Arabidopsis thaliana] gi|17065174|gb|AAL32741.1| Unknown protein [Arabidopsis thaliana] gi|20259952|gb|AAM13323.1| unknown protein [Arabidopsis thaliana] gi|332656709|gb|AEE82109.1| uncharacterized protein AT4G01995 [Arabidopsis thaliana]	258	258	1.00E-113	100.0	84.5	89.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G01995.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G64680.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:873075-874619 FORWARD LENGTH=258	258	258	1.00E-116	100.0	84.5	89.9
Rsa1.0_00652.1.g17519.t1	ref|XP_002872860.1| hypothetical protein ARALYDRAFT_490379 [Arabidopsis lyrata subsp. lyrata] gi|297318697|gb|EFH49119.1| hypothetical protein ARALYDRAFT_490379 [Arabidopsis lyrata subsp. lyrata]	502	500	0	99.6	76.3	87.8	hypothetical protein ARALYDRAFT_490379	gbpln	Arabidopsis lyrata	AT4G01990.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:871268-872885 REVERSE LENGTH=502	502	502	0	100.0	74.1	86.5
Rsa1.0_00652.1.g17520.t1	dbj|BAJ34109.1| unnamed protein product [Thellungiella halophila]	520	521	0	100.2	87.1	94.0	unnamed protein product	----	----	AT4G01950.1 | Symbols: ATGPAT3, GPAT3 | glycerol-3-phosphate acyltransferase 3 | chr4:844597-846710 REVERSE LENGTH=520	520	520	0	100.0	86.7	93.8
Rsa1.0_00652.1.g17521.t1	ref|NP_567219.1| NifU-like protein 1 [Arabidopsis thaliana] gi|75163233|sp|Q93W77.1|NIFU1_ARATH RecName: Full=NifU-like protein 1, chloroplastic; Short=AtCNfu1; Short=AtCnfU-IVb; Flags: Precursor gi|14517434|gb|AAK62607.1| AT4g01940/T7B11_20 [Arabidopsis thaliana] gi|15215670|gb|AAK91380.1| AT4g01940/T7B11_20 [Arabidopsis thaliana] gi|20908090|gb|AAM26728.1| AT4g01940/T7B11_20 [Arabidopsis thaliana] gi|28207816|emb|CAD55558.1| NFU1 protein [Arabidopsis thaliana] gi|332656703|gb|AEE82103.1| NifU-like protein 1 [Arabidopsis thaliana]	229	231	5.00E-96	100.9	85.6	88.2	NifU-like protein 1	gbpln	Arabidopsis thaliana	AT4G01940.1 | Symbols: NFU1, AtCNFU1 | NFU domain protein 1 | chr4:842265-843388 REVERSE LENGTH=231	229	231	2.00E-98	100.9	85.6	88.2
Rsa1.0_00652.1.g17522.t1	gb|AAG52094.1|AC012680_5 putative Mutator-like transposase; 12516-14947 [Arabidopsis thaliana]	352	761	2.00E-59	216.2	41.2	54.0	putative Mutator-like transposase; 12516-14947	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00652.1.g17523.t1	ref|XP_002872902.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata] gi|297318739|gb|EFH49161.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata]	338	356	1.00E-142	105.3	75.7	85.5	hypothetical protein ARALYDRAFT_912111	gbpln	Arabidopsis lyrata	AT4G01220.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr4:513431-515648 REVERSE LENGTH=360	338	360	1.00E-141	106.5	70.4	79.6
Rsa1.0_00652.1.g17524.t1	ref|XP_002872902.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata] gi|297318739|gb|EFH49161.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata]	344	356	1.00E-143	103.5	74.7	81.4	hypothetical protein ARALYDRAFT_912111	gbpln	Arabidopsis lyrata	AT4G01220.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr4:513431-515648 REVERSE LENGTH=360	344	360	1.00E-145	104.7	71.2	76.7
Rsa1.0_00652.1.g17525.t1	gb|EOA19468.1| hypothetical protein CARUB_v10002012mg [Capsella rubella]	196	195	7.00E-86	99.5	82.7	89.3	hypothetical protein CARUB_v10002012mg	gbpln	Capsella rubella	AT4G01900.1 | Symbols: PII, GLB1 | GLNB1 homolog | chr4:821736-823294 FORWARD LENGTH=196	196	196	6.00E-87	100.0	83.2	88.8
Rsa1.0_00652.1.g17526.t1	ref|XP_002872869.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318706|gb|EFH49128.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	147	122	2.00E-50	83.0	69.4	76.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G01897.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF952 (InterPro:IPR009297); Has 763 Blast hits to 763 proteins in 180 species: Archae - 0; Bacteria - 351; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 383 (source: NCBI BLink). | chr4:820487-821466 REVERSE LENGTH=122	147	122	1.00E-50	83.0	66.0	76.2
Rsa1.0_00652.1.g17527.t1	ref|NP_567218.2| systemic acquired resistance (SAR) regulator protein NIMIN-1-like protein [Arabidopsis thaliana] gi|12057175|emb|CAC19852.1| NIMIN-1b protein [Arabidopsis thaliana] gi|109946491|gb|ABG48424.1| At4g01895 [Arabidopsis thaliana] gi|332656692|gb|AEE82092.1| systemic acquired resistance (SAR) regulator protein NIMIN-1-like protein [Arabidopsis thaliana]	130	140	9.00E-26	107.7	60.0	73.8	systemic acquired resistance (SAR) regulator protein NIMIN-1-like protein	gbpln	Arabidopsis thaliana	AT4G01895.1 | Symbols: | systemic acquired resistance (SAR) regulator protein NIMIN-1-related | chr4:819957-820379 FORWARD LENGTH=140	130	140	2.00E-28	107.7	60.0	73.8
Rsa1.0_00652.1.g17528.t2	gb|EOA19709.1| hypothetical protein CARUB_v10003570mg [Capsella rubella]	485	477	0	98.4	75.9	82.9	hypothetical protein CARUB_v10003570mg	gbpln	Capsella rubella	AT4G01890.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:816210-818428 FORWARD LENGTH=468	485	468	0	96.5	73.2	81.4
Rsa1.0_00653.1.g17529.t1	gb|ABD65028.1| hypothetical protein 26.t00082 [Brassica oleracea]	105	220	4.00E-14	209.5	42.9	51.4	hypothetical protein 26.t00082	gbpln	Brassica oleracea	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	105	384	5.00E-12	365.7	26.7	36.2
Rsa1.0_00653.1.g17530.t1	ref|XP_002889446.1| EDGP precursor [Arabidopsis lyrata subsp. lyrata] gi|297335288|gb|EFH65705.1| EDGP precursor [Arabidopsis lyrata subsp. lyrata]	419	433	0	103.3	79.7	88.1	EDGP precursor	gbpln	Arabidopsis lyrata	AT1G03220.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:787143-788444 FORWARD LENGTH=433	419	433	0	103.3	77.8	87.6
Rsa1.0_00653.1.g17531.t1	ref|XP_002889446.1| EDGP precursor [Arabidopsis lyrata subsp. lyrata] gi|297335288|gb|EFH65705.1| EDGP precursor [Arabidopsis lyrata subsp. lyrata]	432	433	0	100.2	85.2	91.0	EDGP precursor	gbpln	Arabidopsis lyrata	AT1G03220.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:787143-788444 FORWARD LENGTH=433	432	433	0	100.2	83.6	90.7
Rsa1.0_00653.1.g17532.t3	ref|XP_002892154.1| hypothetical protein ARALYDRAFT_887478 [Arabidopsis lyrata subsp. lyrata] gi|297337996|gb|EFH68413.1| hypothetical protein ARALYDRAFT_887478 [Arabidopsis lyrata subsp. lyrata]	351	274	1.00E-134	78.1	72.1	74.9	hypothetical protein ARALYDRAFT_887478	gbpln	Arabidopsis lyrata	AT1G03260.1 | Symbols: | SNARE associated Golgi protein family | chr1:795678-798102 REVERSE LENGTH=274	351	274	1.00E-136	78.1	71.5	74.9
Rsa1.0_00653.1.g17533.t1	gb|EOA40220.1| hypothetical protein CARUB_v10008943mg [Capsella rubella]	500	496	0	99.2	87.0	91.2	hypothetical protein CARUB_v10008943mg	gbpln	Capsella rubella	AT1G03270.1 | Symbols: | CBS domain-containing protein with a domain of unknown function (DUF21) | chr1:799191-802436 FORWARD LENGTH=499	500	499	0	99.8	89.8	92.4
Rsa1.0_00653.1.g17534.t1	gb|EOA38324.1| hypothetical protein CARUB_v10009825mg, partial [Capsella rubella]	332	306	4.00E-14	92.2	19.0	21.1	hypothetical protein CARUB_v10009825mg, partial	gbpln	Capsella rubella	AT1G03470.2 | Symbols: | Kinase interacting (KIP1-like) family protein | chr1:866217-867493 REVERSE LENGTH=269	332	269	2.00E-12	81.0	16.6	21.7
Rsa1.0_00653.1.g17535.t2	gb|EOA39421.1| hypothetical protein CARUB_v10012530mg [Capsella rubella]	285	283	1.00E-147	99.3	89.1	94.4	hypothetical protein CARUB_v10012530mg	gbpln	Capsella rubella	AT1G03550.1 | Symbols: | Secretory carrier membrane protein (SCAMP) family protein | chr1:885851-887778 REVERSE LENGTH=283	285	283	1.00E-143	99.3	89.1	93.7
Rsa1.0_00653.1.g17536.t1	gb|EOA38556.1| hypothetical protein CARUB_v10010366mg, partial [Capsella rubella]	158	191	2.00E-78	120.9	87.3	94.3	hypothetical protein CARUB_v10010366mg, partial	gbpln	Capsella rubella	AT1G03650.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr1:910249-911103 REVERSE LENGTH=158	158	158	6.00E-79	100.0	86.1	94.3
Rsa1.0_00653.1.g17537.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00653.1.g17538.t2	sp|Q9XGS0.1|TRXM_BRANA RecName: Full=Thioredoxin M-type, chloroplastic; Short=Trx-M; Flags: Precursor gi|1943720|gb|AAB52409.1| thioredoxin-m [Brassica napus] gi|5566283|gb|AAD45358.1| thioredoxin-m precursor [Brassica napus]	181	177	1.00E-83	97.8	89.0	90.6	RecName: Full=Thioredoxin M-type, chloroplastic; Short=Trx-M; Flags: Precursor gi|1943720|gb|AAB52409.1| thioredoxin-m	gbpln	Brassica napus	AT1G03680.1 | Symbols: ATHM1, TRX-M1, ATM1, THM1 | thioredoxin M-type 1 | chr1:916990-917865 REVERSE LENGTH=179	181	179	1.00E-80	98.9	81.2	88.4
Rsa1.0_00653.1.g17539.t1	gb|EOA37950.1| hypothetical protein CARUB_v10009418mg [Capsella rubella]	385	386	0	100.3	82.6	90.9	hypothetical protein CARUB_v10009418mg	gbpln	Capsella rubella	AT1G03687.1 | Symbols: | DTW domain-containing protein | chr1:918308-920306 FORWARD LENGTH=381	385	381	0	99.0	82.1	89.6
Rsa1.0_00653.1.g17540.t1	ref|NP_563690.1| uncharacterized protein [Arabidopsis thaliana] gi|107738058|gb|ABF83624.1| At1g03730 [Arabidopsis thaliana] gi|332189482|gb|AEE27603.1| uncharacterized protein AT1G03730 [Arabidopsis thaliana]	164	167	9.00E-69	101.8	91.5	95.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G03730.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03600.1); Has 50 Blast hits to 50 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:931017-931520 REVERSE LENGTH=167	164	167	3.00E-71	101.8	91.5	95.1
Rsa1.0_00653.1.g17541.t1	ref|NP_171870.4| protein kinase domain-containing protein [Arabidopsis thaliana] gi|9280653|gb|AAF86522.1|AC002560_15 F21B7.34 [Arabidopsis thaliana] gi|13430452|gb|AAK25848.1|AF360138_1 putative protein kinase [Arabidopsis thaliana] gi|14532736|gb|AAK64069.1| putative protein kinase [Arabidopsis thaliana] gi|332189483|gb|AEE27604.1| protein kinase domain-containing protein [Arabidopsis thaliana]	724	740	0	102.2	75.1	84.3	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G03740.1 | Symbols: | Protein kinase superfamily protein | chr1:934055-936792 FORWARD LENGTH=740	724	740	0	102.2	75.1	84.3
Rsa1.0_00653.1.g17542.t1	ref|XP_002889473.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335315|gb|EFH65732.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	872	876	0	100.5	86.2	93.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G03750.1 | Symbols: CHR9 | switch 2 | chr1:937920-941068 FORWARD LENGTH=862	872	862	0	98.9	85.8	92.3
Rsa1.0_00653.1.g17543.t1	ref|XP_002892523.1| hypothetical protein ARALYDRAFT_334257 [Arabidopsis lyrata subsp. lyrata] gi|297338365|gb|EFH68782.1| hypothetical protein ARALYDRAFT_334257 [Arabidopsis lyrata subsp. lyrata]	323	305	1.00E-70	94.4	48.9	64.4	hypothetical protein ARALYDRAFT_334257	gbpln	Arabidopsis lyrata	AT2G42470.1 | Symbols: | TRAF-like family protein | chr2:17679887-17685187 REVERSE LENGTH=898	323	898	4.00E-61	278.0	40.6	55.7
Rsa1.0_00653.1.g17544.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00653.1.g17545.t1	gb|ABD65112.1| hypothetical protein 31.t00014 [Brassica oleracea]	210	122	5.00E-16	58.1	26.7	33.8	hypothetical protein 31.t00014	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00653.1.g17546.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	593	484	5.00E-86	81.6	26.8	34.1	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00653.1.g17547.t1	gb|AAF79797.1|AC020646_20 T32E20.30 [Arabidopsis thaliana]	148	1397	1.00E-23	943.9	38.5	50.7	T32E20.30	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00654.1.g17548.t1	gb|EOA39129.1| hypothetical protein CARUB_v10012051mg [Capsella rubella]	371	426	0	114.8	98.1	98.4	hypothetical protein CARUB_v10012051mg	gbpln	Capsella rubella	AT1G53750.1 | Symbols: RPT1A | regulatory particle triple-A 1A | chr1:20065921-20068324 REVERSE LENGTH=426	371	426	0	114.8	98.1	98.4
Rsa1.0_00654.1.g17549.t1	gb|EOA28228.1| hypothetical protein CARUB_v10024418mg [Capsella rubella]	96	87	4.00E-26	90.6	78.1	82.3	hypothetical protein CARUB_v10024418mg	gbpln	Capsella rubella	AT2G39705.1 | Symbols: RTFL8, DVL11 | ROTUNDIFOLIA like 8 | chr2:16557038-16557301 FORWARD LENGTH=87	96	87	6.00E-26	90.6	69.8	72.9
Rsa1.0_00654.1.g17550.t1	ref|XP_002881671.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297327510|gb|EFH57930.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	363	438	0	120.7	87.6	94.5	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT2G39710.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:16562051-16563379 REVERSE LENGTH=442	363	442	0	121.8	86.8	93.9
Rsa1.0_00654.1.g17551.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00654.1.g17552.t1	gb|EOA27259.1| hypothetical protein CARUB_v10023378mg [Capsella rubella]	341	393	1.00E-135	115.2	80.4	87.4	hypothetical protein CARUB_v10023378mg	gbpln	Capsella rubella	AT2G39720.1 | Symbols: RHC2A | RING-H2 finger C2A | chr2:16567506-16568711 REVERSE LENGTH=401	341	401	1.00E-119	117.6	70.4	75.1
Rsa1.0_00654.1.g17553.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00654.1.g17554.t1	ref|XP_002881673.1| hypothetical protein ARALYDRAFT_482998 [Arabidopsis lyrata subsp. lyrata] gi|297327512|gb|EFH57932.1| hypothetical protein ARALYDRAFT_482998 [Arabidopsis lyrata subsp. lyrata]	472	474	0	100.4	94.9	97.2	hypothetical protein ARALYDRAFT_482998	gbpln	Arabidopsis lyrata	AT2G39730.1 | Symbols: RCA | rubisco activase | chr2:16570951-16573345 REVERSE LENGTH=474	472	474	0	100.4	93.9	96.2
Rsa1.0_00654.1.g17555.t2	ref|XP_002881674.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297327513|gb|EFH57933.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	710	689	0	97.0	83.4	88.6	dehydration-responsive family protein	gbpln	Arabidopsis lyrata	AT2G39750.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:16578986-16582281 REVERSE LENGTH=694	710	694	0	97.7	82.7	88.3

Rsa1.0_00654.1.g17556.t1	ref|NP_192226.1| AP2/B3 domain-containing protein [Arabidopsis thaliana] gi|75267842|sp|Q9ZR14.1|Y4317_ARATH RecName: Full=Putative B3 domain-containing protein At4g03170 gi|4262145|gb|AAD14445.1| hypothetical protein [Arabidopsis thaliana] gi|7270187|emb|CAB77802.1| hypothetical protein [Arabidopsis thaliana] gi|225898763|dbj|BAH30512.1| hypothetical protein [Arabidopsis thaliana] gi|332656884|gb|AEE82284.1| AP2/B3 domain-containing protein [Arabidopsis thaliana]	209	250	2.00E-23	119.6	35.9	48.8	AP2/B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G03170.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr4:1400832-1401584 FORWARD LENGTH=250	209	250	6.00E-26	119.6	35.9	48.8
Rsa1.0_00654.1.g17557.t1	ref|NP_192226.1| AP2/B3 domain-containing protein [Arabidopsis thaliana] gi|75267842|sp|Q9ZR14.1|Y4317_ARATH RecName: Full=Putative B3 domain-containing protein At4g03170 gi|4262145|gb|AAD14445.1| hypothetical protein [Arabidopsis thaliana] gi|7270187|emb|CAB77802.1| hypothetical protein [Arabidopsis thaliana] gi|225898763|dbj|BAH30512.1| hypothetical protein [Arabidopsis thaliana] gi|332656884|gb|AEE82284.1| AP2/B3 domain-containing protein [Arabidopsis thaliana]	304	250	1.00E-22	82.2	21.7	31.3	AP2/B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G03170.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr4:1400832-1401584 FORWARD LENGTH=250	304	250	3.00E-25	82.2	21.7	31.3
Rsa1.0_00654.1.g17558.t1	ref|XP_002879822.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297325661|gb|EFH56081.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	250	250	1.00E-100	100.0	80.0	85.6	mitochondrial glycoprotein family protein	gbpln	Arabidopsis lyrata	AT2G39795.1 | Symbols: | Mitochondrial glycoprotein family protein | chr2:16597026-16598028 FORWARD LENGTH=250	250	250	1.00E-101	100.0	78.4	85.6
Rsa1.0_00654.1.g17559.t1	gb|AAK01360.1|AF314811_1 delta 1-pyrroline-5-carboxylate synthetase A [Brassica napus]	762	717	0	94.1	93.6	93.8	delta 1-pyrroline-5-carboxylate synthetase A	gbpln	Brassica napus	AT2G39800.4 | Symbols: P5CS1 | delta1-pyrroline-5-carboxylate synthase 1 | chr2:16598516-16602939 REVERSE LENGTH=717	762	717	0	94.1	90.7	92.7
Rsa1.0_00654.1.g17560.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1740	1213	0	69.7	37.8	48.9	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	1740	289	3.00E-77	16.6	7.9	10.7
Rsa1.0_00654.1.g17561.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00654.1.g17562.t1	ref|NP_181513.3| DA1-related protein 2 [Arabidopsis thaliana] gi|122236286|sp|Q0WSN2.1|DAR2_ARATH RecName: Full=Protein DA1-related 2 gi|110735778|dbj|BAE99866.1| hypothetical protein [Arabidopsis thaliana] gi|330254642|gb|AEC09736.1| DA1-related protein 2 [Arabidopsis thaliana]	527	528	0	100.2	89.8	92.8	DA1-related protein 2	gbpln	Arabidopsis thaliana	AT2G39830.1 | Symbols: DAR2 | DA1-related protein 2 | chr2:16619950-16623658 REVERSE LENGTH=528	527	528	0	100.2	89.8	92.8
Rsa1.0_00655.1.g17563.t1	ref|XP_004170560.1| PREDICTED: sugar transport protein 10-like [Cucumis sativus]	53	515	3.00E-13	971.7	79.2	88.7	PREDICTED: sugar transport protein 10-like	gbpln	Cucumis sativus	AT5G23270.1 | Symbols: STP11, ATSTP11 | sugar transporter 11 | chr5:7839132-7840874 FORWARD LENGTH=514	53	514	3.00E-15	969.8	75.5	83.0
Rsa1.0_00655.1.g17564.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00655.1.g17565.t1	ref|XP_002883213.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297329053|gb|EFH59472.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	308	330	1.00E-115	107.1	75.6	82.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G19950.1 | Symbols: | RING/U-box superfamily protein | chr3:6942853-6943839 FORWARD LENGTH=328	308	328	1.00E-114	106.5	76.0	82.8
Rsa1.0_00655.1.g17566.t1	ref|NP_001190727.1| structural constituent of ribosome [Arabidopsis thaliana] gi|332658002|gb|AEE83402.1| structural constituent of ribosome [Arabidopsis thaliana]	323	815	1.00E-74	252.3	50.8	66.9	structural constituent of ribosome	gbpln	Arabidopsis thaliana	AT4G14250.2 | Symbols: | structural constituent of ribosome | chr4:8208985-8213237 REVERSE LENGTH=815	323	815	3.00E-77	252.3	50.8	66.9

Rsa1.0_00655.1.g17567.t1	ref|NP_175454.1| phytochrome-associated serine/threonine protein phosphatase 1 [Arabidopsis thaliana] gi|297847376|ref|XP_002891569.1| hypothetical protein ARALYDRAFT_474164 [Arabidopsis lyrata subsp. lyrata] gi|75314041|sp|Q9SX52.1|FYPP1_ARATH RecName: Full=Phytochrome-associated serine/threonine-protein phosphatase 1; Short=AtFyPP1 gi|5734785|gb|AAD50050.1|AC007980_15 phosphoprotein phosphatase [Arabidopsis thaliana] gi|16226940|gb|AAL16304.1|AF428374_1 At1g50370/F14I3_10 [Arabidopsis thaliana] gi|21593021|gb|AAM64970.1| phosphoprotein phosphatase [Arabidopsis thaliana] gi|56550683|gb|AAV97795.1| At1g50370 [Arabidopsis thaliana] gi|297337411|gb|EFH67828.1| hypothetical protein ARALYDRAFT_474164 [Arabidopsis lyrata subsp. lyrata] gi|332194420|gb|AEE32541.1| phytochrome-associated serine/threonine protein phosphatase 1 [Arabidopsis thaliana] gi|482574158|gb|EOA38345.1| hypothetical protein CARUB_v10009861mg [Capsella rubella]	303	303	1.00E-175	100.0	96.4	99.0	phytochrome-associated serine/threonine protein phosphatase 1	gbpln	Arabidopsis lyrata	AT1G50370.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr1:18658894-18661672 FORWARD LENGTH=303	303	303	1.00E-178	100.0	96.4	99.0
Rsa1.0_00655.1.g17568.t8	ref|NP_188635.1| SNF2 and helicase domain-containing protein [Arabidopsis thaliana] gi|11994776|dbj|BAB03166.1| transcription factor-like protein [Arabidopsis thaliana] gi|332642797|gb|AEE76318.1| SNF2 and helicase domain-containing protein [Arabidopsis thaliana]	280	1047	2.00E-16	373.9	20.0	26.4	SNF2 and helicase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G20010.1 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related | chr3:6971352-6976340 FORWARD LENGTH=1047	280	1047	6.00E-19	373.9	20.0	26.4
Rsa1.0_00655.1.g17569.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00655.1.g17570.t1	gb|EOA29760.1| hypothetical protein CARUB_v10012850mg [Capsella rubella]	88	1138	2.00E-36	1293.2	84.1	90.9	hypothetical protein CARUB_v10012850mg	gbpln	Capsella rubella	AT3G20010.1 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related | chr3:6971352-6976340 FORWARD LENGTH=1047	88	1047	2.00E-38	1189.8	83.0	89.8
Rsa1.0_00655.1.g17571.t2	gb|EOA31967.1| hypothetical protein CARUB_v10015209mg [Capsella rubella]	316	216	5.00E-54	68.4	35.8	46.2	hypothetical protein CARUB_v10015209mg	gbpln	Capsella rubella	AT3G20155.1 | Symbols: | unknown protein; Has 36 Blast hits to 36 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7037251-7038260 FORWARD LENGTH=216	316	216	3.00E-55	68.4	35.4	45.3
Rsa1.0_00655.1.g17572.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00655.1.g17573.t1	dbj|BAJ33773.1| unnamed protein product [Thellungiella halophila]	71	444	2.00E-24	625.4	80.3	80.3	unnamed protein product	----	----	AT2G36530.1 | Symbols: LOS2, ENO2 | Enolase | chr2:15321081-15323786 REVERSE LENGTH=444	71	444	3.00E-27	625.4	80.3	80.3
Rsa1.0_00655.1.g17574.t1	ref|XP_002883236.1| DELTA-VPE [Arabidopsis lyrata subsp. lyrata] gi|297329076|gb|EFH59495.1| DELTA-VPE [Arabidopsis lyrata subsp. lyrata]	187	466	1.00E-63	249.2	69.5	80.2	DELTA-VPE	gbpln	Arabidopsis lyrata	AT3G20210.1 | Symbols: DELTA-VPE, DELTAVPE | delta vacuolar processing enzyme | chr3:7052482-7054525 FORWARD LENGTH=466	187	466	7.00E-66	249.2	69.0	80.7
Rsa1.0_00655.1.g17575.t1	ref|NP_566657.1| EPS15 homology domain 1 protein [Arabidopsis thaliana] gi|79313303|ref|NP_001030731.1| EPS15 homology domain 1 protein [Arabidopsis thaliana] gi|14334440|gb|AAK59418.1| unknown protein [Arabidopsis thaliana] gi|28394001|gb|AAO42408.1| unknown protein [Arabidopsis thaliana] gi|222424046|dbj|BAH19984.1| AT3G20290 [Arabidopsis thaliana] gi|332642838|gb|AEE76359.1| EPS15 homology domain 1 protein [Arabidopsis thaliana] gi|332642839|gb|AEE76360.1| EPS15 homology domain 1 protein [Arabidopsis thaliana]	984	545	0	55.4	51.0	52.4	EPS15 homology domain 1 protein	gbpln	Arabidopsis thaliana	AT3G20290.2 | Symbols: ATEHD1, EHD1 | EPS15 homology domain 1 | chr3:7075057-7078655 REVERSE LENGTH=545	984	545	0	55.4	51.0	52.4

Rsa1.0_00655.1.g17576.t1	gb|EOA30798.1| hypothetical protein CARUB_v10013942mg [Capsella rubella] gi|482566610|gb|EOA30799.1| hypothetical protein CARUB_v10013942mg [Capsella rubella]	598	381	1.00E-151	63.7	46.0	49.7	hypothetical protein CARUB_v10013942mg	gbpln	Capsella rubella	AT3G20320.1 | Symbols: TGD2 | trigalactosyldiacylglycerol2 | chr3:7087657-7089640 REVERSE LENGTH=381	598	381	1.00E-153	63.7	46.0	49.7
Rsa1.0_00655.1.g17577.t2	gb|EOA30740.1| hypothetical protein CARUB_v10013880mg [Capsella rubella]	488	398	1.00E-159	81.6	62.9	68.0	hypothetical protein CARUB_v10013880mg	gbpln	Capsella rubella	AT3G20330.1 | Symbols: PYRB | PYRIMIDINE B | chr3:7090354-7091904 REVERSE LENGTH=390	488	390	1.00E-154	79.9	61.5	66.0
Rsa1.0_00655.1.g17578.t1	ref|XP_002885368.1| hypothetical protein ARALYDRAFT_898447 [Arabidopsis lyrata subsp. lyrata] gi|297331208|gb|EFH61627.1| hypothetical protein ARALYDRAFT_898447 [Arabidopsis lyrata subsp. lyrata]	107	116	2.00E-27	108.4	68.2	81.3	hypothetical protein ARALYDRAFT_898447	gbpln	Arabidopsis lyrata	AT3G20340.1 | Symbols: | Expression of the gene is downregulated in the presence of paraquat, an inducer of photoxidative stress. | chr3:7093075-7093422 REVERSE LENGTH=115	107	115	2.00E-29	107.5	67.3	79.4
Rsa1.0_00655.1.g17579.t2	ref|NP_188671.1| TRAF-like family protein [Arabidopsis thaliana] gi|18087637|gb|AAL58948.1|AF462862_1 AT3g20360/MQC12_11 [Arabidopsis thaliana] gi|332642847|gb|AEE76368.1| TRAF-like family protein [Arabidopsis thaliana]	360	363	1.00E-148	100.8	72.5	84.2	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G20360.1 | Symbols: | TRAF-like family protein | chr3:7099952-7101589 REVERSE LENGTH=363	360	363	1.00E-150	100.8	72.5	84.2
Rsa1.0_00655.1.g17580.t1	ref|XP_002883241.1| hypothetical protein ARALYDRAFT_479561 [Arabidopsis lyrata subsp. lyrata] gi|297329081|gb|EFH59500.1| hypothetical protein ARALYDRAFT_479561 [Arabidopsis lyrata subsp. lyrata]	721	385	1.00E-155	53.4	35.9	40.9	hypothetical protein ARALYDRAFT_479561	gbpln	Arabidopsis lyrata	AT3G20370.1 | Symbols: | TRAF-like family protein | chr3:7105481-7107079 FORWARD LENGTH=379	721	379	1.00E-149	52.6	34.7	40.1
Rsa1.0_00655.1.g17581.t1	gb|EOA29522.1| hypothetical protein CARUB_v10014733mg [Capsella rubella]	156	187	2.00E-53	119.9	66.0	69.9	hypothetical protein CARUB_v10014733mg	gbpln	Capsella rubella	AT3G20390.1 | Symbols: | endoribonuclease L-PSP family protein | chr3:7110227-7111695 REVERSE LENGTH=187	156	187	7.00E-55	119.9	64.7	69.9
Rsa1.0_00655.1.g17582.t1	ref|NP_188676.1| calmodulin-domain protein kinase 9 [Arabidopsis thaliana] gi|75319414|sp|Q38868.1|CDPK9_ARATH RecName: Full=Calcium-dependent protein kinase 9; AltName: Full=Calmodulin-domain protein kinase CDPK isoform 9 gi|1399265|gb|AAB03242.1| calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana] gi|9294561|dbj|BAB02824.1| calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana] gi|21539465|gb|AAM53285.1| calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana] gi|31711962|gb|AAP68337.1| At3g20410 [Arabidopsis thaliana] gi|332642854|gb|AEE76375.1| calmodulin-domain protein kinase 9 [Arabidopsis thaliana]	538	541	0	100.6	93.5	95.5	calmodulin-domain protein kinase 9	gbpln	Arabidopsis thaliana	AT3G20410.1 | Symbols: CPK9 | calmodulin-domain protein kinase 9 | chr3:7116388-7118824 FORWARD LENGTH=541	538	541	0	100.6	93.5	95.5
Rsa1.0_00655.1.g17583.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00655.1.g17584.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00655.1.g17585.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00655.1.g17586.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00656.1.g17587.t1	ref|XP_002887735.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297333576|gb|EFH63994.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	104	110	3.00E-37	105.8	78.8	87.5	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT1G78410.1 | Symbols: | VQ motif-containing protein | chr1:29502728-29503054 FORWARD LENGTH=108	104	108	2.00E-39	103.8	77.9	85.6
Rsa1.0_00656.1.g17588.t1	gb|EOA34325.1| hypothetical protein CARUB_v10021845mg [Capsella rubella]	403	406	0	100.7	77.7	87.8	hypothetical protein CARUB_v10021845mg	gbpln	Capsella rubella	AT1G78400.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:29498281-29499682 REVERSE LENGTH=404	403	404	1.00E-172	100.2	73.0	84.9
Rsa1.0_00656.1.g17589.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00656.1.g17590.t1	gb|EOA34913.1| hypothetical protein CARUB_v10019990mg, partial [Capsella rubella]	610	616	0	101.0	86.1	93.0	hypothetical protein CARUB_v10019990mg, partial	gbpln	Capsella rubella	AT1G78390.1 | Symbols: NCED9, ATNCED9 | nine-cis-epoxycarotenoid dioxygenase 9 | chr1:29490895-29492868 REVERSE LENGTH=657	610	657	0	107.7	86.4	93.4
Rsa1.0_00656.1.g17591.t2	gb|AAD24601.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1633	1319	0	80.8	28.3	40.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1633	575	6.00E-43	35.2	6.8	11.1
Rsa1.0_00656.1.g17592.t1	gb|EEC76289.1| hypothetical protein OsI_13796 [Oryza sativa Indica Group]	84	268	1.00E-23	319.0	76.2	85.7	hypothetical protein OsI_13796	gbpln	Oryza sativa	AT4G18360.2 | Symbols: | Aldolase-type TIM barrel family protein | chr4:10146627-10148386 REVERSE LENGTH=314	84	314	5.00E-25	373.8	76.2	85.7

Rsa1.0_00656.1.g17593.t1	ref|XP_002889189.1| F3F9.11 [Arabidopsis lyrata subsp. lyrata] gi|297335030|gb|EFH65448.1| F3F9.11 [Arabidopsis lyrata subsp. lyrata]	221	646	1.00E-101	292.3	81.9	92.3	F3F9.11	gbpln	Arabidopsis lyrata	AT1G78360.1 | Symbols: ATGSTU21, GSTU21 | glutathione S-transferase TAU 21 | chr1:29482070-29482966 REVERSE LENGTH=222	221	222	1.00E-103	100.5	79.2	90.5
Rsa1.0_00656.1.g17594.t1	ref|XP_002889189.1| F3F9.11 [Arabidopsis lyrata subsp. lyrata] gi|297335030|gb|EFH65448.1| F3F9.11 [Arabidopsis lyrata subsp. lyrata]	220	646	1.00E-104	293.6	82.7	93.2	F3F9.11	gbpln	Arabidopsis lyrata	AT1G78360.1 | Symbols: ATGSTU21, GSTU21 | glutathione S-transferase TAU 21 | chr1:29482070-29482966 REVERSE LENGTH=222	220	222	1.00E-106	100.9	80.9	91.4
Rsa1.0_00656.1.g17595.t1	gb|AAF71799.1|AC013430_8 F3F9.13 [Arabidopsis thaliana]	278	439	3.00E-98	157.9	60.1	64.4	F3F9.13	gbpln	Arabidopsis thaliana	AT1G78340.1 | Symbols: ATGSTU22, GSTU22 | glutathione S-transferase TAU 22 | chr1:29473046-29473797 REVERSE LENGTH=218	278	218	2.00E-99	78.4	60.8	65.5
Rsa1.0_00656.1.g17596.t1	gb|EOA33873.1| hypothetical protein CARUB_v10021365mg [Capsella rubella]	290	316	5.00E-96	109.0	77.6	83.8	hypothetical protein CARUB_v10021365mg	gbpln	Capsella rubella	AT1G78310.1 | Symbols: | VQ motif-containing protein | chr1:29464003-29464938 REVERSE LENGTH=311	290	311	2.00E-87	107.2	81.0	86.6
Rsa1.0_00656.1.g17597.t1	gb|AAK26634.1|AF342780_1 GF14 omega [Brassica napus]	260	260	1.00E-141	100.0	96.2	96.9	GF14 omega	gbpln	Brassica napus	AT1G78300.1 | Symbols: GRF2, 14-3-3OMEGA, GF14 OMEGA | general regulatory factor 2 | chr1:29461883-29463052 FORWARD LENGTH=259	260	259	1.00E-140	99.6	92.7	95.8
Rsa1.0_00656.1.g17598.t2	gb|EOA33589.1| hypothetical protein CARUB_v10019734mg [Capsella rubella]	965	944	0	97.8	84.5	88.8	hypothetical protein CARUB_v10019734mg	gbpln	Capsella rubella	AT1G78280.1 | Symbols: | transferases, transferring glycosyl groups | chr1:29452823-29457118 FORWARD LENGTH=943	965	943	0	97.7	84.0	88.9
Rsa1.0_00656.1.g17599.t1	ref|XP_002890510.1| hypothetical protein ARALYDRAFT_472481 [Arabidopsis lyrata subsp. lyrata] gi|297336352|gb|EFH66769.1| hypothetical protein ARALYDRAFT_472481 [Arabidopsis lyrata subsp. lyrata]	431	527	0	122.3	85.4	88.9	hypothetical protein ARALYDRAFT_472481	gbpln	Arabidopsis lyrata	AT1G22410.1 | Symbols: | Class-II DAHP synthetase family protein | chr1:7912120-7914742 FORWARD LENGTH=527	431	527	0	122.3	84.7	88.6
Rsa1.0_00656.1.g17600.t1	gb|ABD64987.1| hypothetical protein 26.t00003 [Brassica oleracea]	433	330	9.00E-12	76.2	14.3	19.9	hypothetical protein 26.t00003	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00656.1.g17601.t1	ref|NP_565175.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|21537200|gb|AAM61541.1| RNA recognition motif-containing protein SEB-4 [Arabidopsis thaliana] gi|124300976|gb|ABN04740.1| At1g78260 [Arabidopsis thaliana] gi|332197966|gb|AEE36087.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	284	287	1.00E-116	101.1	92.3	95.1	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT1G78260.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:29447317-29450181 FORWARD LENGTH=287	284	287	1.00E-118	101.1	92.3	95.1
Rsa1.0_00657.1.g17602.t1	ref|XP_002871312.1| hypothetical protein ARALYDRAFT_487656 [Arabidopsis lyrata subsp. lyrata] gi|297317149|gb|EFH47571.1| hypothetical protein ARALYDRAFT_487656 [Arabidopsis lyrata subsp. lyrata]	429	407	1.00E-161	94.9	80.2	86.2	hypothetical protein ARALYDRAFT_487656	gbpln	Arabidopsis lyrata	AT5G08200.1 | Symbols: | peptidoglycan-binding LysM domain-containing protein | chr5:2638385-2640508 FORWARD LENGTH=409	429	409	1.00E-163	95.3	80.2	85.5
Rsa1.0_00657.1.g17603.t1	ref|XP_002873350.1| hypothetical protein ARALYDRAFT_908776 [Arabidopsis lyrata subsp. lyrata] gi|297319187|gb|EFH49609.1| hypothetical protein ARALYDRAFT_908776 [Arabidopsis lyrata subsp. lyrata]	426	382	0	89.7	82.6	85.9	hypothetical protein ARALYDRAFT_908776	gbpln	Arabidopsis lyrata	AT5G08280.1 | Symbols: HEMC | hydroxymethylbilane synthase | chr5:2663763-2665596 REVERSE LENGTH=382	426	382	0	89.7	81.7	85.4
Rsa1.0_00657.1.g17604.t1	ref|XP_002871316.1| hypothetical protein ARALYDRAFT_487662 [Arabidopsis lyrata subsp. lyrata] gi|297317153|gb|EFH47575.1| hypothetical protein ARALYDRAFT_487662 [Arabidopsis lyrata subsp. lyrata]	340	347	0	102.1	95.3	97.4	hypothetical protein ARALYDRAFT_487662	gbpln	Arabidopsis lyrata	AT5G08300.1 | Symbols: | Succinyl-CoA ligase, alpha subunit | chr5:2667579-2669672 FORWARD LENGTH=347	340	347	0	102.1	95.0	97.4
Rsa1.0_00657.1.g17605.t1	ref|NP_196448.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|223635617|sp|P0C8Q6.1|PP368_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At5g08310, mitochondrial; Flags: Precursor gi|332003898|gb|AED91281.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	824	832	0	101.0	82.8	89.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G08310.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:2672756-2675254 REVERSE LENGTH=832	824	832	0	101.0	82.8	89.7

Rsa1.0_00657.1.g17606.t1	ref|XP_002871318.1| hypothetical protein ARALYDRAFT_908781 [Arabidopsis lyrata subsp. lyrata] gi|297317155|gb|EFH47577.1| hypothetical protein ARALYDRAFT_908781 [Arabidopsis lyrata subsp. lyrata]	150	150	5.00E-71	100.0	86.0	90.7	hypothetical protein ARALYDRAFT_908781	gbpln	Arabidopsis lyrata	AT5G08320.1 | Symbols: | CONTAINS InterPro DOMAIN/s: E2F-associated phosphoprotein, C-terminal (InterPro:IPR019370); Has 149 Blast hits to 149 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 79; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 35 (source: NCBI BLink). | chr5:2677153-2678603 FORWARD LENGTH=150	150	150	1.00E-72	100.0	84.7	90.0
Rsa1.0_00657.1.g17607.t1	gb|EOA21459.1| hypothetical protein CARUB_v10001850mg [Capsella rubella]	238	238	1.00E-92	100.0	84.0	87.0	hypothetical protein CARUB_v10001850mg	gbpln	Capsella rubella	AT5G08330.1 | Symbols: | TCP family transcription factor | chr5:2680828-2681547 FORWARD LENGTH=239	238	239	3.00E-88	100.4	81.5	84.9
Rsa1.0_00657.1.g17608.t1	ref|XP_002871320.1| prenylcysteine alpha-carboxyl methyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297317157|gb|EFH47579.1| prenylcysteine alpha-carboxyl methyltransferase [Arabidopsis lyrata subsp. lyrata]	182	197	9.00E-91	108.2	88.5	94.5	prenylcysteine alpha-carboxyl methyltransferase	gbpln	Arabidopsis lyrata	AT5G08335.1 | Symbols: ATSTE14B, ATICMTB, ICMTB | Isoprenylcysteine carboxyl methyltransferase (ICMT) family | chr5:2683012-2683605 FORWARD LENGTH=197	182	197	1.00E-92	108.2	86.3	94.5
Rsa1.0_00657.1.g17609.t1	ref|XP_002873354.1| alpha-galactosidase 2 [Arabidopsis lyrata subsp. lyrata] gi|297319191|gb|EFH49613.1| alpha-galactosidase 2 [Arabidopsis lyrata subsp. lyrata]	398	394	0	99.0	89.9	93.5	alpha-galactosidase 2	gbpln	Arabidopsis lyrata	AT5G08370.1 | Symbols: AtAGAL2, AGAL2 | alpha-galactosidase 2 | chr5:2691116-2693441 REVERSE LENGTH=396	398	396	0	99.5	89.7	93.5
Rsa1.0_00657.1.g17610.t1	ref|NP_196455.1| alpha-galactosidase 1 [Arabidopsis thaliana] gi|10178280|emb|CAC08338.1| alpha-galactosidase-like protein [Arabidopsis thaliana] gi|332003909|gb|AED91292.1| alpha-galactosidase 1 [Arabidopsis thaliana]	431	410	0	95.1	83.1	88.9	alpha-galactosidase 1	gbpln	Arabidopsis thaliana	AT5G08380.1 | Symbols: AtAGAL1, AGAL1 | alpha-galactosidase 1 | chr5:2694851-2697616 REVERSE LENGTH=410	431	410	0	95.1	83.1	88.9
Rsa1.0_00657.1.g17611.t1	ref|XP_002871323.1| hypothetical protein ARALYDRAFT_487673 [Arabidopsis lyrata subsp. lyrata] gi|297317160|gb|EFH47582.1| hypothetical protein ARALYDRAFT_487673 [Arabidopsis lyrata subsp. lyrata] gi|482557717|gb|EOA21909.1| hypothetical protein CARUB_v10002392mg [Capsella rubella]	69	69	1.00E-30	100.0	98.6	98.6	hypothetical protein ARALYDRAFT_487673	gbpln	Arabidopsis lyrata	AT5G08391.1 | Symbols: | Protein of unknown function (DUF 3339) | chr5:2699357-2699566 FORWARD LENGTH=69	69	69	5.00E-33	100.0	97.1	98.6
Rsa1.0_00657.1.g17612.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00657.1.g17613.t1	gb|EOA22984.1| hypothetical protein CARUB_v10003725mg [Capsella rubella]	388	395	0	101.8	90.5	93.8	hypothetical protein CARUB_v10003725mg	gbpln	Capsella rubella	AT5G08415.1 | Symbols: | Radical SAM superfamily protein | chr5:2710983-2713101 REVERSE LENGTH=394	388	394	0	101.5	90.2	93.6
Rsa1.0_00657.1.g17614.t1	ref|XP_002871325.1| hypothetical protein ARALYDRAFT_487679 [Arabidopsis lyrata subsp. lyrata] gi|297317162|gb|EFH47584.1| hypothetical protein ARALYDRAFT_487679 [Arabidopsis lyrata subsp. lyrata]	316	391	1.00E-107	123.7	55.4	63.3	hypothetical protein ARALYDRAFT_487679	gbpln	Arabidopsis lyrata	AT5G08420.1 | Symbols: | RNA-binding KH domain-containing protein | chr5:2713555-2716064 FORWARD LENGTH=391	316	391	1.00E-105	123.7	57.9	64.2
Rsa1.0_00657.1.g17615.t2	ref|NP_196460.2| SWIB/MDM2 and Plus-3 and GYF domain-containing protein [Arabidopsis thaliana] gi|73622094|sp|Q9FT92.2|Y5843_ARATH RecName: Full=Uncharacterized protein At5g08430 gi|192807344|gb|ACF06124.1| At5g08430 [Arabidopsis thaliana] gi|332003917|gb|AED91300.1| SWIB/MDM2 and Plus-3 and GYF domain-containing protein [Arabidopsis thaliana]	553	553	0	100.0	73.2	84.6	SWIB/MDM2 and Plus-3 and GYF domain-containing protein	gbpln	Arabidopsis thaliana	AT5G08430.1 | Symbols: | SWIB/MDM2 domain;Plus-3;GYF | chr5:2716974-2720095 FORWARD LENGTH=553	553	553	0	100.0	73.2	84.6
Rsa1.0_00657.1.g17616.t1	dbj|BAJ34067.1| unnamed protein product [Thellungiella halophila]	287	305	1.00E-126	106.3	85.4	93.4	unnamed protein product	----	----	AT5G08520.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr5:2755470-2757741 REVERSE LENGTH=298	287	298	1.00E-125	103.8	83.3	91.6
Rsa1.0_00657.1.g17617.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00657.1.g17618.t5	ref|XP_002285341.2| PREDICTED: topless-related protein 4-like isoform 1 [Vitis vinifera] gi|297738983|emb|CBI28228.3| unnamed protein product [Vitis vinifera]	1162	1133	0	97.5	71.9	81.9	PREDICTED: topless-related protein 4-like isoform 1	gbpln	Vitis vinifera	AT3G15880.2 | Symbols: WSIP2, TPR4 | WUS-interacting protein 2 | chr3:5364454-5371869 REVERSE LENGTH=1137	1162	1137	0	97.8	65.9	78.5
Rsa1.0_00657.1.g17619.t1	gb|EOA22779.1| hypothetical protein CARUB_v10003496mg [Capsella rubella]	552	564	0	102.2	83.0	89.5	hypothetical protein CARUB_v10003496mg	gbpln	Capsella rubella	AT5G08620.1 | Symbols: STRS2, ATRH25 | DEA(D/H)-box RNA helicase family protein | chr5:2794540-2797548 FORWARD LENGTH=563	552	563	0	102.0	81.5	88.8

Rsa1.0_00657.1.g17620.t1	ref|XP_002873375.1| hypothetical protein ARALYDRAFT_487706 [Arabidopsis lyrata subsp. lyrata] gi|297319212|gb|EFH49634.1| hypothetical protein ARALYDRAFT_487706 [Arabidopsis lyrata subsp. lyrata]	694	680	0	98.0	90.9	94.7	hypothetical protein ARALYDRAFT_487706	gbpln	Arabidopsis lyrata	AT5G08650.1 | Symbols: | Small GTP-binding protein | chr5:2806533-2813220 REVERSE LENGTH=681	694	681	0	98.1	91.5	95.1
Rsa1.0_00657.1.g17621.t1	ref|NP_680154.2| uncharacterized protein [Arabidopsis thaliana] gi|13548324|emb|CAC35871.1| putative protein [Arabidopsis thaliana] gi|332003952|gb|AED91335.1| uncharacterized protein AT5G08660 [Arabidopsis thaliana]	640	649	0	101.4	88.1	93.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G08660.1 | Symbols: | Protein of unknown function (DUF668) | chr5:2814526-2817845 FORWARD LENGTH=649	640	649	0	101.4	88.1	93.4
Rsa1.0_00657.1.g17622.t1	gb|EOA20295.1| hypothetical protein CARUB_v10000603mg [Capsella rubella]	181	559	1.00E-101	308.8	99.4	100.0	hypothetical protein CARUB_v10000603mg	gbpln	Capsella rubella	AT5G08680.1 | Symbols: | ATP synthase alpha/beta family protein | chr5:2821992-2824683 FORWARD LENGTH=559	181	559	1.00E-102	308.8	98.3	99.4
Rsa1.0_00658.1.g17623.t1	gb|AAF80658.1|AC012190_14 Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872 [Arabidopsis thaliana]	268	904	7.00E-63	337.3	44.4	64.2	Similar to At2g29230 Mutator-like transposase gi|3980409 from Arabidopsis thaliana gb|AC004561. It is a member of Transposase mutator family PF|00872	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	268	719	1.00E-11	268.3	23.1	43.3
Rsa1.0_00658.1.g17624.t1	ref|XP_002869436.1| hypothetical protein ARALYDRAFT_913570 [Arabidopsis lyrata subsp. lyrata] gi|297315272|gb|EFH45695.1| hypothetical protein ARALYDRAFT_913570 [Arabidopsis lyrata subsp. lyrata]	344	386	5.00E-69	112.2	51.2	63.4	hypothetical protein ARALYDRAFT_913570	gbpln	Arabidopsis lyrata	AT5G39560.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:15841885-15843096 REVERSE LENGTH=403	344	403	8.00E-55	117.2	41.0	57.3
Rsa1.0_00658.1.g17625.t1	gb|EOA40271.1| hypothetical protein CARUB_v10008999mg [Capsella rubella] gi|482576085|gb|EOA40272.1| hypothetical protein CARUB_v10008999mg [Capsella rubella]	436	482	0	110.6	92.2	95.4	hypothetical protein CARUB_v10008999mg	gbpln	Capsella rubella	AT1G50420.1 | Symbols: SCL3, SCL-3 | scarecrow-like 3 | chr1:18678177-18679625 REVERSE LENGTH=482	436	482	0	110.6	91.7	95.9
Rsa1.0_00658.1.g17626.t3	ref|NP_175460.1| 7-dehydrocholesterol reductase [Arabidopsis thaliana] gi|20140296|sp|Q9LDU6.1|ST7R_ARATH RecName: Full=7-dehydrocholesterol reductase; Short=7-DHC reductase; AltName: Full=Protein DWARF 5; AltName: Full=Sterol Delta(7)-reductase gi|7542561|gb|AAF63498.1|AF239701_1 sterol delta7 reductase [Arabidopsis thaliana] gi|9454565|gb|AAF87888.1|AC012561_21 sterol delta7 reductase [Arabidopsis thaliana] gi|20466246|gb|AAM20440.1| sterol delta7 reductase [Arabidopsis thaliana] gi|23198074|gb|AAN15564.1| sterol delta7 reductase [Arabidopsis thaliana] gi|110742801|dbj|BAE99303.1| sterol delta7 reductase [Arabidopsis thaliana] gi|332194426|gb|AEE32547.1| 7-dehydrocholesterol reductase [Arabidopsis thaliana]	455	432	0	94.9	89.9	92.1	7-dehydrocholesterol reductase	gbpln	Arabidopsis thaliana	AT1G50430.1 | Symbols: DWF5, PA, LE, ST7R, 7RED | Ergosterol biosynthesis ERG4/ERG24 family | chr1:18682175-18685555 REVERSE LENGTH=432	455	432	0	94.9	89.9	92.1
Rsa1.0_00658.1.g17627.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00658.1.g17628.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00658.1.g17629.t1	ref|XP_002883225.1| hexokinase [Arabidopsis lyrata subsp. lyrata] gi|297329065|gb|EFH59484.1| hexokinase [Arabidopsis lyrata subsp. lyrata]	92	502	4.00E-29	545.7	72.8	83.7	hexokinase	gbpln	Arabidopsis lyrata	AT1G50460.1 | Symbols: HKL1, ATHKL1 | hexokinase-like 1 | chr1:18694031-18697429 FORWARD LENGTH=498	92	498	1.00E-28	541.3	62.0	66.3
Rsa1.0_00658.1.g17630.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1422	1485	0	104.4	44.4	60.1	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1422	158	1.00E-27	11.1	3.8	5.8
Rsa1.0_00658.1.g17631.t2	ref|XP_002891576.1| hypothetical protein ARALYDRAFT_474175 [Arabidopsis lyrata subsp. lyrata] gi|297337418|gb|EFH67835.1| hypothetical protein ARALYDRAFT_474175 [Arabidopsis lyrata subsp. lyrata]	199	498	1.00E-86	250.3	79.4	84.9	hypothetical protein ARALYDRAFT_474175	gbpln	Arabidopsis lyrata	AT1G50460.1 | Symbols: HKL1, ATHKL1 | hexokinase-like 1 | chr1:18694031-18697429 FORWARD LENGTH=498	199	498	1.00E-87	250.3	78.9	84.4

Rsa1.0_00658.1.g17632.t1	ref|XP_002894257.1| heat-intolerant 1 [Arabidopsis lyrata subsp. lyrata] gi|297340099|gb|EFH70516.1| heat-intolerant 1 [Arabidopsis lyrata subsp. lyrata]	826	828	0	100.2	91.8	95.5	heat-intolerant 1	gbpln	Arabidopsis lyrata	AT1G50500.1 | Symbols: HIT1, ATVPS53, VPS53 | Membrane trafficking VPS53 family protein | chr1:18708217-18715597 REVERSE LENGTH=828	826	828	0	100.2	91.4	95.6
Rsa1.0_00658.1.g17633.t1	gb|EOA37472.1| hypothetical protein CARUB_v10011600mg [Capsella rubella]	680	689	0	101.3	81.5	89.0	hypothetical protein CARUB_v10011600mg	gbpln	Capsella rubella	AT1G50610.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:18742171-18744501 FORWARD LENGTH=686	680	686	0	100.9	80.1	88.2
Rsa1.0_00658.1.g17634.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1355	1838	0	135.6	28.5	35.6	F5M15.26	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1355	158	2.00E-18	11.7	3.5	5.1
Rsa1.0_00658.1.g17635.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17636.t1	gb|EOA15770.1| hypothetical protein CARUB_v10006927mg [Capsella rubella]	506	852	1.00E-149	168.4	65.2	77.3	hypothetical protein CARUB_v10006927mg	gbpln	Capsella rubella	AT4G13820.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:8008535-8010694 REVERSE LENGTH=719	506	719	1.00E-145	142.1	64.0	74.9
Rsa1.0_00659.1.g17637.t2	gb|ABD65088.1| hypothetical protein 27.t00109 [Brassica oleracea]	693	1176	1.00E-106	169.7	39.8	46.6	hypothetical protein 27.t00109	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	693	673	1.00E-11	97.1	6.9	11.5
Rsa1.0_00659.1.g17638.t1	gb|AFK08576.1| glycine-rich RNA binding protein 2a [Camelina sativa] gi|387861099|gb|AFK08579.1| glycine-rich RNA binding protein 2a [Camelina sativa]	150	160	2.00E-53	106.7	68.0	74.0	glycine-rich RNA binding protein 2a	gbpln	Camelina sativa	AT4G13850.1 | Symbols: ATGRP2, GR-RBP2, GRP2 | glycine-rich RNA-binding protein 2 | chr4:8021314-8022065 FORWARD LENGTH=158	150	158	2.00E-53	105.3	66.0	73.3
Rsa1.0_00659.1.g17639.t1	gb|AAC26241.1| F9D12.15 gene product [Arabidopsis thaliana]	177	850	2.00E-27	480.2	44.6	58.8	F9D12.15 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17640.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	161	1024	1.00E-33	636.0	44.7	52.2	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17641.t1	gb|ABW81181.1| gag-pol20 [Arabidopsis cebennensis]	132	498	3.00E-12	377.3	25.8	41.7	gag-pol20	gbpln	Arabidopsis cebennensis	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17642.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17643.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	284	1103	1.00E-116	388.4	70.8	81.7	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17644.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17645.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1502	1496	0	99.6	57.2	70.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1502	1262	1.00E-141	84.0	16.0	22.9
Rsa1.0_00659.1.g17646.t4	emb|CAB40051.1| putative protein [Arabidopsis thaliana] gi|7267781|emb|CAB81184.1| putative protein [Arabidopsis thaliana]	1004	1294	1.00E-168	128.9	30.4	38.8	putative protein	gbpln	Arabidopsis thaliana	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	1004	336	7.00E-47	33.5	9.2	12.6
Rsa1.0_00659.1.g17647.t1	gb|AFK08576.1| glycine-rich RNA binding protein 2a [Camelina sativa] gi|387861099|gb|AFK08579.1| glycine-rich RNA binding protein 2a [Camelina sativa]	144	160	2.00E-53	111.1	70.8	77.1	glycine-rich RNA binding protein 2a	gbpln	Camelina sativa	AT4G13850.3 | Symbols: ATGRP2 | glycine-rich RNA-binding protein 2 | chr4:8021314-8022065 FORWARD LENGTH=144	144	144	4.00E-53	100.0	68.8	75.7
Rsa1.0_00659.1.g17648.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17649.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	1459	1024	2.00E-58	70.2	9.1	12.1	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17650.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00659.1.g17651.t1	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	156	578	2.00E-24	370.5	41.7	51.3	hypothetical protein 27.t00126	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00660.1.g17652.t3	gb|AAO86825.1| hypothetical protein [Arabidopsis thaliana]	231	657	4.00E-43	284.4	48.5	56.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G04680.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:1640188-1642161 FORWARD LENGTH=657	231	657	1.00E-45	284.4	48.5	56.7

Rsa1.0_00660.1.g17653.t1	ref|NP_179559.2| phospholipase A2-beta [Arabidopsis thaliana] gi|75299644|sp|Q8GZB4.1|PLA2B_ARATH RecName: Full=Phospholipase A2-beta; AltName: Full=Secretory phospholipase A2-beta; Short=AtsPLA2-beta; Flags: Precursor gi|25992715|gb|AAN77229.1| phospholipase A2 beta [Arabidopsis thaliana] gi|330251819|gb|AEC06913.1| phospholipase A2-beta [Arabidopsis thaliana]	145	147	1.00E-59	101.4	75.9	79.3	phospholipase A2-beta	gbpln	Arabidopsis thaliana	AT2G19690.1 | Symbols: PLA2-BETA | phospholipase A2-beta | chr2:8503326-8504549 FORWARD LENGTH=147	145	147	4.00E-62	101.4	75.9	79.3
Rsa1.0_00660.1.g17654.t1	gb|EOA29824.1| hypothetical protein CARUB_v10012919mg [Capsella rubella]	937	933	0	99.6	70.5	79.5	hypothetical protein CARUB_v10012919mg	gbpln	Capsella rubella	AT2G19710.1 | Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr2:8506339-8509817 FORWARD LENGTH=937	937	937	0	100.0	71.6	80.5
Rsa1.0_00660.1.g17655.t1	ref|NP_194672.1| 40S ribosomal protein S15a-5 [Arabidopsis thaliana] gi|297803094|ref|XP_002869431.1| RPS15AE [Arabidopsis lyrata subsp. lyrata] gi|75311751|sp|Q9M0E0.1|R15A5_ARATH RecName: Full=40S ribosomal protein S15a-5 gi|7269842|emb|CAB79701.1| ribosomal protein S15a homolog [Arabidopsis thaliana] gi|21553914|gb|AAM62997.1| ribosomal protein S15a homolog [Arabidopsis thaliana] gi|110737866|dbj|BAF00871.1| ribosomal protein S15a homolog [Arabidopsis thaliana] gi|111074474|gb|ABH04610.1| At4g29430 [Arabidopsis thaliana] gi|297315267|gb|EFH45690.1| RPS15AE [Arabidopsis lyrata subsp. lyrata] gi|332660230|gb|AEE85630.1| 40S ribosomal protein S15a-5 [Arabidopsis thaliana] gi|482553463|gb|EOA17656.1| hypothetical protein CARUB_v10006023mg [Capsella rubella]	129	129	2.00E-67	100.0	94.6	99.2	40S ribosomal protein S15a-5	gbpln	Arabidopsis lyrata	AT4G29430.1 | Symbols: rps15ae | ribosomal protein S15A E | chr4:14472440-14473383 FORWARD LENGTH=129	129	129	5.00E-70	100.0	94.6	99.2
Rsa1.0_00660.1.g17656.t1	gb|ACF23027.1| ST45-109 [Eutrema halophilum]	143	143	2.00E-73	100.0	95.8	97.2	ST45-109	gbpln	Eutrema halophilum	AT2G19730.3 | Symbols: | Ribosomal L28e protein family | chr2:8511752-8512995 FORWARD LENGTH=143	143	143	8.00E-71	100.0	89.5	94.4
Rsa1.0_00660.1.g17657.t1	gb|EOA16024.1| hypothetical protein CARUB_v10004149mg [Capsella rubella]	812	815	0	100.4	93.2	97.4	hypothetical protein CARUB_v10004149mg	gbpln	Capsella rubella	AT2G21790.1 | Symbols: R1, RNR1, CLS8, ATRNR1 | ribonucleotide reductase 1 | chr2:9293529-9297580 FORWARD LENGTH=816	812	816	0	100.5	91.6	96.6
Rsa1.0_00660.1.g17658.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	363	1072	5.00E-97	295.3	47.4	63.4	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	363	289	9.00E-75	79.6	37.5	50.7
Rsa1.0_00660.1.g17659.t1	ref|NP_198719.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|75333904|sp|Q9FID5.1|Y5393_ARATH RecName: Full=Probable receptor-like protein kinase At5g39030; Flags: Precursor gi|10177548|dbj|BAB10827.1| receptor protein kinase-like protein [Arabidopsis thaliana] gi|332007006|gb|AED94389.1| putative receptor-like protein kinase [Arabidopsis thaliana]	799	806	0	100.9	66.5	76.2	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G39030.1 | Symbols: | Protein kinase superfamily protein | chr5:15620066-15622486 FORWARD LENGTH=806	799	806	0	100.9	66.5	76.2
Rsa1.0_00660.1.g17660.t1	ref|NP_198719.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|75333904|sp|Q9FID5.1|Y5393_ARATH RecName: Full=Probable receptor-like protein kinase At5g39030; Flags: Precursor gi|10177548|dbj|BAB10827.1| receptor protein kinase-like protein [Arabidopsis thaliana] gi|332007006|gb|AED94389.1| putative receptor-like protein kinase [Arabidopsis thaliana]	802	806	0	100.5	64.2	75.1	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G39030.1 | Symbols: | Protein kinase superfamily protein | chr5:15620066-15622486 FORWARD LENGTH=806	802	806	0	100.5	64.2	75.1

Rsa1.0_00660.1.g17661.t1	ref|NP_179564.1| 60S ribosomal protein L31-1 [Arabidopsis thaliana] gi|297836284|ref|XP_002886024.1| 60S ribosomal protein L31 [Arabidopsis lyrata subsp. lyrata] gi|75266051|sp|Q9SLL7.1|RL311_ARATH RecName: Full=60S ribosomal protein L31-1 gi|3687244|gb|AAC62142.1| 60S ribosomal protein L31 [Arabidopsis thaliana] gi|15450425|gb|AAK96506.1| At2g19740/F6F22.23 [Arabidopsis thaliana] gi|15451072|gb|AAK96807.1| 60S ribosomal protein L31 [Arabidopsis thaliana] gi|16974433|gb|AAL31220.1| At2g19740/F6F22.23 [Arabidopsis thaliana] gi|18377416|gb|AAL66874.1| 60S ribosomal protein L31 [Arabidopsis thaliana] gi|297331864|gb|EFH62283.1| 60S ribosomal protein L31 [Arabidopsis lyrata subsp. lyrata] gi|330251827|gb|AEC06921.1| 60S ribosomal protein L31-1 [Arabidopsis thaliana]	112	119	4.00E-42	106.3	75.9	80.4	60S ribosomal protein L31-1	gbpln	Arabidopsis lyrata	AT2G19740.1 | Symbols: | Ribosomal protein L31e family protein | chr2:8513577-8514346 FORWARD LENGTH=119	112	119	7.00E-45	106.3	75.9	80.4
Rsa1.0_00660.1.g17662.t1	dbj|BAK06364.1| predicted protein [Hordeum vulgare subsp. vulgare]	123	69	2.00E-16	56.1	35.8	38.2	predicted protein	gbpln	Hordeum vulgare	AT5G56670.1 | Symbols: | Ribosomal protein S30 family protein | chr5:22935413-22935981 REVERSE LENGTH=62	123	62	4.00E-13	50.4	36.6	36.6
Rsa1.0_00660.1.g17663.t1	dbj|BAB02625.1| unnamed protein product [Arabidopsis thaliana]	418	420	4.00E-83	100.5	48.1	60.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G28223.1 | Symbols: | F-box family protein | chr3:10527669-10528921 REVERSE LENGTH=391	418	391	3.00E-70	93.5	42.6	53.3
Rsa1.0_00660.1.g17664.t1	gb|EOA31704.1| hypothetical protein CARUB_v10014910mg [Capsella rubella]	131	131	6.00E-63	100.0	89.3	93.9	hypothetical protein CARUB_v10014910mg	gbpln	Capsella rubella	AT2G19760.1 | Symbols: PFN1, PRF1 | profilin 1 | chr2:8517074-8518067 REVERSE LENGTH=131	131	131	1.00E-64	100.0	89.3	92.4
Rsa1.0_00660.1.g17665.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00660.1.g17666.t1	gb|EOA31559.1| hypothetical protein CARUB_v10014752mg, partial [Capsella rubella]	143	179	6.00E-80	125.2	100.0	100.0	hypothetical protein CARUB_v10014752mg, partial	gbpln	Capsella rubella	AT2G19790.1 | Symbols: | SNARE-like superfamily protein | chr2:8527302-8528395 FORWARD LENGTH=143	143	143	2.00E-81	100.0	100.0	100.0
Rsa1.0_00660.1.g17667.t1	ref|XP_002883969.1| myo-inositol oxygenase 2 [Arabidopsis lyrata subsp. lyrata] gi|297329809|gb|EFH60228.1| myo-inositol oxygenase 2 [Arabidopsis lyrata subsp. lyrata]	317	317	1.00E-173	100.0	92.4	95.0	myo-inositol oxygenase 2	gbpln	Arabidopsis lyrata	AT2G19800.1 | Symbols: MIOX2 | myo-inositol oxygenase 2 | chr2:8531106-8533354 REVERSE LENGTH=317	317	317	1.00E-172	100.0	91.2	94.6
Rsa1.0_00661.1.g17668.t1	gb|ACR48181.1| MYB domain protein 29-1 [Brassica rapa subsp. pekinensis]	340	330	1.00E-157	97.1	83.5	88.2	MYB domain protein 29-1	gbpln	Brassica rapa	AT5G07690.1 | Symbols: MYB29, ATMYB29, PMG2 | myb domain protein 29 | chr5:2447090-2448285 FORWARD LENGTH=336	340	336	1.00E-131	98.8	75.6	83.2
Rsa1.0_00661.1.g17669.t18	ref|NP_568183.1| uncharacterized protein [Arabidopsis thaliana] gi|15451038|gb|AAK96790.1| Unknown protein [Arabidopsis thaliana] gi|18377548|gb|AAL66940.1| unknown protein [Arabidopsis thaliana] gi|332003815|gb|AED91198.1| uncharacterized protein AT5G07730 [Arabidopsis thaliana]	231	264	5.00E-61	114.3	70.1	78.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G07730.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61360.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:2457509-2458383 REVERSE LENGTH=264	231	264	2.00E-63	114.3	70.1	78.4
Rsa1.0_00661.1.g17670.t1	sp|Q9FLQ7.3|FH20_ARATH RecName: Full=Formin-like protein 20; Short=AtFH20 gi|332003816|gb|AED91199.1| actin binding protein [Arabidopsis thaliana]	704	1649	2.33E-156	234.2	36.2	41.3	RecName: Full=Formin-like protein 20; Short=AtFH20 gi|332003816|gb|AED91199.1| actin binding protein	gbpln	Arabidopsis thaliana	AT5G07740.1 | Symbols: | actin binding | chr5:2459076-2466580 REVERSE LENGTH=1649	704	1649	1.00E-149	234.2	36.2	41.3
Rsa1.0_00661.1.g17671.t2	sp|Q9FLQ7.3|FH20_ARATH RecName: Full=Formin-like protein 20; Short=AtFH20 gi|332003816|gb|AED91199.1| actin binding protein [Arabidopsis thaliana]	394	1649	1.00E-117	418.5	56.9	64.7	RecName: Full=Formin-like protein 20; Short=AtFH20 gi|332003816|gb|AED91199.1| actin binding protein	gbpln	Arabidopsis thaliana	AT5G07740.1 | Symbols: | actin binding | chr5:2459076-2466580 REVERSE LENGTH=1649	394	1649	1.00E-120	418.5	56.9	64.7
Rsa1.0_00661.1.g17672.t1	ref|XP_002871290.1| hypothetical protein ARALYDRAFT_487610 [Arabidopsis lyrata subsp. lyrata] gi|297317127|gb|EFH47549.1| hypothetical protein ARALYDRAFT_487610 [Arabidopsis lyrata subsp. lyrata]	542	617	1.00E-122	113.8	56.1	69.6	hypothetical protein ARALYDRAFT_487610	gbpln	Arabidopsis lyrata	AT5G07790.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61300.1). | chr5:2484073-2486107 FORWARD LENGTH=616	542	616	1.00E-124	113.7	57.0	69.7

Rsa1.0_00661.1.g17673.t1	ref|NP_001190233.1| 26S proteasome regulatory subunit N8 [Arabidopsis thaliana] gi|332003541|gb|AED90924.1| probable 26S proteasome non-ATPase regulatory subunit 7 [Arabidopsis thaliana]	314	305	8.00E-56	97.1	37.6	42.7	26S proteasome regulatory subunit N8	gbpln	Arabidopsis thaliana	AT5G05780.2 | Symbols: RPN8A | RP non-ATPase subunit 8A | chr5:1735862-1738176 FORWARD LENGTH=305	314	305	2.00E-58	97.1	37.6	42.7
Rsa1.0_00661.1.g17674.t1	gb|AAL67083.1| unknown protein [Arabidopsis thaliana]	224	616	4.00E-25	275.0	25.9	30.4	unknown protein	gbpln	Arabidopsis thaliana	AT5G07790.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61300.1). | chr5:2484073-2486107 FORWARD LENGTH=616	224	616	1.00E-27	275.0	25.9	30.4
Rsa1.0_00661.1.g17675.t1	ref|XP_002873325.1| SNF2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319162|gb|EFH49584.1| SNF2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1180	1194	0	101.2	80.3	89.1	SNF2 domain-containing protein	gbpln	Arabidopsis lyrata	AT5G07810.1 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing protein | chr5:2491412-2498484 REVERSE LENGTH=1190	1180	1190	0	100.8	79.2	88.3
Rsa1.0_00661.1.g17676.t1	ref|XP_002894507.1| hypothetical protein ARALYDRAFT_474610 [Arabidopsis lyrata subsp. lyrata] gi|297340349|gb|EFH70766.1| hypothetical protein ARALYDRAFT_474610 [Arabidopsis lyrata subsp. lyrata]	201	200	2.00E-85	99.5	79.6	86.1	hypothetical protein ARALYDRAFT_474610	gbpln	Arabidopsis lyrata	AT3G13445.1 | Symbols: TBP1, TFIID-1 | TATA binding protein 1 | chr3:4380317-4381869 FORWARD LENGTH=200	201	200	1.00E-87	99.5	79.1	87.1
Rsa1.0_00661.1.g17677.t1	gb|EOA20264.1| hypothetical protein CARUB_v10000566mg [Capsella rubella]	440	579	4.00E-71	131.6	43.6	49.3	hypothetical protein CARUB_v10000566mg	gbpln	Capsella rubella	AT5G07820.1 | Symbols: | Plant calmodulin-binding protein-related | chr5:2498861-2500546 REVERSE LENGTH=561	440	561	1.00E-61	127.5	42.5	48.9
Rsa1.0_00661.1.g17678.t1	ref|NP_196404.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|6562301|emb|CAB62599.1| N-hydroxycinnamoyl/benzoyltransferase-like protein [Arabidopsis thaliana] gi|10176721|dbj|BAB09951.1| N-hydroxycinnamoyl/benzoyltransferase-like protein [Arabidopsis thaliana] gi|332003831|gb|AED91214.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	459	464	0	101.1	72.3	82.6	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT5G07870.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:2513864-2515351 FORWARD LENGTH=464	459	464	0	101.1	72.3	82.6
Rsa1.0_00661.1.g17679.t1	ref|NP_196406.2| myosin heavy chain-like protein [Arabidopsis thaliana] gi|79327239|ref|NP_001031851.1| myosin heavy chain-like protein [Arabidopsis thaliana] gi|222423567|dbj|BAH19753.1| AT5G07890 [Arabidopsis thaliana] gi|332003833|gb|AED91216.1| myosin heavy chain-like protein [Arabidopsis thaliana] gi|332003835|gb|AED91218.1| myosin heavy chain-like protein [Arabidopsis thaliana]	407	409	1.00E-151	100.5	72.5	83.3	myosin heavy chain-like protein	gbpln	Arabidopsis thaliana	AT5G07890.3 | Symbols: | myosin heavy chain-related | chr5:2517718-2519493 REVERSE LENGTH=409	407	409	1.00E-153	100.5	72.5	83.3
Rsa1.0_00661.1.g17680.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	1505	1489	0	98.9	57.7	71.8	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1505	1262	1.00E-172	83.9	19.5	25.5
Rsa1.0_00661.1.g17681.t2	ref|XP_002873330.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297319167|gb|EFH49589.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	268	262	1.00E-129	97.8	86.6	92.2	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT5G07910.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:2521937-2523769 REVERSE LENGTH=262	268	262	1.00E-121	97.8	86.2	91.8
Rsa1.0_00661.1.g17682.t1	ref|XP_002873331.1| hypothetical protein ARALYDRAFT_487625 [Arabidopsis lyrata subsp. lyrata] gi|297319168|gb|EFH49590.1| hypothetical protein ARALYDRAFT_487625 [Arabidopsis lyrata subsp. lyrata]	727	728	0	100.1	90.8	95.6	hypothetical protein ARALYDRAFT_487625	gbpln	Arabidopsis lyrata	AT5G07920.1 | Symbols: DGK1, ATDGK1 | diacylglycerol kinase1 | chr5:2525197-2528396 REVERSE LENGTH=728	727	728	0	100.1	90.2	95.6
Rsa1.0_00661.1.g17683.t1	ref|NP_196419.1| RPA70-kDa subunit B [Arabidopsis thaliana] gi|6562316|emb|CAB62614.1| replication factor A-like protein [Arabidopsis thaliana] gi|332003852|gb|AED91235.1| RPA70-kDa subunit B [Arabidopsis thaliana]	602	604	0	100.3	88.2	94.9	RPA70-kDa subunit B	gbpln	Arabidopsis thaliana	AT5G08020.1 | Symbols: ATRPA70B, RPA70B | RPA70-kDa subunit B | chr5:2572107-2574879 FORWARD LENGTH=604	602	604	0	100.3	88.2	94.9

Rsa1.0_00661.1.g17684.t1	gb|EOA21885.1| hypothetical protein CARUB_v10002362mg, partial [Capsella rubella]	54	84	1.00E-17	155.6	77.8	90.7	hypothetical protein CARUB_v10002362mg, partial	gbpln	Capsella rubella	AT5G08040.1 | Symbols: TOM5 | mitochondrial import receptor subunit TOM5 homolog | chr5:2577358-2578073 REVERSE LENGTH=54	54	54	1.00E-17	100.0	68.5	90.7
Rsa1.0_00661.1.g17685.t1	ref|NP_196422.1| uncharacterized protein [Arabidopsis thaliana] gi|6562319|emb|CAB62617.1| putative protein [Arabidopsis thaliana] gi|332003855|gb|AED91238.1| uncharacterized protein AT5G08050 [Arabidopsis thaliana]	157	158	3.00E-64	100.6	89.8	95.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G08050.1 | Symbols: | Protein of unknown function (DUF1118) | chr5:2578418-2578964 FORWARD LENGTH=158	157	158	9.00E-67	100.6	89.8	95.5
Rsa1.0_00661.1.g17686.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00661.1.g17687.t1	ref|XP_002871323.1| hypothetical protein ARALYDRAFT_487673 [Arabidopsis lyrata subsp. lyrata] gi|297317160|gb|EFH47582.1| hypothetical protein ARALYDRAFT_487673 [Arabidopsis lyrata subsp. lyrata] gi|482557717|gb|EOA21909.1| hypothetical protein CARUB_v10002392mg [Capsella rubella]	69	69	2.00E-30	100.0	97.1	98.6	hypothetical protein ARALYDRAFT_487673	gbpln	Arabidopsis lyrata	AT5G08391.1 | Symbols: | Protein of unknown function (DUF 3339) | chr5:2699357-2699566 FORWARD LENGTH=69	69	69	5.00E-33	100.0	95.7	98.6
Rsa1.0_00661.1.g17688.t1	ref|NP_568194.2| katanin p80 subunit-like protein [Arabidopsis thaliana] gi|332003911|gb|AED91294.1| katanin p80 subunit-like protein [Arabidopsis thaliana]	711	839	0	118.0	85.5	90.4	katanin p80 subunit-like protein	gbpln	Arabidopsis thaliana	AT5G08390.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:2701448-2706910 FORWARD LENGTH=839	711	839	0	118.0	85.5	90.4
Rsa1.0_00661.1.g17689.t1	gb|EOA21100.1| hypothetical protein CARUB_v10001440mg, partial [Capsella rubella]	243	327	1.00E-116	134.6	85.6	92.2	hypothetical protein CARUB_v10001440mg, partial	gbpln	Capsella rubella	AT5G08400.2 | Symbols: | Protein of unknown function (DUF3531) | chr5:2707225-2708911 REVERSE LENGTH=300	243	300	1.00E-118	123.5	84.8	91.8
Rsa1.0_00661.1.g17690.t1	gb|EOA22822.1| hypothetical protein CARUB_v10003540mg [Capsella rubella]	177	184	1.00E-67	104.0	80.8	84.7	hypothetical protein CARUB_v10003540mg	gbpln	Capsella rubella	AT5G08410.1 | Symbols: FTRA2 | ferredoxin/thioredoxin reductase subunit A (variable subunit) 2 | chr5:2709974-2710528 REVERSE LENGTH=184	177	184	8.00E-69	104.0	80.8	87.0
Rsa1.0_00661.1.g17691.t1	emb|CBI27710.3| unnamed protein product [Vitis vinifera]	136	201	7.00E-41	147.8	64.7	74.3	unnamed protein product	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00661.1.g17692.t1	ref|NP_196462.2| uncharacterized protein [Arabidopsis thaliana] gi|30682392|ref|NP_851033.1| uncharacterized protein [Arabidopsis thaliana] gi|79327334|ref|NP_001031857.1| uncharacterized protein [Arabidopsis thaliana] gi|20259547|gb|AAM13893.1| unknown protein [Arabidopsis thaliana] gi|21689693|gb|AAM67468.1| unknown protein [Arabidopsis thaliana] gi|332003920|gb|AED91303.1| uncharacterized protein AT5G08450 [Arabidopsis thaliana] gi|332003921|gb|AED91304.1| uncharacterized protein AT5G08450 [Arabidopsis thaliana] gi|332003922|gb|AED91305.1| uncharacterized protein AT5G08450 [Arabidopsis thaliana]	922	918	0	99.6	82.2	88.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G08450.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Histone deacetylation protein Rxt3 (InterPro:IPR013951); Has 34444 Blast hits to 20801 proteins in 1175 species: Archae - 64; Bacteria - 2390; Metazoa - 15568; Fungi - 3729; Plants - 1886; Viruses - 208; Other Eukaryotes - 10599 (source: NCBI BLink). | chr5:2727970-2732572 REVERSE LENGTH=918	922	918	0	99.6	82.2	88.3
Rsa1.0_00661.1.g17693.t1	ref|XP_002871330.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317167|gb|EFH47589.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	174	175	3.00E-77	100.6	89.7	94.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G08480.2 | Symbols: | VQ motif-containing protein | chr5:2744486-2745007 FORWARD LENGTH=173	174	173	9.00E-75	99.4	87.9	93.7
Rsa1.0_00661.1.g17694.t1	ref|XP_002873361.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319198|gb|EFH49620.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	851	849	0	99.8	82.4	90.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G08490.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:2745208-2747757 REVERSE LENGTH=849	851	849	0	99.8	82.5	90.2
Rsa1.0_00661.1.g17695.t1	dbj|BAJ34067.1| unnamed protein product [Thellungiella halophila]	320	305	1.00E-142	95.3	83.1	89.7	unnamed protein product	----	----	AT5G08520.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr5:2755470-2757741 REVERSE LENGTH=298	320	298	1.00E-135	93.1	80.3	86.6
Rsa1.0_00662.1.g17696.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00662.1.g17697.t1	ref|NP_199286.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|42573575|ref|NP_974884.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|2660676|gb|AAC79147.1| Dreg-2 like protein [Arabidopsis thaliana] gi|9758377|dbj|BAB08826.1| Dreg-2 like protein [Arabidopsis thaliana] gi|106879171|gb|ABF82615.1| At5g44730 [Arabidopsis thaliana] gi|332007769|gb|AED95152.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|332007770|gb|AED95153.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana]	247	255	1.00E-129	103.2	91.1	96.4	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G44730.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:18045588-18046519 REVERSE LENGTH=255	247	255	1.00E-132	103.2	91.1	96.4
Rsa1.0_00662.1.g17698.t1	ref|XP_002865328.1| molybdenum cofactor sulfurase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311163|gb|EFH41587.1| molybdenum cofactor sulfurase family protein [Arabidopsis lyrata subsp. lyrata]	308	308	1.00E-138	100.0	77.6	86.7	molybdenum cofactor sulfurase family protein	gbpln	Arabidopsis lyrata	AT5G44720.1 | Symbols: | Molybdenum cofactor sulfurase family protein | chr5:18043086-18045275 FORWARD LENGTH=308	308	308	1.00E-139	100.0	76.0	85.7
Rsa1.0_00662.1.g17699.t1	ref|XP_002865328.1| molybdenum cofactor sulfurase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311163|gb|EFH41587.1| molybdenum cofactor sulfurase family protein [Arabidopsis lyrata subsp. lyrata]	308	308	1.00E-157	100.0	86.0	93.5	molybdenum cofactor sulfurase family protein	gbpln	Arabidopsis lyrata	AT5G44720.1 | Symbols: | Molybdenum cofactor sulfurase family protein | chr5:18043086-18045275 FORWARD LENGTH=308	308	308	1.00E-155	100.0	82.8	91.2
Rsa1.0_00662.1.g17700.t1	gb|ABL97982.1| putative TRAPP subunit [Brassica rapa]	102	135	2.00E-47	132.4	99.0	99.0	putative TRAPP subunit	gbpln	Brassica rapa	AT1G80500.1 | Symbols: | SNARE-like superfamily protein | chr1:30271195-30272431 FORWARD LENGTH=135	102	135	5.00E-49	132.4	96.1	98.0
Rsa1.0_00662.1.g17701.t1	gb|EOA33803.1| hypothetical protein CARUB_v10021274mg [Capsella rubella]	329	304	7.00E-90	92.4	52.3	60.8	hypothetical protein CARUB_v10021274mg	gbpln	Capsella rubella	AT2G40560.1 | Symbols: | Protein kinase superfamily protein | chr2:16938705-16939616 REVERSE LENGTH=303	329	303	3.00E-74	92.1	45.9	57.4
Rsa1.0_00662.1.g17702.t1	gb|EOA37158.1| hypothetical protein CARUB_v10010491mg, partial [Capsella rubella]	102	167	9.00E-49	163.7	92.2	97.1	hypothetical protein CARUB_v10010491mg, partial	gbpln	Capsella rubella	AT5G44710.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ribosomal protein S27/S33, mitochondrial (InterPro:IPR013219); Has 101 Blast hits to 101 proteins in 55 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 59; Plants - 26; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr5:18041621-18042322 FORWARD LENGTH=102	102	102	2.00E-50	100.0	92.2	96.1
Rsa1.0_00662.1.g17703.t1	gb|EOA40356.1| hypothetical protein CARUB_v10009084mg [Capsella rubella]	435	459	1.00E-147	105.5	70.1	81.8	hypothetical protein CARUB_v10009084mg	gbpln	Capsella rubella	AT1G50040.1 | Symbols: | Protein of unknown function (DUF1005) | chr1:18542236-18543823 FORWARD LENGTH=460	435	460	1.00E-145	105.7	69.4	81.4
Rsa1.0_00662.1.g17704.t1	ref|NP_199276.1| alpha-barbatene synthase [Arabidopsis thaliana] gi|254810224|sp|Q4KSH9.2|BARS_ARATH RecName: Full=Alpha-barbatene synthase; Short=AtBS; AltName: Full=Beta-chamigrene synthase; AltName: Full=Terpendeoid synthase 11; Short=AtTPS11; AltName: Full=Thujopsene synthase gi|126352284|gb|ABO09887.1| At5g44630 [Arabidopsis thaliana] gi|332007757|gb|AED95140.1| alpha-barbatene synthase [Arabidopsis thaliana]	514	557	0	108.4	73.7	84.2	alpha-barbatene synthase	gbpln	Arabidopsis thaliana	AT5G44630.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr5:18003280-18005616 FORWARD LENGTH=557	514	557	0	108.4	73.7	84.2
Rsa1.0_00662.1.g17705.t1	ref|NP_199276.1| alpha-barbatene synthase [Arabidopsis thaliana] gi|254810224|sp|Q4KSH9.2|BARS_ARATH RecName: Full=Alpha-barbatene synthase; Short=AtBS; AltName: Full=Beta-chamigrene synthase; AltName: Full=Terpendeoid synthase 11; Short=AtTPS11; AltName: Full=Thujopsene synthase gi|126352284|gb|ABO09887.1| At5g44630 [Arabidopsis thaliana] gi|332007757|gb|AED95140.1| alpha-barbatene synthase [Arabidopsis thaliana]	298	557	1.00E-62	186.9	38.3	45.3	alpha-barbatene synthase	gbpln	Arabidopsis thaliana	AT5G44630.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr5:18003280-18005616 FORWARD LENGTH=557	298	557	3.00E-65	186.9	38.3	45.3

Rsa1.0_00662.1.g17706.t1	dbj|BAJ33888.1| unnamed protein product [Thellungiella halophila]	244	245	6.00E−37	100.4	42.6	50.4	unnamed protein product	−−−−	−−−−	AT4G20260.3 | Symbols: ATPCAP1, PCAP1 | plasma−membrane associated cation−binding protein 1 | chr4:10941593−10943227 FORWARD LENGTH=225	244	225	4.00E−34	92.2	38.1	45.9
Rsa1.0_00662.1.g17707.t1	ref|XP_002862972.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308761|gb|EFH39231.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	203	223	3.00E−98	109.9	96.6	99.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G44560.1 | Symbols: VPS2.2 | SNF7 family protein | chr5:17946081−17948222 FORWARD LENGTH=222	203	222	1.00E−100	109.4	92.6	96.1
Rsa1.0_00662.1.g17708.t1	ref|NP_176572.1| TIR−NBS−LRR class disease resistance protein [Arabidopsis thaliana] gi|12325006|gb|AAG52448.1|AC010852_5 putative disease resistance protein; 24665−28198 [Arabidopsis thaliana] gi|332196042|gb|AEE34163.1| TIR−NBS−LRR class disease resistance protein [Arabidopsis thaliana]	1018	1017	0	99.9	60.7	72.9	TIR−NBS−LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT1G63880.1 | Symbols: | Disease resistance protein (TIR−NBS−LRR class) family | chr1:23712514−23716047 REVERSE LENGTH=1017	1018	1017	0	99.9	60.7	72.9
Rsa1.0_00662.1.g17709.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00662.1.g17710.t1	ref|NP_199261.1| UDP−arabinose 4−epimerase [Arabidopsis thaliana] gi|75309104|sp|Q9FI17.1|ARAE4_ARATH RecName: Full=Putative UDP−arabinose 4−epimerase 4; AltName: Full=UDP−D−xylose 4−epimerase 4 gi|9758701|dbj|BAB09155.1| unnamed protein product [Arabidopsis thaliana] gi|332007730|gb|AED95113.1| putative UDP−arabinose 4−epimerase 4 [Arabidopsis thaliana]	383	436	0	113.8	95.3	97.9	UDP−arabinose 4−epimerase	gbpln	Arabidopsis thaliana	AT5G44480.1 | Symbols: DUR | NAD(P)−binding Rossmann−fold superfamily protein | chr5:17921515−17923643 FORWARD LENGTH=436	383	436	0	113.8	95.3	97.9
Rsa1.0_00662.1.g17711.t1	ref|XP_002863575.1| hypothetical protein ARALYDRAFT_494541 [Arabidopsis lyrata subsp. lyrata] gi|297309410|gb|EFH39834.1| hypothetical protein ARALYDRAFT_494541 [Arabidopsis lyrata subsp. lyrata]	334	335	1.00E−163	100.3	86.5	91.3	hypothetical protein ARALYDRAFT_494541	gbpln	Arabidopsis lyrata	AT5G44450.1 | Symbols: | methyltransferases | chr5:17914360−17916017 REVERSE LENGTH=334	334	334	1.00E−164	100.0	85.0	90.1
Rsa1.0_00662.1.g17712.t1	gb|EOA13178.1| hypothetical protein CARUB_v10026203mg [Capsella rubella]	530	538	0	101.5	82.8	91.7	hypothetical protein CARUB_v10026203mg	gbpln	Capsella rubella	AT5G44410.1 | Symbols: | FAD−binding Berberine family protein | chr5:17891246−17892853 REVERSE LENGTH=535	530	535	0	100.9	82.8	91.7
Rsa1.0_00662.1.g17713.t1	ref|XP_002863581.1| FAD−binding domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297309416|gb|EFH39840.1| FAD−binding domain−containing protein [Arabidopsis lyrata subsp. lyrata]	481	540	0	112.3	82.1	91.7	FAD−binding domain−containing protein	gbpln	Arabidopsis lyrata	AT5G44400.1 | Symbols: | FAD−binding Berberine family protein | chr5:17886365−17888071 REVERSE LENGTH=537	481	537	0	111.6	82.7	91.3
Rsa1.0_00662.1.g17714.t1	ref|NP_199252.1| FAD−binding and BBE domain−containing protein [Arabidopsis thaliana] gi|10176894|dbj|BAB10124.1| berberine bridge enzyme−like protein [Arabidopsis thaliana] gi|332007721|gb|AED95104.1| FAD−binding and BBE domain−containing protein [Arabidopsis thaliana]	480	542	0	112.9	76.5	89.0	FAD−binding and BBE domain−containing protein	gbpln	Arabidopsis thaliana	AT5G44390.1 | Symbols: | FAD−binding Berberine family protein | chr5:17882329−17884906 REVERSE LENGTH=542	480	542	0	112.9	76.5	89.0
Rsa1.0_00662.1.g17715.t1	ref|XP_002863582.1| FAD−binding domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297309417|gb|EFH39841.1| FAD−binding domain−containing protein [Arabidopsis lyrata subsp. lyrata]	541	541	0	100.0	78.4	88.2	FAD−binding domain−containing protein	gbpln	Arabidopsis lyrata	AT5G44390.1 | Symbols: | FAD−binding Berberine family protein | chr5:17882329−17884906 REVERSE LENGTH=542	541	542	0	100.2	77.1	87.4
Rsa1.0_00662.1.g17716.t1	ref|XP_002863627.1| hypothetical protein ARALYDRAFT_494617 [Arabidopsis lyrata subsp. lyrata] gi|297309462|gb|EFH39886.1| hypothetical protein ARALYDRAFT_494617 [Arabidopsis lyrata subsp. lyrata]	764	833	0	109.0	75.8	82.2	hypothetical protein ARALYDRAFT_494617	gbpln	Arabidopsis lyrata	AT5G43880.1 | Symbols: | Protein of unknown function (DUF3741) | chr5:17639975−17642848 REVERSE LENGTH=836	764	836	0	109.4	75.7	82.5
Rsa1.0_00662.1.g17717.t1	ref|XP_002865397.1| chlorophyll−chlorophyllido hydrolase 2 [Arabidopsis lyrata subsp. lyrata] gi|297311232|gb|EFH41656.1| chlorophyll−chlorophyllido hydrolase 2 [Arabidopsis lyrata subsp. lyrata]	308	318	1.00E−138	103.2	79.5	87.0	chlorophyll−chlorophyllido hydrolase 2	gbpln	Arabidopsis lyrata	AT5G43860.1 | Symbols: ATCLH2, CLH2 | chlorophyllase 2 | chr5:17630492−17632184 FORWARD LENGTH=318	308	318	1.00E−140	103.2	78.9	86.7
Rsa1.0_00662.1.g17718.t1	gb|AAM63708.1| submergence induced protein 2A [Arabidopsis thaliana]	285	187	2.00E−90	65.6	55.1	57.5	submergence induced protein 2A	gbpln	Arabidopsis thaliana	AT5G43850.1 | Symbols: ATARD4, ARD4 | RmlC−like cupins superfamily protein | chr5:17627364−17629122 REVERSE LENGTH=187	285	187	1.00E−92	65.6	54.7	57.9
Rsa1.0_00663.1.g17719.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_00663.1.g17720.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1461	1413	0	96.7	61.3	72.7	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1461	1262	1.00E-173	86.4	20.4	25.9
Rsa1.0_00663.1.g17721.t2	ref|NP_567941.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] gi|17381226|gb|AAL36425.1| unknown protein [Arabidopsis thaliana] gi|20465827|gb|AAM20018.1| unknown protein [Arabidopsis thaliana] gi|21592377|gb|AAM64328.1| putative dioxygenase [Arabidopsis thaliana] gi|332660892|gb|AEE86292.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	299	288	1.00E-154	96.3	86.6	93.3	oxidoreductase, 2OG-Fe(II) oxygenase family protein	gbpln	Arabidopsis thaliana	AT4G33910.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:16256943-16258614 REVERSE LENGTH=288	299	288	1.00E-156	96.3	86.6	93.3
Rsa1.0_00663.1.g17722.t1	dbj|BAB09815.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	337	676	1.00E-110	200.6	55.5	72.4	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17201414-17202323 REVERSE LENGTH=258	337	258	5.00E-71	76.6	39.2	50.1
Rsa1.0_00663.1.g17723.t1	gb|AAK62371.1|AF386926_1 Unknown protein [Arabidopsis thaliana]	583	587	0	100.7	91.3	96.2	Unknown protein	gbpln	Arabidopsis thaliana	AT4G34030.1 | Symbols: MCCB | 3-methylcrotonyl-CoA carboxylase | chr4:16301298-16303949 FORWARD LENGTH=587	583	587	0	100.7	91.4	96.4
Rsa1.0_00663.1.g17724.t1	gb|ABE41833.1| caffeoyl-CoA 3-O-methyltransferase [Brassica rapa subsp. pekinensis]	258	258	1.00E-147	100.0	98.4	98.8	caffeoyl-CoA 3-O-methyltransferase	gbpln	Brassica rapa	AT4G34050.1 | Symbols: CCoAOMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:16310844-16311973 FORWARD LENGTH=259	258	259	1.00E-141	100.4	93.0	94.2
Rsa1.0_00663.1.g17725.t1	ref|XP_002869176.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297315012|gb|EFH45435.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	1060	1108	0	104.5	92.3	95.4	protein binding protein	gbpln	Arabidopsis lyrata	AT4G34100.2 | Symbols: | RING/U-box superfamily protein | chr4:16330590-16334864 FORWARD LENGTH=1107	1060	1107	0	104.4	91.4	95.0
Rsa1.0_00663.1.g17726.t1	ref|XP_002867144.1| hypothetical protein ARALYDRAFT_491284 [Arabidopsis lyrata subsp. lyrata] gi|297312980|gb|EFH43403.1| hypothetical protein ARALYDRAFT_491284 [Arabidopsis lyrata subsp. lyrata]	257	326	2.00E-55	126.8	62.3	73.5	hypothetical protein ARALYDRAFT_491284	gbpln	Arabidopsis lyrata	AT4G33930.1 | Symbols: | Cupredoxin superfamily protein | chr4:16264389-16265420 REVERSE LENGTH=343	257	343	6.00E-50	133.5	38.1	42.8
Rsa1.0_00663.1.g17727.t1	ref|NP_001119113.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332660924|gb|AEE86324.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	833	1107	0	132.9	52.5	59.5	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT4G34100.2 | Symbols: | RING/U-box superfamily protein | chr4:16330590-16334864 FORWARD LENGTH=1107	833	1107	0	132.9	52.5	59.5
Rsa1.0_00663.1.g17728.t1	ref|NP_195137.5| Polyadenylate-binding protein 2 [Arabidopsis thaliana] gi|1171978|sp|P42731.1|PABP2_ARATH RecName: Full=Polyadenylate-binding protein 2; Short=PABP-2; Short=Poly(A)-binding protein 2 gi|304109|gb|AAA61780.1| poly(A)-binding protein [Arabidopsis thaliana] gi|2911051|emb|CAA17561.1| poly(A)-binding protein [Arabidopsis thaliana] gi|7270360|emb|CAB80128.1| poly(A)-binding protein [Arabidopsis thaliana] gi|26983870|gb|AAN86187.1| putative polyadenylate-binding protein 2 (PABP2) [Arabidopsis thaliana] gi|332660925|gb|AEE86325.1| Polyadenylate-binding protein 2 [Arabidopsis thaliana]	620	629	0	101.5	88.4	93.2	Polyadenylate-binding protein 2	gbpln	Arabidopsis thaliana	AT4G34110.1 | Symbols: PAB2, PABP2, ATPAB2 | poly(A) binding protein 2 | chr4:16336732-16339892 FORWARD LENGTH=629	620	629	0	101.5	88.4	93.2
Rsa1.0_00663.1.g17729.t1	ref|XP_002871498.1| hypothetical protein ARALYDRAFT_909147 [Arabidopsis lyrata subsp. lyrata] gi|297317335|gb|EFH47757.1| hypothetical protein ARALYDRAFT_909147 [Arabidopsis lyrata subsp. lyrata]	166	146	9.00E-20	88.0	42.2	54.8	hypothetical protein ARALYDRAFT_909147	gbpln	Arabidopsis lyrata	AT5G11760.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1764, eukaryotic (InterPro:IPR013885); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3789754-3790299 FORWARD LENGTH=181	166	181	1.00E-17	109.0	39.8	54.2
Rsa1.0_00663.1.g17730.t1	ref|XP_002885623.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297331463|gb|EFH61882.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	854	624	0	73.1	61.6	66.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G24000.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:8672774-8674881 FORWARD LENGTH=665	854	665	0	77.9	60.8	65.6

Rsa1.0_00663.1.g17731.t1	ref|XP_002867135.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312971|gb|EFH43394.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	480	482	0	100.4	83.3	91.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G34131.1 | Symbols: UGT73B3 | UDP-glucosyl transferase 73B3 | chr4:16343268-16344713 REVERSE LENGTH=481	480	481	0	100.2	81.0	89.2
Rsa1.0_00663.1.g17732.t1	ref|XP_002867135.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312971|gb|EFH43394.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	482	482	0	100.0	83.4	90.5	predicted protein	gbpln	Arabidopsis lyrata	AT4G34131.1 | Symbols: UGT73B3 | UDP-glucosyl transferase 73B3 | chr4:16343268-16344713 REVERSE LENGTH=481	482	481	0	99.8	81.5	88.8
Rsa1.0_00663.1.g17733.t1	ref|XP_002867133.1| UDP-glucosyl transferase 73B1 [Arabidopsis lyrata subsp. lyrata] gi|297312969|gb|EFH43392.1| UDP-glucosyl transferase 73B1 [Arabidopsis lyrata subsp. lyrata]	490	488	0	99.6	82.4	91.2	UDP-glucosyl transferase 73B1	gbpln	Arabidopsis lyrata	AT4G34138.1 | Symbols: UGT73B1 | UDP-glucosyl transferase 73B1 | chr4:16348267-16349858 REVERSE LENGTH=488	490	488	0	99.6	80.8	91.0
Rsa1.0_00663.1.g17734.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	475	1274	6.00E-76	268.2	36.4	52.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	475	484	6.00E-44	101.9	27.2	44.0
Rsa1.0_00663.1.g17735.t1	ref|XP_002869171.1| hypothetical protein ARALYDRAFT_912986 [Arabidopsis lyrata subsp. lyrata] gi|297315007|gb|EFH45430.1| hypothetical protein ARALYDRAFT_912986 [Arabidopsis lyrata subsp. lyrata]	229	248	6.00E-80	108.3	66.4	71.6	hypothetical protein ARALYDRAFT_912986	gbpln	Arabidopsis lyrata	AT4G34150.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:16355035-16356955 FORWARD LENGTH=247	229	247	3.00E-77	107.9	62.9	69.0
Rsa1.0_00663.1.g17736.t2	ref|NP_195142.1| cyclin-D3-1 [Arabidopsis thaliana] gi|59802919|sp|P42753.3|CCD31_ARATH RecName: Full=Cyclin-D3-1; AltName: Full=Cyclin-delta-3; Short=Cyclin-d3; AltName: Full=G1/S-specific cyclin-D3-1; Short=CycD3;1 gi|2911046|emb|CAA17556.1| cyclin delta-3 [Arabidopsis thaliana] gi|7270365|emb|CAB80133.1| cyclin delta-3 [Arabidopsis thaliana] gi|62320771|dbj|BAD95437.1| cyclin delta-3 [Arabidopsis thaliana] gi|332660935|gb|AEE86335.1| cyclin-D3-1 [Arabidopsis thaliana]	431	376	1.00E-155	87.2	70.5	78.2	cyclin-D3-1	gbpln	Arabidopsis thaliana	AT4G34160.1 | Symbols: CYCD3;1, CYCD3 | CYCLIN D3;1 | chr4:16357903-16359304 FORWARD LENGTH=376	431	376	1.00E-158	87.2	70.5	78.2
Rsa1.0_00664.1.g17737.t1	ref|XP_003527486.1| PREDICTED: RING-box protein 1a-like [Glycine max] gi|83701143|gb|ABC41134.1| RING-box protein [Arachis hypogaea]	116	116	7.00E-57	100.0	90.5	95.7	PREDICTED: RING-box protein 1a-like	gbpln	Arachis hypogaea	AT5G20570.1 | Symbols: ROC1, RBX1, HRT1, ATRBX1 | RING-box 1 | chr5:6956905-6958221 REVERSE LENGTH=118	116	118	9.00E-57	101.7	90.5	96.6
Rsa1.0_00664.1.g17738.t1	ref|NP_197534.1| beta-1,3-glucanase 5 [Arabidopsis thaliana] gi|2808439|emb|CAA56135.1| bg5 [Arabidopsis thaliana] gi|332005450|gb|AED92833.1| beta-1,3-glucanase 5 [Arabidopsis thaliana]	287	354	1.00E-115	123.3	74.9	84.7	beta-1,3-glucanase 5	gbpln	Arabidopsis thaliana	AT5G20340.1 | Symbols: BG5 | beta-1,3-glucanase 5 | chr5:6874787-6875851 FORWARD LENGTH=354	287	354	1.00E-118	123.3	74.9	84.7
Rsa1.0_00664.1.g17739.t1	gb|EOA20662.1| hypothetical protein CARUB_v10000976mg [Capsella rubella]	375	440	1.00E-176	117.3	88.0	92.8	hypothetical protein CARUB_v10000976mg	gbpln	Capsella rubella	AT5G20540.1 | Symbols: ATBRXL4, BRX-LIKE4, BRXL4 | BREVIS RADIX-like 4 | chr5:6947943-6951760 FORWARD LENGTH=384	375	384	1.00E-177	102.4	88.3	92.3
Rsa1.0_00664.1.g17740.t1	ref|NP_568395.1| protein wavy growth 2 / esterase-lipase domain-containing protein [Arabidopsis thaliana] gi|19347881|gb|AAL85997.1| unknown protein [Arabidopsis thaliana] gi|21280815|gb|AAM45057.1| unknown protein [Arabidopsis thaliana] gi|21593162|gb|AAM65111.1| unknown [Arabidopsis thaliana] gi|57157671|dbj|BAD83800.1| Bem46-like protein [Arabidopsis thaliana] gi|332005472|gb|AED92855.1| protein wavy growth 2 / esterase-lipase domain-containing protein [Arabidopsis thaliana]	318	308	1.00E-153	96.9	83.0	89.3	protein wavy growth 2 / esterase-lipase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G20520.1 | Symbols: WAV2 | alpha/beta-Hydrolases superfamily protein | chr5:6943536-6946315 REVERSE LENGTH=308	318	308	1.00E-156	96.9	83.0	89.3
Rsa1.0_00664.1.g17741.t1	gb|EOA22161.1| hypothetical protein CARUB_v10002729mg [Capsella rubella]	298	267	1.00E-103	89.6	74.2	80.2	hypothetical protein CARUB_v10002729mg	gbpln	Capsella rubella	AT5G20510.1 | Symbols: AL5 | alfin-like 5 | chr5:6939991-6942846 REVERSE LENGTH=260	298	260	1.00E-104	87.2	70.5	78.2

Rsa1.0_00664.1.g17742.t1	ref|XP_002883118.1| hypothetical protein ARALYDRAFT_898177 [Arabidopsis lyrata subsp. lyrata] gi|297328958|gb|EFH59377.1| hypothetical protein ARALYDRAFT_898177 [Arabidopsis lyrata subsp. lyrata]	118	536	5.00E-34	454.2	63.6	66.1	hypothetical protein ARALYDRAFT_898177	gbpln	Arabidopsis lyrata	AT3G18190.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:6232226-6233836 FORWARD LENGTH=536	118	536	8.00E-37	454.2	63.6	66.1
Rsa1.0_00664.1.g17743.t1	ref|NP_197550.1| glutaredoxin-C4 [Arabidopsis thaliana] gi|119370637|sp|Q8LFQ6.2|GRXC4_ARATH RecName: Full=Glutaredoxin-C4; Short=AtGrxC4 gi|6735386|emb|CAB69043.1| glutaredoxin [Arabidopsis thaliana] gi|25082927|gb|AAN72016.1| glutaredoxin [Arabidopsis thaliana] gi|25082941|gb|AAN72019.1| glutaredoxin [Arabidopsis thaliana] gi|98960865|gb|ABF58916.1| At5g20500 [Arabidopsis thaliana] gi|332005470|gb|AED92853.1| glutaredoxin-C4 [Arabidopsis thaliana]	281	135	7.00E-32	48.0	23.1	26.7	glutaredoxin-C4	gbpln	Arabidopsis thaliana	AT5G20500.1 | Symbols: | Glutaredoxin family protein | chr5:6938652-6939665 FORWARD LENGTH=135	281	135	2.00E-34	48.0	23.1	26.7
Rsa1.0_00664.1.g17744.t1	ref|XP_002873998.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319835|gb|EFH50257.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1530	1539	0	100.6	94.8	96.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G20490.1 | Symbols: XIK, ATXIK, XI-17 | Myosin family protein with Dil domain | chr5:6927064-6936825 REVERSE LENGTH=1545	1530	1545	0	101.0	94.6	96.4
Rsa1.0_00664.1.g17745.t1	gb|EMJ03759.1| hypothetical protein PRUPE_ppa011299mg [Prunus persica]	222	216	9.00E-81	97.3	67.1	79.3	hypothetical protein PRUPE_ppa011299mg	gbpln	Prunus persica	AT5G45550.1 | Symbols: | Mob1/phocein family protein | chr5:18462284-18464840 FORWARD LENGTH=215	222	215	2.00E-79	96.8	64.4	76.6
Rsa1.0_00664.1.g17746.t1	gb|EOA20550.1| hypothetical protein CARUB_v10000862mg [Capsella rubella]	473	476	0	100.6	91.3	96.6	hypothetical protein CARUB_v10000862mg	gbpln	Capsella rubella	AT5G20410.1 | Symbols: MGD2, ATMGD2 | monogalactosyldiacylglycerol synthase 2 | chr5:6896765-6898581 FORWARD LENGTH=468	473	468	0	98.9	88.8	94.1
Rsa1.0_00664.1.g17747.t2	ref|XP_002873995.1| hypothetical protein ARALYDRAFT_910078 [Arabidopsis lyrata subsp. lyrata] gi|297319832|gb|EFH50254.1| hypothetical protein ARALYDRAFT_910078 [Arabidopsis lyrata subsp. lyrata]	549	517	0	94.2	79.8	84.0	hypothetical protein ARALYDRAFT_910078	gbpln	Arabidopsis lyrata	AT5G20380.1 | Symbols: PHT4;5 | phosphate transporter 4;5 | chr5:6887936-6892358 REVERSE LENGTH=517	549	517	0	94.2	80.0	83.8
Rsa1.0_00664.1.g17748.t1	ref|XP_002873994.1| hypothetical protein ARALYDRAFT_910077 [Arabidopsis lyrata subsp. lyrata] gi|297319831|gb|EFH50253.1| hypothetical protein ARALYDRAFT_910077 [Arabidopsis lyrata subsp. lyrata]	166	169	5.00E-43	101.8	68.1	75.9	hypothetical protein ARALYDRAFT_910077	gbpln	Arabidopsis lyrata	AT5G20370.1 | Symbols: | serine-rich protein-related | chr5:6886931-6887458 REVERSE LENGTH=175	166	175	3.00E-38	105.4	65.7	75.3
Rsa1.0_00664.1.g17749.t1	gb|EOA20179.1| hypothetical protein CARUB_v10000476mg [Capsella rubella]	578	620	0	107.3	93.9	97.4	hypothetical protein CARUB_v10000476mg	gbpln	Capsella rubella	AT5G20350.1 | Symbols: TIP1 | Ankyrin repeat family protein with DHHC zinc finger domain | chr5:6876772-6881102 FORWARD LENGTH=620	578	620	0	107.3	92.9	96.4
Rsa1.0_00664.1.g17750.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1578	1459	0	92.5	48.9	62.6	polyprotein, putative	gbpln	Arabidopsis thaliana	AT5G20340.1 | Symbols: BG5 | beta-1,3-glucanase 5 | chr5:6874787-6875851 FORWARD LENGTH=354	1578	354	1.00E-124	22.4	13.4	14.6
Rsa1.0_00664.1.g17751.t1	ref|XP_002871934.1| beta-1,3-glucanase bg4 [Arabidopsis lyrata subsp. lyrata] gi|297317771|gb|EFH48193.1| beta-1,3-glucanase bg4 [Arabidopsis lyrata subsp. lyrata]	129	345	1.00E-23	267.4	41.1	49.6	beta-1,3-glucanase bg4	gbpln	Arabidopsis lyrata	AT5G20330.1 | Symbols: BETAG4 | beta-1,3-glucanase 4 | chr5:6871620-6872657 FORWARD LENGTH=345	129	345	2.00E-25	267.4	40.3	52.7
Rsa1.0_00665.1.g17752.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00665.1.g17753.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	612	1103	4.00E-66	180.2	20.1	26.0	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00665.1.g17754.t1	ref|XP_002891341.1| hypothetical protein ARALYDRAFT_473874 [Arabidopsis lyrata subsp. lyrata] gi|297337183|gb|EFH67600.1| hypothetical protein ARALYDRAFT_473874 [Arabidopsis lyrata subsp. lyrata]	283	277	1.00E-115	97.9	75.6	78.4	hypothetical protein ARALYDRAFT_473874	gbpln	Arabidopsis lyrata	AT1G47250.1 | Symbols: PAF2 | 20S proteasome alpha subunit F2 | chr1:17319220-17320900 FORWARD LENGTH=277	283	277	1.00E-116	97.9	74.6	77.7
Rsa1.0_00665.1.g17755.t2	gb|AAF67379.1| Hypothetical protein T15F17.k [Arabidopsis thaliana]	308	341	1.00E-91	110.7	61.0	73.7	Hypothetical protein T15F17.k	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00665.1.g17756.t1	gb|ABD65073.1| hypothetical protein 27.t00059 [Brassica oleracea]	307	341	1.00E-19	111.1	20.5	24.1	hypothetical protein 27.t00059	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_00665.1.g17757.t2	gb|AAD20646.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	393	1040	2.00E-90	264.6	45.3	55.2	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00665.1.g17758.t1	ref|XP_002865486.1| hypothetical protein ARALYDRAFT_331125 [Arabidopsis lyrata subsp. lyrata] gi|297311321|gb|EFH41745.1| hypothetical protein ARALYDRAFT_331125 [Arabidopsis lyrata subsp. lyrata]	344	348	1.00E-175	101.2	85.5	92.4	hypothetical protein ARALYDRAFT_331125	gbpln	Arabidopsis lyrata	AT5G42760.1 | Symbols: | Leucine carboxyl methyltransferase | chr5:17148953-17150105 FORWARD LENGTH=348	344	348	1.00E-177	101.2	85.8	91.9
Rsa1.0_00665.1.g17759.t1	dbj|BAA97083.1| unnamed protein product [Arabidopsis thaliana]	186	583	3.00E-17	313.4	32.8	47.3	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00665.1.g17760.t12	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	969	777	7.00E-31	80.2	15.0	24.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00665.1.g17761.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00665.1.g17762.t1	ref|XP_002865493.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297311328|gb|EFH41752.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	430	435	0	101.2	84.7	90.2	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT5G42720.1 | Symbols: | Glycosyl hydrolase family 17 protein | chr5:17130535-17132763 FORWARD LENGTH=438	430	438	0	101.9	84.2	90.2
Rsa1.0_00665.1.g17763.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00666.1.g17764.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00666.1.g17765.t1	ref|XP_002888671.1| hypothetical protein ARALYDRAFT_475977 [Arabidopsis lyrata subsp. lyrata] gi|297334512|gb|EFH64930.1| hypothetical protein ARALYDRAFT_475977 [Arabidopsis lyrata subsp. lyrata]	318	327	4.00E-85	102.8	64.5	74.2	hypothetical protein ARALYDRAFT_475977	gbpln	Arabidopsis lyrata	AT1G68550.2 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:25725810-25726784 REVERSE LENGTH=324	318	324	1.00E-84	101.9	63.2	72.3
Rsa1.0_00666.1.g17766.t1	ref|NP_177020.1| 3-ketoacyl-CoA synthase 6 [Arabidopsis thaliana] gi|75315046|sp|Q9XF43.1|KCS6_ARATH RecName: Full=3-ketoacyl-CoA synthase 6; Short=KCS-6; AltName: Full=Cuticular protein 1; AltName: Full=Very long-chain fatty acid condensing enzyme 6; Short=VLCFA condensing enzyme 6 gi|5001734|gb|AAD37122.1|AF129511_1 very-long-chain fatty acid condensing enzyme CUT1 [Arabidopsis thaliana] gi|12324880|gb|AAG52390.1|AC011915_4 very-long-chain fatty acid condensing enzyme (CUT1); 56079-54227 [Arabidopsis thaliana] gi|332196683|gb|AEE34804.1| 3-ketoacyl-CoA synthase 6 [Arabidopsis thaliana]	497	497	0	100.0	94.8	97.2	3-ketoacyl-CoA synthase 6	gbpln	Arabidopsis thaliana	AT1G68530.1 | Symbols: CUT1, POP1, CER6, G2, KCS6 | 3-ketoacyl-CoA synthase 6 | chr1:25712881-25714733 REVERSE LENGTH=497	497	497	0	100.0	94.8	97.2
Rsa1.0_00666.1.g17767.t1	ref|NP_564932.1| zinc finger protein CONSTANS-LIKE 6 [Arabidopsis thaliana] gi|52840167|sp|Q8LG76.2|COL6_ARATH RecName: Full=Zinc finger protein CONSTANS-LIKE 6 gi|15451090|gb|AAK96816.1| putative B-box zinc finger protein [Arabidopsis thaliana] gi|20148425|gb|AAM10103.1| putative B-box zinc finger protein [Arabidopsis thaliana] gi|332196681|gb|AEE34802.1| zinc finger protein CONSTANS-LIKE 6 [Arabidopsis thaliana]	402	406	1.00E-174	101.0	80.3	88.8	zinc finger protein CONSTANS-LIKE 6	gbpln	Arabidopsis thaliana	AT1G68520.1 | Symbols: | B-box type zinc finger protein with CCT domain | chr1:25709331-25710749 REVERSE LENGTH=406	402	406	1.00E-176	101.0	80.3	88.8
Rsa1.0_00666.1.g17768.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00666.1.g17769.t1	ref|NP_564931.1| uncharacterized protein [Arabidopsis thaliana] gi|12324888|gb|AAG52398.1|AC011915_12 unknown protein; 35272-36292 [Arabidopsis thaliana] gi|21593205|gb|AAM65154.1| unknown [Arabidopsis thaliana] gi|29028824|gb|AAO64791.1| At1g68490 [Arabidopsis thaliana] gi|110736380|dbj|BAF00159.1| hypothetical protein [Arabidopsis thaliana] gi|332196678|gb|AEE34799.1| uncharacterized protein AT1G68490 [Arabidopsis thaliana]	176	183	2.00E-69	104.0	85.8	90.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G68490.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G13390.2); Has 125 Blast hits to 125 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 125; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25693926-25694946 FORWARD LENGTH=183	176	183	6.00E-72	104.0	85.8	90.9

Rsa1.0_00666.1.g17770.t2	ref|XP_002881289.1| hypothetical protein ARALYDRAFT_482302 [Arabidopsis lyrata subsp. lyrata] gi|297327128|gb|EFH57548.1| hypothetical protein ARALYDRAFT_482302 [Arabidopsis lyrata subsp. lyrata]	157	394	6.00E-24	251.0	52.2	56.1	hypothetical protein ARALYDRAFT_482302	gbpln	Arabidopsis lyrata	AT2G33560.2 | Symbols: BUBR1 | BUB1-related (BUB1: budding uninhibited by benzymidazol 1) | chr2:14213810-14215918 REVERSE LENGTH=396	157	396	6.00E-26	252.2	50.3	56.7
Rsa1.0_00666.1.g17771.t1	dbj|BAE43826.1| isopentenyltransferase [Brassica rapa subsp. pekinensis]	298	348	1.00E-142	116.8	86.2	90.3	isopentenyltransferase	gbpln	Brassica rapa	AT1G68460.1 | Symbols: ATIPT1, IPT1 | isopentenyltransferase 1 | chr1:25668976-25670049 REVERSE LENGTH=357	298	357	1.00E-130	119.8	76.5	86.9
Rsa1.0_00667.1.g17772.t1	gb|EOA29659.1| hypothetical protein CARUB_v10015473mg [Capsella rubella]	64	162	1.00E-13	253.1	64.1	70.3	hypothetical protein CARUB_v10015473mg	gbpln	Capsella rubella	AT1G47960.1 | Symbols: C/VIF1, ATC/VIF1 | cell wall / vacuolar inhibitor of fructosidase 1 | chr1:17681954-17683516 REVERSE LENGTH=205	64	205	8.00E-12	320.3	45.3	54.7
Rsa1.0_00667.1.g17773.t1	gb|EOA29659.1| hypothetical protein CARUB_v10015473mg [Capsella rubella]	163	162	3.00E-67	99.4	77.9	84.7	hypothetical protein CARUB_v10015473mg	gbpln	Capsella rubella	AT3G17140.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:5846002-5846589 REVERSE LENGTH=112	163	112	3.00E-46	68.7	50.9	56.4
Rsa1.0_00667.1.g17774.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	151	1142	7.00E-26	756.3	43.7	55.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	151	575	1.00E-11	380.8	25.8	43.0
Rsa1.0_00667.1.g17775.t1	gb|ACJ68115.1| invertase inhibitor-like protein [Brassica napus]	172	153	1.00E-64	89.0	69.8	76.7	invertase inhibitor-like protein	gbpln	Brassica napus	AT3G17152.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:5848812-5849544 FORWARD LENGTH=175	172	175	3.00E-56	101.7	65.1	80.2
Rsa1.0_00667.1.g17776.t1	gb|ACJ68115.1| invertase inhibitor-like protein [Brassica napus]	172	153	4.00E-72	89.0	75.6	83.1	invertase inhibitor-like protein	gbpln	Brassica napus	AT3G17152.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:5848812-5849544 FORWARD LENGTH=175	172	175	2.00E-55	101.7	64.0	79.7
Rsa1.0_00667.1.g17777.t1	gb|ACJ68115.1| invertase inhibitor-like protein [Brassica napus]	152	153	2.00E-54	100.7	67.1	78.9	invertase inhibitor-like protein	gbpln	Brassica napus	AT3G17152.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:5848812-5849544 FORWARD LENGTH=175	152	175	1.00E-50	115.1	62.5	76.3
Rsa1.0_00667.1.g17778.t1	gb|ACJ68115.1| invertase inhibitor-like protein [Brassica napus]	171	153	2.00E-64	89.5	69.0	79.5	invertase inhibitor-like protein	gbpln	Brassica napus	AT3G17152.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:5848812-5849544 FORWARD LENGTH=175	171	175	2.00E-55	102.3	62.0	77.2
Rsa1.0_00667.1.g17779.t1	gb|AAM62870.1| unknown [Arabidopsis thaliana]	301	314	1.00E-122	104.3	82.1	90.4	unknown	gbpln	Arabidopsis thaliana	AT3G17170.1 | Symbols: RFC3 | Translation elongation factor EF1B/ribosomal protein S6 family protein | chr3:5853186-5854853 REVERSE LENGTH=314	301	314	1.00E-124	104.3	82.1	90.7
Rsa1.0_00667.1.g17780.t1	ref|NP_188343.1| protein serine carboxypeptidase-like 33 [Arabidopsis thaliana] gi|334302854|sp|Q9LSM9.2|SCP33_ARATH RecName: Full=Serine carboxypeptidase-like 33; Flags: Precursor gi|332642394|gb|AEE75915.1| protein serine carboxypeptidase-like 33 [Arabidopsis thaliana]	474	478	0	100.8	87.6	94.3	protein serine carboxypeptidase-like 33	gbpln	Arabidopsis thaliana	AT3G17180.1 | Symbols: scpl33 | serine carboxypeptidase-like 33 | chr3:5855861-5859157 REVERSE LENGTH=478	474	478	0	100.8	87.6	94.3
Rsa1.0_00667.1.g17781.t4	gb|EOA15341.1| hypothetical protein CARUB_v10004114mg [Capsella rubella]	190	864	2.00E-50	454.7	52.6	53.7	hypothetical protein CARUB_v10004114mg	gbpln	Capsella rubella	AT4G14330.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:8244228-8247286 FORWARD LENGTH=869	190	869	5.00E-52	457.4	52.1	53.2
Rsa1.0_00667.1.g17782.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	609	536	4.00E-93	88.0	27.4	35.5	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	609	530	7.00E-52	87.0	13.8	17.6
Rsa1.0_00667.1.g17783.t1	ref|XP_002883053.1| hypothetical protein ARALYDRAFT_479191 [Arabidopsis lyrata subsp. lyrata] gi|297328893|gb|EFH59312.1| hypothetical protein ARALYDRAFT_479191 [Arabidopsis lyrata subsp. lyrata]	1054	1029	0	97.6	87.3	92.3	hypothetical protein ARALYDRAFT_479191	gbpln	Arabidopsis lyrata	AT3G17205.3 | Symbols: UPL6 | ubiquitin protein ligase 6 | chr3:5873528-5881132 FORWARD LENGTH=1029	1054	1029	0	97.6	86.4	92.2

Rsa1.0_00667.1.g17784.t1	pdb|1Q53|A Chain A, Solution Structure Of Hypothetical Arabidopsis Thaliana Protein At3g17210. Center For Eukaryotic Structural Genomics Target 13081 gi|159162872|pdb|1Q53|B Chain B, Solution Structure Of Hypothetical Arabidopsis Thaliana Protein At3g17210. Center For Eukaryotic Structural Genomics Target 13081	107	112	4.00E-51	104.7	91.6	97.2	Chain A, Solution Structure Of Hypothetical Arabidopsis Thaliana Protein At3g17210. Center For Eukaryotic Structural Genomics Target 13081 gi|159162872|pdb|1Q53|B Chain B, Solution Structure Of Hypothetical Arabidopsis Thaliana Protein At3g17210. Center For Eukaryotic Structural Genomics Target 13081	----	----	AT3G17210.1 | Symbols: ATHS1, HS1 | heat stable protein 1 | chr3:5882318-5882896 FORWARD LENGTH=109	107	109	8.00E-54	101.9	91.6	97.2
Rsa1.0_00667.1.g17785.t1	gb|EOA32350.1| hypothetical protein CARUB_v10015617mg [Capsella rubella]	180	173	1.00E-42	96.1	52.8	65.6	hypothetical protein CARUB_v10015617mg	gbpln	Capsella rubella	AT3G17220.1 | Symbols: ATPMEI2, PMEI2 | pectin methylesterase inhibitor 2 | chr3:5883328-5883849 REVERSE LENGTH=173	180	173	2.00E-43	96.1	51.1	65.0
Rsa1.0_00667.1.g17786.t2	gb|EOA29133.1| hypothetical protein CARUB_v10025401mg [Capsella rubella]	357	354	6.00E-56	99.2	41.7	59.1	hypothetical protein CARUB_v10025401mg	gbpln	Capsella rubella	AT3G17540.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6002783-6003973 FORWARD LENGTH=396	357	396	4.00E-56	110.9	43.1	59.7
Rsa1.0_00667.1.g17787.t1	ref|XP_002886107.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331947|gb|EFH62366.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	542	337	4.00E-56	62.2	30.1	37.5	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00667.1.g17788.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00668.1.g17789.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00668.1.g17790.t1	gb|ACP30606.1| disease resistance protein [Brassica rapa subsp. pekinensis]	776	836	0	107.7	81.3	88.9	disease resistance protein	gbpln	Brassica rapa	AT4G33300.2 | Symbols: ADR1-L1 | ADR1-like 1 | chr4:16051162-16054005 REVERSE LENGTH=816	776	816	0	105.2	72.0	83.5
Rsa1.0_00668.1.g17791.t1	emb|CAA11819.1| hypothetical protein [Brassica napus]	458	457	0	99.8	97.8	98.9	hypothetical protein	gbpln	Brassica napus	AT4G33270.1 | Symbols: CDC20.1 | Transducin family protein / WD-40 repeat family protein | chr4:16044545-16046590 REVERSE LENGTH=457	458	457	0	99.8	94.5	96.9
Rsa1.0_00668.1.g17792.t1	ref|XP_002867191.1| hypothetical protein ARALYDRAFT_913095 [Arabidopsis lyrata subsp. lyrata] gi|297313027|gb|EFH43450.1| hypothetical protein ARALYDRAFT_913095 [Arabidopsis lyrata subsp. lyrata]	229	228	1.00E-121	99.6	93.0	96.9	hypothetical protein ARALYDRAFT_913095	gbpln	Arabidopsis lyrata	AT4G33250.1 | Symbols: EIF3K, TIF3K1, ATTIF3K1 | eukaryotic translation initiation factor 3K | chr4:16039066-16040617 REVERSE LENGTH=226	229	226	1.00E-121	98.7	92.1	95.2
Rsa1.0_00668.1.g17793.t1	ref|XP_002867192.1| hypothetical protein ARALYDRAFT_491361 [Arabidopsis lyrata subsp. lyrata] gi|297313028|gb|EFH43451.1| hypothetical protein ARALYDRAFT_491361 [Arabidopsis lyrata subsp. lyrata]	1735	1755	0	101.2	86.3	91.1	hypothetical protein ARALYDRAFT_491361	gbpln	Arabidopsis lyrata	AT4G33240.2 | Symbols: FAB1A | 1-phosphatidylinositol-4-phosphate 5-kinases;zinc ion binding;1-phosphatidylinositol-3-phosphate 5-kinases | chr4:16029504-16037278 REVERSE LENGTH=1756	1735	1756	0	101.2	86.1	90.9
Rsa1.0_00668.1.g17794.t1	ref|XP_002869219.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315055|gb|EFH45478.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	505	525	0	104.0	84.6	92.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G33220.1 | Symbols: PME44, ATPME44 | pectin methylesterase 44 | chr4:16022506-16026130 FORWARD LENGTH=525	505	525	0	104.0	84.0	92.1
Rsa1.0_00668.1.g17795.t2	ref|XP_002867194.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313030|gb|EFH43453.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	992	990	0	99.8	89.1	93.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G33210.1 | Symbols: SLOMO | F-box family protein | chr4:16015971-16020697 REVERSE LENGTH=990	992	990	0	99.8	88.5	93.1
Rsa1.0_00668.1.g17796.t1	ref|XP_002867195.1| hypothetical protein ARALYDRAFT_913100 [Arabidopsis lyrata subsp. lyrata] gi|297313031|gb|EFH43454.1| hypothetical protein ARALYDRAFT_913100 [Arabidopsis lyrata subsp. lyrata]	1535	1522	0	99.2	90.4	94.1	hypothetical protein ARALYDRAFT_913100	gbpln	Arabidopsis lyrata	AT4G33200.1 | Symbols: XI-I, ATXI-I, XI-15 | myosin, putative | chr4:16002768-16014792 REVERSE LENGTH=1522	1535	1522	0	99.2	90.5	94.0
Rsa1.0_00668.1.g17797.t2	gb|EOA18803.1| hypothetical protein CARUB_v10007416mg [Capsella rubella]	278	562	2.00E-32	202.2	28.4	33.8	hypothetical protein CARUB_v10007416mg	gbpln	Capsella rubella	AT4G35540.1 | Symbols: | zinc ion binding;transcription regulators | chr4:16873939-16875522 FORWARD LENGTH=527	278	527	6.00E-27	189.6	28.1	33.5

Rsa1.0_00668.1.g17798.t1	ref|XP_002865966.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata] gi|297311801|gb|EFH42225.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata]	577	455	1.00E-95	78.9	38.3	48.0	hypothetical protein ARALYDRAFT_357572	gbpln	Arabidopsis lyrata	AT1G30790.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:10932713-10933912 FORWARD LENGTH=399	577	399	4.00E-74	69.2	30.8	41.4
Rsa1.0_00668.1.g17799.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00668.1.g17800.t1	ref|XP_002867196.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297313032|gb|EFH43455.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	987	997	0	101.0	87.2	93.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G33170.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:15995701-15998673 REVERSE LENGTH=990	987	990	0	100.3	85.1	93.1
Rsa1.0_00668.1.g17801.t1	ref|NP_567915.3| F-box only protein 13 [Arabidopsis thaliana] gi|334302802|sp|Q9SMZ3.2|FBX13_ARATH RecName: Full=F-box only protein 13 gi|332660785|gb|AEE86185.1| F-box only protein 13 [Arabidopsis thaliana]	410	457	0	111.5	78.5	88.0	F-box only protein 13	gbpln	Arabidopsis thaliana	AT4G33160.1 | Symbols: | F-box family protein | chr4:15994160-15995533 FORWARD LENGTH=457	410	457	0	111.5	78.5	88.0
Rsa1.0_00669.1.g17802.t1	gb|AAF79348.1|AC007887_7 F15O4.13 [Arabidopsis thaliana]	271	1887	4.00E-16	696.3	14.0	19.2	F15O4.13	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00669.1.g17803.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00669.1.g17804.t1	emb|CAN66576.1| hypothetical protein VITISV_016964 [Vitis vinifera]	432	1316	1.00E-68	304.6	38.7	53.9	hypothetical protein VITISV_016964	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00669.1.g17805.t2	gb|EOA24720.1| hypothetical protein CARUB_v10017998mg [Capsella rubella]	216	216	1.00E-122	100.0	99.1	100.0	hypothetical protein CARUB_v10017998mg	gbpln	Capsella rubella	AT3G46060.3 | Symbols: ARA3 | RAB GTPase homolog 8A | chr3:16917908-16919740 FORWARD LENGTH=216	216	216	1.00E-124	100.0	99.1	100.0
Rsa1.0_00669.1.g17806.t1	gb|EOA24096.1| hypothetical protein CARUB_v10017326mg [Capsella rubella]	423	422	0	99.8	82.0	90.5	hypothetical protein CARUB_v10017326mg	gbpln	Capsella rubella	AT2G39570.1 | Symbols: | ACT domain-containing protein | chr2:16507963-16509741 FORWARD LENGTH=411	423	411	1.00E-137	97.2	56.0	71.2
Rsa1.0_00669.1.g17807.t1	ref|XP_002891526.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata] gi|297337368|gb|EFH67785.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata]	793	824	1.00E-121	103.9	38.0	53.3	hypothetical protein ARALYDRAFT_337115	gbpln	Arabidopsis lyrata	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	793	452	2.00E-52	57.0	20.8	30.1
Rsa1.0_00669.1.g17808.t1	ref|NP_197073.1| zinc ion binding protein [Arabidopsis thaliana] gi|9755614|emb|CAC01768.1| putative protein [Arabidopsis thaliana] gi|91806864|gb|ABE66159.1| hypothetical protein At5g15690 [Arabidopsis thaliana] gi|332004809|gb|AED92192.1| zinc ion binding protein [Arabidopsis thaliana]	119	169	1.00E-22	142.0	40.3	59.7	zinc ion binding protein	gbpln	Arabidopsis thaliana	AT5G15690.1 | Symbols: | zinc ion binding | chr5:5113823-5114402 REVERSE LENGTH=169	119	169	2.00E-25	142.0	40.3	59.7
Rsa1.0_00669.1.g17809.t1	emb|CAB51200.1| putative protein [Arabidopsis thaliana]	714	739	1.00E-127	103.5	36.1	56.2	putative protein	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	714	785	5.00E-29	109.9	17.9	30.4
Rsa1.0_00669.1.g17810.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	992	1223	0	123.3	42.8	60.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	992	746	3.00E-89	75.2	17.1	23.0
Rsa1.0_00669.1.g17811.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00669.1.g17812.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00669.1.g17813.t2	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	710	1499	1.00E-114	211.1	32.4	41.1	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00670.1.g17814.t1	dbj|BAJ34208.1| unnamed protein product [Thellungiella halophila]	813	895	0	110.1	78.2	84.9	unnamed protein product	----	----	AT3G02170.1 | Symbols: LNG2 | longifolia2 | chr3:396208-399393 REVERSE LENGTH=905	813	905	0	111.3	76.5	83.8
Rsa1.0_00670.1.g17815.t1	gb|EOA31955.1| hypothetical protein CARUB_v10015197mg [Capsella rubella]	205	382	1.00E-14	186.3	28.8	33.7	hypothetical protein CARUB_v10015197mg	gbpln	Capsella rubella	AT3G02160.1 | Symbols: | Bromodomain transcription factor | chr3:394615-395808 FORWARD LENGTH=397	205	397	1.00E-13	193.7	23.4	28.8

Rsa1.0_00670.1.g17816.t1	ref|NP_850501.1| transcription factor TCP13 [Arabidopsis thaliana] gi|75194218|sp|Q9S7W5.1|TCP13_ARATH RecName: Full=Transcription factor TCP13; AltName: Full=Plastid transcription factor 1; AltName: Full=TFPD gi|6041802|gb|AAF02122.1|AC009755_15 unknown protein [Arabidopsis thaliana] gi|6513919|gb|AAF14823.1|AC011664_5 unknown protein [Arabidopsis thaliana] gi|6681577|dbj|BAA88760.1| TFPD [Arabidopsis thaliana] gi|25082706|gb|AAN71993.1| expressed protein [Arabidopsis thaliana] gi|31711844|gb|AAP68278.1| At3g02156 [Arabidopsis thaliana] gi|332640249|gb|AEE73770.1| transcription factor TCP13 [Arabidopsis thaliana]	310	355	1.00E-121	114.5	80.3	85.8	transcription factor TCP13	gbpln	Arabidopsis thaliana	AT3G02150.2 | Symbols: PTF1, TFPD | plastid transcription factor 1 | chr3:391522-392589 FORWARD LENGTH=355	310	355	1.00E-123	114.5	80.3	85.8
Rsa1.0_00670.1.g17817.t1	ref|NP_566162.1| uncharacterized protein [Arabidopsis thaliana] gi|91806371|gb|ABE65913.1| hypothetical protein At3g02125 [Arabidopsis thaliana] gi|332640245|gb|AEE73766.1| uncharacterized protein AT3G02125 [Arabidopsis thaliana]	356	355	2.00E-89	99.7	63.2	73.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G02125.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: pollen tube; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39200.1); Has 2247 Blast hits to 1434 proteins in 202 species: Archae - 4; Bacteria - 111; Metazoa - 942; Fungi - 239; Plants - 140; Viruses - 37; Other Eukaryotes - 774 (source: NCBI BLink). | chr3:378205-379382 FORWARD LENGTH=355	356	355	6.00E-92	99.7	63.2	73.3
Rsa1.0_00670.1.g17818.t4	ref|NP_186859.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75265806|sp|Q9SGA8.1|U83A1_ARATH RecName: Full=UDP-glycosyltransferase 83A1 gi|6513946|gb|AAF14850.1|AC011664_32 putative UDP-glucosyl transferase [Arabidopsis thaliana] gi|332640242|gb|AEE73763.1| UDP-glycosyltransferase 83A1 [Arabidopsis thaliana]	458	464	0	101.3	81.4	88.4	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT3G02100.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:368840-370484 REVERSE LENGTH=464	458	464	0	101.3	81.4	88.4
Rsa1.0_00670.1.g17819.t1	ref|NP_186858.1| mitochondrial processing peptidase [Arabidopsis thaliana] gi|85700445|sp|Q42290.2|MPPB_ARATH RecName: Full=Probable mitochondrial-processing peptidase subunit beta; AltName: Full=Beta-MPP; Flags: Precursor gi|6513923|gb|AAF14827.1|AC011664_9 putative mitochondrial processing peptidase [Arabidopsis thaliana] gi|22022518|gb|AAM83217.1| AT3g02090/F1C9_12 [Arabidopsis thaliana] gi|23397047|gb|AAN31809.1| putative mitochondrial processing peptidase [Arabidopsis thaliana] gi|23463071|gb|AAN33205.1| At3g02090/F1C9_12 [Arabidopsis thaliana] gi|25054848|gb|AAN71914.1| putative mitochondrial processing peptidase [Arabidopsis thaliana] gi|332640240|gb|AEE73761.1| probable mitochondrial-processing peptidase subunit beta [Arabidopsis thaliana]	527	531	0	100.8	90.1	94.7	mitochondrial processing peptidase	gbpln	Arabidopsis thaliana	AT3G02090.1 | Symbols: MPPBETA | Insulinase (Peptidase family M16) protein | chr3:365624-368526 FORWARD LENGTH=531	527	531	0	100.8	90.1	94.7

Rsa1.0_00670.1.g17820.t1	ref|NP_186857.1| 40S ribosomal protein S19-1 [Arabidopsis thaliana] gi|27923843|sp|Q9SGA6.1|RS191_ARATH RecName: Full=40S ribosomal protein S19-1 gi|6513924|gb|AAF14828.1|AC011664_10 putative 40S ribosomal protein S19 [Arabidopsis thaliana] gi|13878029|gb|AAK44092.1|AF370277_1 putative 40S ribosomal protein S19 [Arabidopsis thaliana] gi|17104595|gb|AAL34186.1| putative 40S ribosomal protein S19 [Arabidopsis thaliana] gi|21593712|gb|AAM65679.1| putative 40S ribosomal protein S19 [Arabidopsis thaliana] gi|332640239|gb|AEE73760.1| 40S ribosomal protein S19-1 [Arabidopsis thaliana] gi|482567473|gb|EOA31662.1| hypothetical protein CARUB_v10014866mg [Capsella rubella]	143	143	7.00E-77	100.0	97.9	99.3	40S ribosomal protein S19-1	gbpln	Arabidopsis thaliana	AT3G02080.1 | Symbols: | Ribosomal protein S19e family protein | chr3:364138-365161 REVERSE LENGTH=143	143	143	2.00E-79	100.0	97.9	99.3
Rsa1.0_00670.1.g17821.t4	ref|XP_002884297.1| GAUT13 [Arabidopsis lyrata subsp. lyrata] gi|297330137|gb|EFH60556.1| GAUT13 [Arabidopsis lyrata subsp. lyrata]	545	533	0	97.8	85.5	88.4	GAUT13	gbpln	Arabidopsis lyrata	AT3G01040.1 | Symbols: GAUT13 | galacturonosyltransferase 13 | chr3:9392-11979 FORWARD LENGTH=533	545	533	0	97.8	85.3	87.9
Rsa1.0_00670.1.g17822.t1	ref|NP_186756.1| early nodulin-like protein 16 [Arabidopsis thaliana] gi|6714481|gb|AAF26167.1|AC008261_24 putative lamin [Arabidopsis thaliana] gi|62319463|dbj|BAD94832.1| lamin - like predicted GPI-anchored protein [Arabidopsis thaliana] gi|194708794|gb|ACF88481.1| At3g01070 [Arabidopsis thaliana] gi|332640083|gb|AEE73604.1| early nodulin-like protein 16 [Arabidopsis thaliana]	173	167	5.00E-61	96.5	76.9	84.4	early nodulin-like protein 16	gbpln	Arabidopsis thaliana	AT3G01070.1 | Symbols: ENODL16, AtENODL16 | early nodulin-like protein 16 | chr3:19659-20444 FORWARD LENGTH=167	173	167	2.00E-63	96.5	76.9	84.4
Rsa1.0_00671.1.g17823.t1	gb|EOA26345.1| hypothetical protein CARUB_v10022725mg [Capsella rubella]	166	723	3.00E-71	435.5	78.9	81.9	hypothetical protein CARUB_v10022725mg	gbpln	Capsella rubella	AT2G45340.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:18691739-18694466 FORWARD LENGTH=691	166	691	2.00E-73	416.3	80.1	81.9
Rsa1.0_00671.1.g17824.t1	gb|EOA26625.1| hypothetical protein CARUB_v10022689mg [Capsella rubella] gi|482562436|gb|EOA26626.1| hypothetical protein CARUB_v10022689mg [Capsella rubella]	699	767	0	109.7	87.1	92.0	hypothetical protein CARUB_v10022689mg	gbpln	Capsella rubella	AT2G44830.1 | Symbols: | Protein kinase superfamily protein | chr2:18490398-18492779 FORWARD LENGTH=765	699	765	0	109.4	86.8	91.8
Rsa1.0_00671.1.g17825.t1	gb|EOA27930.1| hypothetical protein CARUB_v10024100mg [Capsella rubella]	196	196	2.00E-49	100.0	53.1	60.2	hypothetical protein CARUB_v10024100mg	gbpln	Capsella rubella	AT2G44820.1 | Symbols: | unknown protein; Has 70 Blast hits to 70 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 9; Fungi - 4; Plants - 47; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr2:18484690-18485517 FORWARD LENGTH=194	196	194	9.00E-46	99.0	52.6	61.2
Rsa1.0_00671.1.g17826.t1	dbj|BAC23081.1| DAD1 [Brassica rapa]	446	446	0	100.0	97.1	99.1	DAD1	gbpln	Brassica rapa	AT2G44810.1 | Symbols: DAD1 | alpha/beta-Hydrolases superfamily protein | chr2:18479095-18480168 FORWARD LENGTH=357	446	357	0	80.0	74.4	78.5
Rsa1.0_00671.1.g17827.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00671.1.g17828.t3	gb|AAD32950.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	404	773	2.00E-34	191.3	16.8	21.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	404	154	1.00E-27	38.1	13.4	20.0
Rsa1.0_00671.1.g17829.t1	ref|XP_002880137.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297325976|gb|EFH56396.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	682	357	0	52.3	43.8	47.8	oxidoreductase	gbpln	Arabidopsis lyrata	AT2G44800.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr2:18467004-18468551 FORWARD LENGTH=357	682	357	0	52.3	43.8	47.7
Rsa1.0_00671.1.g17830.t1	gb|AAB47973.1| blue copper-binding protein II [Arabidopsis thaliana]	202	199	2.00E-57	98.5	66.8	76.7	blue copper-binding protein II	gbpln	Arabidopsis thaliana	AT2G44790.1 | Symbols: UCC2 | uclacyanin 2 | chr2:18462182-18463232 REVERSE LENGTH=202	202	202	8.00E-53	100.0	60.9	71.8
Rsa1.0_00671.1.g17831.t1	ref|XP_002881980.1| hypothetical protein ARALYDRAFT_483605 [Arabidopsis lyrata subsp. lyrata] gi|297327819|gb|EFH58239.1| hypothetical protein ARALYDRAFT_483605 [Arabidopsis lyrata subsp. lyrata]	472	499	0	105.7	86.2	93.6	hypothetical protein ARALYDRAFT_483605	gbpln	Arabidopsis lyrata	AT2G44760.1 | Symbols: | Domain of unknown function (DUF3598) | chr2:18452937-18454785 REVERSE LENGTH=500	472	500	0	105.9	84.5	92.6

<table>
<tr><td>Rsa1.0_00671.1.g17832.t1</td><td>gb|ABK28536.1| unknown [Arabidopsis thaliana]</td><td>215</td><td>219</td><td>7.00E−99</td><td>101.9</td><td>91.6</td><td>94.9</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G44745.1 | Symbols: | WRKY family transcription factor | chr2:18447482-18449004 REVERSE LENGTH=218</td><td>215</td><td>218</td><td>1.00E−101</td><td>101.4</td><td>91.6</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00671.1.g17833.t1</td><td>gb|EOA27921.1| hypothetical protein CARUB_v10024094mg [Capsella rubella]</td><td>199</td><td>199</td><td>3.00E−93</td><td>100.0</td><td>86.9</td><td>92.0</td><td>hypothetical protein CARUB_v10024094mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44740.1 | Symbols: CYCP4;1 | cyclin p4;1 | chr2:18442287-18443304 REVERSE LENGTH=202</td><td>199</td><td>202</td><td>3.00E−93</td><td>101.5</td><td>83.4</td><td>89.4</td></tr>
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<tr><td>Rsa1.0_00671.1.g17835.t1</td><td>gb|EOA29393.1| hypothetical protein CARUB_v10025686mg, partial [Capsella rubella]</td><td>442</td><td>432</td><td>1.00E−159</td><td>97.7</td><td>68.3</td><td>78.5</td><td>hypothetical protein CARUB_v10025686mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G51160.1 | Symbols: | Ankyrin repeat family protein | chr5:20792280-20793681 FORWARD LENGTH=442</td><td>442</td><td>442</td><td>8.00E−41</td><td>100.0</td><td>28.7</td><td>45.7</td></tr>
<tr><td>Rsa1.0_00671.1.g17836.t1</td><td>gb|EOA26431.1| hypothetical protein CARUB_v10025047mg [Capsella rubella]</td><td>285</td><td>395</td><td>5.00E−85</td><td>138.6</td><td>70.9</td><td>81.8</td><td>hypothetical protein CARUB_v10025047mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44730.1 | Symbols: | Alcohol dehydrogenase transcription factor Myb/SANT-like family protein | chr2:18437447-18438565 REVERSE LENGTH=372</td><td>285</td><td>372</td><td>2.00E−85</td><td>130.5</td><td>68.4</td><td>77.5</td></tr>
<tr><td>Rsa1.0_00671.1.g17837.t3</td><td>gb|EOA26601.1| hypothetical protein CARUB_v10022661mg [Capsella rubella]</td><td>210</td><td>798</td><td>4.00E−15</td><td>380.0</td><td>28.6</td><td>33.3</td><td>hypothetical protein CARUB_v10022661mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44710.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:18432902-18436629 FORWARD LENGTH=809</td><td>210</td><td>809</td><td>4.00E−17</td><td>385.2</td><td>21.4</td><td>22.9</td></tr>
<tr><td>Rsa1.0_00671.1.g17838.t1</td><td>ref|XP_002880123.1| hypothetical protein ARALYDRAFT_483580 [Arabidopsis lyrata subsp. lyrata] gi|297325962|gb|EFH56382.1| hypothetical protein ARALYDRAFT_483580 [Arabidopsis lyrata subsp. lyrata]</td><td>94</td><td>170</td><td>6.00E−23</td><td>180.9</td><td>55.3</td><td>57.4</td><td>hypothetical protein ARALYDRAFT_483580</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G44525.1 | Symbols: | Protein of unknown function (DUF498/DUF598) | chr2:18382130-18383320 FORWARD LENGTH=170</td><td>94</td><td>170</td><td>2.00E−25</td><td>180.9</td><td>55.3</td><td>57.4</td></tr>
<tr><td>Rsa1.0_00671.1.g17839.t1</td><td>ref|NP_181978.1| axi 1 protein-like protein [Arabidopsis thaliana] gi|13877693|gb|AAK43924.1|AF370605_1 axi 1 protein-like protein [Arabidopsis thaliana] gi|3128192|gb|AAC16096.1| similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana] gi|330255336|gb|AEC10430.1| axi 1 protein-like protein [Arabidopsis thaliana]</td><td>579</td><td>573</td><td>0</td><td>99.0</td><td>83.4</td><td>86.2</td><td>axi 1 protein-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G44500.1 | Symbols: | O-fucosyltransferase family protein | chr2:18374447-18376435 FORWARD LENGTH=573</td><td>579</td><td>573</td><td>0</td><td>99.0</td><td>83.4</td><td>86.2</td></tr>
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<tr><td>Rsa1.0_00671.1.g17841.t1</td><td>ref|XP_002880113.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325952|gb|EFH56372.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>510</td><td>539</td><td>0</td><td>105.7</td><td>74.3</td><td>85.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G60120.1 | Symbols: BGLU27 | beta glucosidase 27 | chr3:22206238-22208952 FORWARD LENGTH=540</td><td>510</td><td>540</td><td>0</td><td>105.9</td><td>71.2</td><td>83.1</td></tr>
<tr><td>Rsa1.0_00671.1.g17842.t1</td><td>dbj|BAJ34435.1| unnamed protein product [Thellungiella halophila]</td><td>554</td><td>563</td><td>0</td><td>101.6</td><td>95.3</td><td>98.2</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT2G44490.1 | Symbols: PEN2, BGLU26 | Glycosyl hydrolase superfamily protein | chr2:18364872-18367515 FORWARD LENGTH=560</td><td>554</td><td>560</td><td>0</td><td>101.1</td><td>93.5</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00671.1.g17843.t13</td><td>gb|EOA29106.1| hypothetical protein CARUB_v10025373mg, partial [Capsella rubella]</td><td>597</td><td>555</td><td>0</td><td>93.0</td><td>70.0</td><td>78.4</td><td>hypothetical protein CARUB_v10025373mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G24550.1 | Symbols: BGLU32 | beta glucosidase 32 | chr5:8392059-8395302 REVERSE LENGTH=534</td><td>597</td><td>534</td><td>0</td><td>89.4</td><td>66.3</td><td>77.2</td></tr>
<tr><td>Rsa1.0_00671.1.g17844.t1</td><td>gb|EOA32597.1| hypothetical protein CARUB_v10015890mg, partial [Capsella rubella]</td><td>199</td><td>343</td><td>9.00E−51</td><td>172.4</td><td>57.3</td><td>73.4</td><td>hypothetical protein CARUB_v10015890mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G17750.1 | Symbols: NIP1 | NEP-interacting protein 1 | chr2:7709238-7711151 REVERSE LENGTH=396</td><td>199</td><td>396</td><td>1.00E−41</td><td>199.0</td><td>40.2</td><td>52.3</td></tr>
<tr><td>Rsa1.0_00672.1.g17845.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00672.1.g17846.t1</td><td>gb|EOA27770.1| hypothetical protein CARUB_v10023925mg [Capsella rubella]</td><td>249</td><td>248</td><td>1.00E−111</td><td>99.6</td><td>88.0</td><td>93.2</td><td>hypothetical protein CARUB_v10023925mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G36080.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr2:15148612-15151411 REVERSE LENGTH=244</td><td>249</td><td>244</td><td>1.00E−113</td><td>98.0</td><td>86.3</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00672.1.g17847.t1</td><td>ref|NP_001046391.2| Os02g0236500 [Oryza sativa Japonica Group] gi|255670750|dbj|BAF08305.2| Os02g0236500 [Oryza sativa Japonica Group]</td><td>769</td><td>918</td><td>0</td><td>119.4</td><td>45.3</td><td>64.1</td><td>Os02g0236500</td><td>gbpln</td><td>Oryza sativa</td><td>AT4G10200.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr4:6353172-6355591 FORWARD LENGTH=733</td><td>769</td><td>733</td><td>1.00E−179</td><td>95.3</td><td>45.1</td><td>59.0</td></tr>
<tr><td>Rsa1.0_00672.1.g17848.t1</td><td>ref|XP_002881423.1| ATOFP15/OFP15 [Arabidopsis lyrata subsp. lyrata] gi|297327262|gb|EFH57682.1| ATOFP15/OFP15 [Arabidopsis lyrata subsp. lyrata]</td><td>270</td><td>259</td><td>1.00E−88</td><td>95.9</td><td>75.9</td><td>88.5</td><td>ATOFP15/OFP15</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G36050.1 | Symbols: ATOFP15, OFP15 | ovate family protein 15 | chr2:15135852-15136637 REVERSE LENGTH=261</td><td>270</td><td>261</td><td>5.00E−76</td><td>96.7</td><td>72.6</td><td>86.7</td></tr>
<tr><td>Rsa1.0_00672.1.g17849.t1</td><td>gb|EOA29313.1| hypothetical protein CARUB_v10025594mg [Capsella rubella]</td><td>187</td><td>185</td><td>4.00E−63</td><td>98.9</td><td>75.9</td><td>81.8</td><td>hypothetical protein CARUB_v10025594mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G36026.1 | Symbols: | Ovate family protein | chr2:15127265-15127816 FORWARD LENGTH=183</td><td>187</td><td>183</td><td>1.00E−61</td><td>97.9</td><td>73.8</td><td>81.3</td></tr>
<tr><td>Rsa1.0_00672.1.g17850.t1</td><td>ref|XP_002881422.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata] gi|297327261|gb|EFH57681.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>251</td><td>258</td><td>1.00E−120</td><td>102.8</td><td>87.6</td><td>94.8</td><td>abscisic acid-responsive HVA22 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G36020.1 | Symbols: HVA22J | HVA22-like protein J | chr2:15123424-15125140 REVERSE LENGTH=258</td><td>251</td><td>258</td><td>1.00E−121</td><td>102.8</td><td>86.9</td><td>94.8</td></tr>
</table>

Rsa1.0_00672.1.g17851.t1	ref|NP_565829.1| TPX2 (targeting protein for Xklp2)-like protein [Arabidopsis thaliana] gi|16209720|gb|AAL14415.1| At2g35880/F11F19.21 [Arabidopsis thaliana] gi|20197995|gb|AAD21469.2| expressed protein [Arabidopsis thaliana] gi|22655282|gb|AAM98231.1| unknown protein [Arabidopsis thaliana] gi|330254079|gb|AEC09173.1| TPX2 (targeting protein for Xklp2)-like protein [Arabidopsis thaliana]	457	432	1.00E-134	94.5	70.2	76.4	TPX2 (targeting protein for Xklp2)-like protein	gbpln	Arabidopsis thaliana	AT2G35880.1 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr2:15063204-15065259 REVERSE LENGTH=432	457	432	1.00E-137	94.5	70.2	76.4
Rsa1.0_00672.1.g17852.t1	ref|NP_850254.1| RING-H2 finger protein ATL70 [Arabidopsis thaliana] gi|68565230|sp|Q8RX29.1|ATL70_ARATH RecName: Full=RING-H2 finger protein ATL70 gi|20258808|gb|AAM13985.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|21689891|gb|AAM67506.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|330254082|gb|AEC09176.1| RING-H2 finger protein ATL70 [Arabidopsis thaliana]	175	217	3.00E-57	124.0	72.0	78.3	RING-H2 finger protein ATL70	gbpln	Arabidopsis thaliana	AT2G35910.1 | Symbols: | RING/U-box superfamily protein | chr2:15073225-15073878 REVERSE LENGTH=217	175	217	1.00E-59	124.0	72.0	78.3
Rsa1.0_00672.1.g17853.t1	gb|EOA28706.1| hypothetical protein CARUB_v10024934mg [Capsella rubella]	408	408	0	100.0	86.5	91.9	hypothetical protein CARUB_v10024934mg	gbpln	Capsella rubella	AT2G35930.1 | Symbols: PUB23 | plant U-box 23 | chr2:15083101-15084336 REVERSE LENGTH=411	408	411	0	100.7	87.3	92.6
Rsa1.0_00672.1.g17854.t1	gb|ABD65101.1| hypothetical protein 31.t00082 [Brassica oleracea]	250	226	1.00E-89	90.4	64.0	76.0	hypothetical protein 31.t00082	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00672.1.g17855.t1	gb|ABD65117.1| hypothetical protein 31.t00030 [Brassica oleracea]	961	1471	0	153.1	77.8	84.1	hypothetical protein 31.t00030	gbpln	Brassica oleracea	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	961	344	3.00E-84	35.8	16.0	20.9
Rsa1.0_00672.1.g17856.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	519	467	0	90.0	61.7	68.4	hypothetical protein 31.t00031	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	519	566	7.00E-79	109.1	32.2	53.9
Rsa1.0_00673.1.g17857.t1	dbj|BAE98403.1| putative non-LTR reverse transcriptase [Arabidopsis thaliana]	186	278	7.00E-11	149.5	16.7	23.1	putative non-LTR reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00673.1.g17858.t1	gb|EOA37823.1| hypothetical protein CARUB_v10012001mg [Capsella rubella]	232	236	3.00E-89	101.7	75.4	84.5	hypothetical protein CARUB_v10012001mg	gbpln	Capsella rubella	AT1G26100.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane protein family | chr1:9022716-9024081 REVERSE LENGTH=236	232	236	1.00E-89	101.7	74.1	84.5
Rsa1.0_00673.1.g17859.t1	ref|XP_002867139.1| EMB2758 [Arabidopsis lyrata subsp. lyrata] gi|297312975|gb|EFH43398.1| EMB2758 [Arabidopsis lyrata subsp. lyrata]	837	824	0	98.4	81.2	88.5	EMB2758	gbpln	Arabidopsis lyrata	AT4G33990.1 | Symbols: EMB2758 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:16290141-16292612 REVERSE LENGTH=823	837	823	0	98.3	80.6	87.8
Rsa1.0_00673.1.g17860.t1	ref|XP_002882653.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328493|gb|EFH58912.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	202	173	8.00E-28	85.6	36.6	48.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G10116.1 | Symbols: | COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family | chr3:3126023-3126619 FORWARD LENGTH=170	202	170	6.00E-25	84.2	34.7	45.5
Rsa1.0_00673.1.g17861.t1	ref|XP_002874050.1| hypothetical protein ARALYDRAFT_910198 [Arabidopsis lyrata subsp. lyrata] gi|297319887|gb|EFH50309.1| hypothetical protein ARALYDRAFT_910198 [Arabidopsis lyrata subsp. lyrata]	452	450	0	99.6	84.1	90.5	hypothetical protein ARALYDRAFT_910198	gbpln	Arabidopsis lyrata	AT5G22130.1 | Symbols: PNT1 | mannosyltransferase family protein | chr5:7337486-7339831 REVERSE LENGTH=450	452	450	0	99.6	83.8	88.9
Rsa1.0_00673.1.g17862.t1	ref|XP_002874051.1| pyridine nucleotide-disulfide oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319888|gb|EFH50310.1| pyridine nucleotide-disulfide oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	367	365	0	99.5	89.1	94.0	pyridine nucleotide-disulfide oxidoreductase family protein	gbpln	Arabidopsis lyrata	AT5G22140.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr5:7340284-7341657 REVERSE LENGTH=365	367	365	0	99.5	88.3	93.7
Rsa1.0_00673.1.g17863.t1	gb|EOA24755.1| hypothetical protein CARUB_v10018033mg [Capsella rubella]	209	206	1.00E-74	98.6	66.5	76.6	hypothetical protein CARUB_v10018033mg	gbpln	Capsella rubella	AT3G44220.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:15928216-15929645 FORWARD LENGTH=206	209	206	1.00E-76	98.6	66.0	76.1
Rsa1.0_00673.1.g17864.t1	ref|XP_002871996.1| hypothetical protein ARALYDRAFT_351250 [Arabidopsis lyrata subsp. lyrata] gi|297317833|gb|EFH48255.1| hypothetical protein ARALYDRAFT_351250 [Arabidopsis lyrata subsp. lyrata]	155	164	3.00E-63	105.8	81.3	87.7	hypothetical protein ARALYDRAFT_351250	gbpln	Arabidopsis lyrata	AT5G22240.1 | Symbols: ATOFP10, OFP10 | Ovate family protein | chr5:7364689-7365279 FORWARD LENGTH=196	155	196	2.00E-62	126.5	71.6	76.1

Rsa1.0_00673.1.g17865.t1	ref|NP_197617.1| putative CCR4-associated factor 1-11 [Arabidopsis thaliana] gi|75334084|sp|Q9FMS6.1|CAF1K_ARATH RecName: Full=Probable CCR4-associated factor 1 homolog 11 gi|9757805|dbj|BAB08323.1| CCR4-associated factor-like protein [Arabidopsis thaliana] gi|17381058|gb|AAL36341.1| putative CCR4-associated factor [Arabidopsis thaliana] gi|25054979|gb|AAN71961.1| putative CCR4-associated factor [Arabidopsis thaliana] gi|332005618|gb|AED93001.1| putative CCR4-associated factor 1-11 [Arabidopsis thaliana]	278	278	1.00E-130	100.0	83.1	89.6	putative CCR4-associated factor 1-11	gbpln	Arabidopsis thaliana	AT5G22250.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:7365605-7366441 REVERSE LENGTH=278	278	278	1.00E-133	100.0	83.1	89.6
Rsa1.0_00673.1.g17866.t1	ref|XP_002887346.1| hypothetical protein ARALYDRAFT_476243 [Arabidopsis lyrata subsp. lyrata] gi|297333187|gb|EFH63605.1| hypothetical protein ARALYDRAFT_476243 [Arabidopsis lyrata subsp. lyrata]	232	557	1.00E-28	240.1	25.9	28.4	hypothetical protein ARALYDRAFT_476243	gbpln	Arabidopsis lyrata	AT1G71110.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G12400.1); Has 173 Blast hits to 169 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 165; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr1:26818244-26820852 FORWARD LENGTH=557	232	557	2.00E-30	240.1	25.0	28.0
Rsa1.0_00673.1.g17867.t1	ref|NP_197619.1| uncharacterized protein [Arabidopsis thaliana] gi|9757807|dbj|BAB08325.1| unnamed protein product [Arabidopsis thaliana] gi|15450476|gb|AAK96531.1| AT5g22270/MWD9_5 [Arabidopsis thaliana] gi|20466099|gb|AAM19971.1| AT5g22270/MWD9_5 [Arabidopsis thaliana] gi|227206166|dbj|BAH57138.1| AT5G22270 [Arabidopsis thaliana] gi|332005620|gb|AED93003.1| uncharacterized protein AT5G22270 [Arabidopsis thaliana]	88	93	1.00E-14	105.7	59.1	64.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G22270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11600.1); Has 136 Blast hits to 136 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 136; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:7372487-7372768 REVERSE LENGTH=93	88	93	2.00E-17	105.7	59.1	64.8
Rsa1.0_00673.1.g17868.t1	ref|XP_002874058.1| hypothetical protein ARALYDRAFT_489079 [Arabidopsis lyrata subsp. lyrata] gi|297319895|gb|EFH50317.1| hypothetical protein ARALYDRAFT_489079 [Arabidopsis lyrata subsp. lyrata]	108	108	8.00E-51	100.0	93.5	96.3	hypothetical protein ARALYDRAFT_489079	gbpln	Arabidopsis lyrata	AT5G22280.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G44280.1); Has 82 Blast hits to 82 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 82; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:7374211-7375112 REVERSE LENGTH=108	108	108	9.00E-53	100.0	92.6	95.4
Rsa1.0_00673.1.g17869.t2	ref|XP_002874060.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319897|gb|EFH50319.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	515	121	3.00E-22	23.5	10.7	12.8	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00673.1.g17870.t1	gb|ABM55735.1| nitrilase 4 [Brassica rapa]	357	357	0	100.0	95.5	97.5	nitrilase 4	gbpln	Brassica rapa	AT5G22300.1 | Symbols: NIT4, AtNIT4 | nitrilase 4 | chr5:7379401-7381764 FORWARD LENGTH=355	357	355	0	99.4	87.7	92.7
Rsa1.0_00673.1.g17871.t1	gb|EOA20612.1| hypothetical protein CARUB_v10000923mg [Capsella rubella]	458	458	0	100.0	98.5	99.6	hypothetical protein CARUB_v10000923mg	gbpln	Capsella rubella	AT5G22330.1 | Symbols: ATTIP49A, RIN1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:7391026-7394071 REVERSE LENGTH=458	458	458	0	100.0	98.3	99.3
Rsa1.0_00673.1.g17872.t1	ref|XP_002874065.1| hypothetical protein ARALYDRAFT_910225 [Arabidopsis lyrata subsp. lyrata] gi|297319902|gb|EFH50324.1| hypothetical protein ARALYDRAFT_910225 [Arabidopsis lyrata subsp. lyrata]	425	427	0	100.5	90.4	96.0	hypothetical protein ARALYDRAFT_910225	gbpln	Arabidopsis lyrata	AT5G22350.1 | Symbols: ELM1 | Protein of unknown function (DUF1022) | chr5:7397762-7400746 REVERSE LENGTH=427	425	427	0	100.5	89.6	95.8
Rsa1.0_00673.1.g17873.t1	gb|ABM30199.2| synaptobrevin-like protein [Brassica juncea]	221	221	1.00E-122	100.0	95.9	97.7	synaptobrevin-like protein	gbpln	Brassica juncea	AT5G22360.1 | Symbols: ATVAMP714, VAMP714 | vesicle-associated membrane protein 714 | chr5:7404379-7405654 REVERSE LENGTH=221	221	221	1.00E-123	100.0	93.2	98.2
Rsa1.0_00673.1.g17874.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00673.1.g17875.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	589	1142	0	193.9	55.7	70.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	589	575	1.00E-29	97.6	9.8	14.3
Rsa1.0_00674.1.g17876.t1	ref|XP_002864340.1| hypothetical protein ARALYDRAFT_495535 [Arabidopsis lyrata subsp. lyrata] gi|297310175|gb|EFH40599.1| hypothetical protein ARALYDRAFT_495535 [Arabidopsis lyrata subsp. lyrata]	266	335	2.00E-70	125.9	48.9	56.8	hypothetical protein ARALYDRAFT_495535	gbpln	Arabidopsis lyrata	AT5G54550.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22158401-22159480 FORWARD LENGTH=359	266	359	3.00E-70	135.0	47.7	54.5
Rsa1.0_00674.1.g17877.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00674.1.g17878.t1	ref|NP_568793.1| CCT motif family protein [Arabidopsis thaliana] gi|20466574|gb|AAM20604.1| putative protein [Arabidopsis thaliana] gi|23198144|gb|AAN15599.1| putative protein [Arabidopsis thaliana] gi|332008967|gb|AED96350.1| CCT motif family protein [Arabidopsis thaliana]	274	264	1.00E-122	96.4	82.8	86.9	CCT motif family protein	gbpln	Arabidopsis thaliana	AT5G53420.1 | Symbols: | CCT motif family protein | chr5:21673683-21675469 FORWARD LENGTH=264	274	264	1.00E-125	96.4	82.8	86.9
Rsa1.0_00674.1.g17879.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00674.1.g17880.t1	ref|NP_200138.1| Seed maturation protein [Arabidopsis thaliana] gi|9759173|dbj|BAB09788.1| unnamed protein product [Arabidopsis thaliana] gi|332008947|gb|AED96330.1| Seed maturation protein [Arabidopsis thaliana]	187	176	4.00E-59	94.1	65.2	77.5	Seed maturation protein	gbpln	Arabidopsis thaliana	AT5G53260.1 | Symbols: | Seed maturation protein | chr5:21604662-21605674 REVERSE LENGTH=176	187	176	2.00E-61	94.1	65.2	77.5
Rsa1.0_00674.1.g17881.t1	ref|XP_002864231.1| AGP22/ATAGP22 [Arabidopsis lyrata subsp. lyrata] gi|297310066|gb|EFH40490.1| AGP22/ATAGP22 [Arabidopsis lyrata subsp. lyrata]	63	63	6.00E-25	100.0	95.2	98.4	AGP22/ATAGP22	gbpln	Arabidopsis lyrata	AT5G53250.1 | Symbols: AGP22, ATAGP22 | arabinogalactan protein 22 | chr5:21603715-21604007 FORWARD LENGTH=63	63	63	1.00E-26	100.0	93.7	95.2
Rsa1.0_00674.1.g17882.t1	ref|NP_200266.1| uncharacterized protein [Arabidopsis thaliana] gi|9758947|dbj|BAB09334.1| unnamed protein product [Arabidopsis thaliana] gi|332009126|gb|AED96509.1| uncharacterized protein AT5G54550 [Arabidopsis thaliana]	373	359	1.00E-109	96.2	59.0	68.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54550.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22158401-22159480 FORWARD LENGTH=359	373	359	1.00E-112	96.2	59.0	68.6
Rsa1.0_00674.1.g17883.t1	ref|XP_002871160.1| hypothetical protein ARALYDRAFT_908458 [Arabidopsis lyrata subsp. lyrata] gi|297316997|gb|EFH47419.1| hypothetical protein ARALYDRAFT_908458 [Arabidopsis lyrata subsp. lyrata]	526	593	0	112.7	75.9	85.9	hypothetical protein ARALYDRAFT_908458	gbpln	Arabidopsis lyrata	AT5G05450.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:1612077-1615195 FORWARD LENGTH=593	526	593	0	112.7	76.2	86.3
Rsa1.0_00674.1.g17884.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00674.1.g17885.t1	dbj|BAJ34295.1| unnamed protein product [Thellungiella halophila]	356	368	1.00E-147	103.4	86.8	91.3	unnamed protein product	----	----	AT5G53210.1 | Symbols: SPCH | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:21586606-21588941 REVERSE LENGTH=364	356	364	1.00E-127	102.2	88.2	91.6
Rsa1.0_00674.1.g17886.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00674.1.g17887.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00674.1.g17888.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00674.1.g17889.t2	ref|XP_002865955.1| FTSH11 [Arabidopsis lyrata subsp. lyrata] gi|297311790|gb|EFH42214.1| FTSH11 [Arabidopsis lyrata subsp. lyrata]	1133	805	0	71.1	63.0	65.8	FTSH11	gbpln	Arabidopsis lyrata	AT5G53170.1 | Symbols: FTSH11 | FTSH protease 11 | chr5:21563023-21567922 REVERSE LENGTH=806	1133	806	0	71.1	62.8	65.6
Rsa1.0_00674.1.g17890.t1	ref|XP_002864227.1| hypothetical protein ARALYDRAFT_918386 [Arabidopsis lyrata subsp. lyrata] gi|297310062|gb|EFH40486.1| hypothetical protein ARALYDRAFT_918386 [Arabidopsis lyrata subsp. lyrata]	188	193	9.00E-91	102.7	87.8	91.5	hypothetical protein ARALYDRAFT_918386	gbpln	Arabidopsis lyrata	AT5G53160.2 | Symbols: RCAR3, PYL8 | regulatory components of ABA receptor 3 | chr5:21561026-21561953 FORWARD LENGTH=188	188	188	2.00E-92	100.0	88.3	93.6
Rsa1.0_00674.1.g17891.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00675.1.g17892.t1	ref|XP_002881717.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297327556|gb|EFH57976.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	865	757	0	87.5	64.6	68.9	transducin family protein	gbpln	Arabidopsis lyrata	AT2G40360.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:16853123-16856635 REVERSE LENGTH=753	865	753	0	87.1	63.7	68.7

Rsa1.0_00675.1.g17893.t1	ref|NP_182036.1| expansin B4 [Arabidopsis thaliana] gi|20138422|sp|Q9SHD1.1|EXPB4_ARATH RecName: Full=Expansin-B4; Short=At-EXPB4; Short=AtEXPB4; AltName: Full=Ath-ExpBeta-1.1; AltName: Full=Beta-expansin-4; Flags: Precursor gi|330255414|gb|AEC10508.1| expansin B4 [Arabidopsis thaliana]	259	259	1.00E-117	100.0	76.8	88.4	expansin B4	gbpln	Arabidopsis thaliana	AT2G45110.1 | Symbols: ATEXPB4, EXPB4, ATHEXP BETA 1.1 | expansin B4 | chr2:18599575-18601237 FORWARD LENGTH=259	259	259	1.00E-119	100.0	76.8	88.4
Rsa1.0_00675.1.g17894.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1386	1307	0	94.3	58.4	73.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1386	1262	1.00E-106	91.1	14.1	22.4
Rsa1.0_00675.1.g17895.t1	ref|NP_564860.3| putative expansin-B2 [Arabidopsis thaliana] gi|20138423|sp|Q9SHY6.2|EXPB2_ARATH RecName: Full=Putative expansin-B2; Short=At-EXPB2; Short=AtEXPB2; AltName: Full=Ath-ExpBeta-1.4; AltName: Full=Beta-expansin-2; Flags: Precursor gi|332196289|gb|AEE34410.1| putative expansin-B2 [Arabidopsis thaliana]	265	273	1.00E-109	103.0	76.6	84.9	putative expansin-B2	gbpln	Arabidopsis thaliana	AT1G65680.1 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | expansin B2 | chr1:24427266-24428399 FORWARD LENGTH=273	265	273	1.00E-111	103.0	76.6	84.9
Rsa1.0_00675.1.g17896.t1	gb|EOA27868.1| hypothetical protein CARUB_v10024026mg [Capsella rubella]	222	220	1.00E-119	99.1	94.6	97.3	hypothetical protein CARUB_v10024026mg	gbpln	Capsella rubella	AT2G45080.1 | Symbols: cycp3;1 | cyclin p3;1 | chr2:18591688-18592443 FORWARD LENGTH=222	222	222	1.00E-120	100.0	94.1	97.3
Rsa1.0_00675.1.g17897.t1	ref|XP_004133771.1| PREDICTED: protein transport protein Sec61 subunit beta-like isoform 1 [Cucumis sativus] gi|449431968|ref|XP_004133772.1| PREDICTED: protein transport protein Sec61 subunit beta-like isoform 2 [Cucumis sativus] gi|449431970|ref|XP_004133773.1| PREDICTED: protein transport protein Sec61 subunit beta-like isoform 3 [Cucumis sativus]	81	82	5.00E-28	101.2	80.2	87.7	PREDICTED: protein transport protein Sec61 subunit beta-like isoform 1	gbpln	Cucumis sativus	AT2G45070.4 | Symbols: SEC61 BETA | Preprotein translocase Sec, Sec61-beta subunit protein | chr2:18587208-18587456 REVERSE LENGTH=82	81	82	1.00E-29	101.2	84.0	86.4
Rsa1.0_00675.1.g17898.t1	gb|ADK63416.1| GATA type zinc finger protein [Brassica rapa]	258	256	1.00E-109	99.2	84.5	88.8	GATA type zinc finger protein	gbpln	Brassica rapa	AT2G45050.1 | Symbols: GATA2 | GATA transcription factor 2 | chr2:18582958-18583845 FORWARD LENGTH=264	258	264	1.00E-107	102.3	85.3	89.1
Rsa1.0_00675.1.g17899.t1	ref|NP_182030.1| matrix metalloprotease domain-containing protein [Arabidopsis thaliana] gi|26452204|dbj|BAC43190.1| putative metalloproteinase [Arabidopsis thaliana] gi|31711730|gb|AAP68221.1| At2g45040 [Arabidopsis thaliana] gi|330255405|gb|AEC10499.1| matrix metalloprotease domain-containing protein [Arabidopsis thaliana]	337	342	1.00E-159	101.5	81.6	89.3	matrix metalloprotease domain-containing protein	gbpln	Arabidopsis thaliana	AT2G45040.1 | Symbols: | Matrixin family protein | chr2:18577693-18578721 FORWARD LENGTH=342	337	342	1.00E-162	101.5	81.6	89.3
Rsa1.0_00675.1.g17900.t1	gb|EOA26634.1| hypothetical protein CARUB_v10022698mg [Capsella rubella]	757	754	0	99.6	92.7	96.3	hypothetical protein CARUB_v10022698mg	gbpln	Capsella rubella	AT2G45030.1 | Symbols: | Translation elongation factor EFG/EF2 protein | chr2:18572411-18576756 FORWARD LENGTH=754	757	754	0	99.6	92.1	96.6
Rsa1.0_00675.1.g17901.t1	gb|EOA28399.1| hypothetical protein CARUB_v10024605mg [Capsella rubella]	148	166	1.00E-65	112.2	84.5	89.2	hypothetical protein CARUB_v10024605mg	gbpln	Capsella rubella	AT2G28105.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nucleic acid-binding, OB-fold-like (InterPro:IPR016027), Replication factor A, C-terminal (InterPro:IPR013955); Has 20 Blast hits to 20 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:11976764-11977713 FORWARD LENGTH=166	148	166	6.00E-68	112.2	83.8	89.9
Rsa1.0_00675.1.g17902.t3	ref|XP_002880151.1| hypothetical protein ARALYDRAFT_483631 [Arabidopsis lyrata subsp. lyrata] gi|297325990|gb|EFH56410.1| hypothetical protein ARALYDRAFT_483631 [Arabidopsis lyrata subsp. lyrata]	245	244	1.00E-128	99.6	93.5	96.7	hypothetical protein ARALYDRAFT_483631	gbpln	Arabidopsis lyrata	AT2G45010.1 | Symbols: | PLAC8 family protein | chr2:18568045-18569615 FORWARD LENGTH=244	245	244	1.00E-130	99.6	93.5	96.7
Rsa1.0_00675.1.g17903.t2	ref|XP_002881993.1| hypothetical protein ARALYDRAFT_483627 [Arabidopsis lyrata subsp. lyrata] gi|297327832|gb|EFH58252.1| hypothetical protein ARALYDRAFT_483627 [Arabidopsis lyrata subsp. lyrata]	864	873	0	101.0	89.7	94.7	hypothetical protein ARALYDRAFT_483627	gbpln	Arabidopsis lyrata	AT2G44980.2 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein | chr2:18552343-18556669 REVERSE LENGTH=877	864	877	0	101.5	89.4	94.2

Rsa1.0_00675.1.g17904.t1	ref|XP_002881991.1| histone mono-ubiquitination 1 [Arabidopsis lyrata subsp. lyrata] gi|297327830|gb|EFH58250.1| histone mono-ubiquitination 1 [Arabidopsis lyrata subsp. lyrata]	877	878	0	100.1	87.0	93.5	histone mono-ubiquitination 1	gbpln	Arabidopsis lyrata	AT2G44950.1 | Symbols: RDO4, HUB1 | histone mono-ubiquitination 1 | chr2:18542602-18548247 REVERSE LENGTH=878	877	878	0	100.1	86.5	92.9
Rsa1.0_00675.1.g17905.t1	ref|XP_002880148.1| hypothetical protein ARALYDRAFT_483623 [Arabidopsis lyrata subsp. lyrata] gi|297325987|gb|EFH56407.1| hypothetical protein ARALYDRAFT_483623 [Arabidopsis lyrata subsp. lyrata]	296	290	1.00E-107	98.0	74.3	83.4	hypothetical protein ARALYDRAFT_483623	gbpln	Arabidopsis lyrata	AT2G44940.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr2:18537294-18538181 FORWARD LENGTH=295	296	295	1.00E-102	99.7	70.9	80.4
Rsa1.0_00675.1.g17906.t1	gb|AFZ41789.1| putative progesterone 5-beta-reductase [Raphanus sativus]	203	390	2.00E-33	192.1	33.5	35.5	putative progesterone 5-beta-reductase	gbpln	Raphanus sativus	AT4G24220.1 | Symbols: VEP1, AWI31 | NAD(P)-binding Rossmann-fold superfamily protein | chr4:12565219-12566474 FORWARD LENGTH=388	203	388	4.00E-35	191.1	34.0	36.9
Rsa1.0_00675.1.g17907.t2	gb|EOA14700.1| hypothetical protein CARUB_v10027975mg [Capsella rubella]	592	766	0	129.4	58.1	68.9	hypothetical protein CARUB_v10027975mg	gbpln	Capsella rubella	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	592	769	0	129.9	59.0	70.4
Rsa1.0_00675.1.g17908.t1	ref|NP_173766.1| uncharacterized protein [Arabidopsis thaliana] gi|8778585|gb|AAF79593.1|AC007945_13 F28C11.15 [Arabidopsis thaliana] gi|4056435|gb|AAC98008.1| Similar to OBP32pep protein gb|U37698 from Arabidopsis thaliana [Arabidopsis thaliana] gi|332192277|gb|AEE30398.1| uncharacterized protein AT1G23520 [Arabidopsis thaliana]	267	263	9.00E-72	98.5	54.7	71.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23520.1 | Symbols: | Domain of unknown function (DUF220) | chr1:8343571-8344675 REVERSE LENGTH=263	267	263	2.00E-74	98.5	54.7	71.2
Rsa1.0_00676.1.g17909.t1	gb|EOA22792.1| hypothetical protein CARUB_v10003509mg [Capsella rubella]	350	360	1.00E-176	102.9	85.4	93.4	hypothetical protein CARUB_v10003509mg	gbpln	Capsella rubella	AT5G07010.1 | Symbols: ATST2A, ST2A | sulfotransferase 2A | chr5:2174960-2176039 REVERSE LENGTH=359	350	359	1.00E-176	102.6	83.4	92.6
Rsa1.0_00676.1.g17910.t1	ref|NP_196316.1| uncharacterized protein [Arabidopsis thaliana] gi|9759555|dbj|BAB11157.1| unnamed protein product [Arabidopsis thaliana] gi|71905551|gb|AAZ52753.1| expressed protein [Arabidopsis thaliana] gi|332003713|gb|AED91096.1| uncharacterized protein AT5G06990 [Arabidopsis thaliana]	258	261	1.00E-120	101.2	88.8	94.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G06990.1 | Symbols: | Protein of unknown function, DUF617 | chr5:2169699-2170484 FORWARD LENGTH=261	258	261	1.00E-123	101.2	88.8	94.6
Rsa1.0_00676.1.g17911.t1	dbj|BAJ33600.1| unnamed protein product [Thellungiella halophila]	287	286	1.00E-120	99.7	80.5	84.7	unnamed protein product	----	----	AT5G06980.4 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12320.1). | chr5:2167799-2169110 FORWARD LENGTH=279	287	279	6.00E-99	97.2	70.4	78.4
Rsa1.0_00676.1.g17912.t1	ref|XP_002873288.1| hypothetical protein ARALYDRAFT_487516 [Arabidopsis lyrata subsp. lyrata] gi|297319125|gb|EFH49547.1| hypothetical protein ARALYDRAFT_487516 [Arabidopsis lyrata subsp. lyrata]	1127	1101	0	97.7	90.7	93.8	hypothetical protein ARALYDRAFT_487516	gbpln	Arabidopsis lyrata	AT5G06970.1 | Symbols: | Protein of unknown function (DUF810) | chr5:2158431-2166004 REVERSE LENGTH=1101	1127	1101	0	97.7	89.8	93.8
Rsa1.0_00676.1.g17913.t1	gb|EOA21559.1| hypothetical protein CARUB_v10001968mg [Capsella rubella]	213	209	9.00E-96	98.1	79.3	88.7	hypothetical protein CARUB_v10001968mg	gbpln	Capsella rubella	AT3G56180.1 | Symbols: | Protein of unknown function (DUF567) | chr3:20844765-20845548 FORWARD LENGTH=204	213	204	7.00E-36	95.8	36.6	56.3

<table>
<tr><td>Rsa1.0_00676.1.g17914.t1</td><td>ref|NP_196389.1| xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] gi|46576342|sp|Q9LF80.1|GT3_ARATH RecName: Full=Putative glycosyltransferase 3; Short=AtGT3 gi|9716848|emb|CAC01676.1| putative golgi glycosyltransferase [Arabidopsis thaliana] gi|9759594|dbj|BAB11451.1| alpha galactosyltransferase protein [Arabidopsis thaliana] gi|34098851|gb|AAQ56808.1| At5g07720 [Arabidopsis thaliana] gi|110743797|dbj|BAE99734.1| alpha galactosyltransferase protein [Arabidopsis thaliana] gi|332003814|gb|AED91197.1| putative glycosyltransferase 3 [Arabidopsis thaliana]</td><td>456</td><td>457</td><td>0</td><td>100.2</td><td>89.9</td><td>96.1</td><td>xyloglucan 6-xylosyltransferase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07720.1 | Symbols: | Galactosyl transferase GMA12/MNN10 family protein | chr5:2455757-2457130 FORWARD LENGTH=457</td><td>456</td><td>457</td><td>0</td><td>100.2</td><td>89.9</td><td>96.1</td></tr>
<tr><td>Rsa1.0_00676.1.g17915.t7</td><td>gb|EOA23129.1| hypothetical protein CARUB_v100028210mg, partial [Capsella rubella]</td><td>1320</td><td>809</td><td>0</td><td>61.3</td><td>36.5</td><td>41.5</td><td>hypothetical protein CARUB_v100028210mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G07740.1 | Symbols: | actin binding | chr5:2459076-2466580 REVERSE LENGTH=1649</td><td>1320</td><td>1649</td><td>0</td><td>124.9</td><td>32.8</td><td>36.4</td></tr>
<tr><td>Rsa1.0_00676.1.g17916.t1</td><td>ref|NP_196382.2| Actin-binding FH2 protein [Arabidopsis thaliana] gi|332003806|gb|AED91189.1| Actin-binding FH2 protein [Arabidopsis thaliana]</td><td>1296</td><td>815</td><td>0</td><td>62.9</td><td>35.8</td><td>43.8</td><td>Actin-binding FH2 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07650.1 | Symbols: | Actin-binding FH2 protein | chr5:2416375-2421814 REVERSE LENGTH=815</td><td>1296</td><td>815</td><td>0</td><td>62.9</td><td>35.8</td><td>43.8</td></tr>
<tr><td>Rsa1.0_00676.1.g17917.t1</td><td>ref|NP_196397.1| flavin-containing monooxygenase-like protein [Arabidopsis thaliana] gi|75170143|sp|Q9FF12.1|GSXL9_ARATH RecName: Full=Flavin-containing monooxygenase FMO GS-OX-like 9; AltName: Full=Flavin-monooxygenase glucosinolate S-oxygenase-like 9 gi|10176714|dbj|BAB09944.1| dimethylaniline monooxygenase-like protein [Arabidopsis thaliana] gi|332003823|gb|AED91206.1| flavin-containing monooxygenase FMO GS-OX-like 9 [Arabidopsis thaliana]</td><td>461</td><td>460</td><td>0</td><td>99.8</td><td>91.8</td><td>96.5</td><td>flavin-containing monooxygenase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07800.1 | Symbols: | Flavin-binding monooxygenase family protein | chr5:2486717-2489241 REVERSE LENGTH=460</td><td>461</td><td>460</td><td>0</td><td>99.8</td><td>91.8</td><td>96.5</td></tr>
<tr><td>Rsa1.0_00676.1.g17918.t1</td><td>gb|EOA20264.1| hypothetical protein CARUB_v10000566mg [Capsella rubella]</td><td>540</td><td>579</td><td>1.00E-151</td><td>107.2</td><td>69.1</td><td>78.1</td><td>hypothetical protein CARUB_v10000566mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G07820.1 | Symbols: | Plant calmodulin-binding protein-related | chr5:2498861-2500546 REVERSE LENGTH=561</td><td>540</td><td>561</td><td>1.00E-140</td><td>103.9</td><td>67.8</td><td>76.7</td></tr>
<tr><td>Rsa1.0_00676.1.g17919.t1</td><td>emb|CAB62595.1| putative protein [Arabidopsis thaliana]</td><td>522</td><td>521</td><td>0</td><td>99.8</td><td>87.7</td><td>95.4</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07830.1 | Symbols: AtGUS2, GUS2 | glucuronidase 2 | chr5:2504168-2506567 FORWARD LENGTH=543</td><td>522</td><td>543</td><td>0</td><td>104.0</td><td>87.7</td><td>95.4</td></tr>
<tr><td>Rsa1.0_00676.1.g17920.t1</td><td>dbj|BAJ34130.1| unnamed protein product [Thellungiella halophila]</td><td>306</td><td>302</td><td>1.00E-115</td><td>98.7</td><td>72.5</td><td>82.0</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G61210.1 | Symbols: SNAP33, ATSNAP33, SNP33, ATSNAP33B | soluble N-ethylmaleimide-sensitive factor adaptor protein 33 | chr5:24624027-24625366 FORWARD LENGTH=300</td><td>306</td><td>300</td><td>1.00E-112</td><td>98.0</td><td>68.0</td><td>80.1</td></tr>
<tr><td>Rsa1.0_00676.1.g17921.t1</td><td>ref|NP_193725.3| Toll-Interleukin-Resistance domain-containing protein [Arabidopsis thaliana] gi|332658846|gb|AEE84246.1| Toll-Interleukin-Resistance domain-containing protein [Arabidopsis thaliana]</td><td>268</td><td>274</td><td>8.00E-67</td><td>102.2</td><td>49.3</td><td>58.2</td><td>Toll-Interleukin-Resistance domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G19920.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr4:10797392-10798360 REVERSE LENGTH=274</td><td>268</td><td>274</td><td>2.00E-69</td><td>102.2</td><td>49.3</td><td>58.2</td></tr>
<tr><td>Rsa1.0_00676.1.g17922.t1</td><td>ref|NP_196406.2| myosin heavy chain-like protein [Arabidopsis thaliana] gi|79327239|ref|NP_001031851.1| myosin heavy chain-like protein [Arabidopsis thaliana] gi|222423567|dbj|BAH19753.1| AT5G07890 [Arabidopsis thaliana] gi|332003833|gb|AED91216.1| myosin heavy chain-like protein [Arabidopsis thaliana] gi|332003835|gb|AED91218.1| myosin heavy chain-like protein [Arabidopsis thaliana]</td><td>435</td><td>409</td><td>1.00E-149</td><td>94.0</td><td>67.4</td><td>75.6</td><td>myosin heavy chain-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G07890.3 | Symbols: | myosin heavy chain-related | chr5:2517718-2519493 REVERSE LENGTH=409</td><td>435</td><td>409</td><td>1.00E-152</td><td>94.0</td><td>67.4</td><td>75.6</td></tr>
<tr><td>Rsa1.0_00677.1.g17923.t1</td><td>gb|EOA28676.1| hypothetical protein CARUB_v10024900mg [Capsella rubella]</td><td>361</td><td>901</td><td>3.00E-85</td><td>249.6</td><td>42.7</td><td>60.1</td><td>hypothetical protein CARUB_v10024900mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907-10814173 REVERSE LENGTH=337</td><td>361</td><td>337</td><td>6.00E-39</td><td>93.4</td><td>21.9</td><td>32.1</td></tr>
<tr><td>Rsa1.0_00677.1.g17924.t1</td><td>ref|XP_003609074.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula] gi|355510129|gb|AES91271.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula]</td><td>786</td><td>1531</td><td>1.00E-157</td><td>194.8</td><td>35.1</td><td>49.9</td><td>ATP-dependent DNA helicase PIF1</td><td>gbpln</td><td>Medicago truncatula</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_00677.1.g17925.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	802	1489	1.00E-157	185.7	40.6	58.7	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	802	237	1.00E-14	29.6	7.1	12.6
Rsa1.0_00677.1.g17926.t1	gb|AAG52950.1| putative envelope protein [Arabidopsis thaliana]	342	461	3.00E-12	134.8	14.9	25.1	putative envelope protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17927.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	565	484	8.00E-49	85.7	22.7	29.6	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17928.t1	ref|XP_002866410.1| evolutionary conserved C-terminal 3 [Arabidopsis lyrata subsp. lyrata] gi|297312245|gb|EFH42669.1| evolutionary conserved C-terminal 3 [Arabidopsis lyrata subsp. lyrata]	483	498	1.00E-139	103.1	58.0	66.9	evolutionary conserved C-terminal 3	gbpln	Arabidopsis lyrata	AT5G61020.2 | Symbols: ECT3 | evolutionarily conserved C-terminal region 3 | chr5:24557485-24559780 REVERSE LENGTH=493	483	493	1.00E-135	102.1	59.0	68.5
Rsa1.0_00677.1.g17929.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17930.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17931.t1	ref|XP_002875043.1| LOB domain protein 30 [Arabidopsis lyrata subsp. lyrata] gi|297320880|gb|EFH51302.1| LOB domain protein 30 [Arabidopsis lyrata subsp. lyrata]	65	226	6.00E-18	347.7	73.8	78.5	LOB domain protein 30	gbpln	Arabidopsis lyrata	AT4G00220.1 | Symbols: LBD30, JLO | Lateral organ boundaries (LOB) domain family protein | chr4:90147-92087 FORWARD LENGTH=228	65	228	2.00E-20	350.8	72.3	80.0
Rsa1.0_00677.1.g17932.t1	gb|AAF63110.1|AC006423_11 putative retroelement pol polyprotein [Arabidopsis thaliana]	222	1150	4.00E-23	518.0	33.3	43.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17933.t1	ref|XP_002875039.1| hypothetical protein ARALYDRAFT_490540 [Arabidopsis lyrata subsp. lyrata] gi|297320876|gb|EFH51298.1| hypothetical protein ARALYDRAFT_490540 [Arabidopsis lyrata subsp. lyrata]	498	788	0	158.2	76.3	85.7	hypothetical protein ARALYDRAFT_490540	gbpln	Arabidopsis lyrata	AT4G00300.1 | Symbols: | fringe-related protein | chr4:126509-130126 FORWARD LENGTH=785	498	785	0	157.6	75.9	84.5
Rsa1.0_00677.1.g17934.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17935.t1	ref|NP_001190642.1| fringe-related protein [Arabidopsis thaliana] gi|110737285|dbj|BAF00589.1| hypothetical protein [Arabidopsis thaliana] gi|332656452|gb|AEE81852.1| fringe-related protein [Arabidopsis thaliana]	474	478	0	100.8	78.3	86.3	fringe-related protein	gbpln	Arabidopsis thaliana	AT4G00300.2 | Symbols: | fringe-related protein | chr4:128690-130126 FORWARD LENGTH=478	474	478	0	100.8	78.3	86.3
Rsa1.0_00677.1.g17936.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17937.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17938.t1	ref|NP_567167.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332656453|gb|AEE81853.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	126	126	1.00E-46	100.0	75.4	84.1	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT4G00305.1 | Symbols: | RING/U-box superfamily protein | chr4:131550-131930 FORWARD LENGTH=126	126	126	2.00E-49	100.0	75.4	84.1
Rsa1.0_00677.1.g17939.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00677.1.g17940.t1	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	808	695	0	86.0	43.6	44.8	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00678.1.g17941.t2	gb|EOA15973.1| hypothetical protein CARUB_v10004068mg [Capsella rubella] gi|482551781|gb|EOA15974.1| hypothetical protein CARUB_v10004068mg [Capsella rubella] gi|482551782|gb|EOA15975.1| hypothetical protein CARUB_v10004068mg [Capsella rubella]	1017	972	0	95.6	75.8	80.8	hypothetical protein CARUB_v10004068mg	gbpln	Capsella rubella	AT4G35270.1 | Symbols: | Plant regulator RWP-RK family protein | chr4:16777657-16780824 REVERSE LENGTH=963	1017	963	0	94.7	74.6	79.7
Rsa1.0_00678.1.g17942.t1	gb|EOA18908.1| hypothetical protein CARUB_v10007538mg [Capsella rubella]	253	253	1.00E-109	100.0	81.4	92.1	hypothetical protein CARUB_v10007538mg	gbpln	Capsella rubella	AT4G35200.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16749142-16749903 REVERSE LENGTH=253	253	253	1.00E-110	100.0	81.0	91.3
Rsa1.0_00678.1.g17943.t1	gb|EOA18908.1| hypothetical protein CARUB_v10007538mg [Capsella rubella]	196	253	7.00E-57	129.1	72.4	82.7	hypothetical protein CARUB_v10007538mg	gbpln	Capsella rubella	AT4G35200.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16749142-16749903 REVERSE LENGTH=253	196	253	6.00E-57	129.1	70.9	82.7
Rsa1.0_00678.1.g17944.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	784	723	0	92.2	46.2	59.2	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	784	696	1.00E-36	88.8	16.6	30.5

Rsa1.0_00678.1.g17945.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00678.1.g17946.t2	ref|NP_195187.1| BEL1-like homeodomain 6 [Arabidopsis thaliana] gi|186516293|ref|NP_001119116.1| BEL1-like homeodomain 6 [Arabidopsis thaliana] gi|75219970|sp|O65685.1|BLH6_ARATH RecName: Full=BEL1-like homeodomain protein 6; Short=BEL1-like protein 6 gi|3096930|emb|CAA18840.1| Homeodomain-like protein [Arabidopsis thaliana] gi|7270411|emb|CAB80178.1| Homeodomain-like protein [Arabidopsis thaliana] gi|45773948|gb|AAS76778.1| At4g34610 [Arabidopsis thaliana] gi|332660999|gb|AEE86399.1| BEL1-like homeodomain 6 [Arabidopsis thaliana] gi|332661000|gb|AEE86400.1| BEL1-like homeodomain 6 [Arabidopsis thaliana]	532	532	0	100.0	85.0	90.4	BEL1-like homeodomain 6	gbpln	Arabidopsis thaliana	AT4G34610.2 | Symbols: BLH6 | BEL1-like homeodomain 6 | chr4:16530546-16532498 REVERSE LENGTH=532	532	532	0	100.0	85.0	90.4
Rsa1.0_00678.1.g17947.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00678.1.g17948.t1	gb|EOA17614.1| hypothetical protein CARUB_v10005978mg [Capsella rubella]	153	143	8.00E-53	93.5	71.2	75.8	hypothetical protein CARUB_v10005978mg	gbpln	Capsella rubella	AT4G34590.1 | Symbols: ATB2, GBF6, AtbZIP11, BZIP11 | G-box binding factor 6 | chr4:16522449-16522928 FORWARD LENGTH=159	153	159	5.00E-54	103.9	71.2	76.5
Rsa1.0_00678.1.g17949.t2	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	481	1534	1.00E-160	318.9	61.5	74.6	F17L21.7	gbpln	Arabidopsis thaliana	AT5G48050.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G34070.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19472661-19473770 REVERSE LENGTH=369	481	369	1.00E-11	76.7	13.9	21.6
Rsa1.0_00678.1.g17950.t1	gb|EOA17396.1| hypothetical protein CARUB_v10005690mg [Capsella rubella]	222	221	9.00E-85	99.5	80.2	88.7	hypothetical protein CARUB_v10005690mg	gbpln	Capsella rubella	AT4G34560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66440.1); Has 67 Blast hits to 66 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:16507923-16508588 FORWARD LENGTH=221	222	221	2.00E-78	99.5	77.0	84.7
Rsa1.0_00678.1.g17951.t2	gb|EOA18989.1| hypothetical protein CARUB_v10007634mg [Capsella rubella]	236	475	4.00E-21	201.3	20.8	22.0	hypothetical protein CARUB_v10007634mg	gbpln	Capsella rubella	AT4G34490.1 | Symbols: ATCAP1, CAP 1, CAP1 | cyclase associated protein 1 | chr4:16484896-16487355 REVERSE LENGTH=476	236	476	1.00E-23	201.7	20.8	22.0
Rsa1.0_00678.1.g17952.t1	ref|NP_195174.6| glucan endo-1,3-beta-glucosidase 7 [Arabidopsis thaliana] gi|259016223|sp|Q9M069.2|E137_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 7; AltName: Full=(1-3)-beta-glucan endohydrolase 7; Short=(1-3)-beta-glucanase 7; AltName: Full=Beta-1,3-endoglucanase 7; Short=Beta-1,3-glucanase 7; Flags: Precursor gi|332660984|gb|AEE86384.1| glucan endo-1,3-beta-glucosidase 7 [Arabidopsis thaliana]	463	504	0	108.9	82.7	89.0	glucan endo-1,3-beta-glucosidase 7	gbpln	Arabidopsis thaliana	AT4G34480.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr4:16481147-16483988 REVERSE LENGTH=504	463	504	0	108.9	82.7	89.0
Rsa1.0_00678.1.g17953.t1	dbj|BAJ34135.1| unnamed protein product [Thellungiella halophila]	392	377	0	96.2	91.1	93.6	unnamed protein product	––––	––––	AT4G34460.1 | Symbols: AGB1, ELK4, ATAGB1 | GTP binding protein beta 1 | chr4:16477393-16479266 REVERSE LENGTH=377	392	377	0	96.2	88.8	92.6
Rsa1.0_00678.1.g17954.t1	gb|EOA17538.1| hypothetical protein CARUB_v10005889mg [Capsella rubella]	172	172	2.00E-86	100.0	91.3	97.1	hypothetical protein CARUB_v10005889mg	gbpln	Capsella rubella	AT4G34412.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Kinase binding protein CGI-121 (InterPro:IPR013926); Has 275 Blast hits to 275 proteins in 139 species: Archae - 0; Bacteria - 5; Metazoa - 98; Fungi - 109; Plants - 42; Viruses - 0; Other Eukaryotes - 21 (source: NCBI BLink). | chr4:16453099-16454515 REVERSE LENGTH=172	172	172	4.00E-87	100.0	91.9	95.3
Rsa1.0_00678.1.g17955.t1	gb|EOA15869.1| hypothetical protein CARUB_v10007825mg [Capsella rubella]	275	272	4.00E-92	98.9	74.9	82.9	hypothetical protein CARUB_v10007825mg	gbpln	Capsella rubella	AT4G34410.1 | Symbols: RRTF1 | redox responsive transcription factor 1 | chr4:16451992-16452798 FORWARD LENGTH=268	275	268	1.00E-87	97.5	75.6	82.9

Rsa1.0_00678.1.g17956.t1	ref|XP_002869150.1| hypothetical protein ARALYDRAFT_912952 [Arabidopsis lyrata subsp. lyrata] gi|297314986|gb|EFH45409.1| hypothetical protein ARALYDRAFT_912952 [Arabidopsis lyrata subsp. lyrata]	332	373	8.00E-83	112.3	57.5	67.8	hypothetical protein ARALYDRAFT_912952	gbpln	Arabidopsis lyrata	AT3G06160.2 | Symbols: | AP2/B3-like transcriptional factor family protein | chr3:1864326-1867192 FORWARD LENGTH=374	332	374	7.00E-74	112.7	47.0	61.1
Rsa1.0_00678.1.g17957.t1	ref|XP_002869151.1| extra-large GTP-binding protein 2 [Arabidopsis lyrata subsp. lyrata] gi|297314987|gb|EFH45410.1| extra-large GTP-binding protein 2 [Arabidopsis lyrata subsp. lyrata]	820	859	0	104.8	75.1	84.9	extra-large GTP-binding protein 2	gbpln	Arabidopsis lyrata	AT4G34390.1 | Symbols: XLG2 | extra-large GTP-binding protein 2 | chr4:16441579-16444840 FORWARD LENGTH=861	820	861	0	105.0	75.5	85.5
Rsa1.0_00678.1.g17958.t1	gb|EOA18995.1| hypothetical protein CARUB_v10007640mg [Capsella rubella]	493	492	0	99.8	81.9	89.5	hypothetical protein CARUB_v10007640mg	gbpln	Capsella rubella	AT4G34380.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:16438835-16440322 FORWARD LENGTH=495	493	495	0	100.4	79.9	87.8
Rsa1.0_00678.1.g17959.t1	ref|NP_195158.1| uncharacterized protein [Arabidopsis thaliana] gi|75213510|sp|Q9SYZ7.1|U496A_ARATH RecName: Full=UPF0496 protein At4g34320 gi|4455177|emb|CAB36709.1| putative protein [Arabidopsis thaliana] gi|7270382|emb|CAB80149.1| putative protein [Arabidopsis thaliana] gi|332660959|gb|AEE86359.1| uncharacterized protein AT4G34320 [Arabidopsis thaliana]	379	374	0	98.7	90.2	95.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G34320.1 | Symbols: | Protein of unknown function (DUF677) | chr4:16422436-16423824 FORWARD LENGTH=374	379	374	0	98.7	90.2	95.8
Rsa1.0_00678.1.g17960.t1	ref|XP_002869158.1| hypothetical protein ARALYDRAFT_491238 [Arabidopsis lyrata subsp. lyrata] gi|297314994|gb|EFH45417.1| hypothetical protein ARALYDRAFT_491238 [Arabidopsis lyrata subsp. lyrata]	140	144	7.00E-54	102.9	83.6	89.3	hypothetical protein ARALYDRAFT_491238	gbpln	Arabidopsis lyrata	AT4G34290.1 | Symbols: | SWIB/MDM2 domain superfamily protein | chr4:16410883-16412122 FORWARD LENGTH=144	140	144	9.00E-53	102.9	79.3	88.6
Rsa1.0_00678.1.g17961.t1	ref|XP_002869162.1| hypothetical protein ARALYDRAFT_491244 [Arabidopsis lyrata subsp. lyrata] gi|297314998|gb|EFH45421.1| hypothetical protein ARALYDRAFT_491244 [Arabidopsis lyrata subsp. lyrata]	491	493	0	100.4	82.5	91.2	hypothetical protein ARALYDRAFT_491244	gbpln	Arabidopsis lyrata	AT4G34250.1 | Symbols: KCS16 | 3-ketoacyl-CoA synthase 16 | chr4:16394749-16396230 FORWARD LENGTH=493	491	493	0	100.4	82.1	90.2
Rsa1.0_00679.1.g17962.t1	ref|NP_197435.2| uncharacterized protein [Arabidopsis thaliana] gi|40823080|gb|AAR92257.1| At5g19340 [Arabidopsis thaliana] gi|45752682|gb|AAS76239.1| At5g19340 [Arabidopsis thaliana] gi|110738485|dbj|BAF01168.1| hypothetical protein [Arabidopsis thaliana] gi|332005305|gb|AED92688.1| uncharacterized protein AT5G19340 [Arabidopsis thaliana]	251	263	2.00E-62	104.8	78.5	86.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G19340.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G05980.1); Has 1000 Blast hits to 906 proteins in 61 species: Archae - 0; Bacteria - 4; Metazoa - 62; Fungi - 36; Plants - 128; Viruses - 4; Other Eukaryotes - 766 (source: NCBI BLink). | chr5:6515371-6516162 REVERSE LENGTH=263	251	263	5.00E-65	104.8	78.5	86.5
Rsa1.0_00679.1.g17963.t1	ref|XP_002871881.1| hypothetical protein ARALYDRAFT_488820 [Arabidopsis lyrata subsp. lyrata] gi|297317718|gb|EFH48140.1| hypothetical protein ARALYDRAFT_488820 [Arabidopsis lyrata subsp. lyrata]	418	426	0	101.9	84.2	89.0	hypothetical protein ARALYDRAFT_488820	gbpln	Arabidopsis lyrata	AT5G19350.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:6518978-6521295 FORWARD LENGTH=425	418	425	0	101.7	83.7	89.0
Rsa1.0_00679.1.g17964.t1	gb|EOA22641.1| hypothetical protein CARUB_v10003311mg [Capsella rubella]	517	524	0	101.4	94.2	97.5	hypothetical protein CARUB_v10003311mg	gbpln	Capsella rubella	AT5G19360.1 | Symbols: CPK34 | calcium-dependent protein kinase 34 | chr5:6521716-6523780 REVERSE LENGTH=523	517	523	0	101.2	93.8	96.9
Rsa1.0_00679.1.g17965.t3	ref|XP_002871882.1| hypothetical protein ARALYDRAFT_488825 [Arabidopsis lyrata subsp. lyrata] gi|297317719|gb|EFH48141.1| hypothetical protein ARALYDRAFT_488825 [Arabidopsis lyrata subsp. lyrata]	892	870	0	97.5	87.7	91.7	hypothetical protein ARALYDRAFT_488825	gbpln	Arabidopsis lyrata	AT5G19390.2 | Symbols: | Rho GTPase activation protein (RhoGAP) with PH domain | chr5:6531906-6538206 FORWARD LENGTH=870	892	870	0	97.5	87.3	91.4
Rsa1.0_00679.1.g17966.t2	ref|XP_002871883.1| hypothetical protein ARALYDRAFT_488829 [Arabidopsis lyrata subsp. lyrata] gi|297317720|gb|EFH48142.1| hypothetical protein ARALYDRAFT_488829 [Arabidopsis lyrata subsp. lyrata]	1027	1047	0	101.9	77.1	85.3	hypothetical protein ARALYDRAFT_488829	gbpln	Arabidopsis lyrata	AT5G19400.2 | Symbols: SMG7 | Telomerase activating protein Est1 | chr5:6540603-6544262 FORWARD LENGTH=1059	1027	1059	0	103.1	74.6	84.4
Rsa1.0_00679.1.g17967.t1	gb|EOA20169.1| hypothetical protein CARUB_v10000467mg [Capsella rubella]	616	624	0	101.3	83.6	89.1	hypothetical protein CARUB_v10000467mg	gbpln	Capsella rubella	AT5G19410.1 | Symbols: | ABC-2 type transporter family protein | chr5:6545237-6547111 REVERSE LENGTH=624	616	624	0	101.3	83.3	89.1

Rsa1.0_00679.1.g17968.t1	ref|NP_197443.3| regulator of chromosome condensation-like protein with FYVE zinc finger domain [Arabidopsis thaliana] gi|332005320|gb|AED92703.1| regulator of chromosome condensation-like protein with FYVE zinc finger domain [Arabidopsis thaliana]	1098	1105	0	100.6	92.3	96.4	regulator of chromosome condensation-like protein with FYVE zinc finger domain	gbpln	Arabidopsis thaliana	AT5G19420.1 | Symbols: | Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain | chr5:6547945-6552866 REVERSE LENGTH=1105	1098	1105	0	100.6	92.3	96.4
Rsa1.0_00679.1.g17969.t1	ref|XP_002871885.1| hypothetical protein ARALYDRAFT_488833 [Arabidopsis lyrata subsp. lyrata] gi|297317722|gb|EFH48144.1| hypothetical protein ARALYDRAFT_488833 [Arabidopsis lyrata subsp. lyrata]	369	326	1.00E-177	88.3	79.9	84.8	hypothetical protein ARALYDRAFT_488833	gbpln	Arabidopsis lyrata	AT5G19440.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:6556493-6558123 FORWARD LENGTH=326	369	326	1.00E-176	88.3	79.1	83.5
Rsa1.0_00679.1.g17970.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1922	1274	0	66.3	31.3	42.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1922	575	2.00E-71	29.9	9.3	14.6
Rsa1.0_00679.1.g17971.t1	ref|XP_002871885.1| hypothetical protein ARALYDRAFT_488833 [Arabidopsis lyrata subsp. lyrata] gi|297317722|gb|EFH48144.1| hypothetical protein ARALYDRAFT_488833 [Arabidopsis lyrata subsp. lyrata]	326	326	1.00E-169	100.0	87.1	94.2	hypothetical protein ARALYDRAFT_488833	gbpln	Arabidopsis lyrata	AT5G19440.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:6556493-6558123 FORWARD LENGTH=326	326	326	1.00E-169	100.0	85.6	92.9
Rsa1.0_00679.1.g17972.t1	ref|XP_002873948.1| calcium-dependent protein kinase 19 [Arabidopsis lyrata subsp. lyrata] gi|297319785|gb|EFH50207.1| calcium-dependent protein kinase 19 [Arabidopsis lyrata subsp. lyrata]	534	533	0	99.8	94.4	97.6	calcium-dependent protein kinase 19	gbpln	Arabidopsis lyrata	AT5G19450.2 | Symbols: CDPK19, CPK8 | calcium-dependent protein kinase 19 | chr5:6558672-6561471 REVERSE LENGTH=533	534	533	0	99.8	94.2	97.2
Rsa1.0_00679.1.g17973.t1	gb|EOA20848.1| hypothetical protein CARUB_v10001185mg [Capsella rubella]	365	378	1.00E-169	103.6	84.7	90.1	hypothetical protein CARUB_v10001185mg	gbpln	Capsella rubella	AT5G19460.1 | Symbols: atnudt20, NUDT20 | nudix hydrolase homolog 20 | chr5:6563112-6565178 FORWARD LENGTH=374	365	374	1.00E-166	102.5	81.6	88.2
Rsa1.0_00679.1.g17974.t1	ref|XP_002871889.1| hypothetical protein ARALYDRAFT_488840 [Arabidopsis lyrata subsp. lyrata] gi|297317726|gb|EFH48148.1| hypothetical protein ARALYDRAFT_488840 [Arabidopsis lyrata subsp. lyrata]	295	208	5.00E-69	70.5	55.9	62.7	hypothetical protein ARALYDRAFT_488840	gbpln	Arabidopsis lyrata	AT5G19480.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12230.1); Has 15754 Blast hits to 7644 proteins in 441 species: Archae - 6; Bacteria - 451; Metazoa - 7628; Fungi - 1448; Plants - 1196; Viruses - 38; Other Eukaryotes - 4987 (source: NCBI BLink). | chr5:6571828-6572929 FORWARD LENGTH=207	295	207	2.00E-60	70.2	51.9	56.3
Rsa1.0_00679.1.g17975.t1	gb|EOA20537.1| hypothetical protein CARUB_v10000850mg, partial [Capsella rubella]	457	481	0	105.3	89.9	94.3	hypothetical protein CARUB_v10000850mg, partial	gbpln	Capsella rubella	AT5G19485.1 | Symbols: | transferases;nucleotidyltransferases | chr5:6573907-6576352 REVERSE LENGTH=456	457	456	0	99.8	89.3	94.3
Rsa1.0_00679.1.g17976.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00679.1.g17977.t1	gb|EOA19454.1| hypothetical protein CARUB_v10001845mg, partial [Capsella rubella]	221	240	9.00E-99	108.6	84.6	91.9	hypothetical protein CARUB_v10001845mg, partial	gbpln	Capsella rubella	AT5G12110.1 | Symbols: | Glutathione S-transferase, C-terminal-like;Translation elongation factor EF1B/ribosomal protein S6 | chr5:3914483-3915732 FORWARD LENGTH=228	221	228	2.00E-94	103.2	84.6	91.0
Rsa1.0_00679.1.g17978.t1	#	#	#	#	#	#	#	-	----	----	AT5G19520.1 | Symbols: MSL9, ATMSL9 | mechanosensitive channel of small conductance-like 9 | chr5:6586079-6588771 FORWARD LENGTH=742	125	742	1.00E-10	593.6	33.6	40.0
Rsa1.0_00680.1.g17979.t1	emb|CAB89177.1| SLL3 ORF2 protein [Brassica napus var. napus]	170	291	1.00E-36	171.2	48.2	57.1	SLL3 ORF2 protein	gbpln	Brassica napus	#	#	#	#	#	#	#
Rsa1.0_00680.1.g17980.t1	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	134	695	3.00E-60	518.7	91.0	92.5	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00680.1.g17981.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00680.1.g17982.t6	gb|EOA23571.1| hypothetical protein CARUB_v10016766mg [Capsella rubella] gi|482559381|gb|EOA23572.1| hypothetical protein CARUB_v10016766mg [Capsella rubella]	137	693	4.00E-24	505.8	45.3	51.8	hypothetical protein CARUB_v10016766mg	gbpln	Capsella rubella	AT3G26540.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:9744542-9746644 REVERSE LENGTH=700	137	700	7.00E-26	510.9	44.5	50.4
Rsa1.0_00680.1.g17983.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00680.1.g17984.t1	gb|AAG50886.1|AC025294_24 hypothetical protein [Arabidopsis thaliana]	553	629	1.00E-158	113.7	48.5	68.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	553	746	1.00E-106	134.9	36.5	50.5
Rsa1.0_00680.1.g17985.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00680.1.g17986.t3</td><td>ref|XP_002883433.1| hypothetical protein ARALYDRAFT_898865 [Arabidopsis lyrata subsp. lyrata] gi|297329273|gb|EFH59692.1| hypothetical protein ARALYDRAFT_898865 [Arabidopsis lyrata subsp. lyrata]</td><td>778</td><td>867</td><td>0</td><td>111.4</td><td>76.0</td><td>87.0</td><td>hypothetical protein ARALYDRAFT_898865</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G23530.1 | Symbols: | Cyclopropane-fatty-acyl-phospholipid synthase | chr3:8437472-8442597 FORWARD LENGTH=867</td><td>778</td><td>867</td><td>0</td><td>111.4</td><td>75.6</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00680.1.g17987.t1</td><td>ref|NP_178722.1| cycloartenol synthase [Arabidopsis thaliana] gi|21542399|sp|P38605.2|CAS1_ARATH RecName: Full=Cycloartenol synthase; Short=AtCYC; AltName: Full=2,3-epoxysqualene--cycloartenol cyclase gi|20197302|gb|AAM15015.1| cycloartenol synthase [Arabidopsis thaliana] gi|20453056|gb|AAM19773.1| At2g07050/T4E14.16 [Arabidopsis thaliana] gi|24796994|gb|AAN64509.1| At2g07050/T4E14.16 [Arabidopsis thaliana] gi|330250938|gb|AEC06032.1| cycloartenol synthase [Arabidopsis thaliana]</td><td>198</td><td>759</td><td>6.00E-85</td><td>383.3</td><td>80.8</td><td>85.9</td><td>cycloartenol synthase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G07050.1 | Symbols: CAS1 | cycloartenol synthase 1 | chr2:2924629-2930295 FORWARD LENGTH=759</td><td>198</td><td>759</td><td>2.00E-87</td><td>383.3</td><td>80.8</td><td>85.9</td></tr>
<tr><td>Rsa1.0_00680.1.g17988.t1</td><td>ref|NP_182079.1| cytochrome P450 76C4 [Arabidopsis thaliana] gi|5915834|sp|O64635.1|C76C4_ARATH RecName: Full=Cytochrome P450 76C4 gi|2979547|gb|AAC06156.1| putative cytochrome P450 [Arabidopsis thaliana] gi|330255475|gb|AEC10569.1| cytochrome P450 76C4 [Arabidopsis thaliana]</td><td>469</td><td>511</td><td>0</td><td>109.0</td><td>74.8</td><td>85.1</td><td>cytochrome P450 76C4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G45550.1 | Symbols: CYP76C4 | cytochrome P450, family 76, subfamily C, polypeptide 4 | chr2:18773541-18775654 REVERSE LENGTH=511</td><td>469</td><td>511</td><td>0</td><td>109.0</td><td>74.8</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00681.1.g17989.t1</td><td>ref|NP_177887.1| ethylene-responsive transcription factor ERF013 [Arabidopsis thaliana] gi|75262287|sp|Q9CAP4.1|ERF13_ARATH RecName: Full=Ethylene-responsive transcription factor ERF013 gi|12323380|gb|AAG51661.1|AC010704_5 hypothetical protein; 89317-90051 [Arabidopsis thaliana] gi|46931288|gb|AAT06448.1| At1g77640 [Arabidopsis thaliana] gi|48479278|gb|AAT44910.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|332197882|gb|AEE36003.1| ethylene-responsive transcription factor ERF013 [Arabidopsis thaliana]</td><td>237</td><td>244</td><td>3.00E-66</td><td>103.0</td><td>75.1</td><td>82.3</td><td>ethylene-responsive transcription factor ERF013</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G77640.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:29178796-29179530 FORWARD LENGTH=244</td><td>237</td><td>244</td><td>8.00E-69</td><td>103.0</td><td>75.1</td><td>82.3</td></tr>
<tr><td>Rsa1.0_00681.1.g17990.t1</td><td>ref|XP_002889151.1| nucleoside-triphosphatase/ nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] gi|297334992|gb|EFH65410.1| nucleoside-triphosphatase/ nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>1068</td><td>1154</td><td>0</td><td>108.1</td><td>72.0</td><td>83.2</td><td>nucleoside-triphosphatase/ nucleotide binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G77620.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:29167934-29172867 REVERSE LENGTH=1151</td><td>1068</td><td>1151</td><td>0</td><td>107.8</td><td>72.0</td><td>82.7</td></tr>
<tr><td>Rsa1.0_00681.1.g17991.t1</td><td>ref|XP_002862808.1| hypothetical protein ARALYDRAFT_497286 [Arabidopsis lyrata subsp. lyrata] gi|297308543|gb|EFH39066.1| hypothetical protein ARALYDRAFT_497286 [Arabidopsis lyrata subsp. lyrata]</td><td>338</td><td>336</td><td>0</td><td>99.4</td><td>95.9</td><td>98.8</td><td>hypothetical protein ARALYDRAFT_497286</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G77610.1 | Symbols: | EamA-like transporter family protein | chr1:29165489-29167486 FORWARD LENGTH=336</td><td>338</td><td>336</td><td>0</td><td>99.4</td><td>95.6</td><td>98.5</td></tr>
<tr><td>Rsa1.0_00681.1.g17992.t1</td><td>ref|XP_002889148.1| hypothetical protein ARALYDRAFT_476922 [Arabidopsis lyrata subsp. lyrata] gi|297334989|gb|EFH65407.1| hypothetical protein ARALYDRAFT_476922 [Arabidopsis lyrata subsp. lyrata]</td><td>729</td><td>780</td><td>0</td><td>107.0</td><td>72.8</td><td>82.9</td><td>hypothetical protein ARALYDRAFT_476922</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G77580.2 | Symbols: | Plant protein of unknown function (DUF869) | chr1:29144191-29146793 REVERSE LENGTH=779</td><td>729</td><td>779</td><td>0</td><td>106.9</td><td>71.9</td><td>82.3</td></tr>
<tr><td>Rsa1.0_00681.1.g17993.t1</td><td>ref|NP_177876.1| O-methyltransferase family protein [Arabidopsis thaliana] gi|12323395|gb|AAG51676.1|AC010704_20 putative caffeic acid 3-O-methyltransferase; 41078-42528 [Arabidopsis thaliana] gi|332197867|gb|AEE35988.1| O-methyltransferase family protein [Arabidopsis thaliana]</td><td>373</td><td>381</td><td>1.00E-148</td><td>102.1</td><td>67.3</td><td>81.2</td><td>O-methyltransferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G77520.1 | Symbols: | O-methyltransferase family protein | chr1:29130557-29132007 FORWARD LENGTH=381</td><td>373</td><td>381</td><td>1.00E-151</td><td>102.1</td><td>67.3</td><td>81.2</td></tr>
<tr><td>Rsa1.0_00681.1.g17994.t1</td><td>gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]</td><td>117</td><td>149</td><td>7.00E-25</td><td>127.4</td><td>41.9</td><td>64.1</td><td>hypothetical protein CARUB_v10016547mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292</td><td>117</td><td>292</td><td>1.00E-12</td><td>249.6</td><td>30.8</td><td>53.0</td></tr>
</table>

Rsa1.0_00681.1.g17995.t1	gb|ABB17025.1| protein disulfide isomerase [Brassica carinata]	509	509	0	100.0	95.1	98.0	protein disulfide isomerase	gbpln	Brassica carinata	AT1G77510.1 | Symbols: ATPDIL1−2, PDI6, ATPDI6, PDIL1−2 | PDI−like 1−2 | chr1:29126742−29129433 FORWARD LENGTH=508	509	508	0	99.8	84.7	91.2
Rsa1.0_00681.1.g17996.t1	ref|XP_002887687.1| hypothetical protein ARALYDRAFT_476915 [Arabidopsis lyrata subsp. lyrata] gi|297333528|gb|EFH63946.1| hypothetical protein ARALYDRAFT_476915 [Arabidopsis lyrata subsp. lyrata]	876	880	0	100.5	68.8	79.5	hypothetical protein ARALYDRAFT_476915	gbpln	Arabidopsis lyrata	AT1G77500.1 | Symbols: | Protein of unknown function (DUF630 and DUF632) | chr1:29121753−29124937 FORWARD LENGTH=879	876	879	0	100.3	68.3	77.2
Rsa1.0_00681.1.g17997.t1	emb|CCC55737.1| thylakoid−bound ascorbate peroxidase [Brassica rapa subsp. oleifera]	433	437	0	100.9	90.5	92.4	thylakoid−bound ascorbate peroxidase	gbpln	Brassica rapa	AT1G77490.1 | Symbols: TAPX | thylakoidal ascorbate peroxidase | chr1:29117688−29120046 FORWARD LENGTH=426	433	426	0	98.4	80.8	87.3
Rsa1.0_00681.1.g17998.t1	ref|XP_002889144.1| hypothetical protein ARALYDRAFT_476912 [Arabidopsis lyrata subsp. lyrata] gi|297334985|gb|EFH65403.1| hypothetical protein ARALYDRAFT_476912 [Arabidopsis lyrata subsp. lyrata]	466	467	0	100.2	82.0	88.4	hypothetical protein ARALYDRAFT_476912	gbpln	Arabidopsis lyrata	AT1G77480.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:29114705−29117150 REVERSE LENGTH=466	466	466	0	100.0	82.0	88.0
Rsa1.0_00681.1.g17999.t1	gb|EOA35654.1| hypothetical protein CARUB_v10020878mg [Capsella rubella]	227	236	2.00E−72	104.0	77.5	84.1	hypothetical protein CARUB_v10020878mg	gbpln	Capsella rubella	AT1G77400.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF688 (InterPro:IPR007789); BEST Arabidopsis thaliana protein match is: hydroxyproline−rich glycoprotein family protein (TAIR:AT1G21695.1); Has 328 Blast hits to 314 proteins in 61 species: Archae − 0; Bacteria − 12; Metazoa − 130; Fungi − 28; Plants − 92; Viruses − 10; Other Eukaryotes − 56 (source: NCBI BLink). | chr1:29085881−29086579 FORWARD LENGTH=232	227	232	2.00E−74	102.2	79.3	87.2
Rsa1.0_00681.1.g18000.t1	ref|NP_177863.2| cyclin−A1−2 [Arabidopsis thaliana] gi|148887347|sp|Q9FVX0.2|CCA12_ARATH RecName: Full=Cyclin−A1−2; AltName: Full=G2/mitotic−specific cyclin−A1−2; Short=CycA1;2; AltName: Full=Protein TARDY ASYNCHRONOUS MEIOSIS gi|332197851|gb|AEE35972.1| cyclin−A1−2 [Arabidopsis thaliana]	389	442	1.00E−169	113.6	79.2	87.9	cyclin−A1−2	gbpln	Arabidopsis thaliana	AT1G77390.1 | Symbols: TAM, CYCA1;2, DYP, CYCA1 | CYCLIN A1;2 | chr1:29081904−29084137 REVERSE LENGTH=442	389	442	1.00E−172	113.6	79.2	87.9
Rsa1.0_00682.1.g18001.t1	ref|XP_002888847.1| hypothetical protein ARALYDRAFT_476299 [Arabidopsis lyrata subsp. lyrata] gi|297334688|gb|EFH65106.1| hypothetical protein ARALYDRAFT_476299 [Arabidopsis lyrata subsp. lyrata]	255	190	1.00E−48	74.5	36.5	39.6	hypothetical protein ARALYDRAFT_476299	gbpln	Arabidopsis lyrata	AT1G71780.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; Has 34 Blast hits to 34 proteins in 11 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 34; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:26995406−26996638 REVERSE LENGTH=197	255	197	2.00E−49	77.3	34.9	39.6
Rsa1.0_00682.1.g18002.t1	ref|XP_002888846.1| hypothetical protein ARALYDRAFT_339396 [Arabidopsis lyrata subsp. lyrata] gi|297334687|gb|EFH65105.1| hypothetical protein ARALYDRAFT_339396 [Arabidopsis lyrata subsp. lyrata]	686	685	0	99.9	87.3	92.1	hypothetical protein ARALYDRAFT_339396	gbpln	Arabidopsis lyrata	AT1G71770.2 | Symbols: PAB5 | poly(A)−binding protein 5 | chr1:26990777−26993489 REVERSE LENGTH=682	686	682	0	99.4	84.5	90.4
Rsa1.0_00682.1.g18003.t1	ref|NP_177321.1| uncharacterized protein [Arabidopsis thaliana] gi|7239503|gb|AAF43229.1|AC012654_13 F14O23.14 [Arabidopsis thaliana] gi|52354211|gb|AAU44426.1| hypothetical protein AT1G71760 [Arabidopsis thaliana] gi|332197107|gb|AEE35228.1| uncharacterized protein AT1G71760 [Arabidopsis thaliana]	249	259	1.00E−87	104.0	68.7	79.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G71760.1 | Symbols: | unknown protein; Has 92 Blast hits to 92 proteins in 41 species: Archae − 0; Bacteria − 0; Metazoa − 44; Fungi − 0; Plants − 32; Viruses − 0; Other Eukaryotes − 16 (source: NCBI BLink). | chr1:26989414−26990499 FORWARD LENGTH=259	249	259	4.00E−90	104.0	68.7	79.9
Rsa1.0_00682.1.g18004.t1	ref|XP_002888845.1| phosphoribosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334686|gb|EFH65104.1| phosphoribosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	187	187	1.00E−93	100.0	90.4	94.7	phosphoribosyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G71750.1 | Symbols: HGPT | Hypoxanthine−guanine phosphoribosyltransferase | chr1:26987954−26989144 REVERSE LENGTH=188	187	188	2.00E−93	100.5	88.2	94.1

Rsa1.0_00682.1.g18005.t1	ref|NP_177319.1| uncharacterized protein [Arabidopsis thaliana] gi|7239501|gb|AAF43227.1|AC012654_11 F14O23.12 [Arabidopsis thaliana] gi|61742554|gb|AAX55098.1| hypothetical protein At1g71740 [Arabidopsis thaliana] gi|332197104|gb|AEE35225.1| uncharacterized protein AT1G71740 [Arabidopsis thaliana]	138	130	1.00E-52	94.2	74.6	86.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G71740.1 | Symbols: | unknown protein; Has 82 Blast hits to 82 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 82; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26987245-26987637 FORWARD LENGTH=130	138	130	4.00E-55	94.2	74.6	86.2
Rsa1.0_00682.1.g18006.t1	gb|ABL97948.1| unknown [Brassica rapa]	159	157	1.00E-65	98.7	83.6	87.4	unknown	gbpln	Brassica rapa	AT1G71730.1 | Symbols: | unknown protein; Has 52 Blast hits to 52 proteins in 24 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr1:26986298-26986831 REVERSE LENGTH=177	159	177	7.00E-52	111.3	73.0	81.8
Rsa1.0_00682.1.g18007.t1	ref|XP_002887384.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333225|gb|EFH63643.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	503	501	0	99.6	81.3	86.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G71720.1 | Symbols: | Nucleic acid-binding proteins superfamily | chr1:26983744-26985893 FORWARD LENGTH=500	503	500	0	99.4	80.5	87.3
Rsa1.0_00682.1.g18008.t1	dbj|BAJ34469.1| unnamed protein product [Thellungiella halophila]	678	661	0	97.5	84.7	89.8	unnamed protein product	----	----	AT1G71710.1 | Symbols: | DNAse I-like superfamily protein | chr1:26973796-26976774 REVERSE LENGTH=664	678	664	0	97.9	84.5	90.1
Rsa1.0_00682.1.g18009.t2	gb|EOA34450.1| hypothetical protein CARUB_v10021986mg [Capsella rubella]	353	348	0	98.6	86.4	92.1	hypothetical protein CARUB_v10021986mg	gbpln	Capsella rubella	AT1G71697.1 | Symbols: ATCK1, CK, CK1 | choline kinase 1 | chr1:26971537-26973177 FORWARD LENGTH=346	353	346	0	98.0	86.4	91.5
Rsa1.0_00682.1.g18010.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1433	1485	0	103.6	44.0	58.5	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1433	158	8.00E-24	11.0	3.5	5.6
Rsa1.0_00682.1.g18011.t1	dbj|BAJ33705.1| unnamed protein product [Thellungiella halophila]	362	385	0	106.4	90.3	94.5	unnamed protein product	----	----	AT1G71695.1 | Symbols: | Peroxidase superfamily protein | chr1:26964359-26966557 FORWARD LENGTH=358	362	358	0	98.9	88.1	92.8
Rsa1.0_00682.1.g18012.t8	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1969	1274	0	64.7	24.4	32.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1969	575	2.00E-65	29.2	8.7	14.5
Rsa1.0_00682.1.g18013.t1	ref|NP_851232.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|79331627|ref|NP_001032112.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332009965|gb|AED97348.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332009967|gb|AED97350.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	128	494	2.00E-32	385.9	57.0	62.5	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G60580.4 | Symbols: | RING/U-box superfamily protein | chr5:24354298-24356706 FORWARD LENGTH=494	128	494	4.00E-35	385.9	57.0	62.5
Rsa1.0_00682.1.g18014.t1	gb|EOA30046.1| hypothetical protein CARUB_v10013151mg [Capsella rubella]	152	664	1.00E-20	436.8	32.9	34.9	hypothetical protein CARUB_v10013151mg	gbpln	Capsella rubella	AT3G01750.1 | Symbols: | Ankyrin repeat family protein | chr3:270615-272691 FORWARD LENGTH=664	152	664	2.00E-22	436.8	32.2	34.2
Rsa1.0_00683.1.g18015.t1	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	96	1643	4.00E-19	1711.5	45.8	67.7	gag/pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00683.1.g18016.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	97	99	3.00E-42	102.1	90.7	94.8	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18030.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5968527-5968793 FORWARD LENGTH=88	97	88	1.00E-42	90.7	86.6	88.7
Rsa1.0_00683.1.g18017.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	98	99	3.00E-43	101.0	88.8	93.9	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	98	91	5.00E-42	92.9	82.7	87.8
Rsa1.0_00683.1.g18018.t1	gb|EOA21868.1| hypothetical protein CARUB_v10002345mg [Capsella rubella] gi|482557677|gb|EOA21869.1| hypothetical protein CARUB_v10002345mg [Capsella rubella]	92	92	1.00E-40	100.0	85.9	94.6	hypothetical protein CARUB_v10002345mg	gbpln	Capsella rubella	AT5G18030.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5968527-5968793 FORWARD LENGTH=88	92	88	3.00E-38	95.7	79.3	87.0
Rsa1.0_00683.1.g18019.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	98	99	3.00E-41	101.0	85.7	92.9	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	98	91	7.00E-40	92.9	78.6	86.7
Rsa1.0_00683.1.g18020.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	97	99	2.00E-40	102.1	87.6	94.8	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	97	91	3.00E-41	93.8	81.4	86.6

Rsa1.0_00683.1.g18021.t1	ref|NP_197299.1| C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein [Arabidopsis thaliana] gi|9757890|dbj|BAB08397.1| phosphoribosylanthranilate transferase-like protein [Arabidopsis thaliana] gi|332005109|gb|AED92492.1| C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein [Arabidopsis thaliana]	1502	1049	0	69.8	62.1	65.1	C2 calcium/lipid-binding and phosphoribosyltransferase C-terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT5G17980.1 | Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr5:5953596-5956745 FORWARD LENGTH=1049	1502	1049	0	69.8	62.1	65.1
Rsa1.0_00683.1.g18022.t1	ref|NP_197337.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332005160|gb|AED92543.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1201	900	0	74.9	38.4	50.2	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G18360.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6080049-6083027 REVERSE LENGTH=900	1201	900	0	74.9	38.4	50.2
Rsa1.0_00683.1.g18023.t1	ref|XP_002871787.1| cobalamin-independent methionine synthase [Arabidopsis lyrata subsp. lyrata] gi|297317624|gb|EFH48046.1| cobalamin-independent methionine synthase [Arabidopsis lyrata subsp. lyrata]	738	765	0	103.7	92.8	95.0	cobalamin-independent methionine synthase	gbpln	Arabidopsis lyrata	AT5G17920.2 | Symbols: ATCIMS | Cobalamin-independent synthase family protein | chr5:5935771-5939195 FORWARD LENGTH=765	738	765	0	103.7	92.5	94.9
Rsa1.0_00683.1.g18024.t1	gb|EOA19787.1| hypothetical protein CARUB_v10000034mg [Capsella rubella]	1451	1498	0	103.2	72.7	81.0	hypothetical protein CARUB_v10000034mg	gbpln	Capsella rubella	AT5G17910.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29620.1). | chr5:5927906-5932292 FORWARD LENGTH=1342	1451	1342	1.00E-107	92.5	15.0	16.7
Rsa1.0_00683.1.g18025.t1	ref|XP_002871786.1| hypothetical protein ARALYDRAFT_488655 [Arabidopsis lyrata subsp. lyrata] gi|297317623|gb|EFH48045.1| hypothetical protein ARALYDRAFT_488655 [Arabidopsis lyrata subsp. lyrata]	679	435	1.00E-168	64.1	53.0	57.3	hypothetical protein ARALYDRAFT_488655	gbpln	Arabidopsis lyrata	AT4G08580.1 | Symbols: | microfibrillar-associated protein-related | chr4:5462190-5463718 FORWARD LENGTH=435	679	435	1.00E-168	64.1	53.2	57.9
Rsa1.0_00683.1.g18026.t2	dbj|BAB11222.1| disease resistance protein-like [Arabidopsis thaliana]	1350	1251	0	92.7	48.6	56.9	disease resistance protein-like	gbpln	Arabidopsis thaliana	AT5G17890.1 | Symbols: CHS3, DAR4 | DA1-related protein 4 | chr5:5917015-5923160 FORWARD LENGTH=1613	1350	1613	0	119.5	48.6	56.9
Rsa1.0_00683.1.g18027.t1	ref|NP_197290.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332005098|gb|AED92481.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1170	1197	0	102.3	71.8	82.5	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G17880.1 | Symbols: CSA1 | disease resistance protein (TIR-NBS-LRR class) | chr5:5908874-5913096 REVERSE LENGTH=1197	1170	1197	0	102.3	71.8	82.5
Rsa1.0_00683.1.g18028.t1	ref|NP_568358.1| plastid-specific 50S ribosomal protein 6 [Arabidopsis thaliana] gi|75171293|sp|Q9FKP0.1|PSRP6_ARATH RecName: Full=50S ribosomal protein 6, chloroplastic; AltName: Full=CL25; AltName: Full=Plastid-specific 50S ribosomal protein 6; Short=PSRP-6; Flags: Precursor gi|10177888|dbj|BAB11220.1| unnamed protein product [Arabidopsis thaliana] gi|14517428|gb|AAK62604.1| AT5g17870/MPI7_10 [Arabidopsis thaliana] gi|20147339|gb|AAM10383.1| AT5g17870/MPI7_10 [Arabidopsis thaliana] gi|21554906|gb|AAM63726.1| plastid-specific ribosomal protein 6 precursor (Psrp-6)-like [Arabidopsis thaliana] gi|332005097|gb|AED92480.1| plastid-specific 50S ribosomal protein 6 [Arabidopsis thaliana]	106	106	3.00E-48	100.0	91.5	93.4	plastid-specific 50S ribosomal protein 6	gbpln	Arabidopsis thaliana	AT5G17870.1 | Symbols: PSRP6 | plastid-specific 50S ribosomal protein 6 | chr5:5907817-5908137 FORWARD LENGTH=106	106	106	5.00E-51	100.0	91.5	93.4
Rsa1.0_00683.1.g18029.t1	dbj|BAJ34263.1| unnamed protein product [Thellungiella halophila]	575	577	0	100.3	88.3	93.6	unnamed protein product	----	----	AT5G17860.1 | Symbols: CAX7 | calcium exchanger 7 | chr5:5902638-5904350 REVERSE LENGTH=570	575	570	0	99.1	85.9	91.7

Rsa1.0_00683.1.g18030.t1	ref|NP_197287.1| Sodium/calcium exchanger family protein [Arabidopsis thaliana] gi|75171295|sp|Q9FKP2.1|CCX2_ARATH RecName: Full=Cation/calcium exchanger 2; AltName: Full=Protein CATION EXCHANGER 8 gi|10177886|dbj|BAB11218.1| Na/Ca,K-exchanger-like protein [Arabidopsis thaliana] gi|332005095|gb|AED92478.1| Sodium/calcium exchanger family protein [Arabidopsis thaliana]	550	559	0	101.6	84.5	92.0	Sodium/calcium exchanger family protein	gbpln	Arabidopsis thaliana	AT5G17850.1 | Symbols: | Sodium/calcium exchanger family protein | chr5:5899253-5900932 FORWARD LENGTH=559	550	559	0	101.6	84.5	92.0
Rsa1.0_00684.1.g18031.t1	gb|AAF99801.1|AC012463_18 T2E6.13 [Arabidopsis thaliana]	101	165	1.00E-16	163.4	37.6	58.4	T2E6.13	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00684.1.g18032.t1	sp|P34794.1|RUB2_BRANA RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor gi|415925|emb|CAA81736.1| chaperonin-60 alpha subunit [Brassica napus]	603	583	0	96.7	93.2	94.2	RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor gi|415925|emb|CAA81736.1| chaperonin-60 alpha subunit	gbpln	Brassica napus	AT2G28000.1 | Symbols: CPN60A, CH-CPN60A, SLP | chaperonin-60alpha | chr2:11926603-11929184 FORWARD LENGTH=586	603	586	0	97.2	89.6	92.2
Rsa1.0_00684.1.g18033.t2	gb|EOA39500.1| hypothetical protein CARUB_v10008106mg [Capsella rubella]	1260	1260	0	100.0	87.4	93.4	hypothetical protein CARUB_v10008106mg	gbpln	Capsella rubella	AT1G42470.1 | Symbols: | Patched family protein | chr1:15926987-15935128 FORWARD LENGTH=1272	1260	1272	0	101.0	81.5	86.0
Rsa1.0_00684.1.g18034.t31	dbj|BAF36296.1| hypothetical protein [Ipomoea trifida]	82	1291	2.00E-34	1574.4	82.9	85.4	hypothetical protein	gbpln	Ipomoea trifida	AT2G27970.1 | Symbols: CKS2 | CDK-subunit 2 | chr2:11912460-11913112 REVERSE LENGTH=83	82	83	4.00E-37	101.2	85.4	86.6
Rsa1.0_00684.1.g18035.t1	ref|XP_002879127.1| hypothetical protein ARALYDRAFT_901726 [Arabidopsis lyrata subsp. lyrata] gi|297324966|gb|EFH55386.1| hypothetical protein ARALYDRAFT_901726 [Arabidopsis lyrata subsp. lyrata]	836	840	0	100.5	79.4	86.1	hypothetical protein ARALYDRAFT_901726	gbpln	Arabidopsis lyrata	AT2G27950.1 | Symbols: | Ring/U-Box superfamily protein | chr2:11899422-11903171 REVERSE LENGTH=839	836	839	0	100.4	77.9	85.3
Rsa1.0_00684.1.g18036.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00684.1.g18037.t1	ref|NP_180360.4| PLATZ transcription factor family protein [Arabidopsis thaliana] gi|330252967|gb|AEC08061.1| PLATZ transcription factor family protein [Arabidopsis thaliana]	189	189	2.00E-88	100.0	91.0	93.7	PLATZ transcription factor family protein	gbpln	Arabidopsis thaliana	AT2G27930.1 | Symbols: | PLATZ transcription factor family protein | chr2:11892369-11893488 FORWARD LENGTH=189	189	189	7.00E-91	100.0	91.0	93.7
Rsa1.0_00684.1.g18038.t1	ref|XP_002880962.1| hypothetical protein ARALYDRAFT_481718 [Arabidopsis lyrata subsp. lyrata] gi|297326801|gb|EFH57221.1| hypothetical protein ARALYDRAFT_481718 [Arabidopsis lyrata subsp. lyrata]	968	1001	0	103.4	75.5	84.2	hypothetical protein ARALYDRAFT_481718	gbpln	Arabidopsis lyrata	AT2G27880.1 | Symbols: AGO5 | Argonaute family protein | chr2:11871488-11876712 FORWARD LENGTH=997	968	997	0	103.0	75.0	84.5
Rsa1.0_00684.1.g18039.t1	#	#	#	#	#	#	#	-	----	----	AT1G08200.1 | Symbols: AXS2 | UDP-D-apiose/UDP-D-xylose synthase 2 | chr1:2574259-2576609 REVERSE LENGTH=389	105	389	9.00E-13	370.5	41.9	49.5
Rsa1.0_00684.1.g18040.t1	ref|NP_565660.1| uncharacterized protein [Arabidopsis thaliana] gi|3860249|gb|AAC73017.1| expressed protein [Arabidopsis thaliana] gi|17473713|gb|AAL38309.1| unknown protein [Arabidopsis thaliana] gi|21386999|gb|AAM47903.1| unknown protein [Arabidopsis thaliana] gi|21592892|gb|AAM64842.1| unknown [Arabidopsis thaliana] gi|330252957|gb|AEC08051.1| uncharacterized protein AT2G27830 [Arabidopsis thaliana]	196	190	6.00E-80	96.9	79.1	82.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G27830.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G22758.1); Has 131 Blast hits to 131 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 131; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:11860734-11861306 FORWARD LENGTH=190	196	190	2.00E-82	96.9	79.1	82.7
Rsa1.0_00685.1.g18041.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00685.1.g18042.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00685.1.g18043.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00685.1.g18044.t1	gb|EOA30650.1| hypothetical protein CARUB_v10013787mg [Capsella rubella]	380	422	1.00E-153	111.1	82.4	88.4	hypothetical protein CARUB_v10013787mg	gbpln	Capsella rubella	AT3G22190.2 | Symbols: IQD5 | IQ-domain 5 | chr3:7831280-7833512 REVERSE LENGTH=422	380	422	1.00E-155	111.1	82.9	88.2

Rsa1.0_00685.1.g18045.t1	ref|NP_188856.2| far-red elongated hypocotyls 3 protein [Arabidopsis thaliana] gi|186510310|ref|NP_001118673.1| far-red elongated hypocotyls 3 protein [Arabidopsis thaliana] gi|75273369|sp|Q9LIE5.1|FHY3_ARATH RecName: Full=Protein FAR-RED ELONGATED HYPOCOTYL 3 gi|11994736|dbj|BAB03065.1| far-red impaired response protein; Mutator-like transposase-like protein; phytochrome A signaling protein-like [Arabidopsis thaliana] gi|332643075|gb|AEE76596.1| far-red elongated hypocotyls 3 protein [Arabidopsis thaliana] gi|332643076|gb|AEE76597.1| far-red elongated hypocotyls 3 protein [Arabidopsis thaliana]	830	839	0	101.1	84.8	91.6	far-red elongated hypocotyls 3 protein	gbpln	Arabidopsis thaliana	AT3G22170.2 | Symbols: FHY3 | far-red elongated hypocotyls 3 | chr3:7822359-7825414 REVERSE LENGTH=839	830	839	0	101.1	84.8	91.6
Rsa1.0_00685.1.g18046.t1	gb|EOA31512.1| hypothetical protein CARUB_v10014701mg [Capsella rubella]	199	195	9.00E-57	98.0	76.4	83.9	hypothetical protein CARUB_v10014701mg	gbpln	Capsella rubella	AT3G22160.1 | Symbols: | VQ motif-containing protein | chr3:7818148-7818726 REVERSE LENGTH=192	199	192	2.00E-56	96.5	76.9	83.4
Rsa1.0_00685.1.g18047.t1	ref|NP_188854.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75273371|sp|Q9LIE7.1|PP246_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g22150, chloroplastic; Flags: Precursor gi|11994734|dbj|BAB03063.1| selenium-binding protein-like [Arabidopsis thaliana] gi|110739449|dbj|BAF01634.1| hypothetical protein [Arabidopsis thaliana] gi|332643073|gb|AEE76594.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	814	820	0	100.7	86.4	92.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G22150.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:7813028-7815490 FORWARD LENGTH=820	814	820	0	100.7	86.4	92.9
Rsa1.0_00685.1.g18048.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00685.1.g18049.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00685.1.g18050.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00685.1.g18051.t1	ref|XP_002885484.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331324|gb|EFH61743.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	388	722	2.00E-58	186.1	45.9	51.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G22142.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:7803604-7808046 REVERSE LENGTH=1480	388	1480	2.00E-56	381.4	45.4	52.3
Rsa1.0_00686.1.g18052.t2	ref|NP_181854.1| uncharacterized protein [Arabidopsis thaliana] gi|3763934|gb|AAC64314.1| hypothetical protein [Arabidopsis thaliana] gi|110737676|dbj|BAF00777.1| hypothetical protein [Arabidopsis thaliana] gi|330255143|gb|AEC10237.1| uncharacterized protein AT2G43250 [Arabidopsis thaliana]	74	625	7.00E-15	844.6	63.5	77.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G43250.1 | Symbols: | unknown protein; Has 32 Blast hits to 32 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17977619-17979496 FORWARD LENGTH=625	74	625	1.00E-17	844.6	63.5	77.0
Rsa1.0_00686.1.g18053.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00686.1.g18054.t1	emb|CAB43055.1| putative protein [Arabidopsis thaliana] gi|7267819|emb|CAB81221.1| putative protein [Arabidopsis thaliana]	310	462	5.00E-43	149.0	37.1	53.5	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00686.1.g18055.t1	ref|XP_002881893.1| hypothetical protein ARALYDRAFT_903711 [Arabidopsis lyrata subsp. lyrata] gi|297327732|gb|EFH58152.1| hypothetical protein ARALYDRAFT_903711 [Arabidopsis lyrata subsp. lyrata]	225	189	5.00E-20	84.0	24.0	34.2	hypothetical protein ARALYDRAFT_903711	gbpln	Arabidopsis lyrata	AT2G43261.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:17985581-17986559 REVERSE LENGTH=190	225	190	8.00E-18	84.4	24.0	33.3
Rsa1.0_00686.1.g18056.t1	gb|EOA27181.1| hypothetical protein CARUB_v10023282mg [Capsella rubella]	415	423	2.00E-96	101.9	53.7	64.6	hypothetical protein CARUB_v10023282mg	gbpln	Capsella rubella	AT2G43270.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17988207-17989491 REVERSE LENGTH=387	415	387	1.00E-98	93.3	53.5	64.3
Rsa1.0_00686.1.g18057.t1	gb|EOA27181.1| hypothetical protein CARUB_v10023282mg [Capsella rubella]	421	423	1.00E-158	100.5	68.2	80.5	hypothetical protein CARUB_v10023282mg	gbpln	Capsella rubella	AT2G43260.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17983744-17985089 REVERSE LENGTH=420	421	420	1.00E-152	99.8	67.0	79.8
Rsa1.0_00686.1.g18058.t1	gb|EOA26935.1| hypothetical protein CARUB_v10023029mg [Capsella rubella]	503	509	0	101.2	91.5	96.0	hypothetical protein CARUB_v10023029mg	gbpln	Capsella rubella	AT2G43330.1 | Symbols: ATINT1, INT1 | inositol transporter 1 | chr2:18001135-18003854 FORWARD LENGTH=509	503	509	0	101.2	91.7	96.2

<table>
<tr><td>Rsa1.0_00686.1.g18059.t1</td><td>gb|EOA27961.1| hypothetical protein CARUB_v10024131mg [Capsella rubella]</td><td>172</td><td>186</td><td>8.00E-61</td><td>108.1</td><td>77.9</td><td>84.9</td><td>hypothetical protein CARUB_v10024131mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G43340.1 | Symbols: | Protein of unknown function (DUF1685) | chr2:18007769-18008416 FORWARD LENGTH=189</td><td>172</td><td>189</td><td>2.00E-55</td><td>109.9</td><td>79.1</td><td>84.3</td></tr>
<tr><td>Rsa1.0_00686.1.g18060.t1</td><td>gb|EOA27306.1| hypothetical protein CARUB_v10023426mg [Capsella rubella]</td><td>376</td><td>380</td><td>0</td><td>101.1</td><td>94.1</td><td>95.5</td><td>hypothetical protein CARUB_v10023426mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G43360.1 | Symbols: BIO2, BIOB | Radical SAM superfamily protein | chr2:18010918-18013129 REVERSE LENGTH=378</td><td>376</td><td>378</td><td>0</td><td>100.5</td><td>93.4</td><td>95.7</td></tr>
<tr><td>Rsa1.0_00686.1.g18061.t1</td><td>gb|ABD65166.1| F-box domain containing protein [Brassica oleracea]</td><td>356</td><td>391</td><td>1.00E-95</td><td>109.8</td><td>56.7</td><td>69.1</td><td>F-box domain containing protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G43445.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:18041511-18042995 FORWARD LENGTH=405</td><td>356</td><td>405</td><td>1.00E-93</td><td>113.8</td><td>53.7</td><td>69.9</td></tr>
<tr><td>Rsa1.0_00686.1.g18062.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00686.1.g18063.t1</td><td>gb|EOA28793.1| hypothetical protein CARUB_v10025025mg [Capsella rubella]</td><td>619</td><td>624</td><td>0</td><td>100.8</td><td>90.1</td><td>93.1</td><td>hypothetical protein CARUB_v10025025mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G43400.1 | Symbols: ETFQO | electron-transfer flavoprotein:ubiquinone oxidoreductase | chr2:18021304-18025041 FORWARD LENGTH=633</td><td>619</td><td>633</td><td>0</td><td>102.3</td><td>91.0</td><td>93.7</td></tr>
<tr><td>Rsa1.0_00686.1.g18064.t1</td><td>ref|XP_002881902.1| hypothetical protein ARALYDRAFT_483451 [Arabidopsis lyrata subsp. lyrata] gi|297327741|gb|EFH58161.1| hypothetical protein ARALYDRAFT_483451 [Arabidopsis lyrata subsp. lyrata]</td><td>851</td><td>902</td><td>0</td><td>106.0</td><td>81.2</td><td>88.0</td><td>hypothetical protein ARALYDRAFT_483451</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G43410.1 | Symbols: FPA | RNA binding | chr2:18026397-18030989 REVERSE LENGTH=858</td><td>851</td><td>858</td><td>0</td><td>100.8</td><td>81.3</td><td>88.1</td></tr>
<tr><td>Rsa1.0_00686.1.g18065.t1</td><td>ref|NP_565998.1| 3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 3 [Arabidopsis thaliana] gi|229890389|sp|A9X4U2.2|HSDD3_ARATH RecName: Full=3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 3; Short=At3BETAHSD/D3; AltName: Full=4alpha-carboxysterol-C3-dehydrogenase/C4- decarboxylase isoform 1-3; AltName: Full=Reticulon-like protein B20; Short=AtRTNLB20; AltName: Full=Sterol-4-alpha-carboxylate 3-dehydrogenase 3, decarboxylating gi|15027969|gb|AAK76515.1| putative sterol dehydrogenase [Arabidopsis thaliana] gi|20196859|gb|AAB64337.2| putative sterol dehydrogenase [Arabidopsis thaliana] gi|26450922|dbj|BAC42568.1| putative sterol dehydrogenase [Arabidopsis thaliana] gi|330255172|gb|AEC10266.1| 3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 3 [Arabidopsis thaliana]</td><td>606</td><td>561</td><td>0</td><td>92.6</td><td>79.9</td><td>85.1</td><td>3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G43420.1 | Symbols: | 3-beta hydroxysteroid dehydrogenase/isomerase family protein | chr2:18031493-18034936 REVERSE LENGTH=561</td><td>606</td><td>561</td><td>0</td><td>92.6</td><td>79.9</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00686.1.g18066.t3</td><td>ref|NP_565999.1| Hydroxyacylglutathione hydrolase 1 [Arabidopsis thaliana] gi|21264419|sp|O24495.2|GLO2M_ARATH RecName: Full=Hydroxyacylglutathione hydrolase 1, mitochondrial; AltName: Full=Glyoxalase II; Short=Glx II; Flags: Precursor gi|2570338|gb|AAC49865.1| glyoxalase II isozyme [Arabidopsis thaliana] gi|17380664|gb|AAL36162.1| putative glyoxalase II [Arabidopsis thaliana] gi|20196860|gb|AAB64315.2| putative glyoxalase II [Arabidopsis thaliana] gi|20259003|gb|AAM14217.1| putative glyoxalase II [Arabidopsis thaliana] gi|330255174|gb|AEC10268.1| Hydroxyacylglutathione hydrolase 1 [Arabidopsis thaliana]</td><td>337</td><td>331</td><td>1.00E-177</td><td>98.2</td><td>88.7</td><td>94.4</td><td>Hydroxyacylglutathione hydrolase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G43430.1 | Symbols: GLX2-1, GLY1 | glyoxalase 2-1 | chr2:18035569-18038064 REVERSE LENGTH=331</td><td>337</td><td>331</td><td>1.00E-180</td><td>98.2</td><td>88.7</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00686.1.g18067.t1</td><td>ref|NP_001154572.1| RNA-binding ASCH domain protein [Arabidopsis thaliana] gi|330255179|gb|AEC10273.1| RNA-binding ASCH domain protein [Arabidopsis thaliana]</td><td>477</td><td>388</td><td>1.00E-154</td><td>81.3</td><td>57.7</td><td>65.0</td><td>RNA-binding ASCH domain protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G43465.1 | Symbols: | RNA-binding ASCH domain protein | chr2:18047732-18049709 REVERSE LENGTH=388</td><td>477</td><td>388</td><td>1.00E-156</td><td>81.3</td><td>57.7</td><td>65.0</td></tr>
<tr><td>Rsa1.0_00686.1.g18068.t1</td><td>ref|NP_181875.5| uncharacterized protein [Arabidopsis thaliana] gi|330255180|gb|AEC10274.1| uncharacterized protein AT2G43470 [Arabidopsis thaliana]</td><td>245</td><td>210</td><td>2.00E-32</td><td>85.7</td><td>36.7</td><td>48.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G43470.1 | Symbols: | Protein of unknown function (DUF3755) | chr2:18049944-18051218 REVERSE LENGTH=210</td><td>245</td><td>210</td><td>4.00E-35</td><td>85.7</td><td>36.7</td><td>48.2</td></tr>
</table>

Rsa1.0_00687.1.g18069.t1	ref|NP_565065.1| uncharacterized protein [Arabidopsis thaliana] gi|21593462|gb|AAM65429.1| unknown [Arabidopsis thaliana] gi|124301178|gb|ABN04841.1| At1g73470 [Arabidopsis thaliana] gi|332197343|gb|AEE35464.1| uncharacterized protein AT1G73470 [Arabidopsis thaliana]	358	351	1.00E−165	98.0	83.0	90.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G73470.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 72 Blast hits to 72 proteins in 35 species: Archae − 0; Bacteria − 50; Metazoa − 0; Fungi − 0; Plants − 22; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:27625208−27627604 FORWARD LENGTH=351	358	351	1.00E−168	98.0	83.0	90.2
Rsa1.0_00687.1.g18070.t26	ref|XP_002887484.1| hypothetical protein ARALYDRAFT_895203 [Arabidopsis lyrata subsp. lyrata] gi|297333325|gb|EFH63743.1| hypothetical protein ARALYDRAFT_895203 [Arabidopsis lyrata subsp. lyrata]	808	784	0	97.0	84.7	87.5	hypothetical protein ARALYDRAFT_895203	gbpln	Arabidopsis lyrata	AT1G73430.2 | Symbols: | sec34−like family protein | chr1:27604096−27610829 FORWARD LENGTH=784	808	784	0	97.0	84.3	87.1
Rsa1.0_00687.1.g18071.t1	ref|NP_177484.1| myb domain protein 54 [Arabidopsis thaliana] gi|11120806|gb|AAG30986.1|AC012396_22 myb−like transcription factor, putative [Arabidopsis thaliana] gi|41619168|gb|AAS10039.1| MYB transcription factor [Arabidopsis thaliana] gi|89111924|gb|ABD60734.1| At1g73410 [Arabidopsis thaliana] gi|110743027|dbj|BAE99406.1| hypothetical protein [Arabidopsis thaliana] gi|332197337|gb|AEE35458.1| myb domain protein 54 [Arabidopsis thaliana]	234	243	1.00E−106	103.8	86.3	91.9	myb domain protein 54	gbpln	Arabidopsis thaliana	AT1G73410.1 | Symbols: ATMYB54, MYB54 | myb domain protein 54 | chr1:27601852−27603038 FORWARD LENGTH=243	234	243	1.00E−108	103.8	86.3	91.9
Rsa1.0_00687.1.g18072.t1	gb|EOA35177.1| hypothetical protein CARUB_v10020322mg [Capsella rubella]	433	431	1.00E−163	99.5	71.8	82.4	hypothetical protein CARUB_v10020322mg	gbpln	Capsella rubella	AT1G73380.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1308 (InterPro:IPR010733); Has 162 Blast hits to 160 proteins in 67 species: Archae − 0; Bacteria − 2; Metazoa − 120; Fungi − 0; Plants − 34; Viruses − 0; Other Eukaryotes − 6 (source: NCBI BLink). | chr1:27589100−27590657 FORWARD LENGTH=434	433	434	1.00E−154	100.2	71.6	80.6
Rsa1.0_00687.1.g18073.t1	gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]	206	214	3.00E−61	103.9	60.2	72.8	trypsin inhibitor propeptide	gbpln	Brassica oleracea	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410−27548057 REVERSE LENGTH=215	206	215	4.00E−48	104.4	51.0	64.6
Rsa1.0_00687.1.g18074.t1	gb|AAB68964.1| trypsin inhibitor propeptide [Brassica oleracea]	209	214	6.00E−73	102.4	68.9	77.0	trypsin inhibitor propeptide	gbpln	Brassica oleracea	AT1G73260.1 | Symbols: ATKTI1, KTI1 | kunitz trypsin inhibitor 1 | chr1:27547410−27548057 REVERSE LENGTH=215	209	215	4.00E−55	102.9	56.5	65.6
Rsa1.0_00687.1.g18075.t1	gb|EOA33228.1| hypothetical protein CARUB_v10021058mg [Capsella rubella] gi|482569041|gb|EOA33229.1| hypothetical protein CARUB_v10021058mg [Capsella rubella]	166	164	2.00E−73	98.8	91.6	93.4	hypothetical protein CARUB_v10021058mg	gbpln	Capsella rubella	AT1G73230.1 | Symbols: | Nascent polypeptide−associated complex NAC | chr1:27540506−27541364 REVERSE LENGTH=165	166	165	2.00E−74	99.4	91.6	93.4
Rsa1.0_00687.1.g18076.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838−20266 [Arabidopsis thaliana]	367	1142	2.00E−85	311.2	47.1	59.9	reverse transcriptase, putative; 16838−20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	367	575	2.00E−35	156.7	27.5	48.5
Rsa1.0_00687.1.g18077.t1	ref|NP_565059.2| organic cation/carnitine transporter1 [Arabidopsis thaliana] gi|75262291|sp|Q9CAT6.1|OCT1_ARATH RecName: Full=Organic cation/carnitine transporter 1; Short=AtOCT1 gi|12324316|gb|AAG52125.1|AC010556_7 putative transporter; 29320−27598 [Arabidopsis thaliana] gi|27311699|gb|AAO00815.1| putative transporter [Arabidopsis thaliana] gi|31711954|gb|AAP68333.1| At1g73220 [Arabidopsis thaliana] gi|332197310|gb|AEE35431.1| organic cation/carnitine transporter1 [Arabidopsis thaliana]	538	539	0	100.2	86.8	92.4	organic cation/carnitine transporter1	gbpln	Arabidopsis thaliana	AT1G73220.1 | Symbols: AtOCT1, 1−Oct | organic cation/carnitine transporter1 | chr1:27538387−27540109 FORWARD LENGTH=539	538	539	0	100.2	86.8	92.4

Rsa1.0_00687.1.g18078.t1	ref|NP_565059.2| organic cation/carnitine transporter1 [Arabidopsis thaliana] gi|75262291|sp|Q9CAT6.1|OCT1_ARATH RecName: Full=Organic cation/carnitine transporter 1; Short=AtOCT1 gi|12324316|gb|AAG52125.1|AC010556_7 putative transporter; 29320-27598 [Arabidopsis thaliana] gi|27311699|gb|AAO00815.1| putative transporter [Arabidopsis thaliana] gi|31711954|gb|AAP68333.1| At1g73220 [Arabidopsis thaliana] gi|332197310|gb|AEE35431.1| organic cation/carnitine transporter1 [Arabidopsis thaliana]	536	539	0	100.6	87.9	93.3	organic cation/carnitine transporter1	gbpln	Arabidopsis thaliana	AT1G73220.1 | Symbols: AtOCT1, 1-Oct | organic cation/carnitine transporter1 | chr1:27538387-27540109 FORWARD LENGTH=539	536	539	0	100.6	87.9	93.3
Rsa1.0_00687.1.g18079.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00688.1.g18080.t12	gb|EOA28251.1| hypothetical protein CARUB_v10024444mg [Capsella rubella]	78	78	9.00E-34	100.0	96.2	98.7	hypothetical protein CARUB_v10024444mg	gbpln	Capsella rubella	AT2G21820.1 | Symbols: | unknown protein; Has 45 Blast hits to 45 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9302983-9303219 REVERSE LENGTH=78	78	78	5.00E-36	100.0	94.9	97.4
Rsa1.0_00688.1.g18081.t2	gb|ACT33453.1| mercapto-pyruvate sulfurtransferase 1 [Brassica napus]	376	379	0	100.8	88.0	95.2	mercapto-pyruvate sulfurtransferase 1	gbpln	Brassica napus	AT1G79230.1 | Symbols: ST1, ATMST1, MST1, ATRDH1, STR1 | mercaptopyruvate sulfurtransferase 1 | chr1:29800824-29803679 FORWARD LENGTH=379	376	379	0	100.8	85.4	92.0
Rsa1.0_00688.1.g18082.t1	ref|XP_002887773.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297333614|gb|EFH64032.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata]	411	405	1.00E-163	98.5	72.5	83.0	mitochondrial transcription termination factor family protein	gbpln	Arabidopsis lyrata	AT1G79220.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:29799227-29800426 FORWARD LENGTH=399	411	399	1.00E-160	97.1	71.8	82.0
Rsa1.0_00688.1.g18083.t1	ref|NP_173096.1| proteasome subunit alpha type-2-A [Arabidopsis thaliana] gi|79318062|ref|NP_001031057.1| proteasome subunit alpha type-2-A [Arabidopsis thaliana] gi|6093778|sp|O23708.1|PSA2A_ARATH RecName: Full=Proteasome subunit alpha type-2-A; AltName: Full=20S proteasome alpha subunit B; AltName: Full=Proteasome component 3 gi|4966368|gb|AAD34699.1|AC006341_27 Identical to gb|Y13176 Arabidopsis thaliana mRNA for proteasome subunit prc3. ESTs gb|H36972, gb|T22551 and gb|T13800 come from this gene [Arabidopsis thaliana] gi|12083342|gb|AAG48830.1|AF332467_1 putative multicatalytic endopeptidase [Arabidopsis thaliana] gi|2511574|emb|CAA73619.1| multicatalytic endopeptidase [Arabidopsis thaliana] gi|3421075|gb|AAC32056.1| 20S proteasome subunit PAB1 [Arabidopsis thaliana] gi|21617900|gb|AAM66950.1| multicatalytic endopeptidase [Arabidopsis thaliana] gi|222423615|dbj|BAH19776.1| AT1G16470 [Arabidopsis thaliana] gi|222424243|dbj|BAH20079.1| AT1G16470 [Arabidopsis thaliana] gi|332191336|gb|AEE29457.1| proteasome subunit alpha type-2-A [Arabidopsis thaliana]	235	235	1.00E-132	100.0	99.6	99.6	proteasome subunit alpha type-2-A	gbpln	Arabidopsis thaliana	AT1G16470.2 | Symbols: PAB1 | proteasome subunit PAB1 | chr1:5623122-5625439 FORWARD LENGTH=235	235	235	1.00E-135	100.0	99.6	99.6
Rsa1.0_00688.1.g18084.t1	gb|EOA35828.1| hypothetical protein CARUB_v10021069mg [Capsella rubella]	159	162	3.00E-50	101.9	78.0	84.9	hypothetical protein CARUB_v10021069mg	gbpln	Capsella rubella	AT1G79200.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:29794404-29795711 FORWARD LENGTH=159	159	159	4.00E-47	100.0	76.7	83.0
Rsa1.0_00688.1.g18085.t4	gb|AAC17063.1| YUP8H12R.20 [Arabidopsis thaliana]	404	1325	2.00E-42	328.0	24.5	29.0	YUP8H12R.20	gbpln	Arabidopsis thaliana	AT1G79190.1 | Symbols: | ARM repeat superfamily protein | chr1:29788639-29794116 FORWARD LENGTH=1335	404	1335	2.00E-44	330.4	24.3	28.5

Rsa1.0_00688.1.g18086.t1	ref|XP_002887770.1| hypothetical protein ARALYDRAFT_477086 [Arabidopsis lyrata subsp. lyrata] gi|297333611|gb|EFH64029.1| hypothetical protein ARALYDRAFT_477086 [Arabidopsis lyrata subsp. lyrata]	282	290	1.00E-115	102.8	81.2	88.3	hypothetical protein ARALYDRAFT_477086	gbpln	Arabidopsis lyrata	AT1G79180.1 | Symbols: ATMYB63, MYB63 | myb domain protein 63 | chr1:29786509-29787589 FORWARD LENGTH=294	282	294	1.00E-112	104.3	80.5	88.7
Rsa1.0_00688.1.g18087.t1	ref|XP_002889235.1| hypothetical protein ARALYDRAFT_316812 [Arabidopsis lyrata subsp. lyrata] gi|297335076|gb|EFH65494.1| hypothetical protein ARALYDRAFT_316812 [Arabidopsis lyrata subsp. lyrata]	240	238	1.00E-87	99.2	80.0	85.0	hypothetical protein ARALYDRAFT_316812	gbpln	Arabidopsis lyrata	AT1G79160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16500.1); Has 104 Blast hits to 102 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:29779862-29780668 REVERSE LENGTH=239	240	239	1.00E-80	99.6	77.1	82.5
Rsa1.0_00688.1.g18088.t3	ref|XP_002889234.1| hypothetical protein ARALYDRAFT_895820 [Arabidopsis lyrata subsp. lyrata] gi|297335075|gb|EFH65493.1| hypothetical protein ARALYDRAFT_895820 [Arabidopsis lyrata subsp. lyrata]	863	826	0	95.7	79.5	86.9	hypothetical protein ARALYDRAFT_895820	gbpln	Arabidopsis lyrata	AT1G79150.1 | Symbols: | binding | chr1:29772716-29777874 REVERSE LENGTH=830	863	830	0	96.2	77.4	86.0
Rsa1.0_00688.1.g18089.t1	ref|NP_178034.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|3152585|gb|AAC17066.1| Contains similarity to auxin-induced protein TM018A10.6 from A. thaliana BAC gb|AF013294 [Arabidopsis thaliana] gi|89001087|gb|ABD59133.1| At1g79130 [Arabidopsis thaliana] gi|332198087|gb|AEE36208.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	141	134	1.00E-43	95.0	67.4	75.9	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT1G79130.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:29771319-29771723 FORWARD LENGTH=134	141	134	3.00E-46	95.0	67.4	75.9
Rsa1.0_00688.1.g18090.t1	ref|XP_002889232.1| hypothetical protein ARALYDRAFT_477083 [Arabidopsis lyrata subsp. lyrata] gi|297335073|gb|EFH65491.1| hypothetical protein ARALYDRAFT_477083 [Arabidopsis lyrata subsp. lyrata]	376	377	0	100.3	88.6	93.6	hypothetical protein ARALYDRAFT_477083	gbpln	Arabidopsis lyrata	AT1G79120.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr1:29767314-29768555 REVERSE LENGTH=413	376	413	0	109.8	86.7	93.4
Rsa1.0_00688.1.g18091.t1	ref|XP_002887768.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297333609|gb|EFH64027.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	314	346	1.00E-108	110.2	71.3	81.8	protein binding protein	gbpln	Arabidopsis lyrata	AT1G79110.2 | Symbols: | zinc ion binding | chr1:29759345-29760586 FORWARD LENGTH=355	314	355	1.00E-104	113.1	70.1	79.3
Rsa1.0_00688.1.g18092.t1	ref|XP_002889230.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335071|gb|EFH65489.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	550	580	0	105.5	86.2	94.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G79080.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:29747102-29748832 REVERSE LENGTH=576	550	576	0	104.7	84.7	92.9
Rsa1.0_00688.1.g18093.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00689.1.g18094.t1	ref|XP_002892398.1| hypothetical protein ARALYDRAFT_470764 [Arabidopsis lyrata subsp. lyrata] gi|297338240|gb|EFH68657.1| hypothetical protein ARALYDRAFT_470764 [Arabidopsis lyrata subsp. lyrata]	438	437	0	99.8	78.3	84.2	hypothetical protein ARALYDRAFT_470764	gbpln	Arabidopsis lyrata	AT1G07430.1 | Symbols: HAI2 | highly ABA-induced PP2C gene 2 | chr1:2281151-2282656 REVERSE LENGTH=442	438	442	0	100.9	79.0	85.8
Rsa1.0_00689.1.g18095.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00689.1.g18096.t1	ref|XP_002889647.1| sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata] gi|297335489|gb|EFH65906.1| sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata]	204	266	2.00E-70	130.4	62.7	63.7	sterol 4-alpha-methyl-oxidase 2	gbpln	Arabidopsis lyrata	AT1G07420.1 | Symbols: ATSMO2, SMO2-1 | sterol 4-alpha-methyl-oxidase 2-1 | chr1:2277910-2280033 FORWARD LENGTH=266	204	266	6.00E-72	130.4	62.3	63.2
Rsa1.0_00689.1.g18097.t1	gb|EOA39531.1| hypothetical protein CARUB_v10008151mg [Capsella rubella]	1067	1078	0	101.0	80.9	88.1	hypothetical protein CARUB_v10008151mg	gbpln	Capsella rubella	AT1G07390.1 | Symbols: AtRLP1, RLP1 | receptor like protein 1 | chr1:2269893-2274654 FORWARD LENGTH=1034	1067	1034	0	96.9	78.7	85.1
Rsa1.0_00689.1.g18098.t1	sp|Q43124.1|PCNA_BRANA RecName: Full=Proliferating cell nuclear antigen; Short=PCNA gi|408232|gb|AAB27811.1| PCNA [Brassica napus]	264	263	1.00E-148	99.6	97.3	98.1	RecName: Full=Proliferating cell nuclear antigen; Short=PCNA gi|408232|gb|AAB27811.1| PCNA	gbpln	Brassica napus	AT1G07370.1 | Symbols: PCNA1, ATPCNA1 | proliferating cellular nuclear antigen 1 | chr1:2263204-2264382 FORWARD LENGTH=263	264	263	1.00E-149	99.6	98.1	98.1
Rsa1.0_00689.1.g18099.t1	gb|EOA38384.1| hypothetical protein CARUB_v10009944mg [Capsella rubella]	228	283	1.00E-56	124.1	52.6	55.7	hypothetical protein CARUB_v10009944mg	gbpln	Capsella rubella	AT1G07320.2 | Symbols: RPL4 | ribosomal protein L4 | chr1:2249190-2250189 FORWARD LENGTH=280	228	280	5.00E-56	122.8	50.4	55.3

<table>
<tr><td>Rsa1.0_00689.1.g18100.t1</td><td>gb|EOA38103.1| hypothetical protein CARUB_v10009572mg [Capsella rubella]</td><td>341</td><td>355</td><td>1.00E-105</td><td>104.1</td><td>70.7</td><td>77.7</td><td>hypothetical protein CARUB_v10009572mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G07310.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:2247775-2248833 REVERSE LENGTH=352</td><td>341</td><td>352</td><td>1.00E-103</td><td>103.2</td><td>71.6</td><td>77.7</td></tr>
<tr><td>Rsa1.0_00689.1.g18101.t1</td><td>ref|NP_172210.1| josephin protein-like protein [Arabidopsis thaliana] gi|38454076|gb|AAR20732.1| At1g07300 [Arabidopsis thaliana] gi|38603992|gb|AAR24739.1| At1g07300 [Arabidopsis thaliana] gi|332189983|gb|AEE28104.1| josephin protein-like protein [Arabidopsis thaliana]</td><td>131</td><td>128</td><td>1.00E-46</td><td>97.7</td><td>74.0</td><td>80.9</td><td>josephin protein-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G07300.1 | Symbols: | josephin protein-related | chr1:2245914-2246300 REVERSE LENGTH=128</td><td>131</td><td>128</td><td>3.00E-49</td><td>97.7</td><td>74.0</td><td>80.9</td></tr>
<tr><td>Rsa1.0_00689.1.g18102.t1</td><td>gb|EOA38012.1| hypothetical protein CARUB_v10009481mg [Capsella rubella]</td><td>376</td><td>372</td><td>0</td><td>98.9</td><td>87.5</td><td>93.1</td><td>hypothetical protein CARUB_v10009481mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G07290.1 | Symbols: GONST2 | golgi nucleotide sugar transporter 2 | chr1:2242284-2244428 REVERSE LENGTH=375</td><td>376</td><td>375</td><td>0</td><td>99.7</td><td>87.8</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00689.1.g18103.t1</td><td>ref|NP_563784.2| UDP-glucosyl transferase 71C4 [Arabidopsis thaliana] gi|75311371|sp|Q9LML6.2|U71C4_ARATH RecName: Full=UDP-glycosyltransferase 71C4; AltName: Full=Flavonol 3-O-glucosyltransferase UGT71C4; AltName: Full=Flavonol 7-O-glucosyltransferase UGT71C4 gi|10567858|gb|AAG18592.1|AC067971_33 Contains similarity to an unknown flavonol 3-o-glucosyltransferase At2g29750 gi|3582329 from Arabidopsis thaliana BAC T27A16 gb|AC005496. It contains a UDP-glucoronosyl and UDP-glucosyl transferases domain PF|00201. ESTs gb|AI993795, gb|N97301 and gb|Z18063 come from this gene [Arabidopsis thaliana] gi|25054917|gb|AAN71937.1| putative UDP-glucose glucosyltransferase [Arabidopsis thaliana] gi|332189976|gb|AEE28097.1| UDP-glucosyl transferase 71C4 [Arabidopsis thaliana]</td><td>476</td><td>479</td><td>0</td><td>100.6</td><td>79.0</td><td>88.7</td><td>UDP-glucosyl transferase 71C4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G07250.1 | Symbols: UGT71C4 | UDP-glucosyl transferase 71C4 | chr1:2225963-2227402 FORWARD LENGTH=479</td><td>476</td><td>479</td><td>0</td><td>100.6</td><td>79.0</td><td>88.7</td></tr>
<tr><td>Rsa1.0_00689.1.g18104.t1</td><td>ref|NP_172204.1| UDP-glucosyl transferase 71C5 [Arabidopsis thaliana] gi|75308970|sp|Q9FE68.1|U71C5_ARATH RecName: Full=UDP-glycosyltransferase 71C5 gi|10567857|gb|AAG18591.1|AC067971_4 Contains similarity to an unknown flavonol 3-o-glucosyltransferase At2g29750 gi|3582329 from Arabidopsis thaliana BAC T27A16 gb|AC005496. It contains a UDP-glucoronosyl and UDP-glucosyl transferases domain PF|00201. ESTs gb|AI997635, gb|T13644, gb|AV546216 and gb|AI996826 come from this gene [Arabidopsis thaliana] gi|12083248|gb|AAG48783.1|AF332420_1 putative UDP-glucose glucosyltransferase [Arabidopsis thaliana] gi|17473894|gb|AAL38366.1| unknown protein [Arabidopsis thaliana] gi|20259790|gb|AAM13242.1| unknown protein [Arabidopsis thaliana] gi|21594310|gb|AAM65993.1| UDP-glucose glucosyltransferase, putative [Arabidopsis thaliana] gi|332189975|gb|AEE28096.1| UDP-glucosyl transferase 71C5 [Arabidopsis thaliana]</td><td>275</td><td>480</td><td>8.00E-15</td><td>174.5</td><td>22.2</td><td>28.7</td><td>UDP-glucosyl transferase 71C5</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G07240.1 | Symbols: UGT71C5 | UDP-glucosyl transferase 71C5 | chr1:2223889-2225331 FORWARD LENGTH=480</td><td>275</td><td>480</td><td>2.00E-17</td><td>174.5</td><td>22.2</td><td>28.7</td></tr>
<tr><td>Rsa1.0_00689.1.g18105.t1</td><td>gb|EOA40174.1| hypothetical protein CARUB_v10008891mg [Capsella rubella]</td><td>505</td><td>509</td><td>0</td><td>100.8</td><td>88.5</td><td>94.3</td><td>hypothetical protein CARUB_v10008891mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G07220.1 | Symbols: | Arabidopsis thaliana protein of unknown function (DUF821) | chr1:2217073-2219379 REVERSE LENGTH=507</td><td>505</td><td>507</td><td>0</td><td>100.4</td><td>85.9</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00689.1.g18106.t1</td><td>gb|EOA38264.1| hypothetical protein CARUB_v10009750mg [Capsella rubella]</td><td>288</td><td>323</td><td>2.00E-84</td><td>112.2</td><td>63.2</td><td>74.7</td><td>hypothetical protein CARUB_v10009750mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G07210.1 | Symbols: | Ribosomal protein S18 | chr1:2215320-2216668 FORWARD LENGTH=261</td><td>288</td><td>261</td><td>4.00E-81</td><td>90.6</td><td>60.4</td><td>71.9</td></tr>
</table>

Rsa1.0_00689.1.g18107.t1	ref|XP_002892387.1| hypothetical protein ARALYDRAFT_311783 [Arabidopsis lyrata subsp. lyrata] gi|297338229|gb|EFH68646.1| hypothetical protein ARALYDRAFT_311783 [Arabidopsis lyrata subsp. lyrata]	948	977	0	103.1	77.3	85.8	hypothetical protein ARALYDRAFT_311783	gbpln	Arabidopsis lyrata	AT1G07200.2 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr1:2209033-2212316 REVERSE LENGTH=979	948	979	0	103.3	75.7	84.1
Rsa1.0_00689.1.g18108.t2	ref|NP_174267.4| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|332193002|gb|AEE31123.1| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana]	986	1078	0	109.3	85.5	92.6	Leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT1G29740.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10407379-10412997 REVERSE LENGTH=1078	986	1078	0	109.3	85.5	92.6
Rsa1.0_00690.1.g18109.t3	gb|EOA36640.1| hypothetical protein CARUB_v10011892mg [Capsella rubella]	819	1530	0	186.8	92.2	95.8	hypothetical protein CARUB_v10011892mg	gbpln	Capsella rubella	AT1G08730.1 | Symbols: XIC, ATXIC | Myosin family protein with Dil domain | chr1:2779963-2788325 FORWARD LENGTH=1538	819	1538	0	187.8	92.2	96.2
Rsa1.0_00690.1.g18110.t1	ref|NP_563825.1| peptidase C13-like protein [Arabidopsis thaliana] gi|30680805|ref|NP_849616.1| peptidase C13-like protein [Arabidopsis thaliana] gi|42571407|ref|NP_973794.1| peptidase C13-like protein [Arabidopsis thaliana] gi|26450273|dbj|BAC42253.1| putative GPI-anchor transamidase [Arabidopsis thaliana] gi|332190220|gb|AEE28341.1| peptidase C13-like protein [Arabidopsis thaliana] gi|332190221|gb|AEE28342.1| peptidase C13-like protein [Arabidopsis thaliana] gi|332190222|gb|AEE28343.1| peptidase C13-like protein [Arabidopsis thaliana]	392	388	0	99.0	87.8	92.9	peptidase C13-like protein	gbpln	Arabidopsis thaliana	AT1G08750.3 | Symbols: | Peptidase C13 family | chr1:2801283-2804392 FORWARD LENGTH=388	392	388	0	99.0	87.8	92.9
Rsa1.0_00690.1.g18111.t1	dbj|BAJ34479.1| unnamed protein product [Thellungiella halophila]	939	760	0	80.9	63.8	69.2	unnamed protein product	----	----	AT1G08760.1 | Symbols: | Plant protein of unknown function (DUF936) | chr1:2805478-2808409 FORWARD LENGTH=748	939	748	0	79.7	61.1	66.9
Rsa1.0_00690.1.g18112.t1	ref|XP_002892471.1| hypothetical protein ARALYDRAFT_334161 [Arabidopsis lyrata subsp. lyrata] gi|297338313|gb|EFH68730.1| hypothetical protein ARALYDRAFT_334161 [Arabidopsis lyrata subsp. lyrata]	142	129	1.00E-57	90.8	76.1	84.5	hypothetical protein ARALYDRAFT_334161	gbpln	Arabidopsis lyrata	AT1G08780.1 | Symbols: AIP3, PFD4 | ABI3-interacting protein 3 | chr1:2809925-2811126 REVERSE LENGTH=129	142	129	9.00E-60	90.8	76.1	83.1
Rsa1.0_00690.1.g18113.t1	ref|XP_002889715.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335557|gb|EFH65974.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	197	190	4.00E-73	96.4	84.3	88.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G08790.1 | Symbols: | Protein of unknown function (DUF1685) | chr1:2811989-2812646 FORWARD LENGTH=190	197	190	3.00E-75	96.4	84.3	87.8
Rsa1.0_00690.1.g18114.t1	gb|EOA39537.1| hypothetical protein CARUB_v10008154mg [Capsella rubella] gi|482575351|gb|EOA39538.1| hypothetical protein CARUB_v10008154mg [Capsella rubella]	890	1073	0	120.6	66.4	77.5	hypothetical protein CARUB_v10008154mg	gbpln	Capsella rubella	AT1G08800.2 | Symbols: | Protein of unknown function, DUF593 | chr1:2813578-2817078 REVERSE LENGTH=1113	890	1113	0	125.1	52.8	61.9
Rsa1.0_00690.1.g18115.t2	ref|NP_172359.2| vamp/synaptobrevin-associated protein 27-2 [Arabidopsis thaliana] gi|79317397|ref|NP_001031004.1| vamp/synaptobrevin-associated protein 27-2 [Arabidopsis thaliana] gi|313471716|sp|B9DHD7.1|VAP22_ARATH RecName: Full=Vesicle-associated protein 2-2; AltName: Full=Plant VAP homolog 22; Short=AtPVA22; AltName: Full=VAMP-associated protein 2-2; AltName: Full=Vesicle-associated protein 27-2 gi|222424397|dbj|BAH20154.1| AT1G08820 [Arabidopsis thaliana] gi|222424668|dbj|BAH20288.1| AT1G08820 [Arabidopsis thaliana] gi|332190231|gb|AEE28352.1| vamp/synaptobrevin-associated protein 27-2 [Arabidopsis thaliana] gi|332190232|gb|AEE28353.1| vamp/synaptobrevin-associated protein 27-2 [Arabidopsis thaliana]	424	386	1.00E-157	91.0	68.2	75.5	vamp/synaptobrevin-associated protein 27-2	gbpln	Arabidopsis thaliana	AT1G08820.2 | Symbols: VAP27-2 | vamp/synaptobrevin-associated protein 27-2 | chr1:2821810-2824412 REVERSE LENGTH=386	424	386	1.00E-160	91.0	68.2	75.5
Rsa1.0_00690.1.g18116.t1	ref|NP_001154322.1| Ribosomal L.8/L5e family protein [Arabidopsis thaliana] gi|332190238|gb|AEE28359.1| Ribosomal L.8/L5e family protein [Arabidopsis thaliana]	375	234	4.00E-97	62.4	46.4	48.0	Ribosomal L.8/L5e family protein	gbpln	Arabidopsis thaliana	AT1G08845.2 | Symbols: | Ribosomal L18p/L5e family protein | chr1:2838789-2840955 FORWARD LENGTH=234	375	234	1.00E-99	62.4	46.4	48.0

Rsa1.0_00690.1.g18117.t1	ref|XP_002892475.1| hypothetical protein ARALYDRAFT_888122 [Arabidopsis lyrata subsp. lyrata] gi|297338317|gb|EFH68734.1| hypothetical protein ARALYDRAFT_888122 [Arabidopsis lyrata subsp. lyrata]	142	142	8.00E-73	100.0	97.9	98.6	hypothetical protein ARALYDRAFT_888122	gbpln	Arabidopsis lyrata	AT1G08880.1 | Symbols: HTA5, H2AXA, G-H2AX, GAMMA-H2AX | Histone superfamily protein | chr1:2847144-2847676 REVERSE LENGTH=142	142	142	2.00E-74	100.0	96.5	97.9
Rsa1.0_00690.1.g18118.t1	ref|XP_002889721.1| EMB3001 [Arabidopsis lyrata subsp. lyrata] gi|297335563|gb|EFH65980.1| EMB3001 [Arabidopsis lyrata subsp. lyrata]	688	836	1.00E-163	121.5	47.4	54.9	EMB3001	gbpln	Arabidopsis lyrata	AT1G08910.1 | Symbols: EMB3001 | zinc ion binding;zinc ion binding | chr1:2856227-2860816 FORWARD LENGTH=829	688	829	1.00E-147	120.5	44.6	53.6
Rsa1.0_00690.1.g18119.t1	ref|NP_563829.1| sugar transporter ERD6-like 3 [Arabidopsis thaliana] gi|75332302|sp|Q94KE0.1|ERDL3_ARATH RecName: Full=Sugar transporter ERD6-like 3; AltName: Full=Sugar transporter-like protein 2 gi|14194109|gb|AAK56249.1|AF367260_1 At1g08920/F7G19_20 [Arabidopsis thaliana] gi|22137064|gb|AAM91377.1| At1g08920/F7G19_20 [Arabidopsis thaliana] gi|169403716|emb|CAQ16329.1| hexose transporter-like protein [Arabidopsis thaliana] gi|332190246|gb|AEE28367.1| sugar transporter ERD6-like 3 [Arabidopsis thaliana]	470	470	0	100.0	90.0	94.5	sugar transporter ERD6-like 3	gbpln	Arabidopsis thaliana	AT1G08920.1 | Symbols: ESL1 | ERD (early response to dehydration) six-like 1 | chr1:2867446-2870360 FORWARD LENGTH=470	470	470	0	100.0	90.0	94.5
Rsa1.0_00690.1.g18120.t1	ref|XP_002889723.1| hypothetical protein ARALYDRAFT_888127 [Arabidopsis lyrata subsp. lyrata] gi|297335565|gb|EFH65982.1| hypothetical protein ARALYDRAFT_888127 [Arabidopsis lyrata subsp. lyrata]	481	496	0	103.1	86.5	92.9	hypothetical protein ARALYDRAFT_888127	gbpln	Arabidopsis lyrata	AT1G08930.2 | Symbols: ERD6 | Major facilitator superfamily protein | chr1:2873604-2876979 FORWARD LENGTH=496	481	496	0	103.1	86.1	93.3
Rsa1.0_00690.1.g18121.t1	ref|NP_172369.1| Phosphoglycerate mutase-like protein [Arabidopsis thaliana] gi|2342686|gb|AAB70412.1| Similar to Saccharomyces hypothetical protein YDR051c (gb|Z49209). ESTs gb|T44436,gb|42252 come from this gene [Arabidopsis thaliana] gi|332190251|gb|AEE28372.1| Phosphoglycerate mutase-like protein [Arabidopsis thaliana]	280	281	2.33E-156	100.4	89.3	93.9	Phosphoglycerate mutase-like protein	gbpln	Arabidopsis thaliana	AT1G08940.1 | Symbols: | Phosphoglycerate mutase family protein | chr1:2877694-2879104 FORWARD LENGTH=281	280	281	1.00E-148	100.4	89.3	93.9
Rsa1.0_00690.1.g18122.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00690.1.g18123.t1	ref|XP_002892478.1| hypothetical protein ARALYDRAFT_888138 [Arabidopsis lyrata subsp. lyrata] gi|297338320|gb|EFH68737.1| hypothetical protein ARALYDRAFT_888138 [Arabidopsis lyrata subsp. lyrata]	132	139	1.00E-56	105.3	80.3	83.3	hypothetical protein ARALYDRAFT_888138	gbpln	Arabidopsis lyrata	AT1G09030.1 | Symbols: NF-YB4 | nuclear factor Y, subunit B4 | chr1:2908611-2909030 REVERSE LENGTH=139	132	139	6.00E-58	105.3	78.8	82.6
Rsa1.0_00690.1.g18124.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	390	390	7.00E-72	100.0	41.8	59.2	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	390	320	3.00E-29	82.1	22.1	32.8
Rsa1.0_00691.1.g18125.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00691.1.g18126.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00691.1.g18127.t2	dbj|BAB03186.1| En/Spm transposon protein-like [Arabidopsis thaliana]	1862	1516	0	81.4	30.6	35.3	En/Spm transposon protein-like	gbpln	Arabidopsis thaliana	AT1G40087.1 | Symbols: | Plant transposase (Ptta/En/Spm family) | chr1:14999762-15001868 REVERSE LENGTH=390	1862	390	5.00E-11	20.9	3.4	5.9
Rsa1.0_00691.1.g18128.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	211	1142	1.00E-35	541.2	40.8	56.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	211	575	1.00E-15	272.5	27.5	45.5
Rsa1.0_00691.1.g18129.t2	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	1040	190	4.00E-38	18.3	8.5	10.0	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00691.1.g18130.t2	gb|AAD32950.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	337	773	2.00E-22	229.4	21.1	27.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	337	575	5.00E-17	170.6	17.8	29.1
Rsa1.0_00691.1.g18131.t1	ref|NP_001119364.1| uncharacterized protein [Arabidopsis thaliana] gi|332007523|gb|AED94906.1| uncharacterized protein AT5G43066 [Arabidopsis thaliana]	80	74	7.00E-16	92.5	63.8	75.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G43066.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:17284583-17284807 FORWARD LENGTH=74	80	74	1.00E-18	92.5	63.8	75.0

Rsa1.0_00691.1.g18132.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00691.1.g18133.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00692.1.g18134.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1770	1213	0	68.5	25.1	37.0	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1770	626	1.00E-64	35.4	7.6	12.3
Rsa1.0_00692.1.g18135.t1	gb|AAG50886.1|AC025294_24 hypothetical protein [Arabidopsis thaliana]	419	629	9.00E-84	150.1	37.9	48.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	419	746	4.00E-59	178.0	27.0	36.8
Rsa1.0_00692.1.g18136.t2	gb|EOA35144.1| hypothetical protein CARUB_v10020279mg [Capsella rubella]	454	454	0	100.0	89.4	93.0	hypothetical protein CARUB_v10020279mg	gbpln	Capsella rubella	AT1G67320.2 | Symbols: | DNA primase, large subunit family | chr1:25205520-25208966 REVERSE LENGTH=454	454	454	0	100.0	88.8	92.7
Rsa1.0_00692.1.g18137.t1	ref|XP_002888589.1| calmodulin binding protein [Arabidopsis lyrata subsp. lyrata] gi|297334430|gb|EFH64848.1| calmodulin binding protein [Arabidopsis lyrata subsp. lyrata]	1069	1031	0	96.4	67.4	76.0	calmodulin binding protein	gbpln	Arabidopsis lyrata	AT1G67310.1 | Symbols: | Calmodulin-binding transcription activator protein with CG-1 and Ankyrin domains | chr1:25198182-25203126 REVERSE LENGTH=1016	1069	1016	0	95.0	64.8	74.0
Rsa1.0_00692.1.g18138.t1	ref|XP_002888587.1| hypothetical protein ARALYDRAFT_475824 [Arabidopsis lyrata subsp. lyrata] gi|297334428|gb|EFH64846.1| hypothetical protein ARALYDRAFT_475824 [Arabidopsis lyrata subsp. lyrata]	592	599	0	101.2	78.2	88.0	hypothetical protein ARALYDRAFT_475824	gbpln	Arabidopsis lyrata	AT1G67290.1 | Symbols: | glyoxal oxidase-related protein | chr1:25191168-25193160 REVERSE LENGTH=615	592	615	0	103.9	77.2	87.0
Rsa1.0_00692.1.g18139.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	386	1223	2.00E-72	316.8	37.3	55.2	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	386	746	9.00E-49	193.3	31.1	43.8
Rsa1.0_00692.1.g18140.t1	gb|EOA39471.1| hypothetical protein CARUB_v10008066mg [Capsella rubella]	2177	2170	0	99.7	85.8	92.2	hypothetical protein CARUB_v10008066mg	gbpln	Capsella rubella	AT1G20960.2 | Symbols: emb1507 | U5 small nuclear ribonucleoprotein helicase, putative | chr1:7302591-7309914 REVERSE LENGTH=2171	2177	2171	0	99.7	85.9	91.8
Rsa1.0_00692.1.g18141.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00692.1.g18142.t1	gb|EOA21678.1| hypothetical protein CARUB_v10002101mg [Capsella rubella]	173	172	2.00E-67	99.4	73.4	84.4	hypothetical protein CARUB_v10002101mg	gbpln	Capsella rubella	AT4G12340.1 | Symbols: | copper ion binding | chr4:7321492-7322004 REVERSE LENGTH=170	173	170	3.00E-60	98.3	69.4	79.2
Rsa1.0_00693.1.g18143.t1	dbj|BAJ34476.1| unnamed protein product [Thellungiella halophila]	170	172	3.00E-83	101.2	90.6	95.3	unnamed protein product	––––	––––	AT3G60690.1 | Symbols: | SAUR-like auxin-responsive protein family | chr3:22435262-22435774 FORWARD LENGTH=170	170	170	2.00E-81	100.0	85.3	92.4
Rsa1.0_00693.1.g18144.t1	ref|XP_002876575.1| hypothetical protein ARALYDRAFT_907600 [Arabidopsis lyrata subsp. lyrata] gi|297322413|gb|EFH52834.1| hypothetical protein ARALYDRAFT_907600 [Arabidopsis lyrata subsp. lyrata]	398	494	1.00E-141	124.1	74.4	84.2	hypothetical protein ARALYDRAFT_907600	gbpln	Arabidopsis lyrata	AT3G60680.1 | Symbols: | Plant protein of unknown function (DUF641) | chr3:22430246-22431745 FORWARD LENGTH=499	398	499	1.00E-143	125.4	71.9	82.2
Rsa1.0_00693.1.g18145.t1	ref|XP_002878345.1| hypothetical protein ARALYDRAFT_486540 [Arabidopsis lyrata subsp. lyrata] gi|297324183|gb|EFH54604.1| hypothetical protein ARALYDRAFT_486540 [Arabidopsis lyrata subsp. lyrata]	242	245	1.00E-116	101.2	84.7	90.9	hypothetical protein ARALYDRAFT_486540	gbpln	Arabidopsis lyrata	AT3G60670.1 | Symbols: | PLATZ transcription factor family protein | chr3:22424695-22426074 REVERSE LENGTH=245	242	245	1.00E-117	101.2	85.1	90.9
Rsa1.0_00693.1.g18146.t1	ref|NP_191622.1| scarecrow-like protein 22 [Arabidopsis thaliana] gi|75181377|sp|Q9M000.1|SCL22_ARATH RecName: Full=Scarecrow-like protein 22; Short=AtSCL22; AltName: Full=GRAS family protein 21; Short=AtGRAS-21; AltName: Full=SCL6-III gi|7329673|emb|CAB82667.1| scarecrow-like protein [Arabidopsis thaliana] gi|17381212|gb|AAL36418.1| putative scarecrow protein [Arabidopsis thaliana] gi|20465817|gb|AAM20013.1| putative scarecrow protein [Arabidopsis thaliana] gi|332646569|gb|AEE80090.1| scarecrow-like protein 22 [Arabidopsis thaliana]	588	623	0	106.0	72.8	82.5	scarecrow-like protein 22	gbpln	Arabidopsis thaliana	AT3G60630.1 | Symbols: HAM2, ATHAM2, LOM2 | GRAS family transcription factor | chr3:22410496-22412367 REVERSE LENGTH=623	588	623	0	106.0	72.8	82.5
Rsa1.0_00693.1.g18147.t1	#	#	#	#	#	#	#	–	––––	––––	AT2G45150.3 | Symbols: | cytidinediphosphate diacylglycerol synthase 4 | chr2:18613519-18615347 FORWARD LENGTH=382	76	382	2.00E-12	502.6	56.6	64.5

Rsa1.0_00693.1.g18148.t1	ref|NP_974468.1| uncharacterized protein [Arabidopsis thaliana] gi|332646561|gb|AEE80082.1| uncharacterized protein AT3G60590 [Arabidopsis thaliana]	384	404	1.00E−149	105.2	71.4	78.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G60590.3 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G48460.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr3:22398228−22399753 FORWARD LENGTH=404	384	404	1.00E−152	105.2	71.4	78.4
Rsa1.0_00693.1.g18149.t1	sp|Q9M203.2|EXPB5_ARATH RecName: Full=Expansin−B5; Short=At−EXPB5; Short=AtEXPB5; AltName: Full=Ath−ExpBeta−1.3; AltName: Full=Beta−expansin−5; Flags: Precursor	148	264	2.00E−62	178.4	77.0	87.8	RecName: Full=Expansin−B5; Short=At−EXPB5; Short=AtEXPB5; AltName: Full=Ath−ExpBeta−1.3; AltName: Full=Beta−expansin−5; Flags: Precursor	----	----	AT3G60570.1 | Symbols: ATEXPB5, EXPB5, ATHEXP BETA 1.3 | expansin B5 | chr3:22391247−22392463 FORWARD LENGTH=252	148	252	9.00E−63	170.3	74.3	85.1
Rsa1.0_00693.1.g18150.t1	ref|XP_002959357.1| hypothetical protein VOLCADRAFT_100797 [Volvox carteri f. nagariensis] gi|300255236|gb|EFJ39573.1| hypothetical protein VOLCADRAFT_100797 [Volvox carteri f. nagariensis]	138	233	1.00E−11	168.8	29.0	36.2	hypothetical protein VOLCADRAFT_100797	gbpln	Volvox carteri	#	#	#	#	#	#	#
Rsa1.0_00693.1.g18151.t1	ref|XP_002883985.1| hypothetical protein ARALYDRAFT_480516 [Arabidopsis lyrata subsp. lyrata] gi|297329825|gb|EFH60244.1| hypothetical protein ARALYDRAFT_480516 [Arabidopsis lyrata subsp. lyrata]	136	414	7.00E−28	304.4	51.5	53.7	hypothetical protein ARALYDRAFT_480516	gbpln	Arabidopsis lyrata	AT2G19560.1 | Symbols: EER5 | proteasome family protein | chr2:8465924−8469069 REVERSE LENGTH=413	136	413	4.00E−29	303.7	50.7	52.2
Rsa1.0_00693.1.g18152.t1	ref|XP_002876557.1| hypothetical protein ARALYDRAFT_486518 [Arabidopsis lyrata subsp. lyrata] gi|297322395|gb|EFH52816.1| hypothetical protein ARALYDRAFT_486518 [Arabidopsis lyrata subsp. lyrata]	276	274	1.00E−136	99.3	82.6	92.0	hypothetical protein ARALYDRAFT_486518	gbpln	Arabidopsis lyrata	AT3G60450.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:22340982−22342187 FORWARD LENGTH=274	276	274	1.00E−137	99.3	81.9	91.3
Rsa1.0_00693.1.g18153.t1	ref|NP_191603.2| phosphoglycerate mutase−like protein [Arabidopsis thaliana] gi|332646541|gb|AEE80062.1| phosphoglycerate mutase−like protein [Arabidopsis thaliana]	283	291	1.00E−125	102.8	77.7	88.0	phosphoglycerate mutase−like protein	gbpln	Arabidopsis thaliana	AT3G60440.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:22337820−22339145 FORWARD LENGTH=291	283	291	1.00E−127	102.8	77.7	88.0
Rsa1.0_00693.1.g18154.t1	gb|AAL47433.1| AT5g62580/K19B1_19 [Arabidopsis thaliana]	188	615	2.00E−17	327.1	36.2	43.1	AT5g62580/K19B1_19	gbpln	Arabidopsis thaliana	AT5G62580.1 | Symbols: | ARM repeat superfamily protein | chr5:25120010−25122259 FORWARD LENGTH=615	188	615	8.00E−20	327.1	36.2	43.1
Rsa1.0_00693.1.g18155.t1	ref|XP_002876554.1| hypothetical protein ARALYDRAFT_907564 [Arabidopsis lyrata subsp. lyrata] gi|297322392|gb|EFH52813.1| hypothetical protein ARALYDRAFT_907564 [Arabidopsis lyrata subsp. lyrata]	264	274	1.00E−109	103.8	70.5	82.6	hypothetical protein ARALYDRAFT_907564	gbpln	Arabidopsis lyrata	AT3G60420.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:22334446−22335710 FORWARD LENGTH=270	264	270	1.00E−110	102.3	69.7	82.2
Rsa1.0_00693.1.g18156.t1	ref|XP_002876554.1| hypothetical protein ARALYDRAFT_907564 [Arabidopsis lyrata subsp. lyrata] gi|297322392|gb|EFH52813.1| hypothetical protein ARALYDRAFT_907564 [Arabidopsis lyrata subsp. lyrata]	269	274	1.00E−104	101.9	69.1	81.8	hypothetical protein ARALYDRAFT_907564	gbpln	Arabidopsis lyrata	AT3G60420.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:22334446−22335710 FORWARD LENGTH=270	269	270	1.00E−106	100.4	69.9	81.4
Rsa1.0_00693.1.g18157.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00693.1.g18158.t2	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00693.1.g18159.t2	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	659	536	1.00E−89	81.3	25.3	33.1	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC−type) family protein | chr2:3584420−3586278 REVERSE LENGTH=530	659	530	3.00E−49	80.4	15.2	19.9
Rsa1.0_00694.1.g18160.t1		#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00694.1.g18161.t1	dbj|BAJ34017.1| unnamed protein product [Thellungiella halophila]	389	389	0	100.0	98.5	99.2	unnamed protein product	----	----	AT3G27000.1 | Symbols: ARP2, ATARP2, WRM | actin related protein 2 | chr3:9952787−9955784 REVERSE LENGTH=389	389	389	0	100.0	98.2	99.2
Rsa1.0_00694.1.g18162.t1	ref|XP_002875350.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] gi|297321188|gb|EFH51609.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	127	120	9.00E−57	94.5	85.8	92.1	ubiquitin family protein	gbpln	Arabidopsis lyrata	AT3G26980.1 | Symbols: MUB4 | membrane−anchored ubiquitin−fold protein 4 precursor | chr3:9946467−9947444 REVERSE LENGTH=120	127	120	1.00E−58	94.5	85.8	91.3
Rsa1.0_00694.1.g18163.t1	gb|EOA23822.1| hypothetical protein CARUB_v10017036mg [Capsella rubella]	450	513	1.00E−178	114.0	78.9	86.9	hypothetical protein CARUB_v10017036mg	gbpln	Capsella rubella	AT3G26990.1 | Symbols: | ENTH/VHS family protein | chr3:9948426−9951557 REVERSE LENGTH=513	450	513	1.00E−177	114.0	81.6	89.1
Rsa1.0_00694.1.g18164.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#

Rsa1.0_00694.1.g18165.t1	ref|NP_199678.1| agamous-like MADS-box protein AGL80 [Arabidopsis thaliana] gi|75333956|sp|Q9FJK3.1|AGL80_ARATH RecName: Full=Agamous-like MADS-box protein AGL80 gi|10177357|dbj|BAB10700.1| unnamed protein product [Arabidopsis thaliana] gi|67633864|gb|AAY78856.1| MADS-box family protein [Arabidopsis thaliana] gi|89275220|gb|ABD66036.1| MADS box transcription factor AGL80 [Arabidopsis thaliana] gi|332008326|gb|AED95709.1| agamous-like MADS-box protein AGL80 [Arabidopsis thaliana]	322	321	2.00E-52	99.7	42.5	56.2	agamous-like MADS-box protein AGL80	gbpln	Arabidopsis thaliana	AT5G48670.1 | Symbols: FEM111, AGL80 | AGAMOUS-like 80 | chr5:19738825-19739790 REVERSE LENGTH=321	322	321	6.00E-55	99.7	42.5	56.2
Rsa1.0_00694.1.g18166.t1	gb|EOA24039.1| hypothetical protein CARUB_v10017257mg [Capsella rubella]	445	443	0	99.6	88.8	93.7	hypothetical protein CARUB_v10017257mg	gbpln	Capsella rubella	AT3G26935.1 | Symbols: | DHHC-type zinc finger family protein | chr3:9933001-9935218 REVERSE LENGTH=443	445	443	0	99.6	88.8	93.0
Rsa1.0_00694.1.g18167.t1	ref|XP_002877005.1| dsRNA-binding protein 3 [Arabidopsis lyrata subsp. lyrata] gi|297322843|gb|EFH53264.1| dsRNA-binding protein 3 [Arabidopsis lyrata subsp. lyrata]	323	356	1.00E-122	110.2	77.1	82.4	dsRNA-binding protein 3	gbpln	Arabidopsis lyrata	AT3G26932.2 | Symbols: DRB3 | dsRNA-binding protein 3 | chr3:9930460-9931714 REVERSE LENGTH=359	323	359	1.00E-124	111.1	76.8	82.0
Rsa1.0_00694.1.g18168.t1	ref|NP_001078213.1| uncharacterized protein [Arabidopsis thaliana] gi|11994158|dbj|BAB01187.1| unnamed protein product [Arabidopsis thaliana] gi|332643723|gb|AEE77244.1| uncharacterized protein AT3G26934 [Arabidopsis thaliana]	132	153	7.00E-26	115.9	56.1	67.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G26934.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 11 Blast hits to 11 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr3:9928316-9929123 REVERSE LENGTH=153	132	153	2.00E-28	115.9	56.1	67.4
Rsa1.0_00694.1.g18169.t1	sp|Q3EA38.2|FDL48_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At4g13965	377	427	1.00E-101	113.3	57.0	70.8	RecName: Full=Putative F-box/FBD/LRR-repeat protein At4g13965	----	----	AT1G55030.1 | Symbols: | RNI-like superfamily protein | chr1:20530417-20531768 REVERSE LENGTH=422	377	422	2.00E-88	111.9	52.8	65.3
Rsa1.0_00694.1.g18170.t1	gb|EOA23598.1| hypothetical protein CARUB_v10016795mg [Capsella rubella]	660	663	0	100.5	87.9	94.2	hypothetical protein CARUB_v10016795mg	gbpln	Capsella rubella	AT3G26782.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:9850594-9852682 FORWARD LENGTH=659	660	659	0	99.8	87.6	94.1
Rsa1.0_00694.1.g18171.t1	gb|AFG29442.1| inducer of CBF expression 1 protein [Isatis tinctoria]	474	499	1.00E-176	105.3	79.1	82.9	inducer of CBF expression 1 protein	gbpln	Isatis tinctoria	AT3G26744.4 | Symbols: ICE1, ATICE1, SCRM | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:9832953-9834790 REVERSE LENGTH=494	474	494	1.00E-164	104.2	73.2	77.8
Rsa1.0_00694.1.g18172.t1	gb|EOA24196.1| hypothetical protein CARUB_v10017433mg [Capsella rubella]	393	380	1.00E-174	96.7	80.9	86.3	hypothetical protein CARUB_v10017433mg	gbpln	Capsella rubella	AT3G26700.1 | Symbols: | Protein kinase superfamily protein | chr3:9810669-9812356 FORWARD LENGTH=380	393	380	1.00E-177	96.7	80.9	86.5
Rsa1.0_00694.1.g18173.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00694.1.g18174.t1	ref|NP_189295.3| peptide chain release factor eRF subunit 1 [Arabidopsis thaliana] gi|549010|sp|P35614.1|ERF1Z_ARATH RecName: Full=Eukaryotic peptide chain release factor subunit 1-3; Short=Eukaryotic release factor 1-3; Short=eRF1-3; AltName: Full=Omnipotent suppressor protein 1 homolog 3; Short=SUP1 homolog 3 gi|16514|emb|CAA49172.1| unnamed protein product [Arabidopsis thaliana] gi|1402882|emb|CAA66813.1| eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] gi|1495249|emb|CAA66118.1| eRF1-3 [Arabidopsis thaliana] gi|11994297|dbj|BAB01727.1| translation release factor subunit 1 [Arabidopsis thaliana] gi|15215648|gb|AAK91369.1| MFE16.15/MFE16.15 [Arabidopsis thaliana] gi|21435997|gb|AAM51576.1| At3g26618/MFE16.15 [Arabidopsis thaliana] gi|332643666|gb|AEE77187.1| peptide chain release factor eRF subunit 1 [Arabidopsis thaliana]	801	435	0	54.3	52.6	53.4	peptide chain release factor eRF subunit 1	gbpln	Arabidopsis thaliana	AT3G26618.1 | Symbols: ERF1-3 | eukaryotic release factor 1-3 | chr3:9788854-9790161 FORWARD LENGTH=435	801	435	0	54.3	52.6	53.4
Rsa1.0_00694.1.g18175.t1	gb|EOA23652.1| hypothetical protein CARUB_v10016853mg [Capsella rubella]	610	614	0	100.7	81.6	91.0	hypothetical protein CARUB_v10016853mg	gbpln	Capsella rubella	AT3G26600.1 | Symbols: ARO4 | armadillo repeat only 4 | chr3:9769889-9771736 FORWARD LENGTH=615	610	615	0	100.8	83.4	91.3

Rsa1.0_00695.1.g18176.t1	gb|EOA14684.1| hypothetical protein CARUB_v10027956mg [Capsella rubella]	496	496	1.00E-106	100.0	55.0	67.1	hypothetical protein CARUB_v10027956mg	gbpln	Capsella rubella	AT5G53220.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21596824-21598004 FORWARD LENGTH=368	496	368	1.00E-96	74.2	45.8	53.8
Rsa1.0_00695.1.g18177.t1	dbj|BAJ34295.1| unnamed protein product [Thellungiella halophila]	332	368	1.00E-140	110.8	88.6	93.1	unnamed protein product	----	----	AT5G53210.1 | Symbols: SPCH | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:21586606-21588941 REVERSE LENGTH=364	332	364	1.00E-121	109.6	87.0	91.9
Rsa1.0_00695.1.g18178.t3	#	#	#	#	#	#	#	-	----	----	AT5G53170.1 | Symbols: FTSH11 | FTSH protease 11 | chr5:21563023-21567922 REVERSE LENGTH=806	140	806	2.00E-11	575.7	20.7	20.7
Rsa1.0_00695.1.g18179.t2	ref|NP_200128.1| abscisic acid receptor PYL8 [Arabidopsis thaliana] gi|75170450|sp|Q9FGM1.1|PYL8_ARATH RecName: Full=Abscisic acid receptor PYL8; AltName: Full=ABI1-binding protein 1; AltName: Full=PYR1-like protein 8; AltName: Full=Regulatory components of ABA receptor 3 gi|9757997|dbj|BAB08419.1| unnamed protein product [Arabidopsis thaliana] gi|27808528|gb|AAO24544.1| At5g53160 [Arabidopsis thaliana] gi|332008933|gb|AED96316.1| abscisic acid receptor PYL8 [Arabidopsis thaliana]	181	188	1.00E-90	103.9	93.4	95.6	abscisic acid receptor PYL8	gbpln	Arabidopsis thaliana	AT5G53160.2 | Symbols: RCAR3, PYL8 | regulatory components of ABA receptor 3 | chr5:21561026-21561953 FORWARD LENGTH=188	181	188	6.00E-93	103.9	93.4	95.6
Rsa1.0_00695.1.g18180.t2	ref|XP_002864225.1| hypothetical protein ARALYDRAFT_918384 [Arabidopsis lyrata subsp. lyrata] gi|297310060|gb|EFH40484.1| hypothetical protein ARALYDRAFT_918384 [Arabidopsis lyrata subsp. lyrata]	435	420	0	96.6	79.1	84.1	hypothetical protein ARALYDRAFT_918384	gbpln	Arabidopsis lyrata	AT5G53140.1 | Symbols: | Protein phosphatase 2C family protein | chr5:21549228-21552132 FORWARD LENGTH=420	435	420	0	96.6	77.7	83.9
Rsa1.0_00695.1.g18181.t1	ref|NP_190191.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75180796|sp|Q9LX87.1|FBK74_ARATH RecName: Full=Putative F-box/kelch-repeat protein At3g46050 gi|7798993|emb|CAB90932.1| putative protein [Arabidopsis thaliana] gi|332644584|gb|AEE78105.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	335	370	9.00E-58	110.4	45.7	61.2	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G46050.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:16916072-16917184 FORWARD LENGTH=370	335	370	2.00E-60	110.4	45.7	61.2
Rsa1.0_00695.1.g18182.t2	ref|NP_001190533.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana] gi|75262547|sp|Q9FJC1.1|FBD31_ARATH RecName: Full=Putative FBD-associated F-box protein At5g53635 gi|9759202|dbj|BAB09739.1| heat shock transcription factor HSF30-like protein [Arabidopsis thaliana] gi|332009006|gb|AED96389.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana]	431	426	2.00E-96	98.8	51.0	66.1	F-box/RNI-like/FBD-like domains-containing protein	gbpln	Arabidopsis thaliana	AT5G53635.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:21785999-21787444 REVERSE LENGTH=426	431	426	4.00E-99	98.8	51.0	66.1
Rsa1.0_00696.1.g18183.t1	ref|NP_199536.1| putative disease resistance protein [Arabidopsis thaliana] gi|46396007|sp|Q9LVT4.1|DRL37_ARATH RecName: Full=Probable disease resistance protein At5g47250 gi|8809608|dbj|BAA97159.1| NBS/LRR disease resistance protein [Arabidopsis thaliana] gi|110741827|dbj|BAE98856.1| NBS/LRR disease resistance protein [Arabidopsis thaliana] gi|332008108|gb|AED95491.1| putative disease resistance protein [Arabidopsis thaliana]	882	843	0	95.6	56.0	67.7	putative disease resistance protein	gbpln	Arabidopsis thaliana	AT5G47250.1 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr5:19186045-19188576 REVERSE LENGTH=843	882	843	0	95.6	56.0	67.7

Rsa1.0_00696.1.g18184.t1	gb|EOA14559.1| hypothetical protein CARUB_v10027797mg [Capsella rubella]	837	1251	0	149.5	50.7	66.9	hypothetical protein CARUB_v10027797mg	gbpln	Capsella rubella	AT5G47260.1 | Symbols: | ATP binding;GTP binding;nucleotide binding;nucleoside-triphosphatases | chr5:19189411-19192516 FORWARD LENGTH=948	837	948	0	113.3	50.2	65.2
Rsa1.0_00696.1.g18185.t1	ref|NP_199536.1| putative disease resistance protein [Arabidopsis thaliana] gi|46396007|sp|Q9LVT4.1|DRL37_ARATH RecName: Full=Probable disease resistance protein At5g47250 gi|8809608|dbj|BAA97159.1| NBS/LRR disease resistance protein [Arabidopsis thaliana] gi|110741827|dbj|BAE98856.1| NBS/LRR disease resistance protein [Arabidopsis thaliana] gi|332008108|gb|AED95491.1| putative disease resistance protein [Arabidopsis thaliana]	944	843	0	89.3	50.1	62.8	putative disease resistance protein	gbpln	Arabidopsis thaliana	AT5G47250.1 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr5:19186045-19188576 REVERSE LENGTH=843	944	843	0	89.3	50.1	62.8
Rsa1.0_00696.1.g18186.t1	dbj|BAH30638.1| hypothetical protein [Arabidopsis thaliana]	342	556	4.00E-55	162.6	43.3	58.2	hypothetical protein	gbpln	Arabidopsis thaliana	AT5G59390.1 | Symbols: | XH/XS domain-containing protein | chr5:23954934-23957151 FORWARD LENGTH=561	342	561	5.00E-57	164.0	42.7	58.2
Rsa1.0_00696.1.g18187.t7	ref|NP_199537.2| putative disease resistance protein [Arabidopsis thaliana] gi|190358917|sp|Q9LVT3.2|DRL38_ARATH RecName: Full=Probable disease resistance protein At5g47260 gi|332008109|gb|AED95492.1| putative disease resistance protein [Arabidopsis thaliana]	994	948	0	95.4	55.1	65.2	putative disease resistance protein	gbpln	Arabidopsis thaliana	AT5G47260.1 | Symbols: | ATP binding;GTP binding;nucleotide binding;nucleoside-triphosphatases | chr5:19189411-19192516 FORWARD LENGTH=948	994	948	0	95.4	55.1	65.2
Rsa1.0_00696.1.g18188.t1	gb|ABD65033.1| YDG/SRA domain containing protein [Brassica oleracea]	93	498	2.00E-22	535.5	57.0	62.4	YDG/SRA domain containing protein	gbpln	Brassica oleracea	AT5G47160.1 | Symbols: | YDG/SRA domain-containing protein | chr5:19156731-19157978 FORWARD LENGTH=415	93	415	1.00E-15	446.2	39.8	52.7
Rsa1.0_00696.1.g18189.t1	ref|XP_002865469.1| GYF domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311304|gb|EFH41728.1| GYF domain-containing protein [Arabidopsis lyrata subsp. lyrata]	293	1714	3.00E-11	585.0	14.7	18.4	GYF domain-containing protein	gbpln	Arabidopsis lyrata	AT5G42950.1 | Symbols: | GYF domain-containing protein | chr5:17224436-17231044 FORWARD LENGTH=1714	293	1714	2.00E-13	585.0	14.7	18.4
Rsa1.0_00696.1.g18190.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00696.1.g18191.t7	gb|ABD65043.1| hypothetical protein 26.t00101 [Brassica oleracea]	497	189	2.00E-23	38.0	14.9	18.7	hypothetical protein 26.t00101	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00697.1.g18192.t1	gb|EOA16103.1| hypothetical protein CARUB_v10004236mg [Capsella rubella]	480	725	0	151.0	69.4	77.5	hypothetical protein CARUB_v10004236mg	gbpln	Capsella rubella	AT4G24000.1 | Symbols: ATCSLG2, CSLG2 | cellulose synthase like G2 | chr4:12462142-12465471 FORWARD LENGTH=722	480	722	0	150.4	68.8	76.0
Rsa1.0_00697.1.g18193.t1	dbj|BAA85459.1| ORF-a [Brassica rapa]	490	427	9.00E-48	87.1	23.7	25.5	ORF-a	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00697.1.g18194.t1	ref|NP_567692.2| cellulose synthase-like protein G2 [Arabidopsis thaliana] gi|75161526|sp|Q8VYR4.1|CSLG2_ARATH RecName: Full=Cellulose synthase-like protein G2; Short=AtCslG2 gi|17979143|gb|AAL49829.1| unknown protein [Arabidopsis thaliana] gi|20465365|gb|AAM20086.1| unknown protein [Arabidopsis thaliana] gi|332659438|gb|AEE84838.1| cellulose synthase-like protein G2 [Arabidopsis thaliana]	607	722	0	118.9	76.8	86.3	cellulose synthase-like protein G2	gbpln	Arabidopsis thaliana	AT4G24000.1 | Symbols: ATCSLG2, CSLG2 | cellulose synthase like G2 | chr4:12462142-12465471 FORWARD LENGTH=722	607	722	0	118.9	76.8	86.3
Rsa1.0_00697.1.g18195.t1	gb|AFD01307.1| auxin response factor 9-1 [Brassica rapa subsp. pekinensis]	601	602	0	100.2	93.0	95.2	auxin response factor 9-1	gbpln	Brassica rapa	AT4G23980.2 | Symbols: ARF9 | auxin response factor 9 | chr4:12451592-12454737 FORWARD LENGTH=636	601	636	0	105.8	84.2	91.2
Rsa1.0_00697.1.g18196.t1	ref|NP_567691.1| FtsH extracellular protease [Arabidopsis thaliana] gi|2262118|gb|AAB63626.1| cell division protein isolog [Arabidopsis thaliana] gi|4972098|emb|CAB43894.1| cell division protein-like [Arabidopsis thaliana] gi|7269243|emb|CAB81312.1| cell division protein-like [Arabidopsis thaliana] gi|332659430|gb|AEE84830.1| FtsH extracellular protease [Arabidopsis thaliana]	1514	946	0	62.5	52.6	55.4	FtsH extracellular protease	gbpln	Arabidopsis thaliana	AT4G23940.1 | Symbols: | FtsH extracellular protease family | chr4:12437108-12441841 FORWARD LENGTH=946	1514	946	0	62.5	52.6	55.4
Rsa1.0_00697.1.g18197.t1	gb|EOA17481.1| hypothetical protein CARUB_v10005808mg [Capsella rubella]	197	191	9.00E-78	97.0	75.1	86.3	hypothetical protein CARUB_v10005808mg	gbpln	Capsella rubella	AT4G23930.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr4:12436131-12436694 REVERSE LENGTH=187	197	187	2.00E-76	94.9	75.1	84.8

Rsa1.0_00697.1.g18198.t1	ref|XP_002869754.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 2 [Arabidopsis lyrata subsp. lyrata] gi|297315590|gb|EFH46013.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 2 [Arabidopsis lyrata subsp. lyrata]	339	350	0	103.2	92.6	95.0	UDP-D-glucose/UDP-D-galactose 4-epimerase 2	gbpln	Arabidopsis lyrata	AT4G23920.1 | Symbols: UGE2, ATUGE2 | UDP-D-glucose/UDP-D-galactose 4-epimerase 2 | chr4:12431416-12433666 FORWARD LENGTH=350	339	350	0	103.2	91.7	94.7
Rsa1.0_00697.1.g18199.t4	dbj|BAE99702.1| hypothetical protein [Arabidopsis thaliana]	334	138	3.00E-36	41.3	26.0	30.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G23910.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10970.4). | chr4:12427055-12429287 FORWARD LENGTH=198	334	198	2.00E-38	59.3	25.1	29.6
Rsa1.0_00697.1.g18200.t1	ref|NP_567690.1| nucleoside diphosphate kinase IV [Arabidopsis thaliana] gi|45477149|sp|Q8LAH8.2|NDK4_ARATH RecName: Full=Nucleoside diphosphate kinase IV, chloroplastic/mitochondrial; Short=NDK IV; Short=NDP kinase IV; Short=NDPK IV; AltName: Full=Nucleoside diphosphate kinase 4; Flags: Precursor gi|4972094|emb|CAB43890.1| hypothetical protein [Arabidopsis thaliana] gi|7269239|emb|CAB81308.1| hypothetical protein [Arabidopsis thaliana] gi|11990430|dbj|BAB19789.1| nucleoside diphosphate kinase 4 [Arabidopsis thaliana] gi|26450853|dbj|BAC42534.1| unknown protein [Arabidopsis thaliana] gi|105829662|gb|ABF74700.1| At4g23900 [Arabidopsis thaliana] gi|332659424|gb|AEE84824.1| nucleoside diphosphate kinase IV [Arabidopsis thaliana]	319	237	1.00E-119	74.3	65.2	69.3	nucleoside diphosphate kinase IV	gbpln	Arabidopsis thaliana	AT4G23900.1 | Symbols: | Nucleoside diphosphate kinase family protein | chr4:12424505-12426318 FORWARD LENGTH=237	319	237	1.00E-121	74.3	65.2	69.3
Rsa1.0_00697.1.g18201.t1	gb|EOA18489.1| hypothetical protein CARUB_v10007040mg [Capsella rubella]	245	248	1.00E-106	101.2	85.3	91.4	hypothetical protein CARUB_v10007040mg	gbpln	Capsella rubella	AT4G23890.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3252 (InterPro:IPR021659); Has 287 Blast hits to 287 proteins in 81 species: Archae - 0; Bacteria - 118; Metazoa - 12; Fungi - 6; Plants - 40; Viruses - 0; Other Eukaryotes - 111 (source: NCBI BLink). | chr4:12420593-12421345 REVERSE LENGTH=250	245	250	1.00E-108	102.0	83.7	90.2
Rsa1.0_00697.1.g18202.t1	ref|XP_002869758.1| hypothetical protein ARALYDRAFT_914208 [Arabidopsis lyrata subsp. lyrata] gi|297315594|gb|EFH46017.1| hypothetical protein ARALYDRAFT_914208 [Arabidopsis lyrata subsp. lyrata]	75	76	5.00E-27	101.3	85.3	88.0	hypothetical protein ARALYDRAFT_914208	gbpln	Arabidopsis lyrata	AT4G23885.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24165.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12419472-12420240 FORWARD LENGTH=77	75	77	2.00E-28	102.7	85.3	86.7
Rsa1.0_00697.1.g18203.t1	gb|EOA17457.1| hypothetical protein CARUB_v10005780mg [Capsella rubella]	174	197	7.00E-57	113.2	69.5	82.2	hypothetical protein CARUB_v10005780mg	gbpln	Capsella rubella	AT4G23880.1 | Symbols: | unknown protein; Has 73 Blast hits to 69 proteins in 22 species: Archae - 0; Bacteria - 4; Metazoa - 9; Fungi - 2; Plants - 18; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink). | chr4:12415789-12416388 REVERSE LENGTH=199	174	199	7.00E-56	114.4	70.1	82.2

Rsa1.0_00697.1.g18204.t1	ref|NP_194118.1| uncharacterized protein [Arabidopsis thaliana] gi|4972091|emb|CAB43887.1| putative protein [Arabidopsis thaliana] gi|7269236|emb|CAB81305.1| putative protein [Arabidopsis thaliana] gi|15450916|gb|AAK96729.1| putative protein [Arabidopsis thaliana] gi|25084175|gb|AAN72191.1| putative protein [Arabidopsis thaliana] gi|332659416|gb|AEE84816.1| uncharacterized protein AT4G23870 [Arabidopsis thaliana]	117	116	1.00E-39	99.1	84.6	93.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G23870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11020.1); Has 12 Blast hits to 12 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:12414409-12414759 FORWARD LENGTH=116	117	116	2.00E-42	99.1	84.6	93.2
Rsa1.0_00697.1.g18205.t1	ref|XP_002869761.1| hypothetical protein ARALYDRAFT_492483 [Arabidopsis lyrata subsp. lyrata] gi|297315597|gb|EFH46020.1| hypothetical protein ARALYDRAFT_492483 [Arabidopsis lyrata subsp. lyrata]	400	453	1.00E-178	113.3	77.5	86.8	hypothetical protein ARALYDRAFT_492483	gbpln	Arabidopsis lyrata	AT4G23860.3 | Symbols: | PHD finger protein-related | chr4:12409336-12411336 FORWARD LENGTH=452	400	452	1.00E-180	113.0	77.0	86.5
Rsa1.0_00697.1.g18206.t1	emb|CAA64327.1| acyl-CoA synthetase [Brassica napus]	679	667	0	98.2	96.0	97.2	acyl-CoA synthetase	gbpln	Brassica napus	AT4G23850.1 | Symbols: LACS4 | AMP-dependent synthetase and ligase family protein | chr4:12403720-12408263 REVERSE LENGTH=666	679	666	0	98.1	91.5	95.3
Rsa1.0_00697.1.g18207.t1	ref|XP_002867688.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297313524|gb|EFH43947.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	449	444	0	98.9	88.6	94.7	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT4G23820.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:12397217-12400050 REVERSE LENGTH=444	449	444	0	98.9	88.4	94.2
Rsa1.0_00698.1.g18208.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00698.1.g18209.t1	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	586	498	9.00E-29	85.0	15.9	22.5	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00698.1.g18210.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	846	1225	4.00E-80	144.8	18.4	26.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	846	484	9.00E-23	57.2	7.8	11.1
Rsa1.0_00698.1.g18211.t1	gb|AAQ18645.1| division protein [Arabidopsis thaliana]	791	801	0	101.3	87.9	92.4	division protein	gbpln	Arabidopsis thaliana	AT5G42480.1 | Symbols: ARC6 | Chaperone DnaJ-domain superfamily protein | chr5:16985295-16988332 FORWARD LENGTH=801	791	801	0	101.3	88.1	92.7
Rsa1.0_00698.1.g18212.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00698.1.g18213.t1	emb|CAA69271.1| lectin receptor kinase [Arabidopsis thaliana]	148	544	4.00E-57	367.6	72.3	77.0	lectin receptor kinase	gbpln	Arabidopsis thaliana	AT1G48720.1 | Symbols: | unknown protein; Has 229 Blast hits to 229 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 228; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18018148-18018441 FORWARD LENGTH=97	148	97	2.00E-42	65.5	53.4	57.4
Rsa1.0_00698.1.g18214.t1	gb|EOA39165.1| hypothetical protein CARUB_v10012117mg [Capsella rubella]	223	308	6.00E-92	138.1	78.0	87.4	hypothetical protein CARUB_v10012117mg	gbpln	Capsella rubella	AT1G19540.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr1:6765713-6767247 FORWARD LENGTH=310	223	310	4.00E-94	139.0	78.0	88.3
Rsa1.0_00698.1.g18215.t1	ref|XP_002893054.1| hypothetical protein ARALYDRAFT_472181 [Arabidopsis lyrata subsp. lyrata] gi|297338896|gb|EFH69313.1| hypothetical protein ARALYDRAFT_472181 [Arabidopsis lyrata subsp. lyrata]	213	213	5.00E-98	100.0	84.0	89.7	hypothetical protein ARALYDRAFT_472181	gbpln	Arabidopsis lyrata	AT1G19570.1 | Symbols: DHAR1, ATDHAR1, DHAR5 | dehydroascorbate reductase | chr1:6773462-6774413 REVERSE LENGTH=213	213	213	1.00E-100	100.0	84.0	88.7
Rsa1.0_00698.1.g18216.t3	emb|CAB75469.1| copia-type reverse transcriptase-like protein [Arabidopsis thaliana]	1047	1272	0	121.5	82.5	89.3	copia-type reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1047	1262	3.00E-51	120.5	9.2	14.0
Rsa1.0_00698.1.g18217.t5	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00698.1.g18218.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00698.1_g18219.t1	ref|NP_199069.1| 5'-3' exoribonuclease 2 [Arabidopsis thaliana] gi|75262831|sp|Q9FQ02.1|XRN2_ARATH RecName: Full=5'-3' exoribonuclease 2; AltName: Full=Protein EXORIBONUCLEASE 2 gi|11875630|gb|AAG40733.1|AF286720_1 XRN2 [Arabidopsis thaliana] gi|51970342|dbj|BAD43863.1| unnamed protein product [Arabidopsis thaliana] gi|62319144|dbj|BAD94308.1| 5'-3' exoribonuclease 2 [Arabidopsis thaliana] gi|332007441|gb|AED94824.1| 5'-3' exoribonuclease 2 [Arabidopsis thaliana]	995	1012	0	101.7	71.6	83.3	5'-3' exoribonuclease 2	gbpln	Arabidopsis thaliana	AT5G42540.1 | Symbols: XRN2, AtXRN2 | exoribonuclease 2 | chr5:17007513-17014534 FORWARD LENGTH=1012	995	1012	0	101.7	71.6	83.3
Rsa1.0_00698.1_g18220.t3	dbj|BAB01349.1| En/Spm-like transposon protein-like [Arabidopsis thaliana]	1050	714	9.00E-61	68.0	11.5	15.7	En/Spm-like transposon protein-like	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	1050	249	2.00E-26	23.7	6.6	10.2
Rsa1.0_00698.1_g18221.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00698.1_g18222.t1	dbj|BAB01350.1| Mutator-like transposase [Arabidopsis thaliana]	581	811	1.00E-124	139.6	39.4	52.7	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	581	719	5.00E-17	123.8	17.7	33.6
Rsa1.0_00698.1_g18223.t1	gb|EOA13585.1| hypothetical protein CARUB_v10026651mg, partial [Capsella rubella]	290	361	1.00E-137	124.5	87.2	92.1	hypothetical protein CARUB_v10026651mg, partial	gbpln	Capsella rubella	AT5G42560.1 | Symbols: | Abscisic acid-responsive (TB2/DP1, HVA22) family protein | chr5:17015573-17016969 FORWARD LENGTH=296	290	296	1.00E-133	102.1	85.2	90.0
Rsa1.0_00699.1_g18224.t2	ref|XP_002887324.1| hypothetical protein ARALYDRAFT_476197 [Arabidopsis lyrata subsp. lyrata] gi|297333165|gb|EFH63583.1| hypothetical protein ARALYDRAFT_476197 [Arabidopsis lyrata subsp. lyrata]	199	300	1.00E-68	150.8	74.4	82.9	hypothetical protein ARALYDRAFT_476197	gbpln	Arabidopsis lyrata	AT1G70690.1 | Symbols: HWI1, PDLP5 | Receptor-like protein kinase-related family protein | chr1:26652099-26653381 FORWARD LENGTH=299	199	299	1.00E-69	150.3	72.9	81.9
Rsa1.0_00699.1_g18225.t1	ref|NP_177227.5| protein TIFY 7 [Arabidopsis thaliana] gi|342187044|sp|Q8W4J8.2|TIF7_ARATH RecName: Full=Protein TIFY 7; AltName: Full=Jasmonate ZIM domain-containing protein 9 gi|332196980|gb|AEE35101.1| protein TIFY 7 [Arabidopsis thaliana]	266	267	3.00E-90	100.4	69.2	78.2	protein TIFY 7	gbpln	Arabidopsis thaliana	AT1G70700.1 | Symbols: JAZ9, TIFY7 | TIFY domain/Divergent CCT motif family protein | chr1:26654951-26656804 FORWARD LENGTH=267	266	267	9.00E-93	100.4	69.2	78.2
Rsa1.0_00699.1_g18226.t1	gb|EOA35078.1| hypothetical protein CARUB_v10020190mg [Capsella rubella]	496	492	0	99.2	92.7	96.8	hypothetical protein CARUB_v10020190mg	gbpln	Capsella rubella	AT1G70710.1 | Symbols: ATGH9B1, CEL1, GH9B1 | glycosyl hydrolase 9B1 | chr1:26659356-26662962 REVERSE LENGTH=492	496	492	0	99.2	91.3	95.8
Rsa1.0_00699.1_g18227.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1656	1529	0	92.3	46.9	64.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1656	746	1.00E-138	45.0	14.1	18.6
Rsa1.0_00699.1_g18228.t1	ref|NP_177231.2| protein kinase domain-containing protein [Arabidopsis thaliana] gi|193870477|gb|ACF22895.1| At1g70740 [Arabidopsis thaliana] gi|332196987|gb|AEE35108.1| protein kinase domain-containing protein [Arabidopsis thaliana]	600	425	0	70.8	61.7	66.5	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G70740.1 | Symbols: | Protein kinase superfamily protein | chr1:26673847-26675687 REVERSE LENGTH=425	600	425	0	70.8	61.7	66.5
Rsa1.0_00699.1_g18229.t1	ref|XP_002888793.1| hypothetical protein ARALYDRAFT_894893 [Arabidopsis lyrata subsp. lyrata] gi|297334634|gb|EFH65052.1| hypothetical protein ARALYDRAFT_894893 [Arabidopsis lyrata subsp. lyrata]	878	758	1.00E-159	86.3	38.5	42.9	hypothetical protein ARALYDRAFT_894893	gbpln	Arabidopsis lyrata	AT1G70750.1 | Symbols: | Protein of unknown function, DUF593 | chr1:26680728-26683147 REVERSE LENGTH=749	878	749	1.00E-160	85.3	37.7	42.8
Rsa1.0_00699.1_g18230.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00699.1_g18231.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00699.1_g18232.t1	gb|ACG25170.1| hypothetical protein [Zea mays]	98	192	2.00E-26	195.9	68.4	71.4	hypothetical protein	gbenv/gbpln	Zea mays	AT1G70760.1 | Symbols: CRR23 | inorganic carbon transport protein-related | chr1:26687267-26688201 FORWARD LENGTH=191	98	191	2.00E-24	194.9	60.2	65.3

Rsa1.0_00699.1.g18233.t4	dbj|BAJ34604.1| unnamed protein product [Thellungiella halophila]	130	141	3.00E-60	108.5	92.3	93.8	unnamed protein product	----	----	AT1G70780.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23150.1); Has 143 Blast hits to 143 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 143; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26695462-26695975 REVERSE LENGTH=140	130	140	2.00E-61	107.7	90.0	93.8
Rsa1.0_00699.1.g18234.t1	gb|EOA34244.1| hypothetical protein CARUB_v10021755mg [Capsella rubella]	165	159	3.00E-60	96.4	69.1	82.4	hypothetical protein CARUB_v10021755mg	gbpln	Capsella rubella	AT1G70880.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:26723086-26723717 REVERSE LENGTH=159	165	159	1.00E-58	96.4	65.5	78.8
Rsa1.0_00699.1.g18235.t1	ref|NP_001077806.1| MLP-like protein 28 [Arabidopsis thaliana] gi|332197002|gb|AEE35123.1| MLP-like protein 28 [Arabidopsis thaliana]	158	201	1.00E-57	127.2	64.6	81.6	MLP-like protein 28	gbpln	Arabidopsis thaliana	AT1G70830.3 | Symbols: MLP28 | MLP-like protein 28 | chr1:26710203-26711395 REVERSE LENGTH=201	158	201	3.00E-60	127.2	64.6	81.6
Rsa1.0_00699.1.g18236.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00699.1.g18237.t1	ref|NP_565004.1| protein CLAVATA3/ESR-related 17 [Arabidopsis thaliana] gi|145327213|ref|NP_001077808.1| protein CLAVATA3/ESR-related 17 [Arabidopsis thaliana] gi|75154575|sp|Q8L9H6.1|CLE17_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 17; Contains: RecName: Full=CLE17p; Flags: Precursor gi|21618200|gb|AAM67250.1| unknown [Arabidopsis thaliana] gi|88900320|gb|ABD57472.1| At1g70895 [Arabidopsis thaliana] gi|332197014|gb|AEE35135.1| protein CLAVATA3/ESR-related 17 [Arabidopsis thaliana] gi|332197015|gb|AEE35136.1| protein CLAVATA3/ESR-related 17 [Arabidopsis thaliana]	64	99	1.00E-10	154.7	64.1	73.4	protein CLAVATA3/ESR-related 17	gbpln	Arabidopsis thaliana	AT1G70895.2 | Symbols: CLE17 | CLAVATA3/ESR-RELATED 17 | chr1:26728170-26728469 FORWARD LENGTH=99	64	99	2.00E-13	154.7	64.1	73.4
Rsa1.0_00699.1.g18238.t1	gb|EOA35647.1| hypothetical protein CARUB_v10020864mg [Capsella rubella]	244	244	1.00E-133	100.0	93.4	96.7	hypothetical protein CARUB_v10020864mg	gbpln	Capsella rubella	AT1G70900.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23110.4); Has 57 Blast hits to 57 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26732456-26733637 FORWARD LENGTH=244	244	244	1.00E-134	100.0	91.8	96.3
Rsa1.0_00699.1.g18239.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00699.1.g18240.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	224	1142	6.00E-41	509.8	41.1	53.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	224	292	3.00E-13	130.4	22.3	35.3
Rsa1.0_00699.1.g18241.t1	emb|CAC67688.1| efflux carrier, pin3 [Brassica juncea]	628	635	0	101.1	97.6	98.6	efflux carrier, pin3	gbpln	Brassica juncea	AT1G70940.1 | Symbols: PIN3, ATPIN3 | Auxin efflux carrier family protein | chr1:26743170-26745871 FORWARD LENGTH=640	628	640	0	101.9	92.0	96.2
Rsa1.0_00699.1.g18242.t3	ref|NP_177251.2| TPX2 (targeting protein for Xklp2) protein family [Arabidopsis thaliana] gi|51971395|dbj|BAD44362.1| At1g70950 [Arabidopsis thaliana] gi|332197022|gb|AEE35143.1| TPX2 (targeting protein for Xklp2) protein family [Arabidopsis thaliana]	495	478	1.00E-173	96.6	67.7	77.2	TPX2 (targeting protein for Xklp2) protein family	gbpln	Arabidopsis thaliana	AT1G70950.1 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr1:26752779-26755242 FORWARD LENGTH=478	495	478	1.00E-176	96.6	67.7	77.2
Rsa1.0_00699.1.g18243.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1478	1491	0	100.9	56.4	71.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1478	1262	1.00E-140	85.4	17.3	25.0
Rsa1.0_00699.1.g18244.t1	ref|XP_002890553.1| hypothetical protein ARALYDRAFT_472555 [Arabidopsis lyrata subsp. lyrata] gi|297336395|gb|EFH66812.1| hypothetical protein ARALYDRAFT_472555 [Arabidopsis lyrata subsp. lyrata]	103	158	1.00E-18	153.4	52.4	63.1	hypothetical protein ARALYDRAFT_472555	gbpln	Arabidopsis lyrata	AT1G70985.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:26764774-26765181 REVERSE LENGTH=135	103	135	3.00E-17	131.1	52.4	60.2

Rsa1.0_00700.1.g18245.t1	ref|NP_564930.1| uncharacterized protein [Arabidopsis thaliana] gi|6714347|gb|AAF26038.1|AC015986_1 unknown protein; 9003-8083 [Arabidopsis thaliana] gi|16648773|gb|AAL25577.1| At1g68440/T2E12_1 [Arabidopsis thaliana] gi|21592921|gb|AAM64871.1| unknown [Arabidopsis thaliana] gi|21700823|gb|AAM70535.1| At1g68440/T2E12_1 [Arabidopsis thaliana] gi|332196673|gb|AEE34794.1| uncharacterized protein AT1G68440 [Arabidopsis thaliana]	303	306	2.00E-99	101.0	72.6	84.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G68440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G25400.2); Has 86 Blast hits to 86 proteins in 29 species: Archae - 0; Bacteria - 6; Metazoa - 27; Fungi - 11; Plants - 24; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr1:25658115-25659035 FORWARD LENGTH=306	303	306	1.00E-102	101.0	72.6	84.5
Rsa1.0_00700.1.g18246.t1	ref|NP_177014.1| Exostosin family protein [Arabidopsis thaliana] gi|12324886|gb|AAG52396.1|AC011915_10 hypothetical protein; 19613-17891 [Arabidopsis thaliana] gi|332196676|gb|AEE34797.1| Exostosin family protein [Arabidopsis thaliana]	466	455	0	97.6	82.6	89.9	Exostosin family protein	gbpln	Arabidopsis thaliana	AT1G68470.1 | Symbols: | Exostosin family protein | chr1:25676545-25678267 REVERSE LENGTH=455	466	455	0	97.6	82.6	89.9
Rsa1.0_00700.1.g18247.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	843	1223	1.00E-149	145.1	37.7	54.9	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	843	626	1.00E-32	74.3	8.4	14.7
Rsa1.0_00700.1.g18248.t1	ref|XP_002888667.1| hypothetical protein ARALYDRAFT_475967 [Arabidopsis lyrata subsp. lyrata] gi|297334508|gb|EFH64926.1| hypothetical protein ARALYDRAFT_475967 [Arabidopsis lyrata subsp. lyrata]	217	253	9.00E-78	116.6	79.3	83.9	hypothetical protein ARALYDRAFT_475967	gbpln	Arabidopsis lyrata	AT1G68480.1 | Symbols: JAG | C2H2 and C2HC zinc fingers superfamily protein | chr1:25684543-25685932 REVERSE LENGTH=253	217	253	3.00E-78	116.6	77.0	82.9
Rsa1.0_00700.1.g18249.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00700.1.g18250.t1	ref|NP_564931.1| uncharacterized protein [Arabidopsis thaliana] gi|12324888|gb|AAG52398.1|AC011915_12 unknown protein; 35272-36292 [Arabidopsis thaliana] gi|21593205|gb|AAM65154.1| unknown [Arabidopsis thaliana] gi|29028824|gb|AAO64791.1| At1g68490 [Arabidopsis thaliana] gi|110736380|dbj|BAF00159.1| hypothetical protein [Arabidopsis thaliana] gi|332196678|gb|AEE34799.1| uncharacterized protein AT1G68490 [Arabidopsis thaliana]	163	183	9.00E-60	112.3	79.8	88.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G68490.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G13390.2); Has 125 Blast hits to 125 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 125; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25693926-25694946 FORWARD LENGTH=183	163	183	3.00E-62	112.3	79.8	88.3
Rsa1.0_00700.1.g18251.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00700.1.g18252.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00700.1.g18253.t1	ref|NP_177017.2| uncharacterized protein [Arabidopsis thaliana] gi|28393283|gb|AAO42069.1| unknown protein [Arabidopsis thaliana] gi|28973117|gb|AAO63883.1| unknown protein [Arabidopsis thaliana] gi|332196679|gb|AEE34800.1| uncharacterized protein AT1G68500 [Arabidopsis thaliana]	87	93	2.00E-19	106.9	72.4	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G68500.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G25422.1); Has 16 Blast hits to 16 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25702041-25702322 FORWARD LENGTH=93	87	93	3.00E-22	106.9	72.4	83.9
Rsa1.0_00701.1.g18254.t1	ref|NP_188829.1| putative cysteine-rich repeat secretory protein 17 [Arabidopsis thaliana] gi|75273781|sp|Q9LRM2.1|CRR17_ARATH RecName: Full=Putative cysteine-rich repeat secretory protein 17; Flags: Precursor gi|9279742|dbj|BAB01368.1| unnamed protein product [Arabidopsis thaliana] gi|332643044|gb|AEE76565.1| putative cysteine-rich repeat secretory protein 17 [Arabidopsis thaliana]	206	278	5.00E-30	135.0	32.0	41.3	putative cysteine-rich repeat secretory protein 17	gbpln	Arabidopsis thaliana	AT3G21910.1 | Symbols: | Domain of unknown function (DUF26) | chr3:7717372-7718405 FORWARD LENGTH=278	206	278	2.00E-32	135.0	32.0	41.3
Rsa1.0_00701.1.g18255.t1	gb|EOA32183.1| hypothetical protein CARUB_v10015439mg [Capsella rubella]	269	278	6.00E-70	103.3	52.4	70.3	hypothetical protein CARUB_v10015439mg	gbpln	Capsella rubella	AT3G21910.1 | Symbols: | Domain of unknown function (DUF26) | chr3:7717372-7718405 FORWARD LENGTH=278	269	278	2.00E-72	103.3	50.6	69.9

<table>
<tr><td>Rsa1.0_00701.1.g18256.t1</td><td>ref|XP_002885475.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]
gi|297835188|ref|XP_002885476.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]
gi|297331315|gb|EFH61734.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]
gi|297331316|gb|EFH61735.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]</td><td>199</td><td>123</td><td>7.00E-43</td><td>61.8</td><td>46.7</td><td>52.8</td><td>zinc finger (B-box type) family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G21890.1 | Symbols: | B-box type zinc finger family protein | chr3:7709298-7709663 REVERSE LENGTH=121</td><td>199</td><td>121</td><td>4.00E-44</td><td>60.8</td><td>45.2</td><td>51.3</td></tr>
<tr><td>Rsa1.0_00701.1.g18257.t1</td><td>ref|XP_002883322.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]
gi|297329162|gb|EFH59581.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]</td><td>386</td><td>377</td><td>1.00E-156</td><td>97.7</td><td>72.5</td><td>79.8</td><td>zinc finger (B-box type) family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G21880.1 | Symbols: | B-box type zinc finger protein with CCT domain | chr3:7706748-7708093 FORWARD LENGTH=364</td><td>386</td><td>364</td><td>1.00E-152</td><td>94.3</td><td>69.4</td><td>78.5</td></tr>
<tr><td>Rsa1.0_00701.1.g18258.t1</td><td>ref|XP_002885473.1| hypothetical protein ARALYDRAFT_479706 [Arabidopsis lyrata subsp. lyrata]
gi|297331313|gb|EFH61732.1| hypothetical protein ARALYDRAFT_479706 [Arabidopsis lyrata subsp. lyrata]</td><td>254</td><td>282</td><td>1.00E-99</td><td>111.0</td><td>83.1</td><td>87.0</td><td>hypothetical protein ARALYDRAFT_479706</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G21865.1 | Symbols: PEX22 | peroxin 22 | chr3:7701308-7703218 REVERSE LENGTH=283</td><td>254</td><td>283</td><td>1.00E-100</td><td>111.4</td><td>81.1</td><td>86.6</td></tr>
<tr><td>Rsa1.0_00701.1.g18259.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00701.1.g18260.t3</td><td>ref|XP_002883320.1| hypothetical protein ARALYDRAFT_898633 [Arabidopsis lyrata subsp. lyrata]
gi|297329160|gb|EFH59579.1| hypothetical protein ARALYDRAFT_898633 [Arabidopsis lyrata subsp. lyrata]</td><td>484</td><td>436</td><td>1.00E-111</td><td>90.1</td><td>53.3</td><td>62.2</td><td>hypothetical protein ARALYDRAFT_898633</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G21810.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr3:7684852-7688360 FORWARD LENGTH=437</td><td>484</td><td>437</td><td>1.00E-109</td><td>90.3</td><td>51.4</td><td>59.1</td></tr>
<tr><td>Rsa1.0_00701.1.g18261.t1</td><td>ref|XP_002885466.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331306|gb|EFH61725.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>496</td><td>494</td><td>0</td><td>99.6</td><td>70.6</td><td>83.5</td><td>UDP-glucoronosyl/UDP-glucosyl transferase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G21790.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:7676927-7678414 REVERSE LENGTH=495</td><td>496</td><td>495</td><td>0</td><td>99.8</td><td>67.9</td><td>82.1</td></tr>
<tr><td>Rsa1.0_00701.1.g18262.t1</td><td>gb|ACT35472.1| peroxidase 30, partial [Brassica rapa]</td><td>329</td><td>354</td><td>1.00E-172</td><td>107.6</td><td>89.4</td><td>93.6</td><td>peroxidase 30, partial</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G21770.1 | Symbols: | Peroxidase superfamily protein | chr3:7673345-7674661 FORWARD LENGTH=329</td><td>329</td><td>329</td><td>1.00E-173</td><td>100.0</td><td>88.4</td><td>93.3</td></tr>
<tr><td>Rsa1.0_00701.1.g18263.t1</td><td>ref|XP_002883317.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329157|gb|EFH59576.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>467</td><td>485</td><td>0</td><td>103.9</td><td>69.8</td><td>82.2</td><td>UDP-glucoronosyl/UDP-glucosyl transferase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G21760.1 | Symbols: HYR1 | UDP-Glycosyltransferase superfamily protein | chr3:7667099-7668556 FORWARD LENGTH=485</td><td>467</td><td>485</td><td>0</td><td>103.9</td><td>68.7</td><td>81.8</td></tr>
<tr><td>Rsa1.0_00701.1.g18264.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00702.1.g18265.t1</td><td>gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>217</td><td>1225</td><td>4.00E-54</td><td>564.5</td><td>46.5</td><td>68.2</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>217</td><td>626</td><td>2.00E-13</td><td>288.5</td><td>17.5</td><td>30.0</td></tr>
<tr><td>Rsa1.0_00702.1.g18266.t1</td><td>ref|NP_190493.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]
gi|75183725|sp|Q9M3A8.1|PP273_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g49240; AltName: Full=Protein EMBRYO DEFECTIVE 1796
gi|6723394|emb|CAB66403.1| putative protein [Arabidopsis thaliana]
gi|20466250|gb|AAM20442.1| putative protein [Arabidopsis thaliana]
gi|31711738|gb|AAP68225.1| At3g49240 [Arabidopsis thaliana]
gi|58013028|gb|AAW62967.1| mitochondrial embryo-defective 1796 [Arabidopsis thaliana]
gi|332644993|gb|AEE78514.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]</td><td>636</td><td>629</td><td>0</td><td>98.9</td><td>82.7</td><td>90.3</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G49240.1 | Symbols: emb1796 | Pentatricopeptide repeat (PPR) superfamily protein | chr3:18256086-18257975 FORWARD LENGTH=629</td><td>636</td><td>629</td><td>0</td><td>98.9</td><td>82.7</td><td>90.3</td></tr>
<tr><td>Rsa1.0_00702.1.g18267.t1</td><td>gb|EOA25878.1| hypothetical protein CARUB_v10019256mg [Capsella rubella]</td><td>503</td><td>339</td><td>1.00E-135</td><td>67.4</td><td>47.3</td><td>53.7</td><td>hypothetical protein CARUB_v10019256mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G49340.1 | Symbols: | Cysteine proteinases superfamily protein | chr3:18293347-18294577 REVERSE LENGTH=341</td><td>503</td><td>341</td><td>1.00E-136</td><td>67.8</td><td>45.5</td><td>53.1</td></tr>
<tr><td>Rsa1.0_00702.1.g18268.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_00702.1.g18269.t1	ref|NP_190504.2| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|66792662|gb|AAY56433.1| At3g49350 [Arabidopsis thaliana] gi|110738525|dbj|BAF01188.1| GTPase activating -like protein [Arabidopsis thaliana] gi|332645010|gb|AEE78531.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	533	539	0	101.1	88.7	92.7	RabGAP/TBC domain-containing protein	gbpln	Arabidopsis thaliana	AT3G49350.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr3:18297663-18299846 REVERSE LENGTH=539	533	539	0	101.1	88.7	92.7
Rsa1.0_00702.1.g18270.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00702.1.g18271.t1	ref|XP_002877669.1| glucosamine/galactosamine-6-phosphate isomerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297323507|gb|EFH53928.1| glucosamine/galactosamine-6-phosphate isomerase family protein [Arabidopsis lyrata subsp. lyrata]	258	259	1.00E-137	100.4	92.2	96.1	glucosamine/galactosamine-6-phosphate isomerase family protein	gbpln	Arabidopsis lyrata	AT3G49360.1 | Symbols: PGL2 | 6-phosphogluconolactonase 2 | chr3:18303189-18304283 REVERSE LENGTH=259	258	259	1.00E-138	100.4	90.3	95.0
Rsa1.0_00703.1.g18272.t1	gb|EOA29772.1| hypothetical protein CARUB_v10012863mg [Capsella rubella]	298	1102	1.00E-115	369.8	67.8	70.1	hypothetical protein CARUB_v10012863mg	gbpln	Capsella rubella	AT3G06480.1 | Symbols: | DEAD box RNA helicase family protein | chr3:1985697-1989666 REVERSE LENGTH=1088	298	1088	1.00E-117	365.1	67.1	69.8
Rsa1.0_00703.1.g18273.t4	gb|ADF30185.1| boron transporter [Brassica napus]	780	738	0	94.6	91.4	93.1	boron transporter	gbpln	Brassica napus	AT3G06450.2 | Symbols: | HCO3-transporter family | chr3:1976085-1979303 REVERSE LENGTH=732	780	732	0	93.8	86.9	90.1
Rsa1.0_00703.1.g18274.t1	ref|XP_002884578.1| hypothetical protein ARALYDRAFT_477945 [Arabidopsis lyrata subsp. lyrata] gi|297330418|gb|EFH60837.1| hypothetical protein ARALYDRAFT_477945 [Arabidopsis lyrata subsp. lyrata]	119	119	7.00E-59	100.0	90.8	97.5	hypothetical protein ARALYDRAFT_477945	gbpln	Arabidopsis lyrata	AT3G06420.1 | Symbols: ATG8H | Ubiquitin-like superfamily protein | chr3:1955219-1956274 REVERSE LENGTH=119	119	119	2.00E-61	100.0	89.9	97.5
Rsa1.0_00703.1.g18275.t2	gb|ADK63414.1| CCCH type zinc finger protein [Brassica rapa]	620	455	0	73.4	62.7	65.2	CCCH type zinc finger protein	gbpln	Brassica rapa	AT3G06410.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr3:1947471-1949528 REVERSE LENGTH=462	620	462	1.00E-162	74.5	58.2	62.4
Rsa1.0_00703.1.g18276.t1	ref|XP_002884573.1| EMB3004/MEE32 [Arabidopsis lyrata subsp. lyrata] gi|297330413|gb|EFH60832.1| EMB3004/MEE32 [Arabidopsis lyrata subsp. lyrata]	541	603	0	111.5	85.0	91.3	EMB3004/MEE32	gbpln	Arabidopsis lyrata	AT3G06350.1 | Symbols: EMB3004, MEE32 | dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative | chr3:1924536-1927701 REVERSE LENGTH=603	541	603	0	111.5	84.5	90.6
Rsa1.0_00703.1.g18277.t1	ref|XP_002884572.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330412|gb|EFH60831.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	657	671	0	102.1	63.9	75.8	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT3G06340.3 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr3:1920607-1922628 REVERSE LENGTH=673	657	673	0	102.4	65.6	77.2
Rsa1.0_00703.1.g18278.t2	gb|EOA30590.1| hypothetical protein CARUB_v10013722mg [Capsella rubella]	449	440	0	98.0	79.3	84.0	hypothetical protein CARUB_v10013722mg	gbpln	Capsella rubella	AT3G06330.1 | Symbols: | RING/U-box superfamily protein | chr3:1917334-1919709 FORWARD LENGTH=426	449	426	1.00E-173	94.9	74.2	80.2
Rsa1.0_00703.1.g18279.t1	gb|EOA31003.1| hypothetical protein CARUB_v10014146mg [Capsella rubella]	300	334	1.00E-156	111.3	93.3	96.0	hypothetical protein CARUB_v10014146mg	gbpln	Capsella rubella	AT3G06300.1 | Symbols: AT-P4H-2 | P4H isoform 2 | chr3:1907744-1909675 FORWARD LENGTH=299	300	299	1.00E-157	99.7	92.7	95.0
Rsa1.0_00703.1.g18280.t1	ref|XP_002884568.1| hypothetical protein ARALYDRAFT_477928 [Arabidopsis lyrata subsp. lyrata] gi|297330408|gb|EFH60827.1| hypothetical protein ARALYDRAFT_477928 [Arabidopsis lyrata subsp. lyrata]	1649	1703	0	103.3	81.0	87.8	hypothetical protein ARALYDRAFT_477928	gbpln	Arabidopsis lyrata	AT3G06290.1 | Symbols: | SAC3/GANP/Nin1/mts3/eIF-3 p25 family | chr3:1899123-1907297 REVERSE LENGTH=1697	1649	1697	0	102.9	79.0	86.8
Rsa1.0_00703.1.g18281.t1	ref|XP_002882459.1| hypothetical protein ARALYDRAFT_477927 [Arabidopsis lyrata subsp. lyrata] gi|297328299|gb|EFH58718.1| hypothetical protein ARALYDRAFT_477927 [Arabidopsis lyrata subsp. lyrata]	352	348	1.00E-179	98.9	88.6	92.9	hypothetical protein ARALYDRAFT_477927	gbpln	Arabidopsis lyrata	AT3G06270.1 | Symbols: | Protein phosphatase 2C family protein | chr3:1896763-1897887 FORWARD LENGTH=348	352	348	1.00E-180	98.9	88.1	92.3
Rsa1.0_00703.1.g18282.t1	gb|EOA29649.1| hypothetical protein CARUB_v10015151mg [Capsella rubella]	346	351	0	101.4	93.6	97.1	hypothetical protein CARUB_v10015151mg	gbpln	Capsella rubella	AT3G06260.1 | Symbols: GATL4 | galacturonosyltransferase-like 4 | chr3:1893804-1894859 REVERSE LENGTH=351	346	351	0	101.4	94.2	98.0
Rsa1.0_00703.1.g18283.t1	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1079	910	0	84.3	38.6	49.9	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1079	626	4.00E-91	58.0	15.5	22.2
Rsa1.0_00703.1.g18284.t1	gb|AAF79677.1|AC022314_18 F9C16.26 [Arabidopsis thaliana]	511	1902	4.00E-80	372.2	28.2	37.4	F9C16.26	gbpln	Arabidopsis thaliana	AT5G32613.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr5:12263255-12265041 FORWARD LENGTH=457	511	457	2.00E-36	89.4	17.8	23.3

Rsa1.0_00703.1.g18285.t1	gb|EOA17964.1| hypothetical protein CARUB_v10006379mg [Capsella rubella]	393	435	2.00E-57	110.7	36.1	53.2	hypothetical protein CARUB_v10006379mg	gbpln	Capsella rubella	AT4G30030.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr4:14682210-14683484 REVERSE LENGTH=424	393	424	8.00E-60	107.9	36.9	52.2
Rsa1.0_00703.1.g18286.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	386	1142	6.00E-65	295.9	31.6	43.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	386	575	5.00E-27	149.0	19.2	28.2
Rsa1.0_00703.1.g18287.t1	dbj|BAJ34465.1| unnamed protein product [Thellungiella halophila]	118	198	2.00E-48	167.8	82.2	86.4	unnamed protein product	----	----	AT2G34720.1 | Symbols: NF-YA4 | nuclear factor Y, subunit A4 | chr2:14650018-14651255 REVERSE LENGTH=198	118	198	2.00E-50	167.8	82.2	88.1
Rsa1.0_00704.1.g18288.t1	emb|CAB72466.1| putative protein [Arabidopsis thaliana]	700	377	1.00E-127	53.9	33.1	37.6	putative protein	gbpln	Arabidopsis thaliana	AT5G27260.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9603943-9604930 FORWARD LENGTH=303	700	303	4.00E-70	43.3	21.0	27.6
Rsa1.0_00704.1.g18289.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1387	1496	0	107.9	53.5	66.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1387	1262	1.00E-134	91.0	16.1	22.5
Rsa1.0_00704.1.g18290.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00704.1.g18291.t1	ref|XP_002874774.1| hypothetical protein ARALYDRAFT_490049 [Arabidopsis lyrata subsp. lyrata] gi|297320611|gb|EFH51033.1| hypothetical protein ARALYDRAFT_490049 [Arabidopsis lyrata subsp. lyrata]	161	277	1.00E-59	172.0	80.7	83.9	hypothetical protein ARALYDRAFT_490049	gbpln	Arabidopsis lyrata	AT4G12450.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G22560.1); Has 380 Blast hits to 380 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 4; Plants - 374; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr4:7385841-7386674 REVERSE LENGTH=277	161	277	1.00E-61	172.0	82.0	85.1
Rsa1.0_00704.1.g18292.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00704.1.g18293.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00704.1.g18294.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00705.1.g18295.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00705.1.g18296.t1	gb|EOA28140.1| hypothetical protein CARUB_v10024329mg [Capsella rubella]	61	123	2.00E-22	201.6	90.2	95.1	hypothetical protein CARUB_v10024329mg	gbpln	Capsella rubella	AT2G41905.1 | Symbols: | BEST Arabidopsis thaliana protein match is: arabinogalactan protein 23 (TAIR:AT3G57690.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17495766-17495951 FORWARD LENGTH=61	61	61	4.00E-25	100.0	93.4	95.1
Rsa1.0_00705.1.g18297.t1	dbj|BAJ33641.1| unnamed protein product [Thellungiella halophila]	165	723	5.00E-21	438.2	41.8	46.1	unnamed protein product	----	----	AT2G41900.1 | Symbols: | CCCH-type zinc finger protein with ARM repeat domain | chr2:17491352-17493502 FORWARD LENGTH=716	165	716	3.00E-23	433.9	41.8	45.5
Rsa1.0_00705.1.g18298.t1	gb|EOA27653.1| hypothetical protein CARUB_v10023800mg [Capsella rubella]	453	283	1.00E-122	62.5	53.0	54.7	hypothetical protein CARUB_v10023800mg	gbpln	Capsella rubella	AT1G58684.1 | Symbols: | Ribosomal protein S5 family protein | chr1:21770021-21771217 REVERSE LENGTH=284	453	284	1.00E-121	62.7	45.7	47.5
Rsa1.0_00705.1.g18299.t1	gb|EOA24665.1| hypothetical protein CARUB_v10017938mg [Capsella rubella]	225	242	2.00E-31	107.6	51.6	65.8	hypothetical protein CARUB_v10017938mg	gbpln	Capsella rubella	AT3G57440.1 | Symbols: | unknown protein; Has 31 Blast hits to 31 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:21258732-21260249 FORWARD LENGTH=241	225	241	5.00E-33	107.1	52.0	64.9
Rsa1.0_00705.1.g18300.t1	ref|NP_565960.1| uncharacterized protein [Arabidopsis thaliana] gi|2335100|gb|AAC02770.1| expressed protein [Arabidopsis thaliana] gi|15810461|gb|AAL07118.1| unknown protein [Arabidopsis thaliana] gi|330254936|gb|AEC10030.1| uncharacterized protein AT2G41770 [Arabidopsis thaliana]	756	771	0	102.0	89.9	95.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G41770.1 | Symbols: | Protein of unknown function (DUF288) | chr2:17424549-17427042 REVERSE LENGTH=771	756	771	0	102.0	89.9	95.2
Rsa1.0_00705.1.g18301.t1	ref|XP_002879951.1| hypothetical protein ARALYDRAFT_903515 [Arabidopsis lyrata subsp. lyrata] gi|297325790|gb|EFH56210.1| hypothetical protein ARALYDRAFT_903515 [Arabidopsis lyrata subsp. lyrata]	212	221	1.00E-109	104.2	89.2	95.8	hypothetical protein ARALYDRAFT_903515	gbpln	Arabidopsis lyrata	AT2G41760.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function WDYHV (InterPro:IPR019161); Has 201 Blast hits to 201 proteins in 90 species: Archae - 0; Bacteria - 2; Metazoa - 132; Fungi - 10; Plants - 30; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:17422864-17424255 FORWARD LENGTH=221	212	221	1.00E-110	104.2	89.6	94.8

<table>
<tr><td>Rsa1.0_00705.1.g18302.t1</td><td>ref|NP_565958.1| villin 2 [Arabidopsis thaliana]
gi|25091521|sp|O81644.2|VILI2_ARATH RecName: Full=Villin-2
gi|19310558|gb|AAL85012.1| putative villin 2 protein [Arabidopsis thaliana]
gi|20196894|gb|AAC02774.2| putative villin 2 [Arabidopsis thaliana]
gi|22136974|gb|AAM91716.1| putative villin 2 protein [Arabidopsis thaliana]
gi|110742058|dbj|BAE98961.1| putative villin 2 protein [Arabidopsis thaliana]
gi|330254933|gb|AEC10027.1| villin 2 [Arabidopsis thaliana]</td><td>962</td><td>976</td><td>0</td><td>101.5</td><td>88.9</td><td>94.3</td><td>villin 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G41740.1 | Symbols: VLN2, ATVLN2 | villin 2 | chr2:17410962-17416878 REVERSE LENGTH=976</td><td>962</td><td>976</td><td>0</td><td>101.5</td><td>88.9</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00705.1.g18303.t1</td><td>ref|NP_850354.2| ABC transporter A family member 1 [Arabidopsis thaliana]
gi|75327922|sp|Q84M24.2|AB1A_ARATH RecName: Full=ABC transporter A family member 1; Short=ABC transporter ABCA.1; Short=AtABCA1; AltName: Full=ABC one homolog protein 1; Short=AtAOH1
gi|45504175|dbj|BAC75958.2| AtABCA1 [Arabidopsis thaliana]
gi|330254923|gb|AEC10017.1| ABC transporter A family member 1 [Arabidopsis thaliana]</td><td>1850</td><td>1882</td><td>0</td><td>101.7</td><td>90.2</td><td>94.9</td><td>ABC transporter A family member 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G41700.1 | Symbols: ABCA1, AtABCA1 | ATP-binding cassette A1 | chr2:17383239-17396110 REVERSE LENGTH=1882</td><td>1850</td><td>1882</td><td>0</td><td>101.7</td><td>90.2</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00705.1.g18304.t1</td><td>ref|NP_181700.1| heat stress transcription factor B-3 [Arabidopsis thaliana]
gi|75277249|sp|O22230.1|HSFB3_ARATH RecName: Full=Heat stress transcription factor B-3; Short=AtHsfB3; AltName: Full=AtHsf-05
gi|2618703|gb|AAB84350.1| putative heat shock transcription factor [Arabidopsis thaliana]
gi|117958747|gb|ABK59681.1| At2g41690 [Arabidopsis thaliana]
gi|330254922|gb|AEC10016.1| heat stress transcription factor B-3 [Arabidopsis thaliana]</td><td>317</td><td>244</td><td>4.00E-46</td><td>77.0</td><td>35.0</td><td>37.9</td><td>heat stress transcription factor B-3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G41690.1 | Symbols: AT-HSFB3, HSFB3 | heat shock transcription factor B3 | chr2:17381723-17382577 FORWARD LENGTH=244</td><td>317</td><td>244</td><td>1.00E-48</td><td>77.0</td><td>35.0</td><td>37.9</td></tr>
<tr><td>Rsa1.0_00705.1.g18305.t1</td><td>gb|EOA26894.1| hypothetical protein CARUB_v10022987mg [Capsella rubella]</td><td>549</td><td>528</td><td>0</td><td>96.2</td><td>87.1</td><td>89.8</td><td>hypothetical protein CARUB_v10022987mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G41680.1 | Symbols: NTRC | NADPH-dependent thioredoxin reductase C | chr2:17376349-17379028 REVERSE LENGTH=529</td><td>549</td><td>529</td><td>0</td><td>96.4</td><td>86.0</td><td>89.3</td></tr>
<tr><td>Rsa1.0_00705.1.g18306.t2</td><td>gb|AAD28689.1| putative TNP1-like transposon protein [Arabidopsis thaliana]</td><td>245</td><td>984</td><td>3.00E-26</td><td>401.6</td><td>24.1</td><td>33.5</td><td>putative TNP1-like transposon protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00706.1.g18307.t2</td><td>ref|XP_002867786.1| plant UBX domain-containing protein 3 [Arabidopsis lyrata subsp. lyrata]
gi|297313622|gb|EFH44045.1| plant UBX domain-containing protein 3 [Arabidopsis lyrata subsp. lyrata]</td><td>257</td><td>302</td><td>1.00E-112</td><td>117.5</td><td>85.2</td><td>89.5</td><td>plant UBX domain-containing protein 3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22150.1 | Symbols: PUX3 | plant UBX domain-containing protein 3 | chr4:11731272-11732800 REVERSE LENGTH=367</td><td>257</td><td>367</td><td>1.00E-111</td><td>142.8</td><td>82.9</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00706.1.g18308.t1</td><td>ref|XP_002869839.1| hypothetical protein ARALYDRAFT_492649 [Arabidopsis lyrata subsp. lyrata]
gi|297315675|gb|EFH46098.1| hypothetical protein ARALYDRAFT_492649 [Arabidopsis lyrata subsp. lyrata]</td><td>133</td><td>148</td><td>8.00E-30</td><td>111.3</td><td>59.4</td><td>69.2</td><td>hypothetical protein ARALYDRAFT_492649</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22160.1 | Symbols: | unknown protein; Has 42 Blast hits to 42 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11733182-11733610 FORWARD LENGTH=142</td><td>133</td><td>142</td><td>4.00E-31</td><td>106.8</td><td>57.1</td><td>68.4</td></tr>
<tr><td>Rsa1.0_00706.1.g18309.t1</td><td>ref|XP_002869837.1| hypothetical protein ARALYDRAFT_914405 [Arabidopsis lyrata subsp. lyrata]
gi|297315673|gb|EFH46096.1| hypothetical protein ARALYDRAFT_914405 [Arabidopsis lyrata subsp. lyrata]</td><td>339</td><td>384</td><td>1.00E-86</td><td>113.3</td><td>57.8</td><td>71.4</td><td>hypothetical protein ARALYDRAFT_914405</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22180.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr4:11738574-11739782 FORWARD LENGTH=402</td><td>339</td><td>402</td><td>3.00E-80</td><td>118.6</td><td>53.7</td><td>67.8</td></tr>
<tr><td>Rsa1.0_00706.1.g18310.t1</td><td>ref|XP_002869837.1| hypothetical protein ARALYDRAFT_914405 [Arabidopsis lyrata subsp. lyrata]
gi|297315673|gb|EFH46096.1| hypothetical protein ARALYDRAFT_914405 [Arabidopsis lyrata subsp. lyrata]</td><td>388</td><td>384</td><td>1.00E-111</td><td>99.0</td><td>58.0</td><td>68.6</td><td>hypothetical protein ARALYDRAFT_914405</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22170.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr4:11736653-11737744 FORWARD LENGTH=363</td><td>388</td><td>363</td><td>1.00E-104</td><td>93.6</td><td>52.8</td><td>65.5</td></tr>
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Rsa1.0_00706.1.g18311.t1	ref|NP_567650.2| uncharacterized protein [Arabidopsis thaliana] gi|20466282|gb|AAM20458.1| unknown protein [Arabidopsis thaliana] gi|22136352|gb|AAM91254.1| unknown protein [Arabidopsis thaliana] gi|332659170|gb|AEE84570.1| uncharacterized protein AT4G22190 [Arabidopsis thaliana]	336	387	1.00E-135	115.2	82.7	89.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G22190.1 | Symbols: | unknown protein; Has 283 Blast hits to 154 proteins in 44 species: Archae - 0; Bacteria - 2; Metazoa - 24; Fungi - 12; Plants - 48; Viruses - 0; Other Eukaryotes - 197 (source: NCBI BLink). | chr4:11742102-11743265 REVERSE LENGTH=387	336	387	1.00E-137	115.2	82.7	89.6
Rsa1.0_00706.1.g18312.t1	ref|NP_567651.1| Potassium channel AKT2/3 [Arabidopsis thaliana] gi|44887668|sp|Q38898.1|AKT2_ARATH RecName: Full=Potassium channel AKT2/3 gi|1100898|gb|AAA97865.1| potassium channel [Arabidopsis thaliana] gi|110739319|dbj|BAF01572.1| potassium channel [Arabidopsis thaliana] gi|332659171|gb|AEE84571.1| Potassium channel AKT2/3 [Arabidopsis thaliana]	814	802	0	98.5	84.9	90.7	Potassium channel AKT2/3	gbpln	Arabidopsis thaliana	AT4G22200.1 | Symbols: AKT2/3, AKT3, AKT2, KT2/3 | potassium transport 2/3 | chr4:11746666-11750091 REVERSE LENGTH=802	814	802	0	98.5	84.9	90.7
Rsa1.0_00706.1.g18313.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00706.1.g18314.t1	ref|XP_002867782.1| iron-sulfur cluster assembly complex protein [Arabidopsis lyrata subsp. lyrata] gi|297313618|gb|EFH44041.1| iron-sulfur cluster assembly complex protein [Arabidopsis lyrata subsp. lyrata]	158	167	3.00E-86	105.7	96.2	98.7	iron-sulfur cluster assembly complex protein	gbpln	Arabidopsis lyrata	AT4G22220.1 | Symbols: ISU1, ATISU1 | SufE/NifU family protein | chr4:11759444-11760881 REVERSE LENGTH=167	158	167	3.00E-88	105.7	95.6	98.1
Rsa1.0_00706.1.g18315.t1	sp|Q94KU6.1|PAP2_BRACM RecName: Full=Plastid lipid-associated protein 2, chloroplastic; Flags: Precursor gi|14248556|gb|AAK57565.1|AF290567_1 plastid-lipid associated protein PAP2 [Brassica rapa subsp. oleifera]	317	319	1.00E-160	100.6	91.8	95.0	RecName: Full=Plastid lipid-associated protein 2, chloroplastic; Flags: Precursor gi|14248556|gb|AAK57565.1|AF290567_1 plastid-lipid associated protein PAP2	gbpln	Brassica rapa	AT4G22240.1 | Symbols: | Plastid-lipid associated protein PAP / fibrillin family protein | chr4:11766090-11767227 REVERSE LENGTH=310	317	310	1.00E-142	97.8	82.3	86.4
Rsa1.0_00706.1.g18316.t1	ref|XP_002867780.1| hypothetical protein ARALYDRAFT_492641 [Arabidopsis lyrata subsp. lyrata] gi|297313616|gb|EFH44039.1| hypothetical protein ARALYDRAFT_492641 [Arabidopsis lyrata subsp. lyrata]	206	214	4.00E-75	103.9	76.2	83.0	hypothetical protein ARALYDRAFT_492641	gbpln	Arabidopsis lyrata	AT4G22250.1 | Symbols: | RING/U-box superfamily protein | chr4:11767685-11768329 REVERSE LENGTH=214	206	214	4.00E-77	103.9	75.7	81.6
Rsa1.0_00706.1.g18317.t1	gb|EOA16917.1| hypothetical protein CARUB_v10005140mg [Capsella rubella]	351	353	1.00E-169	100.6	84.3	89.7	hypothetical protein CARUB_v10005140mg	gbpln	Capsella rubella	AT4G22260.1 | Symbols: IM, IM1 | Alternative oxidase family protein | chr4:11769967-11772350 REVERSE LENGTH=351	351	351	1.00E-166	100.0	82.6	88.6
Rsa1.0_00706.1.g18318.t1	gb|EOA16619.1| hypothetical protein CARUB_v10004790mg [Capsella rubella]	430	444	0	103.3	90.2	94.4	hypothetical protein CARUB_v10004790mg	gbpln	Capsella rubella	AT4G22270.1 | Symbols: MRB1, ATMRB1 | Protein of unknown function (DUF3537) | chr4:11773396-11775782 FORWARD LENGTH=437	430	437	0	101.6	88.1	93.5
Rsa1.0_00706.1.g18319.t1	gb|EOA16644.1| hypothetical protein CARUB_v10004819mg [Capsella rubella]	414	442	0	106.8	90.3	94.2	hypothetical protein CARUB_v10004819mg	gbpln	Capsella rubella	AT4G22290.1 | Symbols: | Ubiquitin-specific protease family C19-related protein | chr4:11783199-11785730 REVERSE LENGTH=445	414	445	0	107.5	90.1	93.7
Rsa1.0_00706.1.g18320.t1	ref|XP_002867776.1| hypothetical protein ARALYDRAFT_492635 [Arabidopsis lyrata subsp. lyrata] gi|297313612|gb|EFH44035.1| hypothetical protein ARALYDRAFT_492635 [Arabidopsis lyrata subsp. lyrata]	212	234	4.00E-64	110.4	74.1	80.7	hypothetical protein ARALYDRAFT_492635	gbpln	Arabidopsis lyrata	AT4G22320.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G55210.1). | chr4:11793129-11794596 REVERSE LENGTH=237	212	237	5.00E-63	111.8	71.7	80.7
Rsa1.0_00706.1.g18321.t1	gb|EOA17285.1| hypothetical protein CARUB_v10005555mg [Capsella rubella]	255	255	2.33E-156	100.0	96.9	98.8	hypothetical protein CARUB_v10005555mg	gbpln	Capsella rubella	AT4G22330.1 | Symbols: ATCES1 | Alkaline phytoceramidase (aPHC) | chr4:11798483-11799549 FORWARD LENGTH=255	255	255	1.00E-148	100.0	96.5	98.4
Rsa1.0_00706.1.g18322.t1	ref|XP_002867775.1| hypothetical protein ARALYDRAFT_492631 [Arabidopsis lyrata subsp. lyrata] gi|297313611|gb|EFH44034.1| hypothetical protein ARALYDRAFT_492631 [Arabidopsis lyrata subsp. lyrata]	423	423	0	100.0	94.1	96.9	hypothetical protein ARALYDRAFT_492631	gbpln	Arabidopsis lyrata	AT4G22340.3 | Symbols: CDS2 | cytidinediphosphate diacylglycerol synthase 2 | chr4:11800150-11802621 REVERSE LENGTH=447	423	447	0	105.7	93.6	96.5
Rsa1.0_00706.1.g18323.t1	ref|XP_002867774.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313610|gb|EFH44033.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	510	506	0	99.2	88.8	93.1	ubiquitin carboxyl-terminal hydrolase family protein	gbpln	Arabidopsis lyrata	AT4G22350.1 | Symbols: | Ubiquitin C-terminal hydrolases superfamily protein | chr4:11804073-11806939 REVERSE LENGTH=510	510	510	0	100.0	87.8	92.4

<table>
<tr><td>Rsa1.0_00706.1.g18324.t1</td><td>emb|CAA16787.1| hypothetical protein [Arabidopsis thaliana] gi|7269083|emb|CAB79192.1| hypothetical protein [Arabidopsis thaliana]</td><td>279</td><td>205</td><td>4.00E-54</td><td>73.5</td><td>45.2</td><td>52.0</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G22370.1 | Symbols: | unknown protein; Has 12 Blast hits to 12 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11810169-11810957 REVERSE LENGTH=130</td><td>279</td><td>130</td><td>3.00E-50</td><td>46.6</td><td>38.0</td><td>41.6</td></tr>
<tr><td>Rsa1.0_00706.1.g18325.t1</td><td>gb|ABL97959.1| ribosomal protein L7Ae-like [Brassica rapa]</td><td>128</td><td>128</td><td>2.00E-66</td><td>100.0</td><td>98.4</td><td>100.0</td><td>ribosomal protein L7Ae-like</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G20160.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr5:6804075-6805102 REVERSE LENGTH=128</td><td>128</td><td>128</td><td>1.00E-59</td><td>100.0</td><td>95.3</td><td>97.7</td></tr>
<tr><td>Rsa1.0_00706.1.g18326.t1</td><td>ref|XP_002869826.1| hypothetical protein ARALYDRAFT_914375 [Arabidopsis lyrata subsp. lyrata] gi|297315662|gb|EFH46085.1| hypothetical protein ARALYDRAFT_914375 [Arabidopsis lyrata subsp. lyrata]</td><td>246</td><td>246</td><td>1.00E-137</td><td>100.0</td><td>97.2</td><td>98.4</td><td>hypothetical protein ARALYDRAFT_914375</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G12590.1 | Symbols: | Protein of unknown function DUF106, transmembrane | chr4:7451291-7452976 REVERSE LENGTH=246</td><td>246</td><td>246</td><td>1.00E-138</td><td>100.0</td><td>96.3</td><td>97.6</td></tr>
<tr><td>Rsa1.0_00706.1.g18327.t1</td><td>sp|Q3ECR3.3|FB305_ARATH RecName: Full=Putative F-box protein At1g53360</td><td>396</td><td>384</td><td>3.00E-75</td><td>97.0</td><td>44.9</td><td>59.1</td><td>RecName: Full=Putative F-box protein At1g53360</td><td>----</td><td>----</td><td>AT1G53360.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:19907517-19908548 FORWARD LENGTH=343</td><td>396</td><td>343</td><td>2.00E-74</td><td>86.6</td><td>43.4</td><td>56.3</td></tr>
<tr><td>Rsa1.0_00706.1.g18328.t1</td><td>emb|CAA16549.1| putative protein [Arabidopsis thaliana]</td><td>140</td><td>140</td><td>2.00E-34</td><td>100.0</td><td>55.0</td><td>77.9</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G22640.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:11911658-11912008 FORWARD LENGTH=116</td><td>140</td><td>116</td><td>1.00E-27</td><td>82.9</td><td>43.6</td><td>62.1</td></tr>
<tr><td>Rsa1.0_00706.1.g18329.t1</td><td>ref|XP_002869813.1| hypothetical protein ARALYDRAFT_492602 [Arabidopsis lyrata subsp. lyrata] gi|297315649|gb|EFH46072.1| hypothetical protein ARALYDRAFT_492602 [Arabidopsis lyrata subsp. lyrata]</td><td>404</td><td>425</td><td>1.00E-134</td><td>105.2</td><td>63.6</td><td>67.8</td><td>hypothetical protein ARALYDRAFT_492602</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22670.1 | Symbols: AtHip1, HIP1, TPR11 | HSP70-interacting protein 1 | chr4:11918236-11920671 FORWARD LENGTH=441</td><td>404</td><td>441</td><td>1.00E-136</td><td>109.2</td><td>63.4</td><td>67.6</td></tr>
<tr><td>Rsa1.0_00706.1.g18330.t1</td><td>dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]</td><td>1557</td><td>910</td><td>0</td><td>58.4</td><td>29.7</td><td>41.0</td><td>putative reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1557</td><td>626</td><td>1.00E-114</td><td>40.2</td><td>12.9</td><td>19.6</td></tr>
<tr><td>Rsa1.0_00706.1.g18331.t1</td><td>gb|EOA17210.1| hypothetical protein CARUB_v10005483mg [Capsella rubella]</td><td>267</td><td>271</td><td>1.00E-121</td><td>101.5</td><td>81.3</td><td>87.6</td><td>hypothetical protein CARUB_v10005483mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G22680.1 | Symbols: MYB85, AtMYB85 | myb domain protein 85 | chr4:11922789-11924080 REVERSE LENGTH=266</td><td>267</td><td>266</td><td>1.00E-116</td><td>99.6</td><td>79.8</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00706.1.g18332.t1</td><td>ref|XP_002869812.1| hypothetical protein ARALYDRAFT_354499 [Arabidopsis lyrata subsp. lyrata] gi|297315648|gb|EFH46071.1| hypothetical protein ARALYDRAFT_354499 [Arabidopsis lyrata subsp. lyrata]</td><td>524</td><td>524</td><td>0</td><td>100.0</td><td>94.5</td><td>98.1</td><td>hypothetical protein ARALYDRAFT_354499</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22690.1 | Symbols: CYP706A1 | cytochrome P450, family 706, subfamily A, polypeptide 1 | chr4:11929847-11931520 FORWARD LENGTH=557</td><td>524</td><td>557</td><td>0</td><td>106.3</td><td>93.7</td><td>97.7</td></tr>
<tr><td>Rsa1.0_00706.1.g18333.t1</td><td>ref|XP_002869810.1| glycoprotease M22 family protein [Arabidopsis lyrata subsp. lyrata] gi|297315646|gb|EFH46069.1| glycoprotease M22 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>351</td><td>353</td><td>0</td><td>100.6</td><td>95.7</td><td>98.3</td><td>glycoprotease M22 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22720.2 | Symbols: | Actin-like ATPase superfamily protein | chr4:11937467-11938717 FORWARD LENGTH=353</td><td>351</td><td>353</td><td>0</td><td>100.6</td><td>94.9</td><td>98.0</td></tr>
<tr><td>Rsa1.0_00706.1.g18334.t1</td><td>ref|XP_002869809.1| hypothetical protein ARALYDRAFT_492596 [Arabidopsis lyrata subsp. lyrata] gi|297315645|gb|EFH46068.1| hypothetical protein ARALYDRAFT_492596 [Arabidopsis lyrata subsp. lyrata]</td><td>688</td><td>687</td><td>0</td><td>99.9</td><td>87.9</td><td>94.0</td><td>hypothetical protein ARALYDRAFT_492596</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G22730.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:11941384-11943696 FORWARD LENGTH=688</td><td>688</td><td>688</td><td>0</td><td>100.0</td><td>88.7</td><td>93.5</td></tr>
<tr><td>Rsa1.0_00706.1.g18335.t1</td><td>gb|EOA16462.1| hypothetical protein CARUB_v10004615mg [Capsella rubella]</td><td>472</td><td>508</td><td>1.00E-112</td><td>107.6</td><td>52.8</td><td>63.3</td><td>hypothetical protein CARUB_v10004615mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G46000.1 | Symbols: | Mannose-binding lectin superfamily protein | chr5:18654319-18656376 REVERSE LENGTH=396</td><td>472</td><td>396</td><td>3.00E-94</td><td>83.9</td><td>48.7</td><td>56.4</td></tr>
<tr><td>Rsa1.0_00706.1.g18336.t1</td><td>ref|NP_567666.1| glycine-rich protein [Arabidopsis thaliana] gi|30685911|ref|NP_849421.1| glycine-rich protein [Arabidopsis thaliana] gi|15809950|gb|AAL06902.1| AT4g22740/T12H17_130 [Arabidopsis thaliana] gi|19347920|gb|AAL85981.1| unknown protein [Arabidopsis thaliana] gi|21436279|gb|AAM51278.1| unknown protein [Arabidopsis thaliana] gi|332659246|gb|AEE84646.1| glycine-rich protein [Arabidopsis thaliana] gi|332659247|gb|AEE84647.1| glycine-rich protein [Arabidopsis thaliana]</td><td>618</td><td>356</td><td>2.00E-62</td><td>57.6</td><td>23.6</td><td>25.7</td><td>glycine-rich protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G22740.2 | Symbols: | glycine-rich protein | chr4:11944050-11945565 REVERSE LENGTH=356</td><td>618</td><td>356</td><td>4.00E-65</td><td>57.6</td><td>23.6</td><td>25.7</td></tr>
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Rsa1.0_00706.1.g18337.t3	ref|NP_001190801.1| sterol 4-alpha methyl oxidase 1-3 [Arabidopsis thaliana] gi|332659250|gb|AEE84650.1| sterol 4-alpha methyl oxidase 1-3 [Arabidopsis thaliana]	290	581	1.00E-151	200.3	86.9	93.4	sterol 4-alpha methyl oxidase 1-3	gbpln	Arabidopsis thaliana	AT4G22753.2 | Symbols: SMO1-3 | sterol 4-alpha methyl oxidase 1-3 | chr4:11949366-11953609 REVERSE LENGTH=581	290	581	1.00E-153	200.3	86.9	93.4
Rsa1.0_00706.1.g18338.t1	gb|AAF23831.1|AC007234_3 F1E22.12 [Arabidopsis thaliana]	255	1055	5.00E-90	413.7	63.9	75.3	F1E22.12	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17201414-17202323 REVERSE LENGTH=258	255	258	2.00E-66	101.2	47.8	58.0
Rsa1.0_00706.1.g18339.t1	gb|EOA16884.1| hypothetical protein CARUB_v10005108mg [Capsella rubella]	296	362	1.00E-159	122.3	92.2	95.9	hypothetical protein CARUB_v10005108mg	gbpln	Capsella rubella	AT4G22756.1 | Symbols: SMO1-2, ATSMO1, ATSMO1-2, SMO1 | sterol C4-methyl oxidase 1-2 | chr4:11955124-11956695 REVERSE LENGTH=299	296	299	1.00E-159	101.0	90.5	95.6
Rsa1.0_00706.1.g18340.t2	ref|XP_002869806.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315642|gb|EFH46065.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	899	852	0	94.8	70.4	80.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G22760.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:11960553-11962289 FORWARD LENGTH=578	899	578	0	64.3	49.1	56.8
Rsa1.0_00706.1.g18341.t1	ref|NP_194008.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|2827554|emb|CAA16562.1| putative DNA binding protein [Arabidopsis thaliana] gi|7269124|emb|CAB79232.1| putative DNA binding protein [Arabidopsis thaliana] gi|21537115|gb|AAM61456.1| putative DNA binding protein [Arabidopsis thaliana] gi|111074368|gb|ABH04557.1| At4g22770 [Arabidopsis thaliana] gi|119657348|tpd|FAA00273.1| TPA: AT-hook motif nuclear localized protein 2 [Arabidopsis thaliana] gi|225898799|dbj|BAH30530.1| hypothetical protein [Arabidopsis thaliana] gi|332659256|gb|AEE84656.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	210	334	2.00E-81	159.0	81.0	87.1	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT4G22770.1 | Symbols: | AT hook motif DNA-binding family protein | chr4:11963879-11965439 REVERSE LENGTH=334	210	334	7.00E-84	159.0	81.0	87.1
Rsa1.0_00706.1.g18342.t1	ref|NP_175703.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|12324642|gb|AAG52278.1|AC019018_15 putative replication protein; 94555-97079 [Arabidopsis thaliana] gi|332194750|gb|AEE32871.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	506	566	9.00E-96	111.9	34.2	61.7	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	506	566	2.00E-98	111.9	34.2	61.7
Rsa1.0_00706.1.g18343.t3	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	1711	1752	0	102.4	53.9	70.0	putative protein	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1711	331	2.00E-70	19.3	8.1	11.1
Rsa1.0_00706.1.g18344.t1	ref|XP_002867750.1| hypothetical protein ARALYDRAFT_492590 [Arabidopsis lyrata subsp. lyrata] gi|297313586|gb|EFH44009.1| hypothetical protein ARALYDRAFT_492590 [Arabidopsis lyrata subsp. lyrata]	449	449	0	100.0	92.4	96.2	hypothetical protein ARALYDRAFT_492590	gbpln	Arabidopsis lyrata	AT4G22780.1 | Symbols: ACR7 | ACT domain repeat 7 | chr4:11968696-11970956 REVERSE LENGTH=449	449	449	0	100.0	92.9	96.0
Rsa1.0_00706.1.g18345.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	310	1274	5.00E-41	411.0	34.5	48.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	310	303	1.00E-37	97.7	31.3	45.2
Rsa1.0_00706.1.g18346.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00706.1.g18347.t1	ref|XP_002867749.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297313585|gb|EFH44008.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	501	487	0	97.2	81.0	88.4	mate efflux family protein	gbpln	Arabidopsis lyrata	AT4G22790.1 | Symbols: | MATE efflux family protein | chr4:11975153-11976628 REVERSE LENGTH=491	501	491	0	98.0	79.2	88.2
Rsa1.0_00706.1.g18348.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00706.1.g18349.t1</td><td>ref|NP_194012.1| putative AT-hook DNA-binding family protein [Arabidopsis thaliana] gi|2827558|emb|CAA16566.1| putative DNA binding protein [Arabidopsis thaliana] gi|7269128|emb|CAB79236.1| putative DNA binding protein [Arabidopsis thaliana] gi|110738517|dbj|BAF01184.1| putative DNA binding protein [Arabidopsis thaliana] gi|119657392|tpd|FAA00295.1| TPA: AT-hook motif nuclear localized protein 24 [Arabidopsis thaliana] gi|225898801|dbj|BAH30531.1| hypothetical protein [Arabidopsis thaliana] gi|332659260|gb|AEE84660.1| putative AT-hook DNA-binding family protein [Arabidopsis thaliana]</td><td>326</td><td>324</td><td>1.00E-114</td><td>99.4</td><td>86.5</td><td>89.9</td><td>putative AT-hook DNA-binding family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G22810.1 | Symbols: | Predicted AT-hook DNA-binding family protein | chr4:11984432-11985406 FORWARD LENGTH=324</td><td>326</td><td>324</td><td>1.00E-117</td><td>99.4</td><td>86.5</td><td>89.9</td></tr>
<tr><td>Rsa1.0_00707.1.g18350.t1</td><td>ref|NP_181213.1| cytokinin-O-glucosyltransferase 1 [Arabidopsis thaliana] gi|66774040|sp|Q9ZQ99.1|U73C1_ARATH RecName: Full=UDP-glycosyltransferase 73C1; AltName: Full=Cytokinin-O-glucosyltransferase 1; AltName: Full=Zeatin O-glucosyltransferase 1; Short=AtZOG1 gi|4415920|gb|AAD20151.1| putative glucosyl transferase [Arabidopsis thaliana] gi|46318041|gb|AAS87590.1| zeatin O-glucosyltransferase 1 [Arabidopsis thaliana] gi|111074234|gb|ABH04490.1| At2g36750 [Arabidopsis thaliana] gi|330254200|gb|AEC09294.1| cytokinin-O-glucosyltransferase 1 [Arabidopsis thaliana]</td><td>495</td><td>491</td><td>0</td><td>99.2</td><td>82.4</td><td>90.7</td><td>cytokinin-O-glucosyltransferase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G36750.1 | Symbols: UGT73C1 | UDP-glucosyl transferase 73C1 | chr2:15410531-15412006 REVERSE LENGTH=491</td><td>495</td><td>491</td><td>0</td><td>99.2</td><td>82.4</td><td>90.7</td></tr>
<tr><td>Rsa1.0_00707.1.g18351.t1</td><td>ref|XP_002881468.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297327307|gb|EFH57727.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>496</td><td>496</td><td>0</td><td>100.0</td><td>81.3</td><td>90.7</td><td>UDP-glucoronosyl/UDP-glucosyl transferase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G36780.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:15417618-15419108 REVERSE LENGTH=496</td><td>496</td><td>496</td><td>0</td><td>100.0</td><td>82.5</td><td>90.3</td></tr>
<tr><td>Rsa1.0_00707.1.g18352.t1</td><td>ref|XP_002881469.1| don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297327308|gb|EFH57728.1| don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata]</td><td>497</td><td>496</td><td>0</td><td>99.8</td><td>83.3</td><td>91.5</td><td>don-glucosyltransferase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G36800.1 | Symbols: DOGT1, UGT73C5 | don-glucosyltransferase 1 | chr2:15423493-15424980 REVERSE LENGTH=495</td><td>497</td><td>495</td><td>0</td><td>99.6</td><td>81.9</td><td>90.3</td></tr>
<tr><td>Rsa1.0_00707.1.g18353.t1</td><td>gb|EOA26985.1| hypothetical protein CARUB_v10023081mg [Capsella rubella]</td><td>496</td><td>495</td><td>0</td><td>99.8</td><td>83.1</td><td>90.9</td><td>hypothetical protein CARUB_v10023081mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G36800.1 | Symbols: DOGT1, UGT73C5 | don-glucosyltransferase 1 | chr2:15423493-15424980 REVERSE LENGTH=495</td><td>496</td><td>495</td><td>0</td><td>99.8</td><td>81.5</td><td>90.1</td></tr>
<tr><td>Rsa1.0_00707.1.g18354.t1</td><td>gb|EOA28137.1| hypothetical protein CARUB_v10024326mg [Capsella rubella]</td><td>127</td><td>124</td><td>3.00E-60</td><td>97.6</td><td>92.1</td><td>96.1</td><td>hypothetical protein CARUB_v10024326mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G36835.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 26 Blast hits to 26 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15449839-15451307 REVERSE LENGTH=124</td><td>127</td><td>124</td><td>6.00E-62</td><td>97.6</td><td>91.3</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00707.1.g18355.t1</td><td>gb|EOA26452.1| hypothetical protein CARUB_v10022498mg [Capsella rubella]</td><td>1930</td><td>1897</td><td>0</td><td>98.3</td><td>90.3</td><td>94.2</td><td>hypothetical protein CARUB_v10022498mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G36850.1 | Symbols: ATGSL08, GSL8, GSL08, ATGSL8, CHOR | glucan synthase-like 8 | chr2:15454935-15469666 REVERSE LENGTH=1904</td><td>1930</td><td>1904</td><td>0</td><td>98.7</td><td>90.1</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00707.1.g18356.t1</td><td>ref|NP_174450.2| putative copper amine oxidase [Arabidopsis thaliana] gi|332193262|gb|AEE31383.1| putative copper amine oxidase [Arabidopsis thaliana]</td><td>156</td><td>677</td><td>1.00E-59</td><td>434.0</td><td>72.4</td><td>78.2</td><td>putative copper amine oxidase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31690.1 | Symbols: | Copper amine oxidase family protein | chr1:11343980-11347767 FORWARD LENGTH=677</td><td>156</td><td>677</td><td>5.00E-62</td><td>434.0</td><td>72.4</td><td>78.2</td></tr>
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Rsa1.0_00707.1.g18357.t1	ref|NP_181224.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|38605514|sp|Q9SJL9.1|XTH32_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 32; Short=At-XTH32; Short=XTH-32; Flags: Precursor gi|4883603|gb|AAD31572.1| xyloglucan endotransglycosylase, putative [Arabidopsis thaliana] gi|15027967|gb|AAK76514.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|21595304|gb|AAM66089.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|22136872|gb|AAM91780.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|330254214|gb|AEC09308.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana]	299	299	1.00E-167	100.0	94.6	98.0	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT2G36870.1 | Symbols: XTH32 | xyloglucan endotransglucosylase/hydrolase 32 | chr2:15472869-15474630 REVERSE LENGTH=299	299	299	1.00E-170	100.0	94.6	98.0
Rsa1.0_00707.1.g18358.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00707.1.g18359.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	900	1274	0	141.6	47.0	64.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	900	575	1.00E-75	63.9	19.6	30.1
Rsa1.0_00707.1.g18360.t1	sp|P48498.1|METK1_PETHY RecName: Full=S-adenosylmethionine synthase 1; Short=AdoMet synthase 1; AltName: Full=Methionine adenosyltransferase 1; Short=MAT 1 gi|559506|emb|CAA57696.1| methionine adenosyltransferase [Petunia x hybrida]	333	390	1.00E-158	117.1	89.2	94.3	RecName: Full=S-adenosylmethionine synthase 1; Short=AdoMet synthase 1; AltName: Full=Methionine adenosyltransferase 1; Short=MAT 1 gi|559506|emb|CAA57696.1| methionine adenosyltransferase	gbpln	Petunia x	AT3G17390.1 | Symbols: MTO3, SAMS3, MAT4 | S-adenosylmethionine synthetase family protein | chr3:5952484-5953665 REVERSE LENGTH=393	333	393	1.00E-153	118.0	85.0	92.8
Rsa1.0_00707.1.g18361.t1	ref|NP_565853.1| uncharacterized protein [Arabidopsis thaliana] gi|20197943|gb|AAM15322.1| Expressed protein [Arabidopsis thaliana] gi|21555809|gb|AAM63938.1| unknown [Arabidopsis thaliana] gi|26983860|gb|AAN86182.1| unknown protein [Arabidopsis thaliana] gi|330254219|gb|AEC09313.1| uncharacterized protein AT2G36885 [Arabidopsis thaliana]	256	256	1.00E-104	100.0	82.4	87.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G36885.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 172 Blast hits to 172 proteins in 58 species: Archae - 0; Bacteria - 116; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 24 (source: NCBI BLink). | chr2:15482167-15483676 REVERSE LENGTH=256	256	256	1.00E-107	100.0	82.4	87.1
Rsa1.0_00707.1.g18362.t1	gb|EOA27604.1| hypothetical protein CARUB_v10023744mg [Capsella rubella]	292	297	1.00E-118	101.7	82.2	86.3	hypothetical protein CARUB_v10023744mg	gbpln	Capsella rubella	AT2G36890.1 | Symbols: RAX2, MYB38, ATMYB38, BIT1 | Duplicated homeodomain-like superfamily protein | chr2:15485821-15487245 FORWARD LENGTH=298	292	298	1.00E-108	102.1	80.8	85.6
Rsa1.0_00707.1.g18363.t1	ref|XP_002881481.1| MEMB11 [Arabidopsis lyrata subsp. lyrata] gi|297327320|gb|EFH57740.1| MEMB11 [Arabidopsis lyrata subsp. lyrata]	226	225	1.00E-108	99.6	86.7	95.1	MEMB11	gbpln	Arabidopsis lyrata	AT2G36900.1 | Symbols: MEMB11, ATMEMB11 | membrin 11 | chr2:15491615-15492587 REVERSE LENGTH=225	226	225	1.00E-110	99.6	86.7	93.8
Rsa1.0_00707.1.g18364.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00707.1.g18365.t1	gb|ABC69917.1| phenylalanine ammonia-lyase [Brassica napus]	657	719	0	109.4	97.4	98.5	phenylalanine ammonia-lyase	gbpln	Brassica napus	AT2G37040.1 | Symbols: PAL1, ATPAL1 | PHE ammonia lyase 1 | chr2:15557602-15560237 REVERSE LENGTH=725	657	725	0	110.4	94.5	96.7
Rsa1.0_00707.1.g18366.t1	gb|EOA26491.1| hypothetical protein CARUB_v10022540mg [Capsella rubella]	905	1088	0	120.2	86.0	92.0	hypothetical protein CARUB_v10022540mg	gbpln	Capsella rubella	AT2G37050.3 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:15569290-15573477 FORWARD LENGTH=934	905	934	0	103.2	86.0	91.8

Rsa1.0_00707.1.g18367.t1	ref|NP_181245.1| interactor of constitutive active ROPs 2 [Arabidopsis thaliana] gi|75216208|sp|Q9ZQC5.1|ICR2_ARATH RecName: Full=Interactor of constitutive active ROPs 2, chloroplastic; Flags: Precursor gi|4371293|gb|AAD18151.1| putative myosin heavy chain [Arabidopsis thaliana] gi|56461746|gb|AAV91329.1| At2g37080 [Arabidopsis thaliana] gi|56790246|gb|AAW30040.1| At2g37080 [Arabidopsis thaliana] gi|330254255|gb|AEC09349.1| interactor of constitutive active ROPs 2 [Arabidopsis thaliana]	571	583	0	102.1	84.6	91.9	interactor of constitutive active ROPs 2	gbpln	Arabidopsis thaliana	AT2G37080.1 | Symbols: RIP3 | ROP interactive partner 3 | chr2:15581565-15584057 REVERSE LENGTH=583	571	583	0	102.1	84.6	91.9
Rsa1.0_00707.1.g18368.t1	gb|EOA29117.1| hypothetical protein CARUB_v10025384mg [Capsella rubella]	347	352	0	101.4	88.2	94.5	hypothetical protein CARUB_v10025384mg	gbpln	Capsella rubella	AT2G37090.1 | Symbols: IRX9 | Nucleotide-diphospho-sugar transferases superfamily protein | chr2:15587671-15589223 REVERSE LENGTH=351	347	351	0	101.2	87.9	94.5
Rsa1.0_00707.1.g18369.t1	ref|XP_002879651.1| hypothetical protein ARALYDRAFT_482699 [Arabidopsis lyrata subsp. lyrata] gi|297325490|gb|EFH55910.1| hypothetical protein ARALYDRAFT_482699 [Arabidopsis lyrata subsp. lyrata]	292	295	6.00E-75	101.0	68.5	79.1	hypothetical protein ARALYDRAFT_482699	gbpln	Arabidopsis lyrata	AT2G37100.1 | Symbols: | protamine P1 family protein | chr2:15591147-15592040 FORWARD LENGTH=297	292	297	4.00E-75	101.7	65.8	77.7
Rsa1.0_00707.1.g18370.t1	dbj|BAA92260.1| Plasma membrane aquaporin 2b [Raphanus sativus]	283	283	1.00E-160	100.0	100.0	100.0	Plasma membrane aquaporin 2b	gbpln	Raphanus sativus	AT2G37170.1 | Symbols: PIP2B, PIP2;2 | plasma membrane intrinsic protein 2 | chr2:15613624-15614791 REVERSE LENGTH=285	283	285	1.00E-157	100.7	95.4	98.2
Rsa1.0_00707.1.g18371.t1	dbj|BAA92260.1| Plasma membrane aquaporin 2b [Raphanus sativus]	285	283	1.00E-158	99.3	97.5	98.2	Plasma membrane aquaporin 2b	gbpln	Raphanus sativus	AT2G37170.1 | Symbols: PIP2B, PIP2;2 | plasma membrane intrinsic protein 2 | chr2:15613624-15614791 REVERSE LENGTH=285	285	285	1.00E-156	100.0	94.4	97.2
Rsa1.0_00707.1.g18372.t3	gb|EOA26421.1| hypothetical protein CARUB_v10024039mg [Capsella rubella]	446	215	1.00E-108	48.2	43.0	44.6	hypothetical protein CARUB_v10024039mg	gbpln	Capsella rubella	AT2G37210.1 | Symbols: | lysine decarboxylase family protein | chr2:15624253-15626834 REVERSE LENGTH=215	446	215	1.00E-110	48.2	42.6	44.2
Rsa1.0_00707.1.g18373.t1	ref|XP_002881497.1| hypothetical protein ARALYDRAFT_482714 [Arabidopsis lyrata subsp. lyrata] gi|297327336|gb|EFH57756.1| hypothetical protein ARALYDRAFT_482714 [Arabidopsis lyrata subsp. lyrata]	279	289	1.00E-116	103.6	82.4	86.7	hypothetical protein ARALYDRAFT_482714	gbpln	Arabidopsis lyrata	AT2G37220.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:15634980-15636331 REVERSE LENGTH=289	279	289	1.00E-111	103.6	78.5	84.2
Rsa1.0_00707.1.g18374.t1	ref|XP_002881499.1| hypothetical protein ARALYDRAFT_482716 [Arabidopsis lyrata subsp. lyrata] gi|297327338|gb|EFH57758.1| hypothetical protein ARALYDRAFT_482716 [Arabidopsis lyrata subsp. lyrata]	261	248	1.00E-117	95.0	83.9	88.5	hypothetical protein ARALYDRAFT_482716	gbpln	Arabidopsis lyrata	AT2G37240.1 | Symbols: | Thioredoxin superfamily protein | chr2:15640235-15641720 REVERSE LENGTH=248	261	248	1.00E-116	95.0	79.7	82.0
Rsa1.0_00707.1.g18375.t2	ref|NP_181263.2| WRKY transcription factor 44 [Arabidopsis thaliana] gi|29839696|sp|Q9ZUU0.2|WRK44_ARATH RecName: Full=WRKY transcription factor 44; AltName: Full=Protein TRANSPARENT TESTA GLABRA 2; AltName: Full=WRKY DNA-binding protein 44 gi|154090558|dbj|BAF74397.1| WRKY transcription factor [Arabidopsis thaliana] gi|330254279|gb|AEC09373.1| WRKY transcription factor 44 [Arabidopsis thaliana]	410	429	1.00E-172	104.6	77.3	85.6	WRKY transcription factor 44	gbpln	Arabidopsis thaliana	AT2G37260.1 | Symbols: TTG2, ATWRKY44, WRKY44, DSL1 | WRKY family transcription factor family protein | chr2:15645277-15646792 FORWARD LENGTH=429	410	429	1.00E-175	104.6	77.3	85.6
Rsa1.0_00707.1.g18376.t1	gb|EOA27796.1| hypothetical protein CARUB_v10023948mg, partial [Capsella rubella]	207	241	1.00E-115	116.4	98.1	99.0	hypothetical protein CARUB_v10023948mg, partial	gbpln	Capsella rubella	AT2G37270.2 | Symbols: ATRPS5B, RPS5B | ribosomal protein 5B | chr2:15647883-15649042 REVERSE LENGTH=207	207	207	1.00E-117	100.0	97.1	99.0
Rsa1.0_00708.1.g18377.t1	gb|EOA17556.1| hypothetical protein CARUB_v10005915mg [Capsella rubella]	150	162	8.00E-55	108.0	74.7	83.3	hypothetical protein CARUB_v10005915mg	gbpln	Capsella rubella	AT4G21745.1 | Symbols: | PAK-box/P21-Rho-binding family protein | chr4:11549340-11550415 FORWARD LENGTH=156	150	156	4.00E-43	104.0	59.3	66.7
Rsa1.0_00708.1.g18378.t1	ref|XP_002869843.1| hypothetical protein ARALYDRAFT_354556 [Arabidopsis lyrata subsp. lyrata] gi|297315679|gb|EFH46102.1| hypothetical protein ARALYDRAFT_354556 [Arabidopsis lyrata subsp. lyrata]	142	504	1.00E-50	354.9	75.4	81.7	hypothetical protein ARALYDRAFT_354556	gbpln	Arabidopsis lyrata	AT4G21740.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G30515.1); Has 20 Blast hits to 20 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:11545926-11546396 FORWARD LENGTH=156	142	156	3.00E-48	109.9	75.4	79.6

Rsa1.0_00708.1.g18379.t1	gb|EOA17622.1| hypothetical protein CARUB_v10005987mg [Capsella rubella]	138	136	3.00E−48	98.6	82.6	89.9	hypothetical protein CARUB_v10005987mg	gbpln	Capsella rubella	AT4G21720.1 | Symbols: | unknown protein; Has 2692 Blast hits to 975 proteins in 186 species: Archae − 4; Bacteria − 460; Metazoa − 658; Fungi − 93; Plants − 1089; Viruses − 100; Other Eukaryotes − 288 (source: NCBI BLink). | chr4:11542561−11544274 FORWARD LENGTH=139	138	139	1.00E−48	100.7	79.0	88.4
Rsa1.0_00708.1.g18380.t1	ref|XP_002867829.1| hypothetical protein ARALYDRAFT_492703 [Arabidopsis lyrata subsp. lyrata] gi|297313665|gb|EFH44088.1| hypothetical protein ARALYDRAFT_492703 [Arabidopsis lyrata subsp. lyrata]	1289	1188	0	92.2	83.9	85.2	hypothetical protein ARALYDRAFT_492703	gbpln	Arabidopsis lyrata	AT4G21710.1 | Symbols: NRPB2, EMB1989, RPB2 | DNA−directed RNA polymerase family protein | chr4:11535684−11542200 REVERSE LENGTH=1188	1289	1188	0	92.2	83.9	85.1
Rsa1.0_00708.1.g18381.t1	gb|EOA16508.1| hypothetical protein CARUB_v10004666mg [Capsella rubella]	515	492	0	95.5	77.7	86.0	hypothetical protein CARUB_v10004666mg	gbpln	Capsella rubella	AT4G21705.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr4:11533257−11534817 REVERSE LENGTH=492	515	492	0	95.5	77.3	86.0
Rsa1.0_00708.1.g18382.t1	gb|EOA16294.1| hypothetical protein CARUB_v10004438mg [Capsella rubella]	583	586	0	100.5	91.6	95.9	hypothetical protein CARUB_v10004438mg	gbpln	Capsella rubella	AT4G21680.1 | Symbols: NRT1.8 | NITRATE TRANSPORTER 1.8 | chr4:11517540−11519576 REVERSE LENGTH=589	583	589	0	101.0	90.1	95.2
Rsa1.0_00708.1.g18383.t1	ref|XP_002869873.1| hypothetical protein ARALYDRAFT_492708 [Arabidopsis lyrata subsp. lyrata] gi|297315709|gb|EFH46132.1| hypothetical protein ARALYDRAFT_492708 [Arabidopsis lyrata subsp. lyrata]	953	965	0	101.3	84.4	91.0	hypothetical protein ARALYDRAFT_492708	gbpln	Arabidopsis lyrata	AT4G21670.1 | Symbols: CPL1, FRY2, ATCPL1 | C−terminal domain phosphatase−like 1 | chr4:11511511−11516922 FORWARD LENGTH=967	953	967	0	101.5	83.1	89.5
Rsa1.0_00708.1.g18384.t2	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00708.1.g18385.t1	ref|NP_567633.2| Subtilase family protein [Arabidopsis thaliana] gi|27311663|gb|AAO00797.1| subtilisin proteinase − like [Arabidopsis thaliana] gi|332659085|gb|AEE84485.1| Subtilase family protein [Arabidopsis thaliana]	729	766	0	105.1	82.0	88.5	Subtilase family protein	gbpln	Arabidopsis thaliana	AT4G21650.1 | Symbols: | Subtilase family protein | chr4:11501314−11504656 REVERSE LENGTH=766	729	766	0	105.1	82.0	88.5
Rsa1.0_00708.1.g18386.t1	ref|NP_567633.2| Subtilase family protein [Arabidopsis thaliana] gi|27311663|gb|AAO00797.1| subtilisin proteinase − like [Arabidopsis thaliana] gi|332659085|gb|AEE84485.1| Subtilase family protein [Arabidopsis thaliana]	709	766	0	108.0	82.8	88.9	Subtilase family protein	gbpln	Arabidopsis thaliana	AT4G21650.1 | Symbols: | Subtilase family protein | chr4:11501314−11504656 REVERSE LENGTH=766	709	766	0	108.0	82.8	88.9
Rsa1.0_00708.1.g18387.t1	ref|NP_567633.2| Subtilase family protein [Arabidopsis thaliana] gi|27311663|gb|AAO00797.1| subtilisin proteinase − like [Arabidopsis thaliana] gi|332659085|gb|AEE84485.1| Subtilase family protein [Arabidopsis thaliana]	769	766	0	99.6	79.3	87.5	Subtilase family protein	gbpln	Arabidopsis thaliana	AT4G21650.1 | Symbols: | Subtilase family protein | chr4:11501314−11504656 REVERSE LENGTH=766	769	766	0	99.6	79.3	87.5
Rsa1.0_00708.1.g18388.t1	gb|EOA18922.1| hypothetical protein CARUB_v10007555mg [Capsella rubella]	134	133	1.00E−31	99.3	86.6	94.8	hypothetical protein CARUB_v10007555mg	gbpln	Capsella rubella	AT4G21620.1 | Symbols: | glycine−rich protein | chr4:11491519−11491914 FORWARD LENGTH=131	134	131	8.00E−31	97.8	79.1	83.6
Rsa1.0_00708.1.g18389.t2	emb|CAA18718.1| putative protein [Arabidopsis thaliana] gi|7268951|emb|CAB81261.1| putative protein [Arabidopsis thaliana]	137	1240	2.00E−13	905.1	30.7	35.0	putative protein	gbpln	Arabidopsis thaliana	AT4G21530.1 | Symbols: | Transducin/WD40 repeat−like superfamily protein | chr4:11450743−11455862 FORWARD LENGTH=777	137	777	2.00E−14	567.2	30.7	35.0
Rsa1.0_00708.1.g18390.t1	ref|NP_193885.6| sphingosine kinase 1 [Arabidopsis thaliana] gi|75154185|sp|Q8L7L1.1|SPHK1_ARATH RecName: Full=Sphingosine kinase 1 gi|22136030|gb|AAM91597.1| putative protein [Arabidopsis thaliana] gi|30387599|gb|AAP31965.1| At4g21540 [Arabidopsis thaliana] gi|332659065|gb|AEE84465.1| sphingosine kinase 1 [Arabidopsis thaliana]	483	485	0	100.4	84.9	91.9	sphingosine kinase 1	gbpln	Arabidopsis thaliana	AT4G21540.1 | Symbols: SPHK1 | sphingosine kinase 1 | chr4:11459609−11462356 FORWARD LENGTH=485	483	485	0	100.4	84.9	91.9
Rsa1.0_00709.1.g18391.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00709.1.g18392.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00709.1.g18393.t1	gb|EOA28352.1| hypothetical protein CARUB_v10024557mg [Capsella rubella]	91	863	6.00E−12	948.4	41.8	56.0	hypothetical protein CARUB_v10024557mg	gbpln	Capsella rubella	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301−18475574 FORWARD LENGTH=921	91	921	3.00E−14	1012.1	36.3	52.7
Rsa1.0_00709.1.g18394.t1	ref|XP_002870738.1| hypothetical protein ARALYDRAFT_916278 [Arabidopsis lyrata subsp. lyrata] gi|297316574|gb|EFH46997.1| hypothetical protein ARALYDRAFT_916278 [Arabidopsis lyrata subsp. lyrata]	492	467	0	94.9	67.9	78.0	hypothetical protein ARALYDRAFT_916278	gbpln	Arabidopsis lyrata	AT5G12420.1 | Symbols: | O−acyltransferase (WSD1−like) family protein | chr5:4024568−4026715 REVERSE LENGTH=480	492	480	1.00E−157	97.6	55.7	70.9

Rsa1.0_00709.1.g18395.t2	ref|XP_002864303.1| calcium ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297310138|gb|EFH40562.1| calcium ion binding protein [Arabidopsis lyrata subsp. lyrata]	168	437	5.00E-48	260.1	63.1	70.8	calcium ion binding protein	gbpln	Arabidopsis lyrata	AT5G54130.2 | Symbols: | Calcium-binding endonuclease/exonuclease/phosphatase family | chr5:21962900-21965279 FORWARD LENGTH=436	168	436	7.00E-50	259.5	62.5	70.2
Rsa1.0_00709.1.g18396.t1	gb|EOA18868.1| hypothetical protein CARUB_v10007491mg [Capsella rubella]	441	445	0	100.9	84.6	90.5	hypothetical protein CARUB_v10007491mg	gbpln	Capsella rubella	AT5G39990.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:16004494-16006428 FORWARD LENGTH=447	441	447	0	101.4	85.9	90.9
Rsa1.0_00709.1.g18397.t1	ref|NP_198816.1| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332007117|gb|AED94500.1| AAA-type ATPase family protein [Arabidopsis thaliana]	475	470	0	98.9	78.3	88.0	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT5G40000.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:16011072-16012484 REVERSE LENGTH=470	475	470	0	98.9	78.3	88.0
Rsa1.0_00709.1.g18398.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00709.1.g18399.t2	ref|NP_198816.1| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332007117|gb|AED94500.1| AAA-type ATPase family protein [Arabidopsis thaliana]	465	470	1.00E-156	101.1	62.6	73.5	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT5G40000.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:16011072-16012484 REVERSE LENGTH=470	465	470	1.00E-158	101.1	62.6	73.5
Rsa1.0_00709.1.g18400.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00709.1.g18401.t1	ref|NP_189491.1| 60S acidic ribosomal protein P2-3 [Arabidopsis thaliana] gi|75273208|sp|Q9LH85.1|RLA23_ARATH RecName: Full=60S acidic ribosomal protein P2-3 gi|9294100|dbj|BAB01952.1| unnamed protein product [Arabidopsis thaliana] gi|21555286|gb|AAM63824.1| acidic ribosomal protein P2b (rpp2b), putative [Arabidopsis thaliana] gi|28393165|gb|AAO42015.1| putative acidic ribosomal protein P2b (rpp2b) [Arabidopsis thaliana] gi|28827552|gb|AAO50620.1| putative acidic ribosomal protein P2b (rpp2b) [Arabidopsis thaliana] gi|332643932|gb|AEE77453.1| 60S acidic ribosomal protein P2-3 [Arabidopsis thaliana]	113	115	4.00E-32	101.8	77.0	84.1	60S acidic ribosomal protein P2-3	gbpln	Arabidopsis thaliana	AT3G28500.1 | Symbols: | 60S acidic ribosomal protein family | chr3:10682204-10682551 FORWARD LENGTH=115	113	115	7.00E-35	101.8	77.0	84.1
Rsa1.0_00709.1.g18402.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00709.1.g18403.t1	ref|XP_002870728.1| hypothetical protein ARALYDRAFT_355985 [Arabidopsis lyrata subsp. lyrata] gi|297316564|gb|EFH46987.1| hypothetical protein ARALYDRAFT_355985 [Arabidopsis lyrata subsp. lyrata]	504	500	0	99.2	91.3	94.0	hypothetical protein ARALYDRAFT_355985	gbpln	Arabidopsis lyrata	AT5G40030.1 | Symbols: | Protein kinase superfamily protein | chr5:16026227-16028283 FORWARD LENGTH=499	504	499	0	99.0	90.5	93.5
Rsa1.0_00710.1.g18404.t1	gb|AAB61378.1| aquaporin [Brassica rapa subsp. oleifera]	286	286	1.00E-163	100.0	99.7	99.7	aquaporin	gbpln	Brassica rapa	AT2G45960.1 | Symbols: PIP1B, TMP-A, ATHH2, PIP1;2 | plasma membrane intrinsic protein 1B | chr2:18910450-18911703 FORWARD LENGTH=286	286	286	1.00E-164	100.0	98.6	99.3
Rsa1.0_00710.1.g18405.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00710.1.g18406.t1	ref|XP_002880213.1| ATBRM/CHR2 [Arabidopsis lyrata subsp. lyrata] gi|297326052|gb|EFH56472.1| ATBRM/CHR2 [Arabidopsis lyrata subsp. lyrata]	2153	2186	0	101.5	89.3	93.3	ATBRM/CHR2	gbpln	Arabidopsis lyrata	AT2G46020.2 | Symbols: CHR2, ATBRM, BRM, CHA2 | transcription regulatory protein SNF2, putative | chr2:18923304-18931769 FORWARD LENGTH=2193	2153	2193	0	101.9	89.3	93.1

<table>
<tr><td>Rsa1.0_00710.1.g18407.t1</td><td>ref|NP_566062.1| ubiquitin-conjugating enzyme E2 6 [Arabidopsis thaliana] gi|21542470|sp|P42750.2|UBC6_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 6; AltName: Full=Ubiquitin carrier protein 6; AltName: Full=Ubiquitin-conjugating enzyme E2-21 kDa 3; AltName: Full=Ubiquitin-protein ligase 6 gi|807095|gb|AAB32508.1| UBC6=E2-related ubiquitin-conjugating protein [Arabidopsis thaliana, Peptide, 183 aa] gi|3702350|gb|AAC62907.1| E2, ubiquitin-conjugating enzyme 6 (UBC6) [Arabidopsis thaliana] gi|28950697|gb|AAO63272.1| At2g46030 [Arabidopsis thaliana] gi|66354415|gb|AAY44847.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|110736450|dbj|BAF00193.1| putative ubiquitin-conjugating enzyme E2 [Arabidopsis thaliana] gi|330255540|gb|AEC10634.1| ubiquitin-conjugating enzyme E2 6 [Arabidopsis thaliana]</td><td>190</td><td>183</td><td>1.00E-81</td><td>96.3</td><td>75.8</td><td>78.9</td><td>ubiquitin-conjugating enzyme E2 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46030.1 | Symbols: UBC6 | ubiquitin-conjugating enzyme 6 | chr2:18932243-18933421 REVERSE LENGTH=183</td><td>190</td><td>183</td><td>4.00E-84</td><td>96.3</td><td>75.8</td><td>78.9</td></tr>
<tr><td>Rsa1.0_00710.1.g18408.t1</td><td>ref|XP_002882049.1| hypothetical protein ARALYDRAFT_322261 [Arabidopsis lyrata subsp. lyrata] gi|297327888|gb|EFH58308.1| hypothetical protein ARALYDRAFT_322261 [Arabidopsis lyrata subsp. lyrata]</td><td>502</td><td>406</td><td>1.00E-138</td><td>80.9</td><td>51.8</td><td>56.2</td><td>hypothetical protein ARALYDRAFT_322261</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46070.1 | Symbols: ATMPK12, MAPK12, MPK12 | mitogen-activated protein kinase 12 | chr2:18946134-18947770 REVERSE LENGTH=372</td><td>502</td><td>372</td><td>1.00E-139</td><td>74.1</td><td>48.8</td><td>51.6</td></tr>
<tr><td>Rsa1.0_00710.1.g18409.t1</td><td>gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]</td><td>149</td><td>1231</td><td>2.00E-15</td><td>826.2</td><td>30.2</td><td>50.3</td><td>Very similar to retrotransposon reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365</td><td>149</td><td>365</td><td>6.00E-16</td><td>245.0</td><td>31.5</td><td>43.6</td></tr>
<tr><td>Rsa1.0_00710.1.g18410.t1</td><td>gb|EOA39454.1| hypothetical protein CARUB_v10012651mg [Capsella rubella]</td><td>239</td><td>233</td><td>1.00E-122</td><td>97.5</td><td>92.1</td><td>93.7</td><td>hypothetical protein CARUB_v10012651mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G14620.1 | Symbols: DECOY | decoy | chr1:5014948-5016501 REVERSE LENGTH=233</td><td>239</td><td>233</td><td>1.00E-123</td><td>97.5</td><td>90.0</td><td>92.5</td></tr>
<tr><td>Rsa1.0_00710.1.g18411.t1</td><td>gb|EOA28020.1| hypothetical protein CARUB_v10024196mg [Capsella rubella]</td><td>166</td><td>166</td><td>6.00E-81</td><td>100.0</td><td>88.6</td><td>95.8</td><td>hypothetical protein CARUB_v10024196mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G46140.1 | Symbols: | Late embryogenesis abundant protein | chr2:18959163-18960362 FORWARD LENGTH=166</td><td>166</td><td>166</td><td>1.00E-82</td><td>100.0</td><td>88.6</td><td>95.2</td></tr>
<tr><td>Rsa1.0_00710.1.g18412.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00710.1.g18413.t1</td><td>ref|XP_002880225.1| hypothetical protein ARALYDRAFT_483769 [Arabidopsis lyrata subsp. lyrata] gi|297326064|gb|EFH56484.1| hypothetical protein ARALYDRAFT_483769 [Arabidopsis lyrata subsp. lyrata]</td><td>237</td><td>237</td><td>1.00E-103</td><td>100.0</td><td>78.9</td><td>86.9</td><td>hypothetical protein ARALYDRAFT_483769</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46220.1 | Symbols: | Uncharacterized conserved protein (DUF2358) | chr2:18979655-18980557 FORWARD LENGTH=241</td><td>237</td><td>241</td><td>4.00E-99</td><td>101.7</td><td>78.9</td><td>86.9</td></tr>
<tr><td>Rsa1.0_00710.1.g18414.t1</td><td>ref|XP_002880226.1| hypothetical protein ARALYDRAFT_483770 [Arabidopsis lyrata subsp. lyrata] gi|297326065|gb|EFH56485.1| hypothetical protein ARALYDRAFT_483770 [Arabidopsis lyrata subsp. lyrata]</td><td>297</td><td>298</td><td>1.00E-142</td><td>100.3</td><td>87.2</td><td>91.2</td><td>hypothetical protein ARALYDRAFT_483770</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46225.1 | Symbols: ABIL1 | ABI-1-like 1 | chr2:18982113-18984074 FORWARD LENGTH=298</td><td>297</td><td>298</td><td>1.00E-144</td><td>100.3</td><td>86.9</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00710.1.g18415.t1</td><td>ref|NP_566069.1| BTB/POZ/Kelch-associated protein [Arabidopsis thaliana] gi|75220239|sp|O82343.2|Y2626_ARATH RecName: Full=BTB/POZ domain-containing protein At2g46260 gi|15028123|gb|AAK76685.1| unknown protein [Arabidopsis thaliana] gi|19310797|gb|AAL85129.1| unknown protein [Arabidopsis thaliana] gi|20197378|gb|AAC62880.2| expressed protein [Arabidopsis thaliana] gi|330255572|gb|AEC10666.1| BTB/POZ/Kelch-associated protein [Arabidopsis thaliana]</td><td>546</td><td>561</td><td>0</td><td>102.7</td><td>88.6</td><td>93.2</td><td>BTB/POZ/Kelch-associated protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46260.1 | Symbols: | BTB/POZ/Kelch-associated protein | chr2:18996111-18998463 FORWARD LENGTH=561</td><td>546</td><td>561</td><td>0</td><td>102.7</td><td>88.6</td><td>93.2</td></tr>
</table>

Rsa1.0_00710.1.g18416.t1	gb|EOA28724.1| hypothetical protein CARUB_v10024952mg [Capsella rubella]	326	249	3.00E-90	76.4	63.5	68.1	hypothetical protein CARUB_v10024952mg	gbpln	Capsella rubella	AT2G46300.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:19008392-19009247 FORWARD LENGTH=252	326	252	1.00E-92	77.3	61.3	66.9
Rsa1.0_00710.1.g18417.t1	gb|EOA27621.1| hypothetical protein CARUB_v10023769mg [Capsella rubella]	287	290	1.00E-89	101.0	66.2	73.2	hypothetical protein CARUB_v10023769mg	gbpln	Capsella rubella	AT2G46310.1 | Symbols: CRF5 | cytokinin response factor 5 | chr2:19011614-19012498 FORWARD LENGTH=294	287	294	4.00E-85	102.4	65.5	73.2
Rsa1.0_00710.1.g18418.t1	gb|EOA28262.1| hypothetical protein CARUB_v10024456mg [Capsella rubella]	73	73	4.00E-28	100.0	93.2	95.9	hypothetical protein CARUB_v10024456mg	gbpln	Capsella rubella	AT2G46330.1 | Symbols: AGP16, ATAGP16 | arabinogalactan protein 16 | chr2:19018730-19019108 REVERSE LENGTH=73	73	73	1.00E-30	100.0	91.8	94.5
Rsa1.0_00711.1.g18419.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00711.1.g18420.t1	gb|EOA31571.1| hypothetical protein CARUB_v10014763mg [Capsella rubella]	173	176	9.00E-61	101.7	79.2	83.8	hypothetical protein CARUB_v10014763mg	gbpln	Capsella rubella	AT3G15640.1 | Symbols: | Rubredoxin-like superfamily protein | chr3:5299273-5301371 FORWARD LENGTH=176	173	176	3.00E-61	101.7	87.9	90.2
Rsa1.0_00711.1.g18421.t3	ref|NP_566520.1| (6-4)DNA photolyase [Arabidopsis thaliana] gi|306756349|sp|O48652.2|UVR3_ARATH RecName: Full=(6-4)DNA photolyase; AltName: Full=Protein UV repair defective 3 gi|332642182|gb|AEE75703.1| (6-4)DNA photolyase [Arabidopsis thaliana]	538	556	0	103.3	87.0	92.4	(6-4)DNA photolyase	gbpln	Arabidopsis thaliana	AT3G15620.1 | Symbols: UVR3 | DNA photolyase family protein | chr3:5293475-5296548 REVERSE LENGTH=556	538	556	0	103.3	87.0	92.4
Rsa1.0_00711.1.g18422.t1	gb|EOA31692.1| hypothetical protein CARUB_v10014898mg [Capsella rubella]	134	134	2.00E-61	100.0	97.0	98.5	hypothetical protein CARUB_v10014898mg	gbpln	Capsella rubella	AT1G52740.1 | Symbols: HTA9 | histone H2A protein 9 | chr1:19645409-19646221 FORWARD LENGTH=134	134	134	1.00E-61	100.0	94.0	96.3
Rsa1.0_00711.1.g18423.t1	gb|EOA32639.1| hypothetical protein CARUB_v10015934mg [Capsella rubella]	679	708	0	104.3	79.7	86.7	hypothetical protein CARUB_v10015934mg	gbpln	Capsella rubella	AT3G15550.1 | Symbols: | unknown protein; Has 25732 Blast hits to 16979 proteins in 961 species: Archae - 144; Bacteria - 1801; Metazoa - 12681; Fungi - 1868; Plants - 912; Viruses - 94; Other Eukaryotes - 8232 (source: NCBI BLink). | chr3:5267351-5270095 FORWARD LENGTH=729	679	729	0	107.4	80.3	88.7
Rsa1.0_00711.1.g18424.t1	ref|XP_002882971.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297328811|gb|EFH59230.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	163	642	6.00E-21	393.9	54.0	64.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G16010.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr3:5434142-5436244 FORWARD LENGTH=642	163	642	2.00E-22	393.9	49.1	57.7
Rsa1.0_00711.1.g18425.t1	ref|NP_174124.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|12322993|gb|AAG51483.1|AC069471_14 oxidoreductase, putative [Arabidopsis thaliana] gi|332192783|gb|AEE30904.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	323	322	1.00E-138	99.7	72.4	86.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT1G28030.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:9771793-9773345 FORWARD LENGTH=322	323	322	1.00E-141	99.7	72.4	86.1
Rsa1.0_00711.1.g18426.t1	ref|NP_174124.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|12322993|gb|AAG51483.1|AC069471_14 oxidoreductase, putative [Arabidopsis thaliana] gi|332192783|gb|AEE30904.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	325	322	1.00E-116	99.1	65.2	79.4	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT1G28030.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:9771793-9773345 FORWARD LENGTH=322	325	322	1.00E-119	99.1	65.2	79.4
Rsa1.0_00711.1.g18427.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00711.1.g18428.t1	ref|NP_188173.1| auxin-responsive protein IAA19 [Arabidopsis thaliana] gi|17365900|sp|O24409.2|IAA19_ARATH RecName: Full=Auxin-responsive protein IAA19; AltName: Full=Indoleacetic acid-induced protein 19; AltName: Full=Protein MASSUGU 2 gi|7021739|gb|AAF35420.1| early auxin-induced protein, IAA19 [Arabidopsis thaliana] gi|15795119|dbj|BAB02383.1| auxin-regulated protein, IAA19 [Arabidopsis thaliana] gi|49616371|gb|AAT67082.1| IAA19 [Arabidopsis thaliana] gi|88193790|gb|ABD42984.1| At3g15540 [Arabidopsis thaliana] gi|332642169|gb|AEE75690.1| auxin-responsive protein IAA19 [Arabidopsis thaliana]	165	197	1.00E-77	119.4	90.9	95.2	auxin-responsive protein IAA19	gbpln	Arabidopsis thaliana	AT3G15540.1 | Symbols: IAA19, MSG2 | indole-3-acetic acid inducible 19 | chr3:5264100-5265378 FORWARD LENGTH=197	165	197	5.00E-80	119.4	90.9	95.2

Rsa1.0_00711.1.g18429.t1	gb|EOA29538.1| hypothetical protein CARUB_v10015041mg [Capsella rubella]	133	67	2.00E-14	50.4	28.6	36.1	hypothetical protein CARUB_v10015041mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00711.1.g18430.t1	ref|XP_002885092.1| hypothetical protein ARALYDRAFT_479001 [Arabidopsis lyrata subsp. lyrata] gi|297330932|gb|EFH61351.1| hypothetical protein ARALYDRAFT_479001 [Arabidopsis lyrata subsp. lyrata]	400	288	1.00E-150	72.0	68.3	69.8	hypothetical protein ARALYDRAFT_479001	gbpln	Arabidopsis lyrata	AT3G15530.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:5253253-5254193 REVERSE LENGTH=288	400	288	1.00E-145	72.0	68.5	69.5
Rsa1.0_00711.1.g18431.t1	dbj|BAJ34312.1| unnamed protein product [Thellungiella halophila]	362	364	1.00E-157	100.6	86.7	91.2	unnamed protein product	----	----	AT3G15510.1 | Symbols: ATNAC2, ANAC056, NARS1, NAC2 | NAC domain containing protein 2 | chr3:5243696-5245037 FORWARD LENGTH=364	362	364	1.00E-158	100.6	85.4	90.6
Rsa1.0_00711.1.g18432.t1	gb|ABK28184.1| unknown [Arabidopsis thaliana]	176	488	1.00E-54	277.3	55.7	77.8	unknown	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	176	361	3.00E-23	205.1	34.1	54.0
Rsa1.0_00712.1.g18433.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	411	1557	1.00E-74	378.8	38.9	58.2	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	411	575	2.00E-40	139.9	31.9	50.4
Rsa1.0_00712.1.g18434.t2	gb|EOA16247.1| hypothetical protein CARUB_v10004393mg [Capsella rubella]	560	613	0	109.5	82.1	88.0	hypothetical protein CARUB_v10004393mg	gbpln	Capsella rubella	AT4G37670.2 | Symbols: NAGS2 | N-acetyl-l-glutamate synthase 2 | chr4:17696179-17698836 REVERSE LENGTH=613	560	613	0	109.5	80.4	85.0
Rsa1.0_00712.1.g18435.t1	ref|XP_002868977.1| ribosomal protein L12 family protein [Arabidopsis lyrata subsp. lyrata] gi|297314813|gb|EFH45236.1| ribosomal protein L12 family protein [Arabidopsis lyrata subsp. lyrata]	168	167	6.00E-73	99.4	84.5	89.3	ribosomal protein L12 family protein	gbpln	Arabidopsis lyrata	AT4G37660.1 | Symbols: | Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein | chr4:17695543-17696046 FORWARD LENGTH=167	168	167	1.00E-69	99.4	82.7	91.1
Rsa1.0_00712.1.g18436.t1	ref|XP_002868978.1| hypothetical protein ARALYDRAFT_912572 [Arabidopsis lyrata subsp. lyrata] gi|297314814|gb|EFH45237.1| hypothetical protein ARALYDRAFT_912572 [Arabidopsis lyrata subsp. lyrata]	530	531	0	100.2	92.5	94.9	hypothetical protein ARALYDRAFT_912572	gbpln	Arabidopsis lyrata	AT4G37650.1 | Symbols: SHR, SGR7 | GRAS family transcription factor | chr4:17691871-17693466 FORWARD LENGTH=531	530	531	0	100.2	91.9	94.3
Rsa1.0_00712.1.g18437.t1	gb|EOA15958.1| hypothetical protein CARUB_v10004056mg [Capsella rubella] gi|482551766|gb|EOA15959.1| hypothetical protein CARUB_v10004056mg [Capsella rubella]	1017	1014	0	99.7	96.4	98.6	hypothetical protein CARUB_v10004056mg	gbpln	Capsella rubella	AT4G37640.1 | Symbols: ACA2 | calcium ATPase 2 | chr4:17683225-17686808 REVERSE LENGTH=1014	1017	1014	0	99.7	96.0	98.3
Rsa1.0_00712.1.g18438.t1	gb|EOA17000.1| hypothetical protein CARUB_v10005238mg [Capsella rubella]	273	229	8.00E-63	83.9	46.9	50.9	hypothetical protein CARUB_v10005238mg	gbpln	Capsella rubella	AT4G37630.1 | Symbols: CYCD5;1 | cyclin d5;1 | chr4:17679497-17680788 FORWARD LENGTH=323	273	323	7.00E-65	118.3	47.6	51.3
Rsa1.0_00712.1.g18439.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	1551	1489	0	96.0	55.4	70.3	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1551	1262	1.00E-164	81.4	17.7	23.9
Rsa1.0_00712.1.g18440.t1	ref|NP_568031.1| BTB and TAZ domain protein 5 [Arabidopsis thaliana] gi|75255062|sp|Q6EJ98.1|BT5_ARATH RecName: Full=BTB/POZ and TAZ domain-containing protein 5; AltName: Full=BTB and TAZ domain protein 5 gi|36955924|gb|AAQ87008.1| BTB and TAZ domain protein 5 [Arabidopsis thaliana] gi|94442425|gb|ABF19000.1| At4g37610 [Arabidopsis thaliana] gi|332661416|gb|AEE86816.1| BTB and TAZ domain protein 5 [Arabidopsis thaliana]	376	368	0	97.9	83.0	89.6	BTB and TAZ domain protein 5	gbpln	Arabidopsis thaliana	AT4G37610.1 | Symbols: BT5 | BTB and TAZ domain protein 5 | chr4:17670606-17671992 REVERSE LENGTH=368	376	368	0	97.9	83.0	89.6
Rsa1.0_00712.1.g18441.t1	gb|EOA17745.1| hypothetical protein CARUB_v10006133mg [Capsella rubella]	107	88	1.00E-18	82.2	50.5	60.7	hypothetical protein CARUB_v10006133mg	gbpln	Capsella rubella	AT4G37608.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 22 Blast hits to 22 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17669825-17670429 FORWARD LENGTH=87	107	87	5.00E-19	81.3	44.9	55.1
Rsa1.0_00712.1.g18442.t1	gb|AAK96859.1| putative protein [Arabidopsis thaliana] gi|20148337|gb|AAM10059.1| putative protein [Arabidopsis thaliana]	580	580	0	100.0	86.7	93.6	putative protein	gbpln	Arabidopsis thaliana	AT4G37590.1 | Symbols: NPY5 | Phototropic-responsive NPH3 family protein | chr4:17663080-17665299 REVERSE LENGTH=580	580	580	0	100.0	86.6	93.6

Rsa1.0_00712.1.g18443.t1	gb|EOA16747.1| hypothetical protein CARUB_v10004955mg [Capsella rubella]	403	404	0	100.2	91.3	95.5	hypothetical protein CARUB_v10004955mg	gbpln	Capsella rubella	AT4G37580.1 | Symbols: HLS1, COP3, UNS2 | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr4:17658932-17660564 FORWARD LENGTH=403	403	403	0	100.0	91.1	95.0
Rsa1.0_00712.1.g18444.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00712.1.g18445.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00712.1.g18446.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00712.1.g18447.t1	ref|XP_002866942.1| ribonuclease III family protein [Arabidopsis lyrata subsp. lyrata] gi|297312778|gb|EFH43201.1| ribonuclease III family protein [Arabidopsis lyrata subsp. lyrata]	82	537	7.00E-17	654.9	52.4	61.0	ribonuclease III family protein	gbpln	Arabidopsis lyrata	AT4G37510.1 | Symbols: | Ribonuclease III family protein | chr4:17626259-17628854 REVERSE LENGTH=537	82	537	2.00E-19	654.9	52.4	61.0
Rsa1.0_00712.1.g18448.t1	gb|EOA17212.1| hypothetical protein CARUB_v10005485mg [Capsella rubella]	134	271	5.00E-68	202.2	93.3	95.5	hypothetical protein CARUB_v10005485mg	gbpln	Capsella rubella	AT4G37470.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:17617045-17618363 REVERSE LENGTH=270	134	270	3.00E-66	201.5	88.1	94.0
Rsa1.0_00713.1.g18449.t1	ref|XP_002865546.1| hypothetical protein ARALYDRAFT_494806 [Arabidopsis lyrata subsp. lyrata] gi|297311381|gb|EFH41805.1| hypothetical protein ARALYDRAFT_494806 [Arabidopsis lyrata subsp. lyrata]	466	473	0	101.5	78.5	86.5	hypothetical protein ARALYDRAFT_494806	gbpln	Arabidopsis lyrata	AT5G42240.1 | Symbols: scpl42 | serine carboxypeptidase-like 42 | chr5:16888717-16890931 FORWARD LENGTH=473	466	473	0	101.5	78.1	86.1
Rsa1.0_00713.1.g18450.t1	ref|NP_565039.4| uncharacterized protein [Arabidopsis thaliana] gi|332197175|gb|AEE35296.1| uncharacterized protein AT1G72270 [Arabidopsis thaliana]	432	2845	1.00E-131	658.6	63.4	71.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G72270.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ribosome 60S biogenesis N-terminal (InterPro:IPR021714); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27010.1); Has 772 Blast hits to 657 proteins in 120 species: Archae - 0; Bacteria - 0; Metazoa - 344; Fungi - 94; Plants - 322; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr1:27199733-27211122 REVERSE LENGTH=2845	432	2845	1.00E-134	658.6	63.4	71.3
Rsa1.0_00713.1.g18451.t6	ref|XP_002885864.1| hypothetical protein ARALYDRAFT_899550 [Arabidopsis lyrata subsp. lyrata] gi|297835966|ref|XP_002885865.1| hypothetical protein ARALYDRAFT_480295 [Arabidopsis lyrata subsp. lyrata] gi|297331704|gb|EFH62123.1| hypothetical protein ARALYDRAFT_899550 [Arabidopsis lyrata subsp. lyrata] gi|297331705|gb|EFH62124.1| hypothetical protein ARALYDRAFT_480295 [Arabidopsis lyrata subsp. lyrata]	261	256	1.00E-124	98.1	87.0	91.2	hypothetical protein ARALYDRAFT_899550	gbpln	Arabidopsis lyrata	AT2G12646.1 | Symbols: | PLATZ transcription factor family protein | chr2:5167179-5169022 REVERSE LENGTH=256	261	256	1.00E-126	98.1	87.0	91.2
Rsa1.0_00713.1.g18452.t1	dbj|BAJ33858.1| unnamed protein product [Thellungiella halophila]	401	438	0	109.2	98.8	99.5	unnamed protein product	----	----	AT2G13360.2 | Symbols: AGT, AGT1, SGAT | alanine:glyoxylate aminotransferase | chr2:5539417-5540902 REVERSE LENGTH=401	401	401	0	100.0	95.8	98.8
Rsa1.0_00713.1.g18453.t1	ref|XP_002885870.1| hypothetical protein ARALYDRAFT_480303 [Arabidopsis lyrata subsp. lyrata] gi|297331710|gb|EFH62129.1| hypothetical protein ARALYDRAFT_480303 [Arabidopsis lyrata subsp. lyrata]	409	402	0	98.3	86.3	89.5	hypothetical protein ARALYDRAFT_480303	gbpln	Arabidopsis lyrata	AT2G13350.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:5536525-5537730 REVERSE LENGTH=401	409	401	0	98.0	85.6	89.0
Rsa1.0_00713.1.g18454.t1	gb|EOA29945.1| hypothetical protein CARUB_v10013044mg, partial [Capsella rubella]	695	747	0	107.5	89.9	93.4	hypothetical protein CARUB_v10013044mg, partial	gbpln	Capsella rubella	AT2G13440.1 | Symbols: | glucose-inhibited division family A protein | chr2:5593270-5598296 REVERSE LENGTH=723	695	723	0	104.0	86.0	89.8
Rsa1.0_00713.1.g18455.t1	dbj|BAJ34245.1| unnamed protein product [Thellungiella halophila]	870	848	0	97.5	88.9	93.3	unnamed protein product	----	----	AT2G13540.1 | Symbols: ENS, ABH1, CBP80, ATCBP80 | ARM repeat superfamily protein | chr2:5637053-5642813 FORWARD LENGTH=848	870	848	0	97.5	87.5	91.8
Rsa1.0_00713.1.g18456.t1	ref|XP_002885881.1| hypothetical protein ARALYDRAFT_899587 [Arabidopsis lyrata subsp. lyrata] gi|297331721|gb|EFH62140.1| hypothetical protein ARALYDRAFT_899587 [Arabidopsis lyrata subsp. lyrata]	209	213	3.00E-89	101.9	85.6	89.0	hypothetical protein ARALYDRAFT_899587	gbpln	Arabidopsis lyrata	AT2G13570.1 | Symbols: NF-YB7 | nuclear factor Y, subunit B7 | chr2:5655842-5656489 REVERSE LENGTH=215	209	215	6.00E-91	102.9	88.0	91.4
Rsa1.0_00713.1.g18457.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00713.1.g18458.t1	ref|NP_178983.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75206168|sp|Q9SIT7.1|PP151_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g13600 gi|4558664|gb|AAD22682.1| hypothetical protein [Arabidopsis thaliana] gi|330251150|gb|AEC06244.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	697	697	0	100.0	85.4	91.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G13600.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:5671493-5673586 FORWARD LENGTH=697	697	697	0	100.0	85.4	91.4
Rsa1.0_00713.1.g18459.t1	gb|EOA33038.1| hypothetical protein CARUB_v10016369mg [Capsella rubella]	642	649	0	101.1	91.6	94.9	hypothetical protein CARUB_v10016369mg	gbpln	Capsella rubella	AT2G13610.1 | Symbols: | ABC-2 type transporter family protein | chr2:5673827-5675776 REVERSE LENGTH=649	642	649	0	101.1	91.4	94.4
Rsa1.0_00713.1.g18460.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00713.1.g18461.t1	emb|CAA08995.1| MAP3K alpha 1 protein kinase [Brassica napus]	607	591	0	97.4	91.6	93.2	MAP3K alpha 1 protein kinase	gbpln	Brassica napus	AT1G53570.3 | Symbols: MAP3KA, MAPKKK3 | mitogen-activated protein kinase kinase kinase 3 | chr1:19987391-19990733 FORWARD LENGTH=608	607	608	0	100.2	73.6	81.1
Rsa1.0_00713.1.g18462.t1	ref|NP_565359.1| AGD2-like defense response protein 1 [Arabidopsis thaliana] gi|75216244|sp|Q9ZQI7.2|ALD1_ARATH RecName: Full=Aminotransferase ALD1; AltName: Full=AGD2-like defense response protein 1 gi|451928665|pdb|4FL0|A Chain A, Crystal Structure Of Ald1 From Arabidopsis Thaliana gi|451928666|pdb|4FL0|B Chain B, Crystal Structure Of Ald1 From Arabidopsis Thaliana gi|15982838|gb|AAL09766.1| At2g13810/F13J11.16 [Arabidopsis thaliana] gi|20197607|gb|AAD15433.2| putative aspartate aminotransferase [Arabidopsis thaliana] gi|20197797|gb|AAM15253.1| putative aspartate aminotransferase [Arabidopsis thaliana] gi|23505955|gb|AAN28837.1| At2g13810/F13J11.16 [Arabidopsis thaliana] gi|41323505|gb|AAR99910.1| aminotransferase ALD1 [Arabidopsis thaliana] gi|330251167|gb|AEC06261.1| AGD2-like defense response protein 1 [Arabidopsis thaliana]	456	456	0	100.0	87.9	92.8	AGD2-like defense response protein 1	gbpln	Arabidopsis thaliana	AT2G13810.1 | Symbols: ALD1 | AGD2-like defense response protein 1 | chr2:5768489-5772138 FORWARD LENGTH=456	456	456	0	100.0	87.9	92.8
Rsa1.0_00713.1.g18463.t1	ref|NP_565374.1| uncharacterized protein [Arabidopsis thaliana] gi|4544369|gb|AAD22280.1| expressed protein [Arabidopsis thaliana] gi|21592803|gb|AAM64752.1| unknown [Arabidopsis thaliana] gi|115311445|gb|ABI93903.1| At2g15440 [Arabidopsis thaliana] gi|330251307|gb|AEC06401.1| uncharacterized protein AT2G15440 [Arabidopsis thaliana]	330	329	1.00E-128	99.7	79.1	87.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G15440.1 | Symbols: | Protein of unknown function (DUF579) | chr2:6743792-6744781 REVERSE LENGTH=329	330	329	1.00E-131	99.7	79.1	87.0
Rsa1.0_00713.1.g18464.t1	ref|XP_002883897.1| UDP-glucosyl transferase 73B5 [Arabidopsis lyrata subsp. lyrata] gi|297329737|gb|EFH60156.1| UDP-glucosyl transferase 73B5 [Arabidopsis lyrata subsp. lyrata]	472	484	0	102.5	86.4	93.4	UDP-glucosyl transferase 73B5	gbpln	Arabidopsis lyrata	AT2G15480.1 | Symbols: UGT73B5 | UDP-glucosyl transferase 73B5 | chr2:6758817-6760452 FORWARD LENGTH=484	472	484	0	102.5	85.2	92.4
Rsa1.0_00713.1.g18465.t1	ref|XP_002883899.1| hypothetical protein ARALYDRAFT_899764 [Arabidopsis lyrata subsp. lyrata] gi|297329739|gb|EFH60158.1| hypothetical protein ARALYDRAFT_899764 [Arabidopsis lyrata subsp. lyrata]	626	655	0	104.6	89.1	93.1	hypothetical protein ARALYDRAFT_899764	gbpln	Arabidopsis lyrata	AT4G34110.1 | Symbols: PAB2, PABP2, ATPAB2 | poly(A) binding protein 2 | chr4:16336732-16339892 FORWARD LENGTH=629	626	629	0	100.5	80.5	87.7
Rsa1.0_00713.1.g18466.t1	gb|EOA13384.1| hypothetical protein CARUB_v10026424mg, partial [Capsella rubella]	270	437	8.00E-22	161.9	19.6	23.7	hypothetical protein CARUB_v10026424mg, partial	gbpln	Capsella rubella	AT3G06720.2 | Symbols: AT-IMP, ATKAP ALPHA, AIMP ALPHA | importin alpha isoform 1 | chr3:2120559-2123555 FORWARD LENGTH=532	270	532	6.00E-23	197.0	19.6	23.7

Rsa1.0_00714.1.g18467.t1	ref|NP_563718.1| ubiquitin-associated (UBA)/TS-N domain-containing protein [Arabidopsis thaliana] gi|7211981|gb|AAF40452.1|AC004809_10 ESTs gb|N65605, gb|N38087, gb|T20485, gb|T13726, gb|N38339, gb|F15440 and gb|N97201 come from this gene [Arabidopsis thaliana] gi|17065066|gb|AAL32687.1| Unknown protein [Arabidopsis thaliana] gi|21594053|gb|AAM65971.1| unknown [Arabidopsis thaliana] gi|23197878|gb|AAN15466.1| Unknown protein [Arabidopsis thaliana] gi|332189630|gb|AEE27751.1| ubiquitin-associated (UBA)/TS-N domain-containing protein [Arabidopsis thaliana]	123	413	5.00E-66	335.8	97.6	100.0	ubiquitin-associated (UBA)/TS-N domain-containing protein	gbpln	Arabidopsis thaliana	AT1G04850.1 | Symbols: | ubiquitin-associated (UBA)/TS-N domain-containing protein | chr1:1365311-1368706 REVERSE LENGTH=413	123	413	9.00E-69	335.8	97.6	100.0
Rsa1.0_00714.1.g18468.t1	gb|AAF40453.1|AC004809_11 Similar to gi|3217452 F45E6.3 gene product from C. elegans cosmid gb|Z68117 [Arabidopsis thaliana]	440	438	0	99.5	86.8	91.6	Similar to gi|3217452 F45E6.3 gene product from C. elegans cosmid gb|Z68117	gbpln	Arabidopsis thaliana	AT1G04830.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr1:1359087-1361844 REVERSE LENGTH=448	440	448	0	101.8	81.6	86.6
Rsa1.0_00714.1.g18469.t1	ref|NP_563716.3| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|26451052|dbj|BAC42631.1| unknown protein [Arabidopsis thaliana] gi|332189622|gb|AEE27743.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	658	664	0	100.9	89.5	95.3	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G04780.1 | Symbols: | Ankyrin repeat family protein | chr1:1340891-1342965 REVERSE LENGTH=664	658	664	0	100.9	89.5	95.3
Rsa1.0_00714.1.g18470.t1	gb|EOA38336.1| hypothetical protein CARUB_v10009848mg [Capsella rubella]	285	305	1.00E-133	107.0	87.0	90.5	hypothetical protein CARUB_v10009848mg	gbpln	Capsella rubella	AT1G04770.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1336564-1337767 REVERSE LENGTH=303	285	303	1.00E-133	106.3	87.0	90.5
Rsa1.0_00714.1.g18471.t1	gb|EOA37088.1| hypothetical protein CARUB_v10010251mg [Capsella rubella]	219	219	1.00E-126	100.0	99.5	100.0	hypothetical protein CARUB_v10010251mg	gbpln	Capsella rubella	AT1G04750.1 | Symbols: VAMP7B, VAMP721, ATVAMP721, AT VAMP7B | vesicle-associated membrane protein 721 | chr1:1331857-1333426 REVERSE LENGTH=219	219	219	1.00E-128	100.0	98.6	100.0
Rsa1.0_00714.1.g18472.t1	ref|NP_180873.1| 3-ketoacyl-CoA thiolase 2 [Arabidopsis thaliana] gi|73919871|sp|Q56WD9.2|THIK2_ARATH RecName: Full=3-ketoacyl-CoA thiolase 2, peroxisomal; AltName: Full=Acetyl-CoA acyltransferase 2; AltName: Full=Beta-ketothiolase 2; AltName: Full=Peroxisomal 3-oxoacyl-CoA thiolase 2; AltName: Full=Peroxisome defective protein 1; Flags: Precursor gi|11993853|gb|AAG42910.1|AF327529_1 putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|13194830|gb|AAK15577.1|AF349530_1 putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2924779|gb|AAC04908.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2981616|dbj|BAA25248.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2981618|dbj|BAA25249.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|15450669|gb|AAK96606.1| At2g33150/F25I18.11 [Arabidopsis thaliana] gi|17380614|gb|AAL36070.1| At2g33150/F25I18.11 [Arabidopsis thaliana] gi|21593136|gb|AAM65085.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|330253697|gb|AEC08791.1| 3-ketoacyl-CoA thiolase 2 [Arabidopsis thaliana]	443	462	0	104.3	86.7	92.6	3-ketoacyl-CoA thiolase 2	gbpln	Arabidopsis thaliana	AT2G33150.1 | Symbols: PKT3, PED1, KAT2 | peroxisomal 3-ketoacyl-CoA thiolase 3 | chr2:14047814-14050983 REVERSE LENGTH=462	443	462	0	104.3	86.7	92.6
Rsa1.0_00714.1.g18473.t1	gb|EOA39837.1| hypothetical protein CARUB_v10008506mg [Capsella rubella]	667	671	0	100.6	93.1	97.3	hypothetical protein CARUB_v10008506mg	gbpln	Capsella rubella	AT1G50920.1 | Symbols: | Nucleolar GTP-binding protein | chr1:18870555-18872570 FORWARD LENGTH=671	667	671	0	100.6	91.2	96.4
Rsa1.0_00714.1.g18474.t1	gb|EOA38234.1| hypothetical protein CARUB_v10009717mg [Capsella rubella]	328	328	0	100.0	98.2	99.4	hypothetical protein CARUB_v10009717mg	gbpln	Capsella rubella	AT1G04690.1 | Symbols: KAB1, KV-BETA1 | potassium channel beta subunit 1 | chr1:1313662-1315420 FORWARD LENGTH=328	328	328	0	100.0	97.9	99.4

Rsa1.0_00714.1.g18475.t1	ref|NP_563715.1| putative pectate lyase 1 [Arabidopsis thaliana] gi|32129844|sp|Q940Q1.2|PEL1_ARATH RecName: Full=Probable pectate lyase 1; AltName: Full=Pectate lyase A1; Flags: Precursor gi|2494113|gb|AAB80622.1| Strong similarity to Musa pectate lyase (gb|X92943). ESTs gb|AA042458, gb|ATTS4502, gb|N38552 come from this gene [Arabidopsis thaliana] gi|18086433|gb|AAL57671.1| At1g04680/T1G11_6 [Arabidopsis thaliana] gi|21593312|gb|AAM65261.1| putative pectate lyase A11 [Arabidopsis thaliana] gi|332189611|gb|AEE27732.1| putative pectate lyase 1 [Arabidopsis thaliana]	429	431	0	100.5	93.5	95.8	putative pectate lyase 1	gbpln	Arabidopsis thaliana	AT1G04680.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:1304052-1307780 REVERSE LENGTH=431	429	431	0	100.5	93.5	95.8
Rsa1.0_00714.1.g18476.t1	ref|XP_002892235.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338077|gb|EFH68494.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	220	207	3.00E-16	94.1	20.0	22.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G04660.1 | Symbols: | glycine-rich protein | chr1:1300668-1301306 REVERSE LENGTH=212	220	212	4.00E-18	96.4	20.0	22.3
Rsa1.0_00714.1.g18477.t2	ref|NP_171959.2| uncharacterized protein [Arabidopsis thaliana] gi|332189608|gb|AEE27729.1| uncharacterized protein AT1G04650 [Arabidopsis thaliana]	975	997	0	102.3	79.5	89.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G04650.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:1294893-1298903 REVERSE LENGTH=997	975	997	0	102.3	79.5	89.3
Rsa1.0_00714.1.g18478.t2	ref|XP_002889516.1| hypothetical protein ARALYDRAFT_887631 [Arabidopsis lyrata subsp. lyrata] gi|297335358|gb|EFH65775.1| hypothetical protein ARALYDRAFT_887631 [Arabidopsis lyrata subsp. lyrata]	1748	1715	0	98.1	84.4	90.1	hypothetical protein ARALYDRAFT_887631	gbpln	Arabidopsis lyrata	AT1G04600.1 | Symbols: XIA, ATXIA | myosin XI A | chr1:1262123-1272376 FORWARD LENGTH=1730	1748	1730	0	99.0	83.8	89.6
Rsa1.0_00714.1.g18479.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00714.1.g18480.t1	gb|ACB59212.1| unknown protein [Brassica oleracea]	89	610	4.00E-12	685.4	46.1	62.9	unknown protein	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	89	302	3.00E-12	339.3	40.4	51.7
Rsa1.0_00715.1.g18481.t1	ref|NP_179007.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|20197610|gb|AAM15153.1| hypothetical protein [Arabidopsis thaliana] gi|29725844|gb|AAO89210.1| hypothetical protein [Arabidopsis thaliana] gi|60547703|gb|AAX23815.1| hypothetical protein At2g13900 [Arabidopsis thaliana] gi|330251172|gb|AEC06266.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	653	661	0	101.2	59.9	72.4	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G13900.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:5833102-5835087 FORWARD LENGTH=661	653	661	0	101.2	59.9	72.4
Rsa1.0_00715.1.g18482.t1	gb|EOA12717.1| hypothetical protein CARUB_v10028097mg [Capsella rubella]	364	364	1.00E-178	100.0	80.5	91.2	hypothetical protein CARUB_v10028097mg	gbpln	Capsella rubella	AT5G59530.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:23994434-23995715 REVERSE LENGTH=364	364	364	1.00E-179	100.0	80.5	90.7
Rsa1.0_00715.1.g18483.t2	ref|XP_002866336.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297312171|gb|EFH42595.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	727	365	1.00E-174	50.2	40.4	44.3	oxidoreductase	gbpln	Arabidopsis lyrata	AT5G59540.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:23996293-23997576 REVERSE LENGTH=366	727	366	1.00E-173	50.3	39.5	43.9
Rsa1.0_00715.1.g18484.t1	ref|XP_002866336.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297312171|gb|EFH42595.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	366	365	1.00E-178	99.7	80.9	91.0	oxidoreductase	gbpln	Arabidopsis lyrata	AT5G59540.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:23996293-23997576 REVERSE LENGTH=366	366	366	1.00E-180	100.0	80.1	91.0
Rsa1.0_00715.1.g18485.t1	ref|XP_002866336.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297312171|gb|EFH42595.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	379	365	1.00E-179	96.3	78.9	85.5	oxidoreductase	gbpln	Arabidopsis lyrata	AT5G59540.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:23996293-23997576 REVERSE LENGTH=366	379	366	1.00E-179	96.6	77.0	84.7
Rsa1.0_00715.1.g18486.t1	ref|XP_002866337.1| hypothetical protein ARALYDRAFT_496089 [Arabidopsis lyrata subsp. lyrata] gi|297312172|gb|EFH42596.1| hypothetical protein ARALYDRAFT_496089 [Arabidopsis lyrata subsp. lyrata]	393	406	1.00E-147	103.3	76.6	83.5	hypothetical protein ARALYDRAFT_496089	gbpln	Arabidopsis lyrata	AT5G59550.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:23998422-23999645 REVERSE LENGTH=407	393	407	1.00E-144	103.6	76.8	84.2

Rsa1.0_00715.1.g18487.t1	ref|XP_002866339.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312174|gb|EFH42598.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	652	453	0	69.5	57.4	63.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G59580.1 | Symbols: UGT76E1 | UDP-glucosyl transferase 76E1 | chr5:24006239-24007689 REVERSE LENGTH=453	652	453	0	69.5	56.6	63.2
Rsa1.0_00715.1.g18488.t1	ref|XP_002866375.1| APUM18 [Arabidopsis lyrata subsp. lyrata] gi|297312210|gb|EFH42634.1| APUM18 [Arabidopsis lyrata subsp. lyrata]	335	328	2.00E-71	97.9	47.5	60.3	APUM18	gbpln	Arabidopsis lyrata	AT5G60180.1 | Symbols: APUM19, PUM19 | pumilio 19 | chr5:24233024-24234007 REVERSE LENGTH=327	335	327	3.00E-65	97.6	45.7	58.2
Rsa1.0_00715.1.g18489.t1	ref|XP_002866375.1| APUM18 [Arabidopsis lyrata subsp. lyrata] gi|297312210|gb|EFH42634.1| APUM18 [Arabidopsis lyrata subsp. lyrata]	355	328	8.00E-74	92.4	44.5	58.6	APUM18	gbpln	Arabidopsis lyrata	AT5G60180.1 | Symbols: APUM19, PUM19 | pumilio 19 | chr5:24233024-24234007 REVERSE LENGTH=327	355	327	9.00E-66	92.1	40.3	53.2
Rsa1.0_00715.1.g18490.t1	ref|NP_190227.1| uncharacterized protein [Arabidopsis thaliana] gi|22327975|ref|NP_680457.1| uncharacterized protein [Arabidopsis thaliana] gi|334188494|ref|NP_001190570.1| uncharacterized protein [Arabidopsis thaliana] gi|297796915|ref|XP_002866342.1| hypothetical protein ARALYDRAFT_496097 [Arabidopsis lyrata subsp. lyrata] gi|297815794|ref|XP_002875780.1| hypothetical protein ARALYDRAFT_485014 [Arabidopsis lyrata subsp. lyrata] gi|6522622|emb|CAB62034.1| putative protein [Arabidopsis thaliana] gi|17065520|gb|AAL32914.1| Unknown protein [Arabidopsis thaliana] gi|17381284|gb|AAL36060.1| AT3g46430/F18L15_150 [Arabidopsis thaliana] gi|20148461|gb|AAM10121.1| unknown protein [Arabidopsis thaliana] gi|20453375|gb|AAM19926.1| AT3g46430/F18L15_150 [Arabidopsis thaliana] gi|26450436|dbj|BAC42332.1| unknown protein [Arabidopsis thaliana] gi|26451867|dbj|BAC43026.1| unknown protein [Arabidopsis thaliana] gi|297312177|gb|EFH42601.1| hypothetical protein ARALYDRAFT_496097 [Arabidopsis lyrata subsp. lyrata]	55	55	6.00E-23	100.0	96.4	96.4	uncharacterized protein	gbpln	Arabidopsis lyrata	AT5G59613.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrial respiratory chain complex III; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G46430.1). | chr5:24015726-24016500 REVERSE LENGTH=55	55	55	1.00E-25	100.0	96.4	96.4
Rsa1.0_00715.1.g18491.t1	ref|NP_200775.2| Receptor-like protein kinase [Arabidopsis thaliana] gi|75334110|sp|Q9FN94.1|RLK7_ARATH RecName: Full=Receptor-like protein kinase At5g59670; AltName: Full=Leucine-rich repeat receptor-like protein kinase At5g59670; Flags: Precursor gi|9758833|dbj|BAB09505.1| receptor-like protein kinase [Arabidopsis thaliana] gi|20466280|gb|AAM20457.1| serine/threonine-specific protein kinase-like [Arabidopsis thaliana] gi|31711772|gb|AAP68242.1| At5g59670 [Arabidopsis thaliana] gi|224589733|gb|ACN59398.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332009835|gb|AED97218.1| Receptor-like protein kinase [Arabidopsis thaliana]	208	868	7.00E-67	417.3	63.0	70.2	Receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G59670.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24041538-24045478 FORWARD LENGTH=868	208	868	2.00E-69	417.3	63.0	70.2

Rsa1.0_00715.1.g18492.t1	ref|NP_200775.2| Receptor-like protein kinase [Arabidopsis thaliana] gi|75334110|sp|Q9FN94.1|RLK7_ARATH RecName: Full=Receptor-like protein kinase At5g59670; AltName: Full=Leucine-rich repeat receptor-like protein kinase At5g59670; Flags: Precursor gi|9758833|dbj|BAB09505.1| receptor-like protein kinase [Arabidopsis thaliana] gi|20466280|gb|AAM20457.1| serine/threonine-specific protein kinase-like [Arabidopsis thaliana] gi|31711772|gb|AAP68242.1| At5g59670 [Arabidopsis thaliana] gi|224589733|gb|ACN59398.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332009835|gb|AED97218.1| Receptor-like protein kinase [Arabidopsis thaliana]	655	868	0	132.5	62.7	72.4	Receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G59670.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24041538-24045478 FORWARD LENGTH=868	655	868	0	132.5	62.7	72.4
Rsa1.0_00715.1.g18493.t10	gb|EOA12886.1| hypothetical protein CARUB_v10025859mg [Capsella rubella]	979	887	0	90.6	58.8	70.7	hypothetical protein CARUB_v10025859mg	gbpln	Capsella rubella	AT5G59680.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24046792-24050801 FORWARD LENGTH=887	979	887	0	90.6	57.8	69.3
Rsa1.0_00715.1.g18494.t1	gb|EOA12886.1| hypothetical protein CARUB_v10025859mg [Capsella rubella]	440	887	3.00E-82	201.6	35.0	44.1	hypothetical protein CARUB_v10025859mg	gbpln	Capsella rubella	AT5G59680.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24046792-24050801 FORWARD LENGTH=887	440	887	2.00E-84	201.6	33.6	42.7
Rsa1.0_00715.1.g18495.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_00715.1.g18496.t1	ref|NP_568912.2| VIRE2 interacting protein 2 [Arabidopsis thaliana] gi|325530323|sp|Q9FPW4.2|VIP2_ARATH RecName: Full=Probable NOT transcription complex subunit VIP2; AltName: Full=Protein VIRE2 INTERACTING PROTEIN2; Short=AtVIP2 gi|332009839|gb|AED97222.1| VIRE2 interacting protein 2 [Arabidopsis thaliana]	292	614	1.00E-112	210.3	84.6	89.7	VIRE2 interacting protein 2	gbpln	Arabidopsis thaliana	AT5G59710.1 | Symbols: VIP2, AtVIP2 | VIRE2 interacting protein 2 | chr5:24058157-24061736 FORWARD LENGTH=614	292	614	1.00E-115	210.3	84.6	89.7
Rsa1.0_00716.1.g18497.t1	ref|NP_200466.1| oxidative stress 3 [Arabidopsis thaliana] gi|8809630|dbj|BAA97181.1| unnamed protein product [Arabidopsis thaliana] gi|51969112|dbj|BAD43248.1| putative protein [Arabidopsis thaliana] gi|51971389|dbj|BAD44359.1| putative protein [Arabidopsis thaliana] gi|332009397|gb|AED96780.1| oxidative stress 3 [Arabidopsis thaliana]	117	172	5.00E-26	147.0	71.8	78.6	oxidative stress 3	gbpln	Arabidopsis thaliana	AT5G56550.1 | Symbols: OXS3, ATOXS3 | oxidative stress 3 | chr5:22895847-22896502 REVERSE LENGTH=172	117	172	9.00E-29	147.0	71.8	78.6
Rsa1.0_00716.1.g18498.t1	sp|Q9FJV2.2|FBD27_ARATH RecName: Full=Putative FBD-associated F-box protein At5g56560	427	418	1.00E-139	97.9	59.7	73.1	RecName: Full=Putative FBD-associated F-box protein At5g56560	----	----	AT5G56560.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr5:22899724-22901985 FORWARD LENGTH=607	427	607	1.00E-106	142.2	44.3	52.2
Rsa1.0_00716.1.g18499.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00716.1.g18500.t1	gb|EOA14381.1| hypothetical protein CARUB_v10027574mg [Capsella rubella]	517	618	1.00E-145	119.5	59.6	74.9	hypothetical protein CARUB_v10027574mg	gbpln	Capsella rubella	AT5G56560.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr5:22899724-22901985 FORWARD LENGTH=607	517	607	1.00E-140	117.4	57.6	73.1
Rsa1.0_00716.1.g18501.t1	ref|XP_002866159.1| hypothetical protein ARALYDRAFT_495755 [Arabidopsis lyrata subsp. lyrata] gi|297311994|gb|EFH42418.1| hypothetical protein ARALYDRAFT_495755 [Arabidopsis lyrata subsp. lyrata]	319	315	1.00E-162	98.7	85.3	89.0	hypothetical protein ARALYDRAFT_495755	gbpln	Arabidopsis lyrata	AT5G56640.1 | Symbols: MIOX5 | myo-inositol oxygenase 5 | chr5:22927534-22929638 REVERSE LENGTH=314	319	314	1.00E-161	98.4	84.6	88.1

Rsa1.0_00716.1.g18502.t1	ref|NP_194668.1| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|15241895|ref|NP_200478.1| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|18399137|ref|NP_565458.1| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|297796551|ref|XP_002866160.1| 40S ribosomal protein S30 [Arabidopsis lyrata subsp. lyrata] gi|297799054|ref|XP_002867411.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297836282|ref|XP_002886023.1| 40S ribosomal protein S30 [Arabidopsis lyrata subsp. lyrata] gi|22096379|sp|P49689.3|RS30_ARATH RecName: Full=40S ribosomal protein S30 gi|7269837|emb|CAB79697.1| RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana] gi|10176771|dbj|BAB09885.1| 40S ribosomal protein S30 homolog [Arabidopsis thaliana] gi|15450480|gb|AAK96533.1| At2g19750/F6F22.22 [Arabidopsis thaliana] gi|16974467|gb|AAL31237.1| At2g19750/F6F22.22 [Arabidopsis thaliana] gi|20197294|gb|AAC62141.2| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|21618031|gb|AAM67081.1| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|22135964|gb|AAM91564.1| 40S ribosomal protein S30-like protein	62	62	5.00E-26	100.0	100.0	100.0	40S ribosomal protein S30	gbpln	Arabidopsis lyrata	AT5G56670.1 | Symbols: | Ribosomal protein S30 family protein | chr5:22935413-22935981 REVERSE LENGTH=62	62	62	8.00E-29	100.0	100.0	100.0
Rsa1.0_00716.1.g18503.t1	ref|XP_002888797.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata] gi|297334638|gb|EFH65056.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata]	161	335	9.00E-52	208.1	55.9	77.6	bet v I allergen family protein	gbpln	Arabidopsis lyrata	AT1G70830.3 | Symbols: MLP28 | MLP-like protein 28 | chr1:26710203-26711395 REVERSE LENGTH=201	161	201	2.00E-53	124.8	56.5	75.8
Rsa1.0_00716.1.g18504.t1	gb|EOA17998.1| hypothetical protein CARUB_v10006433mg [Capsella rubella]	119	119	1.00E-60	100.0	98.3	99.2	hypothetical protein CARUB_v10006433mg	gbpln	Capsella rubella	AT5G56710.1 | Symbols: | Ribosomal protein L31e family protein | chr5:22944003-22944767 REVERSE LENGTH=119	119	119	2.00E-62	100.0	96.6	99.2
Rsa1.0_00716.1.g18505.t1	ref|XP_002864477.1| ndr family protein [Arabidopsis lyrata subsp. lyrata] gi|297310312|gb|EFH40736.1| ndr family protein [Arabidopsis lyrata subsp. lyrata]	144	346	1.00E-49	240.3	66.7	72.9	ndr family protein	gbpln	Arabidopsis lyrata	AT5G56750.1 | Symbols: NDL1 | N-MYC downregulated-like 1 | chr5:22957986-22960606 FORWARD LENGTH=346	144	346	3.00E-52	240.3	66.7	72.9
Rsa1.0_00716.1.g18506.t1	gb|EOA13035.1| hypothetical protein CARUB_v10026029mg [Capsella rubella]	661	669	0	101.2	89.9	95.0	hypothetical protein CARUB_v10026029mg	gbpln	Capsella rubella	AT5G56790.1 | Symbols: | Protein kinase superfamily protein | chr5:22968610-22971391 FORWARD LENGTH=669	661	669	0	101.2	88.5	94.9
Rsa1.0_00716.1.g18507.t1	ref|NP_200492.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262578|sp|Q9FJT2.1|FDL40_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g56810 gi|10176785|dbj|BAB09899.1| unnamed protein product [Arabidopsis thaliana] gi|332009427|gb|AED96810.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	451	435	2.00E-87	96.5	49.4	62.7	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G56810.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22974520-22975992 FORWARD LENGTH=435	451	435	5.00E-90	96.5	49.4	62.7
Rsa1.0_00716.1.g18508.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00716.1.g18509.t1	ref|XP_002866147.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311982|gb|EFH42406.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	422	423	1.00E-68	100.2	39.6	59.5	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56420.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22850863-22852334 REVERSE LENGTH=422	422	422	8.00E-69	100.0	38.4	59.7
Rsa1.0_00716.1.g18510.t1	gb|EOA13498.1| hypothetical protein CARUB_v10026556mg [Capsella rubella]	392	395	1.00E-134	100.8	80.6	87.0	hypothetical protein CARUB_v10026556mg	gbpln	Capsella rubella	AT5G56860.1 | Symbols: GNC, GATA21 | GATA type zinc finger transcription factor family protein | chr5:22989630-22991351 REVERSE LENGTH=398	392	398	1.00E-135	101.5	79.3	85.5
Rsa1.0_00716.1.g18511.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00717.1.g18512.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1028	1491	0	145.0	61.2	73.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	1028	237	7.00E-31	23.1	6.8	11.1

Rsa1.0_00717.1.g18513.t1	ref|NP_564417.1| 60S ribosomal protein L9-1 [Arabidopsis thaliana] gi|18398761|ref|NP_564418.1| 60S ribosomal protein L9-1 [Arabidopsis thaliana] gi|22096367|sp|P49209.3|RL91_ARATH RecName: Full=60S ribosomal protein L9-1 gi|9665161|gb|AAF97345.1|AC021045_2 Putative 60S ribosomal protein L9 [Arabidopsis thaliana] gi|9665164|gb|AAF97348.1|AC021045_5 Putative 60S ribosomal protein L9 [Arabidopsis thaliana] gi|11692872|gb|AAG40039.1|AF324688_1 At1g33120 [Arabidopsis thaliana] gi|11908052|gb|AAG41455.1|AF326873_1 putative ribosomal protein L9 [Arabidopsis thaliana] gi|12642868|gb|AAK00376.1|AF339694_1 putative ribosomal protein L9 [Arabidopsis thaliana] gi|14030657|gb|AAK53003.1|AF375419_1 At1g33140/T9L6_10 [Arabidopsis thaliana] gi|14517516|gb|AAK62648.1| At1g33140/T9L6_10 [Arabidopsis thaliana] gi|15809778|gb|AAL06817.1| At1g33140/T9L6_10 [Arabidopsis thaliana] gi|16604306|gb|AAL24159.1| At1g33140/T9L6_10 [Arabidopsis thaliana] gi|18253023|gb|AAL62438.1| ribosomal protein L9, putative [Arabidopsis thaliana]	223	194	5.00E-97	87.0	82.1	86.1	60S ribosomal protein L9-1	gbpln	Arabidopsis thaliana	AT1G33140.1 | Symbols: PGY2 | Ribosomal protein L6 family | chr1:12023360-12024502 FORWARD LENGTH=194	223	194	2.00E-99	87.0	82.1	86.1
Rsa1.0_00717.1.g18514.t1	gb|EOA15229.1| hypothetical protein CARUB_v10028623mg [Capsella rubella]	535	535	0	100.0	88.0	93.6	hypothetical protein CARUB_v10028623mg	gbpln	Capsella rubella	AT5G43360.1 | Symbols: PHT3, ATPT4, PHT1;3 | phosphate transporter 1;3 | chr5:17409524-17411214 FORWARD LENGTH=521	535	521	0	97.4	80.6	88.2
Rsa1.0_00717.1.g18515.t1	ref|NP_974876.1| actin-related protein 9 [Arabidopsis thaliana] gi|332007588|gb|AED94971.1| actin-related protein 9 [Arabidopsis thaliana]	541	584	0	107.9	77.4	88.9	actin-related protein 9	gbpln	Arabidopsis thaliana	AT5G43500.2 | Symbols: ATARP9, ARP9 | actin-related protein 9 | chr5:17469991-17473429 FORWARD LENGTH=584	541	584	0	107.9	77.4	88.9
Rsa1.0_00717.1.g18516.t2	gb|AAC14510.1| En/Spm-like transposon protein [Arabidopsis thaliana]	195	292	3.00E-12	149.7	26.2	32.3	En/Spm-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00717.1.g18517.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00717.1.g18518.t1	ref|NP_199184.1| putative alpha-mannosidase I MNS4 [Arabidopsis thaliana] gi|75262426|sp|Q9FG93.1|MNS4_ARATH RecName: Full=Probable alpha-mannosidase I MNS4 gi|13877731|gb|AAK43943.1|AF370128_1 unknown protein [Arabidopsis thaliana] gi|10177939|dbj|BAB11298.1| unnamed protein product [Arabidopsis thaliana] gi|14532840|gb|AAK64102.1| unknown protein [Arabidopsis thaliana] gi|332007616|gb|AED94999.1| putative alpha-mannosidase I MNS4 [Arabidopsis thaliana]	691	624	0	90.3	78.6	81.8	putative alpha-mannosidase I MNS4	gbpln	Arabidopsis thaliana	AT5G43710.1 | Symbols: | Glycosyl hydrolase family 47 protein | chr5:17552252-17556523 REVERSE LENGTH=624	691	624	0	90.3	78.6	81.8
Rsa1.0_00717.1.g18519.t1	gb|AAD17409.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1073	1347	0	125.5	44.9	51.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1073	1262	5.00E-55	117.6	10.2	15.5
Rsa1.0_00717.1.g18520.t1	gb|EOA13697.1| hypothetical protein CARUB_v10026768mg, partial [Capsella rubella]	133	330	4.00E-25	248.1	63.9	70.7	hypothetical protein CARUB_v10026768mg, partial	gbpln	Capsella rubella	AT5G43720.1 | Symbols: | Protein of unknown function (DUF2361) | chr5:17557431-17559238 REVERSE LENGTH=329	133	329	5.00E-25	247.4	63.2	69.2
Rsa1.0_00717.1.g18521.t1	ref|XP_002881264.1| hypothetical protein ARALYDRAFT_902378 [Arabidopsis lyrata subsp. lyrata] gi|297327103|gb|EFH57523.1| hypothetical protein ARALYDRAFT_902378 [Arabidopsis lyrata subsp. lyrata]	103	101	4.00E-24	98.1	60.2	70.9	hypothetical protein ARALYDRAFT_902378	gbpln	Arabidopsis lyrata	AT2G33130.1 | Symbols: RALFL18, RALF18 | ralf-like 18 | chr2:14046521-14046832 REVERSE LENGTH=103	103	103	2.00E-26	100.0	59.2	73.8
Rsa1.0_00717.1.g18522.t1	gb|AAC13582.1| similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana] gi|8843876|dbj|BAA97402.1| mutator-like transposase [Arabidopsis thaliana]	169	806	6.00E-29	476.9	39.1	47.9	similar to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00718.1.g18523.t1	gb|AAG51247.1|AC055769_6 copia-type polyprotein, putative; 28768-32772 [Arabidopsis thaliana]	965	1334	0	138.2	55.1	71.9	copia-type polyprotein, putative; 28768-32772	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	965	1262	9.00E-89	130.8	19.3	29.5
Rsa1.0_00718.1.g18524.t1	ref|XP_002864721.1| hypothetical protein ARALYDRAFT_919360 [Arabidopsis lyrata subsp. lyrata] gi|297310556|gb|EFH40980.1| hypothetical protein ARALYDRAFT_919360 [Arabidopsis lyrata subsp. lyrata]	297	303	7.00E-62	102.0	43.4	49.5	hypothetical protein ARALYDRAFT_919360	gbpln	Arabidopsis lyrata	AT5G61180.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr5:24612867-24614174 FORWARD LENGTH=346	297	346	2.00E-59	116.5	37.0	45.5
Rsa1.0_00718.1.g18525.t1	gb|EOA14082.1| hypothetical protein CARUB_v10027219mg, partial [Capsella rubella]	143	180	4.00E-77	125.9	97.9	99.3	hypothetical protein CARUB_v10027219mg, partial	gbpln	Capsella rubella	AT5G61170.1 | Symbols: | Ribosomal protein S19e family protein | chr5:24611158-24612202 FORWARD LENGTH=143	143	143	1.00E-79	100.0	99.3	99.3
Rsa1.0_00718.1.g18526.t1	#	#	#	#	#	#	#	–	----	----	AT3G22520.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast, chloroplast envelope; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G14840.1); Has 717 Blast hits to 703 proteins in 179 species: Archae - 14; Bacteria - 134; Metazoa - 141; Fungi - 74; Plants - 209; Viruses - 0; Other Eukaryotes - 145 (source: NCBI BLink). | chr3:7974984-7977406 FORWARD LENGTH=600	57	600	7.00E-12	1052.6	59.6	68.4
Rsa1.0_00718.1.g18527.t1	gb|EOA13076.1| hypothetical protein CARUB_v10026081mg [Capsella rubella]	612	626	0	102.3	69.0	73.9	hypothetical protein CARUB_v10026081mg	gbpln	Capsella rubella	AT5G61150.2 | Symbols: VIP4 | leo1-like family protein | chr5:24603846-24607528 REVERSE LENGTH=623	612	623	0	101.8	75.7	82.7
Rsa1.0_00718.1.g18528.t1	gb|EOA14801.1| hypothetical protein CARUB_v10028107mg [Capsella rubella]	2161	2084	0	96.4	87.6	90.9	hypothetical protein CARUB_v10028107mg	gbpln	Capsella rubella	AT5G61140.2 | Symbols: | U5 small nuclear ribonucleoprotein helicase | chr5:24589999-24603311 FORWARD LENGTH=2157	2161	2157	0	99.8	87.0	90.7
Rsa1.0_00718.1.g18529.t1	gb|EOA14034.1| hypothetical protein CARUB_v10027167mg [Capsella rubella]	229	198	5.00E-73	86.5	67.7	74.7	hypothetical protein CARUB_v10027167mg	gbpln	Capsella rubella	AT5G61130.1 | Symbols: PDCB1 | plasmodesmata callose-binding protein 1 | chr5:24587438-24589369 REVERSE LENGTH=201	229	201	4.00E-66	87.8	64.2	69.0
Rsa1.0_00718.1.g18530.t7	emb|CBY05413.1| FRUITFULL-like protein [Aethionema carneum]	508	228	2.00E-91	44.9	34.8	36.2	FRUITFULL-like protein	gbpln	Aethionema carneum	AT5G60910.1 | Symbols: AGL8, FUL | AGAMOUS-like 8 | chr5:24502736-24506013 REVERSE LENGTH=242	508	242	3.00E-93	47.6	32.9	33.7
Rsa1.0_00718.1.g18531.t1	dbj|BAM78216.1| Myb transcription factor BoMyb34 [Brassica oleracea var. viridis]	299	316	1.00E-123	105.7	77.6	86.0	Myb transcription factor BoMyb34	gbpln	Brassica oleracea	AT5G60890.1 | Symbols: ATMYB34, ATR1, MYB34 | myb domain protein 34 | chr5:24495029-24496220 FORWARD LENGTH=295	299	295	1.00E-111	98.7	70.6	80.3
Rsa1.0_00718.1.g18532.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	433	1515	1.00E-172	349.9	64.9	80.1	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	433	1262	2.00E-90	291.5	38.3	55.7
Rsa1.0_00718.1.g18533.t1	gb|AAF69172.1|AC007915_24 F27F5.11 [Arabidopsis thaliana]	753	1313	1.00E-131	174.4	37.6	49.9	F27F5.11	gbpln	Arabidopsis thaliana	AT5G48050.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G34070.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19472661-19473770 REVERSE LENGTH=369	753	369	3.00E-17	49.0	8.2	15.8
Rsa1.0_00718.1.g18534.t1	gb|AAV25873.1| Putative bHLH family protein [Brassica oleracea]	359	240	9.00E-84	66.9	51.5	54.0	Putative bHLH family protein	gbpln	Brassica oleracea	AT5G08130.6 | Symbols: BIM1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:2606655-2609571 REVERSE LENGTH=529	359	529	3.00E-79	147.4	58.5	69.1
Rsa1.0_00718.1.g18535.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00718.1.g18536.t1	gb|AAV25874.1| 2-isopropylmalate synthase [Brassica oleracea]	497	505	0	101.6	92.2	96.2	2-isopropylmalate synthase	gbpln	Brassica oleracea	AT5G23010.1 | Symbols: MAM1, IMS3 | methylthioalkylmalate synthase 1 | chr5:7703173-7706769 FORWARD LENGTH=506	497	506	0	101.8	78.9	86.9
Rsa1.0_00718.1.g18537.t1	gb|AAV25876.1| Putative Sequence-associated protein [Brassica oleracea]	263	263	1.00E-124	100.0	95.1	97.7	Putative Sequence-associated protein	gbpln	Brassica oleracea	AT5G23030.1 | Symbols: TET12 | tetraspanin12 | chr5:7726819-7727709 FORWARD LENGTH=264	263	264	1.00E-108	100.4	80.2	90.9
Rsa1.0_00718.1.g18538.t1	ref|XP_002872040.1| enhancer of ag-4 2 [Arabidopsis lyrata subsp. lyrata] gi|297317877|gb|EFH48299.1| enhancer of ag-4 2 [Arabidopsis lyrata subsp. lyrata]	1358	1398	0	102.9	59.2	64.5	enhancer of ag-4 2	gbpln	Arabidopsis lyrata	AT5G23150.1 | Symbols: HUA2 | Tudor/PWWP/MBT domain-containing protein | chr5:7786173-7792080 FORWARD LENGTH=1392	1358	1392	0	102.5	58.5	64.3

Rsa1.0_00718.1.g18539.t1	emb|CAI23696.1| putative carboxypeptidase [Arabidopsis thaliana] gi|63146754|emb|CAI23698.1| putative carboxypeptidase [Arabidopsis thaliana]	250	271	5.00E-76	108.4	67.2	75.2	putative carboxypeptidase	gbpln	Arabidopsis thaliana	AT5G23160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G08240.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:7795409-7796310 REVERSE LENGTH=271	250	271	2.00E-78	108.4	67.2	75.2
Rsa1.0_00718.1.g18540.t1	ref|XP_002874114.1| CYP86B1 [Arabidopsis lyrata subsp. lyrata] gi|297319951|gb|EFH50373.1| CYP86B1 [Arabidopsis lyrata subsp. lyrata]	520	559	0	107.5	90.2	95.0	CYP86B1	gbpln	Arabidopsis lyrata	AT5G23190.1 | Symbols: CYP86B1 | cytochrome P450, family 86, subfamily B, polypeptide 1 | chr5:7803478-7805659 REVERSE LENGTH=559	520	559	0	107.5	90.4	95.4
Rsa1.0_00718.1.g18541.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1353	1307	0	96.6	55.1	68.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1353	1262	1.00E-105	93.3	14.3	22.8
Rsa1.0_00718.1.g18542.t1	gb|EOA20478.1| hypothetical protein CARUB_v10000790mg [Capsella rubella]	503	499	0	99.2	86.3	91.7	hypothetical protein CARUB_v10000790mg	gbpln	Capsella rubella	AT5G23210.1 | Symbols: SCPL34 | serine carboxypeptidase-like 34 | chr5:7810892-7814837 FORWARD LENGTH=499	503	499	0	99.2	84.5	90.7
Rsa1.0_00718.1.g18543.t1	ref|NP_197714.1| nicotinamidase 2 [Arabidopsis thaliana] gi|10177812|dbj|BAB11178.1| unnamed protein product [Arabidopsis thaliana] gi|28466925|gb|AAO44071.1| At5g23230 [Arabidopsis thaliana] gi|110743859|dbj|BAE99764.1| hypothetical protein [Arabidopsis thaliana] gi|332005756|gb|AED93139.1| nicotinamidase 2 [Arabidopsis thaliana]	198	198	2.00E-89	100.0	80.8	89.9	nicotinamidase 2	gbpln	Arabidopsis thaliana	AT5G23230.1 | Symbols: NIC2 | nicotinamidase 2 | chr5:7826005-7826601 REVERSE LENGTH=198	198	198	8.00E-92	100.0	80.8	89.9
Rsa1.0_00719.1.g18544.t1	gb|EOA23251.1| hypothetical protein CARUB_v10017299mg [Capsella rubella]	421	431	5.00E-32	102.4	20.0	32.8	hypothetical protein CARUB_v10017299mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00719.1.g18545.t4	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	1684	1643	0	97.6	47.9	65.0	gag/pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1684	1262	1.00E-83	74.9	9.9	15.3
Rsa1.0_00719.1.g18546.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1166	1142	0	97.9	37.8	50.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1166	575	2.00E-36	49.3	9.8	13.8
Rsa1.0_00719.1.g18547.t1	emb|CAA70587.1| myrosinase binding protein [Brassica napus]	1015	988	0	97.3	69.5	73.3	myrosinase binding protein	gbpln	Brassica napus	AT1G52030.1 | Symbols: MBP2, MBP1.2, F-ATMBP | myrosinase-binding protein 2 | chr1:19346090-19348282 REVERSE LENGTH=642	1015	642	1.00E-120	63.3	29.3	37.4
Rsa1.0_00719.1.g18548.t1	ref|NP_178048.2| nucleoprotein TPR [Arabidopsis thaliana] gi|302425121|sp|A4GSN8.1|NUA_ARATH RecName: Full=Nuclear-pore anchor; AltName: Full=Protein TRANSLOCATED PROMOTER REGION; Short=AtTPR gi|126594444|gb|ABO21684.1| nuclear-pore anchor [Arabidopsis thaliana] gi|332198105|gb|AEE36226.1| nucleoprotein TPR [Arabidopsis thaliana]	157	2093	2.00E-66	1333.1	84.1	91.1	nucleoprotein TPR	gbpln	Arabidopsis thaliana	AT1G79280.1 | Symbols: NUA, AtTPR | nuclear pore anchor | chr1:29819176-29832809 REVERSE LENGTH=2093	157	2093	7.00E-69	1333.1	84.1	91.1
Rsa1.0_00719.1.g18549.t1	ref|NP_175610.1| putative mitochondrial-processing peptidase subunit alpha-1 [Arabidopsis thaliana] gi|29839695|sp|Q9ZU25.1|MPPA1_ARATH RecName: Full=Probable mitochondrial-processing peptidase subunit alpha-1; AltName: Full=Alpha-MPP 1; Flags: Precursor gi|4220446|gb|AAD12673.1| Strong similarity to gi|2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb|AC001645. ESTs gb|Z18504 and gb|AA395715 come from this gene [Arabidopsis thaliana] gi|17529270|gb|AAL38862.1| putative mitochondrial processing peptidase alpha subunit [Arabidopsis thaliana] gi|20258957|gb|AAM14194.1| putative mitochondrial processing peptidase alpha subunit [Arabidopsis thaliana] gi|332194621|gb|AEE32742.1| putative mitochondrial-processing peptidase subunit alpha-1 [Arabidopsis thaliana]	535	503	0	94.0	82.1	87.7	putative mitochondrial-processing peptidase subunit alpha-1	gbpln	Arabidopsis thaliana	AT1G51980.1 | Symbols: | Insulinase (Peptidase family M16) protein | chr1:19323692-19326771 REVERSE LENGTH=503	535	503	0	94.0	82.1	87.7

Rsa1.0_00719.1.g18550.t1	ref|XP_002891672.1| hypothetical protein ARALYDRAFT_892185 [Arabidopsis lyrata subsp. lyrata] gi|297337514|gb|EFH67931.1| hypothetical protein ARALYDRAFT_892185 [Arabidopsis lyrata subsp. lyrata]	258	268	1.00E−109	103.9	81.4	85.7	hypothetical protein ARALYDRAFT_892185	gbpln	Arabidopsis lyrata	AT1G51950.1 | Symbols: IAA18 | indole−3−acetic acid inducible 18 | chr1:19305670−19307130 FORWARD LENGTH=267	258	267	1.00E−109	103.5	78.3	84.5
Rsa1.0_00719.1.g18551.t1	gb|EOA36821.1| hypothetical protein CARUB_v10008527mg [Capsella rubella]	633	660	0	104.3	88.6	93.2	hypothetical protein CARUB_v10008527mg	gbpln	Capsella rubella	AT1G51940.1 | Symbols: | protein kinase family protein / peptidoglycan−binding LysM domain−containing protein | chr1:19296092−19298941 REVERSE LENGTH=651	633	651	0	102.8	85.0	90.5
Rsa1.0_00720.1.g18552.t1	ref|NP_563969.1| translation machinery associated protein TMA7 [Arabidopsis thaliana] gi|297849952|ref|XP_002892857.1| hypothetical protein ARALYDRAFT_471721 [Arabidopsis lyrata subsp. lyrata] gi|5103825|gb|AAD39655.1|AC007591_20 ESTs gb|AA650895, gb|AA720043 and gb|R29777 come from this gene [Arabidopsis thaliana] gi|12484215|gb|AAG54006.1|AF336925_1 unknown protein [Arabidopsis thaliana] gi|15028107|gb|AAK76677.1| unknown protein [Arabidopsis thaliana] gi|17065256|gb|AAL32782.1| Unknown protein [Arabidopsis thaliana] gi|20260078|gb|AAM13386.1| unknown protein [Arabidopsis thaliana] gi|21592316|gb|AAM64267.1| unknown [Arabidopsis thaliana] gi|297338699|gb|EFH69116.1| hypothetical protein ARALYDRAFT_471721 [Arabidopsis lyrata subsp. lyrata] gi|332191176|gb|AEE29297.1| translation machinery associated protein TMA7 [Arabidopsis thaliana]	64	64	5.00E−24	100.0	95.3	98.4	translation machinery associated protein TMA7	gbpln	Arabidopsis lyrata	AT1G15270.1 | Symbols: | Translation machinery associated TMA7 | chr1:5250833−5252020 REVERSE LENGTH=64	64	64	9.00E−27	100.0	95.3	98.4
Rsa1.0_00720.1.g18553.t1	gb|EOA38631.1| hypothetical protein CARUB_v10010517mg [Capsella rubella]	147	159	3.00E−67	108.2	89.1	91.8	hypothetical protein CARUB_v10010517mg	gbpln	Capsella rubella	AT1G15220.2 | Symbols: ATCCMH, CCMH | cytochrome c biogenesis protein family | chr1:5240471−5241117 REVERSE LENGTH=159	147	159	3.00E−66	108.2	85.7	89.1
Rsa1.0_00720.1.g18554.t1	ref|XP_002892853.1| ATPDR7/PDR7 [Arabidopsis lyrata subsp. lyrata] gi|297338695|gb|EFH69112.1| ATPDR7/PDR7 [Arabidopsis lyrata subsp. lyrata]	1437	1445	0	100.6	90.8	96.6	ATPDR7/PDR7	gbpln	Arabidopsis lyrata	AT1G15210.1 | Symbols: PDR7, ATPDR7 | pleiotropic drug resistance 7 | chr1:5231552−5236573 REVERSE LENGTH=1442	1437	1442	0	100.3	90.3	96.7
Rsa1.0_00720.1.g18555.t1	gb|EOA36212.1| hypothetical protein CARUB_v10010136mg [Capsella rubella]	240	243	2.00E−76	101.3	71.3	79.6	hypothetical protein CARUB_v10010136mg	gbpln	Capsella rubella	AT1G15190.1 | Symbols: | Fasciclin−like arabinogalactan family protein | chr1:5227275−5228021 FORWARD LENGTH=248	240	248	9.00E−76	103.3	70.4	80.0
Rsa1.0_00720.1.g18556.t1	ref|XP_002890091.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297335933|gb|EFH66350.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	479	483	0	100.8	79.7	91.0	mate efflux family protein	gbpln	Arabidopsis lyrata	AT1G15170.1 | Symbols: | MATE efflux family protein | chr1:5220690−5222756 FORWARD LENGTH=481	479	481	0	100.4	78.5	90.4
Rsa1.0_00720.1.g18557.t1	gb|EOA38363.1| hypothetical protein CARUB_v10009891mg [Capsella rubella]	301	295	1.00E−143	98.0	85.7	91.7	hypothetical protein CARUB_v10009891mg	gbpln	Capsella rubella	AT1G15140.1 | Symbols: | FAD/NAD(P)−binding oxidoreductase | chr1:5210403−5212137 REVERSE LENGTH=295	301	295	1.00E−144	98.0	84.1	92.0
Rsa1.0_00720.1.g18558.t1	ref|NP_172964.1| Ubiquinol−cytochrome C reductase hinge protein [Arabidopsis thaliana] gi|110740918|dbj|BAE98555.1| ubiquinol−cytochrome−c reductase like protein [Arabidopsis thaliana] gi|114050691|gb|ABI49495.1| At1g15120 [Arabidopsis thaliana] gi|227204459|dbj|BAH57081.1| AT1G15120 [Arabidopsis thaliana] gi|332191146|gb|AEE29267.1| Ubiquinol−cytochrome C reductase hinge protein [Arabidopsis thaliana]	74	69	2.00E−30	93.2	86.5	89.2	Ubiquinol−cytochrome C reductase hinge protein	gbpln	Arabidopsis thaliana	AT1G15120.1 | Symbols: | Ubiquinol−cytochrome C reductase hinge protein | chr1:5203091−5203897 FORWARD LENGTH=69	74	69	4.00E−33	93.2	86.5	89.2
Rsa1.0_00720.1.g18559.t1	ref|XP_002892848.1| hypothetical protein ARALYDRAFT_888899 [Arabidopsis lyrata subsp. lyrata] gi|297338690|gb|EFH69107.1| hypothetical protein ARALYDRAFT_888899 [Arabidopsis lyrata subsp. lyrata]	601	575	0	95.7	83.4	88.9	hypothetical protein ARALYDRAFT_888899	gbpln	Arabidopsis lyrata	AT1G15060.1 | Symbols: | Uncharacterised conserved protein UCP031088, alpha/beta hydrolase | chr1:5184053−5186856 REVERSE LENGTH=578	601	578	0	96.2	82.9	89.0

Rsa1.0_00720.1.g18560.t1	gb|EOA38634.1| hypothetical protein CARUB_v10010520mg [Capsella rubella]	143	158	2.00E-58	110.5	80.4	84.6	hypothetical protein CARUB_v10010520mg	gbpln	Capsella rubella	AT1G15010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G01300.1); Has 71 Blast hits to 71 proteins in 13 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5171215-5171643 FORWARD LENGTH=142	143	142	2.00E-53	99.3	72.0	77.6
Rsa1.0_00720.1.g18561.t1	dbj|BAJ34090.1| unnamed protein product [Thellungiella halophila]	98	98	1.00E-46	100.0	95.9	98.0	unnamed protein product	----	----	AT1G14980.1 | Symbols: CPN10 | chaperonin 10 | chr1:5165930-5166654 REVERSE LENGTH=98	98	98	3.00E-49	100.0	94.9	98.0
Rsa1.0_00720.1.g18562.t1	ref|XP_002890079.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297335921|gb|EFH66338.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	204	201	1.00E-99	98.5	87.7	93.1	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT1G14890.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:5137045-5137704 FORWARD LENGTH=219	204	219	1.00E-101	107.4	86.3	92.2
Rsa1.0_00720.1.g18563.t8	ref|XP_002892832.1| hypothetical protein ARALYDRAFT_888870 [Arabidopsis lyrata subsp. lyrata] gi|297338674|gb|EFH69091.1| hypothetical protein ARALYDRAFT_888870 [Arabidopsis lyrata subsp. lyrata]	678	614	0	90.6	88.5	89.4	hypothetical protein ARALYDRAFT_888870	gbpln	Arabidopsis lyrata	AT1G14830.1 | Symbols: ADL1C, ADL5, DRP1C, DL1C | DYNAMIN-like 1C | chr1:5107699-5111470 REVERSE LENGTH=614	678	614	0	90.6	87.9	89.4
Rsa1.0_00720.1.g18564.t1	ref|NP_172934.1| semialdehyde dehydrogenase-like protein [Arabidopsis thaliana] gi|17979524|gb|AAL50097.1| At1g14810/F10B6_6 [Arabidopsis thaliana] gi|20856224|gb|AAM26654.1| At1g14810/F10B6_6 [Arabidopsis thaliana] gi|21536731|gb|AAM61063.1| aspartate-semialdehyde dehydrogenase, putative [Arabidopsis thaliana] gi|332191107|gb|AEE29228.1| semialdehyde dehydrogenase-like protein [Arabidopsis thaliana]	375	375	0	100.0	94.4	96.8	semialdehyde dehydrogenase-like protein	gbpln	Arabidopsis thaliana	AT1G14810.1 | Symbols: | semialdehyde dehydrogenase family protein | chr1:5102684-5104633 REVERSE LENGTH=375	375	375	0	100.0	94.4	96.8
Rsa1.0_00720.1.g18565.t1	ref|XP_002892827.1| hypothetical protein ARALYDRAFT_471662 [Arabidopsis lyrata subsp. lyrata] gi|297338669|gb|EFH69086.1| hypothetical protein ARALYDRAFT_471662 [Arabidopsis lyrata subsp. lyrata]	526	581	0	110.5	77.8	84.2	hypothetical protein ARALYDRAFT_471662	gbpln	Arabidopsis lyrata	AT1G14750.1 | Symbols: SDS | Cyclin family protein | chr1:5079674-5082423 REVERSE LENGTH=578	526	578	0	109.9	78.3	85.0
Rsa1.0_00720.1.g18566.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00720.1.g18567.t1	gb|EOA39760.1| hypothetical protein CARUB_v10008407mg [Capsella rubella]	706	738	0	104.5	83.0	89.5	hypothetical protein CARUB_v10008407mg	gbpln	Capsella rubella	AT1G14740.1 | Symbols: | Protein of unknown function (DUF1423) | chr1:5075450-5077732 REVERSE LENGTH=733	706	733	0	103.8	81.7	89.1
Rsa1.0_00720.1.g18568.t2	ref|NP_563957.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|30683962|ref|NP_849663.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|332191091|gb|AEE29212.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|332191092|gb|AEE29213.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana]	585	601	0	102.7	71.6	79.5	hydroxyproline-rich glycoprotein-like protein	gbpln	Arabidopsis thaliana	AT1G14710.2 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:5062168-5064697 REVERSE LENGTH=601	585	601	0	102.7	71.6	79.5
Rsa1.0_00720.1.g18569.t1	ref|NP_172923.3| purple acid phosphatase 3 [Arabidopsis thaliana] gi|75244598|sp|Q8H129.1|PPA3_ARATH RecName: Full=Purple acid phosphatase 3; Flags: Precursor gi|24030193|gb|AAN41277.1| putative purple acid phosphatase [Arabidopsis thaliana] gi|51101268|gb|AAT95435.1| putative purple acid phosphatase [Arabidopsis thaliana] gi|332191089|gb|AEE29210.1| purple acid phosphatase 3 [Arabidopsis thaliana]	268	366	1.00E-134	136.6	86.2	91.8	purple acid phosphatase 3	gbpln	Arabidopsis thaliana	AT1G14700.1 | Symbols: PAP3, ATPAP3 | purple acid phosphatase 3 | chr1:5058680-5060988 FORWARD LENGTH=366	268	366	1.00E-137	136.6	86.2	91.8

Rsa1.0_00720.1.g18570.t2	ref|XP_002890058.1| hypothetical protein ARALYDRAFT_334745 [Arabidopsis lyrata subsp. lyrata] gi|297335900|gb|EFH66317.1| hypothetical protein ARALYDRAFT_334745 [Arabidopsis lyrata subsp. lyrata]	286	310	7.00E-42	108.4	43.0	54.5	hypothetical protein ARALYDRAFT_334745	gbpln	Arabidopsis lyrata	AT1G14688.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: E3 Ubiquitin ligase (InterPro:IPR022170); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:5049654-5050983 REVERSE LENGTH=170	286	170	2.00E-21	59.4	18.9	21.3
Rsa1.0_00720.1.g18571.t1	dbj|BAA11674.1| unnamed protein product [Nicotiana tabacum]	1324	1338	0	101.1	57.4	75.2	unnamed protein product	gbpln	Nicotiana tabacum	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1324	1262	1.00E-94	95.3	14.7	23.2
Rsa1.0_00721.1.g18572.t1	ref|XP_002867360.1| hypothetical protein ARALYDRAFT_491727 [Arabidopsis lyrata subsp. lyrata] gi|297313196|gb|EFH43619.1| hypothetical protein ARALYDRAFT_491727 [Arabidopsis lyrata subsp. lyrata]	211	308	1.00E-80	146.0	81.0	87.2	hypothetical protein ARALYDRAFT_491727	gbpln	Arabidopsis lyrata	AT4G30240.1 | Symbols: | Syntaxin/t-SNARE family protein | chr4:14808359-14809745 REVERSE LENGTH=300	211	300	5.00E-77	142.2	76.8	83.4
Rsa1.0_00721.1.g18573.t1	gb|EOA17247.1| hypothetical protein CARUB_v10005521mg [Capsella rubella]	250	263	2.00E-77	105.2	71.6	82.0	hypothetical protein CARUB_v10005521mg	gbpln	Capsella rubella	AT4G30230.1 | Symbols: | unknown protein; Has 42 Blast hits to 42 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14806376-14807158 FORWARD LENGTH=260	250	260	2.00E-77	104.0	69.2	80.8
Rsa1.0_00721.1.g18574.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	525	1231	1.00E-129	234.5	45.7	63.0	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	525	575	1.00E-81	109.5	31.8	52.0
Rsa1.0_00721.1.g18575.t1	dbj|BAJ33878.1| unnamed protein product [Thellungiella halophila]	709	711	0	100.3	93.9	96.5	unnamed protein product	----	----	AT4G30210.2 | Symbols: ATR2, AR2 | P450 reductase 2 | chr4:14796900-14800578 FORWARD LENGTH=711	709	711	0	100.3	91.3	95.3
Rsa1.0_00721.1.g18576.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00721.1.g18577.t1	ref|XP_002867362.1| hypothetical protein ARALYDRAFT_491730 [Arabidopsis lyrata subsp. lyrata] gi|297313198|gb|EFH43621.1| hypothetical protein ARALYDRAFT_491730 [Arabidopsis lyrata subsp. lyrata]	642	718	0	111.8	82.9	88.9	hypothetical protein ARALYDRAFT_491730	gbpln	Arabidopsis lyrata	AT4G30200.3 | Symbols: VEL1, VIL2 | vernalization5/VIN3-like | chr4:14786852-14790070 REVERSE LENGTH=702	642	702	0	109.3	81.8	88.3
Rsa1.0_00721.1.g18578.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00721.1.g18579.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	146	255	7.00E-34	174.7	55.5	65.1	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	146	302	1.00E-21	206.8	41.1	58.2
Rsa1.0_00721.1.g18580.t1	gb|EOA15440.1| hypothetical protein CARUB_v10004082mg [Capsella rubella]	948	948	0	100.0	94.8	97.8	hypothetical protein CARUB_v10004082mg	gbpln	Capsella rubella	AT4G30190.1 | Symbols: AHA2, PMA2, HA2 | H(+)-ATPase 2 | chr4:14770820-14775920 REVERSE LENGTH=948	948	948	0	100.0	94.8	97.8
Rsa1.0_00721.1.g18581.t1	ref|XP_002869391.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata] gi|297315227|gb|EFH45650.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata]	162	156	3.00E-61	96.3	84.0	89.5	transcription factor/ transcription regulator	gbpln	Arabidopsis lyrata	AT4G30180.1 | Symbols: | sequence-specific DNA binding transcription factors;transcription regulators | chr4:14769028-14769504 FORWARD LENGTH=158	162	158	2.00E-57	97.5	84.0	90.7
Rsa1.0_00722.1.g18582.t1	gb|AAC16262.1| putative CCAAT-binding transcription factor subunit [Arabidopsis thaliana]	243	226	1.00E-63	93.0	50.6	54.7	putative CCAAT-binding transcription factor subunit	gbpln	Arabidopsis thaliana	AT2G34720.1 | Symbols: NF-YA4 | nuclear factor Y, subunit A4 | chr2:14650018-14651255 REVERSE LENGTH=198	243	198	5.00E-66	81.5	48.6	51.9
Rsa1.0_00722.1.g18583.t1	ref|NP_680161.1| protein ATAF2 [Arabidopsis thaliana] gi|75168917|sp|Q9C598.1|NAC81_ARATH RecName: Full=Protein ATAF2; AltName: Full=NAC domain-containing protein 81; Short=ANAC081 gi|13548337|emb|CAC35884.1| ATAF2 protein [Arabidopsis thaliana] gi|19424091|gb|AAL87335.1| unknown protein [Arabidopsis thaliana] gi|22136754|gb|AAM91696.1| unknown protein [Arabidopsis thaliana] gi|110737514|dbj|BAF00699.1| ATAF2 protein [Arabidopsis thaliana] gi|332003967|gb|AED91350.1| protein ATAF2 [Arabidopsis thaliana]	280	283	1.00E-150	101.1	93.9	96.8	protein ATAF2	gbpln	Arabidopsis thaliana	AT5G08790.1 | Symbols: ATAF2, anac081 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr5:2859113-2860144 REVERSE LENGTH=283	280	283	1.00E-153	101.1	93.9	96.8

Rsa1.0_00722.1.g18584.t1	ref|XP_002871359.1| histone H1/H5 family protein [Arabidopsis lyrata subsp. lyrata] gi|297317196|gb|EFH47618.1| histone H1/H5 family protein [Arabidopsis lyrata subsp. lyrata]	451	460	1.00E−148	102.0	65.6	76.7	histone H1/H5 family protein	gbpln	Arabidopsis lyrata	AT5G08780.1 | Symbols: | winged−helix DNA−binding transcription factor family protein | chr5:2856782−2858810 FORWARD LENGTH=457	451	457	1.00E−137	101.3	65.0	75.6
Rsa1.0_00722.1.g18585.t1	gb|EOA22394.1| hypothetical protein CARUB_v10003030mg [Capsella rubella]	305	304	2.00E−92	99.7	75.4	82.0	hypothetical protein CARUB_v10003030mg	gbpln	Capsella rubella	AT5G08770.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:2855638−2856531 REVERSE LENGTH=297	305	297	9.00E−91	97.4	74.8	81.3
Rsa1.0_00722.1.g18586.t1	ref|NP_568206.1| RING/FYVE/PHD zinc finger−containing protein [Arabidopsis thaliana] gi|145334331|ref|NP_001078547.1| RING/FYVE/PHD zinc finger−containing protein [Arabidopsis thaliana] gi|13548333|emb|CAC35880.1| putative protein [Arabidopsis thaliana] gi|26451043|dbj|BAC42627.1| unknown protein [Arabidopsis thaliana] gi|94442419|gb|ABF18997.1| At5g08750 [Arabidopsis thaliana] gi|332003961|gb|AED91344.1| RING/FYVE/PHD zinc finger−containing protein [Arabidopsis thaliana] gi|332003962|gb|AED91345.1| RING/FYVE/PHD zinc finger−containing protein [Arabidopsis thaliana]	370	363	1.00E−167	98.1	82.2	87.0	RING/FYVE/PHD zinc finger−containing protein	gbpln	Arabidopsis thaliana	AT5G08750.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:2853066−2854343 FORWARD LENGTH=363	370	363	1.00E−170	98.1	82.2	87.0
Rsa1.0_00722.1.g18587.t1	sp|Q8GXR9.2|DHNA_ARATH RecName: Full=NADH dehydrogenase C1, chloroplastic/mitochondrial; Flags: Precursor	525	519	0	98.9	86.3	93.0	RecName: Full=NADH dehydrogenase C1, chloroplastic/mitochondrial; Flags: Precursor	−−−−	−−−−	AT5G08740.1 | Symbols: NDC1 | NAD(P)H dehydrogenase C1 | chr5:2848752−2851323 REVERSE LENGTH=519	525	519	0	98.9	85.9	92.6
Rsa1.0_00722.1.g18588.t1	ref|XP_002873380.1| IBR domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319217|gb|EFH49639.1| IBR domain−containing protein [Arabidopsis lyrata subsp. lyrata]	720	497	1.00E−133	69.0	36.3	46.7	IBR domain−containing protein	gbpln	Arabidopsis lyrata	AT5G08730.1 | Symbols: ATARI16, ARI16 | IBR domain−containing protein | chr5:2845824−2847415 REVERSE LENGTH=500	720	500	1.00E−134	69.4	35.8	46.1
Rsa1.0_00722.1.g18589.t1	ref|XP_002873379.1| hypothetical protein ARALYDRAFT_487714 [Arabidopsis lyrata subsp. lyrata] gi|297319216|gb|EFH49638.1| hypothetical protein ARALYDRAFT_487714 [Arabidopsis lyrata subsp. lyrata]	722	722	0	100.0	86.1	90.9	hypothetical protein ARALYDRAFT_487714	gbpln	Arabidopsis lyrata	AT5G08720.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Streptomyces cyclase/dehydrase (InterPro:IPR005031); BEST Arabidopsis thaliana protein match is: Polyketide cyclase / dehydrase and lipid transport protein (TAIR:AT4G01650.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:2841536−2845335 REVERSE LENGTH=719	722	719	0	99.6	85.6	90.2
Rsa1.0_00722.1.g18590.t2	gb|AAD15377.1| putative non−LTR retroelement reverse transcriptase [Arabidopsis thaliana]	679	1044	1.00E−156	153.8	43.6	62.3	putative non−LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G06845.1 | Symbols: | Beta−galactosidase related protein | chr2:2754666−2756008 FORWARD LENGTH=315	679	315	3.00E−42	46.4	15.6	20.5
Rsa1.0_00722.1.g18591.t1	gb|EOA20295.1| hypothetical protein CARUB_v10000603mg [Capsella rubella]	613	559	0	91.2	71.9	73.2	hypothetical protein CARUB_v10000603mg	gbpln	Capsella rubella	AT5G08680.1 | Symbols: | ATP synthase alpha/beta family protein | chr5:2821992−2824683 FORWARD LENGTH=559	613	559	0	91.2	69.8	70.3
Rsa1.0_00722.1.g18592.t1	gb|EOA20295.1| hypothetical protein CARUB_v10000603mg [Capsella rubella]	560	559	0	99.8	90.5	92.1	hypothetical protein CARUB_v10000603mg	gbpln	Capsella rubella	AT5G08680.1 | Symbols: | ATP synthase alpha/beta family protein | chr5:2821992−2824683 FORWARD LENGTH=559	560	559	0	99.8	87.7	88.8
Rsa1.0_00722.1.g18593.t1	ref|NP_568037.1| uncharacterized protein [Arabidopsis thaliana] gi|21593523|gb|AAM65490.1| unknown [Arabidopsis thaliana] gi|23297383|gb|AAN12956.1| unknown protein [Arabidopsis thaliana] gi|332661498|gb|AEE86898.1| uncharacterized protein AT4G38225 [Arabidopsis thaliana]	354	363	1.00E−143	102.5	73.7	81.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G38225.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:17927230−17928613 FORWARD LENGTH=363	354	363	1.00E−145	102.5	73.7	81.4

Rsa1.0_00722.1.g18594.t1	ref|NP_680154.2| uncharacterized protein [Arabidopsis thaliana] gi|13548324|emb|CAC35871.1| putative protein [Arabidopsis thaliana] gi|332003952|gb|AED91335.1| uncharacterized protein AT5G08660 [Arabidopsis thaliana]	639	649	0	101.6	85.8	91.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G08660.1 | Symbols: | Protein of unknown function (DUF668) | chr5:2814526-2817845 FORWARD LENGTH=649	639	649	0	101.6	85.8	91.1
Rsa1.0_00722.1.g18595.t1	gb|EOA21042.1| hypothetical protein CARUB_v10001381mg [Capsella rubella]	336	336	1.00E-180	100.0	90.2	96.1	hypothetical protein CARUB_v10001381mg	gbpln	Capsella rubella	AT5G08640.2 | Symbols: FLS1 | flavonol synthase 1 | chr5:2804009-2805175 FORWARD LENGTH=336	336	336	0	100.0	90.8	95.8
Rsa1.0_00722.1.g18596.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00722.1.g18597.t1	ref|XP_002873374.1| DDT domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319211|gb|EFH49633.1| DDT domain-containing protein [Arabidopsis lyrata subsp. lyrata]	699	722	0	103.3	82.1	88.1	DDT domain-containing protein	gbpln	Arabidopsis lyrata	AT5G08630.1 | Symbols: | DDT domain-containing protein | chr5:2798575-2802138 REVERSE LENGTH=723	699	723	0	103.4	80.4	88.0
Rsa1.0_00722.1.g18598.t1	gb|EOA22779.1| hypothetical protein CARUB_v10003496mg [Capsella rubella]	562	564	0	100.4	89.1	93.2	hypothetical protein CARUB_v10003496mg	gbpln	Capsella rubella	AT5G08620.1 | Symbols: STRS2, ATRH25 | DEA(D/H)-box RNA helicase family protein | chr5:2794540-2797548 FORWARD LENGTH=563	562	563	0	100.2	87.7	92.3
Rsa1.0_00722.1.g18599.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	152	1231	1.00E-26	809.9	40.8	56.6	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00722.1.g18600.t2	gb|EOA19348.1| hypothetical protein CARUB_v10000281mg [Capsella rubella]	728	766	0	105.2	88.3	92.7	hypothetical protein CARUB_v10000281mg	gbpln	Capsella rubella	AT5G08610.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:2790341-2794059 FORWARD LENGTH=850	728	850	0	116.8	85.7	90.1
Rsa1.0_00723.1.g18601.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	520	704	1.00E-139	135.4	49.6	52.1	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00723.1.g18602.t3	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1077	1838	4.00E-52	170.7	12.3	20.7	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00723.1.g18603.t1	gb|AAF04414.1|AC010927_7 hypothetical protein [Arabidopsis thaliana]	903	1004	1.00E-28	111.2	19.8	32.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957	903	957	1.00E-24	106.0	18.8	29.6
Rsa1.0_00723.1.g18604.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	636	1142	1.00E-100	179.6	30.5	40.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	636	575	2.00E-38	90.4	18.7	31.8
Rsa1.0_00723.1.g18605.t1	gb|AAD25557.1|AC005850_14 Hypothetical protein [Arabidopsis thaliana]	374	404	8.00E-12	108.0	10.4	12.0	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00723.1.g18606.t4	ref|NP_567204.3| cysteine-rich receptor-like protein kinase 41 [Arabidopsis thaliana] gi|152013451|sp|O23081.2|CRK41_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 41; Short=Cysteine-rich RLK41; Flags: Precursor gi|332656562|gb|AEE81962.1| cysteine-rich receptor-like protein kinase 41 [Arabidopsis thaliana]	667	665	0	99.7	72.7	82.5	cysteine-rich receptor-like protein kinase 41	gbpln	Arabidopsis thaliana	AT4G00970.1 | Symbols: CRK41 | cysteine-rich RLK (RECEPTOR-like protein kinase) 41 | chr4:418437-421694 FORWARD LENGTH=665	667	665	0	99.7	72.7	82.5
Rsa1.0_00723.1.g18607.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	718	723	0	100.7	52.6	68.0	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	718	696	2.00E-45	96.9	22.6	40.3
Rsa1.0_00723.1.g18608.t8	gb|AAD15376.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1100	962	3.00E-35	87.5	9.7	13.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00723.1.g18609.t1	gb|EOA23025.1| hypothetical protein CARUB_v10003790mg [Capsella rubella]	478	485	0	101.5	84.7	91.2	hypothetical protein CARUB_v10003790mg	gbpln	Capsella rubella	AT4G00910.1 | Symbols: | Aluminium activated malate transporter family protein | chr4:389370-391287 REVERSE LENGTH=497	478	497	0	104.0	84.7	90.4
Rsa1.0_00723.1.g18610.t1	ref|XP_002875008.1| hypothetical protein ARALYDRAFT_490476 [Arabidopsis lyrata subsp. lyrata] gi|297320845|gb|EFH51267.1| hypothetical protein ARALYDRAFT_490476 [Arabidopsis lyrata subsp. lyrata]	184	190	6.00E-54	103.3	73.4	81.0	hypothetical protein ARALYDRAFT_490476	gbpln	Arabidopsis lyrata	AT4G00895.1 | Symbols: | ATPase, F1 complex, OSCP/delta subunit protein | chr4:381823-382398 FORWARD LENGTH=191	184	191	2.00E-51	103.8	69.6	76.1
Rsa1.0_00723.1.g18611.t1	gb|EOA19956.1| hypothetical protein CARUB_v10000206mg [Capsella rubella]	859	854	4.00E-33	99.4	36.0	45.1	hypothetical protein CARUB_v10000206mg	gbpln	Capsella rubella	AT4G00890.1 | Symbols: | proline-rich family protein | chr4:374055-375350 REVERSE LENGTH=431	859	431	3.00E-20	50.2	7.9	8.8
Rsa1.0_00723.1.g18612.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00724.1.g18613.t1	ref|XP_002875078.1| hypothetical protein ARALYDRAFT_322499 [Arabidopsis lyrata subsp. lyrata] gi|297320916|gb|EFH51337.1| hypothetical protein ARALYDRAFT_322499 [Arabidopsis lyrata subsp. lyrata]	141	137	3.00E-58	97.2	83.0	87.2	hypothetical protein ARALYDRAFT_322499	gbpln	Arabidopsis lyrata	AT1G70780.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23150.1); Has 143 Blast hits to 143 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 143; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26695462-26695975 REVERSE LENGTH=140	141	140	8.00E-36	99.3	56.0	68.1
Rsa1.0_00724.1.g18614.t1	gb|AAF02855.1|AC009324_4 Similar to retrotransposon proteins [Arabidopsis thaliana]	1039	1522	0	146.5	60.4	75.8	Similar to retrotransposon proteins	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1039	1262	1.00E-106	121.5	18.8	26.5
Rsa1.0_00724.1.g18615.t1	sp|Q5BN23.1|RGA1_BRACM RecName: Full=DELLA protein RGA1; AltName: Full=BrRGA1; AltName: Full=RGA-like protein 1 gi|60656559|gb|AAX33297.1| DELLA protein [Brassica rapa]	575	573	0	99.7	93.0	94.8	RecName: Full=DELLA protein RGA1; AltName: Full=BrRGA1; AltName: Full=RGA-like protein 1 gi|60656559|gb|AAX33297.1| DELLA protein	gbpln	Brassica rapa	AT2G01570.1 | Symbols: RGA1, RGA | GRAS family transcription factor family protein | chr2:255581-257344 REVERSE LENGTH=587	575	587	0	102.1	85.2	89.7
Rsa1.0_00724.1.g18616.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00724.1.g18617.t1	gb|EOA29259.1| hypothetical protein CARUB_v10025533mg, partial [Capsella rubella]	165	293	2.00E-14	177.6	23.6	27.9	hypothetical protein CARUB_v10025533mg, partial	gbpln	Capsella rubella	AT1G34070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48050.1); Has 648 Blast hits to 647 proteins in 29 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 25; Plants - 607; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12402283-12403209 FORWARD LENGTH=308	165	308	6.00E-14	186.7	20.6	26.1
Rsa1.0_00724.1.g18618.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00724.1.g18619.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00724.1.g18620.t1	ref|XP_002876764.1| hypothetical protein ARALYDRAFT_484074 [Arabidopsis lyrata subsp. lyrata] gi|297322602|gb|EFH53023.1| hypothetical protein ARALYDRAFT_484074 [Arabidopsis lyrata subsp. lyrata]	191	191	6.00E-79	100.0	87.4	95.8	hypothetical protein ARALYDRAFT_484074	gbpln	Arabidopsis lyrata	AT2G01580.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G07510.2); Has 129 Blast hits to 129 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 129; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:265181-265756 REVERSE LENGTH=191	191	191	3.00E-71	100.0	86.9	93.7
Rsa1.0_00724.1.g18621.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	279	1223	8.00E-57	438.4	43.0	60.6	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	279	746	7.00E-36	267.4	30.5	43.7
Rsa1.0_00724.1.g18622.t1	ref|XP_002875082.1| hypothetical protein ARALYDRAFT_904366 [Arabidopsis lyrata subsp. lyrata] gi|297320920|gb|EFH51341.1| hypothetical protein ARALYDRAFT_904366 [Arabidopsis lyrata subsp. lyrata]	556	562	0	101.1	87.4	92.1	hypothetical protein ARALYDRAFT_904366	gbpln	Arabidopsis lyrata	AT2G01600.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr2:268975-272356 FORWARD LENGTH=571	556	571	0	102.7	86.7	91.9
Rsa1.0_00724.1.g18623.t1	gb|AAF22135.1|AF127919_1 high mobility group protein I/Y [Brassica napus]	211	203	2.00E-90	96.2	87.2	90.5	high mobility group protein I/Y	gbpln	Brassica napus	AT1G14900.1 | Symbols: HMGA | high mobility group A | chr1:5138665-5139353 REVERSE LENGTH=204	211	204	3.00E-54	96.7	63.5	70.1
Rsa1.0_00724.1.g18624.t1	gb|EOA25668.1| hypothetical protein CARUB_v10019019mg [Capsella rubella]	215	227	3.00E-50	105.6	55.3	69.8	hypothetical protein CARUB_v10019019mg	gbpln	Capsella rubella	AT2G01610.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr2:274124-274792 REVERSE LENGTH=222	215	222	6.00E-50	103.3	50.7	64.2
Rsa1.0_00724.1.g18625.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00725.1.g18626.t1	ref|NP_188081.1| cytochrome P450, family 72, subfamily A, polypeptide 9 [Arabidopsis thaliana] gi|332642028|gb|AEE75549.1| cytochrome P450, family 72, subfamily A, polypeptide 9 [Arabidopsis thaliana]	508	508	0	100.0	83.7	92.7	cytochrome P450, family 72, subfamily A, polypeptide 9	gbpln	Arabidopsis thaliana	AT3G14630.1 | Symbols: CYP72A9 | cytochrome P450, family 72, subfamily A, polypeptide 9 | chr3:4917498-4919409 FORWARD LENGTH=508	508	508	0	100.0	83.7	92.7
Rsa1.0_00725.1.g18627.t1	ref|XP_002882888.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata] gi|297328728|gb|EFH59147.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata]	512	512	0	100.0	85.2	92.2	CYP72A15	gbpln	Arabidopsis lyrata	AT3G14690.1 | Symbols: CYP72A15 | cytochrome P450, family 72, subfamily A, polypeptide 15 | chr3:4937410-4939310 FORWARD LENGTH=512	512	512	0	100.0	84.2	91.6

Rsa1.0_00725.1.g18628.t1	ref|XP_002882888.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata] gi|297328728|gb|EFH59147.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata]	513	512	0	99.8	88.7	94.5	CYP72A15	gbpln	Arabidopsis lyrata	AT3G14690.1 | Symbols: CYP72A15 | cytochrome P450, family 72, subfamily A, polypeptide 15 | chr3:4937410-4939310 FORWARD LENGTH=512	513	512	0	99.8	88.5	94.3
Rsa1.0_00725.1.g18629.t1	dbj|BAJ33634.1| unnamed protein product [Thellungiella halophila]	718	512	0	71.3	58.8	64.1	unnamed protein product	----	----	AT3G14690.1 | Symbols: CYP72A15 | cytochrome P450, family 72, subfamily A, polypeptide 15 | chr3:4937410-4939310 FORWARD LENGTH=512	718	512	0	71.3	57.1	63.8
Rsa1.0_00725.1.g18630.t1	ref|NP_188090.2| mitogen-activated protein kinase 19 [Arabidopsis thaliana] gi|209572650|sp|Q9LUC3.2|MPK19_ARATH RecName: Full=Mitogen-activated protein kinase 19; Short=AtMPK19; Short=MAP kinase 19 gi|332642038|gb|AEE75559.1| mitogen-activated protein kinase 19 [Arabidopsis thaliana]	554	598	0	107.9	89.0	94.4	mitogen-activated protein kinase 19	gbpln	Arabidopsis thaliana	AT3G14720.1 | Symbols: ATMPK19, MPK19 | MAP kinase 19 | chr3:4946057-4948906 FORWARD LENGTH=598	554	598	0	107.9	89.0	94.4
Rsa1.0_00725.1.g18631.t1	gb|EOA32067.1| hypothetical protein CARUB_v10015310mg [Capsella rubella]	362	335	1.00E-141	92.5	72.7	78.7	hypothetical protein CARUB_v10015310mg	gbpln	Capsella rubella	AT3G14740.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr3:4952185-4953306 REVERSE LENGTH=343	362	343	1.00E-141	94.8	74.3	81.8
Rsa1.0_00725.1.g18632.t1	ref|XP_002885054.1| hypothetical protein ARALYDRAFT_478888 [Arabidopsis lyrata subsp. lyrata] gi|297330894|gb|EFH61313.1| hypothetical protein ARALYDRAFT_478888 [Arabidopsis lyrata subsp. lyrata]	329	329	1.00E-125	100.0	77.2	82.1	hypothetical protein ARALYDRAFT_478888	gbpln	Arabidopsis lyrata	AT3G14750.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67170.1); Has 4036 Blast hits to 3091 proteins in 519 species: Archae - 61; Bacteria - 669; Metazoa - 1503; Fungi - 255; Plants - 421; Viruses - 4; Other Eukaryotes - 1123 (source: NCBI BLink). | chr3:4953765-4955373 REVERSE LENGTH=331	329	331	1.00E-125	100.6	76.3	81.8
Rsa1.0_00725.1.g18633.t1	ref|NP_566493.1| nodulin MtN3-like protein [Arabidopsis thaliana] gi|75273203|sp|Q9LH79.1|SWET2_ARATH RecName: Full=Bidirectional sugar transporter SWEET2; Short=AtSWEET2 gi|11994587|dbj|BAB02642.1| MtN3-like protein [Arabidopsis thaliana] gi|15809923|gb|AAL06889.1| AT3g14770/T21E2_2 [Arabidopsis thaliana] gi|17978879|gb|AAL47411.1| AT3g14770/T21E2_2 [Arabidopsis thaliana] gi|332642044|gb|AEE75565.1| bidirectional sugar transporter SWEET2 [Arabidopsis thaliana]	236	236	1.00E-113	100.0	88.1	94.5	nodulin MtN3-like protein	gbpln	Arabidopsis thaliana	AT3G14770.1 | Symbols: SWEET2, AtSWEET2 | Nodulin MtN3 family protein | chr3:4957787-4959202 REVERSE LENGTH=236	236	236	1.00E-115	100.0	88.1	94.5
Rsa1.0_00725.1.g18634.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00725.1.g18635.t1	gb|EOA30048.1| hypothetical protein CARUB_v10013153mg [Capsella rubella]	665	664	0	99.8	95.3	97.3	hypothetical protein CARUB_v10013153mg	gbpln	Capsella rubella	AT3G14790.1 | Symbols: RHM3, ATRHM3 | rhamnose biosynthesis 3 | chr3:4964791-4966875 FORWARD LENGTH=664	665	664	0	99.8	94.6	96.7
Rsa1.0_00725.1.g18636.t10	ref|XP_002882895.1| hypothetical protein ARALYDRAFT_478897 [Arabidopsis lyrata subsp. lyrata] gi|297328735|gb|EFH59154.1| hypothetical protein ARALYDRAFT_478897 [Arabidopsis lyrata subsp. lyrata]	567	475	0	83.8	68.8	73.2	hypothetical protein ARALYDRAFT_478897	gbpln	Arabidopsis lyrata	AT3G14830.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53450.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:4983386-4985666 FORWARD LENGTH=476	567	476	0	84.0	68.1	72.5
Rsa1.0_00725.1.g18637.t7	ref|NP_188102.5| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|313471762|sp|C0LGN2.1|Y3148_ARATH RecName: Full=Probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840; Flags: Precursor gi|224589567|gb|ACN59317.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332642053|gb|AEE75574.1| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana]	992	1020	0	102.8	76.4	86.3	Leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT3G14840.2 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr3:4988271-4993891 FORWARD LENGTH=1020	992	1020	0	102.8	76.4	86.3
Rsa1.0_00726.1.g18638.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00726.1.g18639.t1	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	516	954	3.00E-54	184.9	27.1	31.2	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_00726.1.g18640.t1	ref|NP_566893.1| HhH-GPD base excision DNA repair protein-related protein [Arabidopsis thaliana] gi|332644814|gb|AEE78335.1| HhH-GPD base excision DNA repair protein-related protein [Arabidopsis thaliana]	287	293	1.00E-138	102.1	84.3	93.0	HhH-GPD base excision DNA repair protein-related protein	gbpln	Arabidopsis thaliana	AT3G47830.1 | Symbols: | DNA glycosylase superfamily protein | chr3:17647069-17648346 FORWARD LENGTH=293	287	293	1.00E-141	102.1	84.3	93.0
Rsa1.0_00726.1.g18641.t1	ref|XP_002875864.1| hypothetical protein ARALYDRAFT_485139 [Arabidopsis lyrata subsp. lyrata] gi|297321702|gb|EFH52123.1| hypothetical protein ARALYDRAFT_485139 [Arabidopsis lyrata subsp. lyrata]	943	935	0	99.2	82.4	89.7	hypothetical protein ARALYDRAFT_485139	gbpln	Arabidopsis lyrata	AT3G47780.1 | Symbols: ATATH6, ATH6 | ABC2 homolog 6 | chr3:17624500-17628972 FORWARD LENGTH=935	943	935	0	99.2	81.9	89.1
Rsa1.0_00726.1.g18642.t1	ref|XP_002875861.1| hypothetical protein ARALYDRAFT_485136 [Arabidopsis lyrata subsp. lyrata] gi|297321699|gb|EFH52120.1| hypothetical protein ARALYDRAFT_485136 [Arabidopsis lyrata subsp. lyrata]	169	937	7.00E-82	554.4	86.4	90.5	hypothetical protein ARALYDRAFT_485136	gbpln	Arabidopsis lyrata	AT3G47760.1 | Symbols: ATATH4, ATH4, ABCA5 | ABC2 homolog 4 | chr3:17611787-17616639 FORWARD LENGTH=872	169	872	1.00E-83	516.0	85.8	90.5
Rsa1.0_00726.1.g18643.t2	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	1004	1089	0	108.5	47.5	54.7	transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00726.1.g18644.t1	gb|AAF71981.1|AC013453_6 Hypothetical protein [Arabidopsis thaliana]	360	399	1.00E-126	110.8	62.5	77.5	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00726.1.g18645.t2	gb|EOA23464.1| hypothetical protein CARUB_v10016655mg [Capsella rubella]	207	933	4.00E-73	450.7	69.1	79.2	hypothetical protein CARUB_v10016655mg	gbpln	Capsella rubella	AT3G47780.1 | Symbols: ATATH6, ATH6 | ABC2 homolog 6 | chr3:17624500-17628972 FORWARD LENGTH=935	207	935	3.00E-75	451.7	66.7	76.8
Rsa1.0_00726.1.g18646.t1	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	453	1463	1.00E-46	323.0	28.5	47.7	F5J5.1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00726.1.g18647.t2	ref|NP_190358.3| ABC transporter A family member 3 [Arabidopsis thaliana] gi|374095510|sp|Q1PEH6.3|AB3A_ARATH RecName: Full=ABC transporter A family member 3; Short=ABC transporter ABCA.3; Short=AtABCA3; AltName: Full=ABC2 homolog 2 gi|332644803|gb|AEE78324.1| ABC transporter A family member 3 [Arabidopsis thaliana]	327	932	1.00E-101	285.0	58.1	68.5	ABC transporter A family member 3	gbpln	Arabidopsis thaliana	AT3G47740.1 | Symbols: ATATH2, ATH2, ABCA3 | ABC2 homolog 2 | chr3:17600651-17604965 FORWARD LENGTH=932	327	932	1.00E-104	285.0	58.1	68.5
Rsa1.0_00726.1.g18648.t5	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00726.1.g18649.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1381	1475	0	106.8	59.9	76.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1381	1262	0	91.4	23.2	29.6
Rsa1.0_00726.1.g18650.t1	gb|AAQ82842.1| At4g20730 [Arabidopsis thaliana] gi|51970840|dbj|BAD44112.1| putative protein [Arabidopsis thaliana]	976	800	6.00E-33	82.0	18.9	32.4	At4g20730	gbpln	Arabidopsis thaliana	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	976	1399	8.00E-29	143.3	17.6	32.1
Rsa1.0_00726.1.g18651.t7	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	474	1838	4.00E-41	387.8	25.1	39.9	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00727.1.g18652.t1	ref|XP_002873002.1| hypothetical protein ARALYDRAFT_486913 [Arabidopsis lyrata subsp. lyrata] gi|297318839|gb|EFH49261.1| hypothetical protein ARALYDRAFT_486913 [Arabidopsis lyrata subsp. lyrata]	170	170	4.00E-85	100.0	89.4	97.1	hypothetical protein ARALYDRAFT_486913	gbpln	Arabidopsis lyrata	AT5G01610.1 | Symbols: | Protein of unknown function, DUF538 | chr5:231075-231994 FORWARD LENGTH=170	170	170	4.00E-87	100.0	88.8	96.5
Rsa1.0_00727.1.g18653.t2	ref|XP_002873001.1| hypothetical protein ARALYDRAFT_486912 [Arabidopsis lyrata subsp. lyrata] gi|297318838|gb|EFH49260.1| hypothetical protein ARALYDRAFT_486912 [Arabidopsis lyrata subsp. lyrata]	453	448	0	98.9	85.0	89.6	hypothetical protein ARALYDRAFT_486912	gbpln	Arabidopsis lyrata	AT5G01620.2 | Symbols: | TRICHOME BIREFRINGENCE-LIKE 35 | chr5:232882-234821 FORWARD LENGTH=449	453	449	0	99.1	85.2	89.8
Rsa1.0_00727.1.g18654.t2	ref|NP_195783.3| breast cancer 2 susceptibility protein [Arabidopsis thaliana] gi|31335362|emb|CAD32572.1| breast cancer susceptibility protein 2b [Arabidopsis thaliana] gi|332002986|gb|AED90369.1| protein BRCA2-like B [Arabidopsis thaliana]	1065	1155	0	108.5	76.2	83.1	breast cancer 2 susceptibility protein	gbpln	Arabidopsis thaliana	AT5G01630.1 | Symbols: BRCA2B, BRCA2(V), ATBRCA2(V) | BRCA2-like B | chr5:235117-240911 REVERSE LENGTH=1155	1065	1155	0	108.5	76.2	83.1
Rsa1.0_00727.1.g18655.t1	gb|EOA19529.1| hypothetical protein CARUB_v10002469mg [Capsella rubella]	213	224	2.00E-85	105.2	78.9	86.4	hypothetical protein CARUB_v10002469mg	gbpln	Capsella rubella	AT5G01640.1 | Symbols: PRA1.B5 | prenylated RAB acceptor 1.B5 | chr5:241442-242113 REVERSE LENGTH=223	213	223	8.00E-86	104.7	76.1	83.6

Rsa1.0_00727.1.g18656.t1	ref|NP_001154692.1| macrophage migration inhibitory factor family protein [Arabidopsis thaliana] gi|332002989|gb|AED90372.1| macrophage migration inhibitory factor family protein [Arabidopsis thaliana]	135	122	4.00E-47	90.4	70.4	74.8	macrophage migration inhibitory factor family protein	gbpln	Arabidopsis thaliana	AT5G01650.2 | Symbols: | Tautomerase/MIF superfamily protein | chr5:243067-244033 REVERSE LENGTH=122	135	122	1.00E-49	90.4	70.4	74.8
Rsa1.0_00727.1.g18657.t1	gb|EOA23003.1| hypothetical protein CARUB_v10003758mg [Capsella rubella]	322	322	1.00E-169	100.0	87.0	95.0	hypothetical protein CARUB_v10003758mg	gbpln	Capsella rubella	AT5G01670.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr5:252000-253856 FORWARD LENGTH=322	322	322	1.00E-170	100.0	86.0	94.7
Rsa1.0_00727.1.g18658.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	99	1231	1.00E-14	1243.4	40.4	53.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00727.1.g18659.t1	ref|XP_002870901.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297316738|gb|EFH47160.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	675	665	0	98.5	83.1	89.8	F-box family protein	gbpln	Arabidopsis lyrata	AT5G01720.1 | Symbols: | RNI-like superfamily protein | chr5:267118-270391 REVERSE LENGTH=665	675	665	0	98.5	83.6	90.2
Rsa1.0_00727.1.g18660.t1	gb|AAM62599.1| unknown [Arabidopsis thaliana]	190	174	4.00E-83	91.6	79.5	84.2	unknown	gbpln	Arabidopsis thaliana	AT5G01750.2 | Symbols: | Protein of unknown function (DUF567) | chr5:290034-291109 FORWARD LENGTH=217	190	217	5.00E-85	114.2	79.5	85.8
Rsa1.0_00727.1.g18661.t1	gb|EOA22786.1| hypothetical protein CARUB_v10003503mg [Capsella rubella]	551	568	0	103.1	75.5	80.4	hypothetical protein CARUB_v10003503mg	gbpln	Capsella rubella	AT5G01760.1 | Symbols: | ENTH/VHS/GAT family protein | chr5:291753-294127 FORWARD LENGTH=542	551	542	0	98.4	71.5	78.6
Rsa1.0_00727.1.g18662.t1	ref|XP_002870897.1| hypothetical protein ARALYDRAFT_907968 [Arabidopsis lyrata subsp. lyrata] gi|297316734|gb|EFH47156.1| hypothetical protein ARALYDRAFT_907968 [Arabidopsis lyrata subsp. lyrata]	191	191	5.00E-54	100.0	68.1	78.0	hypothetical protein ARALYDRAFT_907968	gbpln	Arabidopsis lyrata	AT5G01790.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; Has 121 Blast hits to 121 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 121; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:305057-305683 REVERSE LENGTH=208	191	208	6.00E-56	108.9	67.5	77.5
Rsa1.0_00727.1.g18663.t1	ref|XP_002872989.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297318826|gb|EFH49248.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	235	224	3.00E-68	95.3	64.3	74.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G01860.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:335630-336277 FORWARD LENGTH=215	235	215	1.00E-57	91.5	59.1	66.8
Rsa1.0_00727.1.g18664.t1	ref|XP_002870893.1| hypothetical protein ARALYDRAFT_907956 [Arabidopsis lyrata subsp. lyrata] gi|297316730|gb|EFH47152.1| hypothetical protein ARALYDRAFT_907956 [Arabidopsis lyrata subsp. lyrata]	174	189	6.00E-42	108.6	57.5	63.2	hypothetical protein ARALYDRAFT_907956	gbpln	Arabidopsis lyrata	AT5G01910.1 | Symbols: | unknown protein; Has 66 Blast hits to 66 proteins in 27 species: Archae - 0; Bacteria - 2; Metazoa - 18; Fungi - 7; Plants - 29; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr5:357950-358655 REVERSE LENGTH=180	174	180	4.00E-44	103.4	58.0	63.2
Rsa1.0_00727.1.g18665.t1	dbj|BAC41802.1| unknown protein [Arabidopsis thaliana]	479	504	0	105.2	83.9	91.2	unknown protein	gbpln	Arabidopsis thaliana	AT5G01920.1 | Symbols: STN8 | Protein kinase superfamily protein | chr5:359154-360867 FORWARD LENGTH=495	479	495	0	103.3	83.9	91.2
Rsa1.0_00727.1.g18666.t7	ref|XP_002870892.1| hypothetical protein ARALYDRAFT_349416 [Arabidopsis lyrata subsp. lyrata] gi|297316729|gb|EFH47151.1| hypothetical protein ARALYDRAFT_349416 [Arabidopsis lyrata subsp. lyrata]	694	448	0	64.6	58.2	61.7	hypothetical protein ARALYDRAFT_349416	gbpln	Arabidopsis lyrata	AT5G01930.1 | Symbols: MAN6, AtMAN6 | Glycosyl hydrolase superfamily protein | chr5:361189-362867 REVERSE LENGTH=448	694	448	0	64.6	58.2	61.7
Rsa1.0_00727.1.g18667.t1	ref|XP_002870890.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297316727|gb|EFH47149.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	944	951	0	100.7	88.7	93.4	ATP binding protein	gbpln	Arabidopsis lyrata	AT5G01950.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:365040-369532 REVERSE LENGTH=951	944	951	0	100.7	88.8	93.8
Rsa1.0_00727.1.g18668.t1	sp|C0LGU1.1|Y5374_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At5g37450; Flags: Precursor gi|224589689|gb|ACN59376.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	959	959	0	100.0	80.6	89.3	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At5g37450; Flags: Precursor gi|224589689|gb|ACN59376.1| leucine-rich repeat receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT5G37450.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:14852801-14857098 REVERSE LENGTH=935	959	935	0	97.5	75.5	83.8

Rsa1.0_00728.1.g18669.t1	ref|XP_002871965.1| hypothetical protein ARALYDRAFT_489014 [Arabidopsis lyrata subsp. lyrata] gi|297317802|gb|EFH48224.1| hypothetical protein ARALYDRAFT_489014 [Arabidopsis lyrata subsp. lyrata]	38	353	8.00E-11	928.9	89.5	92.1	hypothetical protein ARALYDRAFT_489014	gbpln	Arabidopsis lyrata	AT5G21050.1 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 8 growth stages; CONTAINS InterPro DOMAIN/s: Hyccin (InterPro:IPR018619); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64090.1); Has 206 Blast hits to 206 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 145; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr5:7147890-7148957 FORWARD LENGTH=355	38	355	4.00E-13	934.2	86.8	92.1
Rsa1.0_00728.1.g18670.t1	ref|NP_197608.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|11762126|gb|AAG40341.1|AF324989_1 AT5g21090 [Arabidopsis thaliana] gi|13899097|gb|AAK48970.1|AF370543_1 Unknown protein [Arabidopsis thaliana] gi|20148427|gb|AAM10104.1| unknown protein [Arabidopsis thaliana] gi|27311823|gb|AAO00877.1| Unknown protein [Arabidopsis thaliana] gi|29294060|gb|AAO73897.1| leucine rich repeat protein (LRP), putative [Arabidopsis thaliana] gi|30023686|gb|AAP13376.1| At5g21090 [Arabidopsis thaliana] gi|222424256|dbj|BAH20085.1| AT5G21090 [Arabidopsis thaliana] gi|332005547|gb|AED92930.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	198	218	3.00E-98	110.1	91.9	94.9	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G21090.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:7164758-7166904 FORWARD LENGTH=218	198	218	1.00E-101	110.1	91.9	94.9
Rsa1.0_00728.1.g18671.t1	ref|NP_197612.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|29294053|gb|AAO73890.1| hypothetical protein [Arabidopsis thaliana] gi|52354467|gb|AAU44554.1| hypothetical protein AT5G21130 [Arabidopsis thaliana] gi|332005555|gb|AED92938.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	308	281	7.00E-87	91.2	54.5	68.8	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT5G21130.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr5:7185968-7186813 FORWARD LENGTH=281	308	281	2.00E-89	91.2	54.5	68.8
Rsa1.0_00728.1.g18672.t1	gb|EOA19730.1| hypothetical protein CARUB_v10003787mg [Capsella rubella]	344	821	4.00E-41	238.7	35.5	43.0	hypothetical protein CARUB_v10003787mg	gbpln	Capsella rubella	AT5G21160.1 | Symbols: | LA RNA-binding protein | chr5:7199191-7203879 REVERSE LENGTH=826	344	826	2.00E-34	240.1	34.6	42.7
Rsa1.0_00728.1.g18673.t1	ref|XP_004251248.1| PREDICTED: calmodulin-like isoform 1 [Solanum lycopersicum]	149	180	4.00E-80	120.8	100.0	100.0	PREDICTED: calmodulin-like isoform 1	gbpln	Solanum lycopersicum	AT2G27030.3 | Symbols: CAM5 | calmodulin 5 | chr2:11532069-11534176 FORWARD LENGTH=181	149	181	6.00E-82	121.5	98.7	100.0
Rsa1.0_00728.1.g18674.t1	ref|NP_680178.1| RNI-like family protein-like protein [Arabidopsis thaliana] gi|13374849|emb|CAC34483.1| DNA excision repair protein [Arabidopsis thaliana] gi|29294068|gb|AAO73905.1| hypothetical protein [Arabidopsis thaliana] gi|53828573|gb|AAU94396.1| At5g21900 [Arabidopsis thaliana] gi|55167908|gb|AAV43786.1| At5g21900 [Arabidopsis thaliana] gi|332005569|gb|AED92952.1| RNI-like family protein-like protein [Arabidopsis thaliana]	574	544	1.00E-148	94.8	48.4	61.3	RNI-like family protein-like protein	gbpln	Arabidopsis thaliana	AT5G21900.1 | Symbols: | RNI-like superfamily protein | chr5:7238239-7240338 FORWARD LENGTH=544	574	544	1.00E-151	94.8	48.4	61.3
Rsa1.0_00728.1.g18675.t1	gb|EOA21421.1| hypothetical protein CARUB_v10001794mg [Capsella rubella]	325	251	1.00E-108	77.2	61.8	66.8	hypothetical protein CARUB_v10001794mg	gbpln	Capsella rubella	AT5G21920.1 | Symbols: YLMG2, ATYLMG2 | YGGT family protein | chr5:7241350-7242765 REVERSE LENGTH=251	325	251	1.00E-108	77.2	60.6	66.2
Rsa1.0_00728.1.g18676.t1	gb|EOA21360.1| hypothetical protein CARUB_v10001723mg [Capsella rubella]	239	267	6.00E-60	111.7	65.3	75.3	hypothetical protein CARUB_v10001723mg	gbpln	Capsella rubella	AT5G21940.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G43850.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7249446-7250353 REVERSE LENGTH=264	239	264	4.00E-56	110.5	63.6	71.1

Rsa1.0_00728.1.g18677.t1	ref|NP_680184.1| ethylene-responsive transcription factor ERF016 [Arabidopsis thaliana] gi|75333357|sp|Q9C591.1|ERF16_ARATH RecName: Full=Ethylene-responsive transcription factor ERF016 gi|13374855|emb|CAC34489.1| putative protein [Arabidopsis thaliana] gi|29294061|gb|AAO73898.1| AP2 domain transcription factor, putative [Arabidopsis thaliana] gi|44021931|gb|AAS46630.1| At5g21960 [Arabidopsis thaliana] gi|45773852|gb|AAS76730.1| At5g21960 [Arabidopsis thaliana] gi|48479324|gb|AAT44933.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|332005578|gb|AED92961.1| ethylene-responsive transcription factor ERF016 [Arabidopsis thaliana]	207	216	2.00E-74	104.3	76.8	85.0	ethylene-responsive transcription factor ERF016	gbpln	Arabidopsis thaliana	AT5G21960.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:7258560-7259210 REVERSE LENGTH=216	207	216	6.00E-77	104.3	76.8	85.0
Rsa1.0_00728.1.g18678.t1	ref|XP_002874039.1| hypothetical protein ARALYDRAFT_489044 [Arabidopsis lyrata subsp. lyrata] gi|297319876|gb|EFH50298.1| hypothetical protein ARALYDRAFT_489044 [Arabidopsis lyrata subsp. lyrata]	248	292	6.00E-73	117.7	71.4	79.4	hypothetical protein ARALYDRAFT_489044	gbpln	Arabidopsis lyrata	AT5G21280.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:7264094-7265514 REVERSE LENGTH=302	248	302	8.00E-74	121.8	72.6	80.2
Rsa1.0_00728.1.g18679.t1	dbj|BAC43348.1| unknown protein [Arabidopsis thaliana]	577	554	0	96.0	83.2	87.9	unknown protein	gbpln	Arabidopsis thaliana	AT5G21990.1 | Symbols: TPR7 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:7273395-7276318 FORWARD LENGTH=554	577	554	0	96.0	83.2	87.7
Rsa1.0_00728.1.g18680.t1	ref|XP_002871983.1| hypothetical protein ARALYDRAFT_489047 [Arabidopsis lyrata subsp. lyrata] gi|297317820|gb|EFH48242.1| hypothetical protein ARALYDRAFT_489047 [Arabidopsis lyrata subsp. lyrata]	296	376	1.00E-116	127.0	83.1	87.2	hypothetical protein ARALYDRAFT_489047	gbpln	Arabidopsis lyrata	AT5G22000.2 | Symbols: RHF2A | RING-H2 group F2A | chr5:7277436-7279553 FORWARD LENGTH=375	296	375	1.00E-115	126.7	82.1	86.1
Rsa1.0_00728.1.g18681.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00728.1.g18682.t1	ref|XP_002874087.1| hypothetical protein ARALYDRAFT_910271 [Arabidopsis lyrata subsp. lyrata] gi|297319924|gb|EFH50346.1| hypothetical protein ARALYDRAFT_910271 [Arabidopsis lyrata subsp. lyrata]	99	261	6.00E-24	263.6	55.6	73.7	hypothetical protein ARALYDRAFT_910271	gbpln	Arabidopsis lyrata	AT5G22791.2 | Symbols: | F-box family protein | chr5:7603579-7604771 REVERSE LENGTH=355	99	355	3.00E-18	358.6	48.5	68.7
Rsa1.0_00728.1.g18683.t1	ref|XP_002874089.1| hypothetical protein ARALYDRAFT_910273 [Arabidopsis lyrata subsp. lyrata] gi|297319926|gb|EFH50348.1| hypothetical protein ARALYDRAFT_910273 [Arabidopsis lyrata subsp. lyrata]	203	393	4.00E-19	193.6	36.5	47.3	hypothetical protein ARALYDRAFT_910273	gbpln	Arabidopsis lyrata	AT5G22791.2 | Symbols: | F-box family protein | chr5:7603579-7604771 REVERSE LENGTH=355	203	355	5.00E-18	174.9	31.5	44.8
Rsa1.0_00728.1.g18684.t17	gb|EOA19946.1| hypothetical protein CARUB_v10000196mg [Capsella rubella]	2221	868	0	39.1	35.1	36.8	hypothetical protein CARUB_v10000196mg	gbpln	Capsella rubella	AT5G22030.1 | Symbols: UBP8 | ubiquitin-specific protease 8 | chr5:7290155-7296344 REVERSE LENGTH=913	2221	913	0	41.1	35.2	36.9
Rsa1.0_00729.1.g18685.t1	gb|EOA17519.1| hypothetical protein CARUB_v10005852mg [Capsella rubella]	136	180	8.00E-47	132.4	75.0	83.1	hypothetical protein CARUB_v10005852mg	gbpln	Capsella rubella	AT4G30410.1 | Symbols: | sequence-specific DNA binding transcription factors | chr4:14871309-14871851 REVERSE LENGTH=180	136	180	1.00E-47	132.4	78.7	84.6
Rsa1.0_00729.1.g18686.t1	ref|NP_567846.1| RING-H2 finger protein ATL13 [Arabidopsis thaliana] gi|68565248|sp|Q940Q4.2|ATL13_ARATH RecName: Full=RING-H2 finger protein ATL13 gi|332660360|gb|AEE85760.1| RING-H2 finger protein ATL13 [Arabidopsis thaliana]	465	472	0	101.5	82.6	87.7	RING-H2 finger protein ATL13	gbpln	Arabidopsis thaliana	AT4G30400.1 | Symbols: | RING/U-box superfamily protein | chr4:14867068-14868486 FORWARD LENGTH=472	465	472	0	101.5	82.6	87.7
Rsa1.0_00729.1.g18687.t1	ref|XP_002867352.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297313188|gb|EFH43611.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	163	169	2.00E-43	103.7	68.1	77.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G30370.1 | Symbols: | RING/U-box superfamily protein | chr4:14858743-14859273 REVERSE LENGTH=176	163	176	2.00E-45	108.0	66.3	76.1

Rsa1.0_00729.1.g18688.t1	ref|NP_194765.2| cyclic nucleotide gated channel [Arabidopsis thaliana] gi|38503044|sp|Q8L7Z0.1|CNG17_ARATH RecName: Full=Probable cyclic nucleotide-gated ion channel 17; AltName: Full=Cyclic nucleotide- and calmodulin-regulated ion channel 17 gi|21703138|gb|AAM74509.1| AT4g30360/F17I23_300 [Arabidopsis thaliana] gi|25090415|gb|AAN72295.1| At4g30360/F17I23_300 [Arabidopsis thaliana] gi|110742607|dbj|BAE99216.1| cyclic nucleotide and calmodulin-regulated ion channel-like protein [Arabidopsis thaliana] gi|332660356|gb|AEE85756.1| cyclic nucleotide-gated channel 17 [Arabidopsis thaliana]	725	720	0	99.3	86.9	91.3	cyclic nucleotide gated channel	gbpln	Arabidopsis thaliana	AT4G30360.1 | Symbols: ATCNGC17, CNGC17 | cyclic nucleotide-gated channel 17 | chr4:14855060-14857779 REVERSE LENGTH=720	725	720	0	99.3	86.9	91.3
Rsa1.0_00729.1.g18689.t1	ref|NP_194764.1| heat shock-related protein [Arabidopsis thaliana] gi|7269935|emb|CAB81028.1| putative protein [Arabidopsis thaliana] gi|332660355|gb|AEE85755.1| heat shock-related protein [Arabidopsis thaliana]	901	924	0	102.6	83.1	88.8	heat shock-related protein	gbpln	Arabidopsis thaliana	AT4G30350.1 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr4:14848031-14850973 FORWARD LENGTH=924	901	924	0	102.6	83.1	88.8
Rsa1.0_00729.1.g18690.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	697	1555	1.00E-107	223.1	26.3	33.4	disease resistance protein	gbpln	Brassica rapa	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	697	575	2.00E-59	82.5	22.2	34.6
Rsa1.0_00729.1.g18691.t1	ref|NP_567845.4| diacylglycerol kinase 7 [Arabidopsis thaliana] gi|487523322|sp|F4JQ95.1|DGK7_ARATH RecName: Full=Diacylglycerol kinase 7; Short=AtDGK7; Short=DAG kinase 7; AltName: Full=Diglyceride kinase 7; Short=DGK 7 gi|332660354|gb|AEE85754.1| diacylglycerol kinase 7 [Arabidopsis thaliana]	493	492	0	99.8	90.5	95.3	diacylglycerol kinase 7	gbpln	Arabidopsis thaliana	AT4G30340.1 | Symbols: ATDGK7, DGK7 | diacylglycerol kinase 7 | chr4:14838465-14840941 REVERSE LENGTH=492	493	492	0	99.8	90.5	95.3
Rsa1.0_00729.1.g18692.t1	gb|EOA18929.1| hypothetical protein CARUB_v10007576mg [Capsella rubella]	168	164	5.00E-73	97.6	80.4	85.1	hypothetical protein CARUB_v10007576mg	gbpln	Capsella rubella	AT4G30320.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:14835833-14836318 FORWARD LENGTH=161	168	161	5.00E-69	95.8	73.8	78.6
Rsa1.0_00729.1.g18693.t1	ref|NP_199618.1| xyloglucan endotransglucosylase/hydrolase protein 20 [Arabidopsis thaliana] gi|38605469|sp|Q9FI31.1|XTH20_ARATH RecName: Full=Xyloglucan endotransglucosylase/hydrolase protein 20; Short=At-XTH20; Short=XTH-20; Flags: Precursor gi|10177758|dbj|BAB11071.1| xyloglucan endo-1,4-beta-D-glucanase [Arabidopsis thaliana] gi|45825157|gb|AAS77486.1| At5g48070 [Arabidopsis thaliana] gi|62320256|dbj|BAD94531.1| xyloglucan endo-1,4-beta-D-glucanase [Arabidopsis thaliana] gi|332008233|gb|AED95616.1| xyloglucan endotransglucosylase/hydrolase protein 20 [Arabidopsis thaliana]	282	282	1.00E-138	100.0	82.3	87.6	xyloglucan endotransglucosylase/hydrolase protein 20	gbpln	Arabidopsis thaliana	AT5G48070.1 | Symbols: ATXTH20, XTH20 | xyloglucan endotransglucosylase/hydrolase 20 | chr5:19482158-19483231 FORWARD LENGTH=282	282	282	1.00E-140	100.0	82.3	87.6
Rsa1.0_00729.1.g18694.t1	ref|XP_002867357.1| ATXTH18/XTH18 [Arabidopsis lyrata subsp. lyrata] gi|297313193|gb|EFH43616.1| ATXTH18/XTH18 [Arabidopsis lyrata subsp. lyrata]	282	282	1.00E-144	100.0	89.0	93.3	ATXTH18/XTH18	gbpln	Arabidopsis lyrata	AT4G30280.1 | Symbols: ATXTH18, XTH18 | xyloglucan endotransglucosylase/hydrolase 18 | chr4:14825958-14826998 REVERSE LENGTH=282	282	282	2.33E-156	100.0	88.7	92.6
Rsa1.0_00729.1.g18695.t1	gb|AEX07595.1| xyloglucosyl transferase 2, partial [Brassica juncea]	282	265	1.00E-153	94.0	91.1	92.2	xyloglucosyl transferase 2, partial	gbpln	Brassica juncea	AT4G30270.1 | Symbols: MERI5B, MERI-5, XTH24, SEN4 | xyloglucan endotransglucosylase/hydrolase 24 | chr4:14819445-14820448 REVERSE LENGTH=269	282	269	1.00E-147	95.4	87.6	91.1
Rsa1.0_00729.1.g18696.t3	gb|EOA15588.1| hypothetical protein CARUB_v10005446mg [Capsella rubella]	176	280	1.00E-68	159.1	84.7	88.6	hypothetical protein CARUB_v10005446mg	gbpln	Capsella rubella	AT4G30260.1 | Symbols: | Integral membrane Yip1 family protein | chr4:14816890-14818722 REVERSE LENGTH=280	176	280	2.00E-63	159.1	84.1	88.1
Rsa1.0_00729.1.g18697.t1	gb|EOA17963.1| hypothetical protein CARUB_v10006378mg [Capsella rubella]	526	523	0	99.4	86.7	92.4	hypothetical protein CARUB_v10006378mg	gbpln	Capsella rubella	AT4G30250.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:14811262-14812821 REVERSE LENGTH=519	526	519	0	98.7	86.7	92.2

<table>
<tr><td>Rsa1.0_00730.1.g18698.t2</td><td>gb|EOA19817.1| hypothetical protein CARUB_v10000063mg [Capsella rubella]</td><td>270</td><td>1207</td><td>6.00E−52</td><td>447.0</td><td>39.6</td><td>44.1</td><td>hypothetical protein CARUB_v10000063mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G05040.1 | Symbols: HST, HST1 | ARM repeat superfamily protein | chr3:1401479−1408095 REVERSE LENGTH=1202</td><td>270</td><td>1202</td><td>8.00E−49</td><td>445.2</td><td>37.0</td><td>40.7</td></tr>
<tr><td>Rsa1.0_00730.1.g18699.t1</td><td>ref|NP_175249.1| MADS−box domain−containing protein [Arabidopsis thaliana] gi|8778530|gb|AAF79538.1|AC023673_26 F21D18.12 [Arabidopsis thaliana] gi|332194135|gb|AEE32256.1| MADS−box domain−containing protein [Arabidopsis thaliana]</td><td>274</td><td>323</td><td>6.00E−61</td><td>117.9</td><td>56.2</td><td>71.2</td><td>MADS−box domain−containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G48150.1 | Symbols: | MADS−box transcription factor family protein | chr1:17785397−17786368 FORWARD LENGTH=323</td><td>274</td><td>323</td><td>2.00E−63</td><td>117.9</td><td>56.2</td><td>71.2</td></tr>
<tr><td>Rsa1.0_00730.1.g18700.t1</td><td>ref|NP_198064.1| putative nucleolar protein 5−1 [Arabidopsis thaliana] gi|147744575|sp|O04658.2|NOP5A_ARATH RecName: Full=Probable nucleolar protein 5−1; AltName: Full=MAR−binding NOP56/58 homolog 1; AltName: Full=NOP58−like protein F108; AltName: Full=Nucleolar protein 58−1 gi|11878185|gb|AAG40836.1|AF302490_1 NOP58−like protein F108 [Arabidopsis thaliana] gi|18377656|gb|AAL66978.1| putative SAR DNA−binding protein [Arabidopsis thaliana] gi|20465699|gb|AAM20318.1| putative SAR DNA−binding protein [Arabidopsis thaliana] gi|332006269|gb|AED93652.1| putative nucleolar protein 5−1 [Arabidopsis thaliana]</td><td>511</td><td>533</td><td>0</td><td>104.3</td><td>73.8</td><td>79.6</td><td>putative nucleolar protein 5−1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G27120.1 | Symbols: | NOP56−like pre RNA processing ribonucleoprotein | chr5:9541287−9543684 FORWARD LENGTH=533</td><td>511</td><td>533</td><td>0</td><td>104.3</td><td>73.8</td><td>79.6</td></tr>
<tr><td>Rsa1.0_00730.1.g18701.t27</td><td>ref|NP_198149.2| armadillo/beta−catenin−like repeat−containing protein [Arabidopsis thaliana] gi|332006370|gb|AED93753.1| armadillo/beta−catenin−like repeat−containing protein [Arabidopsis thaliana]</td><td>1599</td><td>1630</td><td>0</td><td>101.9</td><td>90.2</td><td>93.2</td><td>armadillo/beta−catenin−like repeat−containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G27970.1 | Symbols: | ARM repeat superfamily protein | chr5:10004720−10015429 FORWARD LENGTH=1630</td><td>1599</td><td>1630</td><td>0</td><td>101.9</td><td>90.2</td><td>93.2</td></tr>
<tr><td>Rsa1.0_00730.1.g18702.t1</td><td>ref|NP_198150.1| Seed maturation protein [Arabidopsis thaliana] gi|26452310|dbj|BAC43241.1| putative embryonic abundant protein [Arabidopsis thaliana] gi|332006372|gb|AED93755.1| Seed maturation protein [Arabidopsis thaliana]</td><td>186</td><td>192</td><td>1.00E−71</td><td>103.2</td><td>85.5</td><td>88.7</td><td>Seed maturation protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G27980.1 | Symbols: | Seed maturation protein | chr5:10015883−10016676 REVERSE LENGTH=192</td><td>186</td><td>192</td><td>4.00E−74</td><td>103.2</td><td>85.5</td><td>88.7</td></tr>
<tr><td>Rsa1.0_00730.1.g18703.t1</td><td>ref|XP_002872303.1| cysteine synthase [Arabidopsis lyrata subsp. lyrata] gi|297318140|gb|EFH48562.1| cysteine synthase [Arabidopsis lyrata subsp. lyrata]</td><td>346</td><td>324</td><td>1.00E−157</td><td>93.6</td><td>82.9</td><td>89.0</td><td>cysteine synthase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G28020.6 | Symbols: CYSD2, ATCYSD2 | cysteine synthase D2 | chr5:10026395−10028166 REVERSE LENGTH=323</td><td>346</td><td>323</td><td>1.00E−156</td><td>93.4</td><td>84.4</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00730.1.g18704.t1</td><td>ref|XP_002874422.1| hypothetical protein ARALYDRAFT_489646 [Arabidopsis lyrata subsp. lyrata] gi|297320259|gb|EFH50681.1| hypothetical protein ARALYDRAFT_489646 [Arabidopsis lyrata subsp. lyrata]</td><td>590</td><td>567</td><td>0</td><td>96.1</td><td>81.0</td><td>85.3</td><td>hypothetical protein ARALYDRAFT_489646</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G28290.1 | Symbols: ATNEK3, NEK3 | NIMA−related kinase 3 | chr5:10278880−10281880 REVERSE LENGTH=568</td><td>590</td><td>568</td><td>0</td><td>96.3</td><td>80.3</td><td>84.6</td></tr>
<tr><td>Rsa1.0_00730.1.g18705.t1</td><td>gb|EOA20220.1| hypothetical protein CARUB_v10000523mg [Capsella rubella]</td><td>604</td><td>597</td><td>0</td><td>98.8</td><td>73.2</td><td>80.6</td><td>hypothetical protein CARUB_v10000523mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G28300.1 | Symbols: | Duplicated homeodomain−like superfamily protein | chr5:10292789−10295101 REVERSE LENGTH=619</td><td>604</td><td>619</td><td>0</td><td>102.5</td><td>75.8</td><td>83.1</td></tr>
<tr><td>Rsa1.0_00730.1.g18706.t1</td><td>gb|EOA19400.1| hypothetical protein CARUB_v10001016mg [Capsella rubella]</td><td>436</td><td>429</td><td>0</td><td>98.4</td><td>75.7</td><td>84.9</td><td>hypothetical protein CARUB_v10001016mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G29250.1 | Symbols: | HXXXD−type acyl−transferase family protein | chr4:14420713−14422177 FORWARD LENGTH=460</td><td>436</td><td>460</td><td>4.00E−48</td><td>105.5</td><td>31.7</td><td>51.1</td></tr>
<tr><td>Rsa1.0_00730.1.g18707.t1</td><td>ref|XP_002872312.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318149|gb|EFH48571.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>573</td><td>561</td><td>0</td><td>97.9</td><td>81.3</td><td>90.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G28470.1 | Symbols: | Major facilitator superfamily protein | chr5:10429813−10432357 FORWARD LENGTH=559</td><td>573</td><td>559</td><td>0</td><td>97.6</td><td>79.6</td><td>89.0</td></tr>
<tr><td>Rsa1.0_00730.1.g18708.t1</td><td>ref|NP_198201.1| uncharacterized protein [Arabidopsis thaliana] gi|34851102|gb|AAQ82901.1| light−dependent short hypocotyl 1 [Arabidopsis thaliana] gi|38566596|gb|AAR24188.1| At5g28490 [Arabidopsis thaliana] gi|40824076|gb|AAR92340.1| At5g28490 [Arabidopsis thaliana] gi|332006422|gb|AED93805.1| uncharacterized protein AT5G28490 [Arabidopsis thaliana]</td><td>189</td><td>190</td><td>7.00E−76</td><td>100.5</td><td>91.0</td><td>93.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G28490.1 | Symbols: LSH1 | Protein of unknown function (DUF640) | chr5:10454541−10455113 REVERSE LENGTH=190</td><td>189</td><td>190</td><td>3.00E−78</td><td>100.5</td><td>91.0</td><td>93.1</td></tr>
</table>

Rsa1.0_00731.1.g18709.t4	gb|EOA38742.1| hypothetical protein CARUB_v10010894mg [Capsella rubella]	761	423	0	55.6	49.4	51.8	hypothetical protein CARUB_v10010894mg	gbpln	Capsella rubella	AT1G50710.1 | Symbols: | unknown protein; Has 109 Blast hits to 109 proteins in 44 species: Archae - 0; Bacteria - 2; Metazoa - 61; Fungi - 8; Plants - 36; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:18784719-18787615 REVERSE LENGTH=423	761	423	0	55.6	49.1	51.6
Rsa1.0_00731.1.g18710.t1	ref|XP_002894269.1| hypothetical protein ARALYDRAFT_474200 [Arabidopsis lyrata subsp. lyrata] gi|297340111|gb|EFH70528.1| hypothetical protein ARALYDRAFT_474200 [Arabidopsis lyrata subsp. lyrata]	344	337	1.00E-119	98.0	64.5	77.3	hypothetical protein ARALYDRAFT_474200	gbpln	Arabidopsis lyrata	AT1G50680.1 | Symbols: | AP2/B3 transcription factor family protein | chr1:18777601-18778614 REVERSE LENGTH=337	344	337	1.00E-118	98.0	64.2	75.6
Rsa1.0_00731.1.g18711.t1	gb|EOA36251.1| hypothetical protein CARUB_v10010299mg [Capsella rubella]	208	208	1.00E-116	100.0	96.2	98.1	hypothetical protein CARUB_v10010299mg	gbpln	Capsella rubella	AT1G50670.1 | Symbols: | OTU-like cysteine protease family protein | chr1:18775086-18776552 REVERSE LENGTH=208	208	208	1.00E-116	100.0	94.7	97.1
Rsa1.0_00731.1.g18712.t1	ref|NP_175481.1| uncharacterized protein [Arabidopsis thaliana] gi|9454546|gb|AAF87869.1|AC012561_2 Unknown protein [Arabidopsis thaliana] gi|12322324|gb|AAG51180.1|AC079279_1 unknown protein [Arabidopsis thaliana] gi|332194455|gb|AEE32576.1| uncharacterized protein AT1G50660 [Arabidopsis thaliana]	647	725	0	112.1	88.7	93.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G50660.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G20350.1); Has 21445 Blast hits to 15134 proteins in 1325 species: Archae - 461; Bacteria - 2309; Metazoa - 11052; Fungi - 1737; Plants - 1035; Viruses - 42; Other Eukaryotes - 4809 (source: NCBI BLink). | chr1:18771386-18774385 FORWARD LENGTH=725	647	725	0	112.1	88.7	93.8
Rsa1.0_00731.1.g18713.t1	gb|EOA18953.1| hypothetical protein CARUB_v10007587mg [Capsella rubella]	221	527	7.00E-18	238.5	24.4	31.7	hypothetical protein CARUB_v10007587mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	221	530	6.00E-12	239.8	22.6	29.9
Rsa1.0_00731.1.g18714.t1	ref|XP_002894266.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340108|gb|EFH70525.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	173	173	1.00E-62	100.0	69.9	78.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G50650.1 | Symbols: | Stigma-specific Stig1 family protein | chr1:18763773-18764297 REVERSE LENGTH=174	173	174	2.00E-60	100.6	69.9	77.5
Rsa1.0_00731.1.g18715.t1	emb|CAA20201.1| putative transposable element [Arabidopsis thaliana] gi|7268932|emb|CAB79135.1| putative transposable element [Arabidopsis thaliana]	684	1308	8.00E-75	191.2	21.6	31.3	putative transposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	684	1262	3.00E-24	184.5	12.6	21.2
Rsa1.0_00731.1.g18716.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00731.1.g18717.t1	ref|XP_002894264.1| ATERF3/ERF3 [Arabidopsis lyrata subsp. lyrata] gi|297340106|gb|EFH70523.1| ATERF3/ERF3 [Arabidopsis lyrata subsp. lyrata]	211	224	3.00E-67	106.2	79.1	85.8	ATERF3/ERF3	gbpln	Arabidopsis lyrata	AT1G50640.1 | Symbols: ERF3, ATERF3 | ethylene responsive element binding factor 3 | chr1:18757602-18758279 REVERSE LENGTH=225	211	225	2.00E-58	106.6	73.5	81.0
Rsa1.0_00731.1.g18718.t8	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1630	1197	1.00E-155	73.4	19.9	27.4	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1630	575	4.00E-48	35.3	9.5	15.6
Rsa1.0_00731.1.g18719.t4	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00731.1.g18720.t2	gb|AAN72190.1| Unknown protein [Arabidopsis thaliana] gi|110742754|dbj|BAE99285.1| hypothetical protein [Arabidopsis thaliana]	218	667	6.00E-34	306.0	46.3	53.7	Unknown protein	gbpln	Arabidopsis thaliana	AT3G13460.4 | Symbols: ECT2 | evolutionarily conserved C-terminal region 2 | chr3:4385274-4388220 REVERSE LENGTH=666	218	666	2.00E-36	305.5	46.3	53.7
Rsa1.0_00731.1.g18721.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00732.1.g18722.t1	gb|EOA13888.1| hypothetical protein CARUB_v10026998mg [Capsella rubella]	245	248	1.00E-137	101.2	97.1	98.8	hypothetical protein CARUB_v10026998mg	gbpln	Capsella rubella	AT5G50370.1 | Symbols: | Adenylate kinase family protein | chr5:20509382-20510631 REVERSE LENGTH=248	245	248	1.00E-133	101.2	96.3	98.4
Rsa1.0_00732.1.g18723.t3	ref|XP_002866374.1| hypothetical protein ARALYDRAFT_332278 [Arabidopsis lyrata subsp. lyrata] gi|297312209|gb|EFH42633.1| hypothetical protein ARALYDRAFT_332278 [Arabidopsis lyrata subsp. lyrata]	481	477	0	99.2	92.7	96.3	hypothetical protein ARALYDRAFT_332278	gbpln	Arabidopsis lyrata	AT5G60160.1 | Symbols: | Zn-dependent exopeptidases superfamily protein | chr5:24223887-24226783 REVERSE LENGTH=477	481	477	0	99.2	92.1	95.6
Rsa1.0_00732.1.g18724.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00732.1.g18725.t1	gb|EOA13082.1| hypothetical protein CARUB_v10026087mg [Capsella rubella]	581	622	0	107.1	78.7	84.9	hypothetical protein CARUB_v10026087mg	gbpln	Capsella rubella	AT5G50350.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:20498697-20501611 REVERSE LENGTH=584	581	584	0	100.5	78.7	85.0
Rsa1.0_00732.1.g18726.t1	gb|EOA36657.1| hypothetical protein CARUB_v10011946mg, partial [Capsella rubella]	194	188	4.00E-34	96.9	35.1	53.6	hypothetical protein CARUB_v10011946mg, partial	gbpln	Capsella rubella	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365	194	365	6.00E-36	188.1	41.8	56.2
Rsa1.0_00732.1.g18727.t2	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1563	1365	0	87.3	32.9	45.4	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1563	575	4.00E-64	36.8	8.5	12.0
Rsa1.0_00732.1.g18728.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00732.1.g18729.t1	gb|AAF78267.1|AC020576_11 Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene [Arabidopsis thaliana]	1031	1206	0	117.0	42.0	58.1	Contains weak similarity to 25.7 kDa protein from Cicer arietinum gb|AJ276422 and contains a transposase mutator PF|00872 domain. ESTs gb|T13756, gb|AA712647, gb|AA585980 come from this gene	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	1031	719	1.00E-30	69.7	12.9	21.5
Rsa1.0_00732.1.g18730.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00732.1.g18731.t1	gb|EOA39894.1| hypothetical protein CARUB_v10008573mg [Capsella rubella]	986	630	4.00E-63	63.9	16.7	25.5	hypothetical protein CARUB_v10008573mg	gbpln	Capsella rubella	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	986	673	5.00E-51	68.3	12.7	18.3
Rsa1.0_00732.1.g18732.t1	gb|EOA13075.1| hypothetical protein CARUB_v10026080mg, partial [Capsella rubella]	568	627	0	110.4	81.9	88.4	hypothetical protein CARUB_v10026080mg, partial	gbpln	Capsella rubella	AT5G50340.1 | Symbols: | ATP-dependent peptidases;nucleotide binding;serine-type endopeptidases;DNA helicases;ATP binding;damaged DNA binding;nucleoside-triphosphatases | chr5:20491635-20495830 REVERSE LENGTH=587	568	587	0	103.3	82.7	89.3
Rsa1.0_00732.1.g18733.t1	ref|XP_002883034.1| hypothetical protein ARALYDRAFT_341831 [Arabidopsis lyrata subsp. lyrata] gi|297328874|gb|EFH59293.1| hypothetical protein ARALYDRAFT_341831 [Arabidopsis lyrata subsp. lyrata]	100	401	2.00E-33	401.0	65.0	79.0	hypothetical protein ARALYDRAFT_341831	gbpln	Arabidopsis lyrata	AT5G18460.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:6123205-6126505 FORWARD LENGTH=430	100	430	2.00E-28	430.0	52.0	69.0
Rsa1.0_00732.1.g18734.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00732.1.g18735.t1	ref|XP_002865784.1| hypothetical protein ARALYDRAFT_495092 [Arabidopsis lyrata subsp. lyrata] gi|297311619|gb|EFH42043.1| hypothetical protein ARALYDRAFT_495092 [Arabidopsis lyrata subsp. lyrata]	565	565	0	100.0	99.3	99.6	hypothetical protein ARALYDRAFT_495092	gbpln	Arabidopsis lyrata	AT5G50320.1 | Symbols: ELO3, HAG3, HAC8, ELP3, AtELP3 | radical SAM domain-containing protein / GCN5-related N-acetyltransferase (GNAT) family protein | chr5:20481200-20484811 REVERSE LENGTH=565	565	565	0	100.0	98.9	99.5
Rsa1.0_00732.1.g18736.t1	gb|AAF19546.1|AC007190_14 F23N19.13 [Arabidopsis thaliana]	313	633	2.00E-60	202.2	40.3	50.8	F23N19.13	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00732.1.g18737.t1	ref|NP_187216.1| receptor like protein 32 [Arabidopsis thaliana] gi|6714445|gb|AAF26132.1|AC011620_8 putative disease resistance protein [Arabidopsis thaliana] gi|332640751|gb|AEE74272.1| receptor like protein 32 [Arabidopsis thaliana]	105	868	5.00E-32	826.7	67.6	76.2	receptor like protein 32	gbpln	Arabidopsis thaliana	AT3G05650.1 | Symbols: AtRLP32, RLP32 | receptor like protein 32 | chr3:1645884-1648490 REVERSE LENGTH=868	105	868	7.00E-35	826.7	67.6	76.2
Rsa1.0_00733.1.g18738.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00733.1.g18739.t1	dbj|BAD95789.1| LSD-One-Like 1 [Brassica rapa]	155	155	1.00E-70	100.0	96.8	97.4	LSD-One-Like 1	gbpln	Brassica rapa	AT1G32540.3 | Symbols: LOL1 | lsd one like 1 | chr1:11768043-11769591 FORWARD LENGTH=154	155	154	1.00E-67	99.4	80.0	82.6
Rsa1.0_00733.1.g18740.t2	gb|AAF67369.1| Hypothetical protein T15F17.a [Arabidopsis thaliana]	277	703	3.00E-31	253.8	27.8	40.1	Hypothetical protein T15F17.a	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00733.1.g18741.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	270	1142	3.00E-13	423.0	13.7	19.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00733.1.g18742.t1	ref|XP_002893492.1| hypothetical protein ARALYDRAFT_890322 [Arabidopsis lyrata subsp. lyrata] gi|297339334|gb|EFH69751.1| hypothetical protein ARALYDRAFT_890322 [Arabidopsis lyrata subsp. lyrata]	392	322	2.00E-43	82.1	29.3	39.5	hypothetical protein ARALYDRAFT_890322	gbpln	Arabidopsis lyrata	AT1G61470.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr1:22678185-22679021 FORWARD LENGTH=278	392	278	4.00E-37	70.9	23.5	29.6
Rsa1.0_00733.1.g18743.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	358	1142	1.00E-32	319.0	20.4	27.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	358	256	2.00E-18	71.5	20.7	30.7
Rsa1.0_00733.1.g18744.t1	ref|NP_564404.1| protein ABCI7 [Arabidopsis thaliana] gi|75180162|sp|Q9LQK7.1|AB7I_ARATH RecName: Full=Protein ABCI7, chloroplastic; AltName: Full=ABC transporter I family member 7; Short=ABC transporter ABCI.7; Short=AtABCI7; AltName: Full=Non-intrinsic ABC protein 6; AltName: Full=Plastid SufD-like protein; Flags: Precursor gi|8920626|gb|AAF81348.1|AC007767_28 Contains an uncharacterized protein family (UPF0051) domain PF|01458 [Arabidopsis thaliana] gi|115646721|gb|ABJ17094.1| At1g32500 [Arabidopsis thaliana] gi|332193373|gb|AEE31494.1| protein ABCI7 [Arabidopsis thaliana]	626	475	0	75.9	62.3	66.0	protein ABCI7	gbpln	Arabidopsis thaliana	AT1G32500.1 | Symbols: ATNAP6, NAP6 | non-intrinsic ABC protein 6 | chr1:11750091-11751994 REVERSE LENGTH=475	626	475	0	75.9	62.3	66.0
Rsa1.0_00733.1.g18745.t2	gb|EOA36424.1| hypothetical protein CARUB_v10010941mg [Capsella rubella]	1044	1045	0	100.1	92.9	96.7	hypothetical protein CARUB_v10010941mg	gbpln	Capsella rubella	AT1G32490.1 | Symbols: EMB2733, ESP3 | RNA helicase family protein | chr1:11742356-11749286 REVERSE LENGTH=1044	1044	1044	0	100.0	92.1	96.4
Rsa1.0_00733.1.g18746.t1	ref|NP_174525.1| glycine cleavage system H protein [Arabidopsis thaliana] gi|12644523|sp|Q9LQL0.1|GCSH3_ARATH RecName: Full=Glycine cleavage system H protein 3, mitochondrial; Flags: Precursor gi|8920623|gb|AAF81345.1|AC007767_25 Identical to a glycine cleavage system H-protein precursor from Arabidopsis thaliana gb|P25855. It contains a glycine cleavage H-protein domain PF|01597. ESTs gb|R90208, gb|AI994794, gb|AA605324, gb|N38240, gb|AV533336, gb|AV534187, gb|AA597419 and gb|AA597515 come from this gene [Arabidopsis thaliana] gi|12083338|gb|AAG48828.1|AF332465_1 putative glycine cleavage system H protein precursor [Arabidopsis thaliana] gi|14326572|gb|AAK60330.1|AF385740_1 At1g32470/F5D14_10 [Arabidopsis thaliana] gi|18700238|gb|AAL77729.1| At1g32470/F5D14_10 [Arabidopsis thaliana] gi|332193369|gb|AEE31490.1| glycine decarboxylase complex protein H3 [Arabidopsis thaliana]	166	166	2.00E-79	100.0	94.6	97.6	glycine cleavage system H protein	gbpln	Arabidopsis thaliana	AT1G32470.1 | Symbols: | Single hybrid motif superfamily protein | chr1:11739479-11740246 REVERSE LENGTH=166	166	166	7.00E-82	100.0	94.6	97.6

Rsa1.0_00733.1.g18747.t1	ref|NP_564403.1| uncharacterized protein [Arabidopsis thaliana] gi|8920622|gb|AAF81344.1|AC007767_24 EST gb|AV442603 comes from this gene [Arabidopsis thaliana] gi|12247989|gb|AAG50086.1|AF334380_1 unknown protein [Arabidopsis thaliana] gi|19310544|gb|AAL85005.1| unknown protein [Arabidopsis thaliana] gi|21280909|gb|AAM45075.1| unknown protein [Arabidopsis thaliana] gi|21618055|gb|AAM67105.1| unknown [Arabidopsis thaliana] gi|110743194|dbj|BAE99488.1| hypothetical protein [Arabidopsis thaliana] gi|332193368|gb|AEE31489.1| uncharacterized protein AT1G32460 [Arabidopsis thaliana]	87	92	9.00E-22	105.7	71.3	81.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G32460.1 | Symbols: | unknown protein; Has 19 Blast hits to 19 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:11738859-11739137 FORWARD LENGTH=92	87	92	2.00E-24	105.7	71.3	81.6
Rsa1.0_00734.1.g18748.t9	ref|XP_002890178.1| transcriptional factor B3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297336020|gb|EFH66437.1| transcriptional factor B3 family protein [Arabidopsis lyrata subsp. lyrata]	127	133	3.00E-42	104.7	66.9	76.4	transcriptional factor B3 family protein	gbpln	Arabidopsis lyrata	AT1G16640.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr1:5686763-5687533 FORWARD LENGTH=134	127	134	3.00E-44	105.5	64.6	74.8
Rsa1.0_00734.1.g18749.t1	ref|XP_002890180.1| hypothetical protein ARALYDRAFT_471863 [Arabidopsis lyrata subsp. lyrata] gi|297336022|gb|EFH66439.1| hypothetical protein ARALYDRAFT_471863 [Arabidopsis lyrata subsp. lyrata]	391	391	0	100.0	85.7	93.6	hypothetical protein ARALYDRAFT_471863	gbpln	Arabidopsis lyrata	AT1G16670.1 | Symbols: | Protein kinase superfamily protein | chr1:5697846-5699492 FORWARD LENGTH=390	391	390	0	99.7	85.2	92.3
Rsa1.0_00734.1.g18750.t2	gb|EOA40059.1| hypothetical protein CARUB_v10008751mg [Capsella rubella]	803	554	0	69.0	59.4	62.3	hypothetical protein CARUB_v10008751mg	gbpln	Capsella rubella	AT1G16680.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:5702930-5705537 FORWARD LENGTH=554	803	554	0	69.0	57.8	61.1
Rsa1.0_00734.1.g18751.t1	ref|XP_002890184.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336026|gb|EFH66443.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	2056	1685	0	82.0	45.4	49.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G16710.2 | Symbols: HAC12 | histone acetyltransferase of the CBP family 12 | chr1:5714692-5721782 FORWARD LENGTH=1677	2056	1677	0	81.6	45.1	49.4
Rsa1.0_00734.1.g18752.t1	ref|NP_173118.1| Ribosomal protein L20 [Arabidopsis thaliana] gi|21554397|gb|AAM63502.1| ribosomal protein L20, putative [Arabidopsis thaliana] gi|88011169|gb|ABD38912.1| At1g16740 [Arabidopsis thaliana] gi|332191370|gb|AEE29491.1| Ribosomal protein L20 [Arabidopsis thaliana] gi|482574488|gb|EOA38675.1| hypothetical protein CARUB_v10010647mg [Capsella rubella]	163	126	9.00E-60	77.3	75.5	75.5	Ribosomal protein L20	gbpln	Arabidopsis thaliana	AT1G16740.1 | Symbols: | Ribosomal protein L20 | chr1:5727773-5728950 FORWARD LENGTH=126	163	126	3.00E-62	77.3	75.5	75.5
Rsa1.0_00734.1.g18753.t1	ref|XP_002890187.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336029|gb|EFH66446.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	768	757	0	98.6	84.2	89.7	kinase family protein	gbpln	Arabidopsis lyrata	AT1G16760.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:5734234-5737307 FORWARD LENGTH=758	768	758	0	98.7	82.4	89.2
Rsa1.0_00734.1.g18754.t1	gb|EOA36658.1| hypothetical protein CARUB_v10011947mg [Capsella rubella]	149	144	1.00E-56	96.6	79.2	84.6	hypothetical protein CARUB_v10011947mg	gbpln	Capsella rubella	AT1G16790.1 | Symbols: | ribosomal protein-related | chr1:5744638-5745072 FORWARD LENGTH=144	149	144	3.00E-56	96.6	77.9	84.6
Rsa1.0_00734.1.g18755.t1	gb|EOA36775.1| hypothetical protein CARUB_v10012679mg [Capsella rubella]	137	141	3.00E-52	102.9	89.8	93.4	hypothetical protein CARUB_v10012679mg	gbpln	Capsella rubella	AT1G16810.2 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1754, eukaryotic (InterPro:IPR013865); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:5756150-5756694 FORWARD LENGTH=144	137	144	1.00E-53	105.1	89.1	92.0
Rsa1.0_00734.1.g18756.t1	ref|NP_001154345.1| reticulon-like protein [Arabidopsis thaliana] gi|229891661|sp|P0C941.1|RTNLU_ARATH RecName: Full=Reticulon-like protein B23; Short=AtRTNLB23 gi|332191382|gb|AEE29503.1| reticulon-like protein B23 [Arabidopsis thaliana]	182	155	1.00E-17	85.2	35.7	40.1	reticulon-like protein	gbpln	Arabidopsis thaliana	AT1G16825.1 | Symbols: | Reticulon family protein | chr1:5758877-5760340 FORWARD LENGTH=155	182	155	4.00E-20	85.2	35.7	40.1
Rsa1.0_00734.1.g18757.t1	gb|EOA36834.1| hypothetical protein CARUB_v10008619mg [Capsella rubella]	606	607	0	100.2	67.0	79.2	hypothetical protein CARUB_v10008619mg	gbpln	Capsella rubella	AT1G16830.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:5760793-5762619 FORWARD LENGTH=608	606	608	0	100.3	68.0	79.7

<table>
<tr><td>Rsa1.0_00734.1.g18758.t1</td><td>ref|NP_564007.1| uncharacterized protein [Arabidopsis thaliana] gi|30685032|ref|NP_849677.1| uncharacterized protein [Arabidopsis thaliana] gi|42571511|ref|NP_973846.1| uncharacterized protein [Arabidopsis thaliana] gi|9802780|gb|AAF99849.1|AC051629_16 Unknown protein [Arabidopsis thaliana] gi|15450363|gb|AAK96475.1| At1g16840/F17F16.27 [Arabidopsis thaliana] gi|332191384|gb|AEE29505.1| uncharacterized protein AT1G16840 [Arabidopsis thaliana] gi|332191386|gb|AEE29507.1| uncharacterized protein AT1G16840 [Arabidopsis thaliana] gi|332191387|gb|AEE29508.1| uncharacterized protein AT1G16840 [Arabidopsis thaliana]</td><td>316</td><td>161</td><td>1.00E-55</td><td>50.9</td><td>33.9</td><td>36.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G16840.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G78890.1); Has 71 Blast hits to 71 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 71; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5763111-5763984 REVERSE LENGTH=161</td><td>316</td><td>161</td><td>3.00E-58</td><td>50.9</td><td>33.9</td><td>36.4</td></tr>
<tr><td>Rsa1.0_00734.1.g18759.t1</td><td>gb|EOA40305.1| hypothetical protein CARUB_v10009033mg [Capsella rubella]</td><td>469</td><td>474</td><td>0</td><td>101.1</td><td>89.8</td><td>95.1</td><td>hypothetical protein CARUB_v10009033mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G16860.1 | Symbols: | Ubiquitin-specific protease family C19-related protein | chr1:5768280-5770183 FORWARD LENGTH=474</td><td>469</td><td>474</td><td>0</td><td>101.1</td><td>89.1</td><td>94.5</td></tr>
<tr><td>Rsa1.0_00734.1.g18760.t1</td><td>ref|NP_173131.1| mitochondrial 28S ribosomal protein S29-like protein [Arabidopsis thaliana] gi|17064866|gb|AAL32587.1| Unknown protein [Arabidopsis thaliana] gi|20259906|gb|AAM13300.1| unknown protein [Arabidopsis thaliana] gi|332191391|gb|AEE29512.1| mitochondrial 28S ribosomal protein S29-like protein [Arabidopsis thaliana]</td><td>463</td><td>480</td><td>0</td><td>103.7</td><td>86.4</td><td>92.9</td><td>mitochondrial 28S ribosomal protein S29-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G16870.1 | Symbols: | mitochondrial 28S ribosomal protein S29-related | chr1:5770964-5773157 REVERSE LENGTH=480</td><td>463</td><td>480</td><td>0</td><td>103.7</td><td>86.4</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00734.1.g18761.t1</td><td>ref|XP_002890192.1| hypothetical protein ARALYDRAFT_471888 [Arabidopsis lyrata subsp. lyrata] gi|297336034|gb|EFH66451.1| hypothetical protein ARALYDRAFT_471888 [Arabidopsis lyrata subsp. lyrata]</td><td>288</td><td>290</td><td>1.00E-149</td><td>100.7</td><td>92.0</td><td>96.5</td><td>hypothetical protein ARALYDRAFT_471888</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G16880.1 | Symbols: | uridylyltransferase-related | chr1:5773796-5776125 FORWARD LENGTH=290</td><td>288</td><td>290</td><td>1.00E-151</td><td>100.7</td><td>91.0</td><td>96.5</td></tr>
<tr><td>Rsa1.0_00734.1.g18762.t1</td><td>ref|NP_173134.2| alpha-1,2-mannosyltransferase [Arabidopsis thaliana] gi|75173357|sp|Q9FZ49.1|ALG9_ARATH RecName: Full=Dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase; AltName: Full=Alpha-1,2-mannosyltransferase ALG9; AltName: Full=Asparagine-linked glycosylation protein 9; AltName: Full=Dol-P-Man:Man(8)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase gi|9802774|gb|AAF99843.1|AC051629_10 Hypothetical protein [Arabidopsis thaliana] gi|22655224|gb|AAM98202.1| Ser/Thr protein kinase, putative [Arabidopsis thaliana] gi|34098911|gb|AAQ56838.1| At1g16900 [Arabidopsis thaliana] gi|332191397|gb|AEE29518.1| Dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase [Arabidopsis thaliana]</td><td>702</td><td>570</td><td>0</td><td>81.2</td><td>74.1</td><td>77.2</td><td>alpha-1,2-mannosyltransferase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G16900.1 | Symbols: | Alg9-like mannosyltransferase family | chr1:5779262-5782303 REVERSE LENGTH=570</td><td>702</td><td>570</td><td>0</td><td>81.2</td><td>74.1</td><td>77.2</td></tr>
<tr><td>Rsa1.0_00734.1.g18763.t1</td><td>gb|EOA38457.1| hypothetical protein CARUB_v10010133mg, partial [Capsella rubella]</td><td>232</td><td>243</td><td>1.00E-118</td><td>104.7</td><td>91.4</td><td>92.2</td><td>hypothetical protein CARUB_v10010133mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G16920.1 | Symbols: RAB11, ATRABA1B, RABA1b | RAB GTPase homolog A1B | chr1:5787489-5789147 REVERSE LENGTH=216</td><td>232</td><td>216</td><td>1.00E-120</td><td>93.1</td><td>90.9</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00734.1.g18764.t1</td><td>ref|NP_173137.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana] gi|75263252|sp|Q9FZ52.1|FDL3_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g16930 gi|9802769|gb|AAF99838.1|AC051629_5 Hypothetical protein [Arabidopsis thaliana] gi|332191402|gb|AEE29523.1| F-box/RNI-like/FBD-like domains-containing protein [Arabidopsis thaliana]</td><td>178</td><td>449</td><td>4.00E-20</td><td>252.2</td><td>37.1</td><td>43.3</td><td>F-box/RNI-like/FBD-like domains-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G16930.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:5789987-5791534 FORWARD LENGTH=449</td><td>178</td><td>449</td><td>2.00E-22</td><td>252.2</td><td>37.1</td><td>43.3</td></tr>
<tr><td>Rsa1.0_00735.1.g18765.t5</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_00735.1.g18766.t1	ref|XP_002877589.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297323427|gb|EFH53848.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	402	358	1.00E-180	89.1	82.1	84.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G47990.1 | Symbols: SIS3 | SUGAR-INSENSITIVE 3 | chr3:17713367-17716051 REVERSE LENGTH=358	402	358	1.00E-180	89.1	81.1	84.6
Rsa1.0_00735.1.g18767.t1	ref|XP_002875873.1| integral membrane HPP family protein [Arabidopsis lyrata subsp. lyrata] gi|297321711|gb|EFH52132.1| integral membrane HPP family protein [Arabidopsis lyrata subsp. lyrata]	284	252	6.00E-78	88.7	55.6	63.7	integral membrane HPP family protein	gbpln	Arabidopsis lyrata	AT3G47980.1 | Symbols: | Integral membrane HPP family protein | chr3:17710477-17712631 FORWARD LENGTH=252	284	252	9.00E-76	88.7	58.1	63.7
Rsa1.0_00735.1.g18768.t1	gb|EOA16415.1| hypothetical protein CARUB_v10004569mg [Capsella rubella]	128	530	1.00E-11	414.1	28.1	37.5	hypothetical protein CARUB_v10004569mg	gbpln	Capsella rubella	AT5G41480.1 | Symbols: EMB9, GLA1, ATDFA, DFA | Folylpolyglutamate synthetase family protein | chr5:16595967-16598523 FORWARD LENGTH=530	128	530	6.00E-14	414.1	28.9	37.5
Rsa1.0_00735.1.g18769.t5	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	327	940	5.00E-11	287.5	10.1	17.7	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00735.1.g18770.t1	dbj|BAJ34570.1| unnamed protein product [Thellungiella halophila]	153	623	2.00E-59	407.2	74.5	83.7	unnamed protein product	----	----	AT3G47960.1 | Symbols: | Major facilitator superfamily protein | chr3:17698126-17700771 REVERSE LENGTH=636	153	636	5.00E-60	415.7	73.9	83.0
Rsa1.0_00735.1.g18771.t1	gb|EOA24281.1| hypothetical protein CARUB_v10017521mg [Capsella rubella]	341	356	1.00E-151	104.4	85.6	92.4	hypothetical protein CARUB_v10017521mg	gbpln	Capsella rubella	AT3G47940.1 | Symbols: | DNAJ heat shock family protein | chr3:17688232-17689402 REVERSE LENGTH=350	341	350	1.00E-153	102.6	81.8	89.7
Rsa1.0_00735.1.g18772.t1	ref|NP_190372.3| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana] gi|332644822|gb|AEE78343.1| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana]	1449	1568	0	108.2	49.6	54.8	Ubiquitin carboxyl-terminal hydrolase-related protein	gbpln	Arabidopsis thaliana	AT3G47890.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr3:17667172-17673530 REVERSE LENGTH=1568	1449	1568	0	108.2	49.6	54.8
Rsa1.0_00735.1.g18773.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	1079	695	1.00E-165	64.4	33.8	41.4	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	1079	681	1.00E-12	63.1	3.3	5.1
Rsa1.0_00735.1.g18774.t1	gb|EOA25068.1| hypothetical protein CARUB_v10018376mg [Capsella rubella]	328	364	1.00E-125	111.0	74.1	84.8	hypothetical protein CARUB_v10018376mg	gbpln	Capsella rubella	AT3G47870.1 | Symbols: SCP, LBD27 | LOB domain-containing protein 27 | chr3:17660021-17661007 REVERSE LENGTH=328	328	328	1.00E-100	100.0	64.3	72.0
Rsa1.0_00736.1.g18775.t3	dbj|BAJ34286.1| unnamed protein product [Thellungiella halophila]	161	358	7.00E-19	222.4	37.9	44.1	unnamed protein product	----	----	AT5G60360.1 | Symbols: SAG2, AALP, ALP | aleurain-like protease | chr5:24280044-24282152 FORWARD LENGTH=358	161	358	4.00E-18	222.4	30.4	36.6
Rsa1.0_00736.1.g18776.t1	gb|EOA31566.1| hypothetical protein CARUB_v10014758mg [Capsella rubella]	177	177	3.00E-76	100.0	78.0	92.7	hypothetical protein CARUB_v10014758mg	gbpln	Capsella rubella	AT5G60340.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:24275098-24275891 REVERSE LENGTH=178	177	178	2.00E-75	100.6	72.9	87.6
Rsa1.0_00736.1.g18777.t1	gb|EOA15011.1| hypothetical protein CARUB_v10028361mg [Capsella rubella]	165	166	7.00E-77	100.6	85.5	90.3	hypothetical protein CARUB_v10028361mg	gbpln	Capsella rubella	AT5G60335.1 | Symbols: | Thioesterase superfamily protein | chr5:24273879-24274551 REVERSE LENGTH=166	165	166	9.00E-77	100.6	84.2	89.1
Rsa1.0_00736.1.g18778.t1	ref|NP_179007.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|20197610|gb|AAM15153.1| hypothetical protein [Arabidopsis thaliana] gi|29725844|gb|AAO89210.1| hypothetical protein [Arabidopsis thaliana] gi|60547703|gb|AAX23815.1| hypothetical protein At2g13900 [Arabidopsis thaliana] gi|330251172|gb|AEC06266.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	702	661	0	94.2	52.4	66.2	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G13900.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:5833102-5835087 FORWARD LENGTH=661	702	661	0	94.2	52.4	66.2
Rsa1.0_00736.1.g18779.t2	gb|ABF18679.1| cysteine protease [Medicago sativa]	338	350	4.00E-54	103.6	34.0	45.9	cysteine protease	gbpln	Medicago sativa	AT5G60360.2 | Symbols: AALP, ALP | aleurain-like protease | chr5:24280044-24282152 FORWARD LENGTH=357	338	357	3.00E-56	105.6	34.0	44.1

Rsa1.0_00736.1.g18780.t1	dbj|BAJ34286.1| unnamed protein product [Thellungiella halophila]	343	358	3.00E−36	104.4	23.0	25.4	unnamed protein product	----	----	AT3G45310.2 | Symbols: | Cysteine proteinases superfamily protein | chr3:16628704−16630473 REVERSE LENGTH=357	343	357	5.00E−31	104.1	19.0	24.8
Rsa1.0_00736.1.g18781.t1	ref|NP_200840.1| concanavalin A−like lectin kinase−like protein [Arabidopsis thaliana] gi|75333953|sp|Q9FJI4.1|LK111_ARATH RecName: Full=Putative L−type lectin−domain containing receptor kinase I.11; Short=LecRK−I.11; Flags: Precursor gi|10177723|dbj|BAB10969.1| receptor−like protein kinase [Arabidopsis thaliana] gi|332009925|gb|AED97308.1| concanavalin A−like lectin kinase−like protein [Arabidopsis thaliana]	702	675	0	96.2	77.9	84.2	concanavalin A−like lectin kinase−like protein	gbpln	Arabidopsis thaliana	AT5G60320.1 | Symbols: | Concanavalin A−like lectin protein kinase family protein | chr5:24270808−24272835 FORWARD LENGTH=675	702	675	0	96.2	77.9	84.2
Rsa1.0_00736.1.g18782.t2	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	1907	1274	0	66.8	31.3	43.0	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1907	575	2.00E−63	30.2	8.8	14.1
Rsa1.0_00736.1.g18783.t1	ref|NP_001078773.1| concanavalin A−like lectin kinase−like protein [Arabidopsis thaliana] gi|317411743|sp|Q9LSR8.2|LRK19_ARATH RecName: Full=L−type lectin−domain containing receptor kinase I.9; Short=LecRK−I.9; Short=LecRK79; Flags: Precursor gi|332009923|gb|AED97306.1| concanavalin A−like lectin kinase−like protein [Arabidopsis thaliana]	721	766	0	106.2	77.9	86.1	concanavalin A−like lectin kinase−like protein	gbpln	Arabidopsis thaliana	AT5G60300.3 | Symbols: | Concanavalin A−like lectin protein kinase family protein | chr5:24264862−24267973 FORWARD LENGTH=766	721	766	0	106.2	77.9	86.1
Rsa1.0_00736.1.g18784.t1	ref|NP_200835.1| concanavalin A−like lectin kinase−like protein [Arabidopsis thaliana] gi|75335418|sp|Q9LSS0.1|LRK17_ARATH RecName: Full=L−type lectin−domain containing receptor kinase I.7; Short=LecRK−I.7; Flags: Precursor gi|8885577|dbj|BAA97507.1| receptor−like protein kinase [Arabidopsis thaliana] gi|51969170|dbj|BAD43277.1| receptor like protein kinase [Arabidopsis thaliana] gi|332009918|gb|AED97301.1| concanavalin A−like lectin kinase−like protein [Arabidopsis thaliana]	639	668	0	104.5	78.2	88.3	concanavalin A−like lectin kinase−like protein	gbpln	Arabidopsis thaliana	AT5G60270.1 | Symbols: | Concanavalin A−like lectin protein kinase family protein | chr5:24257761−24259767 FORWARD LENGTH=668	639	668	0	104.5	78.2	88.3
Rsa1.0_00736.1.g18785.t1	ref|XP_002864676.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310511|gb|EFH40935.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	669	668	0	99.9	77.9	87.6	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT5G60270.1 | Symbols: | Concanavalin A−like lectin protein kinase family protein | chr5:24257761−24259767 FORWARD LENGTH=668	669	668	0	99.9	77.7	87.6
Rsa1.0_00736.1.g18786.t1	ref|NP_200833.1| C3H4 type zinc finger protein [Arabidopsis thaliana] gi|8885575|dbj|BAA97505.1| unnamed protein product [Arabidopsis thaliana] gi|332009916|gb|AED97299.1| C3H4 type zinc finger protein [Arabidopsis thaliana]	638	655	0	102.7	61.0	71.3	C3H4 type zinc finger protein	gbpln	Arabidopsis thaliana	AT5G60250.1 | Symbols: | zinc finger (C3HC4−type RING finger) family protein | chr5:24252226−24254710 FORWARD LENGTH=655	638	655	0	102.7	61.0	71.3
Rsa1.0_00736.1.g18787.t1	gb|EOA14477.1| hypothetical protein CARUB_v10027691mg [Capsella rubella]	251	255	1.00E−120	101.6	84.1	91.2	hypothetical protein CARUB_v10027691mg	gbpln	Capsella rubella	AT5G60230.2 | Symbols: SEN2, ATSEN2 | splicing endonuclease 2 | chr5:24250185−24250952 REVERSE LENGTH=255	251	255	1.00E−121	101.6	84.1	91.6
Rsa1.0_00736.1.g18788.t1	ref|XP_002864674.1| hypothetical protein ARALYDRAFT_358240 [Arabidopsis lyrata subsp. lyrata] gi|297310509|gb|EFH40933.1| hypothetical protein ARALYDRAFT_358240 [Arabidopsis lyrata subsp. lyrata]	285	285	1.00E−149	100.0	88.8	95.8	hypothetical protein ARALYDRAFT_358240	gbpln	Arabidopsis lyrata	AT3G45600.1 | Symbols: TET3 | tetraspanin3 | chr3:16733973−16735854 REVERSE LENGTH=285	285	285	1.00E−141	100.0	83.2	90.9

Rsa1.0_00736.1.g18789.t1	ref|NP_200829.5| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|334188518|ref|NP_001190579.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|75180396|sp|Q9LSS5.1|ICR3_ARATH RecName: Full=Interactor of constitutive active ROPs 3 gi|8885572|dbj|BAA97502.1| myosin heavy chain-like [Arabidopsis thaliana] gi|332009910|gb|AED97293.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|332009911|gb|AED97294.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana]	519	564	0	108.7	85.7	93.1	interactor of constitutive active ROPs 3	gbpln	Arabidopsis thaliana	AT5G60210.2 | Symbols: RIP5 | ROP interactive partner 5 | chr5:24243529-24245889 REVERSE LENGTH=564	519	564	0	108.7	85.7	93.1
Rsa1.0_00736.1.g18790.t1	gb|EOA13642.1| hypothetical protein CARUB_v10026713mg [Capsella rubella]	227	344	2.00E-99	151.5	84.6	93.0	hypothetical protein CARUB_v10026713mg	gbpln	Capsella rubella	AT5G60200.1 | Symbols: TMO6 | TARGET OF MONOPTEROS 6 | chr5:24241078-24241951 FORWARD LENGTH=257	227	257	1.00E-101	113.2	81.9	90.7
Rsa1.0_00736.1.g18791.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00736.1.g18792.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00737.1.g18793.t1	ref|XP_002876829.1| hypothetical protein ARALYDRAFT_484186 [Arabidopsis lyrata subsp. lyrata] gi|297322667|gb|EFH53088.1| hypothetical protein ARALYDRAFT_484186 [Arabidopsis lyrata subsp. lyrata]	451	426	0	94.5	88.2	91.1	hypothetical protein ARALYDRAFT_484186	gbpln	Arabidopsis lyrata	AT2G02800.2 | Symbols: APK2B | protein kinase 2B | chr2:796889-799250 REVERSE LENGTH=426	451	426	0	94.5	87.8	91.1
Rsa1.0_00737.1.g18794.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00737.1.g18795.t1	ref|NP_178381.3| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|264664503|sp|C0LGJ9.1|Y2278_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g02780; Flags: Precursor gi|224589501|gb|ACN59284.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|330250529|gb|AEC05623.1| probable LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	725	742	0	102.3	83.4	90.9	leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT2G02780.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:781932-784646 REVERSE LENGTH=742	725	742	0	102.3	83.4	90.9
Rsa1.0_00737.1.g18796.t1	ref|NP_565289.1| ubiquitin-conjugating enzyme E2 A [Arabidopsis thaliana] gi|297814522|ref|XP_002875144.1| ubiquiting-conjugating enzyme 2 [Arabidopsis lyrata subsp. lyrata] gi|1174844|sp|P42745.1|UBC2_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 2; AltName: Full=Ubiquitin carrier protein 2; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 2; AltName: Full=Ubiquitin-protein ligase 2 gi|13899127|gb|AAK48985.1|AF370558_1 putative ubiquitin-conjugating enzyme E2 [Arabidopsis thaliana] gi|431264|gb|AAA32899.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|2689243|emb|CAA73476.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|2947065|gb|AAC05346.1| E2, ubiquitin-conjugating enzyme 2 (UBC2) [Arabidopsis thaliana] gi|18377456|gb|AAL66894.1| putative ubiquitin-conjugating enzyme E2 [Arabidopsis thaliana] gi|66354400|gb|AAY44843.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|118197458|gb|ABK78692.1| ubiquitin conjugating enzyme [Brassica rapa] gi|297320982|gb|EFH51403.1| ubiquiting-conjugating enzyme 2 [Arabidopsis lyrata subsp. lyrata] gi|312281529|dbj|BAJ33630.1| unnamed	152	152	1.00E-84	100.0	100.0	100.0	ubiquitin-conjugating enzyme E2 A	gbpln	Arabidopsis lyrata	AT2G02760.1 | Symbols: ATUBC2, UBC2 | ubiquiting-conjugating enzyme 2 | chr2:774271-775149 FORWARD LENGTH=152	152	152	3.00E-87	100.0	100.0	100.0

<table>
<tr><td>Rsa1.0_00737.1.g18797.t1</td><td>ref|NP_178377.2| ssDNA-binding transcriptional regulator [Arabidopsis thaliana] gi|75115367|sp|Q66GR6.1|WHY3_ARATH RecName: Full=Single-stranded DNA-binding protein WHY3, chloroplastic; AltName: Full=Protein PLASTID TRANSCRIPTIONALLY ACTIVE 11; AltName: Full=Protein WHIRLY 3; Short=AtWHY3; Flags: Precursor gi|51536442|gb|AAU05459.1| At2g02740 [Arabidopsis thaliana] gi|51972072|gb|AAU15140.1| At2g02740 [Arabidopsis thaliana] gi|330250524|gb|AEC05618.1| ssDNA-binding transcriptional regulator [Arabidopsis thaliana]</td><td>172</td><td>268</td><td>1.00E-62</td><td>155.8</td><td>77.3</td><td>84.3</td><td>ssDNA-binding transcriptional regulator</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G02740.1 | Symbols: ATWHY3, PTAC11, WHY3 | ssDNA-binding transcriptional regulator | chr2:769389-770993 FORWARD LENGTH=268</td><td>172</td><td>268</td><td>5.00E-65</td><td>155.8</td><td>77.3</td><td>84.3</td></tr>
<tr><td>Rsa1.0_00737.1.g18798.t2</td><td>ref|NP_178376.1| uncharacterized protein [Arabidopsis thaliana] gi|42570657|ref|NP_973402.1| uncharacterized protein [Arabidopsis thaliana] gi|20196955|gb|AAC05349.2| expressed protein [Arabidopsis thaliana] gi|21618010|gb|AAM67060.1| unknown [Arabidopsis thaliana] gi|26453164|dbj|BAC43658.1| unknown protein [Arabidopsis thaliana] gi|28950835|gb|AAO63341.1| At2g02730 [Arabidopsis thaliana] gi|330250522|gb|AEC05616.1| uncharacterized protein AT2G02730 [Arabidopsis thaliana] gi|330250523|gb|AEC05617.1| uncharacterized protein AT2G02730 [Arabidopsis thaliana]</td><td>288</td><td>276</td><td>1.00E-124</td><td>95.8</td><td>77.1</td><td>87.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G02730.2 | Symbols: | Protein of unknown function (DUF1664) | chr2:765280-767336 REVERSE LENGTH=276</td><td>288</td><td>276</td><td>1.00E-127</td><td>95.8</td><td>77.1</td><td>87.2</td></tr>
<tr><td>Rsa1.0_00737.1.g18799.t1</td><td>ref|XP_002875142.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320980|gb|EFH51401.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>459</td><td>455</td><td>0</td><td>99.1</td><td>83.7</td><td>90.0</td><td>pectate lyase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G02720.1 | Symbols: | Pectate lyase family protein | chr2:763173-764834 FORWARD LENGTH=455</td><td>459</td><td>455</td><td>0</td><td>99.1</td><td>82.8</td><td>89.3</td></tr>
<tr><td>Rsa1.0_00737.1.g18800.t1</td><td>ref|XP_002876825.1| pac motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322663|gb|EFH53084.1| pac motif-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>400</td><td>386</td><td>1.00E-177</td><td>96.5</td><td>80.5</td><td>86.5</td><td>pac motif-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G02710.1 | Symbols: PLP, PLPB | PAS/LOV protein B | chr2:758812-760608 REVERSE LENGTH=399</td><td>400</td><td>399</td><td>1.00E-177</td><td>99.8</td><td>81.0</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00737.1.g18801.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00737.1.g18802.t2</td><td>ref|NP_178361.2| survival of motor neuron-related-splicing factor 30 [Arabidopsis thaliana] gi|30678012|ref|NP_849927.1| survival of motor neuron-related-splicing factor 30 [Arabidopsis thaliana] gi|145328250|ref|NP_001077871.1| survival of motor neuron-related-splicing factor 30 [Arabidopsis thaliana] gi|27754612|gb|AAO22752.1| unknown protein [Arabidopsis thaliana] gi|28393903|gb|AAO42359.1| unknown protein [Arabidopsis thaliana] gi|330250503|gb|AEC05597.1| survival of motor neuron-related-splicing factor 30 [Arabidopsis thaliana] gi|330250504|gb|AEC05598.1| survival of motor neuron-related-splicing factor 30 [Arabidopsis thaliana] gi|330250506|gb|AEC05600.1| survival of motor neuron-related-splicing factor 30 [Arabidopsis thaliana]</td><td>341</td><td>300</td><td>1.00E-136</td><td>88.0</td><td>73.9</td><td>81.2</td><td>survival of motor neuron-related-splicing factor 30</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G02570.4 | Symbols: | nucleic acid binding;RNA binding | chr2:698361-700794 REVERSE LENGTH=300</td><td>341</td><td>300</td><td>1.00E-139</td><td>88.0</td><td>73.9</td><td>81.2</td></tr>
<tr><td>Rsa1.0_00737.1.g18803.t1</td><td>gb|EOA23151.1| hypothetical protein CARUB_v10016592mg [Capsella rubella]</td><td>1239</td><td>1217</td><td>0</td><td>98.2</td><td>94.1</td><td>96.3</td><td>hypothetical protein CARUB_v10016592mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G02560.2 | Symbols: CAND1, ATCAND1, ETA2, TIP120, HVE | cullin-associated and neddylation dissociated | chr2:690345-697342 FORWARD LENGTH=1217</td><td>1239</td><td>1217</td><td>0</td><td>98.2</td><td>93.5</td><td>96.1</td></tr>
<tr><td>Rsa1.0_00737.1.g18804.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00737.1.g18805.t1</td><td>gb|EOA24407.1| hypothetical protein CARUB_v10017657mg [Capsella rubella]</td><td>311</td><td>320</td><td>1.00E-112</td><td>102.9</td><td>74.6</td><td>84.2</td><td>hypothetical protein CARUB_v10017657mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G02540.1 | Symbols: ATHB21, ZFHD4, HB21, ZHD3 | homeobox protein 21 | chr2:684302-685234 FORWARD LENGTH=310</td><td>311</td><td>310</td><td>1.00E-112</td><td>99.7</td><td>75.6</td><td>83.3</td></tr>
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Rsa1.0_00737.1.g18806.t1	ref|NP_565285.1| AAA-type ATPase-like protein [Arabidopsis thaliana] gi|8980710|gb|AAF82285.1|AF264023_1 STICHEL [Arabidopsis thaliana] gi|20197093|gb|AAC18938.2| similar to prokaryotic DNA polymerase III gamma subunit [Arabidopsis thaliana] gi|330250491|gb|AEC05585.1| AAA-type ATPase-like protein [Arabidopsis thaliana]	1237	1218	0	98.5	86.6	91.6	AAA-type ATPase-like protein	gbpln	Arabidopsis thaliana	AT2G02480.1 | Symbols: STI | AAA-type ATPase family protein | chr2:661093-665337 FORWARD LENGTH=1218	1237	1218	0	98.5	86.6	91.6
Rsa1.0_00737.1.g18807.t1	ref|NP_178351.1| protein alfin-like 6 [Arabidopsis thaliana] gi|75248014|sp|Q8S8M9.1|ALFL6_ARATH RecName: Full=PHD finger protein ALFIN-LIKE 6; Short=Protein AL6 gi|20197338|gb|AAM15031.1| putative PHD-type zinc finger protein [Arabidopsis thaliana] gi|28393037|gb|AAO41953.1| putative PHD-type zinc finger protein [Arabidopsis thaliana] gi|28827386|gb|AAO50537.1| putative PHD-type zinc finger protein [Arabidopsis thaliana] gi|330250489|gb|AEC05583.1| protein alfin-like 6 [Arabidopsis thaliana]	245	256	1.00E-107	104.5	87.3	93.1	protein alfin-like 6	gbpln	Arabidopsis thaliana	AT2G02470.1 | Symbols: AL6 | alfin-like 6 | chr2:652837-654621 FORWARD LENGTH=256	245	256	1.00E-109	104.5	87.3	93.1
Rsa1.0_00737.1.g18808.t1	dbj|BAB01217.1| Ta11 non-LTR retroelement protein-like [Arabidopsis thaliana] gi|67633664|gb|AAY78756.1| putative zinc finger protein [Arabidopsis thaliana]	449	487	2.00E-96	108.5	44.1	62.8	Ta11 non-LTR retroelement protein-like	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	449	361	4.00E-27	80.4	14.5	24.3
Rsa1.0_00738.1.g18809.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00738.1.g18810.t2	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	741	1352	1.00E-127	182.5	35.6	47.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	741	746	2.00E-56	100.7	16.7	23.3
Rsa1.0_00738.1.g18811.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	560	1023	1.00E-164	182.7	53.4	68.4	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	560	575	1.00E-37	102.7	17.0	27.3
Rsa1.0_00738.1.g18812.t1	gb|EOA31014.1| hypothetical protein CARUB_v10014159mg [Capsella rubella]	369	330	4.00E-58	89.4	47.2	55.6	hypothetical protein CARUB_v10014159mg	gbpln	Capsella rubella	AT2G17787.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G35940.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:7731374-7732853 FORWARD LENGTH=324	369	324	1.00E-59	87.8	46.1	57.5
Rsa1.0_00738.1.g18813.t2	gb|EOA32604.1| hypothetical protein CARUB_v10015897mg [Capsella rubella]	804	788	0	98.0	89.7	93.7	hypothetical protein CARUB_v10015897mg	gbpln	Capsella rubella	AT2G17790.1 | Symbols: VPS35A, ZIP3 | VPS35 homolog A | chr2:7733685-7739344 FORWARD LENGTH=787	804	787	0	97.9	89.8	93.7
Rsa1.0_00738.1.g18814.t3	ref|XP_004233565.1| PREDICTED: rac-like GTP-binding protein ARAC1-like [Solanum lycopersicum]	616	197	4.00E-86	32.0	27.4	27.9	PREDICTED: rac-like GTP-binding protein ARAC1-like	gbpln	Solanum lycopersicum	AT2G17800.2 | Symbols: ARAC1, ATGP2, ATRAC1, ROP3, ATROP3 | Arabidopsis RAC-like 1 | chr2:7740313-7741942 FORWARD LENGTH=197	616	197	1.00E-84	32.0	27.8	27.9
Rsa1.0_00738.1.g18815.t1	ref|NP_192092.1| ABC transporter B family member 5 [Arabidopsis thaliana] gi|75337855|sp|Q9SYI3.1|AB5B_ARATH RecName: Full=ABC transporter B family member 5; Short=ABC transporter ABCB.5; Short=AtABCB5; AltName: Full=P-glycoprotein 5; AltName: Full=Putative multidrug resistance protein 5 gi|4558552|gb|AAD22645.1|AC007138_9 putative P-glycoprotein-like protein [Arabidopsis thaliana] gi|7268567|emb|CAB80676.1| putative P-glycoprotein-like protein [Arabidopsis thaliana] gi|332656682|gb|AEE82082.1| ABC transporter B family member 5 [Arabidopsis thaliana]	1257	1230	0	97.9	82.0	90.2	ABC transporter B family member 5	gbpln	Arabidopsis thaliana	AT4G01830.1 | Symbols: PGP5 | P-glycoprotein 5 | chr4:785683-790447 REVERSE LENGTH=1230	1257	1230	0	97.9	82.0	90.2
Rsa1.0_00738.1.g18816.t1	gb|EOA29746.1| hypothetical protein CARUB_v10012835mg [Capsella rubella]	1196	1201	0	100.4	89.4	93.9	hypothetical protein CARUB_v10012835mg	gbpln	Capsella rubella	AT2G17820.1 | Symbols: ATHK1, AHK1, HK1 | histidine kinase 1 | chr2:7743133-7748013 REVERSE LENGTH=1207	1196	1207	0	100.9	88.5	93.6
Rsa1.0_00738.1.g18817.t1	gb|EOA34012.1| hypothetical protein CARUB_v10021508mg, partial [Capsella rubella]	156	105	1.00E-11	67.3	28.8	38.5	hypothetical protein CARUB_v10021508mg, partial	gbpln	Capsella rubella	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	156	170	1.00E-11	109.0	24.4	34.0
Rsa1.0_00739.1.g18818.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00739.1.g18819.t1	gb|EOA20649.1| hypothetical protein CARUB_v10000962mg [Capsella rubella]	359	444	4.00E-80	123.7	44.6	47.6	hypothetical protein CARUB_v10000962mg	gbpln	Capsella rubella	AT5G19380.2 | Symbols: CLT1 | CRT (chloroquine-resistance transporter)-like transporter 1 | chr5:6527017-6530445 REVERSE LENGTH=507	359	507	1.00E-81	141.2	43.7	47.4
Rsa1.0_00739.1.g18820.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00739.1.g18821.t1	ref|XP_002871882.1| hypothetical protein ARALYDRAFT_488825 [Arabidopsis lyrata subsp. lyrata] gi|297317719|gb|EFH48141.1| hypothetical protein ARALYDRAFT_488825 [Arabidopsis lyrata subsp. lyrata]	851	870	0	102.2	87.1	91.9	hypothetical protein ARALYDRAFT_488825	gbpln	Arabidopsis lyrata	AT5G19390.2 | Symbols: | Rho GTPase activation protein (RhoGAP) with PH domain | chr5:6531906-6538206 FORWARD LENGTH=870	851	870	0	102.2	86.5	91.7
Rsa1.0_00739.1.g18822.t1	gb|EOA19874.1| hypothetical protein CARUB_v10000123mg [Capsella rubella]	1077	1026	0	95.3	72.3	80.2	hypothetical protein CARUB_v10000123mg	gbpln	Capsella rubella	AT5G19400.2 | Symbols: SMG7 | Telomerase activating protein Est1 | chr5:6540603-6544262 FORWARD LENGTH=1059	1077	1059	0	98.3	70.2	79.5
Rsa1.0_00739.1.g18823.t1	gb|EOA37750.1| hypothetical protein CARUB_v10012565mg [Capsella rubella]	252	679	5.00E-43	269.4	46.8	67.1	hypothetical protein CARUB_v10012565mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00739.1.g18824.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	310	1142	3.00E-97	368.4	58.4	72.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	310	575	9.00E-27	185.5	25.8	36.5
Rsa1.0_00739.1.g18825.t2	ref|NP_197446.1| calcium-dependent protein kinase 19 [Arabidopsis thaliana] gi|30687323|ref|NP_850853.1| calcium-dependent protein kinase 19 [Arabidopsis thaliana] gi|75319668|sp|Q42438.1|CDPK8_ARATH RecName: Full=Calcium-dependent protein kinase 8; AltName: Full=Calcium-dependent protein kinase isoform CDPK19; Short=AtCDPK19 gi|836942|gb|AAA67655.1| calcium-dependent protein kinase [Arabidopsis thaliana] gi|836948|gb|AAA67658.1| calcium-dependent protein kinase [Arabidopsis thaliana] gi|332005325|gb|AED92708.1| calcium-dependent protein kinase 19 [Arabidopsis thaliana] gi|332005326|gb|AED92709.1| calcium-dependent protein kinase 19 [Arabidopsis thaliana]	536	533	0	99.4	94.8	97.4	calcium-dependent protein kinase 19	gbpln	Arabidopsis thaliana	AT5G19450.2 | Symbols: CDPK19, CPK8 | calcium-dependent protein kinase 19 | chr5:6558672-6561471 REVERSE LENGTH=533	536	533	0	99.4	94.8	97.4
Rsa1.0_00739.1.g18826.t1	gb|EOA20537.1| hypothetical protein CARUB_v10000850mg, partial [Capsella rubella]	452	481	0	106.4	92.0	95.8	hypothetical protein CARUB_v10000850mg, partial	gbpln	Capsella rubella	AT5G19485.1 | Symbols: | transferases;nucleotidyltransferases | chr5:6573907-6576352 REVERSE LENGTH=456	452	456	0	100.9	91.4	95.6
Rsa1.0_00739.1.g18827.t1	ref|NP_197450.2| histone 2A domain-containing protein [Arabidopsis thaliana] gi|332005334|gb|AED92717.1| histone 2A domain-containing protein [Arabidopsis thaliana]	256	264	5.00E-86	103.1	73.8	83.2	histone 2A domain-containing protein	gbpln	Arabidopsis thaliana	AT5G19490.1 | Symbols: | Histone superfamily protein | chr5:6576769-6578273 REVERSE LENGTH=264	256	264	1.00E-88	103.1	73.8	83.2
Rsa1.0_00739.1.g18828.t1	ref|XP_002871890.1| tryptophan/tyrosine permease family protein [Arabidopsis lyrata subsp. lyrata] gi|297317727|gb|EFH48149.1| tryptophan/tyrosine permease family protein [Arabidopsis lyrata subsp. lyrata]	496	504	0	101.6	85.5	91.7	tryptophan/tyrosine permease family protein	gbpln	Arabidopsis lyrata	AT5G19500.1 | Symbols: | Tryptophan/tyrosine permease | chr5:6579019-6581699 FORWARD LENGTH=505	496	505	0	101.8	85.7	92.1
Rsa1.0_00739.1.g18829.t1	gb|EOA19454.1| hypothetical protein CARUB_v10001845mg, partial [Capsella rubella]	225	240	1.00E-96	106.7	81.3	89.3	hypothetical protein CARUB_v10001845mg, partial	gbpln	Capsella rubella	AT5G12110.1 | Symbols: | Glutathione S-transferase, C-terminal-like;Translation elongation factor EF1B/ribosomal protein S6 | chr5:3914483-3915732 FORWARD LENGTH=228	225	228	1.00E-94	101.3	84.0	91.1
Rsa1.0_00739.1.g18830.t2	ref|NP_197453.1| mechanosensitive channel of small conductance-like 9 [Arabidopsis thaliana] gi|75147155|sp|Q84M97.1|MSL9_ARATH RecName: Full=Mechanosensitive ion channel protein 9; AltName: Full=Mechanosensitive channel of small conductance-like 9; AltName: Full=MscS-Like protein 9; Short=AtMSL9 gi|30102694|gb|AAP21265.1| At5g19520 [Arabidopsis thaliana] gi|110736360|dbj|BAF00149.1| hypothetical protein [Arabidopsis thaliana] gi|332005337|gb|AED92720.1| mechanosensitive channel of small conductance-like 9 [Arabidopsis thaliana]	745	742	0	99.6	72.9	85.4	mechanosensitive channel of small conductance-like 9	gbpln	Arabidopsis thaliana	AT5G19520.1 | Symbols: MSL9, ATMSL9 | mechanosensitive channel of small conductance-like 9 | chr5:6586079-6588771 FORWARD LENGTH=742	745	742	0	99.6	72.9	85.4

Rsa1.0_00739.1.g18831.t1	dbj|BAB83654.1| spermine synthase [Arabidopsis halleri subsp. gemmifera]	339	339	0	100.0	95.0	97.9	spermine synthase	gbpln	Arabidopsis halleri	AT5G19530.1 | Symbols: ACL5 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:6589176-6591091 REVERSE LENGTH=339	339	339	0	100.0	93.8	97.1
Rsa1.0_00740.1.g18832.t1	sp|Q39290.1|RPAB5_BRANA RecName: Full=DNA-directed RNA polymerases I, II, and III subunit RPABC5; Short=RNA polymerases I, II, and III subunit ABC5; AltName: Full=ABC10; AltName: Full=DNA-directed RNA polymerase III subunit L; AltName: Full=RPB10 homolog gi|533690|gb|AAA21279.1| RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]	77	71	8.00E-22	92.2	68.8	70.1	RecName: Full=DNA-directed RNA polymerases I, II, and III subunit RPABC5; Short=RNA polymerases I, II, and III subunit ABC5; AltName: Full=ABC10; AltName: Full=DNA-directed RNA polymerase III subunit L; AltName: Full=RPB10 homolog gi|533690|gb|AAA21279.1| RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139	gbpln	Brassica napus	AT1G11475.1 | Symbols: NRPB10, NRPD10, NRPE10 | RNA polymerases N / 8 kDa subunit | chr1:3862520-3863805 FORWARD LENGTH=71	77	71	1.00E-23	92.2	66.2	67.5
Rsa1.0_00740.1.g18833.t1	gb|EOA39997.1| hypothetical protein CARUB_v10008685mg [Capsella rubella]	607	581	0	95.7	72.0	80.2	hypothetical protein CARUB_v10008685mg	gbpln	Capsella rubella	AT1G11480.1 | Symbols: | eukaryotic translation initiation factor-related | chr1:3864368-3866750 REVERSE LENGTH=578	607	578	0	95.2	68.9	76.1
Rsa1.0_00740.1.g18834.t1	ref|XP_002892647.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297338489|gb|EFH68906.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	364	362	1.00E-147	99.5	75.3	84.6	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G11490.1 | Symbols: | zinc finger (C2H2 type) family protein | chr1:3868884-3870065 REVERSE LENGTH=365	364	365	1.00E-147	100.3	74.7	83.2
Rsa1.0_00740.1.g18835.t1	ref|XP_002889872.1| At1g11500 [Arabidopsis lyrata subsp. lyrata] gi|297335714|gb|EFH66131.1| At1g11500 [Arabidopsis lyrata subsp. lyrata]	185	184	2.00E-76	99.5	82.2	87.6	At1g11500	gbpln	Arabidopsis lyrata	AT1G11500.1 | Symbols: | Protein of unknown function (DUF1218) | chr1:3870833-3871570 FORWARD LENGTH=184	185	184	1.00E-76	99.5	78.9	83.2
Rsa1.0_00740.1.g18836.t1	gb|EOA36119.1| hypothetical protein CARUB_v10011873mg [Capsella rubella]	409	378	2.00E-67	92.4	48.4	61.4	hypothetical protein CARUB_v10011873mg	gbpln	Capsella rubella	AT1G11510.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:3871778-3872836 REVERSE LENGTH=352	409	352	7.00E-66	86.1	45.5	58.2
Rsa1.0_00740.1.g18837.t1	ref|NP_563892.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|334302869|sp|Q8L9A9.2|XTH8_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 8; Short=At-XTH8; Short=XTH-8; Flags: Precursor gi|110736799|dbj|BAF00360.1| endo-xyloglucan transferase like protein [Arabidopsis thaliana] gi|332190629|gb|AEE28750.1| probable xyloglucan endotransglucosylase/hydrolase protein 8 [Arabidopsis thaliana]	299	305	1.00E-169	102.0	93.0	96.7	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT1G11545.1 | Symbols: XTH8 | xyloglucan endotransglucosylase/hydrolase 8 | chr1:3878689-3880286 REVERSE LENGTH=305	299	305	1.00E-171	102.0	93.0	96.7
Rsa1.0_00740.1.g18838.t1	ref|XP_002889875.1| hypothetical protein ARALYDRAFT_888463 [Arabidopsis lyrata subsp. lyrata] gi|297335717|gb|EFH66134.1| hypothetical protein ARALYDRAFT_888463 [Arabidopsis lyrata subsp. lyrata]	92	89	5.00E-38	96.7	88.0	93.5	hypothetical protein ARALYDRAFT_888463	gbpln	Arabidopsis lyrata	AT1G11572.1 | Symbols: | Plant thionin family protein | chr1:3884455-3884724 FORWARD LENGTH=89	92	89	3.00E-38	96.7	81.5	91.3
Rsa1.0_00740.1.g18839.t3	ref|XP_002874731.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320568|gb|EFH50990.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	830	806	0	97.1	62.9	73.7	predicted protein	gbpln	Arabidopsis lyrata	AT4G11900.1 | Symbols: | S-locus lectin protein kinase family protein | chr4:7150241-7153542 REVERSE LENGTH=849	830	849	0	102.3	61.3	72.8
Rsa1.0_00740.1.g18840.t1	ref|XP_002892652.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338494|gb|EFH68911.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	403	403	1.00E-170	100.0	71.2	84.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G11630.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:3913168-3914385 REVERSE LENGTH=405	403	405	1.00E-166	100.5	70.7	84.1
Rsa1.0_00740.1.g18841.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00740.1.g18842.t1	ref|NP_683299.1| uncharacterized protein [Arabidopsis thaliana] gi|28466815|gb|AAO44016.1| At1g11655 [Arabidopsis thaliana] gi|110743478|dbj|BAE99625.1| hypothetical protein [Arabidopsis thaliana] gi|332190645|gb|AEE28766.1| uncharacterized protein AT1G11655 [Arabidopsis thaliana]	114	113	1.00E-41	99.1	74.6	86.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11655.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G21902.1); Has 22 Blast hits to 22 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:3919338-3919679 FORWARD LENGTH=113	114	113	2.00E-44	99.1	74.6	86.0
Rsa1.0_00740.1.g18843.t1	ref|NP_172631.2| heat shock protein 70 (Hsp 70) family protein [Arabidopsis thaliana] gi|75313135|sp|Q9SAB1.1|HSP7Q_ARATH RecName: Full=Heat shock 70 kDa protein 16; AltName: Full=Heat shock protein 70-16; Short=AtHsp70-16 gi|4835791|gb|AAD30257.1|AC007296_18 Strong similarity to gb|Z70314 heat-shock protein from Arabidopsis thaliana and is a member of the PF|00012 Hsp70 protein family [Arabidopsis thaliana] gi|332190646|gb|AEE28767.1| heat shock protein 70 (Hsp 70) family protein [Arabidopsis thaliana]	755	763	0	101.1	90.6	94.4	heat shock protein 70 (Hsp 70) family protein	gbpln	Arabidopsis thaliana	AT1G11660.1 | Symbols: | heat shock protein 70 (Hsp 70) family protein | chr1:3921056-3924347 FORWARD LENGTH=763	755	763	0	101.1	90.6	94.4
Rsa1.0_00740.1.g18844.t1	ref|NP_172633.1| cytochrome P450, family 51 (sterol 14-demethylase) [Arabidopsis thaliana] gi|75313134|sp|Q9SAA9.1|CP511_ARATH RecName: Full=Sterol 14-demethylase; AltName: Full=Cytochrome P450 51A2; AltName: Full=Cytochrome P450 51G1; Short=AtCYP51; AltName: Full=Obtusifoliol 14-demethylase; AltName: Full=Protein EMBRYO DEFECTIVE 1738 gi|4835788|gb|AAD30254.1|AC007296_15 Strong similarity to gb|U74319 obtusifoliol 14-alpha demethylase (CYP51) from Sorghum bicolor and is a member of the PF|00067 cytochrome P450 family. ESTs gb|AA72030, gb|N65031 and gb|AA651059 come from this gene [Arabidopsis thaliana] gi|15294294|gb|AAK95324.1|AF410338_1 At1g11680/F25C20_17 [Arabidopsis thaliana] gi|14624983|dbj|BAB61873.1| obtusifoliol 14-demethylase [Arabidopsis thaliana] gi|15292853|gb|AAK92797.1| putative obtusifoliol 14-alpha demethylase [Arabidopsis thaliana] gi|20258897|gb|AAM14142.1| putative obtusifoliol 14-alpha demethylase [Arabidopsis thaliana] gi|21536753|gb|AAM61085.1| putative obtusifoliol 14-alpha demethylase	490	488	0	99.6	92.4	97.6	cytochrome P450, family 51 (sterol 14-demethylase)	gbpln	Arabidopsis thaliana	AT1G11680.1 | Symbols: CYP51G1, EMB1738, CYP51A2, CYP51 | CYTOCHROME P450 51G1 | chr1:3938925-3940585 FORWARD LENGTH=488	490	488	0	99.6	92.4	97.6
Rsa1.0_00740.1.g18845.t1	ref|NP_172634.1| uncharacterized protein [Arabidopsis thaliana] gi|4835790|gb|AAD30256.1|AC007296_17 F25C20.16 [Arabidopsis thaliana] gi|225897912|dbj|BAH30288.1| hypothetical protein [Arabidopsis thaliana] gi|332190650|gb|AEE28771.1| uncharacterized protein AT1G11690 [Arabidopsis thaliana]	216	247	2.00E-73	114.4	69.4	82.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11690.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G20350.1); Has 5959 Blast hits to 4807 proteins in 476 species: Archae - 156; Bacteria - 436; Metazoa - 2789; Fungi - 309; Plants - 336; Viruses - 9; Other Eukaryotes - 1924 (source: NCBI BLink). | chr1:3941469-3942212 FORWARD LENGTH=247	216	247	5.00E-76	114.4	69.4	82.9
Rsa1.0_00740.1.g18846.t1	ref|NP_172635.1| uncharacterized protein [Arabidopsis thaliana] gi|4835787|gb|AAD30253.1|AC007296_14 ESTs gb|R65381 and gb|T44635 come from this gene [Arabidopsis thaliana] gi|13194780|gb|AAK15552.1|AF348581_1 unknown protein [Arabidopsis thaliana] gi|27808534|gb|AAO24547.1| At1g11700 [Arabidopsis thaliana] gi|110743662|dbj|BAE99668.1| hypothetical protein [Arabidopsis thaliana] gi|332190651|gb|AEE28772.1| uncharacterized protein AT1G11700 [Arabidopsis thaliana]	212	201	4.00E-76	94.8	82.5	88.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11700.1 | Symbols: | Protein of unknown function, DUF584 | chr1:3945852-3946457 FORWARD LENGTH=201	212	201	1.00E-78	94.8	82.5	88.7
Rsa1.0_00740.1.g18847.t1	gb|EOA37371.1| hypothetical protein CARUB_v10011175mg [Capsella rubella]	1745	1093	0	62.6	53.0	56.5	hypothetical protein CARUB_v10011175mg	gbpln	Capsella rubella	AT1G11720.2 | Symbols: SS3 | starch synthase 3 | chr1:3951597-3956840 FORWARD LENGTH=1094	1745	1094	0	62.7	52.1	56.0

Rsa1.0_00740.1.g18848.t1	ref|NP_172638.1| putative beta-1,3-galactosyltransferase 1 [Arabidopsis thaliana] gi|221222634|sp|Q9SAA4.2|B3GT1_ARATH RecName: Full=Probable beta-1,3-galactosyltransferase 1 gi|332190655|gb|AEE28776.1| putative beta-1,3-galactosyltransferase 1 [Arabidopsis thaliana]	408	384	0	94.1	79.9	86.3	putative beta-1,3-galactosyltransferase 1	gbpln	Arabidopsis thaliana	AT1G11730.1 | Symbols: | Galactosyltransferase family protein | chr1:3957473-3960113 FORWARD LENGTH=384	408	384	0	94.1	79.9	86.3
Rsa1.0_00740.1.g18849.t1	dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	450	1098	1.00E-126	244.0	54.0	67.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	450	237	3.00E-28	52.7	15.1	25.3
Rsa1.0_00740.1.g18850.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1336	1491	0	111.6	58.2	72.4	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1336	1262	1.00E-127	94.5	17.8	26.3
Rsa1.0_00740.1.g18851.t1	ref|NP_563925.1| putative galacturonosyltransferase-like 3 [Arabidopsis thaliana] gi|122223578|sp|Q0V7R1.1|GATL3_ARATH RecName: Full=Probable galacturonosyltransferase-like 3 gi|111074486|gb|ABH04616.1| At1g13250 [Arabidopsis thaliana] gi|332190869|gb|AEE28990.1| putative galacturonosyltransferase-like 3 [Arabidopsis thaliana]	345	345	1.00E-169	100.0	87.8	89.6	putative galacturonosyltransferase-like 3	gbpln	Arabidopsis thaliana	AT1G13250.1 | Symbols: GATL3 | galacturonosyltransferase-like 3 | chr1:4528965-4530002 REVERSE LENGTH=345	345	345	1.00E-172	100.0	87.8	89.6
Rsa1.0_00740.1.g18852.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00740.1.g18853.t9	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00740.1.g18854.t1	ref|NP_172782.2| Piriformospora indica-insensitive protein 2 [Arabidopsis thaliana] gi|75321275|sp|Q5PP26.1|PII2_ARATH RecName: Full=Piriformospora indica-insensitive protein 2; Flags: Precursor gi|56236072|gb|AAV84492.1| At1g13230 [Arabidopsis thaliana] gi|332190867|gb|AEE28988.1| Piriformospora indica-insensitive protein 2 [Arabidopsis thaliana]	421	424	0	100.7	80.3	87.6	Piriformospora indica-insensitive protein 2	gbpln	Arabidopsis thaliana	AT1G13230.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr1:4520679-4522439 FORWARD LENGTH=424	421	424	0	100.7	80.3	87.6
Rsa1.0_00740.1.g18855.t1	gb|EOA39033.1| hypothetical protein CARUB_v10011605mg [Capsella rubella]	1161	1169	0	100.7	80.4	87.3	hypothetical protein CARUB_v10011605mg	gbpln	Capsella rubella	AT1G13220.2 | Symbols: LINC2 | nuclear matrix constituent protein-related | chr1:4515699-4520071 FORWARD LENGTH=1128	1161	1128	0	97.2	76.4	83.8
Rsa1.0_00740.1.g18856.t1	gb|EOA36037.1| hypothetical protein CARUB_v10008116mg [Capsella rubella]	1217	1204	0	98.9	88.8	93.7	hypothetical protein CARUB_v10008116mg	gbpln	Capsella rubella	AT1G13210.1 | Symbols: ACA.l | autoinhibited Ca2+/ATPase II | chr1:4509252-4513774 REVERSE LENGTH=1203	1217	1203	0	98.8	87.8	92.9
Rsa1.0_00740.1.g18857.t1	ref|NP_563922.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|4850408|gb|AAD31078.1|AC007357_27 Contains PF|00097 Zinc finger (C3HC4) ring finger motif [Arabidopsis thaliana] gi|21593124|gb|AAM65073.1| unknown [Arabidopsis thaliana] gi|87116602|gb|ABD19665.1| At1g13195 [Arabidopsis thaliana] gi|110742119|dbj|BAE98989.1| hypothetical protein [Arabidopsis thaliana] gi|332190861|gb|AEE28982.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	258	260	1.00E-136	100.8	93.0	96.9	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT1G13195.1 | Symbols: | RING/U-box superfamily protein | chr1:4501778-4503347 REVERSE LENGTH=260	258	260	1.00E-139	100.8	93.0	96.9

Rsa1.0_00740.1.g18858.t1	ref|NP_172778.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|4850402|gb|AAD31072.1|AC007357_21 Contains similarity to gb|Y12424 SGRP-1 protein frm Solanum commersonii and contains a PF|00076 RNA rocognition motif [Arabidopsis thaliana] gi|17064902|gb|AAL32605.1| Unknown protein [Arabidopsis thaliana] gi|27311939|gb|AAO00935.1| Unknown protein [Arabidopsis thaliana] gi|332190860|gb|AEE28981.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	591	573	0	97.0	80.9	86.8	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT1G13190.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:4499633-4501354 FORWARD LENGTH=573	591	573	0	97.0	80.9	86.8
Rsa1.0_00741.1.g18859.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	950	871	1.00E-87	91.7	29.3	47.6	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	950	874	1.00E-27	92.0	9.7	14.2
Rsa1.0_00741.1.g18860.t3	gb|AAC79133.1| putative Mutator-like transposase, 3' partial [Arabidopsis thaliana]	712	792	1.00E-112	111.2	36.2	53.8	putative Mutator-like transposase, 3' partial	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	712	719	1.00E-21	101.0	12.9	23.7
Rsa1.0_00741.1.g18861.t1	gb|EOA29059.1| hypothetical protein CARUB_v10025314mg [Capsella rubella]	177	587	8.00E-26	331.6	36.2	40.7	hypothetical protein CARUB_v10025314mg	gbpln	Capsella rubella	AT2G38910.1 | Symbols: CPK20 | calcium-dependent protein kinase 20 | chr2:16245214-16247483 REVERSE LENGTH=583	177	583	3.00E-27	329.4	35.0	40.7
Rsa1.0_00741.1.g18862.t1	dbj|BAJ34334.1| unnamed protein product [Thellungiella halophila]	145	141	7.00E-71	97.2	93.1	93.8	unnamed protein product	----	----	AT2G38880.3 | Symbols: NF-YB1 | nuclear factor Y, subunit B1 | chr2:16238685-16240225 FORWARD LENGTH=140	145	140	3.00E-72	96.6	91.0	93.1
Rsa1.0_00741.1.g18863.t1	gb|EEE62437.1| hypothetical protein OsJ_17229 [Oryza sativa Japonica Group]	142	2504	3.00E-43	1763.4	62.7	75.4	hypothetical protein OsJ_17229	gbpln	Oryza sativa	AT1G80070.1 | Symbols: SUS2, EMB33, EMB177, EMB14 | Pre-mRNA-processing-splicing factor | chr1:30118052-30127574 FORWARD LENGTH=2359	142	2359	2.00E-45	1661.3	62.7	75.4
Rsa1.0_00741.1.g18864.t1	ref|NP_178124.2| Pre-mRNA-processing-splicing factor [Arabidopsis thaliana] gi|5902365|gb|AAD55467.1|AC009322_7 Putative splicing factor Prp8 [Arabidopsis thaliana] gi|332198232|gb|AEE36353.1| Pre-mRNA-processing-splicing factor [Arabidopsis thaliana]	2336	2359	0	101.0	89.8	94.6	Pre-mRNA-processing-splicing factor	gbpln	Arabidopsis thaliana	AT1G80070.1 | Symbols: SUS2, EMB33, EMB177, EMB14 | Pre-mRNA-processing-splicing factor | chr1:30118052-30127574 FORWARD LENGTH=2359	2336	2359	0	101.0	89.8	94.6
Rsa1.0_00741.1.g18865.t1	gb|EOA28115.1| hypothetical protein CARUB_v10024299mg [Capsella rubella]	82	134	1.00E-29	163.4	78.0	82.9	hypothetical protein CARUB_v10024299mg	gbpln	Capsella rubella	AT2G38810.2 | Symbols: HTA8 | histone H2A 8 | chr2:16219444-16220679 REVERSE LENGTH=136	82	136	2.00E-32	165.9	78.0	82.9
Rsa1.0_00741.1.g18866.t1	ref|XP_002879765.1| hypothetical protein ARALYDRAFT_482892 [Arabidopsis lyrata subsp. lyrata] gi|297325604|gb|EFH56024.1| hypothetical protein ARALYDRAFT_482892 [Arabidopsis lyrata subsp. lyrata]	520	620	0	119.2	72.1	83.1	hypothetical protein ARALYDRAFT_482892	gbpln	Arabidopsis lyrata	AT2G38800.1 | Symbols: | Plant calmodulin-binding protein-related | chr2:16216999-16218837 FORWARD LENGTH=612	520	612	1.00E-172	117.7	69.4	80.8
Rsa1.0_00741.1.g18867.t1	ref|XP_002881617.1| hypothetical protein ARALYDRAFT_482891 [Arabidopsis lyrata subsp. lyrata] gi|297327456|gb|EFH57876.1| hypothetical protein ARALYDRAFT_482891 [Arabidopsis lyrata subsp. lyrata]	202	203	7.00E-58	100.5	62.9	72.8	hypothetical protein ARALYDRAFT_482891	gbpln	Arabidopsis lyrata	AT2G38790.1 | Symbols: | unknown protein; Has 21 Blast hits to 21 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:16214546-16215160 REVERSE LENGTH=204	202	204	3.00E-57	101.0	61.9	69.8
Rsa1.0_00741.1.g18868.t1	ref|XP_002878163.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297324001|gb|EFH54422.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	365	401	5.00E-90	109.9	52.6	63.3	F-box family protein	gbpln	Arabidopsis lyrata	AT3G57590.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:21330182-21331396 REVERSE LENGTH=404	365	404	3.00E-92	110.7	52.9	63.0
Rsa1.0_00741.1.g18869.t1	ref|XP_002881616.1| hypothetical protein ARALYDRAFT_482889 [Arabidopsis lyrata subsp. lyrata] gi|297327455|gb|EFH57875.1| hypothetical protein ARALYDRAFT_482889 [Arabidopsis lyrata subsp. lyrata]	1546	1512	0	97.8	91.2	94.4	hypothetical protein ARALYDRAFT_482889	gbpln	Arabidopsis lyrata	AT2G38770.1 | Symbols: EMB2765 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:16203185-16210253 REVERSE LENGTH=1509	1546	1509	0	97.6	90.9	93.9
Rsa1.0_00741.1.g18870.t1	dbj|BAJ33731.1| unnamed protein product [Thellungiella halophila]	409	412	0	100.7	89.5	93.9	unnamed protein product	----	----	AT2G26900.1 | Symbols: | Sodium Bile acid symporter family | chr2:11475156-11477870 REVERSE LENGTH=409	409	409	0	100.0	88.3	92.9

Rsa1.0_00741.1.g18871.t1	ref|NP_181407.1| peptidyl-prolyl isomerase H (cyclophilin H) [Arabidopsis thaliana] gi|3785999|gb|AAC67345.1| putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|25083102|gb|AAN72042.1| putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|30102910|gb|AAP21373.1| At2g38730 [Arabidopsis thaliana] gi|45680872|gb|AAS75305.1| single domain cyclophilin type peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|330254484|gb|AEC09578.1| cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana]	205	199	1.00E-106	97.1	90.7	95.6	peptidyl-prolyl isomerase H (cyclophilin H)	gbpln	Arabidopsis thaliana	AT2G38730.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr2:16192579-16194038 REVERSE LENGTH=199	205	199	1.00E-108	97.1	90.7	95.6
Rsa1.0_00741.1.g18872.t1	ref|NP_181403.2| uncharacterized protein [Arabidopsis thaliana] gi|330254476|gb|AEC09570.1| uncharacterized protein AT2G38690 [Arabidopsis thaliana]	217	191	2.00E-43	88.0	56.7	66.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G38690.1 | Symbols: | unknown protein; Has 9 Blast hits to 7 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 2; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:16176905-16177669 REVERSE LENGTH=191	217	191	6.00E-46	88.0	56.7	66.8
Rsa1.0_00741.1.g18873.t1	ref|XP_002879759.1| hypothetical protein ARALYDRAFT_903103 [Arabidopsis lyrata subsp. lyrata] gi|297325598|gb|EFH56018.1| hypothetical protein ARALYDRAFT_903103 [Arabidopsis lyrata subsp. lyrata]	422	421	0	99.8	88.6	93.4	hypothetical protein ARALYDRAFT_903103	gbpln	Arabidopsis lyrata	AT2G38670.1 | Symbols: PECT1 | phosphorylethanolamine cytidylyltransferase 1 | chr2:16168979-16171680 FORWARD LENGTH=421	422	421	0	99.8	88.6	93.6
Rsa1.0_00741.1.g18874.t2	ref|XP_002881608.1| GAUT7/LGT7 [Arabidopsis lyrata subsp. lyrata] gi|297327447|gb|EFH57867.1| GAUT7/LGT7 [Arabidopsis lyrata subsp. lyrata]	630	617	0	97.9	81.3	88.6	GAUT7/LGT7	gbpln	Arabidopsis lyrata	AT2G38650.2 | Symbols: GAUT7 | galacturonosyltransferase 7 | chr2:16161856-16165523 REVERSE LENGTH=619	630	619	0	98.3	80.8	87.6
Rsa1.0_00741.1.g18875.t1	ref|XP_002881606.1| hypothetical protein ARALYDRAFT_482873 [Arabidopsis lyrata subsp. lyrata] gi|297327445|gb|EFH57865.1| hypothetical protein ARALYDRAFT_482873 [Arabidopsis lyrata subsp. lyrata]	195	196	9.00E-98	100.5	87.7	93.3	hypothetical protein ARALYDRAFT_482873	gbpln	Arabidopsis lyrata	AT2G38640.1 | Symbols: | Protein of unknown function (DUF567) | chr2:16157725-16158474 REVERSE LENGTH=196	195	196	7.00E-99	100.5	85.6	93.8
Rsa1.0_00742.1.g18876.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00742.1.g18877.t1	ref|NP_564515.1| uncharacterized protein [Arabidopsis thaliana] gi|30694176|ref|NP_849781.1| uncharacterized protein [Arabidopsis thaliana] gi|9802603|gb|AAF99805.1|AC012463_22 T2E6.7 [Arabidopsis thaliana] gi|17380814|gb|AAL36094.1| unknown protein [Arabidopsis thaliana] gi|20465323|gb|AAM20065.1| unknown protein [Arabidopsis thaliana] gi|21555584|gb|AAM63891.1| unknown [Arabidopsis thaliana] gi|332194097|gb|AEE32218.1| uncharacterized protein AT1G47820 [Arabidopsis thaliana] gi|332194098|gb|AEE32219.1| uncharacterized protein AT1G47820 [Arabidopsis thaliana]	92	96	1.00E-24	104.3	76.1	88.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G47820.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G47813.1); Has 29 Blast hits to 29 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:17612114-17612404 FORWARD LENGTH=96	92	96	2.00E-27	104.3	76.1	88.0
Rsa1.0_00742.1.g18878.t1	gb|EOA38658.1| hypothetical protein CARUB_v10010593mg [Capsella rubella]	142	142	1.00E-74	100.0	99.3	99.3	hypothetical protein CARUB_v10010593mg	gbpln	Capsella rubella	AT1G47830.1 | Symbols: | SNARE-like superfamily protein | chr1:17613346-17614784 REVERSE LENGTH=142	142	142	6.00E-77	100.0	98.6	99.3
Rsa1.0_00742.1.g18879.t1	gb|AAC67205.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1046	1413	0	135.1	52.2	67.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	1046	237	5.00E-32	22.7	8.0	11.6
Rsa1.0_00742.1.g18880.t2	ref|XP_002894073.1| hypothetical protein ARALYDRAFT_314227 [Arabidopsis lyrata subsp. lyrata] gi|297339915|gb|EFH70332.1| hypothetical protein ARALYDRAFT_314227 [Arabidopsis lyrata subsp. lyrata]	515	491	0	95.3	79.2	87.6	hypothetical protein ARALYDRAFT_314227	gbpln	Arabidopsis lyrata	AT1G47840.1 | Symbols: HXK3 | hexokinase 3 | chr1:17616243-17618859 REVERSE LENGTH=493	515	493	0	95.7	78.4	86.4

Rsa1.0_00742.1.g18881.t1	gb|ABK28413.1| unknown [Arabidopsis thaliana]	318	294	2.00E-81	92.5	52.8	63.2	unknown	gbpln	Arabidopsis thaliana	AT1G24380.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10230.1); Has 252 Blast hits to 250 proteins in 33 species: Archae - 0; Bacteria - 4; Metazoa - 16; Fungi - 6; Plants - 180; Viruses - 2; Other Eukaryotes - 44 (source: NCBI BLink). | chr1:8646625-8647609 FORWARD LENGTH=293	318	293	3.00E-83	92.1	52.5	62.9
Rsa1.0_00742.1.g18882.t1	gb|AAD28316.1| hypothetical protein [Arabidopsis thaliana]	191	244	6.00E-54	127.7	64.9	70.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	191	343	3.00E-54	179.6	58.6	66.0
Rsa1.0_00742.1.g18883.t1	gb|AAF99784.1|AC012463_1 T2E6.3 [Arabidopsis thaliana] gi|110737661|dbj|BAF00770.1| hypothetical protein [Arabidopsis thaliana]	417	419	0	100.5	87.5	92.1	T2E6.3	gbpln	Arabidopsis thaliana	AT1G75710.1 | Symbols: | C2H2-like zinc finger protein | chr1:28428806-28431128 FORWARD LENGTH=462	417	462	1.00E-130	110.8	65.5	75.5
Rsa1.0_00742.1.g18884.t4	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	578	1044	7.00E-63	180.6	28.4	37.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	ATMG01250.1 | Symbols: ORF102 | RNA-directed DNA polymerase (reverse transcriptase) | chrM:310514-310882 FORWARD LENGTH=122	578	122	8.00E-13	21.1	5.4	6.4
Rsa1.0_00742.1.g18885.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00742.1.g18886.t1	gb|AAD20433.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	414	889	2.00E-46	214.7	24.9	30.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00742.1.g18887.t2	emb|CAN79683.1| hypothetical protein VITISV_011289 [Vitis vinifera]	565	926	1.00E-108	163.9	41.6	58.9	hypothetical protein VITISV_011289	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00743.1.g18888.t1	gb|EOA28112.1| hypothetical protein CARUB_v10024308mg [Capsella rubella]	128	131	7.00E-60	102.3	89.1	89.8	hypothetical protein CARUB_v10024308mg	gbpln	Capsella rubella	AT2G40590.1 | Symbols: | Ribosomal protein S26e family protein | chr2:16945215-16946345 REVERSE LENGTH=131	128	131	9.00E-62	102.3	87.5	88.3
Rsa1.0_00743.1.g18889.t1	ref|NP_181580.2| uncharacterized protein [Arabidopsis thaliana] gi|75111145|sp|Q5XVC7.1|Y2048_ARATH RecName: Full=WEB family protein At2g40480 gi|52354289|gb|AAU44465.1| hypothetical protein AT2G40480 [Arabidopsis thaliana] gi|330254742|gb|AEC09836.1| uncharacterized protein AT2G40480 [Arabidopsis thaliana]	457	518	1.00E-178	113.3	79.6	89.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G40480.1 | Symbols: | Plant protein of unknown function (DUF827) | chr2:16910425-16912444 FORWARD LENGTH=518	457	518	1.00E-180	113.3	79.6	89.5
Rsa1.0_00743.1.g18890.t1	ref|XP_002881725.1| hypothetical protein ARALYDRAFT_903340 [Arabidopsis lyrata subsp. lyrata] gi|297327564|gb|EFH57984.1| hypothetical protein ARALYDRAFT_903340 [Arabidopsis lyrata subsp. lyrata]	195	192	4.00E-59	98.5	79.0	84.6	hypothetical protein ARALYDRAFT_903340	gbpln	Arabidopsis lyrata	AT2G40475.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G56260.2); Has 477 Blast hits to 219 proteins in 41 species: Archae - 0; Bacteria - 4; Metazoa - 91; Fungi - 61; Plants - 144; Viruses - 0; Other Eukaryotes - 177 (source: NCBI BLink). | chr2:16907222-16907803 REVERSE LENGTH=193	195	193	3.00E-54	99.0	75.9	81.0
Rsa1.0_00743.1.g18891.t2	ref|NP_191076.2| uncharacterized protein [Arabidopsis thaliana] gi|332645826|gb|AEE79347.1| uncharacterized protein AT3G55160 [Arabidopsis thaliana]	2112	2130	0	100.9	84.7	91.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G55160.1 | Symbols: | unknown protein; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2428, death-receptor-like (InterPro:IPR019442); Has 357 Blast hits to 330 proteins in 163 species: Archae - 0; Bacteria - 0; Metazoa - 144; Fungi - 118; Plants - 50; Viruses - 0; Other Eukaryotes - 45 (source: NCBI BLink). | chr3:20445629-20452400 REVERSE LENGTH=2130	2112	2130	0	100.9	84.7	91.0
Rsa1.0_00743.1.g18892.t1	gb|AAG50652.1|AC073433_4 transposase, putative [Arabidopsis thaliana]	309	659	5.00E-93	213.3	57.6	76.1	transposase, putative	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	309	696	9.00E-38	225.2	29.1	50.5
Rsa1.0_00743.1.g18893.t1	ref|XP_002881723.1| hypothetical protein ARALYDRAFT_345842 [Arabidopsis lyrata subsp. lyrata] gi|297327562|gb|EFH57982.1| hypothetical protein ARALYDRAFT_345842 [Arabidopsis lyrata subsp. lyrata]	208	208	3.00E-73	100.0	72.1	83.2	hypothetical protein ARALYDRAFT_345842	gbpln	Arabidopsis lyrata	AT2G40450.1 | Symbols: | BTB/POZ domain-containing protein | chr2:16892024-16892790 REVERSE LENGTH=209	208	209	1.00E-71	100.5	73.1	82.2
Rsa1.0_00743.1.g18894.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00743.1.g18895.t2	ref|XP_002881642.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327481|gb|EFH57901.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	418	405	6.00E-98	96.9	51.0	64.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G49790.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:18436137-18437068 REVERSE LENGTH=283	418	283	1.00E-74	67.7	38.0	48.8
Rsa1.0_00743.1.g18896.t1	ref|XP_002881723.1| hypothetical protein ARALYDRAFT_345842 [Arabidopsis lyrata subsp. lyrata] gi|297327562|gb|EFH57982.1| hypothetical protein ARALYDRAFT_345842 [Arabidopsis lyrata subsp. lyrata]	77	208	4.00E-20	270.1	68.8	77.9	hypothetical protein ARALYDRAFT_345842	gbpln	Arabidopsis lyrata	AT2G40450.1 | Symbols: | BTB/POZ domain-containing protein | chr2:16892024-16892790 REVERSE LENGTH=209	77	209	7.00E-23	271.4	70.1	76.6
Rsa1.0_00743.1.g18897.t2	ref|XP_002881723.1| hypothetical protein ARALYDRAFT_345842 [Arabidopsis lyrata subsp. lyrata] gi|297327562|gb|EFH57982.1| hypothetical protein ARALYDRAFT_345842 [Arabidopsis lyrata subsp. lyrata]	251	208	3.00E-67	82.9	56.2	66.1	hypothetical protein ARALYDRAFT_345842	gbpln	Arabidopsis lyrata	AT2G40450.1 | Symbols: | BTB/POZ domain-containing protein | chr2:16892024-16892790 REVERSE LENGTH=209	251	209	2.00E-62	83.3	56.6	65.3
Rsa1.0_00743.1.g18898.t1	ref|XP_002881715.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata] gi|297327554|gb|EFH57974.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata]	215	215	1.00E-101	100.0	85.1	93.0	bet v I allergen family protein	gbpln	Arabidopsis lyrata	AT2G40330.1 | Symbols: PYL6, RCAR9 | PYR1-like 6 | chr2:16845177-16845824 REVERSE LENGTH=215	215	215	1.00E-103	100.0	85.1	91.2
Rsa1.0_00743.1.g18899.t1	ref|XP_002879863.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325702|gb|EFH56122.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	509	404	0	79.4	65.4	69.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G43080.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:16213995-16215828 REVERSE LENGTH=404	509	404	0	79.4	65.0	69.9
Rsa1.0_00743.1.g18900.t1	gb|AAD24652.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	138	977	5.00E-35	708.0	52.9	70.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	138	746	7.00E-32	540.6	46.4	62.3
Rsa1.0_00743.1.g18901.t1	ref|XP_002893940.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339782|gb|EFH70199.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	403	404	0	100.2	84.6	91.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G43080.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:16213995-16215828 REVERSE LENGTH=404	403	404	0	100.2	83.9	90.1
Rsa1.0_00743.1.g18902.t1	ref|XP_002881712.1| hypothetical protein ARALYDRAFT_483081 [Arabidopsis lyrata subsp. lyrata] gi|297327551|gb|EFH57971.1| hypothetical protein ARALYDRAFT_483081 [Arabidopsis lyrata subsp. lyrata]	343	344	1.00E-174	100.3	93.9	96.8	hypothetical protein ARALYDRAFT_483081	gbpln	Arabidopsis lyrata	AT2G40290.1 | Symbols: | Eukaryotic translation initiation factor 2 subunit 1 | chr2:16829030-16830889 REVERSE LENGTH=344	343	344	1.00E-175	100.3	92.7	96.5
Rsa1.0_00743.1.g18903.t1	ref|XP_002876102.1| hypothetical protein ARALYDRAFT_485528 [Arabidopsis lyrata subsp. lyrata] gi|297321940|gb|EFH52361.1| hypothetical protein ARALYDRAFT_485528 [Arabidopsis lyrata subsp. lyrata]	358	832	8.00E-44	232.4	26.0	27.7	hypothetical protein ARALYDRAFT_485528	gbpln	Arabidopsis lyrata	AT3G51740.1 | Symbols: IMK2 | inflorescence meristem receptor-like kinase 2 | chr3:19189248-19191842 FORWARD LENGTH=836	358	836	4.00E-43	233.5	23.7	24.9
Rsa1.0_00743.1.g18904.t1	gb|EOA26738.1| hypothetical protein CARUB_v10022824mg, partial [Capsella rubella]	581	626	0	107.7	86.4	91.7	hypothetical protein CARUB_v10022824mg, partial	gbpln	Capsella rubella	AT2G40280.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:16825707-16828300 REVERSE LENGTH=589	581	589	0	101.4	87.3	92.1
Rsa1.0_00744.1.g18905.t1	ref|XP_002869436.1| hypothetical protein ARALYDRAFT_913570 [Arabidopsis lyrata subsp. lyrata] gi|297315272|gb|EFH45695.1| hypothetical protein ARALYDRAFT_913570 [Arabidopsis lyrata subsp. lyrata]	401	386	5.00E-98	96.3	56.1	68.1	hypothetical protein ARALYDRAFT_913570	gbpln	Arabidopsis lyrata	AT5G39560.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:15841885-15843096 REVERSE LENGTH=403	401	403	3.00E-68	100.5	45.6	60.6
Rsa1.0_00744.1.g18906.t2	emb|CAA18194.1| putative protein [Arabidopsis thaliana] gi|7270001|emb|CAB79817.1| putative protein [Arabidopsis thaliana]	255	2895	8.00E-65	1135.3	51.0	55.3	putative protein	gbpln	Arabidopsis thaliana	AT4G30996.1 | Symbols: | Protein of unknown function (DUF1068) | chr4:15101464-15102461 FORWARD LENGTH=172	255	172	5.00E-66	67.5	51.0	55.3
Rsa1.0_00744.1.g18907.t1	ref|XP_002869433.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315269|gb|EFH45692.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	1486	1494	0	100.5	92.5	96.1	kinase family protein	gbpln	Arabidopsis lyrata	AT4G29380.1 | Symbols: | protein kinase family protein / WD-40 repeat family protein | chr4:14458822-14464692 FORWARD LENGTH=1494	1486	1494	0	100.5	92.6	95.8

<table>
<tr><td>Rsa1.0_00744.1.g18908.t1</td><td>ref|NP_194668.1| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|15241895|ref|NP_200478.1| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|18399137|ref|NP_565458.1| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|297796551|ref|XP_002866160.1| 40S ribosomal protein S30 [Arabidopsis lyrata subsp. lyrata] gi|297799054|ref|XP_002867411.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297836282|ref|XP_002886023.1| 40S ribosomal protein S30 [Arabidopsis lyrata subsp. lyrata] gi|22096379|sp|P49689.3|RS30_ARATH RecName: Full=40S ribosomal protein S30 gi|7269837|emb|CAB79697.1| RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana] gi|10176771|dbj|BAB09885.1| 40S ribosomal protein S30 homolog [Arabidopsis thaliana] gi|15450480|gb|AAK96533.1| At2g19750/F6F22.22 [Arabidopsis thaliana] gi|16974467|gb|AAL31237.1| At2g19750/F6F22.22 [Arabidopsis thaliana] gi|20197294|gb|AAC62141.2| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|21618031|gb|AAM67081.1| 40S ribosomal protein S30 [Arabidopsis thaliana] gi|22135964|gb|AAM91564.1| 40S ribosomal protein S30–like protein</td><td>62</td><td>62</td><td>5.00E−26</td><td>100.0</td><td>100.0</td><td>100.0</td><td>40S ribosomal protein S30</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G56670.1 | Symbols: | Ribosomal protein S30 family protein | chr5:22935413–22935981 REVERSE LENGTH=62</td><td>62</td><td>62</td><td>8.00E−29</td><td>100.0</td><td>100.0</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00744.1.g18909.t1</td><td>gb|EOA17123.1| hypothetical protein CARUB_v10005384mg [Capsella rubella]</td><td>297</td><td>294</td><td>1.00E−135</td><td>99.0</td><td>80.8</td><td>89.6</td><td>hypothetical protein CARUB_v10005384mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G29400.1 | Symbols: | Protein of unknown function (DUF3531) | chr4:14466350–14467980 FORWARD LENGTH=302</td><td>297</td><td>302</td><td>1.00E−132</td><td>101.7</td><td>79.5</td><td>87.5</td></tr>
<tr><td>Rsa1.0_00744.1.g18910.t1</td><td>ref|XP_002867410.1| 60S ribosomal protein L28 [Arabidopsis lyrata subsp. lyrata] gi|297313246|gb|EFH43669.1| 60S ribosomal protein L28 [Arabidopsis lyrata subsp. lyrata]</td><td>143</td><td>143</td><td>5.00E−72</td><td>100.0</td><td>93.0</td><td>96.5</td><td>60S ribosomal protein L28</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G29410.2 | Symbols: | Ribosomal L28e protein family | chr4:14468439–14469964 REVERSE LENGTH=143</td><td>143</td><td>143</td><td>1.00E−72</td><td>100.0</td><td>90.9</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00744.1.g18911.t1</td><td>gb|EOA16627.1| hypothetical protein CARUB_v10004800mg [Capsella rubella]</td><td>190</td><td>448</td><td>5.00E−64</td><td>235.8</td><td>71.1</td><td>81.6</td><td>hypothetical protein CARUB_v10004800mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G29420.1 | Symbols: | F–box/RNI–like superfamily protein | chr4:14470715–14472204 REVERSE LENGTH=446</td><td>190</td><td>446</td><td>1.00E−61</td><td>234.7</td><td>68.9</td><td>80.0</td></tr>
<tr><td>Rsa1.0_00744.1.g18912.t1</td><td>ref|XP_002866962.1| hypothetical protein ARALYDRAFT_912622 [Arabidopsis lyrata subsp. lyrata] gi|297312798|gb|EFH43221.1| hypothetical protein ARALYDRAFT_912622 [Arabidopsis lyrata subsp. lyrata]</td><td>415</td><td>542</td><td>2.00E−89</td><td>130.6</td><td>44.3</td><td>61.0</td><td>hypothetical protein ARALYDRAFT_912622</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G49000.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19864527–19865645 FORWARD LENGTH=372</td><td>415</td><td>372</td><td>2.00E−51</td><td>89.6</td><td>30.6</td><td>41.9</td></tr>
<tr><td>Rsa1.0_00744.1.g18913.t1</td><td>ref|XP_002867409.1| F–box family protein [Arabidopsis lyrata subsp. lyrata] gi|297313245|gb|EFH43668.1| F–box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>445</td><td>445</td><td>0</td><td>100.0</td><td>77.5</td><td>88.1</td><td>F–box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G29420.1 | Symbols: | F–box/RNI–like superfamily protein | chr4:14470715–14472204 REVERSE LENGTH=446</td><td>445</td><td>446</td><td>0</td><td>100.2</td><td>76.6</td><td>87.4</td></tr>
<tr><td>Rsa1.0_00744.1.g18914.t1</td><td>ref|NP_194672.1| 40S ribosomal protein S15a–5 [Arabidopsis thaliana] gi|297803094|ref|XP_002869431.1| RPS15AE [Arabidopsis lyrata subsp. lyrata] gi|75311751|sp|Q9M0E0.1|R15A5_ARATH RecName: Full=40S ribosomal protein S15a–5 gi|7269842|emb|CAB79701.1| ribosomal protein S15a homolog [Arabidopsis thaliana] gi|21553914|gb|AAM62997.1| ribosomal protein S15a homolog [Arabidopsis thaliana] gi|110737866|dbj|BAF00871.1| ribosomal protein S15a homolog [Arabidopsis thaliana] gi|111074474|gb|ABH04610.1| At4g29430 [Arabidopsis thaliana] gi|297315267|gb|EFH45690.1| RPS15AE [Arabidopsis lyrata subsp. lyrata] gi|332660230|gb|AEE85630.1| 40S ribosomal protein S15a–5 [Arabidopsis thaliana] gi|482553463|gb|EOA17656.1| hypothetical protein CARUB_v10006023mg [Capsella rubella]</td><td>129</td><td>129</td><td>8.00E−69</td><td>100.0</td><td>97.7</td><td>99.2</td><td>40S ribosomal protein S15a–5</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G29430.1 | Symbols: rps15ae | ribosomal protein S15A E | chr4:14472440–14473383 FORWARD LENGTH=129</td><td>129</td><td>129</td><td>2.00E−71</td><td>100.0</td><td>97.7</td><td>99.2</td></tr>
</table>

Rsa1.0_00744.1.g18915.t1	gb|EOA15950.1| hypothetical protein CARUB_v10004047mg [Capsella rubella]	940	1043	0	111.0	72.4	82.9	hypothetical protein CARUB_v10004047mg	gbpln	Capsella rubella	AT4G29440.1 | Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr4:14473942-14477721 REVERSE LENGTH=1090	940	1090	0	116.0	68.3	78.4
Rsa1.0_00744.1.g18916.t1	ref|NP_194675.1| Phospholipase A2 family protein [Arabidopsis thaliana] gi|75264514|sp|Q9M0D7.1|PLA2C_ARATH RecName: Full=Phospholipase A2-gamma; AltName: Full=Secretory phospholipase A2-gamma; Short=AtsPLA2-gamma; Flags: Precursor gi|7269845|emb|CAB79704.1| phospholipase A2-like protein [Arabidopsis thaliana] gi|26006457|gb|AAN63044.1| phospholipase A2 gamma [Arabidopsis thaliana] gi|332660234|gb|AEE85634.1| phospholipase A2-gamma [Arabidopsis thaliana]	194	187	7.00E-82	96.4	76.3	82.0	Phospholipase A2 family protein	gbpln	Arabidopsis thaliana	AT4G29460.1 | Symbols: | Phospholipase A2 family protein | chr4:14483066-14483930 REVERSE LENGTH=187	194	187	3.00E-84	96.4	76.3	82.0
Rsa1.0_00744.1.g18917.t1	ref|NP_194677.1| ATP synthase subunit G protein [Arabidopsis thaliana] gi|11908084|gb|AAG41471.1|AF326889_1 unknown protein [Arabidopsis thaliana] gi|12642892|gb|AAK00388.1|AF339706_1 unknown protein [Arabidopsis thaliana] gi|7269847|emb|CAB79706.1| putative protein [Arabidopsis thaliana] gi|14517504|gb|AAK62642.1| AT4g29480/F17A13_300 [Arabidopsis thaliana] gi|15809754|gb|AAL06805.1| AT4g29480/F17A13_300 [Arabidopsis thaliana] gi|21594744|gb|AAM66039.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana] gi|332660236|gb|AEE85636.1| ATP synthase subunit G protein [Arabidopsis thaliana]	122	122	3.00E-63	100.0	95.9	97.5	ATP synthase subunit G protein	gbpln	Arabidopsis thaliana	AT4G29480.1 | Symbols: | Mitochondrial ATP synthase subunit G protein | chr4:14486265-14487257 REVERSE LENGTH=122	122	122	5.00E-66	100.0	95.9	97.5
Rsa1.0_00744.1.g18918.t1	gb|EOA15795.1| hypothetical protein CARUB_v10007150mg, partial [Capsella rubella]	493	513	0	104.1	91.7	95.3	hypothetical protein CARUB_v10007150mg, partial	gbpln	Capsella rubella	AT4G29490.1 | Symbols: | Metallopeptidase M24 family protein | chr4:14487943-14491321 FORWARD LENGTH=486	493	486	0	98.6	89.9	93.9
Rsa1.0_00744.1.g18919.t1	gb|EOA18714.1| hypothetical protein CARUB_v10007292mg [Capsella rubella]	388	386	0	99.5	93.6	96.1	hypothetical protein CARUB_v10007292mg	gbpln	Capsella rubella	AT4G29510.1 | Symbols: ATPRMT11, PRMT11, ATPRMT1B, PRMT1B | arginine methyltransferase 11 | chr4:14491739-14493752 FORWARD LENGTH=390	388	390	0	100.5	93.3	96.4
Rsa1.0_00744.1.g18920.t1	ref|XP_002869428.1| 2,3-diketo-5-methylthio-1-phosphopentane phosphatase family [Arabidopsis lyrata subsp. lyrata] gi|297315264|gb|EFH45687.1| 2,3-diketo-5-methylthio-1-phosphopentane phosphatase family [Arabidopsis lyrata subsp. lyrata]	230	242	1.00E-105	105.2	83.5	90.0	2,3-diketo-5-methylthio-1-phosphopentane phosphatase family	gbpln	Arabidopsis lyrata	AT4G29530.1 | Symbols: | Pyridoxal phosphate phosphatase-related protein | chr4:14496164-14497310 FORWARD LENGTH=245	230	245	1.00E-107	106.5	83.0	90.4
Rsa1.0_00744.1.g18921.t1	gb|EOA17904.1| hypothetical protein CARUB_v10006313mg [Capsella rubella]	193	183	1.00E-66	94.8	74.1	85.5	hypothetical protein CARUB_v10006313mg	gbpln	Capsella rubella	AT4G29658.1 | Symbols: PRA1.C | prenylated RAB acceptor 1.C | chr4:14533447-14533830 REVERSE LENGTH=127	193	127	1.00E-39	65.8	49.2	54.9
Rsa1.0_00744.1.g18922.t3	ref|NP_567830.1| protein embryo defective 2752 [Arabidopsis thaliana] gi|75166388|sp|Q94K18.1|Y4966_ARATH RecName: Full=Uncharacterized protein At4g29660; AltName: Full=Protein EMBRYO DEFECTIVE 2752 gi|13877545|gb|AAK43850.1|AF370473_1 putative protein [Arabidopsis thaliana] gi|17978761|gb|AAL47374.1| putative protein [Arabidopsis thaliana] gi|21537375|gb|AAM61716.1| unknown [Arabidopsis thaliana] gi|332660258|gb|AEE85658.1| protein embryo defective 2752 [Arabidopsis thaliana]	106	103	6.00E-51	97.2	92.5	93.4	protein embryo defective 2752	gbpln	Arabidopsis thaliana	AT4G29660.1 | Symbols: EMB2752 | embryo defective 2752 | chr4:14534495-14535171 REVERSE LENGTH=103	106	103	1.00E-53	97.2	92.5	93.4
Rsa1.0_00744.1.g18923.t1	ref|XP_002867396.1| type I phosphodiesterase/nucleotide pyrophosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313232|gb|EFH43655.1| type I phosphodiesterase/nucleotide pyrophosphatase family protein [Arabidopsis lyrata subsp. lyrata]	486	496	0	102.1	86.2	93.2	type I phosphodiesterase/nucleotide pyrophosphatase family protein	gbpln	Arabidopsis lyrata	AT4G29680.1 | Symbols: | Alkaline-phosphatase-like family protein | chr4:14538067-14539557 REVERSE LENGTH=496	486	496	0	102.1	85.8	93.4

Rsa1.0_00744.1.g18924.t1	gb|EOA16623.1| hypothetical protein CARUB_v10004793mg [Capsella rubella]	454	451	0	99.3	82.6	88.5	hypothetical protein CARUB_v10004793mg	gbpln	Capsella rubella	AT4G29690.1 | Symbols: | Alkaline-phosphatase-like family protein | chr4:14541084-14542457 REVERSE LENGTH=457	454	457	0	100.7	81.7	87.9
Rsa1.0_00744.1.g18925.t1	gb|EOA16607.1| hypothetical protein CARUB_v10004780mg [Capsella rubella]	313	454	1.00E-148	145.0	78.6	90.1	hypothetical protein CARUB_v10004780mg	gbpln	Capsella rubella	AT4G29700.1 | Symbols: | Alkaline-phosphatase-like family protein | chr4:14543739-14545124 REVERSE LENGTH=461	313	461	2.33E-156	147.3	77.3	88.8
Rsa1.0_00745.1.g18926.t1	gb|ABQ50546.1| hypothetical protein [Brassica rapa]	624	650	0	104.2	77.6	89.3	hypothetical protein	gbpln	Brassica rapa	AT1G12300.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4184163-4186076 REVERSE LENGTH=637	624	637	0	102.1	71.0	83.8
Rsa1.0_00745.1.g18927.t1	ref|NP_001184959.1| uncharacterized protein [Arabidopsis thaliana] gi|332190568|gb|AEE28689.1| uncharacterized protein AT1G11125 [Arabidopsis thaliana]	259	265	8.00E-78	102.3	68.7	77.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11125.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G61170.1). | chr1:3718846-3719643 FORWARD LENGTH=265	259	265	2.00E-80	102.3	68.7	77.2
Rsa1.0_00745.1.g18928.t2	ref|NP_172574.5| uncharacterized protein [Arabidopsis thaliana] gi|332190558|gb|AEE28679.1| uncharacterized protein AT1G11070 [Arabidopsis thaliana]	700	763	0	109.0	67.7	78.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G11070.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Hydroxyproline-rich glycoprotein family protein (TAIR:AT1G61080.1); Has 579 Blast hits to 567 proteins in 152 species: Archae - 0; Bacteria - 68; Metazoa - 159; Fungi - 113; Plants - 172; Viruses - 0; Other Eukaryotes - 67 (source: NCBI BLink). | chr1:3690406-3693648 REVERSE LENGTH=763	700	763	0	109.0	67.7	78.0
Rsa1.0_00745.1.g18929.t1	gb|EOA36046.1| hypothetical protein CARUB_v10008277mg [Capsella rubella]	858	870	0	101.4	85.0	91.5	hypothetical protein CARUB_v10008277mg	gbpln	Capsella rubella	AT1G11060.1 | Symbols: | WAPL (Wings apart-like protein regulation of heterochromatin) protein | chr1:3684568-3689537 FORWARD LENGTH=930	858	930	0	108.4	85.2	90.9
Rsa1.0_00745.1.g18930.t1	ref|NP_172572.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|75317752|sp|O04086.1|Y1105_ARATH RecName: Full=Probable receptor-like protein kinase At1g11050; Flags: Precursor gi|1931642|gb|AAB65477.1| Ser/Thr protein kinase isolog; 46094-44217 [Arabidopsis thaliana] gi|332190556|gb|AEE28677.1| putative receptor-like protein kinase [Arabidopsis thaliana]	624	625	0	100.2	85.3	90.1	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT1G11050.1 | Symbols: | Protein kinase superfamily protein | chr1:3681892-3683769 FORWARD LENGTH=625	624	625	0	100.2	85.3	90.1
Rsa1.0_00745.1.g18931.t1	gb|AAB65494.1| hypothetical protein; 51018-49636 [Arabidopsis thaliana]	273	281	1.00E-91	102.9	71.4	76.6	hypothetical protein; 51018-49636	gbpln	Arabidopsis thaliana	AT1G11020.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:3676968-3678350 FORWARD LENGTH=321	273	321	1.00E-92	117.6	72.2	79.1
Rsa1.0_00745.1.g18932.t1	dbj|BAJ34386.1| unnamed protein product [Thellungiella halophila]	570	574	0	100.7	95.1	97.7	unnamed protein product	----	----	AT1G11000.1 | Symbols: MLO4, ATMLO4 | Seven transmembrane MLO family protein | chr1:3671935-3675909 REVERSE LENGTH=573	570	573	0	100.5	92.8	96.5
Rsa1.0_00745.1.g18933.t1	gb|EOA40564.1| hypothetical protein CARUB_v10009291mg [Capsella rubella]	388	414	1.00E-179	106.7	88.1	93.0	hypothetical protein CARUB_v10009291mg	gbpln	Capsella rubella	AT1G10970.1 | Symbols: ZIP4, ATZIP4 | zinc transporter 4 precursor | chr1:3665201-3666933 REVERSE LENGTH=408	388	408	1.00E-173	105.2	86.6	91.8
Rsa1.0_00745.1.g18934.t1	gb|EOA37821.1| hypothetical protein CARUB_v10011995mg [Capsella rubella]	583	589	0	101.0	96.1	97.4	hypothetical protein CARUB_v10011995mg	gbpln	Capsella rubella	AT1G10950.1 | Symbols: TMN1, AtTMN1 | transmembrane nine 1 | chr1:3659322-3663622 FORWARD LENGTH=589	583	589	0	101.0	94.7	96.9
Rsa1.0_00745.1.g18935.t2	gb|AAA33003.1| serine/threonine protein kinase [Brassica napus] gi|1097353|prf||2113401A protein kinase	359	359	0	100.0	95.3	97.5	serine/threonine protein kinase	gbpln	Brassica napus	AT1G10940.1 | Symbols: ASK1, SNRK2-4, SNRK2.4, SRK2A | Protein kinase superfamily protein | chr1:3656050-3658170 REVERSE LENGTH=363	359	363	0	101.1	94.4	97.5
Rsa1.0_00745.1.g18936.t2	emb|CAC14868.1| DNA Helicase [Arabidopsis thaliana]	1196	1182	0	98.8	82.5	88.3	DNA Helicase	gbpln	Arabidopsis thaliana	AT1G10930.1 | Symbols: ATSGS1, RECQ4A, ATRECQ4A | DNA helicase (RECQl4A) | chr1:3648032-3654997 REVERSE LENGTH=1188	1196	1188	0	99.3	82.5	88.3

Rsa1.0_00745.1.g18937.t1	ref|NP_172559.2| 1-phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana] gi|75208667|sp|Q9SUI2.1|PI5K7_ARATH RecName: Full=Phosphatidylinositol 4-phosphate 5-kinase 7; Short=AtPIP5K7; AltName: Full=1-phosphatidylinositol 4-phosphate kinase 7; AltName: Full=Diphosphoinositide kinase 7; Short=AtP5K2; AltName: Full=PtdIns(4)P-5-kinase 7 gi|5777366|emb|CAB53377.1| phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana] gi|17065284|gb|AAL32796.1| Unknown protein [Arabidopsis thaliana] gi|34098805|gb|AAQ56785.1| At1g10900 [Arabidopsis thaliana] gi|332190540|gb|AEE28661.1| phosphatidylinositol 4-phosphate 5-kinase 7 [Arabidopsis thaliana]	706	754	0	106.8	85.6	89.9	1-phosphatidylinositol-4-phosphate 5-kinase	gbpln	Arabidopsis thaliana	AT1G10900.1 | Symbols: | Phosphatidylinositol-4-phosphate 5-kinase family protein | chr1:3632396-3636416 REVERSE LENGTH=754	706	754	0	106.8	85.6	89.9
Rsa1.0_00746.1.g18938.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00746.1.g18939.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00746.1.g18940.t1	gb|ACN73535.1| 1433-2 [Brassica napus]	263	262	1.00E-144	99.6	97.0	97.3	1433-2	gbpln	Brassica napus	AT2G42590.3 | Symbols: GRF9, GF14 MU | general regulatory factor 9 | chr2:17732164-17733775 REVERSE LENGTH=276	263	276	1.00E-143	104.9	92.8	97.0
Rsa1.0_00746.1.g18941.t1	ref|XP_002879994.1| hypothetical protein ARALYDRAFT_483352 [Arabidopsis lyrata subsp. lyrata] gi|297325833|gb|EFH56253.1| hypothetical protein ARALYDRAFT_483352 [Arabidopsis lyrata subsp. lyrata]	668	688	0	103.0	87.7	92.4	hypothetical protein ARALYDRAFT_483352	gbpln	Arabidopsis lyrata	AT2G42580.1 | Symbols: TTL3, VIT | tetratricopetide-repeat thioredoxin-like 3 | chr2:17728855-17731461 FORWARD LENGTH=691	668	691	0	103.4	86.7	91.0
Rsa1.0_00746.1.g18942.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00746.1.g18943.t1	gb|EOA28713.1| hypothetical protein CARUB_v10024941mg [Capsella rubella]	227	653	6.00E-51	287.7	62.6	69.6	hypothetical protein CARUB_v10024941mg	gbpln	Capsella rubella	AT2G42560.1 | Symbols: | late embryogenesis abundant domain-containing protein / LEA domain-containing protein | chr2:17714813-17716821 REVERSE LENGTH=635	227	635	1.00E-45	279.7	59.5	67.0
Rsa1.0_00746.1.g18944.t1	gb|ABA01003.2| cold-regulated protein [Brassica rapa subsp. chinensis]	521	129	4.00E-51	24.8	20.3	21.1	cold-regulated protein	gbpln	Brassica rapa	AT2G42530.1 | Symbols: COR15B | cold regulated 15b | chr2:17709191-17709873 REVERSE LENGTH=141	521	141	6.00E-43	27.1	17.5	19.8
Rsa1.0_00746.1.g18945.t4	#	#	#	#	#	#	#	-	----	----	AT1G20850.1 | Symbols: XCP2 | xylem cysteine peptidase 2 | chr1:7252208-7253537 FORWARD LENGTH=356	206	356	7.00E-13	172.8	18.9	22.8
Rsa1.0_00746.1.g18946.t1	gb|AAS16843.1| cold-regulated protein [Brassica napus]	66	129	7.00E-27	195.5	92.4	95.5	cold-regulated protein	gbpln	Brassica napus	AT2G42530.1 | Symbols: COR15B | cold regulated 15b | chr2:17709191-17709873 REVERSE LENGTH=141	66	141	4.00E-23	213.6	80.3	84.8
Rsa1.0_00747.1.g18947.t1	gb|AAF67380.1| Hypothetical protein T15F17.I [Arabidopsis thaliana]	432	1141	1.00E-44	264.1	20.1	22.7	Hypothetical protein T15F17.I	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00747.1.g18948.t2	ref|XP_002865249.1| sodium:solute symporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297311084|gb|EFH41508.1| sodium:solute symporter family protein [Arabidopsis lyrata subsp. lyrata]	233	702	1.00E-115	301.3	87.6	90.6	sodium:solute symporter family protein	gbpln	Arabidopsis lyrata	AT5G45380.1 | Symbols: ATDUR3, DUR3 | solute:sodium symporters;urea transmembrane transporters | chr5:18391337-18395696 FORWARD LENGTH=704	233	704	1.00E-116	302.1	88.4	90.6
Rsa1.0_00747.1.g18949.t1	gb|AAC02664.1| polyprotein [Arabidopsis thaliana]	1390	1451	0	104.4	66.4	78.2	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1390	1262	1.00E-110	90.8	14.7	22.4
Rsa1.0_00747.1.g18950.t1	gb|EOA12996.1| hypothetical protein CARUB_v10025985mg [Capsella rubella]	504	705	0	139.9	81.3	87.7	hypothetical protein CARUB_v10025985mg	gbpln	Capsella rubella	AT5G45380.1 | Symbols: ATDUR3, DUR3 | solute:sodium symporters;urea transmembrane transporters | chr5:18391337-18395696 FORWARD LENGTH=704	504	704	0	139.7	81.7	88.9
Rsa1.0_00747.1.g18951.t1	gb|EOA14703.1| hypothetical protein CARUB_v10027980mg [Capsella rubella]	832	842	0	101.2	70.2	80.9	hypothetical protein CARUB_v10027980mg	gbpln	Capsella rubella	AT5G45400.1 | Symbols: RPA70C, ATRPA70C | Replication factor-A protein 1-related | chr5:18398990-18401644 FORWARD LENGTH=853	832	853	0	102.5	69.7	80.3

Rsa1.0_00747.1.g18952.t1	gb|EOA13618.1| hypothetical protein CARUB_v10026685mg [Capsella rubella] gi|482549425|gb|EOA13619.1| hypothetical protein CARUB_v10026685mg [Capsella rubella]	346	353	1.00E−153	102.0	85.8	90.8	hypothetical protein CARUB_v10026685mg	gbpln	Capsella rubella	AT5G45410.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25030.2); Has 124 Blast hits to 124 proteins in 34 species: Archae − 2; Bacteria − 31; Metazoa − 0; Fungi − 0; Plants − 91; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr5:18402071−18403282 REVERSE LENGTH=342	346	342	1.00E−141	98.8	81.2	87.3
Rsa1.0_00747.1.g18953.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00747.1.g18954.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00748.1.g18955.t1	ref|XP_002875393.1| hypothetical protein ARALYDRAFT_905015 [Arabidopsis lyrata subsp. lyrata] gi|297321231|gb|EFH51652.1| hypothetical protein ARALYDRAFT_905015 [Arabidopsis lyrata subsp. lyrata]	505	538	0	106.5	88.1	92.5	hypothetical protein ARALYDRAFT_905015	gbpln	Arabidopsis lyrata	AT3G27640.1 | Symbols: | Transducin/WD40 repeat−like superfamily protein | chr3:10232307−10235467 FORWARD LENGTH=535	505	535	0	105.9	88.3	92.5
Rsa1.0_00748.1.g18956.t2	ref|XP_002877065.1| hypothetical protein ARALYDRAFT_905014 [Arabidopsis lyrata subsp. lyrata] gi|297322903|gb|EFH53324.1| hypothetical protein ARALYDRAFT_905014 [Arabidopsis lyrata subsp. lyrata]	222	106	1.00E−35	47.7	33.3	42.3	hypothetical protein ARALYDRAFT_905014	gbpln	Arabidopsis lyrata	AT5G40460.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27630.1); Has 87 Blast hits to 87 proteins in 12 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 87; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr5:16202465−16202803 FORWARD LENGTH=112	222	112	7.00E−34	50.5	34.7	37.4
Rsa1.0_00748.1.g18957.t1	gb|EOA25560.1| hypothetical protein CARUB_v10018904mg [Capsella rubella]	175	198	2.00E−49	113.1	64.0	75.4	hypothetical protein CARUB_v10018904mg	gbpln	Capsella rubella	AT3G27520.1 | Symbols: | unknown protein; Has 28 Blast hits to 28 proteins in 10 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 28; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:10192484−10193159 FORWARD LENGTH=198	175	198	8.00E−48	113.1	61.7	70.9
Rsa1.0_00748.1.g18958.t1	ref|NP_189384.1| cysteine/histidine−rich C1 domain−containing protein [Arabidopsis thaliana] gi|11994636|dbj|BAA95723.2| CHP−rich zinc finger protein−like [Arabidopsis thaliana] gi|332643805|gb|AEE77326.1| cysteine/histidine−rich C1 domain−containing protein [Arabidopsis thaliana]	668	662	0	99.1	62.6	74.3	cysteine/histidine−rich C1 domain−containing protein	gbpln	Arabidopsis thaliana	AT3G27473.1 | Symbols: | Cysteine/Histidine−rich C1 domain family protein | chr3:10169242−10171230 REVERSE LENGTH=662	668	662	0	99.1	62.6	74.3
Rsa1.0_00748.1.g18959.t1	ref|NP_189383.2| uncharacterized protein [Arabidopsis thaliana] gi|145332703|ref|NP_001078217.1| uncharacterized protein [Arabidopsis thaliana] gi|19698931|gb|AAL91201.1| unknown protein [Arabidopsis thaliana] gi|27311907|gb|AAO00919.1| unknown protein [Arabidopsis thaliana] gi|332643803|gb|AEE77324.1| uncharacterized protein AT3G27470 [Arabidopsis thaliana] gi|332643804|gb|AEE77325.1| uncharacterized protein AT3G27470 [Arabidopsis thaliana]	399	398	0	99.7	91.2	95.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27470.2 | Symbols: | Protein of unknown function (DUF707) | chr3:10163947−10166550 FORWARD LENGTH=398	399	398	0	99.7	91.2	95.2
Rsa1.0_00748.1.g18960.t1	ref|XP_002875388.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321226|gb|EFH51647.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	456	464	0	101.8	91.7	95.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G27440.1 | Symbols: UKL5 | uridine kinase−like 5 | chr3:10155555−10157931 FORWARD LENGTH=465	456	465	0	102.0	90.6	95.0
Rsa1.0_00748.1.g18961.t1	ref|NP_001118720.1| uncharacterized protein [Arabidopsis thaliana] gi|332643794|gb|AEE77315.1| uncharacterized protein AT3G27416 [Arabidopsis thaliana]	171	171	6.00E−12	100.0	53.2	63.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27416.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr3:10147371−10147886 REVERSE LENGTH=171	171	171	2.00E−14	100.0	53.2	63.7

Rsa1.0_00748.1.g18962.t1	ref|XP_002875382.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321220|gb|EFH51641.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	412	412	0	100.0	89.6	95.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G27400.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:10140323-10143023 FORWARD LENGTH=412	412	412	0	100.0	89.8	95.1
Rsa1.0_00748.1.g18963.t1	dbj|BAJ34353.1| unnamed protein product [Thellungiella halophila]	283	279	1.00E-145	98.6	90.5	94.7	unnamed protein product	----	----	AT3G27380.2 | Symbols: SDH2-1 | succinate dehydrogenase 2-1 | chr3:10131209-10132673 REVERSE LENGTH=279	283	279	1.00E-148	98.6	88.7	92.6
Rsa1.0_00748.1.g18964.t1	gb|EOA23814.1| hypothetical protein CARUB_v10017030mg [Capsella rubella]	527	516	0	97.9	93.2	96.4	hypothetical protein CARUB_v10017030mg	gbpln	Capsella rubella	AT3G27300.3 | Symbols: G6PD5 | glucose-6-phosphate dehydrogenase 5 | chr3:10083318-10086288 REVERSE LENGTH=516	527	516	0	97.9	92.2	96.8
Rsa1.0_00748.1.g18965.t1	gb|EOA23946.1| hypothetical protein CARUB_v10017162mg [Capsella rubella]	417	472	1.00E-123	113.2	65.2	76.3	hypothetical protein CARUB_v10017162mg	gbpln	Capsella rubella	AT3G27290.1 | Symbols: | RNI-like superfamily protein | chr3:10080038-10081265 REVERSE LENGTH=382	417	382	1.00E-115	91.6	55.9	65.5
Rsa1.0_00748.1.g18966.t1	ref|NP_189364.1| prohibitin 4 [Arabidopsis thaliana] gi|42572547|ref|NP_974369.1| prohibitin 4 [Arabidopsis thaliana] gi|75273705|sp|Q9LK25.1|PHB4_ARATH RecName: Full=Prohibitin-4, mitochondrial; Short=Atphb4 gi|9294221|dbj|BAB02123.1| prohibitin [Arabidopsis thaliana] gi|332643766|gb|AEE77287.1| prohibitin 4 [Arabidopsis thaliana] gi|332643767|gb|AEE77288.1| prohibitin 4 [Arabidopsis thaliana]	278	279	2.33E-156	100.4	93.5	96.4	prohibitin 4	gbpln	Arabidopsis thaliana	AT3G27280.1 | Symbols: ATPHB4, PHB4 | prohibitin 4 | chr3:10076904-10078051 FORWARD LENGTH=279	278	279	1.00E-149	100.4	93.5	96.4
Rsa1.0_00748.1.g18967.t1	gb|EOA25372.1| hypothetical protein CARUB_v10018703mg [Capsella rubella]	410	433	0	105.6	93.2	97.1	hypothetical protein CARUB_v10018703mg	gbpln	Capsella rubella	AT5G40780.1 | Symbols: LHT1 | lysine histidine transporter 1 | chr5:16323823-16327082 FORWARD LENGTH=446	410	446	0	108.8	88.3	96.1
Rsa1.0_00748.1.g18968.t2	ref|XP_002875368.1| hypothetical protein ARALYDRAFT_484508 [Arabidopsis lyrata subsp. lyrata] gi|297321206|gb|EFH51627.1| hypothetical protein ARALYDRAFT_484508 [Arabidopsis lyrata subsp. lyrata]	687	814	0	118.5	80.8	87.8	hypothetical protein ARALYDRAFT_484508	gbpln	Arabidopsis lyrata	AT3G27260.1 | Symbols: GTE8 | global transcription factor group E8 | chr3:10068411-10072403 FORWARD LENGTH=813	687	813	0	118.3	80.8	88.1
Rsa1.0_00748.1.g18969.t1	ref|XP_002877032.1| AT3g27240/K17E12_6 [Arabidopsis lyrata subsp. lyrata] gi|297322870|gb|EFH53291.1| AT3g27240/K17E12_6 [Arabidopsis lyrata subsp. lyrata]	304	307	1.00E-141	101.0	83.9	86.8	AT3g27240/K17E12_6	gbpln	Arabidopsis lyrata	AT3G27240.1 | Symbols: | Cytochrome C1 family | chr3:10056144-10058370 REVERSE LENGTH=307	304	307	1.00E-144	101.0	84.5	86.8
Rsa1.0_00748.1.g18970.t1	ref|XP_002875365.1| hypothetical protein ARALYDRAFT_904944 [Arabidopsis lyrata subsp. lyrata] gi|297321203|gb|EFH51624.1| hypothetical protein ARALYDRAFT_904944 [Arabidopsis lyrata subsp. lyrata]	415	410	0	98.8	87.5	92.8	hypothetical protein ARALYDRAFT_904944	gbpln	Arabidopsis lyrata	AT3G27230.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:10054224-10055456 FORWARD LENGTH=410	415	410	0	98.8	88.2	91.8
Rsa1.0_00748.1.g18971.t1	gb|EOA23280.1| hypothetical protein CARUB_v10018089mg [Capsella rubella]	190	183	1.00E-75	96.3	84.7	89.5	hypothetical protein CARUB_v10018089mg	gbpln	Capsella rubella	AT3G27160.1 | Symbols: GHS1 | Ribosomal protein S21 family protein | chr3:10017531-10018854 FORWARD LENGTH=183	190	183	3.00E-70	96.3	86.3	90.0
Rsa1.0_00748.1.g18972.t1	ref|NP_189346.2| enhancer of yellow 2 transcription factor [Arabidopsis thaliana] gi|37202032|gb|AAQ89631.1| At3g27100 [Arabidopsis thaliana] gi|51969380|dbj|BAD43382.1| hypothetical protein [Arabidopsis thaliana] gi|332643745|gb|AEE77266.1| enhancer of yellow 2 transcription factor [Arabidopsis thaliana]	139	115	1.00E-46	82.7	69.8	74.8	enhancer of yellow 2 transcription factor	gbpln	Arabidopsis thaliana	AT3G27100.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Transcription factor, enhancer of yellow 2 (InterPro:IPR018783); Has 288 Blast hits to 288 proteins in 94 species: Archae - 0; Bacteria - 0; Metazoa - 197; Fungi - 20; Plants - 51; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink). | chr3:9994743-9995923 REVERSE LENGTH=115	139	115	3.00E-49	82.7	69.8	74.8

Rsa1.0_00749.1.g18973.t1	ref|NP_188169.1| NAC domain-containing protein 55 [Arabidopsis thaliana] gi|75273159|sp|Q9LDY8.1|NAC55_ARATH RecName: Full=NAC domain-containing protein 55; Short=ANAC055; AltName: Full=NAC domain-containing protein 3; Short=AtNAC3 gi|7021735|gb|AAF35416.1| putative jasmonic acid regulatory protein [Arabidopsis thaliana] gi|12060424|dbj|BAB20599.1| AtNAC3 [Arabidopsis thaliana] gi|15795115|dbj|BAB02379.1| jasmonic acid regulatory protein-like [Arabidopsis thaliana] gi|105830298|gb|ABF74720.1| At3g15500 [Arabidopsis thaliana] gi|332642162|gb|AEE75683.1| NAC domain-containing protein 55 [Arabidopsis thaliana]	317	317	1.00E-140	100.0	81.7	86.4	NAC domain-containing protein 55	gbpln	Arabidopsis thaliana	AT3G15500.1 | Symbols: ATNAC3, ANAC055, NAC055, NAC3 | NAC domain containing protein 3 | chr3:5234731-5235882 FORWARD LENGTH=317	317	317	1.00E-142	100.0	81.7	86.4
Rsa1.0_00749.1.g18974.t1	ref|XP_002882945.1| hypothetical protein ARALYDRAFT_318329 [Arabidopsis lyrata subsp. lyrata] gi|297328785|gb|EFH59204.1| hypothetical protein ARALYDRAFT_318329 [Arabidopsis lyrata subsp. lyrata]	273	271	2.00E-79	99.3	57.1	71.1	hypothetical protein ARALYDRAFT_318329	gbpln	Arabidopsis lyrata	AT3G15490.1 | Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr3:5229785-5230646 FORWARD LENGTH=211	273	211	4.00E-58	77.3	43.2	55.7
Rsa1.0_00749.1.g18975.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00749.1.g18976.t1	gb|EOA32735.1| hypothetical protein CARUB_v10016040mg [Capsella rubella]	317	317	1.00E-174	100.0	92.1	96.2	hypothetical protein CARUB_v10016040mg	gbpln	Capsella rubella	AT3G15460.1 | Symbols: | Ribosomal RNA processing Brix domain protein | chr3:5214279-5216188 REVERSE LENGTH=315	317	315	1.00E-169	99.4	89.3	93.1
Rsa1.0_00749.1.g18977.t1	gb|EOA31283.1| hypothetical protein CARUB_v10014455mg [Capsella rubella]	246	253	1.00E-105	102.8	78.9	86.2	hypothetical protein CARUB_v10014455mg	gbpln	Capsella rubella	AT3G15450.1 | Symbols: | Aluminium induced protein with YGL and LRDR motifs | chr3:5213050-5213998 FORWARD LENGTH=253	246	253	1.00E-107	102.8	77.6	86.2
Rsa1.0_00749.1.g18978.t1	ref|XP_002882943.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] gi|297328783|gb|EFH59202.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	491	488	0	99.4	88.4	93.7	regulator of chromosome condensation family protein	gbpln	Arabidopsis lyrata	AT3G15430.2 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:5209408-5211562 FORWARD LENGTH=488	491	488	0	99.4	88.6	93.5
Rsa1.0_00749.1.g18979.t1	gb|AEJ33660.1| ATA20 [Brassica napus]	421	462	6.00E-85	109.7	40.9	42.5	ATA20	gbpln	Brassica napus	AT3G15400.1 | Symbols: ATA20 | anther 20 | chr3:5201678-5202928 FORWARD LENGTH=416	421	416	1.00E-38	98.8	21.4	23.5
Rsa1.0_00749.1.g18980.t2	ref|NP_188158.4| protein silencing defective 5 [Arabidopsis thaliana] gi|15795104|dbj|BAB02368.1| unnamed protein product [Arabidopsis thaliana] gi|332642141|gb|AEE75662.1| protein silencing defective 5 [Arabidopsis thaliana]	503	490	0	97.4	71.0	81.3	protein silencing defective 5	gbpln	Arabidopsis thaliana	AT3G15390.1 | Symbols: SDE5 | silencing defective 5 | chr3:5196689-5199531 REVERSE LENGTH=490	503	490	0	97.4	71.0	81.3
Rsa1.0_00749.1.g18981.t1	ref|XP_002882934.1| ubiquitin-conjugating enzyme 23 [Arabidopsis lyrata subsp. lyrata] gi|297328774|gb|EFH59193.1| ubiquitin-conjugating enzyme 23 [Arabidopsis lyrata subsp. lyrata]	591	605	0	102.4	66.2	75.6	ubiquitin-conjugating enzyme 23	gbpln	Arabidopsis lyrata	AT3G15355.1 | Symbols: UBC25, PFU1 | ubiquitin-conjugating enzyme 25 | chr3:5183858-5186669 FORWARD LENGTH=609	591	609	0	103.0	63.8	72.6
Rsa1.0_00749.1.g18982.t1	dbj|BAC42437.1| putative ubiquitin-conjugating enzyme [Arabidopsis thaliana] gi|29028948|gb|AAO64853.1| At1g53020 [Arabidopsis thaliana]	428	543	1.00E-162	126.9	72.0	82.5	putative ubiquitin-conjugating enzyme	gbpln	Arabidopsis thaliana	AT1G53025.1 | Symbols: | Ubiquitin-conjugating enzyme family protein | chr1:19757072-19759474 REVERSE LENGTH=543	428	543	1.00E-164	126.9	72.0	82.5
Rsa1.0_00749.1.g18983.t1	ref|XP_002882932.1| hypothetical protein ARALYDRAFT_897817 [Arabidopsis lyrata subsp. lyrata] gi|297328772|gb|EFH59191.1| hypothetical protein ARALYDRAFT_897817 [Arabidopsis lyrata subsp. lyrata]	144	144	1.00E-74	100.0	93.8	97.9	hypothetical protein ARALYDRAFT_897817	gbpln	Arabidopsis lyrata	AT3G15358.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53035.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:5178205-5178639 FORWARD LENGTH=144	144	144	2.00E-76	100.0	93.8	97.9

Rsa1.0_00749.1.g18984.t1	gb|AAO22669.1| unknown protein [Arabidopsis thaliana]	170	165	7.00E-72	97.1	76.5	85.3	unknown protein	gbpln	Arabidopsis thaliana	AT3G15351.1 | Symbols: | unknown protein; Has 50 Blast hits to 50 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5176726-5177531 FORWARD LENGTH=165	170	165	3.00E-74	97.1	76.5	85.3
Rsa1.0_00749.1.g18985.t2	dbj|BAJ33836.1| unnamed protein product [Thellungiella halophila]	583	424	0	72.7	61.9	65.7	unnamed protein product	----	----	AT3G15350.2 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr3:5167250-5168882 FORWARD LENGTH=424	583	424	0	72.7	59.3	64.5
Rsa1.0_00749.1.g18986.t1	dbj|BAB02162.1| unnamed protein product [Arabidopsis thaliana]	294	288	5.00E-92	98.0	59.2	69.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT2G04930.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:1733638-1734471 REVERSE LENGTH=277	294	277	6.00E-75	94.2	48.6	62.9
Rsa1.0_00749.1.g18987.t1	ref|XP_002882925.1| hypothetical protein ARALYDRAFT_897805 [Arabidopsis lyrata subsp. lyrata] gi|297328765|gb|EFH59184.1| hypothetical protein ARALYDRAFT_897805 [Arabidopsis lyrata subsp. lyrata]	155	166	5.00E-69	107.1	83.9	91.0	hypothetical protein ARALYDRAFT_897805	gbpln	Arabidopsis lyrata	AT1G53130.1 | Symbols: GRI | Stigma-specific Stig1 family protein | chr1:19794947-19795453 REVERSE LENGTH=168	155	168	3.00E-65	108.4	74.2	88.4
Rsa1.0_00749.1.g18988.t1	ref|NP_188148.1| VQ motif-containing protein [Arabidopsis thaliana] gi|9294257|dbj|BAB02159.1| unnamed protein product [Arabidopsis thaliana] gi|38454098|gb|AAR20743.1| At3g15300 [Arabidopsis thaliana] gi|41349916|gb|AAS00343.1| At3g15300 [Arabidopsis thaliana] gi|332642121|gb|AEE75642.1| VQ motif-containing protein [Arabidopsis thaliana]	227	219	7.00E-81	96.5	80.2	85.9	VQ motif-containing protein	gbpln	Arabidopsis thaliana	AT3G15300.1 | Symbols: | VQ motif-containing protein | chr3:5147551-5148210 REVERSE LENGTH=219	227	219	2.00E-83	96.5	80.2	85.9
Rsa1.0_00749.1.g18989.t1	ref|NP_566504.1| uncharacterized protein [Arabidopsis thaliana] gi|9294255|dbj|BAB02157.1| unnamed protein product [Arabidopsis thaliana] gi|16974611|gb|AAL31208.1| AT3g15280/K7L4_8 [Arabidopsis thaliana] gi|21928105|gb|AAM78081.1| AT3g15280/K7L4_8 [Arabidopsis thaliana] gi|332642119|gb|AEE75640.1| uncharacterized protein AT3G15280 [Arabidopsis thaliana]	120	150	5.00E-12	125.0	31.7	33.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15280.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: L mature pollen stage, 4 anthesis, petal differentiation and expansion stage; Has 36 Blast hits to 36 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 2; Plants - 33; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5144144-5144670 REVERSE LENGTH=150	120	150	9.00E-15	125.0	31.7	33.3
Rsa1.0_00750.1.g18990.t1	ref|XP_002891530.1| phospholipase C [Arabidopsis lyrata subsp. lyrata] gi|297337372|gb|EFH67789.1| phospholipase C [Arabidopsis lyrata subsp. lyrata]	358	359	0	100.3	84.9	89.4	phospholipase C	gbpln	Arabidopsis lyrata	AT1G49740.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr1:18407728-18409468 FORWARD LENGTH=359	358	359	0	100.3	84.6	89.4
Rsa1.0_00750.1.g18991.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00750.1.g18992.t1	ref|XP_002891531.1| PAB8 binding protein 8 [Arabidopsis lyrata subsp. lyrata] gi|297337373|gb|EFH67790.1| PAB8 binding protein 8 [Arabidopsis lyrata subsp. lyrata]	654	669	0	102.3	89.9	93.9	PAB8 binding protein 8	gbpln	Arabidopsis lyrata	AT1G49760.2 | Symbols: PAB8 | poly(A) binding protein 8 | chr1:18416740-18419753 FORWARD LENGTH=671	654	671	0	102.6	88.8	93.0
Rsa1.0_00750.1.g18993.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00750.1.g18994.t1	gb|EOA39304.1| hypothetical protein CARUB_v10012321mg [Capsella rubella]	210	180	1.00E-21	85.7	38.1	47.1	hypothetical protein CARUB_v10012321mg	gbpln	Capsella rubella	AT1G49420.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:18287859-18288650 REVERSE LENGTH=189	210	189	7.00E-24	90.0	25.7	30.0
Rsa1.0_00750.1.g18995.t1	gb|EOA32409.1| hypothetical protein CARUB_v10015681mg [Capsella rubella]	135	131	3.00E-42	97.0	64.4	74.1	hypothetical protein CARUB_v10015681mg	gbpln	Capsella rubella	AT3G03410.1 | Symbols: | EF hand calcium-binding protein family | chr3:811324-811719 REVERSE LENGTH=131	135	131	2.00E-41	97.0	60.0	71.9
Rsa1.0_00750.1.g18996.t1	dbj|BAA77394.1| SAE1-S9-protein [Brassica rapa]	150	255	5.00E-23	170.0	36.7	45.3	SAE1-S9-protein	gbpln	Brassica rapa	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	150	295	7.00E-25	196.7	39.3	54.7
Rsa1.0_00750.1.g18997.t1	gb|AAC32803.2| phosphatidylinositol 4-kinase [Arabidopsis thaliana]	2015	2028	0	100.6	94.1	97.3	phosphatidylinositol 4-kinase	gbpln	Arabidopsis thaliana	AT1G49340.1 | Symbols: ATPI4K ALPHA | Phosphatidylinositol 3- and 4-kinase family protein | chr1:18252355-18263967 FORWARD LENGTH=2028	2015	2028	0	100.6	94.1	97.3
Rsa1.0_00750.1.g18998.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00750.1.g18999.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	502	1529	1.00E-165	304.6	57.4	72.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	502	746	4.00E-87	148.6	34.9	43.8

<table>
<tr><td>Rsa1.0_00750.1.g19000.t1</td><td>gb|ACO54862.1| BURP domain protein [Brassica napus] gi|226427147|gb|ACO54863.1| BURP domain protein [Brassica napus]</td><td>279</td><td>281</td><td>1.00E−140</td><td>100.7</td><td>86.0</td><td>91.8</td><td>BURP domain protein</td><td>gbpln</td><td>Brassica napus</td><td>AT1G49320.1 | Symbols: ATUSPL1, USPL1 | unknown seed protein like 1 | chr1:18246441−18247817 FORWARD LENGTH=280</td><td>279</td><td>280</td><td>1.00E−134</td><td>100.4</td><td>78.1</td><td>89.6</td></tr>
<tr><td>Rsa1.0_00751.1.g19001.t2</td><td>emb|CAB91581.1| putative protein [Arabidopsis thaliana]</td><td>2087</td><td>1752</td><td>0</td><td>83.9</td><td>43.8</td><td>54.8</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G52950.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:19725483−19728007 FORWARD LENGTH=566</td><td>2087</td><td>566</td><td>1.00E−83</td><td>27.1</td><td>8.8</td><td>14.9</td></tr>
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<tr><td>Rsa1.0_00751.1.g19003.t1</td><td>ref|NP_188868.2| Endoplasmic reticulum vesicle transporter protein [Arabidopsis thaliana] gi|13877821|gb|AAK43988.1|AF370173_1 unknown protein [Arabidopsis thaliana] gi|51969000|dbj|BAD43192.1| unknown protein [Arabidopsis thaliana] gi|51970108|dbj|BAD43746.1| unknown protein [Arabidopsis thaliana] gi|51970556|dbj|BAD43970.1| unknown protein [Arabidopsis thaliana] gi|51970734|dbj|BAD44059.1| unknown protein [Arabidopsis thaliana] gi|62319967|dbj|BAD94071.1| hypothetical protein [Arabidopsis thaliana] gi|332643097|gb|AEE76618.1| Endoplasmic reticulum vesicle transporter protein [Arabidopsis thaliana]</td><td>353</td><td>354</td><td>0</td><td>100.3</td><td>94.6</td><td>97.2</td><td>Endoplasmic reticulum vesicle transporter protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G22290.1 | Symbols: | Endoplasmic reticulum vesicle transporter protein | chr3:7882082−7885260 FORWARD LENGTH=354</td><td>353</td><td>354</td><td>0</td><td>100.3</td><td>94.6</td><td>97.2</td></tr>
<tr><td>Rsa1.0_00751.1.g19004.t1</td><td>ref|XP_002885498.1| ATRPABC24.3 [Arabidopsis lyrata subsp. lyrata] gi|297331338|gb|EFH61757.1| ATRPABC24.3 [Arabidopsis lyrata subsp. lyrata]</td><td>206</td><td>205</td><td>1.00E−110</td><td>99.5</td><td>94.7</td><td>97.6</td><td>ATRPABC24.3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G22320.1 | Symbols: ATRPABC24.3, RPB5A, NRPB5, NRPD5 | Eukaryotic rpb5 RNA polymerase subunit family protein | chr3:7891045−7892094 REVERSE LENGTH=205</td><td>206</td><td>205</td><td>1.00E−112</td><td>99.5</td><td>93.7</td><td>98.1</td></tr>
<tr><td>Rsa1.0_00751.1.g19005.t1</td><td>gb|AEB00555.1| mitochondrial alternative oxidase 1a [Brassica juncea]</td><td>342</td><td>360</td><td>1.00E−176</td><td>105.3</td><td>90.6</td><td>94.4</td><td>mitochondrial alternative oxidase 1a</td><td>gbpln</td><td>Brassica juncea</td><td>AT3G22370.1 | Symbols: AOX1A, ATAOX1A | alternative oxidase 1A | chr3:7906890−7908416 FORWARD LENGTH=354</td><td>342</td><td>354</td><td>1.00E−171</td><td>103.5</td><td>86.5</td><td>92.4</td></tr>
<tr><td>Rsa1.0_00751.1.g19006.t1</td><td>ref|XP_002883360.1| time for coffee [Arabidopsis lyrata subsp. lyrata] gi|297329200|gb|EFH59619.1| time for coffee [Arabidopsis lyrata subsp. lyrata]</td><td>1281</td><td>1550</td><td>0</td><td>121.0</td><td>42.2</td><td>46.4</td><td>time for coffee</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G22380.2 | Symbols: TIC | time for coffee | chr3:7913181−7918967 FORWARD LENGTH=1555</td><td>1281</td><td>1555</td><td>0</td><td>121.4</td><td>42.6</td><td>47.2</td></tr>
<tr><td>Rsa1.0_00752.1.g19007.t1</td><td>ref|XP_002879526.1| hypothetical protein ARALYDRAFT_321210 [Arabidopsis lyrata subsp. lyrata] gi|297325365|gb|EFH55785.1| hypothetical protein ARALYDRAFT_321210 [Arabidopsis lyrata subsp. lyrata]</td><td>642</td><td>619</td><td>0</td><td>96.4</td><td>80.2</td><td>86.8</td><td>hypothetical protein ARALYDRAFT_321210</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G34940.1 | Symbols: VSR5, VSR3;2, BP80−3;2 | VACUOLAR SORTING RECEPTOR 5 | chr2:14740497−14743314 FORWARD LENGTH=618</td><td>642</td><td>618</td><td>0</td><td>96.3</td><td>78.3</td><td>86.1</td></tr>
<tr><td>Rsa1.0_00752.1.g19008.t1</td><td>ref|NP_181041.1| cationic amino acid transporter 5 [Arabidopsis thaliana] gi|75278307|sp|O64759.1|CAAT5_ARATH RecName: Full=Cationic amino acid transporter 5 gi|3033391|gb|AAC12835.1| putative amino acid transporter [Arabidopsis thaliana] gi|330253949|gb|AEC09043.1| cationic amino acid transporter 5 [Arabidopsis thaliana]</td><td>572</td><td>569</td><td>0</td><td>99.5</td><td>90.2</td><td>94.2</td><td>cationic amino acid transporter 5</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34960.1 | Symbols: CAT5 | cationic amino acid transporter 5 | chr2:14744175−14745884 REVERSE LENGTH=569</td><td>572</td><td>569</td><td>0</td><td>99.5</td><td>90.2</td><td>94.2</td></tr>
<tr><td>Rsa1.0_00752.1.g19009.t1</td><td>ref|NP_181046.1| thioredoxin O1 [Arabidopsis thaliana] gi|145330362|ref|NP_001078006.1| thioredoxin O1 [Arabidopsis thaliana] gi|75099186|sp|O64764.1|TRXO1_ARATH RecName: Full=Thioredoxin O1, mitochondrial; Short=AtTrxo1; Flags: Precursor gi|3033396|gb|AAC12840.1| putative thioredoxin [Arabidopsis thaliana] gi|107738216|gb|ABF83663.1| At2g35010 [Arabidopsis thaliana] gi|330253954|gb|AEC09048.1| thioredoxin O1 [Arabidopsis thaliana] gi|330253955|gb|AEC09049.1| thioredoxin O1 [Arabidopsis thaliana]</td><td>194</td><td>194</td><td>3.00E−74</td><td>100.0</td><td>73.2</td><td>84.5</td><td>thioredoxin O1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G35010.2 | Symbols: ATO1, TO1 | thioredoxin O1 | chr2:14754398−14755888 FORWARD LENGTH=194</td><td>194</td><td>194</td><td>1.00E−76</td><td>100.0</td><td>73.2</td><td>84.5</td></tr>
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<tr><td>Rsa1.0_00752.1.g19011.t1</td><td>ref|XP_002879531.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325370|gb|EFH55790.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>1255</td><td>1254</td><td>0</td><td>99.9</td><td>80.9</td><td>87.9</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G35050.1 | Symbols: | Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain | chr2:14769708−14774796 FORWARD LENGTH=1257</td><td>1255</td><td>1257</td><td>0</td><td>100.2</td><td>80.7</td><td>87.3</td></tr>
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Rsa1.0_00752.1.g19012.t1	gb|EOA37473.1| hypothetical protein CARUB_v10011614mg, partial [Capsella rubella]	113	287	6.00E-19	254.0	38.1	46.0	hypothetical protein CARUB_v10011614mg, partial	gbpln	Capsella rubella	AT4G19970.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nucleotide-diphospho-sugar transferase, predicted (InterPro:IPR005069); BEST Arabidopsis thaliana protein match is: Nucleotide-diphospho-sugar transferase family protein (TAIR:AT5G44820.1); Has 801 Blast hits to 466 proteins in 35 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 750; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink). | chr4:10818242-10825343 FORWARD LENGTH=715	113	715	8.00E-18	632.7	32.7	41.6
Rsa1.0_00752.1.g19013.t1	gb|EMJ11865.1| hypothetical protein PRUPE_ppa022462mg [Prunus persica]	259	606	5.00E-38	234.0	30.9	44.8	hypothetical protein PRUPE_ppa022462mg	gbpln	Prunus persica	#	#	#	#	#	#	#
Rsa1.0_00752.1.g19014.t1	ref|XP_002881376.1| hypothetical protein ARALYDRAFT_482477 [Arabidopsis lyrata subsp. lyrata] gi|297327215|gb|EFH57635.1| hypothetical protein ARALYDRAFT_482477 [Arabidopsis lyrata subsp. lyrata]	179	156	3.00E-61	87.2	65.9	69.3	hypothetical protein ARALYDRAFT_482477	gbpln	Arabidopsis lyrata	AT2G35120.1 | Symbols: | Single hybrid motif superfamily protein | chr2:14805913-14807274 REVERSE LENGTH=156	179	156	4.00E-63	87.2	65.4	68.7
Rsa1.0_00752.1.g19015.t1	gb|EOA27710.1| hypothetical protein CARUB_v10023864mg [Capsella rubella]	264	263	1.00E-134	99.6	95.5	98.9	hypothetical protein CARUB_v10023864mg	gbpln	Capsella rubella	AT2G35190.1 | Symbols: NPSN11, ATNPSN11, NSPN11 | novel plant snare 11 | chr2:14831087-14832979 FORWARD LENGTH=265	264	265	1.00E-135	100.4	95.5	98.9
Rsa1.0_00752.1.g19016.t1	ref|XP_002879538.1| AGD10/MEE28 [Arabidopsis lyrata subsp. lyrata] gi|297325377|gb|EFH55797.1| AGD10/MEE28 [Arabidopsis lyrata subsp. lyrata]	397	399	1.00E-170	100.5	82.4	88.7	AGD10/MEE28	gbpln	Arabidopsis lyrata	AT2G35210.1 | Symbols: RPA, AGD10, MEE28 | root and pollen arfgap | chr2:14836206-14837946 FORWARD LENGTH=395	397	395	1.00E-171	99.5	81.6	87.7
Rsa1.0_00752.1.g19017.t1	ref|XP_002879539.1| hypothetical protein ARALYDRAFT_902620 [Arabidopsis lyrata subsp. lyrata] gi|297325378|gb|EFH55798.1| hypothetical protein ARALYDRAFT_902620 [Arabidopsis lyrata subsp. lyrata]	100	106	4.00E-34	106.0	73.0	81.0	hypothetical protein ARALYDRAFT_902620	gbpln	Arabidopsis lyrata	AT2G35215.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G46770.1); Has 19 Blast hits to 19 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:14839296-14839616 FORWARD LENGTH=106	100	106	4.00E-36	106.0	70.0	82.0
Rsa1.0_00752.1.g19018.t1	ref|NP_181066.1| VQ motif-containing protein [Arabidopsis thaliana] gi|3668083|gb|AAC61815.1| hypothetical protein [Arabidopsis thaliana] gi|26449749|dbj|BAC41998.1| unknown protein [Arabidopsis thaliana] gi|32189295|gb|AAP75802.1| At2g35230 [Arabidopsis thaliana] gi|330253989|gb|AEC09083.1| VQ motif-containing protein [Arabidopsis thaliana]	358	402	1.00E-107	112.3	70.9	78.5	VQ motif-containing protein	gbpln	Arabidopsis thaliana	AT2G35230.1 | Symbols: IKU1 | VQ motif-containing protein | chr2:14842871-14844079 FORWARD LENGTH=402	358	402	1.00E-110	112.3	70.9	78.5
Rsa1.0_00752.1.g19019.t1	gb|EOA27681.1| hypothetical protein CARUB_v10023834mg, partial [Capsella rubella]	231	273	1.00E-109	118.2	84.8	91.3	hypothetical protein CARUB_v10023834mg, partial	gbpln	Capsella rubella	AT2G35240.1 | Symbols: | plastid developmental protein DAG, putative | chr2:14845099-14846262 REVERSE LENGTH=232	231	232	1.00E-108	100.4	83.1	89.6
Rsa1.0_00752.1.g19020.t1	ref|XP_002879544.1| hypothetical protein ARALYDRAFT_482492 [Arabidopsis lyrata subsp. lyrata] gi|297325383|gb|EFH55803.1| hypothetical protein ARALYDRAFT_482492 [Arabidopsis lyrata subsp. lyrata]	281	287	1.00E-111	102.1	90.4	94.7	hypothetical protein ARALYDRAFT_482492	gbpln	Arabidopsis lyrata	AT2G35270.1 | Symbols: GIK | Predicted AT-hook DNA-binding family protein | chr2:14857021-14857878 FORWARD LENGTH=285	281	285	1.00E-113	101.4	89.7	94.0
Rsa1.0_00752.1.g19021.t1	ref|XP_002881386.1| hypothetical protein ARALYDRAFT_482493 [Arabidopsis lyrata subsp. lyrata] gi|297327225|gb|EFH57645.1| hypothetical protein ARALYDRAFT_482493 [Arabidopsis lyrata subsp. lyrata]	122	121	8.00E-54	99.2	84.4	91.8	hypothetical protein ARALYDRAFT_482493	gbpln	Arabidopsis lyrata	AT2G35290.1 | Symbols: | unknown protein; Has 39 Blast hits to 39 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:14861635-14862000 REVERSE LENGTH=121	122	121	1.00E-55	99.2	82.8	90.2
Rsa1.0_00752.1.g19022.t1	ref|NP_181078.2| protein phosphatase 2C 29 [Arabidopsis thaliana] gi|158514812|sp|O82302.2|P2C29_ARATH RecName: Full=Protein phosphatase 2C 29; Short=AtPP2C29; AltName: Full=Protein POLTERGEIST-LIKE 1; AltName: Full=Protein phosphatase 2C PLL1; Short=PP2C PLL1 gi|330254004|gb|AEC09098.1| protein phosphatase 2C 29 [Arabidopsis thaliana]	750	783	0	104.4	84.1	89.5	protein phosphatase 2C 29	gbpln	Arabidopsis thaliana	AT2G35350.1 | Symbols: PLL1 | poltergeist like 1 | chr2:14881360-14884116 REVERSE LENGTH=783	750	783	0	104.4	84.1	89.5

<table>
<tr><td>Rsa1.0_00753.1.g19023.t1</td><td>gb|EOA21202.1| hypothetical protein CARUB_v10001549mg [Capsella rubella]</td><td>300</td><td>306</td><td>1.00E-135</td><td>102.0</td><td>86.7</td><td>90.7</td><td>hypothetical protein CARUB_v10001549mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G24490.1 | Symbols: | 30S ribosomal protein, putative | chr5:8365690-8367178 FORWARD LENGTH=308</td><td>300</td><td>308</td><td>1.00E-136</td><td>102.7</td><td>87.0</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00753.1.g19024.t1</td><td>gb|AFK38951.1| unknown [Lotus japonicus]</td><td>223</td><td>250</td><td>1.00E-24</td><td>112.1</td><td>30.5</td><td>49.8</td><td>unknown</td><td>gbpln</td><td>Lotus japonicus</td><td>AT5G43830.1 | Symbols: | Aluminium induced protein with YGL and LRDR motifs | chr5:17622593-17624239 REVERSE LENGTH=251</td><td>223</td><td>251</td><td>3.00E-24</td><td>112.6</td><td>30.5</td><td>48.0</td></tr>
<tr><td>Rsa1.0_00753.1.g19025.t4</td><td>gb|EOA26149.1| hypothetical protein CARUB_v10019585mg [Capsella rubella]</td><td>730</td><td>423</td><td>1.00E-124</td><td>57.9</td><td>35.1</td><td>41.5</td><td>hypothetical protein CARUB_v10019585mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G52680.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr3:19527075-19528838 FORWARD LENGTH=456</td><td>730</td><td>456</td><td>1.00E-106</td><td>62.5</td><td>31.8</td><td>39.7</td></tr>
<tr><td>Rsa1.0_00753.1.g19026.t1</td><td>pir||T00910 coproporphyrinogen oxidase (EC 1.3.3.3) F21B7.24 - Arabidopsis thaliana</td><td>128</td><td>362</td><td>3.00E-35</td><td>282.8</td><td>62.5</td><td>67.2</td><td>coproporphyrinogen oxidase (EC 1.3.3.3) F21B7.24 - Arabidopsis thaliana</td><td>----</td><td>----</td><td>AT1G03475.1 | Symbols: LIN2, HEMF1, ATCPO-I | Coproporphyrinogen III oxidase | chr1:869302-871175 REVERSE LENGTH=386</td><td>128</td><td>386</td><td>7.00E-38</td><td>301.6</td><td>62.5</td><td>67.2</td></tr>
<tr><td>Rsa1.0_00753.1.g19027.t2</td><td>gb|ADA58341.1| pseudo-response regulator 5a [Brassica rapa]</td><td>378</td><td>497</td><td>1.00E-113</td><td>131.5</td><td>60.8</td><td>63.0</td><td>pseudo-response regulator 5a</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G24470.1 | Symbols: APRR5, PRR5 | pseudo-response regulator 5 | chr5:8356204-8358873 REVERSE LENGTH=667</td><td>378</td><td>667</td><td>6.00E-83</td><td>176.5</td><td>38.6</td><td>40.7</td></tr>
<tr><td>Rsa1.0_00753.1.g19028.t1</td><td>ref|XP_002872115.1| hypothetical protein ARALYDRAFT_489310 [Arabidopsis lyrata subsp. lyrata] gi|297317952|gb|EFH48374.1| hypothetical protein ARALYDRAFT_489310 [Arabidopsis lyrata subsp. lyrata]</td><td>227</td><td>295</td><td>1.00E-102</td><td>130.0</td><td>87.7</td><td>93.8</td><td>hypothetical protein ARALYDRAFT_489310</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G24460.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8354815-8355717 FORWARD LENGTH=300</td><td>227</td><td>300</td><td>1.00E-101</td><td>132.2</td><td>85.0</td><td>93.0</td></tr>
<tr><td>Rsa1.0_00753.1.g19029.t2</td><td>gb|EOA19681.1| hypothetical protein CARUB_v10003348mg [Capsella rubella]</td><td>332</td><td>321</td><td>1.00E-112</td><td>96.7</td><td>63.9</td><td>74.1</td><td>hypothetical protein CARUB_v10003348mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G24440.1 | Symbols: CID13 | CTC-interacting domain 13 | chr5:8345402-8347776 REVERSE LENGTH=320</td><td>332</td><td>320</td><td>1.00E-110</td><td>96.4</td><td>63.0</td><td>73.8</td></tr>
<tr><td>Rsa1.0_00753.1.g19030.t1</td><td>ref|NP_190693.1| Senescence/dehydration-associated protein-like protein [Arabidopsis thaliana] gi|6562277|emb|CAB62647.1| putative protein [Arabidopsis thaliana] gi|15215688|gb|AAK91390.1| AT3g51250/F24M12_290 [Arabidopsis thaliana] gi|21464565|gb|AAM52237.1| AT3g51250/F24M12_290 [Arabidopsis thaliana] gi|332645247|gb|AEE78768.1| Senescence/dehydration-associated protein-like protein [Arabidopsis thaliana]</td><td>142</td><td>463</td><td>2.00E-45</td><td>326.1</td><td>67.6</td><td>72.5</td><td>Senescence/dehydration-associated protein-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G51250.1 | Symbols: | Senescence/dehydration-associated protein-related | chr3:19028227-19030442 FORWARD LENGTH=463</td><td>142</td><td>463</td><td>4.00E-48</td><td>326.1</td><td>67.6</td><td>72.5</td></tr>
<tr><td>Rsa1.0_00753.1.g19031.t3</td><td>ref|NP_197831.3| calcium dependent protein kinase-like protein [Arabidopsis thaliana] gi|75333922|sp|Q9FIM9.1|CAMK4_ARATH RecName: Full=CDPK-related kinase 4; Short=AtCRK4; AltName: Full=Calcium/calmodulin-dependent protein kinase CRK4 gi|10177904|dbj|BAB11236.1| calcium dependent protein kinase-like protein [Arabidopsis thaliana] gi|332005927|gb|AED93310.1| CDPK-related kinase 4 (AtCRK4) [Arabidopsis thaliana]</td><td>636</td><td>594</td><td>0</td><td>93.4</td><td>84.9</td><td>86.6</td><td>calcium dependent protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G24430.1 | Symbols: | Calcium-dependent protein kinase (CDPK) family protein | chr5:8339390-8342913 REVERSE LENGTH=594</td><td>636</td><td>594</td><td>0</td><td>93.4</td><td>84.9</td><td>86.6</td></tr>
<tr><td>Rsa1.0_00753.1.g19032.t1</td><td>ref|XP_002874195.1| EMB2024 [Arabidopsis lyrata subsp. lyrata] gi|297320032|gb|EFH50454.1| EMB2024 [Arabidopsis lyrata subsp. lyrata]</td><td>252</td><td>327</td><td>1.00E-124</td><td>129.8</td><td>86.5</td><td>94.4</td><td>EMB2024</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G24400.1 | Symbols: EMB2024, PGL3 | NagB/RpiA/CoA transferase-like superfamily protein | chr5:8330532-8331784 REVERSE LENGTH=325</td><td>252</td><td>325</td><td>1.00E-126</td><td>129.0</td><td>85.7</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00753.1.g19033.t1</td><td>ref|NP_001031936.1| O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana] gi|332005907|gb|AED93290.1| O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana]</td><td>509</td><td>458</td><td>0</td><td>90.0</td><td>69.2</td><td>77.2</td><td>O-Glycosyl hydrolases family 17 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G24318.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:8282285-8283956 REVERSE LENGTH=458</td><td>509</td><td>458</td><td>0</td><td>90.0</td><td>69.2</td><td>77.2</td></tr>
<tr><td>Rsa1.0_00753.1.g19034.t1</td><td>gb|EOA20023.1| hypothetical protein CARUB_v10000297mg [Capsella rubella]</td><td>969</td><td>749</td><td>0</td><td>77.3</td><td>66.3</td><td>71.2</td><td>hypothetical protein CARUB_v10000297mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G24260.1 | Symbols: | prolyl oligopeptidase family protein | chr5:8234865-8237810 REVERSE LENGTH=746</td><td>969</td><td>746</td><td>0</td><td>77.0</td><td>66.2</td><td>71.5</td></tr>
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Rsa1.0_00753.1.g19035.t13	ref|NP_193778.2| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|264664499|sp|C0LGQ7.1|Y4245_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g20450; Flags: Precursor gi|224589618|gb|ACN59342.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332658934|gb|AEE84334.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	884	898	0	101.6	61.2	75.0	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT4G20450.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:11024054-11029008 REVERSE LENGTH=898	884	898	0	101.6	61.2	75.0
Rsa1.0_00753.1.g19036.t1	ref|NP_197812.1| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana] gi|10177083|dbj|BAB10389.1| ubiquitin [Arabidopsis thaliana] gi|110741569|dbj|BAE98733.1| ubiquitin [Arabidopsis thaliana] gi|332005891|gb|AED93274.1| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana]	521	574	0	110.2	83.5	91.0	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	gbpln	Arabidopsis thaliana	AT5G24240.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase ;Ubiquitin family protein | chr5:8231110-8232925 REVERSE LENGTH=574	521	574	0	110.2	83.5	91.0
Rsa1.0_00753.1.g19037.t1	gb|EOA20957.1| hypothetical protein CARUB_v10001289mg [Capsella rubella]	337	353	2.00E-76	104.7	49.3	63.8	hypothetical protein CARUB_v10001289mg	gbpln	Capsella rubella	AT5G24220.1 | Symbols: | Lipase class 3-related protein | chr5:8225861-8227551 FORWARD LENGTH=376	337	376	3.00E-75	111.6	46.0	64.4
Rsa1.0_00754.1.g19038.t1	ref|XP_002880752.1| hypothetical protein ARALYDRAFT_901326 [Arabidopsis lyrata subsp. lyrata] gi|297326591|gb|EFH57011.1| hypothetical protein ARALYDRAFT_901326 [Arabidopsis lyrata subsp. lyrata]	250	378	5.00E-77	151.2	61.6	74.8	hypothetical protein ARALYDRAFT_901326	gbpln	Arabidopsis lyrata	AT1G64840.1 | Symbols: | Protein of unknown function (DUF295) | chr1:24094010-24095164 FORWARD LENGTH=384	250	384	3.00E-70	153.6	57.2	70.8
Rsa1.0_00754.1.g19039.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00754.1.g19040.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00754.1.g19041.t1	ref|XP_002880759.1| hypothetical protein ARALYDRAFT_901333 [Arabidopsis lyrata subsp. lyrata] gi|297326598|gb|EFH57018.1| hypothetical protein ARALYDRAFT_901333 [Arabidopsis lyrata subsp. lyrata]	396	529	1.00E-121	133.6	62.4	73.2	hypothetical protein ARALYDRAFT_901333	gbpln	Arabidopsis lyrata	AT1G64840.1 | Symbols: | Protein of unknown function (DUF295) | chr1:24094010-24095164 FORWARD LENGTH=384	396	384	1.00E-100	97.0	52.0	64.6
Rsa1.0_00754.1.g19042.t3	ref|XP_002880759.1| hypothetical protein ARALYDRAFT_901333 [Arabidopsis lyrata subsp. lyrata] gi|297326598|gb|EFH57018.1| hypothetical protein ARALYDRAFT_901333 [Arabidopsis lyrata subsp. lyrata]	972	529	1.00E-124	54.4	25.1	30.0	hypothetical protein ARALYDRAFT_901333	gbpln	Arabidopsis lyrata	AT1G64840.1 | Symbols: | Protein of unknown function (DUF295) | chr1:24094010-24095164 FORWARD LENGTH=384	972	384	1.00E-105	39.5	22.1	27.5
Rsa1.0_00754.1.g19043.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00754.1.g19044.t1	ref|XP_002880759.1| hypothetical protein ARALYDRAFT_901333 [Arabidopsis lyrata subsp. lyrata] gi|297326598|gb|EFH57018.1| hypothetical protein ARALYDRAFT_901333 [Arabidopsis lyrata subsp. lyrata]	399	529	1.00E-118	132.6	61.4	72.4	hypothetical protein ARALYDRAFT_901333	gbpln	Arabidopsis lyrata	AT1G64840.1 | Symbols: | Protein of unknown function (DUF295) | chr1:24094010-24095164 FORWARD LENGTH=384	399	384	2.00E-96	96.2	51.6	64.2
Rsa1.0_00754.1.g19045.t1	gb|EOA28645.1| hypothetical protein CARUB_v10024867mg [Capsella rubella]	275	346	3.00E-53	125.8	50.5	66.2	hypothetical protein CARUB_v10024867mg	gbpln	Capsella rubella	AT1G64840.1 | Symbols: | Protein of unknown function (DUF295) | chr1:24094010-24095164 FORWARD LENGTH=384	275	384	4.00E-33	139.6	30.5	36.0
Rsa1.0_00754.1.g19046.t1	gb|EOA28454.1| hypothetical protein CARUB_v10024663mg [Capsella rubella]	88	933	2.00E-24	1060.2	64.8	68.2	hypothetical protein CARUB_v10024663mg	gbpln	Capsella rubella	AT2G24720.1 | Symbols: ATGLR2.2, GLR2.2 | glutamate receptor 2.2 | chr2:10522783-10525840 REVERSE LENGTH=920	88	920	5.00E-23	1045.5	54.5	63.6
Rsa1.0_00754.1.g19047.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00754.1.g19048.t1	gb|EOA28454.1| hypothetical protein CARUB_v10024663mg [Capsella rubella]	806	933	0	115.8	81.1	90.0	hypothetical protein CARUB_v10024663mg	gbpln	Capsella rubella	AT2G24720.1 | Symbols: ATGLR2.2, GLR2.2 | glutamate receptor 2.2 | chr2:10522783-10525840 REVERSE LENGTH=920	806	920	0	114.1	75.2	87.0
Rsa1.0_00754.1.g19049.t7	sp|Q96361.3|ARF1_BRARP RecName: Full=ADP-ribosylation factor 1 gi|1654142|gb|AAB17725.1| small GTP-binding protein ARF [Brassica rapa subsp. oleifera] gi|482563782|gb|EOA27972.1| hypothetical protein CARUB_v10024146mg [Capsella rubella]	374	182	5.00E-96	48.7	46.3	46.3	RecName: Full=ADP-ribosylation factor 1 gi|1654142|gb|AAB17725.1| small GTP-binding protein ARF	gbpln	Brassica rapa	AT2G24765.1 | Symbols: ARF3, ARL1, ATARL1 | ADP-ribosylation factor 3 | chr2:10562822-10564961 FORWARD LENGTH=182	374	182	4.00E-98	48.7	46.0	46.3

Rsa1.0_00754.1.g19050.t1	gb|AAC35496.1| CONSTANS-like 1 protein [Raphanus sativus]	307	307	1.00E-179	100.0	99.3	99.7	CONSTANS-like 1 protein	gbpln	Raphanus sativus	AT2G24790.1 | Symbols: COL3, ATCOL3 | CONSTANS-like 3 | chr2:10566959-10567946 FORWARD LENGTH=294	307	294	1.00E-115	95.8	72.3	79.5
Rsa1.0_00754.1.g19051.t1	ref|XP_002890900.1| hypothetical protein ARALYDRAFT_473311 [Arabidopsis lyrata subsp. lyrata] gi|297336742|gb|EFH67159.1| hypothetical protein ARALYDRAFT_473311 [Arabidopsis lyrata subsp. lyrata]	221	235	1.00E-72	106.3	70.1	81.9	hypothetical protein ARALYDRAFT_473311	gbpln	Arabidopsis lyrata	AT1G30800.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr1:10936995-10937714 FORWARD LENGTH=239	221	239	2.00E-68	108.1	68.8	79.6
Rsa1.0_00754.1.g19052.t1	ref|NP_001032158.1| NEP1-interacting protein-like 1 [Arabidopsis thaliana] gi|332010773|gb|AED98156.1| NEP1-interacting protein-like 1 [Arabidopsis thaliana]	83	245	7.00E-29	295.2	78.3	86.7	NEP1-interacting protein-like 1	gbpln	Arabidopsis thaliana	AT5G66070.2 | Symbols: | RING/U-box superfamily protein | chr5:26421923-26423033 FORWARD LENGTH=245	83	245	1.00E-31	295.2	78.3	86.7
Rsa1.0_00755.1.g19053.t1	gb|EOA15125.1| hypothetical protein CARUB_v10028500mg [Capsella rubella]	319	982	1.00E-152	307.8	84.3	91.2	hypothetical protein CARUB_v10028500mg	gbpln	Capsella rubella	AT5G57320.1 | Symbols: VLN5 | villin, putative | chr5:23212690-23217549 FORWARD LENGTH=962	319	962	1.00E-147	301.6	82.1	89.7
Rsa1.0_00755.1.g19054.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00755.1.g19055.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	404	657	1.00E-128	162.6	54.2	68.8	T14P8.10	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	404	746	3.00E-70	184.7	34.7	49.0
Rsa1.0_00755.1.g19056.t1	gb|EOA13587.1| hypothetical protein CARUB_v10026653mg [Capsella rubella]	346	361	1.00E-164	104.3	88.2	94.2	hypothetical protein CARUB_v10026653mg	gbpln	Capsella rubella	AT5G57660.1 | Symbols: ATCOL5, COL5 | CONSTANS-like 5 | chr5:23355573-23356729 FORWARD LENGTH=355	346	355	1.00E-160	102.6	84.7	93.1
Rsa1.0_00755.1.g19057.t1	ref|XP_002866222.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297312057|gb|EFH42481.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	579	569	0	98.3	87.2	91.7	ATP binding protein	gbpln	Arabidopsis lyrata	AT5G57670.2 | Symbols: | Protein kinase superfamily protein | chr5:23360531-23363694 REVERSE LENGTH=579	579	579	0	100.0	88.4	94.0
Rsa1.0_00755.1.g19058.t1	ref|XP_002866223.1| hypothetical protein ARALYDRAFT_495865 [Arabidopsis lyrata subsp. lyrata] gi|297312058|gb|EFH42482.1| hypothetical protein ARALYDRAFT_495865 [Arabidopsis lyrata subsp. lyrata]	123	148	5.00E-51	120.3	84.6	91.9	hypothetical protein ARALYDRAFT_495865	gbpln	Arabidopsis lyrata	AT5G57685.1 | Symbols: ATGDU3, GDU3, LSB1 | glutamine dumper 3 | chr5:23366356-23366802 REVERSE LENGTH=148	123	148	5.00E-51	120.3	82.1	90.2
Rsa1.0_00755.1.g19059.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00755.1.g19060.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1141	1223	0	107.2	53.4	70.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1141	746	1.00E-110	65.4	17.9	23.8
Rsa1.0_00755.1.g19061.t3	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00755.1.g19062.t2	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00755.1.g19063.t1	gb|AAZ66942.1| 117M18_23 [Brassica rapa]	119	518	2.00E-33	435.3	66.4	77.3	117M18_23	gbpln	Brassica rapa	AT5G44050.1 | Symbols: | MATE efflux family protein | chr5:17722484-17726209 FORWARD LENGTH=491	119	491	1.00E-33	412.6	63.0	75.6
Rsa1.0_00755.1.g19064.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00756.1.g19065.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00756.1.g19066.t12	gb|AAD25621.1|AC005287_23 Hypothetical protein [Arabidopsis thaliana]	599	1250	3.00E-42	208.7	16.5	22.7	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00756.1.g19067.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	1243	1356	0	109.1	48.5	66.8	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1243	1262	2.00E-64	101.5	12.5	20.0
Rsa1.0_00756.1.g19068.t1	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	161	1463	2.00E-20	908.7	36.6	52.2	F5J5.1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00756.1.g19069.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	387	1024	5.00E-38	264.6	24.8	30.2	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00756.1.g19070.t3	emb|CAN83506.1| hypothetical protein VITISV_027576 [Vitis vinifera]	911	1172	0	128.6	44.5	55.8	hypothetical protein VITISV_027576	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	911	1262	2.00E-72	138.5	14.7	22.2
Rsa1.0_00756.1.g19071.t1	gb|AAF98181.1|AC000107_4 F17F8.5 [Arabidopsis thaliana]	479	872	1.00E-129	182.0	51.4	68.9	F17F8.5	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	479	746	8.00E-55	155.7	25.1	34.4
Rsa1.0_00756.1.g19072.t1	dbj|BAE98403.1| putative non-LTR reverse transcriptase [Arabidopsis thaliana]	143	278	8.00E-28	194.4	39.9	62.9	putative non-LTR reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	143	320	4.00E-14	223.8	30.8	46.9

Rsa1.0_00756.1.g19073.t1	gb|ACQ90230.1| virus-resistance protein [Brassica rapa subsp. chinensis]	181	249	1.00E-100	137.6	95.0	97.2	virus-resistance protein	gbpln	Brassica rapa	AT5G38430.1 | Symbols: | Ribulose bisphosphate carboxylase (small chain) family protein | chr5:15384350-15385155 REVERSE LENGTH=181	181	181	3.00E-99	100.0	92.3	94.5
Rsa1.0_00756.1.g19074.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	618	1274	4.00E-80	206.1	29.6	44.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	618	575	8.00E-57	93.0	26.5	42.4
Rsa1.0_00756.1.g19075.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00757.1.g19076.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00757.1.g19077.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1768	1213	0	68.6	24.5	38.1	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1768	626	6.00E-62	35.4	7.5	12.2
Rsa1.0_00757.1.g19078.t1	ref|XP_002866375.1| APUM18 [Arabidopsis lyrata subsp. lyrata] gi|297312210|gb|EFH42634.1| APUM18 [Arabidopsis lyrata subsp. lyrata]	343	328	1.00E-79	95.6	49.0	61.2	APUM18	gbpln	Arabidopsis lyrata	AT1G21620.1 | Symbols: APUM20, PUM20 | pumilio 20 | chr1:7579129-7580171 FORWARD LENGTH=308	343	308	7.00E-76	89.8	49.3	59.2
Rsa1.0_00757.1.g19079.t1	ref|NP_190227.1| uncharacterized protein [Arabidopsis thaliana] gi|22327975|ref|NP_680457.1| uncharacterized protein [Arabidopsis thaliana] gi|334188494|ref|NP_001190570.1| uncharacterized protein [Arabidopsis thaliana] gi|297796915|ref|XP_002866342.1| hypothetical protein ARALYDRAFT_496097 [Arabidopsis lyrata subsp. lyrata] gi|297815794|ref|XP_002875780.1| hypothetical protein ARALYDRAFT_485014 [Arabidopsis lyrata subsp. lyrata] gi|6522622|emb|CAB62034.1| putative protein [Arabidopsis thaliana] gi|17065520|gb|AAL32914.1| Unknown protein [Arabidopsis thaliana] gi|17381284|gb|AAL36060.1| AT3g46430/F18L15_150 [Arabidopsis thaliana] gi|20148461|gb|AAM10121.1| unknown protein [Arabidopsis thaliana] gi|20453375|gb|AAM19926.1| AT3g46430/F18L15_150 [Arabidopsis thaliana] gi|26450436|dbj|BAC42332.1| unknown protein [Arabidopsis thaliana] gi|26451867|dbj|BAC43026.1| unknown protein [Arabidopsis thaliana] gi|297312177|gb|EFH42601.1| hypothetical protein ARALYDRAFT_496097 [Arabidopsis lyrata subsp. lyrata]	121	55	2.00E-15	45.5	33.1	35.5	uncharacterized protein	gbpln	Arabidopsis lyrata	AT5G59613.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrial respiratory chain complex III; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G46430.1). | chr5:24015726-24016500 REVERSE LENGTH=55	121	55	3.00E-18	45.5	33.1	35.5
Rsa1.0_00757.1.g19080.t1	gb|EOA12886.1| hypothetical protein CARUB_v10025859mg [Capsella rubella]	864	887	0	102.7	65.3	78.2	hypothetical protein CARUB_v10025859mg	gbpln	Capsella rubella	AT5G59670.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24041538-24045478 FORWARD LENGTH=868	864	868	0	100.5	65.6	76.6
Rsa1.0_00757.1.g19081.t1	gb|EOA12886.1| hypothetical protein CARUB_v10025859mg [Capsella rubella]	899	887	0	98.7	77.4	85.0	hypothetical protein CARUB_v10025859mg	gbpln	Capsella rubella	AT5G59680.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24046792-24050801 FORWARD LENGTH=887	899	887	0	98.7	76.4	83.4
Rsa1.0_00757.1.g19082.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_00757.1.g19083.t1	ref|XP_002864648.1| hypothetical protein ARALYDRAFT_496103 [Arabidopsis lyrata subsp. lyrata] gi|297310483|gb|EFH40907.1| hypothetical protein ARALYDRAFT_496103 [Arabidopsis lyrata subsp. lyrata]	608	615	0	101.2	87.8	95.1	hypothetical protein ARALYDRAFT_496103	gbpln	Arabidopsis lyrata	AT5G59710.1 | Symbols: VIP2, AtVIP2 | VIRE2 interacting protein 2 | chr5:24058157-24061736 FORWARD LENGTH=614	608	614	0	101.0	87.3	94.1

Rsa1.0_00757.1.g19084.t1	gb|AAF78436.1|AC018748_15 Contains similarity to 17.6 KD class I heat shock protein from Arabidopsis thaliana gi|P13853 and contains Hsp20/alpha crystallin PF|00011 and signal peptidase I PF|00461 domains. ESTs gb|AI998650, gb|AW004417, gb|AI998904 come from this gene [Arabidopsis thaliana]	152	403	9.00E−70	265.1	82.9	92.8	Contains similarity to 17.6 KD class I heat shock protein from Arabidopsis thaliana gi|P13853 and contains Hsp20/alpha crystallin PF|00011 and signal peptidase I PF|00461 domains. ESTs gb|AI998650, gb|AW004417, gb|AI998904 come from this gene	gbpln	Arabidopsis thaliana	AT5G59720.1 | Symbols: HSP18.2 | heat shock protein 18.2 | chr5:24062632−24063117 FORWARD LENGTH=161	152	161	1.00E−71	105.9	92.8	97.4
Rsa1.0_00757.1.g19085.t1	gb|EOA14941.1| hypothetical protein CARUB_v10028285mg [Capsella rubella]	612	637	0	104.1	74.2	83.3	hypothetical protein CARUB_v10028285mg	gbpln	Capsella rubella	AT5G59730.2 | Symbols: ATEXO70H7, EXO70H7 | exocyst subunit exo70 family protein H7 | chr5:24064096−24066004 REVERSE LENGTH=632	612	632	0	103.3	75.0	83.8
Rsa1.0_00757.1.g19086.t1	ref|XP_002866345.1| hypothetical protein ARALYDRAFT_332244 [Arabidopsis lyrata subsp. lyrata] gi|297312180|gb|EFH42604.1| hypothetical protein ARALYDRAFT_332244 [Arabidopsis lyrata subsp. lyrata]	322	344	1.00E−170	106.8	93.5	96.0	hypothetical protein ARALYDRAFT_332244	gbpln	Arabidopsis lyrata	AT5G59740.1 | Symbols: | UDP−N−acetylglucosamine (UAA) transporter family | chr5:24070310−24072747 REVERSE LENGTH=344	322	344	1.00E−172	106.8	94.1	95.7
Rsa1.0_00757.1.g19087.t3	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	182	255	1.00E−46	140.1	57.7	67.6	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483−17578391 REVERSE LENGTH=302	182	302	2.00E−39	165.9	46.2	61.0
Rsa1.0_00758.1.g19088.t1	gb|EOA15843.1| hypothetical protein CARUB_v10007508mg [Capsella rubella]	502	500	0	99.6	89.2	93.8	hypothetical protein CARUB_v10007508mg	gbpln	Capsella rubella	AT4G38500.1 | Symbols: | Protein of unknown function (DUF616) | chr4:18008418−18010693 FORWARD LENGTH=499	502	499	0	99.4	88.6	93.4
Rsa1.0_00758.1.g19089.t2	ref|NP_195564.2| putative protein phosphatase 2C 64 [Arabidopsis thaliana] gi|42573223|ref|NP_974708.1| putative protein phosphatase 2C 64 [Arabidopsis thaliana] gi|75251246|sp|Q5PNS9.1|P2C64_ARATH RecName: Full=Probable protein phosphatase 2C 64; Short=AtPP2C64 gi|56382009|gb|AAV85723.1| At4g38520 [Arabidopsis thaliana] gi|59958308|gb|AAX12864.1| At4g38520 [Arabidopsis thaliana] gi|332661541|gb|AEE86941.1| putative protein phosphatase 2C 64 [Arabidopsis thaliana] gi|332661542|gb|AEE86942.1| putative protein phosphatase 2C 64 [Arabidopsis thaliana]	389	400	0	102.8	85.9	91.0	putative protein phosphatase 2C 64	gbpln	Arabidopsis thaliana	AT4G38520.2 | Symbols: | Protein phosphatase 2C family protein | chr4:18015999−18017514 REVERSE LENGTH=400	389	400	0	102.8	85.9	91.0
Rsa1.0_00758.1.g19090.t1	ref|XP_002866805.1| ATPLC1 [Arabidopsis lyrata subsp. lyrata] gi|297312641|gb|EFH43064.1| ATPLC1 [Arabidopsis lyrata subsp. lyrata]	578	575	0	99.5	84.9	92.4	ATPLC1	gbpln	Arabidopsis lyrata	AT4G38530.1 | Symbols: ATPLC1, PLC1 | phospholipase C1 | chr4:18020708−18022898 FORWARD LENGTH=564	578	564	0	97.6	83.0	89.4
Rsa1.0_00758.1.g19091.t1	ref|XP_002866806.1| hypothetical protein ARALYDRAFT_490619 [Arabidopsis lyrata subsp. lyrata] gi|297312642|gb|EFH43065.1| hypothetical protein ARALYDRAFT_490619 [Arabidopsis lyrata subsp. lyrata]	402	404	0	100.5	85.1	92.3	hypothetical protein ARALYDRAFT_490619	gbpln	Arabidopsis lyrata	AT4G38540.1 | Symbols: | FAD/NAD(P)−binding oxidoreductase family protein | chr4:18023187−18024827 FORWARD LENGTH=407	402	407	0	101.2	85.6	92.5
Rsa1.0_00758.1.g19092.t1	ref|XP_002880351.1| hypothetical protein ARALYDRAFT_900506 [Arabidopsis lyrata subsp. lyrata] gi|297326190|gb|EFH56610.1| hypothetical protein ARALYDRAFT_900506 [Arabidopsis lyrata subsp. lyrata]	141	140	4.00E−65	99.3	86.5	92.9	hypothetical protein ARALYDRAFT_900506	gbpln	Arabidopsis lyrata	AT2G20930.1 | Symbols: | SNARE−like superfamily protein | chr2:9000790−9001656 REVERSE LENGTH=140	141	140	3.00E−67	99.3	85.8	92.9
Rsa1.0_00758.1.g19093.t2	emb|CAB64750.1| putative beta−galactosidase [Arabidopsis thaliana]	825	887	0	107.5	78.4	85.6	putative beta−galactosidase	gbpln	Arabidopsis thaliana	AT4G38590.1 | Symbols: BGAL14 | beta−galactosidase 14 | chr4:18036395−18040928 FORWARD LENGTH=988	825	988	0	119.8	78.2	85.3
Rsa1.0_00758.1.g19094.t1	gb|ABQ81932.1| transcription factor MYB4 [Brassica rapa subsp. chinensis] gi|326631152|gb|ADZ98868.1| MYB domain protein 12 [Brassica rapa subsp. rapa]	293	294	1.00E−156	100.3	95.2	96.6	transcription factor MYB4	gbpln	Brassica rapa	AT4G38620.1 | Symbols: ATMYB4, MYB4 | myb domain protein 4 | chr4:18053866−18054876 FORWARD LENGTH=282	293	282	1.00E−145	96.2	87.4	90.1
Rsa1.0_00758.1.g19095.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033−105622 [Arabidopsis thaliana]	1631	1557	0	95.5	41.6	55.7	reverse transcriptase, putative; 100033−105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1631	575	8.00E−77	35.3	9.3	13.8

<table>
<tr><td>Rsa1.0_00758.1.g19096.t1</td><td>ref|NP_195575.1| 26S proteasome non-ATPase regulatory subunit 4 [Arabidopsis thaliana] gi|1709794|sp|P55034.1|PSMD4_ARATH RecName: Full=26S proteasome non-ATPase regulatory subunit 4; AltName: Full=26S proteasome regulatory subunit RPN10; AltName: Full=26S proteasome regulatory subunit S5A; AltName: Full=Multiubiquitin chain-binding protein 1; Short=AtMCB1; AltName: Full=Protein REGULATORY PARTICLE NON-ATPASE 10 gi|13430814|gb|AAK26029.1|AF360319_1 putative multiubiquitin chain binding protein MBP1 [Arabidopsis thaliana] gi|1165206|gb|AAA85583.1| MBP1 [Arabidopsis thaliana] gi|4467150|emb|CAB37519.1| multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana] gi|7270846|emb|CAB80527.1| multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana] gi|21281020|gb|AAM44937.1| putative multiubiquitin chain binding protein MBP1 [Arabidopsis thaliana] gi|110735112|gb|ABG89126.1| RPN10 [synthetic construct] gi|332661556|gb|AEE86956.1| 26S proteasome non-ATPase regulatory subunit 4 [Arabidopsis thaliana]</td><td>385</td><td>386</td><td>0</td><td>100.3</td><td>94.8</td><td>97.9</td><td>26S proteasome non-ATPase regulatory subunit 4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G38630.1 | Symbols: RPN10, MCB1, ATMCB1, MBP1 | regulatory particle non-ATPase 10 | chr4:18057357-18059459 REVERSE LENGTH=386</td><td>385</td><td>386</td><td>0</td><td>100.3</td><td>94.8</td><td>97.9</td></tr>
<tr><td>Rsa1.0_00758.1.g19097.t1</td><td>gb|EOA15636.1| hypothetical protein CARUB_v10005879mg [Capsella rubella]</td><td>172</td><td>173</td><td>1.00E-87</td><td>100.6</td><td>91.9</td><td>95.9</td><td>hypothetical protein CARUB_v10005879mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G38740.1 | Symbols: ROC1 | rotamase CYP 1 | chr4:18083620-18084138 REVERSE LENGTH=172</td><td>172</td><td>172</td><td>3.00E-89</td><td>100.0</td><td>90.7</td><td>95.3</td></tr>
<tr><td>Rsa1.0_00758.1.g19098.t27</td><td>ref|NP_195587.5| uncharacterized protein [Arabidopsis thaliana] gi|332661571|gb|AEE86971.1| uncharacterized protein AT4G38760 [Arabidopsis thaliana]</td><td>1971</td><td>1965</td><td>0</td><td>99.7</td><td>81.8</td><td>89.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G38760.1 | Symbols: | Protein of unknown function (DUF3414) | chr4:18085033-18096166 REVERSE LENGTH=1965</td><td>1971</td><td>1965</td><td>0</td><td>99.7</td><td>81.8</td><td>89.9</td></tr>
<tr><td>Rsa1.0_00758.1.g19099.t1</td><td>gb|EOA17208.1| hypothetical protein CARUB_v10005480mg [Capsella rubella]</td><td>273</td><td>273</td><td>1.00E-152</td><td>100.0</td><td>96.3</td><td>98.5</td><td>hypothetical protein CARUB_v10005480mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G38790.1 | Symbols: | ER lumen protein retaining receptor family protein | chr4:18111426-18112977 FORWARD LENGTH=273</td><td>273</td><td>273</td><td>1.00E-151</td><td>100.0</td><td>94.5</td><td>96.3</td></tr>
<tr><td>Rsa1.0_00758.1.g19100.t1</td><td>ref|XP_002868864.1| ATMTN1 [Arabidopsis lyrata subsp. lyrata] gi|297314700|gb|EFH45123.1| ATMTN1 [Arabidopsis lyrata subsp. lyrata]</td><td>244</td><td>266</td><td>1.00E-107</td><td>109.0</td><td>82.8</td><td>88.5</td><td>ATMTN1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38800.1 | Symbols: ATMTN1, ATMTAN1, MTN1, MTAN1 | methylthioadenosine nucleosidase 1 | chr4:18113355-18114996 REVERSE LENGTH=267</td><td>244</td><td>267</td><td>1.00E-107</td><td>109.4</td><td>80.7</td><td>87.7</td></tr>
<tr><td>Rsa1.0_00758.1.g19101.t1</td><td>ref|XP_002868865.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297314701|gb|EFH45124.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]</td><td>378</td><td>373</td><td>0</td><td>98.7</td><td>91.0</td><td>94.4</td><td>calcium-binding EF hand family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38810.2 | Symbols: | Calcium-binding EF-hand family protein | chr4:18115607-18118860 REVERSE LENGTH=375</td><td>378</td><td>375</td><td>0</td><td>99.2</td><td>90.5</td><td>93.7</td></tr>
<tr><td>Rsa1.0_00758.1.g19102.t5</td><td>ref|NP_195594.1| cysteine-rich receptor-like protein kinase 26 [Arabidopsis thaliana] gi|75337951|sp|Q9T0J1.1|CRK26_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 26; Short=Cysteine-rich RLK26; Flags: Precursor gi|4490335|emb|CAB38617.1| receptor-like protein kinase-like protein [Arabidopsis thaliana] gi|7270866|emb|CAB80546.1| receptor-like protein kinase-like protein [Arabidopsis thaliana] gi|332661581|gb|AEE86981.1| cysteine-rich receptor-like protein kinase 26 [Arabidopsis thaliana]</td><td>658</td><td>665</td><td>0</td><td>101.1</td><td>84.3</td><td>91.6</td><td>cysteine-rich receptor-like protein kinase 26</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G38830.1 | Symbols: CRK26 | cysteine-rich RLK (RECEPTOR-like protein kinase) 26 | chr4:18122339-18124943 FORWARD LENGTH=665</td><td>658</td><td>665</td><td>0</td><td>101.1</td><td>84.3</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00758.1.g19103.t1</td><td>gb|EOA18006.1| hypothetical protein CARUB_v10006441mg [Capsella rubella]</td><td>99</td><td>98</td><td>5.00E-41</td><td>99.0</td><td>88.9</td><td>97.0</td><td>hypothetical protein CARUB_v10006441mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G38840.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:18125174-18125473 REVERSE LENGTH=99</td><td>99</td><td>99</td><td>3.00E-41</td><td>100.0</td><td>82.8</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00758.1.g19104.t1</td><td>ref|XP_002866819.1| SAUR_AC1 [Arabidopsis lyrata subsp. lyrata] gi|297312655|gb|EFH43078.1| SAUR_AC1 [Arabidopsis lyrata subsp. lyrata]</td><td>80</td><td>89</td><td>4.00E-33</td><td>111.3</td><td>85.0</td><td>88.8</td><td>SAUR_AC1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38850.1 | Symbols: SAUR_AC1, ATSAUR15, SAUR15, SAUR-AC1 | SAUR-like auxin-responsive protein family | chr4:18126257-18126526 FORWARD LENGTH=89</td><td>80</td><td>89</td><td>4.00E-35</td><td>111.3</td><td>82.5</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00759.1.g19105.t2</td><td>gb|EOA39965.1| hypothetical protein CARUB_v10008653mg, partial [Capsella rubella]</td><td>506</td><td>593</td><td>0</td><td>117.2</td><td>77.1</td><td>84.2</td><td>hypothetical protein CARUB_v10008653mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G45207.2 | Symbols: | Remorin family protein | chr1:17130703-17133548 REVERSE LENGTH=555</td><td>506</td><td>555</td><td>0</td><td>109.7</td><td>74.9</td><td>82.6</td></tr>
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Rsa1.0_00759.1.g19106.t1	ref|NP_564493.1| ubiquitin-conjugating enzyme 15 [Arabidopsis thaliana] gi|26454674|sp|P42743.2|UBC15_ARATH RecName: Full=Ubiquitin-conjugating enzyme 15; AltName: Full=PM42; AltName: Full=Ubiquitin carrier protein; AltName: Full=Ubiquitin-conjugating enzyme E2-18 kDa 15; AltName: Full=Ubiquitin-protein ligase gi|2801442|gb|AAC39324.1| ubiquitin-conjugating enzyme 15 [Arabidopsis thaliana] gi|51971711|dbj|BAD44520.1| At1g45050 [Arabidopsis thaliana] gi|66354440|gb|AAY44855.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|109946565|gb|ABG48461.1| At1g45050 [Arabidopsis thaliana] gi|332193956|gb|AEE32077.1| ubiquitin-conjugating enzyme 15 [Arabidopsis thaliana]	148	161	1.00E-71	108.8	96.6	98.6	ubiquitin-conjugating enzyme 15	gbpln	Arabidopsis thaliana	AT1G45050.1 | Symbols: ATUBC2-1, UBC15 | Ubiquitin-conjugating enzyme family protein | chr1:17031337-17032967 FORWARD LENGTH=161	148	161	3.00E-74	108.8	96.6	98.6
Rsa1.0_00759.1.g19107.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1298	1307	0	100.7	58.6	72.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1298	1262	1.00E-104	97.2	14.3	23.0
Rsa1.0_00759.1.g19108.t2	gb|EOA37881.1| hypothetical protein CARUB_v10009347mg [Capsella rubella]	92	399	3.00E-34	433.7	85.9	87.0	hypothetical protein CARUB_v10009347mg	gbpln	Capsella rubella	AT1G45000.1 | Symbols: | AAA-type ATPase family protein | chr1:17009220-17011607 FORWARD LENGTH=399	92	399	6.00E-37	433.7	85.9	87.0
Rsa1.0_00759.1.g19109.t1	ref|XP_002888606.1| ALDH3H1 [Arabidopsis lyrata subsp. lyrata] gi|297334447|gb|EFH64865.1| ALDH3H1 [Arabidopsis lyrata subsp. lyrata]	482	484	0	100.4	87.6	94.8	ALDH3H1	gbpln	Arabidopsis lyrata	AT1G44170.2 | Symbols: ALDH3H1, ALDH4 | aldehyde dehydrogenase 3H1 | chr1:16796564-16800031 REVERSE LENGTH=484	482	484	0	100.4	85.7	94.6
Rsa1.0_00759.1.g19110.t1	ref|XP_002891286.1| DNAJ chaperone C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297337128|gb|EFH67545.1| DNAJ chaperone C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	230	356	1.00E-105	154.8	84.8	88.7	DNAJ chaperone C-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT1G44160.1 | Symbols: | HSP40/DnaJ peptide-binding protein | chr1:16795032-16796276 FORWARD LENGTH=357	230	357	1.00E-102	155.2	83.9	88.3
Rsa1.0_00759.1.g19111.t2	dbj|BAB02146.1| copia retroelement pol polyprotein-like [Arabidopsis thaliana]	490	526	3.00E-46	107.3	18.6	23.5	copia retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00759.1.g19112.t1	#	#	#	#	#	#	#	-	----	----	AT1G44160.1 | Symbols: | HSP40/DnaJ peptide-binding protein | chr1:16795032-16796276 FORWARD LENGTH=357	77	357	4.00E-11	463.6	37.7	39.0
Rsa1.0_00759.1.g19113.t1	ref|XP_002891285.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297337127|gb|EFH67544.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	2135	2110	0	98.8	81.4	88.7	C2 domain-containing protein	gbpln	Arabidopsis lyrata	AT1G44120.1 | Symbols: | Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein | chr1:16780610-16787414 FORWARD LENGTH=2114	2135	2114	0	99.0	80.4	88.2
Rsa1.0_00759.1.g19114.t1	ref|XP_002893979.1| CYCA1_1 [Arabidopsis lyrata subsp. lyrata] gi|297339821|gb|EFH70238.1| CYCA1_1 [Arabidopsis lyrata subsp. lyrata]	406	467	0	115.0	82.0	86.9	CYCA1_1	gbpln	Arabidopsis lyrata	AT1G44110.1 | Symbols: CYCA1;1 | Cyclin A1;1 | chr1:16775035-16777182 REVERSE LENGTH=460	406	460	0	113.3	80.8	86.2
Rsa1.0_00759.1.g19115.t1	gb|EOA40281.1| hypothetical protein CARUB_v10009009mg [Capsella rubella]	487	480	0	98.6	88.1	94.7	hypothetical protein CARUB_v10009009mg	gbpln	Capsella rubella	AT1G44100.1 | Symbols: AAP5 | amino acid permease 5 | chr1:16764651-16767223 REVERSE LENGTH=480	487	480	0	98.6	84.2	92.6
Rsa1.0_00759.1.g19116.t1	ref|NP_175058.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|8778680|gb|AAF79688.1|AC022314_29 F9C16.7 [Arabidopsis thaliana] gi|332193886|gb|AEE32007.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana]	460	475	0	103.3	72.4	82.0	P-loop containing nucleoside triphosphate hydrolase-like protein	gbpln	Arabidopsis thaliana	AT1G43910.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:16656050-16657628 REVERSE LENGTH=475	460	475	0	103.3	72.4	82.0
Rsa1.0_00759.1.g19117.t1	ref|XP_002893966.1| hypothetical protein ARALYDRAFT_473785 [Arabidopsis lyrata subsp. lyrata] gi|297339808|gb|EFH70225.1| hypothetical protein ARALYDRAFT_473785 [Arabidopsis lyrata subsp. lyrata]	212	212	1.00E-119	100.0	99.5	100.0	hypothetical protein ARALYDRAFT_473785	gbpln	Arabidopsis lyrata	AT1G43890.3 | Symbols: ATRAB18, ATRABC1, RAB18-1, RABC1, ATRAB-C1, RAB18 | RAB GTPASE HOMOLOG B18 | chr1:16646934-16648395 FORWARD LENGTH=212	212	212	1.00E-120	100.0	98.6	99.5
Rsa1.0_00759.1.g19118.t1	gb|EOA38019.1| hypothetical protein CARUB_v10009490mg [Capsella rubella]	362	370	0	102.2	89.8	96.4	hypothetical protein CARUB_v10009490mg	gbpln	Capsella rubella	AT1G43860.1 | Symbols: | sequence-specific DNA binding transcription factors | chr1:16622244-16624385 REVERSE LENGTH=370	362	370	0	102.2	90.3	95.3

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<tr><td>Rsa1.0_00760.1.g19119.t1</td><td>ref|NP_171740.3| uncharacterized protein [Arabidopsis thaliana] gi|9857534|gb|AAG00889.1|AC064879_7 Hypothetical protein [Arabidopsis thaliana] gi|332189301|gb|AEE27422.1| uncharacterized protein AT1G02380 [Arabidopsis thaliana]</td><td>225</td><td>231</td><td>8.00E-75</td><td>102.7</td><td>67.1</td><td>81.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G02380.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01960.1); Has 66 Blast hits to 66 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 66; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:477814-478850 FORWARD LENGTH=231</td><td>225</td><td>231</td><td>3.00E-77</td><td>102.7</td><td>67.1</td><td>81.3</td></tr>
<tr><td>Rsa1.0_00760.1.g19120.t1</td><td>ref|XP_002892103.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297337945|gb|EFH68362.1| expressed protein [Arabidopsis lyrata subsp. lyrata]</td><td>73</td><td>69</td><td>6.00E-11</td><td>94.5</td><td>71.2</td><td>78.1</td><td>expressed protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00760.1.g19121.t1</td><td>ref|NP_563650.1| transcription factor HFR1 [Arabidopsis thaliana] gi|20532238|sp|Q9FE22.1|HFR1_ARATH RecName: Full=Transcription factor HFR1; AltName: Full=Basic helix-loop-helix protein 26; Short=AtbHLH26; Short=bHLH 26; AltName: Full=Protein LONG HYPOCOTYL IN FAR-RED 1; AltName: Full=Protein REDUCED PHYTOCHROME SIGNALING; AltName: Full=Reduced sensitivity to far-red light; AltName: Full=Transcription factor EN 68; AltName: Full=bHLH transcription factor bHLH026 gi|11870115|gb|AAG40617.1|AF324245_1 bHLH-like protein HFR1 [Arabidopsis thaliana] gi|12025106|gb|AAG45733.1|AF288287_1 reduced phytochrome signaling 1 [Arabidopsis thaliana] gi|13183644|gb|AAK15282.1|AF323182_1 basic helix-loop-helix FBI1 protein [Arabidopsis thaliana] gi|332189297|gb|AEE27418.1| transcription factor HFR1 [Arabidopsis thaliana]</td><td>268</td><td>292</td><td>5.00E-94</td><td>109.0</td><td>68.3</td><td>79.5</td><td>transcription factor HFR1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G02340.1 | Symbols: HFR1, RSF1, FBI1, REP1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:465933-467685 REVERSE LENGTH=292</td><td>268</td><td>292</td><td>2.00E-96</td><td>109.0</td><td>68.3</td><td>79.5</td></tr>
<tr><td>Rsa1.0_00760.1.g19122.t1</td><td>gb|AAQ17548.1| TOC33 [Brassica napus]</td><td>297</td><td>297</td><td>1.00E-160</td><td>100.0</td><td>97.0</td><td>98.7</td><td>TOC33</td><td>gbpln</td><td>Brassica napus</td><td>AT1G02280.2 | Symbols: TOC33, ATTOC33, PPI1 | translocon at the outer envelope membrane of chloroplasts 33 | chr1:448665-450246 REVERSE LENGTH=297</td><td>297</td><td>297</td><td>1.00E-162</td><td>100.0</td><td>91.9</td><td>96.6</td></tr>
<tr><td>Rsa1.0_00760.1.g19123.t1</td><td>gb|AAM61631.1| aspartyl aminopeptidase-like protein [Arabidopsis thaliana]</td><td>207</td><td>477</td><td>3.00E-47</td><td>230.4</td><td>42.0</td><td>42.5</td><td>aspartyl aminopeptidase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G60160.1 | Symbols: | Zn-dependent exopeptidases superfamily protein | chr5:24223887-24226783 REVERSE LENGTH=477</td><td>207</td><td>477</td><td>9.00E-50</td><td>230.4</td><td>42.0</td><td>42.5</td></tr>
<tr><td>Rsa1.0_00760.1.g19124.t1</td><td>ref|NP_563646.1| uncharacterized calcium-binding protein [Arabidopsis thaliana] gi|148887024|sp|O81916.2|YC22_ARATH RecName: Full=Uncharacterized calcium-binding protein At1g02270 gi|15450673|gb|AAK96608.1| At1g02270/T6A9_9 [Arabidopsis thaliana] gi|17380606|gb|AAL36066.1| At1g02270/T6A9_9 [Arabidopsis thaliana] gi|332189287|gb|AEE27408.1| uncharacterized calcium-binding protein [Arabidopsis thaliana]</td><td>386</td><td>484</td><td>1.00E-174</td><td>125.4</td><td>80.1</td><td>88.1</td><td>uncharacterized calcium-binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G02270.1 | Symbols: | Calcium-binding endonuclease/exonuclease/phosphatase family | chr1:443301-446197 REVERSE LENGTH=484</td><td>386</td><td>484</td><td>1.00E-176</td><td>125.4</td><td>80.1</td><td>88.1</td></tr>
<tr><td>Rsa1.0_00760.1.g19125.t1</td><td>gb|EOA36878.1| hypothetical protein CARUB_v10008913mg [Capsella rubella]</td><td>501</td><td>504</td><td>0</td><td>100.6</td><td>89.0</td><td>92.4</td><td>hypothetical protein CARUB_v10008913mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G02260.1 | Symbols: | Divalent ion symporter | chr1:440757-442459 REVERSE LENGTH=502</td><td>501</td><td>502</td><td>0</td><td>100.2</td><td>88.4</td><td>91.4</td></tr>
<tr><td>Rsa1.0_00760.1.g19126.t1</td><td>gb|AAC24383.1| Hypothetical protein [Arabidopsis thaliana]</td><td>299</td><td>345</td><td>1.00E-48</td><td>115.4</td><td>35.8</td><td>42.5</td><td>Hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G02230.1 | Symbols: ANAC004, NAC004 | NAC domain containing protein 4 | chr1:435174-436775 REVERSE LENGTH=359</td><td>299</td><td>359</td><td>2.00E-47</td><td>120.1</td><td>33.8</td><td>39.8</td></tr>
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Rsa1.0_00760.1.g19127.t1	ref|NP_171613.1| inorganic pyrophosphatase [Arabidopsis thaliana] gi|297843016|ref|XP_002889389.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|15450699|gb|AAK96621.1| At1g01050/T25K16_5 [Arabidopsis thaliana] gi|16323129|gb|AAL15299.1| At1g01050/T25K16_5 [Arabidopsis thaliana] gi|17473935|gb|AAL38377.1| putative inorganic pyrophosphatase [Arabidopsis thaliana] gi|20148453|gb|AAM10117.1| putative inorganic pyrophosphatase [Arabidopsis thaliana] gi|21537232|gb|AAM61573.1| soluble inorganic pyrophosphatase, putative [Arabidopsis thaliana] gi|24797046|gb|AAN64535.1| At1g01050/T25K16_5 [Arabidopsis thaliana] gi|110741975|dbj|BAE98927.1| putative soluble inorganic pyrophosphatase [Arabidopsis thaliana] gi|225897848|dbj|BAH30256.1| hypothetical protein [Arabidopsis thaliana] gi|297335231|gb|EFH65648.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|332189101|gb|AEE27222.1| inorganic pyrophosphatase [Arabidopsis thaliana]	211	212	1.00E−115	100.5	96.7	98.1	inorganic pyrophosphatase	gbpln	Arabidopsis lyrata	AT1G01050.1 | Symbols: AtPPa1, PPa1 | pyrophosphorylase 1 | chr1:31382−32670 REVERSE LENGTH=212	211	212	1.00E−118	100.5	96.7	98.1
Rsa1.0_00760.1.g19128.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00760.1.g19129.t1	ref|XP_002889387.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297335229|gb|EFH65646.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	354	361	1.00E−168	102.0	81.4	89.3	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT1G01070.1 | Symbols: | nodulin MtN21 /EamA−like transporter family protein | chr1:38898−40877 REVERSE LENGTH=365	354	365	1.00E−168	103.1	80.8	88.7
Rsa1.0_00761.1.g19130.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00761.1.g19131.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00761.1.g19132.t1	gb|ADZ98865.1| MYB domain protein 111 [Brassica rapa subsp. rapa]	343	343	1.00E−176	100.0	91.8	94.5	MYB domain protein 111	gbpln	Brassica rapa	AT5G49330.1 | Symbols: MYB111, ATMYB111, PFG3 | myb domain protein 111 | chr5:19999147−20001293 REVERSE LENGTH=342	343	342	1.00E−149	99.7	77.8	85.1
Rsa1.0_00761.1.g19133.t2	ref|XP_002865732.1| beta−xylosidase 1 [Arabidopsis lyrata subsp. lyrata] gi|297311567|gb|EFH41991.1| beta−xylosidase 1 [Arabidopsis lyrata subsp. lyrata]	1031	774	0	75.1	66.2	68.9	beta−xylosidase 1	gbpln	Arabidopsis lyrata	AT5G49360.1 | Symbols: BXL1, ATBXL1 | beta−xylosidase 1 | chr5:20012179−20016659 REVERSE LENGTH=774	1031	774	0	75.1	66.1	68.4
Rsa1.0_00761.1.g19134.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00761.1.g19135.t1	ref|XP_002314930.1| predicted protein [Populus trichocarpa] gi|222863970|gb|EEF01101.1| predicted protein [Populus trichocarpa]	283	258	2.00E−63	91.2	48.8	55.8	predicted protein	gbpln	Populus trichocarpa	AT5G49400.1 | Symbols: | zinc knuckle (CCHC−type) family protein | chr5:20031154−20031981 FORWARD LENGTH=275	283	275	5.00E−55	97.2	43.8	45.9
Rsa1.0_00761.1.g19136.t1	ref|NP_199754.2| WD40/YVTN repeat and Bromo−WDR9−I−like domain−containing protein [Arabidopsis thaliana] gi|332008427|gb|AED95810.1| WD40/YVTN repeat and Bromo−WDR9−I−like domain−containing protein [Arabidopsis thaliana]	1681	1677	0	99.8	86.4	91.8	WD40/YVTN repeat and Bromo−WDR9−I−like domain−containing protein	gbpln	Arabidopsis thaliana	AT5G49430.1 | Symbols: | WD40/YVTN repeat−like−containing domain;Bromodomain | chr5:20037338−20045454 REVERSE LENGTH=1677	1681	1677	0	99.8	86.4	91.8
Rsa1.0_00761.1.g19137.t1	ref|XP_002863984.1| ATP−citrate lyase B−2 [Arabidopsis lyrata subsp. lyrata] gi|297309819|gb|EFH40243.1| ATP−citrate lyase B−2 [Arabidopsis lyrata subsp. lyrata]	104	608	3.00E−12	584.6	34.6	37.5	ATP−citrate lyase B−2	gbpln	Arabidopsis lyrata	AT5G49460.1 | Symbols: ACLB−2 | ATP citrate lyase subunit B 2 | chr5:20055048−20058195 FORWARD LENGTH=608	104	608	5.00E−15	584.6	34.6	37.5
Rsa1.0_00761.1.g19138.t1	dbj|BAJ33845.1| unnamed protein product [Thellungiella halophila]	139	141	1.00E−56	101.4	82.7	89.9	unnamed protein product	−−−−	−−−−	AT5G49450.1 | Symbols: AtbZIP1, bZIP1 | basic leucine−zipper 1 | chr5:20052145−20052582 FORWARD LENGTH=145	139	145	5.00E−55	104.3	79.9	89.2
Rsa1.0_00761.1.g19139.t1	ref|XP_002863989.1| hypothetical protein ARALYDRAFT_495010 [Arabidopsis lyrata subsp. lyrata] gi|297309824|gb|EFH40248.1| hypothetical protein ARALYDRAFT_495010 [Arabidopsis lyrata subsp. lyrata]	240	195	1.00E−89	81.3	73.3	75.0	hypothetical protein ARALYDRAFT_495010	gbpln	Arabidopsis lyrata	AT5G49510.2 | Symbols: PFD3 | prefoldin 3 | chr5:20080729−20082456 FORWARD LENGTH=195	240	195	3.00E−91	81.3	72.5	74.6

Rsa1.0_00762.1.g19140.t1	ref|NP_199378.1| subtilase family protein [Arabidopsis thaliana] gi|9758669|dbj|BAB09208.1| subtilisin-like protease [Arabidopsis thaliana] gi|26451161|dbj|BAC42684.1| putative subtilisin-like protease [Arabidopsis thaliana] gi|28973549|gb|AAO64099.1| putative subtilisin [Arabidopsis thaliana] gi|332007897|gb|AED95280.1| subtilase family protein [Arabidopsis thaliana]	794	791	0	99.6	86.6	93.1	subtilase family protein	gbpln	Arabidopsis thaliana	AT5G45650.1 | Symbols: | subtilase family protein | chr5:18513520-18518790 REVERSE LENGTH=791	794	791	0	99.6	86.6	93.1
Rsa1.0_00762.1.g19141.t1	gb|ABD65056.1| hypothetical protein 27.t00122 [Brassica oleracea]	207	239	3.00E-28	115.5	32.4	43.5	hypothetical protein 27.t00122	gbpln	Brassica oleracea	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	207	575	5.00E-14	277.8	28.0	48.8
Rsa1.0_00762.1.g19142.t1	ref|NP_199379.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75171192|sp|Q9FK75.1|GDL82_ARATH RecName: Full=GDSL esterase/lipase At5g45670; AltName: Full=Extracellular lipase At5g45670; Flags: Precursor gi|17933312|gb|AAL48238.1|AF446366_1 AT5g45670/MRA19_6 [Arabidopsis thaliana] gi|9758670|dbj|BAB09209.1| GDSL-motif lipase/hydrolase-like protein [Arabidopsis thaliana] gi|20453403|gb|AAM19940.1| AT5g45670/MRA19_6 [Arabidopsis thaliana] gi|332007899|gb|AED95282.1| GDSL esterase/lipase [Arabidopsis thaliana]	361	362	0	100.3	90.0	96.7	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT5G45670.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:18528600-18530164 FORWARD LENGTH=362	361	362	0	100.3	90.0	96.7
Rsa1.0_00762.1.g19143.t1	ref|NP_199380.1| FKBP-type peptidyl-prolyl cis-trans isomerase 3 [Arabidopsis thaliana] gi|21542069|sp|Q9SCY2.2|FKB13_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP13, chloroplastic; Short=PPIase FKBP13; AltName: Full=FK506-binding protein 1; AltName: Full=FK506-binding protein 13; Short=AtFKBP13; AltName: Full=Immunophilin FKBP13; AltName: Full=Rotamase; Flags: Precursor gi|9758671|dbj|BAB09210.1| unnamed protein product [Arabidopsis thaliana] gi|18086457|gb|AAL57682.1| AT5g45680/MRA19_7 [Arabidopsis thaliana] gi|20147125|gb|AAM10279.1| AT5g45680/MRA19_7 [Arabidopsis thaliana] gi|332007900|gb|AED95283.1| FKBP-type peptidyl-prolyl cis-trans isomerase 3 [Arabidopsis thaliana]	207	208	1.00E-99	100.5	87.9	94.2	FKBP-type peptidyl-prolyl cis-trans isomerase 3	gbpln	Arabidopsis thaliana	AT5G45680.1 | Symbols: ATFKBP13, FKBP13 | FK506-binding protein 13 | chr5:18530894-18532128 FORWARD LENGTH=208	207	208	1.00E-102	100.5	87.9	94.2
Rsa1.0_00762.1.g19144.t1	ref|XP_002891072.1| alliinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336914|gb|EFH67331.1| alliinase family protein [Arabidopsis lyrata subsp. lyrata]	468	460	0	98.3	75.9	86.1	alliinase family protein	gbpln	Arabidopsis lyrata	AT1G34060.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr1:12396561-12398299 REVERSE LENGTH=463	468	463	0	98.9	73.3	84.2
Rsa1.0_00762.1.g19145.t1	dbj|BAJ34615.1| unnamed protein product [Thellungiella halophila]	340	345	1.00E-152	101.5	84.1	92.1	unnamed protein product	----	----	AT5G45710.1 | Symbols: AT-HSFA4C, RHA1, HSFA4C | winged-helix DNA-binding transcription factor family protein | chr5:18541576-18542706 FORWARD LENGTH=345	340	345	2.33E-156	101.5	79.4	87.6
Rsa1.0_00762.1.g19146.t1	ref|XP_002863460.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297309295|gb|EFH39719.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	926	970	0	104.8	71.2	80.3	ATP binding protein	gbpln	Arabidopsis lyrata	AT5G45720.1 | Symbols: | AAA-type ATPase family protein | chr5:18543338-18546629 REVERSE LENGTH=966	926	966	0	104.3	71.5	79.8
Rsa1.0_00762.1.g19147.t1	ref|NP_199386.2| Ubiquitin domain-containing protein [Arabidopsis thaliana] gi|332007908|gb|AED95291.1| Ubiquitin domain-containing protein [Arabidopsis thaliana]	118	118	3.00E-57	100.0	90.7	95.8	Ubiquitin domain-containing protein	gbpln	Arabidopsis thaliana	AT5G45740.1 | Symbols: | Ubiquitin domain-containing protein | chr5:18556975-18558097 REVERSE LENGTH=118	118	118	5.00E-60	100.0	90.7	95.8
Rsa1.0_00762.1.g19148.t1	ref|XP_002865226.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297311061|gb|EFH41485.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	350	358	1.00E-172	102.3	88.3	93.7	transducin family protein	gbpln	Arabidopsis lyrata	AT5G45760.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:18561121-18563005 FORWARD LENGTH=360	350	360	1.00E-171	102.9	87.7	93.4
Rsa1.0_00762.1.g19149.t1	gb|EOA16660.1| hypothetical protein CARUB_v10004846mg [Capsella rubella]	419	434	1.00E-121	103.6	62.1	75.4	hypothetical protein CARUB_v10004846mg	gbpln	Capsella rubella	AT5G45770.1 | Symbols: AtRLP55, RLP55 | receptor like protein 55 | chr5:18563568-18564845 FORWARD LENGTH=425	419	425	1.00E-123	101.4	61.8	73.7

Rsa1.0_00762.1.g19150.t1	ref|NP_850376.2| 60S ribosomal protein L11-1 [Arabidopsis thaliana] gi|297791141|ref|XP_002863455.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|297804282|ref|XP_002870025.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|21542441|sp|P42795.2|RL111_ARATH RecName: Full=60S ribosomal protein L11-1; AltName: Full=L16A gi|110737006|dbj|BAF00458.1| 60S ribosomal protein L11B [Arabidopsis thaliana] gi|297309290|gb|EFH39714.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|297315861|gb|EFH46284.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|330255069|gb|AEC10163.1| 60S ribosomal protein L11-1 [Arabidopsis thaliana] gi|482549880|gb|EOA14074.1| hypothetical protein CARUB_v10027211mg [Capsella rubella] gi|482560618|gb|EOA24809.1| hypothetical protein CARUB_v10018095mg [Capsella rubella]	182	182	1.00E-102	100.0	99.5	100.0	60S ribosomal protein L11-1	gbpln	Arabidopsis lyrata	AT2G42740.1 | Symbols: RPL16A | ribosomal protein large subunit 16A | chr2:17791794-17792946 FORWARD LENGTH=182	182	182	1.00E-104	100.0	99.5	100.0
Rsa1.0_00762.1.g19151.t1	gb|ACV41802.1| delay of germination 1, partial [Brassica rapa subsp. pekinensis]	280	258	1.00E-130	92.1	80.4	86.1	delay of germination 1, partial	gbpln	Brassica rapa	AT5G45830.1 | Symbols: DOG1, GSQ5, ATDOG1 | delay of germination 1 | chr5:18589669-18591400 REVERSE LENGTH=291	280	291	1.00E-112	103.9	74.3	83.9
Rsa1.0_00763.1.g19152.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00763.1.g19153.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	606	695	1.00E-143	114.7	54.3	66.5	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	606	681	5.00E-16	112.4	6.4	10.2
Rsa1.0_00763.1.g19154.t4	gb|EOA29246.1| hypothetical protein CARUB_v10025520mg [Capsella rubella]	650	141	6.00E-61	21.7	17.1	19.2	hypothetical protein CARUB_v10025520mg	gbpln	Capsella rubella	AT2G21045.1 | Symbols: | Rhodanese/Cell cycle control phosphatase superfamily protein | chr2:9027858-9028805 FORWARD LENGTH=169	650	169	3.00E-62	26.0	17.2	19.8
Rsa1.0_00763.1.g19155.t12	ref|XP_002884055.1| ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329895|gb|EFH60314.1| ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1005	796	0	79.2	47.9	53.2	ARID/BRIGHT DNA-binding domain-containing protein	gbpln	Arabidopsis lyrata	AT2G17410.1 | Symbols: | ARID/BRIGHT DNA-binding domain-containing protein | chr2:7559869-7563474 FORWARD LENGTH=786	1005	786	0	78.2	45.3	51.8
Rsa1.0_00763.1.g19156.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00763.1.g19157.t1	sp|Q9FMV0.1|FBL91_ARATH RecName: Full=F-box/LRR-repeat protein At5g63520 gi|9758293|dbj|BAB08817.1| unnamed protein product [Arabidopsis thaliana]	510	529	0	103.7	66.1	79.2	RecName: Full=F-box/LRR-repeat protein At5g63520 gi|9758293|dbj|BAB08817.1| unnamed protein product	gbpln	Arabidopsis thaliana	AT5G63520.1 | Symbols: | CONTAINS InterPro DOMAIN/s: F-box domain, Skp2-like (InterPro:IPR022364), FIST C domain (InterPro:IPR019494), FIST domain, N-terminal (InterPro:IPR013702); Has 137 Blast hits to 137 proteins in 56 species: Archae - 0; Bacteria - 88; Metazoa - 6; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr5:25426300-25429093 REVERSE LENGTH=519	510	519	0	101.8	66.1	79.2
Rsa1.0_00763.1.g19158.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00763.1.g19159.t3	ref|NP_191905.3| protein transport protein SEC31 [Arabidopsis thaliana] gi|332646966|gb|AEE80487.1| protein transport protein SEC31 [Arabidopsis thaliana]	259	1102	4.00E-21	425.5	38.6	43.2	protein transport protein SEC31	gbpln	Arabidopsis thaliana	AT3G63460.2 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:23431009-23437241 REVERSE LENGTH=1102	259	1102	1.00E-23	425.5	38.6	43.2

Rsa1.0_00763.1.g19160.t1	ref|XP_002870533.1| hypothetical protein ARALYDRAFT_915876 [Arabidopsis lyrata subsp. lyrata] gi|297316369|gb|EFH46792.1| hypothetical protein ARALYDRAFT_915876 [Arabidopsis lyrata subsp. lyrata]	599	631	1.00E-161	105.3	52.8	69.6	hypothetical protein ARALYDRAFT_915876	gbpln	Arabidopsis lyrata	AT5G37470.1 | Symbols: | Family of unknown function (DUF577) | chr5:14861503-14863392 REVERSE LENGTH=629	599	629	1.00E-161	105.0	52.6	68.9
Rsa1.0_00763.1.g19161.t2	ref|NP_179331.1| ankyrin repeat-containing 2B [Arabidopsis thaliana] gi|89000957|gb|ABD59068.1| At2g17390 [Arabidopsis thaliana] gi|330251526|gb|AEC06620.1| ankyrin repeat-containing 2B [Arabidopsis thaliana]	360	344	1.00E-144	95.6	78.1	83.9	ankyrin repeat-containing 2B	gbpln	Arabidopsis thaliana	AT2G17390.1 | Symbols: AKR2B | ankyrin repeat-containing 2B | chr2:7555870-7557743 FORWARD LENGTH=344	360	344	1.00E-147	95.6	78.1	83.9
Rsa1.0_00763.1.g19162.t1	gb|AAG10812.1|AC018460_6 Putative retroelement polyprotein [Arabidopsis thaliana]	153	1404	3.00E-64	917.6	75.2	84.3	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	153	1262	4.00E-33	824.8	46.4	60.1
Rsa1.0_00764.1.g19163.t1	dbj|BAB01217.1| Ta11 non-LTR retroelement protein-like [Arabidopsis thaliana] gi|67633664|gb|AAY78756.1| putative zinc finger protein [Arabidopsis thaliana]	411	487	1.00E-62	118.5	34.3	48.2	Ta11 non-LTR retroelement protein-like	gbpln	Arabidopsis thaliana	AT2G41590.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25200.1); Has 221 Blast hits to 217 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 221; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17343600-17344703 FORWARD LENGTH=367	411	367	2.00E-13	89.3	10.7	20.0
Rsa1.0_00764.1.g19164.t2	dbj|BAB11196.1| mutator-like transposase [Arabidopsis thaliana]	488	797	1.00E-78	163.3	34.2	48.2	mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	488	719	7.00E-18	147.3	16.8	28.3
Rsa1.0_00764.1.g19165.t3	gb|AAF69717.1|AC016041_22 F27J15.14 [Arabidopsis thaliana]	427	1526	1.00E-58	357.4	30.9	41.2	F27J15.14	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00764.1.g19166.t1	ref|XP_002868443.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314279|gb|EFH44702.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	349	145	2.00E-34	41.5	23.8	31.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	349	921	2.00E-14	263.9	15.5	24.4
Rsa1.0_00764.1.g19167.t1	ref|XP_002893993.1| hypothetical protein ARALYDRAFT_473819 [Arabidopsis lyrata subsp. lyrata] gi|297339835|gb|EFH70252.1| hypothetical protein ARALYDRAFT_473819 [Arabidopsis lyrata subsp. lyrata]	275	271	1.00E-137	98.5	90.2	94.5	hypothetical protein ARALYDRAFT_473819	gbpln	Arabidopsis lyrata	AT1G44770.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G49710.3); Has 81 Blast hits to 81 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 81; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:16907834-16909409 REVERSE LENGTH=271	275	271	1.00E-138	98.5	88.7	94.2
Rsa1.0_00764.1.g19168.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00764.1.g19169.t1	gb|ABV89614.1| universal stress protein family protein [Brassica rapa]	215	215	1.00E-120	100.0	98.6	98.6	universal stress protein family protein	gbpln	Brassica rapa	AT1G44760.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr1:16896894-16898427 REVERSE LENGTH=213	215	213	1.00E-113	99.1	92.1	94.4
Rsa1.0_00764.1.g19170.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	595	723	1.00E-165	121.5	50.1	65.4	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	595	696	2.00E-32	117.0	19.5	37.1
Rsa1.0_00764.1.g19171.t1	gb|EOA38028.1| hypothetical protein CARUB_v10009499mg [Capsella rubella]	444	369	1.00E-178	83.1	75.9	78.4	hypothetical protein CARUB_v10009499mg	gbpln	Capsella rubella	AT1G44750.2 | Symbols: ATPUP11, PUP11 | purine permease 11 | chr1:16893825-16895168 FORWARD LENGTH=367	444	367	1.00E-174	82.7	75.7	78.6
Rsa1.0_00764.1.g19172.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00765.1.g19173.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00765.1.g19174.t1	gb|EOA40579.1| hypothetical protein CARUB_v10009309mg, partial [Capsella rubella]	369	409	1.00E-174	110.8	87.8	91.6	hypothetical protein CARUB_v10009309mg, partial	gbpln	Capsella rubella	AT1G21890.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:7682808-7685581 REVERSE LENGTH=389	369	389	1.00E-171	105.4	87.5	91.3
Rsa1.0_00765.1.g19175.t1	ref|NP_173604.1| SKU5 similar 7 protein [Arabidopsis thaliana] gi|6552744|gb|AAF16543.1|AC013482_17 T26F17.7 [Arabidopsis thaliana] gi|332192042|gb|AEE30163.1| SKU5 similar 7 protein [Arabidopsis thaliana]	274	538	6.00E-32	196.4	28.8	32.5	SKU5 similar 7 protein	gbpln	Arabidopsis thaliana	AT1G21860.1 | Symbols: sks7 | SKU5 similar 7 | chr1:7671028-7674215 REVERSE LENGTH=538	274	538	2.00E-34	196.4	28.8	32.5

Rsa1.0_00765.1.g19176.t1	ref|NP_564149.1| proteasome subunit beta type-3-A [Arabidopsis thaliana] gi|288558823|sp|Q9XI05.2|PSB3A_ARATH RecName: Full=Proteasome subunit beta type-3-A; AltName: Full=20S proteasome beta subunit C-1; AltName: Full=Proteasome component T gi|17473525|gb|AAL38246.1| proteasome subunit [Arabidopsis thaliana] gi|21387087|gb|AAM47947.1| proteasome subunit [Arabidopsis thaliana] gi|110740894|dbj|BAE98543.1| 20S proteasome beta subunit PBC2 like protein [Arabidopsis thaliana] gi|332192025|gb|AEE30146.1| proteasome subunit beta type-3-A [Arabidopsis thaliana]	204	204	1.00E-115	100.0	98.5	100.0	proteasome subunit beta type-3-A	gbpln	Arabidopsis thaliana	AT1G21720.1 | Symbols: PBC1 | proteasome beta subunit C1 | chr1:7626394-7628070 FORWARD LENGTH=204	204	204	1.00E-118	100.0	98.5	100.0
Rsa1.0_00765.1.g19177.t1	ref|XP_002890454.1| hypothetical protein ARALYDRAFT_472409 [Arabidopsis lyrata subsp. lyrata] gi|297336296|gb|EFH66713.1| hypothetical protein ARALYDRAFT_472409 [Arabidopsis lyrata subsp. lyrata]	304	205	2.00E-22	67.4	33.6	39.5	hypothetical protein ARALYDRAFT_472409	gbpln	Arabidopsis lyrata	AT1G21695.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:7619132-7619785 FORWARD LENGTH=217	304	217	1.00E-18	71.4	31.3	35.9
Rsa1.0_00765.1.g19178.t1	ref|XP_002890450.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297336292|gb|EFH66709.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	497	522	0	105.0	76.5	82.7	heat shock protein binding protein	gbpln	Arabidopsis lyrata	AT1G21660.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:7605924-7608835 FORWARD LENGTH=523	497	523	1.00E-177	105.2	75.1	82.1
Rsa1.0_00765.1.g19179.t2	gb|EOA29965.1| hypothetical protein CARUB_v10013068mg [Capsella rubella]	115	722	1.00E-14	627.8	44.3	55.7	hypothetical protein CARUB_v10013068mg	gbpln	Capsella rubella	AT3G16000.1 | Symbols: MFP1 | MAR binding filament-like protein 1 | chr3:5431041-5433613 REVERSE LENGTH=726	115	726	1.00E-16	631.3	45.2	54.8
Rsa1.0_00765.1.g19180.t1	ref|XP_002887678.1| hypothetical protein ARALYDRAFT_316646 [Arabidopsis lyrata subsp. lyrata] gi|297333519|gb|EFH63937.1| hypothetical protein ARALYDRAFT_316646 [Arabidopsis lyrata subsp. lyrata]	396	122	1.00E-26	30.8	16.7	18.4	hypothetical protein ARALYDRAFT_316646	gbpln	Arabidopsis lyrata	AT1G77350.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function KRTCAP2 (InterPro:IPR018614); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:29070497-29071545 FORWARD LENGTH=122	396	122	9.00E-29	30.8	16.4	18.4
Rsa1.0_00765.1.g19181.t1	ref|XP_002893172.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata] gi|297339014|gb|EFH69431.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata]	70	71	1.00E-18	101.4	71.4	77.1	hypothetical protein ARALYDRAFT_472389	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00765.1.g19182.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	474	1365	7.00E-81	288.0	35.2	51.7	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	474	575	6.00E-56	121.3	27.4	46.8
Rsa1.0_00765.1.g19183.t1	ref|XP_002893172.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata] gi|297339014|gb|EFH69431.1| hypothetical protein ARALYDRAFT_472389 [Arabidopsis lyrata subsp. lyrata]	65	71	6.00E-15	109.2	75.4	81.5	hypothetical protein ARALYDRAFT_472389	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00766.1.g19184.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	495	536	3.00E-87	108.3	37.8	52.9	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	495	530	2.00E-49	107.1	17.0	21.2

Rsa1.0_00766.1.g19185.t1	ref|NP_175346.1| RING-H2 finger protein ATL75 [Arabidopsis thaliana] gi|68565250|sp|Q94BY6.1|ATL75_ARATH RecName: Full=RING-H2 finger protein ATL75 gi|14517432|gb|AAK62606.1| At1g49200/F27J15_35 [Arabidopsis thaliana] gi|20147327|gb|AAM10377.1| At1g49200/F27J15_35 [Arabidopsis thaliana] gi|332194283|gb|AEE32404.1| RING-H2 finger protein ATL75 [Arabidopsis thaliana]	288	226	1.00E-108	78.5	64.9	70.1	RING-H2 finger protein ATL75	gbpln	Arabidopsis thaliana	AT1G49200.1 | Symbols: | RING/U-box superfamily protein | chr1:18198298-18198978 FORWARD LENGTH=226	288	226	1.00E-110	78.5	64.9	70.1
Rsa1.0_00766.1.g19186.t1	ref|XP_002891481.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297337323|gb|EFH67740.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	225	226	3.00E-99	100.4	78.7	88.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G49200.1 | Symbols: | RING/U-box superfamily protein | chr1:18198298-18198978 FORWARD LENGTH=226	225	226	1.00E-101	100.4	78.7	88.0
Rsa1.0_00766.1.g19187.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00766.1.g19188.t1	gb|EOA38874.1| hypothetical protein CARUB_v10011239mg [Capsella rubella]	148	216	7.00E-59	145.9	77.7	87.8	hypothetical protein CARUB_v10011239mg	gbpln	Capsella rubella	AT1G49230.1 | Symbols: | RING/U-box superfamily protein | chr1:18209320-18209979 FORWARD LENGTH=219	148	219	9.00E-56	148.0	70.9	81.1
Rsa1.0_00766.1.g19189.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00766.1.g19190.t1	gb|EOA37340.1| hypothetical protein CARUB_v10011065mg [Capsella rubella]	692	691	0	99.9	71.7	75.1	hypothetical protein CARUB_v10011065mg	gbpln	Capsella rubella	AT1G49270.1 | Symbols: | Protein kinase superfamily protein | chr1:18227334-18230227 REVERSE LENGTH=699	692	699	0	101.0	70.7	74.1
Rsa1.0_00766.1.g19191.t1	ref|XP_002894166.1| hypothetical protein ARALYDRAFT_891775 [Arabidopsis lyrata subsp. lyrata] gi|297340008|gb|EFH70425.1| hypothetical protein ARALYDRAFT_891775 [Arabidopsis lyrata subsp. lyrata]	419	333	8.00E-58	79.5	26.0	34.6	hypothetical protein ARALYDRAFT_891775	gbpln	Arabidopsis lyrata	AT1G49290.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13620.1); Has 99 Blast hits to 93 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 97; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18232608-18233624 REVERSE LENGTH=338	419	338	5.00E-56	80.7	23.9	32.9
Rsa1.0_00767.1.g19192.t1	dbj|BAB02492.1| unnamed protein product [Arabidopsis thaliana]	80	540	2.00E-18	675.0	67.5	72.5	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G20840.1 | Symbols: PLT1 | Integrase-type DNA-binding superfamily protein | chr3:7300764-7303370 FORWARD LENGTH=574	80	574	4.00E-21	717.5	67.5	72.5
Rsa1.0_00767.1.g19193.t2	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	331	1463	1.00E-49	442.0	29.0	43.2	F5J5.1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00767.1.g19194.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00767.1.g19195.t1	ref|NP_188722.1| NIMA-related kinase 5 [Arabidopsis thaliana] gi|332642911|gb|AEE76432.1| NIMA-related kinase 5 [Arabidopsis thaliana]	434	427	0	98.4	91.2	95.6	NIMA-related kinase 5	gbpln	Arabidopsis thaliana	AT3G20860.1 | Symbols: ATNEK5, NEK5 | NIMA-related kinase 5 | chr3:7306147-7308434 FORWARD LENGTH=427	434	427	0	98.4	91.2	95.6
Rsa1.0_00767.1.g19196.t1	ref|XP_002885407.1| hypothetical protein ARALYDRAFT_898522 [Arabidopsis lyrata subsp. lyrata] gi|297331247|gb|EFH61666.1| hypothetical protein ARALYDRAFT_898522 [Arabidopsis lyrata subsp. lyrata]	63	64	5.00E-12	101.6	63.5	71.4	hypothetical protein ARALYDRAFT_898522	gbpln	Arabidopsis lyrata	AT3G20865.1 | Symbols: AGP40 | arabinogalactan protein 40 | chr3:7308699-7308887 REVERSE LENGTH=62	63	62	8.00E-13	98.4	61.9	71.4
Rsa1.0_00767.1.g19197.t1	ref|XP_002885408.1| metal transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297331248|gb|EFH61667.1| metal transporter family protein [Arabidopsis lyrata subsp. lyrata]	270	276	1.00E-143	102.2	95.6	98.1	metal transporter family protein	gbpln	Arabidopsis lyrata	AT3G20870.1 | Symbols: ZTP29 | ZIP metal ion transporter family | chr3:7309499-7312476 REVERSE LENGTH=276	270	276	1.00E-145	102.2	95.2	97.4
Rsa1.0_00767.1.g19198.t1	ref|XP_002885409.1| hypothetical protein ARALYDRAFT_318837 [Arabidopsis lyrata subsp. lyrata] gi|297331249|gb|EFH61668.1| hypothetical protein ARALYDRAFT_318837 [Arabidopsis lyrata subsp. lyrata]	354	353	1.00E-147	99.7	79.7	85.9	hypothetical protein ARALYDRAFT_318837	gbpln	Arabidopsis lyrata	AT3G20880.1 | Symbols: WIP4 | WIP domain protein 4 | chr3:7313759-7315792 REVERSE LENGTH=412	354	412	1.00E-149	116.4	78.8	85.0
Rsa1.0_00767.1.g19199.t1	gb|EOA30963.1| hypothetical protein CARUB_v10014109mg [Capsella rubella]	279	342	1.00E-124	122.6	87.5	91.8	hypothetical protein CARUB_v10014109mg	gbpln	Capsella rubella	AT3G20890.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:7319939-7321054 FORWARD LENGTH=292	279	292	1.00E-118	104.7	84.6	88.5
Rsa1.0_00767.1.g19200.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1773	1213	0	68.4	25.1	38.0	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1773	626	1.00E-63	35.3	7.4	12.5

Rsa1.0_00767.1.g19201.t1	ref|XP_002868166.1| hypothetical protein ARALYDRAFT_915171 [Arabidopsis lyrata subsp. lyrata] gi|297314002|gb|EFH44425.1| hypothetical protein ARALYDRAFT_915171 [Arabidopsis lyrata subsp. lyrata]	135	135	2.00E-50	100.0	72.6	81.5	hypothetical protein ARALYDRAFT_915171	gbpln	Arabidopsis lyrata	AT4G15990.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G16024.1); Has 14 Blast hits to 14 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:9061269-9061676 REVERSE LENGTH=135	135	135	2.00E-52	100.0	71.1	83.7
Rsa1.0_00767.1.g19202.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00767.1.g19203.t2	ref|NP_180058.1| tyrosine aminotransferase 3 [Arabidopsis thaliana] gi|75206385|sp|Q9SK47.1|TAT3_ARATH RecName: Full=Probable aminotransferase TAT3; AltName: Full=Tyrosine aminotransferase 3 gi|4559366|gb|AAD23027.1| putative tyrosine aminotransferase [Arabidopsis thaliana] gi|27311739|gb|AAO00835.1| putative tyrosine aminotransferase [Arabidopsis thaliana] gi|30387543|gb|AAP31937.1| At2g24850 [Arabidopsis thaliana] gi|110740890|dbj|BAE98541.1| putative tyrosine aminotransferase [Arabidopsis thaliana] gi|330252542|gb|AEC07636.1| tyrosine aminotransferase 3 [Arabidopsis thaliana]	189	445	9.00E-69	235.4	76.2	85.7	tyrosine aminotransferase 3	gbpln	Arabidopsis thaliana	AT2G24850.1 | Symbols: TAT3, TAT | tyrosine aminotransferase 3 | chr2:10583070-10585152 REVERSE LENGTH=445	189	445	3.00E-71	235.4	76.2	85.7
Rsa1.0_00768.1.g19204.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00768.1.g19205.t1	ref|XP_002889493.1| hypothetical protein ARALYDRAFT_887579 [Arabidopsis lyrata subsp. lyrata] gi|297335335|gb|EFH65752.1| hypothetical protein ARALYDRAFT_887579 [Arabidopsis lyrata subsp. lyrata]	707	1500	0	212.2	60.7	63.4	hypothetical protein ARALYDRAFT_887579	gbpln	Arabidopsis lyrata	AT1G04160.1 | Symbols: XIB, ATXIB, XI-8, XI-B | myosin XI B | chr1:1086495-1096146 FORWARD LENGTH=1500	707	1500	0	212.2	60.5	63.4
Rsa1.0_00768.1.g19206.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00768.1.g19207.t1	ref|XP_002884885.1| hypothetical protein ARALYDRAFT_341336 [Arabidopsis lyrata subsp. lyrata] gi|297330725|gb|EFH61144.1| hypothetical protein ARALYDRAFT_341336 [Arabidopsis lyrata subsp. lyrata]	389	431	4.00E-67	110.8	41.9	54.8	hypothetical protein ARALYDRAFT_341336	gbpln	Arabidopsis lyrata	AT1G50920.1 | Symbols: | Nucleolar GTP-binding protein | chr1:18870555-18872570 FORWARD LENGTH=671	389	671	7.00E-51	172.5	33.4	46.5
Rsa1.0_00768.1.g19208.t2	gb|EOA29401.1| hypothetical protein CARUB_v10025690mg [Capsella rubella]	215	665	3.00E-27	309.3	38.6	55.8	hypothetical protein CARUB_v10025690mg	gbpln	Capsella rubella	AT2G42470.1 | Symbols: | TRAF-like family protein | chr2:17679887-17685187 REVERSE LENGTH=898	215	898	2.00E-24	417.7	35.3	55.3
Rsa1.0_00768.1.g19209.t1	gb|EOA38824.1| hypothetical protein CARUB_v10011153mg [Capsella rubella]	362	636	1.00E-151	175.7	74.3	81.8	hypothetical protein CARUB_v10011153mg	gbpln	Capsella rubella	AT1G04945.2 | Symbols: | HIT-type Zinc finger family protein | chr1:1400969-1402651 FORWARD LENGTH=392	362	392	1.00E-147	108.3	74.6	81.5
Rsa1.0_00768.1.g19210.t1	ref|XP_002870720.1| hypothetical protein ARALYDRAFT_493970 [Arabidopsis lyrata subsp. lyrata] gi|297316556|gb|EFH46979.1| hypothetical protein ARALYDRAFT_493970 [Arabidopsis lyrata subsp. lyrata]	781	793	0	101.5	57.2	70.2	hypothetical protein ARALYDRAFT_493970	gbpln	Arabidopsis lyrata	AT5G40170.1 | Symbols: AtRLP54, RLP54 | receptor like protein 54 | chr5:16065179-16067557 REVERSE LENGTH=792	781	792	0	101.4	56.3	69.3
Rsa1.0_00768.1.g19211.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00768.1.g19212.t1	gb|ABD65089.1| zinc knuckle containing protein [Brassica oleracea]	327	333	1.00E-104	101.8	66.7	73.7	zinc knuckle containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00768.1.g19213.t1	gb|EOA38824.1| hypothetical protein CARUB_v10011153mg [Capsella rubella]	185	636	3.00E-41	343.8	56.2	64.9	hypothetical protein CARUB_v10011153mg	gbpln	Capsella rubella	AT1G04945.2 | Symbols: | HIT-type Zinc finger family protein | chr1:1400969-1402651 FORWARD LENGTH=392	185	392	2.00E-39	211.9	53.5	60.5
Rsa1.0_00768.1.g19214.t1	ref|NP_683276.1| CLAVATA3/ESR-related protein 20 [Arabidopsis thaliana] gi|122215645|sp|Q3EDI6.1|CLE20_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 20; Contains: RecName: Full=CLE20p; Flags: Precursor gi|332189665|gb|AEE27786.1| CLAVATA3/ESR-related protein 20 [Arabidopsis thaliana]	76	83	4.00E-20	109.2	75.0	82.9	CLAVATA3/ESR-related protein 20	gbpln	Arabidopsis thaliana	AT1G05065.1 | Symbols: CLE20 | CLAVATA3/ESR-RELATED 20 | chr1:1454969-1455220 REVERSE LENGTH=83	76	83	6.00E-23	109.2	75.0	82.9
Rsa1.0_00768.1.g19215.t1	ref|XP_003540892.1| PREDICTED: uncharacterized protein LOC100793937 [Glycine max]	768	817	1.00E-112	106.4	27.0	33.7	PREDICTED: uncharacterized protein LOC100793937	gbenv/gbpln	Glycine max	AT1G40087.1 | Symbols: | Plant transposase (Ptta/En/Spm family) | chr1:14999762-15001868 REVERSE LENGTH=390	768	390	2.00E-17	50.8	6.6	10.3
Rsa1.0_00768.1.g19216.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00768.1.g19217.t1	gb|ABV89645.1| auxin resistant 1 [Brassica rapa]	667	522	0	78.3	71.5	74.5	auxin resistant 1	gbpln	Brassica rapa	AT1G05180.1 | Symbols: AXR1 | NAD(P)-binding Rossmann-fold superfamily protein | chr1:1498357-1501775 REVERSE LENGTH=540	667	540	0	81.0	69.6	74.5
Rsa1.0_00768.1.g19218.t1	dbj|BAJ34158.1| unnamed protein product [Thellungiella halophila]	945	954	0	101.0	88.3	94.0	unnamed protein product	----	----	AT1G05200.2 | Symbols: ATGLR3.4, GLR3.4, GLUR3 | glutamate receptor 3.4 | chr1:1505642-1509002 FORWARD LENGTH=959	945	959	0	101.5	87.2	93.4
Rsa1.0_00768.1.g19219.t1	ref|XP_002892274.1| hypothetical protein ARALYDRAFT_470515 [Arabidopsis lyrata subsp. lyrata] gi|297338116|gb|EFH68533.1| hypothetical protein ARALYDRAFT_470515 [Arabidopsis lyrata subsp. lyrata]	87	91	3.00E-42	104.6	98.9	98.9	hypothetical protein ARALYDRAFT_470515	gbpln	Arabidopsis lyrata	AT1G05205.1 | Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1509352-1510249 REVERSE LENGTH=91	87	91	2.00E-44	104.6	96.6	97.7
Rsa1.0_00768.1.g19220.t1	ref|NP_172015.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|30679181|ref|NP_849596.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|334182300|ref|NP_001184911.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|75332091|sp|Q94C37.1|HDG2_ARATH RecName: Full=Homeobox-leucine zipper protein HDG2; AltName: Full=HD-ZIP protein HDG2; AltName: Full=Homeodomain GLABRA 2-like protein 2; AltName: Full=Homeodomain transcription factor HDG2; AltName: Full=Protein HOMEODOMAIN GLABROUS 2 gi|14334996|gb|AAK59762.1| At1g05230/YUP8H12_16 [Arabidopsis thaliana] gi|20147145|gb|AAM10289.1| At1g05230/YUP8H12_16 [Arabidopsis thaliana] gi|222423025|dbj|BAH19495.1| AT1G05230 [Arabidopsis thaliana] gi|332189688|gb|AEE27809.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|332189689|gb|AEE27810.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|332189691|gb|AEE27812.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana]	534	721	0	135.0	91.8	95.3	homeobox-leucine zipper protein HDG2	gbpln	Arabidopsis thaliana	AT1G05230.4 | Symbols: HDG2 | homeodomain GLABROUS 2 | chr1:1513388-1517024 REVERSE LENGTH=721	534	721	0	135.0	91.8	95.3
Rsa1.0_00769.1.g19221.t1	gb|EOA36208.1| hypothetical protein CARUB_v10010124mg [Capsella rubella]	113	245	4.00E-13	216.8	49.6	59.3	hypothetical protein CARUB_v10010124mg	gbpln	Capsella rubella	AT1G49590.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr1:18354997-18356409 FORWARD LENGTH=242	113	242	4.00E-15	214.2	48.7	56.6
Rsa1.0_00769.1.g19222.t1	dbj|BAB09912.1| MADS-box protein-like [Arabidopsis thaliana]	291	368	4.00E-46	126.5	31.3	38.1	MADS-box protein-like	gbpln	Arabidopsis thaliana	AT5G49420.1 | Symbols: | MADS-box transcription factor family protein | chr5:20035166-20036170 REVERSE LENGTH=334	291	334	2.00E-48	114.8	31.3	38.1
Rsa1.0_00769.1.g19223.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00769.1.g19224.t1	ref|XP_002891616.1| hypothetical protein ARALYDRAFT_474225 [Arabidopsis lyrata subsp. lyrata] gi|297337458|gb|EFH67875.1| hypothetical protein ARALYDRAFT_474225 [Arabidopsis lyrata subsp. lyrata]	203	211	7.00E-92	103.9	85.2	91.1	hypothetical protein ARALYDRAFT_474225	gbpln	Arabidopsis lyrata	AT1G51100.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast stroma; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 26 Blast hits to 26 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18934342-18934977 FORWARD LENGTH=211	203	211	4.00E-93	103.9	82.3	89.2

<table>
<tr><td>Rsa1.0_00769.1.g19225.t1</td><td>ref|NP_175522.2| putative plastid-lipid-associated protein 12 [Arabidopsis thaliana] gi|75154826|sp|Q8LAP6.1|PAP12_ARATH RecName: Full=Probable plastid-lipid-associated protein 12, chloroplastic; AltName: Full=Fibrillin-12; Flags: Precursor gi|21593276|gb|AAM65225.1| unknown [Arabidopsis thaliana] gi|26452116|dbj|BAC43147.1| unknown protein [Arabidopsis thaliana] gi|28950975|gb|AAO63411.1| At1g51115 [Arabidopsis thaliana] gi|332194502|gb|AEE32623.1| putative plastid-lipid-associated protein 12 [Arabidopsis thaliana]</td><td>407</td><td>409</td><td>0</td><td>100.5</td><td>87.0</td><td>93.6</td><td>putative plastid-lipid-associated protein 12</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G51110.1 | Symbols: | Plastid-lipid associated protein PAP / fibrillin family protein | chr1:18935380-18937484 FORWARD LENGTH=409</td><td>407</td><td>409</td><td>0</td><td>100.5</td><td>87.0</td><td>93.6</td></tr>
<tr><td>Rsa1.0_00769.1.g19226.t1</td><td>ref|XP_002891618.1| hypothetical protein ARALYDRAFT_474227 [Arabidopsis lyrata subsp. lyrata] gi|297337460|gb|EFH67877.1| hypothetical protein ARALYDRAFT_474227 [Arabidopsis lyrata subsp. lyrata]</td><td>336</td><td>353</td><td>1.00E-130</td><td>105.1</td><td>71.4</td><td>81.5</td><td>hypothetical protein ARALYDRAFT_474227</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G51120.1 | Symbols: | AP2/B3 transcription factor family protein | chr1:18938091-18939149 FORWARD LENGTH=352</td><td>336</td><td>352</td><td>1.00E-130</td><td>104.8</td><td>70.8</td><td>80.7</td></tr>
<tr><td>Rsa1.0_00769.1.g19227.t1</td><td>gb|EOA40599.1| hypothetical protein CARUB_v10009330mg [Capsella rubella]</td><td>404</td><td>402</td><td>1.00E-177</td><td>99.5</td><td>79.2</td><td>86.6</td><td>hypothetical protein CARUB_v10009330mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G51130.1 | Symbols: | Nse4, component of Smc5/6 DNA repair complex | chr1:18939480-18941560 REVERSE LENGTH=403</td><td>404</td><td>403</td><td>1.00E-170</td><td>99.8</td><td>75.2</td><td>84.9</td></tr>
<tr><td>Rsa1.0_00769.1.g19228.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00769.1.g19229.t1</td><td>ref|XP_002894296.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297340138|gb|EFH70555.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]</td><td>372</td><td>378</td><td>1.00E-169</td><td>101.6</td><td>87.9</td><td>90.9</td><td>basic helix-loop-helix family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G51140.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:18943802-18945613 REVERSE LENGTH=379</td><td>372</td><td>379</td><td>1.00E-168</td><td>101.9</td><td>86.8</td><td>89.8</td></tr>
<tr><td>Rsa1.0_00769.1.g19230.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00769.1.g19231.t1</td><td>ref|NP_175528.1| SNARE-like protein [Arabidopsis thaliana] gi|79319655|ref|NP_001031168.1| SNARE-like protein [Arabidopsis thaliana] gi|297847478|ref|XP_002891620.1| hypothetical protein ARALYDRAFT_892078 [Arabidopsis lyrata subsp. lyrata] gi|4836927|gb|AAD30629.1|AC006085_2 Unknown protein [Arabidopsis thaliana] gi|12320789|gb|AAG50544.1|AC079828_15 unknown protein [Arabidopsis thaliana] gi|28466907|gb|AAO44062.1| At1g51160 [Arabidopsis thaliana] gi|110743933|dbj|BAE99800.1| hypothetical protein [Arabidopsis thaliana] gi|297337462|gb|EFH67879.1| hypothetical protein ARALYDRAFT_892078 [Arabidopsis lyrata subsp. lyrata] gi|332194507|gb|AEE32628.1| SNARE-like protein [Arabidopsis thaliana] gi|332194508|gb|AEE32629.1| SNARE-like protein [Arabidopsis thaliana]</td><td>169</td><td>169</td><td>4.00E-94</td><td>100.0</td><td>98.8</td><td>98.8</td><td>SNARE-like protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G51160.2 | Symbols: | SNARE-like superfamily protein | chr1:18950057-18951560 FORWARD LENGTH=169</td><td>169</td><td>169</td><td>2.00E-96</td><td>100.0</td><td>98.8</td><td>98.8</td></tr>
<tr><td>Rsa1.0_00769.1.g19232.t1</td><td>ref|NP_564584.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|4836928|gb|AAD30630.1|AC006085_3 Similar to protein kinases [Arabidopsis thaliana] gi|12320780|gb|AAG50535.1|AC079828_6 serine/threonine protein kinase, putative [Arabidopsis thaliana] gi|110738644|dbj|BAF01247.1| putative serine/threonine protein kinase [Arabidopsis thaliana] gi|115311465|gb|ABI93913.1| At1g51170 [Arabidopsis thaliana] gi|332194509|gb|AEE32630.1| protein kinase domain-containing protein [Arabidopsis thaliana]</td><td>381</td><td>404</td><td>0</td><td>106.0</td><td>87.9</td><td>93.2</td><td>protein kinase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G51170.1 | Symbols: | Protein kinase superfamily protein | chr1:18953625-18954839 REVERSE LENGTH=404</td><td>381</td><td>404</td><td>0</td><td>106.0</td><td>87.9</td><td>93.2</td></tr>
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Rsa1.0_00769.1.g19233.t1	ref|XP_002892480.1| hypothetical protein ARALYDRAFT_311954 [Arabidopsis lyrata subsp. lyrata] gi|297338322|gb|EFH68739.1| hypothetical protein ARALYDRAFT_311954 [Arabidopsis lyrata subsp. lyrata]	248	646	8.00E-19	260.5	27.4	31.5	hypothetical protein ARALYDRAFT_311954	gbpln	Arabidopsis lyrata	AT1G09080.1 | Symbols: BIP3 | Heat shock protein 70 (Hsp 70) family protein | chr1:2929268-2931804 REVERSE LENGTH=675	248	675	7.00E-21	272.2	27.0	31.0
Rsa1.0_00769.1.g19234.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	690	1557	1.00E-151	225.7	45.2	62.6	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	690	361	8.00E-31	52.3	10.4	16.7
Rsa1.0_00770.1.g19235.t1	gb|AAF16534.1|AC013482_8 T26F17.17 [Arabidopsis thaliana]	81	1291	1.00E-33	1593.8	87.7	92.6	T26F17.17	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00770.1.g19236.t1	gb|EOA18959.1| hypothetical protein CARUB_v10007594mg [Capsella rubella]	547	454	0	83.0	72.8	77.0	hypothetical protein CARUB_v10007594mg	gbpln	Capsella rubella	AT4G21250.1 | Symbols: | Sulfite exporter TauE/SafE family protein | chr4:11325030-11326637 FORWARD LENGTH=449	547	449	0	82.1	71.1	76.8
Rsa1.0_00770.1.g19237.t1	dbj|BAF81515.1| oxygen-evolving enhancer protein 3-2 [Brassica rapa]	227	227	1.00E-123	100.0	98.2	99.1	oxygen-evolving enhancer protein 3-2	gbpln	Brassica rapa	AT4G21280.1 | Symbols: PSBQ, PSBQA, PSBQ-1 | photosystem II subunit QA | chr4:11334446-11335587 FORWARD LENGTH=223	227	223	1.00E-102	98.2	83.3	89.4
Rsa1.0_00770.1.g19238.t1	ref|NP_193861.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75207660|sp|Q9STE1.1|PP333_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g21300 gi|3402749|emb|CAA20195.1| putative protein [Arabidopsis thaliana] gi|7268926|emb|CAB79129.1| putative protein [Arabidopsis thaliana] gi|332659037|gb|AEE84437.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	842	857	0	101.8	82.1	90.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G21300.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:11336479-11339052 FORWARD LENGTH=857	842	857	0	101.8	82.1	90.1
Rsa1.0_00770.1.g19239.t1	ref|NP_193862.1| uncharacterized protein [Arabidopsis thaliana] gi|3402750|emb|CAA20196.1| putative protein [Arabidopsis thaliana] gi|7268927|emb|CAB79130.1| putative protein [Arabidopsis thaliana] gi|48310105|gb|AAT41754.1| At4g21310 [Arabidopsis thaliana] gi|50198867|gb|AAT70460.1| At4g21310 [Arabidopsis thaliana] gi|332659038|gb|AEE84438.1| uncharacterized protein AT4G21310 [Arabidopsis thaliana]	168	168	1.00E-86	100.0	92.9	97.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G21310.1 | Symbols: | Protein of unknown function (DUF1218) | chr4:11339134-11339787 REVERSE LENGTH=168	168	168	6.00E-89	100.0	92.9	97.0
Rsa1.0_00770.1.g19240.t1	ref|NP_567624.1| Subtilase family protein [Arabidopsis thaliana] gi|332659040|gb|AEE84440.1| Subtilase family protein [Arabidopsis thaliana]	799	803	0	100.5	74.5	83.9	Subtilase family protein	gbpln	Arabidopsis thaliana	AT4G21323.1 | Symbols: | Subtilase family protein | chr4:11342494-11345632 FORWARD LENGTH=803	799	803	0	100.5	74.5	83.9
Rsa1.0_00770.1.g19241.t1	emb|CCI61494.1| unnamed protein product [Arabidopsis halleri]	755	756	0	100.1	70.7	82.0	unnamed protein product	gbpln	Arabidopsis halleri	AT4G21326.1 | Symbols: ATSBT3.12, SBT3.12 | subtilase 3.12 | chr4:11346685-11349653 FORWARD LENGTH=754	755	754	0	99.9	69.5	81.1
Rsa1.0_00770.1.g19242.t1	gb|ADQ37369.1| unknown [Arabidopsis lyrata]	216	208	6.00E-93	96.3	81.0	87.5	unknown	gbpln	Arabidopsis lyrata	AT4G21330.1 | Symbols: DYT1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:11349922-11350694 FORWARD LENGTH=207	216	207	1.00E-91	95.8	79.2	86.1
Rsa1.0_00770.1.g19243.t1	gb|ADQ37380.1| unknown [Arabidopsis lyrata]	286	301	7.00E-99	105.2	69.2	80.4	unknown	gbpln	Arabidopsis lyrata	AT4G21340.1 | Symbols: B70 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:11353064-11354628 FORWARD LENGTH=301	286	301	1.00E-100	105.2	69.2	80.4
Rsa1.0_00770.1.g19244.t1	gb|ADQ37381.1| unknown [Arabidopsis lyrata]	370	374	0	101.1	91.1	95.7	unknown	gbpln	Arabidopsis lyrata	AT4G21350.1 | Symbols: B80, PUB8 | plant U-box 8 | chr4:11356143-11357267 REVERSE LENGTH=374	370	374	0	101.1	90.0	94.9
Rsa1.0_00770.1.g19245.t1	emb|CAA67145.1| receptor-like kinase [Brassica oleracea var. viridis]	846	847	0	100.1	93.9	97.2	receptor-like kinase	gbpln	Brassica oleracea	AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850	846	850	0	100.5	82.2	88.7
Rsa1.0_00770.1.g19246.t1	emb|CAA73134.1| serine/threonine kinase [Brassica oleracea]	856	850	0	99.3	93.6	96.6	serine/threonine kinase	gbpln	Brassica oleracea	AT4G21390.1 | Symbols: B120 | S-locus lectin protein kinase family protein | chr4:11394458-11397474 REVERSE LENGTH=849	856	849	0	99.2	86.3	92.3
Rsa1.0_00770.1.g19247.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00770.1.g19248.t1	gb|ADQ37395.1| unknown [Capsella rubella]	680	689	0	101.3	86.9	92.4	unknown	gbpln	Capsella rubella	AT4G21410.1 | Symbols: CRK29 | cysteine-rich RLK (RECEPTOR-like protein kinase) 29 | chr4:11402463-11405025 REVERSE LENGTH=679	680	679	0	99.9	85.3	91.5

Rsa1.0_00770.1.g19249.t1	ref|XP_002869889.1| At4g21420 [Arabidopsis lyrata subsp. lyrata] gi|297315725|gb|EFH46148.1| At4g21420 [Arabidopsis lyrata subsp. lyrata]	200	201	6.00E-98	100.5	85.0	94.0	At4g21420	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00770.1.g19250.t1	emb|CCI61488.1| unnamed protein product [Arabidopsis halleri]	968	936	0	96.7	70.5	78.9	unnamed protein product	gbpln	Arabidopsis halleri	AT4G21430.1 | Symbols: B160 | Zinc finger, RING-type;Transcription factor jumonji/aspartyl beta-hydroxylase | chr4:11407835-11412159 REVERSE LENGTH=927	968	927	0	95.8	68.7	77.3
Rsa1.0_00771.1.g19251.t1	ref|NP_188645.1| cytochrome P450, family 705, subfamily A, polypeptide 19 [Arabidopsis thaliana] gi|9293967|dbj|BAB01870.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|15215772|gb|AAK91431.1| AT3g20100/MAL21_14 [Arabidopsis thaliana] gi|27764974|gb|AAO23608.1| At3g20100/MAL21_14 [Arabidopsis thaliana] gi|332642812|gb|AEE76333.1| cytochrome P450, family 705, subfamily A, polypeptide 19 [Arabidopsis thaliana]	465	513	0	110.3	68.2	81.3	cytochrome P450, family 705, subfamily A, polypeptide 19	gbpln	Arabidopsis thaliana	AT3G20100.1 | Symbols: CYP705A19 | cytochrome P450, family 705, subfamily A, polypeptide 19 | chr3:7019014-7020649 FORWARD LENGTH=513	465	513	0	110.3	68.2	81.3
Rsa1.0_00771.1.g19252.t1	ref|NP_188649.1| cytochrome P450, family 705, subfamily A, polypeptide 23 [Arabidopsis thaliana] gi|9293971|dbj|BAB01874.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|91806443|gb|ABE65949.1| cytochrome P450 family protein [Arabidopsis thaliana] gi|332642818|gb|AEE76339.1| cytochrome P450, family 705, subfamily A, polypeptide 23 [Arabidopsis thaliana]	517	510	0	98.6	73.3	81.2	cytochrome P450, family 705, subfamily A, polypeptide 23	gbpln	Arabidopsis thaliana	AT3G20140.1 | Symbols: CYP705A23 | cytochrome P450, family 705, subfamily A, polypeptide 23 | chr3:7029175-7030787 FORWARD LENGTH=510	517	510	0	98.6	73.3	81.2
Rsa1.0_00771.1.g19253.t1	ref|NP_188648.1| cytochrome P450, family 705, subfamily A, polypeptide 22 [Arabidopsis thaliana] gi|9293970|dbj|BAB01873.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|30102724|gb|AAP21280.1| At3g20130 [Arabidopsis thaliana] gi|110736609|dbj|BAF00269.1| putative cytochrome P450 [Arabidopsis thaliana] gi|332642816|gb|AEE76337.1| cytochrome P450, family 705, subfamily A, polypeptide 22 [Arabidopsis thaliana]	517	515	0	99.6	72.1	85.3	cytochrome P450, family 705, subfamily A, polypeptide 22	gbpln	Arabidopsis thaliana	AT3G20130.1 | Symbols: CYP705A22 | cytochrome P450, family 705, subfamily A, polypeptide 22 | chr3:7026982-7028613 FORWARD LENGTH=515	517	515	0	99.6	72.1	85.3
Rsa1.0_00771.1.g19254.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00771.1.g19255.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00771.1.g19256.t1	ref|XP_002868209.1| hypothetical protein ARALYDRAFT_493357 [Arabidopsis lyrata subsp. lyrata] gi|297314045|gb|EFH44468.1| hypothetical protein ARALYDRAFT_493357 [Arabidopsis lyrata subsp. lyrata]	140	757	4.00E-56	540.7	72.9	83.6	hypothetical protein ARALYDRAFT_493357	gbpln	Arabidopsis lyrata	AT4G15370.1 | Symbols: BARS1, PEN2 | baruol synthase 1 | chr4:8773786-8779685 REVERSE LENGTH=759	140	759	1.00E-58	542.1	73.6	82.9
Rsa1.0_00771.1.g19257.t1	gb|EOA18520.1| hypothetical protein CARUB_v10007073mg [Capsella rubella]	556	763	0	137.2	79.0	90.5	hypothetical protein CARUB_v10007073mg	gbpln	Capsella rubella	AT1G78500.1 | Symbols: | Terpenoid cyclases family protein | chr1:29531646-29535177 FORWARD LENGTH=767	556	767	0	137.9	72.7	86.7
Rsa1.0_00771.1.g19258.t1	gb|EOA30474.1| hypothetical protein CARUB_v10013599mg [Capsella rubella]	249	477	8.00E-66	191.6	54.6	60.6	hypothetical protein CARUB_v10013599mg	gbpln	Capsella rubella	AT3G20170.1 | Symbols: | ARM repeat superfamily protein | chr3:7041780-7043207 FORWARD LENGTH=475	249	475	7.00E-67	190.8	54.2	58.6
Rsa1.0_00771.1.g19259.t1	gb|EOA32511.1| hypothetical protein CARUB_v10015791mg [Capsella rubella]	146	121	7.00E-33	82.9	54.1	65.8	hypothetical protein CARUB_v10015791mg	gbpln	Capsella rubella	AT3G20180.1 | Symbols: | Copper transport protein family | chr3:7043385-7043841 REVERSE LENGTH=118	146	118	1.00E-32	80.8	49.3	64.4
Rsa1.0_00771.1.g19260.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	1628	1466	0	90.0	58.2	69.8	copia-like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1628	1262	1.00E-103	77.5	11.0	16.6
Rsa1.0_00771.1.g19261.t1	ref|XP_002883963.1| RNA-dependent RNA polymerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329803|gb|EFH60222.1| RNA-dependent RNA polymerase family protein [Arabidopsis lyrata subsp. lyrata]	735	981	0	133.5	69.7	78.4	RNA-dependent RNA polymerase family protein	gbpln	Arabidopsis lyrata	AT2G19930.1 | Symbols: | RNA-dependent RNA polymerase family protein | chr2:8607533-8612441 REVERSE LENGTH=977	735	977	0	132.9	68.4	77.7
Rsa1.0_00771.1.g19262.t1	sp|O81776.2|GLR24_ARATH RecName: Full=Glutamate receptor 2.4; AltName: Full=Ligand-gated ion channel 2.4; Flags: Precursor	913	896	0	98.1	80.8	89.0	RecName: Full=Glutamate receptor 2.4; AltName: Full=Ligand-gated ion channel 2.4; Flags: Precursor	----	----	AT4G31710.1 | Symbols: ATGLR2.4, GLR2.4 | glutamate receptor 2.4 | chr4:15349121-15352962 FORWARD LENGTH=898	913	898	0	98.4	78.5	86.6

Rsa1.0_00771.1.g19263.t1	gb|EOA29917.1| hypothetical protein CARUB_v10013010mg [Capsella rubella]	798	793	0	99.4	85.2	91.5	hypothetical protein CARUB_v10013010mg	gbpln	Capsella rubella	AT3G20200.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr3:7047895-7051145 FORWARD LENGTH=780	798	780	0	97.7	84.7	90.7
Rsa1.0_00771.1.g19264.t6	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00772.1.g19265.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1190	1223	0	102.8	44.6	63.1	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1190	746	5.00E-88	62.7	14.7	20.0
Rsa1.0_00772.1.g19266.t1	ref|XP_002873852.1| hypothetical protein ARALYDRAFT_909780 [Arabidopsis lyrata subsp. lyrata] gi|297319689|gb|EFH50111.1| hypothetical protein ARALYDRAFT_909780 [Arabidopsis lyrata subsp. lyrata]	281	281	1.00E-152	100.0	92.5	96.8	hypothetical protein ARALYDRAFT_909780	gbpln	Arabidopsis lyrata	AT5G17770.1 | Symbols: ATCBR, CBR1, CBR | NADH:cytochrome B5 reductase 1 | chr5:5864543-5866495 REVERSE LENGTH=281	281	281	1.00E-150	100.0	93.2	97.2
Rsa1.0_00772.1.g19267.t1	gb|EOA20461.1| hypothetical protein CARUB_v10000774mg [Capsella rubella]	480	505	0	105.2	89.8	95.0	hypothetical protein CARUB_v10000774mg	gbpln	Capsella rubella	AT5G17760.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:5860591-5862301 REVERSE LENGTH=505	480	505	0	105.2	88.8	94.6
Rsa1.0_00772.1.g19268.t1	gb|AAB84340.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	803	1094	0	136.2	46.5	64.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	803	575	8.00E-71	71.6	19.4	31.6
Rsa1.0_00772.1.g19269.t1	gb|EOA21102.1| hypothetical protein CARUB_v10001443mg [Capsella rubella]	325	326	1.00E-148	100.3	89.2	93.8	hypothetical protein CARUB_v10001443mg	gbpln	Capsella rubella	AT5G17710.2 | Symbols: EMB1241 | Co-chaperone GrpE family protein | chr5:5839560-5841639 REVERSE LENGTH=326	325	326	1.00E-148	100.3	87.7	91.4
Rsa1.0_00772.1.g19270.t1	ref|NP_197272.2| mate efflux domain-containing protein [Arabidopsis thaliana] gi|20466400|gb|AAM20517.1| putative protein [Arabidopsis thaliana] gi|23198102|gb|AAN15578.1| putative protein [Arabidopsis thaliana] gi|332005074|gb|AED92457.1| mate efflux domain-containing protein [Arabidopsis thaliana]	498	497	0	99.8	87.8	93.6	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT5G17700.1 | Symbols: | MATE efflux family protein | chr5:5831025-5833415 REVERSE LENGTH=497	498	497	0	99.8	87.8	93.6
Rsa1.0_00772.1.g19271.t1	gb|EOA20620.1| hypothetical protein CARUB_v10000932mg [Capsella rubella]	382	455	1.00E-122	119.1	70.2	81.2	hypothetical protein CARUB_v10000932mg	gbpln	Capsella rubella	AT5G17690.1 | Symbols: TFL2, LHP1 | like heterochromatin protein (LHP1) | chr5:5827504-5829537 REVERSE LENGTH=445	382	445	1.00E-113	116.5	71.7	81.4
Rsa1.0_00772.1.g19272.t1	ref|XP_002871778.1| hypothetical protein ARALYDRAFT_488633 [Arabidopsis lyrata subsp. lyrata] gi|297317615|gb|EFH48037.1| hypothetical protein ARALYDRAFT_488633 [Arabidopsis lyrata subsp. lyrata]	1569	1281	0	81.6	63.0	69.6	hypothetical protein ARALYDRAFT_488633	gbpln	Arabidopsis lyrata	AT5G17680.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr5:5822999-5827153 FORWARD LENGTH=1294	1569	1294	0	82.5	62.5	68.4
Rsa1.0_00772.1.g19273.t1	gb|AAM64307.1| nuclear matrix protein 1 [Arabidopsis thaliana]	329	329	0	100.0	97.9	98.8	nuclear matrix protein 1	gbpln	Arabidopsis thaliana	AT5G17620.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Plant nuclear matrix 1 (InterPro:IPR010604); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5805934-5808455 REVERSE LENGTH=329	329	329	0	100.0	97.9	98.8
Rsa1.0_00772.1.g19274.t1	ref|XP_002871775.1| hypothetical protein ARALYDRAFT_488628 [Arabidopsis lyrata subsp. lyrata] gi|297317612|gb|EFH48034.1| hypothetical protein ARALYDRAFT_488628 [Arabidopsis lyrata subsp. lyrata]	122	120	9.00E-50	98.4	82.8	90.2	hypothetical protein ARALYDRAFT_488628	gbpln	Arabidopsis lyrata	AT5G17610.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5804011-5805045 FORWARD LENGTH=121	122	121	3.00E-50	99.2	81.1	87.7
Rsa1.0_00772.1.g19275.t1	gb|EOA22487.1| hypothetical protein CARUB_v10003140mg [Capsella rubella]	138	193	9.00E-39	139.9	76.8	89.1	hypothetical protein CARUB_v10003140mg	gbpln	Capsella rubella	AT5G17590.1 | Symbols: | Putative membrane lipoprotein | chr5:5797371-5797949 REVERSE LENGTH=192	138	192	5.00E-41	139.1	71.0	82.6
Rsa1.0_00772.1.g19276.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1880	1274	0	67.8	36.9	46.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1880	575	3.00E-68	30.6	9.7	14.5

Rsa1.0_00773.1.g19277.t1	ref|XP_002892324.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297338166|gb|EFH68583.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	428	421	0	98.4	82.7	90.0	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT1G06170.2 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:1885146-1886564 REVERSE LENGTH=420	428	420	0	98.1	80.8	90.0
Rsa1.0_00773.1.g19278.t1	ref|NP_172108.1| myb proto-oncogene protein [Arabidopsis thaliana] gi|8844123|gb|AAF80215.1|AC025290_4 Identical to the myb protein from Arabidopsis thaliana gb|Z50869 and contains a myb-like DNA binding PF|00249 domain [Arabidopsis thaliana] gi|41619084|gb|AAS10020.1| MYB transcription factor [Arabidopsis thaliana] gi|92856632|gb|ABE77411.1| At1g06180 [Arabidopsis thaliana] gi|225897886|dbj|BAH30275.1| hypothetical protein [Arabidopsis thaliana] gi|332189834|gb|AEE27955.1| myb domain protein 13 [Arabidopsis thaliana]	253	246	3.00E-98	97.2	74.7	83.8	myb proto-oncogene protein	gbpln	Arabidopsis thaliana	AT1G06180.1 | Symbols: ATMYB13, ATMYBLFGN, MYB13 | myb domain protein 13 | chr1:1889510-1891089 FORWARD LENGTH=246	253	246	1.00E-101	97.2	74.7	83.8
Rsa1.0_00773.1.g19279.t3	gb|EOA39379.1| hypothetical protein CARUB_v10012464mg [Capsella rubella]	205	206	1.00E-105	100.5	88.8	97.1	hypothetical protein CARUB_v10012464mg	gbpln	Capsella rubella	AT1G06200.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr1:1894604-1896852 REVERSE LENGTH=206	205	206	1.00E-107	100.5	87.3	96.6
Rsa1.0_00773.1.g19280.t1	gb|EOA37974.1| hypothetical protein CARUB_v10009444mg [Capsella rubella]	383	381	1.00E-173	99.5	82.8	90.1	hypothetical protein CARUB_v10009444mg	gbpln	Capsella rubella	AT1G06210.1 | Symbols: | ENTH/VHS/GAT family protein | chr1:1897567-1898986 FORWARD LENGTH=383	383	383	1.00E-175	100.0	83.3	90.3
Rsa1.0_00773.1.g19281.t1	gb|EOA38987.1| hypothetical protein CARUB_v10011516mg [Capsella rubella]	83	81	6.00E-24	97.6	69.9	79.5	hypothetical protein CARUB_v10011516mg	gbpln	Capsella rubella	AT1G06225.1 | Symbols: CLE3 | CLAVATA3/ESR-RELATED 3 | chr1:1905975-1906226 FORWARD LENGTH=83	83	83	2.00E-23	100.0	60.2	63.9
Rsa1.0_00773.1.g19282.t1	gb|EOA39708.1| hypothetical protein CARUB_v10008353mg [Capsella rubella]	767	784	0	102.2	76.7	82.5	hypothetical protein CARUB_v10008353mg	gbpln	Capsella rubella	AT1G06230.3 | Symbols: GTE4 | global transcription factor group E4 | chr1:1907626-1910183 FORWARD LENGTH=766	767	766	0	99.9	76.4	80.8
Rsa1.0_00773.1.g19283.t1	gb|EOA39214.1| hypothetical protein CARUB_v10012192mg [Capsella rubella]	402	423	0	105.2	81.3	90.0	hypothetical protein CARUB_v10012192mg	gbpln	Capsella rubella	AT1G06250.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:1913339-1914850 REVERSE LENGTH=423	402	423	0	105.2	79.6	90.3
Rsa1.0_00773.1.g19284.t1	ref|XP_002889596.1| hypothetical protein ARALYDRAFT_887827 [Arabidopsis lyrata subsp. lyrata] gi|297335438|gb|EFH65855.1| hypothetical protein ARALYDRAFT_887827 [Arabidopsis lyrata subsp. lyrata]	345	343	1.00E-157	99.4	76.5	86.7	hypothetical protein ARALYDRAFT_887827	gbpln	Arabidopsis lyrata	AT1G06260.1 | Symbols: | Cysteine proteinases superfamily protein | chr1:1916449-1917585 FORWARD LENGTH=343	345	343	1.00E-158	99.4	75.9	86.1
Rsa1.0_00773.1.g19285.t1	ref|XP_002892331.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338173|gb|EFH68590.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	340	343	0	100.9	92.1	95.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G06270.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:1918242-1919273 REVERSE LENGTH=343	340	343	0	100.9	90.9	95.9
Rsa1.0_00773.1.g19286.t1	gb|EOA39249.1| hypothetical protein CARUB_v10012245mg [Capsella rubella]	677	675	0	99.7	91.3	96.0	hypothetical protein CARUB_v10012245mg	gbpln	Capsella rubella	AT1G06290.1 | Symbols: ACX3, ATACX3 | acyl-CoA oxidase 3 | chr1:1922423-1926002 FORWARD LENGTH=675	677	675	0	99.7	91.3	96.8
Rsa1.0_00773.1.g19287.t1	ref|XP_002892336.1| fatty acid desaturase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338178|gb|EFH68595.1| fatty acid desaturase family protein [Arabidopsis lyrata subsp. lyrata]	300	299	1.00E-134	99.7	79.0	87.0	fatty acid desaturase family protein	gbpln	Arabidopsis lyrata	AT1G06350.1 | Symbols: | Fatty acid desaturase family protein | chr1:1935510-1936789 REVERSE LENGTH=300	300	300	1.00E-136	100.0	78.0	88.0
Rsa1.0_00773.1.g19288.t1	ref|NP_172120.2| acyl-CoA oxidase [Arabidopsis thaliana] gi|62286635|sp|Q9LMI7.1|ACO32_ARATH RecName: Full=Putative acyl-coenzyme A oxidase 3.2, peroxisomal; Flags: Precursor gi|8927669|gb|AAF82160.1|AC068143_2 Contains similarity to an acyl-CoA oxidase (ASX2) mRNA from Arabidopsis thaliana gb|AF057043 and contains an acyl-CoA oxidase PF|01756 domain [Arabidopsis thaliana] gi|332189852|gb|AEE27973.1| acyl-CoA oxidase [Arabidopsis thaliana]	675	675	0	100.0	86.1	93.0	acyl-CoA oxidase	gbpln	Arabidopsis thaliana	AT1G06310.1 | Symbols: ACX6 | acyl-CoA oxidase 6 | chr1:1926802-1930227 FORWARD LENGTH=675	675	675	0	100.0	86.1	93.0

Rsa1.0_00773.1.g19289.t1	ref|XP_002892337.1| fatty acid desaturase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338179|gb|EFH68596.1| fatty acid desaturase family protein [Arabidopsis lyrata subsp. lyrata]	299	299	1.00E-151	100.0	89.0	94.0	fatty acid desaturase family protein	gbpln	Arabidopsis lyrata	AT1G06360.1 | Symbols: | Fatty acid desaturase family protein | chr1:1939173-1940417 REVERSE LENGTH=299	299	299	1.00E-152	100.0	88.3	92.6
Rsa1.0_00773.1.g19290.t1	ref|XP_002889602.1| hypothetical protein ARALYDRAFT_470660 [Arabidopsis lyrata subsp. lyrata] gi|297335444|gb|EFH65861.1| hypothetical protein ARALYDRAFT_470660 [Arabidopsis lyrata subsp. lyrata]	848	851	0	100.4	88.4	94.2	hypothetical protein ARALYDRAFT_470660	gbpln	Arabidopsis lyrata	AT1G06410.1 | Symbols: ATTPS7, TPS7, ATTPSA | trehalose-phosphatase/synthase 7 | chr1:1955413-1958153 FORWARD LENGTH=851	848	851	0	100.4	88.2	94.0
Rsa1.0_00773.1.g19291.t1	gb|EOA38492.1| hypothetical protein CARUB_v10010258mg [Capsella rubella]	241	219	2.00E-29	90.9	46.5	56.0	hypothetical protein CARUB_v10010258mg	gbpln	Capsella rubella	AT1G06420.1 | Symbols: | unknown protein; Has 1017 Blast hits to 654 proteins in 124 species: Archae - 0; Bacteria - 39; Metazoa - 232; Fungi - 69; Plants - 40; Viruses - 0; Other Eukaryotes - 637 (source: NCBI BLink). | chr1:1958987-1959652 FORWARD LENGTH=221	241	221	4.00E-17	91.7	39.4	51.0
Rsa1.0_00773.1.g19292.t1	dbj|BAJ33891.1| unnamed protein product [Thellungiella halophila]	694	693	0	99.9	97.1	98.4	unnamed protein product	----	----	AT1G06430.1 | Symbols: FTSH8 | FTSH protease 8 | chr1:1960214-1962525 REVERSE LENGTH=685	694	685	0	98.7	91.8	93.9
Rsa1.0_00773.1.g19293.t1	gb|EOA37683.1| hypothetical protein CARUB_v10012333mg [Capsella rubella]	386	390	0	101.0	89.4	94.3	hypothetical protein CARUB_v10012333mg	gbpln	Capsella rubella	AT1G06440.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr1:1963733-1964905 REVERSE LENGTH=390	386	390	0	101.0	89.4	94.6
Rsa1.0_00773.1.g19294.t1	gb|ABV89635.1| peroxisomal small heat shock protein ACD31.2 [Brassica rapa]	298	291	1.00E-134	97.7	81.2	86.6	peroxisomal small heat shock protein ACD31.2	gbpln	Brassica rapa	AT1G06460.1 | Symbols: ACD32.1, ACD31.2 | alpha-crystallin domain 32.1 | chr1:1967308-1969414 REVERSE LENGTH=285	298	285	1.00E-109	95.6	73.8	79.2
Rsa1.0_00773.1.g19295.t4	ref|XP_002889605.1| hypothetical protein ARALYDRAFT_887850 [Arabidopsis lyrata subsp. lyrata] gi|297335447|gb|EFH65864.1| hypothetical protein ARALYDRAFT_887850 [Arabidopsis lyrata subsp. lyrata]	399	414	0	103.8	92.2	95.0	hypothetical protein ARALYDRAFT_887850	gbpln	Arabidopsis lyrata	AT1G06470.2 | Symbols: | Nucleotide/sugar transporter family protein | chr1:1970726-1973540 FORWARD LENGTH=414	399	414	0	103.8	90.2	93.5
Rsa1.0_00773.1.g19296.t1	ref|XP_002892344.1| hypothetical protein ARALYDRAFT_470668 [Arabidopsis lyrata subsp. lyrata] gi|297338186|gb|EFH68603.1| hypothetical protein ARALYDRAFT_470668 [Arabidopsis lyrata subsp. lyrata]	87	86	2.00E-26	98.9	70.1	82.8	hypothetical protein ARALYDRAFT_470668	gbpln	Arabidopsis lyrata	AT1G06475.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:1973992-1974273 REVERSE LENGTH=93	87	93	1.00E-21	106.9	63.2	72.4
Rsa1.0_00774.1.g19297.t2	ref|NP_199688.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|9758876|dbj|BAB09430.1| disease resistance protein [Arabidopsis thaliana] gi|332008339|gb|AED95722.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	853	1190	1.00E-117	139.5	28.6	39.7	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G48770.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:19773277-19777242 REVERSE LENGTH=1190	853	1190	1.00E-120	139.5	28.6	39.7
Rsa1.0_00774.1.g19298.t1	ref|NP_177427.2| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|110737528|dbj|BAF00706.1| hypothetical protein [Arabidopsis thaliana] gi|332197259|gb|AEE35380.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	164	1042	5.00E-32	635.4	50.0	66.5	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT1G72840.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr1:27410020-27413485 REVERSE LENGTH=1042	164	1042	2.00E-34	635.4	50.0	66.5
Rsa1.0_00774.1.g19299.t2	gb|ABW81058.1| atlantys transposase [Arabidopsis lyrata subsp. lyrata]	632	777	4.00E-24	122.9	11.1	17.6	atlantys transposase	gbpln	Arabidopsis lyrata	AT4G03830.1 | Symbols: | Protein of unknown function, DUF601 | chr4:1790440-1792458 FORWARD LENGTH=578	632	578	9.00E-25	91.5	10.4	16.3
Rsa1.0_00774.1.g19300.t1	gb|AAD28663.1| hypothetical protein [Arabidopsis thaliana]	329	356	1.00E-12	108.2	12.5	19.1	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00774.1.g19301.t1	gb|AAC28207.1| T24H24.13 gene product [Arabidopsis thaliana] gi|7267161|emb|CAB77873.1| putative transposon protein [Arabidopsis thaliana]	471	681	2.00E-34	144.6	18.5	27.0	T24H24.13 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00774.1.g19302.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00774.1.g19303.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	201	1142	6.00E-23	568.2	33.8	52.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	201	292	4.00E-16	145.3	26.9	47.8
Rsa1.0_00774.1.g19304.t1	ref|XP_004309249.1| PREDICTED: TMV resistance protein N-like [Fragaria vesca subsp. vesca]	164	416	2.00E-25	253.7	37.8	59.8	PREDICTED: TMV resistance protein N-like	gbpln	Fragaria vesca	AT1G65850.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:24494734-24498485 FORWARD LENGTH=1036	164	1036	9.00E-28	631.7	40.9	57.9

Rsa1.0_00774.1.g19305.t1	ref|XP_002868674.1| hypothetical protein ARALYDRAFT_493978 [Arabidopsis lyrata subsp. lyrata] gi|297314510|gb|EFH44933.1| hypothetical protein ARALYDRAFT_493978 [Arabidopsis lyrata subsp. lyrata]	392	434	2.00E-42	110.7	27.6	44.1	hypothetical protein ARALYDRAFT_493978	gbpln	Arabidopsis lyrata	AT4G09420.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr4:5962319-5963776 REVERSE LENGTH=457	392	457	3.00E-44	116.6	29.1	44.6
Rsa1.0_00774.1.g19306.t1	dbj|BAB09567.1| disease resistance protein-like [Arabidopsis thaliana]	505	1295	9.00E-66	256.4	32.3	51.7	disease resistance protein-like	gbpln	Arabidopsis thaliana	AT1G72870.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27421086-27422999 FORWARD LENGTH=512	505	512	2.00E-67	101.4	35.4	53.5
Rsa1.0_00774.1.g19307.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00775.1.g19308.t1	ref|NP_193284.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75277384|sp|O23401.1|U84A3_ARATH RecName: Full=UDP-glycosyltransferase 84A3; AltName: Full=Hydroxycinnamate glucosyltransferase 3; Short=AtHCAGT3 gi|2244906|emb|CAB10327.1| indole-3-acetate beta-glucosyltransferase like protein [Arabidopsis thaliana] gi|7268296|emb|CAB78591.1| indole-3-acetate beta-glucosyltransferase like protein [Arabidopsis thaliana] gi|16323085|gb|AAL15277.1| AT4g15490/dl3785c [Arabidopsis thaliana] gi|18377771|gb|AAL67035.1| putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana] gi|23296972|gb|AAN13214.1| putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana] gi|332658210|gb|AEE83610.1| UDP-glycosyltransferase 84A3 [Arabidopsis thaliana]	284	479	3.00E-70	168.7	45.1	49.3	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT4G15490.1 | Symbols: UGT84A3 | UDP-Glycosyltransferase superfamily protein | chr4:8852864-8854303 REVERSE LENGTH=479	284	479	7.00E-73	168.7	45.1	49.3
Rsa1.0_00775.1.g19309.t1	emb|CAJ77651.1| UDP glucosyltransferase related [Brassica napus]	193	476	4.00E-21	246.6	28.0	31.1	UDP glucosyltransferase related	gbpln	Brassica napus	AT4G15480.1 | Symbols: UGT84A1 | UDP-Glycosyltransferase superfamily protein | chr4:8849000-8850472 REVERSE LENGTH=490	193	490	1.00E-19	253.9	22.3	25.9
Rsa1.0_00775.1.g19310.t1	ref|XP_002870237.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316073|gb|EFH46496.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	321	374	1.00E-152	116.5	85.4	90.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G15450.1 | Symbols: | Senescence/dehydration-associated protein-related | chr4:8839437-8841162 FORWARD LENGTH=381	321	381	1.00E-154	118.7	85.4	91.0
Rsa1.0_00775.1.g19311.t1	gb|EOA18436.1| hypothetical protein CARUB_v10006979mg [Capsella rubella]	655	801	0	122.3	66.9	80.8	hypothetical protein CARUB_v10006979mg	gbpln	Capsella rubella	AT1G62670.1 | Symbols: RPF2 | rna processing factor 2 | chr1:23204773-23206665 REVERSE LENGTH=630	655	630	9.00E-78	96.2	25.3	44.0
Rsa1.0_00775.1.g19312.t4	ref|XP_002870239.1| hypothetical protein ARALYDRAFT_493346 [Arabidopsis lyrata subsp. lyrata] gi|297316075|gb|EFH46498.1| hypothetical protein ARALYDRAFT_493346 [Arabidopsis lyrata subsp. lyrata]	760	761	0	100.1	87.6	92.1	hypothetical protein ARALYDRAFT_493346	gbpln	Arabidopsis lyrata	AT4G15430.2 | Symbols: | ERD (early-responsive to dehydration stress) family protein | chr4:8828214-8831354 FORWARD LENGTH=760	760	760	0	100.0	86.7	91.1
Rsa1.0_00775.1.g19313.t1	gb|EOA16124.1| hypothetical protein CARUB_v10004257mg [Capsella rubella]	109	706	1.00E-19	647.7	48.6	53.2	hypothetical protein CARUB_v10004257mg	gbpln	Capsella rubella	AT4G15420.1 | Symbols: | Ubiquitin fusion degradation UFD1 family protein | chr4:8823822-8825949 FORWARD LENGTH=561	109	561	2.00E-21	514.7	47.7	51.4
Rsa1.0_00775.1.g19314.t1	gb|EOA18385.1| hypothetical protein CARUB_v10006915mg [Capsella rubella]	385	393	1.00E-114	102.1	56.6	70.6	hypothetical protein CARUB_v10006915mg	gbpln	Capsella rubella	AT5G39560.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:15841885-15843096 REVERSE LENGTH=403	385	403	2.00E-76	104.7	49.4	62.9
Rsa1.0_00775.1.g19315.t1	gb|EOA18892.1| hypothetical protein CARUB_v10007521mg [Capsella rubella]	283	284	2.00E-79	100.4	57.2	72.8	hypothetical protein CARUB_v10007521mg	gbpln	Capsella rubella	AT4G15417.1 | Symbols: ATRTL1, RTL1 | RNAse II-like 1 | chr4:8821759-8822991 FORWARD LENGTH=264	283	264	2.00E-79	93.3	53.4	66.8
Rsa1.0_00775.1.g19316.t1	ref|XP_002870241.1| hypothetical protein ARALYDRAFT_329973 [Arabidopsis lyrata subsp. lyrata] gi|297316077|gb|EFH46500.1| hypothetical protein ARALYDRAFT_329973 [Arabidopsis lyrata subsp. lyrata]	492	948	0	192.7	88.4	93.5	hypothetical protein ARALYDRAFT_329973	gbpln	Arabidopsis lyrata	AT4G15415.1 | Symbols: ATB' GAMMA | Protein phosphatase 2A regulatory B subunit family protein | chr4:8817707-8819349 FORWARD LENGTH=522	492	522	0	106.1	88.6	93.7
Rsa1.0_00775.1.g19317.t2	ref|NP_680696.2| cytochrome P450, family 702, subfamily A, polypeptide 6 [Arabidopsis thaliana] gi|332658195|gb|AEE83595.1| cytochrome P450, family 702, subfamily A, polypeptide 6 [Arabidopsis thaliana]	564	475	0	84.2	64.7	73.8	cytochrome P450, family 702, subfamily A, polypeptide 6	gbpln	Arabidopsis thaliana	AT4G15396.1 | Symbols: CYP702A6 | cytochrome P450, family 702, subfamily A, polypeptide 6 | chr4:8807574-8810419 FORWARD LENGTH=475	564	475	0	84.2	64.7	73.8

Rsa1.0_00775.1.g19318.t1	ref|XP_002885880.1| hypothetical protein ARALYDRAFT_899583 [Arabidopsis lyrata subsp. lyrata] gi|297331720|gb|EFH62139.1| hypothetical protein ARALYDRAFT_899583 [Arabidopsis lyrata subsp. lyrata]	183	183	1.00E-13	100.0	30.6	45.4	hypothetical protein ARALYDRAFT_899583	gbpln	Arabidopsis lyrata	AT5G33330.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:12591754-12592896 REVERSE LENGTH=183	183	183	1.00E-14	100.0	27.3	38.8
Rsa1.0_00775.1.g19319.t1	gb|EOA15505.1| hypothetical protein CARUB_v10004825mg [Capsella rubella]	445	441	0	99.1	76.9	87.0	hypothetical protein CARUB_v10004825mg	gbpln	Capsella rubella	AT4G15390.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr4:8792941-8794281 REVERSE LENGTH=446	445	446	0	100.2	74.6	85.4
Rsa1.0_00775.1.g19320.t1	ref|NP_199609.1| BAHD acyltransferase [Arabidopsis thaliana] gi|75170749|sp|Q9FI40.1|BAHD1_ARATH RecName: Full=BAHD acyltransferase At5g47980 gi|10177749|dbj|BAB11062.1| acetyl-CoA:benzylalcohol acetyltranferase-like protein [Arabidopsis thaliana] gi|29028772|gb|AAO64765.1| At5g47980 [Arabidopsis thaliana] gi|110742843|dbj|BAE99320.1| acetyl-CoA:benzylalcohol acetyltranferase-like protein [Arabidopsis thaliana] gi|332008219|gb|AED95602.1| BAHD acyltransferase [Arabidopsis thaliana]	447	443	1.00E-147	99.1	57.5	75.2	BAHD acyltransferase	gbpln	Arabidopsis thaliana	AT5G47980.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:19428970-19430301 FORWARD LENGTH=443	447	443	1.00E-149	99.1	57.5	75.2
Rsa1.0_00775.1.g19321.t1	ref|NP_193263.1| UDP-glucosyl transferase 71B5 [Arabidopsis thaliana] gi|75277377|sp|O23382.1|U71B5_ARATH RecName: Full=UDP-glycosyltransferase 71B5 gi|2244886|emb|CAB10307.1| UTP-glucose glucosyltransferase [Arabidopsis thaliana] gi|7268275|emb|CAB78570.1| UTP-glucose glucosyltransferase [Arabidopsis thaliana] gi|332658180|gb|AEE83580.1| UDP-glucosyl transferase 71B5 [Arabidopsis thaliana]	476	478	0	100.4	74.8	84.0	UDP-glucosyl transferase 71B5	gbpln	Arabidopsis thaliana	AT4G15280.1 | Symbols: UGT71B5 | UDP-glucosyl transferase 71B5 | chr4:8719182-8720618 FORWARD LENGTH=478	476	478	0	100.4	74.8	84.0
Rsa1.0_00775.1.g19322.t1	ref|NP_193263.1| UDP-glucosyl transferase 71B5 [Arabidopsis thaliana] gi|75277377|sp|O23382.1|U71B5_ARATH RecName: Full=UDP-glycosyltransferase 71B5 gi|2244886|emb|CAB10307.1| UTP-glucose glucosyltransferase [Arabidopsis thaliana] gi|7268275|emb|CAB78570.1| UTP-glucose glucosyltransferase [Arabidopsis thaliana] gi|332658180|gb|AEE83580.1| UDP-glucosyl transferase 71B5 [Arabidopsis thaliana]	458	478	0	104.4	71.8	82.8	UDP-glucosyl transferase 71B5	gbpln	Arabidopsis thaliana	AT4G15280.1 | Symbols: UGT71B5 | UDP-glucosyl transferase 71B5 | chr4:8719182-8720618 FORWARD LENGTH=478	458	478	0	104.4	71.8	82.8
Rsa1.0_00775.1.g19323.t1	ref|NP_001031645.1| B-box type zinc finger-containing protein [Arabidopsis thaliana] gi|98962119|gb|ABF59389.1| unknown protein [Arabidopsis thaliana] gi|332658176|gb|AEE83576.1| B-box type zinc finger-containing protein [Arabidopsis thaliana]	97	117	2.00E-36	120.6	80.4	88.7	B-box type zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT4G15248.1 | Symbols: | B-box type zinc finger family protein | chr4:8708881-8709234 FORWARD LENGTH=117	97	117	4.00E-39	120.6	80.4	88.7
Rsa1.0_00775.1.g19324.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	414	1515	1.00E-141	365.9	60.1	75.6	retrotransposon like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00776.1.g19325.t1	ref|NP_974536.1| protein kinase family protein [Arabidopsis thaliana] gi|332657664|gb|AEE83064.1| protein kinase family protein [Arabidopsis thaliana]	361	354	1.00E-149	98.1	71.7	83.1	protein kinase family protein	gbpln	Arabidopsis thaliana	AT4G11890.3 | Symbols: | Protein kinase superfamily protein | chr4:7148269-7149772 FORWARD LENGTH=354	361	354	1.00E-151	98.1	71.7	83.1

Rsa1.0_00776.1.g19326.t1	ref|XP_002866474.1| hypothetical protein ARALYDRAFT_496390 [Arabidopsis lyrata subsp. lyrata] gi|297312309|gb|EFH42733.1| hypothetical protein ARALYDRAFT_496390 [Arabidopsis lyrata subsp. lyrata]	46	238	2.00E-14	517.4	82.6	91.3	hypothetical protein ARALYDRAFT_496390	gbpln	Arabidopsis lyrata	AT5G62140.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; Has 60 Blast hits to 60 proteins in 24 species: Archae - 0; Bacteria - 14; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:24954563-24955376 REVERSE LENGTH=241	46	241	9.00E-16	523.9	76.1	89.1
Rsa1.0_00776.1.g19327.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00776.1.g19328.t1	gb|AAP03023.1| acyl-activating enzyme 12 [Arabidopsis thaliana]	585	578	0	98.8	79.1	87.5	acyl-activating enzyme 12	gbpln	Arabidopsis thaliana	AT1G65890.1 | Symbols: AAE12 | acyl activating enzyme 12 | chr1:24512598-24514611 REVERSE LENGTH=578	585	578	0	98.8	78.8	87.2
Rsa1.0_00776.1.g19329.t1	gb|AAF79483.1|AC022492_27 F1L3.20 [Arabidopsis thaliana]	270	1188	2.00E-45	440.0	44.1	53.7	F1L3.20	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00776.1.g19330.t1	ref|XP_002874729.1| hypothetical protein ARALYDRAFT_490003 [Arabidopsis lyrata subsp. lyrata] gi|297320566|gb|EFH50988.1| hypothetical protein ARALYDRAFT_490003 [Arabidopsis lyrata subsp. lyrata]	140	687	1.00E-19	490.7	45.7	57.9	hypothetical protein ARALYDRAFT_490003	gbpln	Arabidopsis lyrata	AT4G11860.1 | Symbols: | Protein of unknown function (DUF544) | chr4:7134237-7138361 REVERSE LENGTH=682	140	682	9.00E-22	487.1	44.3	57.9
Rsa1.0_00776.1.g19331.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00776.1.g19332.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1090	1142	0	104.8	39.3	56.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1090	575	2.00E-84	52.8	16.0	26.5
Rsa1.0_00776.1.g19333.t1	gb|ACB98704.1| phospholipase D gamma 1 [Brassica oleracea var. capitata]	817	859	0	105.1	78.6	86.2	phospholipase D gamma 1	gbpln	Brassica oleracea	AT4G11850.1 | Symbols: PLDGAMMA1, MEE54 | phospholipase D gamma 1 | chr4:7129352-7132937 REVERSE LENGTH=858	817	858	0	105.0	78.6	86.7
Rsa1.0_00776.1.g19334.t1	gb|AAD29058.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	166	1229	6.00E-56	740.4	61.4	77.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	166	626	4.00E-17	377.1	24.1	34.3
Rsa1.0_00776.1.g19335.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	414	1274	2.00E-64	307.7	39.4	53.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	414	303	4.00E-33	73.2	21.7	31.4
Rsa1.0_00777.1.g19336.t1	ref|XP_002867087.1| O-methyltransferase family 2 protein [Arabidopsis lyrata subsp. lyrata] gi|297312923|gb|EFH43346.1| O-methyltransferase family 2 protein [Arabidopsis lyrata subsp. lyrata]	367	368	0	100.3	82.3	90.7	O-methyltransferase family 2 protein	gbpln	Arabidopsis lyrata	AT4G35160.1 | Symbols: | O-methyltransferase family protein | chr4:16730989-16732808 REVERSE LENGTH=382	367	382	1.00E-177	104.1	81.7	91.8
Rsa1.0_00777.1.g19337.t1	ref|XP_002867087.1| O-methyltransferase family 2 protein [Arabidopsis lyrata subsp. lyrata] gi|297312923|gb|EFH43346.1| O-methyltransferase family 2 protein [Arabidopsis lyrata subsp. lyrata]	367	368	1.00E-175	100.3	79.8	89.6	O-methyltransferase family 2 protein	gbpln	Arabidopsis lyrata	AT4G35160.1 | Symbols: | O-methyltransferase family protein | chr4:16730989-16732808 REVERSE LENGTH=382	367	382	1.00E-172	104.1	79.3	90.7
Rsa1.0_00777.1.g19338.t1	gb|EOA18110.1| hypothetical protein CARUB_v10006571mg [Capsella rubella]	446	457	1.00E-180	102.5	72.9	82.5	hypothetical protein CARUB_v10006571mg	gbpln	Capsella rubella	AT4G15740.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:8964912-8966318 REVERSE LENGTH=468	446	468	1.00E-180	104.9	71.5	81.2
Rsa1.0_00777.1.g19339.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00777.1.g19340.t1	ref|NP_567468.1| PsbP domain-containing protein 1 [Arabidopsis thaliana] gi|13959580|sp|O23403.1|PPD1_ARATH RecName: Full=PsbP domain-containing protein 1, chloroplastic; AltName: Full=OEC23-like protein 3; AltName: Full=PsbP-related thylakoid lumenal protein 1; Flags: Precursor gi|2244908|emb|CAB10329.1| hypothetical protein [Arabidopsis thaliana] gi|7268298|emb|CAB78593.1| hypothetical protein [Arabidopsis thaliana] gi|332658213|gb|AEE83613.1| PsbP domain-containing protein 1 [Arabidopsis thaliana]	207	287	1.00E-100	138.6	89.9	94.7	PsbP domain-containing protein 1	gbpln	Arabidopsis thaliana	AT4G15510.1 | Symbols: | Photosystem II reaction center PsbP family protein | chr4:8860701-8862529 FORWARD LENGTH=287	207	287	1.00E-103	138.6	89.9	94.7

Rsa1.0_00777.1.g19341.t2	ref|XP_002870236.1| hypothetical protein ARALYDRAFT_493344 [Arabidopsis lyrata subsp. lyrata] gi|297316072|gb|EFH46495.1| hypothetical protein ARALYDRAFT_493344 [Arabidopsis lyrata subsp. lyrata]	281	256	1.00E-134	91.1	86.1	90.4	hypothetical protein ARALYDRAFT_493344	gbpln	Arabidopsis lyrata	AT4G15470.1 | Symbols: | Bax inhibitor-1 family protein | chr4:8843661-8845505 FORWARD LENGTH=256	281	256	1.00E-135	91.1	85.8	90.0
Rsa1.0_00777.1.g19342.t1	gb|EOA18595.1| hypothetical protein CARUB_v10007167mg [Capsella rubella]	751	763	0	101.6	91.2	95.2	hypothetical protein CARUB_v10007167mg	gbpln	Capsella rubella	AT4G15430.2 | Symbols: | ERD (early-responsive to dehydration stress) family protein | chr4:8828214-8831354 FORWARD LENGTH=760	751	760	0	101.2	90.1	94.4
Rsa1.0_00777.1.g19343.t1	gb|AAG31651.1| PRLI-interacting factor K [Arabidopsis thaliana]	561	574	0	102.3	90.6	95.5	PRLI-interacting factor K	gbpln	Arabidopsis thaliana	AT4G15420.1 | Symbols: | Ubiquitin fusion degradation UFD1 family protein | chr4:8823822-8825949 FORWARD LENGTH=561	561	561	0	100.0	90.6	95.5
Rsa1.0_00777.1.g19344.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1036	1715	1.00E-154	165.5	30.2	43.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G04625.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr1:1287831-1289820 REVERSE LENGTH=257	1036	257	4.00E-36	24.8	6.8	9.7
Rsa1.0_00777.1.g19345.t1	ref|XP_002871263.1| hypothetical protein ARALYDRAFT_487555 [Arabidopsis lyrata subsp. lyrata] gi|297317100|gb|EFH47522.1| hypothetical protein ARALYDRAFT_487555 [Arabidopsis lyrata subsp. lyrata]	173	587	9.00E-22	339.3	36.4	40.5	hypothetical protein ARALYDRAFT_487555	gbpln	Arabidopsis lyrata	AT5G07300.1 | Symbols: BON2 | Calcium-dependent phospholipid-binding Copine family protein | chr5:2299996-2303040 FORWARD LENGTH=586	173	586	8.00E-24	338.7	34.1	37.6
Rsa1.0_00777.1.g19346.t1	gb|EOA16678.1| hypothetical protein CARUB_v10004870mg [Capsella rubella]	364	427	1.00E-136	117.3	77.7	84.9	hypothetical protein CARUB_v10004870mg	gbpln	Capsella rubella	AT4G15410.1 | Symbols: PUX5 | serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B prime gamma | chr4:8814868-8816596 FORWARD LENGTH=421	364	421	1.00E-135	115.7	75.0	84.1
Rsa1.0_00777.1.g19347.t1	dbj|BAH20736.1| beta-amylase [Raphanus sativus]	498	498	0	100.0	97.8	99.6	beta-amylase	gbpln	Raphanus sativus	AT4G15210.1 | Symbols: ATBETA-AMY, AT-BETA-AMY, RAM1, BMY1, BAM5 | beta-amylase 5 | chr4:8666734-8669357 REVERSE LENGTH=498	498	498	0	100.0	91.4	97.0
Rsa1.0_00777.1.g19348.t1	ref|NP_567460.1| beta-amylase 5 [Arabidopsis thaliana] gi|113782|sp|P25853.1|BAM5_ARATH RecName: Full=Beta-amylase 5; Short=AtBeta-Amy; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Protein REDUCED BETA AMYLASE 1 gi|15983398|gb|AAL11567.1|AF424573_1 unknown protein [Arabidopsis thaliana] gi|166602|gb|AAA32737.1| beta-amylase [Arabidopsis thaliana] gi|22655392|gb|AAM98288.1| At4g15210/At4g15210 [Arabidopsis thaliana] gi|110740808|dbj|BAE98501.1| beta-amylase [Arabidopsis thaliana] gi|332658168|gb|AEE83568.1| beta-amylase 5 [Arabidopsis thaliana] gi|228699|prf||1808329A beta amylase	520	498	0	95.8	80.6	88.7	beta-amylase 5	gbpln	Arabidopsis thaliana	AT4G15210.1 | Symbols: ATBETA-AMY, AT-BETA-AMY, RAM1, BMY1, BAM5 | beta-amylase 5 | chr4:8666734-8669357 REVERSE LENGTH=498	520	498	0	95.8	80.6	88.7
Rsa1.0_00778.1.g19349.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00778.1.g19350.t1	gb|AAD29774.1|AF074021_6 putative polyprotein [Arabidopsis thaliana] gi|7267218|emb|CAB80825.1| putative polyprotein [Arabidopsis thaliana]	292	922	3.00E-55	315.8	45.2	63.4	putative polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00778.1.g19351.t1	gb|EOA29337.1| hypothetical protein CARUB_v10025619mg [Capsella rubella]	343	357	1.00E-159	104.1	78.7	86.9	hypothetical protein CARUB_v10025619mg	gbpln	Capsella rubella	AT2G25710.2 | Symbols: HCS1 | holocarboxylase synthase 1 | chr2:10952719-10955061 FORWARD LENGTH=367	343	367	1.00E-161	107.0	79.6	86.6
Rsa1.0_00778.1.g19352.t2	ref|XP_002888457.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334298|gb|EFH64716.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	345	1058	9.00E-42	306.7	24.1	27.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G65810.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:24477043-24480728 REVERSE LENGTH=1016	345	1016	6.00E-44	294.5	23.5	27.2
Rsa1.0_00778.1.g19353.t1	ref|XP_002873062.1| hypothetical protein ARALYDRAFT_908126 [Arabidopsis lyrata subsp. lyrata] gi|297318899|gb|EFH49321.1| hypothetical protein ARALYDRAFT_908126 [Arabidopsis lyrata subsp. lyrata]	241	99	2.00E-31	41.1	29.0	32.8	hypothetical protein ARALYDRAFT_908126	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00778.1.g19354.t4	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1096	1529	1.00E-102	139.5	22.8	34.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1096	626	2.00E-28	57.1	6.6	10.8
Rsa1.0_00778.1.g19355.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00778.1.g19356.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00778.1.g19357.t1	ref|NP_181490.5| uncharacterized protein [Arabidopsis thaliana] gi|330254602|gb|AEC09696.1| uncharacterized protein AT2G39580 [Arabidopsis thaliana]	254	1577	3.00E-49	620.9	39.4	41.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G39580.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative zinc-finger domain (InterPro:IPR019607); Has 249 Blast hits to 219 proteins in 85 species: Archae - 0; Bacteria - 144; Metazoa - 29; Fungi - 8; Plants - 50; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr2:16510540-16516948 FORWARD LENGTH=1577	254	1577	1.00E-51	620.9	39.4	41.7
Rsa1.0_00778.1.g19358.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00778.1.g19359.t1	gb|EOA39403.1| hypothetical protein CARUB_v10012493mg [Capsella rubella]	183	307	4.00E-46	167.8	63.4	73.8	hypothetical protein CARUB_v10012493mg	gbpln	Capsella rubella	AT3G19950.1 | Symbols: | RING/U-box superfamily protein | chr3:6942853-6943839 FORWARD LENGTH=328	183	328	6.00E-38	179.2	43.7	56.8
Rsa1.0_00778.1.g19360.t16	ref|XP_002891568.1| hypothetical protein ARALYDRAFT_474163 [Arabidopsis lyrata subsp. lyrata] gi|297337410|gb|EFH67827.1| hypothetical protein ARALYDRAFT_474163 [Arabidopsis lyrata subsp. lyrata]	1211	1153	0	95.2	85.5	89.7	hypothetical protein ARALYDRAFT_474163	gbpln	Arabidopsis lyrata	AT1G50360.1 | Symbols: VIIIA, ATVIIIA | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:18650688-18657106 FORWARD LENGTH=1153	1211	1153	0	95.2	85.0	89.8
Rsa1.0_00778.1.g19361.t1	ref|NP_564567.1| oligopeptidase B [Arabidopsis thaliana] gi|5734786|gb|AAD50051.1|AC007980_16 Similar to oligopeptidases [Arabidopsis thaliana] gi|19310465|gb|AAL84967.1| At1g50380/F14I3_27 [Arabidopsis thaliana] gi|332194421|gb|AEE32542.1| prolyl oligopeptidase family protein [Arabidopsis thaliana]	710	710	0	100.0	91.5	95.9	oligopeptidase B	gbpln	Arabidopsis thaliana	AT1G50380.1 | Symbols: | Prolyl oligopeptidase family protein | chr1:18662480-18666185 FORWARD LENGTH=710	710	710	0	100.0	91.5	95.9
Rsa1.0_00778.1.g19362.t1	gb|EOA39090.1| hypothetical protein CARUB_v10011822mg [Capsella rubella]	1038	997	0	96.1	72.4	79.6	hypothetical protein CARUB_v10011822mg	gbpln	Capsella rubella	AT1G50410.1 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related | chr1:18672828-18677365 FORWARD LENGTH=981	1038	981	0	94.5	71.5	79.0
Rsa1.0_00778.1.g19363.t1	gb|EOA40271.1| hypothetical protein CARUB_v10008999mg [Capsella rubella] gi|482576085|gb|EOA40272.1| hypothetical protein CARUB_v10008999mg [Capsella rubella]	444	482	0	108.6	91.0	94.4	hypothetical protein CARUB_v10008999mg	gbpln	Capsella rubella	AT1G50420.1 | Symbols: SCL3, SCL-3 | scarecrow-like 3 | chr1:18678177-18679625 REVERSE LENGTH=482	444	482	0	108.6	90.5	94.8
Rsa1.0_00778.1.g19364.t3	ref|XP_002894253.1| hypothetical protein ARALYDRAFT_474174 [Arabidopsis lyrata subsp. lyrata] gi|297340095|gb|EFH70512.1| hypothetical protein ARALYDRAFT_474174 [Arabidopsis lyrata subsp. lyrata]	422	428	0	101.4	90.0	95.0	hypothetical protein ARALYDRAFT_474174	gbpln	Arabidopsis lyrata	AT1G50450.1 | Symbols: | Saccharopine dehydrogenase | chr1:18687902-18690348 REVERSE LENGTH=428	422	428	0	101.4	88.9	94.3
Rsa1.0_00779.1.g19365.t3	ref|NP_181316.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|330254358|gb|AEC09452.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	297	396	1.00E-39	133.3	27.9	33.3	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G37800.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:15841039-15843610 REVERSE LENGTH=396	297	396	4.00E-42	133.3	27.9	33.3
Rsa1.0_00779.1.g19366.t1	ref|NP_565872.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] gi|15451110|gb|AAK96826.1| Unknown protein [Arabidopsis thaliana] gi|18377476|gb|AAL66904.1| unknown protein [Arabidopsis thaliana] gi|330254366|gb|AEC09460.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	115	115	2.00E-50	100.0	89.6	93.9	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	gbpln	Arabidopsis thaliana	AT2G37870.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr2:15859280-15859723 FORWARD LENGTH=115	115	115	3.00E-53	100.0	89.6	93.9
Rsa1.0_00779.1.g19367.t1	gb|EMJ03944.1| hypothetical protein PRUPE_ppa013206mg [Prunus persica]	143	135	1.00E-20	94.4	38.5	44.8	hypothetical protein PRUPE_ppa013206mg	gbpln	Prunus persica	AT3G54560.1 | Symbols: HTA11 | histone H2A 11 | chr3:20196532-20197466 FORWARD LENGTH=136	143	136	2.00E-22	95.1	37.1	41.3
Rsa1.0_00779.1.g19368.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00779.1.g19369.t1	ref|NP_565872.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] gi|15451110|gb|AAK96826.1| Unknown protein [Arabidopsis thaliana] gi|18377476|gb|AAL66904.1| unknown protein [Arabidopsis thaliana] gi|330254366|gb|AEC09460.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	117	115	4.00E-50	98.3	91.5	93.2	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	gbpln	Arabidopsis thaliana	AT2G37870.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr2:15859280-15859723 FORWARD LENGTH=115	117	115	6.00E-53	98.3	91.5	93.2
Rsa1.0_00779.1.g19370.t1	gb|ABK28527.1| unknown [Arabidopsis thaliana]	251	248	1.00E-111	98.8	85.7	90.8	unknown	gbpln	Arabidopsis thaliana	AT2G37880.1 | Symbols: | Protein of unknown function, DUF617 | chr2:15860705-15861448 FORWARD LENGTH=247	251	247	1.00E-113	98.4	85.7	90.8
Rsa1.0_00779.1.g19371.t1	ref|NP_181325.2| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|22135876|gb|AAM91520.1| putative mitochondrial carrier protein [Arabidopsis thaliana] gi|23197668|gb|AAN15361.1| putative mitochondrial carrier protein [Arabidopsis thaliana] gi|51968418|dbj|BAD42901.1| mitochondrial carrier like protein [Arabidopsis thaliana] gi|51968668|dbj|BAD43026.1| mitochondrial carrier like protein [Arabidopsis thaliana] gi|330254368|gb|AEC09462.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana]	347	337	1.00E-150	97.1	74.9	85.0	Mitochondrial substrate carrier family protein	gbpln	Arabidopsis thaliana	AT2G37890.1 | Symbols: | Mitochondrial substrate carrier family protein | chr2:15862017-15863849 REVERSE LENGTH=337	347	337	1.00E-152	97.1	74.9	85.0
Rsa1.0_00779.1.g19372.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00779.1.g19373.t1	gb|EOA26770.1| hypothetical protein CARUB_v10022857mg [Capsella rubella] gi|482562581|gb|EOA26771.1| hypothetical protein CARUB_v10022857mg [Capsella rubella]	475	597	1.00E-137	125.7	58.7	67.8	hypothetical protein CARUB_v10022857mg	gbpln	Capsella rubella	AT2G37930.1 | Symbols: | Protein of unknown function (DUF3527) | chr2:15873284-15874770 FORWARD LENGTH=467	475	467	1.00E-138	98.3	61.5	72.8
Rsa1.0_00779.1.g19374.t1	ref|XP_002879716.1| hypothetical protein ARALYDRAFT_482800 [Arabidopsis lyrata subsp. lyrata] gi|297325555|gb|EFH55975.1| hypothetical protein ARALYDRAFT_482800 [Arabidopsis lyrata subsp. lyrata]	304	305	1.00E-168	100.3	94.7	98.4	hypothetical protein ARALYDRAFT_482800	gbpln	Arabidopsis lyrata	AT2G37940.1 | Symbols: AtIPCS2 | Arabidopsis Inositol phosphorylceramide synthase 2 | chr2:15877169-15879411 FORWARD LENGTH=305	304	305	1.00E-171	100.3	94.4	98.4
Rsa1.0_00779.1.g19375.t1	ref|XP_002879861.1| hypothetical protein ARALYDRAFT_345820 [Arabidopsis lyrata subsp. lyrata] gi|297325700|gb|EFH56120.1| hypothetical protein ARALYDRAFT_345820 [Arabidopsis lyrata subsp. lyrata]	298	305	1.00E-80	102.3	54.7	67.8	hypothetical protein ARALYDRAFT_345820	gbpln	Arabidopsis lyrata	AT2G20620.1 | Symbols: | Protein of unknown function (DUF626) | chr2:8891929-8893244 REVERSE LENGTH=286	298	286	3.00E-58	96.0	38.3	58.1
Rsa1.0_00779.1.g19376.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1902	1274	0	67.0	36.2	46.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	1902	303	2.00E-45	15.9	6.0	8.3
Rsa1.0_00779.1.g19377.t1	ref|XP_002881708.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327547|gb|EFH57967.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	174	164	1.00E-39	94.3	48.3	64.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G22080.2 | Symbols: | Cysteine proteinases superfamily protein | chr1:7792404-7794089 REVERSE LENGTH=332	174	332	2.00E-18	190.8	30.5	45.4
Rsa1.0_00779.1.g19378.t1	ref|XP_002879859.1| hypothetical protein ARALYDRAFT_903307 [Arabidopsis lyrata subsp. lyrata] gi|297325698|gb|EFH56118.1| hypothetical protein ARALYDRAFT_903307 [Arabidopsis lyrata subsp. lyrata]	306	304	1.00E-79	99.3	53.3	66.3	hypothetical protein ARALYDRAFT_903307	gbpln	Arabidopsis lyrata	AT2G20620.1 | Symbols: | Protein of unknown function (DUF626) | chr2:8891929-8893244 REVERSE LENGTH=286	306	286	2.00E-53	93.5	37.3	54.9
Rsa1.0_00779.1.g19379.t1	ref|XP_002889340.1| hypothetical protein ARALYDRAFT_333453 [Arabidopsis lyrata subsp. lyrata] gi|297335182|gb|EFH65599.1| hypothetical protein ARALYDRAFT_333453 [Arabidopsis lyrata subsp. lyrata]	229	264	3.00E-77	115.3	81.7	87.8	hypothetical protein ARALYDRAFT_333453	gbpln	Arabidopsis lyrata	AT1G02040.1 | Symbols: | C2H2-type zinc finger family protein | chr1:358104-359078 REVERSE LENGTH=324	229	324	7.00E-79	141.5	81.2	87.3

Rsa1.0_00779.1.g19380.t1	gb|ADF43044.1| chalcone synthase 3 protein [Brassica rapa subsp. rapa]	391	393	0	100.5	96.2	98.0	chalcone synthase 3 protein	gbpln	Brassica rapa	AT1G02050.1 | Symbols: LAP6 | Chalcone and stilbene synthase family protein | chr1:359164-360441 REVERSE LENGTH=395	391	395	0	101.0	92.8	96.2
Rsa1.0_00779.1.g19381.t1	ref|XP_002881555.1| hypothetical protein ARALYDRAFT_902985 [Arabidopsis lyrata subsp. lyrata] gi|297327394|gb|EFH57814.1| hypothetical protein ARALYDRAFT_902985 [Arabidopsis lyrata subsp. lyrata]	494	483	1.00E-154	97.8	65.2	75.3	hypothetical protein ARALYDRAFT_902985	gbpln	Arabidopsis lyrata	AT2G37960.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54060.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:15886962-15889180 REVERSE LENGTH=480	494	480	1.00E-154	97.2	64.2	74.9
Rsa1.0_00779.1.g19382.t1	ref|XP_002879719.1| soul heme-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297325558|gb|EFH55978.1| soul heme-binding family protein [Arabidopsis lyrata subsp. lyrata]	245	224	1.00E-100	91.4	78.0	84.9	soul heme-binding family protein	gbpln	Arabidopsis lyrata	AT2G37970.1 | Symbols: SOUL-1 | SOUL heme-binding family protein | chr2:15891027-15891704 FORWARD LENGTH=225	245	225	1.00E-101	91.8	76.3	84.1
Rsa1.0_00779.1.g19383.t1	ref|NP_181334.1| O-fucosyltransferase-like protein [Arabidopsis thaliana] gi|13430694|gb|AAK25969.1|AF360259_1 putative axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana] gi|25054996|gb|AAN71964.1| putative axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana] gi|330254380|gb|AEC09474.1| O-fucosyltransferase-like protein [Arabidopsis thaliana]	625	638	0	102.1	84.5	90.1	O-fucosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT2G37980.1 | Symbols: | O-fucosyltransferase family protein | chr2:15894162-15897452 REVERSE LENGTH=638	625	638	0	102.1	84.5	90.1
Rsa1.0_00780.1.g19384.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00780.1.g19385.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2069	1274	0	61.6	26.4	34.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G51410.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:19059885-19061424 FORWARD LENGTH=325	2069	325	1.00E-152	15.7	12.5	13.0
Rsa1.0_00780.1.g19386.t1	emb|CAA16721.1| MuDR transposable element - like protein [Arabidopsis thaliana] gi|7268634|emb|CAB78843.1| MuDR transposable element-like protein [Arabidopsis thaliana]	156	633	3.00E-31	405.8	46.2	61.5	MuDR transposable element - like protein	gbpln	Arabidopsis thaliana	AT3G30370.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Transposase, MuDR, plant (InterPro:IPR004332); BEST Arabidopsis thaliana protein match is: SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein (TAIR:AT1G18050.1); Has 35 Blast hits to 35 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:11965180-11965719 REVERSE LENGTH=179	156	179	2.00E-24	114.7	37.2	54.5
Rsa1.0_00780.1.g19387.t2	ref|NP_174483.1| uncharacterized protein [Arabidopsis thaliana] gi|75169198|sp|Q9C6X0.1|Y1203_ARATH RecName: Full=B3 domain-containing protein At1g32030 gi|12321462|gb|AAG50787.1|AC074309_4 hypothetical protein [Arabidopsis thaliana] gi|225897992|dbj|BAH30328.1| hypothetical protein [Arabidopsis thaliana] gi|332193307|gb|AEE31428.1| uncharacterized protein AT1G32030 [Arabidopsis thaliana]	315	333	1.00E-65	105.7	50.5	64.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G32030.1 | Symbols: | Domain of unknown function (DUF313) | chr1:11514594-11515595 FORWARD LENGTH=333	315	333	3.00E-68	105.7	50.5	64.4
Rsa1.0_00780.1.g19388.t1	ref|XP_002890959.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336801|gb|EFH67218.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	526	539	0	102.5	89.4	94.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G31970.1 | Symbols: STRS1 | DEA(D/H)-box RNA helicase family protein | chr1:11479921-11482707 FORWARD LENGTH=537	526	537	0	102.1	88.6	93.3
Rsa1.0_00780.1.g19389.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00780.1.g19390.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00780.1.g19391.t1	dbj|BAJ34269.1| unnamed protein product [Thellungiella halophila]	360	472	1.00E-93	131.1	63.6	70.6	unnamed protein product	----	----	AT1G14580.2 | Symbols: | C2H2-like zinc finger protein | chr1:4990070-4992442 FORWARD LENGTH=467	360	467	7.00E-96	129.7	62.8	69.4
Rsa1.0_00780.1.g19392.t1	gb|AEV40788.1| heme oxygenase 1 [Brassica rapa subsp. pekinensis]	235	281	1.00E-117	119.6	90.6	94.9	heme oxygenase 1	gbpln	Brassica rapa	AT2G26670.1 | Symbols: HY1, ATHO1, HO1, TED4, GUN2, HY6 | Plant haem oxygenase (decyclizing) family protein | chr2:11341816-11343394 FORWARD LENGTH=282	235	282	1.00E-111	120.0	83.4	93.2

Rsa1.0_00780.1.g19393.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1462	1501	0	102.7	51.6	66.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1462	1262	2.00E-75	86.3	10.3	14.1
Rsa1.0_00780.1.g19394.t1	gb|EOA19843.1| hypothetical protein CARUB_v10000089mg [Capsella rubella]	441	1102	3.00E-43	249.9	31.1	41.5	hypothetical protein CARUB_v10000089mg	gbpln	Capsella rubella	AT4G00630.1 | Symbols: KEA2, ATKEA2 | K+ efflux antiporter 2 | chr4:261655-267789 REVERSE LENGTH=1174	441	1174	6.00E-44	266.2	30.4	39.0
Rsa1.0_00780.1.g19395.t1	ref|NP_174471.2| protein BREVIS RADIX [Arabidopsis thaliana] gi|229621711|sp|Q17TI5.2|BRX_ARATH RecName: Full=Protein BREVIS RADIX; Short=AtBRX gi|27754447|gb|AAO22671.1| putative major intrinsic protein [Arabidopsis thaliana] gi|28393953|gb|AAO42384.1| putative major intrinsic protein [Arabidopsis thaliana] gi|332193291|gb|AEE31412.1| protein BREVIS RADIX [Arabidopsis thaliana]	342	344	0	100.6	91.8	96.5	protein BREVIS RADIX	gbpln	Arabidopsis thaliana	AT1G31880.1 | Symbols: NLM9, BRX | DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein | chr1:11447804-11450053 FORWARD LENGTH=344	342	344	0	100.6	91.8	96.5
Rsa1.0_00781.1.g19396.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00781.1.g19397.t2	ref|XP_002868543.1| hypothetical protein ARALYDRAFT_330314 [Arabidopsis lyrata subsp. lyrata] gi|297314379|gb|EFH44802.1| hypothetical protein ARALYDRAFT_330314 [Arabidopsis lyrata subsp. lyrata]	442	283	1.00E-139	64.0	53.4	60.0	hypothetical protein ARALYDRAFT_330314	gbpln	Arabidopsis lyrata	AT5G37810.1 | Symbols: NIP4;1, NLM4 | NOD26-like intrinsic protein 4;1 | chr5:15045232-15047807 FORWARD LENGTH=283	442	283	1.00E-140	64.0	52.7	59.5
Rsa1.0_00781.1.g19398.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00781.1.g19399.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	253	258	2.00E-74	102.0	60.5	73.9	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	253	302	2.00E-50	119.4	47.4	68.4
Rsa1.0_00781.1.g19400.t1	gb|ABD65112.1| hypothetical protein 31.t00014 [Brassica oleracea]	119	122	3.00E-34	102.5	63.0	81.5	hypothetical protein 31.t00014	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00781.1.g19401.t1	gb|AAC26250.1| contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana] gi|7267136|emb|CAB80804.1| putative retrotransposon protein [Arabidopsis thaliana]	61	964	2.00E-13	1580.3	60.7	73.8	contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00781.1.g19402.t3	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1776	1142	0	64.3	24.2	33.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1776	575	7.00E-51	32.4	6.1	10.0
Rsa1.0_00782.1.g19403.t2	gb|EOA12827.1| hypothetical protein CARUB_v10025787mg [Capsella rubella]	995	1055	0	106.0	87.7	91.9	hypothetical protein CARUB_v10025787mg	gbpln	Capsella rubella	AT5G64220.2 | Symbols: | Calmodulin-binding transcription activator protein with CG-1 and Ankyrin domains | chr5:25686434-25691903 FORWARD LENGTH=1050	995	1050	0	105.5	86.7	91.6
Rsa1.0_00782.1.g19404.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00782.1.g19405.t1	gb|EOA13614.1| hypothetical protein CARUB_v10026681mg [Capsella rubella]	316	354	1.00E-138	112.0	81.0	85.8	hypothetical protein CARUB_v10026681mg	gbpln	Capsella rubella	AT5G64210.1 | Symbols: AOX2 | alternative oxidase 2 | chr5:25683965-25685664 REVERSE LENGTH=353	316	353	1.00E-139	111.7	80.7	85.4
Rsa1.0_00782.1.g19406.t1	ref|NP_201223.1| uncharacterized protein [Arabidopsis thaliana] gi|9759394|dbj|BAB09849.1| unnamed protein product [Arabidopsis thaliana] gi|15810363|gb|AAL07069.1| unknown protein [Arabidopsis thaliana] gi|21280975|gb|AAM45070.1| unknown protein [Arabidopsis thaliana] gi|332010468|gb|AED97851.1| uncharacterized protein AT5G64180 [Arabidopsis thaliana]	155	158	1.00E-65	101.9	90.3	94.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G64180.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:25677163-25678204 FORWARD LENGTH=158	155	158	5.00E-68	101.9	90.3	94.2
Rsa1.0_00782.1.g19407.t1	ref|NP_568985.1| cAMP-regulated phosphoprotein 19-related protein [Arabidopsis thaliana] gi|16648718|gb|AAL25551.1| AT5g64130/MHJ24_11 [Arabidopsis thaliana] gi|20453353|gb|AAM19915.1| AT5g64130/MHJ24_11 [Arabidopsis thaliana] gi|21618212|gb|AAM67262.1| unknown [Arabidopsis thaliana] gi|332010460|gb|AED97843.1| cAMP-regulated phosphoprotein 19-related protein [Arabidopsis thaliana]	261	115	1.00E-50	44.1	36.8	38.3	cAMP-regulated phosphoprotein 19-related protein	gbpln	Arabidopsis thaliana	AT5G64130.1 | Symbols: | cAMP-regulated phosphoprotein 19-related protein | chr5:25664547-25665339 REVERSE LENGTH=115	261	115	4.00E-53	44.1	36.8	38.3

Rsa1.0_00782.1.g19408.t1	gb|EOA13363.1| hypothetical protein CARUB_v10026400mg [Capsella rubella]	414	445	1.00E-167	107.5	77.3	84.3	hypothetical protein CARUB_v10026400mg	gbpln	Capsella rubella	AT5G64090.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Hyccin (InterPro:IPR018619); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G21050.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:25648069-25649415 FORWARD LENGTH=448	414	448	1.00E-165	108.2	77.8	83.6
Rsa1.0_00782.1.g19409.t1	ref|XP_002866588.1| photosystem I reaction center subunit psi-N [Arabidopsis lyrata subsp. lyrata] gi|297312423|gb|EFH42847.1| photosystem I reaction center subunit psi-N [Arabidopsis lyrata subsp. lyrata]	187	171	2.00E-71	91.4	78.1	81.8	photosystem I reaction center subunit psi-N	gbpln	Arabidopsis lyrata	AT5G64040.1 | Symbols: PSAN | photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN) | chr5:25628724-25629409 REVERSE LENGTH=171	187	171	1.00E-73	91.4	77.5	81.3
Rsa1.0_00782.1.g19410.t1	ref|NP_201203.2| inositol polyphosphate 1-phosphatase [Arabidopsis thaliana] gi|332010442|gb|AED97825.1| bifunctional 3'(2'),5'-bisphosphate nucleotidase and inositol polyphosphate 1-phosphatase [Arabidopsis thaliana]	360	407	1.00E-177	113.1	90.0	93.6	inositol polyphosphate 1-phosphatase	gbpln	Arabidopsis thaliana	AT5G63980.1 | Symbols: SAL1, ALX8, ATSAL1, HOS2, FRY1, RON1 | Inositol monophosphatase family protein | chr5:25609840-25611802 FORWARD LENGTH=407	360	407	1.00E-180	113.1	90.0	93.6
Rsa1.0_00782.1.g19411.t1	ref|XP_002866582.1| hypothetical protein ARALYDRAFT_919691 [Arabidopsis lyrata subsp. lyrata] gi|297312417|gb|EFH42841.1| hypothetical protein ARALYDRAFT_919691 [Arabidopsis lyrata subsp. lyrata]	76	76	2.00E-18	100.0	85.5	90.8	hypothetical protein ARALYDRAFT_919691	gbpln	Arabidopsis lyrata	AT5G63905.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 12 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:25571055-25571503 REVERSE LENGTH=76	76	76	7.00E-16	100.0	86.8	93.4
Rsa1.0_00782.1.g19412.t1	ref|XP_002864874.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310709|gb|EFH41133.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata]	568	555	1.00E-172	97.7	61.4	73.6	PHD finger family protein	gbpln	Arabidopsis lyrata	AT5G63900.1 | Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain | chr5:25568698-25570371 FORWARD LENGTH=557	568	557	1.00E-174	98.1	60.0	73.9
Rsa1.0_00782.1.g19413.t1	sp|P24226.1|HISX_BRAOC RecName: Full=Histidinol dehydrogenase, chloroplastic; Short=HDH; Flags: Precursor gi|167142|gb|AAA32991.1| histidinol dehydrogenase [Brassica oleracea]	473	469	0	99.2	94.1	95.8	RecName: Full=Histidinol dehydrogenase, chloroplastic; Short=HDH; Flags: Precursor gi|167142|gb|AAA32991.1| histidinol dehydrogenase	gbpln	Brassica oleracea	AT5G63890.2 | Symbols: ATHDH, HISN8, HDH | histidinol dehydrogenase | chr5:25565600-25568104 REVERSE LENGTH=466	473	466	0	98.5	89.9	92.6
Rsa1.0_00782.1.g19414.t1	gb|EOA13450.1| hypothetical protein CARUB_v10026492mg [Capsella rubella]	413	412	0	99.8	90.3	94.9	hypothetical protein CARUB_v10026492mg	gbpln	Capsella rubella	AT5G63870.1 | Symbols: PP7, ATPP7 | serine/threonine phosphatase 7 | chr5:25561336-25562908 REVERSE LENGTH=413	413	413	0	100.0	88.1	94.2
Rsa1.0_00782.1.g19415.t1	dbj|BAJ33982.1| unnamed protein product [Thellungiella halophila]	416	440	0	105.8	93.5	96.4	unnamed protein product	----	----	AT5G63860.1 | Symbols: UVR8 | Regulator of chromosome condensation (RCC1) family protein | chr5:25554821-25558587 REVERSE LENGTH=440	416	440	0	105.8	91.8	95.2
Rsa1.0_00782.1.g19416.t1	ref|NP_201189.1| alpha 1,3-glucosidase [Arabidopsis thaliana] gi|10177672|dbj|BAB11032.1| glucosidase II alpha subunit [Arabidopsis thaliana] gi|332010420|gb|AED97803.1| alpha 1,3-glucosidase [Arabidopsis thaliana]	96	921	1.00E-29	959.4	66.7	68.8	alpha 1,3-glucosidase	gbpln	Arabidopsis thaliana	AT5G63840.1 | Symbols: RSW3, PSL5 | Glycosyl hydrolases family 31 protein | chr5:25545056-25548922 FORWARD LENGTH=921	96	921	2.00E-32	959.4	66.7	68.8
Rsa1.0_00782.1.g19417.t1	ref|XP_002864866.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310701|gb|EFH41125.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	336	368	1.00E-144	109.5	83.9	87.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G63780.1 | Symbols: SHA1 | RING/FYVE/PHD zinc finger superfamily protein | chr5:25525160-25526446 FORWARD LENGTH=367	336	367	1.00E-142	109.2	81.0	85.4
Rsa1.0_00782.1.g19418.t1	ref|NP_201177.1| protein kokopelli [Arabidopsis thaliana] gi|10177053|dbj|BAB10465.1| unnamed protein product [Arabidopsis thaliana] gi|332010406|gb|AED97789.1| protein kokopelli [Arabidopsis thaliana]	476	492	1.00E-74	103.4	49.2	63.2	protein kokopelli	gbpln	Arabidopsis thaliana	AT5G63720.1 | Symbols: KPL | kokopelli | chr5:25506349-25508017 FORWARD LENGTH=492	476	492	3.00E-77	103.4	49.2	63.2

Rsa1.0_00782.1.g19419.t1	gb|EOA12496.1| hypothetical protein CARUB_v10026111mg, partial [Capsella rubella]	566	604	0	106.7	66.1	78.4	hypothetical protein CARUB_v10026111mg, partial	gbpln	Capsella rubella	AT5G63700.1 | Symbols: | zinc ion binding;DNA binding | chr5:25493934-25497632 REVERSE LENGTH=602	566	602	0	106.4	65.0	76.5
Rsa1.0_00782.1.g19420.t1	ref|XP_002864862.1| hypothetical protein ARALYDRAFT_919664 [Arabidopsis lyrata subsp. lyrata] gi|297310697|gb|EFH41121.1| hypothetical protein ARALYDRAFT_919664 [Arabidopsis lyrata subsp. lyrata]	510	510	0	100.0	96.1	98.8	hypothetical protein ARALYDRAFT_919664	gbpln	Arabidopsis lyrata	AT5G63680.1 | Symbols: | Pyruvate kinase family protein | chr5:25490507-25492530 FORWARD LENGTH=510	510	510	0	100.0	96.1	98.6
Rsa1.0_00782.1.g19421.t1	dbj|BAJ33958.1| unnamed protein product [Thellungiella halophila]	384	472	1.00E-157	122.9	72.4	75.0	unnamed protein product	––––	––––	AT5G63610.1 | Symbols: HEN3, CDKE;1, ATCDK8 | cyclin-dependent kinase E;1 | chr5:25463645-25465057 REVERSE LENGTH=470	384	470	1.00E-158	122.4	71.1	74.2
Rsa1.0_00782.1.g19422.t1	gb|EOA21042.1| hypothetical protein CARUB_v10001381mg [Capsella rubella]	332	336	1.00E-98	101.2	55.1	69.6	hypothetical protein CARUB_v10001381mg	gbpln	Capsella rubella	AT5G08640.2 | Symbols: FLS1 | flavonol synthase 1 | chr5:2804009-2805175 FORWARD LENGTH=336	332	336	1.00E-101	101.2	55.1	69.6
Rsa1.0_00782.1.g19423.t1	gb|EOA13644.1| hypothetical protein CARUB_v10026716mg [Capsella rubella]	169	343	8.00E-24	203.0	33.1	40.2	hypothetical protein CARUB_v10026716mg	gbpln	Capsella rubella	AT5G43935.1 | Symbols: FLS6, ATFLS6 | flavonol synthase 6 | chr5:17682179-17683446 FORWARD LENGTH=293	169	293	4.00E-26	173.4	34.3	41.4
Rsa1.0_00782.1.g19424.t1	gb|EOA13644.1| hypothetical protein CARUB_v10026716mg [Capsella rubella]	111	343	2.00E-36	309.0	66.7	82.0	hypothetical protein CARUB_v10026716mg	gbpln	Capsella rubella	AT5G08640.2 | Symbols: FLS1 | flavonol synthase 1 | chr5:2804009-2805175 FORWARD LENGTH=336	111	336	1.00E-33	302.7	60.4	71.2
Rsa1.0_00782.1.g19425.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	409	1466	1.00E-153	358.4	64.5	77.3	copia-like polyprotein	gbpln	Arabidopsis thaliana	AT5G48050.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G34070.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19472661-19473770 REVERSE LENGTH=369	409	369	4.00E-22	90.2	18.6	30.6
Rsa1.0_00783.1.g19426.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	353	390	3.00E-63	110.5	39.9	53.0	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	353	320	1.00E-32	90.7	25.2	40.2
Rsa1.0_00783.1.g19427.t1	ref|XP_002887115.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297332956|gb|EFH63374.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	354	375	1.00E-158	105.9	79.7	85.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G67340.1 | Symbols: | HCP-like superfamily protein with MYND-type zinc finger | chr1:25230323-25231622 FORWARD LENGTH=379	354	379	1.00E-154	107.1	77.7	84.7
Rsa1.0_00783.1.g19428.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	155	1142	9.00E-23	736.8	41.3	60.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	155	292	1.00E-10	188.4	26.5	45.8
Rsa1.0_00783.1.g19429.t1	ref|NP_176901.1| uncharacterized protein [Arabidopsis thaliana] gi|9828617|gb|AAG00240.1|AC002130_5 F1N21.15 [Arabidopsis thaliana] gi|40823166|gb|AAR92263.1| At1g67330 [Arabidopsis thaliana] gi|45752704|gb|AAS76250.1| At1g67330 [Arabidopsis thaliana] gi|110742847|dbj|BAE99322.1| hypothetical protein [Arabidopsis thaliana] gi|332196511|gb|AEE34632.1| uncharacterized protein AT1G67330 [Arabidopsis thaliana]	288	291	1.00E-149	101.0	86.8	92.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G67330.1 | Symbols: | Protein of unknown function (DUF579) | chr1:25214118-25214993 FORWARD LENGTH=291	288	291	1.00E-152	101.0	86.8	92.0
Rsa1.0_00783.1.g19430.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00783.1.g19431.t1	emb|CAN65591.1| hypothetical protein VITISV_042091 [Vitis vinifera]	1111	1427	1.00E-152	128.4	29.8	40.5	hypothetical protein VITISV_042091	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1111	1262	5.00E-41	113.6	7.3	11.7
Rsa1.0_00783.1.g19432.t1	gb|ADP76651.1| MYB2 [Brassica oleracea var. botrytis]	185	247	3.00E-61	133.5	64.3	75.1	MYB2	gbpln	Brassica oleracea	AT1G66370.1 | Symbols: MYB113, AtMYB113 | myb domain protein 113 | chr1:24753634-24754604 FORWARD LENGTH=246	185	246	1.00E-53	133.0	59.5	73.0
Rsa1.0_00783.1.g19433.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00783.1.g19434.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00783.1.g19435.t1	ref|XP_004154771.1| PREDICTED: kanadaptin-like [Cucumis sativus]	249	962	3.00E-41	386.3	40.2	52.6	PREDICTED: kanadaptin-like	gbpln	Cucumis sativus	#	#	#	#	#	#	#
Rsa1.0_00783.1.g19436.t2	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#

Rsa1.0_00783.1.g19437.t1	gb|ADP76651.1| MYB2 [Brassica oleracea var. botrytis]	190	247	4.00E-45	130.0	58.4	73.2	MYB2	gbpln	Brassica oleracea	AT1G56650.1 | Symbols: PAP1, MYB75, SIAA1, ATMYB75 | production of anthocyanin pigment 1 | chr1:21233714-21235089 REVERSE LENGTH=248	190	248	4.00E-42	130.5	55.8	68.9
Rsa1.0_00784.1.g19438.t1	ref|XP_002884844.1| AHG3/ATPP2CA [Arabidopsis lyrata subsp. lyrata] gi|297330684|gb|EFH61103.1| AHG3/ATPP2CA [Arabidopsis lyrata subsp. lyrata]	391	396	1.00E-165	101.3	83.4	89.8	AHG3/ATPP2CA	gbpln	Arabidopsis lyrata	AT3G11410.1 | Symbols: ATPP2CA, AHG3, PP2CA | protein phosphatase 2CA | chr3:3584181-3585649 REVERSE LENGTH=399	391	399	1.00E-167	102.0	83.4	90.0
Rsa1.0_00784.1.g19439.t1	ref|NP_187747.1| translation initiation factor eIF-3 subunit 4 [Arabidopsis thaliana] gi|12322907|gb|AAG51445.1|AC008153_18 putative eukaryotic translation initiation factor 3 subunit; 21071-22901 [Arabidopsis thaliana] gi|16226341|gb|AAL16140.1|AF428308_1 AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|9755847|emb|CAC01929.1| translation initiation factor 3, subunit g (eIF3g) [Arabidopsis thaliana] gi|18377870|gb|AAL67121.1| AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|22137220|gb|AAM91455.1| AT3g11400/F24K9_7 [Arabidopsis thaliana] gi|332641520|gb|AEE75041.1| translation initiation factor eIF-3 subunit 4 [Arabidopsis thaliana]	291	294	1.00E-144	101.0	87.6	91.4	translation initiation factor eIF-3 subunit 4	gbpln	Arabidopsis thaliana	AT3G11400.1 | Symbols: EIF3G1, ATEIF3G1 | eukaryotic translation initiation factor 3G1 | chr3:3578536-3580366 FORWARD LENGTH=294	291	294	2.33E-156	101.0	87.6	91.4
Rsa1.0_00784.1.g19440.t1	ref|NP_001189860.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|332641518|gb|AEE75039.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	225	910	2.00E-95	404.4	75.1	78.2	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G11402.2 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:3573516-3577765 FORWARD LENGTH=910	225	910	5.00E-98	404.4	75.1	78.2
Rsa1.0_00784.1.g19441.t1	ref|XP_002871192.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297317029|gb|EFH47451.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	775	780	0	100.6	76.0	85.5	transducin family protein	gbpln	Arabidopsis lyrata	AT5G05970.1 | Symbols: NEDD1 | Transducin/WD40 repeat-like superfamily protein | chr5:1795464-1799313 FORWARD LENGTH=781	775	781	0	100.8	75.0	85.0
Rsa1.0_00784.1.g19442.t1	gb|EOA30568.1| hypothetical protein CARUB_v10013696mg [Capsella rubella]	456	447	0	98.0	75.9	83.8	hypothetical protein CARUB_v10013696mg	gbpln	Capsella rubella	AT3G11340.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:3556728-3558149 FORWARD LENGTH=447	456	447	0	98.0	75.4	82.9
Rsa1.0_00784.1.g19443.t1	ref|NP_187741.2| ras group-related LRR 9 protein [Arabidopsis thaliana] gi|18175638|gb|AAL59901.1| unknown protein [Arabidopsis thaliana] gi|21689861|gb|AAM67491.1| unknown protein [Arabidopsis thaliana] gi|57868160|gb|AAW57418.1| plant intracellular Ras-group-related LRR protein 9 [Arabidopsis thaliana] gi|332641510|gb|AEE75031.1| ras group-related LRR 9 protein [Arabidopsis thaliana]	496	499	0	100.6	81.0	88.9	ras group-related LRR 9 protein	gbpln	Arabidopsis thaliana	AT3G11330.1 | Symbols: PIRL9 | plant intracellular ras group-related LRR 9 | chr3:3552330-3554695 REVERSE LENGTH=499	496	499	0	100.6	81.0	88.9
Rsa1.0_00784.1.g19444.t1	ref|XP_002884840.1| organic anion transporter [Arabidopsis lyrata subsp. lyrata] gi|297330680|gb|EFH61099.1| organic anion transporter [Arabidopsis lyrata subsp. lyrata]	309	308	1.00E-167	99.7	95.1	97.7	organic anion transporter	gbpln	Arabidopsis lyrata	AT3G11320.1 | Symbols: | Nucleotide-sugar transporter family protein | chr3:3547017-3548539 REVERSE LENGTH=308	309	308	1.00E-169	99.7	94.8	97.4
Rsa1.0_00784.1.g19445.t1	gb|EOA32960.1| hypothetical protein CARUB_v10016290mg [Capsella rubella]	559	548	0	98.0	86.9	91.1	hypothetical protein CARUB_v10016290mg	gbpln	Capsella rubella	AT2G38080.1 | Symbols: IRX12, LAC4, ATLMCO4, LMCO4 | Laccase/Diphenol oxidase family protein | chr2:15934540-15937352 FORWARD LENGTH=558	559	558	0	99.8	62.1	78.2
Rsa1.0_00784.1.g19446.t1	ref|XP_002884839.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297330679|gb|EFH61098.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	254	264	1.00E-119	103.9	86.2	90.9	myb family transcription factor	gbpln	Arabidopsis lyrata	AT3G11280.2 | Symbols: | Duplicated homeodomain-like superfamily protein | chr3:3533477-3534393 REVERSE LENGTH=263	254	263	1.00E-122	103.5	86.6	91.3
Rsa1.0_00784.1.g19447.t9	gb|AAG50976.1|AC073395_18 hypothetical protein; 64772-65429 [Arabidopsis thaliana]	146	165	7.00E-57	113.0	81.5	91.8	hypothetical protein; 64772-65429	gbpln	Arabidopsis thaliana	AT3G11260.1 | Symbols: WOX5 | WUSCHEL related homeobox 5 | chr3:3527606-3528263 FORWARD LENGTH=182	146	182	1.00E-57	124.7	81.5	91.8
Rsa1.0_00784.1.g19448.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00784.1.g19449.t1	ref|XP_002884838.1| hypothetical protein ARALYDRAFT_478464 [Arabidopsis lyrata subsp. lyrata] gi|297330678|gb|EFH61097.1| hypothetical protein ARALYDRAFT_478464 [Arabidopsis lyrata subsp. lyrata]	582	602	0	103.4	79.4	88.1	hypothetical protein ARALYDRAFT_478464	gbpln	Arabidopsis lyrata	AT3G11240.1 | Symbols: ATE2, ATATE2 | arginine-tRNA protein transferase 2 | chr3:3518665-3521092 REVERSE LENGTH=605	582	605	0	104.0	77.7	86.6
Rsa1.0_00784.1.g19450.t1	ref|NP_001078135.1| yippee-like protein [Arabidopsis thaliana] gi|332641497|gb|AEE75018.1| yippee-like protein [Arabidopsis thaliana]	130	162	1.00E-65	124.6	93.1	96.9	yippee-like protein	gbpln	Arabidopsis thaliana	AT3G11230.2 | Symbols: | Yippee family putative zinc-binding protein | chr3:3516683-3518193 FORWARD LENGTH=162	130	162	2.00E-68	124.6	93.1	96.9
Rsa1.0_00784.1.g19451.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00785.1.g19452.t1	emb|CAN84021.1| hypothetical protein VITISV_032575 [Vitis vinifera]	484	962	2.00E-95	198.8	36.8	48.6	hypothetical protein VITISV_032575	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00785.1.g19453.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00785.1.g19454.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00785.1.g19455.t1	ref|XP_002883906.1| hypothetical protein ARALYDRAFT_899777 [Arabidopsis lyrata subsp. lyrata] gi|297329746|gb|EFH60165.1| hypothetical protein ARALYDRAFT_899777 [Arabidopsis lyrata subsp. lyrata]	589	585	0	99.3	92.7	96.1	hypothetical protein ARALYDRAFT_899777	gbpln	Arabidopsis lyrata	AT2G15620.1 | Symbols: NIR1, NIR, ATHNIR | nitrite reductase 1 | chr2:6810552-6812666 FORWARD LENGTH=586	589	586	0	99.5	92.7	96.3
Rsa1.0_00785.1.g19456.t1	ref|NP_179165.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75216226|sp|Q9ZQF1.1|PP152_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g15630, mitochondrial; Flags: Precursor gi|4335729|gb|AAD17407.1| putative salt-inducible protein [Arabidopsis thaliana] gi|330251331|gb|AEC06425.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	634	627	0	98.9	80.6	89.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G15630.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:6814521-6816404 FORWARD LENGTH=627	634	627	0	98.9	80.6	89.1
Rsa1.0_00785.1.g19457.t1	ref|XP_002885975.1| hypothetical protein ARALYDRAFT_899795 [Arabidopsis lyrata subsp. lyrata] gi|297331815|gb|EFH62234.1| hypothetical protein ARALYDRAFT_899795 [Arabidopsis lyrata subsp. lyrata]	407	420	0	103.2	90.2	95.1	hypothetical protein ARALYDRAFT_899795	gbpln	Arabidopsis lyrata	AT2G15695.1 | Symbols: | Protein of unknown function DUF829, transmembrane 53 | chr2:6834194-6836336 REVERSE LENGTH=420	407	420	0	103.2	89.4	94.1
Rsa1.0_00785.1.g19458.t1	gb|EOA30954.1| hypothetical protein CARUB_v10014100mg [Capsella rubella]	345	344	0	99.7	93.6	97.1	hypothetical protein CARUB_v10014100mg	gbpln	Capsella rubella	AT2G15730.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:6849797-6851881 FORWARD LENGTH=344	345	344	0	99.7	92.2	95.9
Rsa1.0_00785.1.g19459.t1	ref|NP_198536.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|10178231|dbj|BAB11642.1| unnamed protein product [Arabidopsis thaliana] gi|332006769|gb|AED94152.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	213	217	5.00E-38	101.9	51.2	63.8	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G37200.1 | Symbols: | RING/U-box superfamily protein | chr5:14727832-14728485 FORWARD LENGTH=217	213	217	2.00E-40	101.9	51.2	63.8
Rsa1.0_00785.1.g19460.t1	ref|XP_002885977.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] gi|297331817|gb|EFH62236.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	308	317	1.00E-124	102.9	84.7	89.9	calmodulin-binding protein	gbpln	Arabidopsis lyrata	AT2G15760.1 | Symbols: | Protein of unknown function (DUF1645) | chr2:6865807-6866754 REVERSE LENGTH=315	308	315	1.00E-118	102.3	82.1	87.3
Rsa1.0_00785.1.g19461.t1	gb|AAF79747.1|AC009317_6 T30E16.9 [Arabidopsis thaliana]	242	888	4.00E-49	366.9	51.2	64.0	T30E16.9	gbpln	Arabidopsis thaliana	AT1G59540.1 | Symbols: ZCF125 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:21874083-21879382 FORWARD LENGTH=823	242	823	4.00E-50	340.1	49.2	61.2
Rsa1.0_00785.1.g19462.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00785.1.g19463.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00785.1.g19464.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00786.1.g19465.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00786.1.g19466.t1	#	#	#	#	#	#	#	-	----	----	AT3G51650.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G51640.1); Has 27645 Blast hits to 15097 proteins in 1246 species: Archae - 44; Bacteria - 3367; Metazoa - 10036; Fungi - 2690; Plants - 1205; Viruses - 196; Other Eukaryotes - 10107 (source: NCBI BLink). | chr3:19159449-19162267 FORWARD LENGTH=842	144	842	1.00E-12	584.7	29.9	37.5

Rsa1.0_00786.1.g19467.t1	ref|NP_566955.1| macrophage migration inhibitory factor family protein [Arabidopsis thaliana] gi|297819864|ref|XP_002877815.1| macrophage migration inhibitory factor family protein [Arabidopsis lyrata subsp. lyrata] gi|21536646|gb|AAM60978.1| LS1-like protein [Arabidopsis thaliana] gi|26450314|dbj|BAC42273.1| putative LS1 [Arabidopsis thaliana] gi|28827214|gb|AAO50451.1| putative macrophage migration inhibitory factor (MIF) [Arabidopsis thaliana] gi|297323653|gb|EFH54074.1| macrophage migration inhibitory factor family protein [Arabidopsis lyrata subsp. lyrata] gi|332645303|gb|AEE78824.1| macrophage migration inhibitory factor family protein [Arabidopsis thaliana]	112	112	1.00E-55	100.0	94.6	97.3	macrophage migration inhibitory factor family protein	gbpln	Arabidopsis lyrata	AT3G51660.1 | Symbols: | Tautomerase/MIF superfamily protein | chr3:19164229-19165076 REVERSE LENGTH=112	112	112	2.00E-58	100.0	94.6	97.3
Rsa1.0_00786.1.g19468.t3	dbj|BAJ34003.1| unnamed protein product [Thellungiella halophila]	186	560	2.00E-25	301.1	40.3	46.8	unnamed protein product	----	----	AT4G26640.2 | Symbols: WRKY20, AtWRKY20 | WRKY family transcription factor family protein | chr4:13437298-13440693 REVERSE LENGTH=557	186	557	3.00E-26	299.5	38.7	46.2
Rsa1.0_00786.1.g19469.t1	ref|XP_002876098.1| SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297321936|gb|EFH52357.1| SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata]	438	409	0	93.4	81.5	85.8	SEC14 cytosolic factor family protein	gbpln	Arabidopsis lyrata	AT3G51670.1 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr3:19168912-19170848 FORWARD LENGTH=409	438	409	0	93.4	80.8	85.8
Rsa1.0_00786.1.g19470.t1	ref|XP_002877816.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297323654|gb|EFH54075.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	235	302	3.00E-87	128.5	84.3	89.4	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G51680.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:19173622-19174667 REVERSE LENGTH=303	235	303	1.00E-58	128.9	51.5	51.9
Rsa1.0_00786.1.g19471.t1	ref|XP_002876099.1| hypothetical protein ARALYDRAFT_323720 [Arabidopsis lyrata subsp. lyrata] gi|297321937|gb|EFH52358.1| hypothetical protein ARALYDRAFT_323720 [Arabidopsis lyrata subsp. lyrata]	467	472	0	101.1	79.4	88.9	hypothetical protein ARALYDRAFT_323720	gbpln	Arabidopsis lyrata	AT3G51710.1 | Symbols: | D-mannose binding lectin protein with Apple-like carbohydrate-binding domain | chr3:19182484-19183996 FORWARD LENGTH=476	467	476	0	101.9	79.7	88.4
Rsa1.0_00786.1.g19472.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1686	1274	0	75.6	34.5	45.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1686	575	2.00E-62	34.1	8.7	12.6
Rsa1.0_00786.1.g19473.t1	dbj|BAJ33968.1| unnamed protein product [Thellungiella halophila]	217	213	1.00E-92	98.2	83.9	87.6	unnamed protein product	----	----	AT3G51730.1 | Symbols: | saposin B domain-containing protein | chr3:19186970-19188436 FORWARD LENGTH=213	217	213	7.00E-92	98.2	77.9	87.6
Rsa1.0_00786.1.g19474.t1	ref|XP_002877820.1| hypothetical protein ARALYDRAFT_348272 [Arabidopsis lyrata subsp. lyrata] gi|297323658|gb|EFH54079.1| hypothetical protein ARALYDRAFT_348272 [Arabidopsis lyrata subsp. lyrata]	101	113	2.00E-16	111.9	55.4	73.3	hypothetical protein ARALYDRAFT_348272	gbpln	Arabidopsis lyrata	AT3G51750.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 9 growth stages. | chr3:19196706-19197307 REVERSE LENGTH=110	101	110	2.00E-16	108.9	55.4	71.3
Rsa1.0_00786.1.g19475.t1	dbj|BAJ34198.1| unnamed protein product [Thellungiella halophila]	899	958	0	106.6	91.1	94.3	unnamed protein product	----	----	AT3G51770.2 | Symbols: ETO1 | tetratricopeptide repeat (TPR)-containing protein | chr3:19200328-19203998 REVERSE LENGTH=959	899	959	0	106.7	87.8	92.1
Rsa1.0_00786.1.g19476.t1	ref|XP_002877823.1| hypothetical protein ARALYDRAFT_485533 [Arabidopsis lyrata subsp. lyrata] gi|297323661|gb|EFH54082.1| hypothetical protein ARALYDRAFT_485533 [Arabidopsis lyrata subsp. lyrata]	237	271	7.00E-74	114.3	65.0	77.6	hypothetical protein ARALYDRAFT_485533	gbpln	Arabidopsis lyrata	AT3G51780.1 | Symbols: ATBAG4, BAG4 | BCL-2-associated athanogene 4 | chr3:19207029-19208178 REVERSE LENGTH=269	237	269	1.00E-74	113.5	65.8	78.5
Rsa1.0_00786.1.g19477.t3	ref|NP_001190060.1| metallopeptidase M24 domain-containing protein [Arabidopsis thaliana] gi|332645325|gb|AEE78846.1| metallopeptidase M24 domain-containing protein [Arabidopsis thaliana]	424	385	0	90.8	77.4	83.0	metallopeptidase M24 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G51800.3 | Symbols: ATG2 | metallopeptidase M24 family protein | chr3:19211261-19213568 REVERSE LENGTH=385	424	385	0	90.8	77.4	83.0

Rsa1.0_00786.1.g19478.t1	ref|XP_002876106.1| calcium-dependent protein kinase 13 [Arabidopsis lyrata subsp. lyrata] gi|297321944|gb|EFH52365.1| calcium-dependent protein kinase 13 [Arabidopsis lyrata subsp. lyrata]	575	528	0	91.8	88.3	90.4	calcium-dependent protein kinase 13	gbpln	Arabidopsis lyrata	AT3G51850.1 | Symbols: CPK13 | calcium-dependent protein kinase 13 | chr3:19232667-19235526 FORWARD LENGTH=528	575	528	0	91.8	88.2	90.4
Rsa1.0_00787.1.g19479.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00787.1.g19480.t22	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	958	915	1.00E-143	95.5	25.7	37.3	F22O13.21	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	958	719	2.00E-27	75.1	11.8	22.0
Rsa1.0_00787.1.g19481.t1	emb|CAB87198.1| putative protein [Arabidopsis thaliana] gi|91806512|gb|ABE65983.1| hypothetical protein At3g42810 [Arabidopsis thaliana]	157	154	7.00E-28	98.1	41.4	58.0	putative protein	gbpln	Arabidopsis thaliana	AT4G04775.1 | Symbols: | zinc ion binding | chr4:2431120-2431695 FORWARD LENGTH=150	157	150	2.00E-18	95.5	24.8	33.8
Rsa1.0_00787.1.g19482.t14	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	940	871	6.00E-90	92.7	22.3	29.6	Ulp1 protease family protein	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	940	673	1.00E-31	71.6	11.5	17.3
Rsa1.0_00787.1.g19483.t1	ref|NP_176729.1| uncharacterized protein [Arabidopsis thaliana] gi|50253548|gb|AAT71976.1| At1g65510 [Arabidopsis thaliana] gi|332196270|gb|AEE34391.1| uncharacterized protein AT1G65510 [Arabidopsis thaliana]	80	80	1.00E-20	100.0	77.5	90.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G65510.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: LP.06 six leaves visible, LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage, LP.08 eight leaves visible; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G65486.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:24359456-24359847 FORWARD LENGTH=80	80	80	2.00E-23	100.0	77.5	90.0
Rsa1.0_00787.1.g19484.t1	gb|EOA35650.1| hypothetical protein CARUB_v10020872mg [Capsella rubella]	239	240	1.00E-106	100.4	79.9	90.8	hypothetical protein CARUB_v10020872mg	gbpln	Capsella rubella	AT1G65520.1 | Symbols: ATECI1, ECI1, ECHIC, PEC11 | delta(3), delta(2)-enoyl CoA isomerase 1 | chr1:24361171-24361893 REVERSE LENGTH=240	239	240	1.00E-109	100.4	80.3	90.4
Rsa1.0_00787.1.g19485.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00787.1.g19486.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00787.1.g19487.t1	ref|XP_004295592.1| PREDICTED: uncharacterized protein LOC101291324 [Fragaria vesca subsp. vesca]	172	2122	3.00E-59	1233.7	61.0	74.4	PREDICTED: uncharacterized protein LOC101291324	gbpln	Fragaria vesca	#	#	#	#	#	#	#
Rsa1.0_00787.1.g19488.t1	ref|XP_002888424.1| hypothetical protein ARALYDRAFT_894134 [Arabidopsis lyrata subsp. lyrata] gi|297334265|gb|EFH64683.1| hypothetical protein ARALYDRAFT_894134 [Arabidopsis lyrata subsp. lyrata]	350	350	1.00E-175	100.0	89.7	94.6	hypothetical protein ARALYDRAFT_894134	gbpln	Arabidopsis lyrata	AT1G65560.1 | Symbols: | Zinc-binding dehydrogenase family protein | chr1:24371608-24373673 REVERSE LENGTH=350	350	350	1.00E-177	100.0	88.0	94.6
Rsa1.0_00787.1.g19489.t1	ref|XP_002875882.1| hypothetical protein ARALYDRAFT_323420 [Arabidopsis lyrata subsp. lyrata] gi|297321720|gb|EFH52141.1| hypothetical protein ARALYDRAFT_323420 [Arabidopsis lyrata subsp. lyrata]	127	3832	3.00E-32	3017.3	61.4	70.9	hypothetical protein ARALYDRAFT_323420	gbpln	Arabidopsis lyrata	AT3G48190.1 | Symbols: ATM, ATATM | ataxia-telangiectasia mutated | chr3:17797628-17828361 FORWARD LENGTH=3845	127	3845	4.00E-34	3027.6	59.8	70.9
Rsa1.0_00787.1.g19490.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00787.1.g19491.t1	ref|NP_176738.1| endoglucanase 7 [Arabidopsis thaliana] gi|75218974|sp|O04478.1|GUN7_ARATH RecName: Full=Endoglucanase 7; AltName: Full=Endo-1,4-beta glucanase 7 gi|2190558|gb|AAB60922.1| F5I14.14 [Arabidopsis thaliana] gi|110738678|dbj|BAF01264.1| hypothetical protein [Arabidopsis thaliana] gi|332196279|gb|AEE34400.1| endoglucanase 7 [Arabidopsis thaliana]	630	623	0	98.9	88.4	94.6	endoglucanase 7	gbpln	Arabidopsis thaliana	AT1G65610.1 | Symbols: ATGH9A2, KOR2 | Six-hairpin glycosidases superfamily protein | chr1:24391823-24395261 REVERSE LENGTH=623	630	623	0	98.9	88.4	94.6
Rsa1.0_00788.1.g19492.t1	ref|XP_002881491.1| peroxidase 21 [Arabidopsis lyrata subsp. lyrata] gi|297327330|gb|EFH57750.1| peroxidase 21 [Arabidopsis lyrata subsp. lyrata]	328	327	1.00E-175	99.7	89.0	92.4	peroxidase 21	gbpln	Arabidopsis lyrata	AT2G37130.1 | Symbols: | Peroxidase superfamily protein | chr2:15598225-15600004 REVERSE LENGTH=327	328	327	1.00E-171	99.7	86.0	89.6

Rsa1.0_00788.1.g19493.t1	gb|EOA27785.1| hypothetical protein CARUB_v10023937mg [Capsella rubella]	233	244	1.00E-118	104.7	91.8	96.6	hypothetical protein CARUB_v10023937mg	gbpln	Capsella rubella	AT2G37110.1 | Symbols: | PLAC8 family protein | chr2:15592689-15593726 FORWARD LENGTH=242	233	242	1.00E-119	103.9	90.1	94.4
Rsa1.0_00788.1.g19494.t1	gb|EOA26847.1| hypothetical protein CARUB_v10022940mg [Capsella rubella]	487	546	5.00E-95	112.1	60.6	71.9	hypothetical protein CARUB_v10022940mg	gbpln	Capsella rubella	AT2G37070.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G53320.1); Has 1323 Blast hits to 775 proteins in 176 species: Archae - 0; Bacteria - 113; Metazoa - 351; Fungi - 175; Plants - 115; Viruses - 13; Other Eukaryotes - 556 (source: NCBI BLink). | chr2:15578415-15581125 FORWARD LENGTH=530	487	530	5.00E-92	108.8	57.5	68.2
Rsa1.0_00788.1.g19495.t1	gb|ABC69916.1| phenylalanine ammonia-lyase [Brassica napus]	685	722	0	105.4	97.2	98.5	phenylalanine ammonia-lyase	gbpln	Brassica napus	AT2G37040.1 | Symbols: PAL1, ATPAL1 | PHE ammonia lyase 1 | chr2:15557602-15560237 REVERSE LENGTH=725	685	725	0	105.8	94.5	97.7
Rsa1.0_00788.1.g19496.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00788.1.g19497.t1	ref|XP_002879646.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297325485|gb|EFH55905.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	120	124	3.00E-51	103.3	81.7	90.0	auxin-responsive family protein	gbpln	Arabidopsis lyrata	AT2G37030.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:15553732-15554106 FORWARD LENGTH=124	120	124	8.00E-54	103.3	80.8	89.2
Rsa1.0_00788.1.g19498.t1	ref|NP_568884.4| dehydrodolichyl diphosphate synthase 5 [Arabidopsis thaliana] gi|83305680|sp|Q570Q8.2|DDPS5_ARATH RecName: Full=Dehydrodolichyl diphosphate synthase 5; Short=Dedol-PP synthase 5 gi|8843800|dbj|BAA97348.1| cis-prenyltransferase homolog-like; undecaprenyl phosphate synthetase-like [Arabidopsis thaliana] gi|332009716|gb|AED97099.1| dehydrodolichyl diphosphate synthase 5 [Arabidopsis thaliana]	245	302	4.00E-64	123.3	55.5	69.4	dehydrodolichyl diphosphate synthase 5	gbpln	Arabidopsis thaliana	AT5G58784.1 | Symbols: | Undecaprenyl pyrophosphate synthetase family protein | chr5:23739950-23741267 REVERSE LENGTH=302	245	302	1.00E-66	123.3	55.5	69.4
Rsa1.0_00788.1.g19499.t1	dbj|BAJ34201.1| unnamed protein product [Thellungiella halophila]	542	547	0	100.9	87.5	91.9	unnamed protein product	----	----	AT2G36990.1 | Symbols: SIGF, SIG6, ATSIG6, SOLDAT8 | RNApolymerase sigma-subunit F | chr2:15537502-15540016 REVERSE LENGTH=547	542	547	0	100.9	85.6	91.0
Rsa1.0_00788.1.g19500.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00788.1.g19501.t1	ref|XP_002879635.1| tsl-kinase interacting protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297325474|gb|EFH55894.1| tsl-kinase interacting protein 1 [Arabidopsis lyrata subsp. lyrata]	164	740	7.00E-11	451.2	25.0	29.3	tsl-kinase interacting protein 1	gbpln	Arabidopsis lyrata	AT2G36960.3 | Symbols: TKI1 | TSL-kinase interacting protein 1 | chr2:15523552-15527245 FORWARD LENGTH=744	164	744	1.00E-10	453.7	23.2	28.7
Rsa1.0_00788.1.g19502.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00788.1.g19503.t2	ref|XP_002879634.1| hypothetical protein ARALYDRAFT_482676 [Arabidopsis lyrata subsp. lyrata] gi|297325473|gb|EFH55893.1| hypothetical protein ARALYDRAFT_482676 [Arabidopsis lyrata subsp. lyrata]	397	388	1.00E-136	97.7	77.6	82.9	hypothetical protein ARALYDRAFT_482676	gbpln	Arabidopsis lyrata	AT2G36950.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr2:15515216-15516754 FORWARD LENGTH=386	397	386	1.00E-137	97.2	75.8	81.4
Rsa1.0_00789.1.g19504.t1	gb|EOA31271.1| hypothetical protein CARUB_v10014443mg [Capsella rubella]	252	258	1.00E-103	102.4	78.2	84.5	hypothetical protein CARUB_v10014443mg	gbpln	Capsella rubella	AT3G13540.1 | Symbols: ATMYB5, MYB5 | myb domain protein 5 | chr3:4420239-4421443 FORWARD LENGTH=249	252	249	1.00E-104	98.8	78.6	84.5
Rsa1.0_00789.1.g19505.t2	gb|AAC28197.1| contains similarity to reverse transcriptases [Arabidopsis thaliana] gi|7267156|emb|CAB77868.1| putative reverse transcriptase [Arabidopsis thaliana]	989	1077	1.00E-137	108.9	30.5	39.4	contains similarity to reverse transcriptases	gbpln	Arabidopsis thaliana	AT3G13530.1 | Symbols: MAPKKK7, MAP3KE1 | mitogen-activated protein kinase kinase kinase 7 | chr3:4411934-4419320 REVERSE LENGTH=1368	989	1368	6.00E-23	138.3	5.1	5.8

Rsa1.0_00789.1.g19506.t1	ref|NP_566458.1| arabinogalactan protein 12 [Arabidopsis thaliana] gi|75273536|sp|Q9LJD9.1|AGP12_ARATH RecName: Full=Arabinogalactan peptide 12; Short=AG-peptide 12; Flags: Precursor gi|10880501|gb|AAG24280.1|AF195893_1 arabinogalactan protein [Arabidopsis thaliana] gi|9280304|dbj|BAB01759.1| unnamed protein product [Arabidopsis thaliana] gi|16649109|gb|AAL24406.1| Unknown protein [Arabidopsis thaliana] gi|20148539|gb|AAM10160.1| unknown protein [Arabidopsis thaliana] gi|21554170|gb|AAM63249.1| unknown [Arabidopsis thaliana] gi|332641846|gb|AEE75367.1| arabinogalactan protein 12 [Arabidopsis thaliana]	61	60	1.00E-18	98.4	88.5	91.8	arabinogalactan protein 12	gbpln	Arabidopsis thaliana	AT3G13520.1 | Symbols: AGP12, ATAGP12 | arabinogalactan protein 12 | chr3:4409087-4409269 FORWARD LENGTH=60	61	60	2.00E-21	98.4	88.5	91.8
Rsa1.0_00789.1.g19507.t2	dbj|BAB01757.1| unnamed protein product [Arabidopsis thaliana]	93	117	3.00E-12	125.8	35.5	45.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G13500.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G55365.1); Has 2761 Blast hits to 655 proteins in 118 species: Archae - 5; Bacteria - 503; Metazoa - 856; Fungi - 159; Plants - 239; Viruses - 11; Other Eukaryotes - 988 (source: NCBI BLink). | chr3:4399974-4400306 FORWARD LENGTH=110	93	110	9.00E-13	118.3	30.1	39.8
Rsa1.0_00789.1.g19508.t1	ref|XP_002884969.1| hypothetical protein ARALYDRAFT_478735 [Arabidopsis lyrata subsp. lyrata] gi|297330809|gb|EFH61228.1| hypothetical protein ARALYDRAFT_478735 [Arabidopsis lyrata subsp. lyrata]	603	603	0	100.0	91.4	95.2	hypothetical protein ARALYDRAFT_478735	gbpln	Arabidopsis lyrata	AT3G13490.1 | Symbols: OVA5, ATKRS-2 | Lysyl-tRNA synthetase, class II | chr3:4395984-4399302 REVERSE LENGTH=602	603	602	0	99.8	91.0	95.0
Rsa1.0_00789.1.g19509.t1	gb|EOA33066.1| hypothetical protein CARUB_v10016399mg [Capsella rubella]	155	158	5.00E-49	101.9	71.0	79.4	hypothetical protein CARUB_v10016399mg	gbpln	Capsella rubella	AT3G13480.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G55475.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:4393184-4393848 REVERSE LENGTH=172	155	172	2.00E-44	111.0	69.7	77.4
Rsa1.0_00789.1.g19510.t1	ref|NP_187956.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana] gi|75311214|sp|Q9LJE4.1|CPNB2_ARATH RecName: Full=Chaperonin 60 subunit beta 2, chloroplastic; Short=CPN-60 beta 2; Flags: Precursor gi|9280299|dbj|BAB01754.1| GloEL protein; chaperonin, 60 kDa [Arabidopsis thaliana] gi|332641841|gb|AEE75362.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]	442	596	1.00E-164	134.8	75.3	84.6	TCP-1/cpn60 chaperonin family protein	gbpln	Arabidopsis thaliana	AT3G13470.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:4389685-4392624 FORWARD LENGTH=596	442	596	1.00E-167	134.8	75.3	84.6
Rsa1.0_00789.1.g19511.t1	ref|XP_002884968.1| hypothetical protein ARALYDRAFT_478733 [Arabidopsis lyrata subsp. lyrata] gi|297330808|gb|EFH61227.1| hypothetical protein ARALYDRAFT_478733 [Arabidopsis lyrata subsp. lyrata]	647	677	0	104.6	83.6	90.9	hypothetical protein ARALYDRAFT_478733	gbpln	Arabidopsis lyrata	AT3G13460.1 | Symbols: ECT2 | evolutionarily conserved C-terminal region 2 | chr3:4385274-4388220 REVERSE LENGTH=667	647	667	0	103.1	83.2	90.6
Rsa1.0_00789.1.g19512.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00789.1.g19513.t1	gb|EOA31490.1| hypothetical protein CARUB_v10014676mg [Capsella rubella]	200	200	1.00E-110	100.0	97.5	98.5	hypothetical protein CARUB_v10014676mg	gbpln	Capsella rubella	AT3G13445.1 | Symbols: TBP1, TFIID-1 | TATA binding protein 1 | chr3:4380317-4381869 FORWARD LENGTH=200	200	200	1.00E-112	100.0	97.5	99.0
Rsa1.0_00789.1.g19514.t1	ref|NP_001142677.1| uncharacterized protein LOC100274972 [Zea mays] gi|195608106|gb|ACG25883.1| hypothetical protein [Zea mays]	252	249	1.00E-124	98.8	89.7	95.6	uncharacterized protein LOC100274972	gbenv/gbpln	Zea mays	AT3G13440.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:4378338-4379347 FORWARD LENGTH=278	252	278	1.00E-111	110.3	80.2	88.9

Rsa1.0_00789.1.g19515.t2	gb|EOA31242.1| hypothetical protein CARUB_v10014412mg [Capsella rubella]	286	264	1.00E-102	92.3	68.5	79.4	hypothetical protein CARUB_v10014412mg	gbpln	Capsella rubella	AT3G13420.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G55535.1); Has 66 Blast hits to 66 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 66; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4364723-4365892 FORWARD LENGTH=242	286	242	5.00E-92	84.6	60.5	70.3
Rsa1.0_00789.1.g19516.t3	gb|AAN60225.1| unknown [Arabidopsis thaliana]	347	321	1.00E-156	92.5	81.0	85.3	unknown	gbpln	Arabidopsis thaliana	AT3G13410.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G55546.1); Has 49 Blast hits to 49 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:4362149-4364032 REVERSE LENGTH=321	347	321	1.00E-158	92.5	80.7	84.7
Rsa1.0_00789.1.g19517.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00790.1.g19518.t1	ref|XP_002885398.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331238|gb|EFH61657.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	369	366	2.00E-67	99.2	47.2	62.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G20710.1 | Symbols: | F-box family protein | chr3:7237911-7238999 REVERSE LENGTH=362	369	362	3.00E-68	98.1	45.8	60.4
Rsa1.0_00790.1.g19519.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00790.1.g19520.t2	ref|XP_002885396.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331236|gb|EFH61655.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	367	347	8.00E-74	94.6	47.7	59.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G20710.1 | Symbols: | F-box family protein | chr3:7237911-7238999 REVERSE LENGTH=362	367	362	1.00E-70	98.6	46.3	61.9
Rsa1.0_00790.1.g19521.t1	ref|XP_002885396.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331236|gb|EFH61655.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	366	347	2.00E-73	94.8	48.9	61.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G20710.1 | Symbols: | F-box family protein | chr3:7237911-7238999 REVERSE LENGTH=362	366	362	1.00E-72	98.9	46.2	63.4
Rsa1.0_00790.1.g19522.t1	ref|NP_188707.1| F-box protein [Arabidopsis thaliana] gi|75273302|sp|Q9LHQ0.1|FBK64_ARATH RecName: Full=Putative F-box/kelch-repeat protein At3g20710 gi|9294351|dbj|BAB02248.1| unnamed protein product [Arabidopsis thaliana] gi|332642893|gb|AEE76414.1| F-box protein [Arabidopsis thaliana]	251	362	9.00E-52	144.2	45.8	62.2	F-box protein	gbpln	Arabidopsis thaliana	AT3G20710.1 | Symbols: | F-box family protein | chr3:7237911-7238999 REVERSE LENGTH=362	251	362	2.00E-54	144.2	45.8	62.2
Rsa1.0_00790.1.g19523.t1	ref|XP_002885395.1| hypothetical protein ARALYDRAFT_479594 [Arabidopsis lyrata subsp. lyrata] gi|297331235|gb|EFH61654.1| hypothetical protein ARALYDRAFT_479594 [Arabidopsis lyrata subsp. lyrata]	343	337	1.00E-139	98.3	79.9	88.0	hypothetical protein ARALYDRAFT_479594	gbpln	Arabidopsis lyrata	AT3G20680.1 | Symbols: | Domain of unknown function (DUF1995) | chr3:7230147-7231163 REVERSE LENGTH=338	343	338	1.00E-138	98.5	77.8	86.3
Rsa1.0_00790.1.g19524.t1	gb|EOA29533.1| hypothetical protein CARUB_v10014905mg [Capsella rubella]	134	132	5.00E-66	98.5	97.0	97.8	hypothetical protein CARUB_v10014905mg	gbpln	Capsella rubella	AT3G20670.1 | Symbols: HTA13 | histone H2A 13 | chr3:7229472-7229963 FORWARD LENGTH=132	134	132	4.00E-67	98.5	94.8	97.0
Rsa1.0_00790.1.g19525.t1	ref|NP_188701.2| mRNA cap guanine-N7 methyltransferase 1 [Arabidopsis thaliana] gi|75273308|sp|Q9LHQ7.1|MCES1_ARATH RecName: Full=mRNA cap guanine-N7 methyltransferase 1; AltName: Full=mRNA (guanine-N(7)-)-methyltransferase 1; AltName: Full=mRNA cap methyltransferase 1 gi|9294344|dbj|BAB02241.1| mRNA cap methyltransferase-like protein [Arabidopsis thaliana] gi|28973781|gb|AAO64206.1| unknown protein [Arabidopsis thaliana] gi|29824183|gb|AAP04052.1| unknown protein [Arabidopsis thaliana] gi|110736712|dbj|BAF00319.1| hypothetical protein [Arabidopsis thaliana] gi|332642886|gb|AEE76407.1| mRNA cap guanine-N7 methyltransferase 1 [Arabidopsis thaliana]	374	370	0	98.9	93.3	97.1	mRNA cap guanine-N7 methyltransferase 1	gbpln	Arabidopsis thaliana	AT3G20650.1 | Symbols: | mRNA capping enzyme family protein | chr3:7221168-7223939 REVERSE LENGTH=370	374	370	0	98.9	93.3	97.1

Rsa1.0_00790.1.g19526.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00790.1.g19527.t1	ref|NP_188700.1| transcription factor bHLH123 [Arabidopsis thaliana] gi|75299591|sp|Q8GXT3.1|BH123_ARATH RecName: Full=Transcription factor bHLH123; AltName: Full=Basic helix-loop-helix protein 123; Short=AtbHLH123; Short=bHLH 123; AltName: Full=Transcription factor EN 63; AltName: Full=bHLH transcription factor bHLH123 gi|26451163|dbj|BAC42685.1| putative bHLH transcription factor bHLH123 [Arabidopsis thaliana] gi|30793909|gb|AAP40407.1| unknown protein [Arabidopsis thaliana] gi|332642885|gb|AEE76406.1| transcription factor bHLH123 [Arabidopsis thaliana]	420	454	1.00E-169	108.1	85.5	88.6	transcription factor bHLH123	gbpln	Arabidopsis thaliana	AT3G20640.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:7210654-7213199 REVERSE LENGTH=454	420	454	1.00E-171	108.1	85.5	88.6
Rsa1.0_00790.1.g19528.t1	gb|ABR45916.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939421|gb|ABR45917.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939423|gb|ABR45918.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939425|gb|ABR45919.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939427|gb|ABR45920.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939431|gb|ABR45922.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939433|gb|ABR45923.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939435|gb|ABR45924.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939441|gb|ABR45927.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939443|gb|ABR45928.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939445|gb|ABR45929.1| non-race specific disease resistance 1 [Arabidopsis thaliana] gi|149939447|gb|ABR45930.1| non-race specific disease resistance 1	212	219	5.00E-92	103.3	79.2	88.2	non-race specific disease resistance 1	gbpln	Arabidopsis thaliana	AT3G20600.1 | Symbols: NDR1 | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:7194877-7195536 FORWARD LENGTH=219	212	219	6.00E-93	103.3	77.8	87.7
Rsa1.0_00790.1.g19529.t1	ref|XP_002885386.1| hypothetical protein ARALYDRAFT_479584 [Arabidopsis lyrata subsp. lyrata] gi|297331226|gb|EFH61645.1| hypothetical protein ARALYDRAFT_479584 [Arabidopsis lyrata subsp. lyrata]	672	671	0	99.9	88.5	94.6	hypothetical protein ARALYDRAFT_479584	gbpln	Arabidopsis lyrata	AT3G20580.1 | Symbols: COBL10 | COBRA-like protein 10 precursor | chr3:7188063-7190416 REVERSE LENGTH=672	672	672	0	100.0	87.9	93.9
Rsa1.0_00790.1.g19530.t1	gb|ABB97040.1| unknown [Brassica rapa]	183	204	1.00E-76	111.5	82.5	88.0	unknown	gbpln	Brassica rapa	AT3G20570.1 | Symbols: ENODL9, AtENODL9 | early nodulin-like protein 9 | chr3:7186754-7187453 REVERSE LENGTH=203	183	203	1.00E-66	110.9	78.7	87.4
Rsa1.0_00790.1.g19531.t1	ref|XP_002883257.1| hypothetical protein ARALYDRAFT_898483 [Arabidopsis lyrata subsp. lyrata] gi|297329097|gb|EFH59516.1| hypothetical protein ARALYDRAFT_898483 [Arabidopsis lyrata subsp. lyrata]	131	130	2.00E-53	99.2	80.2	87.8	hypothetical protein ARALYDRAFT_898483	gbpln	Arabidopsis lyrata	AT3G20557.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G50930.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:7180140-7180731 FORWARD LENGTH=130	131	130	3.00E-54	99.2	79.4	85.5
Rsa1.0_00790.1.g19532.t1	ref|XP_002883253.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329093|gb|EFH59512.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	385	383	0	99.5	88.3	92.2	kinase family protein	gbpln	Arabidopsis lyrata	AT3G20530.1 | Symbols: | Protein kinase superfamily protein | chr3:7166318-7167806 FORWARD LENGTH=386	385	386	0	100.3	87.3	91.4
Rsa1.0_00790.1.g19533.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00790.1.g19534.t1	dbj|BAB01869.1| cytochrome P450-like protein [Arabidopsis thaliana]	513	524	0	102.1	79.3	88.1	cytochrome P450-like protein	gbpln	Arabidopsis thaliana	AT4G15360.1 | Symbols: CYP705A3 | cytochrome P450, family 705, subfamily A, polypeptide 3 | chr4:8770185-8771852 FORWARD LENGTH=527	513	527	0	102.7	72.7	82.8
Rsa1.0_00790.1.g19535.t1	ref|XP_002885355.1| ubiquitin-conjugating enzyme 19 [Arabidopsis lyrata subsp. lyrata] gi|297331195|gb|EFH61614.1| ubiquitin-conjugating enzyme 19 [Arabidopsis lyrata subsp. lyrata]	181	181	1.00E-96	100.0	92.8	95.6	ubiquitin-conjugating enzyme 19	gbpln	Arabidopsis lyrata	AT3G20060.1 | Symbols: UBC19 | ubiquitin-conjugating enzyme19 | chr3:7002927-7004283 REVERSE LENGTH=181	181	181	8.00E-92	100.0	91.7	94.5
Rsa1.0_00790.1.g19536.t1	emb|CAB89229.1| putative protein [Arabidopsis thaliana]	392	451	1.00E-107	115.1	57.1	74.5	putative protein	gbpln	Arabidopsis thaliana	AT3G52680.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr3:19527075-19528838 FORWARD LENGTH=456	392	456	1.00E-110	116.3	57.1	74.5
Rsa1.0_00790.1.g19537.t1	gb|EOA32274.1| hypothetical protein CARUB_v10015535mg [Capsella rubella]	529	545	0	103.0	90.0	92.8	hypothetical protein CARUB_v10015535mg	gbpln	Capsella rubella	AT3G20050.1 | Symbols: ATTCP-1, TCP-1 | T-complex protein 1 alpha subunit | chr3:6998544-7002266 REVERSE LENGTH=545	529	545	0	103.0	89.8	92.6
Rsa1.0_00790.1.g19538.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00791.1.g19539.t1	ref|XP_002894122.1| hypothetical protein ARALYDRAFT_474002 [Arabidopsis lyrata subsp. lyrata] gi|297339964|gb|EFH70381.1| hypothetical protein ARALYDRAFT_474002 [Arabidopsis lyrata subsp. lyrata]	246	326	2.00E-76	132.5	63.8	72.0	hypothetical protein ARALYDRAFT_474002	gbpln	Arabidopsis lyrata	AT1G48630.1 | Symbols: RACK1B_AT | receptor for activated C kinase 1B | chr1:17981977-17983268 REVERSE LENGTH=326	246	326	2.00E-78	132.5	63.8	72.0
Rsa1.0_00791.1.g19540.t1	gb|EOA32275.1| hypothetical protein CARUB_v10015536mg [Capsella rubella]	160	483	1.00E-22	301.9	33.8	40.0	hypothetical protein CARUB_v10015536mg	gbpln	Capsella rubella	AT1G47350.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:17358447-17360722 REVERSE LENGTH=528	160	528	2.00E-22	330.0	31.9	37.5
Rsa1.0_00791.1.g19541.t1	gb|ABK78696.1| DNA binding protein [Brassica rapa]	197	185	2.00E-36	93.9	57.9	64.0	DNA binding protein	gbpln	Brassica rapa	AT1G48610.1 | Symbols: | AT hook motif-containing protein | chr1:17971027-17972798 REVERSE LENGTH=212	197	212	1.00E-37	107.6	62.4	71.6
Rsa1.0_00791.1.g19542.t2	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	2302	1270	0	55.2	25.3	33.1	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2302	575	9.00E-46	25.0	5.8	9.1
Rsa1.0_00791.1.g19543.t1	ref|XP_002891444.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297337286|gb|EFH67703.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	179	170	3.00E-85	95.0	84.9	90.5	C2 domain-containing protein	gbpln	Arabidopsis lyrata	AT1G48590.2 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:17962886-17964274 FORWARD LENGTH=200	179	200	2.00E-85	111.7	83.8	89.4
Rsa1.0_00791.1.g19544.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	326	1023	8.00E-27	313.8	26.7	41.7	F27F5.21	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	326	256	2.00E-20	78.5	18.4	26.7
Rsa1.0_00791.1.g19545.t1	gb|ADQ37383.1| unknown [Arabidopsis lyrata]	510	850	0	166.7	76.5	84.7	unknown	gbpln	Arabidopsis lyrata	AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850	510	850	0	166.7	74.5	83.3
Rsa1.0_00791.1.g19546.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00791.1.g19547.t3	ref|XP_002894115.1| T1N15.10 [Arabidopsis lyrata subsp. lyrata] gi|297339957|gb|EFH70374.1| T1N15.10 [Arabidopsis lyrata subsp. lyrata]	1226	1259	0	102.7	73.1	81.6	T1N15.10	gbpln	Arabidopsis lyrata	AT1G48490.3 | Symbols: | Protein kinase superfamily protein | chr1:17922345-17928597 REVERSE LENGTH=1235	1226	1235	0	100.7	71.5	80.9
Rsa1.0_00791.1.g19548.t1	ref|NP_564528.1| receptor-like kinase 1 [Arabidopsis thaliana] gi|75335279|sp|Q9LP77.1|Y1848_ARATH RecName: Full=Probable inactive receptor kinase At1g48480; Flags: Precursor gi|8778688|gb|AAF79696.1|AC020889_4 T1N15.9 [Arabidopsis thaliana] gi|209529789|gb|ACI49789.1| At1g48480 [Arabidopsis thaliana] gi|224589420|gb|ACN59244.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332194177|gb|AEE32298.1| receptor-like kinase 1 [Arabidopsis thaliana]	643	655	0	101.9	87.1	92.7	receptor-like kinase 1	gbpln	Arabidopsis thaliana	AT1G48480.1 | Symbols: RKL1 | receptor-like kinase 1 | chr1:17918475-17920743 FORWARD LENGTH=655	643	655	0	101.9	87.1	92.7
Rsa1.0_00792.1.g19549.t1	ref|XP_002866925.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata] gi|297312761|gb|EFH43184.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	782	787	0	100.6	72.3	78.8	glycine-rich protein	gbpln	Arabidopsis lyrata	AT4G37900.1 | Symbols: | Protein of unknown function (duplicated DUF1399) | chr4:17821737-17824445 REVERSE LENGTH=787	782	787	0	100.6	71.4	78.8

Rsa1.0_00792.1.g19550.t1	gb|EOA16807.1| hypothetical protein CARUB_v10005028mg [Capsella rubella] gi|482552615|gb|EOA16808.1| hypothetical protein CARUB_v10005028mg [Capsella rubella]	325	385	1.00E-126	118.5	73.5	86.8	hypothetical protein CARUB_v10005028mg	gbpln	Capsella rubella	AT2G22690.2 | Symbols: | zinc ion binding | chr2:9649820-9650965 REVERSE LENGTH=381	325	381	1.00E-104	117.2	60.3	80.9
Rsa1.0_00792.1.g19551.t1	gb|EOA17720.1| hypothetical protein CARUB_v10006101mg [Capsella rubella]	102	102	5.00E-51	100.0	97.1	97.1	hypothetical protein CARUB_v10006101mg	gbpln	Capsella rubella	AT4G37830.1 | Symbols: | cytochrome c oxidase-related | chr4:17787672-17788762 REVERSE LENGTH=102	102	102	1.00E-50	100.0	91.2	94.1
Rsa1.0_00792.1.g19552.t1	gb|EOA28316.1| hypothetical protein CARUB_v10024517mg [Capsella rubella]	514	740	4.00E-22	144.0	9.1	10.9	hypothetical protein CARUB_v10024517mg	gbpln	Capsella rubella	AT2G22795.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37820.1); Has 799854 Blast hits to 188815 proteins in 4452 species: Archae - 4529; Bacteria - 144236; Metazoa - 287749; Fungi - 87083; Plants - 43826; Viruses - 3662; Other Eukaryotes - 228769 (source: NCBI BLink). | chr2:9697380-9699584 REVERSE LENGTH=734	514	734	4.00E-22	142.8	9.1	10.3
Rsa1.0_00792.1.g19553.t1	ref|XP_002868962.1| hypothetical protein ARALYDRAFT_353057 [Arabidopsis lyrata subsp. lyrata] gi|297314798|gb|EFH45221.1| hypothetical protein ARALYDRAFT_353057 [Arabidopsis lyrata subsp. lyrata]	134	126	5.00E-50	94.0	79.1	84.3	hypothetical protein ARALYDRAFT_353057	gbpln	Arabidopsis lyrata	AT4G37810.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G10310.1); Has 149 Blast hits to 149 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 149; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:17780970-17781544 FORWARD LENGTH=128	134	128	1.00E-48	95.5	78.4	82.1
Rsa1.0_00792.1.g19554.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	576	1213	1.00E-178	210.6	54.0	68.4	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	576	289	8.00E-73	50.2	23.3	31.3
Rsa1.0_00792.1.g19555.t1	ref|XP_002868963.1| homeobox-leucine zipper protein 22 [Arabidopsis lyrata subsp. lyrata] gi|297314799|gb|EFH45222.1| homeobox-leucine zipper protein 22 [Arabidopsis lyrata subsp. lyrata]	544	283	1.00E-113	52.0	43.8	46.5	homeobox-leucine zipper protein 22	gbpln	Arabidopsis lyrata	AT4G37790.1 | Symbols: HAT22 | Homeobox-leucine zipper protein family | chr4:17768241-17769272 FORWARD LENGTH=278	544	278	1.00E-115	51.1	42.6	45.8
Rsa1.0_00792.1.g19556.t1	gb|ABA42147.1| aintegumenta 2 [Brassica napus]	631	562	0	89.1	78.3	81.3	aintegumenta 2	gbpln	Brassica napus	AT4G37750.1 | Symbols: ANT, DRG, CKC, CKC1 | Integrase-type DNA-binding superfamily protein | chr4:17739782-17742189 FORWARD LENGTH=555	631	555	0	88.0	74.2	77.0
Rsa1.0_00792.1.g19557.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00792.1.g19558.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	244	1164	4.00E-53	477.0	46.3	56.1	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	244	746	2.00E-40	305.7	32.4	46.3
Rsa1.0_00792.1.g19559.t1	ref|NP_195485.1| VQ motif-containing protein [Arabidopsis thaliana] gi|4468996|emb|CAB38310.1| putative protein [Arabidopsis thaliana] gi|7270754|emb|CAB80436.1| putative protein [Arabidopsis thaliana] gi|117168075|gb|ABK32120.1| At4g37710 [Arabidopsis thaliana] gi|332661430|gb|AEE86830.1| VQ motif-containing protein [Arabidopsis thaliana]	122	123	2.00E-45	100.8	79.5	84.4	VQ motif-containing protein	gbpln	Arabidopsis thaliana	AT4G37710.1 | Symbols: | VQ motif-containing protein | chr4:17718234-17718605 FORWARD LENGTH=123	122	123	3.00E-48	100.8	79.5	84.4
Rsa1.0_00792.1.g19560.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1454	1515	0	104.2	56.2	70.5	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1454	1262	1.00E-117	86.8	14.0	20.8
Rsa1.0_00792.1.g19561.t1	ref|XP_002868978.1| hypothetical protein ARALYDRAFT_912572 [Arabidopsis lyrata subsp. lyrata] gi|297314814|gb|EFH45237.1| hypothetical protein ARALYDRAFT_912572 [Arabidopsis lyrata subsp. lyrata]	224	531	1.00E-111	237.1	88.8	92.4	hypothetical protein ARALYDRAFT_912572	gbpln	Arabidopsis lyrata	AT4G37650.1 | Symbols: SHR, SGR7 | GRAS family transcription factor | chr4:17691871-17693466 FORWARD LENGTH=531	224	531	1.00E-112	237.1	87.5	91.5
Rsa1.0_00793.1.g19562.t1	ref|XP_002884591.1| hypothetical protein ARALYDRAFT_477961 [Arabidopsis lyrata subsp. lyrata] gi|297330431|gb|EFH60850.1| hypothetical protein ARALYDRAFT_477961 [Arabidopsis lyrata subsp. lyrata]	543	545	0	100.4	85.3	87.7	hypothetical protein ARALYDRAFT_477961	gbpln	Arabidopsis lyrata	AT3G06550.2 | Symbols: | O-acetyltransferase family protein | chr3:2039408-2042664 REVERSE LENGTH=568	543	568	0	104.6	85.5	89.0

Rsa1.0_00793.1.g19563.t1	ref|XP_002882480.1| polynucleotide adenylyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297328320|gb|EFH58739.1| polynucleotide adenylyltransferase [Arabidopsis lyrata subsp. lyrata]	501	507	0	101.2	78.2	87.8	polynucleotide adenylyltransferase	gbpln	Arabidopsis lyrata	AT3G06560.1 | Symbols: PAPS3 | poly(A) polymerase 3 | chr3:2044443-2047034 FORWARD LENGTH=507	501	507	0	101.2	78.2	88.6
Rsa1.0_00793.1.g19564.t1	ref|XP_002884593.1| hypothetical protein ARALYDRAFT_896791 [Arabidopsis lyrata subsp. lyrata] gi|297330433|gb|EFH60852.1| hypothetical protein ARALYDRAFT_896791 [Arabidopsis lyrata subsp. lyrata]	496	496	0	100.0	91.1	95.4	hypothetical protein ARALYDRAFT_896791	gbpln	Arabidopsis lyrata	AT3G06580.1 | Symbols: GAL1, GALK | Mevalonate/galactokinase family protein | chr3:2049141-2051867 REVERSE LENGTH=496	496	496	0	100.0	90.3	95.0
Rsa1.0_00793.1.g19565.t1	ref|XP_002884594.1| hypothetical protein ARALYDRAFT_477966 [Arabidopsis lyrata subsp. lyrata] gi|297330434|gb|EFH60853.1| hypothetical protein ARALYDRAFT_477966 [Arabidopsis lyrata subsp. lyrata]	230	217	2.00E-66	94.3	68.7	77.4	hypothetical protein ARALYDRAFT_477966	gbpln	Arabidopsis lyrata	AT3G06590.2 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:2054647-2055312 REVERSE LENGTH=221	230	221	6.00E-63	96.1	59.6	66.5
Rsa1.0_00793.1.g19566.t1	ref|NP_187312.1| uncharacterized protein [Arabidopsis thaliana] gi|186509849|ref|NP_001118593.1| uncharacterized protein [Arabidopsis thaliana] gi|12322684|gb|AAG51336.1|AC020580_16 hypothetical protein; 25909-26809 [Arabidopsis thaliana] gi|49660141|gb|AAT68361.1| hypothetical protein At3g06600 [Arabidopsis thaliana] gi|50058941|gb|AAT69215.1| hypothetical protein At3g06600 [Arabidopsis thaliana] gi|332640899|gb|AEE74420.1| uncharacterized protein AT3G06600 [Arabidopsis thaliana] gi|332640900|gb|AEE74421.1| uncharacterized protein AT3G06600 [Arabidopsis thaliana]	183	193	7.00E-48	105.5	63.4	77.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G06600.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:2059558-2060458 REVERSE LENGTH=193	183	193	3.00E-50	105.5	63.4	77.0
Rsa1.0_00793.1.g19567.t1	ref|NP_566288.1| DNA-binding enhancer-like protein [Arabidopsis thaliana] gi|12322682|gb|AAG51334.1|AC020580_14 unknown protein; 25530-24522 [Arabidopsis thaliana] gi|18252855|gb|AAL62354.1| unknown protein [Arabidopsis thaliana] gi|21389699|gb|AAM48048.1| unknown protein [Arabidopsis thaliana] gi|21593830|gb|AAM65797.1| unknown [Arabidopsis thaliana] gi|332640901|gb|AEE74422.1| DNA-binding enhancer-like protein [Arabidopsis thaliana]	115	115	3.00E-53	100.0	92.2	95.7	DNA-binding enhancer-like protein	gbpln	Arabidopsis thaliana	AT3G06610.1 | Symbols: | DNA-binding enhancer protein-related | chr3:2060837-2061845 FORWARD LENGTH=115	115	115	5.00E-56	100.0	92.2	95.7
Rsa1.0_00793.1.g19568.t1	gb|EOA29935.1| hypothetical protein CARUB_v10013028mg [Capsella rubella]	758	769	0	101.5	83.6	90.4	hypothetical protein CARUB_v10013028mg	gbpln	Capsella rubella	AT3G06620.1 | Symbols: | PAS domain-containing protein tyrosine kinase family protein | chr3:2062833-2067138 REVERSE LENGTH=773	758	773	0	102.0	83.8	90.6
Rsa1.0_00793.1.g19569.t1	gb|EOA29935.1| hypothetical protein CARUB_v10013028mg [Capsella rubella]	759	769	0	101.3	67.6	77.9	hypothetical protein CARUB_v10013028mg	gbpln	Capsella rubella	AT3G06620.1 | Symbols: | PAS domain-containing protein tyrosine kinase family protein | chr3:2062833-2067138 REVERSE LENGTH=773	759	773	0	101.8	67.3	78.0
Rsa1.0_00793.1.g19570.t1	ref|XP_002882485.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata] gi|297328325|gb|EFH58744.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata]	235	236	1.00E-115	100.4	87.2	91.1	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	gbpln	Arabidopsis lyrata	AT3G66654.2 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr3:2088694-2090297 FORWARD LENGTH=236	235	236	1.00E-117	100.4	87.2	91.5

Rsa1.0_00793.1.g19571.t1	ref|NP_974242.1| aldehyde dehydrogenase 22A1 [Arabidopsis thaliana] gi|118595572|sp|Q0WSF1.2|AL221_ARATH RecName: Full=Aldehyde dehydrogenase 22A1; AltName: Full=Novel aldehyde dehydrogenase family 22 member A1; Flags: Precursor gi|42406419|emb|CAE48165.1| putative aldehyde dehydrogenase [Arabidopsis thaliana] gi|332640912|gb|AEE74433.1| aldehyde dehydrogenase 22A1 [Arabidopsis thaliana]	628	596	0	94.9	91.7	93.6	aldehyde dehydrogenase 22A1	gbpln	Arabidopsis thaliana	AT3G66658.2 | Symbols: ALDH22A1 | aldehyde dehydrogenase 22A1 | chr3:2095341-2099013 REVERSE LENGTH=596	628	596	0	94.9	91.7	93.6
Rsa1.0_00793.1.g19572.t1	ref|XP_002884603.1| hypothetical protein ARALYDRAFT_896807 [Arabidopsis lyrata subsp. lyrata] gi|297330443|gb|EFH60862.1| hypothetical protein ARALYDRAFT_896807 [Arabidopsis lyrata subsp. lyrata]	859	948	0	110.4	66.9	78.8	hypothetical protein ARALYDRAFT_896807	gbpln	Arabidopsis lyrata	AT4G32670.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr4:15759527-15762847 REVERSE LENGTH=860	859	860	0	100.1	47.6	63.2
Rsa1.0_00793.1.g19573.t1	ref|NP_187323.2| component of IIS longevity pathway SMK-1 domain-containing protein [Arabidopsis thaliana] gi|20453090|gb|AAM19788.1| At3g06670/T8E24.10 [Arabidopsis thaliana] gi|27764910|gb|AAO23576.1| At3g06670/T8E24.10 [Arabidopsis thaliana] gi|332640916|gb|AEE74437.1| component of IIS longevity pathway SMK-1 domain-containing protein [Arabidopsis thaliana]	866	865	0	99.9	89.1	93.4	component of IIS longevity pathway SMK-1 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G06670.1 | Symbols: | binding | chr3:2105908-2113136 REVERSE LENGTH=865	866	865	0	99.9	89.1	93.4
Rsa1.0_00793.1.g19574.t1	ref|NP_187324.2| 60S ribosomal protein L29-2 [Arabidopsis thaliana] gi|332640918|gb|AEE74439.1| 60S ribosomal protein L29-2 [Arabidopsis thaliana]	61	83	8.00E-26	136.1	95.1	96.7	60S ribosomal protein L29-2	gbpln	Arabidopsis thaliana	AT3G06680.1 | Symbols: | Ribosomal L29e protein family | chr3:2114402-2114877 REVERSE LENGTH=83	61	83	1.00E-28	136.1	95.1	96.7
Rsa1.0_00793.1.g19575.t4	ref|XP_002882489.1| hypothetical protein ARALYDRAFT_477988 [Arabidopsis lyrata subsp. lyrata] gi|297328329|gb|EFH58748.1| hypothetical protein ARALYDRAFT_477988 [Arabidopsis lyrata subsp. lyrata]	229	183	6.00E-85	79.9	72.9	76.0	hypothetical protein ARALYDRAFT_477988	gbpln	Arabidopsis lyrata	AT3G06730.1 | Symbols: TRX P, TRX z | Thioredoxin z | chr3:2124276-2125845 FORWARD LENGTH=183	229	183	9.00E-87	79.9	71.6	75.5
Rsa1.0_00794.1.g19576.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00794.1.g19577.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1620	1365	0	84.3	30.9	43.0	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1620	575	1.00E-60	35.5	9.1	14.3
Rsa1.0_00794.1.g19578.t1	ref|NP_174390.2| PLATZ transcription factor family protein [Arabidopsis thaliana] gi|332193187|gb|AEE31308.1| PLATZ transcription factor family protein [Arabidopsis thaliana]	239	243	1.00E-108	101.7	86.6	94.6	PLATZ transcription factor family protein	gbpln	Arabidopsis thaliana	AT1G31040.1 | Symbols: | PLATZ transcription factor family protein | chr1:11069793-11072182 REVERSE LENGTH=243	239	243	1.00E-110	101.7	86.6	94.6
Rsa1.0_00794.1.g19579.t1	ref|NP_199996.1| fructokinase [Arabidopsis thaliana] gi|13878053|gb|AAK44104.1|AF370289_1 putative fructokinase 1 [Arabidopsis thaliana] gi|10177882|dbj|BAB11252.1| fructokinase 1 [Arabidopsis thaliana] gi|17104645|gb|AAL34211.1| putative fructokinase 1 [Arabidopsis thaliana] gi|332008749|gb|AED96132.1| pfkB-like carbohydrate kinase family protein [Arabidopsis thaliana]	124	343	2.00E-13	276.6	37.1	38.7	fructokinase	gbpln	Arabidopsis thaliana	AT5G51830.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr5:21069709-21071450 FORWARD LENGTH=343	124	343	3.00E-16	276.6	37.1	38.7
Rsa1.0_00794.1.g19580.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00794.1.g19581.t1	ref|NP_174391.5| basic helix-loop-helix domain-containing protein [Arabidopsis thaliana] gi|332193188|gb|AEE31309.1| transcription factor bHLH111 [Arabidopsis thaliana]	298	434	1.00E-104	145.6	73.8	81.2	basic helix-loop-helix domain-containing protein	gbpln	Arabidopsis thaliana	AT1G31050.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:11075720-11079140 REVERSE LENGTH=434	298	434	1.00E-106	145.6	73.8	81.2
Rsa1.0_00794.1.g19582.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00794.1.g19583.t2	gb|ADF80194.1| UTP:N-acetylglucosamine-1-P uridylyltransferase-1 [synthetic construct]	136	505	4.00E-42	371.3	73.5	78.7	UTP:N-acetylglucosamine-1-P uridylyltransferase-1	gbenv	synthetic construct	AT1G31070.2 | Symbols: GlcNAc1pUT1 | N-acetylglucosamine-1-phosphate uridylyltransferase 1 | chr1:11084951-11088361 FORWARD LENGTH=505	136	505	1.00E-44	371.3	73.5	78.7
Rsa1.0_00795.1.g19584.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00795.1.g19585.t1	gb|ABD65073.1| hypothetical protein 27.t00059 [Brassica oleracea]	287	341	7.00E-45	118.8	37.6	42.2	hypothetical protein 27.t00059	gbpln	Brassica oleracea	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00795.1.g19586.t1</td><td>gb|AAF79374.1|AC007887_33 F15O4.30 [Arabidopsis thaliana]</td><td>262</td><td>1180</td><td>2.00E-38</td><td>450.4</td><td>44.3</td><td>61.8</td><td>F15O4.30</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00795.1.g19587.t1</td><td>gb|EOA16131.1| hypothetical protein CARUB_v10004266mg [Capsella rubella]</td><td>688</td><td>699</td><td>0</td><td>101.6</td><td>84.4</td><td>89.5</td><td>hypothetical protein CARUB_v10004266mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G05230.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:1899818-1901938 REVERSE LENGTH=706</td><td>688</td><td>706</td><td>0</td><td>102.6</td><td>72.5</td><td>80.4</td></tr>
<tr><td>Rsa1.0_00795.1.g19588.t2</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>502</td><td>1142</td><td>6.00E-35</td><td>227.5</td><td>23.3</td><td>35.3</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>502</td><td>575</td><td>6.00E-18</td><td>114.5</td><td>16.1</td><td>26.3</td></tr>
<tr><td>Rsa1.0_00795.1.g19589.t1</td><td>gb|AAC28207.1| T24H24.13 gene product [Arabidopsis thaliana] gi|7267161|emb|CAB77873.1| putative transposon protein [Arabidopsis thaliana]</td><td>458</td><td>681</td><td>5.00E-56</td><td>148.7</td><td>25.3</td><td>35.4</td><td>T24H24.13 gene product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00795.1.g19590.t2</td><td>gb|AAD28663.1| hypothetical protein [Arabidopsis thaliana]</td><td>353</td><td>356</td><td>2.00E-19</td><td>100.8</td><td>20.1</td><td>34.6</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00795.1.g19591.t1</td><td>ref|XP_002876899.1| nonsense-mediated mRNA decay NMD3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297322737|gb|EFH53158.1| nonsense-mediated mRNA decay NMD3 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>90</td><td>516</td><td>3.00E-11</td><td>573.3</td><td>41.1</td><td>43.3</td><td>nonsense-mediated mRNA decay NMD3 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G03820.1 | Symbols: | nonsense-mediated mRNA decay NMD3 family protein | chr2:1165149-1166699 REVERSE LENGTH=516</td><td>90</td><td>516</td><td>8.00E-14</td><td>573.3</td><td>40.0</td><td>43.3</td></tr>
<tr><td>Rsa1.0_00795.1.g19592.t1</td><td>ref|XP_002870448.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316284|gb|EFH46707.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>376</td><td>449</td><td>0</td><td>119.4</td><td>89.1</td><td>93.4</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G35770.1 | Symbols: SAP | Transducin/WD40 repeat-like superfamily protein | chr5:13936457-13940786 REVERSE LENGTH=446</td><td>376</td><td>446</td><td>0</td><td>118.6</td><td>88.6</td><td>93.6</td></tr>
<tr><td>Rsa1.0_00795.1.g19593.t1</td><td>ref|NP_198426.1| transcriptional regulator STERILE APETALA [Arabidopsis thaliana] gi|30580503|sp|Q9FKH1.1|SAP_ARATH RecName: Full=Transcriptional regulator STERILE APETALA gi|9758652|dbj|BAB09276.1| sterile apetala [Arabidopsis thaliana] gi|332006634|gb|AED94017.1| transcriptional regulator STERILE APETALA [Arabidopsis thaliana]</td><td>82</td><td>446</td><td>6.00E-15</td><td>543.9</td><td>73.2</td><td>79.3</td><td>transcriptional regulator STERILE APETALA</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G35770.1 | Symbols: SAP | Transducin/WD40 repeat-like superfamily protein | chr5:13936457-13940786 REVERSE LENGTH=446</td><td>82</td><td>446</td><td>1.00E-17</td><td>543.9</td><td>73.2</td><td>79.3</td></tr>
<tr><td>Rsa1.0_00795.1.g19594.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00795.1.g19595.t1</td><td>gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]</td><td>187</td><td>543</td><td>2.00E-28</td><td>290.4</td><td>33.7</td><td>51.9</td><td>hypothetical protein CARUB_v10015730mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566</td><td>187</td><td>566</td><td>7.00E-25</td><td>302.7</td><td>29.9</td><td>54.0</td></tr>
<tr><td>Rsa1.0_00795.1.g19596.t1</td><td>gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]</td><td>981</td><td>1024</td><td>2.00E-90</td><td>104.4</td><td>24.5</td><td>33.5</td><td>F5J5.16</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00795.1.g19597.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00795.1.g19598.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00796.1.g19599.t1</td><td>ref|XP_002874165.1| peroxidase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320002|gb|EFH50424.1| peroxidase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>341</td><td>341</td><td>0</td><td>100.0</td><td>92.1</td><td>97.7</td><td>peroxidase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G24070.1 | Symbols: | Peroxidase superfamily protein | chr5:8134301-8135991 REVERSE LENGTH=340</td><td>341</td><td>340</td><td>0</td><td>99.7</td><td>90.9</td><td>95.9</td></tr>
<tr><td>Rsa1.0_00796.1.g19600.t1</td><td>gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]</td><td>888</td><td>1164</td><td>0</td><td>131.1</td><td>53.2</td><td>67.5</td><td>similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>888</td><td>626</td><td>6.00E-67</td><td>70.5</td><td>15.2</td><td>24.3</td></tr>
<tr><td>Rsa1.0_00796.1.g19601.t1</td><td>ref|XP_002890732.1| hypothetical protein ARALYDRAFT_890279 [Arabidopsis lyrata subsp. lyrata] gi|297336574|gb|EFH66991.1| hypothetical protein ARALYDRAFT_890279 [Arabidopsis lyrata subsp. lyrata]</td><td>312</td><td>311</td><td>4.00E-71</td><td>99.7</td><td>44.6</td><td>62.5</td><td>hypothetical protein ARALYDRAFT_890279</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G27570.1 | Symbols: | phosphatidylinositol 3- and 4-kinase family protein | chr1:9575538-9582376 FORWARD LENGTH=649</td><td>312</td><td>649</td><td>6.00E-73</td><td>208.0</td><td>46.5</td><td>63.1</td></tr>
<tr><td>Rsa1.0_00796.1.g19602.t1</td><td>ref|NP_174074.1| uncharacterized protein [Arabidopsis thaliana] gi|5668765|gb|AAD45992.1|AC005916_4 T17H3.4 [Arabidopsis thaliana] gi|332192722|gb|AEE30843.1| uncharacterized protein AT1G27540 [Arabidopsis thaliana]</td><td>392</td><td>413</td><td>1.00E-100</td><td>105.4</td><td>52.6</td><td>65.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G27540.1 | Symbols: | Protein of unknown function (DUF295) | chr1:9566608-9567849 REVERSE LENGTH=413</td><td>392</td><td>413</td><td>1.00E-102</td><td>105.4</td><td>52.6</td><td>65.6</td></tr>
<tr><td>Rsa1.0_00796.1.g19603.t1</td><td>gb|EOA19255.1| hypothetical protein CARUB_v10000189mg, partial [Capsella rubella]</td><td>880</td><td>883</td><td>0</td><td>100.3</td><td>88.6</td><td>93.6</td><td>hypothetical protein CARUB_v10000189mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G24080.1 | Symbols: | Protein kinase superfamily protein | chr5:8139334-8141014 REVERSE LENGTH=470</td><td>880</td><td>470</td><td>0</td><td>53.4</td><td>48.9</td><td>51.9</td></tr>
<tr><td>Rsa1.0_00796.1.g19604.t2</td><td>dbj|BAA21873.1| acidic endochitinase [Arabidopsis thaliana]</td><td>263</td><td>302</td><td>1.00E-117</td><td>114.8</td><td>77.6</td><td>82.5</td><td>acidic endochitinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G24090.1 | Symbols: ATCHIA, CHIA | chitinase A | chr5:8143805-8145153 REVERSE LENGTH=302</td><td>263</td><td>302</td><td>1.00E-119</td><td>114.8</td><td>76.4</td><td>82.1</td></tr>
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Rsa1.0_00796.1.g19606.t1	ref|XP_002874170.1| hypothetical protein ARALYDRAFT_489269 [Arabidopsis lyrata subsp. lyrata] gi|297320007|gb|EFH50429.1| hypothetical protein ARALYDRAFT_489269 [Arabidopsis lyrata subsp. lyrata]	539	517	0	95.9	82.0	87.2	hypothetical protein ARALYDRAFT_489269	gbpln	Arabidopsis lyrata	AT5G24120.1 | Symbols: SIGE, SIG5, ATSIG5 | sigma factor E | chr5:8157794-8159746 REVERSE LENGTH=517	539	517	0	95.9	79.8	86.1
Rsa1.0_00796.1.g19607.t1	ref|XP_002872093.1| hypothetical protein ARALYDRAFT_489270 [Arabidopsis lyrata subsp. lyrata] gi|297317930|gb|EFH48352.1| hypothetical protein ARALYDRAFT_489270 [Arabidopsis lyrata subsp. lyrata]	315	315	1.00E-155	100.0	88.3	94.3	hypothetical protein ARALYDRAFT_489270	gbpln	Arabidopsis lyrata	AT5G24130.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: petal, leaf whorl, flower; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8162247-8163825 FORWARD LENGTH=316	315	316	1.00E-153	100.3	87.3	93.7
Rsa1.0_00796.1.g19608.t1	ref|NP_197802.1| Squalene monooxygenase 2 [Arabidopsis thaliana] gi|6685408|sp|O65403.1|ERG13_ARATH RecName: Full=Squalene monooxygenase 2; AltName: Full=Squalene epoxidase 2; Short=SE 2 gi|3123329|emb|CAA06771.1| squalene epoxidase homologue [Arabidopsis thaliana] gi|10178162|dbj|BAB11574.1| squalene monooxygenase 2 (squalene epoxidase 2) (SE 2) [Arabidopsis thaliana] gi|332005878|gb|AED93261.1| Squalene monooxygenase 2 [Arabidopsis thaliana]	518	516	0	99.6	80.5	88.4	Squalene monooxygenase 2	gbpln	Arabidopsis thaliana	AT5G24140.1 | Symbols: SQP2 | squalene monooxygenase 2 | chr5:8164547-8167669 REVERSE LENGTH=516	518	516	0	99.6	80.5	88.4
Rsa1.0_00796.1.g19609.t1	sp|O65726.1|ERG12_BRANA RecName: Full=Squalene monooxygenase 1,2; AltName: Full=Squalene epoxidase 1,2; Short=SE 1,2 gi|3123352|emb|CAA06770.1| squalene epoxidase homologue [Brassica napus]	514	518	0	100.8	88.1	91.2	RecName: Full=Squalene monooxygenase 1,2; AltName: Full=Squalene epoxidase 1,2; Short=SE 1,2 gi|3123352|emb|CAA06770.1| squalene epoxidase homologue	gbpln	Brassica napus	AT5G24150.1 | Symbols: SQP1, SQE5 | FAD/NAD(P)-binding oxidoreductase family protein | chr5:8172594-8175395 REVERSE LENGTH=516	514	516	0	100.4	74.3	85.6
Rsa1.0_00796.1.g19610.t1	gb|EOA21899.1| hypothetical protein CARUB_v10002380mg [Capsella rubella]	107	75	4.00E-28	70.1	61.7	63.6	hypothetical protein CARUB_v10002380mg	gbpln	Capsella rubella	AT5G24165.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G23885.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:8188622-8189087 FORWARD LENGTH=75	107	75	5.00E-29	70.1	58.9	62.6
Rsa1.0_00796.1.g19611.t1	ref|XP_002874175.1| hypothetical protein ARALYDRAFT_489277 [Arabidopsis lyrata subsp. lyrata] gi|297320012|gb|EFH50434.1| hypothetical protein ARALYDRAFT_489277 [Arabidopsis lyrata subsp. lyrata]	164	163	2.00E-75	99.4	87.2	92.1	hypothetical protein ARALYDRAFT_489277	gbpln	Arabidopsis lyrata	AT5G24170.1 | Symbols: | Got1/Sft2-like vescicle transport protein family | chr5:8189744-8191355 REVERSE LENGTH=163	164	163	1.00E-70	99.4	84.8	89.6

<table>
<tr><td>Rsa1.0_00797.1.g19612.t1</td><td>ref|NP_566914.1| RNA polymerase III subunit RPC82 family protein [Arabidopsis thaliana] gi|20466336|gb|AAM20485.1| RNA polymerase III subunit-like protein [Arabidopsis thaliana] gi|34098883|gb|AAQ56824.1| At3g49000 [Arabidopsis thaliana] gi|332644960|gb|AEE78481.1| RNA polymerase III subunit RPC82 family protein [Arabidopsis thaliana]</td><td>182</td><td>523</td><td>8.00E-74</td><td>287.4</td><td>72.5</td><td>87.9</td><td>RNA polymerase III subunit RPC82 family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G49000.1 | Symbols: | RNA polymerase III subunit RPC82 family protein | chr3:18162903-18165846 FORWARD LENGTH=523</td><td>182</td><td>523</td><td>3.00E-76</td><td>287.4</td><td>72.5</td><td>87.9</td></tr>
<tr><td>Rsa1.0_00797.1.g19613.t1</td><td>ref|XP_002877640.1| AMP-dependent synthetase and ligase family protein [Arabidopsis lyrata subsp. lyrata] gi|297323478|gb|EFH53899.1| AMP-dependent synthetase and ligase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>514</td><td>514</td><td>0</td><td>100.0</td><td>95.9</td><td>98.1</td><td>AMP-dependent synthetase and ligase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G48990.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr3:18159031-18161294 REVERSE LENGTH=514</td><td>514</td><td>514</td><td>0</td><td>100.0</td><td>95.5</td><td>97.5</td></tr>
<tr><td>Rsa1.0_00797.1.g19614.t1</td><td>ref|XP_002875936.1| hypothetical protein ARALYDRAFT_485256 [Arabidopsis lyrata subsp. lyrata] gi|297321774|gb|EFH52195.1| hypothetical protein ARALYDRAFT_485256 [Arabidopsis lyrata subsp. lyrata]</td><td>548</td><td>539</td><td>0</td><td>98.4</td><td>86.5</td><td>90.3</td><td>hypothetical protein ARALYDRAFT_485256</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G48980.1 | Symbols: | Arabidopsis thaliana protein of unknown function (DUF821) | chr3:18155416-18158222 FORWARD LENGTH=539</td><td>548</td><td>539</td><td>0</td><td>98.4</td><td>85.6</td><td>89.6</td></tr>
<tr><td>Rsa1.0_00797.1.g19615.t1</td><td>gb|EOA24919.1| hypothetical protein CARUB_v10018210mg [Capsella rubella]</td><td>140</td><td>140</td><td>1.00E-70</td><td>100.0</td><td>96.4</td><td>100.0</td><td>hypothetical protein CARUB_v10018210mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G48970.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:18152408-18153296 REVERSE LENGTH=140</td><td>140</td><td>140</td><td>7.00E-66</td><td>100.0</td><td>96.4</td><td>98.6</td></tr>
<tr><td>Rsa1.0_00797.1.g19616.t1</td><td>ref|NP_190464.1| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana] gi|6522571|emb|CAB62015.1| endo-polygalacturonase-like protein [Arabidopsis thaliana] gi|67633678|gb|AAY78763.1| glycoside hydrolase family 28 protein [Arabidopsis thaliana] gi|332644955|gb|AEE78476.1| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]</td><td>464</td><td>469</td><td>0</td><td>101.1</td><td>86.6</td><td>94.0</td><td>glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G48950.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:18148017-18149987 FORWARD LENGTH=469</td><td>464</td><td>469</td><td>0</td><td>101.1</td><td>86.6</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00797.1.g19617.t1</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1524</td><td>1529</td><td>0</td><td>100.3</td><td>39.5</td><td>55.8</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>1524</td><td>746</td><td>5.00E-88</td><td>49.0</td><td>11.2</td><td>15.5</td></tr>
<tr><td>Rsa1.0_00797.1.g19618.t1</td><td>ref|XP_002877638.1| remorin family protein [Arabidopsis lyrata subsp. lyrata] gi|297323476|gb|EFH53897.1| remorin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>84</td><td>175</td><td>4.00E-25</td><td>208.3</td><td>77.4</td><td>88.1</td><td>remorin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G48940.1 | Symbols: | Remorin family protein | chr3:18142863-18144163 REVERSE LENGTH=175</td><td>84</td><td>175</td><td>4.00E-25</td><td>208.3</td><td>72.6</td><td>83.3</td></tr>
<tr><td>Rsa1.0_00797.1.g19619.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00797.1.g19620.t1</td><td>ref|XP_002869362.1| 40S ribosomal protein S11 [Arabidopsis lyrata subsp. lyrata] gi|297315198|gb|EFH45621.1| 40S ribosomal protein S11 [Arabidopsis lyrata subsp. lyrata]</td><td>159</td><td>159</td><td>1.00E-79</td><td>100.0</td><td>90.6</td><td>94.3</td><td>40S ribosomal protein S11</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23740.1 | Symbols: RPS11-BETA | ribosomal protein S11-beta | chr5:8008251-8009330 REVERSE LENGTH=159</td><td>159</td><td>159</td><td>2.00E-79</td><td>100.0</td><td>96.2</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00797.1.g19621.t1</td><td>ref|XP_003536473.1| PREDICTED: membrane steroid-binding protein 1-like [Glycine max]</td><td>79</td><td>235</td><td>3.00E-14</td><td>297.5</td><td>48.1</td><td>49.4</td><td>PREDICTED: membrane steroid-binding protein 1-like</td><td>gbenv/gbpln</td><td>Glycine max</td><td>AT5G52240.1 | Symbols: MSBP1, ATMP1, AtMAPR5 | membrane steroid binding protein 1 | chr5:21213121-21214557 FORWARD LENGTH=220</td><td>79</td><td>220</td><td>3.00E-16</td><td>278.5</td><td>45.6</td><td>48.1</td></tr>
<tr><td>Rsa1.0_00797.1.g19622.t1</td><td>ref|XP_002875931.1| membrane-associated progesterone binding protein 3 [Arabidopsis lyrata subsp. lyrata] gi|297321769|gb|EFH52190.1| membrane-associated progesterone binding protein 3 [Arabidopsis lyrata subsp. lyrata]</td><td>224</td><td>232</td><td>1.00E-101</td><td>103.6</td><td>85.7</td><td>90.2</td><td>membrane-associated progesterone binding protein 3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G48890.1 | Symbols: ATMP2, ATMAPR3, MSBP2, MAPR3 | membrane-associated progesterone binding protein 3 | chr3:18129669-18131353 FORWARD LENGTH=233</td><td>224</td><td>233</td><td>3.00E-99</td><td>104.0</td><td>80.8</td><td>84.4</td></tr>
<tr><td>Rsa1.0_00797.1.g19623.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00797.1.g19624.t1</td><td>gb|EOA23157.1| hypothetical protein CARUB_v10016640mg [Capsella rubella]</td><td>930</td><td>977</td><td>0</td><td>105.1</td><td>92.5</td><td>95.4</td><td>hypothetical protein CARUB_v10016640mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G48870.2 | Symbols: HSP93-III | Clp ATPase | chr3:18122363-18125915 REVERSE LENGTH=921</td><td>930</td><td>921</td><td>0</td><td>99.0</td><td>90.8</td><td>93.8</td></tr>
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Rsa1.0_00797.1.g19625.t1	gb|EOA25124.1| hypothetical protein CARUB_v10018432mg [Capsella rubella]	296	574	1.00E-129	193.9	82.1	87.8	hypothetical protein CARUB_v10018432mg	gbpln	Capsella rubella	AT3G48860.2 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23700.1); Has 12429 Blast hits to 9751 proteins in 897 species: Archae - 180; Bacteria - 1190; Metazoa - 6552; Fungi - 1361; Plants - 886; Viruses - 50; Other Eukaryotes - 2210 (source: NCBI BLink). | chr3:18117619-18121853 FORWARD LENGTH=577	296	577	1.00E-130	194.9	81.4	86.8
Rsa1.0_00798.1.g19626.t1	ref|XP_002892523.1| hypothetical protein ARALYDRAFT_334257 [Arabidopsis lyrata subsp. lyrata] gi|297338365|gb|EFH68782.1| hypothetical protein ARALYDRAFT_334257 [Arabidopsis lyrata subsp. lyrata]	282	305	3.00E-45	108.2	44.3	60.3	hypothetical protein ARALYDRAFT_334257	gbpln	Arabidopsis lyrata	AT2G42470.1 | Symbols: | TRAF-like family protein | chr2:17679887-17685187 REVERSE LENGTH=898	282	898	1.00E-41	318.4	39.7	58.5
Rsa1.0_00798.1.g19627.t7	gb|AAC13599.1| similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]	1585	928	1.00E-163	58.5	19.4	25.1	similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31)	gbpln	Arabidopsis thaliana	AT1G02580.1 | Symbols: MEA, EMB173, FIS1, SDG5 | SET domain-containing protein | chr1:544796-548994 FORWARD LENGTH=689	1585	689	2.00E-79	43.5	11.4	15.5
Rsa1.0_00798.1.g19628.t1	gb|EOA36475.1| hypothetical protein CARUB_v10011093mg [Capsella rubella]	698	716	0	102.6	82.1	89.3	hypothetical protein CARUB_v10011093mg	gbpln	Capsella rubella	AT1G02660.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:572187-574746 REVERSE LENGTH=713	698	713	0	102.1	82.2	89.1
Rsa1.0_00798.1.g19629.t1	ref|NP_198686.2| uncharacterized protein [Arabidopsis thaliana] gi|62318737|dbj|BAD93759.1| putative protein [Arabidopsis thaliana] gi|332006968|gb|AED94351.1| uncharacterized protein AT5G38700 [Arabidopsis thaliana]	159	182	2.00E-71	114.5	84.9	90.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G38700.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.04 four leaves visible, LP.10 ten leaves visible, petal differentiation and expansion stage, LP.08 eight leaves visible, LP.12 twelve leaves visible; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02170.1); Has 64 Blast hits to 64 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:15489690-15490238 FORWARD LENGTH=182	159	182	8.00E-74	114.5	84.9	90.6
Rsa1.0_00798.1.g19630.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1389	2726	0	196.3	50.7	68.8	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1389	158	3.00E-30	11.4	4.3	5.2
Rsa1.0_00798.1.g19631.t1	ref|NP_171772.1| galacturonosyltransferase 5 [Arabidopsis thaliana] gi|42571307|ref|NP_973744.1| galacturonosyltransferase 5 [Arabidopsis thaliana] gi|75172933|sp|Q9FWY9.1|GATL5_ARATH RecName: Full=Probable galacturonosyltransferase-like 5 gi|9972380|gb|AAG10630.1|AC022521_8 Unknown protein [Arabidopsis thaliana] gi|25083419|gb|AAN72073.1| Unknown protein [Arabidopsis thaliana] gi|26452192|dbj|BAC43184.1| unknown protein [Arabidopsis thaliana] gi|31711862|gb|AAP68287.1| At1g02720 [Arabidopsis thaliana] gi|332189341|gb|AEE27462.1| galacturonosyltransferase 5 [Arabidopsis thaliana] gi|332189342|gb|AEE27463.1| galacturonosyltransferase 5 [Arabidopsis thaliana]	364	361	1.00E-167	99.2	79.9	87.6	galacturonosyltransferase 5	gbpln	Arabidopsis thaliana	AT1G02720.2 | Symbols: GATL5 | galacturonosyltransferase 5 | chr1:592115-593200 FORWARD LENGTH=361	364	361	1.00E-169	99.2	79.9	87.6
Rsa1.0_00798.1.g19632.t1	ref|NP_171774.2| mortality factor 4-like protein 1 [Arabidopsis thaliana] gi|66792606|gb|AAY56405.1| At1g02740 [Arabidopsis thaliana] gi|332189344|gb|AEE27465.1| MRG family protein [Arabidopsis thaliana]	329	327	1.00E-133	99.4	74.2	84.2	mortality factor 4-like protein 1	gbpln	Arabidopsis thaliana	AT1G02740.1 | Symbols: | MRG family protein | chr1:599734-602021 REVERSE LENGTH=327	329	327	1.00E-136	99.4	74.2	84.2
Rsa1.0_00798.1.g19633.t4	dbj|BAJ33794.1| unnamed protein product [Thellungiella halophila] gi|312281899|dbj|BAJ33815.1| unnamed protein product [Thellungiella halophila]	237	220	7.00E-67	92.8	67.5	79.7	unnamed protein product	----	----	AT1G02750.1 | Symbols: | Drought-responsive family protein | chr1:602673-604134 FORWARD LENGTH=221	237	221	2.00E-59	93.2	59.1	70.0

Rsa1.0_00798.1.g19634.t1	gb|EOA31438.1| hypothetical protein CARUB_v10014622mg [Capsella rubella]	217	210	2.00E-96	96.8	84.3	87.6	hypothetical protein CARUB_v10014622mg	gbpln	Capsella rubella	AT3G16780.1 | Symbols: | Ribosomal protein L19e family protein | chr3:5708982-5710249 FORWARD LENGTH=209	217	209	2.00E-97	96.3	82.9	86.6
Rsa1.0_00798.1.g19635.t1	ref|XP_002892124.1| hypothetical protein ARALYDRAFT_887420 [Arabidopsis lyrata subsp. lyrata] gi|297337966|gb|EFH68383.1| hypothetical protein ARALYDRAFT_887420 [Arabidopsis lyrata subsp. lyrata]	418	422	0	101.0	80.4	90.9	hypothetical protein ARALYDRAFT_887420	gbpln	Arabidopsis lyrata	AT1G02790.1 | Symbols: PGA4 | polygalacturonase 4 | chr1:610681-612225 REVERSE LENGTH=422	418	422	0	101.0	80.4	90.2
Rsa1.0_00798.1.g19636.t1	gb|EOA37572.1| hypothetical protein CARUB_v10011914mg [Capsella rubella]	511	501	0	98.0	85.1	88.8	hypothetical protein CARUB_v10011914mg	gbpln	Capsella rubella	AT1G02800.1 | Symbols: ATCEL2, CEL2 | cellulase 2 | chr1:613386-616103 REVERSE LENGTH=501	511	501	0	98.0	89.2	92.8
Rsa1.0_00798.1.g19637.t1	gb|EOA38526.1| hypothetical protein CARUB_v10010322mg, partial [Capsella rubella]	172	203	1.00E-73	118.0	82.0	86.0	hypothetical protein CARUB_v10010322mg, partial	gbpln	Capsella rubella	AT1G02816.1 | Symbols: | Protein of unknown function, DUF538 | chr1:621637-622137 FORWARD LENGTH=166	172	166	1.00E-73	96.5	79.1	83.1
Rsa1.0_00798.1.g19638.t1	dbj|BAJ34418.1| unnamed protein product [Thellungiella halophila]	123	124	1.00E-41	100.8	78.0	87.0	unnamed protein product	----	----	AT3G05560.3 | Symbols: | Ribosomal L22e protein family | chr3:1614641-1615204 FORWARD LENGTH=124	123	124	8.00E-44	100.8	77.2	87.8
Rsa1.0_00799.1.g19639.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00799.1.g19640.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00799.1.g19641.t1	gb|EOA17311.1| hypothetical protein CARUB_v10005590mg [Capsella rubella]	85	249	1.00E-14	292.9	51.8	64.7	hypothetical protein CARUB_v10005590mg	gbpln	Capsella rubella	AT4G30550.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr4:14925618-14926713 FORWARD LENGTH=249	85	249	2.00E-16	292.9	51.8	62.4
Rsa1.0_00799.1.g19642.t1	gb|EOA15566.1| hypothetical protein CARUB_v10005224mg [Capsella rubella]	388	329	4.00E-49	84.8	30.7	36.3	hypothetical protein CARUB_v10005224mg	gbpln	Capsella rubella	AT4G28430.1 | Symbols: | Reticulon family protein | chr4:14057846-14059772 FORWARD LENGTH=457	388	457	9.00E-51	117.8	30.7	36.3
Rsa1.0_00799.1.g19643.t1	gb|ABD64950.1| GRF zinc finger containing protein [Brassica oleracea]	80	180	1.00E-20	225.0	58.8	61.3	GRF zinc finger containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00799.1.g19644.t11	gb|EOA39134.1| hypothetical protein CARUB_v10012056mg [Capsella rubella]	413	435	9.00E-99	105.3	50.1	64.2	hypothetical protein CARUB_v10012056mg	gbpln	Capsella rubella	AT1G32660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11811040-11812380 FORWARD LENGTH=446	413	446	2.00E-94	108.0	53.3	65.6
Rsa1.0_00799.1.g19645.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00800.1.g19646.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00800.1.g19647.t1	gb|EOA27921.1| hypothetical protein CARUB_v10024094mg [Capsella rubella]	200	199	1.00E-99	99.5	92.0	94.5	hypothetical protein CARUB_v10024094mg	gbpln	Capsella rubella	AT2G44740.1 | Symbols: CYCP4;1 | cyclin p4;1 | chr2:18442287-18443304 REVERSE LENGTH=202	200	202	2.00E-98	101.0	87.5	91.0
Rsa1.0_00800.1.g19648.t1	gb|EOA26431.1| hypothetical protein CARUB_v10025047mg [Capsella rubella]	354	395	1.00E-128	111.6	75.7	83.1	hypothetical protein CARUB_v10025047mg	gbpln	Capsella rubella	AT2G44730.1 | Symbols: | Alcohol dehydrogenase transcription factor Myb/SANT-like family protein | chr2:18437447-18438565 REVERSE LENGTH=372	354	372	1.00E-123	105.1	72.0	79.4
Rsa1.0_00800.1.g19649.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00800.1.g19650.t1	ref|XP_002881976.1| hypothetical protein ARALYDRAFT_483599 [Arabidopsis lyrata subsp. lyrata] gi|297327815|gb|EFH58235.1| hypothetical protein ARALYDRAFT_483599 [Arabidopsis lyrata subsp. lyrata]	281	283	1.00E-125	100.7	82.6	89.0	hypothetical protein ARALYDRAFT_483599	gbpln	Arabidopsis lyrata	AT2G44680.1 | Symbols: CKB4 | casein kinase II beta subunit 4 | chr2:18426898-18428166 REVERSE LENGTH=283	281	283	1.00E-127	100.7	82.6	89.0
Rsa1.0_00800.1.g19651.t1	ref|NP_566023.1| uncharacterized protein [Arabidopsis thaliana] gi|13272435|gb|AAK17156.1|AF325088_1 unknown protein [Arabidopsis thaliana] gi|3341687|gb|AAC27469.1| expressed protein [Arabidopsis thaliana] gi|15081775|gb|AAK82542.1| At2g44670/F16B22.16 [Arabidopsis thaliana] gi|21593625|gb|AAM65592.1| unknown [Arabidopsis thaliana] gi|24797042|gb|AAN64533.1| At2g44670/F16B22.16 [Arabidopsis thaliana] gi|110736091|dbj|BAF00018.1| hypothetical protein [Arabidopsis thaliana] gi|330255359|gb|AEC10453.1| uncharacterized protein AT2G44670 [Arabidopsis thaliana]	94	93	7.00E-38	98.9	85.1	87.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G44670.1 | Symbols: | Protein of unknown function (DUF581) | chr2:18425279-18425673 FORWARD LENGTH=93	94	93	1.00E-40	98.9	85.1	87.2

Rsa1.0_00800.1.g19652.t1	gb|EOA27088.1| hypothetical protein CARUB_v10023185mg [Capsella rubella]	484	455	0	94.0	78.5	85.5	hypothetical protein CARUB_v10023185mg	gbpln	Capsella rubella	AT2G44640.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, chloroplast, plasma membrane, plastid, chloroplast envelope; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3769 (InterPro:IPR022244); BEST Arabidopsis thaliana protein match is: pigment defective 320 (TAIR:AT3G06960.1); Has 49 Blast hits to 48 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:18417286-18419063 FORWARD LENGTH=451	484	451	0	93.2	77.5	84.7
Rsa1.0_00800.1.g19653.t1	ref|XP_002880126.1| mtACP-1 [Arabidopsis lyrata subsp. lyrata] gi|297325965|gb|EFH56385.1| mtACP-1 [Arabidopsis lyrata subsp. lyrata]	120	122	9.00E-55	101.7	89.2	94.2	mtACP-1	gbpln	Arabidopsis lyrata	AT2G44620.1 | Symbols: MTACP-1, MTACP1 | mitochondrial acyl carrier protein 1 | chr2:18414320-18415065 FORWARD LENGTH=122	120	122	1.00E-56	101.7	87.5	94.2
Rsa1.0_00800.1.g19654.t1	ref|NP_181989.1| Ras-related protein RABH1B [Arabidopsis thaliana] gi|297828175|ref|XP_002881970.1| hypothetical protein ARALYDRAFT_903887 [Arabidopsis lyrata subsp. lyrata] gi|75318653|sp|O80501.1|RAH1B_ARATH RecName: Full=Ras-related protein RABH1b; Short=AtRABH1b; AltName: Full=Ras-related protein Rab6A; Short=AtRab6A gi|3341681|gb|AAC27463.1| putative small GTP-binding protein [Arabidopsis thaliana] gi|21593488|gb|AAM65455.1| putative small GTP-binding protein [Arabidopsis thaliana] gi|107738267|gb|ABF83670.1| At2g44610 [Arabidopsis thaliana] gi|110742258|dbj|BAE99055.1| putative small GTP-binding protein [Arabidopsis thaliana] gi|297327809|gb|EFH58229.1| hypothetical protein ARALYDRAFT_903887 [Arabidopsis lyrata subsp. lyrata] gi|330255353|gb|AEC10447.1| Ras-related protein RABH1B [Arabidopsis thaliana] gi|741994|prf||2008312A GTP-binding protein	208	208	1.00E-117	100.0	100.0	100.0	Ras-related protein RABH1B	gbpln	Arabidopsis lyrata	AT2G44610.1 | Symbols: RAB6, ATRABH1B, ATRAB6A, RAB6A | Ras-related small GTP-binding family protein | chr2:18411778-18413883 REVERSE LENGTH=208	208	208	1.00E-120	100.0	100.0	100.0
Rsa1.0_00800.1.g19655.t1	ref|XP_002881965.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata] gi|297327804|gb|EFH58224.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata]	486	494	0	101.6	81.7	87.7	glycosyl hydrolase family 9 protein	gbpln	Arabidopsis lyrata	AT2G44570.1 | Symbols: AtGH9B12, GH9B12 | glycosyl hydrolase 9B12 | chr2:18394425-18396268 REVERSE LENGTH=492	486	492	0	101.2	81.1	87.0
Rsa1.0_00800.1.g19656.t1	gb|EOA27499.1| hypothetical protein CARUB_v10023636mg [Capsella rubella]	130	324	2.00E-25	249.2	72.3	80.0	hypothetical protein CARUB_v10023636mg	gbpln	Capsella rubella	AT2G44510.1 | Symbols: | CDK inhibitor P21 binding protein | chr2:18377411-18379030 FORWARD LENGTH=326	130	326	1.00E-26	250.8	69.2	80.0
Rsa1.0_00800.1.g19657.t1	sp|Q9LJF9.3|FDL44_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	425	434	1.00E-73	102.1	45.6	60.5	RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	----	----	AT1G55030.1 | Symbols: | RNI-like superfamily protein | chr1:20530417-20531768 REVERSE LENGTH=422	425	422	2.00E-67	99.3	42.6	60.2
Rsa1.0_00800.1.g19658.t1	gb|EOA26134.1| hypothetical protein CARUB_v10019567mg [Capsella rubella]	227	381	5.00E-16	167.8	25.1	34.4	hypothetical protein CARUB_v10019567mg	gbpln	Capsella rubella	AT3G26930.1 | Symbols: | Protein with RNI-like/FBD-like domains | chr3:9925931-9927351 FORWARD LENGTH=409	227	409	4.00E-18	180.2	26.4	37.4
Rsa1.0_00800.1.g19659.t1	sp|Q9LJF9.3|FDL44_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	441	434	6.00E-71	98.4	43.8	58.0	RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	----	----	AT4G00160.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:63465-65365 FORWARD LENGTH=453	441	453	2.00E-67	102.7	42.9	55.6
Rsa1.0_00800.1.g19660.t1	ref|NP_001154649.1| leucine rich repeat and F-box domain-containing protein [Arabidopsis thaliana] gi|143015252|sp|Q9LJF8.2|FBL47_ARATH RecName: Full=F-box/LRR-repeat protein At3g26922 gi|332643721|gb|AEE77242.1| leucine rich repeat and F-box domain-containing protein [Arabidopsis thaliana]	209	306	7.00E-21	146.4	40.7	56.0	leucine rich repeat and F-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G26922.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:9922858-9923891 FORWARD LENGTH=306	209	306	2.00E-23	146.4	40.7	56.0
Rsa1.0_00800.1.g19661.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00800.1.g19662.t1	sp|Q9LJF9.3|FDL44_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	294	434	5.00E-44	147.6	36.1	48.6	RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	----	----	AT3G26922.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:9922858-9923891 FORWARD LENGTH=306	294	306	3.00E-39	104.1	35.4	45.2

Rsa1.0_00800.1.g19663.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00800.1.g19664.t1	sp|Q9LJF9.3|FDL44_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	417	434	3.00E-65	104.1	42.4	58.8	RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	----	----	AT3G52680.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr3:19527075-19528838 FORWARD LENGTH=456	417	456	8.00E-65	109.4	42.7	58.5
Rsa1.0_00800.1.g19665.t1	ref|XP_002993757.1| hypothetical protein SELMODRAFT_431804 [Selaginella moellendorffii] gi|300138407|gb|EFJ05176.1| hypothetical protein SELMODRAFT_431804 [Selaginella moellendorffii]	151	276	7.00E-22	182.8	43.7	64.9	hypothetical protein SELMODRAFT_431804	gbpln	Selaginella moellendorffii	AT2G44510.1 | Symbols: | CDK inhibitor P21 binding protein | chr2:18377411-18379030 FORWARD LENGTH=326	151	326	2.00E-23	215.9	34.4	39.1
Rsa1.0_00800.1.g19666.t9	ref|XP_002874089.1| hypothetical protein ARALYDRAFT_910273 [Arabidopsis lyrata subsp. lyrata] gi|297319926|gb|EFH50348.1| hypothetical protein ARALYDRAFT_910273 [Arabidopsis lyrata subsp. lyrata]	377	393	1.00E-104	104.2	57.0	69.2	hypothetical protein ARALYDRAFT_910273	gbpln	Arabidopsis lyrata	AT5G22791.2 | Symbols: | F-box family protein | chr5:7603579-7604771 REVERSE LENGTH=355	377	355	1.00E-75	94.2	45.9	57.6
Rsa1.0_00801.1.g19667.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00801.1.g19668.t1	ref|XP_002876427.1| hypothetical protein ARALYDRAFT_907231 [Arabidopsis lyrata subsp. lyrata] gi|297322265|gb|EFH52686.1| hypothetical protein ARALYDRAFT_907231 [Arabidopsis lyrata subsp. lyrata]	551	547	0	99.3	83.8	91.8	hypothetical protein ARALYDRAFT_907231	gbpln	Arabidopsis lyrata	AT3G57620.1 | Symbols: | glyoxal oxidase-related protein | chr3:21337564-21339207 FORWARD LENGTH=547	551	547	0	99.3	82.6	91.5
Rsa1.0_00801.1.g19669.t1	gb|ACH99803.1| WRKY2 transcription factor [Brassica napus]	676	624	0	92.3	85.4	87.6	WRKY2 transcription factor	gbpln	Brassica napus	AT5G56270.1 | Symbols: WRKY2, ATWRKY2 | WRKY DNA-binding protein 2 | chr5:22780816-22783137 FORWARD LENGTH=687	676	687	0	101.6	82.1	89.6
Rsa1.0_00801.1.g19670.t1	gb|EOA12550.1| hypothetical protein CARUB_v10026800mg [Capsella rubella]	320	317	1.00E-172	99.1	92.2	95.6	hypothetical protein CARUB_v10026800mg	gbpln	Capsella rubella	AT5G56280.1 | Symbols: CSN6A | COP9 signalosome subunit 6A | chr5:22783617-22785530 REVERSE LENGTH=317	320	317	1.00E-173	99.1	91.9	95.0
Rsa1.0_00801.1.g19671.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00801.1.g19672.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1455	1475	0	101.4	61.2	76.4	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1455	1262	0	86.7	22.3	28.1
Rsa1.0_00801.1.g19673.t4	gb|ABB92565.1| peroxisomal import receptor PTS1 [Brassica napus]	324	731	2.00E-66	225.6	42.9	47.2	peroxisomal import receptor PTS1	gbpln	Brassica napus	AT5G56290.1 | Symbols: PEX5, ATPEX5 | peroxin 5 | chr5:22786655-22791972 FORWARD LENGTH=728	324	728	4.00E-67	224.7	41.7	46.6
Rsa1.0_00801.1.g19674.t1	ref|NP_175953.1| protein SKU5 similar 12 [Arabidopsis thaliana] gi|13605853|gb|AAK32912.1|AF367325_1 At1g55570/T5A14_1 [Arabidopsis thaliana] gi|4204257|gb|AAD10638.1| putative pollen specific protein [Arabidopsis thaliana] gi|22137174|gb|AAM91432.1| At1g55570/T5A14_1 [Arabidopsis thaliana] gi|332195146|gb|AEE33267.1| protein SKU5 similar 12 [Arabidopsis thaliana]	554	555	0	100.2	73.6	84.1	protein SKU5 similar 12	gbpln	Arabidopsis thaliana	AT1G55570.1 | Symbols: sks12 | SKU5 similar 12 | chr1:20757882-20759771 FORWARD LENGTH=555	554	555	0	100.2	73.6	84.1
Rsa1.0_00801.1.g19675.t1	ref|NP_200443.1| expansin A14 [Arabidopsis thaliana] gi|20137960|sp|Q9FMA0.1|EXP14_ARATH RecName: Full=Expansin-A14; Short=AtEXPA14; AltName: Full=Alpha-expansin-14; Short=At-EXP14; Short=AtEx14; AltName: Full=Ath-ExpAlpha-1.5; Flags: Precursor gi|10177830|dbj|BAB11259.1| expansin [Arabidopsis thaliana] gi|110740362|dbj|BAF02076.1| Expansin [Arabidopsis thaliana] gi|332009365|gb|AED96748.1| expansin A14 [Arabidopsis thaliana]	271	255	1.00E-134	94.1	84.5	90.4	expansin A14	gbpln	Arabidopsis thaliana	AT5G56320.1 | Symbols: ATEXPA14, EXP14, ATEXP14, ATHEXP ALPHA 1.5, EXPA14 | expansin A14 | chr5:22808854-22809906 FORWARD LENGTH=255	271	255	1.00E-136	94.1	84.5	90.4
Rsa1.0_00801.1.g19676.t1	ref|NP_564398.1| putative FBD-associated F-box protein [Arabidopsis thaliana] gi|302425238|sp|Q9LQM1.2|FBD39_ARATH RecName: Full=Probable FBD-associated F-box protein At1g32375 gi|332193353|gb|AEE31474.1| putative FBD-associated F-box protein [Arabidopsis thaliana]	425	422	1.00E-111	99.3	54.1	68.7	putative FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	425	422	1.00E-113	99.3	54.1	68.7

Rsa1.0_00801.1.g19677.t1	ref|XP_002864451.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310286|gb|EFH40710.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	350	395	1.00E-133	112.9	74.9	85.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G56340.1 | Symbols: ATCRT1 | RING/U-box superfamily protein | chr5:22818254-22819444 FORWARD LENGTH=396	350	396	1.00E-133	113.1	73.4	82.0
Rsa1.0_00801.1.g19678.t1	gb|EOA13135.1| hypothetical protein CARUB_v10026152mg, partial [Capsella rubella]	244	575	1.00E-136	235.7	98.0	99.2	hypothetical protein CARUB_v10026152mg, partial	gbpln	Capsella rubella	AT5G56350.1 | Symbols: | Pyruvate kinase family protein | chr5:22820254-22822529 REVERSE LENGTH=498	244	498	1.00E-138	204.1	97.5	98.8
Rsa1.0_00802.1.g19679.t1	ref|NP_851107.1| uncharacterized protein [Arabidopsis thaliana] gi|10177977|dbj|BAB11383.1| unnamed protein product [Arabidopsis thaliana] gi|17979201|gb|AAL49839.1| unknown protein [Arabidopsis thaliana] gi|21436077|gb|AAM51239.1| unknown protein [Arabidopsis thaliana] gi|332007091|gb|AED94474.1| uncharacterized protein AT5G39785 [Arabidopsis thaliana]	685	606	0	88.5	66.6	72.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G39785.1 | Symbols: | Protein of unknown function (DUF1666) | chr5:15929257-15932215 FORWARD LENGTH=606	685	606	0	88.5	66.6	72.3
Rsa1.0_00802.1.g19680.t2	gb|EOA17166.1| hypothetical protein CARUB_v10005433mg [Capsella rubella]	300	282	1.00E-119	94.0	75.0	81.7	hypothetical protein CARUB_v10005433mg	gbpln	Capsella rubella	AT5G39790.1 | Symbols: | 5'-AMP-activated protein kinase-related | chr5:15932884-15935121 REVERSE LENGTH=273	300	273	1.00E-116	91.0	73.3	79.3
Rsa1.0_00802.1.g19681.t1	ref|XP_002870753.1| hypothetical protein ARALYDRAFT_494007 [Arabidopsis lyrata subsp. lyrata] gi|297316589|gb|EFH47012.1| hypothetical protein ARALYDRAFT_494007 [Arabidopsis lyrata subsp. lyrata]	445	448	0	100.7	93.0	96.2	hypothetical protein ARALYDRAFT_494007	gbpln	Arabidopsis lyrata	AT5G39830.1 | Symbols: DEGP8, DEG8 | Trypsin family protein with PDZ domain | chr5:15942883-15945676 FORWARD LENGTH=448	445	448	0	100.7	92.4	96.0
Rsa1.0_00802.1.g19682.t1	dbj|BAB11679.1| unnamed protein product [Arabidopsis thaliana]	457	457	1.00E-103	100.0	51.6	63.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G22730.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:7551632-7553219 REVERSE LENGTH=466	457	466	1.00E-105	102.0	51.6	63.9
Rsa1.0_00802.1.g19683.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00802.1.g19684.t1	gb|EOA15626.1| hypothetical protein CARUB_v10005777mg [Capsella rubella]	198	198	9.00E-99	100.0	89.4	92.4	hypothetical protein CARUB_v10005777mg	gbpln	Capsella rubella	AT5G39850.1 | Symbols: | Ribosomal protein S4 | chr5:15950053-15951171 FORWARD LENGTH=197	198	197	1.00E-101	99.5	88.9	91.9
Rsa1.0_00802.1.g19685.t1	gb|EOA30606.1| hypothetical protein CARUB_v10013737mg [Capsella rubella]	441	437	0	99.1	71.9	77.6	hypothetical protein CARUB_v10013737mg	gbpln	Capsella rubella	AT3G10450.1 | Symbols: SCPL7 | serine carboxypeptidase-like 7 | chr3:3249544-3252320 FORWARD LENGTH=437	441	437	0	99.1	73.0	81.2
Rsa1.0_00802.1.g19686.t3	ref|XP_002865185.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311020|gb|EFH41444.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	972	1185	0	121.9	41.5	53.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G22690.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:7541369-7544888 FORWARD LENGTH=1008	972	1008	0	103.7	42.7	55.6
Rsa1.0_00802.1.g19687.t1	ref|XP_002868691.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297314527|gb|EFH44950.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	405	414	1.00E-152	102.2	71.6	84.0	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT5G39865.1 | Symbols: | Glutaredoxin family protein | chr5:15965560-15966732 REVERSE LENGTH=390	405	390	1.00E-150	96.3	68.1	79.3
Rsa1.0_00802.1.g19688.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00802.1.g19689.t1	ref|XP_002868690.1| hypothetical protein ARALYDRAFT_493997 [Arabidopsis lyrata subsp. lyrata] gi|297314526|gb|EFH44949.1| hypothetical protein ARALYDRAFT_493997 [Arabidopsis lyrata subsp. lyrata]	320	263	2.00E-70	82.2	43.1	51.9	hypothetical protein ARALYDRAFT_493997	gbpln	Arabidopsis lyrata	AT5G39870.1 | Symbols: | Protein of unknown function (DUF1216) | chr5:15968622-15970011 REVERSE LENGTH=290	320	290	2.00E-70	90.6	41.6	51.6
Rsa1.0_00802.1.g19690.t1	gb|EOA17162.1| hypothetical protein CARUB_v10005430mg [Capsella rubella]	279	285	1.00E-129	102.2	82.8	86.0	hypothetical protein CARUB_v10005430mg	gbpln	Capsella rubella	AT5G39890.1 | Symbols: | Protein of unknown function (DUF1637) | chr5:15974543-15976013 FORWARD LENGTH=276	279	276	1.00E-130	98.9	81.7	86.4
Rsa1.0_00802.1.g19691.t1	gb|AAM67109.1| putative DNA-binding protein [Arabidopsis thaliana]	140	125	2.00E-17	89.3	42.1	60.0	putative DNA-binding protein	gbpln	Arabidopsis thaliana	AT1G77570.1 | Symbols: | Winged helix-turn-helix transcription repressor DNA-binding | chr1:29143350-29143793 FORWARD LENGTH=147	140	147	8.00E-20	105.0	42.1	60.0
Rsa1.0_00802.1.g19692.t1	ref|XP_002868701.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314537|gb|EFH44960.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	338	395	2.00E-65	116.9	49.1	59.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G41200.1 | Symbols: AGL75 | AGAMOUS-like 75 | chr5:16490544-16491536 FORWARD LENGTH=330	338	330	2.00E-53	97.6	44.7	54.1
Rsa1.0_00803.1.g19693.t1	#	#	#	#	#	#	#	-	----	----	AT1G20930.1 | Symbols: CDKB2;2 | cyclin-dependent kinase B2;2 | chr1:7292752-7294664 REVERSE LENGTH=315	74	315	1.00E-10	425.7	55.4	63.5

Rsa1.0_00803.1.g19694.t1	ref|XP_002890416.1| auxin efflux carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297336258|gb|EFH66675.1| auxin efflux carrier family protein [Arabidopsis lyrata subsp. lyrata]	383	386	0	100.8	86.2	93.2	auxin efflux carrier family protein	gbpln	Arabidopsis lyrata	AT1G20925.1 | Symbols: | Auxin efflux carrier family protein | chr1:7289973-7292507 FORWARD LENGTH=472	383	472	0	123.2	85.6	93.2
Rsa1.0_00803.1.g19695.t1	gb|EOA39511.1| hypothetical protein CARUB_v10008128mg [Capsella rubella] gi|482575325|gb|EOA39512.1| hypothetical protein CARUB_v10008128mg [Capsella rubella] gi|482575326|gb|EOA39513.1| hypothetical protein CARUB_v10008128mg [Capsella rubella]	1172	1171	0	99.9	72.1	76.9	hypothetical protein CARUB_v10008128mg	gbpln	Capsella rubella	AT1G20920.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:7285342-7288842 FORWARD LENGTH=1166	1172	1166	0	99.5	72.1	76.8
Rsa1.0_00803.1.g19696.t1	gb|EOA40571.1| hypothetical protein CARUB_v10009301mg [Capsella rubella]	389	410	1.00E-135	105.4	65.0	74.3	hypothetical protein CARUB_v10009301mg	gbpln	Capsella rubella	AT1G20910.1 | Symbols: | ARID/BRIGHT DNA-binding domain-containing protein | chr1:7277209-7280635 REVERSE LENGTH=398	389	398	1.00E-132	102.3	67.9	78.4
Rsa1.0_00803.1.g19697.t1	ref|NP_173514.1| putative DNA-binding protein ESCAROLA [Arabidopsis thaliana] gi|20532086|sp|Q9S7C9.1|ESCA_ARATH RecName: Full=Putative DNA-binding protein ESCAROLA gi|4836899|gb|AAD30602.1|AC007369_12 Unknown protein [Arabidopsis thaliana] gi|6319180|gb|AAF07197.1|AF194974_1 ESCAROLA [Arabidopsis thaliana] gi|30102700|gb|AAP21268.1| At1g20900 [Arabidopsis thaliana] gi|110736548|dbj|BAF00240.1| putative DNA-binding protein [Arabidopsis thaliana] gi|119657398|tpd|FAA00298.1| TPA: AT-hook motif nuclear localized protein 27 [Arabidopsis thaliana] gi|225897950|dbj|BAH30307.1| hypothetical protein [Arabidopsis thaliana] gi|332191917|gb|AEE30038.1| putative DNA-binding protein ESCAROLA [Arabidopsis thaliana]	313	311	1.00E-118	99.4	92.0	93.0	putative DNA-binding protein ESCAROLA	gbpln	Arabidopsis thaliana	AT1G20900.1 | Symbols: ESC, ORE7, AHL27 | Predicted AT-hook DNA-binding family protein | chr1:7273024-7273959 FORWARD LENGTH=311	313	311	1.00E-121	99.4	92.0	93.0
Rsa1.0_00803.1.g19698.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00803.1.g19699.t1	gb|EOA36255.1| hypothetical protein CARUB_v10010341mg [Capsella rubella]	158	197	7.00E-62	124.7	74.1	81.6	hypothetical protein CARUB_v10010341mg	gbpln	Capsella rubella	AT1G20890.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76480.2); Has 33 Blast hits to 33 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7266088-7267060 REVERSE LENGTH=197	158	197	2.00E-58	124.7	70.9	79.1
Rsa1.0_00803.1.g19700.t1	gb|EOA35544.1| hypothetical protein CARUB_v10020749mg [Capsella rubella]	296	285	1.00E-112	96.3	73.0	79.1	hypothetical protein CARUB_v10020749mg	gbpln	Capsella rubella	AT1G76460.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:28686932-28688506 REVERSE LENGTH=285	296	285	1.00E-111	96.3	71.3	78.4
Rsa1.0_00803.1.g19701.t2	ref|XP_002893135.1| hypothetical protein ARALYDRAFT_472323 [Arabidopsis lyrata subsp. lyrata] gi|297338977|gb|EFH69394.1| hypothetical protein ARALYDRAFT_472323 [Arabidopsis lyrata subsp. lyrata]	358	465	2.00E-81	129.9	46.4	53.6	hypothetical protein ARALYDRAFT_472323	gbpln	Arabidopsis lyrata	AT1G20870.1 | Symbols: | HSP20-like chaperones superfamily protein | chr1:7259287-7260775 REVERSE LENGTH=463	358	463	4.00E-79	129.3	45.0	52.0
Rsa1.0_00803.1.g19702.t2	ref|XP_002890413.1| hypothetical protein ARALYDRAFT_472321 [Arabidopsis lyrata subsp. lyrata] gi|297336255|gb|EFH66672.1| hypothetical protein ARALYDRAFT_472321 [Arabidopsis lyrata subsp. lyrata]	201	357	8.00E-16	177.6	20.9	21.9	hypothetical protein ARALYDRAFT_472321	gbpln	Arabidopsis lyrata	AT1G20850.1 | Symbols: XCP2 | xylem cysteine peptidase 2 | chr1:7252208-7253537 FORWARD LENGTH=356	201	356	1.00E-17	177.1	20.4	21.4

Rsa1.0_00803.1.g19703.t1	gb|EOA39766.1| hypothetical protein CARUB_v10008415mg [Capsella rubella] gi|482575580|gb|EOA39767.1| hypothetical protein CARUB_v10008415mg [Capsella rubella] gi|482575581|gb|EOA39768.1| hypothetical protein CARUB_v10008415mg [Capsella rubella]	718	736	0	102.5	88.2	92.8	hypothetical protein CARUB_v10008415mg	gbpln	Capsella rubella	AT1G20840.1 | Symbols: TMT1 | tonoplast monosaccharide transporter1 | chr1:7245107-7247674 REVERSE LENGTH=734	718	734	0	102.2	90.0	94.6
Rsa1.0_00803.1.g19704.t1	ref|XP_002890412.1| hypothetical protein ARALYDRAFT_472319 [Arabidopsis lyrata subsp. lyrata] gi|297336254|gb|EFH66671.1| hypothetical protein ARALYDRAFT_472319 [Arabidopsis lyrata subsp. lyrata]	368	351	1.00E-152	95.4	73.1	83.7	hypothetical protein ARALYDRAFT_472319	gbpln	Arabidopsis lyrata	AT1G20830.1 | Symbols: MCD1 | multiple chloroplast division site 1 | chr1:7242933-7244736 FORWARD LENGTH=349	368	349	1.00E-153	94.8	74.2	82.9
Rsa1.0_00803.1.g19705.t1	gb|ABK56013.1| zinc finger protein [Brassica rapa]	206	196	1.00E-85	95.1	77.7	84.5	zinc finger protein	gbpln	Brassica rapa	AT1G20823.1 | Symbols: | RING/U-box superfamily protein | chr1:7238880-7239473 FORWARD LENGTH=197	206	197	1.00E-83	95.6	83.0	87.4
Rsa1.0_00803.1.g19706.t1	gb|EOA16678.1| hypothetical protein CARUB_v10004870mg [Capsella rubella]	168	427	2.00E-36	254.2	54.8	60.1	hypothetical protein CARUB_v10004870mg	gbpln	Capsella rubella	AT4G15410.1 | Symbols: PUX5 | serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B prime gamma | chr4:8814868-8816596 FORWARD LENGTH=421	168	421	4.00E-35	250.6	44.0	50.0
Rsa1.0_00803.1.g19707.t1	ref|NP_173489.2| protein kinase-like protein [Arabidopsis thaliana] gi|8778594|gb|AAF79602.1|AC027665_3 F5M15.3 [Arabidopsis thaliana] gi|8886951|gb|AAF80637.1|AC069251_30 F2D10.13 [Arabidopsis thaliana] gi|51971194|dbj|BAD44289.1| unknown protein [Arabidopsis thaliana] gi|332191880|gb|AEE30001.1| protein kinase-like protein [Arabidopsis thaliana]	377	381	0	101.1	92.3	95.2	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G20650.1 | Symbols: | Protein kinase superfamily protein | chr1:7158422-7160022 REVERSE LENGTH=381	377	381	0	101.1	92.3	95.2
Rsa1.0_00803.1.g19708.t1	gb|EOA39657.1| hypothetical protein CARUB_v10008300mg [Capsella rubella]	824	844	0	102.4	86.8	92.5	hypothetical protein CARUB_v10008300mg	gbpln	Capsella rubella	AT1G20640.2 | Symbols: | Plant regulator RWP-RK family protein | chr1:7155201-7157986 FORWARD LENGTH=844	824	844	0	102.4	88.7	93.6
Rsa1.0_00804.1.g19709.t1	gb|EOA27773.1| hypothetical protein CARUB_v10023927mg [Capsella rubella]	325	246	1.00E-134	75.7	70.2	73.8	hypothetical protein CARUB_v10023927mg	gbpln	Capsella rubella	AT2G45790.1 | Symbols: ATPMM, PMM | phosphomannomutase | chr2:18855876-18857753 FORWARD LENGTH=246	325	246	1.00E-134	75.7	69.2	73.2
Rsa1.0_00804.1.g19710.t1	ref|XP_002882034.1| LIM domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327873|gb|EFH58293.1| LIM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	228	225	1.00E-110	98.7	84.2	90.4	LIM domain-containing protein	gbpln	Arabidopsis lyrata	AT2G45800.1 | Symbols: | GATA type zinc finger transcription factor family protein | chr2:18858153-18859007 REVERSE LENGTH=226	228	226	1.00E-104	99.1	76.3	82.5
Rsa1.0_00804.1.g19711.t1	ref|XP_002880201.1| hypothetical protein ARALYDRAFT_483719 [Arabidopsis lyrata subsp. lyrata] gi|297326040|gb|EFH56460.1| hypothetical protein ARALYDRAFT_483719 [Arabidopsis lyrata subsp. lyrata]	529	521	0	98.5	80.2	83.0	hypothetical protein ARALYDRAFT_483719	gbpln	Arabidopsis lyrata	AT2G45810.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr2:18859836-18862318 FORWARD LENGTH=528	529	528	0	99.8	79.6	82.8
Rsa1.0_00804.1.g19712.t2	ref|NP_182081.1| cytochrome P450 76C2 [Arabidopsis thaliana] gi|5915832|sp|O64637.1|C76C2_ARATH RecName: Full=Cytochrome P450 76C2 gi|2979549|gb|AAC06158.1| putative cytochrome P450 [Arabidopsis thaliana] gi|17065048|gb|AAL32678.1| putative cytochrome P450 [Arabidopsis thaliana] gi|21387151|gb|AAM47979.1| putative cytochrome P450 [Arabidopsis thaliana] gi|330255478|gb|AEC10572.1| cytochrome P450 76C2 [Arabidopsis thaliana]	358	512	1.00E-147	143.0	73.5	84.1	cytochrome P450 76C2	gbpln	Arabidopsis thaliana	AT2G45570.1 | Symbols: CYP76C2 | cytochrome P450, family 76, subfamily C, polypeptide 2 | chr2:18779935-18781922 REVERSE LENGTH=512	358	512	1.00E-150	143.0	73.5	84.1
Rsa1.0_00804.1.g19713.t1	ref|XP_002880201.1| hypothetical protein ARALYDRAFT_483719 [Arabidopsis lyrata subsp. lyrata] gi|297326040|gb|EFH56460.1| hypothetical protein ARALYDRAFT_483719 [Arabidopsis lyrata subsp. lyrata]	884	521	0	58.9	49.7	50.7	hypothetical protein ARALYDRAFT_483719	gbpln	Arabidopsis lyrata	AT2G45810.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr2:18859836-18862318 FORWARD LENGTH=528	884	528	0	59.7	49.7	51.0

Rsa1.0_00804.1.g19714.t1	ref|NP_182106.1| Remorin [Arabidopsis thaliana] gi|75099946|sp|O80837.1|REMO_ARATH RecName: Full=Remorin; AltName: Full=DNA-binding protein gi|3386612|gb|AAC28542.1| remorin [Arabidopsis thaliana] gi|15028387|gb|AAK76670.1| putative remorin protein [Arabidopsis thaliana] gi|19310659|gb|AAL85060.1| putative remorin protein [Arabidopsis thaliana] gi|330255511|gb|AEC10605.1| Remorin [Arabidopsis thaliana]	195	190	2.00E-79	97.4	86.7	92.8	Remorin	gbpln	Arabidopsis thaliana	AT2G45820.1 | Symbols: | Remorin family protein | chr2:18863147-18864576 REVERSE LENGTH=190	195	190	5.00E-82	97.4	86.7	92.8
Rsa1.0_00804.1.g19715.t3	ref|XP_002880202.1| hypothetical protein ARALYDRAFT_483721 [Arabidopsis lyrata subsp. lyrata] gi|297326041|gb|EFH56461.1| hypothetical protein ARALYDRAFT_483721 [Arabidopsis lyrata subsp. lyrata]	512	520	0	101.6	78.1	84.4	hypothetical protein ARALYDRAFT_483721	gbpln	Arabidopsis lyrata	AT2G45830.1 | Symbols: DTA2 | downstream target of AGL15 2 | chr2:18866324-18868344 FORWARD LENGTH=523	512	523	0	102.1	79.7	86.5
Rsa1.0_00804.1.g19716.t1	ref|XP_002882036.1| DNA-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297327875|gb|EFH58295.1| DNA-binding family protein [Arabidopsis lyrata subsp. lyrata]	313	340	1.00E-123	108.6	79.2	85.0	DNA-binding family protein	gbpln	Arabidopsis lyrata	AT2G45850.2 | Symbols: | AT hook motif DNA-binding family protein | chr2:18871901-18873457 REVERSE LENGTH=348	313	348	1.00E-122	111.2	81.5	87.5
Rsa1.0_00804.1.g19717.t1	ref|NP_182110.1| uncharacterized protein [Arabidopsis thaliana] gi|3386608|gb|AAC28538.1| hypothetical protein [Arabidopsis thaliana] gi|38566524|gb|AAR24152.1| At2g45860 [Arabidopsis thaliana] gi|40823665|gb|AAR92297.1| At2g45860 [Arabidopsis thaliana] gi|330255517|gb|AEC10611.1| uncharacterized protein AT2G45860 [Arabidopsis thaliana]	78	79	4.00E-15	101.3	94.9	97.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G45860.1 | Symbols: | unknown protein; Has 32 Blast hits to 32 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18874913-18875568 REVERSE LENGTH=79	78	79	6.00E-18	101.3	94.9	97.4
Rsa1.0_00804.1.g19718.t1	ref|NP_182111.1| Bestrophin-like protein [Arabidopsis thaliana] gi|20140947|sp|O80832.1|YU87_ARATH RecName: Full=UPF0187 protein At2g45870, chloroplastic; Flags: Precursor gi|3386607|gb|AAC28537.1| hypothetical protein [Arabidopsis thaliana] gi|18491251|gb|AAL69450.1| At2g45870/F4I18.15 [Arabidopsis thaliana] gi|330255518|gb|AEC10612.1| Bestrophin-like protein [Arabidopsis thaliana]	416	410	0	98.6	86.1	90.6	Bestrophin-like protein	gbpln	Arabidopsis thaliana	AT2G45870.1 | Symbols: | Bestrophin-like protein | chr2:18875928-18877440 FORWARD LENGTH=410	416	410	0	98.6	86.1	90.6
Rsa1.0_00804.1.g19719.t4	gb|EOA26641.1| hypothetical protein CARUB_v10022705mg [Capsella rubella]	661	745	0	112.7	70.7	80.8	hypothetical protein CARUB_v10022705mg	gbpln	Capsella rubella	AT2G45900.1 | Symbols: | Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-related | chr2:18886069-18888674 REVERSE LENGTH=720	661	720	0	108.9	70.0	78.4
Rsa1.0_00804.1.g19720.t1	gb|EOA26573.1| hypothetical protein CARUB_v10022633mg [Capsella rubella] gi|482562384|gb|EOA26574.1| hypothetical protein CARUB_v10022633mg [Capsella rubella]	828	839	0	101.3	77.8	84.1	hypothetical protein CARUB_v10022633mg	gbpln	Capsella rubella	AT2G45910.1 | Symbols: | U-box domain-containing protein kinase family protein | chr2:18894520-18898212 FORWARD LENGTH=834	828	834	0	100.7	76.1	83.2
Rsa1.0_00804.1.g19721.t1	gb|AAC28534.1| putative protein kinase [Arabidopsis thaliana]	630	799	4.00E-62	126.8	20.5	21.0	putative protein kinase	gbpln	Arabidopsis thaliana	AT2G45910.1 | Symbols: | U-box domain-containing protein kinase family protein | chr2:18894520-18898212 FORWARD LENGTH=834	630	834	1.00E-64	132.4	20.5	21.0
Rsa1.0_00804.1.g19722.t1	gb|EOA27556.1| hypothetical protein CARUB_v10023694mg, partial [Capsella rubella]	271	307	1.00E-105	113.3	71.2	77.1	hypothetical protein CARUB_v10023694mg, partial	gbpln	Capsella rubella	AT3G61410.1 | Symbols: | BEST Arabidopsis thaliana protein match is: U-box domain-containing protein kinase family protein (TAIR:AT2G45910.1); Has 232 Blast hits to 229 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 13; Fungi - 0; Plants - 218; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:22721112-22722452 FORWARD LENGTH=294	271	294	1.00E-77	108.5	50.6	60.9
Rsa1.0_00804.1.g19723.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	110	387	8.00E-12	351.8	46.4	64.5	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	110	387	1.00E-14	351.8	46.4	64.5

Rsa1.0_00804.1.g19724.t1	emb|CAA64896.1| transmembrane channel protein [Brassica oleracea] gi|7209558|dbj|BAA92259.1| plasma membrane aquaporin 1c [Raphanus sativus] gi|90019596|gb|ABD84431.1| aquaporin PIP1 [Noccaea caerulescens]	288	286	1.00E−152	99.3	93.8	95.1	transmembrane channel protein	gbpln	Brassica oleracea	AT2G45960.1 | Symbols: PIP1B, TMP−A, ATHH2, PIP1;2 | plasma membrane intrinsic protein 1B | chr2:18910450−18911703 FORWARD LENGTH=286	288	286	1.00E−153	99.3	92.7	94.8
Rsa1.0_00804.1.g19725.t1	ref|XP_002882044.1| hypothetical protein ARALYDRAFT_904051 [Arabidopsis lyrata subsp. lyrata] gi|297327883|gb|EFH58303.1| hypothetical protein ARALYDRAFT_904051 [Arabidopsis lyrata subsp. lyrata]	233	265	3.00E−84	113.7	73.4	87.6	hypothetical protein ARALYDRAFT_904051	gbpln	Arabidopsis lyrata	AT2G45980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G00355.2); Has 93 Blast hits to 90 proteins in 15 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 93; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr2:18917680−18918569 REVERSE LENGTH=256	233	256	3.00E−85	109.9	71.2	85.0
Rsa1.0_00804.1.g19726.t1	ref|NP_973671.1| uncharacterized protein [Arabidopsis thaliana] gi|29028790|gb|AAO64774.1| At2g42395 [Arabidopsis thaliana] gi|110743081|dbj|BAE99433.1| hypothetical protein [Arabidopsis thaliana] gi|330255022|gb|AEC10116.1| uncharacterized protein AT2G42395 [Arabidopsis thaliana]	133	104	4.00E−21	78.2	33.8	45.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G42395.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr2:17653566−17653980 REVERSE LENGTH=104	133	104	8.00E−24	78.2	33.8	45.9
Rsa1.0_00804.1.g19727.t1	ref|XP_002882045.1| hypothetical protein ARALYDRAFT_483745 [Arabidopsis lyrata subsp. lyrata] gi|297327884|gb|EFH58304.1| hypothetical protein ARALYDRAFT_483745 [Arabidopsis lyrata subsp. lyrata]	214	206	6.00E−85	96.3	77.1	87.9	hypothetical protein ARALYDRAFT_483745	gbpln	Arabidopsis lyrata	AT2G46000.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Mesoderm development candidate 2 (InterPro:IPR019330); Has 31 Blast hits to 31 proteins in 13 species: Archae − 0; Bacteria − 0; Metazoa − 5; Fungi − 0; Plants − 26; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr2:18921194−18922047 REVERSE LENGTH=208	214	208	1.00E−75	97.2	72.4	79.0
Rsa1.0_00804.1.g19728.t1	ref|XP_002880213.1| ATBRM/CHR2 [Arabidopsis lyrata subsp. lyrata] gi|297326052|gb|EFH56472.1| ATBRM/CHR2 [Arabidopsis lyrata subsp. lyrata]	611	2186	0	357.8	78.9	84.8	ATBRM/CHR2	gbpln	Arabidopsis lyrata	AT2G46020.1 | Symbols: CHR2, ATBRM, BRM, CHA2 | transcription regulatory protein SNF2, putative | chr2:18923304−18931769 FORWARD LENGTH=2192	611	2192	0	358.8	78.7	84.3
Rsa1.0_00805.1.g19729.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00805.1.g19730.t6	gb|AAF79900.1|AC022472_9 Contains a strong similarity to Anther−specific proline−rich protein APG precursor from Arabidopsis thaliana gi|728867 and contains a Lipase/Acylhydrolase domain with GDSL−like motif PF|00657. ESTs gb|AV531882, gb|AV533240, gb|AV534374, gb|AV533394, gb|AV532582, gb|AV533541 come from this gene [Arabidopsis thaliana]	854	1137	0	133.1	51.2	59.3	Contains a strong similarity to Anther−specific proline−rich protein APG precursor from Arabidopsis thaliana gi|728867 and contains a Lipase/Acylhydrolase domain with GDSL−like motif PF|00657. ESTs gb|AV531882, gb|AV533240, gb|AV534374, gb|AV533394, gb|AV532582, gb|AV533541 come from this gene	gbpln	Arabidopsis thaliana	AT1G20132.1 | Symbols: | GDSL−like Lipase/Acylhydrolase superfamily protein | chr1:6981358−6983495 FORWARD LENGTH=383	854	383	1.00E−135	44.8	28.0	32.1
Rsa1.0_00805.1.g19731.t1	ref|XP_002880415.1| hypothetical protein ARALYDRAFT_481069 [Arabidopsis lyrata subsp. lyrata] gi|297326254|gb|EFH56674.1| hypothetical protein ARALYDRAFT_481069 [Arabidopsis lyrata subsp. lyrata]	161	161	1.00E−70	100.0	82.0	87.6	hypothetical protein ARALYDRAFT_481069	gbpln	Arabidopsis lyrata	AT1G20140.1 | Symbols: ASK4, SK4 | SKP1−like 4 | chr1:6986430−6987079 FORWARD LENGTH=163	161	163	4.00E−72	101.2	79.5	86.3
Rsa1.0_00805.1.g19732.t1	gb|EOA39722.1| hypothetical protein CARUB_v10008367mg [Capsella rubella]	751	770	0	102.5	88.1	94.1	hypothetical protein CARUB_v10008367mg	gbpln	Capsella rubella	AT1G20160.1 | Symbols: ATSBT5.2 | Subtilisin−like serine endopeptidase family protein | chr1:6990852−6993854 REVERSE LENGTH=769	751	769	0	102.4	88.7	94.4

Rsa1.0_00805.1.g19733.t1	ref|NP_175654.1| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana] gi|5903057|gb|AAD55616.1|AC008016_26 F6D8.33 [Arabidopsis thaliana] gi|332194687|gb|AEE32808.1| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana]	261	1136	4.00E-37	435.2	40.6	57.9	Ubiquitin carboxyl-terminal hydrolase-related protein	gbpln	Arabidopsis thaliana	AT1G52450.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr1:19541684-19546266 REVERSE LENGTH=1136	261	1136	1.00E-39	435.2	40.6	57.9
Rsa1.0_00805.1.g19734.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00805.1.g19735.t1	gb|AAX23752.1| hypothetical protein At1g20180 [Arabidopsis thaliana]	323	359	1.00E-120	111.1	76.5	85.4	hypothetical protein At1g20180	gbpln	Arabidopsis thaliana	AT1G20180.2 | Symbols: | Protein of unknown function (DUF677) | chr1:6996354-6997779 FORWARD LENGTH=359	323	359	1.00E-122	111.1	76.5	85.1
Rsa1.0_00805.1.g19736.t1	ref|XP_002893092.1| Alpha-expansin 11 precursor [Arabidopsis lyrata subsp. lyrata] gi|297338934|gb|EFH69351.1| Alpha-expansin 11 precursor [Arabidopsis lyrata subsp. lyrata]	252	252	1.00E-137	100.0	94.0	97.2	Alpha-expansin 11 precursor	gbpln	Arabidopsis lyrata	AT1G20190.1 | Symbols: ATEXPA11, EXP11, ATEXP11, ATHEXP ALPHA 1.14, EXPA11 | expansin 11 | chr1:6998762-6999710 REVERSE LENGTH=252	252	252	1.00E-134	100.0	94.8	97.6
Rsa1.0_00805.1.g19737.t1	ref|XP_002893094.1| hypothetical protein ARALYDRAFT_312946 [Arabidopsis lyrata subsp. lyrata] gi|297338936|gb|EFH69353.1| hypothetical protein ARALYDRAFT_312946 [Arabidopsis lyrata subsp. lyrata]	338	529	8.00E-76	156.5	56.8	60.7	hypothetical protein ARALYDRAFT_312946	gbpln	Arabidopsis lyrata	AT1G76010.1 | Symbols: | Alba DNA/RNA-binding protein | chr1:28528505-28530488 REVERSE LENGTH=350	338	350	7.00E-76	103.6	65.4	73.4
Rsa1.0_00805.1.g19738.t1	gb|EOA38448.1| hypothetical protein CARUB_v10010092mg, partial [Capsella rubella]	232	252	1.00E-106	108.6	81.0	90.1	hypothetical protein CARUB_v10010092mg, partial	gbpln	Capsella rubella	AT1G20225.1 | Symbols: | Thioredoxin superfamily protein | chr1:7007966-7009318 REVERSE LENGTH=233	232	233	1.00E-108	100.4	81.0	90.1
Rsa1.0_00805.1.g19739.t1	ref|NP_173449.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|193806503|sp|Q9LNU6.2|PPR53_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g20230 gi|332191832|gb|AEE29953.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	760	760	0	100.0	87.8	94.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G20230.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:7009570-7011852 FORWARD LENGTH=760	760	760	0	100.0	87.8	94.9
Rsa1.0_00805.1.g19740.t1	ref|XP_002890376.1| hypothetical protein ARALYDRAFT_472256 [Arabidopsis lyrata subsp. lyrata] gi|297336218|gb|EFH66635.1| hypothetical protein ARALYDRAFT_472256 [Arabidopsis lyrata subsp. lyrata]	486	487	0	100.2	98.1	99.0	hypothetical protein ARALYDRAFT_472256	gbpln	Arabidopsis lyrata	AT1G20260.1 | Symbols: | ATPase, V1 complex, subunit B protein | chr1:7016971-7020290 FORWARD LENGTH=487	486	487	0	100.2	97.9	98.8
Rsa1.0_00805.1.g19741.t1	gb|EOA38379.1| hypothetical protein CARUB_v10009921mg [Capsella rubella]	291	287	1.00E-161	98.6	95.2	97.6	hypothetical protein CARUB_v10009921mg	gbpln	Capsella rubella	AT1G20270.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:7021383-7022923 REVERSE LENGTH=287	291	287	1.00E-163	98.6	95.2	97.3
Rsa1.0_00805.1.g19742.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00805.1.g19743.t1	gb|EOA38982.1| hypothetical protein CARUB_v10011494mg [Capsella rubella]	537	532	0	99.1	86.0	92.0	hypothetical protein CARUB_v10011494mg	gbpln	Capsella rubella	AT1G20300.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:7029701-7031314 FORWARD LENGTH=537	537	537	0	100.0	86.0	92.2
Rsa1.0_00805.1.g19744.t1	ref|XP_002890378.1| hypothetical protein ARALYDRAFT_472259 [Arabidopsis lyrata subsp. lyrata] gi|297336220|gb|EFH66637.1| hypothetical protein ARALYDRAFT_472259 [Arabidopsis lyrata subsp. lyrata]	261	236	2.00E-73	90.4	64.4	70.9	hypothetical protein ARALYDRAFT_472259	gbpln	Arabidopsis lyrata	AT1G20310.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76070.1); Has 46 Blast hits to 46 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7032308-7033030 FORWARD LENGTH=240	261	240	1.00E-75	92.0	62.1	71.6
Rsa1.0_00805.1.g19745.t1	gb|EOA39020.1| hypothetical protein CARUB_v10011566mg [Capsella rubella]	269	366	1.00E-144	136.1	91.1	95.5	hypothetical protein CARUB_v10011566mg	gbpln	Capsella rubella	AT1G20330.1 | Symbols: SMT2, CVP1, FRL1 | sterol methyltransferase 2 | chr1:7038968-7040053 REVERSE LENGTH=361	269	361	1.00E-145	134.2	91.1	94.8
Rsa1.0_00806.1.g19746.t10	gb|AFK13856.1| Ty3/gypsy retrotransposon protein [Beta vulgaris subsp. vulgaris]	2381	1631	0	68.5	32.0	41.7	Ty3/gypsy retrotransposon protein	gbpln	Beta vulgaris	AT2G35060.1 | Symbols: KUP11 | K+ uptake permease 11 | chr2:14775184-14778184 REVERSE LENGTH=792	2381	792	0	33.3	31.5	32.3
Rsa1.0_00806.1.g19747.t1	ref|XP_002879531.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325370|gb|EFH55790.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	1197	1254	0	104.8	81.2	87.6	kinase family protein	gbpln	Arabidopsis lyrata	AT2G35050.1 | Symbols: | Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain | chr2:14769708-14774796 FORWARD LENGTH=1257	1197	1257	0	105.0	80.9	87.4

Rsa1.0_00806.1.g19748.t1	ref|NP_850240.1| phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP [Arabidopsis thaliana] gi|20268737|gb|AAM14072.1| putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana] gi|22136684|gb|AAM91661.1| putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana] gi|330253960|gb|AEC09054.1| phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP [Arabidopsis thaliana]	621	596	0	96.0	90.3	92.4	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP	gbpln	Arabidopsis thaliana	AT2G35040.1 | Symbols: | AICARFT/IMPCHase bienzyme family protein | chr2:14765347-14768269 REVERSE LENGTH=596	621	596	0	96.0	90.3	92.4
Rsa1.0_00806.1.g19749.t1	ref|NP_850239.1| urease accessory protein D [Arabidopsis thaliana] gi|31096381|emb|CAC85462.1| putative urease accessory protein D [Arabidopsis thaliana] gi|330253958|gb|AEC09052.1| urease accessory protein D [Arabidopsis thaliana]	294	294	1.00E-155	100.0	88.4	94.6	urease accessory protein D	gbpln	Arabidopsis thaliana	AT2G35035.1 | Symbols: URED | urease accessory protein D | chr2:14763387-14765045 REVERSE LENGTH=294	294	294	1.00E-157	100.0	88.4	94.6
Rsa1.0_00806.1.g19750.t1	ref|XP_002881370.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327209|gb|EFH57629.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	635	627	0	98.7	79.7	89.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT2G35030.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:14761080-14762963 REVERSE LENGTH=627	635	627	0	98.7	79.2	88.5
Rsa1.0_00806.1.g19751.t2	gb|EOA28336.1| hypothetical protein CARUB_v10024537mg [Capsella rubella]	503	501	0	99.6	89.9	94.2	hypothetical protein CARUB_v10024537mg	gbpln	Capsella rubella	AT2G35020.1 | Symbols: GlcNAc1pUT2 | N-acetylglucosamine-1-phosphate uridylyltransferase 2 | chr2:14756803-14760477 FORWARD LENGTH=502	503	502	0	99.8	90.9	94.8
Rsa1.0_00806.1.g19752.t1	gb|EOA27336.1| hypothetical protein CARUB_v10023452mg [Capsella rubella]	371	374	1.00E-137	100.8	75.5	83.0	hypothetical protein CARUB_v10023452mg	gbpln	Capsella rubella	AT2G35000.1 | Symbols: | RING/U-box superfamily protein | chr2:14751809-14752945 REVERSE LENGTH=378	371	378	1.00E-127	101.9	72.8	83.0
Rsa1.0_00806.1.g19753.t1	gb|EOA29001.1| hypothetical protein CARUB_v10025254mg [Capsella rubella]	313	311	4.00E-75	99.4	54.0	68.1	hypothetical protein CARUB_v10025254mg	gbpln	Capsella rubella	AT2G34990.1 | Symbols: | RING/U-box superfamily protein | chr2:14750260-14751168 REVERSE LENGTH=302	313	302	3.00E-72	96.5	53.0	64.2
Rsa1.0_00806.1.g19754.t1	ref|NP_181043.1| phosphatidylinositol glycan, class C [Arabidopsis thaliana] gi|3033393|gb|AAC12837.1| putative phosphatidylinositol-glycan synthase [Arabidopsis thaliana] gi|330253951|gb|AEC09045.1| phosphatidylinositol glycan, class C [Arabidopsis thaliana]	307	303	1.00E-125	98.7	87.9	94.5	phosphatidylinositol glycan, class C	gbpln	Arabidopsis thaliana	AT2G34980.1 | Symbols: SETH1 | phosphatidylinositolglycan synthase family protein | chr2:14748967-14749878 FORWARD LENGTH=303	307	303	1.00E-128	98.7	87.9	94.5
Rsa1.0_00806.1.g19755.t1	ref|XP_002879527.1| eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325366|gb|EFH55786.1| eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein [Arabidopsis lyrata subsp. lyrata]	725	726	0	100.1	86.6	92.7	eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein	gbpln	Arabidopsis lyrata	AT2G34970.1 | Symbols: | Trimeric LpxA-like enzyme | chr2:14746340-14748532 FORWARD LENGTH=730	725	730	0	100.7	85.0	92.3
Rsa1.0_00806.1.g19756.t1	dbj|BAJ34318.1| unnamed protein product [Thellungiella halophila]	911	911	0	100.0	86.3	92.0	unnamed protein product	----	----	AT2G34930.1 | Symbols: | disease resistance family protein / LRR family protein | chr2:14737169-14739886 REVERSE LENGTH=905	911	905	0	99.3	82.3	89.7
Rsa1.0_00806.1.g19757.t1	ref|NP_181038.2| embryo sac development arrest 18 protein [Arabidopsis thaliana] gi|330253945|gb|AEC09039.1| embryo sac development arrest 18 protein [Arabidopsis thaliana]	654	652	0	99.7	66.8	76.5	embryo sac development arrest 18 protein	gbpln	Arabidopsis thaliana	AT2G34920.1 | Symbols: EDA18 | RING/U-box superfamily protein | chr2:14728375-14730816 REVERSE LENGTH=652	654	652	0	99.7	66.8	76.5
Rsa1.0_00806.1.g19758.t1	ref|XP_002879524.1| hypothetical protein ARALYDRAFT_902587 [Arabidopsis lyrata subsp. lyrata] gi|297325363|gb|EFH55783.1| hypothetical protein ARALYDRAFT_902587 [Arabidopsis lyrata subsp. lyrata]	297	288	1.00E-109	97.0	75.4	79.8	hypothetical protein ARALYDRAFT_902587	gbpln	Arabidopsis lyrata	AT2G34910.1 | Symbols: | BEST Arabidopsis thaliana protein match is: root hair specific 4 (TAIR:AT1G30850.1); Has 43 Blast hits to 43 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:14726900-14727766 FORWARD LENGTH=288	297	288	1.00E-110	97.0	74.7	80.5
Rsa1.0_00807.1.g19759.t1	gb|EOA16741.1| hypothetical protein CARUB_v10004942mg [Capsella rubella]	406	409	0	100.7	94.6	98.3	hypothetical protein CARUB_v10004942mg	gbpln	Capsella rubella	AT4G24780.2 | Symbols: | Pectin lyase-like superfamily protein | chr4:12770631-12772227 REVERSE LENGTH=408	406	408	0	100.5	93.8	97.5

Rsa1.0_00807.1.g19760.t1	ref|NP_194210.2| AAA-type ATPase family protein [Arabidopsis thaliana] gi|186513264|ref|NP_001119046.1| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332659557|gb|AEE84957.1| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332659558|gb|AEE84958.1| AAA-type ATPase family protein [Arabidopsis thaliana]	845	857	0	101.4	83.6	88.6	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT4G24790.2 | Symbols: | AAA-type ATPase family protein | chr4:12778222-12781345 FORWARD LENGTH=857	845	857	0	101.4	83.6	88.6
Rsa1.0_00807.1.g19761.t2	ref|XP_002867642.1| hypothetical protein ARALYDRAFT_492356 [Arabidopsis lyrata subsp. lyrata] gi|297313478|gb|EFH43901.1| hypothetical protein ARALYDRAFT_492356 [Arabidopsis lyrata subsp. lyrata]	403	387	0	96.0	92.6	94.5	hypothetical protein ARALYDRAFT_492356	gbpln	Arabidopsis lyrata	AT4G24820.2 | Symbols: | 26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain | chr4:12790471-12792599 REVERSE LENGTH=387	403	387	0	96.0	91.8	94.0
Rsa1.0_00807.1.g19762.t1	ref|NP_194214.2| argininosuccinate synthase [Arabidopsis thaliana] gi|78099761|sp|Q9SZX3.3|ASSY_ARATH RecName: Full=Argininosuccinate synthase, chloroplastic; AltName: Full=Citrulline--aspartate ligase; Flags: Precursor gi|17529036|gb|AAL38728.1| putative argininosuccinate synthase [Arabidopsis thaliana] gi|20259085|gb|AAM14258.1| putative argininosuccinate synthase [Arabidopsis thaliana] gi|332659568|gb|AEE84968.1| argininosuccinate synthase [Arabidopsis thaliana]	510	494	0	96.9	88.4	92.7	argininosuccinate synthase	gbpln	Arabidopsis thaliana	AT4G24830.1 | Symbols: | arginosuccinate synthase family | chr4:12793085-12795857 REVERSE LENGTH=494	510	494	0	96.9	88.4	92.7
Rsa1.0_00807.1.g19763.t12	gb|EOA16079.1| hypothetical protein CARUB_v10004211mg [Capsella rubella]	1482	754	0	50.9	44.0	47.1	hypothetical protein CARUB_v10004211mg	gbpln	Capsella rubella	AT4G24840.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein transport, Golgi organization; LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: COG complex component, COG2 (InterPro:IPR009316); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12796525-12800926 REVERSE LENGTH=756	1482	756	0	51.0	43.8	47.1
Rsa1.0_00807.1.g19764.t1	gb|EOA16710.1| hypothetical protein CARUB_v10004911mg [Capsella rubella]	642	418	0	65.1	53.3	56.7	hypothetical protein CARUB_v10004911mg	gbpln	Capsella rubella	AT4G24880.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12808593-12811218 FORWARD LENGTH=417	642	417	0	65.0	53.1	56.9

Rsa1.0_00807.1.g19765.t1	ref|NP_194222.1| protein transport protein sec61 subunit gamma-1 [Arabidopsis thaliana] gi|18423153|ref|NP_568728.1| protein transport protein sec61 subunit gamma-1 [Arabidopsis thaliana] gi|297795847|ref|XP_002865808.1| hypothetical protein ARALYDRAFT_495113 [Arabidopsis lyrata subsp. lyrata] gi|297799504|ref|XP_002867636.1| hypothetical protein ARALYDRAFT_492346 [Arabidopsis lyrata subsp. lyrata] gi|408407792|sp|P0DI74.1|S61G1_ARATH RecName: Full=Protein transport protein Sec61 subunit gamma-1 gi|408407793|sp|P0DI75.1|S61G2_ARATH RecName: Full=Protein transport protein Sec61 subunit gamma-2 gi|13877813|gb|AAK43984.1|AF370169_1 putative protein translocation complex Sec61 gamma chain [Arabidopsis thaliana] gi|4455235|emb|CAB36734.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana] gi|7269342|emb|CAB79401.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana] gi|9758755|dbj|BAB09131.1| protein translocation complex Sec61 gamma chain [Arabidopsis thaliana] gi|16323486|gb|AAL15237.1| putative	69	69	1.00E-30	100.0	100.0	100.0	protein transport protein sec61 subunit gamma-1	gbpln	Arabidopsis lyrata	AT5G50460.1 | Symbols: | secE/sec61-gamma protein transport protein | chr5:20552168-20552509 REVERSE LENGTH=69	69	69	2.00E-33	100.0	100.0	100.0
Rsa1.0_00807.1.g19766.t1	ref|XP_002878483.1| 60S ribosomal protein L7A [Arabidopsis lyrata subsp. lyrata] gi|297324321|gb|EFH54742.1| 60S ribosomal protein L7A [Arabidopsis lyrata subsp. lyrata]	421	256	1.00E-138	60.8	57.2	59.6	60S ribosomal protein L7A	gbpln	Arabidopsis lyrata	AT3G62870.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr3:23242862-23244273 REVERSE LENGTH=256	421	256	1.00E-140	60.8	57.2	59.4
Rsa1.0_00807.1.g19767.t1	gb|ACJ09230.1| HVA22d [Arabidopsis thaliana] gi|210148663|gb|ACJ09237.1| HVA22d [Arabidopsis thaliana] gi|210148671|gb|ACJ09241.1| HVA22d [Arabidopsis thaliana] gi|210148687|gb|ACJ09249.1| HVA22d [Arabidopsis thaliana] gi|210148711|gb|ACJ09261.1| HVA22d [Arabidopsis thaliana]	135	135	5.00E-62	100.0	83.7	91.1	HVA22d	gbpln	Arabidopsis thaliana	AT4G24960.1 | Symbols: ATHVA22D, HVA22D | HVA22 homologue D | chr4:12828060-12828982 FORWARD LENGTH=135	135	135	2.00E-64	100.0	83.7	91.9
Rsa1.0_00807.1.g19768.t1	ref|XP_002869696.1| hypothetical protein ARALYDRAFT_492340 [Arabidopsis lyrata subsp. lyrata] gi|297315532|gb|EFH45955.1| hypothetical protein ARALYDRAFT_492340 [Arabidopsis lyrata subsp. lyrata]	699	709	0	101.4	82.5	89.6	hypothetical protein ARALYDRAFT_492340	gbpln	Arabidopsis lyrata	AT4G24970.1 | Symbols: | Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein | chr4:12831125-12835449 FORWARD LENGTH=707	699	707	0	101.1	80.4	86.8
Rsa1.0_00807.1.g19769.t1	ref|XP_002867630.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297313466|gb|EFH43889.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	274	280	1.00E-132	102.2	88.0	93.1	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT4G25010.1 | Symbols: SWEET14, AtSWEET14 | Nodulin MtN3 family protein | chr4:12854630-12856351 REVERSE LENGTH=281	274	281	1.00E-133	102.6	87.2	91.6
Rsa1.0_00807.1.g19770.t1	ref|XP_002869693.1| hypothetical protein ARALYDRAFT_492335 [Arabidopsis lyrata subsp. lyrata] gi|297315529|gb|EFH45952.1| hypothetical protein ARALYDRAFT_492335 [Arabidopsis lyrata subsp. lyrata]	352	344	1.00E-164	97.7	82.4	90.1	hypothetical protein ARALYDRAFT_492335	gbpln	Arabidopsis lyrata	AT4G25030.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G45410.3); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:12865336-12866638 FORWARD LENGTH=344	352	344	1.00E-162	97.7	83.8	90.6
Rsa1.0_00808.1.g19771.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00808.1.g19772.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00808.1.g19773.t1	gb|EOA37570.1| hypothetical protein CARUB_v10011900mg [Capsella rubella]	365	368	1.00E-166	100.8	83.0	88.2	hypothetical protein CARUB_v10011900mg	gbpln	Capsella rubella	AT1G32770.1 | Symbols: ANAC012, SND1, NST3, NAC012 | NAC domain containing protein 12 | chr1:11865343-11866950 REVERSE LENGTH=358	365	358	1.00E-164	98.1	81.4	87.4
Rsa1.0_00808.1.g19774.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	153	1142	4.00E-30	746.4	42.5	56.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	153	575	3.00E-13	375.8	24.2	41.2

Rsa1.0_00808.1.g19775.t1	ref|XP_002874639.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297320476|gb|EFH50898.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	306	325	1.00E−103	106.2	68.3	78.8	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT1G32760.1 | Symbols: | Glutaredoxin family protein | chr1:11858251−11859195 FORWARD LENGTH=314	306	314	1.00E−102	102.6	72.2	79.4
Rsa1.0_00808.1.g19776.t1	gb|EOA27611.1| hypothetical protein CARUB_v10023752mg [Capsella rubella]	237	295	1.00E−101	124.5	78.1	91.1	hypothetical protein CARUB_v10023752mg	gbpln	Capsella rubella	AT2G26550.2 | Symbols: HO2 | heme oxygenase 2 | chr2:11291584−11293426 REVERSE LENGTH=299	237	299	1.00E−102	126.2	78.5	88.6
Rsa1.0_00808.1.g19777.t1	ref|NP_564407.1| uncharacterized protein [Arabidopsis thaliana] gi|6714274|gb|AAF25970.1|AC017118_7 F6N18.11 [Arabidopsis thaliana] gi|21536980|gb|AAM61321.1| unknown [Arabidopsis thaliana] gi|225897996|dbj|BAH30330.1| hypothetical protein [Arabidopsis thaliana] gi|332193401|gb|AEE31522.1| uncharacterized protein AT1G32730 [Arabidopsis thaliana]	348	327	1.00E−123	94.0	69.3	77.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G32730.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF702 (InterPro:IPR007818); Has 120 Blast hits to 118 proteins in 39 species: Archae − 0; Bacteria − 8; Metazoa − 63; Fungi − 4; Plants − 33; Viruses − 0; Other Eukaryotes − 12 (source: NCBI BLink). | chr1:11841077−11842956 FORWARD LENGTH=327	348	327	1.00E−126	94.0	69.3	77.3
Rsa1.0_00808.1.g19778.t1	dbj|BAB02990.1| retroelement pol polyprotein−like [Arabidopsis thaliana]	646	1250	0	193.5	61.1	75.2	retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	646	1262	4.00E−95	195.4	29.4	46.3
Rsa1.0_00808.1.g19779.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	254	329	2.00E−36	129.5	33.9	44.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	254	575	1.00E−18	226.4	20.9	36.2
Rsa1.0_00808.1.g19780.t1	gb|AAF25968.1|AC017118_5 F6N18.8 [Arabidopsis thaliana]	208	270	1.00E−103	129.8	91.8	95.2	F6N18.8	gbpln	Arabidopsis thaliana	AT1G32700.1 | Symbols: | PLATZ transcription factor family protein | chr1:11827588−11829444 FORWARD LENGTH=213	208	213	1.00E−105	102.4	91.8	95.2
Rsa1.0_00809.1.g19781.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19782.t14	ref|NP_179075.1| myosin heavy chain−related protein [Arabidopsis thaliana] gi|334184229|ref|NP_001189526.1| myosin heavy chain−related protein [Arabidopsis thaliana] gi|3810592|gb|AAC69374.1| unknown protein [Arabidopsis thaliana] gi|330251225|gb|AEC06319.1| myosin heavy chain−related protein [Arabidopsis thaliana] gi|330251227|gb|AEC06321.1| myosin heavy chain−related protein [Arabidopsis thaliana]	172	629	2.00E−80	365.7	87.2	94.8	myosin heavy chain−related protein	gbpln	Arabidopsis thaliana	AT2G14680.3 | Symbols: MEE13 | myosin heavy chain−related | chr2:6278256−6283766 FORWARD LENGTH=629	172	629	9.00E−83	365.7	87.2	94.8
Rsa1.0_00809.1.g19783.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19784.t2	gb|AAC33226.1| putative non−LTR retroelement reverse transcriptase [Arabidopsis thaliana]	777	1529	0	196.8	57.7	74.4	putative non−LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr3:8789471−8793208 FORWARD LENGTH=746	777	746	1.00E−121	96.0	29.0	36.2
Rsa1.0_00809.1.g19785.t12	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	1181	1024	2.00E−66	86.7	14.4	19.9	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19786.t7	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	1000	190	1.00E−32	19.0	8.1	9.7	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19787.t1	dbj|BAB02259.1| retroelement pol polyprotein−like [Arabidopsis thaliana]	418	777	2.00E−17	185.9	12.4	17.7	retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19788.t1	gb|AAD19762.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	266	616	4.00E−19	231.6	26.3	38.7	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19789.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19790.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19791.t2	ref|XP_003566116.1| PREDICTED: uncharacterized protein LOC100833674 [Brachypodium distachyon]	1729	1225	1.00E−148	70.9	19.5	27.7	PREDICTED: uncharacterized protein LOC100833674	gbpln	Brachypodium distachyon	AT3G30820.1 | Symbols: | Arabidopsis retrotransposon ORF−1 protein | chr3:12529843−12531235 FORWARD LENGTH=405	1729	405	3.00E−16	23.4	4.8	8.1
Rsa1.0_00809.1.g19792.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00809.1.g19793.t1	emb|CAN73649.1| hypothetical protein VITISV_036843 [Vitis vinifera]	1305	996	1.00E−173	76.3	26.9	36.9	hypothetical protein VITISV_036843	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00810.1.g19794.t1	ref|XP_002872139.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317976|gb|EFH48398.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	509	515	0	101.2	85.3	90.8	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00810.1.g19795.t1	gb|EOA21643.1| hypothetical protein CARUB_v10002061mg [Capsella rubella]	191	184	4.00E−71	96.3	75.9	82.2	hypothetical protein CARUB_v10002061mg	gbpln	Capsella rubella	AT5G25090.1 | Symbols: ENODL13, AtENODL13 | early nodulin−like protein 13 | chr5:8647117−8647755 REVERSE LENGTH=186	191	186	2.00E−66	97.4	70.2	78.5

Rsa1.0_00810.1.g19796.t1	ref|NP_197890.1| Sas10/Utp3/C1D family protein [Arabidopsis thaliana] gi|14190385|gb|AAK55673.1|AF378870_1 AT5g25080/T11H3_90 [Arabidopsis thaliana] gi|15215877|gb|AAK91482.1| AT5g25080/T11H3_90 [Arabidopsis thaliana] gi|21593008|gb|AAM64957.1| unknown [Arabidopsis thaliana] gi|332006014|gb|AED93397.1| Sas10/Utp3/C1D family protein [Arabidopsis thaliana]	223	217	6.00E-92	97.3	72.6	85.7	Sas10/Utp3/C1D family protein	gbpln	Arabidopsis thaliana	AT5G25080.1 | Symbols: | Sas10/Utp3/C1D family | chr5:8643782-8646306 FORWARD LENGTH=217	223	217	2.00E-94	97.3	72.6	85.7
Rsa1.0_00810.1.g19797.t1	ref|NP_197887.1| major facilitator protein [Arabidopsis thaliana] gi|75104998|sp|Q5FV41.1|FBT2_ARATH RecName: Full=Probable folate-biopterin transporter 2 gi|58331763|gb|AAW70379.1| At5g25050 [Arabidopsis thaliana] gi|332006011|gb|AED93394.1| probable folate-biopterin transporter 2 [Arabidopsis thaliana]	498	499	0	100.2	90.0	94.2	major facilitator protein	gbpln	Arabidopsis thaliana	AT5G25050.1 | Symbols: | Major facilitator superfamily protein | chr5:8632022-8633828 FORWARD LENGTH=499	498	499	0	100.2	90.0	94.2
Rsa1.0_00810.1.g19798.t1	ref|XP_002872135.1| hypothetical protein ARALYDRAFT_910545 [Arabidopsis lyrata subsp. lyrata] gi|297317972|gb|EFH48394.1| hypothetical protein ARALYDRAFT_910545 [Arabidopsis lyrata subsp. lyrata]	294	296	1.00E-107	100.7	63.9	80.3	hypothetical protein ARALYDRAFT_910545	gbpln	Arabidopsis lyrata	AT5G24990.1 | Symbols: | Protein of unknown function (DUF1336) | chr5:8610591-8611475 FORWARD LENGTH=294	294	294	1.00E-106	100.0	62.9	77.6
Rsa1.0_00810.1.g19799.t8	ref|XP_002874233.1| hypothetical protein ARALYDRAFT_489354 [Arabidopsis lyrata subsp. lyrata] gi|297320070|gb|EFH50492.1| hypothetical protein ARALYDRAFT_489354 [Arabidopsis lyrata subsp. lyrata]	431	446	1.00E-176	103.5	75.4	81.7	hypothetical protein ARALYDRAFT_489354	gbpln	Arabidopsis lyrata	AT5G24940.1 | Symbols: | Protein phosphatase 2C family protein | chr5:8591407-8593601 REVERSE LENGTH=447	431	447	1.00E-173	103.7	74.0	82.4
Rsa1.0_00810.1.g19800.t1	ref|NP_197875.2| protein CONSTANS-like 4 [Arabidopsis thaliana] gi|332005996|gb|AED93379.1| zinc finger protein CONSTANS-LIKE 4 [Arabidopsis thaliana]	351	406	1.00E-166	115.7	91.7	94.6	protein CONSTANS-like 4	gbpln	Arabidopsis thaliana	AT5G24930.1 | Symbols: ATCOL4, COL4 | CONSTANS-like 4 | chr5:8589325-8590949 FORWARD LENGTH=406	351	406	1.00E-169	115.7	91.7	94.6
Rsa1.0_00810.1.g19801.t1	gb|EOA21783.1| hypothetical protein CARUB_v10002244mg [Capsella rubella]	130	133	2.00E-41	102.3	66.9	71.5	hypothetical protein CARUB_v10002244mg	gbpln	Capsella rubella	AT5G24920.1 | Symbols: AtGDU5, GDU5 | glutamine dumper 5 | chr5:8584665-8585060 FORWARD LENGTH=131	130	131	7.00E-38	100.8	68.5	73.8
Rsa1.0_00810.1.g19802.t1	gb|EOA20382.1| hypothetical protein CARUB_v10000695mg [Capsella rubella]	533	529	0	99.2	90.6	95.5	hypothetical protein CARUB_v10000695mg	gbpln	Capsella rubella	AT5G24910.1 | Symbols: CYP714A1 | cytochrome P450, family 714, subfamily A, polypeptide 1 | chr5:8567674-8570260 REVERSE LENGTH=532	533	532	0	99.8	90.2	94.0
Rsa1.0_00810.1.g19803.t1	gb|AAO42013.1| unknown protein [Arabidopsis thaliana]	219	240	1.00E-62	109.6	72.6	79.9	unknown protein	gbpln	Arabidopsis thaliana	AT5G24890.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24550.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8558357-8559172 REVERSE LENGTH=240	219	240	4.00E-65	109.6	72.6	79.9
Rsa1.0_00810.1.g19804.t1	gb|EOA22360.1| hypothetical protein CARUB_v10002989mg [Capsella rubella]	417	421	8.00E-98	101.0	66.2	77.2	hypothetical protein CARUB_v10002989mg	gbpln	Capsella rubella	AT5G10660.1 | Symbols: | calmodulin-binding protein-related | chr5:3370553-3371776 FORWARD LENGTH=407	417	407	3.00E-71	97.6	52.5	64.7
Rsa1.0_00811.1.g19805.t1	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	910	1453	0	159.7	47.3	59.7	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	910	1262	1.00E-87	138.7	18.6	28.7
Rsa1.0_00811.1.g19806.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00811.1.g19807.t1	ref|NP_190805.1| fasciclin-like arabinogalactan protein 15 [Arabidopsis thaliana] gi|75172383|sp|Q9FT45.1|FLA15_ARATH RecName: Full=Fasciclin-like arabinogalactan protein 15; Flags: Precursor gi|10045570|emb|CAC07928.1| putative protein [Arabidopsis thaliana] gi|26450296|dbj|BAC42264.1| GPI-anchored protein [Arabidopsis thaliana] gi|109946609|gb|ABG48483.1| At3g52370 [Arabidopsis thaliana] gi|332645418|gb|AEE78939.1| fasciclin-like arabinogalactan protein 15 [Arabidopsis thaliana]	436	436	0	100.0	85.3	89.4	fasciclin-like arabinogalactan protein 15	gbpln	Arabidopsis thaliana	AT3G52370.1 | Symbols: FLA15 | FASCICLIN-like arabinogalactan protein 15 precursor | chr3:19417549-19419549 FORWARD LENGTH=436	436	436	0	100.0	85.3	89.4
Rsa1.0_00811.1.g19808.t1	ref|XP_002876141.1| RNA-binding protein cp33 [Arabidopsis lyrata subsp. lyrata] gi|297321979|gb|EFH52400.1| RNA-binding protein cp33 [Arabidopsis lyrata subsp. lyrata]	310	330	1.00E-118	106.5	73.5	81.0	RNA-binding protein cp33	gbpln	Arabidopsis lyrata	AT3G52380.1 | Symbols: CP33, PDE322 | chloroplast RNA-binding protein 33 | chr3:19421619-19422855 FORWARD LENGTH=329	310	329	1.00E-119	106.1	74.2	81.9
Rsa1.0_00811.1.g19809.t1	gb|EOA24396.1| hypothetical protein CARUB_v10017645mg [Capsella rubella]	302	323	1.00E-165	107.0	90.4	94.7	hypothetical protein CARUB_v10017645mg	gbpln	Capsella rubella	AT3G52390.2 | Symbols: | TatD related DNase | chr3:19423105-19425183 REVERSE LENGTH=323	302	323	1.00E-165	107.0	89.7	94.0
Rsa1.0_00811.1.g19810.t1	dbj|BAJ33859.1| unnamed protein product [Thellungiella halophila]	345	343	1.00E-159	99.4	87.8	93.9	unnamed protein product	----	----	AT3G52400.1 | Symbols: SYP122, ATSYP122 | syntaxin of plants 122 | chr3:19425835-19427032 REVERSE LENGTH=341	345	341	1.00E-144	98.8	81.7	90.1
Rsa1.0_00811.1.g19811.t1	ref|XP_002876143.1| phytoalexin deficient 4 [Arabidopsis lyrata subsp. lyrata] gi|297321981|gb|EFH52402.1| phytoalexin deficient 4 [Arabidopsis lyrata subsp. lyrata]	433	542	1.00E-164	125.2	69.7	77.8	phytoalexin deficient 4	gbpln	Arabidopsis lyrata	AT3G52430.1 | Symbols: PAD4, ATPAD4 | alpha/beta-Hydrolases superfamily protein | chr3:19431566-19434292 FORWARD LENGTH=541	433	541	1.00E-164	124.9	69.3	76.9
Rsa1.0_00811.1.g19812.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	209	1501	2.00E-55	718.2	51.7	65.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	209	1262	8.00E-26	603.8	23.9	40.7
Rsa1.0_00811.1.g19813.t1	dbj|BAJ34414.1| unnamed protein product [Thellungiella halophila]	424	435	0	102.6	91.3	96.0	unnamed protein product	----	----	AT3G52450.1 | Symbols: PUB22 | plant U-box 22 | chr3:19440943-19442250 REVERSE LENGTH=435	424	435	0	102.6	88.0	94.1
Rsa1.0_00812.1.g19814.t1	emb|CAA79989.2| myrosinase, thioglucoside glucohydrolase [Brassica napus]	522	527	0	101.0	79.5	86.2	myrosinase, thioglucoside glucohydrolase	gbpln	Brassica napus	AT5G26000.1 | Symbols: TGG1, BGLU38 | thioglucoside glucohydrolase 1 | chr5:9079678-9082347 REVERSE LENGTH=541	522	541	0	103.6	68.2	78.2
Rsa1.0_00812.1.g19815.t1	gb|EOA30088.1| hypothetical protein CARUB_v10013195mg [Capsella rubella]	607	636	0	104.8	72.7	76.1	hypothetical protein CARUB_v10013195mg	gbpln	Capsella rubella	AT3G22330.1 | Symbols: PMH2, ATRH53 | putative mitochondrial RNA helicase 2 | chr3:7892641-7895145 FORWARD LENGTH=616	607	616	0	101.5	81.1	86.8
Rsa1.0_00812.1.g19816.t1	ref|NP_188875.1| alternative oxidase 1B [Arabidopsis thaliana] gi|3913143|sp|O23913.1|AOX1B_ARATH RecName: Full=Ubiquinol oxidase 1b, mitochondrial; AltName: Full=Alternative oxidase 1b; Flags: Precursor gi|2506082|dbj|BAA22624.1| alternative oxidase [Arabidopsis thaliana] gi|9293871|dbj|BAB01774.1| alternative oxidase 1b precursor [Arabidopsis thaliana] gi|67633654|gb|AAY78751.1| mitochondrial alternative oxidase 1b [Arabidopsis thaliana] gi|332643105|gb|AEE76626.1| alternative oxidase 1B [Arabidopsis thaliana]	332	325	1.00E-165	97.9	87.3	90.7	alternative oxidase 1B	gbpln	Arabidopsis thaliana	AT3G22360.1 | Symbols: AOX1B | alternative oxidase 1B | chr3:7904156-7905384 FORWARD LENGTH=325	332	325	1.00E-167	97.9	87.3	90.7
Rsa1.0_00812.1.g19817.t1	gb|ABA96452.1| GRF zinc finger family protein [Oryza sativa Japonica Group]	73	278	4.00E-35	380.8	97.3	98.6	GRF zinc finger family protein	gbpln	Oryza sativa	AT5G42300.1 | Symbols: UBL5 | ubiquitin-like protein 5 | chr5:16913611-16913832 REVERSE LENGTH=73	73	73	2.00E-36	100.0	98.6	100.0
Rsa1.0_00812.1.g19818.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00812.1.g19819.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00812.1.g19820.t1	ref|XP_002883360.1| time for coffee [Arabidopsis lyrata subsp. lyrata] gi|297329200|gb|EFH59619.1| time for coffee [Arabidopsis lyrata subsp. lyrata]	1509	1550	0	102.7	76.0	82.7	time for coffee	gbpln	Arabidopsis lyrata	AT3G22380.1 | Symbols: TIC | time for coffee | chr3:7913181-7918879 FORWARD LENGTH=1550	1509	1550	0	102.7	75.7	82.9

Rsa1.0_00812.1.g19821.t1	ref|NP_188879.2| lipoxygenase 5 [Arabidopsis thaliana] gi|254810223|sp|Q9LUW0.2|LOX5_ARATH RecName: Full=Linoleate 9S-lipoxygenase 5, chloroplastic; AltName: Full=Lipoxygenase 5; Short=AtLOX5 gi|332643109|gb|AEE76630.1| lipoxygenase 5 [Arabidopsis thaliana]	765	886	0	115.8	92.4	96.5	lipoxygenase 5	gbpln	Arabidopsis thaliana	AT3G22400.1 | Symbols: LOX5 | PLAT/LH2 domain-containing lipoxygenase family protein | chr3:7927011-7931167 FORWARD LENGTH=886	765	886	0	115.8	92.4	96.5
Rsa1.0_00812.1.g19822.t1	ref|XP_002885501.1| hypothetical protein ARALYDRAFT_479753 [Arabidopsis lyrata subsp. lyrata] gi|297331341|gb|EFH61760.1| hypothetical protein ARALYDRAFT_479753 [Arabidopsis lyrata subsp. lyrata]	399	400	0	100.3	81.5	89.7	hypothetical protein ARALYDRAFT_479753	gbpln	Arabidopsis lyrata	AT3G22410.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr3:7933328-7935664 REVERSE LENGTH=400	399	400	0	100.3	81.7	89.2
Rsa1.0_00813.1.g19823.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1352	1307	0	96.7	60.9	75.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1352	1262	1.00E-97	93.3	13.7	22.1
Rsa1.0_00813.1.g19824.t1	gb|EOA38591.1| hypothetical protein CARUB_v10010434mg [Capsella rubella]	176	177	1.00E-62	100.6	65.3	75.0	hypothetical protein CARUB_v10010434mg	gbpln	Capsella rubella	AT1G09370.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:3024901-3025425 FORWARD LENGTH=174	176	174	2.00E-62	98.9	61.9	76.1
Rsa1.0_00813.1.g19825.t1	ref|NP_172407.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|3482911|gb|AAC33196.1| Hypothetical protein [Arabidopsis thaliana] gi|332190312|gb|AEE28433.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	138	188	2.00E-23	136.2	41.3	53.6	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT1G09360.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:3021802-3022368 FORWARD LENGTH=188	138	188	6.00E-26	136.2	41.3	53.6
Rsa1.0_00813.1.g19826.t1	dbj|BAJ33886.1| unnamed protein product [Thellungiella halophila]	378	379	0	100.3	97.9	99.5	unnamed protein product	----	----	AT1G09340.1 | Symbols: CRB, CSP41B, HIP1.3 | chloroplast RNA binding | chr1:3015473-3018035 FORWARD LENGTH=378	378	378	0	100.0	97.1	98.7
Rsa1.0_00813.1.g19827.t2	gb|EOA39357.1| hypothetical protein CARUB_v10012409mg [Capsella rubella]	183	185	6.00E-97	101.1	98.4	98.9	hypothetical protein CARUB_v10012409mg	gbpln	Capsella rubella	AT1G09330.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF846, eukaryotic (InterPro:IPR008564); Has 518 Blast hits to 518 proteins in 206 species: Archae - 0; Bacteria - 0; Metazoa - 193; Fungi - 145; Plants - 73; Viruses - 0; Other Eukaryotes - 107 (source: NCBI BLink). | chr1:3013003-3014903 REVERSE LENGTH=186	183	186	3.00E-99	101.6	98.4	98.9
Rsa1.0_00813.1.g19828.t1	ref|XP_002892499.1| agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338341|gb|EFH68758.1| agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata]	516	518	0	100.4	71.3	83.3	agenet domain-containing protein	gbpln	Arabidopsis lyrata	AT1G09320.1 | Symbols: | agenet domain-containing protein | chr1:3010270-3012228 REVERSE LENGTH=517	516	517	0	100.2	69.6	82.8
Rsa1.0_00813.1.g19829.t1	ref|NP_563841.1| uncharacterized protein [Arabidopsis thaliana] gi|13194796|gb|AAK15560.1|AF348589_1 unknown protein [Arabidopsis thaliana] gi|4337175|gb|AAD18096.1| ESTs gb|T20589, gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457, gb|T20921, gb|AA042762 and gb|AA720210 come from this gene [Arabidopsis thaliana] gi|15028183|gb|AAK76588.1| unknown protein [Arabidopsis thaliana] gi|19310813|gb|AAL85137.1| unknown protein [Arabidopsis thaliana] gi|21536763|gb|AAM61095.1| unknown [Arabidopsis thaliana] gi|332190307|gb|AEE28428.1| uncharacterized protein AT1G09310 [Arabidopsis thaliana]	184	179	2.00E-73	97.3	82.6	88.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G09310.1 | Symbols: | Protein of unknown function, DUF538 | chr1:3009109-3009648 FORWARD LENGTH=179	184	179	7.00E-76	97.3	82.6	88.6

Rsa1.0_00813.1.g19830.t1	ref|NP_563840.1| uncharacterized protein [Arabidopsis thaliana] gi|75164945|sp|Q94AC1.1|STR6_ARATH RecName: Full=Rhodanese–like domain–containing protein 6; AltName: Full=Sulfurtransferase 6; Short=AtStr6 gi|15081791|gb|AAK82550.1| At1g09280/T12M4_1 [Arabidopsis thaliana] gi|133778874|gb|ABO38777.1| At1g09280 [Arabidopsis thaliana] gi|332190303|gb|AEE28424.1| uncharacterized protein AT1G09280 [Arabidopsis thaliana]	593	581	0	98.0	88.9	92.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G09280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Rhodanese–like (InterPro:IPR001763), Serine hydrolase (InterPro:IPR005645); BEST Arabidopsis thaliana protein match is: Rhodanese/Cell cycle control phosphatase superfamily protein (TAIR:AT2G40760.1); Has 5925 Blast hits to 5912 proteins in 1592 species: Archae – 0; Bacteria – 2946; Metazoa – 156; Fungi – 408; Plants – 229; Viruses – 0; Other Eukaryotes – 2186 (source: NCBI BLink). | chr1:2998209–3001253 REVERSE LENGTH=581	593	581	0	98.0	88.9	92.9
Rsa1.0_00813.1.g19831.t1	gb|ABO21639.1| importin alpha–like protein [Brassica napus] gi|126572504|gb|ABO21640.1| importin alpha–like protein [Brassica napus]	538	542	0	100.7	97.2	98.9	importin alpha–like protein	gbpln	Brassica napus	AT1G09270.2 | Symbols: IMPA–4 | importin alpha isoform 4 | chr1:2994506–2997833 FORWARD LENGTH=538	538	538	0	100.0	93.3	96.5
Rsa1.0_00813.1.g19832.t1	ref|NP_172397.1| Chaperone DnaJ–domain–containing protein [Arabidopsis thaliana] gi|3249097|gb|AAC24080.1| Contains similarity to DNAJ homologue gb|D84222 from Thermus thermophilus [Arabidopsis thaliana] gi|332190299|gb|AEE28420.1| Chaperone DnaJ–domain–containing protein [Arabidopsis thaliana]	169	138	8.00E–25	81.7	37.9	53.8	Chaperone DnaJ–domain–containing protein	gbpln	Arabidopsis thaliana	AT1G09260.1 | Symbols: | Chaperone DnaJ–domain superfamily protein | chr1:2993404–2993820 FORWARD LENGTH=138	169	138	3.00E–27	81.7	37.9	53.8
Rsa1.0_00813.1.g19833.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00813.1.g19834.t1	ref|NP_567745.1| antitermination NusB domain–containing protein [Arabidopsis thaliana] gi|15450968|gb|AAK96755.1| putative protein [Arabidopsis thaliana] gi|30984514|gb|AAP42720.1| At4g26370 [Arabidopsis thaliana] gi|332659789|gb|AEE85189.1| antitermination NusB domain–containing protein [Arabidopsis thaliana]	175	301	4.00E–51	172.0	68.0	72.6	antitermination NusB domain–containing protein	gbpln	Arabidopsis thaliana	AT4G26370.1 | Symbols: | antitermination NusB domain–containing protein | chr4:13334099–13336153 REVERSE LENGTH=301	175	301	2.00E–53	172.0	68.0	72.6
Rsa1.0_00813.1.g19835.t1	ref|XP_002889739.1| hypothetical protein ARALYDRAFT_471014 [Arabidopsis lyrata subsp. lyrata] gi|297335581|gb|EFH65998.1| hypothetical protein ARALYDRAFT_471014 [Arabidopsis lyrata subsp. lyrata]	121	198	3.00E–20	163.6	56.2	59.5	hypothetical protein ARALYDRAFT_471014	gbpln	Arabidopsis lyrata	AT1G09250.1 | Symbols: | basic helix–loop–helix (bHLH) DNA–binding superfamily protein | chr1:2989509–2990132 FORWARD LENGTH=207	121	207	1.00E–22	171.1	56.2	59.5
Rsa1.0_00813.1.g19836.t1	emb|CAC82913.1| nicotianamine synthase [Noccaea caerulescens]	322	321	1.00E–164	99.7	89.1	93.8	nicotianamine synthase	gbpln	Noccaea caerulescens	AT1G09240.1 | Symbols: NAS3, ATNAS3 | nicotianamine synthase 3 | chr1:2984950–2985912 FORWARD LENGTH=320	322	320	1.00E–160	99.4	85.7	91.0
Rsa1.0_00813.1.g19837.t1	ref|NP_172394.1| U11/U12 small nuclear ribonucleoprotein 65 kDa protein [Arabidopsis thaliana] gi|20258828|gb|AAM13896.1| unknown protein [Arabidopsis thaliana] gi|21689717|gb|AAM67480.1| unknown protein [Arabidopsis thaliana] gi|332190295|gb|AEE28416.1| RNA–binding (RRM/RBD/RNP motifs) family protein [Arabidopsis thaliana]	448	442	0	98.7	85.3	90.2	U11/U12 small nuclear ribonucleoprotein 65 kDa protein	gbpln	Arabidopsis thaliana	AT1G09230.1 | Symbols: | RNA–binding (RRM/RBD/RNP motifs) family protein | chr1:2979637–2982563 REVERSE LENGTH=442	448	442	0	98.7	85.3	90.2
Rsa1.0_00813.1.g19838.t1	gb|AAM63796.1| putative calcium–binding protein, calreticulin [Arabidopsis thaliana]	423	424	0	100.2	92.7	95.3	putative calcium–binding protein, calreticulin	gbpln	Arabidopsis thaliana	AT1G09210.1 | Symbols: CRT1b, AtCRT1b | calreticulin 1b | chr1:2973217–2976655 REVERSE LENGTH=424	423	424	0	100.2	92.4	95.0
Rsa1.0_00813.1.g19839.t1	gb|EOA34021.1| hypothetical protein CARUB_v10021517mg, partial [Capsella rubella]	193	205	1.00E–104	106.2	95.3	97.4	hypothetical protein CARUB_v10021517mg, partial	gbpln	Capsella rubella	AT1G56330.1 | Symbols: SAR1, ATSAR1, ATSARA1B, ATSAR1B, SAR1B | secretion–associated RAS 1B | chr1:21086845–21088478 REVERSE LENGTH=193	193	193	1.00E–106	100.0	95.3	97.4
Rsa1.0_00813.1.g19840.t1	ref|NP_172391.2| pentatricopeptide repeat–containing protein [Arabidopsis thaliana] gi|75099767|sp|O80488.1|PPR23_ARATH RecName: Full=Pentatricopeptide repeat–containing protein At1g09190 gi|3249103|gb|AAC24086.1| Contains similarity to membrane–associated salt–inducible protein homolog TM021B04.10 gb|2191192 from A. thaliana BAC gb|AF007271 [Arabidopsis thaliana] gi|28393182|gb|AAO42022.1| unknown protein [Arabidopsis thaliana] gi|332190289|gb|AEE28410.1| pentatricopeptide repeat–containing protein [Arabidopsis thaliana]	685	484	0	70.7	62.0	66.4	pentatricopeptide repeat–containing protein	gbpln	Arabidopsis thaliana	AT1G09190.1 | Symbols: | Tetratricopeptide repeat (TPR)–like superfamily protein | chr1:2966263–2967717 REVERSE LENGTH=484	685	484	0	70.7	62.0	66.4

Rsa1.0_00813.1.g19841.t1	ref|XP_002892485.1| phloem protein 2-B15 [Arabidopsis lyrata subsp. lyrata] gi|297338327|gb|EFH68744.1| phloem protein 2-B15 [Arabidopsis lyrata subsp. lyrata]	58	289	4.00E-19	498.3	75.9	82.8	phloem protein 2-B15	gbpln	Arabidopsis lyrata	AT1G09155.1 | Symbols: AtPP2-B15, PP2-B15 | phloem protein 2-B15 | chr1:2949831-2950842 REVERSE LENGTH=289	58	289	1.00E-20	498.3	72.4	79.3
Rsa1.0_00814.1.g19842.t1	ref|XP_002865861.1| hypothetical protein ARALYDRAFT_495214 [Arabidopsis lyrata subsp. lyrata] gi|297311696|gb|EFH42120.1| hypothetical protein ARALYDRAFT_495214 [Arabidopsis lyrata subsp. lyrata]	787	836	0	106.2	94.8	97.7	hypothetical protein ARALYDRAFT_495214	gbpln	Arabidopsis lyrata	AT5G51430.1 | Symbols: EYE | conserved oligomeric Golgi complex component-related / COG complex component-related | chr5:20887044-20890795 REVERSE LENGTH=836	787	836	0	106.2	94.8	97.5
Rsa1.0_00814.1.g19843.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00814.1.g19844.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00814.1.g19845.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00814.1.g19846.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1171	1413	0	120.7	49.4	65.8	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1171	1262	1.00E-96	107.8	15.5	21.5
Rsa1.0_00814.1.g19847.t3	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1354	1223	0	90.3	38.8	52.2	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1354	746	2.00E-90	55.1	12.7	17.4
Rsa1.0_00814.1.g19848.t3	ref|NP_174400.1| uncharacterized protein [Arabidopsis thaliana] gi|4512629|gb|AAD21698.1| EST gb|Z33866 comes from this gene [Arabidopsis thaliana] gi|332193197|gb|AEE31318.1| uncharacterized protein AT1G31150 [Arabidopsis thaliana]	547	673	5.00E-53	123.0	23.2	32.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	547	673	1.00E-55	123.0	23.2	32.2
Rsa1.0_00814.1.g19849.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00814.1.g19850.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00815.1.g19851.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00815.1.g19852.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	239	390	5.00E-28	163.2	34.3	49.4	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	239	320	2.00E-19	133.9	30.5	49.4
Rsa1.0_00815.1.g19853.t1	gb|ABS11038.1| MYC [Brassica oleracea var. gemmifera]	568	610	0	107.4	85.0	90.7	MYC	gbpln	Brassica oleracea	AT1G32640.1 | Symbols: ATMYC2, RD22BP1, JAI1, JIN1, MYC2, ZBF1 | Basic helix-loop-helix (bHLH) DNA-binding family protein | chr1:11799042-11800913 REVERSE LENGTH=623	568	623	0	109.7	83.3	89.1
Rsa1.0_00815.1.g19854.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	808	1142	1.00E-164	141.3	34.9	42.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	808	575	1.00E-39	71.2	13.9	23.6
Rsa1.0_00815.1.g19855.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00815.1.g19856.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00815.1.g19857.t1	ref|XP_002893730.1| hypothetical protein ARALYDRAFT_890836 [Arabidopsis lyrata subsp. lyrata] gi|297339572|gb|EFH69989.1| hypothetical protein ARALYDRAFT_890836 [Arabidopsis lyrata subsp. lyrata]	221	219	3.00E-50	99.1	57.9	67.4	hypothetical protein ARALYDRAFT_890836	gbpln	Arabidopsis lyrata	AT1G32585.1 | Symbols: | VQ motif-containing protein-related | chr1:11788515-11789177 REVERSE LENGTH=220	221	220	1.00E-44	99.5	53.8	63.8
Rsa1.0_00815.1.g19858.t1	ref|NP_187030.1| syntaxin 1B/2/3 [Arabidopsis thaliana] gi|28380139|sp|Q9SRV7.1|SY131_ARATH RecName: Full=Putative syntaxin-131; Short=AtSYP131 gi|6006872|gb|AAF00648.1|AC009540_25 s-syntaxin-like protein [Arabidopsis thaliana] gi|332640474|gb|AEE73995.1| putative syntaxin-131 [Arabidopsis thaliana]	109	306	4.00E-24	280.7	69.7	73.4	syntaxin 1B/2/3	gbpln	Arabidopsis thaliana	AT3G03800.1 | Symbols: SYP131, ATSYP131 | syntaxin of plants 131 | chr3:969314-971460 FORWARD LENGTH=306	109	306	7.00E-27	280.7	69.7	73.4
Rsa1.0_00815.1.g19859.t1	gb|EOA22467.1| hypothetical protein CARUB_v10003115mg [Capsella rubella]	102	515	7.00E-15	504.9	39.2	40.2	hypothetical protein CARUB_v10003115mg	gbpln	Capsella rubella	AT5G01710.1 | Symbols: | methyltransferases | chr5:263709-265250 REVERSE LENGTH=513	102	513	2.00E-17	502.9	39.2	40.2
Rsa1.0_00815.1.g19860.t1	dbj|BAB08713.1| unnamed protein product [Arabidopsis thaliana]	511	439	1.00E-55	85.9	18.6	25.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	511	361	2.00E-17	70.6	10.8	17.4

Rsa1.0_00815.1.g19861.t1	ref|NP_174529.2| NAC domain containing protein 11 [Arabidopsis thaliana] gi|8920628|gb|AAF81350.1|AC007767_30 Contains similarity to a hypothetical protein T6K21.160 gi|7487769 from Arabidopsis thaliana BAC T6K21 gb|AL021889 [Arabidopsis thaliana] gi|332193374|gb|AEE31495.1| NAC domain containing protein 11 [Arabidopsis thaliana]	326	283	1.00E-121	86.8	66.6	74.5	NAC domain containing protein 11	gbpln	Arabidopsis thaliana	AT1G32510.1 | Symbols: ANAC011, NAC011 | NAC domain containing protein 11 | chr1:11757000-11758118 FORWARD LENGTH=283	326	283	1.00E-123	86.8	66.6	74.5
Rsa1.0_00816.1.g19862.t1	ref|XP_002871263.1| hypothetical protein ARALYDRAFT_487555 [Arabidopsis lyrata subsp. lyrata] gi|297317100|gb|EFH47522.1| hypothetical protein ARALYDRAFT_487555 [Arabidopsis lyrata subsp. lyrata]	588	587	0	99.8	85.5	92.5	hypothetical protein ARALYDRAFT_487555	gbpln	Arabidopsis lyrata	AT5G07300.1 | Symbols: BON2 | Calcium-dependent phospholipid-binding Copine family protein | chr5:2299996-2303040 FORWARD LENGTH=586	588	586	0	99.7	84.9	92.2
Rsa1.0_00816.1.g19863.t1	gb|ABK28684.1| unknown [Arabidopsis thaliana]	262	264	1.00E-106	100.8	87.0	90.1	unknown	gbpln	Arabidopsis thaliana	AT5G07310.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:2305684-2306660 FORWARD LENGTH=263	262	263	1.00E-108	100.4	87.0	90.1
Rsa1.0_00816.1.g19864.t1	dbj|BAJ34421.1| unnamed protein product [Thellungiella halophila]	320	355	1.00E-132	110.9	77.8	86.3	unnamed protein product	----	----	AT5G07690.1 | Symbols: MYB29, ATMYB29, PMG2 | myb domain protein 29 | chr5:2447090-2448285 FORWARD LENGTH=336	320	336	1.00E-119	105.0	70.9	80.9
Rsa1.0_00816.1.g19865.t1	ref|XP_002866432.1| hypothetical protein ARALYDRAFT_919384 [Arabidopsis lyrata subsp. lyrata] gi|297312267|gb|EFH42691.1| hypothetical protein ARALYDRAFT_919384 [Arabidopsis lyrata subsp. lyrata]	317	281	1.00E-140	88.6	79.5	82.0	hypothetical protein ARALYDRAFT_919384	gbpln	Arabidopsis lyrata	AT5G61410.2 | Symbols: RPE | D-ribulose-5-phosphate-3-epimerase | chr5:24684085-24685836 REVERSE LENGTH=281	317	281	1.00E-142	88.6	78.9	81.7
Rsa1.0_00816.1.g19866.t1	ref|NP_196388.1| exonuclease family protein [Arabidopsis thaliana] gi|9759593|dbj|BAB11450.1| exonuclease-like protein [Arabidopsis thaliana] gi|332003813|gb|AED91196.1| exonuclease family protein [Arabidopsis thaliana]	474	468	0	98.7	83.5	89.7	exonuclease family protein	gbpln	Arabidopsis thaliana	AT5G07710.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:2453310-2455357 FORWARD LENGTH=468	474	468	0	98.7	83.5	89.7
Rsa1.0_00816.1.g19867.t1	dbj|BAJ34211.1| unnamed protein product [Thellungiella halophila]	339	330	1.00E-153	97.3	85.8	90.6	unnamed protein product	----	----	AT3G12250.2 | Symbols: TGA6, BZIP45 | TGACG motif-binding factor 6 | chr3:3906351-3908583 FORWARD LENGTH=330	339	330	1.00E-150	97.3	84.1	89.4
Rsa1.0_00816.1.g19868.t1	gb|EOA19919.1| hypothetical protein CARUB_v10000169mg, partial [Capsella rubella]	863	908	0	105.2	82.7	90.0	hypothetical protein CARUB_v10000169mg, partial	gbpln	Capsella rubella	AT5G06940.1 | Symbols: | Leucine-rich repeat receptor-like protein kinase family protein | chr5:2148078-2150771 REVERSE LENGTH=872	863	872	0	101.0	81.5	88.6
Rsa1.0_00816.1.g19869.t1	ref|XP_002871241.1| hypothetical protein ARALYDRAFT_487508 [Arabidopsis lyrata subsp. lyrata] gi|297317078|gb|EFH47500.1| hypothetical protein ARALYDRAFT_487508 [Arabidopsis lyrata subsp. lyrata]	716	725	0	101.3	77.1	85.3	hypothetical protein ARALYDRAFT_487508	gbpln	Arabidopsis lyrata	AT5G06930.1 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: nucleolar protein gar2-related (TAIR:AT2G42320.2); Has 3369 Blast hits to 1526 proteins in 313 species: Archae - 2; Bacteria - 910; Metazoa - 754; Fungi - 336; Plants - 137; Viruses - 11; Other Eukaryotes - 1219 (source: NCBI BLink). | chr5:2145139-2147849 FORWARD LENGTH=723	716	723	0	101.0	74.0	82.5
Rsa1.0_00816.1.g19870.t2	gb|ABX46555.1| polygalacturonase inhibitor protein 9 [Brassica napus] gi|227345518|gb|ACP28177.1| polygalacturonase-inhibiting protein 5 [Brassica rapa subsp. pekinensis]	325	336	1.00E-108	103.4	60.0	63.7	polygalacturonase inhibitor protein 9	gbpln	Brassica napus	AT5G06860.1 | Symbols: PGIP1, ATPGIP1 | polygalacturonase inhibiting protein 1 | chr5:2132373-2133434 FORWARD LENGTH=330	325	330	2.00E-86	101.5	46.8	52.6
Rsa1.0_00816.1.g19871.t1	gb|AAX68500.1| polygalacturonase inhibiting protein [Brassica rapa subsp. pekinensis] gi|160693712|gb|ABX46554.1| polygalacturonase inhibitor protein 8 [Brassica napus]	331	332	1.00E-160	100.3	84.6	88.2	polygalacturonase inhibiting protein	gbpln	Brassica napus	AT5G06860.1 | Symbols: PGIP1, ATPGIP1 | polygalacturonase inhibiting protein 1 | chr5:2132373-2133434 FORWARD LENGTH=330	331	330	1.00E-140	99.7	71.3	81.6
Rsa1.0_00816.1.g19872.t1	gb|ABX46555.1| polygalacturonase inhibitor protein 9 [Brassica napus] gi|227345518|gb|ACP28177.1| polygalacturonase-inhibiting protein 5 [Brassica rapa subsp. pekinensis]	335	336	1.00E-170	100.3	88.7	93.4	polygalacturonase inhibitor protein 9	gbpln	Brassica napus	AT5G06860.1 | Symbols: PGIP1, ATPGIP1 | polygalacturonase inhibiting protein 1 | chr5:2132373-2133434 FORWARD LENGTH=330	335	330	1.00E-136	98.5	69.0	79.4
Rsa1.0_00816.1.g19873.t1	gb|ACP28179.1| polygalacturonase-inhibiting protein 4 [Brassica rapa subsp. pekinensis]	334	334	1.00E-168	100.0	88.9	93.1	polygalacturonase-inhibiting protein 4	gbpln	Brassica rapa	AT5G06860.1 | Symbols: PGIP1, ATPGIP1 | polygalacturonase inhibiting protein 1 | chr5:2132373-2133434 FORWARD LENGTH=330	334	330	1.00E-144	98.8	72.8	81.4

<table>
<tr><td>Rsa1.0_00816.1.g19874.t1</td><td>gb|ABX46551.1| polygalacturonase inhibitor protein 5, partial [Brassica napus]</td><td>467</td><td>331</td><td>1.00E-179</td><td>70.9</td><td>68.5</td><td>70.0</td><td>polygalacturonase inhibitor protein 5, partial</td><td>gbpln</td><td>Brassica napus</td><td>AT5G06860.1 | Symbols: PGIP1, ATPGIP1 | polygalacturonase inhibiting protein 1 | chr5:2132373-2133434 FORWARD LENGTH=330</td><td>467</td><td>330</td><td>1.00E-160</td><td>70.7</td><td>57.0</td><td>61.9</td></tr>
<tr><td>Rsa1.0_00816.1.g19875.t2</td><td>ref|NP_001190244.1| bZIP transcription factor-like protein [Arabidopsis thaliana] gi|309952051|gb|ADO95299.1| bZIP65 [Arabidopsis thaliana] gi|332003691|gb|AED91074.1| bZIP transcription factor-like protein [Arabidopsis thaliana]</td><td>449</td><td>460</td><td>0</td><td>102.4</td><td>89.3</td><td>91.5</td><td>bZIP transcription factor-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06839.3 | Symbols: TGA10, bZIP65 | bZIP transcription factor family protein | chr5:2120911-2126217 FORWARD LENGTH=460</td><td>449</td><td>460</td><td>0</td><td>102.4</td><td>89.3</td><td>91.5</td></tr>
<tr><td>Rsa1.0_00816.1.g19876.t1</td><td>gb|EOA22632.1| hypothetical protein CARUB_v10003302mg [Capsella rubella]</td><td>547</td><td>549</td><td>0</td><td>100.4</td><td>89.9</td><td>94.5</td><td>hypothetical protein CARUB_v10003302mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G06830.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF773 (InterPro:IPR008491); Has 365 Blast hits to 359 proteins in 109 species: Archae - 9; Bacteria - 13; Metazoa - 209; Fungi - 7; Plants - 47; Viruses - 0; Other Eukaryotes - 80 (source: NCBI BLink). | chr5:2116882-2119559 REVERSE LENGTH=549</td><td>547</td><td>549</td><td>0</td><td>100.4</td><td>89.6</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00816.1.g19877.t1</td><td>gb|EOA20038.1| hypothetical protein CARUB_v10000312mg [Capsella rubella]</td><td>754</td><td>733</td><td>0</td><td>97.2</td><td>84.9</td><td>90.7</td><td>hypothetical protein CARUB_v10000312mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G06820.1 | Symbols: SRF2 | STRUBBELIG-receptor family 2 | chr5:2112994-2116663 FORWARD LENGTH=735</td><td>754</td><td>735</td><td>0</td><td>97.5</td><td>85.1</td><td>91.0</td></tr>
<tr><td>Rsa1.0_00816.1.g19878.t1</td><td>ref|XP_002871231.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317068|gb|EFH47490.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>534</td><td>1144</td><td>0</td><td>214.2</td><td>71.2</td><td>83.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G06810.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr5:2108493-2112256 FORWARD LENGTH=1141</td><td>534</td><td>1141</td><td>0</td><td>213.7</td><td>70.2</td><td>83.5</td></tr>
<tr><td>Rsa1.0_00816.1.g19879.t2</td><td>ref|XP_002873276.1| hypothetical protein ARALYDRAFT_487487 [Arabidopsis lyrata subsp. lyrata] gi|297319113|gb|EFH49535.1| hypothetical protein ARALYDRAFT_487487 [Arabidopsis lyrata subsp. lyrata]</td><td>357</td><td>374</td><td>1.00E-180</td><td>104.8</td><td>87.4</td><td>91.9</td><td>hypothetical protein ARALYDRAFT_487487</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G06750.3 | Symbols: | Protein phosphatase 2C family protein | chr5:2086403-2088245 REVERSE LENGTH=393</td><td>357</td><td>393</td><td>0</td><td>110.1</td><td>87.1</td><td>91.9</td></tr>
<tr><td>Rsa1.0_00816.1.g19880.t1</td><td>ref|XP_002871229.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317066|gb|EFH47488.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>651</td><td>654</td><td>0</td><td>100.5</td><td>87.9</td><td>93.4</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G06740.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:2084094-2086052 FORWARD LENGTH=652</td><td>651</td><td>652</td><td>0</td><td>100.2</td><td>86.5</td><td>92.8</td></tr>
<tr><td>Rsa1.0_00816.1.g19881.t1</td><td>ref|XP_002272597.2| PREDICTED: double-stranded RNA-binding protein 4-like [Vitis vinifera] gi|296087161|emb|CBI33535.3| unnamed protein product [Vitis vinifera]</td><td>455</td><td>333</td><td>1.00E-26</td><td>73.2</td><td>18.2</td><td>25.3</td><td>PREDICTED: double-stranded RNA-binding protein 4-like</td><td>gbpln</td><td>Vitis vinifera</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00816.1.g19882.t1</td><td>emb|CCJ34833.1| horseradish peroxidase isoenzyme HRP_4663 [Armoracia rusticana]</td><td>359</td><td>358</td><td>1.00E-171</td><td>99.7</td><td>84.7</td><td>90.0</td><td>horseradish peroxidase isoenzyme HRP_4663</td><td>gbpln</td><td>Armoracia rusticana</td><td>AT5G06730.1 | Symbols: | Peroxidase superfamily protein | chr5:2080207-2081621 REVERSE LENGTH=358</td><td>359</td><td>358</td><td>1.00E-171</td><td>99.7</td><td>85.0</td><td>89.7</td></tr>
<tr><td>Rsa1.0_00816.1.g19883.t1</td><td>emb|CCJ34825.1| horseradish peroxidase isoenzyme HRP_A2A [Armoracia rusticana]</td><td>338</td><td>336</td><td>1.00E-174</td><td>99.4</td><td>90.5</td><td>95.9</td><td>horseradish peroxidase isoenzyme HRP_A2A</td><td>gbpln</td><td>Armoracia rusticana</td><td>AT5G06720.1 | Symbols: ATPA2, PA2 | peroxidase 2 | chr5:2077567-2078857 REVERSE LENGTH=335</td><td>338</td><td>335</td><td>1.00E-172</td><td>99.1</td><td>88.5</td><td>95.0</td></tr>
<tr><td>Rsa1.0_00816.1.g19884.t1</td><td>ref|XP_002873274.1| homeobox-leucine zipper protein 14 [Arabidopsis lyrata subsp. lyrata] gi|297319111|gb|EFH49533.1| homeobox-leucine zipper protein 14 [Arabidopsis lyrata subsp. lyrata]</td><td>340</td><td>343</td><td>1.00E-140</td><td>100.9</td><td>82.4</td><td>87.6</td><td>homeobox-leucine zipper protein 14</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G06710.1 | Symbols: HAT14 | homeobox from Arabidopsis thaliana | chr5:2068305-2070284 REVERSE LENGTH=336</td><td>340</td><td>336</td><td>1.00E-141</td><td>98.8</td><td>84.7</td><td>87.9</td></tr>
<tr><td>Rsa1.0_00816.1.g19885.t1</td><td>gb|EOA20195.1| hypothetical protein CARUB_v10000490mg [Capsella rubella]</td><td>601</td><td>613</td><td>0</td><td>102.0</td><td>81.9</td><td>88.2</td><td>hypothetical protein CARUB_v10000490mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G06700.1 | Symbols: TBR | Plant protein of unknown function (DUF828) | chr5:2063638-2065810 FORWARD LENGTH=608</td><td>601</td><td>608</td><td>0</td><td>101.2</td><td>81.5</td><td>87.7</td></tr>
<tr><td>Rsa1.0_00816.1.g19886.t1</td><td>ref|NP_568172.1| thioredoxin-like 3-1 [Arabidopsis thaliana] gi|298286899|sp|Q9FG36.3|TRL31_ARATH RecName: Full=Thioredoxin-like 3-1, chloroplastic; AltName: Full=Thioredoxin WCRKC-1; Flags: Precursor gi|117958721|gb|ABK59676.1| At5g06690 [Arabidopsis thaliana] gi|332003667|gb|AED91050.1| thioredoxin-like 3-1 [Arabidopsis thaliana]</td><td>346</td><td>210</td><td>4.00E-86</td><td>60.7</td><td>44.5</td><td>47.4</td><td>thioredoxin-like 3-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06690.1 | Symbols: WCRKC1 | WCRKC thioredoxin 1 | chr5:2060651-2061956 REVERSE LENGTH=210</td><td>346</td><td>210</td><td>1.00E-88</td><td>60.7</td><td>44.5</td><td>47.4</td></tr>
<tr><td>Rsa1.0_00816.1.g19887.t4</td><td>gb|EOA21499.1| hypothetical protein CARUB_v10001894mg [Capsella rubella]</td><td>195</td><td>227</td><td>3.00E-22</td><td>116.4</td><td>40.0</td><td>53.8</td><td>hypothetical protein CARUB_v10001894mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321</td><td>195</td><td>321</td><td>3.00E-23</td><td>164.6</td><td>35.9</td><td>51.8</td></tr>
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Rsa1.0_00816.1.g19888.t1	gb|EOA21499.1| hypothetical protein CARUB_v10001894mg [Capsella rubella]	217	227	1.00E-34	104.6	42.9	55.8	hypothetical protein CARUB_v10001894mg	gbpln	Capsella rubella	AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321	217	321	8.00E-30	147.9	36.9	51.2
Rsa1.0_00816.1.g19889.t1	ref|XP_002873256.1| hypothetical protein ARALYDRAFT_487451 [Arabidopsis lyrata subsp. lyrata] gi|297319093|gb|EFH49515.1| hypothetical protein ARALYDRAFT_487451 [Arabidopsis lyrata subsp. lyrata]	492	480	0	97.6	73.8	84.8	hypothetical protein ARALYDRAFT_487451	gbpln	Arabidopsis lyrata	AT5G06440.3 | Symbols: | BEST Arabidopsis thaliana protein match is: Polyketide cyclase/dehydrase and lipid transport superfamily protein (TAIR:AT3G11720.3); Has 157 Blast hits to 155 proteins in 41 species: Archae - 0; Bacteria - 6; Metazoa - 5; Fungi - 6; Plants - 99; Viruses - 0; Other Eukaryotes - 41 (source: NCBI BLink). | chr5:1964641-1966807 REVERSE LENGTH=479	492	479	0	97.4	73.4	85.0
Rsa1.0_00816.1.g19890.t1	ref|XP_002871235.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317072|gb|EFH47494.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	198	194	1.00E-86	98.0	81.3	88.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G06430.1 | Symbols: | Thioredoxin superfamily protein | chr5:1963580-1964251 REVERSE LENGTH=194	198	194	3.00E-86	98.0	82.8	89.9
Rsa1.0_00816.1.g19891.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00816.1.g19892.t1	ref|XP_002884859.1| hypothetical protein ARALYDRAFT_478516 [Arabidopsis lyrata subsp. lyrata] gi|297330699|gb|EFH61118.1| hypothetical protein ARALYDRAFT_478516 [Arabidopsis lyrata subsp. lyrata]	557	625	0	112.2	74.5	83.7	hypothetical protein ARALYDRAFT_478516	gbpln	Arabidopsis lyrata	AT3G11710.1 | Symbols: ATKRS-1 | lysyl-tRNA synthetase 1 | chr3:3702359-3705613 REVERSE LENGTH=626	557	626	0	112.4	71.8	83.3
Rsa1.0_00816.1.g19893.t1	ref|XP_002873254.1| hypothetical protein ARALYDRAFT_487450 [Arabidopsis lyrata subsp. lyrata] gi|297319091|gb|EFH49513.1| hypothetical protein ARALYDRAFT_487450 [Arabidopsis lyrata subsp. lyrata]	271	255	1.00E-105	94.1	73.4	81.9	hypothetical protein ARALYDRAFT_487450	gbpln	Arabidopsis lyrata	AT5G06410.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:1959719-1961132 REVERSE LENGTH=252	271	252	1.00E-106	93.0	73.1	81.5
Rsa1.0_00816.1.g19894.t1	ref|XP_002871218.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317055|gb|EFH47477.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	1028	1029	0	100.1	81.2	90.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G06400.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:1955959-1959051 FORWARD LENGTH=1030	1028	1030	0	100.2	80.9	89.9
Rsa1.0_00816.1.g19895.t1	ref|NP_196257.2| fasciclin-like arabinogalactan protein 17 [Arabidopsis thaliana] gi|75115364|sp|Q66GR0.1|FLA17_ARATH RecName: Full=Fasciclin-like arabinogalactan protein 17; Flags: Precursor gi|51536454|gb|AAU05465.1| At5g06390 [Arabidopsis thaliana] gi|56121932|gb|AAV74247.1| At5g06390 [Arabidopsis thaliana] gi|332003626|gb|AED91009.1| fasciclin-like arabinogalactan protein 17 [Arabidopsis thaliana]	502	458	0	91.2	80.3	82.5	fasciclin-like arabinogalactan protein 17	gbpln	Arabidopsis thaliana	AT5G06390.1 | Symbols: FLA17 | FASCICLIN-like arabinogalactan protein 17 precursor | chr5:1952939-1955047 FORWARD LENGTH=458	502	458	0	91.2	80.3	82.5
Rsa1.0_00816.1.g19896.t1	gb|EOA22748.1| hypothetical protein CARUB_v10003460mg [Capsella rubella]	162	154	6.00E-33	95.1	62.3	72.2	hypothetical protein CARUB_v10003460mg	gbpln	Capsella rubella	AT5G06380.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11690.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1949632-1950072 FORWARD LENGTH=146	162	146	1.00E-30	90.1	55.6	66.0
Rsa1.0_00816.1.g19897.t1	ref|XP_002871214.1| ribosomal protein S8e family protein [Arabidopsis lyrata subsp. lyrata] gi|297317051|gb|EFH47473.1| ribosomal protein S8e family protein [Arabidopsis lyrata subsp. lyrata]	260	260	1.00E-140	100.0	93.5	96.2	ribosomal protein S8e family protein	gbpln	Arabidopsis lyrata	AT5G06360.1 | Symbols: | Ribosomal protein S8e family protein | chr5:1944835-1946512 FORWARD LENGTH=260	260	260	1.00E-142	100.0	93.1	96.2
Rsa1.0_00816.1.g19898.t3	gb|EOA19939.1| hypothetical protein CARUB_v10000191mg [Capsella rubella]	909	877	0	96.5	75.8	84.8	hypothetical protein CARUB_v10000191mg	gbpln	Capsella rubella	AT5G06350.1 | Symbols: | ARM repeat superfamily protein | chr5:1938781-1944197 FORWARD LENGTH=877	909	877	0	96.5	74.5	84.2
Rsa1.0_00816.1.g19899.t1	gb|ABL97947.1| bis(5'-nucleosy1)-tetraphosphatase [Brassica rapa]	210	228	1.00E-105	108.6	92.4	96.2	bis(5'-nucleosy1)-tetraphosphatase	gbpln	Brassica rapa	AT5G06340.1 | Symbols: ATNUDX27, NUDX27 | nudix hydrolase homolog 27 | chr5:1936467-1937911 FORWARD LENGTH=227	210	227	1.00E-102	108.1	88.6	92.9
Rsa1.0_00816.1.g19900.t1	dbj|BAJ34098.1| unnamed protein product [Thellungiella halophila]	236	235	1.00E-102	99.6	83.5	90.7	unnamed protein product	----	----	AT5G06320.1 | Symbols: NHL3 | NDR1/HIN1-like 3 | chr5:1931016-1931711 REVERSE LENGTH=231	236	231	9.00E-97	97.9	79.7	88.1

Rsa1.0_00816.1.g19901.t1	ref|XP_002875949.1| hypothetical protein ARALYDRAFT_906172 [Arabidopsis lyrata subsp. lyrata] gi|297321787|gb|EFH52208.1| hypothetical protein ARALYDRAFT_906172 [Arabidopsis lyrata subsp. lyrata]	569	967	1.00E−41	169.9	29.3	42.2	hypothetical protein ARALYDRAFT_906172	gbpln	Arabidopsis lyrata	AT5G12280.1 | Symbols: | SWAP (Suppressor−of−White−APricot)/surp RNA−binding domain−containing protein | chr5:3972014−3973636 REVERSE LENGTH=419	569	419	1.00E−31	73.6	18.3	26.2
Rsa1.0_00816.1.g19902.t1	gb|ACJ49162.1| protection of telomeres 1b protein [Brassica oleracea]	451	450	0	99.8	84.7	92.7	protection of telomeres 1b protein	gbpln	Brassica oleracea	AT5G06310.1 | Symbols: AtPOT1b | Nucleic acid−binding, OB−fold−like protein | chr5:1928468−1930795 FORWARD LENGTH=454	451	454	0	100.7	79.2	89.4
Rsa1.0_00817.1.g19903.t1	gb|AAL49921.1| unknown protein [Arabidopsis thaliana]	442	439	1.00E−163	99.3	64.0	77.1	unknown protein	gbpln	Arabidopsis thaliana	AT3G12700.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:4037136−4039043 FORWARD LENGTH=461	442	461	1.00E−166	104.3	64.0	77.1
Rsa1.0_00817.1.g19904.t1	ref|XP_002884920.1| hypothetical protein ARALYDRAFT_478629 [Arabidopsis lyrata subsp. lyrata] gi|297330760|gb|EFH61179.1| hypothetical protein ARALYDRAFT_478629 [Arabidopsis lyrata subsp. lyrata]	572	578	0	101.0	86.7	90.9	hypothetical protein ARALYDRAFT_478629	gbpln	Arabidopsis lyrata	AT3G12690.3 | Symbols: AGC1.5 | AGC kinase 1.5 | chr3:4030596−4032400 REVERSE LENGTH=577	572	577	0	100.9	86.7	90.7
Rsa1.0_00817.1.g19905.t1	gb|EOA30328.1| hypothetical protein CARUB_v10013453mg [Capsella rubella]	528	523	0	99.1	76.1	82.4	hypothetical protein CARUB_v10013453mg	gbpln	Capsella rubella	AT3G12680.1 | Symbols: HUA1 | floral homeotic protein (HUA1) | chr3:4025276−4028999 REVERSE LENGTH=524	528	524	0	99.2	80.3	87.3
Rsa1.0_00817.1.g19906.t1	gb|EOA30178.1| hypothetical protein CARUB_v10013294mg [Capsella rubella]	592	592	0	100.0	93.2	96.5	hypothetical protein CARUB_v10013294mg	gbpln	Capsella rubella	AT3G12670.1 | Symbols: emb2742 | CTP synthase family protein | chr3:4020351−4024086 REVERSE LENGTH=591	592	591	0	99.8	92.7	96.5
Rsa1.0_00817.1.g19907.t1	ref|NP_187872.1| fasciclin−like arabinogalactan protein 14 [Arabidopsis thaliana] gi|75274151|sp|Q9LTW9.1|FLA14_ARATH RecName: Full=Fasciclin−like arabinogalactan protein 14; Flags: Precursor gi|12321976|gb|AAG51033.1|AC069474_32 hypothetical protein; 8734−7967 [Arabidopsis thaliana] gi|11994407|dbj|BAB02409.1| unnamed protein product [Arabidopsis thaliana] gi|91806417|gb|ABE65936.1| fasciclin−like arabinogalactan family protein [Arabidopsis thaliana] gi|332641708|gb|AEE75229.1| fasciclin−like arabinogalactan protein 14 [Arabidopsis thaliana]	262	255	1.00E−58	97.3	56.5	69.1	fasciclin−like arabinogalactan protein 14	gbpln	Arabidopsis thaliana	AT3G12660.1 | Symbols: FLA14 | FASCICLIN−like arabinogalactan protein 14 precursor | chr3:4019060−4019827 FORWARD LENGTH=255	262	255	4.00E−61	97.3	56.5	69.1
Rsa1.0_00817.1.g19908.t1	gb|EOA31605.1| hypothetical protein CARUB_v10014801mg [Capsella rubella]	157	163	3.00E−66	103.8	85.4	91.7	hypothetical protein CARUB_v10014801mg	gbpln	Capsella rubella	AT3G12630.1 | Symbols: | A20/AN1−like zinc finger family protein | chr3:4012707−4013189 FORWARD LENGTH=160	157	160	4.00E−67	101.9	90.4	96.2
Rsa1.0_00817.1.g19909.t2	dbj|BAJ34487.1| unnamed protein product [Thellungiella halophila]	387	387	0	100.0	94.1	97.2	unnamed protein product	----	----	AT3G12620.2 | Symbols: | Protein phosphatase 2C family protein | chr3:4009510−4010993 REVERSE LENGTH=385	387	385	0	99.5	92.5	96.4
Rsa1.0_00817.1.g19910.t1	ref|XP_002882782.1| hypothetical protein ARALYDRAFT_478618 [Arabidopsis lyrata subsp. lyrata] gi|297328622|gb|EFH59041.1| hypothetical protein ARALYDRAFT_478618 [Arabidopsis lyrata subsp. lyrata]	174	180	2.00E−87	103.4	89.7	94.3	hypothetical protein ARALYDRAFT_478618	gbpln	Arabidopsis lyrata	AT3G12600.1 | Symbols: atnudt16, NUDT16 | nudix hydrolase homolog 16 | chr3:4004809−4005995 FORWARD LENGTH=180	174	180	3.00E−80	103.4	87.4	92.5
Rsa1.0_00817.1.g19911.t1	dbj|BAJ34614.1| unnamed protein product [Thellungiella halophila]	605	637	0	105.3	82.6	89.6	unnamed protein product	----	----	AT3G12560.1 | Symbols: TRFL9, ATTBP2 | TRF−like 9 | chr3:3982272−3984848 REVERSE LENGTH=619	605	619	0	102.3	80.2	87.8
Rsa1.0_00817.1.g19912.t1	ref|XP_002882779.1| hypothetical protein ARALYDRAFT_318024 [Arabidopsis lyrata subsp. lyrata] gi|297328619|gb|EFH59038.1| hypothetical protein ARALYDRAFT_318024 [Arabidopsis lyrata subsp. lyrata]	639	651	0	101.9	82.0	91.2	hypothetical protein ARALYDRAFT_318024	gbpln	Arabidopsis lyrata	AT3G12550.2 | Symbols: | XH/XS domain−containing protein | chr3:3978669−3981372 FORWARD LENGTH=638	639	638	0	99.8	79.8	88.9
Rsa1.0_00817.1.g19913.t2	dbj|BAB02264.1| unnamed protein product [Arabidopsis thaliana]	685	572	0	83.5	64.1	69.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G12540.1 | Symbols: | Protein of unknown function, DUF547 | chr3:3975246−3977247 FORWARD LENGTH=505	685	505	0	73.7	59.6	63.9
Rsa1.0_00817.1.g19914.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00817.1.g19915.t1	sp|Q09023.1|CHI2_BRANA RecName: Full=Endochitinase CH25; Flags: Precursor gi|167130|gb|AAA32986.1| endochitinase [Brassica napus]	322	322	1.00E−172	100.0	95.3	97.2	RecName: Full=Endochitinase CH25; Flags: Precursor gi|167130|gb|AAA32986.1| endochitinase	gbpln	Brassica napus	AT3G12500.1 | Symbols: ATHCHIB, PR3, PR−3, CHI−B, B−CHI, HCHIB | basic chitinase | chr3:3962501−3963984 REVERSE LENGTH=335	322	335	1.00E−158	104.0	83.9	86.3

Rsa1.0_00817.1.g19916.t1	gb|EOA31478.1| hypothetical protein CARUB_v10014664mg [Capsella rubella]	202	203	5.00E-81	100.5	90.1	96.0	hypothetical protein CARUB_v10014664mg	gbpln	Capsella rubella	AT3G12390.1 | Symbols: | Nascent polypeptide-associated complex (NAC), alpha subunit family protein | chr3:3942344-3943595 FORWARD LENGTH=203	202	203	3.00E-75	100.5	84.2	90.6
Rsa1.0_00817.1.g19917.t1	ref|NP_566422.4| actin-related protein 5 [Arabidopsis thaliana] gi|334302767|sp|Q940Z2.2|ARP5_ARATH RecName: Full=Actin-related protein 5 gi|15795157|dbj|BAB03145.1| actin-like protein [Arabidopsis thaliana] gi|257228981|gb|ACV53017.1| actin-related protein 5 [Arabidopsis thaliana] gi|257228983|gb|ACV53018.1| actin-related protein 5 [Arabidopsis thaliana] gi|332641669|gb|AEE75190.1| actin-related protein 5 [Arabidopsis thaliana]	723	724	0	100.1	85.2	92.3	actin-related protein 5	gbpln	Arabidopsis thaliana	AT3G12380.1 | Symbols: ATARP5, ARP5 | actin-related protein 5 | chr3:3938309-3941785 REVERSE LENGTH=724	723	724	0	100.1	85.2	92.3
Rsa1.0_00818.1.g19918.t1	emb|CBI22963.3| unnamed protein product [Vitis vinifera]	409	405	1.00E-100	99.0	45.0	61.6	unnamed protein product	gbpln	Vitis vinifera	AT1G02790.1 | Symbols: PGA4 | polygalacturonase 4 | chr1:610681-612225 REVERSE LENGTH=422	409	422	6.00E-74	103.2	39.4	56.5
Rsa1.0_00818.1.g19919.t1	ref|XP_002865717.1| hypothetical protein ARALYDRAFT_494980 [Arabidopsis lyrata subsp. lyrata] gi|297311552|gb|EFH41976.1| hypothetical protein ARALYDRAFT_494980 [Arabidopsis lyrata subsp. lyrata]	807	807	0	100.0	94.8	97.9	hypothetical protein ARALYDRAFT_494980	gbpln	Arabidopsis lyrata	AT5G49190.1 | Symbols: SUS2, SSA, ATSUS2 | sucrose synthase 2 | chr5:19943369-19947189 REVERSE LENGTH=807	807	807	0	100.0	94.3	97.4
Rsa1.0_00818.1.g19920.t1	ref|NP_199728.1| uncharacterized protein [Arabidopsis thaliana] gi|110737324|dbj|BAF00608.1| hypothetical protein [Arabidopsis thaliana] gi|332008395|gb|AED95778.1| uncharacterized protein AT5G49170 [Arabidopsis thaliana]	195	185	1.00E-58	94.9	66.7	72.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G49170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06840.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19938839-19939482 REVERSE LENGTH=185	195	185	4.00E-61	94.9	66.7	72.8
Rsa1.0_00818.1.g19921.t1	gb|EOA14799.1| hypothetical protein CARUB_v10028105mg [Capsella rubella]	270	329	2.00E-58	121.9	53.0	70.4	hypothetical protein CARUB_v10028105mg	gbpln	Capsella rubella	AT5G49420.1 | Symbols: | MADS-box transcription factor family protein | chr5:20035166-20036170 REVERSE LENGTH=334	270	334	4.00E-60	123.7	45.9	60.0
Rsa1.0_00818.1.g19922.t1	ref|XP_002863963.1| hypothetical protein ARALYDRAFT_917882 [Arabidopsis lyrata subsp. lyrata] gi|297309798|gb|EFH40222.1| hypothetical protein ARALYDRAFT_917882 [Arabidopsis lyrata subsp. lyrata]	70	921	1.00E-16	1315.7	82.9	85.7	hypothetical protein ARALYDRAFT_917882	gbpln	Arabidopsis lyrata	AT5G49150.1 | Symbols: ATGEX2, GEX2 | gamete expressed 2 | chr5:19924760-19928527 FORWARD LENGTH=914	70	914	1.00E-16	1305.7	77.1	82.9
Rsa1.0_00818.1.g19923.t1	ref|NP_199724.1| mate efflux domain-containing protein [Arabidopsis thaliana] gi|29468188|gb|AAO85438.1|AF488694_1 putative transporter NIC3 [Arabidopsis thaliana] gi|10176946|dbj|BAB10095.1| unnamed protein product [Arabidopsis thaliana] gi|332008391|gb|AED95774.1| mate efflux domain-containing protein [Arabidopsis thaliana]	499	502	0	100.6	89.4	94.6	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT5G49130.1 | Symbols: | MATE efflux family protein | chr5:19915904-19917525 FORWARD LENGTH=502	499	502	0	100.6	89.4	94.6
Rsa1.0_00818.1.g19924.t1	ref|NP_199723.1| uncharacterized protein [Arabidopsis thaliana] gi|10176945|dbj|BAB10094.1| unnamed protein product [Arabidopsis thaliana] gi|332008390|gb|AED95773.1| uncharacterized protein AT5G49120 [Arabidopsis thaliana]	134	150	2.00E-33	111.9	69.4	73.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G49120.1 | Symbols: | Protein of unknown function (DUF581) | chr5:19908800-19909332 REVERSE LENGTH=150	134	150	5.00E-36	111.9	69.4	73.9
Rsa1.0_00818.1.g19925.t1	gb|ABO36622.1| copia LTR rider [Solanum lycopersicum] gi|133711819|gb|ABO36636.1| copia LTR rider [Solanum lycopersicum]	513	1307	2.00E-52	254.8	19.5	20.3	copia LTR rider	gbpln	Solanum lycopersicum	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	513	1262	9.00E-17	246.0	8.8	12.1
Rsa1.0_00818.1.g19926.t1	ref|NP_568706.1| uncharacterized protein [Arabidopsis thaliana] gi|10176943|dbj|BAB10092.1| unnamed protein product [Arabidopsis thaliana] gi|18377646|gb|AAL66973.1| unknown protein [Arabidopsis thaliana] gi|22136864|gb|AAM91776.1| unknown protein [Arabidopsis thaliana] gi|332008387|gb|AED95770.1| uncharacterized protein AT5G49100 [Arabidopsis thaliana]	403	396	1.00E-115	98.3	72.2	78.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G49100.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06868.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19897700-19898890 REVERSE LENGTH=396	403	396	1.00E-117	98.3	72.2	78.9

Rsa1.0_00818.1.g19927.t1	dbj|BAB10088.1| DNAJ-like protein [Arabidopsis thaliana]	451	350	1.00E-135	77.6	59.4	67.2	DNAJ-like protein	gbpln	Arabidopsis thaliana	AT5G49060.1 | Symbols: | Heat shock protein DnaJ, N-terminal with domain of unknown function (DUF1977) | chr5:19886764-19888136 FORWARD LENGTH=354	451	354	1.00E-138	78.5	59.4	67.2
Rsa1.0_00818.1.g19928.t1	ref|NP_001190497.1| isoleucyl-tRNA synthetase [Arabidopsis thaliana] gi|332008381|gb|AED95764.1| isoleucyl-tRNA synthetase [Arabidopsis thaliana]	1091	1279	0	117.2	94.0	97.4	isoleucyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT5G49030.3 | Symbols: OVA2 | tRNA synthetase class I (I, L, M and V) family protein | chr5:19875091-19883251 REVERSE LENGTH=1279	1091	1279	0	117.2	94.0	97.4
Rsa1.0_00818.1.g19929.t1	ref|NP_199713.2| histone-arginine methyltransferase CARM1 [Arabidopsis thaliana] gi|152013379|sp|A3KPF2.1|ANM14_ARATH RecName: Full=Probable histone-arginine methyltransferase 1.4; Short=AtPRMT14; AltName: Full=Coactivator-associated methyltransferase 1B; AltName: Full=Protein arginine N-methyltransferase 4A; Short=AtPRMT4A gi|126352276|gb|ABO09883.1| At5g49020 [Arabidopsis thaliana] gi|126352282|gb|ABO09886.1| At5g49020 [Arabidopsis thaliana] gi|332008378|gb|AED95761.1| protein arginine methyltransferase 4A [Arabidopsis thaliana]	656	528	0	80.5	66.6	69.8	histone-arginine methyltransferase CARM1	gbpln	Arabidopsis thaliana	AT5G49020.1 | Symbols: ATPRMT4A, PRMT4A | protein arginine methyltransferase 4A | chr5:19871341-19874683 FORWARD LENGTH=528	656	528	0	80.5	66.6	69.8
Rsa1.0_00818.1.g19930.t1	gb|EOA13912.1| hypothetical protein CARUB_v10027029mg, partial [Capsella rubella]	219	239	2.00E-95	109.1	79.5	90.0	hypothetical protein CARUB_v10027029mg, partial	gbpln	Capsella rubella	AT5G49010.1 | Symbols: SLD5 | DNA replication protein-related | chr5:19866464-19868074 FORWARD LENGTH=220	219	220	8.00E-97	100.5	79.0	89.0
Rsa1.0_00818.1.g19931.t1	ref|XP_002865696.1| hypothetical protein ARALYDRAFT_917838 [Arabidopsis lyrata subsp. lyrata] gi|297311531|gb|EFH41955.1| hypothetical protein ARALYDRAFT_917838 [Arabidopsis lyrata subsp. lyrata]	108	107	4.00E-51	99.1	90.7	95.4	hypothetical protein ARALYDRAFT_917838	gbpln	Arabidopsis lyrata	AT5G24860.1 | Symbols: FPF1, ATFPF1 | flowering promoting factor 1 | chr5:8541822-8542154 FORWARD LENGTH=110	108	110	9.00E-33	101.9	63.0	80.6
Rsa1.0_00818.1.g19932.t1	ref|XP_002865695.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297311530|gb|EFH41954.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	337	338	0	100.3	93.5	97.0	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT5G48970.1 | Symbols: | Mitochondrial substrate carrier family protein | chr5:19857028-19859374 REVERSE LENGTH=339	337	339	0	100.6	92.3	96.1
Rsa1.0_00819.1.g19933.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	389	442	1.00E-155	113.6	68.6	78.1	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	389	343	3.00E-30	88.2	14.7	19.8
Rsa1.0_00819.1.g19934.t2	ref|XP_002876021.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321859|gb|EFH52280.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	408	445	1.00E-149	109.1	67.9	79.4	transferase family protein	gbpln	Arabidopsis lyrata	AT3G50280.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:18637854-18639185 FORWARD LENGTH=443	408	443	1.00E-150	108.6	67.9	78.7
Rsa1.0_00819.1.g19935.t1	ref|XP_002885656.1| hypothetical protein ARALYDRAFT_479971 [Arabidopsis lyrata subsp. lyrata] gi|297331496|gb|EFH61915.1| hypothetical protein ARALYDRAFT_479971 [Arabidopsis lyrata subsp. lyrata]	244	225	3.00E-87	92.2	64.3	67.6	hypothetical protein ARALYDRAFT_479971	gbpln	Arabidopsis lyrata	AT3G24570.1 | Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr3:8966675-8968530 REVERSE LENGTH=235	244	235	2.00E-86	96.3	63.5	67.6
Rsa1.0_00819.1.g19936.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	1820	1333	0	73.2	35.5	47.0	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1820	575	1.00E-102	31.6	11.1	17.3

Rsa1.0_00819.1.g19937.t1	ref|NP_189102.2| chloroplast processing peptidase [Arabidopsis thaliana] gi|160419231|sp|Q8H0W1.2|PLSP1_ARATH RecName: Full=Chloroplast processing peptidase; AltName: Full=Signal peptidase I-3; Flags: Precursor gi|51536582|gb|AAU05529.1| At1g05140 [Arabidopsis thaliana] gi|332643406|gb|AEE76927.1| chloroplast processing peptidase [Arabidopsis thaliana]	302	291	1.00E-122	96.4	79.5	83.1	chloroplast processing peptidase	gbpln	Arabidopsis thaliana	AT3G24590.1 | Symbols: PLSP1 | plastidic type i signal peptidase 1 | chr3:8970694-8972020 FORWARD LENGTH=291	302	291	1.00E-125	96.4	79.5	83.1
Rsa1.0_00819.1.g19938.t1	dbj|BAB02012.1| unnamed protein product [Arabidopsis thaliana]	300	306	1.00E-129	102.0	84.0	90.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G24600.1 | Symbols: | Late embryogenesis abundant protein, group 2 | chr3:8972195-8974867 REVERSE LENGTH=506	300	506	1.00E-106	168.7	69.0	74.7
Rsa1.0_00819.1.g19939.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	328	258	2.00E-46	78.7	34.1	43.0	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	328	302	1.00E-41	92.1	31.4	43.0
Rsa1.0_00819.1.g19940.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	358	442	1.00E-95	123.5	45.8	50.0	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	358	343	6.00E-26	95.8	15.6	19.6
Rsa1.0_00819.1.g19941.t1	ref|XP_002868541.1| hypothetical protein ARALYDRAFT_915930 [Arabidopsis lyrata subsp. lyrata] gi|297314377|gb|EFH44800.1| hypothetical protein ARALYDRAFT_915930 [Arabidopsis lyrata subsp. lyrata]	229	167	9.00E-28	72.9	27.1	32.3	hypothetical protein ARALYDRAFT_915930	gbpln	Arabidopsis lyrata	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	229	256	3.00E-11	111.8	18.8	27.9
Rsa1.0_00819.1.g19942.t1	gb|EOA31239.1| hypothetical protein CARUB_v10014410mg [Capsella rubella]	226	264	1.00E-115	116.8	89.4	91.6	hypothetical protein CARUB_v10014410mg	gbpln	Capsella rubella	AT2G20120.1 | Symbols: COV1 | Protein of unknown function (DUF502) | chr2:8687568-8689321 REVERSE LENGTH=268	226	268	1.00E-105	118.6	80.1	85.8
Rsa1.0_00819.1.g19943.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00819.1.g19944.t1	ref|XP_002885662.1| hypothetical protein ARALYDRAFT_319167 [Arabidopsis lyrata subsp. lyrata] gi|297331502|gb|EFH61921.1| hypothetical protein ARALYDRAFT_319167 [Arabidopsis lyrata subsp. lyrata]	521	524	0	100.6	92.1	95.6	hypothetical protein ARALYDRAFT_319167	gbpln	Arabidopsis lyrata	AT3G24620.1 | Symbols: ATROPGEF8, ROPGEF8 | RHO guanyl-nucleotide exchange factor 8 | chr3:8980695-8982793 REVERSE LENGTH=523	521	523	0	100.4	91.9	95.4
Rsa1.0_00820.1.g19945.t1	ref|XP_002883416.1| hypothetical protein ARALYDRAFT_319045 [Arabidopsis lyrata subsp. lyrata] gi|297329256|gb|EFH59675.1| hypothetical protein ARALYDRAFT_319045 [Arabidopsis lyrata subsp. lyrata]	364	342	3.00E-62	94.0	46.2	59.3	hypothetical protein ARALYDRAFT_319045	gbpln	Arabidopsis lyrata	AT3G23260.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8313334-8314422 FORWARD LENGTH=362	364	362	3.00E-61	99.5	46.4	58.8
Rsa1.0_00820.1.g19946.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1742	1529	0	87.8	41.5	58.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1742	746	1.00E-112	42.8	11.8	15.4

Rsa1.0_00820.1.g19947.t1	ref|NP_567603.1| cysteine-rich repeat secretory protein 54 [Arabidopsis thaliana] gi|18415520|ref|NP_567604.1| cysteine-rich repeat secretory protein 53 [Arabidopsis thaliana] gi|18415540|ref|NP_567613.1| cysteine-rich repeat secretory protein 44 [Arabidopsis thaliana] gi|5262176|emb|CAB45819.1| putative protein [Arabidopsis thaliana] gi|5262177|emb|CAB45820.1| putative protein [Arabidopsis thaliana] gi|5262178|emb|CAB45821.1| putative protein [Arabidopsis thaliana] gi|5262179|emb|CAB45822.1| putative protein [Arabidopsis thaliana] gi|5262180|emb|CAB45823.1| putative protein [Arabidopsis thaliana] gi|5262181|emb|CAB45824.1| putative protein [Arabidopsis thaliana] gi|5262182|emb|CAB45825.1| putative protein [Arabidopsis thaliana] gi|5262183|emb|CAB45826.1| putative protein [Arabidopsis thaliana] gi|5262184|emb|CAB45827.1| putative protein [Arabidopsis thaliana] gi|5262185|emb|CAB45828.1| putative protein [Arabidopsis thaliana] gi|5262186|emb|CAB45829.1| putative protein [Arabidopsis thaliana] gi|5262187|emb|CAB45830.1| putative protein [Arabidopsis thaliana] gi|7268849|emb|CAB79053.1| putative protein [Arabidopsis thaliana]	100	468	3.00E-17	468.0	46.0	59.0	cysteine-rich repeat secretory protein 54	gbpln	Arabidopsis thaliana	AT4G20530.1 | Symbols: | Protein with domains of unknown function (DUF26 and DUF1204) | chr4:11048627-11050975 FORWARD LENGTH=468	100	468	5.00E-20	468.0	46.0	59.0
Rsa1.0_00820.1.g19948.t2	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	321	1223	9.00E-69	381.0	50.2	68.5	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	321	746	6.00E-38	232.4	29.9	42.1
Rsa1.0_00820.1.g19949.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00820.1.g19950.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00820.1.g19951.t1	ref|NP_188957.2| uncharacterized protein [Arabidopsis thaliana] gi|7939524|dbj|BAA95727.1| unnamed protein product [Arabidopsis thaliana] gi|332643204|gb|AEE76725.1| uncharacterized protein AT3G23160 [Arabidopsis thaliana]	492	531	0	107.9	88.6	94.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G23160.1 | Symbols: | Protein of unknown function (DUF668) | chr3:8260059-8261654 REVERSE LENGTH=531	492	531	0	107.9	88.6	94.7
Rsa1.0_00820.1.g19952.t1	gb|AAM67024.1| unknown [Arabidopsis thaliana]	129	107	6.00E-31	82.9	61.2	66.7	unknown	gbpln	Arabidopsis thaliana	AT3G23170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G14450.1); Has 74 Blast hits to 74 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:8268265-8268588 REVERSE LENGTH=107	129	107	8.00E-33	82.9	60.5	65.9
Rsa1.0_00820.1.g19953.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00820.1.g19954.t1	gb|EOA32854.1| hypothetical protein CARUB_v10016168mg [Capsella rubella]	177	180	5.00E-82	101.7	84.7	93.2	hypothetical protein CARUB_v10016168mg	gbpln	Capsella rubella	AT3G23175.1 | Symbols: | HR-like lesion-inducing protein-related | chr3:8274202-8274973 REVERSE LENGTH=169	177	169	2.00E-76	95.5	74.0	86.4
Rsa1.0_00820.1.g19955.t1	ref|NP_188959.3| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana] gi|7939528|dbj|BAA95731.1| HR-like lesion-inducing protein [Arabidopsis thaliana] gi|332643211|gb|AEE76732.1| HR-like lesion-inducing protein-like protein [Arabidopsis thaliana]	217	217	1.00E-100	100.0	79.3	88.9	HR-like lesion-inducing protein-like protein	gbpln	Arabidopsis thaliana	AT3G23180.1 | Symbols: | HR-like lesion-inducing protein-related | chr3:8277131-8278396 FORWARD LENGTH=217	217	217	1.00E-102	100.0	79.3	88.9
Rsa1.0_00820.1.g19956.t1	gb|EOA12359.1| hypothetical protein CARUB_v10016511mg [Capsella rubella]	348	356	4.00E-65	102.3	38.5	48.0	hypothetical protein CARUB_v10016511mg	gbpln	Capsella rubella	AT4G10190.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:6350928-6352031 FORWARD LENGTH=367	348	367	2.00E-52	105.5	33.6	41.4
Rsa1.0_00820.1.g19957.t1	ref|XP_002883411.1| hypothetical protein ARALYDRAFT_898831 [Arabidopsis lyrata subsp. lyrata] gi|297329251|gb|EFH59670.1| hypothetical protein ARALYDRAFT_898831 [Arabidopsis lyrata subsp. lyrata]	154	152	6.00E-68	98.7	84.4	92.9	hypothetical protein ARALYDRAFT_898831	gbpln	Arabidopsis lyrata	AT3G23200.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr3:8281659-8282603 FORWARD LENGTH=152	154	152	3.00E-70	98.7	83.8	92.9

Rsa1.0_00820.1.g19958.t1	gb|AAM10939.1|AF488573_1 putative bHLH transcription factor [Arabidopsis thaliana]	214	291	4.00E−75	136.0	71.5	77.1	putative bHLH transcription factor	gbpln	Arabidopsis thaliana	AT3G23210.1 | Symbols: bHLH34 | basic helix−loop−helix (bHLH) DNA−binding superfamily protein | chr3:8283255−8284915 REVERSE LENGTH=320	214	320	2.00E−77	149.5	71.5	77.1
Rsa1.0_00821.1.g19959.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00821.1.g19960.t1	gb|EMT31378.1| Zinc finger CCCH domain−containing protein 30 [Aegilops tauschii]	110	671	4.00E−60	610.0	92.7	94.5	Zinc finger CCCH domain−containing protein 30	gbpln	Aegilops tauschii	AT2G30000.1 | Symbols: | PHF5−like protein | chr2:12804042−12804374 REVERSE LENGTH=110	110	110	3.00E−59	100.0	99.1	100.0
Rsa1.0_00821.1.g19961.t1	ref|NP_172196.1| putative protein phosphatase 2C 2 [Arabidopsis thaliana] gi|75303253|sp|Q8RX37.1|P2C02_ARATH RecName: Full=Probable protein phosphatase 2C 2; Short=AtPP2C02; AltName: Full=Protein phosphatase AP2C2 gi|20258780|gb|AAM13912.1| putative protein phosphatase 2C [Arabidopsis thaliana] gi|332189963|gb|AEE28084.1| putative protein phosphatase 2C 2 [Arabidopsis thaliana] gi|333891315|gb|AEG21042.1| PP2C−type phosphatase AP2C2 [Arabidopsis thaliana]	380	380	1.00E−155	100.0	76.8	85.0	putative protein phosphatase 2C 2	gbpln	Arabidopsis thaliana	AT1G07160.1 | Symbols: | Protein phosphatase 2C family protein | chr1:2198155−2199678 REVERSE LENGTH=380	380	380	1.00E−158	100.0	76.8	85.0
Rsa1.0_00821.1.g19962.t1	gb|EOA40139.1| hypothetical protein CARUB_v10008850mg [Capsella rubella]	398	523	1.00E−152	131.4	70.6	80.7	hypothetical protein CARUB_v10008850mg	gbpln	Capsella rubella	AT1G07150.2 | Symbols: MAPKKK13 | mitogen−activated protein kinase kinase kinase 13 | chr1:2193983−2195736 REVERSE LENGTH=493	398	493	1.00E−153	123.9	69.3	79.1
Rsa1.0_00821.1.g19963.t1	ref|XP_002887117.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332958|gb|EFH63376.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	470	479	1.00E−100	101.9	46.8	62.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G67390.1 | Symbols: | F−box family protein | chr1:25244690−25247139 FORWARD LENGTH=479	470	479	1.00E−101	101.9	45.7	62.1
Rsa1.0_00821.1.g19964.t1	gb|ABB97039.1| unknown [Brassica rapa]	163	225	2.00E−70	138.0	79.1	80.4	unknown	gbpln	Brassica rapa	AT1G07140.1 | Symbols: SIRANBP | Pleckstrin homology (PH) domain superfamily protein | chr1:2192360−2193688 REVERSE LENGTH=228	163	228	5.00E−71	139.9	77.3	79.1
Rsa1.0_00821.1.g19965.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_00821.1.g19966.t1	ref|XP_002892382.1| hypothetical protein ARALYDRAFT_470734 [Arabidopsis lyrata subsp. lyrata] gi|297338224|gb|EFH68641.1| hypothetical protein ARALYDRAFT_470734 [Arabidopsis lyrata subsp. lyrata]	172	145	8.00E−16	84.3	23.8	29.7	hypothetical protein ARALYDRAFT_470734	gbpln	Arabidopsis lyrata	AT1G07135.1 | Symbols: | glycine−rich protein | chr1:2190157−2190624 REVERSE LENGTH=155	172	155	5.00E−13	90.1	24.4	30.2
Rsa1.0_00821.1.g19967.t1	ref|XP_002892380.1| hypothetical protein ARALYDRAFT_470732 [Arabidopsis lyrata subsp. lyrata] gi|297338222|gb|EFH68639.1| hypothetical protein ARALYDRAFT_470732 [Arabidopsis lyrata subsp. lyrata]	784	743	0	94.8	84.9	89.3	hypothetical protein ARALYDRAFT_470732	gbpln	Arabidopsis lyrata	AT1G07110.1 | Symbols: F2KP, ATF2KP, FKFBP | fructose−2,6−bisphosphatase | chr1:2178363−2183980 REVERSE LENGTH=744	784	744	0	94.9	84.7	89.2
Rsa1.0_00821.1.g19968.t1	ref|NP_563780.1| uncharacterized protein [Arabidopsis thaliana] gi|8954037|gb|AAF82211.1|AC067971_19 Strong similarity to an unknown protein At2g31160 gi|3746060 from Arabidopsis thaliana BAC F7F1 gb|AC005311. EST gb|AI998165 comes from this gene [Arabidopsis thaliana] gi|21555695|gb|AAM63916.1| unknown [Arabidopsis thaliana] gi|28392914|gb|AAO41893.1| unknown protein [Arabidopsis thaliana] gi|56236136|gb|AAV84524.1| At1g07090 [Arabidopsis thaliana] gi|88193786|gb|ABD42982.1| At1g07090 [Arabidopsis thaliana] gi|332189955|gb|AEE28076.1| uncharacterized protein AT1G07090 [Arabidopsis thaliana]	198	196	3.00E−90	99.0	85.9	90.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G07090.1 | Symbols: LSH6 | Protein of unknown function (DUF640) | chr1:2174202−2174792 REVERSE LENGTH=196	198	196	9.00E−93	99.0	85.9	90.4
Rsa1.0_00821.1.g19969.t1	ref|NP_563779.1| GILT domain−containing protein [Arabidopsis thaliana] gi|15146334|gb|AAK83650.1| At1g07080/F10K1_15 [Arabidopsis thaliana] gi|15809756|gb|AAL06806.1| At1g07080/F10K1_15 [Arabidopsis thaliana] gi|332189954|gb|AEE28075.1| GILT domain−containing protein [Arabidopsis thaliana]	262	265	1.00E−119	101.1	80.5	87.8	GILT domain−containing protein	gbpln	Arabidopsis thaliana	AT1G07080.1 | Symbols: | Thioredoxin superfamily protein | chr1:2170069−2171861 FORWARD LENGTH=265	262	265	1.00E−121	101.1	80.5	87.8

Rsa1.0_00821.1.g19970.t1	ref|XP_002892378.1| F10K1.23 [Arabidopsis lyrata subsp. lyrata] gi|297338220|gb|EFH68637.1| F10K1.23 [Arabidopsis lyrata subsp. lyrata]	253	251	1.00E-109	99.2	78.7	87.0	F10K1.23	gbpln	Arabidopsis lyrata	AT1G07060.1 | Symbols: | unknown protein; Has 30 Blast hits to 30 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2167138-2168397 REVERSE LENGTH=233	253	233	7.00E-80	92.1	58.5	65.2
Rsa1.0_00821.1.g19971.t2	ref|XP_002892377.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338219|gb|EFH68636.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	211	194	3.00E-69	91.9	67.8	77.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G07050.1 | Symbols: | CCT motif family protein | chr1:2164327-2165133 REVERSE LENGTH=195	211	195	1.00E-66	92.4	65.4	77.7
Rsa1.0_00821.1.g19972.t1	ref|XP_002892376.1| hypothetical protein ARALYDRAFT_887913 [Arabidopsis lyrata subsp. lyrata] gi|297338218|gb|EFH68635.1| hypothetical protein ARALYDRAFT_887913 [Arabidopsis lyrata subsp. lyrata]	370	371	1.00E-178	100.3	85.7	89.5	hypothetical protein ARALYDRAFT_887913	gbpln	Arabidopsis lyrata	AT1G07040.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27030.1); Has 540 Blast hits to 538 proteins in 187 species: Archae - 0; Bacteria - 333; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 140 (source: NCBI BLink). | chr1:2161225-2163035 REVERSE LENGTH=371	370	371	1.00E-176	100.3	85.1	90.0
Rsa1.0_00821.1.g19973.t1	ref|XP_002892375.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297338217|gb|EFH68634.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	330	326	1.00E-165	98.8	89.1	94.2	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT1G07030.1 | Symbols: | Mitochondrial substrate carrier family protein | chr1:2158631-2160524 REVERSE LENGTH=326	330	326	1.00E-165	98.8	87.9	93.3
Rsa1.0_00821.1.g19974.t1	gb|AFY13519.1| cyclophilin 1 [Aeschynomene evenia] gi|426207762|gb|AFY13520.1| cyclophilin 1 [Aeschynomene evenia] gi|426207764|gb|AFY13521.1| cyclophilin 1 [Aeschynomene evenia] gi|426207766|gb|AFY13522.1| cyclophilin 1 [Aeschynomene evenia] gi|426207768|gb|AFY13523.1| cyclophilin 1 [Aeschynomene evenia] gi|426207770|gb|AFY13524.1| cyclophilin 1 [Aeschynomene evenia]	282	172	1.00E-43	61.0	33.3	40.1	cyclophilin 1	gbpln	Aeschynomene evenia	AT2G16600.1 | Symbols: ROC3 | rotamase CYP 3 | chr2:7200862-7201383 FORWARD LENGTH=173	282	173	7.00E-46	61.3	33.0	40.4
Rsa1.0_00821.1.g19975.t1	ref|XP_002889629.1| hypothetical protein ARALYDRAFT_470724 [Arabidopsis lyrata subsp. lyrata] gi|297335471|gb|EFH65888.1| hypothetical protein ARALYDRAFT_470724 [Arabidopsis lyrata subsp. lyrata]	371	392	0	105.7	87.6	94.9	hypothetical protein ARALYDRAFT_470724	gbpln	Arabidopsis lyrata	AT1G07010.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr1:2152949-2154968 FORWARD LENGTH=389	371	389	0	104.9	89.2	95.1
Rsa1.0_00821.1.g19976.t1	ref|XP_002892371.1| ATEXO70B2 [Arabidopsis lyrata subsp. lyrata] gi|297338213|gb|EFH68630.1| ATEXO70B2 [Arabidopsis lyrata subsp. lyrata]	603	599	0	99.3	86.9	92.9	ATEXO70B2	gbpln	Arabidopsis lyrata	AT1G07000.1 | Symbols: ATEXO70B2, EXO70B2 | exocyst subunit exo70 family protein B2 | chr1:2150398-2152305 REVERSE LENGTH=599	603	599	0	99.3	85.4	92.2
Rsa1.0_00822.1.g19977.t1	gb|ADZ98867.1| MYB domain protein 12 [Brassica rapa subsp. rapa]	377	381	1.00E-148	101.1	76.1	83.6	MYB domain protein 12	gbpln	Brassica rapa	AT2G47460.1 | Symbols: MYB12, ATMYB12, PFG1 | myb domain protein 12 | chr2:19476438-19479242 FORWARD LENGTH=371	377	371	1.00E-142	98.4	74.3	82.0
Rsa1.0_00822.1.g19978.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00822.1.g19979.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00822.1.g19980.t1	gb|ACG60672.1| unknown protein [Brassica oleracea var. alboglabra]	607	288	1.00E-34	47.4	14.8	20.8	unknown protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00822.1.g19981.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00822.1.g19982.t1	ref|XP_002880305.1| hypothetical protein ARALYDRAFT_904222 [Arabidopsis lyrata subsp. lyrata] gi|297326144|gb|EFH56564.1| hypothetical protein ARALYDRAFT_904222 [Arabidopsis lyrata subsp. lyrata]	362	361	0	99.7	93.6	96.1	hypothetical protein ARALYDRAFT_904222	gbpln	Arabidopsis lyrata	AT2G47470.1 | Symbols: ATPDIL2-1, UNE5, MEE30, PDI11, ATPDI11 | thioredoxin family protein | chr2:19481503-19483683 FORWARD LENGTH=361	362	361	0	99.7	92.8	95.3
Rsa1.0_00822.1.g19983.t1	ref|XP_002891574.1| SNF2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297337416|gb|EFH67833.1| SNF2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	92	980	2.00E-38	1065.2	82.6	92.4	SNF2 domain-containing protein	gbpln	Arabidopsis lyrata	AT1G50410.1 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related | chr1:18672828-18677365 FORWARD LENGTH=981	92	981	2.00E-40	1066.3	81.5	92.4

Rsa1.0_00822.1.g19984.t1	ref|NP_850547.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332641290|gb|AEE74811.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	103	341	6.00E-11	331.1	30.1	35.9	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G09770.2 | Symbols: | RING/U-box superfamily protein | chr3:2996629-2997835 REVERSE LENGTH=341	103	341	1.00E-13	331.1	30.1	35.9
Rsa1.0_00822.1.g19985.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00822.1.g19986.t2	gb|EOA27436.1| hypothetical protein CARUB_v10023573mg [Capsella rubella]	256	338	1.00E-140	132.0	96.5	98.8	hypothetical protein CARUB_v10023573mg	gbpln	Capsella rubella	AT3G62870.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr3:23242862-23244273 REVERSE LENGTH=256	256	256	1.00E-142	100.0	96.5	98.4
Rsa1.0_00822.1.g19987.t1	ref|XP_002880821.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297326660|gb|EFH57080.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	328	318	1.00E-102	97.0	58.2	66.8	kinase family protein	gbpln	Arabidopsis lyrata	AT2G41920.1 | Symbols: | Protein kinase superfamily protein | chr2:17499448-17500404 FORWARD LENGTH=318	328	318	2.00E-97	97.0	54.6	66.2
Rsa1.0_00822.1.g19988.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00823.1.g19989.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	319	1142	5.00E-60	358.0	39.2	51.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	319	292	6.00E-29	91.5	27.0	43.9
Rsa1.0_00823.1.g19990.t1	ref|NP_177231.2| protein kinase domain-containing protein [Arabidopsis thaliana] gi|193870477|gb|ACF22895.1| At1g70740 [Arabidopsis thaliana] gi|332196987|gb|AEE35108.1| protein kinase domain-containing protein [Arabidopsis thaliana]	418	425	0	101.7	86.4	91.9	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G70740.1 | Symbols: | Protein kinase superfamily protein | chr1:26673847-26675687 REVERSE LENGTH=425	418	425	0	101.7	86.4	91.9
Rsa1.0_00823.1.g19991.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00823.1.g19992.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1339	1715	0	128.1	31.9	44.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	1339	336	5.00E-87	25.1	10.9	13.5
Rsa1.0_00823.1.g19993.t1	gb|AAM63352.1| unknown [Arabidopsis thaliana]	207	200	1.00E-76	96.6	72.5	83.1	unknown	gbpln	Arabidopsis thaliana	AT1G70720.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:26666427-26667029 FORWARD LENGTH=200	207	200	1.00E-73	96.6	72.5	83.1
Rsa1.0_00823.1.g19994.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00823.1.g19995.t1	ref|NP_177227.5| protein TIFY 7 [Arabidopsis thaliana] gi|342187044|sp|Q8W4J8.2|TIF7_ARATH RecName: Full=Protein TIFY 7; AltName: Full=Jasmonate ZIM domain-containing protein 9 gi|332196980|gb|AEE35101.1| protein TIFY 7 [Arabidopsis thaliana]	277	267	1.00E-100	96.4	73.6	79.8	protein TIFY 7	gbpln	Arabidopsis thaliana	AT1G70700.1 | Symbols: JAZ9, TIFY7 | TIFY domain/Divergent CCT motif family protein | chr1:26654951-26656804 FORWARD LENGTH=267	277	267	1.00E-103	96.4	73.6	79.8
Rsa1.0_00823.1.g19996.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00823.1.g19997.t1	ref|XP_002887324.1| hypothetical protein ARALYDRAFT_476197 [Arabidopsis lyrata subsp. lyrata] gi|297333165|gb|EFH63583.1| hypothetical protein ARALYDRAFT_476197 [Arabidopsis lyrata subsp. lyrata]	262	300	6.00E-96	114.5	66.4	77.1	hypothetical protein ARALYDRAFT_476197	gbpln	Arabidopsis lyrata	AT1G70690.1 | Symbols: HWI1, PDLP5 | Receptor-like protein kinase-related family protein | chr1:26652099-26653381 FORWARD LENGTH=299	262	299	9.00E-97	114.1	65.3	77.5
Rsa1.0_00823.1.g19998.t1	ref|XP_002887322.1| hypothetical protein ARALYDRAFT_894884 [Arabidopsis lyrata subsp. lyrata] gi|297333163|gb|EFH63581.1| hypothetical protein ARALYDRAFT_894884 [Arabidopsis lyrata subsp. lyrata]	189	195	2.00E-91	103.2	85.2	91.5	hypothetical protein ARALYDRAFT_894884	gbpln	Arabidopsis lyrata	AT1G70670.1 | Symbols: | Caleosin-related family protein | chr1:26644830-26645970 FORWARD LENGTH=195	189	195	1.00E-93	103.2	84.1	91.5
Rsa1.0_00823.1.g19999.t1	gb|AAZ67609.1| 80A08_24 [Brassica rapa subsp. pekinensis]	207	475	3.00E-26	229.5	37.2	40.6	80A08_24	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00823.1.g20000.t1	ref|XP_002887321.1| hypothetical protein ARALYDRAFT_476195 [Arabidopsis lyrata subsp. lyrata] gi|297333162|gb|EFH63580.1| hypothetical protein ARALYDRAFT_476195 [Arabidopsis lyrata subsp. lyrata]	177	159	5.00E-73	89.8	77.4	81.9	hypothetical protein ARALYDRAFT_476195	gbpln	Arabidopsis lyrata	AT1G70660.1 | Symbols: MMZ2, UEV1B | MMS ZWEI homologue 2 | chr1:26640755-26641949 FORWARD LENGTH=159	177	159	3.00E-74	89.8	75.7	81.9

Rsa1.0_00824.1.g20001.t1	gb|AAD30632.1|AC006085_5 Hypothetical protein [Arabidopsis thaliana]	1194	1295	1.00E-101	108.5	20.4	27.8	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20002.t2	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	805	1864	1.00E-127	231.6	27.7	33.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	ATMG00750.1 | Symbols: ORF119 | GAG/POL/ENV polyprotein | chrM:220830-221189 FORWARD LENGTH=119	805	119	9.00E-18	14.8	5.0	5.5
Rsa1.0_00824.1.g20003.t1	ref|NP_974372.1| basic helix-loop-helix (bHLH) DNA-binding family protein [Arabidopsis thaliana] gi|9294226|dbj|BAB02128.1| DNA-binding protein-like [Arabidopsis thaliana] gi|88900306|gb|ABD57465.1| At3g28857 [Arabidopsis thaliana] gi|332643976|gb|AEE77497.1| basic helix-loop-helix (bHLH) DNA-binding family protein [Arabidopsis thaliana]	92	92	1.00E-35	100.0	82.6	94.6	basic helix-loop-helix (bHLH) DNA-binding family protein	gbpln	Arabidopsis thaliana	AT3G28857.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding family protein | chr3:10855781-10856313 REVERSE LENGTH=92	92	92	2.00E-38	100.0	82.6	94.6
Rsa1.0_00824.1.g20004.t4	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	1563	1557	0	99.6	42.3	59.1	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1563	575	5.00E-76	36.8	11.0	18.0
Rsa1.0_00824.1.g20005.t1	gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	96	1787	1.00E-25	1861.5	56.3	76.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20006.t2	gb|AAD20646.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	692	1040	5.00E-57	150.3	16.5	19.8	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20007.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20008.t1	ref|XP_002527588.1| hypothetical protein RCOM_1568080 [Ricinus communis] gi|223533034|gb|EEF34796.1| hypothetical protein RCOM_1568080 [Ricinus communis]	295	136	2.00E-17	46.1	14.2	19.7	hypothetical protein RCOM_1568080	gbpln	Ricinus communis	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20009.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20010.t1	ref|XP_002870781.1| hypothetical protein ARALYDRAFT_330553 [Arabidopsis lyrata subsp. lyrata] gi|297316617|gb|EFH47040.1| hypothetical protein ARALYDRAFT_330553 [Arabidopsis lyrata subsp. lyrata]	412	412	0	100.0	89.8	93.4	hypothetical protein ARALYDRAFT_330553	gbpln	Arabidopsis lyrata	AT5G39400.1 | Symbols: ATPTEN1, PTEN1 | Calcium/lipid-binding (CaLB) phosphatase | chr5:15766251-15767922 FORWARD LENGTH=412	412	412	0	100.0	89.6	93.0
Rsa1.0_00824.1.g20011.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20012.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20013.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20014.t1	gb|EOA16478.1| hypothetical protein CARUB_v10004632mg, partial [Capsella rubella]	480	502	0	104.6	98.3	99.4	hypothetical protein CARUB_v10004632mg, partial	gbpln	Capsella rubella	AT5G39320.1 | Symbols: | UDP-glucose 6-dehydrogenase family protein | chr5:15743254-15744696 FORWARD LENGTH=480	480	480	0	100.0	97.3	98.8
Rsa1.0_00824.1.g20015.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	192	1142	1.00E-55	594.8	55.2	66.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	192	626	3.00E-11	326.0	15.6	25.0
Rsa1.0_00824.1.g20016.t1	dbj|BAB01350.1| Mutator-like transposase [Arabidopsis thaliana]	547	811	3.00E-92	148.3	38.8	50.6	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	547	719	8.00E-19	131.4	13.3	20.3
Rsa1.0_00824.1.g20017.t4	gb|AAB61080.1| contains similarity to T. cruzi 3' end fragment (PID:g161956) [Arabidopsis thaliana]	870	707	6.00E-34	81.3	12.4	17.2	contains similarity to T. cruzi 3' end fragment (PID:g161956)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20018.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20019.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00824.1.g20020.t6	gb|AAD15329.1| putative transposon protein [Arabidopsis thaliana] gi|7270696|emb|CAB77858.1| putative transposon protein [Arabidopsis thaliana]	756	696	1.00E-178	92.1	43.5	52.6	putative transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00825.1.g20021.t1	gb|AAM62702.1| unknown [Arabidopsis thaliana]	458	459	1.00E-133	100.2	57.0	71.0	unknown	gbpln	Arabidopsis thaliana	AT5G27750.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:9828430-9829981 FORWARD LENGTH=459	458	459	1.00E-135	100.2	56.6	70.7
Rsa1.0_00825.1.g20022.t1	ref|XP_002874348.1| hypothetical protein ARALYDRAFT_489554 [Arabidopsis lyrata subsp. lyrata] gi|297320185|gb|EFH50607.1| hypothetical protein ARALYDRAFT_489554 [Arabidopsis lyrata subsp. lyrata]	456	457	1.00E-128	100.2	57.7	70.6	hypothetical protein ARALYDRAFT_489554	gbpln	Arabidopsis lyrata	AT5G27750.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:9828430-9829981 FORWARD LENGTH=459	456	459	1.00E-128	100.7	55.5	69.5

Rsa1.0_00825.1.g20023.t1	ref|XP_002874348.1| hypothetical protein ARALYDRAFT_489554 [Arabidopsis lyrata subsp. lyrata] gi|297320185|gb|EFH50607.1| hypothetical protein ARALYDRAFT_489554 [Arabidopsis lyrata subsp. lyrata]	453	457	1.00E-129	100.9	59.2	71.3	hypothetical protein ARALYDRAFT_489554	gbpln	Arabidopsis lyrata	AT5G27750.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:9828430-9829981 FORWARD LENGTH=459	453	459	1.00E-129	101.3	57.8	71.1
Rsa1.0_00825.1.g20024.t1	ref|XP_002892774.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338616|gb|EFH69033.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	885	883	0	99.8	59.3	72.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G13800.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4731056-4733707 REVERSE LENGTH=883	885	883	0	99.8	58.2	72.3
Rsa1.0_00825.1.g20025.t1	ref|NP_172837.1| alpha/beta-hydrolase-like protein [Arabidopsis thaliana] gi|46518397|gb|AAS99680.1| At1g13820 [Arabidopsis thaliana] gi|48310456|gb|AAT41824.1| At1g13820 [Arabidopsis thaliana] gi|110738455|dbj|BAF01153.1| hypothetical protein [Arabidopsis thaliana] gi|332190951|gb|AEE29072.1| alpha/beta-hydrolase-like protein [Arabidopsis thaliana]	340	339	1.00E-177	99.7	87.9	92.6	alpha/beta-hydrolase-like protein	gbpln	Arabidopsis thaliana	AT1G13820.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:4735622-4737617 FORWARD LENGTH=339	340	339	1.00E-180	99.7	87.9	92.6
Rsa1.0_00825.1.g20026.t1	ref|XP_002892776.1| hypothetical protein ARALYDRAFT_471542 [Arabidopsis lyrata subsp. lyrata] gi|297338618|gb|EFH69035.1| hypothetical protein ARALYDRAFT_471542 [Arabidopsis lyrata subsp. lyrata]	189	199	5.00E-50	105.3	69.3	73.0	hypothetical protein ARALYDRAFT_471542	gbpln	Arabidopsis lyrata	AT1G13830.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr1:4739999-4740926 REVERSE LENGTH=197	189	197	1.00E-42	104.2	69.3	73.5
Rsa1.0_00825.1.g20027.t1	ref|NP_172843.1| putative inactive purple acid phosphatase 2 [Arabidopsis thaliana] gi|75264030|sp|Q9LMG7.1|PPA2_ARATH RecName: Full=Probable inactive purple acid phosphatase 2; Flags: Precursor gi|8778406|gb|AAF79414.1|AC068197_24 F16A14.11 [Arabidopsis thaliana] gi|332190960|gb|AEE29081.1| putative inactive purple acid phosphatase 2 [Arabidopsis thaliana]	680	656	0	96.5	75.6	86.5	putative inactive purple acid phosphatase 2	gbpln	Arabidopsis thaliana	AT1G13900.1 | Symbols: | Purple acid phosphatases superfamily protein | chr1:4753494-4755554 REVERSE LENGTH=656	680	656	0	96.5	75.6	86.5
Rsa1.0_00825.1.g20028.t1	ref|XP_002890028.1| remorin family protein [Arabidopsis lyrata subsp. lyrata] gi|297335870|gb|EFH66287.1| remorin family protein [Arabidopsis lyrata subsp. lyrata]	316	345	1.00E-107	109.2	78.5	86.4	remorin family protein	gbpln	Arabidopsis lyrata	AT1G13920.1 | Symbols: | Remorin family protein | chr1:4758188-4759754 FORWARD LENGTH=345	316	345	1.00E-104	109.2	76.3	84.5
Rsa1.0_00825.1.g20029.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00825.1.g20030.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00825.1.g20031.t1	ref|XP_002892784.1| hypothetical protein ARALYDRAFT_334698 [Arabidopsis lyrata subsp. lyrata] gi|297338626|gb|EFH69043.1| hypothetical protein ARALYDRAFT_334698 [Arabidopsis lyrata subsp. lyrata]	66	261	1.00E-14	395.5	63.6	78.8	hypothetical protein ARALYDRAFT_334698	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00825.1.g20032.t1	gb|EOA13293.1| hypothetical protein CARUB_v10026322mg [Capsella rubella]	146	478	2.00E-24	327.4	37.0	37.0	hypothetical protein CARUB_v10026322mg	gbpln	Capsella rubella	AT5G62790.1 | Symbols: DXR, PDE129 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase | chr5:25214358-25217292 REVERSE LENGTH=477	146	477	6.00E-27	326.7	37.0	37.0
Rsa1.0_00825.1.g20033.t1	ref|XP_002892784.1| hypothetical protein ARALYDRAFT_334698 [Arabidopsis lyrata subsp. lyrata] gi|297338626|gb|EFH69043.1| hypothetical protein ARALYDRAFT_334698 [Arabidopsis lyrata subsp. lyrata]	181	261	6.00E-31	144.2	40.9	59.7	hypothetical protein ARALYDRAFT_334698	gbpln	Arabidopsis lyrata	AT1G23201.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: GCK (InterPro:IPR012891); BEST Arabidopsis thaliana protein match is: GCK domain-containing protein (TAIR:AT5G02210.1); Has 106 Blast hits to 71 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 106; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:8230209-8230775 FORWARD LENGTH=188	181	188	5.00E-11	103.9	27.1	45.9
Rsa1.0_00825.1.g20034.t1	gb|ACI14399.1| WRKY4-1 transcription factor [Brassica napus]	483	475	0	98.3	84.1	87.2	WRKY4-1 transcription factor	gbpln	Brassica napus	AT1G13960.1 | Symbols: WRKY4 | WRKY DNA-binding protein 4 | chr1:4776622-4779043 FORWARD LENGTH=514	483	514	0	106.4	83.9	89.4

Rsa1.0_00825.1.g20035.t1	gb|EOA36877.1| hypothetical protein CARUB_v10008911mg [Capsella rubella]	503	504	0	100.2	92.2	96.0	hypothetical protein CARUB_v10008911mg	gbpln	Capsella rubella	AT1G13970.1 | Symbols: | Protein of unknown function (DUF1336) | chr1:4779742-4781882 REVERSE LENGTH=504	503	504	0	100.2	91.3	95.0
Rsa1.0_00825.1.g20036.t1	ref|XP_002890033.1| hypothetical protein ARALYDRAFT_471559 [Arabidopsis lyrata subsp. lyrata] gi|297335875|gb|EFH66292.1| hypothetical protein ARALYDRAFT_471559 [Arabidopsis lyrata subsp. lyrata]	1406	1454	0	103.4	95.3	98.1	hypothetical protein ARALYDRAFT_471559	gbpln	Arabidopsis lyrata	AT1G13980.2 | Symbols: GN | sec7 domain-containing protein | chr1:4789587-4794397 FORWARD LENGTH=1451	1406	1451	0	103.2	95.1	97.9
Rsa1.0_00825.1.g20037.t1	ref|NP_563935.1| uncharacterized protein [Arabidopsis thaliana] gi|14326541|gb|AAK60315.1|AF385724_1 At1g13990/F16A14.28 [Arabidopsis thaliana] gi|21617995|gb|AAM67045.1| unknown [Arabidopsis thaliana] gi|22137314|gb|AAM91502.1| AT4g27310/M4I22_120 [Arabidopsis thaliana] gi|332190973|gb|AEE29094.1| uncharacterized protein AT1G13990 [Arabidopsis thaliana]	278	277	1.00E-117	99.6	87.4	89.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G13990.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3110 (InterPro:IPR021503); Has 25 Blast hits to 25 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4794810-4796476 FORWARD LENGTH=277	278	277	1.00E-120	99.6	87.4	89.2
Rsa1.0_00825.1.g20038.t1	ref|NP_172853.1| VH1-interacting kinase [Arabidopsis thaliana] gi|5080776|gb|AAD39286.1|AC007576_9 Similar to protein kinases [Arabidopsis thaliana] gi|111074450|gb|ABH04598.1| At1g14000 [Arabidopsis thaliana] gi|332190976|gb|AEE29097.1| VH1-interacting kinase [Arabidopsis thaliana]	434	438	0	100.9	96.5	98.8	VH1-interacting kinase	gbpln	Arabidopsis thaliana	AT1G14000.1 | Symbols: VIK | VH1-interacting kinase | chr1:4797606-4800043 FORWARD LENGTH=438	434	438	0	100.9	96.5	98.8
Rsa1.0_00825.1.g20039.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00825.1.g20040.t1	gb|AAF79407.1|AC068197_17 F16A14.26 [Arabidopsis thaliana]	222	841	9.00E-89	378.8	78.8	85.1	F16A14.26	gbpln	Arabidopsis thaliana	AT1G14040.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr1:4810488-4814543 FORWARD LENGTH=813	222	813	3.00E-91	366.2	78.8	85.1
Rsa1.0_00826.1.g20041.t1	dbj|BAH19457.1| AT3G18140 [Arabidopsis thaliana]	82	305	1.00E-31	372.0	78.0	86.6	AT3G18140	gbpln	Arabidopsis thaliana	AT3G18140.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:6212743-6214567 REVERSE LENGTH=305	82	305	2.00E-34	372.0	78.0	86.6
Rsa1.0_00826.1.g20042.t1	ref|XP_002880413.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297326252|gb|EFH56672.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	1276	1276	0	100.0	90.8	95.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G22010.1 | Symbols: RKP | related to KPC1 | chr2:9363946-9368828 REVERSE LENGTH=1280	1276	1280	0	100.3	90.1	94.7
Rsa1.0_00826.1.g20043.t1	gb|EOA28183.1| hypothetical protein CARUB_v10024374mg [Capsella rubella]	95	107	8.00E-20	112.6	72.6	80.0	hypothetical protein CARUB_v10024374mg	gbpln	Capsella rubella	AT2G22000.1 | Symbols: PROPEP6 | elicitor peptide 6 precursor | chr2:9362408-9363002 FORWARD LENGTH=104	95	104	2.00E-14	109.5	60.0	65.3
Rsa1.0_00826.1.g20044.t1	gb|ABD64930.1| hypothetical protein 24.t00076 [Brassica oleracea]	442	407	3.00E-70	92.1	36.4	42.8	hypothetical protein 24.t00076	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00826.1.g20045.t1	gb|EOA18842.1| hypothetical protein CARUB_v10007464mg [Capsella rubella]	730	666	0	91.2	60.8	69.7	hypothetical protein CARUB_v10007464mg	gbpln	Capsella rubella	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	730	1262	0	172.9	57.7	66.4
Rsa1.0_00826.1.g20046.t1	ref|XP_002880432.1| lipid-associated family protein [Arabidopsis lyrata subsp. lyrata] gi|297326271|gb|EFH56691.1| lipid-associated family protein [Arabidopsis lyrata subsp. lyrata]	182	183	2.00E-92	100.5	89.6	95.6	lipid-associated family protein	gbpln	Arabidopsis lyrata	AT2G22170.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr2:9427010-9427742 REVERSE LENGTH=183	182	183	5.00E-94	100.5	88.5	94.5
Rsa1.0_00826.1.g20047.t2	gb|ABD65076.1| SLL3 ORF2 protein, putative [Brassica oleracea]	264	443	3.00E-38	167.8	34.1	44.3	SLL3 ORF2 protein, putative	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00826.1.g20048.t1	gb|EOA26319.1| hypothetical protein CARUB_v10025210mg [Capsella rubella]	288	292	1.00E-126	101.4	81.3	88.9	hypothetical protein CARUB_v10025210mg	gbpln	Capsella rubella	AT2G22180.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr2:9428969-9429844 FORWARD LENGTH=291	288	291	1.00E-125	101.0	83.7	88.5
Rsa1.0_00826.1.g20049.t1	ref|XP_002878603.1| hypothetical protein ARALYDRAFT_481086 [Arabidopsis lyrata subsp. lyrata] gi|297324442|gb|EFH54862.1| hypothetical protein ARALYDRAFT_481086 [Arabidopsis lyrata subsp. lyrata]	224	224	1.00E-101	100.0	87.9	92.0	hypothetical protein ARALYDRAFT_481086	gbpln	Arabidopsis lyrata	AT2G22230.1 | Symbols: | Thioesterase superfamily protein | chr2:9450042-9451427 FORWARD LENGTH=220	224	220	1.00E-101	98.2	83.5	87.9

Rsa1.0_00826.1.g20050.t1	sp|Q9S7U0.1|INO1_WHEAT RecName: Full=Inositol-3-phosphate synthase; Short=MIP synthase; AltName: Full=Myo-inositol 1-phosphate synthase; Short=IPS; Short=MI-1-P synthase gi|4589062|gb|AAD26330.1|AF120146_1 myo-inositol 1-phosphate synthase [Triticum aestivum] gi|4589064|gb|AAD26331.1|AF120147_1 myo-inositol 1-phosphate synthase [Triticum aestivum] gi|4589066|gb|AAD26332.1|AF120148_1 myo-inositol 1-phosphate synthase [Triticum aestivum]	510	510	0	100.0	99.0	99.2	RecName: Full=Inositol-3-phosphate synthase; Short=MIP synthase; AltName: Full=Myo-inositol 1-phosphate synthase; Short=IPS; Short=MI-1-P synthase gi|4589062|gb|AAD26330.1|AF120146_1 myo-inositol 1-phosphate synthase	gbpln	Triticum aestivum	AT2G22240.1 | Symbols: ATMIPS2, MIPS2, ATIPS2 | myo-inositol-1-phosphate synthase 2 | chr2:9451901-9453938 REVERSE LENGTH=510	510	510	0	100.0	96.7	98.8
Rsa1.0_00826.1.g20051.t1	gb|EOA24618.1| hypothetical protein CARUB_v10017886mg [Capsella rubella]	88	255	4.00E-23	289.8	63.6	80.7	hypothetical protein CARUB_v10017886mg	gbpln	Capsella rubella	AT3G57390.1 | Symbols: AGL18 | AGAMOUS-like 18 | chr3:21233910-21235735 FORWARD LENGTH=256	88	256	2.00E-25	290.9	60.2	77.3
Rsa1.0_00826.1.g20052.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00826.1.g20053.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00826.1.g20054.t1	ref|NP_565529.1| aspartate aminotransferase [Arabidopsis thaliana] gi|79322722|ref|NP_001031394.1| aspartate aminotransferase [Arabidopsis thaliana] gi|75206088|sp|Q9SIE1.2|PAT_ARATH RecName: Full=Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase; Short=AtAAT; Short=AtPPA-AT; AltName: Full=Protein MATERNAL EFFECT EMBRYO ARREST 17; Flags: Precursor gi|17381280|gb|AAL36058.1| At2g22250/T26C19.9 [Arabidopsis thaliana] gi|20198151|gb|AAD23617.2| putative aspartate aminotransferase [Arabidopsis thaliana] gi|21700793|gb|AAM70520.1| At2g22250/T26C19.9 [Arabidopsis thaliana] gi|305855255|gb|ADM67558.1| prephenate aminotransferase [Arabidopsis thaliana] gi|330252190|gb|AEC07284.1| aspartate aminotransferase [Arabidopsis thaliana] gi|330252191|gb|AEC07285.1| aspartate aminotransferase [Arabidopsis thaliana]	436	475	0	108.9	86.7	91.7	aspartate aminotransferase	gbpln	Arabidopsis thaliana	AT2G22250.3 | Symbols: ATAAT, AAT, MEE17 | aspartate aminotransferase | chr2:9458011-9460297 REVERSE LENGTH=475	436	475	0	108.9	86.7	91.7
Rsa1.0_00826.1.g20055.t1	gb|EOA28324.1| hypothetical protein CARUB_v10024523mg [Capsella rubella]	290	308	1.00E-124	106.2	80.0	87.6	hypothetical protein CARUB_v10024523mg	gbpln	Capsella rubella	AT2G22260.1 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr2:9461342-9463053 FORWARD LENGTH=314	290	314	1.00E-122	108.3	78.3	86.2
Rsa1.0_00826.1.g20056.t1	ref|XP_002878608.1| hypothetical protein ARALYDRAFT_481093 [Arabidopsis lyrata subsp. lyrata] gi|297324447|gb|EFH54867.1| hypothetical protein ARALYDRAFT_481093 [Arabidopsis lyrata subsp. lyrata]	950	1031	0	108.5	85.3	90.9	hypothetical protein ARALYDRAFT_481093	gbpln	Arabidopsis lyrata	AT2G22300.2 | Symbols: CAMTA3, SR1 | signal responsive 1 | chr2:9471599-9476472 FORWARD LENGTH=1032	950	1032	0	108.6	84.0	90.3
Rsa1.0_00827.1.g20057.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00827.1.g20058.t1	ref|XP_002875475.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297321313|gb|EFH51734.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	415	435	1.00E-156	104.8	75.2	86.5	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT3G28850.1 | Symbols: | Glutaredoxin family protein | chr3:10848669-10849955 FORWARD LENGTH=428	415	428	1.00E-153	103.1	74.5	84.1
Rsa1.0_00827.1.g20059.t1	ref|XP_002875474.1| hypothetical protein ARALYDRAFT_484654 [Arabidopsis lyrata subsp. lyrata] gi|297321312|gb|EFH51733.1| hypothetical protein ARALYDRAFT_484654 [Arabidopsis lyrata subsp. lyrata]	310	388	3.00E-60	125.2	40.3	52.3	hypothetical protein ARALYDRAFT_484654	gbpln	Arabidopsis lyrata	AT3G28840.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10838469-10839734 FORWARD LENGTH=391	310	391	6.00E-62	126.1	34.8	45.2
Rsa1.0_00827.1.g20060.t1	ref|XP_002875472.1| hypothetical protein ARALYDRAFT_484653 [Arabidopsis lyrata subsp. lyrata] gi|297321310|gb|EFH51731.1| hypothetical protein ARALYDRAFT_484653 [Arabidopsis lyrata subsp. lyrata]	661	518	4.00E-65	78.4	19.5	25.0	hypothetical protein ARALYDRAFT_484653	gbpln	Arabidopsis lyrata	AT3G28830.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10831233-10833020 FORWARD LENGTH=539	661	539	8.00E-66	81.5	17.9	22.5
Rsa1.0_00827.1.g20061.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00827.1.g20062.t1	dbj|BAB03175.1| unnamed protein product [Arabidopsis thaliana]	497	614	4.00E-34	123.5	13.3	16.5	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G28780.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10806131-10808369 REVERSE LENGTH=674	497	674	2.00E-35	135.6	13.5	16.7
Rsa1.0_00827.1.g20063.t2	ref|NP_189518.2| uncharacterized protein [Arabidopsis thaliana] gi|27754381|gb|AAO22639.1| unknown protein [Arabidopsis thaliana] gi|28973463|gb|AAO64056.1| unknown protein [Arabidopsis thaliana] gi|332643966|gb|AEE77487.1| uncharacterized protein AT3G28760 [Arabidopsis thaliana]	425	422	0	99.3	83.5	89.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G28760.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: 3-dehydroquinate synthase, prokaryotic-type (InterPro:IPR002812); Has 390 Blast hits to 390 proteins in 131 species: Archae - 144; Bacteria - 105; Metazoa - 0; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 87 (source: NCBI BLink). | chr3:10793126-10795304 REVERSE LENGTH=422	425	422	0	99.3	83.5	89.9
Rsa1.0_00827.1.g20064.t1	ref|XP_002877129.1| hypothetical protein ARALYDRAFT_484650 [Arabidopsis lyrata subsp. lyrata] gi|297322967|gb|EFH53388.1| hypothetical protein ARALYDRAFT_484650 [Arabidopsis lyrata subsp. lyrata]	493	346	8.00E-65	70.2	32.7	42.2	hypothetical protein ARALYDRAFT_484650	gbpln	Arabidopsis lyrata	AT3G28750.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr3:10791772-10792773 REVERSE LENGTH=333	493	333	1.00E-60	67.5	24.1	33.9
Rsa1.0_00827.1.g20065.t1	ref|XP_002877127.1| cytochrome P450 family protein [Arabidopsis lyrata subsp. lyrata] gi|297322965|gb|EFH53386.1| cytochrome P450 family protein [Arabidopsis lyrata subsp. lyrata]	472	501	0	106.1	77.8	84.7	cytochrome P450 family protein	gbpln	Arabidopsis lyrata	AT3G28740.1 | Symbols: CYP81D1 | Cytochrome P450 superfamily protein | chr3:10788764-10790552 REVERSE LENGTH=509	472	509	0	107.8	76.3	85.6
Rsa1.0_00827.1.g20066.t1	gb|EOA23621.1| hypothetical protein CARUB_v10016819mg [Capsella rubella]	642	647	0	100.8	88.3	92.8	hypothetical protein CARUB_v10016819mg	gbpln	Capsella rubella	AT3G28730.1 | Symbols: ATHMG, SSRP1, NFD, HMG | high mobility group | chr3:10784954-10788498 FORWARD LENGTH=646	642	646	0	100.6	87.7	93.0
Rsa1.0_00827.1.g20067.t1	ref|NP_189514.1| uncharacterized protein [Arabidopsis thaliana] gi|11994779|dbj|BAB03169.1| unnamed protein product [Arabidopsis thaliana] gi|332643962|gb|AEE77483.1| uncharacterized protein AT3G28720 [Arabidopsis thaliana]	976	687	0	70.4	51.6	56.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G28720.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G58100.1); Has 1610 Blast hits to 344 proteins in 85 species: Archae - 0; Bacteria - 567; Metazoa - 95; Fungi - 71; Plants - 145; Viruses - 0; Other Eukaryotes - 732 (source: NCBI BLink). | chr3:10782276-10784339 FORWARD LENGTH=687	976	687	0	70.4	51.6	56.4
Rsa1.0_00827.1.g20068.t1	ref|NP_189511.2| uncharacterized protein [Arabidopsis thaliana] gi|95147286|gb|ABF57278.1| At3g28700 [Arabidopsis thaliana] gi|332643957|gb|AEE77478.1| uncharacterized protein AT3G28700 [Arabidopsis thaliana]	479	471	0	98.3	86.6	93.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G28700.1 | Symbols: | Protein of unknown function (DUF185) | chr3:10759580-10761834 FORWARD LENGTH=471	479	471	0	98.3	86.6	93.3
Rsa1.0_00827.1.g20069.t1	ref|NP_566839.1| oxidoreductase, zinc-binding dehydrogenase family protein [Arabidopsis thaliana] gi|15983368|gb|AAL11552.1|AF424558_1 AT3g28670/MZN14_13 [Arabidopsis thaliana] gi|20260470|gb|AAM13133.1| unknown protein [Arabidopsis thaliana] gi|34365729|gb|AAQ65176.1| At3g28670 [Arabidopsis thaliana] gi|332643951|gb|AEE77472.1| oxidoreductase, zinc-binding dehydrogenase family protein [Arabidopsis thaliana]	485	491	0	101.2	81.0	91.5	oxidoreductase, zinc-binding dehydrogenase family protein	gbpln	Arabidopsis thaliana	AT3G28670.1 | Symbols: | oxidoreductase, zinc-binding dehydrogenase family protein | chr3:10744183-10746983 FORWARD LENGTH=491	485	491	0	101.2	81.0	91.5
Rsa1.0_00827.1.g20070.t1	gb|EOA23836.1| hypothetical protein CARUB_v10017051mg [Capsella rubella]	505	507	0	100.4	79.4	88.5	hypothetical protein CARUB_v10017051mg	gbpln	Capsella rubella	AT3G28640.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:10731518-10733032 REVERSE LENGTH=504	505	504	0	99.8	78.0	88.5

Rsa1.0_00828.1.g20071.t1	ref|XP_002864231.1| AGP22/ATAGP22 [Arabidopsis lyrata subsp. lyrata] gi|297310066|gb|EFH40490.1| AGP22/ATAGP22 [Arabidopsis lyrata subsp. lyrata]	99	63	9.00E-25	63.6	59.6	62.6	AGP22/ATAGP22	gbpln	Arabidopsis lyrata	AT5G53250.1 | Symbols: AGP22, ATAGP22 | arabinogalactan protein 22 | chr5:21603715-21604007 FORWARD LENGTH=63	99	63	1.00E-25	63.6	56.6	60.6
Rsa1.0_00828.1.g20072.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00828.1.g20073.t1	ref|NP_200138.1| Seed maturation protein [Arabidopsis thaliana] gi|9759173|dbj|BAB09788.1| unnamed protein product [Arabidopsis thaliana] gi|332008947|gb|AED96330.1| Seed maturation protein [Arabidopsis thaliana]	177	176	5.00E-67	99.4	77.4	85.3	Seed maturation protein	gbpln	Arabidopsis thaliana	AT5G53260.1 | Symbols: | Seed maturation protein | chr5:21604662-21605674 REVERSE LENGTH=176	177	176	2.00E-69	99.4	77.4	85.3
Rsa1.0_00828.1.g20074.t1	ref|XP_002864232.1| hypothetical protein ARALYDRAFT_495401 [Arabidopsis lyrata subsp. lyrata] gi|297310067|gb|EFH40491.1| hypothetical protein ARALYDRAFT_495401 [Arabidopsis lyrata subsp. lyrata]	246	269	1.00E-93	109.3	77.6	85.8	hypothetical protein ARALYDRAFT_495401	gbpln	Arabidopsis lyrata	AT5G53280.1 | Symbols: PDV1 | plastid division1 | chr5:21607586-21609080 FORWARD LENGTH=272	246	272	4.00E-91	110.6	73.6	84.1
Rsa1.0_00828.1.g20075.t1	ref|XP_002873035.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297318872|gb|EFH49294.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	237	264	2.00E-51	111.4	54.4	70.0	mitochondrial glycoprotein family protein	gbpln	Arabidopsis lyrata	AT5G02050.1 | Symbols: | Mitochondrial glycoprotein family protein | chr5:403239-404244 REVERSE LENGTH=267	237	267	1.00E-48	112.7	50.6	67.1
Rsa1.0_00828.1.g20076.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00828.1.g20077.t1	ref|XP_002864232.1| hypothetical protein ARALYDRAFT_495401 [Arabidopsis lyrata subsp. lyrata] gi|297310067|gb|EFH40491.1| hypothetical protein ARALYDRAFT_495401 [Arabidopsis lyrata subsp. lyrata]	266	269	1.00E-109	101.1	78.9	86.5	hypothetical protein ARALYDRAFT_495401	gbpln	Arabidopsis lyrata	AT5G53280.1 | Symbols: PDV1 | plastid division1 | chr5:21607586-21609080 FORWARD LENGTH=272	266	272	1.00E-107	102.3	75.2	85.0
Rsa1.0_00828.1.g20078.t1	ref|NP_200141.1| ethylene-responsive transcription factor CRF3 [Arabidopsis thaliana] gi|75262588|sp|Q9FK12.1|CRF3_ARATH RecName: Full=Ethylene-responsive transcription factor CRF3; AltName: Full=Protein CYTOKININ RESPONSE FACTOR 3 gi|9759176|dbj|BAB09791.1| unnamed protein product [Arabidopsis thaliana] gi|48479348|gb|AAT44945.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|56121914|gb|AAV74238.1| At5g53290 [Arabidopsis thaliana] gi|60543347|gb|AAX22271.1| At5g53290 [Arabidopsis thaliana] gi|332008950|gb|AED96333.1| ethylene-responsive transcription factor CRF3 [Arabidopsis thaliana]	348	354	1.00E-103	101.7	63.5	76.4	ethylene-responsive transcription factor CRF3	gbpln	Arabidopsis thaliana	AT5G53290.1 | Symbols: CRF3 | cytokinin response factor 3 | chr5:21617961-21619025 REVERSE LENGTH=354	348	354	1.00E-105	101.7	63.5	76.4
Rsa1.0_00828.1.g20079.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00828.1.g20080.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00828.1.g20081.t1	ref|NP_568788.1| ubiquitin-conjugating enzyme E2 10 [Arabidopsis thaliana] gi|30696309|ref|NP_851181.1| ubiquitin-conjugating enzyme E2 10 [Arabidopsis thaliana] gi|334188360|ref|NP_001190528.1| ubiquitin-conjugating enzyme E2 10 [Arabidopsis thaliana] gi|297796167|ref|XP_002865968.1| ubiquitin-conjugating enzyme 10 [Arabidopsis lyrata subsp. lyrata] gi|464987|sp|P35133.1|UBC10_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 10; AltName: Full=Ubiquitin carrier protein 10/12; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 10/12; AltName: Full=Ubiquitin-protein ligase 10/12 gi|11692932|gb|AAG40069.1|AF324718_1 AT5g53300 [Arabidopsis thaliana] gi|11762158|gb|AAG40357.1|AF325005_1 AT5g53300 [Arabidopsis thaliana] gi|11908050|gb|AAG41454.1|AF326872_1 putative E2, ubiquitin-conjugating enzyme UBC10 [Arabidopsis thaliana] gi|297878|emb|CAA78715.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|349213|gb|AAA32895.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|9759177|dbj|BAB09792.1| ubiquitin-conjugating enzyme E2-17 kD 10 (ubiquitin-protein ligase 10) (ubiquitin carrier protein 10) [Arabidopsis	148	148	6.00E-82	100.0	99.3	100.0	ubiquitin-conjugating enzyme E2 10	gbpln	Arabidopsis lyrata	AT5G53300.4 | Symbols: UBC10 | ubiquitin-conjugating enzyme 10 | chr5:21632802-21633989 REVERSE LENGTH=148	148	148	2.00E-84	100.0	99.3	100.0
Rsa1.0_00828.1.g20082.t1	gb|EOA13102.1| hypothetical protein CARUB_v10026109mg [Capsella rubella]	609	604	0	99.2	83.6	90.5	hypothetical protein CARUB_v10026109mg	gbpln	Capsella rubella	AT5G53320.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:21636453-21638337 REVERSE LENGTH=601	609	601	0	98.7	80.3	90.0
Rsa1.0_00828.1.g20083.t1	ref|XP_002864236.1| hypothetical protein ARALYDRAFT_918411 [Arabidopsis lyrata subsp. lyrata] gi|297310071|gb|EFH40495.1| hypothetical protein ARALYDRAFT_918411 [Arabidopsis lyrata subsp. lyrata]	221	221	3.00E-79	100.0	77.8	82.8	hypothetical protein ARALYDRAFT_918411	gbpln	Arabidopsis lyrata	AT5G53330.1 | Symbols: | Ubiquitin-associated/translation elongation factor EF1B protein | chr5:21639236-21640716 FORWARD LENGTH=221	221	221	6.00E-80	100.0	75.1	81.4
Rsa1.0_00828.1.g20084.t1	ref|XP_002865972.1| hypothetical protein ARALYDRAFT_918418 [Arabidopsis lyrata subsp. lyrata] gi|297311807|gb|EFH42231.1| hypothetical protein ARALYDRAFT_918418 [Arabidopsis lyrata subsp. lyrata]	454	488	0	107.5	88.8	96.0	hypothetical protein ARALYDRAFT_918418	gbpln	Arabidopsis lyrata	AT5G53390.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:21656951-21659207 REVERSE LENGTH=486	454	486	0	107.0	88.3	95.8
Rsa1.0_00829.1.g20085.t1	gb|EOA35903.1| hypothetical protein CARUB_v10021160mg, partial [Capsella rubella]	119	121	2.00E-22	101.7	48.7	52.1	hypothetical protein CARUB_v10021160mg, partial	gbpln	Capsella rubella	AT1G69325.1 | Symbols: | Remorin family protein | chr1:26063205-26063736 FORWARD LENGTH=120	119	120	7.00E-23	100.8	42.0	44.5
Rsa1.0_00829.1.g20086.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1158	1447	0	125.0	44.8	60.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1158	746	1.00E-105	64.4	17.2	22.1
Rsa1.0_00829.1.g20087.t1	dbj|BAJ34500.1| unnamed protein product [Thellungiella halophila]	296	281	9.00E-99	94.9	76.4	81.4	unnamed protein product	----	----	AT1G69310.2 | Symbols: WRKY57, ATWRKY57 | WRKY DNA-binding protein 57 | chr1:26056118-26057909 REVERSE LENGTH=287	296	287	1.00E-101	97.0	74.0	80.7
Rsa1.0_00829.1.g20088.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00829.1.g20089.t1	gb|EOA35673.1| hypothetical protein CARUB_v10020897mg [Capsella rubella]	216	228	9.00E-60	105.6	75.0	84.7	hypothetical protein CARUB_v10020897mg	gbpln	Capsella rubella	AT1G69295.1 | Symbols: PDCB4 | plasmodesmata callose-binding protein 4 | chr1:26050492-26051843 REVERSE LENGTH=222	216	222	6.00E-49	102.8	40.3	44.4
Rsa1.0_00829.1.g20090.t1	ref|NP_177089.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|193806277|sp|P0C7R4.1|PP110_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g69290 gi|332196785|gb|AEE34906.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	675	658	0	97.5	77.9	85.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G69290.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:26047372-26049348 REVERSE LENGTH=658	675	658	0	97.5	77.9	85.6

Rsa1.0_00829.1.g20091.t1	ref|XP_002888711.1| hypothetical protein ARALYDRAFT_476053 [Arabidopsis lyrata subsp. lyrata] gi|297334552|gb|EFH64970.1| hypothetical protein ARALYDRAFT_476053 [Arabidopsis lyrata subsp. lyrata]	474	537	0	113.3	78.3	85.0	hypothetical protein ARALYDRAFT_476053	gbpln	Arabidopsis lyrata	AT1G69270.1 | Symbols: RPK1 | receptor-like protein kinase 1 | chr1:26040877-26042499 REVERSE LENGTH=540	474	540	0	113.9	78.3	85.0
Rsa1.0_00829.1.g20092.t3	ref|NP_175971.3| transcription initiation factor TFIIH subunit H1 [Arabidopsis thaliana] gi|122215373|sp|Q3ECP0.1|TFB1A_ARATH RecName: Full=Probable RNA polymerase II transcription factor B subunit 1-1; AltName: Full=General transcription and DNA repair factor IIH subunit TFB1-1; Short=AtTFB1-1; Short=TFIIH subunit TFB1-1 gi|110741140|dbj|BAE98663.1| hypothetical protein [Arabidopsis thaliana] gi|332195172|gb|AEE33293.1| probable RNA polymerase II transcription factor B subunit 1-1 [Arabidopsis thaliana]	698	591	0	84.7	73.2	77.8	transcription initiation factor TFIIH subunit H1	gbpln	Arabidopsis thaliana	AT1G55750.1 | Symbols: | BSD domain (BTF2-like transcription factors, Synapse-associated proteins and DOS2-like proteins) | chr1:20840449-20845135 REVERSE LENGTH=591	698	591	0	84.7	73.2	77.8
Rsa1.0_00829.1.g20093.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00829.1.g20094.t1	ref|NP_001031095.1| self-incompatibility protein S1-like protein [Arabidopsis thaliana] gi|332192618|gb|AEE30739.1| self-incompatibility protein S1-like protein [Arabidopsis thaliana]	143	151	1.00E-58	105.6	79.0	86.0	self-incompatibility protein S1-like protein	gbpln	Arabidopsis thaliana	AT1G26796.1 | Symbols: | Plant self-incompatibility protein S1 family | chr1:9278958-9279413 FORWARD LENGTH=151	143	151	4.00E-61	105.6	79.0	86.0
Rsa1.0_00829.1.g20095.t1	ref|NP_177085.1| nuclear transport factor 2 and RNA recognition motif-containing protein [Arabidopsis thaliana] gi|6730639|gb|AAF27060.1|AC008262_9 F4N2.20 [Arabidopsis thaliana] gi|12325079|gb|AAG52488.1|AC018364_6 putative RNA-binding protein; 63745-61607 [Arabidopsis thaliana] gi|30017247|gb|AAP12857.1| At1g69250 [Arabidopsis thaliana] gi|332196781|gb|AEE34902.1| nuclear transport factor 2 and RNA recognition motif-containing protein [Arabidopsis thaliana]	474	427	1.00E-116	90.1	54.0	66.7	nuclear transport factor 2 and RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT1G69250.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr1:26033163-26035301 FORWARD LENGTH=427	474	427	1.00E-118	90.1	54.0	66.7
Rsa1.0_00829.1.g20096.t1	gb|AAF27064.1|AC008262_13 F4N2.19 [Arabidopsis thaliana]	470	456	0	97.0	82.6	88.3	F4N2.19	gbpln	Arabidopsis thaliana	AT1G69240.1 | Symbols: ATMES15, MES15, RHS9 | methyl esterase 15 | chr1:26028115-26030218 REVERSE LENGTH=444	470	444	0	94.5	81.3	87.0
Rsa1.0_00829.1.g20097.t1	dbj|BAJ33884.1| unnamed protein product [Thellungiella halophila]	108	117	7.00E-39	108.3	87.0	91.7	unnamed protein product	----	----	AT1G26355.1 | Symbols: SP1L1 | SPIRAL1-like1 | chr1:9117950-9118611 REVERSE LENGTH=113	108	113	2.00E-39	104.6	75.9	87.0
Rsa1.0_00829.1.g20098.t12	ref|NP_564954.1| uncharacterized protein [Arabidopsis thaliana] gi|13937141|gb|AAK50064.1|AF372924_1 At1g69210/F4N2_11 [Arabidopsis thaliana] gi|22137004|gb|AAM91347.1| At1g69210/F4N2_11 [Arabidopsis thaliana] gi|332196773|gb|AEE34894.1| uncharacterized protein AT1G69210 [Arabidopsis thaliana]	289	305	3.00E-97	105.5	75.1	84.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G69210.1 | Symbols: | Uncharacterised protein family UPF0090 | chr1:26018583-26020058 REVERSE LENGTH=305	289	305	1.00E-100	105.5	75.1	84.8
Rsa1.0_00829.1.g20099.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00829.1.g20100.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00829.1.g20101.t1	ref|XP_002864030.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297309865|gb|EFH40289.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	154	166	4.00E-21	107.8	39.0	51.3	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT5G50070.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:20364556-20365429 FORWARD LENGTH=183	154	183	1.00E-21	118.8	39.0	55.8
Rsa1.0_00829.1.g20102.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00829.1.g20103.t1	ref|NP_177077.3| squamosa promoter-binding-like protein 6 [Arabidopsis thaliana] gi|67461542|sp|Q94JW8.2|SPL6_ARATH RecName: Full=Squamosa promoter-binding-like protein 6 gi|12325078|gb|AAG52487.1|AC018364_5 squamosa promoter binding protein-like 6; 91282-89867 [Arabidopsis thaliana] gi|5931683|emb|CAB56595.1| squamosa promoter binding protein-like 6 [Arabidopsis thaliana] gi|5931685|emb|CAB56596.1| squamosa promoter binding protein-like 6 [Arabidopsis thaliana] gi|30102652|gb|AAP21244.1| At1g69170 [Arabidopsis thaliana] gi|110735912|dbj|BAE99931.1| squamosa promoter binding protein-like 6 [Arabidopsis thaliana] gi|332196769|gb|AEE34890.1| squamosa promoter-binding-like protein 6 [Arabidopsis thaliana]	339	405	1.00E-109	119.5	70.8	79.9	squamosa promoter-binding-like protein 6	gbpln	Arabidopsis thaliana	AT1G69170.1 | Symbols: | Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein | chr1:26005626-26007041 FORWARD LENGTH=405	339	405	1.00E-111	119.5	70.8	79.9
Rsa1.0_00829.1.g20104.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00829.1.g20105.t1	gb|ACG60677.1| hypothetical protein BoB028L01.120 [Brassica oleracea var. alboglabra]	313	322	1.00E-124	102.9	81.8	87.9	hypothetical protein BoB028L01.120	gbpln	Brassica oleracea	AT1G69160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13980.1); Has 173 Blast hits to 172 proteins in 54 species: Archae - 0; Bacteria - 0; Metazoa - 25; Fungi - 33; Plants - 84; Viruses - 2; Other Eukaryotes - 29 (source: NCBI BLink). | chr1:26000315-26001280 FORWARD LENGTH=321	313	321	1.00E-103	102.6	76.7	82.4
Rsa1.0_00829.1.g20106.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00830.1.g20107.t7	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1581	1611	0	101.9	25.1	31.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00830.1.g20108.t1	gb|ACA61613.1| hypothetical protein AP2_E11.1 [Arabidopsis lyrata subsp. petraea]	390	471	1.00E-165	120.8	70.0	84.4	hypothetical protein AP2_E11.1	gbpln	Arabidopsis lyrata	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	390	1262	6.00E-76	323.6	34.9	53.1
Rsa1.0_00830.1.g20109.t1	gb|AAF79692.1|AC022314_33 F9C16.1 [Arabidopsis thaliana]	244	820	3.00E-30	336.1	33.6	45.1	F9C16.1	gbpln	Arabidopsis thaliana	ATMG00820.1 | Symbols: ORF170 | Reverse transcriptase (RNA-dependent DNA polymerase) | chrM:228573-229085 REVERSE LENGTH=170	244	170	1.00E-18	69.7	24.2	32.0
Rsa1.0_00830.1.g20110.t7	gb|EOA25562.1| hypothetical protein CARUB_v10018906mg [Capsella rubella]	282	300	9.00E-86	106.4	62.1	76.2	hypothetical protein CARUB_v10018906mg	gbpln	Capsella rubella	AT3G58360.1 | Symbols: | TRAF-like family protein | chr3:21593505-21594866 REVERSE LENGTH=298	282	298	6.00E-88	105.7	59.9	72.3
Rsa1.0_00830.1.g20111.t1	ref|NP_191395.1| TRAF-like family protein [Arabidopsis thaliana] gi|6735348|emb|CAB68174.1| putative protein [Arabidopsis thaliana] gi|332646252|gb|AEE79773.1| TRAF-like family protein [Arabidopsis thaliana]	287	298	5.00E-91	103.8	61.7	74.6	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G58360.1 | Symbols: | TRAF-like family protein | chr3:21593505-21594866 REVERSE LENGTH=298	287	298	1.00E-93	103.8	61.7	74.6
Rsa1.0_00830.1.g20112.t1	gb|EOA23339.1| hypothetical protein CARUB_v10019412mg [Capsella rubella]	233	287	2.00E-60	123.2	54.9	72.1	hypothetical protein CARUB_v10019412mg	gbpln	Capsella rubella	AT3G58410.1 | Symbols: | TRAF-like family protein | chr3:21604871-21606229 REVERSE LENGTH=328	233	328	1.00E-60	140.8	55.4	70.8
Rsa1.0_00830.1.g20113.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00830.1.g20114.t1	ref|NP_191395.1| TRAF-like family protein [Arabidopsis thaliana] gi|6735348|emb|CAB68174.1| putative protein [Arabidopsis thaliana] gi|332646252|gb|AEE79773.1| TRAF-like family protein [Arabidopsis thaliana]	298	298	1.00E-118	100.0	68.5	84.2	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G58360.1 | Symbols: | TRAF-like family protein | chr3:21593505-21594866 REVERSE LENGTH=298	298	298	1.00E-120	100.0	68.5	84.2
Rsa1.0_00830.1.g20115.t1	ref|XP_002878217.1| hypothetical protein ARALYDRAFT_907320 [Arabidopsis lyrata subsp. lyrata] gi|297324055|gb|EFH54476.1| hypothetical protein ARALYDRAFT_907320 [Arabidopsis lyrata subsp. lyrata]	502	426	3.00E-89	84.9	36.1	39.8	hypothetical protein ARALYDRAFT_907320	gbpln	Arabidopsis lyrata	AT3G58440.1 | Symbols: | TRAF-like superfamily protein | chr3:21618446-21621249 REVERSE LENGTH=601	502	601	2.00E-69	119.7	39.4	55.2
Rsa1.0_00830.1.g20116.t1	ref|NP_191400.1| TRAF-like family protein [Arabidopsis thaliana] gi|6735353|emb|CAB68179.1| putative protein [Arabidopsis thaliana] gi|332646257|gb|AEE79778.1| TRAF-like family protein [Arabidopsis thaliana]	349	328	7.00E-72	94.0	48.7	61.6	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G58410.1 | Symbols: | TRAF-like family protein | chr3:21604871-21606229 REVERSE LENGTH=328	349	328	2.00E-74	94.0	48.7	61.6

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<tr><td>Rsa1.0_00830.1.g20119.t1</td><td>dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]</td><td>1325</td><td>1072</td><td>0</td><td>80.9</td><td>36.2</td><td>47.3</td><td>non-LTR retroelement reverse transcriptase-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G58440.1 | Symbols: | TRAF-like superfamily protein | chr3:21618446-21621249 REVERSE LENGTH=601</td><td>1325</td><td>601</td><td>1.00E-80</td><td>45.4</td><td>15.5</td><td>20.4</td></tr>
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<tr><td>Rsa1.0_00831.1.g20121.t1</td><td>gb|EOA24181.1| hypothetical protein CARUB_v10017418mg [Capsella rubella]</td><td>375</td><td>390</td><td>1.00E-177</td><td>104.0</td><td>86.1</td><td>91.7</td><td>hypothetical protein CARUB_v10017418mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G03590.1 | Symbols: ATUPS1, UPS1 | ureide permease 1 | chr2:1095129-1096711 FORWARD LENGTH=390</td><td>375</td><td>390</td><td>1.00E-178</td><td>104.0</td><td>85.3</td><td>91.5</td></tr>
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<tr><td>Rsa1.0_00831.1.g20124.t1</td><td>gb|EOA12340.1| hypothetical protein CARUB_v10007908mg [Capsella rubella]</td><td>170</td><td>323</td><td>2.00E-41</td><td>190.0</td><td>65.3</td><td>77.1</td><td>hypothetical protein CARUB_v10007908mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G27260.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9603943-9604930 FORWARD LENGTH=303</td><td>170</td><td>303</td><td>2.00E-25</td><td>178.2</td><td>43.5</td><td>67.6</td></tr>
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<tr><td>Rsa1.0_00831.1.g20126.t1</td><td>gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]</td><td>287</td><td>442</td><td>4.00E-93</td><td>154.0</td><td>64.1</td><td>74.9</td><td>hypothetical protein 24.t00017</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343</td><td>287</td><td>343</td><td>4.00E-60</td><td>119.5</td><td>38.3</td><td>50.9</td></tr>
<tr><td>Rsa1.0_00831.1.g20127.t1</td><td>gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]</td><td>283</td><td>255</td><td>2.00E-64</td><td>90.1</td><td>48.8</td><td>62.9</td><td>hypothetical protein 40.t00057</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302</td><td>283</td><td>302</td><td>3.00E-40</td><td>106.7</td><td>37.8</td><td>56.5</td></tr>
<tr><td>Rsa1.0_00831.1.g20128.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00831.1.g20129.t1</td><td>ref|XP_002875207.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297321045|gb|EFH51466.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]</td><td>314</td><td>432</td><td>1.00E-136</td><td>137.6</td><td>86.3</td><td>89.5</td><td>myb family transcription factor</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G03500.1 | Symbols: | Homeodomain-like superfamily protein | chr2:1059926-1062259 FORWARD LENGTH=432</td><td>314</td><td>432</td><td>1.00E-130</td><td>137.6</td><td>85.4</td><td>89.2</td></tr>
<tr><td>Rsa1.0_00831.1.g20130.t1</td><td>dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]</td><td>1620</td><td>910</td><td>0</td><td>56.2</td><td>28.6</td><td>37.6</td><td>putative reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1620</td><td>626</td><td>1.00E-101</td><td>38.6</td><td>11.7</td><td>17.3</td></tr>
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<tr><td>Rsa1.0_00831.1.g20131.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>430</td><td>1274</td><td>1.00E-62</td><td>296.3</td><td>34.4</td><td>51.6</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>430</td><td>575</td><td>7.00E-38</td><td>133.7</td><td>28.4</td><td>44.7</td></tr>
<tr><td>Rsa1.0_00831.1.g20132.t1</td><td>ref|XP_002875206.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321044|gb|EFH51465.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>626</td><td>619</td><td>0</td><td>98.9</td><td>91.4</td><td>96.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G03480.1 | Symbols: QUL2 | QUASIMODO2 LIKE 2 | chr2:1051509-1054090 FORWARD LENGTH=606</td><td>626</td><td>606</td><td>0</td><td>96.8</td><td>90.3</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00832.1.g20133.t1</td><td>ref|XP_002889677.1| SIT4 phosphatase-associated family protein [Arabidopsis lyrata subsp. lyrata] gi|297335519|gb|EFH65936.1| SIT4 phosphatase-associated family protein [Arabidopsis lyrata subsp. lyrata]</td><td>793</td><td>805</td><td>0</td><td>101.5</td><td>86.5</td><td>91.7</td><td>SIT4 phosphatase-associated family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G07990.1 | Symbols: | SIT4 phosphatase-associated family protein | chr1:2477413-2482898 FORWARD LENGTH=802</td><td>793</td><td>802</td><td>0</td><td>101.1</td><td>85.4</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00832.1.g20134.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00832.1.g20135.t1</td><td>gb|EOA36903.1| hypothetical protein CARUB_v10011453mg [Capsella rubella]</td><td>498</td><td>499</td><td>0</td><td>100.2</td><td>83.9</td><td>90.8</td><td>hypothetical protein CARUB_v10011453mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G08030.1 | Symbols: TPST | tyrosylprotein sulfotransferase | chr1:2489575-2492741 REVERSE LENGTH=500</td><td>498</td><td>500</td><td>0</td><td>100.4</td><td>83.5</td><td>89.2</td></tr>
<tr><td>Rsa1.0_00832.1.g20136.t1</td><td>ref|NP_172279.1| GATA transcription factor 11 [Arabidopsis thaliana] gi|145323792|ref|NP_001077485.1| GATA transcription factor 11 [Arabidopsis thaliana] gi|71660879|sp|Q6DBP8.1|GAT11_ARATH RecName: Full=GATA transcription factor 11 gi|50198783|gb|AAT70425.1| At1g08010 [Arabidopsis thaliana] gi|52421283|gb|AAU45211.1| At1g08010 [Arabidopsis thaliana] gi|110738607|dbj|BAF01229.1| putative GATA transcription factor 3 [Arabidopsis thaliana] gi|225897894|dbj|BAH30279.1| hypothetical protein [Arabidopsis thaliana] gi|332190107|gb|AEE28228.1| GATA transcription factor 11 [Arabidopsis thaliana] gi|332190108|gb|AEE28229.1| GATA transcription factor 11 [Arabidopsis thaliana]</td><td>287</td><td>303</td><td>1.00E-102</td><td>105.6</td><td>69.0</td><td>80.8</td><td>GATA transcription factor 11</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G08010.2 | Symbols: GATA11 | GATA transcription factor 11 | chr1:2486202-2487402 REVERSE LENGTH=303</td><td>287</td><td>303</td><td>1.00E-105</td><td>105.6</td><td>69.0</td><td>80.8</td></tr>
<tr><td>Rsa1.0_00832.1.g20137.t1</td><td>ref|XP_002889677.1| SIT4 phosphatase-associated family protein [Arabidopsis lyrata subsp. lyrata] gi|297335519|gb|EFH65936.1| SIT4 phosphatase-associated family protein [Arabidopsis lyrata subsp. lyrata]</td><td>788</td><td>805</td><td>0</td><td>102.2</td><td>87.3</td><td>92.3</td><td>SIT4 phosphatase-associated family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G07990.1 | Symbols: | SIT4 phosphatase-associated family protein | chr1:2477413-2482898 FORWARD LENGTH=802</td><td>788</td><td>802</td><td>0</td><td>101.8</td><td>86.5</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00832.1.g20138.t1</td><td>gb|EOA38222.1| hypothetical protein CARUB_v10009702mg [Capsella rubella]</td><td>144</td><td>330</td><td>3.00E-38</td><td>229.2</td><td>80.6</td><td>86.1</td><td>hypothetical protein CARUB_v10009702mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G07985.1 | Symbols: | Expressed protein | chr1:2475508-2475942 FORWARD LENGTH=144</td><td>144</td><td>144</td><td>9.00E-39</td><td>100.0</td><td>80.6</td><td>86.1</td></tr>
<tr><td>Rsa1.0_00832.1.g20139.t2</td><td>dbj|BAF00898.1| hypothetical protein [Arabidopsis thaliana] gi|110738408|dbj|BAF01130.1| hypothetical protein [Arabidopsis thaliana]</td><td>245</td><td>206</td><td>9.00E-48</td><td>84.1</td><td>44.5</td><td>47.3</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G07980.1 | Symbols: NF-YC10 | nuclear factor Y, subunit C10 | chr1:2473523-2474910 REVERSE LENGTH=206</td><td>245</td><td>206</td><td>2.00E-48</td><td>84.1</td><td>36.7</td><td>39.2</td></tr>
<tr><td>Rsa1.0_00832.1.g20140.t1</td><td>gb|AAF79822.1|AC026875_2 T6D22.2 [Arabidopsis thaliana]</td><td>471</td><td>967</td><td>0</td><td>205.3</td><td>97.0</td><td>98.3</td><td>T6D22.2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G60390.3 | Symbols: | GTP binding Elongation factor Tu family protein | chr5:24289226-24290675 FORWARD LENGTH=449</td><td>471</td><td>449</td><td>0</td><td>95.3</td><td>94.3</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00832.1.g20141.t1</td><td>gb|EOA35617.1| hypothetical protein CARUB_v10020841mg [Capsella rubella] gi|482571430|gb|EOA35618.1| hypothetical protein CARUB_v10020841mg [Capsella rubella]</td><td>250</td><td>252</td><td>1.00E-117</td><td>100.8</td><td>85.2</td><td>90.4</td><td>hypothetical protein CARUB_v10020841mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G62350.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:23056653-23057935 FORWARD LENGTH=196</td><td>250</td><td>196</td><td>4.00E-99</td><td>78.4</td><td>69.6</td><td>75.2</td></tr>
<tr><td>Rsa1.0_00832.1.g20142.t1</td><td>gb|EOA38652.1| hypothetical protein CARUB_v10010571mg [Capsella rubella]</td><td>144</td><td>147</td><td>4.00E-65</td><td>102.1</td><td>85.4</td><td>91.7</td><td>hypothetical protein CARUB_v10010571mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G07960.1 | Symbols: ATPDIL5-1, PDIL5-1 | PDI-like 5-1 | chr1:2467681-2468831 FORWARD LENGTH=146</td><td>144</td><td>146</td><td>5.00E-67</td><td>101.4</td><td>84.0</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00832.1.g20143.t13</td><td>ref|NP_172269.2| RNA ligase [Arabidopsis thaliana] gi|238478403|ref|NP_001154320.1| RNA ligase [Arabidopsis thaliana] gi|110740464|dbj|BAF02126.1| translation elongation factor EF-1 alpha [Arabidopsis thaliana] gi|332190089|gb|AEE28210.1| RNA ligase [Arabidopsis thaliana] gi|332190090|gb|AEE28211.1| RNA ligase [Arabidopsis thaliana]</td><td>547</td><td>1104</td><td>0</td><td>201.8</td><td>65.6</td><td>71.8</td><td>RNA ligase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G07910.2 | Symbols: ATRNL, RNL, AtRLG1 | RNAligase | chr1:2446712-2454386 FORWARD LENGTH=1104</td><td>547</td><td>1104</td><td>0</td><td>201.8</td><td>65.6</td><td>71.8</td></tr>
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Rsa1.0_00832.1.g20144.t4	ref|NP_172269.2| RNA ligase [Arabidopsis thaliana] gi|238478403|ref|NP_001154320.1| RNA ligase [Arabidopsis thaliana] gi|110740464|dbj|BAF02126.1| translation elongation factor EF-1 alpha [Arabidopsis thaliana] gi|332190089|gb|AEE28210.1| RNA ligase [Arabidopsis thaliana] gi|332190090|gb|AEE28211.1| RNA ligase [Arabidopsis thaliana]	1221	1104	0	90.4	72.2	79.1	RNA ligase	gbpln	Arabidopsis thaliana	AT1G07910.2 | Symbols: ATRNL, RNL, AtRLG1 | RNAligase | chr1:2446712-2454386 FORWARD LENGTH=1104	1221	1104	0	90.4	72.2	79.1
Rsa1.0_00832.1.g20145.t1	ref|NP_180417.2| LOB domain-containing protein 11 [Arabidopsis thaliana] gi|334302828|sp|Q9SK08.2|LBD11_ARATH RecName: Full=LOB domain-containing protein 11; AltName: Full=ASYMMETRIC LEAVES 2-like protein 7; Short=AS2-like protein 7 gi|330253037|gb|AEC08131.1| LOB domain-containing protein 11 [Arabidopsis thaliana]	209	232	1.00E-78	111.0	69.4	76.6	LOB domain-containing protein 11	gbpln	Arabidopsis thaliana	AT2G28500.1 | Symbols: LBD11 | LOB domain-containing protein 11 | chr2:12186603-12188110 REVERSE LENGTH=232	209	232	4.00E-81	111.0	69.4	76.6
Rsa1.0_00833.1.g20146.t2	ref|NP_566216.1| FMN binding protein [Arabidopsis thaliana] gi|21553937|gb|AAM63018.1| unknown [Arabidopsis thaliana] gi|222422814|dbj|BAH19395.1| AT3G03890 [Arabidopsis thaliana] gi|332640487|gb|AEE74008.1| FMN binding protein [Arabidopsis thaliana]	269	321	7.00E-69	119.3	53.9	57.6	FMN binding protein	gbpln	Arabidopsis thaliana	AT3G03890.1 | Symbols: | FMN binding | chr3:999667-1001996 REVERSE LENGTH=321	269	321	2.00E-71	119.3	53.9	57.6
Rsa1.0_00833.1.g20147.t1	ref|NP_187040.1| adenylylsulfate kinase [Arabidopsis thaliana] gi|6006852|gb|AAF00628.1|AC009540_5 putative adenylylsulfate kinase [Arabidopsis thaliana] gi|332640489|gb|AEE74010.1| adenosine-5'-phosphosulfate (APS) kinase 3 [Arabidopsis thaliana]	180	208	2.00E-93	115.6	96.1	98.3	adenylylsulfate kinase	gbpln	Arabidopsis thaliana	AT3G03900.1 | Symbols: APK3 | adenosine-5'-phosphosulfate (APS) kinase 3 | chr3:1002975-1004271 REVERSE LENGTH=208	180	208	9.00E-96	115.6	96.1	98.3
Rsa1.0_00833.1.g20148.t1	ref|NP_195066.1| Vacuolar import/degradation, Vid27-related protein [Arabidopsis thaliana] gi|4490307|emb|CAB38798.1| Dem-like protein [Arabidopsis thaliana] gi|7270288|emb|CAB80057.1| Dem-like protein [Arabidopsis thaliana] gi|20465423|gb|AAM20135.1| putative Dem protein [Arabidopsis thaliana] gi|28394003|gb|AAO42409.1| putative Dem protein [Arabidopsis thaliana] gi|332660820|gb|AEE86220.1| Vacuolar import/degradation, Vid27-related protein [Arabidopsis thaliana]	561	645	0	115.0	72.9	79.5	Vacuolar import/degradation, Vid27-related protein	gbpln	Arabidopsis thaliana	AT4G33400.1 | Symbols: | Vacuolar import/degradation, Vid27-related protein | chr4:16078189-16080410 REVERSE LENGTH=645	561	645	0	115.0	72.9	79.5
Rsa1.0_00833.1.g20149.t1	ref|NP_187044.1| protein kinase-like protein [Arabidopsis thaliana] gi|6223639|gb|AAF05853.1|AC011698_4 putative casein kinase [Arabidopsis thaliana] gi|332640493|gb|AEE74014.1| protein kinase-like protein [Arabidopsis thaliana]	701	701	0	100.0	93.9	97.3	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT3G03940.1 | Symbols: | Protein kinase family protein | chr3:1014412-1018244 REVERSE LENGTH=701	701	701	0	100.0	93.9	97.3
Rsa1.0_00833.1.g20150.t1	ref|NP_001030629.1| uncharacterized protein [Arabidopsis thaliana] gi|66351940|gb|AAY44714.1| unknown [Arabidopsis thaliana] gi|222423649|dbj|BAH19792.1| AT3G03950 [Arabidopsis thaliana] gi|332640496|gb|AEE74017.1| uncharacterized protein AT3G03950 [Arabidopsis thaliana]	429	428	0	99.8	77.2	84.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G03950.3 | Symbols: ECT1 | evolutionarily conserved C-terminal region 1 | chr3:1021502-1023767 FORWARD LENGTH=428	429	428	0	99.8	77.2	84.6
Rsa1.0_00833.1.g20151.t1	ref|XP_002882322.1| hypothetical protein ARALYDRAFT_477651 [Arabidopsis lyrata subsp. lyrata] gi|297328162|gb|EFH58581.1| hypothetical protein ARALYDRAFT_477651 [Arabidopsis lyrata subsp. lyrata]	543	546	0	100.6	91.3	95.4	hypothetical protein ARALYDRAFT_477651	gbpln	Arabidopsis lyrata	AT3G03960.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:1024432-1027604 FORWARD LENGTH=549	543	549	0	101.1	91.2	95.4
Rsa1.0_00833.1.g20152.t1	ref|XP_002884422.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330262|gb|EFH60681.1| binding protein [Arabidopsis lyrata subsp. lyrata]	544	555	0	102.0	77.9	87.3	binding protein	gbpln	Arabidopsis lyrata	AT3G03970.2 | Symbols: | ARM repeat superfamily protein | chr3:1028144-1029891 REVERSE LENGTH=554	544	554	0	101.8	78.5	87.9

Rsa1.0_00833.1.g20153.t1	ref|XP_002882324.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328164|gb|EFH58583.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	267	267	1.00E-148	100.0	95.5	97.4	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G03990.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:1033788-1034591 FORWARD LENGTH=267	267	267	1.00E-150	100.0	95.5	97.4
Rsa1.0_00833.1.g20154.t1	ref|XP_002882325.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328165|gb|EFH58584.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	235	274	1.00E-108	116.6	85.5	91.5	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G04000.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:1035500-1036435 FORWARD LENGTH=272	235	272	1.00E-106	115.7	83.4	90.6
Rsa1.0_00833.1.g20155.t1	ref|NP_187051.3| O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana] gi|6223646|gb|AAF05860.1|AC011698_11 putative beta-1,3-glucanase [Arabidopsis thaliana] gi|116325948|gb|ABJ98575.1| At3g04010 [Arabidopsis thaliana] gi|332640504|gb|AEE74025.1| O-Glycosyl hydrolases family 17 protein [Arabidopsis thaliana]	490	491	0	100.2	90.0	94.1	O-Glycosyl hydrolases family 17 protein	gbpln	Arabidopsis thaliana	AT3G04010.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr3:1036879-1039263 REVERSE LENGTH=491	490	491	0	100.2	90.0	94.1
Rsa1.0_00833.1.g20156.t1	gb|EOA31100.1| hypothetical protein CARUB_v10014253mg [Capsella rubella]	304	304	1.00E-148	100.0	85.9	92.4	hypothetical protein CARUB_v10014253mg	gbpln	Capsella rubella	AT3G04020.1 | Symbols: | unknown protein; Has 26 Blast hits to 25 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:1040548-1042377 FORWARD LENGTH=304	304	304	1.00E-150	100.0	84.9	93.4
Rsa1.0_00833.1.g20157.t1	ref|NP_001118567.1| myb family transcription factor [Arabidopsis thaliana] gi|6223653|gb|AAF05867.1|AC011698_18 transfactor-like [Arabidopsis thaliana] gi|332640508|gb|AEE74029.1| myb family transcription factor [Arabidopsis thaliana]	401	394	0	98.3	87.5	92.3	myb family transcription factor	gbpln	Arabidopsis thaliana	AT3G04030.3 | Symbols: | Homeodomain-like superfamily protein | chr3:1042920-1044574 REVERSE LENGTH=394	401	394	0	98.3	87.5	92.3
Rsa1.0_00833.1.g20158.t1	ref|XP_002882328.1| hypothetical protein ARALYDRAFT_340564 [Arabidopsis lyrata subsp. lyrata] gi|297328168|gb|EFH58587.1| hypothetical protein ARALYDRAFT_340564 [Arabidopsis lyrata subsp. lyrata]	493	510	0	103.4	80.5	87.8	hypothetical protein ARALYDRAFT_340564	gbpln	Arabidopsis lyrata	AT3G04050.1 | Symbols: | Pyruvate kinase family protein | chr3:1049795-1051522 FORWARD LENGTH=510	493	510	0	103.4	80.1	87.6
Rsa1.0_00833.1.g20159.t2	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1768	1213	0	68.6	33.3	44.5	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1768	626	2.00E-86	35.4	9.8	14.8
Rsa1.0_00834.1.g20160.t7	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1940	1838	0	94.7	33.1	41.8	F5M15.26	gbpln	Arabidopsis thaliana	AT4G20520.1 | Symbols: | RNA binding;RNA-directed DNA polymerases | chr4:11045912-11047716 FORWARD LENGTH=376	1940	376	4.00E-12	19.4	1.6	2.6
Rsa1.0_00834.1.g20161.t2	gb|AAQ82842.1| At4g20730 [Arabidopsis thaliana] gi|51970840|dbj|BAD44112.1| putative protein [Arabidopsis thaliana]	875	800	1.00E-27	91.4	8.6	13.3	At4g20730	gbpln	Arabidopsis thaliana	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	875	1399	8.00E-29	159.9	9.0	14.2
Rsa1.0_00834.1.g20162.t2	gb|AAD14492.1| Hypothetical protein [Arabidopsis thaliana]	300	240	1.00E-35	80.0	30.0	39.3	Hypothetical protein	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	300	256	2.00E-12	85.3	24.3	35.3
Rsa1.0_00834.1.g20163.t4	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1707	1044	0	61.2	27.7	37.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1707	626	8.00E-31	36.7	6.2	10.1
Rsa1.0_00834.1.g20164.t3	dbj|BAH57285.1| AT5G26850 [Arabidopsis thaliana]	216	896	2.00E-60	414.8	52.3	58.8	AT5G26850	gbpln	Arabidopsis thaliana	AT5G26850.4 | Symbols: | Uncharacterized protein | chr5:9445950-9450584 FORWARD LENGTH=983	216	983	1.00E-62	455.1	52.3	58.8
Rsa1.0_00834.1.g20165.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00834.1.g20166.t16	ref|XP_002888226.1| helicase domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297334067|gb|EFH64485.1| helicase domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1483	1458	0	98.3	72.8	81.5	helicase domain-containing protein	gbpln	Arabidopsis lyrata	AT1G58060.1 | Symbols: | RNA helicase family protein | chr1:21489480-21501775 REVERSE LENGTH=1459	1483	1459	0	98.4	72.6	81.5

<table>
<tr><td>Rsa1.0_00834.1.g20167.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT2G33620.4 | Symbols: | AT hook motif DNA-binding family protein | chr2:14234749-14236563 FORWARD LENGTH=351</td><td>110</td><td>351</td><td>2.00E-12</td><td>319.1</td><td>41.8</td><td>47.3</td></tr>
<tr><td>Rsa1.0_00834.1.g20168.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00835.1.g20169.t1</td><td>gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]</td><td>385</td><td>521</td><td>1.00E-13</td><td>135.3</td><td>12.2</td><td>16.1</td><td>hypothetical protein CARUB_v10017017mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00835.1.g20170.t1</td><td>ref|XP_002886639.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata] gi|297332480|gb|EFH62898.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata]</td><td>537</td><td>537</td><td>0</td><td>100.0</td><td>90.1</td><td>95.3</td><td>xanthine/uracil permease family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G60030.1 | Symbols: ATNAT7, NAT7 | nucleobase-ascorbate transporter 7 | chr1:22113993-22116648 REVERSE LENGTH=538</td><td>537</td><td>538</td><td>0</td><td>100.2</td><td>88.6</td><td>95.2</td></tr>
<tr><td>Rsa1.0_00835.1.g20171.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00835.1.g20172.t1</td><td>ref|NP_564752.1| uncharacterized protein [Arabidopsis thaliana] gi|4249380|gb|AAD14477.1| ESTs gb|Z37637, gb|AA042498 and gb|AA042269 come from this gene [Arabidopsis thaliana] gi|26450481|dbj|BAC42354.1| unknown protein [Arabidopsis thaliana] gi|28827334|gb|AAO50511.1| unknown protein [Arabidopsis thaliana] gi|332195529|gb|AEE33650.1| uncharacterized protein AT1G60010 [Arabidopsis thaliana]</td><td>175</td><td>173</td><td>1.00E-72</td><td>98.9</td><td>81.7</td><td>92.0</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G60010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10530.1); Has 185 Blast hits to 185 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 3; Plants - 180; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:22095660-22096434 REVERSE LENGTH=173</td><td>175</td><td>173</td><td>4.00E-75</td><td>98.9</td><td>81.7</td><td>92.0</td></tr>
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<tr><td>Rsa1.0_00835.1.g20174.t1</td><td>ref|XP_004239004.1| PREDICTED: uncharacterized protein LOC101252686 [Solanum lycopersicum]</td><td>245</td><td>210</td><td>4.00E-38</td><td>85.7</td><td>38.0</td><td>50.6</td><td>PREDICTED: uncharacterized protein LOC101252686</td><td>gbpln</td><td>Solanum lycopersicum</td><td>AT1G20000.1 | Symbols: TAF11b | TBP-associated factor 11B | chr1:6936898-6937666 REVERSE LENGTH=204</td><td>245</td><td>204</td><td>4.00E-38</td><td>83.3</td><td>38.4</td><td>48.2</td></tr>
<tr><td>Rsa1.0_00835.1.g20175.t1</td><td>emb|CCD74528.1| NAC domain containing protein 23 [Arabidopsis halleri subsp. halleri]</td><td>325</td><td>334</td><td>5.00E-94</td><td>102.8</td><td>56.3</td><td>69.5</td><td>NAC domain containing protein 23</td><td>gbpln</td><td>Arabidopsis halleri</td><td>AT1G60280.1 | Symbols: ANAC023, NAC023 | NAC domain containing protein 23 | chr1:22226885-22227928 REVERSE LENGTH=347</td><td>325</td><td>347</td><td>1.00E-93</td><td>106.8</td><td>54.2</td><td>68.9</td></tr>
<tr><td>Rsa1.0_00835.1.g20176.t1</td><td>gb|EOA33233.1| hypothetical protein CARUB_v10021279mg [Capsella rubella]</td><td>595</td><td>583</td><td>0</td><td>98.0</td><td>84.0</td><td>90.1</td><td>hypothetical protein CARUB_v10021279mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G59990.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr1:22090369-22092885 REVERSE LENGTH=581</td><td>595</td><td>581</td><td>0</td><td>97.6</td><td>83.0</td><td>88.7</td></tr>
<tr><td>Rsa1.0_00835.1.g20177.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00835.1.g20178.t1</td><td>gb|EOA40155.1| hypothetical protein CARUB_v10008872mg [Capsella rubella]</td><td>105</td><td>516</td><td>1.00E-48</td><td>491.4</td><td>85.7</td><td>93.3</td><td>hypothetical protein CARUB_v10008872mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G13710.1 | Symbols: CYP78A5, KLU | cytochrome P450, family 78, subfamily A, polypeptide 5 | chr1:4702932-4704592 REVERSE LENGTH=517</td><td>105</td><td>517</td><td>5.00E-49</td><td>492.4</td><td>84.8</td><td>90.5</td></tr>
<tr><td>Rsa1.0_00835.1.g20179.t1</td><td>gb|EOA34331.1| hypothetical protein CARUB_v10021851mg [Capsella rubella]</td><td>459</td><td>496</td><td>0</td><td>108.1</td><td>79.1</td><td>85.8</td><td>hypothetical protein CARUB_v10021851mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G59850.1 | Symbols: | ARM repeat superfamily protein | chr1:22028509-22030207 REVERSE LENGTH=498</td><td>459</td><td>498</td><td>0</td><td>108.5</td><td>78.9</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00835.1.g20180.t1</td><td>gb|EOA34536.1| hypothetical protein CARUB_v10022081mg [Capsella rubella]</td><td>225</td><td>297</td><td>2.00E-97</td><td>132.0</td><td>77.3</td><td>83.6</td><td>hypothetical protein CARUB_v10022081mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G59840.2 | Symbols: CCB4 | cofactor assembly of complex C | chr1:22026569-22028174 FORWARD LENGTH=297</td><td>225</td><td>297</td><td>2.00E-99</td><td>132.0</td><td>77.3</td><td>83.6</td></tr>
<tr><td>Rsa1.0_00835.1.g20181.t1</td><td>ref|NP_176191.1| phospholipid-transporting ATPase 3 [Arabidopsis thaliana] gi|30316321|sp|Q9XIE6.2|ALA3_ARATH RecName: Full=Phospholipid-transporting ATPase 3; Short=AtALA3; AltName: Full=Aminophospholipid ATPase 3; AltName: Full=Aminophospholipid flippase 3; AltName: Full=Protein IRREGULAR TRICHOME BRANCH 2 gi|20147219|gb|AAM10325.1| At1g59820/F23H11_14 [Arabidopsis thaliana] gi|332195500|gb|AEE33621.1| phospholipid-transporting ATPase 3 [Arabidopsis thaliana]</td><td>1216</td><td>1213</td><td>0</td><td>99.8</td><td>95.1</td><td>97.8</td><td>phospholipid-transporting ATPase 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G59820.1 | Symbols: ALA3 | aminophospholipid ATPase 3 | chr1:22011599-22020023 FORWARD LENGTH=1213</td><td>1216</td><td>1213</td><td>0</td><td>99.8</td><td>95.1</td><td>97.8</td></tr>
<tr><td>Rsa1.0_00835.1.g20182.t1</td><td>gb|EOA33686.1| hypothetical protein CARUB_v10019869mg [Capsella rubella]</td><td>619</td><td>725</td><td>0</td><td>117.1</td><td>66.1</td><td>75.8</td><td>hypothetical protein CARUB_v10019869mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G59620.1 | Symbols: CW9 | Disease resistance protein (CC-NBS-LRR class) family | chr1:21902627-21905527 FORWARD LENGTH=842</td><td>619</td><td>842</td><td>0</td><td>136.0</td><td>58.3</td><td>68.0</td></tr>
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Rsa1.0_00835.1_g20183.t1	ref|XP_002872057.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297317894|gb|EFH48316.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	305	302	4.00E-85	99.0	57.7	68.5	NLI interacting factor family protein	gbpln	Arabidopsis lyrata	AT2G02290.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:604453-605361 FORWARD LENGTH=302	305	302	3.00E-86	99.0	58.7	70.8
Rsa1.0_00835.1_g20184.t2	gb|AFD01292.1| auxin response factor 1 [Brassica rapa subsp. pekinensis]	656	665	0	101.4	97.9	98.6	auxin response factor 1	gbpln	Brassica rapa	AT1G59750.2 | Symbols: ARF1 | auxin response factor 1 | chr1:21980414-21984193 FORWARD LENGTH=662	656	662	0	100.9	94.2	96.2
Rsa1.0_00835.1_g20185.t3	ref|NP_176183.1| putative peptide/nitrate transporter [Arabidopsis thaliana] gi|75305727|sp|Q93VV5.1|PTR16_ARATH RecName: Full=Probable peptide/nitrate transporter At1g59740 gi|14334728|gb|AAK59542.1| putative oligopeptide transporter protein [Arabidopsis thaliana] gi|15293215|gb|AAK93718.1| putative oligopeptide transporter protein [Arabidopsis thaliana] gi|332195490|gb|AEE33611.1| probable peptide/nitrate transporter [Arabidopsis thaliana]	491	591	0	120.4	90.6	96.1	putative peptide/nitrate transporter	gbpln	Arabidopsis thaliana	AT1G59740.1 | Symbols: | Major facilitator superfamily protein | chr1:21968227-21972312 FORWARD LENGTH=591	491	591	0	120.4	90.6	96.1
Rsa1.0_00835.1_g20186.t1	dbj|BAJ33912.1| unnamed protein product [Thellungiella halophila]	541	539	0	99.6	91.7	94.6	unnamed protein product	----	----	AT1G58290.1 | Symbols: HEMA1 | Glutamyl-tRNA reductase family protein | chr1:21624028-21626051 REVERSE LENGTH=543	541	543	0	100.4	88.4	93.2
Rsa1.0_00835.1_g20187.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00835.1_g20188.t1	emb|CAN69058.1| hypothetical protein VITISV_022968 [Vitis vinifera]	1066	830	1.00E-114	77.9	21.3	28.0	hypothetical protein VITISV_022968	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00836.1_g20189.t1	ref|XP_002876336.1| sedoheptulose-bisphosphatase [Arabidopsis lyrata subsp. lyrata] gi|297322174|gb|EFH52595.1| sedoheptulose-bisphosphatase [Arabidopsis lyrata subsp. lyrata]	289	393	1.00E-128	136.0	80.3	82.0	sedoheptulose-bisphosphatase	gbpln	Arabidopsis lyrata	AT3G55800.1 | Symbols: SBPASE | sedoheptulose-bisphosphatase | chr3:20709640-20711421 FORWARD LENGTH=393	289	393	1.00E-130	136.0	79.2	82.0
Rsa1.0_00836.1_g20190.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00836.1_g20191.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00836.1_g20192.t1	ref|NP_175500.1| putative F-box protein [Arabidopsis thaliana] gi|75268203|sp|Q9C6J3.1|FB52_ARATH RecName: Full=Putative F-box protein At1g50870 gi|12321805|gb|AAG50947.1|AC079284_22 hypothetical protein [Arabidopsis thaliana] gi|332194475|gb|AEE32596.1| putative F-box protein [Arabidopsis thaliana]	404	396	3.00E-91	98.0	47.8	65.1	putative F-box protein	gbpln	Arabidopsis thaliana	AT1G50870.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:18855147-18856337 FORWARD LENGTH=396	404	396	7.00E-94	98.0	47.8	65.1
Rsa1.0_00836.1_g20193.t1	ref|NP_567027.2| amidohydrolase family protein [Arabidopsis thaliana] gi|332645927|gb|AEE79448.1| amidohydrolase family protein [Arabidopsis thaliana]	593	576	0	97.1	84.5	89.7	amidohydrolase family protein	gbpln	Arabidopsis thaliana	AT3G55850.1 | Symbols: LAF3, LAF3 ISF2 | Amidohydrolase family | chr3:20721866-20725489 REVERSE LENGTH=576	593	576	0	97.1	84.5	89.7
Rsa1.0_00836.1_g20194.t1	ref|XP_003599996.1| hypothetical protein MTR_3g050240 [Medicago truncatula] gi|355489044|gb|AES70247.1| hypothetical protein MTR_3g050240 [Medicago truncatula]	669	496	6.00E-19	74.1	14.8	24.2	hypothetical protein MTR_3g050240	gbpln	Medicago truncatula	AT3G62210.1 | Symbols: EDA32 | Putative endonuclease or glycosyl hydrolase | chr3:23026910-23028113 REVERSE LENGTH=279	669	279	2.00E-19	41.7	8.7	12.6
Rsa1.0_00836.1_g20195.t1	ref|XP_002877981.1| skp1-interacting partner 5 [Arabidopsis lyrata subsp. lyrata] gi|297323819|gb|EFH54240.1| skp1-interacting partner 5 [Arabidopsis lyrata subsp. lyrata]	245	274	1.00E-105	111.8	78.8	83.3	skp1-interacting partner 5	gbpln	Arabidopsis lyrata	AT3G54480.1 | Symbols: SKIP5, SKP5 | SKP1/ASK-interacting protein 5 | chr3:20170883-20173325 REVERSE LENGTH=274	245	274	1.00E-103	111.8	77.1	82.4
Rsa1.0_00836.1_g20196.t1	ref|XP_002877980.1| ump synthase [Arabidopsis lyrata subsp. lyrata] gi|297323818|gb|EFH54239.1| ump synthase [Arabidopsis lyrata subsp. lyrata]	477	476	0	99.8	88.7	93.9	ump synthase	gbpln	Arabidopsis lyrata	AT3G54470.1 | Symbols: | uridine 5'-monophosphate synthase / UMP synthase (PYRE-F) (UMPS) | chr3:20168285-20170245 REVERSE LENGTH=476	477	476	0	99.8	88.7	93.5
Rsa1.0_00836.1_g20197.t1	ref|XP_002877979.1| SNF2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297323817|gb|EFH54238.1| SNF2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1346	1370	0	101.8	79.7	86.8	SNF2 domain-containing protein	gbpln	Arabidopsis lyrata	AT3G54460.1 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / F-box family protein | chr3:20162050-20167186 REVERSE LENGTH=1378	1346	1378	0	102.4	79.5	86.3

Rsa1.0_00836.1.g20198.t1	ref|NP_001030858.1| beta-galactosidase [Arabidopsis thaliana] gi|332645710|gb|AEE79231.1| glycoside hydrolase family 2 protein [Arabidopsis thaliana]	684	1108	0	162.0	90.4	93.7	beta-galactosidase	gbpln	Arabidopsis thaliana	AT3G54440.2 | Symbols: | glycoside hydrolase family 2 protein | chr3:20148494-20157019 REVERSE LENGTH=1108	684	1108	0	162.0	90.4	93.7
Rsa1.0_00836.1.g20199.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00836.1.g20200.t1	ref|XP_002877978.1| hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis lyrata subsp. lyrata] gi|297323816|gb|EFH54237.1| hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis lyrata subsp. lyrata]	713	1107	0	155.3	49.1	53.0	hydrolase, hydrolyzing O-glycosyl compounds	gbpln	Arabidopsis lyrata	AT3G54440.3 | Symbols: | glycoside hydrolase family 2 protein | chr3:20148494-20157019 REVERSE LENGTH=1120	713	1120	0	157.1	48.9	52.6
Rsa1.0_00836.1.g20201.t1	ref|NP_566867.1| putative cysteine proteinase [Arabidopsis thaliana] gi|30315950|sp|Q9LXW3.1|CPR2_ARATH RecName: Full=Probable cysteine proteinase At3g43960; Flags: Precursor gi|7594557|emb|CAB88124.1| cysteine proteinase-like protein [Arabidopsis thaliana] gi|26452289|dbj|BAC43231.1| putative cysteine proteinase [Arabidopsis thaliana] gi|332644328|gb|AEE77849.1| putative cysteine proteinase [Arabidopsis thaliana]	385	376	1.00E-128	97.7	59.2	70.4	putative cysteine proteinase	gbpln	Arabidopsis thaliana	AT3G43960.1 | Symbols: | Cysteine proteinases superfamily protein | chr3:15774122-15775628 REVERSE LENGTH=376	385	376	1.00E-131	97.7	59.2	70.4
Rsa1.0_00836.1.g20202.t1	gb|ABD65073.1| hypothetical protein 27.t00059 [Brassica oleracea]	172	341	4.00E-46	198.3	51.7	61.6	hypothetical protein 27.t00059	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00836.1.g20203.t1	ref|NP_191010.1| chitinase [Arabidopsis thaliana] gi|7288020|emb|CAB81807.1| class IV chitinase (CHIV) [Arabidopsis thaliana] gi|34146830|gb|AAQ62423.1| At3g54420 [Arabidopsis thaliana] gi|51971118|dbj|BAD44251.1| class IV chitinase (CHIV) [Arabidopsis thaliana] gi|332645707|gb|AEE79228.1| chitinase class IV [Arabidopsis thaliana]	91	273	8.00E-12	300.0	39.6	41.8	chitinase	gbpln	Arabidopsis thaliana	AT3G54420.1 | Symbols: ATEP3, ATCHITIV, CHIV, EP3 | homolog of carrot EP3-3 chitinase | chr3:20145935-20147034 FORWARD LENGTH=273	91	273	1.00E-14	300.0	39.6	41.8
Rsa1.0_00836.1.g20204.t1	dbj|BAJ34532.1| unnamed protein product [Thellungiella halophila]	428	428	0	100.0	92.1	96.5	unnamed protein product	----	----	AT3G54400.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:20140291-20142599 REVERSE LENGTH=425	428	425	0	99.3	88.6	93.5
Rsa1.0_00837.1.g20205.t1	gb|EOA22110.1| hypothetical protein CARUB_v10002660mg [Capsella rubella]	260	262	1.00E-120	100.8	78.8	90.4	hypothetical protein CARUB_v10002660mg	gbpln	Capsella rubella	AT5G24410.1 | Symbols: PGL4 | 6-phosphogluconolactonase 4 | chr5:8332690-8333984 REVERSE LENGTH=261	260	261	1.00E-119	100.4	77.3	88.5
Rsa1.0_00837.1.g20206.t1	gb|AAM63366.1| 6-phosphogluconolactonase-like protein [Arabidopsis thaliana]	313	325	1.00E-138	103.8	82.7	89.8	6-phosphogluconolactonase-like protein	gbpln	Arabidopsis thaliana	AT5G24400.1 | Symbols: EMB2024, PGL3 | NagB/RpiA/CoA transferase-like superfamily protein | chr5:8330532-8331784 REVERSE LENGTH=325	313	325	1.00E-140	103.8	83.7	89.8
Rsa1.0_00837.1.g20207.t1	ref|XP_002874194.1| RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297320031|gb|EFH50453.1| RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	541	528	0	97.6	77.1	86.5	RabGAP/TBC domain-containing protein	gbpln	Arabidopsis lyrata	AT5G24390.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr5:8327004-8329238 REVERSE LENGTH=528	541	528	0	97.6	75.8	85.2
Rsa1.0_00837.1.g20208.t1	ref|XP_002872112.1| hypothetical protein ARALYDRAFT_489303 [Arabidopsis lyrata subsp. lyrata] gi|297317949|gb|EFH48371.1| hypothetical protein ARALYDRAFT_489303 [Arabidopsis lyrata subsp. lyrata]	665	664	0	99.8	91.1	95.5	hypothetical protein ARALYDRAFT_489303	gbpln	Arabidopsis lyrata	AT5G24380.1 | Symbols: YSL2, ATYSL2 | YELLOW STRIPE like 2 | chr5:8324098-8326525 FORWARD LENGTH=664	665	664	0	99.8	90.4	95.2
Rsa1.0_00837.1.g20209.t2	ref|XP_002872110.1| hypothetical protein ARALYDRAFT_489300 [Arabidopsis lyrata subsp. lyrata] gi|297317947|gb|EFH48369.1| hypothetical protein ARALYDRAFT_489300 [Arabidopsis lyrata subsp. lyrata]	1173	871	0	74.3	56.2	61.9	hypothetical protein ARALYDRAFT_489300	gbpln	Arabidopsis lyrata	AT5G24360.1 | Symbols: ATIRE1-1, IRE1-1 | inositol requiring 1-1 | chr5:8316627-8319827 FORWARD LENGTH=881	1173	881	0	75.1	56.1	62.3
Rsa1.0_00837.1.g20210.t1	ref|XP_002874190.1| hypothetical protein ARALYDRAFT_489297 [Arabidopsis lyrata subsp. lyrata] gi|297320027|gb|EFH50449.1| hypothetical protein ARALYDRAFT_489297 [Arabidopsis lyrata subsp. lyrata]	347	349	1.00E-175	100.6	87.3	92.2	hypothetical protein ARALYDRAFT_489297	gbpln	Arabidopsis lyrata	AT5G24330.1 | Symbols: ATXR6, SDG34 | ARABIDOPSIS TRITHORAX-RELATED PROTEIN 6 | chr5:8295245-8296997 REVERSE LENGTH=349	347	349	1.00E-173	100.6	87.6	92.8
Rsa1.0_00837.1.g20211.t1	ref|XP_002874189.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320026|gb|EFH50448.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	690	703	0	101.9	78.8	86.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G24320.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:8284858-8287651 REVERSE LENGTH=694	690	694	0	100.6	79.9	87.1

Rsa1.0_00837.1.g20212.t1	ref|XP_002872105.1| PDE225/PTAC7 [Arabidopsis lyrata subsp. lyrata] gi|297317942|gb|EFH48364.1| PDE225/PTAC7 [Arabidopsis lyrata subsp. lyrata]	165	161	4.00E-76	97.6	84.8	89.7	PDE225/PTAC7	gbpln	Arabidopsis lyrata	AT5G24314.1 | Symbols: PDE225, PTAC7 | plastid transcriptionally active7 | chr5:8277750-8279099 FORWARD LENGTH=161	165	161	3.00E-78	97.6	84.2	89.7
Rsa1.0_00837.1.g20213.t1	ref|XP_002874186.1| hypothetical protein ARALYDRAFT_489292 [Arabidopsis lyrata subsp. lyrata] gi|297320023|gb|EFH50445.1| hypothetical protein ARALYDRAFT_489292 [Arabidopsis lyrata subsp. lyrata]	77	83	1.00E-14	107.8	66.2	72.7	hypothetical protein ARALYDRAFT_489292	gbpln	Arabidopsis lyrata	AT5G24313.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:8277106-8277351 REVERSE LENGTH=81	77	81	1.00E-15	105.2	61.0	71.4
Rsa1.0_00837.1.g20214.t1	ref|NP_197819.2| protein ABIL3 [Arabidopsis thaliana] gi|75127037|sp|Q6NMC6.1|ABIL3_ARATH RecName: Full=Protein ABIL3; AltName: Full=Abl interactor-like protein 3; Short=AtABIL3 gi|44917545|gb|AAS49097.1| At5g24310 [Arabidopsis thaliana] gi|57240096|gb|AAW49258.1| Abl interactor-like protein-3 [Arabidopsis thaliana] gi|62321758|dbj|BAD95383.1| hypothetical protein [Arabidopsis thaliana] gi|110737536|dbj|BAF00710.1| hypothetical protein [Arabidopsis thaliana] gi|332005902|gb|AED93285.1| protein ABIL3 [Arabidopsis thaliana]	324	321	1.00E-161	99.1	88.0	92.6	protein ABIL3	gbpln	Arabidopsis thaliana	AT5G24310.1 | Symbols: ABIL3 | ABL interactor-like protein 3 | chr5:8274637-8276325 FORWARD LENGTH=321	324	321	1.00E-163	99.1	88.0	92.6
Rsa1.0_00837.1.g20215.t1	ref|XP_002872103.1| hypothetical protein ARALYDRAFT_489289 [Arabidopsis lyrata subsp. lyrata] gi|297317940|gb|EFH48362.1| hypothetical protein ARALYDRAFT_489289 [Arabidopsis lyrata subsp. lyrata]	657	655	0	99.7	87.2	91.6	hypothetical protein ARALYDRAFT_489289	gbpln	Arabidopsis lyrata	AT5G24300.2 | Symbols: SSI1 | Glycogen/starch synthases, ADP-glucose type | chr5:8266934-8270860 FORWARD LENGTH=652	657	652	0	99.2	87.2	91.5
Rsa1.0_00837.1.g20216.t1	ref|NP_851067.1| vacuolar iron transporter-like protein [Arabidopsis thaliana] gi|332005898|gb|AED93281.1| vacuolar iron transporter-like protein [Arabidopsis thaliana]	531	550	2.33E-156	103.6	61.8	74.2	vacuolar iron transporter-like protein	gbpln	Arabidopsis thaliana	AT5G24290.1 | Symbols: | Vacuolar iron transporter (VIT) family protein | chr5:8263271-8265618 REVERSE LENGTH=550	531	550	1.00E-148	103.6	61.8	74.2
Rsa1.0_00838.1.g20217.t1	gb|ACI14387.1| WRKY20-1 transcription factor [Brassica napus]	529	532	0	100.6	84.1	87.3	WRKY20-1 transcription factor	gbpln	Brassica napus	AT4G26640.2 | Symbols: WRKY20, AtWRKY20 | WRKY family transcription factor family protein | chr4:13437298-13440693 REVERSE LENGTH=557	529	557	0	105.3	79.2	86.2
Rsa1.0_00838.1.g20218.t1	ref|NP_194393.3| DEK domain-containing chromatin associated protein [Arabidopsis thaliana] gi|79325273|ref|NP_001031724.1| DEK domain-containing chromatin associated protein [Arabidopsis thaliana] gi|4938501|emb|CAB43859.1| putative protein [Arabidopsis thaliana] gi|7269515|emb|CAB79518.1| putative protein [Arabidopsis thaliana] gi|332659828|gb|AEE85228.1| DEK domain-containing chromatin associated protein [Arabidopsis thaliana] gi|332659829|gb|AEE85229.1| DEK domain-containing chromatin associated protein [Arabidopsis thaliana]	840	763	0	90.8	62.5	71.1	DEK domain-containing chromatin associated protein	gbpln	Arabidopsis thaliana	AT4G26630.2 | Symbols: | DEK domain-containing chromatin associated protein | chr4:13430873-13434877 REVERSE LENGTH=763	840	763	0	90.8	62.5	71.1
Rsa1.0_00838.1.g20219.t1	ref|XP_002867555.1| hypothetical protein ARALYDRAFT_492146 [Arabidopsis lyrata subsp. lyrata] gi|297313391|gb|EFH43814.1| hypothetical protein ARALYDRAFT_492146 [Arabidopsis lyrata subsp. lyrata]	441	440	0	99.8	89.3	93.7	hypothetical protein ARALYDRAFT_492146	gbpln	Arabidopsis lyrata	AT4G26620.1 | Symbols: | Sucrase/ferredoxin-like family protein | chr4:13427599-13429877 REVERSE LENGTH=443	441	443	0	100.5	90.0	94.6
Rsa1.0_00838.1.g20220.t1	ref|XP_002869601.1| hypothetical protein ARALYDRAFT_492147 [Arabidopsis lyrata subsp. lyrata] gi|297315437|gb|EFH45860.1| hypothetical protein ARALYDRAFT_492147 [Arabidopsis lyrata subsp. lyrata]	511	510	0	99.8	89.2	93.3	hypothetical protein ARALYDRAFT_492147	gbpln	Arabidopsis lyrata	AT4G26610.1 | Symbols: D6PKL1, AGC1-2 | D6 protein kinase like 1 | chr4:13425568-13427188 FORWARD LENGTH=506	511	506	0	99.0	86.9	91.8

Rsa1.0_00838.1.g20221.t1	ref|NP_194390.2| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|17979390|gb|AAL49920.1| unknown protein [Arabidopsis thaliana] gi|22136852|gb|AAM91770.1| unknown protein [Arabidopsis thaliana] gi|332659825|gb|AEE85225.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	627	671	0	107.0	77.8	87.6	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT4G26600.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:13419629-13423418 FORWARD LENGTH=671	627	671	0	107.0	77.8	87.6
Rsa1.0_00838.1.g20222.t1	ref|XP_002867556.1| ATOPT5 [Arabidopsis lyrata subsp. lyrata] gi|297313392|gb|EFH43815.1| ATOPT5 [Arabidopsis lyrata subsp. lyrata]	720	753	0	104.6	88.6	92.9	ATOPT5	gbpln	Arabidopsis lyrata	AT4G26590.1 | Symbols: ATOPT5, OPT5 | oligopeptide transporter 5 | chr4:13414134-13416850 REVERSE LENGTH=753	720	753	0	104.6	86.7	92.4
Rsa1.0_00838.1.g20223.t1	emb|CAB43854.1| putative protein [Arabidopsis thaliana] gi|7269510|emb|CAB79513.1| putative protein [Arabidopsis thaliana]	343	464	1.00E-155	135.3	83.4	88.3	putative protein	gbpln	Arabidopsis thaliana	AT4G26580.2 | Symbols: | RING/U-box superfamily protein | chr4:13411705-13412889 REVERSE LENGTH=335	343	335	1.00E-157	97.7	83.7	88.3
Rsa1.0_00838.1.g20224.t1	dbj|BAJ33834.1| unnamed protein product [Thellungiella halophila]	534	226	1.00E-118	42.3	39.1	40.4	unnamed protein product	----	----	AT4G26570.1 | Symbols: ATCBL3, CBL3 | calcineurin B-like 3 | chr4:13408608-13409998 REVERSE LENGTH=226	534	226	1.00E-120	42.3	39.0	40.4
Rsa1.0_00838.1.g20225.t1	ref|NP_567749.1| Got1/Sft2-like vescicle transport protein [Arabidopsis thaliana] gi|88196739|gb|ABD43012.1| At4g26550 [Arabidopsis thaliana] gi|332659817|gb|AEE85217.1| Got1/Sft2-like vescicle transport protein [Arabidopsis thaliana]	227	225	1.00E-111	99.1	92.1	94.3	Got1/Sft2-like vescicle transport protein	gbpln	Arabidopsis thaliana	AT4G26550.1 | Symbols: | Got1/Sft2-like vescicle transport protein family | chr4:13402755-13404208 REVERSE LENGTH=225	227	225	1.00E-113	99.1	92.1	94.3
Rsa1.0_00838.1.g20226.t1	ref|XP_002867561.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313397|gb|EFH43820.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	1094	1091	0	99.7	85.9	92.4	kinase family protein	gbpln	Arabidopsis lyrata	AT4G26540.1 | Symbols: | Leucine-rich repeat receptor-like protein kinase family protein | chr4:13394673-13398028 REVERSE LENGTH=1091	1094	1091	0	99.7	85.8	92.4
Rsa1.0_00838.1.g20227.t1	gb|EOA16898.1| hypothetical protein CARUB_v10005122mg [Capsella rubella]	358	358	0	100.0	95.0	96.6	hypothetical protein CARUB_v10005122mg	gbpln	Capsella rubella	AT4G26530.2 | Symbols: | Aldolase superfamily protein | chr4:13391566-13392937 FORWARD LENGTH=358	358	358	0	100.0	94.4	96.1
Rsa1.0_00838.1.g20228.t1	ref|NP_567747.4| putative uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|240256079|ref|NP_849448.4| putative uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|298286881|sp|O65583.2|UKL4_ARATH RecName: Full=Uridine kinase-like protein 4; Includes: RecName: Full=Uridine kinase; Short=UK; Includes: RecName: Full=Putative uracil phosphoribosyltransferase; Short=UPRTase; AltName: Full=UMP pyrophosphorylase gi|21554263|gb|AAM63338.1| putative uracil phosphoribosyl transferase [Arabidopsis thaliana] gi|63003884|gb|AAY25471.1| At4g26510 [Arabidopsis thaliana] gi|332659811|gb|AEE85211.1| putative uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|332659812|gb|AEE85212.1| putative uracil phosphoribosyltransferase [Arabidopsis thaliana]	469	469	0	100.0	93.6	97.9	putative uracil phosphoribosyltransferase	gbpln	Arabidopsis thaliana	AT4G26510.2 | Symbols: UKL4 | uridine kinase-like 4 | chr4:13384503-13387920 FORWARD LENGTH=469	469	469	0	100.0	93.6	97.9
Rsa1.0_00838.1.g20229.t1	ref|XP_002867562.1| ATSUFE/CPSUFE/EMB1374 [Arabidopsis lyrata subsp. lyrata] gi|297313398|gb|EFH43821.1| ATSUFE/CPSUFE/EMB1374 [Arabidopsis lyrata subsp. lyrata]	353	368	1.00E-143	104.2	79.9	88.4	ATSUFE/CPSUFE/EMB1374	gbpln	Arabidopsis lyrata	AT4G26500.1 | Symbols: EMB1374, CPSUFE, ATSUFE, SUFE1 | chloroplast sulfur E | chr4:13382456-13383571 REVERSE LENGTH=371	353	371	1.00E-143	105.1	77.6	85.8
Rsa1.0_00838.1.g20230.t1	ref|XP_002869608.1| hypothetical protein ARALYDRAFT_913911 [Arabidopsis lyrata subsp. lyrata] gi|297315444|gb|EFH45867.1| hypothetical protein ARALYDRAFT_913911 [Arabidopsis lyrata subsp. lyrata]	269	269	1.00E-116	100.0	74.0	83.3	hypothetical protein ARALYDRAFT_913911	gbpln	Arabidopsis lyrata	AT4G26490.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr4:13380425-13381231 FORWARD LENGTH=268	269	268	1.00E-115	99.6	72.1	81.8
Rsa1.0_00838.1.g20231.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00838.1.g20232.t1</td><td>ref|NP_567742.1| 6-phosphofructokinase 3 [Arabidopsis thaliana] gi|75164938|sp|Q94AA4.1|K6PF3_ARATH RecName: Full=6-phosphofructokinase 3; AltName: Full=Phosphofructokinase 3; AltName: Full=Phosphohexokinase 3 gi|15146208|gb|AAK83587.1| AT4g26270/T25K17_80 [Arabidopsis thaliana] gi|19699124|gb|AAL90928.1| AT4g26270/T25K17_80 [Arabidopsis thaliana] gi|332659778|gb|AEE85178.1| 6-phosphofructokinase 3 [Arabidopsis thaliana]</td><td>489</td><td>489</td><td>0</td><td>100.0</td><td>95.9</td><td>98.0</td><td>6-phosphofructokinase 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26270.1 | Symbols: PFK3 | phosphofructokinase 3 | chr4:13301094-13304030 REVERSE LENGTH=489</td><td>489</td><td>489</td><td>0</td><td>100.0</td><td>95.9</td><td>98.0</td></tr>
<tr><td>Rsa1.0_00838.1.g20233.t2</td><td>gb|EOA18432.1| hypothetical protein CARUB_v10006975mg [Capsella rubella]</td><td>114</td><td>489</td><td>4.00E-55</td><td>428.9</td><td>88.6</td><td>93.0</td><td>hypothetical protein CARUB_v10006975mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G26270.1 | Symbols: PFK3 | phosphofructokinase 3 | chr4:13301094-13304030 REVERSE LENGTH=489</td><td>114</td><td>489</td><td>1.00E-57</td><td>428.9</td><td>88.6</td><td>92.1</td></tr>
<tr><td>Rsa1.0_00838.1.g20234.t3</td><td>gb|EOA17998.1| hypothetical protein CARUB_v10006433mg [Capsella rubella]</td><td>119</td><td>119</td><td>5.00E-61</td><td>100.0</td><td>99.2</td><td>99.2</td><td>hypothetical protein CARUB_v10006433mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G56710.1 | Symbols: | Ribosomal protein L31e family protein | chr5:22944003-22944767 REVERSE LENGTH=119</td><td>119</td><td>119</td><td>5.00E-63</td><td>100.0</td><td>97.5</td><td>99.2</td></tr>
<tr><td>Rsa1.0_00838.1.g20235.t2</td><td>ref|XP_002869622.1| mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297315458|gb|EFH45881.1| mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata]</td><td>173</td><td>122</td><td>2.00E-56</td><td>70.5</td><td>68.8</td><td>69.4</td><td>mitochondrial ATP synthase g subunit family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G26210.2 | Symbols: | Mitochondrial ATP synthase subunit G protein | chr4:13282370-13283118 FORWARD LENGTH=122</td><td>173</td><td>122</td><td>4.00E-57</td><td>70.5</td><td>66.5</td><td>68.8</td></tr>
<tr><td>Rsa1.0_00838.1.g20236.t1</td><td>ref|NP_850902.1| putative galactinol synthase [Arabidopsis thaliana] gi|403399402|sp|F4KED2.1|GOLSA_ARATH RecName: Full=Galactinol synthase 10; Short=AtGolS10; Short=GolS-10 gi|332006493|gb|AED93876.1| galactinol synthase 10 [Arabidopsis thaliana]</td><td>61</td><td>328</td><td>7.00E-18</td><td>537.7</td><td>77.0</td><td>85.2</td><td>putative galactinol synthase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G30500.1 | Symbols: | Nucleotide-diphospho-sugar transferases superfamily protein | chr5:11615345-11616926 FORWARD LENGTH=328</td><td>61</td><td>328</td><td>1.00E-20</td><td>537.7</td><td>77.0</td><td>85.2</td></tr>
<tr><td>Rsa1.0_00839.1.g20237.t1</td><td>ref|XP_002868185.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314021|gb|EFH44444.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>216</td><td>276</td><td>2.00E-58</td><td>127.8</td><td>60.2</td><td>68.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G16510.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:5617112-5618194 REVERSE LENGTH=360</td><td>216</td><td>360</td><td>2.00E-37</td><td>166.7</td><td>38.0</td><td>48.1</td></tr>
<tr><td>Rsa1.0_00839.1.g20238.t1</td><td>ref|NP_193309.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana] gi|2244930|emb|CAB10352.1| hypothetical protein [Arabidopsis thaliana] gi|7268322|emb|CAB78616.1| hypothetical protein [Arabidopsis thaliana] gi|332658244|gb|AEE83644.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana]</td><td>283</td><td>468</td><td>3.00E-36</td><td>165.4</td><td>30.4</td><td>36.4</td><td>calcium-dependent lipid-binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15740.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:8964912-8966318 REVERSE LENGTH=468</td><td>283</td><td>468</td><td>7.00E-39</td><td>165.4</td><td>30.4</td><td>36.4</td></tr>
<tr><td>Rsa1.0_00839.1.g20239.t1</td><td>ref|NP_193309.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana] gi|2244930|emb|CAB10352.1| hypothetical protein [Arabidopsis thaliana] gi|7268322|emb|CAB78616.1| hypothetical protein [Arabidopsis thaliana] gi|332658244|gb|AEE83644.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana]</td><td>424</td><td>468</td><td>1.00E-162</td><td>110.4</td><td>70.0</td><td>81.1</td><td>calcium-dependent lipid-binding domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15740.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:8964912-8966318 REVERSE LENGTH=468</td><td>424</td><td>468</td><td>1.00E-164</td><td>110.4</td><td>70.0</td><td>81.1</td></tr>
<tr><td>Rsa1.0_00839.1.g20240.t1</td><td>ref|XP_002870213.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297316049|gb|EFH46472.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>614</td><td>608</td><td>0</td><td>99.0</td><td>85.2</td><td>92.0</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G15720.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:8949569-8951419 FORWARD LENGTH=616</td><td>614</td><td>616</td><td>0</td><td>100.3</td><td>84.7</td><td>91.5</td></tr>
<tr><td>Rsa1.0_00839.1.g20241.t1</td><td>ref|XP_002870217.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297316053|gb|EFH46476.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>102</td><td>102</td><td>5.00E-50</td><td>100.0</td><td>94.1</td><td>97.1</td><td>glutaredoxin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G15680.1 | Symbols: | Thioredoxin superfamily protein | chr4:8931813-8932121 FORWARD LENGTH=102</td><td>102</td><td>102</td><td>2.00E-52</td><td>100.0</td><td>92.2</td><td>98.0</td></tr>
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Rsa1.0_00839.1.g20242.t1	ref|NP_193300.2| uncharacterized protein [Arabidopsis thaliana] gi|332658232|gb|AEE83632.1| uncharacterized protein AT4G15650 [Arabidopsis thaliana]	218	261	1.00E-48	119.7	62.4	74.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G15650.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis; Has 5184 Blast hits to 3451 proteins in 562 species: Archae - 30; Bacteria - 838; Metazoa - 1576; Fungi - 798; Plants - 319; Viruses - 111; Other Eukaryotes - 1512 (source: NCBI BLink). | chr4:8922632-8923815 FORWARD LENGTH=261	218	261	3.00E-51	119.7	62.4	74.3
Rsa1.0_00839.1.g20243.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00839.1.g20244.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00839.1.g20245.t1	gb|EOA17464.1| hypothetical protein CARUB_v10005787mg [Capsella rubella]	193	195	3.00E-69	101.0	83.9	89.1	hypothetical protein CARUB_v10005787mg	gbpln	Capsella rubella	AT4G15610.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:8909162-8910641 FORWARD LENGTH=193	193	193	1.00E-66	100.0	77.2	84.5
Rsa1.0_00839.1.g20246.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1703	1529	0	89.8	22.4	33.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1703	746	8.00E-54	43.8	8.5	12.4
Rsa1.0_00839.1.g20247.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00839.1.g20248.t1	pir||D71420 hypothetical protein - Arabidopsis thaliana	684	703	0	102.8	94.7	96.8	hypothetical protein - Arabidopsis thaliana	----	----	AT4G15560.1 | Symbols: CLA1, DEF, CLA, DXS, DXPS2 | Deoxyxylulose-5-phosphate synthase | chr4:8884218-8887254 FORWARD LENGTH=717	684	717	0	104.8	96.3	98.5
Rsa1.0_00839.1.g20249.t1	emb|CAB91608.1| farnesyltransferase subunit A (FTA) [Arabidopsis thaliana]	218	340	2.00E-39	156.0	36.2	42.2	farnesyltransferase subunit A (FTA)	gbpln	Arabidopsis thaliana	AT3G59380.1 | Symbols: FTA, PLP, ATFTA, PFT/PGGT-IALPHA | farnesyltransferase A | chr3:21944209-21945781 FORWARD LENGTH=326	218	326	9.00E-42	149.5	36.2	42.2
Rsa1.0_00839.1.g20250.t1	gb|ABO36622.1| copia LTR rider [Solanum lycopersicum] gi|133711819|gb|ABO36636.1| copia LTR rider [Solanum lycopersicum]	427	1307	3.00E-68	306.1	43.6	54.8	copia LTR rider	gbpln	Solanum lycopersicum	#	#	#	#	#	#	#
Rsa1.0_00839.1.g20251.t1	ref|NP_849391.2| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana] gi|145333150|ref|NP_001078395.1| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana] gi|222423813|dbj|BAH19872.1| AT4G15530 [Arabidopsis thaliana] gi|332658217|gb|AEE83617.1| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana] gi|332658219|gb|AEE83619.1| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana]	86	956	3.00E-29	1111.6	73.3	84.9	pyruvate, phosphate dikinase 1	gbpln	Arabidopsis thaliana	AT4G15530.4 | Symbols: PPDK | pyruvate orthophosphate dikinase | chr4:8864828-8870727 REVERSE LENGTH=956	86	956	5.00E-32	1111.6	73.3	84.9
Rsa1.0_00839.1.g20252.t1	ref|NP_193288.2| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana] gi|222424574|dbj|BAH20242.1| AT4G15530 [Arabidopsis thaliana] gi|332658216|gb|AEE83616.1| pyruvate, phosphate dikinase 1 [Arabidopsis thaliana]	569	875	0	153.8	95.3	97.7	pyruvate, phosphate dikinase 1	gbpln	Arabidopsis thaliana	AT4G15530.2 | Symbols: PPDK | pyruvate orthophosphate dikinase | chr4:8864828-8869183 REVERSE LENGTH=875	569	875	0	153.8	95.3	97.7
Rsa1.0_00840.1.g20253.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00840.1.g20254.t1	ref|XP_002876267.1| hypothetical protein ARALYDRAFT_324005 [Arabidopsis lyrata subsp. lyrata] gi|297322105|gb|EFH52526.1| hypothetical protein ARALYDRAFT_324005 [Arabidopsis lyrata subsp. lyrata]	411	436	1.00E-175	106.1	81.0	86.6	hypothetical protein ARALYDRAFT_324005	gbpln	Arabidopsis lyrata	AT3G54740.2 | Symbols: | Protein of unknown function, DUF593 | chr3:20262949-20264466 FORWARD LENGTH=438	411	438	1.00E-173	106.6	81.0	86.4
Rsa1.0_00840.1.g20255.t1	ref|NP_191029.1| sugar isomerase domain-containing protein [Arabidopsis thaliana] gi|75182157|sp|Q9M1T1.1|SETH3_ARATH RecName: Full=Probable arabinose 5-phosphate isomerase; Short=API; AltName: Full=CBS domain-containing protein CBSSIS1 gi|7258373|emb|CAB77589.1| sugar-phosphate isomerase-like protein [Arabidopsis thaliana] gi|110742297|dbj|BAE99073.1| sugar-phosphate isomerase - like protein [Arabidopsis thaliana] gi|332645746|gb|AEE79267.1| probable arabinose 5-phosphate isomerase [Arabidopsis thaliana]	337	350	1.00E-171	103.9	93.5	96.7	sugar isomerase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G54690.1 | Symbols: | Sugar isomerase (SIS) family protein | chr3:20246586-20247810 FORWARD LENGTH=350	337	350	1.00E-174	103.9	93.5	96.7

Rsa1.0_00840.1.g20256.t1	gb|EOA24747.1| hypothetical protein CARUB_v10018024mg [Capsella rubella]	201	210	3.00E-59	104.5	70.1	76.1	hypothetical protein CARUB_v10018024mg	gbpln	Capsella rubella	AT3G54680.1 | Symbols: | proteophosphoglycan-related | chr3:20244568-20245689 FORWARD LENGTH=211	201	211	5.00E-51	105.0	70.1	79.1
Rsa1.0_00840.1.g20257.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00840.1.g20258.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00840.1.g20259.t1	ref|XP_002877991.1| kinetochore protein [Arabidopsis lyrata subsp. lyrata] gi|297323829|gb|EFH54250.1| kinetochore protein [Arabidopsis lyrata subsp. lyrata]	570	567	0	99.5	73.3	83.2	kinetochore protein	gbpln	Arabidopsis lyrata	AT3G54630.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Kinetochore protein Ndc80 (InterPro:IPR005550); Has 24780 Blast hits to 15608 proteins in 1321 species: Archae - 545; Bacteria - 2969; Metazoa - 12597; Fungi - 2181; Plants - 1581; Viruses - 39; Other Eukaryotes - 4868 (source: NCBI BLink). | chr3:20221195-20222901 REVERSE LENGTH=568	570	568	0	99.6	72.5	82.6
Rsa1.0_00840.1.g20260.t1	ref|NP_191023.1| class I glutamine amidotransferase domain-containing protein [Arabidopsis thaliana] gi|7258363|emb|CAB77580.1| putative protein [Arabidopsis thaliana] gi|20466235|gb|AAM20435.1| putative protein [Arabidopsis thaliana] gi|30725650|gb|AAP37847.1| At3g54600 [Arabidopsis thaliana] gi|332645733|gb|AEE79254.1| class I glutamine amidotransferase domain-containing protein [Arabidopsis thaliana]	447	399	0	89.3	78.3	83.2	class I glutamine amidotransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G54600.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr3:20211048-20212876 FORWARD LENGTH=399	447	399	0	89.3	78.3	83.2
Rsa1.0_00840.1.g20261.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	497	1142	2.00E-44	229.8	19.5	27.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	497	256	6.00E-25	51.5	14.5	20.1
Rsa1.0_00840.1.g20262.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00840.1.g20263.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00840.1.g20264.t1	gb|AFJ66186.1| hypothetical protein 11M19.5 [Arabidopsis halleri]	1371	1557	0	113.6	64.3	77.3	hypothetical protein 11M19.5	gbpln	Arabidopsis halleri	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1371	158	4.00E-29	11.5	4.7	5.9
Rsa1.0_00840.1.g20265.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00841.1.g20266.t1	ref|XP_002886185.1| hypothetical protein ARALYDRAFT_343491 [Arabidopsis lyrata subsp. lyrata] gi|297332025|gb|EFH62444.1| hypothetical protein ARALYDRAFT_343491 [Arabidopsis lyrata subsp. lyrata]	184	185	4.00E-93	100.5	89.1	95.7	hypothetical protein ARALYDRAFT_343491	gbpln	Arabidopsis lyrata	AT4G36800.2 | Symbols: RCE1 | RUB1 conjugating enzyme 1 | chr4:17341237-17342148 REVERSE LENGTH=184	184	184	2.00E-95	100.0	88.0	93.5
Rsa1.0_00841.1.g20267.t1	ref|NP_179453.2| uncharacterized protein [Arabidopsis thaliana] gi|334302873|sp|Q56XQ0.3|U496I_ARATH RecName: Full=UPF0496 protein At2g18630 gi|62320594|dbj|BAD95236.1| hypothetical protein [Arabidopsis thaliana] gi|330251693|gb|AEC06787.1| uncharacterized protein AT2G18630 [Arabidopsis thaliana]	349	393	1.00E-134	112.6	74.5	87.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G18630.1 | Symbols: | Protein of unknown function (DUF677) | chr2:8081154-8082496 FORWARD LENGTH=393	349	393	1.00E-137	112.6	74.5	87.4
Rsa1.0_00841.1.g20268.t1	ref|XP_002886186.1| hypothetical protein ARALYDRAFT_480767 [Arabidopsis lyrata subsp. lyrata] gi|297332026|gb|EFH62445.1| hypothetical protein ARALYDRAFT_480767 [Arabidopsis lyrata subsp. lyrata]	372	372	1.00E-179	100.0	81.7	91.9	hypothetical protein ARALYDRAFT_480767	gbpln	Arabidopsis lyrata	AT2G18640.1 | Symbols: GGPS4 | geranylgeranyl pyrophosphate synthase 4 | chr2:8083754-8084872 REVERSE LENGTH=372	372	372	0	100.0	81.5	92.2
Rsa1.0_00841.1.g20269.t1	ref|XP_002886188.1| hypothetical protein ARALYDRAFT_480768 [Arabidopsis lyrata subsp. lyrata] gi|297332028|gb|EFH62447.1| hypothetical protein ARALYDRAFT_480768 [Arabidopsis lyrata subsp. lyrata]	416	413	1.00E-150	99.3	74.5	80.0	hypothetical protein ARALYDRAFT_480768	gbpln	Arabidopsis lyrata	AT2G18650.1 | Symbols: MEE16 | RING/U-box superfamily protein | chr2:8086860-8088131 REVERSE LENGTH=423	416	423	1.00E-148	101.7	73.1	79.3

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<tr><td>Rsa1.0_00841.1.g20270.t1</td><td>ref|XP_002873943.1| calcium-dependent protein kinase 34 [Arabidopsis lyrata subsp. lyrata] gi|297319780|gb|EFH50202.1| calcium-dependent protein kinase 34 [Arabidopsis lyrata subsp. lyrata]</td><td>148</td><td>525</td><td>2.00E-17</td><td>354.7</td><td>27.7</td><td>30.4</td><td>calcium-dependent protein kinase 34</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G19360.1 | Symbols: CPK34 | calcium-dependent protein kinase 34 | chr5:6521716-6523780 REVERSE LENGTH=523</td><td>148</td><td>523</td><td>6.00E-20</td><td>353.4</td><td>27.7</td><td>30.4</td></tr>
<tr><td>Rsa1.0_00841.1.g20271.t1</td><td>gb|EOA32326.1| hypothetical protein CARUB_v10015598mg [Capsella rubella]</td><td>319</td><td>315</td><td>1.00E-119</td><td>98.7</td><td>69.9</td><td>79.9</td><td>hypothetical protein CARUB_v10015598mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G18680.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G18690.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:8094780-8095643 FORWARD LENGTH=287</td><td>319</td><td>287</td><td>1.00E-110</td><td>90.0</td><td>66.5</td><td>77.1</td></tr>
<tr><td>Rsa1.0_00841.1.g20272.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>1939</td><td>1274</td><td>0</td><td>65.7</td><td>31.7</td><td>43.6</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1939</td><td>575</td><td>1.00E-69</td><td>29.7</td><td>8.9</td><td>13.9</td></tr>
<tr><td>Rsa1.0_00841.1.g20273.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00841.1.g20274.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00841.1.g20275.t1</td><td>ref|XP_002884153.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329993|gb|EFH60412.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>863</td><td>871</td><td>0</td><td>100.9</td><td>90.8</td><td>95.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G18700.1 | Symbols: ATTPS11, TPS11, ATTPSB | trehalose phosphatase/synthase 11 | chr2:8109043-8111799 FORWARD LENGTH=862</td><td>863</td><td>862</td><td>0</td><td>99.9</td><td>89.5</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00841.1.g20276.t1</td><td>gb|EOA30430.1| hypothetical protein CARUB_v10013554mg [Capsella rubella]</td><td>484</td><td>488</td><td>0</td><td>100.8</td><td>89.9</td><td>93.0</td><td>hypothetical protein CARUB_v10013554mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G18730.1 | Symbols: ATDGK3, DGK3 | diacylglycerol kinase 3 | chr2:8118976-8121689 FORWARD LENGTH=488</td><td>484</td><td>488</td><td>0</td><td>100.8</td><td>88.8</td><td>92.4</td></tr>
<tr><td>Rsa1.0_00841.1.g20277.t1</td><td>gb|EOA18429.1| hypothetical protein CARUB_v10006973mg [Capsella rubella]</td><td>426</td><td>411</td><td>1.00E-115</td><td>96.5</td><td>54.7</td><td>70.2</td><td>hypothetical protein CARUB_v10006973mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G22000.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr1:7744189-7747123 FORWARD LENGTH=717</td><td>426</td><td>717</td><td>5.00E-92</td><td>168.3</td><td>48.8</td><td>62.7</td></tr>
<tr><td>Rsa1.0_00841.1.g20278.t1</td><td>gb|ABA96411.1| retrotransposon protein, putative, unclassified [Oryza sativa Japonica Group]</td><td>171</td><td>256</td><td>4.00E-71</td><td>149.7</td><td>73.1</td><td>86.5</td><td>retrotransposon protein, putative, unclassified</td><td>gbpln</td><td>Oryza sativa</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>171</td><td>1262</td><td>1.00E-31</td><td>738.0</td><td>32.7</td><td>49.1</td></tr>
<tr><td>Rsa1.0_00841.1.g20279.t1</td><td>ref|NP_179480.2| transducin/WD-40 repeat-containing protein [Arabidopsis thaliana] gi|330251729|gb|AEC06823.1| transducin/WD-40 repeat-containing protein [Arabidopsis thaliana]</td><td>175</td><td>804</td><td>3.00E-44</td><td>459.4</td><td>57.1</td><td>60.0</td><td>transducin/WD-40 repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G18900.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:8188491-8192409 REVERSE LENGTH=804</td><td>175</td><td>804</td><td>1.00E-46</td><td>459.4</td><td>57.1</td><td>60.0</td></tr>
<tr><td>Rsa1.0_00841.1.g20280.t1</td><td>ref|XP_002884186.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297330026|gb|EFH60445.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]</td><td>202</td><td>131</td><td>3.00E-58</td><td>64.9</td><td>55.4</td><td>58.4</td><td>hydroxyproline-rich glycoprotein family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G18910.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr2:8193016-8194131 REVERSE LENGTH=131</td><td>202</td><td>131</td><td>8.00E-60</td><td>64.9</td><td>54.5</td><td>58.4</td></tr>
<tr><td>Rsa1.0_00841.1.g20281.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>282</td><td>1142</td><td>5.00E-46</td><td>405.0</td><td>37.6</td><td>48.2</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>282</td><td>575</td><td>7.00E-17</td><td>203.9</td><td>20.6</td><td>32.6</td></tr>
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<tr><td>Rsa1.0_00842.1.g20282.t1</td><td>ref|NP_198097.1| mevalonate kinase [Arabidopsis thaliana] gi|30690651|ref|NP_851084.1| mevalonate kinase [Arabidopsis thaliana] gi|334187979|ref|NP_001190411.1| mevalonate kinase [Arabidopsis thaliana] gi|1170660|sp|P46086.1|KIME_ARATH RecName: Full=Mevalonate kinase; Short=MK gi|4883990|gb|AAD31719.1|AF141853_1 mevalonate kinase [Arabidopsis thaliana] gi|456614|emb|CAA54820.1| mevalonate kinase [Arabidopsis thaliana] gi|20260532|gb|AAM13164.1| mevalonate kinase [Arabidopsis thaliana] gi|21536584|gb|AAM60916.1| mevalonate kinase [Arabidopsis thaliana] gi|25083757|gb|AAN72115.1| mevalonate kinase [Arabidopsis thaliana] gi|332006305|gb|AED93688.1| mevalonate kinase [Arabidopsis thaliana] gi|332006306|gb|AED93689.1| mevalonate kinase [Arabidopsis thaliana] gi|332006307|gb|AED93690.1| mevalonate kinase [Arabidopsis thaliana]</td><td>376</td><td>378</td><td>0</td><td>100.5</td><td>88.3</td><td>94.1</td><td>mevalonate kinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G27450.3 | Symbols: MK | mevalonate kinase | chr5:9691051-9692975 FORWARD LENGTH=378</td><td>376</td><td>378</td><td>0</td><td>100.5</td><td>88.3</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00842.1.g20283.t1</td><td>ref|NP_198098.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|122214236|sp|Q3E911.1|PP400_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g27460 gi|332006308|gb|AED93691.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]</td><td>482</td><td>491</td><td>0</td><td>101.9</td><td>76.8</td><td>85.3</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G27460.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:9693262-9694815 REVERSE LENGTH=491</td><td>482</td><td>491</td><td>0</td><td>101.9</td><td>76.8</td><td>85.3</td></tr>
<tr><td>Rsa1.0_00842.1.g20284.t3</td><td>gb|EOA20124.1| hypothetical protein CARUB_v10000404mg, partial [Capsella rubella]</td><td>758</td><td>664</td><td>0</td><td>87.6</td><td>70.3</td><td>76.1</td><td>hypothetical protein CARUB_v10000404mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G27540.2 | Symbols: MIRO1 | MIRO-related GTP-ase 1 | chr5:9722816-9727112 FORWARD LENGTH=648</td><td>758</td><td>648</td><td>0</td><td>85.5</td><td>69.7</td><td>76.1</td></tr>
<tr><td>Rsa1.0_00842.1.g20285.t1</td><td>ref|XP_002893912.1| hypothetical protein ARALYDRAFT_314052 [Arabidopsis lyrata subsp. lyrata] gi|297339754|gb|EFH70171.1| hypothetical protein ARALYDRAFT_314052 [Arabidopsis lyrata subsp. lyrata]</td><td>393</td><td>441</td><td>7.00E-97</td><td>112.2</td><td>49.1</td><td>55.7</td><td>hypothetical protein ARALYDRAFT_314052</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G27470.1 | Symbols: | seryl-tRNA synthetase / serine--tRNA ligase | chr5:9695087-9697154 FORWARD LENGTH=451</td><td>393</td><td>451</td><td>3.00E-91</td><td>114.8</td><td>41.7</td><td>46.8</td></tr>
<tr><td>Rsa1.0_00842.1.g20286.t1</td><td>ref|NP_198104.1| peroxisomal adenine nucleotide carrier 2 [Arabidopsis thaliana] gi|75304483|sp|Q8VZS0.1|PNC2_ARATH RecName: Full=Peroxisomal adenine nucleotide carrier 2 gi|17380872|gb|AAL36248.1| unknown protein [Arabidopsis thaliana] gi|21689661|gb|AAM67452.1| unknown protein [Arabidopsis thaliana] gi|332006313|gb|AED93696.1| peroxisomal adenine nucleotide carrier 2 [Arabidopsis thaliana]</td><td>316</td><td>321</td><td>1.00E-155</td><td>101.6</td><td>84.8</td><td>94.9</td><td>peroxisomal adenine nucleotide carrier 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G27520.1 | Symbols: PNC2 | peroxisomal adenine nucleotide carrier 2 | chr5:9714664-9716244 REVERSE LENGTH=321</td><td>316</td><td>321</td><td>1.00E-158</td><td>101.6</td><td>84.8</td><td>94.9</td></tr>
<tr><td>Rsa1.0_00842.1.g20287.t1</td><td>ref|NP_198106.1| MIRO-related GTP-ase 1 [Arabidopsis thaliana] gi|79328825|ref|NP_001031953.1| MIRO-related GTP-ase 1 [Arabidopsis thaliana] gi|19698867|gb|AAL91169.1| unknown protein [Arabidopsis thaliana] gi|28058938|gb|AAO29970.1| unknown protein [Arabidopsis thaliana] gi|332006315|gb|AED93698.1| MIRO-related GTP-ase 1 [Arabidopsis thaliana] gi|332006316|gb|AED93699.1| MIRO-related GTP-ase 1 [Arabidopsis thaliana]</td><td>721</td><td>648</td><td>0</td><td>89.9</td><td>74.5</td><td>80.7</td><td>MIRO-related GTP-ase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G27540.2 | Symbols: MIRO1 | MIRO-related GTP-ase 1 | chr5:9722816-9727112 FORWARD LENGTH=648</td><td>721</td><td>648</td><td>0</td><td>89.9</td><td>74.5</td><td>80.7</td></tr>
<tr><td>Rsa1.0_00842.1.g20288.t1</td><td>gb|EOA19994.1| hypothetical protein CARUB_v10000259mg [Capsella rubella]</td><td>775</td><td>793</td><td>0</td><td>102.3</td><td>84.6</td><td>90.8</td><td>hypothetical protein CARUB_v10000259mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G27550.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:9727634-9731323 REVERSE LENGTH=765</td><td>775</td><td>765</td><td>0</td><td>98.7</td><td>83.4</td><td>89.8</td></tr>
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Rsa1.0_00842.1.g20289.t1	ref|NP_198114.2| cyclin H;1 [Arabidopsis thaliana] gi|75162701|sp|Q8W5S1.1|CCH11_ARATH RecName: Full=Cyclin-H1-1; Short=CycH1;1 gi|17026115|dbj|BAB72144.1| cyclin H [Arabidopsis thaliana] gi|26452432|dbj|BAC43301.1| putative cyclin H AtCycH1 [Arabidopsis thaliana] gi|332006324|gb|AED93707.1| cyclin H;1 [Arabidopsis thaliana]	723	336	1.00E-172	46.5	41.4	43.2	cyclin H;1	gbpln	Arabidopsis thaliana	AT5G27620.1 | Symbols: CYCH;1 | cyclin H;1 | chr5:9771762-9774684 FORWARD LENGTH=336	723	336	1.00E-175	46.5	41.4	43.2
Rsa1.0_00842.1.g20290.t1	ref|NP_198117.2| PWWP domain-containing protein [Arabidopsis thaliana] gi|332006328|gb|AED93711.1| PWWP domain-containing protein [Arabidopsis thaliana]	1045	1072	0	102.6	73.1	81.3	PWWP domain-containing protein	gbpln	Arabidopsis thaliana	AT5G27650.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr5:9785511-9789094 FORWARD LENGTH=1072	1045	1072	0	102.6	73.1	81.3
Rsa1.0_00842.1.g20291.t1	ref|NP_198119.1| histone H2A 7 [Arabidopsis thaliana] gi|75306451|sp|Q94F49.1|H2A5_ARATH RecName: Full=Probable histone H2A.5; AltName: Full=HTA7 gi|14326516|gb|AAK60303.1|AF385711_1 AT5g27670/F15A18_130 [Arabidopsis thaliana] gi|18700220|gb|AAL77720.1| AT5g27670/F15A18_130 [Arabidopsis thaliana] gi|332006330|gb|AED93713.1| histone H2A 7 [Arabidopsis thaliana]	152	150	5.00E-65	98.7	84.2	91.4	histone H2A 7	gbpln	Arabidopsis thaliana	AT5G27670.1 | Symbols: HTA7 | histone H2A 7 | chr5:9792807-9793365 REVERSE LENGTH=150	152	150	1.00E-67	98.7	84.2	91.4
Rsa1.0_00842.1.g20292.t1	gb|EOA21887.1| hypothetical protein CARUB_v10002364mg [Capsella rubella]	82	82	3.00E-40	100.0	93.9	98.8	hypothetical protein CARUB_v10002364mg	gbpln	Capsella rubella	AT5G27700.1 | Symbols: | Ribosomal protein S21e | chr5:9807541-9808048 REVERSE LENGTH=82	82	82	1.00E-42	100.0	92.7	98.8
Rsa1.0_00842.1.g20293.t6	ref|NP_198123.2| uncharacterized protein [Arabidopsis thaliana] gi|40823291|gb|AAR92273.1| At5g27710 [Arabidopsis thaliana] gi|45752716|gb|AAS76256.1| At5g27710 [Arabidopsis thaliana] gi|332006334|gb|AED93717.1| uncharacterized protein AT5G27710 [Arabidopsis thaliana]	1200	335	1.00E-141	27.9	21.7	23.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G27710.1 | Symbols: | unknown protein; Has 49 Blast hits to 49 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:9813069-9815018 FORWARD LENGTH=335	1200	335	1.00E-144	27.9	21.7	23.9
Rsa1.0_00842.1.g20294.t1	sp|Q43582.1|LSM4_TOBAC RecName: Full=Probable U6 snRNA-associated Sm-like protein LSm4; AltName: Full=Glycine-rich protein 10; Short=GRP 10 gi|790473|emb|CAA58702.1| unnamed protein product [Nicotiana tabacum]	129	146	1.00E-51	113.2	77.5	79.1	RecName: Full=Probable U6 snRNA-associated Sm-like protein LSm4; AltName: Full=Glycine-rich protein 10; Short=GRP 10 gi|790473|emb|CAA58702.1| unnamed protein product	gbpln	Nicotiana tabacum	AT5G27720.1 | Symbols: emb1644 | Small nuclear ribonucleoprotein family protein | chr5:9815904-9817304 FORWARD LENGTH=129	129	129	5.00E-51	100.0	70.5	70.5
Rsa1.0_00842.1.g20295.t11	ref|XP_002874350.1| nucleoside-triphosphatase/ nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] gi|297320187|gb|EFH50609.1| nucleoside-triphosphatase/ nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	448	359	1.00E-109	80.1	49.6	56.3	nucleoside-triphosphatase/ nucleotide binding protein	gbpln	Arabidopsis lyrata	AT5G27740.1 | Symbols: EMB161, EMB2775, EMB251, RFC3 | ATPase family associated with various cellular activities (AAA) | chr5:9823831-9826869 FORWARD LENGTH=354	448	354	1.00E-111	79.0	49.1	56.0
Rsa1.0_00843.1.g20296.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00843.1.g20297.t1	gb|AAD15359.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	272	532	6.00E-21	195.6	25.4	39.0	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00843.1.g20298.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00843.1.g20299.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	206	1142	2.00E-19	554.4	34.0	47.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00843.1.g20300.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00843.1.g20301.t2	gb|AAD36943.1|AF069441_3 putative polyprotein [Arabidopsis thaliana] gi|7267195|emb|CAB77906.1| putative polyprotein [Arabidopsis thaliana]	950	778	5.00E-58	81.9	16.3	23.8	putative polyprotein	gbpln	Arabidopsis thaliana	ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145	950	145	1.00E-19	15.3	4.5	6.9
Rsa1.0_00843.1.g20302.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	210	1225	9.00E-37	583.3	39.0	59.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00843.1.g20303.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	367	1142	2.00E-91	311.2	45.8	61.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	367	575	5.00E-43	156.7	32.2	50.7

Rsa1.0_00843.1.g20304.t1	gb|EOA37712.1| hypothetical protein CARUB_v10012448mg [Capsella rubella]	97	95	6.00E-26	97.9	61.9	78.4	hypothetical protein CARUB_v10012448mg	gbpln	Capsella rubella	AT1G48750.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:18036019-18036303 FORWARD LENGTH=94	97	94	1.00E-28	96.9	68.0	85.6
Rsa1.0_00843.1.g20305.t1	dbj|BAJ33786.1| unnamed protein product [Thellungiella halophila]	122	308	3.00E-41	252.5	73.8	77.9	unnamed protein product	----	----	AT3G63520.1 | Symbols: CCD1, ATCCD1, ATNCED1, NCED1 | carotenoid cleavage dioxygenase 1 | chr3:23452940-23455896 FORWARD LENGTH=538	122	538	3.00E-43	441.0	73.8	77.0
Rsa1.0_00843.1.g20306.t1	gb|EOA38518.1| hypothetical protein CARUB_v10010307mg, partial [Capsella rubella]	162	206	2.00E-41	127.2	71.0	80.9	hypothetical protein CARUB_v10010307mg, partial	gbpln	Capsella rubella	AT3G18295.1 | Symbols: | Protein of unknown function (DUF1639) | chr3:6281268-6282000 FORWARD LENGTH=216	162	216	2.00E-41	133.3	67.9	81.5
Rsa1.0_00843.1.g20307.t2	ref|XP_002894133.1| mov34 family protein [Arabidopsis lyrata subsp. lyrata] gi|297339975|gb|EFH70392.1| mov34 family protein [Arabidopsis lyrata subsp. lyrata]	530	507	0	95.7	81.1	85.3	mov34 family protein	gbpln	Arabidopsis lyrata	AT1G48790.1 | Symbols: AMSH1 | associated molecule with the SH3 domain of STAM 1 | chr1:18043925-18047427 REVERSE LENGTH=507	530	507	0	95.7	80.8	85.1
Rsa1.0_00843.1.g20308.t4	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1122	1225	0	109.2	36.5	48.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1122	575	2.00E-42	51.2	7.8	12.3
Rsa1.0_00844.1.g20309.t1	ref|XP_002892284.1| thiF family protein [Arabidopsis lyrata subsp. lyrata] gi|297338126|gb|EFH68543.1| thiF family protein [Arabidopsis lyrata subsp. lyrata]	106	447	8.00E-17	421.7	50.0	55.7	thiF family protein	gbpln	Arabidopsis lyrata	AT1G05350.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:1560891-1564005 REVERSE LENGTH=431	106	431	4.00E-19	406.6	49.1	54.7
Rsa1.0_00844.1.g20310.t2	gb|AAD25596.1| putative helicase [Arabidopsis thaliana]	1371	1219	0	88.9	26.0	34.1	putative helicase	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1371	331	2.00E-67	24.1	9.9	13.6
Rsa1.0_00844.1.g20311.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	511	490	2.00E-80	95.9	32.7	55.6	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	511	566	8.00E-83	110.8	33.3	57.7
Rsa1.0_00844.1.g20312.t1	gb|EOA17284.1| hypothetical protein CARUB_v10005554mg [Capsella rubella]	238	255	1.00E-102	107.1	80.3	80.7	hypothetical protein CARUB_v10005554mg	gbpln	Capsella rubella	AT4G23470.1 | Symbols: | PLAC8 family protein | chr4:12249289-12251079 FORWARD LENGTH=255	238	255	1.00E-101	107.1	76.5	79.8
Rsa1.0_00844.1.g20313.t1	gb|ACC91275.1| fringe-related protein [Capsella rubella] gi|482552213|gb|EOA16406.1| hypothetical protein CARUB_v10004561mg [Capsella rubella]	536	534	0	99.6	88.6	92.7	fringe-related protein	gbpln	Capsella rubella	AT4G23490.1 | Symbols: | Protein of unknown function (DUF604) | chr4:12251580-12253973 REVERSE LENGTH=526	536	526	0	98.1	88.2	92.2
Rsa1.0_00844.1.g20314.t1	ref|NP_563972.1| uncharacterized protein [Arabidopsis thaliana] gi|30684315|ref|NP_849667.1| uncharacterized protein [Arabidopsis thaliana] gi|21617951|gb|AAM67001.1| unknown [Arabidopsis thaliana] gi|110742955|dbj|BAE99372.1| hypothetical protein [Arabidopsis thaliana] gi|332191186|gb|AEE29307.1| uncharacterized protein AT1G15350 [Arabidopsis thaliana] gi|332191187|gb|AEE29308.1| uncharacterized protein AT1G15350 [Arabidopsis thaliana]	126	154	1.00E-39	122.2	67.5	73.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G15350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G15770.2); Has 148 Blast hits to 148 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 141; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr1:5278481-5279486 REVERSE LENGTH=154	126	154	2.00E-42	122.2	67.5	73.0
Rsa1.0_00844.1.g20315.t1	ref|XP_002867705.1| hypothetical protein ARALYDRAFT_492522 [Arabidopsis lyrata subsp. lyrata] gi|297313541|gb|EFH43964.1| hypothetical protein ARALYDRAFT_492522 [Arabidopsis lyrata subsp. lyrata]	255	86	3.00E-27	33.7	23.1	28.2	hypothetical protein ARALYDRAFT_492522	gbpln	Arabidopsis lyrata	AT4G23493.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12256327-12256693 REVERSE LENGTH=87	255	87	6.00E-29	34.1	23.5	28.2
Rsa1.0_00844.1.g20316.t1	ref|XP_002869777.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297315613|gb|EFH46036.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	542	494	0	91.1	85.2	87.3	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT4G23500.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:12264640-12267074 FORWARD LENGTH=495	542	495	0	91.3	83.4	85.4
Rsa1.0_00844.1.g20317.t1	ref|XP_002890732.1| hypothetical protein ARALYDRAFT_890279 [Arabidopsis lyrata subsp. lyrata] gi|297336574|gb|EFH66991.1| hypothetical protein ARALYDRAFT_890279 [Arabidopsis lyrata subsp. lyrata]	207	311	3.00E-24	150.2	36.7	52.7	hypothetical protein ARALYDRAFT_890279	gbpln	Arabidopsis lyrata	AT3G43950.1 | Symbols: | Protein kinase superfamily protein | chr3:15766361-15767014 FORWARD LENGTH=217	207	217	6.00E-22	104.8	30.0	45.9
Rsa1.0_00844.1.g20318.t1	gb|EOA15864.1| hypothetical protein CARUB_v10007726mg [Capsella rubella]	293	366	8.00E-49	124.9	37.9	51.5	hypothetical protein CARUB_v10007726mg	gbpln	Capsella rubella	AT4G23515.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr4:12271382-12272842 REVERSE LENGTH=331	293	331	2.00E-44	113.0	36.9	50.5

Rsa1.0_00844.1.g20319.t1	gb|AAG28902.1|AC008113_18 F12A21.21 [Arabidopsis thaliana]	364	341	1.00E-104	93.7	59.6	67.3	F12A21.21	gbpln	Arabidopsis thaliana	AT5G25290.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr5:8778592-8779785 FORWARD LENGTH=397	364	397	4.00E-65	109.1	43.7	57.1
Rsa1.0_00844.1.g20320.t2	#	#	#	#	#	#	#	-	----	----	AT4G29060.1 | Symbols: emb2726 | elongation factor Ts family protein | chr4:14317744-14321315 FORWARD LENGTH=953	264	953	9.00E-12	361.0	19.3	22.7
Rsa1.0_00844.1.g20321.t1	gb|EOA21337.1| hypothetical protein CARUB_v10001699mg [Capsella rubella]	300	272	7.00E-17	90.7	22.7	36.7	hypothetical protein CARUB_v10001699mg	gbpln	Capsella rubella	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	300	472	2.00E-13	157.3	16.3	29.3
Rsa1.0_00844.1.g20322.t1	ref|XP_002879675.1| hypothetical protein ARALYDRAFT_345479 [Arabidopsis lyrata subsp. lyrata] gi|297325514|gb|EFH55934.1| hypothetical protein ARALYDRAFT_345479 [Arabidopsis lyrata subsp. lyrata]	139	160	4.00E-19	115.1	37.4	45.3	hypothetical protein ARALYDRAFT_345479	gbpln	Arabidopsis lyrata	AT4G23510.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:12267516-12270526 REVERSE LENGTH=635	139	635	9.00E-12	456.8	25.9	30.9
Rsa1.0_00844.1.g20323.t1	gb|EOA18048.1| hypothetical protein CARUB_v10006494mg [Capsella rubella]	328	351	1.00E-135	107.0	72.3	85.1	hypothetical protein CARUB_v10006494mg	gbpln	Capsella rubella	AT4G23520.1 | Symbols: | Cysteine proteinases superfamily protein | chr4:12274457-12276219 REVERSE LENGTH=356	328	356	1.00E-134	108.5	69.8	82.3
Rsa1.0_00845.1.g20324.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	240	1333	4.00E-51	555.4	42.1	54.2	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	240	575	5.00E-37	239.6	31.3	50.0
Rsa1.0_00845.1.g20325.t1	gb|AAD20434.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	96	507	2.00E-14	528.1	45.8	58.3	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00845.1.g20326.t1	ref|NP_566824.1| carbamoyl phosphate synthetase A [Arabidopsis thaliana] gi|9294479|dbj|BAB02698.1| carbamoyl-phosphate synthetase small subunit [Arabidopsis thaliana] gi|15028109|gb|AAK76678.1| putative carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana] gi|19310631|gb|AAL85046.1| putative carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana] gi|332643837|gb|AEE77358.1| carbamoyl phosphate synthetase A [Arabidopsis thaliana]	425	430	0	101.2	90.8	94.8	carbamoyl phosphate synthetase A	gbpln	Arabidopsis thaliana	AT3G27740.1 | Symbols: CARA | carbamoyl phosphate synthetase A | chr3:10281470-10283792 REVERSE LENGTH=430	425	430	0	101.2	90.8	94.8
Rsa1.0_00845.1.g20327.t3	sp|P04796.2|G3PC_SINAL RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product [Sinapis alba]	203	338	3.00E-29	166.5	33.5	35.0	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product	gbpln	Sinapis alba	AT3G04120.1 | Symbols: GAPC, GAPC-1, GAPC1 | glyceraldehyde-3-phosphate dehydrogenase C subunit 1 | chr3:1081077-1083131 FORWARD LENGTH=338	203	338	1.00E-30	166.5	32.0	35.0
Rsa1.0_00845.1.g20328.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00845.1.g20329.t1	gb|AAF24605.1|AC021046_3 transfactor, putative; 28697-27224 [Arabidopsis thaliana] gi|119360087|gb|ABL66772.1| At1g69580 [Arabidopsis thaliana]	328	332	1.00E-130	101.2	78.4	86.6	transfactor, putative; 28697-27224	gbpln	Arabidopsis thaliana	AT1G69580.1 | Symbols: | Homeodomain-like superfamily protein | chr1:26172127-26173612 FORWARD LENGTH=336	328	336	1.00E-133	102.4	78.4	86.6
Rsa1.0_00845.1.g20330.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00845.1.g20331.t1	gb|EOA33235.1| hypothetical protein CARUB_v10021295mg [Capsella rubella]	119	124	2.00E-35	104.2	66.4	78.2	hypothetical protein CARUB_v10021295mg	gbpln	Capsella rubella	AT1G69588.1 | Symbols: CLE45 | CLAVATA3/ESR-RELATED 45 | chr1:26178150-26178524 FORWARD LENGTH=124	119	124	2.00E-37	104.2	62.2	80.7
Rsa1.0_00845.1.g20332.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00845.1.g20333.t1	gb|EOA35643.1| hypothetical protein CARUB_v10020860mg [Capsella rubella]	231	245	2.00E-97	106.1	81.0	85.7	hypothetical protein CARUB_v10020860mg	gbpln	Capsella rubella	AT1G69600.1 | Symbols: ZFHD1, ATHB29, ZHD11 | zinc finger homeodomain 1 | chr1:26182470-26183198 FORWARD LENGTH=242	231	242	3.00E-98	104.8	77.1	81.8
Rsa1.0_00845.1.g20334.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00845.1_g20335.t1	ref|XP_002887247.1| hypothetical protein ARALYDRAFT_476096 [Arabidopsis lyrata subsp. lyrata] gi|297333088|gb|EFH63506.1| hypothetical protein ARALYDRAFT_476096 [Arabidopsis lyrata subsp. lyrata]	117	630	2.00E-18	538.5	57.3	65.0	hypothetical protein ARALYDRAFT_476096	gbpln	Arabidopsis lyrata	AT1G69610.1 | Symbols: | Protein of unknown function (DUF1666) | chr1:26186954-26189349 FORWARD LENGTH=636	117	636	1.00E-17	543.6	47.0	55.6
Rsa1.0_00846.1_g20336.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00846.1_g20337.t3	gb|AAD36950.1|AF069441_10 putative transposon protein [Arabidopsis thaliana] gi|7267188|emb|CAB77899.1| putative transposon protein [Arabidopsis thaliana]	682	1011	3.00E-19	148.2	7.8	11.3	putative transposon protein	gbpln	Arabidopsis thaliana	AT4G07350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40129.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:4172609-4175227 REVERSE LENGTH=330	682	330	2.00E-19	48.4	5.6	7.5
Rsa1.0_00846.1_g20338.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00846.1_g20339.t1	gb|EOA29932.1| hypothetical protein CARUB_v10013024mg, partial [Capsella rubella]	739	774	0	104.7	93.1	95.5	hypothetical protein CARUB_v10013024mg, partial	gbpln	Capsella rubella	AT2G20000.1 | Symbols: HBT, CDC27b | CDC27 family protein | chr2:8632324-8636900 REVERSE LENGTH=744	739	744	0	100.7	93.1	95.4
Rsa1.0_00846.1_g20340.t1	gb|AAD28689.1| putative TNP1-like transposon protein [Arabidopsis thaliana]	280	984	5.00E-55	351.4	46.8	59.3	putative TNP1-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00846.1_g20341.t1	ref|NP_001077922.1| uncharacterized protein [Arabidopsis thaliana] gi|4580471|gb|AAD24395.1| unknown protein [Arabidopsis thaliana] gi|110737370|dbj|BAF00630.1| hypothetical protein [Arabidopsis thaliana] gi|330251861|gb|AEC06955.1| uncharacterized protein AT2G20010 [Arabidopsis thaliana]	953	952	0	99.9	91.1	95.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G20010.2 | Symbols: | Protein of unknown function (DUF810) | chr2:8637977-8641184 REVERSE LENGTH=952	953	952	0	99.9	91.1	95.5
Rsa1.0_00846.1_g20342.t1	ref|XP_002886005.1| hypothetical protein ARALYDRAFT_480467 [Arabidopsis lyrata subsp. lyrata] gi|297331845|gb|EFH62264.1| hypothetical protein ARALYDRAFT_480467 [Arabidopsis lyrata subsp. lyrata]	740	700	0	94.6	79.7	85.3	hypothetical protein ARALYDRAFT_480467	gbpln	Arabidopsis lyrata	AT2G20020.1 | Symbols: CAF1, ATCAF1 | RNA-binding CRS1 / YhbY (CRM) domain-containing protein | chr2:8644464-8647090 FORWARD LENGTH=701	740	701	0	94.7	77.8	83.9
Rsa1.0_00846.1_g20343.t1	ref|NP_179593.1| putative RING-H2 finger protein ATL12 [Arabidopsis thaliana] gi|68565334|sp|Q9SL78.1|ATL12_ARATH RecName: Full=Putative RING-H2 finger protein ATL12; Flags: Precursor gi|4580469|gb|AAD24393.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|330251863|gb|AEC06957.1| putative RING-H2 finger protein ATL12 [Arabidopsis thaliana]	390	390	1.00E-123	100.0	63.8	74.6	putative RING-H2 finger protein ATL12	gbpln	Arabidopsis thaliana	AT2G20030.1 | Symbols: | RING/U-box superfamily protein | chr2:8647813-8648985 FORWARD LENGTH=390	390	390	1.00E-125	100.0	63.8	74.6
Rsa1.0_00846.1_g20344.t4	gb|EOA32925.1| hypothetical protein CARUB_v10016251mg [Capsella rubella]	1111	1101	0	99.1	88.7	92.9	hypothetical protein CARUB_v10016251mg	gbpln	Capsella rubella	AT2G20050.1 | Symbols: | protein serine/threonine phosphatases;protein kinases;catalytics;cAMP-dependent protein kinase regulators;ATP binding;protein serine/threonine phosphatases | chr2:8649779-8654193 REVERSE LENGTH=1094	1111	1094	0	98.5	88.0	92.5
Rsa1.0_00846.1_g20345.t4	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1564	1449	5.00E-94	92.6	16.2	25.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1564	626	6.00E-60	40.0	7.7	12.9
Rsa1.0_00847.1_g20346.t1	gb|EOA24459.1| hypothetical protein CARUB_v10017716mg [Capsella rubella]	314	303	8.00E-61	96.5	52.9	64.6	hypothetical protein CARUB_v10017716mg	gbpln	Capsella rubella	AT3G55690.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G39870.1); Has 76 Blast hits to 69 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 3; Plants - 69; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:20667035-20668204 FORWARD LENGTH=293	314	293	2.00E-56	93.3	51.0	60.5
Rsa1.0_00847.1_g20347.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00847.1_g20348.t1	ref|XP_002876329.1| hypothetical protein ARALYDRAFT_486006 [Arabidopsis lyrata subsp. lyrata] gi|297322167|gb|EFH52588.1| hypothetical protein ARALYDRAFT_486006 [Arabidopsis lyrata subsp. lyrata]	426	438	0	102.8	86.9	93.0	hypothetical protein ARALYDRAFT_486006	gbpln	Arabidopsis lyrata	AT3G55720.1 | Symbols: | Protein of unknown function (DUF620) | chr3:20679893-20681338 FORWARD LENGTH=438	426	438	0	102.8	85.0	92.5

Rsa1.0_00847.1_g20349.t1	ref|NP_180874.1| glycosyl hydrolase and polygalacturonase domain-containing protein [Arabidopsis thaliana] gi|2924778|gb|AAC04907.1| putative polygalacturonase [Arabidopsis thaliana] gi|330253698|gb|AEC08792.1| glycosyl hydrolase and polygalacturonase domain-containing protein [Arabidopsis thaliana]	155	664	1.00E-35	428.4	43.2	61.9	glycosyl hydrolase and polygalacturonase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G33160.1 | Symbols: | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein | chr2:14053404-14056246 FORWARD LENGTH=664	155	664	4.00E-38	428.4	43.2	61.9
Rsa1.0_00847.1_g20350.t1	ref|NP_191133.1| proline transporter 2 [Arabidopsis thaliana] gi|75220395|sp|P92962.1|PROT2_ARATH RecName: Full=Proline transporter 2; Short=AtPROT2 gi|1769903|emb|CAA65053.1| proline transporter 2 [Arabidopsis thaliana] gi|7263562|emb|CAB81599.1| proline transporter 2 [Arabidopsis thaliana] gi|19698891|gb|AAL91181.1| proline transporter 2 [Arabidopsis thaliana] gi|31376371|gb|AAP49512.1| At3g55740 [Arabidopsis thaliana] gi|332645907|gb|AEE79428.1| proline transporter 2 [Arabidopsis thaliana]	439	439	0	100.0	94.1	98.4	proline transporter 2	gbpln	Arabidopsis thaliana	AT3G55740.1 | Symbols: PROT2, ATPROT2 | proline transporter 2 | chr3:20695786-20698157 FORWARD LENGTH=439	439	439	0	100.0	94.1	98.4
Rsa1.0_00847.1_g20351.t1	gb|EOA24978.1| hypothetical protein CARUB_v10018275mg [Capsella rubella]	111	111	2.00E-56	100.0	96.4	98.2	hypothetical protein CARUB_v10018275mg	gbpln	Capsella rubella	AT1G07070.1 | Symbols: | Ribosomal protein L35Ae family protein | chr1:2168652-2169703 FORWARD LENGTH=112	111	112	1.00E-58	100.9	93.7	99.1
Rsa1.0_00847.1_g20352.t1	ref|XP_003555037.1| PREDICTED: uncharacterized protein LOC100798506 [Glycine max]	831	1010	0	121.5	53.4	67.4	PREDICTED: uncharacterized protein LOC100798506	gbenv/gbpln	Glycine max	#	#	#	#	#	#	#
Rsa1.0_00848.1_g20353.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00848.1_g20354.t1	ref|XP_002877042.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297322880|gb|EFH53301.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	347	917	1.00E-117	264.3	78.1	85.3	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G27330.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr3:10116950-10120516 REVERSE LENGTH=913	347	913	1.00E-119	263.1	76.7	85.3
Rsa1.0_00848.1_g20355.t1	ref|XP_002877042.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297322880|gb|EFH53301.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	543	917	0	168.9	82.9	92.3	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G27330.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr3:10116950-10120516 REVERSE LENGTH=913	543	913	0	168.1	82.3	91.5
Rsa1.0_00848.1_g20356.t1	gb|EOA24915.1| hypothetical protein CARUB_v10018206mg [Capsella rubella]	141	142	5.00E-65	100.7	86.5	91.5	hypothetical protein CARUB_v10018206mg	gbpln	Capsella rubella	AT3G27340.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: oxidation reduction; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Gamma-butyrobetaine dioxygenase/Trimethyllysine dioxygenase, N-terminal (InterPro:IPR010376); Has 1035 Blast hits to 1035 proteins in 399 species: Archae - 0; Bacteria - 765; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 231 (source: NCBI BLink). | chr3:10121303-10122692 FORWARD LENGTH=141	141	141	3.00E-67	100.0	86.5	92.2
Rsa1.0_00848.1_g20357.t1	ref|NP_566816.1| uncharacterized protein [Arabidopsis thaliana] gi|7939507|dbj|BAA95710.1| unnamed protein product [Arabidopsis thaliana] gi|19423986|gb|AAL87277.1| unknown protein [Arabidopsis thaliana] gi|21281155|gb|AAM45003.1| unknown protein [Arabidopsis thaliana] gi|332643784|gb|AEE77305.1| uncharacterized protein AT3G27350 [Arabidopsis thaliana]	282	274	1.00E-83	97.2	64.9	73.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27350.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40700.1); Has 230 Blast hits to 202 proteins in 35 species: Archae - 0; Bacteria - 3; Metazoa - 77; Fungi - 4; Plants - 130; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink). | chr3:10126238-10127600 FORWARD LENGTH=274	282	274	3.00E-86	97.2	64.9	73.4
Rsa1.0_00848.1_g20358.t1	dbj|BAJ34353.1| unnamed protein product [Thellungiella halophila]	223	279	3.00E-67	125.1	64.6	69.1	unnamed protein product	----	----	AT3G27380.2 | Symbols: SDH2-1 | succinate dehydrogenase 2-1 | chr3:10131209-10132673 REVERSE LENGTH=279	223	279	2.00E-68	125.1	63.7	69.5

Rsa1.0_00848.1.g20359.t1	ref|NP_189375.2| uncharacterized protein [Arabidopsis thaliana] gi|332278120|sp|Q8GUM4.2|Y3739_ARATH RecName: Full=Uncharacterized membrane protein At3g27390 gi|332643790|gb|AEE77311.1| uncharacterized protein AT3G27390 [Arabidopsis thaliana]	602	588	0	97.7	72.8	82.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27390.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40640.1); Has 101 Blast hits to 99 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:10133372-10136111 REVERSE LENGTH=588	602	588	0	97.7	72.8	82.4
Rsa1.0_00848.1.g20360.t1	ref|NP_189376.1| pectate lyase [Arabidopsis thaliana] gi|378405210|sp|Q9LTZ0.2|PLY11_ARATH RecName: Full=Putative pectate lyase 11; Flags: Precursor gi|332643791|gb|AEE77312.1| putative pectate lyase 11 [Arabidopsis thaliana]	412	412	0	100.0	92.7	95.9	pectate lyase	gbpln	Arabidopsis thaliana	AT3G27400.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:10140323-10143023 FORWARD LENGTH=412	412	412	0	100.0	92.7	95.9
Rsa1.0_00848.1.g20361.t1	ref|NP_189377.1| uncharacterized protein [Arabidopsis thaliana] gi|7939513|dbj|BAA95716.1| unnamed protein product [Arabidopsis thaliana] gi|67633670|gb|AAY78759.1| unknown [Arabidopsis thaliana] gi|332643792|gb|AEE77313.1| uncharacterized protein AT3G27410 [Arabidopsis thaliana]	125	132	2.00E-22	105.6	61.6	71.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27410.1 | Symbols: | unknown protein; Has 10 Blast hits to 10 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:10145244-10145642 REVERSE LENGTH=132	125	132	3.00E-25	105.6	61.6	71.2
Rsa1.0_00848.1.g20362.t1	ref|XP_002875383.1| hypothetical protein ARALYDRAFT_484531 [Arabidopsis lyrata subsp. lyrata] gi|297321221|gb|EFH51642.1| hypothetical protein ARALYDRAFT_484531 [Arabidopsis lyrata subsp. lyrata]	205	177	9.00E-37	86.3	63.4	68.3	hypothetical protein ARALYDRAFT_484531	gbpln	Arabidopsis lyrata	AT3G27415.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:10147375-10147902 FORWARD LENGTH=175	205	175	2.00E-37	85.4	60.0	66.8
Rsa1.0_00848.1.g20363.t1	ref|XP_002875384.1| hypothetical protein ARALYDRAFT_322871 [Arabidopsis lyrata subsp. lyrata] gi|297321222|gb|EFH51643.1| hypothetical protein ARALYDRAFT_322871 [Arabidopsis lyrata subsp. lyrata]	242	243	2.00E-71	100.4	63.2	77.3	hypothetical protein ARALYDRAFT_322871	gbpln	Arabidopsis lyrata	AT3G27420.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40600.1); Has 43 Blast hits to 43 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:10148949-10150139 FORWARD LENGTH=244	242	244	6.00E-68	100.8	57.9	74.0
Rsa1.0_00848.1.g20364.t1	ref|XP_002875387.1| hypothetical protein ARALYDRAFT_904988 [Arabidopsis lyrata subsp. lyrata] gi|297321225|gb|EFH51646.1| hypothetical protein ARALYDRAFT_904988 [Arabidopsis lyrata subsp. lyrata]	273	273	1.00E-154	100.0	96.3	98.5	hypothetical protein ARALYDRAFT_904988	gbpln	Arabidopsis lyrata	AT3G27430.2 | Symbols: PBB1 | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:10152910-10155052 FORWARD LENGTH=273	273	273	1.00E-156	100.0	96.0	98.5
Rsa1.0_00848.1.g20365.t2	ref|XP_002882056.1| TGF-beta receptor interacting protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297327895|gb|EFH58315.1| TGF-beta receptor interacting protein 1 [Arabidopsis lyrata subsp. lyrata]	343	328	1.00E-167	95.6	82.8	90.1	TGF-beta receptor interacting protein 1	gbpln	Arabidopsis lyrata	AT2G46290.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:19005910-19007797 REVERSE LENGTH=355	343	355	1.00E-167	103.5	81.6	90.4
Rsa1.0_00848.1.g20366.t1	ref|XP_002877057.1| hypothetical protein ARALYDRAFT_484543 [Arabidopsis lyrata subsp. lyrata] gi|297322895|gb|EFH53316.1| hypothetical protein ARALYDRAFT_484543 [Arabidopsis lyrata subsp. lyrata]	917	914	0	99.7	88.7	94.0	hypothetical protein ARALYDRAFT_484543	gbpln	Arabidopsis lyrata	AT3G27530.1 | Symbols: GC6, MAG4 | golgin candidate 6 | chr3:10193778-10199659 REVERSE LENGTH=914	917	914	0	99.7	88.3	93.5
Rsa1.0_00848.1.g20367.t1	gb|EOA23738.1| hypothetical protein CARUB_v10016951mg, partial [Capsella rubella]	533	556	0	104.3	86.1	90.1	hypothetical protein CARUB_v10016951mg, partial	gbpln	Capsella rubella	AT3G27550.1 | Symbols: | RNA-binding CRS1 / YhbY (CRM) domain protein | chr3:10208010-10209899 REVERSE LENGTH=491	533	491	0	92.1	77.1	80.7
Rsa1.0_00848.1.g20368.t1	ref|XP_002877060.1| AT3g27570/MMJ24_12 [Arabidopsis lyrata subsp. lyrata] gi|297322898|gb|EFH53319.1| AT3g27570/MMJ24_12 [Arabidopsis lyrata subsp. lyrata]	365	339	1.00E-159	92.9	79.7	84.9	AT3g27570/MMJ24_12	gbpln	Arabidopsis lyrata	AT3G27570.1 | Symbols: | Sucrase/ferredoxin-like family protein | chr3:10214276-10216681 REVERSE LENGTH=379	365	379	1.00E-157	103.8	79.7	84.7

Rsa1.0_00848.1.g20369.t13	ref|XP_002519722.1| hypothetical protein RCOM_0633850 [Ricinus communis] gi|223541139|gb|EEF42695.1| hypothetical protein RCOM_0633850 [Ricinus communis]	198	216	1.00E-12	109.1	21.2	28.3	hypothetical protein RCOM_0633850	gbpln	Ricinus communis	AT1G78520.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr1:29537976-29538656 REVERSE LENGTH=115	198	115	9.00E-12	58.1	17.2	23.7
Rsa1.0_00848.1.g20370.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	110	149	1.00E-20	135.5	40.9	61.8	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00848.1.g20371.t1	gb|EOA25550.1| hypothetical protein CARUB_v10018895mg [Capsella rubella]	408	362	0	88.7	75.2	79.2	hypothetical protein CARUB_v10018895mg	gbpln	Capsella rubella	AT3G27950.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:10378048-10379771 FORWARD LENGTH=361	408	361	1.00E-180	88.5	74.3	77.5
Rsa1.0_00848.1.g20372.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00848.1.g20373.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1355	1307	0	96.5	61.9	75.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1355	1262	1.00E-102	93.1	14.5	22.7
Rsa1.0_00849.1.g20374.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20375.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20376.t1	gb|AAD17414.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	557	1166	1.00E-168	209.3	54.8	67.1	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	557	1262	1.00E-49	226.6	20.1	30.3
Rsa1.0_00849.1.g20377.t1	ref|NP_567451.1| membrane-associated progesterone binding protein 4 [Arabidopsis thaliana] gi|87116572|gb|ABD19650.1| At4g14965 [Arabidopsis thaliana] gi|110738784|dbj|BAF01315.1| hypothetical protein [Arabidopsis thaliana] gi|332658131|gb|AEE83531.1| membrane-associated progesterone binding protein 4 [Arabidopsis thaliana]	346	245	1.00E-118	70.8	59.5	62.1	membrane-associated progesterone binding protein 4	gbpln	Arabidopsis thaliana	AT4G14965.1 | Symbols: AtMAPR4, MAPR4 | membrane-associated progesterone binding protein 4 | chr4:8551356-8553368 FORWARD LENGTH=245	346	245	1.00E-120	70.8	59.5	62.1
Rsa1.0_00849.1.g20378.t1	gb|EOA20910.1| hypothetical protein CARUB_v10001245mg [Capsella rubella]	123	361	1.00E-22	293.5	46.3	52.0	hypothetical protein CARUB_v10001245mg	gbpln	Capsella rubella	AT5G01160.1 | Symbols: | RING/U-box superfamily protein | chr5:54280-55727 FORWARD LENGTH=360	123	360	8.00E-25	292.7	45.5	53.7
Rsa1.0_00849.1.g20379.t1	ref|NP_187840.7| FKBP-like peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana] gi|380876925|sp|F4J9Q6.1|FKB43_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP43; Short=PPIase FKBP43; AltName: Full=FK506-binding protein 43; Short=AtFKBP43; AltName: Full=Immunophilin FKBP43; AltName: Full=Rotamase gi|332641663|gb|AEE75184.1| FKBP-like peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana]	444	499	1.00E-123	112.4	64.9	77.9	FKBP-like peptidyl-prolyl cis-trans isomerase family protein	gbpln	Arabidopsis thaliana	AT3G12340.1 | Symbols: | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | chr3:3925720-3929346 REVERSE LENGTH=499	444	499	1.00E-126	112.4	64.9	77.9
Rsa1.0_00849.1.g20380.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20381.t1	gb|EOA33021.1| hypothetical protein CARUB_v10016352mg, partial [Capsella rubella]	790	886	1.00E-101	112.2	22.9	32.2	hypothetical protein CARUB_v10016352mg, partial	gbpln	Capsella rubella	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	790	719	1.00E-28	91.0	12.7	22.0
Rsa1.0_00849.1.g20382.t1	gb|EOA13348.1| hypothetical protein CARUB_v10026382mg [Capsella rubella]	271	453	2.00E-12	167.2	22.5	38.0	hypothetical protein CARUB_v10026382mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20383.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20384.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20385.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20386.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20387.t1	gb|ABD65162.1| hypothetical protein 40.t00047 [Brassica oleracea]	165	203	2.00E-45	123.0	55.2	67.3	hypothetical protein 40.t00047	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20388.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20389.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20390.t6	emb|CCD74471.1| myosin heavy chain-like protein [Arabidopsis halleri subsp. halleri]	511	788	2.00E-22	154.2	11.7	18.2	myosin heavy chain-like protein	gbpln	Arabidopsis halleri	AT4G03830.1 | Symbols: | Protein of unknown function, DUF601 | chr4:1790440-1792458 FORWARD LENGTH=578	511	578	5.00E-22	113.1	11.5	17.6
Rsa1.0_00849.1.g20391.t1	gb|AAD28663.1| hypothetical protein [Arabidopsis thaliana]	318	356	7.00E-18	111.9	27.0	42.8	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20392.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	700	672	6.00E-51	96.0	19.9	32.9	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20393.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	630	1838	9.00E-76	291.7	24.0	30.3	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00849.1.g20394.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00850.1.g20395.t1	dbj|BAB02259.1| retroelement pol polyprotein–like [Arabidopsis thaliana]	397	777	9.00E–58	195.7	34.3	45.1	retroelement pol polyprotein–like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00850.1.g20396.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00850.1.g20397.t13	gb|AAD21778.1| putative non–LTR retroelement reverse transcriptase [Arabidopsis thaliana]	214	1715	1.00E–40	801.4	37.9	58.4	putative non–LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G02650.1 | Symbols: | Ribonuclease H–like superfamily protein | chr2:735411–736546 FORWARD LENGTH=365	214	365	8.00E–39	170.6	37.4	55.6
Rsa1.0_00850.1.g20398.t2	ref|NP_198930.1| Myosin heavy chain–related protein [Arabidopsis thaliana] gi|9759160|dbj|BAB09716.1| unnamed protein product [Arabidopsis thaliana] gi|332007262|gb|AED94645.1| Myosin heavy chain–related protein [Arabidopsis thaliana]	873	983	0	112.6	78.4	88.3	Myosin heavy chain–related protein	gbpln	Arabidopsis thaliana	AT5G41140.1 | Symbols: | Myosin heavy chain–related protein | chr5:16468726–16472546 FORWARD LENGTH=983	873	983	0	112.6	78.4	88.3
Rsa1.0_00850.1.g20399.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00850.1.g20400.t1	emb|CAB46043.1| retrotransposon like protein [Arabidopsis thaliana] gi|7268438|emb|CAB80958.1| retrotransposon like protein [Arabidopsis thaliana]	1372	1474	0	107.4	56.6	70.3	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine–rich RLK (RECEPTOR–like protein kinase) 8 | chr4:12129485–12134086 FORWARD LENGTH=1262	1372	1262	2.00E–83	92.0	11.1	16.0
Rsa1.0_00850.1.g20401.t1	ref|NP_198929.2| Esterase/lipase/thioesterase–containing protein [Arabidopsis thaliana] gi|110737476|dbj|BAF00681.1| hypothetical protein [Arabidopsis thaliana] gi|332007260|gb|AED94643.1| Esterase/lipase/thioesterase–containing protein [Arabidopsis thaliana]	689	688	0	99.9	78.7	86.2	Esterase/lipase/thioesterase–containing protein	gbpln	Arabidopsis thaliana	AT5G41130.1 | Symbols: | Esterase/lipase/thioesterase family protein | chr5:16459714–16463241 REVERSE LENGTH=688	689	688	0	99.9	78.7	86.2
Rsa1.0_00850.1.g20402.t2	ref|NP_198927.1| uncharacterized protein [Arabidopsis thaliana] gi|9759157|dbj|BAB09713.1| unnamed protein product [Arabidopsis thaliana] gi|332007257|gb|AED94640.1| uncharacterized protein AT5G41110 [Arabidopsis thaliana]	962	621	0	64.6	41.2	45.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G41110.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G26890.5); Has 1807 Blast hits to 1807 proteins in 277 species: Archae – 0; Bacteria – 0; Metazoa – 736; Fungi – 347; Plants – 385; Viruses – 0; Other Eukaryotes – 339 (source: NCBI BLink). | chr5:16452598–16454989 FORWARD LENGTH=621	962	621	0	64.6	41.2	45.7
Rsa1.0_00851.1.g20403.t1	ref|XP_002874617.1| hypothetical protein ARALYDRAFT_911322 [Arabidopsis lyrata subsp. lyrata] gi|297320454|gb|EFH50876.1| hypothetical protein ARALYDRAFT_911322 [Arabidopsis lyrata subsp. lyrata]	138	140	2.00E–55	101.4	84.8	92.0	hypothetical protein ARALYDRAFT_911322	gbpln	Arabidopsis lyrata	AT4G10280.1 | Symbols: | RmlC–like cupins superfamily protein | chr4:6375220–6375996 REVERSE LENGTH=140	138	140	6.00E–58	101.4	85.5	91.3
Rsa1.0_00851.1.g20404.t1	ref|XP_002874614.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320451|gb|EFH50873.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	323	324	1.00E–179	100.3	95.7	98.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G10260.1 | Symbols: | pfkB–like carbohydrate kinase family protein | chr4:6371486–6372770 REVERSE LENGTH=324	323	324	0	100.3	95.0	97.8
Rsa1.0_00851.1.g20405.t1	gb|AEL00035.1| HSP22 [Raphanus sativus]	197	197	1.00E–104	100.0	97.0	98.5	HSP22	gbpln	Raphanus sativus	AT4G10250.1 | Symbols: ATHSP22.0 | HSP20–like chaperones superfamily protein | chr4:6370537–6371124 FORWARD LENGTH=195	197	195	3.00E–95	99.0	89.8	92.9
Rsa1.0_00851.1.g20406.t1	gb|EOA22704.1| hypothetical protein CARUB_v10003410mg [Capsella rubella]	564	539	0	95.6	85.3	90.6	hypothetical protein CARUB_v10003410mg	gbpln	Capsella rubella	AT4G10180.1 | Symbols: DET1, FUS2, ATDET1 | light–mediated development protein 1 / deetiolated1 (DET1) | chr4:6346543–6349146 FORWARD LENGTH=543	564	543	0	96.3	85.6	91.0
Rsa1.0_00851.1.g20407.t1	gb|EOA21398.1| hypothetical protein CARUB_v10001766mg [Capsella rubella] gi|482557207|gb|EOA21399.1| hypothetical protein CARUB_v10001766mg [Capsella rubella]	248	257	1.00E–105	103.6	81.5	89.9	hypothetical protein CARUB_v10001766mg	gbpln	Capsella rubella	AT4G10170.2 | Symbols: | SNARE–like superfamily protein | chr4:6344587–6345351 FORWARD LENGTH=254	248	254	1.00E–102	102.4	77.4	86.7
Rsa1.0_00851.1.g20408.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	116	149	2.00E–24	128.4	43.1	62.1	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H–like superfamily protein | chr2:14484959–14485837 FORWARD LENGTH=292	116	292	4.00E–11	251.7	31.0	49.1
Rsa1.0_00851.1.g20409.t1	ref|NP_567350.1| protein phosphatase methylesterase 1 [Arabidopsis thaliana] gi|14423412|gb|AAK62388.1|AF386943_1 lipase–like protein [Arabidopsis thaliana] gi|20148343|gb|AAM10062.1| lipase–like protein [Arabidopsis thaliana] gi|332657433|gb|AEE82833.1| esterase/lipase/thioesterase family protein [Arabidopsis thaliana]	368	350	1.00E–178	95.1	85.1	89.7	protein phosphatase methylesterase 1	gbpln	Arabidopsis thaliana	AT4G10050.1 | Symbols: | esterase/lipase/thioesterase family protein | chr4:6284620–6287186 REVERSE LENGTH=350	368	350	0	95.1	85.1	89.7

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<tr><td>Rsa1.0_00851.1.g20411.t1</td><td>ref|NP_192741.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] gi|4539006|emb|CAB39627.1| putative protein [Arabidopsis thaliana] gi|7267699|emb|CAB78126.1| putative protein [Arabidopsis thaliana] gi|21594223|gb|AAM65982.1| unknown [Arabidopsis thaliana] gi|332657431|gb|AEE82831.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]</td><td>96</td><td>380</td><td>6.00E-29</td><td>395.8</td><td>65.6</td><td>66.7</td><td>hydrolase, alpha/beta fold family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G10030.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:6270490-6273098 REVERSE LENGTH=380</td><td>96</td><td>380</td><td>1.00E-31</td><td>395.8</td><td>65.6</td><td>66.7</td></tr>
<tr><td>Rsa1.0_00851.1.g20412.t1</td><td>gb|ACG69526.1| steroleosin SLO2-2 [Brassica napus]</td><td>454</td><td>461</td><td>0</td><td>101.5</td><td>94.7</td><td>97.4</td><td>steroleosin SLO2-2</td><td>gbpln</td><td>Brassica napus</td><td>AT4G10020.1 | Symbols: AtHSD5, HSD5 | hydroxysteroid dehydrogenase 5 | chr4:6268363-6270179 FORWARD LENGTH=389</td><td>454</td><td>389</td><td>0</td><td>85.7</td><td>76.0</td><td>79.5</td></tr>
<tr><td>Rsa1.0_00851.1.g20413.t1</td><td>ref|NP_849351.1| agamous-like MADS-box protein AGL11 [Arabidopsis thaliana] gi|17529110|gb|AAL38765.1| putative MADS-box protein AGL11 [Arabidopsis thaliana] gi|22136706|gb|AAM91672.1| putative MADS-box protein AGL11 [Arabidopsis thaliana] gi|332657416|gb|AEE82816.1| agamous-like MADS-box protein AGL11 [Arabidopsis thaliana]</td><td>217</td><td>216</td><td>1.00E-101</td><td>99.5</td><td>89.4</td><td>95.9</td><td>agamous-like MADS-box protein AGL11</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G09960.2 | Symbols: STK, AGL11 | K-box region and MADS-box transcription factor family protein | chr4:6236713-6239409 REVERSE LENGTH=216</td><td>217</td><td>216</td><td>1.00E-104</td><td>99.5</td><td>89.4</td><td>95.9</td></tr>
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<tr><td>Rsa1.0_00851.1.g20415.t1</td><td>ref|XP_002891747.1| hypothetical protein ARALYDRAFT_892371 [Arabidopsis lyrata subsp. lyrata] gi|297337589|gb|EFH68006.1| hypothetical protein ARALYDRAFT_892371 [Arabidopsis lyrata subsp. lyrata]</td><td>909</td><td>905</td><td>0</td><td>99.6</td><td>74.4</td><td>82.8</td><td>hypothetical protein ARALYDRAFT_892371</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G53350.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:19903899-19907515 FORWARD LENGTH=927</td><td>909</td><td>927</td><td>0</td><td>102.0</td><td>74.8</td><td>82.6</td></tr>
<tr><td>Rsa1.0_00852.1.g20416.t1</td><td>ref|XP_002881925.1| hypothetical protein ARALYDRAFT_903775 [Arabidopsis lyrata subsp. lyrata] gi|297327764|gb|EFH58184.1| hypothetical protein ARALYDRAFT_903775 [Arabidopsis lyrata subsp. lyrata]</td><td>142</td><td>170</td><td>8.00E-20</td><td>119.7</td><td>39.4</td><td>54.2</td><td>hypothetical protein ARALYDRAFT_903775</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G43730.1 | Symbols: | Mannose-binding lectin superfamily protein | chr2:18124821-18125669 REVERSE LENGTH=224</td><td>142</td><td>224</td><td>2.00E-13</td><td>157.7</td><td>31.7</td><td>43.0</td></tr>
<tr><td>Rsa1.0_00852.1.g20417.t4</td><td>gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]</td><td>1423</td><td>1356</td><td>0</td><td>95.3</td><td>48.2</td><td>63.7</td><td>Highly similar to Ta1-3 polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1423</td><td>1262</td><td>6.00E-65</td><td>88.7</td><td>10.6</td><td>17.2</td></tr>
<tr><td>Rsa1.0_00852.1.g20418.t1</td><td>dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]</td><td>528</td><td>1223</td><td>2.00E-81</td><td>231.6</td><td>33.7</td><td>52.5</td><td>non-LTR retroelement reverse transcriptase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>528</td><td>626</td><td>7.00E-36</td><td>118.6</td><td>23.9</td><td>37.1</td></tr>
<tr><td>Rsa1.0_00852.1.g20419.t1</td><td>dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]</td><td>1712</td><td>910</td><td>0</td><td>53.2</td><td>29.3</td><td>38.0</td><td>putative reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1712</td><td>626</td><td>1.00E-128</td><td>36.6</td><td>12.7</td><td>18.5</td></tr>
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Rsa1.0_00852.1.g20420.t1	gb|EOA35535.1| hypothetical protein CARUB_v10020742mg [Capsella rubella]	308	288	1.00E-128	93.5	76.3	83.4	hypothetical protein CARUB_v10020742mg	gbpln	Capsella rubella	AT1G57610.2 | Symbols: | Protein of unknown function (DUF607) | chr1:21337449-21338412 REVERSE LENGTH=293	308	293	1.00E-129	95.1	75.3	84.7
Rsa1.0_00852.1.g20421.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	266	414	3.00E-31	155.6	30.1	35.0	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00852.1.g20422.t3	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	728	704	2.00E-95	96.7	24.2	27.5	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00852.1.g20423.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00852.1.g20424.t1	gb|EOA35193.1| hypothetical protein CARUB_v10020343mg [Capsella rubella]	421	425	0	101.0	88.1	93.3	hypothetical protein CARUB_v10020343mg	gbpln	Capsella rubella	AT1G57590.1 | Symbols: | Pectinacetylesterase family protein | chr1:21327458-21329707 REVERSE LENGTH=444	421	444	0	105.5	86.7	93.1
Rsa1.0_00852.1.g20425.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00852.1.g20426.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1508	1529	0	101.4	43.5	61.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1508	746	4.00E-75	49.5	9.5	12.1
Rsa1.0_00852.1.g20427.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00853.1.g20428.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00853.1.g20429.t1	ref|NP_182191.1| homeobox-leucine zipper protein ATHB-7 [Arabidopsis thaliana] gi|21431751|sp|P46897.2|ATHB7_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-7; AltName: Full=HD-ZIP protein ATHB-7; AltName: Full=Homeodomain transcription factor ATHB-7 gi|3831442|gb|AAC69925.1| homeodomain transcription factor (ATHB-7) [Arabidopsis thaliana] gi|15027939|gb|AAK76500.1| putative homeodomain transcription factor ATHB-7 [Arabidopsis thaliana] gi|20259175|gb|AAM14303.1| putative homeodomain transcription factor protein ATHB-7 [Arabidopsis thaliana] gi|330255645|gb|AEC10739.1| homeobox-leucine zipper protein ATHB-7 [Arabidopsis thaliana]	235	258	2.00E-99	109.8	80.0	86.8	homeobox-leucine zipper protein ATHB-7	gbpln	Arabidopsis thaliana	AT2G46680.1 | Symbols: ATHB-7, ATHB7, HB-7 | homeobox 7 | chr2:19165777-19166773 REVERSE LENGTH=258	235	258	1.00E-102	109.8	80.0	86.8
Rsa1.0_00853.1.g20430.t1	ref|XP_002882080.1| CYP78A6 [Arabidopsis lyrata subsp. lyrata] gi|297327919|gb|EFH58339.1| CYP78A6 [Arabidopsis lyrata subsp. lyrata]	527	530	0	100.6	88.4	93.9	CYP78A6	gbpln	Arabidopsis lyrata	AT2G46660.1 | Symbols: CYP78A6 | cytochrome P450, family 78, subfamily A, polypeptide 6 | chr2:19153602-19155417 REVERSE LENGTH=530	527	530	0	100.6	87.9	93.2
Rsa1.0_00853.1.g20431.t1	ref|XP_002880257.1| B5 #1 [Arabidopsis lyrata subsp. lyrata] gi|297326096|gb|EFH56516.1| B5 #1 [Arabidopsis lyrata subsp. lyrata]	135	132	6.00E-61	97.8	84.4	89.6	B5 #1	gbpln	Arabidopsis lyrata	AT2G46650.1 | Symbols: B5 #1, ATCB5-C, CB5-C | cytochrome B5 isoform C | chr2:19151807-19152394 FORWARD LENGTH=132	135	132	4.00E-57	97.8	84.4	90.4
Rsa1.0_00853.1.g20432.t1	gb|EOA27153.1| hypothetical protein CARUB_v10023250mg [Capsella rubella]	389	433	8.00E-99	111.3	70.7	79.2	hypothetical protein CARUB_v10023250mg	gbpln	Capsella rubella	AT2G46630.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 110095 Blast hits to 59224 proteins in 2216 species: Archae - 177; Bacteria - 15429; Metazoa - 38345; Fungi - 18843; Plants - 13341; Viruses - 3084; Other Eukaryotes - 20876 (source: NCBI BLink). | chr2:19145529-19146713 FORWARD LENGTH=394	389	394	1.00E-100	101.3	72.2	78.7

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<tr><td>Rsa1.0_00853.1.g20433.t1</td><td>ref|NP_566082.1| calcium-binding EF-hand-containing protein [Arabidopsis thaliana] gi|75338835|sp|Q9ZPX9.2|KIC_ARATH RecName: Full=Calcium-binding protein KIC; AltName: Full=KCBP-interacting calcium-binding protein gi|237824052|pdb|3H4S|E Chain E, Structure Of The Complex Of A Mitotic Kinesin With Its Calcium Binding Regulator gi|15294244|gb|AAK95299.1|AF410313_1 At2g46600/F13A10.13 [Arabidopsis thaliana] gi|20147271|gb|AAM10349.1| At2g46600/F13A10.13 [Arabidopsis thaliana] gi|20197776|gb|AAD20170.2| putative caltractin [Arabidopsis thaliana] gi|38325077|gb|AAR17001.1| KCBP interacting Ca2+-binding protein [Arabidopsis thaliana] gi|330255633|gb|AEC10727.1| calcium-binding protein KIC [Arabidopsis thaliana]</td><td>137</td><td>135</td><td>9.00E-61</td><td>98.5</td><td>84.7</td><td>92.7</td><td>calcium-binding EF-hand-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G46600.1 | Symbols: | Calcium-binding EF-hand family protein | chr2:19136070-19136477 FORWARD LENGTH=135</td><td>137</td><td>135</td><td>2.00E-63</td><td>98.5</td><td>84.7</td><td>92.7</td></tr>
<tr><td>Rsa1.0_00853.1.g20434.t1</td><td>gb|EOA27345.1| hypothetical protein CARUB_v10023459mg [Capsella rubella]</td><td>360</td><td>372</td><td>1.00E-167</td><td>103.3</td><td>90.6</td><td>94.4</td><td>hypothetical protein CARUB_v10023459mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G46590.2 | Symbols: DAG2 | Dof-type zinc finger DNA-binding family protein | chr2:19133166-19134905 FORWARD LENGTH=369</td><td>360</td><td>369</td><td>1.00E-149</td><td>102.5</td><td>90.0</td><td>92.8</td></tr>
<tr><td>Rsa1.0_00853.1.g20435.t1</td><td>gb|EOA29206.1| hypothetical protein CARUB_v10025480mg [Capsella rubella]</td><td>199</td><td>213</td><td>2.00E-99</td><td>107.0</td><td>85.9</td><td>92.0</td><td>hypothetical protein CARUB_v10025480mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G46580.1 | Symbols: | Pyridoxamine 5'-phosphate oxidase family protein | chr2:19129409-19130513 REVERSE LENGTH=198</td><td>199</td><td>198</td><td>1.00E-100</td><td>99.5</td><td>84.4</td><td>91.5</td></tr>
<tr><td>Rsa1.0_00853.1.g20436.t1</td><td>ref|XP_002880252.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326091|gb|EFH56511.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>569</td><td>569</td><td>0</td><td>100.0</td><td>89.1</td><td>94.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G46570.1 | Symbols: LAC6 | laccase 6 | chr2:19126872-19129069 FORWARD LENGTH=569</td><td>569</td><td>569</td><td>0</td><td>100.0</td><td>89.1</td><td>94.4</td></tr>
<tr><td>Rsa1.0_00853.1.g20437.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT2G46550.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G01240.3); Has 72 Blast hits to 68 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 71; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19112264-19113457 REVERSE LENGTH=397</td><td>99</td><td>397</td><td>1.00E-10</td><td>401.0</td><td>44.4</td><td>49.5</td></tr>
<tr><td>Rsa1.0_00853.1.g20438.t1</td><td>gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>318</td><td>1555</td><td>5.00E-63</td><td>489.0</td><td>39.0</td><td>54.4</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>318</td><td>303</td><td>8.00E-42</td><td>95.3</td><td>33.3</td><td>48.4</td></tr>
<tr><td>Rsa1.0_00854.1.g20439.t7</td><td>ref|XP_002877348.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323186|gb|EFH53607.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>583</td><td>982</td><td>3.00E-85</td><td>168.4</td><td>33.3</td><td>42.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G57650.1 | Symbols: | ATP binding | chr1:21351291-21354311 FORWARD LENGTH=709</td><td>583</td><td>709</td><td>1.00E-62</td><td>121.6</td><td>31.0</td><td>42.9</td></tr>
<tr><td>Rsa1.0_00854.1.g20440.t1</td><td>emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]</td><td>225</td><td>1515</td><td>1.00E-48</td><td>673.3</td><td>56.4</td><td>68.0</td><td>retrotransposon like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240</td><td>225</td><td>240</td><td>1.00E-25</td><td>106.7</td><td>32.0</td><td>41.8</td></tr>
<tr><td>Rsa1.0_00854.1.g20441.t1</td><td>gb|EOA16859.1| hypothetical protein CARUB_v10005083mg [Capsella rubella]</td><td>345</td><td>369</td><td>1.00E-116</td><td>107.0</td><td>78.0</td><td>83.5</td><td>hypothetical protein CARUB_v10005083mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G36930.1 | Symbols: SPT | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:17414167-17415945 FORWARD LENGTH=373</td><td>345</td><td>373</td><td>1.00E-114</td><td>108.1</td><td>80.0</td><td>83.8</td></tr>
<tr><td>Rsa1.0_00854.1.g20442.t1</td><td>gb|ABE65413.1| hypothetical protein At1g62890 [Arabidopsis thaliana]</td><td>119</td><td>195</td><td>8.00E-20</td><td>163.9</td><td>40.3</td><td>59.7</td><td>hypothetical protein At1g62890</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00854.1.g20443.t1</td><td>gb|EOA16840.1| hypothetical protein CARUB_v10005061mg [Capsella rubella]</td><td>374</td><td>376</td><td>0</td><td>100.5</td><td>82.6</td><td>88.2</td><td>hypothetical protein CARUB_v10005061mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G36880.1 | Symbols: CP1 | cysteine proteinase1 | chr4:17374692-17376180 REVERSE LENGTH=376</td><td>374</td><td>376</td><td>0</td><td>100.5</td><td>88.0</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00854.1.g20444.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00854.1.g20445.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_00854.1.g20446.t1	ref|NP_195443.1| myb domain protein 73 [Arabidopsis thaliana] gi|2464855|emb|CAB16756.1| myb−related protein [Arabidopsis thaliana] gi|7270709|emb|CAB80392.1| myb−related protein [Arabidopsis thaliana] gi|17380912|gb|AAL36268.1| putative myb−related protein [Arabidopsis thaliana] gi|20258981|gb|AAM14206.1| putative myb−related protein [Arabidopsis thaliana] gi|41619352|gb|AAS10083.1| MYB transcription factor [Arabidopsis thaliana] gi|332661374|gb|AEE86774.1| myb domain protein 73 [Arabidopsis thaliana]	283	320	1.00E−116	113.1	84.1	90.1	myb domain protein 73	gbpln	Arabidopsis thaliana	AT4G37260.1 | Symbols: MYB73, ATMYB73 | myb domain protein 73 | chr4:17540602−17541564 FORWARD LENGTH=320	283	320	1.00E−118	113.1	84.1	90.1
Rsa1.0_00854.1.g20447.t1	gb|EOA18862.1| hypothetical protein CARUB_v10007485mg [Capsella rubella]	85	86	1.00E−33	101.2	84.7	89.4	hypothetical protein CARUB_v10007485mg	gbpln	Capsella rubella	AT4G37290.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; LOCATED IN: endomembrane system; EXPRESSED IN: cotyledon, hypocotyl, leaf; EXPRESSED DURING: LP.04 four leaves visible; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G23270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:17549929−17550183 REVERSE LENGTH=84	85	84	1.00E−32	98.8	81.2	85.9
Rsa1.0_00854.1.g20448.t1	gb|EOA18685.1| hypothetical protein CARUB_v10007260mg [Capsella rubella]	86	86	6.00E−33	100.0	79.1	89.5	hypothetical protein CARUB_v10007260mg	gbpln	Capsella rubella	AT4G37295.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: stem, root, leaf; EXPRESSED DURING: LP.06 six leaves visible, LP.04 four leaves visible; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:17553628−17553888 FORWARD LENGTH=86	86	86	1.00E−34	100.0	79.1	88.4
Rsa1.0_00854.1.g20449.t1	ref|NP_195450.1| cytochrome P450, family 81, subfamily D, polypeptide 4 [Arabidopsis thaliana] gi|2464850|emb|CAB16753.1| cytochrome P450−like protein [Arabidopsis thaliana] gi|7270716|emb|CAB80399.1| cytochrome P450−like protein [Arabidopsis thaliana] gi|145651786|gb|ABP88118.1| At4g37330 [Arabidopsis thaliana] gi|332661382|gb|AEE86782.1| cytochrome P450, family 81, subfamily D, polypeptide 4 [Arabidopsis thaliana]	481	492	0	102.3	68.8	81.9	cytochrome P450, family 81, subfamily D, polypeptide 4	gbpln	Arabidopsis thaliana	AT4G37330.1 | Symbols: CYP81D4 | cytochrome P450, family 81, subfamily D, polypeptide 4 | chr4:17562547−17564569 REVERSE LENGTH=492	481	492	0	102.3	68.8	81.9
Rsa1.0_00854.1.g20450.t1	ref|XP_002866956.1| CYP81D5 [Arabidopsis lyrata subsp. lyrata] gi|297312792|gb|EFH43215.1| CYP81D5 [Arabidopsis lyrata subsp. lyrata]	183	495	2.00E−79	270.5	76.0	86.3	CYP81D5	gbpln	Arabidopsis lyrata	AT4G37320.1 | Symbols: CYP81D5 | cytochrome P450, family 81, subfamily D, polypeptide 5 | chr4:17559742−17561690 REVERSE LENGTH=495	183	495	2.00E−81	270.5	75.4	85.8
Rsa1.0_00855.1.g20451.t2	ref|XP_002872517.1| hypothetical protein ARALYDRAFT_911351 [Arabidopsis lyrata subsp. lyrata] gi|297318354|gb|EFH48776.1| hypothetical protein ARALYDRAFT_911351 [Arabidopsis lyrata subsp. lyrata]	554	603	2.00E−83	108.8	44.6	59.0	hypothetical protein ARALYDRAFT_911351	gbpln	Arabidopsis lyrata	AT1G33050.4 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10470.1). | chr1:11968361−11970890 REVERSE LENGTH=693	554	693	5.00E−69	125.1	44.2	58.8

Rsa1.0_00855.1.g20452.t1	ref|NP_192783.1| 60S ribosomal protein L9-2 [Arabidopsis thaliana] gi|75314149|sp|Q9SZX9.1|RL92_ARATH RecName: Full=60S ribosomal protein L9-2 gi|4539405|emb|CAB40038.1| putative ribosomal protein L9, cytosolic [Arabidopsis thaliana] gi|7267742|emb|CAB78168.1| putative ribosomal protein L9, cytosolic [Arabidopsis thaliana] gi|17529050|gb|AAL38735.1| putative ribosomal protein L9 [Arabidopsis thaliana] gi|21436441|gb|AAM51421.1| putative ribosomal protein L9 [Arabidopsis thaliana] gi|21554221|gb|AAM63297.1| putative ribosomal protein L9, cytosolic [Arabidopsis thaliana] gi|332657484|gb|AEE82884.1| 60S ribosomal protein L9-2 [Arabidopsis thaliana]	194	194	1.00E-100	100.0	93.3	95.9	60S ribosomal protein L9-2	gbpln	Arabidopsis thaliana	AT4G10450.1 | Symbols: | Ribosomal protein L6 family | chr4:6463201-6464458 REVERSE LENGTH=194	194	194	1.00E-103	100.0	93.3	95.9
Rsa1.0_00855.1.g20453.t1	ref|XP_002874627.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297320464|gb|EFH50886.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	633	631	0	99.7	91.5	95.9	dehydration-responsive family protein	gbpln	Arabidopsis lyrata	AT4G10440.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:6459728-6461932 REVERSE LENGTH=633	633	633	0	100.0	90.5	95.1
Rsa1.0_00855.1.g20454.t3	ref|NP_567356.1| TMPIT-like protein [Arabidopsis thaliana] gi|42572865|ref|NP_974529.1| TMPIT-like protein [Arabidopsis thaliana] gi|16648995|gb|AAL24349.1| putative protein [Arabidopsis thaliana] gi|20259956|gb|AAM13325.1| putative protein [Arabidopsis thaliana] gi|332657481|gb|AEE82881.1| TMPIT-like protein [Arabidopsis thaliana] gi|332657482|gb|AEE82882.1| TMPIT-like protein [Arabidopsis thaliana]	336	347	1.00E-155	103.3	84.2	91.1	TMPIT-like protein	gbpln	Arabidopsis thaliana	AT4G10430.3 | Symbols: | TMPIT-like protein | chr4:6455110-6457996 REVERSE LENGTH=347	336	347	1.00E-157	103.3	84.2	91.1
Rsa1.0_00855.1.g20455.t1	ref|NP_192777.1| protein kinase family protein [Arabidopsis thaliana] gi|75313924|sp|Q9SV83.1|Y4103_ARATH RecName: Full=Probable receptor-like protein kinase At4g10390 gi|4538968|emb|CAB39792.1| putative protein kinase [Arabidopsis thaliana] gi|7267736|emb|CAB78162.1| putative protein kinase [Arabidopsis thaliana] gi|20260592|gb|AAM13194.1| putative protein kinase [Arabidopsis thaliana] gi|23198076|gb|AAN15565.1| putative protein kinase [Arabidopsis thaliana] gi|332657475|gb|AEE82875.1| probable receptor-like protein kinase [Arabidopsis thaliana]	408	342	1.00E-163	83.8	70.8	75.7	protein kinase family protein	gbpln	Arabidopsis thaliana	AT4G10390.1 | Symbols: | Protein kinase superfamily protein | chr4:6441949-6443161 REVERSE LENGTH=342	408	342	1.00E-165	83.8	70.8	75.7
Rsa1.0_00855.1.g20456.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00855.1.g20457.t1	ref|XP_002874623.1| hypothetical protein ARALYDRAFT_911337 [Arabidopsis lyrata subsp. lyrata] gi|297320460|gb|EFH50882.1| hypothetical protein ARALYDRAFT_911337 [Arabidopsis lyrata subsp. lyrata]	301	304	1.00E-151	101.0	94.0	95.7	hypothetical protein ARALYDRAFT_911337	gbpln	Arabidopsis lyrata	AT4G10380.1 | Symbols: NIP5;1, NLM6, NLM8 | NOD26-like intrinsic protein 5;1 | chr4:6431530-6434510 REVERSE LENGTH=304	301	304	1.00E-153	101.0	94.0	95.7
Rsa1.0_00855.1.g20458.t1	ref|NP_567355.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana] gi|79325051|ref|NP_001031610.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana] gi|16323149|gb|AAL15309.1| AT4g10360/F24G24_160 [Arabidopsis thaliana] gi|21436011|gb|AAM51583.1| AT4g10360/F24G24_160 [Arabidopsis thaliana] gi|222424213|dbj|BAH20065.1| AT4G10360 [Arabidopsis thaliana] gi|332657471|gb|AEE82871.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana] gi|332657472|gb|AEE82872.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana]	261	266	1.00E-127	101.9	86.6	93.5	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	gbpln	Arabidopsis thaliana	AT4G10360.2 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr4:6420679-6422108 FORWARD LENGTH=266	261	266	1.00E-130	101.9	86.6	93.5

Rsa1.0_00855.1.g20459.t1	gb|ABD65086.1| hypothetical protein 27.t00104 [Brassica oleracea]	706	1172	9.00E-42	166.0	14.6	17.4	hypothetical protein 27.t00104	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00856.1.g20460.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00856.1.g20461.t1	ref|XP_002862875.1| hypothetical protein ARALYDRAFT_920182 [Arabidopsis lyrata subsp. lyrata] gi|297308637|gb|EFH39134.1| hypothetical protein ARALYDRAFT_920182 [Arabidopsis lyrata subsp. lyrata]	326	315	4.00E-62	96.6	41.7	53.4	hypothetical protein ARALYDRAFT_920182	gbpln	Arabidopsis lyrata	AT3G19520.2 | Symbols: | Protein of unknown function (DUF626) | chr3:6772773-6774209 FORWARD LENGTH=312	326	312	6.00E-39	95.7	31.0	45.7
Rsa1.0_00856.1.g20462.t6	ref|XP_002894257.1| heat-intolerant 1 [Arabidopsis lyrata subsp. lyrata] gi|297340099|gb|EFH70516.1| heat-intolerant 1 [Arabidopsis lyrata subsp. lyrata]	895	828	0	92.5	86.3	88.9	heat-intolerant 1	gbpln	Arabidopsis lyrata	AT1G50500.1 | Symbols: HIT1, ATVPS53, VPS53 | Membrane trafficking VPS53 family protein | chr1:18708217-18715597 REVERSE LENGTH=828	895	828	0	92.5	85.7	88.8
Rsa1.0_00856.1.g20463.t7	gb|EOA36131.1| hypothetical protein CARUB_v10012430mg [Capsella rubella]	156	517	1.00E-33	331.4	46.2	53.2	hypothetical protein CARUB_v10012430mg	gbpln	Capsella rubella	AT1G50520.1 | Symbols: CYP705A27 | cytochrome P450, family 705, subfamily A, polypeptide 27 | chr1:18719381-18721070 FORWARD LENGTH=533	156	533	2.00E-33	341.7	43.6	51.9
Rsa1.0_00856.1.g20464.t3	ref|XP_002878993.1| hypothetical protein ARALYDRAFT_901441 [Arabidopsis lyrata subsp. lyrata] gi|297324832|gb|EFH55252.1| hypothetical protein ARALYDRAFT_901441 [Arabidopsis lyrata subsp. lyrata]	797	872	0	109.4	67.8	76.0	hypothetical protein ARALYDRAFT_901441	gbpln	Arabidopsis lyrata	AT5G27010.1 | Symbols: | ARM repeat superfamily protein | chr5:9503315-9507569 REVERSE LENGTH=863	797	863	0	108.3	62.0	71.5
Rsa1.0_00856.1.g20465.t1	ref|XP_002870581.1| hypothetical protein ARALYDRAFT_915958 [Arabidopsis lyrata subsp. lyrata] gi|297316417|gb|EFH46840.1| hypothetical protein ARALYDRAFT_915958 [Arabidopsis lyrata subsp. lyrata]	123	269	3.00E-28	218.7	53.7	69.1	hypothetical protein ARALYDRAFT_915958	gbpln	Arabidopsis lyrata	AT5G37870.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr5:15073764-15074851 REVERSE LENGTH=281	123	281	1.00E-27	228.5	48.0	61.0
Rsa1.0_00856.1.g20466.t1	dbj|BAJ33810.1| unnamed protein product [Thellungiella halophila]	513	533	0	103.9	89.1	93.6	unnamed protein product	----	----	AT1G50600.1 | Symbols: SCL5 | scarecrow-like 5 | chr1:18737398-18739547 REVERSE LENGTH=597	513	597	0	116.4	85.8	91.8
Rsa1.0_00856.1.g20467.t1	gb|EOA37472.1| hypothetical protein CARUB_v10011600mg [Capsella rubella]	685	689	0	100.6	81.6	89.1	hypothetical protein CARUB_v10011600mg	gbpln	Capsella rubella	AT1G50610.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:18742171-18744501 FORWARD LENGTH=686	685	686	0	100.1	80.4	88.8
Rsa1.0_00856.1.g20468.t1	gb|EOA39831.1| hypothetical protein CARUB_v10008502mg [Capsella rubella]	657	673	0	102.4	67.6	77.3	hypothetical protein CARUB_v10008502mg	gbpln	Capsella rubella	AT1G50620.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:18748537-18751005 FORWARD LENGTH=629	657	629	0	95.7	66.4	74.4
Rsa1.0_00856.1.g20469.t1	ref|NP_171844.6| serine/threonine-protein phosphatase BSU1 [Arabidopsis thaliana] gi|45476981|sp|Q9LR78.2|BSU1_ARATH RecName: Full=Serine/threonine-protein phosphatase BSU1; AltName: Full=Bri1 suppressor protein 1 gi|38425331|gb|AAR19789.1| BSU1 Ser/Thr phosphatase [Arabidopsis thaliana] gi|332189451|gb|AEE27572.1| serine/threonine-protein phosphatase BSU1 [Arabidopsis thaliana]	717	793	0	110.6	54.4	68.3	serine/threonine-protein phosphatase BSU1	gbpln	Arabidopsis thaliana	AT1G03445.1 | Symbols: BSU1 | Serine/threonine protein phosphatase family protein | chr1:854653-859599 REVERSE LENGTH=793	717	793	0	110.6	54.4	68.3
Rsa1.0_00856.1.g20470.t1	ref|NP_175483.1| RAV-like factor [Arabidopsis thaliana] gi|75268209|sp|Q9C6P5.1|RAVL2_ARATH RecName: Full=AP2/ERF and B3 domain-containing transcription factor At1g50680; AltName: Full=RAV1-like ethylene-responsive transcription factor At1g50680 gi|12322330|gb|AAG51186.1|AC079279_7 RAV-like DNA-binding protein, putative [Arabidopsis thaliana] gi|332194457|gb|AEE32578.1| AP2/ERF and B3 domain-containing transcription factor [Arabidopsis thaliana]	260	337	8.00E-88	129.6	68.5	80.4	RAV-like factor	gbpln	Arabidopsis thaliana	AT1G50680.1 | Symbols: | AP2/B3 transcription factor family protein | chr1:18777601-18778614 REVERSE LENGTH=337	260	337	2.00E-90	129.6	68.5	80.4
Rsa1.0_00856.1.g20471.t1	gb|AAQ82842.1| At4g20730 [Arabidopsis thaliana] gi|51970840|dbj|BAD44112.1| putative protein [Arabidopsis thaliana]	893	800	2.00E-29	89.6	7.6	12.4	At4g20730	gbpln	Arabidopsis thaliana	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	893	1399	7.00E-31	156.7	8.0	12.4
Rsa1.0_00856.1.g20472.t1	gb|AAD20101.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	568	764	7.00E-28	134.5	11.4	17.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00857.1.g20473.t1	gb|ABV89659.1| dehydration-responsive protein-related [Brassica rapa]	687	662	0	96.4	82.1	88.1	dehydration-responsive protein-related	gbpln	Brassica rapa	AT1G78240.2 | Symbols: TSD2, QUA2 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:29433173-29435815 REVERSE LENGTH=684	687	684	0	99.6	78.6	86.6
Rsa1.0_00857.1.g20474.t1	ref|XP_002887730.1| hypothetical protein ARALYDRAFT_476991 [Arabidopsis lyrata subsp. lyrata] gi|297333571|gb|EFH63989.1| hypothetical protein ARALYDRAFT_476991 [Arabidopsis lyrata subsp. lyrata]	553	584	0	105.6	77.4	84.8	hypothetical protein ARALYDRAFT_476991	gbpln	Arabidopsis lyrata	AT1G78230.1 | Symbols: | Outer arm dynein light chain 1 protein | chr1:29430226-29432516 FORWARD LENGTH=681	553	681	0	123.1	76.5	81.6
Rsa1.0_00857.1.g20475.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00857.1.g20476.t1	gb|EOA35470.1| hypothetical protein CARUB_v10020680mg [Capsella rubella]	313	315	1.00E-160	100.6	85.6	95.2	hypothetical protein CARUB_v10020680mg	gbpln	Capsella rubella	AT1G78210.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:29422820-29424294 REVERSE LENGTH=314	313	314	1.00E-161	100.3	86.3	94.9
Rsa1.0_00857.1.g20477.t1	dbj|BAJ34008.1| unnamed protein product [Thellungiella halophila]	282	283	1.00E-129	100.4	80.9	89.7	unnamed protein product	----	----	AT1G78200.2 | Symbols: | Protein phosphatase 2C family protein | chr1:29420483-29421650 FORWARD LENGTH=283	282	283	1.00E-125	100.4	76.6	86.5
Rsa1.0_00857.1.g20478.t1	ref|NP_177943.1| Trm1.2-like protein [Arabidopsis thaliana] gi|47606209|sp|Q9C9R3.1|T112B_ARATH RecName: Full=TRM112-like protein At1g78190 gi|12324252|gb|AAG52099.1|AC012680_10 unknown protein; 53758-53384 [Arabidopsis thaliana] gi|332197958|gb|AEE36079.1| Trm1.2-like protein [Arabidopsis thaliana]	122	124	5.00E-51	101.6	82.8	90.2	Trm1.2-like protein	gbpln	Arabidopsis thaliana	AT1G78190.1 | Symbols: | Trm112p-like protein | chr1:29418620-29418994 REVERSE LENGTH=124	122	124	9.00E-54	101.6	82.8	90.2
Rsa1.0_00857.1.g20479.t1	gb|ABO69625.1| synaptonemal complex protein ZYP1 [Brassica oleracea]	878	876	0	99.8	90.9	94.9	synaptonemal complex protein ZYP1	gbpln	Brassica oleracea	AT1G22260.1 | Symbols: ZYP1a, ZYP1 | Myosin heavy chain-related protein | chr1:7860160-7865142 REVERSE LENGTH=871	878	871	0	99.2	67.4	81.2
Rsa1.0_00857.1.g20480.t3	ref|NP_173321.4| Isochorismate synthase 2 [Arabidopsis thaliana] gi|205830866|sp|Q9M9V6.2|ICS2_ARATH RecName: Full=Isochorismate synthase 2, chloroplastic; Short=AtIcs2; AltName: Full=Isochorismate mutase 2; AltName: Full=menF-like protein 2; Flags: Precursor gi|183229349|gb|ACC60228.1| isochorismate synthase 2 [Arabidopsis thaliana] gi|332191652|gb|AEE29773.1| Isochorismate synthase 2 [Arabidopsis thaliana]	309	562	8.00E-50	181.9	41.4	51.5	Isochorismate synthase 2	gbpln	Arabidopsis thaliana	AT1G18870.1 | Symbols: ICS2, ATICS2 | isochorismate synthase 2 | chr1:6515486-6519176 FORWARD LENGTH=562	309	562	2.00E-52	181.9	41.4	51.5
Rsa1.0_00857.1.g20481.t1	ref|NP_177941.2| uncharacterized protein [Arabidopsis thaliana] gi|28393122|gb|AAO41994.1| unknown protein [Arabidopsis thaliana] gi|28827468|gb|AAO50578.1| unknown protein [Arabidopsis thaliana] gi|332197955|gb|AEE36076.1| uncharacterized protein AT1G78170 [Arabidopsis thaliana]	229	221	2.00E-82	96.5	71.6	78.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G78170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22250.1); Has 66 Blast hits to 66 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 66; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:29414160-29414941 FORWARD LENGTH=221	229	221	7.00E-85	96.5	71.6	78.2
Rsa1.0_00857.1.g20482.t1	gb|AAM63644.1| putative 60S acidic ribosomal protein P0 [Arabidopsis thaliana]	190	320	1.00E-12	168.4	18.4	22.1	putative 60S acidic ribosomal protein P0	gbpln	Arabidopsis thaliana	AT3G09200.1 | Symbols: | Ribosomal protein L10 family protein | chr3:2823364-2825020 REVERSE LENGTH=320	190	320	5.00E-15	168.4	18.4	22.1
Rsa1.0_00857.1.g20483.t1	gb|EOA34555.1| hypothetical protein CARUB_v10022107mg [Capsella rubella]	608	665	0	109.4	80.9	87.8	hypothetical protein CARUB_v10022107mg	gbpln	Capsella rubella	AT1G78160.1 | Symbols: APUM7, PUM7 | pumilio 7 | chr1:29407900-29410184 FORWARD LENGTH=650	608	650	0	106.9	79.9	85.7
Rsa1.0_00858.1.g20484.t2	gb|AAD17414.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	1839	1166	0	63.4	41.2	49.4	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT2G41800.1 | Symbols: | Protein of unknown function, DUF642 | chr2:17436671-17438005 REVERSE LENGTH=370	1839	370	1.00E-179	20.1	16.2	17.2
Rsa1.0_00858.1.g20485.t1	ref|NP_181710.1| insulysin [Arabidopsis thaliana] gi|75097648|sp|O22941.1|PXM16_ARATH RecName: Full=Zinc-metallopeptidase, peroxisomal; AltName: Full=Peroxisomal M16 protease gi|2335108|gb|AAC02769.1| putative zinc protease [Arabidopsis thaliana] gi|330254939|gb|AEC10033.1| zinc-metallopeptidase PXM16 [Arabidopsis thaliana]	940	970	0	103.2	92.1	96.6	insulysin	gbpln	Arabidopsis thaliana	AT2G41790.1 | Symbols: | Insulinase (Peptidase family M16) family protein | chr2:17429453-17436110 REVERSE LENGTH=970	940	970	0	103.2	92.1	96.6

<table>
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<tr><td>Rsa1.0_00858.1.g20487.t1</td><td>gb|EOA28874.1| hypothetical protein CARUB_v10025119mg [Capsella rubella]</td><td>973</td><td>973</td><td>0</td><td>100.0</td><td>90.6</td><td>95.4</td><td>hypothetical protein CARUB_v10025119mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G41740.1 | Symbols: VLN2, ATVLN2 | villin 2 | chr2:17410962-17416878 REVERSE LENGTH=976</td><td>973</td><td>976</td><td>0</td><td>100.3</td><td>89.6</td><td>95.1</td></tr>
<tr><td>Rsa1.0_00858.1.g20488.t1</td><td>ref|NP_181704.1| uncharacterized protein [Arabidopsis thaliana] gi|2335105|gb|AAC02775.1| hypothetical protein [Arabidopsis thaliana] gi|26450207|dbj|BAC42222.1| unknown protein [Arabidopsis thaliana] gi|30793799|gb|AAP40352.1| unknown protein [Arabidopsis thaliana] gi|330254932|gb|AEC10026.1| uncharacterized protein AT2G41730 [Arabidopsis thaliana]</td><td>130</td><td>119</td><td>3.00E-39</td><td>91.5</td><td>63.8</td><td>73.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G41730.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24640.1); Has 25 Blast hits to 25 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17409488-17409847 FORWARD LENGTH=119</td><td>130</td><td>119</td><td>5.00E-42</td><td>91.5</td><td>63.8</td><td>73.8</td></tr>
<tr><td>Rsa1.0_00858.1.g20489.t1</td><td>ref|XP_002881793.1| EMB2654 [Arabidopsis lyrata subsp. lyrata] gi|297327632|gb|EFH58052.1| EMB2654 [Arabidopsis lyrata subsp. lyrata]</td><td>1275</td><td>822</td><td>0</td><td>64.5</td><td>57.3</td><td>60.5</td><td>EMB2654</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G41720.1 | Symbols: EMB2654 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:17403744-17407127 REVERSE LENGTH=822</td><td>1275</td><td>822</td><td>0</td><td>64.5</td><td>57.0</td><td>60.2</td></tr>
<tr><td>Rsa1.0_00858.1.g20490.t1</td><td>ref|NP_565956.1| camphor resistance CrcB-like protein [Arabidopsis thaliana] gi|238479528|ref|NP_001154568.1| camphor resistance CrcB-like protein [Arabidopsis thaliana] gi|20196897|gb|AAM14827.1| Expressed protein [Arabidopsis thaliana] gi|26453266|dbj|BAC43706.1| unknown protein [Arabidopsis thaliana] gi|330254925|gb|AEC10019.1| camphor resistance CrcB-like protein [Arabidopsis thaliana] gi|330254926|gb|AEC10020.1| camphor resistance CrcB-like protein [Arabidopsis thaliana]</td><td>422</td><td>461</td><td>1.00E-160</td><td>109.2</td><td>76.1</td><td>85.1</td><td>camphor resistance CrcB-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G41705.2 | Symbols: | camphor resistance CrcB family protein | chr2:17398083-17399910 FORWARD LENGTH=461</td><td>422</td><td>461</td><td>1.00E-163</td><td>109.2</td><td>76.1</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00858.1.g20491.t1</td><td>gb|EOA26894.1| hypothetical protein CARUB_v10022987mg [Capsella rubella]</td><td>525</td><td>528</td><td>0</td><td>100.6</td><td>95.0</td><td>97.3</td><td>hypothetical protein CARUB_v10022987mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G41680.1 | Symbols: NTRC | NADPH-dependent thioredoxin reductase C | chr2:17376349-17379028 REVERSE LENGTH=529</td><td>525</td><td>529</td><td>0</td><td>100.8</td><td>93.7</td><td>96.8</td></tr>
<tr><td>Rsa1.0_00858.1.g20492.t2</td><td>ref|XP_002879947.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297325786|gb|EFH56206.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]</td><td>381</td><td>386</td><td>0</td><td>101.3</td><td>89.5</td><td>92.9</td><td>GTP-binding family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G41670.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:17374118-17376177 FORWARD LENGTH=386</td><td>381</td><td>386</td><td>0</td><td>101.3</td><td>89.0</td><td>92.7</td></tr>
<tr><td>Rsa1.0_00858.1.g20493.t1</td><td>gb|EOA27590.1| hypothetical protein CARUB_v10023729mg [Capsella rubella]</td><td>293</td><td>300</td><td>1.00E-122</td><td>102.4</td><td>85.3</td><td>92.2</td><td>hypothetical protein CARUB_v10023729mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G41660.1 | Symbols: MIZ1 | Protein of unknown function, DUF617 | chr2:17367945-17368838 FORWARD LENGTH=297</td><td>293</td><td>297</td><td>1.00E-121</td><td>101.4</td><td>82.3</td><td>88.7</td></tr>
<tr><td>Rsa1.0_00859.1.g20494.t1</td><td>gb|AAF99860.1|AC015448_10 Putative protein kinase [Arabidopsis thaliana]</td><td>854</td><td>879</td><td>0</td><td>102.9</td><td>75.2</td><td>85.4</td><td>Putative protein kinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G51910.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19284277-19288385 REVERSE LENGTH=876</td><td>854</td><td>876</td><td>0</td><td>102.6</td><td>74.9</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00859.1.g20495.t3</td><td>ref|NP_179090.1| Regulator of Vps4 activity in the MVB pathway protein [Arabidopsis thaliana] gi|3252806|gb|AAC24176.1| hypothetical protein [Arabidopsis thaliana] gi|330251243|gb|AEC06337.1| Regulator of Vps4 activity in the MVB pathway protein [Arabidopsis thaliana]</td><td>364</td><td>454</td><td>1.00E-79</td><td>124.7</td><td>51.4</td><td>67.6</td><td>Regulator of Vps4 activity in the MVB pathway protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G14830.1 | Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr2:6362524-6365818 FORWARD LENGTH=454</td><td>364</td><td>454</td><td>3.00E-82</td><td>124.7</td><td>51.4</td><td>67.6</td></tr>
<tr><td>Rsa1.0_00859.1.g20496.t2</td><td>emb|CAB40067.1| putative retrotransposon polyprotein [Arabidopsis thaliana] gi|7267797|emb|CAB81200.1| putative retrotransposon polyprotein [Arabidopsis thaliana]</td><td>1325</td><td>1203</td><td>0</td><td>90.8</td><td>34.3</td><td>47.1</td><td>putative retrotransposon polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1325</td><td>1262</td><td>1.00E-167</td><td>95.2</td><td>21.1</td><td>28.5</td></tr>
<tr><td>Rsa1.0_00859.1.g20497.t1</td><td>gb|EOA37370.1| hypothetical protein CARUB_v10011168mg [Capsella rubella]</td><td>208</td><td>884</td><td>2.00E-83</td><td>425.0</td><td>69.7</td><td>82.2</td><td>hypothetical protein CARUB_v10011168mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G51880.1 | Symbols: RHS6 | root hair specific 6 | chr1:19270193-19274068 REVERSE LENGTH=880</td><td>208</td><td>880</td><td>5.00E-82</td><td>423.1</td><td>68.8</td><td>79.8</td></tr>
</table>

Rsa1.0_00859.1.g20498.t4	sp|Q9FZB1.1|Y5188_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g51880; Flags: Precursor gi|9802789|gb|AAF99858.1|AC015448_8 Putative protein kinase [Arabidopsis thaliana] gi|224589432|gb|ACN59250.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	625	872	0	139.5	74.6	83.5	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g51880; Flags: Precursor gi|9802789|gb|AAF99858.1|AC015448_8 Putative protein kinase	gbpln	Arabidopsis thaliana	AT1G51880.1 | Symbols: RHS6 | root hair specific 6 | chr1:19270193-19274068 REVERSE LENGTH=880	625	880	0	140.8	74.6	83.5
Rsa1.0_00859.1.g20499.t1	ref|NP_175598.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|281185489|sp|C0LGG4.2|Y1518_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g51860; Flags: Precursor gi|332194605|gb|AEE32726.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	1036	890	0	85.9	70.1	76.9	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G51860.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19257634-19261479 REVERSE LENGTH=890	1036	890	0	85.9	70.1	76.9
Rsa1.0_00859.1.g20500.t1	gb|AAF99864.1|AC015448_14 Putative protein kinase [Arabidopsis thaliana]	851	875	0	102.8	79.0	87.8	Putative protein kinase	gbpln	Arabidopsis thaliana	AT1G51850.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19252964-19256783 REVERSE LENGTH=865	851	865	0	101.6	77.2	85.7
Rsa1.0_00859.1.g20501.t1	ref|XP_002891661.1| hypothetical protein ARALYDRAFT_337332 [Arabidopsis lyrata subsp. lyrata] gi|297337503|gb|EFH67920.1| hypothetical protein ARALYDRAFT_337332 [Arabidopsis lyrata subsp. lyrata]	88	403	1.00E-12	458.0	39.8	47.7	hypothetical protein ARALYDRAFT_337332	gbpln	Arabidopsis lyrata	AT1G51770.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:19201919-19203224 FORWARD LENGTH=406	88	406	5.00E-14	461.4	37.5	45.5
Rsa1.0_00859.1.g20502.t1	gb|ABB60091.1| IAA-amino acid hydrolase 3 [Brassica rapa]	442	444	0	100.5	93.4	98.2	IAA-amino acid hydrolase 3	gbpln	Brassica rapa	AT1G51760.1 | Symbols: IAR3, JR3 | peptidase M20/M25/M40 family protein | chr1:19199562-19201424 FORWARD LENGTH=440	442	440	0	99.5	86.9	94.1
Rsa1.0_00860.1.g20503.t1	ref|NP_200637.1| regulatory particle triple-A ATPase 3 [Arabidopsis thaliana] gi|297793353|ref|XP_002864561.1| hypothetical protein ARALYDRAFT_495939 [Arabidopsis lyrata subsp. lyrata] gi|28558168|sp|Q9SEI4.1|PRS6B_ARATH RecName: Full=26S protease regulatory subunit 6B homolog; AltName: Full=26S protease subunit 6B homolog; AltName: Full=26S proteasome AAA-ATPase subunit RPT3; AltName: Full=Protein BMAA insensitive morphology 409; AltName: Full=Regulatory particle triple-A ATPase subunit 3 gi|6652882|gb|AAF22523.1|AF123392_1 26S proteasome AAA-ATPase subunit RPT3 [Arabidopsis thaliana] gi|8777330|dbj|BAA96920.1| 26S proteasome AAA-ATPase subunit RPT3 [Arabidopsis thaliana] gi|17979231|gb|AAL49932.1| AT4g10340/F24G24_140 [Arabidopsis thaliana] gi|56382019|gb|AAV85728.1| At5g58290 [Arabidopsis thaliana] gi|297310396|gb|EFH40820.1| hypothetical protein ARALYDRAFT_495939 [Arabidopsis lyrata subsp. lyrata] gi|332009646|gb|AED97029.1| regulatory particle triple-A ATPase 3 [Arabidopsis thaliana] gi|482548338|gb|EOA12532.1|	391	408	0	104.3	96.7	98.0	regulatory particle triple-A ATPase 3	gbpln	Arabidopsis lyrata	AT5G58290.1 | Symbols: RPT3 | regulatory particle triple-A ATPase 3 | chr5:23569155-23571116 FORWARD LENGTH=408	391	408	0	104.3	96.7	98.0

Rsa1.0_00860.1.g20504.t1	ref|NP_200638.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|186532563|ref|NP_001119458.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|75335557|sp|Q9LVM0.1|Y5830_ARATH RecName: Full=Probable inactive receptor kinase At5g58300; Flags: Precursor gi|8777331|dbj|BAA96921.1| receptor-like protein kinase [Arabidopsis thaliana] gi|18086391|gb|AAL57654.1| unknown protein [Arabidopsis thaliana] gi|24797034|gb|AAN64529.1| At5g58299/At5g58299 [Arabidopsis thaliana] gi|224589729|gb|ACN59396.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332009647|gb|AED97030.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|332009648|gb|AED97031.1| putative inactive receptor kinase [Arabidopsis thaliana]	659	654	0	99.2	84.4	90.3	putative inactive receptor kinase	gbpln	Arabidopsis thaliana	AT5G58300.2 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:23572821-23574871 FORWARD LENGTH=654	659	654	0	99.2	84.4	90.3
Rsa1.0_00860.1.g20505.t2	ref|NP_001147011.1| esterase PIR7B [Zea mays] gi|195606450|gb|ACG25055.1| esterase PIR7B [Zea mays]	278	264	1.00E-142	95.0	86.3	89.6	esterase PIR7B	gbenv/gbpln	Zea mays	AT5G58310.1 | Symbols: ATMES18, MES18 | methyl esterase 18 | chr5:23575127-23576007 REVERSE LENGTH=263	278	263	1.00E-123	94.6	73.7	82.0
Rsa1.0_00860.1.g20506.t1	gb|EOA14841.1| hypothetical protein CARUB_v10028155mg [Capsella rubella]	482	556	0	115.4	75.7	86.1	hypothetical protein CARUB_v10028155mg	gbpln	Capsella rubella	AT5G58320.2 | Symbols: | Kinase interacting (KIP1-like) family protein | chr5:23577728-23579641 FORWARD LENGTH=558	482	558	1.00E-178	115.8	73.0	85.3
Rsa1.0_00860.1.g20507.t1	ref|NP_851214.1| lactate/malate dehydrogenase family protein [Arabidopsis thaliana] gi|23297668|gb|AAN13004.1| NADP-dependent malate dehydrogenase [Arabidopsis thaliana] gi|110740830|dbj|BAE98512.1| NADP-dependent malate dehydrogenase [Arabidopsis thaliana] gi|332009655|gb|AED97038.1| lactate/malate dehydrogenase family protein [Arabidopsis thaliana]	443	443	0	100.0	92.6	95.5	lactate/malate dehydrogenase family protein	gbpln	Arabidopsis thaliana	AT5G58330.1 | Symbols: | lactate/malate dehydrogenase family protein | chr5:23580010-23582287 REVERSE LENGTH=443	443	443	0	100.0	92.6	95.5
Rsa1.0_00860.1.g20508.t1	ref|XP_002864565.1| hypothetical protein ARALYDRAFT_495950 [Arabidopsis lyrata subsp. lyrata] gi|297310400|gb|EFH40824.1| hypothetical protein ARALYDRAFT_495950 [Arabidopsis lyrata subsp. lyrata]	560	571	0	102.0	83.9	90.2	hypothetical protein ARALYDRAFT_495950	gbpln	Arabidopsis lyrata	AT5G58350.1 | Symbols: WNK4, ZIK2 | with no lysine (K) kinase 4 | chr5:23585505-23587681 FORWARD LENGTH=571	560	571	0	102.0	82.7	89.5
Rsa1.0_00860.1.g20509.t1	ref|NP_200644.1| ovate family protein 3 [Arabidopsis thaliana] gi|8777337|dbj|BAA96927.1| unnamed protein product [Arabidopsis thaliana] gi|67633890|gb|AAY78869.1| ovate family protein [Arabidopsis thaliana] gi|332009659|gb|AED97042.1| ovate family protein 3 [Arabidopsis thaliana]	401	296	2.00E-73	73.8	44.9	49.9	ovate family protein 3	gbpln	Arabidopsis thaliana	AT5G58360.1 | Symbols: ATOFP3, OFP3 | ovate family protein 3 | chr5:23590079-23590969 REVERSE LENGTH=296	401	296	6.00E-76	73.8	44.9	49.9
Rsa1.0_00860.1.g20510.t1	ref|NP_173961.3| helicase associated domain-containing protein [Arabidopsis thaliana] gi|332192562|gb|AEE30683.1| helicase associated domain-containing protein [Arabidopsis thaliana]	758	717	0	94.6	68.3	76.6	helicase associated domain-containing protein	gbpln	Arabidopsis thaliana	AT1G26370.1 | Symbols: | RNA helicase family protein | chr1:9122030-9125368 REVERSE LENGTH=717	758	717	0	94.6	68.3	76.6
Rsa1.0_00860.1.g20511.t1	ref|NP_200647.1| peroxidase 67 [Arabidopsis thaliana] gi|26397866|sp|Q9LVL2.1|PER67_ARATH RecName: Full=Peroxidase 67; Short=Atperox P67; AltName: Full=ATP44; Flags: Precursor gi|8777340|dbj|BAA96930.1| peroxidase [Arabidopsis thaliana] gi|332009664|gb|AED97047.1| peroxidase 67 [Arabidopsis thaliana]	326	316	1.00E-139	96.9	75.8	85.9	peroxidase 67	gbpln	Arabidopsis thaliana	AT5G58390.1 | Symbols: | Peroxidase superfamily protein | chr5:23599755-23601244 REVERSE LENGTH=316	326	316	1.00E-142	96.9	75.8	85.9
Rsa1.0_00860.1.g20512.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00860.1.g20513.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1116	1213	0	108.7	53.7	70.2	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1116	626	7.00E-70	56.1	12.9	20.2
Rsa1.0_00860.1.g20514.t3	gb|EOA31247.1| hypothetical protein CARUB_v10014418mg [Capsella rubella]	264	262	1.00E-144	99.2	93.9	97.3	hypothetical protein CARUB_v10014418mg	gbpln	Capsella rubella	AT2G17360.1 | Symbols: | Ribosomal protein S4 (RPS4A) family protein | chr2:7546598-7548138 FORWARD LENGTH=261	264	261	1.00E-145	98.9	93.2	97.0

Rsa1.0_00860.1.g20515.t1	gb|EOA15234.1| hypothetical protein CARUB_v10028631mg [Capsella rubella]	621	624	0	100.5	86.2	93.6	hypothetical protein CARUB_v10028631mg	gbpln	Capsella rubella	AT5G58430.1 | Symbols: ATEXO70B1, EXO70B1 | exocyst subunit exo70 family protein B1 | chr5:23621460-23623334 REVERSE LENGTH=624	621	624	0	100.5	86.3	93.7
Rsa1.0_00860.1.g20516.t1	ref|XP_002868499.1| ATCHX24 [Arabidopsis lyrata subsp. lyrata] gi|297314335|gb|EFH44758.1| ATCHX24 [Arabidopsis lyrata subsp. lyrata]	841	861	0	102.4	74.0	86.7	ATCHX24	gbpln	Arabidopsis lyrata	AT5G37060.1 | Symbols: ATCHX24, CHX24 | cation/H+ exchanger 24 | chr5:14642741-14645414 REVERSE LENGTH=859	841	859	0	102.1	72.4	86.1
Rsa1.0_00860.1.g20517.t1	gb|EOA14774.1| hypothetical protein CARUB_v10028073mg, partial [Capsella rubella]	376	918	7.00E-97	244.1	67.0	70.7	hypothetical protein CARUB_v10028073mg, partial	gbpln	Capsella rubella	AT5G58470.2 | Symbols: TAF15b | TBP-associated factor 15B | chr5:23638566-23640854 REVERSE LENGTH=422	376	422	3.00E-93	112.2	63.6	66.5
Rsa1.0_00860.1.g20518.t1	ref|NP_200658.1| uncharacterized protein [Arabidopsis thaliana] gi|10177027|dbj|BAB10265.1| unnamed protein product [Arabidopsis thaliana] gi|34098923|gb|AAQ56844.1| At5g58500 [Arabidopsis thaliana] gi|332009677|gb|AED97060.1| uncharacterized protein AT5G58500 [Arabidopsis thaliana]	181	182	5.00E-81	100.6	86.7	92.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G58500.1 | Symbols: LSH5 | Protein of unknown function (DUF640) | chr5:23645535-23646083 REVERSE LENGTH=182	181	182	2.00E-83	100.6	86.7	92.8
Rsa1.0_00861.1.g20519.t2	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	1055	1356	0	128.5	45.2	59.9	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1055	1262	2.00E-72	119.6	15.5	22.9
Rsa1.0_00861.1.g20520.t1	gb|ADD25169.1| putative dof zinc finger protein [Brassica napus]	435	427	0	98.2	85.1	89.0	putative dof zinc finger protein	gbpln	Brassica napus	AT3G47500.1 | Symbols: CDF3 | cycling DOF factor 3 | chr3:17504276-17505964 REVERSE LENGTH=448	435	448	1.00E-176	103.0	81.4	88.3
Rsa1.0_00861.1.g20521.t1	ref|NP_001190027.1| HNH endonuclease [Arabidopsis thaliana] gi|332644768|gb|AEE78289.1| HNH endonuclease [Arabidopsis thaliana]	210	215	8.00E-91	102.4	82.4	86.7	HNH endonuclease	gbpln	Arabidopsis thaliana	AT3G47490.3 | Symbols: | HNH endonuclease | chr3:17498454-17500731 FORWARD LENGTH=215	210	215	3.00E-93	102.4	82.4	86.7
Rsa1.0_00861.1.g20522.t1	gb|EOA25559.1| hypothetical protein CARUB_v10018903mg [Capsella rubella]	183	183	1.00E-75	100.0	77.6	87.4	hypothetical protein CARUB_v10018903mg	gbpln	Capsella rubella	AT3G47480.1 | Symbols: | Calcium-binding EF-hand family protein | chr3:17496354-17496905 REVERSE LENGTH=183	183	183	3.00E-74	100.0	79.2	89.1
Rsa1.0_00861.1.g20523.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00861.1.g20524.t1	dbj|BAJ33651.1| unnamed protein product [Thellungiella halophila]	250	251	1.00E-140	100.4	98.0	99.2	unnamed protein product	----	----	AT3G47470.1 | Symbols: LHCA4, CAB4 | light-harvesting chlorophyll-protein complex I subunit A4 | chr3:17493622-17494773 REVERSE LENGTH=251	250	251	1.00E-138	100.4	95.2	96.8
Rsa1.0_00861.1.g20525.t1	ref|NP_190330.1| structural maintenance of chromosomes protein 2-2 [Arabidopsis thaliana] gi|75337454|sp|Q9SN90.1|SMC22_ARATH RecName: Full=Structural maintenance of chromosomes protein 2-2; Short=AtSMC2-2; AltName: Full=Chromosome-associated protein E-2; Short=AtCAP-E2 gi|6522529|emb|CAB61972.1| chromosome assembly protein homolog [Arabidopsis thaliana] gi|332644763|gb|AEE78284.1| structural maintenance of chromosomes protein 2-2 [Arabidopsis thaliana]	1131	1171	0	103.5	89.7	95.4	structural maintenance of chromosomes protein 2-2	gbpln	Arabidopsis thaliana	AT3G47460.1 | Symbols: ATSMC2 | Structural maintenance of chromosomes (SMC) family protein | chr3:17486765-17493178 FORWARD LENGTH=1171	1131	1171	0	103.5	89.7	95.4
Rsa1.0_00861.1.g20526.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00861.1.g20527.t1	gb|ACX61572.1| GTPase [Brassica juncea]	309	555	1.00E-129	179.6	82.2	87.4	GTPase	gbpln	Brassica juncea	AT3G47450.2 | Symbols: ATNOS1, NOS1, ATNOA1, NOA1, RIF1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:17483195-17486249 REVERSE LENGTH=561	309	561	1.00E-124	181.6	77.3	83.2
Rsa1.0_00861.1.g20528.t1	gb|EOA24694.1| hypothetical protein CARUB_v10017971mg [Capsella rubella]	226	228	1.00E-110	100.9	89.4	96.5	hypothetical protein CARUB_v10017971mg	gbpln	Capsella rubella	AT3G47430.1 | Symbols: PEX11B | peroxin 11B | chr3:17480798-17481692 FORWARD LENGTH=227	226	227	1.00E-111	100.4	88.9	96.5
Rsa1.0_00862.1.g20529.t1	gb|AAC26241.1| F9D12.15 gene product [Arabidopsis thaliana]	624	850	3.00E-35	136.2	20.7	33.5	F9D12.15 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00862.1.g20530.t1	gb|AAF67366.1| Hypothetical protein T32B20.i [Arabidopsis thaliana]	239	724	5.00E-59	302.9	47.7	64.0	Hypothetical protein T32B20.i	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00862.1.g20531.t1	gb|EOA14193.1| hypothetical protein CARUB_v10027345mg, partial [Capsella rubella]	101	137	9.00E-21	135.6	50.5	64.4	hypothetical protein CARUB_v10027345mg, partial	gbpln	Capsella rubella	AT5G47550.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:19286596-19286964 REVERSE LENGTH=122	101	122	7.00E-19	120.8	44.6	59.4
Rsa1.0_00862.1.g20532.t19	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1165	1365	1.00E-129	117.2	24.2	31.8	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1165	575	5.00E-44	49.4	11.2	17.9

Rsa1.0_00862.1.g20533.t1	ref|NP_192985.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|15724342|gb|AAL06564.1|AF412111_1 AT4g12480/T1P17_70 [Arabidopsis thaliana] gi|871780|gb|AAC37471.1| pEARLI 1 [Arabidopsis thaliana] gi|4725947|emb|CAB41718.1| pEARLI 1 [Arabidopsis thaliana] gi|7267950|emb|CAB78291.1| pEARLI 1 [Arabidopsis thaliana] gi|22137278|gb|AAM91484.1| AT4g12480/T1P17_70 [Arabidopsis thaliana] gi|110740320|dbj|BAF02055.1| pEARLI 1 [Arabidopsis thaliana] gi|332657738|gb|AEE83138.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	269	168	7.00E-22	62.5	18.6	21.6	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT4G12480.1 | Symbols: pEARLI 1 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:7406371-7406877 REVERSE LENGTH=168	269	168	2.00E-24	62.5	18.6	21.6
Rsa1.0_00862.1.g20534.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00862.1.g20535.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	598	536	6.00E-93	89.6	36.5	49.7	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	598	530	7.00E-51	88.6	14.5	17.7
Rsa1.0_00862.1.g20536.t9	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1072	1250	0	116.6	41.3	53.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1072	1262	1.00E-35	117.7	12.1	20.1
Rsa1.0_00862.1.g20537.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00862.1.g20538.t1	ref|XP_002874777.1| hypothetical protein ARALYDRAFT_911650 [Arabidopsis lyrata subsp. lyrata] gi|297320614|gb|EFH51036.1| hypothetical protein ARALYDRAFT_911650 [Arabidopsis lyrata subsp. lyrata]	169	150	3.00E-55	88.8	69.8	78.1	hypothetical protein ARALYDRAFT_911650	gbpln	Arabidopsis lyrata	AT4G12490.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:7409830-7410378 REVERSE LENGTH=182	169	182	5.00E-57	107.7	72.8	81.1
Rsa1.0_00863.1.g20539.t1	ref|XP_002889580.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335422|gb|EFH65839.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	76	79	7.00E-28	103.9	84.2	93.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G06010.1 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1823347-1823670 FORWARD LENGTH=78	76	78	4.00E-28	102.6	81.6	89.5
Rsa1.0_00863.1.g20540.t1	gb|AEW46252.1| salt tolerance protein [Brassica napus] gi|363990306|gb|AEW46253.1| salt tolerance protein [Brassica napus]	244	241	1.00E-101	98.8	78.3	85.7	salt tolerance protein	gbpln	Brassica napus	AT1G06040.1 | Symbols: STO | B-box zinc finger family protein | chr1:1828662-1829659 REVERSE LENGTH=248	244	248	3.00E-96	101.6	75.8	84.4
Rsa1.0_00863.1.g20541.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00863.1.g20542.t1	ref|XP_002889607.1| hypothetical protein ARALYDRAFT_887853 [Arabidopsis lyrata subsp. lyrata] gi|297335449|gb|EFH65866.1| hypothetical protein ARALYDRAFT_887853 [Arabidopsis lyrata subsp. lyrata]	137	139	4.00E-45	101.5	74.5	81.8	hypothetical protein ARALYDRAFT_887853	gbpln	Arabidopsis lyrata	AT1G06500.4 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 25 Blast hits to 25 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1990176-1990586 FORWARD LENGTH=136	137	136	3.00E-44	99.3	69.3	78.8
Rsa1.0_00863.1.g20543.t1	gb|AFB74218.1| 4-hydroxyphenylpyruvate dioxygenase [Brassica napus]	1000	440	0	44.0	41.9	42.8	4-hydroxyphenylpyruvate dioxygenase	gbpln	Brassica napus	AT1G06570.1 | Symbols: PDS1, HPD | phytoene desaturation 1 | chr1:2012015-2013543 REVERSE LENGTH=473	1000	473	0	47.3	40.6	42.3
Rsa1.0_00863.1.g20544.t1	gb|AAF24811.1|AC007592_4 F12K11.7 [Arabidopsis thaliana]	105	819	2.00E-12	780.0	33.3	38.1	F12K11.7	gbpln	Arabidopsis thaliana	AT1G06590.1 | Symbols: | unknown protein; Has 380 Blast hits to 268 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 245; Fungi - 73; Plants - 49; Viruses - 0; Other Eukaryotes - 13 (source: NCBI BLink). | chr1:2016504-2024505 REVERSE LENGTH=916	105	916	3.00E-15	872.4	33.3	38.1
Rsa1.0_00863.1.g20545.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1786	1214	0	68.0	25.3	38.0	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1786	626	2.00E-83	35.1	9.4	14.3
Rsa1.0_00863.1.g20546.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00863.1.g20547.t1	ref|XP_002889612.1| hypothetical protein ARALYDRAFT_470684 [Arabidopsis lyrata subsp. lyrata] gi|297335454|gb|EFH65871.1| hypothetical protein ARALYDRAFT_470684 [Arabidopsis lyrata subsp. lyrata]	368	369	0	100.3	84.5	91.8	hypothetical protein ARALYDRAFT_470684	gbpln	Arabidopsis lyrata	AT1G06650.2 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:2035909-2037186 FORWARD LENGTH=369	368	369	0	100.3	81.5	90.2
Rsa1.0_00863.1.g20548.t1	ref|XP_002889612.1| hypothetical protein ARALYDRAFT_470684 [Arabidopsis lyrata subsp. lyrata] gi|297335454|gb|EFH65871.1| hypothetical protein ARALYDRAFT_470684 [Arabidopsis lyrata subsp. lyrata]	366	369	0	100.8	83.9	92.1	hypothetical protein ARALYDRAFT_470684	gbpln	Arabidopsis lyrata	AT1G06650.2 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:2035909-2037186 FORWARD LENGTH=369	366	369	0	100.8	81.4	90.7
Rsa1.0_00863.1.g20549.t1	ref|XP_002892370.1| hypothetical protein ARALYDRAFT_470720 [Arabidopsis lyrata subsp. lyrata] gi|297338212|gb|EFH68629.1| hypothetical protein ARALYDRAFT_470720 [Arabidopsis lyrata subsp. lyrata]	164	168	1.00E-66	102.4	88.4	92.1	hypothetical protein ARALYDRAFT_470720	gbpln	Arabidopsis lyrata	AT1G06980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: sepal, male gametophyte, carpel; EXPRESSED DURING: 4 anthesis; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30230.1); Has 159 Blast hits to 159 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 159; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2143248-2143757 REVERSE LENGTH=169	164	169	9.00E-68	103.0	87.2	91.5
Rsa1.0_00863.1.g20550.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00863.1.g20551.t1	gb|EOA37828.1| hypothetical protein CARUB_v10012021mg [Capsella rubella]	327	349	1.00E-170	106.7	86.5	92.7	hypothetical protein CARUB_v10012021mg	gbpln	Capsella rubella	AT1G06990.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:2148393-2150009 FORWARD LENGTH=360	327	360	1.00E-168	110.1	84.1	91.7
Rsa1.0_00863.1.g20552.t1	ref|NP_563779.1| GILT domain-containing protein [Arabidopsis thaliana] gi|15146334|gb|AAK83650.1| At1g07080/F10K1_15 [Arabidopsis thaliana] gi|15809756|gb|AAL06806.1| At1g07080/F10K1_15 [Arabidopsis thaliana] gi|332189954|gb|AEE28075.1| GILT domain-containing protein [Arabidopsis thaliana]	265	265	1.00E-117	100.0	81.1	86.8	GILT domain-containing protein	gbpln	Arabidopsis thaliana	AT1G07080.1 | Symbols: | Thioredoxin superfamily protein | chr1:2170069-2171861 FORWARD LENGTH=265	265	265	1.00E-119	100.0	81.1	86.8
Rsa1.0_00863.1.g20553.t1	ref|XP_002892379.1| hypothetical protein ARALYDRAFT_887918 [Arabidopsis lyrata subsp. lyrata] gi|297338221|gb|EFH68638.1| hypothetical protein ARALYDRAFT_887918 [Arabidopsis lyrata subsp. lyrata]	197	198	4.00E-93	100.5	85.8	89.8	hypothetical protein ARALYDRAFT_887918	gbpln	Arabidopsis lyrata	AT1G07090.1 | Symbols: LSH6 | Protein of unknown function (DUF640) | chr1:2174202-2174792 REVERSE LENGTH=196	197	196	8.00E-94	99.5	84.8	88.8
Rsa1.0_00863.1.g20554.t2	ref|XP_002892380.1| hypothetical protein ARALYDRAFT_470732 [Arabidopsis lyrata subsp. lyrata] gi|297338222|gb|EFH68639.1| hypothetical protein ARALYDRAFT_470732 [Arabidopsis lyrata subsp. lyrata]	300	743	2.00E-30	247.7	21.7	21.7	hypothetical protein ARALYDRAFT_470732	gbpln	Arabidopsis lyrata	AT1G07110.1 | Symbols: F2KP, ATF2KP, FKFBP | fructose-2,6-bisphosphatase | chr1:2178363-2183980 REVERSE LENGTH=744	300	744	6.00E-33	248.0	21.7	21.7
Rsa1.0_00863.1.g20555.t3	gb|EOA37624.1| hypothetical protein CARUB_v10012057mg [Capsella rubella]	685	743	0	108.5	87.0	90.5	hypothetical protein CARUB_v10012057mg	gbpln	Capsella rubella	AT1G07110.1 | Symbols: F2KP, ATF2KP, FKFBP | fructose-2,6-bisphosphatase | chr1:2178363-2183980 REVERSE LENGTH=744	685	744	0	108.6	86.7	90.4
Rsa1.0_00863.1.g20556.t1	ref|XP_002892380.1| hypothetical protein ARALYDRAFT_470732 [Arabidopsis lyrata subsp. lyrata] gi|297338222|gb|EFH68639.1| hypothetical protein ARALYDRAFT_470732 [Arabidopsis lyrata subsp. lyrata]	99	743	3.00E-27	750.5	69.7	76.8	hypothetical protein ARALYDRAFT_470732	gbpln	Arabidopsis lyrata	AT1G07110.1 | Symbols: F2KP, ATF2KP, FKFBP | fructose-2,6-bisphosphatase | chr1:2178363-2183980 REVERSE LENGTH=744	99	744	1.00E-29	751.5	69.7	75.8
Rsa1.0_00863.1.g20557.t1	ref|XP_002892382.1| hypothetical protein ARALYDRAFT_470734 [Arabidopsis lyrata subsp. lyrata] gi|297338224|gb|EFH68641.1| hypothetical protein ARALYDRAFT_470734 [Arabidopsis lyrata subsp. lyrata]	126	145	2.00E-20	115.1	61.9	69.0	hypothetical protein ARALYDRAFT_470734	gbpln	Arabidopsis lyrata	AT1G07135.1 | Symbols: | glycine-rich protein | chr1:2190157-2190624 REVERSE LENGTH=155	126	155	1.00E-18	123.0	63.5	72.2
Rsa1.0_00863.1.g20558.t1	gb|ABB97039.1| unknown [Brassica rapa]	225	225	1.00E-113	100.0	96.9	98.2	unknown	gbpln	Brassica rapa	AT1G07140.1 | Symbols: SIRANBP | Pleckstrin homology (PH) domain superfamily protein | chr1:2192360-2193688 REVERSE LENGTH=228	225	228	4.00E-95	101.3	87.1	91.6
Rsa1.0_00864.1.g20559.t1	dbj|BAJ34469.1| unnamed protein product [Thellungiella halophila]	654	661	0	101.1	81.5	88.2	unnamed protein product	----	----	AT1G71710.1 | Symbols: | DNAse I-like superfamily protein | chr1:26973796-26976774 REVERSE LENGTH=664	654	664	0	101.5	81.7	88.4

Rsa1.0_00864.1.g20560.t1	ref|XP_002887382.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333223|gb|EFH63641.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	489	491	0	100.4	84.0	87.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G71696.2 | Symbols: SOL1 | carboxypeptidase D, putative | chr1:26966996-26970364 FORWARD LENGTH=491	489	491	0	100.4	82.2	86.7
Rsa1.0_00864.1.g20561.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00864.1.g20562.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00864.1.g20563.t1	gb|EOA33450.1| hypothetical protein CARUB_v10020947mg [Capsella rubella]	226	211	1.00E-101	93.4	85.4	90.7	hypothetical protein CARUB_v10020947mg	gbpln	Capsella rubella	AT1G71692.1 | Symbols: AGL12, XAL1 | AGAMOUS-like 12 | chr1:26952903-26954939 REVERSE LENGTH=211	226	211	1.00E-104	93.4	85.8	90.3
Rsa1.0_00864.1.g20564.t2	gb|EOA33727.1| hypothetical protein CARUB_v10019921mg [Capsella rubella]	659	658	0	99.8	86.2	91.7	hypothetical protein CARUB_v10019921mg	gbpln	Capsella rubella	AT1G71530.1 | Symbols: | Protein kinase superfamily protein | chr1:26939766-26942306 FORWARD LENGTH=655	659	655	0	99.4	85.0	90.6
Rsa1.0_00864.1.g20565.t1	gb|EOA34833.1| hypothetical protein CARUB_v10022408mg [Capsella rubella]	147	150	1.00E-58	102.0	78.2	85.7	hypothetical protein CARUB_v10022408mg	gbpln	Capsella rubella	AT1G71520.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:26938612-26939043 FORWARD LENGTH=143	147	143	9.00E-61	97.3	78.2	83.7
Rsa1.0_00864.1.g20566.t1	gb|EOA34774.1| hypothetical protein CARUB_v10022349mg [Capsella rubella]	183	182	4.00E-83	99.5	83.6	90.2	hypothetical protein CARUB_v10022349mg	gbpln	Capsella rubella	AT1G71450.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:26927088-26927639 FORWARD LENGTH=183	183	183	4.00E-81	100.0	80.3	86.9
Rsa1.0_00864.1.g20567.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1551	1342	0	86.5	42.5	58.2	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1551	1262	2.00E-82	81.4	11.7	18.2
Rsa1.0_00864.1.g20568.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00865.1.g20569.t1	ref|NP_190926.1| diaminopimelate epimerase [Arabidopsis thaliana] gi|75263858|sp|Q9LFG2.1|DAPF_ARATH RecName: Full=Diaminopimelate epimerase, chloroplastic; Short=DAP epimerase; Flags: Precursor gi|6729509|emb|CAB67665.1| diaminopimelate epimerase-like protein [Arabidopsis thaliana] gi|22022530|gb|AAM83223.1| AT3g53580/F4P12_280 [Arabidopsis thaliana] gi|23505901|gb|AAN28810.1| At3g53580/F4P12_280 [Arabidopsis thaliana] gi|332645592|gb|AEE79113.1| diaminopimelate epimerase [Arabidopsis thaliana]	359	362	1.00E-178	100.8	84.1	90.3	diaminopimelate epimerase	gbpln	Arabidopsis thaliana	AT3G53580.1 | Symbols: | diaminopimelate epimerase family protein | chr3:19864784-19866907 FORWARD LENGTH=362	359	362	1.00E-180	100.8	84.1	90.3
Rsa1.0_00865.1.g20570.t1	gb|ABL97987.1| protein translocase [Brassica rapa]	231	220	6.00E-94	95.2	78.8	85.3	protein translocase	gbpln	Brassica rapa	AT2G37410.2 | Symbols: ATTIM17-2, TIM17, TIM17-2 | translocase inner membrane subunit 17-2 | chr2:15698119-15698850 REVERSE LENGTH=243	231	243	2.00E-81	105.2	72.7	81.4
Rsa1.0_00865.1.g20571.t1	ref|NP_190922.3| uncharacterized protein [Arabidopsis thaliana] gi|332645585|gb|AEE79106.1| uncharacterized protein AT3G53540 [Arabidopsis thaliana]	707	924	1.00E-153	130.7	56.0	70.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G53540.1 | Symbols: | unknown protein; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3741 (InterPro:IPR022212); BEST Arabidopsis thaliana protein match is: Protein of unknown function (DUF3741) (TAIR:AT4G28760.2); Has 1710 Blast hits to 868 proteins in 206 species: Archae - 2; Bacteria - 409; Metazoa - 304; Fungi - 204; Plants - 304; Viruses - 2; Other Eukaryotes - 485 (source: NCBI BLink). | chr3:19846805-19850670 REVERSE LENGTH=924	707	924	1.00E-156	130.7	56.0	70.3
Rsa1.0_00865.1.g20572.t1	gb|EOA28993.1| hypothetical protein CARUB_v10025244mg [Capsella rubella]	278	262	1.00E-98	94.2	71.9	80.2	hypothetical protein CARUB_v10025244mg	gbpln	Capsella rubella	AT2G37390.1 | Symbols: NAKR2 | Chloroplast-targeted copper chaperone protein | chr2:15694300-15695461 FORWARD LENGTH=259	278	259	1.00E-101	93.2	72.3	82.0
Rsa1.0_00865.1.g20573.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	226	1274	7.00E-30	563.7	37.2	49.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315	226	315	1.00E-31	139.4	34.5	45.6
Rsa1.0_00865.1.g20574.t1	dbj|BAE98854.1| hypothetical protein [Arabidopsis thaliana]	302	321	6.00E-91	106.3	78.5	84.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G37380.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G39370.1); Has 1284 Blast hits to 422 proteins in 114 species: Archae - 0; Bacteria - 90; Metazoa - 125; Fungi - 151; Plants - 136; Viruses - 0; Other Eukaryotes - 782 (source: NCBI BLink). | chr2:15686828-15687793 FORWARD LENGTH=321	302	321	6.00E-93	106.3	78.1	84.4

Rsa1.0_00865.1.g20575.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00865.1.g20576.t2	gb|EOA29128.1| hypothetical protein CARUB_v10025396mg [Capsella rubella]	670	679	0	101.3	83.3	89.9	hypothetical protein CARUB_v10025396mg	gbpln	Capsella rubella	AT2G37370.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13560.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae – 12; Bacteria – 1396; Metazoa – 17338; Fungi – 3422; Plants – 5037; Viruses – 0; Other Eukaryotes – 2996 (source: NCBI BLink). | chr2:15679273–15682932 FORWARD LENGTH=669	670	669	0	99.9	81.9	88.2
Rsa1.0_00865.1.g20577.t1	gb|EOA27537.1| hypothetical protein CARUB_v10023676mg, partial [Capsella rubella]	254	313	1.00E–119	123.2	89.8	91.7	hypothetical protein CARUB_v10023676mg, partial	gbpln	Capsella rubella	AT2G37330.1 | Symbols: ALS3 | aluminum sensitive 3 | chr2:15669190–15670172 FORWARD LENGTH=273	254	273	1.00E–119	107.5	87.0	90.9
Rsa1.0_00865.1.g20578.t1	ref|XP_002879661.1| pentatricopeptide repeat–containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325500|gb|EFH55920.1| pentatricopeptide repeat–containing protein [Arabidopsis lyrata subsp. lyrata]	481	500	0	104.0	82.5	91.9	pentatricopeptide repeat–containing protein	gbpln	Arabidopsis lyrata	AT2G37320.1 | Symbols: | Tetratricopeptide repeat (TPR)–like superfamily protein | chr2:15667223–15668725 FORWARD LENGTH=500	481	500	0	104.0	83.0	91.5
Rsa1.0_00865.1.g20579.t23	ref|NP_001189697.1| RabGAP/TBC domain–containing protein [Arabidopsis thaliana] gi|330254285|gb|AEC09379.1| RabGAP/TBC domain–containing protein [Arabidopsis thaliana]	1075	916	0	85.2	58.4	64.7	RabGAP/TBC domain–containing protein	gbpln	Arabidopsis thaliana	AT2G37290.2 | Symbols: | Ypt/Rab–GAP domain of gyp1p superfamily protein | chr2:15656935–15661335 REVERSE LENGTH=916	1075	916	0	85.2	58.4	64.7
Rsa1.0_00865.1.g20580.t1	ref|NP_181265.1| ABC transporter G family member 33 [Arabidopsis thaliana] gi|75339056|sp|Q9ZUT8.1|AB33G_ARATH RecName: Full=ABC transporter G family member 33; Short=ABC transporter ABCG.33; Short=AtABCG33; AltName: Full=Probable pleiotropic drug resistance protein 5 gi|4056482|gb|AAC98048.1| putative ABC transporter [Arabidopsis thaliana] gi|28144327|tpg|DAA00873.1| TPA_exp: PDR5 ABC transporter [Arabidopsis thaliana] gi|330254283|gb|AEC09377.1| ABC transporter G family member 33 [Arabidopsis thaliana]	1423	1413	0	99.3	85.6	92.4	ABC transporter G family member 33	gbpln	Arabidopsis thaliana	AT2G37280.1 | Symbols: PDR5, ATPDR5 | pleiotropic drug resistance 5 | chr2:15650400–15656417 FORWARD LENGTH=1413	1423	1413	0	99.3	85.6	92.4
Rsa1.0_00865.1.g20581.t1	ref|XP_002879660.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325499|gb|EFH55919.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1383	1424	0	103.0	86.0	93.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G37280.1 | Symbols: PDR5, ATPDR5 | pleiotropic drug resistance 5 | chr2:15650400–15656417 FORWARD LENGTH=1413	1383	1413	0	102.2	85.0	92.1
Rsa1.0_00866.1.g20582.t1	gb|AAC95175.1| putative non–LTR retroelement reverse transcriptase [Arabidopsis thaliana]	827	1352	1.00E–154	163.5	35.2	49.9	putative non–LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I–like superfamily protein | chr1:16528880–16531065 REVERSE LENGTH=626	827	626	1.00E–43	75.7	13.5	21.9
Rsa1.0_00866.1.g20583.t1	ref|XP_002886433.1| phloem protein 2–A11 [Arabidopsis lyrata subsp. lyrata] gi|297332274|gb|EFH62692.1| phloem protein 2–A11 [Arabidopsis lyrata subsp. lyrata]	152	287	3.00E–63	188.8	79.6	85.5	phloem protein 2–A11	gbpln	Arabidopsis lyrata	AT1G63090.1 | Symbols: AtPP2–A11, PP2–A11 | phloem protein 2–A11 | chr1:23391283–23392609 REVERSE LENGTH=289	152	289	2.00E–63	190.1	77.0	83.6
Rsa1.0_00866.1.g20584.t1	ref|NP_850282.2| Cystatin/monellin domain–containing protein [Arabidopsis thaliana] gi|61742651|gb|AAX55146.1| hypothetical protein At2g37435 [Arabidopsis thaliana] gi|330254304|gb|AEC09398.1| Cystatin/monellin domain–containing protein [Arabidopsis thaliana]	197	171	2.00E–42	86.8	46.7	62.4	Cystatin/monellin domain–containing protein	gbpln	Arabidopsis thaliana	AT2G37435.1 | Symbols: | Cystatin/monellin superfamily protein | chr2:15709823–15710528 FORWARD LENGTH=171	197	171	6.00E–45	86.8	46.7	62.4
Rsa1.0_00866.1.g20585.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00866.1.g20586.t1	ref|NP_176498.1| scarecrow–like protein 28 [Arabidopsis thaliana] gi|75169917|sp|Q9CAN3.1|SCL28_ARATH RecName: Full=Scarecrow–like protein 28; Short=AtSCL28; AltName: Full=GRAS family protein 8; Short=AtGRAS–8 gi|12323248|gb|AAG51600.1|AC010795_4 transcription factor SCARECROW, putative; 52594–50618 [Arabidopsis thaliana] gi|332195932|gb|AEE34053.1| scarecrow–like protein 28 [Arabidopsis thaliana]	650	658	0	101.2	79.2	86.8	scarecrow–like protein 28	gbpln	Arabidopsis thaliana	AT1G63100.1 | Symbols: | GRAS family transcription factor | chr1:23399391–23401367 REVERSE LENGTH=658	650	658	0	101.2	79.2	86.8

Rsa1.0_00866.1.g20587.t1	ref|NP_850969.2| GPI transamidase subunit PIG−U [Arabidopsis thaliana] gi|332195934|gb|AEE34055.1| GPI transamidase subunit PIG−U [Arabidopsis thaliana]	686	469	0	68.4	60.5	64.3	GPI transamidase subunit PIG−U	gbpln	Arabidopsis thaliana	AT1G63110.1 | Symbols: | GPI transamidase subunit PIG−U | chr1:23404870−23407757 FORWARD LENGTH=469	686	469	0	68.4	60.5	64.3
Rsa1.0_00866.1.g20588.t1	ref|NP_176500.1| rhomboid −like 2 [Arabidopsis thaliana] gi|12323258|gb|AAG51610.1|AC010795_14 membrane protein, putative; 61952−60281 [Arabidopsis thaliana] gi|28393358|gb|AAO42103.1| putative membrane protein [Arabidopsis thaliana] gi|28827620|gb|AAO50654.1| putative membrane protein [Arabidopsis thaliana] gi|77999980|dbj|BAE46871.1| Rhomboid family protein AtRBL2 [Arabidopsis thaliana] gi|332195937|gb|AEE34058.1| rhomboid −like 2 [Arabidopsis thaliana]	318	317	1.00E−158	99.7	91.5	95.6	rhomboid −like 2	gbpln	Arabidopsis thaliana	AT1G63120.1 | Symbols: ATRBL2, RBL2 | RHOMBOID−like 2 | chr1:23409054−23410725 REVERSE LENGTH=317	318	317	1.00E−160	99.7	91.5	95.6
Rsa1.0_00866.1.g20589.t1	gb|EOA33411.1| hypothetical protein CARUB_v10020496mg [Capsella rubella]	367	370	1.00E−158	100.8	73.8	83.7	hypothetical protein CARUB_v10020496mg	gbpln	Capsella rubella	AT1G77520.1 | Symbols: | O−methyltransferase family protein | chr1:29130557−29132007 FORWARD LENGTH=381	367	381	1.00E−158	103.8	71.9	83.1
Rsa1.0_00866.1.g20590.t1	gb|AAO24573.1| At1g77520 [Arabidopsis thaliana] gi|110736212|dbj|BAF00077.1| caffeic acid 3−O−methyltransferase like protein [Arabidopsis thaliana]	341	381	1.00E−134	111.7	70.1	81.8	At1g77520	gbpln	Arabidopsis thaliana	AT1G77520.1 | Symbols: | O−methyltransferase family protein | chr1:29130557−29132007 FORWARD LENGTH=381	341	381	1.00E−136	111.7	69.8	81.5
Rsa1.0_00866.1.g20591.t1	ref|XP_002894649.1| hypothetical protein ARALYDRAFT_892826 [Arabidopsis lyrata subsp. lyrata] gi|297340491|gb|EFH70908.1| hypothetical protein ARALYDRAFT_892826 [Arabidopsis lyrata subsp. lyrata]	338	352	1.00E−137	104.1	68.9	82.5	hypothetical protein ARALYDRAFT_892826	gbpln	Arabidopsis lyrata	AT2G19150.1 | Symbols: | Pectin lyase−like superfamily protein | chr2:8305100−8307444 FORWARD LENGTH=339	338	339	7.00E−67	100.3	40.5	53.0
Rsa1.0_00866.1.g20592.t1	ref|XP_002879672.1| hypothetical protein ARALYDRAFT_345475 [Arabidopsis lyrata subsp. lyrata] gi|297325511|gb|EFH55931.1| hypothetical protein ARALYDRAFT_345475 [Arabidopsis lyrata subsp. lyrata]	212	232	3.00E−32	109.4	41.0	53.3	hypothetical protein ARALYDRAFT_345475	gbpln	Arabidopsis lyrata	AT2G37435.1 | Symbols: | Cystatin/monellin superfamily protein | chr2:15709823−15710528 FORWARD LENGTH=171	212	171	2.00E−28	80.7	34.4	46.2
Rsa1.0_00866.1.g20593.t1	gb|EOA33460.1| hypothetical protein CARUB_v10021114mg [Capsella rubella]	147	147	2.00E−73	100.0	90.5	95.2	hypothetical protein CARUB_v10021114mg	gbpln	Capsella rubella	AT1G63220.1 | Symbols: | Calcium−dependent lipid−binding (CaLB domain) family protein | chr1:23449017−23450244 FORWARD LENGTH=147	147	147	3.00E−75	100.0	89.1	93.9
Rsa1.0_00866.1.g20594.t1	ref|NP_564812.1| uncharacterized protein [Arabidopsis thaliana] gi|15292765|gb|AAK92751.1| unknown protein [Arabidopsis thaliana] gi|21281038|gb|AAM45128.1| unknown protein [Arabidopsis thaliana] gi|332195953|gb|AEE34074.1| uncharacterized protein AT1G63240 [Arabidopsis thaliana]	583	548	1.00E−112	94.0	46.8	58.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G63240.1 | Symbols: | unknown protein; Has 460 Blast hits to 413 proteins in 106 species: Archae − 5; Bacteria − 12; Metazoa − 152; Fungi − 46; Plants − 43; Viruses − 2; Other Eukaryotes − 200 (source: NCBI BLink). | chr1:23456188−23458550 REVERSE LENGTH=548	583	548	1.00E−115	94.0	46.8	58.3
Rsa1.0_00867.1.g20595.t1	ref|XP_002889771.1| hypothetical protein ARALYDRAFT_334263 [Arabidopsis lyrata subsp. lyrata] gi|297335613|gb|EFH66030.1| hypothetical protein ARALYDRAFT_334263 [Arabidopsis lyrata subsp. lyrata]	131	128	2.00E−54	97.7	84.7	93.1	hypothetical protein ARALYDRAFT_334263	gbpln	Arabidopsis lyrata	AT1G09812.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58007.2); Has 93 Blast hits to 93 proteins in 13 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 93; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:3187817−3188580 FORWARD LENGTH=128	131	128	1.00E−53	97.7	83.2	92.4
Rsa1.0_00867.1.g20596.t1	gb|EOA37326.1| hypothetical protein CARUB_v10011018mg [Capsella rubella]	573	532	1.00E−173	92.8	60.6	66.7	hypothetical protein CARUB_v10011018mg	gbpln	Capsella rubella	AT1G09810.1 | Symbols: ECT11 | evolutionarily conserved C−terminal region 11 | chr1:3181138−3183354 REVERSE LENGTH=470	573	470	1.00E−173	82.0	61.1	67.5
Rsa1.0_00867.1.g20597.t1	ref|XP_002879092.1| hypothetical protein ARALYDRAFT_481654 [Arabidopsis lyrata subsp. lyrata] gi|297324931|gb|EFH55351.1| hypothetical protein ARALYDRAFT_481654 [Arabidopsis lyrata subsp. lyrata]	318	330	2.00E−49	103.8	45.0	56.3	hypothetical protein ARALYDRAFT_481654	gbpln	Arabidopsis lyrata	AT2G27505.1 | Symbols: | FBD−like domain family protein | chr2:11756746−11757829 FORWARD LENGTH=298	318	298	2.00E−41	93.7	40.3	54.1

Rsa1.0_00867.1.g20598.t1	ref|XP_002892526.1| hypothetical protein ARALYDRAFT_471082 [Arabidopsis lyrata subsp. lyrata] gi|297338368|gb|EFH68785.1| hypothetical protein ARALYDRAFT_471082 [Arabidopsis lyrata subsp. lyrata]	373	373	0	100.0	83.9	91.4	hypothetical protein ARALYDRAFT_471082	gbpln	Arabidopsis lyrata	AT1G09800.1 | Symbols: | Pseudouridine synthase family protein | chr1:3177121-3180336 REVERSE LENGTH=372	373	372	0	99.7	83.9	90.9
Rsa1.0_00867.1.g20599.t1	gb|EOA39069.1| hypothetical protein CARUB_v10011733mg [Capsella rubella]	407	409	0	100.5	88.0	92.9	hypothetical protein CARUB_v10011733mg	gbpln	Capsella rubella	AT1G09795.1 | Symbols: ATATP-PRT2, HISN1B, ATP-PRT2 | ATP phosphoribosyl transferase 2 | chr1:3173588-3176690 FORWARD LENGTH=413	407	413	0	101.5	87.5	91.6
Rsa1.0_00867.1.g20600.t1	ref|NP_001184952.1| Cox19 family protein (CHCH motif) [Arabidopsis thaliana] gi|332190372|gb|AEE28493.1| Cox19 family protein (CHCH motif) [Arabidopsis thaliana]	63	63	1.00E-25	100.0	95.2	95.2	Cox19 family protein (CHCH motif)	gbpln	Arabidopsis thaliana	AT1G09794.1 | Symbols: | Cox19 family protein (CHCH motif) | chr1:3172196-3173321 FORWARD LENGTH=63	63	63	2.00E-28	100.0	95.2	95.2
Rsa1.0_00867.1.g20601.t2	gb|EOA38932.1| hypothetical protein CARUB_v10011331mg [Capsella rubella]	439	442	0	100.7	83.8	90.7	hypothetical protein CARUB_v10011331mg	gbpln	Capsella rubella	AT1G09790.1 | Symbols: COBL6 | COBRA-like protein 6 precursor | chr1:3168568-3170819 REVERSE LENGTH=454	439	454	0	103.4	80.6	86.6
Rsa1.0_00867.1.g20602.t1	dbj|BAA09598.1| Myb-like DNA binding protein [Arabidopsis thaliana]	803	844	0	105.1	88.3	93.9	Myb-like DNA binding protein	gbpln	Arabidopsis thaliana	AT1G09770.1 | Symbols: ATCDC5, CDC5, ATMYBCDC5 | cell division cycle 5 | chr1:3162002-3165122 FORWARD LENGTH=844	803	844	0	105.1	88.3	93.9
Rsa1.0_00867.1.g20603.t5	ref|NP_172447.1| U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana] gi|19884091|sp|P43333.2|RU2A_ARATH RecName: Full=U2 small nuclear ribonucleoprotein A'; Short=U2 snRNP A' gi|2160183|gb|AAB60746.1| Identical to A. thaliana U2 SnRNP-specific A' protein (gb|X69137). ESTs gb|ATTS0705, gb|ATTS0339 come from this gene [Arabidopsis thaliana] gi|16649065|gb|AAL24384.1| SnRNP-specific A protein [Arabidopsis thaliana] gi|23197870|gb|AAN15462.1| SnRNP-specific A protein [Arabidopsis thaliana] gi|332190368|gb|AEE28489.1| U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana]	868	249	1.00E-124	28.7	26.0	27.1	U2 small nuclear ribonucleoprotein A'	gbpln	Arabidopsis thaliana	AT1G09760.1 | Symbols: U2A' | U2 small nuclear ribonucleoprotein A | chr1:3159476-3161603 REVERSE LENGTH=249	868	249	1.00E-126	28.7	26.0	27.1
Rsa1.0_00867.1.g20604.t1	ref|NP_172445.2| adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana] gi|29028798|gb|AAO64778.1| At1g09740 [Arabidopsis thaliana] gi|110736422|dbj|BAF00178.1| putative ER6 protein [Arabidopsis thaliana] gi|332190366|gb|AEE28487.1| adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana]	81	171	4.00E-32	211.1	80.2	90.1	adenine nucleotide alpha hydrolases-like protein	gbpln	Arabidopsis thaliana	AT1G09740.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr1:3154603-3155834 FORWARD LENGTH=171	81	171	7.00E-35	211.1	80.2	90.1
Rsa1.0_00867.1.g20605.t1	gb|EOA38618.1| hypothetical protein CARUB_v10010470mg [Capsella rubella]	68	171	5.00E-25	251.5	97.1	100.0	hypothetical protein CARUB_v10010470mg	gbpln	Capsella rubella	AT1G09740.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr1:3154603-3155834 FORWARD LENGTH=171	68	171	4.00E-27	251.5	94.1	97.1
Rsa1.0_00867.1.g20606.t2	ref|XP_002892520.1| Ulp1 protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297338362|gb|EFH68779.1| Ulp1 protease family protein [Arabidopsis lyrata subsp. lyrata]	1015	970	0	95.6	70.0	75.9	Ulp1 protease family protein	gbpln	Arabidopsis lyrata	AT1G09730.2 | Symbols: | Cysteine proteinases superfamily protein | chr1:3148017-3154236 REVERSE LENGTH=931	1015	931	0	91.7	68.2	74.8
Rsa1.0_00867.1.g20607.t1	ref|XP_002892519.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] gi|297338361|gb|EFH68778.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]	840	927	0	110.4	82.4	89.5	kinase interacting family protein	gbpln	Arabidopsis lyrata	AT1G09720.1 | Symbols: | Kinase interacting (KIP1-like) family protein | chr1:3144438-3147303 REVERSE LENGTH=928	840	928	0	110.5	77.7	87.0
Rsa1.0_00867.1.g20608.t1	ref|XP_002889766.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297335608|gb|EFH66025.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	593	626	0	105.6	70.0	79.6	DNA binding protein	gbpln	Arabidopsis lyrata	AT1G09710.1 | Symbols: | Homeodomain-like superfamily protein | chr1:3141119-3144232 FORWARD LENGTH=610	593	610	0	102.9	65.9	76.6
Rsa1.0_00867.1.g20609.t1	gb|AAT77416.1| dsRNA-binding protein LH1 [Brassica oleracea var. capitata]	258	283	1.00E-127	109.7	91.1	95.7	dsRNA-binding protein LH1	gbpln	Brassica oleracea	AT1G09700.1 | Symbols: HYL1, DRB1 | dsRNA-binding domain-like superfamily protein | chr1:3137960-3140118 REVERSE LENGTH=419	258	419	1.00E-106	162.4	77.1	86.8
Rsa1.0_00867.1.g20610.t1	ref|XP_002889760.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata] gi|297335602|gb|EFH66019.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata]	80	164	1.00E-37	205.0	96.3	97.5	60S ribosomal protein L21	gbpln	Arabidopsis lyrata	AT1G09690.1 | Symbols: | Translation protein SH3-like family protein | chr1:3136407-3137430 REVERSE LENGTH=164	80	164	2.00E-40	205.0	95.0	97.5

Rsa1.0_00868.1.g20611.t1	ref|XP_002881646.1| jacalin lectin family protein [Arabidopsis lyrata subsp. lyrata] gi|297327485|gb|EFH57905.1| jacalin lectin family protein [Arabidopsis lyrata subsp. lyrata]	155	458	5.00E-43	295.5	67.1	79.4	jacalin lectin family protein	gbpln	Arabidopsis lyrata	AT2G39310.3 | Symbols: | jacalin-related lectin 22 | chr2:16414262-16416323 REVERSE LENGTH=458	155	458	2.00E-45	295.5	67.7	78.7
Rsa1.0_00868.1.g20612.t1	ref|NP_181466.2| SAC3/GANP/Nin1/mts3/eIF-3 p25-family protein [Arabidopsis thaliana] gi|330254569|gb|AEC09663.1| SAC3/GANP/Nin1/mts3/eIF-3 p25-family protein [Arabidopsis thaliana]	1002	1006	0	100.4	79.7	86.7	SAC3/GANP/Nin1/mts3/eIF-3 p25-family protein	gbpln	Arabidopsis thaliana	AT2G39340.1 | Symbols: | SAC3/GANP/Nin1/mts3/eIF-3 p25 family | chr2:16424043-16429771 FORWARD LENGTH=1006	1002	1006	0	100.4	79.7	86.7
Rsa1.0_00868.1.g20613.t1	ref|NP_181469.1| uncharacterized protein [Arabidopsis thaliana] gi|75099835|sp|O80624.1|MAKR4_ARATH RecName: Full=Probable membrane-associated kinase regulator 4 gi|3355466|gb|AAC27828.1| unknown protein [Arabidopsis thaliana] gi|330254572|gb|AEC09666.1| uncharacterized protein AT2G39370 [Arabidopsis thaliana]	310	328	1.00E-112	105.8	81.0	87.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G39370.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G37380.1); Has 184 Blast hits to 178 proteins in 53 species: Archae - 0; Bacteria - 58; Metazoa - 9; Fungi - 0; Plants - 103; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink). | chr2:16444280-16445266 REVERSE LENGTH=328	310	328	1.00E-114	105.8	81.0	87.1
Rsa1.0_00868.1.g20614.t1	ref|XP_002881653.1| Os04g0376000 [Arabidopsis lyrata subsp. lyrata] gi|297327492|gb|EFH57912.1| Os04g0376000 [Arabidopsis lyrata subsp. lyrata]	111	123	2.00E-45	110.8	85.6	91.0	Os04g0376000	gbpln	Arabidopsis lyrata	AT2G39390.1 | Symbols: | Ribosomal L29 family protein | chr2:16450803-16451762 REVERSE LENGTH=123	111	123	4.00E-48	110.8	85.6	90.1
Rsa1.0_00868.1.g20615.t1	gb|EOA27527.1| hypothetical protein CARUB_v10023666mg [Capsella rubella]	626	317	1.00E-167	50.6	45.0	47.8	hypothetical protein CARUB_v10023666mg	gbpln	Capsella rubella	AT2G39410.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:16455667-16458217 FORWARD LENGTH=317	626	317	1.00E-165	50.6	43.8	46.8
Rsa1.0_00868.1.g20616.t1	ref|XP_002879795.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325634|gb|EFH56054.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	317	317	1.00E-171	100.0	90.2	95.0	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT2G39420.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:16460442-16462872 FORWARD LENGTH=317	317	317	1.00E-171	100.0	88.6	94.0
Rsa1.0_00868.1.g20617.t1	ref|NP_001118477.4| Phosphatidylinositol N-acetylglucosaminyltransferase, GPI19/PIG-P subunit [Arabidopsis thaliana] gi|330254584|gb|AEC09678.1| Phosphatidylinositol N-acetylglucosaminyltransferase, GPI19/PIG-P subunit [Arabidopsis thaliana]	123	181	2.00E-36	147.2	65.0	73.2	Phosphatidylinositol N-acetylglucosaminyltransferase, GPI19/PIG-P subunit	gbpln	Arabidopsis thaliana	AT2G39445.1 | Symbols: | Phosphatidylinositol N-acetylglucosaminyltransferase, GPI19/PIG-P subunit | chr2:16470025-16471125 REVERSE LENGTH=181	123	181	3.00E-39	147.2	65.0	73.2
Rsa1.0_00868.1.g20618.t1	ref|XP_002862450.1| cation efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297307975|gb|EFH38708.1| cation efflux family protein [Arabidopsis lyrata subsp. lyrata]	372	394	1.00E-173	105.9	89.5	94.1	cation efflux family protein	gbpln	Arabidopsis lyrata	AT2G39450.1 | Symbols: MTP11, ATMTP11 | Cation efflux family protein | chr2:16471744-16473735 REVERSE LENGTH=394	372	394	1.00E-175	105.9	89.8	94.1
Rsa1.0_00868.1.g20619.t2	dbj|BAJ33853.1| unnamed protein product [Thellungiella halophila]	263	154	2.00E-77	58.6	56.3	56.7	unnamed protein product	----	----	AT3G55280.2 | Symbols: RPL23AB | ribosomal protein L23AB | chr3:20500667-20501519 FORWARD LENGTH=154	263	154	2.00E-56	58.6	45.2	45.6
Rsa1.0_00868.1.g20620.t4	ref|NP_181490.5| uncharacterized protein [Arabidopsis thaliana] gi|330254602|gb|AEC09696.1| uncharacterized protein AT2G39580 [Arabidopsis thaliana]	430	1577	8.00E-41	366.7	29.5	35.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G39580.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative zinc-finger domain (InterPro:IPR019607); Has 249 Blast hits to 219 proteins in 85 species: Archae - 0; Bacteria - 144; Metazoa - 29; Fungi - 8; Plants - 50; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr2:16510540-16516948 FORWARD LENGTH=1577	430	1577	2.00E-43	366.7	29.5	35.3
Rsa1.0_00868.1.g20621.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00869.1.g20622.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	326	1161	2.00E-54	356.1	34.7	51.5	F14N23.4	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	326	332	1.00E-54	101.8	33.7	48.5

Rsa1.0_00869.1.g20623.t1	ref|NP_568335.1| glutamine synthetase cytosolic isozyme 1-4 [Arabidopsis thaliana] gi|75309209|sp|Q9FMD9.1|GLN14_ARATH RecName: Full=Glutamine synthetase cytosolic isozyme 1-4; AltName: Full=Glutamate--ammonia ligase GLN1;4; Short=GLN1;4 gi|10176966|dbj|BAB10184.1| glutamine synthetase [Arabidopsis thaliana] gi|16649125|gb|AAL24414.1| glutamine synthetase [Arabidopsis thaliana] gi|22136142|gb|AAM91149.1| glutamine synthetase [Arabidopsis thaliana] gi|332004929|gb|AED92312.1| glutamine synthetase cytosolic isozyme 1-4 [Arabidopsis thaliana]	356	356	0	100.0	96.6	99.2	glutamine synthetase cytosolic isozyme 1-4	gbpln	Arabidopsis thaliana	AT5G16570.1 | Symbols: GLN1;4 | glutamine synthetase 1;4 | chr5:5421898-5424523 REVERSE LENGTH=356	356	356	0	100.0	96.6	99.2
Rsa1.0_00869.1.g20624.t1	ref|NP_197162.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|75171650|sp|Q9FMD7.1|Y5659_ARATH RecName: Full=Probable inactive receptor kinase At5g16590; Flags: Precursor gi|10176968|dbj|BAB10186.1| receptor-like protein kinase [Arabidopsis thaliana] gi|44917459|gb|AAS49054.1| At5g16590 [Arabidopsis thaliana] gi|45773906|gb|AAS76757.1| At5g16590 [Arabidopsis thaliana] gi|110737672|dbj|BAF00775.1| receptor like protein kinase [Arabidopsis thaliana] gi|224589675|gb|ACN59369.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332004931|gb|AED92314.1| putative inactive receptor kinase [Arabidopsis thaliana]	611	625	0	102.3	86.1	90.8	putative inactive receptor kinase	gbpln	Arabidopsis thaliana	AT5G16590.1 | Symbols: LRR1 | Leucine-rich repeat protein kinase family protein | chr5:5431862-5433921 FORWARD LENGTH=625	611	625	0	102.3	86.1	90.8
Rsa1.0_00869.1.g20625.t1	ref|NP_197163.1| myb domain protein 43 [Arabidopsis thaliana] gi|5823313|gb|AAD53095.1|AF175990_1 putative transcription factor [Arabidopsis thaliana] gi|10176969|dbj|BAB10187.1| transcription factor [Arabidopsis thaliana] gi|27754274|gb|AAO22590.1| unknown protein [Arabidopsis thaliana] gi|41619406|gb|AAS10095.1| MYB transcription factor [Arabidopsis thaliana] gi|332004932|gb|AED92315.1| myb domain protein 43 [Arabidopsis thaliana]	318	327	1.00E-121	102.8	78.6	88.1	myb domain protein 43	gbpln	Arabidopsis thaliana	AT5G16600.1 | Symbols: MYB43, AtMYB43 | myb domain protein 43 | chr5:5438291-5440214 FORWARD LENGTH=327	318	327	1.00E-123	102.8	78.6	88.1
Rsa1.0_00869.1.g20626.t2	ref|XP_002873786.1| hypothetical protein ARALYDRAFT_488520 [Arabidopsis lyrata subsp. lyrata] gi|297319623|gb|EFH50045.1| hypothetical protein ARALYDRAFT_488520 [Arabidopsis lyrata subsp. lyrata]	666	687	0	103.2	72.8	81.5	hypothetical protein ARALYDRAFT_488520	gbpln	Arabidopsis lyrata	AT5G16610.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:5445068-5447945 REVERSE LENGTH=673	666	673	0	101.1	69.8	80.3
Rsa1.0_00869.1.g20627.t3	gb|EOA30606.1| hypothetical protein CARUB_v10013737mg [Capsella rubella]	460	437	1.00E-171	95.0	62.4	75.9	hypothetical protein CARUB_v10013737mg	gbpln	Capsella rubella	AT3G10450.1 | Symbols: SCPL7 | serine carboxypeptidase-like 7 | chr3:3249544-3252320 FORWARD LENGTH=437	460	437	1.00E-173	95.0	61.5	75.7
Rsa1.0_00869.1.g20628.t1	ref|NP_197167.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75171647|sp|Q9FMD3.1|PP389_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g16640, mitochondrial; Flags: Precursor gi|10176973|dbj|BAB10191.1| unnamed protein product [Arabidopsis thaliana] gi|110737318|dbj|BAF00605.1| hypothetical protein [Arabidopsis thaliana] gi|332004938|gb|AED92321.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	489	504	0	103.1	79.3	87.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G16640.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:5461031-5462545 FORWARD LENGTH=504	489	504	0	103.1	79.3	87.3
Rsa1.0_00869.1.g20629.t1	gb|EOA21789.1| hypothetical protein CARUB_v10002253mg [Capsella rubella]	127	128	2.00E-55	100.8	81.9	85.8	hypothetical protein CARUB_v10002253mg	gbpln	Capsella rubella	AT5G16650.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:5463446-5465075 REVERSE LENGTH=128	127	128	9.00E-58	100.8	81.1	85.8

Rsa1.0_00869.1.g20630.t1	ref|XP_002873788.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319625|gb|EFH50047.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	165	167	6.00E-65	101.2	78.8	86.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G16660.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast, membrane, chloroplast envelope; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02900.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5465699-5467006 REVERSE LENGTH=168	165	168	2.00E-64	101.8	77.0	86.1
Rsa1.0_00869.1.g20631.t1	ref|NP_197171.2| origin recognition complex subunit 3 [Arabidopsis thaliana] gi|47681285|gb|AAT37463.1| origin recognition complex protein 3 [Arabidopsis thaliana] gi|332004943|gb|AED92326.1| origin recognition complex subunit 3 [Arabidopsis thaliana]	727	734	0	101.0	86.1	91.9	origin recognition complex subunit 3	gbpln	Arabidopsis thaliana	AT5G16690.1 | Symbols: ORC3, ATORC3 | origin recognition complex subunit 3 | chr5:5474410-5479878 FORWARD LENGTH=734	727	734	0	101.0	86.1	91.9
Rsa1.0_00869.1.g20632.t1	ref|XP_002871731.1| glycosyl hydrolase family 5 protein [Arabidopsis lyrata subsp. lyrata] gi|297317568|gb|EFH47990.1| glycosyl hydrolase family 5 protein [Arabidopsis lyrata subsp. lyrata]	193	488	3.00E-91	252.8	82.9	87.6	glycosyl hydrolase family 5 protein	gbpln	Arabidopsis lyrata	AT5G16700.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr5:5480763-5483045 FORWARD LENGTH=488	193	488	4.00E-92	252.8	80.8	88.1
Rsa1.0_00870.1.g20633.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00870.1.g20634.t1	ref|NP_197953.1| ethylene-responsive transcription factor TINY [Arabidopsis thaliana] gi|48428609|sp|Q39127.1|TINY_ARATH RecName: Full=Ethylene-responsive transcription factor TINY gi|1246403|emb|CAA64359.1| TINY [Arabidopsis thaliana] gi|3406035|gb|AAC29139.1| TINY [Arabidopsis thaliana] gi|48479302|gb|AAT44922.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|90568018|gb|ABD94079.1| At5g25810 [Arabidopsis thaliana] gi|332006107|gb|AED93490.1| ethylene-responsive transcription factor TINY [Arabidopsis thaliana]	223	218	2.00E-80	97.8	80.3	85.2	ethylene-responsive transcription factor TINY	gbpln	Arabidopsis thaliana	AT5G25810.1 | Symbols: tny | Integrase-type DNA-binding superfamily protein | chr5:8986976-8987632 REVERSE LENGTH=218	223	218	6.00E-83	97.8	80.3	85.2
Rsa1.0_00870.1.g20635.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00870.1.g20636.t1	ref|XP_002871479.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317316|gb|EFH47738.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1011	1102	0	109.0	51.2	63.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G11530.1 | Symbols: EMF1 | embryonic flower 1 (EMF1) | chr5:3697140-3700930 FORWARD LENGTH=1096	1011	1096	0	108.4	49.7	62.5
Rsa1.0_00870.1.g20637.t1	ref|NP_197952.2| small RNA degrading nuclease 5 [Arabidopsis thaliana] gi|215274964|sp|Q8L7M4.2|SDN5_ARATH RecName: Full=Small RNA degrading nuclease 5 gi|332006106|gb|AED93489.1| small RNA degrading nuclease 5 [Arabidopsis thaliana]	561	567	0	101.1	81.6	89.8	small RNA degrading nuclease 5	gbpln	Arabidopsis thaliana	AT5G25800.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:8979761-8982724 REVERSE LENGTH=567	561	567	0	101.1	81.6	89.8
Rsa1.0_00870.1.g20638.t1	gb|EOA20503.1| hypothetical protein CARUB_v10000816mg, partial [Capsella rubella]	502	491	1.00E-156	97.8	59.0	68.7	hypothetical protein CARUB_v10000816mg, partial	gbpln	Capsella rubella	AT5G25790.1 | Symbols: | Tesmin/TSO1-like CXC domain-containing protein | chr5:8977233-8979181 REVERSE LENGTH=459	502	459	1.00E-158	91.4	57.8	67.5
Rsa1.0_00870.1.g20639.t1	ref|XP_002872181.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297836036|ref|XP_002885900.1| hypothetical protein ARALYDRAFT_899617 [Arabidopsis lyrata subsp. lyrata] gi|297318018|gb|EFH48440.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331740|gb|EFH62159.1| hypothetical protein ARALYDRAFT_899617 [Arabidopsis lyrata subsp. lyrata]	157	157	9.00E-88	100.0	98.7	98.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G25760.2 | Symbols: PEX4 | peroxin4 | chr5:8967983-8969173 FORWARD LENGTH=157	157	157	3.00E-89	100.0	96.8	98.7

Rsa1.0_00870.1.g20640.t1	gb|EOA20339.1| hypothetical protein CARUB_v10000647mg, partial [Capsella rubella]	523	544	0	104.0	90.4	96.0	hypothetical protein CARUB_v10000647mg, partial	gbpln	Capsella rubella	AT5G25757.1 | Symbols: | RNA polymerase I-associated factor PAF67 | chr5:8965515-8967460 REVERSE LENGTH=514	523	514	0	98.3	89.7	94.6
Rsa1.0_00870.1.g20641.t1	gb|EOA20666.1| hypothetical protein CARUB_v10000978mg, partial [Capsella rubella]	426	439	0	103.1	86.6	92.3	hypothetical protein CARUB_v10000978mg, partial	gbpln	Capsella rubella	AT5G25620.2 | Symbols: YUC6 | Flavin-binding monooxygenase family protein | chr5:8935312-8938200 REVERSE LENGTH=426	426	426	0	100.0	87.3	92.0
Rsa1.0_00870.1.g20642.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	847	1274	0	150.4	48.5	64.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	847	575	9.00E-58	67.9	19.5	31.1
Rsa1.0_00870.1.g20643.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00871.1.g20644.t1	ref|NP_188642.2| protein titan9 [Arabidopsis thaliana] gi|42572493|ref|NP_974342.1| protein titan9 [Arabidopsis thaliana] gi|9293961|dbj|BAB01864.1| unnamed protein product [Arabidopsis thaliana] gi|17380796|gb|AAL36085.1| unknown protein [Arabidopsis thaliana] gi|21689809|gb|AAM67548.1| unknown protein [Arabidopsis thaliana] gi|332642806|gb|AEE76327.1| protein titan9 [Arabidopsis thaliana] gi|332642807|gb|AEE76328.1| protein titan9 [Arabidopsis thaliana]	276	282	3.00E-81	102.2	62.7	74.6	protein titan9	gbpln	Arabidopsis thaliana	AT3G20070.2 | Symbols: TTN9 | titan9 | chr3:7004950-7006625 REVERSE LENGTH=282	276	282	9.00E-84	102.2	62.7	74.6
Rsa1.0_00871.1.g20645.t1	ref|NP_001078193.1| cytochrome P450, family 705, subfamily A, polypeptide 22 [Arabidopsis thaliana] gi|332642817|gb|AEE76338.1| cytochrome P450, family 705, subfamily A, polypeptide 22 [Arabidopsis thaliana]	128	487	2.00E-41	380.5	60.2	75.8	cytochrome P450, family 705, subfamily A, polypeptide 22	gbpln	Arabidopsis thaliana	AT3G20130.2 | Symbols: CYP705A22 | cytochrome P450, family 705, subfamily A, polypeptide 22 | chr3:7026982-7028613 FORWARD LENGTH=487	128	487	4.00E-44	380.5	60.2	75.8
Rsa1.0_00871.1.g20646.t1	ref|XP_002885355.1| ubiquitin-conjugating enzyme 19 [Arabidopsis lyrata subsp. lyrata] gi|297331195|gb|EFH61614.1| ubiquitin-conjugating enzyme 19 [Arabidopsis lyrata subsp. lyrata]	181	181	4.00E-99	100.0	95.6	96.1	ubiquitin-conjugating enzyme 19	gbpln	Arabidopsis lyrata	AT3G20060.1 | Symbols: UBC19 | ubiquitin-conjugating enzyme19 | chr3:7002927-7004283 REVERSE LENGTH=181	181	181	3.00E-94	100.0	94.5	95.0
Rsa1.0_00871.1.g20647.t1	gb|EOA32274.1| hypothetical protein CARUB_v10015535mg [Capsella rubella]	545	545	0	100.0	98.0	99.8	hypothetical protein CARUB_v10015535mg	gbpln	Capsella rubella	AT3G20050.1 | Symbols: ATTCP-1, TCP-1 | T-complex protein 1 alpha subunit | chr3:6998544-7002266 REVERSE LENGTH=545	545	545	0	100.0	97.6	99.6
Rsa1.0_00871.1.g20648.t1	ref|XP_002883225.1| hexokinase [Arabidopsis lyrata subsp. lyrata] gi|297329065|gb|EFH59484.1| hexokinase [Arabidopsis lyrata subsp. lyrata]	505	502	0	99.4	86.5	93.5	hexokinase	gbpln	Arabidopsis lyrata	AT3G20040.1 | Symbols: ATHXK4, HKL2 | Hexokinase | chr3:6995317-6998064 FORWARD LENGTH=502	505	502	0	99.4	87.3	94.1
Rsa1.0_00871.1.g20649.t1	ref|XP_002885352.1| arginine N-methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331192|gb|EFH61611.1| arginine N-methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	428	435	0	101.6	92.5	94.9	arginine N-methyltransferase family protein	gbpln	Arabidopsis lyrata	AT3G20020.1 | Symbols: ATPRMT6, PRMT6 | protein arginine methyltransferase 6 | chr3:6984055-6987945 REVERSE LENGTH=435	428	435	0	101.6	91.1	94.4
Rsa1.0_00871.1.g20650.t1	ref|NP_188636.2| aspartyl protease family protein [Arabidopsis thaliana] gi|75273243|sp|Q9LHE3.1|ASPG2_ARATH RecName: Full=Protein ASPARTIC PROTEASE IN GUARD CELL 2; Short=AtASPG2; Flags: Precursor gi|11994777|dbj|BAB03167.1| nucleoid chloroplast DNA-binding protein-like [Arabidopsis thaliana] gi|28392860|gb|AAO41867.1| unknown protein [Arabidopsis thaliana] gi|332642798|gb|AEE76319.1| protein aspartic protease in guard cell 2 [Arabidopsis thaliana]	466	470	0	100.9	89.1	91.8	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT3G20015.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:6978746-6980158 REVERSE LENGTH=470	466	470	0	100.9	89.1	91.8
Rsa1.0_00871.1.g20651.t1	ref|XP_002883222.1| SNF2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329062|gb|EFH59481.1| SNF2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1118	1046	0	93.6	67.1	75.2	SNF2 domain-containing protein	gbpln	Arabidopsis lyrata	AT3G20010.1 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related | chr3:6971352-6976340 FORWARD LENGTH=1047	1118	1047	0	93.6	66.4	74.4
Rsa1.0_00871.1.g20652.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00872.1.g20653.t1	gb|EOA19038.1| hypothetical protein CARUB_v10007695mg [Capsella rubella]	399	403	0	101.0	84.5	90.5	hypothetical protein CARUB_v10007695mg	gbpln	Capsella rubella	AT1G65570.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:24374098-24375846 REVERSE LENGTH=397	399	397	1.00E-147	99.5	62.2	75.9

Rsa1.0_00872.1.g20654.t2	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1294	1499	0	115.8	62.9	78.5	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1294	158	2.00E-23	12.2	3.9	5.2
Rsa1.0_00872.1.g20655.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00872.1.g20656.t1	ref|NP_568543.1| protease Do-like 10 [Arabidopsis thaliana] gi|75262529|sp|Q9FIV6.1|DGP10_ARATH RecName: Full=Protease Do-like 10, mitochondrial; Flags: Precursor gi|10178214|dbj|BAB11638.1| serine protease-like protein [Arabidopsis thaliana] gi|17978951|gb|AAL47441.1| AT5g36950/MLF18_70 [Arabidopsis thaliana] gi|50897262|gb|AAT85770.1| At5g36950 [Arabidopsis thaliana] gi|332006748|gb|AED94131.1| protease Do-like 10 [Arabidopsis thaliana]	586	586	0	100.0	81.4	88.7	protease Do-like 10	gbpln	Arabidopsis thaliana	AT5G36950.1 | Symbols: DegP10 | DegP protease 10 | chr5:14594992-14598216 FORWARD LENGTH=586	586	586	0	100.0	81.4	88.7
Rsa1.0_00872.1.g20657.t1	ref|NP_198512.1| uncharacterized protein [Arabidopsis thaliana] gi|10178215|dbj|BAB11639.1| unnamed protein product [Arabidopsis thaliana] gi|91806934|gb|ABE66194.1| unknown [Arabidopsis thaliana] gi|332006749|gb|AED94132.1| uncharacterized protein AT5G36960 [Arabidopsis thaliana]	136	137	1.00E-52	100.7	78.7	86.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G36960.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:14598745-14599729 FORWARD LENGTH=137	136	137	3.00E-55	100.7	78.7	86.8
Rsa1.0_00872.1.g20658.t1	ref|NP_198513.1| NDR1/HIN1-like 25 [Arabidopsis thaliana] gi|332006750|gb|AED94133.1| NDR1/HIN1-like 25 [Arabidopsis thaliana]	323	248	1.00E-102	76.8	62.8	66.9	NDR1/HIN1-like 25	gbpln	Arabidopsis thaliana	AT5G36970.1 | Symbols: NHL25 | NDR1/HIN1-like 25 | chr5:14604367-14605194 REVERSE LENGTH=248	323	248	1.00E-105	76.8	62.8	66.9
Rsa1.0_00872.1.g20659.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00872.1.g20660.t1	gb|AAC63678.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	110	1216	9.00E-23	1105.5	45.5	60.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00872.1.g20661.t1	dbj|BAB08970.1| unnamed protein product [Arabidopsis thaliana]	540	559	0	103.5	78.0	86.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G37000.1 | Symbols: | Exostosin family protein | chr5:14618107-14620282 FORWARD LENGTH=547	540	547	0	101.3	74.8	82.4
Rsa1.0_00872.1.g20662.t1	ref|NP_176815.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana] gi|12322267|gb|AAG51162.1|AC074025_12 hypothetical protein [Arabidopsis thaliana] gi|12324403|gb|AAG52170.1|AC020665_15 hypothetical protein; 78831-79679 [Arabidopsis thaliana] gi|225898052|dbj|BAH30358.1| hypothetical protein [Arabidopsis thaliana] gi|332196386|gb|AEE34507.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana]	219	282	1.00E-22	128.8	34.2	45.2	DNA-binding storekeeper protein-related transcriptional regulator	gbpln	Arabidopsis thaliana	AT1G66420.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:24777184-24778032 FORWARD LENGTH=282	219	282	4.00E-25	128.8	34.2	45.2
Rsa1.0_00872.1.g20663.t2	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1330	1475	0	110.9	56.4	72.3	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1330	1262	1.00E-174	94.9	22.3	28.6
Rsa1.0_00872.1.g20664.t1	dbj|BAJ33985.1| unnamed protein product [Thellungiella halophila]	475	478	0	100.6	84.0	89.3	unnamed protein product	----	----	AT2G38400.1 | Symbols: AGT3 | alanine:glyoxylate aminotransferase 3 | chr2:16083779-16085974 FORWARD LENGTH=477	475	477	0	100.4	82.3	88.2
Rsa1.0_00872.1.g20665.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00873.1.g20666.t1	gb|AFZ41789.1| putative progesterone 5-beta-reductase [Raphanus sativus]	103	390	2.00E-31	378.6	62.1	65.0	putative progesterone 5-beta-reductase	gbpln	Raphanus sativus	AT4G24220.2 | Symbols: VEP1, AWI31 | NAD(P)-binding Rossmann-fold superfamily protein | chr4:12565219-12566474 FORWARD LENGTH=387	103	387	1.00E-33	375.7	60.2	65.0
Rsa1.0_00873.1.g20667.t3	ref|XP_002864331.1| hypothetical protein ARALYDRAFT_495522 [Arabidopsis lyrata subsp. lyrata] gi|297310166|gb|EFH40590.1| hypothetical protein ARALYDRAFT_495522 [Arabidopsis lyrata subsp. lyrata]	145	369	1.00E-38	254.5	51.7	59.3	hypothetical protein ARALYDRAFT_495522	gbpln	Arabidopsis lyrata	AT5G54320.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22062805-22063914 FORWARD LENGTH=369	145	369	2.00E-40	254.5	51.0	58.6

<table>
<tr><td>Rsa1.0_00873.1.g20668.t1</td><td>gb|EOA39198.1| hypothetical protein CARUB_v10012166mg [Capsella rubella]</td><td>240</td><td>250</td><td>2.00E-76</td><td>104.2</td><td>70.0</td><td>78.3</td><td>hypothetical protein CARUB_v10012166mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30800.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr1:10936995-10937714 FORWARD LENGTH=239</td><td>240</td><td>239</td><td>2.00E-76</td><td>99.6</td><td>75.0</td><td>82.1</td></tr>
<tr><td>Rsa1.0_00873.1.g20669.t1</td><td>ref|NP_174367.6| transcription factor jumonji and C5HC2 type zinc finger domain-containing protein [Arabidopsis thaliana] gi|334182965|ref|NP_001185118.1| transcription factor jumonji and C5HC2 type zinc finger domain-containing protein [Arabidopsis thaliana] gi|332193153|gb|AEE31274.1| transcription factor jumonji and C5HC2 type zinc finger domain-containing protein [Arabidopsis thaliana] gi|332193154|gb|AEE31275.1| transcription factor jumonji and C5HC2 type zinc finger domain-containing protein [Arabidopsis thaliana]</td><td>784</td><td>819</td><td>0</td><td>104.5</td><td>86.0</td><td>92.6</td><td>transcription factor jumonji and C5HC2 type zinc finger domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30810.2 | Symbols: | Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein | chr1:10938139-10941505 REVERSE LENGTH=819</td><td>784</td><td>819</td><td>0</td><td>104.5</td><td>86.0</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00873.1.g20670.t1</td><td>ref|NP_174370.1| protein root hair specific 4 [Arabidopsis thaliana] gi|4926832|gb|AAD32942.1|AC004135_17 T17H7.17 [Arabidopsis thaliana] gi|55740513|gb|AAV63849.1| hypothetical protein At1g30850 [Arabidopsis thaliana] gi|332193164|gb|AEE31285.1| protein root hair specific 4 [Arabidopsis thaliana]</td><td>250</td><td>300</td><td>2.00E-73</td><td>120.0</td><td>64.0</td><td>76.0</td><td>protein root hair specific 4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30850.1 | Symbols: RSH4 | root hair specific 4 | chr1:10985116-10986018 FORWARD LENGTH=300</td><td>250</td><td>300</td><td>5.00E-76</td><td>120.0</td><td>64.0</td><td>76.0</td></tr>
<tr><td>Rsa1.0_00873.1.g20671.t1</td><td>ref|XP_002893652.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297339494|gb|EFH69911.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>708</td><td>725</td><td>0</td><td>102.4</td><td>68.4</td><td>78.2</td><td>protein binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30860.1 | Symbols: | RING/U-box superfamily protein | chr1:10986696-10989246 REVERSE LENGTH=730</td><td>708</td><td>730</td><td>0</td><td>103.1</td><td>66.8</td><td>76.6</td></tr>
<tr><td>Rsa1.0_00873.1.g20672.t1</td><td>gb|EOA36410.1| hypothetical protein CARUB_v10010885mg [Capsella rubella]</td><td>343</td><td>352</td><td>1.00E-164</td><td>102.6</td><td>82.8</td><td>88.0</td><td>hypothetical protein CARUB_v10010885mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30870.1 | Symbols: | Peroxidase superfamily protein | chr1:10991535-10992885 FORWARD LENGTH=349</td><td>343</td><td>349</td><td>1.00E-160</td><td>101.7</td><td>82.8</td><td>90.7</td></tr>
<tr><td>Rsa1.0_00873.1.g20673.t1</td><td>gb|EOA36340.1| hypothetical protein CARUB_v10010686mg [Capsella rubella]</td><td>122</td><td>118</td><td>3.00E-41</td><td>96.7</td><td>82.8</td><td>85.2</td><td>hypothetical protein CARUB_v10010686mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30880.1 | Symbols: | unknown protein; Has 24 Blast hits to 24 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10993379-10994056 REVERSE LENGTH=120</td><td>122</td><td>120</td><td>2.00E-31</td><td>98.4</td><td>85.2</td><td>87.7</td></tr>
<tr><td>Rsa1.0_00873.1.g20674.t1</td><td>ref|NP_564367.1| integral membrane HRF1-like protein [Arabidopsis thaliana] gi|145324088|ref|NP_001077633.1| integral membrane HRF1-like protein [Arabidopsis thaliana] gi|14532658|gb|AAK64057.1| unknown protein [Arabidopsis thaliana] gi|21280943|gb|AAM44952.1| unknown protein [Arabidopsis thaliana] gi|21554340|gb|AAM63447.1| unknown [Arabidopsis thaliana] gi|332193168|gb|AEE31289.1| integral membrane HRF1-like protein [Arabidopsis thaliana] gi|332193169|gb|AEE31290.1| integral membrane HRF1-like protein [Arabidopsis thaliana]</td><td>271</td><td>269</td><td>2.33E-156</td><td>99.3</td><td>94.1</td><td>96.7</td><td>integral membrane HRF1-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30890.2 | Symbols: | Integral membrane HRF1 family protein | chr1:10994890-10995999 FORWARD LENGTH=269</td><td>271</td><td>269</td><td>1.00E-149</td><td>99.3</td><td>94.1</td><td>96.7</td></tr>
<tr><td>Rsa1.0_00873.1.g20675.t1</td><td>ref|NP_174578.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana] gi|378405165|sp|Q9MAP1.2|FB33_ARATH RecName: Full=Putative F-box protein At1g33020 gi|332193429|gb|AEE31550.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana]</td><td>367</td><td>548</td><td>6.00E-80</td><td>149.3</td><td>50.7</td><td>64.0</td><td>F-box and associated interaction domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G33020.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11962746-11964832 FORWARD LENGTH=548</td><td>367</td><td>548</td><td>2.00E-82</td><td>149.3</td><td>50.7</td><td>64.0</td></tr>
<tr><td>Rsa1.0_00873.1.g20676.t2</td><td>gb|EOA39891.1| hypothetical protein CARUB_v10008569mg [Capsella rubella]</td><td>180</td><td>631</td><td>7.00E-32</td><td>350.6</td><td>48.3</td><td>52.8</td><td>hypothetical protein CARUB_v10008569mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30900.1 | Symbols: VSR6, VSR3;3, BP80-3;3 | VACUOLAR SORTING RECEPTOR 6 | chr1:10997275-11000543 FORWARD LENGTH=631</td><td>180</td><td>631</td><td>3.00E-33</td><td>350.6</td><td>46.7</td><td>52.2</td></tr>
<tr><td>Rsa1.0_00873.1.g20677.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_00874.1.g20678.t1	dbj|BAJ34022.1| unnamed protein product [Thellungiella halophila]	352	395	1.00E-154	112.2	85.8	90.9	unnamed protein product	----	----	AT2G30020.1 | Symbols: | Protein phosphatase 2C family protein | chr2:12814437-12815904 FORWARD LENGTH=396	352	396	1.00E-151	112.5	82.7	89.2
Rsa1.0_00874.1.g20679.t1	ref|NP_180565.1| mitogen-activated protein kinase kinase kinase 14 [Arabidopsis thaliana] gi|3420047|gb|AAC31848.1| putative protein kinase [Arabidopsis thaliana] gi|24030256|gb|AAN41303.1| putative protein kinase [Arabidopsis thaliana] gi|330253244|gb|AEC08338.1| mitogen-activated protein kinase kinase kinase 14 [Arabidopsis thaliana]	434	463	1.00E-150	106.7	65.4	73.7	mitogen-activated protein kinase kinase kinase 14	gbpln	Arabidopsis thaliana	AT2G30040.1 | Symbols: MAPKKK14 | mitogen-activated protein kinase kinase kinase 14 | chr2:12821747-12823138 FORWARD LENGTH=463	434	463	1.00E-153	106.7	65.4	73.7
Rsa1.0_00874.1.g20680.t1	ref|XP_002879246.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297325085|gb|EFH55505.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	302	302	1.00E-161	100.0	91.7	96.0	transducin family protein	gbpln	Arabidopsis lyrata	AT2G30050.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr2:12825540-12826448 FORWARD LENGTH=302	302	302	1.00E-163	100.0	90.7	96.4
Rsa1.0_00874.1.g20681.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1391	1307	0	94.0	58.6	73.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1391	1262	1.00E-97	90.7	13.7	21.4
Rsa1.0_00874.1.g20682.t1	gb|AAC49844.1| putative potassium transporter AtKT1p [Arabidopsis thaliana]	732	712	0	97.3	89.1	93.3	putative potassium transporter AtKT1p	gbpln	Arabidopsis thaliana	AT2G30070.1 | Symbols: ATKT1, ATKT1P, ATKUP1, KUP1, KT1 | potassium transporter 1 | chr2:12835097-12838466 FORWARD LENGTH=712	732	712	0	97.3	89.6	93.9
Rsa1.0_00874.1.g20683.t1	ref|NP_180569.1| zinc transporter 6 [Arabidopsis thaliana] gi|37090161|sp|O64738.1|ZIP6_ARATH RecName: Full=Zinc transporter 6, chloroplastic; AltName: Full=ZRT/IRT-like protein 6; Flags: Precursor gi|17385786|gb|AAL38433.1|AF369910_1 putative metal transporter ZIP6 [Arabidopsis thaliana] gi|3150412|gb|AAC16964.1| putative Fe(II) transport protein [Arabidopsis thaliana] gi|20197229|gb|AAM14983.1| putative Fe(II) transport protein [Arabidopsis thaliana] gi|330253248|gb|AEC08342.1| zinc transporter 6 [Arabidopsis thaliana]	340	341	1.00E-173	100.3	92.4	96.5	zinc transporter 6	gbpln	Arabidopsis thaliana	AT2G30080.1 | Symbols: ZIP6, ATZIP6 | ZIP metal ion transporter family | chr2:12838730-12840112 REVERSE LENGTH=341	340	341	1.00E-176	100.3	92.4	96.5
Rsa1.0_00874.1.g20684.t1	gb|EOA29295.1| hypothetical protein CARUB_v10025573mg [Capsella rubella]	390	392	1.00E-164	100.5	73.8	84.6	hypothetical protein CARUB_v10025573mg	gbpln	Capsella rubella	AT2G30090.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr2:12843583-12845597 REVERSE LENGTH=386	390	386	1.00E-163	99.0	75.6	84.4
Rsa1.0_00874.1.g20685.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	274	368	3.00E-52	134.3	43.8	56.6	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	274	370	2.00E-52	135.0	42.3	56.6
Rsa1.0_00874.1.g20686.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	346	368	5.00E-74	106.4	49.1	61.3	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	346	370	3.00E-65	106.9	43.6	61.3
Rsa1.0_00874.1.g20687.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	366	368	4.00E-75	100.5	45.9	62.0	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	366	370	1.00E-66	101.1	41.8	58.7
Rsa1.0_00874.1.g20688.t1	ref|NP_180585.1| U2 small nuclear ribonucleoprotein B'' [Arabidopsis thaliana] gi|75318049|sp|O22922.1|RU2B1_ARATH RecName: Full=U2 small nuclear ribonucleoprotein B''; Short=U2 snRNP B'' gi|2347192|gb|AAC16931.1| putative small nuclear ribonucleoprotein U2B [Arabidopsis thaliana] gi|27765024|gb|AAO23633.1| At2g30260 [Arabidopsis thaliana] gi|110743428|dbj|BAE99600.1| putative small nuclear ribonucleoprotein U2B [Arabidopsis thaliana] gi|330253269|gb|AEC08363.1| U2 small nuclear ribonucleoprotein B'' [Arabidopsis thaliana]	115	232	3.00E-53	201.7	86.1	92.2	U2 small nuclear ribonucleoprotein B''	gbpln	Arabidopsis thaliana	AT2G30260.1 | Symbols: U2B'' | U2 small nuclear ribonucleoprotein B | chr2:12905557-12907434 REVERSE LENGTH=232	115	232	4.00E-56	201.7	86.1	92.2

Rsa1.0_00875.1.g20689.t1	gb|EOA20700.1| hypothetical protein CARUB_v10001014mg [Capsella rubella]	283	429	4.00E-70	151.6	49.5	54.1	hypothetical protein CARUB_v10001014mg	gbpln	Capsella rubella	AT4G02720.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF926 (InterPro:IPR009269); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:1204545-1205813 REVERSE LENGTH=422	283	422	8.00E-67	149.1	45.2	49.1
Rsa1.0_00875.1.g20690.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00875.1.g20691.t1	dbj|BAA19578.2| water-soluble chlorophyll protein precursor [Lepidium virginicum]	222	223	2.00E-67	100.5	59.9	74.8	water-soluble chlorophyll protein precursor	gbpln	Lepidium virginicum	AT1G72290.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27215852-27216499 FORWARD LENGTH=215	222	215	4.00E-34	96.8	44.1	59.5
Rsa1.0_00875.1.g20692.t1	ref|NP_176586.1| serpin-Z1 [Arabidopsis thaliana] gi|189029934|sp|Q9SH52.2|SPZ1_ARATH RecName: Full=Serpin-Z1; AltName: Full=ArathZ1 gi|332196061|gb|AEE34182.1| serpin-Z1 [Arabidopsis thaliana]	396	385	1.00E-127	97.2	60.4	74.2	serpin-Z1	gbpln	Arabidopsis thaliana	AT1G64030.1 | Symbols: ATSRP3, SRP3 | serpin 3 | chr1:23752873-23754348 REVERSE LENGTH=385	396	385	1.00E-129	97.2	60.4	74.2
Rsa1.0_00875.1.g20693.t1	ref|NP_174170.1| glutaredoxin-C9 [Arabidopsis thaliana] gi|75204928|sp|Q9SGP6.1|GRXC9_ARATH RecName: Full=Glutaredoxin-C9; Short=AtGrxC9; AltName: Full=Protein ROXY 19 gi|6560751|gb|AAF16751.1|AC010155_4 F3M18.8 [Arabidopsis thaliana] gi|11762208|gb|AAG40382.1|AF325030_1 At1g28480 [Arabidopsis thaliana] gi|110738613|dbj|BAF01232.1| hypothetical protein [Arabidopsis thaliana] gi|117168135|gb|ABK32150.1| At1g28480 [Arabidopsis thaliana] gi|226348214|gb|ACO50423.1| glutaredoxin [Arabidopsis thaliana] gi|332192860|gb|AEE30981.1| glutaredoxin-C9 [Arabidopsis thaliana]	125	137	2.00E-47	109.6	79.2	86.4	glutaredoxin-C9	gbpln	Arabidopsis thaliana	AT1G28480.1 | Symbols: GRX480, roxy19 | Thioredoxin superfamily protein | chr1:10013634-10014047 REVERSE LENGTH=137	125	137	4.00E-50	109.6	79.2	86.4
Rsa1.0_00875.1.g20694.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00875.1.g20695.t1	ref|NP_564310.1| syntaxin-61 [Arabidopsis thaliana] gi|297845794|ref|XP_002890778.1| hypothetical protein ARALYDRAFT_473066 [Arabidopsis lyrata subsp. lyrata] gi|28380156|sp|Q946Y7.1|SYP61_ARATH RecName: Full=Syntaxin-61; Short=AtSYP61; AltName: Full=Osmotic stress-sensitive mutant 1 gi|16041650|gb|AAK40222.2|AF355754_1 syntaxin of plants 61 [Arabidopsis thaliana] gi|23297416|gb|AAN12965.1| unknown protein [Arabidopsis thaliana] gi|297336620|gb|EFH67037.1| hypothetical protein ARALYDRAFT_473066 [Arabidopsis lyrata subsp. lyrata] gi|332192861|gb|AEE30982.1| syntaxin-61 [Arabidopsis thaliana]	287	245	1.00E-127	85.4	77.4	81.2	syntaxin-61	gbpln	Arabidopsis lyrata	AT1G28490.1 | Symbols: SYP61, ATSYP61, OSM1 | syntaxin of plants 61 | chr1:10016433-10017842 FORWARD LENGTH=245	287	245	1.00E-129	85.4	77.4	81.2
Rsa1.0_00875.1.g20696.t1	gb|AAG10812.1|AC018460_6 Putative retroelement polyprotein [Arabidopsis thaliana]	334	1404	1.00E-34	420.4	25.4	31.1	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT5G61220.1 | Symbols: | LYR family of Fe/S cluster biogenesis protein | chr5:24626057-24626320 REVERSE LENGTH=87	334	87	5.00E-11	26.0	9.6	10.8
Rsa1.0_00875.1.g20697.t1	ref|XP_002871867.1| hypothetical protein ARALYDRAFT_326316 [Arabidopsis lyrata subsp. lyrata] gi|297317704|gb|EFH48126.1| hypothetical protein ARALYDRAFT_326316 [Arabidopsis lyrata subsp. lyrata]	90	390	4.00E-18	433.3	47.8	67.8	hypothetical protein ARALYDRAFT_326316	gbpln	Arabidopsis lyrata	AT5G19170.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:6445245-6447305 FORWARD LENGTH=391	90	391	5.00E-19	434.4	48.9	68.9
Rsa1.0_00875.1.g20698.t1	gb|EOA36887.1| hypothetical protein CARUB_v10008982mg [Capsella rubella]	477	486	0	101.9	90.1	92.5	hypothetical protein CARUB_v10008982mg	gbpln	Capsella rubella	AT1G28520.2 | Symbols: VOZ1 | vascular plant one zinc finger protein | chr1:10029713-10031479 FORWARD LENGTH=486	477	486	0	101.9	90.1	92.5

Rsa1.0_00875.1.g20699.t1	ref|NP_174177.1| RAB GTPase-like protein A1I [Arabidopsis thaliana] gi|75336857|sp|Q9S810.1|RAA1I_ARATH RecName: Full=Ras-related protein RABA1i; Short=AtRABA1i gi|6560749|gb|AAF16749.1|AC010155_2 F3M18.2 [Arabidopsis thaliana] gi|67633398|gb|AAY78624.1| putative Ras-related GTP-binding protein [Arabidopsis thaliana] gi|332192870|gb|AEE30991.1| ras-related protein RABA1i [Arabidopsis thaliana]	218	218	1.00E-122	100.0	97.2	99.5	RAB GTPase-like protein A1I	gbpln	Arabidopsis thaliana	AT1G28550.1 | Symbols: AtRABA1i, RABA1i | RAB GTPase homolog A1I | chr1:10036966-10037698 REVERSE LENGTH=218	218	218	1.00E-124	100.0	97.2	99.5
Rsa1.0_00875.1.g20700.t1	ref|NP_174180.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75173088|sp|Q9FXJ2.1|GDL7_ARATH RecName: Full=GDSL esterase/lipase At1g28580; AltName: Full=Extracellular lipase At1g28580; Flags: Precursor gi|10764859|gb|AAG22836.1|AC007508_13 F1K23.18 [Arabidopsis thaliana] gi|13605565|gb|AAK32776.1|AF361608_1 At1g28580/F1K23_7 [Arabidopsis thaliana] gi|15027915|gb|AAK76488.1| putative lipase [Arabidopsis thaliana] gi|18491141|gb|AAL69539.1| At1g28580/F1K23_7 [Arabidopsis thaliana] gi|19310791|gb|AAL85126.1| putative lipase [Arabidopsis thaliana] gi|332192875|gb|AEE30996.1| GDSL esterase/lipase [Arabidopsis thaliana]	463	390	1.00E-157	84.2	56.4	67.4	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT1G28580.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:10044603-10046379 REVERSE LENGTH=390	463	390	1.00E-159	84.2	56.4	67.4
Rsa1.0_00875.1.g20701.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	429	411	1.00E-119	95.8	55.9	71.1	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT2G38590.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:16142897-16144171 FORWARD LENGTH=424	429	424	1.00E-114	98.8	54.8	68.1
Rsa1.0_00875.1.g20702.t1	gb|EOA32347.1| hypothetical protein CARUB_v10015614mg [Capsella rubella]	57	97	1.00E-21	170.2	94.7	96.5	hypothetical protein CARUB_v10015614mg	gbpln	Capsella rubella	AT5G18790.1 | Symbols: | Ribosomal protein L33 family protein | chr5:6266324-6266500 REVERSE LENGTH=58	57	58	3.00E-24	101.8	94.7	96.5
Rsa1.0_00875.1.g20703.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00875.1.g20704.t1	ref|XP_002884509.1| hypothetical protein ARALYDRAFT_477824 [Arabidopsis lyrata subsp. lyrata] gi|297330349|gb|EFH60768.1| hypothetical protein ARALYDRAFT_477824 [Arabidopsis lyrata subsp. lyrata]	714	786	0	110.1	60.5	72.1	hypothetical protein ARALYDRAFT_477824	gbpln	Arabidopsis lyrata	AT3G05360.1 | Symbols: AtRLP30, RLP30 | receptor like protein 30 | chr3:1530900-1533260 REVERSE LENGTH=786	714	786	0	110.1	59.8	71.8
Rsa1.0_00875.1.g20705.t1	ref|NP_174180.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75173088|sp|Q9FXJ2.1|GDL7_ARATH RecName: Full=GDSL esterase/lipase At1g28580; AltName: Full=Extracellular lipase At1g28580; Flags: Precursor gi|10764859|gb|AAG22836.1|AC007508_13 F1K23.18 [Arabidopsis thaliana] gi|13605565|gb|AAK32776.1|AF361608_1 At1g28580/F1K23_7 [Arabidopsis thaliana] gi|15027915|gb|AAK76488.1| putative lipase [Arabidopsis thaliana] gi|18491141|gb|AAL69539.1| At1g28580/F1K23_7 [Arabidopsis thaliana] gi|19310791|gb|AAL85126.1| putative lipase [Arabidopsis thaliana] gi|332192875|gb|AEE30996.1| GDSL esterase/lipase [Arabidopsis thaliana]	397	390	0	98.2	79.3	86.9	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT1G28580.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:10044603-10046379 REVERSE LENGTH=390	397	390	0	98.2	79.3	86.9
Rsa1.0_00876.1.g20706.t1	ref|NP_173411.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|10086504|gb|AAG12564.1|AC007797_24 Similar to auxin-induced proteins [Arabidopsis thaliana] gi|26450872|dbj|BAC42543.1| unknown protein [Arabidopsis thaliana] gi|28416847|gb|AAO42954.1| At1g19830 [Arabidopsis thaliana] gi|332191781|gb|AEE29902.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	114	117	9.00E-51	102.6	84.2	90.4	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT1G19830.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:6852230-6852583 FORWARD LENGTH=117	114	117	1.00E-53	102.6	84.2	90.4

<table>
<tr><td>Rsa1.0_00876.1.g20707.t1</td><td>dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]</td><td>696</td><td>1072</td><td>0</td><td>154.0</td><td>49.7</td><td>68.1</td><td>non-LTR retroelement reverse transcriptase-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>696</td><td>746</td><td>5.00E-55</td><td>107.2</td><td>20.0</td><td>27.4</td></tr>
<tr><td>Rsa1.0_00876.1.g20708.t1</td><td>ref|NP_173410.1| trigalactosyldiacylglycerol 1 [Arabidopsis thaliana] gi|42571555|ref|NP_973868.1| trigalactosyldiacylglycerol 1 [Arabidopsis thaliana] gi|42571557|ref|NP_973869.1| trigalactosyldiacylglycerol 1 [Arabidopsis thaliana] gi|75153743|sp|Q8L4R0.1|TGD1_ARATH RecName: Full=Protein TRIGALACTOSYLDIACYLGLYCEROL 1, chloroplastic; AltName: Full=ABC transporter I family member 14; Short=ABC transporter ABCI.14; Short=AtABCI14; Flags: Precursor gi|20465620|gb|AAM20141.1| unknown protein [Arabidopsis thaliana] gi|21281062|gb|AAM45069.1| unknown protein [Arabidopsis thaliana] gi|45680900|gb|AAS75319.1| permease-like protein [Arabidopsis thaliana] gi|222424205|dbj|BAH20061.1| AT1G19800 [Arabidopsis thaliana] gi|332191778|gb|AEE29899.1| trigalactosyldiacylglycerol 1 [Arabidopsis thaliana] gi|332191779|gb|AEE29900.1| trigalactosyldiacylglycerol 1 [Arabidopsis thaliana] gi|332191780|gb|AEE29901.1| trigalactosyldiacylglycerol 1 [Arabidopsis thaliana]</td><td>417</td><td>350</td><td>1.00E-177</td><td>83.9</td><td>75.3</td><td>76.5</td><td>trigalactosyldiacylglycerol 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G19800.1 | Symbols: TGD1 | trigalactosyldiacylglycerol 1 | chr1:6846812-6847954 FORWARD LENGTH=350</td><td>417</td><td>350</td><td>1.00E-179</td><td>83.9</td><td>75.3</td><td>76.5</td></tr>
<tr><td>Rsa1.0_00876.1.g20709.t1</td><td>gb|ADA60977.1| short internode related sequence 7 [Brassica rapa subsp. pekinensis]</td><td>347</td><td>346</td><td>1.00E-164</td><td>99.7</td><td>93.7</td><td>96.0</td><td>short internode related sequence 7</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G19790.2 | Symbols: SRS7 | SHI-related sequence 7 | chr1:6838400-6839831 REVERSE LENGTH=345</td><td>347</td><td>345</td><td>1.00E-142</td><td>99.4</td><td>78.4</td><td>83.6</td></tr>
<tr><td>Rsa1.0_00876.1.g20710.t1</td><td>ref|XP_002510468.1| Transcription initiation factor IIF subunit beta, putative [Ricinus communis] gi|223551169|gb|EEF52655.1| Transcription initiation factor IIF subunit beta, putative [Ricinus communis]</td><td>272</td><td>257</td><td>8.00E-52</td><td>94.5</td><td>43.0</td><td>55.5</td><td>Transcription initiation factor IIF subunit beta, putative</td><td>gbpln</td><td>Ricinus communis</td><td>AT1G75510.1 | Symbols: | Transcription initiation factor IIF, beta subunit | chr1:28347254-28348629 REVERSE LENGTH=261</td><td>272</td><td>261</td><td>2.00E-50</td><td>96.0</td><td>43.0</td><td>55.9</td></tr>
<tr><td>Rsa1.0_00876.1.g20711.t1</td><td>gb|EOA38008.1| hypothetical protein CARUB_v10009477mg [Capsella rubella]</td><td>374</td><td>373</td><td>1.00E-134</td><td>99.7</td><td>69.8</td><td>79.7</td><td>hypothetical protein CARUB_v10009477mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G19770.1 | Symbols: ATPUP14, PUP14 | purine permease 14 | chr1:6832426-6833702 FORWARD LENGTH=393</td><td>374</td><td>393</td><td>1.00E-124</td><td>105.1</td><td>66.6</td><td>77.5</td></tr>
<tr><td>Rsa1.0_00876.1.g20712.t1</td><td>ref|NP_173404.1| ATP-dependent protease La domain-containing protein [Arabidopsis thaliana] gi|10086494|gb|AAG12554.1|AC007797_14 Unknown Protein [Arabidopsis thaliana] gi|22136024|gb|AAM91594.1| unknown protein [Arabidopsis thaliana] gi|23197842|gb|AAN15448.1| unknown protein [Arabidopsis thaliana] gi|332191772|gb|AEE29893.1| ATP-dependent protease La domain-containing protein [Arabidopsis thaliana]</td><td>290</td><td>278</td><td>1.00E-114</td><td>95.9</td><td>83.4</td><td>88.6</td><td>ATP-dependent protease La domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G19740.1 | Symbols: | ATP-dependent protease La (LON) domain protein | chr1:6824396-6825232 FORWARD LENGTH=278</td><td>290</td><td>278</td><td>1.00E-117</td><td>95.9</td><td>83.4</td><td>88.6</td></tr>
<tr><td>Rsa1.0_00876.1.g20713.t1</td><td>sp|Q39362.1|TRXH2_BRANA RecName: Full=Thioredoxin H-type 2; Short=Trx-H-2 gi|1403711|gb|AAB53695.1| thioredoxin-h-like-2 [Brassica napus]</td><td>119</td><td>119</td><td>8.00E-59</td><td>100.0</td><td>93.3</td><td>97.5</td><td>RecName: Full=Thioredoxin H-type 2; Short=Trx-H-2 gi|1403711|gb|AAB53695.1| thioredoxin-h-like-2</td><td>gbpln</td><td>Brassica napus</td><td>AT1G19730.1 | Symbols: ATTRX4, ATH4 | Thioredoxin superfamily protein | chr1:6823163-6824020 REVERSE LENGTH=119</td><td>119</td><td>119</td><td>3.00E-57</td><td>100.0</td><td>86.6</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00876.1.g20714.t1</td><td>gb|EOA38972.1| hypothetical protein CARUB_v10011399mg [Capsella rubella]</td><td>478</td><td>482</td><td>0</td><td>100.8</td><td>88.3</td><td>93.3</td><td>hypothetical protein CARUB_v10011399mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G19710.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:6814920-6816716 FORWARD LENGTH=479</td><td>478</td><td>479</td><td>0</td><td>100.2</td><td>87.7</td><td>93.1</td></tr>
<tr><td>Rsa1.0_00876.1.g20715.t1</td><td>gb|EOA40106.1| hypothetical protein CARUB_v10008805mg [Capsella rubella]</td><td>813</td><td>536</td><td>1.00E-170</td><td>65.9</td><td>43.7</td><td>48.1</td><td>hypothetical protein CARUB_v10008805mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G19700.3 | Symbols: BEL10 | BEL1-like homeodomain 10 | chr1:6809958-6811854 REVERSE LENGTH=538</td><td>813</td><td>538</td><td>1.00E-167</td><td>66.2</td><td>43.9</td><td>48.3</td></tr>
<tr><td>Rsa1.0_00876.1.g20716.t1</td><td>gb|AAN51933.1|AF337544_1 chlorophyllase 1 [Brassica oleracea]</td><td>324</td><td>324</td><td>1.00E-176</td><td>100.0</td><td>92.6</td><td>96.0</td><td>chlorophyllase 1</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G19670.1 | Symbols: ATCLH1, CORI1, ATHCOR1, CLH1 | chlorophyllase 1 | chr1:6803796-6804923 REVERSE LENGTH=324</td><td>324</td><td>324</td><td>1.00E-158</td><td>100.0</td><td>82.7</td><td>88.6</td></tr>
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Rsa1.0_00876.1.g20718.t1	ref|XP_002893058.1| hypothetical protein ARALYDRAFT_472189 [Arabidopsis lyrata subsp. lyrata] gi|297338900|gb|EFH69317.1| hypothetical protein ARALYDRAFT_472189 [Arabidopsis lyrata subsp. lyrata]	623	613	0	98.4	81.4	89.7	hypothetical protein ARALYDRAFT_472189	gbpln	Arabidopsis lyrata	AT1G19650.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:6796431-6799537 REVERSE LENGTH=608	623	608	0	97.6	80.7	87.6
Rsa1.0_00877.1.g20719.t1	ref|NP_851207.1| MIF4G domain and MA3 domain-containing protein [Arabidopsis thaliana] gi|75163823|sp|Q93ZT6.1|IF4G1_ARATH RecName: Full=Eukaryotic translation initiation factor isoform 4G-1; Short=eIF(iso)4G-1 gi|15810455|gb|AAL07115.1| putative eukaryotic initiation factor eIF4 [Arabidopsis thaliana] gi|20258963|gb|AAM14197.1| putative eukaryotic initiation factor 4 [Arabidopsis thaliana] gi|332009581|gb|AED96964.1| MIF4G domain and MA3 domain-containing protein [Arabidopsis thaliana]	775	780	0	100.6	87.9	94.1	MIF4G domain and MA3 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G57870.1 | Symbols: eIFiso4G1 | MIF4G domain-containing protein / MA3 domain-containing protein | chr5:23439755-23443433 FORWARD LENGTH=780	775	780	0	100.6	87.9	94.1
Rsa1.0_00877.1.g20720.t1	ref|XP_002864532.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] gi|297310367|gb|EFH40791.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	113	95	1.00E-34	84.1	71.7	75.2	ubiquitin family protein	gbpln	Arabidopsis lyrata	AT5G57860.2 | Symbols: | Ubiquitin-like superfamily protein | chr5:23437991-23439087 FORWARD LENGTH=95	113	95	7.00E-37	84.1	70.8	75.2
Rsa1.0_00877.1.g20721.t1	ref|XP_002866233.1| hypothetical protein ARALYDRAFT_495879 [Arabidopsis lyrata subsp. lyrata] gi|297312068|gb|EFH42492.1| hypothetical protein ARALYDRAFT_495879 [Arabidopsis lyrata subsp. lyrata]	362	385	1.00E-139	106.4	78.5	87.3	hypothetical protein ARALYDRAFT_495879	gbpln	Arabidopsis lyrata	AT5G57830.1 | Symbols: | Protein of unknown function, DUF593 | chr5:23429406-23430860 REVERSE LENGTH=387	362	387	1.00E-140	106.9	79.6	88.4
Rsa1.0_00877.1.g20722.t1	gb|EOA15016.1| hypothetical protein CARUB_v10028373mg [Capsella rubella]	137	154	2.00E-38	112.4	64.2	76.6	hypothetical protein CARUB_v10028373mg	gbpln	Capsella rubella	AT5G57820.1 | Symbols: | zinc ion binding | chr5:23428601-23429165 FORWARD LENGTH=161	137	161	4.00E-38	117.5	62.8	75.2
Rsa1.0_00877.1.g20723.t2	gb|EOA12639.1| hypothetical protein CARUB_v10027573mg [Capsella rubella]	297	320	1.00E-103	107.7	71.0	74.4	hypothetical protein CARUB_v10027573mg	gbpln	Capsella rubella	AT5G57810.1 | Symbols: TET15 | tetraspanin15 | chr5:23424466-23425589 REVERSE LENGTH=317	297	317	1.00E-101	106.7	70.0	74.1
Rsa1.0_00877.1.g20724.t1	ref|XP_002864528.1| hypothetical protein ARALYDRAFT_495876 [Arabidopsis lyrata subsp. lyrata] gi|297310363|gb|EFH40787.1| hypothetical protein ARALYDRAFT_495876 [Arabidopsis lyrata subsp. lyrata]	630	632	0	100.3	89.8	95.4	hypothetical protein ARALYDRAFT_495876	gbpln	Arabidopsis lyrata	AT5G57800.1 | Symbols: FLP1, YRE, CER3, WAX2 | Fatty acid hydroxylase superfamily | chr5:23420589-23423832 FORWARD LENGTH=632	630	632	0	100.3	89.2	94.8
Rsa1.0_00877.1.g20725.t1	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	360	1453	4.00E-90	403.6	48.6	55.0	polyprotein	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	360	240	3.00E-38	66.7	21.1	27.2
Rsa1.0_00877.1.g20726.t1	gb|EOA14948.1| hypothetical protein CARUB_v10028294mg [Capsella rubella]	414	404	0	97.6	88.6	91.8	hypothetical protein CARUB_v10028294mg	gbpln	Capsella rubella	AT5G57770.1 | Symbols: | Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region | chr5:23401094-23403112 REVERSE LENGTH=406	414	406	0	98.1	89.6	92.0
Rsa1.0_00877.1.g20727.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00877.1.g20728.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00877.1.g20729.t1	gb|AAC02672.1| polyprotein [Arabidopsis arenosa]	621	1390	1.00E-49	223.8	15.3	19.3	polyprotein	gbpln	Arabidopsis arenosa	AT5G57720.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:23389927-23391526 REVERSE LENGTH=300	621	300	4.00E-49	48.3	17.2	21.1
Rsa1.0_00878.1.g20730.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20731.t1	ref|NP_001154354.1| nucleic acid/nucleotide binding protein [Arabidopsis thaliana] gi|332191964|gb|AEE30085.1| nucleic acid/nucleotide binding protein [Arabidopsis thaliana]	242	253	6.00E-92	104.5	73.1	82.6	nucleic acid/nucleotide binding protein	gbpln	Arabidopsis thaliana	AT1G21320.2 | Symbols: | nucleotide binding;nucleic acid binding | chr1:7462834-7466164 REVERSE LENGTH=253	242	253	2.00E-94	104.5	73.1	82.6
Rsa1.0_00878.1.g20732.t1	gb|ABA95266.1| retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa Japonica Group]	1099	1388	0	126.3	41.9	61.4	retrotransposon protein, putative, Ty1-copia subclass	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1099	1262	3.00E-80	114.8	14.3	22.9

Rsa1.0_00878.1.g20733.t1	gb|EOA36400.1| hypothetical protein CARUB_v10010842mg [Capsella rubella]	234	237	5.00E-63	101.3	65.4	76.1	hypothetical protein CARUB_v10010842mg	gbpln	Capsella rubella	AT1G21326.1 | Symbols: | VQ motif-containing protein | chr1:7469002-7469721 REVERSE LENGTH=239	234	239	1.00E-57	102.1	64.1	73.9
Rsa1.0_00878.1.g20734.t2	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	799	657	1.00E-110	82.2	23.8	30.0	T14P8.10	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	799	332	2.00E-65	41.6	15.4	20.0
Rsa1.0_00878.1.g20735.t2	ref|NP_177488.2| protein kinase domain-containing protein [Arabidopsis thaliana] gi|332197342|gb|AEE35463.1| protein kinase domain-containing protein [Arabidopsis thaliana]	162	1169	2.00E-12	721.6	24.7	27.2	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G73460.1 | Symbols: | Protein kinase superfamily protein | chr1:27620122-27624899 FORWARD LENGTH=1169	162	1169	8.00E-15	721.6	24.7	27.2
Rsa1.0_00878.1.g20736.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20737.t1	gb|EJP69747.1| hypothetical protein BBA_01712 [Beauveria bassiana ARSEF 2860]	251	318	4.00E-65	126.7	47.0	66.9	hypothetical protein BBA_01712	gbenv/gbpln	Beauveria bassiana	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20738.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20739.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20740.t1	dbj|BAJ33657.1| unnamed protein product [Thellungiella halophila]	535	595	0	111.2	86.0	93.8	unnamed protein product	----	----	AT1G21450.1 | Symbols: SCL1 | SCARECROW-like 1 | chr1:7509721-7511502 FORWARD LENGTH=593	535	593	0	110.8	84.9	94.0
Rsa1.0_00878.1.g20741.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20742.t1	ref|NP_201166.1| cyclin-dependent kinase E-1 [Arabidopsis thaliana] gi|152013387|sp|Q84TI6.2|CDKE1_ARATH RecName: Full=Cyclin-dependent kinase E-1; Short=CDKE;1; AltName: Full=Cyclin-dependent kinase 8; AltName: Full=Protein HUA ENHANCER 3 gi|10177042|dbj|BAB10454.1| cdc2-like protein kinase-like protein [Arabidopsis thaliana] gi|47607488|gb|AAT36644.1| HUA enhancer 3 [Arabidopsis thaliana] gi|56382025|gb|AAV85731.1| At5g63610 [Arabidopsis thaliana] gi|332010393|gb|AED97776.1| cyclin-dependent kinase E-1 [Arabidopsis thaliana]	132	470	2.00E-45	356.1	68.2	72.0	cyclin-dependent kinase E-1	gbpln	Arabidopsis thaliana	AT5G63610.1 | Symbols: HEN3, CDKE;1, ATCDK8 | cyclin-dependent kinase E;1 | chr5:25463645-25465057 REVERSE LENGTH=470	132	470	4.00E-48	356.1	68.2	72.0
Rsa1.0_00878.1.g20743.t1	ref|XP_002886961.1| hypothetical protein ARALYDRAFT_894161 [Arabidopsis lyrata subsp. lyrata] gi|297332802|gb|EFH63220.1| hypothetical protein ARALYDRAFT_894161 [Arabidopsis lyrata subsp. lyrata]	406	299	2.00E-39	73.6	25.9	35.7	hypothetical protein ARALYDRAFT_894161	gbpln	Arabidopsis lyrata	AT1G19060.1 | Symbols: | Protein of unknown function (DUF626) | chr1:6582066-6583601 REVERSE LENGTH=287	406	287	1.00E-31	70.7	23.2	31.8
Rsa1.0_00878.1.g20744.t1	ref|XP_002893169.1| hypothetical protein ARALYDRAFT_472386 [Arabidopsis lyrata subsp. lyrata] gi|297339011|gb|EFH69428.1| hypothetical protein ARALYDRAFT_472386 [Arabidopsis lyrata subsp. lyrata]	171	126	1.00E-29	73.7	54.4	59.6	hypothetical protein ARALYDRAFT_472386	gbpln	Arabidopsis lyrata	AT1G21500.1 | Symbols: | unknown protein; Has 29 Blast hits to 29 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 27; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7530047-7530954 REVERSE LENGTH=126	171	126	9.00E-31	73.7	53.8	59.6
Rsa1.0_00878.1.g20745.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1295	1496	0	115.5	46.2	59.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1295	1262	1.00E-34	97.5	6.1	8.6
Rsa1.0_00878.1.g20746.t1	ref|XP_002877467.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323305|gb|EFH53726.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	107	186	2.00E-17	173.8	44.9	61.7	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20747.t1	gb|AAD15534.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	439	1664	6.00E-67	379.0	30.3	37.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20748.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20749.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20750.t9	ref|NP_173360.1| TTF-type zinc finger protein with HAT dimerization domain [Arabidopsis thaliana] gi|332191703|gb|AEE29824.1| TTF-type zinc finger protein with HAT dimerization domain [Arabidopsis thaliana]	1004	769	0	76.6	37.0	44.8	TTF-type zinc finger protein with HAT dimerization domain	gbpln	Arabidopsis thaliana	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	1004	769	0	76.6	37.0	44.8
Rsa1.0_00878.1.g20751.t8	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20752.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20753.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00878.1.g20754.t3	emb|CAA73042.1| polyprotein [Ananas comosus]	308	871	1.00E-14	282.8	16.6	24.4	polyprotein	gbpln	Ananas comosus	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20755.t2	gb|ADF81045.1| LEC1-2 transcription factor [Brassica napus]	896	230	2.00E-96	25.7	20.3	20.8	LEC1-2 transcription factor	gbpln	Brassica napus	AT1G21970.1 | Symbols: LEC1, EMB 212, EMB212, NF-YB9 | Histone superfamily protein | chr1:7727750-7729571 REVERSE LENGTH=238	896	238	5.00E-82	26.6	17.9	19.0
Rsa1.0_00878.1.g20756.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00878.1.g20757.t2	gb|EOA36900.1| hypothetical protein CARUB_v10011446mg [Capsella rubella]	388	396	0	102.1	82.2	88.7	hypothetical protein CARUB_v10011446mg	gbpln	Capsella rubella	AT1G22015.1 | Symbols: DD46 | Galactosyltransferase family protein | chr1:7751225-7753425 REVERSE LENGTH=398	388	398	1.00E-180	102.6	81.2	87.1
Rsa1.0_00878.1.g20758.t8	ref|NP_563645.1| COP9 signalosome complex subunit 7 [Arabidopsis thaliana] gi|55976565|sp|Q94JU3.1|CSN7_ARATH RecName: Full=COP9 signalosome complex subunit 7; Short=CSN complex subunit 7; AltName: Full=Protein FUSCA 5 gi|13937161|gb|AAK50074.1|AF372934_1 At1g02090/T7I23_24 [Arabidopsis thaliana] gi|18056671|gb|AAL58109.1|AF395066_1 CSN complex subunit 7ii [Arabidopsis thaliana] gi|21593551|gb|AAM65518.1| FUS5 [Arabidopsis thaliana] gi|22137006|gb|AAM91348.1| At1g02090/T7I23_24 [Arabidopsis thaliana] gi|332189259|gb|AEE27380.1| COP9 signalosome complex subunit 7 [Arabidopsis thaliana]	368	260	1.00E-124	70.7	58.4	65.2	COP9 signalosome complex subunit 7	gbpln	Arabidopsis thaliana	AT1G02090.1 | Symbols: FUS5, CSN7, COP15, ATCSN7 | Proteasome component (PCI) domain protein | chr1:387479-389568 REVERSE LENGTH=260	368	260	1.00E-127	70.7	58.4	65.2
Rsa1.0_00879.1.g20759.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	899	1274	0	141.7	46.9	64.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	899	575	3.00E-56	64.0	18.2	27.7
Rsa1.0_00879.1.g20760.t1	ref|NP_566458.1| arabinogalactan protein 12 [Arabidopsis thaliana] gi|75273536|sp|Q9LJD9.1|AGP12_ARATH RecName: Full=Arabinogalactan peptide 12; Short=AG-peptide 12; Flags: Precursor gi|10880501|gb|AAG24280.1|AF195893_1 arabinogalactan protein [Arabidopsis thaliana] gi|9280304|dbj|BAB01759.1| unnamed protein product [Arabidopsis thaliana] gi|16649109|gb|AAL24406.1| Unknown protein [Arabidopsis thaliana] gi|20148539|gb|AAM10160.1| unknown protein [Arabidopsis thaliana] gi|21554170|gb|AAM63249.1| unknown [Arabidopsis thaliana] gi|332641846|gb|AEE75367.1| arabinogalactan protein 12 [Arabidopsis thaliana]	58	60	9.00E-13	103.4	75.9	84.5	arabinogalactan protein 12	gbpln	Arabidopsis thaliana	AT3G13520.1 | Symbols: AGP12, ATAGP12 | arabinogalactan protein 12 | chr3:4409087-4409269 FORWARD LENGTH=60	58	60	2.00E-15	103.4	75.9	84.5
Rsa1.0_00879.1.g20761.t1	ref|NP_001185237.1| RNA polymerase II transcription mediator [Arabidopsis thaliana] gi|332195107|gb|AEE33228.1| RNA polymerase II transcription mediator [Arabidopsis thaliana]	1885	2001	0	106.2	89.8	93.7	RNA polymerase II transcription mediator	gbpln	Arabidopsis thaliana	AT1G55325.2 | Symbols: GCT | RNA polymerase II transcription mediators | chr1:20637594-20647714 FORWARD LENGTH=2001	1885	2001	0	106.2	89.8	93.7
Rsa1.0_00879.1.g20762.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00879.1.g20763.t4	ref|NP_175929.3| acyl-activating enzyme 18 [Arabidopsis thaliana] gi|75297963|sp|Q84P17.1|AEE18_ARATH RecName: Full=Probable acyl-activating enzyme 18, peroxisomal gi|29893268|gb|AAP03028.1| acyl-activating enzyme 18 [Arabidopsis thaliana] gi|332195104|gb|AEE33225.1| acyl-activating enzyme 18 [Arabidopsis thaliana]	695	727	0	104.6	87.1	93.2	acyl-activating enzyme 18	gbpln	Arabidopsis thaliana	AT1G55320.1 | Symbols: AAE18 | acyl-activating enzyme 18 | chr1:20633371-20636659 FORWARD LENGTH=727	695	727	0	104.6	87.1	93.2
Rsa1.0_00879.1.g20764.t2	ref|XP_002891828.1| hypothetical protein ARALYDRAFT_892527 [Arabidopsis lyrata subsp. lyrata] gi|297337670|gb|EFH68087.1| hypothetical protein ARALYDRAFT_892527 [Arabidopsis lyrata subsp. lyrata]	290	289	4.00E-72	99.7	72.8	77.9	hypothetical protein ARALYDRAFT_892527	gbpln	Arabidopsis lyrata	AT1G55310.3 | Symbols: SR33, SCL33, At-SCL33 | SC35-like splicing factor 33 | chr1:20630676-20632695 FORWARD LENGTH=300	290	300	1.00E-71	103.4	55.9	60.7

Rsa1.0_00879.1.g20765.t2	ref|XP_002894499.1| hypothetical protein ARALYDRAFT_474587 [Arabidopsis lyrata subsp. lyrata] gi|297340341|gb|EFH70758.1| hypothetical protein ARALYDRAFT_474587 [Arabidopsis lyrata subsp. lyrata]	250	202	1.00E-80	80.8	64.4	67.6	hypothetical protein ARALYDRAFT_474587	gbpln	Arabidopsis lyrata	AT1G55300.1 | Symbols: TAF7 | TBP-associated factor 7 | chr1:20628170-20629490 REVERSE LENGTH=203	250	203	8.00E-82	81.2	63.6	67.6
Rsa1.0_00879.1.g20766.t1	ref|XP_002891826.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297337668|gb|EFH68085.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	196	190	1.00E-77	96.9	71.9	81.1	protease inhibitor/seed storage/lipid transfer protein family protein	gbpln	Arabidopsis lyrata	AT1G55260.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:20614663-20616158 FORWARD LENGTH=227	196	227	6.00E-76	115.8	68.9	79.1
Rsa1.0_00879.1.g20767.t1	ref|NP_176964.1| heat stress transcription factor A-8 [Arabidopsis thaliana] gi|11386850|sp|Q9S7U5.1|HSFA8_ARATH RecName: Full=Heat stress transcription factor A-8; Short=AtHsfA8; AltName: Full=AtHsf-03; AltName: Full=Heat shock factor protein 5; Short=HSF 5; AltName: Full=Heat shock transcription factor 5; Short=HSTF 5 gi|12324064|gb|AAG51992.1|AC012563_2 putative heat shock transcription factor; 58077-59546 [Arabidopsis thaliana] gi|6624614|emb|CAB63801.1| heat shock factor 5 [Arabidopsis thaliana] gi|20453060|gb|AAM19775.1| At1g67970/T23K23_18 [Arabidopsis thaliana] gi|332196609|gb|AEE34730.1| heat stress transcription factor A-8 [Arabidopsis thaliana]	223	374	1.00E-35	167.7	36.3	40.4	heat stress transcription factor A-8	gbpln	Arabidopsis thaliana	AT1G67970.1 | Symbols: AT-HSFA8, HSFA8 | heat shock transcription factor A8 | chr1:25484844-25486313 REVERSE LENGTH=374	223	374	3.00E-38	167.7	36.3	40.4
Rsa1.0_00879.1.g20768.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00879.1.g20769.t1	dbj|BAJ34575.1| unnamed protein product [Thellungiella halophila]	125	188	6.00E-61	150.4	91.2	94.4	unnamed protein product	----	----	AT1G55210.2 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr1:20598057-20598620 REVERSE LENGTH=187	125	187	6.00E-63	149.6	90.4	93.6
Rsa1.0_00879.1.g20770.t1	gb|EOA36362.1| hypothetical protein CARUB_v10010738mg [Capsella rubella]	127	97	2.00E-27	76.4	52.8	61.4	hypothetical protein CARUB_v10010738mg	gbpln	Capsella rubella	AT1G55205.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13674.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:20594584-20595094 FORWARD LENGTH=103	127	103	2.00E-25	81.1	54.3	63.0
Rsa1.0_00879.1.g20771.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00879.1.g20772.t1	ref|NP_564679.1| PRA1 family protein F2 [Arabidopsis thaliana] gi|75169467|sp|Q9C889.1|PR1F2_ARATH RecName: Full=PRA1 family protein F2; Short=AtPRA1.F2 gi|12323168|gb|AAG51564.1|AC027034_10 hypothetical protein; 89971-89402 [Arabidopsis thaliana] gi|21554296|gb|AAM63371.1| unknown [Arabidopsis thaliana] gi|28393384|gb|AAO42116.1| unknown protein [Arabidopsis thaliana] gi|28827574|gb|AAO50631.1| unknown protein [Arabidopsis thaliana] gi|332195079|gb|AEE33200.1| PRA1 family protein F2 [Arabidopsis thaliana]	187	189	7.00E-87	101.1	84.0	93.0	PRA1 family protein F2	gbpln	Arabidopsis thaliana	AT1G55190.1 | Symbols: PRA1.F2, PRA7 | PRA1 (Prenylated rab acceptor) family protein | chr1:20588450-20589019 FORWARD LENGTH=189	187	189	2.00E-89	101.1	84.0	93.0
Rsa1.0_00880.1.g20773.t1	ref|XP_002532644.1| conserved hypothetical protein [Ricinus communis] gi|223527635|gb|EEF29747.1| conserved hypothetical protein [Ricinus communis]	338	462	3.00E-28	136.7	19.5	30.8	conserved hypothetical protein	gbpln	Ricinus communis	#	#	#	#	#	#	#

Rsa1.0_00880.1.g20774.t1	ref|XP_002890827.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297336669|gb|EFH67086.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata]	425	471	1.00E−150	110.8	63.5	79.3	pentatricopeptide repeat−containing protein	gbpln	Arabidopsis lyrata	AT1G29710.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr1:10387673−10389100 FORWARD LENGTH=475	425	475	1.00E−143	111.8	60.7	76.7
Rsa1.0_00880.1.g20775.t3	gb|EOA34048.1| hypothetical protein CARUB_v10021547mg, partial [Capsella rubella]	640	626	0	97.8	66.4	76.9	hypothetical protein CARUB_v10021547mg, partial	gbpln	Capsella rubella	AT1G66910.1 | Symbols: | Protein kinase superfamily protein | chr1:24961634−24963941 REVERSE LENGTH=666	640	666	0	104.1	63.0	74.8
Rsa1.0_00880.1.g20776.t1	gb|AAM66042.1| unknown [Arabidopsis thaliana]	164	158	2.00E−44	96.3	71.3	76.2	unknown	gbpln	Arabidopsis thaliana	AT1G66890.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: 50S ribosomal protein−related (TAIR:AT5G16200.1); Has 36 Blast hits to 36 proteins in 7 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 36; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:24957614−24958090 FORWARD LENGTH=158	164	158	7.00E−47	96.3	70.7	75.6
Rsa1.0_00880.1.g20777.t1	dbj|BAF02226.1| wall−associated kinase like protein [Arabidopsis thaliana]	625	705	0	112.8	73.1	83.2	wall−associated kinase like protein	gbpln	Arabidopsis thaliana	AT1G66880.1 | Symbols: | Protein kinase superfamily protein | chr1:24946928−24955438 FORWARD LENGTH=1296	625	1296	0	207.4	71.4	81.0
Rsa1.0_00880.1.g20778.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	278	441	4.00E−31	158.6	33.1	46.8	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr3:8789471−8793208 FORWARD LENGTH=746	278	746	3.00E−16	268.3	14.0	19.1
Rsa1.0_00880.1.g20779.t1	dbj|BAF02226.1| wall−associated kinase like protein [Arabidopsis thaliana]	699	705	0	100.9	69.5	79.5	wall−associated kinase like protein	gbpln	Arabidopsis thaliana	AT1G66880.1 | Symbols: | Protein kinase superfamily protein | chr1:24946928−24955438 FORWARD LENGTH=1296	699	1296	0	185.4	67.0	76.5
Rsa1.0_00880.1.g20780.t2	gb|ACP30617.1| disease resistance protein [Brassica rapa subsp. pekinensis]	105	1297	6.00E−30	1235.2	65.7	71.4	disease resistance protein	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00880.1.g20781.t1	dbj|BAA25680.1| Lipid transfer protein [Brassica rapa]	98	86	6.00E−34	87.8	73.5	77.6	Lipid transfer protein	gbpln	Brassica rapa	AT1G66850.1 | Symbols: | Bifunctional inhibitor/lipid−transfer protein/seed storage 2S albumin superfamily protein | chr1:24936985−24937293 FORWARD LENGTH=102	98	102	3.00E−35	104.1	73.5	81.6
Rsa1.0_00880.1.g20782.t1	gb|EOA33752.1| hypothetical protein CARUB_v10019946mg [Capsella rubella]	602	639	0	106.1	72.9	85.9	hypothetical protein CARUB_v10019946mg	gbpln	Capsella rubella	AT1G66840.1 | Symbols: PMI2, WEB2 | Plant protein of unknown function (DUF827) | chr1:24933998−24936116 REVERSE LENGTH=607	602	607	0	100.8	70.4	82.7
Rsa1.0_00880.1.g20783.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00880.1.g20784.t1	ref|XP_002888549.1| hypothetical protein ARALYDRAFT_475779 [Arabidopsis lyrata subsp. lyrata] gi|297334390|gb|EFH64808.1| hypothetical protein ARALYDRAFT_475779 [Arabidopsis lyrata subsp. lyrata]	670	681	0	101.6	83.6	90.9	hypothetical protein ARALYDRAFT_475779	gbpln	Arabidopsis lyrata	AT1G66830.1 | Symbols: | Leucine−rich repeat protein kinase family protein | chr1:24930700−24932834 REVERSE LENGTH=685	670	685	0	102.2	83.3	91.3
Rsa1.0_00880.1.g20785.t1	ref|XP_002887079.1| hypothetical protein ARALYDRAFT_894384 [Arabidopsis lyrata subsp. lyrata] gi|297332920|gb|EFH63338.1| hypothetical protein ARALYDRAFT_894384 [Arabidopsis lyrata subsp. lyrata]	125	109	6.00E−11	87.2	62.4	70.4	hypothetical protein ARALYDRAFT_894384	gbpln	Arabidopsis lyrata	AT1G66820.1 | Symbols: | glycine−rich protein | chr1:24930093−24930422 FORWARD LENGTH=109	125	109	2.00E−11	87.2	59.2	70.4
Rsa1.0_00880.1.g20786.t1	ref|XP_002888548.1| hypothetical protein ARALYDRAFT_475777 [Arabidopsis lyrata subsp. lyrata] gi|297334389|gb|EFH64807.1| hypothetical protein ARALYDRAFT_475777 [Arabidopsis lyrata subsp. lyrata]	330	327	1.00E−109	99.1	73.6	82.4	hypothetical protein ARALYDRAFT_475777	gbpln	Arabidopsis lyrata	AT1G66810.1 | Symbols: | Zinc finger C−x8−C−x5−C−x3−H type family protein | chr1:24927613−24928619 REVERSE LENGTH=310	330	310	1.00E−101	93.9	67.3	76.1
Rsa1.0_00881.1.g20787.t1	gb|EOA25154.1| hypothetical protein CARUB_v10018465mg [Capsella rubella]	385	469	1.00E−157	121.8	73.5	83.4	hypothetical protein CARUB_v10018465mg	gbpln	Capsella rubella	AT2G01760.1 | Symbols: ARR14, RR14 | response regulator 14 | chr2:333041−334514 FORWARD LENGTH=382	385	382	1.00E−143	99.2	71.7	81.8
Rsa1.0_00881.1.g20788.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00881.1.g20789.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_00881.1.g20790.t1	ref|NP_178282.2| cleavage and polyadenylation specificity factor subunit 3-II [Arabidopsis thaliana] gi|332278175|sp|Q8GUU3.2|CPS3B_ARATH RecName: Full=Cleavage and polyadenylation specificity factor subunit 3-II; AltName: Full=Cleavage and polyadenylation specificity factor 73 kDa subunit II; Short=AtCPSF73-II; Short=CPSF 73 kDa subunit II; AltName: Full=Protein EMBRYO SAC DEVELOPMENT ARREST 26 gi|62320470|dbj|BAD94982.1| putative cleavage and polyadenylation specifity factor [Arabidopsis thaliana] gi|330250395|gb|AEC05489.1| cleavage and polyadenylation specificity factor subunit 3-II [Arabidopsis thaliana]	613	613	0	100.0	89.7	94.6	cleavage and polyadenylation specificity factor subunit 3-II	gbpln	Arabidopsis thaliana	AT2G01730.1 | Symbols: ATCPSF73-II, EDA26, CPSF73-II | cleavage and polyadenylation specificity factor 73 kDa subunit-II | chr2:320597-323845 FORWARD LENGTH=613	613	613	0	100.0	89.7	94.6
Rsa1.0_00881.1.g20791.t1	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	231	1250	6.00E-46	541.1	51.9	64.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	231	1262	1.00E-23	546.3	22.1	31.6
Rsa1.0_00881.1.g20792.t1	ref|XP_002881850.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327689|gb|EFH58109.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	153	308	4.00E-13	201.3	29.4	43.1	predicted protein	gbpln	Arabidopsis lyrata	AT2G42480.1 | Symbols: | TRAF-like family protein | chr2:17685805-17689851 REVERSE LENGTH=743	153	743	2.00E-14	485.6	26.8	39.2
Rsa1.0_00881.1.g20793.t1	gb|EOA23970.1| hypothetical protein CARUB_v10017190mg [Capsella rubella]	467	464	0	99.4	89.5	95.3	hypothetical protein CARUB_v10017190mg	gbpln	Capsella rubella	AT2G01720.1 | Symbols: | Ribophorin I | chr2:317193-320016 REVERSE LENGTH=464	467	464	0	99.4	88.9	94.9
Rsa1.0_00881.1.g20794.t1	gb|EOA24403.1| hypothetical protein CARUB_v10017653mg [Capsella rubella] gi|482560213|gb|EOA24404.1| hypothetical protein CARUB_v10017653mg [Capsella rubella]	306	321	1.00E-134	104.9	78.4	86.9	hypothetical protein CARUB_v10017653mg	gbpln	Capsella rubella	AT2G01710.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr2:315836-316771 FORWARD LENGTH=311	306	311	1.00E-132	101.6	79.7	86.3
Rsa1.0_00881.1.g20795.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00881.1.g20796.t1	ref|NP_565275.1| uncharacterized protein [Arabidopsis thaliana] gi|75268025|sp|Q9ZU97.2|VAC14_ARATH RecName: Full=Protein VAC14 homolog gi|20197546|gb|AAD12702.2| expressed protein [Arabidopsis thaliana] gi|330250391|gb|AEC05485.1| uncharacterized protein AT2G01690 [Arabidopsis thaliana]	702	743	0	105.8	90.5	93.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G01690.1 | Symbols: | ARM repeat superfamily protein | chr2:309144-313499 REVERSE LENGTH=743	702	743	0	105.8	90.5	93.4
Rsa1.0_00881.1.g20797.t4	emb|CAN64427.1| hypothetical protein VITISV_029384 [Vitis vinifera]	1140	1392	1.00E-161	122.1	29.3	41.6	hypothetical protein VITISV_029384	gbpln	Vitis vinifera	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1140	158	7.00E-20	13.9	3.9	5.9
Rsa1.0_00881.1.g20798.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1649	1838	0	111.5	45.9	56.8	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00881.1.g20799.t2	gb|AAQ82842.1| At4g20730 [Arabidopsis thaliana] gi|51970840|dbj|BAD44112.1| putative protein [Arabidopsis thaliana]	994	800	9.00E-27	80.5	7.6	11.1	At4g20730	gbpln	Arabidopsis thaliana	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	994	1399	1.00E-27	140.7	6.9	9.5
Rsa1.0_00882.1.g20800.t1	gb|AAC33963.1| contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]	523	1633	2.33E-156	312.2	50.9	69.0	contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19)	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	523	1262	4.00E-98	241.3	32.7	44.0
Rsa1.0_00882.1.g20801.t1	ref|XP_002879261.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325100|gb|EFH55520.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	359	359	0	100.0	86.9	92.8	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT2G30310.1 | Symbols: | GDSL-like Lipase/Acylhydrolase family protein | chr2:12923055-12924371 FORWARD LENGTH=359	359	359	0	100.0	85.8	92.2
Rsa1.0_00882.1.g20802.t1	ref|XP_002883443.1| hypothetical protein ARALYDRAFT_342502 [Arabidopsis lyrata subsp. lyrata] gi|297329283|gb|EFH59702.1| hypothetical protein ARALYDRAFT_342502 [Arabidopsis lyrata subsp. lyrata]	496	454	0	91.5	66.5	72.4	hypothetical protein ARALYDRAFT_342502	gbpln	Arabidopsis lyrata	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	496	472	5.00E-84	95.2	38.3	51.0
Rsa1.0_00882.1.g20803.t1	gb|EOA28478.1| hypothetical protein CARUB_v10024687mg [Capsella rubella]	361	390	1.00E-156	108.0	85.6	90.9	hypothetical protein CARUB_v10024687mg	gbpln	Capsella rubella	AT2G30250.1 | Symbols: WRKY25, ATWRKY25 | WRKY DNA-binding protein 25 | chr2:12903553-12905089 REVERSE LENGTH=393	361	393	1.00E-149	108.9	84.2	90.6

Rsa1.0_00882.1.g20804.t1	ref|XP_002881092.1| ATCHX13 [Arabidopsis lyrata subsp. lyrata] gi|297326931|gb|EFH57351.1| ATCHX13 [Arabidopsis lyrata subsp. lyrata]	832	830	0	99.8	83.5	91.6	ATCHX13	gbpln	Arabidopsis lyrata	AT2G30240.1 | Symbols: ATCHX13, CHX13 | Cation/hydrogen exchanger family protein | chr2:12899907-12902779 REVERSE LENGTH=831	832	831	0	99.9	82.7	91.7
Rsa1.0_00882.1.g20805.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00882.1.g20806.t1	ref|XP_002879258.1| hypothetical protein ARALYDRAFT_481935 [Arabidopsis lyrata subsp. lyrata] gi|297325097|gb|EFH55517.1| hypothetical protein ARALYDRAFT_481935 [Arabidopsis lyrata subsp. lyrata]	179	177	1.00E-75	98.9	84.9	90.5	hypothetical protein ARALYDRAFT_481935	gbpln	Arabidopsis lyrata	AT2G30230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06980.1); Has 167 Blast hits to 167 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 167; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:12897156-12897689 FORWARD LENGTH=177	179	177	4.00E-77	98.9	83.8	89.9
Rsa1.0_00882.1.g20807.t1	ref|XP_002881090.1| hypothetical protein ARALYDRAFT_481932 [Arabidopsis lyrata subsp. lyrata] gi|297326929|gb|EFH57349.1| hypothetical protein ARALYDRAFT_481932 [Arabidopsis lyrata subsp. lyrata]	570	570	0	100.0	94.9	97.0	hypothetical protein ARALYDRAFT_481932	gbpln	Arabidopsis lyrata	AT2G30210.1 | Symbols: LAC3 | laccase 3 | chr2:12887735-12889827 REVERSE LENGTH=570	570	570	0	100.0	93.5	96.5
Rsa1.0_00882.1.g20808.t1	emb|CAB45522.1| [acyl-carrier protein] S-malonyltransferase [Brassica napus]	370	349	1.00E-176	94.3	86.8	90.8		gbpln	Brassica napus	AT2G30200.1 | Symbols: | catalytics;transferases;[acyl-carrier-protein] S-malonyltransferases;binding | chr2:12883162-12885482 REVERSE LENGTH=393	370	393	1.00E-174	106.2	85.1	88.9
Rsa1.0_00882.1.g20809.t1	gb|AAC68670.1| RING-H2 finger protein RHA1b [Arabidopsis thaliana] gi|21593210|gb|AAM65159.1| RING-H2 finger protein RHA1b [Arabidopsis thaliana]	159	157	9.00E-50	98.7	64.8	75.5	RING-H2 finger protein RHA1b	gbpln	Arabidopsis thaliana	AT4G11360.1 | Symbols: RHA1B | RING-H2 finger A1B | chr4:6906066-6906539 FORWARD LENGTH=157	159	157	1.00E-51	98.7	64.2	74.8
Rsa1.0_00882.1.g20810.t1	gb|AAM62642.1| putative mitochondrial carrier protein [Arabidopsis thaliana]	324	331	1.00E-159	102.2	88.0	94.1	putative mitochondrial carrier protein	gbpln	Arabidopsis thaliana	AT2G30160.1 | Symbols: | Mitochondrial substrate carrier family protein | chr2:12878016-12879377 FORWARD LENGTH=331	324	331	1.00E-161	102.2	87.7	93.8
Rsa1.0_00883.1.g20811.t1	gb|EOA22249.1| hypothetical protein CARUB_v10002838mg [Capsella rubella]	214	358	1.00E-43	167.3	45.8	59.8	hypothetical protein CARUB_v10002838mg	gbpln	Capsella rubella	AT5G22160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22150.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7346944-7349255 FORWARD LENGTH=353	214	353	5.00E-45	165.0	45.8	58.9
Rsa1.0_00883.1.g20812.t1	gb|EOA22505.1| hypothetical protein CARUB_v10003160mg, partial [Capsella rubella]	206	213	2.00E-35	103.4	43.2	60.7	hypothetical protein CARUB_v10003160mg, partial	gbpln	Capsella rubella	AT5G22150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22160.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7342567-7345956 FORWARD LENGTH=330	206	330	2.00E-30	160.2	35.4	49.5
Rsa1.0_00883.1.g20813.t1	ref|NP_680202.1| uncharacterized protein [Arabidopsis thaliana] gi|13374875|emb|CAC34509.1| putative protein [Arabidopsis thaliana] gi|332005608|gb|AED92991.1| uncharacterized protein AT5G22160 [Arabidopsis thaliana]	174	353	7.00E-24	202.9	40.8	52.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G22160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22150.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7346944-7349255 FORWARD LENGTH=353	174	353	3.00E-26	202.9	40.8	52.9
Rsa1.0_00883.1.g20814.t1	gb|EOA22193.1| hypothetical protein CARUB_v10002765mg [Capsella rubella]	143	329	6.00E-11	230.1	28.7	42.7	hypothetical protein CARUB_v10002765mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00883.1.g20815.t1	ref|XP_002871995.1| hypothetical protein ARALYDRAFT_489072 [Arabidopsis lyrata subsp. lyrata] gi|297317832|gb|EFH48254.1| hypothetical protein ARALYDRAFT_489072 [Arabidopsis lyrata subsp. lyrata]	476	457	0	96.0	78.4	84.7	hypothetical protein ARALYDRAFT_489072	gbpln	Arabidopsis lyrata	AT5G22220.2 | Symbols: E2F1, E2FB, ATE2FB | E2F transcription factor 1 | chr5:7360749-7364120 FORWARD LENGTH=469	476	469	0	98.5	77.9	84.5

Rsa1.0_00883.1.g20816.t1	ref|NP_197617.1| putative CCR4-associated factor 1-11 [Arabidopsis thaliana] gi|75334084|sp|Q9FMS6.1|CAF1K_ARATH RecName: Full=Probable CCR4-associated factor 1 homolog 11 gi|9757805|dbj|BAB08323.1| CCR4-associated factor-like protein [Arabidopsis thaliana] gi|17381058|gb|AAL36341.1| putative CCR4-associated factor [Arabidopsis thaliana] gi|25054979|gb|AAN71961.1| putative CCR4-associated factor [Arabidopsis thaliana] gi|332005618|gb|AED93001.1| putative CCR4-associated factor 1-11 [Arabidopsis thaliana]	283	278	1.00E-130	98.2	82.0	89.4	putative CCR4-associated factor 1-11	gbpln	Arabidopsis thaliana	AT5G22250.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:7365605-7366441 REVERSE LENGTH=278	283	278	1.00E-133	98.2	82.0	89.4
Rsa1.0_00883.1.g20817.t1	gb|EOA22197.1| hypothetical protein CARUB_v10002769mg [Capsella rubella]	92	93	2.00E-16	101.1	62.0	66.3	hypothetical protein CARUB_v10002769mg	gbpln	Capsella rubella	AT5G22270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11600.1); Has 136 Blast hits to 136 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 136; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:7372487-7372768 REVERSE LENGTH=93	92	93	2.00E-15	101.1	76.1	82.6
Rsa1.0_00883.1.g20818.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1364	1274	0	93.4	44.9	62.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1364	575	4.00E-68	42.2	12.8	19.6
Rsa1.0_00883.1.g20819.t1	ref|XP_002874058.1| hypothetical protein ARALYDRAFT_489079 [Arabidopsis lyrata subsp. lyrata] gi|297319895|gb|EFH50317.1| hypothetical protein ARALYDRAFT_489079 [Arabidopsis lyrata subsp. lyrata]	110	108	7.00E-48	98.2	91.8	96.4	hypothetical protein ARALYDRAFT_489079	gbpln	Arabidopsis lyrata	AT5G22280.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G44280.1); Has 82 Blast hits to 82 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 82; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:7374211-7375112 REVERSE LENGTH=108	110	108	7.00E-50	98.2	90.9	95.5
Rsa1.0_00883.1.g20820.t1	gb|EOA21023.1| hypothetical protein CARUB_v10001357mg [Capsella rubella]	335	340	1.00E-157	101.5	81.2	89.0	hypothetical protein CARUB_v10001357mg	gbpln	Capsella rubella	AT5G22290.1 | Symbols: anac089, NAC089 | NAC domain containing protein 89 | chr5:7376044-7377498 REVERSE LENGTH=340	335	340	1.00E-158	101.5	80.0	88.4
Rsa1.0_00883.1.g20821.t1	ref|XP_002874061.1| hypothetical protein ARALYDRAFT_489082 [Arabidopsis lyrata subsp. lyrata] gi|297319898|gb|EFH50320.1| hypothetical protein ARALYDRAFT_489082 [Arabidopsis lyrata subsp. lyrata]	466	492	0	105.6	80.5	88.6	hypothetical protein ARALYDRAFT_489082	gbpln	Arabidopsis lyrata	AT5G22310.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11590.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7383742-7385345 REVERSE LENGTH=481	466	481	0	103.2	79.0	87.8
Rsa1.0_00883.1.g20822.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00883.1.g20823.t1	gb|EOA20612.1| hypothetical protein CARUB_v10000923mg [Capsella rubella]	457	458	0	100.2	91.2	94.1	hypothetical protein CARUB_v10000923mg	gbpln	Capsella rubella	AT5G22330.1 | Symbols: ATTIP49A, RIN1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:7391026-7394071 REVERSE LENGTH=458	457	458	0	100.2	91.2	93.9
Rsa1.0_00883.1.g20824.t3	ref|NP_197626.2| uncharacterized protein [Arabidopsis thaliana] gi|29028856|gb|AAO64807.1| At5g22340 [Arabidopsis thaliana] gi|110736593|dbj|BAF00262.1| hypothetical protein [Arabidopsis thaliana] gi|332005630|gb|AED93013.1| uncharacterized protein AT5G22340 [Arabidopsis thaliana]	541	323	1.00E-152	59.7	50.8	54.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G22340.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 58 Blast hits to 58 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:7394509-7396554 FORWARD LENGTH=323	541	323	1.00E-154	59.7	50.8	54.7
Rsa1.0_00883.1.g20825.t1	ref|XP_002874066.1| vesicle-associated membrane protein 714 [Arabidopsis lyrata subsp. lyrata] gi|297319903|gb|EFH50325.1| vesicle-associated membrane protein 714 [Arabidopsis lyrata subsp. lyrata]	193	221	1.00E-104	114.5	94.8	96.9	vesicle-associated membrane protein 714	gbpln	Arabidopsis lyrata	AT5G22360.1 | Symbols: ATVAMP714, VAMP714 | vesicle-associated membrane protein 714 | chr5:7404379-7405654 REVERSE LENGTH=221	193	221	1.00E-105	114.5	93.8	97.4

Rsa1.0_00883.1.g20826.t1	ref|XP_002874067.1| ANAC090 [Arabidopsis lyrata subsp. lyrata] gi|297319904|gb|EFH50326.1| ANAC090 [Arabidopsis lyrata subsp. lyrata]	234	235	1.00E-114	100.4	84.2	91.9	ANAC090	gbpln	Arabidopsis lyrata	AT5G22380.1 | Symbols: anac090, NAC090 | NAC domain containing protein 90 | chr5:7408924-7410038 REVERSE LENGTH=235	234	235	1.00E-113	100.4	81.6	90.6
Rsa1.0_00884.1.g20827.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00884.1.g20828.t1	gb|AAG52026.1|AC022456_7 polyprotein, putative; 77260-80472 [Arabidopsis thaliana]	590	884	1.00E-107	149.8	39.5	51.7	polyprotein, putative; 77260-80472	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00884.1.g20829.t1	gb|AAD24567.1|AF120335_1 putative transposase [Arabidopsis thaliana]	245	577	6.00E-66	235.5	49.4	61.2	putative transposase	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	245	696	8.00E-19	284.1	22.0	38.4
Rsa1.0_00884.1.g20830.t1	ref|XP_002876127.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297321965|gb|EFH52386.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	1371	1386	0	101.1	86.1	91.4	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G52140.1 | Symbols: | tetratricopeptide repeat (TPR)-containing protein | chr3:19333232-19341295 FORWARD LENGTH=1403	1371	1403	0	102.3	84.9	90.7
Rsa1.0_00884.1.g20831.t1	ref|XP_002865992.1| hypothetical protein ARALYDRAFT_918470 [Arabidopsis lyrata subsp. lyrata] gi|297311827|gb|EFH42251.1| hypothetical protein ARALYDRAFT_918470 [Arabidopsis lyrata subsp. lyrata]	345	422	1.00E-124	122.3	64.1	75.9	hypothetical protein ARALYDRAFT_918470	gbpln	Arabidopsis lyrata	AT5G53780.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21839818-21841977 REVERSE LENGTH=376	345	376	1.00E-117	109.0	60.6	71.9
Rsa1.0_00884.1.g20832.t1	ref|XP_002864282.1| hypothetical protein ARALYDRAFT_918479 [Arabidopsis lyrata subsp. lyrata] gi|297310117|gb|EFH40541.1| hypothetical protein ARALYDRAFT_918479 [Arabidopsis lyrata subsp. lyrata]	411	371	1.00E-82	90.3	39.7	46.5	hypothetical protein ARALYDRAFT_918479	gbpln	Arabidopsis lyrata	AT5G53790.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21843501-21845261 FORWARD LENGTH=380	411	380	3.00E-74	92.5	36.7	43.3
Rsa1.0_00884.1.g20833.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00884.1.g20834.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00884.1.g20835.t1	gb|EOA14424.1| hypothetical protein CARUB_v10027626mg [Capsella rubella]	191	186	1.00E-42	97.4	47.1	66.0	hypothetical protein CARUB_v10027626mg	gbpln	Capsella rubella	AT5G46990.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19067692-19068255 REVERSE LENGTH=187	191	187	5.00E-45	97.9	48.2	62.8
Rsa1.0_00884.1.g20836.t1	ref|NP_199510.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|9759441|dbj|BAB10238.1| unnamed protein product [Arabidopsis thaliana] gi|332008072|gb|AED95455.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	183	187	1.00E-41	102.2	49.2	65.6	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT5G46990.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19067692-19068255 REVERSE LENGTH=187	183	187	5.00E-44	102.2	49.2	65.6
Rsa1.0_00884.1.g20837.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00885.1.g20838.t1	ref|NP_001077646.1| RING/FYVE/PHD zinc finger protein [Arabidopsis thaliana] gi|6910567|gb|AAF31272.1|AC006424_1 Location of EST 206I21T7, gb|N37185 [Arabidopsis thaliana] gi|332193410|gb|AEE31531.1| RING/FYVE/PHD zinc finger protein [Arabidopsis thaliana]	984	1068	0	108.5	76.2	84.1	RING/FYVE/PHD zinc finger protein	gbpln	Arabidopsis thaliana	AT1G32810.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:11881810-11885843 FORWARD LENGTH=1068	984	1068	0	108.5	76.2	84.1
Rsa1.0_00885.1.g20839.t1	ref|XP_002865907.1| CYP96A4 [Arabidopsis lyrata subsp. lyrata] gi|297311742|gb|EFH42166.1| CYP96A4 [Arabidopsis lyrata subsp. lyrata]	497	503	0	101.2	80.3	89.3	CYP96A4	gbpln	Arabidopsis lyrata	AT5G52320.1 | Symbols: CYP96A4 | cytochrome P450, family 96, subfamily A, polypeptide 4 | chr5:21245111-21246619 REVERSE LENGTH=502	497	502	0	101.0	79.7	88.3
Rsa1.0_00885.1.g20840.t4	gb|AAD15534.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	804	1664	1.00E-168	207.0	44.7	58.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00885.1.g20841.t2	gb|ABD65624.1| hypothetical protein 23.t00036 [Brassica oleracea]	842	842	1.00E-73	100.0	25.2	36.8	hypothetical protein 23.t00036	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	842	673	6.00E-21	79.9	6.7	9.5
Rsa1.0_00885.1.g20842.t1	gb|EOA12319.1| hypothetical protein CARUB_v10007958mg, partial [Capsella rubella]	842	673	1.00E-141	79.9	28.9	39.7	hypothetical protein CARUB_v10007958mg, partial	gbpln	Capsella rubella	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	842	719	2.00E-33	85.4	14.6	26.5
Rsa1.0_00885.1.g20843.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00885.1.g20844.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1550	1529	0	98.6	44.7	61.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1550	746	5.00E-92	48.1	11.7	15.6

Rsa1.0_00886.1.g20845.t1	ref|XP_002876943.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297322781|gb|EFH53202.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	408	451	1.00E-163	110.5	75.5	82.6	F-box family protein	gbpln	Arabidopsis lyrata	AT3G26000.1 | Symbols: | Ribonuclease inhibitor | chr3:9507042-9508542 REVERSE LENGTH=453	408	453	1.00E-153	111.0	69.6	79.2
Rsa1.0_00886.1.g20846.t3	ref|NP_189224.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana] gi|49660177|gb|AAT68379.1| hypothetical protein At3g25950 [Arabidopsis thaliana] gi|50058971|gb|AAT69230.1| hypothetical protein At3g25950 [Arabidopsis thaliana] gi|332643573|gb|AEE77094.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana]	565	251	1.00E-108	44.4	35.4	38.6	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	gbpln	Arabidopsis thaliana	AT3G25950.1 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr3:9496356-9497111 FORWARD LENGTH=251	565	251	1.00E-111	44.4	35.4	38.6
Rsa1.0_00886.1.g20847.t2	ref|NP_566785.1| universal stress protein (USP) family protein [Arabidopsis thaliana] gi|9279598|dbj|BAB01056.1| unnamed protein product [Arabidopsis thaliana] gi|28466901|gb|AAO44059.1| At3g25930 [Arabidopsis thaliana] gi|110743893|dbj|BAE99781.1| hypothetical protein [Arabidopsis thaliana] gi|332643571|gb|AEE77092.1| universal stress protein (USP) family protein [Arabidopsis thaliana]	138	154	6.00E-48	111.6	73.9	83.3	universal stress protein (USP) family protein	gbpln	Arabidopsis thaliana	AT3G25930.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:9493032-9493871 REVERSE LENGTH=154	138	154	1.00E-50	111.6	73.9	83.3
Rsa1.0_00886.1.g20848.t1	gb|EOA24563.1| hypothetical protein CARUB_v10017825mg [Capsella rubella]	273	273	1.00E-121	100.0	83.2	89.0	hypothetical protein CARUB_v10017825mg	gbpln	Capsella rubella	AT3G25920.1 | Symbols: RPL15 | ribosomal protein L15 | chr3:9491268-9492558 REVERSE LENGTH=277	273	277	1.00E-116	101.5	77.7	83.5
Rsa1.0_00886.1.g20849.t1	gb|EOA25813.1| hypothetical protein CARUB_v10019181mg [Capsella rubella]	334	358	1.00E-121	107.2	74.6	80.5	hypothetical protein CARUB_v10019181mg	gbpln	Capsella rubella	AT3G25910.1 | Symbols: | Protein of unknown function (DUF1644) | chr3:9489836-9490954 FORWARD LENGTH=372	334	372	1.00E-108	111.4	70.1	76.6
Rsa1.0_00886.1.g20850.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00886.1.g20851.t1	ref|XP_002876938.1| hypothetical protein ARALYDRAFT_484357 [Arabidopsis lyrata subsp. lyrata] gi|297322776|gb|EFH53197.1| hypothetical protein ARALYDRAFT_484357 [Arabidopsis lyrata subsp. lyrata]	94	90	6.00E-21	95.7	60.6	69.1	hypothetical protein ARALYDRAFT_484357	gbpln	Arabidopsis lyrata	AT3G25905.1 | Symbols: CLE27 | CLAVATA3/ESR-RELATED 27 | chr3:9486348-9486623 REVERSE LENGTH=91	94	91	4.00E-23	96.8	57.4	70.2
Rsa1.0_00886.1.g20852.t1	sp|A4ZGQ8.1|HMT1_BRAOT RecName: Full=Homocysteine S-methyltransferase 1; Short=BoHMT1 gi|110468086|gb|ABG74913.1| homocysteine methyltransferase 1 [Brassica oleracea var. italica]	306	326	1.00E-170	106.5	97.1	99.3	RecName: Full=Homocysteine S-methyltransferase 1; Short=BoHMT1 gi|110468086|gb|ABG74913.1| homocysteine methyltransferase 1	gbpln	Brassica oleracea	AT3G25900.3 | Symbols: HMT-1 | Homocysteine S-methyltransferase family protein | chr3:9480964-9482684 FORWARD LENGTH=306	306	306	1.00E-167	100.0	92.5	96.1
Rsa1.0_00886.1.g20853.t1	dbj|BAJ34405.1| unnamed protein product [Thellungiella halophila]	317	341	1.00E-131	107.6	80.4	86.8	unnamed protein product	----	----	AT3G25890.2 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:9476052-9477050 FORWARD LENGTH=332	317	332	1.00E-121	104.7	77.6	86.8
Rsa1.0_00886.1.g20854.t1	ref|XP_002876936.1| nim1-interacting 2 [Arabidopsis lyrata subsp. lyrata] gi|297322774|gb|EFH53195.1| nim1-interacting 2 [Arabidopsis lyrata subsp. lyrata]	156	117	7.00E-40	75.0	56.4	62.8	nim1-interacting 2	gbpln	Arabidopsis lyrata	AT3G25882.1 | Symbols: NIMIN-2 | NIM1-interacting 2 | chr3:9470521-9470889 REVERSE LENGTH=122	156	122	3.00E-41	78.2	55.8	61.5
Rsa1.0_00886.1.g20855.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	897	1356	0	151.2	53.6	70.9	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	897	1262	2.00E-71	140.7	17.9	26.4
Rsa1.0_00886.1.g20856.t3	dbj|BAF01550.1| terpene synthase-related protein [Arabidopsis thaliana] gi|227206462|dbj|BAH57286.1| AT3G25820 [Arabidopsis thaliana]	362	395	1.00E-163	109.1	78.5	89.2	terpene synthase-related protein	gbpln	Arabidopsis thaliana	AT3G25830.1 | Symbols: ATTPS-CIN, TPS-CIN | terpene synthase-like sequence-1,8-cineole | chr3:9447545-9450316 FORWARD LENGTH=600	362	600	1.00E-165	165.7	78.2	89.0
Rsa1.0_00886.1.g20857.t11	ref|XP_002876929.1| hypothetical protein ARALYDRAFT_904748 [Arabidopsis lyrata subsp. lyrata] gi|297322767|gb|EFH53188.1| hypothetical protein ARALYDRAFT_904748 [Arabidopsis lyrata subsp. lyrata]	997	587	0	58.9	54.7	56.7	hypothetical protein ARALYDRAFT_904748	gbpln	Arabidopsis lyrata	AT3G25800.1 | Symbols: PDF1, PR 65, PP2AA2 | protein phosphatase 2A subunit A2 | chr3:9422822-9425783 REVERSE LENGTH=587	997	587	0	58.9	54.4	56.6
Rsa1.0_00886.1.g20858.t1	gb|AAM62792.1| unknown [Arabidopsis thaliana]	369	351	1.00E-134	95.1	69.1	78.3	unknown	gbpln	Arabidopsis thaliana	AT3G25790.1 | Symbols: | myb-like transcription factor family protein | chr3:9413196-9414951 FORWARD LENGTH=357	369	357	1.00E-135	96.7	68.0	77.8

Rsa1.0_00886.1.g20859.t1	gb|EOA24619.1| hypothetical protein CARUB_v10017888mg [Capsella rubella]	252	254	1.00E-126	100.8	89.3	93.3	hypothetical protein CARUB_v10017888mg	gbpln	Capsella rubella	AT3G25770.1 | Symbols: AOC2 | allene oxide cyclase 2 | chr3:9406975-9407839 FORWARD LENGTH=253	252	253	1.00E-123	100.4	86.9	90.5
Rsa1.0_00886.1.g20860.t1	gb|EOA25834.1| hypothetical protein CARUB_v10019207mg [Capsella rubella]	681	681	0	100.0	78.4	85.9	hypothetical protein CARUB_v10019207mg	gbpln	Capsella rubella	AT3G25740.1 | Symbols: MAP1B, MAP1C | methionine aminopeptidase 1C | chr3:9397806-9399653 FORWARD LENGTH=344	681	344	1.00E-159	50.5	39.8	43.5
Rsa1.0_00887.1.g20861.t6	ref|NP_001154409.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|240254233|ref|NP_564529.4| protein kinase domain-containing protein [Arabidopsis thaliana] gi|240254235|ref|NP_001031155.4| protein kinase domain-containing protein [Arabidopsis thaliana] gi|332194178|gb|AEE32299.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|332194179|gb|AEE32300.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|332194180|gb|AEE32301.1| protein kinase domain-containing protein [Arabidopsis thaliana]	999	1235	0	123.6	36.3	41.9	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G48490.3 | Symbols: | Protein kinase superfamily protein | chr1:17922345-17928597 REVERSE LENGTH=1235	999	1235	0	123.6	36.3	41.9
Rsa1.0_00887.1.g20862.t9	emb|CAN79325.1| hypothetical protein VITISV_003642 [Vitis vinifera]	1385	1783	0	128.7	31.7	49.4	hypothetical protein VITISV_003642	gbpln	Vitis vinifera	AT1G40087.1 | Symbols: | Plant transposase (Ptta/En/Spm family) | chr1:14999762-15001868 REVERSE LENGTH=390	1385	390	1.00E-131	28.2	16.7	19.4
Rsa1.0_00887.1.g20863.t1	gb|EOA39019.1| hypothetical protein CARUB_v10011565mg [Capsella rubella]	352	354	0	100.6	94.0	98.3	hypothetical protein CARUB_v10011565mg	gbpln	Capsella rubella	AT1G48470.1 | Symbols: GLN1;5 | glutamine synthetase 1;5 | chr1:17913784-17915926 FORWARD LENGTH=353	352	353	0	100.3	91.8	94.3
Rsa1.0_00887.1.g20864.t1	gb|EOA24075.1| hypothetical protein CARUB_v10017303mg [Capsella rubella]	120	430	4.00E-27	358.3	59.2	65.8	hypothetical protein CARUB_v10017303mg	gbpln	Capsella rubella	AT3G58140.1 | Symbols: | phenylalanyl-tRNA synthetase class IIc family protein | chr3:21529988-21532386 REVERSE LENGTH=429	120	429	3.00E-28	357.5	57.5	64.2
Rsa1.0_00887.1.g20865.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	309	1142	5.00E-79	369.6	47.9	61.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	309	626	8.00E-21	202.6	26.2	45.3
Rsa1.0_00887.1.g20866.t1	gb|EOA37329.1| hypothetical protein CARUB_v10011025mg [Capsella rubella]	420	641	3.00E-73	152.6	36.4	41.7	hypothetical protein CARUB_v10011025mg	gbpln	Capsella rubella	AT1G48560.1 | Symbols: | unknown protein; Has 75 Blast hits to 71 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:17952935-17955108 FORWARD LENGTH=643	420	643	4.00E-67	153.1	33.3	39.0
Rsa1.0_00887.1.g20867.t1	dbj|BAB09912.1| MADS-box protein-like [Arabidopsis thaliana]	308	368	2.00E-44	119.5	29.9	40.9	MADS-box protein-like	gbpln	Arabidopsis thaliana	AT5G49420.1 | Symbols: | MADS-box transcription factor family protein | chr5:20035166-20036170 REVERSE LENGTH=334	308	334	8.00E-47	108.4	29.9	40.9
Rsa1.0_00887.1.g20868.t3	ref|NP_175275.3| D-cysteine desulfhydrase [Arabidopsis thaliana] gi|332194169|gb|AEE32290.1| D-cysteine desulfhydrase [Arabidopsis thaliana]	379	401	0	105.8	90.8	95.3	D-cysteine desulfhydrase	gbpln	Arabidopsis thaliana	AT1G48420.1 | Symbols: D-CDES, ATACD1, ACD1 | D-cysteine desulfhydrase | chr1:17896767-17898803 REVERSE LENGTH=401	379	401	0	105.8	90.8	95.3
Rsa1.0_00887.1.g20869.t1	gb|EOA20132.1| hypothetical protein CARUB_v10000420mg [Capsella rubella]	615	651	0	105.9	88.8	94.8	hypothetical protein CARUB_v10000420mg	gbpln	Capsella rubella	AT5G02500.1 | Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 | heat shock cognate protein 70-1 | chr5:554055-556334 REVERSE LENGTH=651	615	651	0	105.9	88.3	94.5
Rsa1.0_00888.1.g20870.t1	ref|XP_002885281.1| ATPLT5 [Arabidopsis lyrata subsp. lyrata] gi|297331121|gb|EFH61540.1| ATPLT5 [Arabidopsis lyrata subsp. lyrata]	528	538	0	101.9	87.7	94.1	ATPLT5	gbpln	Arabidopsis lyrata	AT3G18830.1 | Symbols: ATPLT5, PMT5, ATPMT5 | polyol/monosaccharide transporter 5 | chr3:6489000-6491209 REVERSE LENGTH=539	528	539	0	102.1	87.3	93.9
Rsa1.0_00888.1.g20871.t1	#	#	#	#	#	#	#	-	----	----	AT3G18940.1 | Symbols: | clast3-related | chr3:6527081-6529050 REVERSE LENGTH=281	89	281	2.00E-11	315.7	31.5	38.2
Rsa1.0_00888.1.g20872.t1	ref|XP_002883153.1| hypothetical protein ARALYDRAFT_898258 [Arabidopsis lyrata subsp. lyrata] gi|297328993|gb|EFH59412.1| hypothetical protein ARALYDRAFT_898258 [Arabidopsis lyrata subsp. lyrata]	197	206	1.00E-110	104.6	100.0	100.0	hypothetical protein ARALYDRAFT_898258	gbpln	Arabidopsis lyrata	AT3G18820.1 | Symbols: ATRABG3F, ATRAB7B, RAB71, RABG3F, RAB7B | RAB GTPase homolog G3F | chr3:6484266-6486005 FORWARD LENGTH=206	197	206	1.00E-110	104.6	98.5	99.0
Rsa1.0_00888.1.g20873.t1	ref|XP_002885280.1| hypothetical protein ARALYDRAFT_898257 [Arabidopsis lyrata subsp. lyrata] gi|297331120|gb|EFH61539.1| hypothetical protein ARALYDRAFT_898257 [Arabidopsis lyrata subsp. lyrata]	693	696	0	100.4	68.0	71.9	hypothetical protein ARALYDRAFT_898257	gbpln	Arabidopsis lyrata	AT3G18810.1 | Symbols: | Protein kinase superfamily protein | chr3:6480701-6483593 REVERSE LENGTH=700	693	700	0	101.0	67.2	71.7

Rsa1.0_00888.1.g20874.t1	gb|EOA31115.1| hypothetical protein CARUB_v10014275mg [Capsella rubella] gi|482566927|gb|EOA31116.1| hypothetical protein CARUB_v10014275mg [Capsella rubella]	178	300	7.00E-36	168.5	42.7	44.9	hypothetical protein CARUB_v10014275mg	gbpln	Capsella rubella	AT3G18790.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Isy1-like splicing (InterPro:IPR009360); Has 1147 Blast hits to 965 proteins in 236 species: Archae - 12; Bacteria - 13; Metazoa - 351; Fungi - 230; Plants - 49; Viruses - 9; Other Eukaryotes - 483 (source: NCBI BLink). | chr3:6477853-6478755 FORWARD LENGTH=300	178	300	1.00E-32	168.5	39.3	43.3
Rsa1.0_00888.1.g20875.t1	ref|NP_188508.1| actin 2 [Arabidopsis thaliana] gi|297830536|ref|XP_002883150.1| hypothetical protein ARALYDRAFT_342019 [Arabidopsis lyrata subsp. lyrata] gi|297847210|ref|XP_002891486.1| hypothetical protein ARALYDRAFT_474065 [Arabidopsis lyrata subsp. lyrata] gi|25452790|sp|Q96292.1|ACT2_ARATH RecName: Full=Actin-2 gi|16226780|gb|AAL16260.1|AF428330_1 AT3g18780/MVE11_16 [Arabidopsis thaliana] gi|1669387|gb|AAB37098.1| actin 2 [Arabidopsis thaliana] gi|9293903|dbj|BAB01806.1| actin 2 [Arabidopsis thaliana] gi|17381174|gb|AAL36399.1| putative actin 2 protein [Arabidopsis thaliana] gi|20465835|gb|AAM20022.1| putative actin 2 protein [Arabidopsis thaliana] gi|21593338|gb|AAM65287.1| actin 2 [Arabidopsis thaliana] gi|110740435|dbj|BAF02112.1| actin 2 [Arabidopsis thaliana] gi|222424040|dbj|BAH19981.1| AT3G18780 [Arabidopsis thaliana] gi|241740080|gb|ACS68188.1| actin2.2 [Brassica napus] gi|297328990|gb|EFH59409.1| hypothetical protein ARALYDRAFT_342019 [Arabidopsis lyrata subsp. lyrata]	377	377	0	100.0	100.0	100.0	actin 2	gbpln	Arabidopsis lyrata	AT3G18780.2 | Symbols: ACT2, DER1, LSR2, ENL2 | actin 2 | chr3:6475535-6476832 FORWARD LENGTH=377	377	377	0	100.0	100.0	100.0
Rsa1.0_00888.1.g20876.t1	dbj|BAB01805.1| unnamed protein product [Arabidopsis thaliana]	224	222	4.00E-97	99.1	78.1	85.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT1G49230.1 | Symbols: | RING/U-box superfamily protein | chr1:18209320-18209979 FORWARD LENGTH=219	224	219	6.00E-75	97.8	63.4	72.3
Rsa1.0_00888.1.g20877.t1	dbj|BAJ33918.1| unnamed protein product [Thellungiella halophila]	214	225	7.00E-95	105.1	81.3	88.8	unnamed protein product	----	----	AT3G18773.1 | Symbols: | RING/U-box superfamily protein | chr3:6466304-6466966 FORWARD LENGTH=220	214	220	2.00E-94	102.8	75.2	86.9
Rsa1.0_00888.1.g20878.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00888.1.g20879.t1	gb|EOA28769.1| hypothetical protein CARUB_v10025001mg, partial [Capsella rubella]	587	389	2.00E-81	66.3	30.5	44.3	hypothetical protein CARUB_v10025001mg, partial	gbpln	Capsella rubella	AT3G17530.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6000860-6002026 FORWARD LENGTH=388	587	388	5.00E-84	66.1	29.6	41.4
Rsa1.0_00888.1.g20880.t1	gb|EOA30097.1| hypothetical protein CARUB_v10013207mg [Capsella rubella]	575	629	0	109.4	80.7	88.3	hypothetical protein CARUB_v10013207mg	gbpln	Capsella rubella	AT3G18770.1 | Symbols: | Autophagy-related protein 13 | chr3:6460026-6462510 REVERSE LENGTH=625	575	625	0	108.7	80.0	87.0
Rsa1.0_00888.1.g20881.t1	ref|XP_002885277.1| hypothetical protein ARALYDRAFT_318635 [Arabidopsis lyrata subsp. lyrata] gi|297331117|gb|EFH61536.1| hypothetical protein ARALYDRAFT_318635 [Arabidopsis lyrata subsp. lyrata]	561	571	0	101.8	89.8	93.2	hypothetical protein ARALYDRAFT_318635	gbpln	Arabidopsis lyrata	AT3G18750.3 | Symbols: WNK6 | with no lysine (K) kinase 6 | chr3:6454307-6456830 REVERSE LENGTH=567	561	567	0	101.1	88.2	92.5
Rsa1.0_00888.1.g20882.t1	ref|XP_002883147.1| 60S ribosomal protein L30 [Arabidopsis lyrata subsp. lyrata] gi|297846666|ref|XP_002891214.1| 60S ribosomal protein L30 [Arabidopsis lyrata subsp. lyrata] gi|297328987|gb|EFH59406.1| 60S ribosomal protein L30 [Arabidopsis lyrata subsp. lyrata] gi|297337056|gb|EFH67473.1| 60S ribosomal protein L30 [Arabidopsis lyrata subsp. lyrata]	112	112	1.00E-57	100.0	99.1	100.0	60S ribosomal protein L30	gbpln	Arabidopsis lyrata	AT1G36240.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr1:13614890-13616233 FORWARD LENGTH=112	112	112	1.00E-59	100.0	99.1	99.1

Rsa1.0_00889.1.g20883.t1	ref|XP_002864981.1| hypothetical protein ARALYDRAFT_496816 [Arabidopsis lyrata subsp. lyrata] gi|297310816|gb|EFH41240.1| hypothetical protein ARALYDRAFT_496816 [Arabidopsis lyrata subsp. lyrata]	374	374	1.00E-176	100.0	89.0	93.3	hypothetical protein ARALYDRAFT_496816	gbpln	Arabidopsis lyrata	AT5G65790.1 | Symbols: ATMYB68, MYB68 | myb domain protein 68 | chr5:26323035-26324385 FORWARD LENGTH=374	374	374	1.00E-172	100.0	89.8	93.9
Rsa1.0_00889.1.g20884.t1	ref|NP_680468.1| phosphoenolpyruvate carboxykinase 2 [Arabidopsis thaliana] gi|209529795|gb|ACI49792.1| At5g65690 [Arabidopsis thaliana] gi|332010704|gb|AED98087.1| phosphoenolpyruvate carboxykinase 2 [Arabidopsis thaliana]	667	670	0	100.4	92.2	96.6	phosphoenolpyruvate carboxykinase 2	gbpln	Arabidopsis thaliana	AT5G65690.1 | Symbols: PCK2, PEPCK | phosphoenolpyruvate carboxykinase 2 | chr5:26266477-26269486 FORWARD LENGTH=670	667	670	0	100.4	92.2	96.6
Rsa1.0_00889.1.g20885.t1	gb|EOA12985.1| hypothetical protein CARUB_v10025970mg [Capsella rubella]	707	720	0	101.8	79.3	88.0	hypothetical protein CARUB_v10025970mg	gbpln	Capsella rubella	AT5G65683.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr5:26261472-26263704 FORWARD LENGTH=717	707	717	0	101.4	77.1	87.0
Rsa1.0_00889.1.g20886.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00889.1.g20887.t1	ref|NP_569016.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|75180377|sp|Q9LSK9.1|Y5566_ARATH RecName: Full=Uncharacterized protein At5g65660 gi|8978294|dbj|BAA98185.1| unnamed protein product [Arabidopsis thaliana] gi|21554387|gb|AAM63494.1| unknown [Arabidopsis thaliana] gi|30102568|gb|AAP21202.1| At5g65660 [Arabidopsis thaliana] gi|110743764|dbj|BAE99718.1| hypothetical protein [Arabidopsis thaliana] gi|332010700|gb|AED98083.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	123	136	7.00E-54	110.6	87.8	94.3	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT5G65660.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:26245444-26246245 REVERSE LENGTH=136	123	136	1.00E-56	110.6	87.8	94.3
Rsa1.0_00889.1.g20888.t1	gb|AAM61687.1| unknown [Arabidopsis thaliana]	354	351	2.33E-156	99.2	84.5	89.5	unknown	gbpln	Arabidopsis thaliana	AT5G65640.1 | Symbols: bHLH093 | beta HLH protein 93 | chr5:26237137-26238904 FORWARD LENGTH=351	354	351	1.00E-148	99.2	84.5	89.3
Rsa1.0_00890.1.g20889.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00890.1.g20890.t1	gb|AAF97297.1|AC010164_19 Hypothetical protein [Arabidopsis thaliana]	143	308	2.00E-42	215.4	55.9	70.6	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00890.1.g20891.t1	gb|AAC08049.1| myrosinase-binding protein [Brassica napus]	360	634	1.00E-90	176.1	56.4	68.6	myrosinase-binding protein	gbpln	Brassica napus	AT1G52030.1 | Symbols: MBP2, MBP1.2, F-ATMBP | myrosinase-binding protein 2 | chr1:19346090-19348282 REVERSE LENGTH=642	360	642	3.00E-56	178.3	43.3	56.7
Rsa1.0_00890.1.g20892.t1	gb|AAD15471.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	121	1277	2.00E-11	1055.4	33.1	47.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00890.1.g20893.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1253	1352	0	107.9	39.0	55.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1253	746	5.00E-66	59.5	12.0	16.6
Rsa1.0_00890.1.g20894.t1	gb|EOA39049.1| hypothetical protein CARUB_v10011659mg [Capsella rubella]	930	829	0	89.1	49.0	60.4	hypothetical protein CARUB_v10011659mg	gbpln	Capsella rubella	AT3G16410.1 | Symbols: NSP4 | nitrile specifier protein 4 | chr3:5572145-5574359 FORWARD LENGTH=619	930	619	0	66.6	35.9	46.8
Rsa1.0_00890.1.g20895.t1	gb|EOA27653.1| hypothetical protein CARUB_v10023800mg [Capsella rubella]	93	283	5.00E-18	304.3	48.4	48.4	hypothetical protein CARUB_v10023800mg	gbpln	Capsella rubella	AT1G58684.1 | Symbols: | Ribosomal protein S5 family protein | chr1:21770021-21771217 REVERSE LENGTH=284	93	284	2.00E-20	305.4	47.3	48.4
Rsa1.0_00890.1.g20896.t1	dbj|BAL48824.1| lectin [Arabidopsis thaliana] gi|374346926|dbj|BAL48825.1| lectin [Arabidopsis thaliana] gi|374346930|dbj|BAL48827.1| lectin [Arabidopsis thaliana]	149	157	4.00E-53	105.4	73.8	78.5	lectin	gbpln	Arabidopsis thaliana	AT1G58160.1 | Symbols: | Mannose-binding lectin superfamily protein | chr1:21533757-21534440 FORWARD LENGTH=120	149	120	2.00E-42	80.5	55.7	59.7
Rsa1.0_00890.1.g20897.t1	ref|XP_002894363.1| hypothetical protein ARALYDRAFT_892219 [Arabidopsis lyrata subsp. lyrata] gi|297340205|gb|EFH70622.1| hypothetical protein ARALYDRAFT_892219 [Arabidopsis lyrata subsp. lyrata]	190	188	2.00E-89	98.9	82.6	91.6	hypothetical protein ARALYDRAFT_892219	gbpln	Arabidopsis lyrata	AT1G52200.1 | Symbols: | PLAC8 family protein | chr1:19442271-19443407 REVERSE LENGTH=190	190	190	2.00E-89	100.0	78.9	88.4

Rsa1.0_00890.1.g20898.t1	ref|NP_564603.1| uncharacterized protein [Arabidopsis thaliana] gi|6850346|gb|AAF29409.1|AC022354_8 unknown protein [Arabidopsis thaliana] gi|15294156|gb|AAK95255.1|AF410269_1 At1g52220/F9I5_10 [Arabidopsis thaliana] gi|20453285|gb|AAM19881.1| At1g52220/F9I5_10 [Arabidopsis thaliana] gi|332194648|gb|AEE32769.1| uncharacterized protein AT1G52220 [Arabidopsis thaliana]	146	156	8.00E-61	106.8	82.2	92.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G52220.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: photosystem I P subunit (TAIR:AT2G46820.2); Has 291 Blast hits to 291 proteins in 50 species: Archae - 0; Bacteria - 90; Metazoa - 0; Fungi - 0; Plants - 200; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:19453770-19454605 REVERSE LENGTH=156	146	156	2.00E-63	106.8	82.2	92.5
Rsa1.0_00890.1.g20899.t1	sp|O04006.1|PSAH_BRARA RecName: Full=Photosystem I reaction center subunit VI, chloroplastic; Short=PSI-H; AltName: Full=Light-harvesting complex I 11 kDa protein; Flags: Precursor gi|1916350|gb|AAB51159.1| PSI-H subunit [Brassica rapa]	145	145	2.00E-74	100.0	98.6	99.3	RecName: Full=Photosystem I reaction center subunit VI, chloroplastic; Short=PSI-H; AltName: Full=Light-harvesting complex I 11 kDa protein; Flags: Precursor gi|1916350|gb|AAB51159.1| PSI-H subunit	gbpln	Brassica rapa	AT1G52230.1 | Symbols: PSAH2, PSAH-2, PSI-H | photosystem I subunit H2 | chr1:19454902-19455508 FORWARD LENGTH=145	145	145	1.00E-74	100.0	95.2	97.9
Rsa1.0_00890.1.g20900.t1	ref|XP_002894368.1| hypothetical protein ARALYDRAFT_337379 [Arabidopsis lyrata subsp. lyrata] gi|297340210|gb|EFH70627.1| hypothetical protein ARALYDRAFT_337379 [Arabidopsis lyrata subsp. lyrata]	534	538	0	100.7	89.9	94.4	hypothetical protein ARALYDRAFT_337379	gbpln	Arabidopsis lyrata	AT1G52240.1 | Symbols: ATROPGEF11, ROPGEF11, PIRF1 | RHO guanyl-nucleotide exchange factor 11 | chr1:19455766-19459235 REVERSE LENGTH=607	534	607	0	113.7	87.6	92.1
Rsa1.0_00890.1.g20901.t1	ref|NP_001154419.1| RHO guanyl-nucleotide exchange factor 11 [Arabidopsis thaliana] gi|6850349|gb|AAF29412.1|AC022354_11 dynein light chain, putative [Arabidopsis thaliana] gi|12323118|gb|AAG51538.1|AC037424_3 unknown protein; 73838-74229 [Arabidopsis thaliana] gi|38454092|gb|AAR20740.1| At1g52250 [Arabidopsis thaliana] gi|46402458|gb|AAS92331.1| At1g52250 [Arabidopsis thaliana] gi|332194653|gb|AEE32774.1| RHO guanyl-nucleotide exchange factor 11 [Arabidopsis thaliana]	94	94	1.00E-45	100.0	93.6	96.8	RHO guanyl-nucleotide exchange factor 11	gbpln	Arabidopsis thaliana	AT1G52240.2 | Symbols: ATROPGEF11, ROPGEF11, PIRF1 | RHO guanyl-nucleotide exchange factor 11 | chr1:19458844-19459235 REVERSE LENGTH=94	94	94	2.00E-48	100.0	93.6	96.8
Rsa1.0_00890.1.g20902.t1	ref|XP_002891684.1| hypothetical protein ARALYDRAFT_337380 [Arabidopsis lyrata subsp. lyrata] gi|297337526|gb|EFH67943.1| hypothetical protein ARALYDRAFT_337380 [Arabidopsis lyrata subsp. lyrata]	553	536	0	96.9	78.8	86.4	hypothetical protein ARALYDRAFT_337380	gbpln	Arabidopsis lyrata	AT1G52260.1 | Symbols: ATPDIL1-5, ATPDI3, PDI3, PDIL1-5 | PDI-like 1-5 | chr1:19460694-19463346 FORWARD LENGTH=537	553	537	0	97.1	78.3	86.3

<table>
<tr><td>Rsa1.0_00890.1.g20903.t1</td><td>ref|NP_175638.1| RAB GTPase homolog G3D [Arabidopsis thaliana] gi|297852978|ref|XP_002894370.1| hypothetical protein ARALYDRAFT_474344 [Arabidopsis lyrata subsp. lyrata] gi|75169431|sp|Q9C820.1|RAG3D_ARATH RecName: Full=Ras-related protein RABG3d; Short=AtRABG3d; AltName: Full=Ras-related protein Rab72; Short=AtRab72 gi|12323132|gb|AAG51552.1|AC037424_17 GTP-binding protein RAB7D, putative; 63624-64923 [Arabidopsis thaliana] gi|15718410|dbj|BAB68372.1| AtRab72 [Arabidopsis thaliana] gi|18389228|gb|AAL67057.1| putative GTP-binding protein RAB7D [Arabidopsis thaliana] gi|20465885|gb|AAM20047.1| putative GTP-binding protein RAB7D [Arabidopsis thaliana] gi|297340212|gb|EFH70629.1| hypothetical protein ARALYDRAFT_474344 [Arabidopsis lyrata subsp. lyrata] gi|332194656|gb|AEE32777.1| RAB GTPase homolog G3D [Arabidopsis thaliana]</td><td>206</td><td>206</td><td>1.00E-116</td><td>100.0</td><td>98.5</td><td>99.5</td><td>RAB GTPase homolog G3D</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G52280.1 | Symbols: AtRABG3d, RABG3d | RAB GTPase homolog G3D | chr1:19468150-19469449 REVERSE LENGTH=206</td><td>206</td><td>206</td><td>1.00E-118</td><td>100.0</td><td>98.5</td><td>99.5</td></tr>
<tr><td>Rsa1.0_00890.1.g20904.t1</td><td>gb|EOA21197.1| hypothetical protein CARUB_v10001544mg [Capsella rubella]</td><td>230</td><td>230</td><td>1.00E-127</td><td>100.0</td><td>100.0</td><td>100.0</td><td>hypothetical protein CARUB_v10001544mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G03240.3 | Symbols: UBQ3 | polyubiquitin 3 | chr5:771976-772896 REVERSE LENGTH=306</td><td>230</td><td>306</td><td>1.00E-129</td><td>133.0</td><td>100.0</td><td>100.0</td></tr>
<tr><td>Rsa1.0_00890.1.g20905.t1</td><td>ref|NP_175640.1| 60S ribosomal protein L37-2 [Arabidopsis thaliana] gi|20143906|sp|Q43292.2|RL372_ARATH RecName: Full=60S ribosomal protein L37-2 gi|12323122|gb|AAG51542.1|AC037424_7 60S ribosomal protein L37, putative; 56921-57860 [Arabidopsis thaliana] gi|13877907|gb|AAK44031.1|AF370216_1 putative 60S ribosomal protein L37 [Arabidopsis thaliana] gi|21280805|gb|AAM44969.1| putative 60S ribosomal protein L37 [Arabidopsis thaliana] gi|222423584|dbj|BAH19761.1| AT1G52300 [Arabidopsis thaliana] gi|332194658|gb|AEE32779.1| 60S ribosomal protein L37-2 [Arabidopsis thaliana]</td><td>95</td><td>95</td><td>2.00E-46</td><td>100.0</td><td>98.9</td><td>98.9</td><td>60S ribosomal protein L37-2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G52300.1 | Symbols: | Zinc-binding ribosomal protein family protein | chr1:19475213-19476152 REVERSE LENGTH=95</td><td>95</td><td>95</td><td>4.00E-49</td><td>100.0</td><td>98.9</td><td>98.9</td></tr>
<tr><td>Rsa1.0_00890.1.g20906.t1</td><td>ref|XP_002874584.1| oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297320421|gb|EFH50843.1| oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>362</td><td>362</td><td>1.00E-170</td><td>100.0</td><td>79.0</td><td>87.8</td><td>oxidoreductase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G09670.1 | Symbols: | Oxidoreductase family protein | chr4:6107382-6109049 REVERSE LENGTH=362</td><td>362</td><td>362</td><td>1.00E-172</td><td>100.0</td><td>78.7</td><td>87.6</td></tr>
<tr><td>Rsa1.0_00890.1.g20907.t1</td><td>ref|XP_002891686.1| hypothetical protein ARALYDRAFT_337384 [Arabidopsis lyrata subsp. lyrata] gi|297337528|gb|EFH67945.1| hypothetical protein ARALYDRAFT_337384 [Arabidopsis lyrata subsp. lyrata]</td><td>338</td><td>343</td><td>1.00E-124</td><td>101.5</td><td>74.3</td><td>82.8</td><td>hypothetical protein ARALYDRAFT_337384</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G52315.1 | Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr1:19481212-19482674 FORWARD LENGTH=347</td><td>338</td><td>347</td><td>1.00E-118</td><td>102.7</td><td>72.8</td><td>83.4</td></tr>
<tr><td>Rsa1.0_00890.1.g20908.t1</td><td>ref|XP_002891687.1| hypothetical protein ARALYDRAFT_474348 [Arabidopsis lyrata subsp. lyrata] gi|297337529|gb|EFH67946.1| hypothetical protein ARALYDRAFT_474348 [Arabidopsis lyrata subsp. lyrata]</td><td>743</td><td>800</td><td>0</td><td>107.7</td><td>79.3</td><td>85.2</td><td>hypothetical protein ARALYDRAFT_474348</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G52320.4 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF632 (InterPro:IPR006867); BEST Arabidopsis thaliana protein match is: Protein of unknown function (DUF630 and DUF632) (TAIR:AT5G25590.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:19485399-19487204 FORWARD LENGTH=472</td><td>743</td><td>472</td><td>0</td><td>63.5</td><td>56.8</td><td>59.9</td></tr>
<tr><td>Rsa1.0_00890.1.g20909.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>603</td><td>1142</td><td>1.00E-120</td><td>189.4</td><td>41.3</td><td>58.7</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>603</td><td>575</td><td>4.00E-70</td><td>95.4</td><td>26.4</td><td>45.6</td></tr>
</table>

Rsa1.0_00890.1.g20910.t1	ref|XP_002894375.1| hypothetical protein ARALYDRAFT_474354 [Arabidopsis lyrata subsp. lyrata] gi|297340217|gb|EFH70634.1| hypothetical protein ARALYDRAFT_474354 [Arabidopsis lyrata subsp. lyrata]	284	285	1.00E-134	100.4	83.5	90.5	hypothetical protein ARALYDRAFT_474354	gbpln	Arabidopsis lyrata	AT1G52340.1 | Symbols: ABA2, SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ATSDR1 | NAD(P)-binding Rossmann-fold superfamily protein | chr1:19489997-19491527 REVERSE LENGTH=285	284	285	1.00E-126	100.4	83.1	90.1
Rsa1.0_00890.1.g20911.t1	ref|XP_002894377.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340219|gb|EFH70636.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	234	249	1.00E-97	106.4	83.3	88.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G52343.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32680.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:19494226-19495718 REVERSE LENGTH=249	234	249	4.00E-99	106.4	82.5	88.0
Rsa1.0_00890.1.g20912.t1	ref|NP_175645.1| coatomer subunit beta'-2 [Arabidopsis thaliana] gi|75169434|sp|Q9C827.1|COB22_ARATH RecName: Full=Coatomer subunit beta'-2; AltName: Full=Beta'-coat protein 2; Short=Beta'-COP 2 gi|12323125|gb|AAG51545.1|AC037424_10 coatomer complex subunit, putative; 33791-27676 [Arabidopsis thaliana] gi|332194671|gb|AEE32792.1| coatomer subunit beta'-2 [Arabidopsis thaliana]	948	926	0	97.7	91.5	95.3	coatomer subunit beta'-2	gbpln	Arabidopsis thaliana	AT1G52360.1 | Symbols: | Coatomer, beta' subunit | chr1:19499282-19505397 FORWARD LENGTH=926	948	926	0	97.7	91.5	95.3
Rsa1.0_00890.1.g20913.t1	ref|NP_564606.1| nucleoporin 50 protein [Arabidopsis thaliana] gi|12323129|gb|AAG51549.1|AC037424_14 unknown protein; 23094-21772 [Arabidopsis thaliana] gi|14335002|gb|AAK59765.1| At1g52380/F19K6_4 [Arabidopsis thaliana] gi|16323322|gb|AAL15374.1| At1g52380/F19K6_4 [Arabidopsis thaliana] gi|332194676|gb|AEE32797.1| nucleoporin 50 protein [Arabidopsis thaliana]	413	440	1.00E-156	106.5	77.7	86.0	nucleoporin 50 protein	gbpln	Arabidopsis thaliana	AT1G52380.1 | Symbols: | NUP50 (Nucleoporin 50 kDa) protein | chr1:19509979-19511301 FORWARD LENGTH=440	413	440	1.00E-159	106.5	77.7	86.0
Rsa1.0_00890.1.g20914.t1	gb|EOA13214.1| hypothetical protein CARUB_v10026239mg [Capsella rubella]	215	514	1.00E-71	239.1	73.5	83.3	hypothetical protein CARUB_v10026239mg	gbpln	Capsella rubella	AT5G51670.1 | Symbols: | Protein of unknown function (DUF668) | chr5:20993560-20995096 FORWARD LENGTH=474	215	474	5.00E-68	220.5	71.6	80.5
Rsa1.0_00890.1.g20915.t1	ref|XP_002894386.1| hypothetical protein ARALYDRAFT_337410 [Arabidopsis lyrata subsp. lyrata] gi|297340228|gb|EFH70645.1| hypothetical protein ARALYDRAFT_337410 [Arabidopsis lyrata subsp. lyrata]	132	131	2.00E-53	99.2	85.6	90.2	hypothetical protein ARALYDRAFT_337410	gbpln	Arabidopsis lyrata	AT1G52565.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G15760.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:19580061-19580511 REVERSE LENGTH=129	132	129	2.00E-54	97.7	86.4	89.4
Rsa1.0_00890.1.g20916.t1	ref|NP_175667.1| RHOMBOID-like protein 5 [Arabidopsis thaliana] gi|5903047|gb|AAD55606.1|AC008016_16 F6D8.20 [Arabidopsis thaliana] gi|332194705|gb|AEE32826.1| RHOMBOID-like protein 5 [Arabidopsis thaliana]	314	309	1.00E-160	98.4	88.2	94.6	RHOMBOID-like protein 5	gbpln	Arabidopsis thaliana	AT1G52580.1 | Symbols: ATRBL5, RBL5 | RHOMBOID-like protein 5 | chr1:19587637-19588958 FORWARD LENGTH=309	314	309	1.00E-163	98.4	88.2	94.6
Rsa1.0_00890.1.g20917.t1	gb|EOA28769.1| hypothetical protein CARUB_v10025001mg, partial [Capsella rubella]	265	389	3.00E-40	146.8	37.7	43.4	hypothetical protein CARUB_v10025001mg, partial	gbpln	Capsella rubella	AT3G17540.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6002783-6003973 FORWARD LENGTH=396	265	396	1.00E-40	149.4	34.0	41.5

Rsa1.0_00890.1.g20918.t1	ref|NP_175669.1| signal peptidase, endoplasmic reticulum-type [Arabidopsis thaliana] gi|297847646|ref|XP_002891704.1| hypothetical protein ARALYDRAFT_474386 [Arabidopsis lyrata subsp. lyrata] gi|5903045|gb|AAD55604.1|AC008016_14 Similar to gb|AF108945 signal peptidase 18 kDa subunit from Homo sapiens. ESTs gb|H76629, gb|H76949 and gb|H76216 come from this gene [Arabidopsis thaliana] gi|17381152|gb|AAL36388.1| putative signal peptidase subunit [Arabidopsis thaliana] gi|20465737|gb|AAM20337.1| putative signal peptidase subunit [Arabidopsis thaliana] gi|21536563|gb|AAM60895.1| signal peptidase subunit, putative [Arabidopsis thaliana] gi|297337546|gb|EFH67963.1| hypothetical protein ARALYDRAFT_474386 [Arabidopsis lyrata subsp. lyrata] gi|332194707|gb|AEE32828.1| Peptidase S24/S26A/S26B/S26C family protein [Arabidopsis thaliana]	180	180	3.00E-96	100.0	97.2	98.9	signal peptidase, endoplasmic reticulum-type	gbpln	Arabidopsis lyrata	AT1G52600.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr1:19590612-19592486 FORWARD LENGTH=180	180	180	1.00E-98	100.0	97.2	98.9
Rsa1.0_00890.1.g20919.t1	ref|XP_002891705.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297337547|gb|EFH67964.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	801	823	0	102.7	77.8	87.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G52620.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:19603828-19606287 FORWARD LENGTH=819	801	819	0	102.2	77.0	86.9
Rsa1.0_00890.1.g20920.t1	gb|EOA40269.1| hypothetical protein CARUB_v10008996mg, partial [Capsella rubella]	441	482	0	109.3	91.4	95.7	hypothetical protein CARUB_v10008996mg, partial	gbpln	Capsella rubella	AT1G52630.1 | Symbols: | O-fucosyltransferase family protein | chr1:19606470-19608526 REVERSE LENGTH=439	441	439	0	99.5	90.5	94.8
Rsa1.0_00890.1.g20921.t1	ref|XP_002894392.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297340234|gb|EFH70651.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	529	525	0	99.2	85.4	91.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G52640.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:19608857-19610428 REVERSE LENGTH=523	529	523	0	98.9	85.3	91.1
Rsa1.0_00890.1.g20922.t1	ref|XP_002891706.1| hypothetical protein ARALYDRAFT_337420 [Arabidopsis lyrata subsp. lyrata] gi|297337548|gb|EFH67965.1| hypothetical protein ARALYDRAFT_337420 [Arabidopsis lyrata subsp. lyrata]	373	379	0	101.6	91.7	96.0	hypothetical protein ARALYDRAFT_337420	gbpln	Arabidopsis lyrata	AT1G52660.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:19613475-19614796 FORWARD LENGTH=379	373	379	0	101.6	90.6	96.0
Rsa1.0_00891.1.g20923.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	165	1123	4.00E-28	680.6	36.4	46.1	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00891.1.g20924.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00891.1.g20925.t1	ref|XP_002883963.1| RNA-dependent RNA polymerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329803|gb|EFH60222.1| RNA-dependent RNA polymerase family protein [Arabidopsis lyrata subsp. lyrata]	941	981	0	104.3	74.3	83.6	RNA-dependent RNA polymerase family protein	gbpln	Arabidopsis lyrata	AT2G19930.1 | Symbols: | RNA-dependent RNA polymerase family protein | chr2:8607533-8612441 REVERSE LENGTH=977	941	977	0	103.8	73.0	83.0
Rsa1.0_00891.1.g20926.t3	ref|XP_002883963.1| RNA-dependent RNA polymerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329803|gb|EFH60222.1| RNA-dependent RNA polymerase family protein [Arabidopsis lyrata subsp. lyrata]	1679	981	0	58.4	43.3	48.2	RNA-dependent RNA polymerase family protein	gbpln	Arabidopsis lyrata	AT2G19930.1 | Symbols: | RNA-dependent RNA polymerase family protein | chr2:8607533-8612441 REVERSE LENGTH=977	1679	977	0	58.2	42.6	47.5
Rsa1.0_00891.1.g20927.t1	ref|XP_002886016.1| hypothetical protein ARALYDRAFT_319569 [Arabidopsis lyrata subsp. lyrata] gi|297331856|gb|EFH62275.1| hypothetical protein ARALYDRAFT_319569 [Arabidopsis lyrata subsp. lyrata]	521	521	0	100.0	92.1	95.8	hypothetical protein ARALYDRAFT_319569	gbpln	Arabidopsis lyrata	AT2G19880.2 | Symbols: | Nucleotide-diphospho-sugar transferases superfamily protein | chr2:8581578-8585118 FORWARD LENGTH=520	521	520	0	99.8	91.6	95.6
Rsa1.0_00891.1.g20928.t1	gb|AAM63049.1| unknown [Arabidopsis thaliana]	183	457	5.00E-33	249.7	48.1	55.2	unknown	gbpln	Arabidopsis thaliana	AT4G28430.1 | Symbols: | Reticulon family protein | chr4:14057846-14059772 FORWARD LENGTH=457	183	457	2.00E-35	249.7	48.1	55.2

Rsa1.0_00891.1.g20929.t1	ref|NP_187044.1| protein kinase-like protein [Arabidopsis thaliana] gi|6223639|gb|AAF05853.1|AC011698_4 putative casein kinase [Arabidopsis thaliana] gi|332640493|gb|AEE74014.1| protein kinase-like protein [Arabidopsis thaliana]	107	701	6.00E-21	655.1	50.5	53.3	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT3G03940.1 | Symbols: | Protein kinase family protein | chr3:1014412-1018244 REVERSE LENGTH=701	107	701	9.00E-24	655.1	50.5	53.3
Rsa1.0_00891.1.g20930.t1	gb|EOA30187.1| hypothetical protein CARUB_v10013304mg [Capsella rubella]	564	587	0	104.1	79.6	87.1	hypothetical protein CARUB_v10013304mg	gbpln	Capsella rubella	AT2G19870.1 | Symbols: | tRNA/rRNA methyltransferase (SpoU) family protein | chr2:8576034-8577803 FORWARD LENGTH=589	564	589	0	104.4	77.5	84.4
Rsa1.0_00891.1.g20931.t1	gb|AAL60584.1|AF454962_1 hexokinase [Brassica oleracea]	499	499	0	100.0	96.8	98.6	hexokinase	gbpln	Brassica oleracea	AT4G29130.1 | Symbols: ATHXK1, GIN2, HXK1 | hexokinase 1 | chr4:14352338-14354865 REVERSE LENGTH=496	499	496	0	99.4	88.8	93.4
Rsa1.0_00892.1.g20932.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	1548	1489	0	96.2	52.8	68.9	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1548	1262	1.00E-178	81.5	18.7	25.1
Rsa1.0_00892.1.g20933.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00892.1.g20934.t1	ref|NP_177396.1| lipoxygenase 4 [Arabidopsis thaliana] gi|75309247|sp|Q9FNX8.1|LOX4_ARATH RecName: Full=Lipoxygenase 4, chloroplastic; Short=AtLOX4; AltName: Full=LOX3-like protein; Flags: Precursor gi|12325264|gb|AAG52571.1|AC016529_2 putative lipoxygenase; 4618-640 [Arabidopsis thaliana] gi|11967675|emb|CAC19364.1| lipoxygenase [Arabidopsis thaliana] gi|15810255|gb|AAL07015.1| putative lipoxygenase [Arabidopsis thaliana] gi|20259579|gb|AAM14132.1| putative lipoxygenase [Arabidopsis thaliana] gi|332197213|gb|AEE35334.1| lipoxygenase 4 [Arabidopsis thaliana]	863	926	0	107.3	90.8	95.6	lipoxygenase 4	gbpln	Arabidopsis thaliana	AT1G72520.1 | Symbols: LOX4 | PLAT/LH2 domain-containing lipoxygenase family protein | chr1:27308611-27312589 FORWARD LENGTH=926	863	926	0	107.3	90.8	95.6
Rsa1.0_00892.1.g20935.t1	gb|EOA34366.1| hypothetical protein CARUB_v10021890mg [Capsella rubella]	442	448	0	101.4	86.4	93.0	hypothetical protein CARUB_v10021890mg	gbpln	Capsella rubella	AT1G72540.1 | Symbols: | Protein kinase superfamily protein | chr1:27314932-27316669 REVERSE LENGTH=450	442	450	0	101.8	88.0	93.0
Rsa1.0_00892.1.g20936.t1	gb|AAG51860.1|AC010926_23 putative AP2 domain transcription factor; 79136-76819 [Arabidopsis thaliana]	446	425	0	95.3	74.9	83.9	putative AP2 domain transcription factor; 79136-76819	gbpln	Arabidopsis thaliana	AT1G72570.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:27331381-27333698 FORWARD LENGTH=415	446	415	0	93.0	73.3	81.8
Rsa1.0_00892.1.g20937.t1	gb|AAX35339.1| oxalic acid oxidase [Brassica napus]	208	207	3.00E-96	99.5	92.3	93.8	oxalic acid oxidase	gbpln	Brassica napus	AT1G72610.1 | Symbols: GLP1, ATGER1, GER1 | germin-like protein 1 | chr1:27339302-27339928 REVERSE LENGTH=208	208	208	3.00E-98	100.0	89.9	93.3
Rsa1.0_00892.1.g20938.t1	gb|EOA35867.1| hypothetical protein CARUB_v10021108mg [Capsella rubella]	119	148	7.00E-56	124.4	91.6	94.1	hypothetical protein CARUB_v10021108mg	gbpln	Capsella rubella	AT1G72630.1 | Symbols: ELF4-L2 | ELF4-like 2 | chr1:27344988-27345347 FORWARD LENGTH=119	119	119	3.00E-58	100.0	90.8	95.0
Rsa1.0_00892.1.g20939.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00893.1.g20940.t1	ref|NP_196626.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|79327651|ref|NP_001031869.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|53850555|gb|AAU95454.1| At5g10650 [Arabidopsis thaliana] gi|58652060|gb|AAW80855.1| At5g10650 [Arabidopsis thaliana] gi|332004193|gb|AED91576.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332004194|gb|AED91577.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	456	525	1.00E-138	115.1	69.3	80.3	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G10650.2 | Symbols: | RING/U-box superfamily protein | chr5:3365237-3367263 REVERSE LENGTH=525	456	525	1.00E-140	115.1	69.3	80.3
Rsa1.0_00893.1.g20941.t1	gb|EOA20030.1| hypothetical protein CARUB_v10000304mg [Capsella rubella]	715	741	0	103.6	81.8	87.1	hypothetical protein CARUB_v10000304mg	gbpln	Capsella rubella	AT5G10630.1 | Symbols: | Translation elongation factor EF1A/initiation factor IF2gamma family protein | chr5:3360561-3364414 FORWARD LENGTH=667	715	667	0	93.3	80.4	86.2
Rsa1.0_00893.1.g20942.t1	gb|EOA21978.1| hypothetical protein CARUB_v10002483mg [Capsella rubella]	247	247	1.00E-127	100.0	92.3	95.5	hypothetical protein CARUB_v10002483mg	gbpln	Capsella rubella	AT5G10580.1 | Symbols: | Protein of unknown function, DUF599 | chr5:3347511-3348657 FORWARD LENGTH=246	247	246	1.00E-128	99.6	90.7	94.3

Rsa1.0_00893.1.g20943.t1	ref|NP_196615.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana] gi|75335609|sp|Q9LXA5.1|LRK91_ARATH RecName: Full=L-type lectin-domain containing receptor kinase IX.1; Short=LecRK-IX.1; Flags: Precursor gi|7671450|emb|CAB89390.1| lectin-like protein kinase-like [Arabidopsis thaliana] gi|91806848|gb|ABE66151.1| lectin protein kinase [Arabidopsis thaliana] gi|332004177|gb|AED91560.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana]	653	651	0	99.7	83.8	91.0	concanavalin A-like lectin kinase-like protein	gbpln	Arabidopsis thaliana	AT5G10530.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:3324978-3326933 REVERSE LENGTH=651	653	651	0	99.7	83.8	91.0
Rsa1.0_00893.1.g20944.t1	gb|EOA20560.1| hypothetical protein CARUB_v10000873mg [Capsella rubella]	482	474	0	98.3	82.4	88.6	hypothetical protein CARUB_v10000873mg	gbpln	Capsella rubella	AT5G10520.1 | Symbols: RBK1 | ROP binding protein kinases 1 | chr5:3320584-3322649 REVERSE LENGTH=467	482	467	0	96.9	75.7	84.2
Rsa1.0_00893.1.g20945.t1	ref|XP_002871424.1| hypothetical protein ARALYDRAFT_909007 [Arabidopsis lyrata subsp. lyrata] gi|297317261|gb|EFH47683.1| hypothetical protein ARALYDRAFT_909007 [Arabidopsis lyrata subsp. lyrata]	574	576	0	100.3	89.4	92.3	hypothetical protein ARALYDRAFT_909007	gbpln	Arabidopsis lyrata	AT5G10510.2 | Symbols: AIL6 | AINTEGUMENTA-like 6 | chr5:3315991-3320008 FORWARD LENGTH=581	574	581	0	101.2	89.0	92.9
Rsa1.0_00893.1.g20946.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00893.1.g20947.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00893.1.g20948.t1	gb|AAL85008.1| unknown protein [Arabidopsis thaliana]	453	316	1.00E-161	69.8	61.6	64.5	unknown protein	gbpln	Arabidopsis thaliana	AT5G10460.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:3287822-3289844 FORWARD LENGTH=306	453	306	1.00E-163	67.5	61.6	64.5
Rsa1.0_00893.1.g20949.t1	gb|ADO95308.1| 14-3-3-like protein GF14 Lambda [Eutrema salsugineum]	248	248	1.00E-137	100.0	96.0	98.0	14-3-3-like protein GF14 Lambda	gbpln	Eutrema salsugineum	AT5G10450.1 | Symbols: GRF6, AFT1, 14-3-3lambda | G-box regulating factor 6 | chr5:3284452-3286261 REVERSE LENGTH=248	248	248	1.00E-138	100.0	94.8	97.6
Rsa1.0_00893.1.g20950.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00893.1.g20951.t2	gb|AAZ66942.1| 117M18_23 [Brassica rapa]	342	518	1.00E-142	151.5	76.9	84.2	117M18_23	gbpln	Brassica rapa	AT5G44050.1 | Symbols: | MATE efflux family protein | chr5:17722484-17726209 FORWARD LENGTH=491	342	491	1.00E-138	143.6	72.8	81.6
Rsa1.0_00894.1.g20952.t1	emb|CAA58285.1| cyclin delta-1 [Arabidopsis thaliana]	347	335	2.33E-156	96.5	77.8	81.8	cyclin delta-1	gbpln	Arabidopsis thaliana	AT1G70210.1 | Symbols: CYCD1;1, ATCYCD1;1 | CYCLIN D1;1 | chr1:26440015-26441980 FORWARD LENGTH=339	347	339	2.33E-156	97.7	78.4	82.1
Rsa1.0_00894.1.g20953.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1834	1197	0	65.3	24.8	35.1	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1834	575	5.00E-66	31.4	9.1	14.6
Rsa1.0_00894.1.g20954.t1	ref|XP_002887532.1| hypothetical protein ARALYDRAFT_476560 [Arabidopsis lyrata subsp. lyrata] gi|297333373|gb|EFH63791.1| hypothetical protein ARALYDRAFT_476560 [Arabidopsis lyrata subsp. lyrata]	210	292	2.00E-39	139.0	41.4	47.1	hypothetical protein ARALYDRAFT_476560	gbpln	Arabidopsis lyrata	AT1G74230.1 | Symbols: GR-RBP5 | glycine-rich RNA-binding protein 5 | chr1:27915346-27916857 FORWARD LENGTH=289	210	289	1.00E-41	137.6	41.0	47.1
Rsa1.0_00894.1.g20955.t1	ref|NP_177562.1| uncharacterized protein [Arabidopsis thaliana] gi|12324902|gb|AAG52404.1|AC020579_6 hypothetical protein; 38821-39856 [Arabidopsis thaliana] gi|332197446|gb|AEE35567.1| uncharacterized protein AT1G74220 [Arabidopsis thaliana]	161	316	1.00E-19	196.3	46.6	50.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G74220.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03630.1); Has 383 Blast hits to 347 proteins in 86 species: Archae - 0; Bacteria - 17; Metazoa - 87; Fungi - 65; Plants - 76; Viruses - 2; Other Eukaryotes - 136 (source: NCBI BLink). | chr1:27913099-27914134 REVERSE LENGTH=316	161	316	3.00E-22	196.3	46.6	50.9
Rsa1.0_00894.1.g20956.t1	gb|EOA35749.1| hypothetical protein CARUB_v10020982mg [Capsella rubella]	136	196	2.00E-25	144.1	53.7	66.9	hypothetical protein CARUB_v10020982mg	gbpln	Capsella rubella	AT1G24050.1 | Symbols: | RNA-processing, Lsm domain | chr1:8507057-8508439 FORWARD LENGTH=188	136	188	6.00E-26	138.2	50.7	64.0
Rsa1.0_00894.1.g20957.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	116	149	7.00E-21	128.4	41.4	58.6	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00894.1.g20958.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	503	1023	4.00E-93	203.4	34.2	43.9	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	503	575	3.00E-24	114.3	8.5	12.5

Rsa1.0_00894.1.g20959.t1	ref|XP_002894562.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297340404|gb|EFH70821.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	1139	1031	0	90.5	71.8	78.7	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G56130.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:20994931-21000887 REVERSE LENGTH=1032	1139	1032	0	90.6	70.9	78.7
Rsa1.0_00894.1.g20960.t1	ref|XP_002888765.1| hypothetical protein ARALYDRAFT_894830 [Arabidopsis lyrata subsp. lyrata] gi|297334606|gb|EFH65024.1| hypothetical protein ARALYDRAFT_894830 [Arabidopsis lyrata subsp. lyrata]	772	783	0	101.4	89.6	94.2	hypothetical protein ARALYDRAFT_894830	gbpln	Arabidopsis lyrata	AT1G70300.1 | Symbols: KUP6 | K+ uptake permease 6 | chr1:26477993-26481233 REVERSE LENGTH=782	772	782	0	101.3	89.4	94.4
Rsa1.0_00894.1.g20961.t1	ref|XP_002884056.1| thioredoxin reductase [Arabidopsis lyrata subsp. lyrata] gi|297329896|gb|EFH60315.1| thioredoxin reductase [Arabidopsis lyrata subsp. lyrata]	99	381	1.00E-11	384.8	35.4	36.4	thioredoxin reductase	gbpln	Arabidopsis lyrata	AT2G17420.1 | Symbols: NTRA, ATNTRA, NTR2 | NADPH-dependent thioredoxin reductase A | chr2:7564357-7566219 FORWARD LENGTH=378	99	378	2.00E-14	381.8	35.4	36.4
Rsa1.0_00894.1.g20962.t1	ref|NP_564987.2| equilibrative nucleotide transporter 1 [Arabidopsis thaliana] gi|75161382|sp|Q8VXY7.1|ENT1_ARATH RecName: Full=Equilibrative nucleotide transporter 1; Short=AtENT1; AltName: Full=Nucleoside transporter ENT1 gi|18377783|gb|AAL67041.1| unknown protein [Arabidopsis thaliana] gi|27754746|gb|AAO22816.1| unknown protein [Arabidopsis thaliana] gi|332196925|gb|AEE35046.1| equilibrative nucleotide transporter 1 [Arabidopsis thaliana]	457	450	0	98.5	76.4	83.6	equilibrative nucleotide transporter 1	gbpln	Arabidopsis thaliana	AT1G70330.1 | Symbols: ENT1,AT, ENT1 | equilibrative nucleotide transporter 1 | chr1:26502920-26504360 FORWARD LENGTH=450	457	450	0	98.5	76.4	83.6
Rsa1.0_00894.1.g20963.t1	ref|NP_177192.2| uncharacterized protein [Arabidopsis thaliana] gi|34365593|gb|AAQ65108.1| At1g70350 [Arabidopsis thaliana] gi|51969322|dbj|BAD43353.1| hypothetical protein [Arabidopsis thaliana] gi|51971609|dbj|BAD44469.1| hypothetical protein [Arabidopsis thaliana] gi|332196927|gb|AEE35048.1| uncharacterized protein AT1G70350 [Arabidopsis thaliana]	109	105	9.00E-26	96.3	77.1	86.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G70350.1 | Symbols: | unknown protein; Has 98 Blast hits to 98 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 98; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26507341-26508262 REVERSE LENGTH=105	109	105	1.00E-28	96.3	77.1	86.2
Rsa1.0_00894.1.g20964.t1	ref|XP_002888778.1| hypothetical protein ARALYDRAFT_476161 [Arabidopsis lyrata subsp. lyrata] gi|297334619|gb|EFH65037.1| hypothetical protein ARALYDRAFT_476161 [Arabidopsis lyrata subsp. lyrata]	258	280	1.00E-137	108.5	91.5	95.7	hypothetical protein ARALYDRAFT_476161	gbpln	Arabidopsis lyrata	AT1G70410.1 | Symbols: ATBCA4, BCA4, CA4 | beta carbonic anhydrase 4 | chr1:26534167-26536505 REVERSE LENGTH=258	258	258	1.00E-140	100.0	91.1	94.6
Rsa1.0_00894.1.g20965.t3	ref|XP_002877546.1| hypothetical protein ARALYDRAFT_347817 [Arabidopsis lyrata subsp. lyrata] gi|297323384|gb|EFH53805.1| hypothetical protein ARALYDRAFT_347817 [Arabidopsis lyrata subsp. lyrata]	1441	1022	0	70.9	35.2	45.7	hypothetical protein ARALYDRAFT_347817	gbpln	Arabidopsis lyrata	AT3G47090.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17341512-17344645 REVERSE LENGTH=1009	1441	1009	0	70.0	34.1	45.0
Rsa1.0_00894.1.g20966.t1	ref|XP_002890193.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297336035|gb|EFH66452.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	201	452	2.00E-33	224.9	55.2	64.7	F-box family protein	gbpln	Arabidopsis lyrata	AT1G16930.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:5789987-5791534 FORWARD LENGTH=449	201	449	4.00E-35	223.4	52.7	64.7
Rsa1.0_00894.1.g20967.t6	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1786	1274	0	71.3	28.1	37.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1786	575	4.00E-42	32.2	5.4	8.5
Rsa1.0_00894.1.g20968.t1	pir||A96729 homeotic protein (ATK1), 26548-32058 [imported] - Arabidopsis thaliana gi|12325041|gb|AAG52468.1|AC010796_7 homeotic protein (ATK1); 26548-32058 [Arabidopsis thaliana]	195	311	3.00E-73	159.5	72.8	81.5	homeotic protein (ATK1), 26548-32058	gbpln	Arabidopsis thaliana	AT1G70510.1 | Symbols: KNAT2, ATK1 | KNOTTED-like from Arabidopsis thaliana 2 | chr1:26576635-26582145 FORWARD LENGTH=310	195	310	1.00E-75	159.0	72.8	81.5
Rsa1.0_00894.1.g20969.t1	emb|CAA57122.1| ATK1 [Arabidopsis thaliana] gi|984048|emb|CAA57121.1| ATK1 [Arabidopsis thaliana]	299	311	3.00E-60	104.0	40.1	41.1	ATK1	gbpln	Arabidopsis thaliana	AT1G70510.1 | Symbols: KNAT2, ATK1 | KNOTTED-like from Arabidopsis thaliana 2 | chr1:26576635-26582145 FORWARD LENGTH=310	299	310	2.00E-62	103.7	39.8	41.1
Rsa1.0_00894.1.g20970.t1	gb|EOA33736.1| hypothetical protein CARUB_v10019929mg [Capsella rubella]	638	649	0	101.7	77.1	87.6	hypothetical protein CARUB_v10019929mg	gbpln	Capsella rubella	AT1G70520.1 | Symbols: CRK2 | cysteine-rich RLK (RECEPTOR-like protein kinase) 2 | chr1:26584888-26587334 REVERSE LENGTH=649	638	649	0	101.7	75.7	87.3

Rsa1.0_00894.1.g20971.t1	emb|CAA18463.1| putative protein [Arabidopsis thaliana] gi|7269163|emb|CAB79271.1| putative protein [Arabidopsis thaliana]	240	1240	2.00E-51	516.7	44.2	55.8	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	240	1262	7.00E-54	525.8	44.2	55.8
Rsa1.0_00895.1.g20972.t1	ref|XP_002873800.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319637|gb|EFH50059.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	415	346	1.00E-142	83.4	62.4	66.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G16960.1 | Symbols: | Zinc-binding dehydrogenase family protein | chr5:5574537-5575884 REVERSE LENGTH=346	415	346	1.00E-140	83.4	60.0	64.1
Rsa1.0_00895.1.g20973.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1509	1496	0	99.1	59.1	70.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1509	1262	1.00E-142	83.6	16.0	22.1
Rsa1.0_00895.1.g20974.t2	gb|EOA20473.1| hypothetical protein CARUB_v10000784mg [Capsella rubella]	343	502	1.00E-139	146.4	79.3	82.2	hypothetical protein CARUB_v10000784mg	gbpln	Capsella rubella	AT5G17010.3 | Symbols: | Major facilitator superfamily protein | chr5:5587851-5592332 REVERSE LENGTH=503	343	503	1.00E-140	146.6	79.0	81.6
Rsa1.0_00895.1.g20975.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00895.1.g20976.t1	ref|XP_002871746.1| hypothetical protein ARALYDRAFT_909689 [Arabidopsis lyrata subsp. lyrata] gi|297317583|gb|EFH48005.1| hypothetical protein ARALYDRAFT_909689 [Arabidopsis lyrata subsp. lyrata]	192	1076	6.00E-70	560.4	73.4	75.5	hypothetical protein ARALYDRAFT_909689	gbpln	Arabidopsis lyrata	AT5G17020.1 | Symbols: XPO1A, ATCRM1, ATXPO1, XPO1, HIT2 | exportin 1A | chr5:5594904-5602467 FORWARD LENGTH=1075	192	1075	2.00E-71	559.9	72.4	75.0
Rsa1.0_00895.1.g20977.t1	ref|XP_002866055.1| GAUT12/IRX8/LGT6 [Arabidopsis lyrata subsp. lyrata] gi|297311890|gb|EFH42314.1| GAUT12/IRX8/LGT6 [Arabidopsis lyrata subsp. lyrata]	180	535	1.00E-57	297.2	56.7	58.3	GAUT12/IRX8/LGT6	gbpln	Arabidopsis lyrata	AT5G54690.1 | Symbols: GAUT12, LGT6, IRX8 | galacturonosyltransferase 12 | chr5:22219435-22221769 REVERSE LENGTH=535	180	535	2.00E-59	297.2	56.1	58.3
Rsa1.0_00895.1.g20978.t1	ref|NP_200284.1| autophagy 18F-like protein [Arabidopsis thaliana] gi|75333833|sp|Q9FH32.1|AT18F_ARATH RecName: Full=Autophagy-related protein 18f; Short=AtATG18f gi|10176800|dbj|BAB09939.1| unnamed protein product [Arabidopsis thaliana] gi|332009148|gb|AED96531.1| autophagy 18F-like protein [Arabidopsis thaliana]	685	763	0	111.4	61.8	72.6	autophagy 18F-like protein	gbpln	Arabidopsis thaliana	AT5G54730.1 | Symbols: ATATG18F, ATG18F, G18F | homolog of yeast autophagy 18 (ATG18) F | chr5:22233977-22236804 REVERSE LENGTH=763	685	763	0	111.4	61.8	72.6
Rsa1.0_00895.1.g20979.t1	gb|EOA13973.1| hypothetical protein CARUB_v10027102mg [Capsella rubella]	184	219	6.00E-61	119.0	71.7	76.6	hypothetical protein CARUB_v10027102mg	gbpln	Capsella rubella	AT5G52240.1 | Symbols: MSBP1, ATMP1, AtMAPR5 | membrane steroid binding protein 1 | chr5:21213121-21214557 FORWARD LENGTH=220	184	220	3.00E-58	119.6	66.8	75.0
Rsa1.0_00895.1.g20980.t2	ref|XP_002864354.1| hypothetical protein ARALYDRAFT_918614 [Arabidopsis lyrata subsp. lyrata] gi|297310189|gb|EFH40613.1| hypothetical protein ARALYDRAFT_918614 [Arabidopsis lyrata subsp. lyrata]	340	352	0	103.5	93.8	97.4	hypothetical protein ARALYDRAFT_918614	gbpln	Arabidopsis lyrata	AT5G54770.1 | Symbols: THI1, TZ, THI4 | thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (THI4) | chr5:22246634-22247891 FORWARD LENGTH=349	340	349	0	102.6	92.6	96.2
Rsa1.0_00895.1.g20981.t1	gb|EOA13391.1| hypothetical protein CARUB_v10026437mg [Capsella rubella]	404	432	0	106.9	93.3	96.5	hypothetical protein CARUB_v10026437mg	gbpln	Capsella rubella	AT5G54780.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr5:22248696-22251692 REVERSE LENGTH=432	404	432	0	106.9	92.3	96.3
Rsa1.0_00895.1.g20982.t1	gb|EOA39662.1| hypothetical protein CARUB_v10008304mg [Capsella rubella]	79	840	1.00E-14	1063.3	51.9	58.2	hypothetical protein CARUB_v10008304mg	gbpln	Capsella rubella	AT1G30490.1 | Symbols: PHV, ATHB9 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr1:10796328-10800744 REVERSE LENGTH=841	79	841	4.00E-17	1064.6	51.9	58.2
Rsa1.0_00895.1.g20983.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00895.1.g20984.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00896.1.g20985.t1	gb|AAC28216.1| T24M8.9 gene product [Arabidopsis thaliana] gi|7267147|emb|CAB80815.1| putative protein [Arabidopsis thaliana]	476	463	4.00E-74	97.3	26.3	31.3	T24M8.9 gene product	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	476	530	4.00E-14	111.3	7.8	14.7
Rsa1.0_00896.1.g20986.t1	gb|AAF23228.1|AC013454_15 putative transcriptional regulator [Arabidopsis thaliana]	1064	1132	0	106.4	89.4	92.9	putative transcriptional regulator	gbpln	Arabidopsis thaliana	AT3G06010.1 | Symbols: ATCHR12 | Homeotic gene regulator | chr3:1802435-1807284 REVERSE LENGTH=1102	1064	1102	0	103.6	88.9	92.4

Rsa1.0_00896.1.g20987.t1	ref|NP_187250.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|6671958|gb|AAF23217.1|AC013454_4 hypothetical protein [Arabidopsis thaliana] gi|30102730|gb|AAP21283.1| At3g05990 [Arabidopsis thaliana] gi|110743247|dbj|BAE99514.1| hypothetical protein [Arabidopsis thaliana] gi|332640806|gb|AEE74327.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	534	517	0	96.8	76.0	83.7	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G05990.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:1797116-1799732 REVERSE LENGTH=517	534	517	0	96.8	76.0	83.7
Rsa1.0_00896.1.g20988.t1	ref|XP_002882443.1| hypothetical protein ARALYDRAFT_896702 [Arabidopsis lyrata subsp. lyrata] gi|297328283|gb|EFH58702.1| hypothetical protein ARALYDRAFT_896702 [Arabidopsis lyrata subsp. lyrata]	234	248	1.00E-76	106.0	79.5	87.2	hypothetical protein ARALYDRAFT_896702	gbpln	Arabidopsis lyrata	AT3G05980.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19340.1); Has 202 Blast hits to 202 proteins in 28 species: Archae - 0; Bacteria - 0; Metazoa - 39; Fungi - 4; Plants - 148; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr3:1795514-1796251 FORWARD LENGTH=245	234	245	5.00E-71	104.7	70.1	80.8
Rsa1.0_00896.1.g20989.t1	ref|XP_002884549.1| hypothetical protein ARALYDRAFT_896701 [Arabidopsis lyrata subsp. lyrata] gi|297330389|gb|EFH60808.1| hypothetical protein ARALYDRAFT_896701 [Arabidopsis lyrata subsp. lyrata]	190	189	1.00E-74	99.5	73.7	84.7	hypothetical protein ARALYDRAFT_896701	gbpln	Arabidopsis lyrata	AT3G05975.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:1792145-1792714 REVERSE LENGTH=189	190	189	1.00E-76	99.5	73.2	85.8
Rsa1.0_00896.1.g20990.t1	ref|XP_002884547.1| hypothetical protein ARALYDRAFT_317457 [Arabidopsis lyrata subsp. lyrata] gi|297330387|gb|EFH60806.1| hypothetical protein ARALYDRAFT_317457 [Arabidopsis lyrata subsp. lyrata]	505	507	0	100.4	91.1	96.2	hypothetical protein ARALYDRAFT_317457	gbpln	Arabidopsis lyrata	AT3G05960.1 | Symbols: ATSTP6, STP6 | sugar transporter 6 | chr3:1783587-1785334 REVERSE LENGTH=507	505	507	0	100.4	90.9	96.2
Rsa1.0_00896.1.g20991.t2	ref|XP_002874310.1| hypothetical protein ARALYDRAFT_489475 [Arabidopsis lyrata subsp. lyrata] gi|297320147|gb|EFH50569.1| hypothetical protein ARALYDRAFT_489475 [Arabidopsis lyrata subsp. lyrata]	573	555	0	96.9	93.0	95.8	hypothetical protein ARALYDRAFT_489475	gbpln	Arabidopsis lyrata	AT5G26360.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr5:9255561-9258891 REVERSE LENGTH=555	573	555	0	96.9	93.0	95.8
Rsa1.0_00896.1.g20992.t1	gb|EOA31863.1| hypothetical protein CARUB_v10015090mg [Capsella rubella]	229	229	1.00E-122	100.0	94.3	97.4	hypothetical protein CARUB_v10015090mg	gbpln	Capsella rubella	AT3G05950.1 | Symbols: | RmlC-like cupins superfamily protein | chr3:1781130-1781964 REVERSE LENGTH=229	229	229	1.00E-122	100.0	92.6	96.1
Rsa1.0_00896.1.g20993.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00896.1.g20994.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00896.1.g20995.t1	ref|XP_002882441.1| hypothetical protein ARALYDRAFT_896692 [Arabidopsis lyrata subsp. lyrata] gi|297328281|gb|EFH58700.1| hypothetical protein ARALYDRAFT_896692 [Arabidopsis lyrata subsp. lyrata]	218	219	1.00E-97	100.5	80.7	90.4	hypothetical protein ARALYDRAFT_896692	gbpln	Arabidopsis lyrata	AT3G05930.1 | Symbols: GLP8 | germin-like protein 8 | chr3:1770377-1771183 FORWARD LENGTH=219	218	219	3.00E-98	100.5	79.8	89.4
Rsa1.0_00896.1.g20996.t1	gb|AAM61454.1| unknown [Arabidopsis thaliana]	126	126	4.00E-28	100.0	76.2	79.4	unknown	gbpln	Arabidopsis thaliana	AT3G05920.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1768991-1769522 REVERSE LENGTH=126	126	126	8.00E-31	100.0	76.2	79.4
Rsa1.0_00896.1.g20997.t1	gb|AAF23226.1|AC013454_13 unknown protein [Arabidopsis thaliana] gi|6714403|gb|AAF26092.1|AC012393_18 unknown protein [Arabidopsis thaliana]	366	660	1.00E-45	180.3	31.7	35.8	unknown protein	gbpln	Arabidopsis thaliana	AT3G05900.1 | Symbols: | neurofilament protein-related | chr3:1761408-1763854 REVERSE LENGTH=673	366	673	4.00E-48	183.9	31.7	35.8
Rsa1.0_00896.1.g20998.t1	gb|AFC41201.1| PM-YC3.6-Lti6b [Binary expression vector PM-YC3.6-LTI6b]	55	726	4.00E-23	1320.0	92.7	96.4	PM-YC3.6-Lti6b	----	----	AT3G05890.1 | Symbols: RCI2B | Low temperature and salt responsive protein family | chr3:1758179-1758452 REVERSE LENGTH=54	55	54	4.00E-22	98.2	92.7	96.4
Rsa1.0_00896.1.g20999.t1	ref|NP_180438.2| protein agamous-like 46 [Arabidopsis thaliana] gi|330253067|gb|AEC08161.1| protein agamous-like 46 [Arabidopsis thaliana]	415	329	7.00E-58	79.3	30.4	42.7	protein agamous-like 46	gbpln	Arabidopsis thaliana	AT2G28700.1 | Symbols: AGL46 | AGAMOUS-like 46 | chr2:12317384-12318724 REVERSE LENGTH=329	415	329	2.00E-60	79.3	30.4	42.7
Rsa1.0_00897.1.g21000.t1	ref|NP_172471.1| Ribonuclease H-like protein [Arabidopsis thaliana] gi|332190406|gb|AEE28527.1| Ribonuclease H-like protein [Arabidopsis thaliana]	334	303	2.00E-44	90.7	34.4	46.4	Ribonuclease H-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	334	303	6.00E-47	90.7	34.4	46.4

<table>
<tr><td>Rsa1.0_00897.1.g21001.t2</td><td>ref|NP_194722.2| transcription factor bHLH27 [Arabidopsis thaliana] gi|26450533|dbj|BAC42379.1| putative bHLH transcription factor bHLH027 [Arabidopsis thaliana] gi|29028850|gb|AAO64804.1| At4g29930 [Arabidopsis thaliana] gi|51970544|dbj|BAD43964.1| bHLH transcription factor (bHLH027) – like protein [Arabidopsis thaliana] gi|51970694|dbj|BAD44039.1| bHLH transcription factor (bHLH027) – like protein [Arabidopsis thaliana] gi|110736372|dbj|BAF00155.1| bHLH transcription factor (bHLH027) – like protein [Arabidopsis thaliana] gi|332660294|gb|AEE85694.1| transcription factor bHLH27 [Arabidopsis thaliana]</td><td>206</td><td>254</td><td>1.00E-69</td><td>123.3</td><td>73.3</td><td>79.1</td><td>transcription factor bHLH27</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29930.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:14644108-14647449 FORWARD LENGTH=254</td><td>206</td><td>254</td><td>5.00E-72</td><td>123.3</td><td>73.3</td><td>79.1</td></tr>
<tr><td>Rsa1.0_00897.1.g21002.t1</td><td>ref|NP_194723.1| Pathogenesis-related homeodomain protein [Arabidopsis thaliana] gi|1346790|sp|P48785.1|PRH_ARATH RecName: Full=Pathogenesis-related homeodomain protein; Short=PRHA gi|507220|gb|AAA32843.1| homeodomain protein [Arabidopsis thaliana] gi|2501810|gb|AAC49836.1| PRHA [Arabidopsis thaliana] gi|4914418|emb|CAB43669.1| pathogenesis related homeodomain protein (PRHA) [Arabidopsis thaliana] gi|7269893|emb|CAB79752.1| pathogenesis related homeodomain protein (PRHA) [Arabidopsis thaliana] gi|332660298|gb|AEE85698.1| Pathogenesis-related homeodomain protein [Arabidopsis thaliana]</td><td>854</td><td>796</td><td>0</td><td>93.2</td><td>60.3</td><td>70.6</td><td>Pathogenesis-related homeodomain protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29940.1 | Symbols: PRHA | pathogenesis related homeodomain protein A | chr4:14648346-14652710 REVERSE LENGTH=796</td><td>854</td><td>796</td><td>0</td><td>93.2</td><td>60.3</td><td>70.6</td></tr>
<tr><td>Rsa1.0_00897.1.g21003.t1</td><td>dbj|BAJ34590.1| unnamed protein product [Thellungiella halophila]</td><td>828</td><td>842</td><td>0</td><td>101.7</td><td>84.9</td><td>91.1</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G29950.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr4:14657464-14660370 FORWARD LENGTH=828</td><td>828</td><td>828</td><td>0</td><td>100.0</td><td>80.0</td><td>86.4</td></tr>
<tr><td>Rsa1.0_00897.1.g21004.t1</td><td>ref|NP_567837.1| uncharacterized protein [Arabidopsis thaliana] gi|4914420|emb|CAB43671.1| hypothetical protein [Arabidopsis thaliana] gi|7269895|emb|CAB79754.1| hypothetical protein [Arabidopsis thaliana] gi|20466466|gb|AAM20550.1| unknown protein [Arabidopsis thaliana] gi|21537007|gb|AAM61348.1| unknown [Arabidopsis thaliana] gi|22136434|gb|AAM91295.1| unknown protein [Arabidopsis thaliana] gi|332660302|gb|AEE85702.1| uncharacterized protein AT4G29960 [Arabidopsis thaliana]</td><td>269</td><td>291</td><td>1.00E-101</td><td>108.2</td><td>80.3</td><td>85.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29960.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:14660753-14662274 REVERSE LENGTH=291</td><td>269</td><td>291</td><td>1.00E-103</td><td>108.2</td><td>80.3</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00897.1.g21005.t1</td><td>ref|NP_194729.1| Dihydropterin pyrophosphokinase / Dihydropteroate synthase [Arabidopsis thaliana] gi|4938476|emb|CAB43835.1| dihydropteroate synthase-like protein [Arabidopsis thaliana] gi|7269900|emb|CAB80993.1| dihydropteroate synthase-like protein [Arabidopsis thaliana] gi|192807342|gb|ACF06123.1| At4g30000 [Arabidopsis thaliana] gi|332660306|gb|AEE85706.1| Dihydropterin pyrophosphokinase / Dihydropteroate synthase [Arabidopsis thaliana]</td><td>539</td><td>554</td><td>0</td><td>102.8</td><td>87.4</td><td>93.5</td><td>Dihydropterin pyrophosphokinase / Dihydropteroate synthase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G30000.1 | Symbols: | Dihydropterin pyrophosphokinase / Dihydropteroate synthase | chr4:14670524-14672397 REVERSE LENGTH=554</td><td>539</td><td>554</td><td>0</td><td>102.8</td><td>87.4</td><td>93.5</td></tr>
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Rsa1.0_00897.1_g21006.t1	ref|NP_180139.1| molybdate transporter 1 [Arabidopsis thaliana] gi|75206638|sp|Q9SL95.1|MOT1_ARATH RecName: Full=Molybdate transporter 1; AltName: Full=Sulfate transporter like protein 5.2 gi|4874306|gb|AAD31368.1| hypothetical protein [Arabidopsis thaliana] gi|62320536|dbj|BAD95122.1| hypothetical protein [Arabidopsis thaliana] gi|330252640|gb|AEC07734.1| molybdate transporter 1 [Arabidopsis thaliana]	457	456	0	99.8	87.7	93.4	molybdate transporter 1	gbpln	Arabidopsis thaliana	AT2G25680.1 | Symbols: MOT1 | molybdate transporter 1 | chr2:10933167-10934537 REVERSE LENGTH=456	457	456	0	99.8	87.7	93.4
Rsa1.0_00897.1_g21007.t1	ref|NP_567839.1| PA-domain containing subtilase family protein [Arabidopsis thaliana] gi|4938478|emb|CAB43837.1| proteinase-like protein [Arabidopsis thaliana] gi|7269902|emb|CAB80995.1| AT4g30020 [Arabidopsis thaliana] gi|22655014|gb|AAM98098.1| AT4g30020/F6G3_50 [Arabidopsis thaliana] gi|29028756|gb|AAO64757.1| AT4g30020/F6G3_50 [Arabidopsis thaliana] gi|110740572|dbj|BAE98391.1| hypothetical protein [Arabidopsis thaliana] gi|332660309|gb|AEE85709.1| PA-domain containing subtilase family protein [Arabidopsis thaliana]	816	816	0	100.0	94.2	97.9	PA-domain containing subtilase family protein	gbpln	Arabidopsis thaliana	AT4G30020.1 | Symbols: | PA-domain containing subtilase family protein | chr4:14678251-14681762 FORWARD LENGTH=816	816	816	0	100.0	94.2	97.9
Rsa1.0_00897.1_g21008.t1	gb|EOA17964.1| hypothetical protein CARUB_v10006379mg [Capsella rubella]	433	435	0	100.5	76.7	85.0	hypothetical protein CARUB_v10006379mg	gbpln	Capsella rubella	AT4G30030.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr4:14682210-14683484 REVERSE LENGTH=424	433	424	0	97.9	75.3	84.1
Rsa1.0_00897.1_g21009.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00897.1_g21010.t2	gb|AFD01311.1| auxin response factor 16-1 [Brassica rapa subsp. pekinensis]	632	647	0	102.4	90.8	94.1	auxin response factor 16-1	gbpln	Brassica rapa	AT4G30080.1 | Symbols: ARF16 | auxin response factor 16 | chr4:14703369-14705564 REVERSE LENGTH=670	632	670	0	106.0	90.3	93.8
Rsa1.0_00897.1_g21011.t1	ref|NP_194738.4| protein embryo defective 1353 [Arabidopsis thaliana] gi|332660319|gb|AEE85719.1| protein embryo defective 1353 [Arabidopsis thaliana]	435	388	1.00E-153	89.2	61.8	69.0	protein embryo defective 1353	gbpln	Arabidopsis thaliana	AT4G30090.1 | Symbols: emb1353 | embryo defective 1353 | chr4:14709135-14711612 REVERSE LENGTH=388	435	388	1.00E-156	89.2	61.8	69.0
Rsa1.0_00897.1_g21012.t1	gb|EOA18178.1| hypothetical protein CARUB_v10006656mg [Capsella rubella]	1046	1320	0	126.2	80.8	85.0	hypothetical protein CARUB_v10006656mg	gbpln	Capsella rubella	AT4G30100.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:14714191-14719335 FORWARD LENGTH=1311	1046	1311	0	125.3	80.4	85.3
Rsa1.0_00898.1_g21013.t1	ref|XP_002887483.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333324|gb|EFH63742.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	229	243	1.00E-106	106.1	87.3	93.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G73410.1 | Symbols: ATMYB54, MYB54 | myb domain protein 54 | chr1:27601852-27603038 FORWARD LENGTH=243	229	243	1.00E-108	106.1	86.5	93.4
Rsa1.0_00898.1_g21014.t2	ref|XP_002887484.1| hypothetical protein ARALYDRAFT_895203 [Arabidopsis lyrata subsp. lyrata] gi|297333325|gb|EFH63743.1| hypothetical protein ARALYDRAFT_895203 [Arabidopsis lyrata subsp. lyrata]	823	784	0	95.3	86.8	90.2	hypothetical protein ARALYDRAFT_895203	gbpln	Arabidopsis lyrata	AT1G73430.2 | Symbols: | sec34-like family protein | chr1:27604096-27610829 FORWARD LENGTH=784	823	784	0	95.3	86.5	89.7
Rsa1.0_00898.1_g21015.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1790	1274	0	71.2	38.4	47.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1790	575	2.00E-60	32.1	9.1	14.1
Rsa1.0_00898.1_g21016.t1	ref|XP_002887485.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333326|gb|EFH63744.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	1108	1161	0	104.8	85.1	91.2	kinase family protein	gbpln	Arabidopsis lyrata	AT1G73460.1 | Symbols: | Protein kinase superfamily protein | chr1:27620122-27624899 FORWARD LENGTH=1169	1108	1169	0	105.5	85.4	91.2
Rsa1.0_00898.1_g21017.t2	gb|EOA35116.1| hypothetical protein CARUB_v10020236mg [Capsella rubella]	396	468	0	118.2	86.6	91.7	hypothetical protein CARUB_v10020236mg	gbpln	Capsella rubella	AT1G73480.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:27629266-27632486 FORWARD LENGTH=463	396	463	0	116.9	85.9	91.7
Rsa1.0_00898.1_g21018.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00898.1_g21019.t1	gb|EOA35604.1| hypothetical protein CARUB_v10020817mg, partial [Capsella rubella]	174	261	1.00E-78	150.0	82.2	93.7	hypothetical protein CARUB_v10020817mg, partial	gbpln	Capsella rubella	AT1G73540.1 | Symbols: atnudt21, NUDT21 | nudix hydrolase homolog 21 | chr1:27645880-27646571 REVERSE LENGTH=198	174	198	6.00E-77	113.8	80.5	88.5
Rsa1.0_00898.1_g21020.t1	ref|XP_002888933.1| lipid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297334774|gb|EFH65192.1| lipid binding protein [Arabidopsis lyrata subsp. lyrata]	151	155	2.00E-38	102.6	53.6	74.2	lipid binding protein	gbpln	Arabidopsis lyrata	AT1G73550.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:27647806-27648536 REVERSE LENGTH=152	151	152	2.00E-35	100.7	47.7	65.6

Rsa1.0_00898.1_g21021.t1	gb|ACH91863.1| PIN-FORMED1 [Cardamine hirsuta]	620	623	0	100.5	90.8	93.9	PIN-FORMED1	gbpln	Cardamine hirsuta	AT1G73590.1 | Symbols: PIN1, ATPIN1 | Auxin efflux carrier family protein | chr1:27659772-27662876 FORWARD LENGTH=622	620	622	0	100.3	92.1	94.8
Rsa1.0_00898.1_g21022.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00898.1_g21023.t1	gb|ABK28243.1| unknown [Arabidopsis thaliana]	260	297	6.00E-61	114.2	41.9	65.8	unknown	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	260	332	1.00E-61	127.7	40.8	64.6
Rsa1.0_00898.1_g21024.t3	ref|XP_002887501.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297333342|gb|EFH63760.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	555	512	0	92.3	84.0	87.7	transducin family protein	gbpln	Arabidopsis lyrata	AT1G73720.1 | Symbols: SMU1 | transducin family protein / WD-40 repeat family protein | chr1:27725059-27729722 FORWARD LENGTH=511	555	511	0	92.1	83.1	87.7
Rsa1.0_00898.1_g21025.t1	dbj|BAJ34331.1| unnamed protein product [Thellungiella halophila]	578	585	0	101.2	89.8	95.2	unnamed protein product	----	----	AT1G73730.1 | Symbols: EIL3, SLIM1, ATSLIM, AtEIL3 | ETHYLENE-INSENSITIVE3-like 3 | chr1:27730434-27732363 REVERSE LENGTH=567	578	567	0	98.1	85.3	90.3
Rsa1.0_00898.1_g21026.t1	ref|XP_002887503.1| glycosyl transferase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297333344|gb|EFH63762.1| glycosyl transferase family 28 protein [Arabidopsis lyrata subsp. lyrata]	436	435	0	99.8	83.9	92.7	glycosyl transferase family 28 protein	gbpln	Arabidopsis lyrata	AT1G73740.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:27734451-27736008 FORWARD LENGTH=431	436	431	0	98.9	83.9	91.3
Rsa1.0_00898.1_g21027.t1	ref|NP_565071.1| esterase/lipase domain-containing protein [Arabidopsis thaliana] gi|16930505|gb|AAL31938.1|AF419606_1 At1g73750/F25P22_17 [Arabidopsis thaliana] gi|21360473|gb|AAM47352.1| At1g73750/F25P22_17 [Arabidopsis thaliana] gi|332197383|gb|AEE35504.1| esterase/lipase domain-containing protein [Arabidopsis thaliana]	450	452	0	100.4	80.7	89.3	esterase/lipase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G73750.1 | Symbols: | Uncharacterised conserved protein UCP031088, alpha/beta hydrolase | chr1:27736659-27738887 FORWARD LENGTH=452	450	452	0	100.4	80.7	89.3
Rsa1.0_00898.1_g21028.t4	ref|XP_002877484.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323322|gb|EFH53743.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	277	494	4.00E-37	178.3	32.1	36.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G46450.1 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr3:17093297-17095319 REVERSE LENGTH=486	277	486	1.00E-36	175.5	29.6	33.9
Rsa1.0_00898.1_g21029.t1	gb|ADK63390.1| C3HC4 type zinc finger protein [Brassica rapa]	362	346	1.00E-140	95.6	72.7	79.8	C3HC4 type zinc finger protein	gbpln	Brassica rapa	AT1G73760.1 | Symbols: | RING/U-box superfamily protein | chr1:27739366-27741161 REVERSE LENGTH=367	362	367	1.00E-134	101.4	68.5	81.8
Rsa1.0_00898.1_g21030.t1	ref|NP_177519.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|12324219|gb|AAG52085.1|AC012679_23 putative lipid transfer protein; 71816-72112 [Arabidopsis thaliana] gi|332197387|gb|AEE35508.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	98	98	1.00E-35	100.0	73.5	82.7	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT1G73780.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:27743872-27744168 FORWARD LENGTH=98	98	98	2.00E-38	100.0	73.5	82.7
Rsa1.0_00898.1_g21031.t1	ref|XP_004235364.1| PREDICTED: mitotic-spindle organizing protein 1B-like [Solanum lycopersicum]	70	76	1.00E-21	108.6	72.9	85.7	PREDICTED: mitotic-spindle organizing protein 1B-like	gbpln	Solanum lycopersicum	AT1G73790.1 | Symbols: | Protein of unknown function (DUF3743) | chr1:27745019-27745222 FORWARD LENGTH=67	70	67	3.00E-24	95.7	72.9	81.4
Rsa1.0_00898.1_g21032.t1	ref|XP_002888946.1| hypothetical protein ARALYDRAFT_895244 [Arabidopsis lyrata subsp. lyrata] gi|297334787|gb|EFH65205.1| hypothetical protein ARALYDRAFT_895244 [Arabidopsis lyrata subsp. lyrata]	460	449	0	97.6	73.7	83.9	hypothetical protein ARALYDRAFT_895244	gbpln	Arabidopsis lyrata	AT1G73805.1 | Symbols: | Calmodulin binding protein-like | chr1:27745761-27749178 REVERSE LENGTH=451	460	451	0	98.0	73.3	83.3
Rsa1.0_00899.1_g21033.t3	ref|NP_197803.1| Squalene monooxygenase 1,1 [Arabidopsis thaliana] gi|11467948|sp|O65404.2|ERG11_ARATH RecName: Full=Squalene monooxygenase 1,1; AltName: Full=Squalene epoxidase 1,1; Short=SE 1,1 gi|9757924|dbj|BAB08406.1| squalene monooxygenase [Arabidopsis thaliana] gi|222422883|dbj|BAH19428.1| AT5G24150 [Arabidopsis thaliana] gi|332005879|gb|AED93262.1| Squalene monooxygenase 1,1 [Arabidopsis thaliana]	475	516	0	108.6	69.3	83.8	Squalene monooxygenase 1,1	gbpln	Arabidopsis thaliana	AT5G24150.1 | Symbols: SQP1, SQE5 | FAD/NAD(P)-binding oxidoreductase family protein | chr5:8172594-8175395 REVERSE LENGTH=516	475	516	0	108.6	69.3	83.8

Rsa1.0_00899.1.g21034.t1	ref|NP_179633.2| ROP-interactive CRIB motif-containing protein 6 [Arabidopsis thaliana] gi|91806212|gb|ABE65834.1| p21-rho-binding domain-containing protein [Arabidopsis thaliana] gi|330251912|gb|AEC07006.1| ROP-interactive CRIB motif-containing protein 6 [Arabidopsis thaliana]	203	212	3.00E-76	104.4	79.3	87.2	ROP-interactive CRIB motif-containing protein 6	gbpln	Arabidopsis thaliana	AT2G20430.1 | Symbols: RIC6 | ROP-interactive CRIB motif-containing protein 6 | chr2:8808667-8809781 REVERSE LENGTH=212	203	212	1.00E-78	104.4	79.3	87.2
Rsa1.0_00899.1.g21035.t1	ref|XP_002884197.1| hypothetical protein ARALYDRAFT_480864 [Arabidopsis lyrata subsp. lyrata] gi|297330037|gb|EFH60456.1| hypothetical protein ARALYDRAFT_480864 [Arabidopsis lyrata subsp. lyrata]	128	127	1.00E-50	99.2	76.6	85.9	hypothetical protein ARALYDRAFT_480864	gbpln	Arabidopsis lyrata	AT2G20362.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G63310.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:8789772-8790155 FORWARD LENGTH=127	128	127	6.00E-53	99.2	75.8	86.7
Rsa1.0_00899.1.g21036.t1	ref|XP_002884196.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330036|gb|EFH60455.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata]	403	402	0	99.8	94.0	96.8	catalytic/ coenzyme binding protein	gbpln	Arabidopsis lyrata	AT2G20360.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:8786070-8789098 FORWARD LENGTH=402	403	402	0	99.8	93.8	96.5
Rsa1.0_00899.1.g21037.t1	ref|XP_002884194.1| hypothetical protein ARALYDRAFT_900384 [Arabidopsis lyrata subsp. lyrata] gi|297330034|gb|EFH60453.1| hypothetical protein ARALYDRAFT_900384 [Arabidopsis lyrata subsp. lyrata]	220	479	9.00E-71	217.7	56.8	60.5	hypothetical protein ARALYDRAFT_900384	gbpln	Arabidopsis lyrata	AT2G20340.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr2:8779804-8782490 FORWARD LENGTH=490	220	490	8.00E-72	222.7	55.9	60.0
Rsa1.0_00899.1.g21038.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00899.1.g21039.t1	ref|XP_002886272.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297332112|gb|EFH62531.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	340	743	1.00E-150	218.5	75.9	78.5	kinase family protein	gbpln	Arabidopsis lyrata	AT2G20300.1 | Symbols: ALE2 | Protein kinase superfamily protein | chr2:8756475-8759845 REVERSE LENGTH=744	340	744	1.00E-153	218.8	75.9	78.2
Rsa1.0_00899.1.g21040.t1	gb|EOA30837.1| hypothetical protein CARUB_v10013982mg [Capsella rubella]	426	370	1.00E-155	86.9	64.8	66.4	hypothetical protein CARUB_v10013982mg	gbpln	Capsella rubella	AT2G20280.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr2:8740054-8742349 REVERSE LENGTH=371	426	371	1.00E-157	87.1	64.3	66.2
Rsa1.0_00899.1.g21041.t1	ref|XP_002873362.1| hypothetical protein ARALYDRAFT_908808 [Arabidopsis lyrata subsp. lyrata] gi|297319199|gb|EFH49621.1| hypothetical protein ARALYDRAFT_908808 [Arabidopsis lyrata subsp. lyrata]	751	726	0	96.7	51.9	68.6	hypothetical protein ARALYDRAFT_908808	gbpln	Arabidopsis lyrata	AT4G12570.1 | Symbols: UPL5 | ubiquitin protein ligase 5 | chr4:7445585-7448819 FORWARD LENGTH=873	751	873	1.00E-123	116.2	37.8	58.2
Rsa1.0_00899.1.g21042.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00899.1.g21043.t1	ref|XP_002871344.1| hypothetical protein ARALYDRAFT_908827 [Arabidopsis lyrata subsp. lyrata] gi|297317181|gb|EFH47603.1| hypothetical protein ARALYDRAFT_908827 [Arabidopsis lyrata subsp. lyrata]	277	630	2.00E-71	227.4	55.6	68.6	hypothetical protein ARALYDRAFT_908827	gbpln	Arabidopsis lyrata	AT1G76810.1 | Symbols: | eukaryotic translation initiation factor 2 (eIF-2) family protein | chr1:28831366-28836310 REVERSE LENGTH=1294	277	1294	2.00E-51	467.1	43.7	63.2
Rsa1.0_00900.1.g21044.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00900.1.g21045.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00900.1.g21046.t1	gb|AAM63624.1| DnaJ protein, putative [Arabidopsis thaliana]	154	156	3.00E-71	101.3	90.9	94.2	DnaJ protein, putative	gbpln	Arabidopsis thaliana	AT1G56300.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:21079022-21080168 REVERSE LENGTH=156	154	156	2.00E-72	101.3	89.6	93.5
Rsa1.0_00900.1.g21047.t2	ref|XP_002894636.1| hypothetical protein ARALYDRAFT_337810 [Arabidopsis lyrata subsp. lyrata] gi|297340478|gb|EFH70895.1| hypothetical protein ARALYDRAFT_337810 [Arabidopsis lyrata subsp. lyrata]	252	163	1.00E-52	64.7	42.9	46.8	hypothetical protein ARALYDRAFT_337810	gbpln	Arabidopsis lyrata	AT1G56320.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Glycine-rich protein family (TAIR:AT5G49350.2); Has 60 Blast hits to 60 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 60; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:21085722-21086459 REVERSE LENGTH=163	252	163	2.00E-53	64.7	42.9	46.0
Rsa1.0_00900.1.g21048.t1	sp|O04267.1|SAR1B_BRACM RecName: Full=GTP-binding protein SAR1B gi|2108347|gb|AAC49717.1| small GTP-binding protein Bsar1b [Brassica rapa subsp. oleifera]	195	195	1.00E-108	100.0	97.9	99.5	RecName: Full=GTP-binding protein SAR1B gi|2108347|gb|AAC49717.1| small GTP-binding protein Bsar1b	gbpln	Brassica rapa	AT1G56330.1 | Symbols: SAR1, ATSAR1, ATSARA1B, ATSAR1B, SAR1B | secretion-associated RAS 1B | chr1:21086845-21088478 REVERSE LENGTH=193	195	193	1.00E-109	99.0	97.4	98.5

Rsa1.0_00900.1.g21049.t1	emb|CCD74507.1| hypothetical protein [Arabidopsis halleri subsp. halleri]	193	185	3.00E−70	95.9	76.7	80.3	hypothetical protein	gbpln	Arabidopsis halleri	AT1G56420.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G12530.1); Has 58 Blast hits to 58 proteins in 16 species: Archae − 0; Bacteria − 2; Metazoa − 0; Fungi − 0; Plants − 54; Viruses − 0; Other Eukaryotes − 2 (source: NCBI BLink). | chr1:21122772−21124234 REVERSE LENGTH=183	193	183	7.00E−69	94.8	74.1	78.8
Rsa1.0_00900.1.g21050.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00900.1.g21051.t5	ref|XP_002894647.1| hypothetical protein ARALYDRAFT_474807 [Arabidopsis lyrata subsp. lyrata] gi|297340489|gb|EFH70906.1| hypothetical protein ARALYDRAFT_474807 [Arabidopsis lyrata subsp. lyrata]	608	472	0	77.6	56.1	62.3	hypothetical protein ARALYDRAFT_474807	gbpln	Arabidopsis lyrata	AT1G56440.1 | Symbols: TPR5 | Tetratricopeptide repeat (TPR)−like superfamily protein | chr1:21138765−21141482 REVERSE LENGTH=476	608	476	0	78.3	57.6	63.2
Rsa1.0_00900.1.g21052.t1	gb|EOA35645.1| hypothetical protein CARUB_v10020862mg [Capsella rubella]	256	245	1.00E−133	95.7	89.8	94.5	hypothetical protein CARUB_v10020862mg	gbpln	Capsella rubella	AT1G56450.1 | Symbols: PBG1 | 20S proteasome beta subunit G1 | chr1:21141970−21144186 FORWARD LENGTH=246	256	246	1.00E−132	96.1	87.9	93.4
Rsa1.0_00900.1.g21053.t1	gb|AAG51247.1|AC055769_6 copia−type polyprotein, putative; 28768−32772 [Arabidopsis thaliana]	1340	1334	0	99.6	69.0	82.5	copia−type polyprotein, putative; 28768−32772	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1340	1262	1.00E−104	94.2	14.0	22.7
Rsa1.0_00900.1.g21054.t1	ref|NP_176041.2| HIT zinc finger and PAPA−1−like domain−containing protein [Arabidopsis thaliana] gi|26450456|dbj|BAC42342.1| unknown protein [Arabidopsis thaliana] gi|332195277|gb|AEE33398.1| HIT zinc finger and PAPA−1−like domain−containing protein [Arabidopsis thaliana]	447	502	1.00E−164	112.3	81.0	87.9	HIT zinc finger and PAPA−1−like domain−containing protein	gbpln	Arabidopsis thaliana	AT1G56460.1 | Symbols: | HIT zinc finger ;PAPA−1−like conserved region | chr1:21146765−21149468 FORWARD LENGTH=502	447	502	1.00E−166	112.3	81.0	87.9
Rsa1.0_00900.1.g21055.t1	emb|CCD74494.1| hypothetical protein [Arabidopsis halleri subsp. halleri]	169	352	5.00E−61	208.3	69.2	81.1	hypothetical protein	gbpln	Arabidopsis halleri	AT3G24130.1 | Symbols: | Pectin lyase−like superfamily protein | chr3:8711663−8713361 REVERSE LENGTH=335	169	335	4.00E−36	198.2	44.4	63.9
Rsa1.0_00900.1.g21056.t1	ref|NP_564720.1| uncharacterized protein [Arabidopsis thaliana] gi|9954754|gb|AAG09105.1|AC009323_16 Unknown protein [Arabidopsis thaliana] gi|16648669|gb|AAL25527.1| At1g56580/F25P12_18 [Arabidopsis thaliana] gi|20856239|gb|AAM26655.1| At1g56580/F25P12_18 [Arabidopsis thaliana] gi|332195290|gb|AEE33411.1| uncharacterized protein AT1G56580 [Arabidopsis thaliana]	166	166	5.00E−82	100.0	92.2	94.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G56580.1 | Symbols: SVB | Protein of unknown function, DUF538 | chr1:21198402−21198902 REVERSE LENGTH=166	166	166	2.00E−84	100.0	92.2	94.6
Rsa1.0_00901.1.g21057.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	255	1161	2.00E−65	455.3	45.5	64.3	F14N23.4	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr4:2353989−2355213 REVERSE LENGTH=332	255	332	3.00E−67	130.2	43.9	62.0
Rsa1.0_00901.1.g21058.t1	gb|EOA22775.1| hypothetical protein CARUB_v10003489mg [Capsella rubella]	262	365	1.00E−126	139.3	84.0	90.5	hypothetical protein CARUB_v10003489mg	gbpln	Capsella rubella	AT4G01430.1 | Symbols: | nodulin MtN21 /EamA−like transporter family protein | chr4:585707−587846 FORWARD LENGTH=365	262	365	1.00E−125	139.3	84.0	90.5
Rsa1.0_00901.1.g21059.t1	gb|AAC67205.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	2545	1413	0	55.5	27.8	34.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	2545	1262	6.00E−31	49.6	3.1	4.6
Rsa1.0_00901.1.g21060.t1	gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]	366	863	2.00E−39	235.8	21.3	26.5	Ulp1 protease family protein	gbpln	Brassica oleracea	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301−18475574 FORWARD LENGTH=921	366	921	2.00E−23	251.6	12.8	20.5
Rsa1.0_00901.1.g21061.t1	gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]	117	863	3.00E−18	737.6	38.5	47.0	Ulp1 protease family protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00901.1.g21062.t1	dbj|BAB11196.1| mutator−like transposase [Arabidopsis thaliana]	143	797	9.00E−13	557.3	35.0	53.8	mutator−like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00901.1.g21063.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00901.1.g21064.t1	dbj|BAB01350.1| Mutator−like transposase [Arabidopsis thaliana]	756	811	1.00E−141	107.3	40.5	56.7	Mutator−like transposase	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798−18484233 REVERSE LENGTH=785	756	785	2.00E−19	103.8	13.4	22.1
Rsa1.0_00901.1.g21065.t1	emb|CAB43910.1| putative protein [Arabidopsis thaliana] gi|7269794|emb|CAB79654.1| putative protein [Arabidopsis thaliana]	673	493	2.00E−35	73.3	13.5	21.2	putative protein	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083−2539985 FORWARD LENGTH=249	673	249	1.00E−18	37.0	9.1	11.3

Rsa1.0_00901.1.g21066.t1	ref|XP_002872894.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318731|gb|EFH49153.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	130	1162	8.00E-32	893.8	54.6	57.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G01400.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: COG4 transport (InterPro:IPR013167); Has 465 Blast hits to 425 proteins in 199 species: Archae - 0; Bacteria - 3; Metazoa - 153; Fungi - 166; Plants - 45; Viruses - 0; Other Eukaryotes - 98 (source: NCBI BLink). | chr4:573098-575648 REVERSE LENGTH=738	130	738	5.00E-32	567.7	51.5	55.4
Rsa1.0_00902.1.g21067.t4	dbj|BAJ33974.1| unnamed protein product [Thellungiella halophila]	556	622	0	111.9	89.7	95.5	unnamed protein product	----	----	AT1G69870.1 | Symbols: NRT1.7 | nitrate transporter 1.7 | chr1:26316208-26320097 FORWARD LENGTH=620	556	620	0	111.5	85.8	93.0
Rsa1.0_00902.1.g21068.t1	ref|XP_002863112.1| thioredoxin H-type 8 [Arabidopsis lyrata subsp. lyrata] gi|297308934|gb|EFH39371.1| thioredoxin H-type 8 [Arabidopsis lyrata subsp. lyrata]	147	148	2.00E-52	100.7	70.7	81.0	thioredoxin H-type 8	gbpln	Arabidopsis lyrata	AT1G69880.1 | Symbols: ATH8, TH8 | thioredoxin H-type 8 | chr1:26321540-26322794 FORWARD LENGTH=148	147	148	1.00E-52	100.7	69.4	79.6
Rsa1.0_00902.1.g21069.t1	ref|XP_002863112.1| thioredoxin H-type 8 [Arabidopsis lyrata subsp. lyrata] gi|297308934|gb|EFH39371.1| thioredoxin H-type 8 [Arabidopsis lyrata subsp. lyrata]	140	148	1.00E-50	105.7	70.0	83.6	thioredoxin H-type 8	gbpln	Arabidopsis lyrata	AT1G69880.1 | Symbols: ATH8, TH8 | thioredoxin H-type 8 | chr1:26321540-26322794 FORWARD LENGTH=148	140	148	2.00E-51	105.7	70.7	83.6
Rsa1.0_00902.1.g21070.t1	ref|XP_002863106.1| hypothetical protein ARALYDRAFT_920363 [Arabidopsis lyrata subsp. lyrata] gi|297308928|gb|EFH39365.1| hypothetical protein ARALYDRAFT_920363 [Arabidopsis lyrata subsp. lyrata]	295	284	1.00E-127	96.3	81.7	87.5	hypothetical protein ARALYDRAFT_920363	gbpln	Arabidopsis lyrata	AT1G69890.1 | Symbols: | Protein of unknown function (DUF569) | chr1:26323426-26324527 REVERSE LENGTH=279	295	279	1.00E-128	94.6	80.7	87.5
Rsa1.0_00902.1.g21071.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1378	1307	0	94.8	59.1	73.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1378	1262	1.00E-105	91.6	14.9	23.8
Rsa1.0_00902.1.g21072.t1	gb|AAG52555.1|AC010675_3 putative protein kinase; 23181-21271 [Arabidopsis thaliana]	625	625	0	100.0	83.0	89.4	putative protein kinase; 23181-21271	gbpln	Arabidopsis thaliana	AT1G69910.1 | Symbols: | Protein kinase superfamily protein | chr1:26330166-26332076 FORWARD LENGTH=636	625	636	0	101.8	84.0	90.4
Rsa1.0_00902.1.g21073.t1	ref|XP_002879929.1| hypothetical protein ARALYDRAFT_483212 [Arabidopsis lyrata subsp. lyrata] gi|297325768|gb|EFH56188.1| hypothetical protein ARALYDRAFT_483212 [Arabidopsis lyrata subsp. lyrata]	169	148	2.00E-39	87.6	52.7	64.5	hypothetical protein ARALYDRAFT_483212	gbpln	Arabidopsis lyrata	AT2G41390.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr2:17257416-17257862 FORWARD LENGTH=148	169	148	1.00E-39	87.6	50.9	61.5
Rsa1.0_00902.1.g21074.t1	ref|XP_002863104.1| hypothetical protein ARALYDRAFT_920359 [Arabidopsis lyrata subsp. lyrata] gi|297308926|gb|EFH39363.1| hypothetical protein ARALYDRAFT_920359 [Arabidopsis lyrata subsp. lyrata]	230	254	1.00E-108	110.4	80.4	89.1	hypothetical protein ARALYDRAFT_920359	gbpln	Arabidopsis lyrata	AT1G69920.1 | Symbols: ATGSTU12, GSTU12 | glutathione S-transferase TAU 12 | chr1:26334395-26335537 REVERSE LENGTH=254	230	254	1.00E-109	110.4	79.1	89.1
Rsa1.0_00902.1.g21075.t1	ref|XP_002863103.1| hypothetical protein ARALYDRAFT_497157 [Arabidopsis lyrata subsp. lyrata] gi|297308925|gb|EFH39362.1| hypothetical protein ARALYDRAFT_497157 [Arabidopsis lyrata subsp. lyrata]	234	234	1.00E-129	100.0	95.3	98.3	hypothetical protein ARALYDRAFT_497157	gbpln	Arabidopsis lyrata	AT1G69930.1 | Symbols: ATGSTU11, GSTU11 | glutathione S-transferase TAU 11 | chr1:26337735-26338690 REVERSE LENGTH=234	234	234	1.00E-129	100.0	93.6	96.2
Rsa1.0_00902.1.g21076.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	626	657	0	105.0	53.4	67.3	T14P8.10	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	626	746	2.00E-65	119.2	21.9	31.2

Rsa1.0_00902.1.g21077.t1	ref|NP_177158.1| myb-like transcription factor-like protein [Arabidopsis thaliana] gi|334183796|ref|NP_001185359.1| myb-like transcription factor-like protein [Arabidopsis thaliana] gi|2194137|gb|AAB61112.1| ESTs gb|R29947,gb|H76702 come from this gene [Arabidopsis thaliana] gi|30102606|gb|AAP21221.1| At1g70000 [Arabidopsis thaliana] gi|41618912|gb|AAS09979.1| MYB transcription factor [Arabidopsis thaliana] gi|110743721|dbj|BAE99697.1| hypothetical protein [Arabidopsis thaliana] gi|332196886|gb|AEE35007.1| myb-like transcription factor-like protein [Arabidopsis thaliana] gi|332196887|gb|AEE35008.1| myb-like transcription factor-like protein [Arabidopsis thaliana]	244	261	3.00E-85	107.0	80.7	86.1	myb-like transcription factor-like protein	gbpln	Arabidopsis thaliana	AT1G70000.2 | Symbols: | myb-like transcription factor family protein | chr1:26363674-26364635 REVERSE LENGTH=261	244	261	1.00E-87	107.0	80.7	86.1
Rsa1.0_00903.1.g21078.t1	gb|AAA51659.1| cyclin [Brassica napus]	430	434	0	100.9	90.9	94.4	cyclin	gbpln	Brassica napus	AT1G15570.1 | Symbols: CYCA2;3 | CYCLIN A2;3 | chr1:5363034-5365218 FORWARD LENGTH=450	430	450	0	104.7	83.7	89.3
Rsa1.0_00903.1.g21079.t1	ref|NP_178156.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|12324974|gb|AAG52430.1|AC018848_1 putative RING zinc finger protein; 53384-54880 [Arabidopsis thaliana] gi|17065538|gb|AAL32923.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|23197724|gb|AAN15389.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|222423453|dbj|BAH19697.1| AT1G80400 [Arabidopsis thaliana] gi|332198277|gb|AEE36398.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	256	407	1.00E-34	159.0	38.3	55.1	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT1G80400.1 | Symbols: | RING/U-box superfamily protein | chr1:30225864-30227360 FORWARD LENGTH=407	256	407	3.00E-37	159.0	38.3	55.1
Rsa1.0_00903.1.g21080.t1	ref|NP_173013.1| uncharacterized protein [Arabidopsis thaliana] gi|8072399|gb|AAF71987.1|AC013453_12 Hypothetical protein [Arabidopsis thaliana] gi|60547563|gb|AAX23745.1| hypothetical protein At1g15600 [Arabidopsis thaliana] gi|71905403|gb|AAZ52679.1| hypothetical protein At1g15600 [Arabidopsis thaliana] gi|332191219|gb|AEE29340.1| uncharacterized protein AT1G15600 [Arabidopsis thaliana]	218	220	1.00E-59	100.9	60.6	74.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G15600.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15620.1); Has 227 Blast hits to 227 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 227; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5368923-5369761 FORWARD LENGTH=220	218	220	4.00E-62	100.9	60.6	74.3
Rsa1.0_00903.1.g21081.t1	ref|XP_002890116.1| CENP-C [Arabidopsis lyrata subsp. lyrata] gi|297335958|gb|EFH66375.1| CENP-C [Arabidopsis lyrata subsp. lyrata]	735	708	0	96.3	61.2	71.2	CENP-C	gbpln	Arabidopsis lyrata	AT1G15660.1 | Symbols: CENP-C | centromere protein C | chr1:5381230-5385057 FORWARD LENGTH=705	735	705	0	95.9	59.7	70.3
Rsa1.0_00903.1.g21082.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00903.1.g21083.t1	gb|EOA38066.1| hypothetical protein CARUB_v10009534mg [Capsella rubella]	359	361	1.00E-171	100.6	82.2	90.0	hypothetical protein CARUB_v10009534mg	gbpln	Capsella rubella	AT1G15670.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:5390119-5391198 FORWARD LENGTH=359	359	359	1.00E-169	100.0	79.9	87.5
Rsa1.0_00903.1.g21084.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00903.1.g21085.t1	gb|AET95910.1| AVP1-1 [Brassica rapa]	809	769	0	95.1	93.4	94.3	AVP1-1	gbpln	Brassica rapa	AT1G15690.1 | Symbols: AVP1, ATAVP3, AVP-3, AtVHP1;1 | Inorganic H pyrophosphatase family protein | chr1:5399115-5402185 FORWARD LENGTH=770	809	770	0	95.2	91.0	94.1

Rsa1.0_00903.1.g21086.t1	ref|NP_173025.1| Cobalamin biosynthesis CobW-like protein [Arabidopsis thaliana] gi|8927652|gb|AAF82143.1|AC034256_7 Contains similarity to COBW-like protein from Homo sapiens gb|AF257330 and contains a Viral (Superfamily 1) RNA helicase PF|01443 domain. EST gb|AI997977 comes from this genes [Arabidopsis thaliana] gi|14194111|gb|AAK56250.1|AF367261_1 At1g15730/F7H2_7 [Arabidopsis thaliana] gi|20334730|gb|AAM16226.1| At1g15730/F7H2_7 [Arabidopsis thaliana] gi|23397243|gb|AAN31903.1| putative PRLI-interacting factor L [Arabidopsis thaliana] gi|332191233|gb|AEE29354.1| Cobalamin biosynthesis CobW-like protein [Arabidopsis thaliana]	457	448	0	98.0	80.7	86.4	Cobalamin biosynthesis CobW-like protein	gbpln	Arabidopsis thaliana	AT1G15730.1 | Symbols: | Cobalamin biosynthesis CobW-like protein | chr1:5407535-5409937 REVERSE LENGTH=448	457	448	0	98.0	80.7	86.4
Rsa1.0_00903.1.g21087.t1	gb|EOA38743.1| hypothetical protein CARUB_v10010899mg [Capsella rubella]	579	585	0	101.0	91.5	96.0	hypothetical protein CARUB_v10010899mg	gbpln	Capsella rubella	AT1G15740.1 | Symbols: | Leucine-rich repeat family protein | chr1:5411509-5414544 FORWARD LENGTH=585	579	585	0	101.0	93.6	96.4
Rsa1.0_00903.1.g21088.t1	ref|NP_563981.1| protein TOPLESS [Arabidopsis thaliana] gi|30684518|ref|NP_849672.1| protein TOPLESS [Arabidopsis thaliana] gi|79318004|ref|NP_001031050.1| protein TOPLESS [Arabidopsis thaliana] gi|79318012|ref|NP_001031051.1| protein TOPLESS [Arabidopsis thaliana] gi|75332047|sp|Q94AI7.1|TPL_ARATH RecName: Full=Protein TOPLESS; AltName: Full=WUS-interacting protein 1 gi|15028127|gb|AAK76687.1| unknown protein [Arabidopsis thaliana] gi|23296857|gb|AAN13188.1| unknown protein [Arabidopsis thaliana] gi|332191235|gb|AEE29356.1| protein TOPLESS [Arabidopsis thaliana] gi|332191236|gb|AEE29357.1| protein TOPLESS [Arabidopsis thaliana] gi|332191237|gb|AEE29358.1| protein TOPLESS [Arabidopsis thaliana] gi|332191238|gb|AEE29359.1| protein TOPLESS [Arabidopsis thaliana]	1129	1131	0	100.2	97.0	98.6	protein TOPLESS	gbpln	Arabidopsis thaliana	AT1G15750.4 | Symbols: WSIP1, TPL | Transducin family protein / WD-40 repeat family protein | chr1:5415086-5420359 REVERSE LENGTH=1131	1129	1131	0	100.2	97.0	98.6
Rsa1.0_00904.1.g21089.t1	ref|NP_564510.1| Dof zinc finger protein DOF1.6 [Arabidopsis thaliana] gi|55584006|sp|Q9SX97.1|DOF16_ARATH RecName: Full=Dof zinc finger protein DOF1.6; Short=AtDOF1.6 gi|5668794|gb|AAD46020.1|AC007519_5 Similar to gb|U82230 prolamin box binding factor (PBF) from Zea mays [Arabidopsis thaliana] gi|225898016|dbj|BAH30340.1| hypothetical protein [Arabidopsis thaliana] gi|332194076|gb|AEE32197.1| Dof zinc finger protein DOF1.6 [Arabidopsis thaliana]	223	209	9.00E-61	93.7	70.9	75.8	Dof zinc finger protein DOF1.6	gbpln	Arabidopsis thaliana	AT1G47655.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr1:17525437-17526066 FORWARD LENGTH=209	223	209	3.00E-63	93.7	70.9	75.8
Rsa1.0_00904.1.g21090.t1	ref|XP_002894064.1| hypothetical protein ARALYDRAFT_891562 [Arabidopsis lyrata subsp. lyrata] gi|297339906|gb|EFH70323.1| hypothetical protein ARALYDRAFT_891562 [Arabidopsis lyrata subsp. lyrata]	228	228	1.00E-128	100.0	97.4	100.0	hypothetical protein ARALYDRAFT_891562	gbpln	Arabidopsis lyrata	AT1G47640.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2053, membrane (InterPro:IPR019164); Has 204 Blast hits to 204 proteins in 84 species: Archae - 0; Bacteria - 0; Metazoa - 127; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr1:17518409-17519998 REVERSE LENGTH=228	228	228	1.00E-130	100.0	96.9	99.1
Rsa1.0_00904.1.g21091.t1	gb|ABD64994.1| hypothetical protein 26.t00013 [Brassica oleracea]	121	103	2.00E-14	85.1	34.7	43.8	hypothetical protein 26.t00013	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00904.1.g21092.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00904.1.g21093.t1	ref|NP_191125.1| ROP (rho of plants) guanine nucleotide exchange factor 6 [Arabidopsis thaliana] gi|7263554|emb|CAB81591.1| putative protein [Arabidopsis thaliana] gi|56236088|gb|AAV84500.1| At3g55660 [Arabidopsis thaliana] gi|59958354|gb|AAX12887.1| At3g55660 [Arabidopsis thaliana] gi|332645896|gb|AEE79417.1| ROP (rho of plants) guanine nucleotide exchange factor 6 [Arabidopsis thaliana]	161	579	5.00E−29	359.6	47.8	55.9	ROP (rho of plants) guanine nucleotide exchange factor 6	gbpln	Arabidopsis thaliana	AT3G55660.1 | Symbols: ATROPGEF6, ROPGEF6 | ROP (rho of plants) guanine nucleotide exchange factor 6 | chr3:20649051−20651290 REVERSE LENGTH=579	161	579	2.00E−31	359.6	47.8	55.9
Rsa1.0_00904.1.g21094.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00904.1.g21095.t1	dbj|BAF01332.1| hypothetical protein [Arabidopsis thaliana]	713	478	1.00E−10	67.0	14.2	22.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G32200.1 | Symbols: ASY2 | DNA−binding HORMA family protein | chr4:15548840−15554962 FORWARD LENGTH=1399	713	1399	4.00E−13	196.2	14.2	22.7
Rsa1.0_00904.1.g21096.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	665	1103	2.00E−97	165.9	27.4	31.7	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00904.1.g21097.t1	ref|XP_002891365.1| hypothetical protein ARALYDRAFT_473896 [Arabidopsis lyrata subsp. lyrata] gi|297337207|gb|EFH67624.1| hypothetical protein ARALYDRAFT_473896 [Arabidopsis lyrata subsp. lyrata]	484	484	0	100.0	94.4	98.1	hypothetical protein ARALYDRAFT_473896	gbpln	Arabidopsis lyrata	AT1G47530.1 | Symbols: | MATE efflux family protein | chr1:17451724−17454110 FORWARD LENGTH=484	484	484	0	100.0	94.0	98.1
Rsa1.0_00904.1.g21098.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838−20266 [Arabidopsis thaliana]	277	1142	3.00E−31	412.3	23.8	31.8	reverse transcriptase, putative; 16838−20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00904.1.g21099.t1	gb|AAC62785.1| F11O4.11 [Arabidopsis thaliana] gi|7268192|emb|CAB77719.1| putative transposon protein [Arabidopsis thaliana]	178	577	2.00E−38	324.2	41.6	57.3	F11O4.11	gbpln	Arabidopsis thaliana	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 295; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:12795861−12796871 REVERSE LENGTH=336	178	336	1.00E−17	188.8	25.3	40.4
Rsa1.0_00904.1.g21100.t3	gb|AAD29754.1|AF076243_1 putative transposon protein [Arabidopsis thaliana] gi|7267199|emb|CAB77910.1| putative transposon protein [Arabidopsis thaliana]	677	1008	8.00E−26	148.9	21.1	35.3	putative transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00904.1.g21101.t1	ref|XP_002894051.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297339893|gb|EFH70310.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	329	334	1.00E−164	101.5	85.7	91.5	endonuclease/exonuclease/phosphatase family protein	gbpln	Arabidopsis lyrata	AT1G47510.1 | Symbols: AT5PTASE11, 5PTASE11 | inositol polyphosphate 5−phosphatase 11 | chr1:17435991−17438296 REVERSE LENGTH=334	329	334	1.00E−165	101.5	85.7	90.6
Rsa1.0_00904.1.g21102.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_00905.1.g21103.t1	ref|XP_002866099.1| protein translocase [Arabidopsis lyrata subsp. lyrata] gi|297311934|gb|EFH42358.1| protein translocase [Arabidopsis lyrata subsp. lyrata]	211	213	2.00E−93	100.9	82.9	91.0	protein translocase	gbpln	Arabidopsis lyrata	AT5G55510.1 | Symbols: | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr5:22486525−22487916 REVERSE LENGTH=214	211	214	6.00E−92	101.4	82.5	90.0
Rsa1.0_00905.1.g21104.t1	ref|NP_568825.1| beta−(1,2)−xylosyltransferase [Arabidopsis thaliana] gi|17369167|sp|Q9LDH0.1|XYLT_ARATH RecName: Full=Beta−(1,2)−xylosyltransferase gi|15724166|gb|AAL06475.1|AF411785_1 AT5g55500/MTE17_21 [Arabidopsis thaliana] gi|7671513|emb|CAB89489.1| beta1,2−Xylosyltransferase [Arabidopsis thaliana] gi|7768105|emb|CAB90610.1| beta1,2−xylosyltransferase [Arabidopsis thaliana] gi|9758182|dbj|BAB08567.1| unnamed protein product [Arabidopsis thaliana] gi|23505973|gb|AAN28846.1| At5g55500/MTE17_21 [Arabidopsis thaliana] gi|332009252|gb|AED96635.1| beta−(1,2)−xylosyltransferase [Arabidopsis thaliana]	529	534	0	100.9	85.1	90.9	beta−(1,2)−xylosyltransferase	gbpln	Arabidopsis thaliana	AT5G55500.1 | Symbols: ATXYLT, XYLT | beta−1,2−xylosyltransferase | chr5:22482386−22484417 FORWARD LENGTH=534	529	534	0	100.9	85.1	90.9

Rsa1.0_00905.1.g21105.t1	gb|EOA13111.1| hypothetical protein CARUB_v10026121mg [Capsella rubella]	594	598	0	100.7	75.1	87.0	hypothetical protein CARUB_v10026121mg	gbpln	Capsella rubella	AT5G55490.1 | Symbols: ATGEX1, GEX1 | gamete expressed protein 1 | chr5:22478822-22481071 REVERSE LENGTH=593	594	593	0	99.8	71.0	82.3
Rsa1.0_00905.1.g21106.t1	gb|EMJ25132.1| hypothetical protein PRUPE_ppa014266mg [Prunus persica]	125	77	2.00E-17	61.6	37.6	46.4	hypothetical protein PRUPE_ppa014266mg	gbpln	Prunus persica	AT2G30580.1 | Symbols: DRIP2 | DREB2A-interacting protein 2 | chr2:13026444-13030363 FORWARD LENGTH=420	125	420	1.00E-12	336.0	23.2	24.8
Rsa1.0_00905.1.g21107.t1	ref|NP_198699.1| cysteinyl-tRNA synthetase [Arabidopsis thaliana] gi|192807340|gb|ACF06122.1| At5g38830 [Arabidopsis thaliana] gi|332006981|gb|AED94364.1| cysteinyl-tRNA synthetase [Arabidopsis thaliana]	482	511	0	106.0	73.4	84.2	cysteinyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT5G38830.1 | Symbols: | Cysteinyl-tRNA synthetase, class Ia family protein | chr5:15545764-15548094 REVERSE LENGTH=511	482	511	0	106.0	73.4	84.2
Rsa1.0_00905.1.g21108.t1	gb|EOA14613.1| hypothetical protein CARUB_v10027865mg [Capsella rubella]	67	108	3.00E-26	161.2	83.6	94.0	hypothetical protein CARUB_v10027865mg	gbpln	Capsella rubella	AT5G55410.2 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:22460677-22461009 FORWARD LENGTH=110	67	110	3.00E-27	164.2	77.6	89.6
Rsa1.0_00905.1.g21109.t2	gb|EOA12998.1| hypothetical protein CARUB_v10025988mg [Capsella rubella]	680	702	0	103.2	90.6	95.1	hypothetical protein CARUB_v10025988mg	gbpln	Capsella rubella	AT5G55400.1 | Symbols: | Actin binding Calponin homology (CH) domain-containing protein | chr5:22455535-22458950 REVERSE LENGTH=714	680	714	0	105.0	89.7	95.1
Rsa1.0_00905.1.g21110.t6	gb|EOA12998.1| hypothetical protein CARUB_v10025988mg [Capsella rubella]	563	702	0	124.7	80.5	88.5	hypothetical protein CARUB_v10025988mg	gbpln	Capsella rubella	AT5G55400.1 | Symbols: | Actin binding Calponin homology (CH) domain-containing protein | chr5:22455535-22458950 REVERSE LENGTH=714	563	714	0	126.8	80.6	88.8
Rsa1.0_00905.1.g21111.t1	gb|AAF79268.1|AC023279_17 F12K21.19 [Arabidopsis thaliana]	431	621	1.00E-133	144.1	56.6	74.0	F12K21.19	gbpln	Arabidopsis thaliana	AT5G55350.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr5:22442356-22443393 REVERSE LENGTH=345	431	345	1.00E-100	80.0	43.2	53.6
Rsa1.0_00905.1.g21112.t1	gb|EOA13123.1| hypothetical protein CARUB_v10026142mg [Capsella rubella]	116	584	3.00E-43	503.4	88.8	93.1	hypothetical protein CARUB_v10026142mg	gbpln	Capsella rubella	AT5G55230.2 | Symbols: MAP65-1 | microtubule-associated proteins 65-1 | chr5:22402716-22405182 FORWARD LENGTH=616	116	616	2.00E-45	531.0	88.8	93.1
Rsa1.0_00905.1.g21113.t1	ref|XP_002866082.1| hypothetical protein ARALYDRAFT_331859 [Arabidopsis lyrata subsp. lyrata] gi|297311917|gb|EFH42341.1| hypothetical protein ARALYDRAFT_331859 [Arabidopsis lyrata subsp. lyrata]	166	167	3.00E-55	100.6	73.5	83.7	hypothetical protein ARALYDRAFT_331859	gbpln	Arabidopsis lyrata	AT5G55210.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G22320.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:22396707-22397374 REVERSE LENGTH=168	166	168	4.00E-57	101.2	74.1	83.1
Rsa1.0_00905.1.g21114.t1	ref|XP_002864380.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297310215|gb|EFH40639.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	466	461	0	98.9	85.2	90.8	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT5G55180.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:22388834-22390550 FORWARD LENGTH=460	466	460	0	98.7	87.3	93.3
Rsa1.0_00905.1.g21115.t1	gb|AFP65785.1| SUMO peptide [Gossypium hirsutum]	95	96	2.00E-24	101.1	62.1	71.6	SUMO peptide	gbpln	Gossypium hirsutum	AT4G26840.1 | Symbols: SUM1, SUMO 1, SUMO1, ATSUMO1 | small ubiquitin-like modifier 1 | chr4:13497466-13498458 FORWARD LENGTH=100	95	100	3.00E-26	105.3	63.2	71.6
Rsa1.0_00905.1.g21116.t1	ref|NP_200320.1| mitogen-activated protein kinase kinase kinase 15 [Arabidopsis thaliana] gi|9758106|dbj|BAB08578.1| unnamed protein product [Arabidopsis thaliana] gi|332009196|gb|AED96579.1| mitogen-activated protein kinase kinase kinase 15 [Arabidopsis thaliana]	166	448	9.00E-75	269.9	82.5	89.8	mitogen-activated protein kinase kinase kinase 15	gbpln	Arabidopsis thaliana	AT5G55090.1 | Symbols: MAPKKK15 | mitogen-activated protein kinase kinase kinase 15 | chr5:22356852-22358198 REVERSE LENGTH=448	166	448	3.00E-77	269.9	82.5	89.8
Rsa1.0_00906.1.g21117.t1	gb|AAF79374.1|AC007887_33 F15O4.30 [Arabidopsis thaliana]	1032	1180	0	114.3	75.1	86.4	F15O4.30	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00906.1.g21118.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00906.1.g21119.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	675	695	0	103.0	58.7	71.6	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	675	681	1.00E-12	100.9	5.0	8.7
Rsa1.0_00906.1.g21120.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	1454	1103	0	75.9	28.9	36.0	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00906.1.g21121.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	244	1142	3.00E-57	468.0	51.2	64.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	244	292	2.00E-19	119.7	29.9	48.0
Rsa1.0_00906.1.g21122.t1	gb|EOA30318.1| hypothetical protein CARUB_v10013445mg [Capsella rubella]	329	526	4.00E-36	159.9	27.7	31.9	hypothetical protein CARUB_v10013445mg	gbpln	Capsella rubella	AT3G10440.1 | Symbols: | Shugoshin C terminus | chr3:3245376-3248987 FORWARD LENGTH=572	329	572	1.00E-37	173.9	30.7	36.2
Rsa1.0_00906.1.g21123.t1	gb|EOA19642.1| hypothetical protein CARUB_v10003012mg [Capsella rubella]	363	390	9.00E-71	107.4	47.4	63.4	hypothetical protein CARUB_v10003012mg	gbpln	Capsella rubella	AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378	363	378	2.00E-72	104.1	45.5	61.2
Rsa1.0_00906.1.g21124.t1	ref|XP_002868461.1| hypothetical protein ARALYDRAFT_493662 [Arabidopsis lyrata subsp. lyrata] gi|297314297|gb|EFH44720.1| hypothetical protein ARALYDRAFT_493662 [Arabidopsis lyrata subsp. lyrata]	536	447	0	83.4	69.0	72.6	hypothetical protein ARALYDRAFT_493662	gbpln	Arabidopsis lyrata	AT5G36250.1 | Symbols: | Protein phosphatase 2C family protein | chr5:14282590-14284376 FORWARD LENGTH=448	536	448	0	83.6	68.8	72.6
Rsa1.0_00906.1.g21125.t1	ref|XP_002870475.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316311|gb|EFH46734.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	468	480	0	102.6	84.0	92.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G36260.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:14285068-14288179 REVERSE LENGTH=482	468	482	0	103.0	82.7	92.5
Rsa1.0_00906.1.g21126.t6	ref|XP_002329057.1| predicted protein [Populus trichocarpa] gi|222839728|gb|EEE78051.1| predicted protein [Populus trichocarpa]	371	1462	3.00E-27	394.1	16.2	19.9	predicted protein	gbpln	Populus trichocarpa	AT1G17580.1 | Symbols: MYA1, ATMYA1, XI-1 | myosin 1 | chr1:6039453-6049309 FORWARD LENGTH=1520	371	1520	1.00E-29	409.7	16.2	19.7
Rsa1.0_00906.1.g21127.t2	gb|AAD48963.1|AF147263_5 contains similarity to transposases [Arabidopsis thaliana] gi|7267311|emb|CAB81093.1| AT4g05510 [Arabidopsis thaliana]	475	604	1.00E-127	127.2	56.2	66.9	contains similarity to transposases	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	475	696	1.00E-22	146.5	14.7	24.8
Rsa1.0_00906.1.g21128.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00906.1.g21129.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00906.1.g21130.t2	gb|AAD32756.1| putative replication protein A1 [Arabidopsis thaliana]	381	458	1.00E-49	120.2	33.3	55.4	putative replication protein A1	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	381	566	4.00E-43	148.6	31.5	56.2
Rsa1.0_00906.1.g21131.t4	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	393	490	9.00E-36	124.7	30.3	49.4	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	393	566	2.00E-32	144.0	29.3	51.7
Rsa1.0_00906.1.g21132.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00907.1.g21133.t1	gb|EOA21434.1| hypothetical protein CARUB_v10001809mg [Capsella rubella]	252	248	1.00E-132	98.4	91.7	95.6	hypothetical protein CARUB_v10001809mg	gbpln	Capsella rubella	AT5G10450.1 | Symbols: GRF6, AFT1, 14-3-3lambda | G-box regulating factor 6 | chr5:3284452-3286261 REVERSE LENGTH=248	252	248	1.00E-134	98.4	91.7	95.6
Rsa1.0_00907.1.g21134.t1	ref|XP_002871421.1| hypothetical protein ARALYDRAFT_909001 [Arabidopsis lyrata subsp. lyrata] gi|297317258|gb|EFH47680.1| hypothetical protein ARALYDRAFT_909001 [Arabidopsis lyrata subsp. lyrata]	929	992	0	106.8	73.8	83.4	hypothetical protein ARALYDRAFT_909001	gbpln	Arabidopsis lyrata	AT5G65440.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24610.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26152015-26156896 FORWARD LENGTH=1050	929	1050	0	113.0	65.9	78.4

Rsa1.0_00907.1.g21135.t1	gb|ACC78512.1| PASTICCINO 2 [Brassica rapa subsp. pekinensis]	192	229	1.00E-100	119.3	94.8	96.4	PASTICCINO 2	gbpln	Brassica rapa	AT5G10480.1 | Symbols: PAS2, PEP | Protein-tyrosine phosphatase-like, PTPLA | chr5:3298047-3300048 REVERSE LENGTH=221	192	221	1.00E-101	115.1	92.7	96.9
Rsa1.0_00907.1.g21136.t1	gb|EOA22375.1| hypothetical protein CARUB_v10003006mg [Capsella rubella]	683	676	0	99.0	84.2	88.6	hypothetical protein CARUB_v10003006mg	gbpln	Capsella rubella	AT5G10490.1 | Symbols: MSL2 | MSCS-like 2 | chr5:3300376-3304005 REVERSE LENGTH=673	683	673	0	98.5	81.6	86.8
Rsa1.0_00907.1.g21137.t1	ref|NP_196612.2| kinase interacting-like protein [Arabidopsis thaliana] gi|20453212|gb|AAM19845.1| AT5g10500/F12B17_150 [Arabidopsis thaliana] gi|25090455|gb|AAN72306.1| At5g10500/F12B17_150 [Arabidopsis thaliana] gi|332004171|gb|AED91554.1| kinase interacting-like protein [Arabidopsis thaliana]	894	848	0	94.9	69.6	79.2	kinase interacting-like protein	gbpln	Arabidopsis thaliana	AT5G10500.1 | Symbols: | Kinase interacting (KIP1-like) family protein | chr5:3305418-3308039 FORWARD LENGTH=848	894	848	0	94.9	69.6	79.2
Rsa1.0_00907.1.g21138.t1	ref|XP_002871424.1| hypothetical protein ARALYDRAFT_909007 [Arabidopsis lyrata subsp. lyrata] gi|297317261|gb|EFH47683.1| hypothetical protein ARALYDRAFT_909007 [Arabidopsis lyrata subsp. lyrata]	560	576	0	102.9	86.6	91.8	hypothetical protein ARALYDRAFT_909007	gbpln	Arabidopsis lyrata	AT5G10510.2 | Symbols: AIL6 | AINTEGUMENTA-like 6 | chr5:3315991-3320008 FORWARD LENGTH=581	560	581	0	103.8	83.6	89.1
Rsa1.0_00907.1.g21139.t1	ref|XP_002873463.1| hypothetical protein ARALYDRAFT_487885 [Arabidopsis lyrata subsp. lyrata] gi|297319300|gb|EFH49722.1| hypothetical protein ARALYDRAFT_487885 [Arabidopsis lyrata subsp. lyrata]	490	467	0	95.3	79.8	85.7	hypothetical protein ARALYDRAFT_487885	gbpln	Arabidopsis lyrata	AT5G10520.1 | Symbols: RBK1 | ROP binding protein kinases 1 | chr5:3320584-3322649 REVERSE LENGTH=467	490	467	0	95.3	78.4	84.9
Rsa1.0_00907.1.g21140.t1	ref|NP_196615.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana] gi|75335609|sp|Q9LXA5.1|LRK91_ARATH RecName: Full=L-type lectin-domain containing receptor kinase IX.1; Short=LecRK-IX.1; Flags: Precursor gi|7671450|emb|CAB89390.1| lectin-like protein kinase-like [Arabidopsis thaliana] gi|91806848|gb|ABE66151.1| lectin protein kinase [Arabidopsis thaliana] gi|332004177|gb|AED91560.1| concanavalin A-like lectin kinase-like protein [Arabidopsis thaliana]	122	651	8.00E-25	533.6	51.6	55.7	concanavalin A-like lectin kinase-like protein	gbpln	Arabidopsis thaliana	AT5G10530.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:3324978-3326933 REVERSE LENGTH=651	122	651	1.00E-27	533.6	51.6	55.7
Rsa1.0_00907.1.g21141.t1	ref|XP_002873465.1| glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata] gi|297319302|gb|EFH49724.1| glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata]	782	796	0	101.8	87.0	93.2	glycosyl hydrolase family 3 protein	gbpln	Arabidopsis lyrata	AT5G10560.1 | Symbols: | Glycosyl hydrolase family protein | chr5:3336335-3339351 REVERSE LENGTH=792	782	792	0	101.3	86.7	92.7
Rsa1.0_00907.1.g21142.t1	ref|XP_002871426.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297317263|gb|EFH47685.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	326	314	7.00E-84	96.3	64.7	73.3	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT5G10570.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:3341357-3342877 FORWARD LENGTH=315	326	315	1.00E-85	96.6	66.0	75.2
Rsa1.0_00907.1.g21143.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00908.1.g21144.t1	ref|XP_002883637.1| hypothetical protein ARALYDRAFT_480086 [Arabidopsis lyrata subsp. lyrata] gi|297329477|gb|EFH59896.1| hypothetical protein ARALYDRAFT_480086 [Arabidopsis lyrata subsp. lyrata]	397	402	0	101.3	85.6	92.2	hypothetical protein ARALYDRAFT_480086	gbpln	Arabidopsis lyrata	AT2G04400.1 | Symbols: | Aldolase-type TIM barrel family protein | chr2:1531208-1533578 FORWARD LENGTH=402	397	402	0	101.3	85.6	91.9
Rsa1.0_00908.1.g21145.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00908.1.g21146.t1	gb|EOA39894.1| hypothetical protein CARUB_v10008573mg [Capsella rubella]	1014	630	5.00E-73	62.1	17.2	24.7	hypothetical protein CARUB_v10008573mg	gbpln	Capsella rubella	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	1014	673	9.00E-50	66.4	12.3	17.9
Rsa1.0_00908.1.g21147.t1	#	#	#	#	#	#	#	-	----	----	AT5G15690.1 | Symbols: | zinc ion binding | chr5:5113823-5114402 REVERSE LENGTH=169	99	169	1.00E-10	170.7	36.4	55.6
Rsa1.0_00908.1.g21148.t1	gb|AAD49098.1|AF177535_2 contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]	738	872	1.00E-106	118.2	38.1	55.6	contains similarity to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_00908.1.g21149.t1	ref|XP_002885758.1| hypothetical protein ARALYDRAFT_480089 [Arabidopsis lyrata subsp. lyrata] gi|297331598|gb|EFH62017.1| hypothetical protein ARALYDRAFT_480089 [Arabidopsis lyrata subsp. lyrata]	178	261	4.00E-56	146.6	73.6	79.2	hypothetical protein ARALYDRAFT_480089	gbpln	Arabidopsis lyrata	AT2G04480.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35870.1); Has 38 Blast hits to 38 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:1554282-1555514 REVERSE LENGTH=247	178	247	6.00E-58	138.8	69.1	77.5
Rsa1.0_00908.1.g21150.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	805	1142	0	141.9	48.0	63.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	805	575	2.00E-70	71.4	18.6	29.3
Rsa1.0_00908.1.g21151.t1	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	445	703	8.00E-52	158.0	23.1	27.9	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_00908.1.g21152.t2	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	401	414	2.00E-30	103.2	21.7	29.7	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00908.1.g21153.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00908.1.g21154.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00908.1.g21155.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00909.1.g21156.t3	ref|NP_188424.2| translocon at the outer membrane of chloroplasts 64-III [Arabidopsis thaliana] gi|75335547|sp|Q9LVH5.1|OE64C_ARATH RecName: Full=Outer envelope protein 64, chloroplastic; AltName: Full=Translocon at the outer membrane of chloroplasts 64-III gi|9294499|dbj|BAB02718.1| unnamed protein product [Arabidopsis thaliana] gi|332642509|gb|AEE76030.1| translocon at the outer membrane of chloroplasts 64-III [Arabidopsis thaliana]	545	589	0	108.1	84.4	90.3	translocon at the outer membrane of chloroplasts 64-III	gbpln	Arabidopsis thaliana	AT3G17970.1 | Symbols: atToc64-III, TOC64-III | translocon at the outer membrane of chloroplasts 64-III | chr3:6148030-6151794 FORWARD LENGTH=589	545	589	0	108.1	84.4	90.3
Rsa1.0_00909.1.g21157.t1	ref|NP_188425.2| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana] gi|297830434|ref|XP_002883099.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|9294500|dbj|BAB02719.1| GTPase activating protein-like [Arabidopsis thaliana] gi|62867625|gb|AAY17416.1| At3g17980 [Arabidopsis thaliana] gi|149944327|gb|ABR46206.1| At3g17980 [Arabidopsis thaliana] gi|297328939|gb|EFH59358.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|332642510|gb|AEE76031.1| calcium-dependent lipid-binding domain-containing protein [Arabidopsis thaliana]	273	177	9.00E-89	64.8	59.0	63.0	calcium-dependent lipid-binding domain-containing protein	gbpln	Arabidopsis lyrata	AT3G17980.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:6152417-6153115 FORWARD LENGTH=177	273	177	3.00E-91	64.8	59.0	63.0
Rsa1.0_00909.1.g21158.t1	ref|XP_002862807.1| WOX1 protein [Arabidopsis lyrata subsp. lyrata] gi|297308541|gb|EFH39065.1| WOX1 protein [Arabidopsis lyrata subsp. lyrata]	345	348	1.00E-156	100.9	82.3	87.0	WOX1 protein	gbpln	Arabidopsis lyrata	AT3G18010.1 | Symbols: WOX1 | WUSCHEL related homeobox 1 | chr3:6161155-6163183 REVERSE LENGTH=350	345	350	1.00E-150	101.4	81.2	85.8
Rsa1.0_00909.1.g21159.t1	ref|XP_002885238.1| hypothetical protein ARALYDRAFT_479291 [Arabidopsis lyrata subsp. lyrata] gi|297331078|gb|EFH61497.1| hypothetical protein ARALYDRAFT_479291 [Arabidopsis lyrata subsp. lyrata]	621	480	9.00E-57	77.3	30.6	37.0	hypothetical protein ARALYDRAFT_479291	gbpln	Arabidopsis lyrata	AT3G18035.1 | Symbols: HON4 | winged-helix DNA-binding transcription factor family protein | chr3:6169384-6171558 REVERSE LENGTH=480	621	480	2.00E-54	77.3	28.8	35.4
Rsa1.0_00909.1.g21160.t2	ref|NP_566596.1| uncharacterized protein [Arabidopsis thaliana] gi|9294060|dbj|BAB02017.1| unnamed protein product [Arabidopsis thaliana] gi|15451206|gb|AAK96874.1| Unknown protein [Arabidopsis thaliana] gi|23197698|gb|AAN15376.1| Unknown protein [Arabidopsis thaliana] gi|332642519|gb|AEE76040.1| uncharacterized protein AT3G18050 [Arabidopsis thaliana]	335	335	1.00E-142	100.0	77.6	85.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G18050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G28100.1); Has 67 Blast hits to 66 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6180931-6182593 FORWARD LENGTH=335	335	335	1.00E-145	100.0	77.6	85.1
Rsa1.0_00909.1.g21161.t1	sp|Q9LV20.1|WTR17_ARATH RecName: Full=WAT1-related protein At3g18200 gi|9294076|dbj|BAB02033.1| nodulin-like protein [Arabidopsis thaliana]	304	383	1.00E-143	126.0	89.8	93.1	RecName: Full=WAT1-related protein At3g18200 gi|9294076|dbj|BAB02033.1| nodulin-like protein	gbpln	Arabidopsis thaliana	AT3G18200.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:6234509-6236059 REVERSE LENGTH=360	304	360	2.33E-156	118.4	89.8	93.1

<table>
<tr><td>Rsa1.0_00909.1.g21162.t1</td><td>gb|EOA30759.1| hypothetical protein CARUB_v10013901mg [Capsella rubella]</td><td>380</td><td>392</td><td>0</td><td>103.2</td><td>82.4</td><td>91.6</td><td>hypothetical protein CARUB_v10013901mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G18210.2 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:6238264-6240396 REVERSE LENGTH=394</td><td>380</td><td>394</td><td>0</td><td>103.7</td><td>82.4</td><td>91.8</td></tr>
<tr><td>Rsa1.0_00909.1.g21163.t1</td><td>gb|EOA29837.1| hypothetical protein CARUB_v10012930mg, partial [Capsella rubella]</td><td>890</td><td>910</td><td>0</td><td>102.2</td><td>80.4</td><td>87.1</td><td>hypothetical protein CARUB_v10012930mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G18390.1 | Symbols: EMB1865 | CRS1 / YhbY (CRM) domain-containing protein | chr3:6313572-6317584 FORWARD LENGTH=848</td><td>890</td><td>848</td><td>0</td><td>95.3</td><td>79.1</td><td>86.1</td></tr>
<tr><td>Rsa1.0_00909.1.g21164.t1</td><td>ref|NP_188469.1| NAC domain containing protein 58 [Arabidopsis thaliana] gi|11994103|dbj|BAB01106.1| unnamed protein product [Arabidopsis thaliana] gi|332642571|gb|AEE76092.1| NAC domain containing protein 58 [Arabidopsis thaliana]</td><td>55</td><td>314</td><td>3.00E-22</td><td>570.9</td><td>87.3</td><td>87.3</td><td>NAC domain containing protein 58</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G18400.1 | Symbols: anac058, NAC058 | NAC domain containing protein 58 | chr3:6318745-6320593 REVERSE LENGTH=314</td><td>55</td><td>314</td><td>4.00E-25</td><td>570.9</td><td>87.3</td><td>87.3</td></tr>
<tr><td>Rsa1.0_00909.1.g21165.t1</td><td>gb|EOA30252.1| hypothetical protein CARUB_v10013374mg [Capsella rubella]</td><td>621</td><td>556</td><td>1.00E-130</td><td>89.5</td><td>40.6</td><td>43.2</td><td>hypothetical protein CARUB_v10013374mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G18520.2 | Symbols: HDA15, ATHDA15 | histone deacetylase 15 | chr3:6361605-6365399 FORWARD LENGTH=564</td><td>621</td><td>564</td><td>1.00E-130</td><td>90.8</td><td>39.9</td><td>44.4</td></tr>
<tr><td>Rsa1.0_00909.1.g21166.t1</td><td>gb|EOA29821.1| hypothetical protein CARUB_v10012916mg [Capsella rubella]</td><td>858</td><td>937</td><td>0</td><td>109.2</td><td>91.3</td><td>96.6</td><td>hypothetical protein CARUB_v10012916mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G18524.1 | Symbols: MSH2, ATMSH2 | MUTS homolog 2 | chr3:6368151-6372409 REVERSE LENGTH=937</td><td>858</td><td>937</td><td>0</td><td>109.2</td><td>91.3</td><td>96.4</td></tr>
<tr><td>Rsa1.0_00910.1.g21167.t1</td><td>ref|XP_002880115.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297325954|gb|EFH56374.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata]</td><td>170</td><td>579</td><td>2.00E-83</td><td>340.6</td><td>86.5</td><td>94.1</td><td>glycosyl hydrolase family 1 protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G44460.1 | Symbols: BGLU28 | beta glucosidase 28 | chr2:18346500-18349826 FORWARD LENGTH=582</td><td>170</td><td>582</td><td>1.00E-85</td><td>342.4</td><td>85.9</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00910.1.g21168.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>1910</td><td>1274</td><td>0</td><td>66.7</td><td>30.0</td><td>41.5</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1910</td><td>575</td><td>3.00E-73</td><td>30.1</td><td>9.2</td><td>14.5</td></tr>
<tr><td>Rsa1.0_00910.1.g21169.t1</td><td>ref|NP_181973.1| beta glucosidase 15 [Arabidopsis thaliana] gi|75278312|sp|O64879.1|BGL15_ARATH RecName: Full=Beta-glucosidase 15; Short=AtBGLU15; Flags: Precursor gi|3128187|gb|AAC16091.1| putative beta-glucosidase [Arabidopsis thaliana] gi|330255327|gb|AEC10421.1| beta glucosidase 15 [Arabidopsis thaliana]</td><td>507</td><td>506</td><td>0</td><td>99.8</td><td>93.9</td><td>97.4</td><td>beta glucosidase 15</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G44450.1 | Symbols: BGLU15 | beta glucosidase 15 | chr2:18340966-18343744 FORWARD LENGTH=506</td><td>507</td><td>506</td><td>0</td><td>99.8</td><td>93.9</td><td>97.4</td></tr>
<tr><td>Rsa1.0_00910.1.g21170.t1</td><td>gb|EOA27225.1| hypothetical protein CARUB_v10023334mg [Capsella rubella] gi|482563036|gb|EOA27226.1| hypothetical protein CARUB_v10023334mg [Capsella rubella]</td><td>312</td><td>407</td><td>8.00E-92</td><td>130.4</td><td>70.2</td><td>78.5</td><td>hypothetical protein CARUB_v10023334mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44410.1 | Symbols: | RING/U-box superfamily protein | chr2:18328873-18330114 FORWARD LENGTH=413</td><td>312</td><td>413</td><td>2.00E-82</td><td>132.4</td><td>71.8</td><td>81.4</td></tr>
<tr><td>Rsa1.0_00910.1.g21171.t1</td><td>gb|EOA27519.1| hypothetical protein CARUB_v10023658mg [Capsella rubella]</td><td>422</td><td>320</td><td>1.00E-108</td><td>75.8</td><td>54.7</td><td>60.0</td><td>hypothetical protein CARUB_v10023658mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G44400.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:18327096-18327536 FORWARD LENGTH=146</td><td>422</td><td>146</td><td>2.00E-67</td><td>34.6</td><td>29.1</td><td>31.8</td></tr>
<tr><td>Rsa1.0_00910.1.g21172.t1</td><td>ref|NP_180394.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|4803954|gb|AAD29826.1| unknown protein [Arabidopsis thaliana] gi|330253004|gb|AEC08098.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]</td><td>247</td><td>248</td><td>1.00E-102</td><td>100.4</td><td>75.7</td><td>84.2</td><td>cysteine/histidine-rich C1 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G28270.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:12053652-12054398 FORWARD LENGTH=248</td><td>247</td><td>248</td><td>1.00E-104</td><td>100.4</td><td>75.7</td><td>84.2</td></tr>
<tr><td>Rsa1.0_00910.1.g21173.t1</td><td>ref|NP_181964.1| uncharacterized protein [Arabidopsis thaliana] gi|3128181|gb|AAC16085.1| unknown protein [Arabidopsis thaliana] gi|26452605|dbj|BAC43386.1| unknown protein [Arabidopsis thaliana] gi|28973513|gb|AAO64081.1| unknown protein [Arabidopsis thaliana] gi|330255318|gb|AEC10412.1| uncharacterized protein AT2G44360 [Arabidopsis thaliana]</td><td>137</td><td>135</td><td>3.00E-57</td><td>98.5</td><td>83.2</td><td>88.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G44360.1 | Symbols: | unknown protein; Has 23 Blast hits to 23 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18320855-18321584 REVERSE LENGTH=135</td><td>137</td><td>135</td><td>7.00E-60</td><td>98.5</td><td>83.2</td><td>88.3</td></tr>
<tr><td>Rsa1.0_00910.1.g21174.t1</td><td>ref|NP_566016.1| citrate synthase 4 [Arabidopsis thaliana] gi|14423562|gb|AAK62463.1|AF387018_1 citrate synthase [Arabidopsis thaliana] gi|20197191|gb|AAC16084.2| citrate synthase [Arabidopsis thaliana] gi|30387583|gb|AAP31957.1| At2g44350 [Arabidopsis thaliana] gi|330255316|gb|AEC10410.1| citrate synthase 4 [Arabidopsis thaliana]</td><td>473</td><td>473</td><td>0</td><td>100.0</td><td>97.0</td><td>99.2</td><td>citrate synthase 4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G44350.1 | Symbols: ATCS, CSY4 | Citrate synthase family protein | chr2:18316673-18320524 FORWARD LENGTH=473</td><td>473</td><td>473</td><td>0</td><td>100.0</td><td>97.0</td><td>99.2</td></tr>
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Rsa1.0_00910.1.g21175.t1	ref|XP_002880106.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325945|gb|EFH56365.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	180	169	9.00E-67	93.9	73.9	79.4	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT2G44340.1 | Symbols: | VQ motif-containing protein | chr2:18314279-18314845 FORWARD LENGTH=188	180	188	7.00E-66	104.4	78.9	84.4
Rsa1.0_00910.1.g21176.t1	gb|EOA28472.1| hypothetical protein CARUB_v10024679mg [Capsella rubella]	530	552	0	104.2	84.3	90.9	hypothetical protein CARUB_v10024679mg	gbpln	Capsella rubella	AT2G44260.1 | Symbols: | Plant protein of unknown function (DUF946) | chr2:18295988-18297739 FORWARD LENGTH=553	530	553	0	104.3	83.4	90.4
Rsa1.0_00910.1.g21177.t1	gb|EOA26437.1| hypothetical protein CARUB_v10025447mg [Capsella rubella]	83	394	3.00E-20	474.7	62.7	71.1	hypothetical protein CARUB_v10025447mg	gbpln	Capsella rubella	AT2G44220.1 | Symbols: | Protein of Unknown Function (DUF239) | chr2:18283803-18285690 FORWARD LENGTH=403	83	403	1.00E-22	485.5	62.7	71.1
Rsa1.0_00910.1.g21178.t1	ref|NP_030959.1| uncharacterized protein [Arabidopsis thaliana] gi|3128168|gb|AAC16072.1| expressed protein [Arabidopsis thaliana] gi|15081719|gb|AAK82514.1| At2g44210/F4I1.2 [Arabidopsis thaliana] gi|21593455|gb|AAM65422.1| unknown [Arabidopsis thaliana] gi|22137094|gb|AAM91392.1| At2g44210/F4I1.2 [Arabidopsis thaliana] gi|330255297|gb|AEC10391.1| uncharacterized protein AT2G44210 [Arabidopsis thaliana]	417	415	0	99.5	91.1	94.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G44210.1 | Symbols: | Protein of Unknown Function (DUF239) | chr2:18280809-18282591 FORWARD LENGTH=415	417	415	0	99.5	91.1	94.0
Rsa1.0_00910.1.g21179.t2	ref|NP_197310.1| AP2/B3 domain-containing protein [Arabidopsis thaliana] gi|75171182|sp|Q9FK61.1|Y5809_ARATH RecName: Full=B3 domain-containing protein At5g18090 gi|9758891|dbj|BAB09467.1| unnamed protein product [Arabidopsis thaliana] gi|21618285|gb|AAM67335.1| unknown [Arabidopsis thaliana] gi|28393402|gb|AAO42124.1| unknown protein [Arabidopsis thaliana] gi|28973297|gb|AAO63973.1| unknown protein [Arabidopsis thaliana] gi|332005122|gb|AED92505.1| AP2/B3 domain-containing protein [Arabidopsis thaliana]	259	301	2.00E-48	116.2	46.7	61.4	AP2/B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G18090.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:5985467-5986925 FORWARD LENGTH=301	259	301	5.00E-51	116.2	46.7	61.4
Rsa1.0_00910.1.g21180.t1	gb|EOA26778.1| hypothetical protein CARUB_v10022865mg [Capsella rubella]	583	594	0	101.9	91.4	96.2	hypothetical protein CARUB_v10022865mg	gbpln	Capsella rubella	AT2G44160.1 | Symbols: MTHFR2 | methylenetetrahydrofolate reductase 2 | chr2:18262301-18265185 FORWARD LENGTH=594	583	594	0	101.9	91.3	96.2
Rsa1.0_00910.1.g21181.t1	ref|XP_002862275.1| 60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata] gi|297307611|gb|EFH38533.1| 60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata] gi|482563601|gb|EOA27791.1| hypothetical protein CARUB_v10023943mg [Capsella rubella]	120	242	2.00E-51	201.7	87.5	90.8	60S ribosomal protein L7	gbpln	Arabidopsis lyrata	AT2G44120.2 | Symbols: | Ribosomal protein L30/L7 family protein | chr2:18249227-18250417 REVERSE LENGTH=247	120	247	1.00E-53	205.8	87.5	90.0
Rsa1.0_00911.1.g21182.t1	gb|AAF79236.1|AC006917_21 F10B6.25 [Arabidopsis thaliana]	1425	1475	0	103.5	91.3	95.4	F10B6.25	gbpln	Arabidopsis thaliana	AT1G14850.1 | Symbols: NUP155 | nucleoporin 155 | chr1:5116921-5123259 REVERSE LENGTH=1464	1425	1464	0	102.7	91.1	95.4
Rsa1.0_00911.1.g21183.t1	ref|XP_002892833.1| atmap70-4 [Arabidopsis lyrata subsp. lyrata] gi|297338675|gb|EFH69092.1| atmap70-4 [Arabidopsis lyrata subsp. lyrata]	605	603	0	99.7	90.2	93.9	atmap70-4	gbpln	Arabidopsis lyrata	AT1G14840.1 | Symbols: ATMAP70-4, MAP70-4 | microtubule-associated proteins 70-4 | chr1:5112415-5115299 REVERSE LENGTH=604	605	604	0	99.8	89.3	94.0
Rsa1.0_00911.1.g21184.t1	gb|EOA37031.1| hypothetical protein CARUB_v10010095mg [Capsella rubella]	245	251	1.00E-119	102.4	83.3	91.8	hypothetical protein CARUB_v10010095mg	gbpln	Capsella rubella	AT1G14820.3 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:5105237-5106793 REVERSE LENGTH=252	245	252	1.00E-122	102.9	85.3	91.0
Rsa1.0_00911.1.g21185.t1	ref|NP_172934.1| semialdehyde dehydrogenase-like protein [Arabidopsis thaliana] gi|17979524|gb|AAL50097.1| At1g14810/F10B6_6 [Arabidopsis thaliana] gi|20856224|gb|AAM26654.1| At1g14810/F10B6_6 [Arabidopsis thaliana] gi|21536731|gb|AAM61063.1| aspartate-semialdehyde dehydrogenase, putative [Arabidopsis thaliana] gi|332191107|gb|AEE29228.1| semialdehyde dehydrogenase-like protein [Arabidopsis thaliana]	375	375	0	100.0	93.6	97.3	semialdehyde dehydrogenase-like protein	gbpln	Arabidopsis thaliana	AT1G14810.1 | Symbols: | semialdehyde dehydrogenase family protein | chr1:5102684-5104633 REVERSE LENGTH=375	375	375	0	100.0	93.6	97.3

Rsa1.0_00911.1.g21186.t1	gb|EOA39524.1| hypothetical protein CARUB_v10008144mg [Capsella rubella]	1110	1107	0	99.7	86.1	91.8	hypothetical protein CARUB_v10008144mg	gbpln	Capsella rubella	AT1G14790.1 | Symbols: RDR1, ATRDRP1 | RNA-dependent RNA polymerase 1 | chr1:5094317-5097817 REVERSE LENGTH=1107	1110	1107	0	99.7	86.2	91.1
Rsa1.0_00911.1.g21187.t2	ref|NP_172931.1| MAC/Perforin domain-containing protein [Arabidopsis thaliana] gi|75153917|sp|Q8L612.1|MACP1_ARATH RecName: Full=MACPF domain-containing protein At1g14780 gi|20466444|gb|AAM20539.1| unknown protein [Arabidopsis thaliana] gi|27311987|gb|AAO00959.1| unknown protein [Arabidopsis thaliana] gi|332191104|gb|AEE29225.1| MAC/Perforin domain-containing protein [Arabidopsis thaliana]	624	627	0	100.5	86.4	92.5	MAC/Perforin domain-containing protein	gbpln	Arabidopsis thaliana	AT1G14780.1 | Symbols: | MAC/Perforin domain-containing protein | chr1:5091020-5093873 FORWARD LENGTH=627	624	627	0	100.5	86.4	92.5
Rsa1.0_00911.1.g21188.t3	ref|XP_002892829.1| hypothetical protein ARALYDRAFT_471666 [Arabidopsis lyrata subsp. lyrata] gi|297338671|gb|EFH69088.1| hypothetical protein ARALYDRAFT_471666 [Arabidopsis lyrata subsp. lyrata]	603	412	1.00E-129	68.3	41.1	45.4	hypothetical protein ARALYDRAFT_471666	gbpln	Arabidopsis lyrata	AT1G14770.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:5086867-5088437 REVERSE LENGTH=429	603	429	1.00E-122	71.1	40.5	44.6
Rsa1.0_00911.1.g21189.t1	ref|NP_001154340.1| protein KNATM [Arabidopsis thaliana] gi|332191100|gb|AEE29221.1| protein KNATM [Arabidopsis thaliana]	139	138	2.00E-53	99.3	81.3	89.2	protein KNATM	gbpln	Arabidopsis thaliana	AT1G14760.2 | Symbols: KNATM | KNOX Arabidopsis thaliana meinox | chr1:5084530-5085213 REVERSE LENGTH=138	139	138	5.00E-56	99.3	81.3	89.2
Rsa1.0_00911.1.g21190.t1	ref|XP_002892827.1| hypothetical protein ARALYDRAFT_471662 [Arabidopsis lyrata subsp. lyrata] gi|297338669|gb|EFH69086.1| hypothetical protein ARALYDRAFT_471662 [Arabidopsis lyrata subsp. lyrata]	564	581	0	103.0	77.0	84.4	hypothetical protein ARALYDRAFT_471662	gbpln	Arabidopsis lyrata	AT1G14750.1 | Symbols: SDS | Cyclin family protein | chr1:5079674-5082423 REVERSE LENGTH=578	564	578	0	102.5	77.1	84.4
Rsa1.0_00911.1.g21191.t1	gb|EOA39760.1| hypothetical protein CARUB_v10008407mg [Capsella rubella]	741	738	0	99.6	85.3	90.3	hypothetical protein CARUB_v10008407mg	gbpln	Capsella rubella	AT1G14740.1 | Symbols: | Protein of unknown function (DUF1423) | chr1:5075450-5077732 REVERSE LENGTH=733	741	733	0	98.9	85.0	90.0
Rsa1.0_00911.1.g21192.t1	ref|NP_172926.2| Cytochrome b561/ferric reductase transmembrane-like protein [Arabidopsis thaliana] gi|75116658|sp|Q67ZF6.1|ACFR3_ARATH RecName: Full=Probable transmembrane ascorbate ferrireductase 3; AltName: Full=Artb561-3 gi|51970464|dbj|BAD43924.1| putative cytochrome B561 [Arabidopsis thaliana] gi|332191094|gb|AEE29215.1| probable transmembrane ascorbate ferrireductase 3 [Arabidopsis thaliana]	221	224	1.00E-114	101.4	92.8	96.4	Cytochrome b561/ferric reductase transmembrane-like protein	gbpln	Arabidopsis thaliana	AT1G14730.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane protein family | chr1:5073244-5074568 FORWARD LENGTH=224	221	224	1.00E-116	101.4	92.8	96.4
Rsa1.0_00911.1.g21193.t2	ref|NP_563957.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|30683962|ref|NP_849663.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|332191091|gb|AEE29212.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|332191092|gb|AEE29213.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana]	595	601	0	101.0	68.7	78.0	hydroxyproline-rich glycoprotein-like protein	gbpln	Arabidopsis thaliana	AT1G14710.2 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:5062168-5064697 REVERSE LENGTH=601	595	601	0	101.0	68.7	78.0
Rsa1.0_00911.1.g21194.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	573	1486	1.00E-157	259.3	48.5	67.7	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00911.1.g21195.t1	ref|NP_683306.1| putative clathrin assembly protein [Arabidopsis thaliana] gi|46396002|sp|Q9LQW4.1|CAP15_ARATH RecName: Full=Putative clathrin assembly protein At1g14686 gi|8778241|gb|AAF79250.1|AC006917_35 F10B6.6 [Arabidopsis thaliana] gi|332191084|gb|AEE29205.1| putative clathrin assembly protein [Arabidopsis thaliana]	365	339	1.00E-127	92.9	68.5	78.6	putative clathrin assembly protein	gbpln	Arabidopsis thaliana	AT1G14686.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:5045781-5046800 REVERSE LENGTH=339	365	339	1.00E-129	92.9	68.5	78.6

Rsa1.0_00911.1.g21196.t1	gb|ABC25625.1| GAGA-binding transcriptional activator [Capsella rubella] gi|83616242|gb|ABC25626.1| GAGA-binding transcriptional activator [Capsella rubella] gi|482574222|gb|EOA38409.1| hypothetical protein CARUB_v10009978mg [Capsella rubella] gi|482574223|gb|EOA38410.1| hypothetical protein CARUB_v10009978mg [Capsella rubella]	279	277	1.00E-128	99.3	85.3	91.0	GAGA-binding transcriptional activator	gbpln	Capsella rubella	AT1G14685.1 | Symbols: BPC2, BBR/BPC2, ATBPC2 | basic pentacysteine 2 | chr1:5043086-5043925 FORWARD LENGTH=279	279	279	1.00E-124	100.0	84.6	90.0
Rsa1.0_00911.1.g21197.t1	ref|XP_002890069.1| hypothetical protein ARALYDRAFT_888850 [Arabidopsis lyrata subsp. lyrata] gi|297335911|gb|EFH66328.1| hypothetical protein ARALYDRAFT_888850 [Arabidopsis lyrata subsp. lyrata]	285	289	1.00E-101	101.4	70.2	82.5	hypothetical protein ARALYDRAFT_888850	gbpln	Arabidopsis lyrata	AT1G14680.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G09060.1); Has 8132 Blast hits to 6366 proteins in 685 species: Archae - 171; Bacteria - 671; Metazoa - 4046; Fungi - 445; Plants - 318; Viruses - 23; Other Eukaryotes - 2458 (source: NCBI BLink). | chr1:5040861-5041733 FORWARD LENGTH=290	285	290	1.00E-100	101.8	68.1	81.4
Rsa1.0_00912.1.g21198.t1	ref|XP_002876873.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322711|gb|EFH53132.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	267	203	9.00E-77	76.0	53.2	60.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G03300.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr2:1003468-1004222 REVERSE LENGTH=203	267	203	8.00E-78	76.0	52.8	59.6
Rsa1.0_00912.1.g21199.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	804	1534	1.00E-173	190.8	38.2	47.4	F17L21.7	gbpln	Arabidopsis thaliana	AT1G14010.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:4800385-4801790 REVERSE LENGTH=212	804	212	9.00E-83	26.4	17.3	21.4
Rsa1.0_00912.1.g21200.t1	ref|NP_178423.5| phosphate transporter PHO1-5 [Arabidopsis thaliana] gi|306756300|sp|Q6R8G5.2|PHO15_ARATH RecName: Full=Phosphate transporter PHO1 homolog 5; AltName: Full=Protein PHO1 homolog 5; Short=AtPHO1;H5 gi|330250584|gb|AEC05678.1| phosphate transporter PHO1-5 [Arabidopsis thaliana]	815	823	0	101.0	85.2	92.0	phosphate transporter PHO1-5	gbpln	Arabidopsis thaliana	AT2G03240.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr2:973693-977337 REVERSE LENGTH=823	815	823	0	101.0	85.2	92.0
Rsa1.0_00912.1.g21201.t9	ref|XP_002875191.1| EMB1579 [Arabidopsis lyrata subsp. lyrata] gi|297321029|gb|EFH51450.1| EMB1579 [Arabidopsis lyrata subsp. lyrata]	404	1333	3.00E-45	330.0	25.5	28.7	EMB1579	gbpln	Arabidopsis lyrata	AT2G03150.1 | Symbols: emb1579 | ATP/GTP-binding protein family | chr2:952313-959004 FORWARD LENGTH=1340	404	1340	6.00E-47	331.7	25.0	28.5
Rsa1.0_00912.1.g21202.t4	ref|NP_178414.2| ATP/GTP-binding protein-like protein [Arabidopsis thaliana] gi|330250575|gb|AEC05669.1| ATP/GTP-binding protein-like protein [Arabidopsis thaliana]	110	1340	2.00E-22	1218.2	48.2	50.0	ATP/GTP-binding protein-like protein	gbpln	Arabidopsis thaliana	AT2G03150.1 | Symbols: emb1579 | ATP/GTP-binding protein family | chr2:952313-959004 FORWARD LENGTH=1340	110	1340	3.00E-25	1218.2	48.2	50.0
Rsa1.0_00912.1.g21203.t1	gb|EOA24555.1| hypothetical protein CARUB_v10017813mg, partial [Capsella rubella]	248	275	1.00E-138	110.9	96.8	98.4	hypothetical protein CARUB_v10017813mg, partial	gbpln	Capsella rubella	AT2G03090.1 | Symbols: ATEXPA15, EXP15, ATEXP15, ATHEXP ALPHA 1.3, EXPA15 | expansin A15 | chr2:917361-918554 REVERSE LENGTH=253	248	253	1.00E-138	102.0	95.2	96.8
Rsa1.0_00912.1.g21204.t1	gb|EOA24693.1| hypothetical protein CARUB_v10017969mg [Capsella rubella]	229	230	1.00E-118	100.4	88.2	95.6	hypothetical protein CARUB_v10017969mg	gbpln	Capsella rubella	AT2G02990.1 | Symbols: RNS1, ATRNS1 | ribonuclease 1 | chr2:873714-874667 FORWARD LENGTH=230	229	230	1.00E-118	100.4	89.1	96.1
Rsa1.0_00912.1.g21205.t1	gb|EOA24693.1| hypothetical protein CARUB_v10017969mg [Capsella rubella]	341	230	1.00E-106	67.4	53.1	58.1	hypothetical protein CARUB_v10017969mg	gbpln	Capsella rubella	AT2G02990.1 | Symbols: RNS1, ATRNS1 | ribonuclease 1 | chr2:873714-874667 FORWARD LENGTH=230	341	230	1.00E-107	67.4	54.5	58.7
Rsa1.0_00912.1.g21206.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00913.1.g21207.t1	gb|EOA13229.1| hypothetical protein CARUB_v10026255mg [Capsella rubella]	512	509	0	99.4	84.0	91.0	hypothetical protein CARUB_v10026255mg	gbpln	Capsella rubella	AT5G62570.2 | Symbols: | Calmodulin binding protein-like | chr5:25114934-25116967 FORWARD LENGTH=494	512	494	0	96.5	78.1	85.2
Rsa1.0_00913.1.g21208.t1	ref|XP_002866498.1| hypothetical protein ARALYDRAFT_358455 [Arabidopsis lyrata subsp. lyrata] gi|297312333|gb|EFH42757.1| hypothetical protein ARALYDRAFT_358455 [Arabidopsis lyrata subsp. lyrata]	429	438	1.00E-140	102.1	73.0	81.8	hypothetical protein ARALYDRAFT_358455	gbpln	Arabidopsis lyrata	AT5G62550.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 9 growth stages; Has 14949 Blast hits to 9947 proteins in 971 species: Archae - 43; Bacteria - 3248; Metazoa - 4424; Fungi - 1542; Plants - 562; Viruses - 55; Other Eukaryotes - 5075 (source: NCBI BLink). | chr5:25105839-25107875 REVERSE LENGTH=487	429	487	1.00E-142	113.5	73.4	82.5

Rsa1.0_00913.1.g21209.t2	ref|NP_001051522.1| Os03g0791800 [Oryza sativa Japonica Group] gi|18844990|dbj|BAB85469.1| Rad6 [Oryza sativa Japonica Group] gi|28269456|gb|AAO37999.1| ubiquitin carrier protein [Oryza sativa Japonica Group] gi|108711497|gb|ABF99292.1| Ubiquitin-conjugating enzyme E2-17 kDa, putative, expressed [Oryza sativa Japonica Group] gi|113549993|dbj|BAF13436.1| Os03g0791800 [Oryza sativa Japonica Group] gi|125546000|gb|EAY92139.1| hypothetical protein OsI_13850 [Oryza sativa Indica Group] gi|125588203|gb|EAZ28867.1| hypothetical protein OsJ_12905 [Oryza sativa Japonica Group] gi|215695359|dbj|BAG90550.1| unnamed protein product [Oryza sativa Japonica Group] gi|215767708|dbj|BAG99936.1| unnamed protein product [Oryza sativa Japonica Group] gi|341870591|gb|AEK99335.1| ubiquitin conjugated enzyme [Oryza sativa Japonica Group]	71	152	1.00E-22	214.1	69.0	70.4	Os03g0791800	gbpln	Oryza sativa	AT5G62540.1 | Symbols: UBC3 | ubiquitin-conjugating enzyme 3 | chr5:25104679-25105465 FORWARD LENGTH=150	71	150	1.00E-24	211.3	66.2	69.0
Rsa1.0_00913.1.g21210.t1	dbj|BAJ34440.1| unnamed protein product [Thellungiella halophila]	547	557	0	101.8	94.5	98.0	unnamed protein product	----	----	AT5G62530.1 | Symbols: ALDH12A1, ATP5CDH, P5CDH | aldehyde dehydrogenase 12A1 | chr5:25099768-25103159 REVERSE LENGTH=556	547	556	0	101.6	93.6	97.1
Rsa1.0_00913.1.g21211.t1	gb|EOA14515.1| hypothetical protein CARUB_v10027743mg [Capsella rubella]	330	316	1.00E-131	95.8	72.1	82.1	hypothetical protein CARUB_v10027743mg	gbpln	Capsella rubella	AT5G62520.1 | Symbols: SRO5 | similar to RCD one 5 | chr5:25098071-25099264 FORWARD LENGTH=309	330	309	1.00E-130	93.6	71.5	82.1
Rsa1.0_00913.1.g21212.t1	ref|XP_002864798.1| ATEB1B [Arabidopsis lyrata subsp. lyrata] gi|297310633|gb|EFH41057.1| ATEB1B [Arabidopsis lyrata subsp. lyrata]	292	288	1.00E-142	98.6	83.2	87.3	ATEB1B	gbpln	Arabidopsis lyrata	AT5G62500.1 | Symbols: ATEB1B, ATEB1, EB1B | end binding protein 1B | chr5:25092929-25095006 FORWARD LENGTH=293	292	293	1.00E-145	100.3	83.6	86.3
Rsa1.0_00913.1.g21213.t1	ref|NP_851249.1| glutathione S-transferase tau 9 [Arabidopsis thaliana] gi|75263010|sp|Q9FUT0.1|GSTU9_ARATH RecName: Full=Glutathione S-transferase U9; Short=AtGSTU9; AltName: Full=GST class-tau member 9; AltName: Full=Glutathione S-transferase 14 gi|11095992|gb|AAG30128.1|AF288179_1 glutathione S-transferase [Arabidopsis thaliana] gi|51970564|dbj|BAD43974.1| glutathione S-transferase (GST14) [Arabidopsis thaliana] gi|332010229|gb|AED97612.1| glutathione S-transferase tau 9 [Arabidopsis thaliana]	234	240	1.00E-113	102.6	82.5	92.7	glutathione S-transferase tau 9	gbpln	Arabidopsis thaliana	AT5G62480.1 | Symbols: ATGSTU9, GST14, GST14B, GSTU9 | glutathione S-transferase tau 9 | chr5:25088775-25089566 REVERSE LENGTH=240	234	240	1.00E-115	102.6	82.5	92.7
Rsa1.0_00913.1.g21214.t1	gb|EOA17213.1| hypothetical protein CARUB_v10005487mg [Capsella rubella]	272	271	1.00E-122	99.6	82.0	90.8	hypothetical protein CARUB_v10005487mg	gbpln	Capsella rubella	AT4G28360.1 | Symbols: | Ribosomal protein L22p/L17e family protein | chr4:14029294-14030926 REVERSE LENGTH=271	272	271	1.00E-122	99.6	80.1	91.9
Rsa1.0_00913.1.g21215.t1	ref|NP_568954.2| glutathione S-transferase tau 9 [Arabidopsis thaliana] gi|11095994|gb|AAG30129.1|AF288180_1 glutathione S-transferase [Arabidopsis thaliana] gi|10178079|dbj|BAB11498.1| glutathione S-transferase-like protein [Arabidopsis thaliana] gi|332010230|gb|AED97613.1| glutathione S-transferase tau 9 [Arabidopsis thaliana]	191	214	1.00E-83	112.0	80.6	91.6	glutathione S-transferase tau 9	gbpln	Arabidopsis thaliana	AT5G62480.2 | Symbols: ATGSTU9, GST14, GST14B, GSTU9 | glutathione S-transferase tau 9 | chr5:25088775-25089566 REVERSE LENGTH=214	191	214	4.00E-86	112.0	80.6	91.6
Rsa1.0_00913.1.g21216.t1	gb|EOA17213.1| hypothetical protein CARUB_v10005487mg [Capsella rubella]	220	271	1.00E-89	123.2	79.5	89.1	hypothetical protein CARUB_v10005487mg	gbpln	Capsella rubella	AT4G28360.1 | Symbols: | Ribosomal protein L22p/L17e family protein | chr4:14029294-14030926 REVERSE LENGTH=271	220	271	9.00E-90	123.2	77.7	90.0
Rsa1.0_00913.1.g21217.t1	dbj|BAJ34253.1| unnamed protein product [Thellungiella halophila]	348	355	1.00E-169	102.0	87.4	92.2	unnamed protein product	----	----	AT5G62470.2 | Symbols: MYB96 | myb domain protein 96 | chr5:25079434-25080858 REVERSE LENGTH=352	348	352	1.00E-166	101.1	88.5	91.4
Rsa1.0_00913.1.g21218.t1	gb|EOA13766.1| hypothetical protein CARUB_v10026858mg [Capsella rubella]	308	303	1.00E-113	98.4	83.4	88.6	hypothetical protein CARUB_v10026858mg	gbpln	Capsella rubella	AT5G62460.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:25075545-25077072 FORWARD LENGTH=307	308	307	1.00E-112	99.7	83.4	88.0

Rsa1.0_00913.1.g21219.t1	ref|NP_201050.2| uncharacterized protein [Arabidopsis thaliana] gi|20385491|gb|AAM21312.1|AF371327_1 EMB514 [Arabidopsis thaliana] gi|21593438|gb|AAM65405.1| unknown [Arabidopsis thaliana] gi|30793885|gb|AAP40395.1| unknown protein [Arabidopsis thaliana] gi|30794104|gb|AAP40494.1| unknown protein [Arabidopsis thaliana] gi|51968752|dbj|BAD43068.1| unnamed protein product [Arabidopsis thaliana] gi|110739286|dbj|BAF01556.1| hypothetical protein [Arabidopsis thaliana] gi|332010225|gb|AED97608.1| uncharacterized protein AT5G62440 [Arabidopsis thaliana]	203	202	4.00E−65	99.5	67.5	73.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G62440.1 | Symbols: | Protein of unknown function (DUF3223) | chr5:25072620−25073917 REVERSE LENGTH=202	203	202	1.00E−67	99.5	67.5	73.9
Rsa1.0_00914.1.g21220.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00914.1.g21221.t1	gb|AAM60966.1| unknown [Arabidopsis thaliana]	303	306	1.00E−154	101.0	88.4	94.1	unknown	gbpln	Arabidopsis thaliana	AT1G28120.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ovarian tumour, otubain (InterPro:IPR003323), Ubiquitin thioesterase Otubain (InterPro:IPR016615), Peptidase C65, otubain (InterPro:IPR019400); Has 413 Blast hits to 411 proteins in 139 species: Archae − 0; Bacteria − 0; Metazoa − 184; Fungi − 83; Plants − 88; Viruses − 0; Other Eukaryotes − 58 (source: NCBI BLink). | chr1:9813219−9815143 REVERSE LENGTH=306	303	306	1.00E−155	101.0	88.1	93.7
Rsa1.0_00914.1.g21222.t1	gb|EOA39179.1| hypothetical protein CARUB_v10012143mg [Capsella rubella]	240	244	1.00E−100	101.7	75.0	80.0	hypothetical protein CARUB_v10012143mg	gbpln	Capsella rubella	AT1G28160.1 | Symbols: | Integrase−type DNA−binding superfamily protein | chr1:9839387−9840124 FORWARD LENGTH=245	240	245	1.00E−101	102.1	82.9	88.3
Rsa1.0_00914.1.g21223.t1	gb|EOA36914.1| hypothetical protein CARUB_v10009741mg [Capsella rubella]	326	324	1.00E−139	99.4	72.7	88.0	hypothetical protein CARUB_v10009741mg	gbpln	Capsella rubella	AT1G28170.1 | Symbols: SOT7 | sulphotransferase 7 | chr1:9841332−9842312 FORWARD LENGTH=326	326	326	1.00E−140	100.0	76.7	87.1
Rsa1.0_00914.1.g21224.t1	ref|XP_002893509.1| hypothetical protein ARALYDRAFT_890355 [Arabidopsis lyrata subsp. lyrata] gi|297339351|gb|EFH69768.1| hypothetical protein ARALYDRAFT_890355 [Arabidopsis lyrata subsp. lyrata]	267	263	2.00E−91	98.5	76.0	82.4	hypothetical protein ARALYDRAFT_890355	gbpln	Arabidopsis lyrata	AT1G28190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12340.1); Has 166 Blast hits to 162 proteins in 36 species: Archae − 0; Bacteria − 2; Metazoa − 15; Fungi − 5; Plants − 124; Viruses − 0; Other Eukaryotes − 20 (source: NCBI BLink). | chr1:9847015−9847815 REVERSE LENGTH=266	267	266	2.00E−88	99.6	63.7	68.5
Rsa1.0_00914.1.g21225.t1	gb|EOA38389.1| hypothetical protein CARUB_v10009952mg, partial [Capsella rubella]	258	281	1.00E−120	108.9	83.3	89.1	hypothetical protein CARUB_v10009952mg, partial	gbpln	Capsella rubella	AT1G28200.1 | Symbols: FIP1 | FH interacting protein 1 | chr1:9850395−9852300 REVERSE LENGTH=259	258	259	1.00E−118	100.4	84.1	89.9
Rsa1.0_00914.1.g21226.t1	gb|EOA22230.1| hypothetical protein CARUB_v10002817mg [Capsella rubella]	384	390	3.00E−87	101.6	51.6	66.7	hypothetical protein CARUB_v10002817mg	gbpln	Capsella rubella	AT5G18160.1 | Symbols: | F−box and associated interaction domains−containing protein | chr5:6002770−6003909 FORWARD LENGTH=379	384	379	3.00E−58	98.7	39.8	53.6
Rsa1.0_00914.1.g21227.t1	ref|XP_002873866.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata] gi|297319703|gb|EFH50125.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata]	394	384	4.00E−77	97.5	47.0	61.7	hypothetical protein ARALYDRAFT_909803	gbpln	Arabidopsis lyrata	AT1G50870.1 | Symbols: | F−box and associated interaction domains−containing protein | chr1:18855147−18856337 FORWARD LENGTH=396	394	396	1.00E−51	100.5	36.5	51.5
Rsa1.0_00914.1.g21228.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00914.1.g21229.t1	ref|XP_002873866.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata] gi|297319703|gb|EFH50125.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata]	396	384	3.00E−79	97.0	48.0	62.6	hypothetical protein ARALYDRAFT_909803	gbpln	Arabidopsis lyrata	AT5G18160.1 | Symbols: | F−box and associated interaction domains−containing protein | chr5:6002770−6003909 FORWARD LENGTH=379	396	379	3.00E−57	95.7	38.4	54.0
Rsa1.0_00914.1.g21230.t1	ref|XP_002873866.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata] gi|297319703|gb|EFH50125.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata]	398	384	5.00E−80	96.5	48.0	62.1	hypothetical protein ARALYDRAFT_909803	gbpln	Arabidopsis lyrata	AT1G50870.1 | Symbols: | F−box and associated interaction domains−containing protein | chr1:18855147−18856337 FORWARD LENGTH=396	398	396	2.00E−63	99.5	41.2	59.0

<table>
<tr><td>Rsa1.0_00914.1.g21231.t5</td><td>ref|XP_002890765.1| hypothetical protein ARALYDRAFT_473029 [Arabidopsis lyrata subsp. lyrata] gi|297336607|gb|EFH67024.1| hypothetical protein ARALYDRAFT_473029 [Arabidopsis lyrata subsp. lyrata]</td><td>438</td><td>427</td><td>0</td><td>97.5</td><td>77.2</td><td>83.8</td><td>hypothetical protein ARALYDRAFT_473029</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G28210.1 | Symbols: ATJ1 | DNAJ heat shock family protein | chr1:9854598-9859884 FORWARD LENGTH=408</td><td>438</td><td>408</td><td>0</td><td>93.2</td><td>76.5</td><td>84.0</td></tr>
<tr><td>Rsa1.0_00914.1.g21232.t1</td><td>gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]</td><td>1456</td><td>1459</td><td>0</td><td>100.2</td><td>60.4</td><td>74.2</td><td>polyprotein, putative</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1456</td><td>1262</td><td>1.00E-106</td><td>86.7</td><td>12.7</td><td>19.1</td></tr>
<tr><td>Rsa1.0_00914.1.g21233.t1</td><td>gb|EOA38101.1| hypothetical protein CARUB_v10009570mg [Capsella rubella]</td><td>339</td><td>355</td><td>1.00E-151</td><td>104.7</td><td>79.1</td><td>86.7</td><td>hypothetical protein CARUB_v10009570mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G28230.1 | Symbols: PUP1, ATPUP1 | purine permease 1 | chr1:9862200-9864554 REVERSE LENGTH=356</td><td>339</td><td>356</td><td>1.00E-147</td><td>105.0</td><td>79.4</td><td>86.4</td></tr>
<tr><td>Rsa1.0_00914.1.g21234.t1</td><td>gb|EOA38101.1| hypothetical protein CARUB_v10009570mg [Capsella rubella]</td><td>352</td><td>355</td><td>1.00E-164</td><td>100.9</td><td>83.0</td><td>89.8</td><td>hypothetical protein CARUB_v10009570mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G28230.1 | Symbols: PUP1, ATPUP1 | purine permease 1 | chr1:9862200-9864554 REVERSE LENGTH=356</td><td>352</td><td>356</td><td>1.00E-163</td><td>101.1</td><td>86.1</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00914.1.g21235.t1</td><td>emb|CAB40067.1| putative retrotransposon polyprotein [Arabidopsis thaliana] gi|7267797|emb|CAB81200.1| putative retrotransposon polyprotein [Arabidopsis thaliana]</td><td>1063</td><td>1203</td><td>0</td><td>113.2</td><td>35.3</td><td>42.6</td><td>putative retrotransposon polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1063</td><td>1262</td><td>1.00E-167</td><td>118.7</td><td>27.1</td><td>37.3</td></tr>
<tr><td>Rsa1.0_00915.1.g21236.t1</td><td>ref|XP_002864698.1| hypothetical protein ARALYDRAFT_496218 [Arabidopsis lyrata subsp. lyrata] gi|297310533|gb|EFH40957.1| hypothetical protein ARALYDRAFT_496218 [Arabidopsis lyrata subsp. lyrata]</td><td>851</td><td>844</td><td>0</td><td>99.2</td><td>95.9</td><td>98.5</td><td>hypothetical protein ARALYDRAFT_496218</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G60690.1 | Symbols: REV, IFL, IFL1 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr5:24397734-24401933 FORWARD LENGTH=842</td><td>851</td><td>842</td><td>0</td><td>98.9</td><td>96.2</td><td>98.4</td></tr>
<tr><td>Rsa1.0_00915.1.g21237.t1</td><td>dbj|BAB09843.1| unnamed protein product [Arabidopsis thaliana]</td><td>933</td><td>932</td><td>0</td><td>99.9</td><td>95.4</td><td>97.5</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G60700.1 | Symbols: | glycosyltransferase family protein 2 | chr5:24402329-24404729 REVERSE LENGTH=668</td><td>933</td><td>668</td><td>0</td><td>71.6</td><td>69.1</td><td>70.5</td></tr>
<tr><td>Rsa1.0_00915.1.g21238.t1</td><td>gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1873</td><td>1352</td><td>0</td><td>72.2</td><td>37.4</td><td>49.1</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>1873</td><td>746</td><td>1.00E-116</td><td>39.8</td><td>11.3</td><td>14.5</td></tr>
<tr><td>Rsa1.0_00915.1.g21239.t1</td><td>ref|XP_002882535.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297328375|gb|EFH58794.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>393</td><td>394</td><td>1.00E-180</td><td>100.3</td><td>80.9</td><td>91.6</td><td>F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G07550.2 | Symbols: | RNI-like superfamily protein | chr3:2409946-2411133 FORWARD LENGTH=395</td><td>393</td><td>395</td><td>0</td><td>100.5</td><td>80.7</td><td>91.3</td></tr>
<tr><td>Rsa1.0_00915.1.g21240.t1</td><td>ref|NP_566311.1| formin-like protein 10 [Arabidopsis thaliana] gi|75207382|sp|Q9SRR2.1|FH10_ARATH RecName: Full=Formin-like protein 10; Short=AtFH10; Flags: Precursor gi|6041849|gb|AAF02158.1|AC009853_18 hypothetical protein [Arabidopsis thaliana] gi|17386106|gb|AAL38599.1|AF446866_1 AT3g07540/F21O3_25 [Arabidopsis thaliana] gi|15215734|gb|AAK91412.1| AT3g07540/F21O3_25 [Arabidopsis thaliana] gi|332641037|gb|AEE74558.1| formin-like protein 10 [Arabidopsis thaliana]</td><td>980</td><td>841</td><td>1.00E-176</td><td>85.8</td><td>46.0</td><td>55.3</td><td>formin-like protein 10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G07540.1 | Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr3:2404763-2407464 REVERSE LENGTH=841</td><td>980</td><td>841</td><td>1.00E-179</td><td>85.8</td><td>46.0</td><td>55.3</td></tr>
<tr><td>Rsa1.0_00915.1.g21241.t1</td><td>ref|XP_002882534.1| hypothetical protein ARALYDRAFT_896920 [Arabidopsis lyrata subsp. lyrata] gi|297328374|gb|EFH58793.1| hypothetical protein ARALYDRAFT_896920 [Arabidopsis lyrata subsp. lyrata]</td><td>695</td><td>699</td><td>0</td><td>100.6</td><td>80.7</td><td>88.9</td><td>hypothetical protein ARALYDRAFT_896920</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G07530.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Beta-Casp domain (InterPro:IPR022712); BEST Arabidopsis thaliana protein match is: cleavage and polyadenylation specificity factor 73 kDa subunit-II (TAIR:AT2G01730.1); Has 624 Blast hits to 615 proteins in 160 species: Archae - 54; Bacteria - 6; Metazoa - 333; Fungi - 44; Plants - 93; Viruses - 0; Other Eukaryotes - 94 (source: NCBI BLink). | chr3:2400793-2404280 FORWARD LENGTH=699</td><td>695</td><td>699</td><td>0</td><td>100.6</td><td>81.6</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00915.1.g21242.t1</td><td>ref|NP_850532.1| autophagocytosis-associated family protein [Arabidopsis thaliana] gi|17529020|gb|AAL38720.1| unknown protein [Arabidopsis thaliana] gi|23296729|gb|AAN13156.1| unknown protein [Arabidopsis thaliana] gi|332641035|gb|AEE74556.1| autophagocytosis-associated family protein [Arabidopsis thaliana]</td><td>223</td><td>225</td><td>2.00E-85</td><td>100.9</td><td>72.2</td><td>86.1</td><td>autophagocytosis-associated family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G07525.1 | Symbols: ATG10, ATATG10 | autophagocytosis-associated family protein | chr3:2399277-2400380 REVERSE LENGTH=225</td><td>223</td><td>225</td><td>5.00E-88</td><td>100.9</td><td>72.2</td><td>86.1</td></tr>
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Rsa1.0_00915.1.g21243.t1	ref|NP_566310.1| uncharacterized protein [Arabidopsis thaliana] gi|145331996|ref|NP_001078120.1| uncharacterized protein [Arabidopsis thaliana] gi|13877549|gb|AAK43852.1|AF370475_1 Unknown protein [Arabidopsis thaliana] gi|20148735|gb|AAM10258.1| unknown protein [Arabidopsis thaliana] gi|332641030|gb|AEE74551.1| uncharacterized protein AT3G07510 [Arabidopsis thaliana] gi|332641031|gb|AEE74552.1| uncharacterized protein AT3G07510 [Arabidopsis thaliana]	177	189	1.00E-76	106.8	92.7	96.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G07510.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G01580.1); Has 133 Blast hits to 133 proteins in 14 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 129; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2393895-2394464 REVERSE LENGTH=189	177	189	4.00E-79	106.8	92.7	96.6
Rsa1.0_00915.1.g21244.t1	gb|EOA29636.1| hypothetical protein CARUB_v10014621mg [Capsella rubella]	203	211	3.00E-84	103.9	79.8	83.7	hypothetical protein CARUB_v10014621mg	gbpln	Capsella rubella	AT3G07500.1 | Symbols: | Far-red impaired responsive (FAR1) family protein | chr3:2392387-2393709 FORWARD LENGTH=217	203	217	2.00E-83	106.9	80.3	86.2
Rsa1.0_00915.1.g21245.t1	ref|NP_187405.1| calmodulin-like protein 3 [Arabidopsis thaliana] gi|297829300|ref|XP_002882532.1| ARF-GAP domain 11 [Arabidopsis lyrata subsp. lyrata] gi|75337571|sp|Q9SRR7.1|CML3_ARATH RecName: Full=Calmodulin-like protein 3 gi|6041859|gb|AAF02168.1|AC009853_28 putative calmodulin [Arabidopsis thaliana] gi|297328372|gb|EFH58791.1| ARF-GAP domain 11 [Arabidopsis lyrata subsp. lyrata] gi|332641028|gb|AEE74549.1| calmodulin-like protein 3 [Arabidopsis thaliana]	153	153	6.00E-70	100.0	94.8	99.3	calmodulin-like protein 3	gbpln	Arabidopsis lyrata	AT3G07490.1 | Symbols: AGD11 | ARF-GAP domain 11 | chr3:2391189-2391650 FORWARD LENGTH=153	153	153	2.00E-72	100.0	94.8	99.3
Rsa1.0_00915.1.g21246.t1	ref|NP_566309.1| 2Fe-2S ferredoxin-like protein [Arabidopsis thaliana] gi|297829298|ref|XP_002882531.1| electron carrier/ iron ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|6041858|gb|AAF02167.1|AC009853_27 unknown protein [Arabidopsis thaliana] gi|14423424|gb|AAK62394.1|AF386949_1 Unknown protein [Arabidopsis thaliana] gi|20148369|gb|AAM10075.1| unknown protein [Arabidopsis thaliana] gi|21555779|gb|AAM63932.1| unknown [Arabidopsis thaliana] gi|297328371|gb|EFH58790.1| electron carrier/ iron ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|332641027|gb|AEE74548.1| 2Fe-2S ferredoxin-like protein [Arabidopsis thaliana]	157	159	3.00E-73	101.3	88.5	93.0	2Fe-2S ferredoxin-like protein	gbpln	Arabidopsis lyrata	AT3G07480.1 | Symbols: | 2Fe-2S ferredoxin-like superfamily protein | chr3:2389026-2389505 FORWARD LENGTH=159	157	159	9.00E-76	101.3	88.5	93.0
Rsa1.0_00915.1.g21247.t1	gb|AAF02163.1|AC009853_23 unknown protein [Arabidopsis thaliana]	186	160	1.00E-64	86.0	66.1	71.5	unknown protein	gbpln	Arabidopsis thaliana	AT3G07470.1 | Symbols: | Protein of unknown function, DUF538 | chr3:2387291-2388343 REVERSE LENGTH=169	186	169	5.00E-67	90.9	66.1	71.5
Rsa1.0_00915.1.g21248.t1	gb|EOA32947.1| hypothetical protein CARUB_v10016275mg [Capsella rubella]	103	113	8.00E-40	109.7	78.6	84.5	hypothetical protein CARUB_v10016275mg	gbpln	Capsella rubella	AT3G07450.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:2383610-2383930 REVERSE LENGTH=106	103	106	3.00E-42	102.9	79.6	84.5
Rsa1.0_00915.1.g21249.t1	ref|NP_974247.1| uncharacterized protein [Arabidopsis thaliana] gi|332641020|gb|AEE74541.1| uncharacterized protein AT3G07425 [Arabidopsis thaliana]	98	98	6.00E-43	100.0	89.8	94.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G07425.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:2378350-2378646 FORWARD LENGTH=98	98	98	1.00E-45	100.0	89.8	94.9
Rsa1.0_00915.1.g21250.t1	ref|NP_178368.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|3184275|gb|AAC18922.1| putative reverse transcriptase [Arabidopsis thaliana] gi|330250513|gb|AEC05607.1| RNase H domain-containing protein [Arabidopsis thaliana]	352	365	1.00E-82	103.7	45.2	63.1	RNase H domain-containing protein	gbpln	Arabidopsis thaliana	AT2G02650.1 | Symbols: | Ribonuclease H-like superfamily protein | chr2:735411-736546 FORWARD LENGTH=365	352	365	3.00E-85	103.7	45.2	63.1

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<tr><td>Rsa1.0_00915.1.g21257.t3</td><td>ref|XP_002884640.1| eukaryotic translation initiation factor 2B family protein [Arabidopsis lyrata subsp. lyrata] gi|297330480|gb|EFH60899.1| eukaryotic translation initiation factor 2B family protein [Arabidopsis lyrata subsp. lyrata]</td><td>522</td><td>407</td><td>0</td><td>78.0</td><td>73.0</td><td>75.3</td><td>eukaryotic translation initiation factor 2B family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G07300.2 | Symbols: | NagB/RpiA/CoA transferase-like superfamily protein | chr3:2324967-2327380 REVERSE LENGTH=407</td><td>522</td><td>407</td><td>0</td><td>78.0</td><td>72.6</td><td>75.1</td></tr>
<tr><td>Rsa1.0_00915.1.g21258.t1</td><td>ref|XP_002871678.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297317515|gb|EFH47937.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>375</td><td>430</td><td>4.00E-36</td><td>114.7</td><td>31.2</td><td>46.4</td><td>F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G11590.1 | Symbols: | F-box associated ubiquitination effector family protein | chr4:7008603-7009796 FORWARD LENGTH=397</td><td>375</td><td>397</td><td>4.00E-38</td><td>105.9</td><td>36.3</td><td>52.0</td></tr>
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<tr><td>Rsa1.0_00915.1.g21261.t1</td><td>ref|XP_002882520.1| GTP cyclohydrolase I [Arabidopsis lyrata subsp. lyrata] gi|297328360|gb|EFH58779.1| GTP cyclohydrolase I [Arabidopsis lyrata subsp. lyrata]</td><td>121</td><td>466</td><td>8.00E-27</td><td>385.1</td><td>62.0</td><td>71.9</td><td>GTP cyclohydrolase I</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G07270.2 | Symbols: | GTP cyclohydrolase I | chr3:2314005-2317059 FORWARD LENGTH=466</td><td>121</td><td>466</td><td>3.00E-29</td><td>385.1</td><td>50.4</td><td>57.9</td></tr>
<tr><td>Rsa1.0_00915.1.g21262.t1</td><td>ref|XP_002862662.1| hypothetical protein ARALYDRAFT_920411 [Arabidopsis lyrata subsp. lyrata] gi|297308316|gb|EFH38920.1| hypothetical protein ARALYDRAFT_920411 [Arabidopsis lyrata subsp. lyrata]</td><td>191</td><td>224</td><td>2.00E-34</td><td>117.3</td><td>43.5</td><td>58.6</td><td>hypothetical protein ARALYDRAFT_920411</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G40260.1 | Symbols: SWEET8, AtSWEET8 | Nodulin MtN3 family protein | chr5:16089842-16091527 FORWARD LENGTH=239</td><td>191</td><td>239</td><td>7.00E-28</td><td>125.1</td><td>36.6</td><td>51.8</td></tr>
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<tr><td>Rsa1.0_00915.1.g21263.t1</td><td>ref|NP_187383.1| GTP cyclohydrolase I [Arabidopsis thaliana] gi|6642638|gb|AAF20219.1|AC012395_6 GTP cyclohydrolase I [Arabidopsis thaliana] gi|20466832|gb|AAM20733.1| GTP cyclohydrolase I [Arabidopsis thaliana] gi|30387557|gb|AAP31944.1| At3g07270 [Arabidopsis thaliana] gi|332640999|gb|AEE74520.1| GTP cyclohydrolase I [Arabidopsis thaliana]</td><td>459</td><td>466</td><td>0</td><td>101.5</td><td>84.5</td><td>91.5</td><td>GTP cyclohydrolase I</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G07270.1 | Symbols: | GTP cyclohydrolase I | chr3:2315451-2317059 FORWARD LENGTH=466</td><td>459</td><td>466</td><td>0</td><td>101.5</td><td>84.5</td><td>91.5</td></tr>
<tr><td>Rsa1.0_00915.1.g21264.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00915.1.g21265.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>2030</td><td>1142</td><td>0</td><td>56.3</td><td>28.7</td><td>38.3</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>2030</td><td>575</td><td>6.00E-99</td><td>28.3</td><td>9.6</td><td>14.8</td></tr>
<tr><td>Rsa1.0_00916.1.g21266.t1</td><td>ref|NP_001078388.1| AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein [Arabidopsis thaliana] gi|332658025|gb|AEE83425.1| AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein [Arabidopsis thaliana]</td><td>555</td><td>548</td><td>0</td><td>98.7</td><td>94.1</td><td>96.9</td><td>AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G14350.3 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr4:8256353-8259934 REVERSE LENGTH=548</td><td>555</td><td>548</td><td>0</td><td>98.7</td><td>94.1</td><td>96.9</td></tr>
<tr><td>Rsa1.0_00916.1.g21267.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00916.1.g21268.t1</td><td>ref|XP_004245305.1| PREDICTED: uncharacterized protein At3g23325-like [Solanum lycopersicum]</td><td>87</td><td>87</td><td>5.00E-45</td><td>100.0</td><td>97.7</td><td>100.0</td><td>PREDICTED: uncharacterized protein At3g23325-like</td><td>gbpln</td><td>Solanum lycopersicum</td><td>AT3G23325.1 | Symbols: | Splicing factor 3B subunit 5/RDS3 complex subunit 10 | chr3:8345808-8346856 FORWARD LENGTH=87</td><td>87</td><td>87</td><td>6.00E-47</td><td>100.0</td><td>96.6</td><td>98.9</td></tr>
<tr><td>Rsa1.0_00916.1.g21269.t1</td><td>ref|NP_193170.1| casein kinase I [Arabidopsis thaliana] gi|9965745|gb|AAG10149.1|AF250343_1 casein kinase I [Arabidopsis thaliana] gi|1103318|emb|CAA55395.1| casein kinase I [Arabidopsis thaliana] gi|2244791|emb|CAB10213.1| casein kinase I [Arabidopsis thaliana] gi|7268139|emb|CAB78476.1| casein kinase I [Arabidopsis thaliana] gi|15450525|gb|AAK96555.1| AT4g14340/dl3210c [Arabidopsis thaliana] gi|16974431|gb|AAL31141.1| AT4g14340/dl3210c [Arabidopsis thaliana] gi|62996992|gb|AAY24540.1| casein kinase 1-like protein 11 [Arabidopsis thaliana] gi|332658021|gb|AEE83421.1| casein kinase I [Arabidopsis thaliana]</td><td>460</td><td>457</td><td>0</td><td>99.3</td><td>88.9</td><td>92.6</td><td>casein kinase I</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G14340.1 | Symbols: CKI1, CKL11 | casein kinase I | chr4:8248532-8251668 REVERSE LENGTH=457</td><td>460</td><td>457</td><td>0</td><td>99.3</td><td>88.9</td><td>92.6</td></tr>
<tr><td>Rsa1.0_00916.1.g21270.t1</td><td>ref|XP_002870320.1| hypothetical protein ARALYDRAFT_493473 [Arabidopsis lyrata subsp. lyrata] gi|297316156|gb|EFH46579.1| hypothetical protein ARALYDRAFT_493473 [Arabidopsis lyrata subsp. lyrata]</td><td>870</td><td>869</td><td>0</td><td>99.9</td><td>88.2</td><td>93.1</td><td>hypothetical protein ARALYDRAFT_493473</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G14330.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:8244228-8247286 FORWARD LENGTH=869</td><td>870</td><td>869</td><td>0</td><td>99.9</td><td>87.0</td><td>92.2</td></tr>
<tr><td>Rsa1.0_00916.1.g21271.t1</td><td>gb|AAK94425.1|AF398144_1 60S ribosomal protein L144 [Brassica rapa subsp. pekinensis]</td><td>105</td><td>119</td><td>2.00E-52</td><td>113.3</td><td>100.0</td><td>100.0</td><td>60S ribosomal protein L144</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G14320.1 | Symbols: | Zinc-binding ribosomal protein family protein | chr4:8242684-8243805 REVERSE LENGTH=105</td><td>105</td><td>105</td><td>4.00E-53</td><td>100.0</td><td>96.2</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00916.1.g21272.t1</td><td>ref|NP_172808.1| uncharacterized protein [Arabidopsis thaliana] gi|17381056|gb|AAL36340.1| unknown protein [Arabidopsis thaliana] gi|20465869|gb|AAM20039.1| unknown protein [Arabidopsis thaliana] gi|332190907|gb|AEE29028.1| uncharacterized protein AT1G13510 [Arabidopsis thaliana]</td><td>161</td><td>380</td><td>3.00E-47</td><td>236.0</td><td>70.2</td><td>79.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G13510.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4629459-4630687 REVERSE LENGTH=380</td><td>161</td><td>380</td><td>1.00E-49</td><td>236.0</td><td>70.2</td><td>79.5</td></tr>
<tr><td>Rsa1.0_00916.1.g21273.t1</td><td>gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]</td><td>521</td><td>1463</td><td>2.00E-23</td><td>280.8</td><td>15.9</td><td>25.3</td><td>F5J5.1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00916.1.g21274.t1</td><td>ref|XP_002892681.1| F5O11.3 [Arabidopsis lyrata subsp. lyrata] gi|297338523|gb|EFH68940.1| F5O11.3 [Arabidopsis lyrata subsp. lyrata]</td><td>472</td><td>1713</td><td>1.00E-107</td><td>362.9</td><td>46.2</td><td>51.9</td><td>F5O11.3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G12280.1 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr1:4174875-4177559 REVERSE LENGTH=894</td><td>472</td><td>894</td><td>1.00E-105</td><td>189.4</td><td>46.0</td><td>52.3</td></tr>
<tr><td>Rsa1.0_00916.1.g21275.t1</td><td>ref|XP_002892756.1| hypothetical protein ARALYDRAFT_312360 [Arabidopsis lyrata subsp. lyrata] gi|297338598|gb|EFH69015.1| hypothetical protein ARALYDRAFT_312360 [Arabidopsis lyrata subsp. lyrata]</td><td>325</td><td>772</td><td>1.00E-133</td><td>237.5</td><td>74.5</td><td>84.3</td><td>hypothetical protein ARALYDRAFT_312360</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G13520.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4631857-4633223 REVERSE LENGTH=387</td><td>325</td><td>387</td><td>1.00E-130</td><td>119.1</td><td>76.0</td><td>84.0</td></tr>
</table>

Rsa1.0_00916.1.g21276.t1	gb|EOA36691.1| hypothetical protein CARUB_v10012096mg [Capsella rubella]	328	327	1.00E-126	99.7	66.5	81.1	hypothetical protein CARUB_v10012096mg	gbpln	Capsella rubella	AT5G43690.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273-17547268 FORWARD LENGTH=331	328	331	1.00E-128	100.9	67.7	81.4
Rsa1.0_00917.1.g21277.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00917.1.g21278.t1	dbj|BAJ33984.1| unnamed protein product [Thellungiella halophila]	278	699	1.00E-123	251.4	89.2	91.7	unnamed protein product	----	----	AT5G56000.1 | Symbols: Hsp81.4, AtHsp90.4 | HEAT SHOCK PROTEIN 81.4 | chr5:22677602-22680067 REVERSE LENGTH=699	278	699	1.00E-124	251.4	86.7	91.4
Rsa1.0_00917.1.g21279.t1	dbj|BAJ33916.1| unnamed protein product [Thellungiella halophila]	492	578	0	117.5	81.5	87.6	unnamed protein product	----	----	AT1G32230.1 | Symbols: RCD1, CEO, CEO1, ATP8, AtRCD1 | WWE protein-protein interaction domain protein family | chr1:11613427-11615894 FORWARD LENGTH=589	492	589	0	119.7	78.0	85.0
Rsa1.0_00917.1.g21280.t1	ref|NP_199827.2| ferric reduction oxidase 8 [Arabidopsis thaliana] gi|75161398|sp|Q8VY13.1|FRO8_ARATH RecName: Full=Ferric reduction oxidase 8, mitochondrial; Short=AtFRO8; AltName: Full=Ferric-chelate reductase 8; Flags: Precursor gi|18377668|gb|AAL66984.1| putative FRO1 and FRO2 protein [Arabidopsis thaliana] gi|27754744|gb|AAO22815.1| putative FRO1 and FRO2 protein [Arabidopsis thaliana] gi|332008522|gb|AED95905.1| ferric reduction oxidase 8 [Arabidopsis thaliana]	715	728	0	101.8	79.6	89.2	ferric reduction oxidase 8	gbpln	Arabidopsis thaliana	AT5G50160.1 | Symbols: ATFRO8, FRO8 | ferric reduction oxidase 8 | chr5:20415832-20418582 FORWARD LENGTH=728	715	728	0	101.8	79.6	89.2
Rsa1.0_00917.1.g21281.t1	ref|XP_002893700.1| hypothetical protein ARALYDRAFT_473393 [Arabidopsis lyrata subsp. lyrata] gi|297339542|gb|EFH69959.1| hypothetical protein ARALYDRAFT_473393 [Arabidopsis lyrata subsp. lyrata]	313	317	1.00E-164	101.3	90.1	94.9	hypothetical protein ARALYDRAFT_473393	gbpln	Arabidopsis lyrata	AT1G32100.1 | Symbols: ATPRR1, PRR1 | pinoresinol reductase 1 | chr1:11546472-11547953 REVERSE LENGTH=317	313	317	1.00E-167	101.3	90.1	94.6
Rsa1.0_00917.1.g21282.t1	gb|EOA40160.1| hypothetical protein CARUB_v10008878mg [Capsella rubella]	514	514	0	100.0	91.4	94.2	hypothetical protein CARUB_v10008878mg	gbpln	Capsella rubella	AT1G32080.1 | Symbols: | membrane protein, putative | chr1:11537572-11539756 REVERSE LENGTH=512	514	512	0	99.6	91.2	94.2
Rsa1.0_00917.1.g21283.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1403	1515	0	108.0	58.4	73.3	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1403	1262	1.00E-115	90.0	13.7	20.8
Rsa1.0_00917.1.g21284.t1	ref|XP_002890967.1| hypothetical protein ARALYDRAFT_890765 [Arabidopsis lyrata subsp. lyrata] gi|297336809|gb|EFH67226.1| hypothetical protein ARALYDRAFT_890765 [Arabidopsis lyrata subsp. lyrata]	400	395	0	98.8	93.3	95.8	hypothetical protein ARALYDRAFT_890765	gbpln	Arabidopsis lyrata	AT1G32060.1 | Symbols: PRK | phosphoribulokinase | chr1:11532668-11534406 FORWARD LENGTH=395	400	395	0	98.8	93.3	95.8
Rsa1.0_00917.1.g21285.t2	ref|XP_002868268.1| hypothetical protein ARALYDRAFT_355334 [Arabidopsis lyrata subsp. lyrata] gi|297314104|gb|EFH44527.1| hypothetical protein ARALYDRAFT_355334 [Arabidopsis lyrata subsp. lyrata]	162	237	1.00E-18	146.3	31.5	44.4	hypothetical protein ARALYDRAFT_355334	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00918.1.g21286.t1	ref|NP_974140.1| uncharacterized protein [Arabidopsis thaliana] gi|332197370|gb|AEE35491.1| uncharacterized protein AT1G73650 [Arabidopsis thaliana]	310	302	1.00E-143	97.4	85.2	90.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G73650.3 | Symbols: | Protein of unknown function (DUF1295) | chr1:27688409-27690165 REVERSE LENGTH=302	310	302	2.33E-156	97.4	85.2	90.3
Rsa1.0_00918.1.g21287.t1	dbj|BAJ33800.1| unnamed protein product [Thellungiella halophila]	631	631	0	100.0	92.4	96.4	unnamed protein product	----	----	AT1G73680.1 | Symbols: ALPHA DOX2 | alpha dioxygenase | chr1:27704221-27707417 REVERSE LENGTH=631	631	631	0	100.0	88.7	94.8
Rsa1.0_00918.1.g21288.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00918.1.g21289.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	438	1231	1.00E-32	281.1	21.2	29.7	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	438	292	2.00E-23	66.7	17.1	26.0
Rsa1.0_00918.1.g21290.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00918.1.g21291.t1	ref|XP_002868325.1| hypothetical protein ARALYDRAFT_915512 [Arabidopsis lyrata subsp. lyrata] gi|297314161|gb|EFH44584.1| hypothetical protein ARALYDRAFT_915512 [Arabidopsis lyrata subsp. lyrata]	543	366	1.00E-110	67.4	41.6	48.4	hypothetical protein ARALYDRAFT_915512	gbpln	Arabidopsis lyrata	AT4G36840.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:17352166-17352882 FORWARD LENGTH=238	543	238	1.00E-54	43.8	22.1	27.3

Rsa1.0_00918.1.g21292.t1	ref|XP_002868325.1| hypothetical protein ARALYDRAFT_915512 [Arabidopsis lyrata subsp. lyrata] gi|297314161|gb|EFH44584.1| hypothetical protein ARALYDRAFT_915512 [Arabidopsis lyrata subsp. lyrata]	370	366	1.00E-105	98.9	60.0	70.0	hypothetical protein ARALYDRAFT_915512	gbpln	Arabidopsis lyrata	AT4G36840.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:17352166-17352882 FORWARD LENGTH=238	370	238	1.00E-48	64.3	31.4	39.2
Rsa1.0_00918.1.g21293.t1	gb|EOA28675.1| hypothetical protein CARUB_v10024899mg, partial [Capsella rubella]	522	451	1.00E-131	86.4	46.9	60.5	hypothetical protein CARUB_v10024899mg, partial	gbpln	Capsella rubella	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337-69884 REVERSE LENGTH=515	522	515	1.00E-126	98.7	47.9	65.3
Rsa1.0_00918.1.g21294.t1	gb|AAC63844.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1348	1231	0	91.3	56.3	68.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17201414-17202323 REVERSE LENGTH=258	1348	258	6.00E-92	19.1	11.6	14.1
Rsa1.0_00919.1.g21295.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00919.1.g21296.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00919.1.g21297.t1	gb|AAN62481.1| phosphatidylinositol 3-kinase [Brassica napus]	807	813	0	100.7	93.6	97.3	phosphatidylinositol 3-kinase	gbpln	Brassica napus	AT1G60490.1 | Symbols: ATVPS34, VPS34, PI3K | vacuolar protein sorting 34 | chr1:22285792-22290190 REVERSE LENGTH=814	807	814	0	100.9	91.7	96.7
Rsa1.0_00919.1.g21298.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00919.1.g21299.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00919.1.g21300.t1	gb|EOA15129.1| hypothetical protein CARUB_v10028504mg [Capsella rubella]	351	317	1.00E-168	90.3	78.6	85.5	hypothetical protein CARUB_v10028504mg	gbpln	Capsella rubella	AT5G42180.1 | Symbols: | Peroxidase superfamily protein | chr5:16852702-16854021 FORWARD LENGTH=317	351	317	1.00E-168	90.3	77.2	84.0
Rsa1.0_00919.1.g21301.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00919.1.g21302.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00919.1.g21303.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	351	1142	8.00E-60	325.4	34.8	49.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	351	575	2.00E-22	163.8	23.1	41.6
Rsa1.0_00919.1.g21304.t1	emb|CAN77045.1| hypothetical protein VITISV_035256 [Vitis vinifera]	265	665	9.00E-78	250.9	51.7	66.8	hypothetical protein VITISV_035256	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00919.1.g21305.t2	gb|ABD65112.1| hypothetical protein 31.t00014 [Brassica oleracea]	121	122	2.00E-33	100.8	62.8	74.4	hypothetical protein 31.t00014	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00919.1.g21306.t1	#	#	#	#	#	#	#	-	----	----	AT1G17920.1 | Symbols: HDG12 | homeodomain GLABROUS 12 | chr1:6162214-6165033 REVERSE LENGTH=687	111	687	1.00E-10	618.9	29.7	42.3
Rsa1.0_00920.1.g21307.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	210	940	4.00E-14	447.6	25.7	43.3	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00920.1.g21308.t1	ref|XP_002889171.1| hypothetical protein ARALYDRAFT_476964 [Arabidopsis lyrata subsp. lyrata] gi|297335012|gb|EFH65430.1| hypothetical protein ARALYDRAFT_476964 [Arabidopsis lyrata subsp. lyrata]	154	162	2.00E-60	105.2	82.5	88.3	hypothetical protein ARALYDRAFT_476964	gbpln	Arabidopsis lyrata	AT1G78020.1 | Symbols: | Protein of unknown function (DUF581) | chr1:29338787-29339491 FORWARD LENGTH=162	154	162	6.00E-63	105.2	81.8	87.7
Rsa1.0_00920.1.g21309.t1	ref|NP_177924.3| putative tRNA modification GTPase [Arabidopsis thaliana] gi|51536472|gb|AAU05474.1| At1g78010 [Arabidopsis thaliana] gi|52421301|gb|AAU45220.1| At1g78010 [Arabidopsis thaliana] gi|332197936|gb|AEE36057.1| putative tRNA modification GTPase [Arabidopsis thaliana]	580	560	0	96.6	79.8	86.4	putative tRNA modification GTPase	gbpln	Arabidopsis thaliana	AT1G78010.1 | Symbols: | tRNA modification GTPase, putative | chr1:29333535-29336297 FORWARD LENGTH=560	580	560	0	96.6	79.8	86.4
Rsa1.0_00920.1.g21310.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00920.1.g21311.t1	gb|AFX60923.1| high-affinity sulfate transporter 1;2a [Brassica juncea]	655	655	0	100.0	96.2	98.3	high-affinity sulfate transporter 1;2a	gbpln	Brassica juncea	AT1G78000.2 | Symbols: SULTR1;2, SEL1 | sulfate transporter 1;2 | chr1:29329889-29332877 FORWARD LENGTH=653	655	653	0	99.7	93.3	96.9
Rsa1.0_00920.1.g21312.t2	gb|AAZ08077.2| putative low affinity sulfate transporter [Brassica napus]	660	653	0	98.9	93.6	95.8	putative low affinity sulfate transporter	gbpln	Brassica napus	AT1G77990.1 | Symbols: AST56, SULTR2;2 | STAS domain / Sulfate transporter family | chr1:29317965-29323249 REVERSE LENGTH=677	660	677	0	102.6	87.7	93.5
Rsa1.0_00920.1.g21313.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00920.1.g21314.t1	ref|XP_002889327.1| transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297335168|gb|EFH65586.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	170	252	1.00E-58	148.2	71.8	81.2	transcription factor	gbpln	Arabidopsis lyrata	AT1G77950.2 | Symbols: AGL67 | AGAMOUS-like 67 | chr1:29307029-29309667 FORWARD LENGTH=252	170	252	2.00E-55	148.2	68.2	78.2
Rsa1.0_00920.1.g21315.t1	gb|EOA35848.1| hypothetical protein CARUB_v10021089mg [Capsella rubella]	343	154	7.00E-72	44.9	39.4	40.8	hypothetical protein CARUB_v10021089mg	gbpln	Capsella rubella	AT1G77750.1 | Symbols: | Ribosomal protein S13/S18 family | chr1:29230346-29231490 REVERSE LENGTH=154	343	154	4.00E-74	44.9	39.4	40.8

Rsa1.0_00920.1.g21316.t1	ref|XP_002887697.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333538|gb|EFH63956.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	614	786	0	128.0	80.6	85.5	kinase family protein	gbpln	Arabidopsis lyrata	AT1G77720.1 | Symbols: PPK1 | putative protein kinase 1 | chr1:29210730-29213877 FORWARD LENGTH=777	614	777	0	126.5	80.6	86.0
Rsa1.0_00920.1.g21317.t1	ref|NP_177893.1| pathogenesis-related thaumatin-like protein [Arabidopsis thaliana] gi|12323299|gb|AAG51631.1|AC012193_13 thaumatin-like protein; 12104-13574 [Arabidopsis thaliana] gi|332197890|gb|AEE36011.1| pathogenesis-related thaumatin-like protein [Arabidopsis thaliana]	245	356	1.00E-108	145.3	75.9	82.9	pathogenesis-related thaumatin-like protein	gbpln	Arabidopsis thaliana	AT1G77700.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:29204747-29206217 FORWARD LENGTH=356	245	356	1.00E-111	145.3	75.9	82.9
Rsa1.0_00920.1.g21318.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	153	1231	2.00E-30	804.6	44.4	62.1	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365	153	365	3.00E-13	238.6	26.1	45.1
Rsa1.0_00920.1.g21319.t1	gb|ABK28471.1| unknown [Arabidopsis thaliana]	233	245	5.00E-79	105.2	83.7	89.3	unknown	gbpln	Arabidopsis thaliana	AT1G77200.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:29004357-29005091 REVERSE LENGTH=244	233	244	2.00E-81	104.7	83.7	89.3
Rsa1.0_00920.1.g21320.t2	ref|XP_002889128.1| hypothetical protein ARALYDRAFT_476882 [Arabidopsis lyrata subsp. lyrata] gi|297334969|gb|EFH65387.1| hypothetical protein ARALYDRAFT_476882 [Arabidopsis lyrata subsp. lyrata]	613	610	0	99.5	89.1	93.8	hypothetical protein ARALYDRAFT_476882	gbpln	Arabidopsis lyrata	AT1G77180.2 | Symbols: SKIP | chromatin protein family | chr1:28999791-29001632 REVERSE LENGTH=613	613	613	0	100.0	86.5	92.8
Rsa1.0_00920.1.g21321.t1	ref|XP_002889126.1| hypothetical protein ARALYDRAFT_476879 [Arabidopsis lyrata subsp. lyrata] gi|297334967|gb|EFH65385.1| hypothetical protein ARALYDRAFT_476879 [Arabidopsis lyrata subsp. lyrata]	260	261	2.00E-95	100.4	68.1	82.3	hypothetical protein ARALYDRAFT_476879	gbpln	Arabidopsis lyrata	AT1G77145.1 | Symbols: | Protein of unknown function (DUF506) | chr1:28990178-28991290 REVERSE LENGTH=260	260	260	3.00E-89	100.0	66.2	80.8
Rsa1.0_00920.1.g21322.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00920.1.g21323.t1	ref|XP_002887165.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297333006|gb|EFH63424.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	248	248	1.00E-110	100.0	77.4	87.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G68180.1 | Symbols: | RING/U-box superfamily protein | chr1:25554816-25555562 FORWARD LENGTH=248	248	248	1.00E-110	100.0	74.6	86.7
Rsa1.0_00920.1.g21324.t1	gb|EOA35456.1| hypothetical protein CARUB_v10020665mg [Capsella rubella]	323	320	1.00E-121	99.1	73.4	81.7	hypothetical protein CARUB_v10020665mg	gbpln	Capsella rubella	AT1G68200.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:25562118-25563948 FORWARD LENGTH=308	323	308	1.00E-110	95.4	73.4	82.7
Rsa1.0_00920.1.g21325.t1	gb|EOA34580.1| hypothetical protein CARUB_v10022138mg, partial [Capsella rubella]	565	681	1.00E-104	120.5	48.3	65.7	hypothetical protein CARUB_v10022138mg, partial	gbpln	Capsella rubella	AT1G68210.1 | Symbols: APRR6, PRR6 | pseudo-response regulator 6 | chr1:25565983-25569302 FORWARD LENGTH=755	565	755	2.00E-91	133.6	40.7	57.3
Rsa1.0_00920.1.g21326.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00920.1.g21327.t1	gb|EOA35646.1| hypothetical protein CARUB_v10020863mg, partial [Capsella rubella]	204	244	4.00E-90	119.6	82.8	88.7	hypothetical protein CARUB_v10020863mg, partial	gbpln	Capsella rubella	AT1G68220.1 | Symbols: | Protein of unknown function (DUF1218) | chr1:25570322-25571562 FORWARD LENGTH=201	204	201	1.00E-91	98.5	82.4	88.7
Rsa1.0_00920.1.g21328.t1	gb|EOA35712.1| hypothetical protein CARUB_v10020939mg [Capsella rubella]	188	215	9.00E-86	114.4	83.5	91.0	hypothetical protein CARUB_v10020939mg	gbpln	Capsella rubella	AT1G68230.2 | Symbols: | Reticulon family protein | chr1:25572185-25572921 FORWARD LENGTH=162	188	162	1.00E-54	86.2	59.0	63.8
Rsa1.0_00920.1.g21329.t1	gb|AAM63843.1| unknown [Arabidopsis thaliana]	294	439	7.00E-78	149.3	51.4	51.7	unknown	gbpln	Arabidopsis thaliana	AT5G42090.1 | Symbols: | Lung seven transmembrane receptor family protein | chr5:16826830-16828149 FORWARD LENGTH=439	294	439	1.00E-79	149.3	51.0	51.4
Rsa1.0_00920.1.g21330.t1	gb|EOA35757.1| hypothetical protein CARUB_v10020989mg [Capsella rubella]	200	191	5.00E-84	95.5	77.5	83.0	hypothetical protein CARUB_v10020989mg	gbpln	Capsella rubella	AT1G68260.1 | Symbols: | Thioesterase superfamily protein | chr1:25585976-25587601 REVERSE LENGTH=190	200	190	1.00E-84	95.0	76.0	82.5
Rsa1.0_00920.1.g21331.t2	gb|EOA34326.1| hypothetical protein CARUB_v10021846mg [Capsella rubella]	296	291	1.00E-151	98.3	87.2	92.2	hypothetical protein CARUB_v10021846mg	gbpln	Capsella rubella	AT1G68290.1 | Symbols: ENDO 2 | endonuclease 2 | chr1:25596718-25598264 FORWARD LENGTH=290	296	290	1.00E-150	98.0	84.5	90.2

Rsa1.0_00920.1.g21332.t1	ref|NP_564927.1| universal stress protein domain-containing protein [Arabidopsis thaliana] gi|12325313|gb|AAG52594.1|AC016447_3 unknown protein; 44604-45347 [Arabidopsis thaliana] gi|21555126|gb|AAM63782.1| unknown [Arabidopsis thaliana] gi|28950695|gb|AAO63271.1| At1g68300 [Arabidopsis thaliana] gi|110736101|dbj|BAF00023.1| hypothetical protein [Arabidopsis thaliana] gi|332196657|gb|AEE34778.1| universal stress protein domain-containing protein [Arabidopsis thaliana]	161	160	2.00E-75	99.4	84.5	93.8	universal stress protein domain-containing protein	gbpln	Arabidopsis thaliana	AT1G68300.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr1:25598518-25599261 REVERSE LENGTH=160	161	160	9.00E-78	99.4	84.5	93.8
Rsa1.0_00920.1.g21333.t1	ref|XP_002303444.1| predicted protein [Populus trichocarpa] gi|222840876|gb|EEE78423.1| predicted protein [Populus trichocarpa]	186	159	3.00E-63	85.5	66.7	78.0	predicted protein	gbpln	Populus trichocarpa	AT1G68310.2 | Symbols: AE7 | Protein of unknown function (DUF59) | chr1:25599812-25601239 FORWARD LENGTH=157	186	157	5.00E-63	84.4	66.7	75.3
Rsa1.0_00920.1.g21334.t1	ref|XP_002887176.1| hypothetical protein ARALYDRAFT_339072 [Arabidopsis lyrata subsp. lyrata] gi|297333017|gb|EFH63435.1| hypothetical protein ARALYDRAFT_339072 [Arabidopsis lyrata subsp. lyrata]	289	285	1.00E-117	98.6	79.6	85.1	hypothetical protein ARALYDRAFT_339072	gbpln	Arabidopsis lyrata	AT1G68320.1 | Symbols: MYB62, AtMYB62, BW62B, BW62C | myb domain protein 62 | chr1:25603842-25604884 FORWARD LENGTH=286	289	286	1.00E-118	99.0	78.2	83.7
Rsa1.0_00920.1.g21335.t1	ref|XP_002887177.1| hypothetical protein ARALYDRAFT_475952 [Arabidopsis lyrata subsp. lyrata] gi|297333018|gb|EFH63436.1| hypothetical protein ARALYDRAFT_475952 [Arabidopsis lyrata subsp. lyrata]	266	267	6.00E-92	100.4	80.5	84.2	hypothetical protein ARALYDRAFT_475952	gbpln	Arabidopsis lyrata	AT1G68330.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G48780.1); Has 155 Blast hits to 147 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 19; Fungi - 3; Plants - 126; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr1:25611242-25612048 FORWARD LENGTH=268	266	268	1.00E-93	100.8	80.8	84.6
Rsa1.0_00920.1.g21336.t1	gb|EOA36988.1| hypothetical protein CARUB_v10009968mg [Capsella rubella]	201	278	3.00E-28	138.3	48.8	61.7	hypothetical protein CARUB_v10009968mg	gbpln	Capsella rubella	AT1G25370.1 | Symbols: | Protein of unknown function (DUF1639) | chr1:8898046-8898934 REVERSE LENGTH=263	201	263	4.00E-29	130.8	47.8	63.2
Rsa1.0_00920.1.g21337.t1	ref|XP_002888657.1| hypothetical protein ARALYDRAFT_894600 [Arabidopsis lyrata subsp. lyrata] gi|297334498|gb|EFH64916.1| hypothetical protein ARALYDRAFT_894600 [Arabidopsis lyrata subsp. lyrata]	238	244	2.00E-90	102.5	81.5	87.0	hypothetical protein ARALYDRAFT_894600	gbpln	Arabidopsis lyrata	AT1G68360.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr1:25621678-25622412 REVERSE LENGTH=244	238	244	4.00E-92	102.5	82.8	87.0
Rsa1.0_00920.1.g21338.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	127	1072	9.00E-29	844.1	47.2	70.9	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	127	289	2.00E-31	227.6	45.7	72.4
Rsa1.0_00920.1.g21339.t1	ref|XP_002888672.1| alpha-xylosidase precursor [Arabidopsis lyrata subsp. lyrata] gi|297334513|gb|EFH64931.1| alpha-xylosidase precursor [Arabidopsis lyrata subsp. lyrata]	923	916	0	99.2	88.9	94.1	alpha-xylosidase precursor	gbpln	Arabidopsis lyrata	AT1G68560.1 | Symbols: ATXYL1, XYL1, TRG1 | alpha-xylosidase 1 | chr1:25734435-25737897 REVERSE LENGTH=915	923	915	0	99.1	88.6	93.9
Rsa1.0_00921.1.g21340.t1	ref|NP_190652.1| cold-regulated 413-plasma membrane 2 [Arabidopsis thaliana] gi|75212080|sp|Q9SVL6.1|CRPM2_ARATH RecName: Full=Cold-regulated 413 plasma membrane protein 2; Short=AtCOR413-PM2 gi|10121843|gb|AAG13394.1|AF283005_1 cold acclimation protein WCOR413-like protein beta form [Arabidopsis thaliana] gi|13430786|gb|AAK26015.1|AF360305_1 putative cold acclimation protein [Arabidopsis thaliana] gi|4835234|emb|CAB42912.1| putative cold acclimation protein [Arabidopsis thaliana] gi|15810635|gb|AAL07242.1| putative cold acclimation protein [Arabidopsis thaliana] gi|332645194|gb|AEE78715.1| cold-regulated 413-plasma membrane 2 [Arabidopsis thaliana]	284	203	1.00E-98	71.5	63.4	68.0	cold-regulated 413-plasma membrane 2	gbpln	Arabidopsis thaliana	AT3G50830.1 | Symbols: COR413-PM2, ATCOR413-PM2 | cold-regulated 413-plasma membrane 2 | chr3:18894109-18895355 REVERSE LENGTH=203	284	203	1.00E-101	71.5	63.4	68.0

Rsa1.0_00921.1.g21341.t3	ref|XP_002874843.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata] gi|297320680|gb|EFH51102.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata]	482	610	2.00E-66	126.6	28.8	34.4	hypothetical protein ARALYDRAFT_911810	gbpln	Arabidopsis lyrata	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	482	302	2.00E-61	62.7	26.1	32.6
Rsa1.0_00921.1.g21342.t1	ref|NP_001154670.1| PLATZ transcription factor family protein [Arabidopsis thaliana] gi|254801606|sp|P0CB19.1|Y3081_ARATH RecName: Full=Uncharacterized protein At3g50808 gi|332645191|gb|AEE78712.1| PLATZ transcription factor family protein [Arabidopsis thaliana]	178	110	7.00E-30	61.8	36.5	48.9	PLATZ transcription factor family protein	gbpln	Arabidopsis thaliana	AT3G50808.1 | Symbols: | PLATZ transcription factor family protein | chr3:18887614-18888047 REVERSE LENGTH=110	178	110	3.00E-32	61.8	36.5	48.9
Rsa1.0_00921.1.g21343.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	376	1529	4.00E-31	406.6	17.6	24.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	376	295	2.00E-20	78.5	16.2	22.9
Rsa1.0_00921.1.g21344.t1	ref|XP_002877771.1| hypothetical protein ARALYDRAFT_485427 [Arabidopsis lyrata subsp. lyrata] gi|297323609|gb|EFH54030.1| hypothetical protein ARALYDRAFT_485427 [Arabidopsis lyrata subsp. lyrata]	565	410	0	72.6	64.1	68.0	hypothetical protein ARALYDRAFT_485427	gbpln	Arabidopsis lyrata	AT3G50790.1 | Symbols: | esterase/lipase/thioesterase family protein | chr3:18880074-18881940 REVERSE LENGTH=408	565	408	0	72.2	63.0	67.4
Rsa1.0_00921.1.g21345.t1	ref|NP_190647.1| uncharacterized protein [Arabidopsis thaliana] gi|75212286|sp|Q9SVM0.1|Y3078_ARATH RecName: Full=BTB/POZ domain-containing protein At3g50780 gi|4835229|emb|CAB42907.1| putative protein [Arabidopsis thaliana] gi|27754671|gb|AAO22779.1| unknown protein [Arabidopsis thaliana] gi|28827604|gb|AAO50646.1| unknown protein [Arabidopsis thaliana] gi|332645188|gb|AEE78709.1| uncharacterized protein AT3G50780 [Arabidopsis thaliana]	521	520	0	99.8	85.8	91.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G50780.1 | Symbols: | BEST Arabidopsis thaliana protein match is: BTB/POZ domain-containing protein (TAIR:AT1G63850.1); Has 298 Blast hits to 298 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 10; Fungi - 0; Plants - 287; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:18875662-18877341 REVERSE LENGTH=520	521	520	0	99.8	85.8	91.6
Rsa1.0_00921.1.g21346.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00921.1.g21347.t1	gb|EOA28767.1| hypothetical protein CARUB_v10024999mg [Capsella rubella]	574	834	6.00E-60	145.3	21.4	28.2	hypothetical protein CARUB_v10024999mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00921.1.g21348.t1	gb|EOA25245.1| hypothetical protein CARUB_v10018559mg [Capsella rubella]	233	380	2.00E-73	163.1	64.8	77.3	hypothetical protein CARUB_v10018559mg	gbpln	Capsella rubella	AT1G11620.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3910833-3911924 FORWARD LENGTH=363	233	363	6.00E-23	155.8	33.5	52.4
Rsa1.0_00921.1.g21349.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00921.1.g21350.t3	ref|XP_002877763.1| hypothetical protein ARALYDRAFT_323632 [Arabidopsis lyrata subsp. lyrata] gi|297323601|gb|EFH54022.1| hypothetical protein ARALYDRAFT_323632 [Arabidopsis lyrata subsp. lyrata]	84	375	1.00E-14	446.4	46.4	63.1	hypothetical protein ARALYDRAFT_323632	gbpln	Arabidopsis lyrata	AT3G50720.1 | Symbols: | Protein kinase superfamily protein | chr3:18847519-18849430 REVERSE LENGTH=377	84	377	3.00E-15	448.8	41.7	52.4
Rsa1.0_00921.1.g21351.t1	#	#	#	#	#	#	#	-	----	----	AT1G13880.1 | Symbols: | ELM2 domain-containing protein | chr1:4749603-4750967 FORWARD LENGTH=424	126	424	7.00E-12	336.5	27.0	34.1
Rsa1.0_00921.1.g21352.t1	gb|EOA23993.1| hypothetical protein CARUB_v10017209mg [Capsella rubella]	456	458	0	100.4	82.9	87.3	hypothetical protein CARUB_v10017209mg	gbpln	Capsella rubella	AT3G50700.1 | Symbols: AtIDD2, IDD2 | indeterminate(ID)-domain 2 | chr3:18840945-18842829 FORWARD LENGTH=452	456	452	0	99.1	80.5	85.5
Rsa1.0_00922.1.g21353.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00922.1.g21354.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00922.1.g21355.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00922.1.g21356.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	558	1142	2.00E-84	204.7	29.4	36.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	558	575	2.00E-16	103.0	8.8	12.2
Rsa1.0_00922.1.g21357.t8	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00922.1.g21358.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00922.1.g21359.t1</td><td>ref|XP_002870468.1| hypothetical protein ARALYDRAFT_493654 [Arabidopsis lyrata subsp. lyrata] gi|297316304|gb|EFH46727.1| hypothetical protein ARALYDRAFT_493654 [Arabidopsis lyrata subsp. lyrata]</td><td>175</td><td>176</td><td>9.00E-73</td><td>100.6</td><td>80.6</td><td>87.4</td><td>hypothetical protein ARALYDRAFT_493654</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G36120.1 | Symbols: CCB3, YLMG3, atylmg3 | cofactor assembly, complex C (B6F) | chr5:14198679-14199203 REVERSE LENGTH=174</td><td>175</td><td>174</td><td>4.00E-73</td><td>99.4</td><td>79.4</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00922.1.g21360.t1</td><td>gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>195</td><td>1501</td><td>2.00E-77</td><td>769.7</td><td>69.2</td><td>83.1</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>195</td><td>1262</td><td>9.00E-44</td><td>647.2</td><td>43.1</td><td>64.1</td></tr>
<tr><td>Rsa1.0_00922.1.g21361.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00922.1.g21362.t1</td><td>gb|EOA19172.1| hypothetical protein CARUB_v10007851mg [Capsella rubella]</td><td>931</td><td>955</td><td>0</td><td>102.6</td><td>87.0</td><td>91.9</td><td>hypothetical protein CARUB_v10007851mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G35980.1 | Symbols: YAK1 | yeast YAK1-related gene 1 | chr5:14128551-14135984 FORWARD LENGTH=956</td><td>931</td><td>956</td><td>0</td><td>102.7</td><td>86.3</td><td>91.6</td></tr>
<tr><td>Rsa1.0_00923.1.g21363.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00923.1.g21364.t1</td><td>gb|EOA36548.1| hypothetical protein CARUB_v10011649mg [Capsella rubella]</td><td>199</td><td>261</td><td>1.00E-26</td><td>131.2</td><td>33.7</td><td>51.3</td><td>hypothetical protein CARUB_v10011649mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315</td><td>199</td><td>315</td><td>3.00E-28</td><td>158.3</td><td>34.2</td><td>51.8</td></tr>
<tr><td>Rsa1.0_00923.1.g21365.t1</td><td>ref|XP_002865614.1| hypothetical protein ARALYDRAFT_494871 [Arabidopsis lyrata subsp. lyrata] gi|297311449|gb|EFH41873.1| hypothetical protein ARALYDRAFT_494871 [Arabidopsis lyrata subsp. lyrata]</td><td>149</td><td>156</td><td>1.00E-72</td><td>104.7</td><td>90.6</td><td>94.6</td><td>hypothetical protein ARALYDRAFT_494871</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G48170.1 | Symbols: SLY2 | F-box family protein | chr5:19532729-19533202 REVERSE LENGTH=157</td><td>149</td><td>157</td><td>5.00E-74</td><td>105.4</td><td>89.3</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00923.1.g21366.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00923.1.g21367.t1</td><td>ref|XP_002873217.1| signal recognition particle binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319054|gb|EFH49476.1| signal recognition particle binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>222</td><td>260</td><td>1.00E-106</td><td>117.1</td><td>91.9</td><td>96.4</td><td>signal recognition particle binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05670.1 | Symbols: | signal recognition particle binding | chr5:1695916-1697534 REVERSE LENGTH=260</td><td>222</td><td>260</td><td>1.00E-107</td><td>117.1</td><td>89.6</td><td>95.9</td></tr>
<tr><td>Rsa1.0_00923.1.g21368.t1</td><td>dbj|BAJ34265.1| unnamed protein product [Thellungiella halophila]</td><td>324</td><td>324</td><td>1.00E-171</td><td>100.0</td><td>89.8</td><td>95.4</td><td>unnamed protein product</td><td>––––</td><td>––––</td><td>AT5G48180.1 | Symbols: NSP5 | nitrile specifier protein 5 | chr5:19541283-19542358 REVERSE LENGTH=326</td><td>324</td><td>326</td><td>1.00E-163</td><td>100.6</td><td>84.9</td><td>92.9</td></tr>
<tr><td>Rsa1.0_00923.1.g21369.t1</td><td>ref|NP_568693.1| uncharacterized protein [Arabidopsis thaliana] gi|8777411|dbj|BAA97001.1| unnamed protein product [Arabidopsis thaliana] gi|21536545|gb|AAM60877.1| unknown [Arabidopsis thaliana] gi|332008251|gb|AED95634.1| uncharacterized protein AT5G48210 [Arabidopsis thaliana]</td><td>101</td><td>103</td><td>2.00E-27</td><td>102.0</td><td>61.4</td><td>76.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G48210.1 | Symbols: | Protein of unknown function (DUF1278) | chr5:19548459-19548770 FORWARD LENGTH=103</td><td>101</td><td>103</td><td>3.00E-30</td><td>102.0</td><td>61.4</td><td>76.2</td></tr>
<tr><td>Rsa1.0_00923.1.g21370.t1</td><td>ref|XP_002863880.1| hypothetical protein ARALYDRAFT_494873 [Arabidopsis lyrata subsp. lyrata] gi|297309715|gb|EFH40139.1| hypothetical protein ARALYDRAFT_494873 [Arabidopsis lyrata subsp. lyrata]</td><td>317</td><td>375</td><td>1.00E-171</td><td>118.3</td><td>92.4</td><td>97.2</td><td>hypothetical protein ARALYDRAFT_494873</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G48220.1 | Symbols: | Aldolase-type TIM barrel family protein | chr5:19549930-19552046 FORWARD LENGTH=379</td><td>317</td><td>379</td><td>1.00E-173</td><td>119.6</td><td>92.1</td><td>97.2</td></tr>
<tr><td>Rsa1.0_00923.1.g21371.t1</td><td>ref|NP_568694.2| acetyl-CoA acetyltransferase, cytosolic 1 [Arabidopsis thaliana] gi|73919863|sp|Q8S4Y1.1|THIC1_ARATH RecName: Full=Acetyl-CoA acetyltransferase, cytosolic 1; AltName: Full=Cytosolic acetoacetyl-CoA thiolase 1; Short=Thiolase 1; AltName: Full=Protein EMBRYO DEFECTIVE 1276 gi|19880269|gb|AAM00280.1|AF364059_1 acetoacetyl-CoA thiolase [Arabidopsis thaliana] gi|222423909|dbj|BAH19918.1| AT5G48230 [Arabidopsis thaliana] gi|332008255|gb|AED95638.1| acetyl-CoA acetyltransferase, cytosolic 1 [Arabidopsis thaliana]</td><td>428</td><td>403</td><td>0</td><td>94.2</td><td>90.2</td><td>92.3</td><td>acetyl-CoA acetyltransferase, cytosolic 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G48230.2 | Symbols: EMB1276, ACAT2 | acetoacetyl-CoA thiolase 2 | chr5:19552570-19555122 REVERSE LENGTH=403</td><td>428</td><td>403</td><td>0</td><td>94.2</td><td>90.2</td><td>92.3</td></tr>
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Rsa1.0_00923.1.g21372.t1	ref|NP_199635.2| uncharacterized protein [Arabidopsis thaliana] gi|332008257|gb|AED95640.1| uncharacterized protein AT5G48240 [Arabidopsis thaliana]	311	309	1.00E-121	99.4	77.8	87.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G48240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1665 (InterPro:IPR012459); Has 402 Blast hits to 382 proteins in 162 species: Archae - 0; Bacteria - 4; Metazoa - 139; Fungi - 111; Plants - 54; Viruses - 1; Other Eukaryotes - 93 (source: NCBI BLink). | chr5:19559301-19561153 FORWARD LENGTH=309	311	309	1.00E-123	99.4	77.8	87.8
Rsa1.0_00923.1.g21373.t1	ref|NP_199636.1| zinc finger protein CONSTANS-LIKE 10 [Arabidopsis thaliana] gi|17433067|sp|Q9LUA9.1|COL10_ARATH RecName: Full=Zinc finger protein CONSTANS-LIKE 10 gi|8777415|dbj|BAA97005.1| unnamed protein product [Arabidopsis thaliana] gi|14532666|gb|AAK64061.1| unknown protein [Arabidopsis thaliana] gi|23296810|gb|AAN13176.1| unknown protein [Arabidopsis thaliana] gi|332008260|gb|AED95643.1| zinc finger protein CONSTANS-LIKE 10 [Arabidopsis thaliana]	401	373	1.00E-161	93.0	73.6	81.5	zinc finger protein CONSTANS-LIKE 10	gbpln	Arabidopsis thaliana	AT5G48250.1 | Symbols: | B-box type zinc finger protein with CCT domain | chr5:19561719-19563113 REVERSE LENGTH=373	401	373	1.00E-164	93.0	73.6	81.5
Rsa1.0_00923.1.g21374.t1	ref|XP_002865625.1| hypothetical protein ARALYDRAFT_917720 [Arabidopsis lyrata subsp. lyrata] gi|297311460|gb|EFH41884.1| hypothetical protein ARALYDRAFT_917720 [Arabidopsis lyrata subsp. lyrata]	324	322	1.00E-173	99.4	90.1	94.4	hypothetical protein ARALYDRAFT_917720	gbpln	Arabidopsis lyrata	AT5G48270.1 | Symbols: | Plant protein of unknown function (DUF868) | chr5:19564744-19565712 REVERSE LENGTH=322	324	322	1.00E-174	99.4	89.2	94.8
Rsa1.0_00923.1.g21375.t1	dbj|BAA98186.1| ATFP4-like [Arabidopsis thaliana]	211	157	3.00E-39	74.4	54.5	59.2	ATFP4-like	gbpln	Arabidopsis thaliana	AT5G48290.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:19568980-19569658 FORWARD LENGTH=181	211	181	4.00E-41	85.8	57.8	62.6
Rsa1.0_00923.1.g21376.t1	gb|AAM95647.1| polygalacturonase inhibitory protein [Brassica napus] gi|160693704|gb|ABX46550.1| polygalacturonase inhibitor protein 3 [Brassica napus]	302	331	1.00E-109	109.6	65.9	75.2	polygalacturonase inhibitory protein	gbpln	Brassica napus	AT5G06860.1 | Symbols: PGIP1, ATPGIP1 | polygalacturonase inhibiting protein 1 | chr5:2132373-2133434 FORWARD LENGTH=330	302	330	4.00E-92	109.3	55.6	65.9
Rsa1.0_00923.1.g21377.t1	dbj|BAJ33704.1| unnamed protein product [Thellungiella halophila]	516	523	0	101.4	96.7	97.3	unnamed protein product	----	----	AT5G48300.1 | Symbols: ADG1, APS1 | ADP glucose pyrophosphorylase 1 | chr5:19570326-19572557 FORWARD LENGTH=520	516	520	0	100.8	92.6	96.5
Rsa1.0_00923.1.g21378.t1	gb|EOA20463.1| hypothetical protein CARUB_v10000776mg, partial [Capsella rubella]	385	503	2.00E-97	130.6	59.2	73.5	hypothetical protein CARUB_v10000776mg, partial	gbpln	Capsella rubella	AT5G03780.1 | Symbols: TRFL10 | TRF-like 10 | chr5:999266-1000947 REVERSE LENGTH=420	385	420	7.00E-80	109.1	50.9	63.9
Rsa1.0_00923.1.g21379.t1	gb|EOA30157.1| hypothetical protein CARUB_v10013272mg [Capsella rubella]	330	600	8.00E-93	181.8	67.9	78.2	hypothetical protein CARUB_v10013272mg	gbpln	Capsella rubella	AT3G09360.1 | Symbols: | Cyclin/Brf1-like TBP-binding protein | chr3:2873796-2878432 FORWARD LENGTH=604	330	604	2.00E-93	183.0	67.9	78.5
Rsa1.0_00923.1.g21380.t1	gb|EOA30255.1| hypothetical protein CARUB_v10013377mg, partial [Capsella rubella]	462	553	1.00E-153	119.7	66.0	75.3	hypothetical protein CARUB_v10013377mg, partial	gbpln	Capsella rubella	AT3G09370.2 | Symbols: MYB3R-3 | myb domain protein 3r-3 | chr3:2879534-2882128 FORWARD LENGTH=510	462	510	1.00E-153	110.4	66.7	77.7
Rsa1.0_00923.1.g21381.t1	emb|CAO82943.1| putative pre-mRNA-splicing factor cwc-22 [Oryza sativa Japonica Group]	250	615	4.00E-85	246.0	63.2	77.2	putative pre-mRNA-splicing factor cwc-22	gbpln	Oryza sativa	AT1G80930.1 | Symbols: | MIF4G domain-containing protein / MA3 domain-containing protein | chr1:30405774-30409499 REVERSE LENGTH=900	250	900	1.00E-86	360.0	61.6	78.8
Rsa1.0_00923.1.g21382.t1	dbj|BAA11391.1| metallothionein-like protein [Brassica rapa]	75	80	2.00E-19	106.7	68.0	70.7	metallothionein-like protein	gbpln	Brassica rapa	AT3G09390.1 | Symbols: MT2A, ATMT-K, ATMT-1 | metallothionein 2A | chr3:2889737-2890188 REVERSE LENGTH=81	75	81	7.00E-22	108.0	69.3	70.7

Rsa1.0_00924.1.g21383.t1	ref|NP_194222.1| protein transport protein sec61 subunit gamma-1 [Arabidopsis thaliana] gi|18423153|ref|NP_568728.1| protein transport protein sec61 subunit gamma-1 [Arabidopsis thaliana] gi|297795847|ref|XP_002865808.1| hypothetical protein ARALYDRAFT_495113 [Arabidopsis lyrata subsp. lyrata] gi|297799504|ref|XP_002867636.1| hypothetical protein ARALYDRAFT_492346 [Arabidopsis lyrata subsp. lyrata] gi|408407792|sp|P0DI74.1|S61G1_ARATH RecName: Full=Protein transport protein Sec61 subunit gamma-1 gi|408407793|sp|P0DI75.1|S61G2_ARATH RecName: Full=Protein transport protein Sec61 subunit gamma-2 gi|13877813|gb|AAK43984.1|AF370169_1 putative protein translocation complex Sec61 gamma chain [Arabidopsis thaliana] gi|4455235|emb|CAB36734.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana] gi|7269342|emb|CAB79401.1| PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana] gi|9758755|dbj|BAB09131.1| protein translocation complex Sec61 gamma chain [Arabidopsis thaliana] gi|16323486|gb|AAL15237.1| putative	69	69	2.00E-29	100.0	97.1	98.6	protein transport protein sec61 subunit gamma-1	gbpln	Arabidopsis lyrata	AT5G50460.1 | Symbols: | secE/sec61-gamma protein transport protein | chr5:20552168-20552509 REVERSE LENGTH=69	69	69	3.00E-32	100.0	97.1	98.6
Rsa1.0_00924.1.g21384.t1	ref|NP_199859.1| nuclear transcription factor Y subunit C-6 [Arabidopsis thaliana] gi|75262449|sp|Q9FGP7.1|NFYC6_ARATH RecName: Full=Nuclear transcription factor Y subunit C-6; Short=AtNF-YC-6 gi|9758757|dbj|BAB09133.1| transcription factor Hap5a-like [Arabidopsis thaliana] gi|48310164|gb|AAT41766.1| At5g50480 [Arabidopsis thaliana] gi|50198859|gb|AAT70457.1| At5g50480 [Arabidopsis thaliana] gi|225879106|dbj|BAH30623.1| hypothetical protein [Arabidopsis thaliana] gi|332008567|gb|AED95950.1| nuclear transcription factor Y subunit C-6 [Arabidopsis thaliana]	155	202	9.00E-22	130.3	43.2	59.4	nuclear transcription factor Y subunit C-6	gbpln	Arabidopsis thaliana	AT5G50480.1 | Symbols: NF-YC6 | nuclear factor Y, subunit C6 | chr5:20557856-20558464 REVERSE LENGTH=202	155	202	3.00E-24	130.3	43.2	59.4
Rsa1.0_00924.1.g21385.t1	gb|EOA12730.1| hypothetical protein CARUB_v10028175mg [Capsella rubella]	264	709	1.00E-23	268.6	25.0	34.5	hypothetical protein CARUB_v10028175mg	gbpln	Capsella rubella	AT5G50115.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Molecular chaperone, heat shock protein, Hsp40, DnaJ (InterPro:IPR015609); BEST Arabidopsis thaliana protein match is: Molecular chaperone Hsp40/DnaJ family protein (TAIR:AT5G50510.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:20379489-20381036 FORWARD LENGTH=485	264	485	4.00E-20	183.7	19.7	26.9
Rsa1.0_00924.1.g21386.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1277	1307	0	102.3	58.6	73.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1277	1262	2.00E-81	98.8	14.0	21.6

Rsa1.0_00924.1.g21387.t2	ref|NP_568730.1| major facilitator protein [Arabidopsis thaliana] gi|18423171|ref|NP_568735.1| major facilitator protein [Arabidopsis thaliana] gi|8777386|dbj|BAA96976.1| nodulin-like protein [Arabidopsis thaliana] gi|9758761|dbj|BAB09137.1| nodulin-like protein [Arabidopsis thaliana] gi|14532600|gb|AAK64028.1| putative nodulin protein [Arabidopsis thaliana] gi|23297529|gb|AAN12888.1| putative nodulin protein [Arabidopsis thaliana] gi|332008571|gb|AED95954.1| major facilitator protein [Arabidopsis thaliana] gi|332008587|gb|AED95970.1| major facilitator protein [Arabidopsis thaliana]	566	540	0	95.4	79.0	82.7	major facilitator protein	gbpln	Arabidopsis thaliana	AT5G50520.1 | Symbols: | Major facilitator superfamily protein | chr5:20569680-20571587 REVERSE LENGTH=540	566	540	0	95.4	79.0	82.7
Rsa1.0_00924.1.g21388.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00924.1.g21389.t1	gb|EOA22672.1| hypothetical protein CARUB_v10003375mg [Capsella rubella]	401	738	1.00E-163	184.0	68.1	81.3	hypothetical protein CARUB_v10003375mg	gbpln	Capsella rubella	AT4G02570.4 | Symbols: CUL1 | cullin 1 | chr4:1129315-1133435 FORWARD LENGTH=738	401	738	1.00E-163	184.0	67.3	80.8
Rsa1.0_00924.1.g21390.t1	ref|XP_002865817.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311652|gb|EFH42076.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	545	548	0	100.6	89.9	93.9	CBS domain-containing protein	gbpln	Arabidopsis lyrata	AT5G50530.1 | Symbols: | CBS / octicosapeptide/Phox/Bemp1 (PB1) domains-containing protein | chr5:20571876-20574922 REVERSE LENGTH=548	545	548	0	100.6	89.7	93.9
Rsa1.0_00924.1.g21391.t1	ref|XP_002887537.1| hypothetical protein ARALYDRAFT_895304 [Arabidopsis lyrata subsp. lyrata] gi|297333378|gb|EFH63796.1| hypothetical protein ARALYDRAFT_895304 [Arabidopsis lyrata subsp. lyrata]	758	1103	0	145.5	70.2	78.9	hypothetical protein ARALYDRAFT_895304	gbpln	Arabidopsis lyrata	AT1G74360.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:27954299-27957911 FORWARD LENGTH=1106	758	1106	0	145.9	69.7	78.5
Rsa1.0_00924.1.g21392.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00925.1.g21393.t1	ref|XP_002882700.1| hypothetical protein ARALYDRAFT_897277 [Arabidopsis lyrata subsp. lyrata] gi|297328540|gb|EFH58959.1| hypothetical protein ARALYDRAFT_897277 [Arabidopsis lyrata subsp. lyrata]	223	260	9.00E-26	116.6	38.1	59.6	hypothetical protein ARALYDRAFT_897277	gbpln	Arabidopsis lyrata	AT1G50920.1 | Symbols: | Nucleolar GTP-binding protein | chr1:18870555-18872570 FORWARD LENGTH=671	223	671	7.00E-19	300.9	24.7	39.5
Rsa1.0_00925.1.g21394.t1	ref|NP_187884.1| phosphoglycerate kinase 1 [Arabidopsis thaliana] gi|75273138|sp|Q9LD57.1|PGKH1_ARATH RecName: Full=Phosphoglycerate kinase 1, chloroplastic; Flags: Precursor gi|7839389|gb|AAF70258.1|AF247558_1 phosphoglycerate kinase [Arabidopsis thaliana] gi|13430644|gb|AAK25944.1|AF360234_1 putative phosphoglycerate kinase [Arabidopsis thaliana] gi|16226508|gb|AAL16186.1|AF428418_1 AT3g12780/MBK21_14 [Arabidopsis thaliana] gi|11994421|dbj|BAB02423.1| phosphoglycerate kinase [Arabidopsis thaliana] gi|15010644|gb|AAK73981.1| AT3g12780/MBK21_14 [Arabidopsis thaliana] gi|16648943|gb|AAL24323.1| phosphoglycerate kinase [Arabidopsis thaliana] gi|17065610|gb|AAL33785.1| putative phosphoglycerate kinase [Arabidopsis thaliana] gi|20334796|gb|AAM16259.1| AT3g12780/MBK21_14 [Arabidopsis thaliana] gi|21387107|gb|AAM47957.1| phosphoglycerate kinase [Arabidopsis thaliana] gi|22022520|gb|AAM83218.1| AT3g12780/MBK21_14 [Arabidopsis thaliana] gi|110742702|dbj|BAE99262.1| phosphoglycerate kinase like protein [Arabidopsis thaliana] gi|222423303|dbj|BAH19627.1| AT3G12780 [Arabidopsis thaliana] gi|332641725|gb|AEE75246.1|	503	481	0	95.6	88.7	90.9	phosphoglycerate kinase 1	gbpln	Arabidopsis thaliana	AT3G12780.1 | Symbols: PGK1 | phosphoglycerate kinase 1 | chr3:4061127-4063140 REVERSE LENGTH=481	503	481	0	95.6	88.7	90.9

Rsa1.0_00925.1.g21395.t1	gb|AAK93603.1| unknown protein [Arabidopsis thaliana]	141	250	1.00E-60	177.3	85.8	87.2	unknown protein	gbpln	Arabidopsis thaliana	AT3G12760.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Defective-in-cullin neddylation protein (InterPro:IPR014764), Protein of unknown function DUF298 (InterPro:IPR005176), UBA-like (InterPro:IPR009060); BEST Arabidopsis thaliana protein match is: Domain of unknown function (DUF298) (TAIR:AT1G15860.2); Has 857 Blast hits to 855 proteins in 202 species: Archae - 0; Bacteria - 0; Metazoa - 482; Fungi - 154; Plants - 139; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink). | chr3:4054963-4056826 FORWARD LENGTH=250	141	250	4.00E-63	177.3	85.8	87.2
Rsa1.0_00925.1.g21396.t1	ref|NP_187879.2| myb family transcription factor [Arabidopsis thaliana] gi|17979533|gb|AAL50101.1| AT3g12730/MBK21_9 [Arabidopsis thaliana] gi|23505991|gb|AAN28855.1| At3g12730/MBK21_9 [Arabidopsis thaliana] gi|332641719|gb|AEE75240.1| myb family transcription factor [Arabidopsis thaliana]	234	235	1.00E-111	100.4	84.6	88.5	myb family transcription factor	gbpln	Arabidopsis thaliana	AT3G12730.1 | Symbols: | Homeodomain-like superfamily protein | chr3:4047234-4048356 REVERSE LENGTH=235	234	235	1.00E-113	100.4	84.6	88.5
Rsa1.0_00925.1.g21397.t1	ref|XP_002884922.1| hypothetical protein ARALYDRAFT_897482 [Arabidopsis lyrata subsp. lyrata] gi|297330762|gb|EFH61181.1| hypothetical protein ARALYDRAFT_897482 [Arabidopsis lyrata subsp. lyrata]	294	294	1.00E-139	100.0	84.4	91.8	hypothetical protein ARALYDRAFT_897482	gbpln	Arabidopsis lyrata	AT3G12720.1 | Symbols: ATY53, ATMYB67, MYB67 | myb domain protein 67 | chr3:4043407-4044522 REVERSE LENGTH=307	294	307	1.00E-134	104.4	84.7	92.2
Rsa1.0_00925.1.g21398.t1	ref|XP_002884921.1| methyladenine glycosylase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330761|gb|EFH61180.1| methyladenine glycosylase family protein [Arabidopsis lyrata subsp. lyrata]	312	312	1.00E-157	100.0	85.9	93.9	methyladenine glycosylase family protein	gbpln	Arabidopsis lyrata	AT3G12710.1 | Symbols: | DNA glycosylase superfamily protein | chr3:4040572-4041828 REVERSE LENGTH=312	312	312	1.00E-158	100.0	85.9	93.3
Rsa1.0_00925.1.g21399.t1	ref|NP_187876.2| aspartyl protease family protein [Arabidopsis thaliana] gi|11994412|dbj|BAB02414.1| chloroplast nucleoid DNA binding protein-like [Arabidopsis thaliana] gi|332641715|gb|AEE75236.1| aspartyl protease family protein [Arabidopsis thaliana]	445	461	0	103.6	75.3	85.2	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT3G12700.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:4037136-4039043 FORWARD LENGTH=461	445	461	0	103.6	75.3	85.2
Rsa1.0_00925.1.g21400.t1	gb|EOA31965.1| hypothetical protein CARUB_v10015207mg [Capsella rubella]	572	578	0	101.0	89.5	92.8	hypothetical protein CARUB_v10015207mg	gbpln	Capsella rubella	AT3G12690.3 | Symbols: AGC1.5 | AGC kinase 1.5 | chr3:4030596-4032400 REVERSE LENGTH=577	572	577	0	100.9	89.0	92.3
Rsa1.0_00925.1.g21401.t1	gb|EOA30178.1| hypothetical protein CARUB_v10013294mg [Capsella rubella]	826	592	0	71.7	66.8	68.9	hypothetical protein CARUB_v10013294mg	gbpln	Capsella rubella	AT3G12670.1 | Symbols: emb2742 | CTP synthase family protein | chr3:4020351-4024086 REVERSE LENGTH=591	826	591	0	71.5	66.6	69.0
Rsa1.0_00925.1.g21402.t1	ref|NP_187872.1| fasciclin-like arabinogalactan protein 14 [Arabidopsis thaliana] gi|75274151|sp|Q9LTW9.1|FLA14_ARATH RecName: Full=Fasciclin-like arabinogalactan protein 14; Flags: Precursor gi|12321976|gb|AAG51033.1|AC069474_32 hypothetical protein; 8734-7967 [Arabidopsis thaliana] gi|11994407|dbj|BAB02409.1| unnamed protein product [Arabidopsis thaliana] gi|91806417|gb|ABE65936.1| fasciclin-like arabinogalactan family protein [Arabidopsis thaliana] gi|332641708|gb|AEE75229.1| fasciclin-like arabinogalactan protein 14 [Arabidopsis thaliana]	534	255	6.00E-57	47.8	26.0	32.0	fasciclin-like arabinogalactan protein 14	gbpln	Arabidopsis thaliana	AT3G12660.1 | Symbols: FLA14 | FASCICLIN-like arabinogalactan protein 14 precursor | chr3:4019060-4019827 FORWARD LENGTH=255	534	255	1.00E-59	47.8	26.0	32.0
Rsa1.0_00925.1.g21403.t1	gb|AAG51005.1|AC069474_4 unknown protein; 13339-10119 [Arabidopsis thaliana]	678	674	0	99.4	69.8	78.0	unknown protein; 13339-10119	gbpln	Arabidopsis thaliana	AT3G12640.1 | Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr3:4014455-4017675 FORWARD LENGTH=638	678	638	0	94.1	51.8	56.0
Rsa1.0_00925.1.g21404.t1	gb|EOA31605.1| hypothetical protein CARUB_v10014801mg [Capsella rubella]	155	163	3.00E-64	105.2	85.8	91.0	hypothetical protein CARUB_v10014801mg	gbpln	Capsella rubella	AT3G12630.1 | Symbols: | A20/AN1-like zinc finger family protein | chr3:4012707-4013189 FORWARD LENGTH=160	155	160	2.00E-63	103.2	83.9	89.7
Rsa1.0_00925.1.g21405.t1	dbj|BAJ34487.1| unnamed protein product [Thellungiella halophila]	388	387	0	99.7	93.0	95.4	unnamed protein product	----	----	AT3G12620.2 | Symbols: | Protein phosphatase 2C family protein | chr3:4009510-4010993 REVERSE LENGTH=385	388	385	0	99.2	92.3	94.6
Rsa1.0_00926.1.g21406.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00926.1.g21407.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00926.1.g21408.t1	ref|XP_002879847.1| hypothetical protein ARALYDRAFT_321705 [Arabidopsis lyrata subsp. lyrata] gi|297325686|gb|EFH56106.1| hypothetical protein ARALYDRAFT_321705 [Arabidopsis lyrata subsp. lyrata]	260	189	1.00E-34	72.7	27.3	37.3	hypothetical protein ARALYDRAFT_321705	gbpln	Arabidopsis lyrata	AT4G03160.1 | Symbols: | BEST Arabidopsis thaliana protein match is: AP2/B3-like transcriptional factor family protein (TAIR:AT4G03170.1); Has 46 Blast hits to 46 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 4; Plants - 29; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr4:1397979-1398685 FORWARD LENGTH=192	260	192	7.00E-35	73.8	28.5	36.2
Rsa1.0_00926.1.g21409.t1	ref|XP_002879846.1| phosphoinositide-specific phospholipase C family protein [Arabidopsis lyrata subsp. lyrata] gi|297325685|gb|EFH56105.1| phosphoinositide-specific phospholipase C family protein [Arabidopsis lyrata subsp. lyrata]	603	618	0	102.5	92.7	96.5	phosphoinositide-specific phospholipase C family protein	gbpln	Arabidopsis lyrata	AT2G40116.1 | Symbols: | Phosphoinositide-specific phospholipase C family protein | chr2:16751782-16754311 FORWARD LENGTH=613	603	613	0	101.7	91.9	96.2
Rsa1.0_00926.1.g21410.t1	ref|NP_567772.1| uncharacterized protein [Arabidopsis thaliana] gi|14423404|gb|AAK62384.1|AF386939_1 putative protein [Arabidopsis thaliana] gi|14335172|gb|AAK59866.1| AT4g27390/M4I22_200 [Arabidopsis thaliana] gi|15529163|gb|AAK97676.1| AT4g27390/M4I22_200 [Arabidopsis thaliana] gi|16974363|gb|AAL31107.1| AT4g27390/M4I22_200 [Arabidopsis thaliana] gi|332659931|gb|AEE85331.1| uncharacterized protein AT4G27390 [Arabidopsis thaliana]	197	235	8.00E-13	119.3	18.8	19.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G27390.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13703417-13704655 REVERSE LENGTH=235	197	235	3.00E-15	119.3	18.8	19.8
Rsa1.0_00926.1.g21411.t1	gb|EOA27891.1| hypothetical protein CARUB_v10024065mg [Capsella rubella]	223	208	1.00E-106	93.3	85.2	87.9	hypothetical protein CARUB_v10024065mg	gbpln	Capsella rubella	AT2G40095.1 | Symbols: | Alpha/beta hydrolase related protein | chr2:16743107-16744455 FORWARD LENGTH=209	223	209	1.00E-107	93.7	83.0	87.4
Rsa1.0_00926.1.g21412.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	252	1072	1.00E-42	425.4	37.7	46.8	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	252	289	2.00E-35	114.7	32.9	39.3
Rsa1.0_00926.1.g21413.t5	gb|EOA28219.1| hypothetical protein CARUB_v10024408mg [Capsella rubella]	91	93	1.00E-11	102.2	73.6	79.1	hypothetical protein CARUB_v10024408mg	gbpln	Capsella rubella	AT2G40085.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16736534-16736892 REVERSE LENGTH=93	91	93	4.00E-14	102.2	74.7	80.2
Rsa1.0_00926.1.g21414.t1	ref|NP_565922.1| uncharacterized protein [Arabidopsis thaliana] gi|75096964|sp|O04211.1|ELF4_ARATH RecName: Full=Protein EARLY FLOWERING 4; AltName: Full=Protein ARRHYTHMIC 44 gi|2088659|gb|AAB95293.1| expressed protein [Arabidopsis thaliana] gi|14334558|gb|AAK59687.1| unknown protein [Arabidopsis thaliana] gi|17065630|gb|AAL33809.1| unknown protein [Arabidopsis thaliana] gi|21618014|gb|AAM67064.1| unknown [Arabidopsis thaliana] gi|330254679|gb|AEC09773.1| uncharacterized protein AT2G40080 [Arabidopsis thaliana]	89	111	2.00E-31	124.7	85.4	89.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G40080.1 | Symbols: ELF4 | Protein of unknown function (DUF1313) | chr2:16734545-16734880 REVERSE LENGTH=111	89	111	3.00E-34	124.7	85.4	89.9
Rsa1.0_00926.1.g21415.t1	gb|EOA26753.1| hypothetical protein CARUB_v10022840mg [Capsella rubella]	613	607	0	99.0	86.3	90.5	hypothetical protein CARUB_v10022840mg	gbpln	Capsella rubella	AT2G40070.1 | Symbols: | BEST Arabidopsis thaliana protein match is: proline-rich family protein (TAIR:AT3G09000.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16728378-16731160 REVERSE LENGTH=607	613	607	0	99.0	86.1	90.7
Rsa1.0_00926.1.g21416.t1	gb|AAM65809.1| unknown [Arabidopsis thaliana]	259	258	1.00E-109	99.6	81.5	88.0	unknown	gbpln	Arabidopsis thaliana	AT2G40060.1 | Symbols: | Clathrin light chain protein | chr2:16726564-16728001 FORWARD LENGTH=258	259	258	1.00E-111	99.6	81.5	88.0
Rsa1.0_00926.1.g21417.t1	gb|EOA26451.1| hypothetical protein CARUB_v10022497mg [Capsella rubella]	2074	1959	0	94.5	64.9	70.7	hypothetical protein CARUB_v10022497mg	gbpln	Capsella rubella	AT2G40030.1 | Symbols: NRPD1B, DRD3, ATNRPD1B, DMS5, NRPE1 | nuclear RNA polymerase D1B | chr2:16715089-16723406 FORWARD LENGTH=1976	2074	1976	0	95.3	64.0	69.7
Rsa1.0_00926.1.g21418.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_00926.1.g21419.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1046	1274	1.00E-119	121.8	21.7	29.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT2G17920.1 | Symbols: | nucleic acid binding;zinc ion binding | chr2:7782808-7783731 FORWARD LENGTH=307	1046	307	6.00E-28	29.3	7.1	11.2
Rsa1.0_00926.1.g21420.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00926.1.g21421.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00926.1.g21422.t1	gb|EOA26579.1| hypothetical protein CARUB_v10022638mg [Capsella rubella]	444	837	1.00E-117	188.5	52.5	67.6	hypothetical protein CARUB_v10022638mg	gbpln	Capsella rubella	AT3G27900.1 | Symbols: | Protein of unknown function (DUF1184) | chr3:10352905-10353639 REVERSE LENGTH=244	444	244	2.00E-26	55.0	18.9	26.8
Rsa1.0_00926.1.g21423.t1	ref|XP_002892834.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338676|gb|EFH69093.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	147	152	2.00E-50	103.4	65.3	76.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G14870.1 | Symbols: PCR2 | PLANT CADMIUM RESISTANCE 2 | chr1:5128591-5129458 REVERSE LENGTH=152	147	152	9.00E-53	103.4	65.3	76.9
Rsa1.0_00926.1.g21424.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00926.1.g21425.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00926.1.g21426.t1	gb|EOA26624.1| hypothetical protein CARUB_v10022688mg [Capsella rubella]	759	768	0	101.2	69.2	78.5	hypothetical protein CARUB_v10022688mg	gbpln	Capsella rubella	AT2G39850.1 | Symbols: | Subtilisin-like serine endopeptidase family protein | chr2:16630626-16634100 FORWARD LENGTH=775	759	775	0	102.1	68.9	78.5
Rsa1.0_00926.1.g21427.t1	dbj|BAJ34276.1| unnamed protein product [Thellungiella halophila]	330	318	0	96.4	94.5	94.8	unnamed protein product	----	----	AT2G39840.1 | Symbols: TOPP4 | type one serine/threonine protein phosphatase 4 | chr2:16627430-16628789 FORWARD LENGTH=321	330	321	1.00E-179	97.3	91.8	92.7
Rsa1.0_00926.1.g21428.t1	ref|NP_181513.3| DA1-related protein 2 [Arabidopsis thaliana] gi|122236286|sp|Q0WSN2.1|DAR2_ARATH RecName: Full=Protein DA1-related 2 gi|110735778|dbj|BAE99866.1| hypothetical protein [Arabidopsis thaliana] gi|330254642|gb|AEC09736.1| DA1-related protein 2 [Arabidopsis thaliana]	511	528	0	103.3	89.2	93.5	DA1-related protein 2	gbpln	Arabidopsis thaliana	AT2G39830.1 | Symbols: DAR2 | DA1-related protein 2 | chr2:16619950-16623658 REVERSE LENGTH=528	511	528	0	103.3	89.2	93.5
Rsa1.0_00926.1.g21429.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1360	1342	0	98.7	61.5	76.5	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1360	1262	1.00E-89	92.8	13.4	20.0
Rsa1.0_00926.1.g21430.t1	ref|NP_850322.1| Integral membrane Yip1 family protein [Arabidopsis thaliana] gi|19424015|gb|AAL87303.1| unknown protein [Arabidopsis thaliana] gi|24030452|gb|AAN41379.1| unknown protein [Arabidopsis thaliana] gi|330254638|gb|AEC09732.1| Integral membrane Yip1 family protein [Arabidopsis thaliana]	123	275	7.00E-53	223.6	85.4	93.5	Integral membrane Yip1 family protein	gbpln	Arabidopsis thaliana	AT2G39805.1 | Symbols: | Integral membrane Yip1 family protein | chr2:16610216-16612353 REVERSE LENGTH=275	123	275	1.00E-55	223.6	85.4	93.5
Rsa1.0_00927.1.g21431.t1	gb|AAX94977.1| retrotransposon protein, putative, unclassified [Oryza sativa Japonica Group] gi|77550540|gb|ABA93337.1| retrotransposon protein, putative, unclassified [Oryza sativa Japonica Group]	351	428	1.00E-29	121.9	21.1	31.3	retrotransposon protein, putative, unclassified	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_00927.1.g21432.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00927.1.g21433.t6	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00927.1.g21434.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00927.1.g21435.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00927.1.g21436.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	473	1239	7.00E-51	261.9	20.1	23.5	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	473	1262	8.00E-15	266.8	9.5	14.6
Rsa1.0_00927.1.g21437.t13	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1037	1499	0	144.6	44.4	53.7	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1037	158	3.00E-15	15.2	4.6	6.5
Rsa1.0_00927.1.g21438.t1	dbj|BAB02146.1| copia retroelement pol polyprotein-like [Arabidopsis thaliana]	632	526	5.00E-76	83.2	27.4	36.7	copia retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00927.1.g21439.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00927.1.g21440.t5	gb|AFD01292.1| auxin response factor 1 [Brassica rapa subsp. pekinensis]	659	665	0	100.9	89.7	92.7	auxin response factor 1	gbpln	Brassica rapa	AT1G59750.3 | Symbols: ARF1 | auxin response factor 1 | chr1:21980414-21984193 FORWARD LENGTH=665	659	665	0	100.9	88.3	90.9

Rsa1.0_00927.1.g21441.t2	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	628	1529	1.00E-122	243.5	40.8	59.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	628	746	3.00E-34	118.8	16.7	26.3
Rsa1.0_00928.1.g21442.t1	gb|EOA39638.1| hypothetical protein CARUB_v10008272mg [Capsella rubella]	867	880	0	101.5	78.5	85.9	hypothetical protein CARUB_v10008272mg	gbpln	Capsella rubella	AT1G53470.1 | Symbols: MSL4 | mechanosensitive channel of small conductance-like 4 | chr1:19958587-19961578 FORWARD LENGTH=881	867	881	0	101.6	77.5	85.1
Rsa1.0_00928.1.g21443.t1	ref|NP_175754.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332194827|gb|AEE32948.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	332	304	1.00E-152	91.6	80.7	84.3	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT1G53490.1 | Symbols: | RING/U-box superfamily protein | chr1:19965146-19966811 FORWARD LENGTH=304	332	304	1.00E-155	91.6	80.7	84.3
Rsa1.0_00928.1.g21444.t1	ref|XP_002894444.1| mucilage-modified 4 [Arabidopsis lyrata subsp. lyrata] gi|297340286|gb|EFH70703.1| mucilage-modified 4 [Arabidopsis lyrata subsp. lyrata]	668	668	0	100.0	94.5	96.9	mucilage-modified 4	gbpln	Arabidopsis lyrata	AT1G53500.1 | Symbols: MUM4, RHM2, ATRHM2, ATMUM4 | NAD-dependent epimerase/dehydratase family protein | chr1:19967157-19969239 REVERSE LENGTH=667	668	667	0	99.9	94.0	96.7
Rsa1.0_00928.1.g21445.t1	ref|NP_175756.2| mitogen-activated protein kinase 18 [Arabidopsis thaliana] gi|334302931|sp|Q9C5C0.4|MPK18_ARATH RecName: Full=Mitogen-activated protein kinase 18; Short=AtMPK18; Short=MAP kinase 18 gi|332194829|gb|AEE32950.1| mitogen-activated protein kinase 18 [Arabidopsis thaliana]	595	615	0	103.4	85.2	90.6	mitogen-activated protein kinase 18	gbpln	Arabidopsis thaliana	AT1G53510.1 | Symbols: ATMPK18, MPK18 | mitogen-activated protein kinase 18 | chr1:19970961-19974158 REVERSE LENGTH=615	595	615	0	103.4	85.2	90.6
Rsa1.0_00928.1.g21446.t1	gb|EOA38373.1| hypothetical protein CARUB_v10009906mg [Capsella rubella]	284	291	1.00E-115	102.5	79.6	87.0	hypothetical protein CARUB_v10009906mg	gbpln	Capsella rubella	AT1G53520.1 | Symbols: | Chalcone-flavanone isomerase family protein | chr1:19976485-19977915 REVERSE LENGTH=287	284	287	1.00E-114	101.1	78.2	84.5
Rsa1.0_00928.1.g21447.t2	gb|EOA19968.1| hypothetical protein CARUB_v10000229mg [Capsella rubella]	836	828	0	99.0	88.0	93.8	hypothetical protein CARUB_v10000229mg	gbpln	Capsella rubella	AT1G79930.1 | Symbols: HSP91 | heat shock protein 91 | chr1:30063781-30067067 REVERSE LENGTH=831	836	831	0	99.4	88.2	93.2
Rsa1.0_00928.1.g21448.t1	emb|CAA22150.1| hypothetical protein [Arabidopsis thaliana] gi|7269091|emb|CAB79200.1| hypothetical protein [Arabidopsis thaliana]	327	457	1.00E-14	139.8	14.7	20.2	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00928.1.g21449.t1	ref|XP_002894447.1| hypothetical protein ARALYDRAFT_474484 [Arabidopsis lyrata subsp. lyrata] gi|297340289|gb|EFH70706.1| hypothetical protein ARALYDRAFT_474484 [Arabidopsis lyrata subsp. lyrata]	153	153	2.00E-55	100.0	75.8	85.0	hypothetical protein ARALYDRAFT_474484	gbpln	Arabidopsis lyrata	AT1G53560.1 | Symbols: | Ribosomal protein L18ae family | chr1:19984908-19985960 REVERSE LENGTH=153	153	153	4.00E-51	100.0	74.5	85.6
Rsa1.0_00928.1.g21450.t1	dbj|BAJ34342.1| unnamed protein product [Thellungiella halophila]	289	286	1.00E-129	99.0	83.7	88.2	unnamed protein product	----	----	AT1G53580.1 | Symbols: GLX2-3, ETHE1, GLY3 | glyoxalase II 3 | chr1:19991542-19993250 REVERSE LENGTH=294	289	294	1.00E-124	101.7	79.6	84.4
Rsa1.0_00928.1.g21451.t1	ref|XP_002891763.1| hypothetical protein ARALYDRAFT_314676 [Arabidopsis lyrata subsp. lyrata] gi|297337605|gb|EFH68022.1| hypothetical protein ARALYDRAFT_314676 [Arabidopsis lyrata subsp. lyrata]	725	828	0	114.2	81.1	88.3	hypothetical protein ARALYDRAFT_314676	gbpln	Arabidopsis lyrata	AT1G53600.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:20001263-20003416 FORWARD LENGTH=717	725	717	0	98.9	80.0	88.1
Rsa1.0_00928.1.g21452.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00928.1.g21453.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00928.1.g21454.t2	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	1799	1643	0	91.3	36.4	48.5	gag/pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1799	1262	1.00E-94	70.2	9.8	14.7
Rsa1.0_00929.1.g21455.t1	gb|EOA13662.1| hypothetical protein CARUB_v10026733mg [Capsella rubella]	343	339	1.00E-145	98.8	81.3	86.6	hypothetical protein CARUB_v10026733mg	gbpln	Capsella rubella	AT5G66350.1 | Symbols: SHI | Lateral root primordium (LRP) protein-related | chr5:26504714-26506143 REVERSE LENGTH=331	343	331	1.00E-139	96.5	79.3	86.0
Rsa1.0_00929.1.g21456.t1	ref|NP_191279.3| uncharacterized protein [Arabidopsis thaliana] gi|52354345|gb|AAU44493.1| hypothetical protein AT3G57200 [Arabidopsis thaliana] gi|61742717|gb|AAX55179.1| hypothetical protein At3g57200 [Arabidopsis thaliana] gi|332646105|gb|AEE79626.1| uncharacterized protein AT3G57200 [Arabidopsis thaliana]	116	514	5.00E-30	443.1	51.7	57.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G57200.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41451.1); Has 94 Blast hits to 94 proteins in 31 species: Archae - 0; Bacteria - 12; Metazoa - 0; Fungi - 0; Plants - 77; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr3:21169413-21172103 FORWARD LENGTH=514	116	514	8.00E-33	443.1	51.7	57.8

Rsa1.0_00929.1.g21457.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	292	1142	2.00E-52	391.1	38.7	50.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	292	292	1.00E-20	100.0	24.0	41.4
Rsa1.0_00929.1.g21458.t1	ref|XP_002879014.1| EMB1187 [Arabidopsis lyrata subsp. lyrata] gi|297324853|gb|EFH55273.1| EMB1187 [Arabidopsis lyrata subsp. lyrata]	411	374	1.00E-179	91.0	74.0	78.8	EMB1187	gbpln	Arabidopsis lyrata	AT2G26830.1 | Symbols: emb1187 | Protein kinase superfamily protein | chr2:11443599-11446958 FORWARD LENGTH=374	411	374	0	91.0	73.5	78.8
Rsa1.0_00929.1.g21459.t1	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1020	1044	9.00E-85	102.4	16.0	20.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1020	626	3.00E-30	61.4	9.6	13.9
Rsa1.0_00929.1.g21460.t1	gb|AAB95304.1| putative second messenger-dependent protein kinase [Arabidopsis thaliana]	163	676	2.00E-77	414.7	80.4	82.2	putative second messenger-dependent protein kinase	gbpln	Arabidopsis thaliana	AT2G26695.1 | Symbols: | Ran BP2/NZF zinc finger-like superfamily protein | chr2:11365275-11365789 FORWARD LENGTH=138	163	138	9.00E-76	84.7	80.4	82.2
Rsa1.0_00929.1.g21461.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00929.1.g21462.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00929.1.g21463.t1	ref|XP_002879001.1| hypothetical protein ARALYDRAFT_901457 [Arabidopsis lyrata subsp. lyrata] gi|297324840|gb|EFH55260.1| hypothetical protein ARALYDRAFT_901457 [Arabidopsis lyrata subsp. lyrata]	522	521	0	99.8	91.8	95.4	hypothetical protein ARALYDRAFT_901457	gbpln	Arabidopsis lyrata	AT2G26710.1 | Symbols: BAS1, CYP734A1, CYP72B1 | Cytochrome P450 superfamily protein | chr2:11380700-11383413 FORWARD LENGTH=520	522	520	0	99.6	91.4	95.2
Rsa1.0_00930.1.g21464.t1	ref|XP_002883034.1| hypothetical protein ARALYDRAFT_341831 [Arabidopsis lyrata subsp. lyrata] gi|297328874|gb|EFH59293.1| hypothetical protein ARALYDRAFT_341831 [Arabidopsis lyrata subsp. lyrata]	356	401	4.00E-98	112.6	54.2	68.8	hypothetical protein ARALYDRAFT_341831	gbpln	Arabidopsis lyrata	AT5G19170.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:6445245-6447305 FORWARD LENGTH=391	356	391	1.00E-68	109.8	43.5	57.6
Rsa1.0_00930.1.g21465.t1	gb|EOA20755.1| hypothetical protein CARUB_v10001083mg [Capsella rubella]	405	411	0	101.5	87.9	91.9	hypothetical protein CARUB_v10001083mg	gbpln	Capsella rubella	AT5G26960.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:9484908-9486149 REVERSE LENGTH=413	405	413	0	102.0	88.1	91.9
Rsa1.0_00930.1.g21466.t3	gb|EOA22421.1| hypothetical protein CARUB_v10003065mg [Capsella rubella]	104	125	1.00E-31	120.2	77.9	87.5	hypothetical protein CARUB_v10003065mg	gbpln	Capsella rubella	AT5G26930.1 | Symbols: GATA23 | GATA transcription factor 23 | chr5:9479592-9480061 FORWARD LENGTH=120	104	120	6.00E-29	115.4	64.4	72.1
Rsa1.0_00930.1.g21467.t2	ref|XP_002874326.1| hypothetical protein ARALYDRAFT_489520 [Arabidopsis lyrata subsp. lyrata] gi|297320163|gb|EFH50585.1| hypothetical protein ARALYDRAFT_489520 [Arabidopsis lyrata subsp. lyrata]	809	842	0	104.1	78.4	84.2	hypothetical protein ARALYDRAFT_489520	gbpln	Arabidopsis lyrata	AT5G26910.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G58650.1); Has 1322 Blast hits to 684 proteins in 162 species: Archae - 4; Bacteria - 497; Metazoa - 157; Fungi - 101; Plants - 155; Viruses - 0; Other Eukaryotes - 408 (source: NCBI BLink). | chr5:9466169-9469523 REVERSE LENGTH=853	809	853	0	105.4	77.1	84.2
Rsa1.0_00930.1.g21468.t1	ref|XP_002872241.1| hypothetical protein ARALYDRAFT_489516 [Arabidopsis lyrata subsp. lyrata] gi|297318078|gb|EFH48500.1| hypothetical protein ARALYDRAFT_489516 [Arabidopsis lyrata subsp. lyrata]	984	983	0	99.9	91.0	94.4	hypothetical protein ARALYDRAFT_489516	gbpln	Arabidopsis lyrata	AT5G26850.4 | Symbols: | Uncharacterized protein | chr5:9445950-9450584 FORWARD LENGTH=983	984	983	0	99.9	90.8	94.5
Rsa1.0_00930.1.g21469.t1	gb|EOA19297.1| hypothetical protein CARUB_v10002232mg, partial [Capsella rubella]	111	137	5.00E-48	123.4	84.7	90.1	hypothetical protein CARUB_v10002232mg, partial	gbpln	Capsella rubella	AT5G26800.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; CONTAINS InterPro DOMAIN/s: IGR protein motif (InterPro:IPR019083); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G05810.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9425224-9426485 FORWARD LENGTH=112	111	112	1.00E-48	100.9	84.7	89.2

Rsa1.0_00930.1.g21470.t1	ref|NP_568486.1| Shaggy-related protein kinase alpha [Arabidopsis thaliana] gi|27735207|sp|P43288.3|KSG1_ARATH RecName: Full=Shaggy-related protein kinase alpha; AltName: Full=ASK-alpha gi|16226768|gb|AAL16257.1|AF428327_1 AT5g26750/F2P16_10 [Arabidopsis thaliana] gi|15028149|gb|AAK76698.1| putative shaggy kinase alpha [Arabidopsis thaliana] gi|23296760|gb|AAN13164.1| putative shaggy kinase alpha [Arabidopsis thaliana] gi|332006213|gb|AED93596.1| Shaggy-related protein kinase alpha [Arabidopsis thaliana]	405	405	0	100.0	95.8	97.3	Shaggy-related protein kinase alpha	gbpln	Arabidopsis thaliana	AT5G26751.1 | Symbols: ATSK11, SK 11 | shaggy-related kinase 11 | chr5:9399582-9401839 REVERSE LENGTH=405	405	405	0	100.0	95.8	97.3
Rsa1.0_00930.1.g21471.t1	ref|NP_001154741.1| nucleic acid binding / zinc ion binding protein [Arabidopsis thaliana] gi|332006211|gb|AED93594.1| nucleic acid binding / zinc ion binding protein [Arabidopsis thaliana]	147	147	6.00E-58	100.0	78.9	85.0	nucleic acid binding / zinc ion binding protein	gbpln	Arabidopsis thaliana	AT5G26749.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:9398285-9399239 REVERSE LENGTH=147	147	147	2.00E-60	100.0	78.9	85.0
Rsa1.0_00930.1.g21472.t1	ref|XP_002872231.1| D111/G-patch domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318068|gb|EFH48490.1| D111/G-patch domain-containing protein [Arabidopsis lyrata subsp. lyrata]	299	301	1.00E-144	100.7	89.6	93.6	D111/G-patch domain-containing protein	gbpln	Arabidopsis lyrata	AT5G26610.3 | Symbols: | D111/G-patch domain-containing protein | chr5:9375456-9376991 FORWARD LENGTH=301	299	301	1.00E-141	100.7	89.0	93.3
Rsa1.0_00931.1.g21473.t3	ref|XP_002870965.1| EMB2730 [Arabidopsis lyrata subsp. lyrata] gi|297316802|gb|EFH47224.1| EMB2730 [Arabidopsis lyrata subsp. lyrata]	796	803	0	100.9	90.3	94.8	EMB2730	gbpln	Arabidopsis lyrata	AT5G02250.1 | Symbols: EMB2730, RNR1, ATMTRNASEII | Ribonuclease II/R family protein | chr5:454902-459063 FORWARD LENGTH=803	796	803	0	100.9	89.8	94.7
Rsa1.0_00931.1.g21474.t1	ref|NP_568098.1| NAD(P)-binding Rossmann-fold containing protein [Arabidopsis thaliana] gi|73921137|sp|Q94EG6.1|Y5224_ARATH RecName: Full=Uncharacterized protein At5g02240 gi|15294290|gb|AAK95322.1|AF410336_1 AT5g02240/T7H20_290 [Arabidopsis thaliana] gi|22655434|gb|AAM98309.1| At5g02240/T7H20_290 [Arabidopsis thaliana] gi|23397218|gb|AAN31891.1| unknown protein [Arabidopsis thaliana] gi|62320775|dbj|BAD95439.1| hypothetical protein [Arabidopsis thaliana] gi|332003066|gb|AED90449.1| NAD(P)-binding Rossmann-fold containing protein [Arabidopsis thaliana]	253	253	1.00E-135	100.0	94.5	96.8	NAD(P)-binding Rossmann-fold containing protein	gbpln	Arabidopsis thaliana	AT5G02240.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:451502-452984 FORWARD LENGTH=253	253	253	1.00E-137	100.0	94.5	96.8
Rsa1.0_00931.1.g21475.t1	ref|NP_195843.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|30679562|ref|NP_850754.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|7340697|emb|CAB82996.1| putative protein [Arabidopsis thaliana] gi|107738426|gb|ABF83695.1| At5g02230 [Arabidopsis thaliana] gi|110738717|dbj|BAF01283.1| hypothetical protein [Arabidopsis thaliana] gi|332003064|gb|AED90447.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|332003065|gb|AED90448.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana]	280	280	1.00E-137	100.0	88.2	93.6	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G02230.2 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:449132-450507 FORWARD LENGTH=280	280	280	1.00E-139	100.0	88.2	93.6
Rsa1.0_00931.1.g21476.t1	gb|EOA21900.1| hypothetical protein CARUB_v10002381mg [Capsella rubella]	74	74	1.00E-28	100.0	82.4	91.9	hypothetical protein CARUB_v10002381mg	gbpln	Capsella rubella	AT5G02220.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:441884-442102 REVERSE LENGTH=72	74	72	9.00E-31	97.3	83.8	89.2
Rsa1.0_00931.1.g21477.t1	ref|XP_002870961.1| hypothetical protein ARALYDRAFT_486997 [Arabidopsis lyrata subsp. lyrata] gi|297316798|gb|EFH47220.1| hypothetical protein ARALYDRAFT_486997 [Arabidopsis lyrata subsp. lyrata]	180	181	2.00E-36	100.6	64.4	71.7	hypothetical protein ARALYDRAFT_486997	gbpln	Arabidopsis lyrata	AT5G02200.1 | Symbols: FHL | far-red-elongated hypocotyl1-like | chr5:438221-438852 FORWARD LENGTH=181	180	181	3.00E-35	100.6	60.0	70.0

Rsa1.0_00931.1_g21478.t1	ref|XP_002870959.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297316796|gb|EFH47218.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata]	539	543	0	100.7	87.2	93.1	amino acid transporter family protein	gbpln	Arabidopsis lyrata	AT5G02180.1 | Symbols: | Transmembrane amino acid transporter family protein | chr5:431034-433544 FORWARD LENGTH=550	539	550	0	102.0	86.5	92.8
Rsa1.0_00931.1_g21479.t1	gb|EOA21784.1| hypothetical protein CARUB_v10002245mg [Capsella rubella]	119	132	9.00E-48	110.9	85.7	91.6	hypothetical protein CARUB_v10002245mg	gbpln	Capsella rubella	AT5G02160.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 121 Blast hits to 121 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 121; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:426392-427024 FORWARD LENGTH=129	119	129	1.00E-48	108.4	85.7	89.1
Rsa1.0_00931.1_g21480.t1	gb|EOA22838.1| hypothetical protein CARUB_v10003562mg, partial [Capsella rubella]	219	259	1.00E-106	118.3	90.9	95.0	hypothetical protein CARUB_v10003562mg, partial	gbpln	Capsella rubella	AT5G02140.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr5:423384-424437 FORWARD LENGTH=294	219	294	1.00E-104	134.2	87.2	92.2
Rsa1.0_00931.1_g21481.t1	ref|NP_195833.1| kinesin light chain-like protein [Arabidopsis thaliana] gi|7340687|emb|CAB82986.1| putative protein [Arabidopsis thaliana] gi|98961125|gb|ABF59046.1| At5g02130 [Arabidopsis thaliana] gi|332003051|gb|AED90434.1| kinesin light chain-like protein [Arabidopsis thaliana]	304	420	8.00E-99	138.2	75.7	85.5	kinesin light chain-like protein	gbpln	Arabidopsis thaliana	AT5G02130.1 | Symbols: NDP1 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:419747-421958 REVERSE LENGTH=420	304	420	1.00E-101	138.2	75.7	85.5
Rsa1.0_00931.1_g21482.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1735	1213	0	69.9	25.0	36.4	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1735	746	6.00E-69	43.0	9.2	12.4
Rsa1.0_00931.1_g21483.t1	ref|XP_002870954.1| CYCD7_1 [Arabidopsis lyrata subsp. lyrata] gi|297316791|gb|EFH47213.1| CYCD7_1 [Arabidopsis lyrata subsp. lyrata]	344	341	1.00E-119	99.1	65.4	78.5	CYCD7_1	gbpln	Arabidopsis lyrata	AT5G02110.1 | Symbols: CYCD7;1, CYCD7 | CYCLIN D7;1 | chr5:417087-418553 FORWARD LENGTH=341	344	341	1.00E-121	99.1	64.5	77.9
Rsa1.0_00931.1_g21484.t2	ref|NP_195830.1| Oxysterol-binding family protein [Arabidopsis thaliana] gi|75264475|sp|Q9LZM1.1|ORP3A_ARATH RecName: Full=Oxysterol-binding protein-related protein 3A; AltName: Full=OSBP-related protein 3A; AltName: Full=Protein UNFERTILIZED EMBRYO SAC 18 gi|7340684|emb|CAB82983.1| putative protein [Arabidopsis thaliana] gi|15292811|gb|AAK92774.1| unknown protein [Arabidopsis thaliana] gi|20258867|gb|AAM14105.1| putative oxysterol-binding protein [Arabidopsis thaliana] gi|332003048|gb|AED90431.1| Oxysterol-binding family protein [Arabidopsis thaliana]	451	453	0	100.4	86.5	92.2	Oxysterol-binding family protein	gbpln	Arabidopsis thaliana	AT5G02100.1 | Symbols: UNE18, ORP3A | Oxysterol-binding family protein | chr5:413639-416016 FORWARD LENGTH=453	451	453	0	100.4	86.5	92.2
Rsa1.0_00931.1_g21485.t1	ref|NP_195829.1| uncharacterized protein [Arabidopsis thaliana] gi|7340683|emb|CAB82982.1| putative protein [Arabidopsis thaliana] gi|26451474|dbj|BAC42836.1| unknown protein [Arabidopsis thaliana] gi|28973153|gb|AAO63901.1| unknown protein [Arabidopsis thaliana] gi|332003047|gb|AED90430.1| uncharacterized protein AT5G02090 [Arabidopsis thaliana]	84	85	8.00E-32	101.2	84.5	90.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G02090.1 | Symbols: | unknown protein; Has 30 Blast hits to 30 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:412350-412607 REVERSE LENGTH=85	84	85	1.00E-34	101.2	84.5	90.5
Rsa1.0_00931.1_g21486.t1	ref|XP_002889929.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335771|gb|EFH66188.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	303	317	1.00E-144	104.6	88.8	92.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G12350.1 | Symbols: ATCOAB, COAB | 4-phospho-panto-thenoylcysteine synthetase | chr1:4198870-4200633 FORWARD LENGTH=317	303	317	1.00E-144	104.6	88.1	92.1
Rsa1.0_00931.1_g21487.t1	gb|EOA22834.1| hypothetical protein CARUB_v10003558mg [Capsella rubella]	666	657	0	98.6	88.1	92.9	hypothetical protein CARUB_v10003558mg	gbpln	Capsella rubella	AT5G02070.1 | Symbols: | Protein kinase family protein | chr5:405895-408220 REVERSE LENGTH=657	666	657	0	98.6	88.7	94.0

Rsa1.0_00931.1.g21488.t1	ref|XP_002873035.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297318872|gb|EFH49294.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	266	264	2.00E-98	99.2	73.7	83.1	mitochondrial glycoprotein family protein	gbpln	Arabidopsis lyrata	AT5G02050.1 | Symbols: | Mitochondrial glycoprotein family protein | chr5:403239-404244 REVERSE LENGTH=267	266	267	4.00E-98	100.4	74.8	83.5
Rsa1.0_00932.1.g21489.t1	ref|XP_002870475.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316311|gb|EFH46734.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	470	480	0	102.1	83.0	91.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G36260.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:14285068-14288179 REVERSE LENGTH=482	470	482	0	102.6	82.1	91.7
Rsa1.0_00932.1.g21490.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00932.1.g21491.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00932.1.g21492.t4	gb|EOA28483.1| hypothetical protein CARUB_v10024693mg [Capsella rubella]	1088	676	1.00E-27	62.1	7.4	8.5	hypothetical protein CARUB_v10024693mg	gbpln	Capsella rubella	AT2G33580.1 | Symbols: | Protein kinase superfamily protein | chr2:14219848-14221842 REVERSE LENGTH=664	1088	664	3.00E-30	61.0	7.1	8.5
Rsa1.0_00932.1.g21493.t1	ref|XP_002879622.1| hypothetical protein ARALYDRAFT_902789 [Arabidopsis lyrata subsp. lyrata] gi|297325461|gb|EFH55881.1| hypothetical protein ARALYDRAFT_902789 [Arabidopsis lyrata subsp. lyrata]	90	91	1.00E-18	101.1	61.1	72.2	hypothetical protein ARALYDRAFT_902789	gbpln	Arabidopsis lyrata	AT2G36695.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:15382702-15383298 FORWARD LENGTH=117	90	117	5.00E-19	130.0	54.4	63.3
Rsa1.0_00932.1.g21494.t1	gb|EOA38189.1| hypothetical protein CARUB_v10009666mg [Capsella rubella]	130	337	5.00E-31	259.2	51.5	53.1	hypothetical protein CARUB_v10009666mg	gbpln	Capsella rubella	AT1G48460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G63040.1); Has 60 Blast hits to 60 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 60; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:17911469-17913149 FORWARD LENGTH=340	130	340	3.00E-33	261.5	50.8	52.3
Rsa1.0_00932.1.g21495.t1	ref|XP_002307432.1| predicted protein [Populus trichocarpa] gi|118483791|gb|ABK93788.1| unknown [Populus trichocarpa] gi|222856881|gb|EEE94428.1| predicted protein [Populus trichocarpa]	361	342	3.00E-26	94.7	17.7	18.6	predicted protein	gbpln	Populus trichocarpa	AT1G77610.1 | Symbols: | EamA-like transporter family protein | chr1:29165489-29167486 FORWARD LENGTH=336	361	336	8.00E-29	93.1	17.7	18.6
Rsa1.0_00932.1.g21496.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00932.1.g21497.t1	ref|NP_198513.1| NDR1/HIN1-like 25 [Arabidopsis thaliana] gi|332006750|gb|AED94133.1| NDR1/HIN1-like 25 [Arabidopsis thaliana]	251	248	1.00E-114	98.8	86.9	92.8	NDR1/HIN1-like 25	gbpln	Arabidopsis thaliana	AT5G36970.1 | Symbols: NHL25 | NDR1/HIN1-like 25 | chr5:14604367-14605194 REVERSE LENGTH=248	251	248	1.00E-116	98.8	86.9	92.8
Rsa1.0_00932.1.g21498.t1	emb|CAN73567.1| hypothetical protein VITISV_003451 [Vitis vinifera]	895	1277	1.00E-141	142.7	30.4	37.7	hypothetical protein VITISV_003451	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	895	1262	4.00E-53	141.0	12.5	20.6
Rsa1.0_00932.1.g21499.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00933.1.g21500.t1	gb|EOA38212.1| hypothetical protein CARUB_v10009694mg [Capsella rubella]	459	332	1.00E-169	72.3	65.4	68.4	hypothetical protein CARUB_v10009694mg	gbpln	Capsella rubella	AT1G35190.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:12890544-12892632 FORWARD LENGTH=329	459	329	1.00E-166	71.7	62.7	66.9
Rsa1.0_00933.1.g21501.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00933.1.g21502.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	617	1342	1.00E-135	217.5	39.5	51.9	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	617	1262	6.00E-54	204.5	22.5	34.8

Rsa1.0_00933.1.g21503.t1	dbj|BAC42513.1| unknown protein [Arabidopsis thaliana] gi|28372862|gb|AAO39913.1| At1g35210 [Arabidopsis thaliana]	144	163	9.00E-27	113.2	61.8	71.5	unknown protein	gbpln	Arabidopsis thaliana	AT1G35210.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF740 (InterPro:IPR008004); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22470.1); Has 83 Blast hits to 83 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 81; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:12896914-12897384 REVERSE LENGTH=156	144	156	3.00E-29	108.3	61.8	71.5
Rsa1.0_00933.1.g21504.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	395	1142	1.00E-107	289.1	50.9	65.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	395	575	2.00E-37	145.6	29.6	47.8
Rsa1.0_00933.1.g21505.t1	ref|NP_174759.1| thioesterase family protein [Arabidopsis thaliana] gi|12322944|gb|AAG51460.1|AC069160_6 unknown protein [Arabidopsis thaliana] gi|89111888|gb|ABD60716.1| At1g35250 [Arabidopsis thaliana] gi|332193652|gb|AEE31773.1| thioesterase family protein [Arabidopsis thaliana]	100	188	1.00E-23	188.0	51.0	60.0	thioesterase family protein	gbpln	Arabidopsis thaliana	AT1G35250.1 | Symbols: | Thioesterase superfamily protein | chr1:12933046-12934465 REVERSE LENGTH=188	100	188	2.00E-26	188.0	51.0	60.0
Rsa1.0_00933.1.g21506.t1	ref|XP_002893877.1| cyclin family protein [Arabidopsis lyrata subsp. lyrata] gi|297339719|gb|EFH70136.1| cyclin family protein [Arabidopsis lyrata subsp. lyrata]	297	250	1.00E-109	84.2	64.0	72.7	cyclin family protein	gbpln	Arabidopsis lyrata	AT1G35440.1 | Symbols: CYCT1;1 | cyclin T1;1 | chr1:13035294-13036037 REVERSE LENGTH=247	297	247	1.00E-103	83.2	59.9	70.4
Rsa1.0_00933.1.g21507.t1	gb|EOA36180.1| hypothetical protein CARUB_v10010050mg [Capsella rubella]	248	260	2.00E-91	104.8	81.0	88.7	hypothetical protein CARUB_v10010050mg	gbpln	Capsella rubella	AT1G35460.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:13040092-13041907 FORWARD LENGTH=259	248	259	8.00E-91	104.4	75.0	83.9
Rsa1.0_00933.1.g21508.t1	gb|EOA40293.1| hypothetical protein CARUB_v10009024mg [Capsella rubella]	461	476	0	103.3	79.4	86.8	hypothetical protein CARUB_v10009024mg	gbpln	Capsella rubella	AT1G35470.2 | Symbols: | SPla/RYanodine receptor (SPRY) domain-containing protein | chr1:13051636-13054922 REVERSE LENGTH=467	461	467	0	101.3	77.4	83.3
Rsa1.0_00933.1.g21509.t1	gb|EOA39492.1| hypothetical protein CARUB_v10008097mg [Capsella rubella]	1325	1343	0	101.4	79.9	87.9	hypothetical protein CARUB_v10008097mg	gbpln	Capsella rubella	AT1G35530.2 | Symbols: | DEAD/DEAH box RNA helicase family protein | chr1:13089994-13097078 FORWARD LENGTH=1390	1325	1390	0	104.9	80.8	88.4
Rsa1.0_00933.1.g21510.t1	ref|NP_174791.2| cytosolic invertase 1 [Arabidopsis thaliana] gi|30693225|ref|NP_849750.1| cytosolic invertase 1 [Arabidopsis thaliana] gi|75264169|sp|Q9LQF2.1|CINV1_ARATH RecName: Full=Alkaline/neutral invertase CINV1; AltName: Full=Cytosolic invertase 1; Short=AtCYT-INV1 gi|8778348|gb|AAF79356.1|AC007887_15 F15O4.33 [Arabidopsis thaliana] gi|17529026|gb|AAL38723.1| putative invertase [Arabidopsis thaliana] gi|23296907|gb|AAN13200.1| putative invertase [Arabidopsis thaliana] gi|88193450|emb|CAJ76698.1| putative invertase [Arabidopsis thaliana] gi|332193691|gb|AEE31812.1| cytosolic invertase 1 [Arabidopsis thaliana] gi|332193692|gb|AEE31813.1| cytosolic invertase 1 [Arabidopsis thaliana]	543	551	0	101.5	95.2	97.2	cytosolic invertase 1	gbpln	Arabidopsis thaliana	AT1G35580.2 | Symbols: CINV1 | cytosolic invertase 1 | chr1:13122460-13124808 REVERSE LENGTH=551	543	551	0	101.5	95.2	97.2
Rsa1.0_00934.1.g21511.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1681	1142	0	67.9	27.1	36.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1681	575	2.00E-61	34.2	8.4	12.7
Rsa1.0_00934.1.g21512.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00934.1.g21513.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00934.1.g21514.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00934.1.g21515.t1	ref|XP_002882045.1| hypothetical protein ARALYDRAFT_483745 [Arabidopsis lyrata subsp. lyrata] gi|297327884|gb|EFH58304.1| hypothetical protein ARALYDRAFT_483745 [Arabidopsis lyrata subsp. lyrata]	129	206	3.00E-14	159.7	28.7	31.8	hypothetical protein ARALYDRAFT_483745	gbpln	Arabidopsis lyrata	AT2G46000.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Mesoderm development candidate 2 (InterPro:IPR019330); Has 31 Blast hits to 31 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 5; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18921194-18922047 REVERSE LENGTH=208	129	208	1.00E-16	161.2	29.5	31.0
Rsa1.0_00934.1.g21516.t3	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1208	940	3.00E-47	77.8	8.9	11.8	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00934.1.g21517.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	174	467	3.00E-19	268.4	32.8	43.1	hypothetical protein 31.t00031	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	174	566	1.00E-14	325.3	33.9	57.5
Rsa1.0_00934.1.g21518.t1	ref|XP_002875611.1| hypothetical protein ARALYDRAFT_323091 [Arabidopsis lyrata subsp. lyrata] gi|297321449|gb|EFH51870.1| hypothetical protein ARALYDRAFT_323091 [Arabidopsis lyrata subsp. lyrata]	508	556	2.00E-21	109.4	20.3	27.8	hypothetical protein ARALYDRAFT_323091	gbpln	Arabidopsis lyrata	AT3G43590.1 | Symbols: | zinc knuckle (CCHC-type) family protein | chr3:15509753-15512255 FORWARD LENGTH=551	508	551	1.00E-18	108.5	19.3	26.8
Rsa1.0_00934.1.g21519.t1	gb|AFQ22737.1| growth-regulating factor 1, partial [Brassica rapa subsp. pekinensis]	517	518	0	100.2	94.4	96.3	growth-regulating factor 1, partial	gbpln	Brassica rapa	AT2G22840.1 | Symbols: AtGRF1, GRF1 | growth-regulating factor 1 | chr2:9728841-9731141 FORWARD LENGTH=530	517	530	0	102.5	87.6	92.8
Rsa1.0_00934.1.g21520.t1	ref|XP_002878667.1| hypothetical protein ARALYDRAFT_481192 [Arabidopsis lyrata subsp. lyrata] gi|297324506|gb|EFH54926.1| hypothetical protein ARALYDRAFT_481192 [Arabidopsis lyrata subsp. lyrata]	827	828	0	100.1	71.7	80.3	hypothetical protein ARALYDRAFT_481192	gbpln	Arabidopsis lyrata	AT2G23200.1 | Symbols: | Protein kinase superfamily protein | chr2:9879351-9881855 FORWARD LENGTH=834	827	834	0	100.8	71.3	80.2
Rsa1.0_00934.1.g21521.t1	ref|XP_002863767.1| hypothetical protein ARALYDRAFT_917496 [Arabidopsis lyrata subsp. lyrata] gi|297309602|gb|EFH40026.1| hypothetical protein ARALYDRAFT_917496 [Arabidopsis lyrata subsp. lyrata]	264	343	6.00E-76	129.9	60.2	70.1	hypothetical protein ARALYDRAFT_917496	gbpln	Arabidopsis lyrata	AT1G36675.1 | Symbols: | glycine-rich protein | chr1:13867568-13869490 FORWARD LENGTH=268	264	268	9.00E-31	101.5	34.8	41.7
Rsa1.0_00934.1.g21522.t1	gb|ABD32665.1| Terpenoid cylases/protein prenyltransferase alpha-alpha toroid; Bacterial adhesion [Medicago truncatula]	247	426	1.00E-114	172.5	79.8	83.0	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid; Bacterial adhesion	gbpln	Medicago truncatula	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	247	343	2.00E-18	138.9	16.6	22.3
Rsa1.0_00934.1.g21523.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00934.1.g21524.t1	ref|NP_190352.1| DNA binding protein [Arabidopsis thaliana] gi|4741185|emb|CAB41851.1| hypothetical protein [Arabidopsis thaliana] gi|189303599|gb|ACD85799.1| At3g47680 [Arabidopsis thaliana] gi|332644797|gb|AEE78318.1| DNA binding protein [Arabidopsis thaliana]	251	302	3.00E-16	120.3	27.5	32.7	DNA binding protein	gbpln	Arabidopsis thaliana	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	251	302	8.00E-19	120.3	27.5	32.7
Rsa1.0_00934.1.g21525.t1	ref|XP_002880529.1| hypothetical protein ARALYDRAFT_481243 [Arabidopsis lyrata subsp. lyrata] gi|297326368|gb|EFH56788.1| hypothetical protein ARALYDRAFT_481243 [Arabidopsis lyrata subsp. lyrata]	270	273	1.00E-133	101.1	85.6	93.0	hypothetical protein ARALYDRAFT_481243	gbpln	Arabidopsis lyrata	AT2G23810.1 | Symbols: TET8 | tetraspanin8 | chr2:10135859-10137352 REVERSE LENGTH=273	270	273	1.00E-129	101.1	83.7	90.7
Rsa1.0_00934.1.g21526.t1	emb|CAN65331.1| hypothetical protein VITISV_018654 [Vitis vinifera]	1034	1218	0	117.8	55.0	68.5	hypothetical protein VITISV_018654	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1034	1262	2.00E-52	122.1	11.3	17.9
Rsa1.0_00934.1.g21527.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1561	2726	0	174.6	52.0	70.1	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1561	158	3.00E-36	10.1	4.5	6.1

Rsa1.0_00934.1.g21528.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	519	1142	8.00E-62	220.0	24.1	33.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	519	626	2.00E-18	120.6	17.5	30.8
Rsa1.0_00935.1.g21529.t1	ref|NP_181552.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|4587997|gb|AAD25938.1|AF085279_11 hypothetical protein [Arabidopsis thaliana] gi|21536614|gb|AAM60946.1| putative anthranilate N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana] gi|330254705|gb|AEC09799.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	428	433	0	101.2	89.3	95.8	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT2G40230.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr2:16803285-16804586 REVERSE LENGTH=433	428	433	0	101.2	89.3	95.8
Rsa1.0_00935.1.g21530.t1	ref|NP_181551.1| ethylene-responsive transcription factor ABI4 [Arabidopsis thaliana] gi|156630458|sp|A0MES8.2|ABI4_ARATH RecName: Full=Ethylene-responsive transcription factor ABI4; Short=ERF ABI4; AltName: Full=Protein ABSCISIC ACID INSENSITIVE 4; AltName: Full=Protein GLUCOSE INSENSITIVE 6; AltName: Full=Protein IMPAIRED SUCROSE INDUCTION 3; AltName: Full=Protein SALOBRENO 5; AltName: Full=Protein SUCROSE UNCOUPLED 6; AltName: Full=Protein SUGAR INSENSITIVE 5 gi|4587996|gb|AAD25937.1|AF085279_10 ABI4 [Arabidopsis thaliana] gi|3282693|gb|AAC39489.1| AP2 domain family transcription factor homolog [Arabidopsis thaliana] gi|91806337|gb|ABE65896.1| abscisic acid-insensitive 4 [Arabidopsis thaliana] gi|330254704|gb|AEC09798.1| ethylene-responsive transcription factor ABI4 [Arabidopsis thaliana]	327	328	1.00E-105	100.3	76.5	85.3	ethylene-responsive transcription factor ABI4	gbpln	Arabidopsis thaliana	AT2G40220.1 | Symbols: ABI4, SUN6, SIS5, ISI3, GIN6, SAN5, ATABI4 | Integrase-type DNA-binding superfamily protein | chr2:16796599-16797585 REVERSE LENGTH=328	327	328	1.00E-107	100.3	76.5	85.3
Rsa1.0_00935.1.g21531.t1	ref|NP_181549.1| transcription factor bHLH51 [Arabidopsis thaliana] gi|75315012|sp|Q9XEF0.1|BH051_ARATH RecName: Full=Transcription factor bHLH51; AltName: Full=Basic helix-loop-helix protein 51; Short=AtbHLH51; Short=bHLH 51; AltName: Full=Transcription factor EN 57; AltName: Full=bHLH transcription factor bHLH051 gi|4587994|gb|AAD25935.1|AF085279_8 hypothetical protein [Arabidopsis thaliana] gi|20127047|gb|AAM10943.1|AF488586_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|124300966|gb|ABN04735.1| At2g40200 [Arabidopsis thaliana] gi|124301074|gb|ABN04789.1| At2g40200 [Arabidopsis thaliana] gi|225898581|dbj|BAH30421.1| hypothetical protein [Arabidopsis thaliana] gi|330254701|gb|AEC09795.1| transcription factor bHLH51 [Arabidopsis thaliana]	241	254	6.00E-85	105.4	76.3	86.3	transcription factor bHLH51	gbpln	Arabidopsis thaliana	AT2G40200.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:16791098-16792027 FORWARD LENGTH=254	241	254	2.00E-87	105.4	76.3	86.3
Rsa1.0_00935.1.g21532.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	387	1534	1.00E-100	396.4	49.4	58.7	F17L21.7	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	387	1262	5.00E-39	326.1	27.9	48.3
Rsa1.0_00935.1.g21533.t1	ref|XP_002879887.1| hypothetical protein ARALYDRAFT_903365 [Arabidopsis lyrata subsp. lyrata] gi|297325726|gb|EFH56146.1| hypothetical protein ARALYDRAFT_903365 [Arabidopsis lyrata subsp. lyrata]	626	1359	1.00E-101	217.1	36.3	49.7	hypothetical protein ARALYDRAFT_903365	gbpln	Arabidopsis lyrata	AT3G03360.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:795218-796918 FORWARD LENGTH=481	626	481	8.00E-96	76.8	34.8	45.5
Rsa1.0_00935.1.g21534.t2	ref|XP_002879851.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325690|gb|EFH56110.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	380	392	1.00E-180	103.2	84.2	90.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G40180.1 | Symbols: ATHPP2C5, PP2C5 | phosphatase 2C5 | chr2:16782522-16784014 FORWARD LENGTH=390	380	390	1.00E-177	102.6	83.4	89.5

Rsa1.0_00935.1.g21535.t1	ref|XP_002881700.1| early methionine-labelled 6 [Arabidopsis lyrata subsp. lyrata] gi|297327539|gb|EFH57959.1| early methionine-labelled 6 [Arabidopsis lyrata subsp. lyrata]	91	92	4.00E-31	101.1	83.5	89.0	early methionine-labelled 6	gbpln	Arabidopsis lyrata	AT2G40170.1 | Symbols: ATEM6, GEA6, EM6 | Stress induced protein | chr2:16779792-16780167 REVERSE LENGTH=92	91	92	2.00E-33	101.1	83.5	87.9
Rsa1.0_00935.1.g21536.t1	ref|XP_002879850.1| hypothetical protein ARALYDRAFT_483062 [Arabidopsis lyrata subsp. lyrata] gi|297325689|gb|EFH56109.1| hypothetical protein ARALYDRAFT_483062 [Arabidopsis lyrata subsp. lyrata]	437	427	0	97.7	78.7	87.6	hypothetical protein ARALYDRAFT_483062	gbpln	Arabidopsis lyrata	AT2G40160.1 | Symbols: TBL30 | Plant protein of unknown function (DUF828) | chr2:16777448-16779063 FORWARD LENGTH=427	437	427	0	97.7	77.3	87.0
Rsa1.0_00935.1.g21537.t1	ref|NP_030560.1| trichome birefringence-like 28 protein [Arabidopsis thaliana] gi|13877599|gb|AAK43877.1|AF370500_1 Unknown protein [Arabidopsis thaliana] gi|28059703|gb|AAO30085.1| Unknown protein [Arabidopsis thaliana] gi|330254695|gb|AEC09789.1| trichome birefringence-like 28 protein [Arabidopsis thaliana]	433	424	0	97.9	83.4	88.7	trichome birefringence-like 28 protein	gbpln	Arabidopsis thaliana	AT2G40150.1 | Symbols: TBL28 | TRICHOME BIREFRINGENCE-LIKE 28 | chr2:16775511-16777141 FORWARD LENGTH=424	433	424	0	97.9	83.4	88.7
Rsa1.0_00936.1.g21538.t1	gb|AAF79576.1|AC022464_34 F22G5.13 [Arabidopsis thaliana]	91	126	6.00E-21	138.5	63.7	72.5	F22G5.13	gbpln	Arabidopsis thaliana	AT1G07485.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot apex, embryo, leaf whorl, pedicel; EXPRESSED DURING: 4 anthesis, D bilateral stage; Has 5 Blast hits to 5 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2301505-2301892 FORWARD LENGTH=100	91	100	6.00E-18	109.9	50.5	59.3
Rsa1.0_00936.1.g21539.t1	gb|EOA39018.1| hypothetical protein CARUB_v10011564mg [Capsella rubella]	86	78	1.00E-16	90.7	60.5	68.6	hypothetical protein CARUB_v10011564mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00936.1.g21540.t1	ref|XP_002892404.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338246|gb|EFH68663.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	722	1493	0	206.8	76.9	85.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G07520.1 | Symbols: | GRAS family transcription factor | chr1:2309718-2311805 REVERSE LENGTH=695	722	695	0	96.3	74.8	82.7
Rsa1.0_00936.1.g21541.t1	gb|AAF79547.1|AC022464_5 F22G5.8 [Arabidopsis thaliana]	87	707	1.00E-42	812.6	92.0	95.4	F22G5.8	gbpln	Arabidopsis thaliana	AT1G07540.1 | Symbols: TRFL2 | TRF-like 2 | chr1:2318433-2321048 REVERSE LENGTH=630	87	630	2.00E-41	724.1	87.4	88.5
Rsa1.0_00936.1.g21542.t1	dbj|BAJ34037.1| unnamed protein product [Thellungiella halophila]	335	341	1.00E-171	101.8	85.4	92.8	unnamed protein product	----	----	AT3G44290.1 | Symbols: anac060, NAC060 | NAC domain containing protein 60 | chr3:15972909-15975019 REVERSE LENGTH=335	335	335	1.00E-170	100.0	85.4	91.3
Rsa1.0_00936.1.g21543.t1	ref|NP_172234.2| telomere repeat-binding protein 5 [Arabidopsis thaliana] gi|296439813|sp|Q6R0E3.2|TRP5_ARATH RecName: Full=Telomere repeat-binding protein 5; AltName: Full=Protein TRF-LIKE 2 gi|332190019|gb|AEE28140.1| telomere repeat-binding protein 5 [Arabidopsis thaliana]	612	630	0	102.9	80.1	86.6	telomere repeat-binding protein 5	gbpln	Arabidopsis thaliana	AT1G07540.1 | Symbols: TRFL2 | TRF-like 2 | chr1:2318433-2321048 REVERSE LENGTH=630	612	630	0	102.9	80.1	86.6
Rsa1.0_00936.1.g21544.t1	#	#	#	#	#	#	#	-	----	----	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	77	302	6.00E-11	392.2	35.1	42.9
Rsa1.0_00936.1.g21545.t1	gb|EOA37565.1| hypothetical protein CARUB_v10011886mg [Capsella rubella]	870	870	0	100.0	71.7	83.3	hypothetical protein CARUB_v10011886mg	gbpln	Capsella rubella	AT2G14510.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:6171133-6175052 REVERSE LENGTH=868	870	868	0	99.8	72.0	83.1
Rsa1.0_00936.1.g21546.t1	gb|ADP37975.1| metallothionein-like protein [Brassica napus]	45	45	3.00E-13	100.0	100.0	100.0	metallothionein-like protein	gbpln	Brassica napus	AT1G07610.1 | Symbols: MT1C | metallothionein 1C | chr1:2341603-2341865 FORWARD LENGTH=45	45	45	5.00E-14	100.0	91.1	95.6
Rsa1.0_00936.1.g21547.t1	gb|EOA40013.1| hypothetical protein CARUB_v10008702mg [Capsella rubella]	643	557	0	86.6	57.2	68.6	hypothetical protein CARUB_v10008702mg	gbpln	Capsella rubella	AT1G07620.1 | Symbols: ATOBGM | GTP-binding protein Obg/CgtA | chr1:2344556-2346374 REVERSE LENGTH=552	643	552	0	85.8	59.7	67.8

Rsa1.0_00936.1.g21548.t2	ref|NP_563791.1| putative protein phosphatase 2C 4 [Arabidopsis thaliana] gi|75180175|sp|Q9LQN6.1|P2C04_ARATH RecName: Full=Probable protein phosphatase 2C 4; Short=AtPP2C04; AltName: Full=Protein POLTERGEIST-LIKE 5; AltName: Full=Protein phosphatase 2C PLL5; Short=PP2C PLL5 gi|8439909|gb|AAF75095.1|AC007583_31 It contains protein phosphatase 2C domain PF|00481. ESTs gb|H36120 and gb|36519 come from this gene [Arabidopsis thaliana] gi|332190030|gb|AEE28151.1| putative protein phosphatase 2C 4 [Arabidopsis thaliana]	634	662	0	104.4	80.9	86.8	putative protein phosphatase 2C 4	gbpln	Arabidopsis thaliana	AT1G07630.1 | Symbols: PLL5 | pol-like 5 | chr1:2349189-2351437 FORWARD LENGTH=662	634	662	0	104.4	80.9	86.8
Rsa1.0_00936.1.g21549.t1	gb|EOA38961.1| hypothetical protein CARUB_v10011378mg [Capsella rubella]	323	337	1.00E-125	104.3	77.4	83.0	hypothetical protein CARUB_v10011378mg	gbpln	Capsella rubella	AT1G07640.2 | Symbols: OBP2 | Dof-type zinc finger DNA-binding family protein | chr1:2354707-2355798 REVERSE LENGTH=331	323	331	1.00E-126	102.5	78.0	85.1
Rsa1.0_00936.1.g21550.t1	gb|AAL65634.1| transaldolase-like protein [Arabidopsis thaliana] gi|22497334|gb|AAL65636.1| transaldolase-like protein [Arabidopsis thaliana]	69	375	1.00E-11	543.5	66.7	76.8	transaldolase-like protein	gbpln	Arabidopsis thaliana	AT1G12230.1 | Symbols: | Aldolase superfamily protein | chr1:4148050-4150708 FORWARD LENGTH=405	69	405	6.00E-14	587.0	65.2	76.8
Rsa1.0_00936.1.g21551.t1	ref|NP_172244.2| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|264664462|sp|C0LGE0.1|Y1765_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g07650; Flags: Precursor gi|224589382|gb|ACN59225.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332190034|gb|AEE28155.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	1013	1014	0	100.1	86.1	91.5	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G07650.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:2359817-2366423 REVERSE LENGTH=1014	1013	1014	0	100.1	86.1	91.5
Rsa1.0_00936.1.g21552.t1	ref|XP_002892412.1| lactoylglutathione lyase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338254|gb|EFH68671.1| lactoylglutathione lyase family protein [Arabidopsis lyrata subsp. lyrata]	58	137	7.00E-19	236.2	81.0	81.0	lactoylglutathione lyase family protein	gbpln	Arabidopsis lyrata	AT1G07645.1 | Symbols: ATDSI-1VOC, DSI-1VOC | dessication-induced 1VOC superfamily protein | chr1:2367612-2368349 REVERSE LENGTH=137	58	137	8.00E-21	236.2	79.3	81.0
Rsa1.0_00937.1.g21553.t1	gb|EOA30106.1| hypothetical protein CARUB_v10013217mg [Capsella rubella]	625	626	0	100.2	85.4	92.8	hypothetical protein CARUB_v10013217mg	gbpln	Capsella rubella	AT3G10160.1 | Symbols: ATDFC, DFC, FPGS2 | DHFS-FPGS homolog C | chr3:3139588-3143949 REVERSE LENGTH=625	625	625	0	100.0	86.4	92.8
Rsa1.0_00937.1.g21554.t1	ref|NP_187623.2| uncharacterized protein [Arabidopsis thaliana] gi|26450718|dbj|BAC42468.1| unknown protein [Arabidopsis thaliana] gi|28372890|gb|AAO39927.1| At3g10120 [Arabidopsis thaliana] gi|332641341|gb|AEE74862.1| uncharacterized protein AT3G10120 [Arabidopsis thaliana]	171	173	1.00E-65	101.2	77.2	88.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G10120.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G03890.1); Has 57 Blast hits to 57 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3130155-3130676 FORWARD LENGTH=173	171	173	5.00E-68	101.2	77.2	88.3
Rsa1.0_00937.1.g21555.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	170	1231	9.00E-27	724.1	35.9	55.9	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00937.1.g21556.t1	ref|NP_189068.2| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana] gi|332643359|gb|AEE76880.1| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana]	270	746	5.00E-55	276.3	37.0	51.5	RNA-directed DNA polymerase (reverse transcriptase)-related protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	270	746	1.00E-57	276.3	37.0	51.5
Rsa1.0_00937.1.g21557.t1	gb|EOA32236.1| hypothetical protein CARUB_v10015494mg [Capsella rubella]	226	227	1.00E-107	100.4	87.6	94.2	hypothetical protein CARUB_v10015494mg	gbpln	Capsella rubella	AT3G10080.1 | Symbols: | RmlC-like cupins superfamily protein | chr3:3107476-3108159 REVERSE LENGTH=227	226	227	1.00E-107	100.4	86.7	94.7
Rsa1.0_00937.1.g21558.t1	ref|XP_002884774.1| L-O-methylthreonine resistant 1 [Arabidopsis lyrata subsp. lyrata] gi|297330614|gb|EFH61033.1| L-O-methylthreonine resistant 1 [Arabidopsis lyrata subsp. lyrata]	615	591	0	96.1	83.3	89.9	L-O-methylthreonine resistant 1	gbpln	Arabidopsis lyrata	AT3G10050.1 | Symbols: OMR1 | L-O-methylthreonine resistant 1 | chr3:3099164-3101741 REVERSE LENGTH=592	615	592	0	96.3	82.0	88.6

Rsa1.0_00937.1.g21559.t1	ref|NP_187595.1| cell division control protein 48-A [Arabidopsis thaliana] gi|1705677|sp|P54609.1|CD48A_ARATH RecName: Full=Cell division control protein 48 homolog A; Short=AtCDC48a gi|6681343|gb|AAF23260.1|AC015985_18 putative transitional endoplasmic reticulum ATPase [Arabidopsis thaliana] gi|1019904|gb|AAC49120.1| cell division cycle protein [Arabidopsis thaliana] gi|17473551|gb|AAL38252.1| putative transitional endoplasmic reticulum ATPase [Arabidopsis thaliana] gi|20453130|gb|AAM19807.1| AT3g09840/F8A24_11 [Arabidopsis thaliana] gi|110735114|gb|ABG89127.1| CDC48a [synthetic construct] gi|222424942|dbj|BAH20422.1| AT3G09840 [Arabidopsis thaliana] gi|332641299|gb|AEE74820.1| cell division control protein 48-A [Arabidopsis thaliana]	810	809	0	99.9	98.6	99.3	cell division control protein 48-A	gbpln	Arabidopsis thaliana	AT3G09840.1 | Symbols: CDC48, ATCDC48, CDC48A | cell division cycle 48 | chr3:3019494-3022832 FORWARD LENGTH=809	810	809	0	99.9	98.6	99.3
Rsa1.0_00937.1.g21560.t1	gb|EOA30956.1| hypothetical protein CARUB_v10014102mg [Capsella rubella]	186	344	1.00E-104	184.9	96.8	98.9	hypothetical protein CARUB_v10014102mg	gbpln	Capsella rubella	AT3G09820.1 | Symbols: ADK1, ATADK1 | adenosine kinase 1 | chr3:3012122-3014624 FORWARD LENGTH=344	186	344	1.00E-106	184.9	96.8	98.9
Rsa1.0_00938.1.g21561.t1	ref|XP_002882792.1| hypothetical protein ARALYDRAFT_478649 [Arabidopsis lyrata subsp. lyrata] gi|297328632|gb|EFH59051.1| hypothetical protein ARALYDRAFT_478649 [Arabidopsis lyrata subsp. lyrata]	177	175	4.00E-64	98.9	65.5	74.6	hypothetical protein ARALYDRAFT_478649	gbpln	Arabidopsis lyrata	AT3G12880.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:4095563-4096102 FORWARD LENGTH=179	177	179	5.00E-65	101.1	63.8	72.3
Rsa1.0_00938.1.g21562.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00938.1.g21563.t1	ref|XP_002882793.1| hypothetical protein ARALYDRAFT_478650 [Arabidopsis lyrata subsp. lyrata] gi|297328633|gb|EFH59052.1| hypothetical protein ARALYDRAFT_478650 [Arabidopsis lyrata subsp. lyrata]	243	251	1.00E-116	103.3	86.0	90.9	hypothetical protein ARALYDRAFT_478650	gbpln	Arabidopsis lyrata	AT3G12890.1 | Symbols: ASML2 | activator of spomin::LUC2 | chr3:4099223-4100277 FORWARD LENGTH=251	243	251	1.00E-117	103.3	84.8	89.7
Rsa1.0_00938.1.g21564.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	704	1274	0	181.0	54.4	67.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	704	575	2.00E-64	81.7	25.3	37.6
Rsa1.0_00938.1.g21565.t2	gb|ABK28555.1| unknown [Arabidopsis thaliana]	102	358	1.00E-23	351.0	67.6	78.4	unknown	gbpln	Arabidopsis thaliana	AT3G12900.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:4104576-4106112 FORWARD LENGTH=357	102	357	2.00E-26	350.0	67.6	78.4
Rsa1.0_00938.1.g21566.t1	ref|XP_002882795.1| transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297328635|gb|EFH59054.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	311	303	1.00E-132	97.4	75.2	84.6	transcription factor	gbpln	Arabidopsis lyrata	AT3G12910.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr3:4109417-4110648 FORWARD LENGTH=303	311	303	1.00E-127	97.4	74.0	83.3
Rsa1.0_00938.1.g21567.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00938.1.g21568.t1	ref|NP_566438.1| S-ribonuclease binding protein [Arabidopsis thaliana] gi|15795121|dbj|BAB02499.1| unnamed protein product [Arabidopsis thaliana] gi|26451940|dbj|BAC43062.1| unknown protein [Arabidopsis thaliana] gi|30017303|gb|AAP12885.1| At3g12920 [Arabidopsis thaliana] gi|332641741|gb|AEE75262.1| S-ribonuclease binding protein [Arabidopsis thaliana]	443	335	1.00E-127	75.6	51.7	59.6	S-ribonuclease binding protein	gbpln	Arabidopsis thaliana	AT3G12920.1 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr3:4122127-4123323 REVERSE LENGTH=335	443	335	1.00E-130	75.6	51.7	59.6
Rsa1.0_00938.1.g21569.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	728	657	1.00E-171	90.2	40.5	53.3	T14P8.10	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	728	746	3.00E-54	102.5	18.4	27.9
Rsa1.0_00938.1.g21570.t1	ref|NP_187937.2| varicose-related protein [Arabidopsis thaliana] gi|75335477|sp|Q9LTT9.1|VCR_ARATH RecName: Full=Varicose-related protein gi|9294535|dbj|BAB02798.1| unnamed protein product [Arabidopsis thaliana] gi|332641808|gb|AEE75329.1| varicose-related protein [Arabidopsis thaliana]	593	1340	0	226.0	73.2	82.5	varicose-related protein	gbpln	Arabidopsis thaliana	AT3G13290.1 | Symbols: VCR | varicose-related | chr3:4297529-4303113 FORWARD LENGTH=1340	593	1340	0	226.0	73.2	82.5

Rsa1.0_00938.1.g21571.t1	ref|XP_002884960.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330800|gb|EFH61219.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	157	157	8.00E-58	100.0	77.1	83.4	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT3G13310.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr3:4310827-4311300 REVERSE LENGTH=157	157	157	1.00E-59	100.0	77.1	83.4
Rsa1.0_00938.1.g21572.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00938.1.g21573.t1	ref|NP_566450.1| RNA-binding protein PNO1 [Arabidopsis thaliana] gi|9294528|dbj|BAB02791.1| unnamed protein product [Arabidopsis thaliana] gi|50897250|gb|AAT85764.1| At3g13230 [Arabidopsis thaliana] gi|110738874|dbj|BAF01359.1| hypothetical protein [Arabidopsis thaliana] gi|332641801|gb|AEE75322.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana]	217	215	1.00E-110	99.1	90.3	95.4	RNA-binding protein PNO1	gbpln	Arabidopsis thaliana	AT3G13230.1 | Symbols: | RNA-binding KH domain-containing protein | chr3:4270423-4271070 FORWARD LENGTH=215	217	215	1.00E-112	99.1	90.3	95.4
Rsa1.0_00938.1.g21574.t1	dbj|BAF02082.1| hypothetical protein [Arabidopsis thaliana]	1141	774	0	67.8	43.8	49.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G13300.1 | Symbols: VCS | Transducin/WD40 repeat-like superfamily protein | chr3:4304085-4309949 FORWARD LENGTH=1344	1141	1344	0	117.8	43.8	49.0
Rsa1.0_00938.1.g21575.t1	ref|NP_187939.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|9294537|dbj|BAB02800.1| DnaJ-like protein [Arabidopsis thaliana] gi|21592683|gb|AAM64632.1| DnaJ protein, putative [Arabidopsis thaliana] gi|32815917|gb|AAP88343.1| At3g13310 [Arabidopsis thaliana] gi|332641811|gb|AEE75332.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]	120	157	2.00E-36	130.8	71.7	75.8	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT3G13310.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr3:4310827-4311300 REVERSE LENGTH=157	120	157	3.00E-39	130.8	71.7	75.8
Rsa1.0_00938.1.g21576.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00938.1.g21577.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00939.1.g21578.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1531	1342	0	87.7	43.4	59.8	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1531	1262	5.00E-83	82.4	11.3	17.8
Rsa1.0_00939.1.g21579.t1	ref|NP_564729.1| TRAF-like protein [Arabidopsis thaliana] gi|8979946|gb|AAF82260.1|AC008051_11 Identical to gene ZW9 from Arabidopsis thaliana gb|AB028194 and contains two MATH PF|00917 domains. ESTs gb|AI996327, gb|AI997139, gb|AA712716, gb|BE037713, gb|BE037714, gb|F14095, gb|F14009, gb|N38170, gb|T44357, gb|T45202 come from this gene [Arabidopsis thaliana] gi|12083246|gb|AAG48782.1|AF332419_1 unknown protein [Arabidopsis thaliana] gi|16930453|gb|AAL31912.1|AF419580_1 At1g58270/F19C14_8 [Arabidopsis thaliana] gi|6520139|dbj|BAA87936.1| ZW9 [Arabidopsis thaliana] gi|332195406|gb|AEE33527.1| TRAF-like protein [Arabidopsis thaliana]	176	396	6.00E-63	225.0	73.3	86.9	TRAF-like protein	gbpln	Arabidopsis thaliana	AT1G58270.1 | Symbols: ZW9 | TRAF-like family protein | chr1:21612394-21614089 REVERSE LENGTH=396	176	396	2.00E-65	225.0	73.3	86.9
Rsa1.0_00939.1.g21580.t1	gb|EOA31343.1| hypothetical protein CARUB_v10014517mg [Capsella rubella]	170	238	5.00E-25	140.0	31.2	35.9	hypothetical protein CARUB_v10014517mg	gbpln	Capsella rubella	AT3G07800.1 | Symbols: | Thymidine kinase | chr3:2489944-2490935 REVERSE LENGTH=238	170	238	3.00E-26	140.0	30.0	34.7
Rsa1.0_00939.1.g21581.t1	gb|EOA34484.1| hypothetical protein CARUB_v10022025mg [Capsella rubella]	339	348	1.00E-166	102.7	84.7	92.0	hypothetical protein CARUB_v10022025mg	gbpln	Capsella rubella	AT1G73610.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:27678377-27679807 FORWARD LENGTH=344	339	344	1.00E-158	101.5	79.9	88.2
Rsa1.0_00939.1.g21582.t1	gb|ABV89611.1| thaumatin-like protein [Brassica rapa]	265	245	1.00E-140	92.5	91.7	92.5	thaumatin-like protein	gbpln	Brassica rapa	AT1G73620.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:27681432-27682954 FORWARD LENGTH=264	265	264	1.00E-130	99.6	90.2	93.6
Rsa1.0_00939.1.g21583.t1	gb|EOA35826.1| hypothetical protein CARUB_v10021066mg [Capsella rubella]	160	162	6.00E-71	101.3	81.9	90.0	hypothetical protein CARUB_v10021066mg	gbpln	Capsella rubella	AT1G73630.1 | Symbols: | EF hand calcium-binding protein family | chr1:27684748-27685239 FORWARD LENGTH=163	160	163	9.00E-73	101.9	83.1	90.0

Rsa1.0_00939.1.g21584.t1	ref|XP_002887496.1| hypothetical protein ARALYDRAFT_476500 [Arabidopsis lyrata subsp. lyrata] gi|297333337|gb|EFH63755.1| hypothetical protein ARALYDRAFT_476500 [Arabidopsis lyrata subsp. lyrata]	232	232	1.00E-116	100.0	90.5	95.3	hypothetical protein ARALYDRAFT_476500	gbpln	Arabidopsis lyrata	AT1G73640.1 | Symbols: AtRABA6a, RABA6a | RAB GTPase homolog A6A | chr1:27687033-27687987 FORWARD LENGTH=233	232	233	1.00E-116	100.4	89.7	95.3
Rsa1.0_00939.1.g21585.t1	ref|NP_565068.1| uncharacterized protein [Arabidopsis thaliana] gi|222422963|dbj|BAH19466.1| AT1G73650 [Arabidopsis thaliana] gi|332197369|gb|AEE35490.1| uncharacterized protein AT1G73650 [Arabidopsis thaliana]	293	291	1.00E-143	99.3	88.4	94.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G73650.2 | Symbols: | Protein of unknown function (DUF1295) | chr1:27688549-27690165 REVERSE LENGTH=291	293	291	2.33E-156	99.3	88.4	94.5
Rsa1.0_00939.1.g21586.t1	gb|AAP86285.1| CTR1-like kinase kinase kinase [Brassica juncea] gi|32527769|gb|AAP86286.1| CTR1-like kinase kinase kinase [Brassica juncea]	1000	970	0	97.0	89.6	91.7	CTR1-like kinase kinase kinase	gbpln	Brassica juncea	AT1G73660.1 | Symbols: | protein tyrosine kinase family protein | chr1:27692247-27696718 REVERSE LENGTH=1030	1000	1030	0	103.0	85.0	90.0
Rsa1.0_00939.1.g21587.t1	dbj|BAJ33800.1| unnamed protein product [Thellungiella halophila]	631	631	0	100.0	94.0	97.8	unnamed protein product	----	----	AT1G73680.1 | Symbols: ALPHA DOX2 | alpha dioxygenase | chr1:27704221-27707417 REVERSE LENGTH=631	631	631	0	100.0	90.0	95.4
Rsa1.0_00939.1.g21588.t1	gb|EOA35150.1| hypothetical protein CARUB_v10020289mg, partial [Capsella rubella]	406	449	1.00E-173	110.6	76.1	85.2	hypothetical protein CARUB_v10020289mg, partial	gbpln	Capsella rubella	AT1G73810.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:27752506-27755208 REVERSE LENGTH=418	406	418	1.00E-172	103.0	75.4	84.0
Rsa1.0_00939.1.g21589.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	294	1225	1.00E-57	416.7	41.2	55.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	294	575	3.00E-39	195.6	34.7	53.1
Rsa1.0_00939.1.g21590.t1	ref|XP_002888948.1| hypothetical protein ARALYDRAFT_895246 [Arabidopsis lyrata subsp. lyrata] gi|297334789|gb|EFH65207.1| hypothetical protein ARALYDRAFT_895246 [Arabidopsis lyrata subsp. lyrata]	80	193	2.00E-11	241.3	66.3	77.5	hypothetical protein ARALYDRAFT_895246	gbpln	Arabidopsis lyrata	AT1G73820.1 | Symbols: | Ssu72-like family protein | chr1:27755740-27757158 REVERSE LENGTH=193	80	193	4.00E-14	241.3	66.3	76.3
Rsa1.0_00939.1.g21591.t1	gb|EOA33262.1| hypothetical protein CARUB_v10022206mg [Capsella rubella]	398	388	0	97.5	84.7	88.7	hypothetical protein CARUB_v10022206mg	gbpln	Capsella rubella	AT4G23180.1 | Symbols: CRK10, RLK4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 | chr4:12138171-12140780 FORWARD LENGTH=669	398	669	2.00E-97	168.1	43.0	56.8
Rsa1.0_00939.1.g21592.t1	ref|XP_002887509.1| hypothetical protein ARALYDRAFT_476520 [Arabidopsis lyrata subsp. lyrata] gi|297333350|gb|EFH63768.1| hypothetical protein ARALYDRAFT_476520 [Arabidopsis lyrata subsp. lyrata]	444	263	1.00E-104	59.2	43.9	47.5	hypothetical protein ARALYDRAFT_476520	gbpln	Arabidopsis lyrata	AT1G73830.2 | Symbols: BEE3 | BR enhanced expression 3 | chr1:27760027-27761346 FORWARD LENGTH=260	444	260	1.00E-101	58.6	43.5	47.3
Rsa1.0_00939.1.g21593.t1	ref|NP_177525.2| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|17979388|gb|AAL49919.1| putative proline-rich protein precursor [Arabidopsis thaliana] gi|20465539|gb|AAM20252.1| putative proline-rich protein precursor [Arabidopsis thaliana] gi|332197394|gb|AEE35515.1| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana]	412	388	1.00E-108	94.2	57.5	60.9	hydroxyproline-rich glycoprotein-like protein	gbpln	Arabidopsis thaliana	AT1G73840.1 | Symbols: ESP1 | hydroxyproline-rich glycoprotein family protein | chr1:27763937-27766328 REVERSE LENGTH=388	412	388	1.00E-110	94.2	57.5	60.9
Rsa1.0_00939.1.g21594.t1	gb|AAG52080.1|AC012679_18 unknown protein; 95319-98330 [Arabidopsis thaliana]	631	651	0	103.2	81.9	88.9	unknown protein; 95319-98330	gbpln	Arabidopsis thaliana	AT1G73850.1 | Symbols: | Protein of unknown function (DUF1666) | chr1:27767375-27770386 FORWARD LENGTH=635	631	635	0	100.6	82.9	89.5
Rsa1.0_00939.1.g21595.t1	ref|NP_177527.3| putative Kinesin motor protein-related protein [Arabidopsis thaliana] gi|110739024|dbj|BAF01431.1| kinesin-related protein [Arabidopsis thaliana] gi|332197396|gb|AEE35517.1| putative Kinesin motor protein-related protein [Arabidopsis thaliana]	1036	1025	0	98.9	85.3	92.5	putative Kinesin motor protein-related protein	gbpln	Arabidopsis thaliana	AT1G73860.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:27771188-27775977 REVERSE LENGTH=1025	1036	1025	0	98.9	85.3	92.5

Rsa1.0_00940.1.g21596.t1	ref|NP_568161.1| putative transcriptional regulator RABBIT EARS [Arabidopsis thaliana] gi|41688606|sp|Q9LHS9.2|RBE_ARATH RecName: Full=Probable transcriptional regulator RABBIT EARS gi|37514920|dbj|BAC98433.1| one finger-type zinc finger protein for RABBIT EARS [Arabidopsis thaliana] gi|94442519|gb|ABF19047.1| At5g06070 [Arabidopsis thaliana] gi|332003578|gb|AED90961.1| putative transcriptional regulator RABBIT EARS [Arabidopsis thaliana]	216	226	4.00E-91	104.6	77.8	87.5	putative transcriptional regulator RABBIT EARS	gbpln	Arabidopsis thaliana	AT5G06070.1 | Symbols: RBE, RAB | C2H2 and C2HC zinc fingers superfamily protein | chr5:1828426-1829106 REVERSE LENGTH=226	216	226	1.00E-93	104.6	77.8	87.5
Rsa1.0_00940.1.g21597.t1	gb|EOA20121.1| hypothetical protein CARUB_v10000399mg [Capsella rubella]	486	667	1.00E-176	137.2	73.9	81.7	hypothetical protein CARUB_v10000399mg	gbpln	Capsella rubella	AT5G06110.2 | Symbols: | DnaJ domain ;Myb-like DNA-binding domain | chr5:1841009-1843000 REVERSE LENGTH=663	486	663	1.00E-176	136.4	73.9	81.7
Rsa1.0_00940.1.g21598.t1	gb|EOA20121.1| hypothetical protein CARUB_v10000399mg [Capsella rubella]	485	667	1.00E-173	137.5	73.6	82.1	hypothetical protein CARUB_v10000399mg	gbpln	Capsella rubella	AT5G06110.2 | Symbols: | DnaJ domain ;Myb-like DNA-binding domain | chr5:1841009-1843000 REVERSE LENGTH=663	485	663	1.00E-175	136.7	74.0	82.3
Rsa1.0_00940.1.g21599.t1	gb|EOA36691.1| hypothetical protein CARUB_v10012096mg [Capsella rubella]	323	327	1.00E-136	101.2	71.2	84.5	hypothetical protein CARUB_v10012096mg	gbpln	Capsella rubella	AT5G43690.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273-17547268 FORWARD LENGTH=331	323	331	1.00E-136	102.5	71.5	82.7
Rsa1.0_00940.1.g21600.t1	ref|XP_002873241.1| CYC1BAT [Arabidopsis lyrata subsp. lyrata] gi|297319078|gb|EFH49500.1| CYC1BAT [Arabidopsis lyrata subsp. lyrata]	452	445	0	98.5	83.0	88.7	CYC1BAT	gbpln	Arabidopsis lyrata	AT5G06150.1 | Symbols: CYC1BAT, CYCB1;2 | Cyclin family protein | chr5:1859542-1861570 REVERSE LENGTH=445	452	445	0	98.5	81.9	88.5
Rsa1.0_00940.1.g21601.t1	ref|XP_002882139.1| hypothetical protein ARALYDRAFT_904276 [Arabidopsis lyrata subsp. lyrata] gi|297327978|gb|EFH58398.1| hypothetical protein ARALYDRAFT_904276 [Arabidopsis lyrata subsp. lyrata]	514	529	0	102.9	83.5	90.9	hypothetical protein ARALYDRAFT_904276	gbpln	Arabidopsis lyrata	AT2G47990.1 | Symbols: SWA1, EDA13, EDA19 | transducin family protein / WD-40 repeat family protein | chr2:19637010-19638602 REVERSE LENGTH=530	514	530	0	103.1	83.3	91.2
Rsa1.0_00940.1.g21602.t1	ref|XP_002873242.1| hypothetical protein ARALYDRAFT_487419 [Arabidopsis lyrata subsp. lyrata] gi|297319079|gb|EFH49501.1| hypothetical protein ARALYDRAFT_487419 [Arabidopsis lyrata subsp. lyrata]	537	508	0	94.6	76.5	84.4	hypothetical protein ARALYDRAFT_487419	gbpln	Arabidopsis lyrata	AT5G06160.1 | Symbols: ATO | splicing factor-related | chr5:1862623-1866298 REVERSE LENGTH=504	537	504	0	93.9	74.9	83.2
Rsa1.0_00940.1.g21603.t1	gb|EOA35047.1| hypothetical protein CARUB_v10020153mg [Capsella rubella]	434	514	0	118.4	77.2	86.4	hypothetical protein CARUB_v10020153mg	gbpln	Capsella rubella	AT1G71880.1 | Symbols: SUC1, ATSUC1 | sucrose-proton symporter 1 | chr1:27054334-27056100 FORWARD LENGTH=513	434	513	1.00E-180	118.2	77.4	86.6
Rsa1.0_00940.1.g21604.t1	gb|EOA35047.1| hypothetical protein CARUB_v10020153mg [Capsella rubella]	432	514	1.00E-148	119.0	57.9	65.0	hypothetical protein CARUB_v10020153mg	gbpln	Capsella rubella	AT1G71880.1 | Symbols: SUC1, ATSUC1 | sucrose-proton symporter 1 | chr1:27054334-27056100 FORWARD LENGTH=513	432	513	1.00E-149	118.8	57.9	64.6
Rsa1.0_00940.1.g21605.t1	gb|EOA19925.1| hypothetical protein CARUB_v10000175mg [Capsella rubella]	866	896	0	103.5	87.3	93.0	hypothetical protein CARUB_v10000175mg	gbpln	Capsella rubella	AT5G06220.2 | Symbols: | LETM1-like protein | chr5:1880049-1885366 FORWARD LENGTH=909	866	909	0	105.0	84.6	90.3
Rsa1.0_00940.1.g21606.t1	ref|NP_001119177.1| AP2/B3 domain-containing protein [Arabidopsis thaliana] gi|75171862|sp|Q9FNI3.1|Y5625_ARATH RecName: Full=B3 domain-containing protein At5g06250 gi|9758405|dbj|BAB08947.1| unnamed protein product [Arabidopsis thaliana] gi|332003608|gb|AED90991.1| AP2/B3 domain-containing protein [Arabidopsis thaliana]	283	282	4.00E-97	99.6	76.3	80.2	AP2/B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G06250.2 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:1892714-1894058 REVERSE LENGTH=282	283	282	1.00E-99	99.6	76.3	80.2
Rsa1.0_00940.1.g21607.t1	gb|EOA19710.1| hypothetical protein CARUB_v10003649mg [Capsella rubella]	137	139	2.00E-69	101.5	96.4	99.3	hypothetical protein CARUB_v10003649mg	gbpln	Capsella rubella	AT5G04800.4 | Symbols: | Ribosomal S17 family protein | chr5:1389217-1389642 FORWARD LENGTH=141	137	141	2.00E-65	102.9	88.3	93.4

Rsa1.0_00940.1.g21608.t1	ref|NP_196245.1| uncharacterized protein [Arabidopsis thaliana] gi|9758407|dbj|BAB08949.1| unnamed protein product [Arabidopsis thaliana] gi|21536580|gb|AAM60912.1| unknown [Arabidopsis thaliana] gi|28392887|gb|AAO41880.1| putative B-type cyclin [Arabidopsis thaliana] gi|28827636|gb|AAO50662.1| putative B-type cyclin [Arabidopsis thaliana] gi|332003613|gb|AED90996.1| uncharacterized protein AT5G06270 [Arabidopsis thaliana]	121	122	2.00E-37	100.8	83.5	88.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G06270.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11600.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1912895-1913263 FORWARD LENGTH=122	121	122	4.00E-40	100.8	83.5	88.4
Rsa1.0_00940.1.g21609.t1	gb|AAM95647.1| polygalacturonase inhibitory protein [Brassica napus] gi|160693704|gb|ABX46550.1| polygalacturonase inhibitor protein 3 [Brassica napus]	163	331	2.00E-56	203.1	70.6	73.6	polygalacturonase inhibitory protein	gbpln	Brassica napus	AT5G06860.1 | Symbols: PGIP1, ATPGIP1 | polygalacturonase inhibiting protein 1 | chr5:2132373-2133434 FORWARD LENGTH=330	163	330	1.00E-44	202.5	57.1	63.8
Rsa1.0_00940.1.g21610.t1	gb|EOA22207.1| hypothetical protein CARUB_v10002795mg [Capsella rubella]	362	352	1.00E-139	97.2	74.0	81.2	hypothetical protein CARUB_v10002795mg	gbpln	Capsella rubella	AT5G06920.1 | Symbols: FLA21 | FASCICLIN-like arabinogalactan protein 21 precursor | chr5:2142858-2143919 FORWARD LENGTH=353	362	353	1.00E-140	97.5	73.5	79.6
Rsa1.0_00940.1.g21611.t1	#	#	#	#	#	#	#	-	----	----	AT3G49130.1 | Symbols: | SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein | chr3:18210453-18211708 FORWARD LENGTH=307	193	307	2.00E-11	159.1	22.8	32.1
Rsa1.0_00940.1.g21612.t2	ref|NP_001190233.1| 26S proteasome regulatory subunit N8 [Arabidopsis thaliana] gi|332003541|gb|AED90924.1| probable 26S proteasome non-ATPase regulatory subunit 7 [Arabidopsis thaliana]	260	305	2.00E-55	117.3	47.3	53.1	26S proteasome regulatory subunit N8	gbpln	Arabidopsis thaliana	AT5G05780.2 | Symbols: RPN8A | RP non-ATPase subunit 8A | chr5:1735862-1738176 FORWARD LENGTH=305	260	305	7.00E-58	117.3	47.3	53.1
Rsa1.0_00940.1.g21613.t1	dbj|BAJ33600.1| unnamed protein product [Thellungiella halophila]	63	286	4.00E-21	454.0	79.4	82.5	unnamed protein product	----	----	AT5G06980.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12320.1); Has 30 Blast hits to 29 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:2167799-2169133 FORWARD LENGTH=274	63	274	1.00E-22	434.9	79.4	87.3
Rsa1.0_00940.1.g21614.t1	gb|EOA22792.1| hypothetical protein CARUB_v10003509mg [Capsella rubella]	359	360	1.00E-170	100.3	83.0	90.5	hypothetical protein CARUB_v10003509mg	gbpln	Capsella rubella	AT5G07010.1 | Symbols: ATST2A, ST2A | sulfotransferase 2A | chr5:2174960-2176039 REVERSE LENGTH=359	359	359	1.00E-172	100.0	81.6	90.5
Rsa1.0_00940.1.g21615.t1	dbj|BAB11161.1| nucleoid DNA-binding-like protein [Arabidopsis thaliana] gi|21553652|gb|AAM62745.1| nucleoid DNA-binding-like protein [Arabidopsis thaliana] gi|109134179|gb|ABG25087.1| At5g07030 [Arabidopsis thaliana]	439	439	0	100.0	89.5	94.8	nucleoid DNA-binding-like protein	gbpln	Arabidopsis thaliana	AT5G07030.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:2183600-2185717 REVERSE LENGTH=455	439	455	0	103.6	89.5	94.8
Rsa1.0_00940.1.g21616.t1	gb|EOA13870.1| hypothetical protein CARUB_v10026972mg [Capsella rubella]	341	262	1.00E-148	76.8	74.5	76.0	hypothetical protein CARUB_v10026972mg	gbpln	Capsella rubella	AT5G07090.1 | Symbols: | Ribosomal protein S4 (RPS4A) family protein | chr5:2202410-2203805 FORWARD LENGTH=262	341	262	1.00E-150	76.8	73.9	76.0
Rsa1.0_00940.1.g21617.t1	ref|NP_196329.2| sorting nexin 2B [Arabidopsis thaliana] gi|363805551|sp|B9DFS6.1|SNX2B_ARATH RecName: Full=Sorting nexin 2B gi|222423233|dbj|BAH19593.1| AT5G07120 [Arabidopsis thaliana] gi|332003729|gb|AED91112.1| sorting nexin 2B [Arabidopsis thaliana]	530	572	0	107.9	81.1	90.0	sorting nexin 2B	gbpln	Arabidopsis thaliana	AT5G07120.1 | Symbols: SNX2b | sorting nexin 2B | chr5:2207065-2209355 REVERSE LENGTH=572	530	572	0	107.9	81.1	90.0
Rsa1.0_00941.1.g21618.t2	gb|AAC61291.1| Ac-like transposase [Arabidopsis thaliana]	461	730	2.00E-64	158.4	28.4	39.9	Ac-like transposase	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	461	696	2.00E-12	151.0	11.7	20.6
Rsa1.0_00941.1.g21619.t1	ref|XP_002869250.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315086|gb|EFH45509.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	401	433	1.00E-170	108.0	83.5	91.5	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT4G32720.1 | Symbols: AtLa1, La1 | La protein 1 | chr4:15787313-15789683 FORWARD LENGTH=433	401	433	1.00E-170	108.0	82.5	91.0
Rsa1.0_00941.1.g21620.t1	ref|XP_002869249.1| PC-MYB1 [Arabidopsis lyrata subsp. lyrata] gi|297315085|gb|EFH45508.1| PC-MYB1 [Arabidopsis lyrata subsp. lyrata]	916	995	0	108.6	78.6	85.6	PC-MYB1	gbpln	Arabidopsis lyrata	AT4G32730.2 | Symbols: PC-MYB1, MYB3R-1, ATMYB3R-1, ATMYB3R1 | Homeodomain-like protein | chr4:15791039-15795643 FORWARD LENGTH=995	916	995	0	108.6	77.7	84.9

Rsa1.0_00941.1.g21621.t1	ref|NP_567905.1| uncharacterized protein [Arabidopsis thaliana] gi|21593653|gb|AAM65620.1| unknown [Arabidopsis thaliana] gi|51968854|dbj|BAD43119.1| unknown protein [Arabidopsis thaliana] gi|51970976|dbj|BAD44180.1| unknown protein [Arabidopsis thaliana] gi|109946475|gb|ABG48416.1| At4g32750 [Arabidopsis thaliana] gi|332660713|gb|AEE86113.1| uncharacterized protein AT4G32750 [Arabidopsis thaliana]	106	293	1.00E-49	276.4	89.6	94.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32750.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15796415-15798091 REVERSE LENGTH=293	106	293	2.00E-52	276.4	89.6	94.3
Rsa1.0_00941.1.g21622.t1	ref|NP_195005.1| Exostosin family protein [Arabidopsis thaliana] gi|3063691|emb|CAA18582.1| putative protein [Arabidopsis thaliana] gi|7270226|emb|CAB79996.1| putative protein [Arabidopsis thaliana] gi|332660719|gb|AEE86119.1| Exostosin family protein [Arabidopsis thaliana]	609	593	0	97.4	76.0	81.6	Exostosin family protein	gbpln	Arabidopsis thaliana	AT4G32790.1 | Symbols: | Exostosin family protein | chr4:15812566-15814908 FORWARD LENGTH=593	609	593	0	97.4	76.0	81.6
Rsa1.0_00941.1.g21623.t1	gb|EOA15715.1| hypothetical protein CARUB_v10006567mg [Capsella rubella]	225	228	3.00E-74	101.3	66.7	75.6	hypothetical protein CARUB_v10006567mg	gbpln	Capsella rubella	AT4G32800.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:15819812-15820477 FORWARD LENGTH=221	225	221	8.00E-76	98.2	68.0	78.7
Rsa1.0_00941.1.g21624.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00941.1.g21625.t1	ref|XP_002869240.1| hypothetical protein ARALYDRAFT_913154 [Arabidopsis lyrata subsp. lyrata] gi|297315076|gb|EFH45499.1| hypothetical protein ARALYDRAFT_913154 [Arabidopsis lyrata subsp. lyrata]	317	290	1.00E-158	91.5	84.5	85.8	hypothetical protein ARALYDRAFT_913154	gbpln	Arabidopsis lyrata	AT4G32830.1 | Symbols: AtAUR1, AUR1 | ataurora1 | chr4:15842557-15844354 FORWARD LENGTH=294	317	294	1.00E-158	92.7	83.0	85.2
Rsa1.0_00941.1.g21626.t1	emb|CAB80003.1| putative protein [Arabidopsis thaliana]	239	193	8.00E-85	80.8	67.4	71.1	putative protein	gbpln	Arabidopsis thaliana	AT4G32860.1 | Symbols: | unknown protein; Has 46 Blast hits to 46 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15856710-15857309 REVERSE LENGTH=199	239	199	3.00E-87	83.3	67.4	71.1
Rsa1.0_00941.1.g21627.t2	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1232	1307	0	106.1	58.9	72.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1232	1262	3.00E-81	102.4	13.1	20.5
Rsa1.0_00941.1.g21628.t1	ref|XP_002878905.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324744|gb|EFH55164.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	493	480	6.00E-42	97.4	25.2	43.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	493	384	2.00E-27	77.9	14.2	21.5
Rsa1.0_00942.1.g21629.t1	gb|EOA21216.1| hypothetical protein CARUB_v10001564mg [Capsella rubella]	272	302	1.00E-133	111.0	83.5	90.1	hypothetical protein CARUB_v10001564mg	gbpln	Capsella rubella	AT5G27830.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Folate receptor, conserved region (InterPro:IPR018143); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9861344-9862742 FORWARD LENGTH=300	272	300	1.00E-126	110.3	82.0	89.3
Rsa1.0_00942.1.g21630.t1	ref|NP_187210.1| 60S ribosomal protein L18-2 [Arabidopsis thaliana] gi|21431838|sp|P42791.2|RL182_ARATH RecName: Full=60S ribosomal protein L18-2 gi|6714451|gb|AAF26138.1|AC011620_14 putative 60S ribosomal protein L18 [Arabidopsis thaliana] gi|14335090|gb|AAK59824.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gi|16974509|gb|AAL31164.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] gi|332640742|gb|AEE74263.1| 60S ribosomal protein L18-2 [Arabidopsis thaliana]	187	187	4.00E-96	100.0	94.1	96.8	60S ribosomal protein L18-2	gbpln	Arabidopsis thaliana	AT3G05590.1 | Symbols: RPL18 | ribosomal protein L18 | chr3:1621511-1622775 FORWARD LENGTH=187	187	187	2.00E-98	100.0	94.1	96.8

Rsa1.0_00942.1.g21631.t1	ref|NP_198139.1| pectinesterase 28 [Arabidopsis thaliana] gi|122214224|sp|Q3E8Z8.1|PME28_ARATH RecName: Full=Putative pectinesterase/pectinesterase inhibitor 28; Includes: RecName: Full=Pectinesterase inhibitor 28; AltName: Full=Pectin methylesterase inhibitor 28; Includes: RecName: Full=Pectinesterase 28; Short=PE 28; AltName: Full=Pectin methylesterase 28; Short=AtPME28 gi|332006356|gb|AED93739.1| pectinesterase 28 [Arabidopsis thaliana]	759	732	0	96.4	68.2	76.7	pectinesterase 28	gbpln	Arabidopsis thaliana	AT5G27870.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:9878991-9881806 REVERSE LENGTH=732	759	732	0	96.4	68.2	76.7
Rsa1.0_00942.1.g21632.t1	ref|NP_198140.1| C2H2 and C2HC zinc finger-containing protein [Arabidopsis thaliana] gi|332006357|gb|AED93740.1| C2H2 and C2HC zinc finger-containing protein [Arabidopsis thaliana]	404	278	1.00E-64	68.8	37.9	45.0	C2H2 and C2HC zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT5G27880.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:9885908-9886744 FORWARD LENGTH=278	404	278	3.00E-67	68.8	37.9	45.0
Rsa1.0_00942.1.g21633.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00942.1.g21634.t1	ref|XP_002874341.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297320178|gb|EFH50600.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	266	285	8.00E-48	107.1	47.7	61.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G27880.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:9885908-9886744 FORWARD LENGTH=278	266	278	2.00E-49	104.5	47.7	60.2
Rsa1.0_00942.1.g21635.t1	ref|XP_002872252.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297318089|gb|EFH48511.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	640	642	0	100.3	85.0	91.7	F-box family protein	gbpln	Arabidopsis lyrata	AT5G27920.1 | Symbols: | F-box family protein | chr5:9942063-9944507 REVERSE LENGTH=642	640	642	0	100.3	83.3	90.9
Rsa1.0_00942.1.g21636.t1	dbj|BAJ33753.1| unnamed protein product [Thellungiella halophila]	501	376	0	75.0	69.3	72.1	unnamed protein product	----	----	AT5G27930.2 | Symbols: | Protein phosphatase 2C family protein | chr5:9958199-9960219 REVERSE LENGTH=373	501	373	0	74.5	63.1	66.3
Rsa1.0_00942.1.g21637.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00942.1.g21638.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00942.1.g21639.t1	ref|XP_002872249.1| hypothetical protein ARALYDRAFT_489530 [Arabidopsis lyrata subsp. lyrata] gi|297318086|gb|EFH48508.1| hypothetical protein ARALYDRAFT_489530 [Arabidopsis lyrata subsp. lyrata]	929	987	0	106.2	85.9	91.3	hypothetical protein ARALYDRAFT_489530	gbpln	Arabidopsis lyrata	AT5G27000.1 | Symbols: ATK4, KATD | kinesin 4 | chr5:9498099-9502951 FORWARD LENGTH=987	929	987	0	106.2	85.7	90.9
Rsa1.0_00942.1.g21640.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	149	1311	1.00E-18	879.9	37.6	50.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	149	170	4.00E-17	114.1	33.6	46.3
Rsa1.0_00943.1.g21641.t1	#	#	#	#	#	#	#	-	----	----	AT3G01460.1 | Symbols: MBD9, ATMBD9 | methyl-CPG-binding domain 9 | chr3:173316-182038 FORWARD LENGTH=2176	89	2176	6.00E-12	2444.9	33.7	38.2
Rsa1.0_00943.1.g21642.t1	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	309	1449	3.00E-51	468.9	33.3	50.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	309	746	4.00E-34	241.4	23.9	36.6
Rsa1.0_00943.1.g21643.t1	ref|NP_189427.1| NADPH:quinone oxidoreductase [Arabidopsis thaliana] gi|75273736|sp|Q9LK88.1|NQR_ARATH RecName: Full=NADPH:quinone oxidoreductase gi|11994494|dbj|BAB02535.1| NADPH:quinone oxidoreductase [Arabidopsis thaliana] gi|88193780|gb|ABD42979.1| At3g27890 [Arabidopsis thaliana] gi|332643855|gb|AEE77376.1| NADPH:quinone oxidoreductase [Arabidopsis thaliana]	197	196	2.00E-92	99.5	87.3	92.9	NADPH:quinone oxidoreductase	gbpln	Arabidopsis thaliana	AT3G27890.1 | Symbols: NQR | NADPH:quinone oxidoreductase | chr3:10350807-10351938 REVERSE LENGTH=196	197	196	8.00E-95	99.5	87.3	92.9
Rsa1.0_00943.1.g21644.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00943.1.g21645.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00943.1.g21646.t1	gb|EOA14700.1| hypothetical protein CARUB_v10027975mg [Capsella rubella]	405	766	4.00E-66	189.1	29.9	36.0	hypothetical protein CARUB_v10027975mg	gbpln	Capsella rubella	AT3G29765.1 | Symbols: | General transcription factor 2-related zinc finger protein | chr3:11595467-11597077 REVERSE LENGTH=536	405	536	4.00E-66	132.3	29.6	35.6

Rsa1.0_00943.1.g21647.t1	ref|XP_002891027.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297336869|gb|EFH67286.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	401	493	0	122.9	87.5	94.5	mate efflux family protein	gbpln	Arabidopsis lyrata	AT1G33080.1 | Symbols: | MATE efflux family protein | chr1:11985752-11990327 FORWARD LENGTH=494	401	494	0	123.2	86.5	93.3
Rsa1.0_00943.1.g21648.t1	gb|AAC62785.1| F11O4.11 [Arabidopsis thaliana] gi|7268192|emb|CAB77719.1| putative transposon protein [Arabidopsis thaliana]	742	577	6.00E-70	77.8	15.0	20.5	F11O4.11	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	742	361	9.00E-26	48.7	9.6	13.3
Rsa1.0_00943.1.g21649.t1	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	947	1044	0	110.2	35.3	44.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	947	303	2.00E-46	32.0	11.4	16.4
Rsa1.0_00943.1.g21650.t1	gb|EOA40413.1| hypothetical protein CARUB_v10009139mg [Capsella rubella]	294	444	1.00E-124	151.0	73.8	84.0	hypothetical protein CARUB_v10009139mg	gbpln	Capsella rubella	AT1G33110.2 | Symbols: | MATE efflux family protein | chr1:12005084-12008040 FORWARD LENGTH=404	294	404	1.00E-126	137.4	73.8	84.4
Rsa1.0_00944.1.g21651.t1	gb|EOA19105.1| hypothetical protein CARUB_v10007773mg [Capsella rubella]	818	819	0	100.1	94.6	97.9	hypothetical protein CARUB_v10007773mg	gbpln	Capsella rubella	AT4G39080.1 | Symbols: VHA-A3 | vacuolar proton ATPase A3 | chr4:18209513-18214752 FORWARD LENGTH=821	818	821	0	100.4	93.0	96.8
Rsa1.0_00944.1.g21652.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00944.1.g21653.t2	ref|NP_195618.2| B-box type zinc finger-containing protein [Arabidopsis thaliana] gi|122221558|sp|Q0IGM7.1|BBX20_ARATH RecName: Full=B-box zinc finger protein 20; AltName: Full=Protein SALT TOLERANCE HOMOLOG 7 gi|114050581|gb|ABI49440.1| At4g39070 [Arabidopsis thaliana] gi|332661614|gb|AEE87014.1| putative zinc finger transcription factor BZS1 [Arabidopsis thaliana]	264	242	1.00E-109	91.7	82.2	86.0	B-box type zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT4G39070.1 | Symbols: | B-box zinc finger family protein | chr4:18205061-18206421 REVERSE LENGTH=242	264	242	1.00E-112	91.7	82.2	86.0
Rsa1.0_00944.1.g21654.t1	ref|XP_002866829.1| hypothetical protein ARALYDRAFT_327857 [Arabidopsis lyrata subsp. lyrata] gi|297312665|gb|EFH43088.1| hypothetical protein ARALYDRAFT_327857 [Arabidopsis lyrata subsp. lyrata]	1054	1055	0	100.1	89.1	93.3	hypothetical protein ARALYDRAFT_327857	gbpln	Arabidopsis lyrata	AT4G39050.1 | Symbols: | Kinesin motor family protein | chr4:18193462-18200148 FORWARD LENGTH=1055	1054	1055	0	100.1	89.1	93.3
Rsa1.0_00944.1.g21655.t1	ref|XP_002866827.1| hypothetical protein ARALYDRAFT_327853 [Arabidopsis lyrata subsp. lyrata] gi|297312663|gb|EFH43086.1| hypothetical protein ARALYDRAFT_327853 [Arabidopsis lyrata subsp. lyrata]	375	373	0	99.5	89.1	94.4	hypothetical protein ARALYDRAFT_327853	gbpln	Arabidopsis lyrata	AT4G34660.1 | Symbols: | SH3 domain-containing protein | chr4:16545595-16548294 REVERSE LENGTH=368	375	368	1.00E-155	98.1	72.3	86.1
Rsa1.0_00944.1.g21656.t1	ref|NP_195609.1| uncharacterized protein [Arabidopsis thaliana] gi|4539317|emb|CAB38818.1| putative protein [Arabidopsis thaliana] gi|7270881|emb|CAB80561.1| putative protein [Arabidopsis thaliana] gi|19423914|gb|AAL87343.1| unknown protein [Arabidopsis thaliana] gi|22136964|gb|AAM91711.1| unknown protein [Arabidopsis thaliana] gi|332661604|gb|AEE87004.1| uncharacterized protein AT4G38980 [Arabidopsis thaliana]	264	280	8.00E-89	106.1	68.9	83.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G38980.1 | Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 19 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 8; Plants - 24; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr4:18166898-18167740 REVERSE LENGTH=280	264	280	2.00E-91	106.1	68.9	83.0
Rsa1.0_00944.1.g21657.t1	ref|XP_002868874.1| hypothetical protein ARALYDRAFT_490667 [Arabidopsis lyrata subsp. lyrata] gi|297314710|gb|EFH45133.1| hypothetical protein ARALYDRAFT_490667 [Arabidopsis lyrata subsp. lyrata]	393	393	0	100.0	96.7	99.0	hypothetical protein ARALYDRAFT_490667	gbpln	Arabidopsis lyrata	AT4G38970.1 | Symbols: FBA2 | fructose-bisphosphate aldolase 2 | chr4:18163714-18165659 REVERSE LENGTH=398	393	398	0	101.3	97.2	99.2
Rsa1.0_00944.1.g21658.t1	ref|XP_002866825.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297312661|gb|EFH43084.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	334	368	1.00E-105	110.2	61.7	72.2	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	334	370	1.00E-104	110.8	58.7	71.6
Rsa1.0_00944.1.g21659.t1	gb|EOA17498.1| hypothetical protein CARUB_v10005832mg [Capsella rubella]	180	183	4.00E-96	101.7	96.1	98.3	hypothetical protein CARUB_v10005832mg	gbpln	Capsella rubella	AT4G38960.1 | Symbols: | B-box type zinc finger family protein | chr4:18161576-18163045 FORWARD LENGTH=183	180	183	2.00E-96	101.7	95.0	96.1
Rsa1.0_00944.1.g21660.t1	ref|XP_002313006.1| predicted protein [Populus trichocarpa] gi|222849414|gb|EEE86961.1| predicted protein [Populus trichocarpa]	164	207	6.00E-85	126.2	100.0	100.0	predicted protein	gbpln	Populus trichocarpa	AT4G34720.1 | Symbols: AVA-P1, VHA-C1, ATVHA-C1 | ATPase, F0/V0 complex, subunit C protein | chr4:16568223-16569165 REVERSE LENGTH=164	164	164	4.00E-87	100.0	100.0	100.0

Rsa1.0_00944.1.g21661.t1	gb|ABU63290.1| GAGA-motif binding transcriptional activator, partial [Arabidopsis thaliana]	277	297	1.00E-123	107.2	83.0	92.1	GAGA-motif binding transcriptional activator, partial	gbpln	Arabidopsis thaliana	AT4G38910.2 | Symbols: BPC5 | basic pentacysteine 5 | chr4:18145478-18146429 REVERSE LENGTH=283	277	283	1.00E-125	102.2	83.0	92.1
Rsa1.0_00944.1.g21662.t1	ref|XP_002886677.1| hypothetical protein ARALYDRAFT_893631 [Arabidopsis lyrata subsp. lyrata] gi|297332518|gb|EFH62936.1| hypothetical protein ARALYDRAFT_893631 [Arabidopsis lyrata subsp. lyrata]	183	175	2.00E-45	95.6	54.1	66.7	hypothetical protein ARALYDRAFT_893631	gbpln	Arabidopsis lyrata	AT2G21237.1 | Symbols: | unknown protein; Has 10 Blast hits to 10 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9100684-9101184 REVERSE LENGTH=166	183	166	5.00E-29	90.7	38.8	52.5
Rsa1.0_00944.1.g21663.t1	gb|AAL87314.1| unknown protein [Arabidopsis thaliana]	448	547	1.00E-149	122.1	77.5	83.9	unknown protein	gbpln	Arabidopsis thaliana	AT4G38900.3 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:18139564-18141520 REVERSE LENGTH=547	448	547	1.00E-152	122.1	77.5	83.9
Rsa1.0_00944.1.g21664.t13	gb|EOA22764.1| hypothetical protein CARUB_v10003477mg, partial [Capsella rubella]	331	166	2.00E-16	50.2	17.2	22.4	hypothetical protein CARUB_v10003477mg, partial	gbpln	Capsella rubella	AT1G73490.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:27633496-27634867 REVERSE LENGTH=260	331	260	1.00E-13	78.5	13.9	20.2
Rsa1.0_00945.1.g21665.t1	dbj|BAB10164.1| unnamed protein product [Arabidopsis thaliana]	453	468	0	103.3	85.4	90.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G62030.1 | Symbols: | diphthamide synthesis DPH2 family protein | chr5:24919046-24920407 FORWARD LENGTH=453	453	453	0	100.0	85.4	90.3
Rsa1.0_00945.1.g21666.t1	ref|XP_002864765.1| hypothetical protein ARALYDRAFT_919451 [Arabidopsis lyrata subsp. lyrata] gi|297310600|gb|EFH41024.1| hypothetical protein ARALYDRAFT_919451 [Arabidopsis lyrata subsp. lyrata]	290	299	1.00E-106	103.1	75.2	79.7	hypothetical protein ARALYDRAFT_919451	gbpln	Arabidopsis lyrata	AT5G62020.1 | Symbols: AT-HSFB2A, HSFB2A | heat shock transcription factor B2A | chr5:24916212-24917194 FORWARD LENGTH=299	290	299	1.00E-108	103.1	75.5	80.3
Rsa1.0_00945.1.g21667.t1	gb|AFD01294.1| auxin response factor 2-2 [Brassica rapa subsp. pekinensis]	852	851	0	99.9	94.0	95.5	auxin response factor 2-2	gbpln	Brassica rapa	AT5G62000.3 | Symbols: ARF2, ARF1-BP, HSS, ORE14 | auxin response factor 2 | chr5:24910859-24914680 FORWARD LENGTH=859	852	859	0	100.8	87.1	91.8
Rsa1.0_00945.1.g21668.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00945.1.g21669.t1	gb|EOA12847.1| hypothetical protein CARUB_v10025815mg [Capsella rubella]	970	988	0	101.9	77.8	87.3	hypothetical protein CARUB_v10025815mg	gbpln	Capsella rubella	AT5G61990.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:24900186-24903110 REVERSE LENGTH=974	970	974	0	100.4	73.7	84.4
Rsa1.0_00945.1.g21670.t2	ref|XP_002864762.1| hypothetical protein ARALYDRAFT_496370 [Arabidopsis lyrata subsp. lyrata] gi|297310597|gb|EFH41021.1| hypothetical protein ARALYDRAFT_496370 [Arabidopsis lyrata subsp. lyrata]	624	608	0	97.4	86.2	91.0	hypothetical protein ARALYDRAFT_496370	gbpln	Arabidopsis lyrata	AT5G61970.1 | Symbols: | signal recognition particle-related / SRP-related | chr5:24888920-24893079 FORWARD LENGTH=605	624	605	0	97.0	85.4	90.2
Rsa1.0_00945.1.g21671.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00945.1.g21672.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00945.1.g21673.t5	gb|EOA12879.1| hypothetical protein CARUB_v10025852mg [Capsella rubella]	954	908	0	95.2	76.0	83.4	hypothetical protein CARUB_v10025852mg	gbpln	Capsella rubella	AT5G61960.2 | Symbols: AML1, ML1 | MEI2-like protein 1 | chr5:24879001-24883483 REVERSE LENGTH=915	954	915	0	95.9	77.0	83.6
Rsa1.0_00945.1.g21674.t1	ref|NP_200998.1| uncharacterized protein [Arabidopsis thaliana] gi|186532652|ref|NP_001119474.1| uncharacterized protein [Arabidopsis thaliana] gi|9758391|dbj|BAB08878.1| unnamed protein product [Arabidopsis thaliana] gi|91807090|gb|ABE66272.1| hypothetical protein At5g61920 [Arabidopsis thaliana] gi|332010153|gb|AED97536.1| uncharacterized protein AT5G61920 [Arabidopsis thaliana] gi|332010154|gb|AED97537.1| uncharacterized protein AT5G61920 [Arabidopsis thaliana]	225	238	2.00E-82	105.8	77.8	88.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G61920.2 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67170.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:24864830-24865628 FORWARD LENGTH=238	225	238	7.00E-85	105.8	77.8	88.9
Rsa1.0_00945.1.g21675.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00945.1.g21676.t1	gb|EOA12798.1| hypothetical protein CARUB_v10025752mg [Capsella rubella]	402	1270	0	315.9	90.3	95.0	hypothetical protein CARUB_v10025752mg	gbpln	Capsella rubella	AT5G61910.4 | Symbols: | DCD (Development and Cell Death) domain protein | chr5:24855908-24863729 REVERSE LENGTH=1346	402	1346	0	334.8	89.1	94.8
Rsa1.0_00946.1.g21677.t1	gb|ABK28778.1| unknown [Arabidopsis thaliana]	206	206	1.00E-52	100.0	68.0	74.3	unknown	gbpln	Arabidopsis thaliana	AT1G05450.2 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:1600004-1601086 FORWARD LENGTH=205	206	205	4.00E-55	99.5	68.0	74.3
Rsa1.0_00946.1.g21678.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1285	1501	0	116.8	38.4	48.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1285	1262	1.00E-132	98.2	18.0	26.6

Rsa1.0_00946.1.g21679.t1	gb|EOA37272.1| hypothetical protein CARUB_v10010861mg [Capsella rubella]	229	234	2.00E-73	102.2	76.4	82.1	hypothetical protein CARUB_v10010861mg	gbpln	Capsella rubella	AT1G05420.1 | Symbols: ATOFP12, OFP12 | ovate family protein 12 | chr1:1590073-1590753 FORWARD LENGTH=226	229	226	6.00E-73	98.7	72.9	79.5
Rsa1.0_00946.1.g21680.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00946.1.g21681.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00946.1.g21682.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00946.1.g21683.t1	ref|NP_172029.2| Sec.4-like phosphatidylinositol transfer family protein [Arabidopsis thaliana] gi|332189709|gb|AEE27830.1| Sec.4-like phosphatidylinositol transfer family protein [Arabidopsis thaliana]	415	417	0	100.5	91.1	94.2	Sec.4-like phosphatidylinositol transfer family protein	gbpln	Arabidopsis thaliana	AT1G05370.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:1569418-1572280 REVERSE LENGTH=417	415	417	0	100.5	91.1	94.2
Rsa1.0_00946.1.g21684.t1	ref|XP_002889546.1| hypothetical protein ARALYDRAFT_887721 [Arabidopsis lyrata subsp. lyrata] gi|297335388|gb|EFH65805.1| hypothetical protein ARALYDRAFT_887721 [Arabidopsis lyrata subsp. lyrata]	418	416	0	99.5	87.1	90.0	hypothetical protein ARALYDRAFT_887721	gbpln	Arabidopsis lyrata	AT1G05360.1 | Symbols: | BEST Arabidopsis thaliana protein match is: SNARE associated Golgi protein family (TAIR:AT4G14950.1); Has 332 Blast hits to 326 proteins in 115 species: Archae - 0; Bacteria - 11; Metazoa - 174; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 73 (source: NCBI BLink). | chr1:1564816-1567278 FORWARD LENGTH=416	418	416	0	99.5	86.1	90.0
Rsa1.0_00946.1.g21685.t1	ref|NP_172027.2| ubiquitin-like modifier-activating enzyme 5 [Arabidopsis thaliana] gi|290463407|sp|O23034.2|UBA5_ARATH RecName: Full=Ubiquitin-like modifier-activating enzyme 5; Short=Ubiquitin-activating enzyme 5 gi|332189707|gb|AEE27828.1| ubiquitin-like modifier-activating enzyme 5 [Arabidopsis thaliana]	429	431	0	100.5	93.7	95.8	ubiquitin-like modifier-activating enzyme 5	gbpln	Arabidopsis thaliana	AT1G05350.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:1560891-1564005 REVERSE LENGTH=431	429	431	0	100.5	93.7	95.8
Rsa1.0_00946.1.g21686.t1	gb|EOA37878.1| hypothetical protein CARUB_v10011474mg [Capsella rubella]	524	864	1.00E-132	164.9	51.5	58.8	hypothetical protein CARUB_v10011474mg	gbpln	Capsella rubella	AT1G05320.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: fruit, egg cell; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G32240.1); Has 267444 Blast hits to 119656 proteins in 3886 species: Archae - 3699; Bacteria - 62432; Metazoa - 106542; Fungi - 19875; Plants - 13918; Viruses - 1288; Other Eukaryotes - 59690 (source: NCBI BLink). | chr1:1554856-1557658 FORWARD LENGTH=790	524	790	1.00E-131	150.8	50.4	59.2
Rsa1.0_00947.1.g21687.t1	ref|XP_002894222.1| ring-H2 finger protein RHY1a [Arabidopsis lyrata subsp. lyrata] gi|297340064|gb|EFH70481.1| ring-H2 finger protein RHY1a [Arabidopsis lyrata subsp. lyrata]	244	248	2.00E-81	101.6	77.0	85.7	ring-H2 finger protein RHY1a	gbpln	Arabidopsis lyrata	AT1G49850.1 | Symbols: | RING/U-box superfamily protein | chr1:18455326-18456444 REVERSE LENGTH=250	244	250	2.00E-72	102.5	76.6	85.7
Rsa1.0_00947.1.g21688.t1	gb|EOA39699.1| hypothetical protein CARUB_v10008343mg [Capsella rubella]	824	792	0	96.1	80.7	88.6	hypothetical protein CARUB_v10008343mg	gbpln	Capsella rubella	AT1G42440.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ribosome biogenesis; LOCATED IN: nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: AARP2CN (InterPro:IPR012948), Protein of unknown function DUF663 (InterPro:IPR007034); BEST Arabidopsis thaliana protein match is: P-loop containing nucleoside triphosphate hydrolases superfamily protein (TAIR:AT1G06720.1); Has 2741 Blast hits to 2088 proteins in 291 species: Archae - 2; Bacteria - 131; Metazoa - 833; Fungi - 650; Plants - 171; Viruses - 49; Other Eukaryotes - 905 (source: NCBI BLink). | chr1:15895528-15899939 REVERSE LENGTH=793	824	793	0	96.2	80.5	88.6
Rsa1.0_00947.1.g21689.t1	ref|XP_002894219.1| hypothetical protein ARALYDRAFT_474111 [Arabidopsis lyrata subsp. lyrata] gi|297340061|gb|EFH70478.1| hypothetical protein ARALYDRAFT_474111 [Arabidopsis lyrata subsp. lyrata]	86	102	5.00E-24	118.6	67.4	77.9	hypothetical protein ARALYDRAFT_474111	gbpln	Arabidopsis lyrata	AT1G49800.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: sepal, male gametophyte, stamen; EXPRESSED DURING: 4 anthesis; Has 12 Blast hits to 12 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18438550-18438876 REVERSE LENGTH=108	86	108	2.00E-20	125.6	66.3	80.2

Rsa1.0_00947.1.g21690.t1	ref|NP_175399.2| transcription factor bHLH95 [Arabidopsis thaliana] gi|218563532|sp|Q9FXA3.2|BH095_ARATH RecName: Full=Transcription factor bHLH95; AltName: Full=Basic helix-loop-helix protein 95; Short=AtbHLH95; Short=bHLH 95; AltName: Full=Protein RETARDED GROWTH OF EMBRYO 1; AltName: Full=Transcription factor EN 21; AltName: Full=bHLH transcription factor bHLH095 gi|332194353|gb|AEE32474.1| transcription factor bHLH95 [Arabidopsis thaliana]	313	308	1.00E-116	98.4	71.9	80.2	transcription factor bHLH95	gbpln	Arabidopsis thaliana	AT1G49770.1 | Symbols: RGE1, ZOU | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:18424578-18426531 FORWARD LENGTH=308	313	308	1.00E-119	98.4	71.9	80.2
Rsa1.0_00947.1.g21691.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00947.1.g21692.t1	ref|XP_002894215.1| hypothetical protein ARALYDRAFT_474107 [Arabidopsis lyrata subsp. lyrata] gi|297340057|gb|EFH70474.1| hypothetical protein ARALYDRAFT_474107 [Arabidopsis lyrata subsp. lyrata]	538	478	1.00E-163	88.8	53.9	58.6	hypothetical protein ARALYDRAFT_474107	gbpln	Arabidopsis lyrata	AT4G06744.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:4070870-4072084 REVERSE LENGTH=404	538	404	7.00E-88	75.1	31.4	42.0
Rsa1.0_00947.1.g21693.t1	gb|EOA37582.1| hypothetical protein CARUB_v10011932mg [Capsella rubella]	324	321	1.00E-139	99.1	73.8	84.3	hypothetical protein CARUB_v10011932mg	gbpln	Capsella rubella	AT1G49660.1 | Symbols: AtCXE5, CXE5 | carboxyesterase 5 | chr1:18378777-18379736 REVERSE LENGTH=319	324	319	1.00E-136	98.5	74.1	84.3
Rsa1.0_00947.1.g21694.t2	ref|NP_175438.2| Cysteine/Histidine-rich C1 domain family protein [Arabidopsis thaliana] gi|332194402|gb|AEE32523.1| Cysteine/Histidine-rich C1 domain family protein [Arabidopsis thaliana]	578	619	1.00E-173	107.1	57.1	67.5	Cysteine/Histidine-rich C1 domain family protein	gbpln	Arabidopsis thaliana	AT1G50190.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:18588229-18590799 REVERSE LENGTH=619	578	619	1.00E-176	107.1	57.1	67.5
Rsa1.0_00947.1.g21695.t1	ref|XP_002894197.1| hypothetical protein ARALYDRAFT_474095 [Arabidopsis lyrata subsp. lyrata] gi|297340039|gb|EFH70456.1| hypothetical protein ARALYDRAFT_474095 [Arabidopsis lyrata subsp. lyrata]	423	450	1.00E-179	106.4	83.9	88.9	hypothetical protein ARALYDRAFT_474095	gbpln	Arabidopsis lyrata	AT1G49600.1 | Symbols: ATRBP47A, RBP47A | RNA-binding protein 47A | chr1:18357236-18360150 REVERSE LENGTH=445	423	445	0	105.2	76.4	80.9
Rsa1.0_00947.1.g21696.t2	ref|NP_564549.1| myb family transcription factor [Arabidopsis thaliana] gi|10120417|gb|AAG13042.1|AC011807_1 Hypothetical protein [Arabidopsis thaliana] gi|62320610|dbj|BAD95259.1| hypothetical protein [Arabidopsis thaliana] gi|332194321|gb|AEE32442.1| myb family transcription factor [Arabidopsis thaliana]	312	333	8.00E-94	106.7	70.5	80.1	myb family transcription factor	gbpln	Arabidopsis thaliana	AT1G49560.1 | Symbols: | Homeodomain-like superfamily protein | chr1:18342725-18344101 FORWARD LENGTH=333	312	333	2.00E-96	106.7	70.5	80.1
Rsa1.0_00947.1.g21697.t1	ref|NP_001185180.1| elongator protein 2 [Arabidopsis thaliana] gi|332194320|gb|AEE32441.1| elongator protein 2 [Arabidopsis thaliana]	144	840	1.00E-15	583.3	32.6	37.5	elongator protein 2	gbpln	Arabidopsis thaliana	AT1G49540.2 | Symbols: ELP2, AtELP2 | elongator protein 2 | chr1:18333767-18337382 REVERSE LENGTH=840	144	840	4.00E-18	583.3	32.6	37.5
Rsa1.0_00947.1.g21698.t1	gb|EOA37055.1| hypothetical protein CARUB_v10010157mg [Capsella rubella]	228	238	9.00E-88	104.4	66.2	71.9	hypothetical protein CARUB_v10010157mg	gbpln	Capsella rubella	AT1G49510.1 | Symbols: emb1273 | embryo defective 1273 | chr1:18327026-18328147 FORWARD LENGTH=240	228	240	1.00E-87	105.3	66.2	70.6
Rsa1.0_00948.1.g21699.t1	gb|EOA28482.1| hypothetical protein CARUB_v10024692mg, partial [Capsella rubella]	270	328	1.00E-114	121.5	80.0	86.7	hypothetical protein CARUB_v10024692mg, partial	gbpln	Capsella rubella	AT2G33990.1 | Symbols: iqd9 | IQ-domain 9 | chr2:14360502-14361630 REVERSE LENGTH=263	270	263	1.00E-106	97.4	75.2	81.5
Rsa1.0_00948.1.g21700.t2	dbj|BAF01443.1| hypothetical protein [Arabidopsis thaliana]	250	259	2.00E-93	103.6	72.8	80.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G33980.1 | Symbols: atnudt22, NUDT22 | nudix hydrolase homolog 22 | chr2:14356786-14359840 REVERSE LENGTH=302	250	302	8.00E-96	120.8	72.8	80.4
Rsa1.0_00948.1.g21701.t1	gb|EOA28972.1| hypothetical protein CARUB_v10025224mg, partial [Capsella rubella]	393	408	1.00E-156	103.8	84.0	87.8	hypothetical protein CARUB_v10025224mg, partial	gbpln	Capsella rubella	AT2G33880.1 | Symbols: WOX9, HB-3, STIP | homeobox-3 | chr2:14341639-14343597 REVERSE LENGTH=378	393	378	1.00E-154	96.2	79.4	83.0
Rsa1.0_00948.1.g21702.t1	gb|AFD01296.1| auxin response factor 3-1 [Brassica rapa subsp. pekinensis]	620	605	0	97.6	83.4	85.6	auxin response factor 3-1	gbpln	Brassica rapa	AT2G33860.1 | Symbols: ETT, ARF3 | Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related | chr2:14325444-14328613 REVERSE LENGTH=608	620	608	0	98.1	82.1	87.6
Rsa1.0_00948.1.g21703.t2	ref|NP_001078001.1| uncharacterized protein [Arabidopsis thaliana] gi|98961761|gb|ABF59210.1| unknown protein [Arabidopsis thaliana] gi|330253802|gb|AEC08896.1| uncharacterized protein AT2G33847 [Arabidopsis thaliana]	105	93	6.00E-29	88.6	66.7	71.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G33847.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G28395.4); Has 74 Blast hits to 74 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:14319280-14320522 REVERSE LENGTH=93	105	93	9.00E-32	88.6	66.7	71.4

Rsa1.0_00948.1.g21704.t1	ref|XP_002879475.1| hypothetical protein ARALYDRAFT_482340 [Arabidopsis lyrata subsp. lyrata] gi|297325314|gb|EFH55734.1| hypothetical protein ARALYDRAFT_482340 [Arabidopsis lyrata subsp. lyrata]	181	181	6.00E-77	100.0	81.2	84.0	hypothetical protein ARALYDRAFT_482340	gbpln	Arabidopsis lyrata	AT2G33845.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr2:14317781-14318712 FORWARD LENGTH=182	181	182	1.00E-78	100.6	80.7	82.9
Rsa1.0_00948.1.g21705.t2	ref|XP_002881309.1| frigida-essential 1 [Arabidopsis lyrata subsp. lyrata] gi|297327148|gb|EFH57568.1| frigida-essential 1 [Arabidopsis lyrata subsp. lyrata]	634	590	0	93.1	59.0	68.1	frigida-essential 1	gbpln	Arabidopsis lyrata	AT2G33835.1 | Symbols: FES1 | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr2:14312145-14314566 REVERSE LENGTH=587	634	587	0	92.6	57.9	66.6
Rsa1.0_00948.1.g21706.t1	gb|EOA28182.1| hypothetical protein CARUB_v10024372mg [Capsella rubella]	107	108	1.00E-52	100.9	96.3	99.1	hypothetical protein CARUB_v10024372mg	gbpln	Capsella rubella	AT2G33830.2 | Symbols: | Dormancy/auxin associated family protein | chr2:14309768-14310286 REVERSE LENGTH=108	107	108	2.00E-54	100.9	95.3	97.2
Rsa1.0_00948.1.g21707.t1	ref|XP_002879473.1| hypothetical protein ARALYDRAFT_482334 [Arabidopsis lyrata subsp. lyrata] gi|297325312|gb|EFH55732.1| hypothetical protein ARALYDRAFT_482334 [Arabidopsis lyrata subsp. lyrata]	122	130	2.00E-43	106.6	84.4	87.7	hypothetical protein ARALYDRAFT_482334	gbpln	Arabidopsis lyrata	AT2G33810.1 | Symbols: SPL3 | squamosa promoter binding protein-like 3 | chr2:14305342-14305828 FORWARD LENGTH=131	122	131	4.00E-45	107.4	83.6	87.7
Rsa1.0_00948.1.g21708.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1359	1342	0	98.7	70.9	83.9	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1359	1262	2.00E-85	92.9	13.0	20.3
Rsa1.0_00949.1.g21709.t1	emb|CAB72476.1| putative protein [Arabidopsis thaliana]	179	661	6.00E-37	369.3	45.3	60.9	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00949.1.g21710.t1	ref|NP_171622.1| CBL-interacting serine/threonine-protein kinase 9 [Arabidopsis thaliana] gi|259016207|sp|Q9MAM1.2|CIPK9_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 9; AltName: Full=SNF1-related kinase 3.12; AltName: Full=SOS2-like protein kinase PKS6 gi|332189123|gb|AEE27244.1| CBL-interacting serine/threonine-protein kinase 9 [Arabidopsis thaliana]	465	447	0	96.1	89.7	92.9	CBL-interacting serine/threonine-protein kinase 9	gbpln	Arabidopsis thaliana	AT1G01140.1 | Symbols: CIPK9, SnRK3.12, PKS6 | CBL-interacting protein kinase 9 | chr1:64398-67512 REVERSE LENGTH=447	465	447	0	96.1	89.7	92.9
Rsa1.0_00949.1.g21711.t1	gb|EOA38549.1| hypothetical protein CARUB_v10010354mg [Capsella rubella]	216	195	5.00E-64	90.3	80.6	81.5	hypothetical protein CARUB_v10010354mg	gbpln	Capsella rubella	AT1G01160.1 | Symbols: GIF2 | GRF1-interacting factor 2 | chr1:72583-73883 FORWARD LENGTH=195	216	195	1.00E-59	90.3	76.9	79.6
Rsa1.0_00949.1.g21712.t1	gb|ACF23030.1| ST103-2 [Eutrema halophilum]	54	85	9.00E-21	157.4	88.9	90.7	ST103-2	gbpln	Eutrema halophilum	AT1G01170.2 | Symbols: | Protein of unknown function (DUF1138) | chr1:74105-74443 REVERSE LENGTH=83	54	83	2.00E-22	153.7	85.2	88.9
Rsa1.0_00949.1.g21713.t1	gb|EOA38333.1| hypothetical protein CARUB_v10009834mg [Capsella rubella]	314	308	1.00E-151	98.1	81.5	89.2	hypothetical protein CARUB_v10009834mg	gbpln	Capsella rubella	AT1G01180.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:75633-76556 FORWARD LENGTH=307	314	307	1.00E-151	97.8	81.2	89.2
Rsa1.0_00949.1.g21714.t1	gb|AEX20385.1| cytochrome P450 family 78 subfamily A polypeptide 8 [Brassica napus]	539	534	0	99.1	95.4	97.6	cytochrome P450 family 78 subfamily A polypeptide 8	gbpln	Brassica napus	AT1G01190.1 | Symbols: CYP78A8 | cytochrome P450, family 78, subfamily A, polypeptide 8 | chr1:83045-84864 REVERSE LENGTH=535	539	535	0	99.3	88.1	93.7
Rsa1.0_00949.1.g21715.t1	ref|XP_002889376.1| hypothetical protein ARALYDRAFT_470156 [Arabidopsis lyrata subsp. lyrata] gi|297335218|gb|EFH65635.1| hypothetical protein ARALYDRAFT_470156 [Arabidopsis lyrata subsp. lyrata]	235	237	1.00E-117	100.9	90.2	94.0	hypothetical protein ARALYDRAFT_470156	gbpln	Arabidopsis lyrata	AT1G01200.1 | Symbols: ATRABA3, ATRAB-A3, RABA3 | RAB GTPase homolog A3 | chr1:86715-88145 REVERSE LENGTH=237	235	237	1.00E-117	100.9	88.5	92.8
Rsa1.0_00949.1.g21716.t1	ref|XP_002892079.1| ORMDL family protein [Arabidopsis lyrata subsp. lyrata] gi|297337921|gb|EFH68338.1| ORMDL family protein [Arabidopsis lyrata subsp. lyrata]	421	157	1.00E-86	37.3	35.9	36.6	ORMDL family protein	gbpln	Arabidopsis lyrata	AT1G01230.1 | Symbols: | ORMDL family protein | chr1:97620-99046 FORWARD LENGTH=157	421	157	8.00E-89	37.3	35.6	36.6
Rsa1.0_00949.1.g21717.t1	dbj|BAJ34192.1| unnamed protein product [Thellungiella halophila]	188	197	2.00E-83	104.8	90.4	93.1	unnamed protein product	----	----	AT1G01250.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:104731-105309 REVERSE LENGTH=192	188	192	2.00E-82	102.1	86.7	91.5

Rsa1.0_00949.1.g21718.t1	ref|NP_171634.1| transcription factor bHLH13 [Arabidopsis thaliana] gi|145323702|ref|NP_001077440.1| transcription factor bHLH13 [Arabidopsis thaliana] gi|334182212|ref|NP_001184883.1| transcription factor bHLH13 [Arabidopsis thaliana] gi|75311402|sp|Q9LNJ5.1|BH013_ARATH RecName: Full=Transcription factor bHLH13; AltName: Full=Basic helix-loop-helix protein 13; Short=AtbHLH13; Short=bHLH 13; AltName: Full=Transcription factor EN 39; AltName: Full=bHLH transcription factor bHLH013 gi|9665138|gb|AAF97322.1|AC023628_3 Similar to transcription factors [Arabidopsis thaliana] gi|18026974|gb|AAL55720.1|AF251698_1 putative transcription factor BHLH13 [Arabidopsis thaliana] gi|19310467|gb|AAL84968.1| At1g01260/F6F3_25 [Arabidopsis thaliana] gi|21539515|gb|AAM53310.1| transcription factor MYC7E, putative [Arabidopsis thaliana] gi|28416465|gb|AAO42763.1| At1g01260/F6F3_25 [Arabidopsis thaliana] gi|332189141|gb|AEE27262.1| transcription factor bHLH13 [Arabidopsis thaliana] gi|332189142|gb|AEE27263.1| transcription factor bHLH13		580	590	0	101.7	79.8	87.2	transcription factor bHLH13	gbpln	Arabidopsis thaliana	AT1G01260.3 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:109595-111367 FORWARD LENGTH=590		580	590	0	101.7	79.8	87.2
Rsa1.0_00949.1.g21719.t1	gb|EOA38917.1| hypothetical protein CARUB_v10011315mg [Capsella rubella]		514	510	0	99.2	88.5	94.2	hypothetical protein CARUB_v10011315mg	gbpln	Capsella rubella	AT1G01280.1 | Symbols: CYP703A2, CYP703 | cytochrome P450, family 703, subfamily A, polypeptide 2 | chr1:112290-113905 FORWARD LENGTH=510		514	510	0	99.2	88.1	94.4
Rsa1.0_00949.1.g21720.t1	ref|XP_002892074.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297337916|gb|EFH68333.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]		486	485	0	99.8	90.9	94.9	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT1G01300.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:117065-118522 FORWARD LENGTH=485		486	485	0	99.8	85.6	89.5
Rsa1.0_00950.1.g21721.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00950.1.g21722.t2	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]		1455	910	0	62.5	34.0	43.2	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626		1455	626	1.00E-136	43.0	15.5	22.3
Rsa1.0_00950.1.g21723.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_00950.1.g21724.t1	gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]		408	543	8.00E-65	133.1	34.1	50.5	hypothetical protein CARUB_v10015730mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566		408	566	5.00E-55	138.7	31.1	49.3
Rsa1.0_00950.1.g21725.t1	gb|EOA24857.1| hypothetical protein CARUB_v10018148mg [Capsella rubella]		175	163	8.00E-59	93.1	73.7	81.7	hypothetical protein CARUB_v10018148mg	gbpln	Capsella rubella	AT3G25870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G13360.1); Has 50 Blast hits to 50 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9463665-9464177 REVERSE LENGTH=170		175	170	9.00E-57	97.1	75.4	82.3
Rsa1.0_00950.1.g21726.t1	ref|NP_189215.1| 2-oxoacid dehydrogenases acyltransferase family protein [Arabidopsis thaliana] gi|5881963|gb|AAD55139.1|AF066079_1 dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana] gi|14335166|gb|AAK59863.1| AT3g25860/MPE11_1 [Arabidopsis thaliana] gi|26983848|gb|AAN86176.1| putative dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana] gi|332643559|gb|AEE77080.1| pyruvate decarboxylase E2 subunit [Arabidopsis thaliana]		480	480	0	100.0	90.2	93.3	2-oxoacid dehydrogenases acyltransferase family protein	gbpln	Arabidopsis thaliana	AT3G25860.1 | Symbols: LTA2, PLE2 | 2-oxoacid dehydrogenases acyltransferase family protein | chr3:9460632-9462585 FORWARD LENGTH=480		480	480	0	100.0	90.2	93.3

Rsa1.0_00950.1.g21727.t1	ref|NP_566781.1| Copper transport protein family [Arabidopsis thaliana] gi|21592740|gb|AAM64689.1| unknown [Arabidopsis thaliana] gi|88900374|gb|ABD57499.1| At3g25855 [Arabidopsis thaliana] gi|332643558|gb|AEE77079.1| Copper transport protein family [Arabidopsis thaliana]	118	112	2.00E-41	94.9	74.6	83.9	Copper transport protein family	gbpln	Arabidopsis thaliana	AT3G25855.1 | Symbols: | Copper transport protein family | chr3:9459608-9460267 REVERSE LENGTH=112	118	112	3.00E-44	94.9	74.6	83.9
Rsa1.0_00950.1.g21728.t1	gb|EOA23468.1| hypothetical protein CARUB_v10016659mg [Capsella rubella]	891	916	0	102.8	75.3	81.7	hypothetical protein CARUB_v10016659mg	gbpln	Capsella rubella	AT3G25840.1 | Symbols: | Protein kinase superfamily protein | chr3:9452993-9457446 REVERSE LENGTH=935	891	935	0	104.9	73.3	79.9
Rsa1.0_00950.1.g21729.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00950.1.g21730.t1	ref|XP_002873785.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297319622|gb|EFH50044.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata]	161	503	1.00E-71	312.4	77.6	88.2	glycosyl hydrolase family 1 protein	gbpln	Arabidopsis lyrata	AT4G22100.1 | Symbols: BGLU3 | beta glucosidase 2 | chr4:11707370-11709932 REVERSE LENGTH=507	161	507	3.00E-71	314.9	77.0	85.7
Rsa1.0_00950.1.g21731.t1	gb|EOA18953.1| hypothetical protein CARUB_v10007587mg [Capsella rubella]	379	527	7.00E-19	139.1	14.2	20.1	hypothetical protein CARUB_v10007587mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	379	530	2.00E-20	139.8	11.1	15.0
Rsa1.0_00951.1.g21732.t1	ref|NP_187682.1| pectinesterase 24 [Arabidopsis thaliana] gi|75313421|sp|Q9SG77.1|PME24_ARATH RecName: Full=Putative pectinesterase/pectinesterase inhibitor 24; Includes: RecName: Full=Pectinesterase inhibitor 24; AltName: Full=Pectin methylesterase inhibitor 24; Includes: RecName: Full=Pectinesterase 24; Short=PE 24; AltName: Full=Pectin methylesterase 24; Short=AtPME24 gi|6630559|gb|AAF19578.1|AC011708_21 putative pectinesterase [Arabidopsis thaliana] gi|332641424|gb|AEE74945.1| pectinesterase 24 [Arabidopsis thaliana]	559	561	0	100.4	85.3	92.1	pectinesterase 24	gbpln	Arabidopsis thaliana	AT3G10710.1 | Symbols: RHS12 | root hair specific 12 | chr3:3352289-3354237 FORWARD LENGTH=561	559	561	0	100.4	85.3	92.1
Rsa1.0_00951.1.g21733.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00951.1.g21734.t1	ref|XP_002884802.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297330642|gb|EFH61061.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata]	483	490	0	101.4	83.6	89.4	glycosyl transferase family 1 protein	gbpln	Arabidopsis lyrata	AT3G10630.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:3321722-3323185 REVERSE LENGTH=487	483	487	0	100.8	81.6	87.8
Rsa1.0_00951.1.g21735.t1	gb|AFK34779.1| unknown [Medicago truncatula]	424	454	8.00E-65	107.1	40.3	56.6	unknown	gbpln	Medicago truncatula	AT5G19100.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:6408242-6409417 REVERSE LENGTH=391	424	391	1.00E-52	92.2	37.3	50.2
Rsa1.0_00951.1.g21736.t1	ref|XP_002873929.1| hypothetical protein ARALYDRAFT_909934 [Arabidopsis lyrata subsp. lyrata] gi|297319766|gb|EFH50188.1| hypothetical protein ARALYDRAFT_909934 [Arabidopsis lyrata subsp. lyrata]	326	407	1.00E-35	124.8	41.4	53.4	hypothetical protein ARALYDRAFT_909934	gbpln	Arabidopsis lyrata	AT5G19100.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:6408242-6409417 REVERSE LENGTH=391	326	391	1.00E-35	119.9	41.7	54.3
Rsa1.0_00951.1.g21737.t1	ref|NP_187671.1| cationic amino acid transporter 7 [Arabidopsis thaliana] gi|75313793|sp|Q9SQZ0.1|CAAT7_ARATH RecName: Full=Cationic amino acid transporter 7, chloroplastic; Flags: Precursor gi|12322779|gb|AAG51376.1|AC011560_8 putative amino acid transporter; 33388-30195 [Arabidopsis thaliana] gi|8567793|gb|AAF76365.1| amino acid transporter, putative [Arabidopsis thaliana] gi|332641412|gb|AEE74933.1| cationic amino acid transporter 7 [Arabidopsis thaliana]	581	584	0	100.5	92.1	96.0	cationic amino acid transporter 7	gbpln	Arabidopsis thaliana	AT3G10600.1 | Symbols: CAT7 | cationic amino acid transporter 7 | chr3:3313969-3317162 FORWARD LENGTH=584	581	584	0	100.5	92.1	96.0
Rsa1.0_00951.1.g21738.t1	ref|XP_002884801.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330641|gb|EFH61060.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	221	205	3.00E-46	92.8	45.7	60.6	predicted protein	gbpln	Arabidopsis lyrata	AT3G10595.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr3:3311905-3312815 REVERSE LENGTH=183	221	183	1.00E-38	82.8	41.2	56.1
Rsa1.0_00951.1.g21739.t1	ref|XP_002884801.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330641|gb|EFH61060.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	206	205	2.00E-50	99.5	52.9	67.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G10595.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr3:3311905-3312815 REVERSE LENGTH=183	206	183	7.00E-43	88.8	42.7	57.8

Rsa1.0_00951.1.g21740.t1	ref|NP_187669.1| myb family transcription factor [Arabidopsis thaliana] gi|12322787|gb|AAG51384.1|AC011560_16 hypothetical protein; 39127-40274 [Arabidopsis thaliana] gi|8567789|gb|AAF76361.1| I-box binding factor, putative [Arabidopsis thaliana] gi|332641407|gb|AEE74928.1| myb family transcription factor [Arabidopsis thaliana]	198	287	5.00E-42	144.9	50.0	62.1	myb family transcription factor	gbpln	Arabidopsis thaliana	AT3G10580.1 | Symbols: | Homeodomain-like superfamily protein | chr3:3307083-3308230 REVERSE LENGTH=287	198	287	2.00E-44	144.9	50.0	62.1
Rsa1.0_00951.1.g21741.t1	gb|AAK82552.1| AT5g04590/T32M21_190 [Arabidopsis thaliana] gi|23308385|gb|AAN18162.1| At5g04590/T32M21_190 [Arabidopsis thaliana]	370	416	3.00E-36	112.4	24.1	26.8	AT5g04590/T32M21_190	gbpln	Arabidopsis thaliana	AT5G04590.1 | Symbols: SIR | sulfite reductase | chr5:1319404-1322298 FORWARD LENGTH=642	370	642	4.00E-38	173.5	23.5	26.2
Rsa1.0_00951.1.g21742.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	516	1274	1.00E-111	246.9	44.2	59.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	516	575	6.00E-55	111.4	32.9	47.1
Rsa1.0_00951.1.g21743.t1	ref|NP_187666.5| Myotubularin-like phosphatases II-like protein [Arabidopsis thaliana] gi|332641403|gb|AEE74924.1| Myotubularin-like phosphatases II-like protein [Arabidopsis thaliana]	851	840	0	98.7	88.1	92.1	Myotubularin-like phosphatases II-like protein	gbpln	Arabidopsis thaliana	AT3G10550.1 | Symbols: MTM1, AtMTM1 | Myotubularin-like phosphatases II superfamily | chr3:3293210-3298452 REVERSE LENGTH=840	851	840	0	98.7	88.1	92.1
Rsa1.0_00951.1.g21744.t1	ref|XP_002882680.1| hypothetical protein ARALYDRAFT_897238 [Arabidopsis lyrata subsp. lyrata] gi|297328520|gb|EFH58939.1| hypothetical protein ARALYDRAFT_897238 [Arabidopsis lyrata subsp. lyrata]	483	486	0	100.6	94.4	97.7	hypothetical protein ARALYDRAFT_897238	gbpln	Arabidopsis lyrata	AT3G10540.1 | Symbols: | 3-phosphoinositide-dependent protein kinase | chr3:3289916-3292429 FORWARD LENGTH=486	483	486	0	100.6	93.8	97.1
Rsa1.0_00951.1.g21745.t1	ref|XP_002882679.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297328519|gb|EFH58938.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	533	536	0	100.6	90.6	95.5	transducin family protein	gbpln	Arabidopsis lyrata	AT3G10530.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:3286277-3288670 FORWARD LENGTH=536	533	536	0	100.6	90.8	95.1
Rsa1.0_00951.1.g21746.t1	sp|Q941Q2.1|HBL2_BRANA RecName: Full=Non-symbiotic hemoglobin 2; AltName: Full=BRAna GLB2; AltName: Full=Hb2 gi|15809392|gb|AAK07741.1| class 2 non-symbiotic hemoglobin [Brassica napus]	161	161	1.00E-87	100.0	98.1	98.8	RecName: Full=Non-symbiotic hemoglobin 2; AltName: Full=BRAna GLB2; AltName: Full=Hb2 gi|15809392|gb|AAK07741.1| class 2 non-symbiotic hemoglobin	gbpln	Brassica napus	AT3G10520.1 | Symbols: AHB2, GLB2, ARATH GLB2, NSHB2, ATGLB2, HB2 | haemoglobin 2 | chr3:3276516-3277765 REVERSE LENGTH=158	161	158	3.00E-85	98.1	92.5	96.9
Rsa1.0_00951.1.g21747.t1	ref|XP_002871095.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297316932|gb|EFH47354.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	813	860	0	105.8	65.3	75.2	protein binding protein	gbpln	Arabidopsis lyrata	AT5G04460.3 | Symbols: | RING/U-box superfamily protein | chr5:1260009-1263695 FORWARD LENGTH=863	813	863	0	106.2	64.5	74.7
Rsa1.0_00951.1.g21748.t1	gb|EOA30249.1| hypothetical protein CARUB_v10013370mg [Capsella rubella]	535	558	0	104.3	75.1	82.8	hypothetical protein CARUB_v10013370mg	gbpln	Capsella rubella	AT3G10500.1 | Symbols: anac053, NAC053 | NAC domain containing protein 53 | chr3:3271718-3273887 FORWARD LENGTH=549	535	549	0	102.6	75.0	81.5
Rsa1.0_00951.1.g21749.t1	gb|EOA30567.1| hypothetical protein CARUB_v10013694mg [Capsella rubella]	443	447	0	100.9	81.7	89.4	hypothetical protein CARUB_v10013694mg	gbpln	Capsella rubella	AT3G10490.2 | Symbols: ANAC052, NAC052 | NAC domain containing protein 52 | chr3:3268075-3270608 FORWARD LENGTH=451	443	451	0	101.8	82.4	88.7
Rsa1.0_00951.1.g21750.t3	gb|EOA30567.1| hypothetical protein CARUB_v10013694mg [Capsella rubella]	448	447	0	99.8	78.1	86.4	hypothetical protein CARUB_v10013694mg	gbpln	Capsella rubella	AT3G10490.2 | Symbols: ANAC052, NAC052 | NAC domain containing protein 52 | chr3:3268075-3270608 FORWARD LENGTH=451	448	451	0	100.7	76.6	84.2
Rsa1.0_00951.1.g21751.t1	gb|EOA32729.1| hypothetical protein CARUB_v10016033mg [Capsella rubella]	385	395	1.00E-142	102.6	79.0	84.4	hypothetical protein CARUB_v10016033mg	gbpln	Capsella rubella	AT3G10470.1 | Symbols: | C2H2-type zinc finger family protein | chr3:3260424-3261620 FORWARD LENGTH=398	385	398	1.00E-142	103.4	80.0	86.0
Rsa1.0_00951.1.g21752.t12	gb|EOA30606.1| hypothetical protein CARUB_v10013737mg [Capsella rubella]	539	437	0	81.1	62.0	68.1	hypothetical protein CARUB_v10013737mg	gbpln	Capsella rubella	AT3G10450.1 | Symbols: SCPL7 | serine carboxypeptidase-like 7 | chr3:3249544-3252320 FORWARD LENGTH=437	539	437	0	81.1	60.5	67.0
Rsa1.0_00951.1.g21753.t1	ref|NP_187655.2| shugoshin-like protein [Arabidopsis thaliana] gi|332641386|gb|AEE74907.1| shugoshin-like protein [Arabidopsis thaliana]	403	572	3.00E-56	141.9	33.3	38.5	shugoshin-like protein	gbpln	Arabidopsis thaliana	AT3G10440.1 | Symbols: | Shugoshin C terminus | chr3:3245376-3248987 FORWARD LENGTH=572	403	572	7.00E-59	141.9	33.3	38.5

Rsa1.0_00951.1.g21754.t1	ref|NP_567270.1| putative F-box only protein 15 [Arabidopsis thaliana] gi|75265492|sp|Q9S9V1.1|FBX15_ARATH RecName: Full=Putative F-box only protein 15 gi|5732058|gb|AAD48957.1|AF149414_6 contains similarity to Pfam family PF00646 (F-box domain); score=11/3, E=0.23, N=1 [Arabidopsis thaliana] gi|7267227|emb|CAB80834.1| AT4g04690 [Arabidopsis thaliana] gi|332657012|gb|AEE82412.1| putative F-box only protein 15 [Arabidopsis thaliana]	388	378	2.00E-96	97.4	53.6	67.8	putative F-box only protein 15	gbpln	Arabidopsis thaliana	AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378	388	378	5.00E-99	97.4	53.6	67.8
Rsa1.0_00951.1.g21755.t1	gb|EOA19642.1| hypothetical protein CARUB_v10003012mg [Capsella rubella]	361	390	4.00E-66	108.0	46.5	61.5	hypothetical protein CARUB_v10003012mg	gbpln	Capsella rubella	AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378	361	378	1.00E-68	104.7	44.0	60.7
Rsa1.0_00951.1.g21756.t1	gb|EOA19642.1| hypothetical protein CARUB_v10003012mg [Capsella rubella]	392	390	5.00E-83	99.5	48.5	63.8	hypothetical protein CARUB_v10003012mg	gbpln	Capsella rubella	AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378	392	378	3.00E-82	96.4	46.4	61.5
Rsa1.0_00952.1.g21757.t1	gb|EOA35235.1| hypothetical protein CARUB_v10020395mg [Capsella rubella] gi|482571048|gb|EOA35236.1| hypothetical protein CARUB_v10020395mg [Capsella rubella]	477	406	1.00E-170	85.1	68.1	73.0	hypothetical protein CARUB_v10020395mg	gbpln	Capsella rubella	AT1G78420.2 | Symbols: | RING/U-box superfamily protein | chr1:29505278-29507272 FORWARD LENGTH=401	477	401	1.00E-163	84.1	66.9	72.1
Rsa1.0_00952.1.g21758.t1	ref|NP_565179.1| VQ motif-containing protein [Arabidopsis thaliana] gi|17979514|gb|AAL50092.1| At1g78410/F3F9_27 [Arabidopsis thaliana] gi|20857141|gb|AAM26702.1| At1g78410/F3F9_27 [Arabidopsis thaliana] gi|21618255|gb|AAM67305.1| unknown [Arabidopsis thaliana] gi|55982672|gb|AAV69753.1| tobacco rattle virus-induced protein variant 1 [Arabidopsis thaliana] gi|332197981|gb|AEE36102.1| VQ motif-containing protein [Arabidopsis thaliana]	102	108	7.00E-34	105.9	83.3	88.2	VQ motif-containing protein	gbpln	Arabidopsis thaliana	AT1G78410.1 | Symbols: | VQ motif-containing protein | chr1:29502728-29503054 FORWARD LENGTH=108	102	108	1.00E-36	105.9	83.3	88.2
Rsa1.0_00952.1.g21759.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00952.1.g21760.t1	ref|XP_002862994.1| nine-cis-epoxycarotenoid dioxygenase 9 [Arabidopsis lyrata subsp. lyrata] gi|297308788|gb|EFH39253.1| nine-cis-epoxycarotenoid dioxygenase 9 [Arabidopsis lyrata subsp. lyrata]	571	606	0	106.1	82.5	90.0	nine-cis-epoxycarotenoid dioxygenase 9	gbpln	Arabidopsis lyrata	AT1G78390.1 | Symbols: NCED9, ATNCED9 | nine-cis-epoxycarotenoid dioxygenase 9 | chr1:29490895-29492868 REVERSE LENGTH=657	571	657	0	115.1	82.7	89.8
Rsa1.0_00952.1.g21761.t1	ref|NP_565178.1| glutathione S-transferase TAU 19 [Arabidopsis thaliana] gi|75338923|sp|Q9ZRW8.1|GSTUJ_ARATH RecName: Full=Glutathione S-transferase U19; Short=AtGSTU19; AltName: Full=GST class-tau member 19; AltName: Full=Glutathione S-transferase 8 gi|14326477|gb|AAK60284.1|AF385691_1 At1g78380/F3F9_11 [Arabidopsis thaliana] gi|4006934|emb|CAA10060.1| glutathione transferase [Arabidopsis thaliana] gi|18700206|gb|AAL77713.1| At1g78380/F3F9_11 [Arabidopsis thaliana] gi|332197978|gb|AEE36099.1| glutathione S-transferase TAU 19 [Arabidopsis thaliana]	219	219	1.00E-105	100.0	83.1	90.0	glutathione S-transferase TAU 19	gbpln	Arabidopsis thaliana	AT1G78380.1 | Symbols: ATGSTU19, GST8, GSTU19 | glutathione S-transferase TAU 19 | chr1:29486659-29487819 REVERSE LENGTH=219	219	219	1.00E-107	100.0	83.1	90.0
Rsa1.0_00952.1.g21762.t1	ref|XP_002889184.1| hypothetical protein ARALYDRAFT_476999 [Arabidopsis lyrata subsp. lyrata] gi|297335025|gb|EFH65443.1| hypothetical protein ARALYDRAFT_476999 [Arabidopsis lyrata subsp. lyrata]	206	302	2.00E-42	146.6	62.6	68.4	hypothetical protein ARALYDRAFT_476999	gbpln	Arabidopsis lyrata	AT1G78310.1 | Symbols: | VQ motif-containing protein | chr1:29464003-29464938 REVERSE LENGTH=311	206	311	1.00E-40	151.0	60.7	66.0
Rsa1.0_00952.1.g21763.t1	gb|AAK26634.1|AF342780_1 GF14 omega [Brassica napus]	258	260	1.00E-137	100.8	93.4	95.7	GF14 omega	gbpln	Brassica napus	AT1G78300.1 | Symbols: GRF2, 14-3-3OMEGA, GF14 OMEGA | general regulatory factor 2 | chr1:29461883-29463052 FORWARD LENGTH=259	258	259	1.00E-137	100.4	91.1	95.7

Rsa1.0_00952.1.g21764.t2	gb|EOA33589.1| hypothetical protein CARUB_v10019734mg [Capsella rubella]	230	944	4.00E-67	410.4	64.3	75.2	hypothetical protein CARUB_v10019734mg	gbpln	Capsella rubella	AT1G78280.1 | Symbols: | transferases, transferring glycosyl groups | chr1:29452823-29457118 FORWARD LENGTH=943	230	943	2.00E-69	410.0	63.5	76.1
Rsa1.0_00952.1.g21765.t2	ref|XP_002889182.1| hypothetical protein ARALYDRAFT_476994 [Arabidopsis lyrata subsp. lyrata] gi|297335023|gb|EFH65441.1| hypothetical protein ARALYDRAFT_476994 [Arabidopsis lyrata subsp. lyrata]	598	474	6.00E-86	79.3	25.1	27.3	hypothetical protein ARALYDRAFT_476994	gbpln	Arabidopsis lyrata	AT1G78270.1 | Symbols: AtUGT85A4, UGT85A4 | UDP-glucosyl transferase 85A4 | chr1:29450691-29452223 REVERSE LENGTH=489	598	489	2.00E-88	81.8	24.9	27.3
Rsa1.0_00953.1.g21766.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	157	1023	9.00E-16	651.6	38.2	54.1	F27F5.21	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00953.1.g21767.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00953.1.g21768.t1	ref|NP_192696.3| SNARE associated Golgi protein [Arabidopsis thaliana] gi|75153817|sp|Q8L586.1|Y4958_ARATH RecName: Full=Uncharacterized membrane protein At4g09580 gi|20465630|gb|AAM20146.1| unknown protein [Arabidopsis thaliana] gi|21281237|gb|AAM45090.1| unknown protein [Arabidopsis thaliana] gi|332657367|gb|AEE82767.1| uncharacterized membrane protein [Arabidopsis thaliana]	275	287	1.00E-139	104.4	92.0	94.9	SNARE associated Golgi protein	gbpln	Arabidopsis thaliana	AT4G09580.1 | Symbols: | SNARE associated Golgi protein family | chr4:6052721-6054313 REVERSE LENGTH=287	275	287	1.00E-141	104.4	92.0	94.9
Rsa1.0_00953.1.g21769.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1363	1501	0	110.1	58.8	74.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1363	1262	1.00E-120	92.6	15.8	22.5
Rsa1.0_00953.1.g21770.t1	ref|NP_192673.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana] gi|5881780|emb|CAB55698.1| putative protein [Arabidopsis thaliana] gi|7267577|emb|CAB78058.1| putative protein [Arabidopsis thaliana] gi|332657344|gb|AEE82744.1| chaperone DnaJ-domain containing protein [Arabidopsis thaliana]	224	249	1.00E-106	111.2	83.5	90.6	chaperone DnaJ-domain containing protein	gbpln	Arabidopsis thaliana	AT4G09350.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:5931317-5932152 REVERSE LENGTH=249	224	249	1.00E-109	111.2	83.5	90.6
Rsa1.0_00953.1.g21771.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00953.1.g21772.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00953.1.g21773.t1	gb|EOA21830.1| hypothetical protein CARUB_v10002296mg [Capsella rubella]	87	110	8.00E-39	126.4	88.5	95.4	hypothetical protein CARUB_v10002296mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_00953.1.g21774.t1	ref|NP_001190693.1| T-complex protein 11 [Arabidopsis thaliana] gi|332657328|gb|AEE82728.1| T-complex protein 11 [Arabidopsis thaliana]	1079	1098	0	101.8	84.5	90.5	T-complex protein 11	gbpln	Arabidopsis thaliana	AT4G09150.2 | Symbols: | T-complex protein 11 | chr4:5828753-5833475 FORWARD LENGTH=1098	1079	1098	0	101.8	84.5	90.5
Rsa1.0_00953.1.g21775.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	745	871	8.00E-46	116.9	15.3	20.7	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	745	874	3.00E-17	117.3	7.9	11.4
Rsa1.0_00953.1.g21776.t1	ref|XP_002863253.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309087|gb|EFH39512.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	161	165	1.00E-13	102.5	28.0	39.1	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00953.1.g21777.t1	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	901	915	1.00E-101	101.6	23.8	35.4	F22O13.21	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	901	719	1.00E-15	79.8	5.9	9.5
Rsa1.0_00953.1.g21778.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	383	341	4.00E-61	89.0	30.3	36.8	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00953.1.g21779.t1	ref|XP_002872426.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297318263|gb|EFH48685.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	138	133	2.00E-50	96.4	70.3	78.3	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G09100.1 | Symbols: | RING/U-box superfamily protein | chr4:5811256-5811654 FORWARD LENGTH=132	138	132	9.00E-48	95.7	70.3	76.8
Rsa1.0_00953.1.g21780.t8	emb|CAN76698.1| hypothetical protein VITISV_011792 [Vitis vinifera]	1004	1084	0	108.0	43.3	59.8	hypothetical protein VITISV_011792	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1004	1262	4.00E-52	125.7	13.6	22.9

Rsa1.0_00953.1.g21781.t1	gb|EOA20988.1| hypothetical protein CARUB_v10001320mg [Capsella rubella]	184	346	5.00E-30	188.0	54.9	66.3	hypothetical protein CARUB_v10001320mg	gbpln	Capsella rubella	AT4G09060.1 | Symbols: | unknown protein; LOCATED IN: membrane; EXPRESSED IN: leaf; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G14680.1); Has 8168 Blast hits to 6036 proteins in 601 species: Archae - 151; Bacteria - 570; Metazoa - 4684; Fungi - 544; Plants - 345; Viruses - 91; Other Eukaryotes - 1783 (source: NCBI BLink). | chr4:5797781-5800253 REVERSE LENGTH=341	184	341	2.00E-30	185.3	55.4	66.3
Rsa1.0_00953.1.g21782.t1	gb|ADP20180.1| mutant gag-pol polyprotein [Pisum sativum]	238	1004	6.00E-11	421.8	18.5	32.8	mutant gag-pol polyprotein	gbpln	Pisum sativum	#	#	#	#	#	#	#
Rsa1.0_00954.1.g21783.t1	ref|XP_002883801.1| hypothetical protein ARALYDRAFT_480310 [Arabidopsis lyrata subsp. lyrata] gi|297329641|gb|EFH60060.1| hypothetical protein ARALYDRAFT_480310 [Arabidopsis lyrata subsp. lyrata]	618	622	0	100.6	92.9	97.6	hypothetical protein ARALYDRAFT_480310	gbpln	Arabidopsis lyrata	AT2G13560.1 | Symbols: NAD-ME1 | NAD-dependent malic enzyme 1 | chr2:5650089-5655103 FORWARD LENGTH=623	618	623	0	100.8	92.2	96.9
Rsa1.0_00954.1.g21784.t1	ref|NP_178981.1| nuclear transcription factor Y subunit B-7 [Arabidopsis thaliana] gi|75265909|sp|Q9SIT9.1|NFYB7_ARATH RecName: Full=Nuclear transcription factor Y subunit B-7; Short=AtNF-YB-7 gi|4558662|gb|AAD22680.1| putative CCAAT-box binding trancription factor [Arabidopsis thaliana] gi|91806158|gb|ABE65807.1| CCAAT-box binding transcription factor [Arabidopsis thaliana] gi|94442483|gb|ABF19029.1| At2g13570 [Arabidopsis thaliana] gi|225898106|dbj|BAH30385.1| hypothetical protein [Arabidopsis thaliana] gi|330251149|gb|AEC06243.1| nuclear transcription factor Y subunit B-7 [Arabidopsis thaliana]	208	215	9.00E-86	103.4	82.7	88.5	nuclear transcription factor Y subunit B-7	gbpln	Arabidopsis thaliana	AT2G13570.1 | Symbols: NF-YB7 | nuclear factor Y, subunit B7 | chr2:5655842-5656489 REVERSE LENGTH=215	208	215	3.00E-88	103.4	82.7	88.5
Rsa1.0_00954.1.g21785.t1	ref|NP_175075.1| gibberellin 20-oxidase 5 [Arabidopsis thaliana] gi|67633434|gb|AAY78641.1| gibberellin 20-oxidase family protein [Arabidopsis thaliana] gi|332193897|gb|AEE32018.1| gibberellin 20-oxidase 5 [Arabidopsis thaliana]	357	385	0	107.8	84.3	91.9	gibberellin 20-oxidase 5	gbpln	Arabidopsis thaliana	AT1G44090.1 | Symbols: ATGA20OX5, GA20OX5 | gibberellin 20-oxidase 5 | chr1:16760677-16762486 REVERSE LENGTH=385	357	385	0	107.8	84.3	91.9
Rsa1.0_00954.1.g21786.t1	ref|XP_002883804.1| hypothetical protein ARALYDRAFT_480314 [Arabidopsis lyrata subsp. lyrata] gi|297329644|gb|EFH60063.1| hypothetical protein ARALYDRAFT_480314 [Arabidopsis lyrata subsp. lyrata]	807	823	0	102.0	91.9	96.5	hypothetical protein ARALYDRAFT_480314	gbpln	Arabidopsis lyrata	AT2G13620.1 | Symbols: ATCHX15, CHX15 | cation/hydrogen exchanger 15 | chr2:5678006-5680621 FORWARD LENGTH=821	807	821	0	101.7	91.8	96.5
Rsa1.0_00954.1.g21787.t1	ref|XP_002877500.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323338|gb|EFH53759.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	140	136	5.00E-30	97.1	45.7	60.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	140	320	7.00E-15	228.6	31.4	42.1
Rsa1.0_00954.1.g21788.t1	ref|XP_002883808.1| hypothetical protein ARALYDRAFT_899601 [Arabidopsis lyrata subsp. lyrata] gi|297329648|gb|EFH60067.1| hypothetical protein ARALYDRAFT_899601 [Arabidopsis lyrata subsp. lyrata]	1906	1923	0	100.9	94.4	97.0	hypothetical protein ARALYDRAFT_899601	gbpln	Arabidopsis lyrata	AT2G13680.1 | Symbols: CALS5, GLS2, ATGSL02 | callose synthase 5 | chr2:5695124-5706134 FORWARD LENGTH=1923	1906	1923	0	100.9	94.1	96.5
Rsa1.0_00954.1.g21789.t3	ref|NP_001190233.1| 26S proteasome regulatory subunit N8 [Arabidopsis thaliana] gi|332003541|gb|AED90924.1| probable 26S proteasome non-ATPase regulatory subunit 7 [Arabidopsis thaliana]	218	305	1.00E-18	139.9	20.6	26.6	26S proteasome regulatory subunit N8	gbpln	Arabidopsis thaliana	AT5G05780.2 | Symbols: RPN8A | RP non-ATPase subunit 8A | chr5:1735862-1738176 FORWARD LENGTH=305	218	305	4.00E-21	139.9	20.6	26.6

Rsa1.0_00954.1.g21790.t1	ref|NP_973453.2| putative S-acyltransferase [Arabidopsis thaliana] gi|223635847|sp|Q3EC11.2|ZDHC2_ARATH RecName: Full=Probable S-acyltransferase At2g14255; AltName: Full=Probable palmitoyltransferase At2g14255; AltName: Full=Zinc finger DHHC domain-containing protein At2g14255 gi|330251198|gb|AEC06292.1| putative S-acyltransferase [Arabidopsis thaliana]	558	536	0	96.1	80.1	86.6	putative S-acyltransferase	gbpln	Arabidopsis thaliana	AT2G14255.1 | Symbols: | Ankyrin repeat family protein with DHHC zinc finger domain | chr2:6036974-6040892 FORWARD LENGTH=536	558	536	0	96.1	80.1	86.6
Rsa1.0_00954.1.g21791.t1	ref|NP_850652.1| peroxidase 32 [Arabidopsis thaliana] gi|166898075|sp|Q9LHB9.3|PER32_ARATH RecName: Full=Peroxidase 32; Short=Atperox P32; AltName: Full=ATP16a; AltName: Full=PRXR3; Flags: Precursor gi|9884625|dbj|BAB02631.1| peroxidase [Arabidopsis thaliana] gi|19347733|gb|AAL86292.1| unknown protein [Arabidopsis thaliana] gi|22136690|gb|AAM91664.1| unknown protein [Arabidopsis thaliana] gi|222424403|dbj|BAH20157.1| AT3G32980 [Arabidopsis thaliana] gi|332644186|gb|AEE77707.1| peroxidase 32 [Arabidopsis thaliana]	88	352	8.00E-28	400.0	71.6	76.1	peroxidase 32	gbpln	Arabidopsis thaliana	AT3G32980.1 | Symbols: | Peroxidase superfamily protein | chr3:13526404-13529949 REVERSE LENGTH=352	88	352	1.00E-30	400.0	71.6	76.1
Rsa1.0_00954.1.g21792.t2	ref|XP_002885951.1| hypothetical protein ARALYDRAFT_899735 [Arabidopsis lyrata subsp. lyrata] gi|297331791|gb|EFH62210.1| hypothetical protein ARALYDRAFT_899735 [Arabidopsis lyrata subsp. lyrata]	258	252	1.00E-123	97.7	91.5	93.4	hypothetical protein ARALYDRAFT_899735	gbpln	Arabidopsis lyrata	AT2G15240.1 | Symbols: | UNC-50 family protein | chr2:6615980-6618862 REVERSE LENGTH=252	258	252	1.00E-120	97.7	90.3	92.2
Rsa1.0_00954.1.g21793.t1	gb|ADY76580.1| translocon at inner membrane of chloroplasts 21 [Brassica napus]	292	294	1.00E-130	100.7	84.9	89.0	translocon at inner membrane of chloroplasts 21	gbpln	Brassica napus	AT2G15290.1 | Symbols: ATTIC21, TIC21, CIA5, PIC1 | translocon at inner membrane of chloroplasts 21 | chr2:6642512-6644011 REVERSE LENGTH=296	292	296	1.00E-128	101.4	83.2	88.4
Rsa1.0_00954.1.g21794.t1	ref|XP_002883890.1| hypothetical protein ARALYDRAFT_480399 [Arabidopsis lyrata subsp. lyrata] gi|297329730|gb|EFH60149.1| hypothetical protein ARALYDRAFT_480399 [Arabidopsis lyrata subsp. lyrata]	739	744	0	100.7	71.4	80.0	hypothetical protein ARALYDRAFT_480399	gbpln	Arabidopsis lyrata	AT2G15300.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:6649630-6652010 FORWARD LENGTH=744	739	744	0	100.7	71.6	79.7
Rsa1.0_00954.1.g21795.t1	ref|NP_179134.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|4662629|gb|AAD26901.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|15292805|gb|AAK92771.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|20258861|gb|AAM14102.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|330251293|gb|AEC06387.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	387	382	0	98.7	82.4	91.2	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G15320.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr2:6666527-6667675 REVERSE LENGTH=382	387	382	0	98.7	82.4	91.2
Rsa1.0_00954.1.g21796.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00954.1.g21797.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00954.1.g21798.t2	ref|XP_002885958.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331798|gb|EFH62217.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	513	534	0	104.1	75.0	85.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G14080.1 | Symbols: FUT6, ATFUT6 | fucosyltransferase 6 | chr1:4822580-4824218 FORWARD LENGTH=519	513	519	0	101.2	74.7	86.7
Rsa1.0_00955.1.g21799.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00955.1.g21800.t1	gb|EOA40138.1| hypothetical protein CARUB_v10008849mg, partial [Capsella rubella]	465	523	0	112.5	97.8	99.1	hypothetical protein CARUB_v10008849mg, partial	gbpln	Capsella rubella	AT1G04170.1 | Symbols: EIF2 GAMMA | eukaryotic translation initiation factor 2 gamma subunit | chr1:1097423-1099702 FORWARD LENGTH=465	465	465	0	100.0	97.4	98.9
Rsa1.0_00955.1.g21801.t2	gb|EOA36034.1| hypothetical protein CARUB_v10008089mg [Capsella rubella]	1377	1499	0	108.9	85.0	90.7	hypothetical protein CARUB_v10008089mg	gbpln	Capsella rubella	AT1G04160.1 | Symbols: XIB, ATXIB, XI-8, XI-B | myosin XI B | chr1:1086495-1096146 FORWARD LENGTH=1500	1377	1500	0	108.9	84.0	90.0

Rsa1.0_00955.1.g21802.t1	ref|NP_171911.1| C2 domain-containing protein [Arabidopsis thaliana] gi|3142295|gb|AAC16746.1| Strong similarity to phosphoribosylanthranilate transferase gb|D86180 from Pisum sativum [Arabidopsis thaliana] gi|332189542|gb|AEE27663.1| C2 domain-containing protein [Arabidopsis thaliana]	992	1012	0	102.0	84.4	92.1	C2 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G04150.1 | Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr1:1081208-1084246 REVERSE LENGTH=1012	992	1012	0	102.0	84.4	92.1
Rsa1.0_00955.1.g21803.t1	gb|EOA37524.1| hypothetical protein CARUB_v10011722mg [Capsella rubella]	801	790	0	98.6	84.5	90.0	hypothetical protein CARUB_v10011722mg	gbpln	Capsella rubella	AT1G04140.1 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr1:1075984-1080321 REVERSE LENGTH=790	801	790	0	98.6	83.0	88.9
Rsa1.0_00955.1.g21804.t1	ref|XP_002889492.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297335334|gb|EFH65751.1| binding protein [Arabidopsis lyrata subsp. lyrata]	359	360	0	100.3	85.5	94.2	binding protein	gbpln	Arabidopsis lyrata	AT1G04130.1 | Symbols: TPR2, AtTPR2 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1073465-1075374 FORWARD LENGTH=360	359	360	1.00E-180	100.3	84.4	92.5
Rsa1.0_00955.1.g21805.t1	gb|EOA23557.1| hypothetical protein CARUB_v10016751mg [Capsella rubella]	742	719	0	96.9	54.2	64.3	hypothetical protein CARUB_v10016751mg	gbpln	Capsella rubella	AT2G02955.1 | Symbols: MEE12 | maternal effect embryo arrest 12 | chr2:859592-861772 FORWARD LENGTH=666	742	666	0	89.8	49.7	61.7
Rsa1.0_00955.1.g21806.t1	gb|EOA29382.1| hypothetical protein CARUB_v10025669mg [Capsella rubella]	584	377	1.00E-165	64.6	51.2	56.5	hypothetical protein CARUB_v10025669mg	gbpln	Capsella rubella	AT2G35580.1 | Symbols: | Serine protease inhibitor (SERPIN) family protein | chr2:14933828-14935482 REVERSE LENGTH=374	584	374	1.00E-131	64.0	43.2	49.1
Rsa1.0_00955.1.g21807.t1	ref|XP_002881405.1| hypothetical protein ARALYDRAFT_902667 [Arabidopsis lyrata subsp. lyrata] gi|297327244|gb|EFH57664.1| hypothetical protein ARALYDRAFT_902667 [Arabidopsis lyrata subsp. lyrata]	86	86	7.00E-37	100.0	84.9	91.9	hypothetical protein ARALYDRAFT_902667	gbpln	Arabidopsis lyrata	AT2G35612.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; BEST Arabidopsis thaliana protein match is: Copper amine oxidase family protein (TAIR:AT1G31670.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:14955241-14955501 REVERSE LENGTH=86	86	86	5.00E-39	100.0	83.7	90.7
Rsa1.0_00955.1.g21808.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00956.1.g21809.t1	gb|AAM63070.1| VirE2-interacting protein VIP1 [Arabidopsis thaliana]	333	341	1.00E-127	102.4	77.2	83.2	VirE2-interacting protein VIP1	gbpln	Arabidopsis thaliana	AT1G43700.1 | Symbols: VIP1, SUE3 | VIRE2-interacting protein 1 | chr1:16484352-16486017 FORWARD LENGTH=341	333	341	1.00E-129	102.4	76.9	82.9
Rsa1.0_00956.1.g21810.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00956.1.g21811.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00956.1.g21812.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00956.1.g21813.t2	emb|CAB40024.1| putative reverse-transcriptase-like protein [Arabidopsis thaliana] gi|7267755|emb|CAB78181.1| putative reverse-transcriptase-like protein [Arabidopsis thaliana]	886	1240	7.00E-27	140.0	9.8	13.1	putative reverse-transcriptase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00956.1.g21814.t1	ref|NP_175046.1| serine carboxypeptidase-like 44 [Arabidopsis thaliana] gi|75192450|sp|Q9MAR8.1|SCP44_ARATH RecName: Full=Serine carboxypeptidase-like 44; Flags: Precursor gi|7523661|gb|AAF63101.1|AC006423_2 Putative serine carboxypeptidases [Arabidopsis thaliana] gi|332193875|gb|AEE31996.1| serine carboxypeptidase-like 44 [Arabidopsis thaliana]	478	479	0	100.2	85.6	93.3	serine carboxypeptidase-like 44	gbpln	Arabidopsis thaliana	AT1G43780.1 | Symbols: scpl44 | serine carboxypeptidase-like 44 | chr1:16563811-16567399 FORWARD LENGTH=479	478	479	0	100.2	85.6	93.3
Rsa1.0_00956.1.g21815.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00956.1.g21816.t1	ref|XP_002887198.1| hypothetical protein ARALYDRAFT_315886 [Arabidopsis lyrata subsp. lyrata] gi|297333039|gb|EFH63457.1| hypothetical protein ARALYDRAFT_315886 [Arabidopsis lyrata subsp. lyrata]	173	75	2.00E-18	43.4	27.7	29.5	hypothetical protein ARALYDRAFT_315886	gbpln	Arabidopsis lyrata	AT1G68680.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 16 growth stages; Has 20 Blast hits to 20 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25785627-25786622 FORWARD LENGTH=75	173	75	1.00E-19	43.4	26.6	28.3

Rsa1.0_00956.1.g21817.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1155	1142	1.00E-120	98.9	18.3	21.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1155	575	8.00E-39	49.8	9.0	16.1
Rsa1.0_00956.1.g21818.t1	ref|XP_002893975.1| hypothetical protein ARALYDRAFT_891373 [Arabidopsis lyrata subsp. lyrata] gi|297339817|gb|EFH70234.1| hypothetical protein ARALYDRAFT_891373 [Arabidopsis lyrata subsp. lyrata]	605	258	3.00E-70	42.6	21.7	23.3	hypothetical protein ARALYDRAFT_891373	gbpln	Arabidopsis lyrata	AT1G44000.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11911.1); Has 216 Blast hits to 212 proteins in 76 species: Archae - 0; Bacteria - 96; Metazoa - 0; Fungi - 0; Plants - 118; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:16708201-16709521 REVERSE LENGTH=260	605	260	2.00E-67	43.0	20.3	22.0
Rsa1.0_00956.1.g21819.t1	gb|EOA32818.1| hypothetical protein CARUB_v10016129mg [Capsella rubella]	204	849	2.00E-21	416.2	27.0	32.8	hypothetical protein CARUB_v10016129mg	gbpln	Capsella rubella	AT2G16730.1 | Symbols: BGAL13 | glycosyl hydrolase family 35 protein | chr2:7261986-7266105 REVERSE LENGTH=848	204	848	7.00E-23	415.7	26.0	34.3
Rsa1.0_00957.1.g21820.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	904	1024	2.00E-67	113.3	14.6	18.7	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00957.1.g21821.t1	dbj|BAB10385.1| unnamed protein product [Arabidopsis thaliana]	856	733	0	85.6	61.8	71.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	856	785	7.00E-15	91.7	13.1	23.9
Rsa1.0_00957.1.g21822.t3	gb|AAF79483.1|AC022492_27 F1L3.20 [Arabidopsis thaliana]	1197	1188	0	99.2	50.0	66.2	F1L3.20	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1197	1262	2.00E-62	105.4	11.5	18.3
Rsa1.0_00957.1.g21823.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	407	1225	8.00E-68	301.0	34.6	48.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	407	575	1.00E-38	141.3	25.3	42.5
Rsa1.0_00958.1.g21824.t1	dbj|BAJ34204.1| unnamed protein product [Thellungiella halophila]	507	507	0	100.0	97.6	99.0	unnamed protein product	----	----	AT1G48030.2 | Symbols: mtLPD1 | mitochondrial lipoamide dehydrogenase 1 | chr1:17717432-17719141 REVERSE LENGTH=507	507	507	0	100.0	94.9	98.4
Rsa1.0_00958.1.g21825.t1	dbj|BAJ34104.1| unnamed protein product [Thellungiella halophila]	373	383	0	102.7	91.2	95.4	unnamed protein product	----	----	AT1G48040.1 | Symbols: | Protein phosphatase 2C family protein | chr1:17720064-17721698 REVERSE LENGTH=383	373	383	0	102.7	86.3	92.8
Rsa1.0_00958.1.g21826.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00958.1.g21827.t3	emb|CAA54683.1| acetyl-CoA carboxylase [Brassica napus]	2368	2304	0	97.3	89.9	93.2	acetyl-CoA carboxylase	gbpln	Brassica napus	AT1G36160.2 | Symbols: ACC1 | acetyl-CoA carboxylase 1 | chr1:13534196-13543773 FORWARD LENGTH=2254	2368	2254	0	95.2	80.1	85.7
Rsa1.0_00958.1.g21828.t4	ref|NP_175242.7| calcium-dependent lipid-binding-like protein [Arabidopsis thaliana] gi|332194125|gb|AEE32246.1| calcium-dependent lipid-binding-like protein [Arabidopsis thaliana]	4227	4146	0	98.1	89.1	92.8	calcium-dependent lipid-binding-like protein	gbpln	Arabidopsis thaliana	AT1G48090.1 | Symbols: | calcium-dependent lipid-binding family protein | chr1:17732582-17758194 REVERSE LENGTH=4146	4227	4146	0	98.1	89.1	92.8
Rsa1.0_00958.1.g21829.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	980	1142	0	116.5	55.8	71.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	980	575	4.00E-30	58.7	5.6	8.1
Rsa1.0_00959.1.g21830.t1	ref|XP_002873645.1| mitochondrial phosphate transporter [Arabidopsis lyrata subsp. lyrata] gi|297319482|gb|EFH49904.1| mitochondrial phosphate transporter [Arabidopsis lyrata subsp. lyrata]	357	374	0	104.8	96.1	98.0	mitochondrial phosphate transporter	gbpln	Arabidopsis lyrata	AT5G14040.1 | Symbols: PHT3;1 | phosphate transporter 3;1 | chr5:4531059-4532965 REVERSE LENGTH=375	357	375	0	105.0	93.3	95.8

Rsa1.0_00959.1.g21831.t1	ref|NP_568293.1| translocon-associated protein subunit beta [Arabidopsis thaliana] gi|186522719|ref|NP_001119221.1| translocon-associated protein subunit beta [Arabidopsis thaliana] gi|186522723|ref|NP_001119222.1| translocon-associated protein subunit beta [Arabidopsis thaliana] gi|186522727|ref|NP_001119223.1| translocon-associated protein subunit beta [Arabidopsis thaliana] gi|14517446|gb|AAK62613.1| AT5g14030/MUA22_2 [Arabidopsis thaliana] gi|21553748|gb|AAM62841.1| unknown [Arabidopsis thaliana] gi|22136544|gb|AAM91058.1| AT5g14030/MUA22_2 [Arabidopsis thaliana] gi|332004593|gb|AED91976.1| translocon-associated protein subunit beta [Arabidopsis thaliana] gi|332004594|gb|AED91977.1| translocon-associated protein subunit beta [Arabidopsis thaliana] gi|332004595|gb|AED91978.1| translocon-associated protein subunit beta [Arabidopsis thaliana] gi|332004596|gb|AED91979.1| translocon-associated protein subunit beta [Arabidopsis thaliana]	196	195	4.00E-87	99.5	81.6	91.3	translocon-associated protein subunit beta	gbpln	Arabidopsis thaliana	AT5G14030.4 | Symbols: | translocon-associated protein beta (TRAPB) family protein | chr5:4526878-4528253 FORWARD LENGTH=195	196	195	1.00E-89	99.5	81.6	91.3
Rsa1.0_00959.1.g21832.t1	gb|EOA19740.1| hypothetical protein CARUB_v10003842mg [Capsella rubella]	407	426	0	104.7	76.7	85.7	hypothetical protein CARUB_v10003842mg	gbpln	Capsella rubella	AT5G14020.1 | Symbols: | Endosomal targeting BRO1-like domain-containing protein | chr5:4523730-4525819 REVERSE LENGTH=401	407	401	0	98.5	76.2	86.0
Rsa1.0_00959.1.g21833.t1	ref|NP_568292.1| NAC domain containing protein 84 [Arabidopsis thaliana] gi|10177666|dbj|BAB11128.1| unnamed protein product [Arabidopsis thaliana] gi|20466338|gb|AAM20486.1| unknown protein [Arabidopsis thaliana] gi|30023658|gb|AAP13362.1| At5g14000 [Arabidopsis thaliana] gi|332004589|gb|AED91972.1| NAC domain containing protein 84 [Arabidopsis thaliana]	212	206	1.00E-91	97.2	83.0	89.2	NAC domain containing protein 84	gbpln	Arabidopsis thaliana	AT5G14000.1 | Symbols: anac084, NAC084 | NAC domain containing protein 84 | chr5:4518177-4519034 FORWARD LENGTH=206	212	206	4.00E-94	97.2	83.0	89.2
Rsa1.0_00959.1.g21834.t1	ref|NP_196903.1| exocyst complex component 7 [Arabidopsis thaliana] gi|10177665|dbj|BAB11127.1| leucine zipper protein-like [Arabidopsis thaliana] gi|28392955|gb|AAO41913.1| putative leucine zipper protein [Arabidopsis thaliana] gi|29824345|gb|AAP04133.1| putative leucine zipper protein [Arabidopsis thaliana] gi|332004588|gb|AED91971.1| exocyst subunit exo70 family protein C2 [Arabidopsis thaliana]	682	695	0	101.9	84.9	90.3	exocyst complex component 7	gbpln	Arabidopsis thaliana	AT5G13990.1 | Symbols: ATEXO70C2, EXO70C2 | exocyst subunit exo70 family protein C2 | chr5:4514680-4516767 REVERSE LENGTH=695	682	695	0	101.9	84.9	90.3
Rsa1.0_00959.1.g21835.t1	ref|NP_196901.1| uncharacterized protein [Arabidopsis thaliana] gi|10177663|dbj|BAB11125.1| unnamed protein product [Arabidopsis thaliana] gi|19310486|gb|AAL84977.1| AT5g13970/MAC12_6 [Arabidopsis thaliana] gi|28416455|gb|AAO42758.1| At5g13970/MAC12_6 [Arabidopsis thaliana] gi|332004584|gb|AED91967.1| uncharacterized protein AT5G13970 [Arabidopsis thaliana]	387	404	1.00E-121	104.4	68.2	81.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G13970.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13310.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4506383-4507804 REVERSE LENGTH=404	387	404	1.00E-124	104.4	68.2	81.9

Rsa1.0_00959.1_g21836.t1	gb|EOA19908.1| hypothetical protein CARUB_v10000158mg [Capsella rubella]	906	946	0	104.4	74.8	84.5	hypothetical protein CARUB_v10000158mg	gbpln	Capsella rubella	AT5G13950.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02290.1); Has 147 Blast hits to 145 proteins in 44 species: Archae - 0; Bacteria - 2; Metazoa - 56; Fungi - 6; Plants - 81; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr5:4496196-4500206 REVERSE LENGTH=939	906	939	0	103.6	74.9	82.8
Rsa1.0_00959.1_g21837.t1	gb|ABO21005.1| chalcone synthase [Brassica rapa subsp. chinensis] gi|148610280|gb|ABQ95959.1| chalcone synthase [Brassica rapa var. purpuraria] gi|148610294|gb|ABQ95966.1| chalcone synthase [Brassica rapa subsp. rapa]	395	395	0	100.0	98.7	99.0	chalcone synthase	gbpln	Brassica rapa	AT5G13930.1 | Symbols: CHS, TT4, ATCHS | Chalcone and stilbene synthase family protein | chr5:4488762-4490035 FORWARD LENGTH=395	395	395	0	100.0	95.7	97.2
Rsa1.0_00959.1_g21838.t2	gb|EOA33077.1| hypothetical protein CARUB_v10016414mg, partial [Capsella rubella]	78	531	1.00E-27	680.8	75.6	76.9	hypothetical protein CARUB_v10016414mg, partial	gbpln	Capsella rubella	AT3G16950.2 | Symbols: LPD1, ptlpd1 | lipoamide dehydrogenase 1 | chr3:5786508-5790383 REVERSE LENGTH=623	78	623	5.00E-30	798.7	74.4	76.9
Rsa1.0_00959.1_g21839.t1	gb|EOA21975.1| hypothetical protein CARUB_v10002480mg [Capsella rubella]	328	211	1.00E-67	64.3	48.5	50.3	hypothetical protein CARUB_v10002480mg	gbpln	Capsella rubella	AT5G13910.1 | Symbols: LEP | Integrase-type DNA-binding superfamily protein | chr5:4482450-4483085 REVERSE LENGTH=211	328	211	2.00E-68	64.3	47.9	50.3
Rsa1.0_00959.1_g21840.t1	ref|NP_196893.1| uncharacterized protein [Arabidopsis thaliana] gi|30684647|ref|NP_850816.1| uncharacterized protein [Arabidopsis thaliana] gi|30684651|ref|NP_850817.1| uncharacterized protein [Arabidopsis thaliana] gi|10177655|dbj|BAB11117.1| unnamed protein product [Arabidopsis thaliana] gi|51968634|dbj|BAD43009.1| unknown protein [Arabidopsis thaliana] gi|108385354|gb|ABF85775.1| At5g13890 [Arabidopsis thaliana] gi|332004571|gb|AED91954.1| uncharacterized protein AT5G13890 [Arabidopsis thaliana] gi|332004572|gb|AED91955.1| uncharacterized protein AT5G13890 [Arabidopsis thaliana] gi|332004573|gb|AED91956.1| uncharacterized protein AT5G13890 [Arabidopsis thaliana]	304	310	1.00E-124	102.0	88.5	93.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G13890.3 | Symbols: | Family of unknown function (DUF716) | chr5:4479940-4480872 REVERSE LENGTH=310	304	310	1.00E-127	102.0	88.5	93.8
Rsa1.0_00959.1_g21841.t1	gb|EOA22297.1| hypothetical protein CARUB_v10002898mg [Capsella rubella]	174	188	5.00E-63	108.0	79.3	86.2	hypothetical protein CARUB_v10002898mg	gbpln	Capsella rubella	AT5G13880.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G47920.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4477477-4478043 REVERSE LENGTH=188	174	188	2.00E-62	108.0	75.9	84.5
Rsa1.0_00959.1_g21842.t1	gb|EOA21255.1| hypothetical protein CARUB_v10001606mg [Capsella rubella] gi|482557064|gb|EOA21256.1| hypothetical protein CARUB_v10001606mg [Capsella rubella]	294	293	1.00E-165	99.7	94.9	96.3	hypothetical protein CARUB_v10001606mg	gbpln	Capsella rubella	AT5G13870.1 | Symbols: EXGT-A4, XTH5 | xyloglucan endotransglucosylase/hydrolase 5 | chr5:4475089-4476217 REVERSE LENGTH=293	294	293	1.00E-167	99.7	93.9	96.3
Rsa1.0_00959.1_g21843.t1	gb|EOA21404.1| hypothetical protein CARUB_v10001777mg [Capsella rubella]	374	255	3.00E-87	68.2	44.7	47.6	hypothetical protein CARUB_v10001777mg	gbpln	Capsella rubella	AT5G13830.1 | Symbols: | FtsJ-like methyltransferase family protein | chr5:4467363-4468487 FORWARD LENGTH=224	374	224	1.00E-88	59.9	43.9	46.8
Rsa1.0_00959.1_g21844.t1	ref|XP_002873629.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319466|gb|EFH49888.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	132	124	2.00E-20	93.9	43.9	59.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G13825.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4465099-4465969 REVERSE LENGTH=124	132	124	2.00E-22	93.9	42.4	60.6

Rsa1.0_00959.1.g21845.t1	ref|NP_196886.1| Telomere repeat-binding protein 4 [Arabidopsis thaliana] gi|75333778|sp|Q9FFY9.1|TRP4_ARATH RecName: Full=Telomere repeat-binding protein 4; AltName: Full=H-protein promoter binding factor-1; Short=AtTBP1; AltName: Full=Telomeric DNA-binding protein 1 gi|10177648|dbj|BAB11110.1| H-protein promoter binding factor-1 [Arabidopsis thaliana] gi|13641340|gb|AAK31590.1| telomeric DNA-binding protein 1 [Arabidopsis thaliana] gi|209529761|gb|ACI49775.1| At5g13820 [Arabidopsis thaliana] gi|332004562|gb|AED91945.1| Telomere repeat-binding protein 4 [Arabidopsis thaliana]	591	640	0	108.3	70.6	77.8	Telomere repeat-binding protein 4	gbpln	Arabidopsis thaliana	AT5G13820.1 | Symbols: TBP1, ATBP-1, ATBP1, ATTBP1, HPPBF-1 | telomeric DNA binding protein 1 | chr5:4461694-4464355 FORWARD LENGTH=640	591	640	0	108.3	70.6	77.8
Rsa1.0_00959.1.g21846.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	378	1274	2.00E-50	337.0	31.5	51.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	378	303	1.00E-46	80.2	28.3	41.3
Rsa1.0_00960.1.g21847.t1	ref|NP_174673.3| leucine-rich receptor-like protein kinase [Arabidopsis thaliana] gi|263549150|sp|C0LGF5.2|Y1341_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g34110; Flags: Precursor gi|332193550|gb|AEE31671.1| leucine-rich receptor-like protein kinase [Arabidopsis thaliana]	1105	1072	0	97.0	87.1	91.7	leucine-rich receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT1G34110.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr1:12417331-12421246 REVERSE LENGTH=1072	1105	1072	0	97.0	87.1	91.7
Rsa1.0_00960.1.g21848.t1	gb|EOA21645.1| hypothetical protein CARUB_v10002063mg, partial [Capsella rubella]	152	183	7.00E-83	120.4	98.0	99.3	hypothetical protein CARUB_v10002063mg, partial	gbpln	Capsella rubella	AT4G09800.1 | Symbols: RPS18C | S18 ribosomal protein | chr4:6173818-6174963 FORWARD LENGTH=152	152	152	2.00E-85	100.0	98.7	100.0
Rsa1.0_00960.1.g21849.t1	ref|XP_002891071.1| hypothetical protein ARALYDRAFT_473556 [Arabidopsis lyrata subsp. lyrata] gi|297336913|gb|EFH67330.1| hypothetical protein ARALYDRAFT_473556 [Arabidopsis lyrata subsp. lyrata]	346	335	1.00E-140	96.8	80.3	85.3	hypothetical protein ARALYDRAFT_473556	gbpln	Arabidopsis lyrata	AT1G34020.1 | Symbols: | Nucleotide-sugar transporter family protein | chr1:12367359-12368965 FORWARD LENGTH=335	346	335	1.00E-142	96.8	80.1	85.3
Rsa1.0_00960.1.g21850.t1	dbj|BAJ33748.1| unnamed protein product [Thellungiella halophila]	402	177	2.00E-54	44.0	31.3	32.8	unnamed protein product	----	----	AT1G34000.1 | Symbols: OHP2 | one-helix protein 2 | chr1:12358151-12358902 REVERSE LENGTH=172	402	172	5.00E-56	42.8	32.1	33.1
Rsa1.0_00960.1.g21851.t1	ref|XP_002891069.1| ATUPF3/UPF3 [Arabidopsis lyrata subsp. lyrata] gi|297336911|gb|EFH67328.1| ATUPF3/UPF3 [Arabidopsis lyrata subsp. lyrata]	487	486	0	99.8	77.4	83.6	ATUPF3/UPF3	gbpln	Arabidopsis lyrata	AT1G33980.1 | Symbols: ATUPF3, UPF3 | Smg-4/UPF3 family protein | chr1:12351719-12354401 FORWARD LENGTH=482	487	482	0	99.0	76.6	83.8
Rsa1.0_00960.1.g21852.t1	dbj|BAJ34639.1| unnamed protein product [Thellungiella halophila]	343	343	1.00E-160	100.0	84.3	93.6	unnamed protein product	----	----	AT1G33970.5 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:12349614-12350960 REVERSE LENGTH=342	343	342	1.00E-157	99.7	82.2	92.7
Rsa1.0_00960.1.g21853.t1	ref|NP_564430.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75153901|sp|Q8L5Z1.1|GDL17_ARATH RecName: Full=GDSL esterase/lipase At1g33811; AltName: Full=Extracellular lipase At1g33811; Flags: Precursor gi|20466732|gb|AAM20683.1| unknown protein [Arabidopsis thaliana] gi|23198228|gb|AAN15641.1| unknown protein [Arabidopsis thaliana] gi|332193507|gb|AEE31628.1| GDSL esterase/lipase [Arabidopsis thaliana]	370	370	0	100.0	90.0	94.6	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT1G33811.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:12267918-12269690 FORWARD LENGTH=370	370	370	0	100.0	90.0	94.6
Rsa1.0_00960.1.g21854.t1	emb|CAA31653.1| polyprotein [Arabidopsis thaliana]	700	1291	0	184.4	52.9	71.4	polyprotein	gbpln	Arabidopsis thaliana	ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145	700	145	7.00E-21	20.7	7.3	10.1
Rsa1.0_00960.1.g21855.t1	gb|EOA36221.1| hypothetical protein CARUB_v10010170mg [Capsella rubella]	234	236	1.00E-110	100.9	84.2	91.0	hypothetical protein CARUB_v10010170mg	gbpln	Capsella rubella	AT1G24735.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:8757977-8759448 FORWARD LENGTH=240	234	240	1.00E-106	102.6	76.9	87.2

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<tr><td>Rsa1.0_00960.1.g21856.t1</td><td>ref|NP_176973.1| microtubule-associated proteins 70-1 [Arabidopsis thaliana] gi|75169797|sp|Q9C9X0.1|MP701_ARATH RecName: Full=Microtubule-associated protein 70-1; Short=AtMAP70-1; AltName: Full=70 kDa microtubule-associated protein 1 gi|12324091|gb|AAG52019.1|AC012563_29 unknown protein; 30164-32998 [Arabidopsis thaliana] gi|18377700|gb|AAL67000.1| unknown protein [Arabidopsis thaliana] gi|20465647|gb|AAM20292.1| unknown protein [Arabidopsis thaliana] gi|76058012|emb|CAJ31078.1| 70 kDa microtubule associated protein Type 1 [Arabidopsis thaliana] gi|332196621|gb|AEE34742.1| microtubule-associated proteins 70-1 [Arabidopsis thaliana]</td><td>75</td><td>622</td><td>5.00E-27</td><td>829.3</td><td>84.0</td><td>92.0</td><td>microtubule-associated proteins 70-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68060.1 | Symbols: ATMAP70-1, MAP70-1 | microtubule-associated proteins 70-1 | chr1:25511392-25514226 REVERSE LENGTH=622</td><td>75</td><td>622</td><td>8.00E-30</td><td>829.3</td><td>84.0</td><td>92.0</td></tr>
<tr><td>Rsa1.0_00960.1.g21857.t5</td><td>gb|EOA38356.1| hypothetical protein CARUB_v10009876mg [Capsella rubella]</td><td>295</td><td>299</td><td>1.00E-152</td><td>101.4</td><td>92.9</td><td>95.6</td><td>hypothetical protein CARUB_v10009876mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G33800.1 | Symbols: | Protein of unknown function (DUF579) | chr1:12261480-12262456 FORWARD LENGTH=297</td><td>295</td><td>297</td><td>1.00E-149</td><td>100.7</td><td>91.2</td><td>95.6</td></tr>
<tr><td>Rsa1.0_00960.1.g21858.t1</td><td>gb|EOA39920.1| hypothetical protein CARUB_v10008607mg [Capsella rubella]</td><td>633</td><td>616</td><td>0</td><td>97.3</td><td>86.3</td><td>91.8</td><td>hypothetical protein CARUB_v10008607mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G33770.1 | Symbols: | Protein kinase superfamily protein | chr1:12242126-12244462 FORWARD LENGTH=614</td><td>633</td><td>614</td><td>0</td><td>97.0</td><td>86.9</td><td>91.2</td></tr>
<tr><td>Rsa1.0_00961.1.g21859.t1</td><td>gb|EOA20271.1| hypothetical protein CARUB_v10000575mg [Capsella rubella]</td><td>569</td><td>574</td><td>0</td><td>100.9</td><td>84.4</td><td>92.3</td><td>hypothetical protein CARUB_v10000575mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G13320.1 | Symbols: PBS3, GDG1, WIN3, GH3.12 | Auxin-responsive GH3 family protein | chr5:4268902-4270896 FORWARD LENGTH=575</td><td>569</td><td>575</td><td>0</td><td>101.1</td><td>83.8</td><td>91.7</td></tr>
<tr><td>Rsa1.0_00961.1.g21860.t1</td><td>ref|NP_196835.1| uncharacterized protein [Arabidopsis thaliana] gi|7529286|emb|CAB86638.1| putative protein [Arabidopsis thaliana] gi|21593209|gb|AAM65158.1| unknown [Arabidopsis thaliana] gi|28393126|gb|AAO41996.1| unknown protein [Arabidopsis thaliana] gi|28827470|gb|AAO50579.1| unknown protein [Arabidopsis thaliana] gi|332004496|gb|AED91879.1| uncharacterized protein AT5G13310 [Arabidopsis thaliana]</td><td>383</td><td>370</td><td>1.00E-111</td><td>96.6</td><td>64.5</td><td>77.0</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G13310.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13970.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:4263561-4264989 FORWARD LENGTH=370</td><td>383</td><td>370</td><td>1.00E-113</td><td>96.6</td><td>64.5</td><td>77.0</td></tr>
<tr><td>Rsa1.0_00961.1.g21861.t2</td><td>ref|XP_002873607.1| hypothetical protein ARALYDRAFT_488148 [Arabidopsis lyrata subsp. lyrata] gi|297319444|gb|EFH49866.1| hypothetical protein ARALYDRAFT_488148 [Arabidopsis lyrata subsp. lyrata]</td><td>844</td><td>828</td><td>0</td><td>98.1</td><td>91.9</td><td>95.1</td><td>hypothetical protein ARALYDRAFT_488148</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G13300.1 | Symbols: SFC, VAN3, AGD3 | ARF GTPase-activating protein | chr5:4255923-4262018 REVERSE LENGTH=827</td><td>844</td><td>827</td><td>0</td><td>98.0</td><td>91.0</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00961.1.g21862.t1</td><td>ref|XP_002873606.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319443|gb|EFH49865.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>393</td><td>402</td><td>0</td><td>102.3</td><td>85.2</td><td>88.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G13290.2 | Symbols: SOL2, CRN | Protein kinase superfamily protein | chr5:4252924-4254215 REVERSE LENGTH=401</td><td>393</td><td>401</td><td>0</td><td>102.0</td><td>84.7</td><td>88.8</td></tr>
<tr><td>Rsa1.0_00961.1.g21863.t1</td><td>ref|XP_002871558.1| AK-LYS1 [Arabidopsis lyrata subsp. lyrata] gi|297317395|gb|EFH47817.1| AK-LYS1 [Arabidopsis lyrata subsp. lyrata]</td><td>549</td><td>570</td><td>0</td><td>103.8</td><td>89.1</td><td>93.6</td><td>AK-LYS1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G13280.1 | Symbols: AK-LYS1, AK1, AK | aspartate kinase 1 | chr5:4249516-4252654 FORWARD LENGTH=569</td><td>549</td><td>569</td><td>0</td><td>103.6</td><td>88.5</td><td>93.1</td></tr>
<tr><td>Rsa1.0_00961.1.g21864.t1</td><td>ref|XP_002873605.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319442|gb|EFH49864.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>752</td><td>750</td><td>0</td><td>99.7</td><td>88.0</td><td>93.8</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G13270.1 | Symbols: RARE1 | Pentatricopeptide repeat (PPR) superfamily protein | chr5:4246954-4249212 REVERSE LENGTH=752</td><td>752</td><td>752</td><td>0</td><td>100.0</td><td>87.2</td><td>92.8</td></tr>
<tr><td>Rsa1.0_00961.1.g21865.t1</td><td>gb|EOA19674.1| hypothetical protein CARUB_v10003326mg [Capsella rubella]</td><td>542</td><td>542</td><td>0</td><td>100.0</td><td>87.8</td><td>93.0</td><td>hypothetical protein CARUB_v10003326mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G13260.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48860.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4243164-4246677 FORWARD LENGTH=537</td><td>542</td><td>537</td><td>0</td><td>99.1</td><td>85.1</td><td>89.7</td></tr>
<tr><td>Rsa1.0_00961.1.g21866.t1</td><td>gb|EOA22755.1| hypothetical protein CARUB_v10003467mg, partial [Capsella rubella]</td><td>321</td><td>325</td><td>1.00E-124</td><td>101.2</td><td>76.0</td><td>82.6</td><td>hypothetical protein CARUB_v10003467mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G13250.1 | Symbols: | RING finger protein | chr5:4234486-4241615 FORWARD LENGTH=387</td><td>321</td><td>387</td><td>1.00E-119</td><td>120.6</td><td>76.0</td><td>81.9</td></tr>
</table>

Rsa1.0_00961.1.g21867.t1	gb|EOA21464.1| hypothetical protein CARUB_v10001854mg [Capsella rubella]	224	237	1.00E-123	105.8	95.5	97.3	hypothetical protein CARUB_v10001854mg	gbpln	Capsella rubella	AT5G13240.1 | Symbols: | transcription regulators | chr5:4225261-4227152 REVERSE LENGTH=224	224	224	1.00E-123	100.0	93.8	96.4
Rsa1.0_00961.1.g21868.t1	ref|XP_002871555.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317392|gb|EFH47814.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	820	822	0	100.2	81.7	89.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G13230.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:4222514-4224982 FORWARD LENGTH=822	820	822	0	100.2	81.7	89.1
Rsa1.0_00961.1.g21869.t1	ref|XP_002871554.1| hypothetical protein ARALYDRAFT_488138 [Arabidopsis lyrata subsp. lyrata] gi|297317391|gb|EFH47813.1| hypothetical protein ARALYDRAFT_488138 [Arabidopsis lyrata subsp. lyrata]	196	198	1.00E-83	101.0	81.1	88.8	hypothetical protein ARALYDRAFT_488138	gbpln	Arabidopsis lyrata	AT5G13220.1 | Symbols: JAZ10, TIFY9, JAS1 | jasmonate-zim-domain protein 10 | chr5:4219001-4220502 FORWARD LENGTH=197	196	197	7.00E-85	100.5	80.1	86.7
Rsa1.0_00961.1.g21870.t1	ref|XP_002871553.1| hypothetical protein ARALYDRAFT_488135 [Arabidopsis lyrata subsp. lyrata] gi|297317390|gb|EFH47812.1| hypothetical protein ARALYDRAFT_488135 [Arabidopsis lyrata subsp. lyrata]	639	668	0	104.5	76.7	87.8	hypothetical protein ARALYDRAFT_488135	gbpln	Arabidopsis lyrata	AT5G13210.1 | Symbols: | Uncharacterised conserved protein UCP015417, vWA | chr5:4214567-4216588 FORWARD LENGTH=673	639	673	0	105.3	74.6	85.8
Rsa1.0_00962.1.g21871.t1	ref|XP_004253404.1| PREDICTED: uncharacterized protein LOC101249447, partial [Solanum lycopersicum]	1175	485	1.00E-45	41.3	10.2	11.5	PREDICTED: uncharacterized protein LOC101249447, partial	gbpln	Solanum lycopersicum	#	#	#	#	#	#	#
Rsa1.0_00962.1.g21872.t1	ref|NP_850386.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|30689274|ref|NP_850387.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|42571203|ref|NP_973675.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|75116590|sp|Q67YI9.1|EPN2_ARATH RecName: Full=Clathrin interactor EPSIN 2; AltName: Full=EPSIN-related 2 gi|51970954|dbj|BAD44169.1| unknown protein [Arabidopsis thaliana] gi|51971100|dbj|BAD44242.1| unknown protein [Arabidopsis thaliana] gi|62319865|dbj|BAD93910.1| hypothetical protein [Arabidopsis thaliana] gi|62319867|dbj|BAD93914.1| hypothetical protein [Arabidopsis thaliana] gi|110740368|dbj|BAF02079.1| hypothetical protein [Arabidopsis thaliana] gi|330255122|gb|AEC10216.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|330255123|gb|AEC10217.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|330255124|gb|AEC10218.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana]	1007	895	0	88.9	75.5	78.9	clathrin interactor EPSIN 2	gbpln	Arabidopsis thaliana	AT2G43160.1 | Symbols: | ENTH/VHS family protein | chr2:17948884-17953267 FORWARD LENGTH=895	1007	895	0	88.9	75.5	78.9
Rsa1.0_00962.1.g21873.t1	ref|XP_002880031.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325870|gb|EFH56290.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	793	531	0	67.0	46.9	52.2	UBX domain-containing protein	gbpln	Arabidopsis lyrata	AT2G43210.2 | Symbols: | Ubiquitin-like superfamily protein | chr2:17960942-17963560 FORWARD LENGTH=531	793	531	0	67.0	46.0	51.6
Rsa1.0_00962.1.g21874.t1	ref|NP_181851.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|3763931|gb|AAC64311.1| hypothetical protein [Arabidopsis thaliana] gi|61742677|gb|AAX55159.1| hypothetical protein At2g43220 [Arabidopsis thaliana] gi|330255137|gb|AEC10231.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	544	538	0	98.9	62.5	74.6	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G43220.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:17964340-17965956 FORWARD LENGTH=538	544	538	0	98.9	62.5	74.6
Rsa1.0_00962.1.g21875.t1	ref|XP_002880033.1| hypothetical protein ARALYDRAFT_483429 [Arabidopsis lyrata subsp. lyrata] gi|297325872|gb|EFH56292.1| hypothetical protein ARALYDRAFT_483429 [Arabidopsis lyrata subsp. lyrata]	410	406	0	99.0	89.3	93.9	hypothetical protein ARALYDRAFT_483429	gbpln	Arabidopsis lyrata	AT2G43230.1 | Symbols: | Protein kinase superfamily protein | chr2:17966475-17968446 FORWARD LENGTH=406	410	406	0	99.0	89.3	93.7

Rsa1.0_00962.1.g21876.t1	ref|NP_181853.3| nucleotide-sugar transporter [Arabidopsis thaliana] gi|75151390|sp|Q8GY97.1|CSTR2_ARATH RecName: Full=CMP-sialic acid transporter 2; Short=CMP-SA-Tr 2; Short=CMP-Sia-Tr 2 gi|26450627|dbj|BAC42425.1| unknown protein [Arabidopsis thaliana] gi|51971655|dbj|BAD44492.1| unnamed protein product [Arabidopsis thaliana] gi|330255141|gb|AEC10235.1| nucleotide-sugar transporter [Arabidopsis thaliana]	439	406	0	92.5	86.3	89.1	nucleotide-sugar transporter	gbpln	Arabidopsis thaliana	AT2G43240.1 | Symbols: | Nucleotide-sugar transporter family protein | chr2:17971280-17975300 REVERSE LENGTH=406	439	406	0	92.5	86.3	89.1
Rsa1.0_00962.1.g21877.t1	ref|XP_002880034.1| hypothetical protein ARALYDRAFT_483433 [Arabidopsis lyrata subsp. lyrata] gi|297325873|gb|EFH56293.1| hypothetical protein ARALYDRAFT_483433 [Arabidopsis lyrata subsp. lyrata]	619	625	0	101.0	80.9	89.8	hypothetical protein ARALYDRAFT_483433	gbpln	Arabidopsis lyrata	AT2G43250.1 | Symbols: | unknown protein; Has 32 Blast hits to 32 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17977619-17979496 FORWARD LENGTH=625	619	625	0	101.0	80.1	89.5
Rsa1.0_00962.1.g21878.t1	ref|NP_181857.2| far-red impaired responsive 1-like protein [Arabidopsis thaliana] gi|27754520|gb|AAO22707.1| unknown protein [Arabidopsis thaliana] gi|28393991|gb|AAO42403.1| unknown protein [Arabidopsis thaliana] gi|330255153|gb|AEC10247.1| far-red impaired responsive 1-like protein [Arabidopsis thaliana]	198	206	7.00E-88	104.0	80.3	87.9	far-red impaired responsive 1-like protein	gbpln	Arabidopsis thaliana	AT2G43280.1 | Symbols: | Far-red impaired responsive (FAR1) family protein | chr2:17989739-17990861 FORWARD LENGTH=206	198	206	3.00E-90	104.0	80.3	87.9
Rsa1.0_00962.1.g21879.t1	ref|NP_565996.1| calmodulin-like protein 5 [Arabidopsis thaliana] gi|75318037|sp|O22845.2|CML5_ARATH RecName: Full=Calmodulin-like protein 5; AltName: Full=Protein MULTICOPY SUPPRESSORS OF SNF4 DEFICIENCY IN YEAST 3 gi|9965747|gb|AAG10150.1|AF250344_1 calmodulin-like MSS3 [Arabidopsis thaliana] gi|17065478|gb|AAL32893.1| putative Ca2+-binding protein [Arabidopsis thaliana] gi|20148491|gb|AAM10136.1| putative Ca2+-binding protein [Arabidopsis thaliana] gi|20196862|gb|AAB64310.2| putative calcium binding protein [Arabidopsis thaliana] gi|20197147|gb|AAM14938.1| putative calcium binding protein [Arabidopsis thaliana] gi|21592699|gb|AAM64648.1| putative calcium binding protein [Arabidopsis thaliana] gi|330255154|gb|AEC10248.1| calmodulin-like protein 5 [Arabidopsis thaliana]	171	215	5.00E-80	125.7	86.0	87.7	calmodulin-like protein 5	gbpln	Arabidopsis thaliana	AT2G43290.1 | Symbols: MSS3 | Calcium-binding EF-hand family protein | chr2:17991308-17991955 REVERSE LENGTH=215	171	215	2.00E-82	125.7	86.0	87.7
Rsa1.0_00962.1.g21880.t1	ref|XP_002876435.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322273|gb|EFH52694.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	398	358	4.00E-69	89.9	35.2	44.0	kinase family protein	gbpln	Arabidopsis lyrata	AT3G57740.1 | Symbols: | Protein kinase superfamily protein | chr3:21392671-21393744 FORWARD LENGTH=357	398	357	6.00E-71	89.7	34.7	44.2
Rsa1.0_00962.1.g21881.t1	ref|XP_002888869.1| APUM23 [Arabidopsis lyrata subsp. lyrata] gi|297334710|gb|EFH65128.1| APUM23 [Arabidopsis lyrata subsp. lyrata]	80	753	3.00E-25	941.3	75.0	81.3	APUM23	gbpln	Arabidopsis lyrata	AT1G72320.1 | Symbols: APUM23, PUM23 | pumilio 23 | chr1:27228984-27232580 REVERSE LENGTH=753	80	753	6.00E-25	941.3	68.8	77.5
Rsa1.0_00963.1.g21882.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00963.1.g21883.t2	#	#	#	#	#	#	#	-	----	----	AT2G04115.1 | Symbols: | Plant self-incompatibility protein S1 family | chr2:1385449-1385904 FORWARD LENGTH=151	336	151	2.00E-12	44.9	10.4	16.1
Rsa1.0_00963.1.g21884.t1	ref|NP_178040.5| uncharacterized protein [Arabidopsis thaliana] gi|332198092|gb|AEE36213.1| uncharacterized protein AT1G79190 [Arabidopsis thaliana]	1299	1335	0	102.8	84.4	90.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G79190.1 | Symbols: | ARM repeat superfamily protein | chr1:29788639-29794116 FORWARD LENGTH=1335	1299	1335	0	102.8	84.4	90.9

Rsa1.0_00963.1.g21885.t1	ref|NP_173096.1| proteasome subunit alpha type-2-A [Arabidopsis thaliana] gi|79318062|ref|NP_001031057.1| proteasome subunit alpha type-2-A [Arabidopsis thaliana] gi|6093778|sp|O23708.1|PSA2A_ARATH RecName: Full=Proteasome subunit alpha type-2-A; AltName: Full=20S proteasome alpha subunit B; AltName: Full=Proteasome component 3 gi|4966368|gb|AAD34699.1|AC006341_27 Identical to gb|Y13176 Arabidopsis thaliana mRNA for proteasome subunit prc3. ESTs gb|H36972, gb|T22551 and gb|T13800 come from this gene [Arabidopsis thaliana] gi|12083342|gb|AAG48830.1|AF332467_1 putative multicatalytic endopeptidase [Arabidopsis thaliana] gi|2511574|emb|CAA73619.1| multicatalytic endopeptidase [Arabidopsis thaliana] gi|3421075|gb|AAC32056.1| 20S proteasome subunit PAB1 [Arabidopsis thaliana] gi|21617900|gb|AAM66950.1| multicatalytic endopeptidase [Arabidopsis thaliana] gi|222423615|dbj|BAH19776.1| AT1G16470 [Arabidopsis thaliana] gi|222424243|dbj|BAH20079.1| AT1G16470 [Arabidopsis thaliana] gi|332191336|gb|AEE29457.1| proteasome subunit alpha type-2-A [Arabidopsis thaliana]	235	235	1.00E-133	100.0	100.0	100.0	proteasome subunit alpha type-2-A	gbpln	Arabidopsis thaliana	AT1G16470.2 | Symbols: PAB1 | proteasome subunit PAB1 | chr1:5623122-5625439 FORWARD LENGTH=235	235	235	1.00E-136	100.0	100.0	100.0
Rsa1.0_00963.1.g21886.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00963.1.g21887.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00963.1.g21888.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00963.1.g21889.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00963.1.g21890.t1	ref|XP_002889239.1| hypothetical protein ARALYDRAFT_316818 [Arabidopsis lyrata subsp. lyrata] gi|297335080|gb|EFH65498.1| hypothetical protein ARALYDRAFT_316818 [Arabidopsis lyrata subsp. lyrata]	640	558	0	87.2	67.2	71.1	hypothetical protein ARALYDRAFT_316818	gbpln	Arabidopsis lyrata	AT1G79250.2 | Symbols: AGC1.7 | AGC kinase 1.7 | chr1:29810336-29812186 REVERSE LENGTH=555	640	555	0	86.7	67.2	70.5
Rsa1.0_00963.1.g21891.t1	gb|EOA35837.1| hypothetical protein CARUB_v10021078mg [Capsella rubella]	158	159	5.00E-76	100.6	86.7	93.0	hypothetical protein CARUB_v10021078mg	gbpln	Capsella rubella	AT1G79260.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Domain of unknown function DUF1794 (InterPro:IPR014878); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:29813282-29814066 FORWARD LENGTH=166	158	166	5.00E-78	105.1	86.7	92.4
Rsa1.0_00963.1.g21892.t3	ref|XP_002887776.1| evolutionarily conserved C-terminal region 8 [Arabidopsis lyrata subsp. lyrata] gi|297333617|gb|EFH64035.1| evolutionarily conserved C-terminal region 8 [Arabidopsis lyrata subsp. lyrata]	628	522	0	83.1	62.1	67.2	evolutionarily conserved C-terminal region 8	gbpln	Arabidopsis lyrata	AT1G79270.1 | Symbols: ECT8 | evolutionarily conserved C-terminal region 8 | chr1:29816157-29818811 FORWARD LENGTH=528	628	528	0	84.1	61.3	66.9
Rsa1.0_00963.1.g21893.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00964.1.g21894.t1	gb|EOA20957.1| hypothetical protein CARUB_v10001289mg [Capsella rubella]	327	353	6.00E-87	108.0	54.1	66.4	hypothetical protein CARUB_v10001289mg	gbpln	Capsella rubella	AT5G24180.1 | Symbols: | Lipase class 3-related protein | chr5:8195600-8197119 FORWARD LENGTH=375	327	375	4.00E-89	114.7	52.6	68.5
Rsa1.0_00964.1.g21895.t1	ref|NP_197811.2| lipase class 3-related protein [Arabidopsis thaliana] gi|26453202|dbj|BAC43675.1| unknown protein [Arabidopsis thaliana] gi|28950935|gb|AAO63391.1| At5g24230 [Arabidopsis thaliana] gi|332005890|gb|AED93273.1| lipase class 3-related protein [Arabidopsis thaliana]	365	369	1.00E-179	101.1	86.8	92.3	lipase class 3-related protein	gbpln	Arabidopsis thaliana	AT5G24230.1 | Symbols: | Lipase class 3-related protein | chr5:8229182-8230841 FORWARD LENGTH=369	365	369	0	101.1	86.8	92.3

Rsa1.0_00964.1.g21896.t1	ref|NP_197812.1| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana] gi|10177083|dbj|BAB10389.1| ubiquitin [Arabidopsis thaliana] gi|110741569|dbj|BAE98733.1| ubiquitin [Arabidopsis thaliana] gi|332005891|gb|AED93274.1| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana]	575	574	0	99.8	83.8	90.6	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	gbpln	Arabidopsis thaliana	AT5G24240.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase ;Ubiquitin family protein | chr5:8231110-8232925 REVERSE LENGTH=574	575	574	0	99.8	83.8	90.6
Rsa1.0_00964.1.g21897.t1	emb|CCH26608.1| salt overly sensitive 3 [Arabidopsis thaliana] gi|469401053|emb|CCH26609.1| salt overly sensitive 3 [Arabidopsis thaliana] gi|469401071|emb|CCH26612.1| salt overly sensitive 3 [Arabidopsis thaliana]	221	222	1.00E-113	100.5	91.4	96.8	salt overly sensitive 3	gbpln	Arabidopsis thaliana	AT5G24270.2 | Symbols: SOS3 | Calcium-binding EF-hand family protein | chr5:8238781-8240179 REVERSE LENGTH=222	221	222	1.00E-116	100.5	91.0	96.8
Rsa1.0_00964.1.g21898.t2	gb|EOA19783.1| hypothetical protein CARUB_v10000029mg [Capsella rubella]	1562	1588	0	101.7	70.6	82.5	hypothetical protein CARUB_v10000029mg	gbpln	Capsella rubella	AT5G24280.1 | Symbols: GMI1 | gamma-irradiation and mitomycin c induced 1 | chr5:8251378-8261401 REVERSE LENGTH=1598	1562	1598	0	102.3	65.5	79.2
Rsa1.0_00964.1.g21899.t1	gb|EOA19247.1| hypothetical protein CARUB_v10000030mg [Capsella rubella]	1574	1570	0	99.7	71.2	82.3	hypothetical protein CARUB_v10000030mg	gbpln	Capsella rubella	AT5G24280.1 | Symbols: GMI1 | gamma-irradiation and mitomycin c induced 1 | chr5:8251378-8261401 REVERSE LENGTH=1598	1574	1598	0	101.5	71.6	83.4
Rsa1.0_00964.1.g21900.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	454	530	7.00E-38	116.7	18.1	24.9	predicted protein	gbpln	Arabidopsis lyrata	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	454	530	1.00E-11	116.7	8.4	15.6
Rsa1.0_00964.1.g21901.t1	gb|AAM62487.1| unknown [Arabidopsis thaliana]	70	70	3.00E-22	100.0	85.7	90.0	unknown	gbpln	Arabidopsis thaliana	AT5G24570.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:8405814-8406026 REVERSE LENGTH=70	70	70	2.00E-24	100.0	84.3	88.6
Rsa1.0_00964.1.g21902.t1	ref|NP_568449.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|10177858|dbj|BAB11210.1| unnamed protein product [Arabidopsis thaliana] gi|18175601|gb|AAL59894.1| unknown protein [Arabidopsis thaliana] gi|22136850|gb|AAM91769.1| unknown protein [Arabidopsis thaliana] gi|332005944|gb|AED93327.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana]	307	319	1.00E-109	103.9	80.1	85.0	heavy metal transport/detoxification domain-containing protein	gbpln	Arabidopsis thaliana	AT5G24580.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:8410394-8412087 REVERSE LENGTH=319	307	319	1.00E-112	103.9	80.1	85.0
Rsa1.0_00964.1.g21903.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00964.1.g21904.t1	ref|XP_002874210.1| tip [Arabidopsis lyrata subsp. lyrata] gi|297320047|gb|EFH50469.1| tip [Arabidopsis lyrata subsp. lyrata]	433	461	1.00E-150	106.5	67.9	77.1	tip	gbpln	Arabidopsis lyrata	AT5G24590.2 | Symbols: ANAC091, TIP | TCV-interacting protein | chr5:8416920-8418723 REVERSE LENGTH=451	433	451	1.00E-139	104.2	65.8	74.8
Rsa1.0_00964.1.g21905.t1	ref|NP_197848.1| uncharacterized protein [Arabidopsis thaliana] gi|10177860|dbj|BAB11212.1| unnamed protein product [Arabidopsis thaliana] gi|48310199|gb|AAT41773.1| At5g24600 [Arabidopsis thaliana] gi|50198891|gb|AAT70465.1| At5g24600 [Arabidopsis thaliana] gi|332005949|gb|AED93332.1| uncharacterized protein AT5G24600 [Arabidopsis thaliana]	248	248	1.00E-130	100.0	92.3	94.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G24600.1 | Symbols: | Protein of unknown function, DUF599 | chr5:8421790-8423342 REVERSE LENGTH=248	248	248	1.00E-133	100.0	92.3	94.8
Rsa1.0_00964.1.g21906.t1	gb|EOA21962.1| hypothetical protein CARUB_v10002461mg [Capsella rubella]	189	148	2.00E-62	78.3	65.1	70.4	hypothetical protein CARUB_v10002461mg	gbpln	Capsella rubella	AT5G24610.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G49550.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8428577-8429017 FORWARD LENGTH=146	189	146	3.00E-62	77.2	64.0	68.3

Rsa1.0_00964.1.g21907.t1	ref|NP_197850.2| pathogenesis-related thaumatin-like protein [Arabidopsis thaliana] gi|193788746|gb|ACF20472.1| At5g24620 [Arabidopsis thaliana] gi|332005952|gb|AED93335.1| pathogenesis-related thaumatin-like protein [Arabidopsis thaliana]	405	420	0	103.7	85.4	91.1	pathogenesis-related thaumatin-like protein	gbpln	Arabidopsis thaliana	AT5G24620.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr5:8430918-8432289 FORWARD LENGTH=420	405	420	0	103.7	85.4	91.1
Rsa1.0_00964.1.g21908.t1	ref|NP_001154735.1| DNA-binding protein BIN4 [Arabidopsis thaliana] gi|332005955|gb|AED93338.1| DNA-binding protein BIN4 [Arabidopsis thaliana]	435	432	1.00E-123	99.3	64.8	75.2	DNA-binding protein BIN4	gbpln	Arabidopsis thaliana	AT5G24630.2 | Symbols: BIN4 | double-stranded DNA binding | chr5:8432523-8435682 REVERSE LENGTH=432	435	432	1.00E-125	99.3	64.8	75.2
Rsa1.0_00964.1.g21909.t1	ref|NP_197853.1| Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein [Arabidopsis thaliana] gi|10177865|dbj|BAB11217.1| unnamed protein product [Arabidopsis thaliana] gi|17979479|gb|AAL50076.1| AT5g24650/K18P6_19 [Arabidopsis thaliana] gi|22655440|gb|AAM98312.1| At5g24650/K18P6_19 [Arabidopsis thaliana] gi|89213233|gb|ABD64056.1| At5g24650 [Arabidopsis thaliana] gi|332005961|gb|AED93344.1| Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein [Arabidopsis thaliana]	261	259	1.00E-129	99.2	90.8	95.0	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	gbpln	Arabidopsis thaliana	AT5G24650.1 | Symbols: | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr5:8437123-8438859 FORWARD LENGTH=259	261	259	1.00E-132	99.2	90.8	95.0
Rsa1.0_00964.1.g21910.t1	gb|EOA21866.1| hypothetical protein CARUB_v10002342mg [Capsella rubella]	93	93	6.00E-41	100.0	90.3	96.8	hypothetical protein CARUB_v10002342mg	gbpln	Capsella rubella	AT5G24660.1 | Symbols: LSU2 | response to low sulfur 2 | chr5:8443472-8443756 REVERSE LENGTH=94	93	94	5.00E-42	101.1	90.3	96.8
Rsa1.0_00964.1.g21911.t2	gb|EOA20688.1| hypothetical protein CARUB_v10001002mg, partial [Capsella rubella]	369	433	1.00E-162	117.3	78.6	88.9	hypothetical protein CARUB_v10001002mg, partial	gbpln	Capsella rubella	AT5G24680.1 | Symbols: | Peptidase C78, ubiquitin fold modifier-specific peptidase 1/2 | chr5:8453666-8455358 FORWARD LENGTH=399	369	399	1.00E-164	108.1	82.4	90.2
Rsa1.0_00964.1.g21912.t1	ref|NP_197857.2| uncharacterized protein [Arabidopsis thaliana] gi|13877883|gb|AAK44019.1|AF370204_1 unknown protein [Arabidopsis thaliana] gi|15912313|gb|AAL08290.1| AT5g24690/MXC17_8 [Arabidopsis thaliana] gi|22136914|gb|AAM91801.1| unknown protein [Arabidopsis thaliana] gi|110739396|dbj|BAF01609.1| hypothetical protein [Arabidopsis thaliana] gi|110739479|dbj|BAF01649.1| hypothetical protein [Arabidopsis thaliana] gi|110739599|dbj|BAF01708.1| hypothetical protein [Arabidopsis thaliana] gi|110739615|dbj|BAF01716.1| hypothetical protein [Arabidopsis thaliana] gi|110739722|dbj|BAF01768.1| hypothetical protein [Arabidopsis thaliana] gi|110739756|dbj|BAF01785.1| hypothetical protein [Arabidopsis thaliana] gi|110739958|dbj|BAF01883.1| hypothetical protein [Arabidopsis thaliana] gi|110739966|dbj|BAF01887.1| hypothetical protein [Arabidopsis thaliana] gi|110740027|dbj|BAF01917.1| hypothetical protein [Arabidopsis thaliana] gi|110740029|dbj|BAF01918.1| hypothetical protein [Arabidopsis thaliana] gi|110740431|dbj|BAF02110.1| hypothetical protein [Arabidopsis thaliana] gi|110740452|dbj|BAF02120.1| hypothetical protein [Arabidopsis thaliana] gi|110741324|dbj|BAF02212.1| hypothetical protein [Arabidopsis	529	521	0	98.5	87.1	92.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G24690.1 | Symbols: | Protein of unknown function (DUF3411) | chr5:8455783-8458513 REVERSE LENGTH=521	529	521	0	98.5	87.1	92.1
Rsa1.0_00964.1.g21913.t3	ref|XP_002874217.1| hypothetical protein ARALYDRAFT_489332 [Arabidopsis lyrata subsp. lyrata] gi|297320054|gb|EFH50476.1| hypothetical protein ARALYDRAFT_489332 [Arabidopsis lyrata subsp. lyrata]	1349	1376	0	102.0	90.4	93.8	hypothetical protein ARALYDRAFT_489332	gbpln	Arabidopsis lyrata	AT5G24710.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:8459148-8467920 REVERSE LENGTH=1377	1349	1377	0	102.1	90.8	94.0
Rsa1.0_00964.1.g21914.t17	ref|NP_568451.7| uncharacterized protein [Arabidopsis thaliana] gi|332005969|gb|AED93352.1| uncharacterized protein AT5G24740 [Arabidopsis thaliana]	3787	3464	0	91.5	73.9	80.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G24740.1 | Symbols: | Protein of unknown function (DUF1162) | chr5:8470073-8489703 REVERSE LENGTH=3464	3787	3464	0	91.5	73.9	80.5

Rsa1.0_00964.1.g21915.t1	ref|XP_002872126.1| hypothetical protein ARALYDRAFT_351499 [Arabidopsis lyrata subsp. lyrata] gi|297317963|gb|EFH48385.1| hypothetical protein ARALYDRAFT_351499 [Arabidopsis lyrata subsp. lyrata]	248	247	1.00E-108	99.6	82.3	90.3	hypothetical protein ARALYDRAFT_351499	gbpln	Arabidopsis lyrata	AT5G24790.1 | Symbols: | Protein of unknown function, DUF599 | chr5:8512076-8513064 FORWARD LENGTH=246	248	246	1.00E-111	99.2	82.7	90.7
Rsa1.0_00964.1.g21916.t1	gb|EOA21129.1| hypothetical protein CARUB_v10001471mg [Capsella rubella]	293	320	1.00E-127	109.2	84.0	88.4	hypothetical protein CARUB_v10001471mg	gbpln	Capsella rubella	AT5G24800.1 | Symbols: ATBZIP9, BZO2H2, BZIP9 | basic leucine zipper 9 | chr5:8515259-8516541 FORWARD LENGTH=277	293	277	1.00E-126	94.5	77.5	83.3
Rsa1.0_00964.1.g21917.t1	gb|EOA19667.1| hypothetical protein CARUB_v10003319mg [Capsella rubella]	993	1011	0	101.8	89.4	94.9	hypothetical protein CARUB_v10003319mg	gbpln	Capsella rubella	AT5G24810.1 | Symbols: | ABC1 family protein | chr5:8516902-8522616 REVERSE LENGTH=1009	993	1009	0	101.6	88.2	93.9
Rsa1.0_00964.1.g21918.t1	ref|NP_568459.1| aspartyl protease family protein [Arabidopsis thaliana] gi|67633818|gb|AAY78833.1| aspartyl protease family protein [Arabidopsis thaliana] gi|111074346|gb|ABH04546.1| At5g24820 [Arabidopsis thaliana] gi|332005983|gb|AED93366.1| aspartyl protease family protein [Arabidopsis thaliana]	413	407	1.00E-166	98.5	72.4	81.8	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT5G24820.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:8523406-8525297 FORWARD LENGTH=407	413	407	1.00E-168	98.5	72.4	81.8
Rsa1.0_00965.1.g21919.t14	ref|XP_002892883.1| hypothetical protein ARALYDRAFT_888972 [Arabidopsis lyrata subsp. lyrata] gi|297338725|gb|EFH69142.1| hypothetical protein ARALYDRAFT_888972 [Arabidopsis lyrata subsp. lyrata]	1151	184	2.00E-50	16.0	9.0	11.4	hypothetical protein ARALYDRAFT_888972	gbpln	Arabidopsis lyrata	AT1G15790.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15780.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:5438477-5439820 REVERSE LENGTH=179	1151	179	7.00E-46	15.6	8.1	10.5
Rsa1.0_00965.1.g21920.t11	gb|EOA39491.1| hypothetical protein CARUB_v10008096mg [Capsella rubella]	241	1344	2.00E-58	557.7	45.6	51.0	hypothetical protein CARUB_v10008096mg	gbpln	Capsella rubella	AT1G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10440.1); Has 103701 Blast hits to 43153 proteins in 1828 species: Archae - 30; Bacteria - 7385; Metazoa - 38639; Fungi - 11531; Plants - 7727; Viruses - 307; Other Eukaryotes - 38082 (source: NCBI BLink). | chr1:5430446-5435921 REVERSE LENGTH=1335	241	1335	1.00E-59	553.9	44.8	50.2
Rsa1.0_00965.1.g21921.t1	gb|EOA39491.1| hypothetical protein CARUB_v10008096mg [Capsella rubella]	564	1344	0	238.3	78.5	86.2	hypothetical protein CARUB_v10008096mg	gbpln	Capsella rubella	AT1G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10440.1); Has 103701 Blast hits to 43153 proteins in 1828 species: Archae - 30; Bacteria - 7385; Metazoa - 38639; Fungi - 11531; Plants - 7727; Viruses - 307; Other Eukaryotes - 38082 (source: NCBI BLink). | chr1:5430446-5435921 REVERSE LENGTH=1335	564	1335	0	236.7	79.1	86.3
Rsa1.0_00965.1.g21922.t1	gb|AAF79835.1|AC026875_15 T6D22.19 [Arabidopsis thaliana]	676	745	0	110.2	48.4	63.5	T6D22.19	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	676	696	6.00E-82	103.0	27.5	45.7
Rsa1.0_00965.1.g21923.t1	ref|XP_002892882.1| hypothetical protein ARALYDRAFT_471776 [Arabidopsis lyrata subsp. lyrata] gi|297338724|gb|EFH69141.1| hypothetical protein ARALYDRAFT_471776 [Arabidopsis lyrata subsp. lyrata]	706	1343	0	190.2	56.4	58.5	hypothetical protein ARALYDRAFT_471776	gbpln	Arabidopsis lyrata	AT1G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10440.1); Has 103701 Blast hits to 43153 proteins in 1828 species: Archae - 30; Bacteria - 7385; Metazoa - 38639; Fungi - 11531; Plants - 7727; Viruses - 307; Other Eukaryotes - 38082 (source: NCBI BLink). | chr1:5430446-5435921 REVERSE LENGTH=1335	706	1335	0	189.1	55.7	58.2
Rsa1.0_00965.1.g21924.t4	dbj|BAF01492.1| putative Ser/Thr protein kinase [Arabidopsis thaliana]	414	1025	2.00E-40	247.6	22.0	22.7	putative Ser/Thr protein kinase	gbpln	Arabidopsis thaliana	AT1G16270.2 | Symbols: | Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain | chr1:5563890-5568145 FORWARD LENGTH=1147	414	1147	6.00E-43	277.1	22.0	22.7
Rsa1.0_00965.1.g21925.t1	ref|XP_002892989.1| hypothetical protein ARALYDRAFT_889236 [Arabidopsis lyrata subsp. lyrata] gi|297338831|gb|EFH69248.1| hypothetical protein ARALYDRAFT_889236 [Arabidopsis lyrata subsp. lyrata]	169	167	2.00E-22	98.8	35.5	48.5	hypothetical protein ARALYDRAFT_889236	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#

Rsa1.0_00965.1.g21926.t2	ref|XP_002892882.1| hypothetical protein ARALYDRAFT_471776 [Arabidopsis lyrata subsp. lyrata] gi|297338724|gb|EFH69141.1| hypothetical protein ARALYDRAFT_471776 [Arabidopsis lyrata subsp. lyrata]	239	1343	1.00E-26	561.9	31.0	39.3	hypothetical protein ARALYDRAFT_471776	gbpln	Arabidopsis lyrata	AT1G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10440.1); Has 103701 Blast hits to 43153 proteins in 1828 species: Archae - 30; Bacteria - 7385; Metazoa - 38639; Fungi - 11531; Plants - 7727; Viruses - 307; Other Eukaryotes - 38082 (source: NCBI BLink). | chr1:5430446-5435921 REVERSE LENGTH=1335	239	1335	1.00E-27	558.6	27.2	35.6
Rsa1.0_00965.1.g21927.t1	ref|XP_002892989.1| hypothetical protein ARALYDRAFT_889236 [Arabidopsis lyrata subsp. lyrata] gi|297338831|gb|EFH69248.1| hypothetical protein ARALYDRAFT_889236 [Arabidopsis lyrata subsp. lyrata]	239	167	6.00E-24	69.9	29.3	40.2	hypothetical protein ARALYDRAFT_889236	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00965.1.g21928.t1	gb|EOA39338.1| hypothetical protein CARUB_v10012382mg [Capsella rubella]	209	205	1.00E-86	98.1	75.6	83.7	hypothetical protein CARUB_v10012382mg	gbpln	Capsella rubella	AT1G15760.1 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr1:5425714-5426322 FORWARD LENGTH=202	209	202	1.00E-88	96.7	78.9	87.6
Rsa1.0_00966.1.g21929.t1	gb|EOA24147.1| hypothetical protein CARUB_v10017380mg, partial [Capsella rubella]	351	403	1.00E-151	114.8	74.9	85.2	hypothetical protein CARUB_v10017380mg, partial	gbpln	Capsella rubella	AT3G57740.1 | Symbols: | Protein kinase superfamily protein | chr3:21392671-21393744 FORWARD LENGTH=357	351	357	1.00E-153	101.7	76.4	86.9
Rsa1.0_00966.1.g21930.t1	gb|EOA25819.1| hypothetical protein CARUB_v10019188mg [Capsella rubella]	153	349	8.00E-19	228.1	41.8	54.2	hypothetical protein CARUB_v10019188mg	gbpln	Capsella rubella	AT3G57710.1 | Symbols: | Protein kinase superfamily protein | chr3:21386233-21387288 REVERSE LENGTH=351	153	351	9.00E-21	229.4	41.8	54.9
Rsa1.0_00966.1.g21931.t1	gb|EOA25623.1| hypothetical protein CARUB_v10018971mg [Capsella rubella]	376	360	9.00E-54	95.7	37.5	55.6	hypothetical protein CARUB_v10018971mg	gbpln	Capsella rubella	AT2G34280.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:14470335-14471510 REVERSE LENGTH=391	376	391	3.00E-45	104.0	38.8	54.5
Rsa1.0_00966.1.g21932.t1	gb|EOA28140.1| hypothetical protein CARUB_v10024329mg [Capsella rubella]	61	123	1.00E-15	201.6	78.7	90.2	hypothetical protein CARUB_v10024329mg	gbpln	Capsella rubella	AT2G41905.1 | Symbols: | BEST Arabidopsis thaliana protein match is: arabinogalactan protein 23 (TAIR:AT3G57690.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17495766-17495951 FORWARD LENGTH=61	61	61	6.00E-18	100.0	82.0	90.2
Rsa1.0_00966.1.g21933.t1	ref|NP_191327.4| Peptidase S41 family protein [Arabidopsis thaliana] gi|332646165|gb|AEE79686.1| Peptidase S41 family protein [Arabidopsis thaliana]	515	519	0	100.8	85.8	91.3	Peptidase S41 family protein	gbpln	Arabidopsis thaliana	AT3G57680.1 | Symbols: | Peptidase S41 family protein | chr3:21381054-21383629 FORWARD LENGTH=519	515	519	0	100.8	85.8	91.3
Rsa1.0_00966.1.g21934.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1656	1274	0	76.9	31.8	41.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1656	626	4.00E-25	37.8	5.7	9.5
Rsa1.0_00966.1.g21935.t1	gb|AAO64176.1| putative zinc finger protein [Arabidopsis thaliana] gi|110737098|dbj|BAF00501.1| zinc finger like protein [Arabidopsis thaliana]	376	383	1.00E-168	101.9	90.4	91.8	putative zinc finger protein	gbpln	Arabidopsis thaliana	AT3G57670.1 | Symbols: NTT, WIP2 | C2H2-type zinc finger family protein | chr3:21370936-21373121 FORWARD LENGTH=383	376	383	1.00E-167	101.9	91.0	92.3
Rsa1.0_00966.1.g21936.t1	ref|XP_002876429.1| hypothetical protein ARALYDRAFT_486216 [Arabidopsis lyrata subsp. lyrata] gi|297322267|gb|EFH52688.1| hypothetical protein ARALYDRAFT_486216 [Arabidopsis lyrata subsp. lyrata]	1655	1678	0	101.4	80.8	88.6	hypothetical protein ARALYDRAFT_486216	gbpln	Arabidopsis lyrata	AT3G57660.1 | Symbols: NRPA1 | nuclear RNA polymerase A1 | chr3:21353746-21362814 FORWARD LENGTH=1670	1655	1670	0	100.9	80.3	88.2
Rsa1.0_00966.1.g21937.t1	gb|ADC97478.1| lysophosphatidic acid acyltransferase [Brassica napus] gi|289472613|gb|ADC97480.1| lysophosphatidic acid acyltransferase [Brassica napus]	389	390	0	100.3	98.5	99.5	lysophosphatidic acid acyltransferase	gbpln	Brassica napus	AT3G57650.1 | Symbols: LPAT2 | lysophosphatidyl acyltransferase 2 | chr3:21349751-21352839 FORWARD LENGTH=389	389	389	0	100.0	92.5	96.7
Rsa1.0_00967.1.g21938.t1	ref|XP_002876954.1| CYP71B23 [Arabidopsis lyrata subsp. lyrata] gi|297322792|gb|EFH53213.1| CYP71B23 [Arabidopsis lyrata subsp. lyrata]	436	501	0	114.9	86.7	92.4	CYP71B23	gbpln	Arabidopsis lyrata	AT3G26210.1 | Symbols: CYP71B23 | cytochrome P450, family 71, subfamily B, polypeptide 23 | chr3:9593329-9595202 REVERSE LENGTH=501	436	501	0	114.9	86.2	92.7
Rsa1.0_00967.1.g21939.t1	ref|NP_189253.1| cytochrome P450 71B3 [Arabidopsis thaliana] gi|13878902|sp|O65785.2|C71B3_ARATH RecName: Full=Cytochrome P450 71B3 gi|11994441|dbj|BAB02443.1| cytochrome P450 [Arabidopsis thaliana] gi|332643614|gb|AEE77135.1| cytochrome P450 71B3 [Arabidopsis thaliana]	504	501	0	99.4	76.6	88.3	cytochrome P450 71B3	gbpln	Arabidopsis thaliana	AT3G26220.1 | Symbols: CYP71B3 | cytochrome P450, family 71, subfamily B, polypeptide 3 | chr3:9596208-9597828 REVERSE LENGTH=501	504	501	0	99.4	76.6	88.3

Rsa1.0_00967.1.g21940.t1	ref|XP_002876956.1| CYP71B4 [Arabidopsis lyrata subsp. lyrata] gi|297322794|gb|EFH53215.1| CYP71B4 [Arabidopsis lyrata subsp. lyrata]	496	502	0	101.2	73.8	83.9	CYP71B4	gbpln	Arabidopsis lyrata	AT3G26280.1 | Symbols: CYP71B4 | cytochrome P450, family 71, subfamily B, polypeptide 4 | chr3:9630358-9631970 REVERSE LENGTH=504	496	504	0	101.6	71.8	83.5
Rsa1.0_00967.1.g21941.t1	ref|XP_002876956.1| CYP71B4 [Arabidopsis lyrata subsp. lyrata] gi|297322794|gb|EFH53215.1| CYP71B4 [Arabidopsis lyrata subsp. lyrata]	475	502	0	105.7	72.0	83.6	CYP71B4	gbpln	Arabidopsis lyrata	AT3G26280.1 | Symbols: CYP71B4 | cytochrome P450, family 71, subfamily B, polypeptide 4 | chr3:9630358-9631970 REVERSE LENGTH=504	475	504	0	106.1	70.5	82.5
Rsa1.0_00967.1.g21942.t1	ref|XP_002876962.1| CYP71B34 [Arabidopsis lyrata subsp. lyrata] gi|297322800|gb|EFH53221.1| CYP71B34 [Arabidopsis lyrata subsp. lyrata]	497	500	0	100.6	83.7	92.2	CYP71B34	gbpln	Arabidopsis lyrata	AT3G26300.1 | Symbols: CYP71B34 | cytochrome P450, family 71, subfamily B, polypeptide 34 | chr3:9639199-9640866 REVERSE LENGTH=500	497	500	0	100.6	82.3	92.2
Rsa1.0_00967.1.g21943.t1	ref|XP_002876964.1| CYP71B37 [Arabidopsis lyrata subsp. lyrata] gi|297322802|gb|EFH53223.1| CYP71B37 [Arabidopsis lyrata subsp. lyrata]	498	500	0	100.4	79.3	89.4	CYP71B37	gbpln	Arabidopsis lyrata	AT3G26330.1 | Symbols: CYP71B37 | cytochrome P450, family 71, subfamily B, polypeptide 37 | chr3:9646873-9648536 REVERSE LENGTH=500	498	500	0	100.4	76.9	86.3
Rsa1.0_00967.1.g21944.t1	ref|NP_176122.2| cytochrome p450 79c2 [Arabidopsis thaliana] gi|8979947|gb|AAF82261.1|AC008051_12 Strong similarity to N-hydroxylating multifunctional cytochrome P-450 (CYP79) from Sorghum bicolor gb|U32624 and contains a Cytochrome P450 PF|00067 domain [Arabidopsis thaliana] gi|12321833|gb|AAG50952.1|AC073943_2 cytochrome P450, putative [Arabidopsis thaliana] gi|332195404|gb|AEE33525.1| cytochrome p450 79c2 [Arabidopsis thaliana]	589	530	0	90.0	59.8	66.4	cytochrome p450 79c2	gbpln	Arabidopsis thaliana	AT1G58260.1 | Symbols: CYP79C2, CYP79C3P | cytochrome p450 79c2 | chr1:21605752-21607995 FORWARD LENGTH=530	589	530	0	90.0	59.8	66.4
Rsa1.0_00967.1.g21945.t1	ref|NP_189266.1| uncharacterized protein [Arabidopsis thaliana] gi|9294293|dbj|BAB02195.1| unnamed protein product [Arabidopsis thaliana] gi|91805521|gb|ABE65489.1| unknown [Arabidopsis thaliana] gi|332643627|gb|AEE77148.1| uncharacterized protein AT3G26350 [Arabidopsis thaliana]	365	356	1.00E-121	97.5	70.1	78.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G26350.1 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: root, pedicel, carpel, stamen; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Late embryogenesis abundant protein, group 2 (InterPro:IPR004864); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G13050.1); Has 3534 Blast hits to 2704 proteins in 342 species: Archae - 6; Bacteria - 192; Metazoa - 1076; Fungi - 505; Plants - 1162; Viruses - 224; Other Eukaryotes - 369 (source: NCBI BLink). | chr3:9653660-9654730 REVERSE LENGTH=356	365	356	1.00E-124	97.5	70.1	78.9
Rsa1.0_00967.1.g21946.t1	dbj|BAB02196.1| unnamed protein product [Arabidopsis thaliana]	102	99	1.00E-41	97.1	87.3	91.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G26360.1 | Symbols: | Ribosomal protein S21 family protein | chr3:9655963-9656373 REVERSE LENGTH=101	102	101	3.00E-44	99.0	87.3	91.2
Rsa1.0_00967.1.g21947.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	522	1142	1.00E-123	218.8	41.2	55.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	522	575	8.00E-76	110.2	27.2	43.1
Rsa1.0_00968.1.g21948.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00968.1.g21949.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00968.1.g21950.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	1166	1239	0	106.3	51.7	59.2	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1166	1262	7.00E-86	108.2	14.8	23.6
Rsa1.0_00968.1.g21951.t1	gb|EOA25101.1| hypothetical protein CARUB_v10018408mg [Capsella rubella]	248	245	5.00E-95	98.8	80.2	87.1	hypothetical protein CARUB_v10018408mg	gbpln	Capsella rubella	AT3G30260.1 | Symbols: AGL79 | AGAMOUS-like 79 | chr3:11909119-11912880 FORWARD LENGTH=249	248	249	2.00E-97	100.4	79.4	87.5
Rsa1.0_00968.1.g21952.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	209	1838	1.00E-20	879.4	32.1	51.7	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00968.1.g21953.t1	gb|EOA24256.1| hypothetical protein CARUB_v10017497mg [Capsella rubella]	328	364	1.00E-144	111.0	79.9	85.4	hypothetical protein CARUB_v10017497mg	gbpln	Capsella rubella	AT3G30340.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:11956626-11958969 FORWARD LENGTH=364	328	364	1.00E-145	111.0	77.4	86.3
Rsa1.0_00968.1.g21954.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00968.1.g21955.t2	ref|NP_566853.1| uncharacterized protein [Arabidopsis thaliana] gi|313471490|sp|Q9LI64.2|RGF4_ARATH RecName: Full=Root meristem growth factor 4; Short=AtRGF4; Flags: Precursor gi|332644113|gb|AEE77634.1| uncharacterized protein AT3G30350 [Arabidopsis thaliana]	168	163	1.00E-47	97.0	66.1	76.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G30350.1 | Symbols: RGF4 | Encodes a root meristem growth factor (RGF). Belongs to a family of functionally redundant homologous peptides that are secreted, tyrosine-sulfated, and expressed mainly in the stem cell area and the innermost layer of central columella cells. RGFs are required for maintenance of the root stem cell niche and transit amplifying cell proliferation. Members of this family include: At5g60810 (RGF1), At1g13620 (RGF2), At2g04025 (RGF3), At3g30350 (RGF4), At5g51451 (RGF5), At4g16515 (RGF6), At3g02240 (RGF7), At2g03830 (RGF8) and At5g64770 (RGF9). | chr3:11960552-11961764 REVERSE LENGTH=163	168	163	4.00E-50	97.0	66.1	76.8
Rsa1.0_00968.1.g21956.t1	gb|EOA26153.1| hypothetical protein CARUB_v10019591mg [Capsella rubella]	378	377	0	99.7	89.2	92.3	hypothetical protein CARUB_v10019591mg	gbpln	Capsella rubella	AT3G30380.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:11974424-11976571 FORWARD LENGTH=377	378	377	0	99.7	88.4	91.5
Rsa1.0_00968.1.g21957.t1	gb|EOA25673.1| hypothetical protein CARUB_v10019025mg [Capsella rubella]	457	458	0	100.2	89.1	95.4	hypothetical protein CARUB_v10019025mg	gbpln	Capsella rubella	AT3G30390.2 | Symbols: | Transmembrane amino acid transporter family protein | chr3:11977112-11978827 REVERSE LENGTH=460	457	460	0	100.7	88.8	94.1
Rsa1.0_00969.1.g21958.t1	ref|XP_002887784.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333625|gb|EFH64043.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	82	783	4.00E-40	954.9	92.7	97.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G79400.1 | Symbols: ATCHX2, CHX2 | cation/H+ exchanger 2 | chr1:29864992-29867840 FORWARD LENGTH=783	82	783	5.00E-42	954.9	91.5	96.3
Rsa1.0_00969.1.g21959.t1	ref|XP_002889243.1| hypothetical protein ARALYDRAFT_477106 [Arabidopsis lyrata subsp. lyrata] gi|297335084|gb|EFH65502.1| hypothetical protein ARALYDRAFT_477106 [Arabidopsis lyrata subsp. lyrata]	506	514	0	101.6	82.4	91.5	hypothetical protein ARALYDRAFT_477106	gbpln	Arabidopsis lyrata	AT1G79410.1 | Symbols: AtOCT5, 5-Oct | organic cation/carnitine transporter5 | chr1:29868037-29869584 REVERSE LENGTH=515	506	515	0	101.8	81.8	91.7
Rsa1.0_00969.1.g21960.t1	gb|EOA35357.1| hypothetical protein CARUB_v10020551mg [Capsella rubella]	346	354	0	102.3	94.5	98.0	hypothetical protein CARUB_v10020551mg	gbpln	Capsella rubella	AT1G79430.2 | Symbols: APL, WDY | Homeodomain-like superfamily protein | chr1:29877521-29879135 REVERSE LENGTH=358	346	358	0	103.5	95.4	97.7
Rsa1.0_00969.1.g21961.t2	gb|EOA39471.1| hypothetical protein CARUB_v10008066mg [Capsella rubella]	1079	2170	0	201.1	57.8	63.7	hypothetical protein CARUB_v10008066mg	gbpln	Capsella rubella	AT1G20960.2 | Symbols: emb1507 | U5 small nuclear ribonucleoprotein helicase, putative | chr1:7302591-7309914 REVERSE LENGTH=2171	1079	2171	0	201.2	57.1	63.3
Rsa1.0_00969.1.g21962.t1	ref|XP_002878905.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324744|gb|EFH55164.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	492	480	7.00E-44	97.6	25.0	42.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	492	384	2.00E-26	78.0	13.2	20.9
Rsa1.0_00969.1.g21963.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00969.1.g21964.t1	ref|XP_002864260.1| hypothetical protein ARALYDRAFT_918447 [Arabidopsis lyrata subsp. lyrata] gi|297310095|gb|EFH40519.1| hypothetical protein ARALYDRAFT_918447 [Arabidopsis lyrata subsp. lyrata]	226	231	1.00E-25	102.2	30.5	50.0	hypothetical protein ARALYDRAFT_918447	gbpln	Arabidopsis lyrata	AT2G35280.1 | Symbols: | F-box family protein | chr2:14859709-14860200 REVERSE LENGTH=163	226	163	1.00E-25	72.1	24.8	38.5
Rsa1.0_00969.1.g21965.t1	gb|AAV44035.1| putative helicase [Oryza sativa Japonica Group]	1584	1634	0	103.2	44.5	62.4	putative helicase	gbpln	Oryza sativa	AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907-10814173 REVERSE LENGTH=337	1584	337	2.00E-70	21.3	8.6	11.4
Rsa1.0_00969.1.g21966.t1	ref|XP_002889247.1| hypothetical protein ARALYDRAFT_477115 [Arabidopsis lyrata subsp. lyrata] gi|297335088|gb|EFH65506.1| hypothetical protein ARALYDRAFT_477115 [Arabidopsis lyrata subsp. lyrata]	310	386	1.00E-94	124.5	78.1	84.5	hypothetical protein ARALYDRAFT_477115	gbpln	Arabidopsis lyrata	AT1G79480.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr1:29897905-29899267 REVERSE LENGTH=397	310	397	1.00E-70	128.1	49.4	53.9
Rsa1.0_00970.1.g21967.t1	gb|ACI14393.1| WRKY28-1 transcription factor [Brassica napus]	311	312	2.33E-156	100.3	84.6	89.7	WRKY28-1 transcription factor	gbpln	Brassica napus	AT4G18170.1 | Symbols: WRKY28, ATWRKY28 | WRKY DNA-binding protein 28 | chr4:10061508-10062691 FORWARD LENGTH=318	311	318	1.00E-132	102.3	80.7	88.4
Rsa1.0_00970.1.g21968.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00970.1.g21969.t1	ref|XP_002870064.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315900|gb|EFH46323.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	563	373	1.00E-140	66.3	50.1	52.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G18190.1 | Symbols: ATPUP6, PUP6 | purine permease 6 | chr4:10067939-10069193 FORWARD LENGTH=387	563	387	1.00E-139	68.7	49.7	52.6

Rsa1.0_00970.1.g21970.t1	sp|O49726.2|PUP9_ARATH RecName: Full=Probable purine permease 9; Short=AtPUP9	391	390	0	99.7	80.6	89.8	RecName: Full=Probable purine permease 9; Short=AtPUP9	----	----	AT4G18210.1 | Symbols: ATPUP10, PUP10 | purine permease 10 | chr4:10076175-10077495 FORWARD LENGTH=390	391	390	1.00E-178	99.7	80.3	88.5
Rsa1.0_00970.1.g21971.t1	ref|XP_002868006.1| hypothetical protein ARALYDRAFT_493043 [Arabidopsis lyrata subsp. lyrata] gi|297313842|gb|EFH44265.1| hypothetical protein ARALYDRAFT_493043 [Arabidopsis lyrata subsp. lyrata]	235	233	1.00E-110	99.1	84.3	90.2	hypothetical protein ARALYDRAFT_493043	gbpln	Arabidopsis lyrata	AT4G18230.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Oligosaccharide biosynthesis protein Alg14 like (InterPro:IPR013969); Has 640 Blast hits to 640 proteins in 277 species: Archae - 4; Bacteria - 281; Metazoa - 94; Fungi - 127; Plants - 57; Viruses - 0; Other Eukaryotes - 77 (source: NCBI BLink). | chr4:10080521-10081710 REVERSE LENGTH=233	235	233	1.00E-102	99.1	86.0	90.6
Rsa1.0_00970.1.g21972.t1	ref|XP_002868005.1| hypothetical protein ARALYDRAFT_493041 [Arabidopsis lyrata subsp. lyrata] gi|297313841|gb|EFH44264.1| hypothetical protein ARALYDRAFT_493041 [Arabidopsis lyrata subsp. lyrata]	657	852	0	129.7	71.7	82.8	hypothetical protein ARALYDRAFT_493041	gbpln	Arabidopsis lyrata	AT4G18250.1 | Symbols: | receptor serine/threonine kinase, putative | chr4:10087343-10091963 REVERSE LENGTH=853	657	853	0	129.8	71.2	81.3
Rsa1.0_00970.1.g21973.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00970.1.g21974.t1	gb|AAX19659.1| inward rectifying potassium channel [Brassica rapa subsp. pekinensis]	685	685	0	100.0	94.9	97.4	inward rectifying potassium channel	gbpln	Brassica rapa	AT4G18290.1 | Symbols: KAT2 | potassium channel in Arabidopsis thaliana 2 | chr4:10115418-10118477 FORWARD LENGTH=697	685	697	0	101.8	85.8	90.9
Rsa1.0_00970.1.g21975.t1	ref|XP_002870053.1| hypothetical protein ARALYDRAFT_493032 [Arabidopsis lyrata subsp. lyrata] gi|297315889|gb|EFH46312.1| hypothetical protein ARALYDRAFT_493032 [Arabidopsis lyrata subsp. lyrata]	164	159	3.00E-49	97.0	71.3	79.3	hypothetical protein ARALYDRAFT_493032	gbpln	Arabidopsis lyrata	AT4G18335.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10128869-10129363 FORWARD LENGTH=164	164	164	1.00E-51	100.0	78.0	82.9
Rsa1.0_00970.1.g21976.t1	ref|NP_193568.2| glycosyl hydrolase family 17 protein [Arabidopsis thaliana] gi|21539539|gb|AAM53322.1| beta-1,3-glucanase-like protein [Arabidopsis thaliana] gi|24899809|gb|AAN65119.1| beta-1,3-glucanase-like protein [Arabidopsis thaliana] gi|332658629|gb|AEE84029.1| glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	401	397	0	99.0	89.8	94.5	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis thaliana	AT4G18340.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr4:10130245-10132019 REVERSE LENGTH=397	401	397	0	99.0	89.8	94.5
Rsa1.0_00971.1.g21977.t1	ref|NP_194771.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana] gi|75181441|sp|Q9M0B8.1|WTR37_ARATH RecName: Full=WAT1-related protein At4g30420 gi|7269943|emb|CAB79760.1| nodulin-like protein [Arabidopsis thaliana] gi|332660363|gb|AEE85763.1| nodulin MtN21 /EamA-like transporter family protein [Arabidopsis thaliana]	283	373	1.00E-129	131.8	81.6	88.7	nodulin MtN21 /EamA-like transporter family protein	gbpln	Arabidopsis thaliana	AT4G30420.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:14877069-14878914 FORWARD LENGTH=373	283	373	1.00E-132	131.8	81.6	88.7
Rsa1.0_00971.1.g21978.t1	ref|XP_002867349.1| hypothetical protein ARALYDRAFT_328673 [Arabidopsis lyrata subsp. lyrata] gi|297313185|gb|EFH43608.1| hypothetical protein ARALYDRAFT_328673 [Arabidopsis lyrata subsp. lyrata]	269	272	1.00E-113	101.1	74.3	85.9	hypothetical protein ARALYDRAFT_328673	gbpln	Arabidopsis lyrata	AT4G30430.1 | Symbols: TET9 | tetraspanin9 | chr4:14879029-14880272 REVERSE LENGTH=272	269	272	1.00E-112	101.1	69.5	82.2

Rsa1.0_00971.1.g21979.t1	ref|NP_194773.1| UDP-D-glucuronate 4-epimerase 1 [Arabidopsis thaliana] gi|297798928|ref|XP_002867348.1| UDP-D-glucuronate 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata] gi|75311748|sp|Q9M0B6.1|GAE1_ARATH RecName: Full=UDP-glucuronate 4-epimerase 1; AltName: Full=UDP-glucuronic acid epimerase 1; Short=AtUGlcAE3 gi|7269945|emb|CAB79762.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|15810529|gb|AAL07152.1| putative nucleotide sugar epimerase [Arabidopsis thaliana] gi|20466778|gb|AAM20706.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|21553636|gb|AAM62729.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|23198200|gb|AAN15627.1| nucleotide sugar epimerase-like protein [Arabidopsis thaliana] gi|50429331|gb|AAT77233.1| UDP-D-glucuronate 4-epimerase [Arabidopsis thaliana] gi|297313184|gb|EFH43607.1| UDP-D-glucuronate 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata] gi|332660365|gb|AEE85765.1| UDP-D-glucuronate 4-epimerase 1 [Arabidopsis thaliana] gi|385137886|gb|AFI41204.1| UDP-D-glucuronate 4-epimerase 1	429	429	0	100.0	98.8	99.8	UDP-D-glucuronate 4-epimerase 1	gbpln	Arabidopsis lyrata	AT4G30440.1 | Symbols: GAE1 | UDP-D-glucuronate 4-epimerase 1 | chr4:14881976-14883265 REVERSE LENGTH=429	429	429	0	100.0	98.8	99.8
Rsa1.0_00971.1.g21980.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00971.1.g21981.t1	#	#	#	#	#	#	#	-	----	----	AT4G30460.1 | Symbols: | glycine-rich protein | chr4:14889246-14889734 REVERSE LENGTH=162	164	162	6.00E-11	98.8	17.7	18.9
Rsa1.0_00971.1.g21982.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00971.1.g21983.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00971.1.g21984.t1	ref|NP_199541.1| putative F-box protein [Arabidopsis thaliana] gi|75264281|sp|Q9LVS9.1|FB340_ARATH RecName: Full=Probable F-box protein At5g47300 gi|8809613|dbj|BAA97164.1| unnamed protein product [Arabidopsis thaliana] gi|332008112|gb|AED95495.1| putative F-box protein [Arabidopsis thaliana]	324	416	5.00E-58	128.4	48.1	63.3	putative F-box protein	gbpln	Arabidopsis thaliana	AT5G47300.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:19198125-19199375 FORWARD LENGTH=416	324	416	1.00E-60	128.4	48.1	63.3
Rsa1.0_00971.1.g21985.t7	ref|NP_567820.1| elongation factor Ts family protein [Arabidopsis thaliana] gi|4972052|emb|CAB43920.1| putative protein [Arabidopsis thaliana] gi|7269804|emb|CAB79664.1| putative protein [Arabidopsis thaliana] gi|15983773|gb|AAL10483.1| AT4g29060/F19B15_90 [Arabidopsis thaliana] gi|332660180|gb|AEE85580.1| elongation factor Ts family protein [Arabidopsis thaliana]	207	953	2.00E-17	460.4	26.1	29.5	elongation factor Ts family protein	gbpln	Arabidopsis thaliana	AT4G29060.1 | Symbols: emb2726 | elongation factor Ts family protein | chr4:14317744-14321315 FORWARD LENGTH=953	207	953	8.00E-20	460.4	26.1	29.5
Rsa1.0_00971.1.g21986.t1	ref|NP_195605.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75212071|sp|Q9SVJ9.1|FBK95_ARATH RecName: Full=F-box/kelch-repeat protein At4g38940 gi|4539313|emb|CAB38814.1| putative protein [Arabidopsis thaliana] gi|7270877|emb|CAB80557.1| putative protein [Arabidopsis thaliana] gi|21593554|gb|AAM65521.1| unknown [Arabidopsis thaliana] gi|51968770|dbj|BAD43077.1| unknown protein [Arabidopsis thaliana] gi|51969398|dbj|BAD43391.1| unknown protein [Arabidopsis thaliana] gi|332661596|gb|AEE86996.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	445	370	3.00E-70	83.1	33.7	46.5	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	445	370	8.00E-73	83.1	33.7	46.5
Rsa1.0_00971.1.g21987.t1	gb|AAK50344.1| defense-related protein [Brassica carinata]	250	250	1.00E-138	100.0	96.4	98.4	defense-related protein	gbpln	Brassica carinata	AT4G30530.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr4:14920605-14922286 FORWARD LENGTH=250	250	250	1.00E-131	100.0	88.0	95.6

Rsa1.0_00971.1.g21988.t4	ref|XP_002867337.1| signal recognition particle receptor alpha subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|297313173|gb|EFH43596.1| signal recognition particle receptor alpha subunit family protein [Arabidopsis lyrata subsp. lyrata]	729	633	0	86.8	77.5	80.7	signal recognition particle receptor alpha subunit family protein	gbpln	Arabidopsis lyrata	AT4G30600.1 | Symbols: | signal recognition particle receptor alpha subunit family protein | chr4:14938142-14940600 REVERSE LENGTH=634	729	634	0	87.0	77.2	80.8
Rsa1.0_00971.1.g21989.t1	gb|EOA18618.1| hypothetical protein CARUB_v10007192mg [Capsella rubella]	181	222	2.00E-36	122.7	54.1	68.0	hypothetical protein CARUB_v10007192mg	gbpln	Capsella rubella	AT4G30630.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G57910.1); Has 33 Blast hits to 33 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14951048-14952159 FORWARD LENGTH=237	181	237	2.00E-22	130.9	34.8	38.7
Rsa1.0_00972.1.g21990.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00972.1.g21991.t1	ref|NP_192327.3| AAA-type ATPase family protein [Arabidopsis thaliana] gi|332656970|gb|AEE82370.1| AAA-type ATPase family protein [Arabidopsis thaliana]	984	609	0	61.9	52.1	55.5	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT4G04180.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:2020471-2023673 FORWARD LENGTH=609	984	609	0	61.9	52.1	55.5
Rsa1.0_00972.1.g21992.t2	gb|EOA22965.1| hypothetical protein CARUB_v10003705mg [Capsella rubella]	131	595	2.00E-22	454.2	41.2	45.8	hypothetical protein CARUB_v10003705mg	gbpln	Capsella rubella	AT4G04180.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:2020471-2023673 FORWARD LENGTH=609	131	609	3.00E-20	464.9	40.5	45.8
Rsa1.0_00972.1.g21993.t1	ref|NP_193901.1| uncharacterized protein [Arabidopsis thaliana] gi|4455278|emb|CAB36814.1| hypothetical protein [Arabidopsis thaliana] gi|7268967|emb|CAB81277.1| hypothetical protein [Arabidopsis thaliana] gi|332659091|gb|AEE84491.1| uncharacterized protein AT4G21700 [Arabidopsis thaliana]	597	962	0	161.1	77.9	84.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G21700.1 | Symbols: | Protein of unknown function (DUF2921) | chr4:11529956-11532844 FORWARD LENGTH=962	597	962	0	161.1	77.9	84.9
Rsa1.0_00972.1.g21994.t4	sp|Q56XW8.2|FBL30_ARATH RecName: Full=F-box/LRR-repeat protein At1g48400	178	487	2.00E-31	273.6	43.8	46.6	RecName: Full=F-box/LRR-repeat protein At1g48400	----	----	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	178	513	1.00E-33	288.2	43.8	46.6
Rsa1.0_00972.1.g21995.t1	gb|AAL36413.1| putative peptide transporter protein [Arabidopsis thaliana]	568	582	0	102.5	78.9	86.6	putative peptide transporter protein	gbpln	Arabidopsis thaliana	AT5G46050.1 | Symbols: ATPTR3, PTR3 | peptide transporter 3 | chr5:18675062-18679071 REVERSE LENGTH=582	568	582	0	102.5	78.9	86.6
Rsa1.0_00972.1.g21996.t1	gb|AAC63678.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	102	1216	2.00E-16	1192.2	39.2	62.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00972.1.g21997.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00972.1.g21998.t2	ref|NP_192313.3| pyrophosphate--fructose-6-phosphate 1-phosphotransferase [Arabidopsis thaliana] gi|425936639|sp|F4JGR5.1|PFPB2_ARATH RecName: Full=Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 2; Short=PFP2; AltName: Full=6-phosphofructokinase, pyrophosphate dependent 2; AltName: Full=PPi-PFK 2; AltName: Full=Protein MATERNAL EFFECT EMBRYO ARREST 51; AltName: Full=Pyrophosphate--fructose-6-phosphate 1-phosphotransferase 2; AltName: Full=Pyrophosphate-dependent 6-phosphofructose-1-kinase 2 gi|332656965|gb|AEE82365.1| pyrophosphate--fructose-6-phosphate 1-phosphotransferase [Arabidopsis thaliana]	599	569	0	95.0	85.8	90.8	pyrophosphate--fructose-6-phosphate 1-phosphotransferase	gbpln	Arabidopsis thaliana	AT4G04040.1 | Symbols: MEE51 | Phosphofructokinase family protein | chr4:1939250-1942765 FORWARD LENGTH=569	599	569	0	95.0	85.8	90.8
Rsa1.0_00972.1.g21999.t1	gb|EOA21123.1| hypothetical protein CARUB_v10001463mg [Capsella rubella]	318	322	1.00E-153	101.3	85.8	92.5	hypothetical protein CARUB_v10001463mg	gbpln	Capsella rubella	AT4G04020.1 | Symbols: FIB | fibrillin | chr4:1932161-1933546 FORWARD LENGTH=318	318	318	1.00E-155	100.0	83.6	91.8
Rsa1.0_00973.1.g22000.t1	dbj|BAJ34535.1| unnamed protein product [Thellungiella halophila]	548	552	0	100.7	83.2	90.1	unnamed protein product	----	----	AT3G45680.1 | Symbols: | Major facilitator superfamily protein | chr3:16770995-16772908 FORWARD LENGTH=558	548	558	0	101.8	82.3	90.0
Rsa1.0_00973.1.g22001.t1	gb|EOA29337.1| hypothetical protein CARUB_v10025619mg [Capsella rubella]	355	357	1.00E-176	100.6	84.8	92.7	hypothetical protein CARUB_v10025619mg	gbpln	Capsella rubella	AT2G25710.2 | Symbols: HCS1 | holocarboxylase synthase 1 | chr2:10952719-10955061 FORWARD LENGTH=367	355	367	1.00E-174	103.4	83.4	90.4
Rsa1.0_00973.1.g22002.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00973.1.g22003.t1	gb|EOA33985.1| hypothetical protein CARUB_v10021479mg [Capsella rubella]	327	349	1.00E-114	106.7	73.7	84.4	hypothetical protein CARUB_v10021479mg	gbpln	Capsella rubella	AT1G68150.1 | Symbols: WRKY9, ATWRKY9 | WRKY DNA-binding protein 9 | chr1:25543970-25545615 FORWARD LENGTH=374	327	374	1.00E-115	114.4	73.1	83.8
Rsa1.0_00973.1.g22004.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00973.1.g22005.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00973.1.g22006.t1	ref|XP_002888457.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334298|gb|EFH64716.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1014	1058	0	104.3	77.8	87.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G65810.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:24477043-24480728 REVERSE LENGTH=1050	1014	1050	0	103.6	76.4	85.5
Rsa1.0_00973.1.g22007.t1	ref|XP_002887155.1| hypothetical protein ARALYDRAFT_475905 [Arabidopsis lyrata subsp. lyrata] gi|297332996|gb|EFH63414.1| hypothetical protein ARALYDRAFT_475905 [Arabidopsis lyrata subsp. lyrata]	323	332	1.00E-118	102.8	73.4	82.4	hypothetical protein ARALYDRAFT_475905	gbpln	Arabidopsis lyrata	AT1G68140.3 | Symbols: | Protein of unknown function (DUF1644) | chr1:25539410-25540414 REVERSE LENGTH=334	323	334	1.00E-116	103.4	70.9	80.2
Rsa1.0_00973.1.g22008.t8	ref|NP_176009.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|263711285|sp|C0LGH2.2|Y1561_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g56130; Flags: Precursor gi|332195226|gb|AEE33347.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	483	1032	0	213.7	71.0	81.2	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G56130.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:20994931-21000887 REVERSE LENGTH=1032	483	1032	0	213.7	71.0	81.2
Rsa1.0_00973.1.g22009.t1	ref|NP_197389.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|332005241|gb|AED92624.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	187	295	4.00E-11	157.8	21.9	31.6	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	187	295	1.00E-13	157.8	21.9	31.6
Rsa1.0_00974.1.g22010.t1	gb|AAD32950.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	312	773	4.00E-97	247.8	55.1	69.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	312	575	6.00E-39	184.3	25.6	39.4
Rsa1.0_00974.1.g22011.t1	gb|AAF69709.1|AC016041_14 F27J15.26 [Arabidopsis thaliana] gi|11094814|gb|AAG29743.1|AC084414_11 unknown protein [Arabidopsis thaliana]	589	608	0	103.2	82.7	90.0	F27J15.26	gbpln	Arabidopsis thaliana	AT1G48950.1 | Symbols: | C3HC zinc finger-like | chr1:18107063-18110108 FORWARD LENGTH=594	589	594	0	100.8	82.5	89.6
Rsa1.0_00974.1.g22012.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00974.1.g22013.t1	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	2741	1089	0	39.7	28.0	32.5	transposon protein-like	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2741	575	1.00E-118	21.0	6.9	9.3
Rsa1.0_00974.1.g22014.t1	dbj|BAB09501.1| unnamed protein product [Arabidopsis thaliana]	340	312	1.00E-121	91.8	61.8	73.2	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00974.1.g22015.t1	ref|XP_002878035.1| hypothetical protein ARALYDRAFT_485976 [Arabidopsis lyrata subsp. lyrata] gi|297323873|gb|EFH54294.1| hypothetical protein ARALYDRAFT_485976 [Arabidopsis lyrata subsp. lyrata]	184	185	8.00E-91	100.5	86.4	92.4	hypothetical protein ARALYDRAFT_485976	gbpln	Arabidopsis lyrata	AT3G55490.1 | Symbols: | GINS complex protein | chr3:20572171-20573415 REVERSE LENGTH=185	184	185	6.00E-93	100.5	85.9	92.4
Rsa1.0_00974.1.g22016.t1	gb|EOA28165.1| hypothetical protein CARUB_v10024354mg [Capsella rubella]	114	113	2.00E-45	99.1	88.6	94.7	hypothetical protein CARUB_v10024354mg	gbpln	Capsella rubella	AT2G40080.1 | Symbols: ELF4 | Protein of unknown function (DUF1313) | chr2:16734545-16734880 REVERSE LENGTH=111	114	111	1.00E-47	97.4	88.6	93.0
Rsa1.0_00974.1.g22017.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	180	1142	2.00E-27	634.4	43.3	58.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00974.1.g22018.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00974.1.g22019.t1	ref|XP_002891463.1| hypothetical protein ARALYDRAFT_474037 [Arabidopsis lyrata subsp. lyrata] gi|297337305|gb|EFH67722.1| hypothetical protein ARALYDRAFT_474037 [Arabidopsis lyrata subsp. lyrata]	603	550	2.00E-88	91.2	26.0	31.7	hypothetical protein ARALYDRAFT_474037	gbpln	Arabidopsis lyrata	AT1G48920.1 | Symbols: ATNUC-L1, PARL1, NUC-L1 | nucleolin like 1 | chr1:18098186-18101422 FORWARD LENGTH=557	603	557	1.00E-88	92.4	28.2	34.7
Rsa1.0_00975.1.g22020.t1	gb|AAD15471.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	108	1277	3.00E-14	1182.4	36.1	44.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00975.1.g22021.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	390	1529	2.00E-44	392.1	22.1	36.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	390	530	8.00E-13	135.9	9.0	13.3

Rsa1.0_00975.1.g22022.t1	ref|XP_002863188.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309022|gb|EFH39447.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	388	394	0	101.5	85.8	92.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G12980.1 | Symbols: | Auxin-responsive family protein | chr4:7589670-7591074 REVERSE LENGTH=394	388	394	0	101.5	85.6	90.7
Rsa1.0_00975.1.g22023.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	386	1023	1.00E-20	265.0	17.4	25.1	F27F5.21	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00975.1.g22024.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00975.1.g22025.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00975.1.g22026.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00975.1.g22027.t1	gb|EOA17253.1| hypothetical protein CARUB_v10005528mg [Capsella rubella]	217	261	3.00E-83	120.3	77.4	86.6	hypothetical protein CARUB_v10005528mg	gbpln	Capsella rubella	AT4G27990.1 | Symbols: YLMG1-2, ATYLMG1-2 | YGGT family protein | chr4:13923991-13924647 REVERSE LENGTH=218	217	218	2.00E-81	100.5	77.4	85.3
Rsa1.0_00976.1.g22028.t1	gb|AAF63125.1|AC009526_10 Similar to Athila ORF 1 [Arabidopsis thaliana]	139	823	9.00E-16	592.1	33.1	49.6	Similar to Athila ORF 1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00976.1.g22029.t1	ref|XP_002880836.1| hypothetical protein ARALYDRAFT_481553 [Arabidopsis lyrata subsp. lyrata] gi|297326675|gb|EFH57095.1| hypothetical protein ARALYDRAFT_481553 [Arabidopsis lyrata subsp. lyrata]	460	469	0	102.0	87.0	93.5	hypothetical protein ARALYDRAFT_481553	gbpln	Arabidopsis lyrata	AT2G26800.2 | Symbols: | Aldolase superfamily protein | chr2:11429192-11432290 REVERSE LENGTH=468	460	468	0	101.7	85.9	92.6
Rsa1.0_00976.1.g22030.t1	ref|XP_002878992.1| hypothetical protein ARALYDRAFT_481528 [Arabidopsis lyrata subsp. lyrata] gi|297324831|gb|EFH55251.1| hypothetical protein ARALYDRAFT_481528 [Arabidopsis lyrata subsp. lyrata]	1248	1253	0	100.4	79.6	87.7	hypothetical protein ARALYDRAFT_481528	gbpln	Arabidopsis lyrata	AT2G26610.1 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr2:11318771-11324174 FORWARD LENGTH=1249	1248	1249	0	100.1	78.8	87.3
Rsa1.0_00976.1.g22031.t1	gb|EOA27277.1| hypothetical protein CARUB_v10023397mg [Capsella rubella]	375	388	0	103.5	85.1	89.6	hypothetical protein CARUB_v10023397mg	gbpln	Capsella rubella	AT2G26600.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr2:11316727-11318215 FORWARD LENGTH=388	375	388	0	103.5	83.2	87.2
Rsa1.0_00976.1.g22032.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00976.1.g22033.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00976.1.g22034.t1	ref|NP_680296.1| uncharacterized protein [Arabidopsis thaliana] gi|332006517|gb|AED93900.1| uncharacterized protein AT5G33393 [Arabidopsis thaliana]	156	435	7.00E-13	278.8	26.9	34.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G33393.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:12656430-12658588 REVERSE LENGTH=435	156	435	2.00E-15	278.8	26.9	34.6
Rsa1.0_00976.1.g22035.t8	dbj|BAB02793.1| helicase-like protein [Arabidopsis thaliana]	1355	1428	0	105.4	46.2	60.5	helicase-like protein	gbpln	Arabidopsis thaliana	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	1355	344	9.00E-27	25.4	7.1	10.1
Rsa1.0_00976.1.g22036.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	443	490	1.00E-56	110.6	36.3	55.8	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	443	566	1.00E-52	127.8	33.2	55.1
Rsa1.0_00976.1.g22037.t7	ref|NP_565626.1| regulatory particle non-ATPase 13 [Arabidopsis thaliana] gi|79323128|ref|NP_001031424.1| regulatory particle non-ATPase 13 [Arabidopsis thaliana] gi|79323137|ref|NP_001031425.1| regulatory particle non-ATPase 13 [Arabidopsis thaliana] gi|20196943|gb|AAC14506.2| expressed protein [Arabidopsis thaliana] gi|330252768|gb|AEC07862.1| regulatory particle non-ATPase 13 [Arabidopsis thaliana] gi|330252769|gb|AEC07863.1| regulatory particle non-ATPase 13 [Arabidopsis thaliana] gi|330252770|gb|AEC07864.1| regulatory particle non-ATPase 13 [Arabidopsis thaliana]	458	300	1.00E-133	65.5	52.8	56.6	regulatory particle non-ATPase 13	gbpln	Arabidopsis thaliana	AT2G26590.3 | Symbols: RPN13 | regulatory particle non-ATPase 13 | chr2:11311182-11314717 REVERSE LENGTH=300	458	300	1.00E-136	65.5	52.8	56.6
Rsa1.0_00976.1.g22038.t21	dbj|BAB02147.1| TNP2-like transposon protein-like [Arabidopsis thaliana]	870	786	1.00E-143	90.3	31.5	38.6	TNP2-like transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00977.1.g22039.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00977.1.g22040.t2	ref|XP_002883291.1| Ca2+-transporting ATPase [Arabidopsis lyrata subsp. lyrata] gi|297329131|gb|EFH59550.1| Ca2+-transporting ATPase [Arabidopsis lyrata subsp. lyrata]	1099	1087	0	98.9	94.7	97.4	Ca2+-transporting ATPase	gbpln	Arabidopsis lyrata	AT3G21180.1 | Symbols: ACA9, ATACA9 | autoinhibited Ca(2+)-ATPase 9 | chr3:7425770-7431941 FORWARD LENGTH=1086	1099	1086	0	98.8	94.6	97.3

Rsa1.0_00977.1.g22041.t6	gb|AAC35532.1| contains similarity to proteases [Arabidopsis thaliana]	1562	1392	0	89.1	54.7	67.1	contains similarity to proteases	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1562	1262	1.00E-111	80.8	12.8	19.1
Rsa1.0_00977.1.g22042.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00977.1.g22043.t1	ref|XP_002885421.1| FMN binding protein [Arabidopsis lyrata subsp. lyrata] gi|297331261|gb|EFH61680.1| FMN binding protein [Arabidopsis lyrata subsp. lyrata]	399	387	0	97.0	82.5	87.2	FMN binding protein	gbpln	Arabidopsis lyrata	AT3G21140.1 | Symbols: | Pyridoxamine 5'-phosphate oxidase family protein | chr3:7409696-7412086 REVERSE LENGTH=387	399	387	0	97.0	82.0	86.2
Rsa1.0_00977.1.g22044.t1	gb|EOA40283.1| hypothetical protein CARUB_v10009011mg [Capsella rubella]	466	479	1.00E-176	102.8	70.8	81.8	hypothetical protein CARUB_v10009011mg	gbpln	Capsella rubella	AT1G51550.1 | Symbols: | Kelch repeat-containing F-box family protein | chr1:19117646-19119291 REVERSE LENGTH=478	466	478	1.00E-178	102.6	69.1	80.0
Rsa1.0_00977.1.g22045.t3	gb|AAG52629.1|AC024261_16 unknown protein; 27363-23366 [Arabidopsis thaliana]	425	1036	0	243.8	84.9	91.1	unknown protein; 27363-23366	gbpln	Arabidopsis thaliana	AT1G51540.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:19115702-19117381 FORWARD LENGTH=415	425	415	0	97.6	84.9	91.1
Rsa1.0_00977.1.g22046.t1	ref|NP_188748.1| phosphoribosylaminoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] gi|79313319|ref|NP_001030739.1| phosphoribosylaminoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] gi|26454658|sp|P38025.2|PUR7_ARATH RecName: Full=Phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic; AltName: Full=SAICAR synthetase; Flags: Precursor gi|11994271|dbj|BAB01454.1| 5'-phosphoribosyl-4-(N-succinocarboxamide)-5- aminoimidazole synthetase [Arabidopsis thaliana] gi|27754219|gb|AAO22563.1| putative phosphoribosyamidoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] gi|332642941|gb|AEE76462.1| phosphoribosylaminoimidazole-succinocarboxamide synthase [Arabidopsis thaliana] gi|332642942|gb|AEE76463.1| phosphoribosylaminoimidazole-succinocarboxamide synthase [Arabidopsis thaliana]	156	411	6.00E-46	263.5	57.7	60.9	phosphoribosylaminoimidazole-succinocarboxamide synthase	gbpln	Arabidopsis thaliana	AT3G21110.2 | Symbols: PUR7, PURC | purin 7 | chr3:7402696-7405273 REVERSE LENGTH=411	156	411	2.00E-48	263.5	57.7	60.9
Rsa1.0_00977.1.g22047.t1	ref|NP_974347.1| NAD(H) kinase 1 [Arabidopsis thaliana] gi|94717660|sp|Q56YN3.2|NADK1_ARATH RecName: Full=NAD(H) kinase 1; Short=AtNADK-1 gi|39843359|gb|AAR32133.1| NADK1 [Arabidopsis thaliana] gi|51970406|dbj|BAD43895.1| unnamed protein product [Arabidopsis thaliana] gi|332642935|gb|AEE76456.1| NAD(H) kinase 1 [Arabidopsis thaliana]	582	524	0	90.0	76.6	82.1	NAD(H) kinase 1	gbpln	Arabidopsis thaliana	AT3G21070.2 | Symbols: NADK1 | NAD kinase 1 | chr3:7380434-7383874 REVERSE LENGTH=524	582	524	0	90.0	76.6	82.1
Rsa1.0_00977.1.g22048.t1	gb|EOA33084.1| hypothetical protein CARUB_v10016422mg [Capsella rubella]	81	106	4.00E-31	130.9	85.2	98.8	hypothetical protein CARUB_v10016422mg	gbpln	Capsella rubella	AT3G21055.1 | Symbols: PSBTN | photosystem II subunit T | chr3:7376761-7377072 REVERSE LENGTH=103	81	103	5.00E-33	127.2	88.9	95.1
Rsa1.0_00977.1.g22049.t1	dbj|BAB01447.1| gag-pol polyprotein-like [Arabidopsis thaliana]	401	420	1.00E-126	104.7	57.9	73.8	gag-pol polyprotein-like	gbpln	Arabidopsis thaliana	AT3G21000.1 | Symbols: | Gag-Pol-related retrotransposon family protein | chr3:7363921-7365138 FORWARD LENGTH=405	401	405	1.00E-81	101.0	46.6	61.8
Rsa1.0_00977.1.g22050.t1	#	#	#	#	#	#	#	-	----	----	AT1G28760.1 | Symbols: | Uncharacterized conserved protein (DUF2215) | chr1:10103158-10104588 FORWARD LENGTH=476	76	476	6.00E-13	626.3	43.4	47.4
Rsa1.0_00977.1.g22051.t1	gb|EOA30911.1| hypothetical protein CARUB_v10014058mg [Capsella rubella]	317	356	5.00E-67	112.3	40.7	43.5	hypothetical protein CARUB_v10014058mg	gbpln	Capsella rubella	AT3G20920.1 | Symbols: | translocation protein-related | chr3:7328763-7330698 REVERSE LENGTH=365	317	365	9.00E-68	115.1	40.1	42.0
Rsa1.0_00977.1.g22052.t1	gb|AAC49265.1| CCAAT-binding factor B subunit homolog [Brassica napus] gi|1336840|gb|AAB36222.1| CCAAT-binding factor B subunit [Brassica napus]	255	314	1.00E-110	123.1	79.2	83.9	CCAAT-binding factor B subunit homolog	gbpln	Brassica napus	AT3G20910.1 | Symbols: NF-YA9 | nuclear factor Y, subunit A9 | chr3:7326495-7328369 FORWARD LENGTH=303	255	303	1.00E-104	118.8	73.7	82.4

Rsa1.0_00977.1.g22053.t2	ref|XP_003522346.1| PREDICTED: uncharacterized protein LOC100809302 [Glycine max]	303	531	1.00E-107	175.2	62.7	76.2	PREDICTED: uncharacterized protein LOC100809302	gbenv/gbpln	Glycine max	AT5G35695.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41980.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:13869120-13869941 FORWARD LENGTH=211	303	211	2.00E-55	69.6	36.3	42.6
Rsa1.0_00977.1.g22054.t1	ref|NP_188666.1| ethylene-responsive transcription factor 7 [Arabidopsis thaliana] gi|57012873|sp|Q9LDE4.1|ERF83_ARATH RecName: Full=Ethylene-responsive transcription factor 7; Short=AtERF7; AltName: Full=Ethylene-responsive element-binding factor 7; Short=EREBP-7 gi|8467962|dbj|BAA96653.1| ERF transcription factor 7 [Arabidopsis thaliana] gi|9294548|dbj|BAB02811.1| ethylene responsive element binding factor-like protein [Arabidopsis thaliana] gi|14335150|gb|AAK59855.1| AT3g20310/MQC12_6 [Arabidopsis thaliana] gi|20334802|gb|AAM16262.1| AT3g20310/MQC12_6 [Arabidopsis thaliana] gi|21537240|gb|AAM61581.1| ethylene responsive element binding factor, putative [Arabidopsis thaliana] gi|110736859|dbj|BAF00387.1| putative ethylene responsive element binding factor [Arabidopsis thaliana] gi|332642841|gb|AEE76362.1| ethylene-responsive transcription factor 7 [Arabidopsis thaliana]	203	244	1.00E-62	120.2	80.8	87.2	ethylene-responsive transcription factor 7	gbpln	Arabidopsis thaliana	AT3G20310.1 | Symbols: ATERF-7, ATERF7, ERF7 | ethylene response factor 7 | chr3:7085957-7086691 REVERSE LENGTH=244	203	244	5.00E-65	120.2	80.8	87.2
Rsa1.0_00977.1.g22055.t1	#	#	#	#	#	#	#	-	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	114	575	4.00E-11	504.4	27.2	37.7
Rsa1.0_00977.1.g22056.t1	ref|XP_002885364.1| extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata] gi|297331204|gb|EFH61623.1| extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata]	448	451	0	100.7	90.8	96.0	extracellular ligand-gated ion channel	gbpln	Arabidopsis lyrata	AT3G20300.1 | Symbols: | Protein of unknown function (DUF3537) | chr3:7079832-7081809 REVERSE LENGTH=452	448	452	0	100.9	90.6	95.8
Rsa1.0_00977.1.g22057.t1	gb|EOA30619.1| hypothetical protein CARUB_v10013756mg [Capsella rubella]	433	430	0	99.3	84.5	91.0	hypothetical protein CARUB_v10013756mg	gbpln	Capsella rubella	AT3G20260.1 | Symbols: | Protein of unknown function (DUF1666) | chr3:7064190-7065751 REVERSE LENGTH=437	433	437	0	100.9	84.5	91.0
Rsa1.0_00977.1.g22058.t1	ref|XP_002883238.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297329078|gb|EFH59497.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	350	348	1.00E-174	99.4	88.0	94.3	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT3G20240.1 | Symbols: | Mitochondrial substrate carrier family protein | chr3:7057192-7058716 FORWARD LENGTH=348	350	348	1.00E-177	99.4	88.3	94.0
Rsa1.0_00977.1.g22059.t1	ref|XP_002883234.1| hypothetical protein ARALYDRAFT_479539 [Arabidopsis lyrata subsp. lyrata] gi|297329074|gb|EFH59493.1| hypothetical protein ARALYDRAFT_479539 [Arabidopsis lyrata subsp. lyrata]	681	679	0	99.7	82.7	88.8	hypothetical protein ARALYDRAFT_479539	gbpln	Arabidopsis lyrata	AT3G20190.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:7044997-7047212 FORWARD LENGTH=679	681	679	0	99.7	82.2	88.0
Rsa1.0_00977.1.g22060.t1	gb|EOA30474.1| hypothetical protein CARUB_v10013599mg [Capsella rubella]	508	477	0	93.9	76.2	84.6	hypothetical protein CARUB_v10013599mg	gbpln	Capsella rubella	AT3G20170.1 | Symbols: | ARM repeat superfamily protein | chr3:7041780-7043207 FORWARD LENGTH=475	508	475	0	93.5	76.4	84.6
Rsa1.0_00977.1.g22061.t1	ref|XP_002883232.1| hypothetical protein ARALYDRAFT_898426 [Arabidopsis lyrata subsp. lyrata] gi|297329072|gb|EFH59491.1| hypothetical protein ARALYDRAFT_898426 [Arabidopsis lyrata subsp. lyrata]	351	356	1.00E-154	101.4	78.3	86.6	hypothetical protein ARALYDRAFT_898426	gbpln	Arabidopsis lyrata	AT3G20160.1 | Symbols: | Terpenoid synthases superfamily protein | chr3:7038995-7040029 FORWARD LENGTH=344	351	344	1.00E-147	98.0	75.2	84.9
Rsa1.0_00977.1.g22062.t1	ref|XP_002883230.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] gi|297329070|gb|EFH59489.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	1085	1127	0	103.9	84.9	91.6	kinesin motor family protein	gbpln	Arabidopsis lyrata	AT3G20150.1 | Symbols: | Kinesin motor family protein | chr3:7031412-7036499 FORWARD LENGTH=1114	1085	1114	0	102.7	83.3	90.2

Rsa1.0_00977.1.g22063.t1	gb|EOA30355.1| hypothetical protein CARUB_v10013477mg [Capsella rubella]	506	512	0	101.2	72.7	82.0	hypothetical protein CARUB_v10013477mg	gbpln	Capsella rubella	AT3G20080.2 | Symbols: CYP705A15 | cytochrome P450, family 705, subfamily A, polypeptide 15 | chr3:7008813-7010463 FORWARD LENGTH=523	506	523	0	103.4	71.9	82.2
Rsa1.0_00977.1.g22064.t1	ref|NP_566654.1| cytochrome P450, family 705, subfamily A, polypeptide 15 [Arabidopsis thaliana] gi|42572495|ref|NP_974343.1| cytochrome P450, family 705, subfamily A, polypeptide 15 [Arabidopsis thaliana] gi|9293963|dbj|BAB01866.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|332642809|gb|AEE76330.1| cytochrome P450, family 705, subfamily A, polypeptide 15 [Arabidopsis thaliana] gi|332642810|gb|AEE76331.1| cytochrome P450, family 705, subfamily A, polypeptide 15 [Arabidopsis thaliana]	505	523	0	103.6	72.1	82.0	cytochrome P450, family 705, subfamily A, polypeptide 15	gbpln	Arabidopsis thaliana	AT3G20080.2 | Symbols: CYP705A15 | cytochrome P450, family 705, subfamily A, polypeptide 15 | chr3:7008813-7010463 FORWARD LENGTH=523	505	523	0	103.6	72.1	82.0
Rsa1.0_00977.1.g22065.t1	gb|EOA30355.1| hypothetical protein CARUB_v10013477mg [Capsella rubella]	517	512	0	99.0	65.0	77.9	hypothetical protein CARUB_v10013477mg	gbpln	Capsella rubella	AT3G20080.2 | Symbols: CYP705A15 | cytochrome P450, family 705, subfamily A, polypeptide 15 | chr3:7008813-7010463 FORWARD LENGTH=523	517	523	0	101.2	65.2	77.8
Rsa1.0_00977.1.g22066.t1	dbj|BAB08692.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana] gi|93007380|gb|ABE97193.1| hypothetical protein At5g13655 [Arabidopsis thaliana]	275	385	6.00E-66	140.0	42.5	64.0	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	275	746	3.00E-54	271.3	38.2	54.2
Rsa1.0_00977.1.g22067.t1	gb|EOA30355.1| hypothetical protein CARUB_v10013477mg [Capsella rubella]	525	512	0	97.5	70.3	79.0	hypothetical protein CARUB_v10013477mg	gbpln	Capsella rubella	AT3G20080.2 | Symbols: CYP705A15 | cytochrome P450, family 705, subfamily A, polypeptide 15 | chr3:7008813-7010463 FORWARD LENGTH=523	525	523	0	99.6	68.8	79.4
Rsa1.0_00978.1.g22068.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00978.1.g22069.t1	ref|XP_002882932.1| hypothetical protein ARALYDRAFT_897817 [Arabidopsis lyrata subsp. lyrata] gi|297328772|gb|EFH59191.1| hypothetical protein ARALYDRAFT_897817 [Arabidopsis lyrata subsp. lyrata]	144	144	4.00E-74	100.0	93.1	97.9	hypothetical protein ARALYDRAFT_897817	gbpln	Arabidopsis lyrata	AT3G15358.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53035.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:5178205-5178639 FORWARD LENGTH=144	144	144	6.00E-76	100.0	93.1	97.9
Rsa1.0_00978.1.g22070.t1	gb|EOA25542.1| hypothetical protein CARUB_v10018887mg [Capsella rubella]	272	291	1.00E-101	107.0	69.1	82.4	hypothetical protein CARUB_v10018887mg	gbpln	Capsella rubella	AT3G11470.1 | Symbols: | 4'-phosphopantetheinyl transferase superfamily | chr3:3610261-3612094 REVERSE LENGTH=300	272	300	1.00E-102	110.3	71.0	83.8
Rsa1.0_00978.1.g22071.t1	gb|AFP57435.1| putative metallothionein type 3 [Brassica napus]	67	67	4.00E-27	100.0	94.0	97.0	putative metallothionein type 3	gbpln	Brassica napus	AT3G15353.1 | Symbols: MT3, ATMT3 | metallothionein 3 | chr3:5180825-5181325 REVERSE LENGTH=69	67	69	1.00E-24	103.0	85.1	88.1
Rsa1.0_00978.1.g22072.t1	ref|XP_002882934.1| ubiquitin-conjugating enzyme 23 [Arabidopsis lyrata subsp. lyrata] gi|297328774|gb|EFH59193.1| ubiquitin-conjugating enzyme 23 [Arabidopsis lyrata subsp. lyrata]	542	605	0	111.6	64.9	74.5	ubiquitin-conjugating enzyme 23	gbpln	Arabidopsis lyrata	AT3G15355.1 | Symbols: UBC25, PFU1 | ubiquitin-conjugating enzyme 25 | chr3:5183858-5186669 FORWARD LENGTH=609	542	609	1.00E-178	112.4	64.2	72.9
Rsa1.0_00978.1.g22073.t1	ref|XP_002882935.1| hypothetical protein ARALYDRAFT_478974 [Arabidopsis lyrata subsp. lyrata] gi|297328775|gb|EFH59194.1| hypothetical protein ARALYDRAFT_478974 [Arabidopsis lyrata subsp. lyrata]	154	144	8.00E-19	93.5	42.9	46.8	hypothetical protein ARALYDRAFT_478974	gbpln	Arabidopsis lyrata	AT3G15357.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: shoot apex, hypocotyl, root, leaf; Has 6931 Blast hits to 2036 proteins in 230 species: Archae - 7; Bacteria - 933; Metazoa - 1824; Fungi - 836; Plants - 482; Viruses - 218; Other Eukaryotes - 2631 (source: NCBI BLink). | chr3:5187164-5187595 FORWARD LENGTH=143	154	143	1.00E-20	92.9	42.2	48.1
Rsa1.0_00978.1.g22074.t2	gb|EOA31519.1| hypothetical protein CARUB_v10014709mg [Capsella rubella]	189	193	7.00E-83	102.1	87.3	91.5	hypothetical protein CARUB_v10014709mg	gbpln	Capsella rubella	AT3G15360.1 | Symbols: ATHM4, TRX-M4, ATM4 | thioredoxin M-type 4 | chr3:5188448-5189457 FORWARD LENGTH=193	189	193	7.00E-84	102.1	85.7	91.0
Rsa1.0_00978.1.g22075.t1	gb|EOA32479.1| hypothetical protein CARUB_v10015755mg [Capsella rubella]	702	700	0	99.7	94.7	97.6	hypothetical protein CARUB_v10015755mg	gbpln	Capsella rubella	AT3G15380.1 | Symbols: | Plasma-membrane choline transporter family protein | chr3:5193319-5196435 FORWARD LENGTH=700	702	700	0	99.7	94.4	97.6

<table>
<tr><td>Rsa1.0_00978.1.g22076.t1</td><td>ref|NP_001189900.1| protein silencing defective 5 [Arabidopsis thaliana] gi|332642142|gb|AEE75663.1| protein silencing defective 5 [Arabidopsis thaliana]</td><td>304</td><td>299</td><td>1.00E-119</td><td>98.4</td><td>73.7</td><td>82.6</td><td>protein silencing defective 5</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G15390.2 | Symbols: SDE5 | silencing defective 5 | chr3:5196689-5198445 REVERSE LENGTH=299</td><td>304</td><td>299</td><td>1.00E-122</td><td>98.4</td><td>73.7</td><td>82.6</td></tr>
<tr><td>Rsa1.0_00978.1.g22077.t1</td><td>ref|XP_002885085.1| hypothetical protein ARALYDRAFT_478977 [Arabidopsis lyrata subsp. lyrata] gi|297330925|gb|EFH61344.1| hypothetical protein ARALYDRAFT_478977 [Arabidopsis lyrata subsp. lyrata]</td><td>205</td><td>468</td><td>2.00E-79</td><td>228.3</td><td>73.7</td><td>84.4</td><td>hypothetical protein ARALYDRAFT_478977</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G15390.1 | Symbols: SDE5 | silencing defective 5 | chr3:5196689-5199531 REVERSE LENGTH=490</td><td>205</td><td>490</td><td>3.00E-79</td><td>239.0</td><td>72.7</td><td>82.9</td></tr>
<tr><td>Rsa1.0_00978.1.g22078.t1</td><td>ref|NP_974321.1| uncharacterized protein [Arabidopsis thaliana] gi|42572453|ref|NP_974322.1| uncharacterized protein [Arabidopsis thaliana] gi|79313241|ref|NP_001030700.1| uncharacterized protein [Arabidopsis thaliana] gi|145332587|ref|NP_001078159.1| uncharacterized protein [Arabidopsis thaliana] gi|21593726|gb|AAM65693.1| unknown [Arabidopsis thaliana] gi|111074242|gb|ABH04494.1| At3g15395 [Arabidopsis thaliana] gi|222423962|dbj|BAH19943.1| AT3G15395 [Arabidopsis thaliana] gi|222424311|dbj|BAH20112.1| AT3G15395 [Arabidopsis thaliana] gi|332642143|gb|AEE75664.1| uncharacterized protein AT3G15395 [Arabidopsis thaliana] gi|332642144|gb|AEE75665.1| uncharacterized protein AT3G15395 [Arabidopsis thaliana] gi|332642145|gb|AEE75666.1| uncharacterized protein AT3G15395 [Arabidopsis thaliana] gi|332642146|gb|AEE75667.1| uncharacterized protein AT3G15395 [Arabidopsis thaliana]</td><td>62</td><td>59</td><td>8.00E-20</td><td>95.2</td><td>77.4</td><td>83.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G15395.4 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 31 Blast hits to 31 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5201014-5201307 FORWARD LENGTH=59</td><td>62</td><td>59</td><td>1.00E-22</td><td>95.2</td><td>77.4</td><td>83.9</td></tr>
<tr><td>Rsa1.0_00978.1.g22079.t12</td><td>ref|XP_002862700.1| hypothetical protein ARALYDRAFT_497329 [Arabidopsis lyrata subsp. lyrata] gi|297308375|gb|EFH38958.1| hypothetical protein ARALYDRAFT_497329 [Arabidopsis lyrata subsp. lyrata]</td><td>517</td><td>358</td><td>9.00E-54</td><td>69.2</td><td>33.1</td><td>36.6</td><td>hypothetical protein ARALYDRAFT_497329</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G15400.1 | Symbols: ATA20 | anther 20 | chr3:5201678-5202928 FORWARD LENGTH=416</td><td>517</td><td>416</td><td>4.00E-37</td><td>80.5</td><td>21.1</td><td>23.2</td></tr>
<tr><td>Rsa1.0_00978.1.g22080.t1</td><td>ref|XP_002882943.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] gi|297328783|gb|EFH59202.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]</td><td>511</td><td>488</td><td>0</td><td>95.5</td><td>86.5</td><td>90.6</td><td>regulator of chromosome condensation family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G15430.2 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:5209408-5211562 FORWARD LENGTH=488</td><td>511</td><td>488</td><td>0</td><td>95.5</td><td>86.7</td><td>90.4</td></tr>
<tr><td>Rsa1.0_00978.1.g22081.t1</td><td>gb|EOA31283.1| hypothetical protein CARUB_v10014455mg [Capsella rubella]</td><td>256</td><td>253</td><td>1.00E-130</td><td>98.8</td><td>87.1</td><td>94.1</td><td>hypothetical protein CARUB_v10014455mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G15450.1 | Symbols: | Aluminium induced protein with YGL and LRDR motifs | chr3:5213050-5213998 FORWARD LENGTH=253</td><td>256</td><td>253</td><td>1.00E-132</td><td>98.8</td><td>87.5</td><td>93.4</td></tr>
<tr><td>Rsa1.0_00978.1.g22082.t1</td><td>gb|EOA38143.1| hypothetical protein CARUB_v10009615mg, partial [Capsella rubella]</td><td>337</td><td>346</td><td>1.00E-168</td><td>102.7</td><td>86.4</td><td>91.4</td><td>hypothetical protein CARUB_v10009615mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G15460.1 | Symbols: | Ribosomal RNA processing Brix domain protein | chr3:5214279-5216188 REVERSE LENGTH=315</td><td>337</td><td>315</td><td>1.00E-167</td><td>93.5</td><td>84.9</td><td>88.7</td></tr>
<tr><td>Rsa1.0_00978.1.g22083.t1</td><td>ref|XP_002885089.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297330929|gb|EFH61348.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]</td><td>874</td><td>885</td><td>0</td><td>101.3</td><td>78.7</td><td>85.2</td><td>WD-40 repeat family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G15470.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:5216630-5219868 REVERSE LENGTH=883</td><td>874</td><td>883</td><td>0</td><td>101.0</td><td>78.6</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00979.1.g22084.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00979.1.g22085.t1</td><td>gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]</td><td>436</td><td>657</td><td>3.00E-78</td><td>150.7</td><td>34.2</td><td>45.4</td><td>T14P8.10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332</td><td>436</td><td>332</td><td>8.00E-61</td><td>76.1</td><td>27.3</td><td>37.8</td></tr>
<tr><td>Rsa1.0_00979.1.g22086.t1</td><td>gb|EOA35498.1| hypothetical protein CARUB_v10020705mg [Capsella rubella]</td><td>296</td><td>306</td><td>1.00E-106</td><td>103.4</td><td>83.8</td><td>88.2</td><td>hypothetical protein CARUB_v10020705mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G75240.1 | Symbols: AtHB33, HB33, ZHD5 | homeobox protein 33 | chr1:28241576-28242505 FORWARD LENGTH=309</td><td>296</td><td>309</td><td>7.00E-98</td><td>104.4</td><td>81.1</td><td>86.1</td></tr>
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Rsa1.0_00979.1_g22087.t1	ref|NP_177661.1| RAD-like 6 protein [Arabidopsis thaliana] gi|10092271|gb|AAG12684.1|AC025814_8 myb-related protein; 20671-21051 [Arabidopsis thaliana] gi|41618978|gb|AAS09995.1| MYB transcription factor [Arabidopsis thaliana] gi|109946537|gb|ABG48447.1| At1g75250 [Arabidopsis thaliana] gi|332197572|gb|AEE35693.1| RAD-like 6 protein [Arabidopsis thaliana]	85	126	1.00E-37	148.2	87.1	91.8	RAD-like 6 protein	gbpln	Arabidopsis thaliana	AT1G75250.1 | Symbols: ATRL6, RSM3, RL6 | RAD-like 6 | chr1:28245073-28245453 REVERSE LENGTH=126	85	126	2.00E-40	148.2	87.1	91.8
Rsa1.0_00979.1_g22088.t1	dbj|BAJ34425.1| unnamed protein product [Thellungiella halophila]	312	311	1.00E-138	99.7	75.0	89.7	unnamed protein product	----	----	AT1G75280.1 | Symbols: | NmrA-like negative transcriptional regulator family protein | chr1:28252030-28253355 FORWARD LENGTH=310	312	310	1.00E-130	99.4	71.5	85.3
Rsa1.0_00979.1_g22089.t1	gb|AAM65005.1| GSH-dependent dehydroascorbate reductase 1, putative [Arabidopsis thaliana]	214	213	1.00E-104	99.5	87.4	91.6	GSH-dependent dehydroascorbate reductase 1, putative	gbpln	Arabidopsis thaliana	AT1G75270.1 | Symbols: DHAR2 | dehydroascorbate reductase 2 | chr1:28250255-28251237 REVERSE LENGTH=213	214	213	1.00E-106	99.5	86.9	91.1
Rsa1.0_00979.1_g22090.t1	ref|XP_002889019.1| hypothetical protein ARALYDRAFT_476678 [Arabidopsis lyrata subsp. lyrata] gi|297334860|gb|EFH65278.1| hypothetical protein ARALYDRAFT_476678 [Arabidopsis lyrata subsp. lyrata]	371	375	0	101.1	92.5	94.6	hypothetical protein ARALYDRAFT_476678	gbpln	Arabidopsis lyrata	AT1G75330.1 | Symbols: OTC | ornithine carbamoyltransferase | chr1:28266457-28268383 REVERSE LENGTH=375	371	375	0	101.1	92.2	94.1
Rsa1.0_00979.1_g22091.t1	ref|XP_002887589.1| hypothetical protein ARALYDRAFT_476681 [Arabidopsis lyrata subsp. lyrata] gi|297333430|gb|EFH63848.1| hypothetical protein ARALYDRAFT_476681 [Arabidopsis lyrata subsp. lyrata]	250	294	6.00E-51	117.6	57.2	70.8	hypothetical protein ARALYDRAFT_476681	gbpln	Arabidopsis lyrata	AT1G75360.1 | Symbols: | unknown protein; Has 74 Blast hits to 71 proteins in 15 species: Archae - 0; Bacteria - 4; Metazoa - 4; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr1:28275084-28275956 FORWARD LENGTH=290	250	290	3.00E-44	116.0	49.2	62.0
Rsa1.0_00979.1_g22092.t1	ref|XP_002889022.1| hypothetical protein ARALYDRAFT_476684 [Arabidopsis lyrata subsp. lyrata] gi|297334863|gb|EFH65281.1| hypothetical protein ARALYDRAFT_476684 [Arabidopsis lyrata subsp. lyrata]	320	324	1.00E-158	101.3	87.5	91.6	hypothetical protein ARALYDRAFT_476684	gbpln	Arabidopsis lyrata	AT1G75380.3 | Symbols: ATBBD1, BBD1 | bifunctional nuclease in basal defense response 1 | chr1:28281789-28283631 REVERSE LENGTH=325	320	325	1.00E-160	101.6	87.2	91.6
Rsa1.0_00979.1_g22093.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00979.1_g22094.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00979.1_g22095.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00980.1_g22096.t1	gb|AAC34342.1| Hypothetical protein [Arabidopsis thaliana]	376	374	2.00E-35	99.5	26.1	37.2	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	376	303	5.00E-38	80.6	26.1	37.5
Rsa1.0_00980.1_g22097.t1	ref|XP_002866551.1| hypothetical protein ARALYDRAFT_919627 [Arabidopsis lyrata subsp. lyrata] gi|297312386|gb|EFH42810.1| hypothetical protein ARALYDRAFT_919627 [Arabidopsis lyrata subsp. lyrata]	557	562	0	100.9	87.1	94.4	hypothetical protein ARALYDRAFT_919627	gbpln	Arabidopsis lyrata	AT5G63380.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr5:25387581-25390026 REVERSE LENGTH=562	557	562	0	100.9	85.3	91.9
Rsa1.0_00980.1_g22098.t1	ref|XP_002866550.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297312385|gb|EFH42809.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	615	616	0	100.2	74.6	83.9	kinase family protein	gbpln	Arabidopsis lyrata	AT5G63370.4 | Symbols: | Protein kinase superfamily protein | chr5:25384954-25386792 REVERSE LENGTH=612	615	612	0	99.5	72.7	82.3
Rsa1.0_00980.1_g22099.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00980.1_g22100.t1	ref|XP_002866549.1| hypothetical protein ARALYDRAFT_496519 [Arabidopsis lyrata subsp. lyrata] gi|297312384|gb|EFH42808.1| hypothetical protein ARALYDRAFT_496519 [Arabidopsis lyrata subsp. lyrata]	295	304	1.00E-123	103.1	82.7	89.8	hypothetical protein ARALYDRAFT_496519	gbpln	Arabidopsis lyrata	AT5G63350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48510.1); Has 103 Blast hits to 102 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:25380216-25381124 REVERSE LENGTH=302	295	302	1.00E-115	102.4	82.4	88.8
Rsa1.0_00980.1_g22101.t1	ref|XP_002864845.1| hypothetical protein ARALYDRAFT_496513 [Arabidopsis lyrata subsp. lyrata] gi|297310680|gb|EFH41104.1| hypothetical protein ARALYDRAFT_496513 [Arabidopsis lyrata subsp. lyrata]	166	183	2.00E-50	110.2	62.7	66.9	hypothetical protein ARALYDRAFT_496513	gbpln	Arabidopsis lyrata	AT5G63300.1 | Symbols: | Ribosomal protein S21 family protein | chr5:25371122-25371759 FORWARD LENGTH=185	166	185	7.00E-52	111.4	60.8	63.3

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<tr><td>Rsa1.0_00980.1.g22103.t1</td><td>gb|EOA14592.1| hypothetical protein CARUB_v10027842mg [Capsella rubella]</td><td>80</td><td>81</td><td>4.00E-28</td><td>101.3</td><td>82.5</td><td>87.5</td><td>hypothetical protein CARUB_v10027842mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G63270.1 | Symbols: | RPM1-interacting protein 4 (RIN4) family protein | chr5:25365498-25365949 REVERSE LENGTH=80</td><td>80</td><td>80</td><td>4.00E-28</td><td>100.0</td><td>81.3</td><td>85.0</td></tr>
<tr><td>Rsa1.0_00980.1.g22104.t2</td><td>ref|NP_201122.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75171684|sp|Q9FMK6.1|GDL89_ARATH RecName: Full=GDSL esterase/lipase At5g63170; AltName: Full=Extracellular lipase At5g63170; Flags: Precursor gi|10177298|dbj|BAB10559.1| lipase/acylhydrolase-like protein [Arabidopsis thaliana] gi|332010331|gb|AED97714.1| GDSL esterase/lipase [Arabidopsis thaliana]</td><td>334</td><td>338</td><td>1.00E-162</td><td>101.2</td><td>86.2</td><td>94.3</td><td>GDSL esterase/lipase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G63170.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:25338699-25340096 REVERSE LENGTH=338</td><td>334</td><td>338</td><td>1.00E-165</td><td>101.2</td><td>86.2</td><td>94.3</td></tr>
<tr><td>Rsa1.0_00980.1.g22105.t1</td><td>ref|XP_002866538.1| hypothetical protein ARALYDRAFT_919604 [Arabidopsis lyrata subsp. lyrata] gi|297312373|gb|EFH42797.1| hypothetical protein ARALYDRAFT_919604 [Arabidopsis lyrata subsp. lyrata]</td><td>366</td><td>365</td><td>0</td><td>99.7</td><td>90.2</td><td>94.8</td><td>hypothetical protein ARALYDRAFT_919604</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63160.1 | Symbols: BT1 | BTB and TAZ domain protein 1 | chr5:25333485-25335399 REVERSE LENGTH=365</td><td>366</td><td>365</td><td>0</td><td>99.7</td><td>88.8</td><td>94.0</td></tr>
<tr><td>Rsa1.0_00980.1.g22106.t1</td><td>ref|XP_002885669.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata] gi|297331509|gb|EFH61928.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata]</td><td>81</td><td>467</td><td>2.00E-27</td><td>576.5</td><td>66.7</td><td>75.3</td><td>hypothetical protein ARALYDRAFT_319176</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472</td><td>81</td><td>472</td><td>1.00E-26</td><td>582.7</td><td>59.3</td><td>70.4</td></tr>
<tr><td>Rsa1.0_00980.1.g22107.t1</td><td>ref|NP_201100.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana] gi|334188590|ref|NP_001190602.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana] gi|32815911|gb|AAP88340.1| At5g62950 [Arabidopsis thaliana] gi|110743157|dbj|BAE99470.1| hypothetical protein [Arabidopsis thaliana] gi|332010294|gb|AED97677.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana] gi|332010296|gb|AED97679.1| RNA polymerase II, Rpb4, core protein [Arabidopsis thaliana]</td><td>150</td><td>139</td><td>6.00E-53</td><td>92.7</td><td>68.7</td><td>80.0</td><td>RNA polymerase II, Rpb4, core protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G62950.3 | Symbols: | RNA polymerase II, Rpb4, core protein | chr5:25262355-25263033 REVERSE LENGTH=139</td><td>150</td><td>139</td><td>2.00E-55</td><td>92.7</td><td>68.7</td><td>80.0</td></tr>
<tr><td>Rsa1.0_00980.1.g22108.t1</td><td>gb|EOA13674.1| hypothetical protein CARUB_v10026747mg [Capsella rubella]</td><td>302</td><td>336</td><td>9.00E-80</td><td>111.3</td><td>65.2</td><td>74.5</td><td>hypothetical protein CARUB_v10026747mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G62910.1 | Symbols: | RING/U-box superfamily protein | chr5:25250830-25252015 FORWARD LENGTH=327</td><td>302</td><td>327</td><td>1.00E-78</td><td>108.3</td><td>63.6</td><td>73.2</td></tr>
<tr><td>Rsa1.0_00981.1.g22109.t1</td><td>gb|EOA40458.1| hypothetical protein CARUB_v10009182mg [Capsella rubella]</td><td>441</td><td>435</td><td>0</td><td>98.6</td><td>95.9</td><td>97.3</td><td>hypothetical protein CARUB_v10009182mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G48850.1 | Symbols: EMB1144 | chorismate synthase, putative / 5-enolpyruvylshikimate-3-phosphate phospholyase, putative | chr1:18065154-18067956 REVERSE LENGTH=436</td><td>441</td><td>436</td><td>0</td><td>98.9</td><td>93.9</td><td>96.1</td></tr>
<tr><td>Rsa1.0_00981.1.g22110.t1</td><td>ref|XP_002878309.1| hypothetical protein ARALYDRAFT_907521 [Arabidopsis lyrata subsp. lyrata] gi|297324147|gb|EFH54568.1| hypothetical protein ARALYDRAFT_907521 [Arabidopsis lyrata subsp. lyrata]</td><td>159</td><td>153</td><td>8.00E-50</td><td>96.2</td><td>61.0</td><td>74.2</td><td>hypothetical protein ARALYDRAFT_907521</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G20140.1 | Symbols: ASK4, SK4 | SKP1-like 4 | chr1:6986430-6987079 FORWARD LENGTH=163</td><td>159</td><td>163</td><td>4.00E-49</td><td>102.5</td><td>60.4</td><td>74.2</td></tr>
<tr><td>Rsa1.0_00981.1.g22111.t1</td><td>dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]</td><td>285</td><td>341</td><td>5.00E-80</td><td>119.6</td><td>50.9</td><td>59.6</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00981.1.g22112.t1</td><td>ref|NP_175319.2| protein trichome berefringence-like 7 [Arabidopsis thaliana] gi|332194241|gb|AEE32362.1| protein trichome berefringence-like 7 [Arabidopsis thaliana]</td><td>443</td><td>445</td><td>0</td><td>100.5</td><td>90.5</td><td>95.9</td><td>protein trichome berefringence-like 7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G48880.1 | Symbols: TBL7 | TRICHOME BIREFRINGENCE-LIKE 7 | chr1:18081033-18082650 FORWARD LENGTH=445</td><td>443</td><td>445</td><td>0</td><td>100.5</td><td>90.5</td><td>95.9</td></tr>
<tr><td>Rsa1.0_00981.1.g22113.t1</td><td>gb|EOA18188.1| hypothetical protein CARUB_v10006667mg [Capsella rubella]</td><td>206</td><td>171</td><td>5.00E-16</td><td>83.0</td><td>27.7</td><td>43.2</td><td>hypothetical protein CARUB_v10006667mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G30760.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr4:14982552-14983285 FORWARD LENGTH=191</td><td>206</td><td>191</td><td>2.00E-17</td><td>92.7</td><td>24.3</td><td>38.8</td></tr>
<tr><td>Rsa1.0_00981.1.g22114.t1</td><td>gb|EOA40222.1| hypothetical protein CARUB_v10008947mg [Capsella rubella]</td><td>496</td><td>495</td><td>0</td><td>99.8</td><td>94.4</td><td>97.2</td><td>hypothetical protein CARUB_v10008947mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G48900.1 | Symbols: | Signal recognition particle, SRP54 subunit protein | chr1:18084972-18087743 REVERSE LENGTH=495</td><td>496</td><td>495</td><td>0</td><td>99.8</td><td>94.4</td><td>97.6</td></tr>
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Rsa1.0_00982.1.g22115.t1	emb|CAN61554.1| hypothetical protein VITISV_028479 [Vitis vinifera]	160	1144	5.00E-32	715.0	38.8	48.1	hypothetical protein VITISV_028479	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_00982.1.g22116.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00982.1.g22117.t1	ref|NP_850851.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|238481311|ref|NP_001154719.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|332005268|gb|AED92651.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|332005269|gb|AED92652.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana]	610	465	4.00E-49	76.2	18.2	18.4	heavy metal transport/detoxification domain-containing protein	gbpln	Arabidopsis thaliana	AT5G19090.3 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:6387910-6389855 FORWARD LENGTH=465	610	465	1.00E-51	76.2	18.2	18.4
Rsa1.0_00982.1.g22118.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00982.1.g22119.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00982.1.g22120.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00983.1.g22121.t1	ref|NP_001077797.1| WPP domain-interacting tail-anchored protein 2 [Arabidopsis thaliana] gi|334183748|ref|NP_001185353.1| WPP domain-interacting tail-anchored protein 2 [Arabidopsis thaliana] gi|332196738|gb|AEE34859.1| WPP domain-interacting tail-anchored protein 2 [Arabidopsis thaliana] gi|332196739|gb|AEE34860.1| WPP domain-interacting tail-anchored protein 2 [Arabidopsis thaliana]	597	582	0	97.5	82.9	90.6	WPP domain-interacting tail-anchored protein 2	gbpln	Arabidopsis thaliana	AT1G68910.3 | Symbols: WIT2 | WPP domain-interacting protein 2 | chr1:25908373-25910485 REVERSE LENGTH=582	597	582	0	97.5	82.9	90.6
Rsa1.0_00983.1.g22122.t1	#	#	#	#	#	#	#	-	----	----	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	129	384	1.00E-10	297.7	22.5	26.4
Rsa1.0_00983.1.g22123.t1	ref|NP_001031254.1| putative defensin-like protein 263 [Arabidopsis thaliana] gi|122209605|sp|Q2V4D9.1|DF263_ARATH RecName: Full=Putative defensin-like protein 263; Flags: Precursor gi|332196736|gb|AEE34857.1| putative defensin-like protein 263 [Arabidopsis thaliana]	93	96	5.00E-34	103.2	76.3	84.9	putative defensin-like protein 263	gbpln	Arabidopsis thaliana	AT1G68907.1 | Symbols: | Defensin-like (DEFL) family protein | chr1:25907508-25907891 REVERSE LENGTH=96	93	96	8.00E-37	103.2	76.3	84.9
Rsa1.0_00983.1.g22124.t1	ref|NP_001031253.1| putative defensin-like protein 262 [Arabidopsis thaliana] gi|122209606|sp|Q2V4E0.1|DF262_ARATH RecName: Full=Putative defensin-like protein 262; Flags: Precursor gi|332196735|gb|AEE34856.1| putative defensin-like protein 262 [Arabidopsis thaliana]	90	95	2.00E-14	105.6	54.4	66.7	putative defensin-like protein 262	gbpln	Arabidopsis thaliana	AT1G68905.1 | Symbols: | Defensin-like (DEFL) family protein | chr1:25906716-25907092 REVERSE LENGTH=95	90	95	3.00E-17	105.6	54.4	66.7
Rsa1.0_00983.1.g22125.t1	ref|XP_002865055.1| hypothetical protein ARALYDRAFT_920059 [Arabidopsis lyrata subsp. lyrata] gi|297310890|gb|EFH41314.1| hypothetical protein ARALYDRAFT_920059 [Arabidopsis lyrata subsp. lyrata]	385	398	1.00E-51	103.4	37.7	55.8	hypothetical protein ARALYDRAFT_920059	gbpln	Arabidopsis lyrata	AT5G66670.2 | Symbols: | Protein of unknown function (DUF677) | chr5:26611474-26612700 REVERSE LENGTH=408	385	408	6.00E-49	106.0	36.6	54.0
Rsa1.0_00983.1.g22126.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00983.1.g22127.t1	gb|EOA12536.1| hypothetical protein CARUB_v10026516mg [Capsella rubella]	319	405	1.00E-39	127.0	34.8	54.2	hypothetical protein CARUB_v10026516mg	gbpln	Capsella rubella	AT5G66670.2 | Symbols: | Protein of unknown function (DUF677) | chr5:26611474-26612700 REVERSE LENGTH=408	319	408	3.00E-39	127.9	37.3	57.4
Rsa1.0_00983.1.g22128.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00984.1.g22129.t2	ref|NP_187969.1| calmodulin-binding protein-like protein [Arabidopsis thaliana] gi|11994562|dbj|BAB02602.1| unnamed protein product [Arabidopsis thaliana] gi|332641860|gb|AEE75381.1| calmodulin-binding protein-like protein [Arabidopsis thaliana]	222	605	4.00E-12	272.5	22.1	24.8	calmodulin-binding protein-like protein	gbpln	Arabidopsis thaliana	AT3G13600.1 | Symbols: | calmodulin-binding family protein | chr3:4445102-4447383 FORWARD LENGTH=605	222	605	1.00E-14	272.5	22.1	24.8
Rsa1.0_00984.1.g22130.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1716	1213	0	70.7	26.0	38.6	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1716	626	5.00E-67	36.5	8.6	14.0
Rsa1.0_00984.1.g22131.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	195	478	1.00E-39	245.1	42.1	58.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	195	746	5.00E-35	382.6	34.9	47.7

Rsa1.0_00984.1.g22132.t1	gb|AAD19773.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1576	1335	4.00E-87	84.7	13.1	19.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145	1576	145	4.00E-17	9.2	2.7	3.3
Rsa1.0_00984.1.g22133.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	374	1342	1.00E-103	358.8	51.1	64.7	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	374	1262	9.00E-40	337.4	29.1	47.3
Rsa1.0_00984.1.g22134.t1	ref|XP_002865054.1| hypothetical protein ARALYDRAFT_920058 [Arabidopsis lyrata subsp. lyrata] gi|297310889|gb|EFH41313.1| hypothetical protein ARALYDRAFT_920058 [Arabidopsis lyrata subsp. lyrata]	374	409	5.00E-58	109.4	42.8	60.2	hypothetical protein ARALYDRAFT_920058	gbpln	Arabidopsis lyrata	AT5G66670.2 | Symbols: | Protein of unknown function (DUF677) | chr5:26611474-26612700 REVERSE LENGTH=408	374	408	2.00E-60	109.1	43.0	60.7
Rsa1.0_00984.1.g22135.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00984.1.g22136.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	774	1023	1.00E-133	132.2	28.7	35.5	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	774	575	5.00E-43	74.3	16.4	27.3
Rsa1.0_00985.1.g22137.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00985.1.g22138.t1	ref|NP_189252.1| cytochrome P450 71B23 [Arabidopsis thaliana] gi|13878383|sp|Q9LTM0.1|C71BN_ARATH RecName: Full=Cytochrome P450 71B23 gi|11994440|dbj|BAB02442.1| cytochrome P450 [Arabidopsis thaliana] gi|50897236|gb|AAT85757.1| At3g26210 [Arabidopsis thaliana] gi|332643613|gb|AEE77134.1| cytochrome P450 71B23 [Arabidopsis thaliana]	501	501	0	100.0	82.4	91.8	cytochrome P450 71B23	gbpln	Arabidopsis thaliana	AT3G26210.1 | Symbols: CYP71B23 | cytochrome P450, family 71, subfamily B, polypeptide 23 | chr3:9593329-9595202 REVERSE LENGTH=501	501	501	0	100.0	82.4	91.8
Rsa1.0_00985.1.g22139.t2	ref|XP_002876955.1| cytochrome P450 [Arabidopsis lyrata subsp. lyrata] gi|297322793|gb|EFH53214.1| cytochrome P450 [Arabidopsis lyrata subsp. lyrata]	1085	483	0	44.5	35.2	40.5	cytochrome P450	gbpln	Arabidopsis lyrata	AT3G26230.1 | Symbols: CYP71B24 | cytochrome P450, family 71, subfamily B, polypeptide 24 | chr3:9598200-9599892 REVERSE LENGTH=498	1085	498	0	45.9	34.3	40.0
Rsa1.0_00985.1.g22140.t1	ref|XP_002876962.1| CYP71B34 [Arabidopsis lyrata subsp. lyrata] gi|297322800|gb|EFH53221.1| CYP71B34 [Arabidopsis lyrata subsp. lyrata]	497	500	0	100.6	68.2	84.1	CYP71B34	gbpln	Arabidopsis lyrata	AT3G26300.1 | Symbols: CYP71B34 | cytochrome P450, family 71, subfamily B, polypeptide 34 | chr3:9639199-9640866 REVERSE LENGTH=500	497	500	0	100.6	67.4	83.7
Rsa1.0_00985.1.g22141.t1	ref|XP_002876962.1| CYP71B34 [Arabidopsis lyrata subsp. lyrata] gi|297322800|gb|EFH53221.1| CYP71B34 [Arabidopsis lyrata subsp. lyrata]	500	500	0	100.0	74.0	85.8	CYP71B34	gbpln	Arabidopsis lyrata	AT3G26300.1 | Symbols: CYP71B34 | cytochrome P450, family 71, subfamily B, polypeptide 34 | chr3:9639199-9640866 REVERSE LENGTH=500	500	500	0	100.0	73.8	85.8
Rsa1.0_00985.1.g22142.t1	gb|EOA25001.1| hypothetical protein CARUB_v10018299mg [Capsella rubella]	108	101	3.00E-40	93.5	81.5	85.2	hypothetical protein CARUB_v10018299mg	gbpln	Capsella rubella	AT3G26360.1 | Symbols: | Ribosomal protein S21 family protein | chr3:9655963-9656373 REVERSE LENGTH=101	108	101	1.00E-42	93.5	81.5	84.3
Rsa1.0_00985.1.g22143.t1	ref|XP_002875314.1| hypothetical protein ARALYDRAFT_484400 [Arabidopsis lyrata subsp. lyrata] gi|297321152|gb|EFH51573.1| hypothetical protein ARALYDRAFT_484400 [Arabidopsis lyrata subsp. lyrata]	557	556	0	99.8	95.2	96.8	hypothetical protein ARALYDRAFT_484400	gbpln	Arabidopsis lyrata	AT3G26370.1 | Symbols: | O-fucosyltransferase family protein | chr3:9656886-9659741 FORWARD LENGTH=557	557	557	0	100.0	95.3	96.8
Rsa1.0_00985.1.g22144.t1	gb|EOA23740.1| hypothetical protein CARUB_v10016953mg [Capsella rubella]	565	555	0	98.2	80.5	85.1	hypothetical protein CARUB_v10016953mg	gbpln	Capsella rubella	AT3G26400.1 | Symbols: EIF4B1 | eukaryotic translation initiation factor 4B1 | chr3:9666616-9669081 FORWARD LENGTH=532	565	532	0	94.2	76.6	81.8
Rsa1.0_00985.1.g22145.t1	ref|XP_002876970.1| methyltransferase/ nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297322808|gb|EFH53229.1| methyltransferase/ nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	475	477	0	100.4	93.5	97.7	methyltransferase/ nucleic acid binding protein	gbpln	Arabidopsis lyrata	AT3G26410.1 | Symbols: TRM11, AtTRM11 | methyltransferases;nucleic acid binding | chr3:9669508-9671273 REVERSE LENGTH=477	475	477	0	100.4	93.1	97.5

Rsa1.0_00985.1.g22146.t1	ref|NP_189273.1| RNA recognition motif and CCHC-type zinc finger domain-containing protein [Arabidopsis thaliana] gi|15983477|gb|AAL11606.1|AF424613_1 AT3g26420/F20C19_14 [Arabidopsis thaliana] gi|9294301|dbj|BAB02203.1| unnamed protein product [Arabidopsis thaliana] gi|15451066|gb|AAK96804.1| Unknown protein [Arabidopsis thaliana] gi|18377412|gb|AAL66872.1| unknown protein [Arabidopsis thaliana] gi|62320797|dbj|BAD93728.1| RNA-binding protein [Arabidopsis thaliana] gi|110742443|dbj|BAE99140.1| putative RNA-binding protein [Arabidopsis thaliana] gi|332643635|gb|AEE77156.1| RNA recognition motif and CCHC-type zinc finger domain-containing protein [Arabidopsis thaliana]	246	245	2.00E-98	99.6	85.0	91.1	RNA recognition motif and CCHC-type zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT3G26420.1 | Symbols: ATRZ-1A | RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain | chr3:9671953-9673055 FORWARD LENGTH=245	246	245	1.00E-101	99.6	85.0	91.1
Rsa1.0_00985.1.g22147.t2	ref|NP_189274.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75273423|sp|Q9LIN2.1|GDL53_ARATH RecName: Full=GDSL esterase/lipase At3g26430; AltName: Full=Extracellular lipase At3g26430; Flags: Precursor gi|9294302|dbj|BAB02204.1| nodulin-like protein protein [Arabidopsis thaliana] gi|17064918|gb|AAL32613.1| Unknown protein [Arabidopsis thaliana] gi|20259934|gb|AAM13314.1| unknown protein [Arabidopsis thaliana] gi|332643634|gb|AEE77155.1| GDSL esterase/lipase [Arabidopsis thaliana]	383	380	0	99.2	82.8	91.4	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT3G26430.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:9674419-9675889 FORWARD LENGTH=380	383	380	0	99.2	82.8	91.4
Rsa1.0_00985.1.g22148.t1	gb|EOA33834.1| hypothetical protein CARUB_v10021315mg, partial [Capsella rubella]	167	684	1.00E-61	409.6	65.3	77.8	hypothetical protein CARUB_v10021315mg, partial	gbpln	Capsella rubella	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	167	769	9.00E-57	460.5	59.9	78.4
Rsa1.0_00985.1.g22149.t2	ref|XP_002510773.1| ATP-dependent RNA helicase, putative [Ricinus communis] gi|223551474|gb|EEF52960.1| ATP-dependent RNA helicase, putative [Ricinus communis]	1185	1177	0	99.3	81.3	87.8	ATP-dependent RNA helicase, putative	gbpln	Ricinus communis	AT3G26560.1 | Symbols: | ATP-dependent RNA helicase, putative | chr3:9750122-9753719 REVERSE LENGTH=1168	1185	1168	0	98.6	78.5	80.4
Rsa1.0_00985.1.g22150.t1	ref|XP_002875323.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297321161|gb|EFH51582.1| binding protein [Arabidopsis lyrata subsp. lyrata]	349	349	1.00E-172	100.0	89.1	93.1	binding protein	gbpln	Arabidopsis lyrata	AT3G26580.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:9758933-9760349 FORWARD LENGTH=350	349	350	1.00E-172	100.3	88.0	92.0
Rsa1.0_00985.1.g22151.t1	ref|NP_189291.1| mate efflux domain-containing protein [Arabidopsis thaliana] gi|1402878|emb|CAA66809.1| hypothetical protein [Arabidopsis thaliana] gi|9293938|dbj|BAB01841.1| unnamed protein product [Arabidopsis thaliana] gi|16323121|gb|AAL15295.1| AT3g26590/MFE16_11 [Arabidopsis thaliana] gi|25141209|gb|AAN73299.1| At3g26590/MFE16_11 [Arabidopsis thaliana] gi|332643662|gb|AEE77183.1| mate efflux domain-containing protein [Arabidopsis thaliana]	503	500	0	99.4	87.1	93.4	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT3G26590.1 | Symbols: | MATE efflux family protein | chr3:9761927-9765259 REVERSE LENGTH=500	503	500	0	99.4	87.1	93.4
Rsa1.0_00985.1.g22152.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2114	1274	0	60.3	28.7	38.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2114	575	2.00E-51	27.2	5.5	8.2
Rsa1.0_00986.1.g22153.t1	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	327	1864	3.00E-90	570.0	54.4	68.2	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00986.1.g22154.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	521	940	5.00E-43	180.4	20.2	31.7	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00986.1.g22155.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00986.1.g22156.t1	gb|ABD65085.1| Ulp1 protease family protein [Brassica oleracea]	83	640	5.00E-12	771.1	42.2	48.2	Ulp1 protease family protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00986.1.g22157.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00986.1.g22158.t2	ref|XP_002894562.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297340404|gb|EFH70821.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	1001	1031	0	103.0	75.5	86.2	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G56130.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:20994931-21000887 REVERSE LENGTH=1032	1001	1032	0	103.1	75.0	86.0
Rsa1.0_00986.1.g22159.t1	dbj|BAJ34267.1| unnamed protein product [Thellungiella halophila]	433	422	0	97.5	85.5	90.3	unnamed protein product	----	----	AT5G43270.1 | Symbols: SPL2 | squamosa promoter binding protein-like 2 | chr5:17360527-17362143 REVERSE LENGTH=419	433	419	0	96.8	81.8	86.8
Rsa1.0_00986.1.g22160.t2	gb|ABD65060.1| hypothetical protein 27.t00039 [Brassica oleracea]	282	1367	1.00E-119	484.8	72.7	79.1	hypothetical protein 27.t00039	gbpln	Brassica oleracea	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	282	344	4.00E-43	122.0	31.2	44.0
Rsa1.0_00987.1.g22161.t1	ref|XP_002887110.1| hypothetical protein ARALYDRAFT_338955 [Arabidopsis lyrata subsp. lyrata] gi|297332951|gb|EFH63369.1| hypothetical protein ARALYDRAFT_338955 [Arabidopsis lyrata subsp. lyrata]	292	330	6.00E-57	113.0	37.3	45.2	hypothetical protein ARALYDRAFT_338955	gbpln	Arabidopsis lyrata	AT5G45220.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18298926-18301069 REVERSE LENGTH=546	292	546	2.00E-49	187.0	30.8	39.7
Rsa1.0_00987.1.g22162.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	160	1142	5.00E-35	713.8	50.6	66.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	160	256	1.00E-15	160.0	30.0	43.1
Rsa1.0_00987.1.g22163.t4	ref|XP_002863513.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309348|gb|EFH39772.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	493	1327	1.00E-150	269.2	60.0	72.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G45200.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18283967-18290332 REVERSE LENGTH=1261	493	1261	1.00E-105	255.8	40.2	46.7
Rsa1.0_00987.1.g22164.t1	dbj|BAB11393.1| disease resistance protein RPS4 [Arabidopsis thaliana]	163	1232	2.00E-38	755.8	51.5	66.3	disease resistance protein RPS4	gbpln	Arabidopsis thaliana	AT5G45200.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18283967-18290332 REVERSE LENGTH=1261	163	1261	8.00E-41	773.6	51.5	66.3
Rsa1.0_00987.1.g22165.t1	emb|CAA19715.1| putative protein [Arabidopsis thaliana] gi|7269574|emb|CAB79576.1| putative protein [Arabidopsis thaliana]	519	1318	2.00E-96	253.9	35.6	50.7	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00987.1.g22166.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1358	1342	0	98.8	48.7	67.1	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1358	1262	1.00E-77	92.9	12.8	19.9
Rsa1.0_00987.1.g22167.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00988.1.g22168.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1423	1475	0	103.7	60.6	75.4	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1423	1262	1.00E-162	88.7	21.4	26.9
Rsa1.0_00988.1.g22169.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00988.1.g22170.t1	ref|NP_564171.1| transcription factor bHLH94 [Arabidopsis thaliana] gi|218563531|sp|Q9SK91.2|BH094_ARATH RecName: Full=Transcription factor bHLH94; AltName: Full=Basic helix-loop-helix protein 94; Short=AtbHLH94; Short=bHLH 94; AltName: Full=Transcription factor EN 16; AltName: Full=bHLH transcription factor bHLH094 gi|332192126|gb|AEE30247.1| transcription factor bHLH94 [Arabidopsis thaliana]	303	304	1.00E-122	100.3	79.5	86.5	transcription factor bHLH94	gbpln	Arabidopsis thaliana	AT1G22490.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:7938448-7940489 REVERSE LENGTH=304	303	304	1.00E-124	100.3	79.5	86.5
Rsa1.0_00988.1.g22171.t1	gb|AAM15219.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	259	767	4.00E-32	296.1	25.5	30.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00988.1.g22172.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_00988.1.g22173.t1</td><td>ref|NP_173661.1| cytochrome C oxidase 6B [Arabidopsis thaliana] gi|75193983|sp|Q9S7L9.1|CX6B1_ARATH RecName: Full=Cytochrome c oxidase subunit 6b-1; Short=AtCOX6b-1 gi|6587843|gb|AAF18532.1|AC006551_18 Subunit 6b of cytochrome c oxidase [Arabidopsis thaliana] gi|6518353|dbj|BAA87883.1| subunit 6b of cytochrome c oxidase [Arabidopsis thaliana] gi|17381082|gb|AAL36353.1| putative cytochrome c oxidase subunit [Arabidopsis thaliana] gi|20465723|gb|AAM20330.1| putative cytochrome c oxidase subunit [Arabidopsis thaliana] gi|332192122|gb|AEE30243.1| cytochrome C oxidase 6B [Arabidopsis thaliana]</td><td>188</td><td>191</td><td>5.00E-68</td><td>101.6</td><td>80.3</td><td>85.6</td><td>cytochrome C oxidase 6B</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G22450.1 | Symbols: COX6B, ATCOX6B2 | cytochrome C oxidase 6B | chr1:7925447-7926918 FORWARD LENGTH=191</td><td>188</td><td>191</td><td>2.00E-70</td><td>101.6</td><td>80.3</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00988.1.g22174.t7</td><td>gb|AAD25621.1|AC005287_23 Hypothetical protein [Arabidopsis thaliana]</td><td>495</td><td>1250</td><td>4.00E-15</td><td>252.5</td><td>8.7</td><td>11.5</td><td>Hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907-10814173 REVERSE LENGTH=337</td><td>495</td><td>337</td><td>4.00E-12</td><td>68.1</td><td>7.1</td><td>9.5</td></tr>
<tr><td>Rsa1.0_00988.1.g22175.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00988.1.g22176.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00988.1.g22177.t1</td><td>gb|EOA35441.1| hypothetical protein CARUB_v10020644mg, partial [Capsella rubella]</td><td>291</td><td>327</td><td>1.00E-115</td><td>112.4</td><td>73.5</td><td>80.8</td><td>hypothetical protein CARUB_v10020644mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G78300.1 | Symbols: GRF2, 14-3-3OMEGA, GF14 OMEGA | general regulatory factor 2 | chr1:29461883-29463052 FORWARD LENGTH=259</td><td>291</td><td>259</td><td>1.00E-114</td><td>89.0</td><td>72.9</td><td>79.7</td></tr>
<tr><td>Rsa1.0_00988.1.g22178.t1</td><td>gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]</td><td>147</td><td>1463</td><td>3.00E-31</td><td>995.2</td><td>44.2</td><td>60.5</td><td>F5J5.1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00989.1.g22179.t1</td><td>gb|AAF97298.1|AC007843_1 Hypothetical protein [Arabidopsis thaliana]</td><td>257</td><td>362</td><td>5.00E-69</td><td>140.9</td><td>49.8</td><td>66.1</td><td>Hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00989.1.g22180.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_00989.1.g22181.t1</td><td>ref|XP_002866187.1| ATLIG4 [Arabidopsis lyrata subsp. lyrata] gi|297312022|gb|EFH42446.1| ATLIG4 [Arabidopsis lyrata subsp. lyrata]</td><td>1185</td><td>1221</td><td>0</td><td>103.0</td><td>89.0</td><td>94.0</td><td>ATLIG4</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G57160.1 | Symbols: ATLIG4, LIG4 | DNA ligase IV | chr5:23155150-23161688 REVERSE LENGTH=1219</td><td>1185</td><td>1219</td><td>0</td><td>102.9</td><td>89.2</td><td>94.1</td></tr>
<tr><td>Rsa1.0_00989.1.g22182.t1</td><td>ref|XP_002864502.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297310337|gb|EFH40761.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]</td><td>244</td><td>247</td><td>1.00E-125</td><td>101.2</td><td>93.0</td><td>97.1</td><td>basic helix-loop-helix family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G57150.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:23152361-23154872 FORWARD LENGTH=247</td><td>244</td><td>247</td><td>1.00E-128</td><td>101.2</td><td>93.0</td><td>97.1</td></tr>
<tr><td>Rsa1.0_00989.1.g22183.t1</td><td>gb|EOA15000.1| hypothetical protein CARUB_v10028349mg, partial [Capsella rubella]</td><td>418</td><td>437</td><td>0</td><td>104.5</td><td>79.2</td><td>85.6</td><td>hypothetical protein CARUB_v10028349mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G57140.1 | Symbols: ATPAP28, PAP28 | purple acid phosphatase 28 | chr5:23149926-23151370 FORWARD LENGTH=397</td><td>418</td><td>397</td><td>0</td><td>95.0</td><td>77.5</td><td>85.6</td></tr>
<tr><td>Rsa1.0_00989.1.g22184.t2</td><td>ref|NP_568849.2| Clp amino terminal domain-containing protein [Arabidopsis thaliana] gi|8843815|dbj|BAA97363.1| unnamed protein product [Arabidopsis thaliana] gi|332009468|gb|AED96851.1| Clp amino terminal domain-containing protein [Arabidopsis thaliana]</td><td>1020</td><td>1028</td><td>0</td><td>100.8</td><td>78.9</td><td>86.3</td><td>Clp amino terminal domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G57130.1 | Symbols: | Clp amino terminal domain-containing protein | chr5:23145291-23149395 FORWARD LENGTH=1028</td><td>1020</td><td>1028</td><td>0</td><td>100.8</td><td>78.9</td><td>86.3</td></tr>
<tr><td>Rsa1.0_00989.1.g22185.t1</td><td>gb|EOA18248.1| hypothetical protein CARUB_v10006740mg, partial [Capsella rubella]</td><td>426</td><td>441</td><td>8.00E-65</td><td>103.5</td><td>37.1</td><td>45.8</td><td>hypothetical protein CARUB_v10006740mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>426</td><td>696</td><td>1.00E-10</td><td>163.4</td><td>16.9</td><td>30.8</td></tr>
<tr><td>Rsa1.0_00990.1.g22186.t1</td><td>ref|NP_001189938.1| legumain [Arabidopsis thaliana] gi|332642827|gb|AEE76348.1| delta vacuolar processing enzyme/legumain [Arabidopsis thaliana]</td><td>575</td><td>571</td><td>0</td><td>99.3</td><td>77.6</td><td>86.6</td><td>legumain</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G20210.2 | Symbols: DELTA-VPE | delta vacuolar processing enzyme | chr3:7052482-7055416 FORWARD LENGTH=571</td><td>575</td><td>571</td><td>0</td><td>99.3</td><td>77.6</td><td>86.6</td></tr>
<tr><td>Rsa1.0_00990.1.g22187.t1</td><td>ref|NP_566655.1| Ribosomal L18p/L5e family protein [Arabidopsis thaliana] gi|9293979|dbj|BAB01882.1| unnamed protein product [Arabidopsis thaliana] gi|21554527|gb|AAM63600.1| unknown [Arabidopsis thaliana] gi|24030337|gb|AAN41334.1| unknown protein [Arabidopsis thaliana] gi|222423792|dbj|BAH19862.1| AT3G20230 [Arabidopsis thaliana] gi|332642829|gb|AEE76350.1| Ribosomal L18p/L5e family protein [Arabidopsis thaliana]</td><td>187</td><td>187</td><td>2.00E-99</td><td>100.0</td><td>94.1</td><td>98.4</td><td>Ribosomal L18p/L5e family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G20230.1 | Symbols: | Ribosomal L18p/L5e family protein | chr3:7055639-7056679 REVERSE LENGTH=187</td><td>187</td><td>187</td><td>1.00E-102</td><td>100.0</td><td>94.1</td><td>98.4</td></tr>
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Rsa1.0_00990.1.g22188.t1	ref|NP_188659.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|75311227|sp|Q9LJX5.1|BRTL1_ARATH RecName: Full=Probable mitochondrial adenine nucleotide transporter BTL1; AltName: Full=Adenine nucleotide transporter BT1-like protein 1 gi|9293980|dbj|BAB01883.1| unnamed protein product [Arabidopsis thaliana] gi|29029108|gb|AAO64933.1| At3g20240 [Arabidopsis thaliana] gi|110743061|dbj|BAE99423.1| putative mitochondrial carrier protein [Arabidopsis thaliana] gi|332642830|gb|AEE76351.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana]	346	348	1.00E-177	100.6	90.2	94.5	Mitochondrial substrate carrier family protein	gbpln	Arabidopsis thaliana	AT3G20240.1 | Symbols: | Mitochondrial substrate carrier family protein | chr3:7057192-7058716 FORWARD LENGTH=348	346	348	1.00E-179	100.6	90.2	94.5
Rsa1.0_00990.1.g22189.t2	ref|XP_002885359.1| hypothetical protein ARALYDRAFT_342166 [Arabidopsis lyrata subsp. lyrata] gi|297331199|gb|EFH61618.1| hypothetical protein ARALYDRAFT_342166 [Arabidopsis lyrata subsp. lyrata]	955	965	0	101.0	83.8	89.1	hypothetical protein ARALYDRAFT_342166	gbpln	Arabidopsis lyrata	AT3G20250.1 | Symbols: APUM5, PUM5 | pumilio 5 | chr3:7059098-7062660 REVERSE LENGTH=961	955	961	0	100.6	82.6	88.1
Rsa1.0_00990.1.g22190.t1	gb|EOA30619.1| hypothetical protein CARUB_v10013756mg [Capsella rubella]	431	430	0	99.8	84.0	89.1	hypothetical protein CARUB_v10013756mg	gbpln	Capsella rubella	AT3G20260.1 | Symbols: | Protein of unknown function (DUF1666) | chr3:7064190-7065751 REVERSE LENGTH=437	431	437	0	101.4	83.8	89.6
Rsa1.0_00990.1.g22191.t1	ref|NP_851006.1| lipid-binding serum glycoprotein-like protein [Arabidopsis thaliana] gi|334185491|ref|NP_001189939.1| lipid-binding serum glycoprotein-like protein [Arabidopsis thaliana] gi|332642833|gb|AEE76354.1| lipid-binding serum glycoprotein-like protein [Arabidopsis thaliana] gi|332642835|gb|AEE76356.1| putative BPI/LBP family protein [Arabidopsis thaliana]	722	722	0	100.0	71.7	84.5	lipid-binding serum glycoprotein-like protein	gbpln	Arabidopsis thaliana	AT3G20270.3 | Symbols: | lipid-binding serum glycoprotein family protein | chr3:7067779-7070866 FORWARD LENGTH=722	722	722	0	100.0	71.7	84.5
Rsa1.0_00990.1.g22192.t1	ref|NP_851007.1| PHD finger protein [Arabidopsis thaliana] gi|332642836|gb|AEE76357.1| PHD finger protein [Arabidopsis thaliana]	715	743	0	103.9	62.5	72.9	PHD finger protein	gbpln	Arabidopsis thaliana	AT3G20280.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr3:7071475-7074340 FORWARD LENGTH=743	715	743	0	103.9	62.5	72.9
Rsa1.0_00990.1.g22193.t2	ref|NP_566657.1| EPS15 homology domain 1 protein [Arabidopsis thaliana] gi|79313303|ref|NP_001030731.1| EPS15 homology domain 1 protein [Arabidopsis thaliana] gi|14334440|gb|AAK59418.1| unknown protein [Arabidopsis thaliana] gi|28394001|gb|AAO42408.1| unknown protein [Arabidopsis thaliana] gi|222424046|dbj|BAH19984.1| AT3G20290 [Arabidopsis thaliana] gi|332642838|gb|AEE76359.1| EPS15 homology domain 1 protein [Arabidopsis thaliana] gi|332642839|gb|AEE76360.1| EPS15 homology domain 1 protein [Arabidopsis thaliana]	562	545	0	97.0	86.3	90.4	EPS15 homology domain 1 protein	gbpln	Arabidopsis thaliana	AT3G20290.2 | Symbols: ATEHD1, EHD1 | EPS15 homology domain 1 | chr3:7075057-7078655 REVERSE LENGTH=545	562	545	0	97.0	86.3	90.4
Rsa1.0_00990.1.g22194.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00990.1.g22195.t1	ref|XP_002885364.1| extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata] gi|297331204|gb|EFH61623.1| extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata]	449	451	0	100.4	94.7	96.7	extracellular ligand-gated ion channel	gbpln	Arabidopsis lyrata	AT3G20300.1 | Symbols: | Protein of unknown function (DUF3537) | chr3:7079832-7081809 REVERSE LENGTH=452	449	452	0	100.7	93.5	96.2
Rsa1.0_00990.1.g22196.t5	ref|XP_002885365.1| hypothetical protein ARALYDRAFT_479554 [Arabidopsis lyrata subsp. lyrata] gi|297331205|gb|EFH61624.1| hypothetical protein ARALYDRAFT_479554 [Arabidopsis lyrata subsp. lyrata]	225	233	1.00E-76	103.6	81.8	85.3	hypothetical protein ARALYDRAFT_479554	gbpln	Arabidopsis lyrata	AT3G20310.1 | Symbols: ATERF-7, ATERF7, ERF7 | ethylene response factor 7 | chr3:7085957-7086691 REVERSE LENGTH=244	225	244	2.00E-76	108.4	84.4	87.6
Rsa1.0_00990.1.g22197.t1	gb|EOA30740.1| hypothetical protein CARUB_v10013880mg [Capsella rubella]	393	398	0	101.3	92.1	96.2	hypothetical protein CARUB_v10013880mg	gbpln	Capsella rubella	AT3G20330.1 | Symbols: PYRB | PYRIMIDINE B | chr3:7090354-7091904 REVERSE LENGTH=390	393	390	0	99.2	90.6	94.7

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<tr><td>Rsa1.0_00990.1_g22198.t1</td><td>ref|XP_002885368.1| hypothetical protein ARALYDRAFT_898447 [Arabidopsis lyrata subsp. lyrata] gi|297331208|gb|EFH61627.1| hypothetical protein ARALYDRAFT_898447 [Arabidopsis lyrata subsp. lyrata]</td><td>116</td><td>116</td><td>6.00E-34</td><td>100.0</td><td>70.7</td><td>78.4</td><td>hypothetical protein ARALYDRAFT_898447</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G20340.1 | Symbols: | Expression of the gene is downregulated in the presence of paraquat, an inducer of photoxidative stress. | chr3:7093075-7093422 REVERSE LENGTH=115</td><td>116</td><td>115</td><td>4.00E-36</td><td>99.1</td><td>70.7</td><td>78.4</td></tr>
<tr><td>Rsa1.0_00990.1_g22199.t1</td><td>ref|NP_188670.1| uncharacterized protein [Arabidopsis thaliana] gi|219291108|gb|ACL13988.1| At3g20350 [Arabidopsis thaliana] gi|332642846|gb|AEE76367.1| uncharacterized protein AT3G20350 [Arabidopsis thaliana]</td><td>649</td><td>673</td><td>0</td><td>103.7</td><td>73.7</td><td>82.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G20350.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: cotyledon; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G50660.1); Has 15095 Blast hits to 11224 proteins in 1051 species: Archae - 223; Bacteria - 1586; Metazoa - 7000; Fungi - 1255; Plants - 746; Viruses - 40; Other Eukaryotes - 4245 (source: NCBI BLink). | chr3:7096602-7099372 FORWARD LENGTH=673</td><td>649</td><td>673</td><td>0</td><td>103.7</td><td>73.7</td><td>82.4</td></tr>
<tr><td>Rsa1.0_00991.1_g22200.t1</td><td>gb|EOA36193.1| hypothetical protein CARUB_v10010105mg [Capsella rubella]</td><td>235</td><td>249</td><td>8.00E-73</td><td>106.0</td><td>78.7</td><td>88.1</td><td>hypothetical protein CARUB_v10010105mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G06160.1 | Symbols: ORA59 | octadecanoid-responsive Arabidopsis AP2/ERF 59 | chr1:1883046-1883780 FORWARD LENGTH=244</td><td>235</td><td>244</td><td>2.00E-67</td><td>103.8</td><td>76.2</td><td>85.1</td></tr>
<tr><td>Rsa1.0_00991.1_g22201.t1</td><td>ref|XP_002889587.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335429|gb|EFH65846.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>659</td><td>558</td><td>0</td><td>84.7</td><td>67.2</td><td>74.5</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06140.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:1864796-1866472 FORWARD LENGTH=558</td><td>659</td><td>558</td><td>0</td><td>84.7</td><td>66.6</td><td>73.9</td></tr>
<tr><td>Rsa1.0_00991.1_g22202.t1</td><td>ref|XP_002892321.1| hypothetical protein ARALYDRAFT_311691 [Arabidopsis lyrata subsp. lyrata] gi|297338163|gb|EFH68580.1| hypothetical protein ARALYDRAFT_311691 [Arabidopsis lyrata subsp. lyrata]</td><td>73</td><td>485</td><td>1.00E-12</td><td>664.4</td><td>61.6</td><td>72.6</td><td>hypothetical protein ARALYDRAFT_311691</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06137.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06135.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:1863544-1863750 REVERSE LENGTH=68</td><td>73</td><td>68</td><td>2.00E-13</td><td>93.2</td><td>58.9</td><td>69.9</td></tr>
<tr><td>Rsa1.0_00991.1_g22203.t1</td><td>ref|XP_002892320.1| skp1/ask-interacting protein 16 [Arabidopsis lyrata subsp. lyrata] gi|297338162|gb|EFH68579.1| skp1/ask-interacting protein 16 [Arabidopsis lyrata subsp. lyrata]</td><td>436</td><td>435</td><td>1.00E-171</td><td>99.8</td><td>72.2</td><td>80.0</td><td>skp1/ask-interacting protein 16</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06110.1 | Symbols: SKIP16 | SKP1/ASK-interacting protein 16 | chr1:1853237-1854938 REVERSE LENGTH=436</td><td>436</td><td>436</td><td>1.00E-172</td><td>100.0</td><td>70.6</td><td>79.6</td></tr>
<tr><td>Rsa1.0_00991.1_g22204.t1</td><td>ref|NP_172099.1| delta-9 desaturase-like 1 protein [Arabidopsis thaliana] gi|62510518|sp|Q9LND9.1|ADSL1_ARATH RecName: Full=Delta-9 desaturase-like 1 protein gi|8810471|gb|AAF80132.1|AC024174_14 Contains similarity to delta 9 desaturase mRNA from Arabidopsis thaliana gb|D88536 and contains a fatty acid desaturase PF|01069 domain. ESTs gb|AV546954, gb|AI993202, gb|AV554343, gb|T46147 come from this gene [Arabidopsis thaliana] gi|332189817|gb|AEE27938.1| delta-9 desaturase-like 1 protein [Arabidopsis thaliana]</td><td>297</td><td>299</td><td>1.00E-150</td><td>100.7</td><td>85.2</td><td>90.9</td><td>delta-9 desaturase-like 1 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G06090.1 | Symbols: | Fatty acid desaturase family protein | chr1:1847921-1849500 FORWARD LENGTH=299</td><td>297</td><td>299</td><td>1.00E-152</td><td>100.7</td><td>85.2</td><td>90.9</td></tr>
<tr><td>Rsa1.0_00991.1_g22205.t1</td><td>ref|XP_002889584.1| hypothetical protein ARALYDRAFT_887802 [Arabidopsis lyrata subsp. lyrata] gi|297335426|gb|EFH65843.1| hypothetical protein ARALYDRAFT_887802 [Arabidopsis lyrata subsp. lyrata]</td><td>304</td><td>305</td><td>1.00E-170</td><td>100.3</td><td>94.7</td><td>97.7</td><td>hypothetical protein ARALYDRAFT_887802</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06080.1 | Symbols: ADS1 | delta 9 desaturase 1 | chr1:1843661-1846093 FORWARD LENGTH=305</td><td>304</td><td>305</td><td>1.00E-172</td><td>100.3</td><td>93.8</td><td>97.4</td></tr>
<tr><td>Rsa1.0_00991.1_g22206.t1</td><td>ref|XP_002892318.1| hypothetical protein ARALYDRAFT_887800 [Arabidopsis lyrata subsp. lyrata] gi|297338160|gb|EFH68577.1| hypothetical protein ARALYDRAFT_887800 [Arabidopsis lyrata subsp. lyrata]</td><td>402</td><td>427</td><td>1.00E-150</td><td>106.2</td><td>79.6</td><td>83.8</td><td>hypothetical protein ARALYDRAFT_887800</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G06070.1 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr1:1835201-1837116 REVERSE LENGTH=423</td><td>402</td><td>423</td><td>1.00E-149</td><td>105.2</td><td>78.9</td><td>83.3</td></tr>
</table>

Rsa1.0_00991.1_g22207.t1	ref|XP_002889583.1| hypothetical protein ARALYDRAFT_470618 [Arabidopsis lyrata subsp. lyrata] gi|297335425|gb|EFH65842.1| hypothetical protein ARALYDRAFT_470618 [Arabidopsis lyrata subsp. lyrata]	107	213	6.00E-17	199.1	51.4	62.6	hypothetical protein ARALYDRAFT_470618	gbpln	Arabidopsis lyrata	AT1G06060.1 | Symbols: | LisH and RanBPM domains containing protein | chr1:1833071-1834516 FORWARD LENGTH=213	107	213	2.00E-17	199.1	49.5	60.7
Rsa1.0_00991.1_g22208.t1	ref|XP_002892317.1| hypothetical protein ARALYDRAFT_887798 [Arabidopsis lyrata subsp. lyrata] gi|297338159|gb|EFH68576.1| hypothetical protein ARALYDRAFT_887798 [Arabidopsis lyrata subsp. lyrata]	313	313	1.00E-147	100.0	82.1	89.1	hypothetical protein ARALYDRAFT_887798	gbpln	Arabidopsis lyrata	AT1G06050.1 | Symbols: | Protein of unknown function (DUF1336) | chr1:1830726-1831667 REVERSE LENGTH=313	313	313	1.00E-149	100.0	83.1	89.8
Rsa1.0_00991.1_g22209.t1	gb|ABV89657.1| salt tolerance protein [Brassica rapa]	250	243	1.00E-124	97.2	91.6	96.0	salt tolerance protein	gbpln	Brassica rapa	AT1G06040.1 | Symbols: STO | B-box zinc finger family protein | chr1:1828662-1829659 REVERSE LENGTH=248	250	248	1.00E-116	99.2	85.2	90.8
Rsa1.0_00991.1_g22210.t2	ref|NP_172093.1| fructokinase [Arabidopsis thaliana] gi|75311394|sp|Q9LNE3.1|SCRK2_ARATH RecName: Full=Probable fructokinase-2 gi|8810465|gb|AAF80126.1|AC024174_8 Contains similarity to a fructokinase from Solanum tuberosum gi|585973 and is a member of the pfkB carbohydrate kinase family PF|00294 [Arabidopsis thaliana] gi|20258778|gb|AAM13911.1| putative fructokinase [Arabidopsis thaliana] gi|332189810|gb|AEE27931.1| probable fructokinase-2 [Arabidopsis thaliana]	371	329	1.00E-172	88.7	79.0	83.3	fructokinase	gbpln	Arabidopsis thaliana	AT1G06030.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr1:1826880-1828130 FORWARD LENGTH=329	371	329	1.00E-175	88.7	79.0	83.3
Rsa1.0_00991.1_g22211.t1	gb|ABL97975.1| unknown [Brassica rapa]	201	205	1.00E-96	102.0	84.1	91.5	unknown	gbpln	Brassica rapa	AT1G05970.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:1816253-1816991 REVERSE LENGTH=200	201	200	1.00E-80	99.5	67.2	84.6
Rsa1.0_00991.1_g22212.t1	gb|EOA36797.1| hypothetical protein CARUB_v10008206mg [Capsella rubella]	926	980	0	105.8	83.9	91.5	hypothetical protein CARUB_v10008206mg	gbpln	Capsella rubella	AT1G05960.1 | Symbols: | ARM repeat superfamily protein | chr1:1808478-1815060 REVERSE LENGTH=982	926	982	0	106.0	83.6	91.4
Rsa1.0_00991.1_g22213.t1	ref|NP_172083.1| uncharacterized protein [Arabidopsis thaliana] gi|75108535|sp|Q5RM09.1|Y1592_ARATH RecName: Full=B3 domain-containing protein At1g05920 gi|55824346|gb|AAV66313.1| hypothetical protein At1g05920 [Arabidopsis thaliana] gi|55978681|gb|AAV68802.1| hypothetical protein AT1G05920 [Arabidopsis thaliana] gi|225897884|dbj|BAH30274.1| hypothetical protein [Arabidopsis thaliana] gi|332189797|gb|AEE27918.1| uncharacterized protein AT1G05920 [Arabidopsis thaliana]	220	315	2.00E-37	143.2	39.1	49.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G05920.1 | Symbols: | Domain of unknown function (DUF313) | chr1:1797044-1797991 FORWARD LENGTH=315	220	315	7.00E-40	143.2	39.1	49.5
Rsa1.0_00991.1_g22214.t1	ref|XP_002889576.1| hypothetical protein ARALYDRAFT_470606 [Arabidopsis lyrata subsp. lyrata] gi|297335418|gb|EFH65835.1| hypothetical protein ARALYDRAFT_470606 [Arabidopsis lyrata subsp. lyrata]	1215	1208	0	99.4	87.7	92.7	hypothetical protein ARALYDRAFT_470606	gbpln	Arabidopsis lyrata	AT1G05910.1 | Symbols: | cell division cycle protein 48-related / CDC48-related | chr1:1790796-1796503 FORWARD LENGTH=1210	1215	1210	0	99.6	87.9	92.3
Rsa1.0_00991.1_g22215.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00991.1_g22216.t1	ref|XP_002889573.1| hypothetical protein ARALYDRAFT_470601 [Arabidopsis lyrata subsp. lyrata] gi|297335415|gb|EFH65832.1| hypothetical protein ARALYDRAFT_470601 [Arabidopsis lyrata subsp. lyrata]	452	557	0	123.2	76.5	83.8	hypothetical protein ARALYDRAFT_470601	gbpln	Arabidopsis lyrata	AT1G05890.1 | Symbols: ARI5, ATARI5 | RING/U-box superfamily protein | chr1:1779631-1784166 FORWARD LENGTH=552	452	552	0	122.1	71.7	79.2

Rsa1.0_00991.1.g22217.t1	ref|NP_172147.2| 1-aminocyclopropane-1-carboxylate oxidase-1 [Arabidopsis thaliana] gi|75297894|sp|Q84MB3.1|ACCH1_ARATH RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana] gi|332189889|gb|AEE28010.1| 1-aminocyclopropane-1-carboxylate oxidase-1 [Arabidopsis thaliana]	365	365	0	100.0	83.8	92.6	1-aminocyclopropane-1-carboxylate oxidase-1	gbpln	Arabidopsis thaliana	AT1G06620.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:2025618-2027094 FORWARD LENGTH=365	365	365	0	100.0	83.8	92.6
Rsa1.0_00991.1.g22218.t1	gb|AAF29395.1|AC009999_15 Contains similarity to Ariadne-2 protein from Drosophila melanogaster gb|AJ010169 and contains an IBR PF|01485 and a KE2 PF|01920 domain [Arabidopsis thaliana]	518	512	1.00E-115	98.8	45.9	60.2	Contains similarity to Ariadne-2 protein from Drosophila melanogaster gb|AJ010169 and contains an IBR PF|01485 and a KE2 PF|01920 domain	gbpln	Arabidopsis thaliana	AT1G05880.2 | Symbols: ARI12 | RING/U-box superfamily protein | chr1:1775655-1778330 FORWARD LENGTH=496	518	496	1.00E-112	95.8	44.6	58.1
Rsa1.0_00991.1.g22219.t1	gb|AAM61025.1| unknown [Arabidopsis thaliana]	159	340	2.00E-15	213.8	26.4	27.0	unknown	gbpln	Arabidopsis thaliana	AT3G19910.1 | Symbols: | RING/U-box superfamily protein | chr3:6926497-6929324 FORWARD LENGTH=340	159	340	4.00E-17	213.8	25.8	26.4
Rsa1.0_00991.1.g22220.t2	ref|XP_002892311.1| hypothetical protein ARALYDRAFT_470598 [Arabidopsis lyrata subsp. lyrata] gi|297338153|gb|EFH68570.1| hypothetical protein ARALYDRAFT_470598 [Arabidopsis lyrata subsp. lyrata]	168	187	6.00E-55	111.3	68.5	73.8	hypothetical protein ARALYDRAFT_470598	gbpln	Arabidopsis lyrata	AT1G05870.4 | Symbols: | Protein of unknown function (DUF1685) | chr1:1772454-1773228 REVERSE LENGTH=189	168	189	1.00E-56	112.5	73.8	81.5
Rsa1.0_00991.1.g22221.t1	ref|XP_002889571.1| hypothetical protein ARALYDRAFT_470597 [Arabidopsis lyrata subsp. lyrata] gi|297335413|gb|EFH65830.1| hypothetical protein ARALYDRAFT_470597 [Arabidopsis lyrata subsp. lyrata]	288	277	1.00E-121	96.2	77.1	85.8	hypothetical protein ARALYDRAFT_470597	gbpln	Arabidopsis lyrata	AT1G05860.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G31600.1); Has 101 Blast hits to 100 proteins in 32 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 2; Plants - 66; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr1:1769061-1770349 FORWARD LENGTH=280	288	280	1.00E-118	97.2	76.0	85.4
Rsa1.0_00991.1.g22222.t1	ref|NP_172076.1| chitinase-like protein 1 [Arabidopsis thaliana] gi|75191903|sp|Q9MA41.1|CTL1_ARATH RecName: Full=Chitinase-like protein 1; Short=AtCTL1; AltName: Full=Protein ANION ALTERED ROOT MORPHOLOGY; AltName: Full=Protein ECTOPIC DEPOSITION OF LIGNIN IN PITH 1; AltName: Full=Protein ECTOPIC ROOT HAIR 2; AltName: Full=Protein POM-POM1; AltName: Full=Protein SENSITIVE TO HOT TEMPERATURES 2; Flags: Precursor gi|6850314|gb|AAF29391.1|AC009999_11 Contains similarity to a basic endochitinase from Arabidopis thaliana gb|AB023448, and contains a Chitinases class I PF|00182 domain. ESTs gb|AI995747, gb|AA728545, gb|Z26222, gb|Z25683, gb|T88386, gb|T14122, gb|T04241, gb|N38122 come from this gene [Arabidopsis thaliana] gi|12083324|gb|AAG48821.1|AF332458_1 putative class I chitinase [Arabidopsis thaliana] gi|17226329|gb|AAL37736.1|AF422178_1 chitinase-like protein 1 [Arabidopsis thaliana] gi|17226331|gb|AAL37737.1|AF422179_1 chitinase-like protein 1 [Arabidopsis thaliana] gi|14334488|gb|AAK59442.1| putative class I chitinase [Arabidopsis thaliana] gi|21280935|gb|AAM44973.1| putative class I chitinase [Arabidopsis	379	321	1.00E-178	84.7	77.6	81.0	chitinase-like protein 1	gbpln	Arabidopsis thaliana	AT1G05850.1 | Symbols: POM1, ERH2, ELP1, CTL1, ELP, HOT2, ATCTL1 | Chitinase family protein | chr1:1766833-1768117 REVERSE LENGTH=321	379	321	0	84.7	77.6	81.0

Rsa1.0_00991.1_g22223.t1	dbj|BAJ34259.1| unnamed protein product [Thellungiella halophila]	355	353	1.00E-148	99.4	77.7	82.5	unnamed protein product	----	----	AT1G05805.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:1744843-1747427 FORWARD LENGTH=362	355	362	1.00E-140	102.0	76.3	83.7
Rsa1.0_00992.1_g22224.t1	dbj|BAJ34283.1| unnamed protein product [Thellungiella halophila]	214	395	5.00E-55	184.6	51.4	57.0	unnamed protein product	----	----	AT3G48160.1 | Symbols: DEL1, E2L3, E2FE | DP-E2F-like 1 | chr3:17783641-17785688 FORWARD LENGTH=379	214	379	1.00E-51	177.1	49.1	56.1
Rsa1.0_00992.1_g22225.t1	gb|AAQ55493.1| betaine aldehyde dehydrogenase [Brassica napus]	503	503	0	100.0	96.0	98.4	betaine aldehyde dehydrogenase	gbpln	Brassica napus	AT3G48170.1 | Symbols: ALDH10A9 | aldehyde dehydrogenase 10A9 | chr3:17786290-17789918 REVERSE LENGTH=503	503	503	0	100.0	93.2	97.8
Rsa1.0_00992.1_g22226.t1	gb|EOA25038.1| hypothetical protein CARUB_v10018344mg [Capsella rubella]	82	75	7.00E-20	91.5	70.7	79.3	hypothetical protein CARUB_v10018344mg	gbpln	Capsella rubella	AT3G48180.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G19020.1); Has 84 Blast hits to 84 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 84; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:17790571-17790804 REVERSE LENGTH=77	82	77	2.00E-22	93.9	70.7	79.3
Rsa1.0_00992.1_g22227.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00992.1_g22228.t1	gb|EOA26197.1| hypothetical protein CARUB_v10019635mg [Capsella rubella]	747	824	0	110.3	64.7	77.0	hypothetical protein CARUB_v10019635mg	gbpln	Capsella rubella	AT3G48190.1 | Symbols: ATM, ATATM | ataxia-telangiectasia mutated | chr3:17797628-17828361 FORWARD LENGTH=3845	747	3845	0	514.7	64.8	76.4
Rsa1.0_00992.1_g22229.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00992.1_g22230.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00992.1_g22231.t1	ref|XP_002892774.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338616|gb|EFH69033.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	953	883	0	92.7	41.4	53.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G13800.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4731056-4733707 REVERSE LENGTH=883	953	883	1.00E-178	92.7	40.9	54.6
Rsa1.0_00992.1_g22232.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00992.1_g22233.t1	ref|XP_002892642.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297338484|gb|EFH68901.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata]	607	624	0	102.8	87.8	92.1	ABC1 family protein	gbpln	Arabidopsis lyrata	AT1G11390.1 | Symbols: | Protein kinase superfamily protein | chr1:3834762-3837305 REVERSE LENGTH=624	607	624	0	102.8	87.3	92.4
Rsa1.0_00992.1_g22234.t1	ref|XP_002889863.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335705|gb|EFH66122.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	843	842	0	99.9	73.7	82.8	S-locus lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT1G11330.2 | Symbols: | S-locus lectin protein kinase family protein | chr1:3810372-3813416 FORWARD LENGTH=842	843	842	0	99.9	73.7	82.8
Rsa1.0_00992.1_g22235.t1	ref|NP_001184962.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|322510093|sp|Q9SXB8.3|Y1133_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330; Flags: Precursor gi|332190598|gb|AEE28719.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	834	842	0	101.0	77.2	87.1	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT1G11330.2 | Symbols: | S-locus lectin protein kinase family protein | chr1:3810372-3813416 FORWARD LENGTH=842	834	842	0	101.0	77.2	87.1
Rsa1.0_00992.1_g22236.t1	ref|XP_002889863.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335705|gb|EFH66122.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	834	842	0	101.0	75.7	84.8	S-locus lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT1G11330.2 | Symbols: | S-locus lectin protein kinase family protein | chr1:3810372-3813416 FORWARD LENGTH=842	834	842	0	101.0	76.3	86.1
Rsa1.0_00992.1_g22237.t1	ref|NP_001184962.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|322510093|sp|Q9SXB8.3|Y1133_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330; Flags: Precursor gi|332190598|gb|AEE28719.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	843	842	0	99.9	82.1	90.0	putative receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT1G11330.2 | Symbols: | S-locus lectin protein kinase family protein | chr1:3810372-3813416 FORWARD LENGTH=842	843	842	0	99.9	82.1	90.0

Rsa1.0_00992.1.g22238.t7	gb|AAM08751.1|AC025098_18 Putative copia-type polyprotein [Oryza sativa Japonica Group]	1498	1803	0	120.4	34.5	47.5	Putative copia-type polyprotein	gbpln	Oryza sativa	AT1G34070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48050.1); Has 648 Blast hits to 647 proteins in 29 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 25; Plants - 607; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12402283-12403209 FORWARD LENGTH=308	1498	308	3.00E-78	20.6	9.9	13.0
Rsa1.0_00993.1.g22239.t1	gb|AAF22900.1|AC006932_17 T27G7.17 [Arabidopsis thaliana]	385	526	1.00E-54	136.6	29.1	30.6	T27G7.17	gbpln	Arabidopsis thaliana	AT1G08490.1 | Symbols: ATSUFS, SUFS, ATCPNIFS, ATNFS2, CPNIFS | chloroplastic NIFS-like cysteine desulfurase | chr1:2685980-2688547 REVERSE LENGTH=463	385	463	5.00E-57	120.3	29.1	30.6
Rsa1.0_00993.1.g22240.t1	gb|AAF79687.1|AC022314_28 F9C16.9 [Arabidopsis thaliana]	704	946	0	134.4	55.3	69.2	F9C16.9	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00993.1.g22241.t1	gb|EOA19350.1| hypothetical protein CARUB_v10000283mg [Capsella rubella]	269	763	7.00E-83	283.6	60.2	65.8	hypothetical protein CARUB_v10000283mg	gbpln	Capsella rubella	AT5G23450.2 | Symbols: ATLCBK1, LCBK1 | long-chain base (LCB) kinase 1 | chr5:7905041-7908960 REVERSE LENGTH=763	269	763	3.00E-83	283.6	58.7	65.4
Rsa1.0_00993.1.g22242.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	681	695	0	102.1	54.6	66.5	hypothetical protein 26.t00052	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_00993.1.g22243.t1	gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1738	1787	0	102.8	29.1	37.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00993.1.g22244.t1	gb|EMJ00160.1| hypothetical protein PRUPE_ppa020671mg, partial [Prunus persica]	955	1460	1.00E-177	152.9	33.4	42.2	hypothetical protein PRUPE_ppa020671mg, partial	gbpln	Prunus persica	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	955	158	1.00E-26	16.5	5.7	8.6
Rsa1.0_00993.1.g22245.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	507	1142	1.00E-157	225.2	51.3	64.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	507	626	2.00E-37	123.5	21.1	34.9
Rsa1.0_00993.1.g22246.t1	emb|CAA16721.1| MuDR transposable element - like protein [Arabidopsis thaliana] gi|7268634|emb|CAB78843.1| MuDR transposable element-like protein [Arabidopsis thaliana]	799	633	0	79.2	43.8	54.2	MuDR transposable element - like protein	gbpln	Arabidopsis thaliana	AT3G30370.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Transposase, MuDR, plant (InterPro:IPR004332); BEST Arabidopsis thaliana protein match is: SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein (TAIR:AT1G18050.1); Has 35 Blast hits to 35 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:11965180-11965719 REVERSE LENGTH=179	799	179	9.00E-29	22.4	7.0	9.4
Rsa1.0_00993.1.g22247.t1	emb|CAB87198.1| putative protein [Arabidopsis thaliana] gi|91806512|gb|ABE65983.1| hypothetical protein At3g42810 [Arabidopsis thaliana]	118	154	2.00E-16	130.5	36.4	57.6	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00994.1.g22248.t1	emb|CAF06580.1| SGT1-like protein [Brassica oleracea]	85	355	6.00E-43	417.6	100.0	100.0	SGT1-like protein	gbpln	Brassica oleracea	AT4G11260.1 | Symbols: ATSGT1B, ETA3, RPR1, EDM1, SGT1B | phosphatase-related | chr4:6851515-6853719 REVERSE LENGTH=358	85	358	6.00E-45	421.2	98.8	98.8
Rsa1.0_00994.1.g22249.t1	ref|NP_567375.1| serine/threonine-protein phosphatase PP1 isozyme 6 [Arabidopsis thaliana] gi|148887170|sp|P48486.2|PP16_ARATH RecName: Full=Serine/threonine-protein phosphatase PP1 isozyme 6 gi|19699316|gb|AAL91268.1| AT4g11240/F8L21_30 [Arabidopsis thaliana] gi|21554190|gb|AAM63269.1| protein phosphatase type 1 PP1BG [Arabidopsis thaliana] gi|21689631|gb|AAM67437.1| AT4g11240/F8L21_30 [Arabidopsis thaliana] gi|332657588|gb|AEE82988.1| serine/threonine-protein phosphatase PP1 isozyme 6 [Arabidopsis thaliana]	322	322	1.00E-177	100.0	90.7	97.2	serine/threonine-protein phosphatase PP1 isozyme 6	gbpln	Arabidopsis thaliana	AT4G11240.1 | Symbols: TOPP7 | Calcineurin-like metallo-phosphoesterase superfamily protein | chr4:6847333-6849032 FORWARD LENGTH=322	322	322	1.00E-179	100.0	90.7	97.2
Rsa1.0_00994.1.g22250.t2	ref|NP_176850.2| MATE efflux family protein [Arabidopsis thaliana] gi|332196434|gb|AEE34555.1| MATE efflux family protein [Arabidopsis thaliana]	471	485	0	103.0	87.5	93.2	MATE efflux family protein	gbpln	Arabidopsis thaliana	AT1G66780.1 | Symbols: | MATE efflux family protein | chr1:24909213-24911485 FORWARD LENGTH=485	471	485	0	103.0	87.5	93.2
Rsa1.0_00994.1.g22251.t2	dbj|BAB03046.1| unnamed protein product [Arabidopsis thaliana]	165	402	6.00E-32	243.6	47.9	55.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G21330.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:7507720-7508841 FORWARD LENGTH=373	165	373	4.00E-30	226.1	44.2	49.1

Rsa1.0_00994.1.g22252.t1	ref|XP_002867698.1| hypothetical protein ARALYDRAFT_914233 [Arabidopsis lyrata subsp. lyrata] gi|297313534|gb|EFH43957.1| hypothetical protein ARALYDRAFT_914233 [Arabidopsis lyrata subsp. lyrata]	709	775	0	109.3	88.2	93.7	hypothetical protein ARALYDRAFT_914233	gbpln	Arabidopsis lyrata	AT4G23640.1 | Symbols: TRH1, ATKT3, KUP4 | Potassium transporter family protein | chr4:12320476–12324291 REVERSE LENGTH=775	709	775	0	109.3	87.6	93.2
Rsa1.0_00994.1.g22253.t1	ref|XP_002872559.1| disease resistance–responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297318396|gb|EFH48818.1| disease resistance–responsive family protein [Arabidopsis lyrata subsp. lyrata]	178	184	8.00E–66	103.4	68.5	79.8	disease resistance–responsive family protein	gbpln	Arabidopsis lyrata	AT4G11190.1 | Symbols: | Disease resistance–responsive (dirigent–like protein) family protein | chr4:6826682–6827236 FORWARD LENGTH=184	178	184	1.00E–66	103.4	68.0	79.2
Rsa1.0_00994.1.g22254.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1–3 polyprotein [Arabidopsis thaliana]	233	1356	8.00E–81	582.0	60.1	82.4	Highly similar to Ta1–3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine–rich RLK (RECEPTOR–like protein kinase) 8 | chr4:12129485–12134086 FORWARD LENGTH=1262	233	1262	5.00E–21	541.6	25.8	42.5
Rsa1.0_00994.1.g22255.t1	ref|XP_002877500.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323338|gb|EFH53759.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	156	136	6.00E–17	87.2	28.8	39.7	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00994.1.g22256.t1	gb|EOA16078.1| hypothetical protein CARUB_v10004210mg [Capsella rubella]	726	757	0	104.3	77.1	84.7	hypothetical protein CARUB_v10004210mg	gbpln	Capsella rubella	AT4G26690.1 | Symbols: SHV3, MRH5, GPDL2 | PLC–like phosphodiesterase family protein | chr4:13456793–13459890 REVERSE LENGTH=759	726	759	0	104.5	76.3	84.8
Rsa1.0_00994.1.g22257.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00994.1.g22258.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838–20266 [Arabidopsis thaliana]	127	1142	6.00E–23	899.2	46.5	64.6	reverse transcriptase, putative; 16838–20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H–like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae – 0; Bacteria – 0; Metazoa – 0; Fungi – 0; Plants – 208; Viruses – 0; Other Eukaryotes – 0 (source: NCBI BLink). | chr2:9528910–9529917 FORWARD LENGTH=256	127	256	2.00E–16	201.6	34.6	47.2
Rsa1.0_00994.1.g22259.t1	gb|EOA21758.1| hypothetical protein CARUB_v10002215mg [Capsella rubella]	141	141	5.00E–67	100.0	92.9	95.0	hypothetical protein CARUB_v10002215mg	gbpln	Capsella rubella	AT4G11175.1 | Symbols: | Nucleic acid–binding, OB–fold–like protein | chr4:6818162–6818806 FORWARD LENGTH=141	141	141	1.00E–67	100.0	87.9	93.6
Rsa1.0_00994.1.g22260.t2	dbj|BAB01344.1| reverse transcriptase–like protein [Arabidopsis thaliana]	1215	1115	3.00E–49	91.8	9.3	13.3	reverse transcriptase–like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA–directed DNA polymerase (reverse transcriptase)–related family protein | chr3:8789471–8793208 FORWARD LENGTH=746	1215	746	1.00E–33	61.4	7.4	11.2
Rsa1.0_00995.1.g22261.t2	gb|ACQ44224.1| unknown [Arabis alpina]	507	291	1.00E–35	57.4	15.0	19.5	unknown	gbpln	Arabis alpina	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097–11122412 FORWARD LENGTH=673	507	673	3.00E–11	132.7	7.7	12.2
Rsa1.0_00995.1.g22262.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00995.1.g22263.t1	ref|NP_566886.2| protein plastid transcriptionally active 16 [Arabidopsis thaliana] gi|5541681|emb|CAB51187.1| putative protein [Arabidopsis thaliana] gi|332644683|gb|AEE78204.1| protein plastid transcriptionally active 16 [Arabidopsis thaliana]	511	510	0	99.8	88.1	93.5	protein plastid transcriptionally active 16	gbpln	Arabidopsis thaliana	AT3G46780.1 | Symbols: PTAC16 | plastid transcriptionally active 16 | chr3:17228766–17231021 FORWARD LENGTH=510	511	510	0	99.8	88.1	93.5
Rsa1.0_00995.1.g22264.t1	gb|AAD31079.1| Mutator–like transposase [Arabidopsis thaliana]	524	819	5.00E–65	156.3	25.4	35.7	Mutator–like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756–23849915 FORWARD LENGTH=719	524	719	1.00E–18	137.2	13.4	24.4
Rsa1.0_00995.1.g22265.t8	ref|XP_002891526.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata] gi|297337368|gb|EFH67785.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata]	874	824	1.00E–90	94.3	27.9	43.1	hypothetical protein ARALYDRAFT_337115	gbpln	Arabidopsis lyrata	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367–2988945 FORWARD LENGTH=452	874	452	9.00E–33	51.7	13.7	21.3
Rsa1.0_00995.1.g22266.t1	ref|XP_002877513.1| hypothetical protein ARALYDRAFT_905886 [Arabidopsis lyrata subsp. lyrata] gi|297323351|gb|EFH53772.1| hypothetical protein ARALYDRAFT_905886 [Arabidopsis lyrata subsp. lyrata]	656	657	0	100.2	93.1	95.6	hypothetical protein ARALYDRAFT_905886	gbpln	Arabidopsis lyrata	AT3G46790.1 | Symbols: CRR2 | Tetratricopeptide repeat (TPR)–like superfamily protein | chr3:17231975–17233948 REVERSE LENGTH=657	656	657	0	100.2	92.7	95.9
Rsa1.0_00995.1.g22267.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_00995.1.g22268.t1	#	#	#	#	#	#	#	–	––––	––––	AT1G36970.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:14016385–14018356 REVERSE LENGTH=439	363	439	6.00E–13	120.9	9.1	11.6
Rsa1.0_00996.1.g22269.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#

Rsa1.0_00996.1.g22270.t1	dbj|BAB11447.1| polyprotein-like [Arabidopsis thaliana]	180	509	8.00E-63	282.8	63.3	78.3	polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	180	1262	2.00E-40	701.1	42.2	65.0
Rsa1.0_00996.1.g22271.t1	ref|NP_564537.1| myb/SANT-like DNA-binding domain-containing protein [Arabidopsis thaliana] gi|7770343|gb|AAF69713.1|AC016041_18 F27J15.20 [Arabidopsis thaliana] gi|21555865|gb|AAM63950.1| unknown [Arabidopsis thaliana] gi|41618992|gb|AAS09998.1| MYB transcription factor [Arabidopsis thaliana] gi|89274145|gb|ABD65593.1| At1g49010 [Arabidopsis thaliana] gi|332194260|gb|AEE32381.1| myb/SANT-like DNA-binding domain-containing protein [Arabidopsis thaliana]	297	314	1.00E-123	105.7	84.2	89.9	myb/SANT-like DNA-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G49010.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr1:18132714-18133778 FORWARD LENGTH=314	297	314	1.00E-126	105.7	84.2	89.9
Rsa1.0_00996.1.g22272.t1	ref|NP_001190775.1| K+ uptake permease 9 [Arabidopsis thaliana] gi|38502848|sp|O49423.2|POT9_ARATH RecName: Full=Potassium transporter 9; Short=AtPOT9 gi|332658852|gb|AEE84252.1| K+ uptake permease 9 [Arabidopsis thaliana]	792	807	0	101.9	79.3	89.1	K+ uptake permease 9	gbpln	Arabidopsis thaliana	AT4G19960.2 | Symbols: KUP9 | K+ uptake permease 9 | chr4:10813807-10816997 FORWARD LENGTH=807	792	807	0	101.9	79.3	89.1
Rsa1.0_00996.1.g22273.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1164	1223	0	105.1	50.3	64.2	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1164	746	1.00E-84	64.1	12.5	16.9
Rsa1.0_00996.1.g22274.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00996.1.g22275.t1	ref|XP_002891480.1| hypothetical protein ARALYDRAFT_474061 [Arabidopsis lyrata subsp. lyrata] gi|297337322|gb|EFH67739.1| hypothetical protein ARALYDRAFT_474061 [Arabidopsis lyrata subsp. lyrata]	449	530	1.00E-106	118.0	55.5	73.1	hypothetical protein ARALYDRAFT_474061	gbpln	Arabidopsis lyrata	AT1G49190.1 | Symbols: ARR19, RR19 | response regulator 19 | chr1:18191342-18193598 FORWARD LENGTH=608	449	608	2.00E-61	135.4	28.5	38.8
Rsa1.0_00996.1.g22276.t4	gb|AAD15376.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	785	962	1.00E-19	122.5	6.6	9.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00996.1.g22277.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00996.1.g22278.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00996.1.g22279.t1	ref|XP_002894164.1| hypothetical protein ARALYDRAFT_314341 [Arabidopsis lyrata subsp. lyrata] gi|297340006|gb|EFH70423.1| hypothetical protein ARALYDRAFT_314341 [Arabidopsis lyrata subsp. lyrata]	265	266	1.00E-134	100.4	86.0	92.1	hypothetical protein ARALYDRAFT_314341	gbpln	Arabidopsis lyrata	AT1G49180.2 | Symbols: | protein kinase family protein | chr1:18184814-18187444 REVERSE LENGTH=376	265	376	1.00E-128	141.9	81.9	86.8
Rsa1.0_00996.1.g22280.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_00997.1.g22281.t2	gb|EOA21157.1| hypothetical protein CARUB_v10001503mg [Capsella rubella]	172	314	7.00E-15	182.6	26.7	27.9	hypothetical protein CARUB_v10001503mg	gbpln	Capsella rubella	AT5G06130.2 | Symbols: | chaperone protein dnaJ-related | chr5:1853754-1855763 REVERSE LENGTH=315	172	315	3.00E-16	183.1	26.2	27.9
Rsa1.0_00997.1.g22282.t1	gb|EOA15376.1| hypothetical protein CARUB_v10006095mg [Capsella rubella]	104	104	2.00E-47	100.0	87.5	93.3	hypothetical protein CARUB_v10006095mg	gbpln	Capsella rubella	AT4G34770.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:16591352-16591666 FORWARD LENGTH=104	104	104	5.00E-50	100.0	88.5	92.3
Rsa1.0_00997.1.g22283.t1	ref|XP_002869123.1| ATMTN2 [Arabidopsis lyrata subsp. lyrata] gi|297314959|gb|EFH45382.1| ATMTN2 [Arabidopsis lyrata subsp. lyrata]	267	254	1.00E-131	95.1	86.1	91.0	ATMTN2	gbpln	Arabidopsis lyrata	AT4G34840.1 | Symbols: ATMTN2, ATMTAN2, MTN2, MTAN2 | Phosphorylase superfamily protein | chr4:16606299-16607748 FORWARD LENGTH=254	267	254	1.00E-132	95.1	84.3	90.3
Rsa1.0_00997.1.g22284.t1	gb|ADF43047.1| chalcone synthase 6 protein [Brassica rapa subsp. rapa]	392	392	0	100.0	94.9	97.4	chalcone synthase 6 protein	gbpln	Brassica rapa	AT4G34850.1 | Symbols: LAP5 | Chalcone and stilbene synthase family protein | chr4:16608349-16609720 FORWARD LENGTH=392	392	392	0	100.0	92.9	95.9
Rsa1.0_00997.1.g22285.t1	ref|XP_004289834.1| PREDICTED: uncharacterized protein LOC101301732 [Fragaria vesca subsp. vesca]	469	573	0	122.2	84.4	90.2	PREDICTED: uncharacterized protein LOC101301732	gbpln	Fragaria vesca	AT4G34860.2 | Symbols: | Plant neutral invertase family protein | chr4:16609955-16612019 REVERSE LENGTH=571	469	571	0	121.7	69.3	71.2
Rsa1.0_00997.1.g22286.t1	gb|EOA16221.1| hypothetical protein CARUB_v10004361mg [Capsella rubella]	615	633	0	102.9	84.7	90.7	hypothetical protein CARUB_v10004361mg	gbpln	Capsella rubella	AT4G34910.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:16631661-16634834 FORWARD LENGTH=626	615	626	0	101.8	82.3	88.1
Rsa1.0_00997.1.g22287.t1	gb|AAM65736.1| unknown [Arabidopsis thaliana]	318	318	1.00E-168	100.0	88.4	94.7	unknown	gbpln	Arabidopsis thaliana	AT4G34920.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr4:16635745-16636701 FORWARD LENGTH=318	318	318	1.00E-169	100.0	87.7	94.0

Rsa1.0_00997.1.g22288.t1	ref|NP_195219.1| 1-phosphatidylinositol phosphodiesterase-related protein [Arabidopsis thaliana] gi|5123710|emb|CAB45454.1| putative protein [Arabidopsis thaliana] gi|7270444|emb|CAB80210.1| putative protein [Arabidopsis thaliana] gi|119360157|gb|ABL66807.1| At4g34930 [Arabidopsis thaliana] gi|332661038|gb|AEE86438.1| 1-phosphatidylinositol phosphodiesterase-related protein [Arabidopsis thaliana]	355	391	1.00E-161	110.1	76.9	87.9	1-phosphatidylinositol phosphodiesterase-related protein	gbpln	Arabidopsis thaliana	AT4G34930.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr4:16637551-16638726 FORWARD LENGTH=391	355	391	1.00E-164	110.1	76.9	87.9
Rsa1.0_00997.1.g22289.t1	gb|EOA19138.1| hypothetical protein CARUB_v10007809mg [Capsella rubella]	659	668	0	101.4	93.9	97.6	hypothetical protein CARUB_v10007809mg	gbpln	Capsella rubella	AT4G34940.1 | Symbols: ARO1 | armadillo repeat only 1 | chr4:16639760-16641754 FORWARD LENGTH=664	659	664	0	100.8	94.1	97.6
Rsa1.0_00997.1.g22290.t1	ref|XP_002867099.1| nodulin family protein [Arabidopsis lyrata subsp. lyrata] gi|297312935|gb|EFH43358.1| nodulin family protein [Arabidopsis lyrata subsp. lyrata]	558	567	0	101.6	87.8	94.3	nodulin family protein	gbpln	Arabidopsis lyrata	AT4G34950.1 | Symbols: | Major facilitator superfamily protein | chr4:16642544-16644759 REVERSE LENGTH=567	558	567	0	101.6	85.8	92.3
Rsa1.0_00997.1.g22291.t1	dbj|BAF81521.1| putative peptidyl-prolyl cis-trans isomerase [Brassica rapa]	202	223	1.00E-91	110.4	84.2	89.1	putative peptidyl-prolyl cis-trans isomerase	gbpln	Brassica rapa	AT4G34960.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr4:16648865-16650646 FORWARD LENGTH=224	202	224	4.00E-91	110.9	80.7	88.6
Rsa1.0_00997.1.g22292.t1	gb|EOA17264.1| hypothetical protein CARUB_v10005538mg [Capsella rubella]	261	258	2.00E-96	98.9	77.8	84.3	hypothetical protein CARUB_v10005538mg	gbpln	Capsella rubella	AT4G35040.1 | Symbols: bZIP19 | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:16680821-16681805 FORWARD LENGTH=261	261	261	3.00E-94	100.0	74.3	81.2
Rsa1.0_00998.1.g22293.t1	gb|ABW74585.1| pol polyprotein [Boechera divaricarpa]	158	551	2.00E-47	348.7	59.5	77.8	pol polyprotein	gbpln	Boechera divaricarpa	#	#	#	#	#	#	#
Rsa1.0_00998.1.g22294.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	119	441	2.00E-24	370.6	46.2	64.7	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_00998.1.g22295.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	75	1489	1.00E-12	1985.3	40.0	68.0	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_00998.1.g22296.t1	gb|AAG50886.1|AC025294_24 hypothetical protein [Arabidopsis thaliana]	753	629	1.00E-151	83.5	35.1	49.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	753	746	7.00E-88	99.1	23.2	30.8
Rsa1.0_00998.1.g22297.t1	ref|NP_175610.1| putative mitochondrial-processing peptidase subunit alpha-1 [Arabidopsis thaliana] gi|29839695|sp|Q9ZU25.1|MPPA1_ARATH RecName: Full=Probable mitochondrial-processing peptidase subunit alpha-1; AltName: Full=Alpha-MPP 1; Flags: Precursor gi|4220446|gb|AAD12673.1| Strong similarity to gi|2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb|AC001645. ESTs gb|Z18504 and gb|AA395715 come from this gene [Arabidopsis thaliana] gi|17529270|gb|AAL38862.1| putative mitochondrial processing peptidase alpha subunit [Arabidopsis thaliana] gi|20258957|gb|AAM14194.1| putative mitochondrial processing peptidase alpha subunit [Arabidopsis thaliana] gi|332194621|gb|AEE32742.1| putative mitochondrial-processing peptidase subunit alpha-1 [Arabidopsis thaliana]	507	503	0	99.2	88.6	94.1	putative mitochondrial-processing peptidase subunit alpha-1	gbpln	Arabidopsis thaliana	AT1G51980.1 | Symbols: | Insulinase (Peptidase family M16) protein | chr1:19323692-19326771 REVERSE LENGTH=503	507	503	0	99.2	88.6	94.1
Rsa1.0_00998.1.g22298.t1	ref|XP_002891673.1| IQ-domain 27 [Arabidopsis lyrata subsp. lyrata] gi|297337515|gb|EFH67932.1| IQ-domain 27 [Arabidopsis lyrata subsp. lyrata]	292	345	4.00E-92	118.2	70.5	79.8	IQ-domain 27	gbpln	Arabidopsis lyrata	AT1G51960.1 | Symbols: IQD27 | IQ-domain 27 | chr1:19310355-19311683 FORWARD LENGTH=351	292	351	3.00E-91	120.2	70.5	82.2
Rsa1.0_00998.1.g22299.t1	ref|XP_002891672.1| hypothetical protein ARALYDRAFT_892185 [Arabidopsis lyrata subsp. lyrata] gi|297337514|gb|EFH67931.1| hypothetical protein ARALYDRAFT_892185 [Arabidopsis lyrata subsp. lyrata]	235	268	9.00E-86	114.0	80.0	85.5	hypothetical protein ARALYDRAFT_892185	gbpln	Arabidopsis lyrata	AT1G51950.1 | Symbols: IAA18 | indole-3-acetic acid inducible 18 | chr1:19305670-19307130 FORWARD LENGTH=267	235	267	6.00E-88	113.6	80.0	84.7
Rsa1.0_00998.1.g22300.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_00998.1.g22301.t1	gb|EOA36821.1| hypothetical protein CARUB_v10008527mg [Capsella rubella]	641	660	0	103.0	90.6	94.7	hypothetical protein CARUB_v10008527mg	gbpln	Capsella rubella	AT1G51940.1 | Symbols: | protein kinase family protein / peptidoglycan-binding LysM domain-containing protein | chr1:19296092-19298941 REVERSE LENGTH=651	641	651	0	101.6	88.5	92.5
Rsa1.0_00998.1.g22302.t6	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_00998.1.g22303.t1	ref|NP_001147018.1| ribosomal RNA apurinic site specific lyase [Zea mays] gi|195606500|gb|ACG25080.1| ribosomal RNA apurinic site specific lyase [Zea mays]	224	419	5.00E-44	187.1	45.5	55.4	ribosomal RNA apurinic site specific lyase	gbenv/gbpln	Zea mays	AT4G10400.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:6446335-6447715 REVERSE LENGTH=409	224	409	3.00E-38	182.6	41.1	51.3
Rsa1.0_00998.1.g22304.t1	ref|XP_002894330.1| RWD domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297340172|gb|EFH70589.1| RWD domain-containing protein [Arabidopsis lyrata subsp. lyrata]	258	252	3.00E-16	97.7	16.3	17.4	RWD domain-containing protein	gbpln	Arabidopsis lyrata	AT1G51730.1 | Symbols: | Ubiquitin-conjugating enzyme family protein | chr1:19186812-19188638 REVERSE LENGTH=252	258	252	9.00E-19	97.7	16.3	17.4
Rsa1.0_00999.1.g22305.t1	gb|EOA12951.1| hypothetical protein CARUB_v10025933mg [Capsella rubella]	572	760	0	132.9	85.1	89.5	hypothetical protein CARUB_v10025933mg	gbpln	Capsella rubella	AT5G66850.1 | Symbols: MAPKKK5 | mitogen-activated protein kinase kinase kinase 5 | chr5:26695965-26699159 REVERSE LENGTH=716	572	716	0	125.2	82.7	87.2
Rsa1.0_00999.1.g22306.t1	gb|EOA13733.1| hypothetical protein CARUB_v10026811mg [Capsella rubella]	324	313	1.00E-123	96.6	79.9	85.2	hypothetical protein CARUB_v10026811mg	gbpln	Capsella rubella	AT5G66870.1 | Symbols: ASL1, LBD36 | ASYMMETRIC LEAVES 2-like 1 | chr5:26706621-26707562 FORWARD LENGTH=313	324	313	1.00E-121	96.6	80.6	86.7
Rsa1.0_00999.1.g22307.t2	dbj|BAJ33953.1| unnamed protein product [Thellungiella halophila]	336	361	1.00E-141	107.4	76.2	78.0	unnamed protein product	----	----	AT3G50500.1 | Symbols: SPK-2-2, SNRK2-2, SNRK2.2, SRK2D | SNF1-related protein kinase 2.2 | chr3:18741805-18743904 REVERSE LENGTH=362	336	362	1.00E-135	107.7	70.8	74.7
Rsa1.0_00999.1.g22308.t1	gb|EOA14713.1| hypothetical protein CARUB_v10027991mg [Capsella rubella]	490	814	1.00E-148	166.1	57.1	71.8	hypothetical protein CARUB_v10027991mg	gbpln	Capsella rubella	AT5G66900.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr5:26714931-26717757 REVERSE LENGTH=809	490	809	1.00E-149	165.1	55.7	71.0
Rsa1.0_00999.1.g22309.t2	ref|XP_002866726.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312561|gb|EFH42985.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	659	543	0	82.4	68.1	73.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G66920.1 | Symbols: sks17 | SKU5 similar 17 | chr5:26722963-26725370 FORWARD LENGTH=546	659	546	0	82.9	71.0	76.2
Rsa1.0_00999.1.g22310.t1	gb|EOA13983.1| hypothetical protein CARUB_v10027114mg [Capsella rubella]	213	216	1.00E-105	101.4	89.2	93.9	hypothetical protein CARUB_v10027114mg	gbpln	Capsella rubella	AT5G66930.2 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1649 (InterPro:IPR012445); Has 251 Blast hits to 251 proteins in 113 species: Archae - 0; Bacteria - 0; Metazoa - 91; Fungi - 85; Plants - 58; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr5:26725997-26727549 FORWARD LENGTH=215	213	215	1.00E-106	100.9	87.8	92.0
Rsa1.0_00999.1.g22311.t1	ref|NP_201495.1| Dof zinc finger protein DOF5.8 [Arabidopsis thaliana] gi|55583982|sp|Q9FGD6.1|DOF58_ARATH RecName: Full=Dof zinc finger protein DOF5.8; Short=AtDOF5.8 gi|9758539|dbj|BAB08933.1| DNA binding protein-like [Arabidopsis thaliana] gi|119360101|gb|ABL66779.1| At5g66940 [Arabidopsis thaliana] gi|225879170|dbj|BAH30655.1| hypothetical protein [Arabidopsis thaliana] gi|332010899|gb|AED98282.1| Dof zinc finger protein DOF5.8 [Arabidopsis thaliana]	221	225	5.00E-87	101.8	77.8	87.3	Dof zinc finger protein DOF5.8	gbpln	Arabidopsis thaliana	AT5G66940.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr5:26727989-26728666 REVERSE LENGTH=225	221	225	2.00E-89	101.8	77.8	87.3
Rsa1.0_00999.1.g22312.t1	ref|XP_002866724.1| hypothetical protein ARALYDRAFT_496904 [Arabidopsis lyrata subsp. lyrata] gi|297312559|gb|EFH42983.1| hypothetical protein ARALYDRAFT_496904 [Arabidopsis lyrata subsp. lyrata]	872	871	0	99.9	88.2	93.2	hypothetical protein ARALYDRAFT_496904	gbpln	Arabidopsis lyrata	AT5G66950.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr5:26733333-26735945 FORWARD LENGTH=870	872	870	0	99.8	87.5	92.5
Rsa1.0_00999.1.g22313.t1	ref|XP_002866723.1| transcriptional factor B3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297312558|gb|EFH42982.1| transcriptional factor B3 family protein [Arabidopsis lyrata subsp. lyrata]	328	332	1.00E-102	101.2	60.1	73.5	transcriptional factor B3 family protein	gbpln	Arabidopsis lyrata	AT5G66980.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:26741563-26742826 FORWARD LENGTH=334	328	334	1.00E-100	101.8	58.2	72.0

Rsa1.0_00999.1.g22314.t1	ref|NP_569043.1| uncharacterized protein [Arabidopsis thaliana] gi|21593797|gb|AAM65764.1| unknown [Arabidopsis thaliana] gi|89111824|gb|ABD60684.1| At5g66985 [Arabidopsis thaliana] gi|332010904|gb|AED98287.1| uncharacterized protein AT5G66985 [Arabidopsis thaliana]	89	83	5.00E-26	93.3	76.4	79.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G66985.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26743412-26743663 FORWARD LENGTH=83	89	83	7.00E-29	93.3	76.4	79.8
Rsa1.0_00999.1.g22315.t1	gb|EOA14385.1| hypothetical protein CARUB_v10027579mg [Capsella rubella]	276	277	3.00E-78	100.4	59.8	73.9	hypothetical protein CARUB_v10027579mg	gbpln	Capsella rubella	AT5G66990.1 | Symbols: | RWP-RK domain-containing protein | chr5:26744257-26745362 REVERSE LENGTH=277	276	277	5.00E-77	100.4	59.8	73.6
Rsa1.0_00999.1.g22316.t1	ref|XP_002865034.1| hypothetical protein ARALYDRAFT_332869 [Arabidopsis lyrata subsp. lyrata] gi|297310869|gb|EFH41293.1| hypothetical protein ARALYDRAFT_332869 [Arabidopsis lyrata subsp. lyrata]	145	146	6.00E-52	100.7	75.9	84.8	hypothetical protein ARALYDRAFT_332869	gbpln	Arabidopsis lyrata	AT5G67010.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:26749058-26749616 REVERSE LENGTH=162	145	162	3.00E-52	111.7	71.7	82.1
Rsa1.0_00999.1.g22317.t1	ref|NP_201503.1| uncharacterized protein [Arabidopsis thaliana] gi|9758547|dbj|BAB08941.1| unnamed protein product [Arabidopsis thaliana] gi|115646816|gb|ABJ17128.1| At5g67020 [Arabidopsis thaliana] gi|332010908|gb|AED98291.1| uncharacterized protein AT5G67020 [Arabidopsis thaliana]	388	394	1.00E-177	101.5	80.7	88.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G67020.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G50340.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:26749962-26751146 FORWARD LENGTH=394	388	394	1.00E-180	101.5	80.7	88.7
Rsa1.0_00999.1.g22318.t4	gb|ACM68704.1| zeaxanthin epoxidase [Brassica rapa subsp. pekinensis]	649	668	0	102.9	95.2	96.3	zeaxanthin epoxidase	gbpln	Brassica rapa	AT5G67030.1 | Symbols: ABA1, LOS6, NPQ2, ATABA1, ZEP, IBS3, ATZEP | zeaxanthin epoxidase (ZEP) (ABA1) | chr5:26753745-26757090 REVERSE LENGTH=667	649	667	0	102.8	87.5	92.6
Rsa1.0_01000.1.g22319.t1	ref|XP_002880834.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297326673|gb|EFH57093.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	695	797	0	114.7	62.2	75.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT2G26790.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:11425270-11427669 REVERSE LENGTH=799	695	799	0	115.0	60.6	74.0
Rsa1.0_01000.1.g22320.t1	ref|XP_002880836.1| hypothetical protein ARALYDRAFT_481553 [Arabidopsis lyrata subsp. lyrata] gi|297326675|gb|EFH57095.1| hypothetical protein ARALYDRAFT_481553 [Arabidopsis lyrata subsp. lyrata]	411	469	0	114.1	85.6	92.2	hypothetical protein ARALYDRAFT_481553	gbpln	Arabidopsis lyrata	AT2G26800.2 | Symbols: | Aldolase superfamily protein | chr2:11429192-11432290 REVERSE LENGTH=468	411	468	0	113.9	82.7	91.0
Rsa1.0_01000.1.g22321.t1	gb|EOA26445.1| hypothetical protein CARUB_v10022491mg [Capsella rubella]	2554	2565	0	100.4	91.0	94.9	hypothetical protein CARUB_v10022491mg	gbpln	Capsella rubella	AT2G26890.1 | Symbols: GRV2, KAM2 | DNAJ heat shock N-terminal domain-containing protein | chr2:11462327-11473841 REVERSE LENGTH=2554	2554	2554	0	100.0	90.7	94.8
Rsa1.0_01000.1.g22322.t1	gb|EOA27217.1| hypothetical protein CARUB_v10023327mg, partial [Capsella rubella]	421	408	0	96.9	82.4	87.6	hypothetical protein CARUB_v10023327mg, partial	gbpln	Capsella rubella	AT2G26930.1 | Symbols: ATCDPMEK, PDE277, ISPE, CDPMEK | 4-(cytidine 5'-phospho)-2-C-methyl-D-erithritol kinase | chr2:11491829-11494229 REVERSE LENGTH=383	421	383	0	91.0	80.5	84.6
Rsa1.0_01000.1.g22323.t1	ref|NP_180262.1| C2H2-type zinc finger family protein [Arabidopsis thaliana] gi|3426050|gb|AAC32249.1| putative C2H2-type zinc finger protein [Arabidopsis thaliana] gi|330252815|gb|AEC07909.1| C2H2-type zinc finger family protein [Arabidopsis thaliana]	255	286	1.00E-50	112.2	56.1	64.3	C2H2-type zinc finger family protein	gbpln	Arabidopsis thaliana	AT2G26940.1 | Symbols: | C2H2-type zinc finger family protein | chr2:11496518-11497378 REVERSE LENGTH=286	255	286	3.00E-53	112.2	56.1	64.3
Rsa1.0_01000.1.g22324.t1	ref|XP_002880852.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326691|gb|EFH57111.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	400	387	1.00E-120	96.8	61.5	70.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G26960.1 | Symbols: AtMYB81, MYB81 | myb domain protein 81 | chr2:11506065-11507425 REVERSE LENGTH=427	400	427	1.00E-112	106.8	58.0	66.5

Rsa1.0_01000.1.g22325.t1	ref|NP_850094.1| CBL-interacting serine/threonine-protein kinase 3 [Arabidopsis thaliana] gi|259016206|sp|Q2V452.2|CIPK3_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 3; AltName: Full=SNF1-related kinase 3.17; AltName: Full=SOS2-like protein kinase PKS12 gi|20268690|gb|AAM14049.1| putative protein kinase [Arabidopsis thaliana] gi|23296954|gb|AAN13209.1| putative protein kinase [Arabidopsis thaliana] gi|30349498|gb|AAP22036.1| CBL-interacting protein kinase 3 [Arabidopsis thaliana] gi|330252821|gb|AEC07915.1| CBL-interacting serine/threonine-protein kinase 3 [Arabidopsis thaliana]	430	441	0	102.6	88.6	94.2	CBL-interacting serine/threonine-protein kinase 3	gbpln	Arabidopsis thaliana	AT2G26980.3 | Symbols: CIPK3 | CBL-interacting protein kinase 3 | chr2:11515234-11518205 REVERSE LENGTH=441	430	441	0	102.6	88.6	94.2
Rsa1.0_01000.1.g22326.t1	dbj|BAJ33758.1| unnamed protein product [Thellungiella halophila]	292	439	1.00E-128	150.3	75.0	78.1	unnamed protein product	----	----	AT2G26990.1 | Symbols: FUS12, ATCSN2, COP12, CSN2 | proteasome family protein | chr2:11519684-11522412 REVERSE LENGTH=439	292	439	1.00E-129	150.3	73.6	76.7
Rsa1.0_01000.1.g22327.t1	gb|EOA27572.1| hypothetical protein CARUB_v10023709mg, partial [Capsella rubella]	249	304	1.00E-142	122.1	98.4	99.6	hypothetical protein CARUB_v10023709mg, partial	gbpln	Capsella rubella	AT2G27020.1 | Symbols: PAG1 | 20S proteasome alpha subunit G1 | chr2:11528515-11530858 REVERSE LENGTH=249	249	249	1.00E-144	100.0	98.8	99.6
Rsa1.0_01000.1.g22328.t1	gb|AGA95981.1| argonaute 4 [Brassica rapa subsp. pekinensis]	923	922	0	99.9	95.9	97.9	argonaute 4	gbpln	Brassica rapa	AT2G27040.2 | Symbols: AGO4 | Argonaute family protein | chr2:11536795-11541503 REVERSE LENGTH=924	923	924	0	100.1	88.6	94.4
Rsa1.0_01000.1.g22329.t1	ref|XP_002879042.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297324881|gb|EFH55301.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	959	1022	0	106.6	79.6	87.6	ATP binding protein	gbpln	Arabidopsis lyrata	AT2G27060.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:11551288-11554577 FORWARD LENGTH=1020	959	1020	0	106.4	78.8	86.2
Rsa1.0_01000.1.g22330.t1	ref|NP_180277.1| uncharacterized protein [Arabidopsis thaliana] gi|3885339|gb|AAC77867.1| hypothetical protein [Arabidopsis thaliana] gi|46518491|gb|AAS99727.1| At2g27090 [Arabidopsis thaliana] gi|110741655|dbj|BAE98774.1| hypothetical protein [Arabidopsis thaliana] gi|330252841|gb|AEC07935.1| uncharacterized protein AT2G27090 [Arabidopsis thaliana]	736	743	0	101.0	81.9	87.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G27090.1 | Symbols: | Protein of unknown function (DUF630 and DUF632) | chr2:11567691-11570345 REVERSE LENGTH=743	736	743	0	101.0	81.9	87.9
Rsa1.0_01001.1.g22331.t2	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	621	1447	1.00E-113	233.0	40.7	52.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	621	746	2.00E-69	120.1	26.4	33.3
Rsa1.0_01001.1.g22332.t1	ref|XP_002872976.1| hypothetical protein ARALYDRAFT_912253 [Arabidopsis lyrata subsp. lyrata] gi|297318813|gb|EFH49235.1| hypothetical protein ARALYDRAFT_912253 [Arabidopsis lyrata subsp. lyrata]	190	162	1.00E-49	85.3	61.1	66.8	hypothetical protein ARALYDRAFT_912253	gbpln	Arabidopsis lyrata	AT2G44840.1 | Symbols: ATERF13, EREBP, ERF13 | ethylene-responsive element binding factor 13 | chr2:18495440-18496120 FORWARD LENGTH=226	190	226	8.00E-30	118.9	30.5	36.3
Rsa1.0_01001.1.g22333.t1	gb|EOA31756.1| hypothetical protein CARUB_v10014973mg [Capsella rubella]	112	107	2.00E-40	95.5	77.7	83.9	hypothetical protein CARUB_v10014973mg	gbpln	Capsella rubella	AT3G15420.1 | Symbols: | Transcription factor TFIIIC, tau55-related protein | chr3:5207704-5208289 REVERSE LENGTH=107	112	107	2.00E-42	95.5	75.0	83.9
Rsa1.0_01001.1.g22334.t1	ref|NP_563754.1| cationic amino acid transporter 9 [Arabidopsis thaliana] gi|75308782|sp|Q9C5D6.1|CAAT9_ARATH RecName: Full=Cationic amino acid transporter 9, chloroplastic; Flags: Precursor gi|13430818|gb|AAK26031.1|AF360321_1 unknown protein [Arabidopsis thaliana] gi|21280891|gb|AAM44938.1| unknown protein [Arabidopsis thaliana] gi|332189800|gb|AEE27921.1| cationic amino acid transporter 9 [Arabidopsis thaliana]	573	569	0	99.3	90.1	94.2	cationic amino acid transporter 9	gbpln	Arabidopsis thaliana	AT1G05940.1 | Symbols: CAT9 | cationic amino acid transporter 9 | chr1:1801365-1803942 REVERSE LENGTH=569	573	569	0	99.3	90.1	94.2

Rsa1.0_01001.1.g22335.t1	ref|XP_002872975.1| hypothetical protein ARALYDRAFT_912250 [Arabidopsis lyrata subsp. lyrata] gi|297318812|gb|EFH49234.1| hypothetical protein ARALYDRAFT_912250 [Arabidopsis lyrata subsp. lyrata]	318	270	1.00E-101	84.9	68.2	72.3	hypothetical protein ARALYDRAFT_912250	gbpln	Arabidopsis lyrata	AT4G00026.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Mitochondrial inner membrane translocase complex, subunit Tim21 (InterPro:IPR013261); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:11634-13285 REVERSE LENGTH=269	318	269	1.00E-101	84.6	60.1	61.3
Rsa1.0_01001.1.g22336.t1	ref|XP_002302516.1| predicted protein [Populus trichocarpa] gi|222844242|gb|EEE81789.1| predicted protein [Populus trichocarpa]	451	450	1.00E-147	99.8	60.3	75.4	predicted protein	gbpln	Populus trichocarpa	AT5G07670.1 | Symbols: | RNI-like superfamily protein | chr5:2430421-2432065 FORWARD LENGTH=476	451	476	1.00E-111	105.5	50.1	62.3
Rsa1.0_01001.1.g22337.t1	ref|XP_002875050.1| plastid-lipid associated protein pap [Arabidopsis lyrata subsp. lyrata] gi|297320887|gb|EFH51309.1| plastid-lipid associated protein pap [Arabidopsis lyrata subsp. lyrata]	209	209	1.00E-90	100.0	77.5	88.5	plastid-lipid associated protein pap	gbpln	Arabidopsis lyrata	AT4G00030.1 | Symbols: | Plastid-lipid associated protein PAP / fibrillin family protein | chr4:13565-14366 FORWARD LENGTH=212	209	212	5.00E-93	101.4	78.5	87.1
Rsa1.0_01001.1.g22338.t3	ref|XP_002875048.1| hypothetical protein ARALYDRAFT_912247 [Arabidopsis lyrata subsp. lyrata] gi|297320885|gb|EFH51307.1| hypothetical protein ARALYDRAFT_912247 [Arabidopsis lyrata subsp. lyrata]	388	403	1.00E-137	103.9	78.9	84.3	hypothetical protein ARALYDRAFT_912247	gbpln	Arabidopsis lyrata	AT4G00050.1 | Symbols: UNE10 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:17863-19848 FORWARD LENGTH=399	388	399	1.00E-132	102.8	75.0	80.9
Rsa1.0_01001.1.g22339.t1	gb|EOA21556.1| hypothetical protein CARUB_v10001965mg [Capsella rubella]	175	209	8.00E-79	119.4	84.0	88.0	hypothetical protein CARUB_v10001965mg	gbpln	Capsella rubella	AT4G00080.1 | Symbols: UNE11 | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:32946-33575 FORWARD LENGTH=209	175	209	3.00E-77	119.4	80.6	86.3
Rsa1.0_01002.1.g22340.t1	ref|NP_175369.1| WD40 domain-containing protein [Arabidopsis thaliana] gi|5430755|gb|AAD43155.1|AC007504_10 Hypothetical Protein [Arabidopsis thaliana] gi|332194310|gb|AEE32431.1| WD40 domain-containing protein [Arabidopsis thaliana]	468	471	0	100.6	86.1	93.4	WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G49450.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:18305684-18307099 FORWARD LENGTH=471	468	471	0	100.6	86.1	93.4
Rsa1.0_01002.1.g22341.t3	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1316	1307	0	99.3	59.7	73.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1316	1262	1.00E-101	95.9	13.6	21.9
Rsa1.0_01002.1.g22342.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01002.1.g22343.t1	ref|XP_002891512.1| hypothetical protein ARALYDRAFT_474085 [Arabidopsis lyrata subsp. lyrata] gi|297337354|gb|EFH67771.1| hypothetical protein ARALYDRAFT_474085 [Arabidopsis lyrata subsp. lyrata]	299	302	1.00E-143	101.0	88.0	94.3	hypothetical protein ARALYDRAFT_474085	gbpln	Arabidopsis lyrata	AT1G49470.1 | Symbols: | Family of unknown function (DUF716) | chr1:18310554-18311462 FORWARD LENGTH=302	299	302	2.33E-156	101.0	88.0	93.6
Rsa1.0_01002.1.g22344.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1932	1142	0	59.1	27.5	36.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1932	575	3.00E-76	29.8	9.1	14.3
Rsa1.0_01002.1.g22345.t4	dbj|BAB01019.1| unnamed protein product [Arabidopsis thaliana]	553	355	2.00E-67	64.2	21.5	27.1	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G32904.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G30520.1); Has 249 Blast hits to 117 proteins in 25 species: Archae - 0; Bacteria - 16; Metazoa - 73; Fungi - 5; Plants - 112; Viruses - 0; Other Eukaryotes - 43 (source: NCBI BLink). | chr3:13451438-13452807 REVERSE LENGTH=330	553	330	2.00E-40	59.7	16.6	21.0
Rsa1.0_01002.1.g22346.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01002.1.g22347.t1	ref|NP_683415.2| B3 domain-containing protein [Arabidopsis thaliana] gi|238056770|sp|Q9XIB4.2|Y1475_ARATH RecName: Full=B3 domain-containing protein At1g49475 gi|332194312|gb|AEE32433.1| B3 domain-containing protein [Arabidopsis thaliana]	220	190	4.00E-62	86.4	58.2	71.4	B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G49475.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr1:18312983-18313748 FORWARD LENGTH=190	220	190	1.00E-64	86.4	58.2	71.4

Rsa1.0_01002.1.g22348.t1	dbj|BAB08885.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	115	370	4.00E-18	321.7	36.5	43.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01002.1.g22349.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22350.t1	emb|CAB46043.1| retrotransposon like protein [Arabidopsis thaliana] gi|7268438|emb|CAB80958.1| retrotransposon like protein [Arabidopsis thaliana]	394	1474	6.00E-50	374.1	36.3	49.5	retrotransposon like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22351.t1	ref|NP_564335.3| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|325511374|sp|Q9ASQ6.3|Y1972_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g29720; Flags: Precursor gi|332193000|gb|AEE31121.1| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana]	819	1019	0	124.4	59.2	67.4	Leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	819	1019	0	124.4	59.2	67.4
Rsa1.0_01003.1.g22352.t2	gb|AAD17351.1| contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana] gi|7267432|emb|CAB77944.1| putative polyprotein [Arabidopsis thaliana]	878	1138	2.00E-96	129.6	24.4	32.9	contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22353.t1	gb|EOA39560.1| hypothetical protein CARUB_v10008178mg [Capsella rubella]	414	1022	1.00E-121	246.9	55.1	63.8	hypothetical protein CARUB_v10008178mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	414	1019	1.00E-116	246.1	55.3	62.1
Rsa1.0_01003.1.g22354.t2	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	532	1463	3.00E-27	275.0	11.7	17.5	F5J5.1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22355.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22356.t2	gb|ABW74585.1| pol polyprotein [Boechera divaricarpa]	332	551	4.00E-15	166.0	13.3	18.7	pol polyprotein	gbpln	Boechera divaricarpa	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22357.t7	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22358.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22359.t1	gb|AAD26892.1| Mutator-like transposase [Arabidopsis thaliana]	443	580	4.00E-70	130.9	31.6	48.5	Mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01003.1.g22360.t1	emb|CAB46045.1| retrotransposon like protein [Arabidopsis thaliana] gi|7268441|emb|CAB80961.1| retrotransposon like protein [Arabidopsis thaliana]	382	687	5.00E-55	179.8	24.9	35.1	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT2G07200.1 | Symbols: | Cysteine proteinases superfamily protein | chr2:2989205-2989878 FORWARD LENGTH=151	382	151	4.00E-26	39.5	16.2	24.6
Rsa1.0_01004.1.g22361.t1	gb|ACQ76806.1| WRKY transcription factor 40 [Brassica napus]	294	290	1.00E-155	98.6	91.2	94.9	WRKY transcription factor 40	gbpln	Brassica napus	AT1G80840.1 | Symbols: WRKY40, ATWRKY40 | WRKY DNA-binding protein 40 | chr1:30383834-30385356 FORWARD LENGTH=302	294	302	1.00E-143	102.7	85.7	92.9
Rsa1.0_01004.1.g22362.t1	ref|NP_565246.1| phospholipid N-methyltransferase [Arabidopsis thaliana] gi|42570261|ref|NP_849916.2| phospholipid N-methyltransferase [Arabidopsis thaliana] gi|6503297|gb|AAF14673.1|AC011713_21 ESTs gb|AI994515 and gb|T44237 come from this gene [Arabidopsis thaliana] gi|194708828|gb|ACF88498.1| At1g80860 [Arabidopsis thaliana] gi|332198338|gb|AEE36459.1| phospholipid N-methyltransferase [Arabidopsis thaliana] gi|332198339|gb|AEE36460.1| phospholipid N-methyltransferase [Arabidopsis thaliana]	164	164	4.00E-83	100.0	92.1	97.0	phospholipid N-methyltransferase	gbpln	Arabidopsis thaliana	AT1G80860.1 | Symbols: ATPLMT, PLMT | phospholipid N-methyltransferase | chr1:30388432-30389284 REVERSE LENGTH=164	164	164	1.00E-85	100.0	92.1	97.0
Rsa1.0_01004.1.g22363.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01004.1.g22364.t1	ref|NP_178202.1| protein kinase-like protein [Arabidopsis thaliana] gi|75336903|sp|Q9SAH3.1|Y1887_ARATH RecName: Full=Putative receptor-like protein kinase At1g80870 gi|6503299|gb|AAF14675.1|AC011713_23 Contains similarity to gb|U82481 KI domain interacting kinase 1 from Zea mays and contains PF|00069 Eukaryotic protein kinase domain. ESTs gb|H77140, gb|H76842 and gb|AI994303 come from this gene [Arabidopsis thaliana] gi|332198341|gb|AEE36462.1| putative receptor-like protein kinase [Arabidopsis thaliana]	696	692	0	99.4	82.3	88.5	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G80870.1 | Symbols: | Protein kinase superfamily protein | chr1:30392133-30394211 FORWARD LENGTH=692	696	692	0	99.4	82.3	88.5

Rsa1.0_01004.1.g22365.t1	ref|XP_002887805.1| hypothetical protein ARALYDRAFT_895892 [Arabidopsis lyrata subsp. lyrata] gi|297333646|gb|EFH64064.1| hypothetical protein ARALYDRAFT_895892 [Arabidopsis lyrata subsp. lyrata]	446	443	0	99.3	91.0	94.6	hypothetical protein ARALYDRAFT_895892	gbpln	Arabidopsis lyrata	AT1G80900.1 | Symbols: ATMGT1, MGT1, MRS2-10 | magnesium transporter 1 | chr1:30398289-30399870 REVERSE LENGTH=443	446	443	0	99.3	90.6	94.4
Rsa1.0_01004.1.g22366.t1	gb|EOA35825.1| hypothetical protein CARUB_v10021065mg [Capsella rubella]	152	162	1.00E-69	106.6	90.8	94.1	hypothetical protein CARUB_v10021065mg	gbpln	Capsella rubella	AT1G80920.1 | Symbols: J8 | Chaperone DnaJ-domain superfamily protein | chr1:30403863-30404549 REVERSE LENGTH=163	152	163	2.00E-71	107.2	90.8	94.1
Rsa1.0_01004.1.g22367.t1	ref|NP_178208.1| pre-mRNA-splicing factor CWC22 [Arabidopsis thaliana] gi|6503305|gb|AAF14681.1|AC011713_29 Contains similarity to gb|U19615 LET 858 gene from Caenorhabditis elegans. ESTs gb|AI995150, gb|H76674 and gb|R84035 come from this gene [Arabidopsis thaliana] gi|22654971|gb|AAM98078.1| At1g80930/F23A5_23 [Arabidopsis thaliana] gi|28416525|gb|AAO42793.1| At1g80930/F23A5_23 [Arabidopsis thaliana] gi|332198347|gb|AEE36468.1| MIF4G and MA3 domain-containing protein [Arabidopsis thaliana]	926	900	0	97.2	74.1	79.8	pre-mRNA-splicing factor CWC22	gbpln	Arabidopsis thaliana	AT1G80930.1 | Symbols: | MIF4G domain-containing protein / MA3 domain-containing protein | chr1:30405774-30409499 REVERSE LENGTH=900	926	900	0	97.2	74.1	79.8
Rsa1.0_01004.1.g22368.t1	ref|NP_178085.1| wall-associated receptor kinase-like 22 [Arabidopsis thaliana] gi|75247675|sp|Q8RY17.1|WAKLI_ARATH RecName: Full=Wall-associated receptor kinase-like 22; Flags: Precursor gi|19310447|gb|AAL84959.1| At1g79670/F20B17_27 [Arabidopsis thaliana] gi|332198163|gb|AEE36284.1| wall-associated receptor kinase-like 22 [Arabidopsis thaliana]	763	751	0	98.4	75.4	83.0	wall-associated receptor kinase-like 22	gbpln	Arabidopsis thaliana	AT1G79670.1 | Symbols: RFO1, WAKL22 | Wall-associated kinase family protein | chr1:29976887-29979337 REVERSE LENGTH=751	763	751	0	98.4	75.4	83.0
Rsa1.0_01004.1.g22369.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	76	871	3.00E-25	1146.1	86.8	90.8	Ulp1 protease family protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01004.1.g22370.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01004.1.g22371.t1	gb|EOA34224.1| hypothetical protein CARUB_v10021735mg [Capsella rubella]	480	496	0	103.3	86.9	92.9	hypothetical protein CARUB_v10021735mg	gbpln	Capsella rubella	AT1G79630.1 | Symbols: | Protein phosphatase 2C family protein | chr1:29962931-29965169 REVERSE LENGTH=504	480	504	0	105.0	84.6	91.7
Rsa1.0_01004.1.g22372.t1	gb|EOA33496.1| hypothetical protein CARUB_v10019721mg, partial [Capsella rubella]	994	982	0	98.8	90.4	94.3	hypothetical protein CARUB_v10019721mg, partial	gbpln	Capsella rubella	AT1G79620.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:29957633-29962174 REVERSE LENGTH=971	994	971	0	97.7	89.7	93.6
Rsa1.0_01004.1.g22373.t1	#	#	#	#	#	#	#	-	----	----	AT1G79610.1 | Symbols: ATNHX6, NHX6 | Na+/H+ antiporter 6 | chr1:29953089-29957070 REVERSE LENGTH=535	95	535	3.00E-11	563.2	46.3	51.6
Rsa1.0_01004.1.g22374.t1	gb|EOA34811.1| hypothetical protein CARUB_v10022389mg [Capsella rubella]	714	713	0	99.9	92.6	95.7	hypothetical protein CARUB_v10022389mg	gbpln	Capsella rubella	AT1G79600.1 | Symbols: | Protein kinase superfamily protein | chr1:29950105-29952516 REVERSE LENGTH=711	714	711	0	99.6	91.3	94.8
Rsa1.0_01004.1.g22375.t1	ref|NP_565213.1| syntaxin-52 [Arabidopsis thaliana] gi|79321486|ref|NP_001031301.1| syntaxin-52 [Arabidopsis thaliana] gi|28380159|sp|Q94KK7.1|SYP52_ARATH RecName: Full=Syntaxin-52; Short=AtSYP52 gi|13811646|gb|AAK40224.1|AF355756_1 syntaxin of plants 52 [Arabidopsis thaliana] gi|28393106|gb|AAO41986.1| unknown protein [Arabidopsis thaliana] gi|29824261|gb|AAP04091.1| unknown protein [Arabidopsis thaliana] gi|332198148|gb|AEE36269.1| syntaxin-52 [Arabidopsis thaliana] gi|332198149|gb|AEE36270.1| syntaxin-52 [Arabidopsis thaliana]	235	233	1.00E-121	99.1	93.2	95.7	syntaxin-52	gbpln	Arabidopsis thaliana	AT1G79590.2 | Symbols: SYP52, ATSYP52 | syntaxin of plants 52 | chr1:29947064-29948304 FORWARD LENGTH=233	235	233	1.00E-123	99.1	93.2	95.7
Rsa1.0_01004.1.g22376.t1	gb|EOA35321.1| hypothetical protein CARUB_v10020504mg [Capsella rubella]	63	368	4.00E-29	584.1	96.8	100.0	hypothetical protein CARUB_v10020504mg	gbpln	Capsella rubella	AT1G79580.3 | Symbols: SMB | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:29941020-29942925 REVERSE LENGTH=371	63	371	1.00E-30	588.9	96.8	100.0
Rsa1.0_01005.1.g22377.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_01005.1.g22378.t1</td><td>emb|CAC41369.1| enoyl-[acyl carrier-protein] reductase [Brassica napus]</td><td>396</td><td>387</td><td>1.00E-156</td><td>97.7</td><td>80.6</td><td>83.1</td><td>enoyl-</td><td>gbpln</td><td>Brassica napus</td><td>AT2G05990.2 | Symbols: MOD1, ENR1 | NAD(P)-binding Rossmann-fold superfamily protein | chr2:2322876-2324867 FORWARD LENGTH=390</td><td>396</td><td>390</td><td>1.00E-155</td><td>98.5</td><td>76.3</td><td>81.6</td></tr>
<tr><td>Rsa1.0_01005.1.g22379.t1</td><td>dbj|BAJ34600.1| unnamed protein product [Thellungiella halophila]</td><td>389</td><td>389</td><td>0</td><td>100.0</td><td>92.3</td><td>95.6</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT2G06050.3 | Symbols: OPR3 | oxophytodienoate-reductase 3 | chr2:2359240-2361971 REVERSE LENGTH=391</td><td>389</td><td>391</td><td>0</td><td>100.5</td><td>90.7</td><td>94.9</td></tr>
<tr><td>Rsa1.0_01005.1.g22380.t1</td><td>ref|NP_178674.6| protein early flowering 8 [Arabidopsis thaliana] gi|207079706|tpd|FAA00428.1| TPA: VERNALIZATION INDEPENDENCE 6 [Arabidopsis thaliana] gi|330250911|gb|AEC06005.1| protein early flowering 8 [Arabidopsis thaliana]</td><td>1085</td><td>1091</td><td>0</td><td>100.6</td><td>91.7</td><td>95.1</td><td>protein early flowering 8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G06210.1 | Symbols: ELF8, VIP6 | binding | chr2:2429108-2436588 REVERSE LENGTH=1091</td><td>1085</td><td>1091</td><td>0</td><td>100.6</td><td>91.7</td><td>95.1</td></tr>
<tr><td>Rsa1.0_01005.1.g22381.t6</td><td>gb|EOA31389.1| hypothetical protein CARUB_v10014566mg [Capsella rubella]</td><td>225</td><td>225</td><td>1.00E-111</td><td>100.0</td><td>97.8</td><td>98.7</td><td>hypothetical protein CARUB_v10014566mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G06530.1 | Symbols: VPS2.1 | SNF7 family protein | chr2:2588740-2590285 REVERSE LENGTH=225</td><td>225</td><td>225</td><td>1.00E-113</td><td>100.0</td><td>97.8</td><td>98.2</td></tr>
<tr><td>Rsa1.0_01005.1.g22382.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01005.1.g22383.t1</td><td>ref|XP_002879863.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325702|gb|EFH56122.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>402</td><td>404</td><td>0</td><td>100.5</td><td>85.6</td><td>91.3</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G43080.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:16213995-16215828 REVERSE LENGTH=404</td><td>402</td><td>404</td><td>0</td><td>100.5</td><td>83.8</td><td>90.8</td></tr>
<tr><td>Rsa1.0_01005.1.g22384.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01005.1.g22385.t1</td><td>sp|Q6YDN9.1|XTH_BRAOB RecName: Full=Xyloglucan endotransglucosylase/hydrolase; AltName: Full=BobXET16A; Flags: Precursor gi|37359374|gb|AAO00727.1| xyloglucan endotransglycosylase precursor [Brassica oleracea var. botrytis]</td><td>295</td><td>295</td><td>1.00E-174</td><td>100.0</td><td>98.0</td><td>99.3</td><td>RecName: Full=Xyloglucan endotransglucosylase/hydrolase; AltName: Full=BobXET16A; Flags: Precursor gi|37359374|gb|AAO00727.1| xyloglucan endotransglycosylase precursor</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G06850.1 | Symbols: EXGT-A1, EXT, XTH4 | xyloglucan endotransglucosylase/hydrolase 4 | chr2:2763619-2765490 FORWARD LENGTH=296</td><td>295</td><td>296</td><td>1.00E-172</td><td>100.3</td><td>96.3</td><td>98.0</td></tr>
<tr><td>Rsa1.0_01005.1.g22386.t1</td><td>ref|XP_002883744.1| hypothetical protein ARALYDRAFT_319360 [Arabidopsis lyrata subsp. lyrata] gi|297329584|gb|EFH60003.1| hypothetical protein ARALYDRAFT_319360 [Arabidopsis lyrata subsp. lyrata]</td><td>201</td><td>181</td><td>8.00E-48</td><td>90.0</td><td>61.2</td><td>69.2</td><td>hypothetical protein ARALYDRAFT_319360</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G35320.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:13521893-13523144 FORWARD LENGTH=225</td><td>201</td><td>225</td><td>4.00E-49</td><td>111.9</td><td>58.2</td><td>72.6</td></tr>
<tr><td>Rsa1.0_01005.1.g22387.t1</td><td>ref|XP_002885825.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331665|gb|EFH62084.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>684</td><td>710</td><td>0</td><td>103.8</td><td>76.3</td><td>86.7</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G07020.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr2:2908473-2911198 REVERSE LENGTH=700</td><td>684</td><td>700</td><td>0</td><td>102.3</td><td>73.4</td><td>84.6</td></tr>
<tr><td>Rsa1.0_01005.1.g22388.t4</td><td>ref|XP_002883756.1| cycloartenol synthase [Arabidopsis lyrata subsp. lyrata] gi|297329596|gb|EFH60015.1| cycloartenol synthase [Arabidopsis lyrata subsp. lyrata]</td><td>728</td><td>759</td><td>0</td><td>104.3</td><td>92.2</td><td>95.3</td><td>cycloartenol synthase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G07050.1 | Symbols: CAS1 | cycloartenol synthase 1 | chr2:2924629-2930295 FORWARD LENGTH=759</td><td>728</td><td>759</td><td>0</td><td>104.3</td><td>91.8</td><td>95.5</td></tr>
<tr><td>Rsa1.0_01005.1.g22389.t1</td><td>gb|ABA18104.1| putative plasma membrane ATPase [Capsella rubella] gi|482548056|gb|EOA12258.1| hypothetical protein CARUB_v10008027mg [Capsella rubella]</td><td>412</td><td>948</td><td>0</td><td>230.1</td><td>80.3</td><td>86.7</td><td>putative plasma membrane ATPase</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G07560.1 | Symbols: AHA6, HA6 | H(+)-ATPase 6 | chr2:3170394-3173952 REVERSE LENGTH=949</td><td>412</td><td>949</td><td>0</td><td>230.3</td><td>85.0</td><td>87.6</td></tr>
<tr><td>Rsa1.0_01006.1.g22390.t1</td><td>ref|XP_002887954.1| hypothetical protein ARALYDRAFT_475003 [Arabidopsis lyrata subsp. lyrata] gi|297333795|gb|EFH64213.1| hypothetical protein ARALYDRAFT_475003 [Arabidopsis lyrata subsp. lyrata]</td><td>221</td><td>517</td><td>2.00E-61</td><td>233.9</td><td>59.3</td><td>67.4</td><td>hypothetical protein ARALYDRAFT_475003</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G63520.1 | Symbols: | Protein of unknown function (DUF3527) | chr1:23560205-23561873 FORWARD LENGTH=528</td><td>221</td><td>528</td><td>1.00E-55</td><td>238.9</td><td>56.6</td><td>66.1</td></tr>
<tr><td>Rsa1.0_01006.1.g22391.t1</td><td>ref|XP_002887955.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333796|gb|EFH64214.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>489</td><td>487</td><td>0</td><td>99.6</td><td>95.1</td><td>97.3</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G63500.1 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr1:23556015-23558403 FORWARD LENGTH=487</td><td>489</td><td>487</td><td>0</td><td>99.6</td><td>94.9</td><td>97.3</td></tr>
<tr><td>Rsa1.0_01006.1.g22392.t1</td><td>ref|XP_002886399.1| F2K11.14 [Arabidopsis lyrata subsp. lyrata] gi|297332240|gb|EFH62658.1| F2K11.14 [Arabidopsis lyrata subsp. lyrata]</td><td>1464</td><td>1461</td><td>0</td><td>99.8</td><td>79.4</td><td>86.6</td><td>F2K11.14</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G63490.1 | Symbols: | transcription factor jumonji (jmjC) domain-containing protein | chr1:23544938-23551946 REVERSE LENGTH=1116</td><td>1464</td><td>1116</td><td>0</td><td>76.2</td><td>58.5</td><td>64.5</td></tr>
</table>

Rsa1.0_01006.1.g22393.t1	ref|NP_176536.2| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|26451696|dbj|BAC42943.1| putative DNA-binding protein [Arabidopsis thaliana] gi|28973281|gb|AAO63965.1| putative DNA-binding protein [Arabidopsis thaliana] gi|119657354|tpd|FAA00276.1| TPA: AT-hook motif nuclear localized protein 5 [Arabidopsis thaliana] gi|332195982|gb|AEE34103.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	373	378	2.33E-156	101.3	80.2	86.9	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT1G63470.1 | Symbols: | AT hook motif DNA-binding family protein | chr1:23536831-23538863 REVERSE LENGTH=378	373	378	1.00E-149	101.3	80.2	86.9
Rsa1.0_01006.1.g22394.t1	gb|ACF95839.1| heavy metal P-type ATPase [Arabidopsis thaliana] gi|195362187|gb|ACF95841.1| heavy metal P-type ATPase [Arabidopsis thaliana] gi|195362195|gb|ACF95845.1| heavy metal P-type ATPase [Arabidopsis thaliana] gi|195362205|gb|ACF95850.1| heavy metal P-type ATPase [Arabidopsis thaliana] gi|195362211|gb|ACF95853.1| heavy metal P-type ATPase [Arabidopsis thaliana] gi|195362221|gb|ACF95858.1| heavy metal P-type ATPase [Arabidopsis thaliana] gi|195362233|gb|ACF95864.1| heavy metal P-type ATPase [Arabidopsis thaliana]	1199	995	0	83.0	76.3	79.7	heavy metal P-type ATPase	gbpln	Arabidopsis thaliana	AT1G63440.1 | Symbols: HMA5 | heavy metal atpase 5 | chr1:23527655-23531109 FORWARD LENGTH=995	1199	995	0	83.0	76.2	79.6
Rsa1.0_01006.1.g22395.t1	ref|NP_176532.2| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|263430169|sp|C0LGH8.1|Y1634_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g63430; Flags: Precursor gi|224589459|gb|ACN59263.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332195977|gb|AEE34098.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	679	664	0	97.8	85.4	91.2	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G63430.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:23522896-23526451 FORWARD LENGTH=664	679	664	0	97.8	85.4	91.2
Rsa1.0_01006.1.g22396.t3	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	934	1274	0	136.4	53.0	67.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	934	575	6.00E-63	61.6	16.8	24.3
Rsa1.0_01006.1.g22397.t1	ref|XP_002887961.1| hypothetical protein ARALYDRAFT_475010 [Arabidopsis lyrata subsp. lyrata] gi|297333802|gb|EFH64220.1| hypothetical protein ARALYDRAFT_475010 [Arabidopsis lyrata subsp. lyrata]	579	571	0	98.6	84.8	89.8	hypothetical protein ARALYDRAFT_475010	gbpln	Arabidopsis lyrata	AT1G63420.1 | Symbols: | Arabidopsis thaliana protein of unknown function (DUF821) | chr1:23515874-23518777 FORWARD LENGTH=578	579	578	0	99.8	83.6	90.0
Rsa1.0_01006.1.g22398.t1	ref|XP_002886402.1| hypothetical protein ARALYDRAFT_475012 [Arabidopsis lyrata subsp. lyrata] gi|297332243|gb|EFH62661.1| hypothetical protein ARALYDRAFT_475012 [Arabidopsis lyrata subsp. lyrata]	159	154	8.00E-61	96.9	76.1	83.6	hypothetical protein ARALYDRAFT_475012	gbpln	Arabidopsis lyrata	AT1G63310.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G20362.1); Has 78 Blast hits to 77 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:23486580-23487044 REVERSE LENGTH=154	159	154	6.00E-63	96.9	75.5	83.6
Rsa1.0_01006.1.g22399.t1	gb|AGF69111.1| PPR [Raphanus sativus]	47	479	2.00E-14	1019.1	83.0	83.0	PPR	gbpln	Raphanus sativus	#	#	#	#	#	#	#
Rsa1.0_01006.1.g22400.t1	ref|XP_002886431.1| hypothetical protein ARALYDRAFT_893154 [Arabidopsis lyrata subsp. lyrata] gi|297332272|gb|EFH62690.1| hypothetical protein ARALYDRAFT_893154 [Arabidopsis lyrata subsp. lyrata]	268	317	1.00E-132	118.3	90.3	95.5	hypothetical protein ARALYDRAFT_893154	gbpln	Arabidopsis lyrata	AT1G63120.1 | Symbols: ATRBL2, RBL2 | RHOMBOID-like 2 | chr1:23409054-23410725 REVERSE LENGTH=317	268	317	1.00E-134	118.3	90.3	95.9

Rsa1.0_01006.1.g22401.t1	ref|NP_176498.1| scarecrow-like protein 28 [Arabidopsis thaliana] gi|75169917|sp|Q9CAN3.1|SCL28_ARATH RecName: Full=Scarecrow-like protein 28; Short=AtSCL28; AltName: Full=GRAS family protein 8; Short=AtGRAS-8 gi|12323248|gb|AAG51600.1|AC010795_4 transcription factor SCARECROW, putative; 52594-50618 [Arabidopsis thaliana] gi|332195932|gb|AEE34053.1| scarecrow-like protein 28 [Arabidopsis thaliana]	639	658	0	103.0	77.9	85.8	scarecrow-like protein 28	gbpln	Arabidopsis thaliana	AT1G63100.1 | Symbols: | GRAS family transcription factor | chr1:23399391-23401367 REVERSE LENGTH=658	639	658	0	103.0	77.9	85.8
Rsa1.0_01006.1.g22402.t1	ref|XP_002886433.1| phloem protein 2-A11 [Arabidopsis lyrata subsp. lyrata] gi|297332274|gb|EFH62692.1| phloem protein 2-A11 [Arabidopsis lyrata subsp. lyrata]	292	287	1.00E-139	98.3	81.8	90.1	phloem protein 2-A11	gbpln	Arabidopsis lyrata	AT1G63090.1 | Symbols: AtPP2-A11, PP2-A11 | phloem protein 2-A11 | chr1:23391283-23392609 REVERSE LENGTH=289	292	289	1.00E-133	99.0	80.1	88.0
Rsa1.0_01006.1.g22403.t1	ref|NP_564808.1| uncharacterized protein [Arabidopsis thaliana] gi|12323263|gb|AAG51615.1|AC010795_19 hypothetical protein; 35332-36114 [Arabidopsis thaliana] gi|21593840|gb|AAM65807.1| unknown [Arabidopsis thaliana] gi|28393136|gb|AAO42001.1| unknown protein [Arabidopsis thaliana] gi|28827488|gb|AAO50588.1| unknown protein [Arabidopsis thaliana] gi|332195928|gb|AEE34049.1| uncharacterized protein AT1G63060 [Arabidopsis thaliana]	135	148	1.00E-60	109.6	83.0	87.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G63060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: petal, leaf whorl, male gametophyte, flower; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G07330.1); Has 42 Blast hits to 42 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:23384105-23384887 FORWARD LENGTH=148	135	148	3.00E-63	109.6	83.0	87.4
Rsa1.0_01006.1.g22404.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01006.1.g22405.t1	gb|EOA34651.1| hypothetical protein CARUB_v10022214mg [Capsella rubella]	245	257	5.00E-82	104.9	75.9	82.9	hypothetical protein CARUB_v10022214mg	gbpln	Capsella rubella	AT1G12630.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:4298897-4299475 FORWARD LENGTH=192	245	192	8.00E-41	78.4	41.2	49.4
Rsa1.0_01007.1.g22406.t1	gb|EOA24627.1| hypothetical protein CARUB_v10017898mg [Capsella rubella]	264	252	2.00E-56	95.5	60.6	73.1	hypothetical protein CARUB_v10017898mg	gbpln	Capsella rubella	AT3G27880.1 | Symbols: | Protein of unknown function (DUF1645) | chr3:10338429-10339157 FORWARD LENGTH=242	264	242	1.00E-57	91.7	59.8	71.2
Rsa1.0_01007.1.g22407.t1	ref|NP_189421.1| 50S ribosomal protein L12-1 [Arabidopsis thaliana] gi|548653|sp|P36210.1|RK121_ARATH RecName: Full=50S ribosomal protein L12-1, chloroplastic; AltName: Full=CL12-A; Flags: Precursor gi|468771|emb|CAA48181.1| ribosomal protein L12 [Arabidopsis thaliana] gi|11994488|dbj|BAB02529.1| 50S ribosomal protein L12-like [Arabidopsis thaliana] gi|15450974|gb|AAK96758.1| 50s ribosomal protein L12-like [Arabidopsis thaliana] gi|15810119|gb|AAL07203.1| putative 50S ribosomal protein L12-A [Arabidopsis thaliana] gi|22530940|gb|AAM96974.1| 50S ribosomal protein L12-A [Arabidopsis thaliana] gi|23198422|gb|AAN15738.1| 50S ribosomal protein L12-A [Arabidopsis thaliana] gi|29824165|gb|AAP04043.1| putative 50S ribosomal protein L12-A [Arabidopsis thaliana] gi|30102916|gb|AAP21376.1| At3g27830 [Arabidopsis thaliana] gi|332643847|gb|AEE77368.1| 50S ribosomal protein L12-1 [Arabidopsis thaliana]	191	191	1.00E-69	100.0	84.8	90.1	50S ribosomal protein L12-1	gbpln	Arabidopsis thaliana	AT3G27830.1 | Symbols: RPL12-A, RPL12 | ribosomal protein L12-A | chr3:10318576-10319151 FORWARD LENGTH=191	191	191	5.00E-72	100.0	84.8	90.1
Rsa1.0_01007.1.g22408.t1	gb|EOA23892.1| hypothetical protein CARUB_v10017107mg [Capsella rubella]	486	488	0	100.4	85.2	93.6	hypothetical protein CARUB_v10017107mg	gbpln	Capsella rubella	AT3G27820.1 | Symbols: ATMDAR4, MDAR4 | monodehydroascorbate reductase 4 | chr3:10315249-10317881 FORWARD LENGTH=488	486	488	0	100.4	85.0	93.6

Rsa1.0_01007.1.g22409.t1	ref|NP_189416.2| myb domain protein 118 [Arabidopsis thaliana] gi|9294482|dbj|BAB02701.1| probable MYB-like DNA-binding protein [Arabidopsis thaliana] gi|91806493|gb|ABE65974.1| myb family transcription factor [Arabidopsis thaliana] gi|332643842|gb|AEE77363.1| myb domain protein 118 [Arabidopsis thaliana]	475	437	1.00E-156	92.0	62.5	71.2	myb domain protein 118	gbpln	Arabidopsis thaliana	AT3G27785.1 | Symbols: MYB118, ATMYB118, PGA37 | myb domain protein 118 | chr3:10288767-10290712 REVERSE LENGTH=437	475	437	1.00E-159	92.0	62.5	71.2
Rsa1.0_01007.1.g22410.t1	ref|XP_002877071.1| hypothetical protein ARALYDRAFT_905031 [Arabidopsis lyrata subsp. lyrata] gi|297322909|gb|EFH53330.1| hypothetical protein ARALYDRAFT_905031 [Arabidopsis lyrata subsp. lyrata]	313	321	1.00E-134	102.6	74.4	86.3	hypothetical protein ARALYDRAFT_905031	gbpln	Arabidopsis lyrata	AT3G27770.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G62960.1); Has 158 Blast hits to 157 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 13; Fungi - 0; Plants - 141; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr3:10285818-10287474 REVERSE LENGTH=315	313	315	1.00E-136	100.6	75.4	84.7
Rsa1.0_01007.1.g22411.t21	gb|EOA26124.1| hypothetical protein CARUB_v10019550mg [Capsella rubella]	1126	1130	0	100.4	90.0	94.0	hypothetical protein CARUB_v10019550mg	gbpln	Capsella rubella	AT3G27730.1 | Symbols: RCK, MER3 | ATP binding;ATP-dependent helicases;DNA helicases | chr3:10273952-10280213 REVERSE LENGTH=1133	1126	1133	0	100.6	89.8	93.7
Rsa1.0_01007.1.g22412.t1	ref|XP_002875399.1| hypothetical protein ARALYDRAFT_905025 [Arabidopsis lyrata subsp. lyrata] gi|297321237|gb|EFH51658.1| hypothetical protein ARALYDRAFT_905025 [Arabidopsis lyrata subsp. lyrata]	525	526	0	100.2	65.5	79.2	hypothetical protein ARALYDRAFT_905025	gbpln	Arabidopsis lyrata	AT4G34370.1 | Symbols: ATARI1, ARI1 | RING/U-box superfamily protein | chr4:16434547-16437037 FORWARD LENGTH=597	525	597	0	113.7	63.2	80.0
Rsa1.0_01007.1.g22413.t1	ref|NP_189407.2| zinc finger CCCH domain-containing protein 41 [Arabidopsis thaliana] gi|30688891|ref|NP_851008.1| zinc finger CCCH domain-containing protein 41 [Arabidopsis thaliana] gi|75335571|sp|Q9LVX1.1|C3H41_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 41; Short=AtC3H41 gi|9294475|dbj|BAB02694.1| unnamed protein product [Arabidopsis thaliana] gi|23397275|gb|AAN31919.1| unknown protein [Arabidopsis thaliana] gi|225898683|dbj|BAH30472.1| hypothetical protein [Arabidopsis thaliana] gi|332643832|gb|AEE77353.1| zinc finger CCCH domain-containing protein 41 [Arabidopsis thaliana] gi|332643833|gb|AEE77354.1| zinc finger CCCH domain-containing protein 41 [Arabidopsis thaliana]	876	908	0	103.7	77.1	83.9	zinc finger CCCH domain-containing protein 41	gbpln	Arabidopsis thaliana	AT3G27700.2 | Symbols: | zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein | chr3:10257681-10261330 REVERSE LENGTH=908	876	908	0	103.7	77.1	83.9
Rsa1.0_01007.1.g22414.t1	dbj|BAJ33772.1| unnamed protein product [Thellungiella halophila]	266	266	1.00E-151	100.0	99.2	99.6	unnamed protein product	----	----	AT3G27690.1 | Symbols: LHCB2.4, LHCB2.3, LHCB2 | photosystem II light harvesting complex gene 2.3 | chr3:10256002-10256921 FORWARD LENGTH=266	266	266	1.00E-152	100.0	97.0	98.5
Rsa1.0_01007.1.g22415.t1	gb|ACG69503.1| oleosin S2-1 [Brassica napus]	190	188	5.00E-85	98.9	94.7	95.3	oleosin S2-1	gbpln	Brassica napus	AT3G27660.1 | Symbols: OLEO4, OLE3 | oleosin 4 | chr3:10243851-10244821 FORWARD LENGTH=191	190	191	4.00E-72	100.5	82.6	89.5
Rsa1.0_01008.1.g22416.t1	ref|XP_002885421.1| FMN binding protein [Arabidopsis lyrata subsp. lyrata] gi|297331261|gb|EFH61680.1| FMN binding protein [Arabidopsis lyrata subsp. lyrata]	326	387	1.00E-147	118.7	82.8	85.6	FMN binding protein	gbpln	Arabidopsis lyrata	AT3G21140.1 | Symbols: | Pyridoxamine 5'-phosphate oxidase family protein | chr3:7409696-7412086 REVERSE LENGTH=387	326	387	1.00E-148	118.7	81.3	84.0
Rsa1.0_01008.1.g22417.t1	gb|EOA12359.1| hypothetical protein CARUB_v10016511mg [Capsella rubella]	718	356	1.00E-84	49.6	26.5	33.4	hypothetical protein CARUB_v10016511mg	gbpln	Capsella rubella	AT4G10190.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:6350928-6352031 FORWARD LENGTH=367	718	367	2.00E-80	51.1	24.9	33.7
Rsa1.0_01008.1.g22418.t1	ref|XP_002889490.1| hypothetical protein ARALYDRAFT_333729 [Arabidopsis lyrata subsp. lyrata] gi|297335332|gb|EFH65749.1| hypothetical protein ARALYDRAFT_333729 [Arabidopsis lyrata subsp. lyrata]	611	1328	1.00E-161	217.3	54.3	66.9	hypothetical protein ARALYDRAFT_333729	gbpln	Arabidopsis lyrata	AT1G04080.1 | Symbols: PRP39 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1051803-1056550 FORWARD LENGTH=768	611	768	1.00E-159	125.7	55.0	68.1

Rsa1.0_01008.1.g22419.t1	gb|EOA19601.1| hypothetical protein CARUB_v10002783mg [Capsella rubella]	375	381	1.00E−72	101.6	49.1	62.4	hypothetical protein CARUB_v10002783mg	gbpln	Capsella rubella	AT4G10190.1 | Symbols: | F−box and associated interaction domains−containing protein | chr4:6350928−6352031 FORWARD LENGTH=367	375	367	3.00E−64	97.9	42.9	57.9
Rsa1.0_01008.1.g22420.t1	gb|EOA12359.1| hypothetical protein CARUB_v10016511mg [Capsella rubella]	390	356	7.00E−87	91.3	49.2	61.5	hypothetical protein CARUB_v10016511mg	gbpln	Capsella rubella	AT4G10190.1 | Symbols: | F−box and associated interaction domains−containing protein | chr4:6350928−6352031 FORWARD LENGTH=367	390	367	2.00E−74	94.1	44.9	60.8
Rsa1.0_01008.1.g22421.t1	ref|XP_002872824.1| hypothetical protein ARALYDRAFT_490290 [Arabidopsis lyrata subsp. lyrata] gi|297318661|gb|EFH49083.1| hypothetical protein ARALYDRAFT_490290 [Arabidopsis lyrata subsp. lyrata]	885	888	0	100.3	92.3	96.3	hypothetical protein ARALYDRAFT_490290	gbpln	Arabidopsis lyrata	AT4G02680.1 | Symbols: EOL1 | ETO1−like 1 | chr4:1181202−1184328 REVERSE LENGTH=888	885	888	0	100.3	92.3	96.0
Rsa1.0_01008.1.g22422.t1	gb|EOA19773.1| hypothetical protein CARUB_v10000019mg [Capsella rubella]	3553	3559	0	100.2	81.5	88.5	hypothetical protein CARUB_v10000019mg	gbpln	Capsella rubella	AT4G02660.1 | Symbols: | Beige/BEACH domain ;WD domain, G−beta repeat protein | chr4:1159927−1173791 REVERSE LENGTH=3527	3553	3527	0	99.3	81.0	87.8
Rsa1.0_01008.1.g22423.t1	ref|XP_002866882.1| hypothetical protein ARALYDRAFT_327926 [Arabidopsis lyrata subsp. lyrata] gi|297312718|gb|EFH43141.1| hypothetical protein ARALYDRAFT_327926 [Arabidopsis lyrata subsp. lyrata]	384	864	1.00E−96	225.0	51.8	67.2	hypothetical protein ARALYDRAFT_327926	gbpln	Arabidopsis lyrata	AT4G39756.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18441756−18442880 FORWARD LENGTH=374	384	374	2.00E−96	97.4	50.3	66.7
Rsa1.0_01009.1.g22424.t3	ref|XP_002894283.1| hypothetical protein ARALYDRAFT_474212 [Arabidopsis lyrata subsp. lyrata] gi|297340125|gb|EFH70542.1| hypothetical protein ARALYDRAFT_474212 [Arabidopsis lyrata subsp. lyrata]	514	500	0	97.3	74.1	80.4	hypothetical protein ARALYDRAFT_474212	gbpln	Arabidopsis lyrata	AT1G50910.1 | Symbols: | unknown protein; Has 1105 Blast hits to 802 proteins in 217 species: Archae − 2; Bacteria − 177; Metazoa − 445; Fungi − 210; Plants − 58; Viruses − 6; Other Eukaryotes − 207 (source: NCBI BLink). | chr1:18867083−18869839 REVERSE LENGTH=500	514	500	0	97.3	73.2	80.0
Rsa1.0_01009.1.g22425.t1	ref|NP_564580.1| Ankyrin repeat family protein [Arabidopsis thaliana] gi|75248476|sp|Q8VY88.1|LTD_ARATH RecName: Full=Protein LHCP TRANSLOCATION DEFECT; AltName: Full=Protein GRANA−DEFICIENT CHLOROPLAST 1; Flags: Precursor gi|18252245|gb|AAL61955.1| unknown protein [Arabidopsis thaliana] gi|21386977|gb|AAM47892.1| unknown protein [Arabidopsis thaliana] gi|21553984|gb|AAM63065.1| unknown [Arabidopsis thaliana] gi|332194478|gb|AEE32599.1| Ankyrin repeat family protein [Arabidopsis thaliana]	176	175	3.00E−79	99.4	87.5	92.6	Ankyrin repeat family protein	gbpln	Arabidopsis thaliana	AT1G50900.1 | Symbols: GDC1 | Ankyrin repeat family protein | chr1:18866272−18867014 FORWARD LENGTH=175	176	175	1.00E−81	99.4	87.5	92.6
Rsa1.0_01009.1.g22426.t1	ref|XP_002891598.1| hypothetical protein ARALYDRAFT_474209 [Arabidopsis lyrata subsp. lyrata] gi|297337440|gb|EFH67857.1| hypothetical protein ARALYDRAFT_474209 [Arabidopsis lyrata subsp. lyrata]	224	378	5.00E−26	168.8	30.8	38.8	hypothetical protein ARALYDRAFT_474209	gbpln	Arabidopsis lyrata	AT1G50870.1 | Symbols: | F−box and associated interaction domains−containing protein | chr1:18855147−18856337 FORWARD LENGTH=396	224	396	5.00E−28	176.8	30.4	38.8
Rsa1.0_01009.1.g22427.t1	gb|AAZ66952.1| 117M18_33 [Brassica rapa]	396	681	6.00E−68	172.0	38.4	50.3	117M18_33	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_01009.1.g22428.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	856	1459	0	170.4	59.3	73.9	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	856	1262	1.00E−118	147.4	24.3	34.8
Rsa1.0_01009.1.g22429.t1	ref|XP_002891598.1| hypothetical protein ARALYDRAFT_474209 [Arabidopsis lyrata subsp. lyrata] gi|297337440|gb|EFH67857.1| hypothetical protein ARALYDRAFT_474209 [Arabidopsis lyrata subsp. lyrata]	249	378	9.00E−45	151.8	46.6	64.3	hypothetical protein ARALYDRAFT_474209	gbpln	Arabidopsis lyrata	AT1G48060.1 | Symbols: | F−box and associated interaction domains−containing protein | chr1:17728295−17729448 FORWARD LENGTH=353	249	353	2.00E−36	141.8	41.8	58.6
Rsa1.0_01009.1.g22430.t2	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	1973	1453	0	73.6	35.1	44.1	polyprotein	gbpln	Arabidopsis thaliana	AT1G50830.1 | Symbols: | Aminotransferase−like, plant mobile domain family protein | chr1:18835559−18837865 REVERSE LENGTH=768	1973	768	1.00E−169	38.9	16.1	18.6
Rsa1.0_01009.1.g22431.t1	ref|XP_002891593.1| hypothetical protein ARALYDRAFT_892015 [Arabidopsis lyrata subsp. lyrata] gi|297337435|gb|EFH67852.1| hypothetical protein ARALYDRAFT_892015 [Arabidopsis lyrata subsp. lyrata]	122	119	3.00E−46	97.5	78.7	90.2	hypothetical protein ARALYDRAFT_892015	gbpln	Arabidopsis lyrata	AT1G50740.1 | Symbols: | Transmembrane proteins 14C | chr1:18807861−18808765 FORWARD LENGTH=119	122	119	1.00E−48	97.5	77.9	89.3

Rsa1.0_01009.1.g22432.t1	ref|NP_001185189.1| uncharacterized protein [Arabidopsis thaliana] gi|332194464|gb|AEE32585.1| uncharacterized protein AT1G50732 [Arabidopsis thaliana]	116	118	2.00E-34	101.7	78.4	81.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G50732.1 | Symbols: | unknown protein. | chr1:18802781-18803263 FORWARD LENGTH=118	116	118	3.00E-37	101.7	78.4	81.9
Rsa1.0_01009.1.g22433.t5	ref|NP_175488.2| uncharacterized protein [Arabidopsis thaliana] gi|332194463|gb|AEE32584.1| uncharacterized protein AT1G50730 [Arabidopsis thaliana]	910	923	0	101.4	77.7	85.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G50730.1 | Symbols: | unknown protein; Has 218 Blast hits to 209 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 141; Fungi - 2; Plants - 33; Viruses - 0; Other Eukaryotes - 42 (source: NCBI BLink). | chr1:18795275-18802098 FORWARD LENGTH=923	910	923	0	101.4	77.7	85.8
Rsa1.0_01009.1.g22434.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1295	1307	0	100.9	59.2	73.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1295	1262	9.00E-94	97.5	14.5	22.5
Rsa1.0_01009.1.g22435.t1	gb|EOA37383.1| hypothetical protein CARUB_v10011220mg [Capsella rubella]	149	154	3.00E-59	103.4	80.5	91.3	hypothetical protein CARUB_v10011220mg	gbpln	Capsella rubella	AT1G50720.1 | Symbols: | Stigma-specific Stig1 family protein | chr1:18789180-18789644 REVERSE LENGTH=154	149	154	1.00E-58	103.4	77.9	86.6
Rsa1.0_01010.1.g22436.t1	ref|NP_195451.1| cytochrome P450, family 81, subfamily D, polypeptide 3 [Arabidopsis thaliana] gi|4006851|emb|CAB16769.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|7270717|emb|CAB80400.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|332661383|gb|AEE86783.1| cytochrome P450, family 81, subfamily D, polypeptide 3 [Arabidopsis thaliana]	501	500	0	99.8	77.0	86.2	cytochrome P450, family 81, subfamily D, polypeptide 3	gbpln	Arabidopsis thaliana	AT4G37340.1 | Symbols: CYP81D3 | cytochrome P450, family 81, subfamily D, polypeptide 3 | chr4:17564953-17566706 REVERSE LENGTH=500	501	500	0	99.8	77.0	86.2
Rsa1.0_01010.1.g22437.t1	ref|XP_002866955.1| CYP81D4 [Arabidopsis lyrata subsp. lyrata] gi|297312791|gb|EFH43214.1| CYP81D4 [Arabidopsis lyrata subsp. lyrata]	492	492	0	100.0	79.7	89.8	CYP81D4	gbpln	Arabidopsis lyrata	AT4G37330.1 | Symbols: CYP81D4 | cytochrome P450, family 81, subfamily D, polypeptide 4 | chr4:17562547-17564569 REVERSE LENGTH=492	492	492	0	100.0	78.3	89.6
Rsa1.0_01010.1.g22438.t1	ref|XP_002866957.1| CYP81H1 [Arabidopsis lyrata subsp. lyrata] gi|297312793|gb|EFH43216.1| CYP81H1 [Arabidopsis lyrata subsp. lyrata]	511	519	0	101.6	85.5	91.0	CYP81H1	gbpln	Arabidopsis lyrata	AT4G37310.1 | Symbols: CYP81H1 | cytochrome P450, family 81, subfamily H, polypeptide 1 | chr4:17556152-17558833 REVERSE LENGTH=518	511	518	0	101.4	83.8	89.8
Rsa1.0_01010.1.g22439.t1	ref|XP_002868994.1| hypothetical protein ARALYDRAFT_912615 [Arabidopsis lyrata subsp. lyrata] gi|297314830|gb|EFH45253.1| hypothetical protein ARALYDRAFT_912615 [Arabidopsis lyrata subsp. lyrata]	152	173	5.00E-54	113.8	69.1	71.1	hypothetical protein ARALYDRAFT_912615	gbpln	Arabidopsis lyrata	AT4G37300.1 | Symbols: MEE59 | maternal effect embryo arrest 59 | chr4:17554805-17555498 FORWARD LENGTH=173	152	173	5.00E-56	113.8	69.7	75.0
Rsa1.0_01010.1.g22440.t1	gb|EOA18685.1| hypothetical protein CARUB_v10007260mg [Capsella rubella]	86	86	7.00E-35	100.0	84.9	90.7	hypothetical protein CARUB_v10007260mg	gbpln	Capsella rubella	AT4G37295.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: stem, root, leaf; EXPRESSED DURING: LP.06 six leaves visible, LP.04 four leaves visible; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17553628-17553888 FORWARD LENGTH=86	86	86	2.00E-36	100.0	83.7	90.7
Rsa1.0_01010.1.g22441.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01010.1.g22442.t1	gb|EOA18862.1| hypothetical protein CARUB_v10007485mg [Capsella rubella]	134	86	2.00E-22	64.2	41.8	47.0	hypothetical protein CARUB_v10007485mg	gbpln	Capsella rubella	AT4G37290.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; LOCATED IN: endomembrane system; EXPRESSED IN: cotyledon, hypocotyl, leaf; EXPRESSED DURING: LP.04 four leaves visible; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G23270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:17549929-17550183 REVERSE LENGTH=84	134	84	2.00E-21	62.7	39.6	44.8

Rsa1.0_01010.1.g22443.t1	ref|NP_568021.1| mortality factor 4-like protein 1 [Arabidopsis thaliana] gi|14335028|gb|AAK59778.1| AT4g37280/C7A10_80 [Arabidopsis thaliana] gi|22655420|gb|AAM98302.1| At4g37280/C7A10_80 [Arabidopsis thaliana] gi|332661376|gb|AEE86776.1| MRG family protein [Arabidopsis thaliana]	317	320	1.00E-163	100.9	89.9	95.6	mortality factor 4-like protein 1	gbpln	Arabidopsis thaliana	AT4G37280.1 | Symbols: | MRG family protein | chr4:17546748-17549362 REVERSE LENGTH=320	317	320	1.00E-166	100.9	89.9	95.6
Rsa1.0_01010.1.g22444.t1	gb|AAY34978.1| chloroplast heavy metal P-type ATPase precursor [Arabidopsis thaliana]	790	819	0	103.7	91.0	94.7	chloroplast heavy metal P-type ATPase precursor	gbpln	Arabidopsis thaliana	AT4G37270.1 | Symbols: HMA1, ATHMA1 | heavy metal atpase 1 | chr4:17541987-17546352 REVERSE LENGTH=819	790	819	0	103.7	91.1	94.8
Rsa1.0_01010.1.g22445.t1	ref|NP_195443.1| myb domain protein 73 [Arabidopsis thaliana] gi|2464855|emb|CAB16756.1| myb-related protein [Arabidopsis thaliana] gi|7270709|emb|CAB80392.1| myb-related protein [Arabidopsis thaliana] gi|17380912|gb|AAL36268.1| putative myb-related protein [Arabidopsis thaliana] gi|20258981|gb|AAM14206.1| putative myb-related protein [Arabidopsis thaliana] gi|41619352|gb|AAS10083.1| MYB transcription factor [Arabidopsis thaliana] gi|332661374|gb|AEE86774.1| myb domain protein 73 [Arabidopsis thaliana]	327	320	1.00E-149	97.9	87.5	89.9	myb domain protein 73	gbpln	Arabidopsis thaliana	AT4G37260.1 | Symbols: MYB73, ATMYB73 | myb domain protein 73 | chr4:17540602-17541564 FORWARD LENGTH=320	327	320	1.00E-152	97.9	87.5	89.9
Rsa1.0_01010.1.g22446.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01010.1.g22447.t1	emb|CAB75932.1| putative protein [Arabidopsis thaliana]	1346	1339	0	99.5	54.3	71.2	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1346	1262	1.00E-100	93.8	13.8	22.9
Rsa1.0_01010.1.g22448.t1	gb|AAL57701.1| AT4g37250/C7A10_110 [Arabidopsis thaliana] gi|25090184|gb|AAN72248.1| At4g37250/C7A10_110 [Arabidopsis thaliana]	845	768	0	90.9	74.4	80.4	AT4g37250/C7A10_110	gbpln	Arabidopsis thaliana	AT4G37250.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:17527789-17530191 REVERSE LENGTH=768	845	768	0	90.9	74.4	80.5
Rsa1.0_01010.1.g22449.t1	gb|EOA16840.1| hypothetical protein CARUB_v10005061mg [Capsella rubella]	375	376	0	100.3	81.3	88.5	hypothetical protein CARUB_v10005061mg	gbpln	Capsella rubella	AT4G36880.1 | Symbols: CP1 | cysteine proteinase1 | chr4:17374692-17376180 REVERSE LENGTH=376	375	376	0	100.3	84.0	89.6
Rsa1.0_01011.1.g22450.t1	ref|XP_002887403.1| hypothetical protein ARALYDRAFT_895043 [Arabidopsis lyrata subsp. lyrata] gi|297333244|gb|EFH63662.1| hypothetical protein ARALYDRAFT_895043 [Arabidopsis lyrata subsp. lyrata]	208	225	3.00E-67	108.2	73.1	82.7	hypothetical protein ARALYDRAFT_895043	gbpln	Arabidopsis lyrata	AT1G71970.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22680.1); Has 58 Blast hits to 58 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr1:27093099-27093776 FORWARD LENGTH=225	208	225	1.00E-66	108.2	72.6	82.2
Rsa1.0_01011.1.g22451.t1	gb|AAK62788.1|AC027036_9 polyprotein, putative [Arabidopsis thaliana] gi|18265373|dbj|BAB84015.1| polyprotein [Arabidopsis thaliana]	352	1466	1.00E-100	416.5	53.7	69.9	polyprotein, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01011.1.g22452.t1	ref|XP_002888855.1| hypothetical protein ARALYDRAFT_476326 [Arabidopsis lyrata subsp. lyrata] gi|297334696|gb|EFH65114.1| hypothetical protein ARALYDRAFT_476326 [Arabidopsis lyrata subsp. lyrata]	661	661	0	100.0	86.7	91.8	hypothetical protein ARALYDRAFT_476326	gbpln	Arabidopsis lyrata	AT1G71960.1 | Symbols: ABCG25, ATABCG25 | ATP-binding casette family G25 | chr1:27082587-27088163 REVERSE LENGTH=662	661	662	0	100.2	86.1	92.0
Rsa1.0_01011.1.g22453.t1	ref|XP_002888854.1| hypothetical protein ARALYDRAFT_316165 [Arabidopsis lyrata subsp. lyrata] gi|297334695|gb|EFH65113.1| hypothetical protein ARALYDRAFT_316165 [Arabidopsis lyrata subsp. lyrata]	178	134	2.00E-32	75.3	41.6	45.5	hypothetical protein ARALYDRAFT_316165	gbpln	Arabidopsis lyrata	AT1G71950.1 | Symbols: | Proteinase inhibitor, propeptide | chr1:27080453-27081573 REVERSE LENGTH=136	178	136	1.00E-34	76.4	41.6	45.5
Rsa1.0_01011.1.g22454.t1	gb|EOA35575.1| hypothetical protein CARUB_v10020785mg [Capsella rubella]	272	272	1.00E-144	100.0	94.1	96.7	hypothetical protein CARUB_v10020785mg	gbpln	Capsella rubella	AT1G71940.1 | Symbols: | SNARE associated Golgi protein family | chr1:27078781-27079948 FORWARD LENGTH=272	272	272	2.33E-156	100.0	93.8	96.7

Rsa1.0_01011.1.g22455.t1	ref|NP_177338.1| vascular related NAC-domain protein 7 [Arabidopsis thaliana] gi|12324533|gb|AAG52219.1|AC021665_2 NAM-like protein; 48543-50167 [Arabidopsis thaliana] gi|21553558|gb|AAM62651.1| NAM-like protein [Arabidopsis thaliana] gi|111074362|gb|ABH04554.1| At1g71930 [Arabidopsis thaliana] gi|332197133|gb|AEE35254.1| vascular related NAC-domain protein 7 [Arabidopsis thaliana]	325	324	1.00E-177	99.7	93.2	94.8	vascular related NAC-domain protein 7	gbpln	Arabidopsis thaliana	AT1G71930.1 | Symbols: VND7, ANAC030 | vascular related NAC-domain protein 7 | chr1:27076205-27077829 FORWARD LENGTH=324	325	324	1.00E-180	99.7	93.2	94.8
Rsa1.0_01011.1.g22456.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01011.1.g22457.t1	ref|NP_177336.1| uncharacterized protein [Arabidopsis thaliana] gi|12324544|gb|AAG52230.1|AC021665_13 hypothetical protein; 37561-38082 [Arabidopsis thaliana] gi|26449816|dbj|BAC42031.1| unknown protein [Arabidopsis thaliana] gi|28372892|gb|AAO39928.1| At1g71910 [Arabidopsis thaliana] gi|332197129|gb|AEE35250.1| uncharacterized protein AT1G71910 [Arabidopsis thaliana]	162	173	4.00E-45	106.8	72.2	82.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G71910.1 | Symbols: | unknown protein; Has 28 Blast hits to 28 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27065223-27065744 FORWARD LENGTH=173	162	173	2.00E-47	106.8	72.2	82.7
Rsa1.0_01012.1.g22458.t1	ref|XP_002868963.1| homeobox-leucine zipper protein 22 [Arabidopsis lyrata subsp. lyrata] gi|297314799|gb|EFH45222.1| homeobox-leucine zipper protein 22 [Arabidopsis lyrata subsp. lyrata]	280	283	1.00E-116	101.1	86.8	90.7	homeobox-leucine zipper protein 22	gbpln	Arabidopsis lyrata	AT4G37790.1 | Symbols: HAT22 | Homeobox-leucine zipper protein family | chr4:17768241-17769272 FORWARD LENGTH=278	280	278	1.00E-118	99.3	85.4	89.6
Rsa1.0_01012.1.g22459.t1	#	#	#	#	#	#	#	–	----	----	AT5G38920.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:15581719-15582439 REVERSE LENGTH=192	237	192	1.00E-11	81.0	14.3	21.1
Rsa1.0_01012.1.g22460.t1	gb|ACB86852.1| xyloglucan endotransglycosylase [Brassica rapa subsp. pekinensis]	292	292	1.00E-167	100.0	95.9	98.3	xyloglucan endotransglycosylase	gbpln	Brassica rapa	AT4G37800.1 | Symbols: XTH7 | xyloglucan endotransglucosylase/hydrolase 7 | chr4:17775703-17777372 REVERSE LENGTH=293	292	293	1.00E-164	100.3	93.2	96.6
Rsa1.0_01012.1.g22461.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01012.1.g22462.t1	gb|EOA32164.1| hypothetical protein CARUB_v10015420mg [Capsella rubella]	282	219	8.00E-48	77.7	35.1	45.4	hypothetical protein CARUB_v10015420mg	gbpln	Capsella rubella	AT3G59120.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:21857876-21860221 REVERSE LENGTH=602	282	602	2.00E-33	213.5	33.3	42.9
Rsa1.0_01012.1.g22463.t1	gb|EOA16167.1| hypothetical protein CARUB_v10004303mg [Capsella rubella]	581	671	1.00E-166	115.5	48.2	49.1	hypothetical protein CARUB_v10004303mg	gbpln	Capsella rubella	AT4G37870.1 | Symbols: PCK1, PEPCK | phosphoenolpyruvate carboxykinase 1 | chr4:17802974-17806332 REVERSE LENGTH=671	581	671	1.00E-167	115.5	47.8	48.9
Rsa1.0_01012.1.g22464.t1	ref|NP_567180.1| uncharacterized protein [Arabidopsis thaliana] gi|17380736|gb|AAL36198.1| unknown protein [Arabidopsis thaliana] gi|20258925|gb|AAM14178.1| unknown protein [Arabidopsis thaliana] gi|26452418|dbj|BAC43294.1| unknown protein [Arabidopsis thaliana] gi|332656505|gb|AEE81905.1| uncharacterized protein AT4G00585 [Arabidopsis thaliana]	86	88	3.00E-37	102.3	87.2	93.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G00585.1 | Symbols: | unknown protein; Has 47 Blast hits to 47 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 7; Plants - 33; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:251157-252284 REVERSE LENGTH=88	86	88	6.00E-40	102.3	87.2	93.0
Rsa1.0_01012.1.g22465.t1	ref|NP_849514.1| Zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] gi|332661450|gb|AEE86850.1| Zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	691	711	0	102.9	79.7	87.8	Zinc finger (C3HC4-type RING finger) family protein	gbpln	Arabidopsis thaliana	AT4G37890.2 | Symbols: EDA40 | Zinc finger (C3HC4-type RING finger) family protein | chr4:17812812-17815031 REVERSE LENGTH=711	691	711	0	102.9	79.7	87.8
Rsa1.0_01012.1.g22466.t1	ref|XP_002866925.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata] gi|297312761|gb|EFH43184.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	755	787	0	104.2	73.1	79.5	glycine-rich protein	gbpln	Arabidopsis lyrata	AT4G37900.1 | Symbols: | Protein of unknown function (duplicated DUF1399) | chr4:17821737-17824445 REVERSE LENGTH=787	755	787	0	104.2	73.2	79.2
Rsa1.0_01013.1.g22467.t1	emb|CAN74823.1| hypothetical protein VITISV_034594 [Vitis vinifera]	461	952	4.00E-74	206.5	41.2	56.0	hypothetical protein VITISV_034594	gbpln	Vitis vinifera	#	#	#	#	#	#	#

Rsa1.0_01013.1.g22468.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	741	695	0	93.8	57.9	69.8	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	741	681	1.00E-21	91.9	6.2	10.1
Rsa1.0_01013.1.g22469.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01013.1.g22470.t1	ref|NP_849772.2| triacylglycerol lipase-like 1 protein [Arabidopsis thaliana] gi|22135828|gb|AAM91100.1| At1g45200 [Arabidopsis thaliana] gi|25090355|gb|AAN72283.1| At1g45200/At1g45200 [Arabidopsis thaliana] gi|332193974|gb|AEE32095.1| triacylglycerol lipase-like 1 protein [Arabidopsis thaliana]	248	479	1.00E-122	193.1	83.5	91.1	triacylglycerol lipase-like 1 protein	gbpln	Arabidopsis thaliana	AT1G45201.1 | Symbols: ATTLL1, TLL1 | triacylglycerol lipase-like 1 | chr1:17123889-17128462 FORWARD LENGTH=479	248	479	1.00E-124	193.1	83.5	91.1
Rsa1.0_01013.1.g22471.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01013.1.g22472.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01013.1.g22473.t1	ref|XP_002891317.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297337159|gb|EFH67576.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	600	648	0	108.0	67.0	76.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G45180.1 | Symbols: | RING/U-box superfamily protein | chr1:17099335-17101683 FORWARD LENGTH=645	600	645	0	107.5	66.7	76.0
Rsa1.0_01013.1.g22474.t1	gb|EOA28676.1| hypothetical protein CARUB_v10024900mg [Capsella rubella]	920	901	6.00E-95	97.9	18.6	26.2	hypothetical protein CARUB_v10024900mg	gbpln	Capsella rubella	AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907-10814173 REVERSE LENGTH=337	920	337	2.00E-18	36.6	6.0	8.2
Rsa1.0_01014.1.g22475.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1315	2301	0	175.0	34.5	43.0	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1315	1262	1.00E-107	96.0	14.7	22.1
Rsa1.0_01014.1.g22476.t1	ref|XP_002877792.1| hypothetical protein ARALYDRAFT_485473 [Arabidopsis lyrata subsp. lyrata] gi|297323630|gb|EFH54051.1| hypothetical protein ARALYDRAFT_485473 [Arabidopsis lyrata subsp. lyrata]	196	186	1.00E-76	94.9	77.0	86.2	hypothetical protein ARALYDRAFT_485473	gbpln	Arabidopsis lyrata	AT3G51220.1 | Symbols: | Plant protein of unknown function (DUF827) | chr3:19021943-19022612 REVERSE LENGTH=186	196	186	2.00E-78	94.9	76.5	85.7
Rsa1.0_01014.1.g22477.t1	ref|NP_190687.2| 60S ribosomal protein L8-2 [Arabidopsis thaliana] gi|332278222|sp|Q4PSL7.3|RL82_ARATH RecName: Full=60S ribosomal protein L8-2 gi|67633686|gb|AAY78767.1| 60S ribosomal protein L8 [Arabidopsis thaliana] gi|332645240|gb|AEE78761.1| 60S ribosomal protein L8-2 [Arabidopsis thaliana]	177	260	2.00E-37	146.9	44.1	48.6	60S ribosomal protein L8-2	gbpln	Arabidopsis thaliana	AT3G51190.1 | Symbols: | Ribosomal protein L2 family | chr3:19016606-19017547 REVERSE LENGTH=260	177	260	7.00E-40	146.9	44.1	48.6
Rsa1.0_01014.1.g22478.t1	ref|NP_190685.2| GDP-mannose 4,6 dehydratase 2 [Arabidopsis thaliana] gi|82654938|sp|P93031.3|GMD2_ARATH RecName: Full=GDP-mannose 4,6 dehydratase 2; AltName: Full=GDP-D-mannose dehydratase 2; Short=GMD 2 gi|1764100|gb|AAB51505.1| GDP-D-mannose-4,6-dehydratase [Arabidopsis thaliana] gi|106879167|gb|ABF82613.1| At3g51160 [Arabidopsis thaliana] gi|332645237|gb|AEE78758.1| GDP-mannose 4,6 dehydratase 2 [Arabidopsis thaliana]	364	373	0	102.5	90.9	95.9	GDP-mannose 4,6 dehydratase 2	gbpln	Arabidopsis thaliana	AT3G51160.1 | Symbols: MUR1, MUR_1, GMD2 | NAD(P)-binding Rossmann-fold superfamily protein | chr3:19007232-19008353 REVERSE LENGTH=373	364	373	0	102.5	90.9	95.9
Rsa1.0_01014.1.g22479.t4	ref|XP_002876072.1| hypothetical protein ARALYDRAFT_485468 [Arabidopsis lyrata subsp. lyrata] gi|297321910|gb|EFH52331.1| hypothetical protein ARALYDRAFT_485468 [Arabidopsis lyrata subsp. lyrata]	194	280	7.00E-70	144.3	72.7	82.0	hypothetical protein ARALYDRAFT_485468	gbpln	Arabidopsis lyrata	AT3G51140.1 | Symbols: | Protein of unknown function (DUF3353) | chr3:18998182-18999437 FORWARD LENGTH=278	194	278	5.00E-70	143.3	71.6	82.0

Rsa1.0_01014.1.g22480.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1411	1459	0	103.4	60.5	75.0	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1411	1262	1.00E-115	89.4	14.5	21.7
Rsa1.0_01014.1.g22481.t26	gb|AAM63377.1| Putative UPF0183 protein [Arabidopsis thaliana]	568	409	0	72.0	61.3	63.7	Putative UPF0183 protein	gbpln	Arabidopsis thaliana	AT3G51130.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0183 (InterPro:IPR005373); Has 269 Blast hits to 265 proteins in 123 species: Archae - 0; Bacteria - 0; Metazoa - 131; Fungi - 82; Plants - 37; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink). | chr3:18994219-18997180 FORWARD LENGTH=410	568	410	0	72.2	61.1	63.6
Rsa1.0_01014.1.g22482.t1	ref|XP_002877789.1| hypothetical protein ARALYDRAFT_906461 [Arabidopsis lyrata subsp. lyrata] gi|297323627|gb|EFH54048.1| hypothetical protein ARALYDRAFT_906461 [Arabidopsis lyrata subsp. lyrata]	1270	1292	0	101.7	81.3	87.5	hypothetical protein ARALYDRAFT_906461	gbpln	Arabidopsis lyrata	AT3G51120.1 | Symbols: | DNA binding;zinc ion binding;nucleic acid binding;nucleic acid binding | chr3:18986026-18991886 REVERSE LENGTH=1292	1270	1292	0	101.7	81.8	87.6
Rsa1.0_01015.1.g22483.t1	ref|NP_567820.1| elongation factor Ts family protein [Arabidopsis thaliana] gi|4972052|emb|CAB43920.1| putative protein [Arabidopsis thaliana] gi|7269804|emb|CAB79664.1| putative protein [Arabidopsis thaliana] gi|15983773|gb|AAL10483.1| AT4g29060/F19B15_90 [Arabidopsis thaliana] gi|332660180|gb|AEE85580.1| elongation factor Ts family protein [Arabidopsis thaliana]	1500	953	0	63.5	55.2	58.2	elongation factor Ts family protein	gbpln	Arabidopsis thaliana	AT4G29060.1 | Symbols: emb2726 | elongation factor Ts family protein | chr4:14317744-14321315 FORWARD LENGTH=953	1500	953	0	63.5	55.2	58.2
Rsa1.0_01015.1.g22484.t1	dbj|BAJ33683.1| unnamed protein product [Thellungiella halophila]	285	304	1.00E-129	106.7	88.1	89.8	unnamed protein product	----	----	AT4G29080.1 | Symbols: PAP2, IAA27 | phytochrome-associated protein 2 | chr4:14323665-14325213 REVERSE LENGTH=305	285	305	1.00E-131	107.0	86.3	89.8
Rsa1.0_01015.1.g22485.t1	ref|NP_194639.1| transcription factor bHLH68 [Arabidopsis thaliana] gi|75159400|sp|Q8S3D1.2|BH068_ARATH RecName: Full=Transcription factor bHLH68; AltName: Full=Basic helix-loop-helix protein 68; Short=AtbHLH68; Short=bHLH 68; AltName: Full=Transcription factor EN 60; AltName: Full=bHLH transcription factor bHLH068 gi|22711852|gb|AAM10966.2|AF488634_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|4972056|emb|CAB43924.1| putative protein [Arabidopsis thaliana] gi|7269808|emb|CAB79668.1| putative protein [Arabidopsis thaliana] gi|19698939|gb|AAL91205.1| putative protein [Arabidopsis thaliana] gi|23197826|gb|AAN15440.1| putative protein [Arabidopsis thaliana] gi|332660186|gb|AEE85586.1| transcription factor bHLH68 [Arabidopsis thaliana]	375	407	1.00E-156	108.5	86.1	90.1	transcription factor bHLH68	gbpln	Arabidopsis thaliana	AT4G29100.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:14341140-14344575 FORWARD LENGTH=407	375	407	1.00E-159	108.5	86.1	90.1
Rsa1.0_01015.1.g22486.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01015.1.g22487.t1	gb|ABD65000.1| hypothetical protein 26.t00020 [Brassica oleracea]	296	302	4.00E-65	102.0	48.3	64.9	hypothetical protein 26.t00020	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	296	302	2.00E-52	102.0	41.2	58.8
Rsa1.0_01015.1.g22488.t1	ref|WP_000519654.1| hypothetical protein, partial [Streptococcus agalactiae]	180	183	2.00E-41	101.7	51.1	61.1	hypothetical protein, partial	gbbct	Streptococcus agalactiae	#	#	#	#	#	#	#
Rsa1.0_01016.1.g22489.t1	ref|XP_002886423.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332264|gb|EFH62682.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	79	326	2.00E-11	412.7	40.5	55.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G63190.1 | Symbols: | Cystatin/monellin superfamily protein | chr1:23431835-23433002 FORWARD LENGTH=225	79	225	2.00E-13	284.8	44.3	62.0
Rsa1.0_01016.1.g22490.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	371	1142	4.00E-59	307.8	39.1	50.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	371	575	2.00E-22	155.0	24.8	41.2
Rsa1.0_01016.1.g22491.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01016.1.g22492.t1	ref|XP_002875233.1| hypothetical protein ARALYDRAFT_484297 [Arabidopsis lyrata subsp. lyrata] gi|297321071|gb|EFH51492.1| hypothetical protein ARALYDRAFT_484297 [Arabidopsis lyrata subsp. lyrata]	201	189	2.00E-57	94.0	61.7	73.6	hypothetical protein ARALYDRAFT_484297	gbpln	Arabidopsis lyrata	AT2G03850.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr2:1175653-1176597 FORWARD LENGTH=191	201	191	1.00E-57	95.0	60.7	73.1
Rsa1.0_01016.1.g22493.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	970	1274	0	131.3	49.3	64.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	970	575	1.00E-46	59.3	15.9	24.1
Rsa1.0_01016.1.g22494.t2	ref|XP_002876893.1| hypothetical protein ARALYDRAFT_904656 [Arabidopsis lyrata subsp. lyrata] gi|297322731|gb|EFH53152.1| hypothetical protein ARALYDRAFT_904656 [Arabidopsis lyrata subsp. lyrata]	449	456	0	101.6	82.9	87.8	hypothetical protein ARALYDRAFT_904656	gbpln	Arabidopsis lyrata	AT2G03730.2 | Symbols: ACR5 | ACT domain repeat 5 | chr2:1137820-1139809 REVERSE LENGTH=456	449	456	0	101.6	82.4	87.1
Rsa1.0_01016.1.g22495.t1	ref|XP_002876892.1| hypothetical protein ARALYDRAFT_904655 [Arabidopsis lyrata subsp. lyrata] gi|297322730|gb|EFH53151.1| hypothetical protein ARALYDRAFT_904655 [Arabidopsis lyrata subsp. lyrata]	69	74	2.00E-19	107.2	71.0	76.8	hypothetical protein ARALYDRAFT_904655	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01016.1.g22496.t1	ref|NP_178467.1| adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana] gi|4406763|gb|AAD20074.1| unknown protein [Arabidopsis thaliana] gi|38566668|gb|AAR24224.1| At2g03720 [Arabidopsis thaliana] gi|56381933|gb|AAV85685.1| At2g03720 [Arabidopsis thaliana] gi|330250647|gb|AEC05741.1| adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana]	224	165	9.00E-85	73.7	67.9	70.1	adenine nucleotide alpha hydrolases-like protein	gbpln	Arabidopsis thaliana	AT2G03720.1 | Symbols: MRH6 | Adenine nucleotide alpha hydrolases-like superfamily protein | chr2:1132364-1133225 FORWARD LENGTH=165	224	165	3.00E-87	73.7	67.9	70.1
Rsa1.0_01016.1.g22497.t1	emb|CAD48302.1| MADS-box protein AGL3-a [Brassica oleracea var. botrytis]	256	256	1.00E-139	100.0	93.8	96.1	MADS-box protein AGL3-a	gbpln	Brassica oleracea	AT2G03710.2 | Symbols: SEP4, AGL3 | K-box region and MADS-box transcription factor family protein | chr2:1129622-1131628 FORWARD LENGTH=257	256	257	1.00E-125	100.4	85.2	92.6
Rsa1.0_01016.1.g22498.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01016.1.g22499.t1	ref|XP_002876891.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322729|gb|EFH53150.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	226	226	1.00E-125	100.0	94.7	97.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G03690.1 | Symbols: | coenzyme Q biosynthesis Coq4 family protein / ubiquinone biosynthesis Coq4 family protein | chr2:1122122-1123011 REVERSE LENGTH=226	226	226	1.00E-126	100.0	93.8	97.3
Rsa1.0_01016.1.g22500.t1	gb|EOA23227.1| hypothetical protein CARUB_v10016858mg [Capsella rubella]	605	610	0	100.8	86.3	90.9	hypothetical protein CARUB_v10016858mg	gbpln	Capsella rubella	AT2G03667.1 | Symbols: | Asparagine synthase family protein | chr2:1114179-1117281 FORWARD LENGTH=610	605	610	0	100.8	84.3	90.2
Rsa1.0_01016.1.g22501.t1	gb|EOA25476.1| hypothetical protein CARUB_v10018815mg [Capsella rubella]	408	426	1.00E-125	104.4	64.0	75.0	hypothetical protein CARUB_v10018815mg	gbpln	Capsella rubella	AT2G03640.2 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr2:1104525-1106418 REVERSE LENGTH=423	408	423	1.00E-126	103.7	61.8	75.5
Rsa1.0_01016.1.g22502.t1	ref|NP_178460.1| magnesium transporter MRS2-5 [Arabidopsis thaliana] gi|186499098|ref|NP_001118259.1| magnesium transporter MRS2-5 [Arabidopsis thaliana] gi|75274822|sp|Q9ZPR4.1|MRS25_ARATH RecName: Full=Magnesium transporter MRS2-5; AltName: Full=Magnesium Transporter 3; Short=AtMGT3 gi|20336657|gb|AAM19344.1|AF499434_1 hypothetical protein [Arabidopsis thaliana] gi|4406759|gb|AAD20070.1| hypothetical protein [Arabidopsis thaliana] gi|17979301|gb|AAL49876.1| unknown protein [Arabidopsis thaliana] gi|20465991|gb|AAM20217.1| unknown protein [Arabidopsis thaliana] gi|330250631|gb|AEC05725.1| magnesium transporter MRS2-5 [Arabidopsis thaliana] gi|330250632|gb|AEC05726.1| magnesium transporter MRS2-5 [Arabidopsis thaliana]	421	421	0	100.0	93.1	96.2	magnesium transporter MRS2-5	gbpln	Arabidopsis thaliana	AT2G03620.2 | Symbols: MGT3, MRS2-5 | magnesium transporter 3 | chr2:1100489-1102168 REVERSE LENGTH=421	421	421	0	100.0	93.1	96.2

Rsa1.0_01016.1.g22503.t1	ref|XP_002886688.1| hypothetical protein ARALYDRAFT_893645 [Arabidopsis lyrata subsp. lyrata] gi|297332529|gb|EFH62947.1| hypothetical protein ARALYDRAFT_893645 [Arabidopsis lyrata subsp. lyrata]	161	364	3.00E-19	226.1	32.9	45.3	hypothetical protein ARALYDRAFT_893645	gbpln	Arabidopsis lyrata	AT4G39756.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18441756-18442880 FORWARD LENGTH=374	161	374	1.00E-18	232.3	32.9	44.7
Rsa1.0_01016.1.g22504.t1	ref|XP_002876888.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297322726|gb|EFH53147.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	421	456	1.00E-144	108.3	71.7	82.2	myb family transcription factor	gbpln	Arabidopsis lyrata	AT2G03470.1 | Symbols: | ELM2 domain-containing protein | chr2:1045694-1047130 REVERSE LENGTH=450	421	450	1.00E-140	106.9	68.6	80.3
Rsa1.0_01016.1.g22505.t1	ref|NP_178443.1| nodulin-related protein 1 [Arabidopsis thaliana] gi|4335755|gb|AAD17432.1| unknown protein [Arabidopsis thaliana] gi|22531277|gb|AAM97142.1| unknown protein [Arabidopsis thaliana] gi|330250606|gb|AEC05700.1| nodulin-related protein 1 [Arabidopsis thaliana]	243	187	1.00E-62	77.0	60.5	65.0	nodulin-related protein 1	gbpln	Arabidopsis thaliana	AT2G03440.1 | Symbols: NRP1, ATNRP1 | nodulin-related protein 1 | chr2:1039409-1039972 REVERSE LENGTH=187	243	187	3.00E-65	77.0	60.5	65.0
Rsa1.0_01016.1.g22506.t1	ref|XP_002876881.1| hypothetical protein ARALYDRAFT_904615 [Arabidopsis lyrata subsp. lyrata] gi|297322719|gb|EFH53140.1| hypothetical protein ARALYDRAFT_904615 [Arabidopsis lyrata subsp. lyrata]	333	331	1.00E-168	99.4	86.8	92.5	hypothetical protein ARALYDRAFT_904615	gbpln	Arabidopsis lyrata	AT2G03390.1 | Symbols: | uvrB/uvrC motif-containing protein | chr2:1030635-1032354 REVERSE LENGTH=330	333	330	1.00E-169	99.1	87.4	92.5
Rsa1.0_01016.1.g22507.t1	ref|XP_002875201.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297814638|ref|XP_002875202.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321039|gb|EFH51460.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321040|gb|EFH51461.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	689	708	0	102.8	79.0	85.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G03380.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:1028292-1030361 FORWARD LENGTH=689	689	689	0	100.0	79.0	86.8
Rsa1.0_01016.1.g22508.t1	ref|NP_178435.2| Glycosyltransferase family 61 protein [Arabidopsis thaliana] gi|330250597|gb|AEC05691.1| Glycosyltransferase family 61 protein [Arabidopsis thaliana]	457	451	0	98.7	76.1	86.0	Glycosyltransferase family 61 protein	gbpln	Arabidopsis thaliana	AT2G03360.1 | Symbols: | Glycosyltransferase family 61 protein | chr2:1022287-1024273 REVERSE LENGTH=451	457	451	0	98.7	76.1	86.0
Rsa1.0_01016.1.g22509.t1	ref|XP_002876879.1| hypothetical protein ARALYDRAFT_484243 [Arabidopsis lyrata subsp. lyrata] gi|297322717|gb|EFH53138.1| hypothetical protein ARALYDRAFT_484243 [Arabidopsis lyrata subsp. lyrata]	179	179	2.00E-94	100.0	95.5	98.9	hypothetical protein ARALYDRAFT_484243	gbpln	Arabidopsis lyrata	AT2G03350.1 | Symbols: | Protein of unknown function, DUF538 | chr2:1019733-1021071 REVERSE LENGTH=179	179	179	1.00E-96	100.0	94.4	98.9
Rsa1.0_01016.1.g22510.t1	gb|ACI14395.1| WRKY3-1 transcription factor [Brassica napus]	473	489	0	103.4	89.6	94.7	WRKY3-1 transcription factor	gbpln	Brassica napus	AT2G03340.1 | Symbols: WRKY3 | WRKY DNA-binding protein 3 | chr2:1014724-1016936 REVERSE LENGTH=513	473	513	0	108.5	82.2	88.2
Rsa1.0_01016.1.g22511.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01017.1.g22512.t3	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1331	2726	0	204.8	48.8	64.5	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1331	158	2.00E-28	11.9	4.4	5.8
Rsa1.0_01017.1.g22513.t1	gb|EOA39983.1| hypothetical protein CARUB_v10008671mg [Capsella rubella]	716	585	0	81.7	64.2	70.3	hypothetical protein CARUB_v10008671mg	gbpln	Capsella rubella	AT1G34160.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:12441393-12443225 FORWARD LENGTH=581	716	581	0	81.1	62.7	69.4
Rsa1.0_01017.1.g22514.t1	ref|XP_002891079.1| hypothetical protein ARALYDRAFT_473569 [Arabidopsis lyrata subsp. lyrata] gi|297336921|gb|EFH67338.1| hypothetical protein ARALYDRAFT_473569 [Arabidopsis lyrata subsp. lyrata]	432	443	0	102.5	85.9	91.0	hypothetical protein ARALYDRAFT_473569	gbpln	Arabidopsis lyrata	AT1G34150.1 | Symbols: | Pseudouridine synthase family protein | chr1:12436086-12439237 FORWARD LENGTH=446	432	446	0	103.2	84.3	89.1
Rsa1.0_01017.1.g22515.t1	ref|NP_174578.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana] gi|378405165|sp|Q9MAP1.2|FB33_ARATH RecName: Full=Putative F-box protein At1g33020 gi|332193429|gb|AEE31550.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana]	598	548	8.00E-67	91.6	28.8	37.6	F-box and associated interaction domain-containing protein	gbpln	Arabidopsis thaliana	AT1G33020.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11962746-11964832 FORWARD LENGTH=548	598	548	2.00E-69	91.6	28.8	37.6

Rsa1.0_01017.1.g22516.t1	ref|XP_002891078.1| hypothetical protein ARALYDRAFT_891007 [Arabidopsis lyrata subsp. lyrata] gi|297336920|gb|EFH67337.1| hypothetical protein ARALYDRAFT_891007 [Arabidopsis lyrata subsp. lyrata]	743	738	0	99.3	95.3	97.4	hypothetical protein ARALYDRAFT_891007	gbpln	Arabidopsis lyrata	AT1G34130.1 | Symbols: STT3B | staurosporin and temperature sensitive 3-like b | chr1:12430000-12432985 FORWARD LENGTH=735	743	735	0	98.9	94.2	97.0
Rsa1.0_01017.1.g22517.t1	gb|ABD65022.1| hypothetical protein 26.t00077 [Brassica oleracea]	181	242	1.00E-36	133.7	53.6	65.7	hypothetical protein 26.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01018.1.g22518.t1	gb|EOA23933.1| hypothetical protein CARUB_v10017147mg [Capsella rubella]	485	475	0	97.9	89.5	94.6	hypothetical protein CARUB_v10017147mg	gbpln	Capsella rubella	AT3G61490.3 | Symbols: | Pectin lyase-like superfamily protein | chr3:22758439-22760137 FORWARD LENGTH=476	485	476	0	98.1	88.9	94.2
Rsa1.0_01018.1.g22519.t1	gb|EOA25497.1| hypothetical protein CARUB_v10018840mg, partial [Capsella rubella]	474	496	0	104.6	85.7	92.6	hypothetical protein CARUB_v10018840mg, partial	gbpln	Capsella rubella	AT3G61510.1 | Symbols: ACS1, AT-ACS1 | ACC synthase 1 | chr3:22763495-22765730 REVERSE LENGTH=488	474	488	0	103.0	86.3	92.6
Rsa1.0_01018.1.g22520.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01018.1.g22521.t1	ref|NP_191712.1| Phosphoenolpyruvate carboxylase family protein [Arabidopsis thaliana] gi|42572757|ref|NP_974474.1| Phosphoenolpyruvate carboxylase family protein [Arabidopsis thaliana] gi|6850844|emb|CAB71083.1| 3-methyl-2-oxobutanoate hydroxy-methyl-transferase-like protein [Arabidopsis thaliana] gi|21593121|gb|AAM65070.1| 3-methyl-2-oxobutanoate hydroxy-methyl-transferase-like protein [Arabidopsis thaliana] gi|94442441|gb|ABF19008.1| At3g61530 [Arabidopsis thaliana] gi|332646697|gb|AEE80218.1| Phosphoenolpyruvate carboxylase family protein [Arabidopsis thaliana] gi|332646698|gb|AEE80219.1| Phosphoenolpyruvate carboxylase family protein [Arabidopsis thaliana]	355	354	0	99.7	89.9	94.4	Phosphoenolpyruvate carboxylase family protein	gbpln	Arabidopsis thaliana	AT3G61530.2 | Symbols: PANB2 | Phosphoenolpyruvate carboxylase family protein | chr3:22771692-22773313 REVERSE LENGTH=354	355	354	0	99.7	89.9	94.4
Rsa1.0_01018.1.g22522.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01018.1.g22523.t1	gb|EOA24745.1| hypothetical protein CARUB_v10018022mg [Capsella rubella]	214	211	1.00E-80	98.6	73.8	79.0	hypothetical protein CARUB_v10018022mg	gbpln	Capsella rubella	AT3G61550.1 | Symbols: | RING/U-box superfamily protein | chr3:22776444-22777082 FORWARD LENGTH=212	214	212	1.00E-80	99.1	73.4	79.4
Rsa1.0_01018.1.g22524.t1	ref|XP_002878389.1| hypothetical protein ARALYDRAFT_907697 [Arabidopsis lyrata subsp. lyrata] gi|297324227|gb|EFH54648.1| hypothetical protein ARALYDRAFT_907697 [Arabidopsis lyrata subsp. lyrata]	709	710	0	100.1	83.9	91.3	hypothetical protein ARALYDRAFT_907697	gbpln	Arabidopsis lyrata	AT3G61570.1 | Symbols: GC3, GDAP1 | GRIP-related ARF-binding domain-containing protein 1 | chr3:22779637-22783642 REVERSE LENGTH=712	709	712	0	100.4	82.9	91.1
Rsa1.0_01018.1.g22525.t1	gb|AEW24954.1| delta8-sphingolipid desaturase [Brassica rapa]	449	447	0	99.6	91.1	96.0	delta8-sphingolipid desaturase	gbpln	Brassica rapa	AT3G61580.1 | Symbols: | Fatty acid/sphingolipid desaturase | chr3:22786253-22787602 FORWARD LENGTH=449	449	449	0	100.0	87.5	93.5
Rsa1.0_01018.1.g22526.t1	ref|NP_191718.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|334186190|ref|NP_001190155.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75183486|sp|Q9M310.1|FBK77_ARATH RecName: Full=F-box/kelch-repeat protein At3g61590 gi|14423514|gb|AAK62439.1|AF386994_1 putative protein [Arabidopsis thaliana] gi|6850850|emb|CAB71089.1| putative protein [Arabidopsis thaliana] gi|23197692|gb|AAN15373.1| putative protein [Arabidopsis thaliana] gi|332646706|gb|AEE80227.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|332646707|gb|AEE80228.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	405	411	0	101.5	82.7	92.1	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G61590.2 | Symbols: HWS | Galactose oxidase/kelch repeat superfamily protein | chr3:22792914-22794149 FORWARD LENGTH=411	405	411	0	101.5	82.7	92.1
Rsa1.0_01018.1.g22527.t1	ref|NP_850733.1| POZ/BTB containin G-protein 1 [Arabidopsis thaliana] gi|327488374|sp|Q9FPW6.2|POB1_ARATH RecName: Full=BTB/POZ domain-containing protein POB1; AltName: Full=POZ/BTB CONTAINING-PROTEIN 1; Short=AtPOB1 gi|332646708|gb|AEE80229.1| POZ/BTB containin G-protein 1 [Arabidopsis thaliana]	557	561	0	100.7	73.2	82.2	POZ/BTB containin G-protein 1	gbpln	Arabidopsis thaliana	AT3G61600.1 | Symbols: ATPOB1, POB1 | POZ/BTB containin G-protein 1 | chr3:22795704-22797953 FORWARD LENGTH=561	557	561	0	100.7	73.2	82.2

Rsa1.0_01018.1.g22528.t1	ref|XP_002876625.1| aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322463|gb|EFH52884.1| aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata]	325	317	1.00E-165	97.5	84.9	90.5	aldose 1-epimerase family protein	gbpln	Arabidopsis lyrata	AT3G61610.1 | Symbols: | Galactose mutarotase-like superfamily protein | chr3:22799480-22801029 FORWARD LENGTH=317	325	317	1.00E-168	97.5	84.6	90.2
Rsa1.0_01018.1.g22529.t8	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1480	1223	0	82.6	39.2	52.8	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1480	746	1.00E-89	50.4	11.6	16.8
Rsa1.0_01018.1.g22530.t1	gb|EOA24449.1| hypothetical protein CARUB_v10017705mg [Capsella rubella]	284	306	2.00E-93	107.7	68.7	79.2	hypothetical protein CARUB_v10017705mg	gbpln	Capsella rubella	AT3G61630.1 | Symbols: CRF6 | cytokinin response factor 6 | chr3:22805274-22806221 FORWARD LENGTH=315	284	315	2.00E-86	110.9	66.9	76.8
Rsa1.0_01018.1.g22531.t1	ref|NP_191724.1| tubulin gamma-1 chain [Arabidopsis thaliana] gi|297821024|ref|XP_002878395.1| gamma-tubulin [Arabidopsis lyrata subsp. lyrata] gi|586079|sp|P38557.1|TBG1_ARATH RecName: Full=Tubulin gamma-1 chain; AltName: Full=Gamma-1-tubulin gi|460089|gb|AAA20653.1| g1-tubulin [Arabidopsis thaliana] gi|6850856|emb|CAB71095.1| TUBULIN GAMMA-1 CHAIN [Arabidopsis thaliana] gi|297324233|gb|EFH54654.1| gamma-tubulin [Arabidopsis lyrata subsp. lyrata] gi|332646715|gb|AEE80236.1| tubulin gamma-1 chain [Arabidopsis thaliana] gi|482559746|gb|EOA23937.1| hypothetical protein CARUB_v10017152mg [Capsella rubella]	473	474	0	100.2	98.3	99.6	tubulin gamma-1 chain	gbpln	Arabidopsis lyrata	AT3G61650.1 | Symbols: TUBG1 | gamma-tubulin | chr3:22812601-22815011 REVERSE LENGTH=474	473	474	0	100.2	98.3	99.6
Rsa1.0_01019.1.g22532.t1	dbj|BAH30499.1| hypothetical protein [Arabidopsis thaliana]	308	363	1.00E-103	117.9	71.4	78.2	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G62090.2 | Symbols: PIL2, PIF6 | phytochrome interacting factor 3-like 2 | chr3:22989097-22990546 REVERSE LENGTH=363	308	363	1.00E-100	117.9	67.9	75.0
Rsa1.0_01019.1.g22533.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1022	2301	0	225.1	35.1	44.6	disease resistance protein	gbpln	Brassica rapa	AT3G61970.1 | Symbols: NGA2 | AP2/B3-like transcriptional factor family protein | chr3:22951829-22952728 FORWARD LENGTH=299	1022	299	1.00E-121	29.3	24.0	25.5
Rsa1.0_01019.1.g22534.t1	gb|AAD24601.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	186	1319	1.00E-16	709.1	33.9	46.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01019.1.g22535.t1	ref|XP_002878423.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297324261|gb|EFH54682.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	636	626	0	98.4	81.3	86.2	kinase family protein	gbpln	Arabidopsis lyrata	AT3G61960.1 | Symbols: | Protein kinase superfamily protein | chr3:22941966-22944996 REVERSE LENGTH=626	636	626	0	98.4	80.2	84.9
Rsa1.0_01019.1.g22536.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2011	1274	0	63.4	29.3	40.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2011	575	7.00E-59	28.6	8.0	13.4
Rsa1.0_01020.1.g22537.t1	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	448	695	1.00E-113	155.1	43.5	45.8	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01020.1.g22538.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	521	1838	1.00E-139	352.8	48.8	62.6	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01020.1.g22539.t5	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	641	1089	5.00E-46	169.9	17.8	24.8	transposon protein-like	gbpln	Arabidopsis thaliana	AT4G03740.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr4:1661992-1663515 REVERSE LENGTH=345	641	345	9.00E-13	53.8	5.3	7.3
Rsa1.0_01020.1.g22540.t1	ref|NP_190532.2| 2-oxoglutarate-Fe(II)-dependent oxygenase domain-containing protein [Arabidopsis thaliana] gi|332645047|gb|AEE78568.1| 2-oxoglutarate-Fe(II)-dependent oxygenase domain-containing protein [Arabidopsis thaliana]	333	332	1.00E-160	99.7	82.0	88.9	2-oxoglutarate-Fe(II)-dependent oxygenase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G49630.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:18397759-18400255 FORWARD LENGTH=332	333	332	1.00E-163	99.7	82.0	88.9
Rsa1.0_01020.1.g22541.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01020.1.g22542.t1	gb|ABD65163.1| hypothetical protein 40.t00048 [Brassica oleracea]	263	569	8.00E-28	216.3	27.8	39.9	hypothetical protein 40.t00048	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_01020.1.g22543.t1	ref|XP_002875990.1| ATBCAT-3 [Arabidopsis lyrata subsp. lyrata] gi|297321828|gb|EFH52249.1| ATBCAT-3 [Arabidopsis lyrata subsp. lyrata]	430	418	0	97.2	77.4	87.9	ATBCAT-3	gbpln	Arabidopsis lyrata	AT3G49680.1 | Symbols: ATBCAT-3, BCAT3 | branched-chain aminotransferase 3 | chr3:18422768-18425473 FORWARD LENGTH=413	430	413	0	96.0	76.3	86.5
Rsa1.0_01020.1.g22544.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01020.1.g22545.t1	ref|NP_190538.1| transcription factor RAX3 [Arabidopsis thaliana] gi|75335856|sp|Q9M2Y9.1|RAX3_ARATH RecName: Full=Transcription factor RAX3; AltName: Full=Myb-related protein 84; Short=AtMYB84; AltName: Full=Protein REGULATOR OF AXILLARY MERISTEMS 3 gi|6723414|emb|CAB66907.1| AtMYB84 [Arabidopsis thaliana] gi|41619286|gb|AAS10067.1| MYB transcription factor [Arabidopsis thaliana] gi|116325910|gb|ABJ98556.1| At3g49690 [Arabidopsis thaliana] gi|332645056|gb|AEE78577.1| transcription factor RAX3 [Arabidopsis thaliana]	288	310	1.00E-119	107.6	83.3	88.5	transcription factor RAX3	gbpln	Arabidopsis thaliana	AT3G49690.1 | Symbols: RAX3, MYB84, ATMYB84 | myb domain protein 84 | chr3:18427941-18429100 FORWARD LENGTH=310	288	310	1.00E-121	107.6	83.3	88.5
Rsa1.0_01021.1.g22546.t1	ref|NP_197290.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332005098|gb|AED92481.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	542	1197	0	220.8	66.4	77.9	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G17880.1 | Symbols: CSA1 | disease resistance protein (TIR-NBS-LRR class) | chr5:5908874-5913096 REVERSE LENGTH=1197	542	1197	0	220.8	66.4	77.9
Rsa1.0_01021.1.g22547.t1	ref|NP_197290.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332005098|gb|AED92481.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	590	1197	0	202.9	77.5	87.6	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G17880.1 | Symbols: CSA1 | disease resistance protein (TIR-NBS-LRR class) | chr5:5908874-5913096 REVERSE LENGTH=1197	590	1197	0	202.9	77.5	87.6
Rsa1.0_01021.1.g22548.t1	ref|NP_568358.1| plastid-specific 50S ribosomal protein 6 [Arabidopsis thaliana] gi|75171293|sp|Q9FKP0.1|PSRP6_ARATH RecName: Full=50S ribosomal protein 6, chloroplastic; AltName: Full=CL25; AltName: Full=Plastid-specific 50S ribosomal protein 6; Short=PSRP-6; Flags: Precursor gi|10177888|dbj|BAB11220.1| unnamed protein product [Arabidopsis thaliana] gi|14517428|gb|AAK62604.1| AT5g17870/MPI7_10 [Arabidopsis thaliana] gi|20147339|gb|AAM10383.1| AT5g17870/MPI7_10 [Arabidopsis thaliana] gi|21554906|gb|AAM63726.1| plastid-specific ribosomal protein 6 precursor (Psrp-6)-like [Arabidopsis thaliana] gi|332005097|gb|AED92480.1| plastid-specific 50S ribosomal protein 6 [Arabidopsis thaliana]	106	106	3.00E-46	100.0	87.7	92.5	plastid-specific 50S ribosomal protein 6	gbpln	Arabidopsis thaliana	AT5G17870.1 | Symbols: PSRP6 | plastid-specific 50S ribosomal protein 6 | chr5:5907817-5908137 FORWARD LENGTH=106	106	106	4.00E-49	100.0	87.7	92.5
Rsa1.0_01021.1.g22549.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01021.1.g22550.t1	dbj|BAJ34263.1| unnamed protein product [Thellungiella halophila]	576	577	0	100.2	87.2	92.9	unnamed protein product	----	----	AT5G17860.1 | Symbols: CAX7 | calcium exchanger 7 | chr5:5902638-5904350 REVERSE LENGTH=570	576	570	0	99.0	84.9	92.0
Rsa1.0_01021.1.g22551.t1	gb|EOA18522.1| hypothetical protein CARUB_v10007075mg [Capsella rubella]	388	401	1.00E-118	103.4	58.2	70.6	hypothetical protein CARUB_v10007075mg	gbpln	Capsella rubella	AT4G22180.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr4:11738574-11739782 FORWARD LENGTH=402	388	402	1.00E-108	103.6	54.6	69.3
Rsa1.0_01021.1.g22552.t1	gb|EOA20308.1| hypothetical protein CARUB_v10000616mg [Capsella rubella]	553	554	0	100.2	85.4	91.0	hypothetical protein CARUB_v10000616mg	gbpln	Capsella rubella	AT5G17850.1 | Symbols: | Sodium/calcium exchanger family protein | chr5:5899253-5900932 FORWARD LENGTH=559	553	559	0	101.1	85.4	91.0
Rsa1.0_01021.1.g22553.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01022.1.g22554.t1	gb|EOA29011.1| hypothetical protein CARUB_v10025264mg [Capsella rubella]	348	623	1.00E-127	179.0	66.1	72.1	hypothetical protein CARUB_v10025264mg	gbpln	Capsella rubella	AT2G30290.2 | Symbols: VSR2, AtVSR2 | VACUOLAR SORTING RECEPTOR 2 | chr2:12912569-12915781 REVERSE LENGTH=641	348	641	1.00E-129	184.2	66.1	71.6
Rsa1.0_01022.1.g22555.t1	ref|XP_002865895.1| hypothetical protein ARALYDRAFT_918255 [Arabidopsis lyrata subsp. lyrata] gi|297311730|gb|EFH42154.1| hypothetical protein ARALYDRAFT_918255 [Arabidopsis lyrata subsp. lyrata]	200	204	6.00E-30	102.0	42.0	52.0	hypothetical protein ARALYDRAFT_918255	gbpln	Arabidopsis lyrata	AT5G52140.1 | Symbols: | RING/U-box superfamily protein | chr5:21184566-21186872 REVERSE LENGTH=280	200	280	4.00E-22	140.0	38.0	57.5

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<tr><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></tr>
<tr><td>Rsa1.0_01022.1.g22556.t1</td><td>gb|EOA12587.1| hypothetical protein CARUB_v10027027mg [Capsella rubella]</td><td>233</td><td>240</td><td>1.00E−92</td><td>103.0</td><td>74.7</td><td>85.0</td><td>hypothetical protein CARUB_v10027027mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25570.1 | Symbols: ACYB-2 | Cytochrome b561/ferric reductase transmembrane protein family | chr4:13053887-13055518 REVERSE LENGTH=239</td><td>233</td><td>239</td><td>2.00E−89</td><td>102.6</td><td>68.7</td><td>81.5</td></tr>
<tr><td>Rsa1.0_01022.1.g22557.t1</td><td>sp|Q9FJU2.2|FBD37_ARATH RecName: Full=Putative FBD-associated F-box protein At5g56700</td><td>408</td><td>398</td><td>1.00E−104</td><td>97.5</td><td>57.1</td><td>69.6</td><td>RecName: Full=Putative FBD-associated F-box protein At5g56700</td><td>----</td><td>----</td><td>AT5G60610.1 | Symbols: | F-box/RNI-like superfamily protein | chr5:24364049-24365386 FORWARD LENGTH=388</td><td>408</td><td>388</td><td>1.00E−101</td><td>95.1</td><td>53.4</td><td>66.9</td></tr>
<tr><td>Rsa1.0_01022.1.g22558.t1</td><td>ref|NP_200041.1| Myosin heavy chain-related protein [Arabidopsis thaliana] gi|10177394|dbj|BAB10525.1| hyaluronan mediated motility receptor-like protein [Arabidopsis thaliana] gi|47550677|gb|AAT35237.1| At5g52280 [Arabidopsis thaliana] gi|51970830|dbj|BAD44107.1| hyaluronan mediated motility receptor-like protein [Arabidopsis thaliana] gi|332008812|gb|AED96195.1| Myosin heavy chain-related protein [Arabidopsis thaliana]</td><td>805</td><td>853</td><td>0</td><td>106.0</td><td>84.7</td><td>93.3</td><td>Myosin heavy chain-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G52280.1 | Symbols: | Myosin heavy chain-related protein | chr5:21226959-21230109 FORWARD LENGTH=853</td><td>805</td><td>853</td><td>0</td><td>106.0</td><td>84.7</td><td>93.3</td></tr>
<tr><td>Rsa1.0_01022.1.g22559.t1</td><td>gb|EOA14447.1| hypothetical protein CARUB_v10027650mg [Capsella rubella]</td><td>553</td><td>634</td><td>1.00E−163</td><td>114.6</td><td>72.2</td><td>82.6</td><td>hypothetical protein CARUB_v10027650mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G52300.1 | Symbols: RD29B, LTI65 | CAP160 protein | chr5:21237205-21239404 FORWARD LENGTH=619</td><td>553</td><td>619</td><td>1.00E−158</td><td>111.9</td><td>68.7</td><td>80.5</td></tr>
<tr><td>Rsa1.0_01022.1.g22560.t1</td><td>gb|AAR21079.1| stress responsive protein [Brassica oleracea var. viridis]</td><td>608</td><td>617</td><td>0</td><td>101.5</td><td>77.8</td><td>81.6</td><td>stress responsive protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G52300.1 | Symbols: RD29B, LTI65 | CAP160 protein | chr5:21237205-21239404 FORWARD LENGTH=619</td><td>608</td><td>619</td><td>2.00E−67</td><td>101.8</td><td>45.2</td><td>57.2</td></tr>
<tr><td>Rsa1.0_01022.1.g22561.t2</td><td>ref|XP_002864165.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310000|gb|EFH40424.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>613</td><td>631</td><td>0</td><td>102.9</td><td>95.6</td><td>98.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G52340.1 | Symbols: ATEXO70A2, EXO70A2 | exocyst subunit exo70 family protein A2 | chr5:21250802-21253939 FORWARD LENGTH=631</td><td>613</td><td>631</td><td>0</td><td>102.9</td><td>95.3</td><td>98.2</td></tr>
<tr><td>Rsa1.0_01022.1.g22562.t1</td><td>ref|XP_002865909.1| hypothetical protein ARALYDRAFT_495305 [Arabidopsis lyrata subsp. lyrata] gi|297311744|gb|EFH42168.1| hypothetical protein ARALYDRAFT_495305 [Arabidopsis lyrata subsp. lyrata] gi|482550326|gb|EOA14520.1| hypothetical protein CARUB_v10027750mg [Capsella rubella]</td><td>130</td><td>137</td><td>2.00E−69</td><td>105.4</td><td>98.5</td><td>98.5</td><td>hypothetical protein ARALYDRAFT_495305</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G52360.1 | Symbols: ADF10 | actin depolymerizing factor 10 | chr5:21258157-21259229 REVERSE LENGTH=137</td><td>130</td><td>137</td><td>8.00E−70</td><td>105.4</td><td>95.4</td><td>96.9</td></tr>
<tr><td>Rsa1.0_01022.1.g22563.t1</td><td>ref|XP_002865911.1| hypothetical protein ARALYDRAFT_918281 [Arabidopsis lyrata subsp. lyrata] gi|297311746|gb|EFH42170.1| hypothetical protein ARALYDRAFT_918281 [Arabidopsis lyrata subsp. lyrata]</td><td>210</td><td>192</td><td>1.00E−96</td><td>91.4</td><td>82.4</td><td>87.6</td><td>hypothetical protein ARALYDRAFT_918281</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G52390.1 | Symbols: | PAR1 protein | chr5:21264281-21265173 REVERSE LENGTH=195</td><td>210</td><td>195</td><td>7.00E−97</td><td>92.9</td><td>79.0</td><td>86.2</td></tr>
<tr><td>Rsa1.0_01022.1.g22564.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>918</td><td>1274</td><td>0</td><td>138.8</td><td>51.9</td><td>67.8</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>918</td><td>575</td><td>2.00E−78</td><td>62.6</td><td>20.6</td><td>30.1</td></tr>
<tr><td>Rsa1.0_01023.1.g22565.t1</td><td>ref|XP_002873219.1| hypothetical protein ARALYDRAFT_908485 [Arabidopsis lyrata subsp. lyrata] gi|297319056|gb|EFH49478.1| hypothetical protein ARALYDRAFT_908485 [Arabidopsis lyrata subsp. lyrata]</td><td>480</td><td>472</td><td>0</td><td>98.3</td><td>92.1</td><td>94.4</td><td>hypothetical protein ARALYDRAFT_908485</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05690.1 | Symbols: CPD, CYP90A, CYP90, CBB3, DWF3, CYP90A1 | Cytochrome P450 superfamily protein | chr5:1702907-1706705 REVERSE LENGTH=472</td><td>480</td><td>472</td><td>0</td><td>98.3</td><td>92.3</td><td>94.6</td></tr>
<tr><td>Rsa1.0_01023.1.g22566.t1</td><td>ref|XP_002871176.1| hypothetical protein ARALYDRAFT_487368 [Arabidopsis lyrata subsp. lyrata] gi|297317013|gb|EFH47435.1| hypothetical protein ARALYDRAFT_487368 [Arabidopsis lyrata subsp. lyrata]</td><td>811</td><td>810</td><td>0</td><td>99.9</td><td>87.3</td><td>94.1</td><td>hypothetical protein ARALYDRAFT_487368</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05680.1 | Symbols: MOS7 | nuclear pore complex protein-related | chr5:1698365-1702475 FORWARD LENGTH=810</td><td>811</td><td>810</td><td>0</td><td>99.9</td><td>86.2</td><td>93.1</td></tr>
<tr><td>Rsa1.0_01023.1.g22567.t1</td><td>ref|XP_002873217.1| signal recognition particle binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319054|gb|EFH49476.1| signal recognition particle binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>259</td><td>260</td><td>1.00E−133</td><td>100.4</td><td>91.9</td><td>95.4</td><td>signal recognition particle binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05670.1 | Symbols: | signal recognition particle binding | chr5:1695916-1697534 REVERSE LENGTH=260</td><td>259</td><td>260</td><td>1.00E−134</td><td>100.4</td><td>90.3</td><td>95.4</td></tr>
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Rsa1.0_01023.1.g22568.t1	ref|XP_002873216.1| transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297319053|gb|EFH49475.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	887	880	0	99.2	87.1	92.6	transcription factor	gbpln	Arabidopsis lyrata	AT5G05660.1 | Symbols: ATNFXL2 | sequence-specific DNA binding transcription factors;zinc ion binding;sequence-specific DNA binding transcription factors | chr5:1691113-1695464 REVERSE LENGTH=880	887	880	0	99.2	87.7	93.5
Rsa1.0_01023.1.g22569.t1	ref|XP_002871174.1| amino acid permease family protein [Arabidopsis lyrata subsp. lyrata] gi|297317011|gb|EFH47433.1| amino acid permease family protein [Arabidopsis lyrata subsp. lyrata]	491	488	0	99.4	79.8	90.0	amino acid permease family protein	gbpln	Arabidopsis lyrata	AT5G05630.1 | Symbols: | Amino acid permease family protein | chr5:1682541-1684013 FORWARD LENGTH=490	491	490	0	99.8	78.6	89.6
Rsa1.0_01023.1.g22570.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01023.1.g22571.t1	ref|XP_002873214.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297319051|gb|EFH49473.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata]	238	241	1.00E-106	101.3	88.2	93.7	PHD finger family protein	gbpln	Arabidopsis lyrata	AT5G05610.2 | Symbols: AL1 | alfin-like 1 | chr5:1677331-1678942 REVERSE LENGTH=241	238	241	1.00E-109	101.3	88.2	93.7
Rsa1.0_01023.1.g22572.t1	ref|NP_001190229.1| syntaxin binding protein 5 (tomosyn) [Arabidopsis thaliana] gi|332003508|gb|AED90891.1| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	1085	1099	0	101.3	86.7	92.4	syntaxin binding protein 5 (tomosyn)	gbpln	Arabidopsis thaliana	AT5G05570.2 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:1656766-1663728 FORWARD LENGTH=1099	1085	1099	0	101.3	86.7	92.4
Rsa1.0_01023.1.g22573.t1	emb|CAN83990.1| hypothetical protein VITISV_018454 [Vitis vinifera]	388	1243	2.00E-50	320.4	33.5	50.8	hypothetical protein VITISV_018454	gbpln	Vitis vinifera	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	388	237	2.00E-11	61.1	8.8	13.9
Rsa1.0_01023.1.g22574.t1	gb|EOA21447.1| hypothetical protein CARUB_v10001830mg [Capsella rubella]	251	243	2.00E-74	96.8	65.3	75.7	hypothetical protein CARUB_v10001830mg	gbpln	Capsella rubella	AT5G05550.1 | Symbols: | sequence-specific DNA binding transcription factors | chr5:1639344-1640550 REVERSE LENGTH=246	251	246	2.00E-76	98.0	64.1	75.3
Rsa1.0_01023.1.g22575.t1	ref|NP_568157.1| outer membrane OMP85 family protein [Arabidopsis thaliana] gi|10178129|dbj|BAB11541.1| unnamed protein product [Arabidopsis thaliana] gi|16648863|gb|AAL24283.1| Unknown protein [Arabidopsis thaliana] gi|20259796|gb|AAM13245.1| unknown protein [Arabidopsis thaliana] gi|332003500|gb|AED90883.1| outer membrane OMP85 family protein [Arabidopsis thaliana]	557	524	0	94.1	74.7	83.8	outer membrane OMP85 family protein	gbpln	Arabidopsis thaliana	AT5G05520.1 | Symbols: | Outer membrane OMP85 family protein | chr5:1632912-1635104 FORWARD LENGTH=524	557	524	0	94.1	74.7	83.8
Rsa1.0_01023.1.g22576.t1	ref|NP_196170.1| Mad3/BUB1 homology region 1 [Arabidopsis thaliana] gi|10178128|dbj|BAB11540.1| unnamed protein product [Arabidopsis thaliana] gi|50253522|gb|AAT71963.1| At5g05510 [Arabidopsis thaliana] gi|56381969|gb|AAV85703.1| At5g05510 [Arabidopsis thaliana] gi|332003499|gb|AED90882.1| Mad3/BUB1 homology region 1 [Arabidopsis thaliana]	467	471	0	100.9	85.0	90.8	Mad3/BUB1 homology region 1	gbpln	Arabidopsis thaliana	AT5G05510.1 | Symbols: | Mad3/BUB1 homology region 1 | chr5:1630651-1632568 REVERSE LENGTH=471	467	471	0	100.9	85.0	90.8
Rsa1.0_01023.1.g22577.t1	gb|EOA22611.1| hypothetical protein CARUB_v10003279mg [Capsella rubella]	182	183	5.00E-91	100.5	90.7	95.1	hypothetical protein CARUB_v10003279mg	gbpln	Capsella rubella	AT5G05500.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:1629716-1630267 FORWARD LENGTH=183	182	183	6.00E-88	100.5	88.5	92.9
Rsa1.0_01023.1.g22578.t10	ref|XP_002871163.1| DIF1/SYN1 [Arabidopsis lyrata subsp. lyrata] gi|297317000|gb|EFH47422.1| DIF1/SYN1 [Arabidopsis lyrata subsp. lyrata]	693	619	0	89.3	70.6	76.5	DIF1/SYN1	gbpln	Arabidopsis lyrata	AT5G05490.2 | Symbols: SYN1, DIF1 | Rad21/Rec8-like family protein | chr5:1624712-1629144 FORWARD LENGTH=617	693	617	0	89.0	69.7	75.6
Rsa1.0_01024.1.g22579.t1	ref|NP_001190461.1| COP1-interacting protein-like protein [Arabidopsis thaliana] gi|332007561|gb|AED94944.1| COP1-interacting protein-like protein [Arabidopsis thaliana]	1179	1180	0	100.1	75.4	84.4	COP1-interacting protein-like protein	gbpln	Arabidopsis thaliana	AT5G43310.2 | Symbols: | COP1-interacting protein-related | chr5:17379735-17385387 REVERSE LENGTH=1180	1179	1180	0	100.1	75.4	84.4
Rsa1.0_01024.1.g22580.t1	dbj|BAJ33598.1| unnamed protein product [Thellungiella halophila]	222	604	2.00E-24	272.1	35.1	36.0	unnamed protein product	----	----	AT1G16720.1 | Symbols: HCF173 | high chlorophyll fluorescence phenotype 173 | chr1:5723161-5726248 FORWARD LENGTH=598	222	598	4.00E-26	269.4	32.0	32.9

Rsa1.0_01024.1.g22581.t1	ref|NP_199146.1| casein kinase I-like 8 [Arabidopsis thaliana] gi|13430690|gb|AAK25967.1|AF360257_1 putative casein kinase I [Arabidopsis thaliana] gi|8843885|dbj|BAA97411.1| casein kinase I [Arabidopsis thaliana] gi|14532894|gb|AAK64129.1| putative casein kinase I [Arabidopsis thaliana] gi|62997000|gb|AAY24544.1| casein kinase 1-like protein 8 [Arabidopsis thaliana] gi|332007562|gb|AED94945.1| casein kinase I-like 8 [Arabidopsis thaliana]	472	480	0	101.7	94.3	96.8	casein kinase I-like 8	gbpln	Arabidopsis thaliana	AT5G43320.1 | Symbols: ckl8 | casein kinase I-like 8 | chr5:17386043-17388941 REVERSE LENGTH=480	472	480	0	101.7	94.3	96.8
Rsa1.0_01024.1.g22582.t1	emb|CAN71038.1| hypothetical protein VITISV_011062 [Vitis vinifera]	209	646	2.00E-31	309.1	37.8	50.2	hypothetical protein VITISV_011062	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01024.1.g22583.t1	gb|EOA19533.1| hypothetical protein CARUB_v10002484mg [Capsella rubella]	518	518	0	100.0	80.7	89.6	hypothetical protein CARUB_v10002484mg	gbpln	Capsella rubella	AT5G43340.1 | Symbols: PHT6, PHT1;6 | phosphate transporter 1;6 | chr5:17393598-17395148 REVERSE LENGTH=516	518	516	0	99.6	81.1	89.4
Rsa1.0_01024.1.g22584.t1	gb|EOA14581.1| hypothetical protein CARUB_v10027822mg [Capsella rubella]	521	524	0	100.6	94.6	97.3	hypothetical protein CARUB_v10027822mg	gbpln	Capsella rubella	AT5G43360.1 | Symbols: PHT3, ATPT4, PHT1;3 | phosphate transporter 1;3 | chr5:17409524-17411214 FORWARD LENGTH=521	521	521	0	100.0	94.2	96.7
Rsa1.0_01024.1.g22585.t1	gb|EOA14581.1| hypothetical protein CARUB_v10027822mg [Capsella rubella]	454	524	0	115.4	88.1	91.9	hypothetical protein CARUB_v10027822mg	gbpln	Capsella rubella	AT5G43360.1 | Symbols: PHT3, ATPT4, PHT1;3 | phosphate transporter 1;3 | chr5:17409524-17411214 FORWARD LENGTH=521	454	521	0	114.8	86.8	91.0
Rsa1.0_01024.1.g22586.t5	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01025.1.g22587.t1	ref|NP_200559.1| uncharacterized protein [Arabidopsis thaliana] gi|9758312|dbj|BAB08786.1| unnamed protein product [Arabidopsis thaliana] gi|91805711|gb|ABE65584.1| hypothetical protein At5g57510 [Arabidopsis thaliana] gi|332009526|gb|AED96909.1| uncharacterized protein AT5G57510 [Arabidopsis thaliana]	94	130	8.00E-30	138.3	81.9	84.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G57510.1 | Symbols: | unknown protein; Has 27 Blast hits to 27 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:23289164-23289556 REVERSE LENGTH=130	94	130	1.00E-32	138.3	81.9	84.0
Rsa1.0_01025.1.g22588.t1	gb|EOA14827.1| hypothetical protein CARUB_v10028137mg [Capsella rubella]	173	172	3.00E-62	99.4	79.8	87.9	hypothetical protein CARUB_v10028137mg	gbpln	Capsella rubella	AT5G57420.1 | Symbols: IAA33 | indole-3-acetic acid inducible 33 | chr5:23270024-23270959 FORWARD LENGTH=171	173	171	3.00E-63	98.8	76.9	87.3
Rsa1.0_01025.1.g22589.t1	gb|AAD26943.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1378	1454	0	105.5	67.5	80.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1378	1262	1.00E-162	91.6	21.0	26.5
Rsa1.0_01025.1.g22590.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01025.1.g22591.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1427	1515	0	106.2	53.5	68.3	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1427	1262	1.00E-109	88.4	13.5	20.2
Rsa1.0_01025.1.g22592.t1	ref|XP_002866204.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312039|gb|EFH42463.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	200	202	2.00E-69	101.0	72.0	80.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G25845.1 | Symbols: | BEST Arabidopsis thaliana protein match is: OSBP(oxysterol binding protein)-related protein 4B (TAIR:AT4G25850.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:13142270-13142632 FORWARD LENGTH=120	200	120	4.00E-25	60.0	31.0	38.0
Rsa1.0_01025.1.g22593.t2	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	1751	1557	0	88.9	37.6	50.8	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1751	575	1.00E-91	32.8	11.0	17.2
Rsa1.0_01025.1.g22594.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01026.1.g22595.t1	emb|CAN64512.1| hypothetical protein VITISV_004351 [Vitis vinifera]	190	282	3.00E-29	148.4	34.7	34.7	hypothetical protein VITISV_004351	gbpln	Vitis vinifera	#	#	#	#	#	#	#

Rsa1.0_01026.1.g22596.t1	ref|NP_566710.1| uncharacterized protein [Arabidopsis thaliana] gi|18252913|gb|AAL62383.1| unknown protein [Arabidopsis thaliana] gi|23197926|gb|AAN15490.1| unknown protein [Arabidopsis thaliana] gi|332643129|gb|AEE76650.1| uncharacterized protein AT3G22530 [Arabidopsis thaliana]	188	198	4.00E-65	105.3	79.8	86.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G22530.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G14830.1); Has 77 Blast hits to 77 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 77; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7977774-7978370 REVERSE LENGTH=198	188	198	2.00E-67	105.3	79.8	86.7
Rsa1.0_01026.1.g22597.t1	ref|NP_188891.1| uncharacterized protein [Arabidopsis thaliana] gi|11994284|dbj|BAB01467.1| unnamed protein product [Arabidopsis thaliana] gi|17381094|gb|AAL36359.1| unknown protein [Arabidopsis thaliana] gi|20259295|gb|AAM14383.1| unknown protein [Arabidopsis thaliana] gi|332643128|gb|AEE76649.1| uncharacterized protein AT3G22520 [Arabidopsis thaliana]	578	600	0	103.8	83.0	89.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G22520.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast, chloroplast envelope; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G14840.1); Has 717 Blast hits to 703 proteins in 179 species: Archae - 14; Bacteria - 134; Metazoa - 141; Fungi - 74; Plants - 209; Viruses - 0; Other Eukaryotes - 145 (source: NCBI BLink). | chr3:7974984-7977406 FORWARD LENGTH=600	578	600	0	103.8	83.0	89.3
Rsa1.0_01026.1.g22598.t2	gb|EOA15469.1| hypothetical protein CARUB_v10004386mg [Capsella rubella]	528	619	7.00E-71	117.2	26.5	33.5	hypothetical protein CARUB_v10004386mg	gbpln	Capsella rubella	AT5G41020.1 | Symbols: | myb family transcription factor | chr5:16425883-16427649 REVERSE LENGTH=588	528	588	4.00E-73	111.4	26.1	34.3
Rsa1.0_01026.1.g22599.t1	ref|NP_188890.2| Pre-rRNA-processing protein TSR2 [Arabidopsis thaliana] gi|50897194|gb|AAT85736.1| At3g22510 [Arabidopsis thaliana] gi|51972092|gb|AAU15150.1| At3g22510 [Arabidopsis thaliana] gi|332643127|gb|AEE76648.1| Pre-rRNA-processing protein TSR2 [Arabidopsis thaliana]	126	124	5.00E-46	98.4	77.8	87.3	Pre-rRNA-processing protein TSR2	gbpln	Arabidopsis thaliana	AT3G22510.1 | Symbols: | Pre-rRNA-processing protein TSR2, conserved region | chr3:7973544-7974087 FORWARD LENGTH=124	126	124	1.00E-48	98.4	77.8	87.3
Rsa1.0_01026.1.g22600.t1	ref|NP_188888.1| Seed maturation protein [Arabidopsis thaliana] gi|11994281|dbj|BAB01464.1| seed maturation protein, LEA protein in group 5-like [Arabidopsis thaliana] gi|27754552|gb|AAO22723.1| putative LEA protein [Arabidopsis thaliana] gi|28394023|gb|AAO42419.1| putative LEA protein [Arabidopsis thaliana] gi|332643125|gb|AEE76646.1| Seed maturation protein [Arabidopsis thaliana]	262	262	1.00E-133	100.0	90.5	95.8	Seed maturation protein	gbpln	Arabidopsis thaliana	AT3G22490.1 | Symbols: | Seed maturation protein | chr3:7969785-7970738 REVERSE LENGTH=262	262	262	1.00E-135	100.0	90.5	95.8
Rsa1.0_01026.1.g22601.t1	gb|EOA31644.1| hypothetical protein CARUB_v10014846mg [Capsella rubella] gi|482567456|gb|EOA31645.1| hypothetical protein CARUB_v10014846mg [Capsella rubella]	152	148	6.00E-68	97.4	84.9	92.8	hypothetical protein CARUB_v10014846mg	gbpln	Capsella rubella	AT3G22480.1 | Symbols: PDF2 | prefoldin 2 | chr3:7969080-7969526 FORWARD LENGTH=148	152	148	3.00E-69	97.4	83.6	91.4
Rsa1.0_01026.1.g22602.t4	gb|EOA29663.1| hypothetical protein CARUB_v10015596mg [Capsella rubella]	595	522	1.00E-166	87.7	59.5	69.4	hypothetical protein CARUB_v10015596mg	gbpln	Capsella rubella	AT3G22430.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Domain of unknown function XS (InterPro:IPR005380); BEST Arabidopsis thaliana protein match is: XS domain-containing protein / XS zinc finger domain-containing protein-related (TAIR:AT5G23570.1); Has 565 Blast hits to 510 proteins in 121 species: Archae - 2; Bacteria - 90; Metazoa - 191; Fungi - 32; Plants - 51; Viruses - 4; Other Eukaryotes - 195 (source: NCBI BLink). | chr3:7953455-7957605 FORWARD LENGTH=510	595	510	1.00E-166	85.7	60.0	67.4
Rsa1.0_01026.1.g22603.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01026.1.g22604.t2	ref|XP_002868242.1| hypothetical protein ARALYDRAFT_915339 [Arabidopsis lyrata subsp. lyrata] gi|297314078|gb|EFH44501.1| hypothetical protein ARALYDRAFT_915339 [Arabidopsis lyrata subsp. lyrata]	271	271	1.00E-121	100.0	83.0	90.4	hypothetical protein ARALYDRAFT_915339	gbpln	Arabidopsis lyrata	AT4G14910.1 | Symbols: HISN5B | HISTIDINE BIOSYNTHESIS 5B | chr4:8528451-8530105 REVERSE LENGTH=272	271	272	1.00E-123	100.4	81.9	88.9
Rsa1.0_01026.1.g22605.t1	gb|EOA13578.1| hypothetical protein CARUB_v10026643mg [Capsella rubella]	230	364	2.00E-19	158.3	40.4	54.8	hypothetical protein CARUB_v10026643mg	gbpln	Capsella rubella	AT5G64060.1 | Symbols: anac103, NAC103 | NAC domain containing protein 103 | chr5:25633818-25635152 REVERSE LENGTH=356	230	356	3.00E-17	154.8	34.8	47.8

Rsa1.0_01026.1.g22606.t1	gb|EOA30124.1| hypothetical protein CARUB_v10013233mg [Capsella rubella]	621	621	0	100.0	88.1	93.9	hypothetical protein CARUB_v10013233mg	gbpln	Capsella rubella	AT3G02280.1 | Symbols: | Flavodoxin family protein | chr3:453646-457659 FORWARD LENGTH=623	621	623	0	100.3	87.9	93.7
Rsa1.0_01026.1.g22607.t1	gb|AAG50751.1|AC079733_19 polyprotein, putative [Arabidopsis thaliana]	1441	1468	0	101.9	50.0	68.4	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1441	1262	1.00E-138	87.6	16.6	24.4
Rsa1.0_01026.1.g22608.t10	ref|XP_002883360.1| time for coffee [Arabidopsis lyrata subsp. lyrata] gi|297329200|gb|EFH59619.1| time for coffee [Arabidopsis lyrata subsp. lyrata]	1652	1550	0	93.8	74.8	80.6	time for coffee	gbpln	Arabidopsis lyrata	AT3G22380.2 | Symbols: TIC | time for coffee | chr3:7913181-7918967 FORWARD LENGTH=1555	1652	1555	0	94.1	73.7	80.0
Rsa1.0_01026.1.g22609.t1	gb|AEB00555.1| mitochondrial alternative oxidase 1a [Brassica juncea]	370	360	0	97.3	91.6	93.2	mitochondrial alternative oxidase 1a	gbpln	Brassica juncea	AT3G22370.1 | Symbols: AOX1A, ATAOX1A | alternative oxidase 1A | chr3:7906890-7908416 FORWARD LENGTH=354	370	354	1.00E-175	95.7	83.0	87.0
Rsa1.0_01026.1.g22610.t1	ref|XP_002885498.1| ATRPABC24.3 [Arabidopsis lyrata subsp. lyrata] gi|297331338|gb|EFH61757.1| ATRPABC24.3 [Arabidopsis lyrata subsp. lyrata]	206	205	1.00E-104	99.5	88.3	96.1	ATRPABC24.3	gbpln	Arabidopsis lyrata	AT3G22320.1 | Symbols: ATRPABC24.3, RPB5A, NRPB5, NRPD5 | Eukaryotic rpb5 RNA polymerase subunit family protein | chr3:7891045-7892094 REVERSE LENGTH=205	206	205	1.00E-107	99.5	87.9	96.1
Rsa1.0_01026.1.g22611.t1	gb|EOA30144.1| hypothetical protein CARUB_v10013251mg [Capsella rubella]	600	609	0	101.5	74.0	77.8	hypothetical protein CARUB_v10013251mg	gbpln	Capsella rubella	AT3G22310.1 | Symbols: PMH1, ATRH9 | putative mitochondrial RNA helicase 1 | chr3:7887382-7889806 FORWARD LENGTH=610	600	610	0	101.7	71.5	77.5
Rsa1.0_01026.1.g22612.t2	ref|XP_002883352.1| hypothetical protein ARALYDRAFT_479742 [Arabidopsis lyrata subsp. lyrata] gi|297329192|gb|EFH59611.1| hypothetical protein ARALYDRAFT_479742 [Arabidopsis lyrata subsp. lyrata]	772	354	0	45.9	40.7	41.6	hypothetical protein ARALYDRAFT_479742	gbpln	Arabidopsis lyrata	AT3G22290.1 | Symbols: | Endoplasmic reticulum vesicle transporter protein | chr3:7882082-7885260 FORWARD LENGTH=354	772	354	0	45.9	40.5	41.6
Rsa1.0_01027.1.g22613.t1	ref|NP_180795.1| ubiquitin family protein [Arabidopsis thaliana] gi|3831460|gb|AAC69942.1| hypothetical protein [Arabidopsis thaliana] gi|330253579|gb|AEC08673.1| ubiquitin family protein [Arabidopsis thaliana]	166	175	1.00E-39	105.4	56.6	67.5	ubiquitin family protein	gbpln	Arabidopsis thaliana	AT2G32360.1 | Symbols: | Ubiquitin-like superfamily protein | chr2:13737019-13737546 REVERSE LENGTH=175	166	175	5.00E-42	105.4	56.6	67.5
Rsa1.0_01027.1.g22614.t1	ref|XP_002524172.1| homeobox protein, putative [Ricinus communis] gi|223536541|gb|EEF38187.1| homeobox protein, putative [Ricinus communis]	718	731	0	101.8	55.7	71.9	homeobox protein, putative	gbpln	Ricinus communis	AT1G05230.3 | Symbols: HDG2 | homeodomain GLABROUS 2 | chr1:1513388-1517024 REVERSE LENGTH=719	718	719	0	100.1	55.6	70.9
Rsa1.0_01027.1.g22615.t1	dbj|BAJ34475.1| unnamed protein product [Thellungiella halophila]	1019	921	0	90.4	71.0	78.0	unnamed protein product	----	----	AT2G32400.1 | Symbols: GLR5, GLR3.7, ATGLR3.7 | glutamate receptor 5 | chr2:13752665-13756233 REVERSE LENGTH=921	1019	921	0	90.4	69.7	77.5
Rsa1.0_01027.1.g22616.t5	ref|NP_001184889.1| CCR4-NOT transcription complex subunit 1 [Arabidopsis thaliana] gi|332189257|gb|AEE27378.1| CCR4-NOT transcription complex subunit 1 [Arabidopsis thaliana]	641	2377	1.00E-127	370.8	37.1	39.6	CCR4-NOT transcription complex subunit 1	gbpln	Arabidopsis thaliana	AT1G02080.2 | Symbols: | transcription regulators | chr1:373694-386682 FORWARD LENGTH=2377	641	2377	1.00E-130	370.8	37.1	39.6
Rsa1.0_01027.1.g22617.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	392	387	2.00E-87	98.7	46.9	63.5	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	392	387	6.00E-90	98.7	46.9	63.5
Rsa1.0_01027.1.g22618.t1	ref|NP_189038.1| putative F-box protein [Arabidopsis thaliana] gi|75273446|sp|Q9LIR1.1|FB182_ARATH RecName: Full=Putative F-box protein At3g23960 gi|9294665|dbj|BAB03014.1| unnamed protein product [Arabidopsis thaliana] gi|332643318|gb|AEE76839.1| putative F-box protein [Arabidopsis thaliana]	535	402	7.00E-79	75.1	32.9	47.1	putative F-box protein	gbpln	Arabidopsis thaliana	AT3G23960.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8657736-8658944 FORWARD LENGTH=402	535	402	2.00E-81	75.1	32.9	47.1
Rsa1.0_01027.1.g22619.t1	ref|NP_189038.1| putative F-box protein [Arabidopsis thaliana] gi|75273446|sp|Q9LIR1.1|FB182_ARATH RecName: Full=Putative F-box protein At3g23960 gi|9294665|dbj|BAB03014.1| unnamed protein product [Arabidopsis thaliana] gi|332643318|gb|AEE76839.1| putative F-box protein [Arabidopsis thaliana]	392	402	2.00E-81	102.6	45.9	65.6	putative F-box protein	gbpln	Arabidopsis thaliana	AT3G23960.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8657736-8658944 FORWARD LENGTH=402	392	402	5.00E-84	102.6	45.9	65.6

Rsa1.0_01027.1.g22620.t2	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	453	387	3.00E-76	85.4	37.7	49.0	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	453	387	8.00E-79	85.4	37.7	49.0
Rsa1.0_01027.1.g22621.t6	ref|XP_002881226.1| hypothetical protein ARALYDRAFT_320982 [Arabidopsis lyrata subsp. lyrata] gi|297327065|gb|EFH57485.1| hypothetical protein ARALYDRAFT_320982 [Arabidopsis lyrata subsp. lyrata]	873	891	0	102.1	80.2	87.9	hypothetical protein ARALYDRAFT_320982	gbpln	Arabidopsis lyrata	AT2G32415.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H fold protein with HRDC domain | chr2:13761307-13765421 REVERSE LENGTH=891	873	891	0	102.1	79.8	88.7
Rsa1.0_01027.1.g22622.t1	gb|AAL58845.1|AF411970_1 putative transcription factor MYB101 [Arabidopsis thaliana]	462	490	0	106.1	78.8	86.4	putative transcription factor MYB101	gbpln	Arabidopsis thaliana	AT2G32460.1 | Symbols: MYB101, ATMYB101, ATM1 | myb domain protein 101 | chr2:13782419-13784363 REVERSE LENGTH=490	462	490	0	106.1	78.4	86.4
Rsa1.0_01027.1.g22623.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01028.1.g22624.t1	ref|XP_002893207.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339049|gb|EFH69466.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	334	334	1.00E-157	100.0	89.5	93.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G22030.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein BYPASS related (InterPro:IPR008511); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G77855.1); Has 99 Blast hits to 99 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 96; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7759337-7760415 REVERSE LENGTH=333	334	333	1.00E-154	99.7	87.7	91.0
Rsa1.0_01028.1.g22625.t1	ref|NP_173621.1| serine hydroxymethyltransferase 6 [Arabidopsis thaliana] gi|9280677|gb|AAF86546.1|AC069252_5 F2E2.7 [Arabidopsis thaliana] gi|21928157|gb|AAM78106.1| At1g22020/F2E2_3 [Arabidopsis thaliana] gi|28416495|gb|AAO42778.1| At1g22020/F2E2_3 [Arabidopsis thaliana] gi|332192065|gb|AEE30186.1| serine hydroxymethyltransferase 6 [Arabidopsis thaliana]	595	599	0	100.7	87.7	92.9	serine hydroxymethyltransferase 6	gbpln	Arabidopsis thaliana	AT1G22020.1 | Symbols: SHM6 | serine hydroxymethyltransferase 6 | chr1:7754599-7757087 FORWARD LENGTH=599	595	599	0	100.7	87.7	92.9
Rsa1.0_01028.1.g22626.t1	gb|EOA36900.1| hypothetical protein CARUB_v10011446mg [Capsella rubella]	334	396	1.00E-165	118.6	83.2	90.4	hypothetical protein CARUB_v10011446mg	gbpln	Capsella rubella	AT1G22015.1 | Symbols: DD46 | Galactosyltransferase family protein | chr1:7751225-7753425 REVERSE LENGTH=398	334	398	1.00E-163	119.2	82.9	90.7
Rsa1.0_01028.1.g22627.t1	gb|ADF81045.1| LEC1-2 transcription factor [Brassica napus]	326	230	4.00E-92	70.6	56.1	58.3	LEC1-2 transcription factor	gbpln	Brassica napus	AT1G21970.1 | Symbols: LEC1, EMB 212, EMB212, NF-YB9 | Histone superfamily protein | chr1:7727750-7729571 REVERSE LENGTH=238	326	238	7.00E-87	73.0	49.1	53.7
Rsa1.0_01028.1.g22628.t1	gb|EOA36681.1| hypothetical protein CARUB_v10012034mg, partial [Capsella rubella]	106	132	3.00E-12	124.5	48.1	62.3	hypothetical protein CARUB_v10012034mg, partial	gbpln	Capsella rubella	AT1G21940.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21950.1); Has 19 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7715170-7716975 REVERSE LENGTH=183	106	183	1.00E-13	172.6	42.5	57.5
Rsa1.0_01028.1.g22629.t1	gb|EOA36681.1| hypothetical protein CARUB_v10012034mg, partial [Capsella rubella]	114	132	1.00E-16	115.8	50.0	60.5	hypothetical protein CARUB_v10012034mg, partial	gbpln	Capsella rubella	AT1G21940.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21950.1); Has 19 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7715170-7716975 REVERSE LENGTH=183	114	183	7.00E-18	160.5	43.0	57.9

Rsa1.0_01028.1.g22630.t1	gb|EOA39330.1| hypothetical protein CARUB_v10012374mg [Capsella rubella]	109	127	9.00E-11	116.5	43.1	59.6	hypothetical protein CARUB_v10012374mg	gbpln	Capsella rubella	AT1G21940.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21950.1); Has 19 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7715170-7716975 REVERSE LENGTH=183	109	183	8.00E-12	167.9	39.4	51.4
Rsa1.0_01028.1.g22631.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01028.1.g22632.t1	ref|XP_002890472.1| hypothetical protein ARALYDRAFT_472429 [Arabidopsis lyrata subsp. lyrata] gi|297845196|ref|XP_002890479.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336314|gb|EFH66731.1| hypothetical protein ARALYDRAFT_472429 [Arabidopsis lyrata subsp. lyrata] gi|297336321|gb|EFH66738.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	106	97	3.00E-35	91.5	75.5	77.4	hypothetical protein ARALYDRAFT_472429	gbpln	Arabidopsis lyrata	AT3G42150.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21930.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:14310567-14311465 FORWARD LENGTH=100	106	100	9.00E-38	94.3	71.7	73.6
Rsa1.0_01028.1.g22633.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	1522	1489	0	97.8	57.7	72.1	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1522	1262	1.00E-170	82.9	19.2	24.7
Rsa1.0_01028.1.g22634.t1	gb|EOA40493.1| hypothetical protein CARUB_v10009218mg [Capsella rubella]	423	426	0	100.7	88.4	93.4	hypothetical protein CARUB_v10009218mg	gbpln	Capsella rubella	AT1G21920.1 | Symbols: | Histone H3 K4-specific methyltransferase SET7/9 family protein | chr1:7704454-7705866 REVERSE LENGTH=417	423	417	1.00E-180	98.6	85.3	92.4
Rsa1.0_01029.1.g22635.t1	ref|NP_565974.1| serine/threonine-protein phosphatase PP2A-4 catalytic subunit [Arabidopsis thaliana] gi|297827949|ref|XP_002881857.1| protein phosphatase 2A-4 [Arabidopsis lyrata subsp. lyrata] gi|1352663|sp|Q07100.2|PP2A4_ARATH RecName: Full=Serine/threonine-protein phosphatase PP2A-4 catalytic subunit; AltName: Full=Protein phosphatase 2A isoform 4 gi|466441|gb|AAA64742.1| Ser/Thr protein phosphatase [Arabidopsis thaliana] gi|4567320|gb|AAD23731.1| serine threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] gi|20198072|gb|AAM15383.1| serine/threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] gi|33589738|gb|AAQ22635.1| At2g42500/F14N22.23 [Arabidopsis thaliana] gi|297327696|gb|EFH58116.1| protein phosphatase 2A-4 [Arabidopsis lyrata subsp. lyrata] gi|330255033|gb|AEC10127.1| serine/threonine-protein phosphatase PP2A-4 catalytic subunit [Arabidopsis thaliana] gi|482563348|gb|EOA27538.1| hypothetical protein CARUB_v10023677mg [Capsella rubella]	282	313	1.00E-165	111.0	97.5	99.6	serine/threonine-protein phosphatase PP2A-4 catalytic subunit	gbpln	Arabidopsis lyrata	AT2G42500.1 | Symbols: PP2A-3 | protein phosphatase 2A-3 | chr2:17698099-17701226 REVERSE LENGTH=313	282	313	1.00E-168	111.0	97.5	99.6
Rsa1.0_01029.1.g22636.t5	emb|CAA74662.1| SFR3 [Brassica oleracea var. viridis]	926	841	0	90.8	81.7	85.4	SFR3	gbpln	Brassica oleracea	AT1G65800.1 | Symbols: ARK2, RK2 | receptor kinase 2 | chr1:24473166-24476523 FORWARD LENGTH=847	926	847	0	91.5	67.6	76.7
Rsa1.0_01029.1.g22637.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01029.1.g22638.t1	emb|CAA22150.1| hypothetical protein [Arabidopsis thaliana] gi|7269091|emb|CAB79200.1| hypothetical protein [Arabidopsis thaliana]	144	457	5.00E-17	317.4	37.5	47.9	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01029.1.g22639.t1	gb|EOA26622.1| hypothetical protein CARUB_v10022684mg [Capsella rubella]	757	771	0	101.8	94.6	97.4	hypothetical protein CARUB_v10022684mg	gbpln	Capsella rubella	AT2G42490.1 | Symbols: | Copper amine oxidase family protein | chr2:17691600-17695526 REVERSE LENGTH=776	757	776	0	102.5	93.9	96.7

Rsa1.0_01029.1.g22640.t1	ref|XP_002881850.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327689|gb|EFH58109.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	281	308	5.00E-71	109.6	46.6	61.2	predicted protein	gbpln	Arabidopsis lyrata	AT2G42460.1 | Symbols: | TRAF-like family protein | chr2:17676399-17679247 REVERSE LENGTH=442	281	442	4.00E-65	157.3	43.4	58.7
Rsa1.0_01029.1.g22641.t1	ref|XP_002881848.1| hypothetical protein ARALYDRAFT_346045 [Arabidopsis lyrata subsp. lyrata] gi|297327687|gb|EFH58107.1| hypothetical protein ARALYDRAFT_346045 [Arabidopsis lyrata subsp. lyrata]	308	293	4.00E-89	95.1	60.4	72.4	hypothetical protein ARALYDRAFT_346045	gbpln	Arabidopsis lyrata	AT2G42460.1 | Symbols: | TRAF-like family protein | chr2:17676399-17679247 REVERSE LENGTH=442	308	442	9.00E-72	143.5	45.8	63.3
Rsa1.0_01029.1.g22642.t3	gb|AAG13591.2|AC051633_7 putative gag/pol polyprotein [Oryza sativa Japonica Group]	1231	1417	0	115.1	40.2	52.1	putative gag/pol polyprotein	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1231	1262	2.00E-80	102.5	13.3	19.4
Rsa1.0_01029.1.g22643.t1	ref|NP_565973.1| LOB domain-containing protein 16 [Arabidopsis thaliana] gi|29428045|sp|Q9SLB7.1|LBD16_ARATH RecName: Full=LOB domain-containing protein 16; AltName: Full=ASYMMETRIC LEAVES 2-like protein 18; Short=AS2-like protein 18 gi|13569546|gb|AAK31143.1|AF345339_1 unknown [Arabidopsis thaliana] gi|15294286|gb|AAK95320.1|AF410334_1 At2g42430/MHK10.15 [Arabidopsis thaliana] gi|17227162|gb|AAL38035.1|AF447890_1 LOB DOMAIN 16 [Arabidopsis thaliana] gi|4567314|gb|AAD23725.1| expressed protein [Arabidopsis thaliana] gi|23507799|gb|AAN38703.1| At2g42430/MHK10.15 [Arabidopsis thaliana] gi|110740350|dbj|BAF02070.1| hypothetical protein [Arabidopsis thaliana] gi|219807112|dbj|BAH10562.1| ASYMMETRIC LEAVES2-like 18 protein [Arabidopsis thaliana] gi|330255025|gb|AEC10119.1| LOB domain-containing protein 16 [Arabidopsis thaliana]	129	245	1.00E-51	189.9	84.5	87.6	LOB domain-containing protein 16	gbpln	Arabidopsis thaliana	AT2G42430.1 | Symbols: LBD16, ASL18 | lateral organ boundaries-domain 16 | chr2:17663668-17665153 FORWARD LENGTH=245	129	245	3.00E-54	189.9	84.5	87.6
Rsa1.0_01029.1.g22644.t1	gb|EOA18088.1| hypothetical protein CARUB_v10006540mg [Capsella rubella]	105	551	2.00E-20	524.8	50.5	54.3	hypothetical protein CARUB_v10006540mg	gbpln	Capsella rubella	AT4G14350.2 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr4:8256449-8259934 REVERSE LENGTH=551	105	551	3.00E-23	524.8	50.5	55.2
Rsa1.0_01029.1.g22645.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01029.1.g22646.t1	gb|EOA27725.1| hypothetical protein CARUB_v10023878mg [Capsella rubella]	268	260	5.00E-87	97.0	71.6	76.9	hypothetical protein CARUB_v10023878mg	gbpln	Capsella rubella	AT2G42040.1 | Symbols: | CONTAINS InterPro DOMAIN/s: WRC (InterPro:IPR014977); Has 219 Blast hits to 219 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 215; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:17543282-17545063 FORWARD LENGTH=269	268	269	1.00E-83	100.4	72.4	78.4
Rsa1.0_01029.1.g22647.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	226	255	2.00E-55	112.8	56.6	69.5	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	226	302	3.00E-20	133.6	29.2	39.8
Rsa1.0_01029.1.g22648.t1	ref|XP_002881818.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297327657|gb|EFH58077.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	183	413	2.00E-18	225.7	30.1	33.9	zinc finger family protein	gbpln	Arabidopsis lyrata	AT2G42030.1 | Symbols: | RING/U-box superfamily protein | chr2:17539069-17540346 REVERSE LENGTH=425	183	425	1.00E-19	232.2	27.9	31.7
Rsa1.0_01029.1.g22649.t1	gb|EOA27569.1| hypothetical protein CARUB_v10023706mg [Capsella rubella]	306	305	1.00E-164	99.7	90.8	93.8	hypothetical protein CARUB_v10023706mg	gbpln	Capsella rubella	AT3G58040.1 | Symbols: SINAT2 | seven in absentia of Arabidopsis 2 | chr3:21489612-21491085 FORWARD LENGTH=308	306	308	1.00E-164	100.7	87.9	91.8

Rsa1.0_01029.1.g22650.t1	ref|NP_181728.1| putative protein kinase [Arabidopsis thaliana] gi|75319137|sp|P93749.1|Y2197_ARATH RecName: Full=Probable protein kinase At2g41970 gi|1871186|gb|AAB63546.1| putative protein kinase [Arabidopsis thaliana] gi|38603828|gb|AAR24659.1| At2g41970 [Arabidopsis thaliana] gi|51968610|dbj|BAD42997.1| putative protein kinase [Arabidopsis thaliana] gi|51968682|dbj|BAD43033.1| putative protein kinase [Arabidopsis thaliana] gi|51971150|dbj|BAD44267.1| putative protein kinase [Arabidopsis thaliana] gi|51971369|dbj|BAD44349.1| putative protein kinase [Arabidopsis thaliana] gi|51971789|dbj|BAD44559.1| putative protein kinase [Arabidopsis thaliana] gi|62318717|dbj|BAD93732.1| putative protein kinase [Arabidopsis thaliana] gi|330254963|gb|AEC10057.1| putative protein kinase [Arabidopsis thaliana]	364	365	0	100.3	94.8	98.1	putative protein kinase	gbpln	Arabidopsis thaliana	AT2G41970.1 | Symbols: | Protein kinase superfamily protein | chr2:17520517-17522304 REVERSE LENGTH=365	364	365	0	100.3	94.8	98.1
Rsa1.0_01029.1.g22651.t11	ref|XP_002881811.1| hypothetical protein ARALYDRAFT_321881 [Arabidopsis lyrata subsp. lyrata] gi|297327650|gb|EFH58070.1| hypothetical protein ARALYDRAFT_321881 [Arabidopsis lyrata subsp. lyrata]	1068	1218	0	114.0	39.4	47.3	hypothetical protein ARALYDRAFT_321881	gbpln	Arabidopsis lyrata	AT2G41960.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G58050.1); Has 11991 Blast hits to 7260 proteins in 458 species: Archae - 17; Bacteria - 481; Metazoa - 5028; Fungi - 1325; Plants - 615; Viruses - 38; Other Eukaryotes - 4487 (source: NCBI BLink). | chr2:17514244-17519015 REVERSE LENGTH=1215	1068	1215	0	113.8	38.9	46.8
Rsa1.0_01029.1.g22652.t1	ref|XP_002881810.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327649|gb|EFH58069.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	158	158	8.00E-76	100.0	94.3	96.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G41945.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G04040.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17511071-17512898 REVERSE LENGTH=158	158	158	2.00E-77	100.0	93.7	96.2
Rsa1.0_01029.1.g22653.t1	ref|NP_181725.1| zinc finger protein 8 [Arabidopsis thaliana] gi|1871188|gb|AAB63548.1| putative C2H2-type zinc finger protein [Arabidopsis thaliana] gi|14517524|gb|AAK62652.1| At2g41940/T6D20.16 [Arabidopsis thaliana] gi|15810111|gb|AAL06981.1| At2g41940/T6D20.16 [Arabidopsis thaliana] gi|330254957|gb|AEC10051.1| zinc finger protein 8 [Arabidopsis thaliana]	259	257	5.00E-87	99.2	70.7	80.7	zinc finger protein 8	gbpln	Arabidopsis thaliana	AT2G41940.1 | Symbols: ZFP8 | zinc finger protein 8 | chr2:17507556-17508329 FORWARD LENGTH=257	259	257	1.00E-89	99.2	70.7	80.7
Rsa1.0_01029.1.g22654.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	520	530	3.00E-13	101.9	7.7	11.3	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01029.1.g22655.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	508	1214	8.00E-55	239.0	31.9	49.4	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	508	332	4.00E-35	65.4	16.3	26.2
Rsa1.0_01029.1.g22656.t1	gb|AAO22523.1| HY5 [Brassica rapa subsp. pekinensis]	65	109	1.00E-11	167.7	56.9	58.5	HY5	gbpln	Brassica rapa	AT5G11260.1 | Symbols: HY5, TED 5 | Basic-leucine zipper (bZIP) transcription factor family protein | chr5:3593583-3594800 REVERSE LENGTH=168	65	168	1.00E-13	258.5	55.4	58.5
Rsa1.0_01029.1.g22657.t1	gb|EOA27539.1| hypothetical protein CARUB_v10023678mg [Capsella rubella]	312	312	1.00E-167	100.0	90.1	95.8	hypothetical protein CARUB_v10023678mg	gbpln	Capsella rubella	AT2G41630.1 | Symbols: TFIIB | transcription factor IIB | chr2:17355555-17357400 REVERSE LENGTH=312	312	312	1.00E-167	100.0	89.1	95.5
Rsa1.0_01029.1.g22658.t1	gb|AGC91761.1| glycerol-3-phosphate dehydrogenase 1.1 [Brassica napus] gi|469517559|gb|AGH55534.1| glycerol-3-phosphate dehydrogenase 1 [Brassica napus]	463	462	0	99.8	97.6	98.5	glycerol-3-phosphate dehydrogenase 1.1	gbpln	Brassica napus	AT2G41540.3 | Symbols: GPDHC1 | 6-phosphogluconate dehydrogenase family protein | chr2:17326801-17328654 FORWARD LENGTH=462	463	462	0	99.8	95.9	97.6
Rsa1.0_01029.1.g22659.t1	ref|XP_002881781.1| hypothetical protein ARALYDRAFT_903473 [Arabidopsis lyrata subsp. lyrata] gi|297327620|gb|EFH58040.1| hypothetical protein ARALYDRAFT_903473 [Arabidopsis lyrata subsp. lyrata]	284	284	1.00E-156	100.0	91.9	96.1	hypothetical protein ARALYDRAFT_903473	gbpln	Arabidopsis lyrata	AT2G41530.1 | Symbols: ATSFGH, SFGH | S-formylglutathione hydrolase | chr2:17323656-17325430 REVERSE LENGTH=284	284	284	1.00E-158	100.0	90.8	96.5

Rsa1.0_01029.1.g22660.t1	ref|XP_002879935.1| ATCKX1/CKX1 [Arabidopsis lyrata subsp. lyrata] gi|297325774|gb|EFH56194.1| ATCKX1/CKX1 [Arabidopsis lyrata subsp. lyrata]	545	564	0	103.5	86.6	94.3	ATCKX1/CKX1	gbpln	Arabidopsis lyrata	AT2G41510.1 | Symbols: ATCKX1, CKX1 | cytokinin oxidase/dehydrogenase 1 | chr2:17314626-17316861 FORWARD LENGTH=575	545	575	0	105.5	86.2	94.1
Rsa1.0_01030.1.g22661.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01030.1.g22662.t1	gb|ABW74585.1| pol polyprotein [Boechera divaricarpa]	245	551	1.00E-22	224.9	23.3	29.4	pol polyprotein	gbpln	Boechera divaricarpa	#	#	#	#	#	#	#
Rsa1.0_01030.1.g22663.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	374	1197	7.00E-64	320.1	39.6	55.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	374	575	7.00E-42	153.7	31.3	49.2
Rsa1.0_01030.1.g22664.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	226	1274	6.00E-56	563.7	50.4	67.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01030.1.g22665.t1	gb|EOA25182.1| hypothetical protein CARUB_v10018494mg [Capsella rubella]	168	282	7.00E-15	167.9	33.3	44.6	hypothetical protein CARUB_v10018494mg	gbpln	Capsella rubella	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	168	303	4.00E-16	180.4	28.6	45.8
Rsa1.0_01030.1.g22666.t1	gb|EOA35333.1| hypothetical protein CARUB_v10020515mg [Capsella rubella]	352	364	1.00E-156	103.4	85.8	90.1	hypothetical protein CARUB_v10020515mg	gbpln	Capsella rubella	AT1G68810.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:25861289-25862882 FORWARD LENGTH=368	352	368	1.00E-157	104.5	86.9	91.5
Rsa1.0_01030.1.g22667.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01030.1.g22668.t1	ref|XP_002887207.1| hypothetical protein ARALYDRAFT_476009 [Arabidopsis lyrata subsp. lyrata] gi|297333048|gb|EFH63466.1| hypothetical protein ARALYDRAFT_476009 [Arabidopsis lyrata subsp. lyrata]	506	461	1.00E-155	91.1	62.3	70.2	hypothetical protein ARALYDRAFT_476009	gbpln	Arabidopsis lyrata	AT1G68820.1 | Symbols: | Transmembrane Fragile-X-F-associated protein | chr1:25865852-25868800 FORWARD LENGTH=468	506	468	1.00E-158	92.5	62.3	70.0
Rsa1.0_01030.1.g22669.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01030.1.g22670.t9	ref|XP_002887207.1| hypothetical protein ARALYDRAFT_476009 [Arabidopsis lyrata subsp. lyrata] gi|297333048|gb|EFH63466.1| hypothetical protein ARALYDRAFT_476009 [Arabidopsis lyrata subsp. lyrata]	574	461	1.00E-143	80.3	50.3	57.5	hypothetical protein ARALYDRAFT_476009	gbpln	Arabidopsis lyrata	AT1G68820.1 | Symbols: | Transmembrane Fragile-X-F-associated protein | chr1:25865852-25868800 FORWARD LENGTH=468	574	468	2.33E-156	81.5	51.2	58.2
Rsa1.0_01031.1.g22671.t1	ref|XP_002864842.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310677|gb|EFH41101.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	665	650	0	97.7	88.7	94.0	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G63200.1 | Symbols: | tetratricopeptide repeat (TPR)-containing protein | chr5:25349043-25352899 FORWARD LENGTH=649	665	649	0	97.6	89.0	92.8
Rsa1.0_01031.1.g22672.t1	gb|EOA14404.1| hypothetical protein CARUB_v10027604mg [Capsella rubella]	319	324	1.00E-173	101.6	92.8	97.5	hypothetical protein CARUB_v10027604mg	gbpln	Capsella rubella	AT5G63220.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0363 (InterPro:IPR007317); Has 304 Blast hits to 301 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 110; Fungi - 121; Plants - 35; Viruses - 0; Other Eukaryotes - 38 (source: NCBI BLink). | chr5:25353256-25355410 REVERSE LENGTH=324	319	324	1.00E-175	101.6	91.8	97.2
Rsa1.0_01031.1.g22673.t24	ref|XP_002893783.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339625|gb|EFH70042.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	261	276	3.00E-12	105.7	24.5	37.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321	261	321	7.00E-12	123.0	22.2	34.9
Rsa1.0_01031.1.g22674.t1	ref|XP_002866546.1| hypothetical protein ARALYDRAFT_496512 [Arabidopsis lyrata subsp. lyrata] gi|297312381|gb|EFH42805.1| hypothetical protein ARALYDRAFT_496512 [Arabidopsis lyrata subsp. lyrata]	478	484	0	101.3	88.7	94.6	hypothetical protein ARALYDRAFT_496512	gbpln	Arabidopsis lyrata	AT5G63290.1 | Symbols: | Radical SAM superfamily protein | chr5:25369349-25370894 REVERSE LENGTH=484	478	484	0	101.3	88.5	94.6
Rsa1.0_01031.1.g22675.t1	gb|EOA13406.1| hypothetical protein CARUB_v10026444mg, partial [Capsella rubella]	399	430	1.00E-100	107.8	57.6	67.7	hypothetical protein CARUB_v10026444mg, partial	gbpln	Capsella rubella	AT5G62660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:25156326-25157465 REVERSE LENGTH=379	399	379	1.00E-101	95.0	51.1	60.7
Rsa1.0_01031.1.g22676.t1	ref|XP_002866553.1| hypothetical protein ARALYDRAFT_496525 [Arabidopsis lyrata subsp. lyrata] gi|297312388|gb|EFH42812.1| hypothetical protein ARALYDRAFT_496525 [Arabidopsis lyrata subsp. lyrata]	240	246	1.00E-130	102.5	93.3	97.9	hypothetical protein ARALYDRAFT_496525	gbpln	Arabidopsis lyrata	AT5G63400.1 | Symbols: ADK1 | adenylate kinase 1 | chr5:25393274-25394817 REVERSE LENGTH=246	240	246	1.00E-131	102.5	91.7	97.5

Rsa1.0_01031.1.g22677.t1	gb|EOA13020.1| hypothetical protein CARUB_v10026016mg [Capsella rubella]	676	678	0	100.3	87.0	93.5	hypothetical protein CARUB_v10026016mg	gbpln	Capsella rubella	AT5G63410.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:25395173-25397768 REVERSE LENGTH=680	676	680	0	100.6	88.3	94.1
Rsa1.0_01031.1.g22678.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01031.1.g22679.t1	gb|AAM60854.1| cytochrome P450-like protein [Arabidopsis thaliana]	504	508	0	100.8	87.1	91.7	cytochrome P450-like protein	gbpln	Arabidopsis thaliana	AT5G63450.1 | Symbols: CYP94B1 | cytochrome P450, family 94, subfamily B, polypeptide 1 | chr5:25408987-25410519 REVERSE LENGTH=510	504	510	0	101.2	87.1	91.7
Rsa1.0_01031.1.g22680.t1	dbj|BAB08811.1| unnamed protein product [Arabidopsis thaliana]	161	188	3.00E-62	116.8	75.8	80.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G63460.1 | Symbols: | SAP domain-containing protein | chr5:25413605-25415399 REVERSE LENGTH=162	161	162	5.00E-64	100.6	75.2	79.5
Rsa1.0_01031.1.g22681.t1	gb|EOA14773.1| hypothetical protein CARUB_v10028072mg [Capsella rubella]	543	544	0	100.2	89.5	94.8	hypothetical protein CARUB_v10028072mg	gbpln	Capsella rubella	AT5G63490.1 | Symbols: | CBS / octicosapeptide/Phox/Bemp1 (PB1) domains-containing protein | chr5:25418716-25421970 REVERSE LENGTH=543	543	543	0	100.0	87.3	92.8
Rsa1.0_01031.1.g22682.t1	ref|XP_002864850.1| hypothetical protein ARALYDRAFT_496538 [Arabidopsis lyrata subsp. lyrata] gi|297310685|gb|EFH41109.1| hypothetical protein ARALYDRAFT_496538 [Arabidopsis lyrata subsp. lyrata]	245	252	1.00E-113	102.9	84.9	88.2	hypothetical protein ARALYDRAFT_496538	gbpln	Arabidopsis lyrata	AT5G63510.1 | Symbols: GAMMA CAL1 | gamma carbonic anhydrase like 1 | chr5:25424054-25425612 FORWARD LENGTH=252	245	252	1.00E-113	102.9	83.7	86.9
Rsa1.0_01031.1.g22683.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	1184	1239	0	104.6	43.0	52.4	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1184	1262	1.00E-110	106.6	17.5	26.7
Rsa1.0_01032.1.g22684.t2	gb|ADP20181.1| mutant gag-pol polyprotein [Pisum sativum]	400	572	2.00E-43	143.0	33.5	50.5	mutant gag-pol polyprotein	gbpln	Pisum sativum	#	#	#	#	#	#	#
Rsa1.0_01032.1.g22685.t2	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1290	1529	0	118.5	45.0	63.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1290	746	8.00E-81	57.8	11.8	16.0
Rsa1.0_01032.1.g22686.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1372	1223	0	89.1	41.3	54.5	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1372	746	6.00E-70	54.4	9.9	12.6
Rsa1.0_01032.1.g22687.t1	sp|P0C895.1|Y2010_ARATH RecName: Full=LRR repeats and ubiquitin-like domain-containing protein At2g30105	309	374	1.00E-144	121.0	84.1	90.3	RecName: Full=LRR repeats and ubiquitin-like domain-containing protein At2g30105	----	----	AT2G30105.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Leucine-rich repeat, typical subtype (InterPro:IPR003591), Leucine-rich repeat (InterPro:IPR001611), Ubiquitin (InterPro:IPR000626), Ubiquitin supergroup (InterPro:IPR019955); BEST Arabidopsis thaliana protein match is: Leucine-rich repeat (LRR) family protein (TAIR:AT5G07910.1). | chr2:12849855-12851908 FORWARD LENGTH=367	309	367	1.00E-147	118.8	84.1	90.3
Rsa1.0_01032.1.g22688.t1	ref|XP_002874998.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297320835|gb|EFH51257.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	179	79	4.00E-11	44.1	20.1	23.5	myb family transcription factor	gbpln	Arabidopsis lyrata	AT4G01060.2 | Symbols: ETC3, CPL3 | CAPRICE-like MYB3 | chr4:460534-460967 FORWARD LENGTH=74	179	74	1.00E-12	41.3	19.6	22.9
Rsa1.0_01032.1.g22689.t2	gb|AAC72868.1| contains similarity to human DHHC-domain-containing cysteine-rich protein (GB:U90653) and several S. cerevisiae probable membrane proteins (GB:U20865, Z48758, U43491) [Arabidopsis thaliana]	170	513	1.00E-22	301.8	40.0	41.8	contains similarity to human DHHC-domain-containing cysteine-rich protein (GB:U90653) and several S. cerevisiae probable membrane proteins (GB:U20865, Z48758, U43491)	gbpln	Arabidopsis thaliana	AT4G01730.1 | Symbols: | DHHC-type zinc finger family protein | chr4:749574-752034 FORWARD LENGTH=508	170	508	3.00E-24	298.8	39.4	41.2
Rsa1.0_01032.1.g22690.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01032.1.g22691.t1	gb|ABD65100.1| hypothetical protein 31.t00077 [Brassica oleracea]	422	391	2.00E-61	92.7	32.9	39.3	hypothetical protein 31.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01032.1.g22692.t1	ref|XP_002891409.1| hypothetical protein ARALYDRAFT_336931 [Arabidopsis lyrata subsp. lyrata] gi|297337251|gb|EFH67668.1| hypothetical protein ARALYDRAFT_336931 [Arabidopsis lyrata subsp. lyrata]	389	379	2.00E-36	97.4	25.2	30.1	hypothetical protein ARALYDRAFT_336931	gbpln	Arabidopsis lyrata	AT1G50870.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:18855147-18856337 FORWARD LENGTH=396	389	396	6.00E-38	101.8	23.1	30.3
Rsa1.0_01032.1.g22693.t1	ref|XP_002863555.1| minichromosome maintenance family protein [Arabidopsis lyrata subsp. lyrata] gi|297309390|gb|EFH39814.1| minichromosome maintenance family protein [Arabidopsis lyrata subsp. lyrata]	101	830	3.00E-18	821.8	57.4	65.3	minichromosome maintenance family protein	gbpln	Arabidopsis lyrata	AT5G44635.1 | Symbols: MCM6 | minichromosome maintenance (MCM2/3/5) family protein | chr5:18006431-18010542 REVERSE LENGTH=831	101	831	2.00E-20	822.8	56.4	64.4

Rsa1.0_01032.1.g22694.t10	ref|XP_002876336.1| sedoheptulose-bisphosphatase [Arabidopsis lyrata subsp. lyrata] gi|297322174|gb|EFH52595.1| sedoheptulose-bisphosphatase [Arabidopsis lyrata subsp. lyrata]	381	393	1.00E-38	103.1	25.5	26.5	sedoheptulose-bisphosphatase	gbpln	Arabidopsis lyrata	AT3G55800.1 | Symbols: SBPASE | sedoheptulose-bisphosphatase | chr3:20709640-20711421 FORWARD LENGTH=393	381	393	2.00E-40	103.1	24.9	26.5
Rsa1.0_01032.1.g22695.t1	gb|AAC28207.1| T24H24.13 gene product [Arabidopsis thaliana] gi|7267161|emb|CAB77873.1| putative transposon protein [Arabidopsis thaliana]	786	681	6.00E-17	86.6	6.5	9.8	T24H24.13 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01033.1.g22696.t1	ref|XP_002863453.1| hypothetical protein ARALYDRAFT_494402 [Arabidopsis lyrata subsp. lyrata] gi|297309288|gb|EFH39712.1| hypothetical protein ARALYDRAFT_494402 [Arabidopsis lyrata subsp. lyrata]	663	657	0	99.1	84.2	90.0	hypothetical protein ARALYDRAFT_494402	gbpln	Arabidopsis lyrata	AT5G45800.1 | Symbols: MEE62 | Leucine-rich repeat protein kinase family protein | chr5:18575765-18578972 REVERSE LENGTH=666	663	666	0	100.5	83.9	89.6
Rsa1.0_01033.1.g22697.t1	gb|EOA14707.1| hypothetical protein CARUB_v10027985mg [Capsella rubella]	422	424	0	100.5	83.6	92.9	hypothetical protein CARUB_v10027985mg	gbpln	Capsella rubella	AT5G45790.2 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr5:18572345-18573664 FORWARD LENGTH=439	422	439	0	104.0	82.7	91.0
Rsa1.0_01033.1.g22698.t1	gb|AFO67893.1| leucine-rich repeat receptor-like kinase (mitochondrion) [Brassica rapa subsp. oleifera]	616	615	0	99.8	97.1	98.9	leucine-rich repeat receptor-like kinase (mitochondrion)	gbpln	Brassica rapa	AT5G45780.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:18566946-18569625 REVERSE LENGTH=614	616	614	0	99.7	90.9	95.1
Rsa1.0_01033.1.g22699.t1	ref|NP_973487.2| Toll-Interleukin-Resistance domain-containing protein [Arabidopsis thaliana] gi|330251877|gb|AEC06971.1| Toll-Interleukin-Resistance domain-containing protein [Arabidopsis thaliana]	313	313	1.00E-156	100.0	84.0	92.0	Toll-Interleukin-Resistance domain-containing protein	gbpln	Arabidopsis thaliana	AT2G20142.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr2:8695387-8696566 FORWARD LENGTH=313	313	313	1.00E-159	100.0	84.0	92.0
Rsa1.0_01033.1.g22700.t4	ref|NP_850376.2| 60S ribosomal protein L11-1 [Arabidopsis thaliana] gi|297791141|ref|XP_002863455.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|297804282|ref|XP_002870025.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|21542441|sp|P42795.2|RL111_ARATH RecName: Full=60S ribosomal protein L11-1; AltName: Full=L16A gi|110737006|dbj|BAF00458.1| 60S ribosomal protein L11B [Arabidopsis thaliana] gi|297309290|gb|EFH39714.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|297315861|gb|EFH46284.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|330255069|gb|AEC10163.1| 60S ribosomal protein L11-1 [Arabidopsis thaliana] gi|482549880|gb|EOA14074.1| hypothetical protein CARUB_v10027211mg [Capsella rubella] gi|482560618|gb|EOA24809.1| hypothetical protein CARUB_v10018095mg [Capsella rubella]	261	182	1.00E-102	69.7	69.0	69.7	60S ribosomal protein L11-1	gbpln	Arabidopsis lyrata	AT2G42740.1 | Symbols: RPL16A | ribosomal protein large subunit 16A | chr2:17791794-17792946 FORWARD LENGTH=182	261	182	1.00E-104	69.7	69.0	69.7
Rsa1.0_01033.1.g22701.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	150	1333	2.00E-14	888.7	30.0	42.0	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	150	575	4.00E-13	383.3	26.0	36.0
Rsa1.0_01033.1.g22702.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1647	1501	0	91.1	51.7	65.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1647	1262	1.00E-142	76.6	14.5	20.2
Rsa1.0_01033.1.g22703.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01033.1.g22704.t1	ref|NP_199387.1| Ras-related protein RABA1c [Arabidopsis thaliana] gi|297794685|ref|XP_002865227.1| hypothetical protein ARALYDRAFT_494409 [Arabidopsis lyrata subsp. lyrata] gi|75171186|sp|Q9FK68.1|RAA1C_ARATH RecName: Full=Ras-related protein RABA1c; Short=AtRABA1c gi|13877913|gb|AAK44034.1|AF370219_1 putative Rab-type small GTP-binding protein [Arabidopsis thaliana] gi|9758678|dbj|BAB09217.1| Rab-type small GTP-binding protein-like [Arabidopsis thaliana] gi|16323446|gb|AAL15217.1| putative Rab-type small GTP-binding protein [Arabidopsis thaliana] gi|297311062|gb|EFH41486.1| hypothetical protein ARALYDRAFT_494409 [Arabidopsis lyrata subsp. lyrata] gi|332007909|gb|AED95292.1| Ras-related protein RABA1c [Arabidopsis thaliana]	216	216	1.00E-118	100.0	96.3	98.1	Ras-related protein RABA1c	gbpln	Arabidopsis lyrata	AT5G45750.1 | Symbols: AtRABA1c, RABA1c | RAB GTPase homolog A1C | chr5:18559318-18560639 FORWARD LENGTH=216	216	216	1.00E-121	100.0	96.3	98.1
Rsa1.0_01034.1.g22705.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01034.1.g22706.t1	ref|XP_002878272.1| hypothetical protein ARALYDRAFT_324413 [Arabidopsis lyrata subsp. lyrata] gi|297324110|gb|EFH54531.1| hypothetical protein ARALYDRAFT_324413 [Arabidopsis lyrata subsp. lyrata]	128	457	8.00E-11	357.0	38.3	46.9	hypothetical protein ARALYDRAFT_324413	gbpln	Arabidopsis lyrata	AT3G59430.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 10 growth stages; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:21964484-21965606 REVERSE LENGTH=345	128	345	3.00E-13	269.5	38.3	45.3
Rsa1.0_01034.1.g22707.t1	gb|EOA25120.1| hypothetical protein CARUB_v10018428mg, partial [Capsella rubella]	340	320	1.00E-35	94.1	29.4	44.1	hypothetical protein CARUB_v10018428mg, partial	gbpln	Capsella rubella	AT3G44780.1 | Symbols: | Cysteine proteinases superfamily protein | chr3:16321624-16322604 REVERSE LENGTH=207	340	207	1.00E-15	60.9	13.8	19.4
Rsa1.0_01034.1.g22708.t1	ref|XP_002879859.1| hypothetical protein ARALYDRAFT_903307 [Arabidopsis lyrata subsp. lyrata] gi|297325698|gb|EFH56118.1| hypothetical protein ARALYDRAFT_903307 [Arabidopsis lyrata subsp. lyrata]	217	304	1.00E-57	140.1	53.9	67.3	hypothetical protein ARALYDRAFT_903307	gbpln	Arabidopsis lyrata	AT4G20095.2 | Symbols: | Protein of unknown function (DUF626) | chr4:10871734-10873072 REVERSE LENGTH=249	217	249	6.00E-43	114.7	44.7	61.3
Rsa1.0_01034.1.g22709.t1	gb|ACR56738.1| trans-2,3-enoyl-CoA reductase [Brassica napus] gi|238915413|gb|ACR56737.1| trans-2,3-enoyl-CoA reductase [Brassica napus]	310	310	0	100.0	99.7	100.0	trans-2,3-enoyl-CoA reductase	gbpln	Brassica napus	AT3G55360.1 | Symbols: CER10, ECR, ATTSC13, TSC13 | 3-oxo-5-alpha-steroid 4-dehydrogenase family protein | chr3:20521186-20522856 REVERSE LENGTH=310	310	310	0	100.0	97.4	99.0
Rsa1.0_01034.1.g22710.t1	ref|NP_191095.1| PIF / Ping-Pong family of plant transposase [Arabidopsis thaliana] gi|7076778|emb|CAB75893.1| putative protein [Arabidopsis thaliana] gi|21593300|gb|AAM65249.1| unknown [Arabidopsis thaliana] gi|26449824|dbj|BAC42035.1| unknown protein [Arabidopsis thaliana] gi|32362295|gb|AAP80175.1| At3g55350 [Arabidopsis thaliana] gi|332645850|gb|AEE79371.1| PIF / Ping-Pong family of plant transposase [Arabidopsis thaliana]	406	406	0	100.0	79.3	83.5	PIF / Ping-Pong family of plant transposase	gbpln	Arabidopsis thaliana	AT3G55350.1 | Symbols: | PIF / Ping-Pong family of plant transposases | chr3:20518518-20520690 FORWARD LENGTH=406	406	406	0	100.0	79.3	83.5
Rsa1.0_01034.1.g22711.t1	gb|EOA18469.1| hypothetical protein CARUB_v10007015mg [Capsella rubella]	888	451	1.00E-136	50.8	30.2	36.0	hypothetical protein CARUB_v10007015mg	gbpln	Capsella rubella	AT1G70770.2 | Symbols: | Protein of unknown function DUF2359, transmembrane | chr1:26688622-26691185 REVERSE LENGTH=610	888	610	1.00E-120	68.7	27.3	32.2
Rsa1.0_01034.1.g22712.t1	gb|EOA23583.1| hypothetical protein CARUB_v10016779mg [Capsella rubella]	644	677	0	105.1	70.8	80.7	hypothetical protein CARUB_v10016779mg	gbpln	Capsella rubella	AT3G55340.1 | Symbols: PHIP1 | phragmoplastin interacting protein 1 | chr3:20515672-20517832 FORWARD LENGTH=597	644	597	1.00E-180	92.7	58.9	68.5

Rsa1.0_01034.1.g22713.t1	ref|XP_002876294.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322132|gb|EFH52553.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	288	280	1.00E-123	97.2	78.1	87.8	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G55290.2 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:20502653-20503730 FORWARD LENGTH=279	288	279	1.00E-125	96.9	76.7	87.5
Rsa1.0_01034.1.g22714.t1	gb|ABB97038.1| unknown [Brassica rapa]	154	154	8.00E-79	100.0	99.4	100.0	unknown	gbpln	Brassica rapa	AT3G55280.2 | Symbols: RPL23AB | ribosomal protein L23AB | chr3:20500667-20501519 FORWARD LENGTH=154	154	154	5.00E-61	100.0	94.8	96.8
Rsa1.0_01034.1.g22715.t1	ref|XP_002876290.1| hypothetical protein ARALYDRAFT_348614 [Arabidopsis lyrata subsp. lyrata] gi|297322128|gb|EFH52549.1| hypothetical protein ARALYDRAFT_348614 [Arabidopsis lyrata subsp. lyrata]	106	277	4.00E-28	261.3	64.2	67.9	hypothetical protein ARALYDRAFT_348614	gbpln	Arabidopsis lyrata	AT3G55250.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, chloroplast, nucleus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 46 Blast hits to 46 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:20479302-20480324 FORWARD LENGTH=277	106	277	3.00E-29	261.3	61.3	67.0
Rsa1.0_01034.1.g22716.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01035.1.g22717.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	740	1142	0	154.3	46.2	56.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	740	626	5.00E-38	84.6	15.8	26.1
Rsa1.0_01035.1.g22718.t1	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	547	498	4.00E-66	91.0	24.3	32.9	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	547	336	4.00E-26	61.4	12.4	19.0
Rsa1.0_01035.1.g22719.t1	ref|XP_002874244.1| hypothetical protein ARALYDRAFT_489371 [Arabidopsis lyrata subsp. lyrata] gi|297320081|gb|EFH50503.1| hypothetical protein ARALYDRAFT_489371 [Arabidopsis lyrata subsp. lyrata]	192	183	1.00E-81	95.3	82.8	87.0	hypothetical protein ARALYDRAFT_489371	gbpln	Arabidopsis lyrata	AT5G25190.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:8707007-8707655 REVERSE LENGTH=181	192	181	4.00E-81	94.3	79.2	85.4
Rsa1.0_01035.1.g22720.t1	ref|XP_002867420.1| phosphofructokinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313256|gb|EFH43679.1| phosphofructokinase family protein [Arabidopsis lyrata subsp. lyrata]	229	472	2.00E-79	206.1	65.1	69.0	phosphofructokinase family protein	gbpln	Arabidopsis lyrata	AT4G29220.1 | Symbols: PFK1 | phosphofructokinase 1 | chr4:14403621-14406071 REVERSE LENGTH=473	229	473	5.00E-81	206.6	64.2	68.6
Rsa1.0_01035.1.g22721.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01035.1.g22722.t1	gb|EOA21634.1| hypothetical protein CARUB_v10002045mg [Capsella rubella]	175	188	2.00E-35	107.4	60.6	71.4	hypothetical protein CARUB_v10002045mg	gbpln	Capsella rubella	AT5G25210.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32030.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:8724056-8725465 FORWARD LENGTH=175	175	175	1.00E-29	100.0	52.6	67.4
Rsa1.0_01035.1.g22723.t1	gb|EOA20703.1| hypothetical protein CARUB_v10001020mg [Capsella rubella]	452	427	0	94.5	83.4	85.8	hypothetical protein CARUB_v10001020mg	gbpln	Capsella rubella	AT5G25220.1 | Symbols: KNAT3 | KNOTTED1-like homeobox gene 3 | chr5:8736208-8738115 FORWARD LENGTH=431	452	431	0	95.4	85.2	86.9
Rsa1.0_01035.1.g22724.t1	gb|EOA22342.1| hypothetical protein CARUB_v10002958mg [Capsella rubella]	623	660	0	105.9	80.3	86.4	hypothetical protein CARUB_v10002958mg	gbpln	Capsella rubella	AT5G25270.1 | Symbols: | Ubiquitin-like superfamily protein | chr5:8757577-8762002 REVERSE LENGTH=658	623	658	0	105.6	78.2	83.9
Rsa1.0_01036.1.g22725.t1	gb|EOA33796.1| hypothetical protein CARUB_v10021265mg [Capsella rubella]	141	167	3.00E-69	118.4	89.4	97.2	hypothetical protein CARUB_v10021265mg	gbpln	Capsella rubella	AT1G66360.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:24751431-24752607 FORWARD LENGTH=174	141	174	1.00E-71	123.4	87.9	96.5
Rsa1.0_01036.1.g22726.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	267	1072	4.00E-31	401.5	32.2	50.6	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	267	289	9.00E-33	108.2	33.0	52.1

Rsa1.0_01036.1.g22727.t2	ref|NP_177800.1| uncharacterized protein [Arabidopsis thaliana] gi|6143891|gb|AAF04437.1|AC010718_6 hypothetical protein; 42007−47249 [Arabidopsis thaliana] gi|332197763|gb|AEE35884.1| uncharacterized protein AT1G76740 [Arabidopsis thaliana]	2040	1532	1.00E−173	75.1	22.7	28.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G76740.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76840.1); Has 3683 Blast hits to 2942 proteins in 407 species: Archae − 9; Bacteria − 440; Metazoa − 1472; Fungi − 269; Plants − 192; Viruses − 8; Other Eukaryotes − 1293 (source: NCBI BLink). | chr1:28805235−28810477 FORWARD LENGTH=1532	2040	1532	1.00E−175	75.1	22.7	28.3
Rsa1.0_01036.1.g22728.t1	ref|NP_177802.2| thioredoxin Y1 [Arabidopsis thaliana] gi|75324340|sp|Q6NPF9.1|TRXY1_ARATH RecName: Full=Thioredoxin Y1, chloroplastic; Short=AtTrxy1; Flags: Precursor gi|38454080|gb|AAR20734.1| At1g76760 [Arabidopsis thaliana] gi|38604000|gb|AAR24743.1| At1g76760 [Arabidopsis thaliana] gi|110743067|dbj|BAE99426.1| thioredoxin−like protein [Arabidopsis thaliana] gi|332197765|gb|AEE35886.1| thioredoxin Y1 [Arabidopsis thaliana]	172	172	6.00E−79	100.0	83.1	90.7	thioredoxin Y1	gbpln	Arabidopsis thaliana	AT1G76760.1 | Symbols: ATY1, TRX−Y1, TY1 | thioredoxin Y1 | chr1:28811873−28812948 REVERSE LENGTH=172	172	172	2.00E−81	100.0	83.1	90.7
Rsa1.0_01036.1.g22729.t1	ref|XP_002887656.1| hypothetical protein ARALYDRAFT_339849 [Arabidopsis lyrata subsp. lyrata] gi|297333497|gb|EFH63915.1| hypothetical protein ARALYDRAFT_339849 [Arabidopsis lyrata subsp. lyrata]	245	249	4.00E−58	101.6	66.1	76.3	hypothetical protein ARALYDRAFT_339849	gbpln	Arabidopsis lyrata	AT1G76770.1 | Symbols: | HSP20−like chaperones superfamily protein | chr1:28813569−28814378 FORWARD LENGTH=244	245	244	3.00E−52	99.6	44.1	46.9
Rsa1.0_01036.1.g22730.t1	gb|AGI62245.1| O−methyltransferase family 2 protein [Brassica napus] gi|476002162|gb|AGI62247.1| O−methyltransferase family 2 protein [Brassica napus]	370	370	0	100.0	95.9	97.8	O−methyltransferase family 2 protein	gbpln	Brassica napus	AT1G76790.1 | Symbols: | O−methyltransferase family protein | chr1:28822355−28823630 REVERSE LENGTH=367	370	367	1.00E−167	99.2	80.0	88.6
Rsa1.0_01036.1.g22731.t1	ref|NP_177806.1| vacuolar iron transporter−like protein [Arabidopsis thaliana] gi|75207331|sp|Q9SRD3.1|VITH2_ARATH RecName: Full=Vacuolar iron transporter homolog 2; AltName: Full=Protein NODULIN−LIKE 2 gi|6143895|gb|AAF04441.1|AC010718_10 nodulin−like protein; 66117−66707 [Arabidopsis thaliana] gi|48958481|gb|AAT47793.1| At1g76800 [Arabidopsis thaliana] gi|51972058|gb|AAU15133.1| At1g76800 [Arabidopsis thaliana] gi|332197769|gb|AEE35890.1| vacuolar iron transporter homolog 2 [Arabidopsis thaliana]	194	196	1.00E−87	101.0	91.2	96.9	vacuolar iron transporter−like protein	gbpln	Arabidopsis thaliana	AT1G76800.1 | Symbols: | Vacuolar iron transporter (VIT) family protein | chr1:28829345−28829935 FORWARD LENGTH=196	194	196	4.00E−90	101.0	91.2	96.9
Rsa1.0_01036.1.g22732.t1	ref|XP_002889106.1| hypothetical protein ARALYDRAFT_895567 [Arabidopsis lyrata subsp. lyrata] gi|297334947|gb|EFH65365.1| hypothetical protein ARALYDRAFT_895567 [Arabidopsis lyrata subsp. lyrata]	97	98	3.00E−44	101.0	93.8	95.9	hypothetical protein ARALYDRAFT_895567	gbpln	Arabidopsis lyrata	AT1G76860.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:28854594−28855637 REVERSE LENGTH=98	97	98	1.00E−46	101.0	92.8	95.9
Rsa1.0_01036.1.g22733.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01036.1.g22734.t1	ref|XP_002887660.1| hypothetical protein ARALYDRAFT_895569 [Arabidopsis lyrata subsp. lyrata] gi|297333501|gb|EFH63919.1| hypothetical protein ARALYDRAFT_895569 [Arabidopsis lyrata subsp. lyrata]	555	598	1.00E−175	107.7	67.7	72.8	hypothetical protein ARALYDRAFT_895569	gbpln	Arabidopsis lyrata	AT1G76880.1 | Symbols: | Duplicated homeodomain−like superfamily protein | chr1:28865594−28867931 FORWARD LENGTH=603	555	603	1.00E−175	108.6	66.1	71.9
Rsa1.0_01036.1.g22735.t1	emb|CAA05997.1| GT2 [Arabidopsis thaliana]	569	575	0	101.1	86.3	91.6	GT2	gbpln	Arabidopsis thaliana	AT1G76890.2 | Symbols: GT2, AT−GT2 | Duplicated homeodomain−like superfamily protein | chr1:28873211−28875203 REVERSE LENGTH=575	569	575	0	101.1	86.6	91.9
Rsa1.0_01037.1.g22736.t1	gb|AAF79809.1|AC020646_32 T32E20.9 [Arabidopsis thaliana]	571	1586	3.00E−20	277.8	14.5	22.1	T32E20.9	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01037.1.g22737.t7	dbj|BAB02259.1| retroelement pol polyprotein−like [Arabidopsis thaliana]	1371	777	1.00E−34	56.7	8.0	11.5	retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01037.1.g22738.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	202	940	5.00E−34	465.3	35.6	47.0	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01037.1.g22739.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01037.1.g22740.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01037.1.g22741.t1	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#	
Rsa1.0_01037.1.g22742.t2	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#	
Rsa1.0_01037.1.g22743.t1	ref|XP_002893978.1| hypothetical protein ARALYDRAFT_473798 [Arabidopsis lyrata subsp. lyrata] gi|297339820|gb|EFH70237.1| hypothetical protein ARALYDRAFT_473798 [Arabidopsis lyrata subsp. lyrata]	476	480	0	100.8	79.2	89.3	hypothetical protein ARALYDRAFT_473798	gbpln	Arabidopsis lyrata	AT1G44100.1 | Symbols: AAP5 | amino acid permease 5 | chr1:16764651-16767223 REVERSE LENGTH=480	476	480	0	100.8	77.9	88.7
Rsa1.0_01038.1.g22744.t2	ref|XP_002863555.1| minichromosome maintenance family protein [Arabidopsis lyrata subsp. lyrata] gi|297309390|gb|EFH39814.1| minichromosome maintenance family protein [Arabidopsis lyrata subsp. lyrata]	334	830	3.00E-97	248.5	67.7	73.1	minichromosome maintenance family protein	gbpln	Arabidopsis lyrata	AT5G44635.1 | Symbols: MCM6 | minichromosome maintenance (MCM2/3/5) family protein | chr5:18006431-18010542 REVERSE LENGTH=831	334	831	8.00E-97	248.8	65.9	72.5
Rsa1.0_01038.1.g22745.t1	ref|NP_199276.1| alpha-barbatene synthase [Arabidopsis thaliana] gi|254810224|sp|Q4KSH9.2|BARS_ARATH RecName: Full=Alpha-barbatene synthase; Short=AtBS; AltName: Full=Beta-chamigrene synthase; AltName: Full=Terpendeoid synthase 11; Short=AtTPS11; AltName: Full=Thujopsene synthase gi|126352284|gb|ABO09887.1| At5g44630 [Arabidopsis thaliana] gi|332007757|gb|AED95140.1| alpha-barbatene synthase [Arabidopsis thaliana]	349	557	1.00E-160	159.6	76.8	86.0	alpha-barbatene synthase	gbpln	Arabidopsis thaliana	AT5G44630.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr5:18003280-18005616 FORWARD LENGTH=557	349	557	1.00E-163	159.6	76.8	86.0
Rsa1.0_01038.1.g22746.t1	gb|AAC02666.1| polyprotein [Arabidopsis thaliana]	1346	1451	0	107.8	67.4	79.0	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1346	1262	7.00E-96	93.8	13.2	19.1
Rsa1.0_01038.1.g22747.t1	gb|EOA14843.1| hypothetical protein CARUB_v10028157mg [Capsella rubella]	136	557	1.00E-38	409.6	59.6	69.9	hypothetical protein CARUB_v10028157mg	gbpln	Capsella rubella	AT5G44630.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr5:18003280-18005616 FORWARD LENGTH=557	136	557	4.00E-35	409.6	54.4	65.4
Rsa1.0_01038.1.g22748.t2	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#	
Rsa1.0_01038.1.g22749.t1	dbj|BAJ33888.1| unnamed protein product [Thellungiella halophila]	291	245	8.00E-38	84.2	35.4	42.6	unnamed protein product	----	----	AT4G20260.3 | Symbols: ATPCAP1, PCAP1 | plasma-membrane associated cation-binding protein 1 | chr4:10941593-10943227 FORWARD LENGTH=225	291	225	5.00E-37	77.3	33.3	40.9
Rsa1.0_01038.1.g22750.t1	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#	
Rsa1.0_01038.1.g22751.t1	#	#	#	#	#	#	–	----	----	AT3G17220.1 | Symbols: ATPMEI2, PMEI2 | pectin methylesterase inhibitor 2 | chr3:5883328-5883849 REVERSE LENGTH=173	79	173	9.00E-13	219.0	44.3	54.4	
Rsa1.0_01038.1.g22752.t1	ref|XP_002878762.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324601|gb|EFH55021.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	400	374	8.00E-66	93.5	42.8	58.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G17540.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6002783-6003973 FORWARD LENGTH=396	400	396	3.00E-67	99.0	42.5	59.3
Rsa1.0_01038.1.g22753.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	386	1447	3.00E-85	374.9	42.7	61.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	386	626	4.00E-29	162.2	16.8	28.5
Rsa1.0_01038.1.g22754.t1	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#	
Rsa1.0_01039.1.g22755.t1	ref|XP_002875755.1| hypothetical protein ARALYDRAFT_484967 [Arabidopsis lyrata subsp. lyrata] gi|297321593|gb|EFH52014.1| hypothetical protein ARALYDRAFT_484967 [Arabidopsis lyrata subsp. lyrata]	462	385	1.00E-174	83.3	69.9	72.3	hypothetical protein ARALYDRAFT_484967	gbpln	Arabidopsis lyrata	AT3G45870.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:16867246-16868838 FORWARD LENGTH=385	462	385	1.00E-171	83.3	66.9	69.0
Rsa1.0_01039.1.g22756.t5	ref|XP_002877437.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323275|gb|EFH53696.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	956	912	0	95.4	78.0	82.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G45810.1 | Symbols: | ferric reductase-like transmembrane component family protein | chr3:16832883-16837569 REVERSE LENGTH=912	956	912	0	95.4	77.0	81.9
Rsa1.0_01039.1.g22757.t1	ref|XP_002873380.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319217|gb|EFH49639.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata]	455	497	1.00E-129	109.2	53.8	67.3	IBR domain-containing protein	gbpln	Arabidopsis lyrata	AT5G08730.1 | Symbols: ATARI16, ARI16 | IBR domain-containing protein | chr5:2845824-2847415 REVERSE LENGTH=500	455	500	1.00E-127	109.9	52.1	67.5

Rsa1.0_01039.1.g22758.t2	ref|XP_002877430.1| hypothetical protein ARALYDRAFT_484955 [Arabidopsis lyrata subsp. lyrata] gi|297323268|gb|EFH53689.1| hypothetical protein ARALYDRAFT_484955 [Arabidopsis lyrata subsp. lyrata]	454	680	1.00E-156	149.8	59.5	72.0	hypothetical protein ARALYDRAFT_484955	gbpln	Arabidopsis lyrata	AT3G45750.1 | Symbols: | Nucleotidyltransferase family protein | chr3:16793855-16797380 REVERSE LENGTH=682	454	682	1.00E-156	150.2	58.4	70.9
Rsa1.0_01039.1.g22759.t1	ref|NP_190160.1| haloacid dehalogenase-like hydrolase-like protein [Arabidopsis thaliana] gi|7019640|emb|CAB75787.1| putative protein [Arabidopsis thaliana] gi|110738250|dbj|BAF01054.1| hypothetical protein [Arabidopsis thaliana] gi|332644544|gb|AEE78065.1| haloacid dehalogenase-like hydrolase-like protein [Arabidopsis thaliana]	378	376	0	99.5	85.7	91.3	haloacid dehalogenase-like hydrolase-like protein	gbpln	Arabidopsis thaliana	AT3G45740.1 | Symbols: | hydrolase family protein / HAD-superfamily protein | chr3:16790830-16793280 FORWARD LENGTH=376	378	376	0	99.5	85.7	91.3
Rsa1.0_01039.1.g22760.t1	gb|EOA23731.1| hypothetical protein CARUB_v10016943mg [Capsella rubella]	553	564	0	102.0	89.7	94.9	hypothetical protein CARUB_v10016943mg	gbpln	Capsella rubella	AT3G45650.1 | Symbols: NAXT1 | nitrate excretion transporter1 | chr3:16759253-16761266 FORWARD LENGTH=558	553	558	0	100.9	88.8	93.5
Rsa1.0_01039.1.g22761.t1	gb|AAV34677.1| mitogen-activated protein kinase 3 [Brassica napus]	370	370	0	100.0	98.4	99.5	mitogen-activated protein kinase 3	gbpln	Brassica napus	AT3G45640.1 | Symbols: ATMPK3, MPK3, ATMAPK3 | mitogen-activated protein kinase 3 | chr3:16756918-16758476 FORWARD LENGTH=370	370	370	0	100.0	94.3	97.6
Rsa1.0_01039.1.g22762.t1	gb|AAD24601.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	557	1319	1.00E-113	236.8	39.1	56.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	557	575	3.00E-72	103.2	28.4	45.2
Rsa1.0_01039.1.g22763.t1	ref|XP_002877425.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297323263|gb|EFH53684.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	897	989	0	110.3	76.1	86.0	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT3G45630.1 | Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr3:16748751-16753190 REVERSE LENGTH=989	897	989	0	110.3	74.8	83.7
Rsa1.0_01039.1.g22764.t1	ref|NP_190148.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|6996265|emb|CAB75491.1| putative protein [Arabidopsis thaliana] gi|26450489|dbj|BAC42358.1| unknown protein [Arabidopsis thaliana] gi|28973383|gb|AAO64016.1| unknown protein [Arabidopsis thaliana] gi|332644530|gb|AEE78051.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	502	481	0	95.8	79.3	86.3	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G45620.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:16745918-16747993 FORWARD LENGTH=481	502	481	0	95.8	79.3	86.3
Rsa1.0_01039.1.g22765.t1	gb|EOA25399.1| hypothetical protein CARUB_v10018731mg [Capsella rubella]	542	1119	0	206.5	76.0	83.8	hypothetical protein CARUB_v10018731mg	gbpln	Capsella rubella	AT5G60250.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24252226-24254710 FORWARD LENGTH=655	542	655	1.00E-101	120.8	36.9	54.2
Rsa1.0_01040.1.g22766.t2	gb|ABA98367.2| retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa Japonica Group]	236	1745	6.00E-11	739.4	22.9	34.3	retrotransposon protein, putative, Ty1-copia subclass	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22767.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	100	1142	4.00E-13	1142.0	38.0	53.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22768.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22769.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22770.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22771.t1	ref|XP_004305746.1| PREDICTED: uncharacterized protein LOC101308702 [Fragaria vesca subsp. vesca]	337	1163	2.00E-49	345.1	32.3	43.3	PREDICTED: uncharacterized protein LOC101308702	gbpln	Fragaria vesca	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	337	158	2.00E-14	46.9	13.4	16.9
Rsa1.0_01040.1.g22772.t4	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22773.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	373	414	7.00E-63	111.0	50.7	61.9	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22774.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	895	704	0	78.7	51.3	57.5	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22775.t1	gb|AAD15474.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	716	1466	1.00E-85	204.7	26.4	34.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01040.1.g22776.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01041.1.g22777.t1	gb|AAM62596.1| sucrose cleavage protein-like [Arabidopsis thaliana]	331	333	1.00E-168	100.6	87.3	94.6	sucrose cleavage protein-like	gbpln	Arabidopsis thaliana	AT5G40510.1 | Symbols: | Sucrase/ferredoxin-like family protein | chr5:16229277-16230798 FORWARD LENGTH=333	331	333	1.00E-170	100.6	87.0	94.6

Rsa1.0_01041.1.g22778.t1	ref|XP_002870698.1| hypothetical protein ARALYDRAFT_355933 [Arabidopsis lyrata subsp. lyrata] gi|297316534|gb|EFH46957.1| hypothetical protein ARALYDRAFT_355933 [Arabidopsis lyrata subsp. lyrata]	127	115	1.00E-48	90.6	80.3	84.3	hypothetical protein ARALYDRAFT_355933	gbpln	Arabidopsis lyrata	AT5G40500.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:16227984-16228518 FORWARD LENGTH=123	127	123	4.00E-51	96.9	81.9	85.8
Rsa1.0_01041.1.g22779.t1	ref|XP_002870699.1| hypothetical protein ARALYDRAFT_493936 [Arabidopsis lyrata subsp. lyrata] gi|297316535|gb|EFH46958.1| hypothetical protein ARALYDRAFT_493936 [Arabidopsis lyrata subsp. lyrata]	417	421	1.00E-114	101.0	50.1	53.7	hypothetical protein ARALYDRAFT_493936	gbpln	Arabidopsis lyrata	AT5G40490.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:16225483-16227423 FORWARD LENGTH=423	417	423	1.00E-117	101.4	50.4	53.7
Rsa1.0_01041.1.g22780.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01041.1.g22781.t1	gb|EOA28034.1| hypothetical protein CARUB_v10024220mg [Capsella rubella] gi|482563845|gb|EOA28035.1| hypothetical protein CARUB_v10024220mg [Capsella rubella]	164	160	2.00E-73	97.6	82.3	88.4	hypothetical protein CARUB_v10024220mg	gbpln	Capsella rubella	AT2G44860.2 | Symbols: | Ribosomal protein L24e family protein | chr2:18501034-18502128 REVERSE LENGTH=159	164	159	9.00E-75	97.0	80.5	88.4
Rsa1.0_01041.1.g22782.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01041.1.g22783.t1	ref|NP_198618.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana] gi|30102648|gb|AAP21242.1| At5g38020 [Arabidopsis thaliana] gi|110736083|dbj|BAF00014.1| SAMT-like protein [Arabidopsis thaliana] gi|332006875|gb|AED94258.1| S-adenosyl-L-methionine-dependent methyltransferase-like protein [Arabidopsis thaliana]	306	368	1.00E-144	120.3	81.0	88.9	S-adenosyl-L-methionine-dependent methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT5G38020.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:15165953-15167612 REVERSE LENGTH=368	306	368	2.33E-156	120.3	81.0	88.9
Rsa1.0_01041.1.g22784.t1	ref|XP_003631792.1| PREDICTED: uncharacterized protein LOC100252656 [Vitis vinifera]	383	946	6.00E-68	247.0	40.7	50.9	PREDICTED: uncharacterized protein LOC100252656	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	383	1262	1.00E-10	329.5	10.4	18.5
Rsa1.0_01042.1.g22785.t1	ref|XP_002888762.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297334603|gb|EFH65021.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	373	375	0	100.5	89.5	94.9	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT1G70260.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:26457067-26459338 REVERSE LENGTH=375	373	375	0	100.5	88.7	94.4
Rsa1.0_01042.1.g22786.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1732	1214	0	70.1	24.1	35.7	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1732	626	8.00E-62	36.1	7.7	11.8
Rsa1.0_01042.1.g22787.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01042.1.g22788.t1	gb|AAM63352.1| unknown [Arabidopsis thaliana]	210	200	1.00E-76	95.2	70.5	81.9	unknown	gbpln	Arabidopsis thaliana	AT1G70720.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:26666427-26667029 FORWARD LENGTH=200	210	200	4.00E-73	95.2	70.5	81.9
Rsa1.0_01042.1.g22789.t1	ref|NP_177231.2| protein kinase domain-containing protein [Arabidopsis thaliana] gi|193870477|gb|ACF22895.1| At1g70740 [Arabidopsis thaliana] gi|332196987|gb|AEE35108.1| protein kinase domain-containing protein [Arabidopsis thaliana]	432	425	0	98.4	84.5	91.9	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G70740.1 | Symbols: | Protein kinase superfamily protein | chr1:26673847-26675687 REVERSE LENGTH=425	432	425	0	98.4	84.5	91.9
Rsa1.0_01042.1.g22790.t3	ref|NP_173766.1| uncharacterized protein [Arabidopsis thaliana] gi|8778585|gb|AAF79593.1|AC007945_13 F28C11.15 [Arabidopsis thaliana] gi|4056435|gb|AAC98008.1| Similar to OBP32pep protein gb|U37698 from Arabidopsis thaliana [Arabidopsis thaliana] gi|332192277|gb|AEE30398.1| uncharacterized protein AT1G23520 [Arabidopsis thaliana]	270	263	2.00E-56	97.4	45.9	61.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23520.1 | Symbols: | Domain of unknown function (DUF220) | chr1:8343571-8344675 REVERSE LENGTH=263	270	263	6.00E-59	97.4	45.9	61.5
Rsa1.0_01042.1.g22791.t2	ref|XP_002888794.1| hypothetical protein ARALYDRAFT_476207 [Arabidopsis lyrata subsp. lyrata] gi|297334635|gb|EFH65053.1| hypothetical protein ARALYDRAFT_476207 [Arabidopsis lyrata subsp. lyrata]	125	616	4.00E-40	492.8	66.4	83.2	hypothetical protein ARALYDRAFT_476207	gbpln	Arabidopsis lyrata	AT1G70770.2 | Symbols: | Protein of unknown function DUF2359, transmembrane | chr1:26688622-26691185 REVERSE LENGTH=610	125	610	8.00E-41	488.0	64.8	80.0

Rsa1.0_01042.1.g22792.t1	ref|XP_002888795.1| hypothetical protein ARALYDRAFT_894896 [Arabidopsis lyrata subsp. lyrata] gi|297334636|gb|EFH65054.1| hypothetical protein ARALYDRAFT_894896 [Arabidopsis lyrata subsp. lyrata]	139	140	9.00E-64	100.7	89.9	95.0	hypothetical protein ARALYDRAFT_894896	gbpln	Arabidopsis lyrata	AT1G70780.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23150.1); Has 143 Blast hits to 143 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 143; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26695462-26695975 REVERSE LENGTH=140	139	140	4.00E-66	100.7	90.6	94.2
Rsa1.0_01042.1.g22793.t1	gb|EOA33828.1| hypothetical protein CARUB_v10021307mg [Capsella rubella]	655	515	1.00E-55	78.6	26.6	35.4	hypothetical protein CARUB_v10021307mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	655	530	3.00E-40	80.9	17.9	27.2
Rsa1.0_01042.1.g22794.t1	gb|ADK63412.1| C2 domain-containing protein [Brassica rapa]	185	185	3.00E-94	100.0	89.7	95.1	C2 domain-containing protein	gbpln	Brassica rapa	AT1G70790.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:26700724-26702127 FORWARD LENGTH=185	185	185	3.00E-95	100.0	86.5	96.2
Rsa1.0_01042.1.g22795.t1	ref|NP_001077806.1| MLP-like protein 28 [Arabidopsis thaliana] gi|332197002|gb|AEE35123.1| MLP-like protein 28 [Arabidopsis thaliana]	147	201	1.00E-65	136.7	86.4	93.2	MLP-like protein 28	gbpln	Arabidopsis thaliana	AT1G70830.3 | Symbols: MLP28 | MLP-like protein 28 | chr1:26710203-26711395 REVERSE LENGTH=201	147	201	4.00E-68	136.7	86.4	93.2
Rsa1.0_01042.1.g22796.t1	emb|CAC24691.1| efflux carrier of polar auxin transport [Brassica juncea]	627	639	0	101.9	96.3	97.6	efflux carrier of polar auxin transport	gbpln	Brassica juncea	AT1G70940.1 | Symbols: PIN3, ATPIN3 | Auxin efflux carrier family protein | chr1:26743170-26745871 FORWARD LENGTH=640	627	640	0	102.1	91.9	95.1
Rsa1.0_01042.1.g22797.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01043.1.g22798.t1	gb|EOA36617.1| hypothetical protein CARUB_v10011853mg [Capsella rubella]	173	170	1.00E-44	98.3	54.9	71.7	hypothetical protein CARUB_v10011853mg	gbpln	Capsella rubella	AT1G05291.1 | Symbols: | Protein of unknown function (DUF1218) | chr1:1541348-1542323 REVERSE LENGTH=204	173	204	2.00E-39	117.9	51.4	67.1
Rsa1.0_01043.1.g22799.t1	ref|XP_002892279.1| transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297338121|gb|EFH68538.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	337	370	6.00E-67	109.8	52.2	63.8	transcription factor	gbpln	Arabidopsis lyrata	AT1G05290.1 | Symbols: | CCT motif family protein | chr1:1539152-1540546 REVERSE LENGTH=369	337	369	1.00E-69	109.5	50.4	65.0
Rsa1.0_01043.1.g22800.t1	ref|XP_002892278.1| hypothetical protein ARALYDRAFT_887710 [Arabidopsis lyrata subsp. lyrata] gi|297338120|gb|EFH68537.1| hypothetical protein ARALYDRAFT_887710 [Arabidopsis lyrata subsp. lyrata]	446	462	0	103.6	73.3	83.6	hypothetical protein ARALYDRAFT_887710	gbpln	Arabidopsis lyrata	AT1G05280.1 | Symbols: | Protein of unknown function (DUF604) | chr1:1535444-1537414 REVERSE LENGTH=461	446	461	0	103.4	73.3	82.5
Rsa1.0_01043.1.g22801.t1	ref|XP_002892278.1| hypothetical protein ARALYDRAFT_887710 [Arabidopsis lyrata subsp. lyrata] gi|297338120|gb|EFH68537.1| hypothetical protein ARALYDRAFT_887710 [Arabidopsis lyrata subsp. lyrata]	445	462	0	103.8	72.6	83.1	hypothetical protein ARALYDRAFT_887710	gbpln	Arabidopsis lyrata	AT1G05280.1 | Symbols: | Protein of unknown function (DUF604) | chr1:1535444-1537414 REVERSE LENGTH=461	445	461	0	103.6	72.6	82.0
Rsa1.0_01043.1.g22802.t1	gb|EOA38328.1| hypothetical protein CARUB_v10009829mg [Capsella rubella]	508	309	1.00E-132	60.8	45.5	47.0	hypothetical protein CARUB_v10009829mg	gbpln	Capsella rubella	AT1G05260.1 | Symbols: RCI3, RCI3A | Peroxidase superfamily protein | chr1:1529827-1531271 FORWARD LENGTH=326	508	326	1.00E-133	64.2	44.7	46.5
Rsa1.0_01043.1.g22803.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1772	1274	0	71.9	36.5	48.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1772	575	6.00E-79	32.4	10.6	16.2
Rsa1.0_01043.1.g22804.t1	gb|EOA39455.1| hypothetical protein CARUB_v10012652mg [Capsella rubella]	320	320	1.00E-143	100.0	79.7	86.3	hypothetical protein CARUB_v10012652mg	gbpln	Capsella rubella	AT1G05250.1 | Symbols: | Peroxidase superfamily protein | chr1:1525924-1527169 REVERSE LENGTH=325	320	325	1.00E-120	101.6	69.7	81.6
Rsa1.0_01043.1.g22805.t1	gb|EOA39455.1| hypothetical protein CARUB_v10012652mg [Capsella rubella]	268	320	1.00E-129	119.4	84.0	88.1	hypothetical protein CARUB_v10012652mg	gbpln	Capsella rubella	AT1G05250.1 | Symbols: | Peroxidase superfamily protein | chr1:1525924-1527169 REVERSE LENGTH=325	268	325	1.00E-111	121.3	71.3	81.3
Rsa1.0_01043.1.g22806.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1261	1501	0	119.0	59.5	74.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1261	1262	1.00E-139	100.1	19.3	27.9

Rsa1.0_01043.1.g22807.t1	ref|NP_172015.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|30679181|ref|NP_849596.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|334182300|ref|NP_001184911.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|75332091|sp|Q94C37.1|HDG2_ARATH RecName: Full=Homeobox-leucine zipper protein HDG2; AltName: Full=HD-ZIP protein HDG2; AltName: Full=Homeodomain GLABRA 2-like protein 2; AltName: Full=Homeodomain transcription factor HDG2; AltName: Full=Protein HOMEODOMAIN GLABROUS 2 gi|14334996|gb|AAK59762.1| At1g05230/YUP8H12_16 [Arabidopsis thaliana] gi|20147145|gb|AAM10289.1| At1g05230/YUP8H12_16 [Arabidopsis thaliana] gi|222423025|dbj|BAH19495.1| AT1G05230 [Arabidopsis thaliana] gi|332189688|gb|AEE27809.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|332189689|gb|AEE27810.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana] gi|332189691|gb|AEE27812.1| homeobox-leucine zipper protein HDG2 [Arabidopsis thaliana]	723	721	0	99.7	94.9	97.0	homeobox-leucine zipper protein HDG2	gbpln	Arabidopsis thaliana	AT1G05230.4 | Symbols: HDG2 | homeodomain GLABROUS 2 | chr1:1513388-1517024 REVERSE LENGTH=721	723	721	0	99.7	94.9	97.0
Rsa1.0_01043.1.g22808.t1	ref|XP_002889539.1| hypothetical protein ARALYDRAFT_470516 [Arabidopsis lyrata subsp. lyrata] gi|297335381|gb|EFH65798.1| hypothetical protein ARALYDRAFT_470516 [Arabidopsis lyrata subsp. lyrata]	168	168	6.00E-77	100.0	83.9	92.9	hypothetical protein ARALYDRAFT_470516	gbpln	Arabidopsis lyrata	AT1G05210.1 | Symbols: | Transmembrane protein 97, predicted | chr1:1510469-1511485 FORWARD LENGTH=168	168	168	4.00E-78	100.0	83.3	91.7
Rsa1.0_01043.1.g22809.t1	ref|XP_002892274.1| hypothetical protein ARALYDRAFT_470515 [Arabidopsis lyrata subsp. lyrata] gi|297338116|gb|EFH68533.1| hypothetical protein ARALYDRAFT_470515 [Arabidopsis lyrata subsp. lyrata]	86	91	2.00E-41	105.8	97.7	97.7	hypothetical protein ARALYDRAFT_470515	gbpln	Arabidopsis lyrata	AT1G05205.1 | Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1509352-1510249 REVERSE LENGTH=91	86	91	1.00E-43	105.8	95.3	96.5
Rsa1.0_01043.1.g22810.t1	dbj|BAJ34158.1| unnamed protein product [Thellungiella halophila]	955	954	0	99.9	89.3	94.1	unnamed protein product	----	----	AT1G05200.2 | Symbols: ATGLR3.4, GLR3.4, GLUR3 | glutamate receptor 3.4 | chr1:1505642-1509002 FORWARD LENGTH=959	955	959	0	100.4	87.0	93.3
Rsa1.0_01044.1.g22811.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01044.1.g22812.t1	ref|NP_188940.1| CBL-interacting serine/threonine-protein kinase 7 [Arabidopsis thaliana] gi|75338665|sp|Q9XIW0.1|CIPK7_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 7; AltName: Full=SNF1-related kinase 3.10; AltName: Full=SOS2-like protein kinase PKS7; AltName: Full=Serine/threonine-protein kinase SR2; Short=AtSR2; Short=AtSRPK1 gi|13249113|gb|AAK16682.1|AF290192_1 CBL-interacting protein kinase 7 [Arabidopsis thaliana] gi|13448039|gb|AAK26846.1|AF339148_1 SOS2-like protein kinase PKS7 [Arabidopsis thaliana] gi|5478791|dbj|BAA77716.2| SNF1 related protein kinase [Arabidopsis thaliana] gi|9294189|dbj|BAB02091.1| SNF1 related protein kinase [Arabidopsis thaliana] gi|57222172|gb|AAW38993.1| At3g23000 [Arabidopsis thaliana] gi|114213519|gb|ABI54342.1| At3g23000 [Arabidopsis thaliana] gi|332643183|gb|AEE76704.1| CBL-interacting serine/threonine-protein kinase 7 [Arabidopsis thaliana]	419	429	0	102.4	83.1	90.2	CBL-interacting serine/threonine-protein kinase 7	gbpln	Arabidopsis thaliana	AT3G23000.1 | Symbols: CIPK7, SnRK3.10, PKS7, ATSRPK1, ATSR2 | CBL-interacting protein kinase 7 | chr3:8172654-8173943 FORWARD LENGTH=429	419	429	0	102.4	83.1	90.2

Rsa1.0_01044.1.g22813.t1	ref|NP_188942.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75273922|sp|Q9LS88.1|PP250_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g23020 gi|9294191|dbj|BAB02093.1| unnamed protein product [Arabidopsis thaliana] gi|332643185|gb|AEE76706.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	850	842	0	99.1	86.2	92.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G23020.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:8177215-8179743 REVERSE LENGTH=842	850	842	0	99.1	86.2	92.6
Rsa1.0_01044.1.g22814.t1	ref|XP_002884981.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297330821|gb|EFH61240.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	426	400	6.00E-76	93.9	40.1	52.3	F-box family protein	gbpln	Arabidopsis lyrata	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	426	395	8.00E-74	92.7	37.3	50.5
Rsa1.0_01044.1.g22815.t1	ref|XP_002885540.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297331380|gb|EFH61799.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	173	841	5.00E-80	486.1	84.4	87.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G23020.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:8177215-8179743 REVERSE LENGTH=842	173	842	1.00E-81	486.7	83.8	86.7
Rsa1.0_01044.1.g22816.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01044.1.g22817.t1	ref|XP_002885542.1| indoleacetic acid-induced protein 2 [Arabidopsis lyrata subsp. lyrata] gi|297331382|gb|EFH61801.1| indoleacetic acid-induced protein 2 [Arabidopsis lyrata subsp. lyrata]	171	174	2.00E-76	101.8	86.5	91.8	indoleacetic acid-induced protein 2	gbpln	Arabidopsis lyrata	AT3G23030.1 | Symbols: IAA2 | indole-3-acetic acid inducible 2 | chr3:8181069-8181685 REVERSE LENGTH=174	171	174	5.00E-78	101.8	84.8	90.6
Rsa1.0_01044.1.g22818.t1	gb|AAG00239.1|AC002130_4 F1N21.6 [Arabidopsis thaliana]	257	901	2.00E-52	350.6	47.1	59.1	F1N21.6	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01044.1.g22819.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01045.1.g22820.t1	ref|XP_002876948.1| glycosyl hydrolase family 5 protein [Arabidopsis lyrata subsp. lyrata] gi|297322786|gb|EFH53207.1| glycosyl hydrolase family 5 protein [Arabidopsis lyrata subsp. lyrata]	369	509	1.00E-176	137.9	80.5	87.8	glycosyl hydrolase family 5 protein	gbpln	Arabidopsis lyrata	AT3G26140.1 | Symbols: | Cellulase (glycosyl hydrolase family 5) protein | chr3:9559742-9563070 REVERSE LENGTH=508	369	508	1.00E-175	137.7	78.9	86.4
Rsa1.0_01045.1.g22821.t2	gb|EOA12742.1| hypothetical protein CARUB_v10028251mg [Capsella rubella]	168	618	3.00E-34	367.9	42.9	55.4	hypothetical protein CARUB_v10028251mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	168	696	3.00E-18	414.3	23.8	35.1
Rsa1.0_01045.1.g22822.t1	gb|EOA25800.1| hypothetical protein CARUB_v10019167mg [Capsella rubella]	127	511	3.00E-51	402.4	78.7	85.8	hypothetical protein CARUB_v10019167mg	gbpln	Capsella rubella	AT3G26140.1 | Symbols: | Cellulase (glycosyl hydrolase family 5) protein | chr3:9559742-9563070 REVERSE LENGTH=508	127	508	9.00E-53	400.0	78.0	85.8
Rsa1.0_01045.1.g22823.t1	dbj|BAB02432.1| unnamed protein product [Arabidopsis thaliana]	554	561	0	101.3	82.9	91.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G26130.1 | Symbols: | Cellulase (glycosyl hydrolase family 5) protein | chr3:9553708-9555611 REVERSE LENGTH=551	554	551	0	99.5	81.8	90.6
Rsa1.0_01045.1.g22824.t1	dbj|BAB01438.1| unnamed protein product [Arabidopsis thaliana]	606	708	0	116.8	78.9	86.5	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G26120.1 | Symbols: TEL1 | terminal EAR1-like 1 | chr3:9546398-9549186 FORWARD LENGTH=615	606	615	0	101.5	78.9	86.5
Rsa1.0_01045.1.g22825.t2	dbj|BAB01437.1| unnamed protein product [Arabidopsis thaliana]	730	572	1.00E-177	78.4	42.3	47.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G26115.1 | Symbols: | Pyridoxal-5'-phosphate-dependent enzyme family protein | chr3:9542301-9544246 FORWARD LENGTH=427	730	427	1.00E-179	58.5	42.3	47.1
Rsa1.0_01045.1.g22826.t1	ref|XP_002890798.1| hypothetical protein ARALYDRAFT_890443 [Arabidopsis lyrata subsp. lyrata] gi|297336640|gb|EFH67057.1| hypothetical protein ARALYDRAFT_890443 [Arabidopsis lyrata subsp. lyrata]	440	574	1.00E-144	130.5	71.4	80.9	hypothetical protein ARALYDRAFT_890443	gbpln	Arabidopsis lyrata	AT1G29240.1 | Symbols: | Protein of unknown function (DUF688) | chr1:10217023-10218924 REVERSE LENGTH=577	440	577	1.00E-141	131.1	69.8	79.8
Rsa1.0_01045.1.g22827.t2	ref|NP_001117377.1| O-fucosyltransferase-like protein [Arabidopsis thaliana] gi|332192938|gb|AEE31059.1| O-fucosyltransferase-like protein [Arabidopsis thaliana]	626	611	0	97.6	82.9	88.8	O-fucosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT1G29200.2 | Symbols: | O-fucosyltransferase family protein | chr1:10208002-10210488 FORWARD LENGTH=611	626	611	0	97.6	82.9	88.8
Rsa1.0_01045.1.g22828.t1	emb|CAN83015.1| hypothetical protein VITISV_041694 [Vitis vinifera]	1338	1099	0	82.1	34.1	43.3	hypothetical protein VITISV_041694	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1338	1262	1.00E-135	94.3	17.4	26.1

Rsa1.0_01045.1.g22829.t1	ref|NP_172045.1| uncharacterized protein [Arabidopsis thaliana] gi|8778720|gb|AAF79728.1|AC005106_9 T25N20.19 [Arabidopsis thaliana] gi|332189729|gb|AEE27850.1| uncharacterized protein AT1G05540 [Arabidopsis thaliana]	446	367	4.00E-90	82.3	43.5	55.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G05540.1 | Symbols: | Protein of unknown function (DUF295) | chr1:1639348-1640707 FORWARD LENGTH=367	446	367	1.00E-92	82.3	43.5	55.6
Rsa1.0_01046.1.g22830.t1	gb|EOA30505.1| hypothetical protein CARUB_v10013628mg [Capsella rubella]	329	468	1.00E-127	142.2	76.9	86.6	hypothetical protein CARUB_v10013628mg	gbpln	Capsella rubella	AT3G02990.1 | Symbols: ATHSFA1E, HSFA1E | heat shock transcription factor A1E | chr3:673614-675988 FORWARD LENGTH=468	329	468	1.00E-127	142.2	78.1	87.5
Rsa1.0_01046.1.g22831.t1	ref|NP_186959.2| D-xylose-proton symporter-like 1 [Arabidopsis thaliana] gi|75329736|sp|Q8L6Z8.1|XYLL1_ARATH RecName: Full=D-xylose-proton symporter-like 1 gi|22655210|gb|AAM98195.1| unknown protein [Arabidopsis thaliana] gi|34098871|gb|AAQ56818.1| At3g03090 [Arabidopsis thaliana] gi|332640379|gb|AEE73900.1| D-xylose-proton symporter-like 1 [Arabidopsis thaliana]	610	503	0	82.5	69.8	76.4	D-xylose-proton symporter-like 1	gbpln	Arabidopsis thaliana	AT3G03090.1 | Symbols: AtVGT1, VGT1 | vacuolar glucose transporter 1 | chr3:700749-704579 REVERSE LENGTH=503	610	503	0	82.5	69.8	76.4
Rsa1.0_01046.1.g22832.t1	ref|NP_186959.2| D-xylose-proton symporter-like 1 [Arabidopsis thaliana] gi|75329736|sp|Q8L6Z8.1|XYLL1_ARATH RecName: Full=D-xylose-proton symporter-like 1 gi|22655210|gb|AAM98195.1| unknown protein [Arabidopsis thaliana] gi|34098871|gb|AAQ56818.1| At3g03090 [Arabidopsis thaliana] gi|332640379|gb|AEE73900.1| D-xylose-proton symporter-like 1 [Arabidopsis thaliana]	688	503	0	73.1	62.2	67.9	D-xylose-proton symporter-like 1	gbpln	Arabidopsis thaliana	AT3G03090.1 | Symbols: AtVGT1, VGT1 | vacuolar glucose transporter 1 | chr3:700749-704579 REVERSE LENGTH=503	688	503	0	73.1	62.2	67.9
Rsa1.0_01046.1.g22833.t1	ref|XP_002884361.1| hypothetical protein ARALYDRAFT_896308 [Arabidopsis lyrata subsp. lyrata] gi|297330201|gb|EFH60620.1| hypothetical protein ARALYDRAFT_896308 [Arabidopsis lyrata subsp. lyrata]	117	120	1.00E-46	102.6	83.8	88.9	hypothetical protein ARALYDRAFT_896308	gbpln	Arabidopsis lyrata	AT3G03150.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G17165.1); Has 39 Blast hits to 39 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:727733-729357 REVERSE LENGTH=121	117	121	3.00E-47	103.4	80.3	84.6
Rsa1.0_01046.1.g22834.t1	ref|XP_002882276.1| hypothetical protein ARALYDRAFT_477563 [Arabidopsis lyrata subsp. lyrata] gi|297328116|gb|EFH58535.1| hypothetical protein ARALYDRAFT_477563 [Arabidopsis lyrata subsp. lyrata]	130	130	2.00E-68	100.0	96.2	99.2	hypothetical protein ARALYDRAFT_477563	gbpln	Arabidopsis lyrata	AT3G03160.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular protein transport; LOCATED IN: endomembrane system, integral to membrane, endoplasmic reticulum; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: B-cell receptor-associated 31-like (InterPro:IPR008417); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G17190.1); Has 102 Blast hits to 102 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 102; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:729876-730268 FORWARD LENGTH=130	130	130	4.00E-71	100.0	96.2	99.2
Rsa1.0_01046.1.g22835.t1	ref|NP_566196.1| uncharacterized protein [Arabidopsis thaliana] gi|89001025|gb|ABD59102.1| At3g03170 [Arabidopsis thaliana] gi|332640388|gb|AEE73909.1| uncharacterized protein AT3G03170 [Arabidopsis thaliana]	152	156	4.00E-58	102.6	83.6	90.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G03170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24890.1); Has 184 Blast hits to 184 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 184; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:732066-732729 FORWARD LENGTH=156	152	156	1.00E-60	102.6	83.6	90.1
Rsa1.0_01046.1.g22836.t1	ref|NP_001078100.1| uncharacterized protein [Arabidopsis thaliana] gi|113204476|gb|ABI34031.1| unknown [Arabidopsis thaliana] gi|332640400|gb|AEE73921.1| uncharacterized protein AT3G03272 [Arabidopsis thaliana]	127	120	5.00E-33	94.5	53.5	62.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G03272.1 | Symbols: | Protein of unknown function (DUF1278) | chr3:763833-764195 REVERSE LENGTH=120	127	120	1.00E-35	94.5	53.5	62.2

Rsa1.0_01046.1.g22837.t1	ref|XP_002862609.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308241|gb|EFH38867.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	107	110	1.00E−22	102.8	63.6	72.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G03350.2 | Symbols: | NAD(P)−binding Rossmann−fold superfamily protein | chr3:791273−794553 FORWARD LENGTH=359	107	359	6.00E−18	335.5	57.0	67.3
Rsa1.0_01046.1.g22838.t1	sp|P69198.1|POLC2_BRANA RecName: Full=Polcalcin Bra n 2; AltName: Full=Calcium−binding pollen allergen Bra n 2; AltName: Allergen=Bra n 2 gi|59800146|sp|P69199.1|POLC2_BRARA RecName: Full=Polcalcin Bra r 2; AltName: Full=Calcium−binding pollen allergen Bra r 2; AltName: Allergen=Bra r 2 gi|1255542|dbj|BAA09635.1| calcium−binding protein [Brassica rapa]	83	83	7.00E−39	100.0	96.4	100.0	RecName: Full=Polcalcin Bra n 2; AltName: Full=Calcium−binding pollen allergen Bra n 2; AltName: Allergen=Bra n 2 gi|59800146|sp|P69199.1|POLC2_BRARA RecName: Full=Polcalcin Bra r 2; AltName: Full=Calcium−binding pollen allergen Bra r 2; AltName: Allergen=Bra r 2 gi|1255542|dbj|BAA09635.1| calcium−binding protein	gbpln	Brassica rapa	AT3G03430.1 | Symbols: | Calcium−binding EF−hand family protein | chr3:814481−814732 FORWARD LENGTH=83	83	83	4.00E−40	100.0	92.8	98.8
Rsa1.0_01046.1.g22839.t1	ref|XP_002884382.1| CYP89A9 [Arabidopsis lyrata subsp. lyrata] gi|297330222|gb|EFH60641.1| CYP89A9 [Arabidopsis lyrata subsp. lyrata]	503	514	0	102.2	90.7	96.0	CYP89A9	gbpln	Arabidopsis lyrata	AT3G03470.1 | Symbols: CYP89A9 | cytochrome P450, family 87, subfamily A, polypeptide 9 | chr3:824692−826345 REVERSE LENGTH=511	503	511	0	101.6	90.1	95.2
Rsa1.0_01046.1.g22840.t1	ref|NP_186999.1| peroxin 19−1 [Arabidopsis thaliana] gi|75313803|sp|Q9SRQ3.1|PE191_ARATH RecName: Full=Peroxisome biogenesis protein 19−1; AltName: Full=Peroxin−19−1; Short=AtPEX19−1; AltName: Full=Peroxisomal membrane protein import receptor PEX19−1; Flags: Precursor gi|6017103|gb|AAF01586.1|AC009895_7 unknown protein [Arabidopsis thaliana] gi|46931296|gb|AAT06452.1| At3g03490 [Arabidopsis thaliana] gi|66392759|emb|CAD91898.1| peroxisomal membrane protein Pex19p [Arabidopsis thaliana] gi|332640429|gb|AEE73950.1| peroxin 19−1 [Arabidopsis thaliana]	250	248	1.00E−106	99.2	82.0	90.4	peroxin 19−1	gbpln	Arabidopsis thaliana	AT3G03490.1 | Symbols: PEX19−1, AtPEX19−1 | peroxin 19−1 | chr3:830302−831759 REVERSE LENGTH=248	250	248	1.00E−108	99.2	82.0	90.4
Rsa1.0_01046.1.g22841.t1	ref|XP_002884394.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297330234|gb|EFH60653.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	334	355	1.00E−119	106.3	75.4	85.0	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G03550.1 | Symbols: | RING/U−box superfamily protein | chr3:850391−851461 REVERSE LENGTH=356	334	356	1.00E−112	106.6	71.3	80.2
Rsa1.0_01046.1.g22842.t1	ref|NP_187006.2| uncharacterized protein [Arabidopsis thaliana] gi|332640436|gb|AEE73957.1| uncharacterized protein AT3G03560 [Arabidopsis thaliana]	523	521	0	99.6	87.6	92.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G03560.1 | Symbols: | unknown protein; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23490.1); Has 157 Blast hits to 146 proteins in 38 species: Archae − 3; Bacteria − 14; Metazoa − 8; Fungi − 0; Plants − 120; Viruses − 0; Other Eukaryotes − 12 (source: NCBI BLink). | chr3:853153−856486 REVERSE LENGTH=521	523	521	0	99.6	87.6	92.9
Rsa1.0_01046.1.g22843.t1	ref|XP_002882297.1| hypothetical protein ARALYDRAFT_477602 [Arabidopsis lyrata subsp. lyrata] gi|297328137|gb|EFH58556.1| hypothetical protein ARALYDRAFT_477602 [Arabidopsis lyrata subsp. lyrata]	601	606	0	100.8	88.5	93.3	hypothetical protein ARALYDRAFT_477602	gbpln	Arabidopsis lyrata	AT3G03570.1 | Symbols: | Protein of unknown function (DUF3550/UPF0682) | chr3:857013−860105 FORWARD LENGTH=607	601	607	0	101.0	88.7	93.7
Rsa1.0_01046.1.g22844.t1	ref|XP_002884398.1| hypothetical protein ARALYDRAFT_477605 [Arabidopsis lyrata subsp. lyrata] gi|297330238|gb|EFH60657.1| hypothetical protein ARALYDRAFT_477605 [Arabidopsis lyrata subsp. lyrata]	220	219	1.00E−122	99.5	95.0	98.6	hypothetical protein ARALYDRAFT_477605	gbpln	Arabidopsis lyrata	AT3G03600.1 | Symbols: RPS2 | ribosomal protein S2 | chr3:867847−868506 REVERSE LENGTH=219	220	219	1.00E−123	99.5	93.2	98.6

Rsa1.0_01046.1.g22845.t1	ref|XP_002884404.1| hypothetical protein ARALYDRAFT_477612 [Arabidopsis lyrata subsp. lyrata] gi|297330244|gb|EFH60663.1| hypothetical protein ARALYDRAFT_477612 [Arabidopsis lyrata subsp. lyrata]	323	321	1.00E-149	99.4	81.1	89.2	hypothetical protein ARALYDRAFT_477612	gbpln	Arabidopsis lyrata	AT3G03670.1 | Symbols: | Peroxidase superfamily protein | chr3:901985-903349 REVERSE LENGTH=321	323	321	1.00E-150	99.4	80.5	88.5
Rsa1.0_01046.1.g22846.t1	ref|XP_002882303.1| hypothetical protein ARALYDRAFT_896385 [Arabidopsis lyrata subsp. lyrata] gi|297328143|gb|EFH58562.1| hypothetical protein ARALYDRAFT_896385 [Arabidopsis lyrata subsp. lyrata]	890	922	0	103.6	89.8	92.6	hypothetical protein ARALYDRAFT_896385	gbpln	Arabidopsis lyrata	AT3G03710.1 | Symbols: RIF10, PNP | polyribonucleotide nucleotidyltransferase, putative | chr3:919542-924906 FORWARD LENGTH=922	890	922	0	103.6	88.2	91.3
Rsa1.0_01047.1.g22847.t1	ref|XP_002888575.1| hypothetical protein ARALYDRAFT_894432 [Arabidopsis lyrata subsp. lyrata] gi|297334416|gb|EFH64834.1| hypothetical protein ARALYDRAFT_894432 [Arabidopsis lyrata subsp. lyrata]	225	224	7.00E-89	99.6	74.7	82.2	hypothetical protein ARALYDRAFT_894432	gbpln	Arabidopsis lyrata	AT1G67080.1 | Symbols: ABA4 | abscisic acid (aba)-deficient 4 | chr1:25045405-25046681 REVERSE LENGTH=220	225	220	3.00E-91	97.8	70.2	81.3
Rsa1.0_01047.1.g22848.t1	ref|NP_176880.1| ribulose bisphosphate carboxylase small chain 1A [Arabidopsis thaliana] gi|27735223|sp|P10795.2|RBS1A_ARATH RecName: Full=Ribulose bisphosphate carboxylase small chain 1A, chloroplastic; Short=RuBisCO small subunit 1A; Flags: Precursor gi|11762170|gb|AAG40363.1|AF325011_1 000C10C11 [Arabidopsis thaliana] gi|15294200|gb|AAK95277.1|AF410291_1 F1O19.10/F1O19.10 [Arabidopsis thaliana] gi|4204274|gb|AAD10655.1| ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana] gi|15451002|gb|AAK96772.1| ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana] gi|15809842|gb|AAL06849.1| At1g67090/F1O19.10 [Arabidopsis thaliana] gi|16604426|gb|AAL24219.1| At1g67090/F1O19.10 [Arabidopsis thaliana] gi|16649141|gb|AAL24422.1| ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana] gi|17065072|gb|AAL32690.1| ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana] gi|17065270|gb|AAL32789.1| ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana] gi|17473628|gb|AAL38277.1| ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]	181	180	1.00E-93	99.4	89.0	92.8	ribulose bisphosphate carboxylase small chain 1A	gbpln	Arabidopsis thaliana	AT1G67090.1 | Symbols: RBCS1A | ribulose bisphosphate carboxylase small chain 1A | chr1:25048465-25049249 REVERSE LENGTH=180	181	180	4.00E-96	99.4	89.0	92.8
Rsa1.0_01047.1.g22849.t1	gb|AEJ89929.1| mannose-6-phosphate isomerase-like protein [Brassica rapa subsp. chinensis]	444	444	0	100.0	93.7	96.6	mannose-6-phosphate isomerase-like protein	gbpln	Brassica rapa	AT1G67070.1 | Symbols: DIN9, PMI2 | Mannose-6-phosphate isomerase, type I | chr1:25042324-25044412 FORWARD LENGTH=441	444	441	0	99.3	84.5	90.5
Rsa1.0_01047.1.g22850.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01047.1.g22851.t1	emb|CAB43904.1| putative protein [Arabidopsis thaliana] gi|7269745|emb|CAB81478.1| putative protein [Arabidopsis thaliana]	602	1415	0	235.0	58.0	74.6	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	602	1262	1.00E-46	209.6	15.6	23.6
Rsa1.0_01047.1.g22852.t1	ref|XP_002887098.1| hypothetical protein ARALYDRAFT_475801 [Arabidopsis lyrata subsp. lyrata] gi|297332939|gb|EFH63357.1| hypothetical protein ARALYDRAFT_475801 [Arabidopsis lyrata subsp. lyrata]	234	235	1.00E-129	100.4	99.1	99.1	hypothetical protein ARALYDRAFT_475801	gbpln	Arabidopsis lyrata	AT1G67060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 283 Blast hits to 281 proteins in 136 species: Archae - 0; Bacteria - 145; Metazoa - 0; Fungi - 65; Plants - 41; Viruses - 0; Other Eukaryotes - 32 (source: NCBI BLink). | chr1:25036729-25039123 FORWARD LENGTH=234	234	234	1.00E-130	100.0	97.9	99.1

Rsa1.0_01047.1.g22853.t1	ref|XP_002888573.1| hypothetical protein ARALYDRAFT_475800 [Arabidopsis lyrata subsp. lyrata] gi|297334414|gb|EFH64832.1| hypothetical protein ARALYDRAFT_475800 [Arabidopsis lyrata subsp. lyrata]	272	266	4.00E-86	97.8	75.0	80.9	hypothetical protein ARALYDRAFT_475800	gbpln	Arabidopsis lyrata	AT1G67050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G38320.1); Has 617 Blast hits to 318 proteins in 80 species: Archae - 0; Bacteria - 16; Metazoa - 141; Fungi - 62; Plants - 128; Viruses - 2; Other Eukaryotes - 268 (source: NCBI BLink). | chr1:25028862-25029656 REVERSE LENGTH=264	272	264	7.00E-87	97.1	74.3	79.0
Rsa1.0_01047.1.g22854.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01048.1.g22855.t1	gb|ACQ90602.1| putative C2H2 zinc finger protein [Eutrema halophilum]	195	607	3.00E-92	311.3	92.3	93.3	putative C2H2 zinc finger protein	gbpln	Eutrema halophilum	AT2G02070.1 | Symbols: AtIDD5, IDD5 | indeterminate(ID)-domain 5 | chr2:505523-509154 FORWARD LENGTH=602	195	602	1.00E-89	308.7	92.3	94.4
Rsa1.0_01048.1.g22856.t1	gb|ADQ43194.1| unknown [Eutrema parvulum]	485	519	0	107.0	89.1	92.8	unknown	gbpln	Eutrema parvulum	AT2G02080.1 | Symbols: AtIDD4, IDD4 | indeterminate(ID)-domain 4 | chr2:518328-521170 REVERSE LENGTH=516	485	516	0	106.4	84.5	90.1
Rsa1.0_01048.1.g22857.t1	gb|ACQ90605.1| SWI/SNF helicase-like protein [Eutrema halophilum]	815	768	0	94.2	85.0	88.0	SWI/SNF helicase-like protein	gbpln	Eutrema halophilum	AT2G02090.1 | Symbols: CHR19, CHA19, ETL1 | SNF2 domain-containing protein / helicase domain-containing protein | chr2:523481-526884 FORWARD LENGTH=763	815	763	0	93.6	84.0	87.0
Rsa1.0_01048.1.g22858.t6	ref|XP_002875115.1| hypothetical protein ARALYDRAFT_484136 [Arabidopsis lyrata subsp. lyrata] gi|297320953|gb|EFH51374.1| hypothetical protein ARALYDRAFT_484136 [Arabidopsis lyrata subsp. lyrata]	225	77	7.00E-25	34.2	23.6	26.2	hypothetical protein ARALYDRAFT_484136	gbpln	Arabidopsis lyrata	AT2G02130.1 | Symbols: PDF2.3, LCR68 | low-molecular-weight cysteine-rich 68 | chr2:540071-540407 FORWARD LENGTH=77	225	77	4.00E-26	34.2	22.2	25.3
Rsa1.0_01048.1.g22859.t1	gb|ADQ43199.1| unknown [Eutrema parvulum]	444	1128	0	254.1	85.8	89.9	unknown	gbpln	Eutrema parvulum	AT2G02148.1 | Symbols: | unknown protein. | chr2:547389-549316 REVERSE LENGTH=432	444	432	0	97.3	80.4	86.5
Rsa1.0_01048.1.g22860.t4	ref|XP_002876802.1| hypothetical protein ARALYDRAFT_322556 [Arabidopsis lyrata subsp. lyrata] gi|297322640|gb|EFH53061.1| hypothetical protein ARALYDRAFT_322556 [Arabidopsis lyrata subsp. lyrata]	326	492	5.00E-39	150.9	30.4	37.1	hypothetical protein ARALYDRAFT_322556	gbpln	Arabidopsis lyrata	AT2G02170.2 | Symbols: | Remorin family protein | chr2:556595-558610 REVERSE LENGTH=486	326	486	6.00E-41	149.1	30.4	37.1
Rsa1.0_01048.1.g22861.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01048.1.g22862.t1	ref|XP_002875118.1| hypothetical protein ARALYDRAFT_484143 [Arabidopsis lyrata subsp. lyrata] gi|297320956|gb|EFH51377.1| hypothetical protein ARALYDRAFT_484143 [Arabidopsis lyrata subsp. lyrata]	499	308	1.00E-141	61.7	50.1	52.7	hypothetical protein ARALYDRAFT_484143	gbpln	Arabidopsis lyrata	AT2G02180.1 | Symbols: TOM3 | tobamovirus multiplication protein 3 | chr2:560976-562961 FORWARD LENGTH=303	499	303	1.00E-140	60.7	50.3	52.5
Rsa1.0_01048.1.g22863.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01048.1.g22864.t1	gb|EOA24103.1| hypothetical protein CARUB_v10017334mg [Capsella rubella]	94	418	4.00E-32	444.7	85.1	92.6	hypothetical protein CARUB_v10017334mg	gbpln	Capsella rubella	AT2G02450.2 | Symbols: ANAC034, ANAC035, LOV1, NAC035 | NAC domain containing protein 35 | chr2:648044-650649 FORWARD LENGTH=414	94	414	3.00E-33	440.4	81.9	91.5
Rsa1.0_01049.1.g22865.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01049.1.g22866.t1	ref|XP_002893269.1| hypothetical protein ARALYDRAFT_472578 [Arabidopsis lyrata subsp. lyrata] gi|297339111|gb|EFH69528.1| hypothetical protein ARALYDRAFT_472578 [Arabidopsis lyrata subsp. lyrata]	218	205	5.00E-91	94.0	78.9	87.2	hypothetical protein ARALYDRAFT_472578	gbpln	Arabidopsis lyrata	AT1G23205.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:8234234-8234851 REVERSE LENGTH=205	218	205	2.00E-92	94.0	77.5	87.2
Rsa1.0_01049.1.g22867.t1	gb|EOA38769.1| hypothetical protein CARUB_v10010959mg [Capsella rubella]	497	489	0	98.4	88.7	92.8	hypothetical protein CARUB_v10010959mg	gbpln	Capsella rubella	AT1G23210.1 | Symbols: AtGH9B6, GH9B6 | glycosyl hydrolase 9B6 | chr1:8240174-8242129 FORWARD LENGTH=489	497	489	0	98.4	89.3	93.6
Rsa1.0_01049.1.g22868.t1	ref|XP_002890577.1| dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297336419|gb|EFH66836.1| dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata]	82	129	5.00E-30	157.3	85.4	87.8	dynein light chain type 1 family protein	gbpln	Arabidopsis lyrata	AT1G23220.1 | Symbols: | Dynein light chain type 1 family protein | chr1:8242614-8244136 FORWARD LENGTH=129	82	129	1.00E-31	157.3	84.1	86.6
Rsa1.0_01049.1.g22869.t1	ref|NP_191599.1| Mitochondrial transcription termination factor family protein [Arabidopsis thaliana] gi|7287988|emb|CAB81826.1| putative protein [Arabidopsis thaliana] gi|332646534|gb|AEE80055.1| Mitochondrial transcription termination factor family protein [Arabidopsis thaliana]	206	558	1.00E-14	270.9	20.4	24.8	Mitochondrial transcription termination factor family protein	gbpln	Arabidopsis thaliana	AT3G60400.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr3:22329093-22330769 FORWARD LENGTH=558	206	558	4.00E-17	270.9	20.4	24.8

Rsa1.0_01049.1.g22870.t2	ref|NP_001185071.1| uncharacterized protein [Arabidopsis thaliana] gi|332192239|gb|AEE30360.1| uncharacterized protein AT1G23230 [Arabidopsis thaliana]	1552	1592	0	102.6	85.4	92.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23230.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to salt stress; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Mediator complex subunit Med23 (InterPro:IPR021629). | chr1:8244481-8251741 FORWARD LENGTH=1592	1552	1592	0	102.6	85.4	92.3
Rsa1.0_01049.1.g22871.t1	ref|NP_564191.1| ubiquitin-conjugating enzyme E2 variant 1A [Arabidopsis thaliana] gi|75305892|sp|Q93YP0.1|UEV1A_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 variant 1A; Short=Ubc enzyme variant 1A; AltName: Full=Protein MMS ZWEI HOMOLOG 1 gi|16649053|gb|AAL24378.1| similar to DNA binding protein [Arabidopsis thaliana] gi|20259984|gb|AAM13339.1| similar to DNA binding protein [Arabidopsis thaliana] gi|332192244|gb|AEE30365.1| ubiquitin-conjugating enzyme E2 variant 1A [Arabidopsis thaliana]	158	158	1.00E-85	100.0	95.6	98.1	ubiquitin-conjugating enzyme E2 variant 1A	gbpln	Arabidopsis thaliana	AT1G23260.1 | Symbols: MMZ1, UEV1A | MMS ZWEI homologue 1 | chr1:8257209-8258573 REVERSE LENGTH=158	158	158	4.00E-88	100.0	95.6	98.1
Rsa1.0_01049.1.g22872.t1	gb|EOA36751.1| hypothetical protein CARUB_v10012590mg [Capsella rubella]	242	319	2.00E-27	131.8	41.7	52.9	hypothetical protein CARUB_v10012590mg	gbpln	Capsella rubella	AT1G31460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23270.1); Has 1251 Blast hits to 756 proteins in 185 species: Archae - 0; Bacteria - 295; Metazoa - 374; Fungi - 176; Plants - 58; Viruses - 17; Other Eukaryotes - 331 (source: NCBI BLink). | chr1:11261705-11262610 REVERSE LENGTH=301	242	301	8.00E-24	124.4	42.6	55.4
Rsa1.0_01049.1.g22873.t1	ref|NP_173743.1| 60S ribosomal protein L27a-2 [Arabidopsis thaliana] gi|297845396|ref|XP_002890579.1| RPL27A [Arabidopsis lyrata subsp. lyrata] gi|20143883|sp|Q9LR33.1|R27A2_ARATH RecName: Full=60S ribosomal protein L27a-2 gi|9295692|gb|AAF86998.1|AC005292_7 F26F24.13 [Arabidopsis thaliana] gi|11692928|gb|AAG40067.1|AF324716_1 At1g23290 [Arabidopsis thaliana] gi|13194820|gb|AAK15572.1|AF349525_1 putative 60s ribosomal protein l27a [Arabidopsis thaliana] gi|15294178|gb|AAK95266.1|AF410280_1 At1g23290/F26F24_23 [Arabidopsis thaliana] gi|23308283|gb|AAN18111.1| At1g23290/F26F24_23 [Arabidopsis thaliana] gi|297336421|gb|EFH66838.1| RPL27A [Arabidopsis lyrata subsp. lyrata] gi|332192247|gb|AEE30368.1| 60S ribosomal protein L27a-2 [Arabidopsis thaliana]	146	146	3.00E-74	100.0	94.5	97.3	60S ribosomal protein L27a-2	gbpln	Arabidopsis lyrata	AT1G23290.1 | Symbols: RPL27A, RPL27AB | Ribosomal protein L18e/L15 superfamily protein | chr1:8263007-8263447 FORWARD LENGTH=146	146	146	9.00E-77	100.0	94.5	97.3
Rsa1.0_01049.1.g22874.t5	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01049.1.g22875.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01049.1.g22876.t1	gb|EOA37442.1| hypothetical protein CARUB_v10011523mg [Capsella rubella]	402	388	1.00E-168	96.5	73.4	81.8	hypothetical protein CARUB_v10011523mg	gbpln	Capsella rubella	AT1G23320.1 | Symbols: TAR1 | tryptophan aminotransferase related 1 | chr1:8273423-8275350 REVERSE LENGTH=388	402	388	1.00E-169	96.5	73.6	81.3
Rsa1.0_01050.1.g22877.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01050.1.g22878.t3	gb|AAD25557.1|AC005850_14 Hypothetical protein [Arabidopsis thaliana]	563	404	1.00E-134	71.8	44.4	50.8	Hypothetical protein	gbpln	Arabidopsis thaliana	AT4G10890.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2439 (InterPro:IPR018838); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43722.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:6688833-6692937 FORWARD LENGTH=527	563	527	1.00E-53	93.6	18.3	22.2

Rsa1.0_01050.1.g22879.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	777	1352	3.00E-85	174.0	24.2	35.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	777	626	2.00E-16	80.6	6.8	10.7
Rsa1.0_01050.1.g22880.t1	ref|NP_567241.1| xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] gi|46576207|sp|O22775.1|GT2_ARATH RecName: Full=Putative glycosyltransferase 2; Short=AtGT2 gi|3193287|gb|AAC19271.1| T14P8.23 [Arabidopsis thaliana] gi|9716844|emb|CAC01674.1| putative golgi glycosyltransferase [Arabidopsis thaliana] gi|16209669|gb|AAL14393.1| AT4g02500/T10P11_20 [Arabidopsis thaliana] gi|22655160|gb|AAM98170.1| putative glycosyltransferase [Arabidopsis thaliana] gi|30387559|gb|AAP31945.1| At4g02500 [Arabidopsis thaliana] gi|332656781|gb|AEE82181.1| putative glycosyltransferase 2 [Arabidopsis thaliana]	489	461	0	94.3	89.4	91.8	xyloglucan 6-xylosyltransferase	gbpln	Arabidopsis thaliana	AT4G02500.1 | Symbols: ATXT2, XXT2, XT2 | UDP-xylosyltransferase 2 | chr4:1101638-1103345 FORWARD LENGTH=461	489	461	0	94.3	89.4	91.8
Rsa1.0_01050.1.g22881.t1	ref|NP_567236.1| DNA mismatch repair protein PMS2 [Arabidopsis thaliana] gi|75249525|sp|Q941I6.1|PMS1_ARATH RecName: Full=DNA mismatch repair protein PMS1; AltName: Full=Postmeiotic segregation protein 1; AltName: Full=Protein POSTMEIOTIC SEGREGATION 1 gi|15617225|gb|AAL01156.1| DNA mismatch repair protein [Arabidopsis thaliana] gi|332656775|gb|AEE82175.1| DNA mismatch repair protein PMS1 [Arabidopsis thaliana]	915	923	0	100.9	82.1	89.4	DNA mismatch repair protein PMS2	gbpln	Arabidopsis thaliana	AT4G02460.1 | Symbols: PMS1 | DNA mismatch repair protein, putative | chr4:1076306-1080510 REVERSE LENGTH=923	915	923	0	100.9	82.1	89.4
Rsa1.0_01050.1.g22882.t2	ref|NP_001154201.1| HSP20-like chaperone [Arabidopsis thaliana] gi|332656774|gb|AEE82174.1| HSP20-like chaperone [Arabidopsis thaliana]	361	240	3.00E-58	66.5	29.9	31.9	HSP20-like chaperone	gbpln	Arabidopsis thaliana	AT4G02450.2 | Symbols: | HSP20-like chaperones superfamily protein | chr4:1073987-1075765 REVERSE LENGTH=240	361	240	7.00E-61	66.5	29.9	31.9
Rsa1.0_01050.1.g22883.t1	gb|ACF48822.1| cyclophilin [Gossypium hirsutum]	275	173	9.00E-46	62.9	33.1	43.3	cyclophilin	gbpln	Gossypium hirsutum	AT2G16600.1 | Symbols: ROC3 | rotamase CYP 3 | chr2:7200862-7201383 FORWARD LENGTH=173	275	173	3.00E-47	62.9	32.7	43.6
Rsa1.0_01050.1.g22884.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01050.1.g22885.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01050.1.g22886.t2	gb|ABD65100.1| hypothetical protein 31.t00077 [Brassica oleracea]	304	391	8.00E-29	128.6	23.0	28.6	hypothetical protein 31.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01050.1.g22887.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	299	704	1.00E-104	235.5	59.2	62.5	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01050.1.g22888.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01050.1.g22889.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01051.1.g22890.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01051.1.g22891.t1	ref|XP_002883480.1| hypothetical protein ARALYDRAFT_479917 [Arabidopsis lyrata subsp. lyrata] gi|297329320|gb|EFH59739.1| hypothetical protein ARALYDRAFT_479917 [Arabidopsis lyrata subsp. lyrata]	315	347	1.00E-132	110.2	79.7	87.3	hypothetical protein ARALYDRAFT_479917	gbpln	Arabidopsis lyrata	AT3G24150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32295.1); Has 50 Blast hits to 50 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:8724273-8725586 REVERSE LENGTH=343	315	343	1.00E-132	108.9	81.9	88.6
Rsa1.0_01051.1.g22892.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1286	940	2.00E-90	73.1	15.0	19.7	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01051.1.g22893.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01052.1.g22894.t1	ref|XP_002866030.1| hypothetical protein ARALYDRAFT_357679 [Arabidopsis lyrata subsp. lyrata] gi|297796293|ref|XP_002866031.1| hypothetical protein ARALYDRAFT_331771 [Arabidopsis lyrata subsp. lyrata] gi|297311865|gb|EFH42289.1| hypothetical protein ARALYDRAFT_357679 [Arabidopsis lyrata subsp. lyrata] gi|297311866|gb|EFH42290.1| hypothetical protein ARALYDRAFT_331771 [Arabidopsis lyrata subsp. lyrata]	319	320	1.00E-149	100.3	87.8	92.5	hypothetical protein ARALYDRAFT_357679	gbpln	Arabidopsis lyrata	AT5G54230.1 | Symbols: MYB49, AtMYB49 | myb domain protein 49 | chr5:22016357-22017845 REVERSE LENGTH=319	319	319	1.00E-144	100.0	87.1	92.2
Rsa1.0_01052.1.g22895.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1288	1307	0	101.5	58.4	72.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1288	1262	1.00E-88	98.0	14.4	22.5
Rsa1.0_01052.1.g22896.t1	ref|NP_200105.1| uncharacterized protein [Arabidopsis thaliana] gi|10177107|dbj|BAB10441.1| unnamed protein product [Arabidopsis thaliana] gi|60547939|gb|AAX23933.1| hypothetical protein At5g52930 [Arabidopsis thaliana] gi|71905609|gb|AAZ52782.1| expressed protein [Arabidopsis thaliana] gi|332008896|gb|AED96279.1| uncharacterized protein AT5G52930 [Arabidopsis thaliana]	368	359	1.00E-116	97.6	58.2	68.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G52930.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21470370-21471449 FORWARD LENGTH=359	368	359	1.00E-118	97.6	58.2	68.8
Rsa1.0_01052.1.g22897.t1	ref|NP_200266.1| uncharacterized protein [Arabidopsis thaliana] gi|9758947|dbj|BAB09334.1| unnamed protein product [Arabidopsis thaliana] gi|332009126|gb|AED96509.1| uncharacterized protein AT5G54550 [Arabidopsis thaliana]	243	359	7.00E-76	147.7	63.0	72.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54550.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22158401-22159480 FORWARD LENGTH=359	243	359	2.00E-78	147.7	63.0	72.0
Rsa1.0_01052.1.g22898.t1	ref|NP_200241.1| uncharacterized protein [Arabidopsis thaliana] gi|9759503|dbj|BAB10753.1| cotton fiber expressed protein 1-like protein [Arabidopsis thaliana] gi|20466706|gb|AAM20670.1| cotton fiber expressed protein 1-like protein [Arabidopsis thaliana] gi|23198238|gb|AAN15646.1| cotton fiber expressed protein 1-like protein [Arabidopsis thaliana] gi|332009099|gb|AED96482.1| uncharacterized protein AT5G54300 [Arabidopsis thaliana]	294	326	9.00E-99	110.9	70.7	83.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G54300.1 | Symbols: | Protein of unknown function (DUF761) | chr5:22054270-22055342 REVERSE LENGTH=326	294	326	1.00E-101	110.9	70.7	83.0
Rsa1.0_01052.1.g22899.t1	gb|EOA12434.1| hypothetical protein CARUB_v10028316mg [Capsella rubella]	472	480	0	101.7	87.9	93.4	hypothetical protein CARUB_v10028316mg	gbpln	Capsella rubella	AT5G54310.1 | Symbols: NEV, AGD5 | ARF-GAP domain 5 | chr5:22057262-22061066 REVERSE LENGTH=483	472	483	0	102.3	86.7	92.6
Rsa1.0_01052.1.g22900.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01052.1.g22901.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1514	2726	0	180.1	52.8	71.8	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1514	158	5.00E-35	10.4	4.8	5.7
Rsa1.0_01053.1.g22902.t1	ref|XP_002866937.1| hypothetical protein ARALYDRAFT_490852 [Arabidopsis lyrata subsp. lyrata] gi|297312773|gb|EFH43196.1| hypothetical protein ARALYDRAFT_490852 [Arabidopsis lyrata subsp. lyrata]	379	611	0	161.2	93.7	96.3	hypothetical protein ARALYDRAFT_490852	gbpln	Arabidopsis lyrata	AT4G37670.2 | Symbols: NAGS2 | N-acetyl-l-glutamate synthase 2 | chr4:17696179-17698836 REVERSE LENGTH=613	379	613	0	161.7	93.1	95.8
Rsa1.0_01053.1.g22903.t1	ref|XP_002868978.1| hypothetical protein ARALYDRAFT_912572 [Arabidopsis lyrata subsp. lyrata] gi|297314814|gb|EFH45237.1| hypothetical protein ARALYDRAFT_912572 [Arabidopsis lyrata subsp. lyrata]	530	531	0	100.2	92.8	96.2	hypothetical protein ARALYDRAFT_912572	gbpln	Arabidopsis lyrata	AT4G37650.1 | Symbols: SHR, SGR7 | GRAS family transcription factor | chr4:17691871-17693466 FORWARD LENGTH=531	530	531	0	100.2	92.8	96.0
Rsa1.0_01053.1.g22904.t1	ref|XP_002866939.1| hypothetical protein ARALYDRAFT_490858 [Arabidopsis lyrata subsp. lyrata] gi|297312775|gb|EFH43198.1| hypothetical protein ARALYDRAFT_490858 [Arabidopsis lyrata subsp. lyrata]	375	369	0	98.4	84.8	89.3	hypothetical protein ARALYDRAFT_490858	gbpln	Arabidopsis lyrata	AT4G37610.1 | Symbols: BT5 | BTB and TAZ domain protein 5 | chr4:17670606-17671992 REVERSE LENGTH=368	375	368	0	98.1	83.5	89.3

Rsa1.0_01053.1.g22905.t1	gb|EOA16747.1| hypothetical protein CARUB_v10004955mg [Capsella rubella]	403	404	0	100.2	92.1	95.5	hypothetical protein CARUB_v10004955mg	gbpln	Capsella rubella	AT4G37580.1 | Symbols: HLS1, COP3, UNS2 | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr4:17658932-17660564 FORWARD LENGTH=403	403	403	0	100.0	91.6	95.3
Rsa1.0_01053.1.g22906.t1	gb|ACQ44224.1| unknown [Arabis alpina]	116	291	1.00E-23	250.9	50.0	68.1	unknown	gbpln	Arabis alpina	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	116	673	6.00E-11	580.2	32.8	55.2
Rsa1.0_01053.1.g22907.t1	gb|EOA18482.1| hypothetical protein CARUB_v10007029mg [Capsella rubella]	460	453	0	98.5	90.7	93.9	hypothetical protein CARUB_v10007029mg	gbpln	Capsella rubella	AT4G37560.1 | Symbols: | Acetamidase/Formamidase family protein | chr4:17646489-17648457 FORWARD LENGTH=452	460	452	0	98.3	90.2	93.3
Rsa1.0_01053.1.g22908.t2	ref|NP_568029.1| formamidase [Arabidopsis thaliana] gi|23297225|gb|AAN12921.1| putative formamidase [Arabidopsis thaliana] gi|332661412|gb|AEE86812.1| acetamidase/Formamidase family protein [Arabidopsis thaliana]	467	452	0	96.8	85.9	91.0	formamidase	gbpln	Arabidopsis thaliana	AT4G37560.1 | Symbols: | Acetamidase/Formamidase family protein | chr4:17646489-17648457 FORWARD LENGTH=452	467	452	0	96.8	85.9	91.0
Rsa1.0_01053.1.g22909.t1	gb|AAM64844.1| unknown [Arabidopsis thaliana]	243	240	5.00E-96	98.8	77.4	83.1	unknown	gbpln	Arabidopsis thaliana	AT4G37540.1 | Symbols: LBD39 | LOB domain-containing protein 39 | chr4:17639649-17640509 REVERSE LENGTH=240	243	240	6.00E-98	98.8	76.5	81.1
Rsa1.0_01053.1.g22910.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01053.1.g22911.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01054.1.g22912.t1	emb|CAN72057.1| hypothetical protein VITISV_026927 [Vitis vinifera]	131	417	2.00E-11	318.3	35.9	55.0	hypothetical protein VITISV_026927	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01054.1.g22913.t1	ref|NP_182227.1| pectinesterase 5 [Arabidopsis thaliana] gi|61213926|sp|Q5MFV8.2|PME5_ARATH RecName: Full=Pectinesterase 5; Short=PE 5; AltName: Full=Pectin methylesterase 5; Short=AtPME5; AltName: Full=Pectin methylesterase 67; Short=AtPME67; AltName: Full=Protein VANGUARD 1; Flags: Precursor gi|3522958|gb|AAC34240.1| putative pectinesterase [Arabidopsis thaliana] gi|20147201|gb|AAM10316.1| At2g47040/F14M4.13 [Arabidopsis thaliana] gi|24796998|gb|AAN64511.1| At2g47040/F14M4.13 [Arabidopsis thaliana] gi|330255697|gb|AEC10791.1| pectinesterase 5 [Arabidopsis thaliana]	595	595	0	100.0	84.0	92.9	pectinesterase 5	gbpln	Arabidopsis thaliana	AT2G47040.1 | Symbols: VGD1 | Plant invertase/pectin methylesterase inhibitor superfamily | chr2:19328186-19330060 REVERSE LENGTH=595	595	595	0	100.0	84.0	92.9
Rsa1.0_01054.1.g22914.t1	ref|NP_182228.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|3522940|gb|AAC34222.1| putative pectinesterase [Arabidopsis thaliana] gi|26451376|dbj|BAC42788.1| putative pectinesterase [Arabidopsis thaliana] gi|91806367|gb|ABE65911.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] gi|330255698|gb|AEC10792.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	216	216	1.00E-104	100.0	83.3	91.7	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT2G47050.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr2:19331927-19332577 REVERSE LENGTH=216	216	216	1.00E-106	100.0	83.3	91.7

Rsa1.0_01054.1.g22915.t1	ref|NP_191784.1| ubiquitin-40S ribosomal protein S27a-3 [Arabidopsis thaliana] gi|302393706|sp|P59233.2|R27AC_ARATH RecName: Full=Ubiquitin-40S ribosomal protein S27a-3; Contains: RecName: Full=Ubiquitin; Contains: RecName: Full=40S ribosomal protein S27a-3; Flags: Precursor gi|166934|gb|AAA32906.1| ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] gi|6899935|emb|CAB71885.1| ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] gi|15529190|gb|AAK97689.1| AT3g62250/T17J13_210 [Arabidopsis thaliana] gi|21537196|gb|AAM61537.1| ubiquitin extension protein UBQ5 [Arabidopsis thaliana] gi|22655050|gb|AAM98116.1| At3g62250/T17J13_210 [Arabidopsis thaliana] gi|110742096|dbj|BAE98979.1| ubiquitin extension protein [Arabidopsis thaliana] gi|332646806|gb|AEE80327.1| ubiquitin-40S ribosomal protein S27a-3 [Arabidopsis thaliana]	157	157	1.00E-85	100.0	98.7	99.4	ubiquitin-40S ribosomal protein S27a-3	gbpln	Arabidopsis thaliana	AT3G62250.1 | Symbols: UBQ5 | ubiquitin 5 | chr3:23037138-23037611 FORWARD LENGTH=157	157	157	3.00E-88	100.0	98.7	99.4
Rsa1.0_01054.1.g22916.t1	ref|XP_002882107.1| hypothetical protein ARALYDRAFT_322360 [Arabidopsis lyrata subsp. lyrata] gi|297327946|gb|EFH58366.1| hypothetical protein ARALYDRAFT_322360 [Arabidopsis lyrata subsp. lyrata]	222	298	3.00E-77	134.2	65.8	73.9	hypothetical protein ARALYDRAFT_322360	gbpln	Arabidopsis lyrata	AT2G47115.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10660.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:19345376-19346864 REVERSE LENGTH=300	222	300	2.00E-77	135.1	65.3	72.5
Rsa1.0_01054.1.g22917.t1	gb|AEZ01592.1| 3-beta-hydroxysteroid dehydrogenase 2 [Erysimum crepidifolium]	258	257	1.00E-117	99.6	79.5	87.2	3-beta-hydroxysteroid dehydrogenase 2	gbpln	Erysimum crepidifolium	AT2G47130.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:19349627-19350481 REVERSE LENGTH=257	258	257	1.00E-118	99.6	78.7	86.4
Rsa1.0_01054.1.g22918.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1591	1501	0	94.3	43.6	54.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT2G47130.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:19349627-19350481 REVERSE LENGTH=257	1591	257	1.00E-112	16.2	12.4	13.5
Rsa1.0_01054.1.g22919.t1	gb|ADF30181.1| boron transporter [Brassica napus] gi|294713704|gb|ADF30189.1| boron transporter [Brassica napus]	703	703	0	100.0	98.0	99.0	boron transporter	gbpln	Brassica napus	AT2G47160.1 | Symbols: BOR1 | HCO3- transporter family | chr2:19357740-19360787 REVERSE LENGTH=704	703	704	0	100.1	95.3	98.2
Rsa1.0_01054.1.g22920.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01055.1.g22921.t2	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	866	1501	0	173.3	44.1	54.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	866	1262	1.00E-48	145.7	11.7	17.0
Rsa1.0_01055.1.g22922.t1	ref|NP_176875.1| uncharacterized protein [Arabidopsis thaliana] gi|9755453|gb|AAF98214.1|AC007152_10 Hypothetical protein [Arabidopsis thaliana] gi|332196468|gb|AEE34589.1| uncharacterized protein AT1G67040 [Arabidopsis thaliana]	751	826	0	110.0	74.0	82.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G67040.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26910.3); Has 89 Blast hits to 84 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 5; Fungi - 2; Plants - 82; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25019105-25021922 REVERSE LENGTH=826	751	826	0	110.0	74.0	82.0
Rsa1.0_01055.1.g22923.t1	ref|NP_001185335.1| uncharacterized protein [Arabidopsis thaliana] gi|60547655|gb|AAX23791.1| hypothetical protein At1g67035 [Arabidopsis thaliana] gi|332196467|gb|AEE34588.1| uncharacterized protein AT1G67035 [Arabidopsis thaliana]	226	229	8.00E-46	101.3	51.8	62.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G67035.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G38300.1). | chr1:25018173-25018862 FORWARD LENGTH=229	226	229	3.00E-48	101.3	51.8	62.4
Rsa1.0_01055.1.g22924.t1	gb|EOA34388.1| hypothetical protein CARUB_v10021913mg, partial [Capsella rubella]	861	864	0	100.3	63.2	73.4	hypothetical protein CARUB_v10021913mg, partial	gbpln	Capsella rubella	AT1G67000.1 | Symbols: | Protein kinase superfamily protein | chr1:25004217-25007604 REVERSE LENGTH=892	861	892	0	103.6	63.5	75.5

<table>
<tr><td>Rsa1.0_01055.1.g22925.t7</td><td>ref|XP_002276757.1| PREDICTED: probable glycerophosphoryl diester phosphodiesterase 1 [Vitis vinifera] gi|297737518|emb|CBI26719.3| unnamed protein product [Vitis vinifera]</td><td>960</td><td>757</td><td>0</td><td>78.9</td><td>40.5</td><td>54.2</td><td>PREDICTED: probable glycerophosphoryl diester phosphodiesterase 1</td><td>gbpln</td><td>Vitis vinifera</td><td>AT1G66980.1 | Symbols: SNC4 | suppressor of npr1-1 constitutive 4 | chr1:24997491-25001961 REVERSE LENGTH=1118</td><td>960</td><td>1118</td><td>0</td><td>116.5</td><td>33.1</td><td>37.8</td></tr>
<tr><td>Rsa1.0_01055.1.g22926.t1</td><td>gb|EOA16078.1| hypothetical protein CARUB_v10004210mg [Capsella rubella]</td><td>653</td><td>757</td><td>0</td><td>115.9</td><td>76.4</td><td>87.4</td><td>hypothetical protein CARUB_v10004210mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G66970.1 | Symbols: SVL2 | SHV3-like 2 | chr1:24992746-24996005 REVERSE LENGTH=763</td><td>653</td><td>763</td><td>0</td><td>116.8</td><td>75.5</td><td>86.4</td></tr>
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<tr><td>Rsa1.0_01055.1.g22928.t1</td><td>ref|XP_002888563.1| hypothetical protein ARALYDRAFT_894412 [Arabidopsis lyrata subsp. lyrata] gi|297334404|gb|EFH64822.1| hypothetical protein ARALYDRAFT_894412 [Arabidopsis lyrata subsp. lyrata]</td><td>276</td><td>249</td><td>4.00E-92</td><td>90.2</td><td>62.0</td><td>75.7</td><td>hypothetical protein ARALYDRAFT_894412</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G66940.1 | Symbols: | protein kinase-related | chr1:24973201-24974684 REVERSE LENGTH=332</td><td>276</td><td>332</td><td>7.00E-74</td><td>120.3</td><td>51.4</td><td>62.3</td></tr>
<tr><td>Rsa1.0_01055.1.g22929.t1</td><td>ref|NP_180979.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|3337363|gb|AAC27408.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana] gi|91805481|gb|ABE65469.1| hypothetical protein At2g34320 [Arabidopsis thaliana] gi|330253864|gb|AEC08958.1| RNase H domain-containing protein [Arabidopsis thaliana]</td><td>271</td><td>292</td><td>2.00E-59</td><td>107.7</td><td>41.0</td><td>63.8</td><td>RNase H domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292</td><td>271</td><td>292</td><td>6.00E-62</td><td>107.7</td><td>41.0</td><td>63.8</td></tr>
<tr><td>Rsa1.0_01055.1.g22930.t1</td><td>gb|EOA34832.1| hypothetical protein CARUB_v10022414mg [Capsella rubella]</td><td>220</td><td>635</td><td>5.00E-67</td><td>288.6</td><td>56.8</td><td>69.5</td><td>hypothetical protein CARUB_v10022414mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G66880.1 | Symbols: | Protein kinase superfamily protein | chr1:24946928-24955438 FORWARD LENGTH=1296</td><td>220</td><td>1296</td><td>2.00E-64</td><td>589.1</td><td>56.4</td><td>68.6</td></tr>
<tr><td>Rsa1.0_01055.1.g22931.t1</td><td>gb|EOA34832.1| hypothetical protein CARUB_v10022414mg [Capsella rubella]</td><td>346</td><td>635</td><td>1.00E-158</td><td>183.5</td><td>79.2</td><td>86.1</td><td>hypothetical protein CARUB_v10022414mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G66980.1 | Symbols: SNC4 | suppressor of npr1-1 constitutive 4 | chr1:24997491-25001961 REVERSE LENGTH=1118</td><td>346</td><td>1118</td><td>1.00E-152</td><td>323.1</td><td>74.6</td><td>84.4</td></tr>
<tr><td>Rsa1.0_01055.1.g22932.t1</td><td>gb|EOA34388.1| hypothetical protein CARUB_v10021913mg, partial [Capsella rubella]</td><td>589</td><td>864</td><td>0</td><td>146.7</td><td>64.3</td><td>75.9</td><td>hypothetical protein CARUB_v10021913mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G67000.1 | Symbols: | Protein kinase superfamily protein | chr1:25004217-25007604 REVERSE LENGTH=892</td><td>589</td><td>892</td><td>0</td><td>151.4</td><td>64.9</td><td>74.5</td></tr>
<tr><td>Rsa1.0_01056.1.g22933.t2</td><td>gb|AAC69377.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>922</td><td>1328</td><td>0</td><td>144.0</td><td>37.5</td><td>47.9</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G23450.1 | Symbols: | Protein kinase superfamily protein | chr2:9988926-9991244 REVERSE LENGTH=708</td><td>922</td><td>708</td><td>4.00E-58</td><td>76.8</td><td>11.9</td><td>13.2</td></tr>
<tr><td>Rsa1.0_01056.1.g22934.t1</td><td>gb|EOA18653.1| hypothetical protein CARUB_v10007229mg [Capsella rubella]</td><td>346</td><td>335</td><td>1.00E-143</td><td>96.8</td><td>75.7</td><td>81.2</td><td>hypothetical protein CARUB_v10007229mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G38380.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: Cation efflux family protein (TAIR:AT2G04620.1); Has 123 Blast hits to 121 proteins in 39 species: Archae - 0; Bacteria - 0; Metazoa - 69; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr5:15345660-15348217 FORWARD LENGTH=361</td><td>346</td><td>361</td><td>1.00E-144</td><td>104.3</td><td>76.6</td><td>84.1</td></tr>
<tr><td>Rsa1.0_01056.1.g22935.t1</td><td>gb|EOA16775.1| hypothetical protein CARUB_v10004994mg [Capsella rubella]</td><td>338</td><td>392</td><td>1.00E-160</td><td>116.0</td><td>82.8</td><td>89.3</td><td>hypothetical protein CARUB_v10004994mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G38360.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:15332289-15333556 REVERSE LENGTH=239</td><td>338</td><td>239</td><td>1.00E-111</td><td>70.7</td><td>58.9</td><td>63.0</td></tr>
<tr><td>Rsa1.0_01056.1.g22936.t1</td><td>gb|AAF97981.1|AC000103_31 F21J9.3 [Arabidopsis thaliana]</td><td>273</td><td>457</td><td>4.00E-95</td><td>167.4</td><td>57.5</td><td>66.7</td><td>F21J9.3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343</td><td>273</td><td>343</td><td>2.00E-48</td><td>125.6</td><td>32.6</td><td>38.1</td></tr>
<tr><td>Rsa1.0_01056.1.g22937.t1</td><td>ref|XP_002865041.1| hypothetical protein ARALYDRAFT_920024 [Arabidopsis lyrata subsp. lyrata] gi|297310876|gb|EFH41300.1| hypothetical protein ARALYDRAFT_920024 [Arabidopsis lyrata subsp. lyrata]</td><td>176</td><td>246</td><td>3.00E-40</td><td>139.8</td><td>57.4</td><td>67.6</td><td>hypothetical protein ARALYDRAFT_920024</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G10230.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24380.1); Has 216 Blast hits to 216 proteins in 30 species: Archae - 0; Bacteria - 8; Metazoa - 10; Fungi - 4; Plants - 160; Viruses - 0; Other Eukaryotes - 34 (source: NCBI BLink). | chr4:6366261-6367185 FORWARD LENGTH=273</td><td>176</td><td>273</td><td>9.00E-25</td><td>155.1</td><td>33.0</td><td>49.4</td></tr>
</table>

Rsa1.0_01056.1.g22938.t5	gb|EOA16130.1| hypothetical protein CARUB_v10004265mg [Capsella rubella]	600	701	1.00E-138	116.8	49.7	65.7	hypothetical protein CARUB_v10004265mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	600	696	4.00E-38	116.0	24.5	45.2
Rsa1.0_01056.1.g22939.t1	emb|CAN80895.1| hypothetical protein VITISV_031817 [Vitis vinifera]	165	324	9.00E-58	196.4	64.2	81.2	hypothetical protein VITISV_031817	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01056.1.g22940.t1	ref|XP_002870853.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316689|gb|EFH47112.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	246	241	1.00E-117	98.0	85.0	90.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G38290.2 | Symbols: | Peptidyl-tRNA hydrolase family protein | chr5:15303491-15305381 FORWARD LENGTH=250	246	250	1.00E-118	101.6	84.1	89.4
Rsa1.0_01056.1.g22941.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01056.1.g22942.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01056.1.g22943.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01056.1.g22944.t1	ref|NP_199370.1| Ulp1 protease family protein [Arabidopsis thaliana] gi|10177930|dbj|BAB11195.1| unnamed protein product [Arabidopsis thaliana] gi|332007886|gb|AED95269.1| Ulp1 protease family protein [Arabidopsis thaliana]	188	921	3.00E-37	489.9	37.2	55.9	Ulp1 protease family protein	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	188	921	1.00E-39	489.9	37.2	55.9
Rsa1.0_01057.1.g22945.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01057.1.g22946.t1	ref|XP_002892251.1| hypothetical protein ARALYDRAFT_470476 [Arabidopsis lyrata subsp. lyrata] gi|297338093|gb|EFH68510.1| hypothetical protein ARALYDRAFT_470476 [Arabidopsis lyrata subsp. lyrata]	102	519	1.00E-41	508.8	89.2	92.2	hypothetical protein ARALYDRAFT_470476	gbpln	Arabidopsis lyrata	AT1G04910.1 | Symbols: | O-fucosyltransferase family protein | chr1:1388101-1391074 REVERSE LENGTH=519	102	519	4.00E-43	508.8	87.3	91.2
Rsa1.0_01057.1.g22947.t3	gb|AAC13586.1| F7N22.14 gene product [Arabidopsis thaliana] gi|8843871|dbj|BAA97397.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1055	961	1.00E-63	91.1	13.6	18.6	F7N22.14 gene product	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	1055	921	3.00E-34	87.3	8.0	13.3
Rsa1.0_01057.1.g22948.t1	gb|AAD23022.1| En/Spm-like transposon protein [Arabidopsis thaliana]	155	155	2.00E-32	100.0	47.7	60.6	En/Spm-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01057.1.g22949.t13	gb|AAC13586.1| F7N22.14 gene product [Arabidopsis thaliana] gi|8843871|dbj|BAA97397.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	921	961	5.00E-84	104.3	18.0	23.8	F7N22.14 gene product	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	921	921	1.00E-48	100.0	11.6	17.8
Rsa1.0_01057.1.g22950.t1	ref|XP_002890421.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297336263|gb|EFH66680.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata]	228	246	1.00E-109	107.9	86.8	91.2	zinc-binding family protein	gbpln	Arabidopsis lyrata	AT1G21000.2 | Symbols: | PLATZ transcription factor family protein | chr1:7338013-7339088 FORWARD LENGTH=243	228	243	1.00E-110	106.6	86.0	90.8
Rsa1.0_01057.1.g22951.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01057.1.g22952.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01057.1.g22953.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01057.1.g22954.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01057.1.g22955.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01057.1.g22956.t1	gb|ABD65162.1| hypothetical protein 40.t00047 [Brassica oleracea]	166	203	8.00E-62	122.3	66.9	80.1	hypothetical protein 40.t00047	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01057.1.g22957.t2	gb|AAD31079.1| Mutator-like transposase [Arabidopsis thaliana]	755	819	0	108.5	58.9	73.5	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	755	785	4.00E-24	104.0	16.3	28.5
Rsa1.0_01057.1.g22958.t6	gb|AAN60795.1| ascorbate peroxidase [Brassica juncea]	96	250	4.00E-27	260.4	72.9	79.2	ascorbate peroxidase	gbpln	Brassica juncea	AT1G07890.8 | Symbols: APX1, MEE6, CS1, ATAPX1, ATAPX01 | ascorbate peroxidase 1 | chr1:2438005-2439435 FORWARD LENGTH=250	96	250	4.00E-28	260.4	69.8	77.1
Rsa1.0_01058.1.g22959.t2	ref|NP_177414.1| phospholipid-translocating ATPase [Arabidopsis thaliana] gi|12229669|sp|Q9SGG3.1|ALA5_ARATH RecName: Full=Putative phospholipid-transporting ATPase 5; Short=AtALA5; AltName: Full=Aminophospholipid flippase 5 gi|12323764|gb|AAG51844.1|AC010926_7 putative P-type transporting ATPase; 43607-39026 [Arabidopsis thaliana] gi|332197241|gb|AEE35362.1| putative phospholipid-transporting ATPase 5 [Arabidopsis thaliana]	1321	1228	0	93.0	69.7	72.3	phospholipid-translocating ATPase	gbpln	Arabidopsis thaliana	AT1G72700.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:27366910-27371491 FORWARD LENGTH=1228	1321	1228	0	93.0	69.7	72.3

Rsa1.0_01058.1.g22960.t2	ref|XP_002888888.1| hypothetical protein ARALYDRAFT_895120 [Arabidopsis lyrata subsp. lyrata] gi|297334729|gb|EFH65147.1| hypothetical protein ARALYDRAFT_895120 [Arabidopsis lyrata subsp. lyrata]	355	355	0	100.0	89.9	94.6	hypothetical protein ARALYDRAFT_895120	gbpln	Arabidopsis lyrata	AT1G72680.1 | Symbols: ATCAD1, CAD1 | cinnamyl-alcohol dehydrogenase | chr1:27359346-27360876 REVERSE LENGTH=355	355	355	0	100.0	89.3	94.4
Rsa1.0_01058.1.g22961.t1	ref|XP_002888887.1| IQ-domain 8 [Arabidopsis lyrata subsp. lyrata] gi|297334728|gb|EFH65146.1| IQ-domain 8 [Arabidopsis lyrata subsp. lyrata]	411	414	0	100.7	92.0	95.1	IQ-domain 8	gbpln	Arabidopsis lyrata	AT1G72670.1 | Symbols: iqd8 | IQ-domain 8 | chr1:27356898-27358657 REVERSE LENGTH=414	411	414	0	100.7	92.0	95.4
Rsa1.0_01058.1.g22962.t1	ref|XP_002887445.1| hypothetical protein ARALYDRAFT_476401 [Arabidopsis lyrata subsp. lyrata] gi|297333286|gb|EFH63704.1| hypothetical protein ARALYDRAFT_476401 [Arabidopsis lyrata subsp. lyrata]	1021	399	0	39.1	38.1	38.7	hypothetical protein ARALYDRAFT_476401	gbpln	Arabidopsis lyrata	AT1G72660.3 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:27354161-27356543 FORWARD LENGTH=399	1021	399	0	39.1	37.8	38.4
Rsa1.0_01058.1.g22963.t1	ref|XP_002888886.1| hypothetical protein ARALYDRAFT_476397 [Arabidopsis lyrata subsp. lyrata] gi|297334727|gb|EFH65145.1| hypothetical protein ARALYDRAFT_476397 [Arabidopsis lyrata subsp. lyrata]	385	311	1.00E-144	80.8	67.0	72.7	hypothetical protein ARALYDRAFT_476397	gbpln	Arabidopsis lyrata	AT1G72640.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:27346409-27348147 REVERSE LENGTH=312	385	312	2.33E-156	81.0	67.5	73.2
Rsa1.0_01058.1.g22964.t1	ref|NP_565044.1| protein ELF4-like 2 [Arabidopsis thaliana] gi|75165123|sp|Q94BS8.1|EF4L2_ARATH RecName: Full=Protein ELF4-LIKE 2 gi|14532584|gb|AAK64020.1| unknown protein [Arabidopsis thaliana] gi|19310623|gb|AAL85042.1| unknown protein [Arabidopsis thaliana] gi|332197229|gb|AEE35350.1| protein ELF4-like 2 [Arabidopsis thaliana]	142	119	5.00E-54	83.8	75.4	78.9	protein ELF4-like 2	gbpln	Arabidopsis thaliana	AT1G72630.1 | Symbols: ELF4-L2 | ELF4-like 2 | chr1:27344988-27345347 FORWARD LENGTH=119	142	119	1.00E-56	83.8	75.4	78.9
Rsa1.0_01058.1.g22965.t1	gb|AAX35339.1| oxalic acid oxidase [Brassica napus]	207	207	1.00E-103	100.0	97.1	98.1	oxalic acid oxidase	gbpln	Brassica napus	AT1G72610.1 | Symbols: GLP1, ATGER1, GER1 | germin-like protein 1 | chr1:27339302-27339928 REVERSE LENGTH=208	207	208	4.00E-95	100.5	87.9	93.7
Rsa1.0_01058.1.g22966.t1	gb|EOA35874.1| hypothetical protein CARUB_v10021124mg [Capsella rubella]	67	138	6.00E-11	206.0	53.7	55.2	hypothetical protein CARUB_v10021124mg	gbpln	Capsella rubella	AT1G72600.2 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:27338272-27338679 FORWARD LENGTH=135	67	135	4.00E-12	201.5	73.1	82.1
Rsa1.0_01058.1.g22967.t2	ref|NP_177400.2| protein PAUSED [Arabidopsis thaliana] gi|145327223|ref|NP_001077813.1| protein PAUSED [Arabidopsis thaliana] gi|334183864|ref|NP_001185383.1| protein PAUSED [Arabidopsis thaliana] gi|75140113|sp|Q7PC79.1|XPOT_ARATH RecName: Full=Exportin-T; AltName: Full=Exportin(tRNA); AltName: Full=Protein PAUSED; AltName: Full=tRNA exportin gi|34303902|tpg|DAA01277.1| TPA_exp: exportin-t [Arabidopsis thaliana] gi|332197219|gb|AEE35340.1| protein PAUSED [Arabidopsis thaliana] gi|332197220|gb|AEE35341.1| exportin-T [Arabidopsis thaliana] gi|332197221|gb|AEE35342.1| protein PAUSED [Arabidopsis thaliana]	996	988	0	99.2	80.4	88.0	protein PAUSED	gbpln	Arabidopsis thaliana	AT1G72560.3 | Symbols: PSD | ARM repeat superfamily protein | chr1:27325026-27329467 REVERSE LENGTH=988	996	988	0	99.2	80.4	88.0
Rsa1.0_01058.1.g22968.t1	gb|EOA33525.1| hypothetical protein CARUB_v10019905mg, partial [Capsella rubella]	99	674	3.00E-22	680.8	44.4	60.6	hypothetical protein CARUB_v10019905mg, partial	gbpln	Capsella rubella	AT1G69910.1 | Symbols: | Protein kinase superfamily protein | chr1:26330166-26332076 FORWARD LENGTH=636	99	636	3.00E-24	642.4	43.4	51.5
Rsa1.0_01058.1.g22969.t1	gb|EOA34366.1| hypothetical protein CARUB_v10021890mg [Capsella rubella]	455	448	0	98.5	86.8	93.2	hypothetical protein CARUB_v10021890mg	gbpln	Capsella rubella	AT1G72540.1 | Symbols: | Protein kinase superfamily protein | chr1:27314932-27316669 REVERSE LENGTH=450	455	450	0	98.9	88.6	93.6
Rsa1.0_01058.1.g22970.t3	gb|EOA35762.1| hypothetical protein CARUB_v10020995mg [Capsella rubella]	198	188	2.00E-29	94.9	42.9	51.0	hypothetical protein CARUB_v10020995mg	gbpln	Capsella rubella	AT1G72530.1 | Symbols: | plastid developmental protein DAG, putative | chr1:27312999-27313937 FORWARD LENGTH=188	198	188	3.00E-28	94.9	40.9	48.5
Rsa1.0_01059.1.g22971.t1	gb|EOA20379.1| hypothetical protein CARUB_v10000692mg [Capsella rubella]	539	530	0	98.3	67.9	77.6	hypothetical protein CARUB_v10000692mg	gbpln	Capsella rubella	AT5G04110.1 | Symbols: GYRB3 | DNA GYRASE B3 | chr5:1110757-1114112 REVERSE LENGTH=546	539	546	0	101.3	67.9	79.0
Rsa1.0_01059.1.g22972.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01059.1.g22973.t1	ref|NP_196026.1| putative methyltransferase PMT7 [Arabidopsis thaliana] gi|75181220|sp|Q9LZA4.1|PMT7_ARATH RecName: Full=Probable methyltransferase PMT7 gi|7406416|emb|CAB85526.1| putative protein [Arabidopsis thaliana] gi|18086557|gb|AAL57703.1| AT5g04060/F8F6_270 [Arabidopsis thaliana] gi|332003309|gb|AED90692.1| putative methyltransferase PMT7 [Arabidopsis thaliana]	688	600	0	87.2	75.7	80.4	putative methyltransferase PMT7	gbpln	Arabidopsis thaliana	AT5G04060.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:1099271-1101810 FORWARD LENGTH=600	688	600	0	87.2	75.7	80.4
Rsa1.0_01059.1.g22974.t1	emb|CAB85525.1| maturase-like protein [Arabidopsis thaliana]	755	696	0	92.2	77.5	85.3	maturase-like protein	gbpln	Arabidopsis thaliana	AT5G04050.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase) | chr5:1096092-1097894 FORWARD LENGTH=600	755	600	0	79.5	67.0	73.9
Rsa1.0_01059.1.g22975.t1	gb|AAD09173.1| putative glutamate receptor [Arabidopsis thaliana]	635	808	0	127.2	54.5	63.1	putative glutamate receptor	gbpln	Arabidopsis thaliana	AT3G04110.1 | Symbols: GLR1, ATGLR1.1, GLR1.1 | glutamate receptor 1.1 | chr3:1077361-1080236 FORWARD LENGTH=808	635	808	0	127.2	54.3	63.0
Rsa1.0_01059.1.g22976.t2	ref|NP_196024.1| triacylglycerol lipase SDP1 [Arabidopsis thaliana] gi|75181222|sp|Q9LZA6.1|SDP1_ARATH RecName: Full=Triacylglycerol lipase SDP1; AltName: Full=Protein SUGAR-DEPENDENT 1 gi|7406414|emb|CAB85524.1| putative protein [Arabidopsis thaliana] gi|22531263|gb|AAM97135.1| putative protein [Arabidopsis thaliana] gi|332003304|gb|AED90687.1| triacylglycerol lipase SDP1 [Arabidopsis thaliana]	803	825	0	102.7	88.7	93.3	triacylglycerol lipase SDP1	gbpln	Arabidopsis thaliana	AT5G04040.1 | Symbols: SDP1 | Patatin-like phospholipase family protein | chr5:1090346-1093003 FORWARD LENGTH=825	803	825	0	102.7	88.7	93.3
Rsa1.0_01059.1.g22977.t1	ref|XP_002873132.1| hypothetical protein ARALYDRAFT_908281 [Arabidopsis lyrata subsp. lyrata] gi|297318969|gb|EFH49391.1| hypothetical protein ARALYDRAFT_908281 [Arabidopsis lyrata subsp. lyrata]	82	75	9.00E-16	91.5	53.7	67.1	hypothetical protein ARALYDRAFT_908281	gbpln	Arabidopsis lyrata	AT5G04030.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: egg cell; Has 1807 Blast hits to 1807 proteins in 277 species: Archae – 0; Bacteria – 0; Metazoa – 736; Fungi – 347; Plants – 385; Viruses – 0; Other Eukaryotes – 339 (source: NCBI BLink). | chr5:1088462-1088692 REVERSE LENGTH=76	82	76	1.00E-14	92.7	48.8	63.4
Rsa1.0_01059.1.g22978.t1	ref|XP_002873131.1| hypothetical protein ARALYDRAFT_487182 [Arabidopsis lyrata subsp. lyrata] gi|297318968|gb|EFH49390.1| hypothetical protein ARALYDRAFT_487182 [Arabidopsis lyrata subsp. lyrata]	1542	1459	0	94.6	41.6	48.1	hypothetical protein ARALYDRAFT_487182	gbpln	Arabidopsis lyrata	AT5G04020.1 | Symbols: | calmodulin binding | chr5:1081980-1086546 REVERSE LENGTH=1495	1542	1495	0	97.0	25.9	29.1
Rsa1.0_01059.1.g22979.t4	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01059.1.g22980.t1	#	#	#	#	#	#	#	–	----	----	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	107	303	1.00E-10	283.2	30.8	48.6
Rsa1.0_01059.1.g22981.t1	ref|XP_002523356.1| conserved hypothetical protein [Ricinus communis] gi|223537444|gb|EEF39072.1| conserved hypothetical protein [Ricinus communis]	239	441	5.00E-19	184.5	22.6	29.7	conserved hypothetical protein	gbpln	Ricinus communis	AT3G62210.1 | Symbols: EDA32 | Putative endonuclease or glycosyl hydrolase | chr3:23026910-23028113 REVERSE LENGTH=279	239	279	3.00E-16	116.7	23.4	36.4
Rsa1.0_01059.1.g22982.t1	dbj|BAB10380.1| unnamed protein product [Arabidopsis thaliana]	490	356	3.00E-15	72.7	14.5	22.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G61190.1 | Symbols: | putative endonuclease or glycosyl hydrolase with C2H2-type zinc finger domain | chr5:24615480-24619886 FORWARD LENGTH=995	490	995	2.00E-16	203.1	11.2	18.4
Rsa1.0_01060.1.g22983.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01060.1.g22984.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01060.1.g22985.t1	ref|NP_197534.1| beta-1,3-glucanase 5 [Arabidopsis thaliana] gi|2808439|emb|CAA56135.1| bg5 [Arabidopsis thaliana] gi|332005450|gb|AED92833.1| beta-1,3-glucanase 5 [Arabidopsis thaliana]	491	354	1.00E-152	72.1	54.4	59.5	beta-1,3-glucanase 5	gbpln	Arabidopsis thaliana	AT5G20340.1 | Symbols: BG5 | beta-1,3-glucanase 5 | chr5:6874787-6875851 FORWARD LENGTH=354	491	354	1.00E-155	72.1	54.4	59.5
Rsa1.0_01060.1.g22986.t1	ref|XP_002873973.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297319810|gb|EFH50232.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	614	660	0	107.5	73.5	81.8	transducin family protein	gbpln	Arabidopsis lyrata	AT5G19920.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:6733622-6737266 REVERSE LENGTH=656	614	656	0	106.8	72.5	79.6

Rsa1.0_01060.1.g22987.t1	ref|NP_568388.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|20260444|gb|AAM13120.1| glycine-rich RNA-binding protein, putative [Arabidopsis thaliana] gi|28059296|gb|AAO30045.1| glycine-rich RNA-binding protein, putative [Arabidopsis thaliana] gi|332005391|gb|AED92774.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	356	337	1.00E-116	94.7	68.5	77.0	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT5G19960.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:6744029-6746133 FORWARD LENGTH=337	356	337	1.00E-118	94.7	68.5	77.0
Rsa1.0_01060.1.g22988.t1	ref|XP_002871913.1| hypothetical protein ARALYDRAFT_910035 [Arabidopsis lyrata subsp. lyrata] gi|297317750|gb|EFH48172.1| hypothetical protein ARALYDRAFT_910035 [Arabidopsis lyrata subsp. lyrata]	363	364	0	100.3	89.3	93.9	hypothetical protein ARALYDRAFT_910035	gbpln	Arabidopsis lyrata	AT5G19970.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:6747550-6748641 FORWARD LENGTH=363	363	363	0	100.0	89.0	92.3
Rsa1.0_01060.1.g22989.t1	ref|NP_197498.1| golgi nucleotide sugar transporter 4 [Arabidopsis thaliana] gi|75146970|sp|Q84L08.1|GONS4_ARATH RecName: Full=GDP-mannose transporter GONST4; AltName: Full=Protein GOLGI NUCLEOTIDE SUGAR TRANSPORTER 4 gi|29329823|emb|CAD83088.1| GONST4 Golgi Nucleotide sugar transporter [Arabidopsis thaliana] gi|89000965|gb|ABD59072.1| At5g19980 [Arabidopsis thaliana] gi|332005393|gb|AED92776.1| golgi nucleotide sugar transporter 4 [Arabidopsis thaliana]	362	341	1.00E-109	94.2	55.2	60.2	golgi nucleotide sugar transporter 4	gbpln	Arabidopsis thaliana	AT5G19980.1 | Symbols: GONST4 | golgi nucleotide sugar transporter 4 | chr5:6749907-6750932 REVERSE LENGTH=341	362	341	1.00E-112	94.2	55.2	60.2
Rsa1.0_01060.1.g22990.t1	gb|EOA20731.1| hypothetical protein CARUB_v10001052mg [Capsella rubella]	350	419	0	119.7	99.4	99.7	hypothetical protein CARUB_v10001052mg	gbpln	Capsella rubella	AT5G19990.1 | Symbols: RPT6A, ATSUG1 | regulatory particle triple-A ATPase 6A | chr5:6752144-6754918 FORWARD LENGTH=419	350	419	0	119.7	99.4	99.7
Rsa1.0_01060.1.g22991.t1	ref|NP_197503.1| Plant Tudor-like RNA-binding protein [Arabidopsis thaliana] gi|21553399|gb|AAM62492.1| unknown [Arabidopsis thaliana] gi|27808580|gb|AAO24570.1| At5g20030 [Arabidopsis thaliana] gi|332005398|gb|AED92781.1| Plant Tudor-like RNA-binding protein [Arabidopsis thaliana]	306	326	1.00E-126	106.5	79.4	85.9	Plant Tudor-like RNA-binding protein	gbpln	Arabidopsis thaliana	AT5G20030.1 | Symbols: | Plant Tudor-like RNA-binding protein | chr5:6764971-6766036 REVERSE LENGTH=326	306	326	1.00E-129	106.5	79.4	85.9
Rsa1.0_01060.1.g22992.t1	ref|XP_002873979.1| ATIPT9 [Arabidopsis lyrata subsp. lyrata] gi|297319816|gb|EFH50238.1| ATIPT9 [Arabidopsis lyrata subsp. lyrata]	498	463	0	93.0	74.9	81.5	ATIPT9	gbpln	Arabidopsis lyrata	AT5G20040.1 | Symbols: ATIPT9, IPT9 | isopentenyltransferase 9 | chr5:6767939-6770980 REVERSE LENGTH=463	498	463	0	93.0	74.1	81.5
Rsa1.0_01061.1.g22993.t1	ref|XP_002881608.1| GAUT7/LGT7 [Arabidopsis lyrata subsp. lyrata] gi|297327447|gb|EFH57867.1| GAUT7/LGT7 [Arabidopsis lyrata subsp. lyrata]	225	617	5.00E-39	274.2	36.0	37.8	GAUT7/LGT7	gbpln	Arabidopsis lyrata	AT2G38650.2 | Symbols: GAUT7 | galacturonosyltransferase 7 | chr2:16161856-16165523 REVERSE LENGTH=619	225	619	7.00E-41	275.1	35.6	37.3
Rsa1.0_01061.1.g22994.t1	gb|EOA23044.1| hypothetical protein CARUB_v10003814mg [Capsella rubella]	180	416	1.00E-60	231.1	65.0	77.2	hypothetical protein CARUB_v10003814mg	gbpln	Capsella rubella	AT1G05080.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:1459091-1460579 FORWARD LENGTH=439	180	439	2.00E-43	243.9	55.0	70.0
Rsa1.0_01061.1.g22995.t1	gb|EOA27927.1| hypothetical protein CARUB_v10024098mg [Capsella rubella]	57	197	8.00E-19	345.6	84.2	87.7	hypothetical protein CARUB_v10024098mg	gbpln	Capsella rubella	AT2G38640.1 | Symbols: | Protein of unknown function (DUF567) | chr2:16157725-16158474 REVERSE LENGTH=196	57	196	5.00E-21	343.9	82.5	87.7
Rsa1.0_01061.1.g22996.t1	ref|XP_002881608.1| GAUT7/LGT7 [Arabidopsis lyrata subsp. lyrata] gi|297327447|gb|EFH57867.1| GAUT7/LGT7 [Arabidopsis lyrata subsp. lyrata]	618	617	0	99.8	81.7	90.3	GAUT7/LGT7	gbpln	Arabidopsis lyrata	AT2G38650.2 | Symbols: GAUT7 | galacturonosyltransferase 7 | chr2:16161856-16165523 REVERSE LENGTH=619	618	619	0	100.2	81.7	89.6
Rsa1.0_01061.1.g22997.t1	gb|EOA27393.1| hypothetical protein CARUB_v10023524mg [Capsella rubella]	352	352	0	100.0	88.4	94.6	hypothetical protein CARUB_v10023524mg	gbpln	Capsella rubella	AT2G38660.3 | Symbols: | Amino acid dehydrogenase family protein | chr2:16166392-16168194 FORWARD LENGTH=352	352	352	0	100.0	88.1	93.5
Rsa1.0_01061.1.g22998.t1	ref|XP_002879759.1| hypothetical protein ARALYDRAFT_903103 [Arabidopsis lyrata subsp. lyrata] gi|297325598|gb|EFH56018.1| hypothetical protein ARALYDRAFT_903103 [Arabidopsis lyrata subsp. lyrata]	453	421	0	92.9	83.7	87.0	hypothetical protein ARALYDRAFT_903103	gbpln	Arabidopsis lyrata	AT2G38670.1 | Symbols: PECT1 | phosphorylethanolamine cytidylyltransferase 1 | chr2:16168979-16171680 FORWARD LENGTH=421	453	421	0	92.9	83.7	87.2

Rsa1.0_01061.1.g22999.t1	gb|EOA27880.1| hypothetical protein CARUB_v10024049mg [Capsella rubella]	215	213	1.00E-113	99.1	91.2	94.0	hypothetical protein CARUB_v10024049mg	gbpln	Capsella rubella	AT2G38710.2 | Symbols: | AMMECR1 family | chr2:16184517-16186764 REVERSE LENGTH=214	215	214	1.00E-113	99.5	90.2	94.0
Rsa1.0_01061.1.g23000.t1	gb|EOA26362.1| hypothetical protein CARUB_v10022884mg [Capsella rubella]	573	585	0	102.1	78.7	86.6	hypothetical protein CARUB_v10022884mg	gbpln	Capsella rubella	AT2G38720.1 | Symbols: MAP65-5 | microtubule-associated protein 65-5 | chr2:16188047-16192102 FORWARD LENGTH=587	573	587	0	102.4	76.3	84.6
Rsa1.0_01061.1.g23001.t1	ref|NP_181407.1| peptidyl-prolyl isomerase H (cyclophilin H) [Arabidopsis thaliana] gi|3785999|gb|AAC67345.1| putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|25083102|gb|AAN72042.1| putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|30102910|gb|AAP21373.1| At2g38730 [Arabidopsis thaliana] gi|45680872|gb|AAS75305.1| single domain cyclophilin type peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|330254484|gb|AEC09578.1| cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana]	212	199	1.00E-105	93.9	87.3	92.0	peptidyl-prolyl isomerase H (cyclophilin H)	gbpln	Arabidopsis thaliana	AT2G38730.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr2:16192579-16194038 REVERSE LENGTH=199	212	199	1.00E-107	93.9	87.3	92.0
Rsa1.0_01061.1.g23002.t1	gb|EOA27764.1| hypothetical protein CARUB_v10023919mg [Capsella rubella]	246	249	1.00E-128	101.2	90.7	95.9	hypothetical protein CARUB_v10023919mg	gbpln	Capsella rubella	AT2G38740.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:16194639-16195995 REVERSE LENGTH=244	246	244	1.00E-128	99.2	89.4	94.3
Rsa1.0_01061.1.g23003.t1	gb|ADD74397.1| annexin 4 [Brassica juncea]	316	315	1.00E-159	99.7	87.3	93.7	annexin 4	gbpln	Brassica juncea	AT2G38750.1 | Symbols: ANNAT4 | annexin 4 | chr2:16196582-16198431 REVERSE LENGTH=319	316	319	1.00E-155	100.9	82.9	93.0
Rsa1.0_01061.1.g23004.t1	gb|ACQ65866.1| annexin 3 [Brassica juncea] gi|251747933|gb|ABD47520.2| annexin 3 [Brassica juncea]	319	319	1.00E-174	100.0	93.1	95.6	annexin 3	gbpln	Brassica juncea	AT2G38760.1 | Symbols: ANNAT3, ANN3 | annexin 3 | chr2:16201086-16202490 FORWARD LENGTH=321	319	321	1.00E-159	100.6	83.7	92.2
Rsa1.0_01061.1.g23005.t1	dbj|BAJ33731.1| unnamed protein product [Thellungiella halophila]	409	412	0	100.7	90.5	94.6	unnamed protein product	----	----	AT2G26900.1 | Symbols: | Sodium Bile acid symporter family | chr2:11475156-11477870 REVERSE LENGTH=409	409	409	0	100.0	89.2	93.2
Rsa1.0_01061.1.g23006.t1	gb|EOA26458.1| hypothetical protein CARUB_v10022505mg [Capsella rubella]	146	1508	2.00E-67	1032.9	83.6	85.6	hypothetical protein CARUB_v10022505mg	gbpln	Capsella rubella	AT2G38770.1 | Symbols: EMB2765 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:16203185-16210253 REVERSE LENGTH=1509	146	1509	5.00E-70	1033.6	83.6	85.6
Rsa1.0_01061.1.g23007.t1	gb|EOA27529.1| hypothetical protein CARUB_v10023669mg [Capsella rubella]	320	316	1.00E-123	98.8	73.4	82.8	hypothetical protein CARUB_v10023669mg	gbpln	Capsella rubella	AT2G38820.2 | Symbols: | Protein of unknown function (DUF506) | chr2:16222271-16223393 FORWARD LENGTH=310	320	310	1.00E-116	96.9	70.0	80.0
Rsa1.0_01061.1.g23008.t1	ref|XP_002879767.1| hypothetical protein ARALYDRAFT_482897 [Arabidopsis lyrata subsp. lyrata] gi|297325606|gb|EFH56026.1| hypothetical protein ARALYDRAFT_482897 [Arabidopsis lyrata subsp. lyrata]	210	258	1.00E-49	122.9	61.0	74.8	hypothetical protein ARALYDRAFT_482897	gbpln	Arabidopsis lyrata	AT2G38823.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54520.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16224105-16225245 FORWARD LENGTH=258	210	258	4.00E-51	122.9	59.5	72.9
Rsa1.0_01061.1.g23009.t1	ref|XP_002879768.1| hypothetical protein ARALYDRAFT_903122 [Arabidopsis lyrata subsp. lyrata] gi|297325607|gb|EFH56027.1| hypothetical protein ARALYDRAFT_903122 [Arabidopsis lyrata subsp. lyrata]	366	333	1.00E-128	91.0	62.8	72.1	hypothetical protein ARALYDRAFT_903122	gbpln	Arabidopsis lyrata	AT2G38830.1 | Symbols: | Ubiquitin-conjugating enzyme/RWD-like protein | chr2:16225777-16226772 FORWARD LENGTH=331	366	331	1.00E-123	90.4	59.8	69.4
Rsa1.0_01061.1.g23010.t3	ref|NP_181418.3| guanylate-binding-like protein [Arabidopsis thaliana] gi|330254499|gb|AEC09593.1| guanylate-binding-like protein [Arabidopsis thaliana]	553	602	0	108.9	92.6	96.7	guanylate-binding-like protein	gbpln	Arabidopsis thaliana	AT2G38840.1 | Symbols: | Guanylate-binding family protein | chr2:16227329-16232115 FORWARD LENGTH=602	553	602	0	108.9	92.6	96.7
Rsa1.0_01062.1.g23011.t1	ref|NP_190562.1| C2H2 and C2HC zinc finger-containing protein [Arabidopsis thaliana] gi|6522914|emb|CAB62101.1| zinc-finger-like protein [Arabidopsis thaliana] gi|117168217|gb|ABK32191.1| At3g49930 [Arabidopsis thaliana] gi|332645087|gb|AEE78608.1| C2H2 and C2HC zinc finger-containing protein [Arabidopsis thaliana]	234	215	8.00E-72	91.9	72.6	76.1	C2H2 and C2HC zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT3G49930.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr3:18510246-18510893 FORWARD LENGTH=215	234	215	2.00E-74	91.9	72.6	76.1
Rsa1.0_01062.1.g23012.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	129	1123	2.00E-55	870.5	78.3	89.1	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01062.1.g23013.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	946	657	0	69.5	40.9	51.5	T14P8.10	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	946	626	6.00E-90	66.2	15.9	21.7
Rsa1.0_01062.1.g23014.t1	ref|NP_180096.3| serpin-Z10 [Arabidopsis thaliana] gi|75313479|sp|Q9SIR9.1|SPZ10_ARATH RecName: Full=Serpin-Z10; AltName: Full=ArathZ10 gi|4567253|gb|AAD23667.1| putative serpin [Arabidopsis thaliana] gi|330252581|gb|AEC07675.1| serpin-Z10 [Arabidopsis thaliana]	274	385	1.00E-108	140.5	69.7	79.2	serpin-Z10	gbpln	Arabidopsis thaliana	AT2G25240.1 | Symbols: | Serine protease inhibitor (SERPIN) family protein | chr2:10751872-10753134 REVERSE LENGTH=385	274	385	1.00E-111	140.5	69.7	79.2
Rsa1.0_01062.1.g23015.t1	ref|NP_180096.3| serpin-Z10 [Arabidopsis thaliana] gi|75313479|sp|Q9SIR9.1|SPZ10_ARATH RecName: Full=Serpin-Z10; AltName: Full=ArathZ10 gi|4567253|gb|AAD23667.1| putative serpin [Arabidopsis thaliana] gi|330252581|gb|AEC07675.1| serpin-Z10 [Arabidopsis thaliana]	330	385	1.00E-121	116.7	70.6	79.4	serpin-Z10	gbpln	Arabidopsis thaliana	AT2G25240.1 | Symbols: | Serine protease inhibitor (SERPIN) family protein | chr2:10751872-10753134 REVERSE LENGTH=385	330	385	1.00E-123	116.7	70.6	79.4
Rsa1.0_01062.1.g23016.t1	gb|EOA20772.1| hypothetical protein CARUB_v10001101mg [Capsella rubella]	388	406	1.00E-55	104.6	37.9	54.1	hypothetical protein CARUB_v10001101mg	gbpln	Capsella rubella	AT5G10340.1 | Symbols: | F-box family protein | chr5:3253122-3255045 FORWARD LENGTH=445	388	445	2.00E-53	114.7	36.9	53.6
Rsa1.0_01062.1.g23017.t2	emb|CAN71782.1| hypothetical protein VITISV_028677 [Vitis vinifera]	730	1383	0	189.5	59.9	73.6	hypothetical protein VITISV_028677	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	730	1262	3.00E-38	172.9	18.4	27.7
Rsa1.0_01062.1.g23018.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1913	1142	0	59.7	27.0	37.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1913	575	3.00E-90	30.1	9.6	14.3
Rsa1.0_01062.1.g23019.t1	ref|XP_002876010.1| hypothetical protein ARALYDRAFT_485358 [Arabidopsis lyrata subsp. lyrata] gi|297321848|gb|EFH52269.1| hypothetical protein ARALYDRAFT_485358 [Arabidopsis lyrata subsp. lyrata]	335	405	0	120.9	91.9	93.4	hypothetical protein ARALYDRAFT_485358	gbpln	Arabidopsis lyrata	AT3G50000.1 | Symbols: CKA2, ATCKA2 | casein kinase II, alpha chain 2 | chr3:18534487-18536743 FORWARD LENGTH=403	335	403	0	120.3	91.9	93.1
Rsa1.0_01062.1.g23020.t1	ref|XP_002877723.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297323561|gb|EFH53982.1| binding protein [Arabidopsis lyrata subsp. lyrata]	547	500	0	91.4	81.0	86.3	binding protein	gbpln	Arabidopsis lyrata	AT3G50030.1 | Symbols: | ARM-repeat/Tetratricopeptide repeat (TPR)-like protein | chr3:18546490-18548132 REVERSE LENGTH=501	547	501	0	91.6	79.2	86.1
Rsa1.0_01062.1.g23021.t1	emb|CAB62112.1| putative protein [Arabidopsis thaliana]	407	417	3.00E-88	102.5	53.8	65.8	putative protein	gbpln	Arabidopsis thaliana	AT3G50040.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37440.2); Has 70 Blast hits to 70 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 70; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:18549489-18551019 REVERSE LENGTH=421	407	421	3.00E-89	103.4	53.8	65.8
Rsa1.0_01063.1.g23022.t1	gb|EOA29120.1| hypothetical protein CARUB_v10025387mg [Capsella rubella]	450	476	0	105.8	85.8	89.8	hypothetical protein CARUB_v10025387mg	gbpln	Capsella rubella	AT2G28550.3 | Symbols: RAP2.7 | related to AP2.7 | chr2:12226168-12228251 REVERSE LENGTH=464	450	464	0	103.1	84.0	88.7
Rsa1.0_01063.1.g23023.t2	ref|XP_002879163.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297325002|gb|EFH55422.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	1013	967	0	95.5	66.7	75.6	nucleic acid binding protein	gbpln	Arabidopsis lyrata	AT2G28540.2 | Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr2:12218652-12223594 FORWARD LENGTH=960	1013	960	0	94.8	63.5	73.9
Rsa1.0_01063.1.g23024.t1	ref|XP_002879161.1| VHA-A1 [Arabidopsis lyrata subsp. lyrata] gi|297325000|gb|EFH55420.1| VHA-A1 [Arabidopsis lyrata subsp. lyrata]	795	822	0	103.4	95.8	98.1	VHA-A1	gbpln	Arabidopsis lyrata	AT2G28520.1 | Symbols: VHA-A1 | vacuolar proton ATPase A1 | chr2:12210026-12215532 FORWARD LENGTH=817	795	817	0	102.8	94.1	96.7
Rsa1.0_01063.1.g23025.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01063.1.g23026.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01063.1.g23027.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01063.1.g23028.t1	ref|NP_180417.2| LOB domain-containing protein 11 [Arabidopsis thaliana] gi|334302828|sp|Q9SK08.2|LBD11_ARATH RecName: Full=LOB domain-containing protein 11; AltName: Full=ASYMMETRIC LEAVES 2-like protein 7; Short=AS2-like protein 7 gi|330253037|gb|AEC08131.1| LOB domain-containing protein 11 [Arabidopsis thaliana]	234	232	6.00E-96	99.1	87.2	91.0	LOB domain-containing protein 11	gbpln	Arabidopsis thaliana	AT2G28500.1 | Symbols: LBD11 | LOB domain-containing protein 11 | chr2:12186603-12188110 REVERSE LENGTH=232	234	232	2.00E-98	99.1	87.2	91.0

Rsa1.0_01063.1.g23029.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01063.1.g23030.t1	ref|XP_002880986.1| cupin family protein [Arabidopsis lyrata subsp. lyrata] gi|297326825|gb|EFH57245.1| cupin family protein [Arabidopsis lyrata subsp. lyrata]	452	491	1.00E−122	108.6	48.0	53.3	cupin family protein	gbpln	Arabidopsis lyrata	AT2G28490.1 | Symbols: | RmlC−like cupins superfamily protein | chr2:12178812−12180983 REVERSE LENGTH=511	452	511	1.00E−124	113.1	47.1	53.8
Rsa1.0_01063.1.g23031.t1	gb|AAC98462.1| putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana] gi|20197956|gb|AAM15330.1| putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]	394	389	1.00E−141	98.7	63.7	76.9	putative chloroplast nucleoid DNA binding protein	gbpln	Arabidopsis thaliana	AT2G28040.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:11936203−11937390 REVERSE LENGTH=395	394	395	1.00E−143	100.3	63.7	76.9
Rsa1.0_01064.1.g23032.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01064.1.g23033.t1	ref|NP_189038.1| putative F−box protein [Arabidopsis thaliana] gi|75273446|sp|Q9LIR1.1|FB182_ARATH RecName: Full=Putative F−box protein At3g23960 gi|9294665|dbj|BAB03014.1| unnamed protein product [Arabidopsis thaliana] gi|332643318|gb|AEE76839.1| putative F−box protein [Arabidopsis thaliana]	245	402	4.00E−49	164.1	48.6	66.1	putative F−box protein	gbpln	Arabidopsis thaliana	AT3G23960.1 | Symbols: | F−box and associated interaction domains−containing protein | chr3:8657736−8658944 FORWARD LENGTH=402	245	402	1.00E−51	164.1	48.6	66.1
Rsa1.0_01064.1.g23034.t2	ref|XP_003609074.1| ATP−dependent DNA helicase PIF1 [Medicago truncatula] gi|355510129|gb|AES91271.1| ATP−dependent DNA helicase PIF1 [Medicago truncatula]	1305	1531	0	117.3	42.7	57.0	ATP−dependent DNA helicase PIF1	gbpln	Medicago truncatula	AT5G28780.1 | Symbols: | PIF1 helicase | chr5:10812907−10814173 REVERSE LENGTH=337	1305	337	1.00E−95	25.8	13.6	16.2
Rsa1.0_01064.1.g23035.t1	gb|EOA30626.1| hypothetical protein CARUB_v10013761mg [Capsella rubella]	169	428	9.00E−21	253.3	28.4	30.8	hypothetical protein CARUB_v10013761mg	gbpln	Capsella rubella	AT3G23080.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr3:8207612−8209181 REVERSE LENGTH=419	169	419	1.00E−22	247.9	27.2	30.8
Rsa1.0_01064.1.g23036.t1	gb|AFJ66186.1| hypothetical protein 11M19.5 [Arabidopsis halleri]	1419	1557	0	109.7	64.2	78.2	hypothetical protein 11M19.5	gbpln	Arabidopsis halleri	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916−236392 FORWARD LENGTH=158	1419	158	3.00E−32	11.1	4.7	5.8
Rsa1.0_01064.1.g23037.t1	ref|NP_180705.1| F−box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F−box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F−box protein DOR [Arabidopsis thaliana]	412	387	8.00E−90	93.9	48.3	62.9	F−box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F−box and associated interaction domains−containing protein | chr2:13407492−13408655 REVERSE LENGTH=387	412	387	2.00E−92	93.9	48.3	62.9
Rsa1.0_01064.1.g23038.t1	ref|XP_002874564.1| hypothetical protein ARALYDRAFT_911192 [Arabidopsis lyrata subsp. lyrata] gi|297320401|gb|EFH50823.1| hypothetical protein ARALYDRAFT_911192 [Arabidopsis lyrata subsp. lyrata]	177	664	5.00E−29	375.1	40.1	57.6	hypothetical protein ARALYDRAFT_911192	gbpln	Arabidopsis lyrata	AT1G43722.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28730.1); Has 924 Blast hits to 912 proteins in 109 species: Archae − 0; Bacteria − 0; Metazoa − 222; Fungi − 31; Plants − 661; Viruses − 0; Other Eukaryotes − 10 (source: NCBI BLink). | chr1:16496403−16497377 FORWARD LENGTH=324	177	324	3.00E−20	183.1	25.4	36.7
Rsa1.0_01064.1.g23039.t1	ref|XP_002887108.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297332949|gb|EFH63367.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	860	464	0	54.0	41.3	45.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G67180.1 | Symbols: | zinc finger (C3HC4−type RING finger) family protein / BRCT domain−containing protein | chr1:25130099−25132169 FORWARD LENGTH=453	860	453	0	52.7	39.4	44.0
Rsa1.0_01064.1.g23040.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	317	368	1.00E−48	116.1	43.2	57.7	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848−18153960 FORWARD LENGTH=370	317	370	1.00E−43	116.7	34.4	47.9
Rsa1.0_01064.1.g23041.t1	ref|XP_002887107.1| hypothetical protein ARALYDRAFT_475814 [Arabidopsis lyrata subsp. lyrata] gi|297332948|gb|EFH63366.1| hypothetical protein ARALYDRAFT_475814 [Arabidopsis lyrata subsp. lyrata]	314	364	1.00E−117	115.9	76.1	86.6	hypothetical protein ARALYDRAFT_475814	gbpln	Arabidopsis lyrata	AT1G67170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14750.1); Has 5478 Blast hits to 4354 proteins in 533 species: Archae − 87; Bacteria − 653; Metazoa − 2554; Fungi − 380; Plants − 418; Viruses − 16; Other Eukaryotes − 1370 (source: NCBI BLink). | chr1:25127727−25129145 FORWARD LENGTH=359	314	359	1.00E−117	114.3	75.2	85.4
Rsa1.0_01064.1.g23042.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01065.1.g23043.t1	ref|NP_191013.1| RNA polymerase II fifth largest subunit, E [Arabidopsis thaliana] gi|7258352|emb|CAB77569.1| RNA polymerase 24kDa subunit-like protein [Arabidopsis thaliana] gi|332645717|gb|AEE79238.1| RNA polymerase II fifth largest subunit, E [Arabidopsis thaliana]	279	233	6.00E-98	83.5	63.4	71.3	RNA polymerase II fifth largest subunit, E	gbpln	Arabidopsis thaliana	AT3G54490.1 | Symbols: RPB5E | RNA polymerase II fifth largest subunit, E | chr3:20173673-20175297 FORWARD LENGTH=233	279	233	1.00E-100	83.5	63.4	71.3
Rsa1.0_01065.1.g23044.t3	dbj|BAC41810.1| unknown protein [Arabidopsis thaliana]	164	271	2.00E-43	165.2	64.0	75.0	unknown protein	gbpln	Arabidopsis thaliana	AT3G54500.2 | Symbols: | BEST Arabidopsis thaliana protein match is: dentin sialophosphoprotein-related (TAIR:AT5G64170.1); Has 162 Blast hits to 160 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 23; Fungi - 11; Plants - 118; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr3:20175792-20178275 REVERSE LENGTH=569	164	569	3.00E-41	347.0	58.5	68.9
Rsa1.0_01065.1.g23045.t1	ref|XP_002974570.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii] gi|300157465|gb|EFJ24090.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii]	544	516	2.00E-39	94.9	51.7	59.9	hypothetical protein SELMODRAFT_442529	gbpln	Selaginella moellendorffii	AT4G13390.1 | Symbols: | Proline-rich extensin-like family protein | chr4:7783856-7785145 FORWARD LENGTH=429	544	429	4.00E-18	78.9	42.6	46.5
Rsa1.0_01065.1.g23046.t1	ref|NP_191022.2| hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|332645732|gb|AEE79253.1| hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	192	699	2.00E-17	364.1	28.6	33.3	hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT3G54590.1 | Symbols: ATHRGP1, HRGP1 | hydroxyproline-rich glycoprotein | chr3:20206223-20208472 FORWARD LENGTH=699	192	699	5.00E-20	364.1	28.6	33.3
Rsa1.0_01065.1.g23047.t1	ref|XP_002876258.1| ATGCN4 [Arabidopsis lyrata subsp. lyrata] gi|297322096|gb|EFH52517.1| ATGCN4 [Arabidopsis lyrata subsp. lyrata]	662	723	0	109.2	78.5	87.5	ATGCN4	gbpln	Arabidopsis lyrata	AT3G54540.1 | Symbols: ATGCN4, GCN4 | general control non-repressible 4 | chr3:20190393-20192564 FORWARD LENGTH=723	662	723	0	109.2	78.1	87.2
Rsa1.0_01065.1.g23048.t1	ref|NP_191019.1| histone H2A [Arabidopsis thaliana] gi|297816752|ref|XP_002876259.1| histone H2A.F/Z [Arabidopsis lyrata subsp. lyrata] gi|75277395|sp|O23628.1|H2AV1_ARATH RecName: Full=Histone H2A variant 1; AltName: Full=H2A.F/Z 1; AltName: Full=H2AvAt; AltName: Full=HTA11 gi|2407800|emb|CAA73155.1| histone H2A.F/Z [Arabidopsis thaliana] gi|7258359|emb|CAB77576.1| histone H2A.F/Z [Arabidopsis thaliana] gi|21592838|gb|AAM64788.1| histone H2A.F/Z [Arabidopsis thaliana] gi|28950691|gb|AAO63269.1| At3g54560 [Arabidopsis thaliana] gi|110736078|dbj|BAF00012.1| histone H2A.F/Z [Arabidopsis thaliana] gi|297322097|gb|EFH52518.1| histone H2A.F/Z [Arabidopsis lyrata subsp. lyrata] gi|332645729|gb|AEE79250.1| histone H2A 11 [Arabidopsis thaliana]	136	136	2.00E-63	100.0	97.1	97.8	histone H2A	gbpln	Arabidopsis lyrata	AT3G54560.1 | Symbols: HTA11 | histone H2A 11 | chr3:20196532-20197466 FORWARD LENGTH=136	136	136	4.00E-66	100.0	97.1	97.8
Rsa1.0_01065.1.g23049.t1	gb|EOA12473.1| hypothetical protein CARUB_v10025904mg [Capsella rubella]	68	800	3.00E-16	1176.5	58.8	64.7	hypothetical protein CARUB_v10025904mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01065.1.g23050.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01065.1.g23051.t1	ref|XP_002974570.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii] gi|300157465|gb|EFJ24090.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii]	983	516	4.00E-38	52.5	27.0	30.8	hypothetical protein SELMODRAFT_442529	gbpln	Selaginella moellendorffii	AT4G13390.1 | Symbols: | Proline-rich extensin-like family protein | chr4:7783856-7785145 FORWARD LENGTH=429	983	429	5.00E-14	43.6	21.9	23.0
Rsa1.0_01065.1.g23052.t1	gb|ABD65076.1| SLL3 ORF2 protein, putative [Brassica oleracea]	255	443	1.00E-33	173.7	43.9	58.8	SLL3 ORF2 protein, putative	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01065.1.g23053.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01066.1.g23054.t1	gb|AAD24831.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1130	1524	0	134.9	42.3	59.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1130	575	2.00E-65	50.9	13.5	21.7
Rsa1.0_01066.1.g23055.t3	ref|XP_002876727.1| hypothetical protein ARALYDRAFT_486866 [Arabidopsis lyrata subsp. lyrata] gi|297322565|gb|EFH52986.1| hypothetical protein ARALYDRAFT_486866 [Arabidopsis lyrata subsp. lyrata]	156	550	4.00E-25	352.6	38.5	40.4	hypothetical protein ARALYDRAFT_486866	gbpln	Arabidopsis lyrata	AT3G63520.1 | Symbols: CCD1, ATCCD1, ATNCED1, NCED1 | carotenoid cleavage dioxygenase 1 | chr3:23452940-23455896 FORWARD LENGTH=538	156	538	7.00E-27	344.9	37.8	40.4

Rsa1.0_01066.1.g23056.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	211	341	3.00E-36	161.6	36.0	55.5	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01066.1.g23057.t1	gb|AAL79774.1|AF331849_1 elongation factor 1 alpha [Saccharum hybrid cultivar CP65-357]	248	447	4.00E-30	180.2	28.6	30.6	elongation factor 1 alpha	gbpln	Saccharum hybrid	AT5G60390.3 | Symbols: | GTP binding Elongation factor Tu family protein | chr5:24289226-24290675 FORWARD LENGTH=449	248	449	4.00E-32	181.0	29.8	33.1
Rsa1.0_01066.1.g23058.t2	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	647	1459	1.00E-175	225.5	50.9	63.2	polyprotein, putative	gbpln	Arabidopsis thaliana	AT2G24970.1 | Symbols: | unknown protein; Has 33 Blast hits to 33 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr2:10620215-10621250 REVERSE LENGTH=152	647	152	8.00E-32	23.5	9.4	10.7
Rsa1.0_01067.1.g23059.t1	gb|AAZ86538.1| fructose 1,6-bisphosphatase [Brassica rapa subsp. pekinensis]	340	340	0	100.0	95.6	99.1	fructose 1,6-bisphosphatase	gbpln	Brassica rapa	AT1G43670.1 | Symbols: | Inositol monophosphatase family protein | chr1:16468184-16470347 FORWARD LENGTH=341	340	341	0	100.3	95.0	97.1
Rsa1.0_01067.1.g23060.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01067.1.g23061.t1	gb|AAF81293.1|AC027656_10 Strong similarity to a mutator-like transposase from Arabidopsis thaliana gb|AC006067. It contains a zinc finger, CCHC class domain PF|00098 [Arabidopsis thaliana]	290	753	1.00E-102	259.7	67.6	75.9	Strong similarity to a mutator-like transposase from Arabidopsis thaliana gb|AC006067. It contains a zinc finger, CCHC class domain PF|00098	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01067.1.g23062.t1	gb|EOA38110.1| hypothetical protein CARUB_v10009579mg, partial [Capsella rubella]	111	353	5.00E-34	318.0	85.6	88.3	hypothetical protein CARUB_v10009579mg, partial	gbpln	Capsella rubella	AT1G43650.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:16443861-16446814 REVERSE LENGTH=343	111	343	3.00E-36	309.0	83.8	88.3
Rsa1.0_01067.1.g23063.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1283	1274	0	99.3	38.1	50.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1283	626	1.00E-34	48.8	9.0	15.1
Rsa1.0_01067.1.g23064.t20	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	508	498	3.00E-46	98.0	20.5	27.8	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT5G40595.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:16253510-16254079 FORWARD LENGTH=141	508	141	8.00E-13	27.8	7.7	10.8
Rsa1.0_01067.1.g23065.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01067.1.g23066.t1	ref|XP_002893952.1| hypothetical protein ARALYDRAFT_473769 [Arabidopsis lyrata subsp. lyrata] gi|297339794|gb|EFH70211.1| hypothetical protein ARALYDRAFT_473769 [Arabidopsis lyrata subsp. lyrata]	380	385	0	101.3	85.8	93.7	hypothetical protein ARALYDRAFT_473769	gbpln	Arabidopsis lyrata	AT1G43630.1 | Symbols: | Protein of unknown function (DUF793) | chr1:16436445-16437686 REVERSE LENGTH=413	380	413	0	108.7	85.5	93.2
Rsa1.0_01068.1.g23067.t2	gb|ADI52861.1| chloroplast beta-carbonic anhydrase [Brassica napus]	259	331	1.00E-148	127.8	99.2	99.6	chloroplast beta-carbonic anhydrase	gbpln	Brassica napus	AT3G01500.2 | Symbols: CA1 | carbonic anhydrase 1 | chr3:194853-197873 REVERSE LENGTH=347	259	347	1.00E-147	134.0	96.1	99.2
Rsa1.0_01068.1.g23068.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	270	1274	4.00E-28	471.9	22.6	29.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01068.1.g23069.t1	emb|CAC19877.1| long chain acyl-CoA synthetase [Brassica napus]	251	693	8.00E-34	276.1	27.1	30.7	long chain acyl-CoA synthetase	gbpln	Brassica napus	AT1G77590.1 | Symbols: LACS9 | long chain acyl-CoA synthetase 9 | chr1:29148501-29151776 REVERSE LENGTH=691	251	691	1.00E-27	275.3	25.1	31.5
Rsa1.0_01068.1.g23070.t1	gb|EOA32012.1| hypothetical protein CARUB_v10015255mg [Capsella rubella]	408	410	0	100.5	93.4	97.1	hypothetical protein CARUB_v10015255mg	gbpln	Capsella rubella	AT3G01490.1 | Symbols: | Protein kinase superfamily protein | chr3:191095-193258 REVERSE LENGTH=411	408	411	0	100.7	92.9	96.6
Rsa1.0_01068.1.g23071.t1	ref|XP_002884278.1| hypothetical protein ARALYDRAFT_477375 [Arabidopsis lyrata subsp. lyrata] gi|297330118|gb|EFH60537.1| hypothetical protein ARALYDRAFT_477375 [Arabidopsis lyrata subsp. lyrata]	449	437	0	97.3	78.2	84.0	hypothetical protein ARALYDRAFT_477375	gbpln	Arabidopsis lyrata	AT3G01480.1 | Symbols: CYP38, ATCYP38 | cyclophilin 38 | chr3:188569-190674 FORWARD LENGTH=437	449	437	0	97.3	76.8	83.5
Rsa1.0_01068.1.g23072.t2	dbj|BAJ33940.1| unnamed protein product [Thellungiella halophila] gi|312283511|dbj|BAJ34621.1| unnamed protein product [Thellungiella halophila]	264	274	1.00E-103	103.8	77.7	86.0	unnamed protein product	----	----	AT3G01470.1 | Symbols: ATHB-1, ATHB1, HD-ZIP-1, HAT5, HB-1 | homeobox 1 | chr3:182648-184034 REVERSE LENGTH=272	264	272	4.00E-95	103.0	76.1	84.1

Rsa1.0_01068.1.g23073.t2	ref|NP_566137.1| photosystem II oxygen-evolving enhancer protein [Arabidopsis thaliana] gi|75204862|sp|Q9SGH4.1|PQL2_ARATH RecName: Full=PsbQ-like protein 2, chloroplastic; AltName: Full=Protein photosynthetic NDH subcomplex L 3; Flags: Precursor gi|6692264|gb|AAF24614.1|AC010870_7 hypothetical protein [Arabidopsis thaliana] gi|17979498|gb|AAL50085.1| AT3g01440/T13O15_8 [Arabidopsis thaliana] gi|20147295|gb|AAM10361.1| AT3g01440/T13O15_8 [Arabidopsis thaliana] gi|332640146|gb|AEE73667.1| photosynthetic NDH subcomplex L3 [Arabidopsis thaliana]	221	220	1.00E-99	99.5	81.4	88.7	photosystem II oxygen-evolving enhancer protein	gbpln	Arabidopsis thaliana	AT3G01440.1 | Symbols: PQL1, PQL2 | PsbQ-like 1 | chr3:168478-169407 FORWARD LENGTH=220	221	220	1.00E-102	99.5	81.4	88.7
Rsa1.0_01068.1.g23074.t1	ref|NP_974205.1| uncharacterized protein [Arabidopsis thaliana] gi|75123851|sp|Q6ID77.1|MED11_ARATH RecName: Full=Mediator of RNA polymerase II transcription subunit 11 gi|48310228|gb|AAT41779.1| At3g01435 [Arabidopsis thaliana] gi|52218796|gb|AAU29468.1| At3g01435 [Arabidopsis thaliana] gi|110738543|dbj|BAF01197.1| hypothetical protein [Arabidopsis thaliana] gi|332640145|gb|AEE73666.1| uncharacterized protein AT3G01435 [Arabidopsis thaliana]	116	115	1.00E-45	99.1	75.9	84.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01435.1 | Symbols: | Expressed protein | chr3:166853-167984 REVERSE LENGTH=115	116	115	2.00E-48	99.1	75.9	84.5
Rsa1.0_01068.1.g23075.t2	gb|EOA30078.1| hypothetical protein CARUB_v10013184mg, partial [Capsella rubella]	424	645	0	152.1	81.1	88.7	hypothetical protein CARUB_v10013184mg, partial	gbpln	Capsella rubella	AT3G01420.1 | Symbols: ALPHA-DOX1, DOX1, DIOX1, PADOX-1 | Peroxidase superfamily protein | chr3:159689-162726 REVERSE LENGTH=639	424	639	0	150.7	81.4	87.7
Rsa1.0_01069.1.g23076.t2	emb|CAB41929.1| putative protein [Arabidopsis thaliana] gi|7268021|emb|CAB78361.1| putative protein [Arabidopsis thaliana]	415	405	1.00E-170	97.6	69.9	75.9	putative protein	gbpln	Arabidopsis thaliana	AT4G13190.1 | Symbols: | Protein kinase superfamily protein | chr4:7659435-7661106 REVERSE LENGTH=389	415	389	1.00E-172	93.7	69.6	75.2
Rsa1.0_01069.1.g23077.t1	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	617	498	2.00E-60	80.7	26.9	38.6	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT2G13450.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02000.1); Has 247 Blast hits to 243 proteins in 13 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 2; Plants - 243; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:5598739-5599923 REVERSE LENGTH=394	617	394	3.00E-15	63.9	7.6	12.5
Rsa1.0_01069.1.g23078.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01069.1.g23079.t2	gb|AAM62995.1| unknown [Arabidopsis thaliana]	580	185	5.00E-42	31.9	20.0	22.1	unknown	gbpln	Arabidopsis thaliana	AT4G13200.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: thylakoid, chloroplast thylakoid membrane, chloroplast, plastoglobule; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 97 Blast hits to 97 proteins in 46 species: Archae - 0; Bacteria - 65; Metazoa - 2; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:7668292-7669166 REVERSE LENGTH=185	580	185	8.00E-41	31.9	20.0	22.1
Rsa1.0_01069.1.g23080.t3	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	489	940	6.00E-18	192.2	11.7	17.8	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01069.1.g23081.t1	pir||G85073 probable myosin-like protein [imported] - Arabidopsis thaliana gi|5032276|gb|AAD38224.1|AF147264_7 contains similarity to intermediate filament protein A; may be a pseudogene [Arabidopsis thaliana] gi|7267350|emb|CAB81123.1| putative myosin-like protein [Arabidopsis thaliana]	840	786	6.00E-18	93.6	5.7	8.2	probable myosin-like protein	gbpln	Arabidopsis thaliana	AT4G03830.1 | Symbols: | Protein of unknown function, DUF601 | chr4:1790440-1792458 FORWARD LENGTH=578	840	578	4.00E-19	68.8	6.3	9.0
Rsa1.0_01069.1.g23082.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	656	1838	2.00E-45	280.2	16.2	24.5	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01069.1.g23083.t1	gb|EOA18445.1| hypothetical protein CARUB_v10006988mg [Capsella rubella]	581	683	1.00E-144	117.6	46.8	61.4	hypothetical protein CARUB_v10006988mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	581	696	1.00E-24	119.8	17.2	32.2
Rsa1.0_01069.1.g23084.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01069.1.g23085.t1	ref|NP_001190715.1| putative pectate lyase 14 [Arabidopsis thaliana] gi|357528834|sp|Q9SVQ6.2|PLY14_ARATH RecName: Full=Putative pectate lyase 14; Flags: Precursor gi|332657846|gb|AEE83246.1| putative pectate lyase 14 [Arabidopsis thaliana]	387	438	0	113.2	89.7	93.0	putative pectate lyase 14	gbpln	Arabidopsis thaliana	AT4G13210.2 | Symbols: | Pectin lyase-like superfamily protein | chr4:7670040-7673135 FORWARD LENGTH=438	387	438	0	113.2	89.7	93.0
Rsa1.0_01070.1.g23086.t1	ref|XP_002883351.1| hypothetical protein ARALYDRAFT_479740 [Arabidopsis lyrata subsp. lyrata] gi|297329191|gb|EFH59610.1| hypothetical protein ARALYDRAFT_479740 [Arabidopsis lyrata subsp. lyrata]	777	782	0	100.6	83.4	89.4	hypothetical protein ARALYDRAFT_479740	gbpln	Arabidopsis lyrata	AT3G22270.1 | Symbols: | Topoisomerase II-associated protein PAT1 | chr3:7874480-7877857 FORWARD LENGTH=782	777	782	0	100.6	83.4	89.4
Rsa1.0_01070.1.g23087.t1	ref|NP_566704.1| OTU-like cysteine protease family protein [Arabidopsis thaliana] gi|332643092|gb|AEE76613.1| OTU-like cysteine protease family protein [Arabidopsis thaliana] gi|407080571|gb|AFS88960.1| OTU-containing deubiquitinating enzyme OTU11 isoform ii [Arabidopsis thaliana]	466	240	1.00E-111	51.5	45.9	49.1	OTU-like cysteine protease family protein	gbpln	Arabidopsis thaliana	AT3G22260.1 | Symbols: | Cysteine proteinases superfamily protein | chr3:7871489-7873393 FORWARD LENGTH=240	466	240	1.00E-114	51.5	45.9	49.1
Rsa1.0_01070.1.g23088.t1	gb|EOA32026.1| hypothetical protein CARUB_v10015270mg [Capsella rubella]	159	463	4.00E-77	291.2	86.8	93.1	hypothetical protein CARUB_v10015270mg	gbpln	Capsella rubella	AT3G22250.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:7867806-7870053 FORWARD LENGTH=461	159	461	9.00E-74	289.9	86.8	93.7
Rsa1.0_01070.1.g23089.t1	ref|NP_566703.4| uncharacterized protein [Arabidopsis thaliana] gi|9294090|dbj|BAB01942.1| unnamed protein product [Arabidopsis thaliana] gi|21593174|gb|AAM65123.1| unknown [Arabidopsis thaliana] gi|51969350|dbj|BAD43367.1| unknown protein [Arabidopsis thaliana] gi|51969492|dbj|BAD43438.1| unknown protein [Arabidopsis thaliana] gi|51970550|dbj|BAD43967.1| unknown protein [Arabidopsis thaliana] gi|51970942|dbj|BAD44163.1| unknown protein [Arabidopsis thaliana] gi|51971146|dbj|BAD44265.1| unknown protein [Arabidopsis thaliana] gi|332643090|gb|AEE76611.1| uncharacterized protein AT3G22240 [Arabidopsis thaliana]	71	72	1.00E-16	101.4	76.1	78.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G22240.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G22235.2); Has 177 Blast hits to 177 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 177; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7863788-7864675 REVERSE LENGTH=72	71	72	2.00E-19	101.4	76.1	78.9
Rsa1.0_01070.1.g23090.t1	ref|NP_193236.1| 60S ribosomal protein L27-3 [Arabidopsis thaliana] gi|3123264|sp|P51419.2|RL273_ARATH RecName: Full=60S ribosomal protein L27-3 gi|2244857|emb|CAB10279.1| ribosomal protein [Arabidopsis thaliana] gi|7268246|emb|CAB78542.1| ribosomal protein [Arabidopsis thaliana] gi|17381062|gb|AAL36343.1| putative ribosomal protein [Arabidopsis thaliana] gi|20466061|gb|AAM20365.1| putative ribosomal protein [Arabidopsis thaliana] gi|21553620|gb|AAM62713.1| ribosomal protein [Arabidopsis thaliana] gi|110736737|dbj|BAF00331.1| ribosomal protein [Arabidopsis thaliana] gi|332658135|gb|AEE83535.1| 60S ribosomal protein L27-3 [Arabidopsis thaliana]	135	135	3.00E-69	100.0	96.3	99.3	60S ribosomal protein L27-3	gbpln	Arabidopsis thaliana	AT4G15000.1 | Symbols: | Ribosomal L27e protein family | chr4:8571896-8572303 FORWARD LENGTH=135	135	135	6.00E-72	100.0	96.3	99.3
Rsa1.0_01070.1.g23091.t1	gb|EOA30373.1| hypothetical protein CARUB_v10013496mg [Capsella rubella]	619	505	0	81.6	74.8	77.5	hypothetical protein CARUB_v10013496mg	gbpln	Capsella rubella	AT3G22200.1 | Symbols: POP2, GABA-T, HER1 | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr3:7835286-7838863 FORWARD LENGTH=504	619	504	0	81.4	72.5	76.3
Rsa1.0_01070.1.g23092.t1	gb|EOA30650.1| hypothetical protein CARUB_v10013787mg [Capsella rubella]	299	422	2.00E-94	141.1	68.9	73.2	hypothetical protein CARUB_v10013787mg	gbpln	Capsella rubella	AT3G22190.2 | Symbols: IQD5 | IQ-domain 5 | chr3:7831280-7833512 REVERSE LENGTH=422	299	422	3.00E-95	141.1	67.6	73.2

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<tr><td>Rsa1.0_01070.1.g23093.t1</td><td>ref|XP_002883347.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297329187|gb|EFH59606.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>643</td><td>704</td><td>0</td><td>109.5</td><td>75.1</td><td>84.4</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G22180.1 | Symbols: | DHHC-type zinc finger family protein | chr3:7827190-7830508 FORWARD LENGTH=706</td><td>643</td><td>706</td><td>0</td><td>109.8</td><td>74.3</td><td>84.6</td></tr>
<tr><td>Rsa1.0_01070.1.g23094.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01070.1.g23095.t1</td><td>ref|NP_188856.2| far-red elongated hypocotyls 3 protein [Arabidopsis thaliana] gi|186510310|ref|NP_001118673.1| far-red elongated hypocotyls 3 protein [Arabidopsis thaliana] gi|75273369|sp|Q9LIE5.1|FHY3_ARATH RecName: Full=Protein FAR-RED ELONGATED HYPOCOTYL 3 gi|11994736|dbj|BAB03065.1| far-red impaired response protein; Mutator-like transposase-like protein; phytochrome A signaling protein-like [Arabidopsis thaliana] gi|332643075|gb|AEE76596.1| far-red elongated hypocotyls 3 protein [Arabidopsis thaliana] gi|332643076|gb|AEE76597.1| far-red elongated hypocotyls 3 protein [Arabidopsis thaliana]</td><td>835</td><td>839</td><td>0</td><td>100.5</td><td>82.4</td><td>89.8</td><td>far-red elongated hypocotyls 3 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G22170.2 | Symbols: FHY3 | far-red elongated hypocotyls 3 | chr3:7822359-7825414 REVERSE LENGTH=839</td><td>835</td><td>839</td><td>0</td><td>100.5</td><td>82.4</td><td>89.8</td></tr>
<tr><td>Rsa1.0_01070.1.g23096.t1</td><td>gb|EOA31512.1| hypothetical protein CARUB_v10014701mg [Capsella rubella]</td><td>197</td><td>195</td><td>6.00E-56</td><td>99.0</td><td>77.7</td><td>83.2</td><td>hypothetical protein CARUB_v10014701mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G22160.1 | Symbols: | VQ motif-containing protein | chr3:7818148-7818726 REVERSE LENGTH=192</td><td>197</td><td>192</td><td>5.00E-56</td><td>97.5</td><td>77.7</td><td>83.2</td></tr>
<tr><td>Rsa1.0_01071.1.g23097.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>179</td><td>1307</td><td>5.00E-31</td><td>730.2</td><td>40.8</td><td>50.8</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>179</td><td>1262</td><td>6.00E-17</td><td>705.0</td><td>27.9</td><td>39.7</td></tr>
<tr><td>Rsa1.0_01071.1.g23098.t2</td><td>gb|AAC95173.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>376</td><td>1200</td><td>1.00E-101</td><td>319.1</td><td>53.7</td><td>72.9</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01071.1.g23099.t1</td><td>dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>536</td><td>1250</td><td>0</td><td>233.2</td><td>61.9</td><td>74.3</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>536</td><td>1262</td><td>5.00E-86</td><td>235.4</td><td>30.6</td><td>47.0</td></tr>
<tr><td>Rsa1.0_01071.1.g23100.t1</td><td>ref|NP_191073.1| ABC transporter G family member 19 [Arabidopsis thaliana] gi|75335879|sp|Q9M3D6.1|AB19G_ARATH RecName: Full=ABC transporter G family member 19; Short=ABC transporter ABCG.19; Short=AtABCG19; AltName: Full=White-brown complex homolog protein 19; Short=AtWBC19 gi|7019646|emb|CAB75747.1| ABC transporter-like protein [Arabidopsis thaliana] gi|15028219|gb|AAK76606.1| putative ABC transporter protein [Arabidopsis thaliana] gi|19310775|gb|AAL85118.1| putative ABC transporter protein [Arabidopsis thaliana] gi|332645822|gb|AEE79343.1| ABC transporter G family member 19 [Arabidopsis thaliana]</td><td>715</td><td>725</td><td>0</td><td>101.4</td><td>81.5</td><td>87.8</td><td>ABC transporter G family member 19</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G55130.1 | Symbols: ATWBC19, WBC19 | white-brown complex homolog 19 | chr3:20434111-20436288 REVERSE LENGTH=725</td><td>715</td><td>725</td><td>0</td><td>101.4</td><td>81.5</td><td>87.8</td></tr>
<tr><td>Rsa1.0_01071.1.g23101.t1</td><td>ref|XP_002868466.1| hypothetical protein ARALYDRAFT_493666 [Arabidopsis lyrata subsp. lyrata] gi|297314302|gb|EFH44725.1| hypothetical protein ARALYDRAFT_493666 [Arabidopsis lyrata subsp. lyrata]</td><td>284</td><td>296</td><td>1.00E-134</td><td>104.2</td><td>92.3</td><td>96.5</td><td>hypothetical protein ARALYDRAFT_493666</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G36290.2 | Symbols: | Uncharacterized protein family (UPF0016) | chr5:14302977-14304972 FORWARD LENGTH=293</td><td>284</td><td>293</td><td>1.00E-133</td><td>103.2</td><td>89.4</td><td>94.0</td></tr>
<tr><td>Rsa1.0_01071.1.g23102.t1</td><td>ref|XP_002870476.1| hypothetical protein ARALYDRAFT_915762 [Arabidopsis lyrata subsp. lyrata] gi|297316312|gb|EFH46735.1| hypothetical protein ARALYDRAFT_915762 [Arabidopsis lyrata subsp. lyrata]</td><td>133</td><td>127</td><td>5.00E-54</td><td>95.5</td><td>82.7</td><td>89.5</td><td>hypothetical protein ARALYDRAFT_915762</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G65290.1 | Symbols: mtACP2 | mitochondrial acyl carrier protein 2 | chr1:24249088-24250366 REVERSE LENGTH=126</td><td>133</td><td>126</td><td>2.00E-53</td><td>94.7</td><td>77.4</td><td>87.2</td></tr>
</table>

Rsa1.0_01071.1.g23103.t1	ref|NP_564847.1| uncharacterized protein [Arabidopsis thaliana] gi|30697168|ref|NP_849845.1| uncharacterized protein [Arabidopsis thaliana] gi|42572005|ref|NP_974093.1| uncharacterized protein [Arabidopsis thaliana] gi|3335335|gb|AAC27137.1| ESTs gb|F14113 and gb|T42122 come from this region [Arabidopsis thaliana] gi|27311649|gb|AAO00790.1| expressed protein [Arabidopsis thaliana] gi|30023788|gb|AAP13427.1| At1g65270 [Arabidopsis thaliana] gi|222423330|dbj|BAH19640.1| AT1G65270 [Arabidopsis thaliana] gi|222423443|dbj|BAH19692.1| AT1G65270 [Arabidopsis thaliana] gi|332196229|gb|AEE34350.1| uncharacterized protein AT1G65270 [Arabidopsis thaliana] gi|332196230|gb|AEE34351.1| uncharacterized protein AT1G65270 [Arabidopsis thaliana] gi|332196231|gb|AEE34352.1| uncharacterized protein AT1G65270 [Arabidopsis thaliana]	294	292	1.00E-116	99.3	73.8	81.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G65270.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum, plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; Has 149 Blast hits to 149 proteins in 49 species: Archae - 0; Bacteria - 0; Metazoa - 98; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr1:24241855-24244504 FORWARD LENGTH=292	294	292	1.00E-119	99.3	73.8	81.0
Rsa1.0_01071.1.g23104.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01071.1.g23105.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	73	1123	5.00E-11	1538.4	45.2	52.1	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01071.1.g23106.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01071.1.g23107.t2	#	#	#	#	#	#	#	-	----	----	AT3G01400.1 | Symbols: | ARM repeat superfamily protein | chr3:151920-152987 FORWARD LENGTH=355	72	355	5.00E-12	493.1	51.4	51.4
Rsa1.0_01071.1.g23108.t1	gb|EOA23471.1| hypothetical protein CARUB_v10016663mg [Capsella rubella]	857	911	1.00E-24	106.3	8.9	13.3	hypothetical protein CARUB_v10016663mg	gbpln	Capsella rubella	AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957	857	957	4.00E-23	111.7	8.1	13.1
Rsa1.0_01071.1.g23109.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1477	1838	0	124.4	32.0	40.4	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01072.1.g23110.t1	dbj|BAJ33974.1| unnamed protein product [Thellungiella halophila]	485	622	0	128.2	93.6	97.5	unnamed protein product	----	----	AT1G69870.1 | Symbols: NRT1.7 | nitrate transporter 1.7 | chr1:26316208-26320097 FORWARD LENGTH=620	485	620	0	127.8	86.6	94.0
Rsa1.0_01072.1.g23111.t1	ref|XP_002863106.1| hypothetical protein ARALYDRAFT_920363 [Arabidopsis lyrata subsp. lyrata] gi|297308928|gb|EFH39365.1| hypothetical protein ARALYDRAFT_920363 [Arabidopsis lyrata subsp. lyrata]	275	284	1.00E-125	103.3	84.7	89.1	hypothetical protein ARALYDRAFT_920363	gbpln	Arabidopsis lyrata	AT1G69890.1 | Symbols: | Protein of unknown function (DUF569) | chr1:26323426-26324527 REVERSE LENGTH=279	275	279	1.00E-127	101.5	84.4	90.2
Rsa1.0_01072.1.g23112.t1	gb|EOA33387.1| hypothetical protein CARUB_v10020368mg, partial [Capsella rubella]	392	417	1.00E-180	106.4	82.1	91.6	hypothetical protein CARUB_v10020368mg, partial	gbpln	Capsella rubella	AT1G69900.1 | Symbols: | Actin cross-linking protein | chr1:26326520-26327816 REVERSE LENGTH=397	392	397	1.00E-166	101.3	78.1	86.0
Rsa1.0_01072.1.g23113.t1	gb|AAD32759.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	313	1356	8.00E-37	433.2	27.8	42.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01072.1.g23114.t1	ref|XP_004155336.1| PREDICTED: LOW QUALITY PROTEIN: paired amphipathic helix protein Sin3-like 4-like [Cucumis sativus]	107	1419	3.00E-19	1326.2	49.5	67.3	PREDICTED: LOW QUALITY PROTEIN: paired amphipathic helix protein Sin3-like 4-like	gbpln	Cucumis sativus	AT1G10450.1 | Symbols: SNL6 | SIN3-like 6 | chr1:3432313-3437979 FORWARD LENGTH=1122	107	1122	1.00E-20	1048.6	44.9	66.4
Rsa1.0_01072.1.g23115.t1	ref|XP_002863104.1| hypothetical protein ARALYDRAFT_920359 [Arabidopsis lyrata subsp. lyrata] gi|297308926|gb|EFH39363.1| hypothetical protein ARALYDRAFT_920359 [Arabidopsis lyrata subsp. lyrata]	229	254	1.00E-106	110.9	80.8	89.1	hypothetical protein ARALYDRAFT_920359	gbpln	Arabidopsis lyrata	AT1G69920.1 | Symbols: ATGSTU12, GSTU12 | glutathione S-transferase TAU 12 | chr1:26334395-26335537 REVERSE LENGTH=254	229	254	1.00E-108	110.9	79.5	88.6

Rsa1.0_01072.1.g23116.t1	ref|NP_177151.1| glutathione S-transferase TAU 11 [Arabidopsis thaliana] gi|75333668|sp|Q9CAS6.1|GSTUB_ARATH RecName: Full=Glutathione S-transferase U11; Short=AtGSTU11; AltName: Full=GST class-tau member 11 gi|12325238|gb|AAG52568.1|AC010675_16 putative glutathione transferase; 14657-15612 [Arabidopsis thaliana] gi|26453280|dbj|BAC43713.1| putative glutathione transferase [Arabidopsis thaliana] gi|30017271|gb|AAP12869.1| At1g69930 [Arabidopsis thaliana] gi|332196878|gb|AEE34999.1| glutathione S-transferase TAU 11 [Arabidopsis thaliana]	230	234	1.00E-121	101.7	92.6	96.1	glutathione S-transferase TAU 11	gbpln	Arabidopsis thaliana	AT1G69930.1 | Symbols: ATGSTU11, GSTU11 | glutathione S-transferase TAU 11 | chr1:26337735-26338690 REVERSE LENGTH=234	230	234	1.00E-123	101.7	92.6	96.1
Rsa1.0_01072.1.g23117.t2	gb|EOA35497.1| hypothetical protein CARUB_v10020704mg [Capsella rubella]	480	307	1.00E-175	64.0	61.5	62.7	hypothetical protein CARUB_v10020704mg	gbpln	Capsella rubella	AT1G69960.1 | Symbols: PP2A | serine/threonine protein phosphatase 2A | chr1:26348892-26350511 REVERSE LENGTH=307	480	307	1.00E-178	64.0	61.5	62.3
Rsa1.0_01072.1.g23118.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01073.1.g23119.t1	ref|XP_002866723.1| transcriptional factor B3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297312558|gb|EFH42982.1| transcriptional factor B3 family protein [Arabidopsis lyrata subsp. lyrata]	316	332	2.00E-96	105.1	61.4	73.7	transcriptional factor B3 family protein	gbpln	Arabidopsis lyrata	AT5G66980.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr5:26741563-26742826 FORWARD LENGTH=334	316	334	1.00E-98	105.7	59.8	74.1
Rsa1.0_01073.1.g23120.t1	ref|XP_002865039.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310874|gb|EFH41298.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	791	792	0	100.1	94.4	97.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G66960.1 | Symbols: | Prolyl oligopeptidase family protein | chr5:26736209-26739493 REVERSE LENGTH=792	791	792	0	100.1	93.9	97.7
Rsa1.0_01073.1.g23121.t1	ref|XP_002866724.1| hypothetical protein ARALYDRAFT_496904 [Arabidopsis lyrata subsp. lyrata] gi|297312559|gb|EFH42983.1| hypothetical protein ARALYDRAFT_496904 [Arabidopsis lyrata subsp. lyrata]	875	871	0	99.5	86.2	90.6	hypothetical protein ARALYDRAFT_496904	gbpln	Arabidopsis lyrata	AT5G66950.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr5:26733333-26735945 FORWARD LENGTH=870	875	870	0	99.4	85.9	90.5
Rsa1.0_01073.1.g23122.t1	ref|XP_002865040.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310875|gb|EFH41299.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	213	223	2.00E-72	104.7	77.0	85.0	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT5G66940.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr5:26727989-26728666 REVERSE LENGTH=225	213	225	1.00E-74	105.6	74.2	85.4
Rsa1.0_01073.1.g23123.t1	gb|EOA13983.1| hypothetical protein CARUB_v10027114mg [Capsella rubella]	218	216	1.00E-110	99.1	90.4	94.5	hypothetical protein CARUB_v10027114mg	gbpln	Capsella rubella	AT5G66930.2 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1649 (InterPro:IPR012445); Has 251 Blast hits to 251 proteins in 113 species: Archae - 0; Bacteria - 0; Metazoa - 91; Fungi - 85; Plants - 58; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr5:26725997-26727549 FORWARD LENGTH=215	218	215	1.00E-110	98.6	89.9	92.7
Rsa1.0_01073.1.g23124.t1	ref|XP_002866726.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312561|gb|EFH42985.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	571	543	0	95.1	80.7	84.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G66920.1 | Symbols: sks17 | SKU5 similar 17 | chr5:26722963-26725370 FORWARD LENGTH=546	571	546	0	95.6	80.4	84.8
Rsa1.0_01073.1.g23125.t1	gb|ACP30573.1| disease resistance protein [Brassica rapa subsp. pekinensis]	818	1038	0	126.9	83.4	87.9	disease resistance protein	gbpln	Brassica rapa	AT5G66900.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr5:26714931-26717757 REVERSE LENGTH=809	818	809	0	98.9	76.9	84.8
Rsa1.0_01073.1.g23126.t1	ref|XP_002865045.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310880|gb|EFH41304.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	400	421	1.00E-174	105.3	76.0	88.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G66890.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:26712944-26714383 REVERSE LENGTH=415	400	415	1.00E-171	103.8	73.8	85.8
Rsa1.0_01073.1.g23127.t1	gb|EOA13203.1| hypothetical protein CARUB_v10026228mg [Capsella rubella]	461	522	1.00E-144	113.2	64.4	70.9	hypothetical protein CARUB_v10026228mg	gbpln	Capsella rubella	AT5G66840.1 | Symbols: | SAP domain-containing protein | chr5:26692922-26695296 REVERSE LENGTH=551	461	551	1.00E-136	119.5	65.3	71.4
Rsa1.0_01073.1.g23128.t1	gb|EOA30805.1| hypothetical protein CARUB_v10013949mg [Capsella rubella]	382	381	2.00E-79	99.7	49.2	61.0	hypothetical protein CARUB_v10013949mg	gbpln	Capsella rubella	AT3G08810.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:2675631-2676662 REVERSE LENGTH=343	382	343	6.00E-62	89.8	45.5	55.0

Rsa1.0_01073.1.g23129.t2	ref|XP_002866734.1| hypothetical protein ARALYDRAFT_920040 [Arabidopsis lyrata subsp. lyrata] gi|297312569|gb|EFH42993.1| hypothetical protein ARALYDRAFT_920040 [Arabidopsis lyrata subsp. lyrata]	84	101	8.00E-23	120.2	63.1	73.8	hypothetical protein ARALYDRAFT_920040	gbpln	Arabidopsis lyrata	AT5G66816.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G50610.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26681495-26681800 FORWARD LENGTH=101	84	101	2.00E-22	120.2	63.1	72.6
Rsa1.0_01073.1.g23130.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01074.1.g23131.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01074.1.g23132.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01074.1.g23133.t1	ref|XP_002869790.1| hypothetical protein ARALYDRAFT_492556 [Arabidopsis lyrata subsp. lyrata] gi|297315626|gb|EFH46049.1| hypothetical protein ARALYDRAFT_492556 [Arabidopsis lyrata subsp. lyrata]	384	390	1.00E-122	101.6	60.9	75.0	hypothetical protein ARALYDRAFT_492556	gbpln	Arabidopsis lyrata	AT4G10220.1 | Symbols: | Protein of Unknown Function (DUF239) | chr4:6362189-6365079 FORWARD LENGTH=400	384	400	1.00E-123	104.2	58.6	74.0
Rsa1.0_01074.1.g23134.t1	ref|XP_002867731.1| hypothetical protein ARALYDRAFT_914292 [Arabidopsis lyrata subsp. lyrata] gi|297313567|gb|EFH43990.1| hypothetical protein ARALYDRAFT_914292 [Arabidopsis lyrata subsp. lyrata]	492	491	0	99.8	77.0	87.0	hypothetical protein ARALYDRAFT_914292	gbpln	Arabidopsis lyrata	AT4G23100.3 | Symbols: GSH1 | glutamate-cysteine ligase | chr4:12103458-12106751 REVERSE LENGTH=522	492	522	0	106.1	66.9	78.9
Rsa1.0_01074.1.g23135.t1	dbj|BAJ34068.1| unnamed protein product [Thellungiella halophila]	570	524	0	91.9	82.6	85.6	unnamed protein product	----	----	AT4G23100.3 | Symbols: GSH1 | glutamate-cysteine ligase | chr4:12103458-12106751 REVERSE LENGTH=522	570	522	0	91.6	80.4	84.4
Rsa1.0_01074.1.g23136.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01074.1.g23137.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01074.1.g23138.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01074.1.g23139.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01074.1.g23140.t2	ref|XP_002867728.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313564|gb|EFH43987.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	634	671	0	105.8	74.8	83.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G23130.1 | Symbols: CRK5, RLK6 | cysteine-rich RLK (RECEPTOR-like protein kinase) 5 | chr4:12117688-12120134 REVERSE LENGTH=659	634	659	0	103.9	71.6	81.2
Rsa1.0_01074.1.g23141.t1	gb|EOA16181.1| hypothetical protein CARUB_v10004319mg [Capsella rubella]	651	660	0	101.4	70.5	81.3	hypothetical protein CARUB_v10004319mg	gbpln	Capsella rubella	AT4G23130.2 | Symbols: CRK5, RLK6 | cysteine-rich RLK (RECEPTOR-like protein kinase) 5 | chr4:12117688-12120134 REVERSE LENGTH=663	651	663	0	101.8	63.3	76.3
Rsa1.0_01075.1.g23142.t9	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01075.1.g23143.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01075.1.g23144.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01075.1.g23145.t1	gb|EOA12628.1| hypothetical protein CARUB_v10027518mg [Capsella rubella]	1180	1253	0	106.2	78.1	87.0	hypothetical protein CARUB_v10027518mg	gbpln	Capsella rubella	AT5G44700.1 | Symbols: EDA23, GSO2 | Leucine-rich repeat transmembrane protein kinase | chr5:18033049-18036894 REVERSE LENGTH=1252	1180	1252	0	106.1	78.6	88.1
Rsa1.0_01075.1.g23146.t1	dbj|BAB08824.1| unnamed protein product [Arabidopsis thaliana]	97	108	4.00E-41	111.3	88.7	94.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G44710.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ribosomal protein S27/S33, mitochondrial (InterPro:IPR013219); Has 101 Blast hits to 101 proteins in 55 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 59; Plants - 26; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr5:18041621-18042322 FORWARD LENGTH=102	97	102	7.00E-41	105.2	86.6	91.8
Rsa1.0_01075.1.g23147.t1	ref|XP_002865328.1| molybdenum cofactor sulfurase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311163|gb|EFH41587.1| molybdenum cofactor sulfurase family protein [Arabidopsis lyrata subsp. lyrata]	308	308	1.00E-167	100.0	92.9	96.1	molybdenum cofactor sulfurase family protein	gbpln	Arabidopsis lyrata	AT5G44720.1 | Symbols: | Molybdenum cofactor sulfurase family protein | chr5:18043086-18045275 FORWARD LENGTH=308	308	308	1.00E-167	100.0	90.3	94.5
Rsa1.0_01075.1.g23148.t1	gb|EOA33803.1| hypothetical protein CARUB_v10021274mg [Capsella rubella]	284	304	2.00E-86	107.0	56.3	68.0	hypothetical protein CARUB_v10021274mg	gbpln	Capsella rubella	AT2G40560.1 | Symbols: | Protein kinase superfamily protein | chr2:16938705-16939616 REVERSE LENGTH=303	284	303	7.00E-75	106.7	53.5	69.4
Rsa1.0_01075.1.g23149.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_01075.1.g23150.t1</td><td>ref|XP_002863541.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297309376|gb|EFH39800.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]</td><td>362</td><td>381</td><td>1.00E-138</td><td>105.2</td><td>70.4</td><td>81.2</td><td>glycoside hydrolase family 28 protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G44840.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:18104851-18107127 REVERSE LENGTH=381</td><td>362</td><td>381</td><td>1.00E-139</td><td>105.2</td><td>69.6</td><td>80.4</td></tr>
<tr><td>Rsa1.0_01075.1.g23151.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01075.1.g23152.t1</td><td>ref|XP_002863539.1| hypothetical protein ARALYDRAFT_917078 [Arabidopsis lyrata subsp. lyrata] gi|297791311|ref|XP_002863540.1| hypothetical protein ARALYDRAFT_917082 [Arabidopsis lyrata subsp. lyrata] gi|297309374|gb|EFH39798.1| hypothetical protein ARALYDRAFT_917078 [Arabidopsis lyrata subsp. lyrata] gi|297309375|gb|EFH39799.1| hypothetical protein ARALYDRAFT_917082 [Arabidopsis lyrata subsp. lyrata]</td><td>322</td><td>321</td><td>1.00E-160</td><td>99.7</td><td>91.0</td><td>96.6</td><td>hypothetical protein ARALYDRAFT_917078</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G44860.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G19950.1); Has 233 Blast hits to 227 proteins in 25 species: Archae - 0; Bacteria - 13; Metazoa - 1; Fungi - 0; Plants - 216; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr5:18110688-18111653 REVERSE LENGTH=321</td><td>322</td><td>321</td><td>1.00E-162</td><td>99.7</td><td>90.7</td><td>96.3</td></tr>
<tr><td>Rsa1.0_01075.1.g23153.t1</td><td>gb|ABD64943.1| myb transcription factor, putative [Brassica oleracea]</td><td>342</td><td>327</td><td>1.00E-112</td><td>95.6</td><td>63.7</td><td>70.8</td><td>myb transcription factor, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47390.1 | Symbols: | myb-like transcription factor family protein | chr5:19227001-19228546 FORWARD LENGTH=365</td><td>342</td><td>365</td><td>1.00E-105</td><td>106.7</td><td>64.3</td><td>72.8</td></tr>
<tr><td>Rsa1.0_01075.1.g23154.t2</td><td>ref|NP_199308.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262649|sp|Q9FLA2.1|FDL34_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g44950 gi|10177487|dbj|BAB10878.1| unnamed protein product [Arabidopsis thaliana] gi|332007796|gb|AED95179.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]</td><td>488</td><td>438</td><td>1.00E-127</td><td>89.8</td><td>53.5</td><td>64.8</td><td>putative F-box/FBD/LRR-repeat protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G44950.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:18151665-18153164 FORWARD LENGTH=438</td><td>488</td><td>438</td><td>1.00E-130</td><td>89.8</td><td>53.5</td><td>64.8</td></tr>
<tr><td>Rsa1.0_01075.1.g23155.t1</td><td>ref|XP_002865306.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311141|gb|EFH41565.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>300</td><td>352</td><td>1.00E-141</td><td>117.3</td><td>82.0</td><td>88.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G44990.2 | Symbols: | Glutathione S-transferase family protein | chr5:18163370-18164768 FORWARD LENGTH=350</td><td>300</td><td>350</td><td>1.00E-142</td><td>116.7</td><td>80.0</td><td>87.7</td></tr>
<tr><td>Rsa1.0_01075.1.g23156.t1</td><td>ref|XP_002862977.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308767|gb|EFH39236.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>166</td><td>393</td><td>4.00E-48</td><td>236.7</td><td>56.0</td><td>72.9</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G45080.1 | Symbols: AtPP2-A6, PP2-A6 | phloem protein 2-A6 | chr5:18191575-18193207 REVERSE LENGTH=392</td><td>166</td><td>392</td><td>1.00E-46</td><td>236.1</td><td>54.2</td><td>68.1</td></tr>
<tr><td>Rsa1.0_01075.1.g23157.t2</td><td>gb|EOA14989.1| hypothetical protein CARUB_v10028338mg [Capsella rubella]</td><td>387</td><td>355</td><td>1.00E-125</td><td>91.7</td><td>57.4</td><td>72.1</td><td>hypothetical protein CARUB_v10028338mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G45070.1 | Symbols: AtPP2-A8, PP2-A8 | phloem protein 2-A8 | chr5:18187899-18189362 REVERSE LENGTH=354</td><td>387</td><td>354</td><td>1.00E-117</td><td>91.5</td><td>54.0</td><td>69.5</td></tr>
<tr><td>Rsa1.0_01076.1.g23158.t1</td><td>gb|EOA22172.1| hypothetical protein CARUB_v10002743mg, partial [Capsella rubella]</td><td>459</td><td>510</td><td>1.00E-140</td><td>111.1</td><td>57.1</td><td>72.3</td><td>hypothetical protein CARUB_v10002743mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G14930.2 | Symbols: SAG101 | senescence-associated gene 101 | chr5:4828754-4830769 FORWARD LENGTH=537</td><td>459</td><td>537</td><td>1.00E-137</td><td>117.0</td><td>60.1</td><td>73.9</td></tr>
<tr><td>Rsa1.0_01076.1.g23159.t4</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1826</td><td>1307</td><td>0</td><td>71.6</td><td>44.5</td><td>54.4</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14930.2 | Symbols: SAG101 | senescence-associated gene 101 | chr5:4828754-4830769 FORWARD LENGTH=537</td><td>1826</td><td>537</td><td>1.00E-178</td><td>29.4</td><td>18.5</td><td>22.2</td></tr>
<tr><td>Rsa1.0_01076.1.g23160.t1</td><td>dbj|BAJ34616.1| unnamed protein product [Thellungiella halophila]</td><td>232</td><td>247</td><td>7.00E-37</td><td>106.5</td><td>56.0</td><td>59.9</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G14920.1 | Symbols: | Gibberellin-regulated family protein | chr5:4826598-4827761 FORWARD LENGTH=275</td><td>232</td><td>275</td><td>9.00E-34</td><td>118.5</td><td>25.9</td><td>26.7</td></tr>
<tr><td>Rsa1.0_01076.1.g23161.t1</td><td>ref|NP_196993.2| NHL domain-containing protein [Arabidopsis thaliana] gi|332004703|gb|AED92086.1| NHL domain-containing protein [Arabidopsis thaliana]</td><td>172</td><td>754</td><td>4.00E-81</td><td>438.4</td><td>81.4</td><td>89.0</td><td>NHL domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14890.1 | Symbols: | NHL domain-containing protein | chr5:4818056-4821534 FORWARD LENGTH=754</td><td>172</td><td>754</td><td>2.00E-83</td><td>438.4</td><td>81.4</td><td>89.0</td></tr>
<tr><td>Rsa1.0_01076.1.g23162.t1</td><td>ref|XP_002871635.1| NHL repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317472|gb|EFH47894.1| NHL repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>475</td><td>704</td><td>0</td><td>148.2</td><td>87.4</td><td>91.6</td><td>NHL repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G14890.1 | Symbols: | NHL domain-containing protein | chr5:4818056-4821534 FORWARD LENGTH=754</td><td>475</td><td>754</td><td>0</td><td>158.7</td><td>85.7</td><td>90.7</td></tr>
<tr><td>Rsa1.0_01076.1.g23163.t2</td><td>gb|EOA20060.1| hypothetical protein CARUB_v10000335mg [Capsella rubella]</td><td>714</td><td>712</td><td>0</td><td>99.7</td><td>93.4</td><td>96.4</td><td>hypothetical protein CARUB_v10000335mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G14870.1 | Symbols: CNGC18, ATCNGC18 | cyclic nucleotide-gated channel 18 | chr5:4808268-4810897 REVERSE LENGTH=706</td><td>714</td><td>706</td><td>0</td><td>98.9</td><td>92.7</td><td>95.7</td></tr>
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<tr><td>Rsa1.0_01076.1.g23165.t1</td><td>dbj|BAJ34507.1| unnamed protein product [Thellungiella halophila]</td><td>276</td><td>276</td><td>1.00E-150</td><td>100.0</td><td>97.1</td><td>99.3</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G14800.1 | Symbols: P5CR, AT-P5R, AT-P5C1, EMB2772 | pyrroline-5-carboxylate (P5C) reductase | chr5:4786190-4787618 REVERSE LENGTH=276</td><td>276</td><td>276</td><td>1.00E-145</td><td>100.0</td><td>92.4</td><td>96.4</td></tr>
<tr><td>Rsa1.0_01076.1.g23166.t2</td><td>gb|EOA22474.1| hypothetical protein CARUB_v10003121mg [Capsella rubella]</td><td>771</td><td>358</td><td>0</td><td>46.4</td><td>44.2</td><td>45.4</td><td>hypothetical protein CARUB_v10003121mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G14780.1 | Symbols: FDH | formate dehydrogenase | chr5:4777043-4779190 FORWARD LENGTH=384</td><td>771</td><td>384</td><td>0</td><td>49.8</td><td>43.3</td><td>44.9</td></tr>
<tr><td>Rsa1.0_01076.1.g23167.t1</td><td>ref|XP_002873691.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319528|gb|EFH49950.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>977</td><td>938</td><td>0</td><td>96.0</td><td>77.1</td><td>84.2</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G14770.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:4772881-4775697 REVERSE LENGTH=938</td><td>977</td><td>938</td><td>0</td><td>96.0</td><td>75.9</td><td>83.9</td></tr>
<tr><td>Rsa1.0_01076.1.g23168.t1</td><td>ref|NP_568304.1| L-aspartate oxidase [Arabidopsis thaliana] gi|15010650|gb|AAK73984.1| AT5g14760/T9L3_60 [Arabidopsis thaliana] gi|24111279|gb|AAN46763.1| At5g14760/T9L3_60 [Arabidopsis thaliana] gi|332004691|gb|AED92074.1| L-aspartate oxidase [Arabidopsis thaliana]</td><td>650</td><td>651</td><td>0</td><td>100.2</td><td>91.1</td><td>94.6</td><td>L-aspartate oxidase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G14760.1 | Symbols: AO | L-aspartate oxidase | chr5:4769133-4772012 FORWARD LENGTH=651</td><td>650</td><td>651</td><td>0</td><td>100.2</td><td>91.1</td><td>94.6</td></tr>
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<tr><td>Rsa1.0_01077.1.g23170.t1</td><td>ref|XP_002871357.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297317194|gb|EFH47616.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>220</td><td>369</td><td>1.00E-11</td><td>167.7</td><td>18.2</td><td>19.1</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G08750.3 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:2852912-2854343 FORWARD LENGTH=370</td><td>220</td><td>370</td><td>5.00E-14</td><td>168.2</td><td>18.2</td><td>19.1</td></tr>
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<tr><td>Rsa1.0_01077.1.g23177.t1</td><td>gb|EMJ23027.1| hypothetical protein PRUPE_ppa016255mg [Prunus persica]</td><td>378</td><td>395</td><td>1.00E-151</td><td>104.5</td><td>66.1</td><td>79.6</td><td>hypothetical protein PRUPE_ppa016255mg</td><td>gbpln</td><td>Prunus persica</td><td>AT5G09280.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:2880423-2881597 REVERSE LENGTH=297</td><td>378</td><td>297</td><td>1.00E-142</td><td>78.6</td><td>62.4</td><td>64.6</td></tr>
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<tr><td>Rsa1.0_01077.1.g23181.t1</td><td>ref|NP_568213.2| Potassium transporter 7 [Arabidopsis thaliana] gi|38503183|sp|Q9FY75.2|POT7_ARATH RecName: Full=Potassium transporter 7; Short=AtHAK7; Short=AtPOT7 gi|332004004|gb|AED91387.1| Potassium transporter 7 [Arabidopsis thaliana]</td><td>877</td><td>858</td><td>0</td><td>97.8</td><td>89.5</td><td>94.0</td><td>Potassium transporter 7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G09400.1 | Symbols: KUP7 | K+ uptake permease 7 | chr5:2916377-2920604 FORWARD LENGTH=858</td><td>877</td><td>858</td><td>0</td><td>97.8</td><td>89.5</td><td>94.0</td></tr>
<tr><td>Rsa1.0_01077.1.g23182.t1</td><td>ref|NP_196505.2| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|67633792|gb|AAY78820.1| hydrolase [Arabidopsis thaliana] gi|332004009|gb|AED91392.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana]</td><td>314</td><td>311</td><td>1.00E-170</td><td>99.0</td><td>91.7</td><td>96.8</td><td>alpha/beta-hydrolase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G09430.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:2932162-2933362 FORWARD LENGTH=311</td><td>314</td><td>311</td><td>1.00E-172</td><td>99.0</td><td>91.7</td><td>96.8</td></tr>
<tr><td>Rsa1.0_01077.1.g23183.t1</td><td>ref|NP_196506.1| protein exordium like 4 [Arabidopsis thaliana] gi|9955531|emb|CAC05470.1| putative protein [Arabidopsis thaliana] gi|17473691|gb|AAL38302.1| putative protein [Arabidopsis thaliana] gi|20148463|gb|AAM10122.1| putative protein [Arabidopsis thaliana] gi|21593400|gb|AAM65367.1| phi-1-like protein [Arabidopsis thaliana] gi|332004010|gb|AED91393.1| protein exordium like 4 [Arabidopsis thaliana]</td><td>348</td><td>278</td><td>1.00E-105</td><td>79.9</td><td>60.6</td><td>67.5</td><td>protein exordium like 4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G09440.1 | Symbols: EXL4 | EXORDIUM like 4 | chr5:2938397-2939233 FORWARD LENGTH=278</td><td>348</td><td>278</td><td>1.00E-107</td><td>79.9</td><td>60.6</td><td>67.5</td></tr>
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<tr><td>Rsa1.0_01077.1.g23185.t1</td><td>ref|XP_002873405.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319242|gb|EFH49664.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>152</td><td>152</td><td>3.00E-77</td><td>100.0</td><td>92.8</td><td>96.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G09490.1 | Symbols: | Ribosomal protein S19 family protein | chr5:2952378-2953183 REVERSE LENGTH=152</td><td>152</td><td>152</td><td>7.00E-76</td><td>100.0</td><td>87.5</td><td>95.4</td></tr>
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<tr><td>Rsa1.0_01077.1.g23187.t1</td><td>gb|AAK96839.1| periaxin-like protein [Arabidopsis thaliana]</td><td>340</td><td>370</td><td>3.00E-96</td><td>108.8</td><td>80.0</td><td>88.8</td><td>periaxin-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G09530.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:2960080-2961192 REVERSE LENGTH=370</td><td>340</td><td>370</td><td>4.00E-98</td><td>108.8</td><td>79.4</td><td>88.2</td></tr>
<tr><td>Rsa1.0_01078.1.g23188.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01078.1.g23189.t9</td><td>gb|EOA20547.1| hypothetical protein CARUB_v10000859mg [Capsella rubella]</td><td>478</td><td>477</td><td>0</td><td>99.8</td><td>77.4</td><td>86.8</td><td>hypothetical protein CARUB_v10000859mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G07670.1 | Symbols: | RNI-like superfamily protein | chr5:2430421-2432065 FORWARD LENGTH=476</td><td>478</td><td>476</td><td>0</td><td>99.6</td><td>76.6</td><td>85.8</td></tr>
<tr><td>Rsa1.0_01078.1.g23190.t1</td><td>gb|AAR13700.1| WD-repeat protein [Brassica oleracea]</td><td>857</td><td>458</td><td>0</td><td>53.4</td><td>52.3</td><td>53.2</td><td>WD-repeat protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G07590.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:2401712-2403731 REVERSE LENGTH=458</td><td>857</td><td>458</td><td>0</td><td>53.4</td><td>51.8</td><td>52.9</td></tr>
<tr><td>Rsa1.0_01078.1.g23191.t1</td><td>gb|AAR15436.1| AP2 transcription factor [Sisymbrium irio]</td><td>219</td><td>218</td><td>5.00E-99</td><td>99.5</td><td>89.0</td><td>92.7</td><td>AP2 transcription factor</td><td>gbpln</td><td>Sisymbrium irio</td><td>AT5G07580.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:2399525-2400349 FORWARD LENGTH=274</td><td>219</td><td>274</td><td>1.00E-85</td><td>125.1</td><td>79.0</td><td>84.0</td></tr>
<tr><td>Rsa1.0_01078.1.g23192.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>142</td><td>1142</td><td>3.00E-18</td><td>804.2</td><td>35.2</td><td>45.8</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>142</td><td>303</td><td>4.00E-11</td><td>213.4</td><td>23.2</td><td>36.6</td></tr>
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Rsa1.0_01078.1.g23193.t1	ref|NP_196346.1| MEI2-like protein 4 [Arabidopsis thaliana] gi|75335654|sp|Q9LYN7.1|AML4_ARATH RecName: Full=Protein MEI2-like 4; Short=AML4; AltName: Full=MEI2-like protein 4 gi|7546707|emb|CAB87285.1| Mei2-like protein [Arabidopsis thaliana] gi|110742203|dbj|BAE99028.1| Mei2-like protein [Arabidopsis thaliana] gi|332003750|gb|AED91133.1| MEI2-like protein 4 [Arabidopsis thaliana]	901	907	0	100.7	83.2	90.1	MEI2-like protein 4	gbpln	Arabidopsis thaliana	AT5G07290.1 | Symbols: AML4, ML4 | MEI2-like 4 | chr5:2294248-2298491 FORWARD LENGTH=907	901	907	0	100.7	83.2	90.1
Rsa1.0_01078.1.g23194.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01078.1.g23195.t1	gb|EOA19823.1| hypothetical protein CARUB_v10000068mg [Capsella rubella]	1265	1200	0	94.9	75.2	82.8	hypothetical protein CARUB_v10000068mg	gbpln	Capsella rubella	AT5G07280.1 | Symbols: EMS1, EXS | Leucine-rich repeat transmembrane protein kinase | chr5:2285088-2288666 FORWARD LENGTH=1192	1265	1192	0	94.2	73.0	81.7
Rsa1.0_01078.1.g23196.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01078.1.g23197.t1	ref|NP_196344.2| E3 ubiquitin-protein ligase XBAT33 [Arabidopsis thaliana] gi|122239678|sp|Q4FE45.1|XB33_ARATH RecName: Full=E3 ubiquitin-protein ligase XBAT33; AltName: Full=Ankyrin repeat domain and RING finger-containing protein XBAT33; AltName: Full=Protein XB3 homolog 3 gi|70905089|gb|AAZ14070.1| At5g07270 [Arabidopsis thaliana] gi|117168057|gb|ABK32111.1| At5g07270 [Arabidopsis thaliana] gi|332003748|gb|AED91131.1| E3 ubiquitin-protein ligase XBAT33 [Arabidopsis thaliana]	518	513	0	99.0	90.7	94.6	E3 ubiquitin-protein ligase XBAT33	gbpln	Arabidopsis thaliana	AT5G07270.1 | Symbols: XBAT33 | XB3 ortholog 3 in Arabidopsis thaliana | chr5:2280821-2283384 FORWARD LENGTH=513	518	513	0	99.0	90.7	94.6
Rsa1.0_01078.1.g23198.t1	gb|EOA20989.1| hypothetical protein CARUB_v10001321mg [Capsella rubella]	348	346	1.00E-152	99.4	80.2	88.2	hypothetical protein CARUB_v10001321mg	gbpln	Capsella rubella	AT5G07250.1 | Symbols: ATRBL3, RBL3 | RHOMBOID-like protein 3 | chr5:2274437-2275935 REVERSE LENGTH=346	348	346	2.33E-156	99.4	81.0	87.1
Rsa1.0_01078.1.g23199.t1	gb|EOA20989.1| hypothetical protein CARUB_v10001321mg [Capsella rubella]	348	346	1.00E-139	99.4	72.7	83.9	hypothetical protein CARUB_v10001321mg	gbpln	Capsella rubella	AT5G07250.1 | Symbols: ATRBL3, RBL3 | RHOMBOID-like protein 3 | chr5:2274437-2275935 REVERSE LENGTH=346	348	346	1.00E-132	99.4	73.0	82.2
Rsa1.0_01078.1.g23200.t1	ref|XP_002871260.1| IQ-domain 24 [Arabidopsis lyrata subsp. lyrata] gi|297317097|gb|EFH47519.1| IQ-domain 24 [Arabidopsis lyrata subsp. lyrata]	350	401	1.00E-123	114.6	80.0	85.7	IQ-domain 24	gbpln	Arabidopsis lyrata	AT5G07240.1 | Symbols: IQD24 | IQ-domain 24 | chr5:2272028-2274051 FORWARD LENGTH=401	350	401	1.00E-123	114.6	78.6	85.7
Rsa1.0_01078.1.g23201.t1	gb|AAO85389.1| tapetum-specific protein BcA9 [Brassica rapa subsp. oleifera]	82	103	5.00E-37	125.6	96.3	96.3	tapetum-specific protein BcA9	gbpln	Brassica rapa	AT5G07230.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:2271013-2271408 FORWARD LENGTH=91	82	91	1.00E-28	111.0	75.6	82.9
Rsa1.0_01078.1.g23202.t1	ref|NP_196339.1| BCL-2-associated athanogene 3 [Arabidopsis thaliana] gi|75181093|sp|Q9LYP4.1|BAG3_ARATH RecName: Full=BAG family molecular chaperone regulator 3; AltName: Full=Bcl-2-associated athanogene 3 gi|16226483|gb|AAL16179.1|AF428411_1 AT5g07220/T28J14_160 [Arabidopsis thaliana] gi|7546700|emb|CAB87278.1| putative protein [Arabidopsis thaliana] gi|332003740|gb|AED91123.1| BCL-2-associated athanogene 3 [Arabidopsis thaliana]	308	303	1.00E-140	98.4	82.8	89.3	BCL-2-associated athanogene 3	gbpln	Arabidopsis thaliana	AT5G07220.1 | Symbols: ATBAG3, BAG3 | BCL-2-associated athanogene 3 | chr5:2265545-2266720 REVERSE LENGTH=303	308	303	1.00E-143	98.4	82.8	89.3
Rsa1.0_01078.1.g23203.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01078.1.g23204.t1	ref|NP_196338.1| putative two-component response regulator ARR21 [Arabidopsis thaliana] gi|7546699|emb|CAB87277.1| putative protein [Arabidopsis thaliana] gi|332003739|gb|AED91122.1| putative two-component response regulator ARR21 [Arabidopsis thaliana]	721	621	1.00E-152	86.1	39.0	45.4	putative two-component response regulator ARR21	gbpln	Arabidopsis thaliana	AT5G07210.1 | Symbols: ARR21, RR21 | response regulator 21 | chr5:2252237-2256018 FORWARD LENGTH=621	721	621	1.00E-155	86.1	39.0	45.4
Rsa1.0_01078.1.g23205.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01078.1.g23206.t1	gb|EOA19715.1| hypothetical protein CARUB_v10003732mg [Capsella rubella]	355	381	1.00E-135	107.3	65.9	71.0	hypothetical protein CARUB_v10003732mg	gbpln	Capsella rubella	AT5G07200.1 | Symbols: YAP169, GA20OX3, ATGA20OX3 | gibberellin 20-oxidase 3 | chr5:2243835-2245157 REVERSE LENGTH=380	355	380	1.00E-135	107.0	63.4	67.0

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<tr><td>Rsa1.0_01079.1.g23207.t1</td><td>ref|NP_190576.1| cyclin-D3-3 [Arabidopsis thaliana] gi|75313638|sp|Q9SN11.1|CCD33_ARATH RecName: Full=Cyclin-D3-3; AltName: Full=G1/S-specific cyclin-D3-3; Short=CycD3;3 gi|6522928|emb|CAB62115.1| cyclin D3-like protein [Arabidopsis thaliana] gi|15450595|gb|AAK96569.1| AT3g50070/F3A4_150 [Arabidopsis thaliana] gi|17380632|gb|AAL36079.1| AT3g50070/F3A4_150 [Arabidopsis thaliana] gi|21593092|gb|AAM65041.1| cyclin D3-like protein [Arabidopsis thaliana] gi|332645102|gb|AEE78623.1| cyclin-D3-3 [Arabidopsis thaliana]</td><td>361</td><td>361</td><td>1.00E-131</td><td>100.0</td><td>70.6</td><td>80.1</td><td>cyclin-D3-3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G50070.1 | Symbols: CYCD3;3 | CYCLIN D3;3 | chr3:18565322-18566669 REVERSE LENGTH=361</td><td>361</td><td>361</td><td>1.00E-133</td><td>100.0</td><td>70.6</td><td>80.1</td></tr>
<tr><td>Rsa1.0_01079.1.g23208.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01079.1.g23209.t1</td><td>gb|ABL97967.1| R2R3-MYB transcription factor [Brassica rapa]</td><td>268</td><td>266</td><td>1.00E-116</td><td>99.3</td><td>85.8</td><td>88.4</td><td>R2R3-MYB transcription factor</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G50060.1 | Symbols: MYB77 | myb domain protein 77 | chr3:18558146-18559051 REVERSE LENGTH=301</td><td>268</td><td>301</td><td>1.00E-94</td><td>112.3</td><td>77.2</td><td>84.7</td></tr>
<tr><td>Rsa1.0_01079.1.g23210.t1</td><td>gb|ACP30550.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>855</td><td>818</td><td>0</td><td>95.7</td><td>77.0</td><td>81.1</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G12220.2 | Symbols: RPS5 | Disease resistance protein (CC-NBS-LRR class) family | chr1:4145011-4147680 FORWARD LENGTH=889</td><td>855</td><td>889</td><td>0</td><td>104.0</td><td>59.5</td><td>73.7</td></tr>
<tr><td>Rsa1.0_01079.1.g23211.t1</td><td>dbj|BAA01091.1| casein kinase II catalytic subunit [Arabidopsis thaliana]</td><td>404</td><td>333</td><td>0</td><td>82.4</td><td>79.7</td><td>81.7</td><td>casein kinase II catalytic subunit</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G50000.1 | Symbols: CKA2, ATCKA2 | casein kinase II, alpha chain 2 | chr3:18534487-18536743 FORWARD LENGTH=403</td><td>404</td><td>403</td><td>0</td><td>99.8</td><td>84.4</td><td>86.6</td></tr>
<tr><td>Rsa1.0_01079.1.g23212.t1</td><td>ref|XP_002877714.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323552|gb|EFH53973.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>566</td><td>551</td><td>0</td><td>97.3</td><td>73.9</td><td>86.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G67385.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr5:26884754-26887083 FORWARD LENGTH=604</td><td>566</td><td>604</td><td>0</td><td>106.7</td><td>73.3</td><td>85.7</td></tr>
<tr><td>Rsa1.0_01079.1.g23213.t1</td><td>ref|NP_180096.3| serpin-Z10 [Arabidopsis thaliana] gi|75313479|sp|Q9SIR9.1|SPZ10_ARATH RecName: Full=Serpin-Z10; AltName: Full=ArathZ10 gi|4567253|gb|AAD23667.1| putative serpin [Arabidopsis thaliana] gi|330252581|gb|AEC07675.1| serpin-Z10 [Arabidopsis thaliana]</td><td>384</td><td>385</td><td>1.00E-170</td><td>100.3</td><td>76.0</td><td>85.4</td><td>serpin-Z10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G25240.1 | Symbols: | Serine protease inhibitor (SERPIN) family protein | chr2:10751872-10753134 REVERSE LENGTH=385</td><td>384</td><td>385</td><td>1.00E-173</td><td>100.3</td><td>76.0</td><td>85.4</td></tr>
<tr><td>Rsa1.0_01079.1.g23214.t1</td><td>ref|NP_190564.1| scarecrow-like protein 32 [Arabidopsis thaliana] gi|75206856|sp|Q9SN22.1|SCL32_ARATH RecName: Full=Scarecrow-like protein 32; Short=AtSCL32; AltName: Full=GRAS family protein 18; Short=AtGRAS-18 gi|6522916|emb|CAB62103.1| putative protein [Arabidopsis thaliana] gi|46518431|gb|AAS99697.1| At3g49950 [Arabidopsis thaliana] gi|110741573|dbj|BAE98735.1| hypothetical protein [Arabidopsis thaliana] gi|332645089|gb|AEE78610.1| scarecrow-like protein 32 [Arabidopsis thaliana]</td><td>418</td><td>410</td><td>0</td><td>98.1</td><td>83.0</td><td>89.2</td><td>scarecrow-like protein 32</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G49950.1 | Symbols: | GRAS family transcription factor | chr3:18522570-18523802 FORWARD LENGTH=410</td><td>418</td><td>410</td><td>0</td><td>98.1</td><td>83.0</td><td>89.2</td></tr>
<tr><td>Rsa1.0_01079.1.g23215.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01080.1.g23216.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01080.1.g23217.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>937</td><td>1307</td><td>0</td><td>139.5</td><td>62.6</td><td>76.3</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>937</td><td>1262</td><td>1.00E-100</td><td>134.7</td><td>21.7</td><td>32.3</td></tr>
<tr><td>Rsa1.0_01080.1.g23218.t1</td><td>ref|XP_002894087.1| hypothetical protein ARALYDRAFT_891606 [Arabidopsis lyrata subsp. lyrata] gi|297339929|gb|EFH70346.1| hypothetical protein ARALYDRAFT_891606 [Arabidopsis lyrata subsp. lyrata]</td><td>309</td><td>315</td><td>1.00E-155</td><td>101.9</td><td>87.7</td><td>92.9</td><td>hypothetical protein ARALYDRAFT_891606</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G47980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G62730.1); Has 169 Blast hits to 169 proteins in 41 species: Archae - 0; Bacteria - 68; Metazoa - 0; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:17691985-17693818 REVERSE LENGTH=315</td><td>309</td><td>315</td><td>1.00E-156</td><td>101.9</td><td>86.4</td><td>92.6</td></tr>
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<tr><td>Rsa1.0_01080.1.g23219.t1</td><td>ref|XP_002891403.1| gibberellin 2-oxidase 4 [Arabidopsis lyrata subsp. lyrata] gi|297337245|gb|EFH67662.1| gibberellin 2-oxidase 4 [Arabidopsis lyrata subsp. lyrata]</td><td>325</td><td>321</td><td>1.00E-169</td><td>98.8</td><td>88.0</td><td>92.3</td><td>gibberellin 2-oxidase 4</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G47990.1 | Symbols: ATGA2OX4, GA2OX4 | gibberellin 2-oxidase 4 | chr1:17698655-17700834 FORWARD LENGTH=321</td><td>325</td><td>321</td><td>1.00E-170</td><td>98.8</td><td>87.1</td><td>92.0</td></tr>
<tr><td>Rsa1.0_01080.1.g23220.t1</td><td>gb|EOA39303.1| hypothetical protein CARUB_v10012316mg [Capsella rubella]</td><td>177</td><td>177</td><td>1.00E-77</td><td>100.0</td><td>79.1</td><td>89.3</td><td>hypothetical protein CARUB_v10012316mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G48020.1 | Symbols: PMEI1, ATPMEI1 | pectin methylesterase inhibitor 1 | chr1:17716234-17716764 REVERSE LENGTH=176</td><td>177</td><td>176</td><td>6.00E-77</td><td>99.4</td><td>81.4</td><td>89.8</td></tr>
<tr><td>Rsa1.0_01080.1.g23221.t1</td><td>dbj|BAJ34104.1| unnamed protein product [Thellungiella halophila]</td><td>363</td><td>383</td><td>0</td><td>105.5</td><td>92.0</td><td>95.6</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G48040.1 | Symbols: | Protein phosphatase 2C family protein | chr1:17720064-17721698 REVERSE LENGTH=383</td><td>363</td><td>383</td><td>0</td><td>105.5</td><td>87.9</td><td>93.4</td></tr>
<tr><td>Rsa1.0_01080.1.g23222.t1</td><td>gb|AAF61460.1|AF139817_1 peroxiredoxin antioxidant [Brassica napus]</td><td>215</td><td>216</td><td>1.00E-121</td><td>100.5</td><td>97.2</td><td>100.0</td><td>peroxiredoxin antioxidant</td><td>gbpln</td><td>Brassica napus</td><td>AT1G48130.1 | Symbols: ATPER1, PER1 | 1-cysteine peroxiredoxin 1 | chr1:17780610-17781500 FORWARD LENGTH=216</td><td>215</td><td>216</td><td>1.00E-114</td><td>100.5</td><td>89.3</td><td>94.9</td></tr>
<tr><td>Rsa1.0_01080.1.g23223.t4</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01080.1.g23224.t2</td><td>ref|NP_175260.1| CBL-interacting serine/threonine-protein kinase 17 [Arabidopsis thaliana] gi|75332093|sp|Q94C40.1|CIPKH_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 17; AltName: Full=SNF1-related kinase 3.21; AltName: Full=SOS2-like protein kinase PKS20 gi|14571553|gb|AAK64513.1| CBL-interacting protein kinase 17 [Arabidopsis thaliana] gi|116325942|gb|ABJ98572.1| At1g48260 [Arabidopsis thaliana] gi|332194148|gb|AEE32269.1| CBL-interacting serine/threonine-protein kinase 17 [Arabidopsis thaliana]</td><td>333</td><td>432</td><td>1.00E-158</td><td>129.7</td><td>81.7</td><td>88.3</td><td>CBL-interacting serine/threonine-protein kinase 17</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G48260.1 | Symbols: CIPK17, SnRK3.21 | CBL-interacting protein kinase 17 | chr1:17814226-17817226 REVERSE LENGTH=432</td><td>333</td><td>432</td><td>1.00E-161</td><td>129.7</td><td>81.7</td><td>88.3</td></tr>
<tr><td>Rsa1.0_01081.1.g23225.t1</td><td>ref|XP_002863103.1| hypothetical protein ARALYDRAFT_497157 [Arabidopsis lyrata subsp. lyrata] gi|297308925|gb|EFH39362.1| hypothetical protein ARALYDRAFT_497157 [Arabidopsis lyrata subsp. lyrata]</td><td>234</td><td>234</td><td>1.00E-126</td><td>100.0</td><td>93.2</td><td>96.2</td><td>hypothetical protein ARALYDRAFT_497157</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G69930.1 | Symbols: ATGSTU11, GSTU11 | glutathione S-transferase TAU 11 | chr1:26337735-26338690 REVERSE LENGTH=234</td><td>234</td><td>234</td><td>1.00E-125</td><td>100.0</td><td>91.5</td><td>94.4</td></tr>
<tr><td>Rsa1.0_01081.1.g23226.t1</td><td>ref|XP_002888745.1| hypothetical protein ARALYDRAFT_894783 [Arabidopsis lyrata subsp. lyrata] gi|297334586|gb|EFH65004.1| hypothetical protein ARALYDRAFT_894783 [Arabidopsis lyrata subsp. lyrata]</td><td>122</td><td>191</td><td>1.00E-17</td><td>156.6</td><td>64.8</td><td>72.1</td><td>hypothetical protein ARALYDRAFT_894783</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G69935.1 | Symbols: SHW1 | short hypocotyl in white light1 | chr1:26342072-26343082 REVERSE LENGTH=192</td><td>122</td><td>192</td><td>5.00E-15</td><td>157.4</td><td>51.6</td><td>59.8</td></tr>
<tr><td>Rsa1.0_01081.1.g23227.t1</td><td>gb|AAG52564.1|AC010675_12 unknown protein; 6859-4829 [Arabidopsis thaliana]</td><td>647</td><td>676</td><td>0</td><td>104.5</td><td>75.0</td><td>85.6</td><td>unknown protein; 6859-4829</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>647</td><td>696</td><td>3.00E-87</td><td>107.6</td><td>32.0</td><td>51.6</td></tr>
<tr><td>Rsa1.0_01081.1.g23228.t1</td><td>ref|NP_001117575.1| CLAVATA3/ESR-related 26 protein [Arabidopsis thaliana] gi|332196883|gb|AEE35004.1| CLAVATA3/ESR (CLE)-related protein 26 [Arabidopsis thaliana]</td><td>100</td><td>102</td><td>3.00E-32</td><td>102.0</td><td>71.0</td><td>80.0</td><td>CLAVATA3/ESR-related 26 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G69970.2 | Symbols: CLE26 | CLAVATA3/ESR-RELATED 26 | chr1:26353079-26354256 REVERSE LENGTH=102</td><td>100</td><td>102</td><td>6.00E-35</td><td>102.0</td><td>71.0</td><td>80.0</td></tr>
<tr><td>Rsa1.0_01081.1.g23229.t1</td><td>ref|NP_564982.1| uncharacterized protein [Arabidopsis thaliana] gi|119360057|gb|ABL66757.1| At1g69980 [Arabidopsis thaliana] gi|332196884|gb|AEE35005.1| uncharacterized protein AT1G69980 [Arabidopsis thaliana]</td><td>212</td><td>205</td><td>4.00E-70</td><td>96.7</td><td>68.9</td><td>80.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G69980.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 30 Blast hits to 30 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26356559-26357647 REVERSE LENGTH=205</td><td>212</td><td>205</td><td>1.00E-72</td><td>96.7</td><td>68.9</td><td>80.7</td></tr>
<tr><td>Rsa1.0_01081.1.g23230.t1</td><td>gb|EOA36532.1| hypothetical protein CARUB_v10011581mg [Capsella rubella]</td><td>374</td><td>425</td><td>5.00E-75</td><td>113.6</td><td>48.4</td><td>63.1</td><td>hypothetical protein CARUB_v10011581mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G25150.1 | Symbols: | F-box family protein | chr1:8821027-8822328 FORWARD LENGTH=433</td><td>374</td><td>433</td><td>8.00E-69</td><td>115.8</td><td>44.4</td><td>59.4</td></tr>
</table>

Rsa1.0_01081.1.g23231.t1	ref|NP_177157.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|264664457|sp|C0LGI5.1|Y1699_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g69990; Flags: Precursor gi|224589473|gb|ACN59270.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332196885|gb|AEE35006.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	583	591	0	101.4	76.3	86.1	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G69990.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:26360235-26362010 REVERSE LENGTH=591	583	591	0	101.4	76.3	86.1
Rsa1.0_01081.1.g23232.t1	dbj|BAB01155.1| unnamed protein product [Arabidopsis thaliana] gi|49823524|gb|AAT68745.1| hypothetical protein At3g17200 [Arabidopsis thaliana] gi|60547763|gb|AAX23845.1| hypothetical protein At3g17200 [Arabidopsis thaliana]	397	310	5.00E-57	78.1	28.2	41.1	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	397	746	4.00E-37	187.9	21.7	30.5
Rsa1.0_01081.1.g23233.t1	ref|XP_002887270.1| hypothetical protein ARALYDRAFT_894796 [Arabidopsis lyrata subsp. lyrata] gi|297333111|gb|EFH63529.1| hypothetical protein ARALYDRAFT_894796 [Arabidopsis lyrata subsp. lyrata]	211	177	2.00E-62	83.9	57.3	66.4	hypothetical protein ARALYDRAFT_894796	gbpln	Arabidopsis lyrata	AT1G70040.1 | Symbols: | Protein of unknown function (DUF1163) | chr1:26381233-26381908 FORWARD LENGTH=193	211	193	4.00E-62	91.5	52.6	61.1
Rsa1.0_01081.1.g23234.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01081.1.g23235.t1	gb|EOA33276.1| hypothetical protein CARUB_v10019668mg [Capsella rubella]	1293	1328	0	102.7	82.9	88.9	hypothetical protein CARUB_v10019668mg	gbpln	Capsella rubella	AT1G70060.1 | Symbols: SNL4 | SIN3-like 4 | chr1:26383789-26389568 FORWARD LENGTH=1326	1293	1326	0	102.6	81.7	88.0
Rsa1.0_01081.1.g23236.t1	ref|NP_177164.1| DEAD-box ATP-dependent RNA helicase ISE2 [Arabidopsis thaliana] gi|298351833|sp|B9DFG3.2|ISE2_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase ISE2, chloroplastic; AltName: Full=Protein EMBRYO DEFECTIVE 25; AltName: Full=Protein INCREASED SIZE EXCLUSION LIMIT 2; AltName: Full=Protein PIGMENT DEFECTIVE 317; Flags: Precursor gi|332196892|gb|AEE35013.1| DEAD-box ATP-dependent RNA helicase ISE2 [Arabidopsis thaliana]	1171	1171	0	100.0	90.5	95.7	DEAD-box ATP-dependent RNA helicase ISE2	gbpln	Arabidopsis thaliana	AT1G70070.1 | Symbols: EMB25, PDE317, ISE2 | DEAD/DEAH box helicase, putative | chr1:26390016-26394148 REVERSE LENGTH=1171	1171	1171	0	100.0	90.5	95.7
Rsa1.0_01081.1.g23237.t1	ref|XP_002887288.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333129|gb|EFH63547.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	413	419	0	101.5	88.4	92.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G70230.1 | Symbols: TBL27 | TRICHOME BIREFRINGENCE-LIKE 27 | chr1:26450389-26451724 FORWARD LENGTH=416	413	416	0	100.7	86.4	92.3
Rsa1.0_01081.1.g23238.t1	gb|EOA35311.1| hypothetical protein CARUB_v10020485mg [Capsella rubella]	376	375	0	99.7	85.6	94.1	hypothetical protein CARUB_v10020485mg	gbpln	Capsella rubella	AT1G70260.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:26457067-26459338 REVERSE LENGTH=375	376	375	0	99.7	84.3	92.3
Rsa1.0_01081.1.g23239.t1	ref|XP_002888763.1| NHL repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297334604|gb|EFH65022.1| NHL repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	544	503	0	92.5	76.8	85.1	NHL repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G70280.2 | Symbols: | NHL domain-containing protein | chr1:26466086-26468471 REVERSE LENGTH=509	544	509	0	93.6	74.3	81.3
Rsa1.0_01081.1.g23240.t2	ref|NP_176009.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|263711285|sp|C0LGH2.2|Y1561_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g56130; Flags: Precursor gi|332195226|gb|AEE33347.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	639	1032	0	161.5	82.8	90.9	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G56130.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:20994931-21000887 REVERSE LENGTH=1032	639	1032	0	161.5	82.8	90.9
Rsa1.0_01081.1.g23241.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	166	1142	2.00E-32	688.0	45.2	57.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	166	575	1.00E-13	346.4	25.3	44.6
Rsa1.0_01081.1.g23242.t1	gb|EOA22321.1| hypothetical protein CARUB_v10002922mg [Capsella rubella]	636	713	0	112.1	69.0	80.7	hypothetical protein CARUB_v10002922mg	gbpln	Capsella rubella	AT5G26830.1 | Symbols: | Threonyl-tRNA synthetase | chr5:9437351-9441568 FORWARD LENGTH=709	636	709	0	111.5	67.9	79.9
Rsa1.0_01081.1.g23243.t1	#	#	#	#	#	#	#	-	----	----	AT4G34210.1 | Symbols: ASK11, SK11 | SKP1-like 11 | chr4:16379003-16379461 FORWARD LENGTH=152	159	152	4.00E-11	95.6	28.9	52.8

Rsa1.0_01081.1.g23244.t1	ref|XP_002888765.1| hypothetical protein ARALYDRAFT_894830 [Arabidopsis lyrata subsp. lyrata] gi|297334606|gb|EFH65024.1| hypothetical protein ARALYDRAFT_894830 [Arabidopsis lyrata subsp. lyrata]	783	783	0	100.0	88.8	93.9	hypothetical protein ARALYDRAFT_894830	gbpln	Arabidopsis lyrata	AT1G70300.1 | Symbols: KUP6 | K+ uptake permease 6 | chr1:26477993-26481233 REVERSE LENGTH=782	783	782	0	99.9	88.9	94.0
Rsa1.0_01081.1.g23245.t1	ref|XP_002887300.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333141|gb|EFH63559.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	568	604	0	106.3	77.6	84.3	kinase family protein	gbpln	Arabidopsis lyrata	AT1G70430.1 | Symbols: | Protein kinase superfamily protein | chr1:26545589-26548756 FORWARD LENGTH=594	568	594	0	104.6	77.5	84.3
Rsa1.0_01081.1.g23246.t1	ref|NP_177201.1| SRO3-like protein [Arabidopsis thaliana] gi|338819582|sp|O64592.2|SRO3_ARATH RecName: Full=Probable inactive poly [ADP-ribose] polymerase SRO3; AltName: Full=Protein SIMILAR TO RCD ONE 3 gi|332196941|gb|AEE35062.1| probable inactive poly [ADP-ribose] polymerase SRO3 [Arabidopsis thaliana]	309	305	1.00E-114	98.7	65.7	79.9	SRO3-like protein	gbpln	Arabidopsis thaliana	AT1G70440.1 | Symbols: SRO3 | similar to RCD one 3 | chr1:26549354-26550520 REVERSE LENGTH=305	309	305	1.00E-116	98.7	65.7	79.9
Rsa1.0_01081.1.g23247.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01081.1.g23248.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	1437	1534	0	106.8	64.9	77.1	F17L21.7	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1437	1262	1.00E-97	87.8	13.2	20.0
Rsa1.0_01081.1.g23249.t1	gb|EOA33797.1| hypothetical protein CARUB_v10021266mg [Capsella rubella]	828	691	0	83.5	39.7	43.0	hypothetical protein CARUB_v10021266mg	gbpln	Capsella rubella	AT1G70460.1 | Symbols: RHS10 | root hair specific 10 | chr1:26556155-26558994 FORWARD LENGTH=710	828	710	0	85.7	39.3	43.0
Rsa1.0_01081.1.g23250.t1	ref|XP_002888781.1| hypothetical protein ARALYDRAFT_476167 [Arabidopsis lyrata subsp. lyrata] gi|297334622|gb|EFH65040.1| hypothetical protein ARALYDRAFT_476167 [Arabidopsis lyrata subsp. lyrata]	169	151	3.00E-42	89.3	65.1	72.8	hypothetical protein ARALYDRAFT_476167	gbpln	Arabidopsis lyrata	AT1G23530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G70470.1); Has 38 Blast hits to 38 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:8345861-8346430 FORWARD LENGTH=189	169	189	2.00E-36	111.8	59.2	69.8
Rsa1.0_01081.1.g23251.t1	gb|EOA33842.1| hypothetical protein CARUB_v10021325mg [Capsella rubella]	325	320	1.00E-150	98.5	83.4	90.2	hypothetical protein CARUB_v10021325mg	gbpln	Capsella rubella	AT1G70480.2 | Symbols: | Domain of unknown function (DUF220) | chr1:26562250-26563608 FORWARD LENGTH=338	325	338	1.00E-152	104.0	82.8	90.5
Rsa1.0_01081.1.g23252.t1	ref|NP_177206.1| ADP-ribosylation factor 2 [Arabidopsis thaliana] gi|18395248|ref|NP_564195.1| ADP-ribosylation factor 2 [Arabidopsis thaliana] gi|30698721|ref|NP_850975.1| ADP-ribosylation factor 2 [Arabidopsis thaliana] gi|42572059|ref|NP_974120.1| ADP-ribosylation factor 2 [Arabidopsis thaliana] gi|297845410|ref|XP_002890586.1| hypothetical protein ARALYDRAFT_472612 [Arabidopsis lyrata subsp. lyrata] gi|378548287|sp|P0DH91.1|ARF2B_ARATH RecName: Full=ADP-ribosylation factor 2-B; Short=AtARF2; AltName: Full=ARF1-like protein U5 gi|378548311|sp|Q9LQC8.2|ARF2A_ARATH RecName: Full=ADP-ribosylation factor 2-A; Short=AtARF2 gi|11692864|gb|AAG40035.1|AF324684_1 At1g23490 [Arabidopsis thaliana] gi|11762198|gb|AAG40377.1|AF325025_1 At1g70490 [Arabidopsis thaliana] gi|11993875|gb|AAG42921.1|AF329504_1 putative ADP-ribosylation factor [Arabidopsis thaliana] gi|12325036|gb|AAG52463.1|AC010796_2 putative ADP-ribosylation factor 1; 15065-14075 [Arabidopsis thaliana] gi|13430504|gb|AAK25874.1|AF360164_1 putative ADP-ribosylation factor 1 [Arabidopsis thaliana] gi|13926232|gb|AAK49591.1|AF372875_1	181	181	1.00E-102	100.0	100.0	100.0	ADP-ribosylation factor 2	gbpln	Arabidopsis lyrata	AT1G70490.2 | Symbols: ATARFA1D, ARFA1D | Ras-related small GTP-binding family protein | chr1:26564162-26565152 REVERSE LENGTH=181	181	181	1.00E-105	100.0	100.0	100.0

Rsa1.0_01081.1.g23253.t1	ref|XP_002863817.1| hypothetical protein ARALYDRAFT_917597 [Arabidopsis lyrata subsp. lyrata] gi|297309652|gb|EFH40076.1| hypothetical protein ARALYDRAFT_917597 [Arabidopsis lyrata subsp. lyrata]	1087	1083	0	99.6	83.7	90.3	hypothetical protein ARALYDRAFT_917597	gbpln	Arabidopsis lyrata	AT5G42140.1 | Symbols: | Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain | chr5:16837547-16841640 REVERSE LENGTH=1073	1087	1073	0	98.7	82.0	88.4
Rsa1.0_01081.1.g23254.t4	ref|NP_189609.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|75273808|sp|Q9LRQ8.1|PMAT2_ARATH RecName: Full=Phenolic glucoside malonyltransferase 2 gi|11994477|dbj|BAB02518.1| anthocyanin 5-aromatic acyltransferase/benzoyltransferase-like protein [Arabidopsis thaliana] gi|26452509|dbj|BAC43339.1| putative anthocyanin 5-aromatic acyltransferase [Arabidopsis thaliana] gi|29824113|gb|AAP04017.1| putative anthocyanin 5-aromatic acyltransferase [Arabidopsis thaliana] gi|332644078|gb|AEE77599.1| phenolic glucoside malonyltransferase 2 [Arabidopsis thaliana]	459	451	1.00E-162	98.3	64.3	78.4	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT3G29670.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:11527952-11529307 FORWARD LENGTH=451	459	451	1.00E-164	98.3	64.3	78.4
Rsa1.0_01081.1.g23255.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	171	442	7.00E-52	258.5	61.4	76.0	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	171	343	1.00E-21	200.6	35.7	48.0
Rsa1.0_01081.1.g23256.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1631	1496	0	91.7	52.8	66.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1631	1262	1.00E-143	77.4	15.6	22.7
Rsa1.0_01081.1.g23257.t1	ref|XP_002887314.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297333155|gb|EFH63573.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	341	345	1.00E-160	101.2	83.0	89.4	F-box family protein	gbpln	Arabidopsis lyrata	AT1G70590.1 | Symbols: | F-box family protein | chr1:26618403-26620159 FORWARD LENGTH=351	341	351	1.00E-157	102.9	80.4	88.0
Rsa1.0_01081.1.g23258.t1	gb|ABM30196.1| ribosomal large subunit structural protein [Brassica juncea]	146	146	1.00E-75	100.0	96.6	98.6	ribosomal large subunit structural protein	gbpln	Brassica juncea	AT1G70600.1 | Symbols: | Ribosomal protein L18e/L15 superfamily protein | chr1:26621168-26621608 REVERSE LENGTH=146	146	146	1.00E-77	100.0	95.2	97.9
Rsa1.0_01081.1.g23259.t1	ref|XP_002892897.1| hypothetical protein ARALYDRAFT_471818 [Arabidopsis lyrata subsp. lyrata] gi|297338739|gb|EFH69156.1| hypothetical protein ARALYDRAFT_471818 [Arabidopsis lyrata subsp. lyrata]	232	233	1.00E-100	100.4	88.8	97.0	hypothetical protein ARALYDRAFT_471818	gbpln	Arabidopsis lyrata	AT1G16210.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1014 (InterPro:IPR010422); Has 16107 Blast hits to 8386 proteins in 1107 species: Archae - 26; Bacteria - 3370; Metazoa - 4013; Fungi - 1516; Plants - 526; Viruses - 120; Other Eukaryotes - 6536 (source: NCBI BLink). | chr1:5546352-5547447 REVERSE LENGTH=234	232	234	1.00E-102	100.9	84.5	93.1
Rsa1.0_01081.1.g23260.t1	gb|EOA33216.1| hypothetical protein CARUB_v10019952mg [Capsella rubella]	636	634	0	99.7	80.7	88.7	hypothetical protein CARUB_v10019952mg	gbpln	Capsella rubella	AT1G70630.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr1:26632118-26633991 FORWARD LENGTH=537	636	537	0	84.4	70.0	76.1
Rsa1.0_01081.1.g23261.t1	ref|NP_177221.1| octicosapeptide/Phox/Be.1 domain-containing protein [Arabidopsis thaliana] gi|12324740|gb|AAG52322.1|AC011663_1 unknown protein; 68334-67702 [Arabidopsis thaliana] gi|12325050|gb|AAG52477.1|AC010796_16 unknown protein; 86168-86800 [Arabidopsis thaliana] gi|149944319|gb|ABR46202.1| At1g70640 [Arabidopsis thaliana] gi|332196972|gb|AEE35093.1| octicosapeptide/Phox/Be.1 domain-containing protein [Arabidopsis thaliana]	166	174	1.00E-47	104.8	68.7	74.7	octicosapeptide/Phox/Be.1 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G70640.1 | Symbols: | octicosapeptide/Phox/Bem1p (PB1) domain-containing protein | chr1:26636255-26636887 FORWARD LENGTH=174	166	174	5.00E-50	104.8	68.7	74.7
Rsa1.0_01081.1.g23262.t1	gb|EOA32094.1| hypothetical protein CARUB_v10015343mg [Capsella rubella]	112	103	2.00E-12	92.0	36.6	45.5	hypothetical protein CARUB_v10015343mg	gbpln	Capsella rubella	AT3G01324.1 | Symbols: | ECA1-like gametogenesis related family protein | chr3:122140-122448 REVERSE LENGTH=102	112	102	4.00E-14	91.1	35.7	48.2

Rsa1.0_01081.1.g23263.t2	ref|NP_564993.1| zinc finger (Ran-binding) domain-containing protein [Arabidopsis thaliana] gi|332196973|gb|AEE35094.1| zinc finger (Ran-binding) domain-containing protein [Arabidopsis thaliana]	464	466	0	100.4	77.6	84.5	zinc finger (Ran-binding) domain-containing protein	gbpln	Arabidopsis thaliana	AT1G70650.1 | Symbols: | Ran BP2/NZF zinc finger-like superfamily protein | chr1:26638158-26640126 FORWARD LENGTH=466	464	466	0	100.4	77.6	84.5
Rsa1.0_01081.1.g23264.t1	gb|EOA33452.1| hypothetical protein CARUB_v10020949mg, partial [Capsella rubella]	191	210	3.00E-91	109.9	86.4	92.1	hypothetical protein CARUB_v10020949mg, partial	gbpln	Capsella rubella	AT1G70670.1 | Symbols: | Caleosin-related family protein | chr1:26644830-26645970 FORWARD LENGTH=195	191	195	3.00E-93	102.1	85.9	92.7
Rsa1.0_01082.1.g23265.t1	ref|NP_181463.1| jacalin-related lectin 22 [Arabidopsis thaliana] gi|238479502|ref|NP_001154564.1| jacalin-related lectin 22 [Arabidopsis thaliana] gi|12230237|sp|O80950.1|MB22_ARATH RecName: Full=Myrosinase-binding protein-like At2g39310 gi|3402676|gb|AAC28979.1| putative myrosinase-binding protein [Arabidopsis thaliana] gi|15809784|gb|AAL06820.1| At2g39310/T16B24.5 [Arabidopsis thaliana] gi|17978944|gb|AAL47438.1| At2g39310/T16B24.5 [Arabidopsis thaliana] gi|22655362|gb|AAM98273.1| At2g39310/T16B24.5 [Arabidopsis thaliana] gi|330254564|gb|AEC09658.1| jacalin-related lectin 22 [Arabidopsis thaliana] gi|330254566|gb|AEC09660.1| jacalin-related lectin 22 [Arabidopsis thaliana]	451	458	0	101.6	74.5	85.6	jacalin-related lectin 22	gbpln	Arabidopsis thaliana	AT2G39310.3 | Symbols: | jacalin-related lectin 22 | chr2:16414262-16416323 REVERSE LENGTH=458	451	458	0	101.6	74.5	85.6
Rsa1.0_01082.1.g23266.t1	ref|NP_181462.4| uncharacterized protein [Arabidopsis thaliana] gi|334184821|ref|NP_001189711.1| uncharacterized protein [Arabidopsis thaliana] gi|330254562|gb|AEC09656.1| uncharacterized protein AT2G39300 [Arabidopsis thaliana] gi|330254563|gb|AEC09657.1| uncharacterized protein AT2G39300 [Arabidopsis thaliana]	794	837	0	105.4	69.4	80.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G39300.2 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G55060.1). | chr2:16410109-16412869 REVERSE LENGTH=837	794	837	0	105.4	69.4	80.5
Rsa1.0_01082.1.g23267.t1	gb|EOA27607.1| hypothetical protein CARUB_v10023748mg [Capsella rubella]	305	296	1.00E-122	97.0	78.0	83.0	hypothetical protein CARUB_v10023748mg	gbpln	Capsella rubella	AT2G39290.1 | Symbols: PGPS1, PGP1, PGS1 | phosphatidylglycerolphosphate synthase 1 | chr2:16407274-16408840 FORWARD LENGTH=296	305	296	1.00E-118	97.0	78.7	83.0
Rsa1.0_01082.1.g23268.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01082.1.g23269.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	196	341	9.00E-45	174.0	49.0	65.8	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01082.1.g23270.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	296	368	4.00E-53	124.3	42.6	58.8	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	296	370	7.00E-46	125.0	41.6	56.4
Rsa1.0_01082.1.g23271.t1	ref|NP_178356.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|3184287|gb|AAC18934.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana] gi|330250497|gb|AEC05591.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	175	211	3.00E-17	120.6	24.0	38.3	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT2G02520.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr2:676771-678145 REVERSE LENGTH=211	175	211	1.00E-19	120.6	24.0	38.3
Rsa1.0_01082.1.g23272.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01082.1.g23273.t1	gb|EOA27019.1| hypothetical protein CARUB_v10023117mg [Capsella rubella]	64	478	2.00E-14	746.9	59.4	64.1	hypothetical protein CARUB_v10023117mg	gbpln	Capsella rubella	AT2G38400.2 | Symbols: AGT3 | alanine:glyoxylate aminotransferase 3 | chr2:16083779-16086115 FORWARD LENGTH=493	64	493	9.00E-17	770.3	57.8	64.1
Rsa1.0_01082.1.g23274.t1	ref|XP_002865823.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297311658|gb|EFH42082.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	203	289	6.00E-65	142.4	64.0	81.8	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT5G50790.1 | Symbols: SWEET10, AtSWEET10 | Nodulin MtN3 family protein | chr5:20656461-20657827 REVERSE LENGTH=289	203	289	2.00E-67	142.4	63.5	81.8
Rsa1.0_01082.1.g23275.t1	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1209	910	0	75.3	29.8	40.4	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1209	626	1.00E-108	51.8	17.5	24.7

Rsa1.0_01083.1.g23276.t1	ref|XP_002871573.1| hypothetical protein ARALYDRAFT_488176 [Arabidopsis lyrata subsp. lyrata] gi|297317410|gb|EFH47832.1| hypothetical protein ARALYDRAFT_488176 [Arabidopsis lyrata subsp. lyrata]	290	373	1.00E-114	128.6	70.3	79.0	hypothetical protein ARALYDRAFT_488176	gbpln	Arabidopsis lyrata	AT5G13570.1 | Symbols: DCP2, TDT, ATDCP2 | decapping 2 | chr5:4367532-4369992 FORWARD LENGTH=373	290	373	1.00E-116	128.6	69.7	78.3
Rsa1.0_01083.1.g23277.t1	gb|EOA17696.1| hypothetical protein CARUB_v10006067mg [Capsella rubella]	111	111	4.00E-48	100.0	83.8	89.2	hypothetical protein CARUB_v10006067mg	gbpln	Capsella rubella	AT5G40370.1 | Symbols: | Glutaredoxin family protein | chr5:16147826-16149052 REVERSE LENGTH=111	111	111	1.00E-50	100.0	83.8	87.4
Rsa1.0_01083.1.g23278.t1	ref|XP_002884714.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330554|gb|EFH60973.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	485	492	1.00E-117	101.4	48.9	68.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G09120.1 | Symbols: | Protein of unknown function (DUF674) | chr3:2797556-2798588 REVERSE LENGTH=314	485	314	2.00E-93	64.7	37.5	46.4
Rsa1.0_01083.1.g23279.t1	ref|XP_002870668.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297316504|gb|EFH46927.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	461	466	0	101.1	75.1	82.6	WD-40 repeat family protein	gbpln	Arabidopsis lyrata	AT5G40880.1 | Symbols: | WD-40 repeat family protein / zfwd3 protein (ZFWD3) | chr5:16379481-16381205 FORWARD LENGTH=472	461	472	0	102.4	72.5	80.5
Rsa1.0_01083.1.g23280.t1	ref|XP_002870668.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297316504|gb|EFH46927.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	524	466	0	88.9	63.4	70.6	WD-40 repeat family protein	gbpln	Arabidopsis lyrata	AT5G40880.1 | Symbols: | WD-40 repeat family protein / zfwd3 protein (ZFWD3) | chr5:16379481-16381205 FORWARD LENGTH=472	524	472	0	90.1	63.5	70.8
Rsa1.0_01083.1.g23281.t1	ref|XP_002875410.1| hypothetical protein ARALYDRAFT_484578 [Arabidopsis lyrata subsp. lyrata] gi|297321248|gb|EFH51669.1| hypothetical protein ARALYDRAFT_484578 [Arabidopsis lyrata subsp. lyrata]	234	244	6.00E-36	104.3	54.7	66.7	hypothetical protein ARALYDRAFT_484578	gbpln	Arabidopsis lyrata	AT3G27880.1 | Symbols: | Protein of unknown function (DUF1645) | chr3:10338429-10339157 FORWARD LENGTH=242	234	242	4.00E-37	103.4	50.9	61.5
Rsa1.0_01083.1.g23282.t1	ref|NP_198849.1| transcription factor MYB23 [Arabidopsis thaliana] gi|75332916|sp|Q96276.1|MYB23_ARATH RecName: Full=Transcription factor MYB23; AltName: Full=Myb-related protein 23; Short=AtMYB23 gi|1495253|emb|CAA92281.1| myb-related protein [Arabidopsis thaliana] gi|10178143|dbj|BAB11588.1| Myb-related protein [Arabidopsis thaliana] gi|41619432|gb|AAS10101.1| MYB transcription factor [Arabidopsis thaliana] gi|94442501|gb|ABF19038.1| At5g40330 [Arabidopsis thaliana] gi|332007151|gb|AED94534.1| transcription factor MYB23 [Arabidopsis thaliana]	233	219	1.00E-100	94.0	76.8	82.4	transcription factor MYB23	gbpln	Arabidopsis thaliana	AT5G40330.1 | Symbols: MYB23, ATMYB23, ATMYBRTF | myb domain protein 23 | chr5:16127849-16129468 FORWARD LENGTH=219	233	219	1.00E-102	94.0	76.8	82.4
Rsa1.0_01084.1.g23283.t6	ref|NP_200492.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262578|sp|Q9FJT2.1|FDL40_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g56810 gi|10176785|dbj|BAB09899.1| unnamed protein product [Arabidopsis thaliana] gi|332009427|gb|AED96810.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	692	435	3.00E-95	62.9	32.7	41.8	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G56810.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22974520-22975992 FORWARD LENGTH=435	692	435	6.00E-98	62.9	32.7	41.8
Rsa1.0_01084.1.g23284.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	449	1611	2.00E-19	358.8	18.3	30.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01084.1.g23285.t2	gb|EOA24087.1| hypothetical protein CARUB_v10017318mg [Capsella rubella]	437	424	0	97.0	87.0	92.0	hypothetical protein CARUB_v10017318mg	gbpln	Capsella rubella	AT3G48530.1 | Symbols: KING1 | SNF1-related protein kinase regulatory subunit gamma 1 | chr3:17987559-17989592 FORWARD LENGTH=424	437	424	0	97.0	86.7	91.8
Rsa1.0_01084.1.g23286.t1	gb|EOA25308.1| hypothetical protein CARUB_v10018623mg [Capsella rubella]	227	230	1.00E-119	101.3	89.9	94.7	hypothetical protein CARUB_v10018623mg	gbpln	Capsella rubella	AT3G48540.1 | Symbols: | Cytidine/deoxycytidylate deaminase family protein | chr3:17989798-17992015 REVERSE LENGTH=232	227	232	1.00E-120	102.2	90.3	95.6
Rsa1.0_01084.1.g23287.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01084.1.g23288.t1	gb|AAF97298.1|AC007843_1 Hypothetical protein [Arabidopsis thaliana]	340	362	9.00E-46	106.5	29.1	38.5	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01084.1.g23289.t1	ref|XP_002875912.1| hypothetical protein ARALYDRAFT_485213 [Arabidopsis lyrata subsp. lyrata] gi|297321750|gb|EFH52171.1| hypothetical protein ARALYDRAFT_485213 [Arabidopsis lyrata subsp. lyrata]	161	160	5.00E-67	99.4	88.2	91.3	hypothetical protein ARALYDRAFT_485213	gbpln	Arabidopsis lyrata	AT3G48550.1 | Symbols: | BEST Arabidopsis thaliana protein match is: C2H2-like zinc finger protein (TAIR:AT2G01940.3); Has 78 Blast hits to 78 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:17994048-17994595 FORWARD LENGTH=158	161	158	8.00E-67	98.1	86.3	90.1
Rsa1.0_01085.1.g23290.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01085.1.g23291.t1	ref|NP_200149.1| Putative pectinesterase/pectinesterase inhibitor 61 [Arabidopsis thaliana] gi|75309150|sp|Q9FK05.1|PME61_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 61; Includes: RecName: Full=Pectinesterase inhibitor 61; AltName: Full=Pectin methylesterase inhibitor 61; Includes: RecName: Full=Pectinesterase 61; Short=PE 61; AltName: Full=AtPMEpcrF; AltName: Full=Pectin methylesterase 61; Short=AtPME61 gi|13507549|gb|AAK28637.1|AF360340_1 putative pectinesterase [Arabidopsis thaliana] gi|9759184|dbj|BAB09799.1| pectinesterase [Arabidopsis thaliana] gi|15293287|gb|AAK93754.1| putative pectinesterase [Arabidopsis thaliana] gi|332008962|gb|AED96345.1| Putative pectinesterase/pectinesterase inhibitor 61 [Arabidopsis thaliana]	586	587	0	100.2	86.2	92.8	Putative pectinesterase/pectinesterase inhibitor 61	gbpln	Arabidopsis thaliana	AT5G53370.1 | Symbols: ATPMEPCRF, PMEPCRF | pectin methylesterase PCR fragment F | chr5:21649683-21651530 REVERSE LENGTH=587	586	587	0	100.2	86.2	92.8
Rsa1.0_01085.1.g23292.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01085.1.g23293.t1	ref|NP_568791.1| putative beta-1,3-galactosyltransferase 11 [Arabidopsis thaliana] gi|75165503|sp|Q94F27.1|B3GTB_ARATH RecName: Full=Probable beta-1,3-galactosyltransferase 11 gi|14423410|gb|AAK62387.1|AF386942_1 Avr9 elicitor response protein-like [Arabidopsis thaliana] gi|20148409|gb|AAM10095.1| Avr9 elicitor response protein-like [Arabidopsis thaliana] gi|332008958|gb|AED96341.1| putative beta-1,3-galactosyltransferase 11 [Arabidopsis thaliana]	337	338	1.00E-177	100.3	92.9	96.4	putative beta-1,3-galactosyltransferase 11	gbpln	Arabidopsis thaliana	AT5G53340.1 | Symbols: | Galactosyltransferase family protein | chr5:21641045-21643195 REVERSE LENGTH=338	337	338	1.00E-180	100.3	92.9	96.4
Rsa1.0_01085.1.g23294.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01085.1.g23295.t1	gb|EOA13991.1| hypothetical protein CARUB_v10027123mg [Capsella rubella]	205	213	3.00E-97	103.9	88.8	93.2	hypothetical protein CARUB_v10027123mg	gbpln	Capsella rubella	AT5G53310.1 | Symbols: | myosin heavy chain-related | chr5:21634657-21636094 FORWARD LENGTH=210	205	210	7.00E-97	102.4	85.9	92.7

Rsa1.0_01085.1.g23296.t1	ref|NP_568788.1| ubiquitin-conjugating enzyme E2 10 [Arabidopsis thaliana] gi|30696309|ref|NP_851181.1| ubiquitin-conjugating enzyme E2 10 [Arabidopsis thaliana] gi|334188360|ref|NP_001190528.1| ubiquitin-conjugating enzyme E2 10 [Arabidopsis thaliana] gi|297796167|ref|XP_002865968.1| ubiquitin-conjugating enzyme 10 [Arabidopsis lyrata subsp. lyrata] gi|464987|sp|P35133.1|UBC10_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 10; AltName: Full=Ubiquitin carrier protein 10/12; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 10/12; AltName: Full=Ubiquitin-protein ligase 10/12 gi|11692932|gb|AAG40069.1|AF324718_1 AT5g53300 [Arabidopsis thaliana] gi|11762158|gb|AAG40357.1|AF325005_1 AT5g53300 [Arabidopsis thaliana] gi|11908050|gb|AAG41454.1|AF326872_1 putative E2, ubiquitin-conjugating enzyme UBC10 [Arabidopsis thaliana] gi|297878|emb|CAA78715.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|349213|gb|AAA32895.1| ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|9759177|dbj|BAB09792.1| ubiquitin-conjugating enzyme E2-17 kD 10 (ubiquitin-protein ligase 10) (ubiquitin carrier protein 10) [Arabidopsis	148	148	6.00E-82	100.0	99.3	100.0	ubiquitin-conjugating enzyme E2 10	gbpln	Arabidopsis lyrata	AT5G53300.4 | Symbols: UBC10 | ubiquitin-conjugating enzyme 10 | chr5:21632802-21633989 REVERSE LENGTH=148	148	148	2.00E-84	100.0	99.3	100.0
Rsa1.0_01085.1.g23297.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01085.1.g23298.t1	ref|NP_200141.1| ethylene-responsive transcription factor CRF3 [Arabidopsis thaliana] gi|75262588|sp|Q9FK12.1|CRF3_ARATH RecName: Full=Ethylene-responsive transcription factor CRF3; AltName: Full=Protein CYTOKININ RESPONSE FACTOR 3 gi|9759176|dbj|BAB09791.1| unnamed protein product [Arabidopsis thaliana] gi|48479348|gb|AAT44945.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|56121914|gb|AAV74238.1| At5g53290 [Arabidopsis thaliana] gi|60543347|gb|AAX22271.1| At5g53290 [Arabidopsis thaliana] gi|332008950|gb|AED96333.1| ethylene-responsive transcription factor CRF3 [Arabidopsis thaliana]	355	354	1.00E-118	99.7	70.7	78.9	ethylene-responsive transcription factor CRF3	gbpln	Arabidopsis thaliana	AT5G53290.1 | Symbols: CRF3 | cytokinin response factor 3 | chr5:21617961-21619025 REVERSE LENGTH=354	355	354	1.00E-120	99.7	70.7	78.9
Rsa1.0_01086.1.g23299.t1	gb|EOA12866.1| hypothetical protein CARUB_v10025834mg [Capsella rubella]	926	934	0	100.9	95.0	97.7	hypothetical protein CARUB_v10025834mg	gbpln	Capsella rubella	AT5G60700.1 | Symbols: | glycosyltransferase family protein 2 | chr5:24402329-24404729 REVERSE LENGTH=668	926	668	0	72.1	69.4	70.8
Rsa1.0_01086.1.g23300.t1	ref|XP_002864698.1| hypothetical protein ARALYDRAFT_496218 [Arabidopsis lyrata subsp. lyrata] gi|297310533|gb|EFH40957.1| hypothetical protein ARALYDRAFT_496218 [Arabidopsis lyrata subsp. lyrata]	849	844	0	99.4	92.1	96.5	hypothetical protein ARALYDRAFT_496218	gbpln	Arabidopsis lyrata	AT5G60690.1 | Symbols: REV, IFL, IFL1 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr5:24397734-24401933 FORWARD LENGTH=842	849	842	0	99.2	92.1	96.5
Rsa1.0_01086.1.g23301.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01086.1.g23302.t1	ref|XP_002864697.1| hypothetical protein ARALYDRAFT_496217 [Arabidopsis lyrata subsp. lyrata] gi|297310532|gb|EFH40956.1| hypothetical protein ARALYDRAFT_496217 [Arabidopsis lyrata subsp. lyrata]	168	158	6.00E-51	94.0	72.6	82.1	hypothetical protein ARALYDRAFT_496217	gbpln	Arabidopsis lyrata	AT5G60680.1 | Symbols: | Protein of unknown function, DUF584 | chr5:24386247-24386738 FORWARD LENGTH=163	168	163	4.00E-47	97.0	69.6	80.4
Rsa1.0_01086.1.g23303.t12	ref|XP_002866390.1| hypothetical protein ARALYDRAFT_496216 [Arabidopsis lyrata subsp. lyrata] gi|297312225|gb|EFH42649.1| hypothetical protein ARALYDRAFT_496216 [Arabidopsis lyrata subsp. lyrata]	292	155	5.00E-12	53.1	14.4	15.8	hypothetical protein ARALYDRAFT_496216	gbpln	Arabidopsis lyrata	AT5G60670.1 | Symbols: | Ribosomal protein L11 family protein | chr5:24381066-24381566 REVERSE LENGTH=166	292	166	3.00E-13	56.8	14.4	16.1

Rsa1.0_01087.1.g23304.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	457	1142	6.00E-77	249.9	33.3	47.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	457	575	3.00E-40	125.8	21.2	33.5
Rsa1.0_01087.1.g23305.t1	ref|NP_563715.1| putative pectate lyase 1 [Arabidopsis thaliana] gi|32129844|sp|Q940Q1.2|PEL1_ARATH RecName: Full=Probable pectate lyase 1; AltName: Full=Pectate lyase A1; Flags: Precursor gi|2494113|gb|AAB80622.1| Strong similarity to Musa pectate lyase (gb|X92943). ESTs gb|AA042458, gb|ATTS4502, gb|N38552 come from this gene [Arabidopsis thaliana] gi|18086433|gb|AAL57671.1| At1g04680/T1G11_6 [Arabidopsis thaliana] gi|21593312|gb|AAM65261.1| putative pectate lyase A11 [Arabidopsis thaliana] gi|332189611|gb|AEE27732.1| putative pectate lyase 1 [Arabidopsis thaliana]	431	431	0	100.0	93.3	97.0	putative pectate lyase 1	gbpln	Arabidopsis thaliana	AT1G04680.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:1304052-1307780 REVERSE LENGTH=431	431	431	0	100.0	93.3	97.0
Rsa1.0_01087.1.g23306.t2	gb|ABH09777.1| pollen-preferential protein [Brassica rapa subsp. chinensis]	129	129	5.00E-63	100.0	94.6	95.3	pollen-preferential protein	gbpln	Brassica rapa	AT1G04670.1 | Symbols: | unknown protein; Has 40 Blast hits to 40 proteins in 14 species: Archae - 2; Bacteria - 5; Metazoa - 1; Fungi - 2; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1301985-1302532 FORWARD LENGTH=126	129	126	2.00E-52	97.7	76.7	86.0
Rsa1.0_01087.1.g23307.t1	ref|XP_002892235.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338077|gb|EFH68494.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	215	207	6.00E-17	96.3	20.5	23.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G04660.1 | Symbols: | glycine-rich protein | chr1:1300668-1301306 REVERSE LENGTH=212	215	212	9.00E-19	98.6	20.5	22.8
Rsa1.0_01087.1.g23308.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	331	1447	5.00E-76	437.2	44.1	62.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	331	746	7.00E-53	225.4	34.1	50.5
Rsa1.0_01087.1.g23309.t1	dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	154	1098	3.00E-40	713.0	50.6	62.3	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	154	237	4.00E-17	153.9	32.5	50.0
Rsa1.0_01087.1.g23310.t1	ref|NP_565761.1| NADH dehydrogenase [Arabidopsis thaliana] gi|297823115|ref|XP_002879440.1| hypothetical protein ARALYDRAFT_482258 [Arabidopsis lyrata subsp. lyrata] gi|75219577|sp|O49313.1|NDADB_ARATH RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-B gi|2924772|gb|AAC04901.1| expressed protein [Arabidopsis thaliana] gi|17529030|gb|AAL38725.1| unknown protein [Arabidopsis thaliana] gi|20259081|gb|AAM14256.1| unknown protein [Arabidopsis thaliana] gi|21618056|gb|AAM67106.1| unknown [Arabidopsis thaliana] gi|297325279|gb|EFH55699.1| hypothetical protein ARALYDRAFT_482258 [Arabidopsis lyrata subsp. lyrata] gi|330253707|gb|AEC08801.1| NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-B [Arabidopsis thaliana]	71	143	3.00E-18	201.4	59.2	63.4	NADH dehydrogenase	gbpln	Arabidopsis lyrata	AT2G33220.1 | Symbols: | GRIM-19 protein | chr2:14078974-14079929 FORWARD LENGTH=143	71	143	4.00E-21	201.4	59.2	63.4
Rsa1.0_01087.1.g23311.t1	gb|EOA36577.1| hypothetical protein CARUB_v10011757mg [Capsella rubella]	437	436	0	99.8	92.2	96.1	hypothetical protein CARUB_v10011757mg	gbpln	Capsella rubella	AT1G04610.1 | Symbols: YUC3 | YUCCA 3 | chr1:1279524-1281331 FORWARD LENGTH=437	437	437	0	100.0	90.6	95.9

Rsa1.0_01088.1.g23312.t1	ref|NP_190559.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana] gi|75183315|sp|Q9M2W8.1|Y3990_ARATH RecName: Full=BTB/POZ domain-containing protein At3g49900 gi|6723435|emb|CAB66928.1| putative protein [Arabidopsis thaliana] gi|332645082|gb|AEE78603.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana]	442	517	1.00E-145	117.0	62.9	69.7	Phototropic-responsive NPH3 family protein	gbpln	Arabidopsis thaliana	AT3G49900.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr3:18500635-18502614 REVERSE LENGTH=517	442	517	1.00E-148	117.0	62.9	69.7
Rsa1.0_01088.1.g23313.t1	ref|XP_002893922.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339764|gb|EFH70181.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	132	582	2.00E-26	440.9	57.6	72.7	predicted protein	gbpln	Arabidopsis lyrata	AT4G08510.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G36990.1); Has 888 Blast hits to 321 proteins in 121 species: Archae - 0; Bacteria - 120; Metazoa - 86; Fungi - 24; Plants - 79; Viruses - 0; Other Eukaryotes - 579 (source: NCBI BLink). | chr4:5411023-5413016 FORWARD LENGTH=551	132	551	9.00E-28	417.4	59.8	72.7
Rsa1.0_01088.1.g23314.t1	ref|XP_002865966.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata] gi|297311801|gb|EFH42225.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata]	295	455	1.00E-80	154.2	53.2	68.1	hypothetical protein ARALYDRAFT_357572	gbpln	Arabidopsis lyrata	AT1G30790.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:10932713-10933912 FORWARD LENGTH=399	295	399	8.00E-57	135.3	46.1	61.4
Rsa1.0_01088.1.g23315.t1	ref|NP_190558.1| uncharacterized protein [Arabidopsis thaliana] gi|6723434|emb|CAB66927.1| putative protein [Arabidopsis thaliana] gi|92856611|gb|ABE77408.1| At3g49890 [Arabidopsis thaliana] gi|332645081|gb|AEE78602.1| uncharacterized protein AT3G49890 [Arabidopsis thaliana]	66	220	1.00E-10	333.3	60.6	68.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G49890.1 | Symbols: | unknown protein; Has 27 Blast hits to 27 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:18499296-18500501 FORWARD LENGTH=220	66	220	2.00E-13	333.3	60.6	68.2
Rsa1.0_01088.1.g23316.t1	ref|XP_002876002.1| glycosyl hydrolase family protein 43 [Arabidopsis lyrata subsp. lyrata] gi|297321840|gb|EFH52261.1| glycosyl hydrolase family protein 43 [Arabidopsis lyrata subsp. lyrata]	498	465	0	93.4	78.1	83.7	glycosyl hydrolase family protein 43	gbpln	Arabidopsis lyrata	AT3G49880.1 | Symbols: | glycosyl hydrolase family protein 43 | chr3:18496907-18498398 FORWARD LENGTH=466	498	466	0	93.6	78.9	84.7
Rsa1.0_01088.1.g23317.t1	gb|EOA24466.1| hypothetical protein CARUB_v10017722mg [Capsella rubella]	287	302	4.00E-86	105.2	75.3	83.6	hypothetical protein CARUB_v10017722mg	gbpln	Capsella rubella	AT3G49850.1 | Symbols: TRB3, ATTRB3, TBP2 | telomere repeat binding factor 3 | chr3:18489451-18490731 FORWARD LENGTH=295	287	295	1.00E-85	102.8	72.8	83.6
Rsa1.0_01088.1.g23318.t1	emb|CAB66922.1| putative protein [Arabidopsis thaliana]	115	651	8.00E-12	566.1	55.7	56.5	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01088.1.g23319.t1	ref|XP_002875997.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321835|gb|EFH52256.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	129	141	1.00E-44	109.3	71.3	77.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G49820.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65925.1); Has 23 Blast hits to 23 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:18481237-18481722 FORWARD LENGTH=161	129	161	3.00E-38	124.8	71.3	77.5
Rsa1.0_01088.1.g23320.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01088.1.g23321.t1	gb|EOA19072.1| hypothetical protein CARUB_v10007738mg [Capsella rubella]	170	480	2.00E-32	282.4	40.6	57.1	hypothetical protein CARUB_v10007738mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	170	566	1.00E-34	332.9	38.2	60.6
Rsa1.0_01089.1.g23322.t1	ref|XP_002868337.1| hypothetical protein ARALYDRAFT_493535 [Arabidopsis lyrata subsp. lyrata] gi|297314173|gb|EFH44596.1| hypothetical protein ARALYDRAFT_493535 [Arabidopsis lyrata subsp. lyrata]	91	92	3.00E-37	101.1	86.8	92.3	hypothetical protein ARALYDRAFT_493535	gbpln	Arabidopsis lyrata	AT4G13790.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:7999846-8000124 REVERSE LENGTH=92	91	92	2.00E-39	101.1	84.6	92.3
Rsa1.0_01089.1.g23323.t1	gb|EOA15994.1| hypothetical protein CARUB_v10004113mg [Capsella rubella]	827	866	0	104.7	66.6	79.9	hypothetical protein CARUB_v10004113mg	gbpln	Capsella rubella	AT4G13820.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:8008535-8010694 REVERSE LENGTH=719	827	719	0	86.9	60.2	69.3
Rsa1.0_01089.1.g23324.t1	#	#	#	#	#	#	#	-	----	----	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	123	484	1.00E-11	393.5	23.6	29.3
Rsa1.0_01089.1.g23325.t1	gb|EOA15770.1| hypothetical protein CARUB_v10006927mg [Capsella rubella]	868	852	0	98.2	67.2	79.6	hypothetical protein CARUB_v10006927mg	gbpln	Capsella rubella	AT4G13810.1 | Symbols: AtRLP47, RLP47 | receptor like protein 47 | chr4:8005062-8007287 REVERSE LENGTH=741	868	741	0	85.4	59.4	68.5

Rsa1.0_01089.1.g23326.t1	ref|XP_002868330.1| hypothetical protein ARALYDRAFT_493524 [Arabidopsis lyrata subsp. lyrata] gi|297314166|gb|EFH44589.1| hypothetical protein ARALYDRAFT_493524 [Arabidopsis lyrata subsp. lyrata]	271	286	1.00E-122	105.5	84.5	92.6	hypothetical protein ARALYDRAFT_493524	gbpln	Arabidopsis lyrata	AT4G13870.2 | Symbols: WRNEXO | Werner syndrome-like exonuclease | chr4:8023563-8025542 REVERSE LENGTH=288	271	288	1.00E-125	106.3	83.0	91.1
Rsa1.0_01089.1.g23327.t1	ref|XP_002868327.1| hypothetical protein ARALYDRAFT_915517 [Arabidopsis lyrata subsp. lyrata] gi|297314163|gb|EFH44586.1| hypothetical protein ARALYDRAFT_915517 [Arabidopsis lyrata subsp. lyrata]	471	471	0	100.0	93.6	97.2	hypothetical protein ARALYDRAFT_915517	gbpln	Arabidopsis lyrata	AT4G13930.1 | Symbols: SHM4 | serine hydroxymethyltransferase 4 | chr4:8048013-8050021 REVERSE LENGTH=471	471	471	0	100.0	93.2	96.8
Rsa1.0_01089.1.g23328.t1	gb|AAD17409.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	293	1347	1.00E-102	459.7	61.1	70.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01089.1.g23329.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	116	149	1.00E-23	128.4	44.0	61.2	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01089.1.g23330.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01090.1.g23331.t1	ref|XP_002887896.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333737|gb|EFH64155.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	260	261	6.00E-75	100.4	68.8	77.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G64340.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41810.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:23878125-23880635 FORWARD LENGTH=263	260	263	9.00E-74	101.2	68.5	76.9
Rsa1.0_01090.1.g23332.t1	ref|XP_002887894.1| hypothetical protein ARALYDRAFT_474915 [Arabidopsis lyrata subsp. lyrata] gi|297333735|gb|EFH64153.1| hypothetical protein ARALYDRAFT_474915 [Arabidopsis lyrata subsp. lyrata]	195	198	4.00E-89	101.5	83.6	91.3	hypothetical protein ARALYDRAFT_474915	gbpln	Arabidopsis lyrata	AT1G64355.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3593 (InterPro:IPR021995); Has 301 Blast hits to 301 proteins in 96 species: Archae - 0; Bacteria - 143; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 114 (source: NCBI BLink). | chr1:23886152-23886987 FORWARD LENGTH=199	195	199	9.00E-88	102.1	84.1	89.7
Rsa1.0_01090.1.g23333.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01090.1.g23334.t1	gb|EOA35864.1| hypothetical protein CARUB_v10021104mg [Capsella rubella]	146	150	2.00E-44	102.7	65.1	78.1	hypothetical protein CARUB_v10021104mg	gbpln	Capsella rubella	AT1G64370.1 | Symbols: | unknown protein; Has 773 Blast hits to 375 proteins in 118 species: Archae - 0; Bacteria - 97; Metazoa - 421; Fungi - 108; Plants - 31; Viruses - 0; Other Eukaryotes - 116 (source: NCBI BLink). | chr1:23888967-23889503 FORWARD LENGTH=178	146	178	2.00E-43	121.9	67.1	78.1
Rsa1.0_01090.1.g23335.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01090.1.g23336.t1	ref|XP_002886346.1| hypothetical protein ARALYDRAFT_474912 [Arabidopsis lyrata subsp. lyrata] gi|297332187|gb|EFH62605.1| hypothetical protein ARALYDRAFT_474912 [Arabidopsis lyrata subsp. lyrata]	206	339	2.00E-48	164.6	54.9	57.8	hypothetical protein ARALYDRAFT_474912	gbpln	Arabidopsis lyrata	AT1G64380.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:23890981-23891988 REVERSE LENGTH=335	206	335	2.00E-48	162.6	52.9	55.8
Rsa1.0_01090.1.g23337.t1	gb|EOA35354.1| hypothetical protein CARUB_v10020548mg [Capsella rubella]	354	354	1.00E-110	100.0	68.4	77.4	hypothetical protein CARUB_v10020548mg	gbpln	Capsella rubella	AT1G64385.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 66 Blast hits to 66 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 4; Plants - 51; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr1:23900309-23901956 FORWARD LENGTH=351	354	351	1.00E-112	99.2	67.2	77.7
Rsa1.0_01090.1.g23338.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01090.1.g23339.t1	gb|AAN31840.1| putative endo-beta-1,4-glucanase [Arabidopsis thaliana]	496	620	0	125.0	87.3	91.7	putative endo-beta-1,4-glucanase	gbpln	Arabidopsis thaliana	AT1G64390.1 | Symbols: AtGH9C2, GH9C2 | glycosyl hydrolase 9C2 | chr1:23911329-23914642 FORWARD LENGTH=620	496	620	0	125.0	87.3	91.7
Rsa1.0_01090.1.g23340.t1	gb|EOA33728.1| hypothetical protein CARUB_v10019918mg [Capsella rubella]	660	660	0	100.0	93.6	96.2	hypothetical protein CARUB_v10019918mg	gbpln	Capsella rubella	AT1G64400.1 | Symbols: LACS3 | AMP-dependent synthetase and ligase family protein | chr1:23915802-23919681 REVERSE LENGTH=665	660	665	0	100.8	91.7	95.6

Rsa1.0_01091.1.g23341.t1	gb|EOA13620.1| hypothetical protein CARUB_v10026686mg [Capsella rubella]	48	353	9.00E-12	735.4	75.0	89.6	hypothetical protein CARUB_v10026686mg	gbpln	Capsella rubella	AT5G52470.1 | Symbols: FIB1, FBR1, ATFIB1, ATFBR1, SKIP7 | fibrillarin 1 | chr5:21294290-21296509 FORWARD LENGTH=308	48	308	2.00E-14	641.7	75.0	89.6
Rsa1.0_01091.1.g23342.t1	ref|NP_564237.2| Di-glucose binding protein with Leucine-rich repeat domain [Arabidopsis thaliana] gi|332192522|gb|AEE30643.1| Di-glucose binding protein with Leucine-rich repeat domain [Arabidopsis thaliana]	666	628	0	94.3	79.4	83.9	Di-glucose binding protein with Leucine-rich repeat domain	gbpln	Arabidopsis thaliana	AT1G25570.1 | Symbols: | Di-glucose binding protein with Leucine-rich repeat domain | chr1:8992183-8995430 REVERSE LENGTH=628	666	628	0	94.3	79.4	83.9
Rsa1.0_01091.1.g23343.t1	ref|XP_002890682.1| ANAC008 [Arabidopsis lyrata subsp. lyrata] gi|297336524|gb|EFH66941.1| ANAC008 [Arabidopsis lyrata subsp. lyrata]	469	459	0	97.9	77.4	84.6	ANAC008	gbpln	Arabidopsis lyrata	AT1G25580.1 | Symbols: SOG1, ANAC008 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:8997064-8999600 REVERSE LENGTH=449	469	449	0	95.7	76.5	83.8
Rsa1.0_01091.1.g23344.t2	ref|NP_173930.1| coiled-coil domain-containing protein 130 [Arabidopsis thaliana] gi|12320741|gb|AAG50519.1|AC084221_1 unknown protein [Arabidopsis thaliana] gi|44681478|gb|AAS47679.1| At1g25682 [Arabidopsis thaliana] gi|62320731|dbj|BAD95398.1| hypothetical protein [Arabidopsis thaliana] gi|332192524|gb|AEE30645.1| uncharacterized protein AT1G25682 [Arabidopsis thaliana]	525	310	1.00E-165	59.0	54.1	56.8	coiled-coil domain-containing protein 130	gbpln	Arabidopsis thaliana	AT1G25682.1 | Symbols: | Family of unknown function (DUF572) | chr1:9002532-9004550 REVERSE LENGTH=310	525	310	1.00E-167	59.0	54.1	56.8
Rsa1.0_01091.1.g23345.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01091.1.g23346.t2	ref|NP_564242.1| putative phosphatidylinositol 4-kinase type 2-beta [Arabidopsis thaliana] gi|75169053|sp|Q9C671.1|P4K2B_ARATH RecName: Full=Probable phosphatidylinositol 4-kinase type 2-beta At1g26270; Short=Phosphatidylinositol 4-kinase type II-beta gi|12321173|gb|AAG50675.1|AC079829_8 hypothetical protein [Arabidopsis thaliana] gi|14334682|gb|AAK59519.1| unknown protein [Arabidopsis thaliana] gi|16648787|gb|AAL25584.1| At1g26270/F28B23_7 [Arabidopsis thaliana] gi|18700159|gb|AAL77691.1| At1g26270/F28B23_7 [Arabidopsis thaliana] gi|332192549|gb|AEE30670.1| putative phosphatidylinositol 4-kinase type 2-beta [Arabidopsis thaliana]	231	630	4.00E-45	272.7	42.0	45.0	putative phosphatidylinositol 4-kinase type 2-beta	gbpln	Arabidopsis thaliana	AT1G26270.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase family protein | chr1:9089822-9091714 REVERSE LENGTH=630	231	630	1.00E-47	272.7	42.0	45.0
Rsa1.0_01091.1.g23347.t1	gb|EOA40307.1| hypothetical protein CARUB_v10009035mg [Capsella rubella]	464	473	0	101.9	86.2	91.2	hypothetical protein CARUB_v10009035mg	gbpln	Capsella rubella	AT1G26120.1 | Symbols: ICME-LIKE1 | alpha/beta-Hydrolases superfamily protein | chr1:9028656-9031402 REVERSE LENGTH=476	464	476	0	102.6	84.9	91.4
Rsa1.0_01091.1.g23348.t1	ref|XP_002890674.1| hypothetical protein ARALYDRAFT_472802 [Arabidopsis lyrata subsp. lyrata] gi|297336516|gb|EFH66933.1| hypothetical protein ARALYDRAFT_472802 [Arabidopsis lyrata subsp. lyrata]	858	754	0	87.9	45.2	48.6	hypothetical protein ARALYDRAFT_472802	gbpln	Arabidopsis lyrata	AT1G68690.1 | Symbols: | Protein kinase superfamily protein | chr1:25789192-25791886 FORWARD LENGTH=708	858	708	0	82.5	36.2	42.1
Rsa1.0_01091.1.g23349.t2	ref|NP_173944.1| phosphoribulokinase/uridine kinase-like protein [Arabidopsis thaliana] gi|12321172|gb|AAG50674.1|AC079829_7 hypothetical protein [Arabidopsis thaliana] gi|20259437|gb|AAM14039.1| unknown protein [Arabidopsis thaliana] gi|21436169|gb|AAM51372.1| unknown protein [Arabidopsis thaliana] gi|332192538|gb|AEE30659.1| phosphoribulokinase/uridine kinase-like protein [Arabidopsis thaliana]	672	674	0	100.3	83.8	91.8	phosphoribulokinase/uridine kinase-like protein	gbpln	Arabidopsis thaliana	AT1G26190.1 | Symbols: | Phosphoribulokinase / Uridine kinase family | chr1:9057285-9060433 REVERSE LENGTH=674	672	674	0	100.3	83.8	91.8
Rsa1.0_01091.1.g23350.t1	gb|EOA39890.1| hypothetical protein CARUB_v10008568mg [Capsella rubella]	620	632	0	101.9	87.1	92.9	hypothetical protein CARUB_v10008568mg	gbpln	Capsella rubella	AT1G26270.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase family protein | chr1:9089822-9091714 REVERSE LENGTH=630	620	630	0	101.6	86.6	92.6
Rsa1.0_01091.1.g23351.t1	emb|CAD40837.3| OSJNBa0086B14.9 [Oryza sativa Japonica Group]	61	294	3.00E-18	482.0	75.4	75.4	OSJNBa0086B14.9	gbpln	Oryza sativa	AT4G40030.2 | Symbols: | Histone superfamily protein | chr4:18555840-18556827 REVERSE LENGTH=164	61	164	1.00E-20	268.9	75.4	75.4

Rsa1.0_01092.1.g23352.t1	gb|EOA22057.1| hypothetical protein CARUB_v10002597mg, partial [Capsella rubella]	90	221	2.00E−26	245.6	72.2	77.8	hypothetical protein CARUB_v10002597mg, partial	gbpln	Capsella rubella	AT5G23360.1 | Symbols: | GRAM domain−containing protein / ABA−responsive protein−related | chr5:7861817−7862449 FORWARD LENGTH=210	90	210	2.00E−28	233.3	73.3	80.0
Rsa1.0_01092.1.g23353.t1	gb|EOA20047.1| hypothetical protein CARUB_v10000319mg [Capsella rubella]	729	729	0	100.0	91.2	94.1	hypothetical protein CARUB_v10000319mg	gbpln	Capsella rubella	AT5G23390.1 | Symbols: | Plant protein of unknown function (DUF639) | chr5:7870719−7874283 REVERSE LENGTH=730	729	730	0	100.1	91.5	95.6
Rsa1.0_01092.1.g23354.t1	ref|NP_680211.1| Cox19−like CHCH family protein [Arabidopsis thaliana] gi|26450246|dbj|BAC42240.1| unknown protein [Arabidopsis thaliana] gi|28827550|gb|AAO50619.1| unknown protein [Arabidopsis thaliana] gi|332005776|gb|AED93159.1| Cox19−like CHCH family protein [Arabidopsis thaliana]	162	162	5.00E−58	100.0	80.2	90.1	Cox19−like CHCH family protein	gbpln	Arabidopsis thaliana	AT5G23395.1 | Symbols: MIA40 | Cox19−like CHCH family protein | chr5:7874848−7876091 REVERSE LENGTH=162	162	162	2.00E−60	100.0	80.2	90.1
Rsa1.0_01092.1.g23355.t1	dbj|BAJ34388.1| unnamed protein product [Thellungiella halophila]	587	587	0	100.0	85.0	91.1	unnamed protein product	−−−−	−−−−	AT5G23400.1 | Symbols: | Leucine−rich repeat (LRR) family protein | chr5:7880603−7882372 FORWARD LENGTH=589	587	589	0	100.3	82.6	89.3
Rsa1.0_01092.1.g23356.t1	gb|EOA21466.1| hypothetical protein CARUB_v10001858mg [Capsella rubella]	173	236	2.00E−25	136.4	45.1	53.8	hypothetical protein CARUB_v10001858mg	gbpln	Capsella rubella	AT5G23420.1 | Symbols: HMGB6 | high−mobility group box 6 | chr5:7888712−7890111 REVERSE LENGTH=241	173	241	2.00E−21	139.3	38.2	47.4
Rsa1.0_01092.1.g23357.t1	gb|EOA21466.1| hypothetical protein CARUB_v10001858mg [Capsella rubella]	125	236	3.00E−25	188.8	53.6	61.6	hypothetical protein CARUB_v10001858mg	gbpln	Capsella rubella	AT5G23420.1 | Symbols: HMGB6 | high−mobility group box 6 | chr5:7888712−7890111 REVERSE LENGTH=241	125	241	6.00E−22	192.8	48.8	59.2
Rsa1.0_01092.1.g23358.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01092.1.g23359.t1	ref|NP_851064.1| Katanin p80 WD40 repeat−containing subunit B1−1 [Arabidopsis thaliana] gi|73620972|sp|Q8H0T9.3|KTNB1_ARATH RecName: Full=Katanin p80 WD40 repeat−containing subunit B1 homolog gi|25083345|gb|AAN72064.1| putative protein [Arabidopsis thaliana] gi|332005783|gb|AED93166.1| Katanin p80 WD40 repeat−containing subunit B1−1 [Arabidopsis thaliana]	842	837	0	99.4	90.5	95.1	Katanin p80 WD40 repeat−containing subunit B1−1	gbpln	Arabidopsis thaliana	AT5G23430.1 | Symbols: | Transducin/WD40 repeat−like superfamily protein | chr5:7894073−7899862 REVERSE LENGTH=837	842	837	0	99.4	90.5	95.1
Rsa1.0_01092.1.g23360.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	328	1164	5.00E−50	354.9	36.3	44.2	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I−like superfamily protein | chr1:16528880−16531065 REVERSE LENGTH=626	328	626	8.00E−20	190.9	17.4	27.1
Rsa1.0_01092.1.g23361.t29	ref|XP_002872058.1| hypothetical protein ARALYDRAFT_351368 [Arabidopsis lyrata subsp. lyrata] gi|297317895|gb|EFH48317.1| hypothetical protein ARALYDRAFT_351368 [Arabidopsis lyrata subsp. lyrata]	410	604	2.00E−50	147.3	35.9	48.0	hypothetical protein ARALYDRAFT_351368	gbpln	Arabidopsis lyrata	AT5G23480.1 | Symbols: | SWIB/MDM2 domain;Plus−3;GYF | chr5:7916314−7919155 FORWARD LENGTH=570	410	570	3.00E−49	139.0	27.8	33.9
Rsa1.0_01092.1.g23362.t1	ref|NP_197743.1| smr (Small MutS Related) domain−containing protein [Arabidopsis thaliana] gi|8809708|dbj|BAA97249.1| unnamed protein product [Arabidopsis thaliana] gi|22531192|gb|AAM97100.1| unknown protein [Arabidopsis thaliana] gi|23198016|gb|AAN15535.1| unknown protein [Arabidopsis thaliana] gi|332005795|gb|AED93178.1| smr (Small MutS Related) domain−containing protein [Arabidopsis thaliana]	417	435	1.00E−176	104.3	77.7	85.6	smr (Small MutS Related) domain−containing protein	gbpln	Arabidopsis thaliana	AT5G23520.1 | Symbols: | smr (Small MutS Related) domain−containing protein | chr5:7929591−7931296 REVERSE LENGTH=435	417	435	1.00E−178	104.3	77.7	85.6
Rsa1.0_01092.1.g23363.t1	ref|NP_197744.1| carboxyesterase 18 [Arabidopsis thaliana] gi|75335430|sp|Q9LT10.1|CXE18_ARATH RecName: Full=Probable carboxylesterase 18; AltName: Full=AtCXE18 gi|8809707|dbj|BAA97248.1| unnamed protein product [Arabidopsis thaliana] gi|110742010|dbj|BAE98944.1| hypothetical protein [Arabidopsis thaliana] gi|114050665|gb|ABI49482.1| At5g23530 [Arabidopsis thaliana] gi|332005796|gb|AED93179.1| carboxyesterase 18 [Arabidopsis thaliana]	333	335	1.00E−159	100.6	81.1	91.6	carboxyesterase 18	gbpln	Arabidopsis thaliana	AT5G23530.1 | Symbols: AtCXE18, CXE18 | carboxyesterase 18 | chr5:7933366−7934373 REVERSE LENGTH=335	333	335	1.00E−162	100.6	81.1	91.6

<table>
<tr><td>Rsa1.0_01092.1.g23364.t1</td><td>ref|NP_680212.1| 50S ribosomal protein L24-like protein [Arabidopsis thaliana] gi|297808355|ref|XP_002872061.1| KOW domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|8809706|dbj|BAA97247.1| 50S ribosomal protein L24 [Arabidopsis thaliana] gi|44681334|gb|AAS47607.1| At5g23535 [Arabidopsis thaliana] gi|45773844|gb|AAS76726.1| At5g23535 [Arabidopsis thaliana] gi|110735795|dbj|BAE99874.1| 50S ribosomal protein L24 [Arabidopsis thaliana] gi|297317898|gb|EFH48320.1| KOW domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|332005797|gb|AED93180.1| 50S ribosomal protein L24-like protein [Arabidopsis thaliana]</td><td>159</td><td>159</td><td>2.00E-85</td><td>100.0</td><td>99.4</td><td>99.4</td><td>50S ribosomal protein L24-like protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G23535.1 | Symbols: | KOW domain-containing protein | chr5:7935871-7937127 FORWARD LENGTH=159</td><td>159</td><td>159</td><td>7.00E-88</td><td>100.0</td><td>99.4</td><td>99.4</td></tr>
<tr><td>Rsa1.0_01092.1.g23365.t1</td><td>ref|NP_197745.1| 26S proteasome non-ATPase regulatory subunit 14 [Arabidopsis thaliana] gi|51701846|sp|Q9LT08.1|PSDE_ARATH RecName: Full=26S proteasome non-ATPase regulatory subunit 14; AltName: Full=26S proteasome regulatory subunit rpn11 gi|8809705|dbj|BAA97246.1| 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gi|17979145|gb|AAL49768.1| putative 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gi|20259105|gb|AAM14268.1| putative 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gi|32700040|gb|AAP86670.1| 26S proteasome subunit RPN11A [Arabidopsis thaliana] gi|32700042|gb|AAP86671.1| 26S proteasome subunit RPN11a [Arabidopsis thaliana] gi|32700044|gb|AAP86672.1| 26S proteasome subunit RPN11 [Arabidopsis thaliana] gi|110737189|dbj|BAF00543.1| 26S proteasome, non-ATPase regulatory subunit [Arabidopsis thaliana] gi|332005798|gb|AED93181.1| 26S proteasome non-ATPase regulatory subunit 14 [Arabidopsis thaliana]</td><td>308</td><td>308</td><td>0</td><td>100.0</td><td>100.0</td><td>100.0</td><td>26S proteasome non-ATPase regulatory subunit 14</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G23540.1 | Symbols: | Mov34/MPN/PAD-1 family protein | chr5:7937772-7939339 FORWARD LENGTH=308</td><td>308</td><td>308</td><td>0</td><td>100.0</td><td>100.0</td><td>100.0</td></tr>
<tr><td>Rsa1.0_01093.1.g23366.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01093.1.g23367.t1</td><td>gb|EOA15341.1| hypothetical protein CARUB_v10004114mg [Capsella rubella]</td><td>124</td><td>864</td><td>4.00E-37</td><td>696.8</td><td>58.9</td><td>63.7</td><td>hypothetical protein CARUB_v10004114mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G14330.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:8244228-8247286 FORWARD LENGTH=869</td><td>124</td><td>869</td><td>5.00E-39</td><td>700.8</td><td>58.1</td><td>62.9</td></tr>
<tr><td>Rsa1.0_01093.1.g23368.t1</td><td>ref|NP_193120.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|17933317|gb|AAL48240.1|AF446369_1 AT4g13840/F18A5_230 [Arabidopsis thaliana] gi|4455313|emb|CAB36848.1| fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana] gi|7268088|emb|CAB78426.1| fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana] gi|23308387|gb|AAN18163.1| At4g13840/F18A5_230 [Arabidopsis thaliana] gi|110740566|dbj|BAE98388.1| fatty acid elongase - like protein [Arabidopsis thaliana] gi|332657932|gb|AEE83332.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]</td><td>149</td><td>428</td><td>2.00E-71</td><td>287.2</td><td>83.2</td><td>91.9</td><td>HXXXD-type acyl-transferase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G13840.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr4:8014088-8016326 REVERSE LENGTH=428</td><td>149</td><td>428</td><td>5.00E-74</td><td>287.2</td><td>83.2</td><td>91.9</td></tr>
</table>

Rsa1.0_01093.1.g23369.t1	ref|NP_193120.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|17933317|gb|AAL48240.1|AF446369_1 AT4g13840/F18A5_230 [Arabidopsis thaliana] gi|4455313|emb|CAB36848.1| fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana] gi|7268088|emb|CAB78426.1| fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana] gi|23308387|gb|AAN18163.1| At4g13840/F18A5_230 [Arabidopsis thaliana] gi|110740566|dbj|BAE98388.1| fatty acid elongase - like protein [Arabidopsis thaliana] gi|332657932|gb|AEE83332.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	281	428	1.00E-125	152.3	77.9	89.3	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT4G13840.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr4:8014088-8016326 REVERSE LENGTH=428	281	428	1.00E-128	152.3	77.9	89.3
Rsa1.0_01093.1.g23370.t1	ref|XP_002870353.1| hypothetical protein ARALYDRAFT_493532 [Arabidopsis lyrata subsp. lyrata] gi|297316189|gb|EFH46612.1| hypothetical protein ARALYDRAFT_493532 [Arabidopsis lyrata subsp. lyrata]	201	197	5.00E-91	98.0	83.1	91.5	hypothetical protein ARALYDRAFT_493532	gbpln	Arabidopsis lyrata	AT4G13830.2 | Symbols: J20 | DNAJ-like 20 | chr4:8011518-8012577 FORWARD LENGTH=197	201	197	9.00E-93	98.0	82.1	90.0
Rsa1.0_01093.1.g23371.t1	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	127	954	2.00E-19	751.2	44.9	57.5	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01093.1.g23372.t1	gb|ABD65089.1| zinc knuckle containing protein [Brassica oleracea]	260	333	5.00E-27	128.1	40.8	47.7	zinc knuckle containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01093.1.g23373.t1	gb|EOA15994.1| hypothetical protein CARUB_v10004113mg [Capsella rubella]	905	866	0	95.7	67.1	77.2	hypothetical protein CARUB_v10004113mg	gbpln	Capsella rubella	AT4G13820.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:8008535-8010694 REVERSE LENGTH=719	905	719	0	79.4	60.0	67.6
Rsa1.0_01093.1.g23374.t1	ref|XP_002868336.1| hypothetical protein ARALYDRAFT_493534 [Arabidopsis lyrata subsp. lyrata] gi|297314172|gb|EFH44595.1| hypothetical protein ARALYDRAFT_493534 [Arabidopsis lyrata subsp. lyrata]	332	336	1.00E-164	101.2	91.6	94.9	hypothetical protein ARALYDRAFT_493534	gbpln	Arabidopsis lyrata	AT4G13800.1 | Symbols: | Protein of unknown function (DUF803) | chr4:8002129-8003858 REVERSE LENGTH=336	332	336	1.00E-165	101.2	91.3	94.3
Rsa1.0_01093.1.g23375.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	371	1142	2.00E-58	307.8	40.4	57.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	371	575	9.00E-29	155.0	24.8	40.4
Rsa1.0_01094.1.g23376.t1	ref|XP_002876454.1| seven in absentia family protein [Arabidopsis lyrata subsp. lyrata] gi|297322292|gb|EFH52713.1| seven in absentia family protein [Arabidopsis lyrata subsp. lyrata]	311	309	1.00E-178	99.4	95.5	97.1	seven in absentia family protein	gbpln	Arabidopsis lyrata	AT3G58040.1 | Symbols: SINAT2 | seven in absentia of Arabidopsis 2 | chr3:21489612-21491085 FORWARD LENGTH=308	311	308	1.00E-180	99.0	95.5	96.8
Rsa1.0_01094.1.g23377.t1	gb|EOA24053.1| hypothetical protein CARUB_v10017271mg [Capsella rubella]	394	437	0	110.9	91.6	96.2	hypothetical protein CARUB_v10017271mg	gbpln	Capsella rubella	AT3G58030.4 | Symbols: | RING/U-box superfamily protein | chr3:21485527-21486837 FORWARD LENGTH=436	394	436	0	110.7	89.1	94.7
Rsa1.0_01094.1.g23378.t1	ref|XP_002880160.1| hypothetical protein ARALYDRAFT_483647 [Arabidopsis lyrata subsp. lyrata] gi|297325999|gb|EFH56419.1| hypothetical protein ARALYDRAFT_483647 [Arabidopsis lyrata subsp. lyrata]	240	239	1.00E-113	99.6	89.2	94.6	hypothetical protein ARALYDRAFT_483647	gbpln	Arabidopsis lyrata	AT2G45140.1 | Symbols: PVA12 | plant VAP homolog 12 | chr2:18611029-18612971 FORWARD LENGTH=239	240	239	1.00E-114	99.6	87.9	94.6
Rsa1.0_01094.1.g23379.t1	ref|NP_182041.1| scarecrow-like protein 27 [Arabidopsis thaliana] gi|75276030|sp|Q7XJM8.1|SCL27_ARATH RecName: Full=Scarecrow-like protein 27; Short=AtSCL27; AltName: Full=GRAS family protein 14; Short=AtGRAS-14 gi|58652078|gb|AAW80864.1| At2g45160 [Arabidopsis thaliana] gi|219291105|gb|ACL13987.1| At2g45160 [Arabidopsis thaliana] gi|330255424|gb|AEC10518.1| scarecrow-like protein 27 [Arabidopsis thaliana]	602	640	0	106.3	82.4	89.0	scarecrow-like protein 27	gbpln	Arabidopsis thaliana	AT2G45160.1 | Symbols: HAM1, ATHAM1, LOM1 | GRAS family transcription factor | chr2:18618110-18620032 REVERSE LENGTH=640	602	640	0	106.3	82.4	89.0

Rsa1.0_01094.1.g23380.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1703	1715	0	100.7	40.3	57.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	1703	336	4.00E-87	19.7	9.3	12.9
Rsa1.0_01094.1.g23381.t1	gb|EOA28141.1| hypothetical protein CARUB_v10024330mg [Capsella rubella]	122	122	1.00E-59	100.0	95.1	99.2	hypothetical protein CARUB_v10024330mg	gbpln	Capsella rubella	AT2G45170.2 | Symbols: ATATG8E, ATG8E | AUTOPHAGY 8E | chr2:18624545-18625526 FORWARD LENGTH=122	122	122	2.00E-61	100.0	93.4	98.4
Rsa1.0_01094.1.g23382.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01094.1.g23383.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01094.1.g23384.t1	ref|NP_191352.1| uncharacterized protein [Arabidopsis thaliana] gi|79315480|ref|NP_001030881.1| uncharacterized protein [Arabidopsis thaliana] gi|6729536|emb|CAB67621.1| putative protein [Arabidopsis thaliana] gi|28393650|gb|AAO42243.1| unknown protein [Arabidopsis thaliana] gi|28973601|gb|AAO64125.1| unknown protein [Arabidopsis thaliana] gi|332646197|gb|AEE79718.1| uncharacterized protein AT3G57930 [Arabidopsis thaliana] gi|332646198|gb|AEE79719.1| uncharacterized protein AT3G57930 [Arabidopsis thaliana]	137	141	9.00E-47	102.9	80.3	91.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G57930.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G42190.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:21447250-21447675 REVERSE LENGTH=141	137	141	2.00E-49	102.9	80.3	91.2
Rsa1.0_01094.1.g23385.t1	ref|XP_002878178.1| hypothetical protein ARALYDRAFT_486243 [Arabidopsis lyrata subsp. lyrata] gi|297324016|gb|EFH54437.1| hypothetical protein ARALYDRAFT_486243 [Arabidopsis lyrata subsp. lyrata]	321	347	1.00E-126	108.1	76.9	84.7	hypothetical protein ARALYDRAFT_486243	gbpln	Arabidopsis lyrata	AT3G57920.1 | Symbols: SPL15 | squamosa promoter binding protein-like 15 | chr3:21444450-21445852 REVERSE LENGTH=354	321	354	1.00E-120	110.3	73.8	82.2
Rsa1.0_01094.1.g23386.t1	gb|EOA23174.1| hypothetical protein CARUB_v10017834mg [Capsella rubella]	167	269	8.00E-73	161.1	88.0	93.4	hypothetical protein CARUB_v10017834mg	gbpln	Capsella rubella	AT3G57910.1 | Symbols: | D111/G-patch domain-containing protein | chr3:21442771-21443968 FORWARD LENGTH=265	167	265	1.00E-62	158.7	89.2	94.0
Rsa1.0_01094.1.g23387.t1	gb|AAO64176.1| putative zinc finger protein [Arabidopsis thaliana] gi|110737098|dbj|BAF00501.1| zinc finger like protein [Arabidopsis thaliana]	231	383	2.00E-71	165.8	80.1	86.1	putative zinc finger protein	gbpln	Arabidopsis thaliana	AT3G57670.1 | Symbols: NTT, WIP2 | C2H2-type zinc finger family protein | chr3:21370936-21373121 FORWARD LENGTH=383	231	383	8.00E-71	165.8	80.1	86.1
Rsa1.0_01094.1.g23388.t1	ref|NP_191325.1| DNA-directed RNA polymerase I subunit A1 [Arabidopsis thaliana] gi|4678281|emb|CAB41189.1| DNA-directed RNA polymerase I 190K chain-like protein [Arabidopsis thaliana] gi|332646163|gb|AEE79684.1| nuclear RNA polymerase A1 [Arabidopsis thaliana]	1459	1670	0	114.5	79.9	87.0	DNA-directed RNA polymerase I subunit A1	gbpln	Arabidopsis thaliana	AT3G57660.1 | Symbols: NRPA1 | nuclear RNA polymerase A1 | chr3:21353746-21362814 FORWARD LENGTH=1670	1459	1670	0	114.5	79.9	87.0
Rsa1.0_01094.1.g23389.t1	sp|Q9XFW4.1|LPAT2_BRANA RecName: Full=1-acyl-sn-glycerol-3-phosphate acyltransferase 2; AltName: Full=Lysophosphatidyl acyltransferase 2 gi|4583544|emb|CAB09138.1| acyl-CoA:1-acylglycerol-3-phosphate acyltransferase [Brassica napus]	391	390	0	99.7	97.2	99.0	RecName: Full=1-acyl-sn-glycerol-3-phosphate acyltransferase 2; AltName: Full=Lysophosphatidyl acyltransferase 2 gi|4583544|emb|CAB09138.1| acyl-CoA:1-acylglycerol-3-phosphate acyltransferase	gbpln	Brassica napus	AT3G57650.1 | Symbols: LPAT2 | lysophosphatidyl acyltransferase 2 | chr3:21349751-21352839 FORWARD LENGTH=389	391	389	0	99.5	92.3	96.4
Rsa1.0_01095.1.g23390.t1	gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]	353	527	8.00E-61	149.3	42.8	56.9	hypothetical protein CARUB_v10022820mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	353	735	5.00E-54	208.2	41.1	57.2
Rsa1.0_01095.1.g23391.t1	gb|EOA13223.1| hypothetical protein CARUB_v10026248mg [Capsella rubella]	523	511	0	97.7	75.1	83.0	hypothetical protein CARUB_v10026248mg	gbpln	Capsella rubella	AT5G52050.1 | Symbols: | MATE efflux family protein | chr5:21138933-21140450 FORWARD LENGTH=505	523	505	0	96.6	75.0	83.6
Rsa1.0_01095.1.g23392.t1	gb|AAD15534.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	767	1664	0	216.9	46.8	59.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	767	1262	1.00E-25	164.5	9.0	12.5

Rsa1.0_01095.1.g23393.t1	ref|XP_002864146.1| hypothetical protein ARALYDRAFT_495273 [Arabidopsis lyrata subsp. lyrata] gi|297309981|gb|EFH40405.1| hypothetical protein ARALYDRAFT_495273 [Arabidopsis lyrata subsp. lyrata]	396	404	0	102.0	88.4	92.2	hypothetical protein ARALYDRAFT_495273	gbpln	Arabidopsis lyrata	AT5G52030.2 | Symbols: | TraB family protein | chr5:21128291-21130034 FORWARD LENGTH=402	396	402	0	101.5	85.4	90.7
Rsa1.0_01095.1.g23394.t11	gb|AAF69161.1|AC007915_13 F27F5.19 [Arabidopsis thaliana]	1051	1309	0	124.5	33.8	42.6	F27F5.19	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1051	1262	1.00E-123	120.1	20.6	28.4
Rsa1.0_01095.1.g23395.t1	ref|NP_200009.1| uncharacterized protein [Arabidopsis thaliana] gi|10177731|dbj|BAB11044.1| unnamed protein product [Arabidopsis thaliana] gi|37202072|gb|AAQ89651.1| At5g51960 [Arabidopsis thaliana] gi|51969014|dbj|BAD43199.1| unknown protein [Arabidopsis thaliana] gi|51969196|dbj|BAD43290.1| unknown protein [Arabidopsis thaliana] gi|332008768|gb|AED96151.1| uncharacterized protein AT5G51960 [Arabidopsis thaliana]	94	103	4.00E-33	109.6	78.7	83.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G51960.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Complex 1 LYR protein (InterPro:IPR008011); Has 45 Blast hits to 45 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:21110716-21111116 FORWARD LENGTH=103	94	103	7.00E-36	109.6	78.7	83.0
Rsa1.0_01095.1.g23396.t1	gb|EOA14537.1| hypothetical protein CARUB_v10027769mg [Capsella rubella]	553	587	0	106.1	86.3	93.3	hypothetical protein CARUB_v10027769mg	gbpln	Capsella rubella	AT5G51950.2 | Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr5:21106093-21108348 REVERSE LENGTH=553	553	553	0	100.0	87.0	93.9
Rsa1.0_01095.1.g23397.t1	gb|AAG51404.1|AC009465_4 unknown protein; 32997-32284 [Arabidopsis thaliana]	111	152	8.00E-14	136.9	48.6	54.1	unknown protein; 32997-32284	gbpln	Arabidopsis thaliana	AT3G04950.1 | Symbols: | CONTAINS InterPro DOMAIN/s: SEC-C motif (InterPro:IPR004027); Has 583 Blast hits to 583 proteins in 248 species: Archae - 0; Bacteria - 488; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 61 (source: NCBI BLink). | chr3:1371786-1373300 FORWARD LENGTH=231	111	231	6.00E-16	208.1	45.0	49.5
Rsa1.0_01096.1.g23398.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01096.1.g23399.t1	gb|EOA14432.1| hypothetical protein CARUB_v10027635mg [Capsella rubella]	386	386	0	100.0	95.1	98.2	hypothetical protein CARUB_v10027635mg	gbpln	Capsella rubella	AT5G45620.1 | Symbols: | Proteasome component (PCI) domain protein | chr5:18501590-18503868 FORWARD LENGTH=386	386	386	0	100.0	94.3	97.9
Rsa1.0_01096.1.g23400.t1	ref|XP_002863466.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297309301|gb|EFH39725.1| binding protein [Arabidopsis lyrata subsp. lyrata]	692	633	1.00E-134	91.5	34.5	38.2	binding protein	gbpln	Arabidopsis lyrata	AT5G45610.1 | Symbols: SUV2 | protein dimerizations | chr5:18496397-18499673 REVERSE LENGTH=646	692	646	1.00E-137	93.4	34.1	37.7
Rsa1.0_01096.1.g23401.t1	ref|XP_002870807.1| hypothetical protein ARALYDRAFT_916420 [Arabidopsis lyrata subsp. lyrata] gi|297316643|gb|EFH47066.1| hypothetical protein ARALYDRAFT_916420 [Arabidopsis lyrata subsp. lyrata]	157	168	1.00E-28	107.0	43.9	59.9	hypothetical protein ARALYDRAFT_916420	gbpln	Arabidopsis lyrata	AT5G39010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G39782.1); Has 12 Blast hits to 12 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:15615948-15616457 FORWARD LENGTH=169	157	169	2.00E-22	107.6	41.4	58.0
Rsa1.0_01096.1.g23402.t1	ref|NP_001190475.1| YEATS family protein [Arabidopsis thaliana] gi|332007891|gb|AED95274.1| YEATS family protein [Arabidopsis thaliana]	267	267	1.00E-147	100.0	93.6	98.1	YEATS family protein	gbpln	Arabidopsis thaliana	AT5G45600.2 | Symbols: GAS41 | YEATS family protein | chr5:18488059-18489666 FORWARD LENGTH=267	267	267	1.00E-150	100.0	93.6	98.1
Rsa1.0_01096.1.g23403.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1386	1365	0	98.5	43.1	60.6	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1386	575	5.00E-77	41.5	13.7	20.2
Rsa1.0_01096.1.g23404.t1	gb|AAB61072.1| contains similarity to a DNAJ-like domain [Arabidopsis thaliana]	563	1609	4.00E-77	285.8	25.4	33.4	contains similarity to a DNAJ-like domain	gbpln	Arabidopsis thaliana	AT5G27260.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9603943-9604930 FORWARD LENGTH=303	563	303	1.00E-79	53.8	25.4	33.4

Rsa1.0_01096.1.g23405.t1	ref|NP_199276.1| alpha-barbatene synthase [Arabidopsis thaliana] gi|254810224|sp|Q4KSH9.2|BARS_ARATH RecName: Full=Alpha-barbatene synthase; Short=AtBS; AltName: Full=Beta-chamigrene synthase; AltName: Full=Terpendeoid synthase 11; Short=AtTPS11; AltName: Full=Thujopsene synthase gi|126352284|gb|ABO09887.1| At5g44630 [Arabidopsis thaliana] gi|332007757|gb|AED95140.1| alpha-barbatene synthase [Arabidopsis thaliana]	556	557	0	100.2	73.4	84.7	alpha-barbatene synthase	gbpln	Arabidopsis thaliana	AT5G44630.1 | Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr5:18003280-18005616 FORWARD LENGTH=557	556	557	0	100.2	73.4	84.7
Rsa1.0_01097.1.g23406.t3	ref|XP_002882622.1| ATEXO70H4 [Arabidopsis lyrata subsp. lyrata] gi|297328462|gb|EFH58881.1| ATEXO70H4 [Arabidopsis lyrata subsp. lyrata]	632	628	0	99.4	75.6	85.6	ATEXO70H4	gbpln	Arabidopsis lyrata	AT3G09520.1 | Symbols: ATEXO70H4, EXO70H4 | exocyst subunit exo70 family protein H4 | chr3:2923743-2925629 FORWARD LENGTH=628	632	628	0	99.4	74.8	85.3
Rsa1.0_01097.1.g23407.t1	gb|EOA31721.1| hypothetical protein CARUB_v10014930mg [Capsella rubella]	123	123	2.00E-58	100.0	94.3	98.4	hypothetical protein CARUB_v10014930mg	gbpln	Capsella rubella	AT3G09500.1 | Symbols: | Ribosomal L29 family protein | chr3:2917047-2917895 FORWARD LENGTH=123	123	123	4.00E-61	100.0	94.3	98.4
Rsa1.0_01097.1.g23408.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01097.1.g23409.t1	gb|EOA31010.1| hypothetical protein CARUB_v10014153mg [Capsella rubella]	312	331	1.00E-89	106.1	63.8	75.6	hypothetical protein CARUB_v10014153mg	gbpln	Capsella rubella	AT3G09490.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:2915636-2916640 FORWARD LENGTH=334	312	334	2.00E-91	107.1	64.4	77.9
Rsa1.0_01097.1.g23410.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01097.1.g23411.t1	ref|NP_187552.3| putative pectinacetylesterase [Arabidopsis thaliana] gi|6478931|gb|AAF14036.1|AC011436_20 putative pectinacetylesterase [Arabidopsis thaliana] gi|119935842|gb|ABM06009.1| At3g09410 [Arabidopsis thaliana] gi|332641244|gb|AEE74765.1| putative pectinacetylesterase [Arabidopsis thaliana]	427	427	0	100.0	81.0	88.8	putative pectinacetylesterase	gbpln	Arabidopsis thaliana	AT3G09410.1 | Symbols: | Pectinacetylesterase family protein | chr3:2898243-2900984 REVERSE LENGTH=427	427	427	0	100.0	81.0	88.8
Rsa1.0_01097.1.g23412.t1	gb|EOA32896.1| hypothetical protein CARUB_v10016220mg [Capsella rubella]	204	150	1.00E-32	73.5	34.3	42.2	hypothetical protein CARUB_v10016220mg	gbpln	Capsella rubella	AT3G09380.1 | Symbols: | Protein of unknown function (DUF59) | chr3:2885265-2886116 REVERSE LENGTH=156	204	156	3.00E-35	76.5	35.8	43.1
Rsa1.0_01097.1.g23413.t1	ref|XP_002882616.1| hypothetical protein ARALYDRAFT_317739 [Arabidopsis lyrata subsp. lyrata] gi|297328456|gb|EFH58875.1| hypothetical protein ARALYDRAFT_317739 [Arabidopsis lyrata subsp. lyrata]	493	1245	0	252.5	73.6	80.3	hypothetical protein ARALYDRAFT_317739	gbpln	Arabidopsis lyrata	AT3G09370.1 | Symbols: MYB3R-3, AtMYB3R3 | myb domain protein 3r-3 | chr3:2879534-2882128 FORWARD LENGTH=505	493	505	0	102.4	72.4	78.9
Rsa1.0_01097.1.g23414.t1	ref|XP_002882612.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297328452|gb|EFH58871.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata]	453	456	0	100.7	95.6	97.1	oxysterol-binding family protein	gbpln	Arabidopsis lyrata	AT3G09300.1 | Symbols: ORP3B | OSBP(oxysterol binding protein)-related protein 3B | chr3:2858068-2860462 FORWARD LENGTH=458	453	458	0	101.1	94.9	96.9
Rsa1.0_01097.1.g23415.t1	ref|XP_002862963.1| hypothetical protein ARALYDRAFT_920906 [Arabidopsis lyrata subsp. lyrata] gi|297829458|ref|XP_002882611.1| hypothetical protein ARALYDRAFT_897082 [Arabidopsis lyrata subsp. lyrata] gi|297308750|gb|EFH39222.1| hypothetical protein ARALYDRAFT_920906 [Arabidopsis lyrata subsp. lyrata] gi|297328451|gb|EFH58870.1| hypothetical protein ARALYDRAFT_897082 [Arabidopsis lyrata subsp. lyrata]	171	174	2.00E-67	101.8	80.1	87.1	hypothetical protein ARALYDRAFT_920906	gbpln	Arabidopsis lyrata	AT3G09290.1 | Symbols: TAC1 | telomerase activator1 | chr3:2856141-2856659 FORWARD LENGTH=172	171	172	1.00E-66	100.6	76.0	83.0
Rsa1.0_01097.1.g23416.t1	ref|XP_002869001.1| hypothetical protein ARALYDRAFT_328051 [Arabidopsis lyrata subsp. lyrata] gi|297314837|gb|EFH45260.1| hypothetical protein ARALYDRAFT_328051 [Arabidopsis lyrata subsp. lyrata]	202	787	2.00E-19	389.6	30.7	35.1	hypothetical protein ARALYDRAFT_328051	gbpln	Arabidopsis lyrata	AT4G36950.1 | Symbols: MAPKKK21 | mitogen-activated protein kinase kinase kinase 21 | chr4:17422834-17423844 REVERSE LENGTH=336	202	336	6.00E-21	166.3	31.7	39.1
Rsa1.0_01097.1.g23417.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01097.1.g23418.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	301	657	2.00E-74	218.3	46.8	63.5	T14P8.10	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	301	746	6.00E-47	247.8	33.2	51.5
Rsa1.0_01098.1.g23419.t1	ref|NP_192771.1| glycine-rich protein [Arabidopsis thaliana] gi|4538962|emb|CAB39786.1| hypothetical protein [Arabidopsis thaliana] gi|7267730|emb|CAB78156.1| hypothetical protein [Arabidopsis thaliana] gi|19347875|gb|AAL85995.1| unknown protein [Arabidopsis thaliana] gi|22136796|gb|AAM91742.1| unknown protein [Arabidopsis thaliana] gi|332657468|gb|AEE82868.1| glycine-rich protein [Arabidopsis thaliana]	102	130	4.00E-20	127.5	61.8	69.6	glycine-rich protein	gbpln	Arabidopsis thaliana	AT4G10330.1 | Symbols: | glycine-rich protein | chr4:6406551-6407136 FORWARD LENGTH=130	102	130	6.00E-23	127.5	61.8	69.6
Rsa1.0_01098.1.g23420.t1	gb|AAC63844.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1080	1231	0	114.0	57.5	72.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17201414-17202323 REVERSE LENGTH=258	1080	258	2.00E-78	23.9	13.1	16.4
Rsa1.0_01098.1.g23421.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1642	1342	0	81.7	42.4	57.9	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1642	1262	1.00E-81	76.9	10.8	16.3
Rsa1.0_01098.1.g23422.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01098.1.g23423.t1	ref|XP_002894196.1| nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] gi|297340038|gb|EFH70455.1| nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	815	839	0	102.9	92.8	96.2	nucleotide binding protein	gbpln	Arabidopsis lyrata	AT1G49540.1 | Symbols: ELP2, AtELP2 | elongator protein 2 | chr1:18333767-18337382 REVERSE LENGTH=838	815	838	0	102.8	92.0	96.2
Rsa1.0_01098.1.g23424.t1	gb|EOA40419.1| hypothetical protein CARUB_v10009144mg [Capsella rubella]	678	443	3.00E-63	65.3	23.6	31.3	hypothetical protein CARUB_v10009144mg	gbpln	Capsella rubella	AT1G43770.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:16548509-16550257 FORWARD LENGTH=431	678	431	2.00E-63	63.6	23.6	30.4
Rsa1.0_01098.1.g23425.t1	gb|EOA13223.1| hypothetical protein CARUB_v10026248mg [Capsella rubella]	497	511	1.00E-155	102.8	58.4	69.4	hypothetical protein CARUB_v10026248mg	gbpln	Capsella rubella	AT5G52050.1 | Symbols: | MATE efflux family protein | chr5:21138933-21140450 FORWARD LENGTH=505	497	505	1.00E-155	101.6	56.7	69.4
Rsa1.0_01099.1.g23426.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	71	1123	2.00E-26	1581.7	78.9	90.1	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01099.1.g23427.t1	gb|EOA19882.1| hypothetical protein CARUB_v10000128mg [Capsella rubella]	998	1013	0	101.5	91.2	95.2	hypothetical protein CARUB_v10000128mg	gbpln	Capsella rubella	AT4G11800.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr4:7093666-7098519 REVERSE LENGTH=1013	998	1013	0	101.5	90.9	94.7
Rsa1.0_01099.1.g23428.t3	ref|XP_002872625.1| hypothetical protein ARALYDRAFT_489995 [Arabidopsis lyrata subsp. lyrata] gi|297318462|gb|EFH48884.1| hypothetical protein ARALYDRAFT_489995 [Arabidopsis lyrata subsp. lyrata]	393	425	1.00E-160	108.1	79.1	85.2	hypothetical protein ARALYDRAFT_489995	gbpln	Arabidopsis lyrata	AT4G11790.1 | Symbols: | Pleckstrin homology (PH) domain superfamily protein | chr4:7090456-7093208 FORWARD LENGTH=443	393	443	1.00E-148	112.7	74.6	83.5
Rsa1.0_01099.1.g23429.t1	ref|XP_002872624.1| hypothetical protein ARALYDRAFT_489994 [Arabidopsis lyrata subsp. lyrata] gi|297318461|gb|EFH48883.1| hypothetical protein ARALYDRAFT_489994 [Arabidopsis lyrata subsp. lyrata]	491	477	1.00E-165	97.1	70.1	79.2	hypothetical protein ARALYDRAFT_489994	gbpln	Arabidopsis lyrata	AT4G11780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G23020.2); Has 550 Blast hits to 387 proteins in 92 species: Archae - 0; Bacteria - 32; Metazoa - 132; Fungi - 122; Plants - 80; Viruses - 0; Other Eukaryotes - 184 (source: NCBI BLink). | chr4:7085970-7088212 FORWARD LENGTH=473	491	473	1.00E-166	96.3	69.9	78.8
Rsa1.0_01099.1.g23430.t1	ref|XP_002886390.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata] gi|297332231|gb|EFH62649.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata]	285	298	1.00E-74	104.6	52.6	68.8	hypothetical protein ARALYDRAFT_893070	gbpln	Arabidopsis lyrata	AT2G42470.1 | Symbols: | TRAF-like family protein | chr2:17679887-17685187 REVERSE LENGTH=898	285	898	4.00E-65	315.1	49.5	68.4
Rsa1.0_01099.1.g23431.t1	ref|NP_568884.4| dehydrodolichyl diphosphate synthase 5 [Arabidopsis thaliana] gi|83305680|sp|Q570Q8.2|DDPS5_ARATH RecName: Full=Dehydrodolichyl diphosphate synthase 5; Short=Dedol-PP synthase 5 gi|8843800|dbj|BAA97348.1| cis-prenyltransferase homolog-like; undecaprenyl phosphate synthetase-like [Arabidopsis thaliana] gi|332009716|gb|AED97099.1| dehydrodolichyl diphosphate synthase 5 [Arabidopsis thaliana]	280	302	1.00E-104	107.9	67.1	79.3	dehydrodolichyl diphosphate synthase 5	gbpln	Arabidopsis thaliana	AT5G58784.1 | Symbols: | Undecaprenyl pyrophosphate synthetase family protein | chr5:23739950-23741267 REVERSE LENGTH=302	280	302	1.00E-106	107.9	67.1	79.3

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<tr><td>Rsa1.0_01099.1.g23432.t1</td><td>ref|XP_002877743.1| hypothetical protein ARALYDRAFT_485389 [Arabidopsis lyrata subsp. lyrata] gi|297323581|gb|EFH54002.1| hypothetical protein ARALYDRAFT_485389 [Arabidopsis lyrata subsp. lyrata]</td><td>116</td><td>117</td><td>2.00E-38</td><td>100.9</td><td>69.8</td><td>80.2</td><td>hypothetical protein ARALYDRAFT_485389</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G51360.1 | Symbols: | Transcription elongation factor (TFIIS) family protein | chr5:20871918-20872277 FORWARD LENGTH=119</td><td>116</td><td>119</td><td>3.00E-33</td><td>102.6</td><td>63.8</td><td>77.6</td></tr>
<tr><td>Rsa1.0_01099.1.g23433.t1</td><td>gb|EOA20188.1| hypothetical protein CARUB_v10000484mg, partial [Capsella rubella]</td><td>478</td><td>617</td><td>0</td><td>129.1</td><td>78.2</td><td>87.7</td><td>hypothetical protein CARUB_v10000484mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G11740.1 | Symbols: SAY1 | Ubiquitin-like superfamily protein | chr4:7071955-7075256 FORWARD LENGTH=564</td><td>478</td><td>564</td><td>1.00E-166</td><td>118.0</td><td>78.2</td><td>87.9</td></tr>
<tr><td>Rsa1.0_01099.1.g23434.t1</td><td>sp|Q39242.2|TRXB2_ARATH RecName: Full=Thioredoxin reductase 2; AltName: Full=NADPH-dependent thioredoxin reductase 2; Short=NTR2; AltName: Full=NADPH-dependent thioredoxin reductase A; Short=AtNTRA</td><td>159</td><td>383</td><td>9.00E-34</td><td>240.9</td><td>45.3</td><td>47.2</td><td>RecName: Full=Thioredoxin reductase 2; AltName: Full=NADPH-dependent thioredoxin reductase 2; Short=NTR2; AltName: Full=NADPH-dependent thioredoxin reductase A; Short=AtNTRA</td><td>----</td><td>----</td><td>AT2G17420.1 | Symbols: NTRA, ATNTRA, NTR2 | NADPH-dependent thioredoxin reductase A | chr2:7564357-7566219 FORWARD LENGTH=378</td><td>159</td><td>378</td><td>3.00E-36</td><td>237.7</td><td>45.3</td><td>47.2</td></tr>
<tr><td>Rsa1.0_01099.1.g23435.t1</td><td>gb|EJP69747.1| hypothetical protein BBA_01712 [Beauveria bassiana ARSEF 2860]</td><td>251</td><td>318</td><td>1.00E-63</td><td>126.7</td><td>48.2</td><td>67.3</td><td>hypothetical protein BBA_01712</td><td>gbenv/gbpln</td><td>Beauveria bassiana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01099.1.g23436.t1</td><td>ref|XP_002881638.1| hypothetical protein ARALYDRAFT_321615 [Arabidopsis lyrata subsp. lyrata] gi|297327477|gb|EFH57897.1| hypothetical protein ARALYDRAFT_321615 [Arabidopsis lyrata subsp. lyrata]</td><td>254</td><td>584</td><td>8.00E-71</td><td>229.9</td><td>62.6</td><td>75.6</td><td>hypothetical protein ARALYDRAFT_321615</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G39240.1 | Symbols: | RNA polymerase I specific transcription initiation factor RRN3 protein | chr2:16384786-16387827 REVERSE LENGTH=573</td><td>254</td><td>573</td><td>7.00E-69</td><td>225.6</td><td>59.8</td><td>70.9</td></tr>
<tr><td>Rsa1.0_01099.1.g23437.t1</td><td>ref|NP_192758.1| TTF-type zinc finger protein with HAT dimerization domain [Arabidopsis thaliana] gi|4538984|emb|CAB39772.1| putative protein [Arabidopsis thaliana] gi|7267716|emb|CAB78143.1| putative protein [Arabidopsis thaliana] gi|332657454|gb|AEE82854.1| TTF-type zinc finger protein with HAT dimerization domain [Arabidopsis thaliana]</td><td>642</td><td>733</td><td>0</td><td>114.2</td><td>58.3</td><td>68.8</td><td>TTF-type zinc finger protein with HAT dimerization domain</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G10200.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr4:6353172-6355591 FORWARD LENGTH=733</td><td>642</td><td>733</td><td>0</td><td>114.2</td><td>58.3</td><td>68.8</td></tr>
<tr><td>Rsa1.0_01099.1.g23438.t5</td><td>ref|NP_174347.1| RNA polymerase I specific transcription initiation factor RRN3 protein [Arabidopsis thaliana] gi|332193126|gb|AEE31247.1| RNA polymerase I specific transcription initiation factor RRN3 protein [Arabidopsis thaliana]</td><td>259</td><td>604</td><td>6.00E-97</td><td>233.2</td><td>73.4</td><td>82.2</td><td>RNA polymerase I specific transcription initiation factor RRN3 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30590.1 | Symbols: | RNA polymerase I specific transcription initiation factor RRN3 protein | chr1:10835976-10839524 REVERSE LENGTH=604</td><td>259</td><td>604</td><td>2.00E-99</td><td>233.2</td><td>73.4</td><td>82.2</td></tr>
<tr><td>Rsa1.0_01099.1.g23439.t1</td><td>gb|EOA21441.1| hypothetical protein CARUB_v10001823mg [Capsella rubella]</td><td>244</td><td>244</td><td>1.00E-125</td><td>100.0</td><td>88.9</td><td>93.0</td><td>hypothetical protein CARUB_v10001823mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G11650.1 | Symbols: ATOSM34, OSM34 | osmotin 34 | chr4:7025127-7026113 REVERSE LENGTH=244</td><td>244</td><td>244</td><td>1.00E-127</td><td>100.0</td><td>88.1</td><td>93.0</td></tr>
<tr><td>Rsa1.0_01099.1.g23440.t1</td><td>gb|AAD23020.1| hypothetical protein [Arabidopsis thaliana]</td><td>664</td><td>926</td><td>1.00E-108</td><td>139.5</td><td>39.5</td><td>56.5</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921</td><td>664</td><td>921</td><td>1.00E-50</td><td>138.7</td><td>16.3</td><td>25.6</td></tr>
<tr><td>Rsa1.0_01100.1.g23441.t22</td><td>ref|XP_003551900.1| PREDICTED: glucose-6-phosphate/phosphate translocator 1, chloroplastic-like [Glycine max]</td><td>123</td><td>394</td><td>1.00E-14</td><td>320.3</td><td>45.5</td><td>48.0</td><td>PREDICTED: glucose-6-phosphate/phosphate translocator 1, chloroplastic-like</td><td>gbenv/gbpln</td><td>Glycine max</td><td>AT5G54800.1 | Symbols: GPT1, ATGPT1 | glucose 6-phosphate/phosphate translocator 1 | chr5:22261408-22263562 FORWARD LENGTH=388</td><td>123</td><td>388</td><td>3.00E-15</td><td>315.4</td><td>45.5</td><td>49.6</td></tr>
<tr><td>Rsa1.0_01100.1.g23442.t1</td><td>gb|EOA15489.1| hypothetical protein CARUB_v10004733mg [Capsella rubella]</td><td>313</td><td>470</td><td>1.00E-108</td><td>150.2</td><td>66.5</td><td>70.3</td><td>hypothetical protein CARUB_v10004733mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G27070.1 | Symbols: TSB2 | tryptophan synthase beta-subunit 2 | chr4:13586564-13588619 FORWARD LENGTH=475</td><td>313</td><td>475</td><td>1.00E-110</td><td>151.8</td><td>66.5</td><td>70.6</td></tr>
<tr><td>Rsa1.0_01100.1.g23443.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01100.1.g23444.t1</td><td>ref|NP_174696.2| translation initiation factor IF-3 [Arabidopsis thaliana] gi|45773942|gb|AAS76775.1| At1g34360 [Arabidopsis thaliana] gi|332193581|gb|AEE31702.1| translation initiation factor IF-3 [Arabidopsis thaliana]</td><td>497</td><td>520</td><td>1.00E-170</td><td>104.6</td><td>72.2</td><td>82.1</td><td>translation initiation factor IF-3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G34360.1 | Symbols: | translation initiation factor 3 (IF-3) family protein | chr1:12542986-12546025 FORWARD LENGTH=520</td><td>497</td><td>520</td><td>1.00E-173</td><td>104.6</td><td>72.2</td><td>82.1</td></tr>
<tr><td>Rsa1.0_01100.1.g23445.t1</td><td>ref|NP_001189538.1| splicing factor, CC1-like protein [Arabidopsis thaliana] gi|330251466|gb|AEC06560.1| splicing factor, CC1-like protein [Arabidopsis thaliana]</td><td>554</td><td>610</td><td>0</td><td>110.1</td><td>88.3</td><td>92.1</td><td>splicing factor, CC1-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G16940.2 | Symbols: | Splicing factor, CC1-like | chr2:7342869-7347052 REVERSE LENGTH=610</td><td>554</td><td>610</td><td>0</td><td>110.1</td><td>88.3</td><td>92.1</td></tr>
<tr><td>Rsa1.0_01100.1.g23446.t1</td><td>gb|EOA32915.1| hypothetical protein CARUB_v10016240mg [Capsella rubella]</td><td>573</td><td>565</td><td>0</td><td>98.6</td><td>83.8</td><td>88.7</td><td>hypothetical protein CARUB_v10016240mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G16910.1 | Symbols: AMS | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:7331721-7334077 FORWARD LENGTH=571</td><td>573</td><td>571</td><td>0</td><td>99.7</td><td>86.7</td><td>91.8</td></tr>
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Rsa1.0_01100.1.g23447.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	667	1352	3.00E-36	202.7	17.7	24.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	667	746	1.00E-19	111.8	10.6	15.9
Rsa1.0_01100.1.g23448.t1	ref|NP_565397.1| phospholipase-like protein [Arabidopsis thaliana] gi|20197278|gb|AAC64221.2| expressed protein [Arabidopsis thaliana] gi|330251456|gb|AEC06550.1| phospholipase-like protein [Arabidopsis thaliana]	378	382	1.00E-166	101.1	76.7	88.1	phospholipase-like protein	gbpln	Arabidopsis thaliana	AT2G16900.1 | Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) family | chr2:7323857-7325374 REVERSE LENGTH=382	378	382	1.00E-168	101.1	76.7	88.1
Rsa1.0_01101.1.g23449.t1	gb|AAD14492.1| Hypothetical protein [Arabidopsis thaliana]	83	240	1.00E-17	289.2	56.6	63.9	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01101.1.g23450.t1	gb|AAG50886.1|AC025294_24 hypothetical protein [Arabidopsis thaliana]	470	629	1.00E-102	133.8	45.5	62.6	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	470	746	3.00E-78	158.7	33.4	43.8
Rsa1.0_01101.1.g23451.t1	ref|NP_849898.1| uncharacterized protein [Arabidopsis thaliana] gi|62320812|dbj|BAD93751.1| hypothetical protein [Arabidopsis thaliana] gi|110742469|dbj|BAE99153.1| hypothetical protein [Arabidopsis thaliana] gi|114050645|gb|ABI49472.1| At1g77122 [Arabidopsis thaliana] gi|332197817|gb|AEE35938.1| uncharacterized protein AT1G77122 [Arabidopsis thaliana]	342	323	1.00E-110	94.4	67.0	76.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G77122.1 | Symbols: | Uncharacterised protein family UPF0090 | chr1:28977427-28978674 REVERSE LENGTH=323	342	323	1.00E-113	94.4	67.0	76.9
Rsa1.0_01101.1.g23452.t1	gb|AEC13713.1| alcohol dehydrogenase 1 [Brassica rapa]	377	379	0	100.5	95.2	97.9	alcohol dehydrogenase 1	gbpln	Brassica rapa	AT1G77120.1 | Symbols: ADH1, ADH, ATADH, ATADH1 | alcohol dehydrogenase 1 | chr1:28975509-28977216 FORWARD LENGTH=379	377	379	0	100.5	92.6	96.3
Rsa1.0_01101.1.g23453.t3	ref|XP_002888647.1| hypothetical protein ARALYDRAFT_475925 [Arabidopsis lyrata subsp. lyrata] gi|297334488|gb|EFH64906.1| hypothetical protein ARALYDRAFT_475925 [Arabidopsis lyrata subsp. lyrata]	210	232	1.00E-108	110.5	91.9	94.8	hypothetical protein ARALYDRAFT_475925	gbpln	Arabidopsis lyrata	AT1G67980.1 | Symbols: CCOAMT | caffeoyl-CoA 3-O-methyltransferase | chr1:25487724-25488934 FORWARD LENGTH=232	210	232	1.00E-110	110.5	91.4	94.8
Rsa1.0_01101.1.g23454.t1	ref|XP_002887160.1| hypothetical protein ARALYDRAFT_339050 [Arabidopsis lyrata subsp. lyrata] gi|297333001|gb|EFH63419.1| hypothetical protein ARALYDRAFT_339050 [Arabidopsis lyrata subsp. lyrata]	396	302	1.00E-106	76.3	52.8	60.6	hypothetical protein ARALYDRAFT_339050	gbpln	Arabidopsis lyrata	AT1G68030.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:25500378-25501544 REVERSE LENGTH=314	396	314	1.00E-101	79.3	51.5	59.3
Rsa1.0_01101.1.g23455.t1	ref|XP_002888642.1| S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334483|gb|EFH64901.1| S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	361	362	0	100.3	88.9	94.7	S-adenosyl-L-methionine:carboxyl methyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G68040.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:25502876-25505224 FORWARD LENGTH=363	361	363	0	100.6	86.7	93.4
Rsa1.0_01101.1.g23456.t1	ref|XP_002887158.1| hypothetical protein ARALYDRAFT_475916 [Arabidopsis lyrata subsp. lyrata] gi|297332999|gb|EFH63417.1| hypothetical protein ARALYDRAFT_475916 [Arabidopsis lyrata subsp. lyrata]	343	344	1.00E-165	100.3	83.1	90.4	hypothetical protein ARALYDRAFT_475916	gbpln	Arabidopsis lyrata	AT1G68070.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr1:25515412-25516767 REVERSE LENGTH=343	343	343	1.00E-167	100.0	81.9	89.5
Rsa1.0_01101.1.g23457.t1	gb|EOA34223.1| hypothetical protein CARUB_v10021734mg [Capsella rubella]	601	373	1.00E-142	62.1	44.1	51.9	hypothetical protein CARUB_v10021734mg	gbpln	Capsella rubella	AT1G68110.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:25524901-25526040 FORWARD LENGTH=379	601	379	1.00E-141	63.1	43.6	50.2
Rsa1.0_01101.1.g23458.t1	ref|XP_002888637.1| atidd14-domain 14 [Arabidopsis lyrata subsp. lyrata] gi|297334478|gb|EFH64896.1| atidd14-domain 14 [Arabidopsis lyrata subsp. lyrata]	408	423	0	103.7	87.7	92.4	atidd14-domain 14	gbpln	Arabidopsis lyrata	AT1G68130.1 | Symbols: AtIDD14, IDD14 | indeterminate(ID)-domain 14 | chr1:25532484-25534317 FORWARD LENGTH=419	408	419	0	102.7	85.8	89.7
Rsa1.0_01102.1.g23459.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01102.1.g23460.t1	gb|EOA38904.1| hypothetical protein CARUB_v10011286mg [Capsella rubella]	319	270	3.00E-11	84.6	10.3	12.2	hypothetical protein CARUB_v10011286mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01102.1.g23461.t2	ref|XP_002879921.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297325760|gb|EFH56180.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	652	408	1.00E-139	62.6	40.3	44.8	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT2G41330.1 | Symbols: | Glutaredoxin family protein | chr2:17227067-17228275 FORWARD LENGTH=402	652	402	1.00E-136	61.7	39.0	43.9

Rsa1.0_01102.1.g23462.t1	ref|NP_181668.1| ankyrin repeat and BTB/POZ domain-containing protein [Arabidopsis thaliana] gi|75315939|sp|Q9ZVC2.1|NPR5_ARATH RecName: Full=Regulatory protein NPR5; AltName: Full=BTB/POZ domain-containing protein NPR5; AltName: Full=Protein BLADE ON PETIOLE 2 gi|3894187|gb|AAC78536.1| hypothetical protein [Arabidopsis thaliana] gi|53749156|gb|AAU90063.1| At2g41370 [Arabidopsis thaliana] gi|60545031|gb|AAX22759.1| BLADE-ON-PETIOLE2 [Arabidopsis thaliana] gi|330254872|gb|AEC09966.1| regulatory protein NPR5 [Arabidopsis thaliana]	441	491	0	111.3	91.2	94.3	ankyrin repeat and BTB/POZ domain-containing protein	gbpln	Arabidopsis thaliana	AT2G41370.1 | Symbols: BOP2 | Ankyrin repeat family protein / BTB/POZ domain-containing protein | chr2:17238019-17240203 REVERSE LENGTH=491	441	491	0	111.3	91.2	94.3
Rsa1.0_01102.1.g23463.t1	gb|AAD17395.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	230	1138	2.00E-47	494.8	34.8	49.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01102.1.g23464.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01102.1.g23465.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	470	255	3.00E-64	54.3	28.3	36.8	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	470	302	2.00E-49	64.3	25.5	37.4
Rsa1.0_01102.1.g23466.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01102.1.g23467.t1	gb|EOA22285.1| hypothetical protein CARUB_v10002883mg [Capsella rubella]	149	151	3.00E-19	101.3	34.9	44.3	hypothetical protein CARUB_v10002883mg	gbpln	Capsella rubella	AT5G05020.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr5:1481084-1481548 REVERSE LENGTH=154	149	154	2.00E-14	103.4	27.5	40.9
Rsa1.0_01102.1.g23468.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	946	1274	0	134.7	48.4	66.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	946	575	3.00E-74	60.8	19.5	29.8
Rsa1.0_01102.1.g23469.t1	gb|EOA27696.1| hypothetical protein CARUB_v10023848mg [Capsella rubella]	268	270	1.00E-133	100.7	85.8	92.9	hypothetical protein CARUB_v10023848mg	gbpln	Capsella rubella	AT2G41380.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:17251981-17252886 FORWARD LENGTH=269	268	269	1.00E-135	100.4	84.7	93.7
Rsa1.0_01103.1.g23470.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01103.1.g23471.t1	ref|XP_002872098.1| hypothetical protein ARALYDRAFT_351441 [Arabidopsis lyrata subsp. lyrata] gi|297317935|gb|EFH48357.1| hypothetical protein ARALYDRAFT_351441 [Arabidopsis lyrata subsp. lyrata]	371	375	1.00E-138	101.1	66.0	78.4	hypothetical protein ARALYDRAFT_351441	gbpln	Arabidopsis lyrata	AT5G24220.1 | Symbols: | Lipase class 3-related protein | chr5:8225861-8227551 FORWARD LENGTH=376	371	376	1.00E-137	101.3	63.9	77.4
Rsa1.0_01103.1.g23472.t1	ref|NP_567387.1| uncharacterized protein [Arabidopsis thaliana] gi|14994259|gb|AAK73264.1| putative protein [Arabidopsis thaliana] gi|26451708|dbj|BAC42949.1| unknown protein [Arabidopsis thaliana] gi|332657693|gb|AEE83093.1| uncharacterized protein AT4G12070 [Arabidopsis thaliana]	465	483	0	103.9	91.4	94.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G12070.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:7231941-7234272 FORWARD LENGTH=483	465	483	0	103.9	91.4	94.2
Rsa1.0_01103.1.g23473.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01103.1.g23474.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01103.1.g23475.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01103.1.g23476.t2	ref|NP_192945.2| AT-hook motif nuclear-localized protein 1 [Arabidopsis thaliana] gi|17979485|gb|AAL50079.1| AT4g12080/F16J13_150 [Arabidopsis thaliana] gi|23506149|gb|AAN31086.1| At4g12080/F16J13_150 [Arabidopsis thaliana] gi|118420990|dbj|BAF37220.1| AT-hook motif nuclear localized protein 1 [Arabidopsis thaliana] gi|332657694|gb|AEE83094.1| AT-hook motif nuclear-localized protein 1 [Arabidopsis thaliana]	347	356	1.00E-153	102.6	83.9	88.2	AT-hook motif nuclear-localized protein 1	gbpln	Arabidopsis thaliana	AT4G12080.1 | Symbols: AHL1, ATAHL1 | AT-hook motif nuclear-localized protein 1 | chr4:7239466-7241246 FORWARD LENGTH=356	347	356	1.00E-156	102.6	83.9	88.2
Rsa1.0_01103.1.g23477.t1	ref|XP_002874746.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297320583|gb|EFH51005.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	135	135	2.00E-64	100.0	88.1	94.8	predicted protein	gbpln	Arabidopsis lyrata	AT4G12090.1 | Symbols: | Cornichon family protein | chr4:7242165-7242924 REVERSE LENGTH=135	135	135	2.00E-65	100.0	84.4	94.1
Rsa1.0_01103.1.g23478.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01103.1.g23479.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01103.1.g23480.t1	gb|EOA21411.1| hypothetical protein CARUB_v10001784mg [Capsella rubella]	248	254	4.00E-89	102.4	74.6	83.5	hypothetical protein CARUB_v10001784mg	gbpln	Capsella rubella	AT4G22758.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G27830.1). | chr4:11958477-11959904 FORWARD LENGTH=255	248	255	3.00E-72	102.8	63.7	77.4
Rsa1.0_01103.1.g23481.t2	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	177	341	9.00E-31	192.7	37.3	58.8	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23482.t2	ref|NP_175640.1| 60S ribosomal protein L37-2 [Arabidopsis thaliana] gi|20143906|sp|Q43292.2|RL372_ARATH RecName: Full=60S ribosomal protein L37-2 gi|12323122|gb|AAG51542.1|AC037424_7 60S ribosomal protein L37, putative; 56921-57860 [Arabidopsis thaliana] gi|13877907|gb|AAK44031.1|AF370216_1 putative 60S ribosomal protein L37 [Arabidopsis thaliana] gi|21280805|gb|AAM44969.1| putative 60S ribosomal protein L37 [Arabidopsis thaliana] gi|222423584|dbj|BAH19761.1| AT1G52300 [Arabidopsis thaliana] gi|332194658|gb|AEE32779.1| 60S ribosomal protein L37-2 [Arabidopsis thaliana]	94	95	1.00E-44	101.1	98.9	100.0	60S ribosomal protein L37-2	gbpln	Arabidopsis thaliana	AT1G52300.1 | Symbols: | Zinc-binding ribosomal protein family protein | chr1:19475213-19476152 REVERSE LENGTH=95	94	95	2.00E-47	101.1	98.9	100.0
Rsa1.0_01104.1.g23483.t1	ref|XP_002885130.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297330970|gb|EFH61389.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	514	362	1.00E-156	70.4	51.2	59.5	F-box family protein	gbpln	Arabidopsis lyrata	AT3G16210.1 | Symbols: | F-box family protein | chr3:5494533-5495615 REVERSE LENGTH=360	514	360	1.00E-157	70.0	52.1	58.9
Rsa1.0_01104.1.g23484.t7	ref|NP_001189909.1| putative eukaryotic LigT protein [Arabidopsis thaliana] gi|332642266|gb|AEE75787.1| putative eukaryotic LigT protein [Arabidopsis thaliana]	430	449	0	104.4	80.5	89.1	putative eukaryotic LigT protein	gbpln	Arabidopsis thaliana	AT3G16230.2 | Symbols: | Predicted eukaryotic LigT | chr3:5500563-5503303 FORWARD LENGTH=449	430	449	0	104.4	80.5	89.1
Rsa1.0_01104.1.g23485.t1	dbj|BAA31452.1| delta-VM23 [Raphanus sativus]	248	248	1.00E-128	100.0	96.0	98.8	delta-VM23	gbpln	Raphanus sativus	AT3G16240.1 | Symbols: DELTA-TIP, TIP2;1, DELTA-TIP1, AQP1, ATTIP2;1 | delta tonoplast integral protein | chr3:5505534-5506788 FORWARD LENGTH=250	248	250	1.00E-129	100.8	96.8	99.6
Rsa1.0_01104.1.g23486.t1	ref|XP_002885133.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330973|gb|EFH61392.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	208	212	3.00E-90	101.9	85.1	92.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G16300.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr3:5525491-5526207 REVERSE LENGTH=212	208	212	4.00E-87	101.9	83.2	89.9
Rsa1.0_01104.1.g23487.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23488.t1	gb|AAB63650.1| Myb-related transcription activator (MybSt1) isolog [Arabidopsis thaliana] gi|9279717|dbj|BAB01274.1| Myb-related transcription activator [Arabidopsis thaliana]	200	369	4.00E-66	184.5	74.5	78.5	Myb-related transcription activator (MybSt1) isolog	gbpln	Arabidopsis thaliana	AT3G16350.1 | Symbols: | Homeodomain-like superfamily protein | chr3:5547828-5549397 FORWARD LENGTH=387	200	387	6.00E-64	193.5	74.0	77.5
Rsa1.0_01104.1.g23489.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23490.t1	dbj|BAB01275.1| histidine-containing phosphotransfer protein-like [Arabidopsis thaliana]	144	133	8.00E-68	92.4	85.4	89.6	histidine-containing phosphotransfer protein-like	gbpln	Arabidopsis thaliana	AT3G16360.2 | Symbols: AHP4 | HPT phosphotransmitter 4 | chr3:5554351-5555518 FORWARD LENGTH=145	144	145	2.00E-69	100.7	84.0	88.9
Rsa1.0_01104.1.g23491.t1	ref|XP_002883006.1| pyk10-binding protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297328846|gb|EFH59265.1| pyk10-binding protein 1 [Arabidopsis lyrata subsp. lyrata]	297	298	1.00E-143	100.3	85.2	91.9	pyk10-binding protein 1	gbpln	Arabidopsis lyrata	AT3G16430.2 | Symbols: JAL31 | jacalin-related lectin 31 | chr3:5581830-5582959 FORWARD LENGTH=296	297	296	1.00E-137	99.7	79.8	86.9
Rsa1.0_01104.1.g23492.t1	gb|EOA31381.1| hypothetical protein CARUB_v10014589mg [Capsella rubella]	174	220	5.00E-80	126.4	82.2	88.5	hypothetical protein CARUB_v10014589mg	gbpln	Capsella rubella	AT3G16990.1 | Symbols: | Haem oxygenase-like, multi-helical | chr3:5795937-5796783 REVERSE LENGTH=221	174	221	6.00E-80	127.0	79.9	87.9
Rsa1.0_01104.1.g23493.t1	ref|XP_002883038.1| transcriptional factor B3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297328878|gb|EFH59297.1| transcriptional factor B3 family protein [Arabidopsis lyrata subsp. lyrata]	258	302	5.00E-70	117.1	53.1	72.1	transcriptional factor B3 family protein	gbpln	Arabidopsis lyrata	AT3G17010.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr3:5800460-5802303 FORWARD LENGTH=302	258	302	3.00E-72	117.1	53.9	71.7

Rsa1.0_01104.1.g23494.t1	ref|NP_188326.1| AP2/B3 domain-containing protein [Arabidopsis thaliana] gi|75274019|sp|Q9LSP6.1|Y3701_ARATH RecName: Full=B3 domain-containing protein At3g17010 gi|7670025|dbj|BAA94979.1| unnamed protein product [Arabidopsis thaliana] gi|225898651|dbj|BAH30456.1| hypothetical protein [Arabidopsis thaliana] gi|332642373|gb|AEE75894.1| AP2/B3 domain-containing protein [Arabidopsis thaliana]	277	302	3.00E-77	109.0	58.8	72.2	AP2/B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G17010.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr3:5800460-5802303 FORWARD LENGTH=302	277	302	9.00E-80	109.0	58.8	72.2
Rsa1.0_01104.1.g23495.t1	gb|ABL97971.1| unknown [Brassica rapa]	163	163	7.00E-81	100.0	90.2	92.6	unknown	gbpln	Brassica rapa	AT3G17020.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:5802728-5804063 REVERSE LENGTH=163	163	163	3.00E-81	100.0	85.9	92.6
Rsa1.0_01104.1.g23496.t1	dbj|BAJ34089.1| unnamed protein product [Thellungiella halophila]	1100	1172	0	106.5	86.3	91.7	unnamed protein product	----	----	AT2G18790.1 | Symbols: PHYB, HY3, OOP1 | phytochrome B | chr2:8140079-8144151 FORWARD LENGTH=1172	1100	1172	0	106.5	85.5	91.5
Rsa1.0_01104.1.g23497.t1	gb|EOA32450.1| hypothetical protein CARUB_v10015726mg [Capsella rubella]	344	344	0	100.0	92.4	95.1	hypothetical protein CARUB_v10015726mg	gbpln	Capsella rubella	AT3G17060.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:5816953-5818458 REVERSE LENGTH=344	344	344	0	100.0	91.9	95.1
Rsa1.0_01104.1.g23498.t1	gb|AAM61747.1| protein phosphatase-2c, putative [Arabidopsis thaliana]	380	384	0	101.1	83.9	90.8	protein phosphatase-2c, putative	gbpln	Arabidopsis thaliana	AT3G17090.1 | Symbols: | Protein phosphatase 2C family protein | chr3:5826984-5829327 FORWARD LENGTH=384	380	384	0	101.1	84.7	91.8
Rsa1.0_01104.1.g23499.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23500.t1	ref|XP_002883017.1| hypothetical protein ARALYDRAFT_318437 [Arabidopsis lyrata subsp. lyrata] gi|297328857|gb|EFH59276.1| hypothetical protein ARALYDRAFT_318437 [Arabidopsis lyrata subsp. lyrata]	159	185	3.00E-22	116.4	53.5	67.3	hypothetical protein ARALYDRAFT_318437	gbpln	Arabidopsis lyrata	AT3G16660.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr3:5676904-5677788 FORWARD LENGTH=180	159	180	2.00E-24	113.2	52.2	65.4
Rsa1.0_01104.1.g23501.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23502.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23503.t1	ref|NP_188337.1| uncharacterized protein [Arabidopsis thaliana] gi|42572461|ref|NP_974326.1| uncharacterized protein [Arabidopsis thaliana] gi|18087521|gb|AAL58895.1|AF462799_1 AT3g17120/K14A17_24 [Arabidopsis thaliana] gi|7670036|dbj|BAA94990.1| unnamed protein product [Arabidopsis thaliana] gi|332642385|gb|AEE75906.1| uncharacterized protein AT3G17120 [Arabidopsis thaliana] gi|332642386|gb|AEE75907.1| uncharacterized protein AT3G17120 [Arabidopsis thaliana]	220	219	2.00E-84	99.5	77.7	86.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G17120.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02380.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:5842410-5843246 FORWARD LENGTH=219	220	219	5.00E-87	99.5	77.7	86.4
Rsa1.0_01104.1.g23504.t1	ref|XP_002885187.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297331027|gb|EFH61446.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	183	182	8.00E-74	99.5	80.9	89.6	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT3G17130.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:5844495-5845046 REVERSE LENGTH=183	183	183	4.00E-76	100.0	79.2	88.5
Rsa1.0_01104.1.g23505.t2	gb|EOA29659.1| hypothetical protein CARUB_v10015473mg [Capsella rubella]	134	162	3.00E-46	120.9	71.6	82.8	hypothetical protein CARUB_v10015473mg	gbpln	Capsella rubella	AT3G17140.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr3:5846002-5846589 REVERSE LENGTH=112	134	112	1.00E-46	83.6	65.7	76.1
Rsa1.0_01104.1.g23506.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23507.t1	ref|XP_002885957.1| hypothetical protein ARALYDRAFT_899752 [Arabidopsis lyrata subsp. lyrata] gi|297331797|gb|EFH62216.1| hypothetical protein ARALYDRAFT_899752 [Arabidopsis lyrata subsp. lyrata]	185	187	9.00E-42	101.1	54.1	68.6	hypothetical protein ARALYDRAFT_899752	gbpln	Arabidopsis lyrata	AT3G17230.1 | Symbols: | invertase/pectin methylesterase inhibitor family protein | chr3:5886381-5889236 REVERSE LENGTH=351	185	351	2.00E-39	189.7	53.0	65.4

Rsa1.0_01104.1.g23508.t1	ref|XP_002874950.1| hypothetical protein ARALYDRAFT_490383 [Arabidopsis lyrata subsp. lyrata] gi|297320787|gb|EFH51209.1| hypothetical protein ARALYDRAFT_490383 [Arabidopsis lyrata subsp. lyrata]	251	256	1.00E-125	102.0	88.0	93.6	hypothetical protein ARALYDRAFT_490383	gbpln	Arabidopsis lyrata	AT4G01935.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 37 Blast hits to 37 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr4:841102-842228 FORWARD LENGTH=256	251	256	1.00E-125	102.0	86.1	93.2
Rsa1.0_01104.1.g23509.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23510.t2	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1846	1307	0	70.8	43.5	54.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT3G17800.1 | Symbols: | Protein of unknown function (DUF760) | chr3:6091248-6092873 REVERSE LENGTH=421	1846	421	0	22.8	19.2	20.7
Rsa1.0_01104.1.g23511.t1	ref|NP_188408.1| pyrimidine 1 [Arabidopsis thaliana] gi|9294485|dbj|BAB02704.1| senescencs-related protein; dihydroorotate dehydrogenase-like protein [Arabidopsis thaliana] gi|14334712|gb|AAK59534.1| putative dehydrogenase [Arabidopsis thaliana] gi|16323430|gb|AAL15209.1| putative dehydrogenase [Arabidopsis thaliana] gi|24850451|gb|AAN64919.1| putative dehydrogenase [Arabidopsis thaliana] gi|332642489|gb|AEE76010.1| pyrimidine 1 [Arabidopsis thaliana]	427	426	0	99.8	91.3	96.3	pyrimidine 1	gbpln	Arabidopsis thaliana	AT3G17810.1 | Symbols: PYD1 | pyrimidine 1 | chr3:6094279-6096289 FORWARD LENGTH=426	427	426	0	99.8	91.3	96.3
Rsa1.0_01104.1.g23512.t1	dbj|BAA04994.1| glutamine synthetase [Raphanus sativus]	354	354	0	100.0	95.5	98.6	glutamine synthetase	gbpln	Raphanus sativus	AT3G17820.1 | Symbols: ATGSKB6, GLN1.3, GLN1;3 | glutamine synthetase 1.3 | chr3:6097503-6099408 FORWARD LENGTH=354	354	354	0	100.0	93.5	97.7
Rsa1.0_01104.1.g23513.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01104.1.g23514.t1	ref|XP_002866514.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312349|gb|EFH42773.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	120	406	5.00E-18	338.3	48.3	61.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G26990.1 | Symbols: FUS12, ATCSN2, COP12, CSN2 | proteasome family protein | chr2:11519684-11522412 REVERSE LENGTH=439	120	439	2.00E-19	365.8	45.0	60.0
Rsa1.0_01104.1.g23515.t1	ref|XP_002883095.1| hypothetical protein ARALYDRAFT_898144 [Arabidopsis lyrata subsp. lyrata] gi|297328935|gb|EFH59354.1| hypothetical protein ARALYDRAFT_898144 [Arabidopsis lyrata subsp. lyrata]	768	837	0	109.0	90.0	94.7	hypothetical protein ARALYDRAFT_898144	gbpln	Arabidopsis lyrata	AT3G17900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 45 Blast hits to 44 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 2; Plants - 39; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:6128983-6133069 FORWARD LENGTH=838	768	838	0	109.1	89.7	93.9
Rsa1.0_01105.1.g23516.t1	gb|AAM61622.1| unknown [Arabidopsis thaliana]	113	112	2.00E-49	99.1	83.2	89.4	unknown	gbpln	Arabidopsis thaliana	AT5G09960.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: RPM1-interacting protein 4, defence response (InterPro:IPR008700); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64850.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:3106503-3107658 FORWARD LENGTH=112	113	112	4.00E-52	99.1	83.2	89.4
Rsa1.0_01105.1.g23517.t1	gb|AAZ66921.1| 117M18_2 [Brassica rapa]	204	329	1.00E-77	161.3	72.1	82.8	117M18_2	gbpln	Brassica rapa	AT5G09940.1 | Symbols: | Protein of unknown function (DUF1635) | chr5:3101192-3101833 FORWARD LENGTH=213	204	213	7.00E-44	104.4	57.4	72.5
Rsa1.0_01105.1.g23518.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01105.1.g23519.t1	gb|EOA21762.1| hypothetical protein CARUB_v10002229mg [Capsella rubella]	275	138	2.00E-72	50.2	49.1	49.5	hypothetical protein CARUB_v10002229mg	gbpln	Capsella rubella	AT5G09920.1 | Symbols: RPB15.9, ATRPB15.9, RPB15.9.9, NRPB4 | RNA polymerase II, Rpb4, core protein | chr5:3096276-3097370 FORWARD LENGTH=138	275	138	1.00E-74	50.2	48.7	49.5
Rsa1.0_01105.1.g23520.t1	gb|EOA19397.1| hypothetical protein CARUB_v10000967mg [Capsella rubella]	501	442	0	88.2	86.0	87.2	hypothetical protein CARUB_v10000967mg	gbpln	Capsella rubella	AT5G09900.1 | Symbols: EMB2107, RPN5A, MSA | 26S proteasome regulatory subunit, putative (RPN5) | chr5:3089462-3092434 REVERSE LENGTH=442	501	442	0	88.2	84.4	87.4

Rsa1.0_01105.1.g23521.t1	ref|XP_002873428.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319265|gb|EFH49687.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	550	520	0	94.5	81.1	85.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G09880.1 | Symbols: | Splicing factor, CC1-like | chr5:3081646-3085179 REVERSE LENGTH=527	550	527	0	95.8	81.5	86.2
Rsa1.0_01105.1.g23522.t1	ref|XP_002871388.1| hypothetical protein ARALYDRAFT_908935 [Arabidopsis lyrata subsp. lyrata] gi|297317225|gb|EFH47647.1| hypothetical protein ARALYDRAFT_908935 [Arabidopsis lyrata subsp. lyrata]	583	597	0	102.4	89.9	94.5	hypothetical protein ARALYDRAFT_908935	gbpln	Arabidopsis lyrata	AT5G09860.1 | Symbols: AtTHO1, THO1, AtHPR1, HPR1 | nuclear matrix protein-related | chr5:3066815-3070733 FORWARD LENGTH=599	583	599	0	102.7	89.9	94.7
Rsa1.0_01105.1.g23523.t1	dbj|BAJ34498.1| unnamed protein product [Thellungiella halophila] gi|482556658|gb|EOA20850.1| hypothetical protein CARUB_v10001188mg [Capsella rubella]	377	377	0	100.0	99.7	100.0	unnamed protein product	gbpln	Capsella rubella	AT5G09810.1 | Symbols: ACT7 | actin 7 | chr5:3052809-3054220 FORWARD LENGTH=377	377	377	0	100.0	99.5	99.7
Rsa1.0_01105.1.g23524.t1	gb|EOA20839.1| hypothetical protein CARUB_v10001176mg [Capsella rubella]	396	380	1.00E-157	96.0	72.0	81.8	hypothetical protein CARUB_v10001176mg	gbpln	Capsella rubella	AT5G09790.2 | Symbols: ATXR5, SDG15 | ARABIDOPSIS TRITHORAX-RELATED PROTEIN 5 | chr5:3039204-3040970 REVERSE LENGTH=379	396	379	1.00E-157	95.7	70.2	78.0
Rsa1.0_01105.1.g23525.t1	ref|NP_196538.1| Putative pectinesterase/pectinesterase inhibitor 51 [Arabidopsis thaliana] gi|75180831|sp|Q9LXD9.1|PME51_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 51; Includes: RecName: Full=Pectinesterase inhibitor 51; AltName: Full=Pectin methylesterase inhibitor 51; Includes: RecName: Full=Pectinesterase 51; Short=PE 51; AltName: Full=Pectin methylesterase 51; Short=AtPME51; Flags: Precursor gi|7671413|emb|CAB89354.1| pectin methylesterase-like protein [Arabidopsis thaliana] gi|17979183|gb|AAL49830.1| putative pectin methylesterase [Arabidopsis thaliana] gi|29824167|gb|AAP04044.1| putative pectin methylesterase [Arabidopsis thaliana] gi|332004060|gb|AED91443.1| Putative pectinesterase/pectinesterase inhibitor 51 [Arabidopsis thaliana]	540	551	0	102.0	82.8	88.1	Putative pectinesterase/pectinesterase inhibitor 51	gbpln	Arabidopsis thaliana	AT5G09760.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr5:3032446-3034364 FORWARD LENGTH=551	540	551	0	102.0	82.8	88.1
Rsa1.0_01105.1.g23526.t1	ref|NP_196537.1| transcription factor HEC3 [Arabidopsis thaliana] gi|75311668|sp|Q9LXD8.1|HEC3_ARATH RecName: Full=Transcription factor HEC3; AltName: Full=Basic helix-loop-helix protein 43; Short=AtbHLH43; Short=bHLH 43; AltName: Full=Protein HECATE 3; AltName: Full=Transcription factor EN 119; AltName: Full=bHLH transcription factor bHLH043 gi|7671414|emb|CAB89355.1| putative protein [Arabidopsis thaliana] gi|9759006|dbj|BAB09533.1| unnamed protein product [Arabidopsis thaliana] gi|332004059|gb|AED91442.1| transcription factor HEC3 [Arabidopsis thaliana]	212	224	1.00E-65	105.7	86.8	91.0	transcription factor HEC3	gbpln	Arabidopsis thaliana	AT5G09750.1 | Symbols: HEC3 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:3026401-3027075 REVERSE LENGTH=224	212	224	5.00E-68	105.7	86.8	91.0
Rsa1.0_01106.1.g23527.t1	gb|AAB80620.1| Contains similarity to Glycine protein kinase 6 (gb|M67449) [Arabidopsis thaliana]	371	1029	8.00E-56	277.4	28.8	31.0	Contains similarity to Glycine protein kinase 6 (gb|M67449)	gbpln	Arabidopsis thaliana	AT1G04700.1 | Symbols: | PB1 domain-containing protein tyrosine kinase | chr1:1316919-1320653 FORWARD LENGTH=1042	371	1042	3.00E-58	280.9	28.6	30.5
Rsa1.0_01106.1.g23528.t1	#	#	#	#	#	#	#	-	----	----	AT5G28823.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: Zinc knuckle (CCHC-type) family protein (TAIR:AT2G07760.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:10837849-10839826 REVERSE LENGTH=568	272	568	1.00E-11	208.8	15.8	22.4
Rsa1.0_01106.1.g23529.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01106.1.g23530.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01106.1.g23531.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01106.1.g23532.t1	gb|EOA32395.1| hypothetical protein CARUB_v10015666mg [Capsella rubella]	244	262	4.00E-68	107.4	54.9	69.3	hypothetical protein CARUB_v10015666mg	gbpln	Capsella rubella	AT3G22040.1 | Symbols: | Domain of unknown function (DUF26) | chr3:7761807-7762675 FORWARD LENGTH=257	244	257	2.00E-67	105.3	52.0	69.3
Rsa1.0_01106.1.g23533.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01107.1.g23534.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01107.1.g23535.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01107.1.g23536.t1	gb|AAZ41811.1| 01P13-1 [Brassica rapa subsp. pekinensis]	286	1545	3.00E-70	540.2	44.1	55.2	01P13-1	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	286	1262	4.00E-23	441.3	21.7	35.0
Rsa1.0_01107.1.g23537.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01107.1.g23538.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01107.1.g23539.t1	gb|AAM15254.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	339	930	5.00E-20	274.3	23.9	37.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01107.1.g23540.t12	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	536	777	6.00E-17	145.0	12.3	15.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01107.1.g23541.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01108.1.g23542.t1	gb|EOA27097.1| hypothetical protein CARUB_v10023195mg [Capsella rubella]	399	452	0	113.3	86.0	92.7	hypothetical protein CARUB_v10023195mg	gbpln	Capsella rubella	AT2G22900.1 | Symbols: | Galactosyl transferase GMA12/MNN10 family protein | chr2:9744359-9746193 REVERSE LENGTH=449	399	449	0	112.5	85.2	93.2
Rsa1.0_01108.1.g23543.t1	dbj|BAF34635.1| DNA methyltransferase 1a [Brassica rapa]	1532	1528	0	99.7	87.7	93.1	DNA methyltransferase 1a	gbpln	Brassica rapa	AT5G49160.1 | Symbols: MET1, MET2, METI, DDM2, DMT01, DMT1 | methyltransferase 1 | chr5:19932501-19938186 FORWARD LENGTH=1534	1532	1534	0	100.1	71.7	83.3
Rsa1.0_01108.1.g23544.t1	gb|EOA26510.1| hypothetical protein CARUB_v10022563mg [Capsella rubella]	1015	1015	0	100.0	95.2	97.7	hypothetical protein CARUB_v10022563mg	gbpln	Capsella rubella	AT2G22950.1 | Symbols: | Cation transporter/ E1-E2 ATPase family protein | chr2:9766127-9769766 FORWARD LENGTH=1015	1015	1015	0	100.0	94.2	97.1
Rsa1.0_01108.1.g23545.t1	ref|NP_565527.1| PLAT-plant-stress domain-containing protein [Arabidopsis thaliana] gi|4567207|gb|AAD23623.1| expressed protein [Arabidopsis thaliana] gi|27754389|gb|AAO22643.1| unknown protein [Arabidopsis thaliana] gi|28393941|gb|AAO42378.1| unknown protein [Arabidopsis thaliana] gi|330252180|gb|AEC07274.1| PLAT-plant-stress domain-containing protein [Arabidopsis thaliana]	142	183	1.00E-31	128.9	51.4	65.5	PLAT-plant-stress domain-containing protein	gbpln	Arabidopsis thaliana	AT2G22170.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr2:9427010-9427742 REVERSE LENGTH=183	142	183	3.00E-34	128.9	51.4	65.5
Rsa1.0_01108.1.g23546.t1	emb|CBI29329.3| unnamed protein product [Vitis vinifera]	199	4396	5.00E-25	2209.0	33.2	47.2	unnamed protein product	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01108.1.g23547.t1	gb|AAM62648.1| dehydration stress-induced protein [Arabidopsis thaliana]	156	182	5.00E-31	116.7	48.1	66.7	dehydration stress-induced protein	gbpln	Arabidopsis thaliana	AT2G22170.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr2:9427010-9427742 REVERSE LENGTH=183	156	183	4.00E-33	117.3	47.4	66.7
Rsa1.0_01108.1.g23548.t2	ref|XP_002887955.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333796|gb|EFH64214.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	208	487	5.00E-51	234.1	51.4	55.3	kinase family protein	gbpln	Arabidopsis lyrata	AT1G63500.1 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr1:23556015-23558403 FORWARD LENGTH=487	208	487	3.00E-53	234.1	51.0	55.3
Rsa1.0_01109.1.g23549.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01109.1.g23550.t1	gb|EOA18865.1| hypothetical protein CARUB_v10007488mg, partial [Capsella rubella]	485	509	0	104.9	90.7	94.4	hypothetical protein CARUB_v10007488mg, partial	gbpln	Capsella rubella	AT4G18700.1 | Symbols: CIPK12, SnRK3.9, ATWL4, WL4 | CBL-interacting protein kinase 12 | chr4:10289110-10290579 REVERSE LENGTH=489	485	489	0	100.8	90.3	93.8
Rsa1.0_01109.1.g23551.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01109.1.g23552.t1	ref|NP_193604.2| uncharacterized protein [Arabidopsis thaliana] gi|61742729|gb|AAX55185.1| hypothetical protein At4g18690 [Arabidopsis thaliana] gi|71905519|gb|AAZ52737.1| hypothetical protein At4g18690 [Arabidopsis thaliana] gi|332658676|gb|AEE84076.1| uncharacterized protein AT4G18690 [Arabidopsis thaliana]	288	282	1.00E-109	97.9	67.0	77.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G18690.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G18680.1); Has 522 Blast hits to 522 proteins in 39 species: Archae - 0; Bacteria - 0; Metazoa - 9; Fungi - 0; Plants - 513; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:10282788-10283636 FORWARD LENGTH=282	288	282	1.00E-112	97.9	67.0	77.1
Rsa1.0_01109.1.g23553.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01109.1.g23554.t1	ref|XP_002884509.1| hypothetical protein ARALYDRAFT_477824 [Arabidopsis lyrata subsp. lyrata] gi|297330349|gb|EFH60768.1| hypothetical protein ARALYDRAFT_477824 [Arabidopsis lyrata subsp. lyrata]	754	786	0	104.2	60.7	70.8	hypothetical protein ARALYDRAFT_477824	gbpln	Arabidopsis lyrata	AT3G05370.1 | Symbols: AtRLP31, RLP31 | receptor like protein 31 | chr3:1536134-1538716 REVERSE LENGTH=860	754	860	0	114.1	59.2	73.1
Rsa1.0_01109.1.g23555.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	187	1555	6.00E-32	831.6	42.2	58.8	disease resistance protein	gbpln	Brassica rapa	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	187	170	6.00E-11	90.9	22.5	33.2
Rsa1.0_01109.1.g23556.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	745	940	3.00E-46	126.2	21.9	34.9	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01109.1.g23557.t1	ref|XP_002870033.1| hypothetical protein ARALYDRAFT_914818 [Arabidopsis lyrata subsp. lyrata] gi|297315869|gb|EFH46292.1| hypothetical protein ARALYDRAFT_914818 [Arabidopsis lyrata subsp. lyrata]	195	191	2.00E-84	97.9	89.7	91.3	hypothetical protein ARALYDRAFT_914818	gbpln	Arabidopsis lyrata	AT4G18610.1 | Symbols: LSH9 | Protein of unknown function (DUF640) | chr4:10250794-10251369 FORWARD LENGTH=191	195	191	1.00E-86	97.9	89.2	91.8
Rsa1.0_01109.1.g23558.t1	ref|NP_567562.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] gi|44681468|gb|AAS47674.1| At4g18596 [Arabidopsis thaliana] gi|62320348|dbj|BAD94719.1| pollen-specific protein - like [Arabidopsis thaliana] gi|332658666|gb|AEE84066.1| pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana]	171	172	3.00E-86	100.6	91.2	97.1	pollen Ole e 1 allergen and extensin family protein	gbpln	Arabidopsis thaliana	AT4G18596.1 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr4:10239114-10239728 FORWARD LENGTH=172	171	172	1.00E-88	100.6	91.2	97.1
Rsa1.0_01110.1.g23559.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01110.1.g23560.t1	ref|XP_002877057.1| hypothetical protein ARALYDRAFT_484543 [Arabidopsis lyrata subsp. lyrata] gi|297322895|gb|EFH53316.1| hypothetical protein ARALYDRAFT_484543 [Arabidopsis lyrata subsp. lyrata]	937	914	0	97.5	86.4	90.5	hypothetical protein ARALYDRAFT_484543	gbpln	Arabidopsis lyrata	AT3G27530.1 | Symbols: GC6, MAG4 | golgin candidate 6 | chr3:10193778-10199659 REVERSE LENGTH=914	937	914	0	97.5	86.6	90.7
Rsa1.0_01110.1.g23561.t1	gb|EOA23253.1| hypothetical protein CARUB_v10017415mg [Capsella rubella]	389	390	0	100.3	87.1	94.1	hypothetical protein CARUB_v10017415mg	gbpln	Capsella rubella	AT3G27540.1 | Symbols: | beta-1,4-N-acetylglucosaminyltransferase family protein | chr3:10205489-10206888 FORWARD LENGTH=390	389	390	0	100.3	87.1	94.1
Rsa1.0_01110.1.g23562.t1	gb|EOA23738.1| hypothetical protein CARUB_v10016951mg, partial [Capsella rubella]	546	556	0	101.8	86.8	90.3	hypothetical protein CARUB_v10016951mg, partial	gbpln	Capsella rubella	AT3G27550.1 | Symbols: | RNA-binding CRS1 / YhbY (CRM) domain protein | chr3:10208010-10209899 REVERSE LENGTH=491	546	491	0	89.9	79.3	82.6
Rsa1.0_01110.1.g23563.t1	ref|NP_189393.1| protein kinase family protein [Arabidopsis thaliana] gi|11994183|dbj|BAB01286.1| nearly identical to protein kinase ATN1 [Arabidopsis thaliana] gi|16604328|gb|AAL24170.1| AT3g27560/MMJ24_11 [Arabidopsis thaliana] gi|19699190|gb|AAL90961.1| AT3g27560/MMJ24_11 [Arabidopsis thaliana] gi|332643816|gb|AEE77337.1| protein kinase family protein [Arabidopsis thaliana]	356	356	0	100.0	93.0	95.8	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G27560.1 | Symbols: ATN1 | Protein kinase superfamily protein | chr3:10210597-10212507 REVERSE LENGTH=356	356	356	0	100.0	93.0	95.8
Rsa1.0_01110.1.g23564.t1	ref|XP_002877060.1| AT3g27570/MMJ24_12 [Arabidopsis lyrata subsp. lyrata] gi|297322898|gb|EFH53319.1| AT3g27570/MMJ24_12 [Arabidopsis lyrata subsp. lyrata]	334	339	1.00E-157	101.5	84.4	88.6	AT3g27570/MMJ24_12	gbpln	Arabidopsis lyrata	AT3G27570.1 | Symbols: | Sucrase/ferredoxin-like family protein | chr3:10214276-10216681 REVERSE LENGTH=379	334	379	1.00E-153	113.5	82.3	88.6
Rsa1.0_01110.1.g23565.t1	gb|EOA23693.1| hypothetical protein CARUB_v10016900mg [Capsella rubella]	565	592	0	104.8	83.7	88.1	hypothetical protein CARUB_v10016900mg	gbpln	Capsella rubella	AT3G27580.2 | Symbols: ATPK7 | Protein kinase superfamily protein | chr3:10217671-10219484 REVERSE LENGTH=578	565	578	0	102.3	80.5	85.0
Rsa1.0_01110.1.g23566.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01110.1.g23567.t1	ref|XP_002877083.1| hypothetical protein ARALYDRAFT_484582 [Arabidopsis lyrata subsp. lyrata] gi|297322921|gb|EFH53342.1| hypothetical protein ARALYDRAFT_484582 [Arabidopsis lyrata subsp. lyrata]	425	425	0	100.0	85.2	90.8	hypothetical protein ARALYDRAFT_484582	gbpln	Arabidopsis lyrata	AT3G27930.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; Has 35 Blast hits to 35 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:10369593-10372318 REVERSE LENGTH=425	425	425	0	100.0	83.3	90.1
Rsa1.0_01110.1.g23568.t2	ref|NP_198848.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|10178142|dbj|BAB11587.1| CHP-rich zinc finger protein-like [Arabidopsis thaliana] gi|332007150|gb|AED94533.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	957	594	1.00E-151	62.1	29.9	37.5	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G40320.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:16121757-16123541 FORWARD LENGTH=594	957	594	1.00E-153	62.1	29.9	37.5
Rsa1.0_01110.1.g23569.t1	gb|EOA23597.1| hypothetical protein CARUB_v10016794mg [Capsella rubella]	663	664	0	100.2	88.2	93.4	hypothetical protein CARUB_v10016794mg	gbpln	Capsella rubella	AT3G27960.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:10380513-10382593 REVERSE LENGTH=663	663	663	0	100.0	86.7	93.1
Rsa1.0_01110.1.g23570.t1	gb|ABD65024.1| Zinc knuckle containing protein [Brassica oleracea]	243	324	1.00E-12	133.3	18.9	21.0	Zinc knuckle containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01111.1.g23571.t1	gb|EOA31069.1| hypothetical protein CARUB_v10014221mg [Capsella rubella]	239	314	6.00E-55	131.4	50.6	54.4	hypothetical protein CARUB_v10014221mg	gbpln	Capsella rubella	AT2G16070.2 | Symbols: PDV2 | plastid division2 | chr2:6984072-6985356 REVERSE LENGTH=307	239	307	2.00E-53	128.5	49.8	53.6
Rsa1.0_01111.1.g23572.t1	ref|NP_179215.1| uncharacterized protein [Arabidopsis thaliana] gi|4678214|gb|AAD26960.1| hypothetical protein [Arabidopsis thaliana] gi|52354251|gb|AAU44446.1| hypothetical protein AT2G16190 [Arabidopsis thaliana] gi|61742584|gb|AAX55113.1| hypothetical protein At2g16190 [Arabidopsis thaliana] gi|330251375|gb|AEC06469.1| uncharacterized protein AT2G16190 [Arabidopsis thaliana]	285	303	2.00E-77	106.3	59.3	68.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G16190.1 | Symbols: | BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT1G49330.1); Has 77 Blast hits to 77 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 13; Plants - 56; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:7020689-7021600 REVERSE LENGTH=303	285	303	7.00E-80	106.3	59.3	68.8
Rsa1.0_01111.1.g23573.t3	gb|EOA32510.1| hypothetical protein CARUB_v10015799mg [Capsella rubella]	524	499	0	95.2	78.2	83.6	hypothetical protein CARUB_v10015799mg	gbpln	Capsella rubella	AT2G16230.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr2:7035463-7038326 REVERSE LENGTH=503	524	503	0	96.0	77.1	82.6
Rsa1.0_01111.1.g23574.t1	ref|XP_002884160.1| hypothetical protein ARALYDRAFT_900287 [Arabidopsis lyrata subsp. lyrata] gi|297330000|gb|EFH60419.1| hypothetical protein ARALYDRAFT_900287 [Arabidopsis lyrata subsp. lyrata]	471	511	0	108.5	85.8	92.1	hypothetical protein ARALYDRAFT_900287	gbpln	Arabidopsis lyrata	AT2G16280.1 | Symbols: KCS9 | 3-ketoacyl-CoA synthase 9 | chr2:7051186-7052724 FORWARD LENGTH=512	471	512	0	108.7	85.8	92.4
Rsa1.0_01111.1.g23575.t1	ref|XP_002886215.1| hypothetical protein ARALYDRAFT_900289 [Arabidopsis lyrata subsp. lyrata] gi|297332055|gb|EFH62474.1| hypothetical protein ARALYDRAFT_900289 [Arabidopsis lyrata subsp. lyrata]	364	387	1.00E-116	106.3	62.6	73.9	hypothetical protein ARALYDRAFT_900289	gbpln	Arabidopsis lyrata	AT2G16290.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr2:7058930-7060573 REVERSE LENGTH=415	364	415	1.00E-70	114.0	47.8	61.5
Rsa1.0_01111.1.g23576.t7	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1303	1491	0	114.4	58.5	72.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1303	1262	1.00E-121	96.9	16.3	23.3

Rsa1.0_01111.1.g23577.t1	ref|NP_179235.1| purple acid phosphatase 10 [Arabidopsis thaliana] gi|75265912|sp|Q9SIV9.1|PPA10_ARATH RecName: Full=Purple acid phosphatase 10; Flags: Precursor gi|20257483|gb|AAM15911.1|AF492662_1 purple acid phosphatase [Arabidopsis thaliana] gi|4544387|gb|AAD22297.1| putative purple acid phosphatase precursor [Arabidopsis thaliana] gi|20260674|gb|AAM13235.1| putative purple acid phosphatase precursor [Arabidopsis thaliana] gi|31376393|gb|AAP49523.1| At2g16430 [Arabidopsis thaliana] gi|330251402|gb|AEC06496.1| purple acid phosphatase 10 [Arabidopsis thaliana]	470	468	0	99.6	85.3	91.7	purple acid phosphatase 10	gbpln	Arabidopsis thaliana	AT2G16430.2 | Symbols: PAP10, ATPAP10 | purple acid phosphatase 10 | chr2:7120502-7122772 REVERSE LENGTH=468	470	468	0	99.6	85.3	91.7
Rsa1.0_01111.1.g23578.t1	ref|NP_565388.1| uncharacterized protein [Arabidopsis thaliana] gi|17529264|gb|AAL38859.1| unknown protein [Arabidopsis thaliana] gi|20198032|gb|AAD22294.2| expressed protein [Arabidopsis thaliana] gi|21536621|gb|AAM60953.1| unknown [Arabidopsis thaliana] gi|29824341|gb|AAP04131.1| unknown protein [Arabidopsis thaliana] gi|330251406|gb|AEC06500.1| uncharacterized protein AT2G16460 [Arabidopsis thaliana]	288	230	1.00E-108	79.9	68.8	72.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G16460.1 | Symbols: | Protein of unknown function (DUF1640) | chr2:7133704-7135483 REVERSE LENGTH=230	288	230	1.00E-110	79.9	68.8	72.9
Rsa1.0_01111.1.g23579.t1	ref|NP_189943.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75173224|sp|Q9FYD3.1|GDL56_ARATH RecName: Full=GDSL esterase/lipase At3g43570; AltName: Full=Extracellular lipase At3g43570; Flags: Precursor gi|9967506|emb|CAC05631.1| putative protein [Arabidopsis thaliana] gi|332644285|gb|AEE77806.1| GDSL esterase/lipase [Arabidopsis thaliana]	308	320	1.00E-144	103.9	80.2	89.3	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT3G43570.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:15473345-15474765 FORWARD LENGTH=320	308	320	2.33E-156	103.9	80.2	89.3
Rsa1.0_01111.1.g23580.t1	ref|XP_002890318.1| hypothetical protein ARALYDRAFT_472131 [Arabidopsis lyrata subsp. lyrata] gi|297336160|gb|EFH66577.1| hypothetical protein ARALYDRAFT_472131 [Arabidopsis lyrata subsp. lyrata]	61	755	3.00E-14	1237.7	78.7	82.0	hypothetical protein ARALYDRAFT_472131	gbpln	Arabidopsis lyrata	AT1G19110.1 | Symbols: | inter-alpha-trypsin inhibitor heavy chain-related | chr1:6602270-6605766 FORWARD LENGTH=754	61	754	2.00E-16	1236.1	77.0	82.0
Rsa1.0_01112.1.g23581.t1	emb|CAN74668.1| hypothetical protein VITISV_005686 [Vitis vinifera]	127	480	2.00E-26	378.0	55.1	61.4	hypothetical protein VITISV_005686	gbpln	Vitis vinifera	AT2G12480.2 | Symbols: SCPL43 | serine carboxypeptidase-like 43 | chr2:5069795-5072227 REVERSE LENGTH=443	127	443	1.00E-28	348.8	48.8	52.8
Rsa1.0_01112.1.g23582.t2	ref|XP_002869254.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315090|gb|EFH45513.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	2106	2147	0	101.9	86.4	91.7	predicted protein	gbpln	Arabidopsis lyrata	AT4G32700.2 | Symbols: | helicases;ATP-dependent helicases;nucleic acid binding;ATP binding;DNA-directed DNA polymerases;DNA binding | chr4:15767440-15779185 FORWARD LENGTH=2154	2106	2154	0	102.3	85.7	91.5
Rsa1.0_01112.1.g23583.t1	gb|EOA23152.1| hypothetical protein CARUB_v10016599mg [Capsella rubella]	1074	1174	0	109.3	80.9	84.4	hypothetical protein CARUB_v10016599mg	gbpln	Capsella rubella	AT3G26560.1 | Symbols: | ATP-dependent RNA helicase, putative | chr3:9750122-9753719 REVERSE LENGTH=1168	1074	1168	0	108.8	80.6	84.2
Rsa1.0_01112.1.g23584.t1	ref|NP_567900.1| uncharacterized protein [Arabidopsis thaliana] gi|332660703|gb|AEE86103.1| uncharacterized protein AT4G32680 [Arabidopsis thaliana]	249	282	1.00E-81	113.3	71.1	82.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G32680.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52343.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15763462-15765039 REVERSE LENGTH=282	249	282	3.00E-84	113.3	71.1	82.3
Rsa1.0_01112.1.g23585.t1	ref|NP_195530.2| FAR1-related sequence 9 [Arabidopsis thaliana] gi|334302810|sp|Q9SZL7.2|FRS9_ARATH RecName: Full=Protein FAR1-RELATED SEQUENCE 9 gi|332661489|gb|AEE86889.1| FAR1-related sequence 9 [Arabidopsis thaliana]	520	545	0	104.8	68.8	81.5	FAR1-related sequence 9	gbpln	Arabidopsis thaliana	AT4G38170.1 | Symbols: FRS9 | FAR1-related sequence 9 | chr4:17904613-17906439 FORWARD LENGTH=545	520	545	0	104.8	68.8	81.5
Rsa1.0_01112.1.g23586.t1	dbj|BAH20056.1| AT2G25670 [Arabidopsis thaliana]	316	318	9.00E-63	100.6	73.7	84.5	AT2G25670	gbpln	Arabidopsis thaliana	AT4G32610.1 | Symbols: | copper ion binding | chr4:15728376-15729897 REVERSE LENGTH=315	316	315	7.00E-61	99.7	75.6	85.4

Rsa1.0_01112.1.g23587.t1	gb|EOA16248.1| hypothetical protein CARUB_v10004394mg [Capsella rubella]	584	613	0	105.0	83.0	91.3	hypothetical protein CARUB_v10004394mg	gbpln	Capsella rubella	AT5G40410.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:16171385-16173211 FORWARD LENGTH=608	584	608	0	104.1	81.7	89.9
Rsa1.0_01112.1.g23588.t1	gb|EOA16606.1| hypothetical protein CARUB_v10004779mg [Capsella rubella]	405	454	1.00E-171	112.1	84.2	89.9	hypothetical protein CARUB_v10004779mg	gbpln	Capsella rubella	AT4G32600.1 | Symbols: | RING/U-box superfamily protein | chr4:15724010-15725737 FORWARD LENGTH=453	405	453	1.00E-172	111.9	82.7	88.9
Rsa1.0_01112.1.g23589.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1605	1214	0	75.6	28.1	41.6	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1605	626	1.00E-82	39.0	10.3	15.6
Rsa1.0_01112.1.g23590.t2	ref|XP_002869282.1| hypothetical protein ARALYDRAFT_491495 [Arabidopsis lyrata subsp. lyrata] gi|297315118|gb|EFH45541.1| hypothetical protein ARALYDRAFT_491495 [Arabidopsis lyrata subsp. lyrata]	427	437	1.00E-157	102.3	73.3	79.2	hypothetical protein ARALYDRAFT_491495	gbpln	Arabidopsis lyrata	AT4G32330.3 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr4:15609801-15611867 FORWARD LENGTH=437	427	437	1.00E-158	102.3	71.7	78.2
Rsa1.0_01112.1.g23591.t1	ref|XP_002869284.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297315120|gb|EFH45543.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	830	825	0	99.4	83.5	91.1	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT4G32300.1 | Symbols: SD2-5 | S-domain-2 5 | chr4:15599970-15602435 FORWARD LENGTH=821	830	821	0	98.9	82.8	90.1
Rsa1.0_01112.1.g23592.t1	gb|EOA15559.1| hypothetical protein CARUB_v10005173mg [Capsella rubella]	343	344	1.00E-177	100.3	89.5	95.0	hypothetical protein CARUB_v10005173mg	gbpln	Capsella rubella	AT4G32272.1 | Symbols: | Nucleotide/sugar transporter family protein | chr4:15577195-15579689 REVERSE LENGTH=344	343	344	1.00E-177	100.3	88.6	94.5
Rsa1.0_01112.1.g23593.t1	ref|XP_002872474.1| hypothetical protein ARALYDRAFT_911263 [Arabidopsis lyrata subsp. lyrata] gi|297318311|gb|EFH48733.1| hypothetical protein ARALYDRAFT_911263 [Arabidopsis lyrata subsp. lyrata]	427	417	1.00E-93	97.7	48.7	63.2	hypothetical protein ARALYDRAFT_911263	gbpln	Arabidopsis lyrata	AT3G26010.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:9511901-9513145 FORWARD LENGTH=414	427	414	3.00E-39	97.0	31.1	46.4
Rsa1.0_01112.1.g23594.t1	ref|XP_002867250.1| hypothetical protein ARALYDRAFT_491506 [Arabidopsis lyrata subsp. lyrata] gi|297313086|gb|EFH43509.1| hypothetical protein ARALYDRAFT_491506 [Arabidopsis lyrata subsp. lyrata]	203	237	4.00E-52	116.7	59.6	72.9	hypothetical protein ARALYDRAFT_491506	gbpln	Arabidopsis lyrata	AT4G32270.1 | Symbols: | Ubiquitin-like superfamily protein | chr4:15575015-15576360 REVERSE LENGTH=239	203	239	5.00E-53	117.7	60.1	70.4
Rsa1.0_01112.1.g23595.t1	gb|EOA16255.1| hypothetical protein CARUB_v10004401mg [Capsella rubella] gi|482552063|gb|EOA16256.1| hypothetical protein CARUB_v10004401mg [Capsella rubella]	623	611	0	98.1	76.6	85.1	hypothetical protein CARUB_v10004401mg	gbpln	Capsella rubella	AT4G32250.3 | Symbols: | Protein kinase superfamily protein | chr4:15570285-15572528 REVERSE LENGTH=611	623	611	0	98.1	76.9	85.9
Rsa1.0_01112.1.g23596.t1	ref|XP_002869310.1| hypothetical protein ARALYDRAFT_491553 [Arabidopsis lyrata subsp. lyrata] gi|297315146|gb|EFH45569.1| hypothetical protein ARALYDRAFT_491553 [Arabidopsis lyrata subsp. lyrata]	173	177	7.00E-73	102.3	83.8	88.4	hypothetical protein ARALYDRAFT_491553	gbpln	Arabidopsis lyrata	AT4G31840.1 | Symbols: ENODL15, AtENODL15 | early nodulin-like protein 15 | chr4:15401798-15402426 FORWARD LENGTH=177	173	177	6.00E-74	102.3	82.7	86.7
Rsa1.0_01112.1.g23597.t1	ref|XP_002867277.1| hypothetical protein ARALYDRAFT_913282 [Arabidopsis lyrata subsp. lyrata] gi|297313113|gb|EFH43536.1| hypothetical protein ARALYDRAFT_913282 [Arabidopsis lyrata subsp. lyrata]	100	100	6.00E-49	100.0	96.0	99.0	hypothetical protein ARALYDRAFT_913282	gbpln	Arabidopsis lyrata	AT4G31830.1 | Symbols: | unknown protein; Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15400803-15401105 REVERSE LENGTH=100	100	100	1.00E-51	100.0	96.0	98.0
Rsa1.0_01112.1.g23598.t1	ref|XP_002867278.1| enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313114|gb|EFH43537.1| enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	409	409	0	100.0	89.5	95.6	enoyl-CoA hydratase/isomerase family protein	gbpln	Arabidopsis lyrata	AT4G31810.1 | Symbols: | ATP-dependent caseinolytic (Clp) protease/crotonase family protein | chr4:15387365-15390290 REVERSE LENGTH=409	409	409	0	100.0	88.3	94.4
Rsa1.0_01112.1.g23599.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01112.1.g23600.t1	gb|AAS13378.1| WRKY1 [Brassica rapa subsp. chinensis]	313	308	1.00E-157	98.4	88.8	91.4	WRKY1	gbpln	Brassica rapa	AT4G31800.1 | Symbols: WRKY18, ATWRKY18 | WRKY DNA-binding protein 18 | chr4:15383296-15384812 FORWARD LENGTH=310	313	310	1.00E-138	99.0	79.2	88.5
Rsa1.0_01113.1.g23601.t1	emb|CAB45522.1| [acyl-carrier protein] S-malonyltransferase [Brassica napus]	369	349	0	94.6	90.0	92.4		gbpln	Brassica napus	AT2G30200.1 | Symbols: | catalytics;transferases;[acyl-carrier-protein] S-malonyltransferases;binding | chr2:12883162-12885482 REVERSE LENGTH=393	369	393	0	106.5	86.7	89.7

Rsa1.0_01113.1.g23602.t1	ref|XP_002880821.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297326660|gb|EFH57080.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	330	318	1.00E-104	96.4	56.1	65.2	kinase family protein	gbpln	Arabidopsis lyrata	AT2G41920.1 | Symbols: | Protein kinase superfamily protein | chr2:17499448-17500404 FORWARD LENGTH=318	330	318	4.00E-99	96.4	53.9	66.1
Rsa1.0_01113.1.g23603.t1	ref|XP_002879254.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325093|gb|EFH55513.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	423	455	0	107.6	79.4	89.1	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT2G30140.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:12872200-12873691 FORWARD LENGTH=455	423	455	0	107.6	78.3	87.7
Rsa1.0_01113.1.g23604.t1	gb|ABD65147.1| hypothetical protein 40.t00024 [Brassica oleracea]	405	480	2.00E-13	118.5	16.0	20.2	hypothetical protein 40.t00024	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01113.1.g23605.t1	ref|NP_565695.1| LOB domain-containing protein 12 [Arabidopsis thaliana] gi|29427828|sp|Q8LBW3.2|LBD12_ARATH RecName: Full=LOB domain-containing protein 12; AltName: Full=ASYMMETRIC LEAVES 2-like protein 5; Short=AS2-like protein 5 gi|3150407|gb|AAC16959.1| expressed protein [Arabidopsis thaliana] gi|45330813|dbj|BAD12425.1| ASYMMETRIC LEAVES2-like gene 5 protein [Arabidopsis thaliana] gi|219807086|dbj|BAH10549.1| ASYMMETRIC LEAVES2-like 5 protein [Arabidopsis thaliana] gi|330253255|gb|AEC08349.1| LOB domain-containing protein 12 [Arabidopsis thaliana]	188	193	6.00E-82	102.7	89.4	93.1	LOB domain-containing protein 12	gbpln	Arabidopsis thaliana	AT2G30130.1 | Symbols: ASL5, LBD12, PCK1 | Lateral organ boundaries (LOB) domain family protein | chr2:12868740-12869684 FORWARD LENGTH=193	188	193	2.00E-84	102.7	89.4	93.1
Rsa1.0_01113.1.g23606.t1	ref|XP_002862737.1| hypothetical protein ARALYDRAFT_920315 [Arabidopsis lyrata subsp. lyrata] gi|297308435|gb|EFH38995.1| hypothetical protein ARALYDRAFT_920315 [Arabidopsis lyrata subsp. lyrata]	195	193	3.00E-80	99.0	77.4	79.0	hypothetical protein ARALYDRAFT_920315	gbpln	Arabidopsis lyrata	AT1G07090.1 | Symbols: LSH6 | Protein of unknown function (DUF640) | chr1:2174202-2174792 REVERSE LENGTH=196	195	196	9.00E-71	100.5	69.7	78.5
Rsa1.0_01113.1.g23607.t1	ref|XP_002881085.1| hypothetical protein ARALYDRAFT_481921 [Arabidopsis lyrata subsp. lyrata] gi|297326924|gb|EFH57344.1| hypothetical protein ARALYDRAFT_481921 [Arabidopsis lyrata subsp. lyrata]	1019	1083	0	106.3	95.0	97.8	hypothetical protein ARALYDRAFT_481921	gbpln	Arabidopsis lyrata	AT2G30110.1 | Symbols: ATUBA1, MOS5, UBA1 | ubiquitin-activating enzyme 1 | chr2:12852632-12857369 REVERSE LENGTH=1080	1019	1080	0	106.0	95.1	97.7
Rsa1.0_01113.1.g23608.t1	ref|XP_002886268.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata] gi|297332108|gb|EFH62527.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata]	366	346	7.00E-71	94.5	46.4	62.0	hypothetical protein ARALYDRAFT_900376	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	366	370	8.00E-65	101.1	41.5	58.2
Rsa1.0_01113.1.g23609.t1	ref|XP_002886268.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata] gi|297332108|gb|EFH62527.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata]	243	346	1.00E-42	142.4	46.1	63.8	hypothetical protein ARALYDRAFT_900376	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	243	370	3.00E-41	152.3	42.4	62.1
Rsa1.0_01114.1.g23610.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	361	1225	6.00E-77	339.3	36.8	53.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01114.1.g23611.t1	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	676	521	7.00E-65	77.1	18.3	24.7	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	AT2G17920.1 | Symbols: | nucleic acid binding;zinc ion binding | chr2:7782808-7783731 FORWARD LENGTH=307	676	307	1.00E-22	45.4	8.7	13.3
Rsa1.0_01114.1.g23612.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	112	1024	4.00E-27	914.3	50.9	60.7	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01114.1.g23613.t1	gb|EOA36607.1| hypothetical protein CARUB_v10011815mg [Capsella rubella]	77	80	5.00E-34	103.9	93.5	98.7	hypothetical protein CARUB_v10011815mg	gbpln	Capsella rubella	AT1G48330.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G17580.1); Has 40 Blast hits to 40 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:17863897-17864124 FORWARD LENGTH=75	77	75	2.00E-32	97.4	81.8	84.4
Rsa1.0_01114.1.g23614.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01114.1.g23615.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01114.1.g23616.t1	gb|EOA36133.1| hypothetical protein CARUB_v10012487mg [Capsella rubella]	271	285	1.00E-99	105.2	72.3	85.6	hypothetical protein CARUB_v10012487mg	gbpln	Capsella rubella	AT1G48405.1 | Symbols: | Kinase interacting (KIP1-like) family protein | chr1:17884645-17885614 REVERSE LENGTH=297	271	297	1.00E-100	109.6	74.2	85.2
Rsa1.0_01114.1.g23617.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01114.1.g23618.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	378	1142	2.00E-51	302.1	26.2	37.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	378	626	2.00E-11	165.6	18.3	32.8
Rsa1.0_01114.1.g23619.t1	ref|XP_002884458.1| pre-mRNA cleavage complex family protein [Arabidopsis lyrata subsp. lyrata] gi|297330298|gb|EFH60717.1| pre-mRNA cleavage complex family protein [Arabidopsis lyrata subsp. lyrata]	182	443	2.00E-32	243.4	38.5	43.4	pre-mRNA cleavage complex family protein	gbpln	Arabidopsis lyrata	AT3G04680.2 | Symbols: CLPS3 | CLP-similar protein 3 | chr3:1270053-1272415 REVERSE LENGTH=444	182	444	2.00E-34	244.0	37.9	43.4
Rsa1.0_01114.1.g23620.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01115.1.g23621.t3	ref|NP_178022.1| NADH dehydrogenase [ubiquinone] iron-sulfur protein 8 [Arabidopsis thaliana] gi|297842689|ref|XP_002889226.1| NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial [Arabidopsis lyrata subsp. lyrata] gi|3929364|sp|Q42599.1|NDS8A_ARATH RecName: Full=NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-A, mitochondrial; Flags: Precursor gi|666977|emb|CAA59061.1| NADH dehydrogenase [Arabidopsis thaliana] gi|3152573|gb|AAC17054.1| Match to NADH:ubiquinone oxidoreductase gb|X84318 from A.thaliana. ESTs gb|Z27005, gb|T04711, gb|T45078 and gb|Z28689 come from this gene [Arabidopsis thaliana] gi|15081697|gb|AAK82503.1| At1g79010/YUP8H12R_21 [Arabidopsis thaliana] gi|18252265|gb|AAL62013.1| At1g79010/YUP8H12R_21 [Arabidopsis thaliana] gi|21593880|gb|AAM65847.1| NADH dehydrogenase, putative [Arabidopsis thaliana] gi|110740838|dbj|BAE98516.1| hypothetical protein [Arabidopsis thaliana] gi|297335067|gb|EFH65485.1| NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial [Arabidopsis lyrata subsp. lyrata] gi|332198072|gb|AEE36193.1| NADH dehydrogenase [ubiquinone] iron-sulfur	222	222	1.00E-123	100.0	95.9	98.2	NADH dehydrogenase	gbpln	Arabidopsis lyrata	AT1G79010.1 | Symbols: | Alpha-helical ferredoxin | chr1:29725138-29726933 REVERSE LENGTH=222	222	222	1.00E-125	100.0	95.9	98.2
Rsa1.0_01115.1.g23622.t1	ref|NP_565196.1| uncharacterized protein [Arabidopsis thaliana] gi|21554958|gb|AAM63739.1| unknown [Arabidopsis thaliana] gi|22531253|gb|AAM97130.1| expressed protein [Arabidopsis thaliana] gi|30102864|gb|AAP21350.1| At1g78995 [Arabidopsis thaliana] gi|332198069|gb|AEE36190.1| uncharacterized protein AT1G78995 [Arabidopsis thaliana]	154	159	5.00E-56	103.2	85.1	88.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G78995.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:29715433-29716079 REVERSE LENGTH=159	154	159	2.00E-58	103.2	85.1	88.3
Rsa1.0_01115.1.g23623.t1	ref|XP_002886496.1| hypothetical protein ARALYDRAFT_893290 [Arabidopsis lyrata subsp. lyrata] gi|297332337|gb|EFH62755.1| hypothetical protein ARALYDRAFT_893290 [Arabidopsis lyrata subsp. lyrata]	347	416	7.00E-58	119.9	37.5	48.4	hypothetical protein ARALYDRAFT_893290	gbpln	Arabidopsis lyrata	AT5G65850.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:26346317-26347495 FORWARD LENGTH=392	347	392	1.00E-50	113.0	32.6	43.2
Rsa1.0_01115.1.g23624.t1	dbj|BAJ33720.1| unnamed protein product [Thellungiella halophila]	339	294	1.00E-125	86.7	72.3	77.9	unnamed protein product	----	----	AT1G78600.1 | Symbols: LZF1, STH3, DBB3 | light-regulated zinc finger protein 1 | chr1:29567370-29568662 FORWARD LENGTH=299	339	299	1.00E-119	88.2	68.7	74.3
Rsa1.0_01115.1.g23625.t1	ref|NP_177964.2| ROP interactive partner 2 [Arabidopsis thaliana] gi|374095407|sp|Q9M9F9.2|ICR4_ARATH RecName: Full=Interactor of constitutive active ROPs 4; AltName: Full=ROP interactive partner 2 gi|332197984|gb|AEE36105.1| ROP interactive partner 2 [Arabidopsis thaliana]	320	324	1.00E-123	101.3	78.4	88.1	ROP interactive partner 2	gbpln	Arabidopsis thaliana	AT1G78430.1 | Symbols: RIP2 | ROP interactive partner 2 | chr1:29509605-29510679 FORWARD LENGTH=324	320	324	1.00E-126	101.3	78.4	88.1
Rsa1.0_01115.1.g23626.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01115.1.g23627.t1	ref|XP_002887735.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297333576|gb|EFH63994.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	100	110	2.00E-30	110.0	76.0	86.0	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT1G78410.1 | Symbols: | VQ motif-containing protein | chr1:29502728-29503054 FORWARD LENGTH=108	100	108	9.00E-33	108.0	76.0	86.0
Rsa1.0_01115.1.g23628.t1	ref|NP_177514.1| ethylene insensitive 3-like 3 protein [Arabidopsis thaliana] gi|37078126|sp|O23116.1|EIL3_ARATH RecName: Full=ETHYLENE INSENSITIVE 3-like 3 protein gi|12324201|gb|AAG52067.1|AC012679_5 ethylene-insensitive3-like3 (EIL3); 60307-58378 [Arabidopsis thaliana] gi|2224931|gb|AAC49748.1| ethylene-insensitive3-like3 [Arabidopsis thaliana] gi|17979067|gb|AAL49801.1| putative ethylene-insensitive protein EIL3 [Arabidopsis thaliana] gi|22136858|gb|AAM91773.1| putative ethylene-insensitive protein EIL3 [Arabidopsis thaliana] gi|332197381|gb|AEE35502.1| ethylene insensitive 3-like 3 protein [Arabidopsis thaliana]	305	567	8.00E-68	185.9	51.1	55.7	ethylene insensitive 3-like 3 protein	gbpln	Arabidopsis thaliana	AT1G73730.1 | Symbols: EIL3, SLIM1, ATSLIM, AtEIL3 | ETHYLENE-INSENSITIVE3-like 3 | chr1:27730434-27732363 REVERSE LENGTH=567	305	567	2.00E-70	185.9	51.1	55.7
Rsa1.0_01115.1.g23629.t1	ref|NP_178198.1| metal transporter Nramp1 [Arabidopsis thaliana] gi|29839673|sp|Q9SAH8.1|NRAM1_ARATH RecName: Full=Metal transporter Nramp1; Short=AtNramp1 gi|6503294|gb|AAF14670.1|AC011713_18 Identical to gb|AF181687 metal ion transporter from Arabidopsis thaliana. ESTs gb|Z30530, gb|AA585940, gb|AI998720 and gb|Z33946 come from this gene [Arabidopsis thaliana] gi|7108911|gb|AAF36535.1|AF165125_1 NRAMP1 protein [Arabidopsis thaliana] gi|117168063|gb|ABK32114.1| At1g80830 [Arabidopsis thaliana] gi|332198334|gb|AEE36455.1| metal transporter Nramp1 [Arabidopsis thaliana]	527	532	0	100.9	90.9	95.3	metal transporter Nramp1	gbpln	Arabidopsis thaliana	AT1G80830.1 | Symbols: NRAMP1, PMIT1, ATNRAMP1 | natural resistance-associated macrophage protein 1 | chr1:30373066-30375644 REVERSE LENGTH=532	527	532	0	100.9	90.9	95.3
Rsa1.0_01115.1.g23630.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	145	1142	3.00E-23	787.6	44.1	55.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01115.1.g23631.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01115.1.g23632.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01115.1.g23633.t1	ref|NP_565178.1| glutathione S-transferase TAU 19 [Arabidopsis thaliana] gi|75338923|sp|Q9ZRW8.1|GSTUJ_ARATH RecName: Full=Glutathione S-transferase U19; Short=AtGSTU19; AltName: Full=GST class-tau member 19; AltName: Full=Glutathione S-transferase 8 gi|14326477|gb|AAK60284.1|AF385691_1 At1g78380/F3F9_11 [Arabidopsis thaliana] gi|4006934|emb|CAA10060.1| glutathione transferase [Arabidopsis thaliana] gi|18700206|gb|AAL77713.1| At1g78380/F3F9_11 [Arabidopsis thaliana] gi|332197978|gb|AEE36099.1| glutathione S-transferase TAU 19 [Arabidopsis thaliana]	219	219	1.00E-107	100.0	84.5	91.3	glutathione S-transferase TAU 19	gbpln	Arabidopsis thaliana	AT1G78380.1 | Symbols: ATGSTU19, GST8, GSTU19 | glutathione S-transferase TAU 19 | chr1:29486659-29487819 REVERSE LENGTH=219	219	219	1.00E-109	100.0	84.5	91.3

Rsa1.0_01116.1.g23634.t1	ref|NP_180305.1| uncharacterized protein [Arabidopsis thaliana] gi|75216242|sp|Q9ZQI2.1|CASP3_ARATH RecName: Full=Casparian strip membrane protein 3 gi|5306261|gb|AAD41993.1| unknown protein [Arabidopsis thaliana] gi|20197657|gb|AAM15182.1| unknown protein [Arabidopsis thaliana] gi|27765014|gb|AAO23628.1| At2g27370 [Arabidopsis thaliana] gi|110743400|dbj|BAE99586.1| hypothetical protein [Arabidopsis thaliana] gi|330252892|gb|AEC07986.1| uncharacterized protein AT2G27370 [Arabidopsis thaliana] gi|339515802|gb|AEJ82279.1| casparian strip protein 3 [Cloning vector pCASP3::CASP3:GFP] gi|339515817|gb|AEJ82289.1| casparian strip protein 3 [Cloning vector p35S::CASP3:GFP]	219	221	1.00E-109	100.9	94.1	97.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G27370.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr2:11708628-11709905 REVERSE LENGTH=221	219	221	1.00E-111	100.9	94.1	97.3
Rsa1.0_01116.1.g23635.t1	gb|AAA62850.1| nodulin [Medicago truncatula]	850	549	2.00E-45	64.6	30.7	37.4	nodulin	gbpln	Medicago truncatula	AT3G22142.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:7803604-7808046 REVERSE LENGTH=1480	850	1480	2.00E-25	174.1	46.2	54.4
Rsa1.0_01116.1.g23636.t1	ref|XP_002879088.1| hypothetical protein ARALYDRAFT_344504 [Arabidopsis lyrata subsp. lyrata] gi|297324927|gb|EFH55347.1| hypothetical protein ARALYDRAFT_344504 [Arabidopsis lyrata subsp. lyrata]	304	316	1.00E-136	103.9	79.6	90.8	hypothetical protein ARALYDRAFT_344504	gbpln	Arabidopsis lyrata	AT1G08340.1 | Symbols: | Rho GTPase activating protein with PAK-box/P21-Rho-binding domain | chr1:2631308-2632669 FORWARD LENGTH=331	304	331	1.00E-122	108.9	66.4	75.0
Rsa1.0_01116.1.g23637.t2	gb|EOA27595.1| hypothetical protein CARUB_v10023735mg [Capsella rubella]	315	299	1.00E-166	94.9	90.5	93.3	hypothetical protein CARUB_v10023735mg	gbpln	Capsella rubella	AT2G27450.1 | Symbols: NLP1, ATNLP1, CPA | nitrilase-like protein 1 | chr2:11737666-11739577 REVERSE LENGTH=299	315	299	1.00E-168	94.9	90.2	92.7
Rsa1.0_01116.1.g23638.t1	gb|EOA26640.1| hypothetical protein CARUB_v10022704mg [Capsella rubella]	746	745	0	99.9	91.3	95.3	hypothetical protein CARUB_v10022704mg	gbpln	Capsella rubella	AT2G27460.1 | Symbols: | sec23/sec24 transport family protein | chr2:11740670-11744867 FORWARD LENGTH=745	746	745	0	99.9	91.0	95.6
Rsa1.0_01116.1.g23639.t1	ref|XP_002880924.1| hypothetical protein ARALYDRAFT_901657 [Arabidopsis lyrata subsp. lyrata] gi|297326763|gb|EFH57183.1| hypothetical protein ARALYDRAFT_901657 [Arabidopsis lyrata subsp. lyrata]	148	154	3.00E-68	104.1	83.8	90.5	hypothetical protein ARALYDRAFT_901657	gbpln	Arabidopsis lyrata	AT2G27510.1 | Symbols: ATFD3, FD3 | ferredoxin 3 | chr2:11758281-11758748 REVERSE LENGTH=155	148	155	2.00E-70	104.7	83.8	91.2
Rsa1.0_01116.1.g23640.t1	ref|XP_002879155.1| 60S ribosomal protein L10A [Arabidopsis lyrata subsp. lyrata] gi|297324994|gb|EFH55414.1| 60S ribosomal protein L10A [Arabidopsis lyrata subsp. lyrata]	216	216	1.00E-108	100.0	96.8	98.1	60S ribosomal protein L10A	gbpln	Arabidopsis lyrata	AT2G27530.2 | Symbols: PGY1 | Ribosomal protein L1p/L10e family | chr2:11763443-11764570 REVERSE LENGTH=216	216	216	1.00E-110	100.0	96.3	98.1
Rsa1.0_01116.1.g23641.t1	ref|XP_002869958.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata] gi|297315794|gb|EFH46217.1| hypothetical protein ARALYDRAFT_914664 [Arabidopsis lyrata subsp. lyrata]	408	428	1.00E-130	104.9	61.0	76.7	hypothetical protein ARALYDRAFT_914664	gbpln	Arabidopsis lyrata	AT4G19930.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:10803558-10804853 FORWARD LENGTH=431	408	431	1.00E-114	105.6	57.4	71.6
Rsa1.0_01116.1.g23642.t1	gb|EOA36409.1| hypothetical protein CARUB_v10010878mg [Capsella rubella]	383	305	1.00E-140	79.6	61.9	68.1	hypothetical protein CARUB_v10010878mg	gbpln	Capsella rubella	AT1G08310.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:2619134-2620338 FORWARD LENGTH=315	383	315	1.00E-142	82.2	62.7	69.7
Rsa1.0_01117.1.g23643.t1	ref|XP_002882175.1| hypothetical protein ARALYDRAFT_477362 [Arabidopsis lyrata subsp. lyrata] gi|297328015|gb|EFH58434.1| hypothetical protein ARALYDRAFT_477362 [Arabidopsis lyrata subsp. lyrata]	685	625	0	91.2	67.0	70.5	hypothetical protein ARALYDRAFT_477362	gbpln	Arabidopsis lyrata	AT3G01540.4 | Symbols: DRH1, ATDRH1 | DEAD box RNA helicase 1 | chr3:213077-216142 REVERSE LENGTH=619	685	619	0	90.4	65.3	69.1

Rsa1.0_01117.1.g23644.t1	ref|NP_186817.1| uncharacterized protein [Arabidopsis thaliana] gi|6016725|gb|AAF01551.1|AC009325_21 unknown protein [Arabidopsis thaliana] gi|30725324|gb|AAP37684.1| At3g01680 [Arabidopsis thaliana] gi|110736167|dbj|BAF00055.1| hypothetical protein [Arabidopsis thaliana] gi|307101698|gb|ADN32814.1| sieve element occlusion b [Arabidopsis thaliana] gi|332640181|gb|AEE73702.1| uncharacterized protein AT3G01680 [Arabidopsis thaliana]	735	740	0	100.7	87.9	92.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01680.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Mediator complex subunit Med28 (InterPro:IPR021640); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01670.1); Has 122 Blast hits to 112 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 122; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:252033-255246 FORWARD LENGTH=740	735	740	0	100.7	87.9	92.8
Rsa1.0_01117.1.g23645.t1	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	1649	1752	0	106.2	52.8	66.5	putative protein	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1649	331	3.00E-70	20.1	8.3	11.5
Rsa1.0_01117.1.g23646.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	499	490	9.00E-87	98.2	38.9	56.5	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	499	566	3.00E-83	113.4	34.7	57.3
Rsa1.0_01117.1.g23647.t1	gb|EOA30906.1| hypothetical protein CARUB_v10014053mg [Capsella rubella]	360	357	1.00E-167	99.2	83.6	89.7	hypothetical protein CARUB_v10014053mg	gbpln	Capsella rubella	AT3G01690.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:256753-258379 FORWARD LENGTH=361	360	361	1.00E-166	100.3	85.3	90.0
Rsa1.0_01117.1.g23648.t1	ref|XP_002882166.1| ribosomal protein L13 family protein [Arabidopsis lyrata subsp. lyrata] gi|297328006|gb|EFH58425.1| ribosomal protein L13 family protein [Arabidopsis lyrata subsp. lyrata]	214	205	1.00E-101	95.8	88.3	90.2	ribosomal protein L13 family protein	gbpln	Arabidopsis lyrata	AT3G01790.2 | Symbols: | Ribosomal protein L13 family protein | chr3:283880-285583 REVERSE LENGTH=205	214	205	1.00E-102	95.8	86.4	88.3
Rsa1.0_01117.1.g23649.t1	ref|NP_186852.4| transferase [Arabidopsis thaliana] gi|332640230|gb|AEE73751.1| transferase [Arabidopsis thaliana]	658	662	0	100.6	85.3	91.2	transferase	gbpln	Arabidopsis thaliana	AT3G02030.1 | Symbols: | transferases, transferring acyl groups other than amino-acyl groups;acyltransferases | chr3:345024-348311 FORWARD LENGTH=662	658	662	0	100.6	85.3	91.2
Rsa1.0_01117.1.g23650.t1	ref|NP_566159.1| senescence-related protein [Arabidopsis thaliana] gi|6513927|gb|AAF14831.1|AC011664_13 hypothetical protein [Arabidopsis thaliana] gi|18175909|gb|AAL59949.1| unknown protein [Arabidopsis thaliana] gi|21280829|gb|AAM45121.1| unknown protein [Arabidopsis thaliana] gi|332640231|gb|AEE73752.1| senescence-related protein [Arabidopsis thaliana]	364	361	1.00E-175	99.2	85.4	90.4	senescence-related protein	gbpln	Arabidopsis thaliana	AT3G02040.1 | Symbols: SRG3 | senescence-related gene 3 | chr3:348505-349909 REVERSE LENGTH=361	364	361	1.00E-178	99.2	85.4	90.4
Rsa1.0_01117.1.g23651.t1	ref|XP_002883173.1| hypothetical protein ARALYDRAFT_479449 [Arabidopsis lyrata subsp. lyrata] gi|297329013|gb|EFH59432.1| hypothetical protein ARALYDRAFT_479449 [Arabidopsis lyrata subsp. lyrata]	344	349	1.00E-150	101.5	81.1	88.1	hypothetical protein ARALYDRAFT_479449	gbpln	Arabidopsis lyrata	AT3G19330.3 | Symbols: | Protein of unknown function (DUF677) | chr3:6699423-6700776 FORWARD LENGTH=345	344	345	1.00E-151	100.3	81.1	87.2
Rsa1.0_01117.1.g23652.t1	gb|EOA32984.1| hypothetical protein CARUB_v10016314mg [Capsella rubella]	790	789	0	99.9	82.3	89.1	hypothetical protein CARUB_v10016314mg	gbpln	Capsella rubella	AT3G02050.1 | Symbols: KUP3, ATKUP3, ATKT4 | K+ uptake transporter 3 | chr3:350815-354135 FORWARD LENGTH=789	790	789	0	99.9	83.4	89.7
Rsa1.0_01118.1.g23653.t1	ref|NP_565930.1| uncharacterized protein [Arabidopsis thaliana] gi|30688262|ref|NP_850329.1| uncharacterized protein [Arabidopsis thaliana] gi|15294188|gb|AAK95271.1|AF410285_1 At2g40400/T3G21.17 [Arabidopsis thaliana] gi|4586056|gb|AAD25674.1| chloroplast lumen common protein family [Arabidopsis thaliana] gi|20857082|gb|AAM26698.1| At2g40400/T3G21.17 [Arabidopsis thaliana] gi|330254728|gb|AEC09822.1| uncharacterized protein AT2G40400 [Arabidopsis thaliana] gi|330254729|gb|AEC09823.1| uncharacterized protein AT2G40400 [Arabidopsis thaliana]	617	735	0	119.1	91.6	95.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G40400.2 | Symbols: | Protein of unknown function (DUF399 and DUF3411) | chr2:16869363-16872569 FORWARD LENGTH=735	617	735	0	119.1	91.6	95.1

Rsa1.0_01118.1.g23654.t1	ref|NP_179556.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|44917427|gb|AAS49038.1| At2g19660 [Arabidopsis thaliana] gi|330251815|gb|AEC06909.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	666	662	0	99.4	57.5	71.0	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G19660.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:8496720-8498708 REVERSE LENGTH=662	666	662	0	99.4	57.5	71.0
Rsa1.0_01118.1.g23655.t1	gb|EOA26430.1| hypothetical protein CARUB_v10025046mg [Capsella rubella]	311	302	1.00E-147	97.1	80.4	89.4	hypothetical protein CARUB_v10025046mg	gbpln	Capsella rubella	AT1G74100.1 | Symbols: SOT16, ATSOT16, CORI-7, ATST5A | sulfotransferase 16 | chr1:27864489-27865505 REVERSE LENGTH=338	311	338	2.00E-52	108.7	37.3	58.5
Rsa1.0_01118.1.g23656.t1	ref|XP_002879869.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297325708|gb|EFH56128.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata]	445	440	0	98.9	87.2	94.4	amino acid transporter family protein	gbpln	Arabidopsis lyrata	AT2G40420.1 | Symbols: | Transmembrane amino acid transporter family protein | chr2:16877300-16878982 FORWARD LENGTH=440	445	440	0	98.9	87.2	94.4
Rsa1.0_01118.1.g23657.t1	gb|EOA29100.1| hypothetical protein CARUB_v10025367mg, partial [Capsella rubella]	393	381	1.00E-148	96.9	72.5	81.9	hypothetical protein CARUB_v10025367mg, partial	gbpln	Capsella rubella	AT2G40430.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Tumour suppressor protein Gltscr2 (InterPro:IPR011211), P60-like (InterPro:IPR011687). | chr2:16879466-16882365 REVERSE LENGTH=441	393	441	1.00E-137	112.2	72.3	81.9
Rsa1.0_01118.1.g23658.t1	ref|XP_002893164.1| hypothetical protein ARALYDRAFT_335387 [Arabidopsis lyrata subsp. lyrata] gi|297339006|gb|EFH69423.1| hypothetical protein ARALYDRAFT_335387 [Arabidopsis lyrata subsp. lyrata]	437	279	4.00E-43	63.8	27.0	38.4	hypothetical protein ARALYDRAFT_335387	gbpln	Arabidopsis lyrata	AT4G21570.1 | Symbols: | Protein of unknown function (DUF300) | chr4:11471126-11472269 REVERSE LENGTH=294	437	294	9.00E-44	67.3	18.1	19.0
Rsa1.0_01118.1.g23659.t1	gb|EOA15725.1| hypothetical protein CARUB_v10006633mg, partial [Capsella rubella]	195	483	1.00E-25	247.7	30.3	43.1	hypothetical protein CARUB_v10006633mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	195	566	9.00E-25	290.3	32.3	49.7
Rsa1.0_01118.1.g23660.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01118.1.g23661.t1	gb|AAD50007.1|AC007651_2 Similar to mudrA protein [Arabidopsis thaliana]	132	622	2.00E-13	471.2	29.5	35.6	Similar to mudrA protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01118.1.g23662.t1	dbj|BAJ34566.1| unnamed protein product [Thellungiella halophila]	473	582	0	123.0	90.5	96.8	unnamed protein product	----	----	AT2G40460.1 | Symbols: | Major facilitator superfamily protein | chr2:16897123-16901171 FORWARD LENGTH=583	473	583	0	123.3	91.5	96.6
Rsa1.0_01118.1.g23663.t1	gb|EOA12026.1| hypothetical protein CARUB_v10008039mg [Capsella rubella]	345	709	1.00E-10	205.5	19.1	25.5	hypothetical protein CARUB_v10008039mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01119.1.g23664.t1	gb|EOA23283.1| hypothetical protein CARUB_v10018092mg [Capsella rubella]	174	182	3.00E-33	104.6	63.8	72.4	hypothetical protein CARUB_v10018092mg	gbpln	Capsella rubella	AT2G03310.1 | Symbols: | unknown protein; Has 17 Blast hits to 17 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:1006476-1007089 REVERSE LENGTH=176	174	176	5.00E-33	101.1	62.6	71.8
Rsa1.0_01119.1.g23665.t1	gb|EOA24337.1| hypothetical protein CARUB_v10017574mg [Capsella rubella]	334	342	1.00E-118	102.4	69.5	81.1	hypothetical protein CARUB_v10017574mg	gbpln	Capsella rubella	AT3G11810.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03330.1); Has 141 Blast hits to 141 proteins in 21 species: Archae - 0; Bacteria - 9; Metazoa - 0; Fungi - 0; Plants - 131; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:3727819-3728865 FORWARD LENGTH=348	334	348	1.00E-116	104.2	66.5	77.8
Rsa1.0_01119.1.g23666.t1	ref|NP_001118256.1| Glycosyltransferase family 61 protein [Arabidopsis thaliana] gi|330250598|gb|AEC05692.1| Glycosyltransferase family 61 protein [Arabidopsis thaliana]	390	455	1.00E-176	116.7	74.1	86.7	Glycosyltransferase family 61 protein	gbpln	Arabidopsis thaliana	AT2G03360.2 | Symbols: | Glycosyltransferase family 61 protein | chr2:1022287-1024273 REVERSE LENGTH=455	390	455	1.00E-178	116.7	74.1	86.7
Rsa1.0_01119.1.g23667.t1	gb|EOA23213.1| hypothetical protein CARUB_v10019429mg [Capsella rubella]	510	348	1.00E-174	68.2	59.0	63.3	hypothetical protein CARUB_v10019429mg	gbpln	Capsella rubella	AT2G03410.1 | Symbols: | Mo25 family protein | chr2:1033907-1034953 FORWARD LENGTH=348	510	348	1.00E-174	68.2	58.6	62.4

Rsa1.0_01119.1.g23668.t1	ref|XP_002876885.1| hypothetical protein ARALYDRAFT_904622 [Arabidopsis lyrata subsp. lyrata] gi|297322723|gb|EFH53144.1| hypothetical protein ARALYDRAFT_904622 [Arabidopsis lyrata subsp. lyrata]	168	175	6.00E-74	104.2	86.3	91.7	hypothetical protein ARALYDRAFT_904622	gbpln	Arabidopsis lyrata	AT2G03420.1 | Symbols: | unknown protein; Has 38 Blast hits to 38 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:1035100-1035937 REVERSE LENGTH=170	168	170	1.00E-72	101.2	86.9	92.3
Rsa1.0_01119.1.g23669.t1	ref|NP_178442.2| 26S proteasome non-ATPase regulatory subunit 10 [Arabidopsis thaliana] gi|26449603|dbj|BAC41927.1| putative ankyrin [Arabidopsis thaliana] gi|28950799|gb|AAO63323.1| At2g03430 [Arabidopsis thaliana] gi|330250605|gb|AEC05699.1| Ankyrin repeat family protein [Arabidopsis thaliana]	246	240	1.00E-119	97.6	85.8	91.9	26S proteasome non-ATPase regulatory subunit 10	gbpln	Arabidopsis thaliana	AT2G03430.1 | Symbols: | Ankyrin repeat family protein | chr2:1036192-1037536 REVERSE LENGTH=240	246	240	1.00E-121	97.6	85.8	91.9
Rsa1.0_01119.1.g23670.t1	gb|EOA24282.1| hypothetical protein CARUB_v10017522mg [Capsella rubella]	358	356	0	99.4	91.9	95.5	hypothetical protein CARUB_v10017522mg	gbpln	Capsella rubella	AT2G03510.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr2:1066717-1068934 FORWARD LENGTH=356	358	356	0	99.4	90.5	95.8
Rsa1.0_01119.1.g23671.t1	ref|XP_002875210.1| ureide permease 4 [Arabidopsis lyrata subsp. lyrata] gi|297321048|gb|EFH51469.1| ureide permease 4 [Arabidopsis lyrata subsp. lyrata]	410	407	0	99.3	88.5	92.4	ureide permease 4	gbpln	Arabidopsis lyrata	AT2G03520.1 | Symbols: ATUPS4, UPS4 | ureide permease 4 | chr2:1069494-1071269 FORWARD LENGTH=401	410	401	0	97.8	86.6	91.0
Rsa1.0_01119.1.g23672.t1	ref|XP_002875213.1| hypothetical protein ARALYDRAFT_484264 [Arabidopsis lyrata subsp. lyrata] gi|297321051|gb|EFH51472.1| hypothetical protein ARALYDRAFT_484264 [Arabidopsis lyrata subsp. lyrata]	274	313	1.00E-113	114.2	75.2	85.8	hypothetical protein ARALYDRAFT_484264	gbpln	Arabidopsis lyrata	AT2G03550.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:1077080-1078018 FORWARD LENGTH=312	274	312	1.00E-111	113.9	73.7	83.9
Rsa1.0_01119.1.g23673.t1	ref|NP_565303.1| ureide permease 1 [Arabidopsis thaliana] gi|68566149|sp|Q9ZPR7.1|UPS1_ARATH RecName: Full=Ureide permease 1; Short=AtUPS1 gi|4406756|gb|AAD20067.1| expressed protein [Arabidopsis thaliana] gi|21554091|gb|AAM63172.1| putative integral membrane protein [Arabidopsis thaliana] gi|115646808|gb|ABJ17125.1| At2g03590 [Arabidopsis thaliana] gi|330250624|gb|AEC05718.1| ureide permease 1 [Arabidopsis thaliana]	390	390	0	100.0	92.3	96.4	ureide permease 1	gbpln	Arabidopsis thaliana	AT2G03590.1 | Symbols: ATUPS1, UPS1 | ureide permease 1 | chr2:1095129-1096711 FORWARD LENGTH=390	390	390	0	100.0	92.3	96.4
Rsa1.0_01119.1.g23674.t1	ref|NP_178461.1| uncharacterized protein [Arabidopsis thaliana] gi|4406760|gb|AAD20071.1| hypothetical protein [Arabidopsis thaliana] gi|330250633|gb|AEC05727.1| uncharacterized protein AT2G03630 [Arabidopsis thaliana]	260	252	1.00E-43	96.9	53.1	60.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G03630.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74220.1); Has 126 Blast hits to 126 proteins in 28 species: Archae - 0; Bacteria - 6; Metazoa - 7; Fungi - 5; Plants - 87; Viruses - 0; Other Eukaryotes - 21 (source: NCBI BLink). | chr2:1103205-1103963 FORWARD LENGTH=252	260	252	3.00E-46	96.9	53.1	60.0
Rsa1.0_01119.1.g23675.t1	gb|EOA23669.1| hypothetical protein CARUB_v10016877mg [Capsella rubella]	614	603	0	98.2	86.5	92.2	hypothetical protein CARUB_v10016877mg	gbpln	Capsella rubella	AT2G03670.1 | Symbols: CDC48B | cell division cycle 48B | chr2:1117595-1120361 FORWARD LENGTH=603	614	603	0	98.2	86.0	91.7
Rsa1.0_01119.1.g23676.t1	gb|EOA24844.1| hypothetical protein CARUB_v10018134mg, partial [Capsella rubella]	121	169	3.00E-36	139.7	76.9	81.8	hypothetical protein CARUB_v10018134mg, partial	gbpln	Capsella rubella	AT2G03680.2 | Symbols: SPR1, SKU6 | spiral1 | chr2:1121398-1121850 FORWARD LENGTH=119	121	119	5.00E-38	98.3	83.5	86.8
Rsa1.0_01119.1.g23677.t1	gb|EOA27628.1| hypothetical protein CARUB_v10023776mg [Capsella rubella]	253	288	1.00E-119	113.8	84.6	87.7	hypothetical protein CARUB_v10023776mg	gbpln	Capsella rubella	AT2G45330.2 | Symbols: emb1067 | RNA 2'-phosphotransferase, Tpt1 / KptA family | chr2:18686340-18687874 FORWARD LENGTH=286	253	286	1.00E-113	113.0	85.0	88.9
Rsa1.0_01119.1.g23678.t1	emb|CAD48302.1| MADS-box protein AGL3-a [Brassica oleracea var. botrytis]	226	256	1.00E-107	113.3	85.0	91.2	MADS-box protein AGL3-a	gbpln	Brassica oleracea	AT2G03710.2 | Symbols: SEP4, AGL3 | K-box region and MADS-box transcription factor family protein | chr2:1129622-1131628 FORWARD LENGTH=257	226	257	1.00E-107	113.7	86.3	92.0
Rsa1.0_01119.1.g23679.t1	ref|NP_178467.1| adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana] gi|4406763|gb|AAD20074.1| unknown protein [Arabidopsis thaliana] gi|38566668|gb|AAR24224.1| At2g03720 [Arabidopsis thaliana] gi|56381933|gb|AAV85685.1| At2g03720 [Arabidopsis thaliana] gi|330250647|gb|AEC05741.1| adenine nucleotide alpha hydrolases-like protein [Arabidopsis thaliana]	232	165	5.00E-89	71.1	67.7	69.4	adenine nucleotide alpha hydrolases-like protein	gbpln	Arabidopsis thaliana	AT2G03720.1 | Symbols: MRH6 | Adenine nucleotide alpha hydrolases-like superfamily protein | chr2:1132364-1133225 FORWARD LENGTH=165	232	165	1.00E-91	71.1	67.7	69.4

Rsa1.0_01120.1.g23680.t2	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	688	498	7.00E-74	72.4	21.8	28.9	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT2G17920.1 | Symbols: | nucleic acid binding;zinc ion binding | chr2:7782808-7783731 FORWARD LENGTH=307	688	307	9.00E-22	44.6	8.1	13.7
Rsa1.0_01120.1.g23681.t9	ref|NP_175703.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|12324642|gb|AAG52278.1|AC019018_15 putative replication protein; 94555-97079 [Arabidopsis thaliana] gi|332194750|gb|AEE32871.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	437	566	3.00E-37	129.5	24.9	43.9	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	437	566	8.00E-40	129.5	24.9	43.9
Rsa1.0_01120.1.g23682.t1	gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]	158	198	1.00E-33	125.3	48.7	68.4	hypothetical protein 27.t00041	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01120.1.g23683.t4	gb|AAD15468.1| putative helicase [Arabidopsis thaliana]	1038	1265	0	121.9	55.5	70.4	putative helicase	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1038	331	4.00E-38	31.9	9.1	13.8
Rsa1.0_01120.1.g23684.t1	dbj|BAB10393.1| unnamed protein product [Arabidopsis thaliana]	794	1335	4.00E-55	168.1	19.3	28.2	unnamed protein product	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	794	249	1.00E-38	31.4	11.8	16.8
Rsa1.0_01120.1.g23685.t3	dbj|BAB01350.1| Mutator-like transposase [Arabidopsis thaliana]	571	811	1.00E-89	142.0	31.0	41.0	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G49920.1 | Symbols: | MuDR family transposase | chr1:18481798-18484233 REVERSE LENGTH=785	571	785	5.00E-12	137.5	9.1	14.4
Rsa1.0_01120.1.g23686.t1	ref|XP_002875676.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321514|gb|EFH51935.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	218	1058	3.00E-61	485.3	52.8	60.6	predicted protein	gbpln	Arabidopsis lyrata	AT3G25510.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr3:9260838-9268797 REVERSE LENGTH=1981	218	1981	5.00E-63	908.7	49.1	57.3
Rsa1.0_01120.1.g23687.t4	gb|AAM15254.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	656	930	6.00E-33	141.8	16.0	20.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01120.1.g23688.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01120.1.g23689.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1086	1838	0	169.2	28.5	34.3	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01121.1.g23690.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01121.1.g23691.t1	ref|XP_002876344.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297322182|gb|EFH52603.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	550	551	0	100.2	86.5	92.4	zinc finger (CCCH-type) family protein	gbpln	Arabidopsis lyrata	AT3G55980.1 | Symbols: SZF1, ATSZF1 | salt-inducible zinc finger 1 | chr3:20776857-20778599 FORWARD LENGTH=580	550	580	0	105.5	87.8	93.3
Rsa1.0_01121.1.g23692.t2	ref|XP_002876345.1| hypothetical protein ARALYDRAFT_907033 [Arabidopsis lyrata subsp. lyrata] gi|297322183|gb|EFH52604.1| hypothetical protein ARALYDRAFT_907033 [Arabidopsis lyrata subsp. lyrata]	472	487	0	103.2	90.0	94.3	hypothetical protein ARALYDRAFT_907033	gbpln	Arabidopsis lyrata	AT3G55990.1 | Symbols: ESK1, TBL29 | Plant protein of unknown function (DUF828) | chr3:20780410-20782931 FORWARD LENGTH=487	472	487	0	103.2	90.3	94.1
Rsa1.0_01121.1.g23693.t1	ref|XP_002878056.1| hypothetical protein ARALYDRAFT_907034 [Arabidopsis lyrata subsp. lyrata] gi|297323894|gb|EFH54315.1| hypothetical protein ARALYDRAFT_907034 [Arabidopsis lyrata subsp. lyrata]	523	528	0	101.0	89.3	95.0	hypothetical protein ARALYDRAFT_907034	gbpln	Arabidopsis lyrata	AT3G56000.1 | Symbols: ATCSLA14, CSLA14 | cellulose synthase like A14 | chr3:20783462-20785684 REVERSE LENGTH=535	523	535	0	102.3	87.4	93.9
Rsa1.0_01121.1.g23694.t1	ref|XP_002876346.1| hypothetical protein ARALYDRAFT_907035 [Arabidopsis lyrata subsp. lyrata] gi|297322184|gb|EFH52605.1| hypothetical protein ARALYDRAFT_907035 [Arabidopsis lyrata subsp. lyrata]	209	198	8.00E-74	94.7	71.3	82.3	hypothetical protein ARALYDRAFT_907035	gbpln	Arabidopsis lyrata	AT3G56010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 25 Blast hits to 25 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:20788758-20789656 FORWARD LENGTH=201	209	201	8.00E-72	96.2	71.3	83.3
Rsa1.0_01121.1.g23695.t1	ref|NP_191162.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|218546756|sp|Q9LY43.2|PP283_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g56030 gi|332645947|gb|AEE79468.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	332	351	1.00E-163	105.7	84.9	91.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G56030.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:20791259-20792314 FORWARD LENGTH=351	332	351	1.00E-166	105.7	84.9	91.6

Rsa1.0_01121.1.g23696.t2	gb|EOA25329.1| hypothetical protein CARUB_v10018646mg [Capsella rubella]	881	879	0	99.8	86.9	92.6	hypothetical protein CARUB_v10018646mg	gbpln	Capsella rubella	AT3G56040.1 | Symbols: UGP3 | UDP-glucose pyrophosphorylase 3 | chr3:20792689-20797482 REVERSE LENGTH=883	881	883	0	100.2	88.1	92.8
Rsa1.0_01121.1.g23697.t1	ref|XP_002878058.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297323896|gb|EFH54317.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	500	499	0	99.8	78.8	86.6	kinase family protein	gbpln	Arabidopsis lyrata	AT3G56050.2 | Symbols: | Protein kinase family protein | chr3:20798322-20800706 REVERSE LENGTH=499	500	499	0	99.8	80.0	88.2
Rsa1.0_01121.1.g23698.t1	gb|EOA25148.1| hypothetical protein CARUB_v10018458mg [Capsella rubella]	576	581	0	100.9	82.6	91.8	hypothetical protein CARUB_v10018458mg	gbpln	Capsella rubella	AT3G56060.1 | Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr3:20803328-20805983 REVERSE LENGTH=577	576	577	0	100.2	78.1	87.2
Rsa1.0_01121.1.g23699.t1	ref|XP_002868561.1| AT5g42080/MJC20_19 [Arabidopsis lyrata subsp. lyrata] gi|297314397|gb|EFH44820.1| AT5g42080/MJC20_19 [Arabidopsis lyrata subsp. lyrata]	387	610	1.00E-174	157.6	85.5	90.7	AT5g42080/MJC20_19	gbpln	Arabidopsis lyrata	AT5G42080.1 | Symbols: ADL1, ADL1A, AG68, DRP1A, RSW9, DL1 | dynamin-like protein | chr5:16820661-16824536 REVERSE LENGTH=610	387	610	1.00E-176	157.6	85.3	90.7
Rsa1.0_01121.1.g23700.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01122.1.g23701.t1	dbj|BAK52341.1| S9 Tyrosyl aminopeptidase [Raphanus sativus]	703	685	0	97.4	94.0	95.3	S9 Tyrosyl aminopeptidase	gbpln	Raphanus sativus	AT5G36210.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:14248202-14253272 REVERSE LENGTH=730	703	730	0	103.8	85.5	91.6
Rsa1.0_01122.1.g23702.t1	ref|NP_564694.2| Nuclear pore complex protein [Arabidopsis thaliana] gi|332195141|gb|AEE33262.1| Nuclear pore complex protein [Arabidopsis thaliana]	1821	1816	0	99.7	71.7	78.2	Nuclear pore complex protein	gbpln	Arabidopsis thaliana	AT1G55540.1 | Symbols: emb1011 | Nuclear pore complex protein | chr1:20734759-20743049 REVERSE LENGTH=1816	1821	1816	0	99.7	71.7	78.2
Rsa1.0_01122.1.g23703.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01122.1.g23704.t1	ref|NP_564696.2| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|332195144|gb|AEE33265.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana]	862	859	0	99.7	71.6	79.9	P-loop containing nucleoside triphosphate hydrolase-like protein	gbpln	Arabidopsis thaliana	AT1G55550.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:20748915-20752862 FORWARD LENGTH=859	862	859	0	99.7	71.6	79.9
Rsa1.0_01122.1.g23705.t1	ref|XP_002894511.1| hypothetical protein ARALYDRAFT_474617 [Arabidopsis lyrata subsp. lyrata] gi|297340353|gb|EFH70770.1| hypothetical protein ARALYDRAFT_474617 [Arabidopsis lyrata subsp. lyrata]	549	549	0	100.0	96.4	98.5	hypothetical protein ARALYDRAFT_474617	gbpln	Arabidopsis lyrata	AT1G55560.1 | Symbols: sks14 | SKU5 similar 14 | chr1:20754474-20756527 REVERSE LENGTH=549	549	549	0	100.0	95.3	98.7
Rsa1.0_01122.1.g23706.t1	#	#	#	#	#	#	#	–	----	----	AT1G05470.1 | Symbols: CVP2 | DNAse I-like superfamily protein | chr1:1608558-1611291 REVERSE LENGTH=617	92	617	1.00E-10	670.7	39.1	51.1
Rsa1.0_01122.1.g23707.t1	ref|XP_002891844.1| hypothetical protein ARALYDRAFT_892557 [Arabidopsis lyrata subsp. lyrata] gi|297337686|gb|EFH68103.1| hypothetical protein ARALYDRAFT_892557 [Arabidopsis lyrata subsp. lyrata]	512	555	0	108.4	95.5	97.9	hypothetical protein ARALYDRAFT_892557	gbpln	Arabidopsis lyrata	AT1G55570.1 | Symbols: sks12 | SKU5 similar 12 | chr1:20757882-20759771 FORWARD LENGTH=555	512	555	0	108.4	94.7	97.9
Rsa1.0_01122.1.g23708.t5	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1022	1274	1.00E-118	124.7	20.2	27.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G55600.1 | Symbols: WRKY10, ATWRKY10, MINI3 | WRKY DNA-binding protein 10 | chr1:20774049-20776293 REVERSE LENGTH=485	1022	485	1.00E-35	47.5	8.8	12.0
Rsa1.0_01123.1.g23709.t1	ref|NP_564933.1| uncharacterized protein [Arabidopsis thaliana] gi|21536535|gb|AAM60867.1| unknown [Arabidopsis thaliana] gi|110739339|dbj|BAF01582.1| hypothetical protein [Arabidopsis thaliana] gi|114050551|gb|ABI49425.1| At1g68585 [Arabidopsis thaliana] gi|332196694|gb|AEE34815.1| uncharacterized protein AT1G68585 [Arabidopsis thaliana]	68	116	1.00E-19	170.6	76.5	89.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G68585.1 | Symbols: | unknown protein; Has 23 Blast hits to 23 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25756911-25757426 FORWARD LENGTH=116	68	116	2.00E-22	170.6	76.5	89.7
Rsa1.0_01123.1.g23710.t1	ref|NP_001077793.1| 30S ribosomal protein 3-1 [Arabidopsis thaliana] gi|332196696|gb|AEE34817.1| 30S ribosomal protein 3-1 [Arabidopsis thaliana]	129	163	2.00E-42	126.4	69.8	78.3	30S ribosomal protein 3-1	gbpln	Arabidopsis thaliana	AT1G68590.2 | Symbols: | Ribosomal protein PSRP-3/Ycf65 | chr1:25757593-25758169 REVERSE LENGTH=163	129	163	4.00E-45	126.4	69.8	78.3

<table>
<tr><td>Rsa1.0_01123.1.g23711.t1</td><td>ref|XP_002887194.1| hypothetical protein ARALYDRAFT_475988 [Arabidopsis lyrata subsp. lyrata] gi|297333035|gb|EFH63453.1| hypothetical protein ARALYDRAFT_475988 [Arabidopsis lyrata subsp. lyrata]</td><td>335</td><td>336</td><td>1.00E−150</td><td>100.3</td><td>77.0</td><td>86.0</td><td>hypothetical protein ARALYDRAFT_475988</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68620.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:25766018−25767028 FORWARD LENGTH=336</td><td>335</td><td>336</td><td>1.00E−148</td><td>100.3</td><td>75.5</td><td>84.5</td></tr>
<tr><td>Rsa1.0_01123.1.g23712.t1</td><td>gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]</td><td>284</td><td>1023</td><td>3.00E−32</td><td>360.2</td><td>30.6</td><td>44.7</td><td>F27F5.21</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 208; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr2:9528910−9529917 FORWARD LENGTH=256</td><td>284</td><td>256</td><td>6.00E−15</td><td>90.1</td><td>22.2</td><td>34.2</td></tr>
<tr><td>Rsa1.0_01123.1.g23713.t1</td><td>ref|XP_002888676.1| hypothetical protein ARALYDRAFT_894639 [Arabidopsis lyrata subsp. lyrata] gi|297334517|gb|EFH64935.1| hypothetical protein ARALYDRAFT_894639 [Arabidopsis lyrata subsp. lyrata]</td><td>157</td><td>159</td><td>2.00E−79</td><td>101.3</td><td>95.5</td><td>96.2</td><td>hypothetical protein ARALYDRAFT_894639</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68660.1 | Symbols: | Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein | chr1:25778058−25779083 REVERSE LENGTH=159</td><td>157</td><td>159</td><td>4.00E−81</td><td>101.3</td><td>94.3</td><td>95.5</td></tr>
<tr><td>Rsa1.0_01123.1.g23714.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01123.1.g23715.t1</td><td>ref|NP_564938.1| myb-like transcription factor-like protein [Arabidopsis thaliana] gi|17380860|gb|AAL36242.1| unknown protein [Arabidopsis thaliana] gi|20258929|gb|AAM14180.1| unknown protein [Arabidopsis thaliana] gi|332196705|gb|AEE34826.1| myb-like transcription factor-like protein [Arabidopsis thaliana]</td><td>370</td><td>354</td><td>1.00E−116</td><td>95.7</td><td>70.8</td><td>75.7</td><td>myb-like transcription factor-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68670.1 | Symbols: | myb-like transcription factor family protein | chr1:25782344−25783873 FORWARD LENGTH=354</td><td>370</td><td>354</td><td>1.00E−119</td><td>95.7</td><td>70.8</td><td>75.7</td></tr>
<tr><td>Rsa1.0_01123.1.g23716.t4</td><td>dbj|BAC42528.1| putative deaminase [Arabidopsis thaliana] gi|38564244|gb|AAR23701.1| At1g68720 [Arabidopsis thaliana]</td><td>1377</td><td>1307</td><td>0</td><td>94.9</td><td>62.0</td><td>68.8</td><td>putative deaminase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68720.1 | Symbols: TADA, ATTADA | tRNA arginine adenosine deaminase | chr1:25804547−25808820 FORWARD LENGTH=1307</td><td>1377</td><td>1307</td><td>0</td><td>94.9</td><td>61.9</td><td>68.8</td></tr>
<tr><td>Rsa1.0_01123.1.g23717.t2</td><td>gb|EOA34564.1| hypothetical protein CARUB_v10022115mg [Capsella rubella]</td><td>207</td><td>184</td><td>5.00E−50</td><td>88.9</td><td>54.6</td><td>59.4</td><td>hypothetical protein CARUB_v10022115mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68730.1 | Symbols: | Zim17-type zinc finger protein | chr1:25810321−25811128 REVERSE LENGTH=170</td><td>207</td><td>170</td><td>6.00E−52</td><td>82.1</td><td>52.7</td><td>59.4</td></tr>
<tr><td>Rsa1.0_01123.1.g23718.t1</td><td>gb|EOA33660.1| hypothetical protein CARUB_v10019828mg [Capsella rubella]</td><td>772</td><td>784</td><td>0</td><td>101.6</td><td>90.9</td><td>94.7</td><td>hypothetical protein CARUB_v10019828mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68740.1 | Symbols: PHO1;H1 | EXS (ERD1/XPR1/SYG1) family protein | chr1:25812735−25816574 REVERSE LENGTH=784</td><td>772</td><td>784</td><td>0</td><td>101.6</td><td>90.3</td><td>93.8</td></tr>
<tr><td>Rsa1.0_01124.1.g23719.t1</td><td>dbj|BAJ34508.1| unnamed protein product [Thellungiella halophila]</td><td>507</td><td>502</td><td>0</td><td>99.0</td><td>84.4</td><td>90.7</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G21910.3 | Symbols: | MATE efflux family protein | chr4:11625821−11630964 REVERSE LENGTH=507</td><td>507</td><td>507</td><td>0</td><td>100.0</td><td>83.4</td><td>89.7</td></tr>
<tr><td>Rsa1.0_01124.1.g23720.t8</td><td>dbj|BAJ34508.1| unnamed protein product [Thellungiella halophila]</td><td>644</td><td>502</td><td>0</td><td>78.0</td><td>55.7</td><td>59.2</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT4G21903.1 | Symbols: | MATE efflux family protein | chr4:11621169−11623738 REVERSE LENGTH=504</td><td>644</td><td>504</td><td>0</td><td>78.3</td><td>54.3</td><td>57.6</td></tr>
<tr><td>Rsa1.0_01124.1.g23721.t1</td><td>gb|AAD25646.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1476</td><td>1461</td><td>0</td><td>99.0</td><td>51.5</td><td>67.3</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262</td><td>1476</td><td>1262</td><td>0</td><td>85.5</td><td>21.3</td><td>27.8</td></tr>
<tr><td>Rsa1.0_01124.1.g23722.t1</td><td>ref|XP_002867811.1| hypothetical protein ARALYDRAFT_492676 [Arabidopsis lyrata subsp. lyrata] gi|297313647|gb|EFH44070.1| hypothetical protein ARALYDRAFT_492676 [Arabidopsis lyrata subsp. lyrata]</td><td>118</td><td>128</td><td>1.00E−28</td><td>108.5</td><td>71.2</td><td>81.4</td><td>hypothetical protein ARALYDRAFT_492676</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G21920.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G20340.1); Has 40 Blast hits to 40 proteins in 10 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 40; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr4:11636084−11636473 REVERSE LENGTH=129</td><td>118</td><td>129</td><td>2.00E−28</td><td>109.3</td><td>67.8</td><td>81.4</td></tr>
<tr><td>Rsa1.0_01124.1.g23723.t1</td><td>dbj|BAN04702.1| putative disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>1193</td><td>1325</td><td>0</td><td>111.1</td><td>70.5</td><td>77.9</td><td>putative disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978−3591960 REVERSE LENGTH=1189</td><td>1193</td><td>1189</td><td>0</td><td>99.7</td><td>54.1</td><td>68.6</td></tr>
<tr><td>Rsa1.0_01124.1.g23724.t1</td><td>dbj|BAN04700.1| putative disease resistance protein [Brassica rapa subsp. pekinensis] gi|469403159|dbj|BAN04701.1| putative disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>1335</td><td>1325</td><td>0</td><td>99.3</td><td>68.2</td><td>78.6</td><td>putative disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G69550.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class) | chr1:26148836−26153374 REVERSE LENGTH=1400</td><td>1335</td><td>1400</td><td>0</td><td>104.9</td><td>54.2</td><td>69.5</td></tr>
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Rsa1.0_01124.1.g23725.t1	ref|XP_002869851.1| hypothetical protein ARALYDRAFT_492672 [Arabidopsis lyrata subsp. lyrata] gi|297315687|gb|EFH46110.1| hypothetical protein ARALYDRAFT_492672 [Arabidopsis lyrata subsp. lyrata]	157	158	5.00E-62	100.6	78.3	89.2	hypothetical protein ARALYDRAFT_492672	gbpln	Arabidopsis lyrata	AT4G21970.1 | Symbols: | Protein of unknown function, DUF584 | chr4:11653633-11654106 FORWARD LENGTH=157	157	157	2.00E-59	100.0	73.9	83.4
Rsa1.0_01124.1.g23726.t1	ref|NP_001078424.1| autophagy-related protein 8a [Arabidopsis thaliana] gi|332659138|gb|AEE84538.1| autophagy-related protein 8a [Arabidopsis thaliana]	124	137	2.00E-61	110.5	91.1	96.8	autophagy-related protein 8a	gbpln	Arabidopsis thaliana	AT4G21980.2 | Symbols: APG8A, ATG8A | Ubiquitin-like superfamily protein | chr4:11655868-11656809 FORWARD LENGTH=137	124	137	4.00E-64	110.5	91.1	96.8
Rsa1.0_01124.1.g23727.t1	ref|XP_002867800.1| PRH26 protein [Arabidopsis lyrata subsp. lyrata] gi|297313636|gb|EFH44059.1| PRH26 protein [Arabidopsis lyrata subsp. lyrata]	460	458	0	99.6	91.5	95.7	PRH26 protein	gbpln	Arabidopsis lyrata	AT4G21990.1 | Symbols: APR3, PRH-26, PRH26, ATAPR3 | APS reductase 3 | chr4:11657284-11658973 REVERSE LENGTH=458	460	458	0	99.6	90.9	95.2
Rsa1.0_01124.1.g23728.t1	ref|XP_003531171.1| PREDICTED: uncharacterized protein LOC100806735 isoform 1 [Glycine max] gi|356525114|ref|XP_003531172.1| PREDICTED: uncharacterized protein LOC100806735 isoform 2 [Glycine max]	72	128	2.00E-20	177.8	70.8	76.4	PREDICTED: uncharacterized protein LOC100806735 isoform 1	gbenv/gbpln	Glycine max	AT4G22000.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:11659810-11660202 REVERSE LENGTH=130	72	130	6.00E-20	180.6	61.1	63.9
Rsa1.0_01125.1.g23729.t1	ref|NP_566730.1| mate efflux domain-containing protein [Arabidopsis thaliana] gi|75274226|sp|Q9LUH2.1|ALF5_ARATH RecName: Full=MATE efflux family protein ALF5; AltName: Full=Protein ABERRANT LATERAL ROOT FORMATION 5; AltName: Full=Protein DTX19 gi|13384114|gb|AAK21273.1|AF337954_1 aberrant lateral root formation 5 [Arabidopsis thaliana] gi|9294512|dbj|BAB02774.1| unnamed protein product [Arabidopsis thaliana] gi|17064870|gb|AAL32589.1| Unknown protein [Arabidopsis thaliana] gi|332643256|gb|AEE76777.1| MATE efflux family protein ALF5 [Arabidopsis thaliana]	407	477	1.00E-174	117.2	74.7	80.3	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT3G23560.1 | Symbols: ALF5 | MATE efflux family protein | chr3:8454361-8456588 REVERSE LENGTH=477	407	477	1.00E-177	117.2	74.7	80.3
Rsa1.0_01125.1.g23730.t1	ref|NP_566730.1| mate efflux domain-containing protein [Arabidopsis thaliana] gi|75274226|sp|Q9LUH2.1|ALF5_ARATH RecName: Full=MATE efflux family protein ALF5; AltName: Full=Protein ABERRANT LATERAL ROOT FORMATION 5; AltName: Full=Protein DTX19 gi|13384114|gb|AAK21273.1|AF337954_1 aberrant lateral root formation 5 [Arabidopsis thaliana] gi|9294512|dbj|BAB02774.1| unnamed protein product [Arabidopsis thaliana] gi|17064870|gb|AAL32589.1| Unknown protein [Arabidopsis thaliana] gi|332643256|gb|AEE76777.1| MATE efflux family protein ALF5 [Arabidopsis thaliana]	533	477	0	89.5	70.4	76.7	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT3G23560.1 | Symbols: ALF5 | MATE efflux family protein | chr3:8454361-8456588 REVERSE LENGTH=477	533	477	0	89.5	70.4	76.7
Rsa1.0_01125.1.g23731.t1	ref|XP_002885569.1| hypothetical protein ARALYDRAFT_479865 [Arabidopsis lyrata subsp. lyrata] gi|297331409|gb|EFH61828.1| hypothetical protein ARALYDRAFT_479865 [Arabidopsis lyrata subsp. lyrata]	483	476	0	98.6	79.9	89.6	hypothetical protein ARALYDRAFT_479865	gbpln	Arabidopsis lyrata	AT3G23560.1 | Symbols: ALF5 | MATE efflux family protein | chr3:8454361-8456588 REVERSE LENGTH=477	483	477	0	98.8	80.5	89.4
Rsa1.0_01125.1.g23732.t1	ref|XP_002883434.1| hypothetical protein ARALYDRAFT_898866 [Arabidopsis lyrata subsp. lyrata] gi|297329274|gb|EFH59693.1| hypothetical protein ARALYDRAFT_898866 [Arabidopsis lyrata subsp. lyrata]	525	565	0	107.6	84.4	89.9	hypothetical protein ARALYDRAFT_898866	gbpln	Arabidopsis lyrata	AT3G23540.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:8443665-8448070 FORWARD LENGTH=566	525	566	0	107.8	83.4	88.8
Rsa1.0_01125.1.g23733.t1	gb|EOA40356.1| hypothetical protein CARUB_v10009084mg [Capsella rubella]	439	459	1.00E-147	104.6	69.5	81.5	hypothetical protein CARUB_v10009084mg	gbpln	Capsella rubella	AT1G50040.1 | Symbols: | Protein of unknown function (DUF1005) | chr1:18542236-18543823 FORWARD LENGTH=460	439	460	2.33E-156	104.8	69.0	81.8
Rsa1.0_01125.1.g23734.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	270	1239	2.00E-51	458.9	43.7	53.0	putative pol polyprotein	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_01125.1.g23735.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01126.1.g23736.t1	ref|NP_187842.1| ankyrin repeats-containing protein [Arabidopsis thaliana] gi|75308849|sp|Q9C7A2.1|Y3236_ARATH RecName: Full=Ankyrin repeat-containing protein At3g12360 gi|12321945|gb|AAG51002.1|AC069474_1 ankyrin-like protein; 93648-91299 [Arabidopsis thaliana] gi|332641667|gb|AEE75188.1| ankyrin repeats-containing protein [Arabidopsis thaliana]	279	590	1.00E-153	211.5	95.0	97.1	ankyrin repeats-containing protein	gbpln	Arabidopsis thaliana	AT3G12360.1 | Symbols: ITN1 | Ankyrin repeat family protein | chr3:3934146-3936495 FORWARD LENGTH=590	279	590	1.00E-156	211.5	95.0	97.1
Rsa1.0_01126.1.g23737.t1	ref|XP_002884899.1| ribosomal protein L10 family protein [Arabidopsis lyrata subsp. lyrata] gi|297330739|gb|EFH61158.1| ribosomal protein L10 family protein [Arabidopsis lyrata subsp. lyrata]	209	170	8.00E-17	81.3	31.1	40.2	ribosomal protein L10 family protein	gbpln	Arabidopsis lyrata	AT3G12370.1 | Symbols: | Ribosomal protein L10 family protein | chr3:3937464-3937979 REVERSE LENGTH=171	209	171	8.00E-17	81.8	30.1	40.7
Rsa1.0_01126.1.g23738.t1	gb|EOA31478.1| hypothetical protein CARUB_v10014664mg [Capsella rubella]	203	203	3.00E-82	100.0	90.1	94.6	hypothetical protein CARUB_v10014664mg	gbpln	Capsella rubella	AT3G12390.1 | Symbols: | Nascent polypeptide-associated complex (NAC), alpha subunit family protein | chr3:3942344-3943595 FORWARD LENGTH=203	203	203	2.00E-76	100.0	84.7	90.6
Rsa1.0_01126.1.g23739.t1	gb|EOA31428.1| hypothetical protein CARUB_v10014617mg [Capsella rubella]	217	212	3.00E-66	97.7	59.0	72.4	hypothetical protein CARUB_v10014617mg	gbpln	Capsella rubella	AT3G12410.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr3:3946267-3946959 REVERSE LENGTH=230	217	230	2.00E-61	106.0	55.3	69.1
Rsa1.0_01126.1.g23740.t1	dbj|BAJ34153.1| unnamed protein product [Thellungiella halophila]	291	294	1.00E-117	101.0	85.2	86.6	unnamed protein product	----	----	AT3G12480.1 | Symbols: NF-YC11 | nuclear factor Y, subunit C11 | chr3:3958065-3960278 FORWARD LENGTH=293	291	293	1.00E-110	100.7	79.4	84.2
Rsa1.0_01126.1.g23741.t1	gb|AFW97773.1| cysteine protease inhibitor [Brassica oleracea var. italica]	207	205	1.00E-107	99.0	93.2	95.7	cysteine protease inhibitor	gbpln	Brassica oleracea	AT3G12490.2 | Symbols: ATCYSB, ATCYS6, CYSB | cystatin B | chr3:3960523-3961876 REVERSE LENGTH=234	207	234	1.00E-101	113.0	87.4	91.3
Rsa1.0_01126.1.g23742.t1	dbj|BAJ34362.1| unnamed protein product [Thellungiella halophila]	332	322	1.00E-142	97.0	74.4	80.4	unnamed protein product	----	----	AT3G12500.1 | Symbols: ATHCHIB, PR3, PR-3, CHI-B, B-CHI, HCHIB | basic chitinase | chr3:3962501-3963984 REVERSE LENGTH=335	332	335	1.00E-132	100.9	74.4	81.6
Rsa1.0_01126.1.g23743.t1	dbj|BAJ34362.1| unnamed protein product [Thellungiella halophila]	335	322	1.00E-148	96.1	76.4	81.5	unnamed protein product	----	----	AT3G12500.1 | Symbols: ATHCHIB, PR3, PR-3, CHI-B, B-CHI, HCHIB | basic chitinase | chr3:3962501-3963984 REVERSE LENGTH=335	335	335	1.00E-138	100.0	73.1	78.5
Rsa1.0_01126.1.g23744.t1	gb|ABB83614.1| unknown [Brassica oleracea]	190	158	6.00E-47	83.2	58.4	66.8	unknown	gbpln	Brassica oleracea	AT3G12510.1 | Symbols: | MADS-box family protein | chr3:3967127-3967648 FORWARD LENGTH=173	190	173	4.00E-17	91.1	32.1	43.2
Rsa1.0_01126.1.g23745.t1	ref|NP_187859.2| DNA replication complex GINS protein PSF2 [Arabidopsis thaliana] gi|37999772|sp|Q9C7A8.2|PSF2_ARATH RecName: Full=DNA replication complex GINS protein PSF2 gi|38603928|gb|AAR24709.1| At3g12530 [Arabidopsis thaliana] gi|58652096|gb|AAW80873.1| At3g12530 [Arabidopsis thaliana] gi|332641686|gb|AEE75207.1| DNA replication complex GINS protein PSF2 [Arabidopsis thaliana]	237	210	1.00E-96	88.6	75.1	81.9	DNA replication complex GINS protein PSF2	gbpln	Arabidopsis thaliana	AT3G12530.1 | Symbols: PSF2 | PSF2 | chr3:3972604-3973864 REVERSE LENGTH=210	237	210	3.00E-99	88.6	75.1	81.9
Rsa1.0_01126.1.g23746.t1	ref|XP_002879891.1| RNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297325730|gb|EFH56150.1| RNA binding protein [Arabidopsis lyrata subsp. lyrata]	162	171	2.00E-70	105.6	84.0	91.4	RNA binding protein	gbpln	Arabidopsis lyrata	AT2G40780.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr2:17021875-17022748 FORWARD LENGTH=171	162	171	3.00E-71	105.6	80.2	88.9
Rsa1.0_01126.1.g23747.t1	dbj|BAJ34614.1| unnamed protein product [Thellungiella halophila]	600	637	0	106.2	80.8	89.5	unnamed protein product	----	----	AT3G12560.1 | Symbols: TRFL9, ATTBP2 | TRF-like 9 | chr3:3982272-3984848 REVERSE LENGTH=619	600	619	0	103.2	77.8	85.7
Rsa1.0_01126.1.g23748.t1	gb|EOA30419.1| hypothetical protein CARUB_v10013545mg [Capsella rubella] gi|482566231|gb|EOA30420.1| hypothetical protein CARUB_v10013545mg [Capsella rubella]	490	489	0	99.8	91.2	95.1	hypothetical protein CARUB_v10013545mg	gbpln	Capsella rubella	AT3G12570.4 | Symbols: FYD | FYD | chr3:3989407-3990876 FORWARD LENGTH=489	490	489	0	99.8	90.6	94.7
Rsa1.0_01126.1.g23749.t1	ref|XP_002884912.1| hypothetical protein ARALYDRAFT_897465 [Arabidopsis lyrata subsp. lyrata] gi|297330752|gb|EFH61171.1| hypothetical protein ARALYDRAFT_897465 [Arabidopsis lyrata subsp. lyrata]	651	650	0	99.8	97.1	98.5	hypothetical protein ARALYDRAFT_897465	gbpln	Arabidopsis lyrata	AT3G12580.1 | Symbols: HSP70, ATHSP70 | heat shock protein 70 | chr3:3991487-3993689 REVERSE LENGTH=650	651	650	0	99.8	97.5	98.6

Rsa1.0_01126.1.g23750.t1	ref|NP_187865.6| uncharacterized protein [Arabidopsis thaliana] gi|332641699|gb|AEE75220.1| uncharacterized protein AT3G12590 [Arabidopsis thaliana]	1242	1184	0	95.3	87.0	90.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G12590.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 50 Blast hits to 41 proteins in 15 species: Archae − 0; Bacteria − 0; Metazoa − 2; Fungi − 0; Plants − 43; Viruses − 0; Other Eukaryotes − 5 (source: NCBI BLink). | chr3:3996473−4003657 REVERSE LENGTH=1184	1242	1184	0	95.3	87.0	90.3
Rsa1.0_01126.1.g23751.t1	gb|EOA31556.1| hypothetical protein CARUB_v10014749mg [Capsella rubella]	207	181	5.00E−84	87.4	76.8	79.2	hypothetical protein CARUB_v10014749mg	gbpln	Capsella rubella	AT3G12600.1 | Symbols: atnudt16, NUDT16 | nudix hydrolase homolog 16 | chr3:4004809−4005995 FORWARD LENGTH=180	207	180	4.00E−77	87.0	71.5	77.3
Rsa1.0_01126.1.g23752.t1	dbj|BAJ34133.1| unnamed protein product [Thellungiella halophila]	369	406	0	110.0	89.7	94.6	unnamed protein product	----	----	AT3G12610.1 | Symbols: DRT100 | Leucine−rich repeat (LRR) family protein | chr3:4006661−4007779 REVERSE LENGTH=372	369	372	0	100.8	87.0	93.0
Rsa1.0_01127.1.g23753.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01127.1.g23754.t1	ref|XP_002891334.1| hypothetical protein ARALYDRAFT_891486 [Arabidopsis lyrata subsp. lyrata] gi|297337176|gb|EFH67593.1| hypothetical protein ARALYDRAFT_891486 [Arabidopsis lyrata subsp. lyrata]	83	83	9.00E−20	100.0	66.3	77.1	hypothetical protein ARALYDRAFT_891486	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01127.1.g23755.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01127.1.g23756.t1	gb|AAF79797.1|AC020646_20 T32E20.30 [Arabidopsis thaliana]	239	1397	2.00E−54	584.5	46.4	60.7	T32E20.30	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01127.1.g23757.t2	ref|XP_002887053.1| hypothetical protein ARALYDRAFT_894325 [Arabidopsis lyrata subsp. lyrata] gi|297332894|gb|EFH63312.1| hypothetical protein ARALYDRAFT_894325 [Arabidopsis lyrata subsp. lyrata]	367	455	2.00E−80	124.0	51.2	62.7	hypothetical protein ARALYDRAFT_894325	gbpln	Arabidopsis lyrata	AT5G01140.1 | Symbols: | Protein of unknown function (DUF674) | chr5:49891−51437 FORWARD LENGTH=473	367	473	6.00E−47	128.9	34.9	48.0
Rsa1.0_01127.1.g23758.t2	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1567	1213	0	77.4	27.2	39.3	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr3:8789471−8793208 FORWARD LENGTH=746	1567	746	7.00E−50	47.6	8.0	11.9
Rsa1.0_01127.1.g23759.t1	gb|AAC67331.1| putative non−LTR retroelement reverse transcriptase [Arabidopsis thaliana]	757	1449	5.00E−50	191.4	19.9	28.9	putative non−LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr3:8789471−8793208 FORWARD LENGTH=746	757	746	3.00E−19	98.5	10.7	14.3
Rsa1.0_01127.1.g23760.t1	gb|AAO67369.1| polyprotein 1 [Petunia vein clearing virus]	162	1886	2.00E−12	1164.2	37.0	49.4	polyprotein 1	gbvrl	Petunia vein	#	#	#	#	#	#	#
Rsa1.0_01127.1.g23761.t1	sp|Q6XKE6.1|POLG_PVCV2 RecName: Full=Genome polyprotein; Contains: RecName: Full=Movement protein; Short=MP; Contains: RecName: Full=Capsid protein; Short=CP; Contains: RecName: Full=Aspartic protease; Short=PR; Contains: RecName: Full=Reverse transcriptase; Short=RT gi|34328896|gb|AAO67368.1| polyprotein 1 [Petunia vein clearing virus]	1061	2180	3.00E−97	205.5	26.9	42.3	RecName: Full=Genome polyprotein; Contains: RecName: Full=Movement protein; Short=MP; Contains: RecName: Full=Capsid protein; Short=CP; Contains: RecName: Full=Aspartic protease; Short=PR; Contains: RecName: Full=Reverse transcriptase; Short=RT gi|34328896|gb|AAO67368.1| polyprotein 1	gbvrl	Petunia vein	AT1G37113.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 24 Blast hits to 24 proteins in 7 species: Archae − 0; Bacteria − 0; Metazoa − 4; Fungi − 0; Plants − 14; Viruses − 6; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:14136413−14138245 FORWARD LENGTH=414	1061	414	3.00E−21	39.0	6.7	9.1
Rsa1.0_01127.1.g23762.t1	emb|CAN64509.1| hypothetical protein VITISV_041217 [Vitis vinifera]	1303	1269	0	97.4	48.7	62.5	hypothetical protein VITISV_041217	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1303	1262	2.00E−98	96.9	14.0	21.4
Rsa1.0_01127.1.g23763.t1	gb|AAL60580.1|AF454958_1 senescence−associated cysteine protease [Brassica oleracea]	300	485	1.00E−151	161.7	92.3	96.7	senescence−associated cysteine protease	gbpln	Brassica oleracea	AT1G47128.1 | Symbols: RD21, RD21A | Granulin repeat cysteine protease family protein | chr1:17283139−17285609 REVERSE LENGTH=462	300	462	1.00E−151	154.0	88.0	94.3
Rsa1.0_01127.1.g23764.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01128.1.g23765.t1	dbj|BAB10790.1| retroelement pol polyprotein−like [Arabidopsis thaliana]	2497	1864	0	74.6	27.4	33.6	retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01128.1.g23766.t7	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	1341	1024	8.00E−75	76.4	11.6	16.0	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01128.1.g23767.t2	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01128.1.g23768.t3	emb|CAN84035.1| hypothetical protein VITISV_016995 [Vitis vinifera]	848	965	0	113.8	40.1	52.6	hypothetical protein VITISV_016995	gbpln	Vitis vinifera	#	#	#	#	#	#	#

Rsa1.0_01128.1.g23769.t3	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	883	915	1.00E-120	103.6	24.8	36.8	F22O13.21	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	883	719	1.00E-22	81.4	13.3	23.7
Rsa1.0_01128.1.g23770.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	876	871	6.00E-58	99.4	17.5	26.0	Ulp1 protease family protein	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	876	673	1.00E-25	76.8	8.7	14.8
Rsa1.0_01128.1.g23771.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01128.1.g23772.t1	ref|XP_002890207.1| hypothetical protein ARALYDRAFT_471920 [Arabidopsis lyrata subsp. lyrata] gi|297336049|gb|EFH66466.1| hypothetical protein ARALYDRAFT_471920 [Arabidopsis lyrata subsp. lyrata]	140	218	6.00E-15	155.7	45.0	56.4	hypothetical protein ARALYDRAFT_471920	gbpln	Arabidopsis lyrata	AT1G17170.1 | Symbols: ATGSTU24, GST, GSTU24 | glutathione S-transferase TAU 24 | chr1:5869895-5870691 FORWARD LENGTH=218	140	218	1.00E-16	155.7	42.1	55.7
Rsa1.0_01128.1.g23773.t1	ref|NP_192445.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|7267296|emb|CAB81078.1| putative protein [Arabidopsis thaliana] gi|332657109|gb|AEE82509.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	398	735	4.00E-75	184.7	43.5	58.5	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	398	735	9.00E-78	184.7	43.5	58.5
Rsa1.0_01129.1.g23774.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01129.1.g23775.t1	gb|AAT40486.1| putative polyprotein [Solanum demissum]	216	1065	2.00E-27	493.1	33.3	44.9	putative polyprotein	gbpln	Solanum demissum	#	#	#	#	#	#	#
Rsa1.0_01129.1.g23776.t1	ref|XP_002891032.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297336874|gb|EFH67291.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	645	639	0	99.1	89.0	93.8	dehydration-responsive family protein	gbpln	Arabidopsis lyrata	AT1G33170.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:12027262-12030397 FORWARD LENGTH=639	645	639	0	99.1	88.5	93.6
Rsa1.0_01129.1.g23777.t2	gb|EOA39207.1| hypothetical protein CARUB_v10012177mg [Capsella rubella]	386	347	1.00E-166	89.9	81.6	85.5	hypothetical protein CARUB_v10012177mg	gbpln	Capsella rubella	AT1G33230.1 | Symbols: | TMPIT-like protein | chr1:12046844-12049794 FORWARD LENGTH=347	386	347	1.00E-162	89.9	79.0	81.9
Rsa1.0_01129.1.g23778.t1	ref|NP_174594.1| protein GT-2-like 1 [Arabidopsis thaliana] gi|332193452|gb|AEE31573.1| trihelix transcription factor GTL1 [Arabidopsis thaliana]	646	669	0	103.6	77.2	82.7	protein GT-2-like 1	gbpln	Arabidopsis thaliana	AT1G33240.1 | Symbols: AT-GTL1, AT-GTL2, GTL1 | GT-2-like 1 | chr1:12051859-12054320 REVERSE LENGTH=669	646	669	0	103.6	77.2	82.7
Rsa1.0_01129.1.g23779.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01130.1.g23780.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01130.1.g23781.t2	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1760	1225	1.00E-166	69.6	17.5	23.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1760	575	9.00E-43	32.7	6.8	12.0
Rsa1.0_01130.1.g23782.t1	gb|AAF81343.1|AC007767_23 Contains similarity to a peptide transport protein homolog F17L22.140 gi|7488004 from Arabidopsis thaliana BAC F17L22 gb|AL035527. It contains a POT family domain PF|00854. ESTs gb|BE038248, gb|T22680, gb|T04498, gb|R89961, gb|R30626, gb|R30389, gb|AA713063 and gb|AA585801 come from this gene [Arabidopsis thaliana]	612	606	0	99.0	91.2	95.6	Contains similarity to a peptide transport protein homolog F17L22.140 gi|7488004 from Arabidopsis thaliana BAC F17L22 gb|AL035527. It contains a POT family domain PF|00854. ESTs gb|BE038248, gb|T22680, gb|T04498, gb|R89961, gb|R30626, gb|R30389, gb|AA713063 and gb|AA585801 come from this gene	gbpln	Arabidopsis thaliana	AT1G32450.1 | Symbols: NRT1.5 | nitrate transporter 1.5 | chr1:11715337-11719807 REVERSE LENGTH=614	612	614	0	100.3	90.8	95.3
Rsa1.0_01130.1.g23783.t1	ref|NP_564402.1| plastidial pyruvate kinase 3 [Arabidopsis thaliana] gi|75305901|sp|Q93Z53.1|PKP3_ARATH RecName: Full=Plastidial pyruvate kinase 3, chloroplastic; Short=PKp3; AltName: Full=Pyruvate kinase I; AltName: Full=Pyruvate kinase isozyme B2, chloroplastic; Short=PKP-BETA2; Short=Plastidic pyruvate kinase beta subunit 2; Flags: Precursor gi|16648691|gb|AAL25538.1| At1g32440/F5D14_7 [Arabidopsis thaliana] gi|24797052|gb|AAN64538.1| At1g32440/F5D14_7 [Arabidopsis thaliana] gi|332193366|gb|AEE31487.1| plastidial pyruvate kinase 3 [Arabidopsis thaliana]	576	571	0	99.1	90.5	94.1	plastidial pyruvate kinase 3	gbpln	Arabidopsis thaliana	AT1G32440.1 | Symbols: PKp3 | plastidial pyruvate kinase 3 | chr1:11712205-11714963 FORWARD LENGTH=571	576	571	0	99.1	90.5	94.1

Rsa1.0_01130.1.g23784.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01130.1.g23785.t1	dbj|BAJ34310.1| unnamed protein product [Thellungiella halophila]	268	280	1.00E-127	104.5	91.4	95.5	unnamed protein product	----	----	AT1G32400.3 | Symbols: TOM2A | tobamovirus multiplication 2A | chr1:11689393-11690873 REVERSE LENGTH=280	268	280	1.00E-129	104.5	90.7	95.9
Rsa1.0_01130.1.g23786.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01130.1.g23787.t1	ref|NP_174578.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana] gi|378405165|sp|Q9MAP1.2|FB33_ARATH RecName: Full=Putative F-box protein At1g33020 gi|332193429|gb|AEE31550.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana]	516	548	2.00E-83	106.2	39.3	52.3	F-box and associated interaction domain-containing protein	gbpln	Arabidopsis thaliana	AT1G33020.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11962746-11964832 FORWARD LENGTH=548	516	548	5.00E-86	106.2	39.3	52.3
Rsa1.0_01131.1.g23788.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01131.1.g23789.t3	ref|XP_002884722.1| hypothetical protein ARALYDRAFT_478237 [Arabidopsis lyrata subsp. lyrata] gi|297330562|gb|EFH60981.1| hypothetical protein ARALYDRAFT_478237 [Arabidopsis lyrata subsp. lyrata]	564	567	0	100.5	84.0	89.5	hypothetical protein ARALYDRAFT_478237	gbpln	Arabidopsis lyrata	AT3G09220.1 | Symbols: LAC7 | laccase 7 | chr3:2827434-2830477 REVERSE LENGTH=567	564	567	0	100.5	82.3	88.5
Rsa1.0_01131.1.g23790.t1	ref|XP_002884723.1| hypothetical protein ARALYDRAFT_317726 [Arabidopsis lyrata subsp. lyrata] gi|297330563|gb|EFH60982.1| hypothetical protein ARALYDRAFT_317726 [Arabidopsis lyrata subsp. lyrata]	491	506	0	103.1	84.5	90.4	hypothetical protein ARALYDRAFT_317726	gbpln	Arabidopsis lyrata	AT3G09240.1 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr3:2835668-2837956 REVERSE LENGTH=477	491	477	0	97.1	80.2	86.4
Rsa1.0_01131.1.g23791.t1	dbj|BAJ34410.1| unnamed protein product [Thellungiella halophila]	516	524	0	101.6	86.0	92.1	unnamed protein product	----	----	AT3G09260.1 | Symbols: PYK10, PSR3.1, BGLU23, LEB | Glycosyl hydrolase superfamily protein | chr3:2840657-2843730 REVERSE LENGTH=524	516	524	0	101.6	83.1	89.9
Rsa1.0_01131.1.g23792.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	267	1023	8.00E-38	383.1	33.7	45.7	F27F5.21	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01131.1.g23793.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	497	1274	1.00E-133	256.3	49.7	66.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	497	575	4.00E-54	115.7	31.4	49.9
Rsa1.0_01131.1.g23794.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	277	1555	2.00E-74	561.4	51.6	66.4	disease resistance protein	gbpln	Brassica rapa	AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315	277	315	6.00E-39	113.7	35.7	48.0
Rsa1.0_01132.1.g23795.t1	gb|EOA35101.1| hypothetical protein CARUB_v10020215mg [Capsella rubella]	394	480	0	121.8	87.8	91.9	hypothetical protein CARUB_v10020215mg	gbpln	Capsella rubella	AT1G69790.1 | Symbols: | Protein kinase superfamily protein | chr1:26266838-26268818 FORWARD LENGTH=387	394	387	0	98.2	87.3	91.6
Rsa1.0_01132.1.g23796.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01132.1.g23797.t1	ref|NP_177136.1| homeobox-leucine zipper protein ATHB-13 [Arabidopsis thaliana] gi|118573191|sp|Q8LC03.2|ATB13_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-13; AltName: Full=HD-ZIP protein ATHB-13; AltName: Full=Homeodomain transcription factor ATHB-13 gi|6644295|gb|AAF20996.1|AF208044_1 homeodomain leucine-zipper protein ATHB13 [Arabidopsis thaliana] gi|12325190|gb|AAG52541.1|AC013289_8 homeobox gene 13 protein; 11736-10437 [Arabidopsis thaliana] gi|15982929|gb|AAL09811.1| At1g69780/T6C23_2 [Arabidopsis thaliana] gi|22137260|gb|AAM91475.1| At1g69780/T6C23_2 [Arabidopsis thaliana] gi|332196853|gb|AEE34974.1| homeobox-leucine zipper protein ATHB-13 [Arabidopsis thaliana]	288	294	1.00E-150	102.1	92.4	95.1	homeobox-leucine zipper protein ATHB-13	gbpln	Arabidopsis thaliana	AT1G69780.1 | Symbols: ATHB13 | Homeobox-leucine zipper protein family | chr1:26259166-26260465 FORWARD LENGTH=294	288	294	1.00E-153	102.1	92.4	95.1
Rsa1.0_01132.1.g23798.t1	gb|AAC63678.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	400	1216	1.00E-100	304.0	44.8	62.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	400	626	4.00E-22	156.5	11.5	20.3

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<tr><td>Rsa1.0_01133.1.g23800.t1</td><td>ref|NP_201198.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|75264278|sp|Q9LVP0.1|Y5639_ARATH RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At5g63930; Flags: Precursor gi|8777306|dbj|BAA96896.1| receptor-like protein kinase [Arabidopsis thaliana] gi|224589747|gb|ACN59405.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332010434|gb|AED97817.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]</td><td>1150</td><td>1102</td><td>0</td><td>95.8</td><td>83.4</td><td>88.9</td><td>leucine-rich repeat protein kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G63930.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:25583006-25586392 FORWARD LENGTH=1102</td><td>1150</td><td>1102</td><td>0</td><td>95.8</td><td>83.4</td><td>88.9</td></tr>
<tr><td>Rsa1.0_01133.1.g23801.t3</td><td>gb|ABD65084.1| hypothetical protein 27.t00096 [Brassica oleracea]</td><td>486</td><td>645</td><td>6.00E-97</td><td>132.7</td><td>44.4</td><td>55.3</td><td>hypothetical protein 27.t00096</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921</td><td>486</td><td>921</td><td>2.00E-29</td><td>189.5</td><td>19.8</td><td>31.5</td></tr>
<tr><td>Rsa1.0_01133.1.g23802.t1</td><td>gb|AAD23705.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]</td><td>399</td><td>333</td><td>8.00E-39</td><td>83.5</td><td>22.3</td><td>31.1</td><td>putative Athila retroelement ORF1 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01133.1.g23803.t4</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01133.1.g23804.t1</td><td>gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]</td><td>520</td><td>1103</td><td>5.00E-35</td><td>212.1</td><td>14.4</td><td>16.5</td><td>GagPol3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01133.1.g23805.t3</td><td>ref|NP_176659.6| protein ILITYHIA [Arabidopsis thaliana] gi|332196168|gb|AEE34289.1| protein ILITYHIA [Arabidopsis thaliana]</td><td>2641</td><td>2610</td><td>0</td><td>98.8</td><td>90.6</td><td>94.5</td><td>protein ILITYHIA</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G64790.1 | Symbols: ILA | ILITYHIA | chr1:24065232-24081908 REVERSE LENGTH=2610</td><td>2641</td><td>2610</td><td>0</td><td>98.8</td><td>90.6</td><td>94.5</td></tr>
<tr><td>Rsa1.0_01134.1.g23806.t1</td><td>ref|NP_190893.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|6630745|emb|CAB64228.1| putative protein [Arabidopsis thaliana] gi|332645533|gb|AEE79054.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]</td><td>116</td><td>109</td><td>7.00E-45</td><td>94.0</td><td>83.6</td><td>87.9</td><td>SAUR-like auxin-responsive protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G53250.1 | Symbols: | SAUR-like auxin-responsive protein family | chr3:19742968-19743297 FORWARD LENGTH=109</td><td>116</td><td>109</td><td>1.00E-47</td><td>94.0</td><td>83.6</td><td>87.9</td></tr>
<tr><td>Rsa1.0_01134.1.g23807.t1</td><td>gb|ADL09136.1| phenylanlanine ammonia-lyase [Brassica oleracea var. botrytis]</td><td>707</td><td>723</td><td>0</td><td>102.3</td><td>98.7</td><td>99.6</td><td>phenylanlanine ammonia-lyase</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G53260.1 | Symbols: PAL2, ATPAL2 | phenylalanine ammonia-lyase 2 | chr3:19744256-19746619 REVERSE LENGTH=717</td><td>707</td><td>717</td><td>0</td><td>101.4</td><td>95.3</td><td>98.0</td></tr>
<tr><td>Rsa1.0_01134.1.g23808.t2</td><td>ref|NP_001190076.1| Small nuclear RNA activating complex (SNAPc), subunit SNAP43 protein [Arabidopsis thaliana] gi|332645540|gb|AEE79061.1| Small nuclear RNA activating complex (SNAPc), subunit SNAP43 protein [Arabidopsis thaliana]</td><td>131</td><td>278</td><td>7.00E-26</td><td>212.2</td><td>61.1</td><td>69.5</td><td>Small nuclear RNA activating complex (SNAPc), subunit SNAP43 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G53270.6 | Symbols: | Small nuclear RNA activating complex (SNAPc), subunit SNAP43 protein | chr3:19750406-19752168 REVERSE LENGTH=278</td><td>131</td><td>278</td><td>2.00E-28</td><td>212.2</td><td>61.1</td><td>69.5</td></tr>
<tr><td>Rsa1.0_01134.1.g23809.t1</td><td>gb|EOA31982.1| hypothetical protein CARUB_v10015243mg [Capsella rubella]</td><td>398</td><td>416</td><td>7.00E-73</td><td>104.5</td><td>48.0</td><td>59.8</td><td>hypothetical protein CARUB_v10015243mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G19880.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6911435-6912604 REVERSE LENGTH=389</td><td>398</td><td>389</td><td>8.00E-73</td><td>97.7</td><td>44.2</td><td>57.8</td></tr>
<tr><td>Rsa1.0_01134.1.g23810.t1</td><td>ref|XP_002876198.1| CYP71B5 [Arabidopsis lyrata subsp. lyrata] gi|297322036|gb|EFH52457.1| CYP71B5 [Arabidopsis lyrata subsp. lyrata]</td><td>343</td><td>498</td><td>1.00E-136</td><td>145.2</td><td>72.9</td><td>78.4</td><td>CYP71B5</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G53280.1 | Symbols: CYP71B5 | cytochrome p450 71b5 | chr3:19755749-19757466 FORWARD LENGTH=498</td><td>343</td><td>498</td><td>1.00E-134</td><td>145.2</td><td>67.6</td><td>74.3</td></tr>
<tr><td>Rsa1.0_01134.1.g23811.t1</td><td>ref|NP_851150.1| putative acetyl-CoA acetyltransferase, cytosolic 2 [Arabidopsis thaliana] gi|42573608|ref|NP_974900.1| putative acetyl-CoA acetyltransferase, cytosolic 2 [Arabidopsis thaliana] gi|332008175|gb|AED95558.1| putative acetyl-CoA acetyltransferase, cytosolic 2 [Arabidopsis thaliana] gi|332008178|gb|AED95561.1| putative acetyl-CoA acetyltransferase, cytosolic 2 [Arabidopsis thaliana]</td><td>164</td><td>405</td><td>7.00E-17</td><td>247.0</td><td>33.5</td><td>36.6</td><td>putative acetyl-CoA acetyltransferase, cytosolic 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G47720.1 | Symbols: | Thiolase family protein | chr5:19331762-19334009 FORWARD LENGTH=405</td><td>164</td><td>405</td><td>2.00E-19</td><td>247.0</td><td>33.5</td><td>36.6</td></tr>
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Rsa1.0_01134.1.g23812.t1	ref|XP_002876198.1| CYP71B5 [Arabidopsis lyrata subsp. lyrata] gi|297322036|gb|EFH52457.1| CYP71B5 [Arabidopsis lyrata subsp. lyrata]	191	498	1.00E-89	260.7	90.6	93.2	CYP71B5	gbpln	Arabidopsis lyrata	AT3G53280.1 | Symbols: CYP71B5 | cytochrome p450 71b5 | chr3:19755749-19757466 FORWARD LENGTH=498	191	498	4.00E-91	260.7	89.5	92.7
Rsa1.0_01134.1.g23813.t1	gb|EOA25898.1| hypothetical protein CARUB_v10019277mg [Capsella rubella]	254	281	7.00E-83	110.6	65.4	78.0	hypothetical protein CARUB_v10019277mg	gbpln	Capsella rubella	AT3G53310.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr3:19766927-19768368 REVERSE LENGTH=286	254	286	8.00E-73	112.6	56.3	70.9
Rsa1.0_01134.1.g23814.t2	gb|EOA23668.1| hypothetical protein CARUB_v10016876mg, partial [Capsella rubella]	587	604	0	102.9	68.8	77.5	hypothetical protein CARUB_v10016876mg, partial	gbpln	Capsella rubella	AT3G53320.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G37070.1); Has 11044 Blast hits to 5993 proteins in 551 species: Archae - 8; Bacteria - 1486; Metazoa - 4078; Fungi - 1814; Plants - 348; Viruses - 112; Other Eukaryotes - 3198 (source: NCBI BLink). | chr3:19769397-19772278 REVERSE LENGTH=553	587	553	0	94.2	68.7	77.2
Rsa1.0_01134.1.g23815.t1	ref|XP_002879649.1| hypothetical protein ARALYDRAFT_902841 [Arabidopsis lyrata subsp. lyrata] gi|297325488|gb|EFH55908.1| hypothetical protein ARALYDRAFT_902841 [Arabidopsis lyrata subsp. lyrata]	191	175	5.00E-74	91.6	74.3	80.6	hypothetical protein ARALYDRAFT_902841	gbpln	Arabidopsis lyrata	AT3G53340.1 | Symbols: NF-YB10 | nuclear factor Y, subunit B10 | chr3:19774667-19775991 REVERSE LENGTH=176	191	176	1.00E-74	92.1	78.0	81.7
Rsa1.0_01134.1.g23816.t2	ref|NP_974423.1| interactor of constitutive active ROPs 5 [Arabidopsis thaliana] gi|42572657|ref|NP_974424.1| interactor of constitutive active ROPs 5 [Arabidopsis thaliana] gi|6729486|emb|CAB67642.1| putative protein [Arabidopsis thaliana] gi|332645552|gb|AEE79073.1| interactor of constitutive active ROPs 5 [Arabidopsis thaliana] gi|332645553|gb|AEE79074.1| interactor of constitutive active ROPs 5 [Arabidopsis thaliana]	376	394	1.00E-163	104.8	81.6	89.1	interactor of constitutive active ROPs 5	gbpln	Arabidopsis thaliana	AT3G53350.3 | Symbols: RIP4 | ROP interactive partner 4 | chr3:19780190-19781555 REVERSE LENGTH=394	376	394	1.00E-166	104.8	81.6	89.1
Rsa1.0_01134.1.g23817.t1	ref|XP_002876202.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322040|gb|EFH52461.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	762	769	0	100.9	82.3	89.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G53360.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:19784502-19786808 FORWARD LENGTH=768	762	768	0	100.8	81.4	89.5
Rsa1.0_01134.1.g23818.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01134.1.g23819.t1	ref|NP_565859.1| DNA-binding protein S1FA2 [Arabidopsis thaliana] gi|52000784|sp|Q42337.2|S1FA2_ARATH RecName: Full=DNA-binding protein S1FA2 gi|13926275|gb|AAK49608.1|AF372892_1 At2g37120/T2N18.12 [Arabidopsis thaliana] gi|4371289|gb|AAD18147.1| expressed protein [Arabidopsis thaliana] gi|21553573|gb|AAM62666.1| DNA BINDING PROTEIN S1FA [Arabidopsis thaliana] gi|27363332|gb|AAO11585.1| At2g37120/T2N18.12 [Arabidopsis thaliana] gi|330254259|gb|AEC09353.1| DNA-binding protein S1FA2 [Arabidopsis thaliana]	76	76	3.00E-13	100.0	80.3	85.5	DNA-binding protein S1FA2	gbpln	Arabidopsis thaliana	AT2G37120.1 | Symbols: | S1FA-like DNA-binding protein | chr2:15594250-15594815 REVERSE LENGTH=76	76	76	5.00E-16	100.0	80.3	85.5
Rsa1.0_01134.1.g23820.t3	ref|XP_002876204.1| hypothetical protein ARALYDRAFT_906727 [Arabidopsis lyrata subsp. lyrata] gi|297322042|gb|EFH52463.1| hypothetical protein ARALYDRAFT_906727 [Arabidopsis lyrata subsp. lyrata]	121	465	6.00E-33	384.3	66.1	72.7	hypothetical protein ARALYDRAFT_906727	gbpln	Arabidopsis lyrata	AT3G53400.1 | Symbols: | BEST Arabidopsis thaliana protein match is: conserved peptide upstream open reading frame 47 (TAIR:AT5G03190.1); Has 285 Blast hits to 285 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 279; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr3:19798526-19799926 FORWARD LENGTH=466	121	466	2.00E-33	385.1	63.6	72.7
Rsa1.0_01134.1.g23821.t1	dbj|BAA32778.1| Plasma membrane aquaporin (PAQ2) [Raphanus sativus]	287	287	1.00E-162	100.0	100.0	100.0	Plasma membrane aquaporin (PAQ2)	gbpln	Raphanus sativus	AT3G53420.2 | Symbols: PIP2A, PIP2, PIP2;1 | plasma membrane intrinsic protein 2A | chr3:19803906-19805454 REVERSE LENGTH=287	287	287	1.00E-155	100.0	93.4	96.5
Rsa1.0_01134.1.g23822.t1	ref|XP_002877919.1| 60S ribosomal protein L12 [Arabidopsis lyrata subsp. lyrata] gi|297323757|gb|EFH54178.1| 60S ribosomal protein L12 [Arabidopsis lyrata subsp. lyrata]	166	166	2.00E-88	100.0	99.4	100.0	60S ribosomal protein L12	gbpln	Arabidopsis lyrata	AT3G53430.1 | Symbols: | Ribosomal protein L11 family protein | chr3:19809895-19810395 REVERSE LENGTH=166	166	166	1.00E-90	100.0	99.4	99.4

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<tr><td>Rsa1.0_01135.1.g23824.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01135.1.g23825.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>169</td><td>1142</td><td>7.00E-29</td><td>675.7</td><td>49.7</td><td>60.4</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292</td><td>169</td><td>292</td><td>1.00E-13</td><td>172.8</td><td>32.5</td><td>51.5</td></tr>
<tr><td>Rsa1.0_01135.1.g23826.t1</td><td>ref|NP_565348.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|30678667|ref|NP_849949.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|4662641|gb|AAD26911.1| expressed protein [Arabidopsis thaliana] gi|17473865|gb|AAL38354.1| unknown protein [Arabidopsis thaliana] gi|22022562|gb|AAM83238.1| At2g10940/F15K19.1 [Arabidopsis thaliana] gi|23308313|gb|AAN18126.1| At2g10940/F15K19.1 [Arabidopsis thaliana] gi|330251063|gb|AEC06157.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|330251064|gb|AEC06158.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]</td><td>252</td><td>291</td><td>2.00E-80</td><td>115.5</td><td>80.2</td><td>86.1</td><td>bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G10940.2 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr2:4311160-4312035 REVERSE LENGTH=291</td><td>252</td><td>291</td><td>5.00E-83</td><td>115.5</td><td>80.2</td><td>86.1</td></tr>
<tr><td>Rsa1.0_01135.1.g23827.t1</td><td>gb|EOA30359.1| hypothetical protein CARUB_v10013480mg [Capsella rubella]</td><td>503</td><td>511</td><td>0</td><td>101.6</td><td>83.9</td><td>91.7</td><td>hypothetical protein CARUB_v10013480mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G11520.1 | Symbols: CRCK3 | calmodulin-binding receptor-like cytoplasmic kinase 3 | chr2:4619145-4621448 FORWARD LENGTH=510</td><td>503</td><td>510</td><td>0</td><td>101.4</td><td>83.7</td><td>90.3</td></tr>
<tr><td>Rsa1.0_01135.1.g23828.t1</td><td>gb|EOA30514.1| hypothetical protein CARUB_v10013637mg [Capsella rubella]</td><td>468</td><td>466</td><td>0</td><td>99.6</td><td>89.3</td><td>94.2</td><td>hypothetical protein CARUB_v10013637mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G11810.1 | Symbols: MGDC, MGD3, ATMGD3 | monogalactosyldiacylglycerol synthase type C | chr2:4743388-4746633 FORWARD LENGTH=465</td><td>468</td><td>465</td><td>0</td><td>99.4</td><td>89.1</td><td>93.4</td></tr>
<tr><td>Rsa1.0_01135.1.g23829.t1</td><td>ref|XP_002885847.1| hypothetical protein ARALYDRAFT_899524 [Arabidopsis lyrata subsp. lyrata] gi|297331687|gb|EFH62106.1| hypothetical protein ARALYDRAFT_899524 [Arabidopsis lyrata subsp. lyrata]</td><td>168</td><td>168</td><td>2.00E-30</td><td>100.0</td><td>69.0</td><td>88.1</td><td>hypothetical protein ARALYDRAFT_899524</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G11910.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 92883 Blast hits to 31060 proteins in 1576 species: Archae - 765; Bacteria - 32670; Metazoa - 21164; Fungi - 12252; Plants - 4238; Viruses - 1282; Other Eukaryotes - 20512 (source: NCBI BLink). | chr2:4805862-4807164 REVERSE LENGTH=168</td><td>168</td><td>168</td><td>1.00E-30</td><td>100.0</td><td>67.3</td><td>85.7</td></tr>
<tr><td>Rsa1.0_01135.1.g23830.t1</td><td>gb|EOA33013.1| hypothetical protein CARUB_v10016344mg [Capsella rubella]</td><td>528</td><td>538</td><td>0</td><td>101.9</td><td>83.0</td><td>90.2</td><td>hypothetical protein CARUB_v10016344mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G12400.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25270.1); Has 177 Blast hits to 172 proteins in 23 species: Archae - 0; Bacteria - 2; Metazoa - 3; Fungi - 0; Plants - 164; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr2:5005144-5008140 REVERSE LENGTH=541</td><td>528</td><td>541</td><td>0</td><td>102.5</td><td>83.1</td><td>90.5</td></tr>
<tr><td>Rsa1.0_01135.1.g23831.t1</td><td>ref|XP_004306187.1| PREDICTED: uncharacterized protein LOC101313541 [Fragaria vesca subsp. vesca]</td><td>273</td><td>402</td><td>3.00E-57</td><td>147.3</td><td>45.8</td><td>64.1</td><td>PREDICTED: uncharacterized protein LOC101313541</td><td>gbpln</td><td>Fragaria vesca</td><td>AT5G33406.1 | Symbols: | hAT dimerisation domain-containing protein / transposase-related | chr5:12676126-12678403 REVERSE LENGTH=509</td><td>273</td><td>509</td><td>6.00E-36</td><td>186.4</td><td>31.5</td><td>46.2</td></tr>
<tr><td>Rsa1.0_01136.1.g23832.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_01136.1.g23833.t1	ref|NP_172953.1| serine carboxypeptidase-like 50 [Arabidopsis thaliana] gi|75336113|sp|Q9M9Q6.1|SCP50_ARATH RecName: Full=Serine carboxypeptidase-like 50; Flags: Precursor gi|6899645|gb|AAF31022.1|AC012189_4 Contains similarity to serine-type carboxypeptidase like protein from Arabidopsis thaliana gi|4678929 and contains two Serine carboxypeptidase domains PF|00450 [Arabidopsis thaliana] gi|19715607|gb|AAL91626.1| At1g15000/T15D22_7 [Arabidopsis thaliana] gi|27363234|gb|AAO11536.1| At1g15000/T15D22_7 [Arabidopsis thaliana] gi|332191131|gb|AEE29252.1| serine carboxypeptidase-like 50 [Arabidopsis thaliana]	454	444	0	97.8	82.6	87.9	serine carboxypeptidase-like 50	gbpln	Arabidopsis thaliana	AT1G15000.1 | Symbols: scpl50 | serine carboxypeptidase-like 50 | chr1:5168613-5169947 FORWARD LENGTH=444	454	444	0	97.8	82.6	87.9
Rsa1.0_01136.1.g23834.t1	gb|EOA37149.1| hypothetical protein CARUB_v10010473mg, partial [Capsella rubella]	124	170	3.00E-66	137.1	96.0	98.4	hypothetical protein CARUB_v10010473mg, partial	gbpln	Capsella rubella	AT1G14990.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 34 Blast hits to 34 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5167354-5168151 REVERSE LENGTH=122	124	122	8.00E-68	98.4	93.5	97.6
Rsa1.0_01136.1.g23835.t1	ref|NP_563961.1| chaperonin 10 [Arabidopsis thaliana] gi|297849924|ref|XP_002892843.1| hypothetical protein ARALYDRAFT_471686 [Arabidopsis lyrata subsp. lyrata] gi|461729|sp|P34893.1|CH10_ARATH RecName: Full=10 kDa chaperonin; AltName: Full=Chaperonin 10; Short=CPN10; AltName: Full=Protein groES gi|6899643|gb|AAF31020.1|AC012189_2 Strong similarity to 10 KD chaperonin (protein CPN10) from Arabidopsis thaliana gb|L02843 containing Chaperonins subunit PF|00166. ESTs gb|Z29788, gb|AW004265 come from this gene [Arabidopsis thaliana] gi|166662|gb|AAA32767.1| 10 kDa chaperonin [Arabidopsis thaliana] gi|11990458|dbj|BAA13588.2| mitochondrial chaperonin 10 [Arabidopsis thaliana] gi|17380944|gb|AAL36284.1| putative chaperonin CPN10 protein [Arabidopsis thaliana] gi|20258951|gb|AAM14191.1| putative chaperonin CPN10 protein [Arabidopsis thaliana] gi|21555041|gb|AAM63762.1| chaperonin CPN10 [Arabidopsis thaliana] gi|297338685|gb|EFH69102.1| hypothetical protein ARALYDRAFT_471686 [Arabidopsis lyrata subsp. lyrata]	98	98	8.00E-48	100.0	98.0	99.0	chaperonin 10	gbpln	Arabidopsis lyrata	AT1G14980.1 | Symbols: CPN10 | chaperonin 10 | chr1:5165930-5166654 REVERSE LENGTH=98	98	98	1.00E-50	100.0	98.0	99.0
Rsa1.0_01136.1.g23836.t1	ref|XP_002892842.1| hypothetical protein ARALYDRAFT_471685 [Arabidopsis lyrata subsp. lyrata] gi|297338684|gb|EFH69101.1| hypothetical protein ARALYDRAFT_471685 [Arabidopsis lyrata subsp. lyrata]	573	561	0	97.9	84.5	89.5	hypothetical protein ARALYDRAFT_471685	gbpln	Arabidopsis lyrata	AT1G14970.1 | Symbols: | O-fucosyltransferase family protein | chr1:5162085-5164917 REVERSE LENGTH=562	573	562	0	98.1	83.4	88.8
Rsa1.0_01136.1.g23837.t1	ref|XP_002892841.1| hypothetical protein ARALYDRAFT_471684 [Arabidopsis lyrata subsp. lyrata] gi|297338683|gb|EFH69100.1| hypothetical protein ARALYDRAFT_471684 [Arabidopsis lyrata subsp. lyrata]	144	153	7.00E-45	106.3	65.3	77.1	hypothetical protein ARALYDRAFT_471684	gbpln	Arabidopsis lyrata	AT1G14960.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:5159334-5159992 REVERSE LENGTH=153	144	153	1.00E-46	106.3	65.3	77.8

Rsa1.0_01136.1.g23838.t1	ref|XP_002892840.1| hypothetical protein ARALYDRAFT_471683 [Arabidopsis lyrata subsp. lyrata] gi|297338682|gb|EFH69099.1| hypothetical protein ARALYDRAFT_471683 [Arabidopsis lyrata subsp. lyrata]	149	155	3.00E-68	104.0	83.2	91.3	hypothetical protein ARALYDRAFT_471683	gbpln	Arabidopsis lyrata	AT1G14950.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:5157588-5158144 REVERSE LENGTH=155	149	155	2.00E-70	104.0	82.6	89.9
Rsa1.0_01136.1.g23839.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1406	1475	0	104.9	61.2	76.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1406	1262	0	89.8	21.6	28.7
Rsa1.0_01136.1.g23840.t1	gb|EOA39741.1| hypothetical protein CARUB_v10008396mg [Capsella rubella]	732	742	0	101.4	78.1	84.3	hypothetical protein CARUB_v10008396mg	gbpln	Capsella rubella	AT1G14910.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:5139928-5143571 REVERSE LENGTH=692	732	692	0	94.5	73.0	79.1
Rsa1.0_01136.1.g23841.t1	ref|XP_002890079.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297335921|gb|EFH66338.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	201	201	2.00E-95	100.0	82.6	90.5	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT1G14890.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:5137045-5137704 FORWARD LENGTH=219	201	219	2.00E-97	109.0	82.1	90.5
Rsa1.0_01136.1.g23842.t1	gb|EOA37179.1| hypothetical protein CARUB_v10010549mg [Capsella rubella]	240	152	1.00E-53	63.3	43.3	45.0	hypothetical protein CARUB_v10010549mg	gbpln	Capsella rubella	AT1G14870.1 | Symbols: PCR2 | PLANT CADMIUM RESISTANCE 2 | chr1:5128591-5129458 REVERSE LENGTH=152	240	152	6.00E-56	63.3	42.5	45.8
Rsa1.0_01137.1.g23843.t2	ref|XP_002876320.1| hypothetical protein ARALYDRAFT_485995 [Arabidopsis lyrata subsp. lyrata] gi|297322158|gb|EFH52579.1| hypothetical protein ARALYDRAFT_485995 [Arabidopsis lyrata subsp. lyrata]	141	139	1.00E-46	98.6	76.6	80.9	hypothetical protein ARALYDRAFT_485995	gbpln	Arabidopsis lyrata	AT3G55646.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G39855.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:20645087-20646148 FORWARD LENGTH=146	141	146	1.00E-45	103.5	80.9	86.5
Rsa1.0_01137.1.g23844.t1	gb|EOA23716.1| hypothetical protein CARUB_v10016923mg [Capsella rubella]	572	579	0	101.2	88.8	94.6	hypothetical protein CARUB_v10016923mg	gbpln	Capsella rubella	AT3G55660.1 | Symbols: ATROPGEF6, ROPGEF6 | ROP (rho of plants) guanine nucleotide exchange factor 6 | chr3:20649051-20651290 REVERSE LENGTH=579	572	579	0	101.2	87.4	93.0
Rsa1.0_01137.1.g23845.t1	ref|NP_191129.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75264501|sp|Q9M052.1|U76F1_ARATH RecName: Full=UDP-glycosyltransferase 76F1 gi|7263558|emb|CAB81595.1| glucuronosyl transferase-like protein [Arabidopsis thaliana] gi|111074514|gb|ABH04630.1| At3g55700 [Arabidopsis thaliana] gi|332645903|gb|AEE79424.1| UDP-glycosyltransferase 76F1 [Arabidopsis thaliana]	300	460	2.00E-55	153.3	42.3	52.0	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT3G55700.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:20671202-20673278 FORWARD LENGTH=460	300	460	7.00E-58	153.3	42.3	52.0
Rsa1.0_01137.1.g23846.t1	ref|NP_191129.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75264501|sp|Q9M052.1|U76F1_ARATH RecName: Full=UDP-glycosyltransferase 76F1 gi|7263558|emb|CAB81595.1| glucuronosyl transferase-like protein [Arabidopsis thaliana] gi|111074514|gb|ABH04630.1| At3g55700 [Arabidopsis thaliana] gi|332645903|gb|AEE79424.1| UDP-glycosyltransferase 76F1 [Arabidopsis thaliana]	462	460	0	99.6	78.4	86.1	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT3G55700.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:20671202-20673278 FORWARD LENGTH=460	462	460	0	99.6	78.4	86.1
Rsa1.0_01137.1.g23847.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01137.1.g23848.t1	ref|XP_002876329.1| hypothetical protein ARALYDRAFT_486006 [Arabidopsis lyrata subsp. lyrata] gi|297322167|gb|EFH52588.1| hypothetical protein ARALYDRAFT_486006 [Arabidopsis lyrata subsp. lyrata]	435	438	0	100.7	88.3	93.1	hypothetical protein ARALYDRAFT_486006	gbpln	Arabidopsis lyrata	AT3G55720.1 | Symbols: | Protein of unknown function (DUF620) | chr3:20679893-20681338 FORWARD LENGTH=438	435	438	0	100.7	86.9	92.9

<table>
<tr><td>Rsa1.0_01137.1.g23849.t2</td><td>dbj|BAJ33746.1| unnamed protein product [Thellungiella halophila]</td><td>392</td><td>395</td><td>1.00E−154</td><td>100.8</td><td>77.6</td><td>81.4</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G55730.1 | Symbols: MYB109, AtMYB109 | myb domain protein 109 | chr3:20682114−20683963 REVERSE LENGTH=399</td><td>392</td><td>399</td><td>1.00E−147</td><td>101.8</td><td>73.5</td><td>78.8</td></tr>
<tr><td>Rsa1.0_01137.1.g23850.t1</td><td>dbj|BAB10837.1| retroelement pol polyprotein−like [Arabidopsis thaliana]</td><td>661</td><td>1462</td><td>0</td><td>221.2</td><td>61.7</td><td>76.4</td><td>retroelement pol polyprotein−like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262</td><td>661</td><td>1262</td><td>1.00E−133</td><td>190.9</td><td>34.8</td><td>51.6</td></tr>
<tr><td>Rsa1.0_01137.1.g23851.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>−</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01137.1.g23852.t1</td><td>gb|EOA24978.1| hypothetical protein CARUB_v10018275mg [Capsella rubella]</td><td>146</td><td>111</td><td>2.00E−49</td><td>76.0</td><td>65.1</td><td>65.8</td><td>hypothetical protein CARUB_v10018275mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G07070.1 | Symbols: | Ribosomal protein L35Ae family protein | chr1:2168652−2169703 FORWARD LENGTH=112</td><td>146</td><td>112</td><td>3.00E−51</td><td>76.7</td><td>63.0</td><td>66.4</td></tr>
<tr><td>Rsa1.0_01138.1.g23853.t1</td><td>ref|NP_001031065.1| DNAJ heat shock N−terminal domain−containing protein [Arabidopsis thaliana] gi|332191627|gb|AEE29748.1| DNAJ heat shock N−terminal domain−containing protein [Arabidopsis thaliana]</td><td>1862</td><td>705</td><td>0</td><td>37.9</td><td>30.7</td><td>33.7</td><td>DNAJ heat shock N−terminal domain−containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G18700.2 | Symbols: | DNAJ heat shock N−terminal domain−containing protein | chr1:6437591−6443814 FORWARD LENGTH=705</td><td>1862</td><td>705</td><td>0</td><td>37.9</td><td>30.7</td><td>33.7</td></tr>
<tr><td>Rsa1.0_01138.1.g23854.t1</td><td>ref|NP_173303.1| HNH endonuclease domain−containing protein [Arabidopsis thaliana] gi|6730716|gb|AAF27111.1|AC011809_20 Unknown protein [Arabidopsis thaliana] gi|26451201|dbj|BAC42704.1| unknown protein [Arabidopsis thaliana] gi|28973585|gb|AAO64117.1| unknown protein [Arabidopsis thaliana] gi|332191624|gb|AEE29745.1| HNH endonuclease domain−containing protein [Arabidopsis thaliana]</td><td>186</td><td>186</td><td>2.00E−80</td><td>100.0</td><td>83.9</td><td>87.6</td><td>HNH endonuclease domain−containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G18680.1 | Symbols: | HNH endonuclease domain−containing protein | chr1:6432133−6433434 REVERSE LENGTH=186</td><td>186</td><td>186</td><td>6.00E−83</td><td>100.0</td><td>83.9</td><td>87.6</td></tr>
<tr><td>Rsa1.0_01138.1.g23855.t4</td><td>gb|EOA39803.1| hypothetical protein CARUB_v10008466mg [Capsella rubella]</td><td>821</td><td>699</td><td>0</td><td>85.1</td><td>69.8</td><td>73.7</td><td>hypothetical protein CARUB_v10008466mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G18670.1 | Symbols: IBS1 | Protein kinase superfamily protein | chr1:6427242−6430696 REVERSE LENGTH=709</td><td>821</td><td>709</td><td>0</td><td>86.4</td><td>68.7</td><td>73.7</td></tr>
<tr><td>Rsa1.0_01138.1.g23856.t2</td><td>gb|EOA40258.1| hypothetical protein CARUB_v10008983mg [Capsella rubella]</td><td>486</td><td>486</td><td>0</td><td>100.0</td><td>93.0</td><td>97.3</td><td>hypothetical protein CARUB_v10008983mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G18660.1 | Symbols: | zinc finger (C3HC4−type RING finger) family protein | chr1:6421433−6425565 FORWARD LENGTH=486</td><td>486</td><td>486</td><td>0</td><td>100.0</td><td>92.4</td><td>96.3</td></tr>
<tr><td>Rsa1.0_01138.1.g23857.t1</td><td>gb|AAD26943.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1272</td><td>1454</td><td>0</td><td>114.3</td><td>63.4</td><td>76.6</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262</td><td>1272</td><td>1262</td><td>1.00E−132</td><td>99.2</td><td>19.4</td><td>25.2</td></tr>
<tr><td>Rsa1.0_01138.1.g23858.t1</td><td>gb|ACB59200.1| unknown protein [Brassica oleracea]</td><td>891</td><td>839</td><td>0</td><td>94.2</td><td>80.9</td><td>86.3</td><td>unknown protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G18620.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74160.1); Has 1987 Blast hits to 1263 proteins in 207 species: Archae − 0; Bacteria − 172; Metazoa − 665; Fungi − 149; Plants − 271; Viruses − 6; Other Eukaryotes − 724 (source: NCBI BLink). | chr1:6410719−6414269 FORWARD LENGTH=978</td><td>891</td><td>978</td><td>0</td><td>109.8</td><td>75.0</td><td>84.1</td></tr>
<tr><td>Rsa1.0_01138.1.g23859.t1</td><td>gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]</td><td>419</td><td>1643</td><td>1.00E−167</td><td>392.1</td><td>66.8</td><td>80.2</td><td>gag/pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262</td><td>419</td><td>1262</td><td>1.00E−74</td><td>301.2</td><td>35.8</td><td>53.2</td></tr>
<tr><td>Rsa1.0_01138.1.g23860.t1</td><td>gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]</td><td>377</td><td>467</td><td>5.00E−79</td><td>123.9</td><td>42.4</td><td>55.4</td><td>hypothetical protein 31.t00031</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G52950.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:19725483−19728007 FORWARD LENGTH=566</td><td>377</td><td>566</td><td>4.00E−24</td><td>150.1</td><td>17.8</td><td>31.0</td></tr>
<tr><td>Rsa1.0_01138.1.g23861.t1</td><td>gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]</td><td>137</td><td>198</td><td>9.00E−20</td><td>144.5</td><td>37.2</td><td>43.8</td><td>hypothetical protein 27.t00041</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01138.1.g23862.t1</td><td>gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]</td><td>524</td><td>467</td><td>1.00E−117</td><td>89.1</td><td>42.6</td><td>55.2</td><td>hypothetical protein 31.t00031</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G52950.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:19725483−19728007 FORWARD LENGTH=566</td><td>524</td><td>566</td><td>3.00E−71</td><td>108.0</td><td>29.0</td><td>47.1</td></tr>
<tr><td>Rsa1.0_01138.1.g23863.t4</td><td>gb|ABD65117.1| hypothetical protein 31.t00030 [Brassica oleracea]</td><td>1737</td><td>1471</td><td>0</td><td>84.7</td><td>60.7</td><td>69.1</td><td>hypothetical protein 31.t00030</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443−19181145 REVERSE LENGTH=344</td><td>1737</td><td>344</td><td>4.00E−63</td><td>19.8</td><td>7.4</td><td>10.1</td></tr>
<tr><td>Rsa1.0_01138.1.g23864.t1</td><td>gb|ABD65101.1| hypothetical protein 31.t00082 [Brassica oleracea]</td><td>254</td><td>226</td><td>3.00E−58</td><td>89.0</td><td>46.9</td><td>60.6</td><td>hypothetical protein 31.t00082</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01138.1.g23865.t1</td><td>gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]</td><td>180</td><td>198</td><td>2.00E−50</td><td>110.0</td><td>53.3</td><td>72.2</td><td>hypothetical protein 27.t00041</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G35280.1 | Symbols: | F−box family protein | chr2:14859709−14860200 REVERSE LENGTH=163</td><td>180</td><td>163</td><td>7.00E−12</td><td>90.6</td><td>17.8</td><td>31.1</td></tr>
<tr><td>Rsa1.0_01139.1.g23866.t1</td><td>gb|AAL14644.1|AF417856_1 AOP1.2 [Arabidopsis thaliana]</td><td>127</td><td>321</td><td>6.00E−50</td><td>252.8</td><td>76.4</td><td>86.6</td><td>AOP1.2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G03070.1 | Symbols: AOP1, AOP, AOP1.1 | 2−oxoglutarate (2OG) and Fe(II)−dependent oxygenase superfamily protein | chr4:1358442−1359620 FORWARD LENGTH=322</td><td>127</td><td>322</td><td>1.00E−50</td><td>253.5</td><td>74.0</td><td>85.0</td></tr>
</table>

Rsa1.0_01139.1.g23867.t1	gb|AAF23556.1|AF110458_1 alcohol dehydrogenase [Barbarea vulgaris]	113	379	7.00E-29	335.4	52.2	54.9	alcohol dehydrogenase	gbpln	Barbarea vulgaris	AT1G77120.1 | Symbols: ADH1, ADH, ATADH, ATADH1 | alcohol dehydrogenase 1 | chr1:28975509-28977216 FORWARD LENGTH=379	113	379	3.00E-30	335.4	50.4	54.9
Rsa1.0_01139.1.g23868.t1	gb|AAL14645.1|AF417857_1 AOP1 [Arabidopsis lyrata] gi|16118984|gb|AAL14690.1| 2-oxoglutarate-dependent dioxygenase [Arabidopsis lyrata]	321	318	1.00E-132	99.1	71.3	83.2	AOP1	gbpln	Arabidopsis lyrata	AT4G03070.1 | Symbols: AOP1, AOP, AOP1.1 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:1358442-1359620 FORWARD LENGTH=322	321	322	1.00E-131	100.3	69.8	81.6
Rsa1.0_01139.1.g23869.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	1437	1534	0	106.8	71.0	80.9	F17L21.7	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1437	1262	1.00E-104	87.8	14.3	20.3
Rsa1.0_01139.1.g23870.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1444	1485	0	102.8	43.9	59.2	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1444	158	9.00E-30	10.9	4.1	6.0
Rsa1.0_01139.1.g23871.t1	ref|XP_002872801.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297318638|gb|EFH49060.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	469	493	0	105.1	93.0	95.9	transducin family protein	gbpln	Arabidopsis lyrata	AT4G03020.2 | Symbols: | transducin family protein / WD-40 repeat family protein | chr4:1331704-1334472 REVERSE LENGTH=493	469	493	0	105.1	92.3	95.5
Rsa1.0_01140.1.g23872.t1	ref|NP_175159.1| gamma carbonic anhydrase 2 [Arabidopsis thaliana] gi|75169075|sp|Q9C6B3.1|GCA2_ARATH RecName: Full=Gamma carbonic anhydrase 2, mitochondrial; Short=AtCA2; Short=GAMMA CA2; AltName: Full=Transcription factor APFI; Flags: Precursor gi|12325399|gb|AAG52641.1|AC079677_5 unknown protein; 6976-8939 [Arabidopsis thaliana] gi|15028353|gb|AAK76653.1| unknown protein [Arabidopsis thaliana] gi|21280965|gb|AAM44984.1| unknown protein [Arabidopsis thaliana] gi|332194023|gb|AEE32144.1| gamma carbonic anhydrase 2 [Arabidopsis thaliana]	276	278	1.00E-144	100.7	89.1	95.3	gamma carbonic anhydrase 2	gbpln	Arabidopsis thaliana	AT1G47260.1 | Symbols: APFI, GAMMA CA2 | gamma carbonic anhydrase 2 | chr1:17321384-17323347 REVERSE LENGTH=278	276	278	2.33E-156	100.7	89.1	95.3
Rsa1.0_01140.1.g23873.t1	ref|XP_002891341.1| hypothetical protein ARALYDRAFT_473874 [Arabidopsis lyrata subsp. lyrata] gi|297337183|gb|EFH67600.1| hypothetical protein ARALYDRAFT_473874 [Arabidopsis lyrata subsp. lyrata]	275	277	1.00E-143	100.7	94.9	97.1	hypothetical protein ARALYDRAFT_473874	gbpln	Arabidopsis lyrata	AT1G47250.1 | Symbols: PAF2 | 20S proteasome alpha subunit F2 | chr1:17319220-17320900 FORWARD LENGTH=277	275	277	1.00E-143	100.7	91.6	94.9
Rsa1.0_01140.1.g23874.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01140.1.g23875.t1	gb|EOA40120.1| hypothetical protein CARUB_v10008822mg [Capsella rubella]	534	531	0	99.4	93.6	96.3	hypothetical protein CARUB_v10008822mg	gbpln	Capsella rubella	AT1G47240.1 | Symbols: NRAMP2, ATNRAMP2 | NRAMP metal ion transporter 2 | chr1:17309043-17311308 REVERSE LENGTH=530	534	530	0	99.3	91.9	94.6
Rsa1.0_01140.1.g23876.t1	gb|ABB97043.1| cyclin-dependent protein kinase regulator-like protein [Brassica rapa]	364	365	0	100.3	92.3	95.1	cyclin-dependent protein kinase regulator-like protein	gbpln	Brassica rapa	AT1G47230.1 | Symbols: CYCA3;4 | CYCLIN A3;4 | chr1:17306752-17308587 FORWARD LENGTH=369	364	369	1.00E-175	101.4	82.7	90.4
Rsa1.0_01140.1.g23877.t1	ref|XP_002891337.1| CYCA3_2 [Arabidopsis lyrata subsp. lyrata] gi|297337179|gb|EFH67596.1| CYCA3_2 [Arabidopsis lyrata subsp. lyrata]	365	368	1.00E-175	100.8	82.7	91.5	CYCA3_2	gbpln	Arabidopsis lyrata	AT1G47210.2 | Symbols: CYCA3;2 | cyclin-dependent protein kinase 3;2 | chr1:17301036-17302584 FORWARD LENGTH=372	365	372	1.00E-178	101.9	82.5	91.8
Rsa1.0_01140.1.g23878.t1	dbj|BAB10772.1| unnamed protein product [Arabidopsis thaliana]	176	171	8.00E-40	97.2	44.3	58.0	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01140.1.g23879.t1	gb|AAM62902.1| unknown [Arabidopsis thaliana]	188	180	7.00E-43	95.7	68.1	74.5	unknown	gbpln	Arabidopsis thaliana	AT1G47200.1 | Symbols: WPP2 | WPP domain protein 2 | chr1:17298181-17298723 REVERSE LENGTH=180	188	180	3.00E-45	95.7	66.0	72.3
Rsa1.0_01140.1.g23880.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	305	1072	1.00E-58	351.5	39.7	60.7	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	305	289	1.00E-47	94.8	34.4	48.2
Rsa1.0_01141.1.g23881.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	52	1123	2.00E-20	2159.6	86.5	100.0	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01141.1.g23882.t1	dbj|BAJ33878.1| unnamed protein product [Thellungiella halophila]	709	711	0	100.3	93.8	97.0	unnamed protein product	----	----	AT4G30210.2 | Symbols: ATR2, AR2 | P450 reductase 2 | chr4:14796900-14800578 FORWARD LENGTH=711	709	711	0	100.3	92.2	95.6

Rsa1.0_01141.1.g23883.t1	ref|NP_193031.1| Fasciclin-like arabinogalactan family protein [Arabidopsis thaliana] gi|5123936|emb|CAB45494.1| hypothetical protein [Arabidopsis thaliana] gi|7267997|emb|CAB78337.1| hypothetical protein [Arabidopsis thaliana] gi|91805587|gb|ABE65522.1| hypothetical protein At4g12950 [Arabidopsis thaliana] gi|332657806|gb|AEE83206.1| Fasciclin-like arabinogalactan family protein [Arabidopsis thaliana]	190	176	1.00E-55	92.6	57.4	71.6	Fasciclin-like arabinogalactan family protein	gbpln	Arabidopsis thaliana	AT4G12950.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr4:7576642-7577172 FORWARD LENGTH=176	190	176	4.00E-58	92.6	57.4	71.6
Rsa1.0_01141.1.g23884.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01141.1.g23885.t1	ref|NP_193031.1| Fasciclin-like arabinogalactan family protein [Arabidopsis thaliana] gi|5123936|emb|CAB45494.1| hypothetical protein [Arabidopsis thaliana] gi|7267997|emb|CAB78337.1| hypothetical protein [Arabidopsis thaliana] gi|91805587|gb|ABE65522.1| hypothetical protein At4g12950 [Arabidopsis thaliana] gi|332657806|gb|AEE83206.1| Fasciclin-like arabinogalactan family protein [Arabidopsis thaliana]	202	176	6.00E-32	87.1	31.7	46.0	Fasciclin-like arabinogalactan family protein	gbpln	Arabidopsis thaliana	AT4G12950.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr4:7576642-7577172 FORWARD LENGTH=176	202	176	2.00E-34	87.1	31.7	46.0
Rsa1.0_01141.1.g23886.t1	ref|NP_193028.1| aspartyl protease family protein [Arabidopsis thaliana] gi|5123933|emb|CAB45491.1| putative protein [Arabidopsis thaliana] gi|7267994|emb|CAB78334.1| putative protein [Arabidopsis thaliana] gi|332657803|gb|AEE83203.1| aspartyl protease family protein [Arabidopsis thaliana]	378	389	1.00E-126	102.9	61.9	75.4	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT4G12920.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr4:7568286-7569455 FORWARD LENGTH=389	378	389	1.00E-129	102.9	61.9	75.4
Rsa1.0_01141.1.g23887.t1	ref|NP_001152699.1| PHD finger-like domain-containing protein 5A [Zea mays] gi|226499812|ref|NP_001148557.1| PHD finger-like domain-containing protein 5A [Zea mays] gi|195620406|gb|ACG32033.1| PHD finger-like domain-containing protein 5A [Zea mays] gi|195636738|gb|ACG37837.1| PHD finger-like domain-containing protein 5A [Zea mays] gi|195659129|gb|ACG49032.1| PHD finger-like domain-containing protein 5A [Zea mays] gi|223946749|gb|ACN27458.1| unknown [Zea mays] gi|414584947|tpg|DAA35518.1| TPA: PHD finger-like domain-containing protein 5A isoform 1 [Zea mays] gi|414584948|tpg|DAA35519.1| TPA: PHD finger-like domain-containing protein 5A isoform 2 [Zea mays] gi|414584949|tpg|DAA35520.1| TPA: PHD finger-like domain-containing protein 5A isoform 3 [Zea mays]	81	110	6.00E-31	135.8	93.8	93.8	PHD finger-like domain-containing protein 5A	gbenv/gbpln	Zea mays	AT2G30000.1 | Symbols: | PHF5-like protein | chr2:12804042-12804374 REVERSE LENGTH=110	81	110	2.00E-33	135.8	92.6	93.8
Rsa1.0_01141.1.g23888.t1	ref|NP_193030.1| uncharacterized protein [Arabidopsis thaliana] gi|5123935|emb|CAB45493.1| putative protein [Arabidopsis thaliana] gi|7267996|emb|CAB78336.1| putative protein [Arabidopsis thaliana] gi|117168111|gb|ABK32138.1| At4g12940 [Arabidopsis thaliana] gi|332657805|gb|AEE83205.1| uncharacterized protein AT4G12940 [Arabidopsis thaliana]	121	151	1.00E-37	124.8	65.3	74.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G12940.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12930.1); Has 12 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:7574172-7574627 FORWARD LENGTH=151	121	151	2.00E-40	124.8	65.3	74.4

Rsa1.0_01141.1.g23889.t1	ref|NP_193029.1| uncharacterized protein [Arabidopsis thaliana] gi|5123934|emb|CAB45492.1| hypothetical protein [Arabidopsis thaliana] gi|7267995|emb|CAB78335.1| hypothetical protein [Arabidopsis thaliana] gi|117168195|gb|ABK32180.1| At4g12930 [Arabidopsis thaliana] gi|332657804|gb|AEE83204.1| uncharacterized protein AT4G12930 [Arabidopsis thaliana]	141	141	2.00E-44	100.0	64.5	78.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G12930.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf whorl, sepal, male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G28930.1); Has 12 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:7573281-7573706 REVERSE LENGTH=141	141	141	5.00E-47	100.0	64.5	78.7
Rsa1.0_01141.1.g23890.t1	gb|EOA15440.1| hypothetical protein CARUB_v10004082mg [Capsella rubella]	948	948	0	100.0	92.6	96.1	hypothetical protein CARUB_v10004082mg	gbpln	Capsella rubella	AT4G30190.1 | Symbols: AHA2, PMA2, HA2 | H(+)-ATPase 2 | chr4:14770820-14775920 REVERSE LENGTH=948	948	948	0	100.0	92.5	96.1
Rsa1.0_01142.1.g23891.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01142.1.g23892.t1	ref|XP_002884081.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297329921|gb|EFH60340.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	238	239	1.00E-120	100.4	89.9	94.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G35840.1 | Symbols: | RING/U-box superfamily protein | chr4:16981083-16982266 FORWARD LENGTH=236	238	236	1.00E-115	99.2	82.8	92.0
Rsa1.0_01142.1.g23893.t1	#	#	#	#	#	#	#	–	----	----	AT1G51690.3 | Symbols: B ALPHA | protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform | chr1:19164124-19169974 FORWARD LENGTH=603	139	603	3.00E-11	433.8	23.7	30.9
Rsa1.0_01142.1.g23894.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01142.1.g23895.t1	ref|NP_175139.1| receptor like protein 6 [Arabidopsis thaliana] gi|12321005|gb|AAG50623.1|AC083835_8 disease resistance protein, putative [Arabidopsis thaliana] gi|332193999|gb|AEE32120.1| receptor like protein 6 [Arabidopsis thaliana]	1015	994	0	97.9	65.6	75.6	receptor like protein 6	gbpln	Arabidopsis thaliana	AT1G45616.1 | Symbols: AtRLP6, RLP6 | receptor like protein 6 | chr1:17183550-17186534 REVERSE LENGTH=994	1015	994	0	97.9	65.6	75.6
Rsa1.0_01142.1.g23896.t1	ref|NP_175139.1| receptor like protein 6 [Arabidopsis thaliana] gi|12321005|gb|AAG50623.1|AC083835_8 disease resistance protein, putative [Arabidopsis thaliana] gi|332193999|gb|AEE32120.1| receptor like protein 6 [Arabidopsis thaliana]	990	994	0	100.4	65.9	75.8	receptor like protein 6	gbpln	Arabidopsis thaliana	AT1G45616.1 | Symbols: AtRLP6, RLP6 | receptor like protein 6 | chr1:17183550-17186534 REVERSE LENGTH=994	990	994	0	100.4	65.9	75.8
Rsa1.0_01142.1.g23897.t1	ref|XP_002877467.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323305|gb|EFH53726.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	105	186	5.00E-13	177.1	41.0	53.3	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01142.1.g23898.t1	gb|EOA32800.1| hypothetical protein CARUB_v10016111mg [Capsella rubella]	512	513	0	100.2	87.3	93.9	hypothetical protein CARUB_v10016111mg	gbpln	Capsella rubella	AT2G17760.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:7713488-7716269 FORWARD LENGTH=513	512	513	0	100.2	88.7	95.1
Rsa1.0_01143.1.g23899.t1	ref|XP_002974570.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii] gi|300157465|gb|EFJ24090.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii]	417	516	6.00E-54	123.7	66.9	69.1	hypothetical protein SELMODRAFT_442529	gbpln	Selaginella moellendorffii	AT4G08370.1 | Symbols: | Proline-rich extensin-like family protein | chr4:5301962-5303314 REVERSE LENGTH=350	417	350	8.00E-25	83.9	40.3	47.2
Rsa1.0_01143.1.g23900.t1	gb|EOA39890.1| hypothetical protein CARUB_v10008568mg [Capsella rubella]	111	632	5.00E-34	569.4	63.1	67.6	hypothetical protein CARUB_v10008568mg	gbpln	Capsella rubella	AT1G26270.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase family protein | chr1:9089822-9091714 REVERSE LENGTH=630	111	630	2.00E-34	567.6	60.4	64.0
Rsa1.0_01143.1.g23901.t1	ref|XP_002982842.1| hypothetical protein SELMODRAFT_422106 [Selaginella moellendorffii] gi|300149432|gb|EFJ16087.1| hypothetical protein SELMODRAFT_422106 [Selaginella moellendorffii]	111	386	9.00E-20	347.7	75.7	79.3	hypothetical protein SELMODRAFT_422106	gbpln	Selaginella moellendorffii	#	#	#	#	#	#	#
Rsa1.0_01143.1.g23902.t1	gb|EOA39890.1| hypothetical protein CARUB_v10008568mg [Capsella rubella]	101	632	4.00E-43	625.7	84.2	90.1	hypothetical protein CARUB_v10008568mg	gbpln	Capsella rubella	AT1G26270.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase family protein | chr1:9089822-9091714 REVERSE LENGTH=630	101	630	3.00E-44	623.8	82.2	86.1

Rsa1.0_01143.1.g23903.t1	ref|XP_002974570.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii] gi|300157465|gb|EFJ24090.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii]	360	516	1.00E-45	143.3	65.0	66.7	hypothetical protein SELMODRAFT_442529	gbpln	Selaginella moellendorffii	AT4G08370.1 | Symbols: | Proline-rich extensin-like family protein | chr4:5301962-5303314 REVERSE LENGTH=350	360	350	1.00E-27	97.2	52.8	60.8
Rsa1.0_01143.1.g23904.t1	gb|EOA39890.1| hypothetical protein CARUB_v10008568mg [Capsella rubella]	621	632	0	101.8	83.1	90.2	hypothetical protein CARUB_v10008568mg	gbpln	Capsella rubella	AT1G26270.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase family protein | chr1:9089822-9091714 REVERSE LENGTH=630	621	630	0	101.4	82.1	90.2
Rsa1.0_01143.1.g23905.t1	sp|Q6R4S3.1|CAL_BRARA RecName: Full=Transcription factor CAULIFLOWER; Short=BcrCAL; AltName: Full=Agamous-like MADS-box protein CAL gi|75291799|sp|Q6R4S6.1|CAL_BRARC RecName: Full=Transcription factor CAULIFLOWER; Short=BccCAL; AltName: Full=Agamous-like MADS-box protein CAL gi|45533860|gb|AAS67303.1| DNA binding protein [Brassica rapa subsp. chinensis] gi|45533866|gb|AAS67306.1| DNA binding protein [Brassica rapa subsp. rapa]	254	254	1.00E-140	100.0	95.7	97.6	RecName: Full=Transcription factor CAULIFLOWER; Short=BcrCAL; AltName: Full=Agamous-like MADS-box protein CAL gi|75291799|sp|Q6R4S6.1|CAL_BRARC RecName: Full=Transcription factor CAULIFLOWER; Short=BccCAL; AltName: Full=Agamous-like MADS-box protein CAL gi|45533860|gb|AAS67303.1| DNA binding protein	gbpln	Brassica rapa	AT1G26310.1 | Symbols: CAL, CAL1, AGL10 | K-box region and MADS-box transcription factor family protein | chr1:9100330-9103510 REVERSE LENGTH=255	254	255	1.00E-121	100.4	85.0	91.3
Rsa1.0_01143.1.g23906.t1	ref|NP_173960.2| methyl esterase 13 [Arabidopsis thaliana] gi|395406784|sp|F4IE65.1|MES13_ARATH RecName: Full=Putative methylesterase 13, chloroplastic; Short=AtMES13; Flags: Precursor gi|332192561|gb|AEE30682.1| methyl esterase 13 [Arabidopsis thaliana]	397	444	1.00E-176	111.8	82.9	89.7	methyl esterase 13	gbpln	Arabidopsis thaliana	AT1G26360.1 | Symbols: ATMES13, MES13 | methyl esterase 13 | chr1:9119021-9121203 REVERSE LENGTH=444	397	444	1.00E-179	111.8	82.9	89.7
Rsa1.0_01143.1.g23907.t1	ref|NP_172913.1| Valyl-tRNA synthetase [Arabidopsis thaliana] gi|21542452|sp|P93736.2|SYV_ARATH RecName: Full=Valine--tRNA ligase; AltName: Full=Valyl-tRNA synthetase; Short=ValRS gi|332191069|gb|AEE29190.1| Valyl-tRNA synthetase [Arabidopsis thaliana]	1303	1108	0	85.0	64.8	70.7	Valyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT1G14610.1 | Symbols: TWN2, VALRS | valyl-tRNA synthetase / valine--tRNA ligase (VALRS) | chr1:5008502-5014486 REVERSE LENGTH=1108	1303	1108	0	85.0	64.8	70.7
Rsa1.0_01144.1.g23908.t1	ref|XP_002879302.1| hypothetical protein ARALYDRAFT_482033 [Arabidopsis lyrata subsp. lyrata] gi|297325141|gb|EFH55561.1| hypothetical protein ARALYDRAFT_482033 [Arabidopsis lyrata subsp. lyrata]	82	81	4.00E-29	98.8	89.0	93.9	hypothetical protein ARALYDRAFT_482033	gbpln	Arabidopsis lyrata	AT2G31081.1 | Symbols: CLE4 | CLAVATA3/ESR-RELATED 4 | chr2:13238103-13238345 FORWARD LENGTH=80	82	80	2.00E-30	97.6	87.8	91.5
Rsa1.0_01144.1.g23909.t1	gb|EOA26707.1| hypothetical protein CARUB_v10022794mg [Capsella rubella]	673	664	0	98.7	85.3	89.3	hypothetical protein CARUB_v10022794mg	gbpln	Capsella rubella	AT2G31060.2 | Symbols: | elongation factor family protein | chr2:13213496-13218544 REVERSE LENGTH=667	673	667	0	99.1	84.8	89.3
Rsa1.0_01144.1.g23910.t1	ref|XP_002878835.1| hypothetical protein ARALYDRAFT_901144 [Arabidopsis lyrata subsp. lyrata] gi|297324674|gb|EFH55094.1| hypothetical protein ARALYDRAFT_901144 [Arabidopsis lyrata subsp. lyrata]	336	200	2.00E-57	59.5	36.0	43.8	hypothetical protein ARALYDRAFT_901144	gbpln	Arabidopsis lyrata	AT2G40450.1 | Symbols: | BTB/POZ domain-containing protein | chr2:16892024-16892790 REVERSE LENGTH=209	336	209	2.00E-53	62.2	36.6	43.2
Rsa1.0_01144.1.g23911.t1	gb|AAM64960.1| unknown [Arabidopsis thaliana]	340	350	1.00E-169	102.9	87.4	93.5	unknown	gbpln	Arabidopsis thaliana	AT2G31040.1 | Symbols: | ATP synthase protein I -related | chr2:13209094-13211012 REVERSE LENGTH=350	340	350	1.00E-171	102.9	87.1	93.5
Rsa1.0_01144.1.g23912.t3	ref|NP_180658.3| protein kinase domain-containing protein [Arabidopsis thaliana] gi|334184603|ref|NP_001189646.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|330253382|gb|AEC08476.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|330253383|gb|AEC08477.1| protein kinase domain-containing protein [Arabidopsis thaliana]	799	775	0	97.0	82.1	87.6	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G31010.2 | Symbols: | Protein kinase superfamily protein | chr2:13194939-13199642 FORWARD LENGTH=775	799	775	0	97.0	82.1	87.6

<table>
<tr><td>Rsa1.0_01144.1.g23913.t2</td><td>ref|NP_001031451.1| uncharacterized protein [Arabidopsis thaliana] gi|79567094|ref|NP_180656.3| uncharacterized protein [Arabidopsis thaliana] gi|330253378|gb|AEC08472.1| uncharacterized protein AT2G30990 [Arabidopsis thaliana] gi|330253379|gb|AEC08473.1| uncharacterized protein AT2G30990 [Arabidopsis thaliana]</td><td>534</td><td>593</td><td>0</td><td>111.0</td><td>76.2</td><td>83.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G30990.2 | Symbols: | Protein of unknown function (DUF688) | chr2:13187776-13189761 REVERSE LENGTH=593</td><td>534</td><td>593</td><td>0</td><td>111.0</td><td>76.2</td><td>83.3</td></tr>
<tr><td>Rsa1.0_01144.1.g23914.t1</td><td>ref|XP_002881146.1| hypothetical protein ARALYDRAFT_902112 [Arabidopsis lyrata subsp. lyrata] gi|297326985|gb|EFH57405.1| hypothetical protein ARALYDRAFT_902112 [Arabidopsis lyrata subsp. lyrata]</td><td>411</td><td>412</td><td>0</td><td>100.2</td><td>94.2</td><td>96.1</td><td>hypothetical protein ARALYDRAFT_902112</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G30980.1 | Symbols: ASKdZeta, ATSK23, BIL1, ATSK2-2, SKdZeta | SHAGGY-related protein kinase dZeta | chr2:13182350-13185870 REVERSE LENGTH=412</td><td>411</td><td>412</td><td>0</td><td>100.2</td><td>93.7</td><td>96.1</td></tr>
<tr><td>Rsa1.0_01145.1.g23915.t1</td><td>gb|ACP30551.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>747</td><td>717</td><td>0</td><td>96.0</td><td>66.3</td><td>71.8</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G63350.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:23494935-23497631 REVERSE LENGTH=898</td><td>747</td><td>898</td><td>0</td><td>120.2</td><td>58.4</td><td>72.0</td></tr>
<tr><td>Rsa1.0_01145.1.g23916.t1</td><td>gb|EOA28746.1| hypothetical protein CARUB_v10024977mg [Capsella rubella]</td><td>450</td><td>473</td><td>0</td><td>105.1</td><td>75.8</td><td>86.0</td><td>hypothetical protein CARUB_v10024977mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G36070.1 | Symbols: ATTIM44-2, TIM44-2 | translocase inner membrane subunit 44-2 | chr2:15145119-15147895 REVERSE LENGTH=469</td><td>450</td><td>469</td><td>0</td><td>104.2</td><td>75.3</td><td>86.7</td></tr>
<tr><td>Rsa1.0_01145.1.g23917.t1</td><td>dbj|BAB09991.1| mutator-like transposase-like [Arabidopsis thaliana]</td><td>228</td><td>825</td><td>9.00E-82</td><td>361.8</td><td>64.5</td><td>75.0</td><td>mutator-like transposase-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01145.1.g23918.t1</td><td>ref|XP_002886283.1| hypothetical protein ARALYDRAFT_900407 [Arabidopsis lyrata subsp. lyrata] gi|297332123|gb|EFH62542.1| hypothetical protein ARALYDRAFT_900407 [Arabidopsis lyrata subsp. lyrata]</td><td>130</td><td>136</td><td>3.00E-39</td><td>104.6</td><td>65.4</td><td>77.7</td><td>hypothetical protein ARALYDRAFT_900407</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G20500.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 13 Blast hits to 13 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:8835300-8835710 REVERSE LENGTH=136</td><td>130</td><td>136</td><td>7.00E-41</td><td>104.6</td><td>65.4</td><td>77.7</td></tr>
<tr><td>Rsa1.0_01145.1.g23919.t1</td><td>ref|XP_002884205.1| EDA27/NOP10 [Arabidopsis lyrata subsp. lyrata] gi|297330045|gb|EFH60464.1| EDA27/NOP10 [Arabidopsis lyrata subsp. lyrata]</td><td>64</td><td>64</td><td>2.00E-27</td><td>100.0</td><td>93.8</td><td>96.9</td><td>EDA27/NOP10</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G20490.1 | Symbols: NOP10, EDA27 | nucleolar RNA-binding Nop10p family protein | chr2:8831897-8832723 FORWARD LENGTH=64</td><td>64</td><td>64</td><td>7.00E-30</td><td>100.0</td><td>92.2</td><td>96.9</td></tr>
<tr><td>Rsa1.0_01145.1.g23920.t1</td><td>ref|NP_179634.2| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|238479300|ref|NP_001154525.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|330251913|gb|AEC07007.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|330251914|gb|AEC07008.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana]</td><td>465</td><td>425</td><td>0</td><td>91.4</td><td>83.9</td><td>86.7</td><td>RabGAP/TBC domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G20440.2 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr2:8811034-8813251 REVERSE LENGTH=425</td><td>465</td><td>425</td><td>0</td><td>91.4</td><td>83.9</td><td>86.7</td></tr>
<tr><td>Rsa1.0_01145.1.g23921.t1</td><td>ref|XP_002884199.1| hypothetical protein ARALYDRAFT_900392 [Arabidopsis lyrata subsp. lyrata] gi|297330039|gb|EFH60458.1| hypothetical protein ARALYDRAFT_900392 [Arabidopsis lyrata subsp. lyrata]</td><td>337</td><td>400</td><td>1.00E-86</td><td>118.7</td><td>60.8</td><td>73.6</td><td>hypothetical protein ARALYDRAFT_900392</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G20400.1 | Symbols: | myb-like HTH transcriptional regulator family protein | chr2:8799624-8801621 FORWARD LENGTH=397</td><td>337</td><td>397</td><td>1.00E-80</td><td>117.8</td><td>58.5</td><td>69.4</td></tr>
<tr><td>Rsa1.0_01145.1.g23922.t1</td><td>gb|ABK28502.1| unknown [Arabidopsis thaliana]</td><td>189</td><td>213</td><td>9.00E-57</td><td>112.7</td><td>73.5</td><td>82.0</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G20430.1 | Symbols: RIC6 | ROP-interactive CRIB motif-containing protein 6 | chr2:8808667-8809781 REVERSE LENGTH=212</td><td>189</td><td>212</td><td>4.00E-59</td><td>112.2</td><td>73.5</td><td>82.0</td></tr>
<tr><td>Rsa1.0_01145.1.g23923.t1</td><td>ref|XP_002884197.1| hypothetical protein ARALYDRAFT_480864 [Arabidopsis lyrata subsp. lyrata] gi|297330037|gb|EFH60456.1| hypothetical protein ARALYDRAFT_480864 [Arabidopsis lyrata subsp. lyrata]</td><td>205</td><td>127</td><td>1.00E-41</td><td>62.0</td><td>42.0</td><td>44.9</td><td>hypothetical protein ARALYDRAFT_480864</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G20362.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G63310.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:8789772-8790155 FORWARD LENGTH=127</td><td>205</td><td>127</td><td>4.00E-44</td><td>62.0</td><td>42.0</td><td>44.9</td></tr>
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Rsa1.0_01145.1.g23924.t1	ref|XP_002884196.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] gi|297330036|gb|EFH60455.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata]	403	402	0	99.8	93.8	96.8	catalytic/ coenzyme binding protein	gbpln	Arabidopsis lyrata	AT2G20360.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:8786070-8789098 FORWARD LENGTH=402	403	402	0	99.8	92.6	95.5
Rsa1.0_01145.1.g23925.t2	gb|EOA29723.1| hypothetical protein CARUB_v10012810mg [Capsella rubella]	1775	1513	0	85.2	78.3	81.0	hypothetical protein CARUB_v10012810mg	gbpln	Capsella rubella	AT1G04120.1 | Symbols: ATMRP5, MRP5, ATABCC5, ABCC5 | multidrug resistance-associated protein 5 | chr1:1064848-1070396 REVERSE LENGTH=1514	1775	1514	0	85.3	65.9	73.5
Rsa1.0_01145.1.g23926.t1	ref|XP_002884194.1| hypothetical protein ARALYDRAFT_900384 [Arabidopsis lyrata subsp. lyrata] gi|297330034|gb|EFH60453.1| hypothetical protein ARALYDRAFT_900384 [Arabidopsis lyrata subsp. lyrata]	371	479	0	129.1	89.8	94.9	hypothetical protein ARALYDRAFT_900384	gbpln	Arabidopsis lyrata	AT2G20340.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr2:8779804-8782490 FORWARD LENGTH=490	371	490	0	132.1	89.5	94.1
Rsa1.0_01146.1.g23927.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01146.1.g23928.t1	ref|XP_002882368.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata] gi|297328208|gb|EFH58627.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata]	171	392	4.00E-58	229.2	62.6	75.4	hypothetical protein ARALYDRAFT_896506	gbpln	Arabidopsis lyrata	AT3G04660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:1264794-1265966 FORWARD LENGTH=390	171	390	2.00E-37	228.1	49.7	66.1
Rsa1.0_01146.1.g23929.t1	ref|XP_002882368.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata] gi|297328208|gb|EFH58627.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata]	636	392	1.00E-134	61.6	39.3	48.1	hypothetical protein ARALYDRAFT_896506	gbpln	Arabidopsis lyrata	AT3G04660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:1264794-1265966 FORWARD LENGTH=390	636	390	7.00E-95	61.3	29.6	40.1
Rsa1.0_01146.1.g23930.t1	ref|XP_002882368.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata] gi|297328208|gb|EFH58627.1| hypothetical protein ARALYDRAFT_896506 [Arabidopsis lyrata subsp. lyrata]	384	392	1.00E-129	102.1	63.8	77.3	hypothetical protein ARALYDRAFT_896506	gbpln	Arabidopsis lyrata	AT3G04660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:1264794-1265966 FORWARD LENGTH=390	384	390	6.00E-88	101.6	47.4	65.1
Rsa1.0_01146.1.g23931.t1	ref|NP_001189808.1| ankyrin repeat family protein [Arabidopsis thaliana] gi|332640603|gb|AEE74124.1| ankyrin repeat family protein [Arabidopsis thaliana]	454	680	0	149.8	89.6	95.4	ankyrin repeat family protein	gbpln	Arabidopsis thaliana	AT3G04710.3 | Symbols: TPR10 | ankyrin repeat family protein | chr3:1276948-1280942 FORWARD LENGTH=680	454	680	0	149.8	89.6	95.4
Rsa1.0_01146.1.g23932.t1	gb|ABV89663.1| indoleacetic acid-induced protein 16 [Brassica rapa]	236	231	1.00E-118	97.9	88.6	91.9	indoleacetic acid-induced protein 16	gbpln	Brassica rapa	AT3G04730.1 | Symbols: IAA16 | indoleacetic acid-induced protein 16 | chr3:1288993-1290415 REVERSE LENGTH=236	236	236	1.00E-119	100.0	91.9	94.9
Rsa1.0_01146.1.g23933.t1	gb|EOA31567.1| hypothetical protein CARUB_v10014759mg [Capsella rubella]	176	176	8.00E-96	100.0	96.0	99.4	hypothetical protein CARUB_v10014759mg	gbpln	Capsella rubella	AT3G04780.1 | Symbols: | Protein of unknown function (DUF1000) | chr3:1311447-1313013 REVERSE LENGTH=176	176	176	1.00E-97	100.0	95.5	98.9
Rsa1.0_01146.1.g23934.t1	ref|XP_002882374.1| hypothetical protein ARALYDRAFT_896526 [Arabidopsis lyrata subsp. lyrata] gi|297328214|gb|EFH58633.1| hypothetical protein ARALYDRAFT_896526 [Arabidopsis lyrata subsp. lyrata]	276	276	1.00E-142	100.0	92.8	96.4	hypothetical protein ARALYDRAFT_896526	gbpln	Arabidopsis lyrata	AT3G04790.1 | Symbols: | Ribose 5-phosphate isomerase, type A protein | chr3:1313365-1314195 FORWARD LENGTH=276	276	276	1.00E-143	100.0	91.7	95.7
Rsa1.0_01146.1.g23935.t1	sp|P49396.2|RS3A_BRARA RecName: Full=40S ribosomal protein S3a; AltName: Full=S phase-specific protein BIS289 gi|387909|gb|AAA33013.1| S-phase-specific protein [Brassica rapa] gi|397401|emb|CAA81030.1| unnamed protein product [Brassica rapa]	261	262	1.00E-139	100.4	97.7	98.5	RecName: Full=40S ribosomal protein S3a; AltName: Full=S phase-specific protein BIS289 gi|387909|gb|AAA33013.1| S-phase-specific protein	gbpln	Brassica rapa	AT4G34670.1 | Symbols: | Ribosomal protein S3Ae | chr4:16548724-16550222 FORWARD LENGTH=262	261	262	1.00E-136	100.4	93.1	96.2
Rsa1.0_01146.1.g23936.t1	ref|NP_566240.1| uncharacterized protein [Arabidopsis thaliana] gi|12322843|gb|AAG51405.1|AC009465_5 unknown protein; 64727-65596 [Arabidopsis thaliana] gi|16612261|gb|AAL27500.1|AF439828_1 AT3g04860/T9J14_19 [Arabidopsis thaliana] gi|21928087|gb|AAM78072.1| AT3g04860/T9J14_19 [Arabidopsis thaliana] gi|332640626|gb|AEE74147.1| uncharacterized protein AT3G04860 [Arabidopsis thaliana]	287	289	1.00E-142	100.7	88.2	93.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G04860.1 | Symbols: | Plant protein of unknown function (DUF868) | chr3:1339349-1340218 REVERSE LENGTH=289	287	289	1.00E-145	100.7	88.2	93.4

Rsa1.0_01146.1.g23937.t1	ref|XP_002884488.1| hypothetical protein ARALYDRAFT_477786 [Arabidopsis lyrata subsp. lyrata] gi|297330328|gb|EFH60747.1| hypothetical protein ARALYDRAFT_477786 [Arabidopsis lyrata subsp. lyrata]	1122	1202	0	107.1	48.9	66.4	hypothetical protein ARALYDRAFT_477786	gbpln	Arabidopsis lyrata	AT3G05040.1 | Symbols: HST, HST1 | ARM repeat superfamily protein | chr3:1401479-1408095 REVERSE LENGTH=1202	1122	1202	0	107.1	48.4	66.3
Rsa1.0_01146.1.g23938.t1	ref|NP_974219.1| tryptophanyl-tRNA synthetase [Arabidopsis thaliana] gi|332640583|gb|AEE74104.1| tryptophanyl-tRNA synthetase [Arabidopsis thaliana]	448	402	1.00E-178	89.7	68.8	77.0	tryptophanyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT3G04600.2 | Symbols: | Nucleotidylyl transferase superfamily protein | chr3:1243152-1245958 FORWARD LENGTH=402	448	402	1.00E-180	89.7	68.8	77.0
Rsa1.0_01146.1.g23939.t1	ref|XP_002882383.1| 40S ribosomal protein S24 [Arabidopsis lyrata subsp. lyrata] gi|297328223|gb|EFH58642.1| 40S ribosomal protein S24 [Arabidopsis lyrata subsp. lyrata]	133	133	2.00E-68	100.0	98.5	99.2	40S ribosomal protein S24	gbpln	Arabidopsis lyrata	AT5G28060.1 | Symbols: | Ribosomal protein S24e family protein | chr5:10069791-10070792 REVERSE LENGTH=133	133	133	3.00E-68	100.0	94.0	97.0
Rsa1.0_01146.1.g23940.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1435	1459	0	101.7	63.0	76.0	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1435	1262	1.00E-107	87.9	13.3	19.6
Rsa1.0_01146.1.g23941.t1	ref|NP_187166.2| sugar transporter ERD6-like 8 [Arabidopsis thaliana] gi|117940178|sp|Q0WQ63.1|ERDL8_ARATH RecName: Full=Sugar transporter ERD6-like 8 gi|110737589|dbj|BAF00736.1| putative sugar transporter [Arabidopsis thaliana] gi|332640670|gb|AEE74191.1| sugar transporter ERD6-like 8 [Arabidopsis thaliana]	465	470	0	101.1	92.7	95.9	sugar transporter ERD6-like 8	gbpln	Arabidopsis thaliana	AT3G05150.1 | Symbols: | Major facilitator superfamily protein | chr3:1440216-1443361 FORWARD LENGTH=470	465	470	0	101.1	92.7	95.9
Rsa1.0_01146.1.g23942.t3	gb|EOA23889.1| hypothetical protein CARUB_v10017105mg [Capsella rubella]	620	488	0	78.7	65.3	69.7	hypothetical protein CARUB_v10017105mg	gbpln	Capsella rubella	AT3G42950.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:15015383-15017800 FORWARD LENGTH=484	620	484	0	78.1	62.1	67.1
Rsa1.0_01146.1.g23943.t1	ref|XP_002882393.1| hypothetical protein ARALYDRAFT_317378 [Arabidopsis lyrata subsp. lyrata] gi|297328233|gb|EFH58652.1| hypothetical protein ARALYDRAFT_317378 [Arabidopsis lyrata subsp. lyrata]	330	341	1.00E-161	103.3	85.5	92.1	hypothetical protein ARALYDRAFT_317378	gbpln	Arabidopsis lyrata	AT3G05100.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:1424155-1425667 FORWARD LENGTH=336	330	336	1.00E-158	101.8	83.3	90.0
Rsa1.0_01146.1.g23944.t1	ref|NP_187156.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|6729015|gb|AAF27011.1|AC009177_1 putative cyclin-dependent protein kinase [Arabidopsis thaliana] gi|14532508|gb|AAK63982.1| AT3g05050/T12H1_1 [Arabidopsis thaliana] gi|23506083|gb|AAN28901.1| At3g05050/T12H1_1 [Arabidopsis thaliana] gi|332640659|gb|AEE74180.1| protein kinase domain-containing protein [Arabidopsis thaliana]	586	593	0	101.2	85.5	93.0	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G05050.1 | Symbols: | Protein kinase superfamily protein | chr3:1408789-1411194 REVERSE LENGTH=593	586	593	0	101.2	85.5	93.0
Rsa1.0_01146.1.g23945.t1	sp|P08971.1|ACP5_BRANA RecName: Full=Acyl carrier protein, chloroplastic; Short=ACP; AltName: Full=Clones 28F10, 10H11/11D11, 34F12 and 04F05/05E01; Flags: Precursor gi|17759|emb|CAA31513.1| unnamed protein product [Brassica napus] gi|17763|emb|CAA30782.1| unnamed protein product [Brassica napus]	136	134	2.00E-65	98.5	94.1	96.3	RecName: Full=Acyl carrier protein, chloroplastic; Short=ACP; AltName: Full=Clones 28F10, 10H11/11D11, 34F12 and 04F05/05E01; Flags: Precursor gi|17759|emb|CAA31513.1| unnamed protein product	gbpln	Brassica napus	AT3G05020.1 | Symbols: ACP1, ACP | acyl carrier protein 1 | chr3:1391863-1392878 REVERSE LENGTH=137	136	137	8.00E-56	100.7	80.1	88.2

Rsa1.0_01147.1.g23946.t1	ref|NP_568670.1| mitochondrial carnitine/acylcarnitine carrier-like protein [Arabidopsis thaliana] gi|24211999|sp|Q93XM7.1|MCAT_ARATH RecName: Full=Mitochondrial carnitine/acylcarnitine carrier-like protein; AltName: Full=Carnitine/acylcarnitine translocase-like protein; Short=CAC-like protein; AltName: Full=Protein A BOUT DE SOUFFLE gi|13992452|emb|CAC38047.1| carnitine acyl carrier-like protein [Arabidopsis thaliana] gi|22531072|gb|AAM97040.1| carnitine/acylcarnitine translocase-like protein [Arabidopsis thaliana] gi|23197914|gb|AAN15484.1| carnitine/acylcarnitine translocase-like protein [Arabidopsis thaliana] gi|332008045|gb|AED95428.1| mitochondrial carnitine/acylcarnitine carrier-like protein [Arabidopsis thaliana]	300	300	1.00E-158	100.0	94.0	95.3	mitochondrial carnitine/acylcarnitine carrier-like protein	gbpln	Arabidopsis thaliana	AT5G46800.1 | Symbols: BOU | Mitochondrial substrate carrier family protein | chr5:18988779-18989810 REVERSE LENGTH=300	300	300	1.00E-161	100.0	94.0	95.3
Rsa1.0_01147.1.g23947.t1	gb|AAM61509.1| unknown [Arabidopsis thaliana]	188	191	3.00E-58	101.6	84.6	89.9	unknown	gbpln	Arabidopsis thaliana	AT5G46795.1 | Symbols: MSP2 | microspore-specific promoter 2 | chr5:18987055-18988168 REVERSE LENGTH=192	188	192	7.00E-59	102.1	83.5	89.4
Rsa1.0_01147.1.g23948.t1	ref|XP_002865162.1| hypothetical protein ARALYDRAFT_916750 [Arabidopsis lyrata subsp. lyrata] gi|297310997|gb|EFH41421.1| hypothetical protein ARALYDRAFT_916750 [Arabidopsis lyrata subsp. lyrata]	225	233	1.00E-72	103.6	85.8	91.1	hypothetical protein ARALYDRAFT_916750	gbpln	Arabidopsis lyrata	AT5G46780.2 | Symbols: | VQ motif-containing protein | chr5:18979236-18979949 FORWARD LENGTH=237	225	237	1.00E-72	105.3	85.3	89.3
Rsa1.0_01147.1.g23949.t1	ref|XP_002865163.1| hypothetical protein ARALYDRAFT_916751 [Arabidopsis lyrata subsp. lyrata] gi|297310998|gb|EFH41422.1| hypothetical protein ARALYDRAFT_916751 [Arabidopsis lyrata subsp. lyrata]	133	133	1.00E-53	100.0	78.9	85.0	hypothetical protein ARALYDRAFT_916751	gbpln	Arabidopsis lyrata	AT5G46770.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:18977494-18977895 FORWARD LENGTH=133	133	133	2.00E-53	100.0	76.7	83.5
Rsa1.0_01147.1.g23950.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01147.1.g23951.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01147.1.g23952.t1	ref|XP_002863392.1| ubiquitin-specific protease 21 [Arabidopsis lyrata subsp. lyrata] gi|297309227|gb|EFH39651.1| ubiquitin-specific protease 21 [Arabidopsis lyrata subsp. lyrata]	673	724	0	107.6	62.1	74.7	ubiquitin-specific protease 21	gbpln	Arabidopsis lyrata	AT5G46740.1 | Symbols: UBP21 | ubiquitin-specific protease 21 | chr5:18965410-18968492 REVERSE LENGTH=732	673	732	0	108.8	62.4	73.7
Rsa1.0_01147.1.g23953.t1	gb|EOA17250.1| hypothetical protein CARUB_v10005524mg, partial [Capsella rubella]	226	262	5.00E-76	115.9	64.2	77.0	hypothetical protein CARUB_v10005524mg, partial	gbpln	Capsella rubella	AT4G17900.1 | Symbols: | PLATZ transcription factor family protein | chr4:9946046-9947697 FORWARD LENGTH=227	226	227	2.00E-78	100.4	65.0	76.5
Rsa1.0_01147.1.g23954.t1	ref|NP_199482.1| Tetraspanin family protein [Arabidopsis thaliana] gi|75262522|sp|Q9FIQ5.1|TRN2_ARATH RecName: Full=Protein TORNADO 2; AltName: Full=Protein EKEKO; AltName: Full=TETRASPANIN-1 gi|9758506|dbj|BAB08914.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] gi|56381915|gb|AAV85676.1| At5g46700 [Arabidopsis thaliana] gi|110740669|dbj|BAE98437.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] gi|332008032|gb|AED95415.1| Tetraspanin family protein [Arabidopsis thaliana]	255	269	1.00E-107	105.5	82.0	90.6	Tetraspanin family protein	gbpln	Arabidopsis thaliana	AT5G46700.1 | Symbols: TET1, TRN2 | Tetraspanin family protein | chr5:18951035-18952439 FORWARD LENGTH=269	255	269	1.00E-109	105.5	82.0	90.6
Rsa1.0_01147.1.g23955.t1	gb|EOA34273.1| hypothetical protein CARUB_v10021787mg [Capsella rubella]	289	336	1.00E-156	116.3	92.0	97.2	hypothetical protein CARUB_v10021787mg	gbpln	Capsella rubella	AT1G54870.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:20459011-20460417 FORWARD LENGTH=335	289	335	1.00E-158	115.9	91.7	96.9

Rsa1.0_01147.1.g23956.t1	ref|NP_568665.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|223635755|sp|Q56XR6.2|PP421_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g46680 gi|332008030|gb|AED95413.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	468	468	0	100.0	83.8	92.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G46680.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr5:18941118-18942524 FORWARD LENGTH=468	468	468	0	100.0	83.8	92.5
Rsa1.0_01147.1.g23957.t1	ref|NP_199475.1| AP-2 complex subunit mu-1 [Arabidopsis thaliana] gi|297794577|ref|XP_002865173.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|2271477|gb|AAB88283.1| AP47/50p [Arabidopsis thaliana] gi|9758499|dbj|BAB08907.1| AP47/50p [Arabidopsis thaliana] gi|297311008|gb|EFH41432.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata] gi|332008024|gb|AED95407.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis thaliana]	438	438	0	100.0	99.3	100.0	AP-2 complex subunit mu-1	gbpln	Arabidopsis lyrata	AT5G46630.1 | Symbols: | Clathrin adaptor complexes medium subunit family protein | chr5:18920580-18923252 FORWARD LENGTH=438	438	438	0	100.0	99.3	100.0
Rsa1.0_01147.1.g23958.t1	gb|ABD64968.1| hypothetical protein 25.t00005 [Brassica oleracea]	268	299	8.00E-75	111.6	56.3	70.5	hypothetical protein 25.t00005	gbpln	Brassica oleracea	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	268	264	8.00E-71	98.5	53.4	69.0
Rsa1.0_01148.1.g23959.t1	gb|EOA31492.1| hypothetical protein CARUB_v10014678mg [Capsella rubella]	117	200	8.00E-54	170.9	93.2	97.4	hypothetical protein CARUB_v10014678mg	gbpln	Capsella rubella	AT3G15190.1 | Symbols: | chloroplast 30S ribosomal protein S20, putative | chr3:5116216-5117412 FORWARD LENGTH=202	117	202	4.00E-54	172.6	93.2	95.7
Rsa1.0_01148.1.g23960.t1	ref|NP_188138.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75273407|sp|Q9LIL5.1|PP233_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At3g15200 gi|11994509|dbj|BAB02574.1| unnamed protein product [Arabidopsis thaliana] gi|332642110|gb|AEE75631.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	522	523	0	100.2	76.2	86.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G15200.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:5117489-5119060 REVERSE LENGTH=523	522	523	0	100.2	76.2	86.6
Rsa1.0_01148.1.g23961.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1170	1213	0	103.7	36.9	54.5	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1170	626	4.00E-59	53.5	11.6	19.7
Rsa1.0_01148.1.g23962.t1	ref|XP_002882920.1| ATERF-4/ATERF4/ERF4/RAP2.5 [Arabidopsis lyrata subsp. lyrata] gi|297328760|gb|EFH59179.1| ATERF-4/ATERF4/ERF4/RAP2.5 [Arabidopsis lyrata subsp. lyrata]	219	219	1.00E-85	100.0	79.9	84.9	ATERF-4/ATERF4/ERF4/RAP2.5	gbpln	Arabidopsis lyrata	AT3G15210.1 | Symbols: ATERF-4, ERF4, RAP2.5, ATERF4 | ethylene responsive element binding factor 4 | chr3:5121472-5122140 FORWARD LENGTH=222	219	222	3.00E-79	101.4	75.3	80.8
Rsa1.0_01148.1.g23963.t2	emb|CAA08758.1| BnMAP4K alpha2 [Brassica napus]	841	676	0	80.4	77.4	78.8	BnMAP4K alpha2	gbpln	Brassica napus	AT3G15220.1 | Symbols: | Protein kinase superfamily protein | chr3:5126899-5131752 REVERSE LENGTH=690	841	690	0	82.0	69.2	73.1
Rsa1.0_01148.1.g23964.t1	ref|XP_002882922.1| hypothetical protein ARALYDRAFT_478955 [Arabidopsis lyrata subsp. lyrata] gi|297328762|gb|EFH59181.1| hypothetical protein ARALYDRAFT_478955 [Arabidopsis lyrata subsp. lyrata]	370	360	0	97.3	85.4	88.6	hypothetical protein ARALYDRAFT_478955	gbpln	Arabidopsis lyrata	AT3G15240.2 | Symbols: | Serine/threonine-protein kinase WNK (With No Lysine)-related | chr3:5133681-5135797 FORWARD LENGTH=362	370	362	1.00E-175	97.8	83.5	87.3
Rsa1.0_01148.1.g23965.t1	ref|XP_002885076.1| hypothetical protein ARALYDRAFT_478956 [Arabidopsis lyrata subsp. lyrata] gi|297330916|gb|EFH61335.1| hypothetical protein ARALYDRAFT_478956 [Arabidopsis lyrata subsp. lyrata]	213	224	1.00E-63	105.2	74.6	80.8	hypothetical protein ARALYDRAFT_478956	gbpln	Arabidopsis lyrata	AT3G15250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53163.1); Has 409 Blast hits to 218 proteins in 63 species: Archae - 0; Bacteria - 22; Metazoa - 178; Fungi - 77; Plants - 38; Viruses - 1; Other Eukaryotes - 93 (source: NCBI BLink). | chr3:5136503-5137183 REVERSE LENGTH=226	213	226	1.00E-61	106.1	70.9	76.5
Rsa1.0_01148.1.g23966.t1	ref|XP_002882923.1| hypothetical protein ARALYDRAFT_478958 [Arabidopsis lyrata subsp. lyrata] gi|297328763|gb|EFH59182.1| hypothetical protein ARALYDRAFT_478958 [Arabidopsis lyrata subsp. lyrata]	290	289	1.00E-158	99.7	93.8	96.9	hypothetical protein ARALYDRAFT_478958	gbpln	Arabidopsis lyrata	AT3G15260.2 | Symbols: | Protein phosphatase 2C family protein | chr3:5138842-5140242 FORWARD LENGTH=289	290	289	1.00E-160	99.7	93.8	96.9

Rsa1.0_01148.1.g23967.t1	gb|EOA31451.1| hypothetical protein CARUB_v10014636mg, partial [Capsella rubella]	179	208	2.00E−81	116.2	82.1	89.9	hypothetical protein CARUB_v10014636mg, partial	gbpln	Capsella rubella	AT3G15270.1 | Symbols: SPL5 | squamosa promoter binding protein−like 5 | chr3:5140624−5141256 REVERSE LENGTH=181	179	181	2.00E−78	101.1	86.6	91.1
Rsa1.0_01148.1.g23968.t1	ref|NP_566504.1| uncharacterized protein [Arabidopsis thaliana] gi|9294255|dbj|BAB02157.1| unnamed protein product [Arabidopsis thaliana] gi|16974611|gb|AAL31208.1| AT3g15280/K7L4_8 [Arabidopsis thaliana] gi|21928105|gb|AAM78081.1| AT3g15280/K7L4_8 [Arabidopsis thaliana] gi|332642119|gb|AEE75640.1| uncharacterized protein AT3G15280 [Arabidopsis thaliana]	154	150	1.00E−54	97.4	73.4	80.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15280.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: L mature pollen stage, 4 anthesis, petal differentiation and expansion stage; Has 36 Blast hits to 36 proteins in 15 species: Archae − 0; Bacteria − 0; Metazoa − 1; Fungi − 2; Plants − 33; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:5144144−5144670 REVERSE LENGTH=150	154	150	3.00E−57	97.4	73.4	80.5
Rsa1.0_01148.1.g23969.t1	dbj|BAJ34596.1| unnamed protein product [Thellungiella halophila]	286	297	1.00E−152	103.8	93.0	96.9	unnamed protein product	----	----	AT3G15290.1 | Symbols: | 3−hydroxyacyl−CoA dehydrogenase family protein | chr3:5145054−5146613 FORWARD LENGTH=294	286	294	1.00E−151	102.8	90.9	95.5
Rsa1.0_01148.1.g23970.t1	ref|NP_188148.1| VQ motif−containing protein [Arabidopsis thaliana] gi|9294257|dbj|BAB02159.1| unnamed protein product [Arabidopsis thaliana] gi|38454098|gb|AAR20743.1| At3g15300 [Arabidopsis thaliana] gi|41349916|gb|AAS00343.1| At3g15300 [Arabidopsis thaliana] gi|332642121|gb|AEE75642.1| VQ motif−containing protein [Arabidopsis thaliana]	220	219	5.00E−77	99.5	76.4	81.8	VQ motif−containing protein	gbpln	Arabidopsis thaliana	AT3G15300.1 | Symbols: | VQ motif−containing protein | chr3:5147551−5148210 REVERSE LENGTH=219	220	219	2.00E−79	99.5	76.4	81.8
Rsa1.0_01148.1.g23971.t2	gb|AAD17398.1| putative non−LTR retroelement reverse transcriptase [Arabidopsis thaliana]	392	1225	7.00E−69	312.5	40.8	56.6	putative non−LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	392	575	1.00E−37	146.7	32.7	51.3
Rsa1.0_01148.1.g23972.t1	gb|EOA33180.1| hypothetical protein CARUB_v100133261mg [Capsella rubella] gi|482568992|gb|EOA33181.1| hypothetical protein CARUB_v100133261mg [Capsella rubella] gi|482568993|gb|EOA33182.1| hypothetical protein CARUB_v100133261mg [Capsella rubella]	589	575	0	97.6	68.1	78.9	hypothetical protein CARUB_v100133261mg	gbpln	Capsella rubella	AT3G15340.1 | Symbols: PPI2 | proton pump interactor 2 | chr3:5160016−5162305 REVERSE LENGTH=589	589	589	0	100.0	66.6	79.3
Rsa1.0_01149.1.g23973.t1	ref|XP_002869066.1| hypothetical protein ARALYDRAFT_491076 [Arabidopsis lyrata subsp. lyrata] gi|297314902|gb|EFH45325.1| hypothetical protein ARALYDRAFT_491076 [Arabidopsis lyrata subsp. lyrata]	322	325	2.33E−156	100.9	86.0	94.1	hypothetical protein ARALYDRAFT_491076	gbpln	Arabidopsis lyrata	AT4G35720.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16927972−16928949 FORWARD LENGTH=325	322	325	1.00E−147	100.9	85.1	93.8
Rsa1.0_01149.1.g23974.t1	gb|ABD64940.1| hypothetical protein 24.t00018 [Brassica oleracea]	138	380	8.00E−26	275.4	48.6	56.5	hypothetical protein 24.t00018	gbpln	Brassica oleracea	AT5G41220.1 | Symbols: ATGSTT3, GST10C, GSTT3 | glutathione S−transferase THETA 3 | chr5:16494560−16496969 REVERSE LENGTH=590	138	590	2.00E−21	427.5	36.2	52.9
Rsa1.0_01149.1.g23975.t1	ref|XP_002869069.1| hypothetical protein ARALYDRAFT_912802 [Arabidopsis lyrata subsp. lyrata] gi|297314905|gb|EFH45328.1| hypothetical protein ARALYDRAFT_912802 [Arabidopsis lyrata subsp. lyrata]	175	283	2.00E−72	161.7	81.1	88.0	hypothetical protein ARALYDRAFT_912802	gbpln	Arabidopsis lyrata	AT4G35690.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16921886−16922740 FORWARD LENGTH=284	175	284	2.00E−70	162.3	75.4	80.6
Rsa1.0_01149.1.g23976.t1	ref|NP_195293.1| uncharacterized protein [Arabidopsis thaliana] gi|3367586|emb|CAA20038.1| putative protein [Arabidopsis thaliana] gi|7270519|emb|CAB80284.1| putative protein [Arabidopsis thaliana] gi|332661148|gb|AEE86548.1| uncharacterized protein AT4G35680 [Arabidopsis thaliana]	307	503	1.00E−112	163.8	74.9	83.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G35680.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16917938−16919749 FORWARD LENGTH=503	307	503	1.00E−115	163.8	74.9	83.4
Rsa1.0_01149.1.g23977.t1	ref|NP_195292.2| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana] gi|332661147|gb|AEE86547.1| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	394	394	1.00E−166	100.0	73.1	84.3	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	gbpln	Arabidopsis thaliana	AT4G35670.1 | Symbols: | Pectin lyase−like superfamily protein | chr4:16914996−16917201 FORWARD LENGTH=394	394	394	1.00E−169	100.0	73.1	84.3

Rsa1.0_01149.1.g23978.t1	ref|NP_189164.1| Ribonuclease H-like protein [Arabidopsis thaliana] gi|9294184|dbj|BAB02086.1| reverse transcriptase-like protein [Arabidopsis thaliana] gi|332643482|gb|AEE77003.1| Ribonuclease H-like protein [Arabidopsis thaliana]	342	343	2.00E-82	100.3	43.9	62.0	Ribonuclease H-like protein	gbpln	Arabidopsis thaliana	AT3G25270.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:9203934-9204965 REVERSE LENGTH=343	342	343	6.00E-85	100.3	43.9	62.0
Rsa1.0_01149.1.g23979.t1	ref|XP_002869072.1| hypothetical protein ARALYDRAFT_491080 [Arabidopsis lyrata subsp. lyrata] gi|297314908|gb|EFH45331.1| hypothetical protein ARALYDRAFT_491080 [Arabidopsis lyrata subsp. lyrata]	249	286	1.00E-97	114.9	71.9	81.1	hypothetical protein ARALYDRAFT_491080	gbpln	Arabidopsis lyrata	AT4G35660.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16912792-16913658 FORWARD LENGTH=288	249	288	1.00E-92	115.7	68.3	78.7
Rsa1.0_01149.1.g23980.t1	gb|EOA16659.1| hypothetical protein CARUB_v10004843mg [Capsella rubella]	403	434	1.00E-178	107.7	84.1	88.8	hypothetical protein CARUB_v10004843mg	gbpln	Capsella rubella	AT4G35620.1 | Symbols: CYCB2;2 | Cyclin B2;2 | chr4:16901744-16903766 FORWARD LENGTH=429	403	429	1.00E-174	106.5	84.4	87.6
Rsa1.0_01149.1.g23981.t1	ref|NP_195285.3| putative serine/threonine-protein kinase Cx32 [Arabidopsis thaliana] gi|49066036|sp|P27450.2|CX32_ARATH RecName: Full=Probable serine/threonine-protein kinase Cx32, chloroplastic; Flags: Precursor gi|17529234|gb|AAL38844.1| putative protein kinase [Arabidopsis thaliana] gi|20465931|gb|AAM20151.1| putative protein kinase [Arabidopsis thaliana] gi|332661138|gb|AEE86538.1| putative serine/threonine-protein kinase Cx32 [Arabidopsis thaliana]	364	419	1.00E-151	115.1	76.1	86.0	putative serine/threonine-protein kinase Cx32	gbpln	Arabidopsis thaliana	AT4G35600.1 | Symbols: CONNEXIN 32 | Protein kinase superfamily protein | chr4:16896448-16898714 FORWARD LENGTH=419	364	419	1.00E-154	115.1	76.1	86.0
Rsa1.0_01149.1.g23982.t1	gb|EOA16696.1| hypothetical protein CARUB_v10004888mg [Capsella rubella]	448	424	0	94.6	77.9	85.9	hypothetical protein CARUB_v10004888mg	gbpln	Capsella rubella	AT4G35600.2 | Symbols: CONNEXIN 32 | Protein kinase superfamily protein | chr4:16896448-16898714 FORWARD LENGTH=420	448	420	0	93.8	77.2	85.0
Rsa1.0_01149.1.g23983.t1	ref|XP_002886121.1| hypothetical protein ARALYDRAFT_480649 [Arabidopsis lyrata subsp. lyrata] gi|297331961|gb|EFH62380.1| hypothetical protein ARALYDRAFT_480649 [Arabidopsis lyrata subsp. lyrata]	205	143	2.00E-51	69.8	51.2	59.5	hypothetical protein ARALYDRAFT_480649	gbpln	Arabidopsis lyrata	AT2G17560.2 | Symbols: HMGB4, NFD4, NFD04 | high mobility group B4 | chr2:7642486-7643468 REVERSE LENGTH=138	205	138	1.00E-51	67.3	49.8	60.0
Rsa1.0_01149.1.g23984.t1	gb|EOA18736.1| hypothetical protein CARUB_v10007318mg [Capsella rubella]	1039	1046	0	100.7	83.0	90.4	hypothetical protein CARUB_v10007318mg	gbpln	Capsella rubella	AT4G35560.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:16881562-16886878 FORWARD LENGTH=1049	1039	1049	0	101.0	83.4	90.4
Rsa1.0_01149.1.g23985.t1	ref|XP_002867072.1| ring-H2 finger A3B [Arabidopsis lyrata subsp. lyrata] gi|297312908|gb|EFH43331.1| ring-H2 finger A3B [Arabidopsis lyrata subsp. lyrata]	196	200	2.00E-84	102.0	85.2	92.9	ring-H2 finger A3B	gbpln	Arabidopsis lyrata	AT4G35480.1 | Symbols: RHA3B | RING-H2 finger A3B | chr4:16852233-16852835 REVERSE LENGTH=200	196	200	4.00E-85	102.0	84.7	92.3
Rsa1.0_01149.1.g23986.t2	ref|XP_002869086.1| NADPH-dependent thioredoxin reductase 1 [Arabidopsis lyrata subsp. lyrata] gi|297314922|gb|EFH45345.1| NADPH-dependent thioredoxin reductase 1 [Arabidopsis lyrata subsp. lyrata]	839	375	1.00E-164	44.7	35.9	39.1	NADPH-dependent thioredoxin reductase 1	gbpln	Arabidopsis lyrata	AT4G35460.1 | Symbols: ATNTRB, NTRB, NTR1 | NADPH-dependent thioredoxin reductase B | chr4:16842218-16843740 FORWARD LENGTH=375	839	375	1.00E-164	44.7	35.9	39.0
Rsa1.0_01149.1.g23987.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01149.1.g23988.t1	ref|XP_002877718.1| cytokinin-independent 1 [Arabidopsis lyrata subsp. lyrata] gi|297323556|gb|EFH53977.1| cytokinin-independent 1 [Arabidopsis lyrata subsp. lyrata]	953	1063	0	111.5	68.7	78.1	cytokinin-independent 1	gbpln	Arabidopsis lyrata	AT2G47430.1 | Symbols: CKI1 | Signal transduction histidine kinase | chr2:19459167-19463122 REVERSE LENGTH=1122	953	1122	0	117.7	59.5	65.9
Rsa1.0_01149.1.g23989.t1	gb|AAT70424.1| At4g35335 [Arabidopsis thaliana] gi|51971024|dbj|BAD44204.1| unnamed protein product [Arabidopsis thaliana] gi|53828601|gb|AAU94410.1| At4g35335 [Arabidopsis thaliana]	380	352	0	92.6	88.9	90.8	At4g35335	gbpln	Arabidopsis thaliana	AT4G35335.1 | Symbols: | Nucleotide-sugar transporter family protein | chr4:16807286-16810015 FORWARD LENGTH=352	380	352	0	92.6	88.7	90.5
Rsa1.0_01149.1.g23990.t1	gb|AAZ32751.1| calcium dependent kinase 5 [Brassica oleracea var. alboglabra]	552	535	0	96.9	93.3	95.5	calcium dependent kinase 5	gbpln	Brassica oleracea	AT4G35310.1 | Symbols: CPK5, ATCPK5 | calmodulin-domain protein kinase 5 | chr4:16802436-16804628 FORWARD LENGTH=556	552	556	0	100.7	91.1	95.1

Rsa1.0_01149.1.g23991.t1	ref|NP_195254.1| C2H2-like zinc finger protein [Arabidopsis thaliana] gi|75318572|sp|O65499.1|ZAT3_ARATH RecName: Full=Zinc finger protein ZAT3; AltName: Full=Protein DUO1-ACTIVATED ZINC FINGER 2 gi|3080422|emb|CAA18741.1| putative zinc-finger protein [Arabidopsis thaliana] gi|7270480|emb|CAB80245.1| putative zinc-finger protein [Arabidopsis thaliana] gi|91806770|gb|ABE66112.1| zinc finger family protein [Arabidopsis thaliana] gi|225898853|dbj|BAH30557.1| hypothetical protein [Arabidopsis thaliana] gi|332661089|gb|AEE86489.1| C2H2-like zinc finger protein [Arabidopsis thaliana]	289	284	1.00E-113	98.3	75.1	81.7	C2H2-like zinc finger protein	gbpln	Arabidopsis thaliana	AT4G35280.1 | Symbols: | C2H2-like zinc finger protein | chr4:16787429-16788283 REVERSE LENGTH=284	289	284	1.00E-115	98.3	75.1	81.7
Rsa1.0_01150.1.g23992.t1	#	#	#	#	#	#	#	-	----	----	AT1G67800.2 | Symbols: | Copine (Calcium-dependent phospholipid-binding protein) family | chr1:25421029-25423297 REVERSE LENGTH=453	65	453	8.00E-12	696.9	46.2	47.7
Rsa1.0_01150.1.g23993.t5	ref|NP_849630.3| protein prenylyltransferase [Arabidopsis thaliana] gi|3540189|gb|AAC34339.1| Hypothetical protein [Arabidopsis thaliana] gi|332190420|gb|AEE28541.1| protein prenylyltransferase [Arabidopsis thaliana]	437	420	1.00E-171	96.1	72.1	80.1	protein prenylyltransferase	gbpln	Arabidopsis thaliana	AT1G10095.1 | Symbols: | Protein prenylyltransferase superfamily protein | chr1:3297478-3300353 REVERSE LENGTH=420	437	420	1.00E-174	96.1	72.1	80.1
Rsa1.0_01150.1.g23994.t1	dbj|BAJ34293.1| unnamed protein product [Thellungiella halophila]	433	455	0	105.1	97.0	98.8	unnamed protein product	----	----	AT5G44370.1 | Symbols: PHT4;6 | phosphate transporter 4;6 | chr5:17875147-17876445 REVERSE LENGTH=432	433	432	0	99.8	96.5	98.4
Rsa1.0_01150.1.g23995.t1	gb|EOA14351.1| hypothetical protein CARUB_v10027532mg [Capsella rubella]	547	531	0	97.1	84.3	90.5	hypothetical protein CARUB_v10027532mg	gbpln	Capsella rubella	AT5G44360.1 | Symbols: | FAD-binding Berberine family protein | chr5:17872100-17873698 REVERSE LENGTH=532	547	532	0	97.3	83.7	89.9
Rsa1.0_01150.1.g23996.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	754	1142	1.00E-135	151.5	32.6	45.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	754	575	4.00E-94	76.3	24.9	39.9
Rsa1.0_01150.1.g23997.t1	ref|NP_001118664.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|9294424|dbj|BAB02544.1| unnamed protein product [Arabidopsis thaliana] gi|332642743|gb|AEE76264.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana]	306	307	3.00E-96	100.3	59.8	74.2	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G19595.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr3:6808585-6809508 REVERSE LENGTH=307	306	307	7.00E-99	100.3	59.8	74.2
Rsa1.0_01150.1.g23998.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01150.1.g23999.t1	ref|NP_199252.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana] gi|10176894|dbj|BAB10124.1| berberine bridge enzyme-like protein [Arabidopsis thaliana] gi|332007721|gb|AED95104.1| FAD-binding and BBE domain-containing protein [Arabidopsis thaliana]	543	542	0	99.8	70.7	82.5	FAD-binding and BBE domain-containing protein	gbpln	Arabidopsis thaliana	AT5G44390.1 | Symbols: | FAD-binding Berberine family protein | chr5:17882329-17884906 REVERSE LENGTH=542	543	542	0	99.8	70.7	82.5
Rsa1.0_01150.1.g24000.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01151.1.g24001.t1	gb|EOA40235.1| hypothetical protein CARUB_v10008955mg [Capsella rubella]	114	493	1.00E-48	432.5	83.3	88.6	hypothetical protein CARUB_v10008955mg	gbpln	Capsella rubella	AT1G08210.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:2577119-2580581 REVERSE LENGTH=492	114	492	2.00E-49	431.6	79.8	87.7
Rsa1.0_01151.1.g24002.t1	ref|NP_172306.1| WIP domain protein 3 [Arabidopsis thaliana] gi|6579204|gb|AAF18247.1|AC011438_9 T23G18.15 [Arabidopsis thaliana] gi|18027014|gb|AAL55723.1|AF254448_1 WIP3 protein [Arabidopsis thaliana] gi|20258782|gb|AAM13913.1| unknown protein [Arabidopsis thaliana] gi|26452714|dbj|BAC43439.1| unknown protein [Arabidopsis thaliana] gi|332190149|gb|AEE28270.1| WIP domain protein 3 [Arabidopsis thaliana]	339	337	1.00E-160	99.4	84.1	90.3	WIP domain protein 3	gbpln	Arabidopsis thaliana	AT1G08290.1 | Symbols: WIP3 | WIP domain protein 3 | chr1:2610680-2613180 REVERSE LENGTH=337	339	337	1.00E-163	99.4	84.1	90.3

Rsa1.0_01151.1.g24003.t3	ref|NP_563810.2| bZIP transcription factor-like protein [Arabidopsis thaliana] gi|79317351|ref|NP_001030999.1| bZIP transcription factor-like protein [Arabidopsis thaliana] gi|14272369|emb|CAC40022.1| bZIP transcription factor [Arabidopsis thaliana] gi|309952053|gb|ADO95300.1| bZIP21 [Arabidopsis thaliana] gi|332190154|gb|AEE28275.1| bZIP transcription factor-like protein [Arabidopsis thaliana] gi|332190156|gb|AEE28277.1| bZIP transcription factor-like protein [Arabidopsis thaliana]	479	481	0	100.4	89.4	93.9	bZIP transcription factor-like protein	gbpln	Arabidopsis thaliana	AT1G08320.3 | Symbols: TGA9, bZIP21 | bZIP transcription factor family protein | chr1:2622113-2627451 REVERSE LENGTH=481	479	481	0	100.4	89.4	93.9
Rsa1.0_01151.1.g24004.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01151.1.g24005.t1	ref|NP_172310.1| Rho GTPase activating protein with PAK-box/P21-Rho-binding domain [Arabidopsis thaliana] gi|46931246|gb|AAT06427.1| At1g08340 [Arabidopsis thaliana] gi|48958519|gb|AAT47812.1| At1g08340 [Arabidopsis thaliana] gi|110736318|dbj|BAF00129.1| hypothetical protein [Arabidopsis thaliana] gi|332190157|gb|AEE28278.1| Rho GTPase activating protein with PAK-box/P21-Rho-binding domain [Arabidopsis thaliana]	295	331	4.00E-79	112.2	61.0	70.2	Rho GTPase activating protein with PAK-box/P21-Rho-binding domain	gbpln	Arabidopsis thaliana	AT1G08340.1 | Symbols: | Rho GTPase activating protein with PAK-box/P21-Rho-binding domain | chr1:2631308-2632669 FORWARD LENGTH=331	295	331	1.00E-81	112.2	61.0	70.2
Rsa1.0_01151.1.g24006.t1	gb|EOA38046.1| hypothetical protein CARUB_v10009516mg [Capsella rubella]	381	365	1.00E-141	95.8	74.8	82.7	hypothetical protein CARUB_v10009516mg	gbpln	Capsella rubella	AT1G08370.1 | Symbols: DCP1, ATDCP1 | decapping 1 | chr1:2638355-2640367 FORWARD LENGTH=367	381	367	1.00E-133	96.3	72.4	80.3
Rsa1.0_01151.1.g24007.t1	dbj|BAJ33638.1| unnamed protein product [Thellungiella halophila]	145	142	1.00E-67	97.9	86.9	94.5	unnamed protein product	----	----	AT1G08380.1 | Symbols: PSAO | photosystem I subunit O | chr1:2641004-2641739 REVERSE LENGTH=140	145	140	1.00E-68	96.6	85.5	93.1
Rsa1.0_01151.1.g24008.t2	ref|XP_002889691.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297335533|gb|EFH65950.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]	538	583	0	108.4	88.5	93.9	GTP-binding family protein	gbpln	Arabidopsis lyrata	AT1G08410.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:2646307-2649106 FORWARD LENGTH=589	538	589	0	109.5	88.5	93.3
Rsa1.0_01151.1.g24009.t1	ref|XP_002892457.1| hypothetical protein ARALYDRAFT_888076 [Arabidopsis lyrata subsp. lyrata] gi|297338299|gb|EFH68716.1| hypothetical protein ARALYDRAFT_888076 [Arabidopsis lyrata subsp. lyrata]	429	423	0	98.6	91.1	93.9	hypothetical protein ARALYDRAFT_888076	gbpln	Arabidopsis lyrata	AT1G08450.1 | Symbols: CRT3, PSL1, EBS2, AtCRT3 | calreticulin 3 | chr1:2668008-2671800 REVERSE LENGTH=424	429	424	0	98.8	91.1	93.5
Rsa1.0_01151.1.g24010.t1	ref|NP_563817.1| histone deacetylase 8 [Arabidopsis thaliana] gi|75250015|sp|Q94EJ2.1|HDA8_ARATH RecName: Full=Histone deacetylase 8 gi|15294162|gb|AAK95258.1|AF410272_1 At1g08460/T27G7_7 [Arabidopsis thaliana] gi|20453297|gb|AAM19887.1| At1g08460/T27G7_7 [Arabidopsis thaliana] gi|21360988|gb|AAM49769.1| HDA8 [Arabidopsis thaliana] gi|332190173|gb|AEE28294.1| histone deacetylase 8 [Arabidopsis thaliana]	386	377	0	97.7	87.6	92.7	histone deacetylase 8	gbpln	Arabidopsis thaliana	AT1G08460.1 | Symbols: HDA08, HDA8, ATHDA8 | histone deacetylase 8 | chr1:2672527-2674469 FORWARD LENGTH=377	386	377	0	97.7	87.6	92.7
Rsa1.0_01151.1.g24011.t1	gb|EOA36256.1| hypothetical protein CARUB_v10010384mg [Capsella rubella]	142	188	1.00E-66	132.4	87.3	91.5	hypothetical protein CARUB_v10010384mg	gbpln	Capsella rubella	AT1G08465.1 | Symbols: YAB2 | Plant-specific transcription factor YABBY family protein | chr1:2676033-2679382 FORWARD LENGTH=184	142	184	2.00E-62	129.6	81.0	87.3
Rsa1.0_01152.1.g24012.t2	ref|XP_002879327.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297325166|gb|EFH55586.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	305	179	8.00E-45	58.7	29.2	35.1	invertase/pectin methylesterase inhibitor family protein	gbpln	Arabidopsis lyrata	AT2G31430.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr2:13396293-13396911 FORWARD LENGTH=179	305	179	1.00E-46	58.7	28.9	35.1
Rsa1.0_01152.1.g24013.t2	dbj|BAB01431.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	467	637	5.00E-58	136.4	27.2	37.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	467	295	1.00E-46	63.2	21.8	32.1
Rsa1.0_01152.1.g24014.t1	gb|AFJ66167.1| hypothetical protein 11M19.11 [Arabidopsis halleri]	499	502	0	100.6	94.8	97.2	hypothetical protein 11M19.11	gbpln	Arabidopsis halleri	AT5G51050.1 | Symbols: | Mitochondrial substrate carrier family protein | chr5:20753381-20755714 FORWARD LENGTH=487	499	487	0	97.6	91.8	93.8
Rsa1.0_01152.1.g24015.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01152.1.g24016.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01152.1.g24017.t1	ref|NP_199917.1| uncharacterized protein [Arabidopsis thaliana] gi|9758251|dbj|BAB08750.1| unnamed protein product [Arabidopsis thaliana] gi|98960953|gb|ABF58960.1| At5g51040 [Arabidopsis thaliana] gi|110738284|dbj|BAF01071.1| hypothetical protein [Arabidopsis thaliana] gi|332008641|gb|AED96024.1| uncharacterized protein AT5G51040 [Arabidopsis thaliana]	86	188	2.00E-37	218.6	87.2	91.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G51040.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF339 (InterPro:IPR005631); Has 532 Blast hits to 532 proteins in 207 species: Archae - 0; Bacteria - 285; Metazoa - 16; Fungi - 41; Plants - 40; Viruses - 0; Other Eukaryotes - 150 (source: NCBI BLink). | chr5:20750700-20751790 FORWARD LENGTH=188	86	188	3.00E-40	218.6	87.2	91.9
Rsa1.0_01152.1.g24018.t1	dbj|BAB10837.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1454	1462	0	100.6	68.2	79.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1454	1262	1.00E-134	86.8	16.4	23.3
Rsa1.0_01152.1.g24019.t1	gb|EOA16537.1| hypothetical protein CARUB_v10004697mg [Capsella rubella]	368	484	0	131.5	86.4	92.9	hypothetical protein CARUB_v10004697mg	gbpln	Capsella rubella	AT4G32360.1 | Symbols: | Pyridine nucleotide-disulphide oxidoreductase family protein | chr4:15621550-15624711 FORWARD LENGTH=483	368	483	0	131.3	85.6	91.8
Rsa1.0_01153.1.g24020.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01153.1.g24021.t1	gb|EOA30900.1| hypothetical protein CARUB_v10014047mg [Capsella rubella]	361	359	1.00E-134	99.4	70.9	77.3	hypothetical protein CARUB_v10014047mg	gbpln	Capsella rubella	AT3G29430.1 | Symbols: | Terpenoid synthases superfamily protein | chr3:11311427-11312604 FORWARD LENGTH=357	361	357	1.00E-134	98.9	72.3	80.1
Rsa1.0_01153.1.g24022.t1	dbj|BAJ34446.1| unnamed protein product [Thellungiella halophila]	154	149	3.00E-59	96.8	76.6	88.3	unnamed protein product	----	----	AT3G14560.1 | Symbols: | unknown protein; Has 6 Blast hits to 6 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4889368-4889832 FORWARD LENGTH=154	154	154	9.00E-58	100.0	76.0	87.0
Rsa1.0_01153.1.g24023.t1	gb|EOA29501.1| hypothetical protein CARUB_v10013073mg [Capsella rubella]	686	718	0	104.7	76.7	84.3	hypothetical protein CARUB_v10013073mg	gbpln	Capsella rubella	AT1G53590.1 | Symbols: NTMC2TYPE6.1, NTMC2T6.1 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:19996556-20000127 FORWARD LENGTH=751	686	751	0	109.5	66.6	77.7
Rsa1.0_01153.1.g24024.t1	ref|NP_188079.1| cytochrome P450, family 72, subfamily A, polypeptide 7 [Arabidopsis thaliana] gi|9294383|dbj|BAB02393.1| cytochrome P450 [Arabidopsis thaliana] gi|18252155|gb|AAL61910.1| cytochrome P450 [Arabidopsis thaliana] gi|28059362|gb|AAO30051.1| cytochrome P450 [Arabidopsis thaliana] gi|332642026|gb|AEE75547.1| cytochrome P450, family 72, subfamily A, polypeptide 7 [Arabidopsis thaliana]	509	512	0	100.6	73.7	86.4	cytochrome P450, family 72, subfamily A, polypeptide 7	gbpln	Arabidopsis thaliana	AT3G14610.1 | Symbols: CYP72A7 | cytochrome P450, family 72, subfamily A, polypeptide 7 | chr3:4912565-4914503 FORWARD LENGTH=512	509	512	0	100.6	73.7	86.4
Rsa1.0_01153.1.g24025.t2	ref|NP_188079.1| cytochrome P450, family 72, subfamily A, polypeptide 7 [Arabidopsis thaliana] gi|9294383|dbj|BAB02393.1| cytochrome P450 [Arabidopsis thaliana] gi|18252155|gb|AAL61910.1| cytochrome P450 [Arabidopsis thaliana] gi|28059362|gb|AAO30051.1| cytochrome P450 [Arabidopsis thaliana] gi|332642026|gb|AEE75547.1| cytochrome P450, family 72, subfamily A, polypeptide 7 [Arabidopsis thaliana]	442	512	0	115.8	73.8	85.5	cytochrome P450, family 72, subfamily A, polypeptide 7	gbpln	Arabidopsis thaliana	AT3G14610.1 | Symbols: CYP72A7 | cytochrome P450, family 72, subfamily A, polypeptide 7 | chr3:4912565-4914503 FORWARD LENGTH=512	442	512	0	115.8	73.8	85.5
Rsa1.0_01153.1.g24026.t1	ref|XP_002882888.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata] gi|297328728|gb|EFH59147.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata]	513	512	0	99.8	86.5	92.2	CYP72A15	gbpln	Arabidopsis lyrata	AT3G14690.1 | Symbols: CYP72A15 | cytochrome P450, family 72, subfamily A, polypeptide 15 | chr3:4937410-4939310 FORWARD LENGTH=512	513	512	0	99.8	85.8	91.8
Rsa1.0_01153.1.g24027.t1	ref|XP_002882888.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata] gi|297328728|gb|EFH59147.1| CYP72A15 [Arabidopsis lyrata subsp. lyrata]	512	512	0	100.0	84.0	91.2	CYP72A15	gbpln	Arabidopsis lyrata	AT3G14690.1 | Symbols: CYP72A15 | cytochrome P450, family 72, subfamily A, polypeptide 15 | chr3:4937410-4939310 FORWARD LENGTH=512	512	512	0	100.0	82.2	90.4
Rsa1.0_01153.1.g24028.t1	gb|EOA30165.1| hypothetical protein CARUB_v10013281mg [Capsella rubella]	601	598	0	99.5	91.0	94.7	hypothetical protein CARUB_v10013281mg	gbpln	Capsella rubella	AT3G14720.1 | Symbols: ATMPK19, MPK19 | MAP kinase 19 | chr3:4946057-4948906 FORWARD LENGTH=598	601	598	0	99.5	91.0	94.5

Rsa1.0_01153.1.g24029.t1	ref|XP_002885052.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330892|gb|EFH61311.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	660	652	0	98.8	74.5	84.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G14730.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:4949385-4951346 REVERSE LENGTH=653	660	653	0	98.9	74.5	85.0
Rsa1.0_01153.1.g24030.t1	ref|NP_188094.2| uncharacterized protein [Arabidopsis thaliana] gi|11994586|dbj|BAB02641.1| unnamed protein product [Arabidopsis thaliana] gi|18252977|gb|AAL62415.1| unknown protein [Arabidopsis thaliana] gi|21389655|gb|AAM48026.1| unknown protein [Arabidopsis thaliana] gi|332642043|gb|AEE75564.1| uncharacterized protein AT3G14760 [Arabidopsis thaliana]	183	168	2.00E-62	91.8	71.0	75.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G14760.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: LP.04 four leaves visible, LP.02 two leaves visible; Has 63 Blast hits to 63 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4956440-4957045 FORWARD LENGTH=168	183	168	8.00E-65	91.8	71.0	75.4
Rsa1.0_01153.1.g24031.t1	ref|NP_566493.1| nodulin MtN3-like protein [Arabidopsis thaliana] gi|75273203|sp|Q9LH79.1|SWET2_ARATH RecName: Full=Bidirectional sugar transporter SWEET2; Short=AtSWEET2 gi|11994587|dbj|BAB02642.1| MtN3-like protein [Arabidopsis thaliana] gi|15809923|gb|AAL06889.1| AT3g14770/T21E2_2 [Arabidopsis thaliana] gi|17978879|gb|AAL47411.1| AT3g14770/T21E2_2 [Arabidopsis thaliana] gi|332642044|gb|AEE75565.1| bidirectional sugar transporter SWEET2 [Arabidopsis thaliana]	236	236	1.00E-111	100.0	86.0	93.6	nodulin MtN3-like protein	gbpln	Arabidopsis thaliana	AT3G14770.1 | Symbols: SWEET2, AtSWEET2 | Nodulin MtN3 family protein | chr3:4957787-4959202 REVERSE LENGTH=236	236	236	1.00E-113	100.0	86.0	93.6
Rsa1.0_01153.1.g24032.t1	gb|EOA30048.1| hypothetical protein CARUB_v10013153mg [Capsella rubella]	666	664	0	99.7	94.0	96.7	hypothetical protein CARUB_v10013153mg	gbpln	Capsella rubella	AT3G14790.1 | Symbols: RHM3, ATRHM3 | rhamnose biosynthesis 3 | chr3:4964791-4966875 FORWARD LENGTH=664	666	664	0	99.7	93.5	96.8
Rsa1.0_01154.1.g24033.t1	ref|NP_181377.2| uncharacterized protein [Arabidopsis thaliana] gi|61742655|gb|AAX55148.1| hypothetical protein At2g38430 [Arabidopsis thaliana] gi|330254442|gb|AEC09536.1| uncharacterized protein AT2G38430 [Arabidopsis thaliana]	391	393	1.00E-160	100.5	71.6	83.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G38430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54310.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:16092950-16094810 REVERSE LENGTH=393	391	393	1.00E-163	100.5	71.6	83.6
Rsa1.0_01154.1.g24034.t1	emb|CAG77504.1| peroxidase precursor [Raphanus sativus var. niger]	350	284	1.00E-164	81.1	80.6	80.6	peroxidase precursor	gbpln	Raphanus sativus	AT2G38390.1 | Symbols: | Peroxidase superfamily protein | chr2:16079726-16081381 FORWARD LENGTH=349	350	349	1.00E-161	99.7	77.4	84.6
Rsa1.0_01154.1.g24035.t1	emb|CAG77503.1| peroxidase precursor [Raphanus sativus var. niger]	350	350	0	100.0	99.7	99.7	peroxidase precursor	gbpln	Raphanus sativus	AT2G38390.1 | Symbols: | Peroxidase superfamily protein | chr2:16079726-16081381 FORWARD LENGTH=349	350	349	1.00E-162	99.7	82.6	87.4
Rsa1.0_01154.1.g24036.t1	gb|EOA26871.1| hypothetical protein CARUB_v10022963mg, partial [Capsella rubella]	514	536	1.00E-156	104.3	69.3	80.7	hypothetical protein CARUB_v10022963mg, partial	gbpln	Capsella rubella	AT2G38370.1 | Symbols: | Plant protein of unknown function (DUF827) | chr2:16072184-16074168 REVERSE LENGTH=522	514	522	1.00E-144	101.6	65.6	76.3
Rsa1.0_01154.1.g24037.t1	ref|NP_565888.1| trichome birefringence-like 34 protein [Arabidopsis thaliana] gi|13878095|gb|AAK44125.1|AF370310_1 unknown protein [Arabidopsis thaliana] gi|20197242|gb|AAC28772.2| expressed protein [Arabidopsis thaliana] gi|330254429|gb|AEC09523.1| trichome birefringence-like 34 protein [Arabidopsis thaliana]	413	410	0	99.3	83.1	90.6	trichome birefringence-like 34 protein	gbpln	Arabidopsis thaliana	AT2G38320.1 | Symbols: TBL34 | TRICHOME BIREFRINGENCE-LIKE 34 | chr2:16055488-16057874 FORWARD LENGTH=410	413	410	0	99.3	83.1	90.6
Rsa1.0_01154.1.g24038.t1	gb|EOA29053.1| hypothetical protein CARUB_v10025307mg [Capsella rubella]	204	207	2.00E-98	101.5	92.6	95.6	hypothetical protein CARUB_v10025307mg	gbpln	Capsella rubella	AT2G38310.1 | Symbols: PYL4, RCAR10 | PYR1-like 4 | chr2:16050251-16050874 FORWARD LENGTH=207	204	207	1.00E-100	101.5	92.6	95.6

Rsa1.0_01154.1.g24039.t2	ref|NP_198523.1| uncharacterized protein [Arabidopsis thaliana] gi|10177986|dbj|BAB11359.1| unnamed protein product [Arabidopsis thaliana] gi|34365659|gb|AAQ65141.1| At5g37070 [Arabidopsis thaliana] gi|51970366|dbj|BAD43875.1| putative protein [Arabidopsis thaliana] gi|51971132|dbj|BAD44258.1| putative protein [Arabidopsis thaliana] gi|332006761|gb|AED94144.1| uncharacterized protein AT5G37070 [Arabidopsis thaliana]	166	170	8.00E−89	102.4	96.4	99.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G37070.1 | Symbols: | Protein of unknown function, DUF538 | chr5:14651091−14652147 FORWARD LENGTH=170	166	170	3.00E−91	102.4	96.4	99.4
Rsa1.0_01154.1.g24040.t1	dbj|BAB02422.1| unnamed protein product [Arabidopsis thaliana]	1166	390	3.00E−35	33.4	7.1	8.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G12775.1 | Symbols: | ubiquitin−conjugating enzyme family protein | chr3:4059772−4060944 FORWARD LENGTH=362	1166	362	6.00E−37	31.0	6.9	8.4
Rsa1.0_01154.1.g24041.t1	dbj|BAJ33778.1| unnamed protein product [Thellungiella halophila]	488	490	0	100.4	93.0	95.1	unnamed protein product	−−−−	−−−−	AT2G38290.1 | Symbols: ATAMT2, AMT2;1, AMT2 | ammonium transporter 2 | chr2:16039672−16042291 REVERSE LENGTH=475	488	475	0	97.3	89.1	93.0
Rsa1.0_01155.1.g24042.t1	ref|NP_564021.1| lipoxygenase 3 [Arabidopsis thaliana] gi|75264086|sp|Q9LNR3.1|LOX3_ARATH RecName: Full=Lipoxygenase 3, chloroplastic; Short=AtLOX3; Flags: Precursor gi|8778453|gb|AAF79461.1|AC022492_5 F1L3.11 [Arabidopsis thaliana] gi|19715630|gb|AAL91636.1| At1g17420/F1L3_1 [Arabidopsis thaliana] gi|30102476|gb|AAP21156.1| At1g17420/F1L3_1 [Arabidopsis thaliana] gi|332191464|gb|AEE29585.1| lipoxygenase 3 [Arabidopsis thaliana]	919	919	0	100.0	91.1	96.1	lipoxygenase 3	gbpln	Arabidopsis thaliana	AT1G17420.1 | Symbols: LOX3 | lipoxygenase 3 | chr1:5977512−5981384 FORWARD LENGTH=919	919	919	0	100.0	91.1	96.1
Rsa1.0_01155.1.g24043.t2	ref|XP_002890225.1| hypothetical protein ARALYDRAFT_471948 [Arabidopsis lyrata subsp. lyrata] gi|297336067|gb|EFH66484.1| hypothetical protein ARALYDRAFT_471948 [Arabidopsis lyrata subsp. lyrata]	395	333	1.00E−166	84.3	74.2	78.7	hypothetical protein ARALYDRAFT_471948	gbpln	Arabidopsis lyrata	AT1G17430.1 | Symbols: | alpha/beta−Hydrolases superfamily protein | chr1:5982310−5983919 FORWARD LENGTH=332	395	332	1.00E−168	84.1	73.2	77.5
Rsa1.0_01155.1.g24044.t1	ref|XP_002892989.1| hypothetical protein ARALYDRAFT_889236 [Arabidopsis lyrata subsp. lyrata] gi|297338831|gb|EFH69248.1| hypothetical protein ARALYDRAFT_889236 [Arabidopsis lyrata subsp. lyrata]	149	167	2.00E−12	112.1	26.8	38.9	hypothetical protein ARALYDRAFT_889236	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01155.1.g24045.t1	ref|XP_002892989.1| hypothetical protein ARALYDRAFT_889236 [Arabidopsis lyrata subsp. lyrata] gi|297338831|gb|EFH69248.1| hypothetical protein ARALYDRAFT_889236 [Arabidopsis lyrata subsp. lyrata]	149	167	1.00E−14	112.1	28.2	38.9	hypothetical protein ARALYDRAFT_889236	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01155.1.g24046.t1	gb|EOA40609.1| hypothetical protein CARUB_v10009345mg [Capsella rubella]	111	399	2.00E−32	359.5	57.7	59.5	hypothetical protein CARUB_v10009345mg	gbpln	Capsella rubella	AT1G17470.2 | Symbols: ATDRG1, ATDRG, DRG1 | developmentally regulated G−protein 1 | chr1:6003442−6006155 FORWARD LENGTH=399	111	399	3.00E−35	359.5	57.7	59.5
Rsa1.0_01155.1.g24047.t1	gb|EOA36959.1| hypothetical protein CARUB_v10009890mg [Capsella rubella]	296	295	1.00E−104	99.7	72.3	81.8	hypothetical protein CARUB_v10009890mg	gbpln	Capsella rubella	AT1G17520.1 | Symbols: | Homeodomain−like/winged−helix DNA−binding family protein | chr1:6024959−6027224 REVERSE LENGTH=296	296	296	1.00E−102	100.0	72.3	83.1

Rsa1.0_01155.1.g24048.t1	ref|NP_564028.1| translocase of inner mitochondrial membrane 23 [Arabidopsis thaliana] gi|75175255|sp|Q9LNQ1.1|TI231_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM23-1 gi|8778460|gb|AAF79468.1|AC022492_12 F1L3.24 [Arabidopsis thaliana] gi|15010570|gb|AAK73944.1| At1g17530/F11A6.4 [Arabidopsis thaliana] gi|20147387|gb|AAM10403.1| At1g17530/F11A6.4 [Arabidopsis thaliana] gi|38678776|gb|AAR26373.1| mitochondrial inner membrane translocase TM23-1 [Arabidopsis thaliana] gi|332191481|gb|AEE29602.1| translocase of inner mitochondrial membrane 23 [Arabidopsis thaliana]	187	187	9.00E-70	100.0	74.3	86.6	translocase of inner mitochondrial membrane 23	gbpln	Arabidopsis thaliana	AT1G17530.1 | Symbols: ATTIM23-1, TIM23-1 | translocase of inner mitochondrial membrane 23 | chr1:6027723-6028286 FORWARD LENGTH=187	187	187	3.00E-72	100.0	74.3	86.6
Rsa1.0_01155.1.g24049.t1	ref|NP_173197.2| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana] gi|51969566|dbj|BAD43475.1| putative protein kinase [Arabidopsis thaliana] gi|332191482|gb|AEE29603.1| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana]	706	728	0	103.1	80.5	88.1	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	gbpln	Arabidopsis thaliana	AT1G17540.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:6029551-6032641 REVERSE LENGTH=728	706	728	0	103.1	80.5	88.1
Rsa1.0_01155.1.g24050.t1	ref|XP_002890234.1| hypothetical protein ARALYDRAFT_889163 [Arabidopsis lyrata subsp. lyrata] gi|297336076|gb|EFH66493.1| hypothetical protein ARALYDRAFT_889163 [Arabidopsis lyrata subsp. lyrata]	489	514	0	105.1	87.7	92.8	hypothetical protein ARALYDRAFT_889163	gbpln	Arabidopsis lyrata	AT1G17550.1 | Symbols: HAB2 | homology to ABI2 | chr1:6034917-6036939 FORWARD LENGTH=511	489	511	0	104.5	86.9	92.2
Rsa1.0_01155.1.g24051.t2	ref|XP_002870343.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316179|gb|EFH46602.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	926	966	0	104.3	52.9	66.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G48770.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:19773277-19777242 REVERSE LENGTH=1190	926	1190	0	128.5	44.2	56.6
Rsa1.0_01155.1.g24052.t1	gb|ACP30589.1| disease resistance protein [Brassica rapa subsp. pekinensis]	504	1104	1.00E-129	219.0	52.8	67.5	disease resistance protein	gbpln	Brassica rapa	AT5G48770.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:19773277-19777242 REVERSE LENGTH=1190	504	1190	1.00E-115	236.1	47.6	63.7
Rsa1.0_01156.1.g24053.t1	ref|NP_201414.1| cell cycle checkpoint protein RAD17 [Arabidopsis thaliana] gi|55976607|sp|Q9MBA3.1|RAD17_ARATH RecName: Full=Cell cycle checkpoint protein RAD17; Short=AtRAD17; AltName: Full=Radiation-sensitive protein 17 gi|6855472|dbj|BAA90479.1| AtRAD17 [Arabidopsis thaliana] gi|10177128|dbj|BAB10418.1| AtRAD17 [Arabidopsis thaliana] gi|332010780|gb|AED98163.1| cell cycle checkpoint protein RAD17 [Arabidopsis thaliana]	644	599	0	93.0	72.7	80.9	cell cycle checkpoint protein RAD17	gbpln	Arabidopsis thaliana	AT5G66130.1 | Symbols: ATRAD17, RAD17 | RADIATION SENSITIVE 17 | chr5:26434236-26437091 FORWARD LENGTH=599	644	599	0	93.0	72.7	80.9
Rsa1.0_01156.1.g24054.t1	ref|XP_002865086.1| hypothetical protein ARALYDRAFT_358942 [Arabidopsis lyrata subsp. lyrata] gi|297310921|gb|EFH41345.1| hypothetical protein ARALYDRAFT_358942 [Arabidopsis lyrata subsp. lyrata]	434	443	0	102.1	89.4	93.8	hypothetical protein ARALYDRAFT_358942	gbpln	Arabidopsis lyrata	AT5G66120.2 | Symbols: | 3-dehydroquinate synthase, putative | chr5:26431516-26433649 REVERSE LENGTH=442	434	442	0	101.8	88.0	92.4
Rsa1.0_01156.1.g24055.t1	gb|EOA13364.1| hypothetical protein CARUB_v10026401mg [Capsella rubella]	380	445	1.00E-105	117.1	65.5	75.8	hypothetical protein CARUB_v10026401mg	gbpln	Capsella rubella	AT5G66100.1 | Symbols: | winged-helix DNA-binding transcription factor family protein | chr5:26427639-26429772 FORWARD LENGTH=453	380	453	1.00E-105	119.2	65.0	76.8
Rsa1.0_01156.1.g24056.t2	ref|NP_201407.4| iron ion binding / oxidoreductase/ oxidoreductase protein [Arabidopsis thaliana] gi|332010770|gb|AED98153.1| iron ion binding / oxidoreductase/ oxidoreductase protein [Arabidopsis thaliana]	540	289	1.00E-153	53.5	48.3	50.6	iron ion binding / oxidoreductase/ oxidoreductase protein	gbpln	Arabidopsis thaliana	AT5G66060.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:26419481-26421118 FORWARD LENGTH=289	540	289	1.00E-155	53.5	48.3	50.6
Rsa1.0_01156.1.g24057.t1	gb|AAA32812.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	436	439	1.00E-180	100.7	75.0	81.0	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G66055.1 | Symbols: EMB16, EMB2036, AKRP | ankyrin repeat protein | chr5:26417425-26419234 REVERSE LENGTH=435	436	435	0	99.8	73.6	79.1

Rsa1.0_01156.1.g24058.t1	ref|NP_201406.2| Wound-responsive family protein [Arabidopsis thaliana] gi|26452559|dbj|BAC43364.1| unknown protein [Arabidopsis thaliana] gi|29824181|gb|AAP04051.1| unknown protein [Arabidopsis thaliana] gi|332010765|gb|AED98148.1| Wound-responsive family protein [Arabidopsis thaliana]	363	340	1.00E-138	93.7	76.6	83.2	Wound-responsive family protein	gbpln	Arabidopsis thaliana	AT5G66050.1 | Symbols: | Wound-responsive family protein | chr5:26412333-26414428 REVERSE LENGTH=340	363	340	1.00E-140	93.7	76.6	83.2
Rsa1.0_01156.1.g24059.t1	ref|NP_851278.1| thiosulfate sulfurtransferase [Arabidopsis thaliana] gi|62903514|sp|Q39129.2|STR16_ARATH RecName: Full=Thiosulfate sulfurtransferase 16, chloroplastic; AltName: Full=Rhodanese; AltName: Full=Senescence-associated protein; AltName: Full=Sulfurtransferase 16; Short=AtStr16 gi|10177119|dbj|BAB10409.1| senescence-associated protein sen1-like protein; ketoconazole resistance protein-like [Arabidopsis thaliana] gi|15146322|gb|AAK83644.1| AT5g66040/K2A18_11 [Arabidopsis thaliana] gi|21536991|gb|AAM61332.1| senescence-associated protein [Arabidopsis thaliana] gi|23507795|gb|AAN38701.1| At5g66040/K2A18_11 [Arabidopsis thaliana] gi|332010763|gb|AED98146.1| thiosulfate sulfurtransferase [Arabidopsis thaliana]	121	120	8.00E-48	99.2	75.2	86.8	thiosulfate sulfurtransferase	gbpln	Arabidopsis thaliana	AT5G66040.1 | Symbols: STR16 | sulfurtransferase protein 16 | chr5:26410557-26411139 FORWARD LENGTH=120	121	120	1.00E-50	99.2	75.2	86.8
Rsa1.0_01156.1.g24060.t1	gb|ADD16954.1| SAC-like protein [Brassica rapa]	1364	594	0	43.5	41.6	42.4	SAC-like protein	gbpln	Brassica rapa	AT5G66030.1 | Symbols: ATGRIP, GRIP | Golgi-localized GRIP domain-containing protein | chr5:26405133-26409888 REVERSE LENGTH=788	1364	788	0	57.8	47.2	50.0
Rsa1.0_01156.1.g24061.t1	ref|XP_002866780.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312615|gb|EFH43039.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	619	395	0	63.8	59.9	61.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G65980.1 | Symbols: | Auxin efflux carrier family protein | chr5:26392444-26394232 FORWARD LENGTH=395	619	395	0	63.8	59.8	61.4
Rsa1.0_01156.1.g24062.t1	ref|XP_002866782.1| hypothetical protein ARALYDRAFT_920139 [Arabidopsis lyrata subsp. lyrata] gi|297312617|gb|EFH43041.1| hypothetical protein ARALYDRAFT_920139 [Arabidopsis lyrata subsp. lyrata]	382	394	1.00E-161	103.1	84.6	90.1	hypothetical protein ARALYDRAFT_920139	gbpln	Arabidopsis lyrata	AT5G65960.1 | Symbols: | GTP binding | chr5:26385413-26387197 FORWARD LENGTH=393	382	393	1.00E-156	102.9	82.5	90.8
Rsa1.0_01156.1.g24063.t1	ref|NP_201395.1| 3-hydroxyisobutyryl-CoA hydrolase 1 [Arabidopsis thaliana] gi|75263928|sp|Q9LKJ1.1|HIBC1_ARATH RecName: Full=3-hydroxyisobutyryl-CoA hydrolase 1; AltName: Full=CoA-thioester hydrolase CHY1 gi|8572760|gb|AAF77193.1|AF276301_1 CoA-thioester hydrolase CHY1 [Arabidopsis thaliana] gi|9759578|dbj|BAB11141.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana] gi|24030391|gb|AAN41356.1| putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana] gi|332010745|gb|AED98128.1| 3-hydroxyisobutyryl-CoA hydrolase 1 [Arabidopsis thaliana]	196	378	7.00E-18	192.9	33.2	39.8	3-hydroxyisobutyryl-CoA hydrolase 1	gbpln	Arabidopsis thaliana	AT5G65940.1 | Symbols: CHY1 | beta-hydroxyisobutyryl-CoA hydrolase 1 | chr5:26376830-26379161 REVERSE LENGTH=378	196	378	2.00E-20	192.9	33.2	39.8
Rsa1.0_01157.1.g24064.t3	gb|AAF79275.1|AC023279_24 F12K21.5 [Arabidopsis thaliana]	775	1033	5.00E-92	133.3	23.0	29.0	F12K21.5	gbpln	Arabidopsis thaliana	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	775	673	5.00E-25	86.8	12.8	20.3
Rsa1.0_01157.1.g24065.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	479	1274	1.00E-111	266.0	45.9	62.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	479	575	3.00E-51	120.0	32.4	49.9
Rsa1.0_01157.1.g24066.t1	gb|EOA25511.1| hypothetical protein CARUB_v10018854mg [Capsella rubella]	368	360	1.00E-137	97.8	66.0	79.1	hypothetical protein CARUB_v10018854mg	gbpln	Capsella rubella	AT3G57720.1 | Symbols: | Protein kinase superfamily protein | chr3:21387766-21388845 FORWARD LENGTH=359	368	359	1.00E-139	97.6	66.3	77.7

Rsa1.0_01157.1.g24067.t1	ref|NP_191330.1| protein kinase family protein [Arabidopsis thaliana] gi|4678276|emb|CAB41184.1| putative protein [Arabidopsis thaliana] gi|21537362|gb|AAM61703.1| protein kinase-like protein [Arabidopsis thaliana] gi|51968400|dbj|BAD42892.1| protein kinase - like protein [Arabidopsis thaliana] gi|51969234|dbj|BAD43309.1| protein kinase - like protein [Arabidopsis thaliana] gi|51969278|dbj|BAD43331.1| protein kinase - like protein [Arabidopsis thaliana] gi|332646167|gb|AEE79688.1| protein kinase family protein [Arabidopsis thaliana]	228	351	3.00E-36	153.9	37.7	52.2	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G57710.1 | Symbols: | Protein kinase superfamily protein | chr3:21386233-21387288 REVERSE LENGTH=351	228	351	8.00E-39	153.9	37.7	52.2
Rsa1.0_01157.1.g24068.t1	gb|EOA29259.1| hypothetical protein CARUB_v10025533mg, partial [Capsella rubella]	385	293	8.00E-37	76.1	19.2	21.0	hypothetical protein CARUB_v10025533mg, partial	gbpln	Capsella rubella	AT1G34070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48050.1); Has 648 Blast hits to 647 proteins in 29 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 25; Plants - 607; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12402283-12403209 FORWARD LENGTH=308	385	308	2.00E-30	80.0	14.8	19.5
Rsa1.0_01157.1.g24069.t1	gb|EOA23580.1| hypothetical protein CARUB_v10016776mg [Capsella rubella]	586	679	0	115.9	75.9	85.5	hypothetical protein CARUB_v10016776mg	gbpln	Capsella rubella	AT3G57780.1 | Symbols: | BEST Arabidopsis thaliana protein match is: nucleolar protein gar2-related (TAIR:AT2G42320.2); Has 3163 Blast hits to 2460 proteins in 357 species: Archae - 16; Bacteria - 291; Metazoa - 841; Fungi - 335; Plants - 248; Viruses - 72; Other Eukaryotes - 1360 (source: NCBI BLink). | chr3:21399766-21402329 REVERSE LENGTH=671	586	671	0	114.5	75.9	84.8
Rsa1.0_01157.1.g24070.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01157.1.g24071.t1	ref|NP_567057.2| transcription factor bHLH60 [Arabidopsis thaliana] gi|122214701|sp|Q3EAI1.1|BH060_ARATH RecName: Full=Transcription factor bHLH60; AltName: Full=Basic helix-loop-helix protein 60; Short=AtbHLH60; Short=bHLH 60; AltName: Full=Transcription factor EN 91; AltName: Full=bHLH transcription factor bHLH060 gi|332646181|gb|AEE79702.1| transcription factor bHLH60 [Arabidopsis thaliana]	386	426	1.00E-143	110.4	78.0	84.5	transcription factor bHLH60	gbpln	Arabidopsis thaliana	AT3G57800.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:21408034-21411321 REVERSE LENGTH=426	386	426	2.33E-156	110.4	78.0	84.5
Rsa1.0_01157.1.g24072.t1	gb|ADP37981.1| ubiquitin-protein ligase [Brassica napus]	160	160	2.00E-89	100.0	98.8	99.4	ubiquitin-protein ligase	gbpln	Brassica napus	AT3G57870.1 | Symbols: AHUS5, EMB1637, SCE1, SCE1A, ATSCE1 | sumo conjugation enzyme 1 | chr3:21428831-21430110 REVERSE LENGTH=160	160	160	4.00E-89	100.0	95.6	96.9
Rsa1.0_01157.1.g24073.t1	ref|NP_191347.1| calcium-dependent lipid-binding domain-containing plant phosphoribosyltransferase-like protein [Arabidopsis thaliana] gi|6729531|emb|CAB67616.1| anthranilate phosphoribosyltransferase-like protein [Arabidopsis thaliana] gi|332646191|gb|AEE79712.1| calcium-dependent lipid-binding domain-containing plant phosphoribosyltransferase-like protein [Arabidopsis thaliana]	775	773	0	99.7	95.7	97.8	calcium-dependent lipid-binding domain-containing plant phosphoribosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT3G57880.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein | chr3:21431198-21433519 REVERSE LENGTH=773	775	773	0	99.7	95.7	97.8
Rsa1.0_01158.1.g24074.t1	ref|NP_172933.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|332191106|gb|AEE29227.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	198	384	4.00E-21	193.9	26.8	39.4	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	198	384	1.00E-23	193.9	26.8	39.4
Rsa1.0_01158.1.g24075.t1	ref|XP_002877088.1| hypothetical protein ARALYDRAFT_905062 [Arabidopsis lyrata subsp. lyrata] gi|297322926|gb|EFH53347.1| hypothetical protein ARALYDRAFT_905062 [Arabidopsis lyrata subsp. lyrata]	130	503	9.00E-16	386.9	33.1	37.7	hypothetical protein ARALYDRAFT_905062	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01158.1.g24076.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	260	1023	5.00E-19	393.5	20.8	31.5	F27F5.21	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01158.1.g24077.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01158.1.g24078.t1	ref|YP_004927579.1| orf113a (mitochondrion) [Brassica carinata] gi|335355040|gb|AEH43594.1| orf113a [Brassica carinata]	129	113	2.00E-19	87.6	38.0	38.8	orf113a (mitochondrion)	gbpln	Brassica carinata	ATMG00050.1 | Symbols: ORF131 | hypothetical protein | chrM:16856-17251 FORWARD LENGTH=131	129	131	5.00E-18	101.6	34.1	34.9
Rsa1.0_01158.1.g24079.t1	gb|EOA15091.1| hypothetical protein CARUB_v10028459mg [Capsella rubella]	377	377	0	100.0	99.2	99.5	hypothetical protein CARUB_v10028459mg	gbpln	Capsella rubella	AT3G46520.1 | Symbols: ACT12 | actin-12 | chr3:17128567-17129981 FORWARD LENGTH=377	377	377	0	100.0	99.2	99.5
Rsa1.0_01158.1.g24080.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	989	1499	0	151.6	61.8	75.2	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	989	158	4.00E-22	16.0	5.2	7.0
Rsa1.0_01158.1.g24081.t1	gb|EOA23471.1| hypothetical protein CARUB_v10016663mg [Capsella rubella]	1191	911	1.00E-32	76.5	13.3	20.7	hypothetical protein CARUB_v10016663mg	gbpln	Capsella rubella	AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957	1191	957	4.00E-34	80.4	11.8	20.5
Rsa1.0_01158.1.g24082.t1	gb|AAG51464.1|AC069160_10 gypsy/Ty3 element polyprotein, putative [Arabidopsis thaliana]	429	1447	1.00E-77	337.3	42.7	55.5	gypsy/Ty3 element polyprotein, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01158.1.g24083.t1	ref|XP_002884714.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330554|gb|EFH60973.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	505	492	0	97.4	72.9	83.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G09110.1 | Symbols: | Protein of unknown function (DUF674) | chr3:2794850-2795963 REVERSE LENGTH=343	505	343	1.00E-151	67.9	51.3	58.2
Rsa1.0_01158.1.g24084.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01159.1.g24085.t1	gb|AAF37287.1|AF227978_1 putative G-protein-coupled transmembrane receptor [Brassica oleracea var. botrytis]	231	457	5.00E-50	197.8	55.8	63.6	putative G-protein-coupled transmembrane receptor	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01159.1.g24086.t1	ref|XP_002893598.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339440|gb|EFH69857.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	542	376	0	69.4	60.3	62.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G30080.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr1:10551231-10553167 REVERSE LENGTH=408	542	408	0	75.3	59.4	62.4
Rsa1.0_01159.1.g24087.t6	gb|EOA38497.1| hypothetical protein CARUB_v10010265mg [Capsella rubella]	482	218	1.00E-83	45.2	32.2	34.6	hypothetical protein CARUB_v10010265mg	gbpln	Capsella rubella	AT1G30070.1 | Symbols: | SGS domain-containing protein | chr1:10546794-10548072 REVERSE LENGTH=222	482	222	3.00E-81	46.1	32.2	35.1
Rsa1.0_01159.1.g24088.t1	gb|EOA37925.1| hypothetical protein CARUB_v10009392mg [Capsella rubella]	410	390	1.00E-155	95.1	80.0	85.6	hypothetical protein CARUB_v10009392mg	gbpln	Capsella rubella	AT1G30050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G01970.1); Has 246 Blast hits to 244 proteins in 61 species: Archae - 0; Bacteria - 8; Metazoa - 78; Fungi - 10; Plants - 117; Viruses - 0; Other Eukaryotes - 33 (source: NCBI BLink). | chr1:10543177-10544418 FORWARD LENGTH=389	410	389	1.00E-155	94.9	76.6	83.2
Rsa1.0_01159.1.g24089.t1	dbj|BAG16378.1| gibberellin 2-oxidase family protein [Brassica rapa var. perviridis]	339	338	0	99.7	91.2	94.1	gibberellin 2-oxidase family protein	gbpln	Brassica rapa	AT1G30040.1 | Symbols: ATGA2OX2, GA2OX2 | gibberellin 2-oxidase | chr1:10537769-10539570 FORWARD LENGTH=341	339	341	1.00E-175	100.6	86.4	92.0
Rsa1.0_01160.1.g24090.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01160.1.g24091.t1	gb|EOA25574.1| hypothetical protein CARUB_v10018920mg [Capsella rubella]	135	700	4.00E-60	518.5	80.7	85.9	hypothetical protein CARUB_v10018920mg	gbpln	Capsella rubella	AT3G45420.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:16657263-16659266 REVERSE LENGTH=667	135	667	1.00E-61	494.1	80.7	90.4
Rsa1.0_01160.1.g24092.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01160.1.g24093.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01160.1.g24094.t1	ref|YP_002608359.1| orf104 [Vitis vinifera] gi|209954156|emb|CAQ77593.1| orf104 [Vitis vinifera] gi|239764779|gb|ACS15247.1| ORF104 [Vitis vinifera]	201	103	4.00E-27	51.2	29.9	31.3	orf104	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01160.1.g24095.t1	ref|XP_002886115.1| hypothetical protein ARALYDRAFT_480631 [Arabidopsis lyrata subsp. lyrata] gi|297331955|gb|EFH62374.1| hypothetical protein ARALYDRAFT_480631 [Arabidopsis lyrata subsp. lyrata]	596	591	0	99.2	81.0	87.8	hypothetical protein ARALYDRAFT_480631	gbpln	Arabidopsis lyrata	AT2G17480.1 | Symbols: MLO8, ATMLO8 | Seven transmembrane MLO family protein | chr2:7590559-7593768 REVERSE LENGTH=593	596	593	0	99.5	78.0	85.4
Rsa1.0_01160.1.g24096.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	664	1499	0	225.8	60.2	69.4	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	664	158	3.00E-26	23.8	8.6	10.7

<table>
<tr><td>Rsa1.0_01160.1.g24097.t2</td><td>ref|NP_179338.1| Aluminium activated malate transporter family protein [Arabidopsis thaliana] gi|75205692|sp|Q9SHM1.1|ALMT6_ARATH RecName: Full=Aluminum-activated malate transporter 6; Short=AtALMT6 gi|4914368|gb|AAD32904.1| unknown protein [Arabidopsis thaliana] gi|330251538|gb|AEC06632.1| Aluminium activated malate transporter family protein [Arabidopsis thaliana]</td><td>532</td><td>538</td><td>0</td><td>101.1</td><td>81.2</td><td>86.1</td><td>Aluminium activated malate transporter family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17470.1 | Symbols: | Aluminium activated malate transporter family protein | chr2:7584572-7588008 REVERSE LENGTH=538</td><td>532</td><td>538</td><td>0</td><td>101.1</td><td>81.2</td><td>86.1</td></tr>
<tr><td>Rsa1.0_01161.1.g24098.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01161.1.g24099.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01161.1.g24100.t1</td><td>gb|AAF79375.1|AC007887_34 F15O4.28 [Arabidopsis thaliana]</td><td>206</td><td>570</td><td>1.00E-37</td><td>276.7</td><td>46.1</td><td>67.5</td><td>F15O4.28</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01161.1.g24101.t1</td><td>gb|EOA27937.1| hypothetical protein CARUB_v10024106mg [Capsella rubella]</td><td>250</td><td>195</td><td>4.00E-79</td><td>78.0</td><td>66.4</td><td>70.4</td><td>hypothetical protein CARUB_v10024106mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G27290.1 | Symbols: | Protein of unknown function (DUF1279) | chr2:11678586-11679765 REVERSE LENGTH=201</td><td>250</td><td>201</td><td>2.00E-73</td><td>80.4</td><td>59.6</td><td>66.8</td></tr>
<tr><td>Rsa1.0_01161.1.g24102.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01161.1.g24103.t1</td><td>gb|AAD17414.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1470</td><td>1166</td><td>0</td><td>79.3</td><td>48.2</td><td>58.8</td><td>copia-like retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1470</td><td>1262</td><td>7.00E-79</td><td>85.9</td><td>11.2</td><td>18.4</td></tr>
<tr><td>Rsa1.0_01161.1.g24104.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01161.1.g24105.t1</td><td>ref|XP_002879078.1| hypothetical protein ARALYDRAFT_481623 [Arabidopsis lyrata subsp. lyrata] gi|297324917|gb|EFH55337.1| hypothetical protein ARALYDRAFT_481623 [Arabidopsis lyrata subsp. lyrata]</td><td>190</td><td>243</td><td>1.00E-59</td><td>127.9</td><td>65.8</td><td>77.9</td><td>hypothetical protein ARALYDRAFT_481623</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G27260.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:11669769-11670500 FORWARD LENGTH=243</td><td>190</td><td>243</td><td>1.00E-58</td><td>127.9</td><td>63.7</td><td>75.8</td></tr>
<tr><td>Rsa1.0_01161.1.g24106.t1</td><td>gb|ABD65163.1| hypothetical protein 40.t00048 [Brassica oleracea]</td><td>590</td><td>569</td><td>1.00E-156</td><td>96.4</td><td>52.0</td><td>56.9</td><td>hypothetical protein 40.t00048</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01162.1.g24107.t2</td><td>gb|EOA15220.1| hypothetical protein CARUB_v10028610mg [Capsella rubella]</td><td>507</td><td>424</td><td>0</td><td>83.6</td><td>64.1</td><td>69.8</td><td>hypothetical protein CARUB_v10028610mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G58230.1 | Symbols: MSI1, MEE70, ATMSI1 | Transducin/WD40 repeat-like superfamily protein | chr5:23556112-23557994 FORWARD LENGTH=424</td><td>507</td><td>424</td><td>0</td><td>83.6</td><td>63.7</td><td>70.2</td></tr>
<tr><td>Rsa1.0_01162.1.g24108.t1</td><td>ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>544</td><td>530</td><td>3.00E-39</td><td>97.4</td><td>20.6</td><td>28.7</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530</td><td>544</td><td>530</td><td>1.00E-14</td><td>97.4</td><td>9.2</td><td>17.1</td></tr>
<tr><td>Rsa1.0_01162.1.g24109.t1</td><td>gb|ABD65056.1| hypothetical protein 27.t00122 [Brassica oleracea]</td><td>226</td><td>239</td><td>6.00E-18</td><td>105.8</td><td>23.9</td><td>31.4</td><td>hypothetical protein 27.t00122</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01162.1.g24110.t1</td><td>dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>191</td><td>1491</td><td>1.00E-29</td><td>780.6</td><td>31.4</td><td>42.4</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01162.1.g24111.t1</td><td>ref|XP_002864686.1| MADS-box protein [Arabidopsis lyrata subsp. lyrata] gi|297310521|gb|EFH40945.1| MADS-box protein [Arabidopsis lyrata subsp. lyrata]</td><td>154</td><td>291</td><td>2.00E-22</td><td>189.0</td><td>47.4</td><td>64.3</td><td>MADS-box protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G60440.1 | Symbols: AGL62 | AGAMOUS-like 62 | chr5:24306329-24307520 FORWARD LENGTH=299</td><td>154</td><td>299</td><td>8.00E-24</td><td>194.2</td><td>50.6</td><td>68.2</td></tr>
<tr><td>Rsa1.0_01162.1.g24112.t2</td><td>ref|XP_004292625.1| PREDICTED: uncharacterized protein LOC101299743 [Fragaria vesca subsp. vesca]</td><td>204</td><td>746</td><td>6.00E-49</td><td>365.7</td><td>51.0</td><td>66.2</td><td>PREDICTED: uncharacterized protein LOC101299743</td><td>gbpln</td><td>Fragaria vesca</td><td>AT5G33406.1 | Symbols: | hAT dimerisation domain-containing protein / transposase-related | chr5:12676126-12678403 REVERSE LENGTH=509</td><td>204</td><td>509</td><td>3.00E-29</td><td>249.5</td><td>34.3</td><td>55.9</td></tr>
<tr><td>Rsa1.0_01162.1.g24113.t1</td><td>gb|EOA13855.1| hypothetical protein CARUB_v10026958mg [Capsella rubella]</td><td>455</td><td>268</td><td>7.00E-97</td><td>58.9</td><td>41.3</td><td>47.0</td><td>hypothetical protein CARUB_v10026958mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G58530.1 | Symbols: | Glutaredoxin family protein | chr5:23660428-23661249 FORWARD LENGTH=273</td><td>455</td><td>273</td><td>8.00E-98</td><td>60.0</td><td>40.9</td><td>46.8</td></tr>
<tr><td>Rsa1.0_01162.1.g24114.t1</td><td>ref|XP_002864585.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297310420|gb|EFH40844.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]</td><td>347</td><td>348</td><td>1.00E-163</td><td>100.3</td><td>83.3</td><td>91.4</td><td>oxidoreductase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G58660.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:23701509-23703802 FORWARD LENGTH=352</td><td>347</td><td>352</td><td>1.00E-158</td><td>101.4</td><td>81.0</td><td>90.5</td></tr>
<tr><td>Rsa1.0_01162.1.g24115.t1</td><td>gb|EOA30805.1| hypothetical protein CARUB_v10013949mg [Capsella rubella]</td><td>295</td><td>381</td><td>3.00E-30</td><td>129.2</td><td>28.5</td><td>33.2</td><td>hypothetical protein CARUB_v10013949mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G38670.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:15475786-15476871 FORWARD LENGTH=291</td><td>295</td><td>291</td><td>2.00E-29</td><td>98.6</td><td>35.3</td><td>47.1</td></tr>
<tr><td>Rsa1.0_01162.1.g24116.t1</td><td>ref|XP_002866283.1| ATPLC1 [Arabidopsis lyrata subsp. lyrata] gi|297312118|gb|EFH42542.1| ATPLC1 [Arabidopsis lyrata subsp. lyrata]</td><td>578</td><td>563</td><td>0</td><td>97.4</td><td>84.8</td><td>90.3</td><td>ATPLC1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G58670.1 | Symbols: ATPLC1, ATPLC, PLC1 | phospholipase C1 | chr5:23704457-23706751 REVERSE LENGTH=561</td><td>578</td><td>561</td><td>0</td><td>97.1</td><td>83.2</td><td>89.4</td></tr>
<tr><td>Rsa1.0_01162.1.g24117.t1</td><td>gb|EOA33134.1| hypothetical protein CARUB_v10016476mg [Capsella rubella]</td><td>329</td><td>354</td><td>1.00E-147</td><td>107.6</td><td>80.5</td><td>90.6</td><td>hypothetical protein CARUB_v10016476mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G01400.1 | Symbols: | ARM repeat superfamily protein | chr3:151920-152987 FORWARD LENGTH=355</td><td>329</td><td>355</td><td>1.00E-149</td><td>107.9</td><td>81.8</td><td>91.2</td></tr>
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Rsa1.0_01162.1.g24118.t1	ref|NP_200677.2| phosphoinositide phospholipase C 5 [Arabidopsis thaliana] gi|75306039|sp|Q944C2.2|PLCD5_ARATH RecName: Full=Phosphoinositide phospholipase C 5; AltName: Full=Phosphoinositide phospholipase PLC5; Short=AtPLC5; Short=AtPLCx; Short=PI-PLC5 gi|19855030|gb|AAL30748.2|AF434167_1 phosphoinositide-specific phospholipase C [Arabidopsis thaliana] gi|17065210|gb|AAL32759.1| phosphoinositide-specific phospholipase C-line [Arabidopsis thaliana] gi|34098919|gb|AAQ56842.1| At5g58690 [Arabidopsis thaliana] gi|332009702|gb|AED97085.1| phosphoinositide phospholipase C 5 [Arabidopsis thaliana]	160	578	2.00E-33	361.3	46.3	50.6	phosphoinositide phospholipase C 5	gbpln	Arabidopsis thaliana	AT5G58690.1 | Symbols: ATPLC5, PLC5 | phosphatidylinositol-speciwc phospholipase C5 | chr5:23709676-23712030 REVERSE LENGTH=578	160	578	7.00E-36	361.3	46.3	50.6
Rsa1.0_01162.1.g24119.t1	gb|EOA12385.1| hypothetical protein CARUB_v10026125mg [Capsella rubella]	615	596	0	96.9	84.2	90.6	hypothetical protein CARUB_v10026125mg	gbpln	Capsella rubella	AT5G58700.1 | Symbols: ATPLC4, PLC4 | phosphatidylinositol-speciwc phospholipase C4 | chr5:23713144-23716057 REVERSE LENGTH=597	615	597	0	97.1	82.8	89.9
Rsa1.0_01162.1.g24120.t1	ref|NP_200680.1| smr (Small MutS Related) domain-containing protein [Arabidopsis thaliana] gi|3201477|emb|CAA06808.1| putative PRL1 associated protein [Arabidopsis thaliana] gi|8843792|dbj|BAA97340.1| PRL1 associated protein-like [Arabidopsis thaliana] gi|17065352|gb|AAL32830.1| PRL1 associated protein-like [Arabidopsis thaliana] gi|21387179|gb|AAM47993.1| PRL1-associated protein-like protein [Arabidopsis thaliana] gi|332009706|gb|AED97089.1| smr (Small MutS Related) domain-containing protein [Arabidopsis thaliana]	525	519	0	98.9	76.8	83.4	smr (Small MutS Related) domain-containing protein	gbpln	Arabidopsis thaliana	AT5G58720.1 | Symbols: | smr (Small MutS Related) domain-containing protein | chr5:23719976-23722974 REVERSE LENGTH=519	525	519	0	98.9	76.8	83.4
Rsa1.0_01162.1.g24121.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01163.1.g24122.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01163.1.g24123.t1	gb|AAF64065.1|AF251794_1 putative diacylglycerol acyltransferase [Brassica napus] gi|390980721|gb|AFM31259.1| diacylglycerol O-acyltransferase 1 [Brassica napus]	488	501	0	102.7	94.7	96.7	putative diacylglycerol acyltransferase	gbpln	Brassica napus	AT2G19450.1 | Symbols: TAG1, AS11, ABX45, DGAT1, RDS1, ATDGAT | membrane bound O-acyl transferase (MBOAT) family protein | chr2:8426436-8429455 FORWARD LENGTH=520	488	520	0	106.6	85.9	89.5
Rsa1.0_01163.1.g24124.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01163.1.g24125.t1	gb|EOA30703.1| hypothetical protein CARUB_v10013840mg, partial [Capsella rubella]	377	408	1.00E-161	108.2	86.7	96.0	hypothetical protein CARUB_v10013840mg, partial	gbpln	Capsella rubella	AT2G19480.3 | Symbols: NAP1;2 | nucleosome assembly protein 1;2 | chr2:8438601-8441040 FORWARD LENGTH=372	377	372	1.00E-156	98.7	84.6	94.4
Rsa1.0_01163.1.g24126.t5	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01163.1.g24127.t1	ref|NP_179539.2| DNA repair protein recA-like 3 [Arabidopsis thaliana] gi|209572665|sp|Q9ZUP2.2|RECA3_ARATH RecName: Full=DNA repair protein recA homolog 3, mitochondrial; AltName: Full=Recombinase A homolog 3; Flags: Precursor gi|119935859|gb|ABM06015.1| At2g19490 [Arabidopsis thaliana] gi|330251794|gb|AEC06888.1| DNA repair protein recA-like 3 [Arabidopsis thaliana]	430	430	0	100.0	86.7	91.9	DNA repair protein recA-like 3	gbpln	Arabidopsis thaliana	AT2G19490.1 | Symbols: | recA DNA recombination family protein | chr2:8441732-8444006 FORWARD LENGTH=430	430	430	0	100.0	86.7	91.9
Rsa1.0_01163.1.g24128.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	243	484	7.00E-26	199.2	23.0	34.6	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01163.1.g24129.t1	gb|AAG30905.1|AF303978_1 cytokinin oxidase [Arabidopsis thaliana]	265	501	1.00E-129	189.1	83.0	91.7	cytokinin oxidase	gbpln	Arabidopsis thaliana	AT2G19500.1 | Symbols: CKX2, ATCKX2 | cytokinin oxidase 2 | chr2:8444311-8447301 REVERSE LENGTH=501	265	501	1.00E-132	189.1	83.0	91.7
Rsa1.0_01163.1.g24130.t1	gb|EOA30341.1| hypothetical protein CARUB_v10013466mg, partial [Capsella rubella]	209	516	3.00E-78	246.9	73.2	80.4	hypothetical protein CARUB_v10013466mg, partial	gbpln	Capsella rubella	AT2G19500.1 | Symbols: CKX2, ATCKX2 | cytokinin oxidase 2 | chr2:8444311-8447301 REVERSE LENGTH=501	209	501	1.00E-80	239.7	70.8	79.9
Rsa1.0_01163.1.g24131.t1	gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]	473	543	1.00E-79	114.8	36.6	58.6	hypothetical protein CARUB_v10015730mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	473	566	2.00E-74	119.7	34.7	57.7
Rsa1.0_01163.1.g24132.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01164.1.g24133.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	215	1413	1.00E-36	657.2	36.7	44.7	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01164.1.g24134.t1	gb|EOA29790.1| hypothetical protein CARUB_v10012885mg [Capsella rubella]	493	1012	1.00E-84	205.3	37.1	45.8	hypothetical protein CARUB_v10012885mg	gbpln	Capsella rubella	AT2G15900.1 | Symbols: | Phox-associated domain;Phox-like;Sorting nexin, C-terminal | chr2:6927390-6932535 FORWARD LENGTH=994	493	994	1.00E-86	201.6	33.5	38.9
Rsa1.0_01164.1.g24135.t1	ref|XP_002882838.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328678|gb|EFH59097.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	680	703	0	103.4	91.3	94.1	kinase family protein	gbpln	Arabidopsis lyrata	AT3G13670.1 | Symbols: | Protein kinase family protein | chr3:4469434-4473234 FORWARD LENGTH=703	680	703	0	103.4	91.5	94.4
Rsa1.0_01164.1.g24136.t1	gb|EOA32205.1| hypothetical protein CARUB_v10015462mg [Capsella rubella]	204	216	8.00E-87	105.9	77.5	88.2	hypothetical protein CARUB_v10015462mg	gbpln	Capsella rubella	AT3G13672.1 | Symbols: | TRAF-like superfamily protein | chr3:4473541-4474343 REVERSE LENGTH=216	204	216	1.00E-87	105.9	78.4	86.8
Rsa1.0_01164.1.g24137.t1	ref|XP_002882840.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328680|gb|EFH59099.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	691	752	0	108.8	88.3	91.8	kinase family protein	gbpln	Arabidopsis lyrata	AT3G13690.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr3:4486920-4490011 FORWARD LENGTH=753	691	753	0	109.0	88.1	91.9
Rsa1.0_01164.1.g24138.t1	gb|AAF79353.1|AC007887_12 F15O4.27 [Arabidopsis thaliana]	585	638	0	109.1	67.2	76.4	F15O4.27	gbpln	Arabidopsis thaliana	AT1G35610.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:13143150-13144988 REVERSE LENGTH=612	585	612	0	104.6	67.2	76.4
Rsa1.0_01164.1.g24139.t1	gb|AAF79353.1|AC007887_12 F15O4.27 [Arabidopsis thaliana]	413	638	4.00E-78	154.5	39.5	48.2	F15O4.27	gbpln	Arabidopsis thaliana	AT1G35610.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:13143150-13144988 REVERSE LENGTH=612	413	612	2.00E-80	148.2	39.5	48.2
Rsa1.0_01164.1.g24140.t1	gb|EOA30083.1| hypothetical protein CARUB_v10013189mg [Capsella rubella]	638	641	0	100.5	97.0	97.6	hypothetical protein CARUB_v10013189mg	gbpln	Capsella rubella	AT3G13772.1 | Symbols: TMN7, AtTMN7 | transmembrane nine 7 | chr3:4521712-4524394 REVERSE LENGTH=641	638	641	0	100.5	97.3	98.0
Rsa1.0_01164.1.g24141.t1	ref|XP_002882849.1| metallo-beta-lactamase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328689|gb|EFH59108.1| metallo-beta-lactamase family protein [Arabidopsis lyrata subsp. lyrata]	358	359	0	100.3	88.3	92.7	metallo-beta-lactamase family protein	gbpln	Arabidopsis lyrata	AT3G13800.1 | Symbols: | Metallo-hydrolase/oxidoreductase superfamily protein | chr3:4538879-4541366 FORWARD LENGTH=361	358	361	0	100.8	86.9	92.5
Rsa1.0_01164.1.g24142.t1	ref|XP_002882851.1| hypothetical protein ARALYDRAFT_478784 [Arabidopsis lyrata subsp. lyrata] gi|297328691|gb|EFH59110.1| hypothetical protein ARALYDRAFT_478784 [Arabidopsis lyrata subsp. lyrata]	506	507	0	100.2	81.2	87.7	hypothetical protein ARALYDRAFT_478784	gbpln	Arabidopsis lyrata	AT3G13810.1 | Symbols: AtIDD11, IDD11 | indeterminate(ID)-domain 11 | chr3:4544941-4547300 FORWARD LENGTH=513	506	513	0	101.4	80.6	87.2
Rsa1.0_01165.1.g24143.t1	gb|AAB60771.1| F19K23.19 gene product [Arabidopsis thaliana]	207	486	7.00E-23	234.8	35.3	43.5	F19K23.19 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01165.1.g24144.t1	gb|EOA34475.1| hypothetical protein CARUB_v10022015mg [Capsella rubella]	661	670	0	101.4	79.9	86.1	hypothetical protein CARUB_v10022015mg	gbpln	Capsella rubella	AT1G70110.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr1:26406238-26408323 REVERSE LENGTH=666	661	666	0	100.8	75.0	84.0
Rsa1.0_01165.1.g24145.t1	ref|XP_002887278.1| hypothetical protein ARALYDRAFT_316004 [Arabidopsis lyrata subsp. lyrata] gi|297333119|gb|EFH63537.1| hypothetical protein ARALYDRAFT_316004 [Arabidopsis lyrata subsp. lyrata]	202	179	3.00E-64	88.6	59.9	68.3	hypothetical protein ARALYDRAFT_316004	gbpln	Arabidopsis lyrata	AT1G70120.1 | Symbols: | Protein of unknown function (DUF1163) | chr1:26408921-26409597 FORWARD LENGTH=193	202	193	5.00E-59	95.5	55.0	63.4
Rsa1.0_01165.1.g24146.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01165.1.g24147.t1	ref|NP_177168.1| concanavalin A-like lectin protein kinase [Arabidopsis thaliana] gi|75317843|sp|O04534.1|LRK51_ARATH RecName: Full=Putative L-type lectin-domain containing receptor kinase V.1; Short=Arabidopsis thaliana lectin-receptor kinase b2; Short=AthlecRK-b2; Short=LecRK-V.1; Flags: Precursor gi|2194128|gb|AAB61103.1| Strong similarity to Arabidopsis receptor-like kinase (gb|ATLECGENE) and F20P5.15 [Arabidopsis thaliana] gi|332196900|gb|AEE35021.1| concanavalin A-like lectin protein kinase [Arabidopsis thaliana]	607	666	0	109.7	71.8	80.9	concanavalin A-like lectin protein kinase	gbpln	Arabidopsis thaliana	AT1G70110.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr1:26406238-26408323 REVERSE LENGTH=666	607	666	0	109.7	71.8	80.9

Rsa1.0_01165.1.g24148.t3	ref|XP_002311786.1| SIN3 component, histone deacetylase complex [Populus trichocarpa] gi|222851606|gb|EEE89153.1| SIN3 component, histone deacetylase complex [Populus trichocarpa]	308	1343	7.00E-26	436.0	20.1	31.8	SIN3 component, histone deacetylase complex	gbpln	Populus trichocarpa	AT1G59890.2 | Symbols: SNL5 | SIN3-like 5 | chr1:22044326-22050670 FORWARD LENGTH=1167	308	1167	8.00E-26	378.9	18.8	28.2
Rsa1.0_01165.1.g24149.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01166.1.g24150.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) – Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	1402	1333	0	95.1	46.0	60.8	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) – Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1402	575	5.00E-80	41.0	11.3	17.5
Rsa1.0_01166.1.g24151.t1	gb|EOA40001.1| hypothetical protein CARUB_v10008691mg [Capsella rubella]	573	578	0	100.9	85.5	92.7	hypothetical protein CARUB_v10008691mg	gbpln	Capsella rubella	AT1G11310.1 | Symbols: MLO2, ATMLO2, PMR2 | Seven transmembrane MLO family protein | chr1:3800899-3803870 REVERSE LENGTH=573	573	573	0	100.0	83.8	90.4
Rsa1.0_01166.1.g24152.t1	ref|NP_172592.1| sugar transporter 1 [Arabidopsis thaliana] gi|21542458|sp|P23586.2|STP1_ARATH RecName: Full=Sugar transport protein 1; AltName: Full=Glucose transporter; AltName: Full=Hexose transporter 1 gi|5734730|gb|AAD49995.1|AC007259_8 glucose transporter [Arabidopsis thaliana] gi|15809962|gb|AAL06908.1| At1g11260/T28P6_18 [Arabidopsis thaliana] gi|16604673|gb|AAL24129.1| putative glucose transporter protein [Arabidopsis thaliana] gi|22136870|gb|AAM91779.1| putative glucose transporter protein [Arabidopsis thaliana] gi|332190584|gb|AEE28705.1| sugar transporter 1 [Arabidopsis thaliana]	524	522	0	99.6	95.0	97.5	sugar transporter 1	gbpln	Arabidopsis thaliana	AT1G11260.1 | Symbols: STP1, ATSTP1 | sugar transporter 1 | chr1:3777460-3780133 FORWARD LENGTH=522	524	522	0	99.6	95.0	97.5
Rsa1.0_01166.1.g24153.t1	gb|EOA36707.1| hypothetical protein CARUB_v10012241mg [Capsella rubella]	165	173	4.00E-42	104.8	63.0	75.8	hypothetical protein CARUB_v10012241mg	gbpln	Capsella rubella	AT1G61340.1 | Symbols: | F-box family protein | chr1:22628526-22629741 FORWARD LENGTH=185	165	185	3.00E-30	112.1	54.5	70.9
Rsa1.0_01166.1.g24154.t1	ref|XP_002888093.1| SYP124 [Arabidopsis lyrata subsp. lyrata] gi|297333934|gb|EFH64352.1| SYP124 [Arabidopsis lyrata subsp. lyrata]	298	303	1.00E-159	101.7	91.6	96.3	SYP124	gbpln	Arabidopsis lyrata	AT1G61290.1 | Symbols: SYP124, ATSYP124 | syntaxin of plants 124 | chr1:22605188-22606216 FORWARD LENGTH=303	298	303	1.00E-159	101.7	89.9	96.3
Rsa1.0_01166.1.g24155.t1	gb|EOA37117.1| hypothetical protein CARUB_v10010339mg [Capsella rubella]	199	199	4.00E-61	100.0	75.9	85.9	hypothetical protein CARUB_v10010339mg	gbpln	Capsella rubella	AT1G11240.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Nucleolar protein 12 (InterPro:IPR019186); Has 2484 Blast hits to 1934 proteins in 262 species: Archae – 0; Bacteria – 90; Metazoa – 921; Fungi – 378; Plants – 144; Viruses – 18; Other Eukaryotes – 933 (source: NCBI BLink). | chr1:3766936-3768212 REVERSE LENGTH=200	199	200	6.00E-63	100.5	77.9	86.4
Rsa1.0_01166.1.g24156.t1	gb|AAD50002.1|AC007259_15 Unknown protein [Arabidopsis thaliana]	262	325	2.00E-60	124.0	57.6	69.8	Unknown protein	gbpln	Arabidopsis thaliana	AT1G11220.1 | Symbols: | Protein of unknown function (DUF761) | chr1:3760022-3761165 REVERSE LENGTH=310	262	310	8.00E-63	118.3	57.6	69.8
Rsa1.0_01166.1.g24157.t1	gb|AAM65215.1| unknown [Arabidopsis thaliana]	293	308	2.00E-80	105.1	62.5	75.4	unknown	gbpln	Arabidopsis thaliana	AT1G11210.1 | Symbols: | Protein of unknown function (DUF761) | chr1:3755876-3756911 REVERSE LENGTH=308	293	308	1.00E-82	105.1	62.1	75.4
Rsa1.0_01166.1.g24158.t22	gb|EOA40454.1| hypothetical protein CARUB_v10009178mg [Capsella rubella]	748	438	0	58.6	47.1	50.4	hypothetical protein CARUB_v10009178mg	gbpln	Capsella rubella	AT1G11170.1 | Symbols: | Protein of unknown function (DUF707) | chr1:3741724-3744459 FORWARD LENGTH=438	748	438	0	58.6	47.3	49.7

Rsa1.0_01166.1.g24159.t1	ref|NP_172580.2| protein STRUBBELIG [Arabidopsis thaliana] gi|75158778|sp|Q8RWZ1.1|SUB_ARATH RecName: Full=Protein STRUBBELIG; AltName: Full=Leucine-rich repeat receptor kinase-like protein SUB; AltName: Full=Protein SCRAMBLED; Flags: Precursor gi|33307660|gb|AAQ03031.1|AF399923_1 LRR receptor kinase [Arabidopsis thaliana] gi|20259441|gb|AAM14041.1| unknown protein [Arabidopsis thaliana] gi|21436211|gb|AAM51393.1| unknown protein [Arabidopsis thaliana] gi|110742467|dbj|BAE99152.1| LRR receptor-like protein kinase strubbelig [Arabidopsis thaliana] gi|224589388|gb|ACN59228.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332190569|gb|AEE28690.1| protein STRUBBELIG [Arabidopsis thaliana]	754	768	0	101.9	88.1	93.0	protein STRUBBELIG	gbpln	Arabidopsis thaliana	AT1G11130.1 | Symbols: SUB, SCM, SRF9 | Leucine-rich repeat protein kinase family protein | chr1:3723135-3727178 FORWARD LENGTH=768	754	768	0	101.9	88.1	93.0
Rsa1.0_01167.1.g24160.t1	ref|NP_197172.1| glycosyl hydrolase family 5 protein [Arabidopsis thaliana] gi|9755722|emb|CAC01834.1| putative protein [Arabidopsis thaliana] gi|332004944|gb|AED92327.1| glycosyl hydrolase family 5 protein [Arabidopsis thaliana]	575	488	0	84.9	68.5	73.7	glycosyl hydrolase family 5 protein	gbpln	Arabidopsis thaliana	AT5G16700.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr5:5480763-5483045 FORWARD LENGTH=488	575	488	0	84.9	68.5	73.7
Rsa1.0_01167.1.g24161.t1	ref|XP_002892663.1| hypothetical protein ARALYDRAFT_312221 [Arabidopsis lyrata subsp. lyrata] gi|297338505|gb|EFH68922.1| hypothetical protein ARALYDRAFT_312221 [Arabidopsis lyrata subsp. lyrata]	165	383	8.00E-63	232.1	69.1	70.9	hypothetical protein ARALYDRAFT_312221	gbpln	Arabidopsis lyrata	AT1G11920.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:4023667-4025097 REVERSE LENGTH=384	165	384	2.00E-63	232.7	67.3	69.7
Rsa1.0_01167.1.g24162.t1	gb|EOA36500.1| hypothetical protein CARUB_v10011187mg [Capsella rubella]	372	385	1.00E-167	103.5	78.2	84.9	hypothetical protein CARUB_v10011187mg	gbpln	Capsella rubella	AT1G11920.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:4023667-4025097 REVERSE LENGTH=384	372	384	1.00E-170	103.2	78.2	85.2
Rsa1.0_01167.1.g24163.t1	ref|XP_002889903.1| hypothetical protein ARALYDRAFT_471341 [Arabidopsis lyrata subsp. lyrata] gi|297335745|gb|EFH66162.1| hypothetical protein ARALYDRAFT_471341 [Arabidopsis lyrata subsp. lyrata]	136	329	4.00E-59	241.9	86.0	94.1	hypothetical protein ARALYDRAFT_471341	gbpln	Arabidopsis lyrata	AT1G11915.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G17350.1); Has 261 Blast hits to 261 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 261; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4021830-4023084 FORWARD LENGTH=329	136	329	2.00E-60	241.9	83.8	93.4
Rsa1.0_01167.1.g24164.t1	ref|XP_002878123.1| OBP3-responsive gene 3 [Arabidopsis lyrata subsp. lyrata] gi|297323961|gb|EFH54382.1| OBP3-responsive gene 3 [Arabidopsis lyrata subsp. lyrata]	234	258	1.00E-70	110.3	64.5	78.6	OBP3-responsive gene 3	gbpln	Arabidopsis lyrata	AT3G56970.1 | Symbols: BHLH038, ORG2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:21084204-21085094 REVERSE LENGTH=253	234	253	4.00E-73	108.1	61.1	76.1
Rsa1.0_01167.1.g24165.t1	dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	281	1098	1.00E-41	390.7	37.4	53.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01167.1.g24166.t1	gb|EOA29734.1| hypothetical protein CARUB_v10012821mg [Capsella rubella]	1333	1343	0	100.8	84.5	90.3	hypothetical protein CARUB_v10012821mg	gbpln	Capsella rubella	AT3G23670.1 | Symbols: PAKRP1L, KINESIN-12B | phragmoplast-associated kinesin-related protein, putative | chr3:8519290-8525055 FORWARD LENGTH=1313	1333	1313	0	98.5	84.2	90.0
Rsa1.0_01167.1.g24167.t1	gb|ABD32665.1| Terpenoid cylases/protein prenyltransferase alpha-alpha toroid; Bacterial adhesion [Medicago truncatula]	285	426	1.00E-115	149.5	76.1	85.6	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid; Bacterial adhesion	gbpln	Medicago truncatula	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	285	343	6.00E-36	120.4	31.6	42.8
Rsa1.0_01167.1.g24168.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01167.1.g24169.t1	gb|AAF79675.1|AC022314_16 F9C16.30 [Arabidopsis thaliana]	618	1001	7.00E-55	162.0	22.8	31.7	F9C16.30	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01167.1.g24170.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01168.1.g24171.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_01168.1.g24172.t1</td><td>gb|EOA29791.1| hypothetical protein CARUB_v10012886mg, partial [Capsella rubella]</td><td>899</td><td>1011</td><td>0</td><td>112.5</td><td>77.0</td><td>84.4</td><td>hypothetical protein CARUB_v10012886mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G10310.1 | Symbols: | P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain | chr3:3190208-3195005 FORWARD LENGTH=922</td><td>899</td><td>922</td><td>0</td><td>102.6</td><td>73.6</td><td>81.0</td></tr>
<tr><td>Rsa1.0_01168.1.g24173.t1</td><td>ref|NP_187746.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|12322904|gb|AAG51442.1|AC008153_15 unknown protein; 12363-14495 [Arabidopsis thaliana] gi|332641516|gb|AEE75037.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]</td><td>738</td><td>710</td><td>0</td><td>96.2</td><td>47.8</td><td>54.5</td><td>cysteine/histidine-rich C1 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G11390.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:3569828-3571960 FORWARD LENGTH=710</td><td>738</td><td>710</td><td>0</td><td>96.2</td><td>47.8</td><td>54.5</td></tr>
<tr><td>Rsa1.0_01168.1.g24174.t1</td><td>ref|NP_187746.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|12322904|gb|AAG51442.1|AC008153_15 unknown protein; 12363-14495 [Arabidopsis thaliana] gi|332641516|gb|AEE75037.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]</td><td>621</td><td>710</td><td>0</td><td>114.3</td><td>59.9</td><td>69.9</td><td>cysteine/histidine-rich C1 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G11390.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:3569828-3571960 FORWARD LENGTH=710</td><td>621</td><td>710</td><td>0</td><td>114.3</td><td>59.9</td><td>69.9</td></tr>
<tr><td>Rsa1.0_01168.1.g24175.t1</td><td>ref|XP_002882573.1| hypothetical protein ARALYDRAFT_478161 [Arabidopsis lyrata subsp. lyrata] gi|297328413|gb|EFH58832.1| hypothetical protein ARALYDRAFT_478161 [Arabidopsis lyrata subsp. lyrata]</td><td>311</td><td>315</td><td>1.00E-112</td><td>101.3</td><td>78.5</td><td>87.8</td><td>hypothetical protein ARALYDRAFT_478161</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G08600.1 | Symbols: | Protein of unknown function (DUF1191) | chr3:2612646-2613596 FORWARD LENGTH=316</td><td>311</td><td>316</td><td>1.00E-110</td><td>101.6</td><td>74.9</td><td>82.0</td></tr>
<tr><td>Rsa1.0_01168.1.g24176.t1</td><td>gb|AAP21180.1| At3g08610 [Arabidopsis thaliana]</td><td>65</td><td>73</td><td>1.00E-29</td><td>112.3</td><td>96.9</td><td>98.5</td><td>At3g08610</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G08610.1 | Symbols: | unknown protein; Has 40 Blast hits to 40 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:2616435-2616768 REVERSE LENGTH=65</td><td>65</td><td>65</td><td>3.00E-32</td><td>100.0</td><td>96.9</td><td>98.5</td></tr>
<tr><td>Rsa1.0_01168.1.g24177.t1</td><td>gb|EOA30171.1| hypothetical protein CARUB_v10013288mg [Capsella rubella]</td><td>597</td><td>595</td><td>0</td><td>99.7</td><td>92.0</td><td>96.1</td><td>hypothetical protein CARUB_v10013288mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G08650.2 | Symbols: | ZIP metal ion transporter family | chr3:2624694-2627308 REVERSE LENGTH=619</td><td>597</td><td>619</td><td>0</td><td>103.7</td><td>92.1</td><td>96.0</td></tr>
<tr><td>Rsa1.0_01168.1.g24178.t1</td><td>ref|NP_187478.1| phototropic-responsive NPH3-like protein [Arabidopsis thaliana] gi|75262254|sp|Q9C9Z0.1|Y3866_ARATH RecName: Full=Putative BTB/POZ domain-containing protein At3g08660 gi|12322729|gb|AAG51353.1|AC012562_14 putative non-phototropic hypocotyl; 42053-44089 [Arabidopsis thaliana] gi|332641139|gb|AEE74660.1| phototropic-responsive NPH3-like protein [Arabidopsis thaliana]</td><td>613</td><td>582</td><td>0</td><td>94.9</td><td>71.5</td><td>80.6</td><td>phototropic-responsive NPH3-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G08660.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr3:2631130-2633166 FORWARD LENGTH=582</td><td>613</td><td>582</td><td>0</td><td>94.9</td><td>71.5</td><td>80.6</td></tr>
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Rsa1.0_01168.1.g24179.t3	ref|NP_566331.1| ubiquitin-conjugating enzyme E2 11 [Arabidopsis thaliana] gi|334185174|ref|NP_001189841.1| ubiquitin-conjugating enzyme E2 11 [Arabidopsis thaliana] gi|297829396|ref|XP_002882580.1| ubiquitin-conjugating enzyme 11 [Arabidopsis lyrata subsp. lyrata] gi|12643427|sp|P35134.2|UBC11_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 11; AltName: Full=Ubiquitin carrier protein 11; AltName: Full=Ubiquitin-conjugating enzyme E2-17 kDa 11; AltName: Full=Ubiquitin-protein ligase 11 gi|12322738|gb|AAG51362.1|AC012562_23 putative ubiquitin conjugating enzyme; 52410-53412 [Arabidopsis thaliana] gi|17380790|gb|AAL36225.1| putative E2, ubiquitin-conjugating enzyme UBC11 [Arabidopsis thaliana] gi|20259611|gb|AAM14162.1| putative ubiquitin conjugating enzyme 11 (UBC11) [Arabidopsis thaliana] gi|21554241|gb|AAM63316.1| E2, ubiquitin-conjugating enzyme UBC11 [Arabidopsis thaliana] gi|66354432|gb|AAY44851.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|110736468|dbj|BAF00202.1| putative ubiquitin conjugating enzyme [Arabidopsis thaliana] gi|297328420|gb|EFH58839.1| ubiquitin-conjugating enzyme 11 [Arabidopsis	148	148	8.00E-81	100.0	98.0	100.0	ubiquitin-conjugating enzyme E2 11	gbpln	Arabidopsis lyrata	AT3G08690.2 | Symbols: UBC11 | ubiquitin-conjugating enzyme 11 | chr3:2641487-2642489 FORWARD LENGTH=148	148	148	2.00E-83	100.0	98.0	100.0
Rsa1.0_01168.1.g24180.t1	ref|XP_002882582.1| thioredoxin H-type 9 [Arabidopsis lyrata subsp. lyrata] gi|297328422|gb|EFH58841.1| thioredoxin H-type 9 [Arabidopsis lyrata subsp. lyrata]	140	141	2.00E-70	100.7	89.3	97.9	thioredoxin H-type 9	gbpln	Arabidopsis lyrata	AT3G08710.2 | Symbols: ATH9, TRX H9, TH9 | thioredoxin H-type 9 | chr3:2645590-2646304 FORWARD LENGTH=140	140	140	1.00E-71	100.0	88.6	97.1
Rsa1.0_01168.1.g24181.t1	gb|EOA29639.1| hypothetical protein CARUB_v10014964mg [Capsella rubella]	115	113	5.00E-36	98.3	62.6	78.3	hypothetical protein CARUB_v10014964mg	gbpln	Capsella rubella	AT3G08770.1 | Symbols: LTP6 | lipid transfer protein 6 | chr3:2664349-2664784 REVERSE LENGTH=113	115	113	8.00E-35	98.3	58.3	70.4
Rsa1.0_01168.1.g24182.t2	ref|XP_002884699.1| D-alanine--D-alanine ligase family [Arabidopsis lyrata subsp. lyrata] gi|297330539|gb|EFH60958.1| D-alanine--D-alanine ligase family [Arabidopsis lyrata subsp. lyrata]	975	943	0	96.7	80.5	86.5	D-alanine--D-alanine ligase family	gbpln	Arabidopsis lyrata	AT3G08840.2 | Symbols: | D-alanine--D-alanine ligase family | chr3:2679648-2686157 REVERSE LENGTH=937	975	937	0	96.1	80.2	86.5
Rsa1.0_01169.1.g24183.t1	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	183	1463	5.00E-62	799.5	57.9	69.9	F5J5.1	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	183	1262	9.00E-21	689.6	26.2	37.2
Rsa1.0_01169.1.g24184.t4	gb|EOA23251.1| hypothetical protein CARUB_v10017299mg [Capsella rubella]	468	431	3.00E-28	92.1	17.7	27.4	hypothetical protein CARUB_v10017299mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01169.1.g24185.t1	ref|XP_002884894.1| hypothetical protein ARALYDRAFT_897434 [Arabidopsis lyrata subsp. lyrata] gi|297330734|gb|EFH61153.1| hypothetical protein ARALYDRAFT_897434 [Arabidopsis lyrata subsp. lyrata]	152	435	1.00E-50	286.2	69.7	75.7	hypothetical protein ARALYDRAFT_897434	gbpln	Arabidopsis lyrata	AT3G12230.1 | Symbols: scpl14 | serine carboxypeptidase-like 14 | chr3:3899431-3901879 REVERSE LENGTH=435	152	435	1.00E-52	286.2	70.4	76.3
Rsa1.0_01169.1.g24186.t1	ref|XP_002893642.1| hypothetical protein ARALYDRAFT_473306 [Arabidopsis lyrata subsp. lyrata] gi|297339484|gb|EFH69901.1| hypothetical protein ARALYDRAFT_473306 [Arabidopsis lyrata subsp. lyrata]	611	613	0	100.3	84.1	89.5	hypothetical protein ARALYDRAFT_473306	gbpln	Arabidopsis lyrata	AT1G30755.1 | Symbols: | Protein of unknown function (DUF668) | chr1:10905991-10908773 REVERSE LENGTH=615	611	615	0	100.7	82.0	87.7
Rsa1.0_01169.1.g24187.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01169.1.g24188.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	358	1142	8.00E-45	319.0	34.1	50.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	358	575	2.00E-21	160.6	13.4	19.3
Rsa1.0_01169.1.g24189.t1	gb|EOA40128.1| hypothetical protein CARUB_v10008835mg [Capsella rubella]	534	527	0	98.7	90.8	94.9	hypothetical protein CARUB_v10008835mg	gbpln	Capsella rubella	AT1G30760.1 | Symbols: | FAD-binding Berberine family protein | chr1:10918321-10920441 FORWARD LENGTH=534	534	534	0	100.0	91.4	96.3
Rsa1.0_01169.1.g24190.t2	gb|ABD64964.1| hypothetical protein 25.t00001 [Brassica oleracea]	509	1103	3.00E-35	216.7	15.7	18.5	hypothetical protein 25.t00001	gbpln	Brassica oleracea	AT3G28570.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:10710534-10711889 FORWARD LENGTH=451	509	451	3.00E-26	88.6	12.0	14.5

Rsa1.0_01169.1.g24191.t2	ref|NP_173766.1| uncharacterized protein [Arabidopsis thaliana] gi|8778585|gb|AAF79593.1|AC007945_13 F28C11.15 [Arabidopsis thaliana] gi|4056435|gb|AAC98008.1| Similar to OBP32pep protein gb|U37698 from Arabidopsis thaliana [Arabidopsis thaliana] gi|332192277|gb|AEE30398.1| uncharacterized protein AT1G23520 [Arabidopsis thaliana]	247	263	6.00E−51	106.5	47.4	65.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23520.1 | Symbols: | Domain of unknown function (DUF220) | chr1:8343571−8344675 REVERSE LENGTH=263	247	263	2.00E−53	106.5	47.4	65.2
Rsa1.0_01169.1.g24192.t4	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01169.1.g24193.t2	emb|CAB10225.1| retrovirus−related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus−related like polyprotein [Arabidopsis thaliana]	1262	1489	0	118.0	55.2	68.1	retrovirus−related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1262	1262	2.00E−52	100.0	7.7	10.1
Rsa1.0_01169.1.g24194.t1	ref|NP_173766.1| uncharacterized protein [Arabidopsis thaliana] gi|8778585|gb|AAF79593.1|AC007945_13 F28C11.15 [Arabidopsis thaliana] gi|4056435|gb|AAC98008.1| Similar to OBP32pep protein gb|U37698 from Arabidopsis thaliana [Arabidopsis thaliana] gi|332192277|gb|AEE30398.1| uncharacterized protein AT1G23520 [Arabidopsis thaliana]	223	263	2.00E−48	117.9	53.4	69.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G23520.1 | Symbols: | Domain of unknown function (DUF220) | chr1:8343571−8344675 REVERSE LENGTH=263	223	263	7.00E−51	117.9	53.4	69.5
Rsa1.0_01170.1.g24195.t1	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	1055	1274	0	120.8	48.0	63.8	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	1055	575	4.00E−60	54.5	15.2	24.2
Rsa1.0_01170.1.g24196.t1	gb|EOA19955.1| hypothetical protein CARUB_v10000205mg [Capsella rubella]	863	855	0	99.1	77.5	85.2	hypothetical protein CARUB_v10000205mg	gbpln	Capsella rubella	AT5G16630.2 | Symbols: ATRAD4, RAD4 | DNA repair protein Rad4 family | chr5:5455325−5459461 FORWARD LENGTH=865	863	865	0	100.2	75.6	83.4
Rsa1.0_01170.1.g24197.t2	gb|EOA20659.1| hypothetical protein CARUB_v10000974mg [Capsella rubella]	454	441	0	97.1	80.6	85.5	hypothetical protein CARUB_v10000974mg	gbpln	Capsella rubella	AT5G16620.1 | Symbols: PDE120, TIC40, ATTIC40 | hydroxyproline−rich glycoprotein family protein | chr5:5450808−5454256 FORWARD LENGTH=447	454	447	1.00E−179	98.5	81.9	87.0
Rsa1.0_01170.1.g24198.t1	ref|NP_174394.1| F−box domain−containing protein [Arabidopsis thaliana] gi|75336888|sp|Q9SA02.1|FB26_ARATH RecName: Full=F−box protein At1g31080 gi|4512631|gb|AAD21700.1| Contains similarity to gi|3249080 T13D8.24 MYB transcription factor homolog from A. thaliana BAC gb|AC004473 [Arabidopsis thaliana] gi|67633404|gb|AAY78627.1| F−box family protein [Arabidopsis thaliana] gi|332193191|gb|AEE31312.1| F−box domain−containing protein [Arabidopsis thaliana]	314	355	8.00E−49	113.1	45.5	60.8	F−box domain−containing protein	gbpln	Arabidopsis thaliana	AT1G31080.1 | Symbols: | F−box family protein | chr1:11091832−11092899 FORWARD LENGTH=355	314	355	2.00E−51	113.1	45.5	60.8
Rsa1.0_01170.1.g24199.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1398	1307	0	93.5	59.2	73.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1398	1262	5.00E−96	90.3	13.1	21.0
Rsa1.0_01170.1.g24200.t1	ref|XP_002873779.1| rop−interactive crib motif−containing protein 4 [Arabidopsis lyrata subsp. lyrata] gi|297319616|gb|EFH50038.1| rop−interactive crib motif−containing protein 4 [Arabidopsis lyrata subsp. lyrata]	150	153	3.00E−59	102.0	82.7	90.0	rop−interactive crib motif−containing protein 4	gbpln	Arabidopsis lyrata	AT5G16490.1 | Symbols: RIC4 | ROP−interactive CRIB motif−containing protein 4 | chr5:5384468−5385205 REVERSE LENGTH=153	150	153	2.00E−59	102.0	79.3	86.7
Rsa1.0_01170.1.g24201.t1	ref|XP_002873778.1| hypothetical protein ARALYDRAFT_488502 [Arabidopsis lyrata subsp. lyrata] gi|297319615|gb|EFH50037.1| hypothetical protein ARALYDRAFT_488502 [Arabidopsis lyrata subsp. lyrata]	208	203	1.00E−101	97.6	85.6	90.9	hypothetical protein ARALYDRAFT_488502	gbpln	Arabidopsis lyrata	AT5G16480.1 | Symbols: | Phosphotyrosine protein phosphatases superfamily protein | chr5:5381334−5382618 REVERSE LENGTH=204	208	204	1.00E−102	98.1	85.6	91.3
Rsa1.0_01170.1.g24202.t1	gb|EOA31756.1| hypothetical protein CARUB_v10014973mg [Capsella rubella]	115	107	2.00E−40	93.0	75.7	81.7	hypothetical protein CARUB_v10014973mg	gbpln	Capsella rubella	AT3G15420.1 | Symbols: | Transcription factor TFIIIC, tau55−related protein | chr3:5207704−5208289 REVERSE LENGTH=107	115	107	3.00E−42	93.0	72.2	83.5

Rsa1.0_01170.1.g24203.t1	ref|XP_002884979.1| hypothetical protein ARALYDRAFT_897607 [Arabidopsis lyrata subsp. lyrata] gi|297330819|gb|EFH61238.1| hypothetical protein ARALYDRAFT_897607 [Arabidopsis lyrata subsp. lyrata]	380	398	1.00E-96	104.7	54.5	68.9	hypothetical protein ARALYDRAFT_897607	gbpln	Arabidopsis lyrata	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	380	395	8.00E-97	103.9	54.7	68.7
Rsa1.0_01170.1.g24204.t1	ref|NP_197151.1| C2H2 type zinc finger protein [Arabidopsis thaliana] gi|297807673|ref|XP_002871720.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|9759129|dbj|BAB09614.1| unnamed protein product [Arabidopsis thaliana] gi|27808636|gb|AAO24598.1| At5g16470 [Arabidopsis thaliana] gi|110736298|dbj|BAF00119.1| hypothetical protein [Arabidopsis thaliana] gi|297317557|gb|EFH47979.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|332004914|gb|AED92297.1| C2H2 type zinc finger protein [Arabidopsis thaliana] gi|482557657|gb|EOA21849.1| hypothetical protein CARUB_v10002316mg [Capsella rubella]	129	104	7.00E-44	80.6	77.5	78.3	C2H2 type zinc finger protein	gbpln	Arabidopsis lyrata	AT5G16470.1 | Symbols: | zinc finger (C2H2 type) family protein | chr5:5379516-5379830 FORWARD LENGTH=104	129	104	2.00E-46	80.6	77.5	78.3
Rsa1.0_01170.1.g24205.t1	ref|NP_197150.1| Putative adipose-regulatory protein (Seipin) [Arabidopsis thaliana] gi|9759128|dbj|BAB09613.1| unnamed protein product [Arabidopsis thaliana] gi|332004913|gb|AED92296.1| Putative adipose-regulatory protein (Seipin) [Arabidopsis thaliana]	357	368	1.00E-161	103.1	75.6	82.9	Putative adipose-regulatory protein (Seipin)	gbpln	Arabidopsis thaliana	AT5G16460.1 | Symbols: | Putative adipose-regulatory protein (Seipin) | chr5:5377085-5378533 REVERSE LENGTH=368	357	368	1.00E-164	103.1	75.6	82.9
Rsa1.0_01170.1.g24206.t1	ref|NP_001031891.1| defensin-like protein 24 [Arabidopsis thaliana] gi|122209268|sp|Q2V371.1|DEF24_ARATH RecName: Full=Defensin-like protein 24; Flags: Precursor gi|113204464|gb|ABI34025.1| unknown [Arabidopsis thaliana] gi|332004912|gb|AED92295.1| defensin-like protein 24 [Arabidopsis thaliana]	85	88	7.00E-17	103.5	58.8	75.3	defensin-like protein 24	gbpln	Arabidopsis thaliana	AT5G16453.1 | Symbols: | Defensin-like (DEFL) family protein | chr5:5375543-5375919 REVERSE LENGTH=88	85	88	1.00E-19	103.5	58.8	75.3
Rsa1.0_01170.1.g24207.t1	ref|NP_197145.2| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|50253516|gb|AAT71960.1| At5g16410 [Arabidopsis thaliana] gi|53850537|gb|AAU95445.1| At5g16410 [Arabidopsis thaliana] gi|332004906|gb|AED92289.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	456	480	0	105.3	78.1	86.2	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT5G16410.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:5365685-5367383 REVERSE LENGTH=480	456	480	0	105.3	78.1	86.2
Rsa1.0_01170.1.g24208.t1	ref|NP_197144.1| thioredoxin F2 [Arabidopsis thaliana] gi|11135405|sp|Q9XFH9.1|TRXF2_ARATH RecName: Full=Thioredoxin F2, chloroplastic; Short=AtTrxf2; AltName: Full=Thioredoxin F1; Short=AtTrxf1; Flags: Precursor gi|4973254|gb|AAD35004.1|AF144386_1 thioredoxin f2 [Arabidopsis thaliana] gi|13878187|gb|AAK44171.1|AF370356_1 putative thioredoxin f2 protein [Arabidopsis thaliana] gi|9759122|dbj|BAB09607.1| thioredoxin f2 [Arabidopsis thaliana] gi|16323396|gb|AAL15192.1| putative thioredoxin f2 protein [Arabidopsis thaliana] gi|332004905|gb|AED92288.1| thioredoxin F2 [Arabidopsis thaliana]	188	185	1.00E-82	98.4	80.9	91.0	thioredoxin F2	gbpln	Arabidopsis thaliana	AT5G16400.1 | Symbols: TRXF2, ATF2 | thioredoxin F2 | chr5:5363905-5365249 REVERSE LENGTH=185	188	185	5.00E-85	98.4	80.9	91.0
Rsa1.0_01170.1.g24209.t1	gb|AEI16459.1| chloroplast acetyl-CoA carboxylase biotin-containing subunit [Brassica rapa]	278	276	1.00E-115	99.3	87.1	89.6	chloroplast acetyl-CoA carboxylase biotin-containing subunit	gbpln	Brassica rapa	AT5G16390.1 | Symbols: CAC1, CAC1A, BCCP, BCCP1 | chloroplastic acetylcoenzyme A carboxylase 1 | chr5:5361098-5363020 REVERSE LENGTH=280	278	280	1.00E-105	100.7	83.5	87.8
Rsa1.0_01170.1.g24210.t9	ref|XP_002871712.1| hypothetical protein ARALYDRAFT_909607 [Arabidopsis lyrata subsp. lyrata] gi|297317549|gb|EFH47971.1| hypothetical protein ARALYDRAFT_909607 [Arabidopsis lyrata subsp. lyrata]	953	1030	0	108.1	64.1	71.5	hypothetical protein ARALYDRAFT_909607	gbpln	Arabidopsis lyrata	AT5G16270.1 | Symbols: ATRAD21.3, SYN4 | sister chromatid cohesion 1 protein 4 | chr5:5316783-5322330 FORWARD LENGTH=1031	953	1031	0	108.2	62.9	69.8

<table>
<tr><td>Rsa1.0_01170.1.g24211.t2</td><td>ref|XP_002871711.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317548|gb|EFH47970.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>494</td><td>519</td><td>2.00E-40</td><td>105.1</td><td>15.6</td><td>19.0</td><td>RNA recognition motif-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G16260.1 | Symbols: ELF9 | RNA binding (RRM/RBD/RNP motifs) family protein | chr5:5311363-5315496 FORWARD LENGTH=519</td><td>494</td><td>519</td><td>2.00E-42</td><td>105.1</td><td>15.4</td><td>19.0</td></tr>
<tr><td>Rsa1.0_01170.1.g24212.t1</td><td>gb|AAF79687.1|AC022314_28 F9C16.9 [Arabidopsis thaliana]</td><td>258</td><td>946</td><td>6.00E-42</td><td>366.7</td><td>39.1</td><td>53.1</td><td>F9C16.9</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01170.1.g24213.t1</td><td>gb|ABD64950.1| GRF zinc finger containing protein [Brassica oleracea]</td><td>136</td><td>180</td><td>2.00E-56</td><td>132.4</td><td>77.9</td><td>86.8</td><td>GRF zinc finger containing protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G15690.1 | Symbols: | zinc ion binding | chr5:5113823-5114402 REVERSE LENGTH=169</td><td>136</td><td>169</td><td>1.00E-11</td><td>124.3</td><td>25.0</td><td>36.0</td></tr>
<tr><td>Rsa1.0_01170.1.g24214.t7</td><td>gb|EOA19955.1| hypothetical protein CARUB_v10000205mg [Capsella rubella]</td><td>556</td><td>855</td><td>0</td><td>153.8</td><td>76.3</td><td>83.6</td><td>hypothetical protein CARUB_v10000205mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G16630.2 | Symbols: ATRAD4, RAD4 | DNA repair protein Rad4 family | chr5:5455325-5459461 FORWARD LENGTH=865</td><td>556</td><td>865</td><td>0</td><td>155.6</td><td>71.8</td><td>80.0</td></tr>
<tr><td>Rsa1.0_01171.1.g24215.t1</td><td>gb|EOA35357.1| hypothetical protein CARUB_v10020551mg [Capsella rubella]</td><td>357</td><td>354</td><td>0</td><td>99.2</td><td>93.3</td><td>96.4</td><td>hypothetical protein CARUB_v10020551mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G79430.2 | Symbols: APL, WDY | Homeodomain-like superfamily protein | chr1:29877521-29879135 REVERSE LENGTH=358</td><td>357</td><td>358</td><td>0</td><td>100.3</td><td>95.0</td><td>96.9</td></tr>
<tr><td>Rsa1.0_01171.1.g24216.t1</td><td>ref|NP_178062.1| succinate-semialdehyde dehydrogenase [Arabidopsis thaliana] gi|118575126|sp|Q9SAK4.2|SSDH_ARATH RecName: Full=Succinate-semialdehyde dehydrogenase, mitochondrial; Short=At-SSADH1; AltName: Full=Aldehyde dehydrogenase family 5 member F1; AltName: Full=NAD(+)-dependent succinic semialdehyde dehydrogenase; Flags: Precursor gi|6684442|gb|AAF23590.1|AF117335_1 succinic semialdehyde dehydrogenase [Arabidopsis thaliana] gi|16226915|gb|AAL16297.1|AF428367_1 At1g79440/T8K14_14 [Arabidopsis thaliana] gi|15810165|gb|AAL07226.1| putative succinic semialdehyde dehydrogenase gabD [Arabidopsis thaliana] gi|332198122|gb|AEE36243.1| succinate-semialdehyde dehydrogenase [Arabidopsis thaliana]</td><td>514</td><td>528</td><td>0</td><td>102.7</td><td>91.4</td><td>96.1</td><td>succinate-semialdehyde dehydrogenase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G79440.1 | Symbols: ALDH5F1, SSADH1, SSADH | aldehyde dehydrogenase 5F1 | chr1:29882525-29887275 REVERSE LENGTH=528</td><td>514</td><td>528</td><td>0</td><td>102.7</td><td>91.4</td><td>96.1</td></tr>
<tr><td>Rsa1.0_01171.1.g24217.t3</td><td>ref|NP_178064.1| Ent-kaur-16-ene synthase [Arabidopsis thaliana] gi|62900442|sp|Q9SAK2.1|KSB_ARATH RecName: Full=Ent-kaur-16-ene synthase, chloroplastic; AltName: Full=Ent-kaurene synthase; Short=AtKS; AltName: Full=Ent-kaurene synthase B; Short=KSB; AltName: Full=Protein GA REQUIRING 2; Flags: Precursor gi|4835764|gb|AAD30231.1|AC007202_13 Identical to gb|AF034774 ent-kaurene synthase (GA2) from Arabidopsis thaliana [Arabidopsis thaliana] gi|332198125|gb|AEE36246.1| Ent-kaur-16-ene synthase [Arabidopsis thaliana]</td><td>1178</td><td>785</td><td>0</td><td>66.6</td><td>55.6</td><td>60.9</td><td>Ent-kaur-16-ene synthase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G79460.1 | Symbols: GA2, KS, ATKS, ATKS1, KS1 | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr1:29890568-29894436 FORWARD LENGTH=785</td><td>1178</td><td>785</td><td>0</td><td>66.6</td><td>55.6</td><td>60.9</td></tr>
<tr><td>Rsa1.0_01171.1.g24218.t1</td><td>gb|EOA35064.1| hypothetical protein CARUB_v10020175mg [Capsella rubella]</td><td>503</td><td>503</td><td>0</td><td>100.0</td><td>92.2</td><td>96.6</td><td>hypothetical protein CARUB_v10020175mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G79470.1 | Symbols: | Aldolase-type TIM barrel family protein | chr1:29894772-29896661 REVERSE LENGTH=503</td><td>503</td><td>503</td><td>0</td><td>100.0</td><td>91.3</td><td>96.0</td></tr>
<tr><td>Rsa1.0_01171.1.g24219.t2</td><td>ref|XP_002889247.1| hypothetical protein ARALYDRAFT_477115 [Arabidopsis lyrata subsp. lyrata] gi|297335088|gb|EFH65506.1| hypothetical protein ARALYDRAFT_477115 [Arabidopsis lyrata subsp. lyrata]</td><td>402</td><td>386</td><td>1.00E-124</td><td>96.0</td><td>75.4</td><td>82.3</td><td>hypothetical protein ARALYDRAFT_477115</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G79480.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr1:29897905-29899267 REVERSE LENGTH=397</td><td>402</td><td>397</td><td>3.00E-68</td><td>98.8</td><td>39.1</td><td>41.5</td></tr>
<tr><td>Rsa1.0_01171.1.g24220.t1</td><td>ref|NP_178070.2| Cation efflux family protein [Arabidopsis thaliana] gi|310947336|sp|Q9SAJ7.2|MTP9_ARATH RecName: Full=Metal tolerance protein 9; Short=AtMTP9 gi|332198137|gb|AEE36258.1| Cation efflux family protein [Arabidopsis thaliana]</td><td>401</td><td>402</td><td>0</td><td>100.2</td><td>92.5</td><td>94.8</td><td>Cation efflux family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G79520.1 | Symbols: | Cation efflux family protein | chr1:29912369-29914515 REVERSE LENGTH=402</td><td>401</td><td>402</td><td>0</td><td>100.2</td><td>92.5</td><td>94.8</td></tr>
</table>

Rsa1.0_01171.1.g24221.t1	ref|XP_002889252.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335093|gb|EFH65511.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	786	780	0	99.2	84.1	91.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G79540.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:29920334-29922676 REVERSE LENGTH=780	786	780	0	99.2	84.7	91.7
Rsa1.0_01171.1.g24222.t1	gb|EOA35321.1| hypothetical protein CARUB_v10020504mg [Capsella rubella]	355	368	1.00E-163	103.7	88.5	92.1	hypothetical protein CARUB_v10020504mg	gbpln	Capsella rubella	AT1G79580.3 | Symbols: SMB | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:29941020-29942925 REVERSE LENGTH=371	355	371	1.00E-152	104.5	87.3	91.3
Rsa1.0_01171.1.g24223.t1	ref|XP_002887794.1| hypothetical protein ARALYDRAFT_477131 [Arabidopsis lyrata subsp. lyrata] gi|297333635|gb|EFH64053.1| hypothetical protein ARALYDRAFT_477131 [Arabidopsis lyrata subsp. lyrata]	230	233	1.00E-120	101.3	93.0	97.8	hypothetical protein ARALYDRAFT_477131	gbpln	Arabidopsis lyrata	AT1G79590.2 | Symbols: SYP52, ATSYP52 | syntaxin of plants 52 | chr1:29947064-29948304 FORWARD LENGTH=233	230	233	1.00E-120	101.3	92.2	96.1
Rsa1.0_01172.1.g24224.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01172.1.g24225.t1	ref|XP_002881497.1| hypothetical protein ARALYDRAFT_482714 [Arabidopsis lyrata subsp. lyrata] gi|297327336|gb|EFH57756.1| hypothetical protein ARALYDRAFT_482714 [Arabidopsis lyrata subsp. lyrata]	279	289	1.00E-108	103.6	80.6	84.9	hypothetical protein ARALYDRAFT_482714	gbpln	Arabidopsis lyrata	AT2G37220.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:15634980-15636331 REVERSE LENGTH=289	279	289	1.00E-107	103.6	79.9	84.9
Rsa1.0_01172.1.g24226.t1	ref|XP_002879658.1| ADK/ATPADK1 [Arabidopsis lyrata subsp. lyrata] gi|297325497|gb|EFH55917.1| ADK/ATPADK1 [Arabidopsis lyrata subsp. lyrata]	285	284	1.00E-151	99.6	93.7	96.1	ADK/ATPADK1	gbpln	Arabidopsis lyrata	AT2G37250.1 | Symbols: ADK, ATPADK1 | adenosine kinase | chr2:15641991-15643318 FORWARD LENGTH=284	285	284	1.00E-149	99.6	90.9	95.1
Rsa1.0_01172.1.g24227.t1	gb|EOA27796.1| hypothetical protein CARUB_v10023948mg, partial [Capsella rubella]	207	241	1.00E-116	116.4	98.6	99.5	hypothetical protein CARUB_v10023948mg, partial	gbpln	Capsella rubella	AT2G37270.2 | Symbols: ATRPS5B, RPS5B | ribosomal protein 5B | chr2:15647883-15649042 REVERSE LENGTH=207	207	207	1.00E-118	100.0	98.1	100.0
Rsa1.0_01172.1.g24228.t2	ref|XP_002879660.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325499|gb|EFH55919.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1399	1424	0	101.8	83.2	90.4	predicted protein	gbpln	Arabidopsis lyrata	AT2G37280.1 | Symbols: PDR5, ATPDR5 | pleiotropic drug resistance 5 | chr2:15650400-15656417 FORWARD LENGTH=1413	1399	1413	0	101.0	83.1	89.9
Rsa1.0_01172.1.g24229.t1	gb|EOA27940.1| hypothetical protein CARUB_v10024110mg [Capsella rubella]	166	194	1.00E-43	116.9	72.3	81.3	hypothetical protein CARUB_v10024110mg	gbpln	Capsella rubella	AT2G37300.1 | Symbols: | unknown protein; Has 93 Blast hits to 62 proteins in 29 species: Archae - 0; Bacteria - 6; Metazoa - 13; Fungi - 19; Plants - 25; Viruses - 0; Other Eukaryotes - 30 (source: NCBI BLink). | chr2:15662845-15663547 REVERSE LENGTH=169	166	169	5.00E-40	101.8	71.1	77.7
Rsa1.0_01172.1.g24230.t1	gb|EOA26355.1| hypothetical protein CARUB_v10022801mg [Capsella rubella]	652	656	0	100.6	86.2	93.1	hypothetical protein CARUB_v10022801mg	gbpln	Capsella rubella	AT2G37310.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:15665102-15667075 REVERSE LENGTH=657	652	657	0	100.8	85.0	93.1
Rsa1.0_01172.1.g24231.t1	gb|EOA27537.1| hypothetical protein CARUB_v10023676mg, partial [Capsella rubella]	273	313	1.00E-137	114.7	93.0	97.1	hypothetical protein CARUB_v10023676mg, partial	gbpln	Capsella rubella	AT2G37330.1 | Symbols: ALS3 | aluminum sensitive 3 | chr2:15669190-15670172 FORWARD LENGTH=273	273	273	1.00E-136	100.0	90.1	95.6
Rsa1.0_01172.1.g24232.t1	gb|EOA28485.1| hypothetical protein CARUB_v10024695mg [Capsella rubella]	744	753	0	101.2	89.0	93.7	hypothetical protein CARUB_v10024695mg	gbpln	Capsella rubella	AT2G37360.1 | Symbols: | ABC-2 type transporter family protein | chr2:15673555-15675822 REVERSE LENGTH=755	744	755	0	101.5	85.8	92.3
Rsa1.0_01172.1.g24233.t9	gb|EOA29128.1| hypothetical protein CARUB_v10025396mg [Capsella rubella]	678	679	0	100.1	83.3	89.2	hypothetical protein CARUB_v10025396mg	gbpln	Capsella rubella	AT2G37370.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13560.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:15679273-15682932 FORWARD LENGTH=669	678	669	0	98.7	82.2	87.6
Rsa1.0_01172.1.g24234.t1	ref|NP_001189699.1| Chloroplast-targeted copper chaperone protein [Arabidopsis thaliana] gi|330254298|gb|AEC09392.1| Chloroplast-targeted copper chaperone protein [Arabidopsis thaliana]	267	258	2.00E-97	96.6	71.9	81.6	Chloroplast-targeted copper chaperone protein	gbpln	Arabidopsis thaliana	AT2G37390.2 | Symbols: NAKR2 | Chloroplast-targeted copper chaperone protein | chr2:15694300-15695461 FORWARD LENGTH=258	267	258	1.00E-100	96.6	71.9	81.6
Rsa1.0_01172.1.g24235.t1	ref|XP_002881505.1| hypothetical protein ARALYDRAFT_482732 [Arabidopsis lyrata subsp. lyrata] gi|297327344|gb|EFH57764.1| hypothetical protein ARALYDRAFT_482732 [Arabidopsis lyrata subsp. lyrata]	334	334	1.00E-134	100.0	79.0	86.5	hypothetical protein ARALYDRAFT_482732	gbpln	Arabidopsis lyrata	AT2G37400.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:15696365-15697366 REVERSE LENGTH=333	334	333	1.00E-129	99.7	75.4	83.5

Rsa1.0_01172.1.g24236.t1	ref|NP_850281.1| ATP binding microtubule motor family protein [Arabidopsis thaliana] gi|110737312|dbj|BAF00602.1| putative kinesin heavy chain [Arabidopsis thaliana] gi|330254302|gb|AEC09396.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]	1062	1039	0	97.8	84.8	91.4	ATP binding microtubule motor family protein	gbpln	Arabidopsis thaliana	AT2G37420.1 | Symbols: | ATP binding microtubule motor family protein | chr2:15700550-15705165 FORWARD LENGTH=1039	1062	1039	0	97.8	84.8	91.4
Rsa1.0_01173.1.g24237.t1	gb|AAM67188.1| GS1-like protein [Arabidopsis thaliana]	299	298	1.00E-140	99.7	82.3	87.3	GS1-like protein	gbpln	Arabidopsis thaliana	AT4G25840.1 | Symbols: GPP1 | glycerol-3-phosphatase 1 | chr4:13139026-13140719 FORWARD LENGTH=298	299	298	1.00E-142	99.7	82.9	88.0
Rsa1.0_01173.1.g24238.t1	ref|XP_002867589.1| hypothetical protein ARALYDRAFT_492232 [Arabidopsis lyrata subsp. lyrata] gi|297313425|gb|EFH43848.1| hypothetical protein ARALYDRAFT_492232 [Arabidopsis lyrata subsp. lyrata]	376	389	0	103.5	88.6	92.8	hypothetical protein ARALYDRAFT_492232	gbpln	Arabidopsis lyrata	AT4G25870.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr4:13149831-13151737 REVERSE LENGTH=389	376	389	0	103.5	87.2	92.8
Rsa1.0_01173.1.g24239.t2	ref|XP_002869646.1| hypothetical protein ARALYDRAFT_913980 [Arabidopsis lyrata subsp. lyrata] gi|297315482|gb|EFH45905.1| hypothetical protein ARALYDRAFT_913980 [Arabidopsis lyrata subsp. lyrata]	773	858	0	111.0	78.7	85.4	hypothetical protein ARALYDRAFT_913980	gbpln	Arabidopsis lyrata	AT4G25880.1 | Symbols: APUM6, PUM6 | pumilio 6 | chr4:13155518-13159078 FORWARD LENGTH=861	773	861	0	111.4	78.1	85.5
Rsa1.0_01173.1.g24240.t1	ref|XP_002867586.1| hypothetical protein ARALYDRAFT_492222 [Arabidopsis lyrata subsp. lyrata] gi|297313422|gb|EFH43845.1| hypothetical protein ARALYDRAFT_492222 [Arabidopsis lyrata subsp. lyrata]	108	108	8.00E-50	100.0	92.6	99.1	hypothetical protein ARALYDRAFT_492222	gbpln	Arabidopsis lyrata	AT4G25950.1 | Symbols: VATG3 | vacuolar ATP synthase G3 | chr4:13173815-13174324 REVERSE LENGTH=108	108	108	1.00E-50	100.0	90.7	96.3
Rsa1.0_01173.1.g24241.t1	ref|XP_002869639.1| multidrug resistance protein 2 [Arabidopsis lyrata subsp. lyrata] gi|297315475|gb|EFH45898.1| multidrug resistance protein 2 [Arabidopsis lyrata subsp. lyrata]	1237	1233	0	99.7	87.4	93.3	multidrug resistance protein 2	gbpln	Arabidopsis lyrata	AT4G25960.1 | Symbols: PGP2 | P-glycoprotein 2 | chr4:13177438-13183425 FORWARD LENGTH=1273	1237	1273	0	102.9	87.3	93.3
Rsa1.0_01173.1.g24242.t1	ref|XP_002867585.1| hypothetical protein ARALYDRAFT_354188 [Arabidopsis lyrata subsp. lyrata] gi|297313421|gb|EFH43844.1| hypothetical protein ARALYDRAFT_354188 [Arabidopsis lyrata subsp. lyrata]	400	392	1.00E-104	98.0	62.5	72.3	hypothetical protein ARALYDRAFT_354188	gbpln	Arabidopsis lyrata	AT4G25990.1 | Symbols: CIL | CCT motif family protein | chr4:13191937-13193543 REVERSE LENGTH=394	400	394	1.00E-107	98.5	62.8	72.8
Rsa1.0_01173.1.g24243.t1	ref|XP_002869635.1| hypothetical protein ARALYDRAFT_492216 [Arabidopsis lyrata subsp. lyrata] gi|297315471|gb|EFH45894.1| hypothetical protein ARALYDRAFT_492216 [Arabidopsis lyrata subsp. lyrata]	490	495	0	101.0	83.3	91.0	hypothetical protein ARALYDRAFT_492216	gbpln	Arabidopsis lyrata	AT4G26000.1 | Symbols: PEP | RNA-binding KH domain-containing protein | chr4:13197280-13199539 FORWARD LENGTH=495	490	495	0	101.0	81.6	90.6
Rsa1.0_01173.1.g24244.t1	gb|EOA15699.1| hypothetical protein CARUB_v10006454mg [Capsella rubella]	312	312	1.00E-163	100.0	90.1	95.5	hypothetical protein CARUB_v10006454mg	gbpln	Capsella rubella	AT4G26010.1 | Symbols: | Peroxidase superfamily protein | chr4:13200653-13201688 FORWARD LENGTH=310	312	310	1.00E-156	99.4	85.6	90.4
Rsa1.0_01173.1.g24245.t1	ref|XP_002869633.1| hypothetical protein ARALYDRAFT_354185 [Arabidopsis lyrata subsp. lyrata] gi|297315469|gb|EFH45892.1| hypothetical protein ARALYDRAFT_354185 [Arabidopsis lyrata subsp. lyrata]	312	312	1.00E-148	100.0	82.1	89.1	hypothetical protein ARALYDRAFT_354185	gbpln	Arabidopsis lyrata	AT4G26010.1 | Symbols: | Peroxidase superfamily protein | chr4:13200653-13201688 FORWARD LENGTH=310	312	310	1.00E-140	99.4	75.6	84.9
Rsa1.0_01173.1.g24246.t1	gb|EOA17329.1| hypothetical protein CARUB_v10005600mg [Capsella rubella]	247	247	1.00E-117	100.0	86.2	94.7	hypothetical protein CARUB_v10005600mg	gbpln	Capsella rubella	AT4G26020.1 | Symbols: | unknown protein; Has 17652 Blast hits to 12460 proteins in 982 species: Archae - 248; Bacteria - 2077; Metazoa - 7446; Fungi - 1455; Plants - 656; Viruses - 34; Other Eukaryotes - 5736 (source: NCBI BLink). | chr4:13202249-13204028 REVERSE LENGTH=247	247	247	1.00E-119	100.0	86.6	94.3
Rsa1.0_01173.1.g24247.t1	ref|XP_002884137.1| hypothetical protein ARALYDRAFT_900233 [Arabidopsis lyrata subsp. lyrata] gi|297329977|gb|EFH60396.1| hypothetical protein ARALYDRAFT_900233 [Arabidopsis lyrata subsp. lyrata]	357	333	1.00E-20	93.3	30.3	45.7	hypothetical protein ARALYDRAFT_900233	gbpln	Arabidopsis lyrata	AT5G42640.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:17088695-17089597 FORWARD LENGTH=300	357	300	4.00E-19	84.0	29.7	42.6
Rsa1.0_01173.1.g24248.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01174.1.g24249.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	160	1529	5.00E-33	955.6	43.1	58.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	160	295	1.00E-21	184.4	39.4	55.6
Rsa1.0_01174.1.g24250.t9	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1347	1374	0	102.0	48.8	65.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1347	575	1.00E-120	42.7	14.0	21.2
Rsa1.0_01174.1.g24251.t1	gb|EOA27084.1| hypothetical protein CARUB_v10023180mg [Capsella rubella]	454	456	0	100.4	88.8	94.9	hypothetical protein CARUB_v10023180mg	gbpln	Capsella rubella	AT2G28840.1 | Symbols: XBAT31 | XB3 ortholog 1 in Arabidopsis thaliana | chr2:12378542-12380474 FORWARD LENGTH=456	454	456	0	100.4	89.9	95.8
Rsa1.0_01174.1.g24252.t6	emb|CAN79321.1| hypothetical protein VITISV_018984 [Vitis vinifera]	1313	1521	0	115.8	39.1	56.1	hypothetical protein VITISV_018984	gbpln	Vitis vinifera	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1313	158	5.00E-15	12.0	2.5	4.0
Rsa1.0_01174.1.g24253.t1	dbj|BAD12263.1| protein kinase [Brassica rapa]	384	404	0	105.2	91.4	94.3	protein kinase	gbpln	Brassica rapa	AT2G28930.2 | Symbols: APK1B, PK1B | protein kinase 1B | chr2:12424551-12426565 FORWARD LENGTH=412	384	412	1.00E-180	107.3	79.7	89.6
Rsa1.0_01174.1.g24254.t1	ref|XP_002879205.1| hypothetical protein ARALYDRAFT_901879 [Arabidopsis lyrata subsp. lyrata] gi|297325044|gb|EFH55464.1| hypothetical protein ARALYDRAFT_901879 [Arabidopsis lyrata subsp. lyrata]	176	167	1.00E-57	94.9	80.7	85.8	hypothetical protein ARALYDRAFT_901879	gbpln	Arabidopsis lyrata	AT2G29180.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 34 Blast hits to 33 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:12543081-12543702 FORWARD LENGTH=169	176	169	2.00E-53	96.0	77.8	82.4
Rsa1.0_01174.1.g24255.t1	gb|EOA12750.1| hypothetical protein CARUB_v10028431mg [Capsella rubella]	403	423	1.00E-123	105.0	58.3	72.7	hypothetical protein CARUB_v10028431mg	gbpln	Capsella rubella	AT5G56430.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:22853323-22854575 REVERSE LENGTH=360	403	360	1.00E-101	89.3	43.9	53.1
Rsa1.0_01174.1.g24256.t1	gb|EOA37750.1| hypothetical protein CARUB_v10012565mg [Capsella rubella]	198	679	2.00E-48	342.9	50.5	69.2	hypothetical protein CARUB_v10012565mg	gbpln	Capsella rubella	AT1G18560.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr1:6385614-6388005 FORWARD LENGTH=690	198	690	9.00E-13	348.5	17.2	26.8
Rsa1.0_01175.1.g24257.t1	gb|EOA29622.1| hypothetical protein CARUB_v10014335mg [Capsella rubella]	225	282	3.00E-61	125.3	68.9	76.0	hypothetical protein CARUB_v10014335mg	gbpln	Capsella rubella	AT3G53500.2 | Symbols: RSZ32, RS2Z32, At-RS2Z | RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain | chr3:19834557-19836507 REVERSE LENGTH=284	225	284	6.00E-53	126.2	60.4	71.1
Rsa1.0_01175.1.g24258.t1	ref|XP_002884506.1| hypothetical protein ARALYDRAFT_896610 [Arabidopsis lyrata subsp. lyrata] gi|297330346|gb|EFH60765.1| hypothetical protein ARALYDRAFT_896610 [Arabidopsis lyrata subsp. lyrata]	82	801	1.00E-31	976.8	87.8	93.9	hypothetical protein ARALYDRAFT_896610	gbpln	Arabidopsis lyrata	AT3G05330.1 | Symbols: ATN, ATTAN | cyclin family | chr3:1519162-1521159 REVERSE LENGTH=444	82	444	2.00E-34	541.5	89.0	92.7
Rsa1.0_01175.1.g24259.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01175.1.g24260.t1	dbj|BAJ33929.1| unnamed protein product [Thellungiella halophila]	348	370	1.00E-177	106.3	89.4	94.0	unnamed protein product	----	----	AT5G02760.1 | Symbols: | Protein phosphatase 2C family protein | chr5:625377-626817 FORWARD LENGTH=370	348	370	1.00E-173	106.3	85.3	91.4
Rsa1.0_01175.1.g24261.t1	ref|XP_002873065.1| hypothetical protein ARALYDRAFT_487051 [Arabidopsis lyrata subsp. lyrata] gi|297318902|gb|EFH49324.1| hypothetical protein ARALYDRAFT_487051 [Arabidopsis lyrata subsp. lyrata]	206	214	9.00E-67	103.9	78.6	83.0	hypothetical protein ARALYDRAFT_487051	gbpln	Arabidopsis lyrata	AT5G02770.1 | Symbols: | unknown protein; Has 469 Blast hits to 336 proteins in 126 species: Archae - 0; Bacteria - 54; Metazoa - 249; Fungi - 22; Plants - 47; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink). | chr5:628101-629168 REVERSE LENGTH=214	206	214	1.00E-66	103.9	76.7	82.5
Rsa1.0_01175.1.g24262.t1	ref|XP_002870997.1| ubiquitin-protein ligase 4 [Arabidopsis lyrata subsp. lyrata] gi|297316834|gb|EFH47256.1| ubiquitin-protein ligase 4 [Arabidopsis lyrata subsp. lyrata]	1528	1509	0	98.8	80.8	88.0	ubiquitin-protein ligase 4	gbpln	Arabidopsis lyrata	AT5G02880.1 | Symbols: UPL4 | ubiquitin-protein ligase 4 | chr5:662643-668847 FORWARD LENGTH=1502	1528	1502	0	98.3	79.6	86.8
Rsa1.0_01175.1.g24263.t1	gb|EOA20937.1| hypothetical protein CARUB_v10001270mg [Capsella rubella]	348	357	1.00E-133	102.6	69.5	83.6	hypothetical protein CARUB_v10001270mg	gbpln	Capsella rubella	AT5G02890.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:670207-671454 REVERSE LENGTH=353	348	353	1.00E-129	101.4	67.8	80.2
Rsa1.0_01175.1.g24264.t1	gb|EOA22049.1| hypothetical protein CARUB_v10002589mg, partial [Capsella rubella]	458	393	1.00E-102	85.8	46.9	59.4	hypothetical protein CARUB_v10002589mg, partial	gbpln	Capsella rubella	AT5G02910.1 | Symbols: | F-box/RNI-like superfamily protein | chr5:677120-678907 FORWARD LENGTH=458	458	458	3.00E-89	100.0	44.1	57.2

Rsa1.0_01175.1.g24265.t1	ref|NP_189482.1| F-box domain-containing protein [Arabidopsis thaliana] gi|334302799|sp|Q9LSJ3.2|FBL48_ARATH RecName: Full=Putative F-box/LRR-repeat protein At3g28410 gi|332643920|gb|AEE77441.1| F-box domain-containing protein [Arabidopsis thaliana]	461	465	6.00E-98	100.9	51.2	62.9	F-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G28410.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:10640152-10642071 REVERSE LENGTH=465	461	465	1.00E-100	100.9	51.2	62.9
Rsa1.0_01175.1.g24266.t1	gb|EOA32309.1| hypothetical protein CARUB_v10015571mg, partial [Capsella rubella]	185	161	5.00E-74	87.0	75.1	75.1	hypothetical protein CARUB_v10015571mg, partial	gbpln	Capsella rubella	AT5G02960.1 | Symbols: | Ribosomal protein S12/S23 family protein | chr5:693280-694396 REVERSE LENGTH=142	185	142	8.00E-76	76.8	75.1	75.1
Rsa1.0_01175.1.g24267.t3	ref|NP_568110.2| protein IQ-domain 2 [Arabidopsis thaliana] gi|238481199|ref|NP_001154693.1| protein IQ-domain 2 [Arabidopsis thaliana] gi|334187391|ref|NP_001190211.1| protein IQ-domain 2 [Arabidopsis thaliana] gi|15982840|gb|AAL09767.1| AT5g03040/F15A17_70 [Arabidopsis thaliana] gi|23506103|gb|AAN28911.1| At5g03040/F15A17_70 [Arabidopsis thaliana] gi|332003165|gb|AED90548.1| protein IQ-domain 2 [Arabidopsis thaliana] gi|332003166|gb|AED90549.1| protein IQ-domain 2 [Arabidopsis thaliana] gi|332003167|gb|AED90550.1| protein IQ-domain 2 [Arabidopsis thaliana]	530	461	1.00E-178	87.0	65.7	67.9	protein IQ-domain 2	gbpln	Arabidopsis thaliana	AT5G03040.3 | Symbols: iqd2 | IQ-domain 2 | chr5:710380-712406 REVERSE LENGTH=461	530	461	0	87.0	65.7	67.9
Rsa1.0_01175.1.g24268.t1	ref|XP_002871012.1| hypothetical protein ARALYDRAFT_349596 [Arabidopsis lyrata subsp. lyrata] gi|297316849|gb|EFH47271.1| hypothetical protein ARALYDRAFT_349596 [Arabidopsis lyrata subsp. lyrata]	312	293	2.00E-79	93.9	61.5	69.2	hypothetical protein ARALYDRAFT_349596	gbpln	Arabidopsis lyrata	AT5G03110.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; BEST Arabidopsis thaliana protein match is: protamine P1 family protein (TAIR:AT2G37100.1); Has 81 Blast hits to 73 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 81; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:730346-731197 FORWARD LENGTH=283	312	283	1.00E-78	90.7	60.6	68.3
Rsa1.0_01175.1.g24269.t1	dbj|BAB11200.1| copia-type polyprotein [Arabidopsis thaliana] gi|13872710|emb|CAC37622.1| polyprotein [Arabidopsis thaliana]	1229	1334	0	108.5	68.7	81.6	copia-type polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1229	1262	5.00E-89	102.7	13.9	22.8
Rsa1.0_01175.1.g24270.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01176.1.g24271.t1	gb|EOA23672.1| hypothetical protein CARUB_v10016879mg [Capsella rubella]	595	602	0	101.2	83.4	92.4	hypothetical protein CARUB_v10016879mg	gbpln	Capsella rubella	AT3G53960.1 | Symbols: | Major facilitator superfamily protein | chr3:19978306-19980886 REVERSE LENGTH=602	595	602	0	101.2	81.8	91.4
Rsa1.0_01176.1.g24272.t1	gb|EOA24451.1| hypothetical protein CARUB_v10017709mg [Capsella rubella]	302	306	9.00E-67	101.3	53.3	65.6	hypothetical protein CARUB_v10017709mg	gbpln	Capsella rubella	AT3G53970.1 | Symbols: | proteasome inhibitor-related | chr3:19985208-19987132 FORWARD LENGTH=302	302	302	3.00E-63	100.0	54.0	66.2
Rsa1.0_01176.1.g24273.t1	gb|EOA24974.1| hypothetical protein CARUB_v10018271mg [Capsella rubella]	120	114	9.00E-52	95.0	81.7	87.5	hypothetical protein CARUB_v10018271mg	gbpln	Capsella rubella	AT3G53980.2 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:19987760-19988203 REVERSE LENGTH=114	120	114	2.00E-47	95.0	80.8	88.3
Rsa1.0_01176.1.g24274.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01176.1.g24275.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	1575	1231	0	78.2	37.8	50.8	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1575	575	2.00E-91	36.5	12.1	18.5
Rsa1.0_01176.1.g24276.t3	ref|XP_002870068.1| hypothetical protein ARALYDRAFT_354931 [Arabidopsis lyrata subsp. lyrata] gi|297315904|gb|EFH46327.1| hypothetical protein ARALYDRAFT_354931 [Arabidopsis lyrata subsp. lyrata]	608	567	4.00E-61	93.3	22.7	31.7	hypothetical protein ARALYDRAFT_354931	gbpln	Arabidopsis lyrata	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	608	452	1.00E-38	74.3	15.3	21.1
Rsa1.0_01176.1.g24277.t1	emb|CAB51200.1| putative protein [Arabidopsis thaliana]	673	739	1.00E-107	109.8	35.8	55.7	putative protein	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	673	719	9.00E-21	106.8	12.6	21.0
Rsa1.0_01176.1.g24278.t1	ref|XP_002877951.1| universal stress protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297323789|gb|EFH54210.1| universal stress protein family protein [Arabidopsis lyrata subsp. lyrata]	162	162	3.00E-77	100.0	88.3	92.0	universal stress protein family protein	gbpln	Arabidopsis lyrata	AT3G53990.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:19989658-19991019 REVERSE LENGTH=160	162	160	4.00E-77	98.8	85.8	88.9

Rsa1.0_01177.1.g24279.t1	ref|NP_177441.1| LOB domain-containing protein 7 [Arabidopsis thaliana] gi|29428051|sp|Q9SSM9.1|LBD7_ARATH RecName: Full=LOB domain-containing protein 7; AltName: Full=ASYMMETRIC LEAVES 2-like protein 31; Short=AS2-like protein 31 gi|5903087|gb|AAD55645.1|AC008017_18 Hypothetical protein [Arabidopsis thaliana] gi|219807138|dbj|BAH10575.1| ASYMMETRIC LEAVES2-like 31 protein [Arabidopsis thaliana] gi|332197278|gb|AEE35399.1| LOB domain-containing protein 7 [Arabidopsis thaliana]	197	214	6.00E-52	108.6	58.4	74.6	LOB domain-containing protein 7	gbpln	Arabidopsis thaliana	AT1G72980.1 | Symbols: LBD7 | LOB domain-containing protein 7 | chr1:27456227-27456871 REVERSE LENGTH=214	197	214	2.00E-54	108.6	58.4	74.6
Rsa1.0_01177.1.g24280.t1	dbj|BAA77842.1| ACE [Arabidopsis thaliana]	590	594	0	100.7	92.0	95.8	ACE	gbpln	Arabidopsis thaliana	AT1G72970.1 | Symbols: HTH, EDA17 | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr1:27452872-27455706 FORWARD LENGTH=594	590	594	0	100.7	91.9	95.6
Rsa1.0_01177.1.g24281.t1	ref|NP_177435.1| Toll-Interleukin-Resistance domain-containing protein [Arabidopsis thaliana] gi|5903081|gb|AAD55639.1|AC008017_12 Similar to part of disease resistance protein [Arabidopsis thaliana] gi|332197270|gb|AEE35391.1| Toll-Interleukin-Resistance domain-containing protein [Arabidopsis thaliana]	159	275	1.00E-57	173.0	69.8	78.0	Toll-Interleukin-Resistance domain-containing protein	gbpln	Arabidopsis thaliana	AT1G72920.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr1:27437947-27438868 FORWARD LENGTH=275	159	275	4.00E-60	173.0	69.8	78.0
Rsa1.0_01177.1.g24282.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01177.1.g24283.t8	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1134	1250	0	110.2	33.8	41.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1134	1262	2.00E-85	111.3	15.7	24.2
Rsa1.0_01177.1.g24284.t1	gb|ACP30576.1| disease resistance protein [Brassica rapa subsp. pekinensis]	184	426	2.00E-72	231.5	71.7	80.4	disease resistance protein	gbpln	Brassica rapa	AT1G72890.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27429947-27431717 FORWARD LENGTH=438	184	438	2.00E-66	238.0	66.8	73.9
Rsa1.0_01177.1.g24285.t1	gb|ACP30576.1| disease resistance protein [Brassica rapa subsp. pekinensis]	186	426	6.00E-70	229.0	75.8	84.9	disease resistance protein	gbpln	Brassica rapa	AT1G72890.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27429947-27431717 FORWARD LENGTH=438	186	438	6.00E-71	235.5	76.9	86.0
Rsa1.0_01177.1.g24286.t2	gb|AAD55633.1|AC008017_6 Similar to downy mildew resistance protein RPP5 [Arabidopsis thaliana]	331	1258	1.00E-82	380.1	58.6	71.6	Similar to downy mildew resistance protein RPP5	gbpln	Arabidopsis thaliana	AT5G48770.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:19773277-19777242 REVERSE LENGTH=1190	331	1190	5.00E-43	359.5	37.8	57.4
Rsa1.0_01177.1.g24287.t1	ref|NP_177431.1| survival protein SurE-like phosphatase/nucleotidase [Arabidopsis thaliana] gi|30698907|ref|NP_849880.1| survival protein SurE-like phosphatase/nucleotidase [Arabidopsis thaliana] gi|30102530|gb|AAP21183.1| At1g72880 [Arabidopsis thaliana] gi|110742851|dbj|BAE99324.1| hypothetical protein [Arabidopsis thaliana] gi|332197264|gb|AEE35385.1| survival protein SurE-like phosphatase/nucleotidase [Arabidopsis thaliana] gi|332197265|gb|AEE35386.1| survival protein SurE-like phosphatase/nucleotidase [Arabidopsis thaliana]	380	385	0	101.3	90.0	93.7	survival protein SurE-like phosphatase/nucleotidase	gbpln	Arabidopsis thaliana	AT1G72880.1 | Symbols: | Survival protein SurE-like phosphatase/nucleotidase | chr1:27423678-27425928 REVERSE LENGTH=385	380	385	0	101.3	90.0	93.7
Rsa1.0_01178.1.g24288.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	893	1142	0	127.9	52.1	66.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	893	575	4.00E-65	64.4	16.5	25.5
Rsa1.0_01178.1.g24289.t1	ref|NP_175583.2| glutamate dehydrogenase (NADP+) [Arabidopsis thaliana] gi|332194586|gb|AEE32707.1| amino acid dehydrogenase family protein [Arabidopsis thaliana]	648	637	0	98.3	95.5	97.5	glutamate dehydrogenase (NADP+)	gbpln	Arabidopsis thaliana	AT1G51720.1 | Symbols: | Amino acid dehydrogenase family protein | chr1:19181741-19186297 FORWARD LENGTH=637	648	637	0	98.3	95.5	97.5

Rsa1.0_01178.1.g24290.t1	ref|NP_175584.1| ubiquitin-conjugating enzyme-like protein [Arabidopsis thaliana] gi|12321663|gb|AAG50865.1|AC025294_3 unknown protein [Arabidopsis thaliana] gi|19698889|gb|AAL91180.1| unknown protein [Arabidopsis thaliana] gi|23198350|gb|AAN15702.1| unknown protein [Arabidopsis thaliana] gi|332194587|gb|AEE32708.1| ubiquitin-conjugating enzyme-like protein [Arabidopsis thaliana]	253	252	1.00E-106	99.6	87.4	94.5	ubiquitin-conjugating enzyme-like protein	gbpln	Arabidopsis thaliana	AT1G51730.1 | Symbols: | Ubiquitin-conjugating enzyme family protein | chr1:19186812-19188638 REVERSE LENGTH=252	253	252	1.00E-108	99.6	87.4	94.5
Rsa1.0_01178.1.g24291.t4	ref|NP_001147018.1| ribosomal RNA apurinic site specific lyase [Zea mays] gi|195606500|gb|ACG25080.1| ribosomal RNA apurinic site specific lyase [Zea mays]	219	419	8.00E-35	191.3	37.4	46.6	ribosomal RNA apurinic site specific lyase	gbenv/gbpln	Zea mays	AT4G10400.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:6446335-6447715 REVERSE LENGTH=409	219	409	4.00E-33	186.8	36.1	46.6
Rsa1.0_01178.1.g24292.t3	ref|XP_002894307.1| hypothetical protein ARALYDRAFT_474240 [Arabidopsis lyrata subsp. lyrata] gi|297340149|gb|EFH70566.1| hypothetical protein ARALYDRAFT_474240 [Arabidopsis lyrata subsp. lyrata]	375	376	1.00E-157	100.3	70.9	82.1	hypothetical protein ARALYDRAFT_474240	gbpln	Arabidopsis lyrata	AT1G51260.1 | Symbols: LPAT3 | lysophosphatidyl acyltransferase 3 | chr1:19003460-19005512 REVERSE LENGTH=376	375	376	1.00E-159	100.3	70.1	81.9
Rsa1.0_01178.1.g24293.t1	gb|EOA13258.1| hypothetical protein CARUB_v10026287mg [Capsella rubella]	480	494	0	102.9	87.1	91.9	hypothetical protein CARUB_v10026287mg	gbpln	Capsella rubella	AT1G51310.1 | Symbols: | transferases;tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferases | chr1:19019185-19021735 REVERSE LENGTH=497	480	497	0	103.5	88.3	92.3
Rsa1.0_01179.1.g24294.t1	ref|NP_973528.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|334184418|ref|NP_001189592.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|330252503|gb|AEC07597.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|330252506|gb|AEC07600.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	341	601	1.00E-102	176.2	57.5	67.4	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G24600.4 | Symbols: | Ankyrin repeat family protein | chr2:10452430-10454414 REVERSE LENGTH=601	341	601	1.00E-105	176.2	57.5	67.4
Rsa1.0_01179.1.g24295.t1	ref|XP_002880527.1| hypothetical protein ARALYDRAFT_900864 [Arabidopsis lyrata subsp. lyrata] gi|297326366|gb|EFH56786.1| hypothetical protein ARALYDRAFT_900864 [Arabidopsis lyrata subsp. lyrata]	349	335	1.00E-147	96.0	76.2	85.1	hypothetical protein ARALYDRAFT_900864	gbpln	Arabidopsis lyrata	AT2G23790.1 | Symbols: | Protein of unknown function (DUF607) | chr2:10125692-10127455 REVERSE LENGTH=336	349	336	1.00E-148	96.3	75.9	84.8
Rsa1.0_01179.1.g24296.t1	gb|ADK63399.1| C3HC4 type zinc finger protein [Brassica rapa]	232	227	1.00E-120	97.8	94.0	94.4	C3HC4 type zinc finger protein	gbpln	Brassica rapa	AT2G23780.1 | Symbols: | RING/U-box superfamily protein | chr2:10123551-10124234 REVERSE LENGTH=227	232	227	6.00E-90	97.8	73.3	81.9
Rsa1.0_01179.1.g24297.t1	ref|XP_002880525.1| hypothetical protein ARALYDRAFT_481239 [Arabidopsis lyrata subsp. lyrata] gi|297326364|gb|EFH56784.1| hypothetical protein ARALYDRAFT_481239 [Arabidopsis lyrata subsp. lyrata]	606	611	0	100.8	76.7	86.6	hypothetical protein ARALYDRAFT_481239	gbpln	Arabidopsis lyrata	AT2G23770.1 | Symbols: | protein kinase family protein / peptidoglycan-binding LysM domain-containing protein | chr2:10120242-10122080 REVERSE LENGTH=612	606	612	0	101.0	74.8	86.0
Rsa1.0_01179.1.g24298.t1	dbj|BAJ33897.1| unnamed protein product [Thellungiella halophila]	356	651	1.00E-123	182.9	80.9	83.4	unnamed protein product	----	----	AT2G23760.3 | Symbols: BLH4, SAW2 | BEL1-like homeodomain 4 | chr2:10107951-10112736 REVERSE LENGTH=627	356	627	1.00E-101	176.1	75.6	80.1
Rsa1.0_01179.1.g24299.t1	dbj|BAJ33897.1| unnamed protein product [Thellungiella halophila]	305	651	1.00E-143	213.4	89.5	93.1	unnamed protein product	----	----	AT2G23760.3 | Symbols: BLH4, SAW2 | BEL1-like homeodomain 4 | chr2:10107951-10112736 REVERSE LENGTH=627	305	627	1.00E-128	205.6	82.0	87.2
Rsa1.0_01179.1.g24300.t1	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	630	498	9.00E-67	79.0	22.5	31.6	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	630	336	4.00E-24	53.3	10.3	15.9
Rsa1.0_01180.1.g24301.t1	ref|XP_002876050.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321888|gb|EFH52309.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	279	294	1.00E-110	105.4	79.9	86.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G50870.1 | Symbols: MNP, HAN, GATA18 | GATA type zinc finger transcription factor family protein | chr3:18911112-18912369 FORWARD LENGTH=295	279	295	1.00E-111	105.7	78.1	84.9

Rsa1.0_01180.1.g24302.t1	ref|NP_190658.1| homeobox protein 28 [Arabidopsis thaliana] gi|4835240|emb|CAB42918.1| putative protein [Arabidopsis thaliana] gi|51969440|dbj|BAD43412.1| unknown protein [Arabidopsis thaliana] gi|332645201|gb|AEE78722.1| homeobox protein 28 [Arabidopsis thaliana]	231	249	1.00E-89	107.8	77.9	85.3	homeobox protein 28	gbpln	Arabidopsis thaliana	AT3G50890.1 | Symbols: AtHB28, HB28, ZHD7 | homeobox protein 28 | chr3:18916420-18917169 FORWARD LENGTH=249	231	249	3.00E-92	107.8	77.9	85.3
Rsa1.0_01180.1.g24303.t1	ref|XP_002876053.1| hypothetical protein ARALYDRAFT_906429 [Arabidopsis lyrata subsp. lyrata] gi|297321891|gb|EFH52312.1| hypothetical protein ARALYDRAFT_906429 [Arabidopsis lyrata subsp. lyrata]	237	114	1.00E-24	48.1	32.9	34.6	hypothetical protein ARALYDRAFT_906429	gbpln	Arabidopsis lyrata	AT3G50900.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66490.1); Has 45 Blast hits to 45 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:18918122-18918466 FORWARD LENGTH=114	237	114	1.00E-26	48.1	31.2	33.8
Rsa1.0_01180.1.g24304.t1	dbj|BAJ34117.1| unnamed protein product [Thellungiella halophila]	426	447	1.00E-174	104.9	85.0	89.7	unnamed protein product	----	----	AT3G50910.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66480.1); Has 76 Blast hits to 75 proteins in 28 species: Archae - 0; Bacteria - 10; Metazoa - 7; Fungi - 2; Plants - 49; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr3:18920189-18921999 FORWARD LENGTH=447	426	447	1.00E-168	104.9	79.1	86.2
Rsa1.0_01180.1.g24305.t1	gb|EOA24702.1| hypothetical protein CARUB_v10017980mg [Capsella rubella]	225	225	5.00E-82	100.0	71.6	80.4	hypothetical protein CARUB_v10017980mg	gbpln	Capsella rubella	AT3G50920.2 | Symbols: | Phosphatidic acid phosphatase (PAP2) family protein | chr3:18922403-18923380 REVERSE LENGTH=228	225	228	1.00E-80	101.3	72.0	82.2
Rsa1.0_01180.1.g24306.t1	ref|XP_002876055.1| hypothetical protein ARALYDRAFT_906432 [Arabidopsis lyrata subsp. lyrata] gi|297321893|gb|EFH52314.1| hypothetical protein ARALYDRAFT_906432 [Arabidopsis lyrata subsp. lyrata]	153	268	3.00E-37	175.2	60.1	69.9	hypothetical protein ARALYDRAFT_906432	gbpln	Arabidopsis lyrata	AT5G66440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G34560.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:26530274-26531032 REVERSE LENGTH=252	153	252	7.00E-22	164.7	41.8	52.9
Rsa1.0_01180.1.g24307.t1	gb|EOA23788.1| hypothetical protein CARUB_v10017002mg [Capsella rubella]	503	530	0	105.4	84.1	91.3	hypothetical protein CARUB_v10017002mg	gbpln	Capsella rubella	AT3G50930.1 | Symbols: BCS1 | cytochrome BC1 synthesis | chr3:18929817-18931547 FORWARD LENGTH=576	503	576	0	114.5	84.3	91.7
Rsa1.0_01180.1.g24308.t1	ref|XP_002877783.1| hypothetical protein ARALYDRAFT_485452 [Arabidopsis lyrata subsp. lyrata] gi|297323621|gb|EFH54042.1| hypothetical protein ARALYDRAFT_485452 [Arabidopsis lyrata subsp. lyrata]	753	323	1.00E-163	42.9	36.3	39.2	hypothetical protein ARALYDRAFT_485452	gbpln	Arabidopsis lyrata	AT3G51000.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:18945258-18946499 REVERSE LENGTH=323	753	323	1.00E-165	42.9	36.3	38.9
Rsa1.0_01180.1.g24309.t2	ref|XP_002876064.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297321902|gb|EFH52323.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	131	137	2.00E-43	104.6	74.0	81.7	metal ion binding protein	gbpln	Arabidopsis lyrata	AT3G51020.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66370.1); Has 19 Blast hits to 19 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:18949645-18950221 FORWARD LENGTH=133	131	133	2.00E-38	101.5	69.5	77.9
Rsa1.0_01180.1.g24310.t1	gb|EOA25674.1| hypothetical protein CARUB_v10019026mg [Capsella rubella]	114	114	3.00E-56	100.0	91.2	98.2	hypothetical protein CARUB_v10019026mg	gbpln	Capsella rubella	AT3G51030.1 | Symbols: ATTRX1, ATTRX H1, TRX1 | thioredoxin H-type 1 | chr3:18951123-18951955 REVERSE LENGTH=114	114	114	3.00E-58	100.0	90.4	96.5
Rsa1.0_01180.1.g24311.t1	gb|EOA25276.1| hypothetical protein CARUB_v10018591mg [Capsella rubella]	696	696	0	100.0	93.2	97.6	hypothetical protein CARUB_v10018591mg	gbpln	Capsella rubella	AT3G51050.1 | Symbols: | FG-GAP repeat-containing protein | chr3:18954023-18957698 FORWARD LENGTH=698	696	698	0	100.3	92.8	97.8
Rsa1.0_01181.1.g24312.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	150	390	2.00E-30	260.0	47.3	58.0	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	150	320	2.00E-15	213.3	31.3	50.7
Rsa1.0_01181.1.g24313.t1	gb|EOA40596.1| hypothetical protein CARUB_v10009328mg [Capsella rubella]	400	403	1.00E-147	100.8	85.0	88.3	hypothetical protein CARUB_v10009328mg	gbpln	Capsella rubella	AT1G32240.1 | Symbols: KAN2 | Homeodomain-like superfamily protein | chr1:11625882-11630355 REVERSE LENGTH=388	400	388	1.00E-148	97.0	81.5	84.3
Rsa1.0_01181.1.g24314.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01181.1.g24315.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01181.1.g24316.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_01181.1.g24317.t1</td><td>dbj|BAB10837.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>135</td><td>1462</td><td>1.00E-38</td><td>1083.0</td><td>52.6</td><td>66.7</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237</td><td>135</td><td>237</td><td>7.00E-11</td><td>175.6</td><td>18.5</td><td>32.6</td></tr>
<tr><td>Rsa1.0_01182.1.g24318.t1</td><td>ref|NP_565974.1| serine/threonine-protein phosphatase PP2A-4 catalytic subunit [Arabidopsis thaliana] gi|297827949|ref|XP_002881857.1| protein phosphatase 2A-4 [Arabidopsis lyrata subsp. lyrata] gi|1352663|sp|Q07100.2|PP2A4_ARATH RecName: Full=Serine/threonine-protein phosphatase PP2A-4 catalytic subunit; AltName: Full=Protein phosphatase 2A isoform 4 gi|466441|gb|AAA64742.1| Ser/Thr protein phosphatase [Arabidopsis thaliana] gi|4567320|gb|AAD23731.1| serine threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] gi|20198072|gb|AAM15383.1| serine/threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] gi|33589738|gb|AAQ22635.1| At2g42500/F14N22.23 [Arabidopsis thaliana] gi|297327696|gb|EFH58116.1| protein phosphatase 2A-4 [Arabidopsis lyrata subsp. lyrata] gi|330255033|gb|AEC10127.1| serine/threonine-protein phosphatase PP2A-4 catalytic subunit [Arabidopsis thaliana] gi|482563348|gb|EOA27538.1| hypothetical protein CARUB_v10023677mg [Capsella rubella]</td><td>327</td><td>313</td><td>1.00E-178</td><td>95.7</td><td>92.0</td><td>93.9</td><td>serine/threonine-protein phosphatase PP2A-4 catalytic subunit</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G42500.1 | Symbols: PP2A-3 | protein phosphatase 2A-3 | chr2:17698099-17701226 REVERSE LENGTH=313</td><td>327</td><td>313</td><td>0</td><td>95.7</td><td>92.0</td><td>93.9</td></tr>
<tr><td>Rsa1.0_01182.1.g24319.t1</td><td>gb|EOA25539.1| hypothetical protein CARUB_v10018884mg [Capsella rubella]</td><td>615</td><td>609</td><td>0</td><td>99.0</td><td>80.3</td><td>83.7</td><td>hypothetical protein CARUB_v10018884mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G58510.3 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr3:21640608-21643464 FORWARD LENGTH=612</td><td>615</td><td>612</td><td>0</td><td>99.5</td><td>79.7</td><td>84.2</td></tr>
<tr><td>Rsa1.0_01182.1.g24320.t1</td><td>gb|EOA25772.1| hypothetical protein CARUB_v10019134mg [Capsella rubella]</td><td>395</td><td>418</td><td>0</td><td>105.8</td><td>87.1</td><td>91.1</td><td>hypothetical protein CARUB_v10019134mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G58520.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr3:21643921-21645277 REVERSE LENGTH=418</td><td>395</td><td>418</td><td>0</td><td>105.8</td><td>87.3</td><td>90.1</td></tr>
<tr><td>Rsa1.0_01182.1.g24321.t2</td><td>ref|XP_002876467.1| hypothetical protein ARALYDRAFT_486305 [Arabidopsis lyrata subsp. lyrata] gi|297322305|gb|EFH52726.1| hypothetical protein ARALYDRAFT_486305 [Arabidopsis lyrata subsp. lyrata]</td><td>349</td><td>353</td><td>1.00E-163</td><td>101.1</td><td>84.0</td><td>90.0</td><td>hypothetical protein ARALYDRAFT_486305</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G58530.1 | Symbols: | RNI-like superfamily protein | chr3:21645759-21648219 FORWARD LENGTH=353</td><td>349</td><td>353</td><td>1.00E-156</td><td>101.1</td><td>77.4</td><td>84.0</td></tr>
<tr><td>Rsa1.0_01182.1.g24322.t1</td><td>ref|XP_002878227.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297324065|gb|EFH54486.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>65</td><td>598</td><td>2.00E-16</td><td>920.0</td><td>81.5</td><td>87.7</td><td>endonuclease/exonuclease/phosphatase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G58560.1 | Symbols: | DNAse I-like superfamily protein | chr3:21650880-21653896 REVERSE LENGTH=602</td><td>65</td><td>602</td><td>6.00E-18</td><td>926.2</td><td>78.5</td><td>84.6</td></tr>
<tr><td>Rsa1.0_01182.1.g24323.t2</td><td>ref|NP_191416.1| DEAD-box ATP-dependent RNA helicase 52 [Arabidopsis thaliana] gi|75335836|sp|Q9M2F9.1|RH52_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 52 gi|6735374|emb|CAB68195.1| ATP-dependent RNA helicase-like protein [Arabidopsis thaliana] gi|15146288|gb|AAK83627.1| AT3g58570/F14P22_160 [Arabidopsis thaliana] gi|21593710|gb|AAM65677.1| ATP-dependent RNA helicase-like protein [Arabidopsis thaliana] gi|27363456|gb|AAO11647.1| At3g58570/F14P22_160 [Arabidopsis thaliana] gi|332646279|gb|AEE79800.1| DEAD-box ATP-dependent RNA helicase 52 [Arabidopsis thaliana]</td><td>659</td><td>646</td><td>0</td><td>98.0</td><td>75.4</td><td>78.6</td><td>DEAD-box ATP-dependent RNA helicase 52</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G58570.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:21657099-21660352 FORWARD LENGTH=646</td><td>659</td><td>646</td><td>0</td><td>98.0</td><td>75.4</td><td>78.6</td></tr>
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Rsa1.0_01182.1.g24324.t1	gb|EOA23679.1| hypothetical protein CARUB_v10016885mg [Capsella rubella]	594	600	0	101.0	89.1	92.8	hypothetical protein CARUB_v10016885mg	gbpln	Capsella rubella	AT3G58580.1 | Symbols: | DNAse I-like superfamily protein | chr3:21660866-21663697 REVERSE LENGTH=603	594	603	0	101.5	88.9	93.4
Rsa1.0_01182.1.g24325.t1	gb|EOA23697.1| hypothetical protein CARUB_v10016904mg [Capsella rubella]	585	591	0	101.0	92.6	96.9	hypothetical protein CARUB_v10016904mg	gbpln	Capsella rubella	AT3G58610.3 | Symbols: | ketol-acid reductoisomerase | chr3:21671561-21674639 FORWARD LENGTH=591	585	591	0	101.0	92.6	96.2
Rsa1.0_01182.1.g24326.t1	ref|XP_002876471.1| hypothetical protein ARALYDRAFT_486314 [Arabidopsis lyrata subsp. lyrata] gi|297322309|gb|EFH52730.1| hypothetical protein ARALYDRAFT_486314 [Arabidopsis lyrata subsp. lyrata]	645	685	0	106.2	81.4	88.7	hypothetical protein ARALYDRAFT_486314	gbpln	Arabidopsis lyrata	AT3G58620.1 | Symbols: TTL4 | tetratricopetide-repeat thioredoxin-like 4 | chr3:21680397-21682959 FORWARD LENGTH=682	645	682	0	105.7	81.4	88.7
Rsa1.0_01182.1.g24327.t1	gb|AAS58438.1| DREB2A [Eutrema salsugineum]	325	340	1.00E-108	104.6	70.2	80.0	DREB2A	gbpln	Eutrema salsugineum	AT5G05410.1 | Symbols: DREB2A, DREB2 | DRE-binding protein 2A | chr5:1602650-1603657 FORWARD LENGTH=335	325	335	1.00E-109	103.1	68.3	80.0
Rsa1.0_01182.1.g24328.t1	ref|NP_196159.1| LRR and NB-ARC domain-containing disease resistance protein [Arabidopsis thaliana] gi|46395986|sp|Q9FLB4.1|DRL31_ARATH RecName: Full=Putative disease resistance protein At5g05400 gi|10176752|dbj|BAB09983.1| NBS/LRR disease resistance protein [Arabidopsis thaliana] gi|332003486|gb|AED90869.1| putative disease resistance protein [Arabidopsis thaliana]	302	874	1.00E-111	289.4	69.2	79.5	LRR and NB-ARC domain-containing disease resistance protein	gbpln	Arabidopsis thaliana	AT5G05400.1 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr5:1597745-1600369 REVERSE LENGTH=874	302	874	1.00E-114	289.4	69.2	79.5
Rsa1.0_01182.1.g24329.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1981	1213	0	61.2	32.1	42.0	unknown protein	gbpln	Arabidopsis thaliana	AT5G05390.1 | Symbols: LAC12 | laccase 12 | chr5:1594753-1597042 FORWARD LENGTH=565	1981	565	0	28.5	25.1	25.9
Rsa1.0_01182.1.g24330.t1	ref|XP_002871155.1| prenylated rab receptor 2 [Arabidopsis lyrata subsp. lyrata] gi|297316992|gb|EFH47414.1| prenylated rab receptor 2 [Arabidopsis lyrata subsp. lyrata]	254	216	6.00E-84	85.0	69.3	72.0	prenylated rab receptor 2	gbpln	Arabidopsis lyrata	AT5G05380.1 | Symbols: PRA1.B3 | prenylated RAB acceptor 1.B3 | chr5:1592214-1592867 FORWARD LENGTH=217	254	217	1.00E-85	85.4	70.9	73.2
Rsa1.0_01182.1.g24331.t1	gb|EOA19506.1| hypothetical protein CARUB_v10002333mg [Capsella rubella]	89	97	3.00E-26	109.0	65.2	65.2	hypothetical protein CARUB_v10002333mg	gbpln	Capsella rubella	AT5G05370.1 | Symbols: | Cytochrome b-c1 complex, subunit 8 protein | chr5:1590977-1591869 REVERSE LENGTH=72	89	72	3.00E-28	80.9	62.9	65.2
Rsa1.0_01182.1.g24332.t1	ref|XP_002871154.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297316991|gb|EFH47413.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	77	77	2.00E-33	100.0	94.8	96.1	metal ion binding protein	gbpln	Arabidopsis lyrata	AT5G05365.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:1590125-1590672 FORWARD LENGTH=77	77	77	4.00E-35	100.0	92.2	93.5
Rsa1.0_01182.1.g24333.t1	ref|NP_196155.2| uncharacterized protein [Arabidopsis thaliana] gi|332003481|gb|AED90864.1| uncharacterized protein AT5G05360 [Arabidopsis thaliana]	166	163	2.00E-72	98.2	84.3	87.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G05360.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G38450.1); Has 84 Blast hits to 84 proteins in 24 species: Archae - 0; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr5:1588356-1589178 FORWARD LENGTH=163	166	163	6.00E-75	98.2	84.3	87.3
Rsa1.0_01182.1.g24334.t1	ref|NP_196154.1| PLAC8 family protein [Arabidopsis thaliana] gi|52354439|gb|AAU44540.1| hypothetical protein AT5G05350 [Arabidopsis thaliana] gi|332003479|gb|AED90862.1| PLAC8 family protein [Arabidopsis thaliana]	434	526	0	121.2	80.6	88.0	PLAC8 family protein	gbpln	Arabidopsis thaliana	AT5G05350.1 | Symbols: | PLAC8 family protein | chr5:1585757-1587337 FORWARD LENGTH=526	434	526	0	121.2	80.6	88.0
Rsa1.0_01182.1.g24335.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01182.1.g24336.t1	gb|ACT35473.1| peroxidase 52, partial [Brassica rapa]	325	306	1.00E-172	94.2	91.7	93.8	peroxidase 52, partial	gbpln	Brassica rapa	AT5G05340.1 | Symbols: | Peroxidase superfamily protein | chr5:1579142-1580819 REVERSE LENGTH=324	325	324	1.00E-164	99.7	88.6	94.5
Rsa1.0_01182.1.g24337.t1	ref|XP_002873206.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319043|gb|EFH49465.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	156	188	6.00E-48	120.5	69.2	80.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G05330.1 | Symbols: | HMG-box (high mobility group) DNA-binding family protein | chr5:1577289-1578750 REVERSE LENGTH=220	156	220	1.00E-47	141.0	66.0	80.1
Rsa1.0_01182.1.g24338.t1	ref|NP_850772.1| TLC ATP/ADP transporter [Arabidopsis thaliana] gi|332003473|gb|AED90856.1| TLC ATP/ADP transporter [Arabidopsis thaliana]	525	511	0	97.3	88.0	90.5	TLC ATP/ADP transporter	gbpln	Arabidopsis thaliana	AT5G05310.3 | Symbols: | TLC ATP/ADP transporter | chr5:1571271-1574458 FORWARD LENGTH=511	525	511	0	97.3	88.0	90.5

Rsa1.0_01182.1.g24339.t1	ref|NP_196149.1| uncharacterized protein [Arabidopsis thaliana] gi|10176742|dbj|BAB09973.1| unnamed protein product [Arabidopsis thaliana] gi|332003470|gb|AED90853.1| uncharacterized protein AT5G05300 [Arabidopsis thaliana]	319	102	5.00E-16	32.0	17.6	19.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G05300.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 8 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:1570102-1570410 REVERSE LENGTH=102	319	102	1.00E-18	32.0	17.6	19.7
Rsa1.0_01182.1.g24340.t1	ref|XP_002871148.1| ATEXPA2 [Arabidopsis lyrata subsp. lyrata] gi|297316985|gb|EFH47407.1| ATEXPA2 [Arabidopsis lyrata subsp. lyrata]	201	253	4.00E-89	125.9	77.1	84.1	ATEXPA2	gbpln	Arabidopsis lyrata	AT5G05290.1 | Symbols: ATEXPA2, EXP2, ATEXP2, ATHEXP ALPHA 1.12, EXPA2 | expansin A2 | chr5:1568752-1569712 FORWARD LENGTH=255	201	255	2.00E-91	126.9	77.1	83.6
Rsa1.0_01182.1.g24341.t1	ref|XP_002873203.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297319040|gb|EFH49462.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	175	178	7.00E-70	101.7	76.6	84.6	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G05280.1 | Symbols: | RING/U-box superfamily protein | chr5:1565509-1566039 REVERSE LENGTH=176	175	176	2.00E-71	100.6	77.7	84.0
Rsa1.0_01182.1.g24342.t1	pdb|4DOK|A Chain A, Crystal Structure Of Arabidopsis Thaliana Chalcone-Isomerase Like Protein At5g05270 (Atchil) gi|386783410|pdb|4DOK|B Chain B, Crystal Structure Of Arabidopsis Thaliana Chalcone-Isomerase Like Protein At5g05270 (Atchil)	205	208	1.00E-100	101.5	93.7	97.1	Chain A, Crystal Structure Of Arabidopsis Thaliana Chalcone-Isomerase Like Protein At5g05270 (Atchil) gi|386783410|pdb|4DOK |B Chain B, Crystal Structure Of Arabidopsis Thaliana Chalcone-Isomerase Like Protein At5g05270 (Atchil)	----	----	AT5G05270.2 | Symbols: | Chalcone-flavanone isomerase family protein | chr5:1563543-1564827 FORWARD LENGTH=209	205	209	1.00E-102	102.0	93.7	97.1
Rsa1.0_01183.1.g24343.t1	ref|XP_002880609.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata] gi|297326448|gb|EFH56868.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata]	430	464	1.00E-119	107.9	56.0	69.3	hypothetical protein ARALYDRAFT_901029	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	430	456	1.00E-109	106.0	51.6	67.2
Rsa1.0_01183.1.g24344.t5	ref|XP_002880609.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata] gi|297326448|gb|EFH56868.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata]	411	464	1.00E-107	112.9	54.0	68.9	hypothetical protein ARALYDRAFT_901029	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	411	456	1.00E-104	110.9	53.0	67.4
Rsa1.0_01183.1.g24345.t1	gb|EOA30184.1| hypothetical protein CARUB_v10013301mg [Capsella rubella]	499	589	1.00E-169	118.0	61.7	69.7	hypothetical protein CARUB_v10013301mg	gbpln	Capsella rubella	AT3G18180.1 | Symbols: | Glycosyltransferase family 61 protein | chr3:6230270-6231878 FORWARD LENGTH=470	499	470	1.00E-154	94.2	55.3	64.9
Rsa1.0_01183.1.g24346.t1	gb|EOA30184.1| hypothetical protein CARUB_v10013301mg [Capsella rubella]	503	589	0	117.1	66.2	75.9	hypothetical protein CARUB_v10013301mg	gbpln	Capsella rubella	AT3G18180.1 | Symbols: | Glycosyltransferase family 61 protein | chr3:6230270-6231878 FORWARD LENGTH=470	503	470	1.00E-142	93.4	53.3	64.4
Rsa1.0_01183.1.g24347.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01183.1.g24348.t1	ref|NP_188447.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana] gi|9294075|dbj|BAB02032.1| cytosolic chaperonin, delta-subunit [Arabidopsis thaliana] gi|20466822|gb|AAM20728.1| chaperonin subunit, putative [Arabidopsis thaliana] gi|28059669|gb|AAO30081.1| chaperonin subunit, putative [Arabidopsis thaliana] gi|332642540|gb|AEE76061.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]	534	536	0	100.4	94.4	97.8	TCP-1/cpn60 chaperonin family protein	gbpln	Arabidopsis thaliana	AT3G18190.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:6232226-6233836 FORWARD LENGTH=536	534	536	0	100.4	94.4	97.8
Rsa1.0_01183.1.g24349.t1	gb|EOA30759.1| hypothetical protein CARUB_v10013901mg [Capsella rubella]	381	392	0	102.9	79.0	90.0	hypothetical protein CARUB_v10013901mg	gbpln	Capsella rubella	AT3G18210.2 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:6238264-6240396 REVERSE LENGTH=394	381	394	0	103.4	78.2	89.5
Rsa1.0_01183.1.g24350.t1	ref|XP_002883119.1| hypothetical protein ARALYDRAFT_898182 [Arabidopsis lyrata subsp. lyrata] gi|297328959|gb|EFH59378.1| hypothetical protein ARALYDRAFT_898182 [Arabidopsis lyrata subsp. lyrata]	245	244	1.00E-120	99.6	84.9	92.7	hypothetical protein ARALYDRAFT_898182	gbpln	Arabidopsis lyrata	AT3G18215.1 | Symbols: | Protein of unknown function, DUF599 | chr3:6240968-6242358 FORWARD LENGTH=244	245	244	1.00E-116	99.6	82.9	91.4

Rsa1.0_01183.1.g24351.t2	gb|EOA31855.1| hypothetical protein CARUB_v10015082mg [Capsella rubella]	304	309	1.00E-148	101.6	85.2	91.8	hypothetical protein CARUB_v10015082mg	gbpln	Capsella rubella	AT3G18220.1 | Symbols: | Phosphatidic acid phosphatase (PAP2) family protein | chr3:6248355-6249799 FORWARD LENGTH=308	304	308	1.00E-138	101.3	84.9	91.4
Rsa1.0_01184.1.g24352.t2	gb|EOA26494.1| hypothetical protein CARUB_v10022544mg [Capsella rubella]	1093	1076	0	98.4	85.1	91.9	hypothetical protein CARUB_v10022544mg	gbpln	Capsella rubella	AT2G47980.1 | Symbols: SCC3, ATSCC3 | sister-chromatid cohesion protein 3 | chr2:19631423-19636795 FORWARD LENGTH=1098	1093	1098	0	100.5	84.6	91.0
Rsa1.0_01184.1.g24353.t2	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	230	704	3.00E-84	306.1	66.5	70.0	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01184.1.g24354.t1	ref|XP_002882142.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297327981|gb|EFH58401.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	427	444	0	104.0	81.0	88.3	endonuclease/exonuclease/phosphatase family protein	gbpln	Arabidopsis lyrata	AT2G48030.1 | Symbols: | DNAse I-like superfamily protein | chr2:19647834-19649988 REVERSE LENGTH=438	427	438	0	102.6	79.4	87.1
Rsa1.0_01184.1.g24355.t10	gb|EOA26448.1| hypothetical protein CARUB_v10022493mg [Capsella rubella]	2410	2485	0	103.1	92.2	95.5	hypothetical protein CARUB_v10022493mg	gbpln	Capsella rubella	AT2G48060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: shoot, sperm cell; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3595 (InterPro:IPR021999); Has 533 Blast hits to 341 proteins in 95 species: Archae - 2; Bacteria - 15; Metazoa - 318; Fungi - 0; Plants - 93; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink). | chr2:19651560-19662386 REVERSE LENGTH=2462	2410	2462	0	102.2	91.5	94.6
Rsa1.0_01184.1.g24356.t1	ref|NP_566122.1| resistance to phytophthora 1 protein [Arabidopsis thaliana] gi|30690887|ref|NP_850484.1| resistance to phytophthora 1 protein [Arabidopsis thaliana] gi|15027853|gb|AAK76457.1| unknown protein [Arabidopsis thaliana] gi|19310717|gb|AAL85089.1| unknown protein [Arabidopsis thaliana] gi|20197563|gb|AAD13710.2| expressed protein [Arabidopsis thaliana] gi|330255834|gb|AEC10928.1| resistance to phytophthora 1 protein [Arabidopsis thaliana] gi|330255835|gb|AEC10929.1| resistance to phytophthora 1 protein [Arabidopsis thaliana]	235	197	6.00E-69	83.8	60.9	65.1	resistance to phytophthora 1 protein	gbpln	Arabidopsis thaliana	AT2G48070.2 | Symbols: RPH1 | resistance to phytophthora 1 | chr2:19662863-19663773 FORWARD LENGTH=197	235	197	2.00E-71	83.8	60.9	65.1
Rsa1.0_01184.1.g24357.t3	gb|EOA28914.1| hypothetical protein CARUB_v10025161mg [Capsella rubella]	469	459	1.00E-173	97.9	73.1	79.5	hypothetical protein CARUB_v10025161mg	gbpln	Capsella rubella	AT2G48080.1 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr2:19665192-19667092 REVERSE LENGTH=438	469	438	1.00E-174	93.4	72.1	79.1
Rsa1.0_01184.1.g24358.t1	ref|XP_002882149.1| hypothetical protein ARALYDRAFT_484001 [Arabidopsis lyrata subsp. lyrata] gi|297327988|gb|EFH58408.1| hypothetical protein ARALYDRAFT_484001 [Arabidopsis lyrata subsp. lyrata]	171	163	3.00E-43	95.3	61.4	68.4	hypothetical protein ARALYDRAFT_484001	gbpln	Arabidopsis lyrata	AT2G48090.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: male gametophyte, root, flower, carpel; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19669220-19669729 REVERSE LENGTH=169	171	169	9.00E-42	98.8	59.6	68.4
Rsa1.0_01184.1.g24359.t1	gb|EOA27419.1| hypothetical protein CARUB_v10023554mg [Capsella rubella]	308	345	1.00E-143	112.0	81.2	89.3	hypothetical protein CARUB_v10023554mg	gbpln	Capsella rubella	AT2G48100.3 | Symbols: | Exonuclease family protein | chr2:19671245-19672847 FORWARD LENGTH=344	308	344	1.00E-139	111.7	77.9	87.3
Rsa1.0_01184.1.g24360.t15	ref|XP_002880344.1| hypothetical protein ARALYDRAFT_484005 [Arabidopsis lyrata subsp. lyrata] gi|297326183|gb|EFH56603.1| hypothetical protein ARALYDRAFT_484005 [Arabidopsis lyrata subsp. lyrata]	314	325	1.00E-121	103.5	86.6	91.4	hypothetical protein ARALYDRAFT_484005	gbpln	Arabidopsis lyrata	AT2G48120.1 | Symbols: PAC | pale cress protein (PAC) | chr2:19679870-19681351 FORWARD LENGTH=313	314	313	1.00E-122	99.7	86.6	90.4
Rsa1.0_01185.1.g24361.t1	ref|XP_002889383.1| 3-ketoacyl-CoA synthase 1 [Arabidopsis lyrata subsp. lyrata] gi|297335225|gb|EFH65642.1| 3-ketoacyl-CoA synthase 1 [Arabidopsis lyrata subsp. lyrata]	529	528	0	99.8	91.1	95.1	3-ketoacyl-CoA synthase 1	gbpln	Arabidopsis lyrata	AT1G01120.1 | Symbols: KCS1 | 3-ketoacyl-CoA synthase 1 | chr1:57392-58978 REVERSE LENGTH=528	529	528	0	99.8	91.3	95.1
Rsa1.0_01185.1.g24362.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01185.1.g24363.t1	ref|XP_002892087.1| T25K16.10 [Arabidopsis lyrata subsp. lyrata] gi|297337929|gb|EFH68346.1| T25K16.10 [Arabidopsis lyrata subsp. lyrata]	522	527	0	101.0	84.7	90.2	T25K16.10	gbpln	Arabidopsis lyrata	AT1G01110.2 | Symbols: IQD18 | IQ-domain 18 | chr1:52239-54494 FORWARD LENGTH=527	522	527	0	101.0	84.1	88.9
Rsa1.0_01185.1.g24364.t1	ref|NP_567190.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|30678744|ref|NP_849278.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|41019478|sp|O23095.2|RLA12_ARATH RecName: Full=60S acidic ribosomal protein P1-2 gi|13605597|gb|AAK32792.1|AF361624_1 AT4g00810/A_TM018A10_9 [Arabidopsis thaliana] gi|15777871|gb|AAL05896.1| AT4g00810/A_TM018A10_9 [Arabidopsis thaliana] gi|21554797|gb|AAM63694.1| acidic ribosomal protein p1 [Arabidopsis thaliana] gi|222423235|dbj|BAH19594.1| AT4G00810 [Arabidopsis thaliana] gi|332656537|gb|AEE81937.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|332656538|gb|AEE81938.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana]	113	113	8.00E-36	100.0	84.1	89.4	60S acidic ribosomal protein P1-2	gbpln	Arabidopsis thaliana	AT4G00810.2 | Symbols: | 60S acidic ribosomal protein family | chr4:346179-346957 REVERSE LENGTH=113	113	113	1.00E-38	100.0	84.1	89.4
Rsa1.0_01185.1.g24365.t1	gb|EOA40477.1| hypothetical protein CARUB_v10009201mg [Capsella rubella]	427	430	0	100.7	94.6	97.2	hypothetical protein CARUB_v10009201mg	gbpln	Capsella rubella	AT1G01090.1 | Symbols: PDH-E1 ALPHA | pyruvate dehydrogenase E1 alpha | chr1:47705-49166 REVERSE LENGTH=428	427	428	0	100.2	92.3	96.0
Rsa1.0_01185.1.g24366.t1	gb|EOA36541.1| hypothetical protein CARUB_v10011623mg [Capsella rubella]	268	251	1.00E-75	93.7	54.1	60.1	hypothetical protein CARUB_v10011623mg	gbpln	Capsella rubella	AT3G04430.1 | Symbols: anac049, NAC049 | NAC domain containing protein 49 | chr3:1175506-1176986 REVERSE LENGTH=198	268	198	6.00E-64	73.9	50.7	55.2
Rsa1.0_01185.1.g24367.t1	ref|NP_171727.2| NAC domain-containing protein 5 [Arabidopsis thaliana] gi|238065080|sp|O81914.2|NAC5_ARATH RecName: Full=NAC domain-containing protein 5; Short=ANAC005 gi|225897862|dbj|BAH30263.1| hypothetical protein [Arabidopsis thaliana] gi|332189285|gb|AEE27406.1| NAC domain-containing protein 5 [Arabidopsis thaliana]	382	362	3.00E-86	94.8	54.5	65.2	NAC domain-containing protein 5	gbpln	Arabidopsis thaliana	AT1G02250.1 | Symbols: anac005, NAC005 | NAC domain containing protein 5 | chr1:437951-439559 REVERSE LENGTH=362	382	362	7.00E-89	94.8	54.5	65.2
Rsa1.0_01185.1.g24368.t1	ref|NP_171727.2| NAC domain-containing protein 5 [Arabidopsis thaliana] gi|238065080|sp|O81914.2|NAC5_ARATH RecName: Full=NAC domain-containing protein 5; Short=ANAC005 gi|225897862|dbj|BAH30263.1| hypothetical protein [Arabidopsis thaliana] gi|332189285|gb|AEE27406.1| NAC domain-containing protein 5 [Arabidopsis thaliana]	380	362	9.00E-79	95.3	51.8	64.2	NAC domain-containing protein 5	gbpln	Arabidopsis thaliana	AT1G02250.1 | Symbols: anac005, NAC005 | NAC domain containing protein 5 | chr1:437951-439559 REVERSE LENGTH=362	380	362	2.00E-81	95.3	51.8	64.2
Rsa1.0_01185.1.g24369.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01185.1.g24370.t1	ref|XP_002892094.1| hypothetical protein ARALYDRAFT_333558 [Arabidopsis lyrata subsp. lyrata] gi|297337936|gb|EFH68353.1| hypothetical protein ARALYDRAFT_333558 [Arabidopsis lyrata subsp. lyrata]	318	216	1.00E-56	67.9	42.8	54.1	hypothetical protein ARALYDRAFT_333558	gbpln	Arabidopsis lyrata	AT1G02250.1 | Symbols: anac005, NAC005 | NAC domain containing protein 5 | chr1:437951-439559 REVERSE LENGTH=362	318	362	1.00E-58	113.8	45.3	53.5
Rsa1.0_01185.1.g24371.t1	ref|NP_171727.2| NAC domain-containing protein 5 [Arabidopsis thaliana] gi|238065080|sp|O81914.2|NAC5_ARATH RecName: Full=NAC domain-containing protein 5; Short=ANAC005 gi|225897862|dbj|BAH30263.1| hypothetical protein [Arabidopsis thaliana] gi|332189285|gb|AEE27406.1| NAC domain-containing protein 5 [Arabidopsis thaliana]	399	362	2.00E-84	90.7	50.4	61.9	NAC domain-containing protein 5	gbpln	Arabidopsis thaliana	AT1G02250.1 | Symbols: anac005, NAC005 | NAC domain containing protein 5 | chr1:437951-439559 REVERSE LENGTH=362	399	362	4.00E-87	90.7	50.4	61.9

Rsa1.0_01185.1.g24372.t1	ref|NP_563646.1| uncharacterized calcium-binding protein [Arabidopsis thaliana] gi|148887024|sp|O81916.2|YC22_ARATH RecName: Full=Uncharacterized calcium-binding protein At1g02270 gi|15450673|gb|AAK96608.1| At1g02270/T6A9_9 [Arabidopsis thaliana] gi|17380606|gb|AAL36066.1| At1g02270/T6A9_9 [Arabidopsis thaliana] gi|332189287|gb|AEE27408.1| uncharacterized calcium-binding protein [Arabidopsis thaliana]	491	484	0	98.6	83.5	90.4	uncharacterized calcium-binding protein	gbpln	Arabidopsis thaliana	AT1G02270.1 | Symbols: | Calcium-binding endonuclease/exonuclease/phosphatase family | chr1:443301-446197 REVERSE LENGTH=484	491	484	0	98.6	83.5	90.4
Rsa1.0_01185.1.g24373.t1	gb|EOA36595.1| hypothetical protein CARUB_v10011793mg [Capsella rubella]	314	317	1.00E-143	101.0	86.0	92.4	hypothetical protein CARUB_v10011793mg	gbpln	Capsella rubella	AT2G41610.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17347181-17348113 FORWARD LENGTH=310	314	310	1.00E-129	98.7	81.5	91.7
Rsa1.0_01185.1.g24374.t1	gb|AAQ17548.1| TOC33 [Brassica napus]	297	297	1.00E-169	100.0	98.3	99.3	TOC33	gbpln	Brassica napus	AT1G02280.2 | Symbols: TOC33, ATTOC33, PPI1 | translocon at the outer envelope membrane of chloroplasts 33 | chr1:448665-450246 REVERSE LENGTH=297	297	297	1.00E-167	100.0	94.9	98.0
Rsa1.0_01185.1.g24375.t1	ref|XP_002889395.1| hypothetical protein ARALYDRAFT_887368 [Arabidopsis lyrata subsp. lyrata] gi|297335237|gb|EFH65654.1| hypothetical protein ARALYDRAFT_887368 [Arabidopsis lyrata subsp. lyrata]	361	360	0	99.7	87.3	93.1	hypothetical protein ARALYDRAFT_887368	gbpln	Arabidopsis lyrata	AT1G02305.1 | Symbols: | Cysteine proteinases superfamily protein | chr1:455816-457974 FORWARD LENGTH=362	361	362	0	100.3	87.3	93.6
Rsa1.0_01185.1.g24376.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01185.1.g24377.t1	ref|NP_001190727.1| structural constituent of ribosome [Arabidopsis thaliana] gi|332658002|gb|AEE83402.1| structural constituent of ribosome [Arabidopsis thaliana]	182	815	6.00E-30	447.8	38.5	49.5	structural constituent of ribosome	gbpln	Arabidopsis thaliana	AT4G14250.2 | Symbols: | structural constituent of ribosome | chr4:8208985-8213237 REVERSE LENGTH=815	182	815	2.00E-32	447.8	38.5	49.5
Rsa1.0_01185.1.g24378.t1	ref|XP_002874719.1| hypothetical protein ARALYDRAFT_911537 [Arabidopsis lyrata subsp. lyrata] gi|297320556|gb|EFH50978.1| hypothetical protein ARALYDRAFT_911537 [Arabidopsis lyrata subsp. lyrata]	373	456	1.00E-99	122.3	53.6	64.9	hypothetical protein ARALYDRAFT_911537	gbpln	Arabidopsis lyrata	AT4G36840.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:17352166-17352882 FORWARD LENGTH=238	373	238	9.00E-35	63.8	26.8	37.0
Rsa1.0_01185.1.g24379.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	133	1231	5.00E-17	925.6	35.3	48.9	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01185.1.g24380.t1	ref|NP_171733.2| mannan endo-1,4-beta-mannosidase 1 [Arabidopsis thaliana] gi|75263247|sp|Q9FZ29.1|MAN1_ARATH RecName: Full=Mannan endo-1,4-beta-mannosidase 1; AltName: Full=Beta-mannanase 1; AltName: Full=Endo-beta-1,4-mannanase 1; Short=AtMAN1; Flags: Precursor gi|9857528|gb|AAG00883.1|AC064879_1 Similar to mannan endo-1,4-beta-mannosidase [Arabidopsis thaliana] gi|19699011|gb|AAL91241.1| (1-4)-beta-mannan endohydrolase precursor, putative [Arabidopsis thaliana] gi|25084063|gb|AAN72165.1| (1-4)-beta-mannan endohydrolase precursor, putative [Arabidopsis thaliana] gi|332189293|gb|AEE27414.1| mannan endo-1,4-beta-mannosidase 1 [Arabidopsis thaliana]	408	411	0	100.7	88.5	94.4	mannan endo-1,4-beta-mannosidase 1	gbpln	Arabidopsis thaliana	AT1G02310.1 | Symbols: MAN1 | Glycosyl hydrolase superfamily protein | chr1:458243-460652 REVERSE LENGTH=411	408	411	0	100.7	88.5	94.4
Rsa1.0_01186.1.g24381.t1	dbj|BAJ34051.1| unnamed protein product [Thellungiella halophila]	250	251	1.00E-129	100.4	90.0	96.0	unnamed protein product	----	----	AT5G20700.1 | Symbols: | Protein of unknown function (DUF581) | chr5:7006178-7007003 REVERSE LENGTH=248	250	248	1.00E-129	99.2	88.0	94.0
Rsa1.0_01186.1.g24382.t2	emb|CAB40067.1| putative retrotransposon polyprotein [Arabidopsis thaliana] gi|7267797|emb|CAB81200.1| putative retrotransposon polyprotein [Arabidopsis thaliana]	272	1203	6.00E-79	442.3	59.6	74.3	putative retrotransposon polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	272	1262	3.00E-58	464.0	48.5	66.2
Rsa1.0_01186.1.g24383.t1	gb|EOA23063.1| hypothetical protein CARUB_v10003833mg [Capsella rubella]	641	660	0	103.0	76.3	84.7	hypothetical protein CARUB_v10003833mg	gbpln	Capsella rubella	AT5G20690.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:7002453-7004551 FORWARD LENGTH=659	641	659	0	102.8	74.6	84.6

Rsa1.0_01186.1.g24384.t1	gb|EOA20312.1| hypothetical protein CARUB_v10000619mg [Capsella rubella]	502	554	0	110.4	85.7	91.4	hypothetical protein CARUB_v10000619mg	gbpln	Capsella rubella	AT5G20680.2 | Symbols: | TRICHOME BIREFRINGENCE-LIKE 16 | chr5:6999221-7001596 FORWARD LENGTH=533	502	533	0	106.2	84.1	91.2
Rsa1.0_01186.1.g24385.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1316	1515	0	115.1	53.7	68.8	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1316	1262	2.00E-85	95.9	12.9	19.5
Rsa1.0_01186.1.g24386.t1	ref|NP_197567.1| uncharacterized protein [Arabidopsis thaliana] gi|149944295|gb|ABR46190.1| At5g20670 [Arabidopsis thaliana] gi|332005491|gb|AED92874.1| uncharacterized protein AT5G20670 [Arabidopsis thaliana]	150	153	2.00E-69	102.0	88.0	91.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G20670.1 | Symbols: | Protein of unknown function (DUF1677) | chr5:6993332-6993793 REVERSE LENGTH=153	150	153	6.00E-72	102.0	88.0	91.3
Rsa1.0_01186.1.g24387.t1	gb|EOA21677.1| hypothetical protein CARUB_v10002100mg, partial [Capsella rubella]	143	173	5.00E-69	121.0	88.1	94.4	hypothetical protein CARUB_v10002100mg, partial	gbpln	Capsella rubella	AT5G20650.1 | Symbols: COPT5 | copper transporter 5 | chr5:6985481-6985921 REVERSE LENGTH=146	143	146	6.00E-69	102.1	88.1	93.7
Rsa1.0_01186.1.g24388.t1	gb|ABK28708.1| unknown [Arabidopsis thaliana]	217	216	2.00E-96	99.5	80.2	90.8	unknown	gbpln	Arabidopsis thaliana	AT5G20640.1 | Symbols: | Protein of unknown function (DUF567) | chr5:6984379-6985205 FORWARD LENGTH=215	217	215	6.00E-99	99.1	80.2	90.8
Rsa1.0_01186.1.g24389.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01186.1.g24390.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01186.1.g24391.t1	ref|XP_002874007.1| hypothetical protein ARALYDRAFT_910104 [Arabidopsis lyrata subsp. lyrata] gi|297319844|gb|EFH50266.1| hypothetical protein ARALYDRAFT_910104 [Arabidopsis lyrata subsp. lyrata]	211	211	1.00E-112	100.0	96.2	98.1	hypothetical protein ARALYDRAFT_910104	gbpln	Arabidopsis lyrata	AT5G20630.1 | Symbols: GLP3, GLP3A, GLP3B, ATGER3, GER3 | germin 3 | chr5:6975315-6975950 REVERSE LENGTH=211	211	211	1.00E-112	100.0	93.8	97.2
Rsa1.0_01186.1.g24392.t1	ref|NP_197561.1| uncharacterized protein [Arabidopsis thaliana] gi|332005483|gb|AED92866.1| uncharacterized protein AT5G20610 [Arabidopsis thaliana]	1085	1164	0	107.3	82.1	88.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G20610.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26160.1); Has 918 Blast hits to 759 proteins in 180 species: Archae - 6; Bacteria - 105; Metazoa - 264; Fungi - 89; Plants - 167; Viruses - 5; Other Eukaryotes - 282 (source: NCBI BLink). | chr5:6969184-6972794 FORWARD LENGTH=1164	1085	1164	0	107.3	82.1	88.5
Rsa1.0_01187.1.g24393.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	771	1307	0	169.5	64.9	79.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	771	1262	1.00E-104	163.7	25.4	39.9
Rsa1.0_01187.1.g24394.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01187.1.g24395.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01187.1.g24396.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01187.1.g24397.t2	emb|CAA65042.1| chlorophyll a/b-binding protein CP26 in PS II [Brassica juncea]	158	283	4.00E-78	179.1	90.5	91.1	chlorophyll a/b-binding protein CP26 in PS II	gbpln	Brassica juncea	AT4G10340.1 | Symbols: LHCB5 | light harvesting complex of photosystem II 5 | chr4:6408200-6409496 FORWARD LENGTH=280	158	280	3.00E-63	177.2	86.1	88.6
Rsa1.0_01187.1.g24398.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1025	1307	1.00E-161	127.5	32.3	40.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1025	1262	2.00E-59	123.1	15.8	23.3
Rsa1.0_01187.1.g24399.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1805	1197	1.00E-135	66.3	18.4	28.4	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1805	575	4.00E-78	31.9	10.1	16.0
Rsa1.0_01187.1.g24400.t1	ref|XP_002886107.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331947|gb|EFH62366.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	512	337	3.00E-66	65.8	33.4	40.6	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01188.1.g24401.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	171	704	3.00E-37	411.7	56.1	72.5	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01188.1.g24402.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01188.1.g24403.t1	ref|XP_002865280.1| hypothetical protein ARALYDRAFT_494469 [Arabidopsis lyrata subsp. lyrata] gi|297311115|gb|EFH41539.1| hypothetical protein ARALYDRAFT_494469 [Arabidopsis lyrata subsp. lyrata]	588	586	0	99.7	84.0	90.1	hypothetical protein ARALYDRAFT_494469	gbpln	Arabidopsis lyrata	AT5G45110.1 | Symbols: NPR3, ATNPR3 | NPR1-like protein 3 | chr5:18229319-18231334 FORWARD LENGTH=586	588	586	0	99.7	84.0	90.0
Rsa1.0_01188.1.g24404.t1	gb|EOA15133.1| hypothetical protein CARUB_v10028508mg [Capsella rubella]	580	550	0	94.8	69.8	80.0	hypothetical protein CARUB_v10028508mg	gbpln	Capsella rubella	AT5G45113.1 | Symbols: | mitochondrial transcription termination factor-related / mTERF-related | chr5:18232277-18233521 REVERSE LENGTH=414	580	414	0	71.4	54.5	62.1

Rsa1.0_01188.1.g24405.t1	ref|XP_002880870.1| hypothetical protein ARALYDRAFT_901538 [Arabidopsis lyrata subsp. lyrata] gi|297326709|gb|EFH57129.1| hypothetical protein ARALYDRAFT_901538 [Arabidopsis lyrata subsp. lyrata]	202	323	8.00E-42	159.9	55.4	67.8	hypothetical protein ARALYDRAFT_901538	gbpln	Arabidopsis lyrata	AT1G35890.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:13341300-13341953 FORWARD LENGTH=171	202	171	1.00E-17	84.7	20.3	24.8
Rsa1.0_01188.1.g24406.t1	gb|EOA14027.1| hypothetical protein CARUB_v10027159mg [Capsella rubella]	202	200	1.00E-108	99.0	96.5	97.5	hypothetical protein CARUB_v10027159mg	gbpln	Capsella rubella	AT5G45130.1 | Symbols: ATRAB5A, ATRABF2A, RABF2A, RAB5A, RHA1, ATRAB-F2A, RAB-F2A | RAB homolog 1 | chr5:18244495-18246060 FORWARD LENGTH=200	202	200	1.00E-110	99.0	95.0	96.0
Rsa1.0_01188.1.g24407.t2	ref|XP_002863522.1| hypothetical protein ARALYDRAFT_917015 [Arabidopsis lyrata subsp. lyrata] gi|297309357|gb|EFH39781.1| hypothetical protein ARALYDRAFT_917015 [Arabidopsis lyrata subsp. lyrata]	1134	1165	0	102.7	89.6	94.7	hypothetical protein ARALYDRAFT_917015	gbpln	Arabidopsis lyrata	AT5G45140.1 | Symbols: NRPC2 | nuclear RNA polymerase C2 | chr5:18247416-18257713 REVERSE LENGTH=1161	1134	1161	0	102.4	88.4	93.5
Rsa1.0_01188.1.g24408.t1	ref|XP_002865275.1| root hair defective 3 GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297311110|gb|EFH41534.1| root hair defective 3 GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]	813	833	0	102.5	88.2	94.3	root hair defective 3 GTP-binding family protein	gbpln	Arabidopsis lyrata	AT5G45160.1 | Symbols: | Root hair defective 3 GTP-binding protein (RHD3) | chr5:18264991-18270035 FORWARD LENGTH=834	813	834	0	102.6	87.9	94.0
Rsa1.0_01188.1.g24409.t1	ref|XP_002863521.1| hypothetical protein ARALYDRAFT_494462 [Arabidopsis lyrata subsp. lyrata] gi|297309356|gb|EFH39780.1| hypothetical protein ARALYDRAFT_494462 [Arabidopsis lyrata subsp. lyrata]	374	372	0	99.5	87.7	93.0	hypothetical protein ARALYDRAFT_494462	gbpln	Arabidopsis lyrata	AT5G45170.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:18270555-18273129 REVERSE LENGTH=372	374	372	0	99.5	86.9	91.7
Rsa1.0_01189.1.g24410.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01189.1.g24411.t1	gb|EOA38306.1| hypothetical protein CARUB_v10009810mg [Capsella rubella]	109	313	1.00E-40	287.2	67.9	71.6	hypothetical protein CARUB_v10009810mg	gbpln	Capsella rubella	AT1G25682.1 | Symbols: | Family of unknown function (DUF572) | chr1:9002532-9004550 REVERSE LENGTH=310	109	310	2.00E-43	284.4	67.0	71.6
Rsa1.0_01189.1.g24412.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01189.1.g24413.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01189.1.g24414.t1	gb|EOA20192.1| hypothetical protein CARUB_v10000488mg, partial [Capsella rubella]	76	614	9.00E-32	807.9	90.8	93.4	hypothetical protein CARUB_v10000488mg, partial	gbpln	Capsella rubella	AT4G05020.1 | Symbols: NDB2 | NAD(P)H dehydrogenase B2 | chr4:2572752-2576222 FORWARD LENGTH=582	76	582	5.00E-33	765.8	88.2	90.8
Rsa1.0_01189.1.g24415.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	517	1274	1.00E-107	246.4	45.1	59.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	517	575	2.00E-47	111.2	29.4	46.8
Rsa1.0_01189.1.g24416.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1049	1274	1.00E-149	121.4	27.2	35.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1049	626	1.00E-26	59.7	10.9	18.3
Rsa1.0_01189.1.g24417.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	335	1072	2.00E-83	320.0	45.7	62.1	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	335	289	2.00E-74	86.3	40.3	55.8
Rsa1.0_01189.1.g24418.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	994	1365	0	137.3	44.6	62.4	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	994	575	1.00E-73	57.8	17.5	27.6
Rsa1.0_01190.1.g24419.t1	gb|AAD19773.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1281	1335	0	104.2	59.5	75.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1281	1262	2.00E-83	98.5	14.4	21.7

Rsa1.0_01190.1_g24420.t1	ref|NP_174340.2| acyl-activating enzyme 14 [Arabidopsis thaliana] gi|75304445|sp|Q8VYJ1.1|MENE_ARATH RecName: Full=2-succinylbenzoate--CoA ligase, chloroplastic/peroxisomal; AltName: Full=Acyl-activating enzyme 14; AltName: Full=O-succinylbenzoyl-CoA ligase; Flags: Precursor gi|17979487|gb|AAL50080.1| At1g30520/F26G16_3 [Arabidopsis thaliana] gi|29893264|gb|AAP03026.1| acyl-activating enzyme 14 [Arabidopsis thaliana] gi|34365547|gb|AAQ65085.1| At1g30520/F26G16_3 [Arabidopsis thaliana] gi|332193118|gb|AEE31239.1| acyl-activating enzyme 14 [Arabidopsis thaliana]	554	560	0	101.1	85.9	91.9	acyl-activating enzyme 14	gbpln	Arabidopsis thaliana	AT1G30520.1 | Symbols: AAE14 | acyl-activating enzyme 14 | chr1:10811039-10813546 FORWARD LENGTH=560	554	560	0	101.1	85.9	91.9
Rsa1.0_01190.1_g24421.t1	ref|NP_564356.1| uncharacterized protein [Arabidopsis thaliana] gi|21618079|gb|AAM67129.1| unknown [Arabidopsis thaliana] gi|92856557|gb|ABE77398.1| At1g30515 [Arabidopsis thaliana] gi|332193117|gb|AEE31238.1| uncharacterized protein AT1G30515 [Arabidopsis thaliana]	150	144	1.00E-38	96.0	63.3	74.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G30515.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G21740.1); Has 20 Blast hits to 20 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10809432-10809866 REVERSE LENGTH=144	150	144	4.00E-41	96.0	63.3	74.7
Rsa1.0_01190.1_g24422.t1	gb|EOA37968.1| hypothetical protein CARUB_v10009436mg [Capsella rubella]	387	382	0	98.7	91.5	95.3	hypothetical protein CARUB_v10009436mg	gbpln	Capsella rubella	AT1G30510.2 | Symbols: ATRFNR2, RFNR2 | root FNR 2 | chr1:10807150-10808984 REVERSE LENGTH=382	387	382	0	98.7	92.0	95.3
Rsa1.0_01190.1_g24423.t2	ref|XP_002893628.1| CCAAT-binding transcription factor (CBF-B/NF-YA) family protein [Arabidopsis lyrata subsp. lyrata] gi|297339470|gb|EFH69887.1| CCAAT-binding transcription factor (CBF-B/NF-YA) family protein [Arabidopsis lyrata subsp. lyrata]	193	190	9.00E-65	98.4	73.6	79.3	CCAAT-binding transcription factor (CBF-B/NF-YA) family protein	gbpln	Arabidopsis lyrata	AT1G30500.2 | Symbols: NF-YA7 | nuclear factor Y, subunit A7 | chr1:10804736-10805896 REVERSE LENGTH=190	193	190	4.00E-67	98.4	74.6	79.3
Rsa1.0_01190.1_g24424.t1	dbj|BAJ34344.1| unnamed protein product [Thellungiella halophila]	840	844	0	100.5	95.6	97.9	unnamed protein product	----	----	AT1G30490.1 | Symbols: PHV, ATHB9 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr1:10796328-10800744 REVERSE LENGTH=841	840	841	0	100.1	95.1	98.2
Rsa1.0_01190.1_g24425.t1	gb|EOA37280.1| hypothetical protein CARUB_v10010883mg, partial [Capsella rubella]	268	233	8.00E-28	86.9	30.2	39.9	hypothetical protein CARUB_v10010883mg, partial	gbpln	Capsella rubella	AT1G30473.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr1:10787215-10788107 FORWARD LENGTH=239	268	239	5.00E-27	89.2	28.4	37.7
Rsa1.0_01190.1_g24426.t2	ref|NP_174335.4| SIT4 phosphatase-associated-like protein [Arabidopsis thaliana] gi|332193102|gb|AEE31223.1| SIT4 phosphatase-associated-like protein [Arabidopsis thaliana]	834	811	0	97.2	81.3	86.9	SIT4 phosphatase-associated-like protein	gbpln	Arabidopsis thaliana	AT1G30470.1 | Symbols: | SIT4 phosphatase-associated family protein | chr1:10779423-10786415 FORWARD LENGTH=811	834	811	0	97.2	81.3	86.9
Rsa1.0_01190.1_g24427.t1	ref|NP_174332.1| Phototropic-responsive NPH3-like protein [Arabidopsis thaliana] gi|166228367|sp|Q9S9Q9.2|Y1044_ARATH RecName: Full=BTB/POZ domain-containing protein At1g30440 gi|332193095|gb|AEE31216.1| Phototropic-responsive NPH3-like protein [Arabidopsis thaliana]	657	665	0	101.2	93.5	96.5	Phototropic-responsive NPH3-like protein	gbpln	Arabidopsis thaliana	AT1G30440.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr1:10759475-10762199 FORWARD LENGTH=665	657	665	0	101.2	93.5	96.5
Rsa1.0_01190.1_g24428.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01190.1_g24429.t1	ref|XP_002890866.1| photosystem I reaction center subunit X psaK [Arabidopsis lyrata subsp. lyrata] gi|297336708|gb|EFH67125.1| photosystem I reaction center subunit X psaK [Arabidopsis lyrata subsp. lyrata]	131	131	1.00E-64	100.0	96.2	98.5	photosystem I reaction center subunit X psaK	gbpln	Arabidopsis lyrata	AT1G30380.1 | Symbols: PSAK | photosystem I subunit K | chr1:10722325-10723013 FORWARD LENGTH=130	131	130	1.00E-65	99.2	95.4	98.5
Rsa1.0_01190.1_g24430.t1	ref|NP_174326.1| lipase-3 domain-containing protein [Arabidopsis thaliana] gi|12322127|gb|AAG51101.1|AC025295_9 lipase, putative [Arabidopsis thaliana] gi|332193089|gb|AEE31210.1| lipase-3 domain-containing protein [Arabidopsis thaliana]	529	529	0	100.0	89.8	94.9	lipase-3 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G30370.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:10719169-10720758 REVERSE LENGTH=529	529	529	0	100.0	89.8	94.9

Rsa1.0_01190.1.g24431.t1	gb|ABV89627.1| early-responsive to dehydration 4 [Brassica rapa]	722	723	0	100.1	85.2	93.6	early-responsive to dehydration 4	gbpln	Brassica rapa	AT1G30360.1 | Symbols: ERD4 | Early-responsive to dehydration stress protein (ERD4) | chr1:10715892-10718799 FORWARD LENGTH=724	722	724	0	100.3	80.9	90.9
Rsa1.0_01190.1.g24432.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01190.1.g24433.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01190.1.g24434.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01191.1.g24435.t1	ref|XP_002880635.1| hypothetical protein ARALYDRAFT_481345 [Arabidopsis lyrata subsp. lyrata] gi|297326474|gb|EFH56894.1| hypothetical protein ARALYDRAFT_481345 [Arabidopsis lyrata subsp. lyrata]	226	445	2.00E-88	196.9	72.1	83.2	hypothetical protein ARALYDRAFT_481345	gbpln	Arabidopsis lyrata	AT2G24850.1 | Symbols: TAT3, TAT | tyrosine aminotransferase 3 | chr2:10583070-10585152 REVERSE LENGTH=445	226	445	6.00E-90	196.9	70.8	83.6
Rsa1.0_01191.1.g24436.t1	ref|XP_002880635.1| hypothetical protein ARALYDRAFT_481345 [Arabidopsis lyrata subsp. lyrata] gi|297326474|gb|EFH56894.1| hypothetical protein ARALYDRAFT_481345 [Arabidopsis lyrata subsp. lyrata]	441	445	0	100.9	78.5	88.4	hypothetical protein ARALYDRAFT_481345	gbpln	Arabidopsis lyrata	AT2G24850.1 | Symbols: TAT3, TAT | tyrosine aminotransferase 3 | chr2:10583070-10585152 REVERSE LENGTH=445	441	445	0	100.9	77.8	88.7
Rsa1.0_01191.1.g24437.t2	gb|AAC19277.1| T14P8.8 [Arabidopsis thaliana] gi|7269008|emb|CAB80741.1| AT4g02480 [Arabidopsis thaliana]	329	731	3.00E-16	222.2	26.1	33.1	T14P8.8	gbpln	Arabidopsis thaliana	AT4G02480.1 | Symbols: | AAA-type ATPase family protein | chr4:1082082-1088680 REVERSE LENGTH=1265	329	1265	6.00E-18	384.5	20.7	23.7
Rsa1.0_01191.1.g24438.t1	gb|EOA15951.1| hypothetical protein CARUB_v10004048mg [Capsella rubella]	301	1041	1.00E-139	345.8	84.1	89.7	hypothetical protein CARUB_v10004048mg	gbpln	Capsella rubella	AT4G16060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast stroma; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 42 Blast hits to 42 proteins in 16 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr4:9094424-9096147 FORWARD LENGTH=289	301	289	1.00E-128	96.0	79.7	84.1
Rsa1.0_01191.1.g24439.t1	ref|XP_002870199.1| At4g15930 [Arabidopsis lyrata subsp. lyrata] gi|297316035|gb|EFH46458.1| At4g15930 [Arabidopsis lyrata subsp. lyrata]	98	123	5.00E-32	125.5	81.6	87.8	At4g15930	gbpln	Arabidopsis lyrata	AT4G15930.1 | Symbols: | Dynein light chain type 1 family protein | chr4:9036344-9037825 FORWARD LENGTH=123	98	123	1.00E-34	125.5	81.6	87.8
Rsa1.0_01191.1.g24440.t1	gb|AAO22792.1| putative cytochrome c oxidoreductase [Arabidopsis thaliana]	238	241	1.00E-117	101.3	88.7	94.5	putative cytochrome c oxidoreductase	gbpln	Arabidopsis thaliana	AT4G15920.1 | Symbols: SWEET17, AtSWEET17 | Nodulin MtN3 family protein | chr4:9030742-9033343 REVERSE LENGTH=241	238	241	1.00E-118	101.3	87.8	93.7
Rsa1.0_01191.1.g24441.t1	gb|EOA16548.1| hypothetical protein CARUB_v10004707mg [Capsella rubella]	477	481	0	100.8	92.5	96.6	hypothetical protein CARUB_v10004707mg	gbpln	Capsella rubella	AT4G15900.1 | Symbols: PRL1 | pleiotropic regulatory locus 1 | chr4:9023775-9027443 FORWARD LENGTH=486	477	486	0	101.9	92.7	96.4
Rsa1.0_01191.1.g24442.t1	gb|EOA15906.1| hypothetical protein CARUB_v10003997mg [Capsella rubella]	1331	1318	0	99.0	86.4	91.8	hypothetical protein CARUB_v10003997mg	gbpln	Capsella rubella	AT4G15890.1 | Symbols: | binding | chr4:9017453-9022745 FORWARD LENGTH=1314	1331	1314	0	98.7	87.7	92.8
Rsa1.0_01191.1.g24443.t2	ref|NP_188285.1| kinesin family member 2/24 [Arabidopsis thaliana] gi|30684173|ref|NP_850598.1| kinesin family member 2/24 [Arabidopsis thaliana] gi|15810129|gb|AAL07208.1| putative kinesin protein [Arabidopsis thaliana] gi|110741480|dbj|BAE98696.1| kinesin like protein [Arabidopsis thaliana] gi|332642324|gb|AEE75845.1| kinesin 13A [Arabidopsis thaliana] gi|332642325|gb|AEE75846.1| kinesin family member 2/24 [Arabidopsis thaliana]	929	794	0	85.5	71.2	77.3	kinesin family member 2/24	gbpln	Arabidopsis thaliana	AT3G16630.2 | Symbols: ATKINESIN-13A, KINESIN-13A | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:5662660-5667261 REVERSE LENGTH=794	929	794	0	85.5	71.2	77.3
Rsa1.0_01191.1.g24444.t1	gb|EOA16487.1| hypothetical protein CARUB_v10004645mg [Capsella rubella]	472	498	1.00E-179	105.5	73.1	79.9	hypothetical protein CARUB_v10004645mg	gbpln	Capsella rubella	AT4G15880.1 | Symbols: ESD4, ATESD4 | Cysteine proteinases superfamily protein | chr4:9012769-9015797 FORWARD LENGTH=489	472	489	1.00E-178	103.6	71.8	80.3
Rsa1.0_01191.1.g24445.t1	gb|EOA18019.1| hypothetical protein CARUB_v10006459mg [Capsella rubella]	372	374	1.00E-144	100.5	68.5	78.8	hypothetical protein CARUB_v10006459mg	gbpln	Capsella rubella	AT1G30350.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:10710194-10711664 REVERSE LENGTH=368	372	368	1.00E-142	98.9	64.5	78.5
Rsa1.0_01192.1.g24446.t1	ref|XP_002882474.1| botrytis-susceptible1, myb domain protein 108 [Arabidopsis lyrata subsp. lyrata] gi|297328314|gb|EFH58733.1| botrytis-susceptible1, myb domain protein 108 [Arabidopsis lyrata subsp. lyrata]	322	322	1.00E-143	100.0	85.7	91.6	botrytis-susceptible1, myb domain protein 108	gbpln	Arabidopsis lyrata	AT3G06490.1 | Symbols: MYB108, AtMYB108, BOS1 | myb domain protein 108 | chr3:2004298-2006358 FORWARD LENGTH=323	322	323	1.00E-140	100.3	87.0	93.2

Rsa1.0_01192.1.g24447.t1	ref|NP_566285.1| beta-glucosidase-like SFR2 [Arabidopsis thaliana] gi|75305863|sp|Q93Y07.1|SFR2_ARATH RecName: Full=Beta-glucosidase-like SFR2, chloroplastic; AltName: Full=Protein SENSITIVE TO FREEZING 2; Short=AtSFR2 gi|16649039|gb|AAL24371.1| beta-glucosidase, putative [Arabidopsis thaliana] gi|22077112|emb|CAD36512.1| putative beta-glycosidase [Arabidopsis thaliana] gi|25083735|gb|AAN72111.1| beta-glucosidase, putative [Arabidopsis thaliana] gi|332640883|gb|AEE74404.1| beta-glucosidase-like SFR2 [Arabidopsis thaliana]	1381	622	0	45.0	38.8	42.0	beta-glucosidase-like SFR2	gbpln	Arabidopsis thaliana	AT3G06510.1 | Symbols: SFR2, ATSFR2 | Glycosyl hydrolase superfamily protein | chr3:2016450-2019533 FORWARD LENGTH=622	1381	622	0	45.0	38.8	42.0
Rsa1.0_01192.1.g24448.t1	gb|EOA29708.1| hypothetical protein CARUB_v10012793mg [Capsella rubella]	2140	2208	0	103.2	56.4	62.1	hypothetical protein CARUB_v10012793mg	gbpln	Capsella rubella	AT3G06530.1 | Symbols: | ARM repeat superfamily protein | chr3:2022596-2033637 FORWARD LENGTH=2197	2140	2197	0	102.7	55.9	62.2
Rsa1.0_01192.1.g24449.t1	gb|AAM19852.1| AT3g06540/F5E6_13 [Arabidopsis thaliana] gi|23463085|gb|AAN33212.1| At3g06540/F5E6_13 [Arabidopsis thaliana]	567	563	0	99.3	80.6	89.2	AT3g06540/F5E6_13	gbpln	Arabidopsis thaliana	AT3G06540.1 | Symbols: REP, AthREP | Rab escort protein | chr3:2035201-2037662 REVERSE LENGTH=563	567	563	0	99.3	80.6	89.2
Rsa1.0_01193.1.g24450.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	872	1142	0	131.0	43.7	57.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	872	626	4.00E-29	71.8	10.7	16.4
Rsa1.0_01193.1.g24451.t1	gb|EOA37904.1| hypothetical protein CARUB_v10009370mg [Capsella rubella]	394	394	0	100.0	95.7	97.5	hypothetical protein CARUB_v10009370mg	gbpln	Capsella rubella	AT1G30580.1 | Symbols: | GTP binding | chr1:10831953-10835454 REVERSE LENGTH=394	394	394	0	100.0	95.7	97.2
Rsa1.0_01193.1.g24452.t1	ref|NP_001154386.2| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|332193122|gb|AEE31243.1| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana]	257	221	3.00E-90	86.0	59.9	67.7	S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G30550.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:10822341-10823641 REVERSE LENGTH=221	257	221	1.00E-92	86.0	59.9	67.7
Rsa1.0_01193.1.g24453.t1	ref|XP_002893626.1| hypothetical protein ARALYDRAFT_473274 [Arabidopsis lyrata subsp. lyrata] gi|297339468|gb|EFH69885.1| hypothetical protein ARALYDRAFT_473274 [Arabidopsis lyrata subsp. lyrata]	165	192	3.00E-39	116.4	70.9	78.8	hypothetical protein ARALYDRAFT_473274	gbpln	Arabidopsis lyrata	AT1G30475.1 | Symbols: | BEST Arabidopsis thaliana protein match is: embryo defective 1303 (TAIR:AT1G56200.1); Has 148 Blast hits to 148 proteins in 34 species: Archae - 0; Bacteria - 14; Metazoa - 63; Fungi - 0; Plants - 62; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink). | chr1:10788501-10789943 REVERSE LENGTH=191	165	191	8.00E-40	115.8	70.3	76.4
Rsa1.0_01193.1.g24454.t1	ref|NP_001185116.1| SIT4 phosphatase-associated-like protein [Arabidopsis thaliana] gi|332193104|gb|AEE31225.1| SIT4 phosphatase-associated-like protein [Arabidopsis thaliana]	834	805	0	96.5	81.5	86.3	SIT4 phosphatase-associated-like protein	gbpln	Arabidopsis thaliana	AT1G30470.2 | Symbols: | SIT4 phosphatase-associated family protein | chr1:10779435-10786415 FORWARD LENGTH=805	834	805	0	96.5	81.5	86.3
Rsa1.0_01193.1.g24455.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01193.1.g24456.t2	ref|NP_174333.2| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|30691718|ref|NP_849731.1| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|30691724|ref|NP_849732.1| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|122209111|sp|Q2UVJ5.1|CCC1_ARATH RecName: Full=Cation-chloride cotransporter 1; Short=AtCCC1; AltName: Full=Protein HAPLESS 5 gi|83523648|emb|CAJ34849.1| cation chloride cotransporter [Arabidopsis thaliana] gi|110741532|dbj|BAE98715.1| putative cation-chloride co-transporter [Arabidopsis thaliana] gi|332193096|gb|AEE31217.1| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|332193097|gb|AEE31218.1| cation-chloride co-transporter 1 [Arabidopsis thaliana] gi|332193098|gb|AEE31219.1| cation-chloride co-transporter 1 [Arabidopsis thaliana]	1007	975	0	96.8	90.0	92.2	cation-chloride co-transporter 1	gbpln	Arabidopsis thaliana	AT1G30450.2 | Symbols: CCC1, ATCCC1, HAP5 | cation-chloride co-transporter 1 | chr1:10762905-10769061 FORWARD LENGTH=975	1007	975	0	96.8	90.0	92.2
Rsa1.0_01194.1.g24457.t1	dbj|BAJ33907.1| unnamed protein product [Thellungiella halophila]	513	595	0	116.0	86.9	90.1	unnamed protein product	----	----	AT5G60790.1 | Symbols: ATGCN1, GCN1 | ABC transporter family protein | chr5:24453760-24455767 REVERSE LENGTH=595	513	595	0	116.0	85.8	89.3

Rsa1.0_01194.1.g24458.t1	ref|NP_200886.1| nitrate transporter 2.3 [Arabidopsis thaliana] gi|75262552|sp|Q9FJH7.1|NRT23_ARATH RecName: Full=High affinity nitrate transporter 2.3; Short=AtNRT2:3 gi|10176906|dbj|BAB10099.1| high affinity nitrate transporter [Arabidopsis thaliana] gi|91807076|gb|ABE66265.1| high-affinity nitrate transporter [Arabidopsis thaliana] gi|332009993|gb|AED97376.1| nitrate transporter 2.3 [Arabidopsis thaliana]	536	539	0	100.6	93.3	96.5	nitrate transporter 2.3	gbpln	Arabidopsis thaliana	AT5G60780.1 | Symbols: ATNRT2.3, NRT2.3 | nitrate transporter 2.3 | chr5:24450839-24452756 FORWARD LENGTH=539	536	539	0	100.6	93.3	96.5
Rsa1.0_01194.1.g24459.t1	ref|NP_191137.1| glycosyl hydrolase family 17 protein [Arabidopsis thaliana] gi|7263566|emb|CAB81603.1| beta-1, 3-glucanase-like protein [Arabidopsis thaliana] gi|332645920|gb|AEE79441.1| glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	61	429	1.00E-16	703.3	68.9	77.0	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis thaliana	AT3G55780.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr3:20705627-20707021 FORWARD LENGTH=429	61	429	2.00E-19	703.3	68.9	77.0
Rsa1.0_01194.1.g24460.t1	gb|EOA32375.1| hypothetical protein CARUB_v10015642mg [Capsella rubella]	158	1127	5.00E-26	713.3	34.8	36.7	hypothetical protein CARUB_v10015642mg	gbpln	Capsella rubella	AT3G16830.1 | Symbols: TPR2 | TOPLESS-related 2 | chr3:5731709-5737531 FORWARD LENGTH=1131	158	1131	4.00E-28	715.8	34.8	36.1
Rsa1.0_01194.1.g24461.t1	ref|XP_002864701.1| hypothetical protein ARALYDRAFT_496224 [Arabidopsis lyrata subsp. lyrata] gi|297310536|gb|EFH40960.1| hypothetical protein ARALYDRAFT_496224 [Arabidopsis lyrata subsp. lyrata]	637	739	0	116.0	55.6	58.9	hypothetical protein ARALYDRAFT_496224	gbpln	Arabidopsis lyrata	AT5G60760.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:24438465-24442004 FORWARD LENGTH=738	637	738	1.00E-179	115.9	52.1	56.8
Rsa1.0_01194.1.g24462.t1	ref|XP_002864699.1| anion-transporting ATPase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310534|gb|EFH40958.1| anion-transporting ATPase family protein [Arabidopsis lyrata subsp. lyrata]	829	391	1.00E-174	47.2	41.3	43.1	anion-transporting ATPase family protein	gbpln	Arabidopsis lyrata	AT5G60730.1 | Symbols: | Anion-transporting ATPase | chr5:24422838-24425352 FORWARD LENGTH=391	829	391	1.00E-175	47.2	41.0	42.7
Rsa1.0_01194.1.g24463.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01194.1.g24464.t1	ref|NP_200879.1| C3H4 type zinc finger protein [Arabidopsis thaliana] gi|9759335|dbj|BAB09844.1| retroelement pol polyprotein-like [Arabidopsis thaliana] gi|332009986|gb|AED97369.1| C3H4 type zinc finger protein [Arabidopsis thaliana]	67	704	1.00E-19	1050.7	74.6	80.6	C3H4 type zinc finger protein	gbpln	Arabidopsis thaliana	AT5G60710.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr5:24410953-24414849 REVERSE LENGTH=704	67	704	2.00E-22	1050.7	74.6	80.6
Rsa1.0_01194.1.g24465.t1	gb|AAM53301.1| putative protein [Arabidopsis thaliana] gi|23198328|gb|AAN15691.1| putative protein [Arabidopsis thaliana]	644	704	0	109.3	82.6	89.0	putative protein	gbpln	Arabidopsis thaliana	AT5G60710.1 | Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr5:24410953-24414849 REVERSE LENGTH=704	644	704	0	109.3	82.6	89.0
Rsa1.0_01194.1.g24466.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01195.1.g24467.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01195.1.g24468.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01195.1.g24469.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01195.1.g24470.t1	gb|EOA26809.1| hypothetical protein CARUB_v10022902mg [Capsella rubella]	578	573	0	99.1	85.1	90.3	hypothetical protein CARUB_v10022902mg	gbpln	Capsella rubella	AT2G46500.2 | Symbols: ATPI4K GAMMA 4, UBDK GAMMA 4, PI4K GAMMA 4 | phosphoinositide 4-kinase gamma 4 | chr2:19086741-19088534 REVERSE LENGTH=566	578	566	0	97.9	83.7	89.4
Rsa1.0_01195.1.g24471.t1	ref|XP_002882072.1| hypothetical protein ARALYDRAFT_904117 [Arabidopsis lyrata subsp. lyrata] gi|297327911|gb|EFH58331.1| hypothetical protein ARALYDRAFT_904117 [Arabidopsis lyrata subsp. lyrata]	149	148	3.00E-50	99.3	71.1	85.9	hypothetical protein ARALYDRAFT_904117	gbpln	Arabidopsis lyrata	AT2G46505.1 | Symbols: SDH4 | succinate dehydrogenase subunit 4 | chr2:19090013-19090468 REVERSE LENGTH=151	149	151	3.00E-50	101.3	67.8	84.6
Rsa1.0_01195.1.g24472.t1	gb|EOA27345.1| hypothetical protein CARUB_v10023459mg [Capsella rubella]	356	372	1.00E-161	104.5	87.6	93.3	hypothetical protein CARUB_v10023459mg	gbpln	Capsella rubella	AT2G46590.1 | Symbols: DAG2 | Dof-type zinc finger DNA-binding family protein | chr2:19133832-19134905 FORWARD LENGTH=357	356	357	1.00E-144	100.3	85.1	89.9
Rsa1.0_01195.1.g24473.t1	gb|EOA28618.1| hypothetical protein CARUB_v10024839mg [Capsella rubella]	137	133	6.00E-61	97.1	81.0	94.9	hypothetical protein CARUB_v10024839mg	gbpln	Capsella rubella	AT2G46600.1 | Symbols: | Calcium-binding EF-hand family protein | chr2:19136070-19136477 FORWARD LENGTH=135	137	135	3.00E-63	98.5	82.5	94.2
Rsa1.0_01195.1.g24474.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01195.1.g24475.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01195.1.g24476.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	162	1142	3.00E-31	704.9	45.1	57.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	162	292	1.00E-14	180.2	28.4	46.3

Rsa1.0_01195.1.g24477.t2	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	180	704	5.00E-53	391.1	58.9	63.3	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01195.1.g24478.t1	ref|XP_002862757.1| hypothetical protein ARALYDRAFT_497309 [Arabidopsis lyrata subsp. lyrata] gi|297308467|gb|EFH39015.1| hypothetical protein ARALYDRAFT_497309 [Arabidopsis lyrata subsp. lyrata]	310	312	1.00E-123	100.6	78.7	83.9	hypothetical protein ARALYDRAFT_497309	gbpln	Arabidopsis lyrata	AT2G46870.1 | Symbols: NGA1 | AP2/B3-like transcriptional factor family protein | chr2:19261313-19262245 FORWARD LENGTH=310	310	310	1.00E-126	100.0	77.7	83.9
Rsa1.0_01195.1.g24479.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01196.1.g24480.t1	gb|ABB45859.1| hypothetical protein [Eutrema halophilum]	274	258	1.00E-123	94.2	79.9	87.2	hypothetical protein	gbpln	Eutrema halophilum	AT5G66510.1 | Symbols: GAMMA CA3 | gamma carbonic anhydrase 3 | chr5:26550016-26551496 REVERSE LENGTH=258	274	258	1.00E-119	94.2	75.5	84.7
Rsa1.0_01196.1.g24481.t1	gb|ABB45850.1| hypothetical protein [Eutrema halophilum]	272	296	1.00E-113	108.8	82.4	88.6	hypothetical protein	gbpln	Eutrema halophilum	AT5G66450.1 | Symbols: | Phosphatidic acid phosphatase (PAP2) family protein | chr5:26534801-26535951 FORWARD LENGTH=286	272	286	1.00E-108	105.1	78.3	87.5
Rsa1.0_01196.1.g24482.t1	gb|ABB45857.1| hypothetical protein [Eutrema halophilum]	358	369	0	103.1	93.3	96.4	hypothetical protein	gbpln	Eutrema halophilum	AT5G66280.1 | Symbols: GMD1 | GDP-D-mannose 4,6-dehydratase 1 | chr5:26476434-26477519 FORWARD LENGTH=361	358	361	0	100.8	91.6	95.5
Rsa1.0_01196.1.g24483.t2	emb|CAH65737.1| folate transporter [Arabidopsis thaliana]	293	308	1.00E-138	105.1	86.0	91.5	folate transporter	gbpln	Arabidopsis thaliana	AT5G66380.1 | Symbols: ATFOLT1, FOLT1 | folate transporter 1 | chr5:26513645-26515533 REVERSE LENGTH=308	293	308	1.00E-140	105.1	85.7	91.1
Rsa1.0_01196.1.g24484.t1	gb|ABB45838.1| hypothetical protein [Eutrema halophilum]	337	336	0	99.7	91.1	93.5	hypothetical protein	gbpln	Eutrema halophilum	AT5G66390.1 | Symbols: | Peroxidase superfamily protein | chr5:26516063-26517329 REVERSE LENGTH=336	337	336	0	99.7	89.3	93.5
Rsa1.0_01196.1.g24485.t1	gb|EOA14069.1| hypothetical protein CARUB_v10027206mg [Capsella rubella]	192	184	4.00E-44	95.8	76.0	77.6	hypothetical protein CARUB_v10027206mg	gbpln	Capsella rubella	AT5G66400.1 | Symbols: RAB18, ATDI8 | Dehydrin family protein | chr5:26518511-26519153 REVERSE LENGTH=186	192	186	4.00E-43	96.9	74.5	76.6
Rsa1.0_01196.1.g24486.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1137	1274	0	112.0	55.1	68.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1137	575	6.00E-73	50.6	16.4	24.5
Rsa1.0_01196.1.g24487.t1	gb|EOA12679.1| hypothetical protein CARUB_v10027866mg [Capsella rubella]	378	326	1.00E-165	86.2	76.5	80.2	hypothetical protein CARUB_v10027866mg	gbpln	Capsella rubella	AT5G66240.2 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:26466348-26468201 FORWARD LENGTH=331	378	331	1.00E-166	87.6	75.7	79.4
Rsa1.0_01196.1.g24488.t1	gb|EOA13055.1| hypothetical protein CARUB_v10026056mg [Capsella rubella]	646	651	0	100.8	93.3	96.6	hypothetical protein CARUB_v10026056mg	gbpln	Capsella rubella	AT5G66200.1 | Symbols: ARO2 | armadillo repeat only 2 | chr5:26453648-26455603 REVERSE LENGTH=651	646	651	0	100.8	92.1	95.5
Rsa1.0_01196.1.g24489.t1	ref|NP_201420.1| ferredoxin--NADP+ reductase [Arabidopsis thaliana] gi|75171342|sp|Q9FKW6.1|FNRL1_ARATH RecName: Full=Ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic; AltName: Full=Leaf FNR 1; Short=AtLFNR1; Short=FNR-1; Flags: Precursor gi|10177134|dbj|BAB10424.1| ferredoxin-NADP+ reductase [Arabidopsis thaliana] gi|18175825|gb|AAL59934.1| putative ferredoxin-NADP+ reductase [Arabidopsis thaliana] gi|20465661|gb|AAM20299.1| putative ferredoxin-NADP+ reductase [Arabidopsis thaliana] gi|332010791|gb|AED98174.1| ferredoxin--NADP+ reductase [Arabidopsis thaliana]	361	360	1.00E-180	99.7	92.0	94.7	ferredoxin--NADP+ reductase	gbpln	Arabidopsis thaliana	AT5G66190.1 | Symbols: ATLFNR1, FNR1 | ferredoxin-NADP(+)-oxidoreductase 1 | chr5:26451203-26453012 REVERSE LENGTH=360	361	360	0	99.7	92.0	94.7
Rsa1.0_01196.1.g24490.t1	ref|NP_201419.2| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|332010788|gb|AED98171.1| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana]	387	395	0	102.1	84.2	92.0	S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G66180.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:26448952-26450919 FORWARD LENGTH=395	387	395	0	102.1	84.2	92.0
Rsa1.0_01196.1.g24491.t1	gb|AAM64406.1| senescence-associated protein [Arabidopsis thaliana]	134	136	1.00E-53	101.5	74.6	86.6	senescence-associated protein	gbpln	Arabidopsis thaliana	AT5G66170.3 | Symbols: STR18 | sulfurtransferase 18 | chr5:26447828-26448586 FORWARD LENGTH=136	134	136	4.00E-56	101.5	74.6	85.8

Rsa1.0_01196.1.g24492.t11	dbj|BAJ34496.1| unnamed protein product [Thellungiella halophila]	395	210	9.00E-71	53.2	38.7	43.3	unnamed protein product	----	----	AT5G66090.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: chloroplast, chloroplast stroma; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26425831-26426955 FORWARD LENGTH=210	395	210	5.00E-70	53.2	38.5	43.3
Rsa1.0_01196.1.g24493.t1	ref|XP_002866780.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312615|gb|EFH43039.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	395	395	0	100.0	96.7	98.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G65980.1 | Symbols: | Auxin efflux carrier family protein | chr5:26392444-26394232 FORWARD LENGTH=395	395	395	0	100.0	95.4	97.2
Rsa1.0_01196.1.g24494.t27	ref|XP_002865094.1| hypothetical protein ARALYDRAFT_497034 [Arabidopsis lyrata subsp. lyrata] gi|297310929|gb|EFH41353.1| hypothetical protein ARALYDRAFT_497034 [Arabidopsis lyrata subsp. lyrata]	1741	1261	0	72.4	67.5	69.8	hypothetical protein ARALYDRAFT_497034	gbpln	Arabidopsis lyrata	AT5G65930.2 | Symbols: ZWI, PKCBP, KCBP | kinesin-like calmodulin-binding protein (ZWICHEL) | chr5:26370369-26376394 REVERSE LENGTH=1260	1741	1260	0	72.4	66.9	69.6
Rsa1.0_01196.1.g24495.t5	#	#	#	#	#	#	#	-	----	----	AT5G04410.1 | Symbols: NAC2, anac078 | NAC domain containing protein 2 | chr5:1243980-1246416 FORWARD LENGTH=567	182	567	2.00E-12	311.5	18.1	22.5
Rsa1.0_01197.1.g24496.t2	emb|CAB78060.1| putative protein [Arabidopsis thaliana]	574	666	9.00E-72	116.0	25.4	36.1	putative protein	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	574	249	5.00E-23	43.4	11.1	15.7
Rsa1.0_01197.1.g24497.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01197.1.g24498.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01197.1.g24499.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01197.1.g24500.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1127	1475	0	130.9	59.4	74.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1127	1262	0	112.0	27.5	36.0
Rsa1.0_01197.1.g24501.t1	ref|XP_002890776.1| hypothetical protein ARALYDRAFT_473063 [Arabidopsis lyrata subsp. lyrata] gi|297336618|gb|EFH67035.1| hypothetical protein ARALYDRAFT_473063 [Arabidopsis lyrata subsp. lyrata]	1029	996	0	96.8	72.3	78.8	hypothetical protein ARALYDRAFT_473063	gbpln	Arabidopsis lyrata	AT1G28440.1 | Symbols: HSL1 | HAESA-like 1 | chr1:9996914-10000171 FORWARD LENGTH=996	1029	996	0	96.8	72.0	78.4
Rsa1.0_01197.1.g24502.t3	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1688	1374	0	81.4	37.9	50.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1688	575	1.00E-114	34.1	13.6	19.1
Rsa1.0_01197.1.g24503.t1	pdb|2DRE|A Chain A, Crystal Structure Of Water-Soluble Chlorophyll Protein From Lepidium Virginicum At 2.00 Angstrom Resolution gi|122919966|pdb|2DRE|B Chain B, Crystal Structure Of Water-Soluble Chlorophyll Protein From Lepidium Virginicum At 2.00 Angstrom Resolution gi|122919967|pdb|2DRE|C Chain C, Crystal Structure Of Water-Soluble Chlorophyll Protein From Lepidium Virginicum At 2.00 Angstrom Resolution gi|122919968|pdb|2DRE|D Chain D, Crystal Structure Of Water-Soluble Chlorophyll Protein From Lepidium Virginicum At 2.00 Angstrom Resolution	190	180	2.00E-19	94.7	27.9	34.2	Chain A, Crystal Structure Of Water-Soluble Chlorophyll Protein From Lepidium Virginicum At 2.00 Angstrom Resolution gi|122919966|pdb|2DRE |B Chain B, Crystal Structure Of Water-Soluble Chlorophyll Protein From Lepidium Virginicum At 2.00 Angstrom Resolution gi|122919967|pdb|2DRE |C Chain C, Crystal Structure Of Water-Soluble Chlorophyll Protein From Lepidium Virginicum At 2.00 Angstrom Resolution gi|122919968|pdb|2DRE |D Chain D, Crystal Structure Of Water-Soluble Chlorophyll Protein From Lepidium Virginicum At 2.00 Angstrom Resolution	----	----	AT1G73325.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27567518-27568186 REVERSE LENGTH=222	190	222	9.00E-11	116.8	16.3	28.4

Rsa1.0_01198.1.g24504.t1	ref|XP_002864790.1| hypothetical protein ARALYDRAFT_496418 [Arabidopsis lyrata subsp. lyrata] gi|297310625|gb|EFH41049.1| hypothetical protein ARALYDRAFT_496418 [Arabidopsis lyrata subsp. lyrata]	1134	1175	0	103.6	93.2	96.9	hypothetical protein ARALYDRAFT_496418	gbpln	Arabidopsis lyrata	AT5G62410.1 | Symbols: SMC2, TTN3, ATCAP-E1, ATSMC4 | structural maintenance of chromosomes 2 | chr5:25056308-25062436 FORWARD LENGTH=1175	1134	1175	0	103.6	92.9	96.6
Rsa1.0_01198.1.g24505.t1	gb|EOA14154.1| hypothetical protein CARUB_v10027301mg, partial [Capsella rubella]	122	152	4.00E-62	124.6	96.7	96.7	hypothetical protein CARUB_v10027301mg, partial	gbpln	Capsella rubella	AT3G47370.3 | Symbols: | Ribosomal protein S10p/S20e family protein | chr3:17453671-17454437 REVERSE LENGTH=122	122	122	7.00E-64	100.0	95.9	95.9
Rsa1.0_01198.1.g24506.t1	gb|EOA13325.1| hypothetical protein CARUB_v10026360mg [Capsella rubella]	446	463	1.00E-175	103.8	78.3	87.4	hypothetical protein CARUB_v10026360mg	gbpln	Capsella rubella	AT5G62390.1 | Symbols: ATBAG7, BAG7 | BCL-2-associated athanogene 7 | chr5:25052377-25054170 REVERSE LENGTH=446	446	446	1.00E-166	100.0	75.3	85.7
Rsa1.0_01198.1.g24507.t1	ref|NP_201044.1| NAC-domain protein 101 [Arabidopsis thaliana] gi|8809651|dbj|BAA97202.1| NAM (no apical meristem)-like protein [Arabidopsis thaliana] gi|67633908|gb|AAY78878.1| no apical meristem family protein [Arabidopsis thaliana] gi|111074488|gb|ABH04617.1| At5g62380 [Arabidopsis thaliana] gi|332010219|gb|AED97602.1| NAC-domain protein 101 [Arabidopsis thaliana]	348	348	1.00E-167	100.0	89.7	92.0	NAC-domain protein 101	gbpln	Arabidopsis thaliana	AT5G62380.1 | Symbols: VND6, ANAC101, NAC101 | NAC-domain protein 101 | chr5:25050684-25051858 FORWARD LENGTH=348	348	348	1.00E-170	100.0	89.7	92.0
Rsa1.0_01198.1.g24508.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01198.1.g24509.t1	gb|AAM67138.1| ripening-related protein-like [Arabidopsis thaliana]	204	202	1.00E-99	99.0	86.8	92.6	ripening-related protein-like	gbpln	Arabidopsis thaliana	AT5G62350.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:25037504-25038112 FORWARD LENGTH=202	204	202	3.00E-97	99.0	86.3	92.6
Rsa1.0_01198.1.g24510.t1	gb|EOA15072.1| hypothetical protein CARUB_v10028436mg [Capsella rubella]	240	243	1.00E-104	101.3	85.8	90.4	hypothetical protein CARUB_v10028436mg	gbpln	Capsella rubella	AT5G62320.1 | Symbols: MYB99, ATMYBCU15, ATMYB99 | myb domain protein 99 | chr5:25028885-25029786 REVERSE LENGTH=245	240	245	1.00E-103	102.1	86.7	90.0
Rsa1.0_01198.1.g24511.t1	ref|NP_201037.1| AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein [Arabidopsis thaliana] gi|6729346|dbj|BAA89783.1| IRE [Arabidopsis thaliana] gi|8809644|dbj|BAA97195.1| IRE [Arabidopsis thaliana] gi|332010212|gb|AED97595.1| AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein [Arabidopsis thaliana]	1120	1168	0	104.3	89.6	93.0	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	gbpln	Arabidopsis thaliana	AT5G62310.1 | Symbols: IRE | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr5:25023405-25028414 FORWARD LENGTH=1168	1120	1168	0	104.3	89.6	93.0
Rsa1.0_01198.1.g24512.t1	ref|NP_001119478.1| nucleotide-sensitive chloride conductance regulator family protein [Arabidopsis thaliana] gi|332010209|gb|AED97592.1| chloride conductance regulatory protein ICln [Arabidopsis thaliana]	117	228	1.00E-27	194.9	58.1	61.5	nucleotide-sensitive chloride conductance regulator family protein	gbpln	Arabidopsis thaliana	AT5G62290.2 | Symbols: | nucleotide-sensitive chloride conductance regulator (ICln) family protein | chr5:25019568-25020972 FORWARD LENGTH=228	117	228	2.00E-30	194.9	58.1	61.5
Rsa1.0_01198.1.g24513.t1	gb|EOA12583.1| hypothetical protein CARUB_v10027009mg, partial [Capsella rubella]	181	245	4.00E-57	135.4	75.1	80.1	hypothetical protein CARUB_v10027009mg, partial	gbpln	Capsella rubella	AT5G62280.1 | Symbols: | Protein of unknown function (DUF1442) | chr5:25017165-25017985 FORWARD LENGTH=236	181	236	2.00E-51	130.4	74.0	79.0
Rsa1.0_01198.1.g24514.t1	gb|EOA13508.1| hypothetical protein CARUB_v10026575mg [Capsella rubella]	296	387	1.00E-149	130.7	89.5	96.6	hypothetical protein CARUB_v10026575mg	gbpln	Capsella rubella	AT5G62270.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: mucin-related (TAIR:AT2G02880.1). | chr5:25012227-25014486 FORWARD LENGTH=420	296	420	1.00E-143	141.9	86.8	95.3
Rsa1.0_01198.1.g24515.t1	gb|EOA12533.1| hypothetical protein CARUB_v10026514mg [Capsella rubella]	463	407	1.00E-132	87.9	59.2	62.9	hypothetical protein CARUB_v10026514mg	gbpln	Capsella rubella	AT5G62260.1 | Symbols: | AT hook motif DNA-binding family protein | chr5:25009331-25011348 FORWARD LENGTH=404	463	404	1.00E-128	87.3	58.1	61.8
Rsa1.0_01199.1.g24516.t1	ref|NP_199205.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|9758551|dbj|BAB09052.1| WD-repeat protein-like [Arabidopsis thaliana] gi|110742722|dbj|BAE99272.1| WD-repeat protein-like [Arabidopsis thaliana] gi|148535209|gb|ABQ85545.1| will die slowly [Arabidopsis thaliana] gi|332007645|gb|AED95028.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	529	523	0	98.9	83.6	90.9	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G43920.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:17673397-17675630 FORWARD LENGTH=523	529	523	0	98.9	83.6	90.9

Rsa1.0_01199.1.g24517.t4	gb|ACJ49161.1| protection of telomeres 1a protein [Brassica oleracea]	464	456	0	98.3	71.8	80.0	protection of telomeres 1a protein	gbpln	Brassica oleracea	AT2G05210.3 | Symbols: AtPOT1a | Nucleic acid-binding, OB-fold-like protein | chr2:1891814-1894196 FORWARD LENGTH=467	464	467	1.00E-162	100.6	64.9	76.1
Rsa1.0_01199.1.g24518.t1	ref|NP_198436.1| uncharacterized protein [Arabidopsis thaliana] gi|10176706|dbj|BAB09928.1| unnamed protein product [Arabidopsis thaliana] gi|91805673|gb|ABE65565.1| hypothetical protein At5g35870 [Arabidopsis thaliana] gi|332006639|gb|AED94022.1| uncharacterized protein AT5G35870 [Arabidopsis thaliana]	156	196	4.00E-44	125.6	67.9	80.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G35870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G04480.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:14021022-14021612 FORWARD LENGTH=196	156	196	1.00E-46	125.6	67.9	80.1
Rsa1.0_01199.1.g24519.t2	gb|ACP30577.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1350	1235	0	91.5	69.0	76.1	disease resistance protein	gbpln	Brassica rapa	AT5G11250.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr5:3587978-3591960 REVERSE LENGTH=1189	1350	1189	0	88.1	60.1	70.0
Rsa1.0_01199.1.g24520.t1	ref|XP_002862509.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297308072|gb|EFH38767.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	236	247	8.00E-93	104.7	74.6	86.0	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT5G43650.1 | Symbols: BHLH92 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:17533310-17534758 REVERSE LENGTH=247	236	247	1.00E-88	104.7	71.6	83.1
Rsa1.0_01199.1.g24521.t1	gb|EOA14915.1| hypothetical protein CARUB_v10028256mg [Capsella rubella]	138	137	2.00E-51	99.3	84.8	89.1	hypothetical protein CARUB_v10028256mg	gbpln	Capsella rubella	AT5G43540.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:17496993-17497406 FORWARD LENGTH=137	138	137	5.00E-45	99.3	79.7	84.1
Rsa1.0_01199.1.g24522.t1	gb|ACG24094.1| nicotiana lesion-inducing like [Zea mays]	157	157	3.00E-81	100.0	97.5	98.1	nicotiana lesion-inducing like	gbenv/gbpln	Zea mays	AT1G04340.1 | Symbols: | HR-like lesion-inducing protein-related | chr1:1163345-1164737 REVERSE LENGTH=159	157	159	4.00E-71	101.3	85.4	91.7
Rsa1.0_01199.1.g24523.t1	ref|NP_199157.1| putative 2-oxoglutarate-dependent dioxygenase [Arabidopsis thaliana] gi|75311542|sp|Q9LSW7.1|ACCH9_ARATH RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 9 gi|8843897|dbj|BAA97423.1| 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana] gi|15983809|gb|AAL10501.1| AT5g43440/MWF20_15 [Arabidopsis thaliana] gi|23505905|gb|AAN28812.1| At5g43440/MWF20_15 [Arabidopsis thaliana] gi|332007580|gb|AED94963.1| putative 2-oxoglutarate-dependent dioxygenase [Arabidopsis thaliana]	345	365	1.00E-150	105.8	75.9	84.6	putative 2-oxoglutarate-dependent dioxygenase	gbpln	Arabidopsis thaliana	AT5G43440.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:17455356-17456608 REVERSE LENGTH=365	345	365	1.00E-152	105.8	75.9	84.6
Rsa1.0_01199.1.g24524.t1	gb|EOA14060.1| hypothetical protein CARUB_v10027196mg, partial [Capsella rubella]	130	187	4.00E-38	143.8	65.4	73.8	hypothetical protein CARUB_v10027196mg, partial	gbpln	Capsella rubella	AT1G04340.1 | Symbols: | HR-like lesion-inducing protein-related | chr1:1163345-1164737 REVERSE LENGTH=159	130	159	9.00E-39	122.3	63.8	73.1
Rsa1.0_01199.1.g24525.t1	gb|AAM61464.1| electron transfer flavoprotein beta-subunit-like [Arabidopsis thaliana]	251	251	1.00E-133	100.0	93.2	98.0	electron transfer flavoprotein beta-subunit-like	gbpln	Arabidopsis thaliana	AT5G43430.1 | Symbols: ETFBETA | electron transfer flavoprotein beta | chr5:17453656-17455111 FORWARD LENGTH=251	251	251	1.00E-135	100.0	92.8	97.6
Rsa1.0_01199.1.g24526.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01199.1.g24527.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01199.1.g24528.t1	gb|EOA14898.1| hypothetical protein CARUB_v10028227mg [Capsella rubella]	133	136	3.00E-44	102.3	83.5	88.0	hypothetical protein CARUB_v10028227mg	gbpln	Capsella rubella	AT5G43410.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:17435010-17435405 REVERSE LENGTH=131	133	131	2.00E-45	98.5	83.5	88.7
Rsa1.0_01199.1.g24529.t1	gb|EOA14581.1| hypothetical protein CARUB_v10027822mg [Capsella rubella]	482	524	0	108.7	94.6	97.3	hypothetical protein CARUB_v10027822mg	gbpln	Capsella rubella	AT5G43360.1 | Symbols: PHT3, ATPT4, PHT1;3 | phosphate transporter 1;3 | chr5:17409524-17411214 FORWARD LENGTH=521	482	521	0	108.1	93.4	96.5
Rsa1.0_01199.1.g24530.t1	gb|EOA21445.1| hypothetical protein CARUB_v10001828mg [Capsella rubella]	194	244	1.00E-100	125.8	93.3	97.4	hypothetical protein CARUB_v10001828mg	gbpln	Capsella rubella	AT1G33140.1 | Symbols: PGY2 | Ribosomal protein L6 family | chr1:12023360-12024502 FORWARD LENGTH=194	194	194	1.00E-102	100.0	93.3	97.9
Rsa1.0_01199.1.g24531.t1	ref|XP_002865428.1| hypothetical protein ARALYDRAFT_331059 [Arabidopsis lyrata subsp. lyrata] gi|297311263|gb|EFH41687.1| hypothetical protein ARALYDRAFT_331059 [Arabidopsis lyrata subsp. lyrata]	86	517	1.00E-41	601.2	97.7	98.8	hypothetical protein ARALYDRAFT_331059	gbpln	Arabidopsis lyrata	AT5G43360.1 | Symbols: PHT3, ATPT4, PHT1;3 | phosphate transporter 1;3 | chr5:17409524-17411214 FORWARD LENGTH=521	86	521	9.00E-44	605.8	96.5	97.7
Rsa1.0_01200.1.g24532.t1	ref|XP_003617941.1| 40S ribosomal protein [Medicago truncatula] gi|355519276|gb|AET00900.1| 40S ribosomal protein [Medicago truncatula]	69	230	3.00E-24	333.3	79.7	87.0	40S ribosomal protein	gbpln	Medicago truncatula	AT2G40590.1 | Symbols: | Ribosomal protein S26e family protein | chr2:16945215-16946345 REVERSE LENGTH=131	69	131	1.00E-25	189.9	76.8	76.8

Rsa1.0_01200.1.g24533.t1	gb|EOA26897.1| hypothetical protein CARUB_v10022988mg [Capsella rubella]	530	528	0	99.6	80.8	88.9	hypothetical protein CARUB_v10022988mg	gbpln	Capsella rubella	AT2G40570.1 | Symbols: | initiator tRNA phosphoribosyl transferase family protein | chr2:16941066-16943288 FORWARD LENGTH=521	530	521	0	98.3	79.8	88.7
Rsa1.0_01200.1.g24534.t1	gb|EOA33803.1| hypothetical protein CARUB_v10021274mg [Capsella rubella]	350	304	8.00E-76	86.9	43.4	54.9	hypothetical protein CARUB_v10021274mg	gbpln	Capsella rubella	AT2G40580.1 | Symbols: | Protein kinase superfamily protein | chr2:16943964-16944899 FORWARD LENGTH=311	350	311	4.00E-72	88.9	43.7	56.6
Rsa1.0_01200.1.g24535.t2	ref|XP_002879879.1| hypothetical protein ARALYDRAFT_483112 [Arabidopsis lyrata subsp. lyrata] gi|297325718|gb|EFH56138.1| hypothetical protein ARALYDRAFT_483112 [Arabidopsis lyrata subsp. lyrata]	598	589	0	98.5	84.4	88.8	hypothetical protein ARALYDRAFT_483112	gbpln	Arabidopsis lyrata	AT2G40550.1 | Symbols: ETG1 | E2F target gene 1 | chr2:16934927-16938033 FORWARD LENGTH=589	598	589	0	98.5	83.1	88.3
Rsa1.0_01200.1.g24536.t1	gb|EOA28443.1| hypothetical protein CARUB_v10024650mg [Capsella rubella]	778	795	0	102.2	92.9	96.5	hypothetical protein CARUB_v10024650mg	gbpln	Capsella rubella	AT2G40540.2 | Symbols: KT2, ATKT2, SHY3, KUP2, ATKUP2, TRK2 | potassium transporter 2 | chr2:16931445-16934516 FORWARD LENGTH=794	778	794	0	102.1	92.7	96.5
Rsa1.0_01200.1.g24537.t1	ref|NP_565935.1| uncharacterized protein [Arabidopsis thaliana] gi|2651304|gb|AAB87584.1| expressed protein [Arabidopsis thaliana] gi|88900366|gb|ABD57495.1| At2g40530 [Arabidopsis thaliana] gi|330254750|gb|AEC09844.1| uncharacterized protein AT2G40530 [Arabidopsis thaliana]	101	105	4.00E-23	104.0	71.3	80.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G40530.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf apex, inflorescence meristem, petal, flower; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:16927600-16927917 FORWARD LENGTH=105	101	105	6.00E-26	104.0	71.3	80.2
Rsa1.0_01200.1.g24538.t1	gb|EOA26742.1| hypothetical protein CARUB_v10022828mg [Capsella rubella]	487	619	0	127.1	71.5	81.7	hypothetical protein CARUB_v10022828mg	gbpln	Capsella rubella	AT2G40520.4 | Symbols: | Nucleotidyltransferase family protein | chr2:16923541-16925675 FORWARD LENGTH=502	487	502	1.00E-175	103.1	59.5	74.9
Rsa1.0_01200.1.g24539.t1	ref|NP_181581.1| Uroporphyrinogen decarboxylase 2 [Arabidopsis thaliana] gi|6014937|sp|O22886.1|DCUP2_ARATH RecName: Full=Uroporphyrinogen decarboxylase 2, chloroplastic; Short=UPD2; Short=URO-D2; Flags: Precursor gi|2651307|gb|AAB87587.1| putative uroporphyrinogen decarboxylase [Arabidopsis thaliana] gi|23297097|gb|AAN13092.1| putative uroporphyrinogen decarboxylase [Arabidopsis thaliana] gi|330254743|gb|AEC09837.1| Uroporphyrinogen decarboxylase 2 [Arabidopsis thaliana]	408	394	0	96.6	91.9	94.4	Uroporphyrinogen decarboxylase 2	gbpln	Arabidopsis thaliana	AT2G40490.1 | Symbols: HEME2 | Uroporphyrinogen decarboxylase | chr2:16912961-16914988 FORWARD LENGTH=394	408	394	0	96.6	91.9	94.4
Rsa1.0_01200.1.g24540.t1	ref|NP_181580.2| uncharacterized protein [Arabidopsis thaliana] gi|75111145|sp|Q5XVC7.1|Y2048_ARATH RecName: Full=WEB family protein At2g40480 gi|52354289|gb|AAU44465.1| hypothetical protein AT2G40480 [Arabidopsis thaliana] gi|330254742|gb|AEC09836.1| uncharacterized protein AT2G40480 [Arabidopsis thaliana]	460	518	1.00E-161	112.6	74.6	82.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G40480.1 | Symbols: | Plant protein of unknown function (DUF827) | chr2:16910425-16912444 FORWARD LENGTH=518	460	518	1.00E-164	112.6	74.6	82.4
Rsa1.0_01200.1.g24541.t1	ref|XP_002881725.1| hypothetical protein ARALYDRAFT_903340 [Arabidopsis lyrata subsp. lyrata] gi|297327564|gb|EFH57984.1| hypothetical protein ARALYDRAFT_903340 [Arabidopsis lyrata subsp. lyrata]	185	192	8.00E-50	103.8	73.0	81.1	hypothetical protein ARALYDRAFT_903340	gbpln	Arabidopsis lyrata	AT2G40475.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G56260.2); Has 477 Blast hits to 219 proteins in 41 species: Archae - 0; Bacteria - 4; Metazoa - 91; Fungi - 61; Plants - 144; Viruses - 0; Other Eukaryotes - 177 (source: NCBI BLink). | chr2:16907222-16907803 REVERSE LENGTH=193	185	193	2.00E-46	104.3	71.4	77.8
Rsa1.0_01200.1.g24542.t1	gb|EOA27836.1| hypothetical protein CARUB_v10024002mg [Capsella rubella]	226	226	1.00E-102	100.0	93.4	94.7	hypothetical protein CARUB_v10024002mg	gbpln	Capsella rubella	AT2G40470.1 | Symbols: LBD15, ASL11 | LOB domain-containing protein 15 | chr2:16902430-16903546 REVERSE LENGTH=224	226	224	1.00E-103	99.1	89.8	90.7
Rsa1.0_01201.1.g24543.t1	#	#	#	#	#	#	#	–	----	----	AT2G42210.2 | Symbols: ATOEP16-3, OEP16-3 | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr2:17590600-17591591 FORWARD LENGTH=173	78	173	5.00E-13	221.8	44.9	51.3

Rsa1.0_01201.1.g24544.t1	gb|EOA13997.1| hypothetical protein CARUB_v10027129mg [Capsella rubella]	206	211	2.00E-94	102.4	85.4	90.3	hypothetical protein CARUB_v10027129mg	gbpln	Capsella rubella	AT5G50200.1 | Symbols: WR3, ATNRT3.1, NRT3.1 | nitrate transmembrane transporters | chr5:20436612-20437535 FORWARD LENGTH=210	206	210	6.00E-90	101.9	79.1	86.4
Rsa1.0_01201.1.g24545.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	391	1142	3.00E-69	292.1	40.4	60.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	391	575	5.00E-43	147.1	31.2	51.9
Rsa1.0_01201.1.g24546.t1	emb|CAB39637.1| putative protein [Arabidopsis thaliana] gi|7267665|emb|CAB78093.1| putative protein [Arabidopsis thaliana] gi|91805577|gb|ABE65517.1| hypothetical protein At4g09700 [Arabidopsis thaliana]	449	371	2.00E-39	82.6	17.6	23.8	putative protein	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	449	361	6.00E-17	80.4	10.9	16.5
Rsa1.0_01201.1.g24547.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	617	1311	3.00E-81	212.5	34.8	49.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	ATMG01250.1 | Symbols: ORF102 | RNA-directed DNA polymerase (reverse transcriptase) | chrM:310514-310882 FORWARD LENGTH=122	617	122	3.00E-17	19.8	7.0	9.2
Rsa1.0_01201.1.g24548.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	447	1838	4.00E-43	411.2	21.5	35.6	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01201.1.g24549.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01201.1.g24550.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01201.1.g24551.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	195	1225	8.00E-17	628.2	25.1	38.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01201.1.g24552.t2	ref|NP_199835.2| protein-l-isoaspartate methyltransferase 2 [Arabidopsis thaliana] gi|40950547|gb|AAR97903.1| L-isoaspartyl methyltransferase 2 TIS I alpha-psi [Arabidopsis thaliana] gi|332008532|gb|AED95915.1| protein-l-isoaspartate methyltransferase 2 [Arabidopsis thaliana]	283	309	1.00E-128	109.2	80.6	87.3	protein-l-isoaspartate methyltransferase 2	gbpln	Arabidopsis thaliana	AT5G50240.1 | Symbols: PIMT2, AtPIMT2 | protein-l-isoaspartate methyltransferase 2 | chr5:20451251-20452461 FORWARD LENGTH=309	283	309	1.00E-130	109.2	80.6	87.3
Rsa1.0_01202.1.g24553.t1	gb|AAF99829.1|AC008046_1 Hypothetical protein [Arabidopsis thaliana]	105	529	2.00E-22	503.8	50.5	69.5	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01202.1.g24554.t1	gb|EOA36824.1| hypothetical protein CARUB_v10008545mg [Capsella rubella]	648	648	0	100.0	94.8	97.7	hypothetical protein CARUB_v10008545mg	gbpln	Capsella rubella	AT1G31770.1 | Symbols: ABCG14 | ATP-binding cassette 14 | chr1:11375252-11377644 REVERSE LENGTH=648	648	648	0	100.0	93.8	97.4
Rsa1.0_01202.1.g24555.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01202.1.g24556.t1	gb|EOA39827.1| hypothetical protein CARUB_v10008495mg [Capsella rubella]	681	680	0	99.9	94.1	97.7	hypothetical protein CARUB_v10008495mg	gbpln	Capsella rubella	AT1G31780.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Conserved oligomeric complex COG6 (InterPro:IPR010490); Has 384 Blast hits to 379 proteins in 190 species: Archae - 0; Bacteria - 4; Metazoa - 151; Fungi - 156; Plants - 42; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink). | chr1:11391341-11394610 FORWARD LENGTH=680	681	680	0	99.9	94.3	97.5
Rsa1.0_01202.1.g24557.t2	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1104	1307	0	118.4	57.0	71.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1104	1262	3.00E-60	114.3	13.7	20.1
Rsa1.0_01202.1.g24558.t1	gb|AAL47433.1| AT5g62580/K19B1_19 [Arabidopsis thaliana]	131	615	1.00E-12	469.5	35.9	38.9	AT5g62580/K19B1_19	gbpln	Arabidopsis thaliana	AT5G62580.1 | Symbols: | ARM repeat superfamily protein | chr5:25120010-25122259 FORWARD LENGTH=615	131	615	3.00E-15	469.5	35.9	38.9
Rsa1.0_01203.1.g24559.t1	gb|EOA32667.1| hypothetical protein CARUB_v10015969mg [Capsella rubella]	193	203	2.00E-93	105.2	95.3	99.0	hypothetical protein CARUB_v10015969mg	gbpln	Capsella rubella	AT3G12870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G56120.1); Has 70 Blast hits to 70 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 70; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4094417-4095037 REVERSE LENGTH=206	193	206	2.00E-95	106.7	95.9	99.0
Rsa1.0_01203.1.g24560.t1	ref|XP_002882791.1| hypothetical protein ARALYDRAFT_478647 [Arabidopsis lyrata subsp. lyrata] gi|297328631|gb|EFH59050.1| hypothetical protein ARALYDRAFT_478647 [Arabidopsis lyrata subsp. lyrata]	500	499	0	99.8	91.0	96.4	hypothetical protein ARALYDRAFT_478647	gbpln	Arabidopsis lyrata	AT3G12860.1 | Symbols: | NOP56-like pre RNA processing ribonucleoprotein | chr3:4091678-4093921 FORWARD LENGTH=499	500	499	0	99.8	90.8	95.4
Rsa1.0_01203.1.g24561.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	454	255	2.00E-49	56.2	26.2	32.6	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	454	302	2.00E-39	66.5	23.3	33.5

Rsa1.0_01203.1.g24562.t1	ref|XP_002884929.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297330769|gb|EFH61188.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	132	132	7.00E-56	100.0	82.6	89.4	auxin-responsive family protein	gbpln	Arabidopsis lyrata	AT3G12830.1 | Symbols: | SAUR-like auxin-responsive protein family | chr3:4079117-4079515 REVERSE LENGTH=132	132	132	9.00E-58	100.0	81.8	88.6
Rsa1.0_01203.1.g24563.t1	ref|XP_002882790.1| photoperiod-independent early flowering 1 [Arabidopsis lyrata subsp. lyrata] gi|297328630|gb|EFH59049.1| photoperiod-independent early flowering 1 [Arabidopsis lyrata subsp. lyrata]	2062	2057	0	99.8	85.4	91.0	photoperiod-independent early flowering 1	gbpln	Arabidopsis lyrata	AT3G12810.1 | Symbols: PIE1, SRCAP, chr13 | SNF2 domain-containing protein / helicase domain-containing protein | chr3:4065636-4073992 FORWARD LENGTH=2055	2062	2055	0	99.7	84.5	90.3
Rsa1.0_01203.1.g24564.t1	gb|EOA31122.1| hypothetical protein CARUB_v10014282mg [Capsella rubella]	294	298	1.00E-143	101.4	88.8	93.9	hypothetical protein CARUB_v10014282mg	gbpln	Capsella rubella	AT3G12800.1 | Symbols: SDRB, DECR | short-chain dehydrogenase-reductase B | chr3:4063463-4064757 REVERSE LENGTH=298	294	298	1.00E-138	101.4	87.8	93.9
Rsa1.0_01203.1.g24565.t1	ref|NP_187884.1| phosphoglycerate kinase 1 [Arabidopsis thaliana] gi|75273138|sp|Q9LD57.1|PGKH1_ARATH RecName: Full=Phosphoglycerate kinase 1, chloroplastic; Flags: Precursor gi|7839389|gb|AAF70258.1|AF247558_1 phosphoglycerate kinase [Arabidopsis thaliana] gi|13430644|gb|AAK25944.1|AF360234_1 putative phosphoglycerate kinase [Arabidopsis thaliana] gi|16226508|gb|AAL16186.1|AF428418_1 AT3g12780/MBK21_14 [Arabidopsis thaliana] gi|11994421|dbj|BAB02423.1| phosphoglycerate kinase [Arabidopsis thaliana] gi|15010644|gb|AAK73981.1| AT3g12780/MBK21_14 [Arabidopsis thaliana] gi|16648943|gb|AAL24323.1| phosphoglycerate kinase [Arabidopsis thaliana] gi|17065610|gb|AAL33785.1| putative phosphoglycerate kinase [Arabidopsis thaliana] gi|20334796|gb|AAM16259.1| AT3g12780/MBK21_14 [Arabidopsis thaliana] gi|21387107|gb|AAM47957.1| phosphoglycerate kinase [Arabidopsis thaliana] gi|22022520|gb|AAM83218.1| AT3g12780/MBK21_14 [Arabidopsis thaliana] gi|110742702|dbj|BAE99262.1| phosphoglycerate kinase like protein [Arabidopsis thaliana] gi|222423303|dbj|BAH19627.1| AT3G12780 [Arabidopsis thaliana] gi|332641725|gb|AEE75246.1|	479	481	0	100.4	91.9	94.6	phosphoglycerate kinase 1	gbpln	Arabidopsis thaliana	AT3G12780.1 | Symbols: PGK1 | phosphoglycerate kinase 1 | chr3:4061127-4063140 REVERSE LENGTH=481	479	481	0	100.4	91.9	94.6
Rsa1.0_01203.1.g24566.t1	dbj|BAB02422.1| unnamed protein product [Arabidopsis thaliana]	403	390	1.00E-108	96.8	58.3	70.7	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G12775.1 | Symbols: | ubiquitin-conjugating enzyme family protein | chr3:4059772-4060944 FORWARD LENGTH=362	403	362	1.00E-107	89.8	51.1	61.8
Rsa1.0_01203.1.g24567.t1	ref|XP_002884925.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330765|gb|EFH61184.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	687	694	0	101.0	90.5	94.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G12770.1 | Symbols: MEF22 | mitochondrial editing factor 22 | chr3:4057027-4059193 REVERSE LENGTH=694	687	694	0	101.0	90.2	94.3
Rsa1.0_01203.1.g24568.t1	ref|NP_566436.1| uncharacterized protein [Arabidopsis thaliana] gi|11994418|dbj|BAB02420.1| unnamed protein product [Arabidopsis thaliana] gi|23297357|gb|AAN12949.1| unknown protein [Arabidopsis thaliana] gi|332641722|gb|AEE75243.1| uncharacterized protein AT3G12760 [Arabidopsis thaliana]	246	250	1.00E-120	101.6	87.0	91.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G12760.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Defective-in-cullin neddylation protein (InterPro:IPR014764), Protein of unknown function DUF298 (InterPro:IPR005176), UBA-like (InterPro:IPR009060); BEST Arabidopsis thaliana protein match is: Domain of unknown function (DUF298) (TAIR:AT1G15860.2); Has 857 Blast hits to 855 proteins in 202 species: Archae - 0; Bacteria - 0; Metazoa - 482; Fungi - 154; Plants - 139; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink). | chr3:4054963-4056826 FORWARD LENGTH=250	246	250	1.00E-122	101.6	87.0	91.1
Rsa1.0_01204.1.g24569.t1	ref|XP_002893330.1| IAA-conjugate-resistant 4 [Arabidopsis lyrata subsp. lyrata] gi|297339172|gb|EFH69589.1| IAA-conjugate-resistant 4 [Arabidopsis lyrata subsp. lyrata]	394	393	0	99.7	85.5	93.7	IAA-conjugate-resistant 4	gbpln	Arabidopsis lyrata	AT1G24180.1 | Symbols: IAR4 | Thiamin diphosphate-binding fold (THDP-binding) superfamily protein | chr1:8560777-8563382 REVERSE LENGTH=393	394	393	0	99.7	85.3	93.7
Rsa1.0_01204.1.g24570.t1	gb|EOA35263.1| hypothetical protein CARUB_v10020432mg [Capsella rubella]	389	390	0	100.3	86.9	92.3	hypothetical protein CARUB_v10020432mg	gbpln	Capsella rubella	AT1G70090.2 | Symbols: GATL9, LGT8 | glucosyl transferase family 8 | chr1:26400927-26402099 FORWARD LENGTH=390	389	390	0	100.3	86.1	92.3

Rsa1.0_01204.1.g24571.t1	ref|NP_974118.1| uncharacterized protein [Arabidopsis thaliana] gi|332196898|gb|AEE35019.1| uncharacterized protein AT1G70100 [Arabidopsis thaliana]	476	504	1.00E-154	105.9	69.7	80.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G70100.3 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24160.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:26403736-26405832 FORWARD LENGTH=504	476	504	1.00E-156	105.9	69.7	80.0
Rsa1.0_01204.1.g24572.t1	ref|NP_177168.1| concanavalin A-like lectin protein kinase [Arabidopsis thaliana] gi|75317843|sp|O04534.1|LRK51_ARATH RecName: Full=Putative L-type lectin-domain containing receptor kinase V.1; Short=Arabidopsis thaliana lectin-receptor kinase b2; Short=AthlecRK-b2; Short=LecRK-V.1; Flags: Precursor gi|2194128|gb|AAB61103.1| Strong similarity to Arabidopsis receptor-like kinase (gb|ATLECGENE) and F20P5.15 [Arabidopsis thaliana] gi|332196900|gb|AEE35021.1| concanavalin A-like lectin protein kinase [Arabidopsis thaliana]	98	666	2.00E-34	679.6	74.5	83.7	concanavalin A-like lectin protein kinase	gbpln	Arabidopsis thaliana	AT1G70110.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr1:26406238-26408323 REVERSE LENGTH=666	98	666	3.00E-37	679.6	74.5	83.7
Rsa1.0_01204.1.g24573.t1	ref|XP_002873484.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319321|gb|EFH49743.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	305	603	4.00E-44	197.7	30.8	34.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G10900.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:3436413-3439221 REVERSE LENGTH=600	305	600	9.00E-43	196.7	31.1	34.4
Rsa1.0_01204.1.g24574.t1	ref|XP_002888756.1| hypothetical protein ARALYDRAFT_316005 [Arabidopsis lyrata subsp. lyrata] gi|297334597|gb|EFH65015.1| hypothetical protein ARALYDRAFT_316005 [Arabidopsis lyrata subsp. lyrata]	651	660	0	101.4	84.0	89.7	hypothetical protein ARALYDRAFT_316005	gbpln	Arabidopsis lyrata	AT1G70130.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr1:26409743-26411801 REVERSE LENGTH=656	651	656	0	100.8	82.0	88.8
Rsa1.0_01204.1.g24575.t1	ref|NP_177171.1| formin-like protein 8 [Arabidopsis thaliana] gi|75097064|sp|O04532.1|FH8_ARATH RecName: Full=Formin-like protein 8; Short=AtFH8; Short=AtFORMIN-1; Flags: Precursor gi|2194126|gb|AAB61101.1| EST gb|T43335 comes from this gene [Arabidopsis thaliana] gi|332196903|gb|AEE35024.1| formin-like protein 8 [Arabidopsis thaliana]	788	760	0	96.4	74.5	82.5	formin-like protein 8	gbpln	Arabidopsis thaliana	AT1G70140.1 | Symbols: ATFH8, FH8 | formin 8 | chr1:26412688-26415048 REVERSE LENGTH=760	788	760	0	96.4	74.5	82.5
Rsa1.0_01204.1.g24576.t1	ref|NP_177172.6| zinc ion binding protein [Arabidopsis thaliana] gi|332196904|gb|AEE35025.1| zinc ion binding protein [Arabidopsis thaliana]	377	374	1.00E-176	99.2	78.8	87.5	zinc ion binding protein	gbpln	Arabidopsis thaliana	AT1G70150.1 | Symbols: | zinc ion binding | chr1:26416898-26419521 FORWARD LENGTH=374	377	374	1.00E-178	99.2	78.8	87.5
Rsa1.0_01204.1.g24577.t1	gb|EOA33344.1| hypothetical protein CARUB_v10020126mg [Capsella rubella]	531	531	0	100.0	87.4	92.3	hypothetical protein CARUB_v10020126mg	gbpln	Capsella rubella	AT1G70160.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27020.1); Has 108 Blast hits to 108 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 89; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink). | chr1:26420159-26422345 FORWARD LENGTH=523	531	523	0	98.5	86.8	91.7
Rsa1.0_01204.1.g24578.t1	ref|XP_002884714.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330554|gb|EFH60973.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	482	492	1.00E-116	102.1	50.2	67.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G09120.1 | Symbols: | Protein of unknown function (DUF674) | chr3:2797556-2798588 REVERSE LENGTH=314	482	314	9.00E-95	65.1	38.6	47.5
Rsa1.0_01204.1.g24579.t1	ref|NP_177174.1| matrix metalloproteinase [Arabidopsis thaliana] gi|2194124|gb|AAB61099.1| Similar to Glycine metalloendoproteinase (gb|U63725) [Arabidopsis thaliana] gi|332196906|gb|AEE35027.1| matrix metalloproteinase [Arabidopsis thaliana]	375	378	0	100.8	88.0	91.7	matrix metalloproteinase	gbpln	Arabidopsis thaliana	AT1G70170.1 | Symbols: MMP | matrix metalloproteinase | chr1:26424005-26425141 FORWARD LENGTH=378	375	378	0	100.8	88.0	91.7

Rsa1.0_01205.1.g24580.t1	gb|AAB61111.1| Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb|U12626) [Arabidopsis thaliana]	142	1315	5.00E-42	926.1	56.3	70.4	Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb|U12626)	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	142	1262	5.00E-35	888.7	45.1	52.1
Rsa1.0_01205.1.g24581.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1530	2726	0	178.2	50.7	68.4	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1530	158	5.00E-39	10.3	4.9	6.1
Rsa1.0_01205.1.g24582.t1	ref|XP_002865541.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311376|gb|EFH41800.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	703	711	0	101.1	91.0	94.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G42310.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr5:16915860-16918238 FORWARD LENGTH=709	703	709	0	100.9	89.6	94.7
Rsa1.0_01205.1.g24583.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01205.1.g24584.t6	gb|AAC95212.1| Mutator-like transposase [Arabidopsis thaliana]	1095	915	2.00E-90	83.6	18.4	26.3	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	1095	719	6.00E-23	65.7	11.7	20.6
Rsa1.0_01205.1.g24585.t6	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1404	1611	0	114.7	40.6	53.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1404	158	2.00E-26	11.3	4.4	6.2
Rsa1.0_01205.1.g24586.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01206.1.g24587.t1	ref|XP_003611507.1| Receptor-like protein kinase [Medicago truncatula] gi|355512842|gb|AES94465.1| Receptor-like protein kinase [Medicago truncatula]	115	1109	7.00E-32	964.3	63.5	69.6	Receptor-like protein kinase	gbpln	Medicago truncatula	AT5G65700.2 | Symbols: BAM1 | Leucine-rich receptor-like protein kinase family protein | chr5:26281826-26284945 FORWARD LENGTH=1003	115	1003	2.00E-31	872.2	67.8	73.0
Rsa1.0_01206.1.g24588.t1	gb|EOA30324.1| hypothetical protein CARUB_v10013451mg [Capsella rubella]	440	445	1.00E-121	101.1	51.1	64.3	hypothetical protein CARUB_v10013451mg	gbpln	Capsella rubella	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	440	472	1.00E-119	107.3	51.6	65.9
Rsa1.0_01206.1.g24589.t1	ref|XP_002884960.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330800|gb|EFH61219.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	161	157	2.00E-58	97.5	78.3	84.5	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT3G13310.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr3:4310827-4311300 REVERSE LENGTH=157	161	157	1.00E-57	97.5	73.9	80.7
Rsa1.0_01206.1.g24590.t2	ref|NP_566452.1| vacuolar cation/proton exchanger 2 [Arabidopsis thaliana] gi|122056116|sp|Q39254.2|CAX2_ARATH RecName: Full=Vacuolar cation/proton exchanger 2; AltName: Full=Ca(2+)/H(+) antiporter CAX2; AltName: Full=Ca(2+)/H(+) exchanger 2; AltName: Full=Protein CATION EXCHANGER 2 gi|15983507|gb|AAL11621.1|AF424628_1 AT3g13320/MDC11_10 [Arabidopsis thaliana] gi|20453241|gb|AAM19859.1| AT3g13320/MDC11_10 [Arabidopsis thaliana] gi|332641812|gb|AEE75333.1| vacuolar cation/proton exchanger 2 [Arabidopsis thaliana]	459	441	0	96.1	87.8	90.8	vacuolar cation/proton exchanger 2	gbpln	Arabidopsis thaliana	AT3G13320.1 | Symbols: CAX2, atcax2 | cation exchanger 2 | chr3:4315418-4317997 FORWARD LENGTH=441	459	441	0	96.1	87.8	90.8
Rsa1.0_01206.1.g24591.t1	ref|NP_187941.6| proteasome activator subunit 4 [Arabidopsis thaliana] gi|332641813|gb|AEE75334.1| proteasome activating protein 200 [Arabidopsis thaliana]	1802	1816	0	100.8	92.9	96.5	proteasome activator subunit 4	gbpln	Arabidopsis thaliana	AT3G13330.1 | Symbols: PA200 | proteasome activating protein 200 | chr3:4319804-4330061 REVERSE LENGTH=1816	1802	1816	0	100.8	92.9	96.5
Rsa1.0_01206.1.g24592.t1	gb|EOA30574.1| hypothetical protein CARUB_v10013702mg [Capsella rubella]	351	446	0	127.1	94.0	96.9	hypothetical protein CARUB_v10013702mg	gbpln	Capsella rubella	AT3G13340.2 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:4332370-4334603 FORWARD LENGTH=447	351	447	0	127.4	93.4	96.0
Rsa1.0_01206.1.g24593.t1	dbj|BAB02805.1| unnamed protein product [Arabidopsis thaliana]	454	538	1.00E-141	118.5	67.6	76.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G13360.1 | Symbols: WIP3 | WPP domain interacting protein 3 | chr3:4338472-4339982 REVERSE LENGTH=459	454	459	1.00E-142	101.1	66.3	75.1
Rsa1.0_01206.1.g24594.t1	emb|CAA47177.1| Bplo [Brassica napus]	530	555	0	104.7	94.2	97.5	Bplo	gbpln	Brassica napus	AT1G55570.1 | Symbols: sks12 | SKU5 similar 12 | chr1:20757882-20759771 FORWARD LENGTH=555	530	555	0	104.7	87.2	92.8

Rsa1.0_01206.1.g24595.t1	ref|NP_187948.1| protein SKU5-like 13 [Arabidopsis thaliana] gi|9280290|dbj|BAB01745.1| BNH protein; pectinesterase-like protein; pollen-secific protein-like [Arabidopsis thaliana] gi|15912263|gb|AAL08265.1| AT3g13400/MRP15_3 [Arabidopsis thaliana] gi|18176449|gb|AAL60046.1| putative pollen specific protein [Arabidopsis thaliana] gi|20465921|gb|AAM20113.1| putative pollen-specific protein [Arabidopsis thaliana] gi|332641821|gb|AEE75342.1| protein SKU5-like 13 [Arabidopsis thaliana]	551	551	0	100.0	95.5	98.0	protein SKU5-like 13	gbpln	Arabidopsis thaliana	AT3G13400.1 | Symbols: sks13 | SKU5 similar 13 | chr3:4355257-4357305 FORWARD LENGTH=551	551	551	0	100.0	95.5	98.0
Rsa1.0_01206.1.g24596.t1	gb|AAN60225.1| unknown [Arabidopsis thaliana]	442	321	1.00E-154	72.6	62.7	66.1	unknown	gbpln	Arabidopsis thaliana	AT3G13410.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G55546.1); Has 49 Blast hits to 49 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:4362149-4364032 REVERSE LENGTH=321	442	321	1.00E-155	72.6	62.4	65.6
Rsa1.0_01206.1.g24597.t1	ref|NP_181023.1| fatty acid hydroxylase 1 [Arabidopsis thaliana] gi|75098527|sp|O48916.1|FAH1_ARATH RecName: Full=Fatty acid 2-hydroxylase 1; Short=AtFAH1 gi|2736147|gb|AAB94072.1| fatty acid hydroxylase Fah1p [Arabidopsis thaliana] gi|3132481|gb|AAC16270.1| fatty acid hydroxylase (FAH1) [Arabidopsis thaliana] gi|15215596|gb|AAK91343.1| At2g34770/T29F13.2 [Arabidopsis thaliana] gi|23308163|gb|AAN18051.1| At2g34770/T29F13.2 [Arabidopsis thaliana] gi|330253925|gb|AEC09019.1| fatty acid hydroxylase 1 [Arabidopsis thaliana]	140	237	8.00E-69	169.3	87.9	92.9	fatty acid hydroxylase 1	gbpln	Arabidopsis thaliana	AT2G34770.1 | Symbols: FAH1, ATFAH1 | fatty acid hydroxylase 1 | chr2:14666776-14668061 FORWARD LENGTH=237	140	237	2.00E-71	169.3	87.9	92.9
Rsa1.0_01207.1.g24598.t1	gb|EOA24245.1| hypothetical protein CARUB_v10017480mg [Capsella rubella]	364	366	2.00E-71	100.5	44.2	57.7	hypothetical protein CARUB_v10017480mg	gbpln	Capsella rubella	AT5G54560.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22161134-22162216 FORWARD LENGTH=360	364	360	4.00E-65	98.9	44.8	59.9
Rsa1.0_01207.1.g24599.t1	ref|XP_002864202.1| hypothetical protein ARALYDRAFT_495358 [Arabidopsis lyrata subsp. lyrata] gi|297310037|gb|EFH40461.1| hypothetical protein ARALYDRAFT_495358 [Arabidopsis lyrata subsp. lyrata]	169	355	8.00E-33	210.1	45.0	59.2	hypothetical protein ARALYDRAFT_495358	gbpln	Arabidopsis lyrata	AT5G52930.1 | Symbols: | Protein of unknown function (DUF295) | chr5:21470370-21471449 FORWARD LENGTH=359	169	359	2.00E-32	212.4	43.2	58.6
Rsa1.0_01207.1.g24600.t1	ref|NP_178168.1| nodulin family protein [Arabidopsis thaliana] gi|6730730|gb|AAF27120.1|AC018849_8 nodulin-like protein; 38383-40406 [Arabidopsis thaliana] gi|14334880|gb|AAK59618.1| putative nodulin protein [Arabidopsis thaliana] gi|15810607|gb|AAL07191.1| putative nodulin protein [Arabidopsis thaliana] gi|332198295|gb|AEE36416.1| nodulin family protein [Arabidopsis thaliana]	167	561	2.00E-41	335.9	57.5	61.7	nodulin family protein	gbpln	Arabidopsis thaliana	AT1G80530.1 | Symbols: | Major facilitator superfamily protein | chr1:30278224-30280247 REVERSE LENGTH=561	167	561	9.00E-44	335.9	57.5	61.7
Rsa1.0_01207.1.g24601.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	185	1213	8.00E-56	655.7	54.6	67.6	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	185	746	4.00E-26	403.2	27.0	37.8
Rsa1.0_01207.1.g24602.t1	gb|EOA35711.1| hypothetical protein CARUB_v10020938mg [Capsella rubella]	198	215	5.00E-63	108.6	62.6	68.2	hypothetical protein CARUB_v10020938mg	gbpln	Capsella rubella	AT1G80450.1 | Symbols: | VQ motif-containing protein | chr1:30244155-30244688 REVERSE LENGTH=177	198	177	4.00E-63	89.4	62.1	68.2
Rsa1.0_01207.1.g24603.t1	ref|XP_002880903.1| hypothetical protein ARALYDRAFT_901626 [Arabidopsis lyrata subsp. lyrata] gi|297326742|gb|EFH57162.1| hypothetical protein ARALYDRAFT_901626 [Arabidopsis lyrata subsp. lyrata]	984	1014	0	103.0	69.9	82.2	hypothetical protein ARALYDRAFT_901626	gbpln	Arabidopsis lyrata	AT3G47570.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17527611-17530748 FORWARD LENGTH=1010	984	1010	0	102.6	67.2	80.4

Rsa1.0_01207.1.g24604.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01207.1.g24605.t5	ref|NP_178157.2| tetratricopeptide repeat-containing protein [Arabidopsis thaliana] gi|17381118|gb|AAL36371.1| putative N-terminal acetyltransferase [Arabidopsis thaliana] gi|20259245|gb|AAM14358.1| putative N-terminal acetyltransferase [Arabidopsis thaliana] gi|26451312|dbj|BAC42757.1| putative N-terminal acetyltransferase [Arabidopsis thaliana] gi|332198278|gb|AEE36399.1| tetratricopeptide repeat-containing protein [Arabidopsis thaliana]	1007	897	0	89.1	81.1	84.9	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G80410.1 | Symbols: EMB2753 | tetratricopeptide repeat (TPR)-containing protein | chr1:30227963-30234832 REVERSE LENGTH=897	1007	897	0	89.1	81.1	84.9
Rsa1.0_01207.1.g24606.t1	gb|EOA35146.1| hypothetical protein CARUB_v10020281mg [Capsella rubella]	464	454	0	97.8	79.3	86.0	hypothetical protein CARUB_v10020281mg	gbpln	Capsella rubella	AT1G80380.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:30217332-30219784 FORWARD LENGTH=456	464	456	0	98.3	80.8	88.6
Rsa1.0_01207.1.g24607.t1	ref|NP_178153.1| cyclin-A2-4 [Arabidopsis thaliana] gi|75308908|sp|Q9C968.1|CCA24_ARATH RecName: Full=Cyclin-A2-4; AltName: Full=G2/mitotic-specific cyclin-A2-4; Short=CycA2;4 gi|12324983|gb|AAG52439.1|AC018848_10 putative cyclin; 42214-44381 [Arabidopsis thaliana] gi|332198271|gb|AEE36392.1| cyclin-A2-4 [Arabidopsis thaliana]	459	461	0	100.4	79.3	86.7	cyclin-A2-4	gbpln	Arabidopsis thaliana	AT1G80370.1 | Symbols: CYCA2;4 | Cyclin A2;4 | chr1:30214694-30216861 FORWARD LENGTH=461	459	461	0	100.4	79.3	86.7
Rsa1.0_01207.1.g24608.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01208.1.g24609.t1	gb|EOA38810.1| hypothetical protein CARUB_v10011128mg [Capsella rubella]	324	1008	5.00E-31	311.1	21.6	24.4	hypothetical protein CARUB_v10011128mg	gbpln	Capsella rubella	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	324	1019	3.00E-25	314.5	18.2	21.6
Rsa1.0_01208.1.g24610.t12	gb|AAG10622.1|AC008030_22 Putative receptor-like serine/threonine kinase - partial protein [Arabidopsis thaliana]	1983	1013	1.00E-162	51.1	14.6	16.1	Putative receptor-like serine/threonine kinase - partial protein	gbpln	Arabidopsis thaliana	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	1983	1019	1.00E-163	51.4	14.3	15.7
Rsa1.0_01208.1.g24611.t1	gb|AAG10622.1|AC008030_22 Putative receptor-like serine/threonine kinase - partial protein [Arabidopsis thaliana]	488	1013	0	207.6	77.3	84.2	Putative receptor-like serine/threonine kinase - partial protein	gbpln	Arabidopsis thaliana	AT1G29720.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:10393894-10399771 REVERSE LENGTH=1019	488	1019	0	208.8	78.7	85.7
Rsa1.0_01208.1.g24612.t1	ref|XP_002890805.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336647|gb|EFH67064.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	274	203	4.00E-23	74.1	22.3	32.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G02370.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:474516-476383 FORWARD LENGTH=537	274	537	7.00E-16	196.0	14.6	25.2
Rsa1.0_01208.1.g24613.t2	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1599	1225	1.00E-79	76.6	10.3	14.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G09650.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3125978-3127126 FORWARD LENGTH=382	1599	382	9.00E-27	23.9	5.3	7.3
Rsa1.0_01209.1.g24614.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01209.1.g24615.t1	ref|NP_198762.1| F-box protein [Arabidopsis thaliana] gi|75262687|sp|Q9FLZ1.1|FB272_ARATH RecName: Full=Putative F-box protein At5g39460 gi|10177693|dbj|BAB11019.1| unnamed protein product [Arabidopsis thaliana] gi|332007052|gb|AED94435.1| putative F-box protein [Arabidopsis thaliana]	217	571	4.00E-68	263.1	61.3	71.9	F-box protein	gbpln	Arabidopsis thaliana	AT5G39460.1 | Symbols: | F-box family protein | chr5:15788289-15790004 REVERSE LENGTH=571	217	571	1.00E-70	263.1	61.3	71.9
Rsa1.0_01209.1.g24616.t1	dbj|BAB11018.1| unnamed protein product [Arabidopsis thaliana]	338	576	8.00E-58	170.4	34.9	40.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G39450.1 | Symbols: | F-box family protein | chr5:15786045-15787877 FORWARD LENGTH=579	338	579	2.00E-60	171.3	34.9	40.8
Rsa1.0_01209.1.g24617.t1	gb|EOA14339.1| hypothetical protein CARUB_v10027520mg [Capsella rubella]	533	495	0	92.9	65.7	78.6	hypothetical protein CARUB_v10027520mg	gbpln	Capsella rubella	AT3G62120.2 | Symbols: | Class II aaRS and biotin synthetases superfamily protein | chr3:23001227-23003849 REVERSE LENGTH=530	533	530	0	99.4	60.4	73.7
Rsa1.0_01209.1.g24618.t2	ref|XP_002870776.1| hypothetical protein ARALYDRAFT_494037 [Arabidopsis lyrata subsp. lyrata] gi|297316612|gb|EFH47035.1| hypothetical protein ARALYDRAFT_494037 [Arabidopsis lyrata subsp. lyrata]	1588	1445	0	91.0	79.7	84.7	hypothetical protein ARALYDRAFT_494037	gbpln	Arabidopsis lyrata	AT5G39500.1 | Symbols: GNL1, ERMO1 | GNOM-like 1 | chr5:15815274-15819910 FORWARD LENGTH=1443	1588	1443	0	90.9	78.7	84.4
Rsa1.0_01209.1.g24619.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1727	1213	0	70.2	25.0	37.1	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1727	626	4.00E-66	36.2	8.3	14.1

Rsa1.0_01209.1.g24620.t1	dbj|BAJ34483.1| unnamed protein product [Thellungiella halophila]	227	220	1.00E-106	96.9	85.0	93.4	unnamed protein product	----	----	AT5G39510.1 | Symbols: VTI11, ATVTI1A, ATVTI11, ZIG, SGR4, VTI1A, ZIG1 | Vesicle transport v-SNARE family protein | chr5:15822035-15823591 FORWARD LENGTH=221	227	221	2.00E-93	97.4	80.2	92.1
Rsa1.0_01209.1.g24621.t2	gb|AAM65834.1| unknown [Arabidopsis thaliana]	431	230	1.00E-95	53.4	39.0	42.9	unknown	gbpln	Arabidopsis thaliana	AT5G39520.1 | Symbols: | Protein of unknown function (DUF1997) | chr5:15823920-15825416 REVERSE LENGTH=230	431	230	5.00E-98	53.4	38.7	42.9
Rsa1.0_01209.1.g24622.t1	ref|XP_002868712.1| hypothetical protein ARALYDRAFT_916349 [Arabidopsis lyrata subsp. lyrata] gi|297314548|gb|EFH44971.1| hypothetical protein ARALYDRAFT_916349 [Arabidopsis lyrata subsp. lyrata]	238	242	1.00E-113	101.7	83.2	90.3	hypothetical protein ARALYDRAFT_916349	gbpln	Arabidopsis lyrata	AT5G39530.1 | Symbols: | Protein of unknown function (DUF1997) | chr5:15826285-15827517 REVERSE LENGTH=239	238	239	1.00E-114	100.4	81.9	90.3
Rsa1.0_01209.1.g24623.t1	gb|EOA16722.1| hypothetical protein CARUB_v10004926mg [Capsella rubella]	357	384	1.00E-110	107.6	80.4	85.7	hypothetical protein CARUB_v10004926mg	gbpln	Capsella rubella	AT5G39570.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol, nucleus; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT3G29075.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:15844021-15845827 FORWARD LENGTH=381	357	381	1.00E-105	106.7	73.9	79.8
Rsa1.0_01209.1.g24624.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	169	1142	1.00E-32	675.7	46.2	60.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	169	292	7.00E-17	172.8	30.8	46.2
Rsa1.0_01210.1.g24625.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	189	1342	7.00E-12	710.1	25.9	37.0	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01210.1.g24626.t1	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	541	1463	3.00E-22	270.4	20.5	30.5	F5J5.1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01210.1.g24627.t1	gb|EOA32569.1| hypothetical protein CARUB_v10015859mg [Capsella rubella]	1047	804	0	76.8	65.9	70.3	hypothetical protein CARUB_v10015859mg	gbpln	Capsella rubella	AT3G14205.1 | Symbols: | Phosphoinositide phosphatase family protein | chr3:4716008-4720524 REVERSE LENGTH=808	1047	808	0	77.2	66.6	71.2
Rsa1.0_01210.1.g24628.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	392	387	2.00E-69	98.7	41.6	56.9	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	392	387	4.00E-72	98.7	41.6	56.9
Rsa1.0_01210.1.g24629.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1787	1213	0	67.9	24.8	37.9	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1787	626	3.00E-62	35.0	7.9	13.3
Rsa1.0_01210.1.g24630.t1	gb|EOA29201.1| hypothetical protein CARUB_v10025475mg [Capsella rubella]	242	420	1.00E-70	173.6	55.0	67.8	hypothetical protein CARUB_v10025475mg	gbpln	Capsella rubella	AT4G39753.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18440125-18441297 FORWARD LENGTH=390	242	390	2.00E-71	161.2	55.8	67.4
Rsa1.0_01211.1.g24631.t1	gb|EOA39490.1| hypothetical protein CARUB_v10008095mg [Capsella rubella]	1428	1361	0	95.3	70.4	78.1	hypothetical protein CARUB_v10008095mg	gbpln	Capsella rubella	AT1G20970.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: guard cell, cultured cell; BEST Arabidopsis thaliana protein match is: proton pump interactor 1 (TAIR:AT4G27500.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:7314338-7319246 FORWARD LENGTH=1364	1428	1364	0	95.5	70.6	78.2
Rsa1.0_01211.1.g24632.t1	dbj|BAJ34640.1| unnamed protein product [Thellungiella halophila]	1013	1035	0	102.2	86.9	92.2	unnamed protein product	----	----	AT1G20980.1 | Symbols: SPL14, FBR6, SPL1R2, ATSPL14 | squamosa promoter binding protein-like 14 | chr1:7325042-7328933 FORWARD LENGTH=1035	1013	1035	0	102.2	84.8	90.9
Rsa1.0_01211.1.g24633.t1	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1188	910	0	76.6	37.5	52.3	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1188	626	3.00E-97	52.7	15.2	24.1

Rsa1.0_01211.1.g24634.t1	ref|NP_173523.1| DC1 domain-containing protein [Arabidopsis thaliana] gi|332191930|gb|AEE30051.1| DC1 domain-containing protein [Arabidopsis thaliana]	322	319	1.00E-137	99.1	85.1	92.2	DC1 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G20990.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:7330524-7331946 REVERSE LENGTH=319	322	319	1.00E-140	99.1	85.1	92.2
Rsa1.0_01211.1.g24635.t1	ref|XP_002890421.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297336263|gb|EFH66680.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata]	268	246	1.00E-130	91.8	86.2	88.4	zinc-binding family protein	gbpln	Arabidopsis lyrata	AT1G21000.2 | Symbols: | PLATZ transcription factor family protein | chr1:7338013-7339088 FORWARD LENGTH=243	268	243	1.00E-130	90.7	84.7	87.7
Rsa1.0_01211.1.g24636.t1	ref|XP_002890422.1| hypothetical protein ARALYDRAFT_889558 [Arabidopsis lyrata subsp. lyrata] gi|297336264|gb|EFH66681.1| hypothetical protein ARALYDRAFT_889558 [Arabidopsis lyrata subsp. lyrata]	115	207	2.00E-34	180.0	77.4	84.3	hypothetical protein ARALYDRAFT_889558	gbpln	Arabidopsis lyrata	AT1G21010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76600.1); Has 206 Blast hits to 206 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 206; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7346239-7346871 FORWARD LENGTH=210	115	210	3.00E-35	182.6	75.7	81.7
Rsa1.0_01212.1.g24637.t1	ref|XP_002887531.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333372|gb|EFH63790.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	391	391	0	100.0	88.0	94.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G74210.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr1:27910396-27912785 FORWARD LENGTH=392	391	392	0	100.3	88.5	95.1
Rsa1.0_01212.1.g24638.t2	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	878	966	0	110.0	63.6	76.2	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	878	965	0	109.9	62.0	75.9
Rsa1.0_01212.1.g24639.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01212.1.g24640.t1	ref|XP_002865001.1| hypothetical protein ARALYDRAFT_496850 [Arabidopsis lyrata subsp. lyrata] gi|297310836|gb|EFH41260.1| hypothetical protein ARALYDRAFT_496850 [Arabidopsis lyrata subsp. lyrata]	101	246	3.00E-11	243.6	47.5	61.4	hypothetical protein ARALYDRAFT_496850	gbpln	Arabidopsis lyrata	AT5G67450.1 | Symbols: AZF1, ZF1 | zinc-finger protein 1 | chr5:26919142-26919879 REVERSE LENGTH=245	101	245	2.00E-13	242.6	46.5	60.4
Rsa1.0_01212.1.g24641.t1	gb|AAG52362.1|AC011765_14 putative receptor protein kinase; 10992-14231 [Arabidopsis thaliana]	663	1079	0	162.7	70.3	78.6	putative receptor protein kinase; 10992-14231	gbpln	Arabidopsis thaliana	AT1G74360.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:27954299-27957911 FORWARD LENGTH=1106	663	1106	0	166.8	70.1	78.6
Rsa1.0_01212.1.g24642.t2	gb|EOA35256.1| hypothetical protein CARUB_v10020425mg [Capsella rubella]	371	393	0	105.9	87.9	93.5	hypothetical protein CARUB_v10020425mg	gbpln	Capsella rubella	AT1G74210.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr1:27910396-27912785 FORWARD LENGTH=392	371	392	0	105.7	87.6	93.8
Rsa1.0_01212.1.g24643.t1	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	928	966	0	104.1	66.7	78.2	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	928	965	0	104.0	65.7	77.8
Rsa1.0_01212.1.g24644.t1	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	964	966	0	100.2	70.9	80.8	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	964	965	0	100.1	69.3	79.8
Rsa1.0_01212.1.g24645.t1	ref|XP_002888967.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297334808|gb|EFH65226.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	362	966	1.00E-129	266.9	71.3	81.8	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	362	965	1.00E-127	266.6	69.9	80.9
Rsa1.0_01212.1.g24646.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1531	1501	0	98.0	60.3	73.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1531	1262	1.00E-123	82.4	14.8	20.7
Rsa1.0_01212.1.g24647.t1	ref|NP_177559.1| receptor like protein 15 [Arabidopsis thaliana] gi|12323812|gb|AAG51871.1|AC079678_1 disease resistance protein, putative; 1096-4664 [Arabidopsis thaliana] gi|332197443|gb|AEE35564.1| receptor like protein 15 [Arabidopsis thaliana]	213	965	2.00E-74	453.1	64.3	75.1	receptor like protein 15	gbpln	Arabidopsis thaliana	AT1G74190.1 | Symbols: AtRLP15, RLP15 | receptor like protein 15 | chr1:27902590-27906158 REVERSE LENGTH=965	213	965	5.00E-77	453.1	64.3	75.1
Rsa1.0_01212.1.g24648.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_01212.1.g24649.t1</td><td>ref|XP_002881173.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327012|gb|EFH57432.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>201</td><td>917</td><td>7.00E-12</td><td>456.2</td><td>22.4</td><td>26.9</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G31400.1 | Symbols: GUN1 | genomes uncoupled 1 | chr2:13387201-13390550 REVERSE LENGTH=918</td><td>201</td><td>918</td><td>1.00E-12</td><td>456.7</td><td>21.4</td><td>24.4</td></tr>
<tr><td>Rsa1.0_01212.1.g24650.t1</td><td>gb|ACR10272.1| sulfotransferase 5b [Brassica rapa subsp. pekinensis]</td><td>344</td><td>342</td><td>1.00E-171</td><td>99.4</td><td>84.0</td><td>88.7</td><td>sulfotransferase 5b</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G74090.1 | Symbols: SOT18, ATSOT18, ATST5B | desulfo-glucosinolate sulfotransferase 18 | chr1:27863003-27864055 FORWARD LENGTH=350</td><td>344</td><td>350</td><td>1.00E-153</td><td>101.7</td><td>74.4</td><td>87.2</td></tr>
<tr><td>Rsa1.0_01212.1.g24651.t1</td><td>gb|ACR10272.1| sulfotransferase 5b [Brassica rapa subsp. pekinensis]</td><td>343</td><td>342</td><td>1.00E-175</td><td>99.7</td><td>85.4</td><td>91.3</td><td>sulfotransferase 5b</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G18590.1 | Symbols: SOT17, ATSOT17, ATST5C | sulfotransferase 17 | chr1:6398634-6399674 FORWARD LENGTH=346</td><td>343</td><td>346</td><td>1.00E-149</td><td>100.9</td><td>69.4</td><td>84.3</td></tr>
<tr><td>Rsa1.0_01212.1.g24652.t1</td><td>gb|ACR10272.1| sulfotransferase 5b [Brassica rapa subsp. pekinensis]</td><td>313</td><td>342</td><td>1.00E-138</td><td>109.3</td><td>75.4</td><td>80.2</td><td>sulfotransferase 5b</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G74100.1 | Symbols: SOT16, ATSOT16, CORI-7, ATST5A | sulfotransferase 16 | chr1:27864489-27865505 REVERSE LENGTH=338</td><td>313</td><td>338</td><td>1.00E-126</td><td>108.0</td><td>63.6</td><td>77.3</td></tr>
<tr><td>Rsa1.0_01213.1.g24653.t1</td><td>ref|NP_001185022.1| B-block binding subunit of TFⅢC [Arabidopsis thaliana] gi|332191469|gb|AEE29590.1| B-block binding subunit of TFⅢC [Arabidopsis thaliana]</td><td>1822</td><td>1844</td><td>0</td><td>101.2</td><td>82.1</td><td>89.5</td><td>B-block binding subunit of TFⅢC</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G17450.2 | Symbols: | B-block binding subunit of TFⅢC | chr1:5988579-5996693 REVERSE LENGTH=1844</td><td>1822</td><td>1844</td><td>0</td><td>101.2</td><td>82.1</td><td>89.5</td></tr>
<tr><td>Rsa1.0_01213.1.g24654.t1</td><td>ref|XP_002888930.1| hypothetical protein ARALYDRAFT_895209 [Arabidopsis lyrata subsp. lyrata] gi|297334771|gb|EFH65189.1| hypothetical protein ARALYDRAFT_895209 [Arabidopsis lyrata subsp. lyrata]</td><td>313</td><td>192</td><td>1.00E-16</td><td>61.3</td><td>17.9</td><td>21.7</td><td>hypothetical protein ARALYDRAFT_895209</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G73510.1 | Symbols: | unknown protein; Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27642651-27643118 REVERSE LENGTH=155</td><td>313</td><td>155</td><td>1.00E-11</td><td>49.5</td><td>12.8</td><td>16.0</td></tr>
<tr><td>Rsa1.0_01213.1.g24655.t2</td><td>gb|AAC33963.1| contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]</td><td>1051</td><td>1633</td><td>0</td><td>155.4</td><td>56.5</td><td>69.8</td><td>contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1051</td><td>1262</td><td>1.00E-165</td><td>120.1</td><td>27.5</td><td>37.5</td></tr>
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<tr><td>Rsa1.0_01213.1.g24657.t1</td><td>gb|EOA30679.1| hypothetical protein CARUB_v10013818mg, partial [Capsella rubella]</td><td>397</td><td>414</td><td>0</td><td>104.3</td><td>80.6</td><td>86.1</td><td>hypothetical protein CARUB_v10013818mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G25210.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:9180348-9181487 FORWARD LENGTH=379</td><td>397</td><td>379</td><td>0</td><td>95.5</td><td>80.1</td><td>86.1</td></tr>
<tr><td>Rsa1.0_01213.1.g24658.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01213.1.g24659.t1</td><td>gb|EOA16322.1| hypothetical protein CARUB_v10004472mg [Capsella rubella]</td><td>488</td><td>570</td><td>8.00E-82</td><td>116.8</td><td>39.5</td><td>51.2</td><td>hypothetical protein CARUB_v10004472mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G41690.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:16670126-16674189 REVERSE LENGTH=567</td><td>488</td><td>567</td><td>3.00E-78</td><td>116.2</td><td>37.1</td><td>49.0</td></tr>
<tr><td>Rsa1.0_01214.1.g24660.t1</td><td>ref|NP_565100.1| DNA-3-methyladenine glycosylase Ⅰ [Arabidopsis thaliana] gi|14334652|gb|AAK59504.1| putative DNA-3-methyladenine glycosylase Ⅰ [Arabidopsis thaliana] gi|17104587|gb|AAL34182.1| putative DNA-3-methyladenine glycosylase Ⅰ [Arabidopsis thaliana] gi|332197550|gb|AEE35671.1| putative 3-methyladenine glycosylase Ⅰ [Arabidopsis thaliana]</td><td>316</td><td>329</td><td>1.00E-134</td><td>104.1</td><td>82.0</td><td>88.6</td><td>DNA-3-methyladenine glycosylase Ⅰ</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G75090.1 | Symbols: | DNA glycosylase superfamily protein | chr1:28187647-28189612 REVERSE LENGTH=329</td><td>316</td><td>329</td><td>1.00E-136</td><td>104.1</td><td>82.0</td><td>88.6</td></tr>
<tr><td>Rsa1.0_01214.1.g24661.t1</td><td>gb|AAL57684.1| At1g75080/F9E10_7 [Arabidopsis thaliana] gi|20147315|gb|AAM10371.1| At1g75080/F9E10_7 [Arabidopsis thaliana]</td><td>325</td><td>336</td><td>1.00E-131</td><td>103.4</td><td>91.4</td><td>93.2</td><td>At1g75080/F9E10_7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G75080.2 | Symbols: BZR1 | Brassinosteroid signalling positive regulator (BZR1) family protein | chr1:28185709-28187063 FORWARD LENGTH=336</td><td>325</td><td>336</td><td>1.00E-133</td><td>103.4</td><td>91.1</td><td>93.2</td></tr>
<tr><td>Rsa1.0_01214.1.g24662.t1</td><td>ref|XP_002889006.1| hypothetical protein ARALYDRAFT_476644 [Arabidopsis lyrata subsp. lyrata] gi|297334847|gb|EFH65265.1| hypothetical protein ARALYDRAFT_476644 [Arabidopsis lyrata subsp. lyrata]</td><td>228</td><td>244</td><td>1.00E-100</td><td>107.0</td><td>78.1</td><td>87.3</td><td>hypothetical protein ARALYDRAFT_476644</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G75060.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G19330.2); Has 104 Blast hits to 104 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:28181481-28183285 REVERSE LENGTH=242</td><td>228</td><td>242</td><td>1.00E-100</td><td>106.1</td><td>76.8</td><td>85.5</td></tr>
<tr><td>Rsa1.0_01214.1.g24663.t1</td><td>ref|XP_002887572.1| hypothetical protein ARALYDRAFT_316436 [Arabidopsis lyrata subsp. lyrata] gi|297333413|gb|EFH63831.1| hypothetical protein ARALYDRAFT_316436 [Arabidopsis lyrata subsp. lyrata]</td><td>88</td><td>245</td><td>3.00E-35</td><td>278.4</td><td>83.0</td><td>88.6</td><td>hypothetical protein ARALYDRAFT_316436</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G75050.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:28180116-28181062 FORWARD LENGTH=246</td><td>88</td><td>246</td><td>5.00E-37</td><td>279.5</td><td>84.1</td><td>88.6</td></tr>
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<tr><td>Rsa1.0_01214.1.g24665.t1</td><td>ref|XP_002887572.1| hypothetical protein ARALYDRAFT_316436 [Arabidopsis lyrata subsp. lyrata] gi|297333413|gb|EFH63831.1| hypothetical protein ARALYDRAFT_316436 [Arabidopsis lyrata subsp. lyrata]</td><td>231</td><td>245</td><td>3.00E-98</td><td>106.1</td><td>77.1</td><td>85.7</td><td>hypothetical protein ARALYDRAFT_316436</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G75030.1 | Symbols: ATLP-3, TLP-3 | thaumatin-like protein 3 | chr1:28174418-28175255 FORWARD LENGTH=246</td><td>231</td><td>246</td><td>8.00E-99</td><td>106.5</td><td>76.2</td><td>84.4</td></tr>
<tr><td>Rsa1.0_01214.1.g24666.t1</td><td>gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]</td><td>473</td><td>255</td><td>4.00E-59</td><td>53.9</td><td>28.3</td><td>34.9</td><td>hypothetical protein 40.t00057</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302</td><td>473</td><td>302</td><td>4.00E-47</td><td>63.8</td><td>26.0</td><td>36.8</td></tr>
<tr><td>Rsa1.0_01214.1.g24667.t1</td><td>gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]</td><td>113</td><td>442</td><td>9.00E-33</td><td>391.2</td><td>59.3</td><td>68.1</td><td>hypothetical protein 24.t00017</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343</td><td>113</td><td>343</td><td>4.00E-19</td><td>303.5</td><td>43.4</td><td>55.8</td></tr>
<tr><td>Rsa1.0_01214.1.g24668.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01214.1.g24669.t1</td><td>ref|NP_177638.2| GTP binding protein [Arabidopsis thaliana] gi|327507752|sp|Q6F6B5.2|ARC3_ARATH RecName: Full=Protein ACCUMULATION AND REPLICATION OF CHLOROPLASTS 3; Flags: Precursor gi|332197540|gb|AEE35661.1| protein accumulation and replication of chloroplast 3 [Arabidopsis thaliana]</td><td>743</td><td>741</td><td>0</td><td>99.7</td><td>84.1</td><td>90.7</td><td>GTP binding protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G75010.1 | Symbols: ARC3 | GTP binding | chr1:28164994-28169941 REVERSE LENGTH=741</td><td>743</td><td>741</td><td>0</td><td>99.7</td><td>84.1</td><td>90.7</td></tr>
<tr><td>Rsa1.0_01214.1.g24670.t1</td><td>ref|XP_002887568.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|297333409|gb|EFH63827.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata]</td><td>273</td><td>281</td><td>1.00E-132</td><td>102.9</td><td>88.6</td><td>93.4</td><td>GNS1/SUR4 membrane family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G75000.1 | Symbols: | GNS1/SUR4 membrane protein family | chr1:28163650-28164586 FORWARD LENGTH=281</td><td>273</td><td>281</td><td>1.00E-133</td><td>102.9</td><td>87.9</td><td>91.9</td></tr>
<tr><td>Rsa1.0_01214.1.g24671.t1</td><td>ref|XP_002889004.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297334845|gb|EFH65263.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>132</td><td>137</td><td>9.00E-51</td><td>103.8</td><td>75.0</td><td>86.4</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G74990.1 | Symbols: | RING/U-box superfamily protein | chr1:28159837-28160250 REVERSE LENGTH=137</td><td>132</td><td>137</td><td>1.00E-51</td><td>103.8</td><td>75.0</td><td>86.4</td></tr>
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Rsa1.0_01214.1.g24672.t1	ref|NP_177635.1| 30S ribosomal protein S9 [Arabidopsis thaliana] gi|48428563|sp|Q9XJ27.1|RR9_ARATH RecName: Full=30S ribosomal protein S9, chloroplastic; Flags: Precursor gi|5882726|gb|AAD55279.1|AC008263_10 Identical to gb|AB022676 ribosomal protein S9 from Arabidopsis thaliana. ESTs gb|T13861, gb|AA389790, gb|T42539, gb|AA586013, gb|AA395093 and gb|AA041154 come from this gene [Arabidopsis thaliana] gi|12744979|gb|AAK06869.1|AF344318_1 putative ribosomal protein S9 [Arabidopsis thaliana] gi|5456946|dbj|BAA82396.1| ribosomal protein S9 [Arabidopsis thaliana] gi|15010598|gb|AAK73958.1| ATg74970/F25A4.6 [Arabidopsis thaliana] gi|15027999|gb|AAK76530.1| putative ribosomal protein S9 [Arabidopsis thaliana] gi|20259211|gb|AAM14321.1| putative ribosomal protein S9 [Arabidopsis thaliana] gi|21554316|gb|AAM63421.1| ribosomal protein S9, putative [Arabidopsis thaliana] gi|51968396|dbj|BAD42890.1| putative ribosomal protein S9 [Arabidopsis thaliana] gi|51969144|dbj|BAD43264.1| putative ribosomal protein S9 [Arabidopsis thaliana] gi|51969266|dbj|BAD43325.1| putative ribosomal protein S9 [Arabidopsis	211	208	1.00E-95	98.6	90.0	93.4	30S ribosomal protein S9	gbpln	Arabidopsis thaliana	AT1G74970.1 | Symbols: RPS9, TWN3 | ribosomal protein S9 | chr1:28157761-28159202 REVERSE LENGTH=208	211	208	3.00E-98	98.6	90.0	93.4
Rsa1.0_01214.1.g24673.t1	gb|AAL91174.1| putative 3-ketoacyl-ACP synthase [Arabidopsis thaliana]	542	541	0	99.8	90.2	93.5	putative 3-ketoacyl-ACP synthase	gbpln	Arabidopsis thaliana	AT1G74960.3 | Symbols: FAB1 | fatty acid biosynthesis 1 | chr1:28152564-28155948 REVERSE LENGTH=541	542	541	0	99.8	90.4	93.7
Rsa1.0_01214.1.g24674.t1	dbj|BAJ33919.1| unnamed protein product [Thellungiella halophila]	256	251	3.00E-90	98.0	73.4	82.4	unnamed protein product	----	----	AT1G74950.1 | Symbols: JAZ2, TIFY10B | TIFY domain/Divergent CCT motif family protein | chr1:28148919-28150258 REVERSE LENGTH=249	256	249	1.00E-81	97.3	69.9	80.5
Rsa1.0_01214.1.g24675.t1	ref|NP_565095.1| uncharacterized protein [Arabidopsis thaliana] gi|23306420|gb|AAN17437.1| expressed protein [Arabidopsis thaliana] gi|27311889|gb|AAO00910.1| expressed protein [Arabidopsis thaliana] gi|332197532|gb|AEE35653.1| uncharacterized protein AT1G74940 [Arabidopsis thaliana]	223	222	3.00E-94	99.6	79.8	88.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G74940.1 | Symbols: | Protein of unknown function (DUF581) | chr1:28146284-28147065 FORWARD LENGTH=222	223	222	9.00E-97	99.6	79.8	88.3
Rsa1.0_01215.1.g24676.t1	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	150	695	1.00E-72	463.3	85.3	92.0	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01215.1.g24677.t1	ref|NP_198536.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|10178231|dbj|BAB11642.1| unnamed protein product [Arabidopsis thaliana] gi|332006769|gb|AED94152.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	204	217	1.00E-39	106.4	52.9	65.7	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT5G37200.1 | Symbols: | RING/U-box superfamily protein | chr5:14727832-14728485 FORWARD LENGTH=217	204	217	4.00E-42	106.4	52.9	65.7
Rsa1.0_01215.1.g24678.t1	gb|EOA18545.1| hypothetical protein CARUB_v10007102mg [Capsella rubella]	208	208	4.00E-33	100.0	45.2	62.0	hypothetical protein CARUB_v10007102mg	gbpln	Capsella rubella	AT5G37200.1 | Symbols: | RING/U-box superfamily protein | chr5:14727832-14728485 FORWARD LENGTH=217	208	217	2.00E-30	104.3	41.3	58.2
Rsa1.0_01215.1.g24679.t1	gb|EOA17626.1| hypothetical protein CARUB_v10005991mg [Capsella rubella]	139	136	2.00E-58	97.8	80.6	92.8	hypothetical protein CARUB_v10005991mg	gbpln	Capsella rubella	AT5G37670.1 | Symbols: | HSP20-like chaperones superfamily protein | chr5:14969035-14969448 FORWARD LENGTH=137	139	137	5.00E-59	98.6	84.2	92.1
Rsa1.0_01215.1.g24680.t1	ref|XP_002870553.1| hypothetical protein ARALYDRAFT_915910 [Arabidopsis lyrata subsp. lyrata] gi|297316389|gb|EFH46812.1| hypothetical protein ARALYDRAFT_915910 [Arabidopsis lyrata subsp. lyrata]	184	184	1.00E-101	100.0	98.9	99.5	hypothetical protein ARALYDRAFT_915910	gbpln	Arabidopsis lyrata	AT5G37680.1 | Symbols: ATARLA1A, ARLA1A | ADP-ribosylation factor-like A1A | chr5:14969797-14971098 REVERSE LENGTH=184	184	184	1.00E-103	100.0	97.8	98.9
Rsa1.0_01215.1.g24681.t2	gb|EOA18579.1| hypothetical protein CARUB_v10007145mg [Capsella rubella]	357	357	0	100.0	86.3	93.8	hypothetical protein CARUB_v10007145mg	gbpln	Capsella rubella	AT5G37690.1 | Symbols: | SGNH hydrolase-type esterase superfamily protein | chr5:14973610-14976115 REVERSE LENGTH=356	357	356	0	99.7	87.1	94.1
Rsa1.0_01215.1.g24682.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01215.1.g24683.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01215.1.g24684.t1	dbj|BAB08316.1| calmodulin-binding heat-shock protein [Arabidopsis thaliana]	442	449	0	101.6	88.7	94.6	calmodulin-binding heat-shock protein	gbpln	Arabidopsis thaliana	AT5G37710.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:14979159-14981400 FORWARD LENGTH=436	442	436	0	98.6	88.0	93.9
Rsa1.0_01215.1.g24685.t1	ref|NP_198588.2| THO complex subunit 4 [Arabidopsis thaliana] gi|37201990|gb|AAQ89610.1| At5g37720 [Arabidopsis thaliana] gi|110735849|dbj|BAE99901.1| hypothetical protein [Arabidopsis thaliana] gi|332006839|gb|AED94222.1| THO complex subunit 4 [Arabidopsis thaliana]	298	288	8.00E-86	96.6	75.2	80.9	THO complex subunit 4	gbpln	Arabidopsis thaliana	AT5G37720.1 | Symbols: ALY4 | ALWAYS EARLY 4 | chr5:14981805-14983978 REVERSE LENGTH=288	298	288	2.00E-88	96.6	75.2	80.9
Rsa1.0_01215.1.g24686.t2	ref|XP_002870559.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316395|gb|EFH46818.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	378	121	4.00E-44	32.0	24.6	25.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G37730.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23150.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:14986141-14986884 REVERSE LENGTH=182	378	182	3.00E-46	48.1	23.5	25.7
Rsa1.0_01216.1.g24687.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01216.1.g24688.t1	ref|NP_200294.1| DOMON and dopamine beta-monooxygenase N-terminal domain-containing protein [Arabidopsis thaliana] gi|9758263|dbj|BAB08762.1| unnamed protein product [Arabidopsis thaliana] gi|19699059|gb|AAL90897.1| AT5g54830/MBG8_9 [Arabidopsis thaliana] gi|27363250|gb|AAO11544.1| At5g54830/MBG8_9 [Arabidopsis thaliana] gi|110742339|dbj|BAE99093.1| hypothetical protein [Arabidopsis thaliana] gi|332009162|gb|AED96545.1| DOMON and dopamine beta-monooxygenase N-terminal domain-containing protein [Arabidopsis thaliana]	919	907	0	98.7	88.5	92.9	DOMON and dopamine beta-monooxygenase N-terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT5G54830.1 | Symbols: | DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein | chr5:22273394-22276117 FORWARD LENGTH=907	919	907	0	98.7	88.5	92.9
Rsa1.0_01216.1.g24689.t1	gb|AAM63660.1| glucose-6-phosphate/phosphate translocator [Arabidopsis thaliana]	392	388	0	99.0	89.8	91.8	glucose-6-phosphate/phosphate translocator	gbpln	Arabidopsis thaliana	AT5G54800.1 | Symbols: GPT1, ATGPT1 | glucose 6-phosphate/phosphate translocator 1 | chr5:22261408-22263562 FORWARD LENGTH=388	392	388	0	99.0	90.1	92.1
Rsa1.0_01216.1.g24690.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01216.1.g24691.t1	gb|ABD64940.1| hypothetical protein 24.t00018 [Brassica oleracea]	440	380	5.00E-56	86.4	28.2	36.1	hypothetical protein 24.t00018	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	440	302	5.00E-49	68.6	26.1	36.6
Rsa1.0_01216.1.g24692.t1	ref|XP_002866061.1| hypothetical protein ARALYDRAFT_495560 [Arabidopsis lyrata subsp. lyrata] gi|297311896|gb|EFH42320.1| hypothetical protein ARALYDRAFT_495560 [Arabidopsis lyrata subsp. lyrata]	130	165	4.00E-30	126.9	60.8	70.8	hypothetical protein ARALYDRAFT_495560	gbpln	Arabidopsis lyrata	AT5G54790.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G50930.1); Has 53 Blast hits to 53 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 53; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:22254195-22255489 REVERSE LENGTH=165	130	165	1.00E-30	126.9	62.3	73.1
Rsa1.0_01216.1.g24693.t4	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1608	1529	0	95.1	30.3	46.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1608	626	2.00E-52	38.9	8.0	13.2
Rsa1.0_01217.1.g24694.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01217.1.g24695.t1	ref|XP_002869942.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315778|gb|EFH46201.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	130	211	6.00E-21	162.3	36.9	43.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G20280.1 | Symbols: TAF11 | TBP-associated factor 11 | chr4:10953792-10954664 FORWARD LENGTH=210	130	210	4.00E-23	161.5	36.2	42.3
Rsa1.0_01217.1.g24696.t1	ref|NP_176226.3| RNA-binding protein 25 [Arabidopsis thaliana] gi|18377662|gb|AAL66981.1| unknown protein [Arabidopsis thaliana] gi|25055015|gb|AAN71971.1| unknown protein [Arabidopsis thaliana] gi|332195545|gb|AEE33666.1| splicing factor PWI domain-containing protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	841	899	1.00E-178	106.9	49.9	53.5	RNA-binding protein 25	gbpln	Arabidopsis thaliana	AT1G60200.1 | Symbols: | splicing factor PWI domain-containing protein / RNA recognition motif (RRM)-containing protein | chr1:22200882-22205241 REVERSE LENGTH=899	841	899	0	106.9	49.9	53.5

<table>
<tr><td>Rsa1.0_01217.1.g24697.t1</td><td>ref|XP_002888147.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]
gi|297333988|gb|EFH64406.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]</td><td>685</td><td>686</td><td>0</td><td>100.1</td><td>76.5</td><td>85.8</td><td>armadillo/beta-catenin repeat family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G60190.1 | Symbols: | ARM repeat superfamily protein | chr1:22198403-22200463 FORWARD LENGTH=686</td><td>685</td><td>686</td><td>0</td><td>100.1</td><td>76.4</td><td>85.5</td></tr>
<tr><td>Rsa1.0_01217.1.g24698.t1</td><td>gb|EOA35096.1| hypothetical protein CARUB_v10020207mg, partial [Capsella rubella]</td><td>485</td><td>484</td><td>0</td><td>99.8</td><td>92.8</td><td>97.1</td><td>hypothetical protein CARUB_v10020207mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G60170.1 | Symbols: emb1220 | pre-mRNA processing ribonucleoprotein binding region-containing protein | chr1:22193008-22195177 FORWARD LENGTH=485</td><td>485</td><td>485</td><td>0</td><td>100.0</td><td>91.1</td><td>95.7</td></tr>
<tr><td>Rsa1.0_01217.1.g24699.t1</td><td>ref|NP_176586.1| serpin-Z1 [Arabidopsis thaliana]
gi|189029934|sp|Q9SH52.2|SPZ1_ARATH RecName: Full=Serpin-Z1; AltName: Full=ArathZ1
gi|332196061|gb|AEE34182.1| serpin-Z1 [Arabidopsis thaliana]</td><td>392</td><td>385</td><td>1.00E-103</td><td>98.2</td><td>55.4</td><td>67.9</td><td>serpin-Z1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G64030.1 | Symbols: ATSRP3, SRP3 | serpin 3 | chr1:23752873-23754348 REVERSE LENGTH=385</td><td>392</td><td>385</td><td>1.00E-105</td><td>98.2</td><td>55.4</td><td>67.9</td></tr>
<tr><td>Rsa1.0_01217.1.g24700.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>1212</td><td>1142</td><td>0</td><td>94.2</td><td>30.4</td><td>40.9</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1212</td><td>575</td><td>1.00E-74</td><td>47.4</td><td>13.9</td><td>21.9</td></tr>
<tr><td>Rsa1.0_01217.1.g24701.t1</td><td>gb|EOA19642.1| hypothetical protein CARUB_v10003012mg [Capsella rubella]</td><td>366</td><td>390</td><td>4.00E-67</td><td>106.6</td><td>46.2</td><td>61.5</td><td>hypothetical protein CARUB_v10003012mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378</td><td>366</td><td>378</td><td>7.00E-69</td><td>103.3</td><td>43.7</td><td>60.7</td></tr>
<tr><td>Rsa1.0_01217.1.g24702.t1</td><td>ref|NP_567270.1| putative F-box only protein 15 [Arabidopsis thaliana]
gi|75265492|sp|Q9S9V1.1|FBX15_ARATH RecName: Full=Putative F-box only protein 15
gi|5732058|gb|AAD48957.1|AF149414_6 contains similarity to Pfam family PF00646 (F-box domain); score=11/3, E=0.23, N=1 [Arabidopsis thaliana]
gi|7267227|emb|CAB80834.1| AT4g04690 [Arabidopsis thaliana]
gi|332657012|gb|AEE82412.1| putative F-box only protein 15 [Arabidopsis thaliana]</td><td>134</td><td>378</td><td>3.00E-33</td><td>282.1</td><td>56.7</td><td>68.7</td><td>putative F-box only protein 15</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378</td><td>134</td><td>378</td><td>7.00E-36</td><td>282.1</td><td>56.7</td><td>68.7</td></tr>
<tr><td>Rsa1.0_01217.1.g24703.t1</td><td>ref|NP_176222.2| putative potassium transporter 12 [Arabidopsis thaliana]
gi|38502862|sp|O80739.2|POT12_ARATH RecName: Full=Putative potassium transporter 12; Short=AtPOT12
gi|332195542|gb|AEE33663.1| putative potassium transporter 12 [Arabidopsis thaliana]</td><td>768</td><td>827</td><td>0</td><td>107.7</td><td>86.1</td><td>88.3</td><td>putative potassium transporter 12</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G60160.1 | Symbols: | Potassium transporter family protein | chr1:22188330-22191395 REVERSE LENGTH=827</td><td>768</td><td>827</td><td>0</td><td>107.7</td><td>86.1</td><td>88.3</td></tr>
<tr><td>Rsa1.0_01218.1.g24704.t1</td><td>ref|XP_002893765.1| hypothetical protein ARALYDRAFT_890918 [Arabidopsis lyrata subsp. lyrata]
gi|297339607|gb|EFH70024.1| hypothetical protein ARALYDRAFT_890918 [Arabidopsis lyrata subsp. lyrata]</td><td>89</td><td>93</td><td>2.00E-36</td><td>104.5</td><td>86.5</td><td>94.4</td><td>hypothetical protein ARALYDRAFT_890918</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G10270.1 | Symbols: | Wound-responsive family protein | chr4:6374805-6375077 FORWARD LENGTH=90</td><td>89</td><td>90</td><td>3.00E-29</td><td>101.1</td><td>70.8</td><td>83.1</td></tr>
<tr><td>Rsa1.0_01218.1.g24705.t1</td><td>gb|EOA36610.1| hypothetical protein CARUB_v10011824mg [Capsella rubella]</td><td>653</td><td>652</td><td>0</td><td>99.8</td><td>88.7</td><td>92.0</td><td>hypothetical protein CARUB_v10011824mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G33360.1 | Symbols: | ATP-dependent Clp protease | chr1:12092111-12095789 FORWARD LENGTH=656</td><td>653</td><td>656</td><td>0</td><td>100.5</td><td>88.5</td><td>92.3</td></tr>
<tr><td>Rsa1.0_01218.1.g24706.t1</td><td>ref|NP_174603.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]
gi|75168867|sp|Q9C501.1|PPR70_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g33350
gi|12322383|gb|AAG51215.1|AC051630_12 unknown protein; 15445-13829 [Arabidopsis thaliana]
gi|12322567|gb|AAG51281.1|AC027035_4 PPR-repeat protein, putative [Arabidopsis thaliana]
gi|332193465|gb|AEE31586.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]</td><td>518</td><td>538</td><td>0</td><td>103.9</td><td>85.1</td><td>92.3</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G33350.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:12090071-12091687 REVERSE LENGTH=538</td><td>518</td><td>538</td><td>0</td><td>103.9</td><td>85.1</td><td>92.3</td></tr>
<tr><td>Rsa1.0_01218.1.g24707.t1</td><td>ref|XP_002893762.1| predicted protein [Arabidopsis lyrata subsp. lyrata]
gi|297339604|gb|EFH70021.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>172</td><td>191</td><td>3.00E-69</td><td>111.0</td><td>84.3</td><td>93.0</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G10250.1 | Symbols: ATHSP22.0 | HSP20-like chaperones superfamily protein | chr4:6370537-6371124 FORWARD LENGTH=195</td><td>172</td><td>195</td><td>6.00E-63</td><td>113.4</td><td>68.6</td><td>84.3</td></tr>
<tr><td>Rsa1.0_01218.1.g24708.t1</td><td>gb|AAX51974.1| transposase [Pisum sativum]</td><td>386</td><td>412</td><td>1.00E-122</td><td>106.7</td><td>56.0</td><td>73.6</td><td>transposase</td><td>gbpln</td><td>Pisum sativum</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_01218.1.g24709.t1	gb|AAD20714.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	357	1750	4.00E-40	490.2	28.0	39.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	357	336	4.00E-35	94.1	19.9	27.7
Rsa1.0_01219.1.g24710.t1	gb|EOA21965.1| hypothetical protein CARUB_v10002464mg [Capsella rubella]	219	201	9.00E-42	91.8	48.9	57.5	hypothetical protein CARUB_v10002464mg	gbpln	Capsella rubella	AT3G05685.1 | Symbols: | Cystatin/monellin superfamily protein | chr3:1673780-1674908 REVERSE LENGTH=180	219	180	7.00E-29	82.2	33.8	43.4
Rsa1.0_01219.1.g24711.t2	ref|NP_192270.4| metallo-beta-lactamase domain-containing protein [Arabidopsis thaliana] gi|332656944|gb|AEE82344.1| metallo-beta-lactamase domain-containing protein [Arabidopsis thaliana]	307	303	1.00E-116	98.7	66.4	71.3	metallo-beta-lactamase domain-containing protein	gbpln	Arabidopsis thaliana	AT4G03610.1 | Symbols: | Metallo-hydrolase/oxidoreductase superfamily protein | chr4:1605039-1606917 FORWARD LENGTH=303	307	303	1.00E-118	98.7	66.4	71.3
Rsa1.0_01219.1.g24712.t1	ref|NP_192271.1| myosin heavy chain-like protein [Arabidopsis thaliana] gi|4263049|gb|AAD15318.1| hypothetical protein [Arabidopsis thaliana] gi|7270685|emb|CAB77847.1| hypothetical protein [Arabidopsis thaliana] gi|332656946|gb|AEE82346.1| myosin heavy chain-like protein [Arabidopsis thaliana]	307	342	1.00E-129	111.4	78.2	86.6	myosin heavy chain-like protein	gbpln	Arabidopsis thaliana	AT4G03620.1 | Symbols: | myosin heavy chain-related | chr4:1607040-1608665 REVERSE LENGTH=342	307	342	1.00E-132	111.4	78.2	86.6
Rsa1.0_01219.1.g24713.t1	gb|AAD19773.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1169	1335	0	114.2	53.4	68.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1169	1262	1.00E-58	108.0	12.2	19.3
Rsa1.0_01219.1.g24714.t1	ref|XP_002874843.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata] gi|297320680|gb|EFH51102.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata]	320	610	1.00E-121	190.6	65.3	74.7	hypothetical protein ARALYDRAFT_911810	gbpln	Arabidopsis lyrata	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	320	302	1.00E-95	94.4	57.5	70.9
Rsa1.0_01219.1.g24715.t1	gb|EOA21150.1| hypothetical protein CARUB_v10001497mg [Capsella rubella]	296	315	4.00E-92	106.4	60.1	70.9	hypothetical protein CARUB_v10001497mg	gbpln	Capsella rubella	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	296	302	2.00E-91	102.0	60.5	72.6
Rsa1.0_01219.1.g24716.t1	ref|XP_002874843.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata] gi|297320680|gb|EFH51102.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata]	108	610	1.00E-25	564.8	54.6	61.1	hypothetical protein ARALYDRAFT_911810	gbpln	Arabidopsis lyrata	AT4G05475.1 | Symbols: | RNI-like superfamily protein | chr4:2765962-2767957 REVERSE LENGTH=309	108	309	2.00E-28	286.1	51.9	59.3
Rsa1.0_01219.1.g24717.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1917	1142	0	59.6	27.7	37.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1917	575	1.00E-73	30.0	8.8	14.6
Rsa1.0_01219.1.g24718.t1	ref|XP_002874843.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata] gi|297320680|gb|EFH51102.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata]	283	610	1.00E-110	215.5	69.3	78.8	hypothetical protein ARALYDRAFT_911810	gbpln	Arabidopsis lyrata	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	283	302	2.00E-88	106.7	56.9	67.8
Rsa1.0_01219.1.g24719.t1	gb|EOA21150.1| hypothetical protein CARUB_v10001497mg [Capsella rubella]	336	315	3.00E-98	93.8	58.6	71.1	hypothetical protein CARUB_v10001497mg	gbpln	Capsella rubella	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	336	302	1.00E-89	89.9	53.0	60.4
Rsa1.0_01219.1.g24720.t2	gb|AAM62925.1| MFDX2 precursor [Arabidopsis thaliana]	151	197	1.00E-18	130.5	29.1	30.5	MFDX2 precursor	gbpln	Arabidopsis thaliana	AT4G05450.1 | Symbols: ATMFDX1, MFDX1 | mitochondrial ferredoxin 1 | chr4:2759048-2760634 FORWARD LENGTH=197	151	197	4.00E-21	130.5	29.1	30.5
Rsa1.0_01219.1.g24721.t1	gb|EOA21150.1| hypothetical protein CARUB_v10001497mg [Capsella rubella]	293	315	1.00E-95	107.5	61.4	72.7	hypothetical protein CARUB_v10001497mg	gbpln	Capsella rubella	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	293	302	1.00E-88	103.1	60.8	69.3
Rsa1.0_01219.1.g24722.t1	#	#	#	#	#	#	#	-	----	----	AT4G05450.1 | Symbols: ATMFDX1, MFDX1 | mitochondrial ferredoxin 1 | chr4:2759048-2760634 FORWARD LENGTH=197	70	197	2.00E-11	281.4	45.7	51.4
Rsa1.0_01220.1.g24723.t1	#	#	#	#	#	#	#	-	----	----	AT1G09210.1 | Symbols: CRT1b, AtCRT1b | calreticulin 1b | chr1:2973217-2976655 REVERSE LENGTH=424	95	424	4.00E-11	446.3	32.6	33.7

Rsa1.0_01220.1.g24724.t1	gb|AAG33975.1|AF250961_1 methionine aminopeptidase-like protein [Arabidopsis thaliana]	329	369	1.00E-29	112.2	19.5	19.5	methionine aminopeptidase-like protein	gbpln	Arabidopsis thaliana	AT1G13270.1 | Symbols: MAP1C, MAP1B | methionine aminopeptidase 1B | chr1:4544999-4547155 FORWARD LENGTH=369	329	369	2.00E-31	112.2	18.8	19.5
Rsa1.0_01220.1.g24725.t1	ref|NP_199923.1| Fe superoxide dismutase 2 [Arabidopsis thaliana] gi|75264241|sp|Q9LU64.1|SODF2_ARATH RecName: Full=Superoxide dismutase [Fe] 2, chloroplastic; AltName: Full=Protein ALBINO OR PALE GREEN 8; AltName: Full=Protein FE SUPEROXIDE DISMUTASE 2; Flags: Precursor gi|8843846|dbj|BAA97372.1| unnamed protein product [Arabidopsis thaliana] gi|21537292|gb|AAM61633.1| Fe-superoxide dismutase precursor [Arabidopsis thaliana] gi|28393352|gb|AAO42100.1| putative iron superoxide dismutase [Arabidopsis thaliana] gi|28827610|gb|AAO50649.1| putative iron superoxide dismutase [Arabidopsis thaliana] gi|110737010|dbj|BAF00460.1| hypothetical protein [Arabidopsis thaliana] gi|332008651|gb|AED96034.1| Fe superoxide dismutase 2 [Arabidopsis thaliana]	298	305	1.00E-148	102.3	85.2	89.3	Fe superoxide dismutase 2	gbpln	Arabidopsis thaliana	AT5G51100.1 | Symbols: FSD2 | Fe superoxide dismutase 2 | chr5:20773357-20775635 REVERSE LENGTH=305	298	305	1.00E-150	102.3	85.2	89.3
Rsa1.0_01220.1.g24726.t1	gb|AFA43307.1| FRIGIDA-like protein [Brassica napus]	604	583	0	96.5	76.7	83.8	FRIGIDA-like protein	gbpln	Brassica napus	AT4G00650.1 | Symbols: FRI, FLA | FRIGIDA-like protein | chr4:269026-270363 FORWARD LENGTH=314	604	314	9.00E-84	52.0	27.6	34.4
Rsa1.0_01220.1.g24727.t1	dbj|BAJ34087.1| unnamed protein product [Thellungiella halophila]	933	950	0	101.8	91.0	94.9	unnamed protein product	----	----	AT5G51070.1 | Symbols: ERD1, CLPD, SAG15 | Clp ATPase | chr5:20764479-20768481 FORWARD LENGTH=945	933	945	0	101.3	90.6	94.2
Rsa1.0_01220.1.g24728.t1	ref|XP_002865839.1| hypothetical protein ARALYDRAFT_495172 [Arabidopsis lyrata subsp. lyrata] gi|297311674|gb|EFH42098.1| hypothetical protein ARALYDRAFT_495172 [Arabidopsis lyrata subsp. lyrata]	917	906	0	98.8	91.7	95.4	hypothetical protein ARALYDRAFT_495172	gbpln	Arabidopsis lyrata	AT5G51060.1 | Symbols: RHD2, ATRBOHC, RBOHC | NADPH/respiratory burst oxidase protein D | chr5:20757484-20762175 REVERSE LENGTH=905	917	905	0	98.7	91.6	95.2
Rsa1.0_01220.1.g24729.t1	gb|AFJ66164.1| hypothetical protein 11M19.8 [Arabidopsis halleri]	310	314	1.00E-168	101.3	92.3	96.8	hypothetical protein 11M19.8	gbpln	Arabidopsis halleri	AT5G51030.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:20747862-20749352 REVERSE LENGTH=314	310	314	1.00E-171	101.3	92.3	96.5
Rsa1.0_01220.1.g24730.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01220.1.g24731.t9	gb|EOA26503.1| hypothetical protein CARUB_v10022552mg [Capsella rubella]	1735	1043	0	60.1	28.4	31.2	hypothetical protein CARUB_v10022552mg	gbpln	Capsella rubella	AT2G31660.1 | Symbols: SAD2, URM9 | ARM repeat superfamily protein | chr2:13464519-13471353 FORWARD LENGTH=1040	1735	1040	0	59.9	27.8	30.8
Rsa1.0_01220.1.g24732.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01220.1.g24733.t1	ref|NP_199903.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|9758237|dbj|BAB08736.1| unnamed protein product [Arabidopsis thaliana] gi|58652072|gb|AAW80861.1| At5g50900 [Arabidopsis thaliana] gi|190576485|gb|ACE79043.1| At5g50900 [Arabidopsis thaliana] gi|332008624|gb|AED96007.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	553	555	0	100.4	75.9	88.1	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G50900.1 | Symbols: | ARM repeat superfamily protein | chr5:20705051-20706718 REVERSE LENGTH=555	553	555	0	100.4	75.9	88.1
Rsa1.0_01220.1.g24734.t2	ref|XP_002865827.1| ubiquitin-conjugating enzyme 26 [Arabidopsis lyrata subsp. lyrata] gi|297311662|gb|EFH42086.1| ubiquitin-conjugating enzyme 26 [Arabidopsis lyrata subsp. lyrata]	187	192	3.00E-98	102.7	93.0	98.9	ubiquitin-conjugating enzyme 26	gbpln	Arabidopsis lyrata	AT5G50870.1 | Symbols: UBC27 | ubiquitin-conjugating enzyme 27 | chr5:20699626-20700998 REVERSE LENGTH=192	187	192	1.00E-100	102.7	92.5	97.9
Rsa1.0_01220.1.g24735.t1	ref|NP_199899.1| protein kinase family protein [Arabidopsis thaliana] gi|8953767|dbj|BAA98122.1| cyclin-dependent protein kinase-like [Arabidopsis thaliana] gi|332008619|gb|AED96002.1| protein kinase family protein [Arabidopsis thaliana]	578	580	0	100.3	81.0	86.2	protein kinase family protein	gbpln	Arabidopsis thaliana	AT5G50860.1 | Symbols: | Protein kinase superfamily protein | chr5:20693778-20696983 REVERSE LENGTH=580	578	580	0	100.3	81.0	86.2
Rsa1.0_01220.1.g24736.t1	dbj|BAJ34206.1| unnamed protein product [Thellungiella halophila]	367	366	0	99.7	97.8	98.9	unnamed protein product	----	----	AT5G50850.1 | Symbols: MAB1 | Transketolase family protein | chr5:20689671-20692976 FORWARD LENGTH=363	367	363	0	98.9	95.6	97.8

Rsa1.0_01220.1.g24737.t1	gb|EOA14605.1| hypothetical protein CARUB_v10027856mg [Capsella rubella]	410	406	1.00E-178	99.0	83.7	91.0	hypothetical protein CARUB_v10027856mg	gbpln	Capsella rubella	AT5G50840.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Taxilin (InterPro:IPR019132); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:20685903-20688739 FORWARD LENGTH=404	410	404	1.00E-176	98.5	83.2	89.8
Rsa1.0_01220.1.g24738.t1	gb|EOA14430.1| hypothetical protein CARUB_v10027633mg [Capsella rubella]	278	268	3.00E-86	96.4	68.7	77.7	hypothetical protein CARUB_v10027633mg	gbpln	Capsella rubella	AT5G50830.2 | Symbols: | unknown protein; Has 4750 Blast hits to 3160 proteins in 341 species: Archae - 14; Bacteria - 239; Metazoa - 1329; Fungi - 394; Plants - 197; Viruses - 79; Other Eukaryotes - 2498 (source: NCBI BLink). | chr5:20683452-20684549 FORWARD LENGTH=282	278	282	1.00E-82	101.4	69.8	80.6
Rsa1.0_01220.1.g24739.t2	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1633	1529	1.00E-170	93.6	27.1	41.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1633	626	4.00E-62	38.3	8.2	13.7
Rsa1.0_01220.1.g24740.t1	gb|EOA14264.1| hypothetical protein CARUB_v10027424mg, partial [Capsella rubella]	75	103	3.00E-26	137.3	76.0	89.3	hypothetical protein CARUB_v10027424mg, partial	gbpln	Capsella rubella	AT5G50810.1 | Symbols: TIM8 | translocase inner membrane subunit 8 | chr5:20675875-20676505 REVERSE LENGTH=77	75	77	2.00E-22	102.7	72.0	88.0
Rsa1.0_01220.1.g24741.t1	ref|XP_002865823.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297311658|gb|EFH42082.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	289	289	1.00E-140	100.0	84.8	91.7	nodulin MtN3 family protein	gbpln	Arabidopsis lyrata	AT5G50790.1 | Symbols: SWEET10, AtSWEET10 | Nodulin MtN3 family protein | chr5:20656461-20657827 REVERSE LENGTH=289	289	289	1.00E-142	100.0	84.4	92.0
Rsa1.0_01220.1.g24742.t1	ref|XP_002864076.1| hypothetical protein ARALYDRAFT_495140 [Arabidopsis lyrata subsp. lyrata] gi|297309911|gb|EFH40335.1| hypothetical protein ARALYDRAFT_495140 [Arabidopsis lyrata subsp. lyrata]	759	804	0	105.9	75.1	84.6	hypothetical protein ARALYDRAFT_495140	gbpln	Arabidopsis lyrata	AT5G50780.1 | Symbols: | Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein | chr5:20650269-20654948 FORWARD LENGTH=819	759	819	0	107.9	74.2	84.8
Rsa1.0_01220.1.g24743.t1	gb|EOA14070.1| hypothetical protein CARUB_v10027207mg [Capsella rubella]	179	184	8.00E-51	102.8	67.0	79.3	hypothetical protein CARUB_v10027207mg	gbpln	Capsella rubella	AT5G50760.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:20644780-20645331 FORWARD LENGTH=183	179	183	5.00E-51	102.2	68.7	81.6
Rsa1.0_01221.1.g24744.t1	gb|EOA33975.1| hypothetical protein CARUB_v10021470mg [Capsella rubella]	682	688	0	100.9	88.4	94.4	hypothetical protein CARUB_v10021470mg	gbpln	Capsella rubella	AT1G71460.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:26928247-26930316 REVERSE LENGTH=689	682	689	0	101.0	87.4	93.4
Rsa1.0_01221.1.g24745.t1	gb|EOA34774.1| hypothetical protein CARUB_v10022349mg [Capsella rubella]	183	182	4.00E-82	99.5	83.6	89.1	hypothetical protein CARUB_v10022349mg	gbpln	Capsella rubella	AT1G71450.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:26927088-26927639 FORWARD LENGTH=183	183	183	2.00E-78	100.0	78.7	85.2
Rsa1.0_01221.1.g24746.t1	ref|XP_002888837.1| hypothetical protein ARALYDRAFT_476275 [Arabidopsis lyrata subsp. lyrata] gi|297334678|gb|EFH65096.1| hypothetical protein ARALYDRAFT_476275 [Arabidopsis lyrata subsp. lyrata]	526	531	0	101.0	82.7	91.1	hypothetical protein ARALYDRAFT_476275	gbpln	Arabidopsis lyrata	AT1G71440.1 | Symbols: PFI, TFC E | tubulin folding cofactor E / Pfifferling (PFI) | chr1:26921271-26924373 REVERSE LENGTH=531	526	531	0	101.0	82.7	90.1
Rsa1.0_01221.1.g24747.t1	ref|XP_002887373.1| hypothetical protein ARALYDRAFT_894991 [Arabidopsis lyrata subsp. lyrata] gi|297333214|gb|EFH63632.1| hypothetical protein ARALYDRAFT_894991 [Arabidopsis lyrata subsp. lyrata]	141	163	2.00E-16	115.6	39.7	46.8	hypothetical protein ARALYDRAFT_894991	gbpln	Arabidopsis lyrata	AT1G71430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 64 Blast hits to 64 proteins in 28 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 6; Plants - 42; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:26920564-26921058 FORWARD LENGTH=164	141	164	1.00E-15	116.3	55.3	68.1
Rsa1.0_01221.1.g24748.t1	gb|EOA33249.1| hypothetical protein CARUB_v10021914mg [Capsella rubella]	1647	914	0	55.5	48.9	50.9	hypothetical protein CARUB_v10021914mg	gbpln	Capsella rubella	AT1G71410.1 | Symbols: | ARM repeat superfamily protein | chr1:26913070-26917515 REVERSE LENGTH=909	1647	909	0	55.2	49.1	51.1
Rsa1.0_01221.1.g24749.t1	ref|XP_002887372.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata] gi|297333213|gb|EFH63631.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata]	797	832	0	104.4	66.5	77.8	hypothetical protein ARALYDRAFT_476271	gbpln	Arabidopsis lyrata	AT1G71400.1 | Symbols: AtRLP12, RLP12 | receptor like protein 12 | chr1:26909905-26912448 FORWARD LENGTH=847	797	847	0	106.3	64.6	76.4

Rsa1.0_01221.1.g24750.t1	ref|XP_002887372.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata] gi|297333213|gb|EFH63631.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata]	814	832	0	102.2	64.6	76.0	hypothetical protein ARALYDRAFT_476271	gbpln	Arabidopsis lyrata	AT1G71400.1 | Symbols: AtRLP12, RLP12 | receptor like protein 12 | chr1:26909905-26912448 FORWARD LENGTH=847	814	847	0	104.1	62.8	75.7
Rsa1.0_01221.1.g24751.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01221.1.g24752.t1	ref|NP_177294.1| endoglucanase 9 [Arabidopsis thaliana] gi|75169715|sp|Q9C9H5.1|GUN9_ARATH RecName: Full=Endoglucanase 9; AltName: Full=Cellulase 3; Short=AtCEL3; AltName: Full=Endo-1,4-beta glucanase 9; Flags: Precursor gi|12323721|gb|AAG51817.1|AC016163_6 putative beta-glucanase; 74324-76084 [Arabidopsis thaliana] gi|111074386|gb|ABH04566.1| At1g71380 [Arabidopsis thaliana] gi|332197074|gb|AEE35195.1| endoglucanase 9 [Arabidopsis thaliana]	484	484	0	100.0	90.1	95.0	endoglucanase 9	gbpln	Arabidopsis thaliana	AT1G71380.1 | Symbols: ATGH9B3, ATCEL3, CEL3 | cellulase 3 | chr1:26899989-26901749 REVERSE LENGTH=484	484	484	0	100.0	90.1	95.0
Rsa1.0_01221.1.g24753.t1	gb|EOA34941.1| hypothetical protein CARUB_v10020025mg [Capsella rubella]	561	592	0	105.5	81.3	87.3	hypothetical protein CARUB_v10020025mg	gbpln	Capsella rubella	AT1G71360.1 | Symbols: | Galactose-binding protein | chr1:26892214-26894166 REVERSE LENGTH=596	561	596	0	106.2	79.7	86.1
Rsa1.0_01221.1.g24754.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01221.1.g24755.t1	ref|NP_177291.2| eukaryotic translation initiation factor SUI1-like protein [Arabidopsis thaliana] gi|110742437|dbj|BAE99137.1| hypothetical protein [Arabidopsis thaliana] gi|332197071|gb|AEE35192.1| eukaryotic translation initiation factor SUI1-like protein [Arabidopsis thaliana]	597	597	0	100.0	87.1	92.8	eukaryotic translation initiation factor SUI1-like protein	gbpln	Arabidopsis thaliana	AT1G71350.1 | Symbols: | eukaryotic translation initiation factor SUI1 family protein | chr1:26888525-26891209 REVERSE LENGTH=597	597	597	0	100.0	87.1	92.8
Rsa1.0_01221.1.g24756.t1	ref|NP_851080.1| serine hydroxymethyltransferase 2 [Arabidopsis thaliana] gi|227202628|dbj|BAH56787.1| AT5G26780 [Arabidopsis thaliana] gi|332006219|gb|AED93602.1| serine hydroxymethyltransferase 2 [Arabidopsis thaliana]	512	517	0	101.0	93.6	97.7	serine hydroxymethyltransferase 2	gbpln	Arabidopsis thaliana	AT5G26780.1 | Symbols: SHM2 | serine hydroxymethyltransferase 2 | chr5:9418299-9421725 FORWARD LENGTH=517	512	517	0	101.0	93.6	97.7
Rsa1.0_01222.1.g24757.t2	gb|EOA20809.1| hypothetical protein CARUB_v10001145mg [Capsella rubella]	393	391	0	99.5	89.1	94.7	hypothetical protein CARUB_v10001145mg	gbpln	Capsella rubella	AT4G12230.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:7284645-7287348 FORWARD LENGTH=392	393	392	0	99.7	89.3	93.9
Rsa1.0_01222.1.g24758.t1	ref|NP_197249.1| putative calcium-binding protein CML32 [Arabidopsis thaliana] gi|75334917|sp|Q9LF55.1|CML32_ARATH RecName: Full=Probable calcium-binding protein CML32; AltName: Full=Calmodulin-like protein 32 gi|9755771|emb|CAC01891.1| calmodulin-like protein [Arabidopsis thaliana] gi|332005048|gb|AED92431.1| putative calcium-binding protein CML32 [Arabidopsis thaliana]	68	146	7.00E-19	214.7	63.2	82.4	putative calcium-binding protein CML32	gbpln	Arabidopsis thaliana	AT5G17470.1 | Symbols: | EF hand calcium-binding protein family | chr5:5760966-5761406 REVERSE LENGTH=146	68	146	1.00E-21	214.7	63.2	82.4
Rsa1.0_01222.1.g24759.t1	gb|EOA19751.1| hypothetical protein CARUB_v10003910mg [Capsella rubella]	239	205	2.00E-29	85.8	29.3	36.0	hypothetical protein CARUB_v10003910mg	gbpln	Capsella rubella	AT4G05350.1 | Symbols: | RING/U-box superfamily protein | chr4:2726910-2727530 REVERSE LENGTH=206	239	206	2.00E-31	86.2	36.4	52.3
Rsa1.0_01222.1.g24760.t1	ref|NP_192950.2| glycine cleavage T-protein family protein [Arabidopsis thaliana] gi|22655070|gb|AAM98126.1| putative protein [Arabidopsis thaliana] gi|30725630|gb|AAP37837.1| At4g12130 [Arabidopsis thaliana] gi|332657699|gb|AEE83099.1| glycine cleavage T-protein family protein [Arabidopsis thaliana]	393	393	0	100.0	91.3	95.4	glycine cleavage T-protein family protein	gbpln	Arabidopsis thaliana	AT4G12130.1 | Symbols: | Glycine cleavage T-protein family | chr4:7263640-7265425 FORWARD LENGTH=393	393	393	0	100.0	91.3	95.4
Rsa1.0_01222.1.g24761.t1	gb|EOA32302.1| hypothetical protein CARUB_v10015564mg [Capsella rubella]	79	799	8.00E-17	1011.4	58.2	60.8	hypothetical protein CARUB_v10015564mg	gbpln	Capsella rubella	AT3G07770.1 | Symbols: Hsp89.1, AtHsp90.6, AtHsp90-6 | HEAT SHOCK PROTEIN 89.1 | chr3:2479611-2483970 FORWARD LENGTH=799	79	799	4.00E-18	1011.4	55.7	58.2
Rsa1.0_01222.1.g24762.t1	gb|AAM08751.1|AC025098_18 Putative copia-type polyprotein [Oryza sativa Japonica Group]	1373	1803	0	131.3	44.7	60.8	Putative copia-type polyprotein	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1373	1262	1.00E-111	91.9	14.1	21.4
Rsa1.0_01222.1.g24763.t1	gb|AAD20433.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	109	889	3.00E-23	815.6	45.9	69.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01222.1.g24764.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01222.1.g24765.t1	ref|XP_002888027.1| hypothetical protein ARALYDRAFT_893244 [Arabidopsis lyrata subsp. lyrata] gi|297333868|gb|EFH64286.1| hypothetical protein ARALYDRAFT_893244 [Arabidopsis lyrata subsp. lyrata]	234	271	5.00E-45	115.8	46.2	61.5	hypothetical protein ARALYDRAFT_893244	gbpln	Arabidopsis lyrata	AT5G57870.1 | Symbols: eIFiso4G1 | MIF4G domain-containing protein / MA3 domain-containing protein | chr5:23439755-23443433 FORWARD LENGTH=780	234	780	1.00E-43	333.3	41.0	52.1
Rsa1.0_01222.1.g24766.t1	ref|NP_567388.1| protein transport sec1b [Arabidopsis thaliana] gi|332278220|sp|Q9SZ77.3|SEC1B_ARATH RecName: Full=Protein transport Sec1b; Short=AtSec1b gi|332657698|gb|AEE83098.1| protein transport sec1b [Arabidopsis thaliana]	776	662	0	85.3	70.4	74.2	protein transport sec1b	gbpln	Arabidopsis thaliana	AT4G12120.1 | Symbols: SEC1B, ATSEC1B | Sec1/munc18-like (SM) proteins superfamily | chr4:7256687-7260914 REVERSE LENGTH=662	776	662	0	85.3	70.4	74.2
Rsa1.0_01223.1.g24767.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	559	1225	8.00E-79	219.1	32.2	47.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	559	575	5.00E-36	102.9	14.8	25.8
Rsa1.0_01223.1.g24768.t1	ref|NP_199856.1| MYND-type zinc finger protein [Arabidopsis thaliana] gi|75171164|sp|Q9FK27.1|FB342_ARATH RecName: Full=F-box protein At5g50450 gi|9758927|dbj|BAB09464.1| unnamed protein product [Arabidopsis thaliana] gi|20466554|gb|AAM20594.1| putative protein [Arabidopsis thaliana] gi|23198134|gb|AAN15594.1| putative protein [Arabidopsis thaliana] gi|332008564|gb|AED95947.1| MYND-type zinc finger protein [Arabidopsis thaliana]	323	336	1.00E-149	104.0	85.4	92.0	MYND-type zinc finger protein	gbpln	Arabidopsis thaliana	AT5G50450.1 | Symbols: | HCP-like superfamily protein with MYND-type zinc finger | chr5:20543519-20544698 REVERSE LENGTH=336	323	336	1.00E-151	104.0	85.4	92.0
Rsa1.0_01223.1.g24769.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01223.1.g24770.t1	gb|EOA15279.1| hypothetical protein CARUB_v10028679mg [Capsella rubella]	74	77	1.00E-24	104.1	81.1	89.2	hypothetical protein CARUB_v10028679mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01223.1.g24771.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	509	530	1.00E-35	104.1	19.4	24.6	predicted protein	gbpln	Arabidopsis lyrata	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	509	530	3.00E-14	104.1	8.6	13.2
Rsa1.0_01223.1.g24772.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1187	1213	0	102.2	36.4	54.3	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1187	626	6.00E-73	52.7	13.4	20.9
Rsa1.0_01223.1.g24773.t1	ref|NP_199853.1| peptide-O-fucosyltransferase [Arabidopsis thaliana] gi|9758924|dbj|BAB09461.1| unnamed protein product [Arabidopsis thaliana] gi|133778858|gb|ABO38769.1| At5g50420 [Arabidopsis thaliana] gi|332008558|gb|AED95941.1| O-fucosyltransferase family protein [Arabidopsis thaliana]	533	566	0	106.2	86.1	91.0	peptide-O-fucosyltransferase	gbpln	Arabidopsis thaliana	AT5G50420.1 | Symbols: | O-fucosyltransferase family protein | chr5:20530453-20532635 REVERSE LENGTH=566	533	566	0	106.2	86.1	91.0
Rsa1.0_01223.1.g24774.t1	ref|NP_199852.1| uncharacterized protein [Arabidopsis thaliana] gi|9758923|dbj|BAB09460.1| unnamed protein product [Arabidopsis thaliana] gi|46931304|gb|AAT06456.1| At5g50410 [Arabidopsis thaliana] gi|332008557|gb|AED95940.1| uncharacterized protein AT5G50410 [Arabidopsis thaliana]	252	259	1.00E-114	102.8	82.5	90.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G50410.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:20528446-20529816 REVERSE LENGTH=259	252	259	1.00E-116	102.8	82.5	90.1
Rsa1.0_01223.1.g24775.t2	#	#	#	#	#	#	#	–	----	----	AT1G21840.1 | Symbols: UREF | urease accessory protein F | chr1:7666859-7667581 FORWARD LENGTH=240	122	240	4.00E-11	196.7	23.0	29.5
Rsa1.0_01223.1.g24776.t1	ref|NP_195555.2| protein SKU5 similar 9 [Arabidopsis thaliana] gi|18176392|gb|AAL60036.1| putative pectinesterase [Arabidopsis thaliana] gi|20465521|gb|AAM20243.1| putative pectinesterase [Arabidopsis thaliana] gi|332661527|gb|AEE86927.1| protein SKU5 similar 9 [Arabidopsis thaliana]	548	549	0	100.2	71.5	81.6	protein SKU5 similar 9	gbpln	Arabidopsis thaliana	AT4G38420.1 | Symbols: sks9 | SKU5 similar 9 | chr4:17982840-17985173 FORWARD LENGTH=549	548	549	0	100.2	71.5	81.6
Rsa1.0_01224.1.g24777.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	317	672	3.00E-29	212.0	27.4	42.6	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01224.1.g24778.t1	gb|ABD65091.1| hypothetical protein 31.t00049 [Brassica oleracea]	85	530	4.00E-11	623.5	41.2	50.6	hypothetical protein 31.t00049	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01224.1.g24779.t1	gb|ABD65163.1| hypothetical protein 40.t00048 [Brassica oleracea]	297	569	6.00E-24	191.6	21.2	29.3	hypothetical protein 40.t00048	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_01224.1.g24780.t2	gb|AAD37019.2| putative non-LTR retrolelement reverse transcriptase [Arabidopsis thaliana]	944	855	0	90.6	40.9	52.6	putative non-LTR retrolelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337-69884 REVERSE LENGTH=515	944	515	1.00E-64	54.6	14.6	18.2
Rsa1.0_01224.1.g24781.t1	gb|AAD14492.1| Hypothetical protein [Arabidopsis thaliana]	96	240	2.00E-15	250.0	45.8	55.2	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01224.1.g24782.t5	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	750	190	7.00E-32	25.3	12.9	14.4	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01224.1.g24783.t1	gb|EOA12473.1| hypothetical protein CARUB_v10025904mg [Capsella rubella]	118	800	4.00E-22	678.0	45.8	55.9	hypothetical protein CARUB_v10025904mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01224.1.g24784.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01225.1.g24785.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	294	441	1.00E-43	150.0	28.2	44.2	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	294	746	6.00E-29	253.7	22.1	31.6
Rsa1.0_01225.1.g24786.t1	ref|NP_179810.1| ethylene-responsive transcription factor ERF056 [Arabidopsis thaliana] gi|75265888|sp|Q9SIE4.1|ERF56_ARATH RecName: Full=Ethylene-responsive transcription factor ERF056 gi|4567204|gb|AAD23620.1| AP2 domain transcription factor [Arabidopsis thaliana] gi|330252183|gb|AEC07277.1| ethylene-responsive transcription factor ERF056 [Arabidopsis thaliana]	210	261	2.00E-77	124.3	70.5	84.3	ethylene-responsive transcription factor ERF056	gbpln	Arabidopsis thaliana	AT2G22200.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr2:9443422-9444207 REVERSE LENGTH=261	210	261	8.00E-80	124.3	70.5	84.3
Rsa1.0_01225.1.g24787.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1358	1413	0	104.1	66.2	79.7	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1358	1262	0	92.9	23.4	30.1
Rsa1.0_01225.1.g24788.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01225.1.g24789.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01225.1.g24790.t2	ref|NP_179809.2| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|75116496|sp|Q67X99.1|TPPE_ARATH RecName: Full=Probable trehalose-phosphate phosphatase E; Short=AtTPPE; AltName: Full=Trehalose 6-phosphate phosphatase gi|51972037|dbj|BAD44683.1| putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana] gi|330252182|gb|AEC07276.1| probable trehalose-phosphate phosphatase E [Arabidopsis thaliana]	320	354	1.00E-157	110.6	86.6	88.8	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G22190.1 | Symbols: TPPE | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:9433897-9436482 REVERSE LENGTH=354	320	354	1.00E-160	110.6	86.6	88.8
Rsa1.0_01225.1.g24791.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	305	1555	3.00E-47	509.8	34.4	50.8	disease resistance protein	gbpln	Brassica rapa	AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315	305	315	4.00E-31	103.3	26.2	36.7
Rsa1.0_01225.1.g24792.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01225.1.g24793.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01226.1.g24794.t1	ref|XP_002893747.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297339589|gb|EFH70006.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	389	399	0	102.6	95.1	96.9	galactosyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G32930.1 | Symbols: | Galactosyltransferase family protein | chr1:11931980-11934399 REVERSE LENGTH=399	389	399	0	102.6	94.3	96.9
Rsa1.0_01226.1.g24795.t1	ref|NP_001031132.1| uncharacterized protein [Arabidopsis thaliana] gi|62320897|dbj|BAD93886.1| hypothetical protein [Arabidopsis thaliana] gi|98962165|gb|ABF59412.1| unknown protein [Arabidopsis thaliana] gi|332193419|gb|AEE31540.1| uncharacterized protein AT1G32928 [Arabidopsis thaliana]	79	84	2.00E-20	106.3	68.4	75.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G32928.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G32920.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:11931332-11931586 FORWARD LENGTH=84	79	84	4.00E-23	106.3	68.4	75.9

Rsa1.0_01226.1.g24796.t1	ref|NP_564411.1| uncharacterized protein [Arabidopsis thaliana] gi|15294268|gb|AAK95311.1|AF410325_1 At1g32920/F9L11_25 [Arabidopsis thaliana] gi|15450637|gb|AAK96590.1| At1g32920/F9L11_25 [Arabidopsis thaliana] gi|20147259|gb|AAM10343.1| At1g32920/F9L11_25 [Arabidopsis thaliana] gi|332193418|gb|AEE31539.1| uncharacterized protein AT1G32920 [Arabidopsis thaliana]	76	78	4.00E-23	102.6	77.6	82.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G32920.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to wounding; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G32928.1); Has 42 Blast hits to 42 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:11928901-11929137 FORWARD LENGTH=78	76	78	6.00E-26	102.6	77.6	82.9
Rsa1.0_01226.1.g24797.t1	ref|XP_002893744.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297339586|gb|EFH70003.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	416	427	0	102.6	83.7	91.6	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT1G32860.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr1:11907308-11908803 REVERSE LENGTH=426	416	426	0	102.4	83.2	92.1
Rsa1.0_01226.1.g24798.t1	ref|XP_002891012.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336854|gb|EFH67271.1| ubiquitin carboxyl-terminal hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	876	894	0	102.1	75.5	85.2	ubiquitin carboxyl-terminal hydrolase family protein	gbpln	Arabidopsis lyrata	AT1G32850.1 | Symbols: UBP11 | ubiquitin-specific protease 11 | chr1:11902629-11906900 FORWARD LENGTH=892	876	892	0	101.8	73.1	83.4
Rsa1.0_01226.1.g24799.t1	ref|NP_200045.1| cytochrome P450, family 96, subfamily A, polypeptide 4 [Arabidopsis thaliana] gi|10177398|dbj|BAB10529.1| cytochrome P450 [Arabidopsis thaliana] gi|332008817|gb|AED96200.1| cytochrome P450, family 96, subfamily A, polypeptide 4 [Arabidopsis thaliana]	461	502	0	108.9	81.1	90.0	cytochrome P450, family 96, subfamily A, polypeptide 4	gbpln	Arabidopsis thaliana	AT5G52320.1 | Symbols: CYP96A4 | cytochrome P450, family 96, subfamily A, polypeptide 4 | chr5:21245111-21246619 REVERSE LENGTH=502	461	502	0	108.9	81.1	90.0
Rsa1.0_01226.1.g24800.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01226.1.g24801.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01226.1.g24802.t1	gb|EOA16028.1| hypothetical protein CARUB_v10004157mg [Capsella rubella]	60	812	4.00E-18	1353.3	70.0	80.0	hypothetical protein CARUB_v10004157mg	gbpln	Capsella rubella	AT4G19960.2 | Symbols: KUP9 | K+ uptake permease 9 | chr4:10813807-10816997 FORWARD LENGTH=807	60	807	2.00E-20	1345.0	71.7	76.7
Rsa1.0_01226.1.g24803.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	368	1142	7.00E-19	310.3	14.4	17.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01227.1.g24804.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01227.1.g24805.t3	ref|NP_190288.1| Glycosyl hydrolase family protein [Arabidopsis thaliana] gi|6522585|emb|CAB61950.1| beta-D-glucan exohydrolase-like protein [Arabidopsis thaliana] gi|332644714|gb|AEE78235.1| Glycosyl hydrolase family protein [Arabidopsis thaliana]	626	636	0	101.6	83.7	91.4	Glycosyl hydrolase family protein	gbpln	Arabidopsis thaliana	AT3G47040.1 | Symbols: | Glycosyl hydrolase family protein | chr3:17324231-17327105 REVERSE LENGTH=636	626	636	0	101.6	83.7	91.4
Rsa1.0_01227.1.g24806.t1	ref|NP_193584.3| uncharacterized protein [Arabidopsis thaliana] gi|357529131|sp|P16128.3|Y4849_ARATH RecName: Full=Uncharacterized protein At4g18490 gi|332658652|gb|AEE84052.1| uncharacterized protein AT4G18490 [Arabidopsis thaliana]	201	756	8.00E-36	376.1	37.3	42.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G18490.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10204388-10208197 FORWARD LENGTH=756	201	756	3.00E-38	376.1	37.3	42.3
Rsa1.0_01227.1.g24807.t4	ref|NP_001078254.1| beta-glucosidase [Arabidopsis thaliana] gi|332644717|gb|AEE78238.1| glycosyl hydrolase family protein [Arabidopsis thaliana]	550	447	3.00E-64	81.3	25.8	29.6	beta-glucosidase	gbpln	Arabidopsis thaliana	AT3G47050.2 | Symbols: | Glycosyl hydrolase family protein | chr3:17328684-17330857 REVERSE LENGTH=447	550	447	6.00E-67	81.3	25.8	29.6
Rsa1.0_01227.1.g24808.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01227.1.g24809.t4	gb|ABD65088.1| hypothetical protein 27.t00109 [Brassica oleracea]	635	1176	1.00E-161	185.2	53.1	61.6	hypothetical protein 27.t00109	gbpln	Brassica oleracea	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	635	452	2.00E-26	71.2	11.7	18.7
Rsa1.0_01227.1.g24810.t1	emb|CAE05256.2| OSJNBb0115I09.18 [Oryza sativa Japonica Group]	511	1134	5.00E-98	221.9	45.0	59.5	OSJNBb0115I09.18	gbpln	Oryza sativa	#	#	#	#	#	#	#

Rsa1.0_01227.1.g24811.t2	ref|NP_190320.1| hydroxysteroid dehydrogenase 3 [Arabidopsis thaliana] gi|75313891|sp|Q9STY7.1|HSD3_ARATH RecName: Full=11-beta-hydroxysteroid dehydrogenase-like 3; AltName: Full=17-beta-hydroxysteroid dehydrogenase-like 3; AltName: Full=Hydroxysteroid dehydrogenase 3; Short=AtHSD3 gi|5541703|emb|CAB51208.1| putative protein [Arabidopsis thaliana] gi|332644749|gb|AEE78270.1| hydroxysteroid dehydrogenase 3 [Arabidopsis thaliana]	251	309	1.00E-36	123.1	31.1	32.7	hydroxysteroid dehydrogenase 3	gbpln	Arabidopsis thaliana	AT3G47360.1 | Symbols: ATHSD3, HSD3 | hydroxysteroid dehydrogenase 3 | chr3:17451112-17452843 FORWARD LENGTH=309	251	309	3.00E-39	123.1	31.1	32.7
Rsa1.0_01227.1.g24812.t1	gb|ABD65100.1| hypothetical protein 31.t00077 [Brassica oleracea]	249	391	1.00E-52	157.0	48.6	58.6	hypothetical protein 31.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01227.1.g24813.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01228.1.g24814.t2	#	#	#	#	#	#	#	-	----	----	AT1G64750.2 | Symbols: ATDSS1(I), DSS1(I) | deletion of SUV3 suppressor 1(I) | chr1:24052787-24053712 REVERSE LENGTH=74	83	74	2.00E-11	89.2	77.1	79.5
Rsa1.0_01228.1.g24815.t1	ref|XP_002866410.1| evolutionary conserved C-terminal 3 [Arabidopsis lyrata subsp. lyrata] gi|297312245|gb|EFH42669.1| evolutionary conserved C-terminal 3 [Arabidopsis lyrata subsp. lyrata]	443	498	1.00E-132	112.4	61.2	72.5	evolutionary conserved C-terminal 3	gbpln	Arabidopsis lyrata	AT5G61020.2 | Symbols: ECT3 | evolutionarily conserved C-terminal region 3 | chr5:24557485-24559780 REVERSE LENGTH=493	443	493	1.00E-127	111.3	59.6	69.5
Rsa1.0_01228.1.g24816.t1	ref|XP_002886783.1| hypothetical protein ARALYDRAFT_475499 [Arabidopsis lyrata subsp. lyrata] gi|297332624|gb|EFH63042.1| hypothetical protein ARALYDRAFT_475499 [Arabidopsis lyrata subsp. lyrata]	1195	1203	0	100.7	81.7	89.7	hypothetical protein ARALYDRAFT_475499	gbpln	Arabidopsis lyrata	AT1G64960.1 | Symbols: | ARM repeat superfamily protein | chr1:24129918-24134049 FORWARD LENGTH=1203	1195	1203	0	100.7	79.9	88.2
Rsa1.0_01228.1.g24817.t1	ref|XP_002887112.1| hypothetical protein ARALYDRAFT_894451 [Arabidopsis lyrata subsp. lyrata] gi|297332953|gb|EFH63371.1| hypothetical protein ARALYDRAFT_894451 [Arabidopsis lyrata subsp. lyrata]	863	1022	0	118.4	56.3	67.9	hypothetical protein ARALYDRAFT_894451	gbpln	Arabidopsis lyrata	AT1G67220.1 | Symbols: HAC02, HAC2, ATHPCAT1 | histone acetyltransferase of the CBP family 2 | chr1:25145587-25150450 FORWARD LENGTH=1367	863	1367	0	158.4	55.7	67.6
Rsa1.0_01228.1.g24818.t2	gb|AAG00256.1|AC002130_21 F1N21.7 [Arabidopsis thaliana]	141	303	1.00E-67	214.9	85.8	93.6	F1N21.7	gbpln	Arabidopsis thaliana	AT1G67250.1 | Symbols: | Proteasome maturation factor UMP1 | chr1:25163808-25164967 REVERSE LENGTH=141	141	141	1.00E-69	100.0	86.5	93.6
Rsa1.0_01228.1.g24819.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	779	1231	0	158.0	48.8	64.3	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	779	575	2.00E-97	73.8	24.8	38.3
Rsa1.0_01228.1.g24820.t1	gb|AEW29768.1| TCP1 [Calepina irregularis]	345	354	1.00E-119	102.6	73.0	82.0	TCP1	gbpln	Calepina irregularis	AT1G67260.2 | Symbols: TCP1 | TCP family transcription factor | chr1:25168152-25169307 REVERSE LENGTH=351	345	351	1.00E-111	101.7	66.7	77.1
Rsa1.0_01228.1.g24821.t7	ref|XP_002888589.1| calmodulin binding protein [Arabidopsis lyrata subsp. lyrata] gi|297334430|gb|EFH64848.1| calmodulin binding protein [Arabidopsis lyrata subsp. lyrata]	1191	1031	0	86.6	57.3	66.1	calmodulin binding protein	gbpln	Arabidopsis lyrata	AT1G67310.1 | Symbols: | Calmodulin-binding transcription activator protein with CG-1 and Ankyrin domains | chr1:25198182-25203126 REVERSE LENGTH=1016	1191	1016	0	85.3	56.5	64.8
Rsa1.0_01229.1.g24822.t1	gb|AAF88013.1| contains similarity to mudrA transposase (GB:AAA21566.1); may be a pseudogene [Arabidopsis thaliana]	222	457	7.00E-26	205.9	37.4	48.6	contains similarity to mudrA transposase (GB:AAA21566.1); may be a pseudogene	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01229.1.g24823.t1	ref|XP_002884160.1| hypothetical protein ARALYDRAFT_900287 [Arabidopsis lyrata subsp. lyrata] gi|297330000|gb|EFH60419.1| hypothetical protein ARALYDRAFT_900287 [Arabidopsis lyrata subsp. lyrata]	507	511	0	100.8	92.7	96.1	hypothetical protein ARALYDRAFT_900287	gbpln	Arabidopsis lyrata	AT2G16280.1 | Symbols: KCS9 | 3-ketoacyl-CoA synthase 9 | chr2:7051186-7052724 FORWARD LENGTH=512	507	512	0	101.0	92.7	96.3
Rsa1.0_01229.1.g24824.t2	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1203	1529	0	127.1	39.7	54.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1203	626	3.00E-35	52.0	9.9	16.5
Rsa1.0_01229.1.g24825.t1	gb|AAG50886.1|AC025294_24 hypothetical protein [Arabidopsis thaliana]	358	629	3.00E-64	175.7	31.3	47.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	358	746	3.00E-43	208.4	24.6	33.8
Rsa1.0_01229.1.g24826.t1	ref|XP_002884163.1| 3-ketoacyl-CoA synthase [Arabidopsis lyrata subsp. lyrata] gi|297330003|gb|EFH60422.1| 3-ketoacyl-CoA synthase [Arabidopsis lyrata subsp. lyrata]	386	486	0	125.9	85.0	91.5	3-ketoacyl-CoA synthase	gbpln	Arabidopsis lyrata	AT4G34520.1 | Symbols: FAE1, KCS18 | 3-ketoacyl-CoA synthase 18 | chr4:16494205-16495725 FORWARD LENGTH=506	386	506	1.00E-176	131.1	74.4	86.0

Rsa1.0_01229.1.g24827.t1	ref|WP_001871707.1| hypothetical protein [Streptococcus agalactiae] gi|77173851|gb|EAO76897.1| hypothetical protein SAI_2423 [Streptococcus agalactiae H36B]	164	181	2.00E-31	110.4	44.5	53.0	hypothetical protein	gbbct	Streptococcus agalactiae	#	#	#	#	#	#	#
Rsa1.0_01229.1.g24828.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01229.1.g24829.t1	gb|AAG50553.1|AC074228_8 En/Spm-like transposon protein, putative [Arabidopsis thaliana]	168	1074	3.00E-33	639.3	38.1	51.2	En/Spm-like transposon protein, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01229.1.g24830.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01230.1.g24831.t1	ref|XP_002866380.1| hypothetical protein ARALYDRAFT_496184 [Arabidopsis lyrata subsp. lyrata] gi|297312215|gb|EFH42639.1| hypothetical protein ARALYDRAFT_496184 [Arabidopsis lyrata subsp. lyrata]	97	94	4.00E-24	96.9	67.0	78.4	hypothetical protein ARALYDRAFT_496184	gbpln	Arabidopsis lyrata	AT5G60400.3 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:24291385-24291754 REVERSE LENGTH=91	97	91	2.00E-23	93.8	67.0	77.3
Rsa1.0_01230.1.g24832.t1	gb|ACS68201.1| elongation factor 1 alpha [Brassica napus] gi|482513961|gb|AGK07381.1| elongation factor 1-alpha protein [Brassica oleracea var. botrytis]	293	449	1.00E-160	153.2	92.8	93.2	elongation factor 1 alpha	gbpln	Brassica napus	AT5G60390.3 | Symbols: | GTP binding Elongation factor Tu family protein | chr5:24289226-24290675 FORWARD LENGTH=449	293	449	1.00E-162	153.2	92.2	93.2
Rsa1.0_01230.1.g24833.t1	ref|XP_002866380.1| hypothetical protein ARALYDRAFT_496184 [Arabidopsis lyrata subsp. lyrata] gi|297312215|gb|EFH42639.1| hypothetical protein ARALYDRAFT_496184 [Arabidopsis lyrata subsp. lyrata]	72	94	1.00E-11	130.6	59.7	73.6	hypothetical protein ARALYDRAFT_496184	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01230.1.g24834.t1	gb|ACS68201.1| elongation factor 1 alpha [Brassica napus] gi|482513961|gb|AGK07381.1| elongation factor 1-alpha protein [Brassica oleracea var. botrytis]	238	449	6.00E-88	188.7	71.0	71.0	elongation factor 1 alpha	gbpln	Brassica napus	AT5G60390.3 | Symbols: | GTP binding Elongation factor Tu family protein | chr5:24289226-24290675 FORWARD LENGTH=449	238	449	2.00E-89	188.7	69.7	71.0
Rsa1.0_01230.1.g24835.t1	ref|NP_200845.1| uncharacterized protein [Arabidopsis thaliana] gi|75171272|sp|Q9FKK6.1|EXO5_ARATH RecName: Full=Exonuclease V, chloroplastic; Short=Exo V; Flags: Precursor gi|9757741|dbj|BAB08222.1| unnamed protein product [Arabidopsis thaliana] gi|18175767|gb|AAL59924.1| unknown protein [Arabidopsis thaliana] gi|23296592|gb|AAN13127.1| unknown protein [Arabidopsis thaliana] gi|332009933|gb|AED97316.1| uncharacterized protein AT5G60370 [Arabidopsis thaliana]	407	413	1.00E-175	101.5	80.3	90.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G60370.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Defects-in-morphology protein 1-like, mitochondrial (InterPro:IPR019190); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G57110.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:24282858-24284760 FORWARD LENGTH=413	407	413	1.00E-177	101.5	80.3	90.4
Rsa1.0_01230.1.g24836.t1	dbj|BAJ34286.1| unnamed protein product [Thellungiella halophila]	358	358	0	100.0	88.3	95.0	unnamed protein product	----	----	AT5G60360.1 | Symbols: SAG2, AALP, ALP | aleurain-like protease | chr5:24280044-24282152 FORWARD LENGTH=358	358	358	0	100.0	86.0	94.7
Rsa1.0_01230.1.g24837.t1	gb|EOA25724.1| hypothetical protein CARUB_v10019078mg [Capsella rubella]	99	168	6.00E-18	169.7	56.6	70.7	hypothetical protein CARUB_v10019078mg	gbpln	Capsella rubella	AT3G45320.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G60330.1); Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:16631646-16632146 FORWARD LENGTH=166	99	166	5.00E-20	167.7	55.6	71.7
Rsa1.0_01230.1.g24838.t1	gb|EOA13014.1| hypothetical protein CARUB_v10026008mg [Capsella rubella]	678	683	0	100.7	77.1	85.4	hypothetical protein CARUB_v10026008mg	gbpln	Capsella rubella	AT5G60300.2 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:24264862-24267018 FORWARD LENGTH=718	678	718	0	105.9	71.8	80.2
Rsa1.0_01230.1.g24839.t1	ref|XP_002864676.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310511|gb|EFH40935.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	665	668	0	100.5	81.1	89.3	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT5G60270.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:24257761-24259767 FORWARD LENGTH=668	665	668	0	100.5	80.6	89.3

Rsa1.0_01230.1.g24840.t1	ref|NP_200829.5| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|334188518|ref|NP_001190579.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|75180396|sp|Q9LSS5.1|ICR3_ARATH RecName: Full=Interactor of constitutive active ROPs 3 gi|8885572|dbj|BAA97502.1| myosin heavy chain-like [Arabidopsis thaliana] gi|332009910|gb|AED97293.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana] gi|332009911|gb|AED97294.1| interactor of constitutive active ROPs 3 [Arabidopsis thaliana]	549	564	0	102.7	86.3	92.5	interactor of constitutive active ROPs 3	gbpln	Arabidopsis thaliana	AT5G60210.2 | Symbols: RIP5 | ROP interactive partner 5 | chr5:24243529-24245889 REVERSE LENGTH=564	549	564	0	102.7	86.3	92.5
Rsa1.0_01230.1.g24841.t1	gb|EOA13642.1| hypothetical protein CARUB_v10026713mg [Capsella rubella]	236	344	1.00E-109	145.8	85.2	90.7	hypothetical protein CARUB_v10026713mg	gbpln	Capsella rubella	AT5G60200.1 | Symbols: TMO6 | TARGET OF MONOPTEROS 6 | chr5:24241078-24241951 FORWARD LENGTH=257	236	257	1.00E-108	108.9	83.5	88.1
Rsa1.0_01231.1.g24842.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	240	1529	3.00E-19	637.1	30.8	46.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01231.1.g24843.t1	ref|XP_004133751.1| PREDICTED: cytochrome c1-1, heme protein, mitochondrial-like [Cucumis sativus] gi|449478083|ref|XP_004155217.1| PREDICTED: cytochrome c1-1, heme protein, mitochondrial-like [Cucumis sativus]	203	307	9.00E-80	151.2	77.3	79.8	PREDICTED: cytochrome c1-1, heme protein, mitochondrial-like	gbpln	Cucumis sativus	AT5G40810.1 | Symbols: | Cytochrome C1 family | chr5:16340200-16342327 FORWARD LENGTH=307	203	307	3.00E-71	151.2	80.3	80.8
Rsa1.0_01231.1.g24844.t1	ref|NP_178356.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|3184287|gb|AAC18934.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana] gi|330250497|gb|AEC05591.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	178	211	2.00E-30	118.5	34.3	46.6	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT2G02520.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr2:676771-678145 REVERSE LENGTH=211	178	211	8.00E-33	118.5	34.3	46.6
Rsa1.0_01231.1.g24845.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01231.1.g24846.t1	ref|NP_198896.1| uncharacterized protein [Arabidopsis thaliana] gi|10177959|dbj|BAB11342.1| unnamed protein product [Arabidopsis thaliana] gi|91805685|gb|ABE65571.1| hypothetical protein At5g40800 [Arabidopsis thaliana] gi|332007213|gb|AED94596.1| uncharacterized protein AT5G40800 [Arabidopsis thaliana]	277	272	1.00E-126	98.2	82.3	87.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G40800.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27250.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:16334810-16335628 REVERSE LENGTH=272	277	272	1.00E-129	98.2	82.3	87.0
Rsa1.0_01231.1.g24847.t1	ref|XP_002868637.1| hypothetical protein ARALYDRAFT_916149 [Arabidopsis lyrata subsp. lyrata] gi|297314473|gb|EFH44896.1| hypothetical protein ARALYDRAFT_916149 [Arabidopsis lyrata subsp. lyrata]	314	304	1.00E-106	96.8	65.6	75.2	hypothetical protein ARALYDRAFT_916149	gbpln	Arabidopsis lyrata	AT5G40790.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27250.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:16330115-16331026 REVERSE LENGTH=303	314	303	1.00E-106	96.5	65.3	75.8
Rsa1.0_01231.1.g24848.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	131	1223	5.00E-47	933.6	70.2	77.1	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	131	626	4.00E-11	477.9	23.7	33.6
Rsa1.0_01231.1.g24849.t1	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	2115	1044	0	49.4	22.7	30.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G40780.2 | Symbols: | lysine histidine transporter 1 | chr5:16323823-16327082 FORWARD LENGTH=445	2115	445	0	21.0	19.4	20.4
Rsa1.0_01232.1.g24850.t1	ref|XP_004308303.1| PREDICTED: uncharacterized protein LOC101292460 [Fragaria vesca subsp. vesca]	75	689	1.00E-14	918.7	65.3	70.7	PREDICTED: uncharacterized protein LOC101292460	gbpln	Fragaria vesca	#	#	#	#	#	#	#
Rsa1.0_01232.1.g24851.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	235	1715	2.00E-31	729.8	37.0	45.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01232.1.g24852.t1	ref|NP_180995.1| 60S ribosomal protein L18a-2 [Arabidopsis thaliana] gi|297826909|ref|XP_002881337.1| 60S ribosomal protein L18A [Arabidopsis lyrata subsp. lyrata] gi|21431842|sp|P51418.2|R18A2_ARATH RecName: Full=60S ribosomal protein L18a-2 gi|3128228|gb|AAC26708.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|14596031|gb|AAK68743.1| Unknown protein [Arabidopsis thaliana] gi|20197170|gb|AAM14956.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|21539567|gb|AAM53336.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|23197736|gb|AAN15395.1| 60S ribosomal protein L18A [Arabidopsis thaliana] gi|30102898|gb|AAP21367.1| At2g34480 [Arabidopsis thaliana] gi|297327176|gb|EFH57596.1| 60S ribosomal protein L18A [Arabidopsis lyrata subsp. lyrata] gi|330253886|gb|AEC08980.1| 60S ribosomal protein L18a-2 [Arabidopsis thaliana]	191	178	7.00E-97	93.2	89.5	91.6	60S ribosomal protein L18a-2	gbpln	Arabidopsis lyrata	AT2G34480.1 | Symbols: | Ribosomal protein L18ae/LX family protein | chr2:14532916-14534161 REVERSE LENGTH=178	191	178	3.00E-99	93.2	89.5	91.6
Rsa1.0_01232.1.g24853.t1	ref|XP_003604534.1| NBS-containing resistance-like protein [Medicago truncatula] gi|355505589|gb|AES86731.1| NBS-containing resistance-like protein [Medicago truncatula]	218	1302	3.00E-18	597.2	39.9	53.7	NBS-containing resistance-like protein	gbpln	Medicago truncatula	#	#	#	#	#	#	#
Rsa1.0_01232.1.g24854.t1	ref|NP_181002.1| gibberellin 2-beta-dioxygenase 3 [Arabidopsis thaliana] gi|49035761|sp|O64692.1|G2OX3_ARATH RecName: Full=Gibberellin 2-beta-dioxygenase 3; AltName: Full=GA 2-oxidase 3; AltName: Full=Gibberellin 2-beta-hydroxylase 3; AltName: Full=Gibberellin 2-oxidase 3 gi|4678370|emb|CAB41009.1| GA 2-oxidase [Arabidopsis thaliana] gi|20197080|gb|AAM14908.1| putative gibberellin 2-oxidase [Arabidopsis thaliana] gi|330253895|gb|AEC08989.1| gibberellin 2-beta-dioxygenase 3 [Arabidopsis thaliana]	335	335	1.00E-156	100.0	80.0	89.3	gibberellin 2-beta-dioxygenase 3	gbpln	Arabidopsis thaliana	AT2G34555.1 | Symbols: ATGA2OX3, GA2OX3 | gibberellin 2-oxidase 3 | chr2:14557102-14558682 FORWARD LENGTH=335	335	335	1.00E-159	100.0	80.0	89.3
Rsa1.0_01232.1.g24855.t2	ref|XP_002879503.1| hypothetical protein ARALYDRAFT_482419 [Arabidopsis lyrata subsp. lyrata] gi|297325342|gb|EFH55762.1| hypothetical protein ARALYDRAFT_482419 [Arabidopsis lyrata subsp. lyrata]	353	390	1.00E-174	110.5	89.2	93.5	hypothetical protein ARALYDRAFT_482419	gbpln	Arabidopsis lyrata	AT2G34560.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:14560266-14562695 FORWARD LENGTH=393	353	393	1.00E-174	111.3	87.5	92.4
Rsa1.0_01232.1.g24856.t1	ref|NP_181004.2| PIN domain-containing MEE21 protein [Arabidopsis thaliana] gi|21805693|gb|AAM76754.1| hypothetical protein [Arabidopsis thaliana] gi|61742637|gb|AAX55139.1| hypothetical protein At2g34570 [Arabidopsis thaliana] gi|330253898|gb|AEC08992.1| PIN domain-containing MEE21 protein [Arabidopsis thaliana]	283	281	1.00E-128	99.3	78.8	89.4	PIN domain-containing MEE21 protein	gbpln	Arabidopsis thaliana	AT2G34570.1 | Symbols: MEE21 | PIN domain-like family protein | chr2:14563048-14564681 REVERSE LENGTH=281	283	281	1.00E-130	99.3	78.8	89.4
Rsa1.0_01232.1.g24857.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01232.1.g24858.t1	ref|NP_181007.1| protein TIFY 5B [Arabidopsis thaliana] gi|75099146|sp|O64687.1|TIF5B_ARATH RecName: Full=Protein TIFY 5B; AltName: Full=Jasmonate ZIM domain-containing protein 7 gi|3128215|gb|AAC26695.1| hypothetical protein [Arabidopsis thaliana] gi|38454058|gb|AAR20723.1| At2g34600 [Arabidopsis thaliana] gi|38603996|gb|AAR24741.1| At2g34600 [Arabidopsis thaliana] gi|330253903|gb|AEC08997.1| protein TIFY 5B [Arabidopsis thaliana]	121	148	3.00E-20	122.3	55.4	63.6	protein TIFY 5B	gbpln	Arabidopsis thaliana	AT2G34600.1 | Symbols: JAZ7, TIFY5B | jasmonate-zim-domain protein 7 | chr2:14573172-14573718 FORWARD LENGTH=148	121	148	5.00E-23	122.3	55.4	63.6

Rsa1.0_01232.1.g24859.t1	ref|NP_199643.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|8978336|dbj|BAA98189.1| unnamed protein product [Arabidopsis thaliana] gi|332008268|gb|AED95651.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	553	977	1.00E-162	176.7	54.1	70.0	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G48320.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:19581794-19584727 REVERSE LENGTH=977	553	977	1.00E-165	176.7	54.1	70.0
Rsa1.0_01232.1.g24860.t1	gb|EOA26368.1| hypothetical protein CARUB_v10023285mg [Capsella rubella]	428	422	0	98.6	86.4	91.8	hypothetical protein CARUB_v10023285mg	gbpln	Capsella rubella	AT2G34630.2 | Symbols: GPPS, GPS1 | geranyl diphosphate synthase 1 | chr2:14578689-14581632 FORWARD LENGTH=422	428	422	0	98.6	85.7	91.6
Rsa1.0_01232.1.g24861.t1	gb|EOA26331.1| hypothetical protein CARUB_v10025625mg [Capsella rubella]	644	696	0	108.1	84.9	90.7	hypothetical protein CARUB_v10025625mg	gbpln	Capsella rubella	AT2G34670.2 | Symbols: | Protein of unknown function (DUF630 and DUF632) | chr2:14612741-14615231 REVERSE LENGTH=694	644	694	0	107.8	84.3	89.9
Rsa1.0_01233.1.g24862.t1	ref|XP_002882262.1| MYB107 [Arabidopsis lyrata subsp. lyrata] gi|297328102|gb|EFH58521.1| MYB107 [Arabidopsis lyrata subsp. lyrata]	322	322	1.00E-148	100.0	88.5	94.1	MYB107	gbpln	Arabidopsis lyrata	AT3G02940.1 | Symbols: MYB107, AtMYB107 | myb domain protein 107 | chr3:662141-663830 FORWARD LENGTH=321	322	321	1.00E-148	99.7	87.9	92.9
Rsa1.0_01233.1.g24863.t1	gb|EOA29907.1| hypothetical protein CARUB_v10013001mg [Capsella rubella]	553	803	1.00E-138	145.2	62.7	76.1	hypothetical protein CARUB_v10013001mg	gbpln	Capsella rubella	AT3G02930.1 | Symbols: | Plant protein of unknown function (DUF827) | chr3:655306-658319 FORWARD LENGTH=806	553	806	1.00E-133	145.8	64.6	78.1
Rsa1.0_01233.1.g24864.t1	ref|XP_002884345.1| hypothetical protein ARALYDRAFT_477538 [Arabidopsis lyrata subsp. lyrata] gi|297330185|gb|EFH60604.1| hypothetical protein ARALYDRAFT_477538 [Arabidopsis lyrata subsp. lyrata]	307	278	1.00E-138	90.6	78.2	85.0	hypothetical protein ARALYDRAFT_477538	gbpln	Arabidopsis lyrata	AT3G02920.2 | Symbols: RPA32B | Replication protein A, subunit RPA32 | chr3:651844-654189 REVERSE LENGTH=298	307	298	1.00E-140	97.1	77.9	86.0
Rsa1.0_01233.1.g24865.t1	gb|AAM63759.1| unknown [Arabidopsis thaliana]	190	187	8.00E-86	98.4	86.8	89.5	unknown	gbpln	Arabidopsis thaliana	AT3G02910.1 | Symbols: | AIG2-like (avirulence induced gene) family protein | chr3:649986-650549 FORWARD LENGTH=187	190	187	2.00E-87	98.4	86.3	88.4
Rsa1.0_01233.1.g24866.t3	gb|EOA31660.1| hypothetical protein CARUB_v10014865mg [Capsella rubella]	129	128	1.00E-64	99.2	92.2	96.1	hypothetical protein CARUB_v10014865mg	gbpln	Capsella rubella	AT5G16650.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:5463446-5465075 REVERSE LENGTH=128	129	128	4.00E-56	99.2	79.8	86.0
Rsa1.0_01233.1.g24867.t1	gb|EOA33035.1| hypothetical protein CARUB_v10016366mg [Capsella rubella]	1057	1135	0	107.4	56.7	67.2	hypothetical protein CARUB_v10016366mg	gbpln	Capsella rubella	AT5G16680.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:5467534-5472956 REVERSE LENGTH=1311	1057	1311	1.00E-165	124.0	44.0	58.2
Rsa1.0_01233.1.g24868.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01233.1.g24869.t1	ref|NP_186938.1| putative inactive receptor kinase [Arabidopsis thaliana] gi|75186527|sp|Q9M8T0.1|Y3288_ARATH RecName: Full=Probable inactive receptor kinase At3g02880; Flags: Precursor gi|6728973|gb|AAF26971.1|AC018363_16 putative protein kinase [Arabidopsis thaliana] gi|13937228|gb|AAK50106.1|AF372969_1 AT3g02880/F13E7_17 [Arabidopsis thaliana] gi|30102484|gb|AAP21160.1| At3g02880/F13E7_17 [Arabidopsis thaliana] gi|224589555|gb|ACN59311.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332640352|gb|AEE73873.1| putative inactive receptor kinase [Arabidopsis thaliana]	621	627	0	101.0	84.7	91.1	putative inactive receptor kinase	gbpln	Arabidopsis thaliana	AT3G02880.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:634819-636982 FORWARD LENGTH=627	621	627	0	101.0	84.7	91.1
Rsa1.0_01233.1.g24870.t1	ref|NP_566183.1| zinc finger CCCH domain-containing protein 33 [Arabidopsis thaliana] gi|62901378|sp|Q8GXX7.1|C3H33_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 33; Short=AtC3H33; AltName: Full=Zinc finger CCCH domain-containing protein ZFN1 gi|26451016|dbj|BAC42614.1| putative zinc finger protein 1 zfn1 [Arabidopsis thaliana] gi|109134113|gb|ABG25055.1| At3g02830 [Arabidopsis thaliana] gi|332640343|gb|AEE73864.1| zinc finger CCCH domain-containing protein 33 [Arabidopsis thaliana]	386	397	1.00E-172	102.8	79.5	81.6	zinc finger CCCH domain-containing protein 33	gbpln	Arabidopsis thaliana	AT3G02830.1 | Symbols: ZFN1 | zinc finger protein 1 | chr3:614075-615916 FORWARD LENGTH=397	386	397	1.00E-175	102.8	79.5	81.6

Rsa1.0_01234.1.g24871.t1	ref|XP_002885130.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297330970|gb|EFH61389.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	43	362	5.00E-12	841.9	76.7	90.7	F-box family protein	gbpln	Arabidopsis lyrata	AT3G16210.1 | Symbols: | F-box family protein | chr3:5494533-5495615 REVERSE LENGTH=360	43	360	3.00E-14	837.2	74.4	88.4
Rsa1.0_01234.1.g24872.t1	dbj|BAA31452.1| delta-VM23 [Raphanus sativus]	248	248	1.00E-132	100.0	99.6	99.6	delta-VM23	gbpln	Raphanus sativus	AT3G16240.1 | Symbols: DELTA-TIP, TIP2;1, DELTA-TIP1, AQP1, ATTIP2;1 | delta tonoplast integral protein | chr3:5505534-5506788 FORWARD LENGTH=250	248	250	1.00E-129	100.8	96.0	98.8
Rsa1.0_01234.1.g24873.t1	gb|EOA31467.1| hypothetical protein CARUB_v10014651mg [Capsella rubella]	204	205	1.00E-106	100.5	92.6	95.1	hypothetical protein CARUB_v10014651mg	gbpln	Capsella rubella	AT3G16250.1 | Symbols: NDF4 | NDH-dependent cyclic electron flow 1 | chr3:5507091-5508320 REVERSE LENGTH=204	204	204	1.00E-104	100.0	90.2	93.1
Rsa1.0_01234.1.g24874.t1	ref|NP_188247.2| tRNAse Z4 [Arabidopsis thaliana] gi|332642270|gb|AEE75791.1| tRNAse Z4 [Arabidopsis thaliana]	942	942	0	100.0	84.3	89.9	tRNAse Z4	gbpln	Arabidopsis thaliana	AT3G16260.1 | Symbols: TRZ4 | tRNAse Z4 | chr3:5509397-5513118 FORWARD LENGTH=942	942	942	0	100.0	84.3	89.9
Rsa1.0_01234.1.g24875.t1	gb|EOA32412.1| hypothetical protein CARUB_v10015684mg [Capsella rubella]	831	447	0	53.8	38.7	41.8	hypothetical protein CARUB_v10015684mg	gbpln	Capsella rubella	AT3G16270.1 | Symbols: | ENTH/VHS family protein | chr3:5513701-5516540 FORWARD LENGTH=690	831	690	0	83.0	37.5	39.7
Rsa1.0_01234.1.g24876.t1	dbj|BAB01268.1| transcription factor TINY-like protein [Arabidopsis thaliana]	243	254	4.00E-65	104.5	72.0	80.7	transcription factor TINY-like protein	gbpln	Arabidopsis thaliana	AT3G16280.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:5518355-5519065 FORWARD LENGTH=236	243	236	2.00E-67	97.1	72.0	80.7
Rsa1.0_01234.1.g24877.t1	ref|XP_002885132.1| EMB2083 [Arabidopsis lyrata subsp. lyrata] gi|297330972|gb|EFH61391.1| EMB2083 [Arabidopsis lyrata subsp. lyrata]	890	874	0	98.2	84.7	91.1	EMB2083	gbpln	Arabidopsis lyrata	AT3G16290.1 | Symbols: EMB2083 | AAA-type ATPase family protein | chr3:5521187-5524995 REVERSE LENGTH=876	890	876	0	98.4	84.8	91.1
Rsa1.0_01234.1.g24878.t1	ref|NP_566542.1| nuclear pore complex protein Nup53 [Arabidopsis thaliana] gi|2062172|gb|AAB63646.1| unknown protein [Arabidopsis thaliana] gi|9279713|dbj|BAB01270.1| unnamed protein product [Arabidopsis thaliana] gi|21592552|gb|AAM64501.1| unknown [Arabidopsis thaliana] gi|26983840|gb|AAN86172.1| unknown protein [Arabidopsis thaliana] gi|332642275|gb|AEE75796.1| nuclear pore complex protein Nup53 [Arabidopsis thaliana]	568	329	1.00E-158	57.9	51.1	53.9	nuclear pore complex protein Nup53	gbpln	Arabidopsis thaliana	AT3G16310.1 | Symbols: | mitotic phosphoprotein N' end (MPPN) family protein | chr3:5526593-5528106 REVERSE LENGTH=329	568	329	1.00E-161	57.9	51.1	53.9
Rsa1.0_01234.1.g24879.t1	ref|XP_002882998.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297328838|gb|EFH59257.1| binding protein [Arabidopsis lyrata subsp. lyrata]	726	717	0	98.8	78.8	86.9	binding protein	gbpln	Arabidopsis lyrata	AT3G16320.1 | Symbols: CDC27a | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:5529534-5534465 FORWARD LENGTH=717	726	717	0	98.8	78.2	85.8
Rsa1.0_01234.1.g24880.t1	gb|EOA31439.1| hypothetical protein CARUB_v10014623mg [Capsella rubella]	209	210	6.00E-90	100.5	81.3	89.0	hypothetical protein CARUB_v10014623mg	gbpln	Capsella rubella	AT3G16330.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52140.1); Has 109 Blast hits to 109 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 109; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5535263-5535880 FORWARD LENGTH=205	209	205	1.00E-89	98.1	79.4	86.6
Rsa1.0_01235.1.g24881.t2	ref|NP_190777.1| DNA-directed RNA polymerase II subunit RPB11 [Arabidopsis thaliana] gi|3219858|sp|Q38859.1|RPB11_ARATH RecName: Full=DNA-directed RNA polymerase II subunit RPB11; Short=RNA polymerase II subunit B11; AltName: Full=DNA-directed RNA polymerase II 13.6 kDa polypeptide; AltName: Full=DNA-directed RNA polymerase II subunit J gi|881501|gb|AAB02849.1| RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] gi|4678938|emb|CAB41329.1| DNA-directed RNA polymerase II 13.6K chain [Arabidopsis thaliana] gi|29029080|gb|AAO64919.1| At3g52090 [Arabidopsis thaliana] gi|332645368|gb|AEE78889.1| DNA-directed RNA polymerase II subunit RPB11 [Arabidopsis thaliana]	64	116	1.00E-23	181.3	81.3	87.5	DNA-directed RNA polymerase II subunit RPB11	gbpln	Arabidopsis thaliana	AT3G52090.1 | Symbols: ATRPB13.6, NRPB11, NRPD11, NRPE11 | DNA-directed RNA polymerase, RBP11-like | chr3:19318069-19318998 REVERSE LENGTH=116	64	116	2.00E-26	181.3	81.3	87.5
Rsa1.0_01235.1.g24882.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_01235.1.g24883.t1</td><td>gb|EOA39489.1| hypothetical protein CARUB_v10008092mg [Capsella rubella]</td><td>1428</td><td>1401</td><td>0</td><td>98.1</td><td>76.3</td><td>82.8</td><td>hypothetical protein CARUB_v10008092mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G48120.1 | Symbols: | hydrolases;protein serine/threonine phosphatases | chr1:17774238-17779624 REVERSE LENGTH=1340</td><td>1428</td><td>1340</td><td>0</td><td>93.8</td><td>75.6</td><td>82.1</td></tr>
<tr><td>Rsa1.0_01235.1.g24884.t2</td><td>ref|XP_002894096.1| evolutionarily conserved C-terminal region 7 [Arabidopsis lyrata subsp. lyrata] gi|297339938|gb|EFH70355.1| evolutionarily conserved C-terminal region 7 [Arabidopsis lyrata subsp. lyrata]</td><td>645</td><td>647</td><td>0</td><td>100.3</td><td>76.7</td><td>84.5</td><td>evolutionarily conserved C-terminal region 7</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G48110.2 | Symbols: ECT7 | evolutionarily conserved C-terminal region 7 | chr1:17770339-17772806 REVERSE LENGTH=639</td><td>645</td><td>639</td><td>0</td><td>99.1</td><td>74.3</td><td>83.1</td></tr>
<tr><td>Rsa1.0_01235.1.g24885.t1</td><td>ref|XP_002891410.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297337252|gb|EFH67669.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]</td><td>472</td><td>474</td><td>0</td><td>100.4</td><td>89.6</td><td>93.9</td><td>glycoside hydrolase family 28 protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G48100.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:17766921-17769625 FORWARD LENGTH=475</td><td>472</td><td>475</td><td>0</td><td>100.6</td><td>88.6</td><td>92.8</td></tr>
<tr><td>Rsa1.0_01235.1.g24886.t1</td><td>gb|AAD26943.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>362</td><td>1454</td><td>1.00E-148</td><td>401.7</td><td>71.3</td><td>83.7</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>362</td><td>1262</td><td>1.00E-107</td><td>348.6</td><td>51.7</td><td>65.2</td></tr>
<tr><td>Rsa1.0_01235.1.g24887.t4</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01236.1.g24888.t1</td><td>gb|EOA14225.1| hypothetical protein CARUB_v10027381mg [Capsella rubella]</td><td>123</td><td>123</td><td>2.00E-62</td><td>100.0</td><td>97.6</td><td>99.2</td><td>hypothetical protein CARUB_v10027381mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G42890.1 | Symbols: ATSCP2, SCP2 | sterol carrier protein 2 | chr5:17194458-17195910 REVERSE LENGTH=123</td><td>123</td><td>123</td><td>1.00E-64</td><td>100.0</td><td>95.9</td><td>99.2</td></tr>
<tr><td>Rsa1.0_01236.1.g24889.t1</td><td>ref|NP_001190457.1| phosphatidic acid phosphohydrolase 2 [Arabidopsis thaliana] gi|332007495|gb|AED94878.1| phosphatidic acid phosphohydrolase 2 [Arabidopsis thaliana]</td><td>837</td><td>925</td><td>0</td><td>110.5</td><td>76.5</td><td>85.4</td><td>phosphatidic acid phosphohydrolase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G42870.2 | Symbols: PAH2 | phosphatidic acid phosphohydrolase 2 | chr5:17185719-17189681 REVERSE LENGTH=925</td><td>837</td><td>925</td><td>0</td><td>110.5</td><td>76.5</td><td>85.4</td></tr>
<tr><td>Rsa1.0_01236.1.g24890.t1</td><td>gb|EOA13721.1| hypothetical protein CARUB_v10026791mg [Capsella rubella]</td><td>322</td><td>321</td><td>1.00E-141</td><td>99.7</td><td>89.8</td><td>93.2</td><td>hypothetical protein CARUB_v10026791mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G42860.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G45688.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:17183339-17184857 REVERSE LENGTH=320</td><td>322</td><td>320</td><td>1.00E-143</td><td>99.4</td><td>88.2</td><td>92.5</td></tr>
<tr><td>Rsa1.0_01236.1.g24891.t1</td><td>ref|NP_199096.1| Splicing factor U2af small subunit B [Arabidopsis thaliana] gi|42573547|ref|NP_974870.1| Splicing factor U2af small subunit B [Arabidopsis thaliana] gi|75334092|sp|Q9FMY5.1|U2AFB_ARATH RecName: Full=Splicing factor U2af small subunit B; AltName: Full=U2 auxiliary factor 35 kDa subunit B; AltName: Full=U2 small nuclear ribonucleoprotein auxiliary factor small subunit B; Short=U2 snRNP auxiliary factor small subunit B; AltName: Full=Zinc finger CCCH domain-containing protein 60; Short=AtC3H60 gi|10177285|dbj|BAB10638.1| U2 snRNP auxiliary factor, small subunit [Arabidopsis thaliana] gi|22531195|gb|AAM97101.1| U2 snRNP auxiliary factor small subunit [Arabidopsis thaliana] gi|23198022|gb|AAN15538.1| U2 snRNP auxiliary factor small subunit [Arabidopsis thaliana] gi|332007485|gb|AED94868.1| Splicing factor U2af small subunit B [Arabidopsis thaliana] gi|332007486|gb|AED94869.1| Splicing factor U2af small subunit B [Arabidopsis thaliana]</td><td>287</td><td>283</td><td>1.00E-117</td><td>98.6</td><td>85.7</td><td>88.5</td><td>Splicing factor U2af small subunit B</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G42820.1 | Symbols: ATU2AF35B, U2AF35B | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr5:17170445-17171296 REVERSE LENGTH=283</td><td>287</td><td>283</td><td>1.00E-120</td><td>98.6</td><td>85.7</td><td>88.5</td></tr>
</table>

Rsa1.0_01236.1.g24892.t2	ref|NP_568613.1| inositol-pentakisphosphate 2-kinase [Arabidopsis thaliana] gi|75163638|sp|Q93YN9.1|IPPK_ARATH RecName: Full=Inositol-pentakisphosphate 2-kinase; AltName: Full=Inositol-1,3,4,5,6-pentakisphosphate 2-kinase; AltName: Full=Ins(1,3,4,5,6)P5 2-kinase; Short=AtIPK1; Short=InsP5 2-kinase gi|16649057|gb|AAL24380.1| Unknown protein [Arabidopsis thaliana] gi|20260028|gb|AAM13361.1| unknown protein [Arabidopsis thaliana] gi|74100007|gb|AAZ99216.1| inositol polyphosphate IP4/IP5 2-kinase [Arabidopsis thaliana] gi|332007484|gb|AED94867.1| inositol-pentakisphosphate 2-kinase [Arabidopsis thaliana]	600	451	0	75.2	60.5	64.8	inositol-pentakisphosphate 2-kinase	gbpln	Arabidopsis thaliana	AT5G42810.1 | Symbols: ATIPK1, IPK1 | inositol-pentakisphosphate 2-kinase 1 | chr5:17167073-17169337 FORWARD LENGTH=451	600	451	0	75.2	60.5	64.8
Rsa1.0_01236.1.g24893.t1	ref|XP_004241213.1| PREDICTED: protein TOC75-3, chloroplastic-like [Solanum lycopersicum]	84	812	4.00E-12	966.7	44.0	60.7	PREDICTED: protein TOC75-3, chloroplastic-like	gbpln	Solanum lycopersicum	AT4G09080.1 | Symbols: TOC75-IV, ATTOC75-IV | Outer membrane OMP85 family protein | chr4:5804451-5806093 FORWARD LENGTH=396	84	396	2.00E-14	471.4	44.0	59.5
Rsa1.0_01236.1.g24894.t1	gb|ABF00984.1| disease resistance protein RPP13 variant [Arabidopsis thaliana]	871	843	0	96.8	65.0	78.4	disease resistance protein RPP13 variant	gbpln	Arabidopsis thaliana	AT3G46530.1 | Symbols: RPP13 | NB-ARC domain-containing disease resistance protein | chr3:17130739-17133246 REVERSE LENGTH=835	871	835	0	95.9	65.6	77.6
Rsa1.0_01236.1.g24895.t1	gb|ABL86389.1| dihydroflavonol 4-reductase [Brassica juncea] gi|119656083|gb|ABL86390.1| dihydroflavonol 4-reductase [Brassica juncea]	387	385	0	99.5	94.3	96.1	dihydroflavonol 4-reductase	gbpln	Brassica juncea	AT5G42800.1 | Symbols: DFR, TT3, M318 | dihydroflavonol 4-reductase | chr5:17164296-17165864 REVERSE LENGTH=382	387	382	0	98.7	84.5	91.2
Rsa1.0_01236.1.g24896.t1	ref|XP_002891341.1| hypothetical protein ARALYDRAFT_473874 [Arabidopsis lyrata subsp. lyrata] gi|297337183|gb|EFH67600.1| hypothetical protein ARALYDRAFT_473874 [Arabidopsis lyrata subsp. lyrata]	275	277	1.00E-141	100.7	90.9	94.5	hypothetical protein ARALYDRAFT_473874	gbpln	Arabidopsis lyrata	AT1G47250.1 | Symbols: PAF2 | 20S proteasome alpha subunit F2 | chr1:17319220-17320900 FORWARD LENGTH=277	275	277	1.00E-142	100.7	89.8	93.5
Rsa1.0_01236.1.g24897.t1	ref|NP_680381.1| uncharacterized protein [Arabidopsis thaliana] gi|91806976|gb|ABE66215.1| hypothetical protein At5g42785 [Arabidopsis thaliana] gi|332007480|gb|AED94863.1| uncharacterized protein AT5G42785 [Arabidopsis thaliana]	108	115	6.00E-35	106.5	75.0	81.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G42785.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:17157069-17157693 REVERSE LENGTH=115	108	115	9.00E-38	106.5	75.0	81.5
Rsa1.0_01236.1.g24898.t1	ref|XP_002865484.1| ATHB27 [Arabidopsis lyrata subsp. lyrata] gi|297311319|gb|EFH41743.1| ATHB27 [Arabidopsis lyrata subsp. lyrata]	310	242	4.00E-17	78.1	13.9	14.8	ATHB27	gbpln	Arabidopsis lyrata	AT5G42780.1 | Symbols: AtHB27, HB27, ZHD13 | homeobox protein 27 | chr5:17154841-17155569 FORWARD LENGTH=242	310	242	3.00E-19	78.1	15.2	16.5
Rsa1.0_01236.1.g24899.t1	ref|XP_002865485.1| hypothetical protein ARALYDRAFT_331123 [Arabidopsis lyrata subsp. lyrata] gi|297311320|gb|EFH41744.1| hypothetical protein ARALYDRAFT_331123 [Arabidopsis lyrata subsp. lyrata]	212	206	2.00E-92	97.2	82.1	88.2	hypothetical protein ARALYDRAFT_331123	gbpln	Arabidopsis lyrata	AT5G42770.2 | Symbols: | Maf-like protein | chr5:17152147-17154355 FORWARD LENGTH=233	212	233	9.00E-92	109.9	82.5	89.2
Rsa1.0_01236.1.g24900.t1	ref|NP_568612.1| uncharacterized protein [Arabidopsis thaliana] gi|332007476|gb|AED94859.1| uncharacterized protein AT5G42765 [Arabidopsis thaliana]	224	229	2.00E-83	102.2	77.2	88.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G42765.1 | Symbols: | INVOLVED IN: biological_process unknown; LOCATED IN: thylakoid, chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Twin-arginine translocation pathway, signal sequence (InterPro:IPR006311); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:17150505-17151641 REVERSE LENGTH=229	224	229	7.00E-86	102.2	77.2	88.4
Rsa1.0_01236.1.g24901.t1	dbj|BAB17636.1| cytosolic phosphoglucose isomerase [Arabidopsis thaliana]	542	560	0	103.3	95.2	98.3	cytosolic phosphoglucose isomerase	gbpln	Arabidopsis thaliana	AT5G42740.1 | Symbols: | Sugar isomerase (SIS) family protein | chr5:17136080-17140622 FORWARD LENGTH=560	542	560	0	103.3	95.0	98.2

Rsa1.0_01237.1.g24902.t1	ref|NP_568012.1| Remorin family protein [Arabidopsis thaliana] gi|4006876|emb|CAB16794.1| hypothetical protein [Arabidopsis thaliana] gi|7270646|emb|CAB80363.1| hypothetical protein [Arabidopsis thaliana] gi|23297309|gb|AAN12938.1| unknown protein [Arabidopsis thaliana] gi|332661326|gb|AEE86726.1| Remorin family protein [Arabidopsis thaliana]	414	427	1.00E-120	103.1	71.0	78.3	Remorin family protein	gbpln	Arabidopsis thaliana	AT4G36970.1 | Symbols: | Remorin family protein | chr4:17429826-17431459 REVERSE LENGTH=427	414	427	1.00E-122	103.1	71.0	78.3
Rsa1.0_01237.1.g24903.t1	gb|EOA19051.1| hypothetical protein CARUB_v10007712mg [Capsella rubella]	350	346	1.00E-150	98.9	78.0	85.1	hypothetical protein CARUB_v10007712mg	gbpln	Capsella rubella	AT4G36950.1 | Symbols: MAPKKK21 | mitogen-activated protein kinase kinase kinase 21 | chr4:17422834-17423844 REVERSE LENGTH=336	350	336	1.00E-150	96.0	76.6	84.0
Rsa1.0_01237.1.g24904.t1	gb|EOA16859.1| hypothetical protein CARUB_v10005083mg [Capsella rubella]	342	369	1.00E-107	107.9	74.0	82.2	hypothetical protein CARUB_v10005083mg	gbpln	Capsella rubella	AT4G36930.1 | Symbols: SPT | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:17414167-17415945 FORWARD LENGTH=373	342	373	1.00E-108	109.1	75.7	83.0
Rsa1.0_01237.1.g24905.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01237.1.g24906.t1	emb|CAA05084.1| putative Ckc2 [Arabidopsis thaliana]	185	246	5.00E-39	133.0	53.5	61.1	putative Ckc2	gbpln	Arabidopsis thaliana	AT3G16770.1 | Symbols: RAP2.3, ATEBP, ERF72, EBP | ethylene-responsive element binding protein | chr3:5705784-5706768 FORWARD LENGTH=248	185	248	6.00E-40	134.1	51.4	54.1
Rsa1.0_01237.1.g24907.t1	emb|CAA05084.1| putative Ckc2 [Arabidopsis thaliana]	162	246	5.00E-31	151.9	53.1	60.5	putative Ckc2	gbpln	Arabidopsis thaliana	AT3G16770.1 | Symbols: RAP2.3, ATEBP, ERF72, EBP | ethylene-responsive element binding protein | chr3:5705784-5706768 FORWARD LENGTH=248	162	248	2.00E-31	153.1	51.2	53.7
Rsa1.0_01237.1.g24908.t1	dbj|BAJ33685.1| unnamed protein product [Thellungiella halophila]	434	439	0	101.2	92.9	95.2	unnamed protein product	----	----	AT4G36920.2 | Symbols: AP2 | Integrase-type DNA-binding superfamily protein | chr4:17400998-17403140 FORWARD LENGTH=432	434	432	0	99.5	89.6	92.9
Rsa1.0_01237.1.g24909.t1	gb|AAC49776.1| AP2 domain containing protein RAP2.10 [Arabidopsis thaliana] gi|2632063|emb|CAA05630.1| TINY-like protein [Arabidopsis thaliana]	183	259	1.00E-58	141.5	74.9	78.1	AP2 domain containing protein RAP2.10	gbpln	Arabidopsis thaliana	AT4G36900.1 | Symbols: RAP2.10, DEAR4 | related to AP2 10 | chr4:17389015-17389605 FORWARD LENGTH=196	183	196	2.00E-60	107.1	74.9	78.1
Rsa1.0_01237.1.g24910.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1457	1515	0	104.0	56.9	71.3	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1457	1262	1.00E-108	86.6	12.7	20.0
Rsa1.0_01238.1.g24911.t1	gb|EOA31457.1| hypothetical protein CARUB_v10014643mg [Capsella rubella]	174	206	1.00E-57	118.4	65.5	67.2	hypothetical protein CARUB_v10014643mg	gbpln	Capsella rubella	AT3G24830.1 | Symbols: | Ribosomal protein L13 family protein | chr3:9064613-9065871 FORWARD LENGTH=206	174	206	6.00E-60	118.4	65.5	67.2
Rsa1.0_01238.1.g24912.t1	ref|XP_002867884.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313720|gb|EFH44143.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	175	175	2.00E-82	100.0	85.1	92.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G20370.1 | Symbols: TSF | PEBP (phosphatidylethanolamine-binding protein) family protein | chr4:11001011-11002965 REVERSE LENGTH=175	175	175	1.00E-82	100.0	82.9	89.7
Rsa1.0_01238.1.g24913.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	621	530	4.00E-41	85.3	14.2	18.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	621	530	1.00E-13	85.3	6.0	12.1
Rsa1.0_01238.1.g24914.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01238.1.g24915.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01238.1.g24916.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1798	1213	0	67.5	35.0	46.5	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1798	626	1.00E-74	34.8	9.0	14.0
Rsa1.0_01238.1.g24917.t1	dbj|BAJ34070.1| unnamed protein product [Thellungiella halophila]	408	445	0	109.1	89.0	91.7	unnamed protein product	----	----	AT1G76900.2 | Symbols: AtTLP1, TLP1 | tubby like protein 1 | chr1:28882741-28884377 FORWARD LENGTH=455	408	455	0	111.5	87.0	90.7
Rsa1.0_01239.1.g24918.t1	gb|EOA30637.1| hypothetical protein CARUB_v10013773mg [Capsella rubella]	423	425	0	100.5	74.7	83.5	hypothetical protein CARUB_v10013773mg	gbpln	Capsella rubella	AT3G23840.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:8611177-8612559 FORWARD LENGTH=420	423	420	1.00E-177	99.3	73.5	83.7

Rsa1.0_01239.1.g24919.t1	ref|NP_567603.1| cysteine-rich repeat secretory protein 54 [Arabidopsis thaliana] gi|18415520|ref|NP_567604.1| cysteine-rich repeat secretory protein 53 [Arabidopsis thaliana] gi|18415540|ref|NP_567613.1| cysteine-rich repeat secretory protein 44 [Arabidopsis thaliana] gi|5262176|emb|CAB45819.1| putative protein [Arabidopsis thaliana] gi|5262177|emb|CAB45820.1| putative protein [Arabidopsis thaliana] gi|5262178|emb|CAB45821.1| putative protein [Arabidopsis thaliana] gi|5262179|emb|CAB45822.1| putative protein [Arabidopsis thaliana] gi|5262180|emb|CAB45823.1| putative protein [Arabidopsis thaliana] gi|5262181|emb|CAB45824.1| putative protein [Arabidopsis thaliana] gi|5262182|emb|CAB45825.1| putative protein [Arabidopsis thaliana] gi|5262183|emb|CAB45826.1| putative protein [Arabidopsis thaliana] gi|5262184|emb|CAB45827.1| putative protein [Arabidopsis thaliana] gi|5262185|emb|CAB45828.1| putative protein [Arabidopsis thaliana] gi|5262186|emb|CAB45829.1| putative protein [Arabidopsis thaliana] gi|5262187|emb|CAB45830.1| putative protein [Arabidopsis thaliana] gi|7268849|emb|CAB79053.1| putative protein [Arabidopsis thaliana]	100	468	3.00E-17	468.0	46.0	59.0	cysteine-rich repeat secretory protein 54	gbpln	Arabidopsis thaliana	AT4G20530.1 | Symbols: | Protein with domains of unknown function (DUF26 and DUF1204) | chr4:11048627-11050975 FORWARD LENGTH=468	100	468	5.00E-20	468.0	46.0	59.0
Rsa1.0_01239.1.g24920.t1	ref|XP_002868336.1| hypothetical protein ARALYDRAFT_493534 [Arabidopsis lyrata subsp. lyrata] gi|297314172|gb|EFH44595.1| hypothetical protein ARALYDRAFT_493534 [Arabidopsis lyrata subsp. lyrata]	333	336	1.00E-150	100.9	84.1	90.7	hypothetical protein ARALYDRAFT_493534	gbpln	Arabidopsis lyrata	AT3G23870.1 | Symbols: | Protein of unknown function (DUF803) | chr3:8620253-8621755 FORWARD LENGTH=335	333	335	1.00E-152	100.6	90.1	95.8
Rsa1.0_01239.1.g24921.t1	ref|XP_002885602.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297331442|gb|EFH61861.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	369	347	1.00E-173	94.0	81.6	86.7	F-box family protein	gbpln	Arabidopsis lyrata	AT3G23880.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8622061-8623155 REVERSE LENGTH=364	369	364	1.00E-165	98.6	80.5	85.9
Rsa1.0_01239.1.g24922.t1	ref|XP_002885604.1| hypothetical protein ARALYDRAFT_342541 [Arabidopsis lyrata subsp. lyrata] gi|297331444|gb|EFH61863.1| hypothetical protein ARALYDRAFT_342541 [Arabidopsis lyrata subsp. lyrata]	417	421	1.00E-172	101.0	76.3	86.8	hypothetical protein ARALYDRAFT_342541	gbpln	Arabidopsis lyrata	AT3G23910.1 | Symbols: | BEST Arabidopsis thaliana protein match is: RNA-directed DNA polymerase (reverse transcriptase)-related family protein (TAIR:AT3G24255.2); Has 562 Blast hits to 532 proteins in 147 species: Archae - 28; Bacteria - 51; Metazoa - 157; Fungi - 82; Plants - 85; Viruses - 6; Other Eukaryotes - 153 (source: NCBI BLink). | chr3:8636594-8639344 REVERSE LENGTH=421	417	421	1.00E-171	101.0	74.8	86.1
Rsa1.0_01239.1.g24923.t8	ref|XP_002883472.1| hypothetical protein ARALYDRAFT_898937 [Arabidopsis lyrata subsp. lyrata] gi|297329312|gb|EFH59731.1| hypothetical protein ARALYDRAFT_898937 [Arabidopsis lyrata subsp. lyrata]	368	295	1.00E-44	80.2	35.9	50.0	hypothetical protein ARALYDRAFT_898937	gbpln	Arabidopsis lyrata	AT3G24260.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Histone deacetylase interacting (InterPro:IPR013194); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G28870.1); Has 220 Blast hits to 218 proteins in 65 species: Archae - 7; Bacteria - 6; Metazoa - 43; Fungi - 2; Plants - 115; Viruses - 0; Other Eukaryotes - 47 (source: NCBI BLink). | chr3:8793837-8794961 REVERSE LENGTH=374	368	374	7.00E-32	101.6	24.2	34.5
Rsa1.0_01239.1.g24924.t1	ref|XP_002885607.1| hypothetical protein ARALYDRAFT_479903 [Arabidopsis lyrata subsp. lyrata] gi|297331447|gb|EFH61866.1| hypothetical protein ARALYDRAFT_479903 [Arabidopsis lyrata subsp. lyrata]	1135	1140	0	100.4	90.3	93.6	hypothetical protein ARALYDRAFT_479903	gbpln	Arabidopsis lyrata	AT3G24240.1 | Symbols: | Leucine-rich repeat receptor-like protein kinase family protein | chr3:8780551-8784150 FORWARD LENGTH=1141	1135	1141	0	100.5	88.4	92.0
Rsa1.0_01239.1.g24925.t1	emb|CAN66208.1| hypothetical protein VITISV_035070 [Vitis vinifera]	765	1496	0	195.6	65.4	78.4	hypothetical protein VITISV_035070	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	765	1262	7.00E-44	165.0	15.4	25.2
Rsa1.0_01239.1.g24926.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01239.1.g24927.t1	ref|XP_002870357.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata] gi|297316193|gb|EFH46616.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata]	366	484	1.00E-172	132.2	80.3	88.0	pectate lyase family protein	gbpln	Arabidopsis lyrata	AT4G13710.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:7962550-7966012 FORWARD LENGTH=470	366	470	1.00E-175	128.4	80.1	88.0
Rsa1.0_01240.1.g24928.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01240.1.g24929.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1455	1499	0	103.0	60.2	73.3	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1455	158	4.00E-33	10.9	4.5	5.9
Rsa1.0_01240.1.g24930.t2	ref|NP_680393.1| minichromosome maintenance protein 6 [Arabidopsis thaliana] gi|332007758|gb|AED95141.1| minichromosome maintenance protein 6 [Arabidopsis thaliana]	621	831	4.00E-89	133.8	31.6	35.1	minichromosome maintenance protein 6	gbpln	Arabidopsis thaliana	AT5G44635.1 | Symbols: MCM6 | minichromosome maintenance (MCM2/3/5) family protein | chr5:18006431-18010542 REVERSE LENGTH=831	621	831	9.00E-92	133.8	31.6	35.1
Rsa1.0_01240.1.g24931.t20	dbj|BAM44535.1| polyprotein [Arabidopsis thaliana]	282	1475	4.00E-71	523.0	56.0	66.0	polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01240.1.g24932.t1	gb|EOA14735.1| hypothetical protein CARUB_v10028028mg [Capsella rubella]	336	360	1.00E-126	107.1	80.4	89.0	hypothetical protein CARUB_v10028028mg	gbpln	Capsella rubella	AT5G44660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G20190.1); Has 944 Blast hits to 462 proteins in 141 species: Archae - 2; Bacteria - 370; Metazoa - 161; Fungi - 102; Plants - 64; Viruses - 6; Other Eukaryotes - 239 (source: NCBI BLink). | chr5:18015810-18017081 FORWARD LENGTH=423	336	423	1.00E-113	125.9	78.0	86.6
Rsa1.0_01240.1.g24933.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01240.1.g24934.t1	ref|NP_199281.1| DNA-3-methyladenine glycosylase I [Arabidopsis thaliana] gi|9758372|dbj|BAB08821.1| unnamed protein product [Arabidopsis thaliana] gi|28393027|gb|AAO41948.1| unknown protein [Arabidopsis thaliana] gi|28827242|gb|AAO50465.1| unknown protein [Arabidopsis thaliana] gi|332007763|gb|AED95146.1| putative 3-methyladenine glycosylase I [Arabidopsis thaliana]	349	353	1.00E-171	101.1	85.7	90.5	DNA-3-methyladenine glycosylase I	gbpln	Arabidopsis thaliana	AT5G44680.1 | Symbols: | DNA glycosylase superfamily protein | chr5:18024461-18025893 REVERSE LENGTH=353	349	353	1.00E-173	101.1	85.7	90.5
Rsa1.0_01241.1.g24935.t1	ref|XP_002886130.1| early-responsive to dehydration 7 [Arabidopsis lyrata subsp. lyrata] gi|297331970|gb|EFH62389.1| early-responsive to dehydration 7 [Arabidopsis lyrata subsp. lyrata]	453	450	0	99.3	85.4	92.7	early-responsive to dehydration 7	gbpln	Arabidopsis lyrata	AT2G17840.1 | Symbols: ERD7 | Senescence/dehydration-associated protein-related | chr2:7755923-7757798 REVERSE LENGTH=452	453	452	0	99.8	85.4	92.9
Rsa1.0_01241.1.g24936.t1	ref|XP_002886132.1| hypothetical protein ARALYDRAFT_343407 [Arabidopsis lyrata subsp. lyrata] gi|297331972|gb|EFH62391.1| hypothetical protein ARALYDRAFT_343407 [Arabidopsis lyrata subsp. lyrata]	249	298	1.00E-117	119.7	83.9	89.2	hypothetical protein ARALYDRAFT_343407	gbpln	Arabidopsis lyrata	AT2G17860.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr2:7762257-7763018 REVERSE LENGTH=253	249	253	1.00E-116	101.6	81.1	88.4
Rsa1.0_01241.1.g24937.t1	gb|EOA32089.1| hypothetical protein CARUB_v10015336mg [Capsella rubella]	296	310	7.00E-90	104.7	76.7	82.8	hypothetical protein CARUB_v10015336mg	gbpln	Capsella rubella	AT2G17870.1 | Symbols: ATCSP3, CSP3 | cold shock domain protein 3 | chr2:7764276-7765181 REVERSE LENGTH=301	296	301	8.00E-86	101.7	75.0	82.8
Rsa1.0_01241.1.g24938.t1	ref|NP_179379.1| calcium-dependent protein kinase 16 [Arabidopsis thaliana] gi|75327228|sp|Q7XJR9.1|CDPKG_ARATH RecName: Full=Calcium-dependent protein kinase 16 gi|330251605|gb|AEC06699.1| calcium-dependent protein kinase 16 [Arabidopsis thaliana]	574	571	0	99.5	90.8	94.4	calcium-dependent protein kinase 16	gbpln	Arabidopsis thaliana	AT2G17890.1 | Symbols: CPK16 | calcium-dependent protein kinase 16 | chr2:7769885-7772627 REVERSE LENGTH=571	574	571	0	99.5	90.8	94.4
Rsa1.0_01241.1.g24939.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01241.1.g24940.t1	ref|NP_849969.1| histone-lysine N-methyltransferase ASHR1 [Arabidopsis thaliana] gi|94707144|sp|Q7XJS0.2|ASHR1_ARATH RecName: Full=Histone-lysine N-methyltransferase ASHR1; AltName: Full=ASH1-related protein 1; AltName: Full=Protein SET DOMAIN GROUP 37 gi|145651792|gb|ABP88121.1| At2g17900 [Arabidopsis thaliana] gi|330251606|gb|AEC06700.1| histone-lysine N-methyltransferase ASHR1 [Arabidopsis thaliana]	483	480	0	99.4	87.2	93.4	histone-lysine N-methyltransferase ASHR1	gbpln	Arabidopsis thaliana	AT2G17900.1 | Symbols: SDG37 | SET domain group 37 | chr2:7773420-7776675 REVERSE LENGTH=480	483	480	0	99.4	87.2	93.4
Rsa1.0_01241.1.g24941.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01241.1.g24942.t1	gb|EOA31432.1| hypothetical protein CARUB_v10014611mg [Capsella rubella]	210	214	1.00E-67	101.9	70.5	78.1	hypothetical protein CARUB_v10014611mg	gbpln	Capsella rubella	AT2G17940.1 | Symbols: | Plant protein of unknown function (DUF827) | chr2:7802878-7803815 FORWARD LENGTH=208	210	208	2.00E-67	99.0	73.3	78.1
Rsa1.0_01242.1.g24943.t1	gb|EOA35939.1| hypothetical protein CARUB_v10021196mg [Capsella rubella]	130	103	7.00E-48	79.2	70.8	73.8	hypothetical protein CARUB_v10021196mg	gbpln	Capsella rubella	AT1G57540.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 29 Blast hits to 29 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:21310478-21311215 REVERSE LENGTH=103	130	103	4.00E-50	79.2	70.0	73.1
Rsa1.0_01242.1.g24944.t1	ref|XP_002891994.1| hypothetical protein ARALYDRAFT_314946 [Arabidopsis lyrata subsp. lyrata] gi|297337836|gb|EFH68253.1| hypothetical protein ARALYDRAFT_314946 [Arabidopsis lyrata subsp. lyrata]	534	504	0	94.4	77.0	83.5	hypothetical protein ARALYDRAFT_314946	gbpln	Arabidopsis lyrata	AT1G11910.1 | Symbols: APA1, ATAPA1 | aspartic proteinase A1 | chr1:4017119-4019874 REVERSE LENGTH=506	534	506	1.00E-169	94.8	53.9	65.4
Rsa1.0_01242.1.g24945.t3	ref|XP_002894677.1| membrane bound O-acyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297340519|gb|EFH70936.1| membrane bound O-acyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	979	533	0	54.4	46.6	49.5	membrane bound O-acyl transferase family protein	gbpln	Arabidopsis lyrata	AT1G57600.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr1:21330729-21334596 REVERSE LENGTH=533	979	533	0	54.4	46.2	49.2
Rsa1.0_01242.1.g24946.t1	emb|CAC69066.1| GDP-Mannose transporter [Arabidopsis thaliana]	574	333	1.00E-171	58.0	54.5	55.9	GDP-Mannose transporter	gbpln	Arabidopsis thaliana	AT2G13650.3 | Symbols: GONST1 | golgi nucleotide sugar transporter 1 | chr2:5687584-5690303 REVERSE LENGTH=333	574	333	1.00E-174	58.0	54.5	55.9
Rsa1.0_01242.1.g24947.t1	gb|EOA34968.1| hypothetical protein CARUB_v10020054mg [Capsella rubella]	585	570	0	97.4	92.0	94.9	hypothetical protein CARUB_v10020054mg	gbpln	Capsella rubella	AT1G57770.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr1:21395254-21398135 FORWARD LENGTH=574	585	574	0	98.1	90.3	93.7
Rsa1.0_01242.1.g24948.t1	ref|XP_002894690.1| hypothetical protein ARALYDRAFT_474859 [Arabidopsis lyrata subsp. lyrata] gi|297340532|gb|EFH70949.1| hypothetical protein ARALYDRAFT_474859 [Arabidopsis lyrata subsp. lyrata]	497	499	0	100.4	73.4	86.1	hypothetical protein ARALYDRAFT_474859	gbpln	Arabidopsis lyrata	AT1G57750.1 | Symbols: MAH1, CYP96A15 | cytochrome P450, family 96, subfamily A, polypeptide 15 | chr1:21384186-21385679 REVERSE LENGTH=497	497	497	0	100.0	71.8	83.7
Rsa1.0_01242.1.g24949.t1	ref|NP_195913.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75264447|sp|Q9LYZ2.1|FBL80_ARATH RecName: Full=Putative F-box/LRR-repeat protein At5g02930 gi|7413568|emb|CAB86047.1| putative protein [Arabidopsis thaliana] gi|332003154|gb|AED90537.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	451	469	1.00E-102	104.0	49.2	66.5	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G02930.1 | Symbols: | F-box/RNI-like superfamily protein | chr5:682577-684480 FORWARD LENGTH=469	451	469	1.00E-105	104.0	49.2	66.5
Rsa1.0_01242.1.g24950.t1	ref|NP_195913.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75264447|sp|Q9LYZ2.1|FBL80_ARATH RecName: Full=Putative F-box/LRR-repeat protein At5g02930 gi|7413568|emb|CAB86047.1| putative protein [Arabidopsis thaliana] gi|332003154|gb|AED90537.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	443	469	1.00E-103	105.9	51.0	67.5	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G02930.1 | Symbols: | F-box/RNI-like superfamily protein | chr5:682577-684480 FORWARD LENGTH=469	443	469	1.00E-105	105.9	51.0	67.5
Rsa1.0_01242.1.g24951.t1	ref|XP_002894690.1| hypothetical protein ARALYDRAFT_474859 [Arabidopsis lyrata subsp. lyrata] gi|297340532|gb|EFH70949.1| hypothetical protein ARALYDRAFT_474859 [Arabidopsis lyrata subsp. lyrata]	496	499	0	100.6	81.3	89.9	hypothetical protein ARALYDRAFT_474859	gbpln	Arabidopsis lyrata	AT1G57750.1 | Symbols: MAH1, CYP96A15 | cytochrome P450, family 96, subfamily A, polypeptide 15 | chr1:21384186-21385679 REVERSE LENGTH=497	496	497	0	100.2	77.2	87.3
Rsa1.0_01242.1.g24952.t1	ref|XP_002894690.1| hypothetical protein ARALYDRAFT_474859 [Arabidopsis lyrata subsp. lyrata] gi|297340532|gb|EFH70949.1| hypothetical protein ARALYDRAFT_474859 [Arabidopsis lyrata subsp. lyrata]	471	499	0	105.9	82.6	92.4	hypothetical protein ARALYDRAFT_474859	gbpln	Arabidopsis lyrata	AT1G57750.1 | Symbols: MAH1, CYP96A15 | cytochrome P450, family 96, subfamily A, polypeptide 15 | chr1:21384186-21385679 REVERSE LENGTH=497	471	497	0	105.5	81.7	91.9
Rsa1.0_01243.1.g24953.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01243.1.g24954.t1	gb|EOA20251.1| hypothetical protein CARUB_v10000551mg [Capsella rubella]	485	584	1.00E−176	120.4	67.8	81.2	hypothetical protein CARUB_v10000551mg	gbpln	Capsella rubella	AT4G11560.1 | Symbols: | bromo−adjacent homology (BAH) domain−containing protein | chr4:7000095−7003445 REVERSE LENGTH=587	485	587	1.00E−178	121.0	68.2	80.0
Rsa1.0_01243.1.g24955.t1	ref|NP_192893.2| bromo−adjacent homology (BAH) domain−containing protein [Arabidopsis thaliana] gi|19347810|gb|AAL86355.1| unknown protein [Arabidopsis thaliana] gi|22136724|gb|AAM91681.1| unknown protein [Arabidopsis thaliana] gi|332657624|gb|AEE83024.1| bromo−adjacent homology (BAH) domain−containing protein [Arabidopsis thaliana]	519	587	0	113.1	66.3	78.2	bromo−adjacent homology (BAH) domain−containing protein	gbpln	Arabidopsis thaliana	AT4G11560.1 | Symbols: | bromo−adjacent homology (BAH) domain−containing protein | chr4:7000095−7003445 REVERSE LENGTH=587	519	587	0	113.1	66.3	78.2
Rsa1.0_01243.1.g24956.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838−20266 [Arabidopsis thaliana]	432	1142	4.00E−95	264.4	38.4	50.2	reverse transcriptase, putative; 16838−20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	432	575	6.00E−19	133.1	9.0	13.0
Rsa1.0_01243.1.g24957.t1	gb|ABD65624.1| hypothetical protein 23.t00036 [Brassica oleracea]	937	842	1.00E−122	89.9	35.0	50.2	hypothetical protein 23.t00036	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine−type peptidases;cysteine−type peptidases | chr2:3007102−3011701 REVERSE LENGTH=874	937	874	2.00E−33	93.3	8.5	13.2
Rsa1.0_01243.1.g24958.t1	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	205	326	2.00E−27	159.0	30.2	53.2	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01243.1.g24959.t3	gb|AAC95212.1| Mutator−like transposase [Arabidopsis thaliana]	958	915	1.00E−137	95.5	23.2	33.5	Mutator−like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756−23849915 FORWARD LENGTH=719	958	719	5.00E−30	75.1	10.8	17.8
Rsa1.0_01243.1.g24960.t1	ref|XP_002872537.1| hypothetical protein ARALYDRAFT_489924 [Arabidopsis lyrata subsp. lyrata] gi|297318374|gb|EFH48796.1| hypothetical protein ARALYDRAFT_489924 [Arabidopsis lyrata subsp. lyrata]	292	283	1.00E−108	96.9	71.6	78.8	hypothetical protein ARALYDRAFT_489924	gbpln	Arabidopsis lyrata	AT4G10800.1 | Symbols: | BEST Arabidopsis thaliana protein match is: BTB/POZ domain−containing protein (TAIR:AT3G05675.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr4:6643678−6644529 FORWARD LENGTH=283	292	283	1.00E−107	96.9	69.5	76.7
Rsa1.0_01243.1.g24961.t1	ref|XP_002874150.1| agenet domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319987|gb|EFH50409.1| agenet domain−containing protein [Arabidopsis lyrata subsp. lyrata]	294	552	8.00E−74	187.8	52.4	68.7	agenet domain−containing protein	gbpln	Arabidopsis lyrata	AT5G23800.1 | Symbols: ATDUF10, DUF 10 | DOMAIN OF UNKNOWN FUNCTION 724 10 | chr5:8022216−8024689 REVERSE LENGTH=552	294	552	2.00E−75	187.8	53.1	68.7
Rsa1.0_01243.1.g24962.t1	emb|CAN76546.1| hypothetical protein VITISV_010420 [Vitis vinifera]	561	1288	2.00E−69	229.6	34.2	46.7	hypothetical protein VITISV_010420	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	561	1262	8.00E−43	225.0	20.3	27.5
Rsa1.0_01243.1.g24963.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01243.1.g24964.t2	gb|AAG16628.1| protein serine/threonine kinase BNK1 [Brassica napus]	412	376	1.00E−169	91.3	75.7	79.1	protein serine/threonine kinase BNK1	gbpln	Brassica napus	AT5G02800.1 | Symbols: | Protein kinase superfamily protein | chr5:635545−637374 REVERSE LENGTH=378	412	378	1.00E−164	91.7	76.7	80.3
Rsa1.0_01243.1.g24965.t1	ref|XP_002865752.1| UDP−glucoronosyl/UDP−glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311587|gb|EFH42011.1| UDP−glucoronosyl/UDP−glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	379	515	1.00E−177	135.9	79.7	88.1	UDP−glucoronosyl/UDP−glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT5G49690.1 | Symbols: | UDP−Glycosyltransferase superfamily protein | chr5:20189968−20191350 REVERSE LENGTH=460	379	460	1.00E−178	121.4	79.7	87.1
Rsa1.0_01244.1.g24966.t1	ref|XP_002877968.1| ATVAMP727 [Arabidopsis lyrata subsp. lyrata] gi|297323806|gb|EFH54227.1| ATVAMP727 [Arabidopsis lyrata subsp. lyrata]	70	240	5.00E−32	342.9	95.7	98.6	ATVAMP727	gbpln	Arabidopsis lyrata	AT3G54300.2 | Symbols: ATVAMP727, VAMP727 | vesicle−associated membrane protein 727 | chr3:20108355−20110127 REVERSE LENGTH=240	70	240	1.00E−34	342.9	95.7	97.1
Rsa1.0_01244.1.g24967.t1	ref|XP_002877966.1| hypothetical protein ARALYDRAFT_485826 [Arabidopsis lyrata subsp. lyrata] gi|297323804|gb|EFH54225.1| hypothetical protein ARALYDRAFT_485826 [Arabidopsis lyrata subsp. lyrata]	365	353	1.00E−160	96.7	77.8	84.1	hypothetical protein ARALYDRAFT_485826	gbpln	Arabidopsis lyrata	AT3G54290.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N−terminal protein myristoylation; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Haemerythrin/HHE cation−binding motif (InterPro:IPR012312); Has 59 Blast hits to 59 proteins in 14 species: Archae − 0; Bacteria − 2; Metazoa − 0; Fungi − 0; Plants − 56; Viruses − 0; Other Eukaryotes − 1 (source: NCBI BLink). | chr3:20104623−20105845 REVERSE LENGTH=350	365	350	1.00E−160	95.9	77.0	84.4

Rsa1.0_01244.1.g24968.t1	ref|NP_190996.3| TATA box binding protein associated factor-like protein [Arabidopsis thaliana] gi|197691963|dbj|BAG70033.1| homolog of human BTAF1 [Arabidopsis thaliana] gi|332645686|gb|AEE79207.1| TATA box binding protein associated factor-like protein [Arabidopsis thaliana]	2077	2045	0	98.5	90.1	93.9	TATA box binding protein associated factor-like protein	gbpln	Arabidopsis thaliana	AT3G54280.1 | Symbols: CHR16, CHA16, RGD3, ATBTAF1, BTAF1 | DNA binding;ATP binding;nucleic acid binding;binding;helicases;ATP binding;DNA binding;helicases | chr3:20092361-20103807 FORWARD LENGTH=2045	2077	2045	0	98.5	90.1	93.9
Rsa1.0_01244.1.g24969.t1	ref|NP_190995.2| putative sucrose-phosphatase 3a [Arabidopsis thaliana] gi|206558305|sp|Q93WU4.2|SPP3A_ARATH RecName: Full=Probable sucrose-phosphatase 3a; Short=AtSPP3a gi|332645685|gb|AEE79206.1| putative sucrose-phosphatase 3a [Arabidopsis thaliana]	426	425	0	99.8	81.5	89.7	putative sucrose-phosphatase 3a	gbpln	Arabidopsis thaliana	AT3G54270.1 | Symbols: | sucrose-6F-phosphate phosphohydrolase family protein | chr3:20087419-20089735 REVERSE LENGTH=425	426	425	0	99.8	81.5	89.7
Rsa1.0_01244.1.g24970.t1	ref|NP_566995.1| diphosphomevalonate decarboxylase [Arabidopsis thaliana] gi|332645683|gb|AEE79204.1| diphosphomevalonate decarboxylase [Arabidopsis thaliana]	419	419	0	100.0	94.0	96.4	diphosphomevalonate decarboxylase	gbpln	Arabidopsis thaliana	AT3G54250.1 | Symbols: | GHMP kinase family protein | chr3:20082468-20084688 REVERSE LENGTH=419	419	419	0	100.0	94.0	96.4
Rsa1.0_01244.1.g24971.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01244.1.g24972.t1	gb|ADE44117.1| suppressor of ABI3-5 [Arabidopsis thaliana]	985	1007	0	102.2	80.7	88.3	suppressor of ABI3-5	gbpln	Arabidopsis thaliana	AT3G54230.1 | Symbols: SUA | suppressor of abi3-5 | chr3:20073872-20080142 FORWARD LENGTH=1007	985	1007	0	102.2	80.9	88.5
Rsa1.0_01244.1.g24973.t1	ref|XP_002876247.1| hypothetical protein ARALYDRAFT_485819 [Arabidopsis lyrata subsp. lyrata] gi|297322085|gb|EFH52506.1| hypothetical protein ARALYDRAFT_485819 [Arabidopsis lyrata subsp. lyrata]	635	646	0	101.7	83.1	85.5	hypothetical protein ARALYDRAFT_485819	gbpln	Arabidopsis lyrata	AT3G54220.1 | Symbols: SCR, SGR1 | GRAS family transcription factor | chr3:20070550-20072625 FORWARD LENGTH=653	635	653	0	102.8	83.0	85.2
Rsa1.0_01244.1.g24974.t1	ref|NP_190989.1| 50S ribosomal protein L17 [Arabidopsis thaliana] gi|75311820|sp|Q9M385.1|RK17_ARATH RecName: Full=50S ribosomal protein L17, chloroplastic; AltName: Full=CL17; Flags: Precursor gi|14030669|gb|AAK53009.1|AF375425_1 AT3g54210/F24B22_170 [Arabidopsis thaliana] gi|6822067|emb|CAB70995.1| ribosomal protein L17-like protein [Arabidopsis thaliana] gi|21700779|gb|AAM70513.1| AT3g54210/F24B22_170 [Arabidopsis thaliana] gi|22530904|gb|AAM96956.1| ribosomal protein L17-like protein [Arabidopsis thaliana] gi|23198410|gb|AAN15732.1| ribosomal protein L17-like protein [Arabidopsis thaliana] gi|332645678|gb|AEE79199.1| 50S ribosomal protein L17 [Arabidopsis thaliana]	201	211	5.00E-97	105.0	91.5	94.5	50S ribosomal protein L17	gbpln	Arabidopsis thaliana	AT3G54210.1 | Symbols: | Ribosomal protein L17 family protein | chr3:20067672-20068385 REVERSE LENGTH=211	201	211	2.00E-99	105.0	91.5	94.5
Rsa1.0_01244.1.g24975.t1	ref|XP_002876246.1| hypothetical protein ARALYDRAFT_485817 [Arabidopsis lyrata subsp. lyrata] gi|297322084|gb|EFH52505.1| hypothetical protein ARALYDRAFT_485817 [Arabidopsis lyrata subsp. lyrata]	231	235	3.00E-82	101.7	73.2	89.2	hypothetical protein ARALYDRAFT_485817	gbpln	Arabidopsis lyrata	AT3G54200.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:20065731-20066438 FORWARD LENGTH=235	231	235	8.00E-70	101.7	70.1	85.7
Rsa1.0_01245.1.g24976.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01245.1.g24977.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01245.1.g24978.t1	ref|NP_188216.2| DNA topoisomerase-like protein [Arabidopsis thaliana] gi|9294600|dbj|BAB02881.1| unnamed protein product [Arabidopsis thaliana] gi|21539511|gb|AAM53308.1| unknown protein [Arabidopsis thaliana] gi|24899759|gb|AAN65094.1| unknown protein [Arabidopsis thaliana] gi|332642230|gb|AEE75751.1| DNA topoisomerase-like protein [Arabidopsis thaliana]	749	772	0	103.1	80.0	88.8	DNA topoisomerase-like protein	gbpln	Arabidopsis thaliana	AT3G15950.1 | Symbols: NAI2 | DNA topoisomerase-related | chr3:5397783-5402610 REVERSE LENGTH=772	749	772	0	103.1	80.0	88.8
Rsa1.0_01245.1.g24979.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01245.1.g24980.t1	emb|CAN64334.1| hypothetical protein VITISV_039730 [Vitis vinifera]	168	1098	4.00E-67	653.6	76.8	85.7	hypothetical protein VITISV_039730	gbpln	Vitis vinifera	AT4G14540.1 | Symbols: NF-YB3 | nuclear factor Y, subunit B3 | chr4:8344663-8345148 FORWARD LENGTH=161	168	161	4.00E-68	95.8	81.5	85.1

Rsa1.0_01245.1.g24981.t1	ref|XP_002885116.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297330956|gb|EFH61375.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata]	670	696	0	103.9	84.9	90.9	glycosyl transferase family 1 protein	gbpln	Arabidopsis lyrata	AT3G15940.2 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:5393632-5396187 REVERSE LENGTH=697	670	697	0	104.0	84.2	90.4
Rsa1.0_01245.1.g24982.t3	gb|ABS86965.1| delta-9 fatty acid desaturase [Descurainia sophia]	495	377	4.00E-61	76.2	21.8	27.7	delta-9 fatty acid desaturase	gbpln	Descurainia sophia	AT3G15850.1 | Symbols: FAD5, FADB, JB67, ADS3 | fatty acid desaturase 5 | chr3:5359087-5360998 FORWARD LENGTH=371	495	371	2.00E-61	74.9	22.0	27.9
Rsa1.0_01245.1.g24983.t1	ref|NP_188207.1| uncharacterized protein [Arabidopsis thaliana] gi|52354305|gb|AAU44473.1| hypothetical protein AT3G15860 [Arabidopsis thaliana] gi|55740627|gb|AAV63906.1| hypothetical protein At3g15860 [Arabidopsis thaliana] gi|332642217|gb|AEE75738.1| uncharacterized protein AT3G15860 [Arabidopsis thaliana]	146	170	8.00E-68	116.4	89.7	94.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15860.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: pollen tube; CONTAINS InterPro DOMAIN/s: Plant self-incompatibility S1 (InterPro:IPR010264); BEST Arabidopsis thaliana protein match is: Plant self-incompatibility protein S1 family (TAIR:AT5G26090.1); Has 19 Blast hits to 16 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5361207-5361719 REVERSE LENGTH=170	146	170	2.00E-70	116.4	89.7	94.5
Rsa1.0_01245.1.g24984.t1	gb|EOA30854.1| hypothetical protein CARUB_v10013996mg [Capsella rubella]	374	368	0	98.4	85.0	91.7	hypothetical protein CARUB_v10013996mg	gbpln	Capsella rubella	AT3G15850.1 | Symbols: FAD5, FADB, JB67, ADS3 | fatty acid desaturase 5 | chr3:5359087-5360998 FORWARD LENGTH=371	374	371	1.00E-178	99.2	84.5	90.4
Rsa1.0_01245.1.g24985.t1	ref|NP_566528.1| post-illumination chlorophyll fluorescence increase protein [Arabidopsis thaliana] gi|11994356|dbj|BAB02315.1| unnamed protein product [Arabidopsis thaliana] gi|14334704|gb|AAK59530.1| unknown protein [Arabidopsis thaliana] gi|22136938|gb|AAM91813.1| unknown protein [Arabidopsis thaliana] gi|332642211|gb|AEE75732.1| post-illumination chlorophyll fluorescence increase protein [Arabidopsis thaliana]	293	268	1.00E-142	91.5	85.3	87.7	post-illumination chlorophyll fluorescence increase protein	gbpln	Arabidopsis thaliana	AT3G15840.1 | Symbols: PIFI | post-illumination chlorophyll fluorescence increase | chr3:5356782-5358418 REVERSE LENGTH=268	293	268	1.00E-145	91.5	85.3	87.7
Rsa1.0_01245.1.g24986.t1	ref|XP_002882965.1| hypothetical protein ARALYDRAFT_897881 [Arabidopsis lyrata subsp. lyrata] gi|297328805|gb|EFH59224.1| hypothetical protein ARALYDRAFT_897881 [Arabidopsis lyrata subsp. lyrata]	286	301	1.00E-139	105.2	88.5	94.4	hypothetical protein ARALYDRAFT_897881	gbpln	Arabidopsis lyrata	AT3G15820.1 | Symbols: ROD1 | phosphatidic acid phosphatase-related / PAP2-related | chr3:5351217-5353573 FORWARD LENGTH=301	286	301	1.00E-138	105.2	85.7	93.0
Rsa1.0_01245.1.g24987.t1	ref|XP_002885109.1| hypothetical protein ARALYDRAFT_897880 [Arabidopsis lyrata subsp. lyrata] gi|297330949|gb|EFH61368.1| hypothetical protein ARALYDRAFT_897880 [Arabidopsis lyrata subsp. lyrata]	218	220	1.00E-108	100.9	90.4	93.6	hypothetical protein ARALYDRAFT_897880	gbpln	Arabidopsis lyrata	AT3G15810.1 | Symbols: | Protein of unknown function (DUF567) | chr3:5348054-5349178 REVERSE LENGTH=220	218	220	1.00E-109	100.9	89.4	92.7
Rsa1.0_01245.1.g24988.t1	dbj|BAB02311.1| beta-1,3-glucanase-like protein [Arabidopsis thaliana]	393	391	0	99.5	79.9	83.5	beta-1,3-glucanase-like protein	gbpln	Arabidopsis thaliana	AT3G15800.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr3:5345051-5346988 FORWARD LENGTH=399	393	399	0	101.5	79.4	83.0
Rsa1.0_01246.1.g24989.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	544	1197	1.00E-90	220.0	39.3	53.1	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	544	575	6.00E-48	105.7	26.3	42.1
Rsa1.0_01246.1.g24990.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01246.1.g24991.t1	dbj|BAJ34416.1| unnamed protein product [Thellungiella halophila]	317	334	1.00E-131	105.4	92.4	94.0	unnamed protein product	----	----	AT1G69690.1 | Symbols: | TCP family transcription factor | chr1:26216449-26217426 FORWARD LENGTH=325	317	325	1.00E-120	102.5	87.4	91.5

<table>
<tr><td>Rsa1.0_01246.1.g24992.t1</td><td>ref|NP_564878.1| 60S ribosomal protein L10-3 [Arabidopsis thaliana] gi|297838747|ref|XP_002887255.1| 60S ribosomal protein L10 [Arabidopsis lyrata subsp. lyrata] gi|75249285|sp|Q93W22.1|RL103_ARATH RecName: Full=60S ribosomal protein L10-3 gi|14194141|gb|AAK56265.1|AF367276_1 At1g66580/T12I7_3 [Arabidopsis thaliana] gi|15777885|gb|AAL05903.1| At1g66580/T12I7_3 [Arabidopsis thaliana] gi|21593025|gb|AAM64974.1| 60S ribosomal protein L10, putative [Arabidopsis thaliana] gi|297333096|gb|EFH63514.1| 60S ribosomal protein L10 [Arabidopsis lyrata subsp. lyrata] gi|332196410|gb|AEE34531.1| 60S ribosomal protein L10-3 [Arabidopsis thaliana] gi|482569259|gb|EOA33447.1| hypothetical protein CARUB_v10020922mg [Capsella rubella]</td><td>221</td><td>221</td><td>1.00E-123</td><td>100.0</td><td>96.4</td><td>98.6</td><td>60S ribosomal protein L10-3</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G66580.1 | Symbols: SAG24, RPL10C | senescence associated gene 24 | chr1:24839208-24840439 FORWARD LENGTH=221</td><td>221</td><td>221</td><td>1.00E-126</td><td>100.0</td><td>96.4</td><td>98.6</td></tr>
<tr><td>Rsa1.0_01246.1.g24993.t1</td><td>gb|AAG51175.1|AC079285_8 hypothetical protein [Arabidopsis thaliana]</td><td>94</td><td>135</td><td>6.00E-45</td><td>143.6</td><td>92.6</td><td>94.7</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G66590.1 | Symbols: ATCOX19-1, COX19-1 | cytochrome c oxidase 19-1 | chr1:24841191-24842157 FORWARD LENGTH=98</td><td>94</td><td>98</td><td>4.00E-47</td><td>104.3</td><td>92.6</td><td>94.7</td></tr>
<tr><td>Rsa1.0_01246.1.g24994.t1</td><td>gb|AAM63020.1| unknown [Arabidopsis thaliana]</td><td>180</td><td>177</td><td>6.00E-55</td><td>98.3</td><td>73.3</td><td>82.2</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G69760.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26920.1); Has 51 Blast hits to 51 proteins in 15 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 7; Plants - 29; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr1:26240094-26240627 REVERSE LENGTH=177</td><td>180</td><td>177</td><td>1.00E-56</td><td>98.3</td><td>72.2</td><td>82.2</td></tr>
<tr><td>Rsa1.0_01247.1.g24995.t2</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>922</td><td>1529</td><td>1.00E-115</td><td>165.8</td><td>28.1</td><td>43.3</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>922</td><td>626</td><td>5.00E-33</td><td>67.9</td><td>8.0</td><td>12.9</td></tr>
<tr><td>Rsa1.0_01247.1.g24996.t1</td><td>gb|EOA22023.1| hypothetical protein CARUB_v10002546mg [Capsella rubella]</td><td>131</td><td>251</td><td>2.00E-42</td><td>191.6</td><td>71.8</td><td>83.2</td><td>hypothetical protein CARUB_v10002546mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G24560.1 | Symbols: AtPP2-B12, PP2-B12 | phloem protein 2-B12 | chr5:8402205-8403266 FORWARD LENGTH=251</td><td>131</td><td>251</td><td>6.00E-45</td><td>191.6</td><td>71.8</td><td>83.2</td></tr>
<tr><td>Rsa1.0_01247.1.g24997.t1</td><td>ref|NP_197841.1| downy mildew resistance 6 protein / oxidoreductase [Arabidopsis thaliana] gi|14423476|gb|AAK62420.1|AF386975_1 flavanone 3-hydroxylase-like protein [Arabidopsis thaliana] gi|10177853|dbj|BAB11205.1| flavanone 3-hydroxylase-like protein [Arabidopsis thaliana] gi|20148253|gb|AAM10017.1| flavanone 3-hydroxylase-like protein [Arabidopsis thaliana] gi|332005939|gb|AED93322.1| downy mildew resistance 6 protein / oxidoreductase [Arabidopsis thaliana]</td><td>161</td><td>341</td><td>1.00E-88</td><td>211.8</td><td>92.5</td><td>97.5</td><td>downy mildew resistance 6 protein / oxidoreductase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G24530.1 | Symbols: DMR6 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:8378964-8383154 FORWARD LENGTH=341</td><td>161</td><td>341</td><td>5.00E-91</td><td>211.8</td><td>92.5</td><td>97.5</td></tr>
<tr><td>Rsa1.0_01247.1.g24998.t1</td><td>ref|XP_002872117.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297317954|gb|EFH48376.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]</td><td>149</td><td>341</td><td>6.00E-72</td><td>228.9</td><td>87.2</td><td>93.3</td><td>oxidoreductase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G24530.1 | Symbols: DMR6 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:8378964-8383154 FORWARD LENGTH=341</td><td>149</td><td>341</td><td>3.00E-74</td><td>228.9</td><td>87.2</td><td>93.3</td></tr>
<tr><td>Rsa1.0_01247.1.g24999.t3</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530</td><td>306</td><td>530</td><td>4.00E-12</td><td>173.2</td><td>11.8</td><td>12.1</td></tr>
<tr><td>Rsa1.0_01247.1.g25000.t1</td><td>gb|ADP38078.1| WD40 transcription regulator [Brassica oleracea var. botrytis]</td><td>335</td><td>337</td><td>0</td><td>100.6</td><td>95.5</td><td>97.6</td><td>WD40 transcription regulator</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G24520.2 | Symbols: TTG1, TTG | Transducin/WD40 repeat-like superfamily protein | chr5:8371708-8372733 REVERSE LENGTH=341</td><td>335</td><td>341</td><td>0</td><td>101.8</td><td>93.7</td><td>96.7</td></tr>
<tr><td>Rsa1.0_01247.1.g25001.t1</td><td>gb|ADA58345.1| pseudo-response regulator 5b [Brassica rapa]</td><td>554</td><td>628</td><td>0</td><td>113.4</td><td>94.8</td><td>96.0</td><td>pseudo-response regulator 5b</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G24470.1 | Symbols: APRR5, PRR5 | pseudo-response regulator 5 | chr5:8356204-8358873 REVERSE LENGTH=667</td><td>554</td><td>667</td><td>0</td><td>120.4</td><td>77.8</td><td>84.8</td></tr>
</table>

Rsa1.0_01247.1.g25002.t1	gb|EOA22093.1| hypothetical protein CARUB_v10002643mg [Capsella rubella]	248	294	3.00E-58	118.5	63.7	73.4	hypothetical protein CARUB_v10002643mg	gbpln	Capsella rubella	AT5G24460.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8354815-8355717 FORWARD LENGTH=300	248	300	3.00E-57	121.0	46.8	58.1
Rsa1.0_01247.1.g25003.t3	gb|EOA19681.1| hypothetical protein CARUB_v10003348mg [Capsella rubella]	320	321	1.00E-106	100.3	63.4	73.8	hypothetical protein CARUB_v10003348mg	gbpln	Capsella rubella	AT5G24440.1 | Symbols: CID13 | CTC-interacting domain 13 | chr5:8345402-8347776 REVERSE LENGTH=320	320	320	1.00E-104	100.0	61.9	72.5
Rsa1.0_01247.1.g25004.t1	ref|NP_197831.3| calcium dependent protein kinase-like protein [Arabidopsis thaliana] gi|75333922|sp|Q9FIM9.1|CAMK4_ARATH RecName: Full=CDPK-related kinase 4; Short=AtCRK4; AltName: Full=Calcium/calmodulin-dependent protein kinase CRK4 gi|10177904|dbj|BAB11236.1| calcium dependent protein kinase-like protein [Arabidopsis thaliana] gi|332005927|gb|AED93310.1| CDPK-related kinase 4 (AtCRK4) [Arabidopsis thaliana]	591	594	0	100.5	93.6	95.4	calcium dependent protein kinase-like protein	gbpln	Arabidopsis thaliana	AT5G24430.1 | Symbols: | Calcium-dependent protein kinase (CDPK) family protein | chr5:8339390-8342913 REVERSE LENGTH=594	591	594	0	100.5	93.6	95.4
Rsa1.0_01247.1.g25005.t1	gb|AAK50346.1| putative 6-phosphogluconolactonase [Brassica carinata]	258	258	1.00E-143	100.0	94.2	96.9	putative 6-phosphogluconolactonase	gbpln	Brassica carinata	AT5G24420.1 | Symbols: PGL5 | 6-phosphogluconolactonase 5 | chr5:8336943-8337879 REVERSE LENGTH=252	258	252	1.00E-114	97.7	75.2	85.7
Rsa1.0_01247.1.g25006.t1	gb|AAK50346.1| putative 6-phosphogluconolactonase [Brassica carinata]	258	258	1.00E-126	100.0	83.3	89.1	putative 6-phosphogluconolactonase	gbpln	Brassica carinata	AT5G24420.1 | Symbols: PGL5 | 6-phosphogluconolactonase 5 | chr5:8336943-8337879 REVERSE LENGTH=252	258	252	1.00E-111	97.7	73.6	83.7
Rsa1.0_01248.1.g25007.t1	emb|CAA54683.1| acetyl-CoA carboxylase [Brassica napus]	304	2304	8.00E-75	757.9	62.5	70.1	acetyl-CoA carboxylase	gbpln	Brassica napus	AT1G36180.1 | Symbols: ACC2 | acetyl-CoA carboxylase 2 | chr1:13546047-13558339 FORWARD LENGTH=2355	304	2355	6.00E-59	774.7	51.0	62.2
Rsa1.0_01248.1.g25008.t1	gb|EOA38589.1| hypothetical protein CARUB_v10010420mg [Capsella rubella]	180	180	5.00E-71	100.0	75.6	83.9	hypothetical protein CARUB_v10010420mg	gbpln	Capsella rubella	AT1G36940.1 | Symbols: | unknown protein; Has 21 Blast hits to 21 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:14004158-14004706 FORWARD LENGTH=182	180	182	6.00E-59	101.1	72.8	83.9
Rsa1.0_01248.1.g25009.t1	gb|EOA38576.1| hypothetical protein CARUB_v10010396mg [Capsella rubella]	144	185	6.00E-63	128.5	83.3	83.3	hypothetical protein CARUB_v10010396mg	gbpln	Capsella rubella	AT1G36980.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0220 (InterPro:IPR007919); Has 424 Blast hits to 424 proteins in 159 species: Archae - 0; Bacteria - 0; Metazoa - 228; Fungi - 120; Plants - 62; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink). | chr1:14025084-14026727 FORWARD LENGTH=135	144	135	2.00E-65	93.8	83.3	84.0
Rsa1.0_01248.1.g25010.t4	gb|EOA39197.1| hypothetical protein CARUB_v10012165mg [Capsella rubella]	757	588	0	77.7	68.7	71.6	hypothetical protein CARUB_v10012165mg	gbpln	Capsella rubella	AT1G38131.1 | Symbols: | O-fucosyltransferase family protein | chr1:14293392-14296020 REVERSE LENGTH=589	757	589	0	77.8	67.9	71.5
Rsa1.0_01248.1.g25011.t1	gb|EOA37688.1| hypothetical protein CARUB_v10012340mg [Capsella rubella]	326	326	1.00E-140	100.0	79.1	85.9	hypothetical protein CARUB_v10012340mg	gbpln	Capsella rubella	AT1G60360.1 | Symbols: | RING/U-box superfamily protein | chr1:22242748-22243731 REVERSE LENGTH=327	326	327	1.00E-137	100.3	76.7	84.7
Rsa1.0_01248.1.g25012.t1	gb|EOA39082.1| hypothetical protein CARUB_v10011794mg [Capsella rubella]	113	115	8.00E-36	101.8	84.1	91.2	hypothetical protein CARUB_v10011794mg	gbpln	Capsella rubella	AT2G25720.1 | Symbols: | unknown protein; Has 38 Blast hits to 38 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:10955664-10956017 REVERSE LENGTH=117	113	117	9.00E-35	103.5	78.8	85.8

Rsa1.0_01248.1.g25013.t1	ref|NP_567860.1| ubiquitin carboxyl-terminal hydrolase 24 [Arabidopsis thaliana] gi|42573095|ref|NP_974644.1| ubiquitin carboxyl-terminal hydrolase 24 [Arabidopsis thaliana] gi|334187041|ref|NP_001190875.1| ubiquitin carboxyl-terminal hydrolase 24 [Arabidopsis thaliana] gi|75262799|sp|Q9FPS3.1|UBP24_ARATH RecName: Full=Ubiquitin carboxyl-terminal hydrolase 24; AltName: Full=Deubiquitinating enzyme 24; Short=AtUBP24; AltName: Full=Ubiquitin thioesterase 24; AltName: Full=Ubiquitin-specific-processing protease 24 gi|11993488|gb|AAG42762.1|AF302672_1 ubiquitin-specific protease 24 [Arabidopsis thaliana] gi|332660424|gb|AEE85824.1| ubiquitin carboxyl-terminal hydrolase 24 [Arabidopsis thaliana] gi|332660425|gb|AEE85825.1| ubiquitin carboxyl-terminal hydrolase 24 [Arabidopsis thaliana] gi|332660426|gb|AEE85826.1| ubiquitin carboxyl-terminal hydrolase 24 [Arabidopsis thaliana]	257	551	4.00E-48	214.4	38.1	42.4	ubiquitin carboxyl-terminal hydrolase 24	gbpln	Arabidopsis thaliana	AT4G30890.3 | Symbols: UBP24 | ubiquitin-specific protease 24 | chr4:15036383-15038825 REVERSE LENGTH=551	257	551	1.00E-50	214.4	38.1	42.4
Rsa1.0_01248.1.g25014.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01248.1.g25015.t1	gb|AAZ86538.1| fructose 1,6-bisphosphatase [Brassica rapa subsp. pekinensis]	324	340	0	104.9	98.1	99.1	fructose 1,6-bisphosphatase	gbpln	Brassica rapa	AT1G43670.1 | Symbols: | Inositol monophosphatase family protein | chr1:16468184-16470347 FORWARD LENGTH=341	324	341	0	105.2	95.1	98.1
Rsa1.0_01248.1.g25016.t1	ref|XP_002893962.1| EMB1075 [Arabidopsis lyrata subsp. lyrata] gi|297339804|gb|EFH70221.1| EMB1075 [Arabidopsis lyrata subsp. lyrata]	166	462	2.00E-84	278.3	89.8	92.8	EMB1075	gbpln	Arabidopsis lyrata	AT1G43710.1 | Symbols: emb1075 | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr1:16486534-16488298 REVERSE LENGTH=482	166	482	3.00E-83	290.4	89.2	91.6
Rsa1.0_01248.1.g25017.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01248.1.g25018.t1	ref|XP_002894031.1| vier F-box protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297339873|gb|EFH70290.1| vier F-box protein 1 [Arabidopsis lyrata subsp. lyrata]	228	520	2.00E-51	228.1	53.5	59.6	vier F-box protein 1	gbpln	Arabidopsis lyrata	AT1G47056.1 | Symbols: VFB1 | VIER F-box proteine 1 | chr1:17276103-17277659 REVERSE LENGTH=518	228	518	6.00E-50	227.2	51.8	57.9
Rsa1.0_01249.1.g25019.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01249.1.g25020.t1	ref|XP_002878329.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297324167|gb|EFH54588.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	97	928	7.00E-16	956.7	45.4	56.7	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT3G60350.1 | Symbols: ARABIDILLO-2, ARABIDILLO2 | ARABIDILLO-2 | chr3:22306806-22310596 REVERSE LENGTH=928	97	928	1.00E-16	956.7	41.2	55.7
Rsa1.0_01249.1.g25021.t1	ref|XP_002878329.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297324167|gb|EFH54588.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	154	928	4.00E-18	602.6	28.6	36.4	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT3G60350.1 | Symbols: ARABIDILLO-2, ARABIDILLO2 | ARABIDILLO-2 | chr3:22306806-22310596 REVERSE LENGTH=928	154	928	3.00E-19	602.6	27.3	37.0
Rsa1.0_01249.1.g25022.t1	ref|NP_191594.1| protein ARABIDILLO 2 [Arabidopsis thaliana] gi|75264584|sp|Q9M224.1|ADLO2_ARATH RecName: Full=Protein ARABIDILLO 2 gi|7287983|emb|CAB81821.1| Arm repeat containing protein-like [Arabidopsis thaliana] gi|332646529|gb|AEE80050.1| protein ARABIDILLO 2 [Arabidopsis thaliana]	857	928	0	108.3	63.9	78.2	protein ARABIDILLO 2	gbpln	Arabidopsis thaliana	AT3G60350.1 | Symbols: ARABIDILLO-2, ARABIDILLO2 | ARABIDILLO-2 | chr3:22306806-22310596 REVERSE LENGTH=928	857	928	0	108.3	63.9	78.2
Rsa1.0_01249.1.g25023.t1	gb|EOA24695.1| hypothetical protein CARUB_v10017973mg [Capsella rubella]	228	228	1.00E-115	100.0	88.6	96.1	hypothetical protein CARUB_v10017973mg	gbpln	Capsella rubella	AT3G60360.1 | Symbols: EDA14, UTP11 | embryo sac development arrest 14 | chr3:22312477-22314002 REVERSE LENGTH=228	228	228	1.00E-114	100.0	85.1	94.3
Rsa1.0_01249.1.g25024.t1	gb|AAA56904.1| homeobox protein [Arabidopsis thaliana] gi|549890|gb|AAA56905.1| homeobox protein [Arabidopsis thaliana]	314	315	1.00E-141	100.3	87.3	92.4	homeobox protein	gbpln	Arabidopsis thaliana	AT3G60390.1 | Symbols: HAT3 | homeobox-leucine zipper protein 3 | chr3:22320788-22322370 REVERSE LENGTH=315	314	315	1.00E-138	100.3	86.6	91.7

Rsa1.0_01249.1.g25025.t1	ref|XP_002876552.1| hypothetical protein ARALYDRAFT_907562 [Arabidopsis lyrata subsp. lyrata] gi|297322390|gb|EFH52811.1| hypothetical protein ARALYDRAFT_907562 [Arabidopsis lyrata subsp. lyrata]	919	560	0	60.9	43.6	52.3	hypothetical protein ARALYDRAFT_907562	gbpln	Arabidopsis lyrata	AT3G60400.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr3:22329093-22330769 FORWARD LENGTH=558	919	558	0	60.7	43.2	51.7
Rsa1.0_01249.1.g25026.t1	ref|XP_002876557.1| hypothetical protein ARALYDRAFT_486518 [Arabidopsis lyrata subsp. lyrata] gi|297322395|gb|EFH52816.1| hypothetical protein ARALYDRAFT_486518 [Arabidopsis lyrata subsp. lyrata]	259	274	1.00E-103	105.8	69.5	83.0	hypothetical protein ARALYDRAFT_486518	gbpln	Arabidopsis lyrata	AT3G60450.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:22340982-22342187 FORWARD LENGTH=274	259	274	1.00E-104	105.8	68.3	82.6
Rsa1.0_01249.1.g25027.t1	ref|XP_002876557.1| hypothetical protein ARALYDRAFT_486518 [Arabidopsis lyrata subsp. lyrata] gi|297322395|gb|EFH52816.1| hypothetical protein ARALYDRAFT_486518 [Arabidopsis lyrata subsp. lyrata]	500	274	1.00E-104	54.8	37.8	43.2	hypothetical protein ARALYDRAFT_486518	gbpln	Arabidopsis lyrata	AT3G60450.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:22340982-22342187 FORWARD LENGTH=274	500	274	1.00E-105	54.8	37.2	43.0
Rsa1.0_01249.1.g25028.t2	ref|NP_191605.1| myb proto-oncogene protein, plant [Arabidopsis thaliana] gi|18766549|gb|AAL79015.1|AF469468_1 putative transcription factor [Arabidopsis thaliana] gi|7287994|emb|CAB81832.1| myb protein-like [Arabidopsis thaliana] gi|302589002|gb|ADL59373.1| duo pollen 1 [Arabidopsis thaliana] gi|332646543|gb|AEE80064.1| R2R3 myb transcription factor DUO1 [Arabidopsis thaliana]	269	297	1.00E-105	110.4	80.3	85.9	myb proto-oncogene protein, plant	gbpln	Arabidopsis thaliana	AT3G60460.1 | Symbols: DUO1 | myb-like HTH transcriptional regulator family protein | chr3:22342429-22343491 REVERSE LENGTH=297	269	297	1.00E-107	110.4	80.3	85.9
Rsa1.0_01249.1.g25029.t1	ref|NP_567103.1| Transketolase [Arabidopsis thaliana] gi|75247623|sp|Q8RWV0.1|TKTC1_ARATH RecName: Full=Transketolase-1, chloroplastic; Short=TK; Flags: Precursor gi|20268682|gb|AAM14045.1| putative transketolase [Arabidopsis thaliana] gi|22136900|gb|AAM91794.1| putative transketolase [Arabidopsis thaliana] gi|332646582|gb|AEE80103.1| Transketolase [Arabidopsis thaliana]	746	741	0	99.3	94.0	96.5	Transketolase	gbpln	Arabidopsis thaliana	AT3G60750.1 | Symbols: | Transketolase | chr3:22454004-22456824 FORWARD LENGTH=741	746	741	0	99.3	94.0	96.5
Rsa1.0_01249.1.g25030.t1	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	991	1453	0	146.6	54.4	66.6	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	991	1262	1.00E-101	127.3	18.3	28.3
Rsa1.0_01249.1.g25031.t1	ref|XP_002876581.1| hypothetical protein ARALYDRAFT_486550 [Arabidopsis lyrata subsp. lyrata] gi|297322419|gb|EFH52840.1| hypothetical protein ARALYDRAFT_486550 [Arabidopsis lyrata subsp. lyrata]	218	218	1.00E-106	100.0	86.7	94.0	hypothetical protein ARALYDRAFT_486550	gbpln	Arabidopsis lyrata	AT3G60780.1 | Symbols: | Protein of unknown function (DUF1442) | chr3:22462695-22463630 FORWARD LENGTH=218	218	218	1.00E-104	100.0	82.6	92.2
Rsa1.0_01249.1.g25032.t4	ref|XP_002876582.1| hypothetical protein ARALYDRAFT_486551 [Arabidopsis lyrata subsp. lyrata] gi|297322420|gb|EFH52841.1| hypothetical protein ARALYDRAFT_486551 [Arabidopsis lyrata subsp. lyrata]	471	494	1.00E-130	104.9	54.6	67.7	hypothetical protein ARALYDRAFT_486551	gbpln	Arabidopsis lyrata	AT3G60790.1 | Symbols: | F-box family protein | chr3:22464623-22466948 FORWARD LENGTH=488	471	488	1.00E-119	103.6	51.0	65.0
Rsa1.0_01249.1.g25033.t1	ref|XP_002876582.1| hypothetical protein ARALYDRAFT_486551 [Arabidopsis lyrata subsp. lyrata] gi|297322420|gb|EFH52841.1| hypothetical protein ARALYDRAFT_486551 [Arabidopsis lyrata subsp. lyrata]	462	494	1.00E-119	106.9	53.5	67.1	hypothetical protein ARALYDRAFT_486551	gbpln	Arabidopsis lyrata	AT3G60790.1 | Symbols: | F-box family protein | chr3:22464623-22466948 FORWARD LENGTH=488	462	488	1.00E-103	105.6	48.5	62.8
Rsa1.0_01249.1.g25034.t1	gb|EOA24450.1| hypothetical protein CARUB_v10017708mg [Capsella rubella]	305	306	1.00E-161	100.3	93.1	96.7	hypothetical protein CARUB_v10017708mg	gbpln	Capsella rubella	AT3G60800.1 | Symbols: | DHHC-type zinc finger family protein | chr3:22467486-22469273 REVERSE LENGTH=307	305	307	1.00E-162	100.7	92.8	96.1
Rsa1.0_01249.1.g25035.t1	ref|XP_002876583.1| hypothetical protein ARALYDRAFT_486553 [Arabidopsis lyrata subsp. lyrata] gi|297322421|gb|EFH52842.1| hypothetical protein ARALYDRAFT_486553 [Arabidopsis lyrata subsp. lyrata]	216	216	1.00E-108	100.0	88.4	94.4	hypothetical protein ARALYDRAFT_486553	gbpln	Arabidopsis lyrata	AT3G60810.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1499 (InterPro:IPR010865); Has 444 Blast hits to 444 proteins in 143 species: Archae - 0; Bacteria - 268; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 125 (source: NCBI BLink). | chr3:22470579-22471756 FORWARD LENGTH=214	216	214	1.00E-108	99.1	87.0	93.1

Rsa1.0_01249.1.g25036.t1	emb|CAA47753.1| proteosome subunit [Arabidopsis thaliana]	223	230	1.00E−124	103.1	94.6	98.2	proteosome subunit	gbpln	Arabidopsis thaliana	AT3G60820.3 | Symbols: PBF1 | N−terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:22472038−22473809 REVERSE LENGTH=223	223	223	1.00E−126	100.0	94.6	98.2
Rsa1.0_01249.1.g25037.t1	ref|XP_003534403.1| PREDICTED: actin−related protein 7−like isoform 2 [Glycine max]	183	330	3.00E−47	180.3	58.5	68.3	PREDICTED: actin−related protein 7−like isoform 2	gbenv/gbpln	Glycine max	AT3G60830.1 | Symbols: ATARP7, ARP7 | actin−related protein 7 | chr3:22474298−22476000 FORWARD LENGTH=363	183	363	2.00E−49	198.4	48.1	50.8
Rsa1.0_01249.1.g25038.t1	gb|EOA23610.1| hypothetical protein CARUB_v10016810mg [Capsella rubella] gi|482559420|gb|EOA23611.1| hypothetical protein CARUB_v10016810mg [Capsella rubella]	749	652	0	87.0	63.4	70.5	hypothetical protein CARUB_v10016810mg	gbpln	Capsella rubella	AT3G60850.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 11 growth stages; Has 42 Blast hits to 42 proteins in 12 species: Archae − 0; Bacteria − 0; Metazoa − 4; Fungi − 0; Plants − 37; Viruses − 0; Other Eukaryotes − 1 (source: NCBI BLink). | chr3:22482053−22483999 FORWARD LENGTH=648	749	648	1.00E−176	86.5	41.3	45.1
Rsa1.0_01249.1.g25039.t1	gb|EOA23258.1| hypothetical protein CARUB_v10017487mg [Capsella rubella]	211	365	1.00E−64	173.0	56.9	60.2	hypothetical protein CARUB_v10017487mg	gbpln	Capsella rubella	AT3G60880.2 | Symbols: DHDPS, DHDPS1 | dihydrodipicolinate synthase 1 | chr3:22495086−22496542 FORWARD LENGTH=365	211	365	3.00E−66	173.0	55.0	60.7
Rsa1.0_01249.1.g25040.t1	ref|NP_191649.1| fasciclin−like arabinogalactan protein 10 [Arabidopsis thaliana] gi|38257776|sp|Q9LZX4.1|FLA10_ARATH RecName: Full=Fasciclin−like arabinogalactan protein 10; Flags: Precursor gi|7329700|emb|CAB82694.1| endosperm specific protein−like [Arabidopsis thaliana] gi|21593224|gb|AAM65173.1| endosperm specific protein−like [Arabidopsis thaliana] gi|332646604|gb|AEE80125.1| fasciclin−like arabinogalactan protein 10 [Arabidopsis thaliana]	365	422	1.00E−141	115.6	74.5	78.6	fasciclin−like arabinogalactan protein 10	gbpln	Arabidopsis thaliana	AT3G60900.1 | Symbols: FLA10 | FASCICLIN−like arabinogalactan−protein 10 | chr3:22499573−22500841 REVERSE LENGTH=422	365	422	1.00E−144	115.6	74.5	78.6
Rsa1.0_01250.1.g25041.t1	gb|AAF79253.1|AC023279_2 F12K21.4 [Arabidopsis thaliana]	833	857	0	102.9	48.1	63.5	F12K21.4	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756−23849915 FORWARD LENGTH=719	833	719	7.00E−22	86.3	13.8	23.4
Rsa1.0_01250.1.g25042.t1	gb|AAD46014.1|AC007894_12 F21H2.13 [Arabidopsis thaliana]	1162	993	4.00E−86	85.5	14.8	20.2	F21H2.13	gbpln	Arabidopsis thaliana	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097−11122412 FORWARD LENGTH=673	1162	673	9.00E−23	57.9	9.0	13.8
Rsa1.0_01250.1.g25043.t1	gb|EOA20993.1| hypothetical protein CARUB_v10001326mg [Capsella rubella]	283	345	1.00E−142	121.9	86.6	92.9	hypothetical protein CARUB_v10001326mg	gbpln	Capsella rubella	AT4G08770.1 | Symbols: Prx37 | Peroxidase superfamily protein | chr4:5598259−5600262 REVERSE LENGTH=346	283	346	1.00E−142	122.3	86.6	91.9
Rsa1.0_01250.1.g25044.t1	gb|ACG60682.1| transposon−like ORF [Brassica oleracea var. alboglabra]	558	704	1.00E−126	126.2	42.7	46.8	transposon−like ORF	gbpln	Brassica oleracea	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:6485617−6487009 REVERSE LENGTH=365	558	365	3.00E−30	65.4	13.8	18.8
Rsa1.0_01250.1.g25045.t2	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01250.1.g25046.t1	ref|XP_002874554.1| hypothetical protein ARALYDRAFT_911156 [Arabidopsis lyrata subsp. lyrata] gi|297320391|gb|EFH50813.1| hypothetical protein ARALYDRAFT_911156 [Arabidopsis lyrata subsp. lyrata]	220	307	1.00E−85	139.5	75.0	80.9	hypothetical protein ARALYDRAFT_911156	gbpln	Arabidopsis lyrata	AT4G08790.1 | Symbols: | Nitrilase/cyanide hydratase and apolipoprotein N−acyltransferase family protein | chr4:5608489−5611118 REVERSE LENGTH=307	220	307	7.00E−88	139.5	75.0	81.8
Rsa1.0_01250.1.g25047.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01250.1.g25048.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01250.1.g25049.t1	gb|EOA18064.1| hypothetical protein CARUB_v10006510mg, partial [Capsella rubella]	78	555	2.00E−11	711.5	38.5	59.0	hypothetical protein CARUB_v10006510mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01250.1.g25050.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01251.1.g25051.t1	ref|XP_002889266.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297335107|gb|EFH65525.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	163	489	7.00E−42	300.0	49.7	52.8	aspartyl protease family protein	gbpln	Arabidopsis lyrata	AT1G79720.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:29997259−29998951 REVERSE LENGTH=484	163	484	2.00E−43	296.9	49.1	51.5

Rsa1.0_01251.1.g25052.t1	ref|XP_002887801.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297333642|gb|EFH64060.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata]	494	497	0	100.6	90.5	96.4	integral membrane transporter family protein	gbpln	Arabidopsis lyrata	AT1G79710.1 | Symbols: | Major facilitator superfamily protein | chr1:29995137-29996988 FORWARD LENGTH=497	494	497	0	100.6	89.3	95.7
Rsa1.0_01251.1.g25053.t1	dbj|BAJ33872.1| unnamed protein product [Thellungiella halophila]	305	328	1.00E-130	107.5	83.3	89.2	unnamed protein product	----	----	AT1G79700.2 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:29990440-29993658 REVERSE LENGTH=313	305	313	1.00E-119	102.6	80.0	86.9
Rsa1.0_01251.1.g25054.t1	ref|NP_565218.1| nudix hydrolase 3 [Arabidopsis thaliana] gi|68565909|sp|Q8L831.1|NUDT3_ARATH RecName: Full=Nudix hydrolase 3; Short=AtNUDT3 gi|21539559|gb|AAM53332.1| unknown protein [Arabidopsis thaliana] gi|23197868|gb|AAN15461.1| unknown protein [Arabidopsis thaliana] gi|332198166|gb|AEE36287.1| nudix hydrolase 3 [Arabidopsis thaliana]	776	772	0	99.5	89.4	94.6	nudix hydrolase 3	gbpln	Arabidopsis thaliana	AT1G79690.1 | Symbols: atnudt3, NUDT3 | nudix hydrolase homolog 3 | chr1:29985360-29990171 FORWARD LENGTH=772	776	772	0	99.5	89.4	94.6
Rsa1.0_01251.1.g25055.t1	ref|NP_178086.1| wall-associated receptor kinase-like 10 [Arabidopsis thaliana] gi|75331123|sp|Q8VYA3.1|WAKLJ_ARATH RecName: Full=Wall-associated receptor kinase-like 10; Flags: Precursor gi|18252189|gb|AAL61927.1| wall-associated kinase 2, putative [Arabidopsis thaliana] gi|22136108|gb|AAM91132.1| wall-associated kinase 2, putative [Arabidopsis thaliana] gi|332198165|gb|AEE36286.1| wall-associated receptor kinase-like 10 [Arabidopsis thaliana]	776	769	0	99.1	65.3	76.2	wall-associated receptor kinase-like 10	gbpln	Arabidopsis thaliana	AT1G79680.1 | Symbols: WAKL10, ATWAKL10 | WALL ASSOCIATED KINASE (WAK)-LIKE 10 | chr1:29980188-29982749 REVERSE LENGTH=769	776	769	0	99.1	65.3	76.2
Rsa1.0_01251.1.g25056.t1	gb|AAY86486.1| RFO1 [Arabidopsis thaliana]	756	749	0	99.1	86.2	91.9	RFO1	gbpln	Arabidopsis thaliana	AT1G79670.1 | Symbols: RFO1, WAKL22 | Wall-associated kinase family protein | chr1:29976887-29979337 REVERSE LENGTH=751	756	751	0	99.3	86.2	91.9
Rsa1.0_01251.1.g25057.t1	gb|EOA33804.1| hypothetical protein CARUB_v10021275mg [Capsella rubella]	94	93	4.00E-40	98.9	88.3	93.6	hypothetical protein CARUB_v10021275mg	gbpln	Capsella rubella	AT1G79660.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16170.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:29976294-29976575 FORWARD LENGTH=93	94	93	2.00E-41	98.9	85.1	91.5
Rsa1.0_01251.1.g25058.t1	ref|NP_178082.6| protein kinase domain-containing protein [Arabidopsis thaliana] gi|332198156|gb|AEE36277.1| protein kinase domain-containing protein [Arabidopsis thaliana]	672	687	0	102.2	90.5	94.5	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G79640.1 | Symbols: | Protein kinase superfamily protein | chr1:29966913-29971387 REVERSE LENGTH=687	672	687	0	102.2	90.5	94.5
Rsa1.0_01251.1.g25059.t1	ref|XP_002889260.1| phosphatase 2C family protein [Arabidopsis lyrata subsp. lyrata] gi|297335101|gb|EFH65519.1| phosphatase 2C family protein [Arabidopsis lyrata subsp. lyrata]	496	501	0	101.0	86.1	91.7	phosphatase 2C family protein	gbpln	Arabidopsis lyrata	AT1G79630.1 | Symbols: | Protein phosphatase 2C family protein | chr1:29962931-29965169 REVERSE LENGTH=504	496	504	0	101.6	85.7	92.3
Rsa1.0_01251.1.g25060.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1891	1374	0	72.7	39.8	52.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1891	575	1.00E-177	30.4	15.1	21.5
Rsa1.0_01251.1.g25061.t2	gb|AFV60030.1| Na+/K+-H+ antiporter NHX6, partial [Brassica oleracea]	549	524	0	95.4	90.0	91.1	Na+/K+-H+ antiporter NHX6, partial	gbpln	Brassica oleracea	AT1G79610.1 | Symbols: ATNHX6, NHX6 | Na+/H+ antiporter 6 | chr1:29953089-29957070 REVERSE LENGTH=535	549	535	0	97.4	88.5	91.3
Rsa1.0_01251.1.g25062.t1	gb|EOA31250.1| hypothetical protein CARUB_v10014420mg [Capsella rubella]	218	262	1.00E-85	120.2	72.5	81.7	hypothetical protein CARUB_v10014420mg	gbpln	Capsella rubella	AT3G19184.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr3:6637555-6639035 FORWARD LENGTH=277	218	277	4.00E-81	127.1	71.6	79.8
Rsa1.0_01252.1.g25063.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01252.1.g25064.t1	gb|EMJ09180.1| hypothetical protein PRUPE_ppa015715mg, partial [Prunus persica]	668	1445	1.00E-82	216.3	22.6	28.9	hypothetical protein PRUPE_ppa015715mg, partial	gbpln	Prunus persica	AT1G47350.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:17358447-17360722 REVERSE LENGTH=528	668	528	3.00E-28	79.0	10.2	12.9
Rsa1.0_01252.1.g25065.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01252.1.g25066.t9	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	1408	1024	1.00E-52	72.7	8.7	12.4	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01252.1.g25067.t1	dbj|BAB11308.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	338	1013	1.00E-53	299.7	34.3	55.6	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01252.1.g25068.t1	ref|XP_002894284.1| etfalpha [Arabidopsis lyrata subsp. lyrata] gi|297340126|gb|EFH70543.1| etfalpha [Arabidopsis lyrata subsp. lyrata]	361	365	0	101.1	90.9	95.0	etfalpha	gbpln	Arabidopsis lyrata	AT1G50940.1 | Symbols: ETFALPHA | electron transfer flavoprotein alpha | chr1:18878038-18879939 REVERSE LENGTH=363	361	363	0	100.6	89.5	94.5
Rsa1.0_01252.1.g25069.t1	#	#	#	#	#	#	#	-	----	----	AT5G47880.2 | Symbols: ERF1-1 | eukaryotic release factor 1-1 | chr5:19386555-19387865 REVERSE LENGTH=436	80	436	1.00E-12	545.0	38.8	48.8
Rsa1.0_01252.1.g25070.t2	gb|EOA34301.1| hypothetical protein CARUB_v10021819mg [Capsella rubella]	305	383	3.00E-78	125.6	61.0	73.8	hypothetical protein CARUB_v10021819mg	gbpln	Capsella rubella	AT1G50980.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:18900541-18902057 REVERSE LENGTH=370	305	370	5.00E-67	121.3	53.8	65.2
Rsa1.0_01252.1.g25071.t1	gb|AAG52313.1|AC021666_2 Mutator-like transposase; 53847-56139 [Arabidopsis thaliana]	365	583	1.00E-23	159.7	17.5	23.0	Mutator-like transposase; 53847-56139	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01252.1.g25072.t1	gb|ABD64950.1| GRF zinc finger containing protein [Brassica oleracea]	142	180	1.00E-54	126.8	75.4	83.1	GRF zinc finger containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01252.1.g25073.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	498	723	1.00E-109	145.2	43.6	57.2	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	498	696	1.00E-15	139.8	18.3	32.7
Rsa1.0_01252.1.g25074.t1	ref|XP_002894316.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340158|gb|EFH70575.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	423	424	0	100.2	83.2	89.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G51420.1 | Symbols: ATSPP1, SPP1 | sucrose-phosphatase 1 | chr1:19064852-19066704 REVERSE LENGTH=423	423	423	0	100.0	82.7	89.6
Rsa1.0_01252.1.g25075.t1	ref|XP_004143235.1| PREDICTED: cinnamoyl-CoA reductase 1-like [Cucumis sativus]	245	256	1.00E-101	104.5	71.8	84.5	PREDICTED: cinnamoyl-CoA reductase 1-like	gbpln	Cucumis sativus	AT1G51410.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:19059885-19061424 FORWARD LENGTH=325	245	325	3.00E-68	132.7	49.4	51.0
Rsa1.0_01252.1.g25076.t1	ref|NP_849791.1| myosin-related protein [Arabidopsis thaliana] gi|332194543|gb|AEE32664.1| myosin-related protein [Arabidopsis thaliana]	443	487	0	109.9	81.0	88.5	myosin-related protein	gbpln	Arabidopsis thaliana	AT1G51405.1 | Symbols: | myosin-related | chr1:19057780-19059582 FORWARD LENGTH=487	443	487	0	109.9	81.0	88.5
Rsa1.0_01252.1.g25077.t1	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	581	498	1.00E-54	85.7	20.7	27.4	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	581	336	4.00E-19	57.8	9.6	16.7
Rsa1.0_01253.1.g25078.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01253.1.g25079.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01253.1.g25080.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01253.1.g25081.t1	ref|XP_002876110.1| AT-HSFA7A [Arabidopsis lyrata subsp. lyrata] gi|297321948|gb|EFH52369.1| AT-HSFA7A [Arabidopsis lyrata subsp. lyrata]	73	277	2.00E-17	379.5	76.7	86.3	AT-HSFA7A	gbpln	Arabidopsis lyrata	AT3G51910.1 | Symbols: AT-HSFA7A, HSFA7A | heat shock transcription factor A7A | chr3:19265294-19266619 FORWARD LENGTH=272	73	272	4.00E-18	372.6	69.9	82.2
Rsa1.0_01253.1.g25082.t1	gb|AFO66530.1| putative nucleic acid-binding OB-fold protein [Brassica napus]	273	102	7.00E-11	37.4	12.5	12.8	putative nucleic acid-binding OB-fold protein	gbpln	Brassica napus	#	#	#	#	#	#	#
Rsa1.0_01253.1.g25083.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01253.1.g25084.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01253.1.g25085.t1	gb|AFN85666.1| glucanase 1 [Brassica rapa subsp. pekinensis]	317	341	1.00E-179	107.6	97.8	98.7	glucanase 1	gbpln	Brassica rapa	AT3G57240.1 | Symbols: BG3 | beta-1,3-glucanase 3 | chr3:21181916-21183045 REVERSE LENGTH=341	317	341	1.00E-149	107.6	81.7	87.4
Rsa1.0_01254.1.g25086.t1	gb|ABE68874.1| cinnamate 4-hydroxylase [Brassica rapa subsp. pekinensis]	505	505	0	100.0	91.5	96.0	cinnamate 4-hydroxylase	gbpln	Brassica rapa	AT2G30490.1 | Symbols: ATC4H, C4H, CYP73A5, REF3 | cinnamate-4-hydroxylase | chr2:12993861-12995683 REVERSE LENGTH=505	505	505	0	100.0	88.1	94.7
Rsa1.0_01254.1.g25087.t1	dbj|BAJ34588.1| unnamed protein product [Thellungiella halophila]	751	809	0	107.7	79.0	86.3	unnamed protein product	----	----	AT2G30470.1 | Symbols: HSI2, VAL1 | high-level expression of sugar-inducible gene 2 | chr2:12980904-12984724 REVERSE LENGTH=790	751	790	0	105.2	73.1	83.0

Rsa1.0_01254.1.g25088.t1	ref|NP_180603.2| thylakoidal processing peptidase 1 [Arabidopsis thaliana] gi|75276837|sp|O04348.2|TPP1_ARATH RecName: Full=Thylakoidal processing peptidase 1, chloroplastic; AltName: Full=Signal peptidase I-1; Flags: Precursor gi|2769566|emb|CAA71502.1| chloroplast thylakoidal processing peptidase [Arabidopsis thaliana] gi|22135950|gb|AAM91557.1| putative signal peptidase I [Arabidopsis thaliana] gi|58652110|gb|AAW80880.1| At2g30440 [Arabidopsis thaliana] gi|330253295|gb|AEC08389.1| thylakoidal processing peptidase 1 [Arabidopsis thaliana]	328	340	1.00E-131	103.7	78.0	86.6	thylakoidal processing peptidase 1	gbpln	Arabidopsis thaliana	AT2G30440.1 | Symbols: TPP | thylakoid processing peptide | chr2:12973244-12975027 FORWARD LENGTH=340	328	340	1.00E-134	103.7	78.0	86.6
Rsa1.0_01254.1.g25089.t1	ref|XP_002879263.1| hypothetical protein ARALYDRAFT_481952 [Arabidopsis lyrata subsp. lyrata] gi|297325102|gb|EFH55522.1| hypothetical protein ARALYDRAFT_481952 [Arabidopsis lyrata subsp. lyrata]	287	319	4.00E-94	111.1	70.4	78.0	hypothetical protein ARALYDRAFT_481952	gbpln	Arabidopsis lyrata	AT2G30400.1 | Symbols: ATOFP2, OFP2 | ovate family protein 2 | chr2:12956592-12957554 FORWARD LENGTH=320	287	320	7.00E-90	111.5	72.5	83.3
Rsa1.0_01254.1.g25090.t1	ref|XP_002881107.1| ATOFP17/OFP17 [Arabidopsis lyrata subsp. lyrata] gi|297326946|gb|EFH57366.1| ATOFP17/OFP17 [Arabidopsis lyrata subsp. lyrata]	196	195	4.00E-79	99.5	79.1	84.7	ATOFP17/OFP17	gbpln	Arabidopsis lyrata	AT2G30395.1 | Symbols: ATOFP17, OFP17 | ovate family protein 17 | chr2:12954409-12955083 REVERSE LENGTH=195	196	195	2.00E-79	99.5	77.0	84.2
Rsa1.0_01254.1.g25091.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01254.1.g25092.t1	ref|NP_001189638.1| allergen-related protein [Arabidopsis thaliana] gi|122180229|sp|Q1PEY6.1|EPFL6_ARATH RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 6; Short=EPF-like protein 6; Flags: Precursor gi|91806295|gb|ABE65875.1| allergen-like [Arabidopsis thaliana] gi|330253283|gb|AEC08377.1| epidermal patterning factor-like protein 6 [Arabidopsis thaliana]	107	156	5.00E-30	145.8	66.4	72.0	allergen-related protein	gbpln	Arabidopsis thaliana	AT2G30370.2 | Symbols: CHAL, EPFL6 | allergen-related | chr2:12940577-12942167 REVERSE LENGTH=156	107	156	9.00E-33	145.8	66.4	72.0
Rsa1.0_01254.1.g25093.t1	ref|XP_002881592.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata] gi|297327431|gb|EFH57851.1| hypothetical protein ARALYDRAFT_903069 [Arabidopsis lyrata subsp. lyrata]	376	411	4.00E-90	109.3	53.7	68.6	hypothetical protein ARALYDRAFT_903069	gbpln	Arabidopsis lyrata	AT4G33290.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:16049573-16050865 FORWARD LENGTH=430	376	430	2.00E-87	114.4	50.5	65.2
Rsa1.0_01254.1.g25094.t1	ref|NP_180595.1| CBL-interacting serine/threonine-protein kinase 11 [Arabidopsis thaliana] gi|55976213|sp|O22932.1|CIPKB_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 11; AltName: Full=SNF1-related kinase 3.22; AltName: Full=SOS2-like protein kinase PKS5; AltName: Full=SOS3-interacting protein 4 gi|13249121|gb|AAK16686.1|AF295666_1 CBL-interacting protein kinase 11 [Arabidopsis thaliana] gi|13448035|gb|AAK26844.1|AF339146_1 SOS2-like protein kinase PKS5 [Arabidopsis thaliana] gi|13877673|gb|AAK43914.1|AF370595_1 putative protein kinase [Arabidopsis thaliana] gi|2347199|gb|AAC16938.1| putative protein kinase [Arabidopsis thaliana] gi|27311745|gb|AAO00838.1| putative protein kinase [Arabidopsis thaliana] gi|30387521|gb|AAP31926.1| At2g30360 [Arabidopsis thaliana] gi|330253281|gb|AEC08375.1| CBL-interacting serine/threonine-protein kinase 11 [Arabidopsis thaliana]	434	435	0	100.2	83.2	88.7	CBL-interacting serine/threonine-protein kinase 11	gbpln	Arabidopsis thaliana	AT2G30360.1 | Symbols: CIPK11, PKS5, SIP4, SNRK3.22 | SOS3-interacting protein 4 | chr2:12937265-12938572 REVERSE LENGTH=435	434	435	0	100.2	83.2	88.7

Rsa1.0_01254.1.g25095.t9	ref|NP_850141.1| LOB domain-containing protein 13 [Arabidopsis thaliana] gi|29427981|sp|Q9AT61.2|LBD13_ARATH RecName: Full=LOB domain-containing protein 13; AltName: Full=ASYMMETRIC LEAVES 2-like protein 10; Short=AS2-like protein 10 gi|17227158|gb|AAL38033.1|AF447888_1 LOB DOMAIN 13 [Arabidopsis thaliana] gi|20196885|gb|AAC16936.2| expressed protein [Arabidopsis thaliana] gi|109946459|gb|ABG48408.1| At2g30340 [Arabidopsis thaliana] gi|219807096|dbj|BAH10554.1| ASYMMETRIC LEAVES2-like 10 protein [Arabidopsis thaliana] gi|330253278|gb|AEC08372.1| LOB domain-containing protein 13 [Arabidopsis thaliana]	263	268	2.00E-98	101.9	86.3	91.6	LOB domain-containing protein 13	gbpln	Arabidopsis thaliana	AT2G30340.1 | Symbols: LBD13 | LOB domain-containing protein 13 | chr2:12931306-12932540 REVERSE LENGTH=268	263	268	1.00E-101	101.9	86.3	91.6
Rsa1.0_01255.1.g25096.t1	dbj|BAB08714.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	361	1197	1.00E-77	331.6	40.7	57.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	361	575	3.00E-37	159.3	28.5	46.3
Rsa1.0_01255.1.g25097.t1	gb|AAD25575.1| Mutator-like transposase [Arabidopsis thaliana]	484	607	9.00E-64	125.4	29.5	43.2	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	484	719	1.00E-14	148.6	17.1	29.5
Rsa1.0_01255.1.g25098.t10	ref|XP_002891526.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata] gi|297337368|gb|EFH67785.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata]	915	824	4.00E-90	90.1	26.7	40.9	hypothetical protein ARALYDRAFT_337115	gbpln	Arabidopsis lyrata	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	915	452	3.00E-28	49.4	12.1	18.0
Rsa1.0_01255.1.g25099.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01255.1.g25100.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	515	490	1.00E-89	95.1	37.7	57.7	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	515	566	3.00E-92	109.9	36.5	60.8
Rsa1.0_01255.1.g25101.t1	gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]	195	198	1.00E-44	101.5	51.3	66.7	hypothetical protein 27.t00041	gbpln	Brassica oleracea	AT2G35280.1 | Symbols: | F-box family protein | chr2:14859709-14860200 REVERSE LENGTH=163	195	163	1.00E-11	83.6	17.4	28.2
Rsa1.0_01255.1.g25102.t1	dbj|BAB11364.1| helicase [Arabidopsis thaliana]	627	1523	1.00E-136	242.9	39.6	48.8	helicase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01255.1.g25103.t1	gb|AAB84340.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1755	1094	0	62.3	27.9	39.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1755	575	6.00E-81	32.8	10.2	16.5
Rsa1.0_01255.1.g25104.t1	ref|NP_178999.2| somatic embryogenesis receptor kinase 4 [Arabidopsis thaliana] gi|254814126|sp|Q9SKG5.2|SERK4_ARATH RecName: Full=Somatic embryogenesis receptor kinase 4; Short=AtSERK4; AltName: Full=Protein BAK1-like 1; Short=AtBKK1; AltName: Full=Somatic embryogenesis receptor-like kinase 2; Flags: Precursor gi|15810409|gb|AAL07092.1| unknown protein [Arabidopsis thaliana] gi|224589505|gb|ACN59286.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|330251165|gb|AEC06259.1| somatic embryogenesis receptor kinase 4 [Arabidopsis thaliana]	615	620	0	100.8	81.5	86.0	somatic embryogenesis receptor kinase 4	gbpln	Arabidopsis thaliana	AT2G13790.1 | Symbols: ATSERK4, SERK4, BKK1, BAK7 | somatic embryogenesis receptor-like kinase 4 | chr2:5741979-5746581 FORWARD LENGTH=620	615	620	0	100.8	81.5	86.0
Rsa1.0_01256.1.g25105.t14	gb|AAF69150.1|AC007915_2 F27F5.2 [Arabidopsis thaliana]	944	937	0	99.3	70.6	78.2	F27F5.2	gbpln	Arabidopsis thaliana	AT1G44910.1 | Symbols: ATPRP40A, PRP40A | pre-mRNA-processing protein 40A | chr1:16975930-16982818 FORWARD LENGTH=958	944	958	0	101.5	57.7	64.1
Rsa1.0_01256.1.g25106.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01256.1.g25107.t1	gb|AAK51235.1|AF287471_1 polyprotein [Arabidopsis thaliana]	681	1453	0	213.4	61.7	75.6	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	681	1262	3.00E-82	185.3	25.0	37.7

Rsa1.0_01256.1.g25108.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	507	1466	0	289.2	64.3	77.9	copia-like polyprotein	gbpln	Arabidopsis thaliana	AT1G34070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48050.1); Has 648 Blast hits to 647 proteins in 29 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 25; Plants - 607; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12402283-12403209 FORWARD LENGTH=308	507	308	1.00E-13	60.7	12.6	20.3
Rsa1.0_01256.1.g25109.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01256.1.g25110.t2	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1231	1413	0	114.8	52.7	68.5	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1231	1262	1.00E-150	102.5	21.2	27.9
Rsa1.0_01256.1.g25111.t4	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	216	484	7.00E-14	224.1	22.7	36.1	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01256.1.g25112.t5	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1302	1274	0	97.8	42.6	59.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1302	575	1.00E-34	44.2	10.1	15.2
Rsa1.0_01257.1.g25113.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01257.1.g25114.t1	ref|XP_002887308.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333149|gb|EFH63567.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	445	466	0	104.7	80.2	83.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G70550.1 | Symbols: | Protein of Unknown Function (DUF239) | chr1:26597510-26599888 FORWARD LENGTH=465	445	465	0	104.5	77.8	82.5
Rsa1.0_01257.1.g25115.t1	ref|NP_177210.1| cysteine-rich receptor-like protein kinase 3 [Arabidopsis thaliana] gi|75333658|sp|Q9CAL2.1|CRK3_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 3; Short=Cysteine-rich RLK3; Flags: Precursor gi|12325043|gb|AAG52470.1|AC010796_9 putative protein kinase; 41292-38663 [Arabidopsis thaliana] gi|332196954|gb|AEE35075.1| cysteine-rich receptor-like protein kinase 3 [Arabidopsis thaliana]	618	646	0	104.5	84.1	90.9	cysteine-rich receptor-like protein kinase 3	gbpln	Arabidopsis thaliana	AT1G70530.1 | Symbols: CRK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 3 | chr1:26588750-26591379 REVERSE LENGTH=646	618	646	0	104.5	84.1	90.9
Rsa1.0_01257.1.g25116.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01257.1.g25117.t1	ref|NP_177210.1| cysteine-rich receptor-like protein kinase 3 [Arabidopsis thaliana] gi|75333658|sp|Q9CAL2.1|CRK3_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 3; Short=Cysteine-rich RLK3; Flags: Precursor gi|12325043|gb|AAG52470.1|AC010796_9 putative protein kinase; 41292-38663 [Arabidopsis thaliana] gi|332196954|gb|AEE35075.1| cysteine-rich receptor-like protein kinase 3 [Arabidopsis thaliana]	647	646	0	99.8	85.3	91.7	cysteine-rich receptor-like protein kinase 3	gbpln	Arabidopsis thaliana	AT1G70530.1 | Symbols: CRK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 3 | chr1:26588750-26591379 REVERSE LENGTH=646	647	646	0	99.8	85.3	91.7
Rsa1.0_01257.1.g25118.t1	gb|EOA33736.1| hypothetical protein CARUB_v10019929mg [Capsella rubella]	652	649	0	99.5	85.6	91.0	hypothetical protein CARUB_v10019929mg	gbpln	Capsella rubella	AT1G70520.1 | Symbols: CRK2 | cysteine-rich RLK (RECEPTOR-like protein kinase) 2 | chr1:26584888-26587334 REVERSE LENGTH=649	652	649	0	99.5	85.3	91.0
Rsa1.0_01257.1.g25119.t1	gb|EOA35431.1| hypothetical protein CARUB_v10020633mg [Capsella rubella]	353	330	1.00E-149	93.5	74.8	82.7	hypothetical protein CARUB_v10020633mg	gbpln	Capsella rubella	AT1G70505.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10660.1); Has 141 Blast hits to 140 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 135; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:26570647-26572463 FORWARD LENGTH=358	353	358	1.00E-121	101.4	60.3	67.7
Rsa1.0_01257.1.g25120.t1	ref|XP_002877193.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323031|gb|EFH53452.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	428	453	1.00E-154	105.8	66.1	79.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G29670.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:11527952-11529307 FORWARD LENGTH=451	428	451	1.00E-156	105.4	65.7	80.1

Rsa1.0_01257.1.g25121.t1	ref|NP_175703.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|12324642|gb|AAG52278.1|AC019018_15 putative replication protein; 94555-97079 [Arabidopsis thaliana] gi|332194750|gb|AEE32871.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	512	566	7.00E-92	110.5	36.1	59.2	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	512	566	2.00E-94	110.5	36.1	59.2
Rsa1.0_01257.1.g25122.t3	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	1639	1752	0	106.9	52.4	66.3	putative protein	gbpln	Arabidopsis thaliana	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	1639	344	2.00E-73	21.0	8.5	11.6
Rsa1.0_01258.1.g25123.t1	gb|ACG47680.1| hypothetical protein [Zea mays] gi|413946083|gb|AFW78732.1| hypothetical protein ZEAMMB73_647957 [Zea mays]	56	72	6.00E-17	128.6	75.0	85.7	hypothetical protein	gbenv/gbpln	Zea mays	AT5G14105.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4552169-4552901 REVERSE LENGTH=76	56	76	4.00E-15	135.7	64.3	69.6
Rsa1.0_01258.1.g25124.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01258.1.g25125.t1	ref|NP_190950.1| C2H2 and C2HC zinc finger-containing protein [Arabidopsis thaliana] gi|7630002|emb|CAB88344.1| putative C2H2-type zinc finger protein [Arabidopsis thaliana] gi|67633692|gb|AAY78770.1| zinc finger (C2H2 type) family protein [Arabidopsis thaliana] gi|225898715|dbj|BAH30488.1| hypothetical protein [Arabidopsis thaliana] gi|332645626|gb|AEE79147.1| C2H2 and C2HC zinc finger-containing protein [Arabidopsis thaliana]	139	142	1.00E-57	102.2	80.6	87.1	C2H2 and C2HC zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT3G53820.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr3:19938706-19939134 FORWARD LENGTH=142	139	142	4.00E-60	102.2	80.6	87.1
Rsa1.0_01258.1.g25126.t1	ref|XP_002872057.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297317894|gb|EFH48316.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	256	302	5.00E-68	118.0	60.2	70.3	NLI interacting factor family protein	gbpln	Arabidopsis lyrata	AT2G02290.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:604453-605361 FORWARD LENGTH=302	256	302	1.00E-68	118.0	59.0	71.1
Rsa1.0_01258.1.g25127.t10	ref|NP_190951.2| Regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] gi|332645627|gb|AEE79148.1| Regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana]	466	472	0	101.3	86.5	92.1	Regulator of chromosome condensation (RCC1) family protein	gbpln	Arabidopsis thaliana	AT3G53830.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:19940814-19943592 FORWARD LENGTH=472	466	472	0	101.3	86.5	92.1
Rsa1.0_01258.1.g25128.t4	gb|EOA25028.1| hypothetical protein CARUB_v10018334mg [Capsella rubella]	124	82	1.00E-39	66.1	62.9	64.5	hypothetical protein CARUB_v10018334mg	gbpln	Capsella rubella	AT5G27700.1 | Symbols: | Ribosomal protein S21e | chr5:9807541-9808048 REVERSE LENGTH=82	124	82	8.00E-42	66.1	62.1	63.7
Rsa1.0_01258.1.g25129.t3	emb|CAB83107.1| sigma factor 3 [Sinapis alba]	877	567	0	64.7	56.3	59.2	sigma factor 3	gbpln	Sinapis alba	AT3G53920.1 | Symbols: SIGC, SIG3 | RNApolymerase sigma-subunit C | chr3:19961041-19963820 REVERSE LENGTH=571	877	571	0	65.1	52.2	56.2
Rsa1.0_01258.1.g25130.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01258.1.g25131.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	166	341	1.00E-31	205.4	44.6	62.7	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01258.1.g25132.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01258.1.g25133.t1	gb|EOA25347.1| hypothetical protein CARUB_v10018670mg [Capsella rubella]	717	707	0	98.6	85.9	91.5	hypothetical protein CARUB_v10018670mg	gbpln	Capsella rubella	AT3G53930.2 | Symbols: | Protein kinase superfamily protein | chr3:19966541-19970580 FORWARD LENGTH=712	717	712	0	99.3	84.9	90.9
Rsa1.0_01258.1.g25134.t1	ref|NP_190962.2| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|17064804|gb|AAL32556.1| putative protein [Arabidopsis thaliana] gi|20259828|gb|AAM13261.1| putative protein [Arabidopsis thaliana] gi|332645641|gb|AEE79162.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana]	356	365	1.00E-167	102.5	83.4	90.4	Mitochondrial substrate carrier family protein	gbpln	Arabidopsis thaliana	AT3G53940.1 | Symbols: | Mitochondrial substrate carrier family protein | chr3:19971258-19973564 REVERSE LENGTH=365	356	365	1.00E-169	102.5	83.4	90.4
Rsa1.0_01259.1.g25135.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01259.1.g25136.t1	ref|NP_200165.1| vacuolar protein sorting 26A [Arabidopsis thaliana] gi|75171014|sp|Q9FJD0.1|VP26A_ARATH RecName: Full=Vacuolar protein sorting-associated protein 26A; AltName: Full=Vesicle protein sorting 26A gi|9759192|dbj|BAB09729.1| vacuolar sorting protein-like; embryogenesis protein H beta 58-like protein [Arabidopsis thaliana] gi|110735821|dbj|BAE99887.1| vacuolar sorting protein-like [Arabidopsis thaliana] gi|332008990|gb|AED96373.1| vacuolar protein sorting 26A [Arabidopsis thaliana]	302	302	1.00E-167	100.0	95.0	97.4	vacuolar protein sorting 26A	gbpln	Arabidopsis thaliana	AT5G53530.1 | Symbols: VPS26A | vacuolar protein sorting 26A | chr5:21746275-21748156 REVERSE LENGTH=302	302	302	1.00E-169	100.0	95.0	97.4
Rsa1.0_01259.1.g25137.t1	ref|XP_002864247.1| ATOPT9 [Arabidopsis lyrata subsp. lyrata] gi|297310082|gb|EFH40506.1| ATOPT9 [Arabidopsis lyrata subsp. lyrata]	740	741	0	100.1	91.4	95.8	ATOPT9	gbpln	Arabidopsis lyrata	AT5G53510.1 | Symbols: ATOPT9, OPT9 | oligopeptide transporter 9 | chr5:21738849-21742082 FORWARD LENGTH=741	740	741	0	100.1	90.4	95.4
Rsa1.0_01259.1.g25138.t1	gb|AAF97298.1|AC007843_1 Hypothetical protein [Arabidopsis thaliana]	354	362	1.00E-108	102.3	56.5	72.3	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01260.1.g25139.t1	gb|AAC95173.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1212	1200	0	99.0	55.8	71.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1212	1262	1.00E-89	104.1	14.1	22.3
Rsa1.0_01260.1.g25140.t1	gb|EOA29315.1| hypothetical protein CARUB_v10025596mg [Capsella rubella]	964	971	0	100.7	81.1	88.9	hypothetical protein CARUB_v10025596mg	gbpln	Capsella rubella	AT2G41790.1 | Symbols: | Insulinase (Peptidase family M16) family protein | chr2:17429453-17436110 REVERSE LENGTH=970	964	970	0	100.6	76.8	86.9
Rsa1.0_01260.1.g25141.t1	gb|EOA29315.1| hypothetical protein CARUB_v10025596mg [Capsella rubella]	994	971	0	97.7	80.2	87.4	hypothetical protein CARUB_v10025596mg	gbpln	Capsella rubella	AT2G41790.1 | Symbols: | Insulinase (Peptidase family M16) family protein | chr2:17429453-17436110 REVERSE LENGTH=970	994	970	0	97.6	76.3	86.0
Rsa1.0_01260.1.g25142.t1	gb|EOA23287.1| hypothetical protein CARUB_v10018323mg [Capsella rubella]	97	87	2.00E-30	89.7	78.4	81.4	hypothetical protein CARUB_v10018323mg	gbpln	Capsella rubella	AT3G57450.1 | Symbols: | unknown protein; Has 65 Blast hits to 65 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 65; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:21262028-21262318 FORWARD LENGTH=96	97	96	1.00E-24	99.0	72.2	78.4
Rsa1.0_01260.1.g25143.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01260.1.g25144.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01261.1.g25145.t1	ref|NP_001154751.1| tetracopeptide epeat-containing protein-like protein [Arabidopsis thaliana] gi|332006684|gb|AED94067.1| putative pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	228	284	5.00E-14	124.6	18.0	19.3	tetracopeptide epeat-containing protein-like protein	gbpln	Arabidopsis thaliana	AT5G36300.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:14320668-14322398 FORWARD LENGTH=284	228	284	1.00E-16	124.6	18.0	19.3
Rsa1.0_01261.1.g25146.t1	gb|EOA39397.1| hypothetical protein CARUB_v10012485mg [Capsella rubella]	105	581	4.00E-48	553.3	84.8	94.3	hypothetical protein CARUB_v10012485mg	gbpln	Capsella rubella	AT1G09280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763), Serine hydrolase (InterPro:IPR005645); BEST Arabidopsis thaliana protein match is: Rhodanese/Cell cycle control phosphatase superfamily protein (TAIR:AT2G40760.1); Has 5925 Blast hits to 5912 proteins in 1592 species: Archae - 0; Bacteria - 2946; Metazoa - 156; Fungi - 408; Plants - 229; Viruses - 0; Other Eukaryotes - 2186 (source: NCBI BLink). | chr1:2998209-3001253 REVERSE LENGTH=581	105	581	1.00E-49	553.3	83.8	93.3
Rsa1.0_01261.1.g25147.t1	ref|XP_002868469.1| hypothetical protein ARALYDRAFT_330235 [Arabidopsis lyrata subsp. lyrata] gi|297314305|gb|EFH44728.1| hypothetical protein ARALYDRAFT_330235 [Arabidopsis lyrata subsp. lyrata]	558	448	0	80.3	66.1	71.1	hypothetical protein ARALYDRAFT_330235	gbpln	Arabidopsis lyrata	AT5G42310.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr5:16915860-16918238 FORWARD LENGTH=709	558	709	1.00E-80	127.1	29.0	44.1
Rsa1.0_01261.1.g25148.t7	ref|NP_568540.1| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain [Arabidopsis thaliana] gi|332006726|gb|AED94109.1| Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain [Arabidopsis thaliana]	1082	1179	0	109.0	62.9	72.9	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain	gbpln	Arabidopsis thaliana	AT5G36740.1 | Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein | chr5:14460790-14465727 FORWARD LENGTH=1179	1082	1179	0	109.0	62.9	72.9

Rsa1.0_01261.1.g25149.t1	ref|NP_198495.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|30692947|ref|NP_198485.2| 2-phosphoglycolate phosphatase 1 [Arabidopsis thaliana] gi|186526986|ref|NP_001119316.1| 2-phosphoglycolate phosphatase 1 [Arabidopsis thaliana] gi|186527016|ref|NP_001119318.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|334188040|ref|NP_001190427.1| 2-phosphoglycolate phosphatase 1 [Arabidopsis thaliana] gi|334188042|ref|NP_001190428.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|487522899|sp|P0DKC4.1|PGP1B_ARATH RecName: Full=Phosphoglycolate phosphatase 1B, chloroplastic; Flags: Precursor gi|487523199|sp|P0DKC3.1|PGP1A_ARATH RecName: Full=Phosphoglycolate phosphatase 1A, chloroplastic; Flags: Precursor gi|20453153|gb|AAM19818.1| AT5g36790/f5h8_20 [Arabidopsis thaliana] gi|21689621|gb|AAM67432.1| AT5g36790/f5h8_20 [Arabidopsis thaliana] gi|332006716|gb|AED94099.1| 2-phosphoglycolate phosphatase 1 [Arabidopsis thaliana]	355	362	0	102.0	91.5	95.8	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G36700.4 | Symbols: PGLP1 | 2-phosphoglycolate phosphatase 1 | chr5:14421929-14424430 REVERSE LENGTH=362	355	362	0	102.0	91.5	95.8
Rsa1.0_01261.1.g25150.t1	gb|ABL97950.1| unknown [Brassica rapa]	182	182	4.00E-98	100.0	98.4	98.9	unknown	gbpln	Brassica rapa	AT5G36710.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G36800.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:14425491-14426042 REVERSE LENGTH=183	182	183	2.00E-90	100.5	88.5	95.6
Rsa1.0_01261.1.g25151.t2	ref|XP_002870490.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297316326|gb|EFH46749.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata]	487	490	0	100.6	85.4	92.0	glycosyl hydrolase family 1 protein	gbpln	Arabidopsis lyrata	AT5G36890.1 | Symbols: BGLU42 | beta glucosidase 42 | chr5:14542164-14546090 REVERSE LENGTH=490	487	490	0	100.6	85.0	91.8
Rsa1.0_01262.1.g25152.t1	ref|NP_175557.1| ABC transporter G family member 13 [Arabidopsis thaliana] gi|75333523|sp|Q9C8J8.1|AB13G_ARATH RecName: Full=ABC transporter G family member 13; Short=ABC transporter ABCG.13; Short=AtABCG13; AltName: Full=White-brown complex homolog protein 13; Short=AtWBC13 gi|12325372|gb|AAG52631.1|AC024261_18 ATP-dependent transmembrane transporter, putative; 59412-63615 [Arabidopsis thaliana] gi|332194549|gb|AEE32670.1| ABC transporter G family member 13 [Arabidopsis thaliana]	685	678	0	99.0	87.0	93.4	ABC transporter G family member 13	gbpln	Arabidopsis thaliana	AT1G51460.1 | Symbols: | ABC-2 type transporter family protein | chr1:19077132-19081335 REVERSE LENGTH=678	685	678	0	99.0	87.0	93.4
Rsa1.0_01262.1.g25153.t1	gb|EOA36866.1| hypothetical protein CARUB_v10008858mg [Capsella rubella]	455	521	1.00E-170	114.5	75.4	83.7	hypothetical protein CARUB_v10008858mg	gbpln	Capsella rubella	AT1G51450.1 | Symbols: TRO | TRAUCO | chr1:19074399-19076220 FORWARD LENGTH=509	455	509	1.00E-169	111.9	71.6	78.2
Rsa1.0_01262.1.g25154.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01262.1.g25155.t1	gb|EOA39443.1| hypothetical protein CARUB_v10012613mg [Capsella rubella]	326	345	1.00E-154	105.8	86.2	90.5	hypothetical protein CARUB_v10012613mg	gbpln	Capsella rubella	AT1G51220.1 | Symbols: WIP5 | WIP domain protein 5 | chr1:18989925-18992034 REVERSE LENGTH=337	326	337	1.00E-154	103.4	85.0	89.3
Rsa1.0_01262.1.g25156.t1	ref|XP_002891623.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297337465|gb|EFH67882.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	461	456	0	98.9	70.3	78.3	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT1G51210.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:18987809-18989110 FORWARD LENGTH=433	461	433	0	93.9	65.5	74.2

Rsa1.0_01262.1.g25157.t1	gb|AAD30636.1|AC006085_9 Hypothetical protein [Arabidopsis thaliana]	114	299	6.00E-18	262.3	36.0	36.0	Hypothetical protein	gbpln	Arabidopsis thaliana	AT3G20880.1 | Symbols: WIP4 | WIP domain protein 4 | chr3:7313759-7315792 REVERSE LENGTH=412	114	412	1.00E-20	361.4	36.0	36.0
Rsa1.0_01262.1.g25158.t3	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	1603	1557	0	97.1	42.9	60.0	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1603	575	8.00E-82	35.9	11.5	17.5
Rsa1.0_01262.1.g25159.t1	ref|XP_002877953.1| hypothetical protein ARALYDRAFT_485800 [Arabidopsis lyrata subsp. lyrata] gi|297323791|gb|EFH54212.1| hypothetical protein ARALYDRAFT_485800 [Arabidopsis lyrata subsp. lyrata]	184	183	6.00E-87	99.5	85.9	92.9	hypothetical protein ARALYDRAFT_485800	gbpln	Arabidopsis lyrata	AT3G54040.1 | Symbols: | PAR1 protein | chr3:20014032-20015299 REVERSE LENGTH=183	184	183	2.00E-86	99.5	82.1	92.4
Rsa1.0_01262.1.g25160.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01262.1.g25161.t1	ref|XP_002891623.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297337465|gb|EFH67882.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	463	456	0	98.5	77.1	84.9	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT1G51210.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:18987809-18989110 FORWARD LENGTH=433	463	433	0	93.5	74.3	80.8
Rsa1.0_01262.1.g25162.t1	gb|ABV89666.1| zinc finger an1-like family protein [Brassica rapa]	181	168	2.00E-91	92.8	89.0	91.2	zinc finger an1-like family protein	gbpln	Brassica rapa	AT1G51200.4 | Symbols: | A20/AN1-like zinc finger family protein | chr1:18985690-18986211 FORWARD LENGTH=173	181	173	5.00E-72	95.6	82.9	86.2
Rsa1.0_01262.1.g25163.t1	ref|XP_002870649.1| hypothetical protein ARALYDRAFT_355852 [Arabidopsis lyrata subsp. lyrata] gi|297316485|gb|EFH46908.1| hypothetical protein ARALYDRAFT_355852 [Arabidopsis lyrata subsp. lyrata]	586	634	1.00E-123	108.2	50.7	63.8	hypothetical protein ARALYDRAFT_355852	gbpln	Arabidopsis lyrata	AT5G41690.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:16670126-16674189 REVERSE LENGTH=567	586	567	1.00E-108	96.8	44.7	59.7
Rsa1.0_01263.1.g25164.t1	gb|EOA16688.1| hypothetical protein CARUB_v10004881mg [Capsella rubella]	438	424	0	96.8	78.5	86.1	hypothetical protein CARUB_v10004881mg	gbpln	Capsella rubella	AT4G20960.1 | Symbols: | Cytidine/deoxycytidylate deaminase family protein | chr4:11212077-11213530 FORWARD LENGTH=426	438	426	0	97.3	80.6	87.9
Rsa1.0_01263.1.g25165.t1	gb|EOA17462.1| hypothetical protein CARUB_v10005784mg, partial [Capsella rubella]	165	196	2.00E-59	118.8	75.2	84.8	hypothetical protein CARUB_v10005784mg, partial	gbpln	Capsella rubella	AT4G20970.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:11215259-11216212 FORWARD LENGTH=190	165	190	2.00E-57	115.2	75.2	86.7
Rsa1.0_01263.1.g25166.t14	gb|EOA18536.1| hypothetical protein CARUB_v10007090mg [Capsella rubella]	293	255	4.00E-99	87.0	68.9	77.1	hypothetical protein CARUB_v10007090mg	gbpln	Capsella rubella	AT4G21020.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr4:11228263-11229392 FORWARD LENGTH=266	293	266	1.00E-95	90.8	67.2	77.1
Rsa1.0_01263.1.g25167.t1	ref|XP_002869912.1| hypothetical protein ARALYDRAFT_914579 [Arabidopsis lyrata subsp. lyrata] gi|297315748|gb|EFH46171.1| hypothetical protein ARALYDRAFT_914579 [Arabidopsis lyrata subsp. lyrata]	75	194	8.00E-20	258.7	62.7	76.0	hypothetical protein ARALYDRAFT_914579	gbpln	Arabidopsis lyrata	AT4G21050.1 | Symbols: | Dof-type zinc finger domain-containing protein | chr4:11238441-11239073 FORWARD LENGTH=210	75	210	8.00E-22	280.0	62.7	76.0
Rsa1.0_01263.1.g25168.t1	ref|XP_002869911.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315747|gb|EFH46170.1| Dof-type zinc finger domain-containing protein [Arabidopsis lyrata subsp. lyrata]	259	223	1.00E-52	86.1	50.6	59.1	Dof-type zinc finger domain-containing protein	gbpln	Arabidopsis lyrata	AT4G21050.1 | Symbols: | Dof-type zinc finger domain-containing protein | chr4:11238441-11239073 FORWARD LENGTH=210	259	210	7.00E-41	81.1	37.8	45.9
Rsa1.0_01263.1.g25169.t1	ref|NP_193839.4| protein BREAST CANCER SUSCEPTIBILITY 1-like protein [Arabidopsis thaliana] gi|75158839|sp|Q8RXD4.1|BRCA1_ARATH RecName: Full=Protein BREAST CANCER SUSCEPTIBILITY 1 homolog; Short=AtBRCA1 gi|19698963|gb|AAL91217.1| unknown protein [Arabidopsis thaliana] gi|28372474|gb|AAO39850.1| BRCA1 [Arabidopsis thaliana] gi|34365717|gb|AAQ65170.1| At4g21070 [Arabidopsis thaliana] gi|332658996|gb|AEE84396.1| protein BREAST CANCER SUSCEPTIBILITY 1-like protein [Arabidopsis thaliana]	929	941	0	101.3	72.4	82.0	protein BREAST CANCER SUSCEPTIBILITY 1-like protein	gbpln	Arabidopsis thaliana	AT4G21070.1 | Symbols: ATBRCA1, BRCA1 | breast cancer susceptibility1 | chr4:11248174-11252633 FORWARD LENGTH=941	929	941	0	101.3	72.4	82.0

Rsa1.0_01263.1.g25170.t1	ref|NP_193841.2| ferredoxin 2 [Arabidopsis thaliana] gi|30685306|ref|NP_849415.1| ferredoxin 2 [Arabidopsis thaliana] gi|79325201|ref|NP_001031685.1| ferredoxin 2 [Arabidopsis thaliana] gi|19698259|dbj|BAB86773.1| MFDX2 precursor [Arabidopsis thaliana] gi|28192429|gb|AAL82812.1| adrenodoxin-like ferredoxin 1 [Arabidopsis thaliana] gi|28466923|gb|AAO44070.1| At4g21090 [Arabidopsis thaliana] gi|110743957|dbj|BAE99811.1| mitochondrial ferredoxin [Arabidopsis thaliana] gi|222424373|dbj|BAH20142.1| AT4G21090 [Arabidopsis thaliana] gi|332658998|gb|AEE84398.1| ferredoxin 2 [Arabidopsis thaliana] gi|332658999|gb|AEE84399.1| ferredoxin 2 [Arabidopsis thaliana] gi|332659000|gb|AEE84400.1| ferredoxin 2 [Arabidopsis thaliana]	209	197	1.00E-65	94.3	63.2	69.4	ferredoxin 2	gbpln	Arabidopsis thaliana	AT4G21090.3 | Symbols: ATMFDX2, MFDX2 | MITOCHONDRIAL FERREDOXIN 2 | chr4:11256663-11258269 REVERSE LENGTH=197	209	197	5.00E-68	94.3	63.2	69.4
Rsa1.0_01263.1.g25171.t1	ref|XP_002867863.1| hypothetical protein ARALYDRAFT_492777 [Arabidopsis lyrata subsp. lyrata] gi|297313699|gb|EFH44122.1| hypothetical protein ARALYDRAFT_492777 [Arabidopsis lyrata subsp. lyrata]	1088	1088	0	100.0	91.5	96.1	hypothetical protein ARALYDRAFT_492777	gbpln	Arabidopsis lyrata	AT4G21100.1 | Symbols: DDB1B | damaged DNA binding protein 1B | chr4:11258916-11265309 REVERSE LENGTH=1088	1088	1088	0	100.0	90.0	95.7
Rsa1.0_01263.1.g25172.t1	gb|EOA17786.1| hypothetical protein CARUB_v10006179mg [Capsella rubella]	68	68	8.00E-32	100.0	98.5	100.0	hypothetical protein CARUB_v10006179mg	gbpln	Capsella rubella	AT4G21105.1 | Symbols: | cytochrome-c oxidases;electron carriers | chr4:11266273-11266724 FORWARD LENGTH=68	68	68	4.00E-34	100.0	95.6	100.0
Rsa1.0_01263.1.g25173.t1	gb|EOA17580.1| hypothetical protein CARUB_v10005939mg [Capsella rubella]	168	153	4.00E-66	91.1	73.8	79.2	hypothetical protein CARUB_v10005939mg	gbpln	Capsella rubella	AT4G21110.1 | Symbols: | G10 family protein | chr4:11267673-11268774 FORWARD LENGTH=145	168	145	3.00E-47	86.3	49.4	54.2
Rsa1.0_01263.1.g25174.t1	ref|XP_002869906.1| hypothetical protein ARALYDRAFT_329490 [Arabidopsis lyrata subsp. lyrata] gi|297315742|gb|EFH46165.1| hypothetical protein ARALYDRAFT_329490 [Arabidopsis lyrata subsp. lyrata]	598	599	0	100.2	87.0	93.3	hypothetical protein ARALYDRAFT_329490	gbpln	Arabidopsis lyrata	AT4G21120.1 | Symbols: AAT1, CAT1 | amino acid transporter 1 | chr4:11270318-11273775 FORWARD LENGTH=594	598	594	0	99.3	86.0	92.6
Rsa1.0_01264.1.g25175.t1	ref|XP_002893071.1| hypothetical protein ARALYDRAFT_335233 [Arabidopsis lyrata subsp. lyrata] gi|297338913|gb|EFH69330.1| hypothetical protein ARALYDRAFT_335233 [Arabidopsis lyrata subsp. lyrata]	933	986	0	105.7	84.2	90.7	hypothetical protein ARALYDRAFT_335233	gbpln	Arabidopsis lyrata	AT1G19835.2 | Symbols: | Plant protein of unknown function (DUF869) | chr1:6856212-6859513 REVERSE LENGTH=982	933	982	0	105.3	83.7	90.1
Rsa1.0_01264.1.g25176.t2	ref|XP_002890353.1| ATPUP14 [Arabidopsis lyrata subsp. lyrata] gi|297336195|gb|EFH66612.1| ATPUP14 [Arabidopsis lyrata subsp. lyrata]	704	393	0	55.8	45.5	50.3	ATPUP14	gbpln	Arabidopsis lyrata	AT1G19770.1 | Symbols: ATPUP14, PUP14 | purine permease 14 | chr1:6832426-6833702 FORWARD LENGTH=393	704	393	1.00E-176	55.8	45.2	49.7
Rsa1.0_01264.1.g25177.t1	gb|EOA39312.1| hypothetical protein CARUB_v10012347mg [Capsella rubella]	555	1361	0	245.2	77.3	87.6	hypothetical protein CARUB_v10012347mg	gbpln	Capsella rubella	AT1G19715.1 | Symbols: | Mannose-binding lectin superfamily protein | chr1:6816934-6819432 REVERSE LENGTH=595	555	595	0	107.2	77.8	89.4
Rsa1.0_01264.1.g25178.t4	dbj|BAJ33686.1| unnamed protein product [Thellungiella halophila]	625	554	0	88.6	66.4	72.0	unnamed protein product	----	----	AT1G19700.3 | Symbols: BEL10 | BEL1-like homeodomain 10 | chr1:6809958-6811854 REVERSE LENGTH=538	625	538	0	86.1	62.1	69.1
Rsa1.0_01264.1.g25179.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01264.1.g25180.t1	sp|Q9SBK6.1|JMT_BRARP RecName: Full=Jasmonate O-methyltransferase; AltName: Full=Floral nectary-specific protein 1; AltName: Full=S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase gi|6651395|gb|AAF22289.1|AF179222_1 floral nectary-specific protein [Brassica rapa subsp. pekinensis]	392	392	0	100.0	91.8	95.7	RecName: Full=Jasmonate O-methyltransferase; AltName: Full=Floral nectary-specific protein 1; AltName: Full=S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase gi|6651395|gb|AAF22289.1|AF179222_1 floral nectary-specific protein	gbpln	Brassica rapa	AT1G19640.1 | Symbols: JMT | jasmonic acid carboxyl methyltransferase | chr1:6789166-6791708 REVERSE LENGTH=389	392	389	1.00E-179	99.2	83.2	89.3
Rsa1.0_01264.1.g25181.t1	gb|EOA40276.1| hypothetical protein CARUB_v10009004mg [Capsella rubella]	458	481	0	105.0	68.6	72.7	hypothetical protein CARUB_v10009004mg	gbpln	Capsella rubella	AT1G19630.1 | Symbols: CYP722A1 | cytochrome P450, family 722, subfamily A, polypeptide 1 | chr1:6785427-6787967 REVERSE LENGTH=476	458	476	0	103.9	67.5	72.7

Rsa1.0_01265.1.g25182.t1	ref|XP_002879091.1| calcium ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297324930|gb|EFH55350.1| calcium ion binding protein [Arabidopsis lyrata subsp. lyrata]	183	228	2.00E-75	124.6	79.8	85.8	calcium ion binding protein	gbpln	Arabidopsis lyrata	AT2G27480.1 | Symbols: | Calcium-binding EF-hand family protein | chr2:11746811-11747885 FORWARD LENGTH=228	183	228	3.00E-75	124.6	78.7	84.7
Rsa1.0_01265.1.g25183.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	862	1142	0	132.5	39.3	49.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	862	154	4.00E-38	17.9	8.5	11.5
Rsa1.0_01265.1.g25184.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01265.1.g25185.t2	gb|AAF97297.1|AC010164_19 Hypothetical protein [Arabidopsis thaliana]	320	308	6.00E-25	96.3	16.9	18.8	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01265.1.g25186.t1	ref|XP_002880914.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297326753|gb|EFH57173.1| binding protein [Arabidopsis lyrata subsp. lyrata]	133	440	2.00E-51	330.8	78.2	88.7	binding protein	gbpln	Arabidopsis lyrata	AT2G27430.1 | Symbols: | ARM repeat superfamily protein | chr2:11729914-11733170 REVERSE LENGTH=438	133	438	1.00E-53	329.3	76.7	89.5
Rsa1.0_01265.1.g25187.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	754	1161	8.00E-83	154.0	21.1	28.5	F14N23.4	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	754	626	2.00E-78	83.0	17.5	25.2
Rsa1.0_01265.1.g25188.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	792	657	0	83.0	46.8	61.1	T14P8.10	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	792	332	1.00E-72	41.9	16.0	22.7
Rsa1.0_01265.1.g25189.t1	ref|XP_002880914.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297326753|gb|EFH57173.1| binding protein [Arabidopsis lyrata subsp. lyrata]	282	440	1.00E-134	156.0	86.2	93.3	binding protein	gbpln	Arabidopsis lyrata	AT2G27430.1 | Symbols: | ARM repeat superfamily protein | chr2:11729914-11733170 REVERSE LENGTH=438	282	438	1.00E-135	155.3	85.8	92.9
Rsa1.0_01265.1.g25190.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	206	441	4.00E-50	214.1	45.1	64.1	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	206	746	3.00E-35	362.1	33.0	45.1
Rsa1.0_01265.1.g25191.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01265.1.g25192.t1	ref|NP_001189619.1| uncharacterized protein [Arabidopsis thaliana] gi|330252897|gb|AEC07991.1| uncharacterized protein AT2G27389 [Arabidopsis thaliana]	182	186	4.00E-12	102.2	19.8	24.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G27389.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system. | chr2:11720362-11720922 FORWARD LENGTH=186	182	186	2.00E-14	102.2	19.8	24.7
Rsa1.0_01266.1.g25193.t1	ref|XP_002879716.1| hypothetical protein ARALYDRAFT_482800 [Arabidopsis lyrata subsp. lyrata] gi|297325555|gb|EFH55975.1| hypothetical protein ARALYDRAFT_482800 [Arabidopsis lyrata subsp. lyrata]	307	305	1.00E-168	99.3	94.1	96.7	hypothetical protein ARALYDRAFT_482800	gbpln	Arabidopsis lyrata	AT2G37940.1 | Symbols: AtIPCS2 | Arabidopsis Inositol phosphorylceramide synthase 2 | chr2:15877169-15879411 FORWARD LENGTH=305	307	305	1.00E-170	99.3	93.8	96.7
Rsa1.0_01266.1.g25194.t1	gb|EOA27751.1| hypothetical protein CARUB_v10023904mg [Capsella rubella]	200	253	5.00E-80	126.5	82.5	86.0	hypothetical protein CARUB_v10023904mg	gbpln	Capsella rubella	AT2G37920.1 | Symbols: emb1513 | copper ion transmembrane transporters | chr2:15869269-15870024 REVERSE LENGTH=251	200	251	3.00E-81	125.5	80.5	84.0
Rsa1.0_01266.1.g25195.t1	gb|EOA26793.1| hypothetical protein CARUB_v10022888mg [Capsella rubella]	586	583	0	99.5	85.0	92.0	hypothetical protein CARUB_v10022888mg	gbpln	Capsella rubella	AT2G37900.1 | Symbols: | Major facilitator superfamily protein | chr2:15864396-15866408 REVERSE LENGTH=575	586	575	0	98.1	83.1	90.1
Rsa1.0_01266.1.g25196.t1	ref|NP_565873.1| uncharacterized protein [Arabidopsis thaliana] gi|91806329|gb|ABE65892.1| unknown [Arabidopsis thaliana] gi|330254367|gb|AEC09461.1| uncharacterized protein AT2G37880 [Arabidopsis thaliana]	245	247	1.00E-102	100.8	82.0	89.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G37880.1 | Symbols: | Protein of unknown function, DUF617 | chr2:15860705-15861448 FORWARD LENGTH=247	245	247	1.00E-104	100.8	82.0	89.4
Rsa1.0_01266.1.g25197.t1	gb|AAD17409.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	833	1347	1.00E-100	161.7	22.1	34.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT3G21000.1 | Symbols: | Gag-Pol-related retrotransposon family protein | chr3:7363921-7365138 FORWARD LENGTH=405	833	405	8.00E-43	48.6	13.8	24.6
Rsa1.0_01266.1.g25198.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01266.1.g25199.t1	ref|XP_002879710.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325549|gb|EFH55969.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	663	733	0	110.6	85.4	91.3	kinase family protein	gbpln	Arabidopsis lyrata	AT2G37840.1 | Symbols: | Protein kinase superfamily protein | chr2:15851978-15856047 FORWARD LENGTH=733	663	733	0	110.6	85.4	90.8
Rsa1.0_01266.1.g25200.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01266.1.g25201.t1	ref|NP_181316.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|330254358|gb|AEC09452.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	251	396	1.00E-101	157.8	75.7	84.1	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G37800.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:15841039-15843610 REVERSE LENGTH=396	251	396	1.00E-103	157.8	75.7	84.1
Rsa1.0_01266.1.g25202.t1	ref|NP_001189996.1| V-type proton ATPase subunit d2 [Arabidopsis thaliana] gi|332643961|gb|AEE77482.1| V-type proton ATPase subunit d2 [Arabidopsis thaliana]	178	343	3.00E-11	192.7	34.3	42.7	V-type proton ATPase subunit d2	gbpln	Arabidopsis thaliana	AT3G28715.2 | Symbols: | ATPase, V0/A0 complex, subunit C/D | chr3:10778025-10780350 FORWARD LENGTH=343	178	343	1.00E-13	192.7	34.3	42.7
Rsa1.0_01266.1.g25203.t1	ref|NP_181316.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|330254358|gb|AEC09452.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	328	396	2.00E-70	120.7	38.4	45.7	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G37800.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:15841039-15843610 REVERSE LENGTH=396	328	396	5.00E-73	120.7	38.4	45.7
Rsa1.0_01266.1.g25204.t1	#	#	#	#	#	#	#	-	----	----	AT2G37790.1 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr2:15838838-15840752 FORWARD LENGTH=314	109	314	2.00E-11	288.1	33.0	41.3
Rsa1.0_01266.1.g25205.t1	gb|EOA29194.1| hypothetical protein CARUB_v10025466mg [Capsella rubella]	237	182	2.00E-65	76.8	58.6	62.9	hypothetical protein CARUB_v10025466mg	gbpln	Capsella rubella	AT2G37780.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:15837442-15838302 REVERSE LENGTH=286	237	286	8.00E-64	120.7	51.1	59.1
Rsa1.0_01267.1.g25206.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	198	704	2.00E-18	355.6	20.7	23.2	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01267.1.g25207.t1	gb|EOA38640.1| hypothetical protein CARUB_v10010550mg [Capsella rubella]	152	152	2.00E-77	100.0	92.1	96.7	hypothetical protein CARUB_v10010550mg	gbpln	Capsella rubella	AT1G22990.1 | Symbols: HIPP22 | Heavy metal transport/detoxification superfamily protein | chr1:8139221-8140045 FORWARD LENGTH=152	152	152	2.00E-78	100.0	90.8	94.7
Rsa1.0_01267.1.g25208.t3	gb|AAF69172.1|AC007915_24 F27F5.11 [Arabidopsis thaliana]	329	1313	4.00E-29	399.1	23.7	31.9	F27F5.11	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01267.1.g25209.t2	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1401	2726	0	194.6	68.2	81.4	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1401	158	2.00E-31	11.3	4.7	6.1
Rsa1.0_01267.1.g25210.t7	ref|NP_173708.3| uncharacterized PKHD-type hydroxylase [Arabidopsis thaliana] gi|193806639|sp|Q3ED68.2|Y1295_ARATH RecName: Full=Uncharacterized PKHD-type hydroxylase At1g22950 gi|332192193|gb|AEE30314.1| uncharacterized PKHD-type hydroxylase [Arabidopsis thaliana]	284	397	1.00E-106	139.8	61.3	77.1	uncharacterized PKHD-type hydroxylase	gbpln	Arabidopsis thaliana	AT1G22950.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(Ⅱ)-dependent oxygenase superfamily protein | chr1:8125291-8127168 REVERSE LENGTH=397	284	397	1.00E-109	139.8	61.3	77.1
Rsa1.0_01267.1.g25211.t1	dbj|BAK41511.1| polyprotein [Arabidopsis thaliana]	245	1466	2.00E-43	598.4	39.6	53.1	polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01267.1.g25212.t1	ref|NP_173701.1| endoglucanase 3 [Arabidopsis thaliana] gi|114149313|sp|Q2V4L8.2|GUN3_ARATH RecName: Full=Endoglucanase 3; AltName: Full=Cellulase 5; Short=AtCEL5; AltName: Full=Endo-1,4-beta glucanase 3; Flags: Precursor gi|2462836|gb|AAB72171.1| beta-glucanase [Arabidopsis thaliana] gi|332192178|gb|AEE30299.1| endoglucanase 3 [Arabidopsis thaliana]	509	484	0	95.1	83.5	86.8	endoglucanase 3	gbpln	Arabidopsis thaliana	AT1G22880.1 | Symbols: ATGH9B4, ATCEL5, CEL5 | cellulase 5 | chr1:8095770-8097539 FORWARD LENGTH=484	509	484	0	95.1	83.5	86.8
Rsa1.0_01267.1.g25213.t1	gb|AAD17351.1| contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana] gi|7267432|emb|CAB77944.1| putative polyprotein [Arabidopsis thaliana]	354	1138	2.00E-32	321.5	21.5	31.1	contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1)	gbpln	Arabidopsis thaliana	AT3G13300.2 | Symbols: VCS | Transducin/WD40 repeat-like superfamily protein | chr3:4304085-4309949 FORWARD LENGTH=1309	354	1309	1.00E-24	369.8	20.1	28.2
Rsa1.0_01268.1.g25214.t1	gb|AAD36950.1|AF069441_10 putative transposon protein [Arabidopsis thaliana] gi|7267188|emb|CAB77899.1| putative transposon protein [Arabidopsis thaliana]	769	1011	2.00E-22	131.5	7.3	9.9	putative transposon protein	gbpln	Arabidopsis thaliana	AT4G07350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40129.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:4172609-4175227 REVERSE LENGTH=330	769	330	1.00E-23	42.9	7.0	9.0

Rsa1.0_01268.1.g25215.t1	gb|EOA38822.1| hypothetical protein CARUB_v10011146mg [Capsella rubella]	395	386	1.00E-70	97.7	41.8	60.5	hypothetical protein CARUB_v10011146mg	gbpln	Capsella rubella	AT1G09650.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3125978-3127126 FORWARD LENGTH=382	395	382	2.00E-65	96.7	40.3	57.5
Rsa1.0_01268.1.g25216.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01268.1.g25217.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1353	1307	0	96.6	59.9	74.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1353	1262	1.00E-101	93.3	14.1	22.5
Rsa1.0_01268.1.g25218.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1291	1307	0	101.2	61.7	77.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1291	1262	1.00E-88	97.8	14.3	20.9
Rsa1.0_01268.1.g25219.t1	gb|AAF67379.1| Hypothetical protein T15F17.k [Arabidopsis thaliana]	304	341	4.00E-95	112.2	61.8	75.0	Hypothetical protein T15F17.k	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01268.1.g25220.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01268.1.g25221.t1	gb|AAC26241.1| F9D12.15 gene product [Arabidopsis thaliana]	265	850	7.00E-18	320.8	17.7	29.1	F9D12.15 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01268.1.g25222.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	326	1024	3.00E-35	314.1	26.1	37.4	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01269.1.g25223.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01269.1.g25224.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01269.1.g25225.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	372	1838	3.00E-81	494.1	42.7	59.7	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01269.1.g25226.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	786	1103	1.00E-147	140.3	37.3	49.6	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01269.1.g25227.t1	#	#	#	#	#	#	#	–	----	----	AT2G11010.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT5G32590.1); Has 404 Blast hits to 390 proteins in 105 species: Archae - 10; Bacteria - 61; Metazoa - 184; Fungi - 25; Plants - 79; Viruses - 0; Other Eukaryotes - 45 (source: NCBI BLink). | chr2:4361869-4365919 FORWARD LENGTH=693	559	693	1.00E-10	124.0	8.6	14.1
Rsa1.0_01269.1.g25228.t1	#	#	#	#	#	#	#	–	----	----	AT3G45730.1 | Symbols: | unknown protein; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:16790072-16790290 FORWARD LENGTH=72	74	72	2.00E-13	97.3	51.4	62.2
Rsa1.0_01269.1.g25229.t1	ref|NP_566881.1| putative trans-2-enoyl-CoA reductase [Arabidopsis thaliana] gi|62900587|sp|Q8LCU7.1|MECR_ARATH RecName: Full=Probable trans-2-enoyl-CoA reductase, mitochondrial; Flags: Precursor gi|21592515|gb|AAM64465.1| nuclear receptor binding factor-like protein [Arabidopsis thaliana] gi|332644550|gb|AEE78071.1| putative trans-2-enoyl-CoA reductase [Arabidopsis thaliana]	375	375	0	100.0	88.0	92.5	putative trans-2-enoyl-CoA reductase	gbpln	Arabidopsis thaliana	AT3G45770.1 | Symbols: | Polyketide synthase, enoylreductase family protein | chr3:16805753-16807774 REVERSE LENGTH=375	375	375	0	100.0	88.0	92.5
Rsa1.0_01269.1.g25230.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01269.1.g25231.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01269.1.g25232.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01269.1.g25233.t1	ref|NP_190171.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|334185753|ref|NP_001190017.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|7339486|emb|CAB82809.1| kinesin-related protein-like [Arabidopsis thaliana] gi|332644559|gb|AEE78080.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|332644560|gb|AEE78081.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana]	1055	1058	0	100.3	94.2	97.6	P-loop containing nucleoside triphosphate hydrolase-like protein	gbpln	Arabidopsis thaliana	AT3G45850.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:16855814-16860950 REVERSE LENGTH=1058	1055	1058	0	100.3	94.2	97.6

Rsa1.0_01269.1.g25234.t2	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	382	954	2.00E-51	249.7	42.7	57.9	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01270.1.g25235.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01270.1.g25236.t2	emb|CAA31653.1| polyprotein [Arabidopsis thaliana]	579	1291	1.00E-120	223.0	40.8	56.8	polyprotein	gbpln	Arabidopsis thaliana	ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145	579	145	1.00E-24	25.0	9.5	13.1
Rsa1.0_01270.1.g25237.t1	gb|EOA39820.1| hypothetical protein CARUB_v10008487mg, partial [Capsella rubella]	600	685	0	114.2	80.0	87.5	hypothetical protein CARUB_v10008487mg, partial	gbpln	Capsella rubella	AT1G20670.1 | Symbols: | DNA-binding bromodomain-containing protein | chr1:7164537-7167933 REVERSE LENGTH=652	600	652	0	108.7	77.7	85.2
Rsa1.0_01270.1.g25238.t1	ref|XP_002884894.1| hypothetical protein ARALYDRAFT_897434 [Arabidopsis lyrata subsp. lyrata] gi|297330734|gb|EFH61153.1| hypothetical protein ARALYDRAFT_897434 [Arabidopsis lyrata subsp. lyrata]	422	435	0	103.1	81.0	89.3	hypothetical protein ARALYDRAFT_897434	gbpln	Arabidopsis lyrata	AT3G12230.1 | Symbols: scpl14 | serine carboxypeptidase-like 14 | chr3:3899431-3901879 REVERSE LENGTH=435	422	435	0	103.1	79.1	89.3
Rsa1.0_01270.1.g25239.t2	gb|AAD30292.1|AF139539_1 catalase 3 [Raphanus sativus]	492	492	0	100.0	99.6	99.8	catalase 3	gbpln	Raphanus sativus	AT1G20620.1 | Symbols: CAT3, SEN2, ATCAT3 | catalase 3 | chr1:7143142-7146193 FORWARD LENGTH=492	492	492	0	100.0	98.2	99.2
Rsa1.0_01270.1.g25240.t1	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	585	695	1.00E-154	118.8	45.1	47.4	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01270.1.g25241.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	456	1142	4.00E-96	250.4	40.1	57.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	456	575	2.00E-55	126.1	28.7	48.7
Rsa1.0_01270.1.g25242.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01271.1.g25243.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01271.1.g25244.t1	emb|CAN77974.1| hypothetical protein VITISV_006175 [Vitis vinifera]	268	1501	1.00E-112	560.1	71.3	84.3	hypothetical protein VITISV_006175	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	268	1262	2.00E-25	470.9	25.4	35.8
Rsa1.0_01271.1.g25245.t1	gb|ABD64973.1| Zinc knuckle containing protein [Brassica oleracea]	184	319	4.00E-83	173.4	81.5	89.1	Zinc knuckle containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01271.1.g25246.t1	dbj|BAJ33967.1| unnamed protein product [Thellungiella halophila]	587	530	0	90.3	78.4	82.6	unnamed protein product	----	----	AT2G22830.1 | Symbols: SQE2 | squalene epoxidase 2 | chr2:9723947-9726270 REVERSE LENGTH=585	587	585	0	99.7	77.7	85.0
Rsa1.0_01271.1.g25247.t1	ref|XP_002878639.1| ATPSK2 [Arabidopsis lyrata subsp. lyrata] gi|297324478|gb|EFH54898.1| ATPSK2 [Arabidopsis lyrata subsp. lyrata]	86	86	8.00E-29	100.0	77.9	83.7	ATPSK2	gbpln	Arabidopsis lyrata	AT2G22860.1 | Symbols: ATPSK2, PSK2 | phytosulfokine 2 precursor | chr2:9737666-9738077 FORWARD LENGTH=87	86	87	6.00E-28	101.2	74.4	80.2
Rsa1.0_01271.1.g25248.t1	ref|XP_002878640.1| EMB2001 [Arabidopsis lyrata subsp. lyrata] gi|297324479|gb|EFH54899.1| EMB2001 [Arabidopsis lyrata subsp. lyrata]	304	300	1.00E-148	98.7	86.8	91.1	EMB2001	gbpln	Arabidopsis lyrata	AT2G22870.1 | Symbols: EMB2001 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:9739476-9740921 FORWARD LENGTH=300	304	300	1.00E-147	98.7	85.9	90.5
Rsa1.0_01271.1.g25249.t1	ref|XP_002868207.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314043|gb|EFH44466.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	239	436	7.00E-85	182.4	65.7	77.4	transferase family protein	gbpln	Arabidopsis lyrata	AT4G15400.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr4:8812121-8813428 REVERSE LENGTH=435	239	435	2.00E-84	182.0	63.6	76.6
Rsa1.0_01271.1.g25250.t1	ref|XP_002868207.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314043|gb|EFH44466.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	156	436	3.00E-43	279.5	65.4	75.6	transferase family protein	gbpln	Arabidopsis lyrata	AT4G15400.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr4:8812121-8813428 REVERSE LENGTH=435	156	435	1.00E-44	278.8	63.5	75.0
Rsa1.0_01271.1.g25251.t1	dbj|BAF34636.1| DNA methyltransferase 1b [Brassica rapa]	1507	1519	0	100.8	86.3	91.6	DNA methyltransferase 1b	gbpln	Brassica rapa	AT5G49160.1 | Symbols: MET1, MET2, METI, DDM2, DMT01, DMT1 | methyltransferase 1 | chr5:19932501-19938186 FORWARD LENGTH=1534	1507	1534	0	101.8	67.9	80.7
Rsa1.0_01271.1.g25252.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01272.1.g25253.t1	ref|NP_180475.2| glutamate receptor 2.8 [Arabidopsis thaliana] gi|41017226|sp|Q9C5V5.2|GLR28_ARATH RecName: Full=Glutamate receptor 2.8; AltName: Full=Ligand-gated ion channel 2.8; Flags: Precursor gi|330253118|gb|AEC08212.1| glutamate receptor 2.8 [Arabidopsis thaliana]	865	947	0	109.5	75.1	85.4	glutamate receptor 2.8	gbpln	Arabidopsis thaliana	AT2G29110.1 | Symbols: ATGLR2.8, GLR2.8 | glutamate receptor 2.8 | chr2:12506880-12510552 REVERSE LENGTH=947	865	947	0	109.5	75.1	85.4
Rsa1.0_01272.1.g25254.t1	gb|EOA27010.1| hypothetical protein CARUB_v10023106mg [Capsella rubella]	459	484	0	105.4	86.1	91.7	hypothetical protein CARUB_v10023106mg	gbpln	Capsella rubella	AT2G29090.2 | Symbols: CYP707A2 | cytochrome P450, family 707, subfamily A, polypeptide 2 | chr2:12495038-12499080 REVERSE LENGTH=482	459	482	0	105.0	83.4	86.7

Rsa1.0_01272.1.g25255.t1	ref|XP_002881027.1| hypothetical protein ARALYDRAFT_344684 [Arabidopsis lyrata subsp. lyrata] gi|297326866|gb|EFH57286.1| hypothetical protein ARALYDRAFT_344684 [Arabidopsis lyrata subsp. lyrata]	778	818	0	105.1	90.1	94.0	hypothetical protein ARALYDRAFT_344684	gbpln	Arabidopsis lyrata	AT2G29080.1 | Symbols: ftsh3 | FTSH protease 3 | chr2:12489911-12492999 REVERSE LENGTH=809	778	809	0	104.0	89.7	94.0
Rsa1.0_01272.1.g25256.t1	ref|NP_001189628.1| GRAS family transcription factor [Arabidopsis thaliana] gi|206557919|sp|P0C884.1|SCL34_ARATH RecName: Full=Scarecrow-like protein 34; Short=AtSCL34; AltName: Full=GRAS family protein 12; Short=AtGRAS-12 gi|330253111|gb|AEC08205.1| GRAS family transcription factor [Arabidopsis thaliana]	629	630	0	100.2	78.9	86.8	GRAS family transcription factor	gbpln	Arabidopsis thaliana	AT2G29065.1 | Symbols: | GRAS family transcription factor | chr2:12485049-12486941 FORWARD LENGTH=630	629	630	0	100.2	78.9	86.8
Rsa1.0_01272.1.g25257.t1	ref|XP_002879199.1| scarecrow transcription factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297325038|gb|EFH55458.1| scarecrow transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	715	1321	0	184.8	75.8	84.8	scarecrow transcription factor family protein	gbpln	Arabidopsis lyrata	AT2G29060.1 | Symbols: | GRAS family transcription factor | chr2:12481991-12484075 FORWARD LENGTH=694	715	694	0	97.1	74.5	84.1
Rsa1.0_01272.1.g25258.t1	gb|EOA27304.1| hypothetical protein CARUB_v10023423mg [Capsella rubella]	391	381	0	97.4	85.4	92.6	hypothetical protein CARUB_v10023423mg	gbpln	Capsella rubella	AT2G29050.1 | Symbols: ATRBL1, RBL1 | RHOMBOID-like 1 | chr2:12478245-12480121 FORWARD LENGTH=389	391	389	0	99.5	85.9	93.1
Rsa1.0_01272.1.g25259.t1	ref|XP_002881026.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297326865|gb|EFH57285.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	682	707	0	103.7	82.1	88.3	exostosin family protein	gbpln	Arabidopsis lyrata	AT2G29040.1 | Symbols: | Exostosin family protein | chr2:12472425-12474962 REVERSE LENGTH=720	682	720	0	105.6	80.9	88.9
Rsa1.0_01272.1.g25260.t1	ref|XP_002862803.1| rab5-interacting family protein [Arabidopsis lyrata subsp. lyrata] gi|297822627|ref|XP_002879196.1| rab5-interacting family protein [Arabidopsis lyrata subsp. lyrata] gi|297308535|gb|EFH39061.1| rab5-interacting family protein [Arabidopsis lyrata subsp. lyrata] gi|297325035|gb|EFH55455.1| rab5-interacting family protein [Arabidopsis lyrata subsp. lyrata]	135	132	5.00E-53	97.8	87.4	93.3	rab5-interacting family protein	gbpln	Arabidopsis lyrata	AT5G59410.1 | Symbols: | Rab5-interacting family protein | chr5:23959761-23960730 REVERSE LENGTH=130	135	130	5.00E-54	96.3	75.6	86.7
Rsa1.0_01272.1.g25261.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01272.1.g25262.t1	gb|EOA29069.1| hypothetical protein CARUB_v10025325mg [Capsella rubella]	890	882	0	99.1	82.5	90.2	hypothetical protein CARUB_v10025325mg	gbpln	Capsella rubella	AT2G28960.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:12438058-12442347 REVERSE LENGTH=880	890	880	0	98.9	58.3	73.1
Rsa1.0_01273.1.g25263.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01273.1.g25264.t1	ref|NP_001190627.1| branched-chain-amino-acid aminotransferase 5 [Arabidopsis thaliana] gi|332010724|gb|AED98107.1| branched-chain-amino-acid aminotransferase 5 [Arabidopsis thaliana]	564	1018	1.00E-113	180.5	43.4	54.3	branched-chain-amino-acid aminotransferase 5	gbpln	Arabidopsis thaliana	AT5G65780.2 | Symbols: ATBCAT-5 | branched-chain amino acid aminotransferase 5 / branched-chain amino acid transaminase 5 (BCAT5) | chr5:26311587-26315610 FORWARD LENGTH=1018	564	1018	1.00E-115	180.5	43.4	54.3
Rsa1.0_01273.1.g25265.t1	gb|EOA34618.1| hypothetical protein CARUB_v10022178mg [Capsella rubella]	454	456	0	100.4	88.8	95.2	hypothetical protein CARUB_v10022178mg	gbpln	Capsella rubella	AT1G78990.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:29713531-29714969 REVERSE LENGTH=455	454	455	0	100.2	88.8	95.4
Rsa1.0_01273.1.g25266.t2	ref|XP_002889223.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297335064|gb|EFH65482.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	696	699	0	100.4	89.1	93.5	ATP binding protein	gbpln	Arabidopsis lyrata	AT1G78980.1 | Symbols: SRF5 | STRUBBELIG-receptor family 5 | chr1:29707923-29711266 REVERSE LENGTH=699	696	699	0	100.4	87.9	93.7
Rsa1.0_01273.1.g25267.t1	ref|XP_002887124.1| ATLUP2 [Arabidopsis lyrata subsp. lyrata] gi|297332965|gb|EFH63383.1| ATLUP2 [Arabidopsis lyrata subsp. lyrata]	769	759	0	98.7	90.0	93.6	ATLUP2	gbpln	Arabidopsis lyrata	AT1G78960.1 | Symbols: ATLUP2, LUP2 | lupeol synthase 2 | chr1:29696722-29701024 FORWARD LENGTH=763	769	763	0	99.2	83.4	90.6
Rsa1.0_01273.1.g25268.t1	gb|AAC17080.1| Strong similarity to lupeol synthase gb|U49919 and cycloartenol synthase gb|U02555 from A. thaliana (the third gene with similar homology) [Arabidopsis thaliana]	763	1565	0	205.1	89.1	94.9	Strong similarity to lupeol synthase gb|U49919 and cycloartenol synthase gb|U02555 from A. thaliana (the third gene with similar homology)	gbpln	Arabidopsis thaliana	AT1G78955.1 | Symbols: CAMS1 | camelliol C synthase 1 | chr1:29689153-29694255 REVERSE LENGTH=769	763	769	0	100.8	89.1	94.9

Rsa1.0_01273.1.g25269.t1	ref|XP_002889221.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335062|gb|EFH65480.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	757	752	0	99.3	87.5	92.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G78940.2 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:29680854-29683985 REVERSE LENGTH=754	757	754	0	99.6	86.7	91.7
Rsa1.0_01273.1.g25270.t1	gb|EOA34936.1| hypothetical protein CARUB_v10020021mg [Capsella rubella]	589	594	0	100.8	81.0	89.0	hypothetical protein CARUB_v10020021mg	gbpln	Capsella rubella	AT1G78930.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:29678285-29680648 REVERSE LENGTH=591	589	591	0	100.3	82.2	88.8
Rsa1.0_01273.1.g25271.t1	gb|EOA33649.1| hypothetical protein CARUB_v10019817mg [Capsella rubella]	802	802	0	100.0	97.6	99.1	hypothetical protein CARUB_v10019817mg	gbpln	Capsella rubella	AT1G78920.2 | Symbols: AVP2, AVPL1, AtVHP2;1, VHP2;1, VP2 | vacuolar H+-pyrophosphatase 2 | chr1:29672340-29676761 FORWARD LENGTH=802	802	802	0	100.0	97.4	99.1
Rsa1.0_01274.1.g25272.t1	ref|XP_002283518.1| PREDICTED: nucleolar protein 56-like [Vitis vinifera]	104	558	2.00E-11	536.5	34.6	37.5	PREDICTED: nucleolar protein 56-like	gbpln	Vitis vinifera	AT1G56110.1 | Symbols: NOP56 | homolog of nucleolar protein NOP56 | chr1:20984544-20986893 REVERSE LENGTH=522	104	522	6.00E-13	501.9	34.6	36.5
Rsa1.0_01274.1.g25273.t1	ref|XP_002869304.1| CYP82C4 [Arabidopsis lyrata subsp. lyrata] gi|297315140|gb|EFH45563.1| CYP82C4 [Arabidopsis lyrata subsp. lyrata]	523	524	0	100.2	87.6	93.9	CYP82C4	gbpln	Arabidopsis lyrata	AT4G31940.1 | Symbols: CYP82C4 | cytochrome P450, family 82, subfamily C, polypeptide 4 | chr4:15452040-15453966 FORWARD LENGTH=524	523	524	0	100.2	87.0	95.0
Rsa1.0_01274.1.g25274.t1	dbj|BAB01085.1| unnamed protein product [Arabidopsis thaliana]	272	271	1.00E-85	99.6	61.0	75.0	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G27040.1 | Symbols: | Meprin and TRAF (MATH) homology domain-containing protein | chr3:9974912-9977927 REVERSE LENGTH=358	272	358	4.00E-88	131.6	61.0	75.0
Rsa1.0_01274.1.g25275.t1	ref|XP_002877013.1| hypothetical protein ARALYDRAFT_322831 [Arabidopsis lyrata subsp. lyrata] gi|297322851|gb|EFH53272.1| hypothetical protein ARALYDRAFT_322831 [Arabidopsis lyrata subsp. lyrata]	270	362	2.00E-88	134.1	64.1	77.8	hypothetical protein ARALYDRAFT_322831	gbpln	Arabidopsis lyrata	AT3G27040.1 | Symbols: | Meprin and TRAF (MATH) homology domain-containing protein | chr3:9974912-9977927 REVERSE LENGTH=358	270	358	1.00E-87	132.6	63.0	76.7
Rsa1.0_01274.1.g25276.t1	gb|EOA28252.1| hypothetical protein CARUB_v10024445mg, partial [Capsella rubella]	51	77	6.00E-21	151.0	98.0	98.0	hypothetical protein CARUB_v10024445mg, partial	gbpln	Capsella rubella	AT4G31985.1 | Symbols: | Ribosomal protein L39 family protein | chr4:15469931-15470366 FORWARD LENGTH=51	51	51	3.00E-23	100.0	98.0	98.0
Rsa1.0_01274.1.g25277.t1	gb|EOA17237.1| hypothetical protein CARUB_v10005509mg [Capsella rubella]	255	266	1.00E-61	104.3	64.7	75.7	hypothetical protein CARUB_v10005509mg	gbpln	Capsella rubella	AT4G32030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80610.1); Has 63 Blast hits to 59 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 0; Plants - 53; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr4:15490903-15493007 FORWARD LENGTH=253	255	253	2.00E-63	99.2	64.7	76.1
Rsa1.0_01274.1.g25278.t1	gb|EOA16773.1| hypothetical protein CARUB_v10004992mg [Capsella rubella]	387	393	0	101.6	91.2	95.3	hypothetical protein CARUB_v10004992mg	gbpln	Capsella rubella	AT4G32140.1 | Symbols: | EamA-like transporter family | chr4:15523037-15525195 REVERSE LENGTH=394	387	394	0	101.8	90.7	94.8
Rsa1.0_01274.1.g25279.t1	ref|XP_002867255.1| vesicle-associated membrane protein 7C [Arabidopsis lyrata subsp. lyrata] gi|297313091|gb|EFH43514.1| vesicle-associated membrane protein 7C [Arabidopsis lyrata subsp. lyrata]	219	219	1.00E-115	100.0	95.9	98.2	vesicle-associated membrane protein 7C	gbpln	Arabidopsis lyrata	AT4G32150.1 | Symbols: VAMP711, ATVAMP711 | vesicle-associated membrane protein 711 | chr4:15526407-15527651 REVERSE LENGTH=219	219	219	1.00E-116	100.0	95.0	97.7
Rsa1.0_01274.1.g25280.t1	ref|XP_002869291.1| hypothetical protein ARALYDRAFT_491516 [Arabidopsis lyrata subsp. lyrata] gi|297315127|gb|EFH45550.1| hypothetical protein ARALYDRAFT_491516 [Arabidopsis lyrata subsp. lyrata]	210	241	1.00E-99	114.8	88.1	93.8	hypothetical protein ARALYDRAFT_491516	gbpln	Arabidopsis lyrata	AT4G32175.1 | Symbols: | PNAS-3 related | chr4:15535555-15537537 FORWARD LENGTH=241	210	241	9.00E-99	114.8	86.7	93.8
Rsa1.0_01274.1.g25281.t1	ref|XP_002867254.1| ATPANK2 [Arabidopsis lyrata subsp. lyrata] gi|297313090|gb|EFH43513.1| ATPANK2 [Arabidopsis lyrata subsp. lyrata]	934	902	0	96.6	92.1	93.5	ATPANK2	gbpln	Arabidopsis lyrata	AT4G32180.1 | Symbols: ATPANK2, PANK2 | pantothenate kinase 2 | chr4:15537724-15543715 REVERSE LENGTH=901	934	901	0	96.5	91.3	93.5
Rsa1.0_01275.1.g25282.t1	gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]	195	198	5.00E-44	101.5	51.8	69.2	hypothetical protein 27.t00041	gbpln	Brassica oleracea	AT2G35280.1 | Symbols: | F-box family protein | chr2:14859709-14860200 REVERSE LENGTH=163	195	163	2.00E-14	83.6	17.9	29.7
Rsa1.0_01275.1.g25283.t1	ref|NP_175703.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|12324642|gb|AAG52278.1|AC019018_15 putative replication protein; 94555-97079 [Arabidopsis thaliana] gi|332194750|gb|AEE32871.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	459	566	9.00E-70	123.3	32.2	56.2	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	459	566	2.00E-72	123.3	32.2	56.2
Rsa1.0_01275.1.g25284.t1	emb|CAB86685.1| putative protein [Arabidopsis thaliana]	204	303	1.00E-11	148.5	33.3	55.9	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01275.1.g25285.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01275.1.g25286.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01275.1.g25287.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01275.1.g25288.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	402	1611	2.33E-156	400.7	63.9	77.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01275.1.g25289.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01275.1.g25290.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01275.1.g25291.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01275.1.g25292.t7	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01276.1.g25293.t1	ref|XP_002881749.1| ubiquitin-specific protease 5 [Arabidopsis lyrata subsp. lyrata] gi|297327588|gb|EFH58008.1| ubiquitin-specific protease 5 [Arabidopsis lyrata subsp. lyrata]	928	924	0	99.6	89.5	94.8	ubiquitin-specific protease 5	gbpln	Arabidopsis lyrata	AT2G40930.1 | Symbols: UBP5, ATUBP5, PDE323 | ubiquitin-specific protease 5 | chr2:17076714-17082192 REVERSE LENGTH=924	928	924	0	99.6	89.0	94.4
Rsa1.0_01276.1.g25294.t1	dbj|BAE98403.1| putative non-LTR reverse transcriptase [Arabidopsis thaliana]	174	278	5.00E-35	159.8	46.0	55.2	putative non-LTR reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	174	746	8.00E-27	428.7	35.1	47.1
Rsa1.0_01276.1.g25295.t1	gb|EOA13563.1| hypothetical protein CARUB_v10026624mg [Capsella rubella]	290	368	1.00E-124	126.9	75.5	85.2	hypothetical protein CARUB_v10026624mg	gbpln	Capsella rubella	AT5G42440.1 | Symbols: | Protein kinase superfamily protein | chr5:16973434-16974513 REVERSE LENGTH=359	290	359	1.00E-125	123.8	76.6	85.2
Rsa1.0_01276.1.g25296.t1	gb|EOA27257.1| hypothetical protein CARUB_v10023376mg [Capsella rubella]	531	393	0	74.0	60.6	66.1	hypothetical protein CARUB_v10023376mg	gbpln	Capsella rubella	AT2G40900.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr2:17063396-17065514 REVERSE LENGTH=394	531	394	0	74.2	61.0	66.7
Rsa1.0_01276.1.g25297.t1	ref|NP_850337.1| cytochrome P450 98A3 [Arabidopsis thaliana] gi|5915859|sp|O22203.1|C98A3_ARATH RecName: Full=Cytochrome P450 98A3; AltName: Full=Protein REDUCED EPIDERMAL FLUORESCENCE 8; AltName: Full=p-coumaroylshikimate/quinate 3'-hydrolxylase; Short=C3'H gi|330254799|gb|AEC09893.1| cytochrome P450 98A3 [Arabidopsis thaliana]	508	508	0	100.0	95.1	97.6	cytochrome P450 98A3	gbpln	Arabidopsis thaliana	AT2G40890.1 | Symbols: CYP98A3 | cytochrome P450, family 98, subfamily A, polypeptide 3 | chr2:17058291-17060532 REVERSE LENGTH=508	508	508	0	100.0	95.1	97.6
Rsa1.0_01276.1.g25298.t2	ref|NP_181620.1| cysteine proteinase inhibitor 3 [Arabidopsis thaliana] gi|125991829|sp|Q41906.2|CYT3_ARATH RecName: Full=Cysteine proteinase inhibitor 3; Short=AtCYS-3; Flags: Precursor gi|2623302|gb|AAB86448.1| putative cysteine proteinase inhibitor B (cystatin B) [Arabidopsis thaliana] gi|21536996|gb|AAM61337.1| putative cysteine proteinase inhibitor B (cystatin B) [Arabidopsis thaliana] gi|23297693|gb|AAN13009.1| putative cysteine proteinase inhibitor B (cystatin B) [Arabidopsis thaliana] gi|330254798|gb|AEC09892.1| cysteine proteinase inhibitor 3 [Arabidopsis thaliana]	249	125	1.00E-19	50.2	19.7	21.7	cysteine proteinase inhibitor 3	gbpln	Arabidopsis thaliana	AT2G40880.1 | Symbols: FL3-27, ATCYSA, CYSA | cystatin A | chr2:17057463-17057930 FORWARD LENGTH=125	249	125	4.00E-22	50.2	19.7	21.7
Rsa1.0_01276.1.g25299.t1	gb|AEH20527.1| coumarate 3-hydroxylase [Isatis tinctoria]	61	508	2.00E-23	832.8	83.6	88.5	coumarate 3-hydroxylase	gbpln	Isatis tinctoria	AT2G40890.1 | Symbols: CYP98A3 | cytochrome P450, family 98, subfamily A, polypeptide 3 | chr2:17058291-17060532 REVERSE LENGTH=508	61	508	6.00E-26	832.8	83.6	86.9
Rsa1.0_01276.1.g25300.t1	gb|AAL86314.1| putative cysteine proteinase inhibitor cystatin B [Arabidopsis thaliana]	117	116	8.00E-44	99.1	74.4	85.5	putative cysteine proteinase inhibitor cystatin B	gbpln	Arabidopsis thaliana	AT2G40880.1 | Symbols: FL3-27, ATCYSA, CYSA | cystatin A | chr2:17057463-17057930 FORWARD LENGTH=125	117	125	2.00E-46	106.8	74.4	86.3
Rsa1.0_01276.1.g25301.t1	ref|XP_002873094.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318931|gb|EFH49353.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	241	262	2.00E-25	108.7	35.7	47.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G03495.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:873804-875025 REVERSE LENGTH=226	241	226	8.00E-25	93.8	29.9	41.1
Rsa1.0_01276.1.g25302.t1	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1728	910	0	52.7	26.7	36.6	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1728	626	2.00E-97	36.2	11.0	16.4
Rsa1.0_01276.1.g25303.t1	ref|XP_002879895.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325734|gb|EFH56154.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	275	542	6.00E-82	197.1	68.4	78.5	phosphatidylinositol 3-and 4-kinase family protein	gbpln	Arabidopsis lyrata	AT2G40850.1 | Symbols: ATPI4K GAMMA 1, PI4K GAMMA 1 | phosphoinositide 4-kinase gamma 1 | chr2:17051575-17053260 FORWARD LENGTH=561	275	561	2.00E-84	204.0	68.7	78.2
Rsa1.0_01277.1.g25304.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01277.1.g25305.t1	ref|XP_002882794.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297328634|gb|EFH59053.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	357	357	0	100.0	88.0	94.1	oxidoreductase	gbpln	Arabidopsis lyrata	AT3G12900.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:4104576-4106112 FORWARD LENGTH=357	357	357	0	100.0	86.3	93.3
Rsa1.0_01277.1.g25306.t2	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	133	1231	2.00E-28	925.6	46.6	64.7	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01277.1.g25307.t1	ref|XP_002882793.1| hypothetical protein ARALYDRAFT_478650 [Arabidopsis lyrata subsp. lyrata] gi|297328633|gb|EFH59052.1| hypothetical protein ARALYDRAFT_478650 [Arabidopsis lyrata subsp. lyrata]	249	251	1.00E-118	100.8	84.3	90.8	hypothetical protein ARALYDRAFT_478650	gbpln	Arabidopsis lyrata	AT3G12890.1 | Symbols: ASML2 | activator of spomin::LUC2 | chr3:4099223-4100277 FORWARD LENGTH=251	249	251	1.00E-117	100.8	82.7	89.2
Rsa1.0_01277.1.g25308.t1	gb|EOA32667.1| hypothetical protein CARUB_v10015969mg [Capsella rubella]	202	203	2.00E-89	100.5	90.1	95.0	hypothetical protein CARUB_v10015969mg	gbpln	Capsella rubella	AT3G12870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G56120.1); Has 70 Blast hits to 70 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 70; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4094417-4095037 REVERSE LENGTH=206	202	206	2.00E-91	102.0	90.6	95.5
Rsa1.0_01277.1.g25309.t2	gb|AAF81293.1|AC027656_10 Strong similarity to a mutator-like transposase from Arabidopsis thaliana gb|AC006067. It contains a zinc finger, CCHC class domain PF|00098 [Arabidopsis thaliana]	763	753	0	98.7	70.5	80.5	Strong similarity to a mutator-like transposase from Arabidopsis thaliana gb|AC006067. It contains a zinc finger, CCHC class domain PF|00098	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01277.1.g25310.t1	ref|XP_002884929.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297330769|gb|EFH61188.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	133	132	1.00E-62	99.2	88.7	94.0	auxin-responsive family protein	gbpln	Arabidopsis lyrata	AT3G12830.1 | Symbols: | SAUR-like auxin-responsive protein family | chr3:4079117-4079515 REVERSE LENGTH=132	133	132	4.00E-65	99.2	88.7	94.0
Rsa1.0_01277.1.g25311.t1	ref|XP_002884928.1| AtMYB10 [Arabidopsis lyrata subsp. lyrata] gi|297330768|gb|EFH61187.1| AtMYB10 [Arabidopsis lyrata subsp. lyrata]	218	238	5.00E-72	109.2	73.9	82.1	AtMYB10	gbpln	Arabidopsis lyrata	AT3G12820.1 | Symbols: AtMYB10, MYB10 | myb domain protein 10 | chr3:4074328-4075614 REVERSE LENGTH=239	218	239	1.00E-72	109.6	70.6	82.1
Rsa1.0_01278.1.g25312.t2	emb|CAN71108.1| hypothetical protein VITISV_001478 [Vitis vinifera]	1133	1354	0	119.5	46.3	62.1	hypothetical protein VITISV_001478	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1133	1262	5.00E-95	111.4	15.9	22.8
Rsa1.0_01278.1.g25313.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01278.1.g25314.t1	ref|XP_002874538.1| hypothetical protein ARALYDRAFT_489755 [Arabidopsis lyrata subsp. lyrata] gi|297320375|gb|EFH50797.1| hypothetical protein ARALYDRAFT_489755 [Arabidopsis lyrata subsp. lyrata]	499	621	1.00E-134	124.4	64.7	72.3	hypothetical protein ARALYDRAFT_489755	gbpln	Arabidopsis lyrata	AT4G08500.1 | Symbols: MEKK1, ATMEKK1, MAPKKK8, ARAKIN | MAPK/ERK kinase kinase 1 | chr4:5404272-5407062 REVERSE LENGTH=608	499	608	1.00E-131	121.8	62.1	70.7
Rsa1.0_01278.1.g25315.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	1684	1557	0	92.5	42.0	56.4	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1684	575	4.00E-54	34.1	8.6	12.3
Rsa1.0_01278.1.g25316.t1	gb|AAC19287.1| T14P8.5 [Arabidopsis thaliana] gi|7269005|emb|CAB80738.1| putative protein [Arabidopsis thaliana]	431	262	2.00E-59	60.8	25.3	26.9	T14P8.5	gbpln	Arabidopsis thaliana	AT4G02450.2 | Symbols: | HSP20-like chaperones superfamily protein | chr4:1073987-1075765 REVERSE LENGTH=240	431	240	4.00E-61	55.7	24.8	26.5
Rsa1.0_01278.1.g25317.t1	ref|NP_567238.2| AAA-type ATPase family protein [Arabidopsis thaliana] gi|110739712|dbj|BAF01763.1| hypothetical protein [Arabidopsis thaliana] gi|332656777|gb|AEE82177.1| AAA-type ATPase family protein [Arabidopsis thaliana]	1258	1265	0	100.6	88.6	93.8	AAA-type ATPase family protein	gbpln	Arabidopsis thaliana	AT4G02480.1 | Symbols: | AAA-type ATPase family protein | chr4:1082082-1088680 REVERSE LENGTH=1265	1258	1265	0	100.6	88.6	93.8
Rsa1.0_01278.1.g25318.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01278.1.g25319.t1	ref|NP_567241.1| xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] gi|46576207|sp|O22775.1|GT2_ARATH RecName: Full=Putative glycosyltransferase 2; Short=AtGT2 gi|3193287|gb|AAC19271.1| T14P8.23 [Arabidopsis thaliana] gi|9716844|emb|CAC01674.1| putative golgi glycosyltransferase [Arabidopsis thaliana] gi|16209669|gb|AAL14393.1| AT4g02500/T10P11_20 [Arabidopsis thaliana] gi|22655160|gb|AAM98170.1| putative glycosyltransferase [Arabidopsis thaliana] gi|30387559|gb|AAP31945.1| At4g02500 [Arabidopsis thaliana] gi|332656781|gb|AEE82181.1| putative glycosyltransferase 2 [Arabidopsis thaliana]	470	461	0	98.1	92.6	94.0	xyloglucan 6-xylosyltransferase	gbpln	Arabidopsis thaliana	AT4G02500.1 | Symbols: ATXT2, XXT2, XT2 | UDP-xylosyltransferase 2 | chr4:1101638-1103345 FORWARD LENGTH=461	470	461	0	98.1	92.6	94.0
Rsa1.0_01279.1.g25320.t1	gb|EOA32513.1| hypothetical protein CARUB_v10015793mg [Capsella rubella]	489	487	0	99.6	81.4	88.5	hypothetical protein CARUB_v10015793mg	gbpln	Capsella rubella	AT3G11680.1 | Symbols: | Aluminium activated malate transporter family protein | chr3:3686995-3689329 REVERSE LENGTH=488	489	488	0	99.8	81.0	88.8
Rsa1.0_01279.1.g25321.t2	dbj|BAJ34190.1| unnamed protein product [Thellungiella halophila]	752	806	0	107.2	89.2	94.0	unnamed protein product	----	----	AT3G11670.1 | Symbols: DGD1 | UDP-Glycosyltransferase superfamily protein | chr3:3681090-3684495 REVERSE LENGTH=808	752	808	0	107.4	85.8	90.6
Rsa1.0_01279.1.g25322.t1	ref|XP_002886482.1| C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297332323|gb|EFH62741.1| C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata]	397	385	0	97.0	78.3	84.6	C4-dicarboxylate transporter/malic acid transport family protein	gbpln	Arabidopsis lyrata	AT1G62280.1 | Symbols: SLAH1 | SLAC1 homologue 1 | chr1:23007309-23008540 REVERSE LENGTH=385	397	385	0	97.0	76.8	84.1
Rsa1.0_01279.1.g25323.t1	ref|NP_566396.1| NDR1/HIN1-Like protein 1 [Arabidopsis thaliana] gi|6041819|gb|AAF02134.1|AC009918_6 unknown protein [Arabidopsis thaliana] gi|9502172|gb|AAF88021.1|AF264697_1 NDR1/HIN1-Like protein 1 [Arabidopsis thaliana] gi|21595601|gb|AAM66116.1| harpin-induced protein-like [Arabidopsis thaliana] gi|56381911|gb|AAV85674.1| At3g11660 [Arabidopsis thaliana] gi|58331799|gb|AAW70397.1| At3g11660 [Arabidopsis thaliana] gi|332641559|gb|AEE75080.1| NDR1/HIN1-Like protein 1 [Arabidopsis thaliana]	211	209	5.00E-96	99.1	80.6	89.1	NDR1/HIN1-Like protein 1	gbpln	Arabidopsis thaliana	AT3G11660.1 | Symbols: NHL1 | NDR1/HIN1-like 1 | chr3:3679031-3679660 REVERSE LENGTH=209	211	209	2.00E-98	99.1	80.6	89.1
Rsa1.0_01279.1.g25324.t1	gb|AAP57211.1| methyl transferase [Arabidopsis lyrata subsp. lyrata]	526	380	1.00E-159	72.2	52.1	57.4	methyl transferase	gbpln	Arabidopsis lyrata	AT3G11480.1 | Symbols: BSMT1, ATBSMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:3614544-3617137 FORWARD LENGTH=379	526	379	1.00E-156	72.1	50.6	56.5
Rsa1.0_01279.1.g25325.t1	gb|EOA14700.1| hypothetical protein CARUB_v10027975mg [Capsella rubella]	667	766	0	114.8	67.3	81.7	hypothetical protein CARUB_v10027975mg	gbpln	Capsella rubella	AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769	667	769	0	115.3	67.3	81.0
Rsa1.0_01279.1.g25326.t1	gb|AAD20102.1| hypothetical protein [Arabidopsis thaliana]	93	221	3.00E-12	237.6	40.9	58.1	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01279.1.g25327.t1	ref|NP_187756.1| rac GTPase activating protein [Arabidopsis thaliana] gi|12322911|gb|AAG51449.1|AC008153_22 putative rac GTPase activating protein; 62102-60058 [Arabidopsis thaliana] gi|332641533|gb|AEE75054.1| rac GTPase activating protein [Arabidopsis thaliana]	99	435	2.00E-22	439.4	58.6	63.6	rac GTPase activating protein	gbpln	Arabidopsis thaliana	AT3G11490.1 | Symbols: | rac GTPase activating protein | chr3:3617523-3619567 REVERSE LENGTH=435	99	435	4.00E-25	439.4	58.6	63.6
Rsa1.0_01279.1.g25328.t1	gb|AAP57211.1| methyl transferase [Arabidopsis lyrata subsp. lyrata]	329	380	1.00E-157	115.5	83.3	92.1	methyl transferase	gbpln	Arabidopsis lyrata	AT3G11480.1 | Symbols: BSMT1, ATBSMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:3614544-3617137 FORWARD LENGTH=379	329	379	1.00E-158	115.2	82.4	91.5
Rsa1.0_01279.1.g25329.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01279.1.g25330.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	508	1274	4.00E-96	250.8	40.4	56.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	508	575	1.00E-58	113.2	30.7	49.4

Rsa1.0_01279.1.g25331.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01279.1.g25332.t1	gb|AAD29058.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	898	1229	1.00E-65	136.9	15.8	23.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	898	626	8.00E-21	69.7	6.6	11.1
Rsa1.0_01280.1.g25333.t2	gb|AAC17040.1| Similarity to A. thaliana gene product F21M12.20, gb|AC000132. EST gb|Z25651 comes from this gene [Arabidopsis thaliana]	307	530	1.00E-106	172.6	60.6	65.5	Similarity to A. thaliana gene product F21M12.20, gb|AC000132. EST gb|Z25651 comes from this gene	gbpln	Arabidopsis thaliana	AT1G79270.1 | Symbols: ECT8 | evolutionarily conserved C-terminal region 8 | chr1:29816157-29818811 FORWARD LENGTH=528	307	528	1.00E-109	172.0	60.6	65.5
Rsa1.0_01280.1.g25334.t2	ref|NP_178048.2| nucleoprotein TPR [Arabidopsis thaliana] gi|302425121|sp|A4GSN8.1|NUA_ARATH RecName: Full=Nuclear-pore anchor; AltName: Full=Protein TRANSLOCATED PROMOTER REGION; Short=AtTPR gi|126594444|gb|ABO21684.1| nuclear-pore anchor [Arabidopsis thaliana] gi|332198105|gb|AEE36226.1| nucleoprotein TPR [Arabidopsis thaliana]	2129	2093	0	98.3	77.7	85.0	nucleoprotein TPR	gbpln	Arabidopsis thaliana	AT1G79280.1 | Symbols: NUA, AtTPR | nuclear pore anchor | chr1:29819176-29832809 REVERSE LENGTH=2093	2129	2093	0	98.3	77.7	85.0
Rsa1.0_01280.1.g25335.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01280.1.g25336.t1	gb|EOA35282.1| hypothetical protein CARUB_v10020450mg [Capsella rubella]	391	385	1.00E-163	98.5	77.0	84.1	hypothetical protein CARUB_v10020450mg	gbpln	Capsella rubella	AT1G79330.1 | Symbols: AMC6, ATMCP2B, ATMC5, MC5 | metacaspase 5 | chr1:29838722-29840137 FORWARD LENGTH=410	391	410	1.00E-139	104.9	65.5	78.3
Rsa1.0_01280.1.g25337.t1	ref|NP_178050.1| metacaspase 6 [Arabidopsis thaliana] gi|75219814|sp|O64519.1|MCA6_ARATH RecName: Full=Metacaspase-6; Short=AtMC6; AltName: Full=Metacaspase 2c; Short=AtMCP2c; AltName: Full=Metacaspase-5 gi|3152597|gb|AAC17078.1| Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb|Z75105 [Arabidopsis thaliana] gi|32482826|gb|AAP84713.1| metacaspase 5 [Arabidopsis thaliana] gi|37788555|gb|AAP44519.1| metacaspase 6 precursor [Arabidopsis thaliana] gi|116325926|gb|ABJ98564.1| At1g79320 [Arabidopsis thaliana] gi|332198109|gb|AEE36230.1| metacaspase 6 [Arabidopsis thaliana]	375	368	0	98.1	84.8	92.0	metacaspase 6	gbpln	Arabidopsis thaliana	AT1G79320.1 | Symbols: AtMC6, MC6 | metacaspase 6 | chr1:29836686-29837908 FORWARD LENGTH=368	375	368	0	98.1	84.8	92.0
Rsa1.0_01280.1.g25338.t1	ref|NP_178051.1| metacaspase 5 [Arabidopsis thaliana] gi|75219813|sp|O64518.1|MCA5_ARATH RecName: Full=Metacaspase-5; Short=AtMC5; AltName: Full=Metacaspase 2b; Short=AtMCP2b; AltName: Full=Metacaspase-6 gi|3152557|gb|AAC17038.1| Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb|Z75105. EST gb|T76227 comes from this gene [Arabidopsis thaliana] gi|32482828|gb|AAP84714.1| metacaspase 6 [Arabidopsis thaliana] gi|37788553|gb|AAP44518.1| metacaspase 5 precursor [Arabidopsis thaliana] gi|116325934|gb|ABJ98568.1| At1g79330 [Arabidopsis thaliana] gi|332198110|gb|AEE36231.1| metacaspase 5 [Arabidopsis thaliana]	387	410	1.00E-180	105.9	84.0	91.7	metacaspase 5	gbpln	Arabidopsis thaliana	AT1G79330.1 | Symbols: AMC6, ATMCP2B, ATMC5, MC5 | metacaspase 5 | chr1:29838722-29840137 FORWARD LENGTH=410	387	410	0	105.9	84.0	91.7
Rsa1.0_01280.1.g25339.t1	ref|XP_002887781.1| metacaspase 7 [Arabidopsis lyrata subsp. lyrata] gi|297333622|gb|EFH64040.1| metacaspase 7 [Arabidopsis lyrata subsp. lyrata]	409	418	0	102.2	92.4	97.1	metacaspase 7	gbpln	Arabidopsis lyrata	AT1G79340.1 | Symbols: AtMC4, MC4 | metacaspase 4 | chr1:29842849-29844368 FORWARD LENGTH=418	409	418	0	102.2	91.9	96.1
Rsa1.0_01280.1.g25340.t2	ref|NP_178053.4| RING/FYVE/PHD zinc finger domain-containing protein [Arabidopsis thaliana] gi|332198112|gb|AEE36233.1| RING/FYVE/PHD zinc finger domain-containing protein [Arabidopsis thaliana]	1252	1295	0	103.4	92.4	95.0	RING/FYVE/PHD zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT1G79350.1 | Symbols: EMB1135 | RING/FYVE/PHD zinc finger superfamily protein | chr1:29844829-29853215 REVERSE LENGTH=1295	1252	1295	0	103.4	92.4	95.0

Rsa1.0_01281.1.g25341.t1	ref|NP_187088.2| histone-lysine N-methyltransferase SUVR4 [Arabidopsis thaliana] gi|94730582|sp|Q8W595.2|SUVR4_ARATH RecName: Full=Histone-lysine N-methyltransferase SUVR4; AltName: Full=Protein SET DOMAIN GROUP 31; AltName: Full=Suppressor of variegation 3-9-related protein 4; Short=Su(var)3-9-related protein 4 gi|332640552|gb|AEE74073.1| histone-lysine N-methyltransferase SUVR4 [Arabidopsis thaliana]	659	492	0	74.7	50.1	56.0	histone-lysine N-methyltransferase SUVR4	gbpln	Arabidopsis thaliana	AT3G04380.1 | Symbols: SUVR4, SDG31 | SET-domain containing protein lysine methyltransferase family protein | chr3:1161602-1164539 FORWARD LENGTH=492	659	492	0	74.7	50.1	56.0
Rsa1.0_01281.1.g25342.t1	gb|EOA30795.1| hypothetical protein CARUB_v10013938mg [Capsella rubella]	389	382	1.00E-137	98.2	78.1	84.8	hypothetical protein CARUB_v10013938mg	gbpln	Capsella rubella	AT3G04360.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:1157025-1158200 REVERSE LENGTH=391	389	391	1.00E-138	100.5	79.7	85.9
Rsa1.0_01281.1.g25343.t1	ref|NP_187081.1| uncharacterized protein [Arabidopsis thaliana] gi|6721155|gb|AAF26783.1|AC016829_7 hypothetical protein [Arabidopsis thaliana] gi|332640544|gb|AEE74065.1| uncharacterized protein AT3G04310 [Arabidopsis thaliana]	263	269	1.00E-76	102.3	67.3	78.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G04310.1 | Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:1141581-1142528 REVERSE LENGTH=269	263	269	3.00E-79	102.3	67.3	78.3
Rsa1.0_01281.1.g25344.t1	ref|NP_187080.1| cupin domain-containing protein [Arabidopsis thaliana] gi|6721156|gb|AAF26784.1|AC016829_8 hypothetical protein [Arabidopsis thaliana] gi|37202048|gb|AAQ89639.1| At3g04300 [Arabidopsis thaliana] gi|51968382|dbj|BAD42883.1| unknown protein [Arabidopsis thaliana] gi|332640543|gb|AEE74064.1| cupin domain-containing protein [Arabidopsis thaliana]	98	96	3.00E-43	98.0	88.8	93.9	cupin domain-containing protein	gbpln	Arabidopsis thaliana	AT3G04300.1 | Symbols: | RmlC-like cupins superfamily protein | chr3:1140318-1140723 FORWARD LENGTH=96	98	96	6.00E-46	98.0	88.8	93.9
Rsa1.0_01281.1.g25345.t1	ref|XP_002884438.1| Li-tolerant lipase 1 [Arabidopsis lyrata subsp. lyrata] gi|297330278|gb|EFH60697.1| Li-tolerant lipase 1 [Arabidopsis lyrata subsp. lyrata]	372	366	0	98.4	95.2	96.0	Li-tolerant lipase 1	gbpln	Arabidopsis lyrata	AT3G04290.1 | Symbols: ATLTL1, LTL1 | Li-tolerant lipase 1 | chr3:1133620-1136223 REVERSE LENGTH=366	372	366	0	98.4	94.4	95.7
Rsa1.0_01281.1.g25346.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01281.1.g25347.t1	ref|NP_566601.1| uncharacterized protein [Arabidopsis thaliana] gi|9294078|dbj|BAB02035.1| unnamed protein product [Arabidopsis thaliana] gi|15810371|gb|AAL07073.1| unknown protein [Arabidopsis thaliana] gi|20259213|gb|AAM14322.1| unknown protein [Arabidopsis thaliana] gi|332642545|gb|AEE76066.1| uncharacterized protein AT3G18215 [Arabidopsis thaliana]	116	244	2.00E-58	210.3	90.5	94.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G18215.1 | Symbols: | Protein of unknown function, DUF599 | chr3:6240968-6242358 FORWARD LENGTH=244	116	244	4.00E-61	210.3	90.5	94.8
Rsa1.0_01281.1.g25348.t1	ref|NP_187078.1| two-component response regulator ARR22 [Arabidopsis thaliana] gi|30679083|ref|NP_850511.1| two-component response regulator ARR22 [Arabidopsis thaliana] gi|145331750|ref|NP_001078102.1| two-component response regulator ARR22 [Arabidopsis thaliana] gi|51316101|sp|Q9M8Y4.1|ARR22_ARATH RecName: Full=Two-component response regulator ARR22 gi|6721158|gb|AAF26786.1|AC016829_10 putative response regulator protein (receiver component) [Arabidopsis thaliana] gi|21553766|gb|AAM62859.1| putative response regulator protein (receiver component) [Arabidopsis thaliana] gi|332640539|gb|AEE74060.1| two-component response regulator ARR22 [Arabidopsis thaliana] gi|332640540|gb|AEE74061.1| two-component response regulator ARR22 [Arabidopsis thaliana] gi|332640541|gb|AEE74062.1| two-component response regulator ARR22 [Arabidopsis thaliana]	167	142	5.00E-53	85.0	67.7	73.1	two-component response regulator ARR22	gbpln	Arabidopsis thaliana	AT3G04280.3 | Symbols: ARR22, RR22 | response regulator 22 | chr3:1130138-1130689 REVERSE LENGTH=142	167	142	2.00E-55	85.0	67.7	73.1

Rsa1.0_01281.1.g25349.t1	gb|EOA17608.1| hypothetical protein CARUB_v10005968mg [Capsella rubella] gi|482557559|gb|EOA21751.1| hypothetical protein CARUB_v10002207mg [Capsella rubella]	146	146	3.00E-73	100.0	91.8	94.5	hypothetical protein CARUB_v10005968mg	gbpln	Capsella rubella	AT5G18380.1 | Symbols: | Ribosomal protein S5 domain 2-like superfamily protein | chr5:6090253-6090693 REVERSE LENGTH=146	146	146	2.00E-75	100.0	91.1	94.5
Rsa1.0_01281.1.g25350.t1	gb|EOA29984.1| hypothetical protein CARUB_v10013089mg [Capsella rubella]	643	703	0	109.3	72.3	83.5	hypothetical protein CARUB_v10013089mg	gbpln	Capsella rubella	AT3G04160.1 | Symbols: | unknown protein; Has 1711 Blast hits to 1353 proteins in 195 species: Archae - 0; Bacteria - 64; Metazoa - 693; Fungi - 201; Plants - 207; Viruses - 0; Other Eukaryotes - 546 (source: NCBI BLink). | chr3:1091647-1094296 REVERSE LENGTH=712	643	712	0	110.7	70.5	79.6
Rsa1.0_01281.1.g25351.t1	ref|XP_002882328.1| hypothetical protein ARALYDRAFT_340564 [Arabidopsis lyrata subsp. lyrata] gi|297328168|gb|EFH58587.1| hypothetical protein ARALYDRAFT_340564 [Arabidopsis lyrata subsp. lyrata]	437	510	1.00E-163	116.7	74.6	84.0	hypothetical protein ARALYDRAFT_340564	gbpln	Arabidopsis lyrata	AT3G04050.1 | Symbols: | Pyruvate kinase family protein | chr3:1049795-1051522 FORWARD LENGTH=510	437	510	1.00E-158	116.7	71.9	82.2
Rsa1.0_01281.1.g25352.t1	gb|EOA32860.1| hypothetical protein CARUB_v10016174mg [Capsella rubella]	544	549	0	100.9	96.7	98.7	hypothetical protein CARUB_v10016174mg	gbpln	Capsella rubella	AT3G03960.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:1024432-1027604 FORWARD LENGTH=549	544	549	0	100.9	95.8	98.3
Rsa1.0_01281.1.g25353.t1	gb|EOA29894.1| hypothetical protein CARUB_v10012990mg [Capsella rubella]	812	818	0	100.7	75.0	84.1	hypothetical protein CARUB_v10012990mg	gbpln	Capsella rubella	AT4G04220.1 | Symbols: AtRLP46, RLP46 | receptor like protein 46 | chr4:2033427-2035946 FORWARD LENGTH=811	812	811	0	99.9	67.4	76.2
Rsa1.0_01281.1.g25354.t1	ref|XP_002882315.1| hypothetical protein ARALYDRAFT_477638 [Arabidopsis lyrata subsp. lyrata] gi|297328155|gb|EFH58574.1| hypothetical protein ARALYDRAFT_477638 [Arabidopsis lyrata subsp. lyrata]	255	300	1.00E-121	117.6	83.9	89.8	hypothetical protein ARALYDRAFT_477638	gbpln	Arabidopsis lyrata	AT3G03860.1 | Symbols: ATAPRL5, APRL5 | APR-like 5 | chr3:992465-994315 FORWARD LENGTH=300	255	300	1.00E-121	117.6	82.0	89.0
Rsa1.0_01281.1.g25355.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1502	1499	0	99.8	63.8	78.6	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1502	158	3.00E-32	10.5	4.2	5.9
Rsa1.0_01282.1.g25356.t11	ref|NP_193817.2| tripeptidyl peptidase ii [Arabidopsis thaliana] gi|332658968|gb|AEE84368.1| tripeptidyl peptidase ii [Arabidopsis thaliana]	1390	1380	0	99.3	88.1	91.8	tripeptidyl peptidase ii	gbpln	Arabidopsis thaliana	AT4G20850.1 | Symbols: TPP2 | tripeptidyl peptidase ii | chr4:11160935-11169889 REVERSE LENGTH=1380	1390	1380	0	99.3	88.1	91.8
Rsa1.0_01282.1.g25357.t1	gb|EOA18748.1| hypothetical protein CARUB_v10007331mg [Capsella rubella]	539	555	0	103.0	86.3	93.1	hypothetical protein CARUB_v10007331mg	gbpln	Capsella rubella	AT4G20840.1 | Symbols: | FAD-binding Berberine family protein | chr4:11157916-11159535 FORWARD LENGTH=539	539	539	0	100.0	83.9	90.5
Rsa1.0_01282.1.g25358.t1	gb|EOA18748.1| hypothetical protein CARUB_v10007331mg [Capsella rubella]	534	555	0	103.9	81.5	91.0	hypothetical protein CARUB_v10007331mg	gbpln	Capsella rubella	AT4G20840.1 | Symbols: | FAD-binding Berberine family protein | chr4:11157916-11159535 FORWARD LENGTH=539	534	539	0	100.9	77.3	86.9
Rsa1.0_01282.1.g25359.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01282.1.g25360.t1	gb|EOA18285.1| hypothetical protein CARUB_v10006784mg [Capsella rubella]	514	519	0	101.0	74.1	85.4	hypothetical protein CARUB_v10006784mg	gbpln	Capsella rubella	AT4G20790.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr4:11134775-11136423 REVERSE LENGTH=518	514	518	0	100.8	75.9	85.8
Rsa1.0_01282.1.g25361.t1	ref|NP_193810.1| calcium-binding protein CML42 [Arabidopsis thaliana] gi|75337714|sp|Q9SVG9.1|CML42_ARATH RecName: Full=Calcium-binding protein CML42; AltName: Full=Calmodulin-like protein 42 gi|5262218|emb|CAB45844.1| calcium-binding protein-like [Arabidopsis thaliana] gi|7268874|emb|CAB79078.1| calcium-binding protein-like [Arabidopsis thaliana] gi|26450755|dbj|BAC42486.1| putative calcium-binding protein [Arabidopsis thaliana] gi|28372940|gb|AAO39952.1| At4g20780 [Arabidopsis thaliana] gi|332658960|gb|AEE84360.1| calcium-binding protein CML42 [Arabidopsis thaliana]	191	191	7.00E-85	100.0	85.9	91.6	calcium-binding protein CML42	gbpln	Arabidopsis thaliana	AT4G20780.1 | Symbols: CML42 | calmodulin like 42 | chr4:11133309-11133884 REVERSE LENGTH=191	191	191	3.00E-87	100.0	85.9	91.6
Rsa1.0_01282.1.g25362.t1	dbj|BAD43836.1| unknown protein [Arabidopsis thaliana]	226	254	4.00E-67	112.4	69.9	72.6	unknown protein	gbpln	Arabidopsis thaliana	AT5G44500.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr5:17927505-17928269 FORWARD LENGTH=254	226	254	9.00E-67	112.4	67.3	69.9
Rsa1.0_01282.1.g25363.t1	gb|ABA00707.1| putative tapetum-specific A3 [Brassica napus]	112	139	2.00E-50	124.1	90.2	95.5	putative tapetum-specific A3	gbpln	Brassica napus	AT4G20420.1 | Symbols: | Tapetum specific protein TAP35/TAP44 | chr4:11017041-11017469 FORWARD LENGTH=142	112	142	1.00E-30	126.8	67.0	76.8

Rsa1.0_01282.1.g25364.t1	gb|AAL50982.1|AF453323_1 zinc finger protein LSD2 [Brassica oleracea]	189	193	2.00E-89	102.1	92.1	96.3	zinc finger protein LSD2	gbpln	Brassica oleracea	AT4G20380.7 | Symbols: LSD1 | LSD1 zinc finger family protein | chr4:11005012-11006438 FORWARD LENGTH=189	189	189	1.00E-67	100.0	77.8	85.2
Rsa1.0_01282.1.g25365.t1	gb|EOA18090.1| hypothetical protein CARUB_v10006542mg [Capsella rubella]	475	480	0	101.1	93.5	94.5	hypothetical protein CARUB_v10006542mg	gbpln	Capsella rubella	AT4G20360.1 | Symbols: ATRAB8D, ATRABE1B, RABE1b | RAB GTPase homolog E1B | chr4:10990036-10991466 FORWARD LENGTH=476	475	476	0	100.2	91.8	93.9
Rsa1.0_01282.1.g25366.t1	ref|NP_001078412.2| ribonuclease H2 subunit B [Arabidopsis thaliana] gi|332658907|gb|AEE84307.1| ribonuclease H2 subunit B domain-containing protein [Arabidopsis thaliana]	297	277	1.00E-137	93.3	81.5	86.9	ribonuclease H2 subunit B	gbpln	Arabidopsis thaliana	AT4G20325.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleus; CONTAINS InterPro DOMAIN/s: Ribonuclease H2, subunit B (InterPro:IPR019024); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10980124-10982426 FORWARD LENGTH=277	297	277	1.00E-140	93.3	81.5	86.9
Rsa1.0_01282.1.g25367.t1	ref|XP_002869939.1| CTP synthase [Arabidopsis lyrata subsp. lyrata] gi|297315775|gb|EFH46198.1| CTP synthase [Arabidopsis lyrata subsp. lyrata]	589	597	0	101.4	93.7	96.4	CTP synthase	gbpln	Arabidopsis lyrata	AT4G20320.2 | Symbols: | CTP synthase family protein | chr4:10974980-10978998 FORWARD LENGTH=597	589	597	0	101.4	92.4	96.4
Rsa1.0_01283.1.g25368.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	196	1239	8.00E-57	632.1	50.0	55.6	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	196	1262	1.00E-19	643.9	25.0	35.2
Rsa1.0_01283.1.g25369.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01283.1.g25370.t1	ref|XP_002884121.1| hypothetical protein ARALYDRAFT_480729 [Arabidopsis lyrata subsp. lyrata] gi|297329961|gb|EFH60380.1| hypothetical protein ARALYDRAFT_480729 [Arabidopsis lyrata subsp. lyrata]	251	221	2.00E-82	88.0	62.9	70.1	hypothetical protein ARALYDRAFT_480729	gbpln	Arabidopsis lyrata	AT2G18240.2 | Symbols: | Rer1 family protein | chr2:7935466-7936464 FORWARD LENGTH=220	251	220	5.00E-84	87.6	62.5	69.7
Rsa1.0_01283.1.g25371.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1525	1365	0	89.5	24.3	36.7	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1525	575	6.00E-83	37.7	9.5	13.8
Rsa1.0_01283.1.g25372.t1	ref|XP_002886161.1| inorganic pyrophosphatase [Arabidopsis lyrata subsp. lyrata] gi|297332001|gb|EFH62420.1| inorganic pyrophosphatase [Arabidopsis lyrata subsp. lyrata]	229	218	1.00E-116	95.2	90.8	91.3	inorganic pyrophosphatase	gbpln	Arabidopsis lyrata	AT2G18230.1 | Symbols: AtPPa2, PPa2 | pyrophosphorylase 2 | chr2:7932139-7933560 REVERSE LENGTH=218	229	218	1.00E-117	95.2	90.0	91.3
Rsa1.0_01283.1.g25373.t1	ref|XP_002884119.1| hypothetical protein ARALYDRAFT_480727 [Arabidopsis lyrata subsp. lyrata] gi|297329959|gb|EFH60378.1| hypothetical protein ARALYDRAFT_480727 [Arabidopsis lyrata subsp. lyrata]	774	772	0	99.7	77.0	84.8	hypothetical protein ARALYDRAFT_480727	gbpln	Arabidopsis lyrata	AT2G18220.1 | Symbols: | Noc2p family | chr2:7928254-7931851 FORWARD LENGTH=764	774	764	0	98.7	73.1	80.1
Rsa1.0_01283.1.g25374.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	134	1142	2.00E-23	852.2	44.0	60.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01283.1.g25375.t1	gb|AAC69125.1| Mutator-like transposase [Arabidopsis thaliana]	701	590	6.00E-83	84.2	22.3	30.1	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	701	719	2.00E-20	102.6	9.0	15.1
Rsa1.0_01283.1.g25376.t4	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	570	871	3.00E-33	152.8	12.1	14.9	Ulp1 protease family protein	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	570	673	3.00E-19	118.1	9.6	13.9
Rsa1.0_01283.1.g25377.t1	gb|EOA38015.1| hypothetical protein CARUB_v10009486mg, partial [Capsella rubella]	99	372	3.00E-22	375.8	66.7	71.7	hypothetical protein CARUB_v10009486mg, partial	gbpln	Capsella rubella	AT1G09460.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr1:3053901-3055090 FORWARD LENGTH=330	99	330	1.00E-23	333.3	64.6	70.7
Rsa1.0_01283.1.g25378.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01284.1.g25379.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	993	1142	0	115.0	51.6	64.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	993	575	8.00E-42	57.9	8.8	12.8
Rsa1.0_01284.1.g25380.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01284.1.g25381.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01284.1.g25382.t1	dbj|BAA96887.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	254	1140	5.00E-53	448.8	44.5	58.7	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01284.1.g25383.t1	gb|EOA20915.1| hypothetical protein CARUB_v10001250mg [Capsella rubella]	362	360	1.00E-145	99.4	73.2	84.8	hypothetical protein CARUB_v10001250mg	gbpln	Capsella rubella	AT4G01450.2 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:608586-610487 FORWARD LENGTH=361	362	361	1.00E-143	99.7	75.4	85.9
Rsa1.0_01284.1.g25384.t1	ref|XP_002877467.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323305|gb|EFH53726.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	219	186	1.00E-26	84.9	32.0	45.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	219	295	4.00E-17	134.7	29.2	45.7
Rsa1.0_01284.1.g25385.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01284.1.g25386.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	197	1557	2.00E-14	790.4	29.4	49.7	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT3G27140.1 | Symbols: | Protein phosphatase 2C family protein | chr3:10006891-10008174 REVERSE LENGTH=245	197	245	8.00E-11	124.4	14.7	19.3
Rsa1.0_01284.1.g25387.t1	gb|EOA20915.1| hypothetical protein CARUB_v10001250mg [Capsella rubella]	327	360	1.00E-137	110.1	78.3	90.8	hypothetical protein CARUB_v10001250mg	gbpln	Capsella rubella	AT4G01450.2 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:608586-610487 FORWARD LENGTH=361	327	361	1.00E-132	110.4	80.4	92.4
Rsa1.0_01285.1.g25388.t1	gb|AAP37140.1| WOX11 protein [Arabidopsis thaliana]	265	268	1.00E-115	101.1	86.8	90.6	WOX11 protein	gbpln	Arabidopsis thaliana	AT3G03660.1 | Symbols: WOX11 | WUSCHEL related homeobox 11 | chr3:889515-892162 REVERSE LENGTH=268	265	268	1.00E-117	101.1	86.0	89.8
Rsa1.0_01285.1.g25389.t1	gb|EOA32859.1| hypothetical protein CARUB_v10016173mg [Capsella rubella]	486	508	0	104.5	84.8	92.4	hypothetical protein CARUB_v10016173mg	gbpln	Capsella rubella	AT3G03650.1 | Symbols: EDA5 | Exostosin family protein | chr3:884298-886166 REVERSE LENGTH=499	486	499	0	102.7	86.6	93.2
Rsa1.0_01285.1.g25390.t1	ref|XP_002884399.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297330239|gb|EFH60658.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	479	500	0	104.4	88.3	93.9	mate efflux family protein	gbpln	Arabidopsis lyrata	AT3G03620.1 | Symbols: | MATE efflux family protein | chr3:873904-876252 REVERSE LENGTH=500	479	500	0	104.4	88.5	94.4
Rsa1.0_01285.1.g25391.t1	ref|XP_002882299.1| hypothetical protein ARALYDRAFT_477606 [Arabidopsis lyrata subsp. lyrata] gi|297328139|gb|EFH58558.1| hypothetical protein ARALYDRAFT_477606 [Arabidopsis lyrata subsp. lyrata]	349	322	1.00E-166	92.3	85.1	87.7	hypothetical protein ARALYDRAFT_477606	gbpln	Arabidopsis lyrata	AT3G03610.1 | Symbols: | ELMO/CED-12 family protein | chr3:869479-871687 FORWARD LENGTH=323	349	323	1.00E-166	92.6	84.5	87.1
Rsa1.0_01285.1.g25392.t1	gb|EOA31411.1| hypothetical protein CARUB_v10014591mg [Capsella rubella]	219	219	1.00E-120	100.0	92.7	98.2	hypothetical protein CARUB_v10014591mg	gbpln	Capsella rubella	AT3G03600.1 | Symbols: RPS2 | ribosomal protein S2 | chr3:867847-868506 REVERSE LENGTH=219	219	219	1.00E-122	100.0	92.2	98.2
Rsa1.0_01285.1.g25393.t1	gb|EOA31614.1| hypothetical protein CARUB_v10014811mg [Capsella rubella]	149	154	2.00E-51	103.4	79.9	87.2	hypothetical protein CARUB_v10014811mg	gbpln	Capsella rubella	AT3G03590.1 | Symbols: | SWIB/MDM2 domain superfamily protein | chr3:865341-866669 REVERSE LENGTH=143	149	143	2.00E-51	96.0	75.2	83.2
Rsa1.0_01285.1.g25394.t1	ref|XP_002884396.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297330236|gb|EFH60655.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	881	882	0	100.1	82.4	91.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G03580.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:860695-863343 REVERSE LENGTH=882	881	882	0	100.1	83.3	91.9
Rsa1.0_01285.1.g25395.t1	gb|AAD12055.1| DnaJ protein [Hevea brasiliensis]	123	415	5.00E-17	337.4	34.1	35.0	DnaJ protein	gbpln	Hevea brasiliensis	AT5G22060.1 | Symbols: ATJ2, J2 | DNAJ homologue 2 | chr5:7303798-7305668 REVERSE LENGTH=419	123	419	2.00E-15	340.7	37.4	38.2
Rsa1.0_01285.1.g25396.t5	gb|ABD65153.1| SLL3 ORF2 protein [Brassica oleracea]	295	333	4.00E-27	112.9	20.7	25.1	SLL3 ORF2 protein	gbpln	Brassica oleracea	AT4G03740.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr4:1661992-1663515 REVERSE LENGTH=345	295	345	2.00E-11	116.9	12.2	16.3
Rsa1.0_01285.1.g25397.t1	ref|NP_187002.1| non-specific phospholipase C3 [Arabidopsis thaliana] gi|6017100|gb|AAF01583.1|AC009895_4 unknown protein [Arabidopsis thaliana] gi|23297654|gb|AAN13002.1| unknown protein [Arabidopsis thaliana] gi|24417135|dbj|BAC22510.1| phosphatidylglycerol specific phospholipase C [Arabidopsis thaliana] gi|332640432|gb|AEE73953.1| non-specific phospholipase C3 [Arabidopsis thaliana]	485	523	0	107.8	93.4	96.3	non-specific phospholipase C3	gbpln	Arabidopsis thaliana	AT3G03520.1 | Symbols: NPC3 | non-specific phospholipase C3 | chr3:837972-840511 REVERSE LENGTH=523	485	523	0	107.8	93.4	96.3
Rsa1.0_01285.1.g25398.t1	sp|Q9SRQ5.2|Y3351_ARATH RecName: Full=BTB/POZ domain-containing protein At3g03510	518	508	0	98.1	73.9	83.8	RecName: Full=BTB/POZ domain-containing protein At3g03510	----	----	AT3G03510.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr3:836340-837707 FORWARD LENGTH=455	518	455	0	87.8	67.0	75.7

Rsa1.0_01285.1.g25399.t1	ref|XP_002884383.1| chat-3-HEXEN-1-OL ACETYLTRANSFERASE [Arabidopsis lyrata subsp. lyrata] gi|297330223|gb|EFH60642.1| chat-3-HEXEN-1-OL ACETYLTRANSFERASE [Arabidopsis lyrata subsp. lyrata]	456	453	0	99.3	81.6	90.1	chat-3-HEXEN-1-OL ACETYLTRANSFERASE	gbpln	Arabidopsis lyrata	AT3G03480.1 | Symbols: CHAT | acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase | chr3:828400-829863 REVERSE LENGTH=454	456	454	0	99.6	81.1	88.8
Rsa1.0_01285.1.g25400.t3	ref|XP_002884383.1| chat-3-HEXEN-1-OL ACETYLTRANSFERASE [Arabidopsis lyrata subsp. lyrata] gi|297330223|gb|EFH60642.1| chat-3-HEXEN-1-OL ACETYLTRANSFERASE [Arabidopsis lyrata subsp. lyrata]	388	453	1.00E-143	116.8	71.6	79.9	chat-3-HEXEN-1-OL ACETYLTRANSFERASE	gbpln	Arabidopsis lyrata	AT3G03480.1 | Symbols: CHAT | acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase | chr3:828400-829863 REVERSE LENGTH=454	388	454	1.00E-143	117.0	71.1	79.6
Rsa1.0_01285.1.g25401.t1	gb|AGA16543.1| DELLA protein RGL2, partial [Sisymbrium officinale]	542	533	0	98.3	88.2	90.8	DELLA protein RGL2, partial	gbpln	Sisymbrium officinale	AT3G03450.1 | Symbols: RGL2 | RGA-like 2 | chr3:819636-821279 REVERSE LENGTH=547	542	547	0	100.9	83.4	89.7
Rsa1.0_01285.1.g25402.t1	ref|NP_186994.2| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|332640423|gb|AEE73944.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	286	408	1.00E-133	142.7	89.2	90.6	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G03440.1 | Symbols: | ARM repeat superfamily protein | chr3:815709-818568 FORWARD LENGTH=408	286	408	1.00E-135	142.7	89.2	90.6
Rsa1.0_01285.1.g25403.t1	sp|P69198.1|POLC2_BRANA RecName: Full=Polcalcin Bra n 2; AltName: Full=Calcium-binding pollen allergen Bra n 2; AltName: Allergen=Bra n 2 gi|59800146|sp|P69199.1|POLC2_BRARA RecName: Full=Polcalcin Bra r 2; AltName: Full=Calcium-binding pollen allergen Bra r 2; AltName: Allergen=Bra r 2 gi|1255542|dbj|BAA09635.1| calcium-binding protein [Brassica rapa]	83	83	1.00E-38	100.0	96.4	98.8	RecName: Full=Polcalcin Bra n 2; AltName: Full=Calcium-binding pollen allergen Bra n 2; AltName: Allergen=Bra n 2 gi|59800146|sp|P69199.1|POLC2_BRARA RecName: Full=Polcalcin Bra r 2; AltName: Full=Calcium-binding pollen allergen Bra r 2; AltName: Allergen=Bra r 2 gi|1255542|dbj|BAA09635.1| calcium-binding protein	gbpln	Brassica rapa	AT3G03430.1 | Symbols: | Calcium-binding EF-hand family protein | chr3:814481-814732 FORWARD LENGTH=83	83	83	5.00E-40	100.0	94.0	96.4
Rsa1.0_01285.1.g25404.t1	gb|EOA31513.1| hypothetical protein CARUB_v10014702mg [Capsella rubella]	185	194	2.00E-80	104.9	76.8	78.9	hypothetical protein CARUB_v10014702mg	gbpln	Capsella rubella	AT3G03420.1 | Symbols: | Ku70-binding family protein | chr3:812527-813644 FORWARD LENGTH=194	185	194	3.00E-82	104.9	76.2	78.9
Rsa1.0_01285.1.g25405.t1	gb|EOA29773.1| hypothetical protein CARUB_v10012864mg [Capsella rubella]	1121	1097	0	97.9	91.4	94.8	hypothetical protein CARUB_v10012864mg	gbpln	Capsella rubella	AT3G03380.1 | Symbols: DegP7 | DegP protease 7 | chr3:799720-808319 FORWARD LENGTH=1097	1121	1097	0	97.9	91.1	94.6
Rsa1.0_01285.1.g25406.t1	ref|XP_002862611.1| hypothetical protein ARALYDRAFT_497388 [Arabidopsis lyrata subsp. lyrata] gi|297308243|gb|EFH38869.1| hypothetical protein ARALYDRAFT_497388 [Arabidopsis lyrata subsp. lyrata]	66	70	5.00E-13	106.1	53.0	54.5	hypothetical protein ARALYDRAFT_497388	gbpln	Arabidopsis lyrata	AT3G03341.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:790338-790556 REVERSE LENGTH=72	66	72	8.00E-16	109.1	53.0	54.5
Rsa1.0_01286.1.g25407.t1	gb|EOA31131.1| hypothetical protein CARUB_v10014293mg [Capsella rubella]	299	293	1.00E-117	98.0	69.2	78.3	hypothetical protein CARUB_v10014293mg	gbpln	Capsella rubella	AT2G26540.1 | Symbols: HEMD, UROS, ATUROS, ATDUF3, DUF3 | uroporphyrinogen-III synthase family protein | chr2:11287666-11290224 REVERSE LENGTH=321	299	321	1.00E-117	107.4	70.9	82.3
Rsa1.0_01286.1.g25408.t1	gb|EOA28135.1| hypothetical protein CARUB_v10024324mg [Capsella rubella]	124	125	8.00E-55	100.8	85.5	94.4	hypothetical protein CARUB_v10024324mg	gbpln	Capsella rubella	AT2G26500.1 | Symbols: | cytochrome b6f complex subunit (petM), putative | chr2:11270370-11270747 FORWARD LENGTH=125	124	125	4.00E-57	100.8	84.7	94.4
Rsa1.0_01286.1.g25409.t1	ref|NP_180217.1| WD40 domain-containing protein [Arabidopsis thaliana] gi|2739374|gb|AAC14498.1| En/Spm-like transposon protein [Arabidopsis thaliana] gi|50253512|gb|AAT71958.1| At2g26490 [Arabidopsis thaliana] gi|53850519|gb|AAU95436.1| At2g26490 [Arabidopsis thaliana] gi|330252750|gb|AEC07844.1| WD40 domain-containing protein [Arabidopsis thaliana]	466	465	0	99.8	94.0	96.4	WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G26490.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:11268035-11269432 FORWARD LENGTH=465	466	465	0	99.8	94.0	96.4
Rsa1.0_01286.1.g25410.t2	ref|XP_002880800.1| red family protein [Arabidopsis lyrata subsp. lyrata] gi|297326639|gb|EFH57059.1| red family protein [Arabidopsis lyrata subsp. lyrata]	584	574	0	98.3	85.4	90.2	red family protein	gbpln	Arabidopsis lyrata	AT2G26460.1 | Symbols: SMU2 | RED family protein | chr2:11255049-11258913 REVERSE LENGTH=585	584	585	0	100.2	85.1	89.7

Rsa1.0_01286.1.g25411.t2	ref|NP_180215.2| uncharacterized protein [Arabidopsis thaliana] gi|26449484|dbj|BAC41868.1| unknown protein [Arabidopsis thaliana] gi|29028900|gb|AAO64829.1| At2g26470 [Arabidopsis thaliana] gi|330252748|gb|AEC07842.1| uncharacterized protein AT2G26470 [Arabidopsis thaliana]	405	487	2.33E-156	120.2	65.4	73.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G26470.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF159 (InterPro:IPR003738); Has 3646 Blast hits to 3636 proteins in 1001 species: Archae - 41; Bacteria - 1922; Metazoa - 142; Fungi - 125; Plants - 44; Viruses - 14; Other Eukaryotes - 1358 (source: NCBI BLink). | chr2:11259316-11262362 REVERSE LENGTH=487	405	487	1.00E-149	120.2	65.4	73.3
Rsa1.0_01286.1.g25412.t1	ref|XP_002877696.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297323534|gb|EFH53955.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	115	1188	3.00E-40	1033.0	70.4	80.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G49730.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:18445730-18447646 REVERSE LENGTH=638	115	638	8.00E-42	554.8	69.6	80.0
Rsa1.0_01286.1.g25413.t1	ref|XP_002877935.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297323773|gb|EFH54194.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	325	322	1.00E-130	99.1	73.5	82.8	zinc finger family protein	gbpln	Arabidopsis lyrata	AT3G53690.1 | Symbols: | RING/U-box superfamily protein | chr3:19898997-19900044 REVERSE LENGTH=320	325	320	1.00E-124	98.5	72.3	81.8
Rsa1.0_01286.1.g25414.t1	ref|XP_002866685.1| hypothetical protein ARALYDRAFT_358769 [Arabidopsis lyrata subsp. lyrata] gi|297312520|gb|EFH42944.1| hypothetical protein ARALYDRAFT_358769 [Arabidopsis lyrata subsp. lyrata]	80	914	9.00E-23	1142.5	67.5	73.8	hypothetical protein ARALYDRAFT_358769	gbpln	Arabidopsis lyrata	AT5G65687.1 | Symbols: | Major facilitator superfamily protein | chr5:26270038-26272787 REVERSE LENGTH=492	80	492	1.00E-24	615.0	67.5	72.5
Rsa1.0_01286.1.g25415.t1	ref|XP_002880789.1| hypothetical protein ARALYDRAFT_320430 [Arabidopsis lyrata subsp. lyrata] gi|297326628|gb|EFH57048.1| hypothetical protein ARALYDRAFT_320430 [Arabidopsis lyrata subsp. lyrata]	1315	705	0	53.6	48.7	50.6	hypothetical protein ARALYDRAFT_320430	gbpln	Arabidopsis lyrata	AT2G26420.1 | Symbols: PIP5K3 | 1-phosphatidylinositol-4-phosphate 5-kinase 3 | chr2:11239434-11242239 REVERSE LENGTH=705	1315	705	0	53.6	48.0	50.3
Rsa1.0_01286.1.g25416.t1	ref|XP_002880778.1| hypothetical protein ARALYDRAFT_481492 [Arabidopsis lyrata subsp. lyrata] gi|297326617|gb|EFH57037.1| hypothetical protein ARALYDRAFT_481492 [Arabidopsis lyrata subsp. lyrata]	359	388	1.00E-169	108.1	83.3	88.3	hypothetical protein ARALYDRAFT_481492	gbpln	Arabidopsis lyrata	AT2G26350.1 | Symbols: PEX10, ATPEX10 | peroxin 10 | chr2:11217767-11220415 REVERSE LENGTH=381	359	381	1.00E-170	106.1	83.0	87.7
Rsa1.0_01286.1.g25417.t3	gb|EOA27758.1| hypothetical protein CARUB_v10023913mg [Capsella rubella]	224	251	5.00E-91	112.1	79.9	86.6	hypothetical protein CARUB_v10023913mg	gbpln	Capsella rubella	AT2G26340.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast thylakoid lumen, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 38 Blast hits to 38 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:11215254-11216480 FORWARD LENGTH=253	224	253	1.00E-85	112.9	80.8	88.4
Rsa1.0_01286.1.g25418.t1	ref|XP_002880777.1| hypothetical protein ARALYDRAFT_481491 [Arabidopsis lyrata subsp. lyrata] gi|297326616|gb|EFH57036.1| hypothetical protein ARALYDRAFT_481491 [Arabidopsis lyrata subsp. lyrata]	344	976	0	283.7	93.6	95.3	hypothetical protein ARALYDRAFT_481491	gbpln	Arabidopsis lyrata	AT2G26330.1 | Symbols: ER, QRP1 | Leucine-rich receptor-like protein kinase family protein | chr2:11208367-11213895 REVERSE LENGTH=976	344	976	0	283.7	91.9	94.5
Rsa1.0_01287.1.g25419.t1	gb|AAM60851.1| unknown [Arabidopsis thaliana]	451	453	0	100.4	92.7	96.9	unknown	gbpln	Arabidopsis thaliana	AT5G39410.1 | Symbols: | Saccharopine dehydrogenase | chr5:15768415-15770274 REVERSE LENGTH=454	451	454	0	100.7	92.5	96.7
Rsa1.0_01287.1.g25420.t1	#	#	#	#	#	#	#	-	----	----	AT2G16730.1 | Symbols: BGAL13 | glycosyl hydrolase family 35 protein | chr2:7261986-7266105 REVERSE LENGTH=848	130	848	5.00E-11	652.3	20.0	26.9
Rsa1.0_01287.1.g25421.t1	ref|XP_002868719.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314555|gb|EFH44978.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	508	516	0	101.6	83.7	90.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G39430.1 | Symbols: | Protein of unknown function (DUF1336) | chr5:15775302-15777599 REVERSE LENGTH=511	508	511	0	100.6	80.7	88.8
Rsa1.0_01287.1.g25422.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01287.1.g25423.t1	gb|AAB60731.1| Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene [Arabidopsis thaliana]	168	575	3.00E-21	342.3	31.5	33.3	Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene	gbpln	Arabidopsis thaliana	AT1G09780.1 | Symbols: | Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent | chr1:3165550-3167812 REVERSE LENGTH=557	168	557	1.00E-23	331.5	31.5	33.3
Rsa1.0_01287.1.g25424.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	265	1365	1.00E-16	515.1	17.0	20.0	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	#	#	#	#	#	#	#
Rsa1.0_01287.1.g25425.t4	ref|XP_002870779.1| hypothetical protein ARALYDRAFT_330549 [Arabidopsis lyrata subsp. lyrata] gi|297316615|gb|EFH47038.1| hypothetical protein ARALYDRAFT_330549 [Arabidopsis lyrata subsp. lyrata]	551	491	0	89.1	63.3	73.9	hypothetical protein ARALYDRAFT_330549	gbpln	Arabidopsis lyrata	AT5G39440.1 | Symbols: SnRK1.3 | SNF1-related protein kinase 1.3 | chr5:15781907-15784699 FORWARD LENGTH=494	551	494	0	89.7	62.6	73.9
Rsa1.0_01287.1.g25426.t1	ref|NP_198761.2| F-box protein [Arabidopsis thaliana] gi|75247593|sp|Q8RWD6.1|FB271_ARATH RecName: Full=F-box protein At5g39450 gi|20260530|gb|AAM13163.1| unknown protein [Arabidopsis thaliana] gi|31711988|gb|AAP68350.1| At5g39450 [Arabidopsis thaliana] gi|332007051|gb|AED94434.1| F-box protein [Arabidopsis thaliana]	577	579	0	100.3	70.5	80.8	F-box protein	gbpln	Arabidopsis thaliana	AT5G39450.1 | Symbols: | F-box family protein | chr5:15786045-15787877 FORWARD LENGTH=579	577	579	0	100.3	70.5	80.8
Rsa1.0_01288.1.g25427.t1	gb|EOA38933.1| hypothetical protein CARUB_v10011332mg [Capsella rubella]	80	331	3.00E-27	413.8	78.8	81.3	hypothetical protein CARUB_v10011332mg	gbpln	Capsella rubella	AT1G53345.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G09580.1); Has 201 Blast hits to 201 proteins in 75 species: Archae - 6; Bacteria - 102; Metazoa - 2; Fungi - 0; Plants - 47; Viruses - 7; Other Eukaryotes - 37 (source: NCBI BLink). | chr1:19902561-19903538 FORWARD LENGTH=325	80	325	8.00E-28	406.3	73.8	80.0
Rsa1.0_01288.1.g25428.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1576	1529	0	97.0	44.2	62.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1576	746	1.00E-108	47.3	12.4	16.6
Rsa1.0_01288.1.g25429.t1	gb|EOA28769.1| hypothetical protein CARUB_v10025001mg, partial [Capsella rubella]	147	389	8.00E-24	264.6	46.9	55.8	hypothetical protein CARUB_v10025001mg, partial	gbpln	Capsella rubella	AT3G17540.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6002783-6003973 FORWARD LENGTH=396	147	396	1.00E-23	269.4	44.9	55.8
Rsa1.0_01288.1.g25430.t5	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	2332	1374	0	58.9	31.7	41.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G53380.3 | Symbols: | Plant protein of unknown function (DUF641) | chr1:19913341-19914702 REVERSE LENGTH=453	2332	453	0	19.4	15.7	16.9
Rsa1.0_01288.1.g25431.t1	gb|EOA37713.1| hypothetical protein CARUB_v10012449mg [Capsella rubella]	190	315	2.00E-56	165.8	71.6	83.2	hypothetical protein CARUB_v10012449mg	gbpln	Capsella rubella	AT1G53460.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ran BP2/NZF zinc finger-like superfamily protein (TAIR:AT1G70650.2); Has 485 Blast hits to 413 proteins in 88 species: Archae - 11; Bacteria - 27; Metazoa - 119; Fungi - 17; Plants - 101; Viruses - 2; Other Eukaryotes - 208 (source: NCBI BLink). | chr1:19954558-19956509 REVERSE LENGTH=314	190	314	9.00E-59	165.3	72.6	82.6
Rsa1.0_01288.1.g25432.t1	gb|EOA39638.1| hypothetical protein CARUB_v10008272mg [Capsella rubella]	869	880	0	101.3	87.0	92.6	hypothetical protein CARUB_v10008272mg	gbpln	Capsella rubella	AT1G53470.1 | Symbols: MSL4 | mechanosensitive channel of small conductance-like 4 | chr1:19958587-19961578 FORWARD LENGTH=881	869	881	0	101.4	85.7	92.3
Rsa1.0_01288.1.g25433.t1	ref|NP_175754.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332194827|gb|AEE32948.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	290	304	1.00E-129	104.8	76.9	84.5	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT1G53490.1 | Symbols: | RING/U-box superfamily protein | chr1:19965146-19966811 FORWARD LENGTH=304	290	304	1.00E-132	104.8	76.9	84.5
Rsa1.0_01288.1.g25434.t1	gb|EOA30048.1| hypothetical protein CARUB_v10013153mg [Capsella rubella]	184	664	2.00E-55	360.9	62.5	66.3	hypothetical protein CARUB_v10013153mg	gbpln	Capsella rubella	AT3G14790.1 | Symbols: RHM3, ATRHM3 | rhamnose biosynthesis 3 | chr3:4964791-4966875 FORWARD LENGTH=664	184	664	5.00E-57	360.9	62.0	65.8

Rsa1.0_01288.1.g25435.t1	gb|AAC79110.1| putative polyprotein of LTR transposon [Arabidopsis thaliana] gi|7269781|emb|CAB77781.1| putative polyprotein of LTR transposon [Arabidopsis thaliana]	161	1456	3.00E−43	904.3	52.8	60.9	putative polyprotein of LTR transposon	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	161	1262	6.00E−19	783.9	26.7	43.5
Rsa1.0_01288.1.g25436.t1	ref|XP_002886377.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332218|gb|EFH62636.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	229	934	3.00E−68	407.9	54.1	58.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G63730.1 | Symbols: | Disease resistance protein (TIR−NBS−LRR class) family | chr1:23641770−23645132 FORWARD LENGTH=966	229	966	7.00E−70	421.8	55.5	59.8
Rsa1.0_01289.1.g25437.t1	gb|EOA40076.1| hypothetical protein CARUB_v10008772mg [Capsella rubella]	523	546	0	104.4	79.2	89.1	hypothetical protein CARUB_v10008772mg	gbpln	Capsella rubella	AT1G14080.1 | Symbols: FUT6, ATFUT6 | fucosyltransferase 6 | chr1:4822580−4824218 FORWARD LENGTH=519	523	519	0	99.2	79.2	87.6
Rsa1.0_01289.1.g25438.t3	ref|NP_172857.2| phosphate transporter PHO1−3 [Arabidopsis thaliana] gi|306756302|sp|Q6R8G7.2|PHO13_ARATH RecName: Full=Phosphate transporter PHO1 homolog 3; AltName: Full=Protein PHO1 homolog 3; Short=AtPHO1;H3 gi|332190980|gb|AEE29101.1| phosphate transporter PHO1−3 [Arabidopsis thaliana]	213	813	1.00E−62	381.7	63.4	78.9	phosphate transporter PHO1−3	gbpln	Arabidopsis thaliana	AT1G14040.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr1:4810488−4814543 FORWARD LENGTH=813	213	813	4.00E−65	381.7	63.4	78.9
Rsa1.0_01289.1.g25439.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01289.1.g25440.t2	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	2835	1274	0	44.9	21.8	29.9	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT1G14040.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr1:4810488−4814543 FORWARD LENGTH=813	2835	813	1.00E−124	28.7	8.4	9.2
Rsa1.0_01289.1.g25441.t1	ref|NP_172857.2| phosphate transporter PHO1−3 [Arabidopsis thaliana] gi|306756302|sp|Q6R8G7.2|PHO13_ARATH RecName: Full=Phosphate transporter PHO1 homolog 3; AltName: Full=Protein PHO1 homolog 3; Short=AtPHO1;H3 gi|332190980|gb|AEE29101.1| phosphate transporter PHO1−3 [Arabidopsis thaliana]	596	813	0	136.4	86.7	93.1	phosphate transporter PHO1−3	gbpln	Arabidopsis thaliana	AT1G14040.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr1:4810488−4814543 FORWARD LENGTH=813	596	813	0	136.4	86.7	93.1
Rsa1.0_01290.1.g25442.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01290.1.g25443.t1	gb|AAD24567.1|AF120335_1 putative transposase [Arabidopsis thaliana]	130	577	2.00E−31	443.8	50.8	66.2	putative transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01290.1.g25444.t2	gb|EOA12975.1| hypothetical protein CARUB_v10025964mg [Capsella rubella]	772	725	0	93.9	77.5	85.8	hypothetical protein CARUB_v10025964mg	gbpln	Capsella rubella	AT5G49880.1 | Symbols: | mitotic checkpoint family protein | chr5:20282305−20287775 FORWARD LENGTH=726	772	726	0	94.0	78.2	85.4
Rsa1.0_01290.1.g25445.t2	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01290.1.g25446.t2	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01290.1.g25447.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01290.1.g25448.t1	gb|EOA29112.1| hypothetical protein CARUB_v10025379mg [Capsella rubella]	374	1560	3.00E−57	417.1	44.7	56.7	hypothetical protein CARUB_v10025379mg	gbpln	Capsella rubella	AT2G36490.1 | Symbols: DML1, ROS1 | demeter−like 1 | chr2:15308259−15314272 REVERSE LENGTH=1393	374	1393	5.00E−56	372.5	38.0	47.6
Rsa1.0_01290.1.g25449.t1	gb|AAC26234.1| contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]	505	940	2.00E−32	186.1	13.1	18.6	contains similarity to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01290.1.g25450.t1	gb|ABD65058.1| GRF zinc finger containing protein [Brassica oleracea]	144	172	9.00E−14	119.4	34.0	46.5	GRF zinc finger containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01291.1.g25451.t1	gb|EOA28069.1| hypothetical protein CARUB_v10024251mg [Capsella rubella]	354	151	4.00E−17	42.7	15.5	20.1	hypothetical protein CARUB_v10024251mg	gbpln	Capsella rubella	AT2G38880.7 | Symbols: NF−YB1 | nuclear factor Y, subunit B1 | chr2:16238685−16240316 FORWARD LENGTH=139	354	139	7.00E−19	39.3	15.5	19.5
Rsa1.0_01291.1.g25452.t1	gb|ABL97987.1| protein translocase [Brassica rapa]	466	220	1.00E−104	47.2	44.0	44.6	protein translocase	gbpln	Brassica rapa	AT2G37410.2 | Symbols: ATTIM17−2, TIM17, TIM17−2 | translocase inner membrane subunit 17−2 | chr2:15698119−15698850 REVERSE LENGTH=243	466	243	7.00E−82	52.1	36.1	40.3
Rsa1.0_01291.1.g25453.t1	ref|XP_002879665.1| hypothetical protein ARALYDRAFT_482731 [Arabidopsis lyrata subsp. lyrata] gi|297325504|gb|EFH55924.1| hypothetical protein ARALYDRAFT_482731 [Arabidopsis lyrata subsp. lyrata]	261	312	6.00E−59	119.5	73.2	79.3	hypothetical protein ARALYDRAFT_482731	gbpln	Arabidopsis lyrata	AT2G37380.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G39370.1); Has 1284 Blast hits to 422 proteins in 114 species: Archae − 0; Bacteria − 90; Metazoa − 125; Fungi − 151; Plants − 136; Viruses − 0; Other Eukaryotes − 782 (source: NCBI BLink). | chr2:15686828−15687793 FORWARD LENGTH=321	261	321	5.00E−61	123.0	75.5	81.6

Rsa1.0_01292.1.g25454.t1	ref|NP_566257.1| U4/U6.U5 tri-snRNP component [Arabidopsis thaliana] gi|14517383|gb|AAK62582.1| AT3g05760/F10A16_5 [Arabidopsis thaliana] gi|15450543|gb|AAK96449.1| AT3g05760/F10A16_5 [Arabidopsis thaliana] gi|332640772|gb|AEE74293.1| U4/U6.U5 tri-snRNP component [Arabidopsis thaliana]	201	202	7.00E-88	100.5	93.5	96.5	U4/U6.U5 tri-snRNP component	gbpln	Arabidopsis thaliana	AT3G05760.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr3:1707981-1709910 FORWARD LENGTH=202	201	202	2.00E-90	100.5	93.5	96.5
Rsa1.0_01292.1.g25455.t2	gb|AAD25610.1|AC005287_12 Hypothetical protein [Arabidopsis thaliana]	449	444	3.00E-64	98.9	36.7	45.9	Hypothetical protein	gbpln	Arabidopsis thaliana	AT3G05770.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G54300.1); Has 105 Blast hits to 105 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 99; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr3:1710328-1712165 REVERSE LENGTH=410	449	410	2.00E-63	91.3	36.5	45.7
Rsa1.0_01292.1.g25456.t2	gb|EOA29822.1| hypothetical protein CARUB_v10012917mg [Capsella rubella]	929	937	0	100.9	72.1	81.6	hypothetical protein CARUB_v10012917mg	gbpln	Capsella rubella	AT3G05790.1 | Symbols: LON4 | lon protease 4 | chr3:1720154-1725182 REVERSE LENGTH=942	929	942	0	101.4	73.1	82.1
Rsa1.0_01292.1.g25457.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01292.1.g25458.t1	gb|EOA30990.1| hypothetical protein CARUB_v10014135mg, partial [Capsella rubella]	293	335	5.00E-93	114.3	70.6	79.2	hypothetical protein CARUB_v10014135mg, partial	gbpln	Capsella rubella	AT3G06020.1 | Symbols: | Protein of unknown function (DUF3049) | chr3:1813267-1814169 FORWARD LENGTH=300	293	300	9.00E-85	102.4	71.7	80.5
Rsa1.0_01292.1.g25459.t1	ref|NP_187254.1| mitogen-activated protein kinase kinase kinase 3 [Arabidopsis thaliana] gi|46576859|sp|O22042.1|M3K3_ARATH RecName: Full=Mitogen-activated protein kinase kinase kinase 3; AltName: Full=Arabidopsis NPK1-related protein kinase 3 gi|2342427|dbj|BAA21857.1| NPK1-related protein kinase 3 [Arabidopsis thaliana] gi|7658341|gb|AAF66131.1| NPK1-related protein kinase 3; 8286-4476 [Arabidopsis thaliana] gi|17979012|gb|AAL47465.1| AT3g06030/F24F17_1 [Arabidopsis thaliana] gi|24111309|gb|AAN46778.1| At3g06030/F24F17_1 [Arabidopsis thaliana] gi|332640811|gb|AEE74332.1| mitogen-activated protein kinase kinase kinase 3 [Arabidopsis thaliana]	656	651	0	99.2	87.5	91.5	mitogen-activated protein kinase kinase kinase 3	gbpln	Arabidopsis thaliana	AT3G06030.1 | Symbols: ANP3, MAPKKK12, NP3 | NPK1-related protein kinase 3 | chr3:1818895-1822705 REVERSE LENGTH=651	656	651	0	99.2	87.5	91.5
Rsa1.0_01292.1.g25460.t1	ref|NP_566267.1| glycoprotein membrane precursor GPI-anchored protein [Arabidopsis thaliana] gi|34395875|sp|Q84MC0.1|UGPI4_ARATH RecName: Full=Uncharacterized GPI-anchored protein At3g06035; Flags: Precursor gi|30102608|gb|AAP21222.1| At3g06035 [Arabidopsis thaliana] gi|110735967|dbj|BAE99958.1| hypothetical protein [Arabidopsis thaliana] gi|332640812|gb|AEE74333.1| glycoprotein membrane precursor GPI-anchored protein [Arabidopsis thaliana]	198	200	3.00E-83	101.0	76.3	84.8	glycoprotein membrane precursor GPI-anchored protein	gbpln	Arabidopsis thaliana	AT3G06035.1 | Symbols: | Glycoprotein membrane precursor GPI-anchored | chr3:1823172-1824110 REVERSE LENGTH=200	198	200	1.00E-85	101.0	76.3	84.8
Rsa1.0_01292.1.g25461.t1	gb|EOA31534.1| hypothetical protein CARUB_v10014726mg [Capsella rubella]	191	188	8.00E-78	98.4	83.2	89.5	hypothetical protein CARUB_v10014726mg	gbpln	Capsella rubella	AT3G06040.3 | Symbols: | Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein | chr3:1824516-1825076 REVERSE LENGTH=186	191	186	8.00E-77	97.4	81.2	88.0
Rsa1.0_01292.1.g25462.t1	dbj|BAJ34275.1| unnamed protein product [Thellungiella halophila]	201	201	1.00E-104	100.0	94.0	95.5	unnamed protein product	----	----	AT3G06050.1 | Symbols: PRXIIF, ATPRXIIF | peroxiredoxin IIF | chr3:1826311-1827809 REVERSE LENGTH=201	201	201	1.00E-106	100.0	92.5	96.5
Rsa1.0_01292.1.g25463.t1	ref|XP_002884556.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330396|gb|EFH60815.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	329	326	1.00E-167	99.1	87.5	94.5	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G06060.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:1828296-1830160 REVERSE LENGTH=326	329	326	1.00E-164	99.1	87.8	93.9

<table>
<tr><td>Rsa1.0_01292.1.g25464.t1</td><td>ref|XP_002884557.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330397|gb|EFH60816.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>155</td><td>152</td><td>2.00E-60</td><td>98.1</td><td>78.1</td><td>85.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G06070.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19190.1); Has 33 Blast hits to 33 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:1831305-1831846 REVERSE LENGTH=151</td><td>155</td><td>151</td><td>3.00E-60</td><td>97.4</td><td>78.7</td><td>86.5</td></tr>
<tr><td>Rsa1.0_01292.1.g25465.t1</td><td>gb|EOA30487.1| hypothetical protein CARUB_v10013611mg [Capsella rubella]</td><td>469</td><td>473</td><td>0</td><td>100.9</td><td>84.4</td><td>91.0</td><td>hypothetical protein CARUB_v10013611mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G06080.2 | Symbols: | Plant protein of unknown function (DUF828) | chr3:1834959-1837524 REVERSE LENGTH=469</td><td>469</td><td>469</td><td>0</td><td>100.0</td><td>84.0</td><td>90.6</td></tr>
<tr><td>Rsa1.0_01293.1.g25466.t1</td><td>gb|AAC15700.1| BURP domain containing protein [Brassica napus] gi|226427141|gb|ACO54860.1| BURP domain protein [Brassica napus] gi|226427143|gb|ACO54861.1| BURP domain protein [Brassica napus]</td><td>249</td><td>282</td><td>1.00E-124</td><td>113.3</td><td>84.3</td><td>92.4</td><td>BURP domain containing protein</td><td>gbpln</td><td>Brassica napus</td><td>AT1G49320.1 | Symbols: ATUSPL1, USPL1 | unknown seed protein like 1 | chr1:18246441-18247817 FORWARD LENGTH=280</td><td>249</td><td>280</td><td>1.00E-123</td><td>112.4</td><td>80.7</td><td>92.0</td></tr>
<tr><td>Rsa1.0_01293.1.g25467.t1</td><td>gb|EOA39437.1| hypothetical protein CARUB_v10012580mg, partial [Capsella rubella]</td><td>507</td><td>342</td><td>8.00E-75</td><td>67.5</td><td>25.2</td><td>28.2</td><td>hypothetical protein CARUB_v10012580mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G49330.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:18250043-18251038 FORWARD LENGTH=331</td><td>507</td><td>331</td><td>6.00E-72</td><td>65.3</td><td>24.3</td><td>27.6</td></tr>
<tr><td>Rsa1.0_01293.1.g25468.t1</td><td>gb|AAD43164.1|AC007504_19 Putative Phosphatidylinositol 4-kinase PI4K [Arabidopsis thaliana]</td><td>2023</td><td>2051</td><td>0</td><td>101.4</td><td>93.9</td><td>96.8</td><td>Putative Phosphatidylinositol 4-kinase PI4K</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G49340.1 | Symbols: ATPI4K ALPHA | Phosphatidylinositol 3- and 4-kinase family protein | chr1:18252355-18263967 FORWARD LENGTH=2028</td><td>2023</td><td>2028</td><td>0</td><td>100.2</td><td>93.8</td><td>96.4</td></tr>
<tr><td>Rsa1.0_01293.1.g25469.t1</td><td>gb|EOA32409.1| hypothetical protein CARUB_v10015681mg [Capsella rubella]</td><td>131</td><td>131</td><td>9.00E-45</td><td>100.0</td><td>66.4</td><td>80.2</td><td>hypothetical protein CARUB_v10015681mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G03410.1 | Symbols: | EF hand calcium-binding protein family | chr3:811324-811719 REVERSE LENGTH=131</td><td>131</td><td>131</td><td>6.00E-43</td><td>100.0</td><td>61.8</td><td>77.1</td></tr>
<tr><td>Rsa1.0_01293.1.g25470.t1</td><td>ref|XP_002894180.1| hypothetical protein ARALYDRAFT_891816 [Arabidopsis lyrata subsp. lyrata] gi|297340022|gb|EFH70439.1| hypothetical protein ARALYDRAFT_891816 [Arabidopsis lyrata subsp. lyrata]</td><td>54</td><td>54</td><td>2.00E-20</td><td>100.0</td><td>87.0</td><td>94.4</td><td>hypothetical protein ARALYDRAFT_891816</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G49410.1 | Symbols: TOM6 | translocase of the outer mitochondrial membrane 6 | chr1:18286738-18286902 REVERSE LENGTH=54</td><td>54</td><td>54</td><td>3.00E-23</td><td>100.0</td><td>88.9</td><td>92.6</td></tr>
<tr><td>Rsa1.0_01293.1.g25471.t1</td><td>emb|CAA96523.1| acyl CoA synthetase [Brassica napus]</td><td>666</td><td>666</td><td>0</td><td>100.0</td><td>97.7</td><td>98.9</td><td>acyl CoA synthetase</td><td>gbpln</td><td>Brassica napus</td><td>AT1G49430.1 | Symbols: LACS2, LRD2 | long-chain acyl-CoA synthetase 2 | chr1:18291188-18295641 FORWARD LENGTH=665</td><td>666</td><td>665</td><td>0</td><td>99.8</td><td>91.9</td><td>96.2</td></tr>
<tr><td>Rsa1.0_01293.1.g25472.t1</td><td>dbj|BAJ34322.1| unnamed protein product [Thellungiella halophila]</td><td>269</td><td>226</td><td>5.00E-96</td><td>84.0</td><td>66.5</td><td>72.5</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G49480.1 | Symbols: RTV1 | related to vernalization1 1 | chr1:18314596-18315460 REVERSE LENGTH=226</td><td>269</td><td>226</td><td>5.00E-95</td><td>84.0</td><td>63.6</td><td>72.1</td></tr>
<tr><td>Rsa1.0_01294.1.g25473.t1</td><td>ref|XP_002876357.1| hypothetical protein ARALYDRAFT_486067 [Arabidopsis lyrata subsp. lyrata] gi|297322195|gb|EFH52616.1| hypothetical protein ARALYDRAFT_486067 [Arabidopsis lyrata subsp. lyrata]</td><td>421</td><td>440</td><td>1.00E-133</td><td>104.5</td><td>68.2</td><td>79.3</td><td>hypothetical protein ARALYDRAFT_486067</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G56270.1 | Symbols: | Plant protein of unknown function (DUF827) | chr3:20870220-20871854 FORWARD LENGTH=446</td><td>421</td><td>446</td><td>1.00E-135</td><td>105.9</td><td>67.5</td><td>79.3</td></tr>
<tr><td>Rsa1.0_01294.1.g25474.t1</td><td>ref|NP_001190104.1| uncharacterized protein [Arabidopsis thaliana] gi|44681332|gb|AAS47606.1| At3g56260 [Arabidopsis thaliana] gi|45773858|gb|AAS76733.1| At3g56260 [Arabidopsis thaliana] gi|332645982|gb|AEE79503.1| uncharacterized protein AT3G56260 [Arabidopsis thaliana]</td><td>201</td><td>197</td><td>4.00E-40</td><td>98.0</td><td>57.7</td><td>70.1</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G56260.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G40475.1). | chr3:20868199-20868792 REVERSE LENGTH=197</td><td>201</td><td>197</td><td>1.00E-42</td><td>98.0</td><td>57.7</td><td>70.1</td></tr>
<tr><td>Rsa1.0_01294.1.g25475.t2</td><td>ref|NP_191184.1| uncharacterized protein [Arabidopsis thaliana] gi|7572923|emb|CAB87424.1| putative protein [Arabidopsis thaliana] gi|332645980|gb|AEE79501.1| uncharacterized protein AT3G56250 [Arabidopsis thaliana]</td><td>261</td><td>222</td><td>4.00E-45</td><td>85.1</td><td>51.7</td><td>61.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G56250.1 | Symbols: | unknown protein; Has 109 Blast hits to 83 proteins in 41 species: Archae - 0; Bacteria - 6; Metazoa - 18; Fungi - 20; Plants - 21; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink). | chr3:20866120-20867840 FORWARD LENGTH=222</td><td>261</td><td>222</td><td>1.00E-47</td><td>85.1</td><td>51.7</td><td>61.7</td></tr>
<tr><td>Rsa1.0_01294.1.g25476.t1</td><td>ref|XP_002878075.1| hypothetical protein ARALYDRAFT_486064 [Arabidopsis lyrata subsp. lyrata] gi|297323913|gb|EFH54334.1| hypothetical protein ARALYDRAFT_486064 [Arabidopsis lyrata subsp. lyrata]</td><td>109</td><td>121</td><td>5.00E-48</td><td>111.0</td><td>93.6</td><td>96.3</td><td>hypothetical protein ARALYDRAFT_486064</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G56240.1 | Symbols: CCH | copper chaperone | chr3:20863460-20864402 REVERSE LENGTH=121</td><td>109</td><td>121</td><td>2.00E-49</td><td>111.0</td><td>91.7</td><td>94.5</td></tr>
</table>

Rsa1.0_01294.1.g25477.t1	ref|NP_191182.1| BTB/POZ domain-containing protein [Arabidopsis thaliana] gi|75264422|sp|Q9LYL9.1|Y3623_ARATH RecName: Full=BTB/POZ domain-containing protein At3g56230 gi|7572921|emb|CAB87422.1| putative protein [Arabidopsis thaliana] gi|45825155|gb|AAS77485.1| At3g56230 [Arabidopsis thaliana] gi|51970740|dbj|BAD44062.1| putative protein [Arabidopsis thaliana] gi|332645978|gb|AEE79499.1| BTB/POZ domain-containing protein [Arabidopsis thaliana]	283	282	1.00E-137	99.6	84.8	93.3	BTB/POZ domain-containing protein	gbpln	Arabidopsis thaliana	AT3G56230.1 | Symbols: | BTB/POZ domain-containing protein | chr3:20860899-20862135 REVERSE LENGTH=282	283	282	1.00E-140	99.6	84.8	93.3
Rsa1.0_01294.1.g25478.t1	gb|EOA24875.1| hypothetical protein CARUB_v10018165mg [Capsella rubella]	157	157	3.00E-63	100.0	76.4	86.6	hypothetical protein CARUB_v10018165mg	gbpln	Capsella rubella	AT3G56220.1 | Symbols: | transcription regulators | chr3:20858941-20860302 FORWARD LENGTH=156	157	156	4.00E-65	99.4	76.4	86.6
Rsa1.0_01294.1.g25479.t1	ref|XP_002878073.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297323911|gb|EFH54332.1| binding protein [Arabidopsis lyrata subsp. lyrata]	194	195	4.00E-92	100.5	86.1	93.3	binding protein	gbpln	Arabidopsis lyrata	AT3G56210.4 | Symbols: | ARM repeat superfamily protein | chr3:20853995-20855445 REVERSE LENGTH=191	194	191	1.00E-90	98.5	83.5	90.2
Rsa1.0_01294.1.g25480.t1	ref|XP_002876354.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297322192|gb|EFH52613.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata]	445	435	0	97.8	84.3	91.7	amino acid transporter family protein	gbpln	Arabidopsis lyrata	AT3G56200.1 | Symbols: | Transmembrane amino acid transporter family protein | chr3:20850087-20851779 FORWARD LENGTH=435	445	435	0	97.8	82.5	91.2
Rsa1.0_01294.1.g25481.t5	ref|XP_002876354.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297322192|gb|EFH52613.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata]	852	435	0	51.1	42.4	44.4	amino acid transporter family protein	gbpln	Arabidopsis lyrata	AT3G56200.1 | Symbols: | Transmembrane amino acid transporter family protein | chr3:20850087-20851779 FORWARD LENGTH=435	852	435	0	51.1	41.5	44.1
Rsa1.0_01294.1.g25482.t1	ref|NP_191178.1| alpha-soluble NSF attachment protein 2 [Arabidopsis thaliana] gi|18203446|sp|Q9SPE6.1|SNAA2_ARATH RecName: Full=Alpha-soluble NSF attachment protein 2; Short=Alpha-SNAP2; AltName: Full=N-ethylmaleimide-sensitive factor attachment protein alpha 2 gi|6013204|gb|AAF01284.1|AF177989_1 alpha-soluble NSF attachment protein [Arabidopsis thaliana] gi|7572917|emb|CAB87418.1| alpha-soluble NSF attachment protein [Arabidopsis thaliana] gi|89000917|gb|ABD59048.1| At3g56190 [Arabidopsis thaliana] gi|332645970|gb|AEE79491.1| alpha-soluble NSF attachment protein 2 [Arabidopsis thaliana]	325	289	1.00E-131	88.9	80.6	83.4	alpha-soluble NSF attachment protein 2	gbpln	Arabidopsis thaliana	AT3G56190.1 | Symbols: ALPHA-SNAP2, ASNAP | alpha-soluble NSF attachment protein 2 | chr3:20846119-20848356 REVERSE LENGTH=289	325	289	1.00E-133	88.9	80.6	83.4
Rsa1.0_01294.1.g25483.t1	gb|EOA24383.1| hypothetical protein CARUB_v10017620mg [Capsella rubella]	623	329	1.00E-128	52.8	37.9	42.1	hypothetical protein CARUB_v10017620mg	gbpln	Capsella rubella	AT3G56170.1 | Symbols: CAN | Ca-2+ dependent nuclease | chr3:20842614-20844319 FORWARD LENGTH=323	623	323	1.00E-126	51.8	37.2	40.4
Rsa1.0_01294.1.g25484.t1	gb|ABK28199.1| unknown [Arabidopsis thaliana]	275	315	3.00E-65	114.5	44.7	52.0	unknown	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17201414-17202323 REVERSE LENGTH=258	275	258	9.00E-41	93.8	28.4	34.9
Rsa1.0_01295.1.g25485.t1	gb|AAZ66928.1| 117M18_9 [Brassica rapa]	339	371	1.00E-178	109.4	90.6	93.8	117M18_9	gbpln	Brassica rapa	AT5G10100.1 | Symbols: TPPI | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:3157980-3160275 FORWARD LENGTH=369	339	369	1.00E-174	108.8	87.9	92.9
Rsa1.0_01295.1.g25486.t1	gb|AAZ66929.1| 117M18_10 [Brassica rapa]	293	283	1.00E-100	96.6	75.4	80.2	117M18_10	gbpln	Brassica rapa	AT5G10110.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65120.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:3166660-3167938 REVERSE LENGTH=321	293	321	6.00E-77	109.6	62.1	74.4
Rsa1.0_01295.1.g25487.t1	gb|ACQ44230.1| putative ethylene insensitive 3 protein [Arabis alpina]	477	460	0	96.4	77.6	83.4	putative ethylene insensitive 3 protein	gbpln	Arabis alpina	AT5G10120.1 | Symbols: | Ethylene insensitive 3 family protein | chr5:3169732-3171147 FORWARD LENGTH=471	477	471	0	98.7	74.2	81.3

Rsa1.0_01295.1.g25488.t2	dbj|BAK55645.1| flowering locus C [Raphanus sativus] gi|398802992|gb|AFP19441.1| FLC [Raphanus sativus]	196	197	1.00E-101	100.5	96.9	96.9	flowering locus C	gbpln	Raphanus sativus	AT5G10140.1 | Symbols: FLC, FLF, AGL25 | K-box region and MADS-box transcription factor family protein | chr5:3173724-3179339 REVERSE LENGTH=196	196	196	2.00E-74	100.0	82.1	90.3
Rsa1.0_01295.1.g25489.t1	gb|AAZ66933.1| 117M18_14 [Brassica rapa]	226	224	1.00E-119	99.1	94.7	97.3	117M18_14	gbpln	Brassica rapa	AT5G10160.1 | Symbols: | Thioesterase superfamily protein | chr5:3185819-3187159 FORWARD LENGTH=219	226	219	1.00E-109	96.9	85.8	92.0
Rsa1.0_01295.1.g25490.t1	gb|AAZ66934.1| 117M18_15 [Brassica rapa]	580	608	0	104.8	98.6	99.1	117M18_15	gbpln	Brassica rapa	AT5G10240.1 | Symbols: ASN3 | asparagine synthetase 3 | chr5:3212934-3216418 REVERSE LENGTH=578	580	578	0	99.7	90.9	95.7
Rsa1.0_01295.1.g25491.t1	gb|AAZ66935.1| 117M18_16 [Brassica rapa]	207	216	1.00E-113	104.3	99.5	99.5	117M18_16	gbpln	Brassica rapa	AT5G10260.1 | Symbols: AtRABH1e, RABH1e | RAB GTPase homolog H1E | chr5:3219991-3221301 FORWARD LENGTH=207	207	207	1.00E-111	100.0	90.8	97.6
Rsa1.0_01295.1.g25492.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01295.1.g25493.t1	gb|AAZ66936.1| 117M18_17 [Brassica rapa]	334	384	1.00E-164	115.0	87.7	93.7	117M18_17	gbpln	Brassica rapa	AT5G10280.1 | Symbols: MYB92, ATMYB92, ATMYB64 | myb domain protein 92 | chr5:3232776-3233956 FORWARD LENGTH=334	334	334	1.00E-149	100.0	79.9	88.0
Rsa1.0_01295.1.g25494.t1	gb|AAZ66937.1| 117M18_18 [Brassica rapa]	282	249	1.00E-131	88.3	82.6	83.7	117M18_18	gbpln	Brassica rapa	AT5G10360.1 | Symbols: EMB3010, RPS6B | Ribosomal protein S6e | chr5:3258734-3260142 REVERSE LENGTH=249	282	249	1.00E-130	88.3	80.5	82.3
Rsa1.0_01295.1.g25495.t1	gb|AAZ66938.1| 117M18_19 [Brassica rapa]	1755	1755	0	100.0	93.0	96.5	117M18_19	gbpln	Brassica rapa	AT5G10370.1 | Symbols: | helicase domain-containing protein / IBR domain-containing protein / zinc finger protein-related | chr5:3261245-3267188 FORWARD LENGTH=1775	1755	1775	0	101.1	80.2	88.1
Rsa1.0_01295.1.g25496.t1	tpg|DAA55311.1| TPA: histone H3.2 [Zea mays]	136	245	1.00E-72	180.1	100.0	100.0	TPA: histone H3.2	gbenv/gbpln	Zea mays	AT5G65360.1 | Symbols: | Histone superfamily protein | chr5:26120099-26120509 REVERSE LENGTH=136	136	136	5.00E-74	100.0	100.0	100.0
Rsa1.0_01296.1.g25497.t1	ref|NP_195186.1| uncharacterized protein [Arabidopsis thaliana] gi|3096929|emb|CAA18839.1| putative protein [Arabidopsis thaliana] gi|7270410|emb|CAB80177.1| putative protein [Arabidopsis thaliana] gi|38566572|gb|AAR24176.1| At4g34600 [Arabidopsis thaliana] gi|47550671|gb|AAT35234.1| At4g34600 [Arabidopsis thaliana] gi|332660998|gb|AEE86398.1| uncharacterized protein AT4G34600 [Arabidopsis thaliana]	82	83	6.00E-30	101.2	84.1	91.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G34600.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: pollen tube growth; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: M germinated pollen stage, LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G16385.1); Has 17 Blast hits to 17 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:16529280-16529958 FORWARD LENGTH=83	82	83	1.00E-32	101.2	84.1	91.5
Rsa1.0_01296.1.g25498.t1	ref|XP_002869133.1| hypothetical protein ARALYDRAFT_912921 [Arabidopsis lyrata subsp. lyrata] gi|297314969|gb|EFH45392.1| hypothetical protein ARALYDRAFT_912921 [Arabidopsis lyrata subsp. lyrata]	447	412	0	92.2	78.5	81.7	hypothetical protein ARALYDRAFT_912921	gbpln	Arabidopsis lyrata	AT4G34640.1 | Symbols: SQS1, ERG9 | squalene synthase 1 | chr4:16538489-16541655 FORWARD LENGTH=410	447	410	0	91.7	77.9	81.0
Rsa1.0_01296.1.g25499.t1	ref|XP_002867108.1| SH3 domain-containing protein 2 [Arabidopsis lyrata subsp. lyrata] gi|297312944|gb|EFH43367.1| SH3 domain-containing protein 2 [Arabidopsis lyrata subsp. lyrata]	384	368	0	95.8	88.8	93.0	SH3 domain-containing protein 2	gbpln	Arabidopsis lyrata	AT4G34660.1 | Symbols: | SH3 domain-containing protein | chr4:16545595-16548294 REVERSE LENGTH=368	384	368	0	95.8	88.8	92.4
Rsa1.0_01296.1.g25500.t1	gb|EOA17249.1| hypothetical protein CARUB_v10005523mg [Capsella rubella]	261	262	1.00E-137	100.4	94.6	98.9	hypothetical protein CARUB_v10005523mg	gbpln	Capsella rubella	AT4G34670.1 | Symbols: | Ribosomal protein S3Ae | chr4:16548724-16550222 FORWARD LENGTH=262	261	262	1.00E-137	100.4	93.1	97.3
Rsa1.0_01296.1.g25501.t1	dbj|BAJ33857.1| unnamed protein product [Thellungiella halophila]	263	269	1.00E-123	102.3	86.3	91.6	unnamed protein product	----	----	AT4G34680.2 | Symbols: GATA3 | GATA transcription factor 3 | chr4:16553700-16554610 FORWARD LENGTH=269	263	269	1.00E-114	102.3	83.3	88.6
Rsa1.0_01296.1.g25502.t1	gb|EOA17609.1| hypothetical protein CARUB_v10005980mg, partial [Capsella rubella]	117	140	6.00E-62	119.7	96.6	99.1	hypothetical protein CARUB_v10005980mg, partial	gbpln	Capsella rubella	AT4G34700.1 | Symbols: CIB22, AtCIB22 | LYR family of Fe/S cluster biogenesis protein | chr4:16556874-16558362 FORWARD LENGTH=117	117	117	3.00E-64	100.0	97.4	98.3
Rsa1.0_01296.1.g25503.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01296.1.g25504.t1	gb|AAF26434.1| arginine decarboxylase [Brassica juncea]	699	692	0	99.0	92.7	95.1	arginine decarboxylase	gbpln	Brassica juncea	AT4G34710.2 | Symbols: ADC2, SPE2, ATADC2 | arginine decarboxylase 2 | chr4:16560315-16562450 REVERSE LENGTH=711	699	711	0	101.7	85.1	91.7
Rsa1.0_01296.1.g25505.t1	dbj|BAA77394.1| SAE1-S9-protein [Brassica rapa]	202	255	2.00E-13	126.2	17.8	21.8	SAE1-S9-protein	gbpln	Brassica rapa	AT3G25720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:9380234-9381405 FORWARD LENGTH=282	202	282	3.00E-11	139.6	30.2	46.0

Rsa1.0_01296.1.g25506.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01296.1.g25507.t1	ref|XP_002313006.1| predicted protein [Populus trichocarpa] gi|222849414|gb|EEE86961.1| predicted protein [Populus trichocarpa]	164	207	6.00E-85	126.2	100.0	100.0	predicted protein	gbpln	Populus trichocarpa	AT4G34720.1 | Symbols: AVA-P1, VHA-C1, ATVHA-C1 | ATPase, F0/V0 complex, subunit C protein | chr4:16568223-16569165 REVERSE LENGTH=164	164	164	4.00E-87	100.0	100.0	100.0
Rsa1.0_01297.1.g25508.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01297.1.g25509.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01297.1.g25510.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01297.1.g25511.t1	ref|NP_193303.1| monothiol glutaredoxin-S4 [Arabidopsis thaliana] gi|297804672|ref|XP_002870220.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|75097840|sp|O23419.1|GRXS4_ARATH RecName: Full=Monothiol glutaredoxin-S4; Short=AtGrxS4; AltName: Full=Protein ROXY 13 gi|2244924|emb|CAB10346.1| glutaredoxin [Arabidopsis thaliana] gi|7268316|emb|CAB78610.1| glutaredoxin [Arabidopsis thaliana] gi|21592753|gb|AAM64702.1| glutaredoxin [Arabidopsis thaliana] gi|88900356|gb|ABD57490.1| At4g15680 [Arabidopsis thaliana] gi|226348204|gb|ACO50418.1| glutaredoxin [Arabidopsis thaliana] gi|297316056|gb|EFH46479.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|332658235|gb|AEE83635.1| monothiol glutaredoxin-S4 [Arabidopsis thaliana]	102	102	2.00E-51	100.0	97.1	99.0	monothiol glutaredoxin-S4	gbpln	Arabidopsis lyrata	AT4G15680.1 | Symbols: | Thioredoxin superfamily protein | chr4:8931813-8932121 FORWARD LENGTH=102	102	102	3.00E-54	100.0	97.1	99.0
Rsa1.0_01297.1.g25512.t1	ref|XP_002870217.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297316053|gb|EFH46476.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	101	102	1.00E-45	101.0	89.1	92.1	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT4G15680.1 | Symbols: | Thioredoxin superfamily protein | chr4:8931813-8932121 FORWARD LENGTH=102	101	102	3.00E-48	101.0	89.1	93.1
Rsa1.0_01297.1.g25513.t1	emb|CAB10343.1| kinase like protein [Arabidopsis thaliana] gi|7268313|emb|CAB78607.1| kinase like protein [Arabidopsis thaliana]	612	258	6.00E-51	42.2	22.1	27.5	kinase like protein	gbpln	Arabidopsis thaliana	AT4G15650.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis; Has 5184 Blast hits to 3451 proteins in 562 species: Archae - 30; Bacteria - 838; Metazoa - 1576; Fungi - 798; Plants - 319; Viruses - 111; Other Eukaryotes - 1512 (source: NCBI BLink). | chr4:8922632-8923815 FORWARD LENGTH=261	612	261	2.00E-53	42.6	22.1	27.5
Rsa1.0_01297.1.g25514.t4	gb|EOA19099.1| hypothetical protein CARUB_v10007767mg [Capsella rubella]	195	390	4.00E-45	200.0	53.3	65.1	hypothetical protein CARUB_v10007767mg	gbpln	Capsella rubella	AT4G15640.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G21465.1); Has 38 Blast hits to 38 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:8919245-8921852 REVERSE LENGTH=390	195	390	3.00E-47	200.0	55.9	62.6
Rsa1.0_01297.1.g25515.t1	gb|AAM67044.1| unknown [Arabidopsis thaliana]	190	190	4.00E-85	100.0	82.6	90.5	unknown	gbpln	Arabidopsis thaliana	AT4G15630.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:8917527-8918683 FORWARD LENGTH=190	190	190	6.00E-87	100.0	82.1	91.1
Rsa1.0_01297.1.g25516.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1372	1475	0	107.5	60.3	75.4	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1372	1262	1.00E-173	92.0	21.5	27.8
Rsa1.0_01297.1.g25517.t1	ref|NP_197389.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|332005241|gb|AED92624.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	431	295	4.00E-75	68.4	32.5	45.2	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	431	295	9.00E-78	68.4	32.5	45.2
Rsa1.0_01297.1.g25518.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	328	1447	1.00E-56	441.2	36.6	54.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	328	295	9.00E-50	89.9	33.8	50.3
Rsa1.0_01298.1.g25519.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01298.1.g25520.t12	gb|AAD20433.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	791	889	1.00E-114	112.4	28.2	33.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01298.1.g25521.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	656	695	0	105.9	54.3	66.3	hypothetical protein 26.t00052	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01298.1.g25522.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01298.1.g25523.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	524	627	2.00E-36	119.7	19.8	28.1	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01298.1.g25524.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01298.1.g25525.t1	ref|XP_002870429.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297316265|gb|EFH46688.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	251	737	1.00E-119	293.6	80.5	86.5	kinase family protein	gbpln	Arabidopsis lyrata	AT5G35380.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr5:13593429-13596293 REVERSE LENGTH=731	251	731	1.00E-112	291.2	78.1	84.5
Rsa1.0_01298.1.g25526.t7	gb|EOA16073.1| hypothetical protein CARUB_v10004206mg [Capsella rubella]	181	763	2.00E-73	421.5	72.9	86.7	hypothetical protein CARUB_v10004206mg	gbpln	Capsella rubella	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	181	331	2.00E-51	182.9	54.7	74.0
Rsa1.0_01299.1.g25527.t1	gb|ABO76902.1| high-affinity K+ transporter HAK5 [Eutrema halophilum]	591	790	0	133.7	92.6	96.4	high-affinity K+ transporter HAK5	gbpln	Eutrema halophilum	AT4G13420.1 | Symbols: HAK5, ATHAK5 | high affinity K+ transporter 5 | chr4:7797038-7802174 REVERSE LENGTH=785	591	785	0	132.8	90.2	95.3
Rsa1.0_01299.1.g25528.t2	ref|NP_193066.4| terpenoid synthase 13 [Arabidopsis thaliana] gi|317373358|sp|Q9T0K1.2|GBIS2_ARATH RecName: Full=(Z)-gamma-bisabolene synthase 2; AltName: Full=Terpenoid synthase 13; Short=AtTPS13 gi|332657860|gb|AEE83260.1| terpenoid synthase 13 [Arabidopsis thaliana]	1472	554	0	37.6	28.6	32.4	terpenoid synthase 13	gbpln	Arabidopsis thaliana	AT4G13300.1 | Symbols: ATTPS13, TPS13 | terpenoid synthase 13 | chr4:7742871-7746363 REVERSE LENGTH=554	1472	554	0	37.6	28.6	32.4
Rsa1.0_01299.1.g25529.t1	emb|CAB80843.1| hypothetical protein [Arabidopsis thaliana]	171	381	3.00E-19	222.8	24.0	27.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G04775.1 | Symbols: | zinc ion binding | chr4:2431120-2431695 FORWARD LENGTH=150	171	150	2.00E-21	87.7	29.2	45.6
Rsa1.0_01299.1.g25530.t1	emb|CAA18618.1| hypothetical protein [Arabidopsis thaliana] gi|7268726|emb|CAB78933.1| hypothetical protein [Arabidopsis thaliana]	857	389	2.00E-52	45.4	13.1	18.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	857	673	9.00E-19	78.5	5.1	7.2
Rsa1.0_01299.1.g25531.t1	ref|NP_191042.1| putative aquaporin PIP2-5 [Arabidopsis thaliana] gi|32363433|sp|Q9SV31.1|PIP25_ARATH RecName: Full=Probable aquaporin PIP2-5; AltName: Full=Plasma membrane intrinsic protein 2-5; Short=AtPIP2;5; AltName: Full=Plasma membrane intrinsic protein 2d; Short=PIP2d gi|13878177|gb|AAK44166.1|AF370351_1 putative aquaporin/MIP protein [Arabidopsis thaliana] gi|4678311|emb|CAB41102.1| aquaporin/MIP-like protein [Arabidopsis thaliana] gi|17104533|gb|AAL34155.1| putative aquaporin/MIP protein [Arabidopsis thaliana] gi|21537067|gb|AAM61408.1| aquaporin/MIP-like protein [Arabidopsis thaliana] gi|23397063|gb|AAN31817.1| putative aquaporin/plasma membrane intrinsic protein [Arabidopsis thaliana] gi|332645774|gb|AEE79295.1| putative aquaporin PIP2-5 [Arabidopsis thaliana]	286	286	1.00E-155	100.0	94.1	97.6	putative aquaporin PIP2-5	gbpln	Arabidopsis thaliana	AT3G54820.1 | Symbols: PIP2D, PIP2;5 | plasma membrane intrinsic protein 2;5 | chr3:20302117-20303738 FORWARD LENGTH=286	286	286	1.00E-158	100.0	94.1	97.6
Rsa1.0_01299.1.g25532.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	198	1142	1.00E-26	576.8	35.9	44.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01299.1.g25533.t2	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	779	703	1.00E-134	90.2	30.2	31.1	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_01299.1.g25534.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1615	1352	0	83.7	43.7	58.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1615	746	1.00E-105	46.2	12.3	15.7
Rsa1.0_01299.1.g25535.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01299.1.g25536.t1	ref|NP_191055.1| patatin-like protein 6 [Arabidopsis thaliana] gi|4678298|emb|CAB41089.1| putative protein [Arabidopsis thaliana] gi|110738274|dbj|BAF01066.1| hypothetical protein [Arabidopsis thaliana] gi|332645796|gb|AEE79317.1| patatin-like protein 6 [Arabidopsis thaliana]	482	488	0	101.2	87.8	92.7	patatin-like protein 6	gbpln	Arabidopsis thaliana	AT3G54950.1 | Symbols: PLP7, PLA IIIA | patatin-like protein 6 | chr3:20359076-20360774 REVERSE LENGTH=488	482	488	0	101.2	87.8	92.7
Rsa1.0_01299.1.g25537.t1	# #	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01299.1.g25538.t1	ref|NP_567012.1| tonneau 1 [Arabidopsis thaliana] gi|75262841|sp|Q9FQ25.1|TON1A_ARATH RecName: Full=Protein TONNEAU 1a; AltName: Full=Protein TONNEAU 1 gi|11494364|gb|AAG35779.1|AF280058_1 tonneau 1a [Arabidopsis thaliana] gi|26449686|dbj|BAC41967.1| unknown protein [Arabidopsis thaliana] gi|87116608|gb|ABD19668.1| At3g55000 [Arabidopsis thaliana] gi|332645804|gb|AEE79325.1| protein TONNEAU 1a [Arabidopsis thaliana]	298	260	1.00E-109	87.2	74.2	78.5	tonneau 1	gbpln	Arabidopsis thaliana	AT3G55000.1 | Symbols: TON1A, TON1 | tonneau family protein | chr3:20381612-20383577 FORWARD LENGTH=260	298	260	1.00E-112	87.2	74.2	78.5
Rsa1.0_01299.1.g25539.t1	gb|EOA25829.1| hypothetical protein CARUB_v10019201mg [Capsella rubella]	267	383	1.00E-114	143.4	85.8	92.1	hypothetical protein CARUB_v10019201mg	gbpln	Capsella rubella	AT3G55010.2 | Symbols: ATPURM, PUR5 | phosphoribosylformylglycinamidine cyclo-ligase, chloroplast / phosphoribosyl-aminoimidazole synthetase / AIR synthase (PUR5) | chr3:20386818-20388549 FORWARD LENGTH=389	267	389	1.00E-110	145.7	85.0	90.3
Rsa1.0_01300.1.g25540.t1	ref|XP_002873053.1| hypothetical protein ARALYDRAFT_487025 [Arabidopsis lyrata subsp. lyrata] gi|297318890|gb|EFH49312.1| hypothetical protein ARALYDRAFT_487025 [Arabidopsis lyrata subsp. lyrata]	286	290	1.00E-138	101.4	89.2	91.6	hypothetical protein ARALYDRAFT_487025	gbpln	Arabidopsis lyrata	AT5G02470.3 | Symbols: DPA | Transcription factor DP | chr5:542562-544423 REVERSE LENGTH=292	286	292	1.00E-140	102.1	88.5	92.7
Rsa1.0_01300.1.g25541.t1	ref|XP_002873052.1| hypothetical protein ARALYDRAFT_487022 [Arabidopsis lyrata subsp. lyrata] gi|297318889|gb|EFH49311.1| hypothetical protein ARALYDRAFT_487022 [Arabidopsis lyrata subsp. lyrata]	413	403	1.00E-133	97.6	77.7	83.3	hypothetical protein ARALYDRAFT_487022	gbpln	Arabidopsis lyrata	AT5G02460.1 | Symbols: | Dof-type zinc finger DNA-binding family protein | chr5:539549-541058 REVERSE LENGTH=399	413	399	1.00E-131	96.6	79.4	84.3
Rsa1.0_01300.1.g25542.t1	ref|NP_195863.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|7413632|emb|CAB85980.1| putative protein [Arabidopsis thaliana] gi|332003088|gb|AED90471.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	897	905	0	100.9	80.6	86.8	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G02430.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:526592-529839 FORWARD LENGTH=905	897	905	0	100.9	80.6	86.8
Rsa1.0_01300.1.g25543.t1	ref|NP_195862.1| uncharacterized protein [Arabidopsis thaliana] gi|75181194|sp|Q9LZ60.1|SMR3_ARATH RecName: Full=Cyclin-dependent protein kinase inhibitor SMR3; AltName: Full=Protein SIAMESE-RELATED 3 gi|7413631|emb|CAB85979.1| putative protein [Arabidopsis thaliana] gi|332003087|gb|AED90470.1| uncharacterized protein AT5G02420 [Arabidopsis thaliana]	109	115	8.00E-41	105.5	82.6	89.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G02420.1 | Symbols: | unknown protein; Has 90 Blast hits to 90 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:523501-523848 FORWARD LENGTH=115	109	115	1.00E-43	105.5	82.6	89.9
Rsa1.0_01300.1.g25544.t1	ref|NP_195861.2| alpha-1,2-glucosyltransferase [Arabidopsis thaliana] gi|20466149|gb|AAM20392.1| putative protein [Arabidopsis thaliana] gi|25083857|gb|AAN72128.1| putative protein [Arabidopsis thaliana] gi|332003086|gb|AED90469.1| alpha-1,2-glucosyltransferase [Arabidopsis thaliana]	507	509	0	100.4	82.1	89.0	alpha-1,2-glucosyltransferase	gbpln	Arabidopsis thaliana	AT5G02410.1 | Symbols: | DIE2/ALG10 family | chr5:517319-519634 REVERSE LENGTH=509	507	509	0	100.4	82.1	89.0
Rsa1.0_01300.1.g25545.t1	gb|ADP37973.1| metallothionein protein [Brassica napus]	80	81	8.00E-29	101.3	86.3	90.0	metallothionein protein	gbpln	Brassica napus	AT3G09390.1 | Symbols: MT2A, ATMT-K, ATMT-1 | metallothionein 2A | chr3:2889737-2890188 REVERSE LENGTH=81	80	81	9.00E-22	101.3	58.8	65.0
Rsa1.0_01300.1.g25546.t1	ref|NP_195857.2| kinesin family member 22 [Arabidopsis thaliana] gi|59958334|gb|AAX12877.1| At5g02370 [Arabidopsis thaliana] gi|332003081|gb|AED90464.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]	643	628	0	97.7	78.1	83.4	kinesin family member 22	gbpln	Arabidopsis thaliana	AT5G02370.1 | Symbols: | ATP binding microtubule motor family protein | chr5:503444-506388 FORWARD LENGTH=628	643	628	0	97.7	78.1	83.4

Rsa1.0_01300.1.g25547.t1	ref|NP_195851.2| proteolysis 6 [Arabidopsis thaliana] gi|332003074|gb|AED90457.1| proteolysis 6 [Arabidopsis thaliana]	1904	2006	0	105.4	55.1	60.4	proteolysis 6	gbpln	Arabidopsis thaliana	AT5G02310.1 | Symbols: PRT6 | proteolysis 6 | chr5:474279-482552 FORWARD LENGTH=2006	1904	2006	0	105.4	55.1	60.4
Rsa1.0_01300.1.g25548.t2	ref|XP_002873046.1| hypothetical protein ARALYDRAFT_487008 [Arabidopsis lyrata subsp. lyrata] gi|297318883|gb|EFH49305.1| hypothetical protein ARALYDRAFT_487008 [Arabidopsis lyrata subsp. lyrata]	389	389	0	100.0	86.1	90.7	hypothetical protein ARALYDRAFT_487008	gbpln	Arabidopsis lyrata	AT5G02290.2 | Symbols: NAK | Protein kinase superfamily protein | chr5:470387-472397 REVERSE LENGTH=389	389	389	0	100.0	85.1	90.7
Rsa1.0_01300.1.g25549.t1	ref|NP_195848.1| SNARE-like superfamily protein [Arabidopsis thaliana] gi|297806167|ref|XP_002870967.1| hypothetical protein ARALYDRAFT_908094 [Arabidopsis lyrata subsp. lyrata] gi|7406424|emb|CAB85533.1| putative protein [Arabidopsis thaliana] gi|21618125|gb|AAM67175.1| unknown [Arabidopsis thaliana] gi|28393092|gb|AAO41980.1| unknown protein [Arabidopsis thaliana] gi|28827482|gb|AAO50585.1| unknown protein [Arabidopsis thaliana] gi|297316804|gb|EFH47226.1| hypothetical protein ARALYDRAFT_908094 [Arabidopsis lyrata subsp. lyrata] gi|332003071|gb|AED90454.1| SNARE-like superfamily protein [Arabidopsis thaliana]	141	141	3.00E-75	100.0	95.0	98.6	SNARE-like superfamily protein	gbpln	Arabidopsis lyrata	AT5G02280.1 | Symbols: | SNARE-like superfamily protein | chr5:469377-470129 FORWARD LENGTH=141	141	141	9.00E-78	100.0	95.0	98.6
Rsa1.0_01301.1.g25550.t1	ref|XP_002864360.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297310195|gb|EFH40619.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata]	105	491	3.00E-18	467.6	51.4	56.2	integral membrane transporter family protein	gbpln	Arabidopsis lyrata	AT5G54860.1 | Symbols: | Major facilitator superfamily protein | chr5:22284721-22287025 FORWARD LENGTH=491	105	491	9.00E-21	467.6	50.5	56.2
Rsa1.0_01301.1.g25551.t1	ref|XP_002864357.1| hypothetical protein ARALYDRAFT_331822 [Arabidopsis lyrata subsp. lyrata] gi|297310192|gb|EFH40616.1| hypothetical protein ARALYDRAFT_331822 [Arabidopsis lyrata subsp. lyrata]	472	476	1.00E-102	100.8	45.1	64.0	hypothetical protein ARALYDRAFT_331822	gbpln	Arabidopsis lyrata	AT5G54820.1 | Symbols: | F-box/RNI-like superfamily protein | chr5:22269859-22271777 FORWARD LENGTH=472	472	472	1.00E-104	100.0	44.5	62.9
Rsa1.0_01301.1.g25552.t1	gb|AAM63660.1| glucose-6-phosphate/phosphate translocator [Arabidopsis thaliana]	395	388	0	98.2	87.3	90.4	glucose-6-phosphate/phosphate translocator	gbpln	Arabidopsis thaliana	AT5G54800.1 | Symbols: GPT1, ATGPT1 | glucose 6-phosphate/phosphate translocator 1 | chr5:22261408-22263562 FORWARD LENGTH=388	395	388	0	98.2	87.8	90.6
Rsa1.0_01301.1.g25553.t1	ref|XP_002866060.1| hypothetical protein ARALYDRAFT_495559 [Arabidopsis lyrata subsp. lyrata] gi|297311895|gb|EFH42319.1| hypothetical protein ARALYDRAFT_495559 [Arabidopsis lyrata subsp. lyrata]	433	438	0	101.2	92.4	94.9	hypothetical protein ARALYDRAFT_495559	gbpln	Arabidopsis lyrata	AT5G54780.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr5:22248696-22251692 REVERSE LENGTH=432	433	432	0	99.8	90.5	93.3
Rsa1.0_01301.1.g25554.t1	ref|XP_002864354.1| hypothetical protein ARALYDRAFT_918614 [Arabidopsis lyrata subsp. lyrata] gi|297310189|gb|EFH40613.1| hypothetical protein ARALYDRAFT_918614 [Arabidopsis lyrata subsp. lyrata]	351	352	0	100.3	93.7	96.9	hypothetical protein ARALYDRAFT_918614	gbpln	Arabidopsis lyrata	AT5G54770.1 | Symbols: THI1, TZ, THI4 | thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (THI4) | chr5:22246634-22247891 FORWARD LENGTH=349	351	349	0	99.4	92.0	95.4
Rsa1.0_01301.1.g25555.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01301.1.g25556.t1	ref|XP_002880903.1| hypothetical protein ARALYDRAFT_901626 [Arabidopsis lyrata subsp. lyrata] gi|297326742|gb|EFH57162.1| hypothetical protein ARALYDRAFT_901626 [Arabidopsis lyrata subsp. lyrata]	890	1014	0	113.9	70.7	81.1	hypothetical protein ARALYDRAFT_901626	gbpln	Arabidopsis lyrata	AT3G47570.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17527611-17530748 FORWARD LENGTH=1010	890	1010	0	113.5	67.2	78.7
Rsa1.0_01301.1.g25557.t1	ref|XP_002877365.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323203|gb|EFH53624.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	112	977	1.00E-40	872.3	67.9	83.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G47090.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17341512-17344645 REVERSE LENGTH=1009	112	1009	2.00E-41	900.9	64.3	82.1
Rsa1.0_01301.1.g25558.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1377	1307	0	94.9	59.6	74.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1377	1262	3.00E-99	91.6	14.2	21.7

Rsa1.0_01301.1.g25559.t1	ref|NP_200284.1| autophagy 18F-like protein [Arabidopsis thaliana] gi|75333833|sp|Q9FH32.1|AT18F_ARATH RecName: Full=Autophagy-related protein 18f; Short=AtATG18f gi|10176800|dbj|BAB09939.1| unnamed protein product [Arabidopsis thaliana] gi|332009148|gb|AED96531.1| autophagy 18F-like protein [Arabidopsis thaliana]	747	763	0	102.1	71.4	80.5	autophagy 18F-like protein	gbpln	Arabidopsis thaliana	AT5G54730.1 | Symbols: ATATG18F, ATG18F, G18F | homolog of yeast autophagy 18 (ATG18) F | chr5:22233977-22236804 REVERSE LENGTH=763	747	763	0	102.1	71.4	80.5
Rsa1.0_01301.1.g25560.t1	ref|XP_002864345.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310180|gb|EFH40604.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	80	156	5.00E-24	195.0	68.8	71.3	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT5G54580.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:22171332-22172656 FORWARD LENGTH=156	80	156	9.00E-27	195.0	68.8	71.3
Rsa1.0_01302.1.g25561.t1	ref|XP_002870773.1| hypothetical protein ARALYDRAFT_494030 [Arabidopsis lyrata subsp. lyrata] gi|297316609|gb|EFH47032.1| hypothetical protein ARALYDRAFT_494030 [Arabidopsis lyrata subsp. lyrata]	537	542	0	100.9	82.1	90.7	hypothetical protein ARALYDRAFT_494030	gbpln	Arabidopsis lyrata	AT5G39590.1 | Symbols: | TLD-domain containing nucleolar protein | chr5:15851483-15853768 FORWARD LENGTH=542	537	542	0	100.9	81.6	89.8
Rsa1.0_01302.1.g25562.t1	gb|EOA17624.1| hypothetical protein CARUB_v10005989mg, partial [Capsella rubella]	128	136	5.00E-66	106.3	96.1	98.4	hypothetical protein CARUB_v10005989mg, partial	gbpln	Capsella rubella	AT5G39600.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ribosomal protein L53, mitochondrial (InterPro:IPR019716); Has 50 Blast hits to 50 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr5:15854188-15854771 REVERSE LENGTH=127	128	127	5.00E-68	99.2	94.5	98.4
Rsa1.0_01302.1.g25563.t8	gb|EEE52627.1| hypothetical protein OsJ_34967 [Oryza sativa Japonica Group]	628	1395	2.00E-32	222.1	18.5	31.1	hypothetical protein OsJ_34967	gbpln	Oryza sativa	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	628	154	3.00E-17	24.5	7.5	11.9
Rsa1.0_01302.1.g25564.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01302.1.g25565.t1	ref|XP_002868706.1| ANAC092/ATNAC2/ATNAC6 [Arabidopsis lyrata subsp. lyrata] gi|297314542|gb|EFH44965.1| ANAC092/ATNAC2/ATNAC6 [Arabidopsis lyrata subsp. lyrata]	300	288	1.00E-135	96.0	79.7	85.7	ANAC092/ATNAC2/ATNAC6	gbpln	Arabidopsis lyrata	AT5G39610.1 | Symbols: ATNAC2, ORE1, ANAC092, ATNAC6, NAC2, NAC6 | NAC domain containing protein 6 | chr5:15858591-15859650 REVERSE LENGTH=285	300	285	1.00E-135	95.0	78.7	84.3
Rsa1.0_01302.1.g25566.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01302.1.g25567.t1	gb|AAG50751.1|AC079733_19 polyprotein, putative [Arabidopsis thaliana]	244	1468	3.00E-88	601.6	69.3	78.3	polyprotein, putative	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	244	237	2.00E-25	97.1	19.7	32.4
Rsa1.0_01302.1.g25568.t1	ref|NP_568567.1| Dof zinc finger protein DOF5.2 [Arabidopsis thaliana] gi|30693448|ref|NP_851106.1| Dof zinc finger protein DOF5.2 [Arabidopsis thaliana] gi|55583973|sp|Q93ZL5.2|CDF2_ARATH RecName: Full=Cyclic dof factor 2; AltName: Full=Dof zinc finger protein DOF5.2; Short=AtDOF5.2 gi|53749192|gb|AAU90081.1| At5g39660 [Arabidopsis thaliana] gi|332007077|gb|AED94460.1| Dof zinc finger protein DOF5.2 [Arabidopsis thaliana] gi|332007078|gb|AED94461.1| Dof zinc finger protein DOF5.2 [Arabidopsis thaliana]	439	457	0	104.1	82.5	87.5	Dof zinc finger protein DOF5.2	gbpln	Arabidopsis thaliana	AT5G39660.2 | Symbols: CDF2 | cycling DOF factor 2 | chr5:15878920-15880712 FORWARD LENGTH=457	439	457	0	104.1	82.5	87.5
Rsa1.0_01302.1.g25569.t1	gb|EOA27133.1| hypothetical protein CARUB_v10023232mg [Capsella rubella]	108	439	1.00E-15	406.5	35.2	38.9	hypothetical protein CARUB_v10023232mg	gbpln	Capsella rubella	AT2G42120.1 | Symbols: POLD2 | DNA polymerase delta small subunit | chr2:17563282-17565965 REVERSE LENGTH=441	108	441	1.00E-17	408.3	34.3	38.0
Rsa1.0_01302.1.g25570.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01302.1.g25571.t1	ref|XP_002870769.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297316605|gb|EFH47028.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	200	203	4.00E-87	101.5	84.5	89.5	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT5G39670.1 | Symbols: | Calcium-binding EF-hand family protein | chr5:15883270-15883884 FORWARD LENGTH=204	200	204	5.00E-87	102.0	82.5	90.0

<table>
<tr><td>Rsa1.0_01303.1.g25572.t1</td><td>gb|AAD14492.1| Hypothetical protein [Arabidopsis thaliana]</td><td>159</td><td>240</td><td>2.00E-28</td><td>150.9</td><td>44.0</td><td>53.5</td><td>Hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>159</td><td>575</td><td>2.00E-12</td><td>361.6</td><td>28.9</td><td>44.0</td></tr>
<tr><td>Rsa1.0_01303.1.g25573.t1</td><td>gb|EOA12705.1| hypothetical protein CARUB_v10027998mg [Capsella rubella]</td><td>322</td><td>315</td><td>1.00E-151</td><td>97.8</td><td>83.2</td><td>88.2</td><td>hypothetical protein CARUB_v10027998mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G58220.1 | Symbols: TTL | transthyretin-like protein | chr5:23554546-23555861 REVERSE LENGTH=324</td><td>322</td><td>324</td><td>1.00E-141</td><td>100.6</td><td>79.5</td><td>87.6</td></tr>
<tr><td>Rsa1.0_01303.1.g25574.t1</td><td>ref|NP_001190565.1| metallophosphatase domain-containing protein [Arabidopsis thaliana] gi|332009630|gb|AED97013.1| metallophosphatase domain-containing protein [Arabidopsis thaliana]</td><td>306</td><td>309</td><td>1.00E-136</td><td>101.0</td><td>79.1</td><td>86.9</td><td>metallophosphatase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G58200.2 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:23549605-23551972 FORWARD LENGTH=309</td><td>306</td><td>309</td><td>1.00E-139</td><td>101.0</td><td>79.1</td><td>86.9</td></tr>
<tr><td>Rsa1.0_01303.1.g25575.t1</td><td>ref|XP_002864554.1| hypothetical protein ARALYDRAFT_332107 [Arabidopsis lyrata subsp. lyrata] gi|297310389|gb|EFH40813.1| hypothetical protein ARALYDRAFT_332107 [Arabidopsis lyrata subsp. lyrata]</td><td>529</td><td>549</td><td>0</td><td>103.8</td><td>78.4</td><td>85.4</td><td>hypothetical protein ARALYDRAFT_332107</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G58190.2 | Symbols: ECT10 | evolutionarily conserved C-terminal region 10 | chr5:23546434-23549363 FORWARD LENGTH=528</td><td>529</td><td>528</td><td>0</td><td>99.8</td><td>77.1</td><td>83.6</td></tr>
<tr><td>Rsa1.0_01303.1.g25576.t1</td><td>ref|NP_176624.2| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|79320695|ref|NP_001031231.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|17529266|gb|AAL38860.1| unknown protein [Arabidopsis thaliana] gi|23296917|gb|AAN13202.1| unknown protein [Arabidopsis thaliana] gi|332196118|gb|AEE34239.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|332196119|gb|AEE34240.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]</td><td>262</td><td>559</td><td>1.00E-22</td><td>213.4</td><td>22.5</td><td>27.1</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G64430.2 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:23933541-23936336 FORWARD LENGTH=559</td><td>262</td><td>559</td><td>3.00E-25</td><td>213.4</td><td>22.5</td><td>27.1</td></tr>
<tr><td>Rsa1.0_01303.1.g25577.t1</td><td>gb|EOA14030.1| hypothetical protein CARUB_v10027163mg [Capsella rubella] gi|482549837|gb|EOA14031.1| hypothetical protein CARUB_v10027163mg [Capsella rubella]</td><td>199</td><td>199</td><td>3.00E-83</td><td>100.0</td><td>74.4</td><td>83.9</td><td>hypothetical protein CARUB_v10027163mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G58060.1 | Symbols: YKT61, ATYKT61, ATGP1 | SNARE-like superfamily protein | chr5:23498277-23500128 FORWARD LENGTH=199</td><td>199</td><td>199</td><td>2.00E-84</td><td>100.0</td><td>73.4</td><td>82.9</td></tr>
<tr><td>Rsa1.0_01303.1.g25578.t1</td><td>ref|XP_002866252.1| glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297312087|gb|EFH42511.1| glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>764</td><td>754</td><td>0</td><td>98.7</td><td>80.0</td><td>88.2</td><td>glycerophosphoryl diester phosphodiesterase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G58170.1 | Symbols: SVL5 | SHV3-like 5 | chr5:23540261-23543092 REVERSE LENGTH=750</td><td>764</td><td>750</td><td>0</td><td>98.2</td><td>79.3</td><td>88.2</td></tr>
<tr><td>Rsa1.0_01303.1.g25579.t1</td><td>ref|XP_002864551.1| hypothetical protein ARALYDRAFT_495923 [Arabidopsis lyrata subsp. lyrata] gi|297310386|gb|EFH40810.1| hypothetical protein ARALYDRAFT_495923 [Arabidopsis lyrata subsp. lyrata]</td><td>1307</td><td>1185</td><td>0</td><td>90.7</td><td>38.6</td><td>41.9</td><td>hypothetical protein ARALYDRAFT_495923</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G58160.1 | Symbols: | actin binding | chr5:23533724-23539465 FORWARD LENGTH=1324</td><td>1307</td><td>1324</td><td>0</td><td>101.3</td><td>30.9</td><td>32.4</td></tr>
<tr><td>Rsa1.0_01303.1.g25580.t2</td><td>ref|NP_851210.1| phototropin 2 [Arabidopsis thaliana] gi|30697010|ref|NP_851211.1| phototropin 2 [Arabidopsis thaliana] gi|82593023|sp|P93025.2|PHOT2_ARATH RecName: Full=Phototropin-2; AltName: Full=Defective in chloroplast avoidance protein 1; AltName: Full=Non-phototropic hypocotyl 1-like protein 1; Short=AtKin7; Short=NPH1-like protein 1 gi|5391442|gb|AAC27293.2| non phototropic hypocotyl 1-like [Arabidopsis thaliana] gi|10176790|dbj|BAB09904.1| unnamed protein product [Arabidopsis thaliana] gi|332009619|gb|AED97002.1| phototropin 2 [Arabidopsis thaliana] gi|332009621|gb|AED97004.1| phototropin 2 [Arabidopsis thaliana]</td><td>902</td><td>915</td><td>0</td><td>101.4</td><td>87.9</td><td>91.6</td><td>phototropin 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G58140.1 | Symbols: PHOT2, NPL1 | phototropin 2 | chr5:23524771-23529993 FORWARD LENGTH=915</td><td>902</td><td>915</td><td>0</td><td>101.4</td><td>87.9</td><td>91.6</td></tr>
<tr><td>Rsa1.0_01304.1.g25581.t2</td><td>dbj|BAC76056.1| S receptor kinase [Brassica rapa]</td><td>828</td><td>859</td><td>0</td><td>103.7</td><td>73.8</td><td>82.4</td><td>S receptor kinase</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850</td><td>828</td><td>850</td><td>0</td><td>102.7</td><td>59.7</td><td>73.4</td></tr>
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Rsa1.0_01304.1.g25582.t1	ref|NP_181459.4| RNA binding protein [Arabidopsis thaliana] gi|476007187|sp|F4IUX6.1|RENT2_ARATH RecName: Full=Regulator of nonsense transcripts UPF2; AltName: Full=Nonsense mRNA reducing factor UPF2; AltName: Full=Up-frameshift suppressor 2 homolog; Short=AtUpf2 gi|330254557|gb|AEC09651.1| RNA binding protein [Arabidopsis thaliana]	161	1181	7.00E-23	733.5	34.8	36.6	RNA binding protein	gbpln	Arabidopsis thaliana	AT2G39260.1 | Symbols: | binding;RNA binding | chr2:16392288-16399588 REVERSE LENGTH=1181	161	1181	3.00E-25	733.5	34.8	36.6
Rsa1.0_01304.1.g25583.t4	gb|AAD29058.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1521	1229	1.00E-171	80.8	21.2	28.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G17920.1 | Symbols: | nucleic acid binding;zinc ion binding | chr2:7782808-7783731 FORWARD LENGTH=307	1521	307	3.00E-30	20.2	5.0	8.0
Rsa1.0_01304.1.g25584.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	223	1466	6.00E-57	657.4	51.1	60.5	copia-like polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01304.1.g25585.t1	gb|AAD43604.1|AC005698_3 T3P18.3 [Arabidopsis thaliana]	680	1309	0	192.5	54.0	68.8	T3P18.3	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	680	1262	2.00E-74	185.6	22.4	36.0
Rsa1.0_01304.1.g25586.t1	ref|XP_002879788.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297325627|gb|EFH56047.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	241	867	1.00E-100	359.8	74.7	87.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT2G39230.1 | Symbols: LOJ | LATERAL ORGAN JUNCTION | chr2:16381647-16384250 FORWARD LENGTH=867	241	867	4.00E-97	359.8	71.0	85.9
Rsa1.0_01304.1.g25587.t1	ref|NP_181459.4| RNA binding protein [Arabidopsis thaliana] gi|476007187|sp|F4IUX6.1|RENT2_ARATH RecName: Full=Regulator of nonsense transcripts UPF2; AltName: Full=Nonsense mRNA reducing factor UPF2; AltName: Full=Up-frameshift suppressor 2 homolog; Short=AtUpf2 gi|330254557|gb|AEC09651.1| RNA binding protein [Arabidopsis thaliana]	187	1181	1.00E-66	631.6	74.3	79.7	RNA binding protein	gbpln	Arabidopsis thaliana	AT2G39260.1 | Symbols: | binding;RNA binding | chr2:16392288-16399588 REVERSE LENGTH=1181	187	1181	5.00E-69	631.6	74.3	79.7
Rsa1.0_01305.1.g25588.t1	ref|XP_002881966.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297327805|gb|EFH58225.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	136	145	3.00E-51	106.6	72.1	81.6	protein binding protein	gbpln	Arabidopsis lyrata	AT2G44578.1 | Symbols: | RING/U-box superfamily protein | chr2:18400864-18401301 REVERSE LENGTH=145	136	145	4.00E-53	106.6	71.3	83.8
Rsa1.0_01305.1.g25589.t1	gb|EOA26379.1| hypothetical protein CARUB_v10023367mg [Capsella rubella]	456	396	0	86.8	78.9	81.1	hypothetical protein CARUB_v10023367mg	gbpln	Capsella rubella	AT2G44530.1 | Symbols: | Phosphoribosyltransferase family protein | chr2:18383732-18385974 FORWARD LENGTH=394	456	394	0	86.4	78.3	80.7
Rsa1.0_01305.1.g25590.t1	ref|NP_566019.1| protoheme IX farnesyltransferase [Arabidopsis thaliana] gi|75099253|sp|O64886.4|COX10_ARATH RecName: Full=Protoheme IX farnesyltransferase, mitochondrial; AltName: Full=Cytochrome c oxidase assembly protein COX10; AltName: Full=Heme O synthase; Flags: Precursor gi|15028299|gb|AAK76626.1| putative heme A:farnesyltransferase [Arabidopsis thaliana] gi|20197028|gb|AAC27454.3| putative heme A:farnesyltransferase [Arabidopsis thaliana] gi|20197183|gb|AAM14960.1| putative heme A:farnesyltransferase [Arabidopsis thaliana] gi|21280973|gb|AAM45064.1| putative heme A [Arabidopsis thaliana] gi|330255338|gb|AEC10432.1| protoheme IX farnesyltransferase [Arabidopsis thaliana]	422	431	0	102.1	85.3	89.8	protoheme IX farnesyltransferase	gbpln	Arabidopsis thaliana	AT2G44520.1 | Symbols: COX10 | cytochrome c oxidase 10 | chr2:18379660-18381731 FORWARD LENGTH=431	422	431	0	102.1	85.3	89.8
Rsa1.0_01305.1.g25591.t3	ref|XP_002880121.1| hypothetical protein ARALYDRAFT_903875 [Arabidopsis lyrata subsp. lyrata] gi|297325960|gb|EFH56380.1| hypothetical protein ARALYDRAFT_903875 [Arabidopsis lyrata subsp. lyrata]	321	327	1.00E-135	101.9	80.1	91.3	hypothetical protein ARALYDRAFT_903875	gbpln	Arabidopsis lyrata	AT2G44510.1 | Symbols: | CDK inhibitor P21 binding protein | chr2:18377411-18379030 FORWARD LENGTH=326	321	326	1.00E-137	101.6	80.1	90.3
Rsa1.0_01305.1.g25592.t2	gb|EOA29106.1| hypothetical protein CARUB_v10025373mg, partial [Capsella rubella]	532	555	0	104.3	78.2	87.8	hypothetical protein CARUB_v10025373mg, partial	gbpln	Capsella rubella	AT5G24550.1 | Symbols: BGLU32 | beta glucosidase 32 | chr5:8392059-8395302 REVERSE LENGTH=534	532	534	0	100.4	75.2	87.8
Rsa1.0_01305.1.g25593.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_01305.1.g25594.t1</td><td>ref|XP_002880115.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata] gi|297325954|gb|EFH56374.1| glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata]</td><td>378</td><td>579</td><td>1.00E-174</td><td>153.2</td><td>82.0</td><td>88.6</td><td>glycosyl hydrolase family 1 protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G44460.1 | Symbols: BGLU28 | beta glucosidase 28 | chr2:18346500-18349826 FORWARD LENGTH=582</td><td>378</td><td>582</td><td>1.00E-173</td><td>154.0</td><td>80.4</td><td>86.8</td></tr>
<tr><td>Rsa1.0_01306.1.g25595.t1</td><td>ref|NP_567747.4| putative uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|240256079|ref|NP_849448.4| putative uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|298286881|sp|O65583.2|UKL4_ARATH RecName: Full=Uridine kinase-like protein 4; Includes: RecName: Full=Uridine kinase; Short=UK; Includes: RecName: Full=Putative uracil phosphoribosyltransferase; Short=UPRTase; AltName: Full=UMP pyrophosphorylase gi|21554263|gb|AAM63338.1| putative uracil phosphoribosyl transferase [Arabidopsis thaliana] gi|63003884|gb|AAY25471.1| At4g26510 [Arabidopsis thaliana] gi|332659811|gb|AEE85211.1| putative uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|332659812|gb|AEE85212.1| putative uracil phosphoribosyltransferase [Arabidopsis thaliana]</td><td>152</td><td>469</td><td>8.00E-81</td><td>308.6</td><td>96.7</td><td>99.3</td><td>putative uracil phosphoribosyltransferase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26510.2 | Symbols: UKL4 | uridine kinase-like 4 | chr4:13384503-13387920 FORWARD LENGTH=469</td><td>152</td><td>469</td><td>2.00E-83</td><td>308.6</td><td>96.7</td><td>99.3</td></tr>
<tr><td>Rsa1.0_01306.1.g25596.t1</td><td>ref|XP_002864427.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310262|gb|EFH40686.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>1120</td><td>1090</td><td>0</td><td>97.3</td><td>87.8</td><td>91.4</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G56040.2 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr5:22695050-22698410 FORWARD LENGTH=1090</td><td>1120</td><td>1090</td><td>0</td><td>97.3</td><td>87.0</td><td>91.2</td></tr>
<tr><td>Rsa1.0_01306.1.g25597.t1</td><td>ref|XP_002864201.1| hypothetical protein ARALYDRAFT_495357 [Arabidopsis lyrata subsp. lyrata] gi|297310036|gb|EFH40460.1| hypothetical protein ARALYDRAFT_495357 [Arabidopsis lyrata subsp. lyrata]</td><td>142</td><td>335</td><td>5.00E-39</td><td>235.9</td><td>55.6</td><td>66.2</td><td>hypothetical protein ARALYDRAFT_495357</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G54320.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22062805-22063914 FORWARD LENGTH=369</td><td>142</td><td>369</td><td>8.00E-41</td><td>259.9</td><td>52.1</td><td>64.8</td></tr>
<tr><td>Rsa1.0_01306.1.g25598.t1</td><td>gb|EOA12588.1| hypothetical protein CARUB_v10027067mg [Capsella rubella]</td><td>226</td><td>226</td><td>1.00E-127</td><td>100.0</td><td>98.7</td><td>99.6</td><td>hypothetical protein CARUB_v10027067mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G55990.1 | Symbols: CBL2, ATCBL2 | calcineurin B-like protein 2 | chr5:22672189-22673579 FORWARD LENGTH=226</td><td>226</td><td>226</td><td>1.00E-129</td><td>100.0</td><td>98.2</td><td>99.1</td></tr>
<tr><td>Rsa1.0_01306.1.g25599.t1</td><td>ref|XP_002864421.1| hypothetical protein ARALYDRAFT_918740 [Arabidopsis lyrata subsp. lyrata] gi|297310256|gb|EFH40680.1| hypothetical protein ARALYDRAFT_918740 [Arabidopsis lyrata subsp. lyrata]</td><td>115</td><td>113</td><td>2.00E-31</td><td>98.3</td><td>73.0</td><td>80.0</td><td>hypothetical protein ARALYDRAFT_918740</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G55980.1 | Symbols: | serine-rich protein-related | chr5:22670301-22670642 FORWARD LENGTH=113</td><td>115</td><td>113</td><td>2.00E-31</td><td>98.3</td><td>70.4</td><td>76.5</td></tr>
<tr><td>Rsa1.0_01306.1.g25600.t1</td><td>ref|XP_002864420.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310255|gb|EFH40679.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>303</td><td>343</td><td>1.00E-119</td><td>113.2</td><td>71.6</td><td>80.2</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G55970.2 | Symbols: | RING/U-box superfamily protein | chr5:22668019-22669312 FORWARD LENGTH=343</td><td>303</td><td>343</td><td>1.00E-120</td><td>113.2</td><td>74.9</td><td>85.5</td></tr>
<tr><td>Rsa1.0_01306.1.g25601.t1</td><td>ref|NP_176234.1| NAC domain containing protein 23 [Arabidopsis thaliana] gi|3249075|gb|AAC24059.1| Contains similarity to no-apical-meristem (NAM) protein gb|X92205 from Petunia hybrida [Arabidopsis thaliana] gi|124301174|gb|ABN04839.1| At1g60280 [Arabidopsis thaliana] gi|332195552|gb|AEE33673.1| NAC domain containing protein 23 [Arabidopsis thaliana]</td><td>328</td><td>347</td><td>5.00E-94</td><td>105.8</td><td>57.9</td><td>69.8</td><td>NAC domain containing protein 23</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G60280.1 | Symbols: ANAC023, NAC023 | NAC domain containing protein 23 | chr1:22226885-22227928 REVERSE LENGTH=347</td><td>328</td><td>347</td><td>1.00E-96</td><td>105.8</td><td>57.9</td><td>69.8</td></tr>
<tr><td>Rsa1.0_01306.1.g25602.t2</td><td>ref|XP_002871839.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297317676|gb|EFH48098.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>326</td><td>478</td><td>5.00E-35</td><td>146.6</td><td>29.8</td><td>35.6</td><td>F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G18770.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:6261426-6263172 FORWARD LENGTH=481</td><td>326</td><td>481</td><td>2.00E-33</td><td>147.5</td><td>25.8</td><td>30.7</td></tr>
<tr><td>Rsa1.0_01306.1.g25603.t1</td><td>emb|CCD74528.1| NAC domain containing protein 23 [Arabidopsis halleri subsp. halleri]</td><td>326</td><td>334</td><td>3.00E-93</td><td>102.5</td><td>58.6</td><td>67.8</td><td>NAC domain containing protein 23</td><td>gbpln</td><td>Arabidopsis halleri</td><td>AT1G60300.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:22229780-22230748 REVERSE LENGTH=322</td><td>326</td><td>322</td><td>3.00E-94</td><td>98.8</td><td>57.1</td><td>69.3</td></tr>
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Rsa1.0_01306.1.g25604.t1	ref|NP_568833.1| uncharacterized protein [Arabidopsis thaliana] gi|16648987|gb|AAL24345.1| Unknown protein [Arabidopsis thaliana] gi|28059051|gb|AAO29982.1| Unknown protein [Arabidopsis thaliana] gi|332009320|gb|AED96703.1| uncharacterized protein AT5G55960 [Arabidopsis thaliana]	643	648	0	100.8	91.6	95.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G55960.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0118 (InterPro:IPR002549); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:22662726-22664762 FORWARD LENGTH=648	643	648	0	100.8	91.6	95.3
Rsa1.0_01307.1.g25605.t1	gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]	486	527	4.00E-52	108.4	25.9	34.8	hypothetical protein CARUB_v10022820mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	486	735	5.00E-50	151.2	23.7	35.6
Rsa1.0_01307.1.g25606.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01307.1.g25607.t1	ref|NP_199139.1| nuclear factor Y, subunit C13 [Arabidopsis thaliana] gi|10177387|dbj|BAB10588.1| unnamed protein product [Arabidopsis thaliana] gi|225879084|dbj|BAH30612.1| hypothetical protein [Arabidopsis thaliana] gi|332007548|gb|AED94931.1| nuclear factor Y, subunit C13 [Arabidopsis thaliana]	129	130	2.00E-52	100.8	82.9	89.9	nuclear factor Y, subunit C13	gbpln	Arabidopsis thaliana	AT5G43250.1 | Symbols: NF-YC13 | nuclear factor Y, subunit C13 | chr5:17356174-17356566 REVERSE LENGTH=130	129	130	4.00E-55	100.8	82.9	89.9
Rsa1.0_01307.1.g25608.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01307.1.g25609.t1	gb|AAF13073.1|AC011621_1 putative retroelement pol polyprotein [Arabidopsis thaliana]	1453	1661	0	114.3	54.0	69.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1453	158	1.00E-43	10.9	5.8	6.6
Rsa1.0_01307.1.g25610.t3	gb|EOA30885.1| hypothetical protein CARUB_v10014029mg [Capsella rubella]	265	363	6.00E-41	137.0	40.4	46.4	hypothetical protein CARUB_v10014029mg	gbpln	Capsella rubella	AT3G15890.1 | Symbols: | Protein kinase superfamily protein | chr3:5374389-5376114 FORWARD LENGTH=361	265	361	1.00E-42	136.2	40.4	45.7
Rsa1.0_01307.1.g25611.t1	gb|EOA37750.1| hypothetical protein CARUB_v10012565mg [Capsella rubella]	664	679	1.00E-164	102.3	46.1	63.0	hypothetical protein CARUB_v10012565mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	664	696	1.00E-33	104.8	22.0	42.2
Rsa1.0_01307.1.g25612.t1	gb|EOA14275.1| hypothetical protein CARUB_v10027437mg [Capsella rubella]	98	98	2.00E-42	100.0	85.7	93.9	hypothetical protein CARUB_v10027437mg	gbpln	Capsella rubella	AT5G43260.1 | Symbols: | chaperone protein dnaJ-related | chr5:17357693-17357986 REVERSE LENGTH=97	98	97	2.00E-43	99.0	84.7	92.9
Rsa1.0_01308.1.g25613.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01308.1.g25614.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01308.1.g25615.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	1198	1333	0	111.3	48.2	63.5	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1198	575	1.00E-84	48.0	14.1	23.2
Rsa1.0_01308.1.g25616.t1	dbj|BAB01217.1| Ta11 non-LTR retroelement protein-like [Arabidopsis thaliana] gi|67633664|gb|AAY78756.1| putative zinc finger protein [Arabidopsis thaliana]	421	487	1.00E-80	115.7	45.4	60.8	Ta11 non-LTR retroelement protein-like	gbpln	Arabidopsis thaliana	AT5G18636.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25200.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:6211268-6212371 FORWARD LENGTH=367	421	367	3.00E-17	87.2	15.7	24.9
Rsa1.0_01308.1.g25617.t1	ref|XP_002882730.1| hypothetical protein ARALYDRAFT_478479 [Arabidopsis lyrata subsp. lyrata] gi|297328570|gb|EFH58989.1| hypothetical protein ARALYDRAFT_478479 [Arabidopsis lyrata subsp. lyrata]	506	505	0	99.8	86.0	91.1	hypothetical protein ARALYDRAFT_478479	gbpln	Arabidopsis lyrata	AT3G11420.1 | Symbols: | Protein of unknown function (DUF604) | chr3:3591834-3594323 FORWARD LENGTH=505	506	505	0	99.8	84.4	90.5
Rsa1.0_01308.1.g25618.t1	ref|XP_002882731.1| glycerol-3-phosphate acyltransferase 5 [Arabidopsis lyrata subsp. lyrata] gi|297328571|gb|EFH58990.1| glycerol-3-phosphate acyltransferase 5 [Arabidopsis lyrata subsp. lyrata]	500	502	0	100.4	89.8	94.2	glycerol-3-phosphate acyltransferase 5	gbpln	Arabidopsis lyrata	AT3G11430.1 | Symbols: ATGPAT5, GPAT5 | glycerol-3-phosphate acyltransferase 5 | chr3:3595911-3597678 FORWARD LENGTH=502	500	502	0	100.4	89.4	94.4
Rsa1.0_01308.1.g25619.t1	ref|XP_002882732.1| hypothetical protein ARALYDRAFT_478481 [Arabidopsis lyrata subsp. lyrata] gi|297328572|gb|EFH58991.1| hypothetical protein ARALYDRAFT_478481 [Arabidopsis lyrata subsp. lyrata]	513	551	0	107.4	77.2	83.4	hypothetical protein ARALYDRAFT_478481	gbpln	Arabidopsis lyrata	AT3G11440.1 | Symbols: ATMYB65, MYB65 | myb domain protein 65 | chr3:3603056-3604929 FORWARD LENGTH=553	513	553	0	107.8	76.4	83.6

Rsa1.0_01308.1.g25620.t1	ref|NP_187752.2| DnaJ homolog subfamily C member 2 [Arabidopsis thaliana] gi|332641527|gb|AEE75048.1| DnaJ and Myb-like DNA-binding domain-containing protein [Arabidopsis thaliana]	645	647	0	100.3	86.7	91.9	DnaJ homolog subfamily C member 2	gbpln	Arabidopsis thaliana	AT3G11450.1 | Symbols: | DnaJ domain ;Myb-like DNA-binding domain | chr3:3605459-3607402 REVERSE LENGTH=647	645	647	0	100.3	86.7	91.9
Rsa1.0_01308.1.g25621.t1	ref|NP_187753.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75169981|sp|Q9CAY1.1|PP223_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At3g11460 gi|12322902|gb|AAG51440.1|AC008153_13 hypothetical protein; 50785-52656 [Arabidopsis thaliana] gi|332641528|gb|AEE75049.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	617	623	0	101.0	83.5	90.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G11460.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:3608250-3610121 FORWARD LENGTH=623	617	623	0	101.0	83.5	90.3
Rsa1.0_01308.1.g25622.t1	ref|XP_002884846.1| 4'-phosphopantetheinyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330686|gb|EFH61105.1| 4'-phosphopantetheinyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	238	300	1.00E-103	126.1	74.8	79.8	4'-phosphopantetheinyl transferase family protein	gbpln	Arabidopsis lyrata	AT3G11470.1 | Symbols: | 4'-phosphopantetheinyl transferase superfamily | chr3:3610261-3612094 REVERSE LENGTH=300	238	300	1.00E-101	126.1	71.8	78.6
Rsa1.0_01308.1.g25623.t1	gb|EOA33133.1| hypothetical protein CARUB_v10016475mg [Capsella rubella]	134	1730	2.00E-60	1291.0	82.8	85.8	hypothetical protein CARUB_v10016475mg	gbpln	Capsella rubella	AT3G08530.1 | Symbols: | Clathrin, heavy chain | chr3:2587171-2595411 REVERSE LENGTH=1703	134	1703	2.00E-62	1270.9	82.8	85.8
Rsa1.0_01309.1.g25624.t1	sp|Q2MHE4.1|HT1_ARATH RecName: Full=Serine/threonine-protein kinase HT1; AltName: Full=High leaf temperature protein 1 gi|84875482|dbj|BAE75921.1| HT1 protein kinase [Arabidopsis thaliana]	458	390	0	85.2	79.9	80.8	RecName: Full=Serine/threonine-protein kinase HT1; AltName: Full=High leaf temperature protein 1 gi|84875482|dbj|BAE75921.1| HT1 protein kinase	gbpln	Arabidopsis thaliana	AT1G62400.1 | Symbols: HT1 | Protein kinase superfamily protein | chr1:23090243-23091529 FORWARD LENGTH=345	458	345	0	75.3	73.6	73.8
Rsa1.0_01309.1.g25625.t1	ref|XP_002870666.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316502|gb|EFH46925.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	249	1104	7.00E-58	443.4	45.4	55.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G41750.2 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16694047-16697527 FORWARD LENGTH=1068	249	1068	2.00E-57	428.9	44.2	53.4
Rsa1.0_01309.1.g25626.t1	ref|XP_002886469.1| CDP-diacylglycerol synthase 1 [Arabidopsis lyrata subsp. lyrata] gi|297332310|gb|EFH62728.1| CDP-diacylglycerol synthase 1 [Arabidopsis lyrata subsp. lyrata]	280	421	2.00E-49	150.4	31.4	32.1	CDP-diacylglycerol synthase 1	gbpln	Arabidopsis lyrata	AT1G62430.1 | Symbols: ATCDS1, CDS1 | CDP-diacylglycerol synthase 1 | chr1:23106274-23108923 REVERSE LENGTH=421	280	421	6.00E-52	150.4	31.1	32.1
Rsa1.0_01309.1.g25627.t1	ref|XP_002880958.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326797|gb|EFH57217.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	238	986	6.00E-56	414.3	46.6	58.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G41750.2 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16694047-16697527 FORWARD LENGTH=1068	238	1068	1.00E-55	448.7	46.2	55.5
Rsa1.0_01309.1.g25628.t2	ref|NP_176433.2| phosphatidate cytidylyltransferase [Arabidopsis thaliana] gi|3121836|sp|O04928.1|CDS1_ARATH RecName: Full=Phosphatidate cytidylyltransferase; AltName: Full=CDP-DAG synthase; AltName: Full=CDP-DG synthase; AltName: Full=CDP-diacylglycerol synthase; Short=CDS; AltName: Full=CDP-diglyceride pyrophosphorylase; AltName: Full=CDP-diglyceride synthase; AltName: Full=CTP:phosphatidate cytidylyltransferase gi|7940286|gb|AAF70845.1|AC003113_12 F24O1.17 [Arabidopsis thaliana] gi|2181182|emb|CAA63969.1| CDP-diacylglycerol synthetase [Arabidopsis thaliana] gi|332195846|gb|AEE33967.1| phosphatidate cytidylyltransferase [Arabidopsis thaliana]	404	421	0	104.2	85.9	88.6	phosphatidate cytidylyltransferase	gbpln	Arabidopsis thaliana	AT1G62430.1 | Symbols: ATCDS1, CDS1 | CDP-diacylglycerol synthase 1 | chr1:23106274-23108923 REVERSE LENGTH=421	404	421	0	104.2	85.9	88.6
Rsa1.0_01309.1.g25629.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_01309.1.g25630.t1</td><td>ref|XP_002888025.1| hypothetical protein ARALYDRAFT_475099 [Arabidopsis lyrata subsp. lyrata] gi|297333866|gb|EFH64284.1| hypothetical protein ARALYDRAFT_475099 [Arabidopsis lyrata subsp. lyrata]</td><td>774</td><td>713</td><td>0</td><td>92.1</td><td>47.0</td><td>48.7</td><td>hypothetical protein ARALYDRAFT_475099</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G12040.1 | Symbols: LRX1 | leucine-rich repeat/extensin 1 | chr1:4070160-4072394 FORWARD LENGTH=744</td><td>774</td><td>744</td><td>0</td><td>96.1</td><td>39.1</td><td>42.6</td></tr>
<tr><td>Rsa1.0_01309.1.g25631.t1</td><td>gb|EOA34754.1| hypothetical protein CARUB_v10022325mg [Capsella rubella]</td><td>223</td><td>224</td><td>1.00E-113</td><td>100.4</td><td>92.4</td><td>97.3</td><td>hypothetical protein CARUB_v10022325mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G62450.1 | Symbols: | Immunoglobulin E-set superfamily protein | chr1:23115958-23117370 REVERSE LENGTH=223</td><td>223</td><td>223</td><td>1.00E-109</td><td>100.0</td><td>90.6</td><td>94.6</td></tr>
<tr><td>Rsa1.0_01310.1.g25632.t1</td><td>ref|XP_002871588.1| hypothetical protein ARALYDRAFT_488205 [Arabidopsis lyrata subsp. lyrata] gi|297317425|gb|EFH47847.1| hypothetical protein ARALYDRAFT_488205 [Arabidopsis lyrata subsp. lyrata]</td><td>388</td><td>648</td><td>1.00E-117</td><td>167.0</td><td>70.1</td><td>77.6</td><td>hypothetical protein ARALYDRAFT_488205</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G13820.1 | Symbols: TBP1, ATBP-1, ATBP1, ATTBP1, HPPBF-1 | telomeric DNA binding protein 1 | chr5:4461694-4464355 FORWARD LENGTH=640</td><td>388</td><td>640</td><td>1.00E-116</td><td>164.9</td><td>68.8</td><td>76.3</td></tr>
<tr><td>Rsa1.0_01310.1.g25633.t1</td><td>ref|XP_002871586.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297317423|gb|EFH47845.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>275</td><td>270</td><td>1.00E-117</td><td>98.2</td><td>79.6</td><td>87.3</td><td>glutaredoxin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G13810.1 | Symbols: | Glutaredoxin family protein | chr5:4455769-4456593 FORWARD LENGTH=274</td><td>275</td><td>274</td><td>1.00E-116</td><td>99.6</td><td>78.9</td><td>87.6</td></tr>
<tr><td>Rsa1.0_01310.1.g25634.t1</td><td>gb|EOA20527.1| hypothetical protein CARUB_v10000840mg [Capsella rubella]</td><td>494</td><td>484</td><td>0</td><td>98.0</td><td>79.6</td><td>88.1</td><td>hypothetical protein CARUB_v10000840mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G13800.1 | Symbols: PPH, CRN1 | pheophytinase | chr5:4452063-4454141 REVERSE LENGTH=484</td><td>494</td><td>484</td><td>0</td><td>98.0</td><td>80.0</td><td>88.1</td></tr>
<tr><td>Rsa1.0_01310.1.g25635.t1</td><td>gb|ABD77425.1| agamous-like 15 [Brassica napus]</td><td>253</td><td>264</td><td>1.00E-114</td><td>104.3</td><td>90.1</td><td>93.7</td><td>agamous-like 15</td><td>gbpln</td><td>Brassica napus</td><td>AT5G13790.1 | Symbols: AGL15 | AGAMOUS-like 15 | chr5:4449128-4450802 REVERSE LENGTH=268</td><td>253</td><td>268</td><td>1.00E-92</td><td>105.9</td><td>72.3</td><td>83.4</td></tr>
<tr><td>Rsa1.0_01310.1.g25636.t1</td><td>gb|EOA19567.1| hypothetical protein CARUB_v10002619mg [Capsella rubella]</td><td>478</td><td>479</td><td>0</td><td>100.2</td><td>84.1</td><td>91.4</td><td>hypothetical protein CARUB_v10002619mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G13750.1 | Symbols: ZIFL1 | zinc induced facilitator-like 1 | chr5:4438318-4441289 FORWARD LENGTH=478</td><td>478</td><td>478</td><td>0</td><td>100.0</td><td>83.3</td><td>90.8</td></tr>
<tr><td>Rsa1.0_01310.1.g25637.t1</td><td>gb|AAM12978.1| transporter-like protein [Arabidopsis thaliana] gi|22136244|gb|AAM91200.1| transporter-like protein [Arabidopsis thaliana]</td><td>411</td><td>460</td><td>0</td><td>111.9</td><td>87.3</td><td>92.0</td><td>transporter-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G13740.1 | Symbols: ZIF1 | zinc induced facilitator 1 | chr5:4432689-4436483 FORWARD LENGTH=486</td><td>411</td><td>486</td><td>0</td><td>118.2</td><td>87.3</td><td>92.0</td></tr>
<tr><td>Rsa1.0_01310.1.g25638.t1</td><td>ref|NP_850812.2| receptor-like kinase CORYNE [Arabidopsis thaliana] gi|75335675|sp|Q9LYU7.1|CRN_ARATH RecName: Full=Inactive leucine-rich repeat receptor-like protein kinase CORYNE; AltName: Full=Protein SUPPRESSOR OF OVEREXPRESSION OF LLP1 2; Flags: Precursor gi|7529284|emb|CAB86636.1| protein kinase precursor-like [Arabidopsis thaliana] gi|332004493|gb|AED91876.1| receptor-like kinase CORYNE [Arabidopsis thaliana]</td><td>180</td><td>401</td><td>6.00E-81</td><td>222.8</td><td>82.8</td><td>90.6</td><td>receptor-like kinase CORYNE</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G13290.2 | Symbols: SOL2, CRN | Protein kinase superfamily protein | chr5:4252924-4254215 REVERSE LENGTH=401</td><td>180</td><td>401</td><td>2.00E-83</td><td>222.8</td><td>82.8</td><td>90.6</td></tr>
<tr><td>Rsa1.0_01310.1.g25639.t1</td><td>gb|EOA22755.1| hypothetical protein CARUB_v10003467mg, partial [Capsella rubella]</td><td>276</td><td>325</td><td>1.00E-107</td><td>117.8</td><td>75.7</td><td>83.0</td><td>hypothetical protein CARUB_v10003467mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G13250.1 | Symbols: | RING finger protein | chr5:4234486-4241615 FORWARD LENGTH=387</td><td>276</td><td>387</td><td>1.00E-103</td><td>140.2</td><td>75.7</td><td>82.6</td></tr>
<tr><td>Rsa1.0_01310.1.g25640.t1</td><td>ref|XP_002871554.1| hypothetical protein ARALYDRAFT_488138 [Arabidopsis lyrata subsp. lyrata] gi|297317391|gb|EFH47813.1| hypothetical protein ARALYDRAFT_488138 [Arabidopsis lyrata subsp. lyrata]</td><td>195</td><td>198</td><td>1.00E-77</td><td>101.5</td><td>76.9</td><td>87.2</td><td>hypothetical protein ARALYDRAFT_488138</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G13220.1 | Symbols: JAZ10, TIFY9, JAS1 | jasmonate-zim-domain protein 10 | chr5:4219001-4220502 FORWARD LENGTH=197</td><td>195</td><td>197</td><td>9.00E-78</td><td>101.0</td><td>75.9</td><td>84.6</td></tr>
<tr><td>Rsa1.0_01310.1.g25641.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01310.1.g25642.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01310.1.g25643.t1</td><td>gb|AFI56995.1| NAC5 [Brassica napus]</td><td>249</td><td>249</td><td>1.00E-118</td><td>100.0</td><td>90.4</td><td>94.4</td><td>NAC5</td><td>gbpln</td><td>Brassica napus</td><td>AT5G13180.1 | Symbols: ANAC083, VNI2, NAC083 | NAC domain containing protein 83 | chr5:4196643-4197577 FORWARD LENGTH=252</td><td>249</td><td>252</td><td>1.00E-113</td><td>101.2</td><td>88.0</td><td>94.0</td></tr>
<tr><td>Rsa1.0_01311.1.g25644.t1</td><td>ref|NP_174430.1| aspartyl protease-like protein [Arabidopsis thaliana] gi|12322538|gb|AAG51267.1|AC027135_8 chloroplast nucleoid DNA binding protein, putative [Arabidopsis thaliana] gi|67633408|gb|AAY78629.1| aspartyl protease family protein [Arabidopsis thaliana] gi|332193236|gb|AEE31357.1| aspartyl protease-like protein [Arabidopsis thaliana]</td><td>404</td><td>445</td><td>1.00E-157</td><td>110.1</td><td>72.8</td><td>81.2</td><td>aspartyl protease-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31450.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:11259872-11261209 REVERSE LENGTH=445</td><td>404</td><td>445</td><td>1.00E-159</td><td>110.1</td><td>72.8</td><td>81.2</td></tr>
<tr><td>Rsa1.0_01311.1.g25645.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_01311.1.g25646.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1253	2301	0	183.6	52.0	65.7	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1253	1262	1.00E-107	100.7	14.7	22.5
Rsa1.0_01311.1.g25647.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01311.1.g25648.t1	gb|EOA37770.1| hypothetical protein CARUB_v10012628mg [Capsella rubella]	282	316	3.00E-90	112.1	75.2	85.5	hypothetical protein CARUB_v10012628mg	gbpln	Capsella rubella	AT1G31460.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23270.1); Has 1251 Blast hits to 756 proteins in 185 species: Archae - 0; Bacteria - 295; Metazoa - 374; Fungi - 176; Plants - 58; Viruses - 17; Other Eukaryotes - 331 (source: NCBI BLink). | chr1:11261705-11262610 REVERSE LENGTH=301	282	301	8.00E-83	106.7	67.0	77.3
Rsa1.0_01311.1.g25649.t1	ref|NP_174432.2| nuclear fusion defective 4 protein [Arabidopsis thaliana] gi|332193238|gb|AEE31359.1| nuclear fusion defective 4 protein [Arabidopsis thaliana]	579	582	0	100.5	86.5	92.1	nuclear fusion defective 4 protein	gbpln	Arabidopsis thaliana	AT1G31470.1 | Symbols: NFD4 | Major facilitator superfamily protein | chr1:11262937-11264944 REVERSE LENGTH=582	579	582	0	100.5	86.5	92.1
Rsa1.0_01311.1.g25650.t4	gb|EOA39604.1| hypothetical protein CARUB_v10008231mg [Capsella rubella]	939	937	0	99.8	85.1	91.2	hypothetical protein CARUB_v10008231mg	gbpln	Capsella rubella	AT1G31480.1 | Symbols: SGR2 | shoot gravitropism 2 (SGR2) | chr1:11266225-11271527 FORWARD LENGTH=933	939	933	0	99.4	84.3	89.7
Rsa1.0_01311.1.g25651.t1	ref|NP_174434.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|12322545|gb|AAG51274.1|AC027135_15 N-hydroxycinnamoyl/benzoyltransferase, putative [Arabidopsis thaliana] gi|12597836|gb|AAG60146.1|AC074360_11 hypothetical protein [Arabidopsis thaliana] gi|332193240|gb|AEE31361.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	446	444	0	99.6	85.7	92.6	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT1G31490.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:11271744-11273078 REVERSE LENGTH=444	446	444	0	99.6	85.7	92.6
Rsa1.0_01311.1.g25652.t1	ref|NP_174435.2| carbon catabolite repressor protein 4-like 4 [Arabidopsis thaliana] gi|332193241|gb|AEE31362.1| carbon catabolite repressor protein 4-like 4 [Arabidopsis thaliana]	355	388	1.00E-179	109.3	87.6	93.0	carbon catabolite repressor protein 4-like 4	gbpln	Arabidopsis thaliana	AT1G31500.1 | Symbols: | DNAse I-like superfamily protein | chr1:11273821-11276534 REVERSE LENGTH=388	355	388	0	109.3	87.6	93.0
Rsa1.0_01311.1.g25653.t1	ref|NP_174446.2| RHO guanyl-nucleotide exchange factor 14 [Arabidopsis thaliana] gi|62321355|dbj|BAD94650.1| hypothetical protein [Arabidopsis thaliana] gi|332193259|gb|AEE31380.1| RHO guanyl-nucleotide exchange factor 14 [Arabidopsis thaliana]	351	576	1.00E-175	164.1	85.8	90.0	RHO guanyl-nucleotide exchange factor 14	gbpln	Arabidopsis thaliana	AT1G31650.1 | Symbols: ATROPGEF14, ROPGEF14 | RHO guanyl-nucleotide exchange factor 14 | chr1:11326474-11329767 REVERSE LENGTH=576	351	576	1.00E-177	164.1	85.8	90.0
Rsa1.0_01312.1.g25654.t1	ref|NP_197389.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|332005241|gb|AED92624.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	187	295	2.00E-22	157.8	34.2	44.9	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	187	295	6.00E-25	157.8	34.2	44.9
Rsa1.0_01312.1.g25655.t1	ref|XP_002872853.1| ATIMPALPHA3/MOS6 [Arabidopsis lyrata subsp. lyrata] gi|297318690|gb|EFH49112.1| ATIMPALPHA3/MOS6 [Arabidopsis lyrata subsp. lyrata]	555	534	0	96.2	71.9	81.4	ATIMPALPHA3/MOS6	gbpln	Arabidopsis lyrata	AT4G02150.1 | Symbols: MOS6, ATIMPALPHA3, IMPA-3 | ARM repeat superfamily protein | chr4:950884-953602 REVERSE LENGTH=531	555	531	0	95.7	69.7	79.3
Rsa1.0_01312.1.g25656.t1	gb|AAC02664.1| polyprotein [Arabidopsis thaliana]	784	1451	0	185.1	69.1	78.7	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	784	1262	1.00E-113	161.0	25.1	36.5
Rsa1.0_01312.1.g25657.t1	gb|AAC02666.1| polyprotein [Arabidopsis thaliana]	504	1451	0	287.9	68.3	78.4	polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01312.1.g25658.t2	gb|AFJ66186.1| hypothetical protein 11M19.5 [Arabidopsis halleri]	1546	1557	0	100.7	63.0	75.8	hypothetical protein 11M19.5	gbpln	Arabidopsis halleri	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1546	158	2.00E-28	10.2	4.5	5.5

Rsa1.0_01312.1.g25659.t1	ref|NP_180368.1| aspartyl protease-like protein [Arabidopsis thaliana] gi|4510415|gb|AAD21501.1| putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana] gi|330252975|gb|AEC08069.1| aspartyl protease-like protein [Arabidopsis thaliana]	436	396	1.00E-121	90.8	54.8	67.4	aspartyl protease-like protein	gbpln	Arabidopsis thaliana	AT2G28010.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:11930579-11931769 REVERSE LENGTH=396	436	396	1.00E-123	90.8	54.8	67.4
Rsa1.0_01312.1.g25660.t1	gb|AAD15377.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1421	1044	1.00E-132	73.5	15.6	21.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1421	575	2.00E-28	40.5	4.8	7.5
Rsa1.0_01312.1.g25661.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	708	1214	1.00E-164	171.5	43.8	63.3	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	708	295	6.00E-84	41.7	21.9	28.5
Rsa1.0_01312.1.g25662.t2	ref|NP_565613.1| uncharacterized protein [Arabidopsis thaliana] gi|15294292|gb|AAK95323.1|AF410337_1 At2g25920/F17H15.5 [Arabidopsis thaliana] gi|20197362|gb|AAC42240.2| expressed protein [Arabidopsis thaliana] gi|23507801|gb|AAN38704.1| At2g25920/F17H15.5 [Arabidopsis thaliana] gi|330252679|gb|AEC07773.1| uncharacterized protein AT2G25920 [Arabidopsis thaliana]	269	280	5.00E-99	104.1	74.7	79.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G25920.1 | Symbols: | BEST Arabidopsis thaliana protein match is: 3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein (TAIR:AT2G25910.2); Has 131 Blast hits to 125 proteins in 54 species: Archae - 0; Bacteria - 50; Metazoa - 12; Fungi - 12; Plants - 41; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink). | chr2:11054425-11055916 REVERSE LENGTH=280	269	280	1.00E-101	104.1	74.7	79.9
Rsa1.0_01312.1.g25663.t1	ref|XP_002875851.1| hypothetical protein ARALYDRAFT_323370 [Arabidopsis lyrata subsp. lyrata] gi|297321689|gb|EFH52110.1| hypothetical protein ARALYDRAFT_323370 [Arabidopsis lyrata subsp. lyrata]	250	970	5.00E-66	388.0	50.4	63.6	hypothetical protein ARALYDRAFT_323370	gbpln	Arabidopsis lyrata	AT3G47580.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17532687-17535810 FORWARD LENGTH=1011	250	1011	3.00E-67	404.4	51.2	61.6
Rsa1.0_01313.1.g25664.t1	gb|AAB87721.1| maize gl1 homolog [Arabidopsis thaliana]	645	625	0	96.9	80.9	86.8	maize gl1 homolog	gbpln	Arabidopsis thaliana	AT1G02205.2 | Symbols: CER1 | Fatty acid hydroxylase superfamily | chr1:418818-422154 FORWARD LENGTH=625	645	625	0	96.9	82.3	87.6
Rsa1.0_01313.1.g25665.t9	ref|NP_001077448.1| alpha-1,6-mannosyltransferase [Arabidopsis thaliana] gi|347662308|sp|A8MR93.1|ALG12_ARATH RecName: Full=Dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase; AltName: Full=Alpha-1,6-mannosyltransferase ALG12; AltName: Full=Asparagine-linked glycosylation protein 12; AltName: Full=EMS-mutagenized BRI1 suppressor 4 gi|332189270|gb|AEE27391.1| alpha-1,6-mannosyltransferase [Arabidopsis thaliana]	508	497	0	97.8	85.8	90.6	alpha-1,6-mannosyltransferase	gbpln	Arabidopsis thaliana	AT1G02145.3 | Symbols: ALG12, EBS4 | homolog of asparagine-linked glycosylation 12 | chr1:404627-408485 FORWARD LENGTH=497	508	497	0	97.8	85.8	90.6
Rsa1.0_01313.1.g25666.t10	gb|EOA36262.1| hypothetical protein CARUB_v10010485mg, partial [Capsella rubella]	153	167	4.00E-62	109.2	78.4	84.3	hypothetical protein CARUB_v10010485mg, partial	gbpln	Capsella rubella	AT1G02140.1 | Symbols: MEE63, MAGO, HAP1 | mago nashi family protein | chr1:403467-404401 REVERSE LENGTH=150	153	150	1.00E-62	98.0	75.8	83.7
Rsa1.0_01313.1.g25667.t1	ref|NP_171712.2| Leucine carboxyl methyltransferase [Arabidopsis thaliana] gi|42571301|ref|NP_973741.1| Leucine carboxyl methyltransferase [Arabidopsis thaliana] gi|18377694|gb|AAL66997.1| unknown protein [Arabidopsis thaliana] gi|22136718|gb|AAM91678.1| unknown protein [Arabidopsis thaliana] gi|332189262|gb|AEE27383.1| Leucine carboxyl methyltransferase [Arabidopsis thaliana] gi|332189263|gb|AEE27384.1| Leucine carboxyl methyltransferase [Arabidopsis thaliana]	325	332	1.00E-153	102.2	85.2	90.2	Leucine carboxyl methyltransferase	gbpln	Arabidopsis thaliana	AT1G02100.1 | Symbols: | Leucine carboxyl methyltransferase | chr1:389876-392448 FORWARD LENGTH=332	325	332	1.00E-155	102.2	85.2	90.2
Rsa1.0_01313.1.g25668.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1747	1213	0	69.4	35.7	45.6	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1747	746	1.00E-68	42.7	8.4	12.0
Rsa1.0_01313.1.g25669.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01313.1.g25670.t1	ref|XP_002867599.1| hypothetical protein ARALYDRAFT_492259 [Arabidopsis lyrata subsp. lyrata] gi|297313435|gb|EFH43858.1| hypothetical protein ARALYDRAFT_492259 [Arabidopsis lyrata subsp. lyrata]	205	187	3.00E-18	91.2	25.4	28.3	hypothetical protein ARALYDRAFT_492259	gbpln	Arabidopsis lyrata	AT4G25670.2 | Symbols: | unknown protein; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25690.2). | chr4:13085431-13085997 REVERSE LENGTH=188	205	188	9.00E-20	91.7	25.9	27.8
Rsa1.0_01314.1.g25671.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01314.1.g25672.t2	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01314.1.g25673.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	674	1838	1.00E-132	272.7	45.1	57.6	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01314.1.g25674.t1	gb|ABD65089.1| zinc knuckle containing protein [Brassica oleracea]	508	333	1.00E-39	65.6	20.5	23.2	zinc knuckle containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01314.1.g25675.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01314.1.g25676.t1	gb|EOA20993.1| hypothetical protein CARUB_v10001326mg [Capsella rubella]	362	345	1.00E-162	95.3	79.6	86.5	hypothetical protein CARUB_v10001326mg	gbpln	Capsella rubella	AT4G08770.1 | Symbols: Prx37 | Peroxidase superfamily protein | chr4:5598259-5600262 REVERSE LENGTH=346	362	346	1.00E-160	95.6	77.9	82.6
Rsa1.0_01314.1.g25677.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01315.1.g25678.t1	ref|XP_002874144.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319981|gb|EFH50403.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	292	230	3.00E-71	78.8	47.9	58.2	DNA binding protein	gbpln	Arabidopsis lyrata	AT5G23710.1 | Symbols: | DNA binding;DNA-directed RNA polymerases | chr5:7996528-7997220 REVERSE LENGTH=230	292	230	4.00E-73	78.8	46.6	57.9
Rsa1.0_01315.1.g25679.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	274	1161	2.00E-60	423.7	43.4	54.4	F14N23.4	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	274	332	1.00E-59	121.2	41.2	54.7
Rsa1.0_01315.1.g25680.t1	ref|NP_568435.2| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|75333740|sp|Q9FFA7.1|RUP2_ARATH RecName: Full=WD repeat-containing protein RUP2; AltName: Full=Protein EARLY FLOWERING BY OVEREXPRESSION 2; AltName: Full=Protein EPRESSOR OF UV-B PHOTOMORPHOGENESIS 2 gi|10176840|dbj|BAB10046.1| unnamed protein product [Arabidopsis thaliana] gi|332005822|gb|AED93205.1| WD repeat-containing protein RUP2 [Arabidopsis thaliana]	387	368	1.00E-179	95.1	88.1	91.2	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT5G23730.1 | Symbols: RUP2 | Transducin/WD40 repeat-like superfamily protein | chr5:8005286-8006392 FORWARD LENGTH=368	387	368	0	95.1	88.1	91.2
Rsa1.0_01315.1.g25681.t1	ref|XP_002869362.1| 40S ribosomal protein S11 [Arabidopsis lyrata subsp. lyrata] gi|297315198|gb|EFH45621.1| 40S ribosomal protein S11 [Arabidopsis lyrata subsp. lyrata]	375	159	4.00E-83	42.4	38.9	40.5	40S ribosomal protein S11	gbpln	Arabidopsis lyrata	AT5G23740.1 | Symbols: RPS11-BETA | ribosomal protein S11-beta | chr5:8008251-8009330 REVERSE LENGTH=159	375	159	1.00E-80	42.4	40.3	41.1
Rsa1.0_01315.1.g25682.t1	ref|XP_002874147.1| hypothetical protein ARALYDRAFT_910389 [Arabidopsis lyrata subsp. lyrata] gi|297319984|gb|EFH50406.1| hypothetical protein ARALYDRAFT_910389 [Arabidopsis lyrata subsp. lyrata]	103	103	3.00E-44	100.0	99.0	100.0	hypothetical protein ARALYDRAFT_910389	gbpln	Arabidopsis lyrata	AT5G23760.1 | Symbols: | Copper transport protein family | chr5:8013242-8014129 REVERSE LENGTH=103	103	103	1.00E-46	100.0	98.1	100.0
Rsa1.0_01315.1.g25683.t1	gb|EOA19597.1| hypothetical protein CARUB_v10002779mg [Capsella rubella]	490	467	0	95.3	80.2	87.8	hypothetical protein CARUB_v10002779mg	gbpln	Capsella rubella	AT5G23810.1 | Symbols: AAP7 | amino acid permease 7 | chr5:8028461-8030730 FORWARD LENGTH=467	490	467	0	95.3	78.2	86.1
Rsa1.0_01315.1.g25684.t1	ref|XP_002874560.1| hypothetical protein ARALYDRAFT_911169 [Arabidopsis lyrata subsp. lyrata] gi|297320397|gb|EFH50819.1| hypothetical protein ARALYDRAFT_911169 [Arabidopsis lyrata subsp. lyrata]	65	77	1.00E-12	118.5	60.0	69.2	hypothetical protein ARALYDRAFT_911169	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01315.1.g25685.t1	ref|NP_197779.4| ATP binding microtubule motor family protein [Arabidopsis thaliana] gi|332005850|gb|AED93233.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]	697	701	0	100.6	67.0	76.9	ATP binding microtubule motor family protein	gbpln	Arabidopsis thaliana	AT5G23910.1 | Symbols: | ATP binding microtubule motor family protein | chr5:8068452-8072723 FORWARD LENGTH=701	697	701	0	100.6	67.0	76.9
Rsa1.0_01315.1.g25686.t1	gb|EOA21333.1| hypothetical protein CARUB_v10001693mg [Capsella rubella]	260	273	8.00E-99	105.0	76.2	81.5	hypothetical protein CARUB_v10001693mg	gbpln	Capsella rubella	AT5G23950.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr5:8082789-8083448 FORWARD LENGTH=219	260	219	5.00E-77	84.2	60.8	66.2

Rsa1.0_01315.1.g25687.t1	ref|NP_197785.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|9758221|dbj|BAB08720.1| acetyl-CoA:benzylalcohol acetyltranferase-like protein [Arabidopsis thaliana] gi|111074496|gb|ABH04621.1| At5g23970 [Arabidopsis thaliana] gi|332005857|gb|AED93240.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	436	428	0	98.2	75.7	85.3	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT5G23970.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:8096326-8097612 FORWARD LENGTH=428	436	428	0	98.2	75.7	85.3
Rsa1.0_01315.1.g25688.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1431	1515	0	105.9	55.1	69.2	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1431	1262	1.00E-110	88.2	13.6	20.4
Rsa1.0_01315.1.g25689.t1	gb|EOA20155.1| hypothetical protein CARUB_v10000447mg [Capsella rubella]	561	637	0	113.5	86.1	92.3	hypothetical protein CARUB_v10000447mg	gbpln	Capsella rubella	AT5G24030.1 | Symbols: SLAH3 | SLAC1 homologue 3 | chr5:8118618-8120993 REVERSE LENGTH=635	561	635	0	113.2	87.2	92.3
Rsa1.0_01316.1.g25690.t1	ref|NP_175672.2| O-fucosyltransferase family protein [Arabidopsis thaliana] gi|18491205|gb|AAL69505.1| unknown protein [Arabidopsis thaliana] gi|20465295|gb|AAM20051.1| unknown protein [Arabidopsis thaliana] gi|332194710|gb|AEE32831.1| O-fucosyltransferase family protein [Arabidopsis thaliana]	706	439	0	62.2	48.2	51.8	O-fucosyltransferase family protein	gbpln	Arabidopsis thaliana	AT1G52630.1 | Symbols: | O-fucosyltransferase family protein | chr1:19606470-19608526 REVERSE LENGTH=439	706	439	0	62.2	48.2	51.8
Rsa1.0_01316.1.g25691.t1	ref|NP_566523.1| signal peptidase, endoplasmic reticulum-type [Arabidopsis thaliana] gi|11994343|dbj|BAB02302.1| signal sequence processing protein; peptidase-like protein [Arabidopsis thaliana] gi|50897212|gb|AAT85745.1| At3g15710 [Arabidopsis thaliana] gi|51972110|gb|AAU15159.1| At3g15710 [Arabidopsis thaliana] gi|332642196|gb|AEE75717.1| Peptidase S24/S26A/S26B/S26C family protein [Arabidopsis thaliana]	180	180	4.00E-86	100.0	87.2	94.4	signal peptidase, endoplasmic reticulum-type	gbpln	Arabidopsis thaliana	AT3G15710.1 | Symbols: | Peptidase S24/S26A/S26B/S26C family protein | chr3:5323564-5324785 REVERSE LENGTH=180	180	180	2.00E-88	100.0	87.2	94.4
Rsa1.0_01316.1.g25692.t1	ref|XP_002882972.1| hypothetical protein ARALYDRAFT_341728 [Arabidopsis lyrata subsp. lyrata] gi|297328812|gb|EFH59231.1| hypothetical protein ARALYDRAFT_341728 [Arabidopsis lyrata subsp. lyrata]	388	366	1.00E-112	94.3	55.9	70.4	hypothetical protein ARALYDRAFT_341728	gbpln	Arabidopsis lyrata	AT3G17620.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6026498-6027694 REVERSE LENGTH=398	388	398	1.00E-96	102.6	49.2	64.7
Rsa1.0_01316.1.g25693.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01316.1.g25694.t1	ref|XP_002882972.1| hypothetical protein ARALYDRAFT_341728 [Arabidopsis lyrata subsp. lyrata] gi|297328812|gb|EFH59231.1| hypothetical protein ARALYDRAFT_341728 [Arabidopsis lyrata subsp. lyrata]	376	366	1.00E-119	97.3	62.0	75.0	hypothetical protein ARALYDRAFT_341728	gbpln	Arabidopsis lyrata	AT3G16740.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:5699476-5700651 FORWARD LENGTH=391	376	391	7.00E-97	104.0	50.8	68.9
Rsa1.0_01316.1.g25695.t7	ref|XP_002885106.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297330946|gb|EFH61365.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	418	454	1.00E-171	108.6	70.3	76.3	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT3G15720.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:5325329-5327457 REVERSE LENGTH=456	418	456	1.00E-172	109.1	68.4	74.6
Rsa1.0_01316.1.g25696.t1	#	#	#	#	#	#	#	-	----	----	AT4G38510.4 | Symbols: | ATPase, V1 complex, subunit B protein | chr4:18011155-18014789 REVERSE LENGTH=487	181	487	6.00E-11	269.1	20.4	24.9
Rsa1.0_01316.1.g25697.t1	sp|O82549.1|PLDA1_BRAOC RecName: Full=Phospholipase D alpha 1; Short=PLD 1; AltName: Full=Choline phosphatase 1; AltName: Full=Phosphatidylcholine-hydrolyzing phospholipase D 1; Flags: Precursor gi|3639089|gb|AAC78487.1| phospholipase D1 [Brassica oleracea var. capitata] gi|4324969|gb|AAD17208.1| phospholipase D1 [Brassica oleracea var. capitata]	810	810	0	100.0	97.2	98.9	RecName: Full=Phospholipase D alpha 1; Short=PLD 1; AltName: Full=Choline phosphatase 1; AltName: Full=Phosphatidylcholine-hydrolyzing phospholipase D 1; Flags: Precursor gi|3639089|gb|AAC78487.1| phospholipase D1	gbpln	Brassica oleracea	AT3G15730.1 | Symbols: PLDALPHA1, PLD | phospholipase D alpha 1 | chr3:5330835-5333474 FORWARD LENGTH=810	810	810	0	100.0	94.0	97.8

Rsa1.0_01316.1.g25698.t1	ref|XP_002882960.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328800|gb|EFH59219.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	110	135	3.00E-41	122.7	80.9	91.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G15760.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52565.1); Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5337734-5338219 FORWARD LENGTH=135	110	135	1.00E-38	122.7	72.7	84.5
Rsa1.0_01316.1.g25699.t1	ref|NP_188199.1| uncharacterized protein [Arabidopsis thaliana] gi|11994350|dbj|BAB02309.1| unnamed protein product [Arabidopsis thaliana] gi|17065466|gb|AAL32887.1| Unknown protein [Arabidopsis thaliana] gi|20148569|gb|AAM10175.1| unknown protein [Arabidopsis thaliana] gi|332642205|gb|AEE75726.1| uncharacterized protein AT3G15780 [Arabidopsis thaliana]	307	117	1.00E-16	38.1	24.4	27.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52550.1); Has 20 Blast hits to 20 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5341434-5342351 FORWARD LENGTH=117	307	117	3.00E-19	38.1	24.4	27.0
Rsa1.0_01317.1.g25700.t1	gb|AAD29058.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	293	1229	3.00E-29	419.5	32.1	46.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	293	303	6.00E-31	103.4	33.1	48.1
Rsa1.0_01317.1.g25701.t1	ref|NP_176441.1| uncharacterized protein [Arabidopsis thaliana] gi|5454194|gb|AAD43609.1|AC005698_8 T3P18.8 [Arabidopsis thaliana] gi|28393500|gb|AAO42171.1| unknown protein [Arabidopsis thaliana] gi|28973499|gb|AAO64074.1| unknown protein [Arabidopsis thaliana] gi|332195853|gb|AEE33974.1| uncharacterized protein AT1G62520 [Arabidopsis thaliana]	264	280	1.00E-107	106.1	83.3	91.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G62520.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12450.1); Has 388 Blast hits to 388 proteins in 26 species: Archae - 0; Bacteria - 1; Metazoa - 0; Fungi - 8; Plants - 376; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr1:23144506-23145348 FORWARD LENGTH=280	264	280	1.00E-110	106.1	83.3	91.3
Rsa1.0_01317.1.g25702.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01317.1.g25703.t2	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1711	1270	0	74.2	37.6	48.2	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1711	575	2.00E-76	33.6	9.9	15.8
Rsa1.0_01317.1.g25704.t1	ref|XP_002888015.1| hypothetical protein ARALYDRAFT_475088 [Arabidopsis lyrata subsp. lyrata] gi|297333856|gb|EFH64274.1| hypothetical protein ARALYDRAFT_475088 [Arabidopsis lyrata subsp. lyrata]	908	452	0	49.8	42.7	45.9	hypothetical protein ARALYDRAFT_475088	gbpln	Arabidopsis lyrata	AT1G62600.1 | Symbols: | Flavin-binding monooxygenase family protein | chr1:23179542-23181411 FORWARD LENGTH=452	908	452	0	49.8	42.3	46.0
Rsa1.0_01318.1.g25705.t2	ref|NP_199308.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262649|sp|Q9FLA2.1|FDL34_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g44950 gi|10177487|dbj|BAB10878.1| unnamed protein product [Arabidopsis thaliana] gi|332007796|gb|AED95179.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	646	438	1.00E-86	67.8	30.8	39.3	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G44950.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:18151665-18153164 FORWARD LENGTH=438	646	438	3.00E-89	67.8	30.8	39.3
Rsa1.0_01318.1.g25706.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01318.1.g25707.t1	ref|XP_002863468.1| hypothetical protein ARALYDRAFT_356449 [Arabidopsis lyrata subsp. lyrata] gi|297309303|gb|EFH39727.1| hypothetical protein ARALYDRAFT_356449 [Arabidopsis lyrata subsp. lyrata]	281	280	1.00E-141	99.6	88.3	93.6	hypothetical protein ARALYDRAFT_356449	gbpln	Arabidopsis lyrata	AT5G45580.1 | Symbols: | Homeodomain-like superfamily protein | chr5:18481092-18482598 REVERSE LENGTH=264	281	264	1.00E-134	94.0	82.9	87.9
Rsa1.0_01318.1.g25708.t1	dbj|BAB01431.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	218	637	1.00E-40	292.2	40.4	51.8	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	218	295	1.00E-34	135.3	35.8	50.5
Rsa1.0_01318.1.g25709.t1	ref|NP_199367.1| uncharacterized protein [Arabidopsis thaliana] gi|9758744|dbj|BAB09182.1| unnamed protein product [Arabidopsis thaliana] gi|332007883|gb|AED95266.1| uncharacterized protein AT5G45540 [Arabidopsis thaliana]	774	803	0	103.7	79.8	88.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G45540.1 | Symbols: | Protein of unknown function (DUF594) | chr5:18458294-18460705 REVERSE LENGTH=803	774	803	0	103.7	79.8	88.1

Rsa1.0_01318.1.g25710.t1	ref|XP_002863471.1| hypothetical protein ARALYDRAFT_494430 [Arabidopsis lyrata subsp. lyrata] gi|297309306|gb|EFH39730.1| hypothetical protein ARALYDRAFT_494430 [Arabidopsis lyrata subsp. lyrata]	823	798	0	97.0	76.3	84.3	hypothetical protein ARALYDRAFT_494430	gbpln	Arabidopsis lyrata	AT5G45530.1 | Symbols: | Protein of unknown function (DUF594) | chr5:18454316-18457222 REVERSE LENGTH=798	823	798	0	97.0	76.2	83.8
Rsa1.0_01318.1.g25711.t1	gb|EOA15239.1| hypothetical protein CARUB_v10028636mg [Capsella rubella]	1109	1176	0	106.0	55.1	69.8	hypothetical protein CARUB_v10028636mg	gbpln	Capsella rubella	AT5G45520.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:18449509-18453012 REVERSE LENGTH=1167	1109	1167	0	105.2	56.4	69.3
Rsa1.0_01318.1.g25712.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01319.1.g25713.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1520	1838	0	120.9	27.6	38.4	F5M15.26	gbpln	Arabidopsis thaliana	AT3G01410.2 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr3:153650-155439 REVERSE LENGTH=294	1520	294	2.00E-13	19.3	2.4	3.3
Rsa1.0_01319.1.g25714.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01319.1.g25715.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01319.1.g25716.t1	ref|XP_002868357.1| hypothetical protein ARALYDRAFT_493559 [Arabidopsis lyrata subsp. lyrata] gi|297314193|gb|EFH44616.1| hypothetical protein ARALYDRAFT_493559 [Arabidopsis lyrata subsp. lyrata]	259	265	2.00E-77	102.3	67.2	80.3	hypothetical protein ARALYDRAFT_493559	gbpln	Arabidopsis lyrata	AT4G13530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10080.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:7866808-7868555 FORWARD LENGTH=270	259	270	1.00E-77	104.2	69.1	82.2
Rsa1.0_01319.1.g25717.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01319.1.g25718.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01319.1.g25719.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01319.1.g25720.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1345	1459	0	108.5	53.5	70.3	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1345	1262	1.00E-109	93.8	14.3	20.6
Rsa1.0_01319.1.g25721.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	110	149	2.00E-23	135.5	44.5	65.5	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01319.1.g25722.t1	gb|EOA15614.1| hypothetical protein CARUB_v10005748mg [Capsella rubella]	194	206	4.00E-85	106.2	78.4	88.7	hypothetical protein CARUB_v10005748mg	gbpln	Capsella rubella	AT4G14100.1 | Symbols: | transferases, transferring glycosyl groups | chr4:8120749-8122288 FORWARD LENGTH=206	194	206	4.00E-87	106.2	78.4	87.6
Rsa1.0_01319.1.g25723.t1	gb|EOA18020.1| hypothetical protein CARUB_v10006460mg [Capsella rubella]	898	797	0	88.8	69.9	77.4	hypothetical protein CARUB_v10006460mg	gbpln	Capsella rubella	AT4G14280.1 | Symbols: | ARM repeat superfamily protein | chr4:8222518-8225074 FORWARD LENGTH=798	898	798	0	88.9	69.5	77.2
Rsa1.0_01320.1.g25724.t2	gb|AAD37019.2| putative non-LTR retrolelement reverse transcriptase [Arabidopsis thaliana]	973	855	0	87.9	44.7	57.9	putative non-LTR retrolelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337-69884 REVERSE LENGTH=515	973	515	1.00E-127	52.9	24.9	32.7
Rsa1.0_01320.1.g25725.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01320.1.g25726.t1	gb|EOA39737.1| hypothetical protein CARUB_v10008382mg [Capsella rubella]	750	763	0	101.7	85.3	89.9	hypothetical protein CARUB_v10008382mg	gbpln	Capsella rubella	AT1G21980.1 | Symbols: ATPIP5K1, ATPIPK1, PIP5K1 | phosphatidylinositol-4-phosphate 5-kinase 1 | chr1:7735053-7738309 FORWARD LENGTH=752	750	752	0	100.3	85.1	90.1
Rsa1.0_01320.1.g25727.t1	gb|EOA36900.1| hypothetical protein CARUB_v10011446mg [Capsella rubella]	391	396	0	101.3	84.7	93.1	hypothetical protein CARUB_v10011446mg	gbpln	Capsella rubella	AT1G22015.1 | Symbols: DD46 | Galactosyltransferase family protein | chr1:7751225-7753425 REVERSE LENGTH=398	391	398	0	101.8	84.1	92.1
Rsa1.0_01320.1.g25728.t1	ref|NP_173621.1| serine hydroxymethyltransferase 6 [Arabidopsis thaliana] gi|9280677|gb|AAF86546.1|AC069252_5 F2E2.7 [Arabidopsis thaliana] gi|21928157|gb|AAM78106.1| At1g22020/F2E2_3 [Arabidopsis thaliana] gi|28416495|gb|AAO42778.1| At1g22020/F2E2_3 [Arabidopsis thaliana] gi|332192065|gb|AEE30186.1| serine hydroxymethyltransferase 6 [Arabidopsis thaliana]	363	599	1.00E-138	165.0	65.0	69.1	serine hydroxymethyltransferase 6	gbpln	Arabidopsis thaliana	AT1G22020.1 | Symbols: SHM6 | serine hydroxymethyltransferase 6 | chr1:7754599-7757087 FORWARD LENGTH=599	363	599	1.00E-140	165.0	65.0	69.1
Rsa1.0_01320.1.g25729.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01320.1.g25730.t1	ref|XP_002893207.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339049|gb|EFH69466.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	325	334	1.00E-156	102.8	90.8	93.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G22030.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Protein BYPASS related (InterPro:IPR008511); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G77855.1); Has 99 Blast hits to 99 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 96; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7759337-7760415 REVERSE LENGTH=333	325	333	1.00E-152	102.5	88.6	91.4
Rsa1.0_01320.1.g25731.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01321.1.g25732.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01321.1.g25733.t1	dbj|BAJ34070.1| unnamed protein product [Thellungiella halophila]	455	445	0	97.8	89.9	92.1	unnamed protein product	----	----	AT1G76900.2 | Symbols: AtTLP1, TLP1 | tubby like protein 1 | chr1:28882741-28884377 FORWARD LENGTH=455	455	455	0	100.0	87.9	91.6
Rsa1.0_01321.1.g25734.t1	ref|XP_002867884.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313720|gb|EFH44143.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	176	175	5.00E-83	99.4	84.1	92.6	predicted protein	gbpln	Arabidopsis lyrata	AT4G20370.1 | Symbols: TSF | PEBP (phosphatidylethanolamine-binding protein) family protein | chr4:11001011-11002965 REVERSE LENGTH=175	176	175	9.00E-85	99.4	84.1	90.3
Rsa1.0_01321.1.g25735.t1	ref|NP_173553.1| extensin 3 [Arabidopsis thaliana] gi|334302912|sp|Q9FS16.3|EXTN3_ARATH RecName: Full=Extensin-3; Short=AtExt3; Short=AtExt5; Flags: Precursor gi|8920638|gb|AAF81360.1|AC036104_9 Contains similarity to Extensin (atExt1) from Arabidopsis thaliana gb|U43627 and contains 12 concatamers of 28 amino acids rich in proline. ESTs gb|AA597816, gb|AA712635, gb|N65860, gb|AA598180, gb|H77085, gb|AA394416, gb|AA394413, gb|AA650774, gb|AA650748, gb|Z25975, gb|AA597958, gb|AA597955 come from this gene [Arabidopsis thaliana] gi|332191962|gb|AEE30083.1| extensin 3 [Arabidopsis thaliana]	343	431	4.00E-51	125.7	85.4	87.2	extensin 3	gbpln	Arabidopsis thaliana	AT1G21310.1 | Symbols: ATEXT3, RSH, EXT3 | extensin 3 | chr1:7453693-7454988 REVERSE LENGTH=431	343	431	1.00E-53	125.7	85.4	87.2
Rsa1.0_01321.1.g25736.t3	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	610	1274	1.00E-151	208.9	50.2	65.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	610	154	1.00E-29	25.2	10.3	14.9
Rsa1.0_01321.1.g25737.t1	ref|NP_565144.1| regulator of chromosome condensation and FYVE zinc finger domain-containing protein [Arabidopsis thaliana] gi|15811367|gb|AAL08940.1| zinc finger protein [Arabidopsis thaliana] gi|332197787|gb|AEE35908.1| regulator of chromosome condensation and FYVE zinc finger domain-containing protein [Arabidopsis thaliana]	1320	1103	0	83.6	74.5	78.5	regulator of chromosome condensation and FYVE zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT1G76950.1 | Symbols: PRAF1 | Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain | chr1:28906952-28911325 FORWARD LENGTH=1103	1320	1103	0	83.6	74.5	78.5
Rsa1.0_01322.1.g25738.t4	#	#	#	#	#	#	#	–	----	----	AT5G27750.1 | Symbols: | F-box/FBD-like domains containing protein | chr5:9828430-9829981 FORWARD LENGTH=459	66	459	5.00E-13	695.5	53.0	54.5
Rsa1.0_01322.1.g25739.t3	ref|NP_172830.1| putative inactive purple acid phosphatase 1 [Arabidopsis thaliana] gi|75264050|sp|Q9LMX4.1|PPA1_ARATH RecName: Full=Probable inactive purple acid phosphatase 1; Flags: Precursor gi|8920580|gb|AAF81302.1|AC027656_19 Strong similarity to a hypothetical protein F13M23.30 gi|7485455 from Arabidopsis thaliana BAC F13M23 gb|AL035523. It contains a purple acid phosphatase domain PF|02227 [Arabidopsis thaliana] gi|20466209|gb|AAM20422.1| unknown protein [Arabidopsis thaliana] gi|24899849|gb|AAN65139.1| unknown protein [Arabidopsis thaliana] gi|55982669|gb|AAV69752.1| putative purple acid phosphatase [Arabidopsis thaliana] gi|332190942|gb|AEE29063.1| putative inactive purple acid phosphatase 1 [Arabidopsis thaliana]	610	613	0	100.5	77.9	86.9	putative inactive purple acid phosphatase 1	gbpln	Arabidopsis thaliana	AT1G13750.1 | Symbols: | Purple acid phosphatases superfamily protein | chr1:4715490-4718091 REVERSE LENGTH=613	610	613	0	100.5	77.9	86.9

Rsa1.0_01322.1.g25740.t1	gb|AAL07175.1| unknown protein [Arabidopsis thaliana]	333	348	1.00E-109	104.5	72.1	78.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G13740.1 | Symbols: AFP2 | ABI five binding protein 2 | chr1:4713969-4715158 FORWARD LENGTH=348	333	348	1.00E-111	104.5	72.1	78.7
Rsa1.0_01322.1.g25741.t1	ref|XP_002890018.1| nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata] gi|297335860|gb|EFH66277.1| nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata]	400	438	1.00E-153	109.5	75.3	86.8	nuclear transport factor 2 family protein	gbpln	Arabidopsis lyrata	AT1G13730.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr1:4710519-4712332 FORWARD LENGTH=428	400	428	1.00E-151	107.0	73.0	83.0
Rsa1.0_01322.1.g25742.t1	gb|EOA40155.1| hypothetical protein CARUB_v10008872mg [Capsella rubella]	457	516	0	112.9	84.2	91.7	hypothetical protein CARUB_v10008872mg	gbpln	Capsella rubella	AT1G13710.1 | Symbols: CYP78A5, KLU | cytochrome P450, family 78, subfamily A, polypeptide 5 | chr1:4702932-4704592 REVERSE LENGTH=517	457	517	0	113.1	84.9	89.9
Rsa1.0_01322.1.g25743.t2	ref|XP_002892767.1| glucosamine/galactosamine-6-phosphate isomerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338609|gb|EFH69026.1| glucosamine/galactosamine-6-phosphate isomerase family protein [Arabidopsis lyrata subsp. lyrata]	288	268	1.00E-113	93.1	73.6	79.9	glucosamine/galactosamine-6-phosphate isomerase family protein	gbpln	Arabidopsis lyrata	AT1G13700.1 | Symbols: PGL1 | 6-phosphogluconolactonase 1 | chr1:4694475-4695600 REVERSE LENGTH=268	288	268	1.00E-115	93.1	74.3	78.8
Rsa1.0_01322.1.g25744.t1	gb|EOA37141.1| hypothetical protein CARUB_v10010435mg [Capsella rubella]	181	177	2.00E-88	97.8	87.3	89.5	hypothetical protein CARUB_v10010435mg	gbpln	Capsella rubella	AT1G13690.1 | Symbols: ATE1 | ATPase E1 | chr1:4693380-4694179 FORWARD LENGTH=177	181	177	2.00E-89	97.8	86.2	89.0
Rsa1.0_01322.1.g25745.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01322.1.g25746.t4	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1300	1274	0	98.0	40.9	56.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1300	575	2.00E-54	44.2	12.1	18.4
Rsa1.0_01322.1.g25747.t1	ref|NP_172824.3| phospholipase C/ phosphoric diester hydrolase [Arabidopsis thaliana] gi|8920573|gb|AAF81295.1|AC027656_12 Contains similarity to MAP3K-like protein kinase from Arabidopsis thaliana gb|Z99707 [Arabidopsis thaliana] gi|332190936|gb|AEE29057.1| phospholipase C/ phosphoric diester hydrolase [Arabidopsis thaliana]	347	346	1.00E-161	99.7	77.8	87.6	phospholipase C/ phosphoric diester hydrolase	gbpln	Arabidopsis thaliana	AT1G13680.1 | Symbols: | PLC-like phosphodiesterases superfamily protein | chr1:4690409-4692702 FORWARD LENGTH=346	347	346	1.00E-163	99.7	77.8	87.6
Rsa1.0_01322.1.g25748.t2	ref|XP_002890015.1| hypothetical protein ARALYDRAFT_888738 [Arabidopsis lyrata subsp. lyrata] gi|297335857|gb|EFH66274.1| hypothetical protein ARALYDRAFT_888738 [Arabidopsis lyrata subsp. lyrata]	242	222	1.00E-70	91.7	64.0	70.7	hypothetical protein ARALYDRAFT_888738	gbpln	Arabidopsis lyrata	AT1G13670.1 | Symbols: | unknown protein; Has 22 Blast hits to 22 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4688201-4688878 FORWARD LENGTH=225	242	225	9.00E-72	93.0	62.0	69.8
Rsa1.0_01323.1.g25749.t1	ref|XP_002886292.1| ROOTY/SUPERROOT1 [Arabidopsis lyrata subsp. lyrata] gi|297332132|gb|EFH62551.1| ROOTY/SUPERROOT1 [Arabidopsis lyrata subsp. lyrata]	456	462	0	101.3	88.6	94.1	ROOTY/SUPERROOT 1	gbpln	Arabidopsis lyrata	AT2G20610.1 | Symbols: SUR1, HLS3, RTY, ALF1, RTY1 | Tyrosine transaminase family protein | chr2:8878150-8880298 REVERSE LENGTH=462	456	462	0	101.3	88.4	93.9
Rsa1.0_01323.1.g25750.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	294	329	1.00E-44	111.9	34.0	46.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	294	575	7.00E-28	195.6	21.1	41.2
Rsa1.0_01323.1.g25751.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	651	1374	1.00E-161	211.1	44.1	65.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	651	626	9.00E-23	96.2	13.5	25.5
Rsa1.0_01323.1.g25752.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01323.1.g25753.t1	gb|EOA31768.1| hypothetical protein CARUB_v10014989mg [Capsella rubella]	106	97	8.00E-37	91.5	76.4	81.1	hypothetical protein CARUB_v10014989mg	gbpln	Capsella rubella	AT2G20585.3 | Symbols: NFD6 | nuclear fusion defective 6 | chr2:8865222-8866097 FORWARD LENGTH=95	106	95	5.00E-33	89.6	77.4	81.1

Rsa1.0_01323.1.g25754.t1	ref|NP_565477.1| 26S proteasome regulatory subunit N1 [Arabidopsis thaliana] gi|75265911|sp|Q9SIV2.2|RPN1A_ARATH RecName: Full=26S proteasome non-ATPase regulatory subunit 2 1A; AltName: Full=26S proteasome regulatory subunit RPN1 A; Short=AtRPN1a; AltName: Full=26S proteasome regulatory subunit S2 1A gi|13430608|gb|AAK25926.1|AF360216_1 putative 26S proteasome regulatory subunit S2 [Arabidopsis thaliana] gi|14532874|gb|AAK64119.1| putative 26S proteasome regulatory subunit S2 [Arabidopsis thaliana] gi|20198043|gb|AAD21708.2| 26S proteasome regulatory subunit S2 (RPN1) [Arabidopsis thaliana] gi|32700010|gb|AAP86655.1| 26S proteasome subunit RPN1a [Arabidopsis thaliana] gi|330251938|gb|AEC07032.1| 26S proteasome regulatory subunit S2 1A [Arabidopsis thaliana]	825	891	0	108.0	95.4	98.8	26S proteasome regulatory subunit N1	gbpln	Arabidopsis thaliana	AT2G20580.1 | Symbols: RPN1A, ATRPN1A | 26S proteasome regulatory subunit S2 1A | chr2:8859211-8864699 FORWARD LENGTH=891	825	891	0	108.0	95.4	98.8
Rsa1.0_01323.1.g25755.t1	ref|XP_002884211.1| hypothetical protein ARALYDRAFT_480887 [Arabidopsis lyrata subsp. lyrata] gi|297330051|gb|EFH60470.1| hypothetical protein ARALYDRAFT_480887 [Arabidopsis lyrata subsp. lyrata]	433	412	1.00E-158	95.2	77.8	83.6	hypothetical protein ARALYDRAFT_480887	gbpln	Arabidopsis lyrata	AT2G20570.1 | Symbols: GPRI1, GLK1, ATGLK1 | GBF's pro-rich region-interacting factor 1 | chr2:8855486-8857522 FORWARD LENGTH=420	433	420	1.00E-159	97.0	79.2	85.5
Rsa1.0_01324.1.g25756.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01324.1.g25757.t8	gb|EOA28805.1| hypothetical protein CARUB_v10025037mg [Capsella rubella]	340	509	4.00E-38	149.7	27.1	45.3	hypothetical protein CARUB_v10025037mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	340	566	3.00E-33	166.5	25.6	42.6
Rsa1.0_01324.1.g25758.t2	gb|EOA22562.1| hypothetical protein CARUB_v10003223mg [Capsella rubella]	1070	752	0	70.3	36.5	47.1	hypothetical protein CARUB_v10003223mg	gbpln	Capsella rubella	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1070	331	6.00E-49	30.9	8.5	11.9
Rsa1.0_01324.1.g25759.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01324.1.g25760.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01324.1.g25761.t4	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1523	1529	0	100.4	33.3	46.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1523	746	1.00E-52	49.0	8.5	11.6
Rsa1.0_01324.1.g25762.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1785	1274	0	71.4	38.5	49.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1785	575	8.00E-64	32.2	9.5	15.0
Rsa1.0_01324.1.g25763.t5	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	886	1225	7.00E-62	138.3	14.9	21.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01324.1.g25764.t1	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	150	326	5.00E-12	217.3	28.7	43.3	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01325.1.g25765.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01325.1.g25766.t1	sp|Q06209.2|CHI4_BRANA RecName: Full=Basic endochitinase CHB4; Flags: Precursor gi|17799|emb|CAA43708.1| chitinase [Brassica napus] gi|218436742|dbj|BAH03380.1| chitinase [Brassica rapa subsp. chinensis] gi|244539521|dbj|BAH82668.1| class IV chitinase [Brassica rapa subsp. chinensis]	270	268	1.00E-139	99.3	95.2	95.9	RecName: Full=Basic endochitinase CHB4; Flags: Precursor gi|17799|emb|CAA43708.1| chitinase	gbpln	Brassica napus	AT2G43590.1 | Symbols: | Chitinase family protein | chr2:18081592-18082749 REVERSE LENGTH=264	270	264	1.00E-129	97.8	87.8	90.7
Rsa1.0_01325.1.g25767.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01325.1.g25768.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	585	1239	1.00E-149	211.8	42.1	48.5	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	585	1262	3.00E-46	215.7	16.6	25.5
Rsa1.0_01325.1.g25769.t1	gb|EOA27703.1| hypothetical protein CARUB_v10023857mg [Capsella rubella]	260	265	1.00E-112	101.9	75.4	83.5	hypothetical protein CARUB_v10023857mg	gbpln	Capsella rubella	AT2G43580.1 | Symbols: | Chitinase family protein | chr2:18078817-18080013 REVERSE LENGTH=265	260	265	1.00E-113	101.9	78.8	86.2
Rsa1.0_01325.1.g25770.t1	gb|EOA26406.1| hypothetical protein CARUB_v10023814mg [Capsella rubella]	278	279	1.00E-127	100.4	82.4	88.8	hypothetical protein CARUB_v10023814mg	gbpln	Capsella rubella	AT2G43570.1 | Symbols: CHI | chitinase, putative | chr2:18076389-18077435 REVERSE LENGTH=277	278	277	1.00E-104	99.6	69.4	78.4

Rsa1.0_01326.1.g25771.t1	ref|XP_002889707.1| hypothetical protein ARALYDRAFT_888100 [Arabidopsis lyrata subsp. lyrata] gi|297335549|gb|EFH65966.1| hypothetical protein ARALYDRAFT_888100 [Arabidopsis lyrata subsp. lyrata]	287	284	1.00E-155	99.0	89.5	95.5	hypothetical protein ARALYDRAFT_888100	gbpln	Arabidopsis lyrata	AT1G08650.1 | Symbols: PPCK1, ATPPCK1 | phosphoenolpyruvate carboxylase kinase 1 | chr1:2752206-2753232 FORWARD LENGTH=284	287	284	1.00E-154	99.0	88.5	94.1
Rsa1.0_01326.1.g25772.t4	ref|XP_002892466.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297338308|gb|EFH68725.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	237	294	5.00E-88	124.1	67.9	71.7	heat shock protein binding protein	gbpln	Arabidopsis lyrata	AT1G08640.1 | Symbols: CJD1 | Chloroplast J-like domain 1 | chr1:2748714-2751209 REVERSE LENGTH=294	237	294	7.00E-90	124.1	67.1	72.2
Rsa1.0_01326.1.g25773.t1	ref|NP_563822.1| threonine aldolase [Arabidopsis thaliana] gi|30680733|ref|NP_849614.1| threonine aldolase [Arabidopsis thaliana] gi|30680739|ref|NP_849615.1| threonine aldolase [Arabidopsis thaliana] gi|145322987|ref|NP_001031001.2| threonine aldolase [Arabidopsis thaliana] gi|19347791|gb|AAL86346.1| unknown protein [Arabidopsis thaliana] gi|21436111|gb|AAM51302.1| unknown protein [Arabidopsis thaliana] gi|110739988|dbj|BAF01898.1| hypothetical protein [Arabidopsis thaliana] gi|332190199|gb|AEE28320.1| threonine aldolase [Arabidopsis thaliana] gi|332190200|gb|AEE28321.1| threonine aldolase [Arabidopsis thaliana] gi|332190201|gb|AEE28322.1| threonine aldolase [Arabidopsis thaliana] gi|332190202|gb|AEE28323.1| threonine aldolase [Arabidopsis thaliana]	328	358	1.00E-169	109.1	89.0	93.6	threonine aldolase	gbpln	Arabidopsis thaliana	AT1G08630.4 | Symbols: THA1 | threonine aldolase 1 | chr1:2743948-2745685 REVERSE LENGTH=358	328	358	1.00E-171	109.1	89.0	93.6
Rsa1.0_01326.1.g25774.t1	ref|XP_002889706.1| transcription factor jumonji family protein [Arabidopsis lyrata subsp. lyrata] gi|297335548|gb|EFH65965.1| transcription factor jumonji family protein [Arabidopsis lyrata subsp. lyrata]	1177	1209	0	102.7	83.2	89.7	transcription factor jumonji family protein	gbpln	Arabidopsis lyrata	AT1G08620.2 | Symbols: PKDM7D | Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein | chr1:2737554-2743370 FORWARD LENGTH=1209	1177	1209	0	102.7	83.2	90.3
Rsa1.0_01326.1.g25775.t1	ref|NP_172335.1| leucine-rich receptor-like protein kinase-like protein [Arabidopsis thaliana] gi|75262900|sp|Q9FRS6.1|PXL1_ARATH RecName: Full=Leucine-rich repeat receptor-like protein kinase PXL1; AltName: Full=Protein PHLOEM INTERCALATED WITH XYLEM-LIKE 1; Flags: Precursor gi|9802553|gb|AAF99755.1|AC003981_5 F22O13.7 [Arabidopsis thaliana] gi|224589384|gb|ACN59226.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332190191|gb|AEE28312.1| leucine-rich repeat receptor-like protein kinase PXL1 [Arabidopsis thaliana]	1029	1029	0	100.0	87.9	92.9	leucine-rich receptor-like protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G08590.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr1:2718859-2721948 FORWARD LENGTH=1029	1029	1029	0	100.0	87.9	92.9
Rsa1.0_01326.1.g25776.t1	ref|XP_002892462.1| SYP111 [Arabidopsis lyrata subsp. lyrata] gi|297338304|gb|EFH68721.1| SYP111 [Arabidopsis lyrata subsp. lyrata]	306	310	1.00E-136	101.3	85.0	92.5	SYP111	gbpln	Arabidopsis lyrata	AT1G08560.1 | Symbols: SYP111, KN, ATSYP111 | syntaxin of plants 111 | chr1:2709778-2710710 REVERSE LENGTH=310	306	310	1.00E-137	101.3	84.6	92.8
Rsa1.0_01326.1.g25777.t1	emb|CAB83106.1| sigma factor 2 [Sinapis alba]	580	575	0	99.1	88.4	92.9	sigma factor 2	gbpln	Sinapis alba	AT1G08540.1 | Symbols: SIGB, SIG1, SIG2, SIGA, ATSIG1, ABC1, ATSIG2 | RNApolymerase sigma subunit 2 | chr1:2703461-2706696 FORWARD LENGTH=572	580	572	0	98.6	84.8	90.0
Rsa1.0_01326.1.g25778.t1	gb|AGG14201.1| palmitoyl-ACP-thioesterase [Brassica napus]	415	415	0	100.0	93.7	97.3	palmitoyl-ACP-thioesterase	gbpln	Brassica napus	AT1G08510.1 | Symbols: FATB | fatty acyl-ACP thioesterases B | chr1:2691546-2693409 REVERSE LENGTH=412	415	412	0	99.3	84.8	91.6
Rsa1.0_01326.1.g25779.t1	gb|EOA37063.1| hypothetical protein CARUB_v10010188mg [Capsella rubella]	234	232	1.00E-97	99.1	76.5	84.2	hypothetical protein CARUB_v10010188mg	gbpln	Capsella rubella	AT1G08500.1 | Symbols: ENODL18, AtENODL18 | early nodulin-like protein 18 | chr1:2689110-2689881 FORWARD LENGTH=228	234	228	1.00E-96	97.4	76.9	82.1

Rsa1.0_01326.1.g25780.t2	gb|EOA37187.1| hypothetical protein CARUB_v10010583mg [Capsella rubella]	183	145	6.00E−58	79.2	64.5	68.9	hypothetical protein CARUB_v10010583mg	gbpln	Capsella rubella	AT1G08480.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, plasma membrane, plastid, vacuole; EXPRESSED IN: 27 plant structures; EXPRESSED DURING: 15 growth stages; Has 39 Blast hits to 39 proteins in 13 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 39; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:2684340−2685395 FORWARD LENGTH=142	183	142	3.00E−58	77.6	62.8	67.2
Rsa1.0_01326.1.g25781.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01327.1.g25782.t1	ref|XP_002873724.1| APG6/CLPB−P/CLPB3 [Arabidopsis lyrata subsp. lyrata] gi|297319561|gb|EFH49983.1| APG6/CLPB−P/CLPB3 [Arabidopsis lyrata subsp. lyrata]	250	972	2.00E−44	388.8	36.8	40.0	APG6/CLPB−P/CLPB3	gbpln	Arabidopsis lyrata	AT5G15450.1 | Symbols: APG6, CLPB3, CLPB−P | casein lytic proteinase B3 | chr5:5014399−5018255 REVERSE LENGTH=968	250	968	9.00E−47	387.2	36.4	40.4
Rsa1.0_01327.1.g25783.t1	ref|NP_172797.2| C2H2 and C2HC zinc finger protein [Arabidopsis thaliana] gi|75324672|sp|Q6S592.1|JGL_ARATH RecName: Full=Zinc finger protein JAGGED−like; AltName: Full=Zinc finger protein NUBBIN gi|39726196|gb|AAR30035.1| JAGGED−like [Arabidopsis thaliana] gi|332190891|gb|AEE29012.1| zinc finger protein JAGGED−like/NUBBIN [Arabidopsis thaliana]	191	207	1.00E−35	108.4	48.2	54.5	C2H2 and C2HC zinc finger protein	gbpln	Arabidopsis thaliana	AT1G13400.1 | Symbols: NUB, JGL | C2H2 and C2HC zinc fingers superfamily protein | chr1:4597784−4598911 FORWARD LENGTH=207	191	207	4.00E−38	108.4	48.2	54.5
Rsa1.0_01327.1.g25784.t1	gb|EOA39904.1| hypothetical protein CARUB_v10008584mg [Capsella rubella]	529	625	0	118.1	80.7	90.4	hypothetical protein CARUB_v10008584mg	gbpln	Capsella rubella	AT1G13410.1 | Symbols: | Tetratricopeptide repeat (TPR)−like superfamily protein | chr1:4601526−4603174 FORWARD LENGTH=474	529	474	0	89.6	68.4	76.4
Rsa1.0_01327.1.g25785.t1	sp|P04796.2|G3PC_SINAL RecName: Full=Glyceraldehyde−3−phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product [Sinapis alba]	338	338	0	100.0	99.4	100.0	RecName: Full=Glyceraldehyde−3−phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product	gbpln	Sinapis alba	AT3G04120.1 | Symbols: GAPC, GAPC−1, GAPC1 | glyceraldehyde−3−phosphate dehydrogenase C subunit 1 | chr3:1081077−1083131 FORWARD LENGTH=338	338	338	0	100.0	97.0	99.1
Rsa1.0_01327.1.g25786.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01327.1.g25787.t1	ref|XP_002892756.1| hypothetical protein ARALYDRAFT_312360 [Arabidopsis lyrata subsp. lyrata] gi|297338598|gb|EFH69015.1| hypothetical protein ARALYDRAFT_312360 [Arabidopsis lyrata subsp. lyrata]	383	772	0	201.6	81.5	90.3	hypothetical protein ARALYDRAFT_312360	gbpln	Arabidopsis lyrata	AT1G13520.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4631857−4633223 REVERSE LENGTH=387	383	387	0	101.0	83.6	90.9
Rsa1.0_01327.1.g25788.t1	ref|NP_172692.1| LRR and NB−ARC domain−containing disease resistance protein [Arabidopsis thaliana] gi|46395647|sp|P60838.1|DRL1_ARATH RecName: Full=Probable disease resistance protein At1g12280 gi|332190740|gb|AEE28861.1| probable disease resistance protein [Arabidopsis thaliana]	888	894	0	100.7	77.0	87.5	LRR and NB−ARC domain−containing disease resistance protein	gbpln	Arabidopsis thaliana	AT1G12280.1 | Symbols: | LRR and NB−ARC domains−containing disease resistance protein | chr1:4174875−4177559 REVERSE LENGTH=894	888	894	0	100.7	77.0	87.5
Rsa1.0_01327.1.g25789.t1	ref|NP_199182.1| sulfotransferase family protein [Arabidopsis thaliana] gi|75262427|sp|Q9FG94.1|SOT1_ARATH RecName: Full=Cytosolic sulfotransferase 1; Short=AtSOT1 gi|10177937|dbj|BAB11296.1| steroid sulfotransferase−like [Arabidopsis thaliana] gi|38566684|gb|AAR24232.1| At5g43690 [Arabidopsis thaliana] gi|51536530|gb|AAU05503.1| At5g43690 [Arabidopsis thaliana] gi|332007613|gb|AED94996.1| sulfotransferase 1 [Arabidopsis thaliana]	344	331	1.00E−94	96.2	54.1	63.1	sulfotransferase family protein	gbpln	Arabidopsis thaliana	AT5G43690.1 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273−17547268 FORWARD LENGTH=331	344	331	4.00E−97	96.2	54.1	63.1
Rsa1.0_01327.1.g25790.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01327.1.g25791.t1	ref|XP_002892776.1| hypothetical protein ARALYDRAFT_471542 [Arabidopsis lyrata subsp. lyrata] gi|297338618|gb|EFH69035.1| hypothetical protein ARALYDRAFT_471542 [Arabidopsis lyrata subsp. lyrata]	173	199	6.00E−56	115.0	78.6	84.4	hypothetical protein ARALYDRAFT_471542	gbpln	Arabidopsis lyrata	AT1G13830.1 | Symbols: | Carbohydrate−binding X8 domain superfamily protein | chr1:4739999−4740926 REVERSE LENGTH=197	173	197	1.00E−49	113.9	72.3	78.6

<table>
<tr><td>Rsa1.0_01327.1.g25792.t1</td><td>gb|EOA38350.1| hypothetical protein CARUB_v10009863mg [Capsella rubella]</td><td>225</td><td>302</td><td>1.00E-111</td><td>134.2</td><td>88.0</td><td>95.6</td><td>hypothetical protein CARUB_v10009863mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G13870.1 | Symbols: DRL1, AtKTI12 | calmodulin binding;purine nucleotide binding | chr1:4747437-4748345 REVERSE LENGTH=302</td><td>225</td><td>302</td><td>1.00E-111</td><td>134.2</td><td>86.7</td><td>93.8</td></tr>
<tr><td>Rsa1.0_01327.1.g25793.t1</td><td>ref|XP_002890025.1| ELM2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335867|gb|EFH66284.1| ELM2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>439</td><td>423</td><td>1.00E-159</td><td>96.4</td><td>64.7</td><td>72.7</td><td>ELM2 domain-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G13880.1 | Symbols: | ELM2 domain-containing protein | chr1:4749603-4750967 FORWARD LENGTH=424</td><td>439</td><td>424</td><td>1.00E-157</td><td>96.6</td><td>62.9</td><td>72.0</td></tr>
<tr><td>Rsa1.0_01327.1.g25794.t1</td><td>ref|XP_002892756.1| hypothetical protein ARALYDRAFT_312360 [Arabidopsis lyrata subsp. lyrata] gi|297338598|gb|EFH69015.1| hypothetical protein ARALYDRAFT_312360 [Arabidopsis lyrata subsp. lyrata]</td><td>305</td><td>772</td><td>1.00E-127</td><td>253.1</td><td>73.8</td><td>81.6</td><td>hypothetical protein ARALYDRAFT_312360</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G13520.1 | Symbols: | Protein of unknown function (DUF1262) | chr1:4631857-4633223 REVERSE LENGTH=387</td><td>305</td><td>387</td><td>1.00E-124</td><td>126.9</td><td>75.1</td><td>81.0</td></tr>
<tr><td>Rsa1.0_01327.1.g25795.t1</td><td>ref|XP_002891048.1| hypothetical protein ARALYDRAFT_473526 [Arabidopsis lyrata subsp. lyrata] gi|297336890|gb|EFH67307.1| hypothetical protein ARALYDRAFT_473526 [Arabidopsis lyrata subsp. lyrata]</td><td>180</td><td>798</td><td>6.00E-54</td><td>443.3</td><td>60.0</td><td>70.6</td><td>hypothetical protein ARALYDRAFT_473526</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G47280.1 | Symbols: ADR1-L3 | ADR1-like 3 | chr5:19193157-19195559 FORWARD LENGTH=623</td><td>180</td><td>623</td><td>4.00E-54</td><td>346.1</td><td>55.0</td><td>69.4</td></tr>
<tr><td>Rsa1.0_01327.1.g25796.t1</td><td>gb|EOA36691.1| hypothetical protein CARUB_v10012096mg [Capsella rubella]</td><td>300</td><td>327</td><td>1.00E-116</td><td>109.0</td><td>66.3</td><td>81.7</td><td>hypothetical protein CARUB_v10012096mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G43690.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273-17547268 FORWARD LENGTH=331</td><td>300</td><td>331</td><td>1.00E-118</td><td>110.3</td><td>67.0</td><td>80.7</td></tr>
<tr><td>Rsa1.0_01328.1.g25797.t1</td><td>ref|NP_172472.1| amino acid permease 8 [Arabidopsis thaliana] gi|75223207|sp|O80592.1|AAP8_ARATH RecName: Full=Amino acid permease 8; AltName: Full=Amino acid transporter AAP8 gi|3540179|gb|AAC34329.1| putative amino acid permease [Arabidopsis thaliana] gi|332190407|gb|AEE28528.1| amino acid permease 8 [Arabidopsis thaliana]</td><td>478</td><td>475</td><td>0</td><td>99.4</td><td>83.3</td><td>91.8</td><td>amino acid permease 8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10010.1 | Symbols: AAP8, ATAAP8 | amino acid permease 8 | chr1:3265976-3268726 FORWARD LENGTH=475</td><td>478</td><td>475</td><td>0</td><td>99.4</td><td>83.3</td><td>91.8</td></tr>
<tr><td>Rsa1.0_01328.1.g25798.t1</td><td>ref|XP_002892543.1| hypothetical protein ARALYDRAFT_888260 [Arabidopsis lyrata subsp. lyrata] gi|297338385|gb|EFH68802.1| hypothetical protein ARALYDRAFT_888260 [Arabidopsis lyrata subsp. lyrata]</td><td>465</td><td>461</td><td>0</td><td>99.1</td><td>85.2</td><td>88.2</td><td>hypothetical protein ARALYDRAFT_888260</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10020.1 | Symbols: | Protein of unknown function (DUF1005) | chr1:3269939-3271732 REVERSE LENGTH=461</td><td>465</td><td>461</td><td>0</td><td>99.1</td><td>85.4</td><td>88.6</td></tr>
<tr><td>Rsa1.0_01328.1.g25799.t1</td><td>gb|EOA36321.1| hypothetical protein CARUB_v10010632mg [Capsella rubella]</td><td>97</td><td>129</td><td>2.00E-43</td><td>133.0</td><td>89.7</td><td>92.8</td><td>hypothetical protein CARUB_v10010632mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G10030.1 | Symbols: ERG28 | homolog of yeast ergosterol28 | chr1:3273972-3275631 FORWARD LENGTH=129</td><td>97</td><td>129</td><td>1.00E-44</td><td>133.0</td><td>87.6</td><td>89.7</td></tr>
<tr><td>Rsa1.0_01328.1.g25800.t1</td><td>ref|XP_002889788.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335630|gb|EFH66047.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>387</td><td>383</td><td>0</td><td>99.0</td><td>87.1</td><td>92.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10060.2 | Symbols: ATBCAT-1, BCAT-1 | branched-chain amino acid transaminase 1 | chr1:3284445-3286837 FORWARD LENGTH=384</td><td>387</td><td>384</td><td>0</td><td>99.2</td><td>87.3</td><td>93.3</td></tr>
<tr><td>Rsa1.0_01328.1.g25801.t1</td><td>ref|NP_172478.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|79317492|ref|NP_001031015.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|26391680|sp|Q9M439.1|BCAT2_ARATH RecName: Full=Branched-chain-amino-acid aminotransferase 2, chloroplastic; Short=Atbcat-2; Flags: Precursor gi|13877745|gb|AAK43950.1|AF370135_1 putative tat-binding protein [Arabidopsis thaliana] gi|8249004|emb|CAB93128.1| branched-chain amino acid transaminase [Arabidopsis thaliana] gi|15293209|gb|AAK93715.1| putative tat-binding protein [Arabidopsis thaliana] gi|222424474|dbj|BAH20192.1| AT1G10070 [Arabidopsis thaliana] gi|332190416|gb|AEE28537.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|332190417|gb|AEE28538.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana]</td><td>387</td><td>388</td><td>0</td><td>100.3</td><td>88.4</td><td>95.1</td><td>branched-chain-amino-acid aminotransferase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G10070.2 | Symbols: ATBCAT-2, BCAT-2 | branched-chain amino acid transaminase 2 | chr1:3288255-3290164 FORWARD LENGTH=388</td><td>387</td><td>388</td><td>0</td><td>100.3</td><td>88.4</td><td>95.1</td></tr>
</table>

Rsa1.0_01328.1.g25802.t1	gb|EOA38044.1| hypothetical protein CARUB_v10009514mg [Capsella rubella]	331	365	1.00E-150	110.3	86.4	89.7	hypothetical protein CARUB_v10009514mg	gbpln	Capsella rubella	AT1G10120.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:3304228-3305984 REVERSE LENGTH=366	331	366	1.00E-144	110.6	82.2	85.5
Rsa1.0_01328.1.g25803.t1	ref|XP_002889791.1| Ca2+-ATPase [Arabidopsis lyrata subsp. lyrata] gi|297335633|gb|EFH66050.1| Ca2+-ATPase [Arabidopsis lyrata subsp. lyrata]	997	992	0	99.5	93.2	95.5	Ca2+-ATPase	gbpln	Arabidopsis lyrata	AT1G10130.1 | Symbols: ECA3, ATECA3 | endoplasmic reticulum-type calcium-transporting ATPase 3 | chr1:3311139-3321941 FORWARD LENGTH=998	997	998	0	100.1	93.0	95.2
Rsa1.0_01328.1.g25804.t1	ref|NP_563861.1| uncharacterized protein [Arabidopsis thaliana] gi|4914316|gb|AAD32864.1|AC005489_2 F14N23.2 [Arabidopsis thaliana] gi|21592444|gb|AAM64395.1| unknown [Arabidopsis thaliana] gi|107738163|gb|ABF83653.1| At1g10140 [Arabidopsis thaliana] gi|110740087|dbj|BAF01945.1| hypothetical protein [Arabidopsis thaliana] gi|332190425|gb|AEE28546.1| uncharacterized protein AT1G10140 [Arabidopsis thaliana]	172	167	2.00E-43	97.1	74.4	84.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G10140.1 | Symbols: | Uncharacterised conserved protein UCP031279 | chr1:3322970-3323473 REVERSE LENGTH=167	172	167	9.00E-46	97.1	74.4	84.3
Rsa1.0_01329.1.g25805.t1	ref|XP_002889791.1| Ca2+-ATPase [Arabidopsis lyrata subsp. lyrata] gi|297335633|gb|EFH66050.1| Ca2+-ATPase [Arabidopsis lyrata subsp. lyrata]	903	992	0	109.9	96.3	98.3	Ca2+-ATPase	gbpln	Arabidopsis lyrata	AT1G10130.1 | Symbols: ECA3, ATECA3 | endoplasmic reticulum-type calcium-transporting ATPase 3 | chr1:3311139-3321941 FORWARD LENGTH=998	903	998	0	110.5	96.1	98.0
Rsa1.0_01329.1.g25806.t1	gb|EOA38044.1| hypothetical protein CARUB_v10009514mg [Capsella rubella]	316	365	1.00E-144	115.5	87.3	90.8	hypothetical protein CARUB_v10009514mg	gbpln	Capsella rubella	AT1G10120.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:3304228-3305984 REVERSE LENGTH=366	316	366	1.00E-140	115.8	86.4	89.9
Rsa1.0_01329.1.g25807.t1	ref|NP_172478.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|79317492|ref|NP_001031015.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|26391680|sp|Q9M439.1|BCAT2_ARATH RecName: Full=Branched-chain-amino-acid aminotransferase 2, chloroplastic; Short=Atbcat-2; Flags: Precursor gi|13877745|gb|AAK43950.1|AF370135_1 putative tat-binding protein [Arabidopsis thaliana] gi|8249004|emb|CAB93128.1| branched-chain amino acid transaminase [Arabidopsis thaliana] gi|15293209|gb|AAK93715.1| putative tat-binding protein [Arabidopsis thaliana] gi|222424474|dbj|BAH20192.1| AT1G10070 [Arabidopsis thaliana] gi|332190416|gb|AEE28537.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|332190417|gb|AEE28538.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana]	377	388	1.00E-179	102.9	81.2	87.0	branched-chain-amino-acid aminotransferase 2	gbpln	Arabidopsis thaliana	AT1G10070.2 | Symbols: ATBCAT-2, BCAT-2 | branched-chain amino acid transaminase 2 | chr1:3288255-3290164 FORWARD LENGTH=388	377	388	0	102.9	81.2	87.0
Rsa1.0_01329.1.g25808.t1	gb|AAD26943.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1453	1454	0	100.1	68.3	82.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1453	1262	1.00E-178	86.9	20.8	27.1
Rsa1.0_01329.1.g25809.t1	ref|XP_002889787.1| glycosyl hydrolase family 10 protein [Arabidopsis lyrata subsp. lyrata] gi|297335629|gb|EFH66046.1| glycosyl hydrolase family 10 protein [Arabidopsis lyrata subsp. lyrata]	1089	1063	0	97.6	84.8	90.4	glycosyl hydrolase family 10 protein	gbpln	Arabidopsis lyrata	AT1G10050.1 | Symbols: | glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein | chr1:3279270-3283444 FORWARD LENGTH=1063	1089	1063	0	97.6	83.3	89.4
Rsa1.0_01329.1.g25810.t1	ref|XP_002887971.1| hypothetical protein ARALYDRAFT_893147 [Arabidopsis lyrata subsp. lyrata] gi|297333812|gb|EFH64230.1| hypothetical protein ARALYDRAFT_893147 [Arabidopsis lyrata subsp. lyrata]	188	296	8.00E-28	157.4	39.9	59.6	hypothetical protein ARALYDRAFT_893147	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01330.1.g25811.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01330.1.g25812.t1	ref|XP_002974570.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii] gi|300157465|gb|EFJ24090.1| hypothetical protein SELMODRAFT_442529 [Selaginella moellendorffii]	663	516	3.00E−38	77.8	33.5	39.8	hypothetical protein SELMODRAFT_442529	gbpln	Selaginella moellendorffii	AT4G13390.1 | Symbols: | Proline-rich extensin-like family protein | chr4:7783856-7785145 FORWARD LENGTH=429	663	429	8.00E−41	64.7	47.8	51.9
Rsa1.0_01330.1.g25813.t2	ref|XP_003603826.1| Helicase-like protein [Medicago truncatula] gi|355492874|gb|AES74077.1| Helicase-like protein [Medicago truncatula]	326	1679	4.00E−29	515.0	16.0	26.1	Helicase-like protein	gbpln	Medicago truncatula	#	#	#	#	#	#	#
Rsa1.0_01330.1.g25814.t1	ref|XP_002881777.1| hypothetical protein ARALYDRAFT_483224 [Arabidopsis lyrata subsp. lyrata] gi|297327616|gb|EFH58036.1| hypothetical protein ARALYDRAFT_483224 [Arabidopsis lyrata subsp. lyrata]	128	179	1.00E−24	139.8	49.2	52.3	hypothetical protein ARALYDRAFT_483224	gbpln	Arabidopsis lyrata	AT2G41475.1 | Symbols: | Embryo-specific protein 3, (ATS3) | chr2:17295259-17296329 REVERSE LENGTH=179	128	179	6.00E−26	139.8	46.9	50.8
Rsa1.0_01330.1.g25815.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	517	1023	1.00E−167	197.9	57.8	74.3	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	517	575	3.00E−30	111.2	11.4	17.6
Rsa1.0_01330.1.g25816.t5	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	873	871	1.00E−61	99.8	16.2	22.8	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	873	874	1.00E−31	100.1	10.3	16.0
Rsa1.0_01330.1.g25817.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01330.1.g25818.t1	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	955	915	1.00E−131	95.8	25.5	36.5	F22O13.21	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	955	719	1.00E−29	75.3	12.5	22.5
Rsa1.0_01330.1.g25819.t2	ref|NP_180252.2| uncharacterized protein [Arabidopsis thaliana] gi|26452962|dbj|BAC43557.1| unknown protein [Arabidopsis thaliana] gi|28973431|gb|AAO64040.1| unknown protein [Arabidopsis thaliana] gi|330252802|gb|AEC07896.1| uncharacterized protein AT2G26840 [Arabidopsis thaliana]	426	273	1.00E−106	64.1	45.3	51.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G26840.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G43910.1); Has 835 Blast hits to 835 proteins in 26 species: Archae - 0; Bacteria - 25; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 2; Other Eukaryotes - 768 (source: NCBI BLink). | chr2:11447346-11448871 REVERSE LENGTH=273	426	273	1.00E−109	64.1	45.3	51.2
Rsa1.0_01331.1.g25820.t10	gb|AAD29835.2| putative SNF2 subfamily transcription regulator [Arabidopsis thaliana]	3186	3571	0	112.1	44.9	49.5	putative SNF2 subfamily transcription regulator	gbpln	Arabidopsis thaliana	AT2G28290.2 | Symbols: SYD, CHR3 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:12056771-12072950 FORWARD LENGTH=3529	3186	3529	0	110.8	45.0	49.6
Rsa1.0_01331.1.g25821.t1	ref|XP_002881627.1| hypothetical protein ARALYDRAFT_345680 [Arabidopsis lyrata subsp. lyrata] gi|297327466|gb|EFH57886.1| hypothetical protein ARALYDRAFT_345680 [Arabidopsis lyrata subsp. lyrata]	368	346	1.00E−165	94.0	77.2	81.8	hypothetical protein ARALYDRAFT_345680	gbpln	Arabidopsis lyrata	AT2G39040.1 | Symbols: | Peroxidase superfamily protein | chr2:16299463-16301173 REVERSE LENGTH=350	368	350	1.00E−162	95.1	75.0	79.9
Rsa1.0_01331.1.g25822.t1	ref|XP_002879780.1| hypothetical protein ARALYDRAFT_482921 [Arabidopsis lyrata subsp. lyrata] gi|297325619|gb|EFH56039.1| hypothetical protein ARALYDRAFT_482921 [Arabidopsis lyrata subsp. lyrata]	229	235	1.00E−108	102.6	85.2	88.2	hypothetical protein ARALYDRAFT_482921	gbpln	Arabidopsis lyrata	AT2G39020.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr2:16295392-16296102 FORWARD LENGTH=236	229	236	1.00E−110	103.1	84.3	87.8
Rsa1.0_01331.1.g25823.t1	gb|ABL97985.1| water channel protein [Brassica rapa]	288	288	1.00E−164	100.0	98.6	100.0	water channel protein	gbpln	Brassica rapa	AT2G39010.1 | Symbols: PIP2E, PIP2;6 | plasma membrane intrinsic protein 2E | chr2:16291564-16293746 FORWARD LENGTH=289	288	289	1.00E−157	100.3	93.1	95.8
Rsa1.0_01331.1.g25824.t2	#	#	#	#	#	#	#	–	----	----	AT2G39000.2 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr2:16286647-16287941 REVERSE LENGTH=228	100	228	8.00E−11	228.0	27.0	32.0
Rsa1.0_01331.1.g25825.t1	ref|NP_001189709.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana] gi|330254528|gb|AEC09622.1| O-acyltransferase (WSD1-like) family protein [Arabidopsis thaliana]	471	487	0	103.4	75.8	86.6	O-acyltransferase (WSD1-like) family protein	gbpln	Arabidopsis thaliana	AT2G38995.2 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr2:16282139-16284700 FORWARD LENGTH=487	471	487	0	103.4	75.8	86.6

Rsa1.0_01332.1.g25826.t1	gb|EOA37859.1| hypothetical protein CARUB_v10011456mg [Capsella rubella]	247	310	1.00E-117	125.5	81.8	90.3	hypothetical protein CARUB_v10011456mg	gbpln	Capsella rubella	AT1G27030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27020.1); Has 504 Blast hits to 502 proteins in 169 species: Archae - 0; Bacteria - 299; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 138 (source: NCBI BLink). | chr1:9381842-9383712 FORWARD LENGTH=310	247	310	1.00E-111	125.5	76.9	88.3
Rsa1.0_01332.1.g25827.t1	ref|XP_002890621.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336463|gb|EFH66880.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	559	578	0	103.4	79.6	89.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G27040.1 | Symbols: | Major facilitator superfamily protein | chr1:9386893-9390018 REVERSE LENGTH=567	559	567	0	101.4	77.3	87.1
Rsa1.0_01332.1.g25828.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01332.1.g25829.t1	gb|AAF79854.1|AC000348_7 T7N9.11 [Arabidopsis thaliana]	205	495	1.00E-71	241.5	76.6	81.5	T7N9.11	gbpln	Arabidopsis thaliana	AT1G27050.1 | Symbols: ATHB54, HB54 | homeobox protein 54 | chr1:9393706-9394408 FORWARD LENGTH=205	205	205	5.00E-73	100.0	76.6	81.5
Rsa1.0_01332.1.g25830.t1	gb|EOA37541.1| hypothetical protein CARUB_v10011778mg [Capsella rubella]	567	579	0	102.1	76.2	88.2	hypothetical protein CARUB_v10011778mg	gbpln	Capsella rubella	AT1G27080.1 | Symbols: NRT1.6 | nitrate transporter 1.6 | chr1:9400664-9403789 FORWARD LENGTH=576	567	576	0	101.6	77.1	89.1
Rsa1.0_01332.1.g25831.t2	gb|EOA40157.1| hypothetical protein CARUB_v10008874mg [Capsella rubella]	1095	515	1.00E-154	47.0	27.5	31.8	hypothetical protein CARUB_v10008874mg	gbpln	Capsella rubella	AT1G27100.1 | Symbols: | Actin cross-linking protein | chr1:9407557-9411074 REVERSE LENGTH=519	1095	519	1.00E-151	47.4	27.2	31.5
Rsa1.0_01332.1.g25832.t1	gb|EOA40157.1| hypothetical protein CARUB_v10008874mg [Capsella rubella]	867	515	1.00E-160	59.4	36.0	39.8	hypothetical protein CARUB_v10008874mg	gbpln	Capsella rubella	AT1G27100.1 | Symbols: | Actin cross-linking protein | chr1:9407557-9411074 REVERSE LENGTH=519	867	519	1.00E-158	59.9	35.6	39.3
Rsa1.0_01332.1.g25833.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01333.1.g25834.t1	ref|NP_192059.4| AP2/B3-like transcriptional factor family protein [Arabidopsis thaliana] gi|334302839|sp|O82595.2|NGA4_ARATH RecName: Full=B3 domain-containing transcription factor NGA4; AltName: Full=Protein NGATHA 4 gi|332656633|gb|AEE82033.1| AP2/B3-like transcriptional factor family protein [Arabidopsis thaliana]	318	333	1.00E-110	104.7	70.4	79.9	AP2/B3-like transcriptional factor family protein	gbpln	Arabidopsis thaliana	AT4G01500.1 | Symbols: NGA4 | AP2/B3-like transcriptional factor family protein | chr4:639791-640792 FORWARD LENGTH=333	318	333	1.00E-112	104.7	70.4	79.9
Rsa1.0_01333.1.g25835.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01333.1.g25836.t1	gb|AAD26943.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1448	1454	0	100.4	67.6	81.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1448	1262	1.00E-178	87.2	20.5	26.5
Rsa1.0_01333.1.g25837.t1	gb|EOA23024.1| hypothetical protein CARUB_v10003789mg, partial [Capsella rubella]	129	143	7.00E-49	110.9	79.8	83.7	hypothetical protein CARUB_v10003789mg, partial	gbpln	Capsella rubella	AT4G01575.1 | Symbols: | serine protease inhibitor, Kazal-type family protein | chr4:682040-682474 REVERSE LENGTH=144	129	144	3.00E-50	111.6	80.6	86.0
Rsa1.0_01333.1.g25838.t1	ref|XP_002874967.1| ATEXPA17 [Arabidopsis lyrata subsp. lyrata] gi|297320804|gb|EFH51226.1| ATEXPA17 [Arabidopsis lyrata subsp. lyrata]	255	255	1.00E-139	100.0	93.3	97.3	ATEXPA17	gbpln	Arabidopsis lyrata	AT4G01630.1 | Symbols: ATEXPA17, ATEXP17, ATHEXP ALPHA 1.13, EXPA17 | expansin A17 | chr4:700653-701527 FORWARD LENGTH=255	255	255	1.00E-140	100.0	92.5	96.9
Rsa1.0_01333.1.g25839.t1	ref|NP_192074.1| Polyketide cyclase / dehydrase and lipid transport protein [Arabidopsis thaliana] gi|7268208|emb|CAB77735.1| hypothetical protein [Arabidopsis thaliana] gi|332656656|gb|AEE82056.1| Polyketide cyclase / dehydrase and lipid transport protein [Arabidopsis thaliana]	281	288	1.00E-121	102.5	81.9	88.6	Polyketide cyclase / dehydrase and lipid transport protein	gbpln	Arabidopsis thaliana	AT4G01650.1 | Symbols: | Polyketide cyclase / dehydrase and lipid transport protein | chr4:704578-705866 REVERSE LENGTH=288	281	288	1.00E-123	102.5	81.9	88.6
Rsa1.0_01333.1.g25840.t2	gb|AAD15534.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	938	1664	0	177.4	41.6	50.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	938	1262	4.00E-26	134.5	5.9	9.3
Rsa1.0_01334.1.g25841.t1	gb|EOA35196.1| hypothetical protein CARUB_v10020346mg [Capsella rubella]	168	425	8.00E-54	253.0	63.1	66.7	hypothetical protein CARUB_v10020346mg	gbpln	Capsella rubella	AT1G65320.1 | Symbols: | Cystathionine beta-synthase (CBS) family protein | chr1:24260168-24262644 REVERSE LENGTH=425	168	425	2.00E-54	253.0	61.9	66.7
Rsa1.0_01334.1.g25842.t1	ref|NP_001077775.1| transcription elongation factor SPT6 [Arabidopsis thaliana] gi|332196253|gb|AEE34374.1| transcription elongation factor SPT6-like protein [Arabidopsis thaliana]	1738	1642	0	94.5	75.7	81.5	transcription elongation factor SPT6	gbpln	Arabidopsis thaliana	AT1G65440.2 | Symbols: GTB1 | global transcription factor group B1 | chr1:24306908-24314327 REVERSE LENGTH=1642	1738	1642	0	94.5	75.7	81.5

Rsa1.0_01334.1.g25843.t1	ref|XP_002886918.1| hypothetical protein ARALYDRAFT_315582 [Arabidopsis lyrata subsp. lyrata] gi|297332759|gb|EFH63177.1| hypothetical protein ARALYDRAFT_315582 [Arabidopsis lyrata subsp. lyrata]	165	450	3.00E-74	272.7	83.0	90.3	hypothetical protein ARALYDRAFT_315582	gbpln	Arabidopsis lyrata	AT1G65450.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:24315875-24318895 FORWARD LENGTH=450	165	450	6.00E-75	272.7	80.0	89.7
Rsa1.0_01334.1.g25844.t1	ref|XP_002886918.1| hypothetical protein ARALYDRAFT_315582 [Arabidopsis lyrata subsp. lyrata] gi|297332759|gb|EFH63177.1| hypothetical protein ARALYDRAFT_315582 [Arabidopsis lyrata subsp. lyrata]	287	450	1.00E-143	156.8	86.8	92.3	hypothetical protein ARALYDRAFT_315582	gbpln	Arabidopsis lyrata	AT1G65450.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:24315875-24318895 FORWARD LENGTH=450	287	450	1.00E-144	156.8	86.1	91.3
Rsa1.0_01334.1.g25845.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1830	1274	0	69.6	35.4	45.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1830	575	2.00E-58	31.4	9.4	14.7
Rsa1.0_01334.1.g25846.t1	ref|NP_176725.1| chromatin assembly factor-1 (FASCIATA1) [Arabidopsis thaliana] gi|75213311|sp|Q9SXY0.1|FAS1_ARATH RecName: Full=Chromatin assembly factor 1 subunit FAS1; Short=CAF-1 subunit FAS1; AltName: Full=CAF-1 p150 homolog; AltName: Full=Protein FASCIATA 1 gi|4887626|dbj|BAA77811.1| FAS1 [Arabidopsis thaliana] gi|22022526|gb|AAM83221.1| At1g65470/F5I14_33 [Arabidopsis thaliana] gi|332196258|gb|AEE34379.1| chromatin assembly factor-1 (FASCIATA1) [Arabidopsis thaliana]	815	815	0	100.0	79.8	87.7	chromatin assembly factor-1 (FASCIATA1)	gbpln	Arabidopsis thaliana	AT1G65470.1 | Symbols: FAS1, NFB2 | chromatin assembly factor-1 (FASCIATA1) (FAS1) | chr1:24319906-24323879 REVERSE LENGTH=815	815	815	0	100.0	79.8	87.7
Rsa1.0_01334.1.g25847.t1	gb|ACM69283.1| flowering locus T [Sinapis alba] gi|222877040|gb|ACM69284.1| flowering locus T [Sinapis alba]	175	175	2.00E-92	100.0	94.9	98.3	flowering locus T	gbpln	Sinapis alba	AT1G65480.1 | Symbols: FT | PEBP (phosphatidylethanolamine-binding protein) family protein | chr1:24331510-24333689 FORWARD LENGTH=175	175	175	4.00E-83	100.0	80.6	90.3
Rsa1.0_01334.1.g25848.t1	ref|XP_002888422.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297334263|gb|EFH64681.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	753	747	0	99.2	90.8	94.0	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT1G65540.1 | Symbols: | LETM1-like protein | chr1:24362382-24366011 REVERSE LENGTH=736	753	736	0	97.7	88.0	91.2
Rsa1.0_01334.1.g25849.t1	gb|EOA34845.1| hypothetical protein CARUB_v10022424mg [Capsella rubella]	398	400	0	100.5	83.4	90.5	hypothetical protein CARUB_v10022424mg	gbpln	Capsella rubella	AT1G65570.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:24374098-24375846 REVERSE LENGTH=397	398	397	0	99.7	82.2	89.7
Rsa1.0_01335.1.g25850.t1	gb|EOA39947.1| hypothetical protein CARUB_v10008637mg [Capsella rubella]	476	600	0	126.1	94.7	96.6	hypothetical protein CARUB_v10008637mg	gbpln	Capsella rubella	AT1G55490.2 | Symbols: CPN60B, LEN1 | chaperonin 60 beta | chr1:20715717-20718673 REVERSE LENGTH=600	476	600	0	126.1	94.5	96.6
Rsa1.0_01335.1.g25851.t1	ref|XP_002891836.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297337678|gb|EFH68095.1| binding protein [Arabidopsis lyrata subsp. lyrata]	313	335	1.00E-133	107.0	80.8	85.6	binding protein	gbpln	Arabidopsis lyrata	AT1G55480.1 | Symbols: ZKT | protein containing PDZ domain, a K-box domain, and a TPR region | chr1:20713822-20715351 FORWARD LENGTH=335	313	335	1.00E-135	107.0	81.2	86.3
Rsa1.0_01335.1.g25852.t1	ref|NP_564690.1| DNA/RNA-binding protein Kin17 conserved region-containing protein [Arabidopsis thaliana] gi|13430440|gb|AAK25842.1|AF360132_1 unknown protein [Arabidopsis thaliana] gi|4204268|gb|AAD10649.1| Similar to Kin17 protein [Arabidopsis thaliana] gi|15293155|gb|AAK93688.1| unknown protein [Arabidopsis thaliana] gi|332195127|gb|AEE33248.1| DNA/RNA-binding protein Kin17 conserved region-containing protein [Arabidopsis thaliana]	391	411	0	105.1	85.2	94.1	DNA/RNA-binding protein Kin17 conserved region-containing protein	gbpln	Arabidopsis thaliana	AT1G55460.1 | Symbols: | DNA/RNA-binding protein Kin17, conserved region | chr1:20707567-20708802 FORWARD LENGTH=411	391	411	0	105.1	85.2	94.1
Rsa1.0_01335.1.g25853.t1	ref|XP_002894505.1| hypothetical protein ARALYDRAFT_892538 [Arabidopsis lyrata subsp. lyrata] gi|297340347|gb|EFH70764.1| hypothetical protein ARALYDRAFT_892538 [Arabidopsis lyrata subsp. lyrata]	336	311	1.00E-164	92.6	86.9	90.5	hypothetical protein ARALYDRAFT_892538	gbpln	Arabidopsis lyrata	AT1G55450.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:20705274-20706825 REVERSE LENGTH=311	336	311	1.00E-165	92.6	86.3	90.2

Rsa1.0_01335.1.g25854.t1	ref|XP_002894503.1| hypothetical protein ARALYDRAFT_892534 [Arabidopsis lyrata subsp. lyrata] gi|297340345|gb|EFH70762.1| hypothetical protein ARALYDRAFT_892534 [Arabidopsis lyrata subsp. lyrata]	74	104	7.00E-19	140.5	64.9	78.4	hypothetical protein ARALYDRAFT_892534	gbpln	Arabidopsis lyrata	AT1G55365.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13500.1); Has 29 Blast hits to 29 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:20673983-20674363 REVERSE LENGTH=126	74	126	1.00E-20	170.3	63.5	78.4
Rsa1.0_01335.1.g25855.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01335.1.g25856.t1	gb|AAG51568.1|AC027034_14 unknown protein; 25817-24837 [Arabidopsis thaliana]	256	243	2.00E-89	94.9	68.8	72.7	unknown protein; 25817-24837	gbpln	Arabidopsis thaliana	AT1G55340.1 | Symbols: | Protein of unknown function (DUF1639) | chr1:20652605-20653469 FORWARD LENGTH=205	256	205	5.00E-86	80.1	62.1	64.5
Rsa1.0_01335.1.g25857.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01335.1.g25858.t1	gb|ABB97032.1| unknown [Brassica rapa]	59	59	4.00E-14	100.0	93.2	96.6	unknown	gbpln	Brassica rapa	AT3G13520.1 | Symbols: AGP12, ATAGP12 | arabinogalactan protein 12 | chr3:4409087-4409269 FORWARD LENGTH=60	59	60	3.00E-16	101.7	83.1	83.1
Rsa1.0_01335.1.g25859.t19	ref|NP_001185237.1| RNA polymerase II transcription mediator [Arabidopsis thaliana] gi|332195107|gb|AEE33228.1| RNA polymerase II transcription mediator [Arabidopsis thaliana]	1986	2001	0	100.8	84.4	88.6	RNA polymerase II transcription mediator	gbpln	Arabidopsis thaliana	AT1G55325.2 | Symbols: GCT | RNA polymerase II transcription mediators | chr1:20637594-20647714 FORWARD LENGTH=2001	1986	2001	0	100.8	84.4	88.6
Rsa1.0_01335.1.g25860.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01336.1.g25861.t1	gb|AAD17409.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	190	1347	2.00E-76	708.9	71.6	84.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT3G21000.1 | Symbols: | Gag-Pol-related retrotransposon family protein | chr3:7363921-7365138 FORWARD LENGTH=405	190	405	5.00E-16	213.2	26.8	50.5
Rsa1.0_01336.1.g25862.t1	ref|NP_201491.1| CC-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|46395984|sp|Q9FKZ1.1|DRL42_ARATH RecName: Full=Probable disease resistance protein At5g66900 gi|9758140|dbj|BAB08632.1| disease resistance protein-like [Arabidopsis thaliana] gi|332010893|gb|AED98276.1| CC-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	809	809	0	100.0	57.4	70.6	CC-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT5G66900.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr5:26714931-26717757 REVERSE LENGTH=809	809	809	0	100.0	57.4	70.6
Rsa1.0_01336.1.g25863.t1	ref|XP_002877065.1| hypothetical protein ARALYDRAFT_905014 [Arabidopsis lyrata subsp. lyrata] gi|297322903|gb|EFH53324.1| hypothetical protein ARALYDRAFT_905014 [Arabidopsis lyrata subsp. lyrata]	113	106	8.00E-27	93.8	58.4	75.2	hypothetical protein ARALYDRAFT_905014	gbpln	Arabidopsis lyrata	AT5G40460.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27630.1); Has 87 Blast hits to 87 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 87; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:16202465-16202803 FORWARD LENGTH=112	113	112	2.00E-23	99.1	61.1	72.6
Rsa1.0_01336.1.g25864.t3	ref|XP_002875393.1| hypothetical protein ARALYDRAFT_905015 [Arabidopsis lyrata subsp. lyrata] gi|297321231|gb|EFH51652.1| hypothetical protein ARALYDRAFT_905015 [Arabidopsis lyrata subsp. lyrata]	1164	538	0	46.2	36.2	38.2	hypothetical protein ARALYDRAFT_905015	gbpln	Arabidopsis lyrata	AT3G27640.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:10232307-10235467 FORWARD LENGTH=535	1164	535	0	46.0	35.7	38.1
Rsa1.0_01336.1.g25865.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1687	1352	0	80.1	35.3	49.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1687	746	2.00E-85	44.2	10.3	14.2
Rsa1.0_01336.1.g25866.t1	gb|EOA24946.1| hypothetical protein CARUB_v10018238mg [Capsella rubella]	132	128	2.00E-64	97.0	90.2	91.7	hypothetical protein CARUB_v10018238mg	gbpln	Capsella rubella	AT3G27650.1 | Symbols: LBD25 | LOB domain-containing protein 25 | chr3:10238731-10240346 FORWARD LENGTH=159	132	159	4.00E-66	120.5	88.6	90.2
Rsa1.0_01336.1.g25867.t1	ref|XP_002875396.1| hypothetical protein ARALYDRAFT_484555 [Arabidopsis lyrata subsp. lyrata] gi|297321234|gb|EFH51655.1| hypothetical protein ARALYDRAFT_484555 [Arabidopsis lyrata subsp. lyrata]	1844	1847	0	100.2	85.4	91.5	hypothetical protein ARALYDRAFT_484555	gbpln	Arabidopsis lyrata	AT3G27670.1 | Symbols: RST1 | ARM repeat superfamily protein | chr3:10245338-10253158 FORWARD LENGTH=1841	1844	1841	0	99.8	84.4	90.7
Rsa1.0_01336.1.g25868.t1	dbj|BAJ33772.1| unnamed protein product [Thellungiella halophila]	266	266	1.00E-152	100.0	99.2	100.0	unnamed protein product	----	----	AT3G27690.1 | Symbols: LHCB2.4, LHCB2.3, LHCB2 | photosystem II light harvesting complex gene 2.3 | chr3:10256002-10256921 FORWARD LENGTH=266	266	266	1.00E-153	100.0	97.4	98.9

Rsa1.0_01336.1.g25869.t1	ref|NP_189407.2| zinc finger CCCH domain-containing protein 41 [Arabidopsis thaliana] gi|30688891|ref|NP_851008.1| zinc finger CCCH domain-containing protein 41 [Arabidopsis thaliana] gi|75335571|sp|Q9LVX1.1|C3H41_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 41; Short=AtC3H41 gi|9294475|dbj|BAB02694.1| unnamed protein product [Arabidopsis thaliana] gi|23397275|gb|AAN31919.1| unknown protein [Arabidopsis thaliana] gi|225898683|dbj|BAH30472.1| hypothetical protein [Arabidopsis thaliana] gi|332643832|gb|AEE77353.1| zinc finger CCCH domain-containing protein 41 [Arabidopsis thaliana] gi|332643833|gb|AEE77354.1| zinc finger CCCH domain-containing protein 41 [Arabidopsis thaliana]	884	908	0	102.7	80.3	86.4	zinc finger CCCH domain-containing protein 41	gbpln	Arabidopsis thaliana	AT3G27700.2 | Symbols: | zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein | chr3:10257681-10261330 REVERSE LENGTH=908	884	908	0	102.7	80.3	86.4
Rsa1.0_01336.1.g25870.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	223	1274	5.00E-33	571.3	35.9	54.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	223	303	1.00E-31	135.9	35.0	53.4
Rsa1.0_01337.1.g25871.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01337.1.g25872.t3	gb|ABV89614.1| universal stress protein family protein [Brassica rapa]	117	215	1.00E-23	183.8	50.4	53.8	universal stress protein family protein	gbpln	Brassica rapa	AT1G44760.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr1:16896894-16898427 REVERSE LENGTH=213	117	213	4.00E-25	182.1	48.7	52.1
Rsa1.0_01337.1.g25873.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1063	1459	0	137.3	43.1	54.3	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1063	1262	1.00E-93	118.7	18.1	26.0
Rsa1.0_01337.1.g25874.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1312	1496	0	114.0	42.5	53.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1312	1262	1.00E-107	96.2	16.2	22.8
Rsa1.0_01337.1.g25875.t1	emb|CAN60947.1| hypothetical protein VITISV_015758 [Vitis vinifera]	264	1306	1.00E-72	494.7	52.7	68.2	hypothetical protein VITISV_015758	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01337.1.g25876.t1	emb|CAN77974.1| hypothetical protein VITISV_006175 [Vitis vinifera]	355	1501	1.00E-127	422.8	61.7	76.6	hypothetical protein VITISV_006175	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	355	1262	3.00E-20	355.5	23.4	38.3
Rsa1.0_01337.1.g25877.t1	gb|EOA40468.1| hypothetical protein CARUB_v10009193mg [Capsella rubella]	279	432	7.00E-40	154.8	41.2	49.5	hypothetical protein CARUB_v10009193mg	gbpln	Capsella rubella	AT1G26590.1 | Symbols: | C2H2-like zinc finger protein | chr1:9189624-9190709 FORWARD LENGTH=361	279	361	3.00E-36	129.4	38.7	46.2
Rsa1.0_01337.1.g25878.t1	ref|XP_002893995.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297339837|gb|EFH70254.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	391	370	0	94.6	84.1	89.8	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT1G44800.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:16914342-16916858 REVERSE LENGTH=370	391	370	0	94.6	83.9	89.5
Rsa1.0_01337.1.g25879.t2	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	273	1643	9.00E-80	601.8	60.4	74.7	gag/pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01338.1.g25880.t1	ref|NP_181163.2| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|21805705|gb|AAM76758.1| hypothetical protein [Arabidopsis thaliana] gi|50058811|gb|AAT69150.1| hypothetical protein At2g36210 [Arabidopsis thaliana] gi|330254123|gb|AEC09217.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	127	135	5.00E-56	106.3	87.4	94.5	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT2G36210.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:15186326-15186733 REVERSE LENGTH=135	127	135	1.00E-58	106.3	87.4	94.5
Rsa1.0_01338.1.g25881.t1	ref|XP_002881430.1| hypothetical protein ARALYDRAFT_482593 [Arabidopsis lyrata subsp. lyrata] gi|297327269|gb|EFH57689.1| hypothetical protein ARALYDRAFT_482593 [Arabidopsis lyrata subsp. lyrata]	212	1046	4.00E-15	493.4	21.2	22.2	hypothetical protein ARALYDRAFT_482593	gbpln	Arabidopsis lyrata	AT2G36200.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:15180078-15185189 REVERSE LENGTH=1009	212	1009	4.00E-17	475.9	20.8	21.7
Rsa1.0_01338.1.g25882.t1	ref|XP_002881429.1| ATCWINV4 [Arabidopsis lyrata subsp. lyrata] gi|297327268|gb|EFH57688.1| ATCWINV4 [Arabidopsis lyrata subsp. lyrata]	540	591	0	109.4	85.9	93.5	ATCWINV4	gbpln	Arabidopsis lyrata	AT2G36190.1 | Symbols: AtcwINV4, cwINV4 | cell wall invertase 4 | chr2:15174951-15177785 REVERSE LENGTH=591	540	591	0	109.4	85.0	92.4

Rsa1.0_01338.1.g25883.t1	ref|XP_004156525.1| PREDICTED: ubiquitin-60S ribosomal protein L40-like [Cucumis sativus]	128	208	3.00E-69	162.5	100.0	100.0	PREDICTED: ubiquitin-60S ribosomal protein L40-like	gbpln	Cucumis sativus	AT3G52590.1 | Symbols: UBQ1, EMB2167, ERD16, HAP4 | ubiquitin extension protein 1 | chr3:19505668-19506681 FORWARD LENGTH=128	128	128	6.00E-71	100.0	99.2	99.2
Rsa1.0_01338.1.g25884.t1	gb|AAO41731.1| cytoplasmic ribosomal protein S14 [Brassica napus]	150	150	1.00E-80	100.0	99.3	100.0	cytoplasmic ribosomal protein S14	gbpln	Brassica napus	AT3G11510.1 | Symbols: | Ribosomal protein S11 family protein | chr3:3623757-3624866 REVERSE LENGTH=150	150	150	5.00E-75	100.0	89.3	92.0
Rsa1.0_01338.1.g25885.t1	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	773	1449	2.00E-62	187.5	19.5	28.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	773	746	9.00E-21	96.5	9.4	13.1
Rsa1.0_01338.1.g25886.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1860	1270	0	68.3	36.5	47.4	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1860	575	1.00E-98	30.9	11.0	16.3
Rsa1.0_01338.1.g25887.t1	ref|XP_002881417.1| hypothetical protein ARALYDRAFT_902702 [Arabidopsis lyrata subsp. lyrata] gi|297327256|gb|EFH57676.1| hypothetical protein ARALYDRAFT_902702 [Arabidopsis lyrata subsp. lyrata]	184	192	9.00E-71	104.3	77.2	84.8	hypothetical protein ARALYDRAFT_902702	gbpln	Arabidopsis lyrata	AT2G35900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleus; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; Has 32 Blast hits to 32 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15070203-15071540 REVERSE LENGTH=192	184	192	4.00E-71	104.3	75.0	83.7
Rsa1.0_01338.1.g25888.t1	ref|XP_002893723.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339565|gb|EFH69982.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	368	385	1.00E-103	104.6	54.1	70.4	predicted protein	gbpln	Arabidopsis lyrata	AT2G14710.1 | Symbols: | F-box family protein | chr2:6298936-6300024 FORWARD LENGTH=362	368	362	1.00E-100	98.4	53.5	66.0
Rsa1.0_01338.1.g25889.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	507	1142	1.00E-66	225.2	31.4	44.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	507	575	4.00E-40	113.4	25.2	41.0
Rsa1.0_01338.1.g25890.t1	ref|NP_565829.1| TPX2 (targeting protein for Xklp2)-like protein [Arabidopsis thaliana] gi|16209720|gb|AAL14415.1| At2g35880/F11F19.21 [Arabidopsis thaliana] gi|20197995|gb|AAD21469.2| expressed protein [Arabidopsis thaliana] gi|22655282|gb|AAM98231.1| unknown protein [Arabidopsis thaliana] gi|330254079|gb|AEC09173.1| TPX2 (targeting protein for Xklp2)-like protein [Arabidopsis thaliana]	422	432	1.00E-130	102.4	74.4	81.5	TPX2 (targeting protein for Xklp2)-like protein	gbpln	Arabidopsis thaliana	AT2G35880.1 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr2:15063204-15065259 REVERSE LENGTH=432	422	432	1.00E-133	102.4	74.4	81.5
Rsa1.0_01338.1.g25891.t1	gb|EOA27118.1| hypothetical protein CARUB_v10023217mg [Capsella rubella]	427	445	0	104.2	87.8	92.0	hypothetical protein CARUB_v10023217mg	gbpln	Capsella rubella	AT2G35860.1 | Symbols: FLA16 | FASCICLIN-like arabinogalactan protein 16 precursor | chr2:15059859-15061810 FORWARD LENGTH=445	427	445	0	104.2	85.2	88.8
Rsa1.0_01338.1.g25892.t1	ref|XP_002879580.1| hypothetical protein ARALYDRAFT_482556 [Arabidopsis lyrata subsp. lyrata] gi|297325419|gb|EFH55839.1| hypothetical protein ARALYDRAFT_482556 [Arabidopsis lyrata subsp. lyrata]	91	82	7.00E-20	90.1	65.9	73.6	hypothetical protein ARALYDRAFT_482556	gbpln	Arabidopsis lyrata	AT2G35850.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G52360.1); Has 42 Blast hits to 42 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15056753-15056995 FORWARD LENGTH=80	91	80	9.00E-22	87.9	65.9	73.6
Rsa1.0_01338.1.g25893.t3	gb|EOA26591.1| hypothetical protein CARUB_v10022650mg [Capsella rubella]	819	821	0	100.2	86.4	90.7	hypothetical protein CARUB_v10022650mg	gbpln	Capsella rubella	AT2G35800.1 | Symbols: | mitochondrial substrate carrier family protein | chr2:15044437-15048352 FORWARD LENGTH=823	819	823	0	100.5	86.2	90.5
Rsa1.0_01338.1.g25894.t1	gb|EOA28167.1| hypothetical protein CARUB_v10024357mg [Capsella rubella]	112	112	9.00E-55	100.0	93.8	96.4	hypothetical protein CARUB_v10024357mg	gbpln	Capsella rubella	AT2G35795.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr2:15042321-15043334 FORWARD LENGTH=112	112	112	1.00E-56	100.0	92.9	95.5
Rsa1.0_01339.1.g25895.t1	ref|XP_002881266.1| hypothetical protein ARALYDRAFT_482252 [Arabidopsis lyrata subsp. lyrata] gi|297327105|gb|EFH57525.1| hypothetical protein ARALYDRAFT_482252 [Arabidopsis lyrata subsp. lyrata]	1119	1120	0	100.1	87.1	91.9	hypothetical protein ARALYDRAFT_482252	gbpln	Arabidopsis lyrata	AT2G33170.1 | Symbols: | Leucine-rich repeat receptor-like protein kinase family protein | chr2:14056371-14059829 REVERSE LENGTH=1124	1119	1124	0	100.4	85.5	91.2

<table>
<tr><td>Rsa1.0_01339.1.g25896.t1</td><td>ref|NP_180874.1| glycosyl hydrolase and polygalacturonase domain-containing protein [Arabidopsis thaliana] gi|2924778|gb|AAC04907.1| putative polygalacturonase [Arabidopsis thaliana] gi|330253698|gb|AEC08792.1| glycosyl hydrolase and polygalacturonase domain-containing protein [Arabidopsis thaliana]</td><td>407</td><td>664</td><td>1.00E-174</td><td>163.1</td><td>72.2</td><td>83.5</td><td>glycosyl hydrolase and polygalacturonase domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G33160.1 | Symbols: | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein | chr2:14053404-14056246 FORWARD LENGTH=664</td><td>407</td><td>664</td><td>1.00E-177</td><td>163.1</td><td>72.2</td><td>83.5</td></tr>
<tr><td>Rsa1.0_01339.1.g25897.t1</td><td>ref|NP_180873.1| 3-ketoacyl-CoA thiolase 2 [Arabidopsis thaliana] gi|73919871|sp|Q56WD9.2|THIK2_ARATH RecName: Full=3-ketoacyl-CoA thiolase 2, peroxisomal; AltName: Full=Acetyl-CoA acyltransferase 2; AltName: Full=Beta-ketothiolase 2; AltName: Full=Peroxisomal 3-oxoacyl-CoA thiolase 2; AltName: Full=Peroxisome defective protein 1; Flags: Precursor gi|11993853|gb|AAG42910.1|AF327529_1 putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|13194830|gb|AAK15577.1|AF349530_1 putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2924779|gb|AAC04908.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2981616|dbj|BAA25248.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2981618|dbj|BAA25249.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|15450669|gb|AAK96606.1| At2g33150/F25I18.11 [Arabidopsis thaliana] gi|17380614|gb|AAL36070.1| At2g33150/F25I18.11 [Arabidopsis thaliana] gi|21593136|gb|AAM65085.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|330253697|gb|AEC08791.1| 3-ketoacyl-CoA thiolase 2 [Arabidopsis thaliana]</td><td>462</td><td>462</td><td>0</td><td>100.0</td><td>95.0</td><td>98.3</td><td>3-ketoacyl-CoA thiolase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G33150.1 | Symbols: PKT3, PED1, KAT2 | peroxisomal 3-ketoacyl-CoA thiolase 3 | chr2:14047814-14050983 REVERSE LENGTH=462</td><td>462</td><td>462</td><td>0</td><td>100.0</td><td>95.0</td><td>98.3</td></tr>
<tr><td>Rsa1.0_01339.1.g25898.t1</td><td>gb|EOA27866.1| hypothetical protein CARUB_v10024024mg [Capsella rubella]</td><td>221</td><td>221</td><td>1.00E-105</td><td>100.0</td><td>88.7</td><td>96.4</td><td>hypothetical protein CARUB_v10024024mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G33120.1 | Symbols: SAR1, VAMP722, ATVAMP722 | synaptobrevin-related protein 1 | chr2:14043785-14045337 REVERSE LENGTH=221</td><td>221</td><td>221</td><td>1.00E-107</td><td>100.0</td><td>89.1</td><td>96.4</td></tr>
<tr><td>Rsa1.0_01339.1.g25899.t1</td><td>ref|XP_002881261.1| hypothetical protein ARALYDRAFT_482247 [Arabidopsis lyrata subsp. lyrata] gi|297327100|gb|EFH57520.1| hypothetical protein ARALYDRAFT_482247 [Arabidopsis lyrata subsp. lyrata]</td><td>1023</td><td>1036</td><td>0</td><td>101.3</td><td>94.6</td><td>97.1</td><td>hypothetical protein ARALYDRAFT_482247</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G33100.1 | Symbols: ATCSLD1, CSLD1 | cellulose synthase-like D1 | chr2:14036494-14040044 REVERSE LENGTH=1036</td><td>1023</td><td>1036</td><td>0</td><td>101.3</td><td>94.6</td><td>97.2</td></tr>
<tr><td>Rsa1.0_01339.1.g25900.t1</td><td>dbj|BAF01195.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana]</td><td>811</td><td>779</td><td>0</td><td>96.1</td><td>63.0</td><td>72.1</td><td>putative leucine-rich repeat disease resistance protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G33020.1 | Symbols: AtRLP24, RLP24 | receptor like protein 24 | chr2:14013874-14016516 REVERSE LENGTH=864</td><td>811</td><td>864</td><td>0</td><td>106.5</td><td>61.2</td><td>71.8</td></tr>
<tr><td>Rsa1.0_01339.1.g25901.t1</td><td>ref|NP_180863.1| ATP synthase subunit gamma [Arabidopsis thaliana] gi|3334123|sp|Q96250.1|ATPG3_ARATH RecName: Full=ATP synthase subunit gamma, mitochondrial; AltName: Full=F-ATPase gamma subunit; Flags: Precursor gi|1655480|dbj|BAA13599.1| gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] gi|2924787|gb|AAC04916.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|14517358|gb|AAK62570.1| At2g33040/F25I18.22 [Arabidopsis thaliana] gi|17065102|gb|AAL32705.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|20196990|gb|AAM14859.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|20857422|gb|AAM26719.1| At2g33040/F25I18.22 [Arabidopsis thaliana] gi|21554962|gb|AAM63740.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|330253683|gb|AEC08777.1| ATP synthase subunit gamma [Arabidopsis thaliana]</td><td>325</td><td>325</td><td>0</td><td>100.0</td><td>98.2</td><td>99.7</td><td>ATP synthase subunit gamma</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G33040.1 | Symbols: ATP3 | gamma subunit of Mt ATP synthase | chr2:14018978-14021047 REVERSE LENGTH=325</td><td>325</td><td>325</td><td>0</td><td>100.0</td><td>98.2</td><td>99.7</td></tr>
</table>

Rsa1.0_01339.1.g25902.t1	ref|NP_189137.1| receptor like protein 41 [Arabidopsis thaliana] gi|9293982|dbj|BAB01885.1| leucine-rich repeat disease resistance protein-like [Arabidopsis thaliana] gi|332643443|gb|AEE76964.1| receptor like protein 41 [Arabidopsis thaliana]	848	881	0	103.9	62.1	73.2	receptor like protein 41	gbpln	Arabidopsis thaliana	AT3G25010.1 | Symbols: AtRLP41, RLP41 | receptor like protein 41 | chr3:9110103-9112748 REVERSE LENGTH=881	848	881	0	103.9	62.1	73.2
Rsa1.0_01339.1.g25903.t1	gb|AAC04914.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana]	829	800	0	96.5	60.0	68.6	putative leucine-rich repeat disease resistance protein	gbpln	Arabidopsis thaliana	AT2G33060.1 | Symbols: AtRLP27, RLP27 | receptor like protein 27 | chr2:14025661-14028087 FORWARD LENGTH=808	829	808	0	97.5	60.0	68.6
Rsa1.0_01339.1.g25904.t1	gb|EOA26884.1| hypothetical protein CARUB_v10022977mg [Capsella rubella]	527	531	0	100.8	90.9	94.5	hypothetical protein CARUB_v10022977mg	gbpln	Capsella rubella	AT2G32990.1 | Symbols: AtGH9B8, GH9B8 | glycosyl hydrolase 9B8 | chr2:14003361-14005844 FORWARD LENGTH=525	527	525	0	99.6	93.9	97.3
Rsa1.0_01340.1.g25905.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	321	1611	3.00E-30	501.9	19.9	35.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01340.1.g25906.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01340.1.g25907.t1	gb|EOA24442.1| hypothetical protein CARUB_v10017699mg [Capsella rubella]	97	308	1.00E-46	317.5	93.8	94.8	hypothetical protein CARUB_v10017699mg	gbpln	Capsella rubella	AT2G02410.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF901 (InterPro:IPR010298); Has 1151 Blast hits to 1151 proteins in 597 species: Archae - 0; Bacteria - 1105; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr2:632713-634613 FORWARD LENGTH=308	97	308	6.00E-49	317.5	92.8	94.8
Rsa1.0_01340.1.g25908.t1	gb|AFK13856.1| Ty3/gypsy retrotransposon protein [Beta vulgaris subsp. vulgaris]	1280	1631	0	127.4	53.3	71.0	Ty3/gypsy retrotransposon protein	gbpln	Beta vulgaris	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1280	158	1.00E-36	12.3	5.9	7.2
Rsa1.0_01340.1.g25909.t1	ref|NP_178346.2| uncharacterized protein [Arabidopsis thaliana] gi|26449562|dbj|BAC41907.1| unknown protein [Arabidopsis thaliana] gi|28950879|gb|AAO63363.1| At2g02410 [Arabidopsis thaliana] gi|330250483|gb|AEC05577.1| uncharacterized protein AT2G02410 [Arabidopsis thaliana]	201	308	5.00E-84	153.2	87.6	92.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G02410.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF901 (InterPro:IPR010298); Has 1151 Blast hits to 1151 proteins in 597 species: Archae - 0; Bacteria - 1105; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr2:632713-634613 FORWARD LENGTH=308	201	308	2.00E-86	153.2	87.6	92.0
Rsa1.0_01340.1.g25910.t1	gb|AAO60042.1| glutathione S-transferase zeta [Brassica napus]	268	221	1.00E-118	82.5	78.4	81.0	glutathione S-transferase zeta	gbpln	Brassica napus	AT2G02390.1 | Symbols: ATGSTZ1, GST18, GSTZ1 | glutathione S-transferase zeta 1 | chr2:629015-630955 FORWARD LENGTH=221	268	221	1.00E-113	82.5	72.4	78.0
Rsa1.0_01340.1.g25911.t1	ref|NP_565283.1| SNARE associated Golgi protein [Arabidopsis thaliana] gi|145328248|ref|NP_001077870.1| SNARE associated Golgi protein [Arabidopsis thaliana] gi|13605571|gb|AAK32779.1|AF361611_1 At2g02370/T16F16.16 [Arabidopsis thaliana] gi|16323326|gb|AAL15376.1| At2g02370/T16F16.16 [Arabidopsis thaliana] gi|20197339|gb|AAC78519.2| expressed protein [Arabidopsis thaliana] gi|23505925|gb|AAN28822.1| At2g02370/T16F16.16 [Arabidopsis thaliana] gi|330250476|gb|AEC05570.1| SNARE associated Golgi protein [Arabidopsis thaliana] gi|330250477|gb|AEC05571.1| SNARE associated Golgi protein [Arabidopsis thaliana]	325	320	1.00E-158	98.5	87.4	92.3	SNARE associated Golgi protein	gbpln	Arabidopsis thaliana	AT2G02370.2 | Symbols: | SNARE associated Golgi protein family | chr2:621841-623084 FORWARD LENGTH=320	325	320	1.00E-161	98.5	87.4	92.3
Rsa1.0_01340.1.g25912.t1	ref|XP_002876816.1| phloem protein 2-B10 [Arabidopsis lyrata subsp. lyrata] gi|297322654|gb|EFH53075.1| phloem protein 2-B10 [Arabidopsis lyrata subsp. lyrata]	302	273	1.00E-107	90.4	61.6	72.8	phloem protein 2-B10	gbpln	Arabidopsis lyrata	AT2G02360.1 | Symbols: AtPP2-B10, PP2-B10 | phloem protein 2-B10 | chr2:619699-620736 REVERSE LENGTH=272	302	272	1.00E-106	90.1	60.6	73.2

Rsa1.0_01340.1.g25913.t1	ref|NP_178341.1| F-box protein PP2-B10 [Arabidopsis thaliana] gi|75268076|sp|Q9ZVQ6.1|P2B10_ARATH RecName: Full=F-box protein PP2-B10; AltName: Full=Protein PHLOEM PROTEIN 2-LIKE B10; Short=AtPP2-B10 gi|3894168|gb|AAC78518.1| putative phloem-specific lectin [Arabidopsis thaliana] gi|107738391|gb|ABF83689.1| At2g02360 [Arabidopsis thaliana] gi|110742667|dbj|BAE99245.1| putative phloem-specific lectin [Arabidopsis thaliana] gi|330250475|gb|AEC05569.1| F-box protein PP2-B10 [Arabidopsis thaliana]	262	272	3.00E-82	103.8	58.8	72.1	F-box protein PP2-B10	gbpln	Arabidopsis thaliana	AT2G02360.1 | Symbols: AtPP2-B10, PP2-B10 | phloem protein 2-B10 | chr2:619699-620736 REVERSE LENGTH=272	262	272	9.00E-85	103.8	58.8	72.1
Rsa1.0_01340.1.g25914.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1399	1515	0	108.3	38.1	46.2	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1399	1262	2.00E-94	90.2	12.2	19.5
Rsa1.0_01340.1.g25915.t1	ref|NP_178332.2| phloem protein 2-B2 [Arabidopsis thaliana] gi|334302847|sp|Q9ZVR5.2|PP2B2_ARATH RecName: Full=Putative F-box protein PP2-B2; AltName: Full=Protein PHLOEM PROTEIN 2-LIKE B2; Short=AtPP2-B2 gi|330250467|gb|AEC05561.1| phloem protein 2-B2 [Arabidopsis thaliana]	285	310	1.00E-120	108.8	71.2	85.3	phloem protein 2-B2	gbpln	Arabidopsis thaliana	AT2G02250.1 | Symbols: AtPP2-B2, PP2-B2 | phloem protein 2-B2 | chr2:594655-595825 REVERSE LENGTH=310	285	310	1.00E-122	108.8	71.2	85.3
Rsa1.0_01341.1.g25916.t2	ref|NP_180882.2| myosin XI D [Arabidopsis thaliana] gi|330253710|gb|AEC08804.1| myosin XI D [Arabidopsis thaliana]	1749	1770	0	101.2	84.7	91.8	myosin XI D	gbpln	Arabidopsis thaliana	AT2G33240.1 | Symbols: XID, ATXID | myosin XI D | chr2:14086942-14096914 REVERSE LENGTH=1770	1749	1770	0	101.2	84.7	91.8
Rsa1.0_01341.1.g25917.t1	ref|NP_850204.2| Haloacid dehalogenase-like hydrolase [Arabidopsis thaliana] gi|20196855|gb|AAM14806.1| unknown protein [Arabidopsis thaliana] gi|330253712|gb|AEC08806.1| Haloacid dehalogenase-like hydrolase [Arabidopsis thaliana]	260	245	1.00E-127	94.2	85.8	90.4	Haloacid dehalogenase-like hydrolase	gbpln	Arabidopsis thaliana	AT2G33255.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:14098795-14100358 FORWARD LENGTH=245	260	245	1.00E-130	94.2	85.8	90.4
Rsa1.0_01341.1.g25918.t1	dbj|BAJ34122.1| unnamed protein product [Thellungiella halophila]	249	249	1.00E-107	100.0	90.0	92.4	unnamed protein product	----	----	AT2G33310.3 | Symbols: IAA13 | auxin-induced protein 13 | chr2:14114569-14115757 REVERSE LENGTH=246	249	246	1.00E-106	98.8	89.6	93.2
Rsa1.0_01341.1.g25919.t1	gb|EOA21157.1| hypothetical protein CARUB_v10001503mg [Capsella rubella]	154	314	2.00E-45	203.9	66.2	69.5	hypothetical protein CARUB_v10001503mg	gbpln	Capsella rubella	AT5G06130.2 | Symbols: | chaperone protein dnaJ-related | chr5:1853754-1855763 REVERSE LENGTH=315	154	315	2.00E-47	204.5	66.2	70.8
Rsa1.0_01341.1.g25920.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01341.1.g25921.t1	ref|XP_002888139.1| dynamin family protein [Arabidopsis lyrata subsp. lyrata] gi|297333980|gb|EFH64398.1| dynamin family protein [Arabidopsis lyrata subsp. lyrata]	649	659	0	101.5	71.5	83.4	dynamin family protein	gbpln	Arabidopsis lyrata	AT1G60500.1 | Symbols: DRP4C | Dynamin related protein 4C | chr1:22291582-22293822 FORWARD LENGTH=669	649	669	0	103.1	69.5	82.0
Rsa1.0_01341.1.g25922.t1	ref|NP_180894.1| uncharacterized protein [Arabidopsis thaliana] gi|2459419|gb|AAB80654.1| hypothetical protein [Arabidopsis thaliana] gi|219291116|gb|ACL13991.1| At2g33360 [Arabidopsis thaliana] gi|330253728|gb|AEC08822.1| uncharacterized protein AT2G33360 [Arabidopsis thaliana]	541	603	0	111.5	74.9	82.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G33360.1 | Symbols: | Protein of unknown function (DUF3527) | chr2:14140901-14142870 FORWARD LENGTH=603	541	603	0	111.5	74.9	82.1
Rsa1.0_01341.1.g25923.t1	gb|EOA27806.1| hypothetical protein CARUB_v10023959mg [Capsella rubella]	133	239	6.00E-62	179.7	81.2	91.0	hypothetical protein CARUB_v10023959mg	gbpln	Capsella rubella	AT2G33380.1 | Symbols: RD20, CLO-3 | Caleosin-related family protein | chr2:14144984-14146374 REVERSE LENGTH=236	133	236	3.00E-60	177.4	78.9	88.0
Rsa1.0_01341.1.g25924.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01341.1.g25925.t1	gb|ACG69528.1| caleosin CLO3-2 [Brassica napus]	98	239	1.00E-42	243.9	82.7	85.7	caleosin CLO3-2	gbpln	Brassica napus	AT2G33380.1 | Symbols: RD20, CLO-3 | Caleosin-related family protein | chr2:14144984-14146374 REVERSE LENGTH=236	98	236	1.00E-41	240.8	77.6	80.6
Rsa1.0_01342.1.g25926.t1	gb|ACB59199.1| copia-like protein [Brassica oleracea]	95	975	3.00E-25	1026.3	63.2	69.5	copia-like protein	gbpln	Brassica oleracea	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	95	240	2.00E-11	252.6	28.4	43.2
Rsa1.0_01342.1.g25927.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	242	255	3.00E-28	105.4	40.9	47.5	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	242	302	1.00E-15	124.8	19.0	27.3

Rsa1.0_01342.1.g25928.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01342.1.g25929.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01342.1.g25930.t2	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	342	190	7.00E-19	55.6	17.8	21.1	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01342.1.g25931.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01342.1.g25932.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01343.1.g25933.t1	gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]	373	527	6.00E-82	141.3	47.5	60.6	hypothetical protein CARUB_v10022820mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	373	735	5.00E-76	197.1	45.6	59.5
Rsa1.0_01343.1.g25934.t1	ref|XP_002890788.1| hypothetical protein ARALYDRAFT_313572 [Arabidopsis lyrata subsp. lyrata] gi|297336630|gb|EFH67047.1| hypothetical protein ARALYDRAFT_313572 [Arabidopsis lyrata subsp. lyrata]	159	341	4.00E-30	214.5	59.7	76.1	hypothetical protein ARALYDRAFT_313572	gbpln	Arabidopsis lyrata	AT1G29041.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 4 Blast hits to 4 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10135451-10135987 FORWARD LENGTH=178	159	178	7.00E-26	111.9	55.3	74.2
Rsa1.0_01343.1.g25935.t1	ref|XP_002893546.1| hypothetical protein ARALYDRAFT_473111 [Arabidopsis lyrata subsp. lyrata] gi|297339388|gb|EFH69805.1| hypothetical protein ARALYDRAFT_473111 [Arabidopsis lyrata subsp. lyrata]	739	380	0	51.4	44.1	46.3	hypothetical protein ARALYDRAFT_473111	gbpln	Arabidopsis lyrata	AT1G29050.1 | Symbols: TBL38 | TRICHOME BIREFRINGENCE-LIKE 38 | chr1:10136376-10139082 REVERSE LENGTH=380	739	380	0	51.4	43.7	46.0
Rsa1.0_01343.1.g25936.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1158	1142	0	98.6	50.9	64.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1158	575	2.00E-57	49.7	13.5	21.7
Rsa1.0_01343.1.g25937.t1	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	541	498	7.00E-72	92.1	26.2	34.6	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	541	336	8.00E-23	62.1	12.0	18.1
Rsa1.0_01343.1.g25938.t1	ref|NP_567434.1| protein transport protein SFT1 [Arabidopsis thaliana] gi|75248462|sp|Q8VXX9.1|BETL1_ARATH RecName: Full=Bet1-like protein At4g14600 gi|18389246|gb|AAL67066.1| unknown protein [Arabidopsis thaliana] gi|20259643|gb|AAM14339.1| unknown protein [Arabidopsis thaliana] gi|21554084|gb|AAM63165.1| unknown [Arabidopsis thaliana] gi|26452326|dbj|BAC43249.1| unknown protein [Arabidopsis thaliana] gi|332658064|gb|AEE83464.1| Bet1-like protein [Arabidopsis thaliana]	65	137	3.00E-21	210.8	80.0	84.6	protein transport protein SFT1	gbpln	Arabidopsis thaliana	AT4G14600.1 | Symbols: | Target SNARE coiled-coil domain protein | chr4:8376562-8378078 FORWARD LENGTH=137	65	137	4.00E-24	210.8	80.0	84.6
Rsa1.0_01343.1.g25939.t3	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	935	1250	1.00E-166	133.7	36.3	49.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	935	1262	1.00E-32	135.0	8.8	13.5
Rsa1.0_01343.1.g25940.t1	gb|AAD17352.1| contains similarity to retrovirus-related polyproteins [Arabidopsis thaliana] gi|7267379|emb|CAB77940.1| putative polyprotein [Arabidopsis thaliana]	1595	1366	0	85.6	33.0	46.3	contains similarity to retrovirus-related polyproteins	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1595	1262	1.00E-168	79.1	17.7	23.3
Rsa1.0_01343.1.g25941.t1	gb|EOA39013.1| hypothetical protein CARUB_v10011567mg [Capsella rubella]	229	342	7.00E-23	149.3	24.0	27.9	hypothetical protein CARUB_v10011567mg	gbpln	Capsella rubella	AT2G34080.1 | Symbols: | Cysteine proteinases superfamily protein | chr2:14393431-14394777 REVERSE LENGTH=345	229	345	8.00E-24	150.7	22.7	27.1
Rsa1.0_01344.1.g25942.t1	ref|XP_002890502.1| hypothetical protein ARALYDRAFT_335467 [Arabidopsis lyrata subsp. lyrata] gi|297336344|gb|EFH66761.1| hypothetical protein ARALYDRAFT_335467 [Arabidopsis lyrata subsp. lyrata]	465	525	1.00E-174	112.9	70.1	81.1	hypothetical protein ARALYDRAFT_335467	gbpln	Arabidopsis lyrata	AT1G22240.1 | Symbols: APUM8, PUM8 | pumilio 8 | chr1:7853084-7854963 FORWARD LENGTH=515	465	515	1.00E-175	110.8	69.7	80.4

Rsa1.0_01344.1.g25943.t1	gb|EOA36928.1| hypothetical protein CARUB_v10009798mg [Capsella rubella]	318	315	1.00E-103	99.1	74.8	81.1	hypothetical protein CARUB_v10009798mg	gbpln	Capsella rubella	AT1G22230.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G78110.1); Has 2358 Blast hits to 1759 proteins in 159 species: Archae - 2; Bacteria - 36; Metazoa - 1046; Fungi - 203; Plants - 157; Viruses - 72; Other Eukaryotes - 842 (source: NCBI BLink). | chr1:7850093-7851037 FORWARD LENGTH=314	318	314	1.00E-102	98.7	74.2	82.7
Rsa1.0_01344.1.g25944.t1	gb|EOA38282.1| hypothetical protein CARUB_v10009775mg [Capsella rubella]	319	318	1.00E-134	99.7	78.1	89.3	hypothetical protein CARUB_v10009775mg	gbpln	Capsella rubella	AT1G22220.1 | Symbols: | F-box family protein | chr1:7846694-7847638 FORWARD LENGTH=314	319	314	1.00E-126	98.4	74.6	85.0
Rsa1.0_01344.1.g25945.t1	ref|NP_564162.1| Endoplasmic reticulum vesicle transporter protein [Arabidopsis thaliana] gi|9454530|gb|AAF87853.1|AC073942_7 Contains similarity to a PR00989 protein from Homo sapiens gi|7959731. EST gb|AI995648 comes from this gene [Arabidopsis thaliana] gi|13878151|gb|AAK44153.1|AF370338_1 unknown protein [Arabidopsis thaliana] gi|21281042|gb|AAM44956.1| unknown protein [Arabidopsis thaliana] gi|21553754|gb|AAM62847.1| unknown [Arabidopsis thaliana] gi|332192089|gb|AEE30210.1| Endoplasmic reticulum vesicle transporter protein [Arabidopsis thaliana]	425	386	0	90.8	83.3	87.3	Endoplasmic reticulum vesicle transporter protein	gbpln	Arabidopsis thaliana	AT1G22200.1 | Symbols: | Endoplasmic reticulum vesicle transporter protein | chr1:7837857-7840602 REVERSE LENGTH=386	425	386	0	90.8	83.3	87.3
Rsa1.0_01344.1.g25946.t1	ref|XP_002890498.1| hypothetical protein ARALYDRAFT_472454 [Arabidopsis lyrata subsp. lyrata] gi|297336340|gb|EFH66757.1| hypothetical protein ARALYDRAFT_472454 [Arabidopsis lyrata subsp. lyrata]	264	261	8.00E-93	98.9	74.2	78.8	hypothetical protein ARALYDRAFT_472454	gbpln	Arabidopsis lyrata	AT1G22190.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:7836245-7837030 FORWARD LENGTH=261	264	261	3.00E-88	98.9	68.6	75.8
Rsa1.0_01344.1.g25947.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01344.1.g25948.t2	ref|XP_002893212.1| hypothetical protein ARALYDRAFT_313100 [Arabidopsis lyrata subsp. lyrata] gi|297339054|gb|EFH69471.1| hypothetical protein ARALYDRAFT_313100 [Arabidopsis lyrata subsp. lyrata]	434	454	2.00E-97	104.6	56.0	68.2	hypothetical protein ARALYDRAFT_313100	gbpln	Arabidopsis lyrata	AT1G22120.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:7806655-7809632 REVERSE LENGTH=462	434	462	1.00E-92	106.5	53.0	66.4
Rsa1.0_01344.1.g25949.t1	ref|NP_173630.1| structural constituent of ribosome [Arabidopsis thaliana] gi|9280688|gb|AAF86557.1|AC069252_16 F2E2.18 [Arabidopsis thaliana] gi|52354139|gb|AAU44390.1| hypothetical protein AT1G22110 [Arabidopsis thaliana] gi|55740505|gb|AAV63845.1| hypothetical protein At1g22110 [Arabidopsis thaliana] gi|332192077|gb|AEE30198.1| structural constituent of ribosome [Arabidopsis thaliana]	283	282	3.00E-70	99.6	69.6	77.4	structural constituent of ribosome	gbpln	Arabidopsis thaliana	AT1G22110.1 | Symbols: | structural constituent of ribosome | chr1:7801625-7802473 REVERSE LENGTH=282	283	282	8.00E-73	99.6	69.6	77.4
Rsa1.0_01344.1.g25950.t1	gb|ABU96774.1| bZIP transcription factor [Brassica juncea]	384	386	0	100.5	93.0	95.6	bZIP transcription factor	gbpln	Brassica juncea	AT1G22070.1 | Symbols: TGA3 | TGA1A-related gene 3 | chr1:7789651-7791821 FORWARD LENGTH=384	384	384	0	100.0	84.1	90.4
Rsa1.0_01344.1.g25951.t1	gb|EOA36270.1| hypothetical protein CARUB_v10010515mg [Capsella rubella]	73	159	3.00E-22	217.8	75.3	82.2	hypothetical protein CARUB_v10010515mg	gbpln	Capsella rubella	AT1G22065.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G77885.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:7785889-7786107 FORWARD LENGTH=72	73	72	4.00E-21	98.6	74.0	82.2

Rsa1.0_01344.1.g25952.t1	ref|XP_002893209.1| hypothetical protein ARALYDRAFT_889705 [Arabidopsis lyrata subsp. lyrata] gi|297339051|gb|EFH69468.1| hypothetical protein ARALYDRAFT_889705 [Arabidopsis lyrata subsp. lyrata]	1946	2000	0	102.8	83.8	90.4	hypothetical protein ARALYDRAFT_889705	gbpln	Arabidopsis lyrata	AT1G22060.1 | Symbols: | LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: FBD, F-box and Leucine Rich Repeat domains containing protein (TAIR:AT1G22000.1); Has 84739 Blast hits to 38714 proteins in 2257 species: Archae - 1436; Bacteria - 11314; Metazoa - 40747; Fungi - 7706; Plants - 4675; Viruses - 308; Other Eukaryotes - 18553 (source: NCBI BLink). | chr1:7773373-7780586 REVERSE LENGTH=1999	1946	1999	0	102.7	83.1	90.0
Rsa1.0_01344.1.g25953.t1	ref|XP_002890488.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] gi|297336330|gb|EFH66747.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	112	119	2.00E-46	106.3	82.1	87.5	ubiquitin family protein	gbpln	Arabidopsis lyrata	AT1G22050.1 | Symbols: MUB6 | membrane-anchored ubiquitin-fold protein 6 precursor | chr1:7771897-7772843 FORWARD LENGTH=119	112	119	9.00E-49	106.3	80.4	86.6
Rsa1.0_01344.1.g25954.t1	ref|XP_002890487.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297336329|gb|EFH66746.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	482	478	0	99.2	83.4	89.6	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT1G22040.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:7768370-7769797 FORWARD LENGTH=475	482	475	0	98.5	83.2	89.8
Rsa1.0_01344.1.g25955.t1	ref|NP_189531.1| receptor like protein 43 [Arabidopsis thaliana] gi|238479928|ref|NP_001154652.1| receptor like protein 43 [Arabidopsis thaliana] gi|9294230|dbj|BAB02132.1| disease resistance protein-like [Arabidopsis thaliana] gi|332643980|gb|AEE77501.1| receptor like protein 43 [Arabidopsis thaliana] gi|332643981|gb|AEE77502.1| receptor like protein 43 [Arabidopsis thaliana]	746	711	1.00E-160	95.3	49.5	62.1	receptor like protein 43	gbpln	Arabidopsis thaliana	AT3G28890.2 | Symbols: AtRLP43, RLP43 | receptor like protein 43 | chr3:10896706-10898841 REVERSE LENGTH=711	746	711	1.00E-162	95.3	49.5	62.1
Rsa1.0_01345.1.g25956.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01345.1.g25957.t2	gb|EOA19360.1| hypothetical protein CARUB_v10000407mg [Capsella rubella]	648	662	0	102.2	74.1	82.9	hypothetical protein CARUB_v10000407mg	gbpln	Capsella rubella	AT4G11470.1 | Symbols: CRK31 | cysteine-rich RLK (RECEPTOR-like protein kinase) 31 | chr4:6967729-6970161 FORWARD LENGTH=666	648	666	0	102.8	73.1	80.7
Rsa1.0_01345.1.g25958.t1	gb|EMJ25392.1| hypothetical protein PRUPE_ppa017155mg, partial [Prunus persica]	906	916	1.00E-131	101.1	31.3	47.9	hypothetical protein PRUPE_ppa017155mg, partial	gbpln	Prunus persica	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	906	575	9.00E-51	63.5	12.1	18.4
Rsa1.0_01345.1.g25959.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	565	530	9.00E-41	93.8	16.3	20.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	565	530	4.00E-17	93.8	7.4	14.3
Rsa1.0_01345.1.g25960.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	1112	1164	0	104.7	36.1	54.2	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1112	626	4.00E-69	56.3	12.2	20.0
Rsa1.0_01345.1.g25961.t1	ref|XP_002872592.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318429|gb|EFH48851.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1149	668	0	58.1	41.0	46.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G11480.1 | Symbols: CRK32 | cysteine-rich RLK (RECEPTOR-like protein kinase) 32 | chr4:6971408-6973799 FORWARD LENGTH=656	1149	656	0	57.1	34.0	41.7
Rsa1.0_01345.1.g25962.t1	ref|XP_002872592.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318429|gb|EFH48851.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	131	668	2.00E-48	509.9	82.4	90.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G11530.1 | Symbols: CRK34 | cysteine-rich RLK (RECEPTOR-like protein kinase) 34 | chr4:6987093-6989599 FORWARD LENGTH=669	131	669	6.00E-46	510.7	75.6	85.5
Rsa1.0_01345.1.g25963.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01345.1.g25964.t1	ref|XP_002872595.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318432|gb|EFH48854.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	645	674	0	104.5	62.9	74.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667	645	667	0	103.4	56.4	70.1
Rsa1.0_01346.1.g25965.t1	ref|XP_002893763.1| hypothetical protein ARALYDRAFT_473510 [Arabidopsis lyrata subsp. lyrata] gi|297339605|gb|EFH70022.1| hypothetical protein ARALYDRAFT_473510 [Arabidopsis lyrata subsp. lyrata]	372	371	1.00E-179	99.7	83.1	88.4	hypothetical protein ARALYDRAFT_473510	gbpln	Arabidopsis lyrata	AT1G33340.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:12087628-12088752 FORWARD LENGTH=374	372	374	1.00E-179	100.5	82.0	89.0

Rsa1.0_01346.1.g25966.t2	ref|NP_174601.2| Class I peptide chain release factor [Arabidopsis thaliana] gi|12322576|gb|AAG51290.1|AC027035_13 unknown protein [Arabidopsis thaliana] gi|26450075|dbj|BAC42157.1| putative peptide chain release factor [Arabidopsis thaliana] gi|29824307|gb|AAP04114.1| putative peptide chain release factor [Arabidopsis thaliana] gi|332193463|gb|AEE31584.1| Class I peptide chain release factor [Arabidopsis thaliana]	277	257	1.00E-103	92.8	72.9	79.1	Class I peptide chain release factor	gbpln	Arabidopsis thaliana	AT1G33330.1 | Symbols: | Class I peptide chain release factor | chr1:12084968-12086238 FORWARD LENGTH=257	277	257	1.00E-105	92.8	72.9	79.1
Rsa1.0_01346.1.g25967.t1	ref|XP_002893770.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297339612|gb|EFH70029.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	600	599	0	99.8	91.7	94.7	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G33440.1 | Symbols: | Major facilitator superfamily protein | chr1:12127712-12130327 REVERSE LENGTH=601	600	601	0	100.2	91.8	95.0
Rsa1.0_01346.1.g25968.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01346.1.g25969.t3	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	593	1864	1.00E-17	314.3	9.3	14.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01346.1.g25970.t1	gb|EOA32853.1| hypothetical protein CARUB_v10016179mg, partial [Capsella rubella]	130	312	3.00E-12	240.0	26.9	43.8	hypothetical protein CARUB_v10016179mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01346.1.g25971.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01347.1.g25972.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01347.1.g25973.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01347.1.g25974.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01347.1.g25975.t1	ref|XP_002872837.1| hypothetical protein ARALYDRAFT_490324 [Arabidopsis lyrata subsp. lyrata] gi|297318674|gb|EFH49096.1| hypothetical protein ARALYDRAFT_490324 [Arabidopsis lyrata subsp. lyrata]	232	259	5.00E-76	111.6	78.4	84.5	hypothetical protein ARALYDRAFT_490324	gbpln	Arabidopsis lyrata	AT4G02425.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 29 Blast hits to 28 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:1067531-1068663 REVERSE LENGTH=262	232	262	2.00E-74	112.9	77.2	84.5
Rsa1.0_01347.1.g25976.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01347.1.g25977.t1	ref|XP_002863767.1| hypothetical protein ARALYDRAFT_917496 [Arabidopsis lyrata subsp. lyrata] gi|297309602|gb|EFH40026.1| hypothetical protein ARALYDRAFT_917496 [Arabidopsis lyrata subsp. lyrata]	353	343	5.00E-44	97.2	26.3	33.7	hypothetical protein ARALYDRAFT_917496	gbpln	Arabidopsis lyrata	AT1G36675.1 | Symbols: | glycine-rich protein | chr1:13867568-13869490 FORWARD LENGTH=268	353	268	8.00E-16	75.9	17.3	22.7
Rsa1.0_01347.1.g25978.t1	ref|XP_002874916.1| hypothetical protein ARALYDRAFT_327556 [Arabidopsis lyrata subsp. lyrata] gi|297320753|gb|EFH51175.1| hypothetical protein ARALYDRAFT_327556 [Arabidopsis lyrata subsp. lyrata]	223	281	3.00E-66	126.0	66.4	69.1	hypothetical protein ARALYDRAFT_327556	gbpln	Arabidopsis lyrata	AT1G02840.3 | Symbols: SR1, ATSRP34, SRP34, SR34, At-SR34 | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:626918-629583 FORWARD LENGTH=303	223	303	1.00E-66	135.9	62.8	67.7
Rsa1.0_01347.1.g25979.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	848	1023	6.00E-76	120.6	19.0	25.1	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	848	575	2.00E-26	67.8	8.6	14.4
Rsa1.0_01348.1.g25980.t1	gb|ABD64987.1| hypothetical protein 26.t00003 [Brassica oleracea]	389	330	2.00E-15	84.8	12.3	14.1	hypothetical protein 26.t00003	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01348.1.g25981.t1	ref|XP_002871479.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317316|gb|EFH47738.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	998	1102	0	110.4	71.7	80.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G11530.1 | Symbols: EMF1 | embryonic flower 1 (EMF1) | chr5:3697140-3700930 FORWARD LENGTH=1096	998	1096	0	109.8	69.5	79.4
Rsa1.0_01348.1.g25982.t1	ref|XP_002873518.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319355|gb|EFH49777.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	584	584	0	100.0	88.9	94.5	FAD-binding domain-containing protein	gbpln	Arabidopsis lyrata	AT5G11540.1 | Symbols: | D-arabinono-1,4-lactone oxidase family protein | chr5:3703002-3704981 REVERSE LENGTH=585	584	585	0	100.2	88.2	94.7
Rsa1.0_01348.1.g25983.t1	ref|XP_002873520.1| hypothetical protein ARALYDRAFT_487993 [Arabidopsis lyrata subsp. lyrata] gi|297319357|gb|EFH49779.1| hypothetical protein ARALYDRAFT_487993 [Arabidopsis lyrata subsp. lyrata]	1314	982	0	74.7	68.3	71.9	hypothetical protein ARALYDRAFT_487993	gbpln	Arabidopsis lyrata	AT5G11560.1 | Symbols: | catalytics | chr5:3709734-3713994 REVERSE LENGTH=982	1314	982	0	74.7	68.1	71.8

Rsa1.0_01348.1.g25984.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01348.1.g25985.t1	emb|CAB87718.1| putative protein [Arabidopsis thaliana]		504	541	0	107.3	86.3	91.9	putative protein	gbpln	Arabidopsis thaliana	AT5G11580.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr5:3718913-3721125 FORWARD LENGTH=553	504	553	0	109.7	86.3	91.9
Rsa1.0_01348.1.g25986.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01349.1.g25987.t1	gb|EOA38519.1| hypothetical protein CARUB_v10010308mg [Capsella rubella]		171	206	2.00E-22	120.5	36.3	48.0	hypothetical protein CARUB_v10010308mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01349.1.g25988.t1	ref|XP_002885646.1| hypothetical protein ARALYDRAFT_479953 [Arabidopsis lyrata subsp. lyrata] gi|297331486|gb|EFH61905.1| hypothetical protein ARALYDRAFT_479953 [Arabidopsis lyrata subsp. lyrata]		600	603	0	100.5	75.7	85.5	hypothetical protein ARALYDRAFT_479953	gbpln	Arabidopsis lyrata	AT3G24440.1 | Symbols: VRN5, VIL1 | Fibronectin type III domain-containing protein | chr3:8876207-8878171 REVERSE LENGTH=602	600	602	0	100.3	73.3	83.3
Rsa1.0_01349.1.g25989.t1	gb|AAC67331.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		710	1449	1.00E-63	204.1	21.3	31.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	710	746	3.00E-49	105.1	14.6	20.3
Rsa1.0_01349.1.g25990.t1	ref|NP_189085.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] gi|11994705|dbj|BAB02943.1| hydrolase-like protein [Arabidopsis thaliana] gi|51536428|gb|AAU05452.1| At3g24420 [Arabidopsis thaliana] gi|53828585|gb|AAU94402.1| At3g24420 [Arabidopsis thaliana] gi|110738305|dbj|BAF01081.1| hypothetical protein [Arabidopsis thaliana] gi|332643375|gb|AEE76896.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]		273	273	1.00E-143	100.0	91.2	96.3	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis thaliana	AT3G24420.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:8863111-8864883 REVERSE LENGTH=273	273	273	2.33E-156	100.0	91.2	96.3
Rsa1.0_01349.1.g25991.t1	ref|NP_189078.2| syntaxin-32 [Arabidopsis thaliana] gi|28380163|sp|Q9LK09.1|SYP32_ARATH RecName: Full=Syntaxin-32; Short=AtSYP32 gi|11994697|dbj|BAB02935.1| probable t-SNARE (soluble NSF attachment protein receptor) SED5; ER to Golgi transport [Arabidopsis thaliana] gi|28393777|gb|AAO42298.1| putative syntaxin SYP32 [Arabidopsis thaliana] gi|30793955|gb|AAP40429.1| putative syntaxin SYP32 [Arabidopsis thaliana] gi|332643371|gb|AEE76892.1| syntaxin-32 [Arabidopsis thaliana]		339	347	1.00E-147	102.4	83.5	90.9	syntaxin-32	gbpln	Arabidopsis thaliana	AT3G24350.1 | Symbols: SYP32, ATSYP32 | syntaxin of plants 32 | chr3:8837733-8839402 FORWARD LENGTH=347	339	347	1.00E-149	102.4	83.5	90.9
Rsa1.0_01350.1.g25992.t1	ref|NP_191084.1| uncharacterized protein [Arabidopsis thaliana] gi|297820286|ref|XP_002878026.1| hypothetical protein ARALYDRAFT_485945 [Arabidopsis lyrata subsp. lyrata] gi|7019657|emb|CAB75758.1| putative protein [Arabidopsis thaliana] gi|19310583|gb|AAL85022.1| unknown protein [Arabidopsis thaliana] gi|24030411|gb|AAN41364.1| unknown protein [Arabidopsis thaliana] gi|297323864|gb|EFH54285.1| hypothetical protein ARALYDRAFT_485945 [Arabidopsis lyrata subsp. lyrata] gi|332645835|gb|AEE79356.1| uncharacterized protein AT3G55240 [Arabidopsis thaliana]		95	95	8.00E-45	100.0	95.8	98.9	uncharacterized protein	gbpln	Arabidopsis lyrata	AT3G55240.1 | Symbols: | Plant protein 1589 of unknown function | chr3:20473876-20474705 REVERSE LENGTH=95	95	95	1.00E-47	100.0	95.8	98.9
Rsa1.0_01350.1.g25993.t1	ref|XP_002876289.1| hypothetical protein ARALYDRAFT_485944 [Arabidopsis lyrata subsp. lyrata] gi|297322127|gb|EFH52548.1| hypothetical protein ARALYDRAFT_485944 [Arabidopsis lyrata subsp. lyrata]		309	297	1.00E-142	96.1	83.5	86.7	hypothetical protein ARALYDRAFT_485944	gbpln	Arabidopsis lyrata	AT3G55230.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr3:20471824-20472744 FORWARD LENGTH=306	309	306	1.00E-138	99.0	87.4	91.3
Rsa1.0_01350.1.g25994.t9	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01350.1.g25995.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01350.1.g25996.t1	ref|NP_191075.2| exocyst complex component 7 [Arabidopsis thaliana] gi|18377618|gb|AAL66959.1| unknown protein [Arabidopsis thaliana] gi|20465379|gb|AAM20093.1| unknown protein [Arabidopsis thaliana] gi|332645825|gb|AEE79346.1| exocyst subunit exo70 family protein H1 [Arabidopsis thaliana]	635	636	0	100.2	87.7	93.5	exocyst complex component 7	gbpln	Arabidopsis thaliana	AT3G55150.1 | Symbols: ATEXO70H1, EXO70H1 | exocyst subunit exo70 family protein H1 | chr3:20440655-20442565 REVERSE LENGTH=636	635	636	0	100.2	87.7	93.5
Rsa1.0_01350.1.g25997.t1	ref|NP_191074.2| pectate lyase [Arabidopsis thaliana] gi|190886519|gb|ACE95182.1| At3g55140 [Arabidopsis thaliana] gi|192571722|gb|ACF04806.1| At3g55140 [Arabidopsis thaliana] gi|332645823|gb|AEE79344.1| pectate lyase [Arabidopsis thaliana]	331	331	0	100.0	93.1	96.7	pectate lyase	gbpln	Arabidopsis thaliana	AT3G55140.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:20438819-20440225 FORWARD LENGTH=331	331	331	0	100.0	93.1	96.7
Rsa1.0_01350.1.g25998.t1	gb|EOA25071.1| hypothetical protein CARUB_v10018379mg [Capsella rubella]	723	725	0	100.3	85.9	91.8	hypothetical protein CARUB_v10018379mg	gbpln	Capsella rubella	AT3G55130.1 | Symbols: ATWBC19, WBC19 | white-brown complex homolog 19 | chr3:20434111-20436288 REVERSE LENGTH=725	723	725	0	100.3	85.1	91.3
Rsa1.0_01351.1.g25999.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01351.1.g26000.t1	ref|NP_680210.2| alanyl-tRNA synthetase [Arabidopsis thaliana] gi|322510075|sp|Q9FFC7.2|SYAP_ARATH RecName: Full=Probable alanine--tRNA ligase, chloroplastic; AltName: Full=Alanyl-tRNA synthetase; Short=AlaRS; AltName: Full=Protein EMBRYO DEFECTIVE 1030; AltName: Full=Protein EMBRYO DEFECTIVE 263; AltName: Full=Protein EMBRYO DEFECTIVE 86; Flags: Precursor gi|332005698|gb|AED93081.1| probable alanine--tRNA ligase [Arabidopsis thaliana]	975	978	0	100.3	89.9	95.8	alanyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT5G22800.1 | Symbols: EMB86, EMB1030, EMB263 | Alanyl-tRNA synthetase, class IIc | chr5:7616221-7619961 REVERSE LENGTH=978	975	978	0	100.3	89.9	95.8
Rsa1.0_01351.1.g26001.t1	sp|Q9FFC6.3|GDL78_ARATH RecName: Full=GDSL esterase/lipase At5g22810; AltName: Full=Extracellular lipase At5g22810; Flags: Precursor	362	362	0	100.0	89.5	94.5	RecName: Full=GDSL esterase/lipase At5g22810; AltName: Full=Extracellular lipase At5g22810; Flags: Precursor	----	----	AT5G22810.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:7621568-7623367 FORWARD LENGTH=337	362	337	0	93.1	84.8	89.8
Rsa1.0_01351.1.g26002.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01351.1.g26003.t1	ref|NP_176495.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75169919|sp|Q9CAN6.1|PPR97_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g63070, mitochondrial; Flags: Precursor gi|12323265|gb|AAG51617.1|AC010795_21 unknown protein; 38394-36551 [Arabidopsis thaliana] gi|332195929|gb|AEE34050.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	507	590	0	116.4	66.3	79.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G63070.1 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:23385324-23387167 REVERSE LENGTH=590	507	590	0	116.4	66.3	79.1
Rsa1.0_01351.1.g26004.t1	ref|XP_002874094.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319931|gb|EFH50353.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	545	531	0	97.4	73.4	82.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G22820.2 | Symbols: | ARM repeat superfamily protein | chr5:7623886-7626943 REVERSE LENGTH=534	545	534	0	98.0	73.4	81.8
Rsa1.0_01351.1.g26005.t1	gb|EOA20351.1| hypothetical protein CARUB_v10000659mg [Capsella rubella]	529	540	0	102.1	88.5	93.4	hypothetical protein CARUB_v10000659mg	gbpln	Capsella rubella	AT5G22840.1 | Symbols: | Protein kinase superfamily protein | chr5:7631103-7633103 REVERSE LENGTH=538	529	538	0	101.7	88.8	93.2
Rsa1.0_01351.1.g26006.t1	ref|NP_197676.2| aspartyl protease family protein [Arabidopsis thaliana] gi|110736370|dbj|BAF00154.1| protease-like protein [Arabidopsis thaliana] gi|332005704|gb|AED93087.1| aspartyl protease family protein [Arabidopsis thaliana]	505	493	0	97.6	90.3	94.5	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT5G22850.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:7633717-7636298 REVERSE LENGTH=493	505	493	0	97.6	90.3	94.5
Rsa1.0_01351.1.g26007.t1	ref|XP_002874097.1| serine carboxypeptidase S28 family protein [Arabidopsis lyrata subsp. lyrata] gi|297319934|gb|EFH50356.1| serine carboxypeptidase S28 family protein [Arabidopsis lyrata subsp. lyrata]	467	501	0	107.3	79.9	85.9	serine carboxypeptidase S28 family protein	gbpln	Arabidopsis lyrata	AT5G22860.1 | Symbols: | Serine carboxypeptidase S28 family protein | chr5:7639511-7642945 REVERSE LENGTH=502	467	502	0	107.5	79.2	85.0
Rsa1.0_01351.1.g26008.t1	gb|AAM61502.1| prolylcarboxypeptidase-like protein [Arabidopsis thaliana]	453	502	1.00E-134	110.8	54.1	59.8	prolylcarboxypeptidase-like protein	gbpln	Arabidopsis thaliana	AT5G22860.1 | Symbols: | Serine carboxypeptidase S28 family protein | chr5:7639511-7642945 REVERSE LENGTH=502	453	502	1.00E-136	110.8	53.9	59.8

Rsa1.0_01351.1.g26009.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	451	1142	1.00E-101	253.2	38.4	49.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	451	626	9.00E-37	138.8	25.5	41.9
Rsa1.0_01352.1.g26010.t1	ref|XP_002869407.1| hypothetical protein ARALYDRAFT_491771 [Arabidopsis lyrata subsp. lyrata] gi|297315243|gb|EFH45666.1| hypothetical protein ARALYDRAFT_491771 [Arabidopsis lyrata subsp. lyrata]	163	173	9.00E-77	106.1	89.6	97.5	hypothetical protein ARALYDRAFT_491771	gbpln	Arabidopsis lyrata	AT4G29870.1 | Symbols: | Oligosaccharyltransferase complex/magnesium transporter family protein | chr4:14606012-14606530 FORWARD LENGTH=172	163	172	1.00E-77	105.5	89.6	96.3
Rsa1.0_01352.1.g26011.t1	gb|EOA27289.1| hypothetical protein CARUB_v10023406mg [Capsella rubella]	390	386	0	99.0	86.2	90.8	hypothetical protein CARUB_v10023406mg	gbpln	Capsella rubella	AT4G29860.1 | Symbols: EMB2757, TAN | Transducin/WD40 repeat-like superfamily protein | chr4:14603296-14605704 REVERSE LENGTH=386	390	386	0	99.0	85.6	90.3
Rsa1.0_01352.1.g26012.t1	ref|NP_194714.1| uncharacterized protein [Arabidopsis thaliana] gi|4914409|emb|CAB43660.1| putative protein [Arabidopsis thaliana] gi|7269884|emb|CAB79743.1| putative protein [Arabidopsis thaliana] gi|88900368|gb|ABD57496.1| At4g29850 [Arabidopsis thaliana] gi|332660285|gb|AEE85685.1| uncharacterized protein AT4G29850 [Arabidopsis thaliana]	103	103	7.00E-48	100.0	91.3	97.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G29850.1 | Symbols: | Eukaryotic protein of unknown function (DUF872) | chr4:14601818-14602874 REVERSE LENGTH=103	103	103	1.00E-50	100.0	91.3	97.1
Rsa1.0_01352.1.g26013.t1	ref|NP_194713.1| threonine synthase 1 [Arabidopsis thaliana] gi|20140904|sp|Q9S7B5.1|THRC1_ARATH RecName: Full=Threonine synthase 1, chloroplastic; AltName: Full=Protein METHIONINE OVER-ACCUMULATOR 2; Flags: Precursor gi|4850369|dbj|BAA77707.1| threonine synthase [Arabidopsis thaliana] gi|4914408|emb|CAB43659.1| threonine synthase [Arabidopsis thaliana] gi|7269883|emb|CAB79742.1| threonine synthase [Arabidopsis thaliana] gi|332660284|gb|AEE85684.1| threonine synthase 1 [Arabidopsis thaliana]	500	526	0	105.2	90.8	93.2	threonine synthase 1	gbpln	Arabidopsis thaliana	AT4G29840.1 | Symbols: MTO2, TS | Pyridoxal-5'-phosphate-dependent enzyme family protein | chr4:14599434-14601014 REVERSE LENGTH=526	500	526	0	105.2	90.8	93.2
Rsa1.0_01352.1.g26014.t1	gb|EOA27427.1| hypothetical protein CARUB_v10023560mg, partial [Capsella rubella]	321	343	1.00E-180	106.9	98.1	99.1	hypothetical protein CARUB_v10023560mg, partial	gbpln	Capsella rubella	AT4G29830.1 | Symbols: VIP3 | Transducin/WD40 repeat-like superfamily protein | chr4:14597728-14599157 FORWARD LENGTH=321	321	321	0	100.0	98.1	99.7
Rsa1.0_01352.1.g26015.t4	gb|EOA27858.1| hypothetical protein CARUB_v10024016mg [Capsella rubella]	220	222	1.00E-105	100.9	85.9	92.7	hypothetical protein CARUB_v10024016mg	gbpln	Capsella rubella	AT4G29820.1 | Symbols: CFIM-25, ATCFIM-25 | homolog of CFIM-25 | chr4:14596047-14597317 REVERSE LENGTH=222	220	222	1.00E-106	100.9	85.5	90.9
Rsa1.0_01352.1.g26016.t1	gb|ADZ75456.1| mitogen-associated protein kinase kinase 1 [Brassica napus]	364	364	0	100.0	97.5	98.9	mitogen-associated protein kinase kinase 1	gbpln	Brassica napus	AT4G29810.1 | Symbols: ATMKK2, MKK2, MK1 | MAP kinase kinase 2 | chr4:14593299-14595241 REVERSE LENGTH=363	364	363	0	99.7	92.0	96.2
Rsa1.0_01352.1.g26017.t1	gb|EOA26885.1| hypothetical protein CARUB_v10022979mg [Capsella rubella]	533	530	0	99.4	92.7	95.3	hypothetical protein CARUB_v10022979mg	gbpln	Capsella rubella	AT4G29800.2 | Symbols: PLP8 | PATATIN-like protein 8 | chr4:14590862-14592536 REVERSE LENGTH=526	533	526	0	98.7	91.6	94.6
Rsa1.0_01352.1.g26018.t3	ref|NP_194708.1| uncharacterized protein [Arabidopsis thaliana] gi|4914403|emb|CAB43654.1| putative protein [Arabidopsis thaliana] gi|7269878|emb|CAB79737.1| putative protein [Arabidopsis thaliana] gi|15810173|gb|AAL06988.1| AT4g29790/F27B13_30 [Arabidopsis thaliana] gi|27363444|gb|AAO11641.1| At4g29790/F27B13_30 [Arabidopsis thaliana] gi|332660276|gb|AEE85676.1| uncharacterized protein AT4G29790 [Arabidopsis thaliana]	1199	1211	0	101.0	83.8	90.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G29790.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G19390.1); Has 538 Blast hits to 357 proteins in 124 species: Archae - 0; Bacteria - 74; Metazoa - 109; Fungi - 58; Plants - 105; Viruses - 2; Other Eukaryotes - 190 (source: NCBI BLink). | chr4:14584228-14590123 FORWARD LENGTH=1211	1199	1211	0	101.0	83.8	90.2
Rsa1.0_01352.1.g26019.t1	ref|NP_567834.2| uncharacterized protein [Arabidopsis thaliana] gi|27754582|gb|AAO22738.1| unknown protein [Arabidopsis thaliana] gi|28973634|gb|AAO64139.1| unknown protein [Arabidopsis thaliana] gi|332660275|gb|AEE85675.1| uncharacterized protein AT4G29780 [Arabidopsis thaliana]	528	540	0	102.3	85.6	91.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G29780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12010.1); Has 945 Blast hits to 944 proteins in 87 species: Archae - 0; Bacteria - 0; Metazoa - 519; Fungi - 43; Plants - 365; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr4:14579859-14581481 FORWARD LENGTH=540	528	540	0	102.3	85.6	91.3
Rsa1.0_01352.1.g26020.t1	gb|EOA20120.1| hypothetical protein CARUB_v10000398mg [Capsella rubella]	724	667	1.00E-140	92.1	39.2	51.1	hypothetical protein CARUB_v10000398mg	gbpln	Capsella rubella	AT5G22355.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:7401762-7403756 FORWARD LENGTH=664	724	664	1.00E-141	91.7	40.6	51.5

Rsa1.0_01352.1.g26021.t1	ref|XP_002867391.1| hypothetical protein ARALYDRAFT_491789 [Arabidopsis lyrata subsp. lyrata] gi|297313227|gb|EFH43650.1| hypothetical protein ARALYDRAFT_491789 [Arabidopsis lyrata subsp. lyrata]		494	488	0	98.8	80.2	86.8	hypothetical protein ARALYDRAFT_491789	gbpln	Arabidopsis lyrata	AT4G29730.1 | Symbols: NFC5, MSI5 | nucleosome/chromatin assembly factor group C5 | chr4:14559255-14562522 REVERSE LENGTH=487		494	487	0	98.6	76.9	84.6
Rsa1.0_01352.1.g26022.t1	gb|AAO16558.1| putative polyamine oxidase [Brassica juncea]		542	541	0	99.8	88.6	93.4	putative polyamine oxidase	gbpln	Brassica juncea	AT4G29720.1 | Symbols: ATPAO5, PAO5 | polyamine oxidase 5 | chr4:14553456-14555057 REVERSE LENGTH=533		542	533	0	98.3	82.5	89.3
Rsa1.0_01353.1.g26023.t1	ref|XP_002866092.1| hypothetical protein ARALYDRAFT_495620 [Arabidopsis lyrata subsp. lyrata] gi|297311927|gb|EFH42351.1| hypothetical protein ARALYDRAFT_495620 [Arabidopsis lyrata subsp. lyrata]		339	345	1.00E-141	101.8	74.6	81.7	hypothetical protein ARALYDRAFT_495620	gbpln	Arabidopsis lyrata	AT5G55350.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr5:22442356-22443393 REVERSE LENGTH=345		339	345	1.00E-140	101.8	72.0	81.4
Rsa1.0_01353.1.g26024.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_01353.1.g26025.t1	ref|XP_002866091.1| long-chain-alcohol O-fatty-acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311926|gb|EFH42350.1| long-chain-alcohol O-fatty-acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]		333	335	1.00E-161	100.6	84.7	91.6	long-chain-alcohol O-fatty-acyltransferase family protein	gbpln	Arabidopsis lyrata	AT5G55340.1 | Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr5:22439985-22440986 REVERSE LENGTH=333		333	333	1.00E-160	100.0	83.2	90.1
Rsa1.0_01353.1.g26026.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_01353.1.g26027.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		905	1529	0	169.0	44.5	63.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746		905	746	5.00E-87	82.4	18.8	25.1
Rsa1.0_01353.1.g26028.t1	ref|NP_564315.1| nucleotide-diphospho-sugar transferase domain-containing protein [Arabidopsis thaliana] gi|334182926|ref|NP_001185108.1| nucleotide-diphospho-sugar transferase domain-containing protein [Arabidopsis thaliana] gi|10764852|gb|AAG22832.1|AC007508_5 F1K23.9 [Arabidopsis thaliana] gi|15027991|gb|AAK76526.1| unknown protein [Arabidopsis thaliana] gi|20259205|gb|AAM14318.1| unknown protein [Arabidopsis thaliana] gi|332192896|gb|AEE31017.1| nucleotide-diphospho-sugar transferase domain-containing protein [Arabidopsis thaliana] gi|332192898|gb|AEE31019.1| nucleotide-diphospho-sugar transferase domain-containing protein [Arabidopsis thaliana]		340	340	1.00E-153	100.0	78.2	85.3	nucleotide-diphospho-sugar transferase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G28710.3 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr1:10086850-10088025 REVERSE LENGTH=340		340	340	1.00E-155	100.0	78.2	85.3
Rsa1.0_01353.1.g26029.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_01354.1.g26030.t2	gb|EOA29867.1| hypothetical protein CARUB_v10012964mg [Capsella rubella]		80	857	1.00E-13	1071.3	48.8	51.3	hypothetical protein CARUB_v10012964mg	gbpln	Capsella rubella	AT2G19210.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase protein | chr2:8335639-8339307 REVERSE LENGTH=881		80	881	5.00E-16	1101.3	47.5	50.0
Rsa1.0_01354.1.g26031.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_01354.1.g26032.t4	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_01354.1.g26033.t1	dbj|BAB10319.1| unnamed protein product [Arabidopsis thaliana]		67	598	1.00E-10	892.5	49.3	49.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G48960.1 | Symbols: | HAD-superfamily hydrolase, subfamily IG, 5'-nucleotidase | chr5:19849645-19853382 FORWARD LENGTH=642		67	642	2.00E-13	958.2	49.3	49.3
Rsa1.0_01354.1.g26034.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]		1208	1239	0	102.6	48.3	62.4	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262		1208	1262	1.00E-101	104.5	15.9	24.7
Rsa1.0_01354.1.g26035.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	

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<tr><td>Rsa1.0_01354.1.g26036.t1</td><td>ref|NP_179337.1| RING-H2 finger protein ATL44 [Arabidopsis thaliana] gi|51316192|sp|O22755.1|ATL44_ARATH RecName: Full=RING-H2 finger protein ATL44; AltName: Full=RING-H2 zinc finger protein RHA3a gi|13877953|gb|AAK44054.1|AF370239_1 putative RING zinc finger protein [Arabidopsis thaliana] gi|3790573|gb|AAC68673.1| RING-H2 finger protein RHA3a [Arabidopsis thaliana] gi|4914367|gb|AAD32903.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|17065626|gb|AAL33807.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|330251537|gb|AEC06631.1| RING-H2 finger protein ATL44 [Arabidopsis thaliana]</td><td>184</td><td>185</td><td>3.00E-73</td><td>100.5</td><td>81.5</td><td>88.6</td><td>RING-H2 finger protein ATL44</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17450.1 | Symbols: RHA3A | RING-H2 finger A3A | chr2:7576640-7577197 REVERSE LENGTH=185</td><td>184</td><td>185</td><td>1.00E-75</td><td>100.5</td><td>81.5</td><td>88.6</td></tr>
<tr><td>Rsa1.0_01354.1.g26037.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01354.1.g26038.t1</td><td>gb|ABD64930.1| hypothetical protein 24.t00076 [Brassica oleracea]</td><td>513</td><td>407</td><td>6.00E-13</td><td>79.3</td><td>9.0</td><td>9.7</td><td>hypothetical protein 24.t00076</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01354.1.g26039.t1</td><td>gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]</td><td>399</td><td>627</td><td>3.00E-32</td><td>157.1</td><td>21.3</td><td>36.6</td><td>putative gag-protease polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01354.1.g26040.t1</td><td>emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]</td><td>166</td><td>1489</td><td>4.00E-24</td><td>897.0</td><td>32.5</td><td>50.6</td><td>retrovirus-related like polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237</td><td>166</td><td>237</td><td>9.00E-14</td><td>142.8</td><td>21.7</td><td>38.0</td></tr>
<tr><td>Rsa1.0_01355.1.g26041.t2</td><td>ref|XP_002893050.1| hypothetical protein ARALYDRAFT_889381 [Arabidopsis lyrata subsp. lyrata] gi|297338892|gb|EFH69309.1| hypothetical protein ARALYDRAFT_889381 [Arabidopsis lyrata subsp. lyrata]</td><td>128</td><td>249</td><td>2.00E-46</td><td>194.5</td><td>73.4</td><td>82.0</td><td>hypothetical protein ARALYDRAFT_889381</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G16550.1 | Symbols: | HSP20-like chaperone | chr4:9318442-9324254 REVERSE LENGTH=743</td><td>128</td><td>743</td><td>3.00E-46</td><td>580.5</td><td>68.8</td><td>78.1</td></tr>
<tr><td>Rsa1.0_01355.1.g26042.t1</td><td>gb|EOA16421.1| hypothetical protein CARUB_v10004575mg [Capsella rubella]</td><td>238</td><td>505</td><td>2.00E-70</td><td>212.2</td><td>64.7</td><td>73.1</td><td>hypothetical protein CARUB_v10004575mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23210.2 | Symbols: CRK13 | cysteine-rich RLK (RECEPTOR-like protein kinase) 13 | chr4:12149499-12151418 REVERSE LENGTH=524</td><td>238</td><td>524</td><td>5.00E-66</td><td>220.2</td><td>59.7</td><td>71.8</td></tr>
<tr><td>Rsa1.0_01355.1.g26043.t1</td><td>gb|EOA17306.1| hypothetical protein CARUB_v10005579mg [Capsella rubella]</td><td>255</td><td>250</td><td>8.00E-79</td><td>98.0</td><td>79.6</td><td>85.1</td><td>hypothetical protein CARUB_v10005579mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G16530.1 | Symbols: | Family of unknown function (DUF577) | chr4:9311355-9315554 FORWARD LENGTH=803</td><td>255</td><td>803</td><td>5.00E-68</td><td>314.9</td><td>75.3</td><td>81.6</td></tr>
<tr><td>Rsa1.0_01355.1.g26044.t2</td><td>gb|EOA17672.1| hypothetical protein CARUB_v10006041mg [Capsella rubella]</td><td>136</td><td>121</td><td>1.00E-58</td><td>89.0</td><td>83.1</td><td>86.0</td><td>hypothetical protein CARUB_v10006041mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G16520.2 | Symbols: ATG8F | Ubiquitin-like superfamily protein | chr4:9306882-9308113 REVERSE LENGTH=121</td><td>136</td><td>121</td><td>3.00E-60</td><td>89.0</td><td>81.6</td><td>84.6</td></tr>
<tr><td>Rsa1.0_01355.1.g26045.t1</td><td>gb|EOA18186.1| hypothetical protein CARUB_v10006665mg [Capsella rubella]</td><td>81</td><td>86</td><td>3.00E-26</td><td>106.2</td><td>80.2</td><td>88.9</td><td>hypothetical protein CARUB_v10006665mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G16515.1 | Symbols: RGF6 | Encodes a root meristem growth factor (RGF). Belongs to a family of functionally redundant homologous peptides that are secreted, tyrosine-sulfated, and expressed mainly in the stem cell area and the innermost layer of central columella cells. RGFs are required for maintenance of the root stem cell niche and transit amplifying cell proliferation. Members of this family include: At5g60810 (RGF1), At1g13620 (RGF2), At2g04025 (RGF3), At3g30350 (RGF4), At5g51451 (RGF5), At4g16515 (RGF6), At3g02240 (RGF7), At2g03830 (RGF8) and At5g64770 (RGF9). | chr4:9305386-9305646 REVERSE LENGTH=86</td><td>81</td><td>86</td><td>8.00E-25</td><td>106.2</td><td>76.5</td><td>86.4</td></tr>
<tr><td>Rsa1.0_01355.1.g26046.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT5G47550.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:19286596-19286964 REVERSE LENGTH=122</td><td>116</td><td>122</td><td>7.00E-12</td><td>105.2</td><td>28.4</td><td>42.2</td></tr>
<tr><td>Rsa1.0_01355.1.g26047.t1</td><td>gb|EOA15472.1| hypothetical protein CARUB_v10004447mg [Capsella rubella]</td><td>582</td><td>582</td><td>0</td><td>100.0</td><td>92.6</td><td>96.4</td><td>hypothetical protein CARUB_v10004447mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G16480.1 | Symbols: ATINT4, INT4 | inositol transporter 4 | chr4:9291246-9293083 FORWARD LENGTH=582</td><td>582</td><td>582</td><td>0</td><td>100.0</td><td>93.1</td><td>96.2</td></tr>
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Rsa1.0_01355.1_g26049.t1	gb|EOA17704.1| hypothetical protein CARUB_v10006076mg [Capsella rubella]	110	108	2.00E-47	98.2	88.2	90.9	hypothetical protein CARUB_v10006076mg	gbpln	Capsella rubella	AT4G16450.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: photorespiration; LOCATED IN: mitochondrion, mitochondrial membrane, mitochondrial respiratory chain complex I, respiratory chain complex I; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages. | chr4:9280132-9280541 FORWARD LENGTH=106	110	106	2.00E-49	96.4	87.3	90.0
Rsa1.0_01355.1_g26050.t1	gb|EOA19014.1| hypothetical protein CARUB_v10007665mg [Capsella rubella]	126	125	2.00E-47	99.2	84.9	92.1	hypothetical protein CARUB_v10007665mg	gbpln	Capsella rubella	AT4G16447.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9278829-9279206 FORWARD LENGTH=125	126	125	5.00E-46	99.2	82.5	91.3
Rsa1.0_01355.1_g26051.t1	emb|CAB10420.1| LET1 like protein [Arabidopsis thaliana] gi|7268394|emb|CAB78686.1| LET1 like protein [Arabidopsis thaliana]	366	578	3.00E-87	157.9	50.8	60.4	LET1 like protein	gbpln	Arabidopsis thaliana	AT4G16442.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:9272042-9272970 REVERSE LENGTH=182	366	182	2.00E-73	49.7	36.1	42.3
Rsa1.0_01355.1_g26052.t1	ref|NP_193376.1| transcription factor bHLH3 [Arabidopsis thaliana] gi|75318117|sp|O23487.1|BH003_ARATH RecName: Full=Transcription factor bHLH3; AltName: Full=Basic helix-loop-helix protein 3; Short=AtbHLH3; Short=bHLH 3; AltName: Full=Transcription factor EN 34; AltName: Full=bHLH transcription factor bHLH003 gi|16226919|gb|AAL16298.1|AF428368_1 AT4g16430/dl4240w [Arabidopsis thaliana] gi|18026954|gb|AAL55710.1|AF251688_1 putative transcription factor BHLH3 [Arabidopsis thaliana] gi|2244999|emb|CAB10419.1| transcription factor like protein [Arabidopsis thaliana] gi|7268393|emb|CAB78685.1| transcription factor like protein [Arabidopsis thaliana] gi|16323045|gb|AAL15257.1| AT4g16430/dl4240w [Arabidopsis thaliana] gi|25141207|gb|AAN73298.1| At4g16430/dl4240w [Arabidopsis thaliana] gi|332658347|gb|AEE83747.1| transcription factor bHLH3 [Arabidopsis thaliana]	453	467	0	103.1	78.8	85.7	transcription factor bHLH3	gbpln	Arabidopsis thaliana	AT4G16430.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:9267599-9269002 FORWARD LENGTH=467	453	467	0	103.1	78.8	85.7
Rsa1.0_01355.1_g26053.t3	emb|CAB10418.1| transcriptional adaptor like protein [Arabidopsis thaliana] gi|7268392|emb|CAB78684.1| transcriptional adaptor like protein [Arabidopsis thaliana]	131	480	4.00E-36	366.4	60.3	71.0	transcriptional adaptor like protein	gbpln	Arabidopsis thaliana	AT4G16420.1 | Symbols: ADA2B, PRZ1 | homolog of yeast ADA2 2B | chr4:9262805-9265775 REVERSE LENGTH=487	131	487	3.00E-37	371.8	58.8	70.2
Rsa1.0_01355.1_g26054.t1	ref|NP_567494.1| uncharacterized protein [Arabidopsis thaliana] gi|17381194|gb|AAL36409.1| unknown protein [Arabidopsis thaliana] gi|21436425|gb|AAM51413.1| unknown protein [Arabidopsis thaliana] gi|332658343|gb|AEE83743.1| uncharacterized protein AT4G16410 [Arabidopsis thaliana]	191	185	7.00E-64	96.9	71.2	80.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G16410.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF751 (InterPro:IPR008470); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9262019-9262576 REVERSE LENGTH=185	191	185	3.00E-66	96.9	71.2	80.1

Rsa1.0_01355.1.g26055.t1	emb|CAB10417.1| hypothetical protein [Arabidopsis thaliana] gi|7268389|emb|CAB78682.1| hypothetical protein [Arabidopsis thaliana]	88	209	3.00E-33	237.5	75.0	90.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G16400.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13175.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9260564-9262102 FORWARD LENGTH=218	88	218	8.00E-36	247.7	75.0	89.8
Rsa1.0_01355.1.g26056.t1	ref|NP_974559.5| metal ion binding protein [Arabidopsis thaliana] gi|332658339|gb|AEE83739.1| metal ion binding protein [Arabidopsis thaliana]	255	254	2.00E-58	99.6	69.8	74.5	metal ion binding protein	gbpln	Arabidopsis thaliana	AT4G16380.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr4:9254638-9255955 FORWARD LENGTH=254	255	254	6.00E-61	99.6	69.8	74.5
Rsa1.0_01355.1.g26057.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	793	2301	0	290.2	57.3	71.9	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	793	1262	1.00E-116	159.1	24.6	37.5
Rsa1.0_01356.1.g26058.t1	gb|AAC63839.1| unknown protein [Arabidopsis thaliana]	230	164	5.00E-73	71.3	60.0	61.3	unknown protein	gbpln	Arabidopsis thaliana	AT2G31110.2 | Symbols: | Plant protein of unknown function (DUF828) | chr2:13258522-13262071 REVERSE LENGTH=364	230	364	7.00E-75	158.3	60.0	60.4
Rsa1.0_01356.1.g26059.t1	gb|EOA27374.1| hypothetical protein CARUB_v10023492mg [Capsella rubella]	213	364	1.00E-113	170.9	90.6	94.8	hypothetical protein CARUB_v10023492mg	gbpln	Capsella rubella	AT2G31110.2 | Symbols: | Plant protein of unknown function (DUF828) | chr2:13258522-13262071 REVERSE LENGTH=364	213	364	1.00E-114	170.9	90.6	93.9
Rsa1.0_01356.1.g26060.t1	sp|O82274.2|PLA19_ARATH RecName: Full=Phospholipase A1-IIbeta	414	414	0	100.0	82.1	88.6	RecName: Full=Phospholipase A1-IIbeta	----	----	AT2G31100.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:13256738-13258174 REVERSE LENGTH=414	414	414	0	100.0	82.1	88.6
Rsa1.0_01356.1.g26061.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01356.1.g26062.t1	gb|EOA29350.1| hypothetical protein CARUB_v10025636mg [Capsella rubella]	70	81	4.00E-24	115.7	78.6	85.7	hypothetical protein CARUB_v10025636mg	gbpln	Capsella rubella	AT2G31085.1 | Symbols: CLE6 | CLAVATA3/ESR-RELATED 6 | chr2:13254263-13254508 FORWARD LENGTH=81	70	81	7.00E-25	115.7	72.9	84.3
Rsa1.0_01356.1.g26063.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01356.1.g26064.t1	gb|EOA26707.1| hypothetical protein CARUB_v10022794mg [Capsella rubella]	592	664	0	112.2	93.8	97.0	hypothetical protein CARUB_v10022794mg	gbpln	Capsella rubella	AT2G31060.2 | Symbols: | elongation factor family protein | chr2:13213496-13218544 REVERSE LENGTH=667	592	667	0	112.7	92.6	96.6
Rsa1.0_01356.1.g26065.t1	ref|XP_002879301.1| hypothetical protein ARALYDRAFT_902122 [Arabidopsis lyrata subsp. lyrata] gi|297325140|gb|EFH55560.1| hypothetical protein ARALYDRAFT_902122 [Arabidopsis lyrata subsp. lyrata]	211	195	6.00E-76	92.4	70.6	79.1	hypothetical protein ARALYDRAFT_902122	gbpln	Arabidopsis lyrata	AT5G26330.1 | Symbols: | Cupredoxin superfamily protein | chr5:9241614-9242635 REVERSE LENGTH=187	211	187	2.00E-26	88.6	24.6	39.3
Rsa1.0_01356.1.g26066.t1	ref|XP_002881149.1| hypothetical protein ARALYDRAFT_482029 [Arabidopsis lyrata subsp. lyrata] gi|297326988|gb|EFH57408.1| hypothetical protein ARALYDRAFT_482029 [Arabidopsis lyrata subsp. lyrata]	103	350	4.00E-31	339.8	74.8	80.6	hypothetical protein ARALYDRAFT_482029	gbpln	Arabidopsis lyrata	AT2G31040.1 | Symbols: | ATP synthase protein I -related | chr2:13209094-13211012 REVERSE LENGTH=350	103	350	2.00E-33	339.8	73.8	79.6
Rsa1.0_01356.1.g26067.t1	gb|ABK28201.1| unknown [Arabidopsis thaliana]	83	84	2.00E-27	101.2	73.5	86.7	unknown	gbpln	Arabidopsis thaliana	AT2G31035.1 | Symbols: | BEST Arabidopsis thaliana protein match is: OSBP(oxysterol binding protein)-related protein 1B (TAIR:AT2G31030.1); Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:13208667-13208918 FORWARD LENGTH=83	83	83	4.00E-30	100.0	73.5	86.7
Rsa1.0_01356.1.g26068.t2	ref|XP_002879298.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297325137|gb|EFH55557.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata]	83	488	3.00E-29	588.0	73.5	88.0	oxysterol-binding family protein	gbpln	Arabidopsis lyrata	AT2G31035.1 | Symbols: | BEST Arabidopsis thaliana protein match is: OSBP(oxysterol binding protein)-related protein 1B (TAIR:AT2G31030.1); Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:13208667-13208918 FORWARD LENGTH=83	83	83	1.00E-31	100.0	74.7	89.2
Rsa1.0_01356.1.g26069.t1	ref|XP_002879296.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325135|gb|EFH55555.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	519	764	2.33E-156	147.2	47.6	48.7	kinase family protein	gbpln	Arabidopsis lyrata	AT2G31010.2 | Symbols: | Protein kinase superfamily protein | chr2:13194939-13199642 FORWARD LENGTH=775	519	775	1.00E-149	149.3	47.6	48.6
Rsa1.0_01357.1.g26070.t1	gb|ACG60669.1| copia-type polyprotein-like protein [Brassica oleracea var. alboglabra]	77	196	1.00E-31	254.5	85.7	92.2	copia-type polyprotein-like protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_01357.1.g26071.t1	dbj|BAF00526.1| hypothetical protein [Arabidopsis thaliana]	170	202	8.00E-75	118.8	81.8	85.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G27385.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF493 (InterPro:IPR007454); Has 76 Blast hits to 76 proteins in 23 species: Archae - 0; Bacteria - 6; Metazoa - 0; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:9511129-9512820 REVERSE LENGTH=202	170	202	9.00E-77	118.8	81.2	85.3
Rsa1.0_01357.1.g26072.t1	ref|XP_002893465.1| F17L21.18 [Arabidopsis lyrata subsp. lyrata] gi|297339307|gb|EFH69724.1| F17L21.18 [Arabidopsis lyrata subsp. lyrata]	214	205	6.00E-78	95.8	69.2	79.4	F17L21.18	gbpln	Arabidopsis lyrata	AT1G27390.1 | Symbols: TOM20-2 | translocase outer membrane 20-2 | chr1:9513469-9514912 REVERSE LENGTH=210	214	210	1.00E-69	98.1	64.0	75.2
Rsa1.0_01357.1.g26073.t7	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	897	871	0	97.1	64.7	75.6	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	897	874	1.00E-39	97.4	10.1	16.8
Rsa1.0_01357.1.g26074.t3	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	911	915	1.00E-130	100.4	26.7	38.1	F22O13.21	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	911	719	9.00E-25	78.9	12.2	22.3
Rsa1.0_01357.1.g26075.t1	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	295	326	8.00E-11	110.5	11.9	23.1	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01357.1.g26076.t4	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1297	1496	0	115.3	39.2	49.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1297	1262	1.00E-138	97.3	18.7	26.3
Rsa1.0_01357.1.g26077.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01357.1.g26078.t1	gb|ADE80749.1| cold shock domain protein 2 [Eutrema salsugineum]	177	201	6.00E-42	113.6	73.4	81.4	cold shock domain protein 2	gbpln	Eutrema salsugineum	AT2G21060.1 | Symbols: ATGRP2B, ATCSP4, GRP2B | glycine-rich protein 2B | chr2:9036983-9037588 REVERSE LENGTH=201	177	201	3.00E-43	113.6	71.2	78.0
Rsa1.0_01357.1.g26079.t2	gb|EOA35774.1| hypothetical protein CARUB_v10021005mg, partial [Capsella rubella]	240	185	2.00E-95	77.1	70.4	70.8	hypothetical protein CARUB_v10021005mg, partial	gbpln	Capsella rubella	AT1G67430.1 | Symbols: | Ribosomal protein L22p/L17e family protein | chr1:25262209-25263627 FORWARD LENGTH=175	240	175	7.00E-98	72.9	70.4	70.8
Rsa1.0_01357.1.g26080.t2	ref|XP_003555102.1| PREDICTED: uncharacterized protein LOC100796026 [Glycine max]	1425	1109	1.00E-120	77.8	18.0	25.0	PREDICTED: uncharacterized protein LOC100796026	gbenv/gbpln	Glycine max	#	#	#	#	#	#	#
Rsa1.0_01358.1.g26081.t1	gb|ABW24665.1| pollen-specific polygalacturonase [Brassica rapa subsp. oleifera]	414	421	0	101.7	94.2	97.3	pollen-specific polygalacturonase	gbpln	Brassica rapa	AT1G02790.1 | Symbols: PGA4 | polygalacturonase 4 | chr1:610681-612225 REVERSE LENGTH=422	414	422	0	101.9	80.9	89.4
Rsa1.0_01358.1.g26082.t1	gb|EOA33828.1| hypothetical protein CARUB_v10021307mg [Capsella rubella]	71	515	7.00E-25	725.4	70.4	83.1	hypothetical protein CARUB_v10021307mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01358.1.g26083.t1	gb|ABW24665.1| pollen-specific polygalacturonase [Brassica rapa subsp. oleifera]	421	421	0	100.0	94.1	97.4	pollen-specific polygalacturonase	gbpln	Brassica rapa	AT1G02790.1 | Symbols: PGA4 | polygalacturonase 4 | chr1:610681-612225 REVERSE LENGTH=422	421	422	0	100.2	80.8	89.1
Rsa1.0_01358.1.g26084.t1	ref|XP_002873866.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata] gi|297319703|gb|EFH50125.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata]	391	384	9.00E-74	98.2	46.5	60.1	hypothetical protein ARALYDRAFT_909803	gbpln	Arabidopsis lyrata	AT1G50870.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:18855147-18856337 FORWARD LENGTH=396	391	396	5.00E-65	101.3	41.7	59.1
Rsa1.0_01358.1.g26085.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01358.1.g26086.t2	gb|EOA37762.1| hypothetical protein CARUB_v10012601mg [Capsella rubella]	157	544	1.00E-29	346.5	44.6	47.8	hypothetical protein CARUB_v10012601mg	gbpln	Capsella rubella	AT1G27980.1 | Symbols: DPL1, ATDPL1 | dihydrosphingosine phosphate lyase | chr1:9748812-9752618 FORWARD LENGTH=544	157	544	1.00E-27	346.5	43.3	47.1
Rsa1.0_01358.1.g26087.t1	gb|ABR45948.1| coronitine insensitive 1 [Arabidopsis thaliana]	558	592	1.00E-118	106.1	41.9	62.0	coronitine insensitive 1	gbpln	Arabidopsis thaliana	AT2G39940.1 | Symbols: COI1 | RNI-like superfamily protein | chr2:16672848-16675486 REVERSE LENGTH=592	558	592	1.00E-120	106.1	41.9	62.0

Rsa1.0_01358.1.g26088.t1	ref|NP_192226.1| AP2/B3 domain-containing protein [Arabidopsis thaliana] gi|75267842|sp|Q9ZR14.1|Y4317_ARATH RecName: Full=Putative B3 domain-containing protein At4g03170 gi|4262145|gb|AAD14445.1| hypothetical protein [Arabidopsis thaliana] gi|7270187|emb|CAB77802.1| hypothetical protein [Arabidopsis thaliana] gi|225898763|dbj|BAH30512.1| hypothetical protein [Arabidopsis thaliana] gi|332656884|gb|AEE82284.1| AP2/B3 domain-containing protein [Arabidopsis thaliana]	167	250	2.00E-22	149.7	37.7	53.3	AP2/B3 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G03170.1 | Symbols: | AP2/B3-like transcriptional factor family protein | chr4:1400832-1401584 FORWARD LENGTH=250	167	250	7.00E-25	149.7	37.7	53.3
Rsa1.0_01358.1.g26089.t2	ref|XP_002873866.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata] gi|297319703|gb|EFH50125.1| hypothetical protein ARALYDRAFT_909803 [Arabidopsis lyrata subsp. lyrata]	253	384	3.00E-15	151.8	21.7	27.7	hypothetical protein ARALYDRAFT_909803	gbpln	Arabidopsis lyrata	AT5G18160.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:6002770-6003909 FORWARD LENGTH=379	253	379	3.00E-14	149.8	17.4	26.9
Rsa1.0_01359.1.g26090.t1	ref|XP_002866438.1| hypothetical protein ARALYDRAFT_496307 [Arabidopsis lyrata subsp. lyrata] gi|297312273|gb|EFH42697.1| hypothetical protein ARALYDRAFT_496307 [Arabidopsis lyrata subsp. lyrata]	1022	1037	0	101.5	85.5	91.0	hypothetical protein ARALYDRAFT_496307	gbpln	Arabidopsis lyrata	AT5G61480.1 | Symbols: PXY | Leucine-rich repeat protein kinase family protein | chr5:24724541-24727842 REVERSE LENGTH=1041	1022	1041	0	101.9	84.1	89.6
Rsa1.0_01359.1.g26091.t1	gb|EOA12449.1| hypothetical protein CARUB_v10028614mg [Capsella rubella]	261	291	1.00E-52	111.5	51.3	67.8	hypothetical protein CARUB_v10028614mg	gbpln	Capsella rubella	AT5G61470.1 | Symbols: | C2H2-like zinc finger protein | chr5:24722870-24723784 FORWARD LENGTH=304	261	304	8.00E-52	116.5	54.4	69.0
Rsa1.0_01359.1.g26092.t4	ref|XP_002866437.1| hypothetical protein ARALYDRAFT_496305 [Arabidopsis lyrata subsp. lyrata] gi|297312272|gb|EFH42696.1| hypothetical protein ARALYDRAFT_496305 [Arabidopsis lyrata subsp. lyrata]	1025	1057	0	103.1	90.0	95.0	hypothetical protein ARALYDRAFT_496305	gbpln	Arabidopsis lyrata	AT5G61460.1 | Symbols: MIM, ATRAD18, SMC6B | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:24714551-24721841 REVERSE LENGTH=1057	1025	1057	0	103.1	88.7	94.1
Rsa1.0_01359.1.g26093.t1	gb|EOA14349.1| hypothetical protein CARUB_v10027529mg [Capsella rubella]	160	222	3.00E-47	138.8	69.4	85.0	hypothetical protein CARUB_v10027529mg	gbpln	Capsella rubella	AT5G51860.2 | Symbols: | K-box region and MADS-box transcription factor family protein | chr5:21081844-21084126 REVERSE LENGTH=202	160	202	8.00E-27	126.3	43.8	56.3
Rsa1.0_01359.1.g26094.t1	gb|EOA15711.1| hypothetical protein CARUB_v10006544mg [Capsella rubella]	61	179	2.00E-23	293.4	85.2	98.4	hypothetical protein CARUB_v10006544mg	gbpln	Capsella rubella	AT5G51860.2 | Symbols: | K-box region and MADS-box transcription factor family protein | chr5:21081844-21084126 REVERSE LENGTH=202	61	202	2.00E-25	331.1	82.0	96.7
Rsa1.0_01359.1.g26095.t2	ref|NP_200953.1| 2-phosphoglycerate kinase-related protein [Arabidopsis thaliana] gi|10177175|dbj|BAB10444.1| unnamed protein product [Arabidopsis thaliana] gi|332010087|gb|AED97470.1| 2-phosphoglycerate kinase-related protein [Arabidopsis thaliana]	455	447	0	98.2	84.2	89.9	2-phosphoglycerate kinase-related protein	gbpln	Arabidopsis thaliana	AT5G61450.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:24710240-24712882 REVERSE LENGTH=447	455	447	0	98.2	84.2	89.9
Rsa1.0_01359.1.g26096.t1	ref|NP_200952.1| thioredoxin-like 1-2 [Arabidopsis thaliana] gi|51702163|sp|Q9XFI1.1|TRL12_ARATH RecName: Full=Thioredoxin-like 1-2, chloroplastic; AltName: Full=Atypical cysteine/histidine-rich thioredoxin 5; Short=AtACHT5; AltName: Full=Lilium-type thioredoxin 1-2; Flags: Precursor gi|4973260|gb|AAD35007.1|AF144389_1 thioredoxin-like 3 [Arabidopsis thaliana] gi|9757866|dbj|BAB08500.1| thioredoxin-like 3 [Arabidopsis thaliana] gi|87116568|gb|ABD19648.1| At5g61440 [Arabidopsis thaliana] gi|110737981|dbj|BAF00926.1| thioredoxin-like 3 [Arabidopsis thaliana] gi|332010086|gb|AED97469.1| thioredoxin-like 1-2 [Arabidopsis thaliana]	275	245	1.00E-101	89.1	71.6	76.0	thioredoxin-like 1-2	gbpln	Arabidopsis thaliana	AT5G61440.1 | Symbols: ACHT5 | atypical CYS HIS rich thioredoxin 5 | chr5:24707658-24708684 FORWARD LENGTH=245	275	245	1.00E-104	89.1	71.6	76.0
Rsa1.0_01359.1.g26097.t1	gb|EOA27690.1| hypothetical protein CARUB_v10023843mg, partial [Capsella rubella]	200	271	2.00E-29	135.5	37.0	53.0	hypothetical protein CARUB_v10023843mg, partial	gbpln	Capsella rubella	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	200	303	6.00E-19	151.5	26.5	46.0
Rsa1.0_01359.1.g26098.t1	ref|XP_002878553.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324392|gb|EFH54812.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	126	819	8.00E-19	650.0	33.3	34.9	predicted protein	gbpln	Arabidopsis lyrata	AT2G21410.1 | Symbols: VHA-A2 | vacuolar proton ATPase A2 | chr2:9162703-9168141 FORWARD LENGTH=821	126	821	1.00E-15	651.6	30.2	31.7

Rsa1.0_01359.1.g26099.t1	emb|CCD74489.1| Zinc knuckle (CCHC-type) family protein / Plant mobile domain protein family [Arabidopsis halleri subsp. halleri]	108	700	5.00E-11	648.1	38.0	52.8	Zinc knuckle (CCHC-type) family protein / Plant mobile domain protein family	gbpln	Arabidopsis halleri	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	108	735	9.00E-13	680.6	38.9	51.9
Rsa1.0_01360.1.g26100.t1	gb|EOA23949.1| hypothetical protein CARUB_v10017166mg [Capsella rubella]	454	472	0	104.0	86.8	92.7	hypothetical protein CARUB_v10017166mg	gbpln	Capsella rubella	AT2G02870.3 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:838378-839781 FORWARD LENGTH=467	454	467	0	102.9	87.7	92.3
Rsa1.0_01360.1.g26101.t1	gb|AAD38033.1|AF149053_1 phytochrome kinase substrate 1 [Arabidopsis thaliana]	418	439	1.00E-159	105.0	76.8	84.7	phytochrome kinase substrate 1	gbpln	Arabidopsis thaliana	AT2G02950.1 | Symbols: PKS1 | phytochrome kinase substrate 1 | chr2:855149-856468 REVERSE LENGTH=439	418	439	1.00E-161	105.0	76.8	84.4
Rsa1.0_01360.1.g26102.t1	gb|ABD65076.1| SLL3 ORF2 protein, putative [Brassica oleracea]	140	443	6.00E-18	316.4	32.9	38.6	SLL3 ORF2 protein, putative	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01360.1.g26103.t1	gb|EOA24478.1| hypothetical protein CARUB_v10017735mg [Capsella rubella]	294	298	1.00E-121	101.4	82.3	87.4	hypothetical protein CARUB_v10017735mg	gbpln	Capsella rubella	AT2G02960.3 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:862346-863980 REVERSE LENGTH=271	294	271	1.00E-116	92.2	78.2	81.6
Rsa1.0_01360.1.g26104.t1	ref|NP_565293.1| GDA1/CD39 nucleoside phosphatase-like protein [Arabidopsis thaliana] gi|75099829|sp|O80612.2|APY6_ARATH RecName: Full=Probable apyrase 6; Short=AtAPY6; AltName: Full=ATP-diphosphatase; AltName: Full=ATP-diphosphohydrolase; AltName: Full=Adenosine diphosphatase; Short=ADPase; AltName: Full=NTPDase; AltName: Full=Nucleoside triphosphate diphosphohydrolase 6 gi|20197095|gb|AAC32915.2| putative nucleoside triphosphatase [Arabidopsis thaliana] gi|330250556|gb|AEC05650.1| probable apyrase 6 [Arabidopsis thaliana] gi|339283650|gb|AEJ38087.1| nucleoside triphosphate diphosphohydrolase 6 [Arabidopsis thaliana]	554	555	0	100.2	83.9	91.5	GDA1/CD39 nucleoside phosphatase-like protein	gbpln	Arabidopsis thaliana	AT2G02970.1 | Symbols: | GDA1/CD39 nucleoside phosphatase family protein | chr2:865395-868007 REVERSE LENGTH=555	554	555	0	100.2	83.9	91.5
Rsa1.0_01360.1.g26105.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01360.1.g26106.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01360.1.g26107.t1	gb|EOA24693.1| hypothetical protein CARUB_v10017969mg [Capsella rubella]	228	230	1.00E-116	100.9	86.8	96.5	hypothetical protein CARUB_v10017969mg	gbpln	Capsella rubella	AT2G02990.1 | Symbols: RNS1, ATRNS1 | ribonuclease 1 | chr2:873714-874667 FORWARD LENGTH=230	228	230	1.00E-115	100.9	87.3	96.9
Rsa1.0_01360.1.g26108.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01360.1.g26109.t1	gb|EOA25885.1| hypothetical protein CARUB_v10019265mg [Capsella rubella]	284	285	1.00E-143	100.4	89.1	95.1	hypothetical protein CARUB_v10019265mg	gbpln	Capsella rubella	AT2G03050.1 | Symbols: EMB93, SOLDAT10 | Mitochondrial transcription termination factor family protein | chr2:900094-900945 REVERSE LENGTH=283	284	283	1.00E-144	99.6	88.4	94.7
Rsa1.0_01360.1.g26110.t1	ref|XP_002875185.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321023|gb|EFH51444.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	374	376	1.00E-178	100.5	82.1	89.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G03060.2 | Symbols: AGL30 | AGAMOUS-like 30 | chr2:901614-903569 FORWARD LENGTH=386	374	386	1.00E-165	103.2	79.1	86.9
Rsa1.0_01361.1.g26111.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	354	1142	1.00E-91	322.6	49.2	63.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	354	575	3.00E-39	162.4	28.8	50.3
Rsa1.0_01361.1.g26112.t1	ref|NP_001189567.1| ribosomal RNA large subunit methyltransferase F [Arabidopsis thaliana] gi|330252026|gb|AEC07120.1| ribosomal RNA large subunit methyltransferase F [Arabidopsis thaliana]	452	513	0	113.5	81.2	86.5	ribosomal RNA large subunit methyltransferase F	gbpln	Arabidopsis thaliana	AT2G21070.3 | Symbols: FIO1 | methyltransferases | chr2:9040940-9043500 FORWARD LENGTH=513	452	513	0	113.5	81.2	86.5
Rsa1.0_01361.1.g26113.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01361.1.g26114.t3	gb|EOA29035.1| hypothetical protein CARUB_v10025289mg [Capsella rubella]	593	597	0	100.7	83.6	91.6	hypothetical protein CARUB_v10025289mg	gbpln	Capsella rubella	AT2G21090.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr2:9045695-9047488 REVERSE LENGTH=597	593	597	0	100.7	82.5	90.6
Rsa1.0_01361.1.g26115.t1	ref|NP_181951.3| uncharacterized protein [Arabidopsis thaliana] gi|330255299|gb|AEC10393.1| uncharacterized protein AT2G44220 [Arabidopsis thaliana]	410	403	1.00E-138	98.3	59.0	72.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G44220.1 | Symbols: | Protein of Unknown Function (DUF239) | chr2:18283803-18285690 FORWARD LENGTH=403	410	403	1.00E-141	98.3	59.0	72.9

Rsa1.0_01361.1.g26116.t1	ref|XP_002880360.1| hypothetical protein ARALYDRAFT_900523 [Arabidopsis lyrata subsp. lyrata] gi|297326199|gb|EFH56619.1| hypothetical protein ARALYDRAFT_900523 [Arabidopsis lyrata subsp. lyrata]	356	332	1.00E-106	93.3	72.8	77.8	hypothetical protein ARALYDRAFT_900523	gbpln	Arabidopsis lyrata	AT2G21140.1 | Symbols: ATPRP2, PRP2 | proline-rich protein 2 | chr2:9060868-9062035 REVERSE LENGTH=321	356	321	1.00E-104	90.2	69.4	75.3
Rsa1.0_01361.1.g26117.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01362.1.g26118.t1	gb|EOA15441.1| hypothetical protein CARUB_v10004083mg [Capsella rubella]	184	948	4.00E-96	515.2	91.3	92.4	hypothetical protein CARUB_v10004083mg	gbpln	Capsella rubella	AT4G31490.1 | Symbols: | Coatomer, beta subunit | chr4:15269460-15272693 FORWARD LENGTH=948	184	948	3.00E-97	515.2	90.2	91.3
Rsa1.0_01362.1.g26119.t1	gb|EOA17791.1| hypothetical protein CARUB_v10006185mg [Capsella rubella]	197	2598	6.00E-44	1318.8	50.3	66.5	hypothetical protein CARUB_v10006185mg	gbpln	Capsella rubella	AT4G30990.2 | Symbols: | ARM repeat superfamily protein | chr4:15084456-15097860 FORWARD LENGTH=2620	197	2620	5.00E-42	1329.9	46.7	65.5
Rsa1.0_01362.1.g26120.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01362.1.g26121.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01362.1.g26122.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01362.1.g26123.t1	gb|EOA36365.1| hypothetical protein CARUB_v10010751mg [Capsella rubella]	90	94	5.00E-32	104.4	80.0	81.1	hypothetical protein CARUB_v10010751mg	gbpln	Capsella rubella	AT1G26945.1 | Symbols: KDR | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:9351571-9352474 FORWARD LENGTH=94	90	94	3.00E-34	104.4	78.9	81.1
Rsa1.0_01362.1.g26124.t1	ref|XP_002893370.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata] gi|297339212|gb|EFH69629.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata]	226	226	1.00E-120	100.0	92.5	96.0	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	gbpln	Arabidopsis lyrata	AT1G26940.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr1:9343193-9344962 FORWARD LENGTH=226	226	226	1.00E-121	100.0	92.0	94.7
Rsa1.0_01362.1.g26125.t1	gb|EOA40529.1| hypothetical protein CARUB_v10009257mg [Capsella rubella]	438	419	0	95.7	83.8	88.6	hypothetical protein CARUB_v10009257mg	gbpln	Capsella rubella	AT1G26930.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9336211-9337476 REVERSE LENGTH=421	438	421	0	96.1	82.4	88.6
Rsa1.0_01363.1.g26126.t1	gb|EOA20109.1| hypothetical protein CARUB_v10000388mg, partial [Capsella rubella]	561	674	0	120.1	94.7	97.5	hypothetical protein CARUB_v10000388mg, partial	gbpln	Capsella rubella	AT5G04590.1 | Symbols: SIR | sulfite reductase | chr5:1319404-1322298 FORWARD LENGTH=642	561	642	0	114.4	94.1	97.7
Rsa1.0_01363.1.g26127.t1	gb|EOA30567.1| hypothetical protein CARUB_v10013694mg [Capsella rubella]	485	447	1.00E-170	92.2	69.3	77.3	hypothetical protein CARUB_v10013694mg	gbpln	Capsella rubella	AT3G10480.1 | Symbols: ANAC050, NAC050 | NAC domain containing protein 50 | chr3:3264410-3266781 FORWARD LENGTH=447	485	447	1.00E-165	92.2	68.0	77.1
Rsa1.0_01363.1.g26128.t1	gb|EOA30567.1| hypothetical protein CARUB_v10013694mg [Capsella rubella]	462	447	0	96.8	75.5	83.8	hypothetical protein CARUB_v10013694mg	gbpln	Capsella rubella	AT3G10490.2 | Symbols: ANAC052, NAC052 | NAC domain containing protein 52 | chr3:3268075-3270608 FORWARD LENGTH=451	462	451	0	97.6	74.9	83.3
Rsa1.0_01363.1.g26129.t1	ref|NP_567270.1| putative F-box only protein 15 [Arabidopsis thaliana] gi|75265492|sp|Q9S9V1.1|FBX15_ARATH RecName: Full=Putative F-box only protein 15 gi|5732058|gb|AAD48957.1|AF149414_6 contains similarity to Pfam family PF00646 (F-box domain); score=11/3, E=0.23, N=1 [Arabidopsis thaliana] gi|7267227|emb|CAB80834.1| AT4g04690 [Arabidopsis thaliana] gi|332657012|gb|AEE82412.1| putative F-box only protein 15 [Arabidopsis thaliana]	392	378	1.00E-76	96.4	44.9	57.9	putative F-box only protein 15	gbpln	Arabidopsis thaliana	AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378	392	378	3.00E-79	96.4	44.9	57.9
Rsa1.0_01363.1.g26130.t2	gb|AAB04606.1| carboxypeptidase Y-like protein [Arabidopsis thaliana] gi|445120|prf||1908426A carboxypeptidase Y	723	539	0	74.6	60.6	64.7	carboxypeptidase Y-like protein	gbpln	Arabidopsis thaliana	AT3G10410.1 | Symbols: SCPL49, CPY | SERINE CARBOXYPEPTIDASE-LIKE 49 | chr3:3235518-3238063 REVERSE LENGTH=516	723	516	0	71.4	60.0	63.9
Rsa1.0_01363.1.g26131.t1	ref|NP_187650.4| lysine-specific histone demethylase 1 [Arabidopsis thaliana] gi|332641378|gb|AEE74899.1| lysine-specific histone demethylase 1 homolog 3 [Arabidopsis thaliana]	895	884	0	98.8	82.7	87.4	lysine-specific histone demethylase 1	gbpln	Arabidopsis thaliana	AT3G10390.1 | Symbols: FLD | Flavin containing amine oxidoreductase family protein | chr3:3229293-3232345 FORWARD LENGTH=884	895	884	0	98.8	82.7	87.4
Rsa1.0_01363.1.g26132.t2	ref|XP_002884791.1| hypothetical protein ARALYDRAFT_897214 [Arabidopsis lyrata subsp. lyrata] gi|297330631|gb|EFH61050.1| hypothetical protein ARALYDRAFT_897214 [Arabidopsis lyrata subsp. lyrata]	1067	1053	0	98.7	87.9	91.1	hypothetical protein ARALYDRAFT_897214	gbpln	Arabidopsis lyrata	AT3G10380.1 | Symbols: SEC8, ATSEC8 | subunit of exocyst complex 8 | chr3:3219922-3228356 REVERSE LENGTH=1053	1067	1053	0	98.7	88.1	91.4

Rsa1.0_01363.1.g26133.t1	ref|XP_002884790.1| hypothetical protein ARALYDRAFT_897212 [Arabidopsis lyrata subsp. lyrata] gi|297330630|gb|EFH61049.1| hypothetical protein ARALYDRAFT_897212 [Arabidopsis lyrata subsp. lyrata]	935	1005	0	107.5	85.7	90.7	hypothetical protein ARALYDRAFT_897212	gbpln	Arabidopsis lyrata	AT3G10360.1 | Symbols: APUM4, PUM4 | pumilio 4 | chr3:3211276-3215144 REVERSE LENGTH=1003	935	1003	0	107.3	85.5	90.8
Rsa1.0_01363.1.g26134.t1	ref|XP_002882661.1| transcription initiation factor IIB-2 [Arabidopsis lyrata subsp. lyrata] gi|297328501|gb|EFH58920.1| transcription initiation factor IIB-2 [Arabidopsis lyrata subsp. lyrata] gi|482566884|gb|EOA31073.1| hypothetical protein CARUB_v10014225mg [Capsella rubella]	312	312	0	100.0	99.0	99.7	transcription initiation factor IIB-2	gbpln	Arabidopsis lyrata	AT3G10330.1 | Symbols: | Cyclin-like family protein | chr3:3199907-3201642 FORWARD LENGTH=312	312	312	0	100.0	98.7	99.4
Rsa1.0_01364.1.g26135.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	243	1142	8.00E-22	470.0	28.0	41.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	243	292	3.00E-14	120.2	16.0	27.2
Rsa1.0_01364.1.g26136.t5	gb|AFJ66169.1| hypothetical protein 11M19.13 [Arabidopsis halleri]	766	1273	9.00E-77	166.2	22.8	30.5	hypothetical protein 11M19.13	gbpln	Arabidopsis halleri	#	#	#	#	#	#	#
Rsa1.0_01364.1.g26137.t1	ref|XP_002864021.1| hypothetical protein ARALYDRAFT_331396 [Arabidopsis lyrata subsp. lyrata] gi|297309856|gb|EFH40280.1| hypothetical protein ARALYDRAFT_331396 [Arabidopsis lyrata subsp. lyrata]	463	707	0	152.7	80.6	89.8	hypothetical protein ARALYDRAFT_331396	gbpln	Arabidopsis lyrata	AT5G49945.1 | Symbols: | Protein of unknown function (DUF1682) | chr5:20317418-20319432 FORWARD LENGTH=480	463	480	0	103.7	79.5	87.3
Rsa1.0_01364.1.g26138.t1	ref|NP_568717.2| pyridoxin (pyrodoxamine) 5'-phosphate oxidase [Arabidopsis thaliana] gi|75180502|sp|Q9LTX3.1|PPOX1_ARATH RecName: Full=Pyridoxine/pyridoxamine 5'-phosphate oxidase 1, chloroplastic; Short=AtPPOX1; Includes: RecName: Full=Pyridoxine/pyridoxamine 5'-phosphate oxidase; AltName: Full=PNP/PMP oxidase; Short=PNPOx; AltName: Full=Pyridoxal 5'-phosphate synthase; Includes: RecName: Full=Probable NAD(P)HX epimerase; Flags: Precursor gi|8777428|dbj|BAA97018.1| unnamed protein product [Arabidopsis thaliana] gi|332008496|gb|AED95879.1| pyridoxin (pyrodoxamine) 5'-phosphate oxidase [Arabidopsis thaliana]	460	530	0	115.2	89.6	95.0	pyridoxin (pyrodoxamine) 5'-phosphate oxidase	gbpln	Arabidopsis thaliana	AT5G49970.1 | Symbols: ATPPOX, PDX3, PPOX | pyridoxin (pyrodoxamine) 5'-phosphate oxidase | chr5:20329213-20332900 FORWARD LENGTH=530	460	530	0	115.2	89.6	95.0
Rsa1.0_01364.1.g26139.t1	ref|XP_002865768.1| auxin F-box protein 5 [Arabidopsis lyrata subsp. lyrata] gi|297311603|gb|EFH42027.1| auxin F-box protein 5 [Arabidopsis lyrata subsp. lyrata]	624	608	0	97.4	87.8	91.0	auxin F-box protein 5	gbpln	Arabidopsis lyrata	AT5G49980.1 | Symbols: AFB5 | auxin F-box protein 5 | chr5:20334420-20336531 REVERSE LENGTH=619	624	619	0	99.2	88.3	92.0
Rsa1.0_01364.1.g26140.t1	gb|EOA13509.1| hypothetical protein CARUB_v10026576mg [Capsella rubella]	408	386	0	94.6	91.2	92.4	hypothetical protein CARUB_v10026576mg	gbpln	Capsella rubella	AT5G50000.1 | Symbols: | Protein kinase superfamily protein | chr5:20342838-20345033 REVERSE LENGTH=385	408	385	0	94.4	89.7	91.7
Rsa1.0_01365.1.g26141.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01365.1.g26142.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01365.1.g26143.t3	gb|AAC28531.1| hypothetical protein [Arabidopsis thaliana]	423	439	1.00E-132	103.8	58.2	66.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G45940.1 | Symbols: | Protein of unknown function (DUF295) | chr2:18903032-18904181 FORWARD LENGTH=352	423	352	1.00E-134	83.2	56.3	65.0
Rsa1.0_01365.1.g26144.t1	ref|NP_193344.5| uncharacterized protein [Arabidopsis thaliana] gi|332658291|gb|AEE83691.1| uncharacterized protein AT4G16090 [Arabidopsis thaliana]	355	268	9.00E-95	75.5	50.4	57.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G16090.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G45930.1); Has 76 Blast hits to 76 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 76; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:9103078-9103965 FORWARD LENGTH=268	355	268	2.00E-97	75.5	50.4	57.2
Rsa1.0_01365.1.g26145.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	318	1142	8.00E-50	359.1	42.5	57.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	318	575	5.00E-24	180.8	28.0	43.1

Rsa1.0_01365.1.g26146.t1	ref|XP_002880209.1| hypothetical protein ARALYDRAFT_904046 [Arabidopsis lyrata subsp. lyrata] gi|297326048|gb|EFH56468.1| hypothetical protein ARALYDRAFT_904046 [Arabidopsis lyrata subsp. lyrata]	744	352	1.00E-124	47.3	30.6	35.9	hypothetical protein ARALYDRAFT_904046	gbpln	Arabidopsis lyrata	AT2G45940.1 | Symbols: | Protein of unknown function (DUF295) | chr2:18903032-18904181 FORWARD LENGTH=352	744	352	1.00E-126	47.3	30.5	35.2
Rsa1.0_01365.1.g26147.t2	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	275	1838	2.00E-43	668.4	34.5	45.8	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01365.1.g26148.t1	ref|NP_001190632.1| Chalcone-flavanone isomerase family protein [Arabidopsis thaliana] gi|332010800|gb|AED98183.1| Chalcone-flavanone isomerase family protein [Arabidopsis thaliana]	163	545	1.00E-13	334.4	34.4	41.1	Chalcone-flavanone isomerase family protein	gbpln	Arabidopsis thaliana	AT5G66230.2 | Symbols: | Chalcone-flavanone isomerase family protein | chr5:26461177-26463873 FORWARD LENGTH=545	163	545	4.00E-16	334.4	34.4	41.1
Rsa1.0_01365.1.g26149.t1	dbj|BAB10876.1| polyprotein [Arabidopsis thaliana]	1408	1429	0	101.5	59.1	73.1	polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1408	1262	1.00E-116	89.6	14.6	21.8
Rsa1.0_01365.1.g26150.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01365.1.g26151.t1	ref|XP_002882042.1| hypothetical protein ARALYDRAFT_483735 [Arabidopsis lyrata subsp. lyrata] gi|297327881|gb|EFH58301.1| hypothetical protein ARALYDRAFT_483735 [Arabidopsis lyrata subsp. lyrata]	341	334	1.00E-134	97.9	78.6	86.2	hypothetical protein ARALYDRAFT_483735	gbpln	Arabidopsis lyrata	AT2G45950.1 | Symbols: ASK20, SK20 | SKP1-like 20 | chr2:18904611-18906967 REVERSE LENGTH=342	341	342	1.00E-135	100.3	76.8	85.0
Rsa1.0_01366.1.g26152.t1	ref|XP_002866219.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] gi|297312054|gb|EFH42478.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	227	646	4.00E-14	284.6	18.5	20.7	calmodulin-binding protein	gbpln	Arabidopsis lyrata	AT5G57580.1 | Symbols: | Calmodulin-binding protein | chr5:23314994-23317683 REVERSE LENGTH=647	227	647	2.00E-16	285.0	18.1	20.3
Rsa1.0_01366.1.g26153.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	889	1239	0	139.4	42.1	48.1	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	889	1262	3.00E-24	142.0	7.9	11.0
Rsa1.0_01366.1.g26154.t1	gb|EOA34747.1| hypothetical protein CARUB_v10022319mg [Capsella rubella]	306	310	1.00E-103	101.3	61.8	74.5	hypothetical protein CARUB_v10022319mg	gbpln	Capsella rubella	AT1G32600.1 | Symbols: | F-box associated ubiquitination effector family protein | chr1:11794802-11795683 FORWARD LENGTH=293	306	293	1.00E-91	95.8	56.2	72.2
Rsa1.0_01366.1.g26155.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01366.1.g26156.t1	ref|XP_002876270.1| BME3/BME3-ZF [Arabidopsis lyrata subsp. lyrata] gi|297322108|gb|EFH52529.1| BME3/BME3-ZF [Arabidopsis lyrata subsp. lyrata]	334	319	1.00E-128	95.5	82.6	87.7	BME3/BME3-ZF	gbpln	Arabidopsis lyrata	AT3G54810.1 | Symbols: BME3-ZF, BME3, GATA8 | Plant-specific GATA-type zinc finger transcription factor family protein | chr3:20296957-20298236 FORWARD LENGTH=322	334	322	1.00E-129	96.4	83.2	88.3
Rsa1.0_01366.1.g26157.t4	dbj|BAB11308.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	668	1013	1.00E-10	151.6	5.8	8.1	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01367.1.g26158.t1	gb|AAF98418.1|AC026238_10 Hypothetical protein [Arabidopsis thaliana]	684	742	0	108.5	87.6	92.7	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G18560.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr1:6385614-6388005 FORWARD LENGTH=690	684	690	0	100.9	87.6	92.7
Rsa1.0_01367.1.g26159.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01367.1.g26160.t2	gb|ACR48187.1| MYB domain protein 51-1 [Brassica rapa subsp. pekinensis]	350	320	1.00E-133	91.4	77.1	82.0	MYB domain protein 51-1	gbpln	Brassica rapa	AT1G18570.1 | Symbols: MYB51, AtMYB51, BW51A, BW51B, HIG1 | myb domain protein 51 | chr1:6389765-6391026 FORWARD LENGTH=352	350	352	1.00E-122	100.6	71.7	79.4
Rsa1.0_01367.1.g26161.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01367.1.g26162.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01368.1.g26163.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01368.1.g26164.t1	ref|NP_567275.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|16604679|gb|AAL24132.1| putative WD-repeat membrane protein [Arabidopsis thaliana] gi|20465603|gb|AAM20284.1| putative WD-repeat membrane protein [Arabidopsis thaliana] gi|332657045|gb|AEE82445.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	1130	910	0	80.5	72.5	77.1	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G04940.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr4:2511212-2517052 REVERSE LENGTH=910	1130	910	0	80.5	72.5	77.1

Rsa1.0_01368.1.g26165.t1	ref|NP_567274.1| homeobox-leucine zipper protein PROTODERMAL FACTOR 2 [Arabidopsis thaliana] gi|75331628|sp|Q93V99.1|PDF2_ARATH RecName: Full=Homeobox-leucine zipper protein PROTODERMAL FACTOR 2; AltName: Full=HD-ZIP protein PDF2; AltName: Full=Homeodomain transcription factor PDF2 gi|15983372|gb|AAL11554.1|AF424560_1 AT4g04890/T1J1_3 [Arabidopsis thaliana] gi|14276060|dbj|BAB58961.1| protodermal factor2 [Arabidopsis thaliana] gi|17064998|gb|AAL32653.1| Unknown protein [Arabidopsis thaliana] gi|23197872|gb|AAN15463.1| Unknown protein [Arabidopsis thaliana] gi|332657038|gb|AEE82438.1| homeobox-leucine zipper protein PROTODERMAL FACTOR 2 [Arabidopsis thaliana]	742	743	0	100.1	93.7	96.9	homeobox-leucine zipper protein PROTODERMAL FACTOR 2	gbpln	Arabidopsis thaliana	AT4G04890.1 | Symbols: PDF2 | protodermal factor 2 | chr4:2476970-2480090 REVERSE LENGTH=743	742	743	0	100.1	93.7	96.9
Rsa1.0_01368.1.g26166.t1	gb|AAF22272.1|AF162913_1 S-locus related 1 [Raphanus raphanistrum subsp. raphanistrum]	433	364	0	84.1	83.1	83.8	S-locus related 1	gbpln	Raphanus raphanistrum	AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850	433	850	1.00E-158	196.3	62.1	75.1
Rsa1.0_01368.1.g26167.t2	ref|NP_564398.1| putative FBD-associated F-box protein [Arabidopsis thaliana] gi|302425238|sp|Q9LQM1.2|FBD39_ARATH RecName: Full=Probable FBD-associated F-box protein At1g32375 gi|332193353|gb|AEE31474.1| putative FBD-associated F-box protein [Arabidopsis thaliana]	434	422	1.00E-96	97.2	50.9	63.4	putative FBD-associated F-box protein	gbpln	Arabidopsis thaliana	AT1G32375.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:11679230-11680679 FORWARD LENGTH=422	434	422	3.00E-99	97.2	50.9	63.4
Rsa1.0_01368.1.g26168.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1479	1499	0	101.4	62.8	77.9	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1479	158	3.00E-33	10.7	4.7	5.9
Rsa1.0_01369.1.g26169.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01369.1.g26170.t1	ref|XP_002868776.1| ribulose bisphosphate carboxylase [Arabidopsis lyrata subsp. lyrata] gi|297314612|gb|EFH45035.1| ribulose bisphosphate carboxylase [Arabidopsis lyrata subsp. lyrata]	181	181	1.00E-101	100.0	96.7	98.9	ribulose bisphosphate carboxylase	gbpln	Arabidopsis lyrata	AT5G38430.1 | Symbols: | Ribulose bisphosphate carboxylase (small chain) family protein | chr5:15384350-15385155 REVERSE LENGTH=181	181	181	1.00E-101	100.0	94.5	97.2
Rsa1.0_01369.1.g26171.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	96	1142	2.00E-15	1189.6	42.7	56.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01369.1.g26172.t1	emb|CAZ40327.1| hypothetical protein [Raphanus sativus]	79	401	2.00E-11	507.6	48.1	58.2	hypothetical protein	gbpln	Raphanus sativus	#	#	#	#	#	#	#
Rsa1.0_01369.1.g26173.t1	ref|XP_002868774.1| CYP735A1 [Arabidopsis lyrata subsp. lyrata] gi|297314610|gb|EFH45033.1| CYP735A1 [Arabidopsis lyrata subsp. lyrata]	460	518	0	112.6	92.2	96.5	CYP735A1	gbpln	Arabidopsis lyrata	AT5G38450.1 | Symbols: CYP735A1 | cytochrome P450, family 735, subfamily A, polypeptide 1 | chr5:15394000-15397233 REVERSE LENGTH=518	460	518	0	112.6	91.3	95.2
Rsa1.0_01370.1.g26174.t1	ref|XP_002893943.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339785|gb|EFH70202.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	432	432	0	100.0	95.6	98.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G43190.2 | Symbols: PTB3 | polypyrimidine tract-binding protein 3 | chr1:16275432-16278185 REVERSE LENGTH=432	432	432	0	100.0	94.9	98.1
Rsa1.0_01370.1.g26175.t1	ref|XP_002893941.1| hypothetical protein ARALYDRAFT_473756 [Arabidopsis lyrata subsp. lyrata] gi|297339783|gb|EFH70200.1| hypothetical protein ARALYDRAFT_473756 [Arabidopsis lyrata subsp. lyrata]	260	261	1.00E-139	100.4	93.5	96.5	hypothetical protein ARALYDRAFT_473756	gbpln	Arabidopsis lyrata	AT1G43130.1 | Symbols: LCV2 | like COV 2 | chr1:16228661-16231158 REVERSE LENGTH=261	260	261	1.00E-141	100.4	93.1	96.5
Rsa1.0_01370.1.g26176.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	499	1239	1.00E-168	248.3	56.3	64.1	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	499	1262	1.00E-68	252.9	28.1	43.5
Rsa1.0_01370.1.g26177.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	385	1142	2.00E-71	296.6	32.5	40.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	385	575	3.00E-30	149.4	15.1	21.0

Rsa1.0_01370.1.g26178.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	854	1023	1.00E-66	119.8	14.6	19.7	F27F5.21	gbpln	Arabidopsis thaliana	AT1G76660.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT5G52430.1); Has 353 Blast hits to 231 proteins in 60 species: Archae - 0; Bacteria - 6; Metazoa - 57; Fungi - 22; Plants - 125; Viruses - 4; Other Eukaryotes - 139 (source: NCBI BLink). | chr1:28769157-28771036 REVERSE LENGTH=431	854	431	9.00E-31	50.5	10.4	13.0
Rsa1.0_01370.1.g26179.t1	gb|AAF97279.1|AC010164_1 Hypothetical protein [Arabidopsis thaliana]	110	352	4.00E-14	320.0	39.1	60.0	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01370.1.g26180.t1	ref|XP_002890242.1| hypothetical protein ARALYDRAFT_335032 [Arabidopsis lyrata subsp. lyrata] gi|297336084|gb|EFH66501.1| hypothetical protein ARALYDRAFT_335032 [Arabidopsis lyrata subsp. lyrata]	333	775	5.00E-32	232.7	31.2	45.9	hypothetical protein ARALYDRAFT_335032	gbpln	Arabidopsis lyrata	AT2G07200.1 | Symbols: | Cysteine proteinases superfamily protein | chr2:2989205-2989878 FORWARD LENGTH=151	333	151	3.00E-21	45.3	17.4	26.4
Rsa1.0_01371.1.g26181.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01371.1.g26182.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01371.1.g26183.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01371.1.g26184.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01371.1.g26185.t1	emb|CAA54951.1| ribosomal protein S19 [Arabidopsis thaliana] gi|459422|emb|CAA54965.1| mitochondrial ribosomal protein S19, nuclear encoded [Arabidopsis thaliana]	206	212	6.00E-97	102.9	86.9	92.7	ribosomal protein S19	gbpln	Arabidopsis thaliana	AT5G47320.1 | Symbols: RPS19 | ribosomal protein S19 | chr5:19203801-19204951 FORWARD LENGTH=212	206	212	1.00E-98	102.9	86.4	92.2
Rsa1.0_01371.1.g26186.t2	gb|AAC63844.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1699	1231	0	72.5	42.0	52.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G23810.1 | Symbols: SAHH2, ATSAHH2 | S-adenosyl-l-homocysteine (SAH) hydrolase 2 | chr3:8588013-8589671 REVERSE LENGTH=485	1699	485	0	28.5	28.0	28.1
Rsa1.0_01371.1.g26187.t1	ref|NP_566740.1| protein ralf-like 24 [Arabidopsis thaliana] gi|75273714|sp|Q9LK37.1|RLF24_ARATH RecName: Full=Protein RALF-like 24; Flags: Precursor gi|9293954|dbj|BAB01857.1| unnamed protein product [Arabidopsis thaliana] gi|332643295|gb|AEE76816.1| protein ralf-like 24 [Arabidopsis thaliana]	118	118	2.00E-48	100.0	85.6	94.1	protein ralf-like 24	gbpln	Arabidopsis thaliana	AT3G23805.1 | Symbols: RALFL24 | ralf-like 24 | chr3:8586467-8586823 FORWARD LENGTH=118	118	118	4.00E-51	100.0	85.6	94.1
Rsa1.0_01371.1.g26188.t1	gb|EOA32655.1| hypothetical protein CARUB_v10015952mg [Capsella rubella]	478	476	0	99.6	87.0	93.1	hypothetical protein CARUB_v10015952mg	gbpln	Capsella rubella	AT3G23770.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr3:8565556-8567196 FORWARD LENGTH=476	478	476	0	99.6	84.7	89.1
Rsa1.0_01372.1.g26189.t1	ref|XP_002887604.1| hypothetical protein ARALYDRAFT_476705 [Arabidopsis lyrata subsp. lyrata] gi|297333445|gb|EFH63863.1| hypothetical protein ARALYDRAFT_476705 [Arabidopsis lyrata subsp. lyrata]	108	108	3.00E-54	100.0	94.4	97.2	hypothetical protein ARALYDRAFT_476705	gbpln	Arabidopsis lyrata	AT1G75580.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:28377530-28377856 FORWARD LENGTH=108	108	108	2.00E-56	100.0	93.5	96.3
Rsa1.0_01372.1.g26190.t1	gb|AAC62132.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	608	1137	1.00E-141	187.0	49.8	67.1	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	608	1262	3.00E-36	207.6	18.3	29.3
Rsa1.0_01372.1.g26191.t1	ref|NP_177687.1| glycine-rich protein [Arabidopsis thaliana] gi|9369369|gb|AAF87118.1|AC006434_14 F10A5.23 [Arabidopsis thaliana] gi|332197611|gb|AEE35732.1| glycine-rich protein [Arabidopsis thaliana]	144	167	5.00E-42	116.0	77.1	82.6	glycine-rich protein	gbpln	Arabidopsis thaliana	AT1G75550.1 | Symbols: | glycine-rich protein | chr1:28369437-28369940 REVERSE LENGTH=167	144	167	1.00E-44	116.0	77.1	82.6
Rsa1.0_01372.1.g26192.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01372.1.g26193.t1	gb|EOA35448.1| hypothetical protein CARUB_v10020651mg [Capsella rubella]	92	325	4.00E-27	353.3	72.8	80.4	hypothetical protein CARUB_v10020651mg	gbpln	Capsella rubella	AT1G75540.1 | Symbols: STH2 | salt tolerance homolog2 | chr1:28366059-28367398 FORWARD LENGTH=331	92	331	6.00E-29	359.8	71.7	77.2
Rsa1.0_01372.1.g26194.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1657	1213	0	73.2	26.5	38.9	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1657	626	1.00E-57	37.8	7.5	12.6
Rsa1.0_01372.1.g26195.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01373.1.g26196.t1	ref|XP_002880160.1| hypothetical protein ARALYDRAFT_483647 [Arabidopsis lyrata subsp. lyrata] gi|297325999|gb|EFH56419.1| hypothetical protein ARALYDRAFT_483647 [Arabidopsis lyrata subsp. lyrata]	116	239	1.00E-23	206.0	46.6	53.4	hypothetical protein ARALYDRAFT_483647	gbpln	Arabidopsis lyrata	AT2G45140.1 | Symbols: PVA12 | plant VAP homolog 12 | chr2:18611029-18612971 FORWARD LENGTH=239	116	239	4.00E-26	206.0	46.6	53.4
Rsa1.0_01373.1.g26197.t6	gb|EOA29123.1| hypothetical protein CARUB_v10025390mg [Capsella rubella]	729	440	1.00E-180	60.4	45.1	47.6	hypothetical protein CARUB_v10025390mg	gbpln	Capsella rubella	AT2G45150.3 | Symbols: | cytidinediphosphate diacylglycerol synthase 4 | chr2:18613519-18615347 FORWARD LENGTH=382	729	382	1.00E-174	52.4	43.9	46.1
Rsa1.0_01373.1.g26198.t1	gb|EOA28527.1| hypothetical protein CARUB_v10024743mg [Capsella rubella]	597	638	0	106.9	79.9	86.1	hypothetical protein CARUB_v10024743mg	gbpln	Capsella rubella	AT2G45160.1 | Symbols: HAM1, ATHAM1, LOM1 | GRAS family transcription factor | chr2:18618110-18620032 REVERSE LENGTH=640	597	640	0	107.2	78.7	86.6
Rsa1.0_01373.1.g26199.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	341	1274	4.00E-47	373.6	33.4	46.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	341	303	2.00E-45	88.9	30.2	44.3
Rsa1.0_01373.1.g26200.t1	gb|EOA28141.1| hypothetical protein CARUB_v10024330mg [Capsella rubella]	122	122	2.00E-59	100.0	93.4	98.4	hypothetical protein CARUB_v10024330mg	gbpln	Capsella rubella	AT2G45170.2 | Symbols: ATATG8E, ATG8E | AUTOPHAGY 8E | chr2:18624545-18625526 FORWARD LENGTH=122	122	122	4.00E-61	100.0	91.8	97.5
Rsa1.0_01373.1.g26201.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	295	1274	2.00E-61	431.9	41.4	57.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	295	303	8.00E-25	102.7	19.7	27.8
Rsa1.0_01373.1.g26202.t1	gb|EOA28114.1| hypothetical protein CARUB_v10024298mg [Capsella rubella]	131	134	5.00E-48	102.3	90.8	95.4	hypothetical protein CARUB_v10024298mg	gbpln	Capsella rubella	AT2G45180.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr2:18626377-18626781 FORWARD LENGTH=134	131	134	8.00E-49	102.3	87.0	94.7
Rsa1.0_01374.1.g26203.t1	ref|NP_200507.1| cytokinin dehydrogenase 3 [Arabidopsis thaliana] gi|20138027|sp|Q9LTS3.1|CKX3_ARATH RecName: Full=Cytokinin dehydrogenase 3; AltName: Full=Cytokinin oxidase 3; Short=AtCKX3; Short=CKO 3; Flags: Precursor gi|11120510|gb|AAG30906.1|AF303979_1 cytokinin oxidase [Arabidopsis thaliana] gi|8777437|dbj|BAA97027.1| cytokinin oxidase [Arabidopsis thaliana] gi|190016002|gb|ACE62889.1| At5g56970 [Arabidopsis thaliana] gi|332009445|gb|AED96828.1| cytokinin dehydrogenase 3 [Arabidopsis thaliana]	519	523	0	100.8	85.7	94.0	cytokinin dehydrogenase 3	gbpln	Arabidopsis thaliana	AT5G56970.1 | Symbols: CKX3, ATCKX3 | cytokinin oxidase 3 | chr5:23044944-23048245 REVERSE LENGTH=523	519	523	0	100.8	85.7	94.0
Rsa1.0_01374.1.g26204.t1	gb|EOA13542.1| hypothetical protein CARUB_v10026605mg [Capsella rubella]	378	376	1.00E-165	99.5	90.5	96.6	hypothetical protein CARUB_v10026605mg	gbpln	Capsella rubella	AT5G56950.1 | Symbols: NFA03, NFA3, NAP1;3 | nucleosome assembly protein 1;3 | chr5:23032618-23035299 FORWARD LENGTH=374	378	374	1.00E-167	98.9	89.2	95.8
Rsa1.0_01374.1.g26205.t2	ref|XP_002863022.1| ribosomal protein S16 family protein [Arabidopsis lyrata subsp. lyrata] gi|297793207|ref|XP_002864488.1| ribosomal protein S16 family protein [Arabidopsis lyrata subsp. lyrata] gi|297308822|gb|EFH39281.1| ribosomal protein S16 family protein [Arabidopsis lyrata subsp. lyrata] gi|297310323|gb|EFH40747.1| ribosomal protein S16 family protein [Arabidopsis lyrata subsp. lyrata]	73	135	2.00E-26	184.9	84.9	87.7	ribosomal protein S16 family protein	gbpln	Arabidopsis lyrata	AT5G56940.1 | Symbols: | Ribosomal protein S16 family protein | chr5:23030879-23032200 FORWARD LENGTH=135	73	135	7.00E-29	184.9	83.6	87.7
Rsa1.0_01374.1.g26206.t1	ref|NP_850984.4| Heat shock protein 70 [Arabidopsis thaliana] gi|378548352|sp|F4HQD4.1|HSP7P_ARATH RecName: Full=Heat shock 70 kDa protein 15; AltName: Full=Heat shock protein 70-15; Short=AtHsp70-15 gi|332198204|gb|AEE36325.1| Heat shock protein 70 [Arabidopsis thaliana]	136	831	7.00E-47	611.0	64.7	66.2	Heat shock protein 70	gbpln	Arabidopsis thaliana	AT1G79920.1 | Symbols: | Heat shock protein 70 (Hsp 70) family protein | chr1:30058935-30062224 REVERSE LENGTH=831	136	831	2.00E-49	611.0	64.7	66.2
Rsa1.0_01374.1.g26207.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01375.1.g26208.t1	ref|XP_002876168.1| hypothetical protein ARALYDRAFT_485652 [Arabidopsis lyrata subsp. lyrata] gi|297322006|gb|EFH52427.1| hypothetical protein ARALYDRAFT_485652 [Arabidopsis lyrata subsp. lyrata]	134	169	1.00E-23	126.1	53.0	59.0	hypothetical protein ARALYDRAFT_485652	gbpln	Arabidopsis lyrata	AT2G36320.1 | Symbols: | A20/AN1-like zinc finger family protein | chr2:15229388-15229873 FORWARD LENGTH=161	134	161	7.00E-26	120.1	50.0	55.2

Rsa1.0_01375.1.g26209.t1	gb|AAF63124.1|AC009526_9 Hypothetical protein [Arabidopsis thaliana]	491	408	2.00E-47	83.1	21.8	27.3	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G43722.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28730.1); Has 924 Blast hits to 912 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 222; Fungi - 31; Plants - 661; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:16496403-16497377 FORWARD LENGTH=324	491	324	5.00E-50	66.0	21.8	27.3
Rsa1.0_01375.1.g26210.t1	ref|XP_002877827.1| acyl-CoA oxidase 4 [Arabidopsis lyrata subsp. lyrata] gi|297323665|gb|EFH54086.1| acyl-CoA oxidase 4 [Arabidopsis lyrata subsp. lyrata]	439	436	0	99.3	87.5	93.6	acyl-CoA oxidase 4	gbpln	Arabidopsis lyrata	AT3G51840.1 | Symbols: ACX4, ATSCX, ATG6 | acyl-CoA oxidase 4 | chr3:19225653-19229008 REVERSE LENGTH=436	439	436	0	99.3	87.5	93.2
Rsa1.0_01375.1.g26211.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01375.1.g26212.t1	ref|XP_002876106.1| calcium-dependent protein kinase 13 [Arabidopsis lyrata subsp. lyrata] gi|297321944|gb|EFH52365.1| calcium-dependent protein kinase 13 [Arabidopsis lyrata subsp. lyrata]	528	528	0	100.0	97.0	98.5	calcium-dependent protein kinase 13	gbpln	Arabidopsis lyrata	AT3G51850.1 | Symbols: CPK13 | calcium-dependent protein kinase 13 | chr3:19232667-19235526 FORWARD LENGTH=528	528	528	0	100.0	96.8	98.5
Rsa1.0_01375.1.g26213.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	205	149	3.00E-24	72.7	24.9	35.1	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01376.1.g26214.t1	ref|NP_199548.1| homeobox-leucine zipper protein HAT2 [Arabidopsis thaliana] gi|12643283|sp|P46601.2|HAT2_ARATH RecName: Full=Homeobox-leucine zipper protein HAT2; AltName: Full=Homeodomain-leucine zipper protein HAT2; Short=HD-ZIP protein 2 gi|16226634|gb|AAL16219.1|AF428450_1 AT5g47370/MQL5_23 [Arabidopsis thaliana] gi|8809620|dbj|BAA97171.1| homeobox-leucine zipper protein-like [Arabidopsis thaliana] gi|15208392|dbj|BAB63202.1| homeodomain leucine-zipper protein HAT2 [Arabidopsis thaliana] gi|15450447|gb|AAK96517.1| AT5g47370/MQL5_23 [Arabidopsis thaliana] gi|16974455|gb|AAL31231.1| AT5g47370/MQL5_23 [Arabidopsis thaliana] gi|18857720|emb|CAD24013.1| homeodomain-leucine zipper protein HAT2 [Arabidopsis thaliana] gi|332008120|gb|AED95503.1| homeobox-leucine zipper protein HAT2 [Arabidopsis thaliana]	354	283	1.00E-126	79.9	66.1	69.8	homeobox-leucine zipper protein HAT2	gbpln	Arabidopsis thaliana	AT5G47370.1 | Symbols: HAT2 | Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein | chr5:19216482-19217647 REVERSE LENGTH=283	354	283	1.00E-129	79.9	66.1	69.8
Rsa1.0_01376.1.g26215.t1	gb|EOA13727.1| hypothetical protein CARUB_v10026804mg [Capsella rubella]	318	316	2.33E-156	99.4	78.3	85.2	hypothetical protein CARUB_v10026804mg	gbpln	Capsella rubella	AT5G47330.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:19207170-19208711 FORWARD LENGTH=314	318	314	1.00E-147	98.7	77.0	87.1
Rsa1.0_01376.1.g26216.t1	gb|ABD64947.1| ethylene responsive element binding factor, putative [Brassica oleracea]	277	296	1.00E-133	106.9	88.8	94.2	ethylene responsive element binding factor, putative	gbpln	Brassica oleracea	AT5G47230.1 | Symbols: ERF5, ATERF-5, ATERF5 | ethylene responsive element binding factor 5 | chr5:19180072-19180974 FORWARD LENGTH=300	277	300	1.00E-104	108.3	76.5	85.2
Rsa1.0_01376.1.g26217.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01376.1.g26218.t1	gb|ABD64951.1| ethylene responsive element binding factor, putative [Brassica oleracea]	228	240	3.00E-96	105.3	85.1	90.4	ethylene responsive element binding factor, putative	gbpln	Brassica oleracea	AT5G47220.1 | Symbols: ATERF2, ATERF-2, ERF2 | ethylene responsive element binding factor 2 | chr5:19172023-19172754 REVERSE LENGTH=243	228	243	8.00E-73	106.6	68.0	77.2
Rsa1.0_01376.1.g26219.t1	gb|ABD64914.1| nuclear RNA binding protein, putative [Brassica oleracea]	372	336	1.00E-126	90.3	79.3	82.8	nuclear RNA binding protein, putative	gbpln	Brassica oleracea	AT4G17520.1 | Symbols: | Hyaluronan / mRNA binding family | chr4:9771496-9773313 FORWARD LENGTH=360	372	360	2.00E-85	96.8	55.9	68.3
Rsa1.0_01376.1.g26220.t1	gb|EOA14024.1| hypothetical protein CARUB_v10027156mg [Capsella rubella]	202	202	1.00E-115	100.0	99.0	100.0	hypothetical protein CARUB_v10027156mg	gbpln	Capsella rubella	AT5G47200.1 | Symbols: ATRABD2B, ATRAB1A, RAB1A | RAB GTPase homolog 1A | chr5:19167029-19168718 FORWARD LENGTH=202	202	202	1.00E-117	100.0	98.5	99.5
Rsa1.0_01376.1.g26221.t2	gb|ABD64915.1| plastid ribosomal protein L19, putative [Brassica oleracea]	201	214	4.00E-40	106.5	47.3	48.3	plastid ribosomal protein L19, putative	gbpln	Brassica oleracea	AT4G17560.1 | Symbols: | Ribosomal protein L19 family protein | chr4:9780343-9781752 FORWARD LENGTH=225	201	225	2.00E-40	111.9	45.8	47.3

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<tr><td>Rsa1.0_01376.1.g26223.t1</td><td>gb|ABD64917.1| GATA zinc finger containing protein [Brassica oleracea]</td><td>485</td><td>466</td><td>0</td><td>96.1</td><td>85.2</td><td>89.7</td><td>GATA zinc finger containing protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47140.1 | Symbols: GATA27 | GATA transcription factor 27 | chr5:19145108-19147303 FORWARD LENGTH=470</td><td>485</td><td>470</td><td>1.00E-172</td><td>96.9</td><td>72.8</td><td>82.1</td></tr>
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<tr><td>Rsa1.0_01376.1.g26225.t1</td><td>gb|ABD64919.1| Lil3 protein, putative [Brassica oleracea]</td><td>268</td><td>248</td><td>1.00E-115</td><td>92.5</td><td>82.1</td><td>84.3</td><td>Lil3 protein, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47110.1 | Symbols: LIL3:2 | Chlorophyll A-B binding family protein | chr5:19134218-19135238 REVERSE LENGTH=258</td><td>268</td><td>258</td><td>1.00E-114</td><td>96.3</td><td>81.7</td><td>87.3</td></tr>
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<tr><td>Rsa1.0_01377.1.g26228.t1</td><td>ref|XP_002867311.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313147|gb|EFH43570.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>412</td><td>412</td><td>0</td><td>100.0</td><td>94.4</td><td>98.3</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G31170.3 | Symbols: | Protein kinase superfamily protein | chr4:15153499-15154846 REVERSE LENGTH=412</td><td>412</td><td>412</td><td>0</td><td>100.0</td><td>94.2</td><td>98.1</td></tr>
<tr><td>Rsa1.0_01377.1.g26229.t1</td><td>emb|CAA16530.1| hypothetical protein [Arabidopsis thaliana] gi|7270029|emb|CAB79845.1| hypothetical protein [Arabidopsis thaliana]</td><td>313</td><td>291</td><td>1.00E-100</td><td>93.0</td><td>64.9</td><td>78.0</td><td>hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G31270.1 | Symbols: | sequence-specific DNA binding transcription factors | chr4:15183291-15184503 REVERSE LENGTH=294</td><td>313</td><td>294</td><td>1.00E-101</td><td>93.9</td><td>64.9</td><td>78.0</td></tr>
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<tr><td>Rsa1.0_01377.1.g26231.t1</td><td>gb|EOA17355.1| hypothetical protein CARUB_v10005646mg [Capsella rubella]</td><td>233</td><td>233</td><td>1.00E-134</td><td>100.0</td><td>100.0</td><td>100.0</td><td>hypothetical protein CARUB_v10005646mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G31300.3 | Symbols: PBA1 | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr4:15188927-15190935 FORWARD LENGTH=233</td><td>233</td><td>233</td><td>1.00E-135</td><td>100.0</td><td>99.1</td><td>99.6</td></tr>
<tr><td>Rsa1.0_01377.1.g26232.t1</td><td>gb|EOA18510.1| hypothetical protein CARUB_v10007062mg [Capsella rubella]</td><td>183</td><td>191</td><td>9.00E-83</td><td>104.4</td><td>85.2</td><td>90.7</td><td>hypothetical protein CARUB_v10007062mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G31320.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:15193993-15194562 REVERSE LENGTH=189</td><td>183</td><td>189</td><td>4.00E-82</td><td>103.3</td><td>81.4</td><td>89.1</td></tr>
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<tr><td>Rsa1.0_01377.1.g26235.t1</td><td>ref|NP_197748.1| calmodulin-like domain protein kinase 9 [Arabidopsis thaliana] gi|75319661|sp|Q42396.1|CDPKC_ARATH RecName: Full=Calcium-dependent protein kinase 12; AltName: Full=Calcium-dependent protein kinase isoform CDPK9; Short=AtCDPK9 gi|836938|gb|AAA67653.1| calcium-dependent protein kinase [Arabidopsis thaliana] gi|836946|gb|AAA67657.1| calcium-dependent protein kinase [Arabidopsis thaliana] gi|8809701|dbj|BAA97242.1| calcium-dependent protein kinase [Arabidopsis thaliana] gi|110738049|dbj|BAF00959.1| calcium-dependent protein kinase [Arabidopsis thaliana] gi|111074232|gb|ABH04489.1| At5g23580 [Arabidopsis thaliana] gi|332005803|gb|AED93186.1| calmodulin-like domain protein kinase 9 [Arabidopsis thaliana]</td><td>199</td><td>490</td><td>3.00E-45</td><td>246.2</td><td>48.7</td><td>53.8</td><td>calmodulin-like domain protein kinase 9</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G23580.1 | Symbols: CDPK9, ATCDPK9, CPK12, ATCPK12 | calmodulin-like domain protein kinase 9 | chr5:7950388-7952433 REVERSE LENGTH=490</td><td>199</td><td>490</td><td>1.00E-47</td><td>246.2</td><td>48.7</td><td>53.8</td></tr>
<tr><td>Rsa1.0_01377.1.g26236.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT4G21790.1 | Symbols: TOM1, ATTOM1 | tobamovirus multiplication 1 | chr4:11569924-11572163 FORWARD LENGTH=291</td><td>117</td><td>291</td><td>4.00E-13</td><td>248.7</td><td>34.2</td><td>43.6</td></tr>
<tr><td>Rsa1.0_01378.1.g26237.t1</td><td>ref|XP_002894513.1| WRKY10 [Arabidopsis lyrata subsp. lyrata] gi|297340355|gb|EFH70772.1| WRKY10 [Arabidopsis lyrata subsp. lyrata]</td><td>400</td><td>495</td><td>2.00E-80</td><td>123.8</td><td>49.3</td><td>71.3</td><td>WRKY10</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G55600.1 | Symbols: WRKY10, ATWRKY10, MINI3 | WRKY DNA-binding protein 10 | chr1:20774049-20776293 REVERSE LENGTH=485</td><td>400</td><td>485</td><td>2.00E-65</td><td>121.3</td><td>45.0</td><td>66.0</td></tr>
<tr><td>Rsa1.0_01378.1.g26238.t1</td><td>dbj|BAE98403.1| putative non-LTR reverse transcriptase [Arabidopsis thaliana]</td><td>276</td><td>278</td><td>5.00E-34</td><td>100.7</td><td>30.1</td><td>46.7</td><td>putative non-LTR reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295</td><td>276</td><td>295</td><td>1.00E-28</td><td>106.9</td><td>25.7</td><td>44.6</td></tr>
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<tr><td>Rsa1.0_01378.1.g26240.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01378.1.g26241.t1</td><td>gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]</td><td>198</td><td>578</td><td>1.00E-30</td><td>291.9</td><td>34.8</td><td>47.5</td><td>hypothetical protein 27.t00126</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G20400.1 | Symbols: | Protein of unknown function (DUF1204) | chr1:7072192-7075838 REVERSE LENGTH=944</td><td>198</td><td>944</td><td>1.00E-16</td><td>476.8</td><td>22.7</td><td>38.9</td></tr>
<tr><td>Rsa1.0_01379.1.g26242.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01379.1.g26243.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01379.1.g26244.t1</td><td>emb|CAN72236.1| hypothetical protein VITISV_032806 [Vitis vinifera]</td><td>337</td><td>513</td><td>2.00E-36</td><td>152.2</td><td>31.2</td><td>44.2</td><td>hypothetical protein VITISV_032806</td><td>gbpln</td><td>Vitis vinifera</td><td>ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158</td><td>337</td><td>158</td><td>1.00E-12</td><td>46.9</td><td>9.8</td><td>14.2</td></tr>
<tr><td>Rsa1.0_01379.1.g26245.t1</td><td>gb|EOA23731.1| hypothetical protein CARUB_v10016943mg [Capsella rubella]</td><td>552</td><td>564</td><td>0</td><td>102.2</td><td>79.0</td><td>87.1</td><td>hypothetical protein CARUB_v10016943mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G45650.1 | Symbols: NAXT1 | nitrate excretion transporter1 | chr3:16759253-16761266 FORWARD LENGTH=558</td><td>552</td><td>558</td><td>0</td><td>101.1</td><td>78.4</td><td>86.4</td></tr>
<tr><td>Rsa1.0_01379.1.g26246.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01379.1.g26247.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01379.1.g26248.t1</td><td>gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>544</td><td>1611</td><td>2.00E-34</td><td>296.1</td><td>14.0</td><td>17.6</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01380.1.g26249.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01380.1.g26250.t1</td><td>ref|XP_002866069.1| pyruvate decarboxylase-2 [Arabidopsis lyrata subsp. lyrata] gi|297311904|gb|EFH42328.1| pyruvate decarboxylase-2 [Arabidopsis lyrata subsp. lyrata]</td><td>607</td><td>607</td><td>0</td><td>100.0</td><td>93.7</td><td>97.5</td><td>pyruvate decarboxylase-2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G54960.1 | Symbols: PDC2 | pyruvate decarboxylase-2 | chr5:22310858-22312681 REVERSE LENGTH=607</td><td>607</td><td>607</td><td>0</td><td>100.0</td><td>93.6</td><td>97.0</td></tr>
<tr><td>Rsa1.0_01380.1.g26251.t16</td><td>gb|EOA15966.1| hypothetical protein CARUB_v10004061mg [Capsella rubella]</td><td>885</td><td>995</td><td>0</td><td>112.4</td><td>56.7</td><td>68.7</td><td>hypothetical protein CARUB_v10004061mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G26970.1 | Symbols: ACO2 | aconitase 2 | chr4:13543077-13548427 FORWARD LENGTH=995</td><td>885</td><td>995</td><td>0</td><td>112.4</td><td>56.0</td><td>68.2</td></tr>
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Rsa1.0_01380.1.g26252.t1	dbj|BAJ34327.1| unnamed protein product [Thellungiella halophila]	112	112	1.00E-52	100.0	89.3	95.5	unnamed protein product	----	----	AT5G54940.2 | Symbols: | Translation initiation factor SUI1 family protein | chr5:22308420-22308758 REVERSE LENGTH=112	112	112	3.00E-55	100.0	91.1	94.6
Rsa1.0_01380.1.g26253.t1	ref|XP_002866066.1| AT hook motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311901|gb|EFH42325.1| AT hook motif-containing protein [Arabidopsis lyrata subsp. lyrata]	258	286	2.00E-92	110.9	76.0	84.1	AT hook motif-containing protein	gbpln	Arabidopsis lyrata	AT5G54930.1 | Symbols: | AT hook motif-containing protein | chr5:22305897-22306839 REVERSE LENGTH=286	258	286	9.00E-91	110.9	72.5	82.2
Rsa1.0_01380.1.g26254.t1	gb|EOA14381.1| hypothetical protein CARUB_v10027574mg [Capsella rubella]	518	618	1.00E-144	119.3	57.3	72.6	hypothetical protein CARUB_v10027574mg	gbpln	Capsella rubella	AT5G56560.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr5:22899724-22901985 FORWARD LENGTH=607	518	607	1.00E-139	117.2	55.4	71.2
Rsa1.0_01380.1.g26255.t1	ref|XP_002866065.1| hypothetical protein ARALYDRAFT_495573 [Arabidopsis lyrata subsp. lyrata] gi|297311900|gb|EFH42324.1| hypothetical protein ARALYDRAFT_495573 [Arabidopsis lyrata subsp. lyrata]	809	741	0	91.6	74.0	81.6	hypothetical protein ARALYDRAFT_495573	gbpln	Arabidopsis lyrata	AT5G54910.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr5:22298668-22301719 REVERSE LENGTH=739	809	739	0	91.3	73.3	81.3
Rsa1.0_01380.1.g26256.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01381.1.g26257.t1	gb|ABD65065.1| hypothetical protein 27.t00043 [Brassica oleracea]	86	117	5.00E-13	136.0	64.0	76.7	hypothetical protein 27.t00043	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01381.1.g26258.t1	ref|XP_002868819.1| seven in absentia family protein [Arabidopsis lyrata subsp. lyrata] gi|297314655|gb|EFH45078.1| seven in absentia family protein [Arabidopsis lyrata subsp. lyrata]	312	350	3.00E-89	112.2	50.3	62.8	seven in absentia family protein	gbpln	Arabidopsis lyrata	AT5G37930.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr5:15102239-15103651 REVERSE LENGTH=349	312	349	5.00E-86	111.9	47.4	58.3
Rsa1.0_01381.1.g26259.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01381.1.g26260.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01381.1.g26261.t3	gb|AAD24831.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1226	1524	0	124.3	32.1	46.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1226	575	1.00E-61	46.9	10.0	14.9
Rsa1.0_01381.1.g26262.t1	ref|NP_198623.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana] gi|8885610|dbj|BAA97540.1| unnamed protein product [Arabidopsis thaliana] gi|63025166|gb|AAY27056.1| At5g38070 [Arabidopsis thaliana] gi|70905091|gb|AAZ14071.1| At5g38070 [Arabidopsis thaliana] gi|117958789|gb|ABK59693.1| At5g38070 [Arabidopsis thaliana] gi|332006881|gb|AED94264.1| RING/FYVE/PHD zinc finger-containing protein [Arabidopsis thaliana]	243	259	1.00E-106	106.6	81.9	89.7	RING/FYVE/PHD zinc finger-containing protein	gbpln	Arabidopsis thaliana	AT5G38070.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:15190254-15191588 FORWARD LENGTH=259	243	259	1.00E-109	106.6	81.9	89.7
Rsa1.0_01381.1.g26263.t1	ref|XP_002885632.1| hypothetical protein ARALYDRAFT_319134 [Arabidopsis lyrata subsp. lyrata] gi|297331472|gb|EFH61891.1| hypothetical protein ARALYDRAFT_319134 [Arabidopsis lyrata subsp. lyrata]	410	357	1.00E-108	87.1	53.9	67.1	hypothetical protein ARALYDRAFT_319134	gbpln	Arabidopsis lyrata	AT3G28223.1 | Symbols: | F-box family protein | chr3:10527669-10528921 REVERSE LENGTH=391	410	391	5.00E-85	95.4	46.1	62.2
Rsa1.0_01382.1.g26264.t1	ref|XP_002891736.1| F12M16.10 [Arabidopsis lyrata subsp. lyrata] gi|297337578|gb|EFH67995.1| F12M16.10 [Arabidopsis lyrata subsp. lyrata]	447	510	1.00E-179	114.1	81.7	85.9	F12M16.10	gbpln	Arabidopsis lyrata	AT1G53190.2 | Symbols: | RING/U-box superfamily protein | chr1:19838072-19840003 FORWARD LENGTH=494	447	494	1.00E-177	110.5	78.1	82.8
Rsa1.0_01382.1.g26265.t1	gb|EOA39937.1| hypothetical protein CARUB_v10008627mg [Capsella rubella]	104	603	5.00E-12	579.8	44.2	59.6	hypothetical protein CARUB_v10008627mg	gbpln	Capsella rubella	AT1G53200.1 | Symbols: | unknown protein; Has 21 Blast hits to 21 proteins in 9 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:19840486-19843169 REVERSE LENGTH=613	104	613	5.00E-11	589.4	38.5	54.8
Rsa1.0_01382.1.g26266.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01382.1.g26267.t1	ref|NP_564623.2| calcium-binding EF-hand domain-containing protein [Arabidopsis thaliana] gi|20466169|gb|AAM20402.1| unknown protein [Arabidopsis thaliana] gi|332194787|gb|AEE32908.1| calcium-binding EF-hand domain-containing protein [Arabidopsis thaliana]	584	585	0	100.2	94.7	97.3	calcium-binding EF-hand domain-containing protein	gbpln	Arabidopsis thaliana	AT1G53210.1 | Symbols: | sodium/calcium exchanger family protein / calcium-binding EF hand family protein | chr1:19844790-19847533 FORWARD LENGTH=585	584	585	0	100.2	94.7	97.3

Rsa1.0_01382.1.g26268.t1	gb|EOA38168.1| hypothetical protein CARUB_v10009646mg [Capsella rubella]	342	341	0	99.7	95.3	98.2	hypothetical protein CARUB_v10009646mg	gbpln	Capsella rubella	AT1G53240.1 | Symbols: mMDH1 | Lactate/malate dehydrogenase family protein | chr1:19854966-19856802 REVERSE LENGTH=341	342	341	0	99.7	94.2	98.0
Rsa1.0_01382.1.g26269.t1	gb|EOA40513.1| hypothetical protein CARUB_v10009243mg [Capsella rubella] gi|482576327|gb|EOA40514.1| hypothetical protein CARUB_v10009243mg [Capsella rubella]	417	422	1.00E-144	101.2	75.3	81.5	hypothetical protein CARUB_v10009243mg	gbpln	Capsella rubella	AT3G15010.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:5052844-5054058 FORWARD LENGTH=404	417	404	1.00E-137	96.9	70.0	77.5
Rsa1.0_01382.1.g26270.t1	ref|XP_002891738.1| F12M16.15 [Arabidopsis lyrata subsp. lyrata] gi|297337580|gb|EFH67997.1| F12M16.15 [Arabidopsis lyrata subsp. lyrata]	369	357	1.00E-141	96.7	74.5	82.4	F12M16.15	gbpln	Arabidopsis lyrata	AT1G53250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53800.1); Has 11909 Blast hits to 7704 proteins in 757 species: Archae - 51; Bacteria - 1338; Metazoa - 4550; Fungi - 987; Plants - 464; Viruses - 24; Other Eukaryotes - 4495 (source: NCBI BLink). | chr1:19857468-19859156 FORWARD LENGTH=371	369	371	1.00E-135	100.5	72.9	81.8
Rsa1.0_01382.1.g26271.t1	ref|NP_190213.2| protein kinase-like protein [Arabidopsis thaliana] gi|26450306|dbj|BAC42269.1| unknown protein [Arabidopsis thaliana] gi|332644621|gb|AEE78142.1| protein kinase-like protein [Arabidopsis thaliana]	523	471	2.00E-84	90.1	36.5	45.3	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT3G46280.1 | Symbols: | protein kinase-related | chr3:17005672-17008410 REVERSE LENGTH=471	523	471	4.00E-87	90.1	36.5	45.3
Rsa1.0_01382.1.g26272.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	235	627	5.00E-18	266.8	25.1	38.7	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01382.1.g26273.t1	ref|XP_002891738.1| F12M16.15 [Arabidopsis lyrata subsp. lyrata] gi|297337580|gb|EFH67997.1| F12M16.15 [Arabidopsis lyrata subsp. lyrata]	258	357	5.00E-86	138.4	65.1	73.6	F12M16.15	gbpln	Arabidopsis lyrata	AT1G53250.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53800.1); Has 11909 Blast hits to 7704 proteins in 757 species: Archae - 51; Bacteria - 1338; Metazoa - 4550; Fungi - 987; Plants - 464; Viruses - 24; Other Eukaryotes - 4495 (source: NCBI BLink). | chr1:19857468-19859156 FORWARD LENGTH=371	258	371	6.00E-77	143.8	63.2	71.7
Rsa1.0_01382.1.g26274.t1	ref|NP_564626.1| 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis [Arabidopsis thaliana] gi|75192181|sp|Q9MAH3.1|DJ1B_ARATH RecName: Full=Protein DJ-1 homolog B; Short=AtDJ1B; Flags: Precursor gi|7769869|gb|AAF69547.1|AC008007_22 F12M16.18 [Arabidopsis thaliana] gi|15810459|gb|AAL07117.1| unknown protein [Arabidopsis thaliana] gi|20259561|gb|AAM14123.1| unknown protein [Arabidopsis thaliana] gi|332194795|gb|AEE32916.1| DJ1-like protein B [Arabidopsis thaliana]	393	438	0	111.5	90.6	94.7	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis	gbpln	Arabidopsis thaliana	AT1G53280.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr1:19864942-19867341 REVERSE LENGTH=438	393	438	0	111.5	90.6	94.7
Rsa1.0_01382.1.g26275.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	1428	1466	0	102.7	48.4	60.6	copia-like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1428	1262	6.00E-73	88.4	9.7	16.1
Rsa1.0_01383.1.g26276.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	172	1142	3.00E-30	664.0	39.5	52.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	172	575	1.00E-14	334.3	26.7	47.1
Rsa1.0_01383.1.g26277.t1	gb|EOA34301.1| hypothetical protein CARUB_v10021819mg [Capsella rubella]	410	383	1.00E-106	93.4	54.9	67.8	hypothetical protein CARUB_v10021819mg	gbpln	Capsella rubella	AT1G50980.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:18900541-18902057 REVERSE LENGTH=370	410	370	3.00E-87	90.2	46.6	58.3
Rsa1.0_01383.1.g26278.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01383.1.g26279.t1	gb|EOA34301.1| hypothetical protein CARUB_v10021819mg [Capsella rubella]	415	383	1.00E-102	92.3	52.3	65.3	hypothetical protein CARUB_v10021819mg	gbpln	Capsella rubella	AT1G50980.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:18900541-18902057 REVERSE LENGTH=370	415	370	5.00E-85	89.2	46.3	57.3
Rsa1.0_01383.1.g26280.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01383.1.g26281.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	1373	1356	0	98.8	51.1	68.1	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1373	1262	9.00E-81	91.9	12.7	19.6
Rsa1.0_01384.1.g26282.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01384.1.g26283.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	257	1529	7.00E-35	594.9	34.2	50.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	257	295	6.00E-37	114.8	35.4	51.4

Rsa1.0_01384.1.g26284.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	329	1225	8.00E-33	372.3	21.3	31.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01384.1.g26285.t2	dbj|BAJ33923.1| unnamed protein product [Thellungiella halophila]	695	676	0	97.3	88.1	92.1	unnamed protein product	----	----	AT3G52640.1 | Symbols: | Zn-dependent exopeptidases superfamily protein | chr3:19515078-19520290 REVERSE LENGTH=676	695	676	0	97.3	86.2	91.1
Rsa1.0_01384.1.g26286.t1	ref|XP_002877875.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323713|gb|EFH54134.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	523	590	0	112.8	89.1	94.8	predicted protein	gbpln	Arabidopsis lyrata	AT3G52600.1 | Symbols: AtcwINV2, CWINV2 | cell wall invertase 2 | chr3:19507080-19509273 REVERSE LENGTH=590	523	590	0	112.8	88.0	94.1
Rsa1.0_01384.1.g26287.t1	ref|XP_004156525.1| PREDICTED: ubiquitin-60S ribosomal protein L40-like [Cucumis sativus]	128	208	3.00E-69	162.5	100.0	100.0	PREDICTED: ubiquitin-60S ribosomal protein L40-like	gbpln	Cucumis sativus	AT3G52590.1 | Symbols: UBQ1, EMB2167, ERD16, HAP4 | ubiquitin extension protein 1 | chr3:19505668-19506681 FORWARD LENGTH=128	128	128	6.00E-71	100.0	99.2	99.2
Rsa1.0_01384.1.g26288.t3	gb|EOA15725.1| hypothetical protein CARUB_v10006633mg, partial [Capsella rubella]	306	483	2.00E-29	157.8	21.6	33.3	hypothetical protein CARUB_v10006633mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	306	566	1.00E-21	185.0	17.3	32.0
Rsa1.0_01384.1.g26289.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01384.1.g26290.t1	dbj|BAB01155.1| unnamed protein product [Arabidopsis thaliana] gi|49823524|gb|AAT68745.1| hypothetical protein At3g17200 [Arabidopsis thaliana] gi|60547763|gb|AAX23845.1| hypothetical protein At3g17200 [Arabidopsis thaliana]	156	310	2.00E-24	198.7	30.8	53.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	156	746	2.00E-14	478.2	25.6	35.3
Rsa1.0_01384.1.g26291.t1	gb|AAD21699.1| Contains reverse transcriptase domain (rvt) PF|00078 [Arabidopsis thaliana]	218	1253	1.00E-24	574.8	25.2	39.9	Contains reverse transcriptase domain (rvt) PF|00078	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	218	295	4.00E-25	135.3	26.6	40.4
Rsa1.0_01385.1.g26292.t1	ref|XP_002888577.1| CYP735A2 [Arabidopsis lyrata subsp. lyrata] gi|297334418|gb|EFH64836.1| CYP735A2 [Arabidopsis lyrata subsp. lyrata]	517	512	0	99.0	90.9	95.4	CYP735A2	gbpln	Arabidopsis lyrata	AT1G67110.1 | Symbols: CYP735A2 | cytochrome P450, family 735, subfamily A, polypeptide 2 | chr1:25061836-25065355 REVERSE LENGTH=512	517	512	0	99.0	90.1	95.0
Rsa1.0_01385.1.g26293.t10	ref|NP_176883.5| AAA ATPase containing von Willebrand factor type A domain-containing protein [Arabidopsis thaliana] gi|332196477|gb|AEE34598.1| AAA ATPase containing von Willebrand factor type A domain-containing protein [Arabidopsis thaliana]	5390	5393	0	100.1	82.1	89.8	AAA ATPase containing von Willebrand factor type A domain-containing protein	gbpln	Arabidopsis thaliana	AT1G67120.1 | Symbols: | ATPases;nucleotide binding;ATP binding;nucleoside-triphosphatases;transcription factor binding | chr1:25069727-25095526 REVERSE LENGTH=5393	5390	5393	0	100.1	82.1	89.8
Rsa1.0_01385.1.g26294.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01385.1.g26295.t1	ref|XP_002874768.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297320605|gb|EFH51027.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	157	161	2.00E-32	102.5	52.2	66.9	protease inhibitor/seed storage/lipid transfer protein family protein	gbpln	Arabidopsis lyrata	AT4G12360.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:7328164-7329104 REVERSE LENGTH=161	157	161	2.00E-26	102.5	42.0	56.1
Rsa1.0_01386.1.g26296.t1	gb|EOA33837.1| hypothetical protein CARUB_v10021318mg, partial [Capsella rubella]	142	290	5.00E-12	204.2	34.5	47.9	hypothetical protein CARUB_v10021318mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01386.1.g26297.t1	ref|NP_001118636.1| uncharacterized protein [Arabidopsis thaliana] gi|332642168|gb|AEE75689.1| uncharacterized protein AT3G15534 [Arabidopsis thaliana]	68	68	2.00E-29	100.0	95.6	97.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G15534.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52855.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:5258876-5259082 FORWARD LENGTH=68	68	68	3.00E-32	100.0	95.6	97.1

<table>
<tr><td>Rsa1.0_01386.1.g26298.t1</td><td>ref|NP_188173.1| auxin-responsive protein IAA19 [Arabidopsis thaliana] gi|17365900|sp|O24409.2|IAA19_ARATH RecName: Full=Auxin-responsive protein IAA19; AltName: Full=Indoleacetic acid-induced protein 19; AltName: Full=Protein MASSUGU 2 gi|7021739|gb|AAF35420.1| early auxin-induced protein, IAA19 [Arabidopsis thaliana] gi|15795119|dbj|BAB02383.1| auxin-regulated protein, IAA19 [Arabidopsis thaliana] gi|49616371|gb|AAT67082.1| IAA19 [Arabidopsis thaliana] gi|88193790|gb|ABD42984.1| At3g15540 [Arabidopsis thaliana] gi|332642169|gb|AEE75690.1| auxin-responsive protein IAA19 [Arabidopsis thaliana]</td><td>195</td><td>197</td><td>3.00E-97</td><td>101.0</td><td>90.3</td><td>94.4</td><td>auxin-responsive protein IAA19</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G15540.1 | Symbols: IAA19, MSG2 | indole-3-acetic acid inducible 19 | chr3:5264100-5265378 FORWARD LENGTH=197</td><td>195</td><td>197</td><td>1.00E-99</td><td>101.0</td><td>90.3</td><td>94.4</td></tr>
<tr><td>Rsa1.0_01386.1.g26299.t1</td><td>dbj|BAA97099.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>553</td><td>1098</td><td>1.00E-165</td><td>198.6</td><td>56.6</td><td>69.4</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237</td><td>553</td><td>237</td><td>7.00E-25</td><td>42.9</td><td>12.7</td><td>21.2</td></tr>
<tr><td>Rsa1.0_01386.1.g26300.t1</td><td>gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]</td><td>836</td><td>695</td><td>1.00E-63</td><td>83.1</td><td>13.4</td><td>15.7</td><td>En/Spm-related transposon protein</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01386.1.g26301.t1</td><td>ref|NP_174124.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|12322993|gb|AAG51483.1|AC069471_14 oxidoreductase, putative [Arabidopsis thaliana] gi|332192783|gb|AEE30904.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]</td><td>323</td><td>322</td><td>1.00E-128</td><td>99.7</td><td>70.3</td><td>82.0</td><td>2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G28030.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:9771793-9773345 FORWARD LENGTH=322</td><td>323</td><td>322</td><td>1.00E-130</td><td>99.7</td><td>70.3</td><td>82.0</td></tr>
<tr><td>Rsa1.0_01386.1.g26302.t1</td><td>gb|EOA32639.1| hypothetical protein CARUB_v10015934mg [Capsella rubella]</td><td>362</td><td>708</td><td>0</td><td>195.6</td><td>89.2</td><td>93.6</td><td>hypothetical protein CARUB_v10015934mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G15550.1 | Symbols: | unknown protein; Has 25732 Blast hits to 16979 proteins in 961 species: Archae - 144; Bacteria - 1801; Metazoa - 12681; Fungi - 1868; Plants - 912; Viruses - 94; Other Eukaryotes - 8232 (source: NCBI BLink). | chr3:5267351-5270095 FORWARD LENGTH=729</td><td>362</td><td>729</td><td>0</td><td>201.4</td><td>88.4</td><td>93.9</td></tr>
<tr><td>Rsa1.0_01387.1.g26303.t1</td><td>ref|NP_199669.1| FK506-binding protein 2-2 [Arabidopsis thaliana] gi|23396587|sp|Q38936.2|FK152_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP15-2; Short=PPIase FKBP15-2; AltName: Full=15 kDa FK506-binding protein; Short=15 kDa FKBP; AltName: Full=FK506-binding protein 15-2; Short=AtFKBP15-2; AltName: Full=FK506-binding protein 2-2; AltName: Full=Immunophilin FKBP15-2; AltName: Full=Rotamase; Flags: Precursor gi|13877793|gb|AAK43974.1|AF370159_1 putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|10177348|dbj|BAB10691.1| peptidyl-prolyl cis-trans isomerase-like protein [Arabidopsis thaliana] gi|16323516|gb|AAL15252.1| putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] gi|21553433|gb|AAM62526.1| peptidyl-prolyl cis-trans isomerase-like protein [Arabidopsis thaliana] gi|332008308|gb|AED95691.1| FK506-binding protein 2-2 [Arabidopsis thaliana]</td><td>165</td><td>163</td><td>7.00E-71</td><td>98.8</td><td>84.2</td><td>89.7</td><td>FK506-binding protein 2-2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G48580.1 | Symbols: FKBP15-2 | FK506- and rapamycin-binding protein 15 kD-2 | chr5:19696156-19697304 REVERSE LENGTH=163</td><td>165</td><td>163</td><td>2.00E-73</td><td>98.8</td><td>84.2</td><td>89.7</td></tr>
<tr><td>Rsa1.0_01387.1.g26304.t1</td><td>dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>1261</td><td>1250</td><td>0</td><td>99.1</td><td>59.6</td><td>75.5</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1261</td><td>1262</td><td>3.00E-99</td><td>100.1</td><td>14.7</td><td>22.8</td></tr>
</table>

Rsa1.0_01387.1.g26305.t2	gb|EOA12366.1| hypothetical protein CARUB_v10025753mg [Capsella rubella]	451	1263	1.00E-63	280.0	42.8	56.3	hypothetical protein CARUB_v10025753mg	gbpln	Capsella rubella	AT5G51630.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:20970069-20974666 FORWARD LENGTH=1229	451	1229	3.00E-62	272.5	35.7	49.9
Rsa1.0_01387.1.g26306.t1	ref|NP_187383.1| GTP cyclohydrolase I [Arabidopsis thaliana] gi|6642638|gb|AAF20219.1|AC012395_6 GTP cyclohydrolase I [Arabidopsis thaliana] gi|20466832|gb|AAM20733.1| GTP cyclohydrolase I [Arabidopsis thaliana] gi|30387557|gb|AAP31944.1| At3g07270 [Arabidopsis thaliana] gi|332640999|gb|AEE74520.1| GTP cyclohydrolase I [Arabidopsis thaliana]	423	466	1.00E-172	110.2	73.8	85.8	GTP cyclohydrolase I	gbpln	Arabidopsis thaliana	AT3G07270.1 | Symbols: | GTP cyclohydrolase I | chr3:2315451-2317059 FORWARD LENGTH=466	423	466	1.00E-175	110.2	73.8	85.8
Rsa1.0_01387.1.g26307.t1	gb|AAF23577.1|AF112102_1 chalcone synthase [Fourraea alpina]	394	395	0	100.3	91.4	95.9	chalcone synthase	gbpln	Fourraea alpina	AT5G13930.1 | Symbols: CHS, TT4, ATCHS | Chalcone and stilbene synthase family protein | chr5:4488762-4490035 FORWARD LENGTH=395	394	395	0	100.3	86.8	93.4
Rsa1.0_01387.1.g26308.t1	gb|AAF23577.1|AF112102_1 chalcone synthase [Fourraea alpina]	161	395	1.00E-47	245.3	55.3	60.2	chalcone synthase	gbpln	Fourraea alpina	AT5G13930.1 | Symbols: CHS, TT4, ATCHS | Chalcone and stilbene synthase family protein | chr5:4488762-4490035 FORWARD LENGTH=395	161	395	8.00E-46	245.3	52.8	55.3
Rsa1.0_01387.1.g26309.t1	ref|NP_199674.1| cyclin-C1-2 [Arabidopsis thaliana] gi|75309141|sp|Q9FJK7.1|CCC12_ARATH RecName: Full=Cyclin-C1-2; Short=CycC1;2 gi|10177353|dbj|BAB10696.1| cyclin C-like protein [Arabidopsis thaliana] gi|21554107|gb|AAM63187.1| cyclin C-like protein [Arabidopsis thaliana] gi|87116580|gb|ABD19654.1| At5g48630 [Arabidopsis thaliana] gi|332008316|gb|AED95699.1| cyclin-C1-2 [Arabidopsis thaliana]	253	253	1.00E-141	100.0	93.7	99.2	cyclin-C1-2	gbpln	Arabidopsis thaliana	AT5G48630.1 | Symbols: | Cyclin family protein | chr5:19721663-19723200 REVERSE LENGTH=253	253	253	1.00E-143	100.0	93.7	99.2
Rsa1.0_01387.1.g26310.t1	gb|EOA24625.1| hypothetical protein CARUB_v10017896mg [Capsella rubella]	243	252	1.00E-130	103.7	93.0	97.9	hypothetical protein CARUB_v10017896mg	gbpln	Capsella rubella	AT5G48640.1 | Symbols: | Cyclin family protein | chr5:19723653-19725641 REVERSE LENGTH=253	243	253	1.00E-130	104.1	93.0	97.5
Rsa1.0_01387.1.g26311.t1	gb|AAM61659.1| unknown [Arabidopsis thaliana]	191	203	8.00E-56	106.3	72.3	78.0	unknown	gbpln	Arabidopsis thaliana	AT5G48655.3 | Symbols: | RING/U-box superfamily protein | chr5:19731575-19732486 REVERSE LENGTH=203	191	203	1.00E-57	106.3	69.6	77.0
Rsa1.0_01387.1.g26312.t1	gb|EOA13977.1| hypothetical protein CARUB_v10027107mg [Capsella rubella]	219	217	9.00E-98	99.1	85.8	92.7	hypothetical protein CARUB_v10027107mg	gbpln	Capsella rubella	AT5G48660.1 | Symbols: | B-cell receptor-associated protein 31-like | chr5:19736986-19738327 FORWARD LENGTH=219	219	219	4.00E-91	100.0	91.8	96.8
Rsa1.0_01387.1.g26313.t1	ref|NP_001154770.1| protein XRI1 [Arabidopsis thaliana] gi|239977726|sp|Q6NLW5.2|XRI1_ARATH RecName: Full=Protein XRI1; AltName: Full=Protein X-RAY INDUCED 1 gi|332008333|gb|AED95716.1| protein XRI1 [Arabidopsis thaliana]	304	300	1.00E-121	98.7	77.3	85.2	protein XRI1	gbpln	Arabidopsis thaliana	AT5G48720.2 | Symbols: XRI, XRI1 | x-ray induced transcript 1 | chr5:19759233-19761621 FORWARD LENGTH=300	304	300	1.00E-124	98.7	77.3	85.2
Rsa1.0_01387.1.g26314.t1	ref|XP_002865669.1| 60S ribosomal protein L13A [Arabidopsis lyrata subsp. lyrata] gi|297311504|gb|EFH41928.1| 60S ribosomal protein L13A [Arabidopsis lyrata subsp. lyrata]	206	206	1.00E-112	100.0	96.1	98.1	60S ribosomal protein L13A	gbpln	Arabidopsis lyrata	AT5G48760.2 | Symbols: | Ribosomal protein L13 family protein | chr5:19771315-19772686 REVERSE LENGTH=206	206	206	1.00E-113	100.0	95.1	97.6
Rsa1.0_01388.1.g26315.t2	dbj|BAJ33720.1| unnamed protein product [Thellungiella halophila]	295	294	1.00E-135	99.7	88.8	91.9	unnamed protein product	----	----	AT1G78600.1 | Symbols: LZF1, STH3, DBB3 | light-regulated zinc finger protein 1 | chr1:29567370-29568662 FORWARD LENGTH=299	295	299	1.00E-130	101.4	84.7	89.2
Rsa1.0_01388.1.g26316.t1	ref|NP_177982.1| mechanosensitive channel of small conductance-like 6 [Arabidopsis thaliana] gi|75213461|sp|Q9SYM1.1|MSL6_ARATH RecName: Full=Mechanosensitive ion channel protein 6; AltName: Full=Mechanosensitive channel of small conductance-like 6; AltName: Full=MscS-Like protein 6 gi|4836872|gb|AAD30575.1|AC007260_6 Hypothetical protein [Arabidopsis thaliana] gi|332198006|gb|AEE36127.1| mechanosensitive channel of small conductance-like 6 [Arabidopsis thaliana]	865	856	0	99.0	85.0	90.4	mechanosensitive channel of small conductance-like 6	gbpln	Arabidopsis thaliana	AT1G78610.1 | Symbols: MSL6 | mechanosensitive channel of small conductance-like 6 | chr1:29569226-29572126 REVERSE LENGTH=856	865	856	0	99.0	85.0	90.4
Rsa1.0_01388.1.g26317.t1	gb|EOA35423.1| hypothetical protein CARUB_v10020623mg [Capsella rubella]	445	335	1.00E-103	75.3	41.8	42.9	hypothetical protein CARUB_v10020623mg	gbpln	Capsella rubella	AT1G78620.2 | Symbols: | Protein of unknown function DUF92, transmembrane | chr1:29573862-29575758 REVERSE LENGTH=342	445	342	1.00E-105	76.9	41.6	43.1

<table>
<tr><td>Rsa1.0_01388.1.g26318.t1</td><td>ref|XP_002887748.1| EMB1473 [Arabidopsis lyrata subsp. lyrata] gi|297333589|gb|EFH64007.1| EMB1473 [Arabidopsis lyrata subsp. lyrata]</td><td>244</td><td>242</td><td>1.00E-130</td><td>99.2</td><td>93.9</td><td>95.9</td><td>EMB1473</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G78630.1 | Symbols: emb1473 | Ribosomal protein L13 family protein | chr1:29575997-29577406 FORWARD LENGTH=241</td><td>244</td><td>241</td><td>1.00E-123</td><td>98.8</td><td>91.8</td><td>93.9</td></tr>
<tr><td>Rsa1.0_01388.1.g26319.t2</td><td>ref|NP_565185.1| DNA-directed DNA polymerase [Arabidopsis thaliana] gi|4836868|gb|AAD30571.1|AC007260_2 Hypothetical protein [Arabidopsis thaliana] gi|332198011|gb|AEE36132.1| DNA-directed DNA polymerase [Arabidopsis thaliana]</td><td>753</td><td>509</td><td>1.00E-175</td><td>67.6</td><td>47.3</td><td>52.2</td><td>DNA-directed DNA polymerase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G78650.1 | Symbols: POLD3 | DNA-directed DNA polymerases | chr1:29582987-29585508 FORWARD LENGTH=509</td><td>753</td><td>509</td><td>1.00E-178</td><td>67.6</td><td>47.3</td><td>52.2</td></tr>
<tr><td>Rsa1.0_01388.1.g26320.t1</td><td>ref|XP_002886496.1| hypothetical protein ARALYDRAFT_893290 [Arabidopsis lyrata subsp. lyrata] gi|297332337|gb|EFH62755.1| hypothetical protein ARALYDRAFT_893290 [Arabidopsis lyrata subsp. lyrata]</td><td>392</td><td>416</td><td>3.00E-97</td><td>106.1</td><td>51.8</td><td>66.6</td><td>hypothetical protein ARALYDRAFT_893290</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387</td><td>392</td><td>387</td><td>4.00E-83</td><td>98.7</td><td>46.7</td><td>62.0</td></tr>
<tr><td>Rsa1.0_01388.1.g26321.t1</td><td>ref|NP_565186.2| gamma-glutamyl hydrolase 2 [Arabidopsis thaliana] gi|26454629|sp|O65355.2|GGH_ARATH RecName: Full=Gamma-glutamyl hydrolase; AltName: Full=Conjugase; AltName: Full=GH; AltName: Full=Gamma-Glu-X carboxypeptidase; Flags: Precursor gi|17979073|gb|AAL49804.1| putative gamma glutamyl hydrolase [Arabidopsis thaliana] gi|20465329|gb|AAM20068.1| putative gamma glutamyl hydrolase [Arabidopsis thaliana] gi|332198016|gb|AEE36137.1| gamma-glutamyl hydrolase 2 [Arabidopsis thaliana]</td><td>381</td><td>347</td><td>1.00E-155</td><td>91.1</td><td>73.5</td><td>79.8</td><td>gamma-glutamyl hydrolase 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G78680.1 | Symbols: ATGGH2, GGH2 | gamma-glutamyl hydrolase 2 | chr1:29593933-29596037 FORWARD LENGTH=347</td><td>381</td><td>347</td><td>1.00E-158</td><td>91.1</td><td>73.5</td><td>79.8</td></tr>
<tr><td>Rsa1.0_01388.1.g26322.t1</td><td>ref|XP_002887753.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333594|gb|EFH64012.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>678</td><td>284</td><td>1.00E-143</td><td>41.9</td><td>35.8</td><td>39.4</td><td>phospholipid/glycerol acyltransferase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G78690.1 | Symbols: | Phospholipid/glycerol acyltransferase family protein | chr1:29597002-29598409 FORWARD LENGTH=284</td><td>678</td><td>284</td><td>1.00E-140</td><td>41.9</td><td>35.3</td><td>38.3</td></tr>
<tr><td>Rsa1.0_01388.1.g26323.t1</td><td>ref|NP_177996.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75268062|sp|Q9ZV93.1|FDL10_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g78750 gi|3834319|gb|AAC83035.1| Similar to gi|2244754 heat shock transcription factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig gb|Z97335 [Arabidopsis thaliana] gi|332198025|gb|AEE36146.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]</td><td>471</td><td>458</td><td>1.00E-117</td><td>97.2</td><td>50.1</td><td>64.1</td><td>F-box/FBD/LRR-repeat protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G78750.1 | Symbols: | F-box/RNI-like superfamily protein | chr1:29613122-29614695 REVERSE LENGTH=458</td><td>471</td><td>458</td><td>1.00E-119</td><td>97.2</td><td>50.1</td><td>64.1</td></tr>
<tr><td>Rsa1.0_01388.1.g26324.t1</td><td>ref|NP_177121.1| F-box/LRR-repeat protein 13 [Arabidopsis thaliana] gi|75263128|sp|Q9FWZ1.1|FBL13_ARATH RecName: Full=F-box/LRR-repeat protein 13 gi|10092292|gb|AAG12704.1|AC021046_5 hypothetical protein; 7662-9196 [Arabidopsis thaliana] gi|12325183|gb|AAG52534.1|AC013289_1 hypothetical protein; 77728-79262 [Arabidopsis thaliana] gi|91806059|gb|ABE65758.1| F-box family protein [Arabidopsis thaliana] gi|332196836|gb|AEE34957.1| F-box/LRR-repeat protein 13 [Arabidopsis thaliana]</td><td>449</td><td>451</td><td>1.00E-155</td><td>100.4</td><td>65.0</td><td>78.6</td><td>F-box/LRR-repeat protein 13</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G69630.1 | Symbols: | F-box/RNI-like superfamily protein | chr1:26191640-26193174 REVERSE LENGTH=451</td><td>449</td><td>451</td><td>1.00E-158</td><td>100.4</td><td>65.0</td><td>78.6</td></tr>
<tr><td>Rsa1.0_01389.1.g26325.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01389.1.g26326.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01389.1.g26327.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_01389.1_g26328.t1	ref|NP_566958.3| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|79314769|ref|NP_001030841.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|17979394|gb|AAL49922.1| unknown protein [Arabidopsis thaliana] gi|22136722|gb|AAM91680.1| unknown protein [Arabidopsis thaliana] gi|332645382|gb|AEE78903.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|332645383|gb|AEE78904.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	261	253	1.00E-113	96.9	80.8	89.7	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT3G52150.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:19342074-19343090 FORWARD LENGTH=253	261	253	1.00E-116	96.9	80.8	89.7
Rsa1.0_01389.1_g26329.t1	dbj|BAD90706.1| plastid DNA-binding protein [Brassica napus]	490	476	1.00E-173	97.1	70.8	76.7	plastid DNA-binding protein	gbpln	Brassica napus	AT3G52170.2 | Symbols: | DNA binding | chr3:19347039-19349099 REVERSE LENGTH=499	490	499	1.00E-143	101.8	62.4	73.1
Rsa1.0_01389.1_g26330.t1	gb|AAL27495.1|AF439823_1 AT3g52180/F4F15_290 [Arabidopsis thaliana] gi|23505915|gb|AAN28817.1| At3g52180/F4F15_290 [Arabidopsis thaliana]	392	379	0	96.7	82.7	86.7	AT3g52180/F4F15_290	gbpln	Arabidopsis thaliana	AT3G52180.1 | Symbols: ATPTPKIS1, DSP4, SEX4, ATSEX4 | dual specificity protein phosphatase (DsPTP1) family protein | chr3:19349884-19353459 REVERSE LENGTH=379	392	379	0	96.7	83.2	87.2
Rsa1.0_01389.1_g26331.t1	ref|XP_002883579.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329419|gb|EFH59838.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	295	345	6.00E-79	116.9	59.3	74.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G24850.1 | Symbols: | Domain of unknown function (DUF313) | chr3:9071105-9072184 FORWARD LENGTH=359	295	359	1.00E-70	121.7	47.1	57.6
Rsa1.0_01389.1_g26332.t1	ref|NP_566961.1| SEC12-like protein 1 [Arabidopsis thaliana] gi|85687563|sp|Q8GYE0.2|PHF1_ARATH RecName: Full=SEC12-like protein 1; AltName: Full=Protein PHOSPHATE TRANSPORTER TRAFFIC FACILITATOR 1; Short=PHF-1 gi|4678948|emb|CAB41339.1| putative protein [Arabidopsis thaliana] gi|114050625|gb|ABI49462.1| At3g52190 [Arabidopsis thaliana] gi|332645390|gb|AEE78911.1| SEC12-like protein 1 [Arabidopsis thaliana]	397	398	0	100.3	92.2	96.5	SEC12-like protein 1	gbpln	Arabidopsis thaliana	AT3G52190.1 | Symbols: PHF1 | phosphate transporter traffic facilitator1 | chr3:19354117-19356910 REVERSE LENGTH=398	397	398	0	100.3	92.2	96.5
Rsa1.0_01389.1_g26333.t1	gb|EOA23635.1| hypothetical protein CARUB_v10016833mg [Capsella rubella] gi|482559445|gb|EOA23636.1| hypothetical protein CARUB_v10016833mg [Capsella rubella]	641	636	0	99.2	87.7	91.7	hypothetical protein CARUB_v10016833mg	gbpln	Capsella rubella	AT3G52200.1 | Symbols: LTA3 | Dihydrolipoamide acetyltransferase, long form protein | chr3:19360317-19366091 FORWARD LENGTH=637	641	637	0	99.4	87.5	92.0
Rsa1.0_01389.1_g26334.t1	ref|XP_002877850.1| hypothetical protein ARALYDRAFT_323774 [Arabidopsis lyrata subsp. lyrata] gi|297323688|gb|EFH54109.1| hypothetical protein ARALYDRAFT_323774 [Arabidopsis lyrata subsp. lyrata]	668	688	0	103.0	74.6	85.2	hypothetical protein ARALYDRAFT_323774	gbpln	Arabidopsis lyrata	AT3G52240.1 | Symbols: | unknown protein; Has 220 Blast hits to 193 proteins in 66 species: Archae - 0; Bacteria - 15; Metazoa - 53; Fungi - 33; Plants - 66; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink). | chr3:19372902-19375799 REVERSE LENGTH=680	668	680	0	101.8	71.6	82.6
Rsa1.0_01389.1_g26335.t1	gb|EOA24074.1| hypothetical protein CARUB_v10017302mg [Capsella rubella]	449	430	1.00E-170	95.8	77.1	84.4	hypothetical protein CARUB_v10017302mg	gbpln	Capsella rubella	AT3G52290.1 | Symbols: IQD3 | IQ-domain 3 | chr3:19394441-19396196 FORWARD LENGTH=430	449	430	1.00E-169	95.8	75.9	84.4
Rsa1.0_01390.1_g26336.t1	ref|XP_002887845.1| hypothetical protein ARALYDRAFT_477244 [Arabidopsis lyrata subsp. lyrata] gi|297333686|gb|EFH64104.1| hypothetical protein ARALYDRAFT_477244 [Arabidopsis lyrata subsp. lyrata]	309	300	4.00E-95	97.1	72.2	80.9	hypothetical protein ARALYDRAFT_477244	gbpln	Arabidopsis lyrata	AT1G80130.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:30141250-30142478 REVERSE LENGTH=305	309	305	7.00E-95	98.7	66.7	75.4
Rsa1.0_01390.1_g26337.t1	ref|NP_001077850.1| epidermal patterning factor-like protein 8 [Arabidopsis thaliana] gi|122178729|sp|Q1G3V9.1|EPFL8_ARATH RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 8; Short=EPF-like protein 8; Flags: Precursor gi|98961733|gb|ABF59196.1| unknown protein [Arabidopsis thaliana] gi|332198240|gb|AEE36361.1| epidermal patterning factor-like protein 8 [Arabidopsis thaliana]	103	99	6.00E-30	96.1	62.1	74.8	epidermal patterning factor-like protein 8	gbpln	Arabidopsis thaliana	AT1G80133.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; Has 154 Blast hits to 154 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 154; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:30143868-30144255 REVERSE LENGTH=99	103	99	1.00E-32	96.1	62.1	74.8

Rsa1.0_01390.1.g26338.t4	ref|XP_002889307.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335148|gb|EFH65566.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	1242	397	1.00E-175	32.0	24.3	26.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G80150.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:30148738-30149931 FORWARD LENGTH=397	1242	397	1.00E-176	32.0	24.1	26.2
Rsa1.0_01390.1.g26339.t1	ref|NP_565233.1| uncharacterized protein [Arabidopsis thaliana] gi|5902372|gb|AAD55474.1|AC009322_14 Unknown protein [Arabidopsis thaliana] gi|14532496|gb|AAK63976.1| At1g80180/F18B13_26 [Arabidopsis thaliana] gi|18655371|gb|AAL76141.1| At1g80180/F18B13_26 [Arabidopsis thaliana] gi|21593068|gb|AAM65017.1| unknown [Arabidopsis thaliana] gi|332198246|gb|AEE36367.1| uncharacterized protein AT1G80180 [Arabidopsis thaliana]	115	138	3.00E-29	120.0	69.6	71.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G80180.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15400.3); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:30157057-30157473 REVERSE LENGTH=138	115	138	5.00E-32	120.0	69.6	71.3
Rsa1.0_01390.1.g26340.t1	ref|NP_178136.1| GINS complex subunit 1 [Arabidopsis thaliana] gi|5902373|gb|AAD55475.1|AC009322_15 Unknown protein [Arabidopsis thaliana] gi|34365591|gb|AAQ65107.1| At1g80190 [Arabidopsis thaliana] gi|51969246|dbj|BAD43315.1| At1g80190 [Arabidopsis thaliana] gi|332198247|gb|AEE36368.1| GINS complex subunit 1-like protein [Arabidopsis thaliana]	220	201	2.00E-96	91.4	75.5	82.7	GINS complex subunit 1	gbpln	Arabidopsis thaliana	AT1G80190.1 | Symbols: PSF1 | partner of SLD five 1 | chr1:30159476-30161115 FORWARD LENGTH=201	220	201	5.00E-99	91.4	75.5	82.7
Rsa1.0_01390.1.g26341.t1	gb|AAT69224.1| hypothetical protein At1g80200 [Arabidopsis thaliana]	199	235	8.00E-61	118.1	68.8	80.9	hypothetical protein At1g80200	gbpln	Arabidopsis thaliana	AT1G80200.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G11280.1); Has 49 Blast hits to 49 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:30162034-30162999 FORWARD LENGTH=234	199	234	5.00E-59	117.6	68.8	80.9
Rsa1.0_01390.1.g26342.t1	emb|CCD74552.1| predicted protein [Arabidopsis halleri subsp. halleri]	268	249	5.00E-58	92.9	44.8	54.9	predicted protein	gbpln	Arabidopsis halleri	AT1G15430.2 | Symbols: | Protein of unknown function (DUF1644) | chr1:5305011-5305790 FORWARD LENGTH=259	268	259	1.00E-51	96.6	37.7	47.0
Rsa1.0_01390.1.g26343.t17	ref|XP_002889303.1| hypothetical protein ARALYDRAFT_316935 [Arabidopsis lyrata subsp. lyrata] gi|297335144|gb|EFH65562.1| hypothetical protein ARALYDRAFT_316935 [Arabidopsis lyrata subsp. lyrata]	170	137	5.00E-36	80.6	47.6	52.4	hypothetical protein ARALYDRAFT_316935	gbpln	Arabidopsis lyrata	AT1G80245.3 | Symbols: | Spc97 / Spc98 family of spindle pole body (SBP) component | chr1:30174547-30175217 FORWARD LENGTH=127	170	127	3.00E-37	74.7	47.1	52.4
Rsa1.0_01390.1.g26344.t1	ref|XP_002887837.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297333678|gb|EFH64096.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	613	639	0	104.2	80.3	87.9	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT1G80280.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:30183839-30186141 REVERSE LENGTH=647	613	647	0	105.5	82.2	89.4
Rsa1.0_01391.1.g26345.t1	ref|NP_179573.1| vacuolar protein sorting-associated protein 32-1 [Arabidopsis thaliana] gi|75100551|sp|O82197.1|VP321_ARATH RecName: Full=Vacuolar protein sorting-associated protein 32 homolog 1; Short=AtVPS32-1; AltName: Full=Charged multivesicular body protein 4 homolog 1; AltName: Full=ESCRT-III complex subunit VPS32 homolog 1 gi|3687235|gb|AAC62133.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana] gi|15028177|gb|AAK76585.1| putative copia retroelement pol polyprotein [Arabidopsis thaliana] gi|19310843|gb|AAL85152.1| putative copia retroelement pol polyprotein [Arabidopsis thaliana] gi|330251837|gb|AEC06931.1| vacuolar protein sorting-associated protein 32-1 [Arabidopsis thaliana]	214	213	1.00E-72	99.5	75.2	87.9	vacuolar protein sorting-associated protein 32-1	gbpln	Arabidopsis thaliana	AT2G19830.1 | Symbols: SNF7.2, VPS32 | SNF7 family protein | chr2:8558101-8559389 REVERSE LENGTH=213	214	213	4.00E-75	99.5	75.2	87.9

Rsa1.0_01391.1.g26346.t1	emb|CAB41922.1| putative protein (possibly fragment) [Arabidopsis thaliana] gi|7268014|emb|CAB78354.1| putative protein (possibly fragment) [Arabidopsis thaliana]	781	770	1.00E-139	98.6	31.1	40.2	putative protein (possibly fragment)	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	781	696	9.00E-36	89.1	15.5	26.6
Rsa1.0_01391.1.g26347.t1	dbj|BAJ34229.1| unnamed protein product [Thellungiella halophila]	356	359	1.00E-180	100.8	88.8	91.3	unnamed protein product	----	----	AT2G19810.1 | Symbols: | CCCH-type zinc finger family protein | chr2:8550419-8551498 FORWARD LENGTH=359	356	359	1.00E-156	100.8	80.6	87.9
Rsa1.0_01391.1.g26348.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	365	1529	2.00E-42	418.9	26.6	39.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	365	295	2.00E-35	80.8	22.7	33.7
Rsa1.0_01391.1.g26349.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01391.1.g26350.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	185	484	7.00E-31	261.6	34.6	43.8	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01392.1.g26351.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01392.1.g26352.t5	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	815	1239	1.00E-128	152.0	32.3	42.8	putative pol polyprotein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01392.1.g26353.t1	emb|CAM31954.1| glucosyltransferase [Brassica napus]	483	482	0	99.8	94.2	96.7	glucosyltransferase	gbpln	Brassica napus	AT4G01070.1 | Symbols: GT72B1, UGT72B1 | UDP-Glycosyltransferase superfamily protein | chr4:461858-463300 REVERSE LENGTH=480	483	480	0	99.4	82.0	89.9
Rsa1.0_01392.1.g26354.t3	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	462	1463	2.00E-32	316.7	30.3	47.0	F5J5.1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01392.1.g26355.t8	gb|AAZ41811.1| 01P13-1 [Brassica rapa subsp. pekinensis]	1209	1545	0	127.8	63.6	76.8	01P13-1	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1209	1262	3.00E-78	104.4	14.5	20.3
Rsa1.0_01392.1.g26356.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01392.1.g26357.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01392.1.g26358.t2	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	536	695	3.00E-84	129.7	35.4	43.8	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT4G03830.1 | Symbols: | Protein of unknown function, DUF601 | chr4:1790440-1792458 FORWARD LENGTH=578	536	578	2.00E-12	107.8	5.2	7.8
Rsa1.0_01392.1.g26359.t1	gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	684	1787	1.00E-156	261.3	44.9	59.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01393.1.g26360.t1	gb|ACP30573.1| disease resistance protein [Brassica rapa subsp. pekinensis]	181	1038	4.00E-12	573.5	41.4	47.5	disease resistance protein	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_01393.1.g26361.t1	ref|XP_002892277.1| TraB family protein [Arabidopsis lyrata subsp. lyrata] gi|297338119|gb|EFH68536.1| TraB family protein [Arabidopsis lyrata subsp. lyrata]	110	372	5.00E-42	338.2	71.8	92.7	TraB family protein	gbpln	Arabidopsis lyrata	AT1G05270.1 | Symbols: | TraB family protein | chr1:1531806-1534305 REVERSE LENGTH=371	110	371	3.00E-43	337.3	68.2	92.7
Rsa1.0_01393.1.g26362.t1	gb|AAT72298.1| CBRCI35 [Capsella bursa-pastoris]	326	326	1.00E-178	100.0	91.4	96.6	CBRCI35	gbpln	Capsella bursa-pastoris	AT1G05260.1 | Symbols: RCI3, RCI3A | Peroxidase superfamily protein | chr1:1529827-1531271 FORWARD LENGTH=326	326	326	1.00E-178	100.0	90.2	96.0
Rsa1.0_01393.1.g26363.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01393.1.g26364.t1	gb|EOA39455.1| hypothetical protein CARUB_v10012652mg [Capsella rubella]	340	320	1.00E-135	94.1	68.8	81.2	hypothetical protein CARUB_v10012652mg	gbpln	Capsella rubella	AT1G05250.1 | Symbols: | Peroxidase superfamily protein | chr1:1525924-1527169 REVERSE LENGTH=325	340	325	1.00E-124	95.6	61.2	72.9
Rsa1.0_01393.1.g26365.t1	gb|EOA39455.1| hypothetical protein CARUB_v10012652mg [Capsella rubella]	321	320	1.00E-164	99.7	88.5	92.8	hypothetical protein CARUB_v10012652mg	gbpln	Capsella rubella	AT1G05250.1 | Symbols: | Peroxidase superfamily protein | chr1:1525924-1527169 REVERSE LENGTH=325	321	325	1.00E-137	101.2	76.3	86.6
Rsa1.0_01393.1.g26366.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2437	1274	0	52.3	26.1	34.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT2G34090.2 | Symbols: MEE18 | maternal effect embryo arrest 18 | chr2:14396283-14399170 REVERSE LENGTH=471	2437	471	1.00E-130	19.3	9.8	10.2
Rsa1.0_01393.1.g26367.t1	ref|XP_002881322.1| hypothetical protein ARALYDRAFT_321134 [Arabidopsis lyrata subsp. lyrata] gi|297327161|gb|EFH57581.1| hypothetical protein ARALYDRAFT_321134 [Arabidopsis lyrata subsp. lyrata]	342	345	9.00E-14	100.9	19.6	23.7	hypothetical protein ARALYDRAFT_321134	gbpln	Arabidopsis lyrata	AT2G34100.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: sperm cell, flower; EXPRESSED DURING: petal differentiation and expansion stage; Has 10185 Blast hits to 4535 proteins in 413 species: Archae - 41; Bacteria - 4951; Metazoa - 1579; Fungi - 1007; Plants - 277; Viruses - 100; Other Eukaryotes - 2230 (source: NCBI BLink). | chr2:14399705-14401655 REVERSE LENGTH=345	342	345	2.00E-15	100.9	9.9	12.0

Rsa1.0_01393.1.g26368.t1	ref|XP_002883131.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297328971|gb|EFH59390.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	175	175	3.00E-88	100.0	91.4	97.1	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT3G18430.2 | Symbols: | Calcium-binding EF-hand family protein | chr3:6326180-6327476 FORWARD LENGTH=175	175	175	2.00E-90	100.0	90.9	97.1
Rsa1.0_01393.1.g26369.t1	ref|XP_002881325.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327164|gb|EFH57584.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	155	802	3.00E-43	517.4	61.3	64.5	predicted protein	gbpln	Arabidopsis lyrata	AT2G34150.1 | Symbols: ATRANGAP2, ATSCAR1, SCAR1, WAVE1 | SCAR family protein | chr2:14419432-14422361 REVERSE LENGTH=700	155	700	5.00E-43	451.6	58.7	61.9
Rsa1.0_01394.1.g26370.t1	gb|EOA18841.1| hypothetical protein CARUB_v10007463mg [Capsella rubella]	386	382	0	99.0	86.3	90.9	hypothetical protein CARUB_v10007463mg	gbpln	Capsella rubella	AT4G12840.2 | Symbols: | Protein of unknown function (DUF707) | chr4:7533621-7536263 REVERSE LENGTH=395	386	395	0	102.3	85.0	91.7
Rsa1.0_01394.1.g26371.t1	ref|NP_567394.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] gi|15912319|gb|AAL08293.1| AT4g12830/T20K18_180 [Arabidopsis thaliana] gi|19699240|gb|AAL90986.1| AT4g12830/T20K18_180 [Arabidopsis thaliana] gi|332657790|gb|AEE83190.1| hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	393	393	0	100.0	89.6	94.7	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis thaliana	AT4G12830.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:7531189-7533327 FORWARD LENGTH=393	393	393	0	100.0	89.6	94.7
Rsa1.0_01394.1.g26372.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01394.1.g26373.t1	gb|ACG24344.1| photosystem I reaction center subunit XI [Zea mays]	219	219	1.00E-100	100.0	91.3	95.9	photosystem I reaction center subunit XI	gbenv/gbpln	Zea mays	AT4G12800.1 | Symbols: PSAL | photosystem I subunit l | chr4:7521469-7522493 FORWARD LENGTH=219	219	219	3.00E-96	100.0	91.8	96.3
Rsa1.0_01394.1.g26374.t2	gb|AAD36941.1|AF069441_1 hypothetical protein [Arabidopsis thaliana] gi|7267197|emb|CAB77908.1| hypothetical protein [Arabidopsis thaliana]	353	735	3.00E-25	208.2	18.4	25.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	353	249	6.00E-18	70.5	12.7	16.4
Rsa1.0_01394.1.g26375.t1	gb|AAC34356.1| Hypothetical protein [Arabidopsis thaliana]	188	1250	9.00E-59	664.9	58.5	61.7	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G77260.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:29023961-29026699 REVERSE LENGTH=655	188	655	1.00E-60	348.4	58.5	61.7
Rsa1.0_01394.1.g26376.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01394.1.g26377.t1	emb|CAN79264.1| hypothetical protein VITISV_034881 [Vitis vinifera]	689	1360	1.00E-122	197.4	37.7	49.6	hypothetical protein VITISV_034881	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	689	1262	1.00E-23	183.2	8.4	14.2
Rsa1.0_01394.1.g26378.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	158	1142	7.00E-26	722.8	41.1	57.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT3G32050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14780.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:13067626-13068582 REVERSE LENGTH=175	158	175	8.00E-11	110.8	17.7	22.2
Rsa1.0_01395.1.g26379.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1438	1529	0	106.3	42.8	58.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1438	746	3.00E-87	51.9	12.2	15.9
Rsa1.0_01395.1.g26380.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01395.1.g26381.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1422	1485	0	104.4	45.0	60.4	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1422	158	5.00E-26	11.1	3.5	5.7
Rsa1.0_01395.1.g26382.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01396.1.g26383.t16	ref|XP_002891633.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297337475|gb|EFH67892.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	748	666	0	89.0	74.9	79.7	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT1G51350.1 | Symbols: | ARM repeat superfamily protein | chr1:19035851-19038738 FORWARD LENGTH=666	748	666	0	89.0	74.1	79.4
Rsa1.0_01396.1.g26384.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01396.1.g26385.t1	gb|AFL91695.1| RNA binding protein [Raphanus sativus var. raphanistroides]	99	200	2.00E-35	202.0	76.8	83.8	RNA binding protein	gbpln	Raphanus sativus	AT1G51510.1 | Symbols: Y14 | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:19103072-19104753 REVERSE LENGTH=202	99	202	2.00E-34	204.0	72.7	82.8

Rsa1.0_01396.1.g26386.t6	ref|NP_197352.1| Aminotransferase-like, plant mobile domain family protein [Arabidopsis thaliana] gi|91805645|gb|ABE65551.1| hypothetical protein At5g18510 [Arabidopsis thaliana] gi|332005190|gb|AED92573.1| Aminotransferase-like, plant mobile domain family protein [Arabidopsis thaliana]	271	702	5.00E-22	259.0	24.0	28.4	Aminotransferase-like, plant mobile domain family protein	gbpln	Arabidopsis thaliana	AT5G18510.1 | Symbols: | Aminotransferase-like, plant mobile domain family protein | chr5:6141778-6143886 REVERSE LENGTH=702	271	702	1.00E-24	259.0	24.0	28.4
Rsa1.0_01396.1.g26387.t1	ref|NP_175494.1| Plant mobile domain protein family [Arabidopsis thaliana] gi|12321786|gb|AAG50928.1|AC079284_3 hypothetical protein [Arabidopsis thaliana] gi|91805349|gb|ABE65404.1| hypothetical protein At1g50790 [Arabidopsis thaliana] gi|332194470|gb|AEE32591.1| Plant mobile domain protein family [Arabidopsis thaliana]	765	812	1.00E-167	106.1	45.6	59.0	Plant mobile domain protein family	gbpln	Arabidopsis thaliana	AT1G50790.1 | Symbols: | Plant mobile domain protein family | chr1:18824050-18826488 REVERSE LENGTH=812	765	812	1.00E-169	106.1	45.6	59.0
Rsa1.0_01396.1.g26388.t1	gb|EOA39656.1| hypothetical protein CARUB_v10008295mg [Capsella rubella]	205	850	1.00E-25	414.6	30.2	38.5	hypothetical protein CARUB_v10008295mg	gbpln	Capsella rubella	AT4G16050.1 | Symbols: | Aminotransferase-like, plant mobile domain family protein | chr4:9092243-9094243 FORWARD LENGTH=666	205	666	2.00E-27	324.9	44.4	58.0
Rsa1.0_01396.1.g26389.t1	gb|EOA36539.1| hypothetical protein CARUB_v10011613mg [Capsella rubella]	880	545	1.00E-156	61.9	32.2	38.3	hypothetical protein CARUB_v10011613mg	gbpln	Capsella rubella	AT1G50820.1 | Symbols: | Aminotransferase-like, plant mobile domain family protein | chr1:18833275-18834861 REVERSE LENGTH=528	880	528	1.00E-156	60.0	32.5	40.3
Rsa1.0_01396.1.g26390.t1	gb|EOA39011.1| hypothetical protein CARUB_v10011554mg, partial [Capsella rubella]	779	874	1.00E-154	112.2	42.0	57.3	hypothetical protein CARUB_v10011554mg, partial	gbpln	Capsella rubella	AT1G50820.1 | Symbols: | Aminotransferase-like, plant mobile domain family protein | chr1:18833275-18834861 REVERSE LENGTH=528	779	528	1.00E-155	67.8	36.5	45.7
Rsa1.0_01396.1.g26391.t1	ref|XP_002894325.1| hypothetical protein ARALYDRAFT_474272 [Arabidopsis lyrata subsp. lyrata] gi|297340167|gb|EFH70584.1| hypothetical protein ARALYDRAFT_474272 [Arabidopsis lyrata subsp. lyrata]	562	560	0	99.6	91.1	95.2	hypothetical protein ARALYDRAFT_474272	gbpln	Arabidopsis lyrata	AT1G51590.1 | Symbols: MNS1, MANIB | alpha-mannosidase 1 | chr1:19128315-19132132 REVERSE LENGTH=560	562	560	0	99.6	91.1	94.1
Rsa1.0_01396.1.g26392.t1	#	#	#	#	#	#	#	-	----	----	AT1G51600.2 | Symbols: ZML2, TIFY2A, GATA28 | ZIM-LIKE 2 | chr1:19133176-19135252 FORWARD LENGTH=302	64	302	1.00E-11	471.9	56.3	60.9
Rsa1.0_01396.1.g26393.t1	gb|EOA37777.1| hypothetical protein CARUB_v10012642mg [Capsella rubella]	798	457	0	57.3	44.2	46.0	hypothetical protein CARUB_v10012642mg	gbpln	Capsella rubella	AT1G51610.1 | Symbols: | Cation efflux family protein | chr1:19136625-19139621 FORWARD LENGTH=457	798	457	0	57.3	43.4	45.6
Rsa1.0_01396.1.g26394.t1	gb|EOA40507.1| hypothetical protein CARUB_v10009235mg [Capsella rubella]	418	423	0	101.2	92.8	96.2	hypothetical protein CARUB_v10009235mg	gbpln	Capsella rubella	AT1G51630.1 | Symbols: | O-fucosyltransferase family protein | chr1:19142141-19144082 REVERSE LENGTH=423	418	423	0	101.2	92.3	95.7
Rsa1.0_01397.1.g26395.t1	ref|NP_173534.1| O-methyltransferase-like protein [Arabidopsis thaliana] gi|8886991|gb|AAF80651.1|AC012190_7 Contains similarity to O-Methyltransferase 1 from Arabidopsis thaliana gb|U70424. It is a member of O-methyltransferase family. ESTs gb|AI994826, gb|N65066 and gb|N38589 come from this gene [Arabidopsis thaliana] gi|12744975|gb|AAK06867.1|AF344316_1 putative O-methyltransferase [Arabidopsis thaliana] gi|15982844|gb|AAL09769.1| At1g21100/T22I11_7 [Arabidopsis thaliana] gi|23506107|gb|AAN28913.1| At1g21100/T22I11_7 [Arabidopsis thaliana] gi|332191943|gb|AEE30064.1| O-methyltransferase-like protein [Arabidopsis thaliana]	278	373	2.33E-156	134.2	93.2	96.0	O-methyltransferase-like protein	gbpln	Arabidopsis thaliana	AT1G21100.1 | Symbols: | O-methyltransferase family protein | chr1:7386991-7388318 REVERSE LENGTH=373	278	373	1.00E-148	134.2	93.2	96.0
Rsa1.0_01397.1.g26396.t1	ref|XP_002893153.1| hypothetical protein ARALYDRAFT_472352 [Arabidopsis lyrata subsp. lyrata] gi|297338995|gb|EFH69412.1| hypothetical protein ARALYDRAFT_472352 [Arabidopsis lyrata subsp. lyrata]	326	373	1.00E-165	114.4	89.0	92.3	hypothetical protein ARALYDRAFT_472352	gbpln	Arabidopsis lyrata	AT1G21100.1 | Symbols: | O-methyltransferase family protein | chr1:7386991-7388318 REVERSE LENGTH=373	326	373	1.00E-167	114.4	87.7	91.7

Rsa1.0_01397.1.g26397.t1	ref|NP_173536.1| O-methyltransferase family protein [Arabidopsis thaliana] gi|8886989|gb|AAF80649.1|AC012190_5 Contains similarity to O-Methyltransferase 1 from Arabidopsis thaliana gb|U70424. It is a member of O-methyltransferase family. ESTs gb|AI993288 and gb|Z18076 come from this gene [Arabidopsis thaliana] gi|12744973|gb|AAK06866.1|AF344315_1 putative ATPase [Arabidopsis thaliana] gi|332191945|gb|AEE30066.1| O-methyltransferase family protein [Arabidopsis thaliana]	374	373	0	99.7	93.3	96.8	O-methyltransferase family protein	gbpln	Arabidopsis thaliana	AT1G21120.1 | Symbols: | O-methyltransferase family protein | chr1:7395331-7396640 REVERSE LENGTH=373	374	373	0	99.7	93.3	96.8
Rsa1.0_01397.1.g26398.t1	ref|NP_189952.1| vacuolar iron transporter-like protein [Arabidopsis thaliana] gi|75182792|sp|Q9M2C0.1|VITH4_ARATH RecName: Full=Vacuolar iron transporter homolog 4; AltName: Full=Protein NODULIN-LIKE 4 gi|7362791|emb|CAB83067.1| nodulin-like protein [Arabidopsis thaliana] gi|34365643|gb|AAQ65133.1| At3g43660 [Arabidopsis thaliana] gi|51970300|dbj|BAD43842.1| nodulin -like protein [Arabidopsis thaliana] gi|332644295|gb|AEE77816.1| vacuolar iron transporter homolog 4 [Arabidopsis thaliana]	205	198	2.00E-82	96.6	75.1	83.4	vacuolar iron transporter-like protein	gbpln	Arabidopsis thaliana	AT3G43660.1 | Symbols: | Vacuolar iron transporter (VIT) family protein | chr3:15565332-15565928 FORWARD LENGTH=198	205	198	6.00E-85	96.6	75.1	83.4
Rsa1.0_01397.1.g26399.t1	ref|NP_173540.2| eukaryotic translation initiation factor 2-like protein [Arabidopsis thaliana] gi|225897954|dbj|BAH30309.1| hypothetical protein [Arabidopsis thaliana] gi|332191950|gb|AEE30071.1| eukaryotic translation initiation factor 2-like protein [Arabidopsis thaliana]	1037	1092	0	105.3	66.1	79.1	eukaryotic translation initiation factor 2-like protein	gbpln	Arabidopsis thaliana	AT1G21160.1 | Symbols: | eukaryotic translation initiation factor 2 (eIF-2) family protein | chr1:7408121-7412455 REVERSE LENGTH=1092	1037	1092	0	105.3	66.1	79.1
Rsa1.0_01397.1.g26400.t1	gb|EOA40426.1| hypothetical protein CARUB_v10009151mg [Capsella rubella] gi|482576240|gb|EOA40427.1| hypothetical protein CARUB_v10009151mg [Capsella rubella]	345	442	1.00E-143	128.1	83.8	89.0	hypothetical protein CARUB_v10009151mg	gbpln	Capsella rubella	AT1G21200.1 | Symbols: | sequence-specific DNA binding transcription factors | chr1:7421483-7422814 FORWARD LENGTH=443	345	443	1.00E-140	128.4	82.9	87.8
Rsa1.0_01397.1.g26401.t2	gb|EOA36812.1| hypothetical protein CARUB_v10008422mg [Capsella rubella]	718	734	0	102.2	69.9	81.2	hypothetical protein CARUB_v10008422mg	gbpln	Capsella rubella	AT1G21250.1 | Symbols: WAK1, PRO25 | cell wall-associated kinase | chr1:7439512-7441892 FORWARD LENGTH=735	718	735	0	102.4	68.8	80.8
Rsa1.0_01397.1.g26402.t1	gb|AAS99677.1| At1g21220 [Arabidopsis thaliana] gi|48310400|gb|AAT41813.1| At1g21220 [Arabidopsis thaliana]	234	227	1.00E-76	97.0	60.7	76.1	At1g21220	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	234	237	2.00E-66	101.3	53.0	68.4
Rsa1.0_01397.1.g26403.t1	gb|EOA36812.1| hypothetical protein CARUB_v10008422mg [Capsella rubella]	738	734	0	99.5	71.5	81.6	hypothetical protein CARUB_v10008422mg	gbpln	Capsella rubella	AT1G21230.1 | Symbols: WAK5 | wall associated kinase 5 | chr1:7429980-7432346 FORWARD LENGTH=733	738	733	0	99.3	70.5	82.0
Rsa1.0_01397.1.g26404.t1	gb|EOA19925.1| hypothetical protein CARUB_v10000175mg [Capsella rubella]	149	896	2.00E-45	601.3	67.8	77.9	hypothetical protein CARUB_v10000175mg	gbpln	Capsella rubella	AT5G06220.1 | Symbols: | LETM1-like protein | chr5:1880049-1885366 FORWARD LENGTH=832	149	832	6.00E-47	558.4	68.5	75.2
Rsa1.0_01397.1.g26405.t6	ref|NP_173577.2| zinc finger CCCH domain-containing protein [Arabidopsis thaliana] gi|332191999|gb|AEE30120.1| zinc finger CCCH domain-containing protein [Arabidopsis thaliana]	1495	2166	0	144.9	40.9	46.9	zinc finger CCCH domain-containing protein	gbpln	Arabidopsis thaliana	AT1G21580.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:7557822-7565655 REVERSE LENGTH=2166	1495	2166	0	144.9	40.9	46.9
Rsa1.0_01397.1.g26406.t1	ref|NP_173578.2| adenine nucleotide alpha hydrolases-domain containing protein kinase [Arabidopsis thaliana] gi|18086338|gb|AAL57632.1| At1g21590/F24J8_9 [Arabidopsis thaliana] gi|22655342|gb|AAM98263.1| At1g21590/F24J8_9 [Arabidopsis thaliana] gi|332192000|gb|AEE30121.1| adenine nucleotide alpha hydrolases-domain containing protein kinase [Arabidopsis thaliana]	707	756	0	106.9	79.9	89.4	adenine nucleotide alpha hydrolases-domain containing protein kinase	gbpln	Arabidopsis thaliana	AT1G21590.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:7566613-7569694 REVERSE LENGTH=756	707	756	0	106.9	79.9	89.4
Rsa1.0_01397.1.g26407.t1	dbj|BAJ53190.1| JMS09K11.8 [Jatropha curcas]	286	332	3.00E-41	116.1	44.8	58.7	JMS09K11.8	gbpln	Jatropha curcas	AT1G21600.2 | Symbols: PTAC6 | plastid transcriptionally active 6 | chr1:7571514-7573782 REVERSE LENGTH=328	286	328	2.00E-33	114.7	25.5	28.3

Rsa1.0_01397.1.g26408.t1	ref|NP_173582.2| calcium-binding EF-hand-containing protein [Arabidopsis thaliana] gi|332192007|gb|AEE30128.1| calcium-binding EF-hand-containing protein [Arabidopsis thaliana]	1199	1218	0	101.6	82.3	86.7	calcium-binding EF-hand-containing protein	gbpln	Arabidopsis thaliana	AT1G21630.1 | Symbols: | Calcium-binding EF hand family protein | chr1:7581457-7587796 FORWARD LENGTH=1218	1199	1218	0	101.6	82.3	86.7
Rsa1.0_01397.1.g26409.t2	ref|NP_001185059.1| preprotein translocase secA-like protein [Arabidopsis thaliana] gi|363805541|sp|D8WUA4.1|SECA2_ARATH RecName: Full=Protein translocase subunit SECA2, chloroplastic; Flags: Precursor gi|298108793|gb|ADI56650.1| plastid SecA2 [Arabidopsis thaliana] gi|332192013|gb|AEE30134.1| preprotein translocase secA-like protein [Arabidopsis thaliana]	1038	1058	0	101.9	93.0	96.5	preprotein translocase secA-like protein	gbpln	Arabidopsis thaliana	AT1G21650.2 | Symbols: SECA2 | Preprotein translocase SecA family protein | chr1:7592891-7600590 REVERSE LENGTH=1058	1038	1058	0	101.9	93.0	96.5
Rsa1.0_01397.1.g26410.t1	gb|EOA35901.1| hypothetical protein CARUB_v10021156mg [Capsella rubella]	121	121	2.00E-55	100.0	90.1	96.7	hypothetical protein CARUB_v10021156mg	gbpln	Capsella rubella	AT1G77350.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function KRTCAP2 (InterPro:IPR018614); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:29070497-29071545 FORWARD LENGTH=122	121	122	2.00E-56	100.8	90.1	96.7
Rsa1.0_01397.1.g26411.t2	ref|XP_002890453.1| EMB1968 [Arabidopsis lyrata subsp. lyrata] gi|297336295|gb|EFH66712.1| EMB1968 [Arabidopsis lyrata subsp. lyrata]	326	339	1.00E-175	104.0	92.0	96.0	EMB1968	gbpln	Arabidopsis lyrata	AT1G21690.1 | Symbols: EMB1968, RFC4 | ATPase family associated with various cellular activities (AAA) | chr1:7615675-7618362 FORWARD LENGTH=339	326	339	1.00E-176	104.0	91.1	95.7
Rsa1.0_01397.1.g26412.t1	gb|EOA36733.1| hypothetical protein CARUB_v10012527mg, partial [Capsella rubella]	810	833	0	102.8	76.4	81.7	hypothetical protein CARUB_v10012527mg, partial	gbpln	Capsella rubella	AT1G21700.1 | Symbols: ATSWI3C, CHB4, SWI3C | SWITCH/sucrose nonfermenting 3C | chr1:7620156-7623978 REVERSE LENGTH=807	810	807	0	99.6	76.2	81.7
Rsa1.0_01398.1.g26413.t1	ref|XP_002870037.1| hypothetical protein ARALYDRAFT_493003 [Arabidopsis lyrata subsp. lyrata] gi|297315873|gb|EFH46296.1| hypothetical protein ARALYDRAFT_493003 [Arabidopsis lyrata subsp. lyrata]	84	636	7.00E-18	757.1	51.2	51.2	hypothetical protein ARALYDRAFT_493003	gbpln	Arabidopsis lyrata	AT4G18570.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:10231439-10234534 FORWARD LENGTH=642	84	642	2.00E-20	764.3	50.0	51.2
Rsa1.0_01398.1.g26414.t2	gb|EOA16130.1| hypothetical protein CARUB_v10004265mg [Capsella rubella]	674	701	0	104.0	52.2	68.7	hypothetical protein CARUB_v10004265mg	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	674	696	2.00E-52	103.3	22.3	39.0
Rsa1.0_01398.1.g26415.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	311	1529	1.00E-54	491.6	37.6	55.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	311	746	2.00E-42	239.9	30.5	41.8
Rsa1.0_01398.1.g26416.t1	gb|ABD65624.1| hypothetical protein 23.t00036 [Brassica oleracea]	963	842	1.00E-158	87.4	41.0	54.0	hypothetical protein 23.t00036	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	963	673	2.00E-35	69.9	11.9	17.9
Rsa1.0_01398.1.g26417.t1	gb|ABD65615.1| hypothetical protein 23.t00033 [Brassica oleracea]	371	326	2.00E-26	87.9	15.4	25.3	hypothetical protein 23.t00033	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01398.1.g26418.t3	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	216	484	1.00E-30	224.1	30.1	36.6	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01398.1.g26419.t1	gb|EOA20474.1| hypothetical protein CARUB_v10000785mg [Capsella rubella]	501	501	0	100.0	95.4	97.4	hypothetical protein CARUB_v10000785mg	gbpln	Capsella rubella	AT4G09570.1 | Symbols: CPK4, ATCPK4 | calcium-dependent protein kinase 4 | chr4:6049560-6052184 FORWARD LENGTH=501	501	501	0	100.0	95.8	97.4
Rsa1.0_01398.1.g26420.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01398.1.g26421.t1	ref|XP_002886268.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata] gi|297332108|gb|EFH62527.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata]	366	346	3.00E-80	94.5	49.2	62.6	hypothetical protein ARALYDRAFT_900376	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	366	370	5.00E-78	101.1	46.7	63.7
Rsa1.0_01399.1.g26422.t1	ref|XP_002883414.1| AtMYB15/AtY19/MYB15 [Arabidopsis lyrata subsp. lyrata] gi|297329254|gb|EFH59673.1| AtMYB15/AtY19/MYB15 [Arabidopsis lyrata subsp. lyrata]	288	285	1.00E-135	99.0	82.3	87.2	AtMYB15/AtY19/MYB15	gbpln	Arabidopsis lyrata	AT3G23250.1 | Symbols: MYB15, ATY19, ATMYB15 | myb domain protein 15 | chr3:8309492-8310624 FORWARD LENGTH=285	288	285	1.00E-136	99.0	80.9	87.2

<table>
<tr><td>Rsa1.0_01399.1.g26423.t1</td><td>gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]</td><td>533</td><td>723</td><td>1.00E-119</td><td>135.6</td><td>40.5</td><td>54.4</td><td>Tam3-like transposon protein; 93317-95488</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>533</td><td>696</td><td>9.00E-30</td><td>130.6</td><td>16.9</td><td>29.3</td></tr>
<tr><td>Rsa1.0_01399.1.g26424.t3</td><td>gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]</td><td>424</td><td>1239</td><td>1.00E-106</td><td>292.2</td><td>48.3</td><td>59.9</td><td>putative pol polyprotein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>424</td><td>1262</td><td>8.00E-45</td><td>297.6</td><td>26.4</td><td>40.8</td></tr>
<tr><td>Rsa1.0_01399.1.g26425.t1</td><td>gb|AAD24601.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>400</td><td>1319</td><td>4.00E-49</td><td>329.8</td><td>28.8</td><td>41.0</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292</td><td>400</td><td>292</td><td>1.00E-29</td><td>73.0</td><td>22.5</td><td>33.3</td></tr>
<tr><td>Rsa1.0_01399.1.g26426.t1</td><td>gb|EOA32154.1| hypothetical protein CARUB_v10015406mg [Capsella rubella]</td><td>137</td><td>143</td><td>1.00E-55</td><td>104.4</td><td>89.1</td><td>94.9</td><td>hypothetical protein CARUB_v10015406mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G23230.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:8289647-8290066 REVERSE LENGTH=139</td><td>137</td><td>139</td><td>2.00E-54</td><td>101.5</td><td>88.3</td><td>93.4</td></tr>
<tr><td>Rsa1.0_01399.1.g26427.t1</td><td>gb|EOA31669.1| hypothetical protein CARUB_v10014873mg [Capsella rubella]</td><td>124</td><td>141</td><td>1.00E-38</td><td>113.7</td><td>71.0</td><td>77.4</td><td>hypothetical protein CARUB_v10014873mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G23220.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr3:8287969-8288388 FORWARD LENGTH=139</td><td>124</td><td>139</td><td>4.00E-33</td><td>112.1</td><td>67.7</td><td>72.6</td></tr>
<tr><td>Rsa1.0_01400.1.g26428.t1</td><td>ref|XP_002873348.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319185|gb|EFH49607.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>231</td><td>252</td><td>2.00E-66</td><td>109.1</td><td>61.0</td><td>71.4</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G08240.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23160.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 1; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:2651382-2652336 REVERSE LENGTH=258</td><td>231</td><td>258</td><td>4.00E-67</td><td>111.7</td><td>62.3</td><td>73.6</td></tr>
<tr><td>Rsa1.0_01400.1.g26429.t1</td><td>gb|EOA20753.1| hypothetical protein CARUB_v10001081mg [Capsella rubella]</td><td>134</td><td>411</td><td>9.00E-39</td><td>306.7</td><td>81.3</td><td>84.3</td><td>hypothetical protein CARUB_v10001081mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G08200.1 | Symbols: | peptidoglycan-binding LysM domain-containing protein | chr5:2638385-2640508 FORWARD LENGTH=409</td><td>134</td><td>409</td><td>9.00E-41</td><td>305.2</td><td>80.6</td><td>84.3</td></tr>
<tr><td>Rsa1.0_01400.1.g26430.t1</td><td>ref|NP_196434.1| agmatine deiminase [Arabidopsis thaliana] gi|73622159|sp|Q8GWW7.2|AGUA_ARATH RecName: Full=Agmatine deiminase; AltName: Full=Agmatine iminohydrolase; AltName: Full=Protein EMBRYO DEFECTIVE 1873 gi|8346554|emb|CAB93718.1| putative protein [Arabidopsis thaliana] gi|332003878|gb|AED91261.1| agmatine deiminase [Arabidopsis thaliana]</td><td>461</td><td>383</td><td>0</td><td>83.1</td><td>73.1</td><td>79.2</td><td>agmatine deiminase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G08170.1 | Symbols: EMB1873, ATAIH | porphyromonas-type peptidyl-arginine deiminase family protein | chr5:2628663-2631047 REVERSE LENGTH=383</td><td>461</td><td>383</td><td>0</td><td>83.1</td><td>73.1</td><td>79.2</td></tr>
<tr><td>Rsa1.0_01400.1.g26431.t1</td><td>ref|NP_196433.1| serine/threonine protein kinase 3 [Arabidopsis thaliana] gi|11762274|gb|AAG40409.1|AF325057_1 AT5g08160 [Arabidopsis thaliana] gi|2109293|gb|AAB69123.1| serine/threonine protein kinase [Arabidopsis thaliana] gi|8346553|emb|CAB93717.1| serine/threonine protein kinase [Arabidopsis thaliana] gi|24417498|gb|AAN60359.1| unknown [Arabidopsis thaliana] gi|94442405|gb|ABF18990.1| At5g08160 [Arabidopsis thaliana] gi|332003876|gb|AED91259.1| serine/threonine protein kinase 3 [Arabidopsis thaliana]</td><td>346</td><td>347</td><td>0</td><td>100.3</td><td>94.2</td><td>96.8</td><td>serine/threonine protein kinase 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G08160.1 | Symbols: ATPK3, PK3 | serine/threonine protein kinase 3 | chr5:2625903-2627942 REVERSE LENGTH=347</td><td>346</td><td>347</td><td>0</td><td>100.3</td><td>94.2</td><td>96.8</td></tr>
<tr><td>Rsa1.0_01400.1.g26432.t1</td><td>ref|XP_002873343.1| hypothetical protein ARALYDRAFT_908765 [Arabidopsis lyrata subsp. lyrata] gi|297319180|gb|EFH49602.1| hypothetical protein ARALYDRAFT_908765 [Arabidopsis lyrata subsp. lyrata]</td><td>142</td><td>140</td><td>7.00E-25</td><td>98.6</td><td>59.9</td><td>66.9</td><td>hypothetical protein ARALYDRAFT_908765</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G08150.1 | Symbols: SOB5 | suppressor of phytochrome b 5 | chr5:2622164-2622598 REVERSE LENGTH=144</td><td>142</td><td>144</td><td>3.00E-20</td><td>101.4</td><td>61.3</td><td>70.4</td></tr>
<tr><td>Rsa1.0_01400.1.g26433.t2</td><td>ref|XP_002871317.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317154|gb|EFH47576.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>409</td><td>313</td><td>8.00E-29</td><td>76.5</td><td>21.3</td><td>29.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G03480.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:869208-870855 REVERSE LENGTH=321</td><td>409</td><td>321</td><td>3.00E-25</td><td>78.5</td><td>18.6</td><td>26.7</td></tr>
<tr><td>Rsa1.0_01400.1.g26434.t1</td><td>gb|EOA20721.1| hypothetical protein CARUB_v10001041mg [Capsella rubella]</td><td>300</td><td>422</td><td>4.00E-77</td><td>140.7</td><td>69.0</td><td>80.7</td><td>hypothetical protein CARUB_v10001041mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G08139.1 | Symbols: | RING/U-box superfamily protein | chr5:2616487-2617617 FORWARD LENGTH=376</td><td>300</td><td>376</td><td>3.00E-76</td><td>125.3</td><td>67.3</td><td>81.0</td></tr>
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Rsa1.0_01400.1.g26435.t1	gb|EOA20347.1| hypothetical protein CARUB_v10000655mg [Capsella rubella]	474	541	1.00E-177	114.1	81.9	87.3	hypothetical protein CARUB_v10000655mg	gbpln	Capsella rubella	AT5G08130.5 | Symbols: BIM1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:2606655-2609571 REVERSE LENGTH=532	474	532	1.00E-172	112.2	78.1	84.6
Rsa1.0_01400.1.g26436.t1	dbj|BAJ34155.1| unnamed protein product [Thellungiella halophila]	311	315	1.00E-159	101.3	88.7	93.6	unnamed protein product	----	----	AT5G08100.1 | Symbols: | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr5:2593242-2594586 REVERSE LENGTH=315	311	315	1.00E-155	101.3	85.5	92.3
Rsa1.0_01400.1.g26437.t1	ref|NP_196426.1| uncharacterized protein [Arabidopsis thaliana] gi|8346546|emb|CAB93710.1| hypothetical protein [Arabidopsis thaliana] gi|332003862|gb|AED91245.1| uncharacterized protein AT5G08090 [Arabidopsis thaliana]	109	322	7.00E-17	295.4	44.0	62.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G08090.1 | Symbols: | unknown protein; Has 13 Blast hits to 13 proteins in 8 species: Archae - 0; Bacteria - 4; Metazoa - 6; Fungi - 2; Plants - 1; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:2591711-2592899 FORWARD LENGTH=322	109	322	1.00E-19	295.4	44.0	62.4
Rsa1.0_01400.1.g26438.t1	ref|NP_196426.1| uncharacterized protein [Arabidopsis thaliana] gi|8346546|emb|CAB93710.1| hypothetical protein [Arabidopsis thaliana] gi|332003862|gb|AED91245.1| uncharacterized protein AT5G08090 [Arabidopsis thaliana]	157	322	1.00E-17	205.1	28.7	35.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G08090.1 | Symbols: | unknown protein; Has 13 Blast hits to 13 proteins in 8 species: Archae - 0; Bacteria - 4; Metazoa - 6; Fungi - 2; Plants - 1; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:2591711-2592899 FORWARD LENGTH=322	157	322	5.00E-20	205.1	28.7	35.7
Rsa1.0_01400.1.g26439.t1	gb|EOA21213.1| hypothetical protein CARUB_v10001560mg [Capsella rubella]	239	304	2.00E-90	127.2	93.3	96.7	hypothetical protein CARUB_v10001560mg	gbpln	Capsella rubella	AT5G08080.1 | Symbols: SYP132, ATSYP132 | syntaxin of plants 132 | chr5:2588532-2591106 FORWARD LENGTH=304	239	304	4.00E-91	127.2	91.6	96.2
Rsa1.0_01401.1.g26440.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01401.1.g26441.t1	gb|EOA12297.1| hypothetical protein CARUB_v10007977mg [Capsella rubella]	353	417	2.00E-51	118.1	35.4	54.7	hypothetical protein CARUB_v10007977mg	gbpln	Capsella rubella	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	353	575	1.00E-36	162.9	28.6	47.0
Rsa1.0_01401.1.g26442.t1	ref|XP_002887290.1| hypothetical protein ARALYDRAFT_476150 [Arabidopsis lyrata subsp. lyrata] gi|297333131|gb|EFH63549.1| hypothetical protein ARALYDRAFT_476150 [Arabidopsis lyrata subsp. lyrata]	85	86	6.00E-27	101.2	77.6	85.9	hypothetical protein ARALYDRAFT_476150	gbpln	Arabidopsis lyrata	AT1G70270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23965.1); Has 20 Blast hits to 20 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26464427-26464687 FORWARD LENGTH=86	85	86	3.00E-28	101.2	75.3	84.7
Rsa1.0_01401.1.g26443.t1	ref|NP_177183.2| nodulin MtN21 /EamA-like transporter protein [Arabidopsis thaliana] gi|460425434|sp|F4I5D5.1|WTR11_ARATH RecName: Full=WAT1-related protein At1g70260 gi|332196917|gb|AEE35038.1| WAT1-related protein [Arabidopsis thaliana]	345	375	0	108.7	89.9	95.9	nodulin MtN21 /EamA-like transporter protein	gbpln	Arabidopsis thaliana	AT1G70260.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:26457067-26459338 REVERSE LENGTH=375	345	375	0	108.7	89.9	95.9
Rsa1.0_01401.1.g26444.t1	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	1770	1643	0	92.8	47.1	62.3	gag/pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1770	1262	2.00E-82	71.3	9.3	14.1
Rsa1.0_01401.1.g26445.t1	gb|AAF18631.1|AC006228_2 F5J5.2 [Arabidopsis thaliana]	434	463	2.00E-37	106.7	23.7	39.4	F5J5.2	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01401.1.g26446.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01401.1.g26447.t1	ref|NP_177175.2| Sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana] gi|17473774|gb|AAL38323.1| unknown protein [Arabidopsis thaliana] gi|32189311|gb|AAP75810.1| At1g70180 [Arabidopsis thaliana] gi|332196908|gb|AEE35029.1| Sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	550	460	1.00E-113	83.6	57.3	65.3	Sterile alpha motif (SAM) domain-containing protein	gbpln	Arabidopsis thaliana	AT1G70180.2 | Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr1:26426768-26429097 FORWARD LENGTH=460	550	460	1.00E-116	83.6	57.3	65.3
Rsa1.0_01401.1.g26448.t1	ref|NP_564985.1| uncharacterized protein [Arabidopsis thaliana] gi|13430576|gb|AAK25910.1|AF360200_1 unknown protein [Arabidopsis thaliana] gi|15293161|gb|AAK93691.1| unknown protein [Arabidopsis thaliana] gi|332196905|gb|AEE35026.1| uncharacterized protein AT1G70160 [Arabidopsis thaliana]	526	523	0	99.4	90.1	93.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G70160.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27020.1); Has 108 Blast hits to 108 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 89; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink). | chr1:26420159-26422345 FORWARD LENGTH=523	526	523	0	99.4	90.1	93.2

Rsa1.0_01401.1.g26449.t1	ref|XP_002887278.1| hypothetical protein ARALYDRAFT_316004 [Arabidopsis lyrata subsp. lyrata] gi|297333119|gb|EFH63537.1| hypothetical protein ARALYDRAFT_316004 [Arabidopsis lyrata subsp. lyrata]	144	179	6.00E-50	124.3	66.7	75.7	hypothetical protein ARALYDRAFT_316004	gbpln	Arabidopsis lyrata	AT1G70040.1 | Symbols: | Protein of unknown function (DUF1163) | chr1:26381233-26381908 FORWARD LENGTH=193	144	193	4.00E-46	134.0	59.7	70.8
Rsa1.0_01402.1.g26450.t1	ref|NP_001189636.1| uncharacterized protein [Arabidopsis thaliana] gi|330253251|gb|AEC08345.1| uncharacterized protein AT2G30105 [Arabidopsis thaliana]	363	367	0	101.1	88.2	93.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G30105.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Leucine-rich repeat, typical subtype (InterPro:IPR003591), Leucine-rich repeat (InterPro:IPR001611), Ubiquitin (InterPro:IPR000626), Ubiquitin supergroup (InterPro:IPR019955); BEST Arabidopsis thaliana protein match is: Leucine-rich repeat (LRR) family protein (TAIR:AT5G07910.1). | chr2:12849855-12851908 FORWARD LENGTH=367	363	367	0	101.1	88.2	93.7
Rsa1.0_01402.1.g26451.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	506	368	2.00E-76	72.7	33.6	45.3	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	506	370	9.00E-66	73.1	30.6	42.5
Rsa1.0_01402.1.g26452.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	359	368	1.00E-68	102.5	44.3	60.2	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	359	370	2.00E-67	103.1	40.4	58.5
Rsa1.0_01402.1.g26453.t1	ref|NP_563963.1| FAD/NAD(P)-binding oxidoreductase [Arabidopsis thaliana] gi|5103813|gb|AAD39643.1|AC007591_8 Contains a PF|00175 Oxidoreductase FAD/NADH-binding domain. ESTs gb|H76345 and gb|AA651465 come from this gene [Arabidopsis thaliana] gi|12744999|gb|AAK06879.1|AF344328_1 unknown protein [Arabidopsis thaliana] gi|15451092|gb|AAK96817.1| Unknown protein [Arabidopsis thaliana] gi|18377448|gb|AAL66890.1| unknown protein [Arabidopsis thaliana] gi|332191150|gb|AEE29271.1| FAD/NAD(P)-binding oxidoreductase [Arabidopsis thaliana]	172	295	9.00E-34	171.5	38.4	44.8	FAD/NAD(P)-binding oxidoreductase	gbpln	Arabidopsis thaliana	AT1G15140.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase | chr1:5210403-5212137 REVERSE LENGTH=295	172	295	4.00E-36	171.5	38.4	44.8
Rsa1.0_01402.1.g26454.t1	ref|XP_002866825.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297312661|gb|EFH43084.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	73	368	4.00E-11	504.1	43.8	57.5	kelch repeat-containing F-box family protein	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	73	370	2.00E-13	506.8	42.5	56.2
Rsa1.0_01402.1.g26455.t1	ref|XP_002881085.1| hypothetical protein ARALYDRAFT_481921 [Arabidopsis lyrata subsp. lyrata] gi|297326924|gb|EFH57344.1| hypothetical protein ARALYDRAFT_481921 [Arabidopsis lyrata subsp. lyrata]	1057	1083	0	102.5	91.3	95.6	hypothetical protein ARALYDRAFT_481921	gbpln	Arabidopsis lyrata	AT2G30110.1 | Symbols: ATUBA1, MOS5, UBA1 | ubiquitin-activating enzyme 1 | chr2:12852632-12857369 REVERSE LENGTH=1080	1057	1080	0	102.2	91.2	95.4
Rsa1.0_01402.1.g26456.t1	ref|XP_002862737.1| hypothetical protein ARALYDRAFT_920315 [Arabidopsis lyrata subsp. lyrata] gi|297308435|gb|EFH38995.1| hypothetical protein ARALYDRAFT_920315 [Arabidopsis lyrata subsp. lyrata]	185	193	1.00E-80	104.3	78.9	82.7	hypothetical protein ARALYDRAFT_920315	gbpln	Arabidopsis lyrata	AT1G07090.1 | Symbols: LSH6 | Protein of unknown function (DUF640) | chr1:2174202-2174792 REVERSE LENGTH=196	185	196	8.00E-73	105.9	73.5	81.1
Rsa1.0_01402.1.g26457.t1	ref|NP_565695.1| LOB domain-containing protein 12 [Arabidopsis thaliana] gi|29427828|sp|Q8LBW3.2|LBD12_ARATH RecName: Full=LOB domain-containing protein 12; AltName: Full=ASYMMETRIC LEAVES 2-like protein 5; Short=AS2-like protein 5 gi|3150407|gb|AAC16959.1| expressed protein [Arabidopsis thaliana] gi|45330813|dbj|BAD12425.1| ASYMMETRIC LEAVES2-like gene 5 protein [Arabidopsis thaliana] gi|219807086|dbj|BAH10549.1| ASYMMETRIC LEAVES2-like 5 protein [Arabidopsis thaliana] gi|330253255|gb|AEC08349.1| LOB domain-containing protein 12 [Arabidopsis thaliana]	192	193	5.00E-85	100.5	93.8	95.3	LOB domain-containing protein 12	gbpln	Arabidopsis thaliana	AT2G30130.1 | Symbols: ASL5, LBD12, PCK1 | Lateral organ boundaries (LOB) domain family protein | chr2:12868740-12869684 FORWARD LENGTH=193	192	193	2.00E-87	100.5	93.8	95.3

<table>
<tr><td>Rsa1.0_01403.1.g26458.t1</td><td>ref|NP_564386.1| uncharacterized protein [Arabidopsis thaliana] gi|17978974|gb|AAL47448.1| At1g31940/F5M6.6 [Arabidopsis thaliana] gi|20334862|gb|AAM16187.1| At1g31940/F5M6.6 [Arabidopsis thaliana] gi|21554317|gb|AAM63422.1| unknown [Arabidopsis thaliana] gi|332193299|gb|AEE31420.1| uncharacterized protein AT1G31940 [Arabidopsis thaliana]</td><td>146</td><td>158</td><td>2.00E-59</td><td>108.2</td><td>90.4</td><td>92.5</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31940.1 | Symbols: | unknown protein; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35585.1); Has 67 Blast hits to 67 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:11470293-11471154 REVERSE LENGTH=158</td><td>146</td><td>158</td><td>6.00E-62</td><td>108.2</td><td>90.4</td><td>92.5</td></tr>
<tr><td>Rsa1.0_01403.1.g26459.t1</td><td>gb|ABK28020.1| unknown [Arabidopsis thaliana]</td><td>83</td><td>86</td><td>1.00E-19</td><td>103.6</td><td>66.3</td><td>77.1</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01403.1.g26460.t2</td><td>gb|EOA31957.1| hypothetical protein CARUB_v10015199mg [Capsella rubella]</td><td>168</td><td>1115</td><td>4.00E-16</td><td>663.7</td><td>34.5</td><td>51.2</td><td>hypothetical protein CARUB_v10015199mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G11910.1 | Symbols: UBP13 | ubiquitin-specific protease 13 | chr3:3761758-3770290 REVERSE LENGTH=1115</td><td>168</td><td>1115</td><td>7.00E-18</td><td>663.7</td><td>33.9</td><td>51.2</td></tr>
<tr><td>Rsa1.0_01403.1.g26461.t5</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01403.1.g26462.t1</td><td>gb|EOA36802.1| hypothetical protein CARUB_v10008296mg [Capsella rubella]</td><td>838</td><td>849</td><td>0</td><td>101.3</td><td>86.8</td><td>92.1</td><td>hypothetical protein CARUB_v10008296mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G31930.3 | Symbols: XLG3 | extra-large GTP-binding protein 3 | chr1:11465832-11468961 FORWARD LENGTH=848</td><td>838</td><td>848</td><td>0</td><td>101.2</td><td>87.5</td><td>92.8</td></tr>
<tr><td>Rsa1.0_01403.1.g26463.t1</td><td>ref|NP_174474.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75169173|sp|Q9C6T2.1|PPR68_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g31920 gi|12321292|gb|AAG50713.1|AC079041_6 PPR-repeat protein, putative [Arabidopsis thaliana] gi|332193295|gb|AEE31416.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]</td><td>611</td><td>606</td><td>0</td><td>99.2</td><td>80.9</td><td>89.9</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31920.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:11461864-11463684 REVERSE LENGTH=606</td><td>611</td><td>606</td><td>0</td><td>99.2</td><td>80.9</td><td>89.9</td></tr>
<tr><td>Rsa1.0_01403.1.g26464.t1</td><td>ref|NP_196125.1| cystatin/monellin-related protein [Arabidopsis thaliana] gi|10178045|dbj|BAB11528.1| unnamed protein product [Arabidopsis thaliana] gi|14334522|gb|AAK59458.1| unknown protein [Arabidopsis thaliana] gi|17104561|gb|AAL34169.1| unknown protein [Arabidopsis thaliana] gi|332003440|gb|AED90823.1| cystatin/monellin-related protein [Arabidopsis thaliana]</td><td>142</td><td>172</td><td>4.00E-41</td><td>121.1</td><td>60.6</td><td>78.2</td><td>cystatin/monellin-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G05060.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:1494334-1494999 REVERSE LENGTH=172</td><td>142</td><td>172</td><td>9.00E-44</td><td>121.1</td><td>60.6</td><td>78.2</td></tr>
<tr><td>Rsa1.0_01403.1.g26465.t1</td><td>ref|NP_174472.2| aquaporin NIP3-1 [Arabidopsis thaliana] gi|259016288|sp|Q9C6T0.2|NIP31_ARATH RecName: Full=Aquaporin NIP3-1; AltName: Full=NOD26-like intrinsic protein 3-1; Short=AtNIP3;1 gi|332193292|gb|AEE31413.1| aquaporin NIP3-1 [Arabidopsis thaliana]</td><td>323</td><td>323</td><td>1.00E-145</td><td>100.0</td><td>77.1</td><td>87.0</td><td>aquaporin NIP3-1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31885.1 | Symbols: NIP3;1 | NOD26-like intrinsic protein 3;1 | chr1:11450460-11451985 FORWARD LENGTH=323</td><td>323</td><td>323</td><td>1.00E-148</td><td>100.0</td><td>77.1</td><td>87.0</td></tr>
<tr><td>Rsa1.0_01403.1.g26466.t1</td><td>ref|NP_174471.2| protein BREVIS RADIX [Arabidopsis thaliana] gi|229621711|sp|Q17TI5.2|BRX_ARATH RecName: Full=Protein BREVIS RADIX; Short=AtBRX gi|27754447|gb|AAO22671.1| putative major intrinsic protein [Arabidopsis thaliana] gi|28393953|gb|AAO42384.1| putative major intrinsic protein [Arabidopsis thaliana] gi|332193291|gb|AEE31412.1| protein BREVIS RADIX [Arabidopsis thaliana]</td><td>437</td><td>344</td><td>1.00E-164</td><td>78.7</td><td>63.4</td><td>68.4</td><td>protein BREVIS RADIX</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G31880.1 | Symbols: NLM9, BRX | DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein | chr1:11447804-11450053 FORWARD LENGTH=344</td><td>437</td><td>344</td><td>1.00E-167</td><td>78.7</td><td>63.4</td><td>68.4</td></tr>
<tr><td>Rsa1.0_01403.1.g26467.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01403.1.g26468.t1</td><td>gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]</td><td>593</td><td>1557</td><td>2.00E-87</td><td>262.6</td><td>34.9</td><td>55.6</td><td>reverse transcriptase, putative; 100033-105622</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G17920.1 | Symbols: | nucleic acid binding;zinc ion binding | chr2:7782808-7783731 FORWARD LENGTH=307</td><td>593</td><td>307</td><td>6.00E-35</td><td>51.8</td><td>12.0</td><td>20.6</td></tr>
<tr><td>Rsa1.0_01404.1.g26469.t1</td><td>gb|ACB59223.1| glutathione S-transferase [Brassica oleracea]</td><td>102</td><td>523</td><td>1.00E-28</td><td>512.7</td><td>61.8</td><td>77.5</td><td>glutathione S-transferase</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01404.1.g26470.t1</td><td>ref|XP_002885842.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297331682|gb|EFH62101.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]</td><td>156</td><td>194</td><td>3.00E-65</td><td>124.4</td><td>76.9</td><td>85.9</td><td>invertase/pectin methylesterase inhibitor family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G10970.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr2:4332948-4333532 REVERSE LENGTH=194</td><td>156</td><td>194</td><td>1.00E-66</td><td>124.4</td><td>76.9</td><td>85.9</td></tr>
<tr><td>Rsa1.0_01404.1.g26471.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01404.1.g26472.t2</td><td>dbj|BAB88750.1| gag protein [Silene latifolia]</td><td>690</td><td>196</td><td>5.00E-20</td><td>28.4</td><td>6.7</td><td>11.2</td><td>gag protein</td><td>gbpln</td><td>Silene latifolia</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_01404.1.g26473.t1	emb|CAN83240.1| hypothetical protein VITISV_021676 [Vitis vinifera]	312	549	8.00E-30	176.0	29.8	46.8	hypothetical protein VITISV_021676	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01404.1.g26474.t2	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1433	777	2.00E-66	54.2	9.2	12.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01404.1.g26475.t1	dbj|BAB88750.1| gag protein [Silene latifolia]	169	196	8.00E-13	116.0	18.9	37.3	gag protein	gbpln	Silene latifolia	#	#	#	#	#	#	#
Rsa1.0_01404.1.g26476.t2	emb|CAN67675.1| hypothetical protein VITISV_020901 [Vitis vinifera]	542	508	6.00E-38	93.7	23.4	38.2	hypothetical protein VITISV_020901	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01404.1.g26477.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01404.1.g26478.t1	ref|XP_003633313.1| PREDICTED: uncharacterized protein LOC100854367 [Vitis vinifera]	2032	955	8.00E-98	47.0	11.5	17.1	PREDICTED: uncharacterized protein LOC100854367	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01405.1.g26479.t1	gb|EOA30423.1| hypothetical protein CARUB_v10013549mg [Capsella rubella]	489	489	0	100.0	86.9	92.4	hypothetical protein CARUB_v10013549mg	gbpln	Capsella rubella	AT3G01300.1 | Symbols: | Protein kinase superfamily protein | chr3:90817-93335 REVERSE LENGTH=490	489	490	0	100.2	82.4	87.3
Rsa1.0_01405.1.g26480.t1	ref|XP_002882188.1| band 7 family protein [Arabidopsis lyrata subsp. lyrata] gi|297328028|gb|EFH58447.1| band 7 family protein [Arabidopsis lyrata subsp. lyrata]	286	287	1.00E-159	100.3	94.8	98.3	band 7 family protein	gbpln	Arabidopsis lyrata	AT3G01290.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr3:88252-89356 REVERSE LENGTH=285	286	285	1.00E-161	99.7	95.1	97.9
Rsa1.0_01405.1.g26481.t1	gb|AAW22621.1| outer mitochondrial membrane protein porin 1 [Brassica napus]	276	276	1.00E-143	100.0	91.3	96.7	outer mitochondrial membrane protein porin 1	gbpln	Brassica napus	AT3G01280.1 | Symbols: VDAC1, ATVDAC1 | voltage dependent anion channel 1 | chr3:85754-87612 FORWARD LENGTH=276	276	276	1.00E-135	100.0	83.0	94.6
Rsa1.0_01405.1.g26482.t1	ref|NP_186774.1| uncharacterized protein [Arabidopsis thaliana] gi|6714463|gb|AAF26149.1|AC008261_6 hypothetical protein [Arabidopsis thaliana] gi|194708802|gb|ACF88485.1| At3g01250 [Arabidopsis thaliana] gi|332640108|gb|AEE73629.1| uncharacterized protein AT3G01250 [Arabidopsis thaliana]	161	164	3.00E-54	101.9	72.7	83.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01250.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; Has 50 Blast hits to 50 proteins in 23 species: Archae - 0; Bacteria - 28; Metazoa - 15; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:79404-79898 FORWARD LENGTH=164	161	164	1.00E-56	101.9	72.7	83.9
Rsa1.0_01405.1.g26483.t1	ref|XP_002882191.1| hypothetical protein ARALYDRAFT_477404 [Arabidopsis lyrata subsp. lyrata] gi|297328031|gb|EFH58450.1| hypothetical protein ARALYDRAFT_477404 [Arabidopsis lyrata subsp. lyrata]	157	129	6.00E-35	82.2	52.2	64.3	hypothetical protein ARALYDRAFT_477404	gbpln	Arabidopsis lyrata	AT3G01240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01230.1); Has 12 Blast hits to 12 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:78545-78937 REVERSE LENGTH=130	157	130	2.00E-37	82.8	51.6	65.6
Rsa1.0_01405.1.g26484.t1	ref|XP_002882192.1| hypothetical protein ARALYDRAFT_896138 [Arabidopsis lyrata subsp. lyrata] gi|297328032|gb|EFH58451.1| hypothetical protein ARALYDRAFT_896138 [Arabidopsis lyrata subsp. lyrata]	126	126	3.00E-40	100.0	66.7	81.7	hypothetical protein ARALYDRAFT_896138	gbpln	Arabidopsis lyrata	AT3G01230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01240.1); Has 11 Blast hits to 11 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:76937-77317 REVERSE LENGTH=126	126	126	5.00E-41	100.0	64.3	81.7
Rsa1.0_01405.1.g26485.t1	ref|XP_002884288.1| ATHB20 [Arabidopsis lyrata subsp. lyrata] gi|297330128|gb|EFH60547.1| ATHB20 [Arabidopsis lyrata subsp. lyrata]	304	283	1.00E-134	93.1	77.6	83.9	ATHB20	gbpln	Arabidopsis lyrata	AT3G01220.1 | Symbols: ATHB20, HB20 | homeobox protein 20 | chr3:73599-75295 FORWARD LENGTH=286	304	286	1.00E-134	94.1	75.3	81.6
Rsa1.0_01405.1.g26486.t1	ref|XP_002882193.1| hypothetical protein ARALYDRAFT_477409 [Arabidopsis lyrata subsp. lyrata] gi|297328033|gb|EFH58452.1| hypothetical protein ARALYDRAFT_477409 [Arabidopsis lyrata subsp. lyrata]	376	378	1.00E-173	100.5	81.4	88.0	hypothetical protein ARALYDRAFT_477409	gbpln	Arabidopsis lyrata	AT3G01200.1 | Symbols: AtRP2, RP2 | PPDK regulatory protein 2 | chr3:69826-71348 REVERSE LENGTH=377	376	377	1.00E-175	100.3	80.6	88.6
Rsa1.0_01405.1.g26487.t1	gb|EOA32852.1| hypothetical protein CARUB_v10016167mg, partial [Capsella rubella]	319	318	1.00E-166	99.7	87.8	94.7	hypothetical protein CARUB_v10016167mg, partial	gbpln	Capsella rubella	AT3G01190.1 | Symbols: | Peroxidase superfamily protein | chr3:67236-68477 REVERSE LENGTH=321	319	321	1.00E-167	100.6	87.8	94.0

Rsa1.0_01405.1.g26488.t1	ref|XP_002882195.1| hypothetical protein ARALYDRAFT_477411 [Arabidopsis lyrata subsp. lyrata] gi|297328035|gb|EFH58454.1| hypothetical protein ARALYDRAFT_477411 [Arabidopsis lyrata subsp. lyrata]	791	796	0	100.6	89.3	93.6	hypothetical protein ARALYDRAFT_477411	gbpln	Arabidopsis lyrata	AT3G01180.1 | Symbols: AtSS2, SS2 | starch synthase 2 | chr3:62456-65678 REVERSE LENGTH=792	791	792	0	100.1	86.9	92.2
Rsa1.0_01405.1.g26489.t1	gb|EOA31860.1| hypothetical protein CARUB_v10015087mg [Capsella rubella]	206	227	1.00E-90	110.2	83.0	90.3	hypothetical protein CARUB_v10015087mg	gbpln	Capsella rubella	AT3G01170.1 | Symbols: | Ribosomal protein L34e superfamily protein | chr3:58043-58690 FORWARD LENGTH=215	206	215	8.00E-93	104.4	82.5	89.3
Rsa1.0_01405.1.g26490.t1	ref|NP_566132.2| uncharacterized protein [Arabidopsis thaliana] gi|6714472|gb|AAF26158.1|AC008261_15 hypothetical protein [Arabidopsis thaliana] gi|332640097|gb|AEE73618.1| uncharacterized protein AT3G01160 [Arabidopsis thaliana]	685	713	0	104.1	60.1	75.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G01160.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NUC153 (InterPro:IPR012580); Has 36638 Blast hits to 21323 proteins in 1057 species: Archae - 109; Bacteria - 2369; Metazoa - 13796; Fungi - 4858; Plants - 1657; Viruses - 489; Other Eukaryotes - 13360 (source: NCBI BLink). | chr3:54655-57449 REVERSE LENGTH=713	685	713	0	104.1	60.1	75.6
Rsa1.0_01405.1.g26491.t1	gb|EOA30737.1| hypothetical protein CARUB_v10013877mg [Capsella rubella]	399	399	0	100.0	93.2	95.7	hypothetical protein CARUB_v10013877mg	gbpln	Capsella rubella	AT3G01150.1 | Symbols: PTB, ATPTB1, PTB1 | polypyrimidine tract-binding protein 1 | chr3:51732-54344 FORWARD LENGTH=399	399	399	0	100.0	91.5	95.0
Rsa1.0_01405.1.g26492.t1	ref|NP_180368.1| aspartyl protease-like protein [Arabidopsis thaliana] gi|4510415|gb|AAD21501.1| putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana] gi|330252975|gb|AEC08069.1| aspartyl protease-like protein [Arabidopsis thaliana]	452	396	1.00E-138	87.6	55.3	68.1	aspartyl protease-like protein	gbpln	Arabidopsis thaliana	AT2G28010.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:11930579-11931769 REVERSE LENGTH=396	452	396	1.00E-141	87.6	55.3	68.1
Rsa1.0_01405.1.g26493.t1	ref|XP_002882197.1| hypothetical protein ARALYDRAFT_477416 [Arabidopsis lyrata subsp. lyrata] gi|297328037|gb|EFH58456.1| hypothetical protein ARALYDRAFT_477416 [Arabidopsis lyrata subsp. lyrata]	318	390	1.00E-144	122.6	84.6	88.1	hypothetical protein ARALYDRAFT_477416	gbpln	Arabidopsis lyrata	AT3G01140.1 | Symbols: MYB106, NOK, AtMYB106 | myb domain protein 106 | chr3:46619-48143 REVERSE LENGTH=388	318	388	1.00E-141	122.0	82.1	86.8
Rsa1.0_01406.1.g26494.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01406.1.g26495.t1	gb|AAX92941.1| retrotransposon protein, putative, Ty1-copia sub-class [Oryza sativa Japonica Group] gi|77548751|gb|ABA91548.1| retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa Japonica Group]	1223	2340	0	191.3	31.4	40.7	retrotransposon protein, putative, Ty1-copia sub-class	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1223	1262	1.00E-77	103.2	14.2	22.2
Rsa1.0_01406.1.g26496.t4	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	778	1463	3.00E-83	188.0	24.7	33.8	F5J5.1	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	778	1262	7.00E-22	162.2	12.0	18.0
Rsa1.0_01406.1.g26497.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01406.1.g26498.t1	gb|EOA36607.1| hypothetical protein CARUB_v10011815mg [Capsella rubella]	77	80	1.00E-32	103.9	90.9	96.1	hypothetical protein CARUB_v10011815mg	gbpln	Capsella rubella	AT1G48330.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G17580.1); Has 40 Blast hits to 40 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:17863897-17864124 FORWARD LENGTH=75	77	75	9.00E-32	97.4	79.2	81.8
Rsa1.0_01406.1.g26499.t1	gb|EOA15725.1| hypothetical protein CARUB_v10006633mg, partial [Capsella rubella]	185	483	2.00E-18	261.1	35.1	47.0	hypothetical protein CARUB_v10006633mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01406.1.g26500.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	215	1555	7.00E-24	723.3	25.6	38.1	disease resistance protein	gbpln	Brassica rapa	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	215	575	9.00E-13	267.4	20.0	31.2
Rsa1.0_01407.1.g26501.t1	emb|CAN66208.1| hypothetical protein VITISV_035070 [Vitis vinifera]	854	1496	0	175.2	48.6	61.2	hypothetical protein VITISV_035070	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	854	1262	3.00E-65	147.8	17.9	28.9

Rsa1.0_01407.1.g26502.t1	ref|NP_192966.5| copper amine oxidase family protein [Arabidopsis thaliana] gi|22654995|gb|AAM98089.1| AT4g12290/T4C9_130 [Arabidopsis thaliana] gi|28416507|gb|AAO42784.1| AT4g12290/T4C9_130 [Arabidopsis thaliana] gi|332657711|gb|AEE83111.1| copper amine oxidase family protein [Arabidopsis thaliana]	743	741	0	99.7	87.1	92.5	copper amine oxidase family protein	gbpln	Arabidopsis thaliana	AT4G12290.1 | Symbols: | Copper amine oxidase family protein | chr4:7304434-7306973 FORWARD LENGTH=741	743	741	0	99.7	87.1	92.5
Rsa1.0_01407.1.g26503.t1	ref|NP_192967.1| cytochrome P450, family 706, subfamily A, polypeptide 4 [Arabidopsis thaliana] gi|5281041|emb|CAB45977.1| flavonoid 3', 5'-hydroxylase-like protein [Arabidopsis thaliana] gi|7267931|emb|CAB78273.1| flavonoid 3', 5'-hydroxylase-like protein [Arabidopsis thaliana] gi|26452581|dbj|BAC43375.1| putative flavonoid 3',5'-hydroxylase [Arabidopsis thaliana] gi|28973099|gb|AAO63874.1| putative cytochrome p450 [Arabidopsis thaliana] gi|332657712|gb|AEE83112.1| cytochrome P450, family 706, subfamily A, polypeptide 4 [Arabidopsis thaliana]	519	516	0	99.4	84.8	91.3	cytochrome P450, family 706, subfamily A, polypeptide 4	gbpln	Arabidopsis thaliana	AT4G12300.1 | Symbols: CYP706A4 | cytochrome P450, family 706, subfamily A, polypeptide 4 | chr4:7308016-7309692 REVERSE LENGTH=516	519	516	0	99.4	84.8	91.3
Rsa1.0_01407.1.g26504.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01407.1.g26505.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01408.1.g26506.t1	gb|EOA29290.1| hypothetical protein CARUB_v10025565mg [Capsella rubella]	370	371	0	100.3	92.4	96.5	hypothetical protein CARUB_v10025565mg	gbpln	Capsella rubella	AT2G41810.1 | Symbols: | Protein of unknown function, DUF642 | chr2:17439414-17441296 REVERSE LENGTH=370	370	370	0	100.0	91.4	94.6
Rsa1.0_01408.1.g26507.t1	ref|NP_181713.1| Leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|75097645|sp|O22938.1|Y2182_ARATH RecName: Full=Leucine-rich repeat receptor-like tyrosine-protein kinase At2g41820; Flags: Precursor gi|2335097|gb|AAC02766.1| putative receptor-like protein kinase [Arabidopsis thaliana] gi|224589547|gb|ACN59307.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|330254942|gb|AEC10036.1| leucine-rich repeat receptor-like tyrosine-protein kinase [Arabidopsis thaliana]	890	890	0	100.0	90.6	94.0	Leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT2G41820.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:17447170-17449914 FORWARD LENGTH=890	890	890	0	100.0	90.6	94.0
Rsa1.0_01408.1.g26508.t1	ref|XP_002881801.1| hypothetical protein ARALYDRAFT_483264 [Arabidopsis lyrata subsp. lyrata] gi|297327640|gb|EFH58060.1| hypothetical protein ARALYDRAFT_483264 [Arabidopsis lyrata subsp. lyrata]	204	1025	4.00E-20	502.5	24.0	26.5	hypothetical protein ARALYDRAFT_483264	gbpln	Arabidopsis lyrata	AT2G41830.1 | Symbols: | Uncharacterized protein | chr2:17450431-17456453 REVERSE LENGTH=1025	204	1025	2.00E-22	502.5	24.0	26.5
Rsa1.0_01408.1.g26509.t1	gb|EOA27653.1| hypothetical protein CARUB_v10023800mg [Capsella rubella]	283	283	1.00E-124	100.0	77.7	79.9	hypothetical protein CARUB_v10023800mg	gbpln	Capsella rubella	AT1G58380.1 | Symbols: XW6 | Ribosomal protein S5 family protein | chr1:21689115-21690085 FORWARD LENGTH=284	283	284	1.00E-123	100.4	75.6	78.4
Rsa1.0_01408.1.g26510.t1	emb|CAC05657.1| endopolygalacturonase [Brassica napus] gi|9967520|emb|CAC05658.1| endopolygalacturonase [Brassica napus]	435	434	0	99.8	86.7	93.1	endopolygalacturonase	gbpln	Brassica napus	AT2G41850.1 | Symbols: PGAZAT, ADPG2 | polygalacturonase abscission zone A. thaliana | chr2:17461918-17464059 REVERSE LENGTH=433	435	433	0	99.5	82.5	90.1
Rsa1.0_01408.1.g26511.t1	ref|XP_002881805.1| calcium-dependent protein kinase 14 [Arabidopsis lyrata subsp. lyrata] gi|297327644|gb|EFH58064.1| calcium-dependent protein kinase 14 [Arabidopsis lyrata subsp. lyrata]	809	531	0	65.6	57.5	62.2	calcium-dependent protein kinase 14	gbpln	Arabidopsis lyrata	AT2G41860.1 | Symbols: CPK14 | calcium-dependent protein kinase 14 | chr2:17467646-17469786 REVERSE LENGTH=530	809	530	0	65.5	57.1	61.8
Rsa1.0_01408.1.g26512.t1	gb|EOA28140.1| hypothetical protein CARUB_v10024329mg [Capsella rubella]	61	123	9.00E-23	201.6	91.8	96.7	hypothetical protein CARUB_v10024329mg	gbpln	Capsella rubella	AT2G41905.1 | Symbols: | BEST Arabidopsis thaliana protein match is: arabinogalactan protein 23 (TAIR:AT3G57690.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17495766-17495951 FORWARD LENGTH=61	61	61	2.00E-25	100.0	95.1	96.7
Rsa1.0_01408.1.g26513.t1	gb|EOA21072.1| hypothetical protein CARUB_v10001410mg [Capsella rubella]	362	330	1.00E-76	91.2	44.8	61.6	hypothetical protein CARUB_v10001410mg	gbpln	Capsella rubella	AT3G57740.1 | Symbols: | Protein kinase superfamily protein | chr3:21392671-21393744 FORWARD LENGTH=357	362	357	3.00E-74	98.6	48.6	59.9

Rsa1.0_01408.1.g26514.t1	ref|NP_850360.2| protein kinase domain-containing protein [Arabidopsis thaliana] gi|1871189|gb|AAB63549.1| putative protein kinase [Arabidopsis thaliana] gi|330254956|gb|AEC10050.1| protein kinase domain-containing protein [Arabidopsis thaliana]	320	351	1.00E-119	109.7	63.8	76.9	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G41930.1 | Symbols: | Protein kinase superfamily protein | chr2:17501629-17502684 FORWARD LENGTH=351	320	351	1.00E-121	109.7	63.8	76.9
Rsa1.0_01408.1.g26515.t1	ref|NP_181725.1| zinc finger protein 8 [Arabidopsis thaliana] gi|1871188|gb|AAB63548.1| putative C2H2-type zinc finger protein [Arabidopsis thaliana] gi|14517524|gb|AAK62652.1| At2g41940/T6D20.16 [Arabidopsis thaliana] gi|15810111|gb|AAL06981.1| At2g41940/T6D20.16 [Arabidopsis thaliana] gi|330254957|gb|AEC10051.1| zinc finger protein 8 [Arabidopsis thaliana]	248	257	1.00E-90	103.6	76.2	83.5	zinc finger protein 8	gbpln	Arabidopsis thaliana	AT2G41940.1 | Symbols: ZFP8 | zinc finger protein 8 | chr2:17507556-17508329 FORWARD LENGTH=257	248	257	4.00E-93	103.6	76.2	83.5
Rsa1.0_01409.1.g26516.t1	ref|XP_002876726.1| hypothetical protein ARALYDRAFT_486864 [Arabidopsis lyrata subsp. lyrata] gi|297322564|gb|EFH52985.1| hypothetical protein ARALYDRAFT_486864 [Arabidopsis lyrata subsp. lyrata]	71	405	1.00E-14	570.4	53.5	56.3	hypothetical protein ARALYDRAFT_486864	gbpln	Arabidopsis lyrata	AT3G63510.1 | Symbols: | FMN-linked oxidoreductases superfamily protein | chr3:23450542-23452682 FORWARD LENGTH=419	71	419	9.00E-17	590.1	52.1	56.3
Rsa1.0_01409.1.g26517.t13	ref|NP_567149.2| FMN-linked oxidoreductase-like protein protein [Arabidopsis thaliana] gi|24030197|gb|AAN41279.1| unknown protein [Arabidopsis thaliana] gi|332646975|gb|AEE80496.1| FMN-linked oxidoreductase-like protein protein [Arabidopsis thaliana]	2277	419	1.00E-172	18.4	13.3	14.1	FMN-linked oxidoreductase-like protein protein	gbpln	Arabidopsis thaliana	AT3G63510.1 | Symbols: | FMN-linked oxidoreductases superfamily protein | chr3:23450542-23452682 FORWARD LENGTH=419	2277	419	1.00E-175	18.4	13.3	14.1
Rsa1.0_01409.1.g26518.t1	ref|XP_002887355.1| UDP-glucose:glycoprotein glucosyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297333196|gb|EFH63614.1| UDP-glucose:glycoprotein glucosyltransferase [Arabidopsis lyrata subsp. lyrata]	1619	1616	0	99.8	91.7	94.8	UDP-glucose:glycoprotein glucosyltransferase	gbpln	Arabidopsis lyrata	AT1G71220.2 | Symbols: EBS1 | UDP-glucose:glycoprotein glucosyltransferases;transferases, transferring hexosyl groups;transferases, transferring glycosyl groups | chr1:26841664-26851730 FORWARD LENGTH=1614	1619	1614	0	99.7	91.0	94.5
Rsa1.0_01409.1.g26519.t1	ref|XP_002888826.1| hypothetical protein ARALYDRAFT_894959 [Arabidopsis lyrata subsp. lyrata] gi|297334667|gb|EFH65085.1| hypothetical protein ARALYDRAFT_894959 [Arabidopsis lyrata subsp. lyrata]	868	868	0	100.0	78.3	87.9	hypothetical protein ARALYDRAFT_894959	gbpln	Arabidopsis lyrata	AT1G71210.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:26838850-26841489 REVERSE LENGTH=879	868	879	0	101.3	77.0	86.9
Rsa1.0_01409.1.g26520.t1	ref|XP_002888825.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334666|gb|EFH65084.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	208	235	2.00E-67	113.0	74.0	82.2	predicted protein	gbpln	Arabidopsis lyrata	AT1G71200.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:26835973-26837308 REVERSE LENGTH=234	208	234	5.00E-68	112.5	72.1	80.3
Rsa1.0_01409.1.g26521.t1	#	#	#	#	#	#	#	-	----	----	AT1G71160.1 | Symbols: KCS7 | 3-ketoacyl-CoA synthase 7 | chr1:26828788-26830170 REVERSE LENGTH=460	118	460	2.00E-12	389.8	25.4	29.7
Rsa1.0_01409.1.g26522.t1	ref|NP_177271.1| uncharacterized protein [Arabidopsis thaliana] gi|12323430|gb|AAG51693.1|AC016972_12 unknown protein; 51945-53271 [Arabidopsis thaliana] gi|49823492|gb|AAT68729.1| hypothetical protein At1g71150 [Arabidopsis thaliana] gi|332197045|gb|AEE35166.1| uncharacterized protein AT1G71150 [Arabidopsis thaliana]	357	351	1.00E-148	98.3	76.2	82.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G71150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22970.1); Has 105 Blast hits to 103 proteins in 41 species: Archae - 0; Bacteria - 2; Metazoa - 42; Fungi - 6; Plants - 48; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink). | chr1:26827189-26828515 FORWARD LENGTH=351	357	351	1.00E-151	98.3	76.2	82.6
Rsa1.0_01409.1.g26523.t1	gb|EOA35095.1| hypothetical protein CARUB_v10020206mg [Capsella rubella]	490	485	0	99.0	84.3	90.4	hypothetical protein CARUB_v10020206mg	gbpln	Capsella rubella	AT1G71140.1 | Symbols: | MATE efflux family protein | chr1:26824762-26826748 FORWARD LENGTH=485	490	485	0	99.0	80.4	88.8
Rsa1.0_01409.1.g26524.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01409.1.g26525.t1	ref|XP_002887346.1| hypothetical protein ARALYDRAFT_476243 [Arabidopsis lyrata subsp. lyrata] gi|297333187|gb|EFH63605.1| hypothetical protein ARALYDRAFT_476243 [Arabidopsis lyrata subsp. lyrata]	553	557	0	100.7	81.7	88.8	hypothetical protein ARALYDRAFT_476243	gbpln	Arabidopsis lyrata	AT1G71110.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G12400.1); Has 173 Blast hits to 169 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 165; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr1:26818244-26820852 FORWARD LENGTH=557	553	557	0	100.7	80.3	88.4
Rsa1.0_01410.1.g26526.t1	gb|ABD65000.1| hypothetical protein 26.t00020 [Brassica oleracea]	342	302	5.00E-82	88.3	46.8	58.5	hypothetical protein 26.t00020	gbpln	Brassica oleracea	AT5G41220.1 | Symbols: ATGSTT3, GST10C, GSTT3 | glutathione S-transferase THETA 3 | chr5:16494560-16496969 REVERSE LENGTH=590	342	590	4.00E-44	172.5	28.1	38.3
Rsa1.0_01410.1.g26527.t1	ref|XP_002887115.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297332956|gb|EFH63374.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	372	375	1.00E-170	100.8	83.3	88.7	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G67340.1 | Symbols: | HCP-like superfamily protein with MYND-type zinc finger | chr1:25230323-25231622 FORWARD LENGTH=379	372	379	1.00E-170	101.9	81.7	88.4
Rsa1.0_01410.1.g26528.t1	gb|EOA33466.1| hypothetical protein CARUB_v10021120mg, partial [Capsella rubella]	91	141	3.00E-43	154.9	93.4	97.8	hypothetical protein CARUB_v10021120mg, partial	gbpln	Capsella rubella	AT1G67350.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: photorespiration; LOCATED IN: mitochondrial membrane, mitochondrial respiratory chain complex I, respiratory chain complex I; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25235826-25236122 FORWARD LENGTH=98	91	98	1.00E-44	107.7	90.1	93.4
Rsa1.0_01410.1.g26529.t1	gb|AAN37925.1|AF410429_1 aysnaptic 1 [Brassica oleracea var. alboglabra]	600	599	0	99.8	92.3	96.0	aysnaptic 1	gbpln	Brassica oleracea	AT1G67370.1 | Symbols: ASY1, ATASY1 | DNA-binding HORMA family protein | chr1:25239347-25243713 REVERSE LENGTH=596	600	596	0	99.3	83.2	90.5
Rsa1.0_01410.1.g26530.t3	ref|NP_001185342.1| Zn-dependent exopeptidase-like protein [Arabidopsis thaliana] gi|332196522|gb|AEE34643.1| Zn-dependent exopeptidase-like protein [Arabidopsis thaliana]	875	922	0	105.4	87.2	92.9	Zn-dependent exopeptidase-like protein	gbpln	Arabidopsis thaliana	AT1G67420.2 | Symbols: | Zn-dependent exopeptidases superfamily protein | chr1:25255264-25260358 FORWARD LENGTH=922	875	922	0	105.4	87.2	92.9
Rsa1.0_01410.1.g26531.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01410.1.g26532.t1	gb|EOA35774.1| hypothetical protein CARUB_v10021005mg, partial [Capsella rubella]	202	185	1.00E-101	91.6	89.1	91.1	hypothetical protein CARUB_v10021005mg, partial	gbpln	Capsella rubella	AT1G67430.1 | Symbols: | Ribosomal protein L22p/L17e family protein | chr1:25262209-25263627 FORWARD LENGTH=175	202	175	1.00E-100	86.6	85.1	86.1
Rsa1.0_01410.1.g26533.t1	ref|NP_176911.2| Minichromosome maintenance (MCM2/3/5) protein [Arabidopsis thaliana] gi|66792692|gb|AAY56448.1| At1g67440 [Arabidopsis thaliana] gi|332196525|gb|AEE34646.1| Minichromosome maintenance (MCM2/3/5) protein [Arabidopsis thaliana]	488	433	0	88.7	73.8	79.1	Minichromosome maintenance (MCM2/3/5) protein	gbpln	Arabidopsis thaliana	AT1G67440.1 | Symbols: emb1688 | Minichromosome maintenance (MCM2/3/5) family protein | chr1:25263905-25265551 REVERSE LENGTH=433	488	433	0	88.7	73.8	79.1
Rsa1.0_01410.1.g26534.t1	gb|EOA35305.1| hypothetical protein CARUB_v10020480mg [Capsella rubella] gi|482571118|gb|EOA35306.1| hypothetical protein CARUB_v10020480mg [Capsella rubella]	298	376	1.00E-151	126.2	85.6	92.6	hypothetical protein CARUB_v10020480mg	gbpln	Capsella rubella	AT1G67480.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:25277294-25278529 FORWARD LENGTH=376	298	376	1.00E-151	126.2	85.9	91.3
Rsa1.0_01411.1.g26535.t1	gb|AAZ66922.1| 117M18_3 [Brassica rapa]	85	87	5.00E-17	102.4	69.4	84.7	117M18_3	gbpln	Brassica rapa	AT5G09980.1 | Symbols: PROPEP4 | elicitor peptide 4 precursor | chr5:3122790-3123728 FORWARD LENGTH=81	85	81	2.00E-12	95.3	56.5	68.2
Rsa1.0_01411.1.g26536.t1	ref|XP_002871398.1| hypothetical protein ARALYDRAFT_487822 [Arabidopsis lyrata subsp. lyrata] gi|297317235|gb|EFH47657.1| hypothetical protein ARALYDRAFT_487822 [Arabidopsis lyrata subsp. lyrata]	85	85	2.00E-17	100.0	64.7	77.6	hypothetical protein ARALYDRAFT_487822	gbpln	Arabidopsis lyrata	AT5G09990.1 | Symbols: PROPEP5 | elicitor peptide 5 precursor | chr5:3124623-3124976 FORWARD LENGTH=86	85	86	7.00E-19	101.2	62.4	76.5
Rsa1.0_01411.1.g26537.t1	ref|NP_974759.1| uncharacterized protein [Arabidopsis thaliana] gi|332004094|gb|AED91477.1| uncharacterized protein AT5G09995 [Arabidopsis thaliana]	256	257	1.00E-102	100.4	79.3	84.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G09995.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G08530.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:3125185-3126302 REVERSE LENGTH=257	256	257	1.00E-104	100.4	79.3	84.0

Rsa1.0_01411.1.g26538.t1	gb|EOA22624.1| hypothetical protein CARUB_v10003293mg [Capsella rubella]	140	144	6.00E−47	102.9	70.7	78.6	hypothetical protein CARUB_v10003293mg	gbpln	Capsella rubella	AT5G10000.1 | Symbols: ATFD4, FD4 | ferredoxin 4 | chr5:3126709−3127155 FORWARD LENGTH=148	140	148	4.00E−48	105.7	68.6	77.9
Rsa1.0_01411.1.g26539.t1	gb|AAZ66923.1| 117M18_4 [Brassica rapa]	435	424	0	97.5	81.6	87.8	117M18_4	gbpln	Brassica rapa	AT5G10010.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64910.1); Has 33260 Blast hits to 16857 proteins in 1270 species: Archae − 88; Bacteria − 3040; Metazoa − 11915; Fungi − 3137; Plants − 1371; Viruses − 424; Other Eukaryotes − 13285 (source: NCBI BLink). | chr5:3128098−3131452 FORWARD LENGTH=434	435	434	1.00E−173	99.8	74.0	85.1
Rsa1.0_01411.1.g26540.t1	ref|XP_002871400.1| hypothetical protein ARALYDRAFT_487827 [Arabidopsis lyrata subsp. lyrata] gi|297317237|gb|EFH47659.1| hypothetical protein ARALYDRAFT_487827 [Arabidopsis lyrata subsp. lyrata]	1059	1051	0	99.2	85.1	91.4	hypothetical protein ARALYDRAFT_487827	gbpln	Arabidopsis lyrata	AT5G10020.1 | Symbols: | Leucine−rich receptor−like protein kinase family protein | chr5:3133514−3136949 FORWARD LENGTH=1048	1059	1048	0	99.0	83.2	89.7
Rsa1.0_01411.1.g26541.t1	gb|AAZ67587.1| 80A08_2 [Brassica rapa subsp. pekinensis]	366	364	0	99.5	93.4	96.7	80A08_2	gbpln	Brassica rapa	AT5G10030.2 | Symbols: TGA4 | TGACG motif−binding factor 4 | chr5:3137648−3139295 REVERSE LENGTH=364	366	364	0	99.5	87.7	93.2
Rsa1.0_01411.1.g26542.t1	gb|AAZ67588.1| 80A08_3 [Brassica rapa subsp. pekinensis]	74	74	3.00E−26	100.0	82.4	90.5	80A08_3	gbpln	Brassica rapa	AT5G10040.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65207.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:3143723−3143986 FORWARD LENGTH=87	74	87	6.00E−15	117.6	60.8	71.6
Rsa1.0_01411.1.g26543.t1	gb|AAK59619.1| putative RNA helicase [Arabidopsis thaliana]	229	563	8.00E−23	245.9	27.5	28.4	putative RNA helicase	gbpln	Arabidopsis thaliana	AT5G08620.1 | Symbols: STRS2, ATRH25 | DEA(D/H)−box RNA helicase family protein | chr5:2794540−2797548 FORWARD LENGTH=563	229	563	3.00E−25	245.9	27.5	28.4
Rsa1.0_01411.1.g26544.t1	gb|AAZ67589.1| 80A08_4 [Brassica rapa subsp. pekinensis]	294	449	1.00E−142	152.7	89.1	93.5	80A08_4	gbpln	Brassica rapa	AT5G10070.1 | Symbols: | RNase L inhibitor protein−related | chr5:3148684−3150324 REVERSE LENGTH=264	294	264	1.00E−122	89.8	75.2	78.9
Rsa1.0_01411.1.g26545.t1	gb|AAZ67590.1| 80A08_5 [Brassica rapa subsp. pekinensis]	527	632	0	119.9	84.4	90.9	80A08_5	gbpln	Brassica rapa	AT5G10080.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:3150843−3153380 FORWARD LENGTH=528	527	528	0	100.2	78.0	85.4
Rsa1.0_01411.1.g26546.t1	gb|AAZ67592.1| 80A08_7 [Brassica rapa subsp. pekinensis]	549	560	0	102.0	92.9	95.1	80A08_7	gbpln	Brassica rapa	AT5G10090.1 | Symbols: TPR13 | Tetratricopeptide repeat (TPR)−like superfamily protein | chr5:3153722−3155745 REVERSE LENGTH=594	549	594	0	108.2	83.1	90.3
Rsa1.0_01411.1.g26547.t1	gb|AAZ67593.1| 80A08_8 [Brassica rapa subsp. pekinensis]	266	365	1.00E−140	137.2	92.1	95.9	80A08_8	gbpln	Brassica rapa	AT5G10100.1 | Symbols: TPPI | Haloacid dehalogenase−like hydrolase (HAD) superfamily protein | chr5:3157980−3160275 FORWARD LENGTH=369	266	369	1.00E−113	138.7	77.4	86.5
Rsa1.0_01412.1.g26548.t1	gb|ABD36807.1| glutathione S−transferase [Brassica napus]	217	217	1.00E−121	100.0	98.2	98.6	glutathione S−transferase	gbpln	Brassica napus	AT1G78370.1 | Symbols: ATGSTU20, GSTU20 | glutathione S−transferase TAU 20 | chr1:29484428−29485204 REVERSE LENGTH=217	217	217	1.00E−113	100.0	88.9	94.5
Rsa1.0_01412.1.g26549.t1	gb|AAF71799.1|AC013430_8 F3F9.13 [Arabidopsis thaliana]	218	439	1.00E−113	201.4	87.6	93.6	F3F9.13	gbpln	Arabidopsis thaliana	AT1G78340.1 | Symbols: ATGSTU22, GSTU22 | glutathione S−transferase TAU 22 | chr1:29473046−29473797 REVERSE LENGTH=218	218	218	1.00E−115	100.0	88.5	94.5
Rsa1.0_01412.1.g26550.t1	gb|EOA35683.1| hypothetical protein CARUB_v10020906mg, partial [Capsella rubella]	220	225	1.00E−108	102.3	85.5	92.7	hypothetical protein CARUB_v10020906mg, partial	gbpln	Capsella rubella	AT1G78320.1 | Symbols: ATGSTU23, GSTU23 | glutathione S−transferase TAU 23 | chr1:29467581−29468358 REVERSE LENGTH=220	220	220	1.00E−109	100.0	84.5	92.7
Rsa1.0_01412.1.g26551.t1	gb|AAK26634.1|AF342780_1 GF14 omega [Brassica napus]	260	260	1.00E−147	100.0	98.5	98.8	GF14 omega	gbpln	Brassica napus	AT1G78300.1 | Symbols: GRF2, 14−3−3OMEGA, GF14 OMEGA | general regulatory factor 2 | chr1:29461883−29463052 FORWARD LENGTH=259	260	259	1.00E−145	99.6	95.0	97.7
Rsa1.0_01412.1.g26552.t1	gb|EOA35386.1| hypothetical protein CARUB_v10020582mg [Capsella rubella]	342	345	1.00E−160	100.9	83.6	87.7	hypothetical protein CARUB_v10020582mg	gbpln	Capsella rubella	AT1G78290.3 | Symbols: | Protein kinase superfamily protein | chr1:29457457−29458909 REVERSE LENGTH=343	342	343	1.00E−161	100.3	79.2	83.0
Rsa1.0_01412.1.g26553.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1449	1496	0	103.2	54.9	69.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1449	1262	1.00E−128	87.1	16.3	24.6

Rsa1.0_01412.1.g26554.t1	ref|NP_974169.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|110736924|dbj|BAF00419.1| hypothetical protein [Arabidopsis thaliana] gi|332197967|gb|AEE36088.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	269	271	3.00E-92	100.7	79.2	84.8	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT1G78260.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:29447317-29449246 FORWARD LENGTH=271	269	271	9.00E-95	100.7	79.2	84.8
Rsa1.0_01412.1.g26555.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01412.1.g26556.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01412.1.g26557.t1	gb|ABV89659.1| dehydration-responsive protein-related [Brassica rapa]	670	662	0	98.8	86.3	92.2	dehydration-responsive protein-related	gbpln	Brassica rapa	AT1G78240.2 | Symbols: TSD2, QUA2 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:29433173-29435815 REVERSE LENGTH=684	670	684	0	102.1	85.7	91.9
Rsa1.0_01413.1.g26558.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01413.1.g26559.t1	ref|NP_181105.2| LRR receptor-like serine/threonine-protein kinase FEI 2 [Arabidopsis thaliana] gi|334184705|ref|NP_001189684.1| LRR receptor-like serine/threonine-protein kinase FEI 2 [Arabidopsis thaliana] gi|263419018|sp|C0LGL9.1|FEI2_ARATH RecName: Full=LRR receptor-like serine/threonine-protein kinase FEI 2; Flags: Precursor gi|224589541|gb|ACN59304.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|330254037|gb|AEC09131.1| LRR receptor-like serine/threonine-protein kinase FEI 2 [Arabidopsis thaliana] gi|330254038|gb|AEC09132.1| LRR receptor-like serine/threonine-protein kinase FEI 2 [Arabidopsis thaliana]	596	589	0	98.8	86.7	91.8	LRR receptor-like serine/threonine-protein kinase FEI 2	gbpln	Arabidopsis thaliana	AT2G35620.2 | Symbols: FEI2 | Leucine-rich repeat protein kinase family protein | chr2:14961187-14964640 REVERSE LENGTH=589	596	589	0	98.8	86.7	91.8
Rsa1.0_01413.1.g26560.t1	ref|NP_850251.1| aspartyl protease-like protein [Arabidopsis thaliana] gi|122215044|sp|Q3EBM5.1|ASPR1_ARATH RecName: Full=Probable aspartic protease At2g35615; Flags: Precursor gi|330254036|gb|AEC09130.1| probable aspartic protease [Arabidopsis thaliana]	447	447	0	100.0	83.0	89.7	aspartyl protease-like protein	gbpln	Arabidopsis thaliana	AT2G35615.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:14959391-14960734 FORWARD LENGTH=447	447	447	0	100.0	83.0	89.7
Rsa1.0_01413.1.g26561.t1	ref|XP_002881405.1| hypothetical protein ARALYDRAFT_902667 [Arabidopsis lyrata subsp. lyrata] gi|297327244|gb|EFH57664.1| hypothetical protein ARALYDRAFT_902667 [Arabidopsis lyrata subsp. lyrata]	85	86	8.00E-39	101.2	89.4	96.5	hypothetical protein ARALYDRAFT_902667	gbpln	Arabidopsis lyrata	AT2G35612.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; BEST Arabidopsis thaliana protein match is: Copper amine oxidase family protein (TAIR:AT1G31670.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:14955241-14955501 REVERSE LENGTH=86	85	86	1.00E-40	101.2	87.1	94.1
Rsa1.0_01413.1.g26562.t1	gb|EOA26720.1| hypothetical protein CARUB_v10022808mg [Capsella rubella]	671	645	0	96.1	86.4	90.6	hypothetical protein CARUB_v10022808mg	gbpln	Capsella rubella	AT2G35610.1 | Symbols: XEG113 | xyloglucanase 113 | chr2:14947617-14951106 REVERSE LENGTH=644	671	644	0	96.0	86.7	90.2
Rsa1.0_01413.1.g26563.t1	ref|XP_002881403.1| hypothetical protein ARALYDRAFT_902664 [Arabidopsis lyrata subsp. lyrata] gi|297327242|gb|EFH57662.1| hypothetical protein ARALYDRAFT_902664 [Arabidopsis lyrata subsp. lyrata]	310	330	1.00E-148	106.5	84.8	91.0	hypothetical protein ARALYDRAFT_902664	gbpln	Arabidopsis lyrata	AT2G35600.1 | Symbols: ATBRXL1, BRXL1 | BREVIS RADIX-like 1 | chr2:14941092-14943281 REVERSE LENGTH=331	310	331	1.00E-144	106.8	84.5	90.3
Rsa1.0_01413.1.g26564.t1	ref|XP_002879558.1| hypothetical protein ARALYDRAFT_902663 [Arabidopsis lyrata subsp. lyrata] gi|297325397|gb|EFH55817.1| hypothetical protein ARALYDRAFT_902663 [Arabidopsis lyrata subsp. lyrata]	147	155	3.00E-39	105.4	59.9	66.7	hypothetical protein ARALYDRAFT_902663	gbpln	Arabidopsis lyrata	AT2G35585.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G31940.1); Has 67 Blast hits to 67 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:14936889-14937873 FORWARD LENGTH=156	147	156	4.00E-40	106.1	57.8	63.3
Rsa1.0_01413.1.g26565.t1	gb|EOA27264.1| hypothetical protein CARUB_v10023384mg [Capsella rubella]	349	392	1.00E-113	112.3	61.3	73.6	hypothetical protein CARUB_v10023384mg	gbpln	Capsella rubella	AT2G35580.1 | Symbols: | Serine protease inhibitor (SERPIN) family protein | chr2:14933828-14935482 REVERSE LENGTH=374	349	374	1.00E-102	107.2	58.5	69.9

Rsa1.0_01413.1.g26566.t1	gb|EOA29382.1| hypothetical protein CARUB_v10025669mg [Capsella rubella]	377	377	1.00E-135	100.0	67.9	80.6	hypothetical protein CARUB_v10025669mg	gbpln	Capsella rubella	AT2G35580.1 | Symbols: | Serine protease inhibitor (SERPIN) family protein | chr2:14933828-14935482 REVERSE LENGTH=374	377	374	1.00E-115	99.2	61.0	72.9
Rsa1.0_01413.1.g26567.t2	ref|NP_181097.2| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] gi|330254025|gb|AEC09119.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	463	590	1.00E-145	127.4	66.7	77.3	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis thaliana	AT2G35540.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:14927158-14928930 FORWARD LENGTH=590	463	590	1.00E-148	127.4	66.7	77.3
Rsa1.0_01413.1.g26568.t3	gb|EOA26810.1| hypothetical protein CARUB_v10022903mg [Capsella rubella]	567	572	0	100.9	67.2	78.0	hypothetical protein CARUB_v10022903mg	gbpln	Capsella rubella	AT2G35510.1 | Symbols: SRO1 | similar to RCD one 1 | chr2:14916898-14919198 REVERSE LENGTH=568	567	568	0	100.2	67.2	76.5
Rsa1.0_01413.1.g26569.t1	gb|EOA27282.1| hypothetical protein CARUB_v10023400mg [Capsella rubella]	384	388	0	101.0	91.9	95.3	hypothetical protein CARUB_v10023400mg	gbpln	Capsella rubella	AT2G35500.1 | Symbols: SKL2 | shikimate kinase like 2 | chr2:14914038-14915909 FORWARD LENGTH=387	384	387	0	100.8	90.4	93.5
Rsa1.0_01414.1.g26570.t1	ref|NP_191788.1| ADP-ribosylation factor A1E [Arabidopsis thaliana] gi|334186204|ref|NP_001190161.1| ADP-ribosylation factor A1E [Arabidopsis thaliana] gi|334186206|ref|NP_001190162.1| ADP-ribosylation factor A1E [Arabidopsis thaliana] gi|297824803|ref|XP_002880284.1| ADP-ribosylation factor A1E [Arabidopsis lyrata subsp. lyrata] gi|13926302|gb|AAK49618.1|AF372902_1 AT3g62290/T17J13_250 [Arabidopsis thaliana] gi|6899939|emb|CAB71889.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] gi|16323248|gb|AAL15358.1| AT3g62290/T17J13_250 [Arabidopsis thaliana] gi|21553518|gb|AAM62611.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] gi|119720788|gb|ABL97964.1| ADP-ribosylation factor-like protein [Brassica rapa] gi|297326123|gb|EFH56543.1| ADP-ribosylation factor A1E [Arabidopsis lyrata subsp. lyrata] gi|332646811|gb|AEE80332.1| ADP-ribosylation factor A1E [Arabidopsis thaliana] gi|332646812|gb|AEE80333.1| ADP-ribosylation factor A1E [Arabidopsis thaliana] gi|332646813|gb|AEE80334.1| ADP-	181	181	1.00E-102	100.0	100.0	100.0	ADP-ribosylation factor A1E	gbpln	Arabidopsis lyrata	AT3G62290.3 | Symbols: ARFA1E | ADP-ribosylation factor A1E | chr3:23052287-23053545 FORWARD LENGTH=181	181	181	1.00E-105	100.0	100.0	100.0
Rsa1.0_01414.1.g26571.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01414.1.g26572.t2	ref|NP_182247.1| putative pre-mRNA-splicing factor ATP-dependent RNA helicase [Arabidopsis thaliana] gi|3913425|sp|O22899.1|DHX15_ARATH RecName: Full=Probable pre-mRNA-splicing factor ATP-dependent RNA helicase gi|2275203|gb|AAB63825.1| putative pre-mRNA splicing factor RNA helicase [Arabidopsis thaliana] gi|22135845|gb|AAM91108.1| At2g47250/T8I13.9 [Arabidopsis thaliana] gi|28416499|gb|AAO42780.1| At2g47250/T8I13.9 [Arabidopsis thaliana] gi|330255726|gb|AEC10820.1| putative pre-mRNA-splicing factor ATP-dependent RNA helicase [Arabidopsis thaliana]	767	729	0	95.0	89.0	92.0	putative pre-mRNA-splicing factor ATP-dependent RNA helicase	gbpln	Arabidopsis thaliana	AT2G47250.1 | Symbols: | RNA helicase family protein | chr2:19399923-19402981 REVERSE LENGTH=729	767	729	0	95.0	89.0	92.0
Rsa1.0_01414.1.g26573.t1	dbj|BAF01862.1| beta-galactosidase like protein [Arabidopsis thaliana]	120	578	6.00E-49	481.7	78.3	80.8	beta-galactosidase like protein	gbpln	Arabidopsis thaliana	AT4G36360.2 | Symbols: BGAL3 | beta-galactosidase 3 | chr4:17176840-17181143 REVERSE LENGTH=855	120	855	2.00E-51	712.5	78.3	80.8
Rsa1.0_01414.1.g26574.t1	gb|EOA29119.1| hypothetical protein CARUB_v10025386mg [Capsella rubella]	101	102	9.00E-42	101.0	87.1	94.1	hypothetical protein CARUB_v10025386mg	gbpln	Capsella rubella	AT2G47270.1 | Symbols: UPB1 | sequence-specific DNA binding transcription factors;transcription regulators | chr2:19411741-19412049 REVERSE LENGTH=102	101	102	2.00E-44	101.0	86.1	95.0
Rsa1.0_01414.1.g26575.t2	gb|EOA27835.1| hypothetical protein CARUB_v10023992mg [Capsella rubella]	496	230	1.00E-100	46.4	38.7	42.7	hypothetical protein CARUB_v10023992mg	gbpln	Capsella rubella	AT2G47320.1 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr2:19427711-19428839 FORWARD LENGTH=230	496	230	1.00E-100	46.4	37.7	41.9

Rsa1.0_01414.1.g26576.t1	ref|XP_002882116.1| hypothetical protein ARALYDRAFT_483908 [Arabidopsis lyrata subsp. lyrata] gi|297327955|gb|EFH58375.1| hypothetical protein ARALYDRAFT_483908 [Arabidopsis lyrata subsp. lyrata]	67	739	5.00E−13	1103.0	71.6	83.6	hypothetical protein ARALYDRAFT_483908	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01414.1.g26577.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01414.1.g26578.t1	ref|XP_002880296.1| hypothetical protein ARALYDRAFT_904210 [Arabidopsis lyrata subsp. lyrata] gi|297326135|gb|EFH56555.1| hypothetical protein ARALYDRAFT_904210 [Arabidopsis lyrata subsp. lyrata]	475	487	1.00E−180	102.5	75.2	81.9	hypothetical protein ARALYDRAFT_904210	gbpln	Arabidopsis lyrata	AT2G47350.1 | Symbols: | HIT zinc finger ;PAPA−1−like conserved region | chr2:19434588−19437045 FORWARD LENGTH=486	475	486	1.00E−177	102.3	73.7	79.8
Rsa1.0_01414.1.g26579.t1	ref|XP_002862722.1| cytochrome c oxidase subunit VC family protein [Arabidopsis lyrata subsp. lyrata] gi|297817580|ref|XP_002876673.1| cytochrome c oxidase subunit VC family protein [Arabidopsis lyrata subsp. lyrata] gi|297308410|gb|EFH38980.1| cytochrome c oxidase subunit VC family protein [Arabidopsis lyrata subsp. lyrata] gi|297322511|gb|EFH52932.1| cytochrome c oxidase subunit VC family protein [Arabidopsis lyrata subsp. lyrata]	64	64	2.00E−27	100.0	92.2	98.4	cytochrome c oxidase subunit VC family protein	gbpln	Arabidopsis lyrata	AT5G61310.4 | Symbols: | Cytochrome c oxidase subunit Vc family protein | chr5:24653543−24653737 REVERSE LENGTH=64	64	64	1.00E−27	100.0	82.8	92.2
Rsa1.0_01414.1.g26580.t1	gb|EOA28136.1| hypothetical protein CARUB_v10024325mg [Capsella rubella]	125	124	7.00E−57	99.2	88.0	92.8	hypothetical protein CARUB_v10024325mg	gbpln	Capsella rubella	AT2G47400.1 | Symbols: CP12−1, CP12 | CP12 domain−containing protein 1 | chr2:19446889−19447263 FORWARD LENGTH=124	125	124	8.00E−55	99.2	88.8	92.8
Rsa1.0_01414.1.g26581.t1	ref|NP_182264.1| dimethyladenosine transferase [Arabidopsis thaliana] gi|2529685|gb|AAC62868.1| putative dimethyladenosine transferase [Arabidopsis thaliana] gi|14532650|gb|AAK64053.1| putative dimethyladenosine transferase [Arabidopsis thaliana] gi|21280901|gb|AAM44912.1| putative dimethyladenosine transferase [Arabidopsis thaliana] gi|330255745|gb|AEC10839.1| dimethyladenosine transferase [Arabidopsis thaliana]	140	353	3.00E−61	252.1	87.1	87.1	dimethyladenosine transferase	gbpln	Arabidopsis thaliana	AT2G47420.1 | Symbols: | Ribosomal RNA adenine dimethylase family protein | chr2:19457574−19458777 FORWARD LENGTH=353	140	353	9.00E−64	252.1	87.1	87.1
Rsa1.0_01415.1.g26582.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01415.1.g26583.t1	gb|EOA28804.1| hypothetical protein CARUB_v10025036mg [Capsella rubella]	58	200	2.00E−15	344.8	69.0	72.4	hypothetical protein CARUB_v10025036mg	gbpln	Capsella rubella	AT2G39900.1 | Symbols: | GATA type zinc finger transcription factor family protein | chr2:16659136−16660267 FORWARD LENGTH=200	58	200	8.00E−18	344.8	65.5	75.9
Rsa1.0_01415.1.g26584.t1	ref|XP_002870177.1| ATOEP16−2/ATOEP16−S [Arabidopsis lyrata subsp. lyrata] gi|297316013|gb|EFH46436.1| ATOEP16−2/ATOEP16−S [Arabidopsis lyrata subsp. lyrata]	184	178	1.00E−88	96.7	89.1	92.9	ATOEP16−2/ATOEP16−S	gbpln	Arabidopsis lyrata	AT4G16160.2 | Symbols: ATOEP16−2, ATOEP16−S | Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr4:9157545−9158738 FORWARD LENGTH=178	184	178	2.00E−90	96.7	88.6	92.4
Rsa1.0_01415.1.g26585.t1	ref|NP_193350.5| calmodulin−binding transcription activator 5 [Arabidopsis thaliana] gi|85718631|sp|O23463.2|CMTA5_ARATH RecName: Full=Calmodulin−binding transcription activator 5; AltName: Full=Ethylene−induced calmodulin−binding protein f; Short=EICBP.f; AltName: Full=Signal−responsive protein 6 gi|332658303|gb|AEE83703.1| calmodulin−binding transcription activator 5 [Arabidopsis thaliana]	938	923	0	98.4	85.8	91.2	calmodulin−binding transcription activator 5	gbpln	Arabidopsis thaliana	AT4G16150.1 | Symbols: | calmodulin binding;transcription regulators | chr4:9148225−9153048 FORWARD LENGTH=923	938	923	0	98.4	85.8	91.2
Rsa1.0_01415.1.g26586.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01415.1.g26587.t1	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	2033	1274	0	62.7	35.7	44.9	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	2033	575	8.00E−62	28.3	8.0	12.7
Rsa1.0_01415.1.g26588.t5	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_01416.1.g26589.t1</td><td>ref|NP_187255.1| ribosomal protein L12/ ATP-dependent Clp protease adaptor protein [Arabidopsis thaliana] gi|42572277|ref|NP_974234.1| ribosomal protein L12/ ATP-dependent Clp protease adaptor protein [Arabidopsis thaliana] gi|145331982|ref|NP_001078113.1| ribosomal protein L12/ ATP-dependent Clp protease adaptor protein [Arabidopsis thaliana] gi|7658342|gb|AAF66132.1| hypothetical protein; 10657-10097 [Arabidopsis thaliana] gi|17381070|gb|AAL36347.1| unknown protein [Arabidopsis thaliana] gi|20465711|gb|AAM20324.1| unknown protein [Arabidopsis thaliana] gi|332640813|gb|AEE74334.1| ribosomal protein L12/ ATP-dependent Clp protease adaptor protein [Arabidopsis thaliana] gi|332640814|gb|AEE74335.1| ribosomal protein L12/ ATP-dependent Clp protease adaptor protein [Arabidopsis thaliana] gi|332640815|gb|AEE74336.1| ribosomal protein L12/ ATP-dependent Clp protease adaptor protein [Arabidopsis thaliana]</td><td>105</td><td>186</td><td>2.00E-14</td><td>177.1</td><td>38.1</td><td>41.9</td><td>ribosomal protein L12/ ATP-dependent Clp protease adaptor protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G06040.3 | Symbols: | Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein | chr3:1824516-1825076 REVERSE LENGTH=186</td><td>105</td><td>186</td><td>4.00E-17</td><td>177.1</td><td>38.1</td><td>41.9</td></tr>
<tr><td>Rsa1.0_01416.1.g26590.t1</td><td>ref|NP_175241.2| TRX domain-containing protein [Arabidopsis thaliana] gi|40822802|gb|AAR92240.1| At1g48070 [Arabidopsis thaliana] gi|45752670|gb|AAS76233.1| At1g48070 [Arabidopsis thaliana] gi|332194123|gb|AEE32244.1| TRX domain-containing protein [Arabidopsis thaliana]</td><td>285</td><td>144</td><td>1.00E-32</td><td>50.5</td><td>27.0</td><td>34.0</td><td>TRX domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G48070.1 | Symbols: | Thioredoxin superfamily protein | chr1:17730568-17731103 REVERSE LENGTH=144</td><td>285</td><td>144</td><td>3.00E-35</td><td>50.5</td><td>27.0</td><td>34.0</td></tr>
<tr><td>Rsa1.0_01416.1.g26591.t1</td><td>gb|EOA37655.1| hypothetical protein CARUB_v10012196mg [Capsella rubella]</td><td>586</td><td>578</td><td>0</td><td>98.6</td><td>87.4</td><td>92.2</td><td>hypothetical protein CARUB_v10012196mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G52980.1 | Symbols: | GTP-binding family protein | chr1:19737493-19740201 FORWARD LENGTH=576</td><td>586</td><td>576</td><td>0</td><td>98.3</td><td>88.7</td><td>93.9</td></tr>
<tr><td>Rsa1.0_01416.1.g26592.t1</td><td>ref|XP_002891724.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297337566|gb|EFH67983.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>177</td><td>177</td><td>5.00E-78</td><td>100.0</td><td>83.6</td><td>89.8</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G53010.1 | Symbols: | RING/U-box superfamily protein | chr1:19747847-19748383 FORWARD LENGTH=178</td><td>177</td><td>178</td><td>5.00E-79</td><td>100.6</td><td>83.1</td><td>89.3</td></tr>
<tr><td>Rsa1.0_01416.1.g26593.t1</td><td>ref|NP_001185207.1| Ubiquitin-conjugating enzyme family protein [Arabidopsis thaliana] gi|205828971|sp|Q8GY87.2|UBC26_ARATH RecName: Full=Probable ubiquitin-conjugating enzyme E2 26; AltName: Full=Ubiquitin carrier protein 26 gi|9454541|gb|AAF87864.1|AC022520_8 Similar to ubiquitin-conjugating enzymes [Arabidopsis thaliana] gi|51970226|dbj|BAD43805.1| putative ubiquitin-conjugating enzyme [Arabidopsis thaliana] gi|66354460|gb|AAY44865.1| ubiquitinating enzyme [Arabidopsis thaliana] gi|332194757|gb|AEE32878.1| Ubiquitin-conjugating enzyme family protein [Arabidopsis thaliana]</td><td>521</td><td>543</td><td>0</td><td>104.2</td><td>68.5</td><td>77.9</td><td>Ubiquitin-conjugating enzyme family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G53025.1 | Symbols: | Ubiquitin-conjugating enzyme family protein | chr1:19757072-19759474 REVERSE LENGTH=543</td><td>521</td><td>543</td><td>0</td><td>104.2</td><td>68.5</td><td>77.9</td></tr>
<tr><td>Rsa1.0_01416.1.g26594.t1</td><td>ref|NP_175711.1| Cytochrome C oxidase copper chaperone (COX17) [Arabidopsis thaliana] gi|14794886|gb|AAK73497.1|AF349685_1 copper chaperone COX17-2 [Arabidopsis thaliana] gi|332194758|gb|AEE32879.1| Cytochrome C oxidase copper chaperone (COX17) [Arabidopsis thaliana]</td><td>75</td><td>72</td><td>7.00E-28</td><td>96.0</td><td>85.3</td><td>90.7</td><td>Cytochrome C oxidase copper chaperone (COX17)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G53030.1 | Symbols: | Cytochrome C oxidase copper chaperone (COX17) | chr1:19760224-19760442 REVERSE LENGTH=72</td><td>75</td><td>72</td><td>1.00E-30</td><td>96.0</td><td>85.3</td><td>90.7</td></tr>
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Rsa1.0_01416.1.g26595.t1	ref|NP_564621.1| uncharacterized protein [Arabidopsis thaliana] gi|14190517|gb|AAK55739.1|AF380658_1 At1g53031 [Arabidopsis thaliana] gi|15809782|gb|AAL06819.1| At1g53031 [Arabidopsis thaliana] gi|26453132|dbj|BAC43642.1| unknown protein [Arabidopsis thaliana] gi|332194759|gb|AEE32880.1| uncharacterized protein AT1G53035 [Arabidopsis thaliana]	150	150	5.00E-78	100.0	95.3	98.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G53035.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G15358.1); Has 49 Blast hits to 49 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:19761866-19762318 REVERSE LENGTH=150	150	150	2.00E-80	100.0	95.3	98.0
Rsa1.0_01416.1.g26596.t2	ref|NP_175712.2| uncharacterized protein [Arabidopsis thaliana] gi|42571845|ref|NP_974013.1| uncharacterized protein [Arabidopsis thaliana] gi|110738523|dbj|BAF01187.1| hypothetical protein [Arabidopsis thaliana] gi|332194761|gb|AEE32882.1| uncharacterized protein AT1G53040 [Arabidopsis thaliana] gi|332194762|gb|AEE32883.1| uncharacterized protein AT1G53040 [Arabidopsis thaliana]	529	540	0	102.1	90.0	94.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G53040.2 | Symbols: | Protein of unknown function (DUF616) | chr1:19764567-19766870 REVERSE LENGTH=540	529	540	0	102.1	90.0	94.1
Rsa1.0_01416.1.g26597.t1	gb|EOA38429.1| hypothetical protein CARUB_v10010019mg [Capsella rubella]	274	268	1.00E-114	97.8	75.2	85.4	hypothetical protein CARUB_v10010019mg	gbpln	Capsella rubella	AT1G53070.1 | Symbols: | Legume lectin family protein | chr1:19778371-19779189 FORWARD LENGTH=272	274	272	1.00E-114	99.3	78.5	88.3
Rsa1.0_01416.1.g26598.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01416.1.g26599.t2	gb|EOA38429.1| hypothetical protein CARUB_v10010019mg [Capsella rubella]	274	268	1.00E-112	97.8	75.5	86.1	hypothetical protein CARUB_v10010019mg	gbpln	Capsella rubella	AT1G53070.1 | Symbols: | Legume lectin family protein | chr1:19778371-19779189 FORWARD LENGTH=272	274	272	1.00E-113	99.3	79.2	87.6
Rsa1.0_01417.1.g26600.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01417.1.g26601.t2	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	973	1491	1.00E-162	153.2	30.3	39.3	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	973	1262	2.00E-51	129.7	9.4	13.8
Rsa1.0_01417.1.g26602.t1	ref|NP_177684.1| SHI-related sequence 5 [Arabidopsis thaliana] gi|9369370|gb|AAF87119.1|AC006434_15 F10A5.26 [Arabidopsis thaliana] gi|55978789|gb|AAV68856.1| hypothetical protein AT1G75520 [Arabidopsis thaliana] gi|60547683|gb|AAX23805.1| hypothetical protein At1g75520 [Arabidopsis thaliana] gi|332197608|gb|AEE35729.1| SHI-related sequence 5 [Arabidopsis thaliana]	334	346	1.00E-147	103.6	84.4	90.1	SHI-related sequence 5	gbpln	Arabidopsis thaliana	AT1G75520.1 | Symbols: SRS5 | SHI-related sequence 5 | chr1:28351779-28353179 REVERSE LENGTH=346	334	346	1.00E-150	103.6	84.4	90.1
Rsa1.0_01417.1.g26603.t1	ref|XP_002889029.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334870|gb|EFH65288.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	268	260	1.00E-106	97.0	72.4	82.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G75510.1 | Symbols: | Transcription initiation factor IIF, beta subunit | chr1:28347254-28348629 REVERSE LENGTH=261	268	261	1.00E-103	97.4	70.5	79.1
Rsa1.0_01417.1.g26604.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01417.1.g26605.t1	ref|XP_002889028.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297334869|gb|EFH65287.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	389	391	0	100.5	97.2	97.9	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT1G75500.2 | Symbols: WAT1 | Walls Are Thin 1 | chr1:28338282-28340091 REVERSE LENGTH=389	389	389	0	100.0	96.1	97.4
Rsa1.0_01417.1.g26606.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1376	1515	0	110.1	57.4	72.6	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1376	1262	1.00E-118	91.7	14.5	21.2
Rsa1.0_01418.1.g26607.t1	gb|ABD64941.1| Ulp1 protease family protein [Brassica oleracea]	496	871	4.00E-54	175.6	27.0	38.5	Ulp1 protease family protein	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	496	874	2.00E-34	176.2	17.7	24.0
Rsa1.0_01418.1.g26608.t1	gb|EOA19720.1| hypothetical protein CARUB_v10003767mg [Capsella rubella]	252	252	1.00E-134	100.0	97.2	98.8	hypothetical protein CARUB_v10003767mg	gbpln	Capsella rubella	AT4G01470.1 | Symbols: GAMMA-TIP3, TIP1;3, ATTIP1.3 | tonoplast intrinsic protein 1;3 | chr4:625092-625850 REVERSE LENGTH=252	252	252	1.00E-135	100.0	96.8	98.4
Rsa1.0_01418.1.g26609.t2	gb|EOA38508.1| hypothetical protein CARUB_v10010288mg [Capsella rubella]	210	212	1.00E-110	101.0	92.4	94.8	hypothetical protein CARUB_v10010288mg	gbpln	Capsella rubella	AT1G01050.1 | Symbols: AtPPa1, PPa1 | pyrophosphorylase 1 | chr1:31382-32670 REVERSE LENGTH=212	210	212	1.00E-113	101.0	92.9	96.2

Rsa1.0_01418.1.g26610.t1	gb|AAD21699.1| Contains reverse transcriptase domain (rvt) PF|00078 [Arabidopsis thaliana]	261	1253	1.00E-33	480.1	36.0	52.1	Contains reverse transcriptase domain (rvt) PF|00078	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	261	746	6.00E-23	285.8	18.4	26.8
Rsa1.0_01418.1.g26611.t1	gb|AAD08951.1| putative reverse transcriptase [Arabidopsis thaliana] gi|20197043|gb|AAM14892.1| putative reverse transcriptase [Arabidopsis thaliana]	628	1412	1.00E-178	224.8	50.5	67.8	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	628	746	3.00E-75	118.8	25.8	34.7
Rsa1.0_01418.1.g26612.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01418.1.g26613.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01418.1.g26614.t1	ref|XP_002874976.1| hypothetical protein ARALYDRAFT_912083 [Arabidopsis lyrata subsp. lyrata] gi|297320813|gb|EFH51235.1| hypothetical protein ARALYDRAFT_912083 [Arabidopsis lyrata subsp. lyrata]	302	332	1.00E-112	109.9	71.5	81.8	hypothetical protein ARALYDRAFT_912083	gbpln	Arabidopsis lyrata	AT4G01500.1 | Symbols: NGA4 | AP2/B3-like transcriptional factor family protein | chr4:639791-640792 FORWARD LENGTH=333	302	333	1.00E-112	110.3	68.2	80.5
Rsa1.0_01418.1.g26615.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	662	723	0	109.2	55.4	72.1	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	662	696	1.00E-39	105.1	23.9	42.7
Rsa1.0_01419.1.g26616.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01419.1.g26617.t1	ref|XP_002887591.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297333432|gb|EFH63850.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	177	173	5.00E-72	97.7	80.8	85.3	bZIP transcription factor family protein	gbpln	Arabidopsis lyrata	AT1G75390.1 | Symbols: AtbZIP44, bZIP44 | basic leucine-zipper 44 | chr1:28292224-28292745 FORWARD LENGTH=173	177	173	2.00E-73	97.7	80.2	84.7
Rsa1.0_01419.1.g26618.t1	gb|AAC63678.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	272	1216	5.00E-18	447.1	25.4	38.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01419.1.g26619.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	951	1274	0	134.0	46.9	63.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	951	575	2.00E-58	60.5	17.0	27.3
Rsa1.0_01419.1.g26620.t2	gb|EOA34909.1| hypothetical protein CARUB_v10019999mg [Capsella rubella]	357	612	1.00E-155	171.4	80.4	87.7	hypothetical protein CARUB_v10019999mg	gbpln	Capsella rubella	AT1G75370.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:28276657-28279798 REVERSE LENGTH=612	357	612	1.00E-154	171.4	80.7	85.4
Rsa1.0_01419.1.g26621.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01419.1.g26622.t1	gb|EOA33528.1| hypothetical protein CARUB_v10019936mg [Capsella rubella]	651	647	0	99.4	86.5	92.5	hypothetical protein CARUB_v10019936mg	gbpln	Capsella rubella	AT1G75200.1 | Symbols: | flavodoxin family protein / radical SAM domain-containing protein | chr1:28220849-28223597 REVERSE LENGTH=647	651	647	0	99.4	85.3	90.9
Rsa1.0_01419.1.g26623.t1	gb|EOA35457.1| hypothetical protein CARUB_v10020666mg [Capsella rubella] gi|482571270|gb|EOA35458.1| hypothetical protein CARUB_v10020666mg [Capsella rubella]	319	318	1.00E-154	99.7	88.1	92.8	hypothetical protein CARUB_v10020666mg	gbpln	Capsella rubella	AT1G75180.3 | Symbols: | Erythronate-4-phosphate dehydrogenase family protein | chr1:28216150-28217911 REVERSE LENGTH=315	319	315	1.00E-153	98.7	86.5	91.2
Rsa1.0_01419.1.g26624.t1	gb|EOA35962.1| hypothetical protein CARUB_v10021223mg [Capsella rubella]	88	86	3.00E-26	97.7	78.4	85.2	hypothetical protein CARUB_v10021223mg	gbpln	Capsella rubella	AT1G61570.1 | Symbols: TIM13 | translocase of the inner mitochondrial membrane 13 | chr1:22718897-22719473 REVERSE LENGTH=87	88	87	2.00E-26	98.9	69.3	80.7
Rsa1.0_01419.1.g26625.t1	ref|XP_002875878.1| aminoacyl-t-RNA synthetase [Arabidopsis lyrata subsp. lyrata] gi|297321716|gb|EFH52137.1| aminoacyl-t-RNA synthetase [Arabidopsis lyrata subsp. lyrata]	716	1083	0	151.3	62.0	63.8	aminoacyl-t-RNA synthetase	gbpln	Arabidopsis lyrata	AT3G48110.1 | Symbols: EDD1, EDD | glycine-tRNA ligases | chr3:17763111-17770964 FORWARD LENGTH=1067	716	1067	0	149.0	62.0	63.7
Rsa1.0_01419.1.g26626.t1	ref|NP_177652.2| uncharacterized protein [Arabidopsis thaliana] gi|332197557|gb|AEE35678.1| uncharacterized protein AT1G75160 [Arabidopsis thaliana]	165	395	3.00E-85	239.4	88.5	95.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G75160.1 | Symbols: | Protein of unknown function (DUF620) | chr1:28209534-28211624 FORWARD LENGTH=395	165	395	1.00E-87	239.4	88.5	95.2
Rsa1.0_01419.1.g26627.t1	gb|EOA21466.1| hypothetical protein CARUB_v10001858mg [Capsella rubella]	113	236	1.00E-28	208.8	61.1	69.9	hypothetical protein CARUB_v10001858mg	gbpln	Capsella rubella	AT5G23420.1 | Symbols: HMGB6 | high-mobility group box 6 | chr5:7888712-7890111 REVERSE LENGTH=241	113	241	6.00E-18	213.3	53.1	67.3
Rsa1.0_01419.1.g26628.t1	ref|XP_002887574.1| hypothetical protein ARALYDRAFT_895383 [Arabidopsis lyrata subsp. lyrata] gi|297333415|gb|EFH63833.1| hypothetical protein ARALYDRAFT_895383 [Arabidopsis lyrata subsp. lyrata]	272	395	1.00E-121	145.2	80.5	82.7	hypothetical protein ARALYDRAFT_895383	gbpln	Arabidopsis lyrata	AT1G75160.1 | Symbols: | Protein of unknown function (DUF620) | chr1:28209534-28211624 FORWARD LENGTH=395	272	395	1.00E-123	145.2	80.1	82.4

Rsa1.0_01419.1.g26629.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01419.1.g26630.t1	ref|NP_177650.1| uncharacterized protein [Arabidopsis thaliana] gi|332278241|sp|Q9FRK5.3|Y1514_ARATH RecName: Full=Uncharacterized membrane protein At1g75140 gi|10092281|gb|AAG12694.1|AC025814_18 unknown protein; 62105-63958 [Arabidopsis thaliana] gi|332197555|gb|AEE35676.1| uncharacterized protein AT1G75140 [Arabidopsis thaliana]	576	617	0	107.1	73.3	83.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G75140.1 | Symbols: | unknown protein; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G19370.1); Has 51 Blast hits to 49 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr1:28202166-28204019 REVERSE LENGTH=617	576	617	0	107.1	73.3	83.0
Rsa1.0_01419.1.g26631.t1	ref|NP_565102.1| Nucleotide-diphospho-sugar transferase family protein [Arabidopsis thaliana] gi|12323891|gb|AAG51917.1|AC013258_11 unknown protein; 7482-9019 [Arabidopsis thaliana] gi|14517393|gb|AAK62587.1| At1g75110/F9E10_4 [Arabidopsis thaliana] gi|20857366|gb|AAM26715.1| At1g75110/F9E10_4 [Arabidopsis thaliana] gi|332197552|gb|AEE35673.1| Nucleotide-diphospho-sugar transferase family protein [Arabidopsis thaliana]	428	428	0	100.0	86.4	93.9	Nucleotide-diphospho-sugar transferase family protein	gbpln	Arabidopsis thaliana	AT1G75110.1 | Symbols: RRA2 | Nucleotide-diphospho-sugar transferase family protein | chr1:28194348-28195885 REVERSE LENGTH=428	428	428	0	100.0	86.4	93.9
Rsa1.0_01419.1.g26632.t1	gb|EOA33700.1| hypothetical protein CARUB_v10019884mg [Capsella rubella]	569	701	0	123.2	73.6	81.7	hypothetical protein CARUB_v10019884mg	gbpln	Capsella rubella	AT1G75100.1 | Symbols: JAC1 | J-domain protein required for chloroplast accumulation response 1 | chr1:28191108-28193769 REVERSE LENGTH=651	569	651	0	114.4	74.3	82.2
Rsa1.0_01419.1.g26633.t1	gb|AAL57684.1| At1g75080/F9E10_7 [Arabidopsis thaliana] gi|20147315|gb|AAM10371.1| At1g75080/F9E10_7 [Arabidopsis thaliana]	333	336	1.00E-153	100.9	94.0	96.1	At1g75080/F9E10_7	gbpln	Arabidopsis thaliana	AT1G75080.2 | Symbols: BZR1 | Brassinosteroid signalling positive regulator (BZR1) family protein | chr1:28185709-28187063 FORWARD LENGTH=336	333	336	1.00E-155	100.9	93.7	96.1
Rsa1.0_01419.1.g26634.t1	ref|XP_002887572.1| hypothetical protein ARALYDRAFT_316436 [Arabidopsis lyrata subsp. lyrata] gi|297333413|gb|EFH63831.1| hypothetical protein ARALYDRAFT_316436 [Arabidopsis lyrata subsp. lyrata]	201	245	1.00E-93	121.9	89.6	93.5	hypothetical protein ARALYDRAFT_316436	gbpln	Arabidopsis lyrata	AT1G75050.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:28180116-28181062 FORWARD LENGTH=246	201	246	1.00E-92	122.4	87.6	93.0
Rsa1.0_01419.1.g26635.t1	ref|XP_002887572.1| hypothetical protein ARALYDRAFT_316436 [Arabidopsis lyrata subsp. lyrata] gi|297333413|gb|EFH63831.1| hypothetical protein ARALYDRAFT_316436 [Arabidopsis lyrata subsp. lyrata]	244	245	4.00E-99	100.4	72.1	82.4	hypothetical protein ARALYDRAFT_316436	gbpln	Arabidopsis lyrata	AT1G75050.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:28180116-28181062 FORWARD LENGTH=246	244	246	1.00E-100	100.8	72.1	82.4
Rsa1.0_01420.1.g26636.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01420.1.g26637.t1	ref|NP_193095.2| uncharacterized protein [Arabidopsis thaliana] gi|308191636|sp|Q9T0H9.2|GDT12_ARATH RecName: Full=GDT1-like protein 2, chloroplastic; Flags: Precursor gi|332657899|gb|AEE83299.1| uncharacterized protein AT4G13590 [Arabidopsis thaliana]	351	359	1.00E-168	102.3	90.0	95.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G13590.1 | Symbols: | Uncharacterized protein family (UPF0016) | chr4:7901369-7903792 REVERSE LENGTH=359	351	359	1.00E-171	102.3	90.0	95.2
Rsa1.0_01420.1.g26638.t1	ref|XP_002870373.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297316209|gb|EFH46632.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata]	244	244	1.00E-132	100.0	97.5	98.0	disease resistance-responsive family protein	gbpln	Arabidopsis lyrata	AT4G13580.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr4:7900427-7901161 FORWARD LENGTH=244	244	244	1.00E-134	100.0	97.1	97.1
Rsa1.0_01420.1.g26639.t1	gb|EOA30761.1| hypothetical protein CARUB_v10013903mg [Capsella rubella]	328	392	1.00E-60	119.5	52.1	69.2	hypothetical protein CARUB_v10013903mg	gbpln	Capsella rubella	AT1G61730.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:22793447-22794577 REVERSE LENGTH=376	328	376	4.00E-61	114.6	48.2	63.1
Rsa1.0_01420.1.g26640.t1	#	#	#	#	#	#	#	-	----	----	AT3G24860.1 | Symbols: | Homeodomain-like superfamily protein | chr3:9073642-9074574 FORWARD LENGTH=310	98	310	3.00E-13	316.3	44.9	52.0
Rsa1.0_01420.1.g26641.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01420.1.g26642.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01420.1.g26643.t1	ref|NP_193087.1| ammonium transporter 1;1 [Arabidopsis thaliana] gi|1703292|sp|P54144.1|AMT11_ARATH RecName: Full=Ammonium transporter 1 member 1; Short=AtAMT1;1 gi|551219|emb|CAA53473.1| amt1 [Arabidopsis thaliana] gi|4678377|emb|CAB41109.1| ammonium transport protein (AMT1) [Arabidopsis thaliana] gi|7268054|emb|CAB78393.1| ammonium transport protein (AMT1) [Arabidopsis thaliana] gi|332657887|gb|AEE83287.1| ammonium transporter 1;1 [Arabidopsis thaliana]	503	501	0	99.6	91.8	95.4	ammonium transporter 1;1	gbpln	Arabidopsis thaliana	AT4G13510.1 | Symbols: AMT1;1, ATAMT1, ATAMT1;1 | ammonium transporter 1;1 | chr4:7858220-7859725 FORWARD LENGTH=501	503	501	0	99.6	91.8	95.4
Rsa1.0_01420.1.g26644.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01421.1.g26645.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	387	490	1.00E-46	126.6	30.7	50.9	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	387	566	2.00E-47	146.3	28.9	48.8
Rsa1.0_01421.1.g26646.t1	gb|AAC23765.1| Mutator-like transposase [Arabidopsis thaliana]	424	784	1.00E-138	184.9	54.7	72.9	Mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	424	719	6.00E-16	169.6	20.8	38.9
Rsa1.0_01421.1.g26647.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01421.1.g26648.t1	ref|XP_002863918.1| hypothetical protein ARALYDRAFT_357086 [Arabidopsis lyrata subsp. lyrata] gi|297309753|gb|EFH40177.1| hypothetical protein ARALYDRAFT_357086 [Arabidopsis lyrata subsp. lyrata]	129	123	8.00E-15	95.3	34.1	42.6	hypothetical protein ARALYDRAFT_357086	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01421.1.g26649.t3	ref|XP_002868430.1| hypothetical protein ARALYDRAFT_493625 [Arabidopsis lyrata subsp. lyrata] gi|297314266|gb|EFH44689.1| hypothetical protein ARALYDRAFT_493625 [Arabidopsis lyrata subsp. lyrata]	241	445	7.00E-80	184.6	73.4	82.2	hypothetical protein ARALYDRAFT_493625	gbpln	Arabidopsis lyrata	AT5G35670.1 | Symbols: iqd33 | IQ-domain 33 | chr5:13856170-13857910 FORWARD LENGTH=442	241	442	3.00E-71	183.4	68.9	78.8
Rsa1.0_01421.1.g26650.t1	ref|XP_002870440.1| hypothetical protein ARALYDRAFT_915692 [Arabidopsis lyrata subsp. lyrata] gi|297316276|gb|EFH46699.1| hypothetical protein ARALYDRAFT_915692 [Arabidopsis lyrata subsp. lyrata]	145	145	3.00E-72	100.0	93.8	97.2	hypothetical protein ARALYDRAFT_915692	gbpln	Arabidopsis lyrata	AT2G04520.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr2:1574802-1575239 REVERSE LENGTH=145	145	145	5.00E-73	100.0	97.9	99.3
Rsa1.0_01421.1.g26651.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	185	1142	1.00E-61	617.3	57.8	77.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	185	575	9.00E-20	310.8	20.5	29.2
Rsa1.0_01421.1.g26652.t1	gb|EOA16232.1| hypothetical protein CARUB_v10004374mg [Capsella rubella]	558	626	0	112.2	78.9	87.5	hypothetical protein CARUB_v10004374mg	gbpln	Capsella rubella	AT5G35690.1 | Symbols: | CONTAINS InterPro DOMAIN/s: WLM (InterPro:IPR013536), PUB domain (InterPro:IPR018997), PUG domain (InterPro:IPR006567); BEST Arabidopsis thaliana protein match is: zinc ion binding (TAIR:AT1G55915.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:13865027-13868117 REVERSE LENGTH=603	558	603	0	108.1	78.7	86.0
Rsa1.0_01421.1.g26653.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01421.1.g26654.t2	ref|NP_198420.1| fimbrin-like protein 2 [Arabidopsis thaliana] gi|59797968|sp|Q9FKI0.1|FIMB2_ARATH RecName: Full=Fimbrin-like protein 2 gi|9758643|dbj|BAB09267.1| fimbrin [Arabidopsis thaliana] gi|15027847|gb|AAK76454.1| putative fimbrin protein [Arabidopsis thaliana] gi|23296651|gb|AAN13139.1| putative fimbrin protein [Arabidopsis thaliana] gi|332006624|gb|AED94007.1| fimbrin-like protein 2 [Arabidopsis thaliana]	690	687	0	99.6	92.2	95.5	fimbrin-like protein 2	gbpln	Arabidopsis thaliana	AT5G35700.1 | Symbols: FIM2, FIM5 | fimbrin-like protein 2 | chr5:13872833-13876432 REVERSE LENGTH=687	690	687	0	99.6	92.2	95.5
Rsa1.0_01422.1.g26655.t1	ref|XP_002890679.1| cytochrome B561 family protein [Arabidopsis lyrata subsp. lyrata] gi|297336521|gb|EFH66938.1| cytochrome B561 family protein [Arabidopsis lyrata subsp. lyrata]	232	236	1.00E-104	101.7	85.8	91.8	cytochrome B561 family protein	gbpln	Arabidopsis lyrata	AT1G26100.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane protein family | chr1:9022716-9024081 REVERSE LENGTH=236	232	236	1.00E-106	101.7	84.9	91.4

<table>
<tr><td>Rsa1.0_01422.1.g26656.t1</td><td>gb|EOA36601.1| hypothetical protein CARUB_v10011801mg [Capsella rubella]</td><td>407</td><td>456</td><td>1.00E-168</td><td>112.0</td><td>80.3</td><td>84.8</td><td>hypothetical protein CARUB_v10011801mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G26090.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:9020509-9022619 FORWARD LENGTH=455</td><td>407</td><td>455</td><td>1.00E-168</td><td>111.8</td><td>77.9</td><td>84.8</td></tr>
<tr><td>Rsa1.0_01422.1.g26657.t1</td><td>ref|XP_002870549.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316385|gb|EFH46808.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>605</td><td>614</td><td>1.00E-169</td><td>101.5</td><td>52.4</td><td>69.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G37650.1 | Symbols: | Family of unknown function (DUF577) | chr5:14954011-14955834 REVERSE LENGTH=607</td><td>605</td><td>607</td><td>1.00E-162</td><td>100.3</td><td>51.2</td><td>68.3</td></tr>
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<tr><td>Rsa1.0_01422.1.g26661.t1</td><td>gb|EOA40307.1| hypothetical protein CARUB_v10009035mg [Capsella rubella]</td><td>456</td><td>473</td><td>0</td><td>103.7</td><td>86.4</td><td>92.5</td><td>hypothetical protein CARUB_v10009035mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G26120.1 | Symbols: ICME-LIKE1 | alpha/beta-Hydrolases superfamily protein | chr1:9028656-9031402 REVERSE LENGTH=476</td><td>456</td><td>476</td><td>0</td><td>104.4</td><td>86.4</td><td>92.8</td></tr>
<tr><td>Rsa1.0_01422.1.g26662.t1</td><td>ref|XP_002890673.1| metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297336515|gb|EFH66932.1| metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>366</td><td>254</td><td>1.00E-106</td><td>69.4</td><td>54.6</td><td>57.4</td><td>metal-dependent phosphohydrolase HD domain-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G26160.1 | Symbols: | Metal-dependent phosphohydrolase | chr1:9044784-9046945 REVERSE LENGTH=258</td><td>366</td><td>258</td><td>1.00E-108</td><td>70.5</td><td>54.4</td><td>56.8</td></tr>
<tr><td>Rsa1.0_01422.1.g26663.t2</td><td>ref|NP_173943.2| uncharacterized protein [Arabidopsis thaliana] gi|18252157|gb|AAL61911.1| unknown protein [Arabidopsis thaliana] gi|21386935|gb|AAM47871.1| unknown protein [Arabidopsis thaliana] gi|332192537|gb|AEE30658.1| uncharacterized protein AT1G26180 [Arabidopsis thaliana]</td><td>316</td><td>289</td><td>1.00E-130</td><td>91.5</td><td>78.5</td><td>82.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G26180.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2232, membrane (InterPro:IPR018710); Has 285 Blast hits to 285 proteins in 90 species: Archae - 0; Bacteria - 140; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink). | chr1:9054824-9056526 FORWARD LENGTH=289</td><td>316</td><td>289</td><td>1.00E-133</td><td>91.5</td><td>78.5</td><td>82.6</td></tr>
<tr><td>Rsa1.0_01422.1.g26664.t1</td><td>ref|NP_173944.1| phosphoribulokinase/uridine kinase-like protein [Arabidopsis thaliana] gi|12321172|gb|AAG50674.1|AC079829_7 hypothetical protein [Arabidopsis thaliana] gi|20259437|gb|AAM14039.1| unknown protein [Arabidopsis thaliana] gi|21436169|gb|AAM51372.1| unknown protein [Arabidopsis thaliana] gi|332192538|gb|AEE30659.1| phosphoribulokinase/uridine kinase-like protein [Arabidopsis thaliana]</td><td>630</td><td>674</td><td>0</td><td>107.0</td><td>89.4</td><td>95.1</td><td>phosphoribulokinase/uridine kinase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G26190.1 | Symbols: | Phosphoribulokinase / Uridine kinase family | chr1:9057285-9060433 REVERSE LENGTH=674</td><td>630</td><td>674</td><td>0</td><td>107.0</td><td>89.4</td><td>95.1</td></tr>
<tr><td>Rsa1.0_01422.1.g26665.t2</td><td>ref|NP_001154368.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana] gi|332192539|gb|AEE30660.1| TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein [Arabidopsis thaliana]</td><td>309</td><td>312</td><td>1.00E-147</td><td>101.0</td><td>83.2</td><td>91.3</td><td>TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G26200.1 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr1:9063471-9064914 REVERSE LENGTH=312</td><td>309</td><td>312</td><td>1.00E-150</td><td>101.0</td><td>83.2</td><td>91.3</td></tr>
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<tr><td>Rsa1.0_01423.1.g26668.t1</td><td>gb|ACG60672.1| unknown protein [Brassica oleracea var. alboglabra]</td><td>49</td><td>288</td><td>4.00E-12</td><td>587.8</td><td>73.5</td><td>85.7</td><td>unknown protein</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<tr><td>Rsa1.0_01424.1.g26682.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<tr><td>Rsa1.0_01424.1.g26684.t1</td><td>dbj|BAJ33887.1| unnamed protein product [Thellungiella halophila]</td><td>680</td><td>688</td><td>0</td><td>101.2</td><td>92.4</td><td>96.6</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G65110.1 | Symbols: ACX2, ATACX2 | acyl-CoA oxidase 2 | chr5:26009821-26012482 REVERSE LENGTH=692</td><td>680</td><td>692</td><td>0</td><td>101.8</td><td>90.4</td><td>95.4</td></tr>
<tr><td>Rsa1.0_01424.1.g26685.t1</td><td>ref|XP_002866646.1| nucleotide-sugar transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297312481|gb|EFH42905.1| nucleotide-sugar transporter family protein [Arabidopsis lyrata subsp. lyrata]</td><td>444</td><td>325</td><td>1.00E-159</td><td>73.2</td><td>67.1</td><td>69.8</td><td>nucleotide-sugar transporter family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G65000.1 | Symbols: | Nucleotide-sugar transporter family protein | chr5:25965123-25967307 REVERSE LENGTH=325</td><td>444</td><td>325</td><td>1.00E-162</td><td>73.2</td><td>66.9</td><td>69.6</td></tr>
<tr><td>Rsa1.0_01425.1.g26686.t1</td><td>dbj|BAB08885.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>171</td><td>370</td><td>1.00E-40</td><td>216.4</td><td>46.8</td><td>60.2</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237</td><td>171</td><td>237</td><td>1.00E-16</td><td>138.6</td><td>26.9</td><td>43.3</td></tr>
<tr><td>Rsa1.0_01425.1.g26687.t1</td><td>ref|XP_002866916.1| hypothetical protein ARALYDRAFT_490803 [Arabidopsis lyrata subsp. lyrata] gi|297312752|gb|EFH43175.1| hypothetical protein ARALYDRAFT_490803 [Arabidopsis lyrata subsp. lyrata]</td><td>246</td><td>239</td><td>1.00E-102</td><td>97.2</td><td>77.2</td><td>82.9</td><td>hypothetical protein ARALYDRAFT_490803</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G38090.1 | Symbols: | Ribosomal protein S5 domain 2-like superfamily protein | chr4:17883757-17884702 REVERSE LENGTH=234</td><td>246</td><td>234</td><td>1.00E-103</td><td>95.1</td><td>76.8</td><td>82.5</td></tr>
<tr><td>Rsa1.0_01425.1.g26688.t1</td><td>ref|NP_566995.1| diphosphomevalonate decarboxylase [Arabidopsis thaliana] gi|332645683|gb|AEE79204.1| diphosphomevalonate decarboxylase [Arabidopsis thaliana]</td><td>419</td><td>419</td><td>0</td><td>100.0</td><td>94.7</td><td>97.4</td><td>diphosphomevalonate decarboxylase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G54250.1 | Symbols: | GHMP kinase family protein | chr3:20082468-20084688 REVERSE LENGTH=419</td><td>419</td><td>419</td><td>0</td><td>100.0</td><td>94.7</td><td>97.4</td></tr>
<tr><td>Rsa1.0_01425.1.g26689.t1</td><td>ref|NP_566996.1| protein trichome birefringence-like 36 [Arabidopsis thaliana] gi|15451108|gb|AAK96825.1| putative protein [Arabidopsis thaliana] gi|20148379|gb|AAM10080.1| putative protein [Arabidopsis thaliana] gi|332645684|gb|AEE79205.1| protein trichome birefringence-like 36 [Arabidopsis thaliana]</td><td>373</td><td>379</td><td>0</td><td>101.6</td><td>86.9</td><td>91.7</td><td>protein trichome birefringence-like 36</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G54260.1 | Symbols: TBL36 | TRICHOME BIREFRINGENCE-LIKE 36 | chr3:20085097-20086745 REVERSE LENGTH=379</td><td>373</td><td>379</td><td>0</td><td>101.6</td><td>86.9</td><td>91.7</td></tr>
<tr><td>Rsa1.0_01425.1.g26690.t1</td><td>ref|NP_680429.1| uncharacterized protein [Arabidopsis thaliana] gi|44917523|gb|AAS49086.1| At5g53895 [Arabidopsis thaliana] gi|332009041|gb|AED96424.1| uncharacterized protein AT5G53895 [Arabidopsis thaliana]</td><td>134</td><td>129</td><td>2.00E-42</td><td>96.3</td><td>76.1</td><td>84.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G53895.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27530.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21880626-21881116 FORWARD LENGTH=129</td><td>134</td><td>129</td><td>4.00E-45</td><td>96.3</td><td>76.1</td><td>84.3</td></tr>
</table>

Rsa1.0_01425.1.g26691.t1	ref|NP_566997.1| uncharacterized protein [Arabidopsis thaliana] gi|20260600|gb|AAM13198.1| unknown protein [Arabidopsis thaliana] gi|31711834|gb|AAP68273.1| At3g54290 [Arabidopsis thaliana] gi|332645688|gb|AEE79209.1| uncharacterized protein AT3G54290 [Arabidopsis thaliana]	329	350	1.00E-145	106.4	80.5	90.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G54290.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Haemerythrin/HHE cation-binding motif (InterPro:IPR012312); Has 59 Blast hits to 59 proteins in 14 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:20104623-20105845 REVERSE LENGTH=350	329	350	1.00E-148	106.4	80.5	90.0
Rsa1.0_01425.1.g26692.t1	ref|XP_002877968.1| ATVAMP727 [Arabidopsis lyrata subsp. lyrata] gi|297323806|gb|EFH54227.1| ATVAMP727 [Arabidopsis lyrata subsp. lyrata]	243	240	1.00E-127	98.8	94.2	96.7	ATVAMP727	gbpln	Arabidopsis lyrata	AT3G54300.2 | Symbols: ATVAMP727, VAMP727 | vesicle-associated membrane protein 727 | chr3:20108355-20110127 REVERSE LENGTH=240	243	240	1.00E-129	98.8	93.4	96.3
Rsa1.0_01425.1.g26693.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01425.1.g26694.t1	gb|AAF28894.1|AF124814_1 APETALA3 [Brassica napus] gi|48375197|gb|AAT42251.1| floral homeotic protein APETALA3 [Brassica rapa subsp. chinensis] gi|87133586|gb|ABD24435.1| APETALA3-4 [Brassica napus]	302	224	1.00E-117	74.2	68.2	69.5	APETALA3	gbpln	Brassica napus	AT3G54340.1 | Symbols: AP3, ATAP3 | K-box region and MADS-box transcription factor family protein | chr3:20119428-20121087 REVERSE LENGTH=232	302	232	1.00E-112	76.8	64.9	67.5
Rsa1.0_01425.1.g26695.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01426.1.g26696.t1	ref|NP_192607.2| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|84778464|dbj|BAE73259.1| xylogen like protein 3 [Arabidopsis thaliana] gi|332657267|gb|AEE82667.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	139	208	2.00E-12	149.6	36.0	41.7	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT4G08670.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:5536765-5538210 REVERSE LENGTH=208	139	208	5.00E-15	149.6	36.0	41.7
Rsa1.0_01426.1.g26697.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01426.1.g26698.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01426.1.g26699.t3	gb|AAD20433.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1555	889	1.00E-165	57.2	21.6	29.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01426.1.g26700.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	662	695	0	105.0	59.7	70.7	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT3G43148.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT5G32590.1); Has 145 Blast hits to 140 proteins in 36 species: Archae - 0; Bacteria - 9; Metazoa - 37; Fungi - 11; Plants - 72; Viruses - 1; Other Eukaryotes - 15 (source: NCBI BLink). | chr3:15139995-15143123 FORWARD LENGTH=673	662	673	1.00E-17	101.7	9.2	14.4
Rsa1.0_01426.1.g26701.t1	ref|NP_189946.1| aldehyde oxidase 2 [Arabidopsis thaliana] gi|62899865|sp|Q7G192.2|ALDO2_ARATH RecName: Full=Indole-3-acetaldehyde oxidase; Short=IAA oxidase; AltName: Full=Aldehyde oxidase 2; Short=AO-2; Short=AtAO-2; Short=AtAO3 gi|3172025|dbj|BAA28625.1| aldehyde oxidase [Arabidopsis thaliana] gi|9967509|emb|CAC05634.1| aldehyde oxidase [Arabidopsis thaliana] gi|332644291|gb|AEE77812.1| aldehyde oxidase 2 [Arabidopsis thaliana]	137	1321	4.00E-37	964.2	57.7	65.0	aldehyde oxidase 2	gbpln	Arabidopsis thaliana	AT3G43600.1 | Symbols: AAO2, AO3, atAO-2, AOgamma, AtAO3 | aldehyde oxidase 2 | chr3:15512778-15517375 REVERSE LENGTH=1321	137	1321	1.00E-39	964.2	57.7	65.0
Rsa1.0_01426.1.g26702.t1	gb|EOA31081.1| hypothetical protein CARUB_v10014232mg [Capsella rubella]	290	310	3.00E-94	106.9	67.6	83.4	hypothetical protein CARUB_v10014232mg	gbpln	Capsella rubella	AT5G48670.1 | Symbols: FEM111, AGL80 | AGAMOUS-like 80 | chr5:19738825-19739790 REVERSE LENGTH=321	290	321	6.00E-93	110.7	66.6	79.7
Rsa1.0_01426.1.g26703.t1	gb|ABL97959.1| ribosomal protein L7Ae-like [Brassica rapa]	128	128	8.00E-67	100.0	99.2	100.0	ribosomal protein L7Ae-like	gbpln	Brassica rapa	AT5G20160.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr5:6804075-6805102 REVERSE LENGTH=128	128	128	4.00E-60	100.0	96.1	97.7

Rsa1.0_01427.1.g26704.t1	ref|NP_564065.1| uncharacterized protein [Arabidopsis thaliana] gi|6730701|gb|AAF27096.1|AC011809_5 Unknown protein [Arabidopsis thaliana] gi|15810347|gb|AAL07061.1| unknown protein [Arabidopsis thaliana] gi|20465593|gb|AAM20279.1| unknown protein [Arabidopsis thaliana] gi|332191650|gb|AEE29771.1| uncharacterized protein AT1G18850 [Arabidopsis thaliana]	141	399	1.00E-14	283.0	43.3	51.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G18850.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 40 Blast hits to 40 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6504928-6506127 REVERSE LENGTH=399	141	399	4.00E-17	283.0	43.3	51.8
Rsa1.0_01427.1.g26705.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01427.1.g26706.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	324	940	1.00E-32	290.1	24.7	35.2	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01427.1.g26707.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	569	940	2.00E-16	165.2	8.6	15.5	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01427.1.g26708.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01427.1.g26709.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01427.1.g26710.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01427.1.g26711.t1	gb|AAF99763.1|AC003981_13 F22O13.21 [Arabidopsis thaliana] gi|9293930|dbj|BAB01833.1| Mutator-like transposase [Arabidopsis thaliana] gi|10177478|dbj|BAB10869.1| mutator-like transposase [Arabidopsis thaliana]	348	915	8.00E-55	262.9	35.6	51.1	F22O13.21	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01427.1.g26712.t1	ref|XP_002893018.1| hypothetical protein ARALYDRAFT_472107 [Arabidopsis lyrata subsp. lyrata] gi|297338860|gb|EFH69277.1| hypothetical protein ARALYDRAFT_472107 [Arabidopsis lyrata subsp. lyrata]	87	88	2.00E-37	101.1	90.8	94.3	hypothetical protein ARALYDRAFT_472107	gbpln	Arabidopsis lyrata	AT1G18835.1 | Symbols: MIF3 | mini zinc finger | chr1:6496106-6496372 REVERSE LENGTH=88	87	88	1.00E-35	101.1	89.7	94.3
Rsa1.0_01428.1.g26713.t8	dbj|BAB01217.1| Ta11 non-LTR retroelement protein-like [Arabidopsis thaliana] gi|67633664|gb|AAY78756.1| putative zinc finger protein [Arabidopsis thaliana]	786	487	2.00E-61	62.0	20.9	29.9	Ta11 non-LTR retroelement protein-like	gbpln	Arabidopsis thaliana	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365	786	365	7.00E-17	46.4	6.5	9.5
Rsa1.0_01428.1.g26714.t1	gb|EOA31093.1| hypothetical protein CARUB_v10014242mg [Capsella rubella]	298	307	1.00E-113	103.0	70.8	82.9	hypothetical protein CARUB_v10014242mg	gbpln	Capsella rubella	AT3G24860.1 | Symbols: | Homeodomain-like superfamily protein | chr3:9073642-9074574 FORWARD LENGTH=310	298	310	1.00E-108	104.0	66.8	77.9
Rsa1.0_01428.1.g26715.t5	ref|NP_189132.2| Helicase/SANT-associated, DNA binding protein [Arabidopsis thaliana] gi|332643436|gb|AEE76957.1| Helicase/SANT-associated, DNA binding protein [Arabidopsis thaliana]	1887	1957	0	103.7	75.4	83.0	Helicase/SANT-associated, DNA binding protein	gbpln	Arabidopsis thaliana	AT3G24880.1 | Symbols: | Helicase/SANT-associated, DNA binding protein | chr3:9086457-9095537 REVERSE LENGTH=1957	1887	1957	0	103.7	75.4	83.0
Rsa1.0_01428.1.g26716.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01428.1.g26717.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01428.1.g26718.t1	ref|NP_189139.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|79313365|ref|NP_001030762.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|9293985|dbj|BAB01888.1| unnamed protein product [Arabidopsis thaliana] gi|48958487|gb|AAT47796.1| At3g25030 [Arabidopsis thaliana] gi|51536564|gb|AAU05520.1| At3g25030 [Arabidopsis thaliana] gi|332643448|gb|AEE76969.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332643449|gb|AEE76970.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	267	250	6.00E-95	93.6	71.2	80.1	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT3G25030.2 | Symbols: | RING/U-box superfamily protein | chr3:9122650-9123402 FORWARD LENGTH=250	267	250	2.00E-97	93.6	71.2	80.1
Rsa1.0_01429.1.g26719.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01429.1.g26720.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	610	1142	1.00E-172	187.2	50.5	63.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	610	626	2.00E-23	102.6	14.3	24.8

Rsa1.0_01429.1.g26721.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01429.1.g26722.t1	gb|AAF79687.1|AC022314_28 F9C16.9 [Arabidopsis thaliana]	781	946	0	121.1	49.3	65.7	F9C16.9	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	781	719	4.00E-23	92.1	14.6	28.3
Rsa1.0_01429.1.g26723.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	687	1024	2.00E-54	149.1	22.9	31.7	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01429.1.g26724.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01429.1.g26725.t1	dbj|BAF01102.1| putative proline-rich protein [Arabidopsis thaliana]	309	315	1.00E-81	101.9	78.3	83.2	putative proline-rich protein	gbpln	Arabidopsis thaliana	AT1G28290.2 | Symbols: AGP31 | arabinogalactan protein 31 | chr1:9889331-9890843 REVERSE LENGTH=315	309	315	6.00E-81	101.9	78.6	83.5
Rsa1.0_01429.1.g26726.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01429.1.g26727.t1	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1014	1250	0	123.3	46.8	59.1	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1014	1262	8.00E-52	124.5	14.6	23.0
Rsa1.0_01429.1.g26728.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	165	1142	7.00E-20	692.1	33.3	49.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01430.1.g26729.t1	ref|NP_190260.1| protein kinase family protein [Arabidopsis thaliana] gi|75266317|sp|Q9STF0.1|LRKS3_ARATH RecName: Full=Receptor like protein kinase S.3; Short=LecRK-S.3 gi|5541683|emb|CAB51189.1| receptor like protein kinase [Arabidopsis thaliana] gi|332644680|gb|AEE78201.1| receptor like protein kinase S.3 [Arabidopsis thaliana]	329	337	1.00E-175	102.4	93.9	96.0	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G46760.1 | Symbols: | Protein kinase superfamily protein | chr3:17222027-17223040 FORWARD LENGTH=337	329	337	1.00E-178	102.4	93.9	96.0
Rsa1.0_01430.1.g26730.t1	gb|EOA25635.1| hypothetical protein CARUB_v10018984mg [Capsella rubella]	343	389	1.00E-141	113.4	80.2	87.5	hypothetical protein CARUB_v10018984mg	gbpln	Capsella rubella	AT3G46750.1 | Symbols: | unknown protein; Has 2631 Blast hits to 1984 proteins in 271 species: Archae - 6; Bacteria - 163; Metazoa - 1232; Fungi - 253; Plants - 141; Viruses - 8; Other Eukaryotes - 828 (source: NCBI BLink). | chr3:17219944-17221461 FORWARD LENGTH=388	343	388	1.00E-142	113.1	79.3	86.3
Rsa1.0_01430.1.g26731.t2	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	259	414	2.00E-13	159.8	21.2	26.3	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01430.1.g26732.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01430.1.g26733.t1	ref|XP_002877506.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297323344|gb|EFH53765.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	269	452	9.00E-66	168.0	59.5	74.0	UDP-glucoronosyl/UDP-glucosyl transferase family protein	gbpln	Arabidopsis lyrata	AT3G46680.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:17195318-17196743 REVERSE LENGTH=449	269	449	2.00E-67	166.9	59.1	72.5
Rsa1.0_01430.1.g26734.t1	ref|NP_566885.1| UDP-glucosyl transferase 76E12 [Arabidopsis thaliana] gi|75249778|sp|Q94AB5.1|U7E12_ARATH RecName: Full=UDP-glycosyltransferase 76E12 gi|15081809|gb|AAK82559.1| AT3g46660/F12A12_180 [Arabidopsis thaliana] gi|21539473|gb|AAM53289.1| glucosyltransferase-like protein [Arabidopsis thaliana] gi|23198296|gb|AAN15675.1| glucosyltransferase-like protein [Arabidopsis thaliana] gi|27363270|gb|AAO11554.1| At3g46660/F12A12_180 [Arabidopsis thaliana] gi|332644669|gb|AEE78190.1| UDP-glucosyl transferase 76E12 [Arabidopsis thaliana]	360	458	1.00E-83	127.2	43.1	48.9	UDP-glucosyl transferase 76E12	gbpln	Arabidopsis thaliana	AT3G46660.1 | Symbols: UGT76E12 | UDP-glucosyl transferase 76E12 | chr3:17189406-17190862 REVERSE LENGTH=458	360	458	3.00E-86	127.2	43.1	48.9

Rsa1.0_01430.1.g26735.t1	ref|NP_190248.1| protein phytoclock 1 [Arabidopsis thaliana] gi|79314533|ref|NP_001030823.1| protein phytoclock 1 [Arabidopsis thaliana] gi|6523067|emb|CAB62334.1| putative protein [Arabidopsis thaliana] gi|30102630|gb|AAP21233.1| At3g46640 [Arabidopsis thaliana] gi|71067050|dbj|BAE16277.1| PHYTOCLOCK 1 [Arabidopsis thaliana] gi|110743672|dbj|BAE99673.1| hypothetical protein [Arabidopsis thaliana] gi|332644665|gb|AEE78186.1| protein phytoclock 1 [Arabidopsis thaliana] gi|332644666|gb|AEE78187.1| protein phytoclock 1 [Arabidopsis thaliana]	293	323	1.00E-120	110.2	82.3	86.7	protein phytoclock 1	gbpln	Arabidopsis thaliana	AT3G46640.2 | Symbols: PCL1 | Homeodomain-like superfamily protein | chr3:17183248-17184219 FORWARD LENGTH=323	293	323	1.00E-122	110.2	82.3	86.7
Rsa1.0_01430.1.g26736.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01430.1.g26737.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01430.1.g26738.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01430.1.g26739.t1	ref|NP_192445.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|7267296|emb|CAB81078.1| putative protein [Arabidopsis thaliana] gi|332657109|gb|AEE82509.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	334	735	4.00E-48	220.1	40.7	52.4	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	334	735	9.00E-51	220.1	40.7	52.4
Rsa1.0_01430.1.g26740.t1	dbj|BAJ33797.1| unnamed protein product [Thellungiella halophila]	609	592	0	97.2	82.9	88.0	unnamed protein product	----	----	AT3G46600.1 | Symbols: | GRAS family transcription factor | chr3:17158048-17159799 FORWARD LENGTH=583	609	583	0	95.7	81.8	87.0
Rsa1.0_01431.1.g26741.t1	gb|ABK28243.1| unknown [Arabidopsis thaliana]	366	297	3.00E-70	81.1	35.8	48.9	unknown	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	366	332	1.00E-72	90.7	35.8	48.9
Rsa1.0_01431.1.g26742.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01431.1.g26743.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	213	1142	3.00E-41	536.2	45.5	59.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	213	292	5.00E-22	137.1	30.0	50.7
Rsa1.0_01431.1.g26744.t1	ref|XP_002884043.1| hypothetical protein ARALYDRAFT_480607 [Arabidopsis lyrata subsp. lyrata] gi|297329883|gb|EFH60302.1| hypothetical protein ARALYDRAFT_480607 [Arabidopsis lyrata subsp. lyrata]	146	142	3.00E-32	97.3	54.1	57.5	hypothetical protein ARALYDRAFT_480607	gbpln	Arabidopsis lyrata	AT2G17240.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G24506.1); Has 2795 Blast hits to 943 proteins in 155 species: Archae - 0; Bacteria - 388; Metazoa - 809; Fungi - 72; Plants - 153; Viruses - 54; Other Eukaryotes - 1319 (source: NCBI BLink). | chr2:7498178-7498996 FORWARD LENGTH=140	146	140	8.00E-30	95.9	54.1	56.8
Rsa1.0_01431.1.g26745.t1	ref|NP_179316.2| CCAAT-binding factor [Arabidopsis thaliana] gi|330251509|gb|AEC06603.1| CCAAT-binding factor [Arabidopsis thaliana]	619	577	0	93.2	78.2	85.3	CCAAT-binding factor	gbpln	Arabidopsis thaliana	AT2G17250.1 | Symbols: EMB2762 | CCAAT-binding factor | chr2:7499573-7502957 FORWARD LENGTH=577	619	577	0	93.2	78.2	85.3
Rsa1.0_01431.1.g26746.t1	gb|AAF21901.1|AF109392_1 ligand gated channel-like protein [Brassica napus]	908	912	0	100.4	95.6	97.7	ligand gated channel-like protein	gbpln	Brassica napus	AT2G17260.1 | Symbols: GLR2, ATGLR2, GLR3.1, ATGLR3.1 | glutamate receptor 2 | chr2:7504780-7508266 FORWARD LENGTH=951	908	951	0	104.7	87.8	93.8
Rsa1.0_01431.1.g26747.t1	ref|XP_002884047.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] gi|297329887|gb|EFH60306.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	309	309	1.00E-173	100.0	95.1	98.4	mitochondrial substrate carrier family protein	gbpln	Arabidopsis lyrata	AT2G17270.1 | Symbols: PHT3;3 | phosphate transporter 3;3 | chr2:7510456-7512118 FORWARD LENGTH=309	309	309	1.00E-174	100.0	94.2	97.7
Rsa1.0_01431.1.g26748.t1	ref|NP_190293.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|6522590|emb|CAB61955.1| receptor kinase-like protein [Arabidopsis thaliana] gi|332644721|gb|AEE78242.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]	997	1009	0	101.2	70.8	81.9	leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT3G47090.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17341512-17344645 REVERSE LENGTH=1009	997	1009	0	101.2	70.8	81.9
Rsa1.0_01431.1.g26749.t1	gb|AAZ32753.1| putative calcium dependent kinase 6 [Brassica napus]	551	535	0	97.1	90.9	92.6	putative calcium dependent kinase 6	gbpln	Brassica napus	AT2G17290.1 | Symbols: CPK6, ATCDPK3, ATCPK6 | Calcium-dependent protein kinase family protein | chr2:7517005-7519239 FORWARD LENGTH=544	551	544	0	98.7	88.9	92.4

Rsa1.0_01431.1.g26750.t1	ref|NP_179322.1| uncharacterized protein [Arabidopsis thaliana] gi|45476533|gb|AAS65932.1| At2g17300 [Arabidopsis thaliana] gi|46359819|gb|AAS88773.1| At2g17300 [Arabidopsis thaliana] gi|330251516|gb|AEC06610.1| uncharacterized protein AT2G17300 [Arabidopsis thaliana]	142	139	2.00E-34	97.9	77.5	83.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G17300.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G35320.1); Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:7522465-7522884 REVERSE LENGTH=139	142	139	6.00E-37	97.9	77.5	83.1
Rsa1.0_01431.1.g26751.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01431.1.g26752.t1	ref|XP_002884053.1| 3-hydroxy-3-methylglutaryl-CoA reductase 2 [Arabidopsis lyrata subsp. lyrata] gi|297329893|gb|EFH60312.1| 3-hydroxy-3-methylglutaryl-CoA reductase 2 [Arabidopsis lyrata subsp. lyrata]	558	564	0	101.1	81.2	88.0	3-hydroxy-3-methylglutaryl-CoA reductase 2	gbpln	Arabidopsis lyrata	AT2G17370.1 | Symbols: HMG2, HMGR2 | 3-hydroxy-3-methylglutaryl-CoA reductase 2 | chr2:7550007-7551981 FORWARD LENGTH=562	558	562	0	100.7	79.2	87.6
Rsa1.0_01431.1.g26753.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01431.1.g26754.t1	ref|XP_002884054.1| hypothetical protein ARALYDRAFT_480622 [Arabidopsis lyrata subsp. lyrata] gi|297329894|gb|EFH60313.1| hypothetical protein ARALYDRAFT_480622 [Arabidopsis lyrata subsp. lyrata] gi|482567420|gb|EOA31609.1| hypothetical protein CARUB_v10014806mg [Capsella rubella]	182	161	1.00E-87	88.5	87.9	87.9	hypothetical protein ARALYDRAFT_480622	gbpln	Arabidopsis lyrata	AT2G17380.1 | Symbols: AP19 | associated protein 19 | chr2:7553122-7554887 FORWARD LENGTH=161	182	161	2.00E-89	88.5	87.4	87.4
Rsa1.0_01431.1.g26755.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01431.1.g26756.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01431.1.g26757.t1	gb|AAG10812.1|AC018460_6 Putative retroelement polyprotein [Arabidopsis thaliana]	294	1404	1.00E-84	477.6	49.0	53.1	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01432.1.g26758.t1	ref|XP_002876566.1| CYCP3_2 [Arabidopsis lyrata subsp. lyrata] gi|297322404|gb|EFH52825.1| CYCP3_2 [Arabidopsis lyrata subsp. lyrata]	230	227	1.00E-112	98.7	86.1	91.7	CYCP3_2	gbpln	Arabidopsis lyrata	AT3G60550.1 | Symbols: CYCP3;2 | cyclin p3;2 | chr3:22379846-22380641 FORWARD LENGTH=230	230	230	1.00E-111	100.0	87.0	92.6
Rsa1.0_01432.1.g26759.t1	ref|XP_002874461.1| hypothetical protein ARALYDRAFT_351855 [Arabidopsis lyrata subsp. lyrata] gi|297320298|gb|EFH50720.1| hypothetical protein ARALYDRAFT_351855 [Arabidopsis lyrata subsp. lyrata]	512	446	3.00E-13	87.1	10.5	13.9	hypothetical protein ARALYDRAFT_351855	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01432.1.g26760.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01432.1.g26761.t1	dbj|BAJ34282.1| unnamed protein product [Thellungiella halophila]	243	247	1.00E-103	101.6	86.8	91.4	unnamed protein product	----	----	AT3G60530.1 | Symbols: GATA4 | GATA transcription factor 4 | chr3:22373348-22374147 FORWARD LENGTH=240	243	240	2.00E-94	98.8	80.7	87.2
Rsa1.0_01432.1.g26762.t1	ref|XP_002457629.1| hypothetical protein SORBIDRAFT_03g010730 [Sorghum bicolor] gi|241929604|gb|EES02749.1| hypothetical protein SORBIDRAFT_03g010730 [Sorghum bicolor]	97	240	1.00E-10	247.4	36.1	45.4	hypothetical protein SORBIDRAFT_03g010730	gbpln	Sorghum bicolor	AT3G12490.1 | Symbols: ATCYSB, ATCYS6, CYSB | cystatin B | chr3:3960523-3961777 REVERSE LENGTH=201	97	201	1.00E-12	207.2	34.0	41.2
Rsa1.0_01432.1.g26763.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01432.1.g26764.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01432.1.g26765.t1	ref|NP_197389.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|332005241|gb|AED92624.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	184	295	2.00E-31	160.3	45.1	59.8	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	184	295	9.00E-34	160.3	45.1	59.8
Rsa1.0_01433.1.g26766.t1	gb|ADG45874.1| UDP-glucosyltransferase [Isatis tinctoria]	479	476	0	99.4	83.1	90.8	UDP-glucosyltransferase	gbpln	Isatis tinctoria	AT4G15550.1 | Symbols: IAGLU | indole-3-acetate beta-D-glucosyltransferase | chr4:8877877-8879301 REVERSE LENGTH=474	479	474	0	99.0	77.2	88.7

<table>
<tr><td>Rsa1.0_01433.1.g26767.t9</td><td>gb|EOA17272.1| hypothetical protein CARUB_v10005545mg [Capsella rubella]</td><td>282</td><td>257</td><td>1.00E-106</td><td>91.1</td><td>68.1</td><td>74.8</td><td>hypothetical protein CARUB_v10005545mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G15563.1 | Symbols: | unknown protein; Has 36 Blast hits to 36 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:8891771-8892348 FORWARD LENGTH=167</td><td>282</td><td>167</td><td>6.00E-68</td><td>59.2</td><td>44.3</td><td>47.9</td></tr>
<tr><td>Rsa1.0_01433.1.g26768.t1</td><td>ref|NP_193292.3| protein MAGATAMA 3 [Arabidopsis thaliana] gi|384950687|sp|B6SFA4.1|MAA3_ARATH RecName: Full=Probable helicase MAGATAMA 3; AltName: Full=SEN1-like protein gi|209574484|gb|ACI63222.1| MAA3 [Arabidopsis thaliana] gi|332658227|gb|AEE83627.1| probable helicase MAGATAMA 3 [Arabidopsis thaliana]</td><td>815</td><td>818</td><td>0</td><td>100.4</td><td>77.4</td><td>87.1</td><td>protein MAGATAMA 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15570.1 | Symbols: MAA3 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:8893043-8898858 FORWARD LENGTH=818</td><td>815</td><td>818</td><td>0</td><td>100.4</td><td>77.4</td><td>87.1</td></tr>
<tr><td>Rsa1.0_01433.1.g26769.t1</td><td>ref|NP_974004.1| O-methyltransferase-like 2 protein [Arabidopsis thaliana] gi|332194624|gb|AEE32745.1| O-methyltransferase-like 2 protein [Arabidopsis thaliana]</td><td>145</td><td>363</td><td>5.00E-51</td><td>250.3</td><td>69.0</td><td>79.3</td><td>O-methyltransferase-like 2 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G51990.2 | Symbols: | O-methyltransferase family protein | chr1:19330949-19332667 FORWARD LENGTH=363</td><td>145</td><td>363</td><td>1.00E-53</td><td>250.3</td><td>69.0</td><td>79.3</td></tr>
<tr><td>Rsa1.0_01433.1.g26770.t1</td><td>ref|NP_175611.1| O-methyltransferase-like 2 protein [Arabidopsis thaliana] gi|4220447|gb|AAD12674.1| Strong similarity to gb|X74814 cafeic acid 3-O-methyl transferase from Eucalyptus gunnii [Arabidopsis thaliana] gi|332194623|gb|AEE32744.1| O-methyltransferase-like 2 protein [Arabidopsis thaliana]</td><td>367</td><td>363</td><td>1.00E-153</td><td>98.9</td><td>71.4</td><td>83.7</td><td>O-methyltransferase-like 2 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G51990.1 | Symbols: | O-methyltransferase family protein | chr1:19330949-19332667 FORWARD LENGTH=363</td><td>367</td><td>363</td><td>1.00E-156</td><td>98.9</td><td>71.4</td><td>83.7</td></tr>
<tr><td>Rsa1.0_01433.1.g26771.t1</td><td>gb|EOA17718.1| hypothetical protein CARUB_v10006099mg [Capsella rubella]</td><td>102</td><td>102</td><td>4.00E-51</td><td>100.0</td><td>97.1</td><td>97.1</td><td>hypothetical protein CARUB_v10006099mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G15680.1 | Symbols: | Thioredoxin superfamily protein | chr4:8931813-8932121 FORWARD LENGTH=102</td><td>102</td><td>102</td><td>1.00E-53</td><td>100.0</td><td>95.1</td><td>98.0</td></tr>
<tr><td>Rsa1.0_01433.1.g26772.t4</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>1320</td><td>1274</td><td>0</td><td>96.5</td><td>41.8</td><td>52.3</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15680.1 | Symbols: | Thioredoxin superfamily protein | chr4:8931813-8932121 FORWARD LENGTH=102</td><td>1320</td><td>102</td><td>6.00E-51</td><td>7.7</td><td>7.3</td><td>7.3</td></tr>
<tr><td>Rsa1.0_01433.1.g26773.t1</td><td>ref|XP_002870217.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297316053|gb|EFH46476.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]</td><td>96</td><td>102</td><td>1.00E-46</td><td>106.3</td><td>93.8</td><td>96.9</td><td>glutaredoxin family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G15680.1 | Symbols: | Thioredoxin superfamily protein | chr4:8931813-8932121 FORWARD LENGTH=102</td><td>96</td><td>102</td><td>7.00E-49</td><td>106.3</td><td>91.7</td><td>96.9</td></tr>
<tr><td>Rsa1.0_01433.1.g26774.t1</td><td>ref|NP_193308.2| CW-type zinc-finger protein [Arabidopsis thaliana] gi|26450789|dbj|BAC42503.1| unknown protein [Arabidopsis thaliana] gi|30102754|gb|AAP21295.1| At4g15730 [Arabidopsis thaliana] gi|332658241|gb|AEE83641.1| CW-type zinc-finger protein [Arabidopsis thaliana]</td><td>963</td><td>1059</td><td>0</td><td>110.0</td><td>45.8</td><td>52.9</td><td>CW-type zinc-finger protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15730.1 | Symbols: | CW-type Zinc Finger | chr4:8951887-8957214 REVERSE LENGTH=1059</td><td>963</td><td>1059</td><td>0</td><td>110.0</td><td>45.8</td><td>52.9</td></tr>
<tr><td>Rsa1.0_01434.1.g26775.t1</td><td>gb|EOA31605.1| hypothetical protein CARUB_v10014801mg [Capsella rubella]</td><td>160</td><td>163</td><td>6.00E-63</td><td>101.9</td><td>81.9</td><td>88.8</td><td>hypothetical protein CARUB_v10014801mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G12630.1 | Symbols: | A20/AN1-like zinc finger family protein | chr3:4012707-4013189 FORWARD LENGTH=160</td><td>160</td><td>160</td><td>5.00E-62</td><td>100.0</td><td>81.3</td><td>88.1</td></tr>
<tr><td>Rsa1.0_01434.1.g26776.t1</td><td>ref|XP_002882784.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328624|gb|EFH59043.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>625</td><td>664</td><td>0</td><td>106.2</td><td>76.3</td><td>84.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G12640.1 | Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr3:4014455-4017675 FORWARD LENGTH=638</td><td>625</td><td>638</td><td>0</td><td>102.1</td><td>72.5</td><td>80.6</td></tr>
<tr><td>Rsa1.0_01434.1.g26777.t1</td><td>gb|EOA32788.1| hypothetical protein CARUB_v10016097mg [Capsella rubella]</td><td>236</td><td>238</td><td>1.00E-100</td><td>100.8</td><td>79.2</td><td>87.3</td><td>hypothetical protein CARUB_v10016097mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G12650.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; Has 31 Blast hits to 31 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4017881-4018597 REVERSE LENGTH=238</td><td>236</td><td>238</td><td>3.00E-96</td><td>100.8</td><td>77.5</td><td>85.6</td></tr>
<tr><td>Rsa1.0_01434.1.g26778.t1</td><td>gb|ABK28554.1| unknown [Arabidopsis thaliana]</td><td>268</td><td>256</td><td>6.00E-61</td><td>95.5</td><td>53.7</td><td>65.3</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G12660.1 | Symbols: FLA14 | FASCICLIN-like arabinogalactan protein 14 precursor | chr3:4019060-4019827 FORWARD LENGTH=255</td><td>268</td><td>255</td><td>2.00E-63</td><td>95.1</td><td>53.7</td><td>65.3</td></tr>
</table>

Rsa1.0_01434.1.g26779.t1	gb|AAB71467.1| Similar to Saccharomyces RAD16 (gb|X78993) [Arabidopsis thaliana]	210	822	9.00E-35	391.4	34.8	37.1	Similar to Saccharomyces RAD16 (gb|X78993)	gbpln	Arabidopsis thaliana	AT1G05120.1 | Symbols: | Helicase protein with RING/U-box domain | chr1:1471624-1476067 REVERSE LENGTH=833	210	833	4.00E-37	396.7	34.8	37.1
Rsa1.0_01434.1.g26780.t1	gb|EOA30178.1| hypothetical protein CARUB_v10013294mg [Capsella rubella]	615	592	0	96.3	88.9	92.2	hypothetical protein CARUB_v10013294mg	gbpln	Capsella rubella	AT3G12670.1 | Symbols: emb2742 | CTP synthase family protein | chr3:4020351-4024086 REVERSE LENGTH=591	615	591	0	96.1	89.4	92.2
Rsa1.0_01434.1.g26781.t1	gb|EOA30566.1| hypothetical protein CARUB_v10013693mg [Capsella rubella]	481	448	0	93.1	71.3	80.0	hypothetical protein CARUB_v10013693mg	gbpln	Capsella rubella	AT3G12700.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:4037136-4039043 FORWARD LENGTH=461	481	461	0	95.8	71.3	78.4
Rsa1.0_01434.1.g26782.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01434.1.g26783.t1	gb|EOA30935.1| hypothetical protein CARUB_v10014082mg [Capsella rubella]	349	349	1.00E-170	100.0	81.4	87.1	hypothetical protein CARUB_v10014082mg	gbpln	Capsella rubella	AT3G12740.1 | Symbols: ALIS1 | ALA-interacting subunit 1 | chr3:4049739-4051561 FORWARD LENGTH=350	349	350	1.00E-168	100.3	79.4	86.0
Rsa1.0_01434.1.g26784.t4	ref|NP_566436.1| uncharacterized protein [Arabidopsis thaliana] gi|11994418|dbj|BAB02420.1| unnamed protein product [Arabidopsis thaliana] gi|23297357|gb|AAN12949.1| unknown protein [Arabidopsis thaliana] gi|332641722|gb|AEE75243.1| uncharacterized protein AT3G12760 [Arabidopsis thaliana]	315	250	1.00E-128	79.4	72.4	76.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G12760.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Defective-in-cullin neddylation protein (InterPro:IPR014764), Protein of unknown function DUF298 (InterPro:IPR005176), UBA-like (InterPro:IPR009060); BEST Arabidopsis thaliana protein match is: Domain of unknown function (DUF298) (TAIR:AT1G15860.2); Has 857 Blast hits to 855 proteins in 202 species: Archae - 0; Bacteria - 0; Metazoa - 482; Fungi - 154; Plants - 139; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink). | chr3:4054963-4056826 FORWARD LENGTH=250	315	250	1.00E-130	79.4	72.4	76.2
Rsa1.0_01434.1.g26785.t1	dbj|BAB02422.1| unnamed protein product [Arabidopsis thaliana]	415	390	1.00E-108	94.0	48.4	60.0	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G12775.1 | Symbols: | ubiquitin-conjugating enzyme family protein | chr3:4059772-4060944 FORWARD LENGTH=362	415	362	1.00E-101	87.2	44.8	54.7
Rsa1.0_01434.1.g26786.t1	gb|EOA30457.1| hypothetical protein CARUB_v10013582mg [Capsella rubella]	480	481	0	100.2	93.3	96.0	hypothetical protein CARUB_v10013582mg	gbpln	Capsella rubella	AT3G12780.1 | Symbols: PGK1 | phosphoglycerate kinase 1 | chr3:4061127-4063140 REVERSE LENGTH=481	480	481	0	100.2	93.3	95.4
Rsa1.0_01434.1.g26787.t1	gb|EOA29809.1| hypothetical protein CARUB_v10012903mg [Capsella rubella]	836	964	0	115.3	66.3	74.9	hypothetical protein CARUB_v10012903mg	gbpln	Capsella rubella	AT3G11010.1 | Symbols: AtRLP34, RLP34 | receptor like protein 34 | chr3:3450988-3453672 REVERSE LENGTH=894	836	894	0	106.9	66.9	75.0
Rsa1.0_01434.1.g26788.t1	gb|EOA31122.1| hypothetical protein CARUB_v10014282mg [Capsella rubella]	73	298	2.00E-31	408.2	90.4	97.3	hypothetical protein CARUB_v10014282mg	gbpln	Capsella rubella	AT3G12800.1 | Symbols: SDRB, DECR | short-chain dehydrogenase-reductase B | chr3:4063463-4064757 REVERSE LENGTH=298	73	298	1.00E-33	408.2	89.0	97.3
Rsa1.0_01435.1.g26789.t1	ref|XP_002891526.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata] gi|297337368|gb|EFH67785.1| hypothetical protein ARALYDRAFT_337115 [Arabidopsis lyrata subsp. lyrata]	361	824	2.00E-30	228.3	23.5	30.2	hypothetical protein ARALYDRAFT_337115	gbpln	Arabidopsis lyrata	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	361	452	3.00E-30	125.2	21.9	33.0
Rsa1.0_01435.1.g26790.t1	gb|EOA38027.1| hypothetical protein CARUB_v10009497mg [Capsella rubella]	356	369	1.00E-171	103.7	87.1	92.1	hypothetical protein CARUB_v10009497mg	gbpln	Capsella rubella	AT1G09540.1 | Symbols: MYB61, ATMYB61 | myb domain protein 61 | chr1:3086333-3087689 FORWARD LENGTH=366	356	366	1.00E-165	102.8	87.6	91.0
Rsa1.0_01435.1.g26791.t3	gb|EOA38926.1| hypothetical protein CARUB_v10011324mg [Capsella rubella]	409	391	1.00E-138	95.6	62.6	72.1	hypothetical protein CARUB_v10011324mg	gbpln	Capsella rubella	AT1G09550.1 | Symbols: | Pectinacetylesterase family protein | chr1:3089733-3092254 REVERSE LENGTH=388	409	388	1.00E-139	94.9	62.8	71.6
Rsa1.0_01435.1.g26792.t1	ref|XP_002889758.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335600|gb|EFH66017.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	220	219	1.00E-102	99.5	85.5	92.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G09560.1 | Symbols: GLP5 | germin-like protein 5 | chr1:3093896-3094639 FORWARD LENGTH=219	220	219	1.00E-104	99.5	85.9	92.7
Rsa1.0_01435.1.g26793.t1	gb|EOA38463.1| hypothetical protein CARUB_v10010159mg, partial [Capsella rubella]	213	238	1.00E-101	111.7	80.8	92.0	hypothetical protein CARUB_v10010159mg, partial	gbpln	Capsella rubella	AT1G09580.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:3104657-3106092 FORWARD LENGTH=217	213	217	1.00E-102	101.9	79.8	91.1
Rsa1.0_01435.1.g26794.t1	ref|XP_002889760.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata] gi|297335602|gb|EFH66019.1| 60S ribosomal protein L21 [Arabidopsis lyrata subsp. lyrata]	164	164	1.00E-88	100.0	98.2	98.8	60S ribosomal protein L21	gbpln	Arabidopsis lyrata	AT1G09690.1 | Symbols: | Translation protein SH3-like family protein | chr1:3136407-3137430 REVERSE LENGTH=164	164	164	2.00E-90	100.0	97.0	98.2
Rsa1.0_01435.1.g26795.t1	gb|AAC33218.1| Similar to cdc2 protein kinases [Arabidopsis thaliana]	952	967	0	101.6	78.0	84.2	Similar to cdc2 protein kinases	gbpln	Arabidopsis thaliana	AT1G09600.1 | Symbols: | Protein kinase superfamily protein | chr1:3108617-3111318 FORWARD LENGTH=714	952	714	0	75.0	51.7	56.0
Rsa1.0_01435.1.g26796.t14	ref|XP_002892512.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297338354|gb|EFH68771.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	1185	1091	0	92.1	70.5	74.6	ATP binding protein	gbpln	Arabidopsis lyrata	AT1G09620.1 | Symbols: | ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases | chr1:3113077-3116455 REVERSE LENGTH=1091	1185	1091	0	92.1	67.8	72.9

Rsa1.0_01435.1.g26797.t1	ref|XP_002889762.1| hypothetical protein ARALYDRAFT_471063 [Arabidopsis lyrata subsp. lyrata] gi|297335604|gb|EFH66021.1| hypothetical protein ARALYDRAFT_471063 [Arabidopsis lyrata subsp. lyrata]	413	414	0	100.2	87.7	94.2	hypothetical protein ARALYDRAFT_471063	gbpln	Arabidopsis lyrata	AT1G09640.1 | Symbols: | Translation elongation factor EF1B, gamma chain | chr1:3120162-3122152 FORWARD LENGTH=414	413	414	0	100.2	86.7	94.2
Rsa1.0_01435.1.g26798.t2	ref|NP_563848.1| elongation factor EF-1 gamma subunit [Arabidopsis thaliana] gi|13626364|sp|O04487.1|EF1G1_ARATH RecName: Full=Probable elongation factor 1-gamma 1; Short=EF-1-gamma 1; AltName: Full=eEF-1B gamma 1 gi|2160158|gb|AAB60721.1| Similar to elongation factor 1-gamma (gb|EF1G_XENLA). ESTs gb|T20564,gb|T45940,gb|T04527 come from this gene [Arabidopsis thaliana] gi|222424502|dbj|BAH20206.1| AT1G09640 [Arabidopsis thaliana] gi|332190351|gb|AEE28472.1| elongation factor EF-1 gamma subunit [Arabidopsis thaliana]	413	414	0	100.2	85.7	93.0	elongation factor EF-1 gamma subunit	gbpln	Arabidopsis thaliana	AT1G09640.1 | Symbols: | Translation elongation factor EF1B, gamma chain | chr1:3120162-3122152 FORWARD LENGTH=414	413	414	0	100.2	85.7	93.0
Rsa1.0_01435.1.g26799.t1	ref|XP_002877446.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323284|gb|EFH53705.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	127	132	4.00E-14	103.9	39.4	55.9	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01436.1.g26800.t10	gb|EOA38142.1| hypothetical protein CARUB_v10009614mg [Capsella rubella]	488	346	1.00E-152	70.9	57.8	63.9	hypothetical protein CARUB_v10009614mg	gbpln	Capsella rubella	AT1G54180.1 | Symbols: ATBRXL3, BRX-LIKE3 | BREVIS RADIX-like 3 | chr1:20227697-20229728 FORWARD LENGTH=370	488	370	1.00E-149	75.8	58.2	64.1
Rsa1.0_01436.1.g26801.t2	ref|XP_002894481.1| ctc-interacting domain 3 [Arabidopsis lyrata subsp. lyrata] gi|297340323|gb|EFH70740.1| ctc-interacting domain 3 [Arabidopsis lyrata subsp. lyrata]	590	587	0	99.5	70.7	78.1	ctc-interacting domain 3	gbpln	Arabidopsis lyrata	AT1G54170.1 | Symbols: CID3 | CTC-interacting domain 3 | chr1:20221353-20224919 REVERSE LENGTH=587	590	587	0	99.5	67.6	76.3
Rsa1.0_01436.1.g26802.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01436.1.g26803.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1415	1223	0	86.4	41.2	54.9	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1415	746	7.00E-80	52.7	10.8	14.5
Rsa1.0_01436.1.g26804.t1	ref|NP_175818.1| nuclear transcription factor Y subunit A-5 [Arabidopsis thaliana] gi|75213441|sp|Q9SYH4.1|NFYA5_ARATH RecName: Full=Nuclear transcription factor Y subunit A-5; Short=AtNF-YA-5 gi|4587559|gb|AAD25790.1|AC006577_26 Contains similarity to gb|Y13722 Hap2c Transcription factor from Arabidopsis thaliana [Arabidopsis thaliana] gi|14423440|gb|AAK62402.1|AF386957_1 Unknown protein [Arabidopsis thaliana] gi|20148233|gb|AAM10007.1| unknown protein [Arabidopsis thaliana] gi|332194935|gb|AEE33056.1| nuclear transcription factor Y subunit A-5 [Arabidopsis thaliana]	281	308	2.00E-96	109.6	74.0	79.0	nuclear transcription factor Y subunit A-5	gbpln	Arabidopsis thaliana	AT1G54160.1 | Symbols: NFYA5, NF-YA5 | nuclear factor Y, subunit A5 | chr1:20217581-20218706 REVERSE LENGTH=308	281	308	4.00E-99	109.6	74.0	79.0
Rsa1.0_01436.1.g26805.t1	ref|XP_002891793.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297337635|gb|EFH68052.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	384	378	1.00E-155	98.4	73.4	83.1	zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G54150.1 | Symbols: | E3 Ubiquitin ligase family protein | chr1:20215480-20217303 FORWARD LENGTH=383	384	383	1.00E-157	99.7	73.7	83.1
Rsa1.0_01436.1.g26806.t1	ref|NP_564652.2| RELA/SPOT homolog 3 [Arabidopsis thaliana] gi|4587556|gb|AAD25787.1|AC006577_23 Similar to gi|1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb|D90911. EST gb|W43807 comes from this gene [Arabidopsis thaliana] gi|110742595|dbj|BAE99211.1| RSH3 [Arabidopsis thaliana] gi|332194932|gb|AEE33053.1| RELA/SPOT homolog 3 [Arabidopsis thaliana]	652	715	0	109.7	86.5	92.5	RELA/SPOT homolog 3	gbpln	Arabidopsis thaliana	AT1G54130.1 | Symbols: RSH3, AT-RSH3, ATRSH3 | RELA/SPOT homolog 3 | chr1:20211177-20213761 FORWARD LENGTH=715	652	715	0	109.7	86.5	92.5

Rsa1.0_01436.1.g26807.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	274	1142	5.00E-66	416.8	47.4	63.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	274	575	4.00E-28	209.9	29.9	50.7
Rsa1.0_01437.1.g26808.t1	gb|ACG60672.1| unknown protein [Brassica oleracea var. alboglabra]	163	288	7.00E-30	176.7	44.8	66.3	unknown protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01437.1.g26809.t1	ref|XP_002864686.1| MADS-box protein [Arabidopsis lyrata subsp. lyrata] gi|297310521|gb|EFH40945.1| MADS-box protein [Arabidopsis lyrata subsp. lyrata]	191	291	1.00E-40	152.4	50.3	64.9	MADS-box protein	gbpln	Arabidopsis lyrata	AT5G60440.1 | Symbols: AGL62 | AGAMOUS-like 62 | chr5:24306329-24307520 FORWARD LENGTH=299	191	299	4.00E-39	156.5	48.2	63.9
Rsa1.0_01437.1.g26810.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01437.1.g26811.t1	ref|XP_002864686.1| MADS-box protein [Arabidopsis lyrata subsp. lyrata] gi|297310521|gb|EFH40945.1| MADS-box protein [Arabidopsis lyrata subsp. lyrata]	265	291	1.00E-60	109.8	53.6	71.7	MADS-box protein	gbpln	Arabidopsis lyrata	AT5G60440.1 | Symbols: AGL62 | AGAMOUS-like 62 | chr5:24306329-24307520 FORWARD LENGTH=299	265	299	2.00E-62	112.8	54.0	71.3
Rsa1.0_01437.1.g26812.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01437.1.g26813.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	1534	1489	0	97.1	55.3	70.3	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1534	1262	1.00E-164	82.3	18.5	23.9
Rsa1.0_01437.1.g26814.t2	ref|XP_002864685.1| ATSIZ1/SIZ1 [Arabidopsis lyrata subsp. lyrata] gi|297310520|gb|EFH40944.1| ATSIZ1/SIZ1 [Arabidopsis lyrata subsp. lyrata]	882	898	0	101.8	84.0	90.0	ATSIZ1/SIZ1	gbpln	Arabidopsis lyrata	AT5G60410.5 | Symbols: ATSIZ1, SIZ1 | DNA-binding protein with MIZ/SP-RING zinc finger, PHD-finger and SAP domain | chr5:24295226-24300792 FORWARD LENGTH=885	882	885	0	100.3	83.2	89.1
Rsa1.0_01437.1.g26815.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01438.1.g26816.t1	ref|XP_002876790.1| hypothetical protein ARALYDRAFT_904415 [Arabidopsis lyrata subsp. lyrata] gi|297322628|gb|EFH53049.1| hypothetical protein ARALYDRAFT_904415 [Arabidopsis lyrata subsp. lyrata]	337	592	4.00E-88	175.7	46.9	47.2	hypothetical protein ARALYDRAFT_904415	gbpln	Arabidopsis lyrata	AT2G01970.1 | Symbols: | Endomembrane protein 70 protein family | chr2:452197-454819 REVERSE LENGTH=592	337	592	5.00E-89	175.7	46.3	46.9
Rsa1.0_01438.1.g26817.t28	gb|ACA50526.1| putative salt overly sensitive 1 [Brassica napus]	1158	1142	0	98.6	92.9	94.6	putative salt overly sensitive 1	gbpln	Brassica napus	AT2G01980.1 | Symbols: SOS1, ATSOS1, ATNHX7 | sodium proton exchanger, putative (NHX7) (SOS1) | chr2:457070-463145 FORWARD LENGTH=1146	1158	1146	0	99.0	81.2	87.9
Rsa1.0_01438.1.g26818.t1	gb|ACQ90595.1| putative glutamate decarboxylase [Eutrema halophilum]	493	493	0	100.0	97.0	98.6	putative glutamate decarboxylase	gbpln	Eutrema halophilum	AT2G02010.1 | Symbols: GAD4 | glutamate decarboxylase 4 | chr2:474375-476495 REVERSE LENGTH=493	493	493	0	100.0	95.7	97.2
Rsa1.0_01438.1.g26819.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01438.1.g26820.t1	gb|ACQ90596.1| putative peptide transporter [Eutrema halophilum]	576	631	0	109.5	76.4	85.6	putative peptide transporter	gbpln	Eutrema halophilum	AT1G62200.1 | Symbols: | Major facilitator superfamily protein | chr1:22982147-22984334 REVERSE LENGTH=590	576	590	0	102.4	74.0	86.1
Rsa1.0_01438.1.g26821.t1	ref|NP_178313.1| peptide transporter PTR2 [Arabidopsis thaliana] gi|1172704|sp|P46032.1|PTR2_ARATH RecName: Full=Peptide transporter PTR2; AltName: Full=Histidine-transporting protein gi|13937185|gb|AAK50086.1|AF372946_1 At2g02040/F14H20.11 [Arabidopsis thaliana] gi|633940|gb|AAB00858.1| transport protein [Arabidopsis thaliana] gi|4406786|gb|AAD20096.1| histidine transport protein (PTR2-B) [Arabidopsis thaliana] gi|23506067|gb|AAN28893.1| At2g02040/F14H20.11 [Arabidopsis thaliana] gi|330250444|gb|AEC05538.1| peptide transporter PTR2 [Arabidopsis thaliana]	583	585	0	100.3	95.0	97.9	peptide transporter PTR2	gbpln	Arabidopsis thaliana	AT2G02040.1 | Symbols: ATPTR2-B, NTR1, PTR2-B, PTR2, ATPTR2 | peptide transporter 2 | chr2:487542-489707 FORWARD LENGTH=585	583	585	0	100.3	95.0	97.9
Rsa1.0_01438.1.g26822.t1	gb|ACQ90599.1| putative NADH dehydrogenase [Eutrema halophilum]	103	102	3.00E-51	99.0	98.1	99.0	putative NADH dehydrogenase	gbpln	Eutrema halophilum	AT2G02050.1 | Symbols: | NADH-ubiquinone oxidoreductase B18 subunit, putative | chr2:490024-490335 FORWARD LENGTH=103	103	103	2.00E-49	100.0	88.3	93.2
Rsa1.0_01438.1.g26823.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01439.1.g26824.t3	ref|XP_002876038.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297321876|gb|EFH52297.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	1440	1579	0	109.7	67.0	69.5	transducin family protein	gbpln	Arabidopsis lyrata	AT3G50590.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:18771292-18779220 FORWARD LENGTH=1614	1440	1614	0	112.1	67.2	69.8

Rsa1.0_01439.1.g26825.t1	ref|XP_002870946.1| hypothetical protein ARALYDRAFT_486978 [Arabidopsis lyrata subsp. lyrata] gi|297316783|gb|EFH47205.1| hypothetical protein ARALYDRAFT_486978 [Arabidopsis lyrata subsp. lyrata]	99	546	2.00E-16	551.5	57.6	67.7	hypothetical protein ARALYDRAFT_486978	gbpln	Arabidopsis lyrata	AT5G02010.1 | Symbols: ATROPGEF7, ROPGEF7 | RHO guanyl-nucleotide exchange factor 7 | chr5:383493-385698 FORWARD LENGTH=546	99	546	9.00E-14	551.5	52.5	63.6
Rsa1.0_01439.1.g26826.t1	ref|XP_002877752.1| hypothetical protein ARALYDRAFT_485404 [Arabidopsis lyrata subsp. lyrata] gi|297323590|gb|EFH54011.1| hypothetical protein ARALYDRAFT_485404 [Arabidopsis lyrata subsp. lyrata]	231	189	1.00E-75	81.8	63.6	73.2	hypothetical protein ARALYDRAFT_485404	gbpln	Arabidopsis lyrata	AT3G50570.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr3:18766918-18767487 REVERSE LENGTH=189	231	189	6.00E-72	81.8	64.1	71.4
Rsa1.0_01439.1.g26827.t1	gb|EOA24556.1| hypothetical protein CARUB_v10017814mg [Capsella rubella]	273	275	1.00E-137	100.7	94.5	96.3	hypothetical protein CARUB_v10017814mg	gbpln	Capsella rubella	AT3G50560.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:18761247-18763835 REVERSE LENGTH=272	273	272	1.00E-137	99.6	93.4	94.9
Rsa1.0_01439.1.g26828.t1	ref|XP_002876036.1| hypothetical protein ARALYDRAFT_485401 [Arabidopsis lyrata subsp. lyrata] gi|297321874|gb|EFH52295.1| hypothetical protein ARALYDRAFT_485401 [Arabidopsis lyrata subsp. lyrata]	601	597	0	99.3	92.3	94.3	hypothetical protein ARALYDRAFT_485401	gbpln	Arabidopsis lyrata	AT3G50530.1 | Symbols: CRK | CDPK-related kinase | chr3:18753833-18756487 FORWARD LENGTH=601	601	601	0	100.0	91.8	94.3
Rsa1.0_01440.1.g26829.t2	ref|XP_002884859.1| hypothetical protein ARALYDRAFT_478516 [Arabidopsis lyrata subsp. lyrata] gi|297330699|gb|EFH61118.1| hypothetical protein ARALYDRAFT_478516 [Arabidopsis lyrata subsp. lyrata]	395	625	1.00E-175	158.2	82.3	89.4	hypothetical protein ARALYDRAFT_478516	gbpln	Arabidopsis lyrata	AT3G11710.1 | Symbols: ATKRS-1 | lysyl-tRNA synthetase 1 | chr3:3702359-3705613 REVERSE LENGTH=626	395	626	1.00E-176	158.5	80.0	88.9
Rsa1.0_01440.1.g26830.t1	ref|XP_002884860.1| hypothetical protein ARALYDRAFT_478517 [Arabidopsis lyrata subsp. lyrata] gi|297330700|gb|EFH61119.1| hypothetical protein ARALYDRAFT_478517 [Arabidopsis lyrata subsp. lyrata]	537	545	0	101.5	66.1	78.6	hypothetical protein ARALYDRAFT_478517	gbpln	Arabidopsis lyrata	AT3G11720.3 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr3:3705991-3708721 REVERSE LENGTH=596	537	596	0	111.0	65.9	78.6
Rsa1.0_01440.1.g26831.t1	ref|XP_002884863.1| hypothetical protein ARALYDRAFT_478521 [Arabidopsis lyrata subsp. lyrata] gi|297330703|gb|EFH61122.1| hypothetical protein ARALYDRAFT_478521 [Arabidopsis lyrata subsp. lyrata]	153	146	2.00E-58	95.4	78.4	84.3	hypothetical protein ARALYDRAFT_478521	gbpln	Arabidopsis lyrata	AT3G11750.1 | Symbols: FOLB1 | Dihydroneopterin aldolase | chr3:3715071-3715904 REVERSE LENGTH=146	153	146	8.00E-60	95.4	76.5	83.0
Rsa1.0_01440.1.g26832.t1	ref|NP_187783.1| DnaQ-like 3'-5' exonuclease domain-containing protein [Arabidopsis thaliana] gi|6671933|gb|AAF23193.1|AC016795_6 unknown protein [Arabidopsis thaliana] gi|27808516|gb|AAO24538.1| At3g11770 [Arabidopsis thaliana] gi|110736243|dbj|BAF00092.1| hypothetical protein [Arabidopsis thaliana] gi|332641574|gb|AEE75095.1| DnaQ-like 3'-5' exonuclease domain-containing protein [Arabidopsis thaliana]	201	200	2.00E-99	99.5	88.1	92.5	DnaQ-like 3'-5' exonuclease domain-containing protein	gbpln	Arabidopsis thaliana	AT3G11770.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr3:3721490-3722092 REVERSE LENGTH=200	201	200	1.00E-102	99.5	88.1	92.5
Rsa1.0_01440.1.g26833.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01440.1.g26834.t1	ref|NP_566400.1| MD-2-related lipid recognition domain-containing protein [Arabidopsis thaliana] gi|6671934|gb|AAF23194.1|AC016795_7 unknown protein [Arabidopsis thaliana] gi|14334430|gb|AAK59413.1| unknown protein [Arabidopsis thaliana] gi|28393843|gb|AAO42329.1| unknown protein [Arabidopsis thaliana] gi|332641577|gb|AEE75098.1| MD-2-related lipid recognition domain-containing protein [Arabidopsis thaliana]	133	153	2.00E-46	115.0	68.4	76.7	MD-2-related lipid recognition domain-containing protein	gbpln	Arabidopsis thaliana	AT3G11780.1 | Symbols: | MD-2-related lipid recognition domain-containing protein / ML domain-containing protein | chr3:3724326-3725476 REVERSE LENGTH=153	133	153	4.00E-49	115.0	68.4	76.7

Rsa1.0_01440.1.g26835.t2	gb|EOA31323.1| hypothetical protein CARUB_v10014494mg [Capsella rubella]	289	244	1.00E-113	84.4	73.0	79.9	hypothetical protein CARUB_v10014494mg	gbpln	Capsella rubella	AT3G11800.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G44150.1); Has 74 Blast hits to 73 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 72; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr3:3726154-3727562 FORWARD LENGTH=246	289	246	1.00E-113	85.1	71.6	79.6
Rsa1.0_01440.1.g26836.t1	gb|EOA32683.1| hypothetical protein CARUB_v10015981mg [Capsella rubella]	317	333	5.00E-66	105.0	48.6	60.9	hypothetical protein CARUB_v10015981mg	gbpln	Capsella rubella	AT2G40210.1 | Symbols: AGL48 | AGAMOUS-like 48 | chr2:16793213-16794328 REVERSE LENGTH=371	317	371	5.00E-64	117.0	47.3	63.7
Rsa1.0_01440.1.g26837.t1	ref|XP_002884867.1| SYP121 [Arabidopsis lyrata subsp. lyrata] gi|297330707|gb|EFH61126.1| SYP121 [Arabidopsis lyrata subsp. lyrata]	336	342	1.00E-149	101.8	87.2	90.8	SYP121	gbpln	Arabidopsis lyrata	AT3G11820.1 | Symbols: SYP121, AT-SYR1, ATSYP121, SYR1, ATSYR1, PEN1 | syntaxin of plants 121 | chr3:3729540-3730868 REVERSE LENGTH=346	336	346	1.00E-145	103.0	89.0	93.2
Rsa1.0_01440.1.g26838.t1	ref|NP_187789.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana] gi|6671939|gb|AAF23199.1|AC016795_12 putative T-complex protein 1, ETA subunit [Arabidopsis thaliana] gi|17979243|gb|AAL49938.1| AT3g11830/F26K24_12 [Arabidopsis thaliana] gi|20857172|gb|AAM26704.1| AT3g11830/F26K24_12 [Arabidopsis thaliana] gi|332641584|gb|AEE75105.1| TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]	547	557	0	101.8	94.7	95.4	TCP-1/cpn60 chaperonin family protein	gbpln	Arabidopsis thaliana	AT3G11830.1 | Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:3732734-3736156 FORWARD LENGTH=557	547	557	0	101.8	94.7	95.4
Rsa1.0_01440.1.g26839.t1	ref|XP_002884868.1| U-box domain-containing protein 24 [Arabidopsis lyrata subsp. lyrata] gi|297330708|gb|EFH61127.1| U-box domain-containing protein 24 [Arabidopsis lyrata subsp. lyrata]	473	463	0	97.9	78.6	88.4	U-box domain-containing protein 24	gbpln	Arabidopsis lyrata	AT3G11840.1 | Symbols: PUB24 | plant U-box 24 | chr3:3736578-3738250 REVERSE LENGTH=470	473	470	0	99.4	77.2	86.7
Rsa1.0_01440.1.g26840.t2	gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]	348	543	1.00E-28	156.0	17.8	27.6	hypothetical protein CARUB_v10015730mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	348	566	4.00E-24	162.6	15.2	27.9
Rsa1.0_01440.1.g26841.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	522	490	1.00E-88	93.9	36.2	56.3	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	522	566	3.00E-84	108.4	32.2	55.6
Rsa1.0_01440.1.g26842.t1	gb|ABD65063.1| hypothetical protein 27.t00041 [Brassica oleracea]	195	198	4.00E-45	101.5	52.8	70.3	hypothetical protein 27.t00041	gbpln	Brassica oleracea	AT2G35280.1 | Symbols: | F-box family protein | chr2:14859709-14860200 REVERSE LENGTH=163	195	163	2.00E-14	83.6	17.9	29.7
Rsa1.0_01440.1.g26843.t1	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	768	1752	0	228.1	41.1	54.3	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01441.1.g26844.t1	ref|NP_177294.1| endoglucanase 9 [Arabidopsis thaliana] gi|75169715|sp|Q9C9H5.1|GUN9_ARATH RecName: Full=Endoglucanase 9; AltName: Full=Cellulase 3; Short=AtCEL3; AltName: Full=Endo-1,4-beta glucanase 9; Flags: Precursor gi|12323721|gb|AAG51817.1|AC016163_6 putative beta-glucanase; 74324-76084 [Arabidopsis thaliana] gi|111074386|gb|ABH04566.1| At1g71380 [Arabidopsis thaliana] gi|332197074|gb|AEE35195.1| endoglucanase 9 [Arabidopsis thaliana]	449	484	1.00E-115	107.8	49.7	56.3	endoglucanase 9	gbpln	Arabidopsis thaliana	AT1G71380.1 | Symbols: ATGH9B3, ATCEL3, CEL3 | cellulase 3 | chr1:26899989-26901749 REVERSE LENGTH=484	449	484	1.00E-118	107.8	49.7	56.3
Rsa1.0_01441.1.g26845.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01441.1.g26846.t2	ref|NP_177294.1| endoglucanase 9 [Arabidopsis thaliana] gi|75169715|sp|Q9C9H5.1|GUN9_ARATH RecName: Full=Endoglucanase 9; AltName: Full=Cellulase 3; Short=AtCEL3; AltName: Full=Endo-1,4-beta glucanase 9; Flags: Precursor gi|12323721|gb|AAG51817.1|AC016163_6 putative beta-glucanase; 74324-76084 [Arabidopsis thaliana] gi|111074386|gb|ABH04566.1| At1g71380 [Arabidopsis thaliana] gi|332197074|gb|AEE35195.1| endoglucanase 9 [Arabidopsis thaliana]	449	484	1.00E-175	107.8	72.8	84.0	endoglucanase 9	gbpln	Arabidopsis thaliana	AT1G71380.1 | Symbols: ATGH9B3, ATCEL3, CEL3 | cellulase 3 | chr1:26899989-26901749 REVERSE LENGTH=484	449	484	1.00E-178	107.8	72.8	84.0
Rsa1.0_01441.1.g26847.t1	ref|XP_002888846.1| hypothetical protein ARALYDRAFT_339396 [Arabidopsis lyrata subsp. lyrata] gi|297334687|gb|EFH65105.1| hypothetical protein ARALYDRAFT_339396 [Arabidopsis lyrata subsp. lyrata]	672	685	0	101.9	78.7	86.3	hypothetical protein ARALYDRAFT_339396	gbpln	Arabidopsis lyrata	AT1G71770.2 | Symbols: PAB5 | poly(A)-binding protein 5 | chr1:26990777-26993489 REVERSE LENGTH=682	672	682	0	101.5	76.2	84.4
Rsa1.0_01441.1.g26848.t1	gb|EOA34351.1| hypothetical protein CARUB_v10021875mg [Capsella rubella]	461	458	0	99.3	80.0	85.0	hypothetical protein CARUB_v10021875mg	gbpln	Capsella rubella	AT1G71800.1 | Symbols: CSTF64 | cleavage stimulating factor 64 | chr1:26999606-27001850 FORWARD LENGTH=461	461	461	0	100.0	77.0	82.6
Rsa1.0_01441.1.g26849.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01441.1.g26850.t1	ref|NP_850465.1| cytochrome P450, family 709, subfamily B, polypeptide 1 [Arabidopsis thaliana] gi|330255683|gb|AEC10777.1| cytochrome P450, family 709, subfamily B, polypeptide 1 [Arabidopsis thaliana]	239	403	1.00E-105	168.6	74.9	89.1	cytochrome P450, family 709, subfamily B, polypeptide 1	gbpln	Arabidopsis thaliana	AT2G46960.1 | Symbols: CYP709B1 | cytochrome P450, family 709, subfamily B, polypeptide 1 | chr2:19292295-19293765 REVERSE LENGTH=403	239	403	1.00E-108	168.6	74.9	89.1
Rsa1.0_01442.1.g26851.t1	ref|NP_176809.1| DELLA protein RGL1 [Arabidopsis thaliana] gi|75169613|sp|Q9C8Y3.1|RGL1_ARATH RecName: Full=DELLA protein RGL1; AltName: Full=GRAS family protein 9; Short=AtGRAS-9; AltName: Full=RGA-like protein 1; Short=RGA-like protein gi|12324404|gb|AAG52171.1|AC020665_16 gibberellin regulatory protein, putative; 49974-51509 [Arabidopsis thaliana] gi|15777857|gb|AAL05911.1| RGL1 protein [Arabidopsis thaliana] gi|17979049|gb|AAL49792.1| putative gibberellin regulatory protein [Arabidopsis thaliana] gi|20465941|gb|AAM20156.1| putative gibberellin regulatory protein [Arabidopsis thaliana] gi|332196378|gb|AEE34499.1| DELLA protein RGL1 [Arabidopsis thaliana]	464	511	0	110.1	86.0	90.5	DELLA protein RGL1	gbpln	Arabidopsis thaliana	AT1G66350.1 | Symbols: RGL1, RGL | RGA-like 1 | chr1:24748327-24749862 FORWARD LENGTH=511	464	511	0	110.1	86.0	90.5
Rsa1.0_01442.1.g26852.t1	ref|NP_849849.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|122215314|sp|Q3ECH5.1|PP107_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g66345, mitochondrial; Flags: Precursor gi|332196377|gb|AEE34498.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	543	544	0	100.2	73.5	86.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G66345.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:24737719-24739353 FORWARD LENGTH=544	543	544	0	100.2	73.5	86.6
Rsa1.0_01442.1.g26853.t1	ref|XP_002888495.1| hypothetical protein ARALYDRAFT_475736 [Arabidopsis lyrata subsp. lyrata] gi|297334336|gb|EFH64754.1| hypothetical protein ARALYDRAFT_475736 [Arabidopsis lyrata subsp. lyrata]	609	416	1.00E-177	68.3	56.5	59.4	hypothetical protein ARALYDRAFT_475736	gbpln	Arabidopsis lyrata	AT1G66330.2 | Symbols: | senescence-associated family protein | chr1:24729880-24732144 REVERSE LENGTH=417	609	417	1.00E-179	68.5	56.3	59.1
Rsa1.0_01442.1.g26854.t1	ref|XP_002887020.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297332861|gb|EFH63279.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	504	503	0	99.8	88.9	92.7	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT1G66250.1 | Symbols: | O-Glycosyl hydrolases family 17 protein | chr1:24693063-24695416 FORWARD LENGTH=505	504	505	0	100.2	87.9	92.7
Rsa1.0_01442.1.g26855.t2	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	609	190	5.00E-13	31.2	6.7	7.6	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01442.1.g26856.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01442.1.g26857.t1	gb|AAB84334.1| hypothetical protein [Arabidopsis thaliana]	82	960	9.00E-25	1170.7	65.9	69.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G41520.2 | Symbols: TPR15 | Heat shock protein DnaJ with tetratricopeptide repeat | chr2:17317662-17322705 FORWARD LENGTH=1077	82	1077	2.00E-27	1313.4	65.9	69.5

Rsa1.0_01443.1.g26858.t8	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	588	672	3.00E-24	114.3	8.5	12.6	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01443.1.g26859.t1	gb|ABD65091.1| hypothetical protein 31.t00049 [Brassica oleracea]	479	530	3.00E-97	110.6	42.2	57.6	hypothetical protein 31.t00049	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01443.1.g26860.t3	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	1132	1231	1.00E-66	108.7	11.9	16.8	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1132	575	6.00E-37	50.8	9.0	14.8
Rsa1.0_01443.1.g26861.t4	ref|NP_174767.2| ATP-dependent protease La (LON) domain-containing protein [Arabidopsis thaliana] gi|51968886|dbj|BAD43135.1| unknown protein [Arabidopsis thaliana] gi|332193662|gb|AEE31783.1| ATP-dependent protease La (LON) domain-containing protein [Arabidopsis thaliana]	459	316	1.00E-129	68.8	54.2	58.6	ATP-dependent protease La (LON) domain-containing protein	gbpln	Arabidopsis thaliana	AT1G35340.1 | Symbols: | ATP-dependent protease La (LON) domain protein | chr1:12977768-12979749 FORWARD LENGTH=316	459	316	1.00E-131	68.8	54.2	58.6
Rsa1.0_01444.1.g26862.t1	ref|XP_002888445.1| hypothetical protein ARALYDRAFT_315605 [Arabidopsis lyrata subsp. lyrata] gi|297334286|gb|EFH64704.1| hypothetical protein ARALYDRAFT_315605 [Arabidopsis lyrata subsp. lyrata]	428	590	5.00E-75	137.9	57.9	66.8	hypothetical protein ARALYDRAFT_315605	gbpln	Arabidopsis lyrata	AT1G65710.1 | Symbols: | unknown protein; INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G37010.1); Has 2241 Blast hits to 1776 proteins in 164 species: Archae - 0; Bacteria - 29; Metazoa - 1759; Fungi - 94; Plants - 93; Viruses - 17; Other Eukaryotes - 249 (source: NCBI BLink). | chr1:24437057-24438424 REVERSE LENGTH=455	428	455	3.00E-73	106.3	61.7	69.9
Rsa1.0_01444.1.g26863.t1	dbj|BAJ34575.1| unnamed protein product [Thellungiella halophila]	189	188	1.00E-88	99.5	83.6	89.4	unnamed protein product	----	----	AT1G55210.2 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr1:20598057-20598620 REVERSE LENGTH=187	189	187	2.00E-87	98.9	81.5	88.9
Rsa1.0_01444.1.g26864.t2	gb|EOA36362.1| hypothetical protein CARUB_v10010738mg [Capsella rubella]	110	97	2.00E-28	88.2	61.8	74.5	hypothetical protein CARUB_v10010738mg	gbpln	Capsella rubella	AT1G55205.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13674.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:20594584-20595094 FORWARD LENGTH=103	110	103	5.00E-27	93.6	67.3	79.1
Rsa1.0_01444.1.g26865.t1	ref|XP_002894494.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297340336|gb|EFH70753.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	599	672	0	112.2	85.3	90.2	kinase family protein	gbpln	Arabidopsis lyrata	AT1G55200.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:20589309-20592049 REVERSE LENGTH=676	599	676	0	112.9	85.1	90.8
Rsa1.0_01444.1.g26866.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	243	414	8.00E-43	170.4	46.1	51.0	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01444.1.g26867.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01444.1.g26868.t1	gb|EOA40568.1| hypothetical protein CARUB_v10009297mg [Capsella rubella]	412	412	0	100.0	98.3	99.8	hypothetical protein CARUB_v10009297mg	gbpln	Capsella rubella	AT3G13920.1 | Symbols: EIF4A1, RH4, TIF4A1 | eukaryotic translation initiation factor 4A1 | chr3:4592635-4594128 REVERSE LENGTH=412	412	412	0	100.0	97.3	99.5
Rsa1.0_01444.1.g26869.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	835	1356	1.00E-176	162.4	44.6	63.4	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145	835	145	6.00E-28	17.4	6.2	9.6
Rsa1.0_01444.1.g26870.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	317	1342	1.00E-107	423.3	56.2	74.4	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	317	1262	1.00E-31	398.1	25.6	43.8
Rsa1.0_01444.1.g26871.t1	gb|AAG51858.1|AC010926_21 putative DNA-binding protein; 27830-29933 [Arabidopsis thaliana]	69	289	5.00E-17	418.8	59.4	75.4	putative DNA-binding protein; 27830-29933	gbpln	Arabidopsis thaliana	AT1G72740.1 | Symbols: | Homeodomain-like/winged-helix DNA-binding family protein | chr1:27380499-27382687 REVERSE LENGTH=287	69	287	8.00E-20	415.9	59.4	75.4

Rsa1.0_01444.1.g26872.t1	ref|NP_974022.1| ribosomal protein L18ae family protein [Arabidopsis thaliana] gi|238478859|ref|NP_001154424.1| ribosomal protein L18ae family protein [Arabidopsis thaliana] gi|62319776|dbj|BAD93772.1| hypothetical protein [Arabidopsis thaliana] gi|332194943|gb|AEE33064.1| ribosomal protein L18ae family protein [Arabidopsis thaliana] gi|332194945|gb|AEE33066.1| ribosomal protein L18ae family protein [Arabidopsis thaliana]	102	102	2.00E-33	100.0	85.3	92.2	ribosomal protein L18ae family protein	gbpln	Arabidopsis thaliana	AT1G54217.3 | Symbols: | Ribosomal protein L18ae family | chr1:20244346-20245005 REVERSE LENGTH=102	102	102	4.00E-36	100.0	85.3	92.2
Rsa1.0_01444.1.g26873.t1	ref|NP_850086.2| proteasome component ECM29 [Arabidopsis thaliana] gi|330252792|gb|AEC07886.1| ARM repeat superfamily protein [Arabidopsis thaliana]	1859	1826	0	98.2	85.2	89.6	proteasome component ECM29	gbpln	Arabidopsis thaliana	AT2G26780.1 | Symbols: | ARM repeat superfamily protein | chr2:11410125-11423598 FORWARD LENGTH=1826	1859	1826	0	98.2	85.2	89.6
Rsa1.0_01444.1.g26874.t1	ref|NP_001046391.2| Os02g0236500 [Oryza sativa Japonica Group] gi|255670750|dbj|BAF08305.2| Os02g0236500 [Oryza sativa Japonica Group]	687	918	1.00E-166	133.6	44.5	62.6	Os02g0236500	gbpln	Oryza sativa	AT4G10200.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr4:6353172-6355591 FORWARD LENGTH=733	687	733	1.00E-162	106.7	47.0	61.4
Rsa1.0_01445.1.g26875.t22	ref|NP_565750.1| cyclin-dependent kinase inhibitor 4 [Arabidopsis thaliana] gi|152032532|sp|Q8GYJ3.2|KRP4_ARATH RecName: Full=Cyclin-dependent kinase inhibitor 4; AltName: Full=Inhibitor/interactor of CDK protein 7; AltName: Full=KIP-related protein 4 gi|11907566|gb|AAG41215.1|AF123315_1 cyclin-dependent kinase inhibitor [Arabidopsis thaliana] gi|20197065|gb|AAC04492.2| expressed protein [Arabidopsis thaliana] gi|193885151|gb|ACF28389.1| At2g32710 [Arabidopsis thaliana] gi|330253634|gb|AEC08728.1| cyclin-dependent kinase inhibitor 4 [Arabidopsis thaliana]	110	289	3.00E-38	262.7	74.5	79.1	cyclin-dependent kinase inhibitor 4	gbpln	Arabidopsis thaliana	AT2G32710.1 | Symbols: KRP4, ACK2, ICK7 | Cyclin-dependent kinase inhibitor family protein | chr2:13873496-13875350 FORWARD LENGTH=289	110	289	5.00E-41	262.7	74.5	79.1
Rsa1.0_01445.1.g26876.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1891	1374	0	72.7	40.1	53.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1891	575	1.00E-173	30.4	14.7	21.0
Rsa1.0_01445.1.g26877.t1	#	#	#	#	#	#	#	-	----	----	AT2G02790.1 | Symbols: IQD29 | IQ-domain 29 | chr2:788708-790946 FORWARD LENGTH=636	71	636	7.00E-11	895.8	43.7	46.5
Rsa1.0_01445.1.g26878.t2	ref|NP_181004.2| PIN domain-containing MEE21 protein [Arabidopsis thaliana] gi|21805693|gb|AAM76754.1| hypothetical protein [Arabidopsis thaliana] gi|61742637|gb|AAX55139.1| hypothetical protein At2g34570 [Arabidopsis thaliana] gi|330253898|gb|AEC08992.1| PIN domain-containing MEE21 protein [Arabidopsis thaliana]	196	281	3.00E-22	143.4	33.2	42.3	PIN domain-containing MEE21 protein	gbpln	Arabidopsis thaliana	AT2G34570.1 | Symbols: MEE21 | PIN domain-like family protein | chr2:14563048-14564681 REVERSE LENGTH=281	196	281	1.00E-24	143.4	33.2	42.3
Rsa1.0_01445.1.g26879.t1	ref|NP_001154548.1| glycine-rich protein 23 [Arabidopsis thaliana] gi|330253625|gb|AEC08719.1| glycine-rich protein 23 [Arabidopsis thaliana]	201	172	1.00E-10	85.6	14.4	15.9	glycine-rich protein 23	gbpln	Arabidopsis thaliana	AT2G32690.4 | Symbols: ATGRP23, GRP23 | glycine-rich protein 23 | chr2:13863934-13864539 REVERSE LENGTH=172	201	172	3.00E-13	85.6	14.4	15.9
Rsa1.0_01445.1.g26880.t1	ref|NP_180861.1| receptor like protein 24 [Arabidopsis thaliana] gi|2924789|gb|AAC04918.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|20196994|gb|AAM14862.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] gi|330253681|gb|AEC08775.1| receptor like protein 24 [Arabidopsis thaliana]	795	864	0	108.7	61.1	73.6	receptor like protein 24	gbpln	Arabidopsis thaliana	AT2G33020.1 | Symbols: AtRLP24, RLP24 | receptor like protein 24 | chr2:14013874-14016516 REVERSE LENGTH=864	795	864	0	108.7	61.1	73.6
Rsa1.0_01445.1.g26881.t2	gb|EOA39215.1| hypothetical protein CARUB_v10012187mg [Capsella rubella]	258	220	1.00E-110	85.3	77.5	82.2	hypothetical protein CARUB_v10012187mg	gbpln	Capsella rubella	AT1G04760.1 | Symbols: ATVAMP726, VAMP726 | vesicle-associated membrane protein 726 | chr1:1334760-1336070 FORWARD LENGTH=220	258	220	1.00E-108	85.3	78.7	82.6

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<tr><td>Rsa1.0_01445.1.g26883.t1</td><td>gb|EOA29389.1| hypothetical protein CARUB_v10025677mg [Capsella rubella]</td><td>610</td><td>627</td><td>0</td><td>102.8</td><td>79.2</td><td>89.7</td><td>hypothetical protein CARUB_v10025677mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G32630.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr2:13844834-13846708 FORWARD LENGTH=624</td><td>610</td><td>624</td><td>0</td><td>102.3</td><td>78.2</td><td>87.2</td></tr>
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<tr><td>Rsa1.0_01446.1.g26885.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01446.1.g26886.t1</td><td>ref|XP_002887102.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332943|gb|EFH63361.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>249</td><td>233</td><td>1.00E-102</td><td>93.6</td><td>81.1</td><td>83.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G67100.1 | Symbols: LBD40 | LOB domain-containing protein 40 | chr1:25053801-25054659 FORWARD LENGTH=233</td><td>249</td><td>233</td><td>1.00E-100</td><td>93.6</td><td>82.7</td><td>85.1</td></tr>
<tr><td>Rsa1.0_01446.1.g26887.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>346</td><td>1142</td><td>9.00E-97</td><td>330.1</td><td>50.3</td><td>69.1</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>346</td><td>575</td><td>2.00E-37</td><td>166.2</td><td>28.6</td><td>47.7</td></tr>
<tr><td>Rsa1.0_01446.1.g26888.t1</td><td>ref|NP_198659.1| ribulose bisphosphate carboxylase small chain 1B [Arabidopsis thaliana] gi|132090|sp|P10796.1|RBS1B_ARATH RecName: Full=Ribulose bisphosphate carboxylase small chain 1B, chloroplastic; Short=RuBisCO small subunit 1B; Flags: Precursor gi|15294184|gb|AAK95269.1|AF410283_1 F1O19.10/F1O19.10 [Arabidopsis thaliana] gi|16193|emb|CAA32700.1| ribulose bisphosphate carboxylase [Arabidopsis thaliana] gi|9758821|dbj|BAB09355.1| ribulose bisphosphate carboxylase small chain 1b precursor (RuBisCO small subunit 1b) [Arabidopsis thaliana] gi|23505787|gb|AAN28753.1| At5g38430/F1O19.10 [Arabidopsis thaliana] gi|332006932|gb|AED94315.1| ribulose bisphosphate carboxylase small chain 1B [Arabidopsis thaliana]</td><td>170</td><td>181</td><td>1.00E-69</td><td>106.5</td><td>73.5</td><td>80.0</td><td>ribulose bisphosphate carboxylase small chain 1B</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G38430.1 | Symbols: | Ribulose bisphosphate carboxylase (small chain) family protein | chr5:15384350-15385155 REVERSE LENGTH=181</td><td>170</td><td>181</td><td>5.00E-72</td><td>106.5</td><td>73.5</td><td>80.0</td></tr>
<tr><td>Rsa1.0_01446.1.g26889.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01447.1.g26890.t1</td><td>gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]</td><td>802</td><td>1356</td><td>1.00E-170</td><td>169.1</td><td>34.9</td><td>45.1</td><td>Highly similar to Ta1-3 polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G75620.1 | Symbols: | glyoxal oxidase-related protein | chr1:28394951-28396594 REVERSE LENGTH=547</td><td>802</td><td>547</td><td>1.00E-143</td><td>68.2</td><td>30.3</td><td>35.5</td></tr>
<tr><td>Rsa1.0_01447.1.g26891.t1</td><td>gb|AFW86017.1| histone H3 [Zea mays]</td><td>136</td><td>227</td><td>1.00E-72</td><td>166.9</td><td>100.0</td><td>100.0</td><td>histone H3</td><td>gbenv/gbpln</td><td>Zea mays</td><td>AT4G40030.2 | Symbols: | Histone superfamily protein | chr4:18555840-18556827 REVERSE LENGTH=164</td><td>136</td><td>164</td><td>9.00E-75</td><td>120.6</td><td>100.0</td><td>100.0</td></tr>
<tr><td>Rsa1.0_01447.1.g26892.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01447.1.g26893.t1</td><td>gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]</td><td>458</td><td>1023</td><td>2.00E-95</td><td>223.4</td><td>40.0</td><td>52.8</td><td>F27F5.21</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>458</td><td>575</td><td>4.00E-29</td><td>125.5</td><td>11.4</td><td>17.2</td></tr>
<tr><td>Rsa1.0_01447.1.g26894.t1</td><td>dbj|BAJ34271.1| unnamed protein product [Thellungiella halophila]</td><td>152</td><td>152</td><td>1.00E-65</td><td>100.0</td><td>86.8</td><td>90.8</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT1G75590.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:28383250-28383714 REVERSE LENGTH=154</td><td>152</td><td>154</td><td>2.00E-66</td><td>101.3</td><td>86.8</td><td>91.4</td></tr>
<tr><td>Rsa1.0_01447.1.g26895.t2</td><td>emb|CAN79321.1| hypothetical protein VITISV_018984 [Vitis vinifera]</td><td>1995</td><td>1521</td><td>0</td><td>76.2</td><td>32.0</td><td>44.4</td><td>hypothetical protein VITISV_018984</td><td>gbpln</td><td>Vitis vinifera</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1995</td><td>1262</td><td>2.00E-60</td><td>63.3</td><td>6.5</td><td>10.5</td></tr>
<tr><td>Rsa1.0_01448.1.g26896.t1</td><td>ref|XP_002869328.1| hypothetical protein ARALYDRAFT_491601 [Arabidopsis lyrata subsp. lyrata] gi|297315164|gb|EFH45587.1| hypothetical protein ARALYDRAFT_491601 [Arabidopsis lyrata subsp. lyrata]</td><td>134</td><td>344</td><td>2.00E-42</td><td>256.7</td><td>66.4</td><td>73.9</td><td>hypothetical protein ARALYDRAFT_491601</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G31400.1 | Symbols: CTF7 | damaged DNA binding;DNA-directed DNA polymerases | chr4:15237411-15239266 FORWARD LENGTH=345</td><td>134</td><td>345</td><td>4.00E-43</td><td>257.5</td><td>67.9</td><td>74.6</td></tr>
<tr><td>Rsa1.0_01448.1.g26897.t1</td><td>gb|AAG51247.1|AC055769_6 copia-type polyprotein, putative; 28768-32772 [Arabidopsis thaliana]</td><td>1338</td><td>1334</td><td>0</td><td>99.7</td><td>53.7</td><td>70.9</td><td>copia-type polyprotein, putative; 28768-32772</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1338</td><td>1262</td><td>1.00E-101</td><td>94.3</td><td>14.3</td><td>22.2</td></tr>
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Rsa1.0_01448.1.g26898.t1	ref|XP_002869328.1| hypothetical protein ARALYDRAFT_491601 [Arabidopsis lyrata subsp. lyrata] gi|297315164|gb|EFH45587.1| hypothetical protein ARALYDRAFT_491601 [Arabidopsis lyrata subsp. lyrata]	209	344	1.00E-79	164.6	72.7	79.4	hypothetical protein ARALYDRAFT_491601	gbpln	Arabidopsis lyrata	AT4G31400.1 | Symbols: CTF7 | damaged DNA binding;DNA-directed DNA polymerases | chr4:15237411-15239266 FORWARD LENGTH=345	209	345	9.00E-79	165.1	72.2	78.9
Rsa1.0_01448.1.g26899.t1	ref|NP_194866.2| protein kinase family protein [Arabidopsis thaliana] gi|55978825|gb|AAV68874.1| hypothetical protein AT4G31380 [Arabidopsis thaliana] gi|60547875|gb|AAX23901.1| hypothetical protein At4g31380 [Arabidopsis thaliana] gi|332660502|gb|AEE85902.1| protein kinase family protein [Arabidopsis thaliana]	123	181	6.00E-51	147.2	89.4	94.3	protein kinase family protein	gbpln	Arabidopsis thaliana	AT4G31380.1 | Symbols: FLP1 | FPF1-like protein 1 | chr4:15229837-15230382 FORWARD LENGTH=181	123	181	1.00E-53	147.2	89.4	94.3
Rsa1.0_01448.1.g26900.t1	gb|EOA19145.1| hypothetical protein CARUB_v10007817mg [Capsella rubella]	302	286	1.00E-105	94.7	69.9	78.1	hypothetical protein CARUB_v10007817mg	gbpln	Capsella rubella	AT4G31370.1 | Symbols: FLA5 | FASCICLIN-like arabinogalactan protein 5 precursor | chr4:15223838-15224674 REVERSE LENGTH=278	302	278	2.00E-99	92.1	61.6	71.5
Rsa1.0_01448.1.g26901.t1	gb|EOA16656.1| hypothetical protein CARUB_v10004835mg [Capsella rubella]	161	434	3.00E-39	269.6	46.6	49.1	hypothetical protein CARUB_v10004835mg	gbpln	Capsella rubella	AT4G31340.2 | Symbols: | myosin heavy chain-related | chr4:15205662-15208895 FORWARD LENGTH=420	161	420	1.00E-41	260.9	46.6	48.4
Rsa1.0_01448.1.g26902.t1	ref|NP_567872.1| uncharacterized protein [Arabidopsis thaliana] gi|13507569|gb|AAK28647.1|AF360350_1 unknown protein [Arabidopsis thaliana] gi|15293233|gb|AAK93727.1| unknown protein [Arabidopsis thaliana] gi|332660492|gb|AEE85892.1| uncharacterized protein AT4G31330 [Arabidopsis thaliana]	241	239	1.00E-123	99.2	89.2	94.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G31330.1 | Symbols: | Protein of unknown function, DUF599 | chr4:15202354-15203151 FORWARD LENGTH=239	241	239	1.00E-125	99.2	89.2	94.6
Rsa1.0_01448.1.g26903.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	318	1274	3.00E-52	400.6	37.7	55.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	318	303	2.00E-43	95.3	33.6	48.1
Rsa1.0_01448.1.g26904.t1	gb|EOA18510.1| hypothetical protein CARUB_v10007062mg [Capsella rubella]	191	191	1.00E-86	100.0	83.8	90.1	hypothetical protein CARUB_v10007062mg	gbpln	Capsella rubella	AT4G31320.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:15193993-15194562 REVERSE LENGTH=189	191	189	4.00E-86	99.0	79.1	88.0
Rsa1.0_01448.1.g26905.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1624	1529	0	94.2	46.3	62.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1624	746	1.00E-115	45.9	12.7	16.1
Rsa1.0_01448.1.g26906.t2	ref|XP_002869336.1| hypothetical protein ARALYDRAFT_491611 [Arabidopsis lyrata subsp. lyrata] gi|297315172|gb|EFH45595.1| hypothetical protein ARALYDRAFT_491611 [Arabidopsis lyrata subsp. lyrata]	175	172	9.00E-79	98.3	83.4	92.6	hypothetical protein ARALYDRAFT_491611	gbpln	Arabidopsis lyrata	AT4G31310.1 | Symbols: | AIG2-like (avirulence induced gene) family protein | chr4:15191325-15192337 FORWARD LENGTH=172	175	172	2.00E-78	98.3	80.0	90.9
Rsa1.0_01448.1.g26907.t1	gb|EOA17355.1| hypothetical protein CARUB_v10005646mg [Capsella rubella]	233	233	1.00E-133	100.0	99.1	100.0	hypothetical protein CARUB_v10005646mg	gbpln	Capsella rubella	AT4G31300.3 | Symbols: PBA1 | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr4:15188927-15190935 FORWARD LENGTH=233	233	233	1.00E-134	100.0	98.3	99.6
Rsa1.0_01448.1.g26908.t1	ref|XP_002867309.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313145|gb|EFH43568.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	771	765	0	99.2	83.4	92.1	kinase family protein	gbpln	Arabidopsis lyrata	AT4G31230.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr4:15173071-15176109 REVERSE LENGTH=764	771	764	0	99.1	82.1	90.9
Rsa1.0_01449.1.g26909.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01449.1.g26910.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01449.1.g26911.t5	gb|ABD65100.1| hypothetical protein 31.t00077 [Brassica oleracea]	412	391	9.00E-57	94.9	31.6	36.7	hypothetical protein 31.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01449.1.g26912.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01449.1.g26913.t2	ref|NP_179692.1| phospholipase-like protein (PEARLI 4) domain-containing protein [Arabidopsis thaliana] gi|4803947|gb|AAD29820.1| pEARLI 4 protein [Arabidopsis thaliana] gi|16648887|gb|AAL24295.1| pEARLI 4 protein [Arabidopsis thaliana] gi|20197697|gb|AAM15210.1| pEARLI 4 protein [Arabidopsis thaliana] gi|23197604|gb|AAN15329.1| pEARLI 4 protein [Arabidopsis thaliana] gi|330252011|gb|AEC07105.1| phospholipase-like protein (PEARLI 4) domain-containing protein [Arabidopsis thaliana]	523	748	1.00E-134	143.0	61.4	74.6	phospholipase-like protein (PEARLI 4) domain-containing protein	gbpln	Arabidopsis thaliana	AT2G20960.1 | Symbols: pEARLI4 | Arabidopsis phospholipase-like protein (PEARLI 4) family | chr2:9007089-9009611 FORWARD LENGTH=748	523	748	1.00E-137	143.0	61.4	74.6
Rsa1.0_01449.1.g26914.t1	ref|NP_179694.2| minichromosome maintenance protein 10 [Arabidopsis thaliana] gi|52354259|gb|AAU44450.1| hypothetical protein AT2G20980 [Arabidopsis thaliana] gi|60547717|gb|AAX23822.1| hypothetical protein At2g20980 [Arabidopsis thaliana] gi|330252014|gb|AEC07108.1| minichromosome maintenance protein 10 [Arabidopsis thaliana]	394	396	1.00E-180	100.5	82.7	87.1	minichromosome maintenance protein 10	gbpln	Arabidopsis thaliana	AT2G20980.1 | Symbols: MCM10 | minichromosome maintenance 10 | chr2:9011654-9013856 REVERSE LENGTH=396	394	396	0	100.5	82.7	87.1
Rsa1.0_01449.1.g26915.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01449.1.g26916.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1757	1274	0	72.5	34.3	46.1	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1757	575	1.00E-60	32.7	9.1	14.8
Rsa1.0_01449.1.g26917.t1	gb|EOA27008.1| hypothetical protein CARUB_v10023108mg [Capsella rubella]	483	483	0	100.0	96.5	98.1	hypothetical protein CARUB_v10023108mg	gbpln	Capsella rubella	AT2G21050.1 | Symbols: LAX2 | like AUXIN RESISTANT 2 | chr2:9034289-9036439 FORWARD LENGTH=483	483	483	0	100.0	96.5	98.1
Rsa1.0_01450.1.g26918.t5	gb|EOA25292.1| hypothetical protein CARUB_v10018607mg [Capsella rubella]	2592	2587	0	99.8	70.3	80.6	hypothetical protein CARUB_v10018607mg	gbpln	Capsella rubella	AT4G30990.1 | Symbols: | ARM repeat superfamily protein | chr4:15084456-15097860 FORWARD LENGTH=2599	2592	2599	0	100.3	61.7	75.7
Rsa1.0_01450.1.g26919.t1	ref|XP_002890615.1| hypothetical protein ARALYDRAFT_889991 [Arabidopsis lyrata subsp. lyrata] gi|297336457|gb|EFH66874.1| hypothetical protein ARALYDRAFT_889991 [Arabidopsis lyrata subsp. lyrata]	577	575	0	99.7	80.9	88.2	hypothetical protein ARALYDRAFT_889991	gbpln	Arabidopsis lyrata	AT1G27200.1 | Symbols: | Domain of unknown function (DUF23) | chr1:9449812-9451539 REVERSE LENGTH=575	577	575	0	99.7	81.6	87.9
Rsa1.0_01450.1.g26920.t1	gb|EOA17996.1| hypothetical protein CARUB_v10006430mg, partial [Capsella rubella]	1151	1227	0	106.6	69.6	80.4	hypothetical protein CARUB_v10006430mg, partial	gbpln	Capsella rubella	AT4G19510.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr4:10633685-10637841 FORWARD LENGTH=1210	1151	1210	0	105.1	64.7	76.5
Rsa1.0_01450.1.g26921.t1	gb|EOA29845.1| hypothetical protein CARUB_v10012938mg [Capsella rubella]	81	896	9.00E-12	1106.2	38.3	38.3	hypothetical protein CARUB_v10012938mg	gbpln	Capsella rubella	AT3G09090.3 | Symbols: DEX1 | defective in exine formation protein (DEX1) | chr3:2782833-2787552 REVERSE LENGTH=891	81	891	1.00E-14	1100.0	38.3	38.3
Rsa1.0_01450.1.g26922.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01450.1.g26923.t5	gb|EOA39486.1| hypothetical protein CARUB_v10008094mg [Capsella rubella] gi|482575300|gb|EOA39487.1| hypothetical protein CARUB_v10008094mg [Capsella rubella]	2142	1371	0	64.0	46.2	53.6	hypothetical protein CARUB_v10008094mg	gbpln	Capsella rubella	AT1G27170.1 | Symbols: | transmembrane receptors;ATP binding | chr1:9434718-9439219 FORWARD LENGTH=1384	2142	1384	0	64.6	45.6	52.9
Rsa1.0_01450.1.g26924.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01450.1.g26925.t2	gb|EOA39486.1| hypothetical protein CARUB_v10008094mg [Capsella rubella] gi|482575300|gb|EOA39487.1| hypothetical protein CARUB_v10008094mg [Capsella rubella]	173	1371	8.00E-38	792.5	52.0	66.5	hypothetical protein CARUB_v10008094mg	gbpln	Capsella rubella	AT1G27180.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr1:9439859-9445818 FORWARD LENGTH=1556	173	1556	7.00E-38	899.4	51.4	67.6

Rsa1.0_01450.1.g26926.t1	ref|NP_564272.1| uncharacterized protein [Arabidopsis thaliana] gi|325530321|sp|Q94K98.2|Y1720_ARATH RecName: Full=UPF0392 protein At1g27200 gi|8778872|gb|AAF79871.1|AC000348_24 T7N9.26 [Arabidopsis thaliana] gi|23297605|gb|AAN12989.1| unknown protein [Arabidopsis thaliana] gi|332192672|gb|AEE30793.1| uncharacterized protein AT1G27200 [Arabidopsis thaliana] gi|385137870|gb|AFI41196.1| DUF23/GT0, partial [Arabidopsis thaliana]	164	575	1.00E-85	350.6	89.6	97.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G27200.1 | Symbols: | Domain of unknown function (DUF23) | chr1:9449812-9451539 REVERSE LENGTH=575	164	575	4.00E-88	350.6	89.6	97.0
Rsa1.0_01450.1.g26927.t1	gb|EOA39486.1| hypothetical protein CARUB_v10008094mg [Capsella rubella] gi|482575300|gb|EOA39487.1| hypothetical protein CARUB_v10008094mg [Capsella rubella]	349	1371	1.00E-119	392.8	66.2	78.8	hypothetical protein CARUB_v10008094mg	gbpln	Capsella rubella	AT1G27180.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr1:9439859-9445818 FORWARD LENGTH=1556	349	1556	1.00E-113	445.8	64.8	77.7
Rsa1.0_01450.1.g26928.t1	#	#	#	#	#	#	#	–	----	----	AT1G26910.1 | Symbols: RPL10B | Ribosomal protein L16p/L10e family protein | chr1:9321709-9322813 FORWARD LENGTH=221	58	221	6.00E-11	381.0	50.0	55.2
Rsa1.0_01450.1.g26929.t1	ref|NP_174010.1| 60S ribosomal protein L34-1 [Arabidopsis thaliana] gi|297850990|ref|XP_002893376.1| hypothetical protein ARALYDRAFT_472716 [Arabidopsis lyrata subsp. lyrata] gi|2500376|sp|Q42351.1|RL341_ARATH RecName: Full=60S ribosomal protein L34-1 gi|4262177|gb|AAD14494.1| 60s ribosomal protein L34 [Arabidopsis thaliana] gi|19310599|gb|AAL85030.1| putative 60s ribosomal protein L34 [Arabidopsis thaliana] gi|21436403|gb|AAM51402.1| putative 60S ribosomal protein L34 [Arabidopsis thaliana] gi|297339218|gb|EFH69635.1| hypothetical protein ARALYDRAFT_472716 [Arabidopsis lyrata subsp. lyrata] gi|332192632|gb|AEE30753.1| 60S ribosomal protein L34-1 [Arabidopsis thaliana] gi|482571901|gb|EOA36088.1| hypothetical protein CARUB_v10010667mg [Capsella rubella]	120	120	3.00E-56	100.0	91.7	95.8	60S ribosomal protein L34-1	gbpln	Arabidopsis lyrata	AT1G26880.1 | Symbols: | Ribosomal protein L34e superfamily protein | chr1:9315640-9316681 REVERSE LENGTH=120	120	120	5.00E-59	100.0	91.7	95.8
Rsa1.0_01450.1.g26930.t1	ref|XP_002890630.1| hypothetical protein ARALYDRAFT_335709 [Arabidopsis lyrata subsp. lyrata] gi|297336472|gb|EFH66889.1| hypothetical protein ARALYDRAFT_335709 [Arabidopsis lyrata subsp. lyrata]	419	416	0	99.3	84.7	89.5	hypothetical protein ARALYDRAFT_335709	gbpln	Arabidopsis lyrata	AT1G26870.1 | Symbols: FEZ, ANAC009 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:9312856-9314983 FORWARD LENGTH=425	419	425	0	101.4	84.5	89.3
Rsa1.0_01451.1.g26931.t1	gb|EOA33759.1| hypothetical protein CARUB_v10019954mg [Capsella rubella]	623	633	0	101.6	85.7	91.2	hypothetical protein CARUB_v10019954mg	gbpln	Capsella rubella	AT1G71020.1 | Symbols: | ARM repeat superfamily protein | chr1:26790825-26793105 REVERSE LENGTH=628	623	628	0	100.8	84.1	90.0
Rsa1.0_01451.1.g26932.t1	gb|EOA35754.1| hypothetical protein CARUB_v10020986mg [Capsella rubella]	194	193	3.00E-74	99.5	80.4	89.2	hypothetical protein CARUB_v10020986mg	gbpln	Capsella rubella	AT1G71015.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G01340.1); Has 85 Blast hits to 85 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 85; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:26789389-26790061 REVERSE LENGTH=195	194	195	4.00E-75	100.5	79.4	87.1
Rsa1.0_01451.1.g26933.t1	gb|EOA33480.1| hypothetical protein CARUB_v10019654mg [Capsella rubella] gi|482569293|gb|EOA33481.1| hypothetical protein CARUB_v10019654mg [Capsella rubella]	551	1651	0	299.6	74.8	80.9	hypothetical protein CARUB_v10019654mg	gbpln	Capsella rubella	AT1G71010.1 | Symbols: FAB1C | FORMS APLOID AND BINUCLEATE CELLS 1C | chr1:26782839-26788712 FORWARD LENGTH=1648	551	1648	0	299.1	74.6	80.6
Rsa1.0_01451.1.g26934.t1	gb|AAF19226.1|AC007505_2 Highly similar to Ta1-3 polyprotein [Arabidopsis thaliana]	1321	1356	0	102.6	55.6	74.0	Highly similar to Ta1-3 polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1321	1262	2.00E-85	95.5	14.2	21.0

Rsa1.0_01451.1.g26935.t1	ref|XP_002887343.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333184|gb|EFH63602.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	60	1653	9.00E-24	2755.0	83.3	90.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G71010.1 | Symbols: FAB1C | FORMS APLOID AND BINUCLEATE CELLS 1C | chr1:26782839-26788712 FORWARD LENGTH=1648	60	1648	7.00E-26	2746.7	81.7	90.0
Rsa1.0_01451.1.g26936.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01451.1.g26937.t1	gb|EOA35811.1| hypothetical protein CARUB_v10021047mg [Capsella rubella]	170	168	1.00E-76	98.8	81.8	88.2	hypothetical protein CARUB_v10021047mg	gbpln	Capsella rubella	AT1G71000.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:26769336-26770111 REVERSE LENGTH=165	170	165	3.00E-75	97.1	80.0	86.5
Rsa1.0_01451.1.g26938.t1	ref|XP_002888811.1| hypothetical protein ARALYDRAFT_476229 [Arabidopsis lyrata subsp. lyrata] gi|297334652|gb|EFH65070.1| hypothetical protein ARALYDRAFT_476229 [Arabidopsis lyrata subsp. lyrata]	131	134	2.00E-33	102.3	76.3	81.7	hypothetical protein ARALYDRAFT_476229	gbpln	Arabidopsis lyrata	AT1G70990.1 | Symbols: | proline-rich family protein | chr1:26767520-26768050 REVERSE LENGTH=176	131	176	9.00E-34	134.4	73.3	80.2
Rsa1.0_01451.1.g26939.t1	ref|NP_565006.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|21536546|gb|AAM60878.1| unknown [Arabidopsis thaliana] gi|332197026|gb|AEE35147.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	90	135	7.00E-15	150.0	48.9	56.7	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT1G70985.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:26764774-26765181 REVERSE LENGTH=135	90	135	1.00E-17	150.0	48.9	56.7
Rsa1.0_01452.1.g26940.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01452.1.g26941.t1	gb|EOA20468.1| hypothetical protein CARUB_v10000781mg [Capsella rubella]	502	502	0	100.0	95.0	98.6	hypothetical protein CARUB_v10000781mg	gbpln	Capsella rubella	AT5G17330.1 | Symbols: GAD, GAD1 | glutamate decarboxylase | chr5:5711141-5714839 FORWARD LENGTH=502	502	502	0	100.0	94.6	97.8
Rsa1.0_01452.1.g26942.t1	gb|AAD24197.1|AF136223_1 M3.4 protein [Brassica napus]	208	218	1.00E-72	104.8	76.9	79.8	M3.4 protein	gbpln	Brassica napus	AT5G17340.1 | Symbols: | Putative membrane lipoprotein | chr5:5715736-5716218 REVERSE LENGTH=160	208	160	7.00E-35	76.9	38.0	47.6
Rsa1.0_01452.1.g26943.t1	gb|AAD24197.1|AF136223_1 M3.4 protein [Brassica napus]	142	218	5.00E-36	153.5	60.6	71.1	M3.4 protein	gbpln	Brassica napus	AT5G17340.1 | Symbols: | Putative membrane lipoprotein | chr5:5715736-5716218 REVERSE LENGTH=160	142	160	5.00E-22	112.7	48.6	65.5
Rsa1.0_01452.1.g26944.t1	ref|XP_002871762.1| hypothetical protein ARALYDRAFT_488600 [Arabidopsis lyrata subsp. lyrata] gi|297317599|gb|EFH48021.1| hypothetical protein ARALYDRAFT_488600 [Arabidopsis lyrata subsp. lyrata]	182	184	4.00E-73	101.1	84.6	91.2	hypothetical protein ARALYDRAFT_488600	gbpln	Arabidopsis lyrata	AT5G17350.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 8 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03280.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5718853-5719404 FORWARD LENGTH=183	182	183	8.00E-74	100.5	85.2	91.2
Rsa1.0_01452.1.g26945.t1	gb|EOA22180.1| hypothetical protein CARUB_v10002751mg [Capsella rubella]	172	177	1.00E-58	102.9	77.3	86.6	hypothetical protein CARUB_v10002751mg	gbpln	Capsella rubella	AT5G17360.1 | Symbols: | BEST Arabidopsis thaliana protein match is: DNA LIGASE 6 (TAIR:AT1G66730.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5720620-5721147 FORWARD LENGTH=175	172	175	2.00E-53	101.7	74.4	86.6
Rsa1.0_01452.1.g26946.t1	ref|NP_197240.1| 2-hydroxyacyl-CoA lyase [Arabidopsis thaliana] gi|75174050|sp|Q9LF46.1|HACL_ARATH RecName: Full=2-hydroxyacyl-CoA lyase; AltName: Full=2-hydroxyphytanoyl-CoA lyase; Short=2-HPCL; AltName: Full=Oxalyl-CoA decarboxylase gi|9755761|emb|CAC01733.1| 2-hydroxyphytanoyl-CoA lyase-like protein [Arabidopsis thaliana] gi|20466616|gb|AAM20625.1| 2-hydroxyphytanoyl-CoA lyase-like protein [Arabidopsis thaliana] gi|23198152|gb|AAN15603.1| 2-hydroxyphytanoyl-CoA lyase-like protein [Arabidopsis thaliana] gi|332005036|gb|AED92419.1| 2-hydroxyacyl-CoA lyase [Arabidopsis thaliana]	572	572	0	100.0	91.3	95.5	2-hydroxyacyl-CoA lyase	gbpln	Arabidopsis thaliana	AT5G17380.1 | Symbols: | Thiamine pyrophosphate dependent pyruvate decarboxylase family protein | chr5:5724920-5726720 REVERSE LENGTH=572	572	572	0	100.0	91.3	95.5

Rsa1.0_01452.1.g26947.t1	ref|NP_197241.1| universal stress protein (USP) family protein [Arabidopsis thaliana] gi|9755762|emb|CAC01734.1| putative protein [Arabidopsis thaliana] gi|332005037|gb|AED92420.1| universal stress protein (USP) family protein [Arabidopsis thaliana]	291	285	1.00E-115	97.9	83.5	87.3	universal stress protein (USP) family protein	gbpln	Arabidopsis thaliana	AT5G17390.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr5:5727640-5728688 FORWARD LENGTH=285	291	285	1.00E-118	97.9	83.5	87.3
Rsa1.0_01452.1.g26948.t1	dbj|BAF00609.1| ADP/ATP translocase-like protein [Arabidopsis thaliana]	228	146	3.00E-23	64.0	25.9	29.8	ADP/ATP translocase-like protein	gbpln	Arabidopsis thaliana	AT5G17400.1 | Symbols: ER-ANT1 | endoplasmic reticulum-adenine nucleotide transporter 1 | chr5:5729015-5730104 REVERSE LENGTH=306	228	306	2.00E-25	134.2	25.9	29.8
Rsa1.0_01452.1.g26949.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01452.1.g26950.t2	sp|Q8LSN2.1|BBM2_BRANA RecName: Full=AP2-like ethylene-responsive transcription factor BBM2; Short=BnBBM2; AltName: Full=Protein BABY BOOM 2 gi|21069053|gb|AAM33801.1|AF317905_1 AP2/EREBP transcription factor BABY BOOM2 [Brassica napus]	567	579	0	102.1	86.6	91.4	RecName: Full=AP2-like ethylene-responsive transcription factor BBM2; Short=BnBBM2; AltName: Full=Protein BABY BOOM 2 gi|21069053|gb|AAM33801.1|AF317905_1 AP2/EREBP transcription factor BABY BOOM2	gbpln	Brassica napus	AT5G17430.1 | Symbols: BBM | Integrase-type DNA-binding superfamily protein | chr5:5742542-5745568 REVERSE LENGTH=584	567	584	0	103.0	79.4	86.1
Rsa1.0_01452.1.g26951.t2	ref|NP_568347.1| LUC7 related protein [Arabidopsis thaliana] gi|15450599|gb|AAK96571.1| AT5g17440/K3M16_10 [Arabidopsis thaliana] gi|17380624|gb|AAL36075.1| AT5g17440/K3M16_10 [Arabidopsis thaliana] gi|332005043|gb|AED92426.1| LUC7 related protein [Arabidopsis thaliana]	428	404	1.00E-174	94.4	80.4	81.5	LUC7 related protein	gbpln	Arabidopsis thaliana	AT5G17440.1 | Symbols: | LUC7 related protein | chr5:5749849-5753415 FORWARD LENGTH=404	428	404	1.00E-176	94.4	80.4	81.5
Rsa1.0_01452.1.g26952.t1	gb|EOA22986.1| hypothetical protein CARUB_v10003727mg [Capsella rubella]	73	73	9.00E-32	100.0	93.2	95.9	hypothetical protein CARUB_v10003727mg	gbpln	Capsella rubella	AT3G03341.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:790338-790556 REVERSE LENGTH=72	73	72	5.00E-29	98.6	80.8	84.9
Rsa1.0_01453.1.g26953.t5	ref|NP_191175.2| Sodium bile acid symporter family protein [Arabidopsis thaliana] gi|403399721|sp|F4IZC4.1|BASS4_ARATH RecName: Full=Probable sodium/metabolite cotransporter BASS4, chloroplastic; AltName: Full=Bile acid transporter 4; AltName: Full=Bile acid-sodium symporter family protein 4; Flags: Precursor gi|332645967|gb|AEE79488.1| probable sodium/metabolite cotransporter BASS4 [Arabidopsis thaliana]	253	436	1.00E-105	172.3	84.2	90.1	Sodium bile acid symporter family protein	gbpln	Arabidopsis thaliana	AT3G56160.1 | Symbols: | Sodium Bile acid symporter family | chr3:20837733-20841541 REVERSE LENGTH=436	253	436	1.00E-108	172.3	84.2	90.1
Rsa1.0_01453.1.g26954.t1	ref|NP_191174.1| translation initiation factor eIF-3 subunit 8 [Arabidopsis thaliana] gi|334186011|ref|NP_001190102.1| translation initiation factor eIF-3 subunit 8 [Arabidopsis thaliana] gi|23503063|sp|O49160.2|EIF3C_ARATH RecName: Full=Eukaryotic translation initiation factor 3 subunit C; Short=eIF3c; AltName: Full=Eukaryotic translation initiation factor 3 subunit 8; AltName: Full=eIF3 p110; AltName: Full=p105 gi|7572913|emb|CAB87414.1| PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 8 [Arabidopsis thaliana] gi|17381100|gb|AAL36362.1| putative eukaryotic translation initiation factor 3 subunit 8 [Arabidopsis thaliana] gi|25054977|gb|AAN71960.1| putative eukaryotic translation initiation factor 3 subunit 8 [Arabidopsis thaliana] gi|332645965|gb|AEE79486.1| translation initiation factor eIF-3 subunit 8 [Arabidopsis thaliana] gi|332645966|gb|AEE79487.1| eukaryotic translation initiation factor 3 subunit C [Arabidopsis thaliana]	896	900	0	100.4	87.3	93.0	translation initiation factor eIF-3 subunit 8	gbpln	Arabidopsis thaliana	AT3G56150.2 | Symbols: EIF3C | eukaryotic translation initiation factor 3C | chr3:20833790-20836820 REVERSE LENGTH=900	896	900	0	100.4	87.3	93.0

Rsa1.0_01453.1.g26955.t1	gb|EOA12870.1| hypothetical protein CARUB_v10025839mg [Capsella rubella]	922	926	0	100.4	80.0	87.7	hypothetical protein CARUB_v10025839mg	gbpln	Capsella rubella	AT5G51350.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase family protein | chr5:20867860-20870621 REVERSE LENGTH=895	922	895	0	97.1	76.9	85.1
Rsa1.0_01453.1.g26956.t1	ref|XP_002876350.1| biotin/lipoyl attachment domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322188|gb|EFH52609.1| biotin/lipoyl attachment domain-containing protein [Arabidopsis lyrata subsp. lyrata]	265	281	1.00E-115	106.0	79.6	89.1	biotin/lipoyl attachment domain-containing protein	gbpln	Arabidopsis lyrata	AT3G56130.4 | Symbols: | biotin/lipoyl attachment domain-containing protein | chr3:20826852-20829007 FORWARD LENGTH=274	265	274	1.00E-116	103.4	79.2	87.5
Rsa1.0_01453.1.g26957.t1	gb|EOA25608.1| hypothetical protein CARUB_v10018956mg [Capsella rubella]	473	462	0	97.7	82.5	89.0	hypothetical protein CARUB_v10018956mg	gbpln	Capsella rubella	AT3G56120.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:20823243-20826357 FORWARD LENGTH=468	473	468	0	98.9	82.9	89.4
Rsa1.0_01453.1.g26958.t1	ref|XP_002878068.1| prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata] gi|297323906|gb|EFH54327.1| prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata]	203	209	2.00E-92	103.0	86.7	91.6	prenylated rab acceptor family protein	gbpln	Arabidopsis lyrata	AT3G56110.2 | Symbols: PRA1.B1 | prenylated RAB acceptor 1.B1 | chr3:20822228-20822857 REVERSE LENGTH=209	203	209	4.00E-94	103.0	86.2	91.6
Rsa1.0_01453.1.g26959.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1866	1274	0	68.3	30.2	41.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1866	575	2.00E-74	30.8	9.9	14.5
Rsa1.0_01453.1.g26960.t1	dbj|BAJ34006.1| unnamed protein product [Thellungiella halophila]	259	263	1.00E-133	101.5	93.4	96.1	unnamed protein product	----	----	AT3G56090.1 | Symbols: ATFER3, FER3 | ferritin 3 | chr3:20814350-20815984 REVERSE LENGTH=259	259	259	1.00E-118	100.0	88.0	92.7
Rsa1.0_01453.1.g26961.t1	gb|EOA24828.1| hypothetical protein CARUB_v10018115mg [Capsella rubella]	176	175	5.00E-90	99.4	90.3	94.9	hypothetical protein CARUB_v10018115mg	gbpln	Capsella rubella	AT3G56070.2 | Symbols: ROC2 | rotamase cyclophilin 2 | chr3:20806987-20807517 REVERSE LENGTH=176	176	176	4.00E-89	100.0	88.6	92.6
Rsa1.0_01453.1.g26962.t2	ref|NP_567032.1| Glucose-methanol-choline (GMC) oxidoreductase family protein [Arabidopsis thaliana] gi|15982755|gb|AAL09718.1| AT3g56060/F18O21_20 [Arabidopsis thaliana] gi|332645951|gb|AEE79472.1| Glucose-methanol-choline (GMC) oxidoreductase family protein [Arabidopsis thaliana]	567	577	0	101.8	84.5	91.7	Glucose-methanol-choline (GMC) oxidoreductase family protein	gbpln	Arabidopsis thaliana	AT3G56060.1 | Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr3:20803328-20805983 REVERSE LENGTH=577	567	577	0	101.8	84.5	91.7
Rsa1.0_01453.1.g26963.t1	gb|EOA25148.1| hypothetical protein CARUB_v10018458mg [Capsella rubella]	185	581	1.00E-88	314.1	82.2	93.0	hypothetical protein CARUB_v10018458mg	gbpln	Capsella rubella	AT3G56060.1 | Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr3:20803328-20805983 REVERSE LENGTH=577	185	577	7.00E-90	311.9	81.6	90.8
Rsa1.0_01453.1.g26964.t2	gb|EOA21081.1| hypothetical protein CARUB_v10001419mg [Capsella rubella]	211	329	6.00E-20	155.9	29.9	39.8	hypothetical protein CARUB_v10001419mg	gbpln	Capsella rubella	AT4G17700.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17990.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:9854322-9855227 FORWARD LENGTH=164	211	164	1.00E-16	77.7	22.3	30.8
Rsa1.0_01454.1.g26965.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	171	1123	1.00E-66	656.7	70.8	80.1	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01454.1.g26966.t1	gb|EOA33009.1| hypothetical protein CARUB_v10016339mg, partial [Capsella rubella]	98	188	9.00E-15	191.8	38.8	57.1	hypothetical protein CARUB_v10016339mg, partial	gbpln	Capsella rubella	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365	98	365	1.00E-15	372.4	36.7	52.0
Rsa1.0_01454.1.g26967.t2	gb|AAF79797.1|AC020646_20 T32E20.30 [Arabidopsis thaliana]	1455	1397	0	96.0	45.2	59.8	T32E20.30	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1455	158	7.00E-38	10.9	5.1	6.4
Rsa1.0_01454.1.g26968.t1	gb|ABD65038.1| nuclear RNA binding protein, putative [Brassica oleracea]	342	336	1.00E-121	98.2	86.0	87.4	nuclear RNA binding protein, putative	gbpln	Brassica oleracea	AT4G17520.1 | Symbols: | Hyaluronan / mRNA binding family | chr4:9771496-9773313 FORWARD LENGTH=360	342	360	8.00E-91	105.3	62.6	74.3
Rsa1.0_01454.1.g26969.t1	gb|EOA14024.1| hypothetical protein CARUB_v10027156mg [Capsella rubella]	311	202	1.00E-111	65.0	62.7	63.7	hypothetical protein CARUB_v10027156mg	gbpln	Capsella rubella	AT5G47200.1 | Symbols: ATRABD2B, ATRAB1A, RAB1A | RAB GTPase homolog 1A | chr5:19167029-19168718 FORWARD LENGTH=202	311	202	1.00E-113	65.0	62.4	63.3
Rsa1.0_01454.1.g26970.t1	#	#	#	#	#	#	#	–	----	----	AT1G21720.1 | Symbols: PBC1 | proteasome beta subunit C1 | chr1:7626394-7628070 FORWARD LENGTH=204	96	204	7.00E-11	212.5	29.2	33.3

Rsa1.0_01454.1.g26971.t2	gb|AAD19773.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1278	1335	0	104.5	56.7	75.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1278	1262	4.00E-74	98.7	13.3	20.8
Rsa1.0_01454.1.g26972.t1	gb|ABD65040.1| vesicle-associated membrane protein, putative [Brassica oleracea]	218	228	1.00E-118	104.6	97.2	98.6	vesicle-associated membrane protein, putative	gbpln	Brassica oleracea	AT5G47180.2 | Symbols: | Plant VAMP (vesicle-associated membrane protein) family protein | chr5:19161384-19163265 REVERSE LENGTH=220	218	220	1.00E-119	100.9	95.0	97.2
Rsa1.0_01454.1.g26973.t1	gb|ABD65041.1| SET-related protein [Brassica oleracea]	243	283	5.00E-86	116.5	72.4	81.9	SET-related protein	gbpln	Brassica oleracea	AT5G47150.1 | Symbols: | YDG/SRA domain-containing protein | chr5:19150807-19151793 FORWARD LENGTH=328	243	328	1.00E-55	135.0	42.8	56.0
Rsa1.0_01454.1.g26974.t1	gb|ABD65041.1| SET-related protein [Brassica oleracea]	285	283	1.00E-132	99.3	84.2	90.5	SET-related protein	gbpln	Brassica oleracea	AT5G47150.1 | Symbols: | YDG/SRA domain-containing protein | chr5:19150807-19151793 FORWARD LENGTH=328	285	328	1.00E-87	115.1	59.3	75.1
Rsa1.0_01454.1.g26975.t1	dbj|BAB01350.1| Mutator-like transposase [Arabidopsis thaliana]	334	811	2.00E-64	242.8	42.8	63.2	Mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01455.1.g26976.t1	ref|XP_002870473.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316309|gb|EFH46732.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	323	502	1.00E-175	155.4	92.3	95.4	predicted protein	gbpln	Arabidopsis lyrata	AT5G36220.1 | Symbols: CYP81D1, CYP91A1 | cytochrome p450 81d1 | chr5:14253827-14256015 REVERSE LENGTH=502	323	502	1.00E-174	155.4	89.8	94.4
Rsa1.0_01455.1.g26977.t2	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	381	1611	7.00E-14	422.8	12.1	21.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01455.1.g26978.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01455.1.g26979.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01455.1.g26980.t3	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	941	940	1.00E-89	99.9	17.6	23.1	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01455.1.g26981.t14	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1902	1225	0	64.4	24.9	35.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G36170.1 | Symbols: HCF109, ATPRFB | high chlorophyll fluorescent 109 | chr5:14236083-14237974 REVERSE LENGTH=456	1902	456	0	24.0	20.1	21.4
Rsa1.0_01455.1.g26982.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01455.1.g26983.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01455.1.g26984.t1	ref|NP_176667.1| uncharacterized protein [Arabidopsis thaliana] gi|5042422|gb|AAD38261.1|AC006193_17 Hypothetical Protein [Arabidopsis thaliana] gi|91805371|gb|ABE65415.1| hypothetical protein At1g64870 [Arabidopsis thaliana] gi|332196179|gb|AEE34300.1| uncharacterized protein AT1G64870 [Arabidopsis thaliana]	294	304	1.00E-106	103.4	66.0	80.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G64870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G45200.1); Has 99 Blast hits to 91 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 99; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:24102917-24103831 FORWARD LENGTH=304	294	304	1.00E-109	103.4	66.0	80.6
Rsa1.0_01456.1.g26985.t4	ref|NP_191500.2| non-specific serine/threonine protein kinase [Arabidopsis thaliana] gi|68052253|sp|Q9LX30.2|GCN2_ARATH RecName: Full=Probable serine/threonine-protein kinase GCN2 gi|24940154|emb|CAD30860.1| GCN2 homologue [Arabidopsis thaliana] gi|332646397|gb|AEE79918.1| non-specific serine/threonine protein kinase [Arabidopsis thaliana]	1283	1241	0	96.7	85.3	89.8	non-specific serine/threonine protein kinase	gbpln	Arabidopsis thaliana	AT3G59410.1 | Symbols: GCN2 | protein kinase family protein | chr3:21950575-21959151 FORWARD LENGTH=1241	1283	1241	0	96.7	85.3	89.8
Rsa1.0_01456.1.g26986.t1	ref|XP_002878271.1| hypothetical protein ARALYDRAFT_486409 [Arabidopsis lyrata subsp. lyrata] gi|297324109|gb|EFH54530.1| hypothetical protein ARALYDRAFT_486409 [Arabidopsis lyrata subsp. lyrata]	886	894	0	100.9	89.1	93.0	hypothetical protein ARALYDRAFT_486409	gbpln	Arabidopsis lyrata	AT3G59420.1 | Symbols: ACR4, CR4 | crinkly4 | chr3:21959871-21962558 REVERSE LENGTH=895	886	895	0	101.0	88.8	92.7
Rsa1.0_01456.1.g26987.t1	ref|NP_191502.1| uncharacterized protein [Arabidopsis thaliana] gi|42572731|ref|NP_974461.1| uncharacterized protein [Arabidopsis thaliana] gi|7801693|emb|CAB91613.1| hypothetical protein [Arabidopsis thaliana] gi|63003806|gb|AAY25432.1| At3g59430 [Arabidopsis thaliana] gi|71143094|gb|AAZ23938.1| At3g59430 [Arabidopsis thaliana] gi|332646400|gb|AEE79921.1| uncharacterized protein AT3G59430 [Arabidopsis thaliana] gi|332646401|gb|AEE79922.1| uncharacterized protein AT3G59430 [Arabidopsis thaliana]	413	451	1.00E-156	109.2	76.8	84.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G59430.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 10 growth stages; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:21964484-21966497 REVERSE LENGTH=451	413	451	1.00E-158	109.2	76.8	84.0

Rsa1.0_01456.1.g26988.t1	gb|EOA24726.1| hypothetical protein CARUB_v10018003mg, partial [Capsella rubella]	197	216	6.00E-99	109.6	92.9	94.9	hypothetical protein CARUB_v10018003mg, partial	gbpln	Capsella rubella	AT3G59440.1 | Symbols: | Calcium-binding EF-hand family protein | chr3:21970423-21971010 FORWARD LENGTH=195	197	195	8.00E-98	99.0	89.8	91.4
Rsa1.0_01456.1.g26989.t1	gb|EOA24572.1| hypothetical protein CARUB_v10017836mg [Capsella rubella]	289	269	1.00E-127	93.1	79.9	85.1	hypothetical protein CARUB_v10017836mg	gbpln	Capsella rubella	AT3G59470.2 | Symbols: | Far-red impaired responsive (FAR1) family protein | chr3:21979099-21980097 REVERSE LENGTH=251	289	251	1.00E-126	86.9	77.2	80.3
Rsa1.0_01456.1.g26990.t1	ref|XP_002876506.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322344|gb|EFH52765.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	326	326	1.00E-180	100.0	94.8	97.5	pfkB-type carbohydrate kinase family protein	gbpln	Arabidopsis lyrata	AT3G59480.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr3:21983103-21984440 FORWARD LENGTH=326	326	326	0	100.0	94.5	97.2
Rsa1.0_01456.1.g26991.t1	ref|NP_175139.1| receptor like protein 6 [Arabidopsis thaliana] gi|12321005|gb|AAG50623.1|AC083835_8 disease resistance protein, putative [Arabidopsis thaliana] gi|332193999|gb|AEE32120.1| receptor like protein 6 [Arabidopsis thaliana]	950	994	0	104.6	65.3	76.8	receptor like protein 6	gbpln	Arabidopsis thaliana	AT1G45616.1 | Symbols: AtRLP6, RLP6 | receptor like protein 6 | chr1:17183550-17186534 REVERSE LENGTH=994	950	994	0	104.6	65.3	76.8
Rsa1.0_01456.1.g26992.t2	ref|NP_175225.1| receptor like protein 7 [Arabidopsis thaliana] gi|12323625|gb|AAG51781.1|AC079679_1 disease resistance protein, putative; 3954-7013 [Arabidopsis thaliana] gi|332194104|gb|AEE32225.1| receptor like protein 7 [Arabidopsis thaliana]	1105	1019	0	92.2	40.5	50.4	receptor like protein 7	gbpln	Arabidopsis thaliana	AT1G47890.1 | Symbols: AtRLP7, RLP7 | receptor like protein 7 | chr1:17643976-17647035 FORWARD LENGTH=1019	1105	1019	0	92.2	40.5	50.4
Rsa1.0_01456.1.g26993.t1	gb|EOA24578.1| hypothetical protein CARUB_v10017840mg [Capsella rubella]	272	269	1.00E-144	98.9	92.6	95.2	hypothetical protein CARUB_v10017840mg	gbpln	Capsella rubella	AT3G59500.1 | Symbols: | Integral membrane HRF1 family protein | chr3:21987110-21988169 FORWARD LENGTH=269	272	269	2.33E-156	98.9	92.3	95.2
Rsa1.0_01457.1.g26994.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01457.1.g26995.t1	gb|EOA39448.1| hypothetical protein CARUB_v10012624mg [Capsella rubella]	499	626	1.00E-135	125.5	52.1	54.5	hypothetical protein CARUB_v10012624mg	gbpln	Capsella rubella	AT1G48930.1 | Symbols: AtGH9C1, GH9C1 | glycosyl hydrolase 9C1 | chr1:18101782-18104587 REVERSE LENGTH=627	499	627	1.00E-135	125.7	51.7	54.3
Rsa1.0_01457.1.g26996.t1	ref|XP_002891463.1| hypothetical protein ARALYDRAFT_474037 [Arabidopsis lyrata subsp. lyrata] gi|297337305|gb|EFH67722.1| hypothetical protein ARALYDRAFT_474037 [Arabidopsis lyrata subsp. lyrata]	476	550	2.00E-88	115.5	34.5	39.7	hypothetical protein ARALYDRAFT_474037	gbpln	Arabidopsis lyrata	AT3G18610.1 | Symbols: PARLL1, ATNUC-L2, NUC-L2 | nucleolin like 2 | chr3:6404270-6407822 REVERSE LENGTH=636	476	636	3.00E-71	133.6	32.1	41.4
Rsa1.0_01457.1.g26997.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01457.1.g26998.t1	ref|XP_002891461.1| flavin-containing monooxygenase family protein [Arabidopsis lyrata subsp. lyrata] gi|297337303|gb|EFH67720.1| flavin-containing monooxygenase family protein [Arabidopsis lyrata subsp. lyrata]	94	382	2.00E-39	406.4	80.9	89.4	flavin-containing monooxygenase family protein	gbpln	Arabidopsis lyrata	AT1G48910.1 | Symbols: YUC10 | Flavin-containing monooxygenase family protein | chr1:18091681-18093774 FORWARD LENGTH=383	94	383	5.00E-41	407.4	79.8	87.2
Rsa1.0_01458.1.g26999.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01458.1.g27000.t1	dbj|BAJ34241.1| unnamed protein product [Thellungiella halophila]	798	800	0	100.3	80.5	85.8	unnamed protein product	----	----	AT2G33050.1 | Symbols: AtRLP26, RLP26 | receptor like protein 26 | chr2:14021870-14024272 FORWARD LENGTH=800	798	800	0	100.3	72.6	80.1
Rsa1.0_01458.1.g27001.t1	ref|NP_180865.2| receptor like protein 27 [Arabidopsis thaliana] gi|330253685|gb|AEC08779.1| receptor like protein 27 [Arabidopsis thaliana]	803	808	0	100.6	74.6	84.1	receptor like protein 27	gbpln	Arabidopsis thaliana	AT2G33060.1 | Symbols: AtRLP27, RLP27 | receptor like protein 27 | chr2:14025661-14028087 FORWARD LENGTH=808	803	808	0	100.6	74.6	84.1
Rsa1.0_01458.1.g27002.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01458.1.g27003.t1	gb|AAF79835.1|AC026875_15 T6D22.19 [Arabidopsis thaliana]	374	745	9.00E-45	199.2	24.3	33.4	T6D22.19	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01458.1.g27004.t1	gb|AAC04914.1| putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana]	811	800	0	98.6	64.4	75.7	putative leucine-rich repeat disease resistance protein	gbpln	Arabidopsis thaliana	AT2G33060.1 | Symbols: AtRLP27, RLP27 | receptor like protein 27 | chr2:14025661-14028087 FORWARD LENGTH=808	811	808	0	99.6	64.4	75.7
Rsa1.0_01458.1.g27005.t1	ref|NP_180865.2| receptor like protein 27 [Arabidopsis thaliana] gi|330253685|gb|AEC08779.1| receptor like protein 27 [Arabidopsis thaliana]	783	808	0	103.2	63.5	74.2	receptor like protein 27	gbpln	Arabidopsis thaliana	AT2G33060.1 | Symbols: AtRLP27, RLP27 | receptor like protein 27 | chr2:14025661-14028087 FORWARD LENGTH=808	783	808	0	103.2	63.5	74.2
Rsa1.0_01458.1.g27006.t1	ref|NP_180869.1| cellulose synthase-like protein D1 [Arabidopsis thaliana] gi|75219583|sp|O49323.1|CSLD1_ARATH RecName: Full=Cellulose synthase-like protein D1; Short=AtCslD1 gi|2924781|gb|AAC04910.1| putative cellulose synthase [Arabidopsis thaliana] gi|330253691|gb|AEC08785.1| cellulose synthase-like protein D1 [Arabidopsis thaliana]	95	1036	1.00E-42	1090.5	92.6	95.8	cellulose synthase-like protein D1	gbpln	Arabidopsis thaliana	AT2G33100.1 | Symbols: ATCSLD1, CSLD1 | cellulose synthase-like D1 | chr2:14036494-14040044 REVERSE LENGTH=1036	95	1036	2.00E-45	1090.5	92.6	95.8

Rsa1.0_01458.1.g27007.t1	ref|NP_180865.2| receptor like protein 27 [Arabidopsis thaliana] gi|330253685|gb|AEC08779.1| receptor like protein 27 [Arabidopsis thaliana]	755	808	0	107.0	73.6	83.2	receptor like protein 27	gbpln	Arabidopsis thaliana	AT2G33060.1 | Symbols: AtRLP27, RLP27 | receptor like protein 27 | chr2:14025661-14028087 FORWARD LENGTH=808	755	808	0	107.0	73.6	83.2
Rsa1.0_01458.1.g27008.t1	ref|NP_180869.1| cellulose synthase-like protein D1 [Arabidopsis thaliana] gi|75219583|sp|O49323.1|CSLD1_ARATH RecName: Full=Cellulose synthase-like protein D1; Short=AtCslD1 gi|2924781|gb|AAC04910.1| putative cellulose synthase [Arabidopsis thaliana] gi|330253691|gb|AEC08785.1| cellulose synthase-like protein D1 [Arabidopsis thaliana]	1035	1036	0	100.1	93.4	96.8	cellulose synthase-like protein D1	gbpln	Arabidopsis thaliana	AT2G33100.1 | Symbols: ATCSLD1, CSLD1 | cellulose synthase-like D1 | chr2:14036494-14040044 REVERSE LENGTH=1036	1035	1036	0	100.1	93.4	96.8
Rsa1.0_01458.1.g27009.t1	gb|EOA27866.1| hypothetical protein CARUB_v10024024mg [Capsella rubella]	223	221	1.00E-125	99.1	97.3	97.8	hypothetical protein CARUB_v10024024mg	gbpln	Capsella rubella	AT2G33120.1 | Symbols: SAR1, VAMP722, ATVAMP722 | synaptobrevin-related protein 1 | chr2:14043785-14045337 REVERSE LENGTH=221	223	221	1.00E-128	99.1	96.9	97.8
Rsa1.0_01458.1.g27010.t1	ref|NP_180873.1| 3-ketoacyl-CoA thiolase 2 [Arabidopsis thaliana] gi|73919871|sp|Q56WD9.2|THIK2_ARATH RecName: Full=3-ketoacyl-CoA thiolase 2, peroxisomal; AltName: Full=Acetyl-CoA acyltransferase 2; AltName: Full=Beta-ketothiolase 2; AltName: Full=Peroxisomal 3-oxoacyl-CoA thiolase 2; AltName: Full=Peroxisome defective protein 1; Flags: Precursor gi|11993853|gb|AAG42910.1|AF327529_1 putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|13194830|gb|AAK15577.1|AF349530_1 putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2924779|gb|AAC04908.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2981616|dbj|BAA25248.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|2981618|dbj|BAA25249.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|15450669|gb|AAK96606.1| At2g33150/F25I18.11 [Arabidopsis thaliana] gi|17380614|gb|AAL36070.1| At2g33150/F25I18.11 [Arabidopsis thaliana] gi|21593136|gb|AAM65085.1| 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] gi|330253697|gb|AEC08791.1| 3-ketoacyl-CoA thiolase 2 [Arabidopsis thaliana]	464	462	0	99.6	96.3	98.1	3-ketoacyl-CoA thiolase 2	gbpln	Arabidopsis thaliana	AT2G33150.1 | Symbols: PKT3, PED1, KAT2 | peroxisomal 3-ketoacyl-CoA thiolase 3 | chr2:14047814-14050983 REVERSE LENGTH=462	464	462	0	99.6	96.3	98.1
Rsa1.0_01458.1.g27011.t2	ref|XP_002889521.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335363|gb|EFH65780.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	843	1043	1.00E-172	123.7	34.6	38.2	kinase family protein	gbpln	Arabidopsis lyrata	AT1G04700.1 | Symbols: | PB1 domain-containing protein tyrosine kinase | chr1:1316919-1320653 FORWARD LENGTH=1042	843	1042	1.00E-173	123.6	34.6	38.0
Rsa1.0_01458.1.g27012.t2	gb|EOA26453.1| hypothetical protein CARUB_v10022500mg [Capsella rubella]	1885	1752	0	92.9	52.0	57.2	hypothetical protein CARUB_v10022500mg	gbpln	Capsella rubella	AT2G33240.1 | Symbols: XID, ATXID | myosin XI D | chr2:14086942-14096914 REVERSE LENGTH=1770	1885	1770	0	93.9	53.3	57.6
Rsa1.0_01458.1.g27013.t1	gb|ACT33452.1| SU(VAR)3-9-like protein 2 [Brassica rapa subsp. pekinensis]	600	635	1.00E-156	105.8	45.0	55.7	SU(VAR)3-9-like protein 2	gbpln	Brassica rapa	AT2G33290.1 | Symbols: SUVH2, SDG3, ATSUVH2 | SU(VAR)3-9 homolog 2 | chr2:14110078-14112033 FORWARD LENGTH=651	600	651	1.00E-149	108.5	46.8	60.7
Rsa1.0_01458.1.g27014.t2	dbj|BAJ34122.1| unnamed protein product [Thellungiella halophila]	61	249	1.00E-27	408.2	95.1	96.7	unnamed protein product	----	----	AT2G33310.2 | Symbols: IAA13 | auxin-induced protein 13 | chr2:14114569-14115757 REVERSE LENGTH=247	61	247	2.00E-29	404.9	93.4	96.7
Rsa1.0_01459.1.g27015.t1	ref|XP_002893897.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339739|gb|EFH70156.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	372	492	3.00E-34	132.3	21.8	33.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G36510.1 | Symbols: | Nucleic acid-binding proteins superfamily | chr1:13761926-13764265 FORWARD LENGTH=351	372	351	8.00E-28	94.4	22.6	35.5
Rsa1.0_01459.1.g27016.t1	gb|ABV89621.1| Lag1 longevity assurance-like 3 [Brassica rapa]	68	251	2.00E-26	369.1	88.2	92.6	Lag1 longevity assurance-like 3	gbpln	Brassica rapa	AT3G25540.1 | Symbols: LAG1 | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr3:9274752-9276261 FORWARD LENGTH=310	68	310	7.00E-25	455.9	83.8	88.2
Rsa1.0_01459.1.g27017.t1	gb|EOA25599.1| hypothetical protein CARUB_v10018947mg [Capsella rubella]	170	169	2.00E-55	99.4	71.8	81.8	hypothetical protein CARUB_v10018947mg	gbpln	Capsella rubella	AT2G04038.1 | Symbols: AtbZIP48, bZIP48 | basic leucine-zipper 48 | chr2:1331919-1332419 FORWARD LENGTH=166	170	166	7.00E-56	97.6	72.4	79.4

Rsa1.0_01459.1.g27018.t1	ref|XP_002875249.1| hypothetical protein ARALYDRAFT_904694 [Arabidopsis lyrata subsp. lyrata] gi|297321087|gb|EFH51508.1| hypothetical protein ARALYDRAFT_904694 [Arabidopsis lyrata subsp. lyrata]	117	91	3.00E-11	77.8	29.1	38.5	hypothetical protein ARALYDRAFT_904694	gbpln	Arabidopsis lyrata	AT2G04034.1 | Symbols: | Putative membrane lipoprotein | chr2:1297161-1297543 FORWARD LENGTH=92	117	92	1.00E-12	78.6	28.2	36.8
Rsa1.0_01459.1.g27019.t1	gb|EOA25349.1| hypothetical protein CARUB_v10018672mg [Capsella rubella]	796	781	0	98.1	93.0	96.4	hypothetical protein CARUB_v10018672mg	gbpln	Capsella rubella	AT2G04030.1 | Symbols: CR88, EMB1956, HSP90.5, Hsp88.1, AtHsp90.5 | Chaperone protein htpG family protein | chr2:1281983-1285909 FORWARD LENGTH=780	796	780	0	98.0	93.6	96.6
Rsa1.0_01459.1.g27020.t1	ref|XP_002875239.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321077|gb|EFH51498.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	368	366	1.00E-158	99.5	74.5	85.6	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT2G03980.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr2:1260907-1262408 FORWARD LENGTH=367	368	367	1.00E-156	99.7	69.0	81.0
Rsa1.0_01459.1.g27021.t1	ref|XP_002875236.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321074|gb|EFH51495.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	646	650	0	100.6	91.6	96.1	phosphatidylinositol 3- and 4-kinase family protein	gbpln	Arabidopsis lyrata	AT2G03890.1 | Symbols: ATPI4K GAMMA 7, UBDK GAMMA 7, PI4K GAMMA 7 | phosphoinositide 4-kinase gamma 7 | chr2:1186199-1188151 FORWARD LENGTH=650	646	650	0	100.6	90.4	96.0
Rsa1.0_01459.1.g27022.t1	ref|NP_178481.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75206038|sp|Q9SI53.1|PP147_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g03880, mitochondrial; Flags: Precursor gi|4582435|gb|AAD24821.1| putative selenium-binding protein [Arabidopsis thaliana] gi|330250668|gb|AEC05762.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	630	630	0	100.0	88.6	94.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G03880.1 | Symbols: REME1 | Pentatricopeptide repeat (PPR) superfamily protein | chr2:1181560-1183452 FORWARD LENGTH=630	630	630	0	100.0	88.6	94.4
Rsa1.0_01459.1.g27023.t1	ref|XP_002875234.1| hypothetical protein ARALYDRAFT_484298 [Arabidopsis lyrata subsp. lyrata] gi|297321072|gb|EFH51493.1| hypothetical protein ARALYDRAFT_484298 [Arabidopsis lyrata subsp. lyrata]	129	99	8.00E-41	76.7	72.1	72.9	hypothetical protein ARALYDRAFT_484298	gbpln	Arabidopsis lyrata	AT2G03870.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr2:1180306-1181256 FORWARD LENGTH=99	129	99	1.00E-42	76.7	71.3	72.1
Rsa1.0_01460.1.g27024.t2	ref|NP_001154446.1| ubiquitin-conjugating enzyme E2 28 [Arabidopsis thaliana] gi|334183622|ref|NP_001185308.1| ubiquitin-conjugating enzyme E2 28 [Arabidopsis thaliana] gi|332196094|gb|AEE34215.1| ubiquitin-conjugating enzyme E2 28 [Arabidopsis thaliana] gi|332196095|gb|AEE34216.1| ubiquitin-conjugating enzyme E2 28 [Arabidopsis thaliana]	184	190	2.00E-76	103.3	80.4	85.3	ubiquitin-conjugating enzyme E2 28	gbpln	Arabidopsis thaliana	AT1G64230.5 | Symbols: UBC28 | ubiquitin-conjugating enzyme 28 | chr1:23833792-23835220 FORWARD LENGTH=190	184	190	8.00E-79	103.3	80.4	85.3
Rsa1.0_01460.1.g27025.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01460.1.g27026.t1	ref|NP_194524.2| ethylene-responsive transcription factor CRF4 [Arabidopsis thaliana] gi|334302779|sp|Q9SUE3.2|CRF4_ARATH RecName: Full=Ethylene-responsive transcription factor CRF4; AltName: Full=Protein CYTOKININ RESPONSE FACTOR 4 gi|192571732|gb|ACF04811.1| At4g27950 [Arabidopsis thaliana] gi|332660012|gb|AEE85412.1| ethylene-responsive transcription factor CRF4 [Arabidopsis thaliana]	338	335	1.00E-118	99.1	68.9	80.5	ethylene-responsive transcription factor CRF4	gbpln	Arabidopsis thaliana	AT4G27950.1 | Symbols: CRF4 | cytokinin response factor 4 | chr4:13909732-13910739 REVERSE LENGTH=335	338	335	1.00E-121	99.1	68.9	80.5
Rsa1.0_01460.1.g27027.t1	gb|EOA14254.1| hypothetical protein CARUB_v10027412mg [Capsella rubella]	71	109	1.00E-18	153.5	63.4	74.6	hypothetical protein CARUB_v10027412mg	gbpln	Capsella rubella	AT5G53200.1 | Symbols: TRY | Homeodomain-like superfamily protein | chr5:21582913-21583960 FORWARD LENGTH=106	71	106	3.00E-21	149.3	59.2	70.4

Rsa1.0_01460.1.g27028.t1	ref|NP_567790.1| manganese tracking factor for mitochondrial SOD2 [Arabidopsis thaliana] gi|75306049|sp|Q944H5.1|MTM1_ARATH RecName: Full=Mitochondrial carrier protein MTM1; AltName: Full=Manganese tracking factor for mitochondrial SOD2 gi|16226567|gb|AAL16202.1|AF428433_1 AT4g27940/T13J8_50 [Arabidopsis thaliana] gi|21553497|gb|AAM62590.1| unknown [Arabidopsis thaliana] gi|21928061|gb|AAM78059.1| AT4g27940/T13J8_50 [Arabidopsis thaliana] gi|332660011|gb|AEE85411.1| manganese tracking factor for mitochondrial SOD2 [Arabidopsis thaliana]	415	413	0	99.5	80.7	86.5	manganese tracking factor for mitochondrial SOD2	gbpln	Arabidopsis thaliana	AT4G27940.1 | Symbols: ATMTM1, MTM1 | manganese tracking factor for mitochondrial SOD2 | chr4:13904745-13907036 FORWARD LENGTH=413	415	413	0	99.5	80.7	86.5
Rsa1.0_01460.1.g27029.t1	ref|XP_002869531.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315367|gb|EFH45790.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	202	182	9.00E-79	90.1	73.8	79.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G27920.1 | Symbols: PYL10, RCAR4 | PYR1-like 10 | chr4:13901220-13901939 FORWARD LENGTH=183	202	183	3.00E-80	90.6	69.3	80.2
Rsa1.0_01460.1.g27030.t1	gb|EOA18541.1| hypothetical protein CARUB_v10007095mg [Capsella rubella]	291	301	1.00E-119	103.4	78.4	88.7	hypothetical protein CARUB_v10007095mg	gbpln	Capsella rubella	AT4G27890.1 | Symbols: | HSP20-like chaperones superfamily protein | chr4:13886033-13887220 FORWARD LENGTH=293	291	293	1.00E-121	100.7	78.0	90.0
Rsa1.0_01460.1.g27031.t1	gb|EOA17008.1| hypothetical protein CARUB_v10005243mg [Capsella rubella]	322	324	1.00E-169	100.6	90.7	94.4	hypothetical protein CARUB_v10005243mg	gbpln	Capsella rubella	AT4G27880.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr4:13883623-13884927 FORWARD LENGTH=327	322	327	1.00E-170	101.6	91.6	94.7
Rsa1.0_01460.1.g27032.t2	ref|XP_002869536.1| hypothetical protein ARALYDRAFT_328905 [Arabidopsis lyrata subsp. lyrata] gi|297315372|gb|EFH45795.1| hypothetical protein ARALYDRAFT_328905 [Arabidopsis lyrata subsp. lyrata]	863	777	0	90.0	60.6	70.2	hypothetical protein ARALYDRAFT_328905	gbpln	Arabidopsis lyrata	AT4G27870.1 | Symbols: | Vacuolar iron transporter (VIT) family protein | chr4:13878983-13882679 FORWARD LENGTH=761	863	761	0	88.2	57.0	66.2
Rsa1.0_01460.1.g27033.t1	ref|NP_001190855.1| vacuolar iron transporter-like protein [Arabidopsis thaliana] gi|332660002|gb|AEE85402.1| vacuolar iron transporter-like protein [Arabidopsis thaliana]	603	596	0	98.8	64.3	73.8	vacuolar iron transporter-like protein	gbpln	Arabidopsis thaliana	AT4G27860.2 | Symbols: | vacuolar iron transporter (VIT) family protein | chr4:13873808-13876240 FORWARD LENGTH=596	603	596	0	98.8	64.3	73.8
Rsa1.0_01460.1.g27034.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	234	329	2.00E-21	140.6	30.8	40.2	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01461.1.g27035.t1	ref|XP_002874843.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata] gi|297320680|gb|EFH51102.1| hypothetical protein ARALYDRAFT_911810 [Arabidopsis lyrata subsp. lyrata]	291	610	2.00E-96	209.6	60.5	70.1	hypothetical protein ARALYDRAFT_911810	gbpln	Arabidopsis lyrata	AT4G05460.1 | Symbols: | RNI-like superfamily protein | chr4:2761106-2762400 REVERSE LENGTH=302	291	302	3.00E-92	103.8	58.1	67.0
Rsa1.0_01461.1.g27036.t1	ref|NP_192819.1| uncharacterized protein [Arabidopsis thaliana] gi|4539355|emb|CAB40049.1| putative protein [Arabidopsis thaliana] gi|7267779|emb|CAB81182.1| putative protein [Arabidopsis thaliana] gi|17380756|gb|AAL36208.1| unknown protein [Arabidopsis thaliana] gi|21595220|gb|AAM66082.1| unknown [Arabidopsis thaliana] gi|21689817|gb|AAM67552.1| unknown protein [Arabidopsis thaliana] gi|332657531|gb|AEE82931.1| uncharacterized protein AT4G10810 [Arabidopsis thaliana]	86	81	3.00E-29	94.2	82.6	86.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G10810.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24026.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr4:6645986-6646231 REVERSE LENGTH=81	86	81	6.00E-32	94.2	82.6	86.0
Rsa1.0_01461.1.g27037.t1	ref|NP_192817.1| UBX domain-containing protein [Arabidopsis thaliana] gi|7267777|emb|CAB81180.1| predicted protein of unknown function [Arabidopsis thaliana] gi|332657529|gb|AEE82929.1| UBX domain-containing protein [Arabidopsis thaliana]	468	480	0	102.6	84.8	88.5	UBX domain-containing protein	gbpln	Arabidopsis thaliana	AT4G10790.1 | Symbols: | UBX domain-containing protein | chr4:6640752-6643035 REVERSE LENGTH=480	468	480	0	102.6	84.8	88.5
Rsa1.0_01461.1.g27038.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01461.1.g27039.t5	ref|XP_002874646.1| EMB1706 [Arabidopsis lyrata subsp. lyrata] gi|297320483|gb|EFH50905.1| EMB1706 [Arabidopsis lyrata subsp. lyrata]	449	689	3.00E-41	153.5	24.9	28.5	EMB1706	gbpln	Arabidopsis lyrata	AT4G10760.1 | Symbols: EMB1706, MTA | mRNAadenosine methylase | chr4:6619947-6623312 REVERSE LENGTH=685	449	685	7.00E-44	152.6	24.9	28.5

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<tr><td>Rsa1.0_01461.1.g27040.t1</td><td>ref|NP_192809.1| FACT complex subunit SPT16 [Arabidopsis thaliana] gi|75220257|sp|O82491.1|SPT16_ARATH RecName: Full=FACT complex subunit SPT16; AltName: Full=Facilitates chromatin transcription complex subunit SPT16 gi|3600033|gb|AAC35521.1| contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana] gi|7267769|emb|CAB81172.1| putative transcriptional regulator [Arabidopsis thaliana] gi|225898771|dbj|BAH30516.1| hypothetical protein [Arabidopsis thaliana] gi|332657519|gb|AEE82919.1| FACT complex subunit SPT16 [Arabidopsis thaliana]</td><td>1085</td><td>1074</td><td>0</td><td>99.0</td><td>87.4</td><td>93.3</td><td>FACT complex subunit SPT16</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G10710.1 | Symbols: SPT16 | global transcription factor C | chr4:6602226-6605450 REVERSE LENGTH=1074</td><td>1085</td><td>1074</td><td>0</td><td>99.0</td><td>87.4</td><td>93.3</td></tr>
<tr><td>Rsa1.0_01461.1.g27041.t1</td><td>ref|XP_002867679.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297313515|gb|EFH43938.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]</td><td>486</td><td>498</td><td>0</td><td>102.5</td><td>79.4</td><td>88.1</td><td>hydrolase, alpha/beta fold family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G24140.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:12530032-12533664 REVERSE LENGTH=498</td><td>486</td><td>498</td><td>0</td><td>102.5</td><td>79.2</td><td>88.3</td></tr>
<tr><td>Rsa1.0_01461.1.g27042.t1</td><td>ref|NP_192802.2| protein IQ-domain 16 [Arabidopsis thaliana] gi|33589696|gb|AAQ22614.1| At4g10640 [Arabidopsis thaliana] gi|110736628|dbj|BAF00278.1| hypothetical protein [Arabidopsis thaliana] gi|332657512|gb|AEE82912.1| protein IQ-domain 16 [Arabidopsis thaliana]</td><td>422</td><td>423</td><td>0</td><td>100.2</td><td>79.4</td><td>86.0</td><td>protein IQ-domain 16</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G10640.1 | Symbols: IQD16 | IQ-domain 16 | chr4:6571999-6574312 FORWARD LENGTH=423</td><td>422</td><td>423</td><td>0</td><td>100.2</td><td>79.4</td><td>86.0</td></tr>
<tr><td>Rsa1.0_01461.1.g27043.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01461.1.g27044.t1</td><td>gb|ABD64940.1| hypothetical protein 24.t00018 [Brassica oleracea]</td><td>292</td><td>380</td><td>3.00E-73</td><td>130.1</td><td>52.1</td><td>67.8</td><td>hypothetical protein 24.t00018</td><td>gbpln</td><td>Brassica oleracea</td><td>AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302</td><td>292</td><td>302</td><td>9.00E-52</td><td>103.4</td><td>41.1</td><td>59.6</td></tr>
<tr><td>Rsa1.0_01461.1.g27045.t2</td><td>gb|ACB59212.1| unknown protein [Brassica oleracea]</td><td>286</td><td>610</td><td>3.00E-56</td><td>213.3</td><td>48.6</td><td>58.4</td><td>unknown protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343</td><td>286</td><td>343</td><td>2.00E-17</td><td>119.9</td><td>16.1</td><td>19.6</td></tr>
<tr><td>Rsa1.0_01462.1.g27046.t1</td><td>pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)</td><td>790</td><td>1365</td><td>1.00E-126</td><td>172.8</td><td>28.9</td><td>39.4</td><td>RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)</td><td>----</td><td>----</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>790</td><td>575</td><td>7.00E-58</td><td>72.8</td><td>15.8</td><td>23.9</td></tr>
<tr><td>Rsa1.0_01462.1.g27047.t1</td><td>ref|XP_002881569.1| hypothetical protein ARALYDRAFT_482825 [Arabidopsis lyrata subsp. lyrata] gi|297327408|gb|EFH57828.1| hypothetical protein ARALYDRAFT_482825 [Arabidopsis lyrata subsp. lyrata]</td><td>466</td><td>463</td><td>0</td><td>99.4</td><td>87.6</td><td>92.3</td><td>hypothetical protein ARALYDRAFT_482825</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G38170.1 | Symbols: CAX1, ATCAX1, RCI4 | cation exchanger 1 | chr2:15989429-15993178 REVERSE LENGTH=463</td><td>466</td><td>463</td><td>0</td><td>99.4</td><td>86.9</td><td>92.5</td></tr>
<tr><td>Rsa1.0_01462.1.g27048.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01462.1.g27049.t1</td><td>ref|XP_002881568.1| hypothetical protein ARALYDRAFT_903014 [Arabidopsis lyrata subsp. lyrata] gi|297327407|gb|EFH57827.1| hypothetical protein ARALYDRAFT_903014 [Arabidopsis lyrata subsp. lyrata]</td><td>396</td><td>404</td><td>0</td><td>102.0</td><td>82.1</td><td>91.4</td><td>hypothetical protein ARALYDRAFT_903014</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G38152.1 | Symbols: | alpha 1,4-glycosyltransferase family protein | chr2:15984062-15985278 REVERSE LENGTH=380</td><td>396</td><td>380</td><td>0</td><td>96.0</td><td>79.3</td><td>87.1</td></tr>
<tr><td>Rsa1.0_01462.1.g27050.t1</td><td>ref|XP_002881567.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327406|gb|EFH57826.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>404</td><td>750</td><td>0</td><td>185.6</td><td>79.0</td><td>86.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G38150.1 | Symbols: | alpha 1,4-glycosyltransferase family protein | chr2:15981700-15982917 REVERSE LENGTH=405</td><td>404</td><td>405</td><td>0</td><td>100.2</td><td>79.0</td><td>88.4</td></tr>
<tr><td>Rsa1.0_01462.1.g27051.t1</td><td>gb|EOA29429.1| hypothetical protein CARUB_v10025723mg [Capsella rubella]</td><td>119</td><td>118</td><td>1.00E-35</td><td>99.2</td><td>85.7</td><td>90.8</td><td>hypothetical protein CARUB_v10025723mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G38140.1 | Symbols: PSRP4 | plastid-specific ribosomal protein 4 | chr2:15980948-15981459 FORWARD LENGTH=118</td><td>119</td><td>118</td><td>1.00E-36</td><td>99.2</td><td>84.0</td><td>89.9</td></tr>
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Rsa1.0_01462.1.g27052.t2	ref|XP_002881566.1| hypothetical protein ARALYDRAFT_321517 [Arabidopsis lyrata subsp. lyrata] gi|297327405|gb|EFH57825.1| hypothetical protein ARALYDRAFT_321517 [Arabidopsis lyrata subsp. lyrata]	200	190	3.00E-90	95.0	81.5	88.0	hypothetical protein ARALYDRAFT_321517	gbpln	Arabidopsis lyrata	AT2G38130.2 | Symbols: ATMAK3 | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr2:15978639-15980145 REVERSE LENGTH=190	200	190	3.00E-88	95.0	77.5	84.5
Rsa1.0_01462.1.g27053.t1	gb|ACZ67478.1| auxin resistant 1 protein [Brassica rapa subsp. oleifera]	493	493	0	100.0	97.6	98.6	auxin resistant 1 protein	gbpln	Brassica rapa	AT2G38120.1 | Symbols: AUX1, WAV5, PIR1, MAP1 | Transmembrane amino acid transporter family protein | chr2:15973493-15976792 FORWARD LENGTH=485	493	485	0	98.4	93.3	95.7
Rsa1.0_01463.1.g27054.t1	ref|NP_177373.1| trypsin inhibitor (Kunitz) domain-containing protein [Arabidopsis thaliana] gi|12323668|gb|AAG51801.1|AC067754_17 drought induced protein, putative; 79797-80444 [Arabidopsis thaliana] gi|21536624|gb|AAM60956.1| drought induced protein, putative [Arabidopsis thaliana] gi|94442485|gb|ABF19030.1| At1g72290 [Arabidopsis thaliana] gi|332197178|gb|AEE35299.1| trypsin inhibitor (Kunitz) domain-containing protein [Arabidopsis thaliana]	209	215	6.00E-38	102.9	46.9	61.7	trypsin inhibitor (Kunitz) domain-containing protein	gbpln	Arabidopsis thaliana	AT1G72290.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27215852-27216499 FORWARD LENGTH=215	209	215	2.00E-40	102.9	46.9	61.7
Rsa1.0_01463.1.g27055.t1	dbj|BAM14713.1| water soluble chlorophyll protein [Brassica oleracea var. gemmifera]	221	218	2.00E-41	98.6	50.7	62.4	water soluble chlorophyll protein	gbpln	Brassica oleracea	AT1G72290.1 | Symbols: | Kunitz family trypsin and protease inhibitor protein | chr1:27215852-27216499 FORWARD LENGTH=215	221	215	2.00E-37	97.3	43.9	57.5
Rsa1.0_01463.1.g27056.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01463.1.g27057.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01463.1.g27058.t1	ref|XP_002888867.1| hypothetical protein ARALYDRAFT_476358 [Arabidopsis lyrata subsp. lyrata] gi|297334708|gb|EFH65126.1| hypothetical protein ARALYDRAFT_476358 [Arabidopsis lyrata subsp. lyrata]	1087	1096	0	100.8	84.4	90.2	hypothetical protein ARALYDRAFT_476358	gbpln	Arabidopsis lyrata	AT1G72300.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr1:27217679-27220966 REVERSE LENGTH=1095	1087	1095	0	100.7	83.7	90.2
Rsa1.0_01463.1.g27059.t1	ref|XP_002887428.1| hypothetical protein ARALYDRAFT_476359 [Arabidopsis lyrata subsp. lyrata] gi|297333269|gb|EFH63687.1| hypothetical protein ARALYDRAFT_476359 [Arabidopsis lyrata subsp. lyrata]	320	324	1.00E-123	101.3	77.5	85.0	hypothetical protein ARALYDRAFT_476359	gbpln	Arabidopsis lyrata	AT1G72310.1 | Symbols: ATL3 | RING/U-box superfamily protein | chr1:27226405-27227379 FORWARD LENGTH=324	320	324	1.00E-121	101.3	75.6	84.7
Rsa1.0_01464.1.g27060.t1	ref|XP_002875819.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321657|gb|EFH52078.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	426	457	2.00E-75	107.3	43.0	55.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G12100.1 | Symbols: | Cullin family protein | chr4:7246453-7248127 REVERSE LENGTH=434	426	434	1.00E-46	101.9	32.6	45.5
Rsa1.0_01464.1.g27061.t1	gb|AEX31284.1| phytoene synthase [Brassica rapa]	404	414	0	102.5	90.6	95.0	phytoene synthase	gbpln	Brassica rapa	AT5G17230.2 | Symbols: PSY | PHYTOENE SYNTHASE | chr5:5659839-5662087 REVERSE LENGTH=422	404	422	0	104.5	86.4	91.8
Rsa1.0_01464.1.g27062.t1	gb|EOA20368.1| hypothetical protein CARUB_v10000682mg [Capsella rubella]	718	533	4.00E-84	74.2	29.8	34.3	hypothetical protein CARUB_v10000682mg	gbpln	Capsella rubella	AT5G17160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03130.1); Has 14330 Blast hits to 10381 proteins in 896 species: Archae - 94; Bacteria - 2881; Metazoa - 4019; Fungi - 1576; Plants - 515; Viruses - 110; Other Eukaryotes - 5135 (source: NCBI BLink). | chr5:5639843-5642427 REVERSE LENGTH=569	718	569	4.00E-84	79.2	32.3	37.6
Rsa1.0_01464.1.g27063.t1	gb|EOA19671.1| hypothetical protein CARUB_v10003324mg [Capsella rubella]	400	232	9.00E-46	58.0	27.0	36.0	hypothetical protein CARUB_v10003324mg	gbpln	Capsella rubella	AT5G17090.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:5621604-5622475 REVERSE LENGTH=230	400	230	1.00E-42	57.5	22.3	27.5
Rsa1.0_01464.1.g27064.t1	gb|EOA19671.1| hypothetical protein CARUB_v10003324mg [Capsella rubella]	223	232	1.00E-52	104.0	52.5	67.7	hypothetical protein CARUB_v10003324mg	gbpln	Capsella rubella	AT5G17120.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:5628529-5629324 REVERSE LENGTH=207	223	207	3.00E-46	92.8	41.3	51.6
Rsa1.0_01464.1.g27065.t1	gb|EOA19671.1| hypothetical protein CARUB_v10003324mg [Capsella rubella]	304	232	1.00E-50	76.3	37.2	47.4	hypothetical protein CARUB_v10003324mg	gbpln	Capsella rubella	AT5G17120.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:5628529-5629324 REVERSE LENGTH=207	304	207	3.00E-43	68.1	26.6	35.9
Rsa1.0_01464.1.g27066.t1	gb|EOA19671.1| hypothetical protein CARUB_v10003324mg [Capsella rubella]	149	232	6.00E-33	155.7	49.0	59.1	hypothetical protein CARUB_v10003324mg	gbpln	Capsella rubella	AT5G17090.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:5621604-5622475 REVERSE LENGTH=230	149	230	5.00E-31	154.4	45.6	57.0
Rsa1.0_01464.1.g27067.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01464.1.g27068.t1	gb|EOA19671.1| hypothetical protein CARUB_v10003324mg [Capsella rubella]	97	232	1.00E-26	239.2	58.8	69.1	hypothetical protein CARUB_v10003324mg	gbpln	Capsella rubella	AT5G17150.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:5638801-5639592 REVERSE LENGTH=202	97	202	2.00E-25	208.2	54.6	69.1
Rsa1.0_01464.1.g27069.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01464.1.g27070.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01464.1.g27071.t1	gb|EOA19671.1| hypothetical protein CARUB_v10003324mg [Capsella rubella]	244	232	6.00E–38	95.1	43.9	56.1	hypothetical protein CARUB_v10003324mg	gbpln	Capsella rubella	AT5G17090.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:5621604–5622475 REVERSE LENGTH=230	244	230	8.00E–33	94.3	29.9	37.3
Rsa1.0_01465.1.g27072.t1	dbj|BAA12711.1| VM23 [Raphanus sativus]	253	253	1.00E–137	100.0	100.0	100.0	VM23	gbpln	Raphanus sativus	AT3G26520.1 | Symbols: TIP2, SITIP, GAMMA–TIP2, TIP1;2 | tonoplast intrinsic protein 2 | chr3:9722770–9723703 REVERSE LENGTH=253	253	253	1.00E–128	100.0	90.9	94.9
Rsa1.0_01465.1.g27073.t2	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	931	910	1.00E–133	97.7	27.4	40.0	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I–like superfamily protein | chr1:16528880–16531065 REVERSE LENGTH=626	931	626	5.00E–63	67.2	14.2	23.0
Rsa1.0_01465.1.g27074.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01465.1.g27075.t1	gb|EOA25649.1| hypothetical protein CARUB_v10018998mg [Capsella rubella]	185	194	3.00E–67	104.9	88.1	93.0	hypothetical protein CARUB_v10018998mg	gbpln	Capsella rubella	AT3G26510.4 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr3:9711886–9712588 REVERSE LENGTH=196	185	196	8.00E–67	105.9	87.0	90.3
Rsa1.0_01465.1.g27076.t1	ref|NP_189280.1| Phototropic–responsive NPH3 family protein [Arabidopsis thaliana] gi|75273418|sp|Q9LIM6.1|Y3649_ARATH RecName: Full=BTB/POZ domain–containing protein At3g26490 gi|9294308|dbj|BAB02210.1| unnamed protein product [Arabidopsis thaliana] gi|332643645|gb|AEE77166.1| Phototropic–responsive NPH3 family protein [Arabidopsis thaliana]	568	588	0	103.5	84.5	91.7	Phototropic–responsive NPH3 family protein	gbpln	Arabidopsis thaliana	AT3G26490.1 | Symbols: | Phototropic–responsive NPH3 family protein | chr3:9704142–9706161 FORWARD LENGTH=588	568	588	0	103.5	84.5	91.7
Rsa1.0_01465.1.g27077.t1	ref|NP_001154500.1| TTF–type zinc finger protein with HAT dimerisation domain [Arabidopsis thaliana] gi|330250920|gb|AEC06014.1| TTF–type zinc finger protein with HAT dimerisation domain [Arabidopsis thaliana]	301	564	1.00E–118	187.4	71.1	83.1	TTF–type zinc finger protein with HAT dimerisation domain	gbpln	Arabidopsis thaliana	AT2G06541.2 | Symbols: | TTF–type zinc finger protein with HAT dimerisation domain | chr2:2598222–2600326 REVERSE LENGTH=564	301	564	1.00E–121	187.4	71.1	83.1
Rsa1.0_01465.1.g27078.t1	gb|EOA33131.1| hypothetical protein CARUB_v10016470mg [Capsella rubella]	289	723	1.00E–100	250.2	66.8	82.7	hypothetical protein CARUB_v10016470mg	gbpln	Capsella rubella	AT2G06541.2 | Symbols: | TTF–type zinc finger protein with HAT dimerisation domain | chr2:2598222–2600326 REVERSE LENGTH=564	289	564	4.00E–92	195.2	60.6	77.9
Rsa1.0_01466.1.g27079.t1	gb|EOA22636.1| hypothetical protein CARUB_v10003306mg [Capsella rubella]	670	664	0	99.1	81.5	90.9	hypothetical protein CARUB_v10003306mg	gbpln	Capsella rubella	AT5G04940.2 | Symbols: SUVH1 | SU(VAR)3–9 homolog 1 | chr5:1454616–1456628 REVERSE LENGTH=670	670	670	0	100.0	80.9	88.7
Rsa1.0_01466.1.g27080.t1	ref|NP_568146.1| phospholipid–transporting ATPase 1 [Arabidopsis thaliana] gi|12229646|sp|P98204.1|ALA1_ARATH RecName: Full=Phospholipid–transporting ATPase 1; Short=AtALA1; AltName: Full=Aminophospholipid flippase 1 gi|9909198|gb|AAG01899.1|AF175769_1 aminophospholipid flippase [Arabidopsis thaliana] gi|10178032|dbj|BAB11515.1| ATPase [Arabidopsis thaliana] gi|332003422|gb|AED90805.1| phospholipid–transporting ATPase 1 [Arabidopsis thaliana]	1150	1158	0	100.7	92.7	95.7	phospholipid–transporting ATPase 1	gbpln	Arabidopsis thaliana	AT5G04930.1 | Symbols: ALA1 | aminophospholipid ATPase 1 | chr5:1445509–1449568 FORWARD LENGTH=1158	1150	1158	0	100.7	92.7	95.7
Rsa1.0_01466.1.g27081.t10	gb|AAF02824.1|AC009400_20 hypothetical protein [Arabidopsis thaliana]	96	634	3.00E–12	660.4	50.0	55.2	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G10180.1 | Symbols: | P–loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:3146393–3154644 REVERSE LENGTH=1273	96	1273	5.00E–15	1326.0	50.0	55.2
Rsa1.0_01466.1.g27082.t1	ref|XP_002871120.1| hypothetical protein ARALYDRAFT_487275 [Arabidopsis lyrata subsp. lyrata] gi|297316957|gb|EFH47379.1| hypothetical protein ARALYDRAFT_487275 [Arabidopsis lyrata subsp. lyrata]	371	366	1.00E–110	98.7	63.3	72.8	hypothetical protein ARALYDRAFT_487275	gbpln	Arabidopsis lyrata	AT5G04890.1 | Symbols: RTM2 | HSP20–like chaperones superfamily protein | chr5:1427217–1428390 FORWARD LENGTH=366	371	366	7.00E–91	98.7	59.8	69.3
Rsa1.0_01466.1.g27083.t1	ref|XP_002871119.1| glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata] gi|297316956|gb|EFH47378.1| glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata]	669	668	0	99.9	89.8	95.2	glycosyl hydrolase family 3 protein	gbpln	Arabidopsis lyrata	AT5G04885.1 | Symbols: | Glycosyl hydrolase family protein | chr5:1423369–1426628 FORWARD LENGTH=665	669	665	0	99.4	87.6	94.3
Rsa1.0_01466.1.g27084.t1	gb|ABE73345.1| putative calcium–dependent protein kinase 2 [Isatis tinctoria] gi|92110524|gb|ABE73346.1| putative calcium–dependent protein kinase 2 [Isatis tinctoria]	603	625	0	103.6	91.5	94.7	putative calcium–dependent protein kinase 2	gbpln	Isatis tinctoria	AT5G04870.1 | Symbols: CPK1, ATCPK1 | calcium dependent protein kinase 1 | chr5:1417015–1419877 REVERSE LENGTH=610	603	610	0	101.2	89.6	92.7

<table>
<tr><td>Rsa1.0_01466.1.g27085.t1</td><td>gb|EOA21471.1| hypothetical protein CARUB_v10001863mg [Capsella rubella]</td><td>238</td><td>235</td><td>1.00E-121</td><td>98.7</td><td>92.4</td><td>95.4</td><td>hypothetical protein CARUB_v10001863mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G04850.1 | Symbols: VPS60.2 | SNF7 family protein | chr5:1408246-1409806 REVERSE LENGTH=235</td><td>238</td><td>235</td><td>1.00E-122</td><td>98.7</td><td>91.2</td><td>95.0</td></tr>
<tr><td>Rsa1.0_01466.1.g27086.t1</td><td>gb|EOA21611.1| hypothetical protein CARUB_v10002023mg [Capsella rubella]</td><td>194</td><td>194</td><td>3.00E-93</td><td>100.0</td><td>86.1</td><td>91.8</td><td>hypothetical protein CARUB_v10002023mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G04830.2 | Symbols: | Nuclear transport factor 2 (NTF2) family protein | chr5:1402294-1403671 REVERSE LENGTH=178</td><td>194</td><td>178</td><td>1.00E-91</td><td>91.8</td><td>80.4</td><td>85.1</td></tr>
<tr><td>Rsa1.0_01466.1.g27087.t1</td><td>ref|XP_002871113.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297316950|gb|EFH47372.1| binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>754</td><td>637</td><td>0</td><td>84.5</td><td>68.6</td><td>74.4</td><td>binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G04780.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:1384540-1386447 FORWARD LENGTH=635</td><td>754</td><td>635</td><td>0</td><td>84.2</td><td>68.0</td><td>74.1</td></tr>
<tr><td>Rsa1.0_01466.1.g27088.t1</td><td>ref|NP_196097.1| cationic amino acid transporter 6 [Arabidopsis thaliana] gi|75311713|sp|Q9LZ20.1|CAAT6_ARATH RecName: Full=Cationic amino acid transporter 6, chloroplastic; Flags: Precursor gi|13430548|gb|AAK25896.1|AF360186_1 putative amino acid transport protein [Arabidopsis thaliana] gi|7413539|emb|CAB86019.1| amino acid transport-like protein [Arabidopsis thaliana] gi|9758452|dbj|BAB08981.1| amino acid transporter-like protein [Arabidopsis thaliana] gi|14532754|gb|AAK64078.1| putative amino acid transport protein [Arabidopsis thaliana] gi|21553707|gb|AAM62800.1| amino acid transport-like protein [Arabidopsis thaliana] gi|332003399|gb|AED90782.1| cationic amino acid transporter 6 [Arabidopsis thaliana]</td><td>480</td><td>583</td><td>0</td><td>121.5</td><td>92.3</td><td>95.2</td><td>cationic amino acid transporter 6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G04770.1 | Symbols: ATCAT6, CAT6 | cationic amino acid transporter 6 | chr5:1379118-1382304 FORWARD LENGTH=583</td><td>480</td><td>583</td><td>0</td><td>121.5</td><td>92.3</td><td>95.2</td></tr>
<tr><td>Rsa1.0_01467.1.g27089.t1</td><td>ref|XP_002886385.1| hypothetical protein ARALYDRAFT_893060 [Arabidopsis lyrata subsp. lyrata] gi|297332226|gb|EFH62644.1| hypothetical protein ARALYDRAFT_893060 [Arabidopsis lyrata subsp. lyrata]</td><td>295</td><td>294</td><td>1.00E-140</td><td>99.7</td><td>80.3</td><td>91.5</td><td>hypothetical protein ARALYDRAFT_893060</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G63780.1 | Symbols: IMP4 | Ribosomal RNA processing Brix domain protein | chr1:23665045-23667243 REVERSE LENGTH=294</td><td>295</td><td>294</td><td>1.00E-139</td><td>99.7</td><td>78.3</td><td>91.5</td></tr>
<tr><td>Rsa1.0_01467.1.g27090.t1</td><td>ref|XP_002873623.1| aba-overly sensitive 1 [Arabidopsis lyrata subsp. lyrata] gi|297319460|gb|EFH49882.1| aba-overly sensitive 1 [Arabidopsis lyrata subsp. lyrata]</td><td>198</td><td>1317</td><td>2.00E-46</td><td>665.2</td><td>55.1</td><td>59.6</td><td>aba-overly sensitive 1</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G13680.1 | Symbols: ELO2, ABO1 | IKI3 family protein | chr5:4410522-4415471 REVERSE LENGTH=1319</td><td>198</td><td>1319</td><td>7.00E-49</td><td>666.2</td><td>54.5</td><td>59.1</td></tr>
<tr><td>Rsa1.0_01467.1.g27091.t1</td><td>ref|XP_002884202.1| hypothetical protein ARALYDRAFT_480870 [Arabidopsis lyrata subsp. lyrata] gi|297330042|gb|EFH60461.1| hypothetical protein ARALYDRAFT_480870 [Arabidopsis lyrata subsp. lyrata]</td><td>421</td><td>421</td><td>0</td><td>100.0</td><td>96.4</td><td>98.3</td><td>hypothetical protein ARALYDRAFT_480870</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G20420.1 | Symbols: | ATP citrate lyase (ACL) family protein | chr2:8805574-8807858 FORWARD LENGTH=421</td><td>421</td><td>421</td><td>0</td><td>100.0</td><td>95.5</td><td>98.6</td></tr>
<tr><td>Rsa1.0_01467.1.g27092.t1</td><td>ref|NP_001185303.1| Peptidase M1 family protein [Arabidopsis thaliana] gi|332196026|gb|AEE34147.1| Peptidase M1 family protein [Arabidopsis thaliana]</td><td>1005</td><td>1013</td><td>0</td><td>100.8</td><td>91.4</td><td>95.4</td><td>Peptidase M1 family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G63770.5 | Symbols: | Peptidase M1 family protein | chr1:23657791-23664243 REVERSE LENGTH=1013</td><td>1005</td><td>1013</td><td>0</td><td>100.8</td><td>91.4</td><td>95.4</td></tr>
<tr><td>Rsa1.0_01467.1.g27093.t4</td><td>emb|CAZ40338.1| putative disease resistance protein [Raphanus sativus]</td><td>1006</td><td>2100</td><td>0</td><td>208.7</td><td>89.1</td><td>89.2</td><td>putative disease resistance protein</td><td>gbpln</td><td>Raphanus sativus</td><td>AT1G63730.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:23641770-23645132 FORWARD LENGTH=966</td><td>1006</td><td>966</td><td>0</td><td>96.0</td><td>63.1</td><td>74.2</td></tr>
<tr><td>Rsa1.0_01467.1.g27094.t1</td><td>gb|AAN72085.1| putative aminopeptidase [Arabidopsis thaliana] gi|34098843|gb|AAQ56804.1| At1g63770 [Arabidopsis thaliana] gi|62003356|gb|AAX59049.1| M1 aminopeptidase [Arabidopsis thaliana]</td><td>153</td><td>883</td><td>1.00E-39</td><td>577.1</td><td>60.1</td><td>70.6</td><td>putative aminopeptidase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G63770.5 | Symbols: | Peptidase M1 family protein | chr1:23657791-23664243 REVERSE LENGTH=1013</td><td>153</td><td>1013</td><td>5.00E-42</td><td>662.1</td><td>50.3</td><td>53.6</td></tr>
<tr><td>Rsa1.0_01467.1.g27095.t1</td><td>emb|CAZ40337.1| hypothetical protein [Raphanus sativus]</td><td>347</td><td>342</td><td>1.00E-175</td><td>98.6</td><td>94.8</td><td>95.1</td><td>hypothetical protein</td><td>gbpln</td><td>Raphanus sativus</td><td>AT1G63720.1 | Symbols: | BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT5G52430.1); Has 490 Blast hits to 394 proteins in 96 species: Archae - 0; Bacteria - 2; Metazoa - 132; Fungi - 88; Plants - 175; Viruses - 14; Other Eukaryotes - 79 (source: NCBI BLink). | chr1:23636122-23637348 REVERSE LENGTH=358</td><td>347</td><td>358</td><td>1.00E-120</td><td>103.2</td><td>74.1</td><td>83.0</td></tr>
<tr><td>Rsa1.0_01467.1.g27096.t1</td><td>gb|AAP86200.1| pentatricopeptide repeat-containing protein [Raphanus sativus]</td><td>143</td><td>654</td><td>2.00E-77</td><td>457.3</td><td>100.0</td><td>100.0</td><td>pentatricopeptide repeat-containing protein</td><td>gbpln</td><td>Raphanus sativus</td><td>AT1G64100.2 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:23791585-23795563 FORWARD LENGTH=806</td><td>143</td><td>806</td><td>2.00E-34</td><td>563.6</td><td>46.2</td><td>54.5</td></tr>
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Rsa1.0_01468.1.g27097.t1	gb|EOA32480.1| hypothetical protein CARUB_v10015759mg [Capsella rubella]	329	350	8.00E-88	106.4	49.8	69.6	hypothetical protein CARUB_v10015759mg	gbpln	Capsella rubella	AT2G17305.1 | Symbols: | CONTAINS InterPro DOMAIN/s: FBD (InterPro:IPR013596), FBD-like (InterPro:IPR006566); BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT3G62230.1); Has 81 Blast hits to 54 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 81; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:7527676-7528853 FORWARD LENGTH=271	329	271	1.00E-88	82.4	44.7	62.0
Rsa1.0_01468.1.g27098.t1	gb|EOA16621.1| hypothetical protein CARUB_v10004791mg [Capsella rubella]	451	452	0	100.2	95.1	97.3	hypothetical protein CARUB_v10004791mg	gbpln	Capsella rubella	AT3G42050.1 | Symbols: | vacuolar ATP synthase subunit H family protein | chr3:14228846-14232228 REVERSE LENGTH=441	451	441	0	97.8	92.0	94.9
Rsa1.0_01468.1.g27099.t1	gb|EOA17260.1| hypothetical protein CARUB_v10005534mg [Capsella rubella]	260	259	1.00E-123	99.6	85.4	88.8	hypothetical protein CARUB_v10005534mg	gbpln	Capsella rubella	AT4G34180.1 | Symbols: | Cyclase family protein | chr4:16370060-16371383 REVERSE LENGTH=255	260	255	1.00E-121	98.1	83.8	88.5
Rsa1.0_01468.1.g27100.t1	ref|NP_567987.1| uncharacterized protein [Arabidopsis thaliana] gi|21593821|gb|AAM65788.1| unknown [Arabidopsis thaliana] gi|332661153|gb|AEE86553.1| uncharacterized protein AT4G35725 [Arabidopsis thaliana]	75	123	2.00E-11	164.0	60.0	68.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G35725.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: embryo, sepal; EXPRESSED DURING: 4 anthesis, C globular stage; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16930028-16930485 REVERSE LENGTH=123	75	123	4.00E-14	164.0	60.0	68.0
Rsa1.0_01468.1.g27101.t1	ref|NP_567987.1| uncharacterized protein [Arabidopsis thaliana] gi|21593821|gb|AAM65788.1| unknown [Arabidopsis thaliana] gi|332661153|gb|AEE86553.1| uncharacterized protein AT4G35725 [Arabidopsis thaliana]	81	123	2.00E-16	151.9	59.3	69.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G35725.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: embryo, sepal; EXPRESSED DURING: 4 anthesis, C globular stage; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16930028-16930485 REVERSE LENGTH=123	81	123	3.00E-19	151.9	59.3	69.1
Rsa1.0_01468.1.g27102.t1	ref|XP_002867129.1| hypothetical protein ARALYDRAFT_491252 [Arabidopsis lyrata subsp. lyrata] gi|297312965|gb|EFH43388.1| hypothetical protein ARALYDRAFT_491252 [Arabidopsis lyrata subsp. lyrata]	599	603	0	100.7	91.5	94.8	hypothetical protein ARALYDRAFT_491252	gbpln	Arabidopsis lyrata	AT4G34200.1 | Symbols: EDA9 | D-3-phosphoglycerate dehydrogenase | chr4:16374041-16376561 REVERSE LENGTH=603	599	603	0	100.7	91.3	94.3
Rsa1.0_01468.1.g27103.t1	gb|EOA24678.1| hypothetical protein CARUB_v10017951mg [Capsella rubella]	240	239	1.00E-117	99.6	87.9	94.6	hypothetical protein CARUB_v10017951mg	gbpln	Capsella rubella	AT3G57230.1 | Symbols: AGL16 | AGAMOUS-like 16 | chr3:21177710-21180671 FORWARD LENGTH=240	240	240	1.00E-117	100.0	86.7	92.5

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<tr><td>Rsa1.0_01468.1.g27104.t1</td><td>ref|NP_195149.1| cinnamyl alcohol dehydrogenase 5 [Arabidopsis thaliana] gi|13626131|sp|O49482.1|CADH5_ARATH RecName: Full=Cinnamyl alcohol dehydrogenase 5; Short=AtCAD5; AltName: Full=Cinnamyl alcohol dehydrogenase D gi|134104089|pdb|2CF5|A Chain A, Crystal Structures Of The Arabidopsis Cinnamyl Alcohol Dehydrogenases, Atcad5 gi|134104090|pdb|2CF6|A Chain A, Crystal Structures Of The Arabidopsis Cinnamyl Alcohol Dehydrogenases Atcad5 gi|2911039|emb|CAA17549.1| cinnamyl alcohol dehydrogenase-like protein [Arabidopsis thaliana] gi|7270373|emb|CAB80140.1| cinnamyl alcohol dehydrogenase-like protein [Arabidopsis thaliana] gi|14334456|gb|AAK59426.1| putative cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|21280925|gb|AAM44967.1| putative cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|31880043|gb|AAP59435.1| cinnamyl alcohol dehydrogenase [Arabidopsis thaliana] gi|332660944|gb|AEE86344.1| cinnamyl alcohol dehydrogenase 5 [Arabidopsis thaliana]</td><td>357</td><td>357</td><td>1.00E-173</td><td>100.0</td><td>93.8</td><td>98.3</td><td>cinnamyl alcohol dehydrogenase 5</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G34230.1 | Symbols: CAD5, ATCAD5, CAD-5 | cinnamyl alcohol dehydrogenase 5 | chr4:16386898-16388666 REVERSE LENGTH=357</td><td>357</td><td>357</td><td>1.00E-175</td><td>100.0</td><td>93.8</td><td>98.3</td></tr>
<tr><td>Rsa1.0_01468.1.g27105.t1</td><td>ref|XP_002869164.1| hypothetical protein ARALYDRAFT_328320 [Arabidopsis lyrata subsp. lyrata] gi|297315000|gb|EFH45423.1| hypothetical protein ARALYDRAFT_328320 [Arabidopsis lyrata subsp. lyrata]</td><td>492</td><td>467</td><td>0</td><td>94.9</td><td>82.9</td><td>86.4</td><td>hypothetical protein ARALYDRAFT_328320</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G73700.1 | Symbols: | MATE efflux family protein | chr1:27717554-27719630 REVERSE LENGTH=476</td><td>492</td><td>476</td><td>0</td><td>96.7</td><td>74.6</td><td>83.1</td></tr>
<tr><td>Rsa1.0_01469.1.g27106.t5</td><td>dbj|BAB09523.1| unnamed protein product [Arabidopsis thaliana]</td><td>212</td><td>275</td><td>2.00E-82</td><td>129.7</td><td>75.9</td><td>83.0</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G09680.2 | Symbols: RLF | reduced lateral root formation | chr5:2999362-3000185 REVERSE LENGTH=211</td><td>212</td><td>211</td><td>1.00E-84</td><td>99.5</td><td>75.9</td><td>83.0</td></tr>
<tr><td>Rsa1.0_01469.1.g27107.t1</td><td>ref|XP_002873415.1| hypothetical protein ARALYDRAFT_908918 [Arabidopsis lyrata subsp. lyrata] gi|297319252|gb|EFH49674.1| hypothetical protein ARALYDRAFT_908918 [Arabidopsis lyrata subsp. lyrata]</td><td>492</td><td>546</td><td>0</td><td>111.0</td><td>75.6</td><td>82.3</td><td>hypothetical protein ARALYDRAFT_908918</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G09670.1 | Symbols: | loricrin-related | chr5:2996109-2997749 REVERSE LENGTH=546</td><td>492</td><td>546</td><td>0</td><td>111.0</td><td>75.6</td><td>81.3</td></tr>
<tr><td>Rsa1.0_01469.1.g27108.t1</td><td>sp|Q9XFW3.1|MDHG2_BRANA RecName: Full=Malate dehydrogenase 2, glyoxysomal; Flags: Precursor gi|4995091|emb|CAB43995.1| malate dehydrogenase 2 [Brassica napus]</td><td>358</td><td>358</td><td>0</td><td>100.0</td><td>99.2</td><td>99.7</td><td>RecName: Full=Malate dehydrogenase 2, glyoxysomal; Flags: Precursor gi|4995091|emb|CAB43995.1| malate dehydrogenase 2</td><td>gbpln</td><td>Brassica napus</td><td>AT5G09660.1 | Symbols: PMDH2 | peroxisomal NAD-malate dehydrogenase 2 | chr5:2993645-2995551 REVERSE LENGTH=354</td><td>358</td><td>354</td><td>0</td><td>98.9</td><td>95.8</td><td>97.8</td></tr>
<tr><td>Rsa1.0_01469.1.g27109.t1</td><td>gb|EOA31114.1| hypothetical protein CARUB_v10014274mg [Capsella rubella]</td><td>296</td><td>300</td><td>1.00E-149</td><td>101.4</td><td>89.2</td><td>92.6</td><td>hypothetical protein CARUB_v10014274mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G09650.1 | Symbols: AtPPa6, PPa6 | pyrophosphorylase 6 | chr5:2991331-2993117 REVERSE LENGTH=300</td><td>296</td><td>300</td><td>1.00E-150</td><td>101.4</td><td>88.5</td><td>92.6</td></tr>
<tr><td>Rsa1.0_01469.1.g27110.t1</td><td>emb|CAM91991.1| sinapoylglucose:choline sinapoyltransferase [Brassica napus var. napus]</td><td>413</td><td>466</td><td>0</td><td>112.8</td><td>81.6</td><td>84.3</td><td>sinapoylglucose:choline sinapoyltransferase</td><td>gbpln</td><td>Brassica napus</td><td>AT5G09640.1 | Symbols: SNG2, SCPL19 | serine carboxypeptidase-like 19 | chr5:2988373-2990966 FORWARD LENGTH=465</td><td>413</td><td>465</td><td>1.00E-171</td><td>112.6</td><td>74.1</td><td>79.9</td></tr>
<tr><td>Rsa1.0_01469.1.g27111.t1</td><td>gb|EOA21533.1| hypothetical protein CARUB_v10001939mg [Capsella rubella]</td><td>214</td><td>216</td><td>8.00E-89</td><td>100.9</td><td>78.0</td><td>84.6</td><td>hypothetical protein CARUB_v10001939mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G09600.3 | Symbols: SDH3-1 | succinate dehydrogenase 3-1 | chr5:2979220-2980527 FORWARD LENGTH=213</td><td>214</td><td>213</td><td>7.00E-89</td><td>99.5</td><td>77.1</td><td>85.0</td></tr>
<tr><td>Rsa1.0_01469.1.g27112.t1</td><td>dbj|BAJ34398.1| unnamed protein product [Thellungiella halophila]</td><td>652</td><td>683</td><td>0</td><td>104.8</td><td>94.6</td><td>97.4</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G09590.1 | Symbols: MTHSC70-2, HSC70-5 | mitochondrial HSO70 2 | chr5:2975721-2978508 FORWARD LENGTH=682</td><td>652</td><td>682</td><td>0</td><td>104.6</td><td>92.9</td><td>96.9</td></tr>
<tr><td>Rsa1.0_01469.1.g27113.t1</td><td>ref|NP_196520.1| uncharacterized protein [Arabidopsis thaliana] gi|7671431|emb|CAB89372.1| putative protein [Arabidopsis thaliana] gi|98961675|gb|ABF59167.1| unknown protein [Arabidopsis thaliana] gi|332004029|gb|AED91412.1| uncharacterized protein AT5G09580 [Arabidopsis thaliana]</td><td>353</td><td>393</td><td>1.00E-152</td><td>111.3</td><td>77.9</td><td>87.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G09580.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53345.1); Has 53 Blast hits to 53 proteins in 12 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:2972639-2974438 FORWARD LENGTH=393</td><td>353</td><td>393</td><td>1.00E-154</td><td>111.3</td><td>77.9</td><td>87.3</td></tr>
</table>

Rsa1.0_01469.1.g27114.t3	ref|XP_002885880.1| hypothetical protein ARALYDRAFT_899583 [Arabidopsis lyrata subsp. lyrata] gi|297331720|gb|EFH62139.1| hypothetical protein ARALYDRAFT_899583 [Arabidopsis lyrata subsp. lyrata]	567	183	5.00E-13	32.3	11.1	17.1	hypothetical protein ARALYDRAFT_899583	gbpln	Arabidopsis lyrata	AT3G60040.1 | Symbols: | F-box family protein | chr3:22175937-22179728 REVERSE LENGTH=838	567	838	6.00E-13	147.8	8.6	12.0
Rsa1.0_01469.1.g27115.t1	gb|EOA22581.1| hypothetical protein CARUB_v10003247mg [Capsella rubella]	445	445	0	100.0	97.3	98.2	hypothetical protein CARUB_v10003247mg	gbpln	Capsella rubella	AT5G09550.1 | Symbols: | GDP dissociation inhibitor family protein / Rab GTPase activator family protein | chr5:2963850-2966465 FORWARD LENGTH=445	445	445	0	100.0	96.9	98.0
Rsa1.0_01470.1.g27116.t3	emb|CAN70013.1| hypothetical protein VITISV_017116 [Vitis vinifera]	468	947	1.00E-65	202.4	36.1	54.7	hypothetical protein VITISV_017116	gbpln	Vitis vinifera	ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145	468	145	2.00E-26	31.0	11.1	16.2
Rsa1.0_01470.1.g27117.t1	gb|EOA28140.1| hypothetical protein CARUB_v10024329mg [Capsella rubella]	61	123	1.00E-17	201.6	83.6	93.4	hypothetical protein CARUB_v10024329mg	gbpln	Capsella rubella	AT2G41905.1 | Symbols: | BEST Arabidopsis thaliana protein match is: arabinogalactan protein 23 (TAIR:AT3G57690.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:17495766-17495951 FORWARD LENGTH=61	61	61	3.00E-20	100.0	86.9	93.4
Rsa1.0_01470.1.g27118.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01470.1.g27119.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	290	467	1.00E-36	161.0	31.4	41.4	hypothetical protein 31.t00031	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	290	566	9.00E-20	195.2	16.2	27.9
Rsa1.0_01470.1.g27120.t1	ref|XP_002876436.1| hypothetical protein ARALYDRAFT_486225 [Arabidopsis lyrata subsp. lyrata] gi|297322274|gb|EFH52695.1| hypothetical protein ARALYDRAFT_486225 [Arabidopsis lyrata subsp. lyrata]	336	334	1.00E-165	99.4	84.5	92.3	hypothetical protein ARALYDRAFT_486225	gbpln	Arabidopsis lyrata	AT3G57750.2 | Symbols: | Protein kinase superfamily protein | chr3:21394050-21395054 FORWARD LENGTH=334	336	334	1.00E-167	99.4	84.8	92.3
Rsa1.0_01470.1.g27121.t1	ref|XP_002876437.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322275|gb|EFH52696.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	372	377	1.00E-180	101.3	83.3	90.3	kinase family protein	gbpln	Arabidopsis lyrata	AT3G57760.3 | Symbols: | Protein kinase superfamily protein | chr3:21395983-21397119 FORWARD LENGTH=378	372	378	1.00E-174	101.6	82.5	89.2
Rsa1.0_01471.1.g27122.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01471.1.g27123.t1	ref|NP_177044.1| nudix hydrolase 1 [Arabidopsis thaliana] gi|68565931|sp|Q9CA40.1|NUDT1_ARATH RecName: Full=Nudix hydrolase 1; Short=AtNUDT1; AltName: Full=7,8-dihydro-8-oxoguanine-triphosphatase; AltName: Full=8-oxo-dGTP diphosphatase; Short=8-oxo-dGTPase; AltName: Full=Dihydroneopterin triphosphate pyrophosphohydrolase; Short=DHNTP pyrophosphohydrolase; AltName: Full=NADH pyrophosphatase gi|12324137|gb|AAG52038.1|AC011914_8 putative mutT protein; 68398-67881 [Arabidopsis thaliana] gi|21593739|gb|AAM65706.1| putative mutT protein [Arabidopsis thaliana] gi|26450213|dbj|BAC42225.1| putative mutT protein [Arabidopsis thaliana] gi|28827456|gb|AAO50572.1| putative mutT protein [Arabidopsis thaliana] gi|51971967|dbj|BAD44648.1| mutT like protein [Arabidopsis thaliana] gi|332196715|gb|AEE34836.1| nudix hydrolase 1 [Arabidopsis thaliana]	144	147	6.00E-62	102.1	78.5	88.2	nudix hydrolase 1	gbpln	Arabidopsis thaliana	AT1G68760.1 | Symbols: ATNUDT1, ATNUDX1, NUDX1 | nudix hydrolase 1 | chr1:25829090-25829607 FORWARD LENGTH=147	144	147	2.00E-64	102.1	78.5	88.2
Rsa1.0_01471.1.g27124.t1	ref|NP_564941.1| protein IDA [Arabidopsis thaliana] gi|75154765|sp|Q8LAD7.1|IDA_ARATH RecName: Full=Protein IDA; AltName: Full=Protein INFLORESCENCE DEFICIENT IN ABSCISSION; Flags: Precursor gi|21593468|gb|AAM65435.1| unknown [Arabidopsis thaliana] gi|94807658|gb|ABF47126.1| At1g68765 [Arabidopsis thaliana] gi|332196716|gb|AEE34837.1| protein IDA [Arabidopsis thaliana]	72	77	6.00E-17	106.9	75.0	87.5	protein IDA	gbpln	Arabidopsis thaliana	AT1G68765.1 | Symbols: IDA | Putative membrane lipoprotein | chr1:25830157-25830390 REVERSE LENGTH=77	72	77	1.00E-19	106.9	75.0	87.5

<table>
<tr><td>Rsa1.0_01471.1.g27125.t1</td><td>ref|NP_177046.1| little nuclei3 protein [Arabidopsis thaliana] gi|12324133|gb|AAG52034.1|AC011914_4 putative nuclear matrix constituent protein 1 (NMCP1); 58331-62556 [Arabidopsis thaliana] gi|332196718|gb|AEE34839.1| little nuclei3 protein [Arabidopsis thaliana]</td><td>997</td><td>1085</td><td>0</td><td>108.8</td><td>58.1</td><td>71.0</td><td>little nuclei3 protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68790.1 | Symbols: LINC3 | little nuclei3 | chr1:25834932-25839157 REVERSE LENGTH=1085</td><td>997</td><td>1085</td><td>0</td><td>108.8</td><td>58.1</td><td>71.0</td></tr>
<tr><td>Rsa1.0_01471.1.g27126.t2</td><td>pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]</td><td>1462</td><td>1333</td><td>0</td><td>91.2</td><td>41.3</td><td>56.2</td><td>RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1462</td><td>575</td><td>2.00E-95</td><td>39.3</td><td>13.3</td><td>19.9</td></tr>
<tr><td>Rsa1.0_01471.1.g27127.t1</td><td>ref|NP_564943.1| protein CLAVATA3/ESR-related 12 [Arabidopsis thaliana] gi|122196653|sp|Q29PU4.1|CLE12_ARATH RecName: Full=CLAVATA3/ESR (CLE)-related protein 12; Contains: RecName: Full=CLE12p; Flags: Precursor gi|89111846|gb|ABD60695.1| At1g68795 [Arabidopsis thaliana] gi|332196719|gb|AEE34840.1| protein CLAVATA3/ESR-related 12 [Arabidopsis thaliana]</td><td>115</td><td>118</td><td>1.00E-23</td><td>102.6</td><td>67.8</td><td>72.2</td><td>protein CLAVATA3/ESR-related 12</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68795.1 | Symbols: CLE12 | CLAVATA3/ESR-RELATED 12 | chr1:25841079-25841435 REVERSE LENGTH=118</td><td>115</td><td>118</td><td>2.00E-26</td><td>102.6</td><td>67.8</td><td>72.2</td></tr>
<tr><td>Rsa1.0_01471.1.g27128.t1</td><td>gb|EOA26043.1| hypothetical protein CARUB_v10019457mg, partial [Capsella rubella]</td><td>348</td><td>489</td><td>4.00E-48</td><td>140.5</td><td>25.9</td><td>27.3</td><td>hypothetical protein CARUB_v10019457mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G53520.1 | Symbols: UXS1, ATUXS1 | UDP-glucuronic acid decarboxylase 1 | chr3:19841635-19844057 FORWARD LENGTH=435</td><td>348</td><td>435</td><td>2.00E-50</td><td>125.0</td><td>25.9</td><td>27.3</td></tr>
<tr><td>Rsa1.0_01471.1.g27129.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01472.1.g27130.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT3G60450.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:22340982-22342187 FORWARD LENGTH=274</td><td>114</td><td>274</td><td>1.00E-12</td><td>240.4</td><td>28.1</td><td>30.7</td></tr>
<tr><td>Rsa1.0_01472.1.g27131.t1</td><td>ref|NP_199009.2| RabGAP/TBC domain-containing protein [Arabidopsis thaliana] gi|51971014|dbj|BAD44199.1| GTPase activator protein of Rab-like small GTPases-like protein [Arabidopsis thaliana] gi|332007362|gb|AED94745.1| RabGAP/TBC domain-containing protein [Arabidopsis thaliana]</td><td>337</td><td>549</td><td>3.00E-38</td><td>162.9</td><td>26.7</td><td>30.0</td><td>RabGAP/TBC domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G41940.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr5:16782039-16785451 FORWARD LENGTH=549</td><td>337</td><td>549</td><td>8.00E-41</td><td>162.9</td><td>26.7</td><td>30.0</td></tr>
<tr><td>Rsa1.0_01472.1.g27132.t2</td><td>ref|XP_002883443.1| hypothetical protein ARALYDRAFT_342502 [Arabidopsis lyrata subsp. lyrata] gi|297329283|gb|EFH59702.1| hypothetical protein ARALYDRAFT_342502 [Arabidopsis lyrata subsp. lyrata]</td><td>323</td><td>454</td><td>7.00E-13</td><td>140.6</td><td>14.9</td><td>20.4</td><td>hypothetical protein ARALYDRAFT_342502</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472</td><td>323</td><td>472</td><td>1.00E-10</td><td>146.1</td><td>11.5</td><td>18.0</td></tr>
<tr><td>Rsa1.0_01472.1.g27133.t1</td><td>ref|NP_195459.1| cytochrome P450 81F1 [Arabidopsis thaliana] gi|12643629|sp|O65790.2|C81F1_ARATH RecName: Full=Cytochrome P450 81F1 gi|4468809|emb|CAB38210.1| cytochrome P450 monooxygenase (CYP91A2) [Arabidopsis thaliana] gi|7270725|emb|CAB80408.1| cytochrome P450 monooxygenase (CYP91A2) [Arabidopsis thaliana] gi|14532440|gb|AAK63948.1| AT4g37430/F6G17_80 [Arabidopsis thaliana] gi|332661392|gb|AEE86792.1| cytochrome P450 81F1 [Arabidopsis thaliana]</td><td>400</td><td>500</td><td>1.00E-151</td><td>125.0</td><td>64.5</td><td>70.8</td><td>cytochrome P450 81F1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G37430.1 | Symbols: CYP91A2, CYP81F1 | cytochrome P450, family 91, subfamily A, polypeptide 2 | chr4:17597242-17598829 FORWARD LENGTH=500</td><td>400</td><td>500</td><td>1.00E-154</td><td>125.0</td><td>64.5</td><td>70.8</td></tr>
</table>

Rsa1.0_01472.1.g27134.t1	ref|NP_195459.1| cytochrome P450 81F1 [Arabidopsis thaliana] gi|12643629|sp|O65790.2|C81F1_ARATH RecName: Full=Cytochrome P450 81F1 gi|4468809|emb|CAB38210.1| cytochrome P450 monooxygenase (CYP91A2) [Arabidopsis thaliana] gi|7270725|emb|CAB80408.1| cytochrome P450 monooxygenase (CYP91A2) [Arabidopsis thaliana] gi|14532440|gb|AAK63948.1| AT4g37430/F6G17_80 [Arabidopsis thaliana] gi|332661392|gb|AEE86792.1| cytochrome P450 81F1 [Arabidopsis thaliana]	498	500	0	100.4	83.9	93.8	cytochrome P450 81F1	gbpln	Arabidopsis thaliana	AT4G37430.1 | Symbols: CYP91A2, CYP81F1 | cytochrome P450, family 91, subfamily A, polypeptide 2 | chr4:17597242-17598829 FORWARD LENGTH=500	498	500	0	100.4	83.9	93.8
Rsa1.0_01472.1.g27135.t1	ref|NP_195458.1| uncharacterized protein [Arabidopsis thaliana] gi|4468808|emb|CAB38209.1| putative protein [Arabidopsis thaliana] gi|7270724|emb|CAB80407.1| putative protein [Arabidopsis thaliana] gi|332661391|gb|AEE86791.1| uncharacterized protein AT4G37420 [Arabidopsis thaliana]	584	588	0	100.7	81.3	86.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G37420.1 | Symbols: | Domain of unknown function (DUF23) | chr4:17593123-17594889 FORWARD LENGTH=588	584	588	0	100.7	81.3	86.3
Rsa1.0_01472.1.g27136.t1	ref|XP_002868991.1| CYP81F3 [Arabidopsis lyrata subsp. lyrata] gi|297314827|gb|EFH45250.1| CYP81F3 [Arabidopsis lyrata subsp. lyrata]	498	499	0	100.2	89.6	95.0	CYP81F3	gbpln	Arabidopsis lyrata	AT4G37400.1 | Symbols: CYP81F3 | cytochrome P450, family 81, subfamily F, polypeptide 3 | chr4:17584096-17586197 FORWARD LENGTH=501	498	501	0	100.6	89.8	95.4
Rsa1.0_01472.1.g27137.t1	gb|EOA16267.1| hypothetical protein CARUB_v10004412mg [Capsella rubella]	593	603	0	101.7	94.8	97.6	hypothetical protein CARUB_v10004412mg	gbpln	Capsella rubella	AT4G37390.1 | Symbols: YDK1, GH3.2, BRU6, GH3-2, AUR3 | Auxin-responsive GH3 family protein | chr4:17579722-17581768 FORWARD LENGTH=603	593	603	0	101.7	94.1	97.3
Rsa1.0_01473.1.g27138.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1055	2726	0	258.4	51.0	67.4	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1055	158	8.00E-35	15.0	6.6	8.5
Rsa1.0_01473.1.g27139.t1	#	#	#	#	#	#	#	–	––––	––––	AT3G54470.1 | Symbols: | uridine 5'-monophosphate synthase / UMP synthase (PYRE-F) (UMPS) | chr3:20168285-20170245 REVERSE LENGTH=476	123	476	5.00E-11	387.0	25.2	27.6
Rsa1.0_01473.1.g27140.t1	gb|ABD65606.1| hypothetical protein 23.t00002 [Brassica oleracea]	373	433	4.00E-43	116.1	34.3	51.5	hypothetical protein 23.t00002	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01473.1.g27141.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01473.1.g27142.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01473.1.g27143.t1	ref|NP_173247.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|79318119|ref|NP_001031063.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|21539549|gb|AAM53327.1| putative guanine nucleotide regulatory protein [Arabidopsis thaliana] gi|31711944|gb|AAP68328.1| At1g18070 [Arabidopsis thaliana] gi|332191549|gb|AEE29670.1| G1 to S phase transition protein [Arabidopsis thaliana] gi|332191550|gb|AEE29671.1| Translation elongation factor EF1A/initiation factor IF2gamma family protein [Arabidopsis thaliana]	506	532	0	105.1	85.0	92.3	G1 to S phase transition protein	gbpln	Arabidopsis thaliana	AT1G18070.2 | Symbols: | Translation elongation factor EF1A/initiation factor IF2gamma family protein | chr1:6214236-6218211 REVERSE LENGTH=532	506	532	0	105.1	85.0	92.3
Rsa1.0_01473.1.g27144.t2	ref|NP_201199.1| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana] gi|8777307|dbj|BAA96897.1| unnamed protein product [Arabidopsis thaliana] gi|20260318|gb|AAM13057.1| unknown protein [Arabidopsis thaliana] gi|31711746|gb|AAP68229.1| At5g63940 [Arabidopsis thaliana] gi|332010435|gb|AED97818.1| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain [Arabidopsis thaliana]	681	705	0	103.5	88.7	93.5	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	gbpln	Arabidopsis thaliana	AT5G63940.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr5:25588254-25591229 FORWARD LENGTH=705	681	705	0	103.5	88.7	93.5
Rsa1.0_01473.1.g27145.t1	gb|EOA12873.1| hypothetical protein CARUB_v10025845mg [Capsella rubella]	938	919	0	98.0	88.7	92.8	hypothetical protein CARUB_v10025845mg	gbpln	Capsella rubella	AT5G63920.1 | Symbols: TOP3A, AtTOP3alpha | topoisomerase 3alpha | chr5:25574533-25581230 FORWARD LENGTH=926	938	926	0	98.7	89.1	93.3

Rsa1.0_01473.1.g27146.t1	ref|XP_002887884.1| hypothetical protein ARALYDRAFT_892963 [Arabidopsis lyrata subsp. lyrata] gi|297333725|gb|EFH64143.1| hypothetical protein ARALYDRAFT_892963 [Arabidopsis lyrata subsp. lyrata]	396	443	1.00E-104	111.9	55.3	67.7	hypothetical protein ARALYDRAFT_892963	gbpln	Arabidopsis lyrata	AT3G27900.1 | Symbols: | Protein of unknown function (DUF1184) | chr3:10352905-10353639 REVERSE LENGTH=244	396	244	3.00E-32	61.6	26.0	34.3
Rsa1.0_01473.1.g27147.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01474.1.g27148.t1	ref|XP_002887811.1| hypothetical protein ARALYDRAFT_477170 [Arabidopsis lyrata subsp. lyrata] gi|297333652|gb|EFH64070.1| hypothetical protein ARALYDRAFT_477170 [Arabidopsis lyrata subsp. lyrata]	305	305	1.00E-169	100.0	96.7	99.7	hypothetical protein ARALYDRAFT_477170	gbpln	Arabidopsis lyrata	AT1G80760.1 | Symbols: NIP6;1, NIP6, NLM7 | NOD26-like intrinsic protein 6;1 | chr1:30350640-30352015 REVERSE LENGTH=305	305	305	1.00E-170	100.0	95.7	99.0
Rsa1.0_01474.1.g27149.t3	gb|AFK13856.1| Ty3/gypsy retrotransposon protein [Beta vulgaris subsp. vulgaris]	1752	1631	0	93.1	43.6	57.1	Ty3/gypsy retrotransposon protein	gbpln	Beta vulgaris	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1752	158	5.00E-37	9.0	4.1	5.4
Rsa1.0_01474.1.g27150.t1	ref|XP_002889273.1| PDE318 [Arabidopsis lyrata subsp. lyrata] gi|297335114|gb|EFH65532.1| PDE318 [Arabidopsis lyrata subsp. lyrata]	227	449	1.00E-87	197.8	81.1	89.0	PDE318	gbpln	Arabidopsis lyrata	AT1G80770.1 | Symbols: PDE318 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:30355266-30357786 FORWARD LENGTH=451	227	451	9.00E-88	198.7	78.4	89.0
Rsa1.0_01474.1.g27151.t1	ref|XP_002887521.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333362|gb|EFH63780.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	207	211	1.00E-48	101.9	50.2	67.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G80990.1 | Symbols: | XH domain-containing protein | chr1:30424421-30425192 FORWARD LENGTH=229	207	229	3.00E-13	110.6	27.1	42.0
Rsa1.0_01474.1.g27152.t1	ref|NP_001185452.1| putative CCR4-associated factor 1-6 [Arabidopsis thaliana] gi|332198329|gb|AEE36450.1| putative CCR4-associated factor 1-6 [Arabidopsis thaliana]	299	286	1.00E-145	95.7	83.9	87.3	putative CCR4-associated factor 1-6	gbpln	Arabidopsis thaliana	AT1G80780.3 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr1:30358517-30359583 FORWARD LENGTH=286	299	286	1.00E-148	95.7	83.9	87.3
Rsa1.0_01474.1.g27153.t1	gb|AAF14668.1|AC011713_16 ESTs gb|Z34732, gb|R89948 and gb|Z33946 come from this gene [Arabidopsis thaliana]	872	780	0	89.4	49.0	55.8	ESTs gb|Z34732, gb|R89948 and gb|Z33946 come from this gene	gbpln	Arabidopsis thaliana	AT1G80810.2 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr1:30365575-30368898 FORWARD LENGTH=774	872	774	0	88.8	46.6	53.6
Rsa1.0_01474.1.g27154.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01474.1.g27155.t1	gb|AEK27168.1| cinnamoyl-CoA reductase 2-1A [Brassica rapa subsp. oleifera] gi|340026102|gb|AEK27169.1| cinnamoyl-CoA reductase 2-1A [Brassica rapa subsp. oleifera]	337	332	1.00E-180	98.5	90.8	91.4	cinnamoyl-CoA reductase 2-1A	gbpln	Brassica rapa	AT1G80820.1 | Symbols: CCR2, ATCCR2 | cinnamoyl coa reductase | chr1:30370646-30372460 FORWARD LENGTH=332	337	332	1.00E-169	98.5	88.1	89.9
Rsa1.0_01474.1.g27156.t1	ref|XP_002887809.1| NRAMP1 [Arabidopsis lyrata subsp. lyrata] gi|297333650|gb|EFH64068.1| NRAMP1 [Arabidopsis lyrata subsp. lyrata]	509	526	0	103.3	87.2	94.5	NRAMP1	gbpln	Arabidopsis lyrata	AT1G80830.1 | Symbols: NRAMP1, PMIT1, ATNRAMP1 | natural resistance-associated macrophage protein 1 | chr1:30373066-30375644 REVERSE LENGTH=532	509	532	0	104.5	86.4	93.7
Rsa1.0_01474.1.g27157.t1	gb|ACI14400.1| WRKY40-1 transcription factor [Brassica napus]	295	301	1.00E-150	102.0	92.5	96.6	WRKY40-1 transcription factor	gbpln	Brassica napus	AT1G80840.1 | Symbols: WRKY40, ATWRKY40 | WRKY DNA-binding protein 40 | chr1:30383834-30385356 FORWARD LENGTH=302	295	302	1.00E-147	102.4	88.1	93.2
Rsa1.0_01474.1.g27158.t1	gb|EOA35462.1| hypothetical protein CARUB_v10020671mg [Capsella rubella]	323	318	1.00E-135	98.5	83.6	88.9	hypothetical protein CARUB_v10020671mg	gbpln	Capsella rubella	AT1G80850.1 | Symbols: | DNA glycosylase superfamily protein | chr1:30385607-30387272 REVERSE LENGTH=327	323	327	1.00E-137	101.2	84.5	89.8
Rsa1.0_01475.1.g27159.t1	gb|ADD09861.1| chloride channel C [Eutrema halophilum]	807	775	0	96.0	88.5	91.8	chloride channel C	gbpln	Eutrema halophilum	AT5G49890.1 | Symbols: CLC-C, ATCLC-C | chloride channel C | chr5:20288489-20292143 REVERSE LENGTH=779	807	779	0	96.5	87.6	91.3
Rsa1.0_01475.1.g27160.t1	gb|AAD20646.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	220	1040	7.00E-44	472.7	41.8	49.5	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01475.1.g27161.t1	gb|AAD20646.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	252	1040	2.00E-35	412.7	38.1	50.4	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01475.1.g27162.t1	ref|XP_002865763.1| hypothetical protein ARALYDRAFT_331392 [Arabidopsis lyrata subsp. lyrata] gi|297311598|gb|EFH42022.1| hypothetical protein ARALYDRAFT_331392 [Arabidopsis lyrata subsp. lyrata]	952	956	0	100.4	91.1	95.1	hypothetical protein ARALYDRAFT_331392	gbpln	Arabidopsis lyrata	AT5G49900.1 | Symbols: | Beta-glucosidase, GBA2 type family protein | chr5:20297235-20302019 REVERSE LENGTH=957	952	957	0	100.5	91.5	95.5
Rsa1.0_01475.1.g27163.t1	ref|XP_002865764.1| octicosapeptide/Phox/Bem1p domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311599|gb|EFH42023.1| octicosapeptide/Phox/Bem1p domain-containing protein [Arabidopsis lyrata subsp. lyrata]	276	285	1.00E-100	103.3	72.5	80.8	octicosapeptide/Phox/Bem1p domain-containing protein	gbpln	Arabidopsis lyrata	AT5G49920.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr5:20306637-20307583 REVERSE LENGTH=288	276	288	1.00E-101	104.3	73.2	82.6

Rsa1.0_01475.1.g27164.t1	ref|XP_002865765.1| EMB1441 [Arabidopsis lyrata subsp. lyrata] gi|297311600|gb|EFH42024.1| EMB1441 [Arabidopsis lyrata subsp. lyrata]	1094	1080	0	98.7	88.1	92.1	EMB1441	gbpln	Arabidopsis lyrata	AT5G49930.1 | Symbols: emb1441 | zinc knuckle (CCHC-type) family protein | chr5:20308260-20312736 REVERSE LENGTH=1080	1094	1080	0	98.7	88.0	92.0
Rsa1.0_01476.1.g27165.t1	ref|XP_002878520.1| hypothetical protein ARALYDRAFT_349401 [Arabidopsis lyrata subsp. lyrata] gi|297324358|gb|EFH54779.1| hypothetical protein ARALYDRAFT_349401 [Arabidopsis lyrata subsp. lyrata]	1147	1169	0	101.9	73.3	80.6	hypothetical protein ARALYDRAFT_349401	gbpln	Arabidopsis lyrata	AT3G63500.2 | Symbols: | Protein of unknown function (DUF1423) | chr3:23446331-23449991 REVERSE LENGTH=1162	1147	1162	0	101.3	71.9	80.1
Rsa1.0_01476.1.g27166.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01476.1.g27167.t3	ref|XP_002888823.1| beta-ketoacyl-CoA synthase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334664|gb|EFH65082.1| beta-ketoacyl-CoA synthase family protein [Arabidopsis lyrata subsp. lyrata]	452	460	0	101.8	85.4	93.1	beta-ketoacyl-CoA synthase family protein	gbpln	Arabidopsis lyrata	AT1G71160.1 | Symbols: KCS7 | 3-ketoacyl-CoA synthase 7 | chr1:26828788-26830170 REVERSE LENGTH=460	452	460	0	101.8	83.2	92.3
Rsa1.0_01476.1.g27168.t1	gb|EOA35095.1| hypothetical protein CARUB_v10020206mg [Capsella rubella]	489	485	0	99.2	82.6	90.0	hypothetical protein CARUB_v10020206mg	gbpln	Capsella rubella	AT1G71140.1 | Symbols: | MATE efflux family protein | chr1:26824762-26826748 FORWARD LENGTH=485	489	485	0	99.2	81.2	89.6
Rsa1.0_01476.1.g27169.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01476.1.g27170.t1	gb|AAG03119.1|AC004133_13 F5A9.24 [Arabidopsis thaliana]	131	1254	1.00E-12	957.3	32.1	45.8	F5A9.24	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01476.1.g27171.t1	ref|NP_177227.5| protein TIFY 7 [Arabidopsis thaliana] gi|342187044|sp|Q8W4J8.2|TIF7_ARATH RecName: Full=Protein TIFY 7; AltName: Full=Jasmonate ZIM domain-containing protein 9 gi|332196980|gb|AEE35101.1| protein TIFY 7 [Arabidopsis thaliana]	224	267	3.00E-66	119.2	68.3	78.1	protein TIFY 7	gbpln	Arabidopsis thaliana	AT1G70700.1 | Symbols: JAZ9, TIFY7 | TIFY domain/Divergent CCT motif family protein | chr1:26654951-26656804 FORWARD LENGTH=267	224	267	9.00E-69	119.2	68.3	78.1
Rsa1.0_01476.1.g27172.t3	ref|NP_563963.1| FAD/NAD(P)-binding oxidoreductase [Arabidopsis thaliana] gi|5103813|gb|AAD39643.1|AC007591_8 Contains a PF|00175 Oxidoreductase FAD/NADH-binding domain. ESTs gb|H76345 and gb|AA651465 come from this gene [Arabidopsis thaliana] gi|12744999|gb|AAK06879.1|AF344328_1 unknown protein [Arabidopsis thaliana] gi|15451092|gb|AAK96817.1| Unknown protein [Arabidopsis thaliana] gi|18377448|gb|AAL66890.1| unknown protein [Arabidopsis thaliana] gi|332191150|gb|AEE29271.1| FAD/NAD(P)-binding oxidoreductase [Arabidopsis thaliana]	203	295	9.00E-31	145.3	31.0	35.5	FAD/NAD(P)-binding oxidoreductase	gbpln	Arabidopsis thaliana	AT1G15140.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase | chr1:5210403-5212137 REVERSE LENGTH=295	203	295	3.00E-33	145.3	31.0	35.5
Rsa1.0_01476.1.g27173.t1	ref|NP_564995.1| Caleosin-related family protein [Arabidopsis thaliana] gi|75333639|sp|Q9CAB7.1|PXG4_ARATH RecName: Full=Probable peroxygenase 4; Short=AtPXG4; AltName: Full=Caleosin-4 gi|12324758|gb|AAG52340.1|AC011663_19 unknown protein; 59759-58619 [Arabidopsis thaliana] gi|15810177|gb|AAL06990.1| At1g70670/F5A18_15 [Arabidopsis thaliana] gi|23505789|gb|AAN28754.1| At1g70670/F5A18_15 [Arabidopsis thaliana] gi|332196977|gb|AEE35098.1| Caleosin-related family protein [Arabidopsis thaliana]	242	195	3.00E-92	80.6	68.2	71.9	Caleosin-related family protein	gbpln	Arabidopsis thaliana	AT1G70670.1 | Symbols: | Caleosin-related family protein | chr1:26644830-26645970 FORWARD LENGTH=195	242	195	8.00E-95	80.6	68.2	71.9
Rsa1.0_01476.1.g27174.t1	ref|NP_173742.1| MAK16 protein-like protein [Arabidopsis thaliana] gi|332192246|gb|AEE30367.1| MAK16 protein-like protein [Arabidopsis thaliana]	304	303	1.00E-107	99.7	75.0	82.6	MAK16 protein-like protein	gbpln	Arabidopsis thaliana	AT1G23280.1 | Symbols: | MAK16 protein-related | chr1:8260865-8262650 REVERSE LENGTH=303	304	303	1.00E-109	99.7	75.0	82.6
Rsa1.0_01476.1.g27175.t3	ref|XP_002887316.1| ATTAP1 [Arabidopsis lyrata subsp. lyrata] gi|297333157|gb|EFH63575.1| ATTAP1 [Arabidopsis lyrata subsp. lyrata]	767	700	0	91.3	79.0	84.4	ATTAP1	gbpln	Arabidopsis lyrata	AT1G70610.1 | Symbols: ATTAP1, TAP1 | transporter associated with antigen processing protein 1 | chr1:26622086-26626331 FORWARD LENGTH=700	767	700	0	91.3	79.1	84.0
Rsa1.0_01476.1.g27176.t1	gb|ABM30196.1| ribosomal large subunit structural protein [Brassica juncea]	146	146	3.00E-76	100.0	96.6	99.3	ribosomal large subunit structural protein	gbpln	Brassica juncea	AT1G70600.1 | Symbols: | Ribosomal protein L18e/L15 superfamily protein | chr1:26621168-26621608 REVERSE LENGTH=146	146	146	1.00E-78	100.0	96.6	98.6

Rsa1.0_01476.1.g27177.t1	gb|ABM30196.1| ribosomal large subunit structural protein [Brassica juncea]	411	146	1.00E-38	35.5	19.2	20.0	ribosomal large subunit structural protein	gbpln	Brassica juncea	AT1G70600.1 | Symbols: | Ribosomal protein L18e/L15 superfamily protein | chr1:26621168-26621608 REVERSE LENGTH=146	411	146	2.00E-40	35.5	19.0	19.7
Rsa1.0_01476.1.g27178.t1	ref|NP_680115.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|332644891|gb|AEE78412.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	541	619	1.00E-138	114.4	50.3	63.6	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G48400.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:17923678-17925589 FORWARD LENGTH=619	541	619	1.00E-141	114.4	50.3	63.6
Rsa1.0_01476.1.g27179.t1	ref|NP_177206.1| ADP-ribosylation factor 2 [Arabidopsis thaliana] gi|18395248|ref|NP_564195.1| ADP-ribosylation factor 2 [Arabidopsis thaliana] gi|30698721|ref|NP_850975.1| ADP-ribosylation factor 2 [Arabidopsis thaliana] gi|42572059|ref|NP_974120.1| ADP-ribosylation factor 2 [Arabidopsis thaliana] gi|297845410|ref|XP_002890586.1| hypothetical protein ARALYDRAFT_472612 [Arabidopsis lyrata subsp. lyrata] gi|378548287|sp|P0DH91.1|ARF2B_ARATH RecName: Full=ADP-ribosylation factor 2-B; Short=AtARF2; AltName: Full=ARF1-like protein U5 gi|378548311|sp|Q9LQC8.2|ARF2A_ARATH RecName: Full=ADP-ribosylation factor 2-A; Short=AtARF2 gi|11692864|gb|AAG40035.1|AF324684_1 At1g23490 [Arabidopsis thaliana] gi|11762198|gb|AAG40377.1|AF325025_1 At1g70490 [Arabidopsis thaliana] gi|11993875|gb|AAG42921.1|AF329504_1 putative ADP-ribosylation factor [Arabidopsis thaliana] gi|12325036|gb|AAG52463.1|AC010796_2 putative ADP-ribosylation factor 1; 15065-14075 [Arabidopsis thaliana] gi|13430504|gb|AAK25874.1|AF360164_1 putative ADP-ribosylation factor 1 [Arabidopsis thaliana] gi|13926232|gb|AAK49591.1|AF372875_1	181	181	1.00E-95	100.0	92.8	96.7	ADP-ribosylation factor 2	gbpln	Arabidopsis lyrata	AT1G70490.2 | Symbols: ATARFA1D, ARFA1D | Ras-related small GTP-binding family protein | chr1:26564162-26565152 REVERSE LENGTH=181	181	181	4.00E-98	100.0	92.8	96.7
Rsa1.0_01476.1.g27180.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01476.1.g27181.t1	gb|AAF79253.1|AC023279_2 F12K21.4 [Arabidopsis thaliana]	211	857	1.00E-74	406.2	61.6	73.5	F12K21.4	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01476.1.g27182.t1	ref|NP_850976.1| MLP-like protein 34 [Arabidopsis thaliana] gi|79321108|ref|NP_001031265.1| MLP-like protein 34 [Arabidopsis thaliana] gi|21542143|sp|Q9SSK7.1|MLP34_ARATH RecName: Full=MLP-like protein 34 gi|5902401|gb|AAD55503.1|AC008148_13 Unknown protein [Arabidopsis thaliana] gi|13926294|gb|AAK49615.1|AF372899_1 At1g70850/F15H11_10 [Arabidopsis thaliana] gi|16197688|emb|CAC83579.1| major latex-like protein [Arabidopsis thaliana] gi|16323244|gb|AAL15356.1| At1g70850/F15H11_10 [Arabidopsis thaliana] gi|110740285|dbj|BAF02039.1| hypothetical protein [Arabidopsis thaliana] gi|332197006|gb|AEE35127.1| MLP-like protein 34 [Arabidopsis thaliana] gi|332197008|gb|AEE35129.1| MLP-like protein 34 [Arabidopsis thaliana]	147	316	2.00E-57	215.0	77.6	85.0	MLP-like protein 34	gbpln	Arabidopsis thaliana	AT1G70850.3 | Symbols: MLP34 | MLP-like protein 34 | chr1:26715429-26716744 REVERSE LENGTH=316	147	316	5.00E-60	215.0	77.6	85.0
Rsa1.0_01477.1.g27183.t1	ref|XP_002865764.1| octicosapeptide/Phox/Bem1p domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311599|gb|EFH42023.1| octicosapeptide/Phox/Bem1p domain-containing protein [Arabidopsis lyrata subsp. lyrata]	275	285	1.00E-107	103.6	74.2	82.9	octicosapeptide/Phox/Bem1p domain-containing protein	gbpln	Arabidopsis lyrata	AT5G49920.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr5:20306637-20307583 REVERSE LENGTH=288	275	288	1.00E-100	104.7	72.4	82.9
Rsa1.0_01477.1.g27184.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01477.1.g27185.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01477.1.g27186.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01477.1.g27187.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01477.1.g27188.t1	gb|ADD09861.1| chloride channel C [Eutrema halophilum]	775	775	0	100.0	94.6	97.8	chloride channel C	gbpln	Eutrema halophilum	AT5G49890.1 | Symbols: CLC-C, ATCLC-C | chloride channel C | chr5:20288489-20292143 REVERSE LENGTH=779	775	779	0	100.5	94.1	97.4
Rsa1.0_01478.1.g27189.t3	ref|NP_179764.4| uncharacterized protein [Arabidopsis thaliana] gi|330252120|gb|AEC07214.1| uncharacterized protein AT2G21720 [Arabidopsis thaliana]	730	734	0	100.5	77.8	84.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G21720.1 | Symbols: | Plant protein of unknown function (DUF639) | chr2:9273696-9276802 FORWARD LENGTH=734	730	734	0	100.5	77.8	84.5
Rsa1.0_01478.1.g27190.t1	ref|NP_001190964.1| phenylalanyl-tRNA synthetase alpha chain [Arabidopsis thaliana] gi|332661651|gb|AEE87051.1| probable phenylalanine--tRNA ligase alpha subunit [Arabidopsis thaliana]	818	485	0	59.3	46.6	51.3	phenylalanyl-tRNA synthetase alpha chain	gbpln	Arabidopsis thaliana	AT4G39280.2 | Symbols: | phenylalanyl-tRNA synthetase, putative / phenylalanine--tRNA ligase, putative | chr4:18280292-18284831 REVERSE LENGTH=485	818	485	0	59.3	46.6	51.3
Rsa1.0_01478.1.g27191.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01478.1.g27192.t1	ref|NP_180542.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75100652|sp|O82375.1|FBK39_ARATH RecName: Full=Putative F-box/kelch-repeat protein At2g29810 gi|3582323|gb|AAC35220.1| hypothetical protein [Arabidopsis thaliana] gi|330253213|gb|AEC08307.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	384	383	4.00E-87	99.7	47.9	62.5	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT2G29810.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:12726102-12727253 REVERSE LENGTH=383	384	383	1.00E-89	99.7	47.9	62.5
Rsa1.0_01478.1.g27193.t1	sp|P49311.1|GRP2_SINAL RecName: Full=Glycine-rich RNA-binding protein GRP2A gi|496237|gb|AAA59213.1| homology with RNA-binding proteins in meristematic tissue [Sinapis alba]	170	169	3.00E-42	99.4	47.6	49.4	RecName: Full=Glycine-rich RNA-binding protein GRP2A gi|496237|gb|AAA59213.1| homology with RNA-binding proteins in meristematic tissue	gbpln	Sinapis alba	AT2G21660.2 | Symbols: ATGRP7, CCR2 | cold, circadian rhythm, and rna binding 2 | chr2:9265477-9266316 REVERSE LENGTH=159	170	159	2.00E-41	93.5	44.1	49.4
Rsa1.0_01478.1.g27194.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1096	1142	0	104.2	48.7	63.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1096	575	6.00E-98	52.5	18.5	27.2
Rsa1.0_01479.1.g27195.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	130	1123	1.00E-53	863.8	76.2	88.5	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01479.1.g27196.t3	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1572	1142	1.00E-164	72.6	19.0	26.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1572	575	1.00E-83	36.6	11.8	18.5
Rsa1.0_01479.1.g27197.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01479.1.g27198.t1	gb|ABW81182.1| gag-pol-polyprotein3-gypsy-like [Arabidopsis cebennensis]	471	297	5.00E-41	63.1	19.7	28.5	gag-pol-polyprotein3-gypsy-like	gbpln	Arabidopsis cebennensis	#	#	#	#	#	#	#
Rsa1.0_01479.1.g27199.t9	gb|ABD65091.1| hypothetical protein 31.t00049 [Brassica oleracea]	1113	530	2.00E-53	47.6	14.3	21.1	hypothetical protein 31.t00049	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01479.1.g27200.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01479.1.g27201.t3	ref|NP_175064.2| pentatricopeptide repeat-containing protein-like protein [Arabidopsis thaliana] gi|332193889|gb|AEE32010.1| pentatricopeptide repeat-containing protein-like protein [Arabidopsis thaliana]	827	621	0	75.1	44.3	50.3	pentatricopeptide repeat-containing protein-like protein	gbpln	Arabidopsis thaliana	AT1G43980.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:16687637-16689502 REVERSE LENGTH=621	827	621	0	75.1	44.3	50.3
Rsa1.0_01480.1.g27202.t1	gb|AAD28647.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana]	601	627	1.00E-16	104.3	10.6	14.1	putative Ta11-like non-LTR retroelement protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01480.1.g27203.t1	ref|XP_002876294.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322132|gb|EFH52553.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	284	280	1.00E-138	98.6	85.2	93.0	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G55290.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:20502653-20503730 FORWARD LENGTH=280	284	280	1.00E-139	98.6	83.8	92.3
Rsa1.0_01480.1.g27204.t1	ref|XP_002876294.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322132|gb|EFH52553.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	318	280	1.00E-119	88.1	67.9	74.5	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G55290.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:20502653-20503730 FORWARD LENGTH=280	318	280	1.00E-120	88.1	67.3	73.9
Rsa1.0_01480.1.g27205.t1	gb|ABB97038.1| unknown [Brassica rapa]	154	154	3.00E-78	100.0	98.7	99.4	unknown	gbpln	Brassica rapa	AT3G55280.2 | Symbols: RPL23AB | ribosomal protein L23AB | chr3:20500667-20501519 FORWARD LENGTH=154	154	154	2.00E-60	100.0	94.2	96.1
Rsa1.0_01480.1.g27206.t1	ref|XP_002876292.1| map kinase phosphatase [Arabidopsis lyrata subsp. lyrata] gi|297322130|gb|EFH52551.1| map kinase phosphatase [Arabidopsis lyrata subsp. lyrata]	741	786	0	106.1	82.5	88.3	map kinase phosphatase	gbpln	Arabidopsis lyrata	AT3G55270.1 | Symbols: MKP1, ATMKP1 | mitogen-activated protein kinase phosphatase 1 | chr3:20496775-20499408 FORWARD LENGTH=784	741	784	0	105.8	81.8	87.7

Rsa1.0_01480.1_g27207.t1	ref|NP_567017.2| beta-hexosaminidase 1 [Arabidopsis thaliana] gi|426020918|sp|A7WM73.1|HEXO1_ARATH RecName: Full=Beta-hexosaminidase 1; AltName: Full=Beta-GlcNAcase 1; AltName: Full=Beta-N-acetylhexosaminidase 1; AltName: Full=Beta-hexosaminidase 2; Short=AtHEX2; AltName: Full=N-acetyl-beta-glucosaminidase 1; Flags: Precursor gi|157154097|emb|CAM35467.1| beta-N-acetylhexosaminidase [Arabidopsis thaliana] gi|332645839|gb|AEE79360.1| beta-hexosaminidase 1 [Arabidopsis thaliana]	547	541	0	98.9	89.8	94.1	beta-hexosaminidase 1	gbpln	Arabidopsis thaliana	AT3G55260.1 | Symbols: HEXO1, ATHEX2 | beta-hexosaminidase 1 | chr3:20489317-20492858 FORWARD LENGTH=541	547	541	0	98.9	89.8	94.1
Rsa1.0_01480.1_g27208.t1	ref|XP_002876290.1| hypothetical protein ARALYDRAFT_348614 [Arabidopsis lyrata subsp. lyrata] gi|297322128|gb|EFH52549.1| hypothetical protein ARALYDRAFT_348614 [Arabidopsis lyrata subsp. lyrata]	282	277	1.00E-141	98.2	90.4	93.6	hypothetical protein ARALYDRAFT_348614	gbpln	Arabidopsis lyrata	AT3G55250.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, chloroplast, nucleus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 46 Blast hits to 46 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:20479302-20480324 FORWARD LENGTH=277	282	277	1.00E-135	98.2	87.9	91.8
Rsa1.0_01481.1_g27209.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01481.1_g27210.t1	ref|NP_565844.1| zinc finger A20 and AN1 domain-containing stress-associated protein 4 [Arabidopsis thaliana] gi|73921295|sp|Q9SJM6.1|SAP4_ARATH RecName: Full=Zinc finger A20 and AN1 domain-containing stress-associated protein 4; Short=AtSAP4 gi|4510345|gb|AAD21434.1| expressed protein [Arabidopsis thaliana] gi|21592464|gb|AAM64415.1| zinc finger-like protein [Arabidopsis thaliana] gi|114050557|gb|ABI49428.1| At2g36320 [Arabidopsis thaliana] gi|330254138|gb|AEC09232.1| zinc finger A20 and AN1 domain-containing stress-associated protein 4 [Arabidopsis thaliana]	167	161	6.00E-68	96.4	79.6	86.2	zinc finger A20 and AN1 domain-containing stress-associated protein 4	gbpln	Arabidopsis thaliana	AT2G36320.1 | Symbols: | A20/AN1-like zinc finger family protein | chr2:15229388-15229873 FORWARD LENGTH=161	167	161	2.00E-70	96.4	79.6	86.2
Rsa1.0_01481.1_g27211.t1	ref|XP_002879603.1| hydrolase, acting on ester bonds [Arabidopsis lyrata subsp. lyrata] gi|297325442|gb|EFH55862.1| hydrolase, acting on ester bonds [Arabidopsis lyrata subsp. lyrata]	348	356	1.00E-131	102.3	64.7	75.9	hydrolase, acting on ester bonds	gbpln	Arabidopsis lyrata	AT2G36325.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr2:15231409-15233224 FORWARD LENGTH=356	348	356	1.00E-127	102.3	62.4	73.3
Rsa1.0_01481.1_g27212.t1	ref|XP_002880339.1| hypothetical protein ARALYDRAFT_904279 [Arabidopsis lyrata subsp. lyrata] gi|297326178|gb|EFH56598.1| hypothetical protein ARALYDRAFT_904279 [Arabidopsis lyrata subsp. lyrata]	622	613	0	98.6	84.7	89.9	hypothetical protein ARALYDRAFT_904279	gbpln	Arabidopsis lyrata	AT2G48010.1 | Symbols: RKF3 | receptor-like kinase in in flowers 3 | chr2:19641465-19643318 FORWARD LENGTH=617	622	617	0	99.2	83.9	90.2
Rsa1.0_01481.1_g27213.t1	ref|XP_002879608.1| ATPDR6/PDR6 [Arabidopsis lyrata subsp. lyrata] gi|297325447|gb|EFH55867.1| ATPDR6/PDR6 [Arabidopsis lyrata subsp. lyrata]	735	1452	0	197.6	73.6	77.4	ATPDR6/PDR6	gbpln	Arabidopsis lyrata	AT2G36380.1 | Symbols: PDR6, ATPDR6 | pleiotropic drug resistance 6 | chr2:15257583-15263627 FORWARD LENGTH=1453	735	1453	0	197.7	72.5	76.9
Rsa1.0_01481.1_g27214.t1	dbj|BAC42083.1| unknown protein [Arabidopsis thaliana]	378	398	1.00E-158	105.3	84.4	88.1	unknown protein	gbpln	Arabidopsis thaliana	AT2G36400.1 | Symbols: AtGRF3, GRF3 | growth-regulating factor 3 | chr2:15270300-15272617 REVERSE LENGTH=398	378	398	1.00E-155	105.3	83.1	86.8
Rsa1.0_01481.1_g27215.t1	gb|EOA28004.1| hypothetical protein CARUB_v10024181mg [Capsella rubella]	176	170	2.00E-69	96.6	80.1	87.5	hypothetical protein CARUB_v10024181mg	gbpln	Capsella rubella	AT2G36410.1 | Symbols: | Family of unknown function (DUF662) | chr2:15279041-15280270 FORWARD LENGTH=195	176	195	4.00E-55	110.8	66.5	81.8
Rsa1.0_01481.1_g27216.t1	gb|EOA27598.1| hypothetical protein CARUB_v10023738mg [Capsella rubella]	304	298	1.00E-149	98.0	84.9	90.5	hypothetical protein CARUB_v10023738mg	gbpln	Capsella rubella	AT3G53000.1 | Symbols: AtPP2-A15, PP2-A15 | phloem protein 2-A15 | chr3:19654278-19655801 FORWARD LENGTH=300	304	300	1.00E-134	98.7	77.3	85.9
Rsa1.0_01481.1_g27217.t1	gb|EOA27054.1| hypothetical protein CARUB_v10023149mg [Capsella rubella]	158	467	4.00E-56	295.6	84.2	86.1	hypothetical protein CARUB_v10023149mg	gbpln	Capsella rubella	AT2G36630.1 | Symbols: | Sulfite exporter TauE/SafE family protein | chr2:15352767-15355050 REVERSE LENGTH=459	158	459	1.00E-58	290.5	85.4	87.3

Rsa1.0_01481.1.g27218.t1	gb|EOA28539.1| hypothetical protein CARUB_v10024756mg [Capsella rubella]	496	496	0	100.0	77.0	87.7	hypothetical protein CARUB_v10024756mg	gbpln	Capsella rubella	AT2G36780.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:15417618-15419108 REVERSE LENGTH=496	496	496	0	100.0	75.8	86.9
Rsa1.0_01481.1.g27219.t1	ref|NP_181215.1| UDP-glucosyl transferase 73C [Arabidopsis thaliana] gi|75315658|sp|Q9ZQ97.1|U73C4_ARATH RecName: Full=UDP-glycosyltransferase 73C4 gi|4415922|gb|AAD20153.1| putative glucosyl transferase [Arabidopsis thaliana] gi|20856890|gb|AAM26689.1| At2g36770/F13K3.17 [Arabidopsis thaliana] gi|25090305|gb|AAN72273.1| At2g36770/F13K3.17 [Arabidopsis thaliana] gi|330254202|gb|AEC09296.1| UDP-glucosyl transferase 73C4 [Arabidopsis thaliana]	497	496	0	99.8	81.7	92.2	UDP-glucosyl transferase 73C	gbpln	Arabidopsis thaliana	AT2G36770.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:15415227-15416717 REVERSE LENGTH=496	497	496	0	99.8	81.7	92.2
Rsa1.0_01481.1.g27220.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01481.1.g27221.t1	ref|XP_002881469.1| don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297327308|gb|EFH57728.1| don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata]	496	496	0	100.0	87.7	94.2	don-glucosyltransferase	gbpln	Arabidopsis lyrata	AT2G36800.1 | Symbols: DOGT1, UGT73C5 | don-glucosyltransferase 1 | chr2:15423493-15424980 REVERSE LENGTH=495	496	495	0	99.8	85.5	92.5
Rsa1.0_01481.1.g27222.t1	ref|NP_181224.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|38605514|sp|Q9SJL9.1|XTH32_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 32; Short=At-XTH32; Short=XTH-32; Flags: Precursor gi|4883603|gb|AAD31572.1| xyloglucan endotransglycosylase, putative [Arabidopsis thaliana] gi|15027967|gb|AAK76514.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|21595304|gb|AAM66089.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|22136872|gb|AAM91780.1| putative xyloglucan endo-transglycosylase [Arabidopsis thaliana] gi|330254214|gb|AEC09308.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana]	299	299	1.00E-160	100.0	90.0	96.3	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT2G36870.1 | Symbols: XTH32 | xyloglucan endotransglucosylase/hydrolase 32 | chr2:15472869-15474630 REVERSE LENGTH=299	299	299	1.00E-163	100.0	90.0	96.3
Rsa1.0_01482.1.g27223.t1	ref|NP_192825.1| uncharacterized protein [Arabidopsis thaliana] gi|3513732|gb|AAC33948.1| F8M12.4 gene product [Arabidopsis thaliana] gi|4539361|emb|CAB40055.1| putative protein [Arabidopsis thaliana] gi|7267785|emb|CAB81188.1| putative protein [Arabidopsis thaliana] gi|332657538|gb|AEE82938.1| uncharacterized protein AT4G10870 [Arabidopsis thaliana]	169	173	3.00E-18	102.4	41.4	54.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G10870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr4:6683555-6684076 REVERSE LENGTH=173	169	173	1.00E-20	102.4	41.4	54.4
Rsa1.0_01482.1.g27224.t1	ref|XP_002865380.1| hypothetical protein ARALYDRAFT_917203 [Arabidopsis lyrata subsp. lyrata] gi|297311215|gb|EFH41639.1| hypothetical protein ARALYDRAFT_917203 [Arabidopsis lyrata subsp. lyrata]	229	238	1.00E-108	103.9	85.6	91.3	hypothetical protein ARALYDRAFT_917203	gbpln	Arabidopsis lyrata	AT5G44170.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:17780394-17781098 FORWARD LENGTH=234	229	234	1.00E-111	102.2	84.3	91.7
Rsa1.0_01482.1.g27225.t1	gb|AAN60339.1| unknown [Arabidopsis thaliana]	252	247	1.00E-101	98.0	71.8	81.0	unknown	gbpln	Arabidopsis thaliana	AT5G44130.1 | Symbols: FLA13 | FASCICLIN-like arabinogalactan protein 13 precursor | chr5:17761128-17761871 FORWARD LENGTH=247	252	247	7.00E-99	98.0	79.4	86.1
Rsa1.0_01482.1.g27226.t1	ref|XP_002863610.1| hypothetical protein ARALYDRAFT_494585 [Arabidopsis lyrata subsp. lyrata] gi|297309445|gb|EFH39869.1| hypothetical protein ARALYDRAFT_494585 [Arabidopsis lyrata subsp. lyrata]	283	282	1.00E-143	99.6	93.6	97.2	hypothetical protein ARALYDRAFT_494585	gbpln	Arabidopsis lyrata	AT5G44110.1 | Symbols: ATPOP1, ATNAP2, POP1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17754222-17755672 REVERSE LENGTH=282	283	282	1.00E-145	99.6	93.3	96.8

<table>
<tr><td>Rsa1.0_01482.1.g27227.t1</td><td>ref|XP_002863242.1| hypothetical protein ARALYDRAFT_358968 [Arabidopsis lyrata subsp. lyrata] gi|297309076|gb|EFH39501.1| hypothetical protein ARALYDRAFT_358968 [Arabidopsis lyrata subsp. lyrata]</td><td>155</td><td>192</td><td>9.00E-63</td><td>123.9</td><td>76.8</td><td>84.5</td><td>hypothetical protein ARALYDRAFT_358968</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G13440.1 | Symbols: | Calcium-binding EF-hand family protein | chr4:7810215-7810679 FORWARD LENGTH=154</td><td>155</td><td>154</td><td>3.00E-65</td><td>99.4</td><td>76.8</td><td>84.5</td></tr>
<tr><td>Rsa1.0_01482.1.g27228.t23</td><td>ref|NP_178162.2| F-box/RNI-like/FBD-like domain-containing protein [Arabidopsis thaliana] gi|332198288|gb|AEE36409.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]</td><td>463</td><td>481</td><td>1.00E-130</td><td>103.9</td><td>53.6</td><td>70.4</td><td>F-box/RNI-like/FBD-like domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G80470.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:30256185-30257916 FORWARD LENGTH=481</td><td>463</td><td>481</td><td>1.00E-133</td><td>103.9</td><td>53.6</td><td>70.4</td></tr>
<tr><td>Rsa1.0_01482.1.g27229.t1</td><td>dbj|BAB85602.1| phytochelatin synthase 1 [Brassica juncea]</td><td>171</td><td>485</td><td>2.00E-34</td><td>283.6</td><td>44.4</td><td>52.0</td><td>phytochelatin synthase 1</td><td>gbpln</td><td>Brassica juncea</td><td>AT5G44070.1 | Symbols: CAD1, ARA8, ATPCS1, PCS1 | phytochelatin synthase 1 (PCS1) | chr5:17734876-17737672 FORWARD LENGTH=485</td><td>171</td><td>485</td><td>4.00E-35</td><td>283.6</td><td>43.3</td><td>52.0</td></tr>
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<tr><td>Rsa1.0_01483.1.g27232.t1</td><td>ref|NP_175260.1| CBL-interacting serine/threonine-protein kinase 17 [Arabidopsis thaliana] gi|75332093|sp|Q94C40.1|CIPKH_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 17; AltName: Full=SNF1-related kinase 3.21; AltName: Full=SOS2-like protein kinase PKS20 gi|14571553|gb|AAK64513.1| CBL-interacting protein kinase 17 [Arabidopsis thaliana] gi|116325942|gb|ABJ98572.1| At1g48260 [Arabidopsis thaliana] gi|332194148|gb|AEE32269.1| CBL-interacting serine/threonine-protein kinase 17 [Arabidopsis thaliana]</td><td>425</td><td>432</td><td>0</td><td>101.6</td><td>82.1</td><td>90.8</td><td>CBL-interacting serine/threonine-protein kinase 17</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G48260.1 | Symbols: CIPK17, SnRK3.21 | CBL-interacting protein kinase 17 | chr1:17814226-17817226 REVERSE LENGTH=432</td><td>425</td><td>432</td><td>0</td><td>101.6</td><td>82.1</td><td>90.8</td></tr>
<tr><td>Rsa1.0_01483.1.g27233.t1</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>697</td><td>1529</td><td>0</td><td>219.4</td><td>57.0</td><td>74.3</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>697</td><td>746</td><td>1.00E-115</td><td>107.0</td><td>29.7</td><td>38.3</td></tr>
<tr><td>Rsa1.0_01483.1.g27234.t3</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1446</td><td>1529</td><td>0</td><td>105.7</td><td>46.5</td><td>63.4</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>1446</td><td>746</td><td>1.00E-67</td><td>51.6</td><td>10.2</td><td>14.5</td></tr>
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<tr><td>Rsa1.0_01483.1.g27237.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01483.1.g27238.t1</td><td>gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]</td><td>1538</td><td>1838</td><td>0</td><td>119.5</td><td>43.6</td><td>55.9</td><td>F5M15.26</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01483.1.g27239.t1</td><td>gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]</td><td>901</td><td>1838</td><td>0</td><td>204.0</td><td>41.7</td><td>52.2</td><td>F5M15.26</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
</table>

Rsa1.0_01484.1.g27240.t1	ref|NP_200637.1| regulatory particle triple-A ATPase 3 [Arabidopsis thaliana] gi|297793353|ref|XP_002864561.1| hypothetical protein ARALYDRAFT_495939 [Arabidopsis lyrata subsp. lyrata] gi|28558168|sp|Q9SEI4.1|PRS6B_ARATH RecName: Full=26S protease regulatory subunit 6B homolog; AltName: Full=26S protease subunit 6B homolog; AltName: Full=26S proteasome AAA-ATPase subunit RPT3; AltName: Full=Protein BMAA insensitive morphology 409; AltName: Full=Regulatory particle triple-A ATPase subunit 3 gi|6652882|gb|AAF22523.1|AF123392_1 26S proteasome AAA-ATPase subunit RPT3 [Arabidopsis thaliana] gi|8777330|dbj|BAA96920.1| 26S proteasome AAA-ATPase subunit RPT3 [Arabidopsis thaliana] gi|17979231|gb|AAL49932.1| AT4g10340/F24G24_140 [Arabidopsis thaliana] gi|56382019|gb|AAV85728.1| At5g58290 [Arabidopsis thaliana] gi|297310396|gb|EFH40820.1| hypothetical protein ARALYDRAFT_495939 [Arabidopsis lyrata subsp. lyrata] gi|332009646|gb|AED97029.1| regulatory particle triple-A ATPase 3 [Arabidopsis thaliana] gi|482548338|gb|EOA12532.1|	284	408	1.00E-154	143.7	97.9	98.9	regulatory particle triple-A ATPase 3	gbpln	Arabidopsis lyrata	AT5G58290.1 | Symbols: RPT3 | regulatory particle triple-A ATPase 3 | chr5:23569155-23571116 FORWARD LENGTH=408	284	408	1.00E-157	143.7	97.9	98.9
Rsa1.0_01484.1.g27241.t1	gb|EOA14841.1| hypothetical protein CARUB_v10028155mg [Capsella rubella]	525	556	0	105.9	80.8	91.2	hypothetical protein CARUB_v10028155mg	gbpln	Capsella rubella	AT5G58320.2 | Symbols: | Kinase interacting (KIP1-like) family protein | chr5:23577728-23579641 FORWARD LENGTH=558	525	558	0	106.3	79.4	91.0
Rsa1.0_01484.1.g27242.t1	ref|NP_851214.1| lactate/malate dehydrogenase family protein [Arabidopsis thaliana] gi|23297668|gb|AAN13004.1| NADP-dependent malate dehydrogenase [Arabidopsis thaliana] gi|110740830|dbj|BAE98512.1| NADP-dependent malate dehydrogenase [Arabidopsis thaliana] gi|332009655|gb|AED97038.1| lactate/malate dehydrogenase family protein [Arabidopsis thaliana]	445	443	0	99.6	93.9	96.4	lactate/malate dehydrogenase family protein	gbpln	Arabidopsis thaliana	AT5G58330.1 | Symbols: | lactate/malate dehydrogenase family protein | chr5:23580010-23582287 REVERSE LENGTH=443	445	443	0	99.6	93.9	96.4
Rsa1.0_01484.1.g27243.t1	ref|XP_002864565.1| hypothetical protein ARALYDRAFT_495950 [Arabidopsis lyrata subsp. lyrata] gi|297310400|gb|EFH40824.1| hypothetical protein ARALYDRAFT_495950 [Arabidopsis lyrata subsp. lyrata]	832	571	0	68.6	54.3	57.7	hypothetical protein ARALYDRAFT_495950	gbpln	Arabidopsis lyrata	AT5G58350.1 | Symbols: WNK4, ZIK2 | with no lysine (K) kinase 4 | chr5:23585505-23587681 FORWARD LENGTH=571	832	571	0	68.6	52.3	56.5
Rsa1.0_01484.1.g27244.t1	ref|NP_200644.1| ovate family protein 3 [Arabidopsis thaliana] gi|8777337|dbj|BAA96927.1| unnamed protein product [Arabidopsis thaliana] gi|67633890|gb|AAY78869.1| ovate family protein [Arabidopsis thaliana] gi|332009659|gb|AED97042.1| ovate family protein 3 [Arabidopsis thaliana]	338	296	7.00E-84	87.6	59.2	66.9	ovate family protein 3	gbpln	Arabidopsis thaliana	AT5G58360.1 | Symbols: ATOFP3, OFP3 | ovate family protein 3 | chr5:23590079-23590969 REVERSE LENGTH=296	338	296	2.00E-86	87.6	59.2	66.9
Rsa1.0_01484.1.g27245.t1	ref|XP_002864570.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310405|gb|EFH40829.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	488	467	0	95.7	75.0	79.9	predicted protein	gbpln	Arabidopsis lyrata	AT5G58370.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:23593358-23595645 FORWARD LENGTH=465	488	465	0	95.3	74.6	80.3
Rsa1.0_01484.1.g27246.t1	ref|XP_002864571.1| hypothetical protein ARALYDRAFT_495954 [Arabidopsis lyrata subsp. lyrata] gi|297310406|gb|EFH40830.1| hypothetical protein ARALYDRAFT_495954 [Arabidopsis lyrata subsp. lyrata]	94	85	9.00E-26	90.4	64.9	70.2	hypothetical protein ARALYDRAFT_495954	gbpln	Arabidopsis lyrata	AT5G58375.1 | Symbols: | Methyltransferase-related protein | chr5:23596369-23596705 FORWARD LENGTH=85	94	85	1.00E-27	90.4	63.8	69.1
Rsa1.0_01484.1.g27247.t1	gb|EOA12435.1| hypothetical protein CARUB_v10028322mg [Capsella rubella]	458	472	0	103.1	86.7	92.4	hypothetical protein CARUB_v10028322mg	gbpln	Capsella rubella	AT5G58380.1 | Symbols: CIPK10, PKS2, SIP1, SNRK3.8 | SOS3-interacting protein 1 | chr5:23597092-23598531 REVERSE LENGTH=479	458	479	0	104.6	86.0	91.9

Rsa1.0_01484.1.g27248.t2	ref|XP_002864573.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297310408|gb|EFH40832.1| binding protein [Arabidopsis lyrata subsp. lyrata]	2185	1871	0	85.6	71.4	76.9	binding protein	gbpln	Arabidopsis lyrata	AT5G58410.1 | Symbols: | HEAT/U-box domain-containing protein | chr5:23609663-23617343 FORWARD LENGTH=1873	2185	1873	0	85.7	70.6	76.8
Rsa1.0_01484.1.g27249.t1	ref|XP_002864575.1| hypothetical protein ARALYDRAFT_358061 [Arabidopsis lyrata subsp. lyrata] gi|297310410|gb|EFH40834.1| hypothetical protein ARALYDRAFT_358061 [Arabidopsis lyrata subsp. lyrata]	366	1018	0	278.1	91.5	97.0	hypothetical protein ARALYDRAFT_358061	gbpln	Arabidopsis lyrata	AT5G58450.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:23626826-23632071 FORWARD LENGTH=1065	366	1065	0	291.0	91.3	96.7
Rsa1.0_01485.1.g27250.t2	ref|XP_002882022.1| CYP76C3 [Arabidopsis lyrata subsp. lyrata] gi|297327861|gb|EFH58281.1| CYP76C3 [Arabidopsis lyrata subsp. lyrata]	769	513	1.00E-169	66.7	38.6	46.0	CYP76C3	gbpln	Arabidopsis lyrata	AT2G45580.1 | Symbols: CYP76C3 | cytochrome P450, family 76, subfamily C, polypeptide 3 | chr2:18782388-18784286 REVERSE LENGTH=515	769	515	1.00E-168	67.0	39.5	48.1
Rsa1.0_01485.1.g27251.t1	ref|XP_002880185.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297326024|gb|EFH56444.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	546	681	0	124.7	73.1	77.3	kinase family protein	gbpln	Arabidopsis lyrata	AT2G45590.1 | Symbols: | Protein kinase superfamily protein | chr2:18786725-18788776 FORWARD LENGTH=683	546	683	0	125.1	72.2	76.7
Rsa1.0_01485.1.g27252.t1	ref|XP_002880188.1| hypothetical protein ARALYDRAFT_483698 [Arabidopsis lyrata subsp. lyrata] gi|297326027|gb|EFH56447.1| hypothetical protein ARALYDRAFT_483698 [Arabidopsis lyrata subsp. lyrata]	814	757	0	93.0	69.5	74.9	hypothetical protein ARALYDRAFT_483698	gbpln	Arabidopsis lyrata	AT2G45620.1 | Symbols: | Nucleotidyltransferase family protein | chr2:18792943-18795750 FORWARD LENGTH=764	814	764	0	93.9	67.2	73.5
Rsa1.0_01485.1.g27253.t1	gb|AFM77891.1| MADS-box protein AGL20/SOC1 [Brassica napus]	206	213	1.00E-106	103.4	92.7	94.7	MADS-box protein AGL20/SOC1	gbpln	Brassica napus	AT2G45660.1 | Symbols: AGL20, SOC1, ATSOC1 | AGAMOUS-like 20 | chr2:18807799-18810193 REVERSE LENGTH=214	206	214	1.00E-100	103.9	92.2	94.7
Rsa1.0_01485.1.g27254.t1	ref|NP_566051.1| lysophosphatidylcholine acyltransferase / lyso-PAF acetyltransferase [Arabidopsis thaliana] gi|20197054|gb|AAM14898.1| unknown protein; alternative splicing isoform [Arabidopsis thaliana] gi|51971062|dbj|BAD44223.1| unknown protein [Arabidopsis thaliana] gi|330255490|gb|AEC10584.1| calcineurin B subunit-related protein [Arabidopsis thaliana]	538	539	0	100.2	83.8	91.3	lysophosphatidylcholine acyltransferase / lyso-PAF acetyltransferase	gbpln	Arabidopsis thaliana	AT2G45670.1 | Symbols: | calcineurin B subunit-related | chr2:18815070-18818382 REVERSE LENGTH=539	538	539	0	100.2	83.8	91.3
Rsa1.0_01485.1.g27255.t1	gb|EOA28195.1| hypothetical protein CARUB_v10024387mg [Capsella rubella]	99	101	7.00E-45	102.0	91.9	97.0	hypothetical protein CARUB_v10024387mg	gbpln	Capsella rubella	AT2G45695.1 | Symbols: | Ubiquitin related modifier 1 | chr2:18826043-18826744 FORWARD LENGTH=101	99	101	3.00E-47	102.0	89.9	97.0
Rsa1.0_01485.1.g27256.t1	ref|NP_182094.1| sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana] gi|3386625|gb|AAC28555.1| hypothetical protein [Arabidopsis thaliana] gi|20197051|gb|AAM14896.1| hypothetical protein [Arabidopsis thaliana] gi|28973723|gb|AAO64178.1| unknown protein [Arabidopsis thaliana] gi|29824257|gb|AAP04089.1| unknown protein [Arabidopsis thaliana] gi|110736829|dbj|BAF00373.1| hypothetical protein [Arabidopsis thaliana] gi|330255495|gb|AEC10589.1| sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	723	723	0	100.0	79.5	86.2	sterile alpha motif (SAM) domain-containing protein	gbpln	Arabidopsis thaliana	AT2G45700.1 | Symbols: | sterile alpha motif (SAM) domain-containing protein | chr2:18827216-18830505 REVERSE LENGTH=723	723	723	0	100.0	79.5	86.2
Rsa1.0_01485.1.g27257.t1	gb|EOA24972.1| hypothetical protein CARUB_v10018269mg, partial [Capsella rubella]	84	115	4.00E-41	136.9	95.2	97.6	hypothetical protein CARUB_v10018269mg, partial	gbpln	Capsella rubella	AT3G61110.1 | Symbols: ARS27A, RS27A | ribosomal protein S27 | chr3:22611710-22612632 FORWARD LENGTH=86	84	86	7.00E-43	102.4	94.0	97.6
Rsa1.0_01485.1.g27258.t1	gb|ABV72578.1| dehydration-responsive family protein S51 [Brassica rapa]	633	632	0	99.8	90.8	94.2	dehydration-responsive family protein S51	gbpln	Brassica rapa	AT2G45750.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:18842655-18845343 FORWARD LENGTH=631	633	631	0	99.7	88.3	92.9
Rsa1.0_01485.1.g27259.t1	gb|ADK63418.1| C3HC4 type zinc finger protein [Brassica rapa]	316	363	3.00E-98	114.9	59.5	66.1	C3HC4 type zinc finger protein	gbpln	Brassica rapa	AT3G61180.1 | Symbols: | RING/U-box superfamily protein | chr3:22645680-22647290 FORWARD LENGTH=379	316	379	7.00E-85	119.9	58.9	73.4

Rsa1.0_01485.1.g27260.t1	ref|NP_182100.2| BON1-associated protein 2 [Arabidopsis thaliana] gi|75103850|sp|Q58FX0.1|BAP2_ARATH RecName: Full=BON1-associated protein 2; AltName: Full=Protein BON1-ASSOCIATED PROTEIN 1-LIKE gi|61742689|gb|AAX55165.1| hypothetical protein At2g45760 [Arabidopsis thaliana] gi|94442457|gb|ABF19016.1| At2g45760 [Arabidopsis thaliana] gi|330255504|gb|AEC10598.1| BON1-associated protein 2 [Arabidopsis thaliana]	205	207	7.00E-72	101.0	72.2	80.0	BON1-associated protein 2	gbpln	Arabidopsis thaliana	AT2G45760.1 | Symbols: BAP2, BAL | BON association protein 2 | chr2:18847125-18847748 REVERSE LENGTH=207	205	207	2.00E-74	101.0	72.2	80.0
Rsa1.0_01485.1.g27261.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01486.1.g27262.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	273	672	1.00E-41	246.2	29.7	44.3	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01486.1.g27263.t3	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	748	1142	4.00E-87	152.7	27.3	39.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	748	292	2.00E-29	39.0	10.6	18.0
Rsa1.0_01486.1.g27264.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	397	1142	1.00E-156	287.7	65.7	78.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	397	626	4.00E-18	157.7	12.3	17.9
Rsa1.0_01486.1.g27265.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1412	1501	0	106.3	58.2	73.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1412	1262	1.00E-131	89.4	15.9	22.7
Rsa1.0_01486.1.g27266.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	160	1311	1.00E-10	819.4	31.3	43.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	160	170	4.00E-12	106.3	30.0	43.8
Rsa1.0_01486.1.g27267.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01486.1.g27268.t5	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1645	940	2.00E-66	57.1	8.5	11.3	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01487.1.g27269.t1	ref|XP_002867281.1| hypothetical protein ARALYDRAFT_491566 [Arabidopsis lyrata subsp. lyrata] gi|297313117|gb|EFH43540.1| hypothetical protein ARALYDRAFT_491566 [Arabidopsis lyrata subsp. lyrata]	323	311	1.00E-169	96.3	92.0	93.2	hypothetical protein ARALYDRAFT_491566	gbpln	Arabidopsis lyrata	AT4G31750.1 | Symbols: WIN2 | HOPW1-1-interacting 2 | chr4:15364657-15367207 REVERSE LENGTH=311	323	311	1.00E-171	96.3	91.6	93.2
Rsa1.0_01487.1.g27270.t1	ref|XP_002869314.1| ATSLY1 [Arabidopsis lyrata subsp. lyrata] gi|297315150|gb|EFH45573.1| ATSLY1 [Arabidopsis lyrata subsp. lyrata]	570	606	0	106.3	74.9	84.7	ATSLY1	gbpln	Arabidopsis lyrata	AT2G17980.1 | Symbols: ATSLY1 | Sec1/munc18-like (SM) proteins superfamily | chr2:7824352-7826404 FORWARD LENGTH=627	570	627	0	110.0	68.9	81.1
Rsa1.0_01487.1.g27271.t1	ref|XP_002874162.1| hypothetical protein ARALYDRAFT_910422 [Arabidopsis lyrata subsp. lyrata] gi|297319999|gb|EFH50421.1| hypothetical protein ARALYDRAFT_910422 [Arabidopsis lyrata subsp. lyrata]	368	357	1.00E-125	97.0	66.6	77.2	hypothetical protein ARALYDRAFT_910422	gbpln	Arabidopsis lyrata	AT5G24040.1 | Symbols: | Protein of unknown function (DUF295) | chr5:8126045-8127336 REVERSE LENGTH=373	368	373	1.00E-123	101.4	59.2	73.9
Rsa1.0_01487.1.g27272.t1	ref|XP_002869317.1| hypothetical protein ARALYDRAFT_353659 [Arabidopsis lyrata subsp. lyrata] gi|297315153|gb|EFH45576.1| hypothetical protein ARALYDRAFT_353659 [Arabidopsis lyrata subsp. lyrata]	381	339	1.00E-162	89.0	73.2	77.4	hypothetical protein ARALYDRAFT_353659	gbpln	Arabidopsis lyrata	AT1G77520.1 | Symbols: | O-methyltransferase family protein | chr1:29130557-29132007 FORWARD LENGTH=381	381	381	1.00E-163	100.0	70.6	81.6
Rsa1.0_01487.1.g27273.t1	gb|AAF18643.1|AC006228_14 F5J5.14 [Arabidopsis thaliana]	274	743	1.00E-47	271.2	44.2	65.7	F5J5.14	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01487.1.g27274.t1	dbj|BAJ33661.1| unnamed protein product [Thellungiella halophila]	244	134	4.00E-47	54.9	46.3	49.6	unnamed protein product	––––	––––	AT4G31720.1 | Symbols: TAFII15, TAF10, STG1 | TBP-associated factor II 15 | chr4:15354223-15355704 REVERSE LENGTH=134	244	134	7.00E-44	54.9	48.0	49.6
Rsa1.0_01487.1.g27275.t1	ref|XP_002867283.1| hypothetical protein ARALYDRAFT_913296 [Arabidopsis lyrata subsp. lyrata] gi|297313119|gb|EFH43542.1| hypothetical protein ARALYDRAFT_913296 [Arabidopsis lyrata subsp. lyrata]	847	394	1.00E-138	46.5	30.7	37.2	hypothetical protein ARALYDRAFT_913296	gbpln	Arabidopsis lyrata	AT4G00260.1 | Symbols: MEE45 | Transcriptional factor B3 family protein | chr4:114971-117051 FORWARD LENGTH=528	847	528	1.00E-94	62.3	25.3	33.2

<table>
<tr><td>Rsa1.0_01487.1.g27276.t1</td><td>ref|NP_177876.1| O-methyltransferase family protein [Arabidopsis thaliana] gi|12323395|gb|AAG51676.1|AC010704_20 putative caffeic acid 3-O-methyltransferase; 41078-42528 [Arabidopsis thaliana] gi|332197867|gb|AEE35988.1| O-methyltransferase family protein [Arabidopsis thaliana]</td><td>382</td><td>381</td><td>1.00E-160</td><td>99.7</td><td>70.7</td><td>83.5</td><td>O-methyltransferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G77520.1 | Symbols: | O-methyltransferase family protein | chr1:29130557-29132007 FORWARD LENGTH=381</td><td>382</td><td>381</td><td>1.00E-163</td><td>99.7</td><td>70.7</td><td>83.5</td></tr>
<tr><td>Rsa1.0_01487.1.g27277.t1</td><td>gb|EOA16311.1| hypothetical protein CARUB_v10004462mg [Capsella rubella]</td><td>110</td><td>574</td><td>1.00E-27</td><td>521.8</td><td>53.6</td><td>62.7</td><td>hypothetical protein CARUB_v10004462mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G24690.1 | Symbols: | Transcriptional factor B3 family protein | chr2:10499551-10503110 REVERSE LENGTH=777</td><td>110</td><td>777</td><td>4.00E-21</td><td>706.4</td><td>38.2</td><td>53.6</td></tr>
<tr><td>Rsa1.0_01487.1.g27278.t1</td><td>gb|EOA40281.1| hypothetical protein CARUB_v10009009mg [Capsella rubella]</td><td>461</td><td>480</td><td>0</td><td>104.1</td><td>85.0</td><td>92.6</td><td>hypothetical protein CARUB_v10009009mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G44100.1 | Symbols: AAP5 | amino acid permease 5 | chr1:16764651-16767223 REVERSE LENGTH=480</td><td>461</td><td>480</td><td>0</td><td>104.1</td><td>82.2</td><td>91.5</td></tr>
<tr><td>Rsa1.0_01487.1.g27279.t1</td><td>gb|AAD24567.1|AF120335_1 putative transposase [Arabidopsis thaliana]</td><td>472</td><td>577</td><td>1.00E-154</td><td>122.2</td><td>54.9</td><td>71.6</td><td>putative transposase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>472</td><td>696</td><td>3.00E-52</td><td>147.5</td><td>25.2</td><td>44.7</td></tr>
<tr><td>Rsa1.0_01488.1.g27280.t1</td><td>dbj|BAJ33830.1| unnamed protein product [Thellungiella halophila]</td><td>349</td><td>351</td><td>0</td><td>100.6</td><td>91.4</td><td>96.3</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G16970.1 | Symbols: AT-AER, AER | alkenal reductase | chr5:5576291-5578001 REVERSE LENGTH=345</td><td>349</td><td>345</td><td>1.00E-175</td><td>98.9</td><td>84.5</td><td>90.5</td></tr>
<tr><td>Rsa1.0_01488.1.g27281.t1</td><td>ref|NP_197197.1| uncharacterized protein [Arabidopsis thaliana] gi|13926247|gb|AAK49597.1|AF372881_1 AT5g16950/F2K13_100 [Arabidopsis thaliana] gi|9755696|emb|CAC01708.1| putative protein [Arabidopsis thaliana] gi|16323228|gb|AAL15348.1| AT5g16950/F2K13_100 [Arabidopsis thaliana] gi|332004979|gb|AED92362.1| uncharacterized protein AT5G16950 [Arabidopsis thaliana]</td><td>106</td><td>99</td><td>5.00E-40</td><td>93.4</td><td>79.2</td><td>86.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G16950.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:5572640-5572939 FORWARD LENGTH=99</td><td>106</td><td>99</td><td>8.00E-43</td><td>93.4</td><td>79.2</td><td>86.8</td></tr>
<tr><td>Rsa1.0_01488.1.g27282.t1</td><td>ref|NP_197196.1| carbon-sulfur lyase [Arabidopsis thaliana] gi|238481283|ref|NP_001154714.1| carbon-sulfur lyase [Arabidopsis thaliana] gi|9755695|emb|CAC01707.1| putative protein [Arabidopsis thaliana] gi|26451264|dbj|BAC42734.1| unknown protein [Arabidopsis thaliana] gi|28973087|gb|AAO63868.1| unknown protein [Arabidopsis thaliana] gi|332004977|gb|AED92360.1| carbon-sulfur lyase [Arabidopsis thaliana] gi|332004978|gb|AED92361.1| carbon-sulfur lyase [Arabidopsis thaliana]</td><td>137</td><td>135</td><td>1.00E-66</td><td>98.5</td><td>86.9</td><td>93.4</td><td>carbon-sulfur lyase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G16940.2 | Symbols: | carbon-sulfur lyases | chr5:5571797-5572204 REVERSE LENGTH=135</td><td>137</td><td>135</td><td>3.00E-69</td><td>98.5</td><td>86.9</td><td>93.4</td></tr>
<tr><td>Rsa1.0_01488.1.g27283.t1</td><td>ref|XP_002871740.1| VHS domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317577|gb|EFH47999.1| VHS domain-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>407</td><td>406</td><td>0</td><td>99.8</td><td>88.2</td><td>93.4</td><td>VHS domain-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G16880.2 | Symbols: | Target of Myb protein 1 | chr5:5549658-5551274 FORWARD LENGTH=407</td><td>407</td><td>407</td><td>0</td><td>100.0</td><td>88.9</td><td>94.3</td></tr>
<tr><td>Rsa1.0_01488.1.g27284.t1</td><td>gb|EOA30133.1| hypothetical protein CARUB_v10013239mg [Capsella rubella]</td><td>614</td><td>618</td><td>0</td><td>100.7</td><td>85.2</td><td>93.0</td><td>hypothetical protein CARUB_v10013239mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G20790.1 | Symbols: | clathrin adaptor complexes medium subunit family protein | chr2:8950162-8952613 REVERSE LENGTH=613</td><td>614</td><td>613</td><td>0</td><td>99.8</td><td>85.3</td><td>92.5</td></tr>
<tr><td>Rsa1.0_01488.1.g27285.t1</td><td>gb|EOA19437.1| hypothetical protein CARUB_v10001749mg [Capsella rubella]</td><td>265</td><td>260</td><td>1.00E-116</td><td>98.1</td><td>83.8</td><td>89.4</td><td>hypothetical protein CARUB_v10001749mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G16840.3 | Symbols: BPA1 | binding partner of acd11 1 | chr5:5536042-5538026 FORWARD LENGTH=257</td><td>265</td><td>257</td><td>1.00E-119</td><td>97.0</td><td>84.2</td><td>89.1</td></tr>
<tr><td>Rsa1.0_01488.1.g27286.t2</td><td>gb|ABB83612.1| syntaxin-like protein [Brassica oleracea]</td><td>258</td><td>276</td><td>1.00E-115</td><td>107.0</td><td>87.2</td><td>89.9</td><td>syntaxin-like protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G16830.1 | Symbols: SYP21, ATSYP21, PEP12, ATPEP12, PEP12P | syntaxin of plants 21 | chr5:5533076-5535152 REVERSE LENGTH=279</td><td>258</td><td>279</td><td>1.00E-104</td><td>108.1</td><td>77.5</td><td>85.7</td></tr>
<tr><td>Rsa1.0_01488.1.g27287.t1</td><td>ref|XP_002875819.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321657|gb|EFH52078.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>305</td><td>457</td><td>2.00E-28</td><td>149.8</td><td>23.0</td><td>28.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G12100.1 | Symbols: | Cullin family protein | chr4:7246453-7248127 REVERSE LENGTH=434</td><td>305</td><td>434</td><td>2.00E-15</td><td>142.3</td><td>17.4</td><td>25.2</td></tr>
</table>

Rsa1.0_01488.1.g27288.t1	gb|EOA37895.1| hypothetical protein CARUB_v10009363mg, partial [Capsella rubella]	340	396	1.00E-139	116.5	87.1	94.1	hypothetical protein CARUB_v10009363mg, partial	gbpln	Capsella rubella	AT1G45688.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G42860.1); Has 258 Blast hits to 242 proteins in 39 species: Archae - 0; Bacteria - 11; Metazoa - 10; Fungi - 14; Plants - 198; Viruses - 17; Other Eukaryotes - 8 (source: NCBI BLink). | chr1:17191502-17192870 FORWARD LENGTH=342	340	342	1.00E-141	100.6	89.4	94.1
Rsa1.0_01488.1.g27289.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01488.1.g27290.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01489.1.g27291.t1	dbj|BAJ33752.1| unnamed protein product [Thellungiella halophila]	383	393	0	102.6	87.2	92.4	unnamed protein product	----	----	AT3G63260.1 | Symbols: ATMRK1 | Protein kinase superfamily protein | chr3:23373090-23374747 REVERSE LENGTH=391	383	391	0	102.1	85.4	91.1
Rsa1.0_01489.1.g27292.t1	ref|NP_567144.1| uncharacterized protein [Arabidopsis thaliana] gi|13878075|gb|AAK44115.1|AF370300_1 unknown protein [Arabidopsis thaliana] gi|17104745|gb|AAL34261.1| unknown protein [Arabidopsis thaliana] gi|332646938|gb|AEE80459.1| uncharacterized protein AT3G63270 [Arabidopsis thaliana]	385	396	0	102.9	84.7	89.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G63270.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); BEST Arabidopsis thaliana protein match is: PIF / Ping-Pong family of plant transposases (TAIR:AT3G55350.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:23375932-23377398 REVERSE LENGTH=396	385	396	0	102.9	84.7	89.4
Rsa1.0_01489.1.g27293.t4	gb|EOA25915.1| hypothetical protein CARUB_v10019295mg [Capsella rubella]	395	431	1.00E-159	109.1	75.2	82.5	hypothetical protein CARUB_v10019295mg	gbpln	Capsella rubella	AT3G63290.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:23381713-23383059 FORWARD LENGTH=403	395	403	1.00E-156	102.0	72.7	81.8
Rsa1.0_01489.1.g27294.t1	ref|NP_191889.2| protein forked1 [Arabidopsis thaliana] gi|17064860|gb|AAL32584.1| putative protein [Arabidopsis thaliana] gi|25083665|gb|AAN72103.1| putative protein [Arabidopsis thaliana] gi|332646943|gb|AEE80464.1| protein forked1 [Arabidopsis thaliana]	490	498	0	101.6	88.2	94.3	protein forked1	gbpln	Arabidopsis thaliana	AT3G63300.1 | Symbols: FKD1 | FORKED 1 | chr3:23385033-23387625 FORWARD LENGTH=498	490	498	0	101.6	88.2	94.3
Rsa1.0_01489.1.g27295.t1	gb|EOA25588.1| hypothetical protein CARUB_v10018936mg [Capsella rubella]	239	239	1.00E-120	100.0	92.5	96.7	hypothetical protein CARUB_v10018936mg	gbpln	Capsella rubella	AT3G63310.1 | Symbols: BIL4 | Bax inhibitor-1 family protein | chr3:23387938-23388882 REVERSE LENGTH=239	239	239	1.00E-121	100.0	91.6	95.8
Rsa1.0_01489.1.g27296.t1	ref|NP_567145.2| putative protein phosphatase 2C 51 [Arabidopsis thaliana] gi|332646947|gb|AEE80468.1| putative protein phosphatase 2C 51 [Arabidopsis thaliana]	1051	1041	0	99.0	82.7	87.6	putative protein phosphatase 2C 51	gbpln	Arabidopsis thaliana	AT3G63340.1 | Symbols: | Protein phosphatase 2C family protein | chr3:23392181-23397999 REVERSE LENGTH=1041	1051	1041	0	99.0	82.7	87.6
Rsa1.0_01489.1.g27297.t1	sp|Q9M1V3.2|PP296_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g63370	997	960	0	96.3	78.3	84.6	RecName: Full=Pentatricopeptide repeat-containing protein At3g63370	----	----	AT3G63370.1 | Symbols: OTP86 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:23402080-23405180 FORWARD LENGTH=884	997	884	0	88.7	69.6	75.6
Rsa1.0_01489.1.g27298.t1	ref|NP_191897.1| Ca2+-transporting ATPase [Arabidopsis thaliana] gi|12229659|sp|Q9LY77.1|ACA12_ARATH RecName: Full=Calcium-transporting ATPase 12, plasma membrane-type; AltName: Full=Ca(2+)-ATPase isoform 12 gi|7573321|emb|CAB87791.1| Ca2+-transporting ATPase-like protein [Arabidopsis thaliana] gi|332646952|gb|AEE80473.1| putative calcium-transporting ATPase 12 [Arabidopsis thaliana]	1030	1033	0	100.3	94.2	97.6	Ca2+-transporting ATPase	gbpln	Arabidopsis thaliana	AT3G63380.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr3:23407112-23410213 REVERSE LENGTH=1033	1030	1033	0	100.3	94.2	97.6
Rsa1.0_01489.1.g27299.t1	dbj|BAH57223.1| AT3G63400 [Arabidopsis thaliana]	578	570	1.00E-169	98.6	70.8	78.2	AT3G63400	gbpln	Arabidopsis thaliana	AT3G63400.3 | Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr3:23412449-23415435 FORWARD LENGTH=570	578	570	1.00E-171	98.6	70.6	78.2
Rsa1.0_01489.1.g27300.t2	ref|XP_002876721.1| G-protein gamma-subunit 1 [Arabidopsis lyrata subsp. lyrata] gi|297322559|gb|EFH52980.1| G-protein gamma-subunit 1 [Arabidopsis lyrata subsp. lyrata]	97	96	5.00E-32	99.0	77.3	80.4	G-protein gamma-subunit 1	gbpln	Arabidopsis lyrata	AT3G63420.2 | Symbols: AGG1, ATAGG1, GG1 | Ggamma-subunit 1 | chr3:23417383-23418405 FORWARD LENGTH=98	97	98	6.00E-34	101.0	73.2	76.3

Rsa1.0_01489.1.g27301.t1	ref|XP_002878518.1| EMB2221 [Arabidopsis lyrata subsp. lyrata] gi|297324356|gb|EFH54777.1| EMB2221 [Arabidopsis lyrata subsp. lyrata]	1113	1104	0	99.2	88.6	93.1	EMB2221	gbpln	Arabidopsis lyrata	AT3G63460.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:23431009-23437241 REVERSE LENGTH=1104	1113	1104	0	99.2	88.5	92.8
Rsa1.0_01490.1.g27302.t1	gb|EOA14817.1| hypothetical protein CARUB_v10028132mg [Capsella rubella]	130	628	5.00E-32	483.1	60.0	63.1	hypothetical protein CARUB_v10028132mg	gbpln	Capsella rubella	AT5G51820.1 | Symbols: PGM, ATPGMP, PGM1, STF1 | phosphoglucomutase | chr5:21063531-21067933 REVERSE LENGTH=623	130	623	2.00E-34	479.2	59.2	63.8
Rsa1.0_01490.1.g27303.t1	ref|NP_199994.1| gibberellin 20 oxidase 2 [Arabidopsis thaliana] gi|60390167|sp|Q39111.1|GAOX2_ARATH RecName: Full=Gibberellin 20 oxidase 2; AltName: Full=GA 20-oxidase 2; AltName: Full=Gibberellin C-20 oxidase 2 gi|1109697|emb|CAA58294.1| gibberellin 20-oxidase [Arabidopsis thaliana] gi|10177880|dbj|BAB11250.1| gibberellin 20-oxidase [Arabidopsis thaliana] gi|332008746|gb|AED96129.1| gibberellin 20 oxidase 2 [Arabidopsis thaliana]	379	378	0	99.7	89.7	94.7	gibberellin 20 oxidase 2	gbpln	Arabidopsis thaliana	AT5G51810.1 | Symbols: GA20OX2, AT2353, ATGA20OX2 | gibberellin 20 oxidase 2 | chr5:21055389-21056746 REVERSE LENGTH=378	379	378	0	99.7	89.7	94.7
Rsa1.0_01490.1.g27304.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01490.1.g27305.t1	gb|AAF69172.1|AC007915_24 F27F5.11 [Arabidopsis thaliana]	468	1313	1.00E-15	280.6	14.1	21.2	F27F5.11	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01490.1.g27306.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01491.1.g27307.t2	gb|AAX55106.1| hypothetical protein At2g05290 [Arabidopsis thaliana]	232	383	8.00E-18	165.1	24.1	35.8	hypothetical protein At2g05290	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01491.1.g27308.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01491.1.g27309.t1	ref|NP_001077941.1| uncharacterized protein [Arabidopsis thaliana] gi|330252178|gb|AEC07272.1| uncharacterized protein AT2G22155 [Arabidopsis thaliana]	156	101	7.00E-19	64.7	29.5	39.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G22155.1 | Symbols: | Encodes a ECA1 gametogenesis related family protein | chr2:9423869-9424174 FORWARD LENGTH=101	156	101	2.00E-21	64.7	29.5	39.1
Rsa1.0_01491.1.g27310.t1	gb|EOA29032.1| hypothetical protein CARUB_v10025286mg [Capsella rubella]	570	551	0	96.7	70.7	77.9	hypothetical protein CARUB_v10025286mg	gbpln	Capsella rubella	AT2G22140.1 | Symbols: ATEME1B, EME1B | essential meiotic endonuclease 1B | chr2:9414895-9418584 REVERSE LENGTH=551	570	551	0	96.7	69.5	76.3
Rsa1.0_01491.1.g27311.t1	ref|XP_002878591.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297324430|gb|EFH54850.1| binding protein [Arabidopsis lyrata subsp. lyrata]	2156	2154	0	99.9	95.8	98.4	binding protein	gbpln	Arabidopsis lyrata	AT2G22125.1 | Symbols: CSI1 | binding | chr2:9406793-9414223 FORWARD LENGTH=2150	2156	2150	0	99.7	95.6	98.0
Rsa1.0_01491.1.g27312.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01491.1.g27313.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01491.1.g27314.t1	gb|EOA27501.1| hypothetical protein CARUB_v10023640mg [Capsella rubella]	323	323	1.00E-175	100.0	95.4	98.5	hypothetical protein CARUB_v10023640mg	gbpln	Capsella rubella	AT2G22120.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:9394026-9396979 FORWARD LENGTH=363	323	363	1.00E-176	112.4	95.0	97.8
Rsa1.0_01492.1.g27315.t1	ref|XP_002864843.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297310678|gb|EFH41102.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	404	434	1.00E-162	107.4	78.5	86.6	zinc finger (CCCH-type) family protein	gbpln	Arabidopsis lyrata	AT5G63260.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr5:25361900-25364453 FORWARD LENGTH=435	404	435	1.00E-164	107.7	77.2	85.9
Rsa1.0_01492.1.g27316.t1	ref|XP_002866545.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312380|gb|EFH42804.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	90	80	6.00E-24	88.9	66.7	70.0	predicted protein	gbpln	Arabidopsis lyrata	AT5G63270.1 | Symbols: | RPM1-interacting protein 4 (RIN4) family protein | chr5:25365498-25365949 REVERSE LENGTH=80	90	80	3.00E-25	88.9	64.4	68.9

Rsa1.0_01492.1.g27317.t1	ref|NP_568970.2| nucleoside diphosphate kinase II [Arabidopsis thaliana] gi|12644076|sp|O64903.2|NDK2_ARATH RecName: Full=Nucleoside diphosphate kinase II, chloroplastic; Short=NDK II; Short=NDP kinase II; Short=NDPK II; Short=NDPK Ia; Flags: Precursor gi|6065740|emb|CAB58230.1| nucleotide diphosphate kinase Ia [Arabidopsis thaliana] gi|10177312|dbj|BAB10573.1| nucleotide diphosphate kinase Ia [Arabidopsis thaliana] gi|16209700|gb|AAL14407.1| AT5g63310/MDC12_28 [Arabidopsis thaliana] gi|17529114|gb|AAL38767.1| putative nucleotide diphosphate kinase Ia [Arabidopsis thaliana] gi|21436481|gb|AAM51441.1| putative nucleotide diphosphate kinase Ia [Arabidopsis thaliana] gi|110742634|dbj|BAE99229.1| nucleoside diphosphate kinase Ia [Arabidopsis thaliana] gi|332010348|gb|AED97731.1| nucleoside diphosphate kinase II [Arabidopsis thaliana]	356	231	1.00E-104	64.9	56.5	59.0	nucleoside diphosphate kinase II	gbpln	Arabidopsis thaliana	AT5G63310.1 | Symbols: NDPK2, NDPK1A, NDPK IA IA, NDPK IA, ATNDPK2 | nucleoside diphosphate kinase 2 | chr5:25372122-25373838 REVERSE LENGTH=231	356	231	1.00E-107	64.9	56.5	59.0
Rsa1.0_01492.1.g27318.t1	ref|XP_002866549.1| hypothetical protein ARALYDRAFT_496519 [Arabidopsis lyrata subsp. lyrata] gi|297312384|gb|EFH42808.1| hypothetical protein ARALYDRAFT_496519 [Arabidopsis lyrata subsp. lyrata]	296	304	1.00E-121	102.7	82.1	87.2	hypothetical protein ARALYDRAFT_496519	gbpln	Arabidopsis lyrata	AT5G63350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48510.1); Has 103 Blast hits to 102 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:25380216-25381124 REVERSE LENGTH=302	296	302	1.00E-110	102.0	80.4	86.1
Rsa1.0_01492.1.g27319.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01492.1.g27320.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1401	1214	0	86.7	32.2	46.8	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1401	626	2.00E-81	44.7	11.5	17.9
Rsa1.0_01492.1.g27321.t1	ref|XP_002866552.1| hypothetical protein ARALYDRAFT_332561 [Arabidopsis lyrata subsp. lyrata] gi|297312387|gb|EFH42811.1| hypothetical protein ARALYDRAFT_332561 [Arabidopsis lyrata subsp. lyrata]	561	559	0	99.6	87.0	91.8	hypothetical protein ARALYDRAFT_332561	gbpln	Arabidopsis lyrata	AT5G63390.1 | Symbols: | O-fucosyltransferase family protein | chr5:25390512-25392591 REVERSE LENGTH=559	561	559	0	99.6	87.3	92.3
Rsa1.0_01492.1.g27322.t1	ref|XP_002864846.1| EMB2746 [Arabidopsis lyrata subsp. lyrata] gi|297310681|gb|EFH41105.1| EMB2746 [Arabidopsis lyrata subsp. lyrata]	906	927	0	102.3	89.8	94.2	EMB2746	gbpln	Arabidopsis lyrata	AT5G63420.1 | Symbols: emb2746 | RNA-metabolising metallo-beta-lactamase family protein | chr5:25400515-25405807 FORWARD LENGTH=911	906	911	0	100.6	89.5	93.9
Rsa1.0_01492.1.g27323.t2	gb|EOA13932.1| hypothetical protein CARUB_v10027050mg [Capsella rubella]	254	232	1.00E-127	91.3	89.0	91.3	hypothetical protein CARUB_v10027050mg	gbpln	Capsella rubella	AT5G63440.2 | Symbols: | Protein of unknown function (DUF167) | chr5:25406360-25408195 FORWARD LENGTH=232	254	232	1.00E-129	91.3	88.6	90.9
Rsa1.0_01492.1.g27324.t1	gb|AAM60854.1| cytochrome P450-like protein [Arabidopsis thaliana]	507	508	0	100.2	84.4	90.5	cytochrome P450-like protein	gbpln	Arabidopsis thaliana	AT5G63450.1 | Symbols: CYP94B1 | cytochrome P450, family 94, subfamily B, polypeptide 1 | chr5:25408987-25410519 REVERSE LENGTH=510	507	510	0	100.6	84.8	91.5
Rsa1.0_01493.1.g27325.t1	ref|XP_002883665.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297329505|gb|EFH59924.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	287	398	2.00E-69	138.7	54.7	70.0	F-box family protein	gbpln	Arabidopsis lyrata	AT2G04810.1 | Symbols: | Protein of unknown function (DUF295) | chr2:1688773-1689966 FORWARD LENGTH=397	287	397	5.00E-68	138.3	53.0	67.6
Rsa1.0_01493.1.g27326.t1	gb|EOA20295.1| hypothetical protein CARUB_v10000603mg [Capsella rubella]	557	559	0	100.4	95.9	97.7	hypothetical protein CARUB_v10000603mg	gbpln	Capsella rubella	AT5G08680.1 | Symbols: | ATP synthase alpha/beta family protein | chr5:2821992-2824683 FORWARD LENGTH=559	557	559	0	100.4	92.6	93.9
Rsa1.0_01493.1.g27327.t1	ref|XP_002873374.1| DDT domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319211|gb|EFH49633.1| DDT domain-containing protein [Arabidopsis lyrata subsp. lyrata]	714	722	0	101.1	82.9	89.6	DDT domain-containing protein	gbpln	Arabidopsis lyrata	AT5G08630.1 | Symbols: | DDT domain-containing protein | chr5:2798575-2802138 REVERSE LENGTH=723	714	723	0	101.3	82.4	89.9
Rsa1.0_01493.1.g27328.t1	ref|XP_002871349.1| hypothetical protein ARALYDRAFT_908839 [Arabidopsis lyrata subsp. lyrata] gi|297317186|gb|EFH47608.1| hypothetical protein ARALYDRAFT_908839 [Arabidopsis lyrata subsp. lyrata]	327	351	1.00E-157	107.3	87.8	92.4	hypothetical protein ARALYDRAFT_908839	gbpln	Arabidopsis lyrata	AT5G08590.1 | Symbols: ASK2, SNRK2-1, SNRK2.1, SRK2G | SNF1-related protein kinase 2.1 | chr5:2783537-2785869 FORWARD LENGTH=353	327	353	1.00E-160	108.0	87.8	92.4

Rsa1.0_01493.1.g27329.t2	ref|XP_002873373.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] gi|297319210|gb|EFH49632.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	513	391	1.00E-115	76.2	43.9	46.4	calcium-binding EF hand family protein	gbpln	Arabidopsis lyrata	AT5G08580.1 | Symbols: | Calcium-binding EF hand family protein | chr5:2780976-2782961 REVERSE LENGTH=391	513	391	1.00E-117	76.2	43.7	46.2
Rsa1.0_01493.1.g27330.t1	ref|XP_002871348.1| hypothetical protein ARALYDRAFT_487699 [Arabidopsis lyrata subsp. lyrata] gi|297317185|gb|EFH47607.1| hypothetical protein ARALYDRAFT_487699 [Arabidopsis lyrata subsp. lyrata]	510	510	0	100.0	95.3	97.5	hypothetical protein ARALYDRAFT_487699	gbpln	Arabidopsis lyrata	AT5G08570.1 | Symbols: | Pyruvate kinase family protein | chr5:2778433-2780300 FORWARD LENGTH=510	510	510	0	100.0	94.9	97.3
Rsa1.0_01493.1.g27331.t1	ref|XP_002871347.1| positive transcription elongation factor/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297317184|gb|EFH47606.1| positive transcription elongation factor/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	116	116	2.00E-55	100.0	86.2	94.0	positive transcription elongation factor/ zinc ion binding protein	gbpln	Arabidopsis lyrata	AT5G08565.1 | Symbols: | Transcription initiation Spt4-like protein | chr5:2775964-2777154 FORWARD LENGTH=116	116	116	4.00E-58	100.0	87.1	92.2
Rsa1.0_01493.1.g27332.t1	gb|EOA15427.1| hypothetical protein CARUB_v10003965mg [Capsella rubella]	2253	2083	0	92.5	55.4	61.7	hypothetical protein CARUB_v10003965mg	gbpln	Capsella rubella	AT4G17330.1 | Symbols: ATG2484-1, G2484-1 | G2484-1 protein | chr4:9689263-9697172 REVERSE LENGTH=2037	2253	2037	0	90.4	55.0	61.5
Rsa1.0_01493.1.g27333.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1497	1499	0	100.1	61.9	75.3	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1497	158	2.00E-30	10.6	4.2	5.5
Rsa1.0_01493.1.g27334.t2	ref|XP_004287287.1| PREDICTED: topless-related protein 4-like [Fragaria vesca subsp. vesca]	582	1120	1.00E-130	192.4	39.9	50.5	PREDICTED: topless-related protein 4-like	gbpln	Fragaria vesca	AT1G80490.1 | Symbols: TPR1 | TOPLESS-related 1 | chr1:30261094-30266446 REVERSE LENGTH=1119	582	1119	1.00E-123	192.3	35.7	46.6
Rsa1.0_01493.1.g27335.t1	gb|ACP30622.1| disease resistance protein [Brassica rapa subsp. pekinensis]	223	1459	1.00E-97	654.3	80.7	88.8	disease resistance protein	gbpln	Brassica rapa	AT5G18370.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6085036-6088926 REVERSE LENGTH=1210	223	1210	2.00E-76	542.6	60.1	76.7
Rsa1.0_01494.1.g27336.t2	ref|XP_002873609.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297319446|gb|EFH49868.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	626	625	0	99.8	94.7	97.0	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT5G13400.1 | Symbols: | Major facilitator superfamily protein | chr5:4296854-4299079 REVERSE LENGTH=624	626	624	0	99.7	93.9	96.5
Rsa1.0_01494.1.g27337.t2	ref|XP_002871567.1| hypothetical protein ARALYDRAFT_488158 [Arabidopsis lyrata subsp. lyrata] gi|297317404|gb|EFH47826.1| hypothetical protein ARALYDRAFT_488158 [Arabidopsis lyrata subsp. lyrata]	1096	1123	0	102.5	92.1	96.6	hypothetical protein ARALYDRAFT_488158	gbpln	Arabidopsis lyrata	AT5G13390.1 | Symbols: NEF1 | no exine formation 1 | chr5:4292809-4296572 FORWARD LENGTH=1123	1096	1123	0	102.5	91.6	96.2
Rsa1.0_01494.1.g27338.t1	ref|NP_196841.2| auxin-responsive GH3 family protein [Arabidopsis thaliana] gi|26449584|dbj|BAC41918.1| putative auxin responsive protein [Arabidopsis thaliana] gi|29028956|gb|AAO64857.1| At5g13370 [Arabidopsis thaliana] gi|332004504|gb|AED91887.1| auxin-responsive GH3 family protein [Arabidopsis thaliana]	577	595	0	103.1	79.0	90.6	auxin-responsive GH3 family protein	gbpln	Arabidopsis thaliana	AT5G13370.1 | Symbols: | Auxin-responsive GH3 family protein | chr5:4286996-4289424 FORWARD LENGTH=595	577	595	0	103.1	79.0	90.6
Rsa1.0_01494.1.g27339.t2	gb|AAD19773.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1297	1335	0	102.9	53.0	69.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1297	1262	4.00E-60	97.3	12.4	19.0
Rsa1.0_01494.1.g27340.t1	dbj|BAJ34121.1| unnamed protein product [Thellungiella halophila]	244	231	9.00E-76	94.7	73.0	78.7	unnamed protein product	----	----	AT5G13330.1 | Symbols: Rap2.6L | related to AP2 6l | chr5:4272384-4274461 FORWARD LENGTH=212	244	212	6.00E-68	86.9	56.6	61.5
Rsa1.0_01494.1.g27341.t1	gb|EOA20271.1| hypothetical protein CARUB_v10000575mg [Capsella rubella]	570	574	0	100.7	85.6	92.3	hypothetical protein CARUB_v10000575mg	gbpln	Capsella rubella	AT5G13320.1 | Symbols: PBS3, GDG1, WIN3, GH3.12 | Auxin-responsive GH3 family protein | chr5:4268902-4270896 FORWARD LENGTH=575	570	575	0	100.9	84.4	91.4
Rsa1.0_01494.1.g27342.t1	ref|XP_002873606.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319443|gb|EFH49865.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	389	402	1.00E-161	103.3	79.4	84.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G13290.2 | Symbols: SOL2, CRN | Protein kinase superfamily protein | chr5:4252924-4254215 REVERSE LENGTH=401	389	401	1.00E-161	103.1	77.9	84.1

Rsa1.0_01494.1.g27343.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	723	1274	1.00E-68	176.2	22.1	34.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	723	303	6.00E-47	41.9	14.5	21.2
Rsa1.0_01494.1.g27344.t1	gb|EOA22271.1| hypothetical protein CARUB_v10002867mg [Capsella rubella]	263	333	9.00E-73	126.6	51.7	68.1	hypothetical protein CARUB_v10002867mg	gbpln	Capsella rubella	AT5G17080.1 | Symbols: | Cysteine proteinases superfamily protein | chr5:5619594-5620949 FORWARD LENGTH=298	263	298	2.00E-51	113.3	41.4	60.5
Rsa1.0_01495.1.g27345.t1	ref|XP_002881431.1| hypothetical protein ARALYDRAFT_902732 [Arabidopsis lyrata subsp. lyrata] gi|297327270|gb|EFH57690.1| hypothetical protein ARALYDRAFT_902732 [Arabidopsis lyrata subsp. lyrata]	123	134	4.00E-44	108.9	79.7	87.0	hypothetical protein ARALYDRAFT_902732	gbpln	Arabidopsis lyrata	AT2G36210.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:15186326-15186733 REVERSE LENGTH=135	123	135	2.00E-46	109.8	77.2	87.0
Rsa1.0_01495.1.g27346.t1	ref|XP_002881431.1| hypothetical protein ARALYDRAFT_902732 [Arabidopsis lyrata subsp. lyrata] gi|297327270|gb|EFH57690.1| hypothetical protein ARALYDRAFT_902732 [Arabidopsis lyrata subsp. lyrata]	123	134	2.00E-44	108.9	77.2	86.2	hypothetical protein ARALYDRAFT_902732	gbpln	Arabidopsis lyrata	AT2G36210.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:15186326-15186733 REVERSE LENGTH=135	123	135	3.00E-47	109.8	76.4	86.2
Rsa1.0_01495.1.g27347.t1	emb|CAN73924.1| hypothetical protein VITISV_041509 [Vitis vinifera]	1381	1434	0	103.8	38.5	55.0	hypothetical protein VITISV_041509	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1381	1262	1.00E-114	91.4	15.4	21.1
Rsa1.0_01495.1.g27348.t1	gb|AAM61505.1| unknown [Arabidopsis thaliana]	246	263	1.00E-74	106.9	73.2	78.5	unknown	gbpln	Arabidopsis thaliana	AT2G36220.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G52710.1); Has 74 Blast hits to 74 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15192556-15193347 FORWARD LENGTH=263	246	263	4.00E-76	106.9	73.2	78.9
Rsa1.0_01495.1.g27349.t1	ref|XP_002881433.1| hypothetical protein ARALYDRAFT_902736 [Arabidopsis lyrata subsp. lyrata] gi|297327272|gb|EFH57692.1| hypothetical protein ARALYDRAFT_902736 [Arabidopsis lyrata subsp. lyrata]	477	479	0	100.4	89.5	93.1	hypothetical protein ARALYDRAFT_902736	gbpln	Arabidopsis lyrata	AT2G36250.2 | Symbols: FTSZ2-1, ATFTSZ2-1 | Tubulin/FtsZ family protein | chr2:15197661-15199932 REVERSE LENGTH=478	477	478	0	100.2	89.5	92.9
Rsa1.0_01495.1.g27350.t1	ref|NP_565840.1| protein abscisic acid-insensitive 5 [Arabidopsis thaliana] gi|75313515|sp|Q9SJN0.1|ABI5_ARATH RecName: Full=Protein ABSCISIC ACID-INSENSITIVE 5; AltName: Full=Dc3 promoter-binding factor 1; Short=AtDPBF1; AltName: Full=Protein GROWTH-INSENSITIVITY TO ABA 1; AltName: Full=bZIP transcription factor 39; Short=AtbZIP39 gi|4510349|gb|AAD21438.1| abscisic acid insensitive 5 (ABI5) [Arabidopsis thaliana] gi|13346151|gb|AAK19599.1| bZIP protein [Arabidopsis thaliana] gi|111074502|gb|ABH04624.1| At2g36270 [Arabidopsis thaliana] gi|330254132|gb|AEC09226.1| protein abscisic acid-insensitive 5 [Arabidopsis thaliana]	138	442	5.00E-67	320.3	93.5	96.4	protein abscisic acid-insensitive 5	gbpln	Arabidopsis thaliana	AT2G36270.1 | Symbols: ABI5, GIA1 | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:15204980-15206571 REVERSE LENGTH=442	138	442	1.00E-69	320.3	93.5	96.4
Rsa1.0_01495.1.g27351.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1445	1475	0	102.1	50.0	65.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1445	1262	0	87.3	24.7	29.3
Rsa1.0_01495.1.g27352.t1	gb|AFZ45968.1| ABA insensitve 5-like protein [Brassica oleracea var. capitata]	236	425	1.00E-74	180.1	76.3	81.8	ABA insensitve 5-like protein	gbpln	Brassica oleracea	AT2G36270.1 | Symbols: ABI5, GIA1 | Basic-leucine zipper (bZIP) transcription factor family protein | chr2:15204980-15206571 REVERSE LENGTH=442	236	442	4.00E-61	187.3	72.5	78.0
Rsa1.0_01495.1.g27353.t1	gb|EOA26311.1| hypothetical protein CARUB_v10024924mg [Capsella rubella]	118	115	2.00E-30	97.5	63.6	73.7	hypothetical protein CARUB_v10024924mg	gbpln	Capsella rubella	AT2G36295.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:15211755-15212096 FORWARD LENGTH=113	118	113	5.00E-27	95.8	59.3	66.9

<table>
<tr><td>Rsa1.0_01495.1.g27354.t1</td><td>ref|XP_002881437.1| hypothetical protein ARALYDRAFT_482602 [Arabidopsis lyrata subsp. lyrata] gi|297327276|gb|EFH57696.1| hypothetical protein ARALYDRAFT_482602 [Arabidopsis lyrata subsp. lyrata]</td><td>196</td><td>255</td><td>3.00E-75</td><td>130.1</td><td>76.0</td><td>82.7</td><td>hypothetical protein ARALYDRAFT_482602</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G52760.1 | Symbols: | Integral membrane Yip1 family protein | chr3:19553932-19554705 REVERSE LENGTH=257</td><td>196</td><td>257</td><td>4.00E-77</td><td>131.1</td><td>77.0</td><td>84.7</td></tr>
<tr><td>Rsa1.0_01495.1.g27355.t2</td><td>gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1412</td><td>1496</td><td>0</td><td>105.9</td><td>57.7</td><td>71.4</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1412</td><td>1262</td><td>1.00E-141</td><td>89.4</td><td>16.8</td><td>23.7</td></tr>
<tr><td>Rsa1.0_01496.1.g27356.t1</td><td>gb|EOA36979.1| hypothetical protein CARUB_v10009943mg [Capsella rubella]</td><td>276</td><td>283</td><td>1.00E-88</td><td>102.5</td><td>66.3</td><td>79.3</td><td>hypothetical protein CARUB_v10009943mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34610.1); Has 56 Blast hits to 56 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr1:10618966-10619802 FORWARD LENGTH=278</td><td>276</td><td>278</td><td>8.00E-90</td><td>100.7</td><td>66.7</td><td>79.7</td></tr>
<tr><td>Rsa1.0_01496.1.g27357.t2</td><td>ref|XP_002893607.1| ATINT2 [Arabidopsis lyrata subsp. lyrata] gi|297339449|gb|EFH69866.1| ATINT2 [Arabidopsis lyrata subsp. lyrata]</td><td>695</td><td>580</td><td>6.00E-13</td><td>83.5</td><td>5.3</td><td>6.0</td><td>ATINT2</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30220.1 | Symbols: ATINT2, INT2 | inositol transporter 2 | chr1:10632957-10635439 REVERSE LENGTH=580</td><td>695</td><td>580</td><td>8.00E-14</td><td>83.5</td><td>4.9</td><td>5.9</td></tr>
<tr><td>Rsa1.0_01496.1.g27358.t1</td><td>ref|NP_564352.1| uncharacterized protein [Arabidopsis thaliana] gi|12320849|gb|AAG50559.1|AC073506_1 hypothetical protein [Arabidopsis thaliana] gi|16323184|gb|AAL15326.1| At1g30260/F12P21_9 [Arabidopsis thaliana] gi|21436007|gb|AAM51581.1| At1g30260/F12P21_9 [Arabidopsis thaliana] gi|332193079|gb|AEE31200.1| uncharacterized protein AT1G30260 [Arabidopsis thaliana]</td><td>92</td><td>97</td><td>2.00E-25</td><td>105.4</td><td>82.6</td><td>85.9</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G30260.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Galactosyltransferase family protein (TAIR:AT4G21060.1); Has 30 Blast hits to 30 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10651159-10651452 FORWARD LENGTH=97</td><td>92</td><td>97</td><td>3.00E-28</td><td>105.4</td><td>82.6</td><td>85.9</td></tr>
<tr><td>Rsa1.0_01496.1.g27359.t5</td><td>gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]</td><td>259</td><td>1557</td><td>2.00E-26</td><td>601.2</td><td>36.7</td><td>56.8</td><td>reverse transcriptase, putative; 100033-105622</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>259</td><td>575</td><td>5.00E-13</td><td>222.0</td><td>20.5</td><td>34.0</td></tr>
<tr><td>Rsa1.0_01496.1.g27360.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01496.1.g27361.t1</td><td>gb|EOA39265.1| hypothetical protein CARUB_v10012271mg [Capsella rubella]</td><td>476</td><td>484</td><td>0</td><td>101.7</td><td>90.8</td><td>94.3</td><td>hypothetical protein CARUB_v10012271mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30270.1 | Symbols: CIPK23, SnRK3.23, ATCIPK23, LKS1 | CBL-interacting protein kinase 23 | chr1:10655270-10658524 FORWARD LENGTH=482</td><td>476</td><td>482</td><td>0</td><td>101.3</td><td>92.0</td><td>95.0</td></tr>
<tr><td>Rsa1.0_01496.1.g27362.t1</td><td>ref|XP_002893610.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297339452|gb|EFH69869.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>439</td><td>455</td><td>1.00E-170</td><td>103.6</td><td>80.6</td><td>88.4</td><td>heat shock protein binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30280.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr1:10662851-10664570 REVERSE LENGTH=455</td><td>439</td><td>455</td><td>1.00E-168</td><td>103.6</td><td>79.7</td><td>87.5</td></tr>
<tr><td>Rsa1.0_01497.1.g27363.t1</td><td>gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>700</td><td>1225</td><td>1.00E-132</td><td>175.0</td><td>41.7</td><td>57.6</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>700</td><td>575</td><td>7.00E-45</td><td>82.1</td><td>19.1</td><td>29.6</td></tr>
<tr><td>Rsa1.0_01497.1.g27364.t1</td><td>gb|EOA30132.1| hypothetical protein CARUB_v10013238mg, partial [Capsella rubella]</td><td>187</td><td>619</td><td>3.00E-21</td><td>331.0</td><td>30.5</td><td>33.7</td><td>hypothetical protein CARUB_v10013238mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G13490.1 | Symbols: OVA5, ATKRS-2 | Lysyl-tRNA synthetase, class II | chr3:4395984-4399302 REVERSE LENGTH=602</td><td>187</td><td>602</td><td>2.00E-22</td><td>321.9</td><td>29.9</td><td>32.6</td></tr>
<tr><td>Rsa1.0_01497.1.g27365.t1</td><td>ref|NP_198579.2| condensin complex subunit 3 [Arabidopsis thaliana] gi|332006829|gb|AED94212.1| embryo defective protein 2656 [Arabidopsis thaliana]</td><td>1047</td><td>1051</td><td>0</td><td>100.4</td><td>86.2</td><td>92.1</td><td>condensin complex subunit 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G37630.1 | Symbols: EMB2656 | ARM repeat superfamily protein | chr5:14947407-14952546 FORWARD LENGTH=1051</td><td>1047</td><td>1051</td><td>0</td><td>100.4</td><td>86.2</td><td>92.1</td></tr>
<tr><td>Rsa1.0_01497.1.g27366.t2</td><td>ref|XP_002892277.1| TraB family protein [Arabidopsis lyrata subsp. lyrata] gi|297338119|gb|EFH68536.1| TraB family protein [Arabidopsis lyrata subsp. lyrata]</td><td>178</td><td>372</td><td>2.00E-35</td><td>209.0</td><td>53.4</td><td>60.1</td><td>TraB family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G05270.1 | Symbols: | TraB family protein | chr1:1531806-1534305 REVERSE LENGTH=371</td><td>178</td><td>371</td><td>2.00E-37</td><td>208.4</td><td>52.8</td><td>59.6</td></tr>
<tr><td>Rsa1.0_01497.1.g27367.t1</td><td>dbj|BAA04996.1| glutamine synthetase [Raphanus sativus]</td><td>356</td><td>356</td><td>0</td><td>100.0</td><td>98.6</td><td>99.4</td><td>glutamine synthetase</td><td>gbpln</td><td>Raphanus sativus</td><td>AT5G37600.1 | Symbols: ATGSR1, GLN1;1, GSR 1, ATGLN1;1 | glutamine synthase clone R1 | chr5:14933574-14935656 REVERSE LENGTH=356</td><td>356</td><td>356</td><td>0</td><td>100.0</td><td>96.1</td><td>98.9</td></tr>
<tr><td>Rsa1.0_01498.1.g27368.t1</td><td>ref|XP_002876953.1| CYP71B21 [Arabidopsis lyrata subsp. lyrata] gi|297322791|gb|EFH53212.1| CYP71B21 [Arabidopsis lyrata subsp. lyrata]</td><td>96</td><td>499</td><td>4.00E-24</td><td>519.8</td><td>55.2</td><td>57.3</td><td>CYP71B21</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G26190.1 | Symbols: CYP71B21 | cytochrome P450, family 71, subfamily B, polypeptide 21 | chr3:9583475-9585083 REVERSE LENGTH=499</td><td>96</td><td>499</td><td>2.00E-26</td><td>519.8</td><td>55.2</td><td>57.3</td></tr>
</table>

Rsa1.0_01498.1.g27369.t1	ref|NP_198850.1| PWWP domain-containing protein [Arabidopsis thaliana] gi|10178144|dbj|BAB11589.1| unnamed protein product [Arabidopsis thaliana] gi|332007152|gb|AED94535.1| PWWP domain-containing protein [Arabidopsis thaliana]	327	1008	6.00E-23	308.3	20.8	25.1	PWWP domain-containing protein	gbpln	Arabidopsis thaliana	AT5G40340.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr5:16131654-16134680 REVERSE LENGTH=1008	327	1008	1.00E-25	308.3	20.8	25.1
Rsa1.0_01498.1.g27370.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01498.1.g27371.t1	ref|XP_002876952.1| CYP71B19 [Arabidopsis lyrata subsp. lyrata] gi|297322790|gb|EFH53211.1| CYP71B19 [Arabidopsis lyrata subsp. lyrata]	500	502	0	100.4	86.2	92.6	CYP71B19	gbpln	Arabidopsis lyrata	AT3G26170.1 | Symbols: CYP71B19 | cytochrome P450, family 71, subfamily B, polypeptide 19 | chr3:9573542-9575129 REVERSE LENGTH=502	500	502	0	100.4	85.4	92.8
Rsa1.0_01498.1.g27372.t1	gb|EOA25800.1| hypothetical protein CARUB_v10019167mg [Capsella rubella]	195	511	2.00E-58	262.1	57.4	64.1	hypothetical protein CARUB_v10019167mg	gbpln	Capsella rubella	AT3G26140.1 | Symbols: | Cellulase (glycosyl hydrolase family 5) protein | chr3:9559742-9563070 REVERSE LENGTH=508	195	508	6.00E-58	260.5	55.4	63.6
Rsa1.0_01498.1.g27373.t1	dbj|BAB01438.1| unnamed protein product [Arabidopsis thaliana]	598	708	0	118.4	78.9	85.6	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G26120.1 | Symbols: TEL1 | terminal EAR1-like 1 | chr3:9546398-9549186 FORWARD LENGTH=615	598	615	0	102.8	78.9	85.6
Rsa1.0_01498.1.g27374.t1	ref|XP_002875308.1| hypothetical protein ARALYDRAFT_484375 [Arabidopsis lyrata subsp. lyrata] gi|297321146|gb|EFH51567.1| hypothetical protein ARALYDRAFT_484375 [Arabidopsis lyrata subsp. lyrata]	118	128	4.00E-25	108.5	65.3	72.9	hypothetical protein ARALYDRAFT_484375	gbpln	Arabidopsis lyrata	AT3G26110.1 | Symbols: | Anther-specific protein agp1-like | chr3:9541573-9541959 FORWARD LENGTH=128	118	128	4.00E-21	108.5	61.0	72.0
Rsa1.0_01498.1.g27375.t1	ref|XP_002875307.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] gi|297321145|gb|EFH51566.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	535	533	0	99.6	88.6	93.5	regulator of chromosome condensation family protein	gbpln	Arabidopsis lyrata	AT3G26100.2 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:9538063-9540149 FORWARD LENGTH=532	535	532	0	99.4	87.9	93.5
Rsa1.0_01499.1.g27376.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01499.1.g27377.t1	ref|XP_002893808.1| At1g34065 [Arabidopsis lyrata subsp. lyrata] gi|297339650|gb|EFH70067.1| At1g34065 [Arabidopsis lyrata subsp. lyrata]	324	321	1.00E-163	99.1	89.2	93.2	At1g34065	gbpln	Arabidopsis lyrata	AT1G34065.1 | Symbols: SAMC2 | S-adenosylmethionine carrier 2 | chr1:12398717-12401036 REVERSE LENGTH=345	324	345	1.00E-165	106.5	88.3	92.6
Rsa1.0_01499.1.g27378.t1	ref|XP_002891076.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336918|gb|EFH67335.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	441	352	1.00E-173	79.8	66.0	72.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G09760.1 | Symbols: | Protein kinase superfamily protein | chr4:6148955-6151150 REVERSE LENGTH=346	441	346	1.00E-159	78.5	59.4	68.0
Rsa1.0_01499.1.g27379.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01499.1.g27380.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01499.1.g27381.t1	ref|NP_190057.1| uncharacterized protein [Arabidopsis thaliana] gi|6967119|emb|CAB72473.1| putative protein [Arabidopsis thaliana] gi|30725352|gb|AAP37698.1| At3g44710 [Arabidopsis thaliana] gi|110743781|dbj|BAE99726.1| hypothetical protein [Arabidopsis thaliana] gi|332644413|gb|AEE77934.1| uncharacterized protein AT3G44710 [Arabidopsis thaliana]	458	504	1.00E-155	110.0	62.0	78.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G44710.1 | Symbols: | Plant protein of unknown function (DUF247) | chr3:16251942-16253456 REVERSE LENGTH=504	458	504	1.00E-158	110.0	62.0	78.4
Rsa1.0_01500.1.g27382.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01500.1.g27383.t1	ref|NP_683459.2| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|49823486|gb|AAT68726.1| hypothetical protein At1g62305 [Arabidopsis thaliana] gi|58743302|gb|AAW81729.1| At1g62305 [Arabidopsis thaliana] gi|60547649|gb|AAX23788.1| hypothetical protein At1g62305 [Arabidopsis thaliana] gi|61656151|gb|AAX49378.1| At1g62305 [Arabidopsis thaliana] gi|332195830|gb|AEE33951.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]	401	378	1.00E-179	94.3	79.1	84.0	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	gbpln	Arabidopsis thaliana	AT1G62305.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:23026989-23029189 REVERSE LENGTH=378	401	378	0	94.3	79.1	84.0
Rsa1.0_01500.1.g27384.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01500.1.g27385.t2	dbj|BAB70678.1| subtilisin-like serine protease [Arabidopsis thaliana]	1429	832	0	58.2	46.5	50.9	subtilisin-like serine protease	gbpln	Arabidopsis thaliana	AT1G62340.1 | Symbols: ALE1, ALE | PA-domain containing subtilase family protein | chr1:23051123-23055656 REVERSE LENGTH=832	1429	832	0	58.2	46.3	50.5
Rsa1.0_01500.1.g27386.t7	ref|NP_188660.3| pumilio 5 [Arabidopsis thaliana] gi|313471415|sp|Q9LJX4.2|PUM5_ARATH RecName: Full=Pumilio homolog 5; Short=APUM-5; Short=AtPUM5 gi|332642831|gb|AEE76352.1| pumilio 5 [Arabidopsis thaliana]	125	961	1.00E-40	768.8	63.2	66.4	pumilio 5	gbpln	Arabidopsis thaliana	AT3G20250.1 | Symbols: APUM5, PUM5 | pumilio 5 | chr3:7059098-7062660 REVERSE LENGTH=961	125	961	2.00E-43	768.8	63.2	66.4
Rsa1.0_01500.1.g27387.t16	emb|CAA19715.1| putative protein [Arabidopsis thaliana] gi|7269574|emb|CAB79576.1| putative protein [Arabidopsis thaliana]	1690	1318	0	78.0	33.1	40.8	putative protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1690	1262	8.00E-72	74.7	9.3	14.0
Rsa1.0_01500.1.g27388.t1	ref|XP_002888031.1| hypothetical protein ARALYDRAFT_893249 [Arabidopsis lyrata subsp. lyrata] gi|297333872|gb|EFH64290.1| hypothetical protein ARALYDRAFT_893249 [Arabidopsis lyrata subsp. lyrata]	212	202	3.00E-76	95.3	73.1	79.7	hypothetical protein ARALYDRAFT_893249	gbpln	Arabidopsis lyrata	AT1G62370.1 | Symbols: | RING/U-box superfamily protein | chr1:23072575-23073189 FORWARD LENGTH=204	212	204	5.00E-77	96.2	72.2	79.7
Rsa1.0_01501.1.g27389.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1492	1213	0	81.3	24.5	36.9	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1492	626	7.00E-62	42.0	9.8	16.4
Rsa1.0_01501.1.g27390.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1850	1274	0	68.9	32.6	44.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1850	575	3.00E-68	31.1	9.2	14.4
Rsa1.0_01501.1.g27391.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01501.1.g27392.t1	ref|XP_002891635.1| hypothetical protein ARALYDRAFT_892105 [Arabidopsis lyrata subsp. lyrata] gi|297337477|gb|EFH67894.1| hypothetical protein ARALYDRAFT_892105 [Arabidopsis lyrata subsp. lyrata]	364	253	4.00E-66	69.5	35.4	45.3	hypothetical protein ARALYDRAFT_892105	gbpln	Arabidopsis lyrata	AT2G31670.1 | Symbols: | Stress responsive alpha-beta barrel domain protein | chr2:13472699-13473490 REVERSE LENGTH=263	364	263	2.00E-68	72.3	35.7	45.1
Rsa1.0_01501.1.g27393.t1	ref|NP_175549.1| DEAD-box ATP-dependent RNA helicase 34 [Arabidopsis thaliana] gi|108861889|sp|Q9C8J1.2|RH34_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 34 gi|4836949|gb|AAD30651.1|AC006085_24 RNA helicase [Arabidopsis thaliana] gi|16604541|gb|AAL24276.1| At1g51380/F11M15_24 [Arabidopsis thaliana] gi|18958046|gb|AAL79596.1| At1g51380/F11M15_24 [Arabidopsis thaliana] gi|332194539|gb|AEE32660.1| DEAD-box ATP-dependent RNA helicase 34 [Arabidopsis thaliana]	406	392	0	96.6	89.9	93.8	DEAD-box ATP-dependent RNA helicase 34	gbpln	Arabidopsis thaliana	AT1G51380.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr1:19047960-19049967 FORWARD LENGTH=392	406	392	0	96.6	89.9	93.8
Rsa1.0_01501.1.g27394.t1	ref|XP_002872983.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297318820|gb|EFH49242.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	456	494	1.00E-160	108.3	74.1	80.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G01980.1 | Symbols: | RING/U-box superfamily protein | chr5:375542-377023 FORWARD LENGTH=493	456	493	1.00E-163	108.1	74.1	80.0
Rsa1.0_01501.1.g27395.t3	gb|EOA33008.1| hypothetical protein CARUB_v10016338mg [Capsella rubella]	456	430	0	94.3	83.8	87.5	hypothetical protein CARUB_v10016338mg	gbpln	Capsella rubella	AT5G01990.1 | Symbols: | Auxin efflux carrier family protein | chr5:377373-379600 REVERSE LENGTH=431	456	431	0	94.5	82.5	86.0
Rsa1.0_01502.1.g27396.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01502.1.g27397.t1	ref|XP_002868643.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] gi|297314479|gb|EFH44902.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	168	162	1.00E-64	96.4	85.1	87.5	ubiquitin family protein	gbpln	Arabidopsis lyrata	AT5G40630.1 | Symbols: | Ubiquitin-like superfamily protein | chr5:16271402-16272429 REVERSE LENGTH=165	168	165	9.00E-67	98.2	84.5	86.9
Rsa1.0_01502.1.g27398.t2	ref|NP_001078680.1| putative DNA repair protein RAD23-4 [Arabidopsis thaliana] gi|332006939|gb|AED94322.1| putative DNA repair protein RAD23-4 [Arabidopsis thaliana]	236	332	6.00E-12	140.7	17.8	21.6	putative DNA repair protein RAD23-4	gbpln	Arabidopsis thaliana	AT5G38470.2 | Symbols: RAD23D | Rad23 UV excision repair protein family | chr5:15404720-15407251 FORWARD LENGTH=332	236	332	2.00E-14	140.7	17.8	21.6

Rsa1.0_01502.1.g27399.t1	gb|EOA16295.1| hypothetical protein CARUB_v10004439mg [Capsella rubella]	760	585	0	77.0	69.1	72.5	hypothetical protein CARUB_v10004439mg	gbpln	Capsella rubella	AT5G40640.1 | Symbols: | unknown protein; LOCATED IN: plasma membrane; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27390.1); Has 104 Blast hits to 102 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:16277345-16280258 FORWARD LENGTH=586	760	586	0	77.1	68.8	72.1
Rsa1.0_01502.1.g27400.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01502.1.g27401.t1	ref|XP_002868641.1| hypothetical protein ARALYDRAFT_493916 [Arabidopsis lyrata subsp. lyrata] gi|297314477|gb|EFH44900.1| hypothetical protein ARALYDRAFT_493916 [Arabidopsis lyrata subsp. lyrata]	364	328	1.00E-156	90.1	79.4	84.3	hypothetical protein ARALYDRAFT_493916	gbpln	Arabidopsis lyrata	AT5G40660.1 | Symbols: | ATP12 protein-related | chr5:16283650-16285161 REVERSE LENGTH=325	364	325	1.00E-158	89.3	78.3	84.1
Rsa1.0_01502.1.g27402.t1	ref|NP_198883.1| cystinosin [Arabidopsis thaliana] gi|13124057|sp|P57758.1|CTNS_ARATH RecName: Full=Cystinosin homolog gi|9758095|dbj|BAB08539.1| unnamed protein product [Arabidopsis thaliana] gi|15529266|gb|AAK97727.1| AT5g40670/MNF13_190 [Arabidopsis thaliana] gi|16974419|gb|AAL31135.1| AT5g40670/MNF13_190 [Arabidopsis thaliana] gi|332007197|gb|AED94580.1| cystinosin homolog [Arabidopsis thaliana]	270	270	1.00E-144	100.0	91.9	96.3	cystinosin	gbpln	Arabidopsis thaliana	AT5G40670.1 | Symbols: | PQ-loop repeat family protein / transmembrane family protein | chr5:16285968-16287591 FORWARD LENGTH=270	270	270	1.00E-147	100.0	91.9	96.3
Rsa1.0_01502.1.g27403.t1	ref|XP_002870685.1| hypothetical protein ARALYDRAFT_493913 [Arabidopsis lyrata subsp. lyrata] gi|297316521|gb|EFH46944.1| hypothetical protein ARALYDRAFT_493913 [Arabidopsis lyrata subsp. lyrata]	210	213	4.00E-89	101.4	85.7	91.4	hypothetical protein ARALYDRAFT_493913	gbpln	Arabidopsis lyrata	AT5G40690.1 | Symbols: | CONTAINS InterPro DOMAIN/s: EF-Hand 1, calcium-binding site (InterPro:IPR018247); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41730.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:16290770-16291402 FORWARD LENGTH=210	210	210	1.00E-84	100.0	83.8	91.4
Rsa1.0_01502.1.g27404.t1	ref|NP_198886.2| uncharacterized protein [Arabidopsis thaliana] gi|9758098|dbj|BAB08542.1| unnamed protein product [Arabidopsis thaliana] gi|332007200|gb|AED94583.1| uncharacterized protein AT5G40700 [Arabidopsis thaliana]	288	302	3.00E-84	104.9	65.3	72.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G40700.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27350.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:16292047-16293443 REVERSE LENGTH=302	288	302	9.00E-87	104.9	65.3	72.6
Rsa1.0_01503.1.g27405.t1	ref|NP_179383.3| transformation/transcription domain-associated protein [Arabidopsis thaliana] gi|330251608|gb|AEC06702.1| phosphatidylinositol 3- and 4-kinase family protein with FAT domain [Arabidopsis thaliana]	3859	3858	0	100.0	95.3	97.3	transformation/transcription domain-associated protein	gbpln	Arabidopsis thaliana	AT2G17930.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase family protein with FAT domain | chr2:7784455-7802230 REVERSE LENGTH=3858	3859	3858	0	100.0	95.3	97.3
Rsa1.0_01503.1.g27406.t2	ref|XP_002886134.1| hypothetical protein ARALYDRAFT_480688 [Arabidopsis lyrata subsp. lyrata] gi|297331974|gb|EFH62393.1| hypothetical protein ARALYDRAFT_480688 [Arabidopsis lyrata subsp. lyrata]	325	158	3.00E-47	48.6	36.6	39.4	hypothetical protein ARALYDRAFT_480688	gbpln	Arabidopsis lyrata	AT2G17880.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr2:7767176-7767658 REVERSE LENGTH=160	325	160	1.00E-48	49.2	36.3	39.1
Rsa1.0_01503.1.g27407.t1	gb|EOA31014.1| hypothetical protein CARUB_v10014159mg [Capsella rubella]	351	330	8.00E-63	94.0	49.0	59.8	hypothetical protein CARUB_v10014159mg	gbpln	Capsella rubella	AT2G17787.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G35940.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:7731374-7732853 FORWARD LENGTH=324	351	324	6.00E-63	92.3	50.1	61.5
Rsa1.0_01503.1.g27408.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1421	1459	0	102.7	59.6	74.2	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1421	1262	1.00E-114	88.8	14.1	21.0

Rsa1.0_01503.1.g27409.t1	gb|AAK32909.1|AF367322_1 AT4g35920/F4B14_190 [Arabidopsis thaliana] gi|22137178|gb|AAM91434.1| AT4g35920/F4B14_190 [Arabidopsis thaliana]	113	440	2.00E−49	389.4	85.8	90.3	AT4g35920/F4B14_190	gbpln	Arabidopsis thaliana	AT4G35920.2 | Symbols: MCA1 | PLAC8 family protein | chr4:17012106−17014192 REVERSE LENGTH=421	113	421	3.00E−52	372.6	85.8	90.3
Rsa1.0_01504.1.g27410.t1	gb|AAM64382.1| unknown [Arabidopsis thaliana]	367	372	1.00E−165	101.4	84.2	89.6	unknown	gbpln	Arabidopsis thaliana	AT2G16800.1 | Symbols: | high−affinity nickel−transport family protein | chr2:7285824−7287188 FORWARD LENGTH=372	367	372	1.00E−166	101.4	83.7	89.1
Rsa1.0_01504.1.g27411.t1	ref|NP_001031359.1| transportin 1 [Arabidopsis thaliana] gi|75244583|sp|Q8H0U4.1|TNPO1_ARATH RecName: Full=Transportin−1; Short=AtTRN1; AltName: Full=Importin beta−2; AltName: Full=Karyopherin beta−2 gi|25083223|gb|AAN72052.1| putative transportin [Arabidopsis thaliana] gi|31711774|gb|AAP68243.1| At2g16950 [Arabidopsis thaliana] gi|330251468|gb|AEC06562.1| transportin 1 [Arabidopsis thaliana]	931	891	0	95.7	87.6	91.4	transportin 1	gbpln	Arabidopsis thaliana	AT2G16950.2 | Symbols: TRN1, ATTRN1 | transportin 1 | chr2:7353939−7360637 FORWARD LENGTH=891	931	891	0	95.7	87.6	91.4
Rsa1.0_01504.1.g27412.t1	ref|NP_565400.1| F−box/LRR−repeat protein 10 [Arabidopsis thaliana] gi|75337079|sp|Q9SDA8.1|FBL10_ARATH RecName: Full=F−box/LRR−repeat protein 10 gi|13605809|gb|AAK32890.1|AF367303_1 At2g17020 [Arabidopsis thaliana] gi|22137200|gb|AAM91445.1| At2g17020/At2g17020 [Arabidopsis thaliana] gi|330251479|gb|AEC06573.1| F−box/LRR−repeat protein 10 [Arabidopsis thaliana]	716	656	0	91.6	75.4	81.6	F−box/LRR−repeat protein 10	gbpln	Arabidopsis thaliana	AT2G17020.1 | Symbols: | F−box/RNI−like superfamily protein | chr2:7396559−7398787 REVERSE LENGTH=656	716	656	0	91.6	75.4	81.6
Rsa1.0_01504.1.g27413.t1	dbj|BAJ34393.1| unnamed protein product [Thellungiella halophila]	285	285	2.33E−156	100.0	89.5	94.4	unnamed protein product	−−−−	−−−−	AT2G17040.1 | Symbols: anac036, NAC036 | NAC domain containing protein 36 | chr2:7407123−7408120 FORWARD LENGTH=276	285	276	1.00E−136	96.8	83.5	88.8
Rsa1.0_01504.1.g27414.t1	ref|XP_002886095.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331935|gb|EFH62354.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	462	468	0	101.3	68.2	84.2	kinase family protein	gbpln	Arabidopsis lyrata	AT2G17090.1 | Symbols: SSP | Protein kinase protein with tetratricopeptide repeat domain | chr2:7435088−7437298 REVERSE LENGTH=465	462	465	0	100.6	67.7	83.1
Rsa1.0_01504.1.g27415.t1	ref|NP_179311.1| ubiquitin−like protein [Arabidopsis thaliana] gi|4584343|gb|AAD25138.1| putative ubiquitin−like protein [Arabidopsis thaliana] gi|23296306|gb|AAN13037.1| putative ubiquitin protein [Arabidopsis thaliana] gi|110735104|gb|ABG89122.1| Dsk2a [synthetic construct] gi|330251503|gb|AEC06597.1| UBL/UBA protein DSK2b [Arabidopsis thaliana]	557	551	0	98.9	85.3	90.1	ubiquitin−like protein	gbpln	Arabidopsis thaliana	AT2G17200.1 | Symbols: DSK2 | ubiquitin family protein | chr2:7482133−7485090 REVERSE LENGTH=551	557	551	0	98.9	85.3	90.1
Rsa1.0_01504.1.g27416.t1	gb|AAD14492.1| Hypothetical protein [Arabidopsis thaliana]	164	240	5.00E−24	146.3	39.0	50.6	Hypothetical protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	164	575	1.00E−10	350.6	27.4	40.2
Rsa1.0_01504.1.g27417.t1	ref|XP_002886105.1| hypothetical protein ARALYDRAFT_480605 [Arabidopsis lyrata subsp. lyrata] gi|297331945|gb|EFH62364.1| hypothetical protein ARALYDRAFT_480605 [Arabidopsis lyrata subsp. lyrata]	397	414	0	104.3	84.6	89.4	hypothetical protein ARALYDRAFT_480605	gbpln	Arabidopsis lyrata	AT2G17220.2 | Symbols: | Protein kinase superfamily protein | chr2:7487866−7489768 REVERSE LENGTH=413	397	413	0	104.0	85.1	89.7
Rsa1.0_01504.1.g27418.t1	ref|XP_002884044.1| hypothetical protein ARALYDRAFT_480608 [Arabidopsis lyrata subsp. lyrata] gi|297329884|gb|EFH60303.1| hypothetical protein ARALYDRAFT_480608 [Arabidopsis lyrata subsp. lyrata]	598	582	0	97.3	83.3	90.3	hypothetical protein ARALYDRAFT_480608	gbpln	Arabidopsis lyrata	AT2G17250.1 | Symbols: EMB2762 | CCAAT−binding factor | chr2:7499573−7502957 FORWARD LENGTH=577	598	577	0	96.5	81.6	88.1
Rsa1.0_01504.1.g27419.t1	ref|NP_179357.1| RPM1−interacting protein 4−like protein [Arabidopsis thaliana] gi|11762120|gb|AAG40338.1|AF324986_1 At2g17660 [Arabidopsis thaliana] gi|115646839|gb|ABJ17136.1| At2g17660 [Arabidopsis thaliana] gi|330251568|gb|AEC06662.1| RPM1−interacting protein 4−like protein [Arabidopsis thaliana]	69	69	4.00E−29	100.0	89.9	97.1	RPM1−interacting protein 4−like protein	gbpln	Arabidopsis thaliana	AT2G17660.1 | Symbols: | RPM1−interacting protein 4 (RIN4) family protein | chr2:7673359−7673568 FORWARD LENGTH=69	69	69	7.00E−32	100.0	89.9	97.1

Rsa1.0_01504.1.g27420.t1	gb|AAM62704.1| unknown [Arabidopsis thaliana]	463	463	0	100.0	74.3	85.3	unknown	gbpln	Arabidopsis thaliana	AT2G17670.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:7674420-7675811 FORWARD LENGTH=463	463	463	0	100.0	74.1	85.1	
Rsa1.0_01504.1.g27421.t1	ref|NP_179359.1| uncharacterized protein [Arabidopsis thaliana] gi|25347770|pir||B84555 hypothetical protein At2g17680 [imported] - Arabidopsis thaliana gi|50058923|gb|AAT69206.1| hypothetical protein At2g17680 [Arabidopsis thaliana] gi|330251571|gb|AEC06665.1| uncharacterized protein AT2G17680 [Arabidopsis thaliana]	288	292	1.00E-121	101.4	76.0	87.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G17680.1 | Symbols: | Arabidopsis protein of unknown function (DUF241) | chr2:7679241-7680119 FORWARD LENGTH=292	288	292	1.00E-123	101.4	76.0	87.5	
Rsa1.0_01504.1.g27422.t2	gb|EOA30274.1| hypothetical protein CARUB_v10013395mg [Capsella rubella]	1150	546	0	47.5	44.1	45.8	hypothetical protein CARUB_v10013395mg	gbpln	Capsella rubella	AT2G17700.1 | Symbols: | ACT-like protein tyrosine kinase family protein | chr2:7685778-7689278 REVERSE LENGTH=546	1150	546	0	47.5	43.8	45.5	
Rsa1.0_01504.1.g27423.t2	ref|NP_175139.1| receptor like protein 6 [Arabidopsis thaliana] gi|12321005|gb|AAG50623.1|AC083835_8 disease resistance protein, putative [Arabidopsis thaliana] gi|332193999|gb|AEE32120.1| receptor like protein 6 [Arabidopsis thaliana]	493	994	2.00E-75	201.6	35.1	43.6	receptor like protein 6	gbpln	Arabidopsis thaliana	AT1G45616.1 | Symbols: AtRLP6, RLP6 | receptor like protein 6 | chr1:17183550-17186534 REVERSE LENGTH=994	493	994	5.00E-78	201.6	35.1	43.6	
Rsa1.0_01504.1.g27424.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1380	1515	0	109.8	56.9	71.0	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1380	1262	1.00E-102	91.4	13.7	20.7	
Rsa1.0_01504.1.g27425.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_01505.1.g27426.t1	gb|EOA12907.1| hypothetical protein CARUB_v10025883mg [Capsella rubella]	576	833	0	144.6	81.3	87.2	hypothetical protein CARUB_v10025883mg	gbpln	Capsella rubella	AT5G57590.1 | Symbols: BIO1 | adenosylmethionine-8-amino-7-oxononanoate transaminases | chr5:23318593-23322687 REVERSE LENGTH=833	576	833	0	144.6	81.6	87.8	
Rsa1.0_01505.1.g27427.t4	gb|AAG50652.1|AC073433_4 transposase, putative [Arabidopsis thaliana]	306	659	3.00E-42	215.4	32.7	43.5	transposase, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#	
Rsa1.0_01505.1.g27428.t1	ref|NP_568860.1| CBL-interacting serine/threonine-protein kinase 21 [Arabidopsis thaliana] gi|75332106|sp|Q94CG0.1|CIPKL_ARATH RecName: Full=CBL-interacting serine/threonine-protein kinase 21; AltName: Full=SNF1-related kinase 3.4; AltName: Full=SOS2-like protein kinase PKS23 gi|14334390|gb|AAK59696.1| CBL-interacting protein kinase 21 [Arabidopsis thaliana] gi|332009545|gb|AED96928.1| CBL-interacting serine/threonine-protein kinase 21 [Arabidopsis thaliana]	441	416	0	94.3	87.8	90.9	CBL-interacting serine/threonine-protein kinase 21	gbpln	Arabidopsis thaliana	AT5G57630.1 | Symbols: CIPK21, SnRK3.4 | CBL-interacting protein kinase 21 | chr5:23341092-23343143 REVERSE LENGTH=416	441	416	0	94.3	87.8	90.9	
Rsa1.0_01505.1.g27429.t3	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	731	1270	1.00E-137	173.7	43.8	57.7	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	731	575	1.00E-45	78.7	15.7	23.5	
Rsa1.0_01505.1.g27430.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_01505.1.g27431.t2	ref|NP_200572.1| GCK domain-containing protein [Arabidopsis thaliana] gi|9758326|dbj|BAB08800.1| unnamed protein product [Arabidopsis thaliana] gi|52354575|gb|AAU44608.1| hypothetical protein AT5G57640 [Arabidopsis thaliana] gi|60547959|gb|AAX23943.1| hypothetical protein At5g57640 [Arabidopsis thaliana] gi|332009546|gb|AED96929.1| GCK domain-containing protein [Arabidopsis thaliana]	246	226	1.00E-16	91.9	27.2	33.7	GCK domain-containing protein	gbpln	Arabidopsis thaliana	AT5G57640.1 | Symbols: | GCK domain-containing protein | chr5:23344766-23345446 FORWARD LENGTH=226	246	226	3.00E-19	91.9	27.2	33.7	
Rsa1.0_01505.1.g27432.t1	gb|EOA13987.1| hypothetical protein CARUB_v10027120mg [Capsella rubella]	242	215	4.00E-40	88.8	47.9	63.2	hypothetical protein CARUB_v10027120mg	gbpln	Capsella rubella	AT5G57640.1 | Symbols: | GCK domain-containing protein | chr5:23344766-23345446 FORWARD LENGTH=226	242	226	3.00E-40	93.4	46.7	60.3	
Rsa1.0_01505.1.g27433.t1	gb|AAM08751.1|AC025098_18 Putative copia-type polyprotein [Oryza sativa Japonica Group]	1209	1803	0	149.1	42.5	57.6	Putative copia-type polyprotein	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1209	1262	1.00E-113	104.4	17.2	26.1	

Rsa1.0_01505.1.g27434.t1	ref|XP_002864523.1| xylose isomerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310358|gb|EFH40782.1| xylose isomerase family protein [Arabidopsis lyrata subsp. lyrata]	477	477	0	100.0	94.5	97.7	xylose isomerase family protein	gbpln	Arabidopsis lyrata	AT5G57655.2 | Symbols: | xylose isomerase family protein | chr5:23347030-23349805 FORWARD LENGTH=477	477	477	0	100.0	94.3	97.3
Rsa1.0_01505.1.g27435.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01506.1.g27436.t1	ref|XP_002871700.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317537|gb|EFH47959.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	248	338	1.00E-109	136.3	83.1	88.7	predicted protein	gbpln	Arabidopsis lyrata	AT5G16030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02500.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5238242-5240578 FORWARD LENGTH=339	248	339	1.00E-110	136.7	82.3	88.3
Rsa1.0_01506.1.g27437.t6	ref|NP_197105.1| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein [Arabidopsis thaliana] gi|14190513|gb|AAK55737.1|AF380656_1 AT5g16010/F1N13_150 [Arabidopsis thaliana] gi|9755647|emb|CAC01800.1| steroid 5alpha-reductase-like protein [Arabidopsis thaliana] gi|24797018|gb|AAN64521.1| At5g16010/F1N13_150 [Arabidopsis thaliana] gi|332004851|gb|AED92234.1| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein [Arabidopsis thaliana]	485	268	1.00E-112	55.3	42.3	47.8	3-oxo-5-alpha-steroid 4-dehydrogenase family protein	gbpln	Arabidopsis thaliana	AT5G16010.1 | Symbols: | 3-oxo-5-alpha-steroid 4-dehydrogenase family protein | chr5:5227982-5229012 FORWARD LENGTH=268	485	268	1.00E-114	55.3	42.3	47.8
Rsa1.0_01506.1.g27438.t1	gb|ACV74393.1| cold resistance protein 1 [Brassica oleracea var. viridis] gi|258548930|gb|ACV74394.1| cold resistance protein 1 [Brassica oleracea var. viridis] gi|258548932|gb|ACV74395.1| cold resistance protein 1 [Brassica oleracea var. botrytis] gi|258548934|gb|ACV74396.1| cold resistance protein 1 [Brassica oleracea var. capitata]	65	65	4.00E-22	100.0	87.7	92.3	cold resistance protein 1	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01506.1.g27439.t1	ref|NP_197098.2| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana] gi|332004843|gb|AED92226.1| Rossmann-fold NAD(P)-binding domain-containing protein [Arabidopsis thaliana]	183	364	5.00E-68	198.9	67.2	77.6	Rossmann-fold NAD(P)-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT5G15940.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:5202801-5204715 FORWARD LENGTH=364	183	364	2.00E-70	198.9	67.2	77.6
Rsa1.0_01506.1.g27440.t1	emb|CAN66863.1| hypothetical protein VITISV_013500 [Vitis vinifera]	1331	1112	0	83.5	42.5	54.7	hypothetical protein VITISV_013500	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1331	1262	1.00E-109	94.8	16.5	23.5
Rsa1.0_01506.1.g27441.t2	gb|EOA20857.1| hypothetical protein CARUB_v10001194mg [Capsella rubella]	168	376	3.00E-62	223.8	72.0	81.5	hypothetical protein CARUB_v10001194mg	gbpln	Capsella rubella	AT5G15940.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:5202801-5204715 FORWARD LENGTH=364	168	364	2.00E-64	216.7	70.8	82.7
Rsa1.0_01506.1.g27442.t1	ref|XP_002871692.1| hypothetical protein ARALYDRAFT_488442 [Arabidopsis lyrata subsp. lyrata] gi|297317529|gb|EFH47951.1| hypothetical protein ARALYDRAFT_488442 [Arabidopsis lyrata subsp. lyrata]	359	354	0	98.6	90.8	95.3	hypothetical protein ARALYDRAFT_488442	gbpln	Arabidopsis lyrata	AT5G15930.1 | Symbols: PAM1 | plant adhesion molecule 1 | chr5:5200329-5202250 FORWARD LENGTH=356	359	356	0	99.2	90.8	95.0
Rsa1.0_01506.1.g27443.t3	ref|NP_568323.1| dehydrogenase-related protein [Arabidopsis thaliana] gi|15292961|gb|AAK93591.1| unknown protein [Arabidopsis thaliana] gi|21280841|gb|AAM44918.1| unknown protein [Arabidopsis thaliana] gi|332004840|gb|AED92223.1| dehydrogenase-related protein [Arabidopsis thaliana]	259	269	1.00E-115	103.9	90.7	94.6	dehydrogenase-related protein	gbpln	Arabidopsis thaliana	AT5G15910.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:5193207-5195202 FORWARD LENGTH=269	259	269	1.00E-117	103.9	90.7	94.6
Rsa1.0_01506.1.g27444.t1	gb|AAP42646.1| putative beta-glucan elicitor receptor [Brassica napus]	672	752	0	111.9	81.3	89.6	putative beta-glucan elicitor receptor	gbpln	Brassica napus	AT5G15870.1 | Symbols: | glycosyl hydrolase family 81 protein | chr5:5182641-5184878 REVERSE LENGTH=745	672	745	0	110.9	79.9	88.4
Rsa1.0_01506.1.g27445.t1	ref|XP_002873025.1| hypothetical protein ARALYDRAFT_486965 [Arabidopsis lyrata subsp. lyrata] gi|297318862|gb|EFH49284.1| hypothetical protein ARALYDRAFT_486965 [Arabidopsis lyrata subsp. lyrata]	518	503	1.00E-163	97.1	59.7	73.4	hypothetical protein ARALYDRAFT_486965	gbpln	Arabidopsis lyrata	AT5G01150.1 | Symbols: | Protein of unknown function (DUF674) | chr5:51988-53649 FORWARD LENGTH=501	518	501	1.00E-154	96.7	58.3	70.7

Rsa1.0_01507.1.g27446.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033–105622 [Arabidopsis thaliana]	1028	1557	0	151.5	45.4	59.3	reverse transcriptase, putative; 100033–105622	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691–14272776 FORWARD LENGTH=361	1028	361	2.00E–32	35.1	6.8	11.4
Rsa1.0_01507.1.g27447.t1	gb|EOA12297.1| hypothetical protein CARUB_v10007977mg [Capsella rubella]	349	417	1.00E–53	119.5	40.4	58.2	hypothetical protein CARUB_v10007977mg	gbpln	Capsella rubella	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528–14335255 FORWARD LENGTH=575	349	575	6.00E–35	164.8	27.8	43.8
Rsa1.0_01507.1.g27448.t1	ref|NP_567362.1| subtilisin–like protease [Arabidopsis thaliana] gi|22136594|gb|AAM91616.1| putative subtilisin serine protease [Arabidopsis thaliana] gi|332657496|gb|AEE82896.1| subtilisin–like protease [Arabidopsis thaliana]	787	778	0	98.9	75.6	84.2	subtilisin–like protease	gbpln	Arabidopsis thaliana	AT4G10550.1 | Symbols: | Subtilase family protein | chr4:6516613–6519767 REVERSE LENGTH=778	787	778	0	98.9	75.6	84.2
Rsa1.0_01507.1.g27449.t1	gb|EOA19618.1| hypothetical protein CARUB_v10002928mg [Capsella rubella]	752	910	0	121.0	68.8	80.2	hypothetical protein CARUB_v10002928mg	gbpln	Capsella rubella	AT4G10570.1 | Symbols: UBP9 | ubiquitin-specific protease 9 | chr4:6523657–6528058 REVERSE LENGTH=923	752	923	0	122.7	68.4	80.7
Rsa1.0_01507.1.g27450.t1	ref|NP_192811.4| protein kinase–like protein [Arabidopsis thaliana] gi|332657522|gb|AEE82922.1| protein kinase–like protein [Arabidopsis thaliana]	886	711	0	80.2	60.9	65.2	protein kinase–like protein	gbpln	Arabidopsis thaliana	AT4G10730.1 | Symbols: | Protein kinase superfamily protein | chr4:6609793–6614786 REVERSE LENGTH=711	886	711	0	80.2	60.9	65.2
Rsa1.0_01507.1.g27451.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01507.1.g27452.t2	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1307	1307	0	100.0	57.8	73.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR–like protein kinase) 8 | chr4:12129485–12134086 FORWARD LENGTH=1262	1307	1262	9.00E–95	96.6	14.9	22.4
Rsa1.0_01507.1.g27453.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	443	1164	1.00E–75	262.8	32.1	48.1	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA–directed DNA polymerase (reverse transcriptase)–related family protein | chr3:8789471–8793208 FORWARD LENGTH=746	443	746	2.00E–55	168.4	27.8	40.9
Rsa1.0_01508.1.g27454.t1	emb|CAB89379.1| putative protein [Arabidopsis thaliana]	141	804	2.00E–17	570.2	31.9	32.6	putative protein	gbpln	Arabidopsis thaliana	AT5G10630.2 | Symbols: | Translation elongation factor EF1A/initiation factor IF2gamma family protein | chr5:3360561–3364414 FORWARD LENGTH=668	141	668	5.00E–20	473.8	31.9	32.6
Rsa1.0_01508.1.g27455.t1	ref|XP_002887337.1| hypothetical protein ARALYDRAFT_476226 [Arabidopsis lyrata subsp. lyrata] gi|297333178|gb|EFH63596.1| hypothetical protein ARALYDRAFT_476226 [Arabidopsis lyrata subsp. lyrata]	205	208	8.00E–73	101.5	79.5	85.9	hypothetical protein ARALYDRAFT_476226	gbpln	Arabidopsis lyrata	AT1G70920.1 | Symbols: ATHB18, HB18 | homeobox–leucine zipper protein 18 | chr1:26736126–26738419 FORWARD LENGTH=206	205	206	6.00E–73	100.5	78.5	84.9
Rsa1.0_01508.1.g27456.t1	ref|XP_002862565.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308168|gb|EFH38823.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	297	87	5.00E–13	29.3	12.1	13.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G70900.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23110.4); Has 57 Blast hits to 57 proteins in 14 species: Archae – 0; Bacteria – 0; Metazoa – 0; Fungi – 0; Plants – 57; Viruses – 0; Other Eukaryotes – 0 (source: NCBI BLink). | chr1:26732456–26733637 FORWARD LENGTH=244	297	244	3.00E–15	82.2	12.5	13.1
Rsa1.0_01508.1.g27457.t1	gb|AAF97298.1|AC007843_1 Hypothetical protein [Arabidopsis thaliana]	316	362	9.00E–82	114.6	51.6	67.4	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01508.1.g27458.t2	gb|AAB82639.1| putative non–LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1012	1374	1.00E–113	135.8	21.5	31.0	putative non–LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I–like superfamily protein | chr1:16528880–16531065 REVERSE LENGTH=626	1012	626	3.00E–33	61.9	9.9	15.8
Rsa1.0_01508.1.g27459.t1	gb|EOA35840.1| hypothetical protein CARUB_v10021082mg [Capsella rubella]	137	158	3.00E–46	115.3	73.0	80.3	hypothetical protein CARUB_v10021082mg	gbpln	Capsella rubella	AT1G70830.3 | Symbols: MLP28 | MLP–like protein 28 | chr1:26710203–26711395 REVERSE LENGTH=201	137	201	6.00E–47	146.7	70.1	83.9
Rsa1.0_01508.1.g27460.t1	gb|EOA34647.1| hypothetical protein CARUB_v10022227mg [Capsella rubella]	146	149	4.00E–74	102.1	95.2	99.3	hypothetical protein CARUB_v10022227mg	gbpln	Capsella rubella	AT1G70870.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:26721020–26721563 REVERSE LENGTH=139	146	139	7.00E–61	95.2	80.1	84.9
Rsa1.0_01508.1.g27461.t1	gb|EOA34244.1| hypothetical protein CARUB_v10021755mg [Capsella rubella]	138	159	3.00E–60	115.2	84.1	93.5	hypothetical protein CARUB_v10021755mg	gbpln	Capsella rubella	AT1G70880.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:26723086–26723717 REVERSE LENGTH=159	138	159	5.00E–59	115.2	80.4	89.9
Rsa1.0_01509.1.g27462.t1	gb|EOA24063.1| hypothetical protein CARUB_v10017283mg [Capsella rubella]	436	435	0	99.8	90.6	94.5	hypothetical protein CARUB_v10017283mg	gbpln	Capsella rubella	AT3G27925.1 | Symbols: DEGP1, Deg1 | DegP protease 1 | chr3:10366659–10368864 REVERSE LENGTH=439	436	439	0	100.7	87.2	90.8
Rsa1.0_01509.1.g27463.t1	dbj|BAM44633.1| glabrous 1 [Raphanus sativus var. niger]	210	210	1.00E–122	100.0	100.0	100.0	glabrous 1	gbpln	Raphanus sativus	AT3G27920.1 | Symbols: GL1, ATMYB0, ATGL1, MYB0 | myb domain protein 0 | chr3:10361945–10363506 REVERSE LENGTH=228	210	228	2.00E–80	108.6	73.3	83.3
Rsa1.0_01509.1.g27464.t1	sp|Q9LK86.2|FBK71_ARATH RecName: Full=Putative F–box/kelch–repeat protein At3g27910	343	384	1.00E–117	112.0	63.6	77.3	RecName: Full=Putative F–box/kelch–repeat protein At3g27910	----	----	AT4G39240.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18269599–18270726 REVERSE LENGTH=375	343	375	3.00E–89	109.3	51.3	65.9

Rsa1.0_01509.1.g27465.t1	gb|EOA25131.1| hypothetical protein CARUB_v10018440mg [Capsella rubella]	196	196	9.00E-98	100.0	91.3	98.0	hypothetical protein CARUB_v10018440mg	gbpln	Capsella rubella	AT3G27890.1 | Symbols: NQR | NADPH:quinone oxidoreductase | chr3:10350807-10351938 REVERSE LENGTH=196	196	196	3.00E-99	100.0	91.8	97.4
Rsa1.0_01509.1.g27466.t1	ref|NP_566827.1| uncharacterized protein [Arabidopsis thaliana] gi|11994493|dbj|BAB02534.1| unnamed protein product [Arabidopsis thaliana] gi|21553599|gb|AAM62692.1| unknown [Arabidopsis thaliana] gi|110741968|dbj|BAE98924.1| hypothetical protein [Arabidopsis thaliana] gi|111074300|gb|ABH04523.1| At3g27880 [Arabidopsis thaliana] gi|332643854|gb|AEE77375.1| uncharacterized protein AT3G27880 [Arabidopsis thaliana]	249	242	2.00E-61	97.2	64.7	75.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27880.1 | Symbols: | Protein of unknown function (DUF1645) | chr3:10338429-10339157 FORWARD LENGTH=242	249	242	5.00E-64	97.2	64.7	75.5
Rsa1.0_01509.1.g27467.t1	ref|NP_189425.2| phospholipid-translocating ATPase [Arabidopsis thaliana] gi|12229655|sp|Q9LK90.1|ALA8_ARATH RecName: Full=Putative phospholipid-transporting ATPase 8; Short=AtALA8; AltName: Full=Aminophospholipid flippase 8 gi|11994492|dbj|BAB02533.1| P-type transporting ATPase-like protein [Arabidopsis thaliana] gi|332643853|gb|AEE77374.1| putative phospholipid-transporting ATPase 8 [Arabidopsis thaliana]	1185	1189	0	100.3	89.7	95.1	phospholipid-translocating ATPase	gbpln	Arabidopsis thaliana	AT3G27870.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr3:10330950-10335288 FORWARD LENGTH=1189	1185	1189	0	100.3	89.7	95.1
Rsa1.0_01509.1.g27468.t1	ref|XP_002875407.1| hypothetical protein ARALYDRAFT_484576 [Arabidopsis lyrata subsp. lyrata] gi|297321245|gb|EFH51666.1| hypothetical protein ARALYDRAFT_484576 [Arabidopsis lyrata subsp. lyrata]	610	661	0	108.4	60.7	76.7	hypothetical protein ARALYDRAFT_484576	gbpln	Arabidopsis lyrata	AT3G27860.1 | Symbols: | Tudor/PWWP/MBT superfamily protein | chr3:10326128-10328086 FORWARD LENGTH=652	610	652	1.00E-168	106.9	58.0	73.1
Rsa1.0_01509.1.g27469.t1	gb|EOA24784.1| hypothetical protein CARUB_v10018063mg [Capsella rubella]	201	191	6.00E-57	95.0	68.7	72.6	hypothetical protein CARUB_v10018063mg	gbpln	Capsella rubella	AT3G27830.1 | Symbols: RPL12-A, RPL12 | ribosomal protein L12-A | chr3:10318576-10319151 FORWARD LENGTH=191	201	191	2.00E-59	95.0	68.7	72.1
Rsa1.0_01509.1.g27470.t1	gb|EOA24744.1| hypothetical protein CARUB_v10018021mg, partial [Capsella rubella]	192	211	7.00E-72	109.9	85.4	89.1	hypothetical protein CARUB_v10018021mg, partial	gbpln	Capsella rubella	AT3G27830.1 | Symbols: RPL12-A, RPL12 | ribosomal protein L12-A | chr3:10318576-10319151 FORWARD LENGTH=191	192	191	1.00E-73	99.5	85.9	90.1
Rsa1.0_01509.1.g27471.t1	gb|EOA23892.1| hypothetical protein CARUB_v10017107mg [Capsella rubella]	496	488	0	98.4	89.7	95.6	hypothetical protein CARUB_v10017107mg	gbpln	Capsella rubella	AT3G27820.1 | Symbols: ATMDAR4, MDAR4 | monodehydroascorbate reductase 4 | chr3:10315249-10317881 FORWARD LENGTH=488	496	488	0	98.4	89.7	96.0
Rsa1.0_01510.1.g27472.t1	dbj|BAF91403.1| S-locus receptor kinase (kinase domain) [Brassica oleracea]	394	424	0	107.6	94.4	97.0	S-locus receptor kinase (kinase domain)	gbpln	Brassica oleracea	AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850	394	850	1.00E-155	215.7	70.1	81.0
Rsa1.0_01510.1.g27473.t11	ref|XP_002887071.1| ATP dependent DNA ligase family protein [Arabidopsis lyrata subsp. lyrata] gi|297332912|gb|EFH63330.1| ATP dependent DNA ligase family protein [Arabidopsis lyrata subsp. lyrata]	1418	1413	0	99.6	80.5	86.5	ATP dependent DNA ligase family protein	gbpln	Arabidopsis lyrata	AT1G66730.1 | Symbols: AtLIG6, LIG6 | DNA LIGASE 6 | chr1:24884991-24891823 FORWARD LENGTH=1396	1418	1396	0	98.4	80.3	86.7
Rsa1.0_01510.1.g27474.t1	gb|EOA35744.1| hypothetical protein CARUB_v10020977mg [Capsella rubella] gi|482571557|gb|EOA35745.1| hypothetical protein CARUB_v10020977mg [Capsella rubella]	217	198	8.00E-88	91.2	79.7	82.9	hypothetical protein CARUB_v10020977mg	gbpln	Capsella rubella	AT1G66740.1 | Symbols: AtSP7, SP7, SGA2, ASF1A | ASF1 like histone chaperone | chr1:24892586-24893548 FORWARD LENGTH=196	217	196	4.00E-89	90.3	77.0	81.6

Rsa1.0_01510.1.g27475.t1	ref|NP_176847.1| cyclin-dependent kinase D-2 [Arabidopsis thaliana] gi|75333580|sp|Q9C9M7.1|CDKD2_ARATH RecName: Full=Cyclin-dependent kinase D-2; Short=CDKD;2; AltName: Full=CDK-activating kinase 4-At; Short=CAK4-At gi|12597763|gb|AAG60076.1|AC013288_10 cell division protein kinase, putative [Arabidopsis thaliana] gi|20521157|dbj|BAB91558.1| cdk-activating kinase 4 [Arabidopsis thaliana] gi|22531034|gb|AAM97021.1| cell division protein kinase, putative [Arabidopsis thaliana] gi|23197980|gb|AAN15517.1| cell division protein kinase, putative [Arabidopsis thaliana] gi|332196430|gb|AEE34551.1| cyclin-dependent kinase D-2 [Arabidopsis thaliana]	347	348	0	100.3	97.1	98.6	cyclin-dependent kinase D-2	gbpln	Arabidopsis thaliana	AT1G66750.1 | Symbols: CDKD1;2, CAK4AT, AT;CDKD;2, CDKD;2, CAK4 | CDK-activating kinase 4 | chr1:24894775-24897015 FORWARD LENGTH=348	347	348	0	100.3	97.1	98.6
Rsa1.0_01510.1.g27476.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01510.1.g27477.t7	ref|NP_176662.1| MATE efflux family protein [Arabidopsis thaliana] gi|91806023|gb|ABE65740.1| MATE efflux family protein [Arabidopsis thaliana] gi|332196173|gb|AEE34294.1| MATE efflux family protein [Arabidopsis thaliana]	494	502	0	101.6	77.1	88.5	MATE efflux family protein	gbpln	Arabidopsis thaliana	AT1G64820.1 | Symbols: | MATE efflux family protein | chr1:24088605-24090558 FORWARD LENGTH=502	494	502	0	101.6	77.1	88.5
Rsa1.0_01510.1.g27478.t1	ref|XP_002886769.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332610|gb|EFH63028.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	261	500	1.00E-115	191.6	80.8	89.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G64820.1 | Symbols: | MATE efflux family protein | chr1:24088605-24090558 FORWARD LENGTH=502	261	502	1.00E-116	192.3	79.7	90.4
Rsa1.0_01510.1.g27479.t1	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	680	536	6.00E-91	78.8	32.2	44.7	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	680	530	1.00E-49	77.9	15.7	21.5
Rsa1.0_01510.1.g27480.t1	ref|XP_002887076.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297332917|gb|EFH63335.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	111	493	6.00E-40	444.1	74.8	82.0	mate efflux family protein	gbpln	Arabidopsis lyrata	AT1G64820.1 | Symbols: | MATE efflux family protein | chr1:24088605-24090558 FORWARD LENGTH=502	111	502	4.00E-39	452.3	69.4	81.1
Rsa1.0_01510.1.g27481.t1	ref|XP_002886769.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332610|gb|EFH63028.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	427	500	1.00E-126	117.1	52.9	73.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G66760.1 | Symbols: | MATE efflux family protein | chr1:24902110-24904054 FORWARD LENGTH=466	427	466	1.00E-160	109.1	65.6	80.3
Rsa1.0_01511.1.g27482.t1	ref|NP_197812.1| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana] gi|10177083|dbj|BAB10389.1| ubiquitin [Arabidopsis thaliana] gi|110741569|dbj|BAE98733.1| ubiquitin [Arabidopsis thaliana] gi|332005891|gb|AED93274.1| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana]	427	574	1.00E-180	134.4	69.8	74.2	phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	gbpln	Arabidopsis thaliana	AT5G24240.1 | Symbols: | Phosphatidylinositol 3- and 4-kinase ;Ubiquitin family protein | chr5:8231110-8232925 REVERSE LENGTH=574	427	574	0	134.4	69.8	74.2
Rsa1.0_01511.1.g27483.t1	gb|EOA20957.1| hypothetical protein CARUB_v10001289mg [Capsella rubella]	366	353	2.00E-97	96.4	50.3	66.1	hypothetical protein CARUB_v10001289mg	gbpln	Capsella rubella	AT5G24220.1 | Symbols: | Lipase class 3-related protein | chr5:8225861-8227551 FORWARD LENGTH=376	366	376	5.00E-94	102.7	48.4	65.3
Rsa1.0_01511.1.g27484.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01511.1.g27485.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1369	1342	0	98.0	47.1	65.0	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1369	1262	1.00E-75	92.2	11.5	19.4
Rsa1.0_01511.1.g27486.t1	gb|EOA20957.1| hypothetical protein CARUB_v10001289mg [Capsella rubella]	355	353	8.00E-96	99.4	51.8	66.5	hypothetical protein CARUB_v10001289mg	gbpln	Capsella rubella	AT5G24220.1 | Symbols: | Lipase class 3-related protein | chr5:8225861-8227551 FORWARD LENGTH=376	355	376	2.00E-93	105.9	50.4	66.8
Rsa1.0_01511.1.g27487.t1	sp|O65727.1|ERG11_BRANA RecName: Full=Squalene monooxygenase 1,1; AltName: Full=Squalene epoxidase 1,1; Short=SE 1,1 gi|3123354|emb|CAA06773.1| squalene epoxidase homologue [Brassica napus]	518	506	0	97.7	90.3	93.1	RecName: Full=Squalene monooxygenase 1,1; AltName: Full=Squalene epoxidase 1,1; Short=SE 1,1 gi|3123354|emb|CAA06773.1| squalene epoxidase homologue	gbpln	Brassica napus	AT5G24150.1 | Symbols: SQP1, SQE5 | FAD/NAD(P)-binding oxidoreductase family protein | chr5:8172594-8175395 REVERSE LENGTH=516	518	516	0	99.6	84.7	92.7

Rsa1.0_01511.1.g27488.t1	ref|XP_002874170.1| hypothetical protein ARALYDRAFT_489269 [Arabidopsis lyrata subsp. lyrata] gi|297320007|gb|EFH50429.1| hypothetical protein ARALYDRAFT_489269 [Arabidopsis lyrata subsp. lyrata]	515	517	0	100.4	86.6	92.0	hypothetical protein ARALYDRAFT_489269	gbpln	Arabidopsis lyrata	AT5G24120.1 | Symbols: SIGE, SIG5, ATSIG5 | sigma factor E | chr5:8157794-8159746 REVERSE LENGTH=517	515	517	0	100.4	86.0	90.9
Rsa1.0_01511.1.g27489.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1407	1274	0	90.5	25.5	34.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1407	626	1.00E-41	44.5	8.4	13.9
Rsa1.0_01512.1.g27490.t1	gb|EOA39186.1| hypothetical protein CARUB_v10012153mg [Capsella rubella]	125	508	2.00E-33	406.4	61.6	72.0	hypothetical protein CARUB_v10012153mg	gbpln	Capsella rubella	AT1G21060.1 | Symbols: | Protein of unknown function, DUF547 | chr1:7371799-7374085 FORWARD LENGTH=505	125	505	3.00E-32	404.0	57.6	71.2
Rsa1.0_01512.1.g27491.t1	gb|EOA21233.1| hypothetical protein CARUB_v10001580mg [Capsella rubella]	299	298	1.00E-169	99.7	97.3	98.7	hypothetical protein CARUB_v10001580mg	gbpln	Capsella rubella	AT5G19760.1 | Symbols: | Mitochondrial substrate carrier family protein | chr5:6679591-6681845 REVERSE LENGTH=298	299	298	1.00E-167	99.7	94.0	96.3
Rsa1.0_01512.1.g27492.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01512.1.g27493.t1	ref|NP_197478.1| tubulin alpha-3/alpha-5 chain [Arabidopsis thaliana] gi|15241179|ref|NP_197479.1| tubulin alpha-3/alpha-5 chain [Arabidopsis thaliana] gi|297808045|ref|XP_002871906.1| tubulin alpha-3 [Arabidopsis lyrata subsp. lyrata] gi|297812159|ref|XP_002873963.1| tubulin alpha-3 [Arabidopsis lyrata subsp. lyrata] gi|408407916|sp|Q56WH1.2|TBA3_ARATH RecName: Full=Tubulin alpha-3 chain gi|408407918|sp|B9DHQ0.2|TBA5_ARATH RecName: Full=Tubulin alpha-5 chain gi|13605805|gb|AAK32888.1|AF367301_1 AT5g19770/T29J13_190 [Arabidopsis thaliana] gi|166912|gb|AAA32888.1| alpha-tubulin [Arabidopsis thaliana] gi|166918|gb|AAA32891.1| alpha-5 tubulin [Arabidopsis thaliana] gi|14532776|gb|AAK64169.1| putative tubulin alpha-5 chain [Arabidopsis thaliana] gi|17473826|gb|AAL38340.1| unknown protein [Arabidopsis thaliana] gi|19310733|gb|AAL85097.1| putative tubulin alpha-5 chain [Arabidopsis thaliana] gi|23397154|gb|AAN31860.1| putative tubulin alpha-5 chain [Arabidopsis thaliana] gi|23397156|gb|AAN31861.1| putative tubulin alpha-5 chain [Arabidopsis thaliana] gi|23505949|gb|AAN28834.1| At5g19770/T29J13_190 [Arabidopsis	450	450	0	100.0	99.8	100.0	tubulin alpha-3/alpha-5 chain	gbpln	Arabidopsis lyrata	AT5G19780.1 | Symbols: TUA5 | tubulin alpha-5 | chr5:6687212-6688926 FORWARD LENGTH=450	450	450	0	100.0	99.8	100.0
Rsa1.0_01512.1.g27494.t1	gb|EOA22165.1| hypothetical protein CARUB_v10002733mg [Capsella rubella]	252	252	1.00E-104	100.0	81.3	88.5	hypothetical protein CARUB_v10002733mg	gbpln	Capsella rubella	AT5G19790.1 | Symbols: RAP2.11 | related to AP2 11 | chr5:6689271-6690032 REVERSE LENGTH=253	252	253	1.00E-104	100.4	81.0	88.5
Rsa1.0_01512.1.g27495.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01512.1.g27496.t1	gb|EOA19838.1| hypothetical protein CARUB_v10000085mg [Capsella rubella]	1114	1116	0	100.2	95.2	98.3	hypothetical protein CARUB_v10000085mg	gbpln	Capsella rubella	AT5G19820.1 | Symbols: emb2734 | ARM repeat superfamily protein | chr5:6695731-6701247 REVERSE LENGTH=1116	1114	1116	0	100.2	94.7	98.0
Rsa1.0_01512.1.g27497.t1	ref|XP_002871909.1| transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297317746|gb|EFH48168.1| transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata]	109	505	2.00E-18	463.3	50.5	59.6	transcription factor jumonji domain-containing protein	gbpln	Arabidopsis lyrata	AT5G19840.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:6705372-6709382 FORWARD LENGTH=505	109	505	1.00E-20	463.3	49.5	59.6
Rsa1.0_01512.1.g27498.t1	gb|EOA22088.1| hypothetical protein CARUB_v10002631mg [Capsella rubella]	199	204	2.00E-92	102.5	86.4	93.0	hypothetical protein CARUB_v10002631mg	gbpln	Capsella rubella	AT5G19855.1 | Symbols: | Chaperonin-like RbcX protein | chr5:6712166-6713445 REVERSE LENGTH=203	199	203	5.00E-94	102.0	83.9	91.0
Rsa1.0_01512.1.g27499.t1	gb|EOA22521.1| hypothetical protein CARUB_v10003176mg [Capsella rubella]	215	170	6.00E-67	79.1	60.5	65.6	hypothetical protein CARUB_v10003176mg	gbpln	Capsella rubella	AT5G19860.1 | Symbols: | Protein of unknown function, DUF538 | chr5:6714533-6715837 REVERSE LENGTH=181	215	181	1.00E-66	84.2	62.8	67.4
Rsa1.0_01512.1.g27500.t1	gb|EOA22866.1| hypothetical protein CARUB_v10003597mg [Capsella rubella]	281	302	1.00E-141	107.5	90.0	95.4	hypothetical protein CARUB_v10003597mg	gbpln	Capsella rubella	AT5G19870.1 | Symbols: | Family of unknown function (DUF716) | chr5:6716182-6717012 REVERSE LENGTH=276	281	276	1.00E-143	98.2	90.0	95.7
Rsa1.0_01513.1.g27501.t5	gb|EOA19792.1| hypothetical protein CARUB_v10000037mg [Capsella rubella]	1378	1456	0	105.7	78.9	85.1	hypothetical protein CARUB_v10000037mg	gbpln	Capsella rubella	AT5G01400.1 | Symbols: ESP4 | HEAT repeat-containing protein | chr5:162803-171072 REVERSE LENGTH=1467	1378	1467	0	106.5	76.9	83.4

Rsa1.0_01513.1.g27502.t1	gb|EOA21182.1| hypothetical protein CARUB_v10001526mg [Capsella rubella]	298	309	1.00E-157	103.7	93.6	96.3	hypothetical protein CARUB_v10001526mg	gbpln	Capsella rubella	AT5G01410.1 | Symbols: PDX1, ATPDX1.3, RSR4, PDX1.3, ATPDX1 | Aldolase-type TIM barrel family protein | chr5:172576-173505 REVERSE LENGTH=309	298	309	1.00E-158	103.7	93.0	96.0
Rsa1.0_01513.1.g27503.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01513.1.g27504.t2	ref|XP_002870921.1| hypothetical protein ARALYDRAFT_486934 [Arabidopsis lyrata subsp. lyrata] gi|297316758|gb|EFH47180.1| hypothetical protein ARALYDRAFT_486934 [Arabidopsis lyrata subsp. lyrata]	513	405	1.00E-132	78.9	51.3	57.7	hypothetical protein ARALYDRAFT_486934	gbpln	Arabidopsis lyrata	AT5G01420.1 | Symbols: | Glutaredoxin family protein | chr5:174886-176091 REVERSE LENGTH=401	513	401	1.00E-129	78.2	49.3	56.9
Rsa1.0_01513.1.g27505.t1	ref|XP_002873011.1| hypothetical protein ARALYDRAFT_486928 [Arabidopsis lyrata subsp. lyrata] gi|297318848|gb|EFH49270.1| hypothetical protein ARALYDRAFT_486928 [Arabidopsis lyrata subsp. lyrata]	249	245	1.00E-120	98.4	83.9	91.2	hypothetical protein ARALYDRAFT_486928	gbpln	Arabidopsis lyrata	AT5G01470.2 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:190953-192462 FORWARD LENGTH=245	249	245	1.00E-121	98.4	83.1	90.4
Rsa1.0_01513.1.g27506.t1	gb|EOA29494.1| hypothetical protein CARUB_v10012960mg [Capsella rubella]	1258	864	0	68.7	59.1	61.9	hypothetical protein CARUB_v10012960mg	gbpln	Capsella rubella	AT2G04660.1 | Symbols: APC2 | anaphase-promoting complex/cyclosome 2 | chr2:1624933-1629039 FORWARD LENGTH=865	1258	865	0	68.8	59.6	62.0
Rsa1.0_01513.1.g27507.t1	dbj|BAJ33665.1| unnamed protein product [Thellungiella halophila]	286	288	1.00E-148	100.7	90.9	92.0	unnamed protein product	----	----	AT3G08940.2 | Symbols: LHCB4.2 | light harvesting complex photosystem II | chr3:2717717-2718665 FORWARD LENGTH=287	286	287	1.00E-148	100.3	87.8	90.9
Rsa1.0_01513.1.g27508.t1	ref|NP_195775.1| Lectin-domain containing receptor kinase A4.2 [Arabidopsis thaliana] gi|75335729|sp|Q9M020.1|LRK63_ARATH RecName: Full=Lectin-domain containing receptor kinase VI.3; Short=LecRK-VI.3; AltName: Full=Lectin receptor kinase A4.2; Flags: Precursor gi|7327814|emb|CAB82271.1| receptor like protein kinase [Arabidopsis thaliana] gi|332002976|gb|AED90359.1| Lectin-domain containing receptor kinase A4.2 [Arabidopsis thaliana]	694	688	0	99.1	75.8	85.3	Lectin-domain containing receptor kinase A4.2	gbpln	Arabidopsis thaliana	AT5G01550.1 | Symbols: LECRKA4.2 | lectin receptor kinase a4.1 | chr5:214517-216583 REVERSE LENGTH=688	694	688	0	99.1	75.8	85.3
Rsa1.0_01513.1.g27509.t1	ref|XP_002870903.1| protein phosphatase type 2C [Arabidopsis lyrata subsp. lyrata] gi|297316740|gb|EFH47162.1| protein phosphatase type 2C [Arabidopsis lyrata subsp. lyrata]	360	382	0	106.1	86.7	94.4	protein phosphatase type 2C	gbpln	Arabidopsis lyrata	AT5G01700.2 | Symbols: | Protein phosphatase 2C family protein | chr5:260848-262492 REVERSE LENGTH=382	360	382	0	106.1	86.9	93.6
Rsa1.0_01513.1.g27510.t1	ref|XP_002870902.1| hypothetical protein ARALYDRAFT_486898 [Arabidopsis lyrata subsp. lyrata] gi|297316739|gb|EFH47161.1| hypothetical protein ARALYDRAFT_486898 [Arabidopsis lyrata subsp. lyrata]	492	513	0	104.3	84.3	91.3	hypothetical protein ARALYDRAFT_486898	gbpln	Arabidopsis lyrata	AT5G01710.1 | Symbols: | methyltransferases | chr5:263709-265250 REVERSE LENGTH=513	492	513	0	104.3	83.3	89.6
Rsa1.0_01514.1.g27511.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01514.1.g27512.t1	ref|XP_002876246.1| hypothetical protein ARALYDRAFT_485817 [Arabidopsis lyrata subsp. lyrata] gi|297322084|gb|EFH52505.1| hypothetical protein ARALYDRAFT_485817 [Arabidopsis lyrata subsp. lyrata]	214	235	1.00E-73	109.8	72.4	88.8	hypothetical protein ARALYDRAFT_485817	gbpln	Arabidopsis lyrata	AT3G54200.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:20065731-20066438 FORWARD LENGTH=235	214	235	2.00E-63	109.8	68.2	85.5
Rsa1.0_01514.1.g27513.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01514.1.g27514.t1	ref|XP_002876247.1| hypothetical protein ARALYDRAFT_485819 [Arabidopsis lyrata subsp. lyrata] gi|297322085|gb|EFH52506.1| hypothetical protein ARALYDRAFT_485819 [Arabidopsis lyrata subsp. lyrata]	593	646	0	108.9	75.5	78.4	hypothetical protein ARALYDRAFT_485819	gbpln	Arabidopsis lyrata	AT3G54220.1 | Symbols: SCR, SGR1 | GRAS family transcription factor | chr3:20070550-20072625 FORWARD LENGTH=653	593	653	0	110.1	74.9	77.7
Rsa1.0_01514.1.g27515.t3	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1199	910	1.00E-107	75.9	15.8	19.9	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	1199	332	4.00E-78	27.7	11.0	15.3
Rsa1.0_01514.1.g27516.t1	ref|XP_002876249.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] gi|297322087|gb|EFH52508.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	350	350	0	100.0	88.0	93.7	hydrolase, alpha/beta fold family protein	gbpln	Arabidopsis lyrata	AT3G54240.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:20080926-20082145 FORWARD LENGTH=350	350	350	0	100.0	87.7	94.0

Rsa1.0_01514.1.g27517.t1	ref|NP_566995.1| diphosphomevalonate decarboxylase [Arabidopsis thaliana] gi|332645683|gb|AEE79204.1| diphosphomevalonate decarboxylase [Arabidopsis thaliana]	419	419	0	100.0	90.9	95.2	diphosphomevalonate decarboxylase	gbpln	Arabidopsis thaliana	AT3G54250.1 | Symbols: | GHMP kinase family protein | chr3:20082468-20084688 REVERSE LENGTH=419	419	419	0	100.0	90.9	95.2
Rsa1.0_01514.1.g27518.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	160	1142	9.00E-33	713.8	50.0	63.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	160	256	1.00E-15	160.0	30.0	43.1
Rsa1.0_01514.1.g27519.t2	ref|XP_002878937.1| CYP711A1 [Arabidopsis lyrata subsp. lyrata] gi|297324776|gb|EFH55196.1| CYP711A1 [Arabidopsis lyrata subsp. lyrata]	552	522	0	94.6	71.4	75.4	CYP711A1	gbpln	Arabidopsis lyrata	AT2G26170.2 | Symbols: CYP711A1 | cytochrome P450, family 711, subfamily A, polypeptide 1 | chr2:11141703-11143270 FORWARD LENGTH=439	552	439	0	79.5	71.2	75.2
Rsa1.0_01515.1.g27520.t1	dbj|BAJ34311.1| unnamed protein product [Thellungiella halophila]	545	554	0	101.7	84.4	92.7	unnamed protein product	----	----	AT5G18070.1 | Symbols: DRT101 | phosphoglucosamine mutase-related | chr5:5981117-5982787 FORWARD LENGTH=556	545	556	0	102.0	82.8	92.7
Rsa1.0_01515.1.g27521.t1	gb|EOA22896.1| hypothetical protein CARUB_v10003628mg [Capsella rubella]	92	90	3.00E-37	97.8	83.7	91.3	hypothetical protein CARUB_v10003628mg	gbpln	Capsella rubella	AT5G18030.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5968527-5968793 FORWARD LENGTH=88	92	88	4.00E-39	95.7	82.6	90.2
Rsa1.0_01515.1.g27522.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01515.1.g27523.t1	gb|EOA19546.1| hypothetical protein CARUB_v10002518mg [Capsella rubella]	97	90	1.00E-36	92.8	81.4	86.6	hypothetical protein CARUB_v10002518mg	gbpln	Capsella rubella	AT5G18080.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5983840-5984112 FORWARD LENGTH=90	97	90	2.00E-37	92.8	78.4	84.5
Rsa1.0_01515.1.g27524.t1	gb|EOA22896.1| hypothetical protein CARUB_v10003628mg [Capsella rubella]	92	90	4.00E-38	97.8	85.9	92.4	hypothetical protein CARUB_v10003628mg	gbpln	Capsella rubella	AT5G18030.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5968527-5968793 FORWARD LENGTH=88	92	88	8.00E-40	95.7	84.8	91.3
Rsa1.0_01515.1.g27525.t1	dbj|BAA25434.1| SAUR [Raphanus sativus]	92	95	4.00E-38	103.3	90.2	92.4	SAUR	gbpln	Raphanus sativus	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	92	91	6.00E-40	98.9	84.8	89.1
Rsa1.0_01515.1.g27526.t1	dbj|BAA25434.1| SAUR [Raphanus sativus]	97	95	7.00E-34	97.9	74.2	85.6	SAUR	gbpln	Raphanus sativus	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	97	91	2.00E-34	93.8	74.2	82.5
Rsa1.0_01515.1.g27527.t1	dbj|BAA25434.1| SAUR [Raphanus sativus]	64	95	2.00E-17	148.4	82.8	90.6	SAUR	gbpln	Raphanus sativus	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	64	91	8.00E-19	142.2	73.4	85.9
Rsa1.0_01515.1.g27528.t1	ref|XP_002871787.1| cobalamin-independent methionine synthase [Arabidopsis lyrata subsp. lyrata] gi|297317624|gb|EFH48046.1| cobalamin-independent methionine synthase [Arabidopsis lyrata subsp. lyrata]	909	765	0	84.2	75.6	76.6	cobalamin-independent methionine synthase	gbpln	Arabidopsis lyrata	AT5G17920.2 | Symbols: ATCIMS | Cobalamin-independent synthase family protein | chr5:5935771-5939195 FORWARD LENGTH=765	909	765	0	84.2	75.4	76.5
Rsa1.0_01515.1.g27529.t1	ref|NP_197293.1| uncharacterized protein [Arabidopsis thaliana] gi|334187738|ref|NP_001190328.1| uncharacterized protein [Arabidopsis thaliana] gi|10177893|dbj|BAB11225.1| unnamed protein product [Arabidopsis thaliana] gi|332005101|gb|AED92484.1| uncharacterized protein AT5G17910 [Arabidopsis thaliana] gi|332005102|gb|AED92485.1| uncharacterized protein AT5G17910 [Arabidopsis thaliana]	1526	1342	0	87.9	59.2	68.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G17910.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29620.1). | chr5:5927906-5932292 FORWARD LENGTH=1342	1526	1342	0	87.9	59.2	68.7
Rsa1.0_01515.1.g27530.t18	gb|EMJ12921.1| hypothetical protein PRUPE_ppa005985mg [Prunus persica]	485	433	1.00E-142	89.3	64.1	75.7	hypothetical protein PRUPE_ppa005985mg	gbpln	Prunus persica	AT4G08580.1 | Symbols: | microfibrillar-associated protein-related | chr4:5462190-5463718 FORWARD LENGTH=435	485	435	1.00E-133	89.7	50.5	52.4
Rsa1.0_01516.1.g27531.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01516.1.g27532.t6	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01516.1.g27533.t1	emb|CAN83959.1| hypothetical protein VITISV_013448 [Vitis vinifera]	1248	878	0	70.4	30.9	43.1	hypothetical protein VITISV_013448	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01516.1.g27534.t3	gb|AAF63106.1|AC006423_7 Hypothetical protein [Arabidopsis thaliana]	561	570	6.00E-22	101.6	22.5	39.0	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01516.1.g27535.t6	ref|XP_003638451.1| hypothetical protein MTR_132s0010, partial [Medicago truncatula] gi|355504386|gb|AES85589.1| hypothetical protein MTR_132s0010, partial [Medicago truncatula]	750	1458	7.00E-64	194.4	22.8	26.3	hypothetical protein MTR_132s0010, partial	gbpln	Medicago truncatula	#	#	#	#	#	#	#

Rsa1.0_01516.1.g27536.t3	ref|XP_002333318.1| predicted protein [Populus trichocarpa] gi|222836199|gb|EEE74620.1| predicted protein [Populus trichocarpa]	228	63	5.00E-11	27.6	19.3	20.2	predicted protein	gbpln	Populus trichocarpa	#	#	#	#	#	#	#
Rsa1.0_01516.1.g27537.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01516.1.g27538.t1	ref|NP_192292.1| uncharacterized protein [Arabidopsis thaliana] gi|7267138|emb|CAB80806.1| hypothetical protein [Arabidopsis thaliana] gi|332656955|gb|AEE82355.1| uncharacterized protein AT4G03830 [Arabidopsis thaliana]	476	578	1.00E-12	121.4	9.0	14.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G03830.1 | Symbols: | Protein of unknown function, DUF601 | chr4:1790440-1792458 FORWARD LENGTH=578	476	578	3.00E-15	121.4	9.0	14.1
Rsa1.0_01516.1.g27539.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01517.1.g27540.t1	ref|XP_002893652.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297339494|gb|EFH69911.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	696	725	0	104.2	67.5	78.2	protein binding protein	gbpln	Arabidopsis lyrata	AT1G30860.1 | Symbols: | RING/U-box superfamily protein | chr1:10986696-10989246 REVERSE LENGTH=730	696	730	0	104.9	66.5	76.9
Rsa1.0_01517.1.g27541.t1	gb|EOA36410.1| hypothetical protein CARUB_v10010885mg [Capsella rubella]	347	352	1.00E-166	101.4	84.1	89.6	hypothetical protein CARUB_v10010885mg	gbpln	Capsella rubella	AT1G30870.1 | Symbols: | Peroxidase superfamily protein | chr1:10991535-10992885 FORWARD LENGTH=349	347	349	1.00E-162	100.6	80.1	88.5
Rsa1.0_01517.1.g27542.t1	gb|EOA36340.1| hypothetical protein CARUB_v10010686mg [Capsella rubella]	120	118	7.00E-44	98.3	85.8	90.8	hypothetical protein CARUB_v10010686mg	gbpln	Capsella rubella	AT1G30880.1 | Symbols: | unknown protein; Has 24 Blast hits to 24 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10993379-10994056 REVERSE LENGTH=120	120	120	3.00E-34	100.0	87.5	91.7
Rsa1.0_01517.1.g27543.t1	ref|NP_174375.1| vacuolar sorting receptor 6 [Arabidopsis thaliana] gi|374095475|sp|Q9FYH7.3|VSR6_ARATH RecName: Full=Vacuolar-sorting receptor 6; Short=AtVSR6; AltName: Full=BP80-like protein d; Short=AtBP80d; AltName: Full=Epidermal growth factor receptor-like protein 6; Short=AtELP6; Flags: Precursor gi|332193170|gb|AEE31291.1| vacuolar sorting receptor 6 [Arabidopsis thaliana]	629	631	0	100.3	94.0	96.8	vacuolar sorting receptor 6	gbpln	Arabidopsis thaliana	AT1G30900.1 | Symbols: VSR6, VSR3;3, BP80-3;3 | VACUOLAR SORTING RECEPTOR 6 | chr1:10997275-11000543 FORWARD LENGTH=631	629	631	0	100.3	94.0	96.8
Rsa1.0_01517.1.g27544.t1	ref|XP_002893669.1| GTP-binding protein [Arabidopsis lyrata subsp. lyrata] gi|297339511|gb|EFH69928.1| GTP-binding protein [Arabidopsis lyrata subsp. lyrata]	420	435	0	103.6	86.7	91.9	GTP-binding protein	gbpln	Arabidopsis lyrata	AT1G30960.1 | Symbols: | GTP-binding family protein | chr1:11037755-11039977 REVERSE LENGTH=437	420	437	0	104.0	86.7	91.7
Rsa1.0_01517.1.g27545.t1	gb|AAM62833.1| putative zinc finger protein [Arabidopsis thaliana]	356	367	1.00E-164	103.1	86.2	89.3	putative zinc finger protein	gbpln	Arabidopsis thaliana	AT1G30970.1 | Symbols: SUF4 | zinc finger (C2H2 type) family protein | chr1:11040613-11043593 REVERSE LENGTH=367	356	367	1.00E-166	103.1	86.0	89.3
Rsa1.0_01517.1.g27546.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	345	1557	8.00E-14	451.3	16.8	26.4	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT1G30974.1 | Symbols: | Plant thionin family protein | chr1:11047031-11047270 FORWARD LENGTH=79	345	79	8.00E-16	22.9	9.9	11.9
Rsa1.0_01518.1.g27547.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01518.1.g27548.t1	gb|ABD64940.1| hypothetical protein 24.t00018 [Brassica oleracea]	162	380	9.00E-28	234.6	46.3	61.7	hypothetical protein 24.t00018	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	162	302	9.00E-25	186.4	36.4	46.3
Rsa1.0_01518.1.g27549.t1	gb|EOA38733.1| hypothetical protein CARUB_v10010875mg [Capsella rubella]	735	462	0	62.9	45.6	51.3	hypothetical protein CARUB_v10010875mg	gbpln	Capsella rubella	AT1G33590.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr1:12177788-12179221 FORWARD LENGTH=477	735	477	0	64.9	42.6	50.5
Rsa1.0_01518.1.g27550.t1	ref|NP_177852.2| adenine nucleotide alpha hydrolases-domain containing protein kinase [Arabidopsis thaliana] gi|332197836|gb|AEE35957.1| adenine nucleotide alpha hydrolases-domain containing protein kinase [Arabidopsis thaliana]	661	794	0	120.1	80.5	88.7	adenine nucleotide alpha hydrolases-domain containing protein kinase	gbpln	Arabidopsis thaliana	AT1G77280.1 | Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:29031468-29035882 REVERSE LENGTH=794	661	794	0	120.1	80.5	88.7
Rsa1.0_01518.1.g27551.t1	ref|NP_174618.1| F-box protein [Arabidopsis thaliana] gi|75268383|sp|Q9C800.1|FB34_ARATH RecName: Full=Putative F-box protein At1g33530 gi|12322373|gb|AAG51205.1|AC051630_2 hypothetical protein; 83642-85072 [Arabidopsis thaliana] gi|332193482|gb|AEE31603.1| F-box protein [Arabidopsis thaliana]	405	441	1.00E-117	108.9	59.3	74.3	F-box protein	gbpln	Arabidopsis thaliana	AT1G33530.1 | Symbols: | F-box family protein | chr1:12159884-12161314 FORWARD LENGTH=441	405	441	1.00E-120	108.9	59.3	74.3
Rsa1.0_01518.1.g27552.t1	dbj|BAJ34354.1| unnamed protein product [Thellungiella halophila]	437	453	0	103.7	82.8	90.8	unnamed protein product	----	----	AT1G33520.1 | Symbols: MOS2 | D111/G-patch domain-containing protein | chr1:12157488-12158876 REVERSE LENGTH=462	437	462	0	105.7	80.8	89.7

Rsa1.0_01518.1.g27553.t1	gb|AAG51223.1|AC051630_20 hypothetical protein; 76532-78443 [Arabidopsis thaliana]	276	254	1.00E-121	92.0	80.1	87.3	hypothetical protein; 76532-78443	gbpln	Arabidopsis thaliana	AT1G33500.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:12152774-12154680 FORWARD LENGTH=276	276	276	1.00E-111	100.0	73.6	80.8
Rsa1.0_01518.1.g27554.t2	ref|NP_973958.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|14532532|gb|AAK63994.1| At1g33470/F10C21_14 [Arabidopsis thaliana] gi|18655391|gb|AAL76151.1| At1g33470/F10C21_14 [Arabidopsis thaliana] gi|332193476|gb|AEE31597.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	244	244	1.00E-119	100.0	88.5	92.6	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT1G33470.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:12144632-12146040 FORWARD LENGTH=244	244	244	1.00E-121	100.0	88.5	92.6
Rsa1.0_01518.1.g27555.t1	gb|EOA37022.1| hypothetical protein CARUB_v10010074mg [Capsella rubella]	208	254	1.00E-71	122.1	71.6	79.3	hypothetical protein CARUB_v10010074mg	gbpln	Capsella rubella	AT4G10150.1 | Symbols: | RING/U-box superfamily protein | chr4:6328136-6329558 FORWARD LENGTH=236	208	236	1.00E-70	113.5	63.0	78.4
Rsa1.0_01518.1.g27556.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01518.1.g27557.t1	ref|NP_188377.1| F-box associated protein [Arabidopsis thaliana] gi|332642440|gb|AEE75961.1| F-box associated protein [Arabidopsis thaliana]	397	438	3.00E-69	110.3	44.1	59.7	F-box associated protein	gbpln	Arabidopsis thaliana	AT3G17500.1 | Symbols: | F-box family protein | chr3:5986685-5988498 FORWARD LENGTH=438	397	438	7.00E-72	110.3	44.1	59.7
Rsa1.0_01519.1.g27558.t1	gb|AAM62950.1| unknown [Arabidopsis thaliana]	227	235	3.00E-99	103.5	83.7	90.7	unknown	gbpln	Arabidopsis thaliana	AT5G07020.1 | Symbols: | proline-rich family protein | chr5:2180669-2182284 REVERSE LENGTH=235	227	235	3.00E-99	103.5	79.7	86.8
Rsa1.0_01519.1.g27559.t1	gb|EOA20615.1| hypothetical protein CARUB_v10000927mg [Capsella rubella]	439	457	0	104.1	91.6	97.5	hypothetical protein CARUB_v10000927mg	gbpln	Capsella rubella	AT5G07030.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:2183600-2185717 REVERSE LENGTH=455	439	455	0	103.6	91.6	97.0
Rsa1.0_01519.1.g27560.t1	ref|NP_196321.1| putative RING-H2 finger protein ATL69 [Arabidopsis thaliana] gi|68565291|sp|Q9FL42.1|ATL69_ARATH RecName: Full=Putative RING-H2 finger protein ATL69 gi|9759560|dbj|BAB11162.1| C3HC4-type RING zinc finger protein-like [Arabidopsis thaliana] gi|332003718|gb|AED91101.1| putative RING-H2 finger protein ATL69 [Arabidopsis thaliana]	157	159	3.00E-72	101.3	88.5	93.0	putative RING-H2 finger protein ATL69	gbpln	Arabidopsis thaliana	AT5G07040.1 | Symbols: | RING/U-box superfamily protein | chr5:2190344-2190823 FORWARD LENGTH=159	157	159	9.00E-75	101.3	88.5	93.0
Rsa1.0_01519.1.g27561.t1	ref|XP_002873292.1| hypothetical protein ARALYDRAFT_487525 [Arabidopsis lyrata subsp. lyrata] gi|297319129|gb|EFH49551.1| hypothetical protein ARALYDRAFT_487525 [Arabidopsis lyrata subsp. lyrata]	402	404	0	100.5	88.3	92.5	hypothetical protein ARALYDRAFT_487525	gbpln	Arabidopsis lyrata	AT5G07050.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:2191533-2193416 REVERSE LENGTH=402	402	402	0	100.0	88.3	93.3
Rsa1.0_01519.1.g27562.t2	ref|XP_002873294.1| hypothetical protein ARALYDRAFT_325322 [Arabidopsis lyrata subsp. lyrata] gi|297319131|gb|EFH49553.1| hypothetical protein ARALYDRAFT_325322 [Arabidopsis lyrata subsp. lyrata]	301	301	1.00E-104	100.0	75.7	81.7	hypothetical protein ARALYDRAFT_325322	gbpln	Arabidopsis lyrata	AT3G12480.1 | Symbols: NF-YC11 | nuclear factor Y, subunit C11 | chr3:3958065-3960278 FORWARD LENGTH=293	301	293	3.00E-83	97.3	60.1	66.8
Rsa1.0_01519.1.g27563.t2	ref|XP_002866260.1| cbl-interacting protein kinase 10 [Arabidopsis lyrata subsp. lyrata] gi|297312095|gb|EFH42519.1| cbl-interacting protein kinase 10 [Arabidopsis lyrata subsp. lyrata]	463	462	0	99.8	68.7	80.6	cbl-interacting protein kinase 10	gbpln	Arabidopsis lyrata	AT5G58380.1 | Symbols: CIPK10, PKS2, SIP1, SNRK3.8 | SOS3-interacting protein 1 | chr5:23597092-23598531 REVERSE LENGTH=479	463	479	0	103.5	68.3	80.8
Rsa1.0_01519.1.g27564.t1	gb|EOA22250.1| hypothetical protein CARUB_v10002839mg [Capsella rubella]	570	455	0	79.8	66.3	72.1	hypothetical protein CARUB_v10002839mg	gbpln	Capsella rubella	AT5G07070.1 | Symbols: CIPK2, SnRK3.2 | CBL-interacting protein kinase 2 | chr5:2196743-2198113 REVERSE LENGTH=456	570	456	0	80.0	65.4	71.2

Rsa1.0_01519.1.g27565.t1	ref|NP_196325.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|7546686|emb|CAB87264.1| putative protein [Arabidopsis thaliana] gi|9759564|dbj|BAB11166.1| hypersensitivity related protein-like [Arabidopsis thaliana] gi|15810289|gb|AAL07032.1| unknown protein [Arabidopsis thaliana] gi|21436093|gb|AAM51247.1| unknown protein [Arabidopsis thaliana] gi|332003723|gb|AED91106.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	448	450	0	100.4	80.8	89.5	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT5G07080.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:2200353-2201975 FORWARD LENGTH=450	448	450	0	100.4	80.8	89.5
Rsa1.0_01519.1.g27566.t1	gb|EOA31247.1| hypothetical protein CARUB_v10014418mg [Capsella rubella]	262	262	1.00E-149	100.0	97.7	99.6	hypothetical protein CARUB_v10014418mg	gbpln	Capsella rubella	AT5G07090.1 | Symbols: | Ribosomal protein S4 (RPS4A) family protein | chr5:2202410-2203805 FORWARD LENGTH=262	262	262	1.00E-150	100.0	96.6	99.6
Rsa1.0_01519.1.g27567.t1	ref|NP_196329.2| sorting nexin 2B [Arabidopsis thaliana] gi|363805551|sp|B9DFS6.1|SNX2B_ARATH RecName: Full=Sorting nexin 2B gi|222423233|dbj|BAH19593.1| AT5G07120 [Arabidopsis thaliana] gi|332003729|gb|AED91112.1| sorting nexin 2B [Arabidopsis thaliana]	566	572	0	101.1	83.6	89.6	sorting nexin 2B	gbpln	Arabidopsis thaliana	AT5G07120.1 | Symbols: SNX2b | sorting nexin 2B | chr5:2207065-2209355 REVERSE LENGTH=572	566	572	0	101.1	83.6	89.6
Rsa1.0_01519.1.g27568.t1	gb|EOA22079.1| hypothetical protein CARUB_v10002622mg [Capsella rubella]	133	568	1.00E-49	427.1	70.7	75.2	hypothetical protein CARUB_v10002622mg	gbpln	Capsella rubella	AT5G07130.1 | Symbols: LAC13 | laccase 13 | chr5:2210567-2212525 FORWARD LENGTH=569	133	569	2.00E-51	427.8	70.7	75.9
Rsa1.0_01520.1.g27569.t5	ref|NP_190233.2| iron ion binding / oxidoreductase/ oxidoreductase protein [Arabidopsis thaliana] gi|332644644|gb|AEE78165.1| iron ion binding / oxidoreductase/ oxidoreductase protein [Arabidopsis thaliana]	308	330	1.00E-102	107.1	59.4	65.9	iron ion binding / oxidoreductase/ oxidoreductase protein	gbpln	Arabidopsis thaliana	AT3G46490.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:17115629-17119451 FORWARD LENGTH=330	308	330	1.00E-105	107.1	59.4	65.9
Rsa1.0_01520.1.g27570.t1	ref|NP_191181.1| transcription regulator [Arabidopsis thaliana] gi|7572920|emb|CAB87421.1| putative protein [Arabidopsis thaliana] gi|28466843|gb|AAO44030.1| At3g56220 [Arabidopsis thaliana] gi|110736048|dbj|BAE99996.1| hypothetical protein [Arabidopsis thaliana] gi|332645977|gb|AEE79498.1| transcription regulator [Arabidopsis thaliana]	157	156	8.00E-64	99.4	79.6	87.9	transcription regulator	gbpln	Arabidopsis thaliana	AT3G56220.1 | Symbols: | transcription regulators | chr3:20858941-20860302 FORWARD LENGTH=156	157	156	3.00E-66	99.4	79.6	87.9
Rsa1.0_01520.1.g27571.t1	gb|EOA23128.1| hypothetical protein CARUB_v100024710mg, partial [Capsella rubella]	225	488	2.00E-17	216.9	20.4	23.1	hypothetical protein CARUB_v100024710mg , partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01520.1.g27572.t1	gb|AAD21699.1| Contains reverse transcriptase domain (rvt) PF|00078 [Arabidopsis thaliana]	1019	1253	1.00E-174	123.0	37.0	54.4	Contains reverse transcriptase domain (rvt) PF|00078	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1019	626	6.00E-61	61.4	13.2	21.1
Rsa1.0_01520.1.g27573.t1	ref|XP_002862436.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297307949|gb|EFH38694.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	618	530	2.00E-38	85.8	17.5	25.7	predicted protein	gbpln	Arabidopsis lyrata	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	618	530	2.00E-13	85.8	6.3	10.8
Rsa1.0_01520.1.g27574.t3	ref|NP_001030872.1| alpha-soluble NSF attachment protein 2 [Arabidopsis thaliana] gi|332645971|gb|AEE79492.1| alpha-soluble NSF attachment protein 2 [Arabidopsis thaliana]	209	240	2.00E-95	114.8	84.2	88.5	alpha-soluble NSF attachment protein 2	gbpln	Arabidopsis thaliana	AT3G56190.2 | Symbols: ALPHA-SNAP2, ASNAP | alpha-soluble NSF attachment protein 2 | chr3:20846119-20848213 REVERSE LENGTH=240	209	240	5.00E-98	114.8	84.2	88.5
Rsa1.0_01520.1.g27575.t1	emb|CAB87417.1| putative protein [Arabidopsis thaliana]	208	208	1.00E-105	100.0	86.5	94.7	putative protein	gbpln	Arabidopsis thaliana	AT3G56180.1 | Symbols: | Protein of unknown function (DUF567) | chr3:20844765-20845548 FORWARD LENGTH=204	208	204	1.00E-104	98.1	84.6	92.8
Rsa1.0_01520.1.g27576.t1	ref|XP_002876351.1| hypothetical protein ARALYDRAFT_486055 [Arabidopsis lyrata subsp. lyrata] gi|297322189|gb|EFH52610.1| hypothetical protein ARALYDRAFT_486055 [Arabidopsis lyrata subsp. lyrata]	740	744	0	100.5	91.2	94.7	hypothetical protein ARALYDRAFT_486055	gbpln	Arabidopsis lyrata	AT3G56140.1 | Symbols: | Protein of unknown function (DUF399 and DUF3411) | chr3:20829407-20832669 FORWARD LENGTH=745	740	745	0	100.7	90.1	93.9
Rsa1.0_01520.1.g27577.t1	ref|XP_002878068.1| prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata] gi|297323906|gb|EFH54327.1| prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata]	209	209	3.00E-93	100.0	90.9	96.2	prenylated rab acceptor family protein	gbpln	Arabidopsis lyrata	AT3G56110.2 | Symbols: PRA1.B1 | prenylated RAB acceptor 1.B1 | chr3:20822228-20822857 REVERSE LENGTH=209	209	209	6.00E-95	100.0	90.4	96.2
Rsa1.0_01521.1.g27578.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01521.1.g27579.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01521.1.g27580.t1	gb|ADY76580.1| translocon at inner membrane of chloroplasts 21 [Brassica napus]	285	294	1.00E-143	103.2	94.4	96.1	translocon at inner membrane of chloroplasts 21	gbpln	Brassica napus	AT2G15290.1 | Symbols: ATTIC21, TIC21, CIA5, PIC1 | translocon at inner membrane of chloroplasts 21 | chr2:6642512-6644011 REVERSE LENGTH=296	285	296	1.00E-139	103.9	90.9	94.7
Rsa1.0_01521.1.g27581.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01521.1.g27582.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	941	1225	0	130.2	40.3	53.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	941	626	2.00E-26	66.5	11.5	19.1
Rsa1.0_01521.1.g27583.t1	ref|XP_002883895.1| RBP36A [Arabidopsis lyrata subsp. lyrata] gi|297329735|gb|EFH60154.1| RBP36A [Arabidopsis lyrata subsp. lyrata]	320	319	1.00E-173	99.7	93.1	95.9	RBP36A	gbpln	Arabidopsis lyrata	AT2G15430.1 | Symbols: RBP36A, RPB35.5A, NRPB3, NRPD3, NRPE3A | DNA-directed RNA polymerase family protein | chr2:6733661-6735482 FORWARD LENGTH=319	320	319	1.00E-175	99.7	93.1	95.9
Rsa1.0_01521.1.g27584.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01521.1.g27585.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	96	255	2.00E-16	265.6	51.0	65.6	hypothetical protein 40.t00057	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01521.1.g27586.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	194	442	3.00E-61	227.8	63.9	72.2	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	194	343	5.00E-26	176.8	34.0	45.9
Rsa1.0_01521.1.g27587.t1	ref|XP_002883897.1| UDP-glucosyl transferase 73B5 [Arabidopsis lyrata subsp. lyrata] gi|297329737|gb|EFH60156.1| UDP-glucosyl transferase 73B5 [Arabidopsis lyrata subsp. lyrata]	485	484	0	99.8	88.7	94.0	UDP-glucosyl transferase 73B5	gbpln	Arabidopsis lyrata	AT2G15480.1 | Symbols: UGT73B5 | UDP-glucosyl transferase 73B5 | chr2:6758817-6760452 FORWARD LENGTH=484	485	484	0	99.8	87.8	93.4
Rsa1.0_01521.1.g27588.t1	gb|ABE65512.1| hypothetical protein At4g04650 [Arabidopsis thaliana]	268	296	1.00E-14	110.4	17.2	27.2	hypothetical protein At4g04650	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	268	332	3.00E-17	123.9	17.2	27.2
Rsa1.0_01521.1.g27589.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1202	1274	0	106.0	55.8	71.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1202	575	1.00E-64	47.8	14.1	22.0
Rsa1.0_01521.1.g27590.t1	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	560	777	2.00E-14	138.8	7.3	10.2	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01521.1.g27591.t1	gb|EGV96854.1| Keratin-associated protein 4-3 [Cricetulus griseus]	185	224	1.00E-11	121.1	28.1	34.6	Keratin-associated protein 4-3	gbrod	Cricetulus griseus	#	#	#	#	#	#	#
Rsa1.0_01521.1.g27592.t8	gb|AAF99785.1|AC012463_2 T2E6.4 [Arabidopsis thaliana]	590	740	3.00E-96	125.4	30.2	45.4	T2E6.4	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	590	746	2.00E-31	126.4	13.2	19.3
Rsa1.0_01521.1.g27593.t1	ref|XP_002883899.1| hypothetical protein ARALYDRAFT_899764 [Arabidopsis lyrata subsp. lyrata] gi|297329739|gb|EFH60158.1| hypothetical protein ARALYDRAFT_899764 [Arabidopsis lyrata subsp. lyrata]	641	655	0	102.2	87.4	90.6	hypothetical protein ARALYDRAFT_899764	gbpln	Arabidopsis lyrata	AT4G34110.1 | Symbols: PAB2, PABP2, ATPAB2 | poly(A) binding protein 2 | chr4:16336732-16339892 FORWARD LENGTH=629	641	629	0	98.1	78.3	86.0
Rsa1.0_01522.1.g27594.t1	ref|XP_002884714.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330554|gb|EFH60973.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	385	492	1.00E-138	127.8	69.6	81.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G09110.1 | Symbols: | Protein of unknown function (DUF674) | chr3:2794850-2795963 REVERSE LENGTH=343	385	343	1.00E-110	89.1	52.5	62.9
Rsa1.0_01522.1.g27595.t1	ref|XP_002885806.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331646|gb|EFH62065.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	761	752	0	98.8	89.4	94.0	predicted protein	gbpln	Arabidopsis lyrata	AT2G05920.1 | Symbols: | Subtilase family protein | chr2:2269831-2272207 REVERSE LENGTH=754	761	754	0	99.1	88.3	92.6
Rsa1.0_01522.1.g27596.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01522.1.g27597.t5	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1082	1838	1.00E-165	169.9	32.3	44.5	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01522.1.g27598.t1	gb|AAD29768.1|AF076243_15 putative polyprotein [Arabidopsis thaliana] gi|7267198|emb|CAB77909.1| putative polyprotein [Arabidopsis thaliana]	286	1017	8.00E-57	355.6	46.9	58.7	putative polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01522.1.g27599.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01522.1.g27600.t1	gb|ABD65022.1| hypothetical protein 26.t00077 [Brassica oleracea]	139	242	7.00E-31	174.1	51.8	59.7	hypothetical protein 26.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_01522.1.g27601.t1	gb|EOA37510.1| hypothetical protein CARUB_v10011684mg, partial [Capsella rubella]	675	273	5.00E-25	40.4	7.9	11.6	hypothetical protein CARUB_v10011684mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	675	336	3.00E-14	49.8	7.0	10.7
Rsa1.0_01522.1.g27602.t1	ref|XP_002885808.1| hypothetical protein ARALYDRAFT_899389 [Arabidopsis lyrata subsp. lyrata] gi|297331648|gb|EFH62067.1| hypothetical protein ARALYDRAFT_899389 [Arabidopsis lyrata subsp. lyrata]	464	472	0	101.7	89.0	93.8	hypothetical protein ARALYDRAFT_899389	gbpln	Arabidopsis lyrata	AT2G05940.1 | Symbols: | Protein kinase superfamily protein | chr2:2287514-2289270 REVERSE LENGTH=462	464	462	0	99.6	87.5	91.8
Rsa1.0_01522.1.g27603.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	152	1103	6.00E-37	725.7	53.3	66.4	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01522.1.g27604.t3	emb|CCD74471.1| myosin heavy chain-like protein [Arabidopsis halleri subsp. halleri]	503	788	8.00E-22	156.7	13.5	20.5	myosin heavy chain-like protein	gbpln	Arabidopsis halleri	AT5G32590.1 | Symbols: | myosin heavy chain-related | chr5:12221589-12224322 REVERSE LENGTH=761	503	761	2.00E-20	151.3	12.5	19.5
Rsa1.0_01522.1.g27605.t1	gb|AAG10812.1|AC018460_6 Putative retroelement polyprotein [Arabidopsis thaliana]	138	1404	3.00E-23	1017.4	37.0	47.8	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01523.1.g27606.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01523.1.g27607.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01523.1.g27608.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01523.1.g27609.t1	ref|NP_565813.1| putative mannan synthase 7 [Arabidopsis thaliana] gi|75216274|sp|Q9ZQN8.2|CSLA7_ARATH RecName: Full=Probable mannan synthase 7; AltName: Full=Cellulose synthase-like protein A7; Short=AtCslA7 gi|16604559|gb|AAL24081.1| putative glucosyltransferase [Arabidopsis thaliana] gi|20197522|gb|AAD15455.2| putative glucosyltransferase [Arabidopsis thaliana] gi|22136794|gb|AAM91741.1| putative glucosyltransferase [Arabidopsis thaliana] gi|28551964|emb|CAD32548.1| glycosyltransferase [Arabidopsis thaliana] gi|330254042|gb|AEC09136.1| putative mannan synthase 7 [Arabidopsis thaliana]	501	556	0	111.0	84.2	90.2	putative mannan synthase 7	gbpln	Arabidopsis thaliana	AT2G35650.1 | Symbols: ATCSLA07, CSLA07, ATCSLA7, CSLA7 | cellulose synthase like | chr2:14985625-14988187 FORWARD LENGTH=556	501	556	0	111.0	84.2	90.2
Rsa1.0_01523.1.g27610.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01523.1.g27611.t1	gb|EOA28974.1| hypothetical protein CARUB_v10025226mg [Capsella rubella]	446	440	0	98.7	86.8	91.9	hypothetical protein CARUB_v10025226mg	gbpln	Capsella rubella	AT2G35660.1 | Symbols: CTF2A | FAD/NAD(P)-binding oxidoreductase family protein | chr2:14988499-14990320 FORWARD LENGTH=439	446	439	0	98.4	85.4	91.9
Rsa1.0_01523.1.g27612.t2	dbj|BAJ34185.1| unnamed protein product [Thellungiella halophila]	364	334	1.00E-154	91.8	75.5	83.0	unnamed protein product	----	----	AT2G35680.1 | Symbols: | Phosphotyrosine protein phosphatases superfamily protein | chr2:14997004-14998590 REVERSE LENGTH=337	364	337	1.00E-156	92.6	74.5	83.0
Rsa1.0_01523.1.g27613.t5	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1533	1225	0	79.9	23.9	30.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	1533	484	6.00E-35	31.6	6.7	9.1
Rsa1.0_01523.1.g27614.t1	ref|XP_002879568.1| hypothetical protein ARALYDRAFT_482537 [Arabidopsis lyrata subsp. lyrata] gi|297325407|gb|EFH55827.1| hypothetical protein ARALYDRAFT_482537 [Arabidopsis lyrata subsp. lyrata]	198	189	9.00E-70	95.5	73.2	79.3	hypothetical protein ARALYDRAFT_482537	gbpln	Arabidopsis lyrata	AT2G35700.1 | Symbols: ATERF38, ERF38 | ERF family protein 38 | chr2:15005205-15005789 FORWARD LENGTH=194	198	194	3.00E-64	98.0	73.2	79.8

Rsa1.0_01524.1.g27615.t1	ref|NP_566720.1| Pyruvate kinase family protein [Arabidopsis thaliana] gi|75311203|sp|Q9LIK0.1|PKP1_ARATH RecName: Full=Plastidial pyruvate kinase 1, chloroplastic; Short=PK1; Short=PKp1; AltName: Full=Pyruvate kinase II; AltName: Full=Pyruvate kinase isozyme A; Short=PKP-ALPHA; Flags: Precursor gi|11994727|dbj|BAB03043.1| pyruvate kinase [Arabidopsis thaliana] gi|15983775|gb|AAL10484.1| AT3g22960/F5N5_15 [Arabidopsis thaliana] gi|16604372|gb|AAL24192.1| AT3g22960/F5N5_15 [Arabidopsis thaliana] gi|26983820|gb|AAN86162.1| putative pyruvate kinase [Arabidopsis thaliana] gi|332643176|gb|AEE76697.1| Pyruvate kinase family protein [Arabidopsis thaliana]	571	596	0	104.4	92.5	96.0	Pyruvate kinase family protein	gbpln	Arabidopsis thaliana	AT3G22960.1 | Symbols: PKP1, PKP-ALPHA | Pyruvate kinase family protein | chr3:8139369-8141771 FORWARD LENGTH=596	571	596	0	104.4	92.5	96.0
Rsa1.0_01524.1.g27616.t1	ref|NP_173742.1| MAK16 protein-like protein [Arabidopsis thaliana] gi|332192246|gb|AEE30367.1| MAK16 protein-like protein [Arabidopsis thaliana]	298	303	1.00E-102	101.7	72.5	83.2	MAK16 protein-like protein	gbpln	Arabidopsis thaliana	AT1G23280.1 | Symbols: | MAK16 protein-related | chr1:8260865-8262650 REVERSE LENGTH=303	298	303	1.00E-105	101.7	72.5	83.2
Rsa1.0_01524.1.g27617.t1	gb|ACX43275.1| GTP binding protein gamma subunit [Brassica napus]	100	100	4.00E-50	100.0	98.0	98.0	GTP binding protein gamma subunit	gbpln	Brassica napus	AT3G22942.1 | Symbols: AGG2 | G-protein gamma subunit 2 | chr3:8134475-8135667 FORWARD LENGTH=100	100	100	3.00E-43	100.0	92.0	93.0
Rsa1.0_01524.1.g27618.t1	ref|NP_188933.1| calmodulin-like protein 11 [Arabidopsis thaliana] gi|75335042|sp|Q9LIK5.1|CML11_ARATH RecName: Full=Calmodulin-like protein 11 gi|16226344|gb|AAL16141.1|AF428309_1 AT3g22930/F5N5_10 [Arabidopsis thaliana] gi|11994722|dbj|BAB03038.1| unnamed protein product [Arabidopsis thaliana] gi|21436047|gb|AAM51601.1| AT3g22930/F5N5_10 [Arabidopsis thaliana] gi|332643171|gb|AEE76692.1| calmodulin-like protein 11 [Arabidopsis thaliana]	154	173	1.00E-73	112.3	89.6	92.9	calmodulin-like protein 11	gbpln	Arabidopsis thaliana	AT3G22930.1 | Symbols: CML11 | calmodulin-like 11 | chr3:8124286-8125835 REVERSE LENGTH=173	154	173	5.00E-76	112.3	89.6	92.9
Rsa1.0_01524.1.g27619.t2	emb|CAA11417.1| ATP sulfurylase [Brassica juncea]	298	461	1.00E-173	154.7	98.7	99.3	ATP sulfurylase	gbpln	Brassica juncea	AT3G22890.1 | Symbols: APS1 | ATP sulfurylase 1 | chr3:8112837-8114734 FORWARD LENGTH=463	298	463	1.00E-172	155.4	95.6	98.0
Rsa1.0_01524.1.g27620.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	787	1534	0	194.9	57.8	68.4	F17L21.7	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	787	1262	1.00E-109	160.4	25.9	38.5
Rsa1.0_01524.1.g27621.t1	emb|CAA11417.1| ATP sulfurylase [Brassica juncea]	166	461	2.00E-81	277.7	92.8	95.2	ATP sulfurylase	gbpln	Brassica juncea	AT3G22890.1 | Symbols: APS1 | ATP sulfurylase 1 | chr3:8112837-8114734 FORWARD LENGTH=463	166	463	2.00E-76	278.9	87.3	94.0
Rsa1.0_01524.1.g27622.t1	gb|EOA30955.1| hypothetical protein CARUB_v10014101mg [Capsella rubella]	324	344	1.00E-169	106.2	92.6	97.5	hypothetical protein CARUB_v10014101mg	gbpln	Capsella rubella	AT3G22880.1 | Symbols: ATDMC1, DMC1, ARLIM15 | DNA repair (Rad51) family protein | chr3:8097948-8100740 REVERSE LENGTH=344	324	344	1.00E-167	106.2	92.0	96.6
Rsa1.0_01524.1.g27623.t1	gb|EOA32838.1| hypothetical protein CARUB_v10016151mg [Capsella rubella]	183	248	7.00E-94	135.5	90.2	95.1	hypothetical protein CARUB_v10016151mg	gbpln	Capsella rubella	AT3G22850.1 | Symbols: | Aluminium induced protein with YGL and LRDR motifs | chr3:8089067-8090275 FORWARD LENGTH=248	183	248	3.00E-93	135.5	86.3	93.4
Rsa1.0_01525.1.g27624.t1	ref|XP_002889143.1| hypothetical protein ARALYDRAFT_476911 [Arabidopsis lyrata subsp. lyrata] gi|297334984|gb|EFH65402.1| hypothetical protein ARALYDRAFT_476911 [Arabidopsis lyrata subsp. lyrata]	361	369	0	102.2	92.2	96.1	hypothetical protein ARALYDRAFT_476911	gbpln	Arabidopsis lyrata	AT1G77470.1 | Symbols: RFC3, RFC5 | replication factor C subunit 3 | chr1:29112194-29114323 REVERSE LENGTH=369	361	369	0	102.2	90.6	95.3
Rsa1.0_01525.1.g27625.t1	gb|EOA33479.1| hypothetical protein CARUB_v10019648mg [Capsella rubella]	2212	2137	0	96.6	87.1	91.2	hypothetical protein CARUB_v10019648mg	gbpln	Capsella rubella	AT1G77460.2 | Symbols: | Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein | chr1:29104378-29111580 FORWARD LENGTH=2136	2212	2136	0	96.6	86.6	90.7
Rsa1.0_01525.1.g27626.t2	gb|EOA35294.1| hypothetical protein CARUB_v10020464mg [Capsella rubella]	346	382	1.00E-164	110.4	79.5	88.4	hypothetical protein CARUB_v10020464mg	gbpln	Capsella rubella	AT1G77420.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:29093641-29095442 FORWARD LENGTH=382	346	382	1.00E-166	110.4	80.1	87.9
Rsa1.0_01525.1.g27627.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01525.1.g27628.t1	ref|NP_565154.1| aminocyclopropanecarboxylate oxidase [Arabidopsis thaliana] gi|122246564|sp|Q0WPW4.1|ACCO5_ARATH RecName: Full=1-aminocyclopropane-1-carboxylate oxidase 5; Short=ACC oxidase 5; Short=AtACO5 gi|110737793|dbj|BAF00835.1| hypothetical protein [Arabidopsis thaliana] gi|111074356|gb|ABH04551.1| At1g77330 [Arabidopsis thaliana] gi|332197844|gb|AEE35965.1| 1-aminocyclopropane-1-carboxylate oxidase 5 [Arabidopsis thaliana]	312	307	1.00E-163	98.4	90.4	93.6	aminocyclopropanecarboxylate oxidase	gbpln	Arabidopsis thaliana	AT1G77330.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:29063215-29064447 REVERSE LENGTH=307	312	307	1.00E-165	98.4	90.4	93.6
Rsa1.0_01525.1.g27629.t1	ref|NP_200585.3| uncharacterized protein [Arabidopsis thaliana] gi|332009565|gb|AED96948.1| uncharacterized protein AT5G57770 [Arabidopsis thaliana]	102	406	1.00E-12	398.0	33.3	38.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G57770.1 | Symbols: | Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region | chr5:23401094-23403112 REVERSE LENGTH=406	102	406	2.00E-15	398.0	33.3	38.2
Rsa1.0_01525.1.g27630.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01525.1.g27631.t2	ref|NP_177855.4| uncharacterized protein [Arabidopsis thaliana] gi|332197841|gb|AEE35962.1| uncharacterized protein AT1G77310 [Arabidopsis thaliana]	671	717	0	106.9	69.3	78.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G77310.1 | Symbols: | BEST Arabidopsis thaliana protein match is: wound-responsive family protein (TAIR:AT1G21610.1); Has 493 Blast hits to 482 proteins in 163 species: Archae - 0; Bacteria - 100; Metazoa - 172; Fungi - 66; Plants - 65; Viruses - 7; Other Eukaryotes - 83 (source: NCBI BLink). | chr1:29051671-29056179 FORWARD LENGTH=717	671	717	0	106.9	69.3	78.5
Rsa1.0_01526.1.g27632.t1	ref|XP_002882022.1| CYP76C3 [Arabidopsis lyrata subsp. lyrata] gi|297327861|gb|EFH58281.1| CYP76C3 [Arabidopsis lyrata subsp. lyrata]	485	513	0	105.8	78.6	87.4	CYP76C3	gbpln	Arabidopsis lyrata	AT2G45580.1 | Symbols: CYP76C3 | cytochrome P450, family 76, subfamily C, polypeptide 3 | chr2:18782388-18784286 REVERSE LENGTH=515	485	515	0	106.2	77.7	87.0
Rsa1.0_01526.1.g27633.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01526.1.g27634.t1	ref|NP_182078.1| beige-related and WD-40 repeat-containing protein [Arabidopsis thaliana] gi|2979554|gb|AAC06163.1| unknown protein [Arabidopsis thaliana] gi|330255473|gb|AEC10567.1| beige-related and WD-40 repeat-containing protein [Arabidopsis thaliana]	2967	2946	0	99.3	90.9	94.6	beige-related and WD-40 repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G45540.1 | Symbols: | WD-40 repeat family protein / beige-related | chr2:18757881-18772229 REVERSE LENGTH=2946	2967	2946	0	99.3	90.9	94.6
Rsa1.0_01526.1.g27635.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01526.1.g27636.t1	ref|XP_002880182.1| CYP704A2 [Arabidopsis lyrata subsp. lyrata] gi|297326021|gb|EFH56441.1| CYP704A2 [Arabidopsis lyrata subsp. lyrata]	513	511	0	99.6	87.3	93.4	CYP704A2	gbpln	Arabidopsis lyrata	AT2G45510.1 | Symbols: CYP704A2 | cytochrome P450, family 704, subfamily A, polypeptide 2 | chr2:18753085-18754944 FORWARD LENGTH=511	513	511	0	99.6	86.4	92.8
Rsa1.0_01526.1.g27637.t7	ref|XP_002882017.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327856|gb|EFH58276.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	567	491	0	86.6	74.3	78.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G45500.1 | Symbols: | AAA-type ATPase family protein | chr2:18749973-18752636 REVERSE LENGTH=491	567	491	0	86.6	73.9	78.1
Rsa1.0_01526.1.g27638.t1	gb|AAM66074.1| endosperm-specific protein-like protein [Arabidopsis thaliana]	416	420	0	101.0	87.3	94.2	endosperm-specific protein-like protein	gbpln	Arabidopsis thaliana	AT2G45470.1 | Symbols: FLA8, AGP8 | FASCICLIN-like arabinogalactan protein 8 | chr2:18742797-18744059 REVERSE LENGTH=420	416	420	0	101.0	87.0	94.2
Rsa1.0_01526.1.g27639.t1	gb|EOA26547.1| hypothetical protein CARUB_v10022606mg [Capsella rubella]	852	897	0	105.3	76.6	85.9	hypothetical protein CARUB_v10022606mg	gbpln	Capsella rubella	AT2G45460.2 | Symbols: | SMAD/FHA domain-containing protein | chr2:18737054-18741690 REVERSE LENGTH=902	852	902	0	105.9	78.4	86.7
Rsa1.0_01526.1.g27640.t1	ref|XP_002882013.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297327852|gb|EFH58272.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	92	92	2.00E-27	100.0	83.7	94.6	expressed protein	gbpln	Arabidopsis lyrata	AT3G60890.2 | Symbols: ZPR2 | protein binding | chr3:22497024-22497442 REVERSE LENGTH=106	92	106	1.00E-18	115.2	59.8	77.2

Rsa1.0_01526.1.g27641.t1	ref|NP_182068.1| dihydrodipicolinate synthase [Arabidopsis thaliana] gi|14547964|sp|Q9FVC8.2|DAPA2_ARATH RecName: Full=4-hydroxy-tetrahydrodipicolinate synthase 2, chloroplastic; Short=HTPA synthase 2; Flags: Precursor gi|2583111|gb|AAB82620.1| putative dihydrodipicolinate synthase [Arabidopsis thaliana] gi|28466961|gb|AAO44089.1| At2g45440 [Arabidopsis thaliana] gi|110735769|dbj|BAE99862.1| putative dihydrodipicolinate synthase [Arabidopsis thaliana] gi|330255460|gb|AEC10554.1| dihydrodipicolinate synthase [Arabidopsis thaliana]	366	365	0	99.7	89.9	95.1	dihydrodipicolinate synthase	gbpln	Arabidopsis thaliana	AT2G45440.1 | Symbols: DHDPS2 | dihydrodipicolinate synthase | chr2:18731294-18732867 FORWARD LENGTH=365	366	365	0	99.7	89.9	95.1
Rsa1.0_01527.1.g27642.t2	gb|EOA37093.1| hypothetical protein CARUB_v10010274mg [Capsella rubella]	193	216	3.00E-65	111.9	70.5	80.3	hypothetical protein CARUB_v10010274mg	gbpln	Capsella rubella	AT1G59590.1 | Symbols: ZCF37 | ZCF37 | chr1:21887860-21888495 FORWARD LENGTH=211	193	211	2.00E-57	109.3	62.7	74.6
Rsa1.0_01527.1.g27643.t1	#	#	#	#	#	#	#	-	----	----	AT3G27080.1 | Symbols: TOM20-3 | translocase of outer membrane 20 kDa subunit 3 | chr3:9985212-9986560 REVERSE LENGTH=202	112	202	1.00E-11	180.4	25.9	35.7
Rsa1.0_01527.1.g27644.t1	ref|XP_002882294.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297328134|gb|EFH58553.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	331	408	2.00E-65	123.3	38.4	39.3	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT3G03440.1 | Symbols: | ARM repeat superfamily protein | chr3:815709-818568 FORWARD LENGTH=408	331	408	4.00E-67	123.3	38.1	39.0
Rsa1.0_01527.1.g27645.t1	ref|XP_002892557.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338399|gb|EFH68816.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	202	412	1.00E-62	204.0	65.8	71.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G10280.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:3366795-3368739 REVERSE LENGTH=412	202	412	6.00E-65	204.0	65.8	71.3
Rsa1.0_01527.1.g27646.t5	gb|AAF22291.1|AF180732_1 dynamin-like protein 6 [Arabidopsis thaliana]	915	914	0	99.9	93.4	97.3	dynamin-like protein 6	gbpln	Arabidopsis thaliana	AT1G10290.1 | Symbols: ADL6, DRP2A | dynamin-like protein 6 | chr1:3370774-3377120 FORWARD LENGTH=914	915	914	0	99.9	93.3	97.2
Rsa1.0_01527.1.g27647.t2	ref|XP_002872263.1| serine-type peptidase/ trypsin [Arabidopsis lyrata subsp. lyrata] gi|297318100|gb|EFH48522.1| serine-type peptidase/ trypsin [Arabidopsis lyrata subsp. lyrata]	327	428	6.00E-41	130.9	28.7	41.6	serine-type peptidase/ trypsin	gbpln	Arabidopsis lyrata	AT5G27660.1 | Symbols: | Trypsin family protein with PDZ domain | chr5:9789835-9792235 REVERSE LENGTH=428	327	428	9.00E-43	130.9	28.1	41.6
Rsa1.0_01527.1.g27648.t1	gb|EOA20680.1| hypothetical protein CARUB_v10000993mg [Capsella rubella]	324	435	4.00E-38	134.3	28.1	40.1	hypothetical protein CARUB_v10000993mg	gbpln	Capsella rubella	AT5G27660.1 | Symbols: | Trypsin family protein with PDZ domain | chr5:9789835-9792235 REVERSE LENGTH=428	324	428	1.00E-39	132.1	27.8	39.5
Rsa1.0_01528.1.g27649.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	228	1123	1.00E-97	492.5	75.9	86.0	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	228	1262	3.00E-11	553.5	30.3	43.9
Rsa1.0_01528.1.g27650.t1	ref|NP_001185315.1| DNA mismatch repair protein MutS2 [Arabidopsis thaliana] gi|6227005|gb|AAF06041.1|AC009360_6 Contains similarity to gb|D90908 DNA mismatch repair protein MutS2 from Synechocystis sp. and is a member of PF|00488 Muts family of mismatch repair proteins [Arabidopsis thaliana] gi|332196205|gb|AEE34326.1| DNA mismatch repair protein MutS2 [Arabidopsis thaliana]	1133	876	0	77.3	61.8	68.6	DNA mismatch repair protein MutS2	gbpln	Arabidopsis thaliana	AT1G65070.2 | Symbols: | DNA mismatch repair protein MutS, type 2 | chr1:24173047-24176244 REVERSE LENGTH=876	1133	876	0	77.3	61.8	68.6
Rsa1.0_01528.1.g27651.t1	ref|NP_176688.3| ALBINO3-like protein 2 [Arabidopsis thaliana] gi|38372237|sp|Q8L718.2|ALB32_ARATH RecName: Full=ALBINO3-like protein 2, chloroplastic; Short=Ath5; Flags: Precursor gi|6227006|gb|AAF06042.1|AC009360_7 F16G16.8 [Arabidopsis thaliana] gi|332196206|gb|AEE34327.1| ALBINO3-like protein 2 [Arabidopsis thaliana]	585	525	0	89.7	72.8	75.9	ALBINO3-like protein 2	gbpln	Arabidopsis thaliana	AT1G65080.1 | Symbols: | Membrane insertion protein, OxaA/YidC with tetratricopeptide repeat domain | chr1:24176619-24180729 FORWARD LENGTH=525	585	525	0	89.7	72.8	75.9

Rsa1.0_01528.1.g27652.t2	ref|XP_002888307.1| hypothetical protein ARALYDRAFT_338601 [Arabidopsis lyrata subsp. lyrata] gi|297334148|gb|EFH64566.1| hypothetical protein ARALYDRAFT_338601 [Arabidopsis lyrata subsp. lyrata]	329	326	1.00E-100	99.1	68.1	76.6	hypothetical protein ARALYDRAFT_338601	gbpln	Arabidopsis lyrata	AT1G65090.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G36100.1); Has 1234 Blast hits to 904 proteins in 178 species: Archae - 0; Bacteria - 58; Metazoa - 431; Fungi - 95; Plants - 83; Viruses - 38; Other Eukaryotes - 529 (source: NCBI BLink). | chr1:24180973-24182668 REVERSE LENGTH=379	329	379	1.00E-101	115.2	69.6	79.9
Rsa1.0_01528.1.g27653.t1	ref|XP_002886801.1| hypothetical protein ARALYDRAFT_315473 [Arabidopsis lyrata subsp. lyrata] gi|297332642|gb|EFH63060.1| hypothetical protein ARALYDRAFT_315473 [Arabidopsis lyrata subsp. lyrata]	258	247	1.00E-109	95.7	84.1	89.5	hypothetical protein ARALYDRAFT_315473	gbpln	Arabidopsis lyrata	AT2G44870.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 15 growth stages; Has 39 Blast hits to 39 proteins in 18 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18503250-18504422 FORWARD LENGTH=248	258	248	1.00E-106	96.1	82.6	88.4
Rsa1.0_01528.1.g27654.t3	ref|XP_002874833.1| hypothetical protein ARALYDRAFT_911781 [Arabidopsis lyrata subsp. lyrata] gi|297320670|gb|EFH51092.1| hypothetical protein ARALYDRAFT_911781 [Arabidopsis lyrata subsp. lyrata]	906	418	0	46.1	35.4	38.9	hypothetical protein ARALYDRAFT_911781	gbpln	Arabidopsis lyrata	AT4G05120.1 | Symbols: ENT3, FUR1, ATENT3 | Major facilitator superfamily protein | chr4:2632886-2634824 REVERSE LENGTH=418	906	418	0	46.1	35.0	38.7
Rsa1.0_01528.1.g27655.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01528.1.g27656.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1283	1307	0	101.9	57.9	72.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1283	1262	2.00E-67	98.4	11.4	19.0
Rsa1.0_01528.1.g27657.t1	ref|XP_002877546.1| hypothetical protein ARALYDRAFT_347817 [Arabidopsis lyrata subsp. lyrata] gi|297323384|gb|EFH53805.1| hypothetical protein ARALYDRAFT_347817 [Arabidopsis lyrata subsp. lyrata]	1031	1022	0	99.1	71.3	81.8	hypothetical protein ARALYDRAFT_347817	gbpln	Arabidopsis lyrata	AT3G47110.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17347103-17350296 REVERSE LENGTH=1025	1031	1025	0	99.4	69.8	80.8
Rsa1.0_01529.1.g27658.t1	gb|ABD65150.1| hypothetical protein 40.t00029 [Brassica oleracea]	312	311	1.00E-133	99.7	82.7	86.5	hypothetical protein 40.t00029	gbpln	Brassica oleracea	AT4G17680.1 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr4:9842903-9844095 REVERSE LENGTH=314	312	314	1.00E-103	100.6	67.6	76.3
Rsa1.0_01529.1.g27659.t1	gb|ABD65149.1| hypothetical protein 40.t00027 [Brassica oleracea]	173	168	3.00E-70	97.1	89.6	90.8	hypothetical protein 40.t00027	gbpln	Brassica oleracea	AT4G17670.1 | Symbols: | Protein of unknown function (DUF581) | chr4:9833948-9834663 REVERSE LENGTH=159	173	159	4.00E-53	91.9	72.8	80.3
Rsa1.0_01529.1.g27660.t1	ref|XP_002870094.1| hypothetical protein ARALYDRAFT_354992 [Arabidopsis lyrata subsp. lyrata] gi|297315930|gb|EFH46353.1| hypothetical protein ARALYDRAFT_354992 [Arabidopsis lyrata subsp. lyrata]	1406	1299	0	92.4	69.2	75.6	hypothetical protein ARALYDRAFT_354992	gbpln	Arabidopsis lyrata	AT4G17616.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:9819608-9821632 FORWARD LENGTH=674	1406	674	0	47.9	37.5	41.7
Rsa1.0_01529.1.g27661.t1	emb|CAB10540.1| hypothetical protein [Arabidopsis thaliana] gi|7268512|emb|CAB78763.1| hypothetical protein [Arabidopsis thaliana]	241	350	1.00E-103	145.2	81.7	88.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G17600.1 | Symbols: LIL3:1 | Chlorophyll A-B binding family protein | chr4:9803759-9804714 FORWARD LENGTH=262	241	262	1.00E-105	108.7	81.7	88.0
Rsa1.0_01529.1.g27662.t2	gb|EOA19009.1| hypothetical protein CARUB_v10007660mg [Capsella rubella]	150	391	1.00E-26	260.7	46.7	60.7	hypothetical protein CARUB_v10007660mg	gbpln	Capsella rubella	AT5G47120.1 | Symbols: ATBI-1, BI-1, ATBI1, BI1 | BAX inhibitor 1 | chr5:19136071-19137585 FORWARD LENGTH=247	150	247	7.00E-28	164.7	46.0	61.3
Rsa1.0_01529.1.g27663.t1	gb|ABD65148.1| transporter, putative [Brassica oleracea]	358	527	0	147.2	92.5	94.1	transporter, putative	gbpln	Brassica oleracea	AT4G17550.1 | Symbols: | Major facilitator superfamily protein | chr4:9777938-9779738 REVERSE LENGTH=544	358	544	1.00E-173	152.0	86.3	91.6
Rsa1.0_01530.1.g27664.t1	ref|XP_002885241.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297331081|gb|EFH61500.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|482566910|gb|EOA31099.1| hypothetical protein CARUB_v10014252mg [Capsella rubella]	305	305	1.00E-179	100.0	98.0	99.3	transducin family protein	gbpln	Arabidopsis lyrata	AT3G18140.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:6212743-6214567 REVERSE LENGTH=305	305	305	1.00E-180	100.0	97.4	98.7

Rsa1.0_01530.1.g27665.t1	gb|AAW62966.1| chloroplast embryo-defective 1270 [Arabidopsis thaliana]	1751	1429	0	81.6	73.8	77.4	chloroplast embryo-defective 1270	gbpln	Arabidopsis thaliana	AT3G18110.1 | Symbols: EMB1270 | Pentatricopeptide repeat (PPR) superfamily protein | chr3:6204940-6209691 REVERSE LENGTH=1440	1751	1440	0	82.2	73.8	77.4
Rsa1.0_01530.1.g27666.t17	ref|XP_002883109.1| MYB4R1 [Arabidopsis lyrata subsp. lyrata] gi|297328949|gb|EFH59368.1| MYB4R1 [Arabidopsis lyrata subsp. lyrata]	900	809	0	89.9	64.1	74.4	MYB4R1	gbpln	Arabidopsis lyrata	AT3G18100.1 | Symbols: MYB4R1, AtMYB4R1 | myb domain protein 4r1 | chr3:6200689-6204583 FORWARD LENGTH=847	900	847	0	94.1	64.9	75.2
Rsa1.0_01530.1.g27667.t1	gb|EOA30146.1| hypothetical protein CARUB_v10013253mg [Capsella rubella]	585	609	0	104.1	91.5	96.2	hypothetical protein CARUB_v10013253mg	gbpln	Capsella rubella	AT3G18060.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:6183880-6186788 FORWARD LENGTH=609	585	609	0	104.1	90.8	95.7
Rsa1.0_01530.1.g27668.t1	gb|ABD65099.1| hypothetical protein 31.t00074 [Brassica oleracea]	261	258	7.00E-58	98.9	51.7	68.2	hypothetical protein 31.t00074	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	261	302	8.00E-48	115.7	44.1	62.8
Rsa1.0_01530.1.g27669.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	394	442	1.00E-143	112.2	65.0	77.9	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	394	343	3.00E-64	87.1	34.8	45.2
Rsa1.0_01530.1.g27670.t1	ref|NP_566596.1| uncharacterized protein [Arabidopsis thaliana] gi|9294060|dbj|BAB02017.1| unnamed protein product [Arabidopsis thaliana] gi|15451206|gb|AAK96874.1| Unknown protein [Arabidopsis thaliana] gi|23197698|gb|AAN15376.1| Unknown protein [Arabidopsis thaliana] gi|332642519|gb|AEE76040.1| uncharacterized protein AT3G18050 [Arabidopsis thaliana]	337	335	1.00E-154	99.4	83.1	89.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G18050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G28100.1); Has 67 Blast hits to 66 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6180931-6182593 FORWARD LENGTH=335	337	335	1.00E-157	99.4	83.1	89.3
Rsa1.0_01530.1.g27671.t1	gb|EOA30100.1| hypothetical protein CARUB_v10013210mg [Capsella rubella]	603	628	0	104.1	90.9	95.7	hypothetical protein CARUB_v10013210mg	gbpln	Capsella rubella	AT3G18040.1 | Symbols: MPK9 | MAP kinase 9 | chr3:6174800-6178150 FORWARD LENGTH=510	603	510	0	84.6	78.6	80.8
Rsa1.0_01531.1.g27672.t1	gb|EOA37955.1| hypothetical protein CARUB_v10009422mg [Capsella rubella]	174	384	1.00E-64	220.7	71.3	78.7	hypothetical protein CARUB_v10009422mg	gbpln	Capsella rubella	AT1G29050.1 | Symbols: TBL38 | TRICHOME BIREFRINGENCE-LIKE 38 | chr1:10136376-10139082 REVERSE LENGTH=380	174	380	8.00E-66	218.4	72.4	77.0
Rsa1.0_01531.1.g27673.t1	ref|XP_002893546.1| hypothetical protein ARALYDRAFT_473111 [Arabidopsis lyrata subsp. lyrata] gi|297339388|gb|EFH69805.1| hypothetical protein ARALYDRAFT_473111 [Arabidopsis lyrata subsp. lyrata]	168	380	3.00E-88	226.2	91.1	95.2	hypothetical protein ARALYDRAFT_473111	gbpln	Arabidopsis lyrata	AT1G29050.1 | Symbols: TBL38 | TRICHOME BIREFRINGENCE-LIKE 38 | chr1:10136376-10139082 REVERSE LENGTH=380	168	380	2.00E-89	226.2	89.3	94.6
Rsa1.0_01531.1.g27674.t1	ref|NP_174197.2| EF-hand, calcium binding motif-containing protein [Arabidopsis thaliana] gi|332192908|gb|AEE31029.1| EF-hand, calcium binding motif-containing protein [Arabidopsis thaliana]	585	564	0	96.4	70.9	83.1	EF-hand, calcium binding motif-containing protein	gbpln	Arabidopsis thaliana	AT1G29020.1 | Symbols: | Calcium-binding EF-hand family protein | chr1:10120497-10122902 REVERSE LENGTH=564	585	564	0	96.4	70.9	83.1
Rsa1.0_01531.1.g27675.t1	ref|NP_174196.2| uncharacterized protein [Arabidopsis thaliana] gi|6691220|gb|AAF24558.1|AC007508_21 F1K23.3 [Arabidopsis thaliana] gi|91805881|gb|ABE65669.1| unknown [Arabidopsis thaliana] gi|332192907|gb|AEE31028.1| uncharacterized protein AT1G29010 [Arabidopsis thaliana]	254	300	3.00E-81	118.1	68.1	77.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G29010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34010.1); Has 18 Blast hits to 17 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10117715-10118973 FORWARD LENGTH=300	254	300	1.00E-83	118.1	68.1	77.6
Rsa1.0_01531.1.g27676.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01531.1.g27677.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01531.1.g27678.t2	gb|EOA14807.1| hypothetical protein CARUB_v10028114mg [Capsella rubella]	162	335	1.00E-37	206.8	48.8	60.5	hypothetical protein CARUB_v10028114mg	gbpln	Capsella rubella	AT5G64920.1 | Symbols: CIP8 | COP1-interacting protein 8 | chr5:25944338-25945342 REVERSE LENGTH=334	162	334	4.00E-37	206.2	47.5	58.6
Rsa1.0_01531.1.g27679.t1	gb|EOA38764.1| hypothetical protein CARUB_v10010950mg [Capsella rubella]	117	118	2.00E-35	100.9	67.5	78.6	hypothetical protein CARUB_v10010950mg	gbpln	Capsella rubella	AT1G28815.1 | Symbols: | unknown protein; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10095812-10096244 FORWARD LENGTH=115	117	115	2.00E-32	98.3	62.4	76.1

Rsa1.0_01531.1.g27680.t1	gb|EOA23054.1| hypothetical protein CARUB_v10003824mg [Capsella rubella]	171	307	3.00E−18	179.5	40.9	52.0	hypothetical protein CARUB_v10003824mg	gbpln	Capsella rubella	AT5G28180.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:10162783−10163943 FORWARD LENGTH=352	171	352	7.00E−19	205.8	41.5	55.0
Rsa1.0_01531.1.g27681.t1	sp|P52425.1|GPDA_CUPLA RecName: Full=Glycerol−3−phosphate dehydrogenase [NAD(+)] gi|840731|emb|CAA56125.1| glycerol−3−phosphate dehydrogenase (NAD+) [Cuphea lanceolata]	81	372	5.00E−16	459.3	60.5	67.9	RecName: Full=Glycerol−3−phosphate dehydrogenase	gbpln	Cuphea lanceolata	AT5G40610.1 | Symbols: | NAD−dependent glycerol−3−phosphate dehydrogenase family protein | chr5:16265071−16267258 REVERSE LENGTH=400	81	400	4.00E−18	493.8	61.7	71.6
Rsa1.0_01532.1.g27682.t1	ref|NP_001078362.1| ECA1 gametogenesis related family protein [Arabidopsis thaliana] gi|332657363|gb|AEE82763.1| ECA1 gametogenesis related family protein [Arabidopsis thaliana] gi|371782144|emb|CCE46138.1| cysteine rich peptide [Arabidopsis thaliana]	120	122	1.00E−34	101.7	62.5	74.2	ECA1 gametogenesis related family protein	gbpln	Arabidopsis thaliana	AT4G09545.1 | Symbols: | ECA1 gametogenesis related family protein | chr4:6037569−6037937 FORWARD LENGTH=122	120	122	2.00E−37	101.7	62.5	74.2
Rsa1.0_01532.1.g27683.t1	emb|CAB81573.1| putative protein [Arabidopsis thaliana]	185	510	4.00E−28	275.7	40.5	59.5	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01532.1.g27684.t1	ref|NP_001078362.1| ECA1 gametogenesis related family protein [Arabidopsis thaliana] gi|332657363|gb|AEE82763.1| ECA1 gametogenesis related family protein [Arabidopsis thaliana] gi|371782144|emb|CCE46138.1| cysteine rich peptide [Arabidopsis thaliana]	111	122	2.00E−33	109.9	64.9	76.6	ECA1 gametogenesis related family protein	gbpln	Arabidopsis thaliana	AT4G09545.1 | Symbols: | ECA1 gametogenesis related family protein | chr4:6037569−6037937 FORWARD LENGTH=122	111	122	4.00E−36	109.9	64.9	76.6
Rsa1.0_01532.1.g27685.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	378	414	2.00E−77	109.5	53.2	60.3	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01532.1.g27686.t10	gb|AAF06087.1|AC007918_11 Similar to gi|4325351 T25H8.2 TNP2 protein homolog from Arabidopsis thaliana BAC gb|AF128394 [Arabidopsis thaliana]	375	1121	2.00E−62	298.9	41.1	57.6	Similar to gi|4325351 T25H8.2 TNP2 protein homolog from Arabidopsis thaliana BAC gb|AF128394	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01532.1.g27687.t5	ref|NP_175242.7| calcium−dependent lipid−binding−like protein [Arabidopsis thaliana] gi|332194125|gb|AEE32246.1| calcium−dependent lipid−binding−like protein [Arabidopsis thaliana]	4230	4146	0	98.0	88.0	92.2	calcium−dependent lipid−binding−like protein	gbpln	Arabidopsis thaliana	AT1G48090.1 | Symbols: | calcium−dependent lipid−binding family protein | chr1:17732582−17758194 REVERSE LENGTH=4146	4230	4146	0	98.0	88.0	92.2
Rsa1.0_01533.1.g27688.t4	ref|XP_002893241.1| hypothetical protein ARALYDRAFT_472501 [Arabidopsis lyrata subsp. lyrata] gi|297339083|gb|EFH69500.1| hypothetical protein ARALYDRAFT_472501 [Arabidopsis lyrata subsp. lyrata]	1288	911	0	70.7	64.4	67.9	hypothetical protein ARALYDRAFT_472501	gbpln	Arabidopsis lyrata	AT1G22620.1 | Symbols: ATSAC1 | Phosphoinositide phosphatase family protein | chr1:7997889−8002787 REVERSE LENGTH=912	1288	912	0	70.8	64.1	67.9
Rsa1.0_01533.1.g27689.t1	ref|NP_973886.1| protein AGAMOUS−like 87 [Arabidopsis thaliana] gi|32402464|gb|AAN52814.1| MADS−box protein AGL87 [Arabidopsis thaliana] gi|332192137|gb|AEE30258.1| protein AGAMOUS−like 87 [Arabidopsis thaliana]	162	163	1.00E−61	100.6	70.4	87.0	protein AGAMOUS−like 87	gbpln	Arabidopsis thaliana	AT1G22590.2 | Symbols: AGL87 | AGAMOUS−like 87 | chr1:7983511−7984002 FORWARD LENGTH=163	162	163	4.00E−64	100.6	70.4	87.0
Rsa1.0_01533.1.g27690.t1	ref|XP_002874461.1| hypothetical protein ARALYDRAFT_351855 [Arabidopsis lyrata subsp. lyrata] gi|297320298|gb|EFH50720.1| hypothetical protein ARALYDRAFT_351855 [Arabidopsis lyrata subsp. lyrata]	279	446	7.00E−13	159.9	20.8	28.3	hypothetical protein ARALYDRAFT_351855	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01533.1.g27691.t2	dbj|BAJ34104.1| unnamed protein product [Thellungiella halophila]	169	383	5.00E−17	226.6	28.4	31.4	unnamed protein product	−−−−	−−−−	AT1G48040.1 | Symbols: | Protein phosphatase 2C family protein | chr1:17720064−17721698 REVERSE LENGTH=383	169	383	2.00E−18	226.6	27.8	30.8
Rsa1.0_01533.1.g27692.t1	emb|CAB40051.1| putative protein [Arabidopsis thaliana] gi|7267781|emb|CAB81184.1| putative protein [Arabidopsis thaliana]	744	1294	1.00E−110	173.9	30.9	44.5	putative protein	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H−like superfamily protein | chr3:2921804−2923258 FORWARD LENGTH=484	744	484	1.00E−31	65.1	11.0	15.6
Rsa1.0_01534.1.g27693.t1	ref|NP_001078624.1| Putative membrane lipoprotein [Arabidopsis thaliana] gi|332006178|gb|AED93561.1| Putative membrane lipoprotein [Arabidopsis thaliana]	75	100	5.00E−12	133.3	49.3	60.0	Putative membrane lipoprotein	gbpln	Arabidopsis thaliana	AT5G26673.1 | Symbols: | Putative membrane lipoprotein | chr5:9279309−9279611 FORWARD LENGTH=100	75	100	9.00E−15	133.3	49.3	60.0
Rsa1.0_01534.1.g27694.t1	emb|CAA09196.1| RNA helicase [Arabidopsis thaliana]	111	748	2.00E−20	673.9	73.9	74.8	RNA helicase	gbpln	Arabidopsis thaliana	AT5G26742.1 | Symbols: emb1138 | DEAD box RNA helicase (RH3) | chr5:9285540−9288871 REVERSE LENGTH=747	111	747	1.00E−10	673.0	24.3	24.3

Rsa1.0_01534.1.g27695.t1	ref|XP_002872219.1| hypothetical protein ARALYDRAFT_489488 [Arabidopsis lyrata subsp. lyrata] gi|297318056|gb|EFH48478.1| hypothetical protein ARALYDRAFT_489488 [Arabidopsis lyrata subsp. lyrata]	103	102	1.00E−22	99.0	75.7	82.5	hypothetical protein ARALYDRAFT_489488	gbpln	Arabidopsis lyrata	AT5G26731.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:9295676−9295975 FORWARD LENGTH=99	103	99	2.00E−23	96.1	64.1	71.8
Rsa1.0_01534.1.g27696.t1	gb|EOA19657.1| hypothetical protein CARUB_v10003200mg [Capsella rubella]	146	271	6.00E−56	185.6	74.0	87.0	hypothetical protein CARUB_v10003200mg	gbpln	Capsella rubella	AT5G26730.1 | Symbols: | Fasciclin−like arabinogalactan family protein | chr5:9300422−9301990 FORWARD LENGTH=268	146	268	6.00E−57	183.6	69.9	82.9
Rsa1.0_01534.1.g27697.t1	ref|NP_850874.1| glutamyl−tRNA synthetase [Arabidopsis thaliana] gi|3435196|gb|AAC36469.1| glutamyl−tRNA synthetase [Arabidopsis thaliana] gi|20466252|gb|AAM20443.1| glutamyl−tRNA synthetase [Arabidopsis thaliana] gi|23198080|gb|AAN15567.1| glutamyl−tRNA synthetase [Arabidopsis thaliana] gi|110740992|dbj|BAE98590.1| glutamyl−tRNA synthetase [Arabidopsis thaliana] gi|332006190|gb|AED93573.1| glutamyl/glutaminyl−tRNA synthetase, class Ic [Arabidopsis thaliana]	796	719	0	90.3	77.0	82.7	glutamyl−tRNA synthetase	gbpln	Arabidopsis thaliana	AT5G26710.1 | Symbols: | Glutamyl/glutaminyl−tRNA synthetase, class Ic | chr5:9305673−9308247 FORWARD LENGTH=719	796	719	0	90.3	77.0	82.7
Rsa1.0_01534.1.g27698.t1	gb|EOA22223.1| hypothetical protein CARUB_v10002810mg [Capsella rubella]	218	216	2.00E−95	99.1	79.8	91.7	hypothetical protein CARUB_v10002810mg	gbpln	Capsella rubella	AT5G26700.1 | Symbols: | RmlC−like cupins superfamily protein | chr5:9308439−9309548 REVERSE LENGTH=213	218	213	9.00E−98	97.7	80.7	88.1
Rsa1.0_01534.1.g27699.t1	#	#	#	#	#	#	#	−	----	----	AT5G26680.2 | Symbols: | 5'−3' exonuclease family protein | chr5:9311882−9315458 REVERSE LENGTH=383	87	383	2.00E−11	440.2	37.9	37.9
Rsa1.0_01534.1.g27700.t1	ref|XP_002872227.1| hypothetical protein ARALYDRAFT_489494 [Arabidopsis lyrata subsp. lyrata] gi|297318064|gb|EFH48486.1| hypothetical protein ARALYDRAFT_489494 [Arabidopsis lyrata subsp. lyrata]	416	416	0	100.0	90.6	94.7	hypothetical protein ARALYDRAFT_489494	gbpln	Arabidopsis lyrata	AT5G26670.1 | Symbols: | Pectinacetylesterase family protein | chr5:9318456−9320816 FORWARD LENGTH=416	416	416	0	100.0	90.9	95.4
Rsa1.0_01534.1.g27701.t1	ref|NP_850879.1| transcription factor MYB86 [Arabidopsis thaliana] gi|56749347|sp|Q8LPH6.1|MYB86_ARATH RecName: Full=Transcription factor MYB86; AltName: Full=Myb homolog 4; Short=AtMyb4; AltName: Full=Myb−related protein 86; Short=AtMYB86 gi|20466622|gb|AAM20628.1| transcription factor ATMYB4 [Arabidopsis thaliana] gi|30984580|gb|AAP42753.1| At5g26655 [Arabidopsis thaliana] gi|41619424|gb|AAS10099.1| MYB transcription factor [Arabidopsis thaliana] gi|332006197|gb|AED93580.1| transcription factor MYB86 [Arabidopsis thaliana]	345	352	1.00E−159	102.0	85.8	91.3	transcription factor MYB86	gbpln	Arabidopsis thaliana	AT5G26660.1 | Symbols: ATMYB86, MYB86 | myb domain protein 86 | chr5:9331775−9333044 REVERSE LENGTH=352	345	352	1.00E−162	102.0	85.8	91.3
Rsa1.0_01534.1.g27702.t1	dbj|BAF00918.1| putative reverse transcriptase [Arabidopsis thaliana]	1497	910	0	60.8	26.6	36.5	putative reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I−like superfamily protein | chr1:16528880−16531065 REVERSE LENGTH=626	1497	626	6.00E−77	41.8	10.8	16.5
Rsa1.0_01534.1.g27703.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01534.1.g27704.t1	gb|ABE65560.1| hypothetical protein At5g26620 [Arabidopsis thaliana]	83	88	3.00E−29	106.0	80.7	90.4	hypothetical protein At5g26620	gbpln	Arabidopsis thaliana	AT5G26620.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G05858.1); Has 48 Blast hits to 48 proteins in 8 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 48; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr5:9366697−9366963 REVERSE LENGTH=74	83	74	2.00E−27	89.2	71.1	78.3
Rsa1.0_01535.1.g27705.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01535.1.g27706.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	301	940	1.00E−63	312.3	44.9	63.8	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01535.1.g27707.t1	gb|ABA98030.2| retrotransposon protein, putative, Ty1−copia subclass [Oryza sativa Japonica Group]	377	1310	3.00E−42	347.5	31.8	47.7	retrotransposon protein, putative, Ty1−copia subclass	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_01535.1.g27708.t1	ref|XP_002864014.1| leucine−rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297309849|gb|EFH40273.1| leucine−rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	953	953	0	100.0	85.1	91.5	leucine−rich repeat family protein	gbpln	Arabidopsis lyrata	AT5G49760.1 | Symbols: | Leucine−rich repeat protein kinase family protein | chr5:20216679−20221052 FORWARD LENGTH=953	953	953	0	100.0	84.8	91.3

Rsa1.0_01535.1.g27709.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01535.1.g27710.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01535.1.g27711.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01535.1.g27712.t1	ref|XP_002864014.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297309849|gb|EFH40273.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	919	953	0	103.7	80.1	87.4	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT5G49760.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:20216679-20221052 FORWARD LENGTH=953	919	953	0	103.7	79.4	87.3
Rsa1.0_01536.1.g27713.t1	gb|EOA30360.1| hypothetical protein CARUB_v10013481mg [Capsella rubella]	532	511	0	96.1	76.9	82.7	hypothetical protein CARUB_v10013481mg	gbpln	Capsella rubella	AT2G15860.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:6905712-6909282 REVERSE LENGTH=512	532	512	0	96.2	76.1	82.7
Rsa1.0_01536.1.g27714.t1	gb|EOA34479.1| hypothetical protein CARUB_v10022019mg [Capsella rubella]	318	312	9.00E-84	98.1	50.6	65.4	hypothetical protein CARUB_v10022019mg	gbpln	Capsella rubella	AT1G65140.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr1:24201620-24203226 FORWARD LENGTH=317	318	317	2.00E-80	99.7	50.3	64.5
Rsa1.0_01536.1.g27715.t1	ref|NP_179188.1| Pollen-specific leucine-rich repeat extensin-like protein 3 [Arabidopsis thaliana] gi|75338652|sp|Q9XIL9.1|PLRX3_ARATH RecName: Full=Pollen-specific leucine-rich repeat extensin-like protein 3; Short=AtPEX3; Short=Pollen-specific LRR/EXTENSIN3; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor gi|5306245|gb|AAD41978.1| unknown protein [Arabidopsis thaliana] gi|330251349|gb|AEC06443.1| Pollen-specific leucine-rich repeat extensin-like protein 3 [Arabidopsis thaliana]	865	727	0	84.0	44.2	46.8	Pollen-specific leucine-rich repeat extensin-like protein 3	gbpln	Arabidopsis thaliana	AT2G15880.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr2:6918039-6920319 REVERSE LENGTH=727	865	727	0	84.0	44.2	46.8
Rsa1.0_01536.1.g27716.t1	ref|NP_565383.1| maternal effect embryo arrest 14 protein [Arabidopsis thaliana] gi|11692922|gb|AAG40064.1|AF324713_1 At2g15890 [Arabidopsis thaliana] gi|12642940|gb|AAK00412.1|AF339730_1 unknown protein [Arabidopsis thaliana] gi|5306244|gb|AAD41977.1| expressed protein [Arabidopsis thaliana] gi|17473578|gb|AAL38262.1| unknown protein [Arabidopsis thaliana] gi|21592568|gb|AAM64517.1| unknown [Arabidopsis thaliana] gi|30725564|gb|AAP37804.1| At2g15890 [Arabidopsis thaliana] gi|330251350|gb|AEC06444.1| maternal effect embryo arrest 14 protein [Arabidopsis thaliana]	201	203	6.00E-81	101.0	81.1	90.0	maternal effect embryo arrest 14 protein	gbpln	Arabidopsis thaliana	AT2G15890.1 | Symbols: MEE14 | maternal effect embryo arrest 14 | chr2:6921196-6921978 REVERSE LENGTH=203	201	203	2.00E-83	101.0	81.1	90.0
Rsa1.0_01536.1.g27717.t1	gb|EOA32338.1| hypothetical protein CARUB_v10015605mg, partial [Capsella rubella]	242	247	1.00E-111	102.1	81.4	86.0	hypothetical protein CARUB_v10015605mg, partial	gbpln	Capsella rubella	AT2G15910.1 | Symbols: | CSL zinc finger domain-containing protein | chr2:6932917-6935333 REVERSE LENGTH=367	242	367	1.00E-109	151.7	81.4	85.5
Rsa1.0_01536.1.g27718.t1	ref|NP_179191.1| CSL zinc finger domain-containing protein [Arabidopsis thaliana] gi|5306242|gb|AAD41975.1| unknown protein [Arabidopsis thaliana] gi|330251353|gb|AEC06447.1| CSL zinc finger domain-containing protein [Arabidopsis thaliana]	84	367	1.00E-37	436.9	88.1	91.7	CSL zinc finger domain-containing protein	gbpln	Arabidopsis thaliana	AT2G15910.1 | Symbols: | CSL zinc finger domain-containing protein | chr2:6932917-6935333 REVERSE LENGTH=367	84	367	2.00E-40	436.9	88.1	91.7
Rsa1.0_01536.1.g27719.t1	dbj|BAJ34348.1| unnamed protein product [Thellungiella halophila]	74	76	4.00E-27	102.7	82.4	90.5	unnamed protein product	----	----	AT2G15960.1 | Symbols: | unknown protein; Has 14 Blast hits to 14 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:6947353-6947586 FORWARD LENGTH=77	74	77	8.00E-26	104.1	82.4	89.2
Rsa1.0_01536.1.g27720.t1	gb|ABV89655.1| cold regulated 413 plasma membrane 1 [Brassica rapa]	197	197	1.00E-106	100.0	97.5	98.5	cold regulated 413 plasma membrane 1	gbpln	Brassica rapa	AT2G15970.1 | Symbols: COR413-PM1, WCOR413, WCOR413-LIKE, ATCOR413-PM1, FL3-5A3, ATCYP19 | cold regulated 413 plasma membrane 1 | chr2:6950163-6951012 FORWARD LENGTH=197	197	197	8.00E-85	100.0	80.7	89.3

Rsa1.0_01536.1.g27721.t1	ref|XP_002872780.1| hypothetical protein ARALYDRAFT_911862 [Arabidopsis lyrata subsp. lyrata] gi|297318617|gb|EFH49039.1| hypothetical protein ARALYDRAFT_911862 [Arabidopsis lyrata subsp. lyrata]	592	591	0	99.8	84.1	90.4	hypothetical protein ARALYDRAFT_911862	gbpln	Arabidopsis lyrata	AT4G03400.1 | Symbols: DFL2, GH3-10 | Auxin-responsive GH3 family protein | chr4:1497675-1499729 REVERSE LENGTH=591	592	591	0	99.8	83.8	90.2
Rsa1.0_01536.1.g27722.t1	gb|EOA31069.1| hypothetical protein CARUB_v10014221mg [Capsella rubella]	305	314	1.00E-121	103.0	80.3	86.2	hypothetical protein CARUB_v10014221mg	gbpln	Capsella rubella	AT2G16070.2 | Symbols: PDV2 | plastid division2 | chr2:6984072-6985356 REVERSE LENGTH=307	305	307	1.00E-122	100.7	80.0	88.2
Rsa1.0_01536.1.g27723.t1	ref|XP_002866147.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311982|gb|EFH42406.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	351	423	1.00E-36	120.5	37.9	54.1	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56420.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22850863-22852334 REVERSE LENGTH=422	351	422	9.00E-38	120.2	36.8	53.8
Rsa1.0_01536.1.g27724.t1	ref|XP_002893862.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata] gi|297339704|gb|EFH70121.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata]	151	152	2.00E-59	100.7	74.8	84.8	bet v I allergen family protein	gbpln	Arabidopsis lyrata	AT1G35260.1 | Symbols: MLP165 | MLP-like protein 165 | chr1:12937059-12937689 REVERSE LENGTH=152	151	152	5.00E-61	100.7	73.5	84.8
Rsa1.0_01536.1.g27725.t2	ref|XP_002886213.1| hypothetical protein ARALYDRAFT_480795 [Arabidopsis lyrata subsp. lyrata] gi|297332053|gb|EFH62472.1| hypothetical protein ARALYDRAFT_480795 [Arabidopsis lyrata subsp. lyrata]	568	907	0	159.7	75.4	81.0	hypothetical protein ARALYDRAFT_480795	gbpln	Arabidopsis lyrata	AT2G16250.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:7039682-7042933 REVERSE LENGTH=915	568	915	0	161.1	73.4	80.5
Rsa1.0_01537.1.g27726.t1	gb|EOA37197.1| hypothetical protein CARUB_v10010654mg [Capsella rubella]	124	124	1.00E-60	100.0	87.9	96.0	hypothetical protein CARUB_v10010654mg	gbpln	Capsella rubella	AT1G09815.1 | Symbols: POLD4 | polymerase delta 4 | chr1:3189460-3190050 FORWARD LENGTH=124	124	124	9.00E-63	100.0	86.3	95.2
Rsa1.0_01537.1.g27727.t1	ref|NP_172453.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75276860|sp|O04504.1|PPR27_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g09820 gi|2160173|gb|AAB60736.1| Similar to N. tabacum salt-inducible protein (gb|U08285) [Arabidopsis thaliana] gi|332190378|gb|AEE28499.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	606	606	0	100.0	80.7	90.3	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G09820.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:3190594-3192414 REVERSE LENGTH=606	606	606	0	100.0	80.7	90.3
Rsa1.0_01537.1.g27728.t1	ref|NP_172454.1| phosphoribosylamine--glycine ligase [Arabidopsis thaliana] gi|12644306|sp|P52420.2|PUR2_ARATH RecName: Full=Phosphoribosylamine--glycine ligase, chloroplastic; AltName: Full=Glycinamide ribonucleotide synthetase; Short=GARS; AltName: Full=Phosphoribosylglycinamide synthetase; Flags: Precursor gi|2160174|gb|AAB60737.1| Identical to A. thaliana PUR2 (gb|X74766). ESTs gb|ATTS3927,gb|N96446 come from this gene [Arabidopsis thaliana] gi|15292773|gb|AAK92755.1| putative phosphoribosylglycinamide synthetase [Arabidopsis thaliana] gi|20259251|gb|AAM14361.1| putative phosphoribosylglycinamide synthetase [Arabidopsis thaliana] gi|332190379|gb|AEE28500.1| phosphoribosylamine--glycine ligase [Arabidopsis thaliana]	529	532	0	100.6	87.5	92.4	phosphoribosylamine--glycine ligase	gbpln	Arabidopsis thaliana	AT1G09830.1 | Symbols: | Glycinamide ribonucleotide (GAR) synthetase | chr1:3192783-3194936 REVERSE LENGTH=532	529	532	0	100.6	87.5	92.4
Rsa1.0_01537.1.g27729.t1	ref|XP_002892530.1| hypothetical protein ARALYDRAFT_471093 [Arabidopsis lyrata subsp. lyrata] gi|297338372|gb|EFH68789.1| hypothetical protein ARALYDRAFT_471093 [Arabidopsis lyrata subsp. lyrata]	546	421	0	77.1	72.0	73.8	hypothetical protein ARALYDRAFT_471093	gbpln	Arabidopsis lyrata	AT1G09840.6 | Symbols: ATSK41, SK41 | shaggy-like protein kinase 41 | chr1:3196114-3199524 REVERSE LENGTH=421	546	421	0	77.1	72.0	73.6
Rsa1.0_01537.1.g27730.t1	ref|XP_002889773.1| hypothetical protein ARALYDRAFT_471096 [Arabidopsis lyrata subsp. lyrata] gi|297335615|gb|EFH66032.1| hypothetical protein ARALYDRAFT_471096 [Arabidopsis lyrata subsp. lyrata]	446	439	0	98.4	87.0	90.4	hypothetical protein ARALYDRAFT_471096	gbpln	Arabidopsis lyrata	AT1G09850.1 | Symbols: XBCP3 | xylem bark cysteine peptidase 3 | chr1:3201848-3203875 FORWARD LENGTH=437	446	437	0	98.0	83.9	87.2
Rsa1.0_01537.1.g27731.t1	gb|EOA37380.1| hypothetical protein CARUB_v10011209mg [Capsella rubella]	386	383	1.00E-159	99.2	81.3	87.6	hypothetical protein CARUB_v10011209mg	gbpln	Capsella rubella	AT1G09860.1 | Symbols: ATPUP16, PUP16 | purine permease 16 | chr1:3204136-3205287 REVERSE LENGTH=383	386	383	1.00E-161	99.2	81.1	87.0

Rsa1.0_01537.1_g27732.t1	ref|XP_002889774.1| histidine acid phosphatase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335616|gb|EFH66033.1| histidine acid phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	487	487	0	100.0	92.0	95.1	histidine acid phosphatase family protein	gbpln	Arabidopsis lyrata	AT1G09870.1 | Symbols: | histidine acid phosphatase family protein | chr1:3205817-3208444 FORWARD LENGTH=487	487	487	0	100.0	91.8	94.7
Rsa1.0_01537.1_g27733.t1	ref|XP_002892532.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338374|gb|EFH68791.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	695	664	0	95.5	82.4	89.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G09880.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr1:3208828-3211653 REVERSE LENGTH=631	695	631	0	90.8	77.7	84.6
Rsa1.0_01537.1_g27734.t1	ref|XP_002892533.1| hypothetical protein ARALYDRAFT_334271 [Arabidopsis lyrata subsp. lyrata] gi|297338375|gb|EFH68792.1| hypothetical protein ARALYDRAFT_334271 [Arabidopsis lyrata subsp. lyrata]	633	633	0	100.0	94.0	97.9	hypothetical protein ARALYDRAFT_334271	gbpln	Arabidopsis lyrata	AT1G09890.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr1:3214237-3217386 REVERSE LENGTH=617	633	617	0	97.5	91.0	95.3
Rsa1.0_01537.1_g27735.t1	ref|XP_002889775.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297335617|gb|EFH66034.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	597	598	0	100.2	90.6	95.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G09900.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:3218133-3219929 FORWARD LENGTH=598	597	598	0	100.2	89.8	94.8
Rsa1.0_01537.1_g27736.t1	ref|NP_172462.2| rhamnogalacturonate lyase-like protein [Arabidopsis thaliana] gi|332190392|gb|AEE28513.1| rhamnogalacturonate lyase-like protein [Arabidopsis thaliana]	684	675	0	98.7	89.8	92.7	rhamnogalacturonate lyase-like protein	gbpln	Arabidopsis thaliana	AT1G09910.1 | Symbols: | Rhamnogalacturonate lyase family protein | chr1:3220151-3224451 REVERSE LENGTH=675	684	675	0	98.7	89.8	92.7
Rsa1.0_01537.1_g27737.t1	gb|EOA38541.1| hypothetical protein CARUB_v10010346mg [Capsella rubella]	200	197	1.00E-98	98.5	85.5	93.0	hypothetical protein CARUB_v10010346mg	gbpln	Capsella rubella	AT1G09920.1 | Symbols: | TRAF-type zinc finger-related | chr1:3224863-3226860 REVERSE LENGTH=192	200	192	2.00E-97	96.0	83.5	90.0
Rsa1.0_01537.1_g27738.t1	ref|XP_002892536.1| hypothetical protein ARALYDRAFT_312036 [Arabidopsis lyrata subsp. lyrata] gi|297338378|gb|EFH68795.1| hypothetical protein ARALYDRAFT_312036 [Arabidopsis lyrata subsp. lyrata]	192	259	1.00E-61	134.9	63.5	74.5	hypothetical protein ARALYDRAFT_312036	gbpln	Arabidopsis lyrata	AT1G09932.1 | Symbols: | Phosphoglycerate mutase family protein | chr1:3230716-3233027 REVERSE LENGTH=260	192	260	4.00E-59	135.4	60.9	71.9
Rsa1.0_01537.1_g27739.t1	gb|EOA40544.1| hypothetical protein CARUB_v10009272mg [Capsella rubella]	341	416	1.00E-129	122.0	72.7	85.0	hypothetical protein CARUB_v10009272mg	gbpln	Capsella rubella	AT1G10150.1 | Symbols: | Carbohydrate-binding protein | chr1:3326160-3327404 FORWARD LENGTH=414	341	414	1.00E-128	121.4	71.0	83.3
Rsa1.0_01537.1_g27740.t1	ref|NP_683296.1| phloem protein 2-A10 [Arabidopsis thaliana] gi|332190427|gb|AEE28548.1| phloem protein 2-A10 [Arabidopsis thaliana]	188	184	2.00E-90	97.9	85.1	91.5	phloem protein 2-A10	gbpln	Arabidopsis thaliana	AT1G10155.1 | Symbols: ATPP2-A10, PP2-A10 | phloem protein 2-A10 | chr1:3327637-3328448 REVERSE LENGTH=184	188	184	9.00E-93	97.9	85.1	91.5
Rsa1.0_01537.1_g27741.t1	ref|XP_002892551.1| NF-X1 type zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297338393|gb|EFH68810.1| NF-X1 type zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	1112	1134	0	102.0	85.1	89.5	NF-X1 type zinc finger family protein	gbpln	Arabidopsis lyrata	AT1G10170.1 | Symbols: ATNFXL1, NFXL1 | NF-X-like 1 | chr1:3333925-3337491 REVERSE LENGTH=1188	1112	1188	0	106.8	85.2	90.3
Rsa1.0_01537.1_g27742.t1	gb|EOA25215.1| hypothetical protein CARUB_v10018528mg, partial [Capsella rubella]	118	103	1.00E-21	87.3	41.5	56.8	hypothetical protein CARUB_v10018528mg, partial	gbpln	Capsella rubella	AT5G66870.1 | Symbols: ASL1, LBD36 | ASYMMETRIC LEAVES 2-like 1 | chr5:26706621-26707562 FORWARD LENGTH=313	118	313	6.00E-21	265.3	39.0	58.5
Rsa1.0_01537.1_g27743.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01537.1_g27744.t1	ref|NP_172491.1| transcription factor lim1 [Arabidopsis thaliana] gi|13926190|gb|AAK49575.1|AF370569_1 similar to transcription factor SF3 (pir|IS37656) [Arabidopsis thaliana] gi|21553513|gb|AAM62606.1| putative transcription factor [Arabidopsis thaliana] gi|332190431|gb|AEE28552.1| transcription factor lim1 [Arabidopsis thaliana]	191	190	1.00E-105	99.5	98.4	99.0	transcription factor lim1	gbpln	Arabidopsis thaliana	AT1G10200.1 | Symbols: WLIM1 | GATA type zinc finger transcription factor family protein | chr1:3346677-3347763 REVERSE LENGTH=190	191	190	1.00E-108	99.5	98.4	99.0

Rsa1.0_01537.1.g27745.t2	ref|NP_172492.1| mitogen-activated protein kinase 1 [Arabidopsis thaliana] gi|79317509|ref|NP_001031017.1| mitogen-activated protein kinase 1 [Arabidopsis thaliana] gi|21431792|sp|Q39021.2|MPK1_ARATH RecName: Full=Mitogen-activated protein kinase 1; Short=AtMPK1; Short=MAP kinase 1 gi|4914323|gb|AAD32871.1|AC005489_9 F14N23.9 [Arabidopsis thaliana] gi|16649135|gb|AAL24419.1| putative mitogen-activated protein kinase homolog 7 [Arabidopsis thaliana] gi|23197708|gb|AAN15381.1| putative mitogen-activated protein kinase homolog 7 [Arabidopsis thaliana] gi|332190432|gb|AEE28553.1| mitogen-activated protein kinase 1 [Arabidopsis thaliana] gi|332190433|gb|AEE28554.1| mitogen-activated protein kinase 1 [Arabidopsis thaliana]	180	370	9.00E-94	205.6	91.7	94.4	mitogen-activated protein kinase 1	gbpln	Arabidopsis thaliana	AT1G10210.2 | Symbols: ATMPK1, MPK1 | mitogen-activated protein kinase 1 | chr1:3349579-3350776 FORWARD LENGTH=370	180	370	4.00E-96	205.6	91.7	94.4
Rsa1.0_01537.1.g27746.t1	gb|EOA37093.1| hypothetical protein CARUB_v10010274mg [Capsella rubella]	208	216	9.00E-71	103.8	73.6	84.1	hypothetical protein CARUB_v10010274mg	gbpln	Capsella rubella	AT1G59590.1 | Symbols: ZCF37 | ZCF37 | chr1:21887860-21888495 FORWARD LENGTH=211	208	211	6.00E-60	101.4	57.7	70.7
Rsa1.0_01538.1.g27747.t1	ref|XP_002888655.1| hypothetical protein ARALYDRAFT_894597 [Arabidopsis lyrata subsp. lyrata] gi|297334496|gb|EFH64914.1| hypothetical protein ARALYDRAFT_894597 [Arabidopsis lyrata subsp. lyrata]	198	251	4.00E-33	126.8	56.1	67.2	hypothetical protein ARALYDRAFT_894597	gbpln	Arabidopsis lyrata	AT1G68340.1 | Symbols: | Protein of unknown function (DUF1639) | chr1:25614440-25615335 REVERSE LENGTH=246	198	246	2.00E-32	124.2	52.0	66.2
Rsa1.0_01538.1.g27748.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01538.1.g27749.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1310	2726	0	208.1	54.5	72.1	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1310	158	2.00E-34	12.1	5.3	6.6
Rsa1.0_01538.1.g27750.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1999	1274	0	63.7	26.1	36.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1999	575	3.00E-63	28.8	8.1	12.4
Rsa1.0_01538.1.g27751.t1	emb|CAC41366.1| enoyl-[acyl-carrier protein] reductase [Brassica napus]	368	385	0	104.6	97.0	97.6	enoyl-	gbpln	Brassica napus	AT2G05990.2 | Symbols: MOD1, ENR1 | NAD(P)-binding Rossmann-fold superfamily protein | chr2:2322876-2324867 FORWARD LENGTH=390	368	390	0	106.0	91.0	95.1
Rsa1.0_01539.1.g27752.t1	gb|ABD65112.1| hypothetical protein 31.t00014 [Brassica oleracea]	82	122	2.00E-16	148.8	50.0	62.2	hypothetical protein 31.t00014	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01539.1.g27753.t1	dbj|BAJ34000.1| unnamed protein product [Thellungiella halophila]	268	274	1.00E-112	102.2	81.7	85.8	unnamed protein product	----	----	AT1G08570.1 | Symbols: ACHT4 | atypical CYS HIS rich thioredoxin 4 | chr1:2713059-2714312 FORWARD LENGTH=275	268	275	1.00E-113	102.6	78.0	82.8
Rsa1.0_01539.1.g27754.t1	ref|NP_172334.1| uncharacterized protein [Arabidopsis thaliana] gi|9802580|gb|AAF99782.1|AC003981_32 F22O13.6 [Arabidopsis thaliana] gi|38454044|gb|AAR20716.1| At1g08580 [Arabidopsis thaliana] gi|41349904|gb|AAS00337.1| At1g08580 [Arabidopsis thaliana] gi|332190190|gb|AEE28311.1| uncharacterized protein AT1G08580 [Arabidopsis thaliana]	123	123	3.00E-43	100.0	88.6	92.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G08580.1 | Symbols: | unknown protein; Has 39 Blast hits to 39 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr1:2715296-2716351 REVERSE LENGTH=123	123	123	6.00E-46	100.0	88.6	92.7
Rsa1.0_01539.1.g27755.t1	ref|NP_001184937.1| DEAD-like helicase domain-containing protein [Arabidopsis thaliana] gi|334182393|ref|NP_001184938.1| DEAD-like helicase domain-containing protein [Arabidopsis thaliana] gi|334182395|ref|NP_001184939.1| DEAD-like helicase domain-containing protein [Arabidopsis thaliana] gi|332190193|gb|AEE28314.1| DEAD-like helicase domain-containing protein [Arabidopsis thaliana] gi|332190194|gb|AEE28315.1| DEAD-like helicase domain-containing protein [Arabidopsis thaliana] gi|332190195|gb|AEE28316.1| DEAD-like helicase domain-containing protein [Arabidopsis thaliana]	1391	1479	0	106.3	71.2	80.0	DEAD-like helicase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G08600.2 | Symbols: ATRX | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:2724562-2733431 FORWARD LENGTH=1479	1391	1479	0	106.3	71.2	80.0

Rsa1.0_01539.1.g27756.t1	ref|XP_002892464.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338306|gb|EFH68723.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	534	555	0	103.9	77.3	89.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G08610.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:2733788-2735467 REVERSE LENGTH=559	534	559	0	104.7	74.0	86.0
Rsa1.0_01539.1.g27757.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01539.1.g27758.t2	ref|XP_002892465.1| hypothetical protein ARALYDRAFT_470930 [Arabidopsis lyrata subsp. lyrata] gi|297338307|gb|EFH68724.1| hypothetical protein ARALYDRAFT_470930 [Arabidopsis lyrata subsp. lyrata]	357	358	0	100.3	91.6	95.8	hypothetical protein ARALYDRAFT_470930	gbpln	Arabidopsis lyrata	AT1G08630.4 | Symbols: THA1 | threonine aldolase 1 | chr1:2743948-2745685 REVERSE LENGTH=358	357	358	0	100.3	90.5	95.8
Rsa1.0_01539.1.g27759.t4	ref|XP_002892467.1| glycosyl transferase family 29 protein [Arabidopsis lyrata subsp. lyrata] gi|297338309|gb|EFH68726.1| glycosyl transferase family 29 protein [Arabidopsis lyrata subsp. lyrata]	490	474	0	96.7	82.2	86.5	glycosyl transferase family 29 protein	gbpln	Arabidopsis lyrata	AT1G08660.1 | Symbols: MGP2 | MALE GAMETOPHYTE DEFECTIVE 2 | chr1:2757116-2759677 REVERSE LENGTH=474	490	474	0	96.7	82.2	86.5
Rsa1.0_01539.1.g27760.t1	gb|ABD65112.1| hypothetical protein 31.t00014 [Brassica oleracea]	137	122	7.00E-32	89.1	54.7	67.9	hypothetical protein 31.t00014	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01540.1.g27761.t2	ref|XP_002877961.1| hypothetical protein ARALYDRAFT_906825 [Arabidopsis lyrata subsp. lyrata] gi|297323799|gb|EFH54220.1| hypothetical protein ARALYDRAFT_906825 [Arabidopsis lyrata subsp. lyrata]	471	467	0	99.2	96.6	97.7	hypothetical protein ARALYDRAFT_906825	gbpln	Arabidopsis lyrata	AT3G54190.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:20061759-20063880 REVERSE LENGTH=467	471	467	0	99.2	95.8	97.7
Rsa1.0_01540.1.g27762.t3	ref|XP_002876244.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322082|gb|EFH52503.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	380	336	1.00E-143	88.4	73.4	79.5	predicted protein	gbpln	Arabidopsis lyrata	AT3G54170.1 | Symbols: ATFIP37, FIP37 | FKBP12 interacting protein 37 | chr3:20056848-20059396 FORWARD LENGTH=330	380	330	1.00E-135	86.8	70.5	76.8
Rsa1.0_01540.1.g27763.t1	gb|EOA25633.1| hypothetical protein CARUB_v10018982mg [Capsella rubella]	310	311	1.00E-155	100.3	85.2	93.2	hypothetical protein CARUB_v10018982mg	gbpln	Capsella rubella	AT3G54150.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:20050802-20052742 REVERSE LENGTH=323	310	323	1.00E-154	104.2	83.2	91.3
Rsa1.0_01540.1.g27764.t1	gb|EOA25617.1| hypothetical protein CARUB_v10018965mg [Capsella rubella]	284	281	1.00E-128	98.9	85.9	93.7	hypothetical protein CARUB_v10018965mg	gbpln	Capsella rubella	AT3G54130.1 | Symbols: | Josephin family protein | chr3:20042895-20044429 REVERSE LENGTH=280	284	280	1.00E-128	98.6	84.5	91.5
Rsa1.0_01540.1.g27765.t1	gb|EOA25084.1| hypothetical protein CARUB_v10018392mg [Capsella rubella]	203	203	3.00E-82	100.0	78.8	87.2	hypothetical protein CARUB_v10018392mg	gbpln	Capsella rubella	AT3G54120.1 | Symbols: | Reticulon family protein | chr3:20041269-20042133 REVERSE LENGTH=203	203	203	1.00E-81	100.0	79.3	87.7
Rsa1.0_01540.1.g27766.t1	gb|EOA24448.1| hypothetical protein CARUB_v10017704mg [Capsella rubella]	305	306	1.00E-166	100.3	93.8	97.4	hypothetical protein CARUB_v10017704mg	gbpln	Capsella rubella	AT3G54110.1 | Symbols: ATPUMP1, UCP, PUMP1, ATUCP1, UCP1 | plant uncoupling mitochondrial protein 1 | chr3:20038890-20040996 FORWARD LENGTH=306	305	306	1.00E-168	100.3	94.1	97.4
Rsa1.0_01540.1.g27767.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01540.1.g27768.t2	ref|XP_002877955.1| hypothetical protein ARALYDRAFT_906813 [Arabidopsis lyrata subsp. lyrata] gi|297323793|gb|EFH54214.1| hypothetical protein ARALYDRAFT_906813 [Arabidopsis lyrata subsp. lyrata]	648	637	0	98.3	85.5	90.9	hypothetical protein ARALYDRAFT_906813	gbpln	Arabidopsis lyrata	AT3G54100.1 | Symbols: | O-fucosyltransferase family protein | chr3:20034451-20037874 REVERSE LENGTH=638	648	638	0	98.5	84.1	90.1
Rsa1.0_01540.1.g27769.t1	gb|EOA23931.1| hypothetical protein CARUB_v10017145mg [Capsella rubella]	461	475	0	103.0	88.5	94.4	hypothetical protein CARUB_v10017145mg	gbpln	Capsella rubella	AT3G54090.1 | Symbols: FLN1 | fructokinase-like 1 | chr3:20028145-20029835 FORWARD LENGTH=471	461	471	0	102.2	87.6	94.8
Rsa1.0_01540.1.g27770.t1	gb|EOA25032.1| hypothetical protein CARUB_v10018338mg [Capsella rubella]	101	78	6.00E-31	77.2	63.4	71.3	hypothetical protein CARUB_v10018338mg	gbpln	Capsella rubella	AT3G54085.2 | Symbols: | Yos1-like protein | chr3:20026780-20027016 REVERSE LENGTH=78	101	78	1.00E-32	77.2	62.4	69.3
Rsa1.0_01540.1.g27771.t1	ref|XP_002876239.1| hypothetical protein ARALYDRAFT_348499 [Arabidopsis lyrata subsp. lyrata] gi|297322077|gb|EFH52498.1| hypothetical protein ARALYDRAFT_348499 [Arabidopsis lyrata subsp. lyrata]	329	436	2.00E-96	132.5	64.4	73.3	hypothetical protein ARALYDRAFT_348499	gbpln	Arabidopsis lyrata	AT3G54080.1 | Symbols: | Concanavalin A-like lectin family protein | chr3:20025397-20026449 FORWARD LENGTH=350	329	350	4.00E-90	106.4	59.6	69.0
Rsa1.0_01540.1.g27772.t1	gb|EOA24108.1| hypothetical protein CARUB_v10017339mg [Capsella rubella]	416	415	0	99.8	91.3	95.7	hypothetical protein CARUB_v10017339mg	gbpln	Capsella rubella	AT3G54050.2 | Symbols: HCEF1 | high cyclic electron flow 1 | chr3:20016951-20018527 FORWARD LENGTH=417	416	417	0	100.2	85.8	88.9

Rsa1.0_01540.1.g27773.t1	ref|XP_002877953.1| hypothetical protein ARALYDRAFT_485800 [Arabidopsis lyrata subsp. lyrata] gi|297323791|gb|EFH54212.1| hypothetical protein ARALYDRAFT_485800 [Arabidopsis lyrata subsp. lyrata]	182	183	3.00E-89	100.5	89.6	95.6	hypothetical protein ARALYDRAFT_485800	gbpln	Arabidopsis lyrata	AT3G54040.1 | Symbols: | PAR1 protein | chr3:20014032-20015299 REVERSE LENGTH=183	182	183	4.00E-89	100.5	85.7	95.1
Rsa1.0_01541.1.g27774.t1	ref|XP_002867688.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297313524|gb|EFH43947.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	240	444	1.00E-116	185.0	84.6	90.4	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT4G23820.1 | Symbols: | Pectin lyase-like superfamily protein | chr4:12397217-12400050 REVERSE LENGTH=444	240	444	1.00E-118	185.0	84.6	90.0
Rsa1.0_01541.1.g27775.t1	ref|XP_002869762.1| hypothetical protein ARALYDRAFT_492485 [Arabidopsis lyrata subsp. lyrata] gi|297315598|gb|EFH46021.1| hypothetical protein ARALYDRAFT_492485 [Arabidopsis lyrata subsp. lyrata]	606	590	0	97.4	77.1	85.3	hypothetical protein ARALYDRAFT_492485	gbpln	Arabidopsis lyrata	AT4G23840.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:12400379-12403190 FORWARD LENGTH=597	606	597	0	98.5	77.1	85.1
Rsa1.0_01541.1.g27776.t1	ref|NP_194118.1| uncharacterized protein [Arabidopsis thaliana] gi|4972091|emb|CAB43887.1| putative protein [Arabidopsis thaliana] gi|7269236|emb|CAB81305.1| putative protein [Arabidopsis thaliana] gi|15450916|gb|AAK96729.1| putative protein [Arabidopsis thaliana] gi|25084175|gb|AAN72191.1| putative protein [Arabidopsis thaliana] gi|332659416|gb|AEE84816.1| uncharacterized protein AT4G23870 [Arabidopsis thaliana]	113	116	9.00E-38	102.7	85.8	92.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G23870.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11020.1); Has 12 Blast hits to 12 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:12414409-12414759 FORWARD LENGTH=116	113	116	1.00E-40	102.7	85.8	92.9
Rsa1.0_01541.1.g27777.t1	gb|EOA17457.1| hypothetical protein CARUB_v10005780mg [Capsella rubella]	199	197	7.00E-76	99.0	72.9	81.4	hypothetical protein CARUB_v10005780mg	gbpln	Capsella rubella	AT4G23880.1 | Symbols: | unknown protein; Has 73 Blast hits to 69 proteins in 22 species: Archae - 0; Bacteria - 4; Metazoa - 9; Fungi - 2; Plants - 18; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink). | chr4:12415789-12416388 REVERSE LENGTH=199	199	199	4.00E-73	100.0	72.9	82.4
Rsa1.0_01541.1.g27778.t1	ref|XP_002869758.1| hypothetical protein ARALYDRAFT_914208 [Arabidopsis lyrata subsp. lyrata] gi|297315594|gb|EFH46017.1| hypothetical protein ARALYDRAFT_914208 [Arabidopsis lyrata subsp. lyrata]	174	76	4.00E-11	43.7	21.8	22.4	hypothetical protein ARALYDRAFT_914208	gbpln	Arabidopsis lyrata	AT4G23885.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24165.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12419472-12420240 FORWARD LENGTH=77	174	77	1.00E-12	44.3	20.1	21.3
Rsa1.0_01541.1.g27779.t1	gb|EOA18489.1| hypothetical protein CARUB_v10007040mg [Capsella rubella]	73	248	1.00E-30	339.7	91.8	94.5	hypothetical protein CARUB_v10007040mg	gbpln	Capsella rubella	AT4G23890.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3252 (InterPro:IPR021659); Has 287 Blast hits to 287 proteins in 81 species: Archae - 0; Bacteria - 118; Metazoa - 12; Fungi - 6; Plants - 40; Viruses - 0; Other Eukaryotes - 111 (source: NCBI BLink). | chr4:12420593-12421345 REVERSE LENGTH=250	73	250	2.00E-33	342.5	91.8	94.5
Rsa1.0_01541.1.g27780.t1	ref|NP_974602.1| Pleckstrin homology (PH) domain-containing protein [Arabidopsis thaliana] gi|145333884|ref|NP_001078437.1| Pleckstrin homology (PH) domain-containing protein [Arabidopsis thaliana] gi|332659421|gb|AEE84821.1| Pleckstrin homology (PH) domain-containing protein [Arabidopsis thaliana] gi|332659422|gb|AEE84822.1| Pleckstrin homology (PH) domain-containing protein [Arabidopsis thaliana]	253	247	1.00E-111	97.6	82.2	89.3	Pleckstrin homology (PH) domain-containing protein	gbpln	Arabidopsis thaliana	AT4G23895.2 | Symbols: | Pleckstrin homology (PH) domain-containing protein | chr4:12422883-12424146 FORWARD LENGTH=247	253	247	1.00E-114	97.6	82.2	89.3

Rsa1.0_01541.1.g27781.t2	ref|XP_002869754.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 2 [Arabidopsis lyrata subsp. lyrata] gi|297315590|gb|EFH46013.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 2 [Arabidopsis lyrata subsp. lyrata]	348	350	0	100.6	92.2	95.1	UDP-D-glucose/UDP-D-galactose 4-epimerase 2	gbpln	Arabidopsis lyrata	AT4G23920.1 | Symbols: UGE2, ATUGE2 | UDP-D-glucose/UDP-D-galactose 4-epimerase 2 | chr4:12431416-12433666 FORWARD LENGTH=350	348	350	0	100.6	91.1	94.8
Rsa1.0_01541.1.g27782.t1	gb|AFD01308.1| auxin response factor 9 [Brassica rapa subsp. pekinensis]	638	629	0	98.6	92.8	94.7	auxin response factor 9	gbpln	Brassica rapa	AT4G23980.2 | Symbols: ARF9 | auxin response factor 9 | chr4:12451592-12454737 FORWARD LENGTH=636	638	636	0	99.7	81.8	88.7
Rsa1.0_01542.1.g27783.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01542.1.g27784.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01542.1.g27785.t1	emb|CAN71052.1| hypothetical protein VITISV_003719 [Vitis vinifera]	258	944	2.00E-47	365.9	39.1	48.1	hypothetical protein VITISV_003719	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01542.1.g27786.t1	gb|ABD65073.1| hypothetical protein 27.t00059 [Brassica oleracea]	178	341	2.00E-45	191.6	49.4	59.6	hypothetical protein 27.t00059	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01542.1.g27787.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	1106	1103	1.00E-169	99.7	29.7	36.0	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01542.1.g27788.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	669	695	1.00E-173	103.9	55.9	68.8	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	669	681	1.00E-14	101.8	4.9	8.2
Rsa1.0_01542.1.g27789.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1168	1838	1.00E-165	157.4	25.0	32.4	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01542.1.g27790.t5	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1779	1838	1.00E-166	103.3	18.5	24.6	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01542.1.g27791.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01543.1.g27792.t1	gb|EOA16045.1| hypothetical protein CARUB_v10004170mg [Capsella rubella]	792	792	0	100.0	81.2	86.0	hypothetical protein CARUB_v10004170mg	gbpln	Capsella rubella	AT4G14990.1 | Symbols: | Topoisomerase II-associated protein PAT1 | chr4:8566259-8569511 REVERSE LENGTH=787	792	787	0	99.4	81.1	85.6
Rsa1.0_01543.1.g27793.t1	ref|NP_193236.1| 60S ribosomal protein L27-3 [Arabidopsis thaliana] gi|3123264|sp|P51419.2|RL273_ARATH RecName: Full=60S ribosomal protein L27-3 gi|2244857|emb|CAB10279.1| ribosomal protein [Arabidopsis thaliana] gi|7268246|emb|CAB78542.1| ribosomal protein [Arabidopsis thaliana] gi|17381062|gb|AAL36343.1| putative ribosomal protein [Arabidopsis thaliana] gi|20466061|gb|AAM20365.1| putative ribosomal protein [Arabidopsis thaliana] gi|21553620|gb|AAM62713.1| ribosomal protein [Arabidopsis thaliana] gi|110736737|dbj|BAF00331.1| ribosomal protein [Arabidopsis thaliana] gi|332658135|gb|AEE83535.1| 60S ribosomal protein L27-3 [Arabidopsis thaliana]	135	135	2.00E-69	100.0	96.3	99.3	60S ribosomal protein L27-3	gbpln	Arabidopsis thaliana	AT4G15000.1 | Symbols: | Ribosomal L27e protein family | chr4:8571896-8572303 FORWARD LENGTH=135	135	135	5.00E-72	100.0	96.3	99.3

<table>
<tr><td>Rsa1.0_01543.1.g27794.t1</td><td>ref|NP_567453.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|42572913|ref|NP_974553.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|42572915|ref|NP_974554.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|15451218|gb|AAK96880.1| Unknown protein [Arabidopsis thaliana] gi|30725620|gb|AAP37832.1| At4g15610 [Arabidopsis thaliana] gi|222424236|dbj|BAH20076.1| AT4G15010 [Arabidopsis thaliana] gi|332658137|gb|AEE83537.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|332658138|gb|AEE83538.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana] gi|332658139|gb|AEE83539.1| Mitochondrial substrate carrier family protein [Arabidopsis thaliana]</td><td>379</td><td>378</td><td>0</td><td>99.7</td><td>91.6</td><td>95.5</td><td>Mitochondrial substrate carrier family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15010.2 | Symbols: | Mitochondrial substrate carrier family protein | chr4:8573125-8574864 REVERSE LENGTH=378</td><td>379</td><td>378</td><td>0</td><td>99.7</td><td>91.6</td><td>95.5</td></tr>
<tr><td>Rsa1.0_01543.1.g27795.t1</td><td>gb|AAM98154.1| putative protein [Arabidopsis thaliana]</td><td>773</td><td>768</td><td>0</td><td>99.4</td><td>77.5</td><td>85.8</td><td>putative protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15020.2 | Symbols: | hAT transposon superfamily | chr4:8575806-8578372 FORWARD LENGTH=768</td><td>773</td><td>768</td><td>0</td><td>99.4</td><td>77.4</td><td>85.8</td></tr>
<tr><td>Rsa1.0_01543.1.g27796.t1</td><td>ref|XP_002870265.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297316101|gb|EFH46524.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>290</td><td>245</td><td>3.00E-98</td><td>84.5</td><td>68.3</td><td>72.1</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G15030.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Folate-sensitive fragile site protein Fra10Ac1 (InterPro:IPR019129); Has 8455 Blast hits to 5700 proteins in 376 species: Archae - 6; Bacteria - 264; Metazoa - 3820; Fungi - 744; Plants - 645; Viruses - 76; Other Eukaryotes - 2900 (source: NCBI BLink). | chr4:8578989-8581180 FORWARD LENGTH=278</td><td>290</td><td>278</td><td>1.00E-100</td><td>95.9</td><td>67.2</td><td>70.7</td></tr>
<tr><td>Rsa1.0_01543.1.g27797.t1</td><td>ref|XP_002868235.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314071|gb|EFH44494.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>403</td><td>403</td><td>1.00E-152</td><td>100.0</td><td>63.0</td><td>78.4</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G10190.1 | Symbols: | Protein of Unknown Function (DUF239) | chr1:3343765-3345591 REVERSE LENGTH=396</td><td>403</td><td>396</td><td>1.00E-149</td><td>98.3</td><td>61.0</td><td>75.7</td></tr>
<tr><td>Rsa1.0_01543.1.g27798.t1</td><td>gb|EOA18357.1| hypothetical protein CARUB_v10006878mg, partial [Capsella rubella]</td><td>436</td><td>567</td><td>1.00E-114</td><td>130.0</td><td>53.7</td><td>66.3</td><td>hypothetical protein CARUB_v10006878mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G00315.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:137404-138888 FORWARD LENGTH=441</td><td>436</td><td>441</td><td>1.00E-111</td><td>101.1</td><td>52.8</td><td>69.3</td></tr>
<tr><td>Rsa1.0_01543.1.g27799.t1</td><td>gb|EOA16119.1| hypothetical protein CARUB_v10004251mg [Capsella rubella]</td><td>720</td><td>715</td><td>0</td><td>99.3</td><td>85.0</td><td>90.6</td><td>hypothetical protein CARUB_v10004251mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G15080.1 | Symbols: | DHHC-type zinc finger family protein | chr4:8609085-8612229 REVERSE LENGTH=718</td><td>720</td><td>718</td><td>0</td><td>99.7</td><td>84.9</td><td>90.4</td></tr>
<tr><td>Rsa1.0_01543.1.g27800.t1</td><td>gb|EOA19229.1| hypothetical protein CARUB_v100041781mg, partial [Capsella rubella]</td><td>111</td><td>118</td><td>5.00E-15</td><td>106.3</td><td>36.9</td><td>40.5</td><td>hypothetical protein CARUB_v100041781mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G15090.1 | Symbols: FAR1 | FRS (FAR1 Related Sequences) transcription factor family | chr4:8614806-8617870 FORWARD LENGTH=827</td><td>111</td><td>827</td><td>5.00E-15</td><td>745.0</td><td>49.5</td><td>64.9</td></tr>
<tr><td>Rsa1.0_01543.1.g27801.t1</td><td>ref|NP_567458.1| VQ motif-containing protein [Arabidopsis thaliana] gi|2244869|emb|CAB10291.1| hypothetical protein [Arabidopsis thaliana] gi|7268258|emb|CAB78554.1| hypothetical protein [Arabidopsis thaliana] gi|26450073|dbj|BAC42156.1| unknown protein [Arabidopsis thaliana] gi|28973003|gb|AAO63826.1| unknown protein [Arabidopsis thaliana] gi|332658158|gb|AEE83558.1| VQ motif-containing protein [Arabidopsis thaliana]</td><td>181</td><td>193</td><td>1.00E-44</td><td>106.6</td><td>72.4</td><td>84.0</td><td>VQ motif-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G15120.1 | Symbols: | VQ motif-containing protein | chr4:8634779-8635360 FORWARD LENGTH=193</td><td>181</td><td>193</td><td>4.00E-47</td><td>106.6</td><td>72.4</td><td>84.0</td></tr>
<tr><td>Rsa1.0_01543.1.g27802.t1</td><td>gb|EOA17119.1| hypothetical protein CARUB_v10005379mg [Capsella rubella]</td><td>226</td><td>294</td><td>5.00E-98</td><td>130.1</td><td>81.4</td><td>90.3</td><td>hypothetical protein CARUB_v10005379mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G15130.1 | Symbols: ATCCT2, CCT2 | phosphorylcholine cytidylyltransferase2 | chr4:8637793-8639388 FORWARD LENGTH=304</td><td>226</td><td>304</td><td>1.00E-97</td><td>134.5</td><td>81.9</td><td>92.5</td></tr>
<tr><td>Rsa1.0_01544.1.g27803.t1</td><td>ref|XP_002877772.1| hypothetical protein ARALYDRAFT_906415 [Arabidopsis lyrata subsp. lyrata] gi|297323610|gb|EFH54031.1| hypothetical protein ARALYDRAFT_906415 [Arabidopsis lyrata subsp. lyrata]</td><td>156</td><td>154</td><td>2.00E-56</td><td>98.7</td><td>82.7</td><td>86.5</td><td>hypothetical protein ARALYDRAFT_906415</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G50800.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66580.1); Has 249 Blast hits to 249 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 249; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:18882444-18882902 REVERSE LENGTH=152</td><td>156</td><td>152</td><td>5.00E-58</td><td>97.4</td><td>81.4</td><td>85.9</td></tr>
</table>

Rsa1.0_01544.1.g27804.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01544.1.g27805.t1	gb|EOA24769.1| hypothetical protein CARUB_v10018048mg [Capsella rubella]	179	202	4.00E-78	112.8	86.6	89.9	hypothetical protein CARUB_v10018048mg	gbpln	Capsella rubella	AT3G50770.1 | Symbols: CML41 | calmodulin-like 41 | chr3:18873987-18874604 FORWARD LENGTH=205	179	205	1.00E-77	114.5	84.4	89.4
Rsa1.0_01544.1.g27806.t1	ref|NP_190645.3| putative galacturonosyltransferase-like 2 [Arabidopsis thaliana] gi|75193862|sp|Q9S7G2.1|GATL2_ARATH RecName: Full=Probable galacturonosyltransferase-like 2 gi|4835227|emb|CAB42905.1| glycosyltransferase-like protein [Arabidopsis thaliana] gi|6561979|emb|CAB62445.1| putative protein [Arabidopsis thaliana] gi|44917561|gb|AAS49105.1| At3g50760 [Arabidopsis thaliana] gi|62320344|dbj|BAD94712.1| hypothetical protein [Arabidopsis thaliana] gi|332645185|gb|AEE78706.1| putative galacturonosyltransferase-like 2 [Arabidopsis thaliana]	342	341	0	99.7	90.9	95.3	putative galacturonosyltransferase-like 2	gbpln	Arabidopsis thaliana	AT3G50760.1 | Symbols: GATL2 | galacturonosyltransferase-like 2 | chr3:18868074-18869099 FORWARD LENGTH=341	342	341	0	99.7	90.9	95.3
Rsa1.0_01544.1.g27807.t1	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	171	954	1.00E-21	557.9	33.9	41.5	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01544.1.g27808.t1	ref|XP_002878187.1| hypothetical protein ARALYDRAFT_348875 [Arabidopsis lyrata subsp. lyrata] gi|297324025|gb|EFH54446.1| hypothetical protein ARALYDRAFT_348875 [Arabidopsis lyrata subsp. lyrata]	205	309	5.00E-31	150.7	35.6	42.0	hypothetical protein ARALYDRAFT_348875	gbpln	Arabidopsis lyrata	AT3G58090.1 | Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr3:21512479-21513905 REVERSE LENGTH=271	205	271	3.00E-27	132.2	34.6	40.0
Rsa1.0_01544.1.g27809.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01544.1.g27810.t1	emb|CAB62318.1| putative protein [Arabidopsis thaliana]	424	466	1.00E-177	109.9	76.9	86.1	putative protein	gbpln	Arabidopsis thaliana	AT3G50390.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:18702137-18703546 FORWARD LENGTH=469	424	469	1.00E-180	110.6	76.9	86.1
Rsa1.0_01544.1.g27811.t1	gb|AAU44488.1| hypothetical protein AT3G50170 [Arabidopsis thaliana]	513	541	0	105.5	77.0	86.0	hypothetical protein AT3G50170	gbpln	Arabidopsis thaliana	AT3G50170.1 | Symbols: | Plant protein of unknown function (DUF247) | chr3:18601857-18603738 REVERSE LENGTH=541	513	541	0	105.5	76.8	85.8
Rsa1.0_01544.1.g27812.t1	gb|EOA23207.1| hypothetical protein CARUB_v10019135mg [Capsella rubella]	593	553	0	93.3	68.3	75.2	hypothetical protein CARUB_v10019135mg	gbpln	Capsella rubella	AT3G50140.1 | Symbols: | Plant protein of unknown function (DUF247) | chr3:18592472-18594562 REVERSE LENGTH=539	593	539	0	90.9	66.9	75.0
Rsa1.0_01544.1.g27813.t1	ref|XP_002877730.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323568|gb|EFH53989.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	581	564	0	97.1	75.7	80.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G50130.1 | Symbols: | Plant protein of unknown function (DUF247) | chr3:18589111-18591222 REVERSE LENGTH=564	581	564	0	97.1	74.9	80.9
Rsa1.0_01544.1.g27814.t1	gb|EOA23237.1| hypothetical protein CARUB_v10016996mg [Capsella rubella]	531	532	0	100.2	88.7	95.5	hypothetical protein CARUB_v10016996mg	gbpln	Capsella rubella	AT3G50120.1 | Symbols: | Plant protein of unknown function (DUF247) | chr3:18585157-18587246 REVERSE LENGTH=531	531	531	0	100.0	88.9	95.1
Rsa1.0_01545.1.g27815.t1	gb|EOA13275.1| hypothetical protein CARUB_v10026304mg [Capsella rubella]	189	486	3.00E-86	257.1	81.5	90.5	hypothetical protein CARUB_v10026304mg	gbpln	Capsella rubella	AT5G65380.1 | Symbols: | MATE efflux family protein | chr5:26123241-26126352 REVERSE LENGTH=486	189	486	2.00E-88	257.1	82.5	89.9
Rsa1.0_01545.1.g27816.t1	ref|NP_201341.1| mate efflux domain-containing protein [Arabidopsis thaliana] gi|14030731|gb|AAK53040.1|AF375456_1 AT5g65380/MNA5_11 [Arabidopsis thaliana] gi|9759618|dbj|BAB11560.1| unnamed protein product [Arabidopsis thaliana] gi|23506079|gb|AAN28899.1| At5g65380/MNA5_11 [Arabidopsis thaliana] gi|332010662|gb|AED98045.1| mate efflux domain-containing protein [Arabidopsis thaliana]	486	486	0	100.0	88.9	93.8	mate efflux domain-containing protein	gbpln	Arabidopsis thaliana	AT5G65380.1 | Symbols: | MATE efflux family protein | chr5:26123241-26126352 REVERSE LENGTH=486	486	486	0	100.0	88.9	93.8
Rsa1.0_01545.1.g27817.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01545.1.g27818.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01545.1.g27819.t1	dbj|BAJ34581.1| unnamed protein product [Thellungiella halophila]	298	286	1.00E-106	96.0	78.9	80.5	unnamed protein product	----	----	AT5G65410.1 | Symbols: ATHB25, ZFHD2, HB25, ZHD1 | homeobox protein 25 | chr5:26136179-26137018 FORWARD LENGTH=279	298	279	8.00E-98	93.6	76.5	77.5
Rsa1.0_01545.1.g27820.t1	gb|EOA13734.1| hypothetical protein CARUB_v10026812mg [Capsella rubella]	316	312	1.00E-149	98.7	84.8	89.9	hypothetical protein CARUB_v10026812mg	gbpln	Capsella rubella	AT5G65420.1 | Symbols: CYCD4;1 | CYCLIN D4;1 | chr5:26141592-26143750 REVERSE LENGTH=308	316	308	2.33E-156	97.5	83.2	88.3

Rsa1.0_01545.1_g27821.t1	ref|NP_851274.1| 14-3-3-like protein GF14 kappa [Arabidopsis thaliana] gi|12643286|sp|P48348.2|14338_ARATH RecName: Full=14-3-3-like protein GF14 kappa; AltName: Full=General regulatory factor 8 gi|5802794|gb|AAD51783.1|AF145300_1 14-3-3 protein GF14 kappa [Arabidopsis thaliana] gi|15293125|gb|AAK93673.1| putative 14-3-3 protein GF14kappa grf8 [Arabidopsis thaliana] gi|19310701|gb|AAL85081.1| putative 14-3-3 protein GF14kappa [Arabidopsis thaliana] gi|21537301|gb|AAM61642.1| 14-3-3 protein GF14kappa (grf8) [Arabidopsis thaliana] gi|332010669|gb|AED98052.1| 14-3-3-like protein GF14 kappa [Arabidopsis thaliana]	248	248	1.00E-137	100.0	96.0	98.4	14-3-3-like protein GF14 kappa	gbpln	Arabidopsis thaliana	AT5G65430.1 | Symbols: GRF8, 14-3-3KAPPA, GF14 KAPPA | general regulatory factor 8 | chr5:26148546-26150255 REVERSE LENGTH=248	248	248	1.00E-139	100.0	96.0	98.4
Rsa1.0_01545.1_g27822.t1	ref|XP_002864956.1| hypothetical protein ARALYDRAFT_332760 [Arabidopsis lyrata subsp. lyrata] gi|297310791|gb|EFH41215.1| hypothetical protein ARALYDRAFT_332760 [Arabidopsis lyrata subsp. lyrata]	744	1091	0	146.6	52.6	54.3	hypothetical protein ARALYDRAFT_332760	gbpln	Arabidopsis lyrata	AT5G65440.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24610.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26152015-26156896 FORWARD LENGTH=1050	744	1050	0	141.1	51.7	54.3
Rsa1.0_01545.1_g27823.t1	ref|XP_002864957.1| hypothetical protein ARALYDRAFT_332761 [Arabidopsis lyrata subsp. lyrata] gi|297310792|gb|EFH41216.1| hypothetical protein ARALYDRAFT_332761 [Arabidopsis lyrata subsp. lyrata]	511	731	0	143.1	70.1	80.6	hypothetical protein ARALYDRAFT_332761	gbpln	Arabidopsis lyrata	AT5G65450.1 | Symbols: UBP17 | ubiquitin-specific protease 17 | chr5:26157863-26161096 FORWARD LENGTH=731	511	731	0	143.1	70.8	79.3
Rsa1.0_01546.1_g27824.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01546.1_g27825.t1	ref|NP_174690.1| lectin protein kinase-like protein [Arabidopsis thaliana] gi|75338636|sp|Q9XID3.1|Y1343_ARATH RecName: Full=G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300; Flags: Precursor gi|5091617|gb|AAD39605.1|AC007454_4 Contains similarity to gi|479356 protein kinase PK1 from Zea mays, is a member of the PF|00954 S-locus glycoprotein family and contains a PF|00069 Eukaryotic protein kinase domain [Arabidopsis thaliana] gi|19699084|gb|AAL90909.1| At1g34300/F23M19_5 [Arabidopsis thaliana] gi|24111429|gb|AAN46865.1| At1g34300/F23M19_5 [Arabidopsis thaliana] gi|332193573|gb|AEE31694.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	772	829	0	107.4	60.9	74.0	lectin protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G34300.1 | Symbols: | lectin protein kinase family protein | chr1:12503450-12505939 FORWARD LENGTH=829	772	829	0	107.4	60.9	74.0
Rsa1.0_01546.1_g27826.t1	gb|EMJ23759.1| hypothetical protein PRUPE_ppa008371mg [Prunus persica]	145	335	7.00E-16	231.0	26.2	28.3	hypothetical protein PRUPE_ppa008371mg	gbpln	Prunus persica	AT5G55190.1 | Symbols: RAN3, ATRAN3 | RAN GTPase 3 | chr5:22392285-22393957 FORWARD LENGTH=221	145	221	3.00E-18	152.4	26.2	28.3
Rsa1.0_01546.1_g27827.t1	gb|AAN08437.1| hypothetical protein [Arabidopsis thaliana]	720	538	1.00E-136	74.7	37.8	46.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G43220.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:17964340-17965956 FORWARD LENGTH=538	720	538	1.00E-139	74.7	37.8	46.4
Rsa1.0_01546.1_g27828.t1	ref|XP_002872455.1| hypothetical protein ARALYDRAFT_489817 [Arabidopsis lyrata subsp. lyrata] gi|297318292|gb|EFH48714.1| hypothetical protein ARALYDRAFT_489817 [Arabidopsis lyrata subsp. lyrata]	234	233	1.00E-114	99.6	86.8	94.0	hypothetical protein ARALYDRAFT_489817	gbpln	Arabidopsis lyrata	AT4G09650.1 | Symbols: ATPD | ATP synthase delta-subunit gene | chr4:6100799-6101503 FORWARD LENGTH=234	234	234	1.00E-114	100.0	86.3	93.6

Rsa1.0_01546.1.g27829.t1	ref|NP_567007.1| glutamate carboxypeptidase II [Arabidopsis thaliana] gi|332278204|sp|Q9M1S8.3|GCP2_ARATH RecName: Full=Probable glutamate carboxypeptidase 2; AltName: Full=Probable glutamate carboxypeptidase II gi|209529809|gb|ACI49799.1| At3g54720 [Arabidopsis thaliana] gi|332645749|gb|AEE79270.1| probable glutamate carboxypeptidase II [Arabidopsis thaliana]	124	705	4.00E-27	568.5	54.0	56.5	glutamate carboxypeptidase II	gbpln	Arabidopsis thaliana	AT3G54720.1 | Symbols: AMP1, COP2, HPT, PT, MFO1 | Peptidase M28 family protein | chr3:20254852-20257815 REVERSE LENGTH=705	124	705	7.00E-30	568.5	54.0	56.5
Rsa1.0_01546.1.g27830.t1	gb|EOA20906.1| hypothetical protein CARUB_v10001242mg [Capsella rubella]	362	362	0	100.0	92.0	96.7	hypothetical protein CARUB_v10001242mg	gbpln	Capsella rubella	AT4G09670.1 | Symbols: | Oxidoreductase family protein | chr4:6107382-6109049 REVERSE LENGTH=362	362	362	0	100.0	90.9	96.1
Rsa1.0_01546.1.g27831.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01547.1.g27832.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	554	1142	1.00E-170	206.1	51.8	69.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	554	575	3.00E-32	103.8	13.7	21.1
Rsa1.0_01547.1.g27833.t1	gb|ACP30588.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1270	1108	0	87.2	42.0	48.7	disease resistance protein	gbpln	Brassica rapa	AT4G19500.2 | Symbols: | nucleoside-triphosphatases;transmembrane receptors;nucleotide binding;ATP binding | chr4:10627364-10631532 FORWARD LENGTH=834	1270	834	0	65.7	32.1	41.3
Rsa1.0_01547.1.g27834.t1	ref|NP_193687.3| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana] gi|332658794|gb|AEE84194.1| TIR-NBS-LRR class disease resistance protein [Arabidopsis thaliana]	1034	1744	0	168.7	57.5	69.9	TIR-NBS-LRR class disease resistance protein	gbpln	Arabidopsis thaliana	AT4G19520.1 | Symbols: | disease resistance protein (TIR-NBS-LRR class) family | chr4:10639488-10647070 REVERSE LENGTH=1744	1034	1744	0	168.7	57.5	69.9
Rsa1.0_01547.1.g27835.t1	dbj|BAA97083.1| unnamed protein product [Arabidopsis thaliana]	519	583	2.00E-27	112.3	24.1	40.1	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01547.1.g27836.t2	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	874	190	1.00E-32	21.7	11.7	13.5	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01548.1.g27837.t1	gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]	375	527	1.00E-35	140.5	22.1	28.0	hypothetical protein CARUB_v10022820mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	375	735	1.00E-37	196.0	25.1	31.2
Rsa1.0_01548.1.g27838.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01548.1.g27839.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01548.1.g27840.t1	ref|NP_199499.3| homeobox-leucine zipper protein HDG5 [Arabidopsis thaliana] gi|322510124|sp|Q9FJS2.3|HDG5_ARATH RecName: Full=Homeobox-leucine zipper protein HDG5; AltName: Full=HD-ZIP protein HDG5; AltName: Full=Homeodomain GLABRA 2-like protein 5; AltName: Full=Homeodomain transcription factor HDG5; AltName: Full=Protein HOMEODOMAIN GLABROUS 5 gi|332008060|gb|AED95443.1| homeobox-leucine zipper protein HDG5 [Arabidopsis thaliana]	825	826	0	100.1	86.3	91.9	homeobox-leucine zipper protein HDG5	gbpln	Arabidopsis thaliana	AT5G46880.1 | Symbols: HB-7, HDG5 | homeobox-7 | chr5:19031540-19035388 FORWARD LENGTH=826	825	826	0	100.1	86.3	91.9
Rsa1.0_01548.1.g27841.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1760	1274	0	72.4	19.7	26.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1760	626	7.00E-41	35.6	6.5	10.8
Rsa1.0_01548.1.g27842.t1	gb|EOA15138.1| hypothetical protein CARUB_v10028513mg [Capsella rubella]	128	129	3.00E-46	100.8	75.8	86.7	hypothetical protein CARUB_v10028513mg	gbpln	Capsella rubella	AT5G46890.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:19036437-19036820 REVERSE LENGTH=127	128	127	1.00E-41	99.2	75.0	86.7
Rsa1.0_01549.1.g27843.t1	dbj|BAJ34051.1| unnamed protein product [Thellungiella halophila]	248	251	1.00E-130	101.2	92.3	95.2	unnamed protein product	----	----	AT5G20700.1 | Symbols: | Protein of unknown function (DUF581) | chr5:7006178-7007003 REVERSE LENGTH=248	248	248	1.00E-124	100.0	87.9	92.3
Rsa1.0_01549.1.g27844.t1	gb|EOA23063.1| hypothetical protein CARUB_v10003833mg [Capsella rubella]	645	660	0	102.3	77.5	87.0	hypothetical protein CARUB_v10003833mg	gbpln	Capsella rubella	AT5G20690.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:7002453-7004551 FORWARD LENGTH=659	645	659	0	102.2	76.9	87.0
Rsa1.0_01549.1.g27845.t1	gb|EOA20311.1| hypothetical protein CARUB_v10000619mg [Capsella rubella]	556	536	0	96.4	80.0	87.9	hypothetical protein CARUB_v10000619mg	gbpln	Capsella rubella	AT5G20680.3 | Symbols: | TRICHOME BIREFRINGENCE-LIKE 16 | chr5:6998946-7001596 FORWARD LENGTH=551	556	551	0	99.1	79.7	88.3

Rsa1.0_01549.1.g27846.t1	ref|NP_197567.1| uncharacterized protein [Arabidopsis thaliana] gi|149944295|gb|ABR46190.1| At5g20670 [Arabidopsis thaliana] gi|332005491|gb|AED92874.1| uncharacterized protein AT5G20670 [Arabidopsis thaliana]	156	153	6.00E-67	98.1	87.8	91.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G20670.1 | Symbols: | Protein of unknown function (DUF1677) | chr5:6993332-6993793 REVERSE LENGTH=153	156	153	2.00E-69	98.1	87.8	91.0
Rsa1.0_01549.1.g27847.t1	gb|EOA21677.1| hypothetical protein CARUB_v10002100mg, partial [Capsella rubella]	144	173	4.00E-68	120.1	88.2	93.1	hypothetical protein CARUB_v10002100mg, partial	gbpln	Capsella rubella	AT5G20650.1 | Symbols: COPT5 | copper transporter 5 | chr5:6985481-6985921 REVERSE LENGTH=146	144	146	2.00E-69	101.4	86.8	91.7
Rsa1.0_01549.1.g27848.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01549.1.g27849.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01549.1.g27850.t1	sp|P45854.1|GLP1_SINAL RecName: Full=Germin-like protein 1; Flags: Precursor gi|683488|emb|CAA59257.1| Glp1 [Sinapis alba]	211	211	1.00E-107	100.0	94.3	95.3	RecName: Full=Germin-like protein 1; Flags: Precursor gi|683488|emb|CAA59257.1| Glp1	gbpln	Sinapis alba	AT5G20630.1 | Symbols: GLP3, GLP3A, GLP3B, ATGER3, GER3 | germin 3 | chr5:6975315-6975950 REVERSE LENGTH=211	211	211	1.00E-107	100.0	91.0	94.8
Rsa1.0_01549.1.g27851.t1	ref|NP_197561.1| uncharacterized protein [Arabidopsis thaliana] gi|332005483|gb|AED92866.1| uncharacterized protein AT5G20610 [Arabidopsis thaliana]	1123	1164	0	103.7	77.7	86.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G20610.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26160.1); Has 918 Blast hits to 759 proteins in 180 species: Archae - 6; Bacteria - 105; Metazoa - 264; Fungi - 89; Plants - 167; Viruses - 5; Other Eukaryotes - 282 (source: NCBI BLink). | chr5:6969184-6972794 FORWARD LENGTH=1164	1123	1164	0	103.7	77.7	86.3
Rsa1.0_01549.1.g27852.t1	ref|NP_197560.2| uncharacterized protein [Arabidopsis thaliana] gi|19310469|gb|AAL84969.1| AT5g20600/F7C8_190 [Arabidopsis thaliana] gi|28416463|gb|AAO42762.1| At5g20600/F7C8_190 [Arabidopsis thaliana] gi|110738085|dbj|BAF00976.1| hypothetical protein [Arabidopsis thaliana] gi|332005482|gb|AED92865.1| uncharacterized protein AT5G20600 [Arabidopsis thaliana]	535	532	0	99.4	77.8	86.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G20600.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: rRNA processing; LOCATED IN: preribosome, small subunit precursor; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nucleolar, Nop52 (InterPro:IPR010301); Has 543 Blast hits to 530 proteins in 201 species: Archae - 0; Bacteria - 10; Metazoa - 211; Fungi - 164; Plants - 46; Viruses - 0; Other Eukaryotes - 112 (source: NCBI BLink). | chr5:6966345-6967943 REVERSE LENGTH=532	535	532	0	99.4	77.8	86.0
Rsa1.0_01549.1.g27853.t1	dbj|BAE98654.1| hypothetical protein [Arabidopsis thaliana]	187	329	4.00E-84	175.9	78.1	82.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT5G20590.1 | Symbols: TBL5 | TRICHOME BIREFRINGENCE-LIKE 5 | chr5:6963517-6966006 FORWARD LENGTH=485	187	485	4.00E-86	259.4	78.1	82.4
Rsa1.0_01550.1.g27854.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1082	1223	0	113.0	53.3	70.0	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1082	746	1.00E-100	68.9	17.0	23.4
Rsa1.0_01550.1.g27855.t1	ref|NP_190870.1| 60S ribosomal protein L24-2 [Arabidopsis thaliana] gi|26454659|sp|P38666.2|RL242_ARATH RecName: Full=60S ribosomal protein L24-2; AltName: Full=Protein SHORT VALVE 1 gi|7529726|emb|CAB86906.1| 60S ribosomal protein-like [Arabidopsis thaliana] gi|16648706|gb|AAL25545.1| AT3g53020/F8J2_190 [Arabidopsis thaliana] gi|20260562|gb|AAM13179.1| 60S ribosomal protein-like [Arabidopsis thaliana] gi|30102870|gb|AAP21353.1| At3g53020 [Arabidopsis thaliana] gi|80750876|dbj|BAE48150.1| ribosomal protein L24 [Arabidopsis thaliana] gi|332645505|gb|AEE79026.1| 60S ribosomal protein L24-2 [Arabidopsis thaliana]	162	163	1.00E-67	100.6	85.2	88.3	60S ribosomal protein L24-2	gbpln	Arabidopsis thaliana	AT3G53020.1 | Symbols: STV1, RPL24B, RPL24 | Ribosomal protein L24e family protein | chr3:19660749-19661912 REVERSE LENGTH=163	162	163	4.00E-70	100.6	85.2	88.3
Rsa1.0_01550.1.g27856.t1	emb|CAB86903.1| pyruvate kinase-like protein [Arabidopsis thaliana]	412	514	1.00E-145	124.8	61.4	62.1	pyruvate kinase-like protein	gbpln	Arabidopsis thaliana	AT3G52990.2 | Symbols: | Pyruvate kinase family protein | chr3:19649336-19652237 FORWARD LENGTH=474	412	474	1.00E-148	115.0	61.4	62.1
Rsa1.0_01550.1.g27857.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01550.1.g27858.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01550.1.g27859.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01550.1.g27860.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1314	2726	0	207.5	55.7	72.4	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1314	158	7.00E-20	12.0	4.2	5.3
Rsa1.0_01551.1.g27861.t9	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	612	703	1.00E-153	114.9	48.7	56.5	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#

Rsa1.0_01551.1.g27862.t1	ref|XP_002865377.1| hypothetical protein ARALYDRAFT_494572 [Arabidopsis lyrata subsp. lyrata] gi|297311212|gb|EFH41636.1| hypothetical protein ARALYDRAFT_494572 [Arabidopsis lyrata subsp. lyrata]	202	199	1.00E-68	98.5	68.8	77.2	hypothetical protein ARALYDRAFT_494572	gbpln	Arabidopsis lyrata	AT5G44210.1 | Symbols: ERF9, ATERF9, ATERF-9 | erf domain protein 9 | chr5:17806742-17807344 FORWARD LENGTH=200	202	200	2.00E-67	99.0	67.3	76.7
Rsa1.0_01551.1.g27863.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01551.1.g27864.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01551.1.g27865.t4	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	580	954	3.00E-36	164.5	19.8	26.4	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	AT5G32590.1 | Symbols: | myosin heavy chain-related | chr5:12221589-12224322 REVERSE LENGTH=761	580	761	1.00E-10	131.2	7.2	12.1
Rsa1.0_01551.1.g27866.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01552.1.g27867.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01552.1.g27868.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1100	1142	0	103.8	36.1	46.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1100	626	1.00E-37	56.9	10.3	17.8
Rsa1.0_01552.1.g27869.t16	gb|EOA31734.1| hypothetical protein CARUB_v10014948mg [Capsella rubella]	119	119	5.00E-55	100.0	91.6	95.8	hypothetical protein CARUB_v10014948mg	gbpln	Capsella rubella	AT3G20510.1 | Symbols: | Transmembrane proteins 14C | chr3:7160884-7161991 FORWARD LENGTH=119	119	119	1.00E-57	100.0	91.6	95.8
Rsa1.0_01552.1.g27870.t1	ref|XP_002883254.1| POLGAMMA1 [Arabidopsis lyrata subsp. lyrata] gi|297329094|gb|EFH59513.1| POLGAMMA1 [Arabidopsis lyrata subsp. lyrata]	1196	1044	0	87.3	72.4	78.2	POLGAMMA1	gbpln	Arabidopsis lyrata	AT3G20540.1 | Symbols: POLGAMMA1 | polymerase gamma 1 | chr3:7168261-7173357 FORWARD LENGTH=1034	1196	1034	0	86.5	72.1	77.3
Rsa1.0_01552.1.g27871.t1	ref|XP_002883257.1| hypothetical protein ARALYDRAFT_898483 [Arabidopsis lyrata subsp. lyrata] gi|297329097|gb|EFH59516.1| hypothetical protein ARALYDRAFT_898483 [Arabidopsis lyrata subsp. lyrata]	127	130	1.00E-48	102.4	79.5	88.2	hypothetical protein ARALYDRAFT_898483	gbpln	Arabidopsis lyrata	AT3G20557.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G50930.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:7180140-7180731 FORWARD LENGTH=130	127	130	1.00E-48	102.4	78.0	85.8
Rsa1.0_01552.1.g27872.t1	ref|NP_566664.1| protein PDI-like 5-3 [Arabidopsis thaliana] gi|75273652|sp|Q9LJU2.1|PDI53_ARATH RecName: Full=Protein disulfide-isomerase 5-3; Short=AtPDIL5-3; AltName: Full=Protein disulfide-isomerase 12; Short=PDI12; AltName: Full=Protein disulfide-isomerase 8-1; Short=AtPDIL8-1; Flags: Precursor gi|11994143|dbj|BAB01164.1| unnamed protein product [Arabidopsis thaliana] gi|15215847|gb|AAK91468.1| AT3g20560/K10D20_9 [Arabidopsis thaliana] gi|332642877|gb|AEE76398.1| protein PDI-like 5-3 [Arabidopsis thaliana]	517	483	0	93.4	73.1	80.5	protein PDI-like 5-3	gbpln	Arabidopsis thaliana	AT3G20560.1 | Symbols: ATPDIL5-3, PDI12, ATPDI12, PDIL5-3 | PDI-like 5-3 | chr3:7182182-7186390 FORWARD LENGTH=483	517	483	0	93.4	73.1	80.5
Rsa1.0_01552.1.g27873.t1	gb|ABB97040.1| unknown [Brassica rapa]	208	204	8.00E-91	98.1	86.5	89.9	unknown	gbpln	Brassica rapa	AT3G20570.1 | Symbols: ENODL9, AtENODL9 | early nodulin-like protein 9 | chr3:7186754-7187453 REVERSE LENGTH=203	208	203	9.00E-81	97.6	79.8	86.1
Rsa1.0_01552.1.g27874.t1	ref|NP_188694.2| COBRA-like protein 10 [Arabidopsis thaliana] gi|34222649|sp|Q9LJU0.1|CBL10_ARATH RecName: Full=COBRA-like protein 10; Flags: Precursor gi|11994145|dbj|BAB01166.1| unnamed protein product [Arabidopsis thaliana] gi|26452233|dbj|BAC43204.1| GPI-anchored protein [Arabidopsis thaliana] gi|29029016|gb|AAO64887.1| At3g20580 [Arabidopsis thaliana] gi|332642879|gb|AEE76400.1| COBRA-like protein 10 [Arabidopsis thaliana]	248	672	1.00E-101	271.0	77.8	83.1	COBRA-like protein 10	gbpln	Arabidopsis thaliana	AT3G20580.1 | Symbols: COBL10 | COBRA-like protein 10 precursor | chr3:7188063-7190416 REVERSE LENGTH=672	248	672	1.00E-104	271.0	77.8	83.1
Rsa1.0_01552.1.g27875.t1	gb|EOA31419.1| hypothetical protein CARUB_v10014599mg [Capsella rubella]	209	218	5.00E-70	104.3	66.0	78.5	hypothetical protein CARUB_v10014599mg	gbpln	Capsella rubella	AT3G20600.1 | Symbols: NDR1 | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:7194877-7195536 FORWARD LENGTH=219	209	219	2.00E-71	104.8	65.6	78.0

Rsa1.0_01552.1.g27876.t1	dbj|BAF00669.1| retrotransposon like protein [Arabidopsis thaliana]	517	392	2.00E−91	75.8	34.0	43.1	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT1G34070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48050.1); Has 648 Blast hits to 647 proteins in 29 species: Archae − 0; Bacteria − 0; Metazoa − 16; Fungi − 25; Plants − 607; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:12402283−12403209 FORWARD LENGTH=308	517	308	2.00E−16	59.6	14.3	25.3
Rsa1.0_01553.1.g27877.t1	ref|XP_002882419.1| rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297328259|gb|EFH58678.1| rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata]	246	246	1.00E−122	100.0	93.5	97.6	rubber elongation factor family protein	gbpln	Arabidopsis lyrata	AT3G05500.1 | Symbols: | Rubber elongation factor protein (REF) | chr3:1593540−1594802 FORWARD LENGTH=246	246	246	1.00E−124	100.0	93.1	97.6
Rsa1.0_01553.1.g27878.t1	ref|XP_002882421.1| alpha subunit of F−actin capping protein [Arabidopsis lyrata subsp. lyrata] gi|297328261|gb|EFH58680.1| alpha subunit of F−actin capping protein [Arabidopsis lyrata subsp. lyrata]	324	308	1.00E−160	95.1	86.7	90.1	alpha subunit of F−actin capping protein	gbpln	Arabidopsis lyrata	AT3G05520.2 | Symbols: | Subunits of heterodimeric actin filament capping protein Capz superfamily | chr3:1598611−1601437 FORWARD LENGTH=382	324	382	1.00E−155	117.9	83.0	86.1
Rsa1.0_01553.1.g27879.t1	dbj|BAB21595.1| Tat binding protein like protein [Brassica rapa]	351	424	1.00E−162	120.8	80.3	81.2	Tat binding protein like protein	gbpln	Brassica rapa	AT3G05530.1 | Symbols: RPT5A, ATS6A.2 | regulatory particle triple−A ATPase 5A | chr3:1603540−1605993 FORWARD LENGTH=424	351	424	1.00E−164	120.8	80.1	80.9
Rsa1.0_01553.1.g27880.t1	ref|XP_002882423.1| hypothetical protein ARALYDRAFT_477844 [Arabidopsis lyrata subsp. lyrata] gi|297328263|gb|EFH58682.1| hypothetical protein ARALYDRAFT_477844 [Arabidopsis lyrata subsp. lyrata]	427	428	1.00E−157	100.2	78.7	85.5	hypothetical protein ARALYDRAFT_477844	gbpln	Arabidopsis lyrata	AT3G05545.1 | Symbols: | RING/U−box superfamily protein | chr3:1609436−1612133 FORWARD LENGTH=425	427	425	1.00E−157	99.5	78.0	84.1
Rsa1.0_01553.1.g27881.t1	dbj|BAJ34418.1| unnamed protein product [Thellungiella halophila]	124	124	1.00E−55	100.0	96.8	100.0	unnamed protein product	----	----	AT3G05560.3 | Symbols: | Ribosomal L22e protein family | chr3:1614641−1615204 FORWARD LENGTH=124	124	124	5.00E−58	100.0	96.8	99.2
Rsa1.0_01553.1.g27882.t1	gb|EOA32863.1| hypothetical protein CARUB_v10016176mg [Capsella rubella]	150	207	5.00E−36	138.0	52.7	72.0	hypothetical protein CARUB_v10016176mg	gbpln	Capsella rubella	AT2G33720.1 | Symbols: | AP2/B3−like transcriptional factor family protein | chr2:14263776−14264989 FORWARD LENGTH=326	150	326	6.00E−22	217.3	36.7	51.3
Rsa1.0_01553.1.g27883.t2	ref|XP_002882426.1| hypothetical protein ARALYDRAFT_896643 [Arabidopsis lyrata subsp. lyrata] gi|297328266|gb|EFH58685.1| hypothetical protein ARALYDRAFT_896643 [Arabidopsis lyrata subsp. lyrata]	357	271	2.00E−65	75.9	39.5	49.6	hypothetical protein ARALYDRAFT_896643	gbpln	Arabidopsis lyrata	AT5G27830.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Folate receptor, conserved region (InterPro:IPR018143); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:9861344−9862742 FORWARD LENGTH=300	357	300	2.00E−51	84.0	32.2	42.9
Rsa1.0_01553.1.g27884.t1	ref|XP_002882426.1| hypothetical protein ARALYDRAFT_896643 [Arabidopsis lyrata subsp. lyrata] gi|297328266|gb|EFH58685.1| hypothetical protein ARALYDRAFT_896643 [Arabidopsis lyrata subsp. lyrata]	254	271	1.00E−57	106.7	52.0	61.4	hypothetical protein ARALYDRAFT_896643	gbpln	Arabidopsis lyrata	AT5G27830.4 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Folate receptor, conserved region (InterPro:IPR018143). | chr5:9861203−9862742 FORWARD LENGTH=322	254	322	2.00E−45	126.8	42.5	51.2
Rsa1.0_01553.1.g27885.t1	gb|EOA31060.1| hypothetical protein CARUB_v10014212mg [Capsella rubella]	318	318	1.00E−176	100.0	94.0	98.4	hypothetical protein CARUB_v10014212mg	gbpln	Capsella rubella	AT3G05580.1 | Symbols: | Calcineurin−like metallo−phosphoesterase superfamily protein | chr3:1618216−1619850 REVERSE LENGTH=318	318	318	1.00E−178	100.0	93.4	98.4
Rsa1.0_01553.1.g27886.t1	ref|XP_002882427.1| hypothetical protein ARALYDRAFT_477850 [Arabidopsis lyrata subsp. lyrata] gi|297328267|gb|EFH58686.1| hypothetical protein ARALYDRAFT_477850 [Arabidopsis lyrata subsp. lyrata]	187	187	1.00E−100	100.0	97.3	99.5	hypothetical protein ARALYDRAFT_477850	gbpln	Arabidopsis lyrata	AT3G05590.1 | Symbols: RPL18 | ribosomal protein L18 | chr3:1621511−1622775 FORWARD LENGTH=187	187	187	1.00E−102	100.0	97.3	98.9
Rsa1.0_01553.1.g27887.t1	ref|XP_002884519.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297330359|gb|EFH60778.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	622	671	0	107.9	84.2	92.8	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT3G05610.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:1625876−1627976 REVERSE LENGTH=669	622	669	0	107.6	82.5	90.8

Rsa1.0_01553.1.g27888.t1	ref|XP_002882429.1| hypothetical protein ARALYDRAFT_477854 [Arabidopsis lyrata subsp. lyrata] gi|297328269|gb|EFH58688.1| hypothetical protein ARALYDRAFT_477854 [Arabidopsis lyrata subsp. lyrata]	1050	1057	0	100.7	89.8	95.0	hypothetical protein ARALYDRAFT_477854	gbpln	Arabidopsis lyrata	AT3G05630.1 | Symbols: PLDP2, PDLZ2, PLDZETA2 | phospholipase D P2 | chr3:1635321-1640105 FORWARD LENGTH=1046	1050	1046	0	99.6	89.5	95.2
Rsa1.0_01553.1.g27889.t1	ref|XP_002884522.1| hypothetical protein ARALYDRAFT_477856 [Arabidopsis lyrata subsp. lyrata] gi|297330362|gb|EFH60781.1| hypothetical protein ARALYDRAFT_477856 [Arabidopsis lyrata subsp. lyrata]	349	357	0	102.3	87.4	94.3	hypothetical protein ARALYDRAFT_477856	gbpln	Arabidopsis lyrata	AT3G05640.2 | Symbols: | Protein phosphatase 2C family protein | chr3:1640610-1642227 REVERSE LENGTH=358	349	358	0	102.6	86.8	94.6
Rsa1.0_01554.1.g27890.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01554.1.g27891.t1	gb|ACQ90589.1| putative C2H2 zinc finger protein [Eutrema halophilum]	447	442	0	98.9	85.0	89.3	putative C2H2 zinc finger protein	gbpln	Eutrema halophilum	AT2G01940.1 | Symbols: SGR5, ATIDD15 | C2H2-like zinc finger protein | chr2:432652-434917 FORWARD LENGTH=445	447	445	0	99.6	84.3	88.4
Rsa1.0_01554.1.g27892.t1	gb|ADQ43184.1| leucine-rich receptor kinase [Eutrema parvulum]	1208	1141	0	94.5	86.8	90.9	leucine-rich receptor kinase	gbpln	Eutrema parvulum	AT2G01950.1 | Symbols: VH1, BRL2 | BRI1-like 2 | chr2:440805-444236 REVERSE LENGTH=1143	1208	1143	0	94.6	86.3	90.3
Rsa1.0_01554.1.g27893.t1	ref|NP_178306.1| putative endomembrane protein 70 [Arabidopsis thaliana] gi|4406780|gb|AAD20090.1| putative endosomal protein [Arabidopsis thaliana] gi|16604501|gb|AAL24256.1| At2g01970/F14H20.4 [Arabidopsis thaliana] gi|110741070|dbj|BAE98629.1| putative endosomal protein [Arabidopsis thaliana] gi|330250434|gb|AEC05528.1| putative endomembrane protein 70 [Arabidopsis thaliana]	270	592	1.00E-155	219.3	99.3	100.0	putative endomembrane protein 70	gbpln	Arabidopsis thaliana	AT2G01970.1 | Symbols: | Endomembrane protein 70 protein family | chr2:452197-454819 REVERSE LENGTH=592	270	592	1.00E-157	219.3	99.3	100.0
Rsa1.0_01554.1.g27894.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01554.1.g27895.t1	ref|NP_178313.1| peptide transporter PTR2 [Arabidopsis thaliana] gi|1172704|sp|P46032.1|PTR2_ARATH RecName: Full=Peptide transporter PTR2; AltName: Full=Histidine-transporting protein gi|13937185|gb|AAK50086.1|AF372946_1 At2g02040/F14H20.11 [Arabidopsis thaliana] gi|633940|gb|AAB00858.1| transport protein [Arabidopsis thaliana] gi|4406786|gb|AAD20096.1| histidine transport protein (PTR2-B) [Arabidopsis thaliana] gi|23506067|gb|AAN28893.1| At2g02040/F14H20.11 [Arabidopsis thaliana] gi|330250444|gb|AEC05538.1| peptide transporter PTR2 [Arabidopsis thaliana]	583	585	0	100.3	95.5	99.0	peptide transporter PTR2	gbpln	Arabidopsis thaliana	AT2G02040.1 | Symbols: ATPTR2-B, NTR1, PTR2-B, PTR2, ATPTR2 | peptide transporter 2 | chr2:487542-489707 FORWARD LENGTH=585	583	585	0	100.3	95.5	99.0
Rsa1.0_01555.1.g27896.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01555.1.g27897.t1	ref|XP_002878408.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324246|gb|EFH54667.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	696	359	1.00E-137	51.6	35.8	40.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G61730.1 | Symbols: RMF | reduced male fertility | chr3:22848427-22850475 REVERSE LENGTH=354	696	354	1.00E-134	50.9	34.9	39.5
Rsa1.0_01555.1.g27898.t1	gb|EOA25290.1| hypothetical protein CARUB_v10018605mg [Capsella rubella]	644	656	0	101.9	86.0	92.7	hypothetical protein CARUB_v10018605mg	gbpln	Capsella rubella	AT3G61680.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:22824630-22826926 FORWARD LENGTH=649	644	649	0	100.8	84.8	91.9
Rsa1.0_01555.1.g27899.t1	ref|XP_002878398.1| hypothetical protein ARALYDRAFT_324601 [Arabidopsis lyrata subsp. lyrata] gi|297324236|gb|EFH54657.1| hypothetical protein ARALYDRAFT_324601 [Arabidopsis lyrata subsp. lyrata]	276	271	4.00E-84	98.2	64.1	75.4	hypothetical protein ARALYDRAFT_324601	gbpln	Arabidopsis lyrata	AT2G46400.1 | Symbols: WRKY46, ATWRKY46 | WRKY DNA-binding protein 46 | chr2:19043676-19044754 REVERSE LENGTH=295	276	295	3.00E-70	106.9	54.7	72.5

Rsa1.0_01555.1.g27900.t1	ref|NP_191723.1| arabinogalactan protein 20 [Arabidopsis thaliana] gi|75183616|sp|Q9M373.1|AGP20_ARATH RecName: Full=Arabinogalactan peptide 20; Short=AG-peptide 20; Flags: Precursor gi|6850855|emb|CAB71094.1| putative protein [Arabidopsis thaliana] gi|21536871|gb|AAM61203.1| unknown [Arabidopsis thaliana] gi|98960995|gb|ABF58981.1| At3g61640 [Arabidopsis thaliana] gi|332646714|gb|AEE80235.1| arabinogalactan protein 20 [Arabidopsis thaliana]	65	74	2.00E-19	113.8	80.0	86.2	arabinogalactan protein 20	gbpln	Arabidopsis thaliana	AT3G61640.1 | Symbols: AGP20, AtAGP20 | arabinogalactan protein 20 | chr3:22810283-22810629 REVERSE LENGTH=74	65	74	3.00E-22	113.8	80.0	86.2
Rsa1.0_01555.1.g27901.t1	ref|NP_191718.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|334186190|ref|NP_001190155.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75183486|sp|Q9M310.1|FBK77_ARATH RecName: Full=F-box/kelch-repeat protein At3g61590 gi|14423514|gb|AAK62439.1|AF386994_1 putative protein [Arabidopsis thaliana] gi|6850850|emb|CAB71089.1| putative protein [Arabidopsis thaliana] gi|23197692|gb|AAN15373.1| putative protein [Arabidopsis thaliana] gi|332646706|gb|AEE80227.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|332646707|gb|AEE80228.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	417	411	0	98.6	84.4	90.4	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G61590.2 | Symbols: HWS | Galactose oxidase/kelch repeat superfamily protein | chr3:22792914-22794149 FORWARD LENGTH=411	417	411	0	98.6	84.4	90.4
Rsa1.0_01555.1.g27902.t1	gb|AEW24952.1| delta8-sphingolipid desaturase [Brassica rapa]	449	449	0	100.0	98.7	99.6	delta8-sphingolipid desaturase	gbpln	Brassica rapa	AT3G61580.1 | Symbols: | Fatty acid/sphingolipid desaturase | chr3:22786253-22787602 FORWARD LENGTH=449	449	449	0	100.0	88.9	94.2
Rsa1.0_01555.1.g27903.t1	gb|ABV21212.1| Ty1_Copia-element protein [Arabidopsis thaliana]	460	438	1.00E-76	95.2	34.8	50.0	Ty1_Copia-element protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	460	746	1.00E-51	162.2	26.1	39.6
Rsa1.0_01555.1.g27904.t1	ref|XP_002878369.1| hypothetical protein ARALYDRAFT_486595 [Arabidopsis lyrata subsp. lyrata] gi|297324207|gb|EFH54628.1| hypothetical protein ARALYDRAFT_486595 [Arabidopsis lyrata subsp. lyrata]	168	179	5.00E-57	106.5	68.5	79.8	hypothetical protein ARALYDRAFT_486595	gbpln	Arabidopsis lyrata	AT3G61190.1 | Symbols: BAP1 | BON association protein 1 | chr3:22650837-22651415 REVERSE LENGTH=192	168	192	6.00E-59	114.3	69.6	80.4
Rsa1.0_01555.1.g27905.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1215	1274	0	104.9	42.6	59.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1215	575	2.00E-67	47.3	13.8	21.8
Rsa1.0_01555.1.g27906.t1	gb|AAD17395.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	314	1138	9.00E-44	362.4	31.2	45.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	314	575	8.00E-38	183.1	25.8	42.4
Rsa1.0_01555.1.g27907.t1	ref|XP_002875792.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321630|gb|EFH52051.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	137	764	5.00E-14	557.7	26.3	36.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	137	295	3.00E-16	215.3	24.8	35.0
Rsa1.0_01556.1.g27908.t1	ref|XP_002884040.1| peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329880|gb|EFH60299.1| peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	142	356	3.00E-43	250.7	63.4	74.6	peptidoglycan-binding LysM domain-containing protein	gbpln	Arabidopsis lyrata	AT2G17120.1 | Symbols: LYM2 | lysm domain GPI-anchored protein 2 precursor | chr2:7459156-7460648 FORWARD LENGTH=350	142	350	2.00E-45	246.5	62.7	74.6
Rsa1.0_01556.1.g27909.t1	gb|ADZ96432.1| transcription factor LAS [Brassica oleracea]	338	439	1.00E-170	129.9	93.5	95.6	transcription factor LAS	gbpln	Brassica oleracea	AT1G55580.1 | Symbols: LAS, SCL18 | GRAS family transcription factor | chr1:20764106-20765443 FORWARD LENGTH=445	338	445	1.00E-164	131.7	88.8	91.7
Rsa1.0_01556.1.g27910.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01556.1.g27911.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_01556.1.g27912.t1</td><td>ref|XP_002891844.1| hypothetical protein ARALYDRAFT_892557 [Arabidopsis lyrata subsp. lyrata] gi|297337686|gb|EFH68103.1| hypothetical protein ARALYDRAFT_892557 [Arabidopsis lyrata subsp. lyrata]</td><td>555</td><td>555</td><td>0</td><td>100.0</td><td>93.5</td><td>96.2</td><td>hypothetical protein ARALYDRAFT_892557</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G55570.1 | Symbols: sks12 | SKU5 similar 12 | chr1:20757882-20759771 FORWARD LENGTH=555</td><td>555</td><td>555</td><td>0</td><td>100.0</td><td>92.8</td><td>96.2</td></tr>
<tr><td>Rsa1.0_01556.1.g27913.t1</td><td>ref|XP_002892644.1| hypothetical protein ARALYDRAFT_888450 [Arabidopsis lyrata subsp. lyrata] gi|297338486|gb|EFH68903.1| hypothetical protein ARALYDRAFT_888450 [Arabidopsis lyrata subsp. lyrata]</td><td>144</td><td>169</td><td>1.00E-32</td><td>117.4</td><td>53.5</td><td>70.1</td><td>hypothetical protein ARALYDRAFT_888450</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G11470.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:3859874-3860522 REVERSE LENGTH=150</td><td>144</td><td>150</td><td>2.00E-18</td><td>104.2</td><td>38.9</td><td>53.5</td></tr>
<tr><td>Rsa1.0_01556.1.g27914.t1</td><td>ref|XP_002892632.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297338474|gb|EFH68891.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>268</td><td>309</td><td>4.00E-32</td><td>115.3</td><td>23.9</td><td>28.4</td><td>F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G11270.2 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3785715-3786653 REVERSE LENGTH=312</td><td>268</td><td>312</td><td>3.00E-32</td><td>116.4</td><td>22.8</td><td>26.5</td></tr>
<tr><td>Rsa1.0_01556.1.g27915.t1</td><td>gb|EOA38105.1| hypothetical protein CARUB_v10009573mg [Capsella rubella]</td><td>443</td><td>355</td><td>1.00E-151</td><td>80.1</td><td>62.8</td><td>69.5</td><td>hypothetical protein CARUB_v10009573mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G55370.2 | Symbols: NDF5 | NDH-dependent cyclic electron flow 5 | chr1:20674852-20676071 FORWARD LENGTH=354</td><td>443</td><td>354</td><td>1.00E-143</td><td>79.9</td><td>60.0</td><td>69.1</td></tr>
<tr><td>Rsa1.0_01556.1.g27916.t1</td><td>ref|XP_002894503.1| hypothetical protein ARALYDRAFT_892534 [Arabidopsis lyrata subsp. lyrata] gi|297340345|gb|EFH70762.1| hypothetical protein ARALYDRAFT_892534 [Arabidopsis lyrata subsp. lyrata]</td><td>135</td><td>104</td><td>2.00E-28</td><td>77.0</td><td>42.2</td><td>49.6</td><td>hypothetical protein ARALYDRAFT_892534</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G55365.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13500.1); Has 29 Blast hits to 29 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:20673983-20674363 REVERSE LENGTH=126</td><td>135</td><td>126</td><td>1.00E-30</td><td>93.3</td><td>50.4</td><td>60.7</td></tr>
<tr><td>Rsa1.0_01556.1.g27917.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01556.1.g27918.t1</td><td>ref|NP_175932.2| calpain-type cysteine protease [Arabidopsis thaliana] gi|30695926|ref|NP_850965.1| calpain-type cysteine protease [Arabidopsis thaliana] gi|30695928|ref|NP_850966.1| calpain-type cysteine protease [Arabidopsis thaliana] gi|30695930|ref|NP_850967.1| calpain-type cysteine protease [Arabidopsis thaliana] gi|20268660|gb|AAL38186.1| calpain-like protein [Arabidopsis thaliana] gi|332195111|gb|AEE33232.1| calpain-type cysteine protease [Arabidopsis thaliana] gi|332195112|gb|AEE33233.1| calpain-type cysteine protease [Arabidopsis thaliana] gi|332195113|gb|AEE33234.1| calpain-type cysteine protease [Arabidopsis thaliana] gi|332195114|gb|AEE33235.1| calpain-type cysteine protease [Arabidopsis thaliana]</td><td>2163</td><td>2151</td><td>0</td><td>99.4</td><td>93.7</td><td>96.7</td><td>calpain-type cysteine protease</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G55350.4 | Symbols: DEK1, ATDEK1 | calpain-type cysteine protease family | chr1:20654463-20664501 REVERSE LENGTH=2151</td><td>2163</td><td>2151</td><td>0</td><td>99.4</td><td>93.7</td><td>96.7</td></tr>
<tr><td>Rsa1.0_01556.1.g27919.t2</td><td>ref|XP_002891830.1| hypothetical protein ARALYDRAFT_474592 [Arabidopsis lyrata subsp. lyrata] gi|297337672|gb|EFH68089.1| hypothetical protein ARALYDRAFT_474592 [Arabidopsis lyrata subsp. lyrata]</td><td>220</td><td>205</td><td>1.00E-86</td><td>93.2</td><td>76.8</td><td>80.0</td><td>hypothetical protein ARALYDRAFT_474592</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G55340.1 | Symbols: | Protein of unknown function (DUF1639) | chr1:20652605-20653469 FORWARD LENGTH=205</td><td>220</td><td>205</td><td>3.00E-87</td><td>93.2</td><td>75.0</td><td>79.1</td></tr>
<tr><td>Rsa1.0_01557.1.g27920.t1</td><td>emb|CAA52069.1| acyl-ACP thioesterase [Brassica napus]</td><td>257</td><td>366</td><td>1.00E-147</td><td>142.4</td><td>96.9</td><td>98.4</td><td>acyl-ACP thioesterase</td><td>gbpln</td><td>Brassica napus</td><td>AT4G13050.1 | Symbols: | Acyl-ACP thioesterase | chr4:7617739-7619355 FORWARD LENGTH=367</td><td>257</td><td>367</td><td>1.00E-142</td><td>142.8</td><td>92.6</td><td>96.1</td></tr>
<tr><td>Rsa1.0_01557.1.g27921.t1</td><td>ref|NP_001119398.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75170771|sp|Q9FI70.1|FK122_ARATH RecName: Full=F-box/kelch-repeat protein At5g49000 gi|10177190|dbj|BAB10324.1| unnamed protein product [Arabidopsis thaliana] gi|119360043|gb|ABL66750.1| At5g49000 [Arabidopsis thaliana] gi|332008372|gb|AED95755.1| F-box/kelch-repeat protein [Arabidopsis thaliana]</td><td>355</td><td>372</td><td>3.00E-90</td><td>104.8</td><td>51.8</td><td>70.7</td><td>F-box/kelch-repeat protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G49000.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19864527-19865645 FORWARD LENGTH=372</td><td>355</td><td>372</td><td>7.00E-93</td><td>104.8</td><td>51.8</td><td>70.7</td></tr>
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Rsa1.0_01557.1.g27922.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1441	2301	0	159.7	59.2	73.8	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1441	1262	1.00E-107	87.6	13.5	19.3
Rsa1.0_01557.1.g27923.t1	ref|NP_189132.2| Helicase/SANT-associated, DNA binding protein [Arabidopsis thaliana] gi|332643436|gb|AEE76957.1| Helicase/SANT-associated, DNA binding protein [Arabidopsis thaliana]	1902	1957	0	102.9	60.9	72.3	Helicase/SANT-associated, DNA binding protein	gbpln	Arabidopsis thaliana	AT3G24880.1 | Symbols: | Helicase/SANT-associated, DNA binding protein | chr3:9086457-9095537 REVERSE LENGTH=1957	1902	1957	0	102.9	60.9	72.3
Rsa1.0_01558.1.g27924.t1	ref|NP_565613.1| uncharacterized protein [Arabidopsis thaliana] gi|15294292|gb|AAK95323.1|AF410337_1 At2g25920/F17H15.5 [Arabidopsis thaliana] gi|20197362|gb|AAC42240.2| expressed protein [Arabidopsis thaliana] gi|23507801|gb|AAN38704.1| At2g25920/F17H15.5 [Arabidopsis thaliana] gi|330252679|gb|AEC07773.1| uncharacterized protein AT2G25920 [Arabidopsis thaliana]	122	280	2.00E-20	229.5	45.9	53.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G25920.1 | Symbols: | BEST Arabidopsis thaliana protein match is: 3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein (TAIR:AT2G25910.2); Has 131 Blast hits to 125 proteins in 54 species: Archae - 0; Bacteria - 50; Metazoa - 12; Fungi - 12; Plants - 41; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink). | chr2:11054425-11055916 REVERSE LENGTH=280	122	280	3.00E-23	229.5	45.9	53.3
Rsa1.0_01558.1.g27925.t1	gb|EOA32134.1| hypothetical protein CARUB_v10015385mg, partial [Capsella rubella]	262	581	2.00E-75	221.8	58.8	66.8	hypothetical protein CARUB_v10015385mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01558.1.g27926.t1	ref|NP_192120.4| transcription coactivator protein [Arabidopsis thaliana] gi|363548502|sp|O04251.3|Y4211_ARATH RecName: Full=BRCT domain-containing protein At4g02110 gi|332656725|gb|AEE82125.1| BRCT domain-containing protein [Arabidopsis thaliana]	1292	1329	0	102.9	69.5	78.8	transcription coactivator protein	gbpln	Arabidopsis thaliana	AT4G02110.1 | Symbols: | transcription coactivators | chr4:935191-940191 FORWARD LENGTH=1329	1292	1329	0	102.9	69.5	78.8
Rsa1.0_01558.1.g27927.t1	ref|XP_002867921.1| hypothetical protein ARALYDRAFT_492890 [Arabidopsis lyrata subsp. lyrata] gi|297313757|gb|EFH44180.1| hypothetical protein ARALYDRAFT_492890 [Arabidopsis lyrata subsp. lyrata]	369	371	1.00E-140	100.5	66.7	79.4	hypothetical protein ARALYDRAFT_492890	gbpln	Arabidopsis lyrata	AT4G19760.1 | Symbols: | Glycosyl hydrolase family protein with chitinase insertion domain | chr4:10750381-10752028 FORWARD LENGTH=369	369	369	1.00E-137	100.0	67.5	79.1
Rsa1.0_01558.1.g27928.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01558.1.g27929.t1	ref|XP_002874939.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297320776|gb|EFH51198.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	543	544	0	100.2	89.3	93.0	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT4G02100.1 | Symbols: | Heat shock protein DnaJ with tetratricopeptide repeat | chr4:930228-932049 FORWARD LENGTH=546	543	546	0	100.6	88.6	92.6
Rsa1.0_01558.1.g27930.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1470	1413	0	96.1	65.4	78.2	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1470	1262	0	85.9	22.1	27.8
Rsa1.0_01558.1.g27931.t1	ref|NP_192117.1| GTP-binding protein SAR1A [Arabidopsis thaliana] gi|3334323|sp|O04834.1|SAR1A_ARATH RecName: Full=GTP-binding protein SAR1A gi|1314860|gb|AAA99827.1| Sar1 homolog [Arabidopsis thaliana] gi|2104532|gb|AAC78700.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|2104550|gb|AAB57799.1| AGAA.4 [Arabidopsis thaliana] gi|7268592|emb|CAB80701.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|17529144|gb|AAL38798.1| putative SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|20465729|gb|AAM20333.1| putative SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|21618030|gb|AAM67080.1| SAR1/GTP-binding secretory factor [Arabidopsis thaliana] gi|332656722|gb|AEE82122.1| GTP-binding protein SAR1A [Arabidopsis thaliana]	193	193	1.00E-107	100.0	97.9	99.5	GTP-binding protein SAR1A	gbpln	Arabidopsis thaliana	AT4G02080.1 | Symbols: ASAR1, ATSARA1C, ATSAR2, SAR2 | secretion-associated RAS super family 2 | chr4:921554-922547 FORWARD LENGTH=193	193	193	1.00E-110	100.0	97.9	99.5

Rsa1.0_01559.1.g27932.t1	ref|XP_002873346.1| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis lyrata subsp. lyrata] gi|297319183|gb|EFH49605.1| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis lyrata subsp. lyrata]	155	156	6.00E-76	100.6	92.3	99.4	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	gbpln	Arabidopsis lyrata	AT5G08180.2 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr5:2631843-2633374 REVERSE LENGTH=156	155	156	2.00E-77	100.6	91.0	98.7
Rsa1.0_01559.1.g27933.t1	ref|XP_002873343.1| hypothetical protein ARALYDRAFT_908765 [Arabidopsis lyrata subsp. lyrata] gi|297319180|gb|EFH49602.1| hypothetical protein ARALYDRAFT_908765 [Arabidopsis lyrata subsp. lyrata]	133	140	1.00E-30	105.3	72.9	83.5	hypothetical protein ARALYDRAFT_908765	gbpln	Arabidopsis lyrata	AT5G08150.1 | Symbols: SOB5 | suppressor of phytochrome b 5 | chr5:2622164-2622598 REVERSE LENGTH=144	133	144	1.00E-25	108.3	69.2	81.2
Rsa1.0_01559.1.g27934.t2	gb|AAB38778.1| myosin heavy chain-like protein [Arabidopsis thaliana]	200	209	9.00E-45	104.5	46.5	55.0	myosin heavy chain-like protein	gbpln	Arabidopsis thaliana	AT5G08120.1 | Symbols: MPB2C | movement protein binding protein 2C | chr5:2600743-2602678 REVERSE LENGTH=326	200	326	7.00E-47	163.0	46.5	55.0
Rsa1.0_01559.1.g27935.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	190	1274	2.00E-26	670.5	42.1	59.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	190	303	5.00E-24	159.5	41.1	56.3
Rsa1.0_01559.1.g27936.t1	dbj|BAJ33766.1| unnamed protein product [Thellungiella halophila]	843	843	0	100.0	97.9	99.5	unnamed protein product	----	----	AT1G56070.1 | Symbols: LOS1 | Ribosomal protein S5/Elongation factor G/III/V family protein | chr1:20968245-20971077 REVERSE LENGTH=843	843	843	0	100.0	96.7	98.3
Rsa1.0_01559.1.g27937.t1	dbj|BAB01155.1| unnamed protein product [Arabidopsis thaliana] gi|49823524|gb|AAT68745.1| hypothetical protein At3g17200 [Arabidopsis thaliana] gi|60547763|gb|AAX23845.1| hypothetical protein At3g17200 [Arabidopsis thaliana]	250	310	9.00E-52	124.0	38.8	54.8	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	250	746	5.00E-42	298.4	31.6	44.4
Rsa1.0_01559.1.g27938.t1	gb|EOA21213.1| hypothetical protein CARUB_v10001560mg [Capsella rubella]	303	304	1.00E-141	100.3	95.0	99.3	hypothetical protein CARUB_v10001560mg	gbpln	Capsella rubella	AT5G08080.1 | Symbols: SYP132, ATSYP132 | syntaxin of plants 132 | chr5:2588532-2591106 FORWARD LENGTH=304	303	304	1.00E-141	100.3	94.1	98.3
Rsa1.0_01559.1.g27939.t1	ref|XP_002871305.1| hypothetical protein ARALYDRAFT_487638 [Arabidopsis lyrata subsp. lyrata] gi|297317142|gb|EFH47564.1| hypothetical protein ARALYDRAFT_487638 [Arabidopsis lyrata subsp. lyrata]	131	131	2.00E-59	100.0	80.2	91.6	hypothetical protein ARALYDRAFT_487638	gbpln	Arabidopsis lyrata	AT5G08060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 16 growth stages; Has 42 Blast hits to 42 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr5:2580588-2580983 FORWARD LENGTH=131	131	131	6.00E-62	100.0	80.2	91.6
Rsa1.0_01559.1.g27940.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01559.1.g27941.t1	ref|XP_002871297.1| hypothetical protein ARALYDRAFT_487629 [Arabidopsis lyrata subsp. lyrata] gi|297317134|gb|EFH47556.1| hypothetical protein ARALYDRAFT_487629 [Arabidopsis lyrata subsp. lyrata]	107	107	4.00E-54	100.0	95.3	97.2	hypothetical protein ARALYDRAFT_487629	gbpln	Arabidopsis lyrata	AT5G07960.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0139 (InterPro:IPR005351); Has 193 Blast hits to 193 proteins in 75 species: Archae - 0; Bacteria - 0; Metazoa - 130; Fungi - 0; Plants - 52; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr5:2542350-2543253 FORWARD LENGTH=107	107	107	9.00E-57	100.0	94.4	96.3
Rsa1.0_01559.1.g27942.t1	ref|NP_568186.1| uncharacterized protein [Arabidopsis thaliana] gi|21593576|gb|AAM65543.1| unknown [Arabidopsis thaliana] gi|332003845|gb|AED91228.1| uncharacterized protein AT5G07950 [Arabidopsis thaliana]	312	303	1.00E-108	97.1	64.7	74.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G07950.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 9 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:2540530-2542047 REVERSE LENGTH=303	312	303	1.00E-111	97.1	64.7	74.4

Rsa1.0_01559.1.g27943.t2	ref|XP_002871296.1| hypothetical protein ARALYDRAFT_487627 [Arabidopsis lyrata subsp. lyrata] gi|297317133|gb|EFH47555.1| hypothetical protein ARALYDRAFT_487627 [Arabidopsis lyrata subsp. lyrata]	1405	1523	0	108.4	72.8	81.9	hypothetical protein ARALYDRAFT_487627	gbpln	Arabidopsis lyrata	AT5G07940.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: pollen tube; BEST Arabidopsis thaliana protein match is: dentin sialophosphoprotein-related (TAIR:AT5G07980.1). | chr5:2534720-2540086 FORWARD LENGTH=1526	1405	1526	0	108.6	73.5	82.3
Rsa1.0_01559.1.g27944.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01559.1.g27945.t1	ref|NP_196410.1| MEI2 C-terminal RRM only like 2 [Arabidopsis thaliana] gi|6562307|emb|CAB62605.1| putative protein [Arabidopsis thaliana] gi|10176727|dbj|BAB09957.1| unnamed protein product [Arabidopsis thaliana] gi|332003839|gb|AED91222.1| MEI2 C-terminal RRM only like 2 [Arabidopsis thaliana]	277	282	2.00E-73	101.8	56.0	68.6	MEI2 C-terminal RRM only like 2	gbpln	Arabidopsis thaliana	AT5G07930.1 | Symbols: MCT2 | MEI2 C-terminal RRM only like 2 | chr5:2530865-2532216 FORWARD LENGTH=282	277	282	5.00E-76	101.8	56.0	68.6
Rsa1.0_01560.1.g27946.t8	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	790	1342	5.00E-62	169.9	13.8	17.7	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	790	1262	1.00E-19	159.7	6.5	9.1
Rsa1.0_01560.1.g27947.t1	gb|EOA37301.1| hypothetical protein CARUB_v10010954mg [Capsella rubella]	802	815	0	101.6	78.8	86.8	hypothetical protein CARUB_v10010954mg	gbpln	Capsella rubella	AT1G11280.3 | Symbols: | S-locus lectin protein kinase family protein | chr1:3787456-3790621 REVERSE LENGTH=808	802	808	0	100.7	79.2	87.4
Rsa1.0_01560.1.g27948.t1	ref|XP_002878862.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324701|gb|EFH55121.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	634	664	0	104.7	73.5	83.4	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT2G25560.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:10881790-10883760 FORWARD LENGTH=656	634	656	0	103.5	70.3	80.8
Rsa1.0_01560.1.g27949.t1	ref|XP_002878866.1| hypothetical protein ARALYDRAFT_344161 [Arabidopsis lyrata subsp. lyrata] gi|297324705|gb|EFH55125.1| hypothetical protein ARALYDRAFT_344161 [Arabidopsis lyrata subsp. lyrata]	315	377	1.00E-119	119.7	76.2	84.8	hypothetical protein ARALYDRAFT_344161	gbpln	Arabidopsis lyrata	AT4G32440.1 | Symbols: | Plant Tudor-like RNA-binding protein | chr4:15657295-15658692 FORWARD LENGTH=377	315	377	1.00E-106	119.7	68.6	79.4
Rsa1.0_01560.1.g27950.t1	gb|EOA25748.1| hypothetical protein CARUB_v10019110mg [Capsella rubella]	346	360	3.00E-91	104.0	53.2	65.6	hypothetical protein CARUB_v10019110mg	gbpln	Capsella rubella	AT2G44630.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:18415829-18416947 REVERSE LENGTH=372	346	372	4.00E-90	107.5	54.9	65.9
Rsa1.0_01560.1.g27951.t1	ref|NP_181998.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|142995062|sp|Q84RE1.2|FBK48_ARATH RecName: Full=F-box/kelch-repeat protein At2g44700 gi|3341690|gb|AAC27472.1| hypothetical protein [Arabidopsis thaliana] gi|55740615|gb|AAV63900.1| hypothetical protein At2g44700 [Arabidopsis thaliana] gi|330255363|gb|AEC10457.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	350	368	1.00E-91	105.1	53.1	66.6	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT2G44700.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:18431015-18432121 FORWARD LENGTH=368	350	368	3.00E-94	105.1	53.1	66.6
Rsa1.0_01560.1.g27952.t1	ref|NP_850062.1| uncharacterized protein [Arabidopsis thaliana] gi|45752742|gb|AAS76269.1| At2g25605 [Arabidopsis thaliana] gi|62320911|dbj|BAD93906.1| hypothetical protein [Arabidopsis thaliana] gi|330252629|gb|AEC07723.1| uncharacterized protein AT2G25605 [Arabidopsis thaliana]	197	200	8.00E-96	101.5	90.9	93.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G25605.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 75 Blast hits to 75 proteins in 20 species: Archae - 2; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 33 (source: NCBI BLink). | chr2:10899541-10900875 FORWARD LENGTH=200	197	200	3.00E-98	101.5	90.9	93.4
Rsa1.0_01560.1.g27953.t1	ref|NP_850063.1| uncharacterized protein [Arabidopsis thaliana] gi|20197506|gb|AAM15100.1| Expressed protein [Arabidopsis thaliana] gi|21593816|gb|AAM65783.1| unknown [Arabidopsis thaliana] gi|110742673|dbj|BAE99248.1| hypothetical protein [Arabidopsis thaliana] gi|330252633|gb|AEC07727.1| uncharacterized protein AT2G25625 [Arabidopsis thaliana]	148	152	3.00E-55	102.7	75.0	84.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G25625.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.06 six leaves visible, LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; Has 24 Blast hits to 24 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:10906562-10907099 FORWARD LENGTH=152	148	152	7.00E-58	102.7	75.0	84.5

Rsa1.0_01560.1.g27954.t2	ref|NP_180135.2| SPOC domain / Transcription elongation factor S-II protein [Arabidopsis thaliana] gi|330252635|gb|AEC07729.1| SPOC domain / Transcription elongation factor S-II protein [Arabidopsis thaliana]	826	745	0	90.2	57.6	64.6	SPOC domain / Transcription elongation factor S-II protein	gbpln	Arabidopsis thaliana	AT2G25640.1 | Symbols: | SPOC domain / Transcription elongation factor S-II protein | chr2:10910836-10913908 FORWARD LENGTH=745	826	745	0	90.2	57.6	64.6
Rsa1.0_01561.1.g27955.t1	gb|EOA36086.1| hypothetical protein CARUB_v10010474mg [Capsella rubella]	171	170	4.00E-59	99.4	63.7	69.6	hypothetical protein CARUB_v10010474mg	gbpln	Capsella rubella	AT1G18210.2 | Symbols: | Calcium-binding EF-hand family protein | chr1:6268273-6268785 REVERSE LENGTH=170	171	170	1.00E-60	99.4	62.0	67.8
Rsa1.0_01561.1.g27956.t1	gb|EOA36627.1| hypothetical protein CARUB_v10011865mg [Capsella rubella]	370	228	1.00E-109	61.6	54.6	56.8	hypothetical protein CARUB_v10011865mg	gbpln	Capsella rubella	AT1G18200.1 | Symbols: AtRABA6b, RABA6b | RAB GTPase homolog A6B | chr1:6265416-6266659 REVERSE LENGTH=229	370	229	1.00E-111	61.9	53.8	56.8
Rsa1.0_01561.1.g27957.t1	ref|XP_002892985.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338827|gb|EFH69244.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	590	579	0	98.1	89.7	93.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G18150.3 | Symbols: ATMPK8 | Protein kinase superfamily protein | chr1:6244641-6247582 REVERSE LENGTH=589	590	589	0	99.8	90.3	94.6
Rsa1.0_01561.1.g27958.t1	ref|XP_002892984.1| hypothetical protein ARALYDRAFT_889226 [Arabidopsis lyrata subsp. lyrata] gi|297338826|gb|EFH69243.1| hypothetical protein ARALYDRAFT_889226 [Arabidopsis lyrata subsp. lyrata]	578	581	0	100.5	88.4	93.8	hypothetical protein ARALYDRAFT_889226	gbpln	Arabidopsis lyrata	AT1G18140.1 | Symbols: LAC1, ATLAC1 | laccase 1 | chr1:6238986-6241393 REVERSE LENGTH=581	578	581	0	100.5	89.3	93.6
Rsa1.0_01561.1.g27959.t1	ref|XP_002890260.1| hypothetical protein ARALYDRAFT_889222 [Arabidopsis lyrata subsp. lyrata] gi|297336102|gb|EFH66519.1| hypothetical protein ARALYDRAFT_889222 [Arabidopsis lyrata subsp. lyrata]	588	577	0	98.1	78.7	83.7	hypothetical protein ARALYDRAFT_889222	gbpln	Arabidopsis lyrata	AT1G18090.2 | Symbols: | 5'-3' exonuclease family protein | chr1:6224539-6227715 FORWARD LENGTH=577	588	577	0	98.1	77.4	82.8
Rsa1.0_01561.1.g27960.t1	gb|EOA38237.1| hypothetical protein CARUB_v10009720mg [Capsella rubella]	328	328	0	100.0	95.4	97.9	hypothetical protein CARUB_v10009720mg	gbpln	Capsella rubella	AT1G18080.1 | Symbols: ATARCA, RACK1A_AT, RACK1A | Transducin/WD40 repeat-like superfamily protein | chr1:6222325-6223901 FORWARD LENGTH=327	328	327	0	99.7	95.1	97.6
Rsa1.0_01561.1.g27961.t20	gb|EOA37322.1| hypothetical protein CARUB_v10011009mg [Capsella rubella]	226	230	1.00E-111	101.8	87.2	94.7	hypothetical protein CARUB_v10011009mg	gbpln	Capsella rubella	AT1G18060.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 74 Blast hits to 74 proteins in 29 species: Archae - 0; Bacteria - 19; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:6212065-6213314 REVERSE LENGTH=226	226	226	1.00E-104	100.0	78.3	85.4
Rsa1.0_01561.1.g27962.t1	ref|XP_002892978.1| cyclin-dependent kinase D1_3 [Arabidopsis lyrata subsp. lyrata] gi|297338820|gb|EFH69237.1| cyclin-dependent kinase D1_3 [Arabidopsis lyrata subsp. lyrata]	425	393	0	92.5	83.3	87.5	cyclin-dependent kinase D1_3	gbpln	Arabidopsis lyrata	AT1G18040.1 | Symbols: CDKD1;3, AT;CDCKD;3, CAK2AT | cyclin-dependent kinase D1;3 | chr1:6207128-6209299 REVERSE LENGTH=391	425	391	0	92.0	82.4	86.4
Rsa1.0_01561.1.g27963.t1	ref|XP_002892977.1| nucleotidyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297338819|gb|EFH69236.1| nucleotidyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	690	716	0	103.8	87.0	93.2	nucleotidyltransferase family protein	gbpln	Arabidopsis lyrata	AT1G17980.1 | Symbols: PAPS1 | poly(A) polymerase 1 | chr1:6187742-6191418 REVERSE LENGTH=713	690	713	0	103.3	84.2	91.2
Rsa1.0_01561.1.g27964.t1	gb|EOA38056.1| hypothetical protein CARUB_v10009526mg [Capsella rubella]	366	363	1.00E-140	99.2	75.7	81.7	hypothetical protein CARUB_v10009526mg	gbpln	Capsella rubella	AT1G17970.1 | Symbols: | RING/U-box superfamily protein | chr1:6185032-6187202 FORWARD LENGTH=368	366	368	1.00E-131	100.5	73.0	81.4
Rsa1.0_01561.1.g27965.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01562.1.g27966.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01562.1.g27967.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01562.1.g27968.t1	gb|EOA35193.1| hypothetical protein CARUB_v10020343mg [Capsella rubella]	415	425	1.00E-170	102.4	69.9	81.4	hypothetical protein CARUB_v10020343mg	gbpln	Capsella rubella	AT1G57590.1 | Symbols: | Pectinacetylesterase family protein | chr1:21327458-21329707 REVERSE LENGTH=444	415	444	1.00E-172	107.0	69.4	81.0
Rsa1.0_01562.1.g27969.t1	gb|EOA15316.1| hypothetical protein CARUB_v100277371mg, partial [Capsella rubella]	437	413	1.00E-59	94.5	30.9	46.7	hypothetical protein CARUB_v100277371mg , partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	437	566	1.00E-37	129.5	21.7	37.8
Rsa1.0_01562.1.g27970.t2	ref|XP_003631153.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula] gi|355525175|gb|AET05629.1| ATP-dependent DNA helicase PIF1 [Medicago truncatula]	1351	1050	0	77.7	29.1	40.9	ATP-dependent DNA helicase PIF1	gbpln	Medicago truncatula	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1351	331	3.00E-67	24.5	11.1	15.3

Rsa1.0_01562.1.g27971.t1	ref|XP_002892284.1| thiF family protein [Arabidopsis lyrata subsp. lyrata] gi|297338126|gb|EFH68543.1| thiF family protein [Arabidopsis lyrata subsp. lyrata]	144	447	2.00E-23	310.4	49.3	58.3	thiF family protein	gbpln	Arabidopsis lyrata	AT1G05350.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:1560891-1564005 REVERSE LENGTH=431	144	431	6.00E-25	299.3	43.1	48.6
Rsa1.0_01562.1.g27972.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01562.1.g27973.t1	ref|XP_002878329.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297324167|gb|EFH54588.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	160	928	2.00E-15	580.0	27.5	33.1	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT3G60350.1 | Symbols: ARABIDILLO-2, ARABIDILLO2 | ARABIDILLO-2 | chr3:22306806-22310596 REVERSE LENGTH=928	160	928	4.00E-17	580.0	25.0	32.5
Rsa1.0_01563.1.g27974.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1747	1307	0	74.8	47.9	59.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT3G61390.2 | Symbols: | RING/U-box superfamily protein | chr3:22716418-22718270 FORWARD LENGTH=435	1747	435	1.00E-132	24.9	14.6	16.5
Rsa1.0_01563.1.g27975.t1	ref|XP_002876611.1| hypothetical protein ARALYDRAFT_486614 [Arabidopsis lyrata subsp. lyrata] gi|297322449|gb|EFH52870.1| hypothetical protein ARALYDRAFT_486614 [Arabidopsis lyrata subsp. lyrata]	286	295	6.00E-98	103.1	72.4	80.8	hypothetical protein ARALYDRAFT_486614	gbpln	Arabidopsis lyrata	AT3G61410.1 | Symbols: | BEST Arabidopsis thaliana protein match is: U-box domain-containing protein kinase family protein (TAIR:AT2G45910.1); Has 232 Blast hits to 229 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 13; Fungi - 0; Plants - 218; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:22721112-22722452 FORWARD LENGTH=294	286	294	2.00E-98	102.8	69.6	77.6
Rsa1.0_01563.1.g27976.t1	gb|EOA24331.1| hypothetical protein CARUB_v10017571mg [Capsella rubella]	286	343	1.00E-163	119.9	98.6	99.3	hypothetical protein CARUB_v10017571mg	gbpln	Capsella rubella	AT3G61430.2 | Symbols: PIP1A, ATPIP1, PIP1, PIP1;1 | plasma membrane intrinsic protein 1A | chr3:22733657-22735113 FORWARD LENGTH=286	286	286	1.00E-164	100.0	98.6	99.0
Rsa1.0_01563.1.g27977.t1	ref|NP_191703.1| cysteine synthase C1 [Arabidopsis thaliana] gi|75193637|sp|Q9S757.1|CYSC1_ARATH RecName: Full=Bifunctional L-3-cyanoalanine synthase/cysteine synthase C1, mitochondrial; AltName: Full=Beta-substituted Ala synthase 3;1; Short=ARAth-Bsas3;1; AltName: Full=Cysteine synthase C1; Short=AtCYSC1; AltName: Full=O-acetylserine (thiol)-lyase 5; Flags: Precursor gi|4996616|dbj|BAA78560.1| cysteine synthase [Arabidopsis thaliana] gi|5824334|emb|CAB54830.1| cysteine synthase [Arabidopsis thaliana] gi|6850835|emb|CAB71074.1| cysteine synthase AtcysC1 [Arabidopsis thaliana] gi|20260390|gb|AAM13093.1| cysteine synthase AtcysC1 [Arabidopsis thaliana] gi|21592815|gb|AAM64764.1| cysteine synthase AtcysC1 [Arabidopsis thaliana] gi|22136208|gb|AAM91182.1| cysteine synthase AtcysC1 [Arabidopsis thaliana] gi|110741540|dbj|BAE98719.1| cysteine synthase [Arabidopsis thaliana] gi|332646682|gb|AEE80203.1| cysteine synthase C1 [Arabidopsis thaliana]	368	368	0	100.0	91.8	95.9	cysteine synthase C1	gbpln	Arabidopsis thaliana	AT3G61440.1 | Symbols: ATCYSC1, ARATH;BSAS3;1, CYSC1 | cysteine synthase C1 | chr3:22735885-22737792 FORWARD LENGTH=368	368	368	0	100.0	91.8	95.9
Rsa1.0_01563.1.g27978.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01563.1_g27979.t1	ref|NP_191705.1| brassinosteroid-responsive RING-H2 [Arabidopsis thaliana] gi|297820998|ref|XP_002878382.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata] gi|4689366|gb|AAD27870.1|AF134155_1 BRH1 RING finger protein [Arabidopsis thaliana] gi|6850837|emb|CAB71076.1| RING finger protein [Arabidopsis thaliana] gi|17644157|gb|AAL38776.1| putative RING finger protein [Arabidopsis thaliana] gi|21436189|gb|AAM51382.1| putative RING finger protein [Arabidopsis thaliana] gi|21554590|gb|AAM63625.1| RING finger protein [Arabidopsis thaliana] gi|297324220|gb|EFH54641.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata] gi|332646687|gb|AEE80208.1| brassinosteroid-responsive RING-H2 [Arabidopsis thaliana]	166	170	2.00E-79	102.4	89.8	94.6	brassinosteroid-responsive RING-H2	gbpln	Arabidopsis lyrata	AT3G61460.1 | Symbols: BRH1 | brassinosteroid-responsive RING-H2 | chr3:22741701-22742213 REVERSE LENGTH=170	166	170	6.00E-82	102.4	89.8	94.6
Rsa1.0_01563.1_g27980.t2	ref|NP_001147224.1| chlorophyll a-b binding protein [Zea mays] gi|195608716|gb|ACG26188.1| chlorophyll a-b binding protein [Zea mays]	533	256	1.00E-137	48.0	44.3	44.5	chlorophyll a-b binding protein	gbenv/gbpln	Zea mays	AT3G61470.1 | Symbols: LHCA2 | photosystem I light harvesting complex gene 2 | chr3:22745736-22747032 FORWARD LENGTH=257	533	257	1.00E-129	48.2	40.9	41.8
Rsa1.0_01563.1_g27981.t1	gb|EOA24745.1| hypothetical protein CARUB_v10018022mg [Capsella rubella]	217	211	1.00E-86	97.2	74.7	77.9	hypothetical protein CARUB_v10018022mg	gbpln	Capsella rubella	AT3G61550.1 | Symbols: | RING/U-box superfamily protein | chr3:22776444-22777082 FORWARD LENGTH=212	217	212	2.00E-86	97.7	73.7	78.8
Rsa1.0_01564.1_g27982.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	889	1374	2.00E-82	154.6	21.8	31.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	889	575	4.00E-25	64.7	8.9	15.2
Rsa1.0_01564.1_g27983.t2	gb|AFN85666.1| glucanase 1 [Brassica rapa subsp. pekinensis]	86	341	4.00E-24	396.5	62.8	74.4	glucanase 1	gbpln	Brassica rapa	AT3G57240.1 | Symbols: BG3 | beta-1,3-glucanase 3 | chr3:21181916-21183045 REVERSE LENGTH=341	86	341	3.00E-24	396.5	57.0	68.6
Rsa1.0_01564.1_g27984.t1	gb|AAX76839.1| beta-1,3-glucanase [Brassica rapa subsp. chinensis]	344	363	1.00E-165	105.5	85.8	92.2	beta-1,3-glucanase	gbpln	Brassica rapa	AT3G57260.1 | Symbols: BGL2, PR2, BG2, PR-2 | beta-1,3-glucanase 2 | chr3:21188709-21189822 REVERSE LENGTH=339	344	339	1.00E-109	98.5	61.3	76.2
Rsa1.0_01564.1_g27985.t1	ref|XP_002878144.1| hypothetical protein ARALYDRAFT_486171 [Arabidopsis lyrata subsp. lyrata] gi|297323982|gb|EFH54403.1| hypothetical protein ARALYDRAFT_486171 [Arabidopsis lyrata subsp. lyrata]	441	441	0	100.0	95.5	98.0	hypothetical protein ARALYDRAFT_486171	gbpln	Arabidopsis lyrata	AT3G57290.1 | Symbols: EIF3E, TIF3E1, ATEIF3E-1, INT-6, ATINT6, INT6 | eukaryotic translation initiation factor 3E | chr3:21196786-21199073 REVERSE LENGTH=441	441	441	0	100.0	93.9	97.5
Rsa1.0_01564.1_g27986.t1	ref|NP_191295.4| uncharacterized protein [Arabidopsis thaliana] gi|50198814|gb|AAT70440.1| At3g57360 [Arabidopsis thaliana] gi|51972142|gb|AAU15175.1| At3g57360 [Arabidopsis thaliana] gi|332646125|gb|AEE79646.1| uncharacterized protein AT3G57360 [Arabidopsis thaliana]	243	254	1.00E-104	104.5	82.3	88.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G57360.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02370.2); Has 122 Blast hits to 122 proteins in 54 species: Archae - 0; Bacteria - 0; Metazoa - 74; Fungi - 4; Plants - 41; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:21225571-21226621 FORWARD LENGTH=254	243	254	1.00E-107	104.5	82.3	88.1
Rsa1.0_01564.1_g27987.t1	ref|XP_002881787.1| hypothetical protein ARALYDRAFT_903484 [Arabidopsis lyrata subsp. lyrata] gi|297327626|gb|EFH58046.1| hypothetical protein ARALYDRAFT_903484 [Arabidopsis lyrata subsp. lyrata]	203	312	2.00E-16	153.7	27.6	43.8	hypothetical protein ARALYDRAFT_903484	gbpln	Arabidopsis lyrata	AT2G41630.1 | Symbols: TFIIB | transcription factor IIB | chr2:17355555-17357400 REVERSE LENGTH=312	203	312	4.00E-18	153.7	27.1	43.8
Rsa1.0_01565.1_g27988.t1	gb|EOA24130.1| hypothetical protein CARUB_v10017363mg [Capsella rubella]	150	408	2.00E-71	272.0	86.0	95.3	hypothetical protein CARUB_v10017363mg	gbpln	Capsella rubella	AT3G48460.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:17949496-17951082 FORWARD LENGTH=381	150	381	3.00E-71	254.0	82.7	95.3
Rsa1.0_01565.1_g27989.t2	gb|EOA23443.1| hypothetical protein CARUB_v10016628mg [Capsella rubella]	1055	1011	0	95.8	82.0	88.1	hypothetical protein CARUB_v10016628mg	gbpln	Capsella rubella	AT3G48470.1 | Symbols: EMB2423 | embryo defective 2423 | chr3:17951689-17956754 FORWARD LENGTH=1027	1055	1027	0	97.3	79.8	87.0
Rsa1.0_01565.1_g27990.t3	gb|EOA24353.1| hypothetical protein CARUB_v10017593mg, partial [Capsella rubella]	275	328	1.00E-100	119.3	68.7	80.7	hypothetical protein CARUB_v10017593mg, partial	gbpln	Capsella rubella	AT3G48480.1 | Symbols: | Cysteine proteinases superfamily protein | chr3:17957326-17959062 REVERSE LENGTH=298	275	298	3.00E-99	108.4	69.5	78.2

Rsa1.0_01565.1.g27991.t1	ref|NP_193153.3| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|223635637|sp|Q5XEY7.2|PP309_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g14170 gi|332657989|gb|AEE83389.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	477	477	0	100.0	78.2	86.2	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT4G14170.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:8176709-8178142 REVERSE LENGTH=477	477	477	0	100.0	78.2	86.2
Rsa1.0_01565.1.g27992.t1	ref|XP_002877614.1| hypothetical protein ARALYDRAFT_485209 [Arabidopsis lyrata subsp. lyrata] gi|297323452|gb|EFH53873.1| hypothetical protein ARALYDRAFT_485209 [Arabidopsis lyrata subsp. lyrata]	302	293	1.00E-107	97.0	73.2	81.5	hypothetical protein ARALYDRAFT_485209	gbpln	Arabidopsis lyrata	AT3G48510.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G63350.1); Has 98 Blast hits to 98 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 98; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:17967568-17968452 REVERSE LENGTH=294	302	294	1.00E-108	97.4	73.5	80.8
Rsa1.0_01565.1.g27993.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01565.1.g27994.t1	gb|AAF23831.1|AC007234_3 F1E22.12 [Arabidopsis thaliana]	473	1055	1.00E-148	223.0	53.9	70.4	F1E22.12	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:17201414-17202323 REVERSE LENGTH=258	473	258	2.00E-57	54.5	24.3	29.8
Rsa1.0_01565.1.g27995.t1	gb|EOA23627.1| hypothetical protein CARUB_v10016824mg [Capsella rubella]	564	593	0	105.1	81.4	86.7	hypothetical protein CARUB_v10016824mg	gbpln	Capsella rubella	AT5G63370.4 | Symbols: | Protein kinase superfamily protein | chr5:25384954-25386792 REVERSE LENGTH=612	564	612	0	108.5	65.1	77.7
Rsa1.0_01565.1.g27996.t1	ref|NP_190421.1| cytochrome P450, family 94, subfamily B, polypeptide 3 [Arabidopsis thaliana] gi|6523083|emb|CAB62341.1| cytochrome P450-like protein [Arabidopsis thaliana] gi|51536434|gb|AAU05455.1| At3g48520 [Arabidopsis thaliana] gi|53828589|gb|AAU94404.1| At3g48520 [Arabidopsis thaliana] gi|110740781|dbj|BAE98488.1| cytochrome P450 like protein [Arabidopsis thaliana] gi|332644905|gb|AEE78426.1| cytochrome P450, family 94, subfamily B, polypeptide 3 [Arabidopsis thaliana]	491	506	0	103.1	87.4	91.6	cytochrome P450, family 94, subfamily B, polypeptide 3	gbpln	Arabidopsis thaliana	AT3G48520.1 | Symbols: CYP94B3 | cytochrome P450, family 94, subfamily B, polypeptide 3 | chr3:17975104-17976624 REVERSE LENGTH=506	491	506	0	103.1	87.4	91.6
Rsa1.0_01565.1.g27997.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	506	1239	0	244.9	81.4	92.1	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	506	1262	2.00E-93	249.4	34.4	52.8
Rsa1.0_01565.1.g27998.t1	gb|EOA30279.1| hypothetical protein CARUB_v10013406mg [Capsella rubella]	544	539	0	99.1	85.5	92.3	hypothetical protein CARUB_v10013406mg	gbpln	Capsella rubella	AT2G05160.1 | Symbols: | CCCH-type zinc fingerfamily protein with RNA-binding domain | chr2:1859011-1860931 REVERSE LENGTH=536	544	536	0	98.5	82.2	90.6
Rsa1.0_01565.1.g27999.t1	ref|XP_002885794.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297331634|gb|EFH62053.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	691	700	0	101.3	85.1	90.6	DNAJ heat shock N-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT2G05230.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:1899818-1901938 REVERSE LENGTH=706	691	706	0	102.2	84.4	89.6
Rsa1.0_01565.1.g28000.t1	ref|NP_178601.2| beta-1,2-N-acetylglucosaminyltransferase II [Arabidopsis thaliana] gi|10183645|emb|CAC08806.1| beta-1,2-N-acetylglucosaminyltransferase II [Arabidopsis thaliana] gi|330250822|gb|AEC05916.1| beta-1,2-N-acetylglucosaminyltransferase II [Arabidopsis thaliana]	434	430	0	99.1	80.0	87.6	beta-1,2-N-acetylglucosaminyltransferase II	gbpln	Arabidopsis thaliana	AT2G05320.1 | Symbols: | beta-1,2-N-acetylglucosaminyltransferase II | chr2:1936016-1937308 FORWARD LENGTH=430	434	430	0	99.1	80.0	87.6
Rsa1.0_01566.1.g28001.t6	ref|NP_198055.3| Topless-related protein 3 [Arabidopsis thaliana] gi|75327840|sp|Q84JM4.1|TPR3_ARATH RecName: Full=Topless-related protein 3 gi|28393287|gb|AAO42071.1| unknown protein [Arabidopsis thaliana] gi|28827708|gb|AAO50698.1| unknown protein [Arabidopsis thaliana] gi|332006259|gb|AED93642.1| Topless-related protein 3 [Arabidopsis thaliana]	1304	1108	0	85.0	68.6	73.2	Topless-related protein 3	gbpln	Arabidopsis thaliana	AT5G27030.1 | Symbols: TPR3 | TOPLESS-related 3 | chr5:9508913-9515263 REVERSE LENGTH=1108	1304	1108	0	85.0	68.6	73.2

Rsa1.0_01566.1.g28002.t10	ref|NP_568491.1| kinesin 4 [Arabidopsis thaliana] gi|34921410|sp|O81635.2|ATK4_ARATH RecName: Full=Kinesin-4; AltName: Full=Kinesin-like protein D gi|332006256|gb|AED93639.1| kinesin 4 [Arabidopsis thaliana]	956	987	0	103.2	79.1	85.6	kinesin 4	gbpln	Arabidopsis thaliana	AT5G27000.1 | Symbols: ATK4, KATD | kinesin 4 | chr5:9498099-9502951 FORWARD LENGTH=987	956	987	0	103.2	79.1	85.6
Rsa1.0_01566.1.g28003.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01566.1.g28004.t1	gb|EOA21513.1| hypothetical protein CARUB_v10001910mg [Capsella rubella]	224	222	3.00E-82	99.1	74.1	82.1	hypothetical protein CARUB_v10001910mg	gbpln	Capsella rubella	AT5G26990.1 | Symbols: | Drought-responsive family protein | chr5:9491366-9493639 FORWARD LENGTH=222	224	222	5.00E-80	99.1	75.0	82.6
Rsa1.0_01566.1.g28005.t1	gb|EOA21136.1| hypothetical protein CARUB_v10001480mg [Capsella rubella] gi|482556945|gb|EOA21137.1| hypothetical protein CARUB_v10001480mg [Capsella rubella]	328	318	1.00E-138	97.0	76.2	86.0	hypothetical protein CARUB_v10001480mg	gbpln	Capsella rubella	AT5G26940.4 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:9481429-9482647 FORWARD LENGTH=316	328	316	1.00E-139	96.3	76.8	85.1
Rsa1.0_01566.1.g28006.t2	gb|EOA19384.1| hypothetical protein CARUB_v10000582mg [Capsella rubella]	676	571	0	84.5	51.8	62.6	hypothetical protein CARUB_v10000582mg	gbpln	Capsella rubella	AT5G26920.1 | Symbols: CBP60G | Cam-binding protein 60-like G | chr5:9475860-9478448 FORWARD LENGTH=563	676	563	0	83.3	50.9	61.2
Rsa1.0_01567.1.g28007.t1	dbj|BAJ34270.1| unnamed protein product [Thellungiella halophila]	445	459	0	103.1	83.6	91.5	unnamed protein product	----	----	AT5G52180.1 | Symbols: | LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Transmembrane protein 161AB, predicted (InterPro:IPR019395); Has 82 Blast hits to 82 proteins in 35 species: Archae - 0; Bacteria - 0; Metazoa - 47; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr5:21200165-21201541 REVERSE LENGTH=458	445	458	0	102.9	82.2	90.6
Rsa1.0_01567.1.g28008.t1	gb|EOA14997.1| hypothetical protein CARUB_v10028346mg [Capsella rubella]	689	683	0	99.1	77.4	86.4	hypothetical protein CARUB_v10028346mg	gbpln	Capsella rubella	AT5G52170.1 | Symbols: HDG7 | homeodomain GLABROUS 7 | chr5:21196974-21199959 FORWARD LENGTH=682	689	682	0	99.0	77.5	85.6
Rsa1.0_01567.1.g28009.t3	gb|EOA23500.1| hypothetical protein CARUB_v10016692mg [Capsella rubella]	291	819	4.00E-47	281.4	39.2	44.7	hypothetical protein CARUB_v10016692mg	gbpln	Capsella rubella	AT3G49650.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:18405260-18409402 REVERSE LENGTH=813	291	813	4.00E-49	279.4	35.7	37.8
Rsa1.0_01567.1.g28010.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1450	1307	0	90.1	54.5	69.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1450	1262	5.00E-99	87.0	13.2	21.3
Rsa1.0_01567.1.g28011.t1	gb|ABA70759.1| baby boom interacting protein 1B [Brassica napus]	275	711	8.00E-82	258.5	58.5	63.6	baby boom interacting protein 1B	gbpln	Brassica napus	AT1G73360.1 | Symbols: HDG11, EDT1, ATHDG11 | homeodomain GLABROUS 11 | chr1:27578893-27581820 REVERSE LENGTH=722	275	722	7.00E-67	262.5	53.1	58.2
Rsa1.0_01567.1.g28012.t1	gb|EOA14892.1| hypothetical protein CARUB_v10028221mg [Capsella rubella]	95	96	2.00E-31	101.1	71.6	82.1	hypothetical protein CARUB_v10028221mg	gbpln	Capsella rubella	AT5G52160.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:21195140-21195430 FORWARD LENGTH=96	95	96	7.00E-30	101.1	60.0	64.2
Rsa1.0_01567.1.g28013.t2	ref|XP_002865896.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297311731|gb|EFH42155.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	233	280	4.00E-57	120.2	58.4	69.1	protein binding protein	gbpln	Arabidopsis lyrata	AT5G52140.1 | Symbols: | RING/U-box superfamily protein | chr5:21184566-21186872 REVERSE LENGTH=280	233	280	5.00E-52	120.2	54.1	64.8
Rsa1.0_01568.1.g28014.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01568.1.g28015.t1	gb|EOA23460.1| hypothetical protein CARUB_v10016649mg [Capsella rubella]	920	947	0	102.9	79.1	88.0	hypothetical protein CARUB_v10016649mg	gbpln	Capsella rubella	AT2G01820.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:357664-360681 REVERSE LENGTH=943	920	943	0	102.5	78.0	87.6
Rsa1.0_01568.1.g28016.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01568.1.g28017.t1	gb|AAZ41811.1| 01P13-1 [Brassica rapa subsp. pekinensis]	787	1545	1.00E-154	196.3	36.2	43.1	01P13-1	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	787	1262	3.00E-57	160.4	14.2	22.1
Rsa1.0_01568.1.g28018.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01568.1.g28019.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	262	1274	1.00E-38	486.3	38.5	54.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	262	303	3.00E-34	115.6	33.6	48.1

Rsa1.0_01568.1.g28020.t1	ref|XP_002875095.1| endoxyloglucan transferase [Arabidopsis lyrata subsp. lyrata] gi|297320933|gb|EFH51354.1| endoxyloglucan transferase [Arabidopsis lyrata subsp. lyrata]	333	333	0	100.0	91.6	95.5	endoxyloglucan transferase	gbpln	Arabidopsis lyrata	AT2G01850.1 | Symbols: EXGT-A3, XTH27, ATXTH27 | endoxyloglucan transferase A3 | chr2:385374-387138 FORWARD LENGTH=333	333	333	1.00E-179	100.0	88.6	93.7
Rsa1.0_01569.1.g28021.t1	ref|NP_179096.1| gibberellin-regulated protein [Arabidopsis thaliana] gi|75100623|sp|O82328.1|GASA7_ARATH RecName: Full=Gibberellin-regulated protein 7; AltName: Full=GAST1 protein homolog 7; Flags: Precursor gi|3650032|gb|AAC61287.1| similar to gibberellin-regulated proteins [Arabidopsis thaliana] gi|27754546|gb|AAO22720.1| putative gibberellin-regulated protein [Arabidopsis thaliana] gi|28394019|gb|AAO42417.1| putative gibberellin-regulated protein [Arabidopsis thaliana] gi|330251254|gb|AEC06348.1| gibberellin-regulated protein [Arabidopsis thaliana]	77	108	2.00E-20	140.3	58.4	71.4	gibberellin-regulated protein	gbpln	Arabidopsis thaliana	AT2G14900.1 | Symbols: | Gibberellin-regulated family protein | chr2:6404210-6405043 FORWARD LENGTH=108	77	108	4.00E-23	140.3	58.4	71.4
Rsa1.0_01569.1.g28022.t1	gb|EOA30442.1| hypothetical protein CARUB_v10013565mg [Capsella rubella]	452	484	0	107.1	92.5	96.0	hypothetical protein CARUB_v10013565mg	gbpln	Capsella rubella	AT3G19540.1 | Symbols: | Protein of unknown function (DUF620) | chr3:6780762-6782633 FORWARD LENGTH=485	452	485	0	107.3	92.5	95.8
Rsa1.0_01569.1.g28023.t1	ref|XP_002885314.1| hypothetical protein ARALYDRAFT_479468 [Arabidopsis lyrata subsp. lyrata] gi|297331154|gb|EFH61573.1| hypothetical protein ARALYDRAFT_479468 [Arabidopsis lyrata subsp. lyrata]	210	110	3.00E-30	52.4	34.3	39.0	hypothetical protein ARALYDRAFT_479468	gbpln	Arabidopsis lyrata	AT3G19550.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; Has 36 Blast hits to 36 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6787462-6788165 REVERSE LENGTH=110	210	110	7.00E-32	52.4	32.9	37.6
Rsa1.0_01569.1.g28024.t1	ref|NP_188589.1| Amino acid permease family protein [Arabidopsis thaliana] gi|75311166|sp|Q9LH39.1|PHSD_ARATH RecName: Full=Probable polyamine transporter At3g19553 gi|9294126|dbj|BAB01977.1| unnamed protein product [Arabidopsis thaliana] gi|332642736|gb|AEE76257.1| Amino acid permease family protein [Arabidopsis thaliana]	479	479	0	100.0	91.6	95.0	Amino acid permease family protein	gbpln	Arabidopsis thaliana	AT3G19553.1 | Symbols: | Amino acid permease family protein | chr3:6790988-6792507 REVERSE LENGTH=479	479	479	0	100.0	91.6	95.0
Rsa1.0_01569.1.g28025.t2	ref|NP_850614.1| uncharacterized protein [Arabidopsis thaliana] gi|26451622|dbj|BAC42908.1| unknown protein [Arabidopsis thaliana] gi|28973259|gb|AAO63954.1| unknown protein [Arabidopsis thaliana] gi|332642739|gb|AEE76260.1| uncharacterized protein AT3G19570 [Arabidopsis thaliana]	615	644	0	104.7	75.1	82.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G19570.2 | Symbols: SCO3, QWRF1 | Family of unknown function (DUF566) | chr3:6797778-6801344 FORWARD LENGTH=644	615	644	0	104.7	75.1	82.1
Rsa1.0_01569.1.g28026.t1	gb|ABI74621.1| C2H2 zinc finger protein 1 [Eutrema halophilum] gi|312282663|dbj|BAJ34197.1| unnamed protein product [Thellungiella halophila]	257	276	5.00E-76	107.4	76.7	83.3	C2H2 zinc finger protein 1	gbpln	Eutrema halophilum	AT3G19580.2 | Symbols: AZF2, ZF2 | zinc-finger protein 2 | chr3:6803293-6804114 REVERSE LENGTH=273	257	273	3.00E-74	106.2	75.5	81.7
Rsa1.0_01569.1.g28027.t1	gb|EOA30976.1| hypothetical protein CARUB_v10014121mg [Capsella rubella]	341	339	0	99.4	92.4	95.9	hypothetical protein CARUB_v10014121mg	gbpln	Capsella rubella	AT3G19590.1 | Symbols: BUB3.1 | Transducin/WD40 repeat-like superfamily protein | chr3:6805798-6808374 FORWARD LENGTH=340	341	340	0	99.7	92.4	95.6
Rsa1.0_01569.1.g28028.t1	ref|NP_001118664.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|9294424|dbj|BAB02544.1| unnamed protein product [Arabidopsis thaliana] gi|332642743|gb|AEE76264.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana]	235	307	2.00E-76	130.6	66.8	75.7	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G19595.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr3:6808585-6809508 REVERSE LENGTH=307	235	307	7.00E-79	130.6	66.8	75.7
Rsa1.0_01569.1.g28029.t1	ref|XP_002885318.1| hypothetical protein ARALYDRAFT_479477 [Arabidopsis lyrata subsp. lyrata] gi|297331158|gb|EFH61577.1| hypothetical protein ARALYDRAFT_479477 [Arabidopsis lyrata subsp. lyrata]	81	613	2.00E-13	756.8	49.4	54.3	hypothetical protein ARALYDRAFT_479477	gbpln	Arabidopsis lyrata	AT3G19610.1 | Symbols: | Plant protein of unknown function (DUF936) | chr3:6812493-6814660 REVERSE LENGTH=640	81	640	2.00E-15	790.1	48.1	53.1

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<tr><td>Rsa1.0_01569.1.g28030.t1</td><td>gb|EOA33039.1| hypothetical protein CARUB_v10016371mg [Capsella rubella]</td><td>100</td><td>93</td><td>2.00E−32</td><td>93.0</td><td>75.0</td><td>77.0</td><td>hypothetical protein CARUB_v10016371mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G19615.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 10 Blast hits to 10 proteins in 5 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 10; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:6815073−6815354 REVERSE LENGTH=93</td><td>100</td><td>93</td><td>1.00E−34</td><td>93.0</td><td>73.0</td><td>77.0</td></tr>
<tr><td>Rsa1.0_01570.1.g28031.t1</td><td>gb|AAF79677.1|AC022314_18 F9C16.26 [Arabidopsis thaliana]</td><td>165</td><td>1902</td><td>3.00E−19</td><td>1152.7</td><td>27.9</td><td>42.4</td><td>F9C16.26</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G05095.1 | Symbols: | BEST Arabidopsis thaliana protein match is: RNA−directed DNA polymerase (reverse transcriptase)−related family protein (TAIR:AT4G04650.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr4:2613798−2614214 REVERSE LENGTH=138</td><td>165</td><td>138</td><td>1.00E−18</td><td>83.6</td><td>24.8</td><td>41.2</td></tr>
<tr><td>Rsa1.0_01570.1.g28032.t1</td><td>gb|ABL97978.1| metal ion binding [Brassica rapa]</td><td>135</td><td>139</td><td>2.00E−38</td><td>103.0</td><td>65.9</td><td>77.8</td><td>metal ion binding</td><td>gbpln</td><td>Brassica rapa</td><td>AT5G52760.1 | Symbols: | Copper transport protein family | chr5:21386919−21387540 FORWARD LENGTH=126</td><td>135</td><td>126</td><td>1.00E−30</td><td>93.3</td><td>58.5</td><td>71.1</td></tr>
<tr><td>Rsa1.0_01570.1.g28033.t1</td><td>gb|EOA27224.1| hypothetical protein CARUB_v10023333mg [Capsella rubella]</td><td>453</td><td>407</td><td>1.00E−175</td><td>89.8</td><td>71.3</td><td>76.4</td><td>hypothetical protein CARUB_v10023333mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G25840.2 | Symbols: OVA4 | Nucleotidylyl transferase superfamily protein | chr2:11021924−11025158 FORWARD LENGTH=412</td><td>453</td><td>412</td><td>1.00E−163</td><td>90.9</td><td>64.5</td><td>68.9</td></tr>
<tr><td>Rsa1.0_01570.1.g28034.t1</td><td>ref|XP_004297977.1| PREDICTED: uncharacterized protein LOC101305167 [Fragaria vesca subsp. vesca]</td><td>764</td><td>934</td><td>0</td><td>122.3</td><td>45.0</td><td>59.4</td><td>PREDICTED: uncharacterized protein LOC101305167</td><td>gbpln</td><td>Fragaria vesca</td><td>AT4G10200.1 | Symbols: | TTF−type zinc finger protein with HAT dimerisation domain | chr4:6353172−6355591 FORWARD LENGTH=733</td><td>764</td><td>733</td><td>1.00E−161</td><td>95.9</td><td>42.3</td><td>55.2</td></tr>
<tr><td>Rsa1.0_01570.1.g28035.t1</td><td>gb|EOA13610.1| hypothetical protein CARUB_v10026677mg, partial [Capsella rubella]</td><td>322</td><td>355</td><td>1.00E−145</td><td>110.2</td><td>85.7</td><td>91.0</td><td>hypothetical protein CARUB_v10026677mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G52660.2 | Symbols: | Homeodomain−like superfamily protein | chr5:21359423−21362037 REVERSE LENGTH=331</td><td>322</td><td>331</td><td>1.00E−147</td><td>102.8</td><td>86.6</td><td>90.7</td></tr>
<tr><td>Rsa1.0_01570.1.g28036.t1</td><td>gb|EOA13969.1| hypothetical protein CARUB_v10027094mg, partial [Capsella rubella]</td><td>180</td><td>220</td><td>4.00E−77</td><td>122.2</td><td>88.3</td><td>90.6</td><td>hypothetical protein CARUB_v10027094mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G25740.1 | Symbols: | RNA binding Plectin/S10 domain−containing protein | chr4:13107488−13108751 REVERSE LENGTH=177</td><td>180</td><td>177</td><td>1.00E−69</td><td>98.3</td><td>88.3</td><td>91.1</td></tr>
<tr><td>Rsa1.0_01570.1.g28037.t1</td><td>gb|AAF14064.1|AF048841_1 MYB82 [Arabidopsis thaliana]</td><td>195</td><td>201</td><td>7.00E−84</td><td>103.1</td><td>82.1</td><td>88.7</td><td>MYB82</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G52600.1 | Symbols: AtMYB82, MYB82 | myb domain protein 82 | chr5:21343197−21343968 REVERSE LENGTH=201</td><td>195</td><td>201</td><td>3.00E−86</td><td>103.1</td><td>82.1</td><td>88.7</td></tr>
<tr><td>Rsa1.0_01570.1.g28038.t2</td><td>ref|XP_002865917.1| hypothetical protein ARALYDRAFT_918304 [Arabidopsis lyrata subsp. lyrata] gi|297311752|gb|EFH42176.1| hypothetical protein ARALYDRAFT_918304 [Arabidopsis lyrata subsp. lyrata]</td><td>591</td><td>464</td><td>0</td><td>78.5</td><td>66.7</td><td>71.2</td><td>hypothetical protein ARALYDRAFT_918304</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G52540.1 | Symbols: | Protein of unknown function (DUF819) | chr5:21321672−21323702 REVERSE LENGTH=461</td><td>591</td><td>461</td><td>0</td><td>78.0</td><td>66.7</td><td>71.6</td></tr>
<tr><td>Rsa1.0_01571.1.g28039.t1</td><td>gb|EOA25193.1| hypothetical protein CARUB_v10018504mg [Capsella rubella]</td><td>98</td><td>92</td><td>1.00E−17</td><td>93.9</td><td>56.1</td><td>69.4</td><td>hypothetical protein CARUB_v10018504mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G59930.1 | Symbols: | Encodes a defensin−like (DEFL) family protein. | chr3:22139772−22140127 REVERSE LENGTH=80</td><td>98</td><td>80</td><td>1.00E−14</td><td>81.6</td><td>48.0</td><td>60.2</td></tr>
<tr><td>Rsa1.0_01571.1.g28040.t1</td><td>gb|EOA16735.1| hypothetical protein CARUB_v10004938mg [Capsella rubella]</td><td>406</td><td>410</td><td>0</td><td>101.0</td><td>85.5</td><td>91.9</td><td>hypothetical protein CARUB_v10004938mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G41060.1 | Symbols: | DHHC−type zinc finger family protein | chr5:16435602−16437540 FORWARD LENGTH=410</td><td>406</td><td>410</td><td>0</td><td>101.0</td><td>83.7</td><td>91.9</td></tr>
<tr><td>Rsa1.0_01571.1.g28041.t1</td><td>gb|EOA16772.1| hypothetical protein CARUB_v10004991mg [Capsella rubella]</td><td>376</td><td>393</td><td>1.00E−134</td><td>104.5</td><td>71.8</td><td>78.7</td><td>hypothetical protein CARUB_v10004991mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G41070.1 | Symbols: DRB5 | dsRNA−binding protein 5 | chr5:16438547−16439916 FORWARD LENGTH=393</td><td>376</td><td>393</td><td>1.00E−130</td><td>104.5</td><td>70.7</td><td>79.0</td></tr>
<tr><td>Rsa1.0_01571.1.g28042.t1</td><td>ref|XP_002870654.1| glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297316490|gb|EFH46913.1| glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>376</td><td>375</td><td>0</td><td>99.7</td><td>87.0</td><td>93.6</td><td>glycerophosphoryl diester phosphodiesterase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G41080.1 | Symbols: | PLC−like phosphodiesterases superfamily protein | chr5:16441858−16443835 FORWARD LENGTH=374</td><td>376</td><td>374</td><td>0</td><td>99.5</td><td>86.2</td><td>92.3</td></tr>
<tr><td>Rsa1.0_01571.1.g28043.t1</td><td>ref|XP_002878091.1| hypothetical protein ARALYDRAFT_324164 [Arabidopsis lyrata subsp. lyrata] gi|297323929|gb|EFH54350.1| hypothetical protein ARALYDRAFT_324164 [Arabidopsis lyrata subsp. lyrata]</td><td>261</td><td>167</td><td>2.00E−29</td><td>64.0</td><td>25.3</td><td>32.6</td><td>hypothetical protein ARALYDRAFT_324164</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G56520.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr3:20947107−20947731 REVERSE LENGTH=175</td><td>261</td><td>175</td><td>3.00E−31</td><td>67.0</td><td>24.5</td><td>30.3</td></tr>
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Rsa1.0_01571.1.g28044.t1	ref|NP_172436.1| F-box/LRR and kelch-repeat containing protein [Arabidopsis thaliana] gi|75218978|sp|O04488.1|FBLK1_ARATH RecName: Full=F-box/LRR-repeat/kelch-repeat protein At1g09650 gi|2160159|gb|AAB60722.1| F21M12.4 gene product [Arabidopsis thaliana] gi|110738143|dbj|BAF01003.1| hypothetical protein [Arabidopsis thaliana] gi|332190354|gb|AEE28475.1| F-box/LRR and kelch-repeat containing protein [Arabidopsis thaliana]	251	382	1.00E-62	152.2	54.2	64.9	F-box/LRR and kelch-repeat containing protein	gbpln	Arabidopsis thaliana	AT1G09650.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3125978-3127126 FORWARD LENGTH=382	251	382	4.00E-65	152.2	54.2	64.9
Rsa1.0_01571.1.g28045.t1	ref|NP_174428.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75169458|sp|Q9C866.1|PPR65_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g31430 gi|12322531|gb|AAG51260.1|AC027135_1 PPR-repeat protein [Arabidopsis thaliana] gi|332193234|gb|AEE31355.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	379	570	8.00E-36	150.4	33.8	41.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G31430.1 | Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:11254025-11255737 REVERSE LENGTH=570	379	570	2.00E-38	150.4	33.8	41.4
Rsa1.0_01571.1.g28046.t1	gb|EOA28508.1| hypothetical protein CARUB_v10024723mg [Capsella rubella]	283	384	5.00E-74	135.7	50.5	52.7	hypothetical protein CARUB_v10024723mg	gbpln	Capsella rubella	AT2G41670.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:17374118-17376177 FORWARD LENGTH=386	283	386	9.00E-75	136.4	49.8	51.9
Rsa1.0_01571.1.g28047.t5	gb|AAC28216.1| T24M8.9 gene product [Arabidopsis thaliana] gi|7267147|emb|CAB80815.1| putative protein [Arabidopsis thaliana]	397	463	6.00E-20	116.6	12.1	17.1	T24M8.9 gene product	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	397	530	1.00E-13	133.5	9.6	15.4
Rsa1.0_01572.1.g28048.t1	ref|NP_564790.3| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|14334426|gb|AAK59411.1| unknown protein [Arabidopsis thaliana] gi|27754742|gb|AAO22814.1| unknown protein [Arabidopsis thaliana] gi|332195798|gb|AEE33919.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	616	624	0	101.3	84.9	88.6	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G62050.1 | Symbols: | Ankyrin repeat family protein | chr1:22936323-22938874 REVERSE LENGTH=624	616	624	0	101.3	84.9	88.6
Rsa1.0_01572.1.g28049.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	195	1491	7.00E-68	764.6	60.5	77.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	195	237	1.00E-27	121.5	30.8	49.7
Rsa1.0_01572.1.g28050.t1	gb|EOA35216.1| hypothetical protein CARUB_v10020367mg [Capsella rubella]	387	417	1.00E-140	107.8	66.9	82.2	hypothetical protein CARUB_v10020367mg	gbpln	Capsella rubella	AT1G61990.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:22911453-22912697 FORWARD LENGTH=414	387	414	1.00E-139	107.0	65.6	81.4
Rsa1.0_01572.1.g28051.t1	gb|ABD65076.1| SLL3 ORF2 protein, putative [Brassica oleracea]	364	443	2.00E-20	121.7	19.2	24.7	SLL3 ORF2 protein, putative	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01572.1.g28052.t2	#	#	#	#	#	#	#	-	----	----	AT1G20200.1 | Symbols: EMB2719, HAP15 | PAM domain (PCI/PINT associated module) protein | chr1:7001409-7004154 REVERSE LENGTH=488	159	488	6.00E-11	306.9	17.6	20.8
Rsa1.0_01572.1.g28053.t1	gb|ABD65163.1| hypothetical protein 40.t00048 [Brassica oleracea]	201	569	1.00E-10	283.1	27.9	38.8	hypothetical protein 40.t00048	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01572.1.g28054.t1	ref|NP_176386.2| calcium-dependent protein kinase 19 [Arabidopsis thaliana] gi|122231654|sp|Q1PFH8.1|CDPKJ_ARATH RecName: Full=Calcium-dependent protein kinase 19 gi|91806009|gb|ABE65733.1| calcium-dependent protein kinase/CDPK [Arabidopsis thaliana] gi|332195785|gb|AEE33906.1| calcium-dependent protein kinase 19 [Arabidopsis thaliana]	1451	551	0	38.0	31.4	33.2	calcium-dependent protein kinase 19	gbpln	Arabidopsis thaliana	AT1G61950.1 | Symbols: CPK19 | calcium-dependent protein kinase 19 | chr1:22899417-22901941 FORWARD LENGTH=551	1451	551	0	38.0	31.4	33.2
Rsa1.0_01572.1.g28055.t1	ref|XP_002868389.1| hypothetical protein ARALYDRAFT_493566 [Arabidopsis lyrata subsp. lyrata] gi|297314225|gb|EFH44648.1| hypothetical protein ARALYDRAFT_493566 [Arabidopsis lyrata subsp. lyrata]	124	264	1.00E-11	212.9	36.3	40.3	hypothetical protein ARALYDRAFT_493566	gbpln	Arabidopsis lyrata	AT5G32440.3 | Symbols: | Ubiquitin system component Cue protein | chr5:12077014-12078396 FORWARD LENGTH=265	124	265	7.00E-14	213.7	33.9	37.9
Rsa1.0_01572.1.g28056.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01572.1.g28057.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01572.1.g28058.t1	emb|CAN62506.1| hypothetical protein VITISV_010654 [Vitis vinifera]	225	458	1.00E-21	203.6	28.9	46.2	hypothetical protein VITISV_010654	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01573.1.g28059.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01573.1.g28060.t1	dbj|BAJ34214.1| unnamed protein product [Thellungiella halophila]	614	638	0	103.9	78.3	86.3	unnamed protein product	----	----	AT5G23570.1 | Symbols: SGS3, ATSGS3 | XS domain-containing protein / XS zinc finger domain-containing protein-related | chr5:7943621-7945874 FORWARD LENGTH=625	614	625	0	101.8	75.1	84.2
Rsa1.0_01573.1.g28061.t1	ref|NP_680213.1| transmembrane CLPTM1 family protein [Arabidopsis thaliana] gi|17381232|gb|AAL36035.1| AT5g08500/MAH20_6 [Arabidopsis thaliana] gi|23506007|gb|AAN28863.1| At5g08500/MAH20_6 [Arabidopsis thaliana] gi|332005802|gb|AED93185.1| transmembrane CLPTM1 family protein [Arabidopsis thaliana]	590	593	0	100.5	92.0	95.6	transmembrane CLPTM1 family protein	gbpln	Arabidopsis thaliana	AT5G23575.1 | Symbols: | Transmembrane CLPTM1 family protein | chr5:7946563-7950041 FORWARD LENGTH=593	590	593	0	100.5	92.0	95.6
Rsa1.0_01573.1.g28062.t1	gb|EOA20507.1| hypothetical protein CARUB_v10000821mg [Capsella rubella]	491	490	0	99.8	89.0	94.7	hypothetical protein CARUB_v10000821mg	gbpln	Capsella rubella	AT5G23580.1 | Symbols: CDPK9, ATCDPK9, CPK12, ATCPK12 | calmodulin-like domain protein kinase 9 | chr5:7950388-7952433 REVERSE LENGTH=490	491	490	0	99.8	88.8	94.3
Rsa1.0_01573.1.g28063.t1	ref|XP_002872065.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317902|gb|EFH48324.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	327	327	2.00E-88	100.0	54.1	68.5	predicted protein	gbpln	Arabidopsis lyrata	AT5G23650.1 | Symbols: | Homeodomain-like transcriptional regulator | chr5:7969812-7971019 FORWARD LENGTH=337	327	337	4.00E-87	103.1	53.2	67.0
Rsa1.0_01573.1.g28064.t1	ref|XP_002877428.1| hypothetical protein ARALYDRAFT_484952 [Arabidopsis lyrata subsp. lyrata] gi|297323266|gb|EFH53687.1| hypothetical protein ARALYDRAFT_484952 [Arabidopsis lyrata subsp. lyrata]	287	285	1.00E-138	99.3	84.7	90.6	hypothetical protein ARALYDRAFT_484952	gbpln	Arabidopsis lyrata	AT5G23660.1 | Symbols: MTN3, SWEET12, AtSWEET12 | homolog of Medicago truncatula MTN3 | chr5:7971936-7973796 REVERSE LENGTH=285	287	285	1.00E-140	99.3	84.0	90.2
Rsa1.0_01573.1.g28065.t2	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	934	1501	0	160.7	54.8	71.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	934	237	1.00E-29	25.4	7.6	12.5
Rsa1.0_01573.1.g28066.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	423	1501	0	354.8	72.6	86.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	423	1262	1.00E-111	298.3	44.4	62.4
Rsa1.0_01574.1.g28067.t5	gb|AAD30632.1|AC006085_5 Hypothetical protein [Arabidopsis thaliana]	995	1295	1.00E-130	130.2	28.0	39.3	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01574.1.g28068.t4	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01574.1.g28069.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01574.1.g28070.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01574.1.g28071.t2	ref|XP_002878995.1| SPX domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324834|gb|EFH55254.1| SPX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	310	288	1.00E-126	92.9	79.7	85.5	SPX domain-containing protein	gbpln	Arabidopsis lyrata	AT2G26660.1 | Symbols: ATSPX2, SPX2 | SPX domain gene 2 | chr2:11338932-11340703 FORWARD LENGTH=287	310	287	1.00E-128	92.6	80.0	85.5
Rsa1.0_01574.1.g28072.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	97	1142	2.00E-17	1177.3	45.4	58.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01574.1.g28073.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01574.1.g28074.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01574.1.g28075.t1	emb|CAN77967.1| hypothetical protein VITISV_027331 [Vitis vinifera]	312	491	7.00E-16	157.4	17.9	30.1	hypothetical protein VITISV_027331	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01574.1.g28076.t9	gb|AAC69377.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1767	1328	0	75.2	26.8	35.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1767	158	1.00E-24	8.9	3.4	4.9
Rsa1.0_01575.1.g28077.t1	ref|XP_002887353.1| 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297333194|gb|EFH63612.1| 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	307	299	1.00E-133	97.4	82.4	88.3	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein	gbpln	Arabidopsis lyrata	AT1G71170.1 | Symbols: | 6-phosphogluconate dehydrogenase family protein | chr1:26830673-26831572 FORWARD LENGTH=299	307	299	1.00E-130	97.4	81.8	88.3

Rsa1.0_01575.1.g28078.t1	ref|NP_189164.1| Ribonuclease H-like protein [Arabidopsis thaliana] gi|9294184|dbj|BAB02086.1| reverse transcriptase-like protein [Arabidopsis thaliana] gi|332643482|gb|AEE77003.1| Ribonuclease H-like protein [Arabidopsis thaliana]	328	343	7.00E-85	104.6	46.3	66.8	Ribonuclease H-like protein	gbpln	Arabidopsis thaliana	AT3G25270.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:9203934-9204965 REVERSE LENGTH=343	328	343	2.00E-87	104.6	46.3	66.8
Rsa1.0_01575.1.g28079.t1	gb|EOA33322.1| hypothetical protein CARUB_v10021968mg [Capsella rubella]	444	460	0	103.6	89.2	96.6	hypothetical protein CARUB_v10021968mg	gbpln	Capsella rubella	AT1G71160.1 | Symbols: KCS7 | 3-ketoacyl-CoA synthase 7 | chr1:26828788-26830170 REVERSE LENGTH=460	444	460	0	103.6	88.3	95.9
Rsa1.0_01575.1.g28080.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01575.1.g28081.t1	ref|NP_177270.1| MATE efflux family protein [Arabidopsis thaliana] gi|12323428|gb|AAG51691.1|AC016972_10 hypothetical protein; 49518-51504 [Arabidopsis thaliana] gi|332197044|gb|AEE35165.1| MATE efflux family protein [Arabidopsis thaliana]	482	485	0	100.6	80.7	89.0	MATE efflux family protein	gbpln	Arabidopsis thaliana	AT1G71140.1 | Symbols: | MATE efflux family protein | chr1:26824762-26826748 FORWARD LENGTH=485	482	485	0	100.6	80.7	89.0
Rsa1.0_01575.1.g28082.t1	gb|EOA35095.1| hypothetical protein CARUB_v10020206mg [Capsella rubella]	482	485	0	100.6	84.6	91.1	hypothetical protein CARUB_v10020206mg	gbpln	Capsella rubella	AT1G71140.1 | Symbols: | MATE efflux family protein | chr1:26824762-26826748 FORWARD LENGTH=485	482	485	0	100.6	83.4	91.1
Rsa1.0_01575.1.g28083.t1	ref|NP_565012.1| ethylene-responsive transcription factor ERF070 [Arabidopsis thaliana] gi|75333560|sp|Q9C995.1|ERF70_ARATH RecName: Full=Ethylene-responsive transcription factor ERF070 gi|12323426|gb|AAG51689.1|AC016972_8 hypothetical protein; 47633-48118 [Arabidopsis thaliana] gi|51969298|dbj|BAD43341.1| unknown protein [Arabidopsis thaliana] gi|51969508|dbj|BAD43446.1| unknown protein [Arabidopsis thaliana] gi|51969622|dbj|BAD43503.1| unknown protein [Arabidopsis thaliana] gi|51969690|dbj|BAD43537.1| unknown protein [Arabidopsis thaliana] gi|51970004|dbj|BAD43694.1| unknown protein [Arabidopsis thaliana] gi|51970228|dbj|BAD43806.1| unknown protein [Arabidopsis thaliana] gi|51970430|dbj|BAD43907.1| unknown protein [Arabidopsis thaliana] gi|51970702|dbj|BAD44043.1| unknown protein [Arabidopsis thaliana] gi|98961105|gb|ABF59036.1| At1g71130 [Arabidopsis thaliana] gi|332197043|gb|AEE35164.1| ethylene-responsive transcription factor ERF070 [Arabidopsis thaliana]	167	161	7.00E-58	96.4	74.9	83.8	ethylene-responsive transcription factor ERF070	gbpln	Arabidopsis thaliana	AT1G71130.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:26822877-26823362 FORWARD LENGTH=161	167	161	3.00E-60	96.4	74.9	83.8
Rsa1.0_01576.1.g28084.t1	ref|XP_002887145.1| hypothetical protein ARALYDRAFT_475882 [Arabidopsis lyrata subsp. lyrata] gi|297332986|gb|EFH63404.1| hypothetical protein ARALYDRAFT_475882 [Arabidopsis lyrata subsp. lyrata]	518	527	0	101.7	65.4	79.5	hypothetical protein ARALYDRAFT_475882	gbpln	Arabidopsis lyrata	AT1G67780.1 | Symbols: | Zinc-finger domain of monoamine-oxidase A repressor R1 protein | chr1:25412816-25415530 FORWARD LENGTH=512	518	512	1.00E-178	98.8	64.7	78.2
Rsa1.0_01576.1.g28085.t1	gb|AEW29768.1| TCP1 [Calepina irregularis]	342	354	1.00E-131	103.5	72.5	81.9	TCP1	gbpln	Calepina irregularis	AT1G67260.1 | Symbols: TCP1 | TCP family transcription factor | chr1:25168228-25169307 REVERSE LENGTH=359	342	359	1.00E-124	105.0	69.0	78.9
Rsa1.0_01576.1.g28086.t1	gb|EOA33467.1| hypothetical protein CARUB_v10021121mg [Capsella rubella]	170	141	1.00E-63	82.9	73.5	79.4	hypothetical protein CARUB_v10021121mg	gbpln	Capsella rubella	AT1G67250.1 | Symbols: | Proteasome maturation factor UMP1 | chr1:25163808-25164967 REVERSE LENGTH=141	170	141	7.00E-65	82.9	71.8	78.2
Rsa1.0_01576.1.g28087.t1	ref|NP_176892.1| protein little nuclei1 [Arabidopsis thaliana] gi|332196494|gb|AEE34615.1| protein little nuclei1 [Arabidopsis thaliana]	1076	1132	0	105.2	78.2	87.7	protein little nuclei1	gbpln	Arabidopsis thaliana	AT1G67230.1 | Symbols: LINC1 | little nuclei1 | chr1:25151561-25156032 REVERSE LENGTH=1132	1076	1132	0	105.2	78.2	87.7
Rsa1.0_01576.1.g28088.t1	ref|XP_002887112.1| hypothetical protein ARALYDRAFT_894451 [Arabidopsis lyrata subsp. lyrata] gi|297332953|gb|EFH63371.1| hypothetical protein ARALYDRAFT_894451 [Arabidopsis lyrata subsp. lyrata]	1053	1022	0	97.1	60.4	72.2	hypothetical protein ARALYDRAFT_894451	gbpln	Arabidopsis lyrata	AT1G67220.1 | Symbols: HAC02, HAC2, ATHPCAT1 | histone acetyltransferase of the CBP family 2 | chr1:25145587-25150450 FORWARD LENGTH=1367	1053	1367	0	129.8	50.8	59.5
Rsa1.0_01576.1.g28089.t1	gb|EOA35180.1| hypothetical protein CARUB_v10020325mg [Capsella rubella]	434	431	1.00E-169	99.3	76.5	82.5	hypothetical protein CARUB_v10020325mg	gbpln	Capsella rubella	AT1G67210.1 | Symbols: | Proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein | chr1:25141339-25143774 FORWARD LENGTH=405	434	405	1.00E-157	93.3	70.7	77.9

Rsa1.0_01577.1.g28090.t1	gb|EOA12330.1| hypothetical protein CARUB_v10007925mg, partial [Capsella rubella]	393	539	3.00E-46	137.2	22.1	31.0	hypothetical protein CARUB_v10007925mg, partial	gbpln	Capsella rubella	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	393	696	3.00E-12	177.1	14.2	22.6
Rsa1.0_01577.1.g28091.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	671	723	0	107.7	55.6	71.7	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	671	696	2.00E-45	103.7	21.9	38.2
Rsa1.0_01577.1.g28092.t6	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01577.1.g28093.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01577.1.g28094.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01577.1.g28095.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	717	1024	2.00E-82	142.8	26.1	33.9	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01577.1.g28096.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01578.1.g28097.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01578.1.g28098.t2	gb|EOA38210.1| hypothetical protein CARUB_v10009689mg [Capsella rubella]	1204	333	1.00E-140	27.7	20.8	23.2	hypothetical protein CARUB_v10009689mg	gbpln	Capsella rubella	AT1G23560.1 | Symbols: | Domain of unknown function (DUF220) | chr1:8352802-8354145 REVERSE LENGTH=332	1204	332	1.00E-140	27.6	20.3	22.3
Rsa1.0_01578.1.g28099.t2	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	620	695	1.00E-158	112.1	48.1	51.3	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01578.1.g28100.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	213	1142	1.00E-42	536.2	46.5	60.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	213	292	8.00E-22	137.1	30.0	50.7
Rsa1.0_01578.1.g28101.t3	ref|NP_173785.1| beta carbonic anhydrase 3 [Arabidopsis thaliana] gi|4056455|gb|AAC98028.1| Similar to gb|L19255 carbonic anhydrase from Nicotiana tabacum and a member of the prokaryotic-type carbonic anhydrase family PF|00484. EST gb|Z235745 comes from this gene [Arabidopsis thaliana] gi|19698837|gb|AAL91154.1| putative carbonic anhydrase [Arabidopsis thaliana] gi|21386933|gb|AAM47870.1| putative carbonic anhydrase [Arabidopsis thaliana] gi|332192305|gb|AEE30426.1| beta carbonic anhydrase 3 [Arabidopsis thaliana]	266	258	1.00E-133	97.0	85.7	94.0	beta carbonic anhydrase 3	gbpln	Arabidopsis thaliana	AT1G23730.1 | Symbols: ATBCA3, BCA3 | beta carbonic anhydrase 3 | chr1:8395965-8398014 FORWARD LENGTH=258	266	258	1.00E-135	97.0	85.7	94.0
Rsa1.0_01578.1.g28102.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01578.1.g28103.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01578.1.g28104.t1	ref|NP_564202.1| OB-fold nucleic acid binding domain-containing protein [Arabidopsis thaliana] gi|4056457|gb|AAC98030.1| ESTs gb|234051 and gb|F13722 come from this gene [Arabidopsis thaliana] gi|21553633|gb|AAM62726.1| unknown [Arabidopsis thaliana] gi|27754651|gb|AAO22770.1| unknown protein [Arabidopsis thaliana] gi|28394047|gb|AAO42431.1| unknown protein [Arabidopsis thaliana] gi|332192307|gb|AEE30428.1| OB-fold nucleic acid binding domain-containing protein [Arabidopsis thaliana]	136	137	3.00E-68	100.7	92.6	97.1	OB-fold nucleic acid binding domain-containing protein	gbpln	Arabidopsis thaliana	AT1G23750.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:8400638-8401171 FORWARD LENGTH=137	136	137	6.00E-71	100.7	92.6	97.1
Rsa1.0_01578.1.g28105.t1	gb|EOA37583.1| hypothetical protein CARUB_v10011933mg [Capsella rubella]	468	481	1.00E-164	102.8	67.1	79.5	hypothetical protein CARUB_v10011933mg	gbpln	Capsella rubella	AT1G23780.1 | Symbols: | F-box family protein | chr1:8407053-8408480 REVERSE LENGTH=475	468	475	1.00E-152	101.5	65.4	77.6
Rsa1.0_01578.1.g28106.t1	ref|NP_173794.2| spermidine synthase 1 [Arabidopsis thaliana] gi|332192315|gb|AEE30436.1| spermidine synthase 1 [Arabidopsis thaliana]	297	378	1.00E-148	127.3	90.6	94.9	spermidine synthase 1	gbpln	Arabidopsis thaliana	AT1G23820.1 | Symbols: SPDS1 | spermidine synthase 1 | chr1:8420278-8422724 FORWARD LENGTH=378	297	378	1.00E-151	127.3	90.6	94.9
Rsa1.0_01578.1.g28107.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01579.1.g28108.t2	gb|EOA26734.1| hypothetical protein CARUB_v10022820mg [Capsella rubella]	510	527	1.00E-103	103.3	47.3	58.0	hypothetical protein CARUB_v10022820mg	gbpln	Capsella rubella	AT4G05360.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=735	510	735	2.00E-59	144.1	28.2	38.0
Rsa1.0_01579.1.g28109.t1	gb|EOA12533.1| hypothetical protein CARUB_v10026514mg [Capsella rubella]	398	407	1.00E-144	102.3	77.4	84.7	hypothetical protein CARUB_v10026514mg	gbpln	Capsella rubella	AT5G62260.1 | Symbols: | AT hook motif DNA-binding family protein | chr5:25009331-25011348 FORWARD LENGTH=404	398	404	1.00E-138	101.5	72.4	77.1

Rsa1.0_01579.1_g28110.t1	gb|EOA15100.1| hypothetical protein CARUB_v10028468mg [Capsella rubella]	541	540	0	99.8	85.0	90.9	hypothetical protein CARUB_v10028468mg	gbpln	Capsella rubella	AT5G62250.1 | Symbols: MAP65-9 | microtubule-associated protein 65-9 | chr5:25005756-25008096 FORWARD LENGTH=549	541	549	0	101.5	85.0	91.9
Rsa1.0_01579.1_g28111.t1	ref|XP_002866481.1| hypothetical protein ARALYDRAFT_496400 [Arabidopsis lyrata subsp. lyrata] gi|297312316|gb|EFH42740.1| hypothetical protein ARALYDRAFT_496400 [Arabidopsis lyrata subsp. lyrata]	371	379	1.00E-142	102.2	73.9	80.9	hypothetical protein ARALYDRAFT_496400	gbpln	Arabidopsis lyrata	AT5G62240.1 | Symbols: | Cell cycle regulated microtubule associated protein | chr5:25002541-25004569 REVERSE LENGTH=377	371	377	1.00E-133	101.6	70.4	79.0
Rsa1.0_01579.1_g28112.t1	gb|EOA12485.1| hypothetical protein CARUB_v10026032mg [Capsella rubella]	656	668	0	101.8	69.4	77.0	hypothetical protein CARUB_v10026032mg	gbpln	Capsella rubella	AT5G62190.1 | Symbols: PRH75 | DEAD box RNA helicase (PRH75) | chr5:24980542-24983879 REVERSE LENGTH=671	656	671	0	102.3	68.6	75.8
Rsa1.0_01579.1_g28113.t1	gb|EOA39029.1| hypothetical protein CARUB_v10011599mg [Capsella rubella]	323	329	1.00E-144	101.9	76.5	85.4	hypothetical protein CARUB_v10011599mg	gbpln	Capsella rubella	AT5G62180.1 | Symbols: AtCXE20, CXE20 | carboxyesterase 20 | chr5:24978866-24979849 REVERSE LENGTH=327	323	327	1.00E-147	101.2	75.5	86.1
Rsa1.0_01579.1_g28114.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01579.1_g28115.t1	gb|EOA13406.1| hypothetical protein CARUB_v10026444mg, partial [Capsella rubella]	432	430	1.00E-109	99.5	54.2	63.2	hypothetical protein CARUB_v10026444mg, partial	gbpln	Capsella rubella	AT5G62660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr5:25156326-25157465 REVERSE LENGTH=379	432	379	1.00E-106	87.7	48.4	58.3
Rsa1.0_01579.1_g28116.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01579.1_g28117.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01580.1_g28118.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1389	1307	0	94.1	58.9	74.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1389	1262	2.00E-98	90.9	13.8	21.2
Rsa1.0_01580.1_g28119.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01580.1_g28120.t1	gb|ABD64959.1| ethylene responsive element binding factor [Brassica oleracea]	304	307	2.33E-156	101.0	88.2	92.1	ethylene responsive element binding factor	gbpln	Brassica oleracea	AT5G47230.1 | Symbols: ERF5, ATERF-5, ATERF5 | ethylene responsive element binding factor 5 | chr5:19180072-19180974 FORWARD LENGTH=300	304	300	1.00E-112	98.7	75.3	80.3
Rsa1.0_01580.1_g28121.t1	gb|ABD64957.1| hydrolase, NUDIX family protein [Brassica oleracea]	361	366	0	101.4	95.6	97.2	hydrolase, NUDIX family protein	gbpln	Brassica oleracea	AT5G47240.1 | Symbols: atnudt8, NUDT8 | nudix hydrolase homolog 8 | chr5:19183806-19185467 FORWARD LENGTH=369	361	369	1.00E-180	102.2	86.1	92.2
Rsa1.0_01580.1_g28122.t1	gb|ABD64953.1| hypothetical protein 25.t00041 [Brassica oleracea]	242	243	1.00E-136	100.4	97.5	99.2	hypothetical protein 25.t00041	gbpln	Brassica oleracea	AT5G47310.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr5:19201325-19202674 FORWARD LENGTH=245	242	245	1.00E-122	101.2	90.1	94.6
Rsa1.0_01580.1_g28123.t1	gb|ABD64963.1| palmitoyl protein thioesterase family protein [Brassica oleracea]	367	328	1.00E-148	89.4	71.4	71.4	palmitoyl protein thioesterase family protein	gbpln	Brassica oleracea	AT5G47330.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:19207170-19208711 FORWARD LENGTH=314	367	314	1.00E-125	85.6	57.8	64.0
Rsa1.0_01580.1_g28124.t1	gb|ABD64952.1| hypothetical protein 25.t00038 [Brassica oleracea]	266	217	2.00E-62	81.6	53.4	60.9	hypothetical protein 25.t00038	gbpln	Brassica oleracea	AT2G01560.1 | Symbols: | Plant protein 1589 of unknown function | chr2:250392-251806 REVERSE LENGTH=301	266	301	9.00E-19	113.2	33.8	53.0
Rsa1.0_01580.1_g28125.t1	gb|ABD64962.1| PPR repeat containing protein [Brassica oleracea]	162	345	6.00E-47	213.0	64.2	65.4	PPR repeat containing protein	gbpln	Brassica oleracea	AT5G47360.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:19214445-19215878 REVERSE LENGTH=477	162	477	3.00E-43	294.4	55.6	61.1
Rsa1.0_01581.1_g28126.t1	gb|EOA27612.1| hypothetical protein CARUB_v10023753mg [Capsella rubella]	306	295	1.00E-139	96.4	81.4	85.9	hypothetical protein CARUB_v10023753mg	gbpln	Capsella rubella	AT2G32080.2 | Symbols: PUR ALPHA-1 | purin-rich alpha 1 | chr2:13642716-13644036 REVERSE LENGTH=295	306	295	1.00E-140	96.4	81.4	84.6
Rsa1.0_01581.1_g28127.t1	gb|EOA27677.1| hypothetical protein CARUB_v10023830mg [Capsella rubella]	275	275	1.00E-151	100.0	92.4	97.5	hypothetical protein CARUB_v10023830mg	gbpln	Capsella rubella	AT2G32070.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:13640829-13641656 REVERSE LENGTH=275	275	275	1.00E-153	100.0	92.4	97.5
Rsa1.0_01581.1_g28128.t1	gb|EOA27677.1| hypothetical protein CARUB_v10023830mg [Capsella rubella]	271	275	1.00E-105	101.5	71.2	81.2	hypothetical protein CARUB_v10023830mg	gbpln	Capsella rubella	AT2G32070.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:13640829-13641656 REVERSE LENGTH=275	271	275	1.00E-107	101.5	71.6	81.2
Rsa1.0_01581.1_g28129.t1	gb|EOA36301.1| hypothetical protein CARUB_v10010589mg [Capsella rubella]	169	142	1.00E-70	84.0	79.9	80.5	hypothetical protein CARUB_v10010589mg	gbpln	Capsella rubella	AT2G32060.2 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr2:13639228-13640104 REVERSE LENGTH=144	169	144	7.00E-62	85.2	65.7	71.0

Rsa1.0_01581.1.g28130.t1	ref|NP_565734.1| major facilitator protein [Arabidopsis thaliana] gi|75206588|sp|Q9SKZ5.2|FBT1_ARATH RecName: Full=Folate-biopterin transporter 1, chloroplastic; Flags: Precursor gi|19698919|gb|AAL91195.1| unknown protein [Arabidopsis thaliana] gi|20197619|gb|AAD15400.2| expressed protein [Arabidopsis thaliana] gi|21553656|gb|AAM62749.1| unknown [Arabidopsis thaliana] gi|28059039|gb|AAO29981.1| unknown protein [Arabidopsis thaliana] gi|330253531|gb|AEC08625.1| folate-biopterin transporter 1 [Arabidopsis thaliana]	553	560	0	101.3	91.0	93.7	major facilitator protein	gbpln	Arabidopsis thaliana	AT2G32040.1 | Symbols: | Major facilitator superfamily protein | chr2:13635116-13637592 FORWARD LENGTH=560	553	560	0	101.3	91.0	93.7
Rsa1.0_01581.1.g28131.t1	ref|XP_002881211.1| hypothetical protein ARALYDRAFT_902251 [Arabidopsis lyrata subsp. lyrata] gi|297327050|gb|EFH57470.1| hypothetical protein ARALYDRAFT_902251 [Arabidopsis lyrata subsp. lyrata]	184	183	9.00E-90	99.5	88.6	92.9	hypothetical protein ARALYDRAFT_902251	gbpln	Arabidopsis lyrata	AT2G32020.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr2:13631193-13631744 REVERSE LENGTH=183	184	183	8.00E-91	99.5	87.5	92.9
Rsa1.0_01581.1.g28132.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	390	387	3.00E-79	99.2	46.7	62.6	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	390	387	7.00E-82	99.2	46.7	62.6
Rsa1.0_01581.1.g28133.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	404	387	8.00E-91	95.8	50.2	64.6	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	404	387	2.00E-93	95.8	50.2	64.6
Rsa1.0_01581.1.g28134.t1	ref|XP_002886496.1| hypothetical protein ARALYDRAFT_893290 [Arabidopsis lyrata subsp. lyrata] gi|297332337|gb|EFH62755.1| hypothetical protein ARALYDRAFT_893290 [Arabidopsis lyrata subsp. lyrata]	405	416	7.00E-86	102.7	48.6	63.0	hypothetical protein ARALYDRAFT_893290	gbpln	Arabidopsis lyrata	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	405	387	2.00E-88	95.6	47.2	59.8
Rsa1.0_01581.1.g28135.t1	ref|XP_002881208.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297327047|gb|EFH57467.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	477	458	0	96.0	70.9	78.6	exostosin family protein	gbpln	Arabidopsis lyrata	AT2G31990.1 | Symbols: | Exostosin family protein | chr2:13611500-13613551 REVERSE LENGTH=479	477	479	0	100.4	72.7	83.0
Rsa1.0_01581.1.g28136.t1	ref|XP_002879356.1| hypothetical protein ARALYDRAFT_482124 [Arabidopsis lyrata subsp. lyrata] gi|297325195|gb|EFH55615.1| hypothetical protein ARALYDRAFT_482124 [Arabidopsis lyrata subsp. lyrata]	2096	1936	0	92.4	85.2	87.5	hypothetical protein ARALYDRAFT_482124	gbpln	Arabidopsis lyrata	AT2G31960.2 | Symbols: GSL03 | glucan synthase-like 3 | chr2:13589545-13600066 FORWARD LENGTH=1950	2096	1950	0	93.0	86.2	88.5
Rsa1.0_01582.1.g28137.t1	gb|EOA22705.1| hypothetical protein CARUB_v10003411mg [Capsella rubella]	703	652	1.00E-178	92.7	43.1	51.6	hypothetical protein CARUB_v10003411mg	gbpln	Capsella rubella	AT5G10530.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:3324978-3326933 REVERSE LENGTH=651	703	651	1.00E-179	92.6	42.1	51.4
Rsa1.0_01582.1.g28138.t1	gb|EOA14568.1| hypothetical protein CARUB_v10027807mg [Capsella rubella]	223	611	5.00E-79	274.0	63.7	73.1	hypothetical protein CARUB_v10027807mg	gbpln	Capsella rubella	AT5G10530.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:3324978-3326933 REVERSE LENGTH=651	223	651	4.00E-71	291.9	60.1	70.9
Rsa1.0_01582.1.g28139.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	202	490	1.00E-16	242.6	29.7	45.0	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	202	566	3.00E-17	280.2	22.8	39.1
Rsa1.0_01582.1.g28140.t2	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	303	1089	4.00E-48	359.4	36.0	48.2	transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01582.1.g28141.t1	ref|XP_002890830.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297336672|gb|EFH67089.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	129	221	7.00E−53	171.3	84.5	89.9	NLI interacting factor family protein	gbpln	Arabidopsis lyrata	AT1G29780.1 | Symbols: | Haloacid dehalogenase−like hydrolase (HAD) superfamily protein | chr1:10426950−10427615 FORWARD LENGTH=221	129	221	2.00E−54	171.3	82.9	89.1
Rsa1.0_01582.1.g28142.t1	ref|XP_002890829.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297336671|gb|EFH67088.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	268	277	1.00E−124	103.4	84.3	91.4	NLI interacting factor family protein	gbpln	Arabidopsis lyrata	AT1G29770.1 | Symbols: | Haloacid dehalogenase−like hydrolase (HAD) superfamily protein | chr1:10424806−10425642 FORWARD LENGTH=278	268	278	1.00E−124	103.7	83.6	90.7
Rsa1.0_01582.1.g28143.t1	ref|NP_174267.4| Leucine−rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|332193002|gb|AEE31123.1| Leucine−rich repeat transmembrane protein kinase [Arabidopsis thaliana]	903	1078	0	119.4	86.7	92.5	Leucine−rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT1G29740.1 | Symbols: | Leucine−rich repeat transmembrane protein kinase | chr1:10407379−10412997 REVERSE LENGTH=1078	903	1078	0	119.4	86.7	92.5
Rsa1.0_01583.1.g28144.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01583.1.g28145.t1	gb|AAZ66937.1| 117M18_18 [Brassica rapa]	242	249	1.00E−127	102.9	95.5	97.1	117M18_18	gbpln	Brassica rapa	AT5G10360.1 | Symbols: EMB3010, RPS6B | Ribosomal protein S6e | chr5:3258734−3260142 REVERSE LENGTH=249	242	249	1.00E−125	102.9	92.6	95.0
Rsa1.0_01583.1.g28146.t1	gb|ADG03603.1| galactinol synthase [Brassica napus]	313	342	1.00E−167	109.3	93.9	97.8	galactinol synthase	gbpln	Brassica napus	AT2G47180.1 | Symbols: AtGolS1, GolS1 | galactinol synthase 1 | chr2:19369049−19370372 REVERSE LENGTH=344	313	344	1.00E−152	109.9	87.2	91.7
Rsa1.0_01583.1.g28147.t1	ref|NP_191788.1| ADP−ribosylation factor A1E [Arabidopsis thaliana] gi|334186204|ref|NP_001190161.1| ADP−ribosylation factor A1E [Arabidopsis thaliana] gi|334186206|ref|NP_001190162.1| ADP−ribosylation factor A1E [Arabidopsis thaliana] gi|297824803|ref|XP_002880284.1| ADP−ribosylation factor A1E [Arabidopsis lyrata subsp. lyrata] gi|13926302|gb|AAK49618.1|AF372902_1 AT3g62290/T17J13_250 [Arabidopsis thaliana] gi|6899939|emb|CAB71889.1| ADP−ribosylation factor−like protein [Arabidopsis thaliana] gi|16323248|gb|AAL15358.1| AT3g62290/T17J13_250 [Arabidopsis thaliana] gi|21553518|gb|AAM62611.1| ADP−ribosylation factor−like protein [Arabidopsis thaliana] gi|119720788|gb|ABL97964.1| ADP−ribosylation factor−like protein [Brassica rapa] gi|297326123|gb|EFH56543.1| ADP−ribosylation factor A1E [Arabidopsis lyrata subsp. lyrata] gi|332646811|gb|AEE80332.1| ADP−ribosylation factor A1E [Arabidopsis thaliana] gi|332646812|gb|AEE80333.1| ADP−ribosylation factor A1E [Arabidopsis thaliana] gi|332646813|gb|AEE80334.1| ADP−ribosylation factor A1E [Arabidopsis	181	181	1.00E−102	100.0	99.4	100.0	ADP−ribosylation factor A1E	gbpln	Arabidopsis lyrata	AT3G62290.3 | Symbols: ARFA1E | ADP−ribosylation factor A1E | chr3:23052287−23053545 FORWARD LENGTH=181	181	181	1.00E−104	100.0	99.4	100.0
Rsa1.0_01583.1.g28148.t1	dbj|BAB09379.1| non−LTR retroelement reverse transcriptase−like protein [Arabidopsis thaliana]	697	1223	0	175.5	59.8	74.0	non−LTR retroelement reverse transcriptase−like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr3:8789471−8793208 FORWARD LENGTH=746	697	746	1.00E−117	107.0	29.8	38.9
Rsa1.0_01583.1.g28149.t1	gb|ADF30179.1| boron transporter [Brassica napus] gi|294713700|gb|ADF30187.1| boron transporter [Brassica napus]	697	701	0	100.6	97.6	98.9	boron transporter	gbpln	Brassica napus	AT2G47160.1 | Symbols: BOR1 | HCO3− transporter family | chr2:19357740−19360787 REVERSE LENGTH=704	697	704	0	101.0	96.3	98.9
Rsa1.0_01583.1.g28150.t1	emb|CBI37899.3| unnamed protein product [Vitis vinifera]	465	541	2.00E−80	116.3	45.8	63.2	unnamed protein product	gbpln	Vitis vinifera	AT5G66200.1 | Symbols: ARO2 | armadillo repeat only 2 | chr5:26453648−26455603 REVERSE LENGTH=651	465	651	3.00E−56	140.0	25.8	33.3

Rsa1.0_01583.1.g28151.t1	ref|NP_182228.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|3522940|gb|AAC34222.1| putative pectinesterase [Arabidopsis thaliana] gi|26451376|dbj|BAC42788.1| putative pectinesterase [Arabidopsis thaliana] gi|91806367|gb|ABE65911.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] gi|330255698|gb|AEC10792.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	216	216	1.00E-105	100.0	85.6	91.7	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT2G47050.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr2:19331927-19332577 REVERSE LENGTH=216	216	216	1.00E-108	100.0	85.6	91.7
Rsa1.0_01584.1.g28152.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01584.1.g28153.t4	gb|AAD36950.1|AF069441_10 putative transposon protein [Arabidopsis thaliana] gi|7267188|emb|CAB77899.1| putative transposon protein [Arabidopsis thaliana]	757	1011	5.00E-16	133.6	6.5	8.2	putative transposon protein	gbpln	Arabidopsis thaliana	AT4G07350.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40129.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:4172609-4175227 REVERSE LENGTH=330	757	330	1.00E-18	43.6	7.3	9.4
Rsa1.0_01584.1.g28154.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01584.1.g28155.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01584.1.g28156.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01584.1.g28157.t1	gb|EOA16045.1| hypothetical protein CARUB_v10004170mg [Capsella rubella]	131	792	3.00E-37	604.6	68.7	71.0	hypothetical protein CARUB_v10004170mg	gbpln	Capsella rubella	AT4G14990.1 | Symbols: | Topoisomerase II-associated protein PAT1 | chr4:8566259-8569511 REVERSE LENGTH=787	131	787	6.00E-34	600.8	59.5	62.6
Rsa1.0_01584.1.g28158.t1	gb|EOA16045.1| hypothetical protein CARUB_v10004170mg [Capsella rubella]	710	792	0	111.5	85.4	90.4	hypothetical protein CARUB_v10004170mg	gbpln	Capsella rubella	AT4G14990.1 | Symbols: | Topoisomerase II-associated protein PAT1 | chr4:8566259-8569511 REVERSE LENGTH=787	710	787	0	110.8	84.8	89.0
Rsa1.0_01584.1.g28159.t2	gb|AAD17395.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1634	1138	0	69.6	27.8	39.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1634	575	6.00E-69	35.2	9.7	15.7
Rsa1.0_01584.1.g28160.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01584.1.g28161.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01584.1.g28162.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01585.1.g28163.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01585.1.g28164.t5	ref|NP_201456.2| Maf-like protein [Arabidopsis thaliana] gi|332010845|gb|AED98228.1| Maf-like protein [Arabidopsis thaliana]	239	207	4.00E-87	86.6	69.0	77.0	Maf-like protein	gbpln	Arabidopsis thaliana	AT5G66550.1 | Symbols: | Maf-like protein | chr5:26559752-26561162 REVERSE LENGTH=207	239	207	1.00E-89	86.6	69.0	77.0
Rsa1.0_01585.1.g28165.t1	ref|NP_201457.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana] gi|338819810|sp|Q94A73.2|Y5656_ARATH RecName: Full=BTB/POZ domain-containing protein At5g66560 gi|332010846|gb|AED98229.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana]	694	668	0	96.3	82.6	87.0	Phototropic-responsive NPH3 family protein	gbpln	Arabidopsis thaliana	AT5G66560.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr5:26564368-26566662 FORWARD LENGTH=668	694	668	0	96.3	82.6	87.0
Rsa1.0_01585.1.g28166.t1	gb|AAT65501.1| photosystem II protein [Brassica oleracea]	332	347	0	104.5	96.4	97.9	photosystem II protein	gbpln	Brassica oleracea	AT5G66570.1 | Symbols: PSBO-1, OEE1, OEE33, OE33, PSBO1, MSP-1 | PS II oxygen-evolving complex 1 | chr5:26568744-26570124 FORWARD LENGTH=332	332	332	0	100.0	94.9	97.9
Rsa1.0_01585.1.g28167.t1	gb|EOA14145.1| hypothetical protein CARUB_v10027290mg [Capsella rubella]	157	156	3.00E-59	99.4	80.9	89.8	hypothetical protein CARUB_v10027290mg	gbpln	Capsella rubella	AT5G66580.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G50800.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:26572724-26573194 FORWARD LENGTH=156	157	156	1.00E-60	99.4	79.0	88.5

<table>
<tr><td>Rsa1.0_01585.1.g28168.t1</td><td>ref|NP_201461.1| uncharacterized protein [Arabidopsis thaliana] gi|186532816|ref|NP_001119511.1| uncharacterized protein [Arabidopsis thaliana] gi|10177541|dbj|BAB10936.1| unnamed protein product [Arabidopsis thaliana] gi|61742773|gb|AAX55207.1| hypothetical protein At5g66600 [Arabidopsis thaliana] gi|332010850|gb|AED98233.1| uncharacterized protein AT5G66600 [Arabidopsis thaliana] gi|332010852|gb|AED98235.1| uncharacterized protein AT5G66600 [Arabidopsis thaliana]</td><td>608</td><td>614</td><td>0</td><td>101.0</td><td>85.4</td><td>90.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G66600.3 | Symbols: | Protein of unknown function, DUF547 | chr5:26575105-26578315 REVERSE LENGTH=614</td><td>608</td><td>614</td><td>0</td><td>101.0</td><td>85.4</td><td>90.8</td></tr>
<tr><td>Rsa1.0_01585.1.g28169.t1</td><td>gb|EOA14276.1| hypothetical protein CARUB_v10027438mg [Capsella rubella]</td><td>101</td><td>97</td><td>1.00E-28</td><td>96.0</td><td>65.3</td><td>78.2</td><td>hypothetical protein CARUB_v10027438mg</td><td>gbpln</td><td>Capsella rubella</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01585.1.g28170.t6</td><td>gb|AAF79687.1|AC022314_28 F9C16.9 [Arabidopsis thaliana]</td><td>1326</td><td>946</td><td>0</td><td>71.3</td><td>30.4</td><td>35.8</td><td>F9C16.9</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G66620.1 | Symbols: DAR6 | DA1-related protein 6 | chr5:26588585-26592006 FORWARD LENGTH=644</td><td>1326</td><td>644</td><td>0</td><td>48.6</td><td>26.4</td><td>32.0</td></tr>
<tr><td>Rsa1.0_01585.1.g28171.t1</td><td>gb|AAO24595.1| At5g66630 [Arabidopsis thaliana] gi|110743610|dbj|BAE99642.1| hypothetical protein [Arabidopsis thaliana]</td><td>715</td><td>702</td><td>0</td><td>98.2</td><td>60.3</td><td>72.4</td><td>At5g66630</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G66630.1 | Symbols: DAR5 | DA1-related protein 5 | chr5:26592720-26595691 FORWARD LENGTH=702</td><td>715</td><td>702</td><td>0</td><td>98.2</td><td>60.3</td><td>72.4</td></tr>
<tr><td>Rsa1.0_01586.1.g28172.t1</td><td>dbj|BAA85452.1| S-locus protein 3 [Brassica rapa]</td><td>113</td><td>249</td><td>2.00E-55</td><td>220.4</td><td>93.8</td><td>96.5</td><td>S-locus protein 3</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G66510.2 | Symbols: | AAR2 protein family | chr1:24812881-24815804 FORWARD LENGTH=399</td><td>113</td><td>399</td><td>6.00E-56</td><td>353.1</td><td>88.5</td><td>93.8</td></tr>
<tr><td>Rsa1.0_01586.1.g28173.t6</td><td>emb|CAB89182.1| SIAH1 protein [Brassica napus var. napus]</td><td>833</td><td>351</td><td>1.00E-132</td><td>42.1</td><td>33.6</td><td>37.0</td><td>SIAH1 protein</td><td>gbpln</td><td>Brassica napus</td><td>AT1G66620.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr1:24852806-24854044 REVERSE LENGTH=313</td><td>833</td><td>313</td><td>4.00E-94</td><td>37.6</td><td>20.2</td><td>24.7</td></tr>
<tr><td>Rsa1.0_01586.1.g28174.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01586.1.g28175.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01586.1.g28176.t1</td><td>ref|NP_176835.1| E3 ubiquitin-protein ligase SINA-like 2 [Arabidopsis thaliana] gi|75169112|sp|Q9C6H3.1|SINL2_ARATH RecName: Full=E3 ubiquitin-protein ligase SINA-like 2; AltName: Full=Seven in absentia-like protein 2 gi|12322296|gb|AAG51178.1|AC079285_11 hypothetical protein [Arabidopsis thaliana] gi|332196416|gb|AEE34537.1| E3 ubiquitin-protein ligase SINA-like 2 [Arabidopsis thaliana]</td><td>306</td><td>313</td><td>1.00E-107</td><td>102.3</td><td>61.4</td><td>73.9</td><td>E3 ubiquitin-protein ligase SINA-like 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G66620.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr1:24852806-24854044 REVERSE LENGTH=313</td><td>306</td><td>313</td><td>1.00E-110</td><td>102.3</td><td>61.4</td><td>73.9</td></tr>
<tr><td>Rsa1.0_01586.1.g28177.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>387</td><td>1142</td><td>4.00E-56</td><td>295.1</td><td>30.0</td><td>39.8</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>387</td><td>575</td><td>1.00E-30</td><td>148.6</td><td>14.2</td><td>19.4</td></tr>
<tr><td>Rsa1.0_01586.1.g28178.t1</td><td>emb|CAB89183.1| AtPP protein [Brassica napus var. napus]</td><td>353</td><td>353</td><td>1.00E-178</td><td>100.0</td><td>89.2</td><td>93.8</td><td>AtPP protein</td><td>gbpln</td><td>Brassica napus</td><td>AT1G66700.1 | Symbols: PXMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:24873460-24874690 REVERSE LENGTH=353</td><td>353</td><td>353</td><td>1.00E-170</td><td>100.0</td><td>79.9</td><td>88.4</td></tr>
<tr><td>Rsa1.0_01586.1.g28179.t1</td><td>ref|XP_002888526.1| hypothetical protein ARALYDRAFT_894342 [Arabidopsis lyrata subsp. lyrata] gi|297334367|gb|EFH64785.1| hypothetical protein ARALYDRAFT_894342 [Arabidopsis lyrata subsp. lyrata]</td><td>366</td><td>342</td><td>2.00E-85</td><td>93.4</td><td>45.1</td><td>56.3</td><td>hypothetical protein ARALYDRAFT_894342</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G66660.2 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr1:24862056-24863332 REVERSE LENGTH=348</td><td>366</td><td>348</td><td>8.00E-83</td><td>95.1</td><td>49.2</td><td>63.1</td></tr>
<tr><td>Rsa1.0_01586.1.g28180.t1</td><td>emb|CAC80640.1| ClpP putative protein [Brassica napus]</td><td>312</td><td>313</td><td>1.00E-166</td><td>100.3</td><td>90.4</td><td>93.3</td><td>ClpP putative protein</td><td>gbpln</td><td>Brassica napus</td><td>AT1G66670.1 | Symbols: CLPP3, NCLPP3 | CLP protease proteolytic subunit 3 | chr1:24863995-24865646 REVERSE LENGTH=309</td><td>312</td><td>309</td><td>1.00E-153</td><td>99.0</td><td>84.9</td><td>90.7</td></tr>
<tr><td>Rsa1.0_01586.1.g28181.t1</td><td>dbj|BAA77395.1| SLL2-S9-protein [Brassica rapa]</td><td>338</td><td>337</td><td>0</td><td>99.7</td><td>98.5</td><td>99.4</td><td>SLL2-S9-protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G66680.1 | Symbols: AR401 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:24866352-24868888 REVERSE LENGTH=358</td><td>338</td><td>358</td><td>1.00E-175</td><td>105.9</td><td>93.8</td><td>96.2</td></tr>
<tr><td>Rsa1.0_01586.1.g28182.t1</td><td>dbj|BAC24068.1| S-locus glycoprotein [Brassica oleracea]</td><td>442</td><td>428</td><td>0</td><td>96.8</td><td>82.8</td><td>88.9</td><td>S-locus glycoprotein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT4G21380.1 | Symbols: ARK3, RK3 | receptor kinase 3 | chr4:11389219-11393090 REVERSE LENGTH=850</td><td>442</td><td>850</td><td>1.00E-154</td><td>192.3</td><td>60.4</td><td>70.8</td></tr>
<tr><td>Rsa1.0_01587.1.g28183.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01587.1.g28184.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_01587.1.g28185.t1	gb|ADO95301.1| 14-3-3-like protein GF14 Upsilon [Eutrema salsugineum]	212	268	5.00E-54	126.4	57.1	74.5	14-3-3-like protein GF14 Upsilon	gbpln	Eutrema salsugineum	AT3G02520.1 | Symbols: GRF7, GF14 NU | general regulatory factor 7 | chr3:526800-527915 REVERSE LENGTH=265	212	265	3.00E-53	125.0	54.7	73.1
Rsa1.0_01587.1.g28186.t1	dbj|BAJ34283.1| unnamed protein product [Thellungiella halophila]	393	395	0	100.5	86.0	92.6	unnamed protein product	----	----	AT3G48160.2 | Symbols: DEL1, E2L3, E2FE | DP-E2F-like 1 | chr3:17783641-17785846 FORWARD LENGTH=403	393	403	1.00E-174	102.5	81.4	89.8
Rsa1.0_01587.1.g28187.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|dbj|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	197	390	1.00E-35	198.0	43.7	56.9	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	197	295	2.00E-21	149.7	33.0	52.3
Rsa1.0_01587.1.g28188.t1	gb|EOA23715.1| hypothetical protein CARUB_v10016922mg [Capsella rubella]	170	579	7.00E-52	340.6	60.6	67.6	hypothetical protein CARUB_v10016922mg	gbpln	Capsella rubella	AT3G48150.1 | Symbols: APC8, CDC23 | anaphase-promoting complex subunit 8 | chr3:17779800-17782565 REVERSE LENGTH=579	170	579	5.00E-53	340.6	59.4	67.1
Rsa1.0_01588.1.g28189.t1	ref|XP_002882118.1| serine-type peptidase [Arabidopsis lyrata subsp. lyrata] gi|297327957|gb|EFH58377.1| serine-type peptidase [Arabidopsis lyrata subsp. lyrata]	948	962	0	101.5	93.7	95.8	serine-type peptidase	gbpln	Arabidopsis lyrata	AT2G47390.1 | Symbols: | Prolyl oligopeptidase family protein | chr2:19442278-19446253 REVERSE LENGTH=961	948	961	0	101.4	92.6	95.1
Rsa1.0_01588.1.g28190.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01588.1.g28191.t1	ref|NP_565392.1| calcium-dependent phosphotriesterase-like protein [Arabidopsis thaliana] gi|4581119|gb|AAD24609.1| expressed protein [Arabidopsis thaliana] gi|21537036|gb|AAM61377.1| unknown [Arabidopsis thaliana] gi|26451541|dbj|BAC42868.1| unknown protein [Arabidopsis thaliana] gi|28973387|gb|AAO64018.1| unknown protein [Arabidopsis thaliana] gi|330251441|gb|AEC06535.1| calcium-dependent phosphotriesterase-like protein [Arabidopsis thaliana]	327	327	1.00E-156	100.0	85.6	92.7	calcium-dependent phosphotriesterase-like protein	gbpln	Arabidopsis thaliana	AT2G16760.1 | Symbols: | Calcium-dependent phosphotriesterase superfamily protein | chr2:7275739-7277122 FORWARD LENGTH=327	327	327	1.00E-159	100.0	85.6	92.7
Rsa1.0_01588.1.g28192.t1	ref|XP_002880297.1| hypothetical protein ARALYDRAFT_904211 [Arabidopsis lyrata subsp. lyrata] gi|297326136|gb|EFH56556.1| hypothetical protein ARALYDRAFT_904211 [Arabidopsis lyrata subsp. lyrata]	309	305	1.00E-117	98.7	79.3	86.7	hypothetical protein ARALYDRAFT_904211	gbpln	Arabidopsis lyrata	AT2G47360.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02570.1); Has 58 Blast hits to 55 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19437820-19438731 FORWARD LENGTH=303	309	303	1.00E-117	98.1	79.0	85.8
Rsa1.0_01588.1.g28193.t1	ref|NP_850472.1| flowering time control protein-like protein [Arabidopsis thaliana] gi|50897178|gb|AAT85728.1| At2g47310 [Arabidopsis thaliana] gi|53793649|gb|AAU93571.1| At2g47310 [Arabidopsis thaliana] gi|110738579|dbj|BAF01215.1| putative FCA-related protein [Arabidopsis thaliana] gi|330255732|gb|AEC10826.1| flowering time control protein-like protein [Arabidopsis thaliana]	428	512	1.00E-97	119.6	47.4	52.3	flowering time control protein-like protein	gbpln	Arabidopsis thaliana	AT2G47310.1 | Symbols: | flowering time control protein-related / FCA gamma-related | chr2:19423791-19426846 FORWARD LENGTH=512	428	512	1.00E-100	119.6	47.4	52.3
Rsa1.0_01588.1.g28194.t1	ref|XP_002862591.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata] gi|297828465|ref|XP_002882115.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata] gi|297308212|gb|EFH38849.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata] gi|297327954|gb|EFH58374.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata]	104	103	2.00E-42	99.0	84.6	92.3	transcription factor/ transcription regulator	gbpln	Arabidopsis lyrata	AT2G47270.1 | Symbols: UPB1 | sequence-specific DNA binding transcription factors;transcription regulators | chr2:19411741-19412049 REVERSE LENGTH=102	104	102	4.00E-44	98.1	81.7	91.3
Rsa1.0_01588.1.g28195.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01588.1.g28196.t1	ref|XP_002882114.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297327953|gb|EFH58373.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	331	337	1.00E-127	101.8	78.5	84.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G47260.1 | Symbols: WRKY23, ATWRKY23 | WRKY DNA-binding protein 23 | chr2:19405045-19406446 REVERSE LENGTH=337	331	337	1.00E-118	101.8	76.4	82.8

Rsa1.0_01588.1.g28197.t1	ref|NP_182246.1| long chain acyl-CoA synthetase 1 [Arabidopsis thaliana] gi|79324939|ref|NP_001031554.1| long chain acyl-CoA synthetase 1 [Arabidopsis thaliana] gi|75097627|sp|O22898.1|LACS1_ARATH RecName: Full=Long chain acyl-CoA synthetase 1; AltName: Full=Protein ECERIFERUM 8 gi|20805863|gb|AAM28868.1|AF503751_1 long chain acyl-CoA synthetase 1 [Arabidopsis thaliana] gi|2275202|gb|AAB63824.1| putative acyl-CoA synthetase [Arabidopsis thaliana] gi|15912205|gb|AAL08236.1| At2g47240/T8I13.8 [Arabidopsis thaliana] gi|22137266|gb|AAM91478.1| At2g47240/T8I13.8 [Arabidopsis thaliana] gi|222424060|dbj|BAH19991.1| AT2G47240 [Arabidopsis thaliana] gi|330255724|gb|AEC10818.1| long chain acyl-CoA synthetase 1 [Arabidopsis thaliana] gi|330255725|gb|AEC10819.1| long chain acyl-CoA synthetase 1 [Arabidopsis thaliana]	660	660	0	100.0	90.9	96.2	long chain acyl-CoA synthetase 1	gbpln	Arabidopsis thaliana	AT2G47240.2 | Symbols: LACS1 | AMP-dependent synthetase and ligase family protein | chr2:19393835-19397616 FORWARD LENGTH=660	660	660	0	100.0	90.9	96.2
Rsa1.0_01588.1.g28198.t1	ref|XP_002880288.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326127|gb|EFH56547.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	695	703	1.00E-132	101.2	42.9	57.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G47230.1 | Symbols: DUF6, ATDUF6 | DOMAIN OF UNKNOWN FUNCTION 724 6 | chr2:19387126-19390011 FORWARD LENGTH=701	695	701	1.00E-134	100.9	42.7	58.6
Rsa1.0_01588.1.g28199.t1	ref|XP_002880287.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297326126|gb|EFH56546.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	446	441	0	98.9	89.9	93.7	myb family transcription factor	gbpln	Arabidopsis lyrata	AT2G47210.1 | Symbols: | myb-like transcription factor family protein | chr2:19379039-19382204 FORWARD LENGTH=441	446	441	0	98.9	89.5	93.0
Rsa1.0_01588.1.g28200.t1	ref|XP_002882113.1| hypothetical protein ARALYDRAFT_322367 [Arabidopsis lyrata subsp. lyrata] gi|297327952|gb|EFH58372.1| hypothetical protein ARALYDRAFT_322367 [Arabidopsis lyrata subsp. lyrata]	72	89	2.00E-19	123.6	66.7	75.0	hypothetical protein ARALYDRAFT_322367	gbpln	Arabidopsis lyrata	AT2G47200.1 | Symbols: | unknown protein; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19377884-19378150 REVERSE LENGTH=88	72	88	4.00E-22	122.2	68.1	73.6
Rsa1.0_01589.1.g28201.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01589.1.g28202.t2	gb|AFP57436.1| putative metallothionein type 4 [Brassica napus]	84	86	2.00E-33	102.4	92.9	96.4	putative metallothionein type 4	gbpln	Brassica napus	AT2G23240.2 | Symbols: | Plant EC metallothionein-like protein, family 15 | chr2:9895995-9896325 REVERSE LENGTH=84	84	84	1.00E-26	100.0	75.0	82.1
Rsa1.0_01589.1.g28203.t1	ref|XP_002879963.1| hypothetical protein ARALYDRAFT_903544 [Arabidopsis lyrata subsp. lyrata] gi|297325802|gb|EFH56222.1| hypothetical protein ARALYDRAFT_903544 [Arabidopsis lyrata subsp. lyrata]	327	298	1.00E-119	91.1	74.9	78.3	hypothetical protein ARALYDRAFT_903544	gbpln	Arabidopsis lyrata	AT2G41990.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Late embryogenesis abundant protein, group 2 (InterPro:IPR004864); BEST Arabidopsis thaliana protein match is: Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (TAIR:AT4G35170.1); Has 172 Blast hits to 168 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 172; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17527396-17528527 FORWARD LENGTH=297	327	297	1.00E-121	90.8	73.7	78.6
Rsa1.0_01589.1.g28204.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01589.1.g28205.t1	emb|CAN63034.1| hypothetical protein VITISV_044052 [Vitis vinifera]	771	820	1.00E-133	106.4	36.6	49.4	hypothetical protein VITISV_044052	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	771	1262	3.00E-23	163.7	9.7	14.8
Rsa1.0_01589.1.g28206.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01589.1.g28207.t3	gb|EOA27633.1| hypothetical protein CARUB_v10023781mg [Capsella rubella]	408	287	1.00E-123	70.3	57.1	61.0	hypothetical protein CARUB_v10023781mg	gbpln	Capsella rubella	AT2G20920.1 | Symbols: | Protein of unknown function (DUF3353) | chr2:8998728-8999789 FORWARD LENGTH=287	408	287	1.00E-123	70.3	56.6	60.0
Rsa1.0_01590.1.g28208.t1	gb|EOA24062.1| hypothetical protein CARUB_v10017282mg [Capsella rubella]	425	435	0	102.4	89.2	94.1	hypothetical protein CARUB_v10017282mg	gbpln	Capsella rubella	AT3G52820.1 | Symbols: ATPAP22, PAP22 | purple acid phosphatase 22 | chr3:19574236-19576938 REVERSE LENGTH=434	425	434	0	102.1	87.3	92.9
Rsa1.0_01590.1.g28209.t2	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	278	478	8.00E-69	171.9	45.7	65.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	278	746	5.00E-60	268.3	39.9	55.8

Rsa1.0_01590.1.g28210.t1	ref|NP_565844.1| zinc finger A20 and AN1 domain-containing stress-associated protein 4 [Arabidopsis thaliana] gi|73921295|sp|Q9SJM6.1|SAP4_ARATH RecName: Full=Zinc finger A20 and AN1 domain-containing stress-associated protein 4; Short=AtSAP4 gi|4510345|gb|AAD21434.1| expressed protein [Arabidopsis thaliana] gi|21592464|gb|AAM64415.1| zinc finger-like protein [Arabidopsis thaliana] gi|114050557|gb|ABI49428.1| At2g36320 [Arabidopsis thaliana] gi|330254138|gb|AEC09232.1| zinc finger A20 and AN1 domain-containing stress-associated protein 4 [Arabidopsis thaliana]	176	161	6.00E-65	91.5	69.9	77.8	zinc finger A20 and AN1 domain-containing stress-associated protein 4	gbpln	Arabidopsis thaliana	AT2G36320.1 | Symbols: | A20/AN1-like zinc finger family protein | chr2:15229388-15229873 FORWARD LENGTH=161	176	161	2.00E-67	91.5	69.9	77.8
Rsa1.0_01590.1.g28211.t1	gb|EOA25380.1| hypothetical protein CARUB_v10018720mg [Capsella rubella]	426	429	0	100.7	82.6	90.8	hypothetical protein CARUB_v10018720mg	gbpln	Capsella rubella	AT3G52780.1 | Symbols: ATPAP20, PAP20 | Purple acid phosphatases superfamily protein | chr3:19561525-19564195 REVERSE LENGTH=427	426	427	0	100.2	81.5	91.5
Rsa1.0_01590.1.g28212.t1	gb|EOA25012.1| hypothetical protein CARUB_v10018310mg, partial [Capsella rubella]	70	95	9.00E-22	135.7	84.3	90.0	hypothetical protein CARUB_v10018310mg, partial	gbpln	Capsella rubella	AT3G52770.1 | Symbols: ZPR3 | protein binding | chr3:19557891-19558094 REVERSE LENGTH=67	70	67	7.00E-19	95.7	64.3	67.1
Rsa1.0_01590.1.g28213.t1	gb|EOA23950.1| hypothetical protein CARUB_v10017167mg [Capsella rubella]	469	472	0	100.6	87.2	92.1	hypothetical protein CARUB_v10017167mg	gbpln	Capsella rubella	AT3G52750.1 | Symbols: FTSZ2-2 | Tubulin/FtsZ family protein | chr3:19549841-19552435 REVERSE LENGTH=473	469	473	0	100.9	85.7	91.7
Rsa1.0_01590.1.g28214.t1	ref|NP_566972.1| uncharacterized protein [Arabidopsis thaliana] gi|17386128|gb|AAL38610.1|AF446877_1 AT3g52740/F3C22_140 [Arabidopsis thaliana] gi|7669948|emb|CAB89235.1| putative protein [Arabidopsis thaliana] gi|15450655|gb|AAK96599.1| AT3g52740/F3C22_140 [Arabidopsis thaliana] gi|332645467|gb|AEE78988.1| uncharacterized protein AT3G52740 [Arabidopsis thaliana]	139	140	1.00E-55	100.7	82.0	89.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G52740.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G44450.1); Has 65 Blast hits to 65 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 65; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:19546446-19546868 REVERSE LENGTH=140	139	140	3.00E-58	100.7	82.0	89.2
Rsa1.0_01591.1.g28215.t1	ref|XP_002893723.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339565|gb|EFH69982.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	408	385	1.00E-136	94.4	58.8	70.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G32430.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11704932-11706325 REVERSE LENGTH=380	408	380	1.00E-123	93.1	54.4	68.6
Rsa1.0_01591.1.g28216.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01591.1.g28217.t1	gb|EOA30347.1| hypothetical protein CARUB_v10013470mg [Capsella rubella]	516	515	0	99.8	87.0	93.4	hypothetical protein CARUB_v10013470mg	gbpln	Capsella rubella	AT3G10570.1 | Symbols: CYP77A6 | cytochrome P450, family 77, subfamily A, polypeptide 6 | chr3:3302156-3303697 FORWARD LENGTH=513	516	513	0	99.4	86.2	91.9
Rsa1.0_01591.1.g28218.t4	ref|XP_002882684.1| hypothetical protein ARALYDRAFT_478393 [Arabidopsis lyrata subsp. lyrata] gi|297328524|gb|EFH58943.1| hypothetical protein ARALYDRAFT_478393 [Arabidopsis lyrata subsp. lyrata]	332	334	1.00E-140	100.6	78.6	86.1	hypothetical protein ARALYDRAFT_478393	gbpln	Arabidopsis lyrata	AT3G10572.1 | Symbols: | 3-phosphoinositide-dependent protein kinase-1, putative | chr3:3304346-3306306 FORWARD LENGTH=333	332	333	1.00E-142	100.3	77.7	85.5
Rsa1.0_01591.1.g28219.t2	ref|NP_564870.1| homolog of anti-oxidant 1 [Arabidopsis thaliana] gi|14532548|gb|AAK64002.1| At1g66240/T6J19_6 [Arabidopsis thaliana] gi|18655401|gb|AAL76156.1| At1g66240/T6J19_6 [Arabidopsis thaliana] gi|332196360|gb|AEE34481.1| homolog of anti-oxidant 1 [Arabidopsis thaliana]	87	106	4.00E-29	121.8	71.3	77.0	homolog of anti-oxidant 1	gbpln	Arabidopsis thaliana	AT1G66240.1 | Symbols: ATX1, ATATX1 | homolog of anti-oxidant 1 | chr1:24686445-24687327 REVERSE LENGTH=106	87	106	6.00E-32	121.8	71.3	77.0
Rsa1.0_01591.1.g28220.t1	ref|NP_683474.1| uncharacterized protein [Arabidopsis thaliana] gi|91805373|gb|ABE65416.1| hypothetical protein At1g66245 [Arabidopsis thaliana] gi|332196363|gb|AEE34484.1| uncharacterized protein AT1G66245 [Arabidopsis thaliana]	274	287	1.00E-88	104.7	75.2	84.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G66245.1 | Symbols: | unknown protein; Has 390 Blast hits to 336 proteins in 78 species: Archae - 0; Bacteria - 22; Metazoa - 81; Fungi - 35; Plants - 39; Viruses - 2; Other Eukaryotes - 211 (source: NCBI BLink). | chr1:24690444-24691307 FORWARD LENGTH=287	274	287	4.00E-91	104.7	75.2	84.7

Rsa1.0_01591.1.g28221.t1	ref|NP_192683.1| SANT DNA-binding domain-containing protein [Arabidopsis thaliana] gi|7267587|emb|CAB78068.1| putative protein [Arabidopsis thaliana] gi|21689645|gb|AAM67444.1| unknown protein [Arabidopsis thaliana] gi|332657349|gb|AEE82749.1| SANT DNA-binding domain-containing protein [Arabidopsis thaliana]	177	200	2.00E-38	113.0	51.4	63.8	SANT DNA-binding domain-containing protein	gbpln	Arabidopsis thaliana	AT4G09450.1 | Symbols: | Duplicated homeodomain-like superfamily protein | chr4:5983277-5984500 FORWARD LENGTH=200	177	200	7.00E-41	113.0	51.4	63.8
Rsa1.0_01591.1.g28222.t1	ref|XP_002882688.1| 40S ribosomal protein S17 [Arabidopsis lyrata subsp. lyrata] gi|297328528|gb|EFH58947.1| 40S ribosomal protein S17 [Arabidopsis lyrata subsp. lyrata]	139	138	1.00E-66	99.3	92.1	93.5	40S ribosomal protein S17	gbpln	Arabidopsis lyrata	AT3G10610.1 | Symbols: | Ribosomal S17 family protein | chr3:3319459-3319881 FORWARD LENGTH=140	139	140	3.00E-68	100.7	90.6	93.5
Rsa1.0_01591.1.g28223.t1	ref|XP_002863885.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] gi|297309720|gb|EFH40144.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	661	454	0	68.7	51.0	56.1	regulator of chromosome condensation family protein	gbpln	Arabidopsis lyrata	AT5G48330.2 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr5:19585989-19587729 FORWARD LENGTH=454	661	454	1.00E-180	68.7	51.1	56.6
Rsa1.0_01591.1.g28224.t1	ref|NP_187677.1| calmodulin-domain protein kinase cdpk isoform 2 [Arabidopsis thaliana] gi|75319416|sp|Q38870.1|CDPK2_ARATH RecName: Full=Calcium-dependent protein kinase 2; AltName: Full=Calmodulin-domain protein kinase CDPK isoform 2 gi|9837343|gb|AAG00535.1|AF286222_1 calcium-dependent protein kinase isoform 2 [Arabidopsis thaliana] gi|12322803|gb|AAG51400.1|AC011560_32 calmodulin-domain protein kinase CDPK isoform 2; 13089-15758 [Arabidopsis thaliana] gi|1399271|gb|AAB03244.1| calmodulin-domain protein kinase CDPK isoform 2 [Arabidopsis thaliana] gi|8567800|gb|AAF76372.1| calmodulin-domain protein kinase CDPK isoform 2 [Arabidopsis thaliana] gi|209529779|gb|ACI49784.1| At3g10660 [Arabidopsis thaliana] gi|332641419|gb|AEE74940.1| calmodulin-domain protein kinase cdpk isoform 2 [Arabidopsis thaliana]	634	646	0	101.9	89.9	93.5	calmodulin-domain protein kinase cdpk isoform 2	gbpln	Arabidopsis thaliana	AT3G10660.1 | Symbols: CPK2, ATCPK2 | calmodulin-domain protein kinase cdpk isoform 2 | chr3:3331599-3334268 REVERSE LENGTH=646	634	646	0	101.9	89.9	93.5
Rsa1.0_01591.1.g28225.t1	gb|EOA30977.1| hypothetical protein CARUB_v10014123mg [Capsella rubella]	333	338	1.00E-157	101.5	88.3	91.3	hypothetical protein CARUB_v10014123mg	gbpln	Capsella rubella	AT3G10670.1 | Symbols: ATNAP7, NAP7 | non-intrinsic ABC protein 7 | chr3:3335325-3337304 REVERSE LENGTH=338	333	338	1.00E-159	101.5	88.9	91.0
Rsa1.0_01591.1.g28226.t1	ref|XP_002882690.1| hypothetical protein ARALYDRAFT_341204 [Arabidopsis lyrata subsp. lyrata] gi|297328530|gb|EFH58949.1| hypothetical protein ARALYDRAFT_341204 [Arabidopsis lyrata subsp. lyrata]	515	489	1.00E-140	95.0	56.5	68.9	hypothetical protein ARALYDRAFT_341204	gbpln	Arabidopsis lyrata	AT3G10680.1 | Symbols: | HSP20-like chaperones superfamily protein | chr3:3337773-3339345 FORWARD LENGTH=490	515	490	1.00E-142	95.1	56.5	69.3
Rsa1.0_01591.1.g28227.t5	gb|AAF19579.1|AC011708_22 galactokinase-like protein [Arabidopsis thaliana]	415	412	1.00E-178	99.3	81.0	87.0	galactokinase-like protein	gbpln	Arabidopsis thaliana	AT3G10700.1 | Symbols: GalAK | galacturonic acid kinase | chr3:3346789-3350863 REVERSE LENGTH=424	415	424	1.00E-175	102.2	80.2	86.0
Rsa1.0_01591.1.g28228.t1	gb|EOA32419.1| hypothetical protein CARUB_v10015693mg [Capsella rubella]	461	457	0	99.1	75.3	85.0	hypothetical protein CARUB_v10015693mg	gbpln	Capsella rubella	AT3G10730.1 | Symbols: SUN2, ATSUN2 | SAD1/UNC-84 domain protein 2 | chr3:3358556-3360522 REVERSE LENGTH=455	461	455	0	98.7	75.7	84.8
Rsa1.0_01591.1.g28229.t1	gb|EOA32148.1| hypothetical protein CARUB_v10015399mg, partial [Capsella rubella]	428	419	7.00E-83	97.9	47.9	61.4	hypothetical protein CARUB_v10015399mg, partial	gbpln	Capsella rubella	AT1G05080.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:1459091-1460579 FORWARD LENGTH=439	428	439	8.00E-71	102.6	42.1	59.3
Rsa1.0_01591.1.g28230.t1	gb|EOA33837.1| hypothetical protein CARUB_v10021318mg, partial [Capsella rubella]	166	290	6.00E-31	174.7	41.6	57.2	hypothetical protein CARUB_v10021318mg, partial	gbpln	Capsella rubella	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	166	332	4.00E-25	200.0	35.5	53.0
Rsa1.0_01591.1.g28231.t1	gb|EOA18354.1| hypothetical protein CARUB_v10006874mg, partial [Capsella rubella]	386	430	1.00E-70	111.4	44.8	60.1	hypothetical protein CARUB_v10006874mg, partial	gbpln	Capsella rubella	AT1G05080.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:1459091-1460579 FORWARD LENGTH=439	386	439	4.00E-61	113.7	43.5	58.0
Rsa1.0_01591.1.g28232.t1	gb|EOA30989.1| hypothetical protein CARUB_v10014134mg [Capsella rubella]	224	335	5.00E-91	149.6	90.2	94.2	hypothetical protein CARUB_v10014134mg	gbpln	Capsella rubella	AT3G10760.1 | Symbols: | Homeodomain-like superfamily protein | chr3:3369814-3370821 FORWARD LENGTH=335	224	335	2.00E-83	149.6	86.2	90.6

Rsa1.0_01592.1.g28233.t1	ref|NP_197954.1| Exostosin family protein [Arabidopsis thaliana] gi|110738111|dbj|BAF00988.1| hypothetical protein [Arabidopsis thaliana] gi|332006108|gb|AED93491.1| Exostosin family protein [Arabidopsis thaliana]	610	654	0	107.2	79.0	86.9	Exostosin family protein	gbpln	Arabidopsis thaliana	AT5G25820.1 | Symbols: | Exostosin family protein | chr5:8997248-8999574 REVERSE LENGTH=654	610	654	0	107.2	79.0	86.9
Rsa1.0_01592.1.g28234.t1	ref|NP_197955.1| GATA transcription factor 12 [Arabidopsis thaliana] gi|71660770|sp|P69781.1|GAT12_ARATH RecName: Full=GATA transcription factor 12 gi|225898931|dbj|BAH30596.1| hypothetical protein [Arabidopsis thaliana] gi|332006109|gb|AED93492.1| GATA transcription factor 12 [Arabidopsis thaliana]	310	331	1.00E-111	106.8	73.2	82.3	GATA transcription factor 12	gbpln	Arabidopsis thaliana	AT5G25830.1 | Symbols: GATA12 | GATA transcription factor 12 | chr5:9004398-9005502 REVERSE LENGTH=331	310	331	1.00E-114	106.8	73.2	82.3
Rsa1.0_01592.1.g28235.t1	gb|AAM63896.1| unknown [Arabidopsis thaliana]	176	173	2.00E-82	98.3	86.9	90.9	unknown	gbpln	Arabidopsis thaliana	AT5G25840.1 | Symbols: | Protein of unknown function (DUF1677) | chr5:9010909-9011430 REVERSE LENGTH=173	176	173	1.00E-84	98.3	86.9	90.9
Rsa1.0_01592.1.g28236.t1	gb|ADB93665.1| indole-3-acetic acid inducible 28 [Arabidopsis thaliana] gi|284794593|gb|ADB93669.1| indole-3-acetic acid inducible 28 [Arabidopsis thaliana]	147	168	1.00E-61	114.3	84.4	91.8	indole-3-acetic acid inducible 28	gbpln	Arabidopsis thaliana	AT5G25890.1 | Symbols: IAA28, IAR2 | indole-3-acetic acid inducible 28 | chr5:9033480-9034554 FORWARD LENGTH=175	147	175	3.00E-64	119.0	84.4	91.8
Rsa1.0_01592.1.g28237.t1	gb|AAD40130.1|AF149413_11 T1N24.10 gene product [Arabidopsis thaliana]	156	375	4.00E-61	240.4	73.1	87.8	T1N24.10 gene product	gbpln	Arabidopsis thaliana	AT5G26050.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:9103395-9103877 REVERSE LENGTH=160	156	160	8.00E-63	102.6	73.1	87.8
Rsa1.0_01592.1.g28238.t1	ref|XP_002874298.1| hypothetical protein ARALYDRAFT_489454 [Arabidopsis lyrata subsp. lyrata] gi|297320135|gb|EFH50557.1| hypothetical protein ARALYDRAFT_489454 [Arabidopsis lyrata subsp. lyrata]	193	326	6.00E-66	168.9	61.7	68.4	hypothetical protein ARALYDRAFT_489454	gbpln	Arabidopsis lyrata	AT5G26090.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:9109026-9113235 REVERSE LENGTH=401	193	401	2.00E-68	207.8	61.1	68.4
Rsa1.0_01592.1.g28239.t1	gb|AAD40131.1|AF149413_12 T1N24.11 gene product [Arabidopsis thaliana]	303	258	1.00E-74	85.1	43.6	49.5	T1N24.11 gene product	gbpln	Arabidopsis thaliana	AT5G26090.1 | Symbols: | Plant self-incompatibility protein S1 family | chr5:9109026-9113235 REVERSE LENGTH=401	303	401	1.00E-75	132.3	42.9	48.8
Rsa1.0_01592.1.g28240.t2	gb|EOA24760.1| hypothetical protein CARUB_v10018038mg [Capsella rubella] gi|482560570|gb|EOA24761.1| hypothetical protein CARUB_v10018038mg [Capsella rubella]	190	205	1.00E-88	107.9	87.9	92.6	hypothetical protein CARUB_v10018038mg	gbpln	Capsella rubella	AT5G11950.2 | Symbols: | Putative lysine decarboxylase family protein | chr5:3855072-3856815 FORWARD LENGTH=216	190	216	7.00E-87	113.7	83.7	91.6
Rsa1.0_01593.1.g28241.t1	ref|XP_002868537.1| hypothetical protein ARALYDRAFT_355725 [Arabidopsis lyrata subsp. lyrata] gi|297314373|gb|EFH44796.1| hypothetical protein ARALYDRAFT_355725 [Arabidopsis lyrata subsp. lyrata]	599	1370	1.00E-128	228.7	50.4	59.1	hypothetical protein ARALYDRAFT_355725	gbpln	Arabidopsis lyrata	AT2G33435.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:14166037-14169492 FORWARD LENGTH=979	599	979	1.00E-112	163.4	48.6	57.4
Rsa1.0_01593.1.g28242.t1	ref|XP_002872140.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata] gi|297317977|gb|EFH48399.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata]	496	496	0	100.0	79.8	90.7	CYP71B11	gbpln	Arabidopsis lyrata	AT5G25120.1 | Symbols: CYP71B11 | ytochrome p450, family 71, subfamily B, polypeptide 11 | chr5:8662851-8664432 FORWARD LENGTH=496	496	496	0	100.0	78.8	90.1
Rsa1.0_01593.1.g28243.t2	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1128	1250	0	110.8	56.6	73.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1128	1262	4.00E-83	111.9	14.9	23.2
Rsa1.0_01593.1.g28244.t1	ref|NP_001189662.1| uncharacterized protein [Arabidopsis thaliana] gi|330253675|gb|AEC08769.1| uncharacterized protein AT2G32970 [Arabidopsis thaliana]	678	690	0	101.8	82.6	92.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G32970.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages. | chr2:13991744-13995065 REVERSE LENGTH=690	678	690	0	101.8	82.6	92.2
Rsa1.0_01593.1.g28245.t1	ref|XP_002881256.1| hypothetical protein ARALYDRAFT_345055 [Arabidopsis lyrata subsp. lyrata] gi|297327095|gb|EFH57515.1| hypothetical protein ARALYDRAFT_345055 [Arabidopsis lyrata subsp. lyrata]	287	291	1.00E-141	101.4	89.2	92.3	hypothetical protein ARALYDRAFT_345055	gbpln	Arabidopsis lyrata	AT2G32980.1 | Symbols: | unknown protein; Has 158 Blast hits to 154 proteins in 73 species: Archae - 0; Bacteria - 61; Metazoa - 0; Fungi - 0; Plants - 55; Viruses - 28; Other Eukaryotes - 14 (source: NCBI BLink). | chr2:13997569-13999715 REVERSE LENGTH=296	287	296	1.00E-141	103.1	88.2	92.0

Rsa1.0_01593.1.g28246.t1	ref|NP_193213.5| TESMIN/TSO1-like CXC 2 [Arabidopsis thaliana] gi|395455099|sp|F4JIF5.1|TCX2_ARATH RecName: Full=Protein tesmin/TSO1-like CXC 2; Short=AtTCX2; AltName: Full=Protein TSO1-like 2; Short=Protein SOL2 gi|332658096|gb|AEE83496.1| TESMIN/TSO1-like CXC 2 [Arabidopsis thaliana]	535	674	4.00E-47	126.0	18.5	22.8	TESMIN/TSO1-like CXC 2	gbpln	Arabidopsis thaliana	AT4G14770.1 | Symbols: TCX2, ATTCX2 | TESMIN/TSO1-like CXC 2 | chr4:8481522-8484825 REVERSE LENGTH=674	535	674	1.00E-49	126.0	18.5	22.8
Rsa1.0_01593.1.g28247.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01593.1.g28248.t1	ref|NP_180863.1| ATP synthase subunit gamma [Arabidopsis thaliana] gi|3334123|sp|Q96250.1|ATPG3_ARATH RecName: Full=ATP synthase subunit gamma, mitochondrial; AltName: Full=F-ATPase gamma subunit; Flags: Precursor gi|1655480|dbj|BAA13599.1| gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] gi|2924787|gb|AAC04916.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|14517358|gb|AAK62570.1| At2g33040/F25I18.22 [Arabidopsis thaliana] gi|17065102|gb|AAL32705.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|20196990|gb|AAM14859.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|20857422|gb|AAM26719.1| At2g33040/F25I18.22 [Arabidopsis thaliana] gi|21554962|gb|AAM63740.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|330253683|gb|AEC08777.1| ATP synthase subunit gamma [Arabidopsis thaliana]	158	325	1.00E-64	205.7	85.4	91.8	ATP synthase subunit gamma	gbpln	Arabidopsis thaliana	AT2G33040.1 | Symbols: ATP3 | gamma subunit of Mt ATP synthase | chr2:14018978-14021047 REVERSE LENGTH=325	158	325	4.00E-67	205.7	85.4	91.8
Rsa1.0_01593.1.g28249.t1	ref|NP_180863.1| ATP synthase subunit gamma [Arabidopsis thaliana] gi|3334123|sp|Q96250.1|ATPG3_ARATH RecName: Full=ATP synthase subunit gamma, mitochondrial; AltName: Full=F-ATPase gamma subunit; Flags: Precursor gi|1655480|dbj|BAA13599.1| gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] gi|2924787|gb|AAC04916.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|14517358|gb|AAK62570.1| At2g33040/F25I18.22 [Arabidopsis thaliana] gi|17065102|gb|AAL32705.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|20196990|gb|AAM14859.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|20857422|gb|AAM26719.1| At2g33040/F25I18.22 [Arabidopsis thaliana] gi|21554962|gb|AAM63740.1| mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis thaliana] gi|330253683|gb|AEC08777.1| ATP synthase subunit gamma [Arabidopsis thaliana]	266	325	1.00E-149	122.2	97.7	99.6	ATP synthase subunit gamma	gbpln	Arabidopsis thaliana	AT2G33040.1 | Symbols: ATP3 | gamma subunit of Mt ATP synthase | chr2:14018978-14021047 REVERSE LENGTH=325	266	325	1.00E-152	122.2	97.7	99.6
Rsa1.0_01594.1.g28250.t1	gb|EOA32164.1| hypothetical protein CARUB_v10015420mg [Capsella rubella]	142	219	4.00E-32	154.2	46.5	59.9	hypothetical protein CARUB_v10015420mg	gbpln	Capsella rubella	AT3G11402.2 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:3573516-3577765 FORWARD LENGTH=910	142	910	3.00E-18	640.8	33.8	43.7
Rsa1.0_01594.1.g28251.t1	ref|NP_179593.1| putative RING-H2 finger protein ATL12 [Arabidopsis thaliana] gi|68565334|sp|Q9SL78.1|ATL12_ARATH RecName: Full=Putative RING-H2 finger protein ATL12; Flags: Precursor gi|4580469|gb|AAD24393.1| putative RING zinc finger protein [Arabidopsis thaliana] gi|330251863|gb|AEC06957.1| putative RING-H2 finger protein ATL12 [Arabidopsis thaliana]	402	390	1.00E-151	97.0	69.7	79.4	putative RING-H2 finger protein ATL12	gbpln	Arabidopsis thaliana	AT2G20030.1 | Symbols: | RING/U-box superfamily protein | chr2:8647813-8648985 FORWARD LENGTH=390	402	390	1.00E-154	97.0	69.7	79.4

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<tr><td>Rsa1.0_01594.1.g28252.t1</td><td>gb|AAM62769.1| 50S ribosomal protein L4 [Arabidopsis thaliana]</td><td>512</td><td>300</td><td>1.00E-148</td><td>58.6</td><td>50.8</td><td>54.1</td><td>50S ribosomal protein L4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G20060.1 | Symbols: | Ribosomal protein L4/L1 family | chr2:8659384-8661227 FORWARD LENGTH=300</td><td>512</td><td>300</td><td>1.00E-151</td><td>58.6</td><td>50.6</td><td>54.1</td></tr>
<tr><td>Rsa1.0_01594.1.g28253.t1</td><td>ref|XP_002873363.1| hypothetical protein ARALYDRAFT_908813 [Arabidopsis lyrata subsp. lyrata] gi|297319200|gb|EFH49622.1| hypothetical protein ARALYDRAFT_908813 [Arabidopsis lyrata subsp. lyrata]</td><td>258</td><td>275</td><td>1.00E-69</td><td>106.6</td><td>56.2</td><td>68.6</td><td>hypothetical protein ARALYDRAFT_908813</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G76810.1 | Symbols: | eukaryotic translation initiation factor 2 (eIF-2) family protein | chr1:28831366-28836310 REVERSE LENGTH=1294</td><td>258</td><td>1294</td><td>4.00E-48</td><td>501.6</td><td>39.9</td><td>55.4</td></tr>
<tr><td>Rsa1.0_01594.1.g28254.t1</td><td>gb|EOA32941.1| hypothetical protein CARUB_v10016269mg [Capsella rubella]</td><td>182</td><td>180</td><td>1.00E-66</td><td>98.9</td><td>79.7</td><td>89.0</td><td>hypothetical protein CARUB_v10016269mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G20080.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G28840.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:8663115-8664735 REVERSE LENGTH=178</td><td>182</td><td>178</td><td>5.00E-69</td><td>97.8</td><td>80.8</td><td>86.8</td></tr>
<tr><td>Rsa1.0_01594.1.g28255.t1</td><td>gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]</td><td>275</td><td>484</td><td>2.00E-24</td><td>176.0</td><td>28.7</td><td>39.3</td><td>hypothetical protein 27.t00116</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01595.1.g28256.t1</td><td>ref|NP_567749.1| Got1/Sft2-like vescicle transport protein [Arabidopsis thaliana] gi|88196739|gb|ABD43012.1| At4g26550 [Arabidopsis thaliana] gi|332659817|gb|AEE85217.1| Got1/Sft2-like vescicle transport protein [Arabidopsis thaliana]</td><td>230</td><td>225</td><td>1.00E-114</td><td>97.8</td><td>91.7</td><td>95.2</td><td>Got1/Sft2-like vescicle transport protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26550.1 | Symbols: | Got1/Sft2-like vescicle transport protein family | chr4:13402755-13404208 REVERSE LENGTH=225</td><td>230</td><td>225</td><td>1.00E-116</td><td>97.8</td><td>91.7</td><td>95.2</td></tr>
<tr><td>Rsa1.0_01595.1.g28257.t1</td><td>ref|NP_567750.1| FKBP-like peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana] gi|75306033|sp|Q944B0.1|FK161_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP16-1, chloroplastic; Short=PPIase FKBP16-1; AltName: Full=FK506-binding protein 16-1; Short=AtFKBP16-1; AltName: Full=Immunophilin FKBP16-1; AltName: Full=Rotamase; Flags: Precursor gi|16612240|gb|AAL27493.1|AF439821_1 AT4g26550/M3E9_20 [Arabidopsis thaliana] gi|21928091|gb|AAM78074.1| AT4g26550/M3E9_20 [Arabidopsis thaliana] gi|26450730|dbj|BAC42474.1| unknown protein [Arabidopsis thaliana] gi|332659818|gb|AEE85218.1| FKBP-like peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana]</td><td>191</td><td>207</td><td>5.00E-79</td><td>108.4</td><td>79.1</td><td>84.3</td><td>FKBP-like peptidyl-prolyl cis-trans isomerase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26555.1 | Symbols: | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | chr4:13404622-13406178 REVERSE LENGTH=207</td><td>191</td><td>207</td><td>2.00E-81</td><td>108.4</td><td>79.1</td><td>84.3</td></tr>
<tr><td>Rsa1.0_01595.1.g28258.t1</td><td>ref|NP_194387.1| calcineurin B-like 3 [Arabidopsis thaliana] gi|56748808|sp|Q8LEM7.2|CNBL3_ARATH RecName: Full=Calcineurin B-like protein 3; AltName: Full=SOS3-like calcium-binding protein 6 gi|3309086|gb|AAC26010.1| calcineurin B-like protein 3 [Arabidopsis thaliana] gi|4938495|emb|CAB43853.1| calcineurin B-like protein 3 [Arabidopsis thaliana] gi|7269509|emb|CAB79512.1| calcineurin B-like protein 3 [Arabidopsis thaliana] gi|18253013|gb|AAL62433.1| calcineurin B-like protein 3 [Arabidopsis thaliana] gi|22136404|gb|AAM91280.1| calcineurin B-like protein 3 [Arabidopsis thaliana] gi|332659820|gb|AEE85220.1| calcineurin B-like 3 [Arabidopsis thaliana] gi|482553189|gb|EOA17382.1| hypothetical protein CARUB_v10005674mg [Capsella rubella]</td><td>226</td><td>226</td><td>1.00E-125</td><td>100.0</td><td>96.9</td><td>99.1</td><td>calcineurin B-like 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G26570.1 | Symbols: ATCBL3, CBL3 | calcineurin B-like 3 | chr4:13408608-13409998 REVERSE LENGTH=226</td><td>226</td><td>226</td><td>1.00E-127</td><td>100.0</td><td>96.9</td><td>99.1</td></tr>
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Rsa1.0_01595.1.g28259.t1	ref|NP_194389.1| oligopeptide transporter 5 [Arabidopsis thaliana] gi|67460976|sp|Q9SUA4.1|OPT5_ARATH RecName: Full=Oligopeptide transporter 5; Short=AtOPT5 gi|13430760|gb|AAK26002.1|AF360292_1 putative isp4 protein [Arabidopsis thaliana] gi|4938497|emb|CAB43855.1| isp4 like protein [Arabidopsis thaliana] gi|7269511|emb|CAB79514.1| isp4 like protein [Arabidopsis thaliana] gi|15293229|gb|AAK93725.1| putative isp4 protein [Arabidopsis thaliana] gi|332659824|gb|AEE85224.1| oligopeptide transporter 5 [Arabidopsis thaliana]	754	753	0	99.9	84.4	91.1	oligopeptide transporter 5	gbpln	Arabidopsis thaliana	AT4G26590.1 | Symbols: ATOPT5, OPT5 | oligopeptide transporter 5 | chr4:13414134-13416850 REVERSE LENGTH=753	754	753	0	99.9	84.4	91.1
Rsa1.0_01595.1.g28260.t7	dbj|BAJ34003.1| unnamed protein product [Thellungiella halophila]	586	560	2.00E-40	95.6	15.9	17.6	unnamed protein product	----	----	AT4G26640.2 | Symbols: WRKY20, AtWRKY20 | WRKY family transcription factor family protein | chr4:13437298-13440693 REVERSE LENGTH=557	586	557	1.00E-40	95.1	14.3	16.7
Rsa1.0_01595.1.g28261.t1	ref|NP_567753.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|16930503|gb|AAL31937.1|AF419605_1 AT4g26650/T15N24_100 [Arabidopsis thaliana] gi|20453245|gb|AAM19861.1| AT4g26650/T15N24_100 [Arabidopsis thaliana] gi|332659832|gb|AEE85232.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	481	455	0	94.6	82.7	86.9	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT4G26650.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:13445552-13447592 FORWARD LENGTH=455	481	455	0	94.6	82.7	86.9
Rsa1.0_01595.1.g28262.t2	ref|XP_002867546.1| MRH5/SHV3 [Arabidopsis lyrata subsp. lyrata] gi|297313382|gb|EFH43805.1| MRH5/SHV3 [Arabidopsis lyrata subsp. lyrata]	759	756	0	99.6	82.1	89.1	MRH5/SHV3	gbpln	Arabidopsis lyrata	AT4G26690.1 | Symbols: SHV3, MRH5, GPDL2 | PLC-like phosphodiesterase family protein | chr4:13456793-13459890 REVERSE LENGTH=759	759	759	0	100.0	81.2	89.3
Rsa1.0_01595.1.g28263.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1531	2726	0	178.1	54.9	73.2	disease resistance protein	gbpln	Brassica rapa	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1531	158	3.00E-40	10.3	5.0	6.5
Rsa1.0_01595.1.g28264.t1	ref|XP_002869593.1| hypothetical protein ARALYDRAFT_492129 [Arabidopsis lyrata subsp. lyrata] gi|297315429|gb|EFH45852.1| hypothetical protein ARALYDRAFT_492129 [Arabidopsis lyrata subsp. lyrata]	243	231	1.00E-115	95.1	81.5	88.9	hypothetical protein ARALYDRAFT_492129	gbpln	Arabidopsis lyrata	AT2G16030.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:6974196-6974891 REVERSE LENGTH=231	243	231	1.00E-116	95.1	80.2	88.5
Rsa1.0_01595.1.g28265.t1	ref|XP_002867545.1| protein phosphatase x-1 [Arabidopsis lyrata subsp. lyrata] gi|297313381|gb|EFH43804.1| protein phosphatase x-1 [Arabidopsis lyrata subsp. lyrata]	305	305	1.00E-175	100.0	96.1	98.0	protein phosphatase x-1	gbpln	Arabidopsis lyrata	AT4G26720.1 | Symbols: PPX1, PPX-1 | protein phosphatase X 1 | chr4:13470397-13472154 REVERSE LENGTH=305	305	305	1.00E-177	100.0	95.7	97.7
Rsa1.0_01595.1.g28266.t1	ref|XP_002869594.1| ATP synthase subunit H family protein [Arabidopsis lyrata subsp. lyrata] gi|297315430|gb|EFH45853.1| ATP synthase subunit H family protein [Arabidopsis lyrata subsp. lyrata]	70	70	3.00E-29	100.0	94.3	97.1	ATP synthase subunit H family protein	gbpln	Arabidopsis lyrata	AT4G26710.2 | Symbols: | ATPase, V0 complex, subunit E | chr4:13468705-13469668 FORWARD LENGTH=70	70	70	6.00E-31	100.0	91.4	95.7
Rsa1.0_01595.1.g28267.t1	ref|XP_002892884.1| hypothetical protein ARALYDRAFT_312568 [Arabidopsis lyrata subsp. lyrata] gi|297338726|gb|EFH69143.1| hypothetical protein ARALYDRAFT_312568 [Arabidopsis lyrata subsp. lyrata]	289	308	5.00E-59	106.6	57.1	65.7	hypothetical protein ARALYDRAFT_312568	gbpln	Arabidopsis lyrata	AT1G15800.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80610.1); Has 56 Blast hits to 52 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:5441425-5443584 REVERSE LENGTH=207	289	207	6.00E-31	71.6	24.2	29.4
Rsa1.0_01595.1.g28268.t1	ref|XP_002892882.1| hypothetical protein ARALYDRAFT_471776 [Arabidopsis lyrata subsp. lyrata] gi|297338724|gb|EFH69141.1| hypothetical protein ARALYDRAFT_471776 [Arabidopsis lyrata subsp. lyrata]	141	1343	1.00E-31	952.5	51.8	61.7	hypothetical protein ARALYDRAFT_471776	gbpln	Arabidopsis lyrata	AT1G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10440.1); Has 103701 Blast hits to 43153 proteins in 1828 species: Archae - 30; Bacteria - 7385; Metazoa - 38639; Fungi - 11531; Plants - 7727; Viruses - 307; Other Eukaryotes - 38082 (source: NCBI BLink). | chr1:5430446-5435921 REVERSE LENGTH=1335	141	1335	1.00E-33	946.8	48.9	56.7

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<tr><td>Rsa1.0_01595.1.g28269.t2</td><td>emb|CAH67061.1| H0112G12.6 [Oryza sativa Indica Group]</td><td>960</td><td>811</td><td>1.00E-152</td><td>84.5</td><td>28.3</td><td>35.7</td><td>H0112G12.6</td><td>gbpln</td><td>Oryza sativa</td><td>AT1G34070.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48050.1); Has 648 Blast hits to 647 proteins in 29 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 25; Plants - 607; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12402283-12403209 FORWARD LENGTH=308</td><td>960</td><td>308</td><td>5.00E-77</td><td>32.1</td><td>15.0</td><td>19.4</td></tr>
<tr><td>Rsa1.0_01595.1.g28270.t4</td><td>ref|XP_002892882.1| hypothetical protein ARALYDRAFT_471776 [Arabidopsis lyrata subsp. lyrata] gi|297338724|gb|EFH69141.1| hypothetical protein ARALYDRAFT_471776 [Arabidopsis lyrata subsp. lyrata]</td><td>1307</td><td>1343</td><td>0</td><td>102.8</td><td>81.0</td><td>86.9</td><td>hypothetical protein ARALYDRAFT_471776</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G15780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G10440.1); Has 103701 Blast hits to 43153 proteins in 1828 species: Archae - 30; Bacteria - 7385; Metazoa - 38639; Fungi - 11531; Plants - 7727; Viruses - 307; Other Eukaryotes - 38082 (source: NCBI BLink). | chr1:5430446-5435921 REVERSE LENGTH=1335</td><td>1307</td><td>1335</td><td>0</td><td>102.1</td><td>29.6</td><td>31.1</td></tr>
<tr><td>Rsa1.0_01595.1.g28271.t1</td><td>gb|AAF79348.1|AC007887_7 F15O4.13 [Arabidopsis thaliana]</td><td>505</td><td>1887</td><td>1.00E-14</td><td>373.7</td><td>7.7</td><td>10.5</td><td>F15O4.13</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01596.1.g28272.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01596.1.g28273.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01596.1.g28274.t1</td><td>gb|AAM15254.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>484</td><td>930</td><td>2.00E-46</td><td>192.1</td><td>25.2</td><td>36.4</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01596.1.g28275.t1</td><td>gb|EOA16183.1| hypothetical protein CARUB_v10004321mg [Capsella rubella]</td><td>249</td><td>660</td><td>2.00E-88</td><td>265.1</td><td>67.5</td><td>77.5</td><td>hypothetical protein CARUB_v10004321mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G23180.1 | Symbols: CRK10, RLK4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 | chr4:12138171-12140780 FORWARD LENGTH=669</td><td>249</td><td>669</td><td>2.00E-85</td><td>268.7</td><td>63.1</td><td>70.7</td></tr>
<tr><td>Rsa1.0_01596.1.g28276.t1</td><td>ref|XP_002863244.1| hypothetical protein ARALYDRAFT_332986 [Arabidopsis lyrata subsp. lyrata] gi|297309078|gb|EFH39503.1| hypothetical protein ARALYDRAFT_332986 [Arabidopsis lyrata subsp. lyrata]</td><td>438</td><td>418</td><td>0</td><td>95.4</td><td>85.8</td><td>89.0</td><td>hypothetical protein ARALYDRAFT_332986</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G13360.1 | Symbols: | ATP-dependent caseinolytic (Clp) protease/crotonase family protein | chr4:7775133-7777701 FORWARD LENGTH=421</td><td>438</td><td>421</td><td>0</td><td>96.1</td><td>84.7</td><td>88.1</td></tr>
<tr><td>Rsa1.0_01596.1.g28277.t1</td><td>ref|XP_002863137.1| hypothetical protein ARALYDRAFT_497045 [Arabidopsis lyrata subsp. lyrata] gi|297308971|gb|EFH39396.1| hypothetical protein ARALYDRAFT_497045 [Arabidopsis lyrata subsp. lyrata]</td><td>536</td><td>672</td><td>0</td><td>125.4</td><td>80.2</td><td>88.1</td><td>hypothetical protein ARALYDRAFT_497045</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G13370.1 | Symbols: | Plant protein of unknown function (DUF936) | chr4:7777916-7780334 REVERSE LENGTH=673</td><td>536</td><td>673</td><td>0</td><td>125.6</td><td>79.5</td><td>87.5</td></tr>
<tr><td>Rsa1.0_01597.1.g28278.t1</td><td>gb|EOA26975.1| hypothetical protein CARUB_v10023072mg [Capsella rubella] gi|482562786|gb|EOA26976.1| hypothetical protein CARUB_v10023072mg [Capsella rubella]</td><td>331</td><td>497</td><td>0</td><td>150.2</td><td>92.4</td><td>96.7</td><td>hypothetical protein CARUB_v10023072mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G39220.1 | Symbols: PLP6, PLA IIB | PATATIN-like protein 6 | chr2:16375055-16376663 REVERSE LENGTH=499</td><td>331</td><td>499</td><td>1.00E-180</td><td>150.8</td><td>92.4</td><td>95.5</td></tr>
<tr><td>Rsa1.0_01597.1.g28279.t2</td><td>ref|XP_002881640.1| RNA binding protein [Arabidopsis lyrata subsp. lyrata] gi|297327479|gb|EFH57899.1| RNA binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>2963</td><td>1181</td><td>0</td><td>39.9</td><td>34.5</td><td>35.9</td><td>RNA binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G39260.1 | Symbols: | binding;RNA binding | chr2:16392288-16399588 REVERSE LENGTH=1181</td><td>2963</td><td>1181</td><td>0</td><td>39.9</td><td>34.2</td><td>35.7</td></tr>
<tr><td>Rsa1.0_01597.1.g28280.t2</td><td>gb|AAC63678.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>473</td><td>1216</td><td>7.00E-87</td><td>257.1</td><td>46.5</td><td>60.7</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>473</td><td>746</td><td>8.00E-42</td><td>157.7</td><td>20.7</td><td>26.2</td></tr>
<tr><td>Rsa1.0_01598.1.g28281.t2</td><td>gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]</td><td>587</td><td>442</td><td>1.00E-78</td><td>75.3</td><td>24.7</td><td>29.8</td><td>hypothetical protein 24.t00017</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343</td><td>587</td><td>343</td><td>6.00E-33</td><td>58.4</td><td>10.2</td><td>13.5</td></tr>
<tr><td>Rsa1.0_01598.1.g28282.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01598.1.g28283.t2</td><td>gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]</td><td>2498</td><td>1213</td><td>0</td><td>48.6</td><td>26.7</td><td>34.1</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G46240.1 | Symbols: KAT1 | potassium channel in Arabidopsis thaliana 1 | chr5:18743652-18746561 REVERSE LENGTH=677</td><td>2498</td><td>677</td><td>0</td><td>27.1</td><td>23.2</td><td>24.3</td></tr>
<tr><td>Rsa1.0_01598.1.g28284.t1</td><td>gb|EOA14036.1| hypothetical protein CARUB_v10027170mg [Capsella rubella]</td><td>144</td><td>197</td><td>2.00E-63</td><td>136.8</td><td>76.4</td><td>91.0</td><td>hypothetical protein CARUB_v10027170mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G46230.1 | Symbols: | Protein of unknown function, DUF538 | chr5:18742593-18743024 REVERSE LENGTH=143</td><td>144</td><td>143</td><td>3.00E-62</td><td>99.3</td><td>73.6</td><td>88.9</td></tr>
<tr><td>Rsa1.0_01598.1.g28285.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_01598.1.g28286.t1	dbj|BAA97290.1| non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	476	1072	1.00E-114	225.2	45.8	60.3	non-LTR retroelement reverse transcriptase-like	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	476	289	3.00E-67	60.7	27.3	36.6
Rsa1.0_01598.1.g28287.t1	ref|XP_002873095.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318932|gb|EFH49354.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	251	227	2.00E-12	90.4	19.5	26.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G03495.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:873804-875025 REVERSE LENGTH=226	251	226	9.00E-14	90.0	19.1	29.1
Rsa1.0_01598.1.g28288.t1	ref|XP_002879895.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325734|gb|EFH56154.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	126	542	4.00E-44	430.2	71.4	78.6	phosphatidylinositol 3-and 4-kinase family protein	gbpln	Arabidopsis lyrata	AT2G40850.1 | Symbols: ATPI4K GAMMA 1, PI4K GAMMA 1 | phosphoinositide 4-kinase gamma 1 | chr2:17051575-17053260 FORWARD LENGTH=561	126	561	4.00E-46	445.2	70.6	77.8
Rsa1.0_01598.1.g28289.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01599.1.g28290.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	644	1213	1.00E-116	188.4	38.0	53.3	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	644	746	4.00E-38	115.8	17.2	25.3
Rsa1.0_01599.1.g28291.t1	ref|XP_002866360.1| hypothetical protein ARALYDRAFT_919236 [Arabidopsis lyrata subsp. lyrata] gi|297312195|gb|EFH42619.1| hypothetical protein ARALYDRAFT_919236 [Arabidopsis lyrata subsp. lyrata]	237	241	3.00E-97	101.7	83.5	90.3	hypothetical protein ARALYDRAFT_919236	gbpln	Arabidopsis lyrata	AT5G59990.1 | Symbols: | CCT motif family protein | chr5:24151206-24153084 REVERSE LENGTH=241	237	241	5.00E-92	101.7	84.0	90.7
Rsa1.0_01599.1.g28292.t1	ref|NP_001154789.1| ribonuclease P subunit Rpp30 [Arabidopsis thaliana] gi|332009879|gb|AED97262.1| ribonuclease P subunit Rpp30 [Arabidopsis thaliana]	648	705	0	108.8	69.8	79.6	ribonuclease P subunit Rpp30	gbpln	Arabidopsis thaliana	AT5G59980.2 | Symbols: | Polymerase/histidinol phosphatase-like | chr5:24147207-24149783 FORWARD LENGTH=705	648	705	0	108.8	69.8	79.6
Rsa1.0_01600.1.g28293.t1	gb|EOA37264.1| hypothetical protein CARUB_v10010834mg [Capsella rubella]	441	448	0	101.6	80.5	87.1	hypothetical protein CARUB_v10010834mg	gbpln	Capsella rubella	AT1G26761.1 | Symbols: | Arabinanase/levansucrase/invertase | chr1:9250269-9251603 REVERSE LENGTH=444	441	444	0	100.7	81.2	86.8
Rsa1.0_01600.1.g28294.t1	ref|NP_173998.2| SET domain protein 35 [Arabidopsis thaliana] gi|332192607|gb|AEE30728.1| SET domain protein 35 [Arabidopsis thaliana]	539	545	0	101.1	82.0	90.5	SET domain protein 35	gbpln	Arabidopsis thaliana	AT1G26760.1 | Symbols: ATXR1, SDG35 | SET domain protein 35 | chr1:9248304-9249941 REVERSE LENGTH=545	539	545	0	101.1	82.0	90.5
Rsa1.0_01600.1.g28295.t1	gb|EOA38546.1| hypothetical protein CARUB_v10010351mg [Capsella rubella]	224	195	6.00E-71	87.1	67.0	75.9	hypothetical protein CARUB_v10010351mg	gbpln	Capsella rubella	AT1G26750.1 | Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:9246857-9248053 FORWARD LENGTH=195	224	195	1.00E-71	87.1	66.1	74.6
Rsa1.0_01600.1.g28296.t1	gb|EOA38665.1| hypothetical protein CARUB_v10010602mg [Capsella rubella]	172	140	8.00E-55	81.4	68.6	71.5	hypothetical protein CARUB_v10010602mg	gbpln	Capsella rubella	AT1G26740.1 | Symbols: | Ribosomal L32p protein family | chr1:9245280-9246555 REVERSE LENGTH=134	172	134	1.00E-55	77.9	66.3	70.3
Rsa1.0_01600.1.g28297.t1	ref|NP_173995.1| phosphate transporter PHO1-7 [Arabidopsis thaliana] gi|75127837|sp|Q6R8G3.1|PHO17_ARATH RecName: Full=Phosphate transporter PHO1 homolog 7; AltName: Full=Protein PHO1 homolog 7; Short=AtPHO1;H7 gi|41079282|gb|AAR99489.1| PHO1-like protein [Arabidopsis thaliana] gi|332192604|gb|AEE30725.1| phosphate transporter PHO1-7 [Arabidopsis thaliana]	737	750	0	101.8	81.8	90.0	phosphate transporter PHO1-7	gbpln	Arabidopsis thaliana	AT1G26730.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr1:9241435-9244650 FORWARD LENGTH=750	737	750	0	101.8	81.8	90.0
Rsa1.0_01600.1.g28298.t1	ref|XP_002893385.1| hypothetical protein ARALYDRAFT_472736 [Arabidopsis lyrata subsp. lyrata] gi|297339227|gb|EFH69644.1| hypothetical protein ARALYDRAFT_472736 [Arabidopsis lyrata subsp. lyrata]	560	555	0	99.1	87.9	92.7	hypothetical protein ARALYDRAFT_472736	gbpln	Arabidopsis lyrata	AT1G26700.1 | Symbols: MLO14, ATMLO14 | Seven transmembrane MLO family protein | chr1:9228300-9232237 FORWARD LENGTH=554	560	554	0	98.9	86.8	91.6
Rsa1.0_01600.1.g28299.t1	ref|XP_002890648.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336490|gb|EFH66907.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	214	214	1.00E-107	100.0	87.9	93.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G26690.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:9224299-9225682 REVERSE LENGTH=214	214	214	1.00E-109	100.0	87.4	93.5
Rsa1.0_01600.1.g28300.t1	ref|XP_002893387.1| T24P13.6 [Arabidopsis lyrata subsp. lyrata] gi|297339229|gb|EFH69646.1| T24P13.6 [Arabidopsis lyrata subsp. lyrata]	528	1003	1.00E-140	190.0	54.0	68.9	T24P13.6	gbpln	Arabidopsis lyrata	AT1G26680.1 | Symbols: | transcriptional factor B3 family protein | chr1:9219552-9223193 FORWARD LENGTH=920	528	920	1.00E-130	174.2	51.9	65.2

Rsa1.0_01600.1.g28301.t1	ref|XP_002893387.1| T24P13.6 [Arabidopsis lyrata subsp. lyrata] gi|297339229|gb|EFH69646.1| T24P13.6 [Arabidopsis lyrata subsp. lyrata]	537	1003	1.00E-128	186.8	49.5	66.1	T24P13.6	gbpln	Arabidopsis lyrata	AT1G26680.1 | Symbols: | transcriptional factor B3 family protein | chr1:9219552-9223193 FORWARD LENGTH=920	537	920	1.00E-125	171.3	47.5	63.7
Rsa1.0_01600.1.g28302.t1	ref|XP_002893387.1| T24P13.6 [Arabidopsis lyrata subsp. lyrata] gi|297339229|gb|EFH69646.1| T24P13.6 [Arabidopsis lyrata subsp. lyrata]	534	1003	1.00E-125	187.8	50.2	65.2	T24P13.6	gbpln	Arabidopsis lyrata	AT1G26680.1 | Symbols: | transcriptional factor B3 family protein | chr1:9219552-9223193 FORWARD LENGTH=920	534	920	1.00E-121	172.3	48.5	61.8
Rsa1.0_01600.1.g28303.t1	ref|XP_002890649.1| hypothetical protein ARALYDRAFT_890071 [Arabidopsis lyrata subsp. lyrata] gi|297336491|gb|EFH66908.1| hypothetical protein ARALYDRAFT_890071 [Arabidopsis lyrata subsp. lyrata]	181	175	3.00E-42	96.7	56.4	68.0	hypothetical protein ARALYDRAFT_890071	gbpln	Arabidopsis lyrata	AT2G27260.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:11669769-11670500 FORWARD LENGTH=243	181	243	8.00E-18	134.3	28.2	48.1
Rsa1.0_01600.1.g28304.t2	ref|NP_564253.2| Prefoldin chaperone subunit family protein [Arabidopsis thaliana] gi|17381132|gb|AAL36378.1| unknown protein [Arabidopsis thaliana] gi|20465553|gb|AAM20259.1| unknown protein [Arabidopsis thaliana] gi|332192594|gb|AEE30715.1| Prefoldin chaperone subunit family protein [Arabidopsis thaliana]	178	152	6.00E-66	85.4	74.2	78.1	Prefoldin chaperone subunit family protein	gbpln	Arabidopsis thaliana	AT1G26660.1 | Symbols: | Prefoldin chaperone subunit family protein | chr1:9212298-9213765 FORWARD LENGTH=152	178	152	2.00E-68	85.4	74.2	78.1
Rsa1.0_01601.1.g28305.t1	gb|EMJ01464.1| hypothetical protein PRUPE_ppa015000mg [Prunus persica]	160	1493	1.00E-31	933.1	43.8	64.4	hypothetical protein PRUPE_ppa015000mg	gbpln	Prunus persica	#	#	#	#	#	#	#
Rsa1.0_01601.1.g28306.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	217	1142	6.00E-22	526.3	26.3	36.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01601.1.g28307.t1	ref|XP_002891300.1| hypothetical protein ARALYDRAFT_473826 [Arabidopsis lyrata subsp. lyrata] gi|297337142|gb|EFH67559.1| hypothetical protein ARALYDRAFT_473826 [Arabidopsis lyrata subsp. lyrata]	304	285	1.00E-101	93.8	65.8	77.0	hypothetical protein ARALYDRAFT_473826	gbpln	Arabidopsis lyrata	AT1G44890.1 | Symbols: | BEST Arabidopsis thaliana protein match is: homolog of yeast oxidase assembly 1 (OXA1) (TAIR:AT5G62050.1); Has 40 Blast hits to 40 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:16963358-16964818 FORWARD LENGTH=281	304	281	4.00E-99	92.4	65.1	76.0
Rsa1.0_01601.1.g28308.t1	ref|NP_175105.2| YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein [Arabidopsis thaliana] gi|26451543|dbj|BAC42869.1| unknown protein [Arabidopsis thaliana] gi|28973135|gb|AAO63892.1| unknown protein [Arabidopsis thaliana] gi|332193936|gb|AEE32057.1| YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein [Arabidopsis thaliana]	306	307	1.00E-137	100.3	82.0	88.6	YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein	gbpln	Arabidopsis thaliana	AT1G44835.1 | Symbols: | YbaK/aminoacyl-tRNA synthetase-associated domain | chr1:16939909-16942337 FORWARD LENGTH=307	306	307	1.00E-139	100.3	82.0	88.6
Rsa1.0_01601.1.g28309.t7	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	478	521	2.00E-39	109.0	20.1	26.4	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	AT5G40595.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:16253510-16254079 FORWARD LENGTH=141	478	141	8.00E-15	29.5	8.4	12.3
Rsa1.0_01601.1.g28310.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	647	1142	9.00E-87	176.5	27.0	34.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	647	575	5.00E-31	88.9	14.5	25.0
Rsa1.0_01601.1.g28311.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01602.1.g28312.t1	ref|NP_187113.1| Alba DNA/RNA-binding protein [Arabidopsis thaliana] gi|6175166|gb|AAF04892.1|AC011437_7 unknown protein [Arabidopsis thaliana] gi|38454036|gb|AAR20712.1| At3g04620 [Arabidopsis thaliana] gi|38604012|gb|AAR24749.1| At3g04620 [Arabidopsis thaliana] gi|332640586|gb|AEE74107.1| Alba DNA/RNA-binding protein [Arabidopsis thaliana]	164	164	2.00E-63	100.0	87.2	90.9	Alba DNA/RNA-binding protein	gbpln	Arabidopsis thaliana	AT3G04620.1 | Symbols: | Alba DNA/RNA-binding protein | chr3:1255660-1256739 REVERSE LENGTH=164	164	164	7.00E-66	100.0	87.2	90.9
Rsa1.0_01602.1.g28313.t1	gb|EOA30196.1| hypothetical protein CARUB_v10013313mg [Capsella rubella]	544	582	0	107.0	75.4	84.9	hypothetical protein CARUB_v10013313mg	gbpln	Capsella rubella	AT4G03460.1 | Symbols: | Ankyrin repeat family protein | chr4:1536404-1540111 REVERSE LENGTH=677	544	677	1.00E-45	124.4	29.0	45.0
Rsa1.0_01602.1.g28314.t1	gb|EOA29585.1| hypothetical protein CARUB_v10013041mg [Capsella rubella]	740	750	0	101.4	90.7	95.3	hypothetical protein CARUB_v10013041mg	gbpln	Capsella rubella	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	740	719	1.00E-41	97.2	17.8	31.4

Rsa1.0_01602.1.g28315.t1	gb|ACT33454.1| histone deacetylase 1 [Brassica rapa subsp. pekinensis]	505	502	0	99.4	96.4	98.0	histone deacetylase 1	gbpln	Brassica rapa	AT4G38130.1 | Symbols: HD1, ATHD1, HDA1, RPD3A, HDA19, ATHDA19 | histone deacetylase 1 | chr4:17896493-17899057 REVERSE LENGTH=501	505	501	0	99.2	94.9	96.2
Rsa1.0_01602.1.g28316.t1	dbj|BAB08360.1| Ta11-like non-LTR retroelement protein-like [Arabidopsis thaliana]	645	655	0	101.6	57.2	68.8	Ta11-like non-LTR retroelement protein-like	gbpln	Arabidopsis thaliana	AT5G59920.1 | Symbols: ULI3 | Cysteine/Histidine-rich C1 domain family protein | chr5:24128756-24130888 FORWARD LENGTH=710	645	710	0	110.1	55.7	66.8
Rsa1.0_01602.1.g28317.t1	dbj|BAB08360.1| Ta11-like non-LTR retroelement protein-like [Arabidopsis thaliana]	643	655	0	101.9	56.1	69.1	Ta11-like non-LTR retroelement protein-like	gbpln	Arabidopsis thaliana	AT5G59920.1 | Symbols: ULI3 | Cysteine/Histidine-rich C1 domain family protein | chr5:24128756-24130888 FORWARD LENGTH=710	643	710	0	110.4	54.4	66.9
Rsa1.0_01602.1.g28318.t1	ref|XP_002882364.1| tRNA synthetase class I family protein [Arabidopsis lyrata subsp. lyrata] gi|297328204|gb|EFH58623.1| tRNA synthetase class I family protein [Arabidopsis lyrata subsp. lyrata]	405	402	0	99.3	94.8	97.5	tRNA synthetase class I family protein	gbpln	Arabidopsis lyrata	AT3G04600.2 | Symbols: | Nucleotidylyl transferase superfamily protein | chr3:1243152-1245958 FORWARD LENGTH=402	405	402	0	99.3	94.3	96.5
Rsa1.0_01602.1.g28319.t1	gb|EOA30721.1| hypothetical protein CARUB_v10013864mg [Capsella rubella]	394	402	1.00E-142	102.0	78.9	84.8	hypothetical protein CARUB_v10013864mg	gbpln	Capsella rubella	AT3G04590.2 | Symbols: | AT hook motif DNA-binding family protein | chr3:1239245-1241603 REVERSE LENGTH=411	394	411	1.00E-134	104.3	76.6	82.2
Rsa1.0_01602.1.g28320.t1	gb|EOA29937.1| hypothetical protein CARUB_v10013030mg [Capsella rubella]	765	766	0	100.1	94.6	97.6	hypothetical protein CARUB_v10013030mg	gbpln	Capsella rubella	AT3G04580.2 | Symbols: EIN4 | Signal transduction histidine kinase, hybrid-type, ethylene sensor | chr3:1235576-1237965 REVERSE LENGTH=766	765	766	0	100.1	94.6	97.6
Rsa1.0_01602.1.g28321.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01602.1.g28322.t1	gb|AAY86771.1| putative DNA-binding protein [Noccaea caerulescens]	312	312	1.00E-113	100.0	93.3	95.8	putative DNA-binding protein	gbpln	Noccaea caerulescens	AT3G04570.1 | Symbols: AHL19 | AT-hook motif nuclear-localized protein 19 | chr3:1231221-1232168 FORWARD LENGTH=315	312	315	1.00E-114	101.0	90.4	92.3
Rsa1.0_01602.1.g28323.t1	gb|EOA32167.1| hypothetical protein CARUB_v10015423mg [Capsella rubella]	392	446	0	113.8	82.7	91.8	hypothetical protein CARUB_v10015423mg	gbpln	Capsella rubella	AT3G04550.1 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28500.1); Has 110 Blast hits to 110 proteins in 51 species: Archae - 0; Bacteria - 67; Metazoa - 1; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:1225961-1227310 FORWARD LENGTH=449	392	449	0	114.5	83.2	90.6
Rsa1.0_01603.1.g28324.t1	ref|XP_002882955.1| hypothetical protein ARALYDRAFT_479016 [Arabidopsis lyrata subsp. lyrata] gi|297328795|gb|EFH59214.1| hypothetical protein ARALYDRAFT_479016 [Arabidopsis lyrata subsp. lyrata]	196	177	3.00E-63	90.3	78.1	80.1	hypothetical protein ARALYDRAFT_479016	gbpln	Arabidopsis lyrata	AT3G15640.1 | Symbols: | Rubredoxin-like superfamily protein | chr3:5299273-5301371 FORWARD LENGTH=176	196	176	6.00E-65	89.8	78.6	80.1
Rsa1.0_01603.1.g28325.t1	gb|AAG51754.1|AC068667_33 reverse transcriptase, putative; 100033-105622 [Arabidopsis thaliana]	1763	1557	0	88.3	38.9	51.8	reverse transcriptase, putative; 100033-105622	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1763	575	2.00E-93	32.6	10.7	16.5
Rsa1.0_01603.1.g28326.t1	gb|EOA38678.1| hypothetical protein CARUB_v10010650mg [Capsella rubella]	114	126	3.00E-30	110.5	64.0	77.2	hypothetical protein CARUB_v10010650mg	gbpln	Capsella rubella	AT3G15630.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52720.1); Has 61 Blast hits to 61 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 61; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5297188-5297511 REVERSE LENGTH=107	114	107	8.00E-33	93.9	68.4	74.6
Rsa1.0_01603.1.g28327.t1	gb|EOA30559.1| hypothetical protein CARUB_v10013684mg [Capsella rubella]	407	453	0	111.3	87.0	92.6	hypothetical protein CARUB_v10013684mg	gbpln	Capsella rubella	AT3G15570.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr3:5270267-5271700 REVERSE LENGTH=452	407	452	0	111.1	85.7	90.9
Rsa1.0_01603.1.g28328.t1	gb|EOA31503.1| hypothetical protein CARUB_v10014689mg [Capsella rubella]	194	197	1.00E-97	101.5	91.8	93.3	hypothetical protein CARUB_v10014689mg	gbpln	Capsella rubella	AT3G15540.1 | Symbols: IAA19, MSG2 | indole-3-acetic acid inducible 19 | chr3:5264100-5265378 FORWARD LENGTH=197	194	197	1.00E-100	101.5	91.2	93.8
Rsa1.0_01603.1.g28329.t1	dbj|BAJ34312.1| unnamed protein product [Thellungiella halophila]	351	364	1.00E-151	103.7	85.2	89.5	unnamed protein product	----	----	AT3G15510.1 | Symbols: ATNAC2, ANAC056, NARS1, NAC2 | NAC domain containing protein 2 | chr3:5243696-5245037 FORWARD LENGTH=364	351	364	1.00E-152	103.7	84.3	90.0

<table>
<tr><td>Rsa1.0_01603.1.g28330.t1</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>938</td><td>1529</td><td>0</td><td>163.0</td><td>38.4</td><td>48.8</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G15500.1 | Symbols: ATNAC3, ANAC055, NAC055, NAC3 | NAC domain containing protein 3 | chr3:5234731-5235882 FORWARD LENGTH=317</td><td>938</td><td>317</td><td>1.00E-115</td><td>33.8</td><td>23.9</td><td>25.8</td></tr>
<tr><td>Rsa1.0_01603.1.g28331.t1</td><td>gb|EOA32735.1| hypothetical protein CARUB_v10016040mg [Capsella rubella]</td><td>317</td><td>317</td><td>1.00E-170</td><td>100.0</td><td>90.5</td><td>95.6</td><td>hypothetical protein CARUB_v10016040mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G15460.1 | Symbols: | Ribosomal RNA processing Brix domain protein | chr3:5214279-5216188 REVERSE LENGTH=315</td><td>317</td><td>315</td><td>1.00E-166</td><td>99.4</td><td>88.0</td><td>93.4</td></tr>
<tr><td>Rsa1.0_01603.1.g28332.t1</td><td>ref|NP_974321.1| uncharacterized protein [Arabidopsis thaliana] gi|42572453|ref|NP_974322.1| uncharacterized protein [Arabidopsis thaliana] gi|79313241|ref|NP_001030700.1| uncharacterized protein [Arabidopsis thaliana] gi|145332587|ref|NP_001078159.1| uncharacterized protein [Arabidopsis thaliana] gi|21593726|gb|AAM65693.1| unknown [Arabidopsis thaliana] gi|111074242|gb|ABH04494.1| At3g15395 [Arabidopsis thaliana] gi|222423962|dbj|BAH19943.1| AT3G15395 [Arabidopsis thaliana] gi|222424311|dbj|BAH20112.1| AT3G15395 [Arabidopsis thaliana] gi|332642143|gb|AEE75664.1| uncharacterized protein AT3G15395 [Arabidopsis thaliana] gi|332642144|gb|AEE75665.1| uncharacterized protein AT3G15395 [Arabidopsis thaliana] gi|332642145|gb|AEE75666.1| uncharacterized protein AT3G15395 [Arabidopsis thaliana] gi|332642146|gb|AEE75667.1| uncharacterized protein AT3G15395 [Arabidopsis thaliana]</td><td>63</td><td>59</td><td>5.00E-20</td><td>93.7</td><td>76.2</td><td>85.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G15395.4 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 31 Blast hits to 31 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5201014-5201307 FORWARD LENGTH=59</td><td>63</td><td>59</td><td>8.00E-23</td><td>93.7</td><td>76.2</td><td>85.7</td></tr>
<tr><td>Rsa1.0_01603.1.g28333.t1</td><td>gb|EOA32479.1| hypothetical protein CARUB_v10015755mg [Capsella rubella]</td><td>569</td><td>700</td><td>0</td><td>123.0</td><td>92.8</td><td>95.6</td><td>hypothetical protein CARUB_v10015755mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G15380.1 | Symbols: | Plasma-membrane choline transporter family protein | chr3:5193319-5196435 FORWARD LENGTH=700</td><td>569</td><td>700</td><td>0</td><td>123.0</td><td>91.9</td><td>95.6</td></tr>
<tr><td>Rsa1.0_01604.1.g28334.t4</td><td>gb|EOA27544.1| hypothetical protein CARUB_v10023683mg [Capsella rubella]</td><td>104</td><td>311</td><td>8.00E-26</td><td>299.0</td><td>72.1</td><td>82.7</td><td>hypothetical protein CARUB_v10023683mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G43140.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:17932376-17935639 REVERSE LENGTH=297</td><td>104</td><td>297</td><td>7.00E-27</td><td>285.6</td><td>76.0</td><td>83.7</td></tr>
<tr><td>Rsa1.0_01604.1.g28335.t1</td><td>emb|CAB40067.1| putative retrotransposon polyprotein [Arabidopsis thaliana] gi|7267797|emb|CAB81200.1| putative retrotransposon polyprotein [Arabidopsis thaliana]</td><td>363</td><td>1203</td><td>1.00E-115</td><td>331.4</td><td>59.0</td><td>75.5</td><td>putative retrotransposon polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>363</td><td>1262</td><td>1.00E-108</td><td>347.7</td><td>54.5</td><td>71.1</td></tr>
<tr><td>Rsa1.0_01604.1.g28336.t1</td><td>ref|XP_004253404.1| PREDICTED: uncharacterized protein LOC101249447, partial [Solanum lycopersicum]</td><td>1037</td><td>485</td><td>3.00E-46</td><td>46.8</td><td>11.8</td><td>13.4</td><td>PREDICTED: uncharacterized protein LOC101249447, partial</td><td>gbpln</td><td>Solanum lycopersicum</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_01604.1.g28337.t1	ref|NP_850386.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|30689274|ref|NP_850387.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|42571203|ref|NP_973675.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|75116590|sp|Q67YI9.1|EPN2_ARATH RecName: Full=Clathrin interactor EPSIN 2; AltName: Full=EPSIN-related 2 gi|51970954|dbj|BAD44169.1| unknown protein [Arabidopsis thaliana] gi|51971100|dbj|BAD44242.1| unknown protein [Arabidopsis thaliana] gi|62319865|dbj|BAD93910.1| hypothetical protein [Arabidopsis thaliana] gi|62319867|dbj|BAD93914.1| hypothetical protein [Arabidopsis thaliana] gi|110740368|dbj|BAF02079.1| hypothetical protein [Arabidopsis thaliana] gi|330255122|gb|AEC10216.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|330255123|gb|AEC10217.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana] gi|330255124|gb|AEC10218.1| clathrin interactor EPSIN 2 [Arabidopsis thaliana]	937	895	0	95.5	81.0	84.3	clathrin interactor EPSIN 2	gbpln	Arabidopsis thaliana	AT2G43160.1 | Symbols: | ENTH/VHS family protein | chr2:17948884-17953267 FORWARD LENGTH=895	937	895	0	95.5	81.0	84.3
Rsa1.0_01604.1.g28338.t1	gb|EOA27022.1| hypothetical protein CARUB_v10023119mg [Capsella rubella]	476	477	0	100.2	81.7	90.3	hypothetical protein CARUB_v10023119mg	gbpln	Capsella rubella	AT2G43180.1 | Symbols: | Phosphoenolpyruvate carboxylase family protein | chr2:17953719-17955774 REVERSE LENGTH=479	476	479	0	100.6	82.8	89.3
Rsa1.0_01605.1.g28339.t1	ref|XP_002890037.1| F16A14.28 [Arabidopsis lyrata subsp. lyrata] gi|297335879|gb|EFH66296.1| F16A14.28 [Arabidopsis lyrata subsp. lyrata]	584	1125	0	192.6	72.6	82.2	F16A14.28	gbpln	Arabidopsis lyrata	AT1G14080.1 | Symbols: FUT6, ATFUT6 | fucosyltransferase 6 | chr1:4822580-4824218 FORWARD LENGTH=519	584	519	0	88.9	71.6	80.3
Rsa1.0_01605.1.g28340.t2	ref|NP_001077531.1| fucosyltransferase 8 [Arabidopsis thaliana] gi|334302812|sp|Q9XI78.2|FUT8_ARATH RecName: Full=Probable fucosyltransferase 8; Short=AtFUT8 gi|332190985|gb|AEE29106.1| fucosyltransferase 8 [Arabidopsis thaliana]	669	516	0	77.1	53.8	60.4	fucosyltransferase 8	gbpln	Arabidopsis thaliana	AT1G14100.1 | Symbols: FUT8 | fucosyltransferase 8 | chr1:4827961-4829587 FORWARD LENGTH=516	669	516	0	77.1	53.8	60.4
Rsa1.0_01605.1.g28341.t1	ref|NP_172864.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|5080788|gb|AAD39298.1|AC007576_21 Very similar to adventitious rooting related oxygenase [Arabidopsis thaliana] gi|21553384|gb|AAM62477.1| dioxygenase-like protein [Arabidopsis thaliana] gi|24030341|gb|AAN41336.1| putative dioxygenase [Arabidopsis thaliana] gi|332190987|gb|AEE29108.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	229	312	1.00E-87	136.2	65.5	82.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT1G14120.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:4833648-4834833 REVERSE LENGTH=312	229	312	4.00E-90	136.2	65.5	82.1
Rsa1.0_01605.1.g28342.t1	ref|NP_172865.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|5080789|gb|AAD39299.1|AC007576_22 Very similar to adventitious rooting related oxygenase [Arabidopsis thaliana] gi|26451604|dbj|BAC42899.1| putative dioxygenase [Arabidopsis thaliana] gi|28973391|gb|AAO64020.1| putative dioxygenase [Arabidopsis thaliana] gi|332190988|gb|AEE29109.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana]	303	308	1.00E-148	101.7	84.2	90.8	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT1G14130.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:4836041-4837040 REVERSE LENGTH=308	303	308	1.00E-151	101.7	84.2	90.8
Rsa1.0_01605.1.g28343.t1	ref|XP_002890040.1| hypothetical protein ARALYDRAFT_471574 [Arabidopsis lyrata subsp. lyrata] gi|297335882|gb|EFH66299.1| hypothetical protein ARALYDRAFT_471574 [Arabidopsis lyrata subsp. lyrata]	188	189	5.00E-91	100.5	86.7	93.1	hypothetical protein ARALYDRAFT_471574	gbpln	Arabidopsis lyrata	AT1G14150.1 | Symbols: PQL1, PQL2 | PsbQ-like 2 | chr1:4839885-4840632 FORWARD LENGTH=190	188	190	8.00E-90	101.1	85.6	90.4

Rsa1.0_01605.1.g28344.t1	ref|NP_001117282.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana] gi|5080792|gb|AAD39302.1|AC007576_25 Unknown protein [Arabidopsis thaliana] gi|332190995|gb|AEE29116.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana]	473	479	0	101.3	86.7	93.2	RNA-binding KH domain-containing protein	gbpln	Arabidopsis thaliana	AT1G14170.3 | Symbols: | RNA-binding KH domain-containing protein | chr1:4843463-4845253 REVERSE LENGTH=479	473	479	0	101.3	86.7	93.2
Rsa1.0_01605.1.g28345.t1	gb|EOA38108.1| hypothetical protein CARUB_v10009576mg [Capsella rubella]	241	354	9.00E-73	146.9	55.2	63.1	hypothetical protein CARUB_v10009576mg	gbpln	Capsella rubella	AT1G14180.1 | Symbols: | RING/U-box superfamily protein | chr1:4847828-4848970 FORWARD LENGTH=348	241	348	6.00E-72	144.4	56.0	62.7
Rsa1.0_01605.1.g28346.t1	gb|EOA36716.1| hypothetical protein CARUB_v10012348mg [Capsella rubella]	205	205	1.00E-62	100.0	66.8	79.0	hypothetical protein CARUB_v10012348mg	gbpln	Capsella rubella	AT1G14200.1 | Symbols: | RING/U-box superfamily protein | chr1:4854532-4855071 REVERSE LENGTH=179	205	179	2.00E-56	87.3	59.0	73.7
Rsa1.0_01605.1.g28347.t1	ref|NP_172877.1| GDA1/CD39 nucleoside phosphatase family protein [Arabidopsis thaliana] gi|75127157|sp|Q6NQA8.1|APY5_ARATH RecName: Full=Probable apyrase 5; Short=AtAPY5; AltName: Full=ATP-diphosphatase; AltName: Full=ATP-diphosphohydrolase; AltName: Full=Adenosine diphosphatase; Short=ADPase; AltName: Full=NTPDase; AltName: Full=Nucleoside triphosphate diphosphohydrolase 5 gi|34365723|gb|AAQ65173.1| At1g14250 [Arabidopsis thaliana] gi|51968412|dbj|BAD42898.1| hypothetical protein [Arabidopsis thaliana] gi|51969180|dbj|BAD43282.1| hypothetical protein [Arabidopsis thaliana] gi|332191010|gb|AEE29131.1| probable apyrase 5 [Arabidopsis thaliana] gi|339283648|gb|AEJ38086.1| nucleoside triphosphate diphosphohydrolase 5 [Arabidopsis thaliana]	469	488	0	104.1	74.0	84.9	GDA1/CD39 nucleoside phosphatase family protein	gbpln	Arabidopsis thaliana	AT1G14250.1 | Symbols: | GDA1/CD39 nucleoside phosphatase family protein | chr1:4868675-4871203 FORWARD LENGTH=488	469	488	0	104.1	74.0	84.9
Rsa1.0_01605.1.g28348.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1201	1491	0	124.1	58.5	71.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1201	1262	1.00E-57	105.1	8.9	12.7
Rsa1.0_01606.1.g28349.t1	gb|AFX68809.1| tetrapyrrole-binding protein [Brassica oleracea]	255	256	1.00E-109	100.4	89.4	92.5	tetrapyrrole-binding protein	gbpln	Brassica oleracea	AT3G59400.1 | Symbols: GUN4 | enzyme binding;tetrapyrrole binding | chr3:21948881-21949678 REVERSE LENGTH=265	255	265	1.00E-94	103.9	75.3	83.1
Rsa1.0_01606.1.g28350.t1	ref|XP_002878266.1| UDP-galactose transporter 6 [Arabidopsis lyrata subsp. lyrata] gi|297324104|gb|EFH54525.1| UDP-galactose transporter 6 [Arabidopsis lyrata subsp. lyrata]	426	405	0	95.1	87.1	91.1	UDP-galactose transporter 6	gbpln	Arabidopsis lyrata	AT3G59360.2 | Symbols: UTR6, ATUTR6 | UDP-galactose transporter 6 | chr3:21935826-21939642 REVERSE LENGTH=405	426	405	0	95.1	86.2	90.4
Rsa1.0_01606.1.g28351.t1	ref|XP_002876497.1| hypothetical protein ARALYDRAFT_486400 [Arabidopsis lyrata subsp. lyrata] gi|297322335|gb|EFH52756.1| hypothetical protein ARALYDRAFT_486400 [Arabidopsis lyrata subsp. lyrata]	404	405	0	100.2	91.1	94.8	hypothetical protein ARALYDRAFT_486400	gbpln	Arabidopsis lyrata	AT3G59350.3 | Symbols: | Protein kinase superfamily protein | chr3:21932930-21934883 FORWARD LENGTH=408	404	408	0	101.0	91.1	94.3
Rsa1.0_01606.1.g28352.t1	ref|NP_567080.1| pentatricopeptide repeat-containing protein-like protein [Arabidopsis thaliana] gi|15292859|gb|AAK92800.1| unknown protein [Arabidopsis thaliana] gi|20258901|gb|AAM14144.1| unknown protein [Arabidopsis thaliana] gi|332646380|gb|AEE79901.1| pentatricopeptide repeat-containing protein-like protein [Arabidopsis thaliana]	457	459	0	100.4	92.3	95.6	pentatricopeptide repeat-containing protein-like protein	gbpln	Arabidopsis thaliana	AT3G59300.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:21918667-21921877 FORWARD LENGTH=459	457	459	0	100.4	92.3	95.6
Rsa1.0_01606.1.g28353.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01606.1.g28354.t1	gb|EOA24964.1| hypothetical protein CARUB_v10018261mg [Capsella rubella]	116	116	6.00E-56	100.0	92.2	95.7	hypothetical protein CARUB_v10018261mg	gbpln	Capsella rubella	AT3G59280.1 | Symbols: TXR1 | Protein Transporter, Pam16 | chr3:21909266-21910519 REVERSE LENGTH=116	116	116	1.00E-56	100.0	87.9	95.7
Rsa1.0_01606.1.g28355.t1	ref|XP_002876494.1| hypothetical protein ARALYDRAFT_324401 [Arabidopsis lyrata subsp. lyrata] gi|297322332|gb|EFH52753.1| hypothetical protein ARALYDRAFT_324401 [Arabidopsis lyrata subsp. lyrata]	284	285	1.00E-127	100.4	76.8	88.4	hypothetical protein ARALYDRAFT_324401	gbpln	Arabidopsis lyrata	AT3G59260.1 | Symbols: | pirin, putative | chr3:21903839-21905188 FORWARD LENGTH=271	284	271	1.00E-120	95.4	71.5	80.6

Rsa1.0_01606.1.g28356.t1	ref|NP_191481.1| pirin [Arabidopsis thaliana] gi|14195011|sp|Q9LX49.1|PRN1_ARATH RecName: Full=Pirin-1; AltName: Full=AtPirin1 gi|19070663|gb|AAL83949.1|AF353716_1 pirin [Arabidopsis thaliana] gi|7801672|emb|CAB91592.1| pirin-like protein [Arabidopsis thaliana] gi|109946467|gb|ABG48412.1| At3g59220 [Arabidopsis thaliana] gi|332646372|gb|AEE79893.1| pirin [Arabidopsis thaliana]	288	287	1.00E-136	99.7	82.3	89.6	pirin	gbpln	Arabidopsis thaliana	AT3G59220.1 | Symbols: PRN, PRN1, ATPIRIN1 | pirin | chr3:21894205-21895501 FORWARD LENGTH=287	288	287	1.00E-139	99.7	82.3	89.6
Rsa1.0_01606.1.g28357.t1	ref|NP_191479.1| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75264308|sp|Q9LX51.1|FBL64_ARATH RecName: Full=F-box/LRR-repeat protein At3g59200 gi|7801670|emb|CAB91590.1| putative protein [Arabidopsis thaliana] gi|26450835|dbj|BAC42525.1| unknown protein [Arabidopsis thaliana] gi|29028916|gb|AAO64837.1| At3g59200 [Arabidopsis thaliana] gi|332646367|gb|AEE79888.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	484	520	1.00E-177	107.4	67.4	78.3	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT3G59200.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21887484-21889214 FORWARD LENGTH=520	484	520	1.00E-179	107.4	67.4	78.3
Rsa1.0_01606.1.g28358.t2	gb|EOA23806.1| hypothetical protein CARUB_v10017021mg [Capsella rubella]	506	520	1.00E-125	102.8	51.4	65.8	hypothetical protein CARUB_v10017021mg	gbpln	Capsella rubella	AT1G58310.1 | Symbols: | F-box/RNI-like superfamily protein | chr1:21631947-21633642 FORWARD LENGTH=505	506	505	1.00E-127	99.8	51.8	67.0
Rsa1.0_01607.1.g28359.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28360.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28361.t1	emb|CAN79085.1| hypothetical protein VITISV_027044 [Vitis vinifera]	334	1000	1.00E-52	299.4	36.2	47.0	hypothetical protein VITISV_027044	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28362.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28363.t5	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28364.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28365.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	812	1024	8.00E-50	126.1	21.4	35.3	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28366.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28367.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1387	1838	0	132.5	32.2	46.0	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28368.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01607.1.g28369.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01608.1.g28370.t1	ref|NP_189510.2| putative protein kinase [Arabidopsis thaliana] gi|193788736|gb|ACF20467.1| At3g28690 [Arabidopsis thaliana] gi|332643954|gb|AEE77475.1| putative protein kinase [Arabidopsis thaliana]	137	376	3.00E-16	274.5	31.4	32.8	putative protein kinase	gbpln	Arabidopsis thaliana	AT3G28690.1 | Symbols: | Protein kinase superfamily protein | chr3:10756002-10757494 FORWARD LENGTH=376	137	376	7.00E-19	274.5	31.4	32.8
Rsa1.0_01608.1.g28371.t1	ref|XP_002883993.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329833|gb|EFH60252.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	817	797	0	97.6	82.1	88.7	kinase family protein	gbpln	Arabidopsis lyrata	AT2G19410.1 | Symbols: | U-box domain-containing protein kinase family protein | chr2:8404901-8409012 REVERSE LENGTH=801	817	801	0	98.0	82.0	88.1
Rsa1.0_01608.1.g28372.t2	ref|XP_002883994.1| hypothetical protein ARALYDRAFT_343256 [Arabidopsis lyrata subsp. lyrata] gi|297329834|gb|EFH60253.1| hypothetical protein ARALYDRAFT_343256 [Arabidopsis lyrata subsp. lyrata]	622	527	0	84.7	73.2	76.0	hypothetical protein ARALYDRAFT_343256	gbpln	Arabidopsis lyrata	AT2G19400.1 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr2:8399523-8402481 REVERSE LENGTH=527	622	527	0	84.7	72.3	75.6
Rsa1.0_01608.1.g28373.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	363	1274	1.00E-55	351.0	37.7	53.2	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	363	575	4.00E-30	158.4	29.2	45.7
Rsa1.0_01608.1.g28374.t1	ref|XP_002883995.1| hypothetical protein ARALYDRAFT_480532 [Arabidopsis lyrata subsp. lyrata] gi|297329835|gb|EFH60254.1| hypothetical protein ARALYDRAFT_480532 [Arabidopsis lyrata subsp. lyrata]	1228	1212	0	98.7	79.2	85.6	hypothetical protein ARALYDRAFT_480532	gbpln	Arabidopsis lyrata	AT2G19390.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G29790.1); Has 203 Blast hits to 188 proteins in 60 species: Archae - 0; Bacteria - 11; Metazoa - 24; Fungi - 34; Plants - 93; Viruses - 0; Other Eukaryotes - 41 (source: NCBI BLink). | chr2:8390136-8396477 REVERSE LENGTH=1211	1228	1211	0	98.6	77.9	85.1

Rsa1.0_01608.1.g28375.t1	ref|XP_002886044.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] gi|297331884|gb|EFH62303.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	277	283	1.00E-112	102.2	79.4	87.0	nucleic acid binding protein	gbpln	Arabidopsis lyrata	AT2G19385.1 | Symbols: | zinc ion binding | chr2:8387149-8388581 FORWARD LENGTH=275	277	275	1.00E-110	99.3	76.5	87.4
Rsa1.0_01608.1.g28376.t1	ref|XP_002886047.1| hypothetical protein ARALYDRAFT_480536 [Arabidopsis lyrata subsp. lyrata] gi|297331887|gb|EFH62306.1| hypothetical protein ARALYDRAFT_480536 [Arabidopsis lyrata subsp. lyrata]	89	103	5.00E-27	115.7	67.4	70.8	hypothetical protein ARALYDRAFT_480536	gbpln	Arabidopsis lyrata	AT2G19350.1 | Symbols: | Eukaryotic protein of unknown function (DUF872) | chr2:8376329-8377097 FORWARD LENGTH=103	89	103	8.00E-29	115.7	66.3	68.5
Rsa1.0_01608.1.g28377.t1	ref|NP_178545.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|4544429|gb|AAD22338.1| unknown protein [Arabidopsis thaliana] gi|55740549|gb|AAV63867.1| hypothetical protein At2g04680 [Arabidopsis thaliana] gi|330250761|gb|AEC05855.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	557	657	1.00E-168	118.0	59.1	68.2	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT2G04680.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:1640188-1642161 FORWARD LENGTH=657	557	657	1.00E-171	118.0	59.1	68.2
Rsa1.0_01608.1.g28378.t1	emb|CAA66376.1| light repressible receptor protein kinase [Arabidopsis thaliana]	489	876	1.00E-171	179.1	61.8	74.0	light repressible receptor protein kinase	gbpln	Arabidopsis thaliana	AT4G29990.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase protein | chr4:14665802-14669438 REVERSE LENGTH=876	489	876	1.00E-173	179.1	61.6	74.0
Rsa1.0_01608.1.g28379.t1	gb|EOA30726.1| hypothetical protein CARUB_v10013863mg [Capsella rubella]	385	402	3.00E-94	104.4	50.4	65.7	hypothetical protein CARUB_v10013863mg	gbpln	Capsella rubella	AT3G18720.1 | Symbols: | F-box family protein | chr3:6444433-6445751 REVERSE LENGTH=380	385	380	7.00E-91	98.7	50.1	64.7
Rsa1.0_01609.1.g28380.t1	gb|EOA29601.1| hypothetical protein CARUB_v10013401mg, partial [Capsella rubella]	504	543	0	107.7	82.5	88.9	hypothetical protein CARUB_v10013401mg, partial	gbpln	Capsella rubella	AT3G13810.1 | Symbols: AtIDD11, IDD11 | indeterminate(ID)-domain 11 | chr3:4544941-4547300 FORWARD LENGTH=513	504	513	0	101.8	83.3	89.3
Rsa1.0_01609.1.g28381.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1852	1213	0	65.5	21.1	28.6	unknown protein	gbpln	Arabidopsis thaliana	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	1852	395	9.00E-93	21.3	10.2	12.9
Rsa1.0_01609.1.g28382.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01609.1.g28383.t1	gb|EOA30760.1| hypothetical protein CARUB_v10013902mg [Capsella rubella]	340	392	5.00E-91	115.3	52.9	67.4	hypothetical protein CARUB_v10013902mg	gbpln	Capsella rubella	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	340	395	3.00E-89	116.2	52.9	65.3
Rsa1.0_01609.1.g28384.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01609.1.g28385.t1	gb|EOA30999.1| hypothetical protein CARUB_v10014142mg [Capsella rubella]	261	334	1.00E-113	128.0	82.4	88.9	hypothetical protein CARUB_v10014142mg	gbpln	Capsella rubella	AT3G13850.1 | Symbols: LBD22 | LOB domain-containing protein 22 | chr3:4559910-4560716 FORWARD LENGTH=268	261	268	1.00E-114	102.7	82.8	91.6
Rsa1.0_01609.1.g28386.t1	gb|EGG05881.1| hypothetical protein MELLADRAFT_87680 [Melampsora larici-populina 98AG31]	468	535	2.33E-156	114.3	61.1	73.7	hypothetical protein MELLADRAFT_87680	gbpln	Melampsora larici-populina	AT4G05320.4 | Symbols: UBQ10 | polyubiquitin 10 | chr4:2718559-2719932 FORWARD LENGTH=457	468	457	1.00E-147	97.6	60.5	73.1
Rsa1.0_01609.1.g28387.t1	ref|NP_188004.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75273848|sp|Q9LRV9.1|PP228_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g13880 gi|9294611|dbj|BAB02912.1| probable selenium-binding protein [Arabidopsis thaliana] gi|332641909|gb|AEE75430.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	747	748	0	100.1	76.2	85.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G13880.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:4572180-4574426 FORWARD LENGTH=748	747	748	0	100.1	76.2	85.5
Rsa1.0_01609.1.g28388.t2	gb|EOA32487.1| hypothetical protein CARUB_v10015767mg [Capsella rubella]	361	357	1.00E-141	98.9	80.3	84.8	hypothetical protein CARUB_v10015767mg	gbpln	Capsella rubella	AT3G13890.1 | Symbols: MYB26, ATMYB26, MS35 | myb domain protein 26 | chr3:4576744-4578027 REVERSE LENGTH=367	361	367	1.00E-141	101.7	81.7	85.6
Rsa1.0_01610.1.g28389.t2	ref|XP_002886534.1| hypothetical protein ARALYDRAFT_315221 [Arabidopsis lyrata subsp. lyrata] gi|297332375|gb|EFH62793.1| hypothetical protein ARALYDRAFT_315221 [Arabidopsis lyrata subsp. lyrata]	602	586	0	97.3	82.1	88.9	hypothetical protein ARALYDRAFT_315221	gbpln	Arabidopsis lyrata	AT1G61560.1 | Symbols: MLO6, ATMLO6 | Seven transmembrane MLO family protein | chr1:22708875-22712032 REVERSE LENGTH=583	602	583	0	96.8	80.7	88.2
Rsa1.0_01610.1.g28390.t1	gb|EOA35572.1| hypothetical protein CARUB_v10020781mg [Capsella rubella]	271	273	1.00E-138	100.7	95.2	97.8	hypothetical protein CARUB_v10020781mg	gbpln	Capsella rubella	AT1G61520.3 | Symbols: LHCA3 | photosystem I light harvesting complex gene 3 | chr1:22700152-22701149 FORWARD LENGTH=273	271	273	1.00E-140	100.7	94.5	97.0

Rsa1.0_01610.1.g28391.t1	ref|XP_002886541.1| hypothetical protein ARALYDRAFT_475177 [Arabidopsis lyrata subsp. lyrata] gi|297332382|gb|EFH62800.1| hypothetical protein ARALYDRAFT_475177 [Arabidopsis lyrata subsp. lyrata]	800	804	0	100.5	78.3	87.9	hypothetical protein ARALYDRAFT_475177	gbpln	Arabidopsis lyrata	AT1G61500.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:22689729-22692881 REVERSE LENGTH=804	800	804	0	100.5	79.4	87.1
Rsa1.0_01610.1.g28392.t1	ref|XP_002877808.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297323646|gb|EFH54067.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	447	446	1.00E-152	99.8	64.4	78.1	F-box family protein	gbpln	Arabidopsis lyrata	AT3G51530.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr3:19112873-19114497 REVERSE LENGTH=455	447	455	1.00E-147	101.8	62.2	75.2
Rsa1.0_01610.1.g28393.t5	ref|XP_002886541.1| hypothetical protein ARALYDRAFT_475177 [Arabidopsis lyrata subsp. lyrata] gi|297332382|gb|EFH62800.1| hypothetical protein ARALYDRAFT_475177 [Arabidopsis lyrata subsp. lyrata]	690	804	0	116.5	73.9	84.8	hypothetical protein ARALYDRAFT_475177	gbpln	Arabidopsis lyrata	AT1G61490.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:22685154-22688267 REVERSE LENGTH=804	690	804	0	116.5	74.8	85.1
Rsa1.0_01610.1.g28394.t2	ref|XP_002886541.1| hypothetical protein ARALYDRAFT_475177 [Arabidopsis lyrata subsp. lyrata] gi|297332382|gb|EFH62800.1| hypothetical protein ARALYDRAFT_475177 [Arabidopsis lyrata subsp. lyrata]	808	804	0	99.5	76.9	87.1	hypothetical protein ARALYDRAFT_475177	gbpln	Arabidopsis lyrata	AT1G61480.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:22681420-22684404 REVERSE LENGTH=809	808	809	0	100.1	77.0	86.4
Rsa1.0_01611.1.g28395.t1	gb|AAF20931.1|AF206721_1 ascorbate oxidase [Brassica juncea]	572	574	0	100.3	81.8	89.7	ascorbate oxidase	gbpln	Brassica juncea	AT5G21100.1 | Symbols: | Plant L-ascorbate oxidase | chr5:7168312-7170719 FORWARD LENGTH=573	572	573	0	100.2	80.9	90.0
Rsa1.0_01611.1.g28396.t1	gb|EOA22050.1| hypothetical protein CARUB_v10002590mg, partial [Capsella rubella]	153	254	4.00E-29	166.0	41.2	58.8	hypothetical protein CARUB_v10002590mg, partial	gbpln	Capsella rubella	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	153	292	1.00E-30	190.8	39.9	57.5
Rsa1.0_01611.1.g28397.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	327	441	1.00E-72	134.9	45.6	66.1	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	327	746	2.00E-52	228.1	35.5	50.2
Rsa1.0_01611.1.g28398.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01611.1.g28399.t1	ref|NP_197608.1| leucine-rich repeat-containing protein [Arabidopsis thaliana] gi|11762126|gb|AAG40341.1|AF324989_1 AT5g21090 [Arabidopsis thaliana] gi|13899097|gb|AAK48970.1|AF370543_1 Unknown protein [Arabidopsis thaliana] gi|20148427|gb|AAM10104.1| unknown protein [Arabidopsis thaliana] gi|27311823|gb|AAO00877.1| Unknown protein [Arabidopsis thaliana] gi|29294060|gb|AAO73897.1| leucine rich repeat protein (LRP), putative [Arabidopsis thaliana] gi|30023686|gb|AAP13376.1| At5g21090 [Arabidopsis thaliana] gi|222424256|dbj|BAH20085.1| AT5G21090 [Arabidopsis thaliana] gi|332005547|gb|AED92930.1| leucine-rich repeat-containing protein [Arabidopsis thaliana]	219	218	1.00E-101	99.5	84.0	89.0	leucine-rich repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G21090.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:7164758-7166904 FORWARD LENGTH=218	219	218	1.00E-104	99.5	84.0	89.0
Rsa1.0_01611.1.g28400.t2	gb|EOA19872.1| hypothetical protein CARUB_v10000121mg [Capsella rubella]	1022	1026	0	100.4	88.9	93.5	hypothetical protein CARUB_v10000121mg	gbpln	Capsella rubella	AT5G21080.1 | Symbols: | Uncharacterized protein | chr5:7158035-7162906 REVERSE LENGTH=1025	1022	1025	0	100.3	88.0	92.7
Rsa1.0_01611.1.g28401.t1	ref|NP_197606.1| uncharacterized protein [Arabidopsis thaliana] gi|15809944|gb|AAL06899.1| AT5g21070/T10F18_100 [Arabidopsis thaliana] gi|18958048|gb|AAL79597.1| AT5g21070/T10F18_100 [Arabidopsis thaliana] gi|332005545|gb|AED92928.1| uncharacterized protein AT5G21070 [Arabidopsis thaliana]	225	225	1.00E-118	100.0	96.4	97.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G21070.1 | Symbols: | unknown protein; Has 115 Blast hits to 115 proteins in 34 species: Archae - 1; Bacteria - 36; Metazoa - 0; Fungi - 0; Plants - 60; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr5:7156356-7157490 FORWARD LENGTH=225	225	225	1.00E-120	100.0	96.4	97.8
Rsa1.0_01611.1.g28402.t1	ref|XP_002863374.1| hypothetical protein ARALYDRAFT_494276 [Arabidopsis lyrata subsp. lyrata] gi|297309209|gb|EFH39633.1| hypothetical protein ARALYDRAFT_494276 [Arabidopsis lyrata subsp. lyrata]	111	888	7.00E-23	800.0	48.6	49.5	hypothetical protein ARALYDRAFT_494276	gbpln	Arabidopsis lyrata	AT5G47040.1 | Symbols: LON2 | lon protease 2 | chr5:19093356-19098678 REVERSE LENGTH=888	111	888	1.00E-25	800.0	48.6	49.5

Rsa1.0_01611.1.g28403.t1	ref|XP_002871964.1| BTB-POZ and math domain 5 [Arabidopsis lyrata subsp. lyrata] gi|297317801|gb|EFH48223.1| BTB-POZ and math domain 5 [Arabidopsis lyrata subsp. lyrata]	413	410	0	99.3	85.2	91.8	BTB-POZ and math domain 5	gbpln	Arabidopsis lyrata	AT5G21010.1 | Symbols: ATBPM5, BPM5 | BTB-POZ and MATH domain 5 | chr5:7136062-7138374 FORWARD LENGTH=410	413	410	0	99.3	84.5	91.0
Rsa1.0_01612.1.g28404.t1	emb|CAB46045.1| retrotransposon like protein [Arabidopsis thaliana] gi|7268441|emb|CAB80961.1| retrotransposon like protein [Arabidopsis thaliana]	203	687	2.00E-57	338.4	58.1	78.8	retrotransposon like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01612.1.g28405.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01612.1.g28406.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01612.1.g28407.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	1436	1499	0	104.4	61.0	75.3	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1436	158	9.00E-34	11.0	4.7	6.1
Rsa1.0_01612.1.g28408.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01612.1.g28409.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1097	1142	0	104.1	49.0	63.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1097	575	1.00E-43	52.4	13.1	20.6
Rsa1.0_01612.1.g28410.t1	ref|NP_179998.1| myrcene/ocimene synthase [Arabidopsis thaliana] gi|75216785|sp|Q9ZUH4.1|TPSA_ARATH RecName: Full=Tricyclene synthase, chloroplastic; AltName: Full=(E)-beta-ocimene synthase 0e23; AltName: Full=Myrcene synthase 1; AltName: Full=Terpenoid synthase 10; Short=AtTPS10; Flags: Precursor gi|4115381|gb|AAD03382.1| putative limonene cyclase [Arabidopsis thaliana] gi|194306668|gb|ACF41947.1| At2g24210 [Arabidopsis thaliana] gi|330252449|gb|AEC07543.1| terpene synthase 10 [Arabidopsis thaliana]	244	591	6.00E-85	242.2	65.6	77.9	myrcene/ocimene synthase	gbpln	Arabidopsis thaliana	AT2G24210.1 | Symbols: TPS10 | terpene synthase 10 | chr2:10294330-10297401 FORWARD LENGTH=591	244	591	2.00E-87	242.2	65.6	77.9
Rsa1.0_01612.1.g28411.t1	ref|XP_002878522.1| hypothetical protein ARALYDRAFT_907941 [Arabidopsis lyrata subsp. lyrata] gi|297324360|gb|EFH54781.1| hypothetical protein ARALYDRAFT_907941 [Arabidopsis lyrata subsp. lyrata]	237	229	1.00E-113	96.6	86.9	91.6	hypothetical protein ARALYDRAFT_907941	gbpln	Arabidopsis lyrata	AT3G63540.1 | Symbols: | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | chr3:23459372-23459803 REVERSE LENGTH=143	237	143	5.00E-75	60.3	55.7	58.2
Rsa1.0_01612.1.g28412.t5	emb|CAH66022.1| OSIGBa0105O19.1 [Oryza sativa Indica Group]	494	944	3.00E-31	191.1	26.9	39.5	OSIGBa0105O19.1	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_01612.1.g28413.t1	ref|XP_002880584.1| hypothetical protein ARALYDRAFT_481301 [Arabidopsis lyrata subsp. lyrata] gi|297326423|gb|EFH56843.1| hypothetical protein ARALYDRAFT_481301 [Arabidopsis lyrata subsp. lyrata]	280	279	1.00E-129	99.6	90.0	94.6	hypothetical protein ARALYDRAFT_481301	gbpln	Arabidopsis lyrata	AT2G24450.1 | Symbols: FLA3 | FASCICLIN-like arabinogalactan protein 3 precursor | chr2:10393019-10393861 REVERSE LENGTH=280	280	280	1.00E-125	100.0	88.2	93.2
Rsa1.0_01612.1.g28414.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01612.1.g28415.t1	ref|XP_001537841.1| predicted protein [Ajellomyces capsulatus NAm1] gi|150415449|gb|EDN10802.1| predicted protein [Ajellomyces capsulatus NAm1]	334	801	2.00E-18	239.8	24.9	38.0	predicted protein	gbenv/gbpln	Ajellomyces capsulatus	#	#	#	#	#	#	#
Rsa1.0_01613.1.g28416.t1	gb|EOA12558.1| hypothetical protein CARUB_v10026825mg [Capsella rubella]	309	309	1.00E-119	100.0	66.3	78.6	hypothetical protein CARUB_v10026825mg	gbpln	Capsella rubella	AT5G63590.1 | Symbols: FLS3, ATFLS3 | flavonol synthase 3 | chr5:25457172-25458427 REVERSE LENGTH=308	309	308	1.00E-121	99.7	65.4	77.7
Rsa1.0_01613.1.g28417.t1	ref|XP_002864854.1| hypothetical protein ARALYDRAFT_332577 [Arabidopsis lyrata subsp. lyrata] gi|297310689|gb|EFH41113.1| hypothetical protein ARALYDRAFT_332577 [Arabidopsis lyrata subsp. lyrata]	254	539	3.00E-53	212.2	63.0	72.8	hypothetical protein ARALYDRAFT_332577	gbpln	Arabidopsis lyrata	AT5G63550.2 | Symbols: | DEK domain-containing chromatin associated protein | chr5:25444805-25447934 FORWARD LENGTH=531	254	531	2.00E-53	209.1	63.4	70.5

Rsa1.0_01613.1.g28418.t3	ref|NP_201164.1| flavonol synthase 3 [Arabidopsis thaliana] gi|75309039|sp|Q9FFQ5.1|FLS3_ARATH RecName: Full=Flavonol synthase 3 gi|10177040|dbj|BAB10452.1| flavonol synthase [Arabidopsis thaliana] gi|27808572|gb|AAO24566.1| At5g63590 [Arabidopsis thaliana] gi|110736555|dbj|BAF00243.1| flavonol synthase [Arabidopsis thaliana] gi|332010389|gb|AED97772.1| flavonol synthase 3 [Arabidopsis thaliana]	334	308	2.00E-83	92.2	50.6	61.7	flavonol synthase 3	gbpln	Arabidopsis thaliana	AT5G63590.1 | Symbols: FLS3, ATFLS3 | flavonol synthase 3 | chr5:25457172-25458427 REVERSE LENGTH=308	334	308	4.00E-86	92.2	50.6	61.7
Rsa1.0_01613.1.g28419.t1	ref|XP_002864854.1| hypothetical protein ARALYDRAFT_332577 [Arabidopsis lyrata subsp. lyrata] gi|297310689|gb|EFH41113.1| hypothetical protein ARALYDRAFT_332577 [Arabidopsis lyrata subsp. lyrata]	179	539	3.00E-31	301.1	36.9	40.8	hypothetical protein ARALYDRAFT_332577	gbpln	Arabidopsis lyrata	AT5G63550.2 | Symbols: | DEK domain-containing chromatin associated protein | chr5:25444805-25447934 FORWARD LENGTH=531	179	531	6.00E-33	296.6	36.3	40.8
Rsa1.0_01613.1.g28420.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01613.1.g28421.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01613.1.g28422.t1	ref|XP_002885669.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata] gi|297331509|gb|EFH61928.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata]	593	467	1.00E-110	78.8	37.9	47.6	hypothetical protein ARALYDRAFT_319176	gbpln	Arabidopsis lyrata	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	593	472	1.00E-110	79.6	36.6	45.9
Rsa1.0_01613.1.g28423.t1	ref|NP_201093.1| Rac-like GTP-binding protein ARAC10 [Arabidopsis thaliana] gi|297793877|ref|XP_002864823.1| hypothetical protein ARALYDRAFT_496470 [Arabidopsis lyrata subsp. lyrata] gi|51701730|sp|O82481.1|RAC10_ARATH RecName: Full=Rac-like GTP-binding protein ARAC10; AltName: Full=GTPase protein ROP11 gi|7211193|gb|AAF40238.1|AF115467_1 Arac10 [Arabidopsis thaliana] gi|3702964|gb|AAC63014.1| rac GTP binding protein Arac10 [Arabidopsis thaliana] gi|10177466|dbj|BAB10857.1| rac GTP binding protein Arac10 [Arabidopsis thaliana] gi|27754724|gb|AAO22805.1| putative GTP binding protein Arac10 [Arabidopsis thaliana] gi|28394091|gb|AAO42453.1| putative GTP binding protein Arac10 [Arabidopsis thaliana] gi|51971983|dbj|BAD44656.1| Arac10 [Arabidopsis thaliana] gi|297310658|gb|EFH41082.1| hypothetical protein ARALYDRAFT_496470 [Arabidopsis lyrata subsp. lyrata] gi|332010284|gb|AED97667.1| Rac-like GTP-binding protein ARAC10 [Arabidopsis thaliana]	193	215	2.00E-96	111.4	97.9	99.5	Rac-like GTP-binding protein ARAC10	gbpln	Arabidopsis lyrata	AT5G62880.1 | Symbols: ARAC10, ATRAC10, ATROP11, RAC10 | RAC-like 10 | chr5:25237236-25238939 FORWARD LENGTH=215	193	215	6.00E-99	111.4	97.9	99.5
Rsa1.0_01613.1.g28424.t1	ref|XP_002864822.1| hypothetical protein ARALYDRAFT_496469 [Arabidopsis lyrata subsp. lyrata] gi|297310657|gb|EFH41081.1| hypothetical protein ARALYDRAFT_496469 [Arabidopsis lyrata subsp. lyrata]	159	360	2.00E-54	226.4	75.5	82.4	hypothetical protein ARALYDRAFT_496469	gbpln	Arabidopsis lyrata	AT5G62865.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48020.1). | chr5:25234064-25234567 FORWARD LENGTH=167	159	167	7.00E-50	105.0	76.1	84.3
Rsa1.0_01613.1.g28425.t1	gb|EOA37836.1| hypothetical protein CARUB_v10012023mg [Capsella rubella]	400	389	5.00E-52	97.3	38.5	53.0	hypothetical protein CARUB_v10012023mg	gbpln	Capsella rubella	AT5G50220.1 | Symbols: | F-box family protein | chr5:20446068-20447200 REVERSE LENGTH=357	400	357	1.00E-46	89.3	36.5	50.0
Rsa1.0_01613.1.g28426.t1	ref|NP_201091.2| nodulin MtN3-like protein [Arabidopsis thaliana] gi|322967651|sp|Q9FM10.2|SWEET5_ARATH RecName: Full=Bidirectional sugar transporter SWEET5; Short=AtSWEET5; AltName: Full=Protein VEGETATIVE CELL EXPRESSED 1; Short=AtVEX1 gi|332010281|gb|AED97664.1| bidirectional sugar transporter SWEET5 [Arabidopsis thaliana]	240	240	1.00E-107	100.0	77.9	88.3	nodulin MtN3-like protein	gbpln	Arabidopsis thaliana	AT5G62850.1 | Symbols: AtVEX1, SWEET5, AtSWEET5 | Nodulin MtN3 family protein | chr5:25230204-25231527 REVERSE LENGTH=240	240	240	1.00E-110	100.0	77.9	88.3

Rsa1.0_01613.1.g28427.t1	ref|NP_201091.2| nodulin MtN3-like protein [Arabidopsis thaliana] gi|322967651|sp|Q9FM10.2|SWET5_ARATH RecName: Full=Bidirectional sugar transporter SWEET5; Short=AtSWEET5; AltName: Full=Protein VEGETATIVE CELL EXPRESSED 1; Short=AtVEX1 gi|332010281|gb|AED97664.1| bidirectional sugar transporter SWEET5 [Arabidopsis thaliana]	240	240	1.00E-116	100.0	83.8	90.8	nodulin MtN3-like protein	gbpln	Arabidopsis thaliana	AT5G62850.1 | Symbols: AtVEX1, SWEET5, AtSWEET5 | Nodulin MtN3 family protein | chr5:25230204-25231527 REVERSE LENGTH=240	240	240	1.00E-119	100.0	83.8	90.8
Rsa1.0_01613.1.g28428.t1	gb|EOA12737.1| hypothetical protein CARUB_v10028245mg [Capsella rubella]	276	297	1.00E-108	107.6	78.3	86.2	hypothetical protein CARUB_v10028245mg	gbpln	Capsella rubella	AT5G62820.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr5:25223828-25224898 REVERSE LENGTH=297	276	297	1.00E-110	107.6	77.2	84.1
Rsa1.0_01613.1.g28429.t1	gb|EOA13719.1| hypothetical protein CARUB_v10026788mg [Capsella rubella]	262	287	1.00E-140	109.5	94.7	96.6	hypothetical protein CARUB_v10026788mg	gbpln	Capsella rubella	AT5G62740.1 | Symbols: HIR1, ATHIR1 | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr5:25201320-25202535 FORWARD LENGTH=286	262	286	1.00E-141	109.2	92.7	96.6
Rsa1.0_01613.1.g28430.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01614.1.g28431.t2	gb|EOA13068.1| hypothetical protein CARUB_v10026072mg [Capsella rubella]	493	637	1.00E-144	129.2	63.1	75.3	hypothetical protein CARUB_v10026072mg	gbpln	Capsella rubella	AT5G46550.1 | Symbols: | DNA-binding bromodomain-containing protein | chr5:18884439-18886503 REVERSE LENGTH=494	493	494	1.00E-129	100.2	56.8	69.2
Rsa1.0_01614.1.g28432.t1	dbj|BAJ34635.1| unnamed protein product [Thellungiella halophila]	201	206	1.00E-58	102.5	57.2	70.6	unnamed protein product	----	----	AT2G34690.1 | Symbols: ACD11 | Glycolipid transfer protein (GLTP) family protein | chr2:14630425-14631779 FORWARD LENGTH=206	201	206	2.00E-58	102.5	53.7	71.1
Rsa1.0_01614.1.g28433.t1	gb|EOA14092.1| hypothetical protein CARUB_v10027229mg, partial [Capsella rubella]	157	176	2.00E-77	112.1	91.7	94.9	hypothetical protein CARUB_v10027229mg, partial	gbpln	Capsella rubella	AT5G46530.1 | Symbols: | AWPM-19-like family protein | chr5:18875576-18876779 FORWARD LENGTH=157	157	157	1.00E-79	100.0	91.1	95.5
Rsa1.0_01614.1.g28434.t1	ref|XP_002865179.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311014|gb|EFH41438.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1139	1113	0	97.7	62.8	76.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G08450.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:5365610-5371101 FORWARD LENGTH=1234	1139	1234	0	108.3	54.5	70.3
Rsa1.0_01614.1.g28435.t1	dbj|BAB01217.1| Ta11 non-LTR retroelement protein-like [Arabidopsis thaliana] gi|67633664|gb|AAY78756.1| putative zinc finger protein [Arabidopsis thaliana]	195	487	5.00E-30	249.7	39.0	51.3	Ta11 non-LTR retroelement protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01614.1.g28436.t1	ref|XP_002865177.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311012|gb|EFH41436.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	126	199	4.00E-39	157.9	60.3	77.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G34690.1 | Symbols: ACD11 | Glycolipid transfer protein (GLTP) family protein | chr2:14630425-14631779 FORWARD LENGTH=206	126	206	4.00E-41	163.5	57.1	78.6
Rsa1.0_01614.1.g28437.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	124	1274	3.00E-38	1027.4	65.3	75.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01615.1.g28438.t1	dbj|BAB02146.1| copia retroelement pol polyprotein-like [Arabidopsis thaliana]	930	526	5.00E-70	56.6	18.7	24.5	copia retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01615.1.g28439.t1	gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	176	1787	8.00E-18	1015.3	26.7	38.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01615.1.g28440.t1	gb|AAM93462.1| putative reverse transcriptase [Oryza sativa Japonica Group]	442	566	4.00E-30	128.1	16.7	25.8	putative reverse transcriptase	gbpln	Oryza sativa	ATMG00310.1 | Symbols: ORF154 | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chrM:90883-91347 REVERSE LENGTH=154	442	154	8.00E-12	34.8	7.2	11.5
Rsa1.0_01615.1.g28441.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01615.1.g28442.t1	gb|AAM15254.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	335	930	3.00E-45	277.6	32.5	43.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01615.1.g28443.t1	gb|AAC69377.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	815	1328	2.00E-18	162.9	9.4	12.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01615.1.g28444.t1	emb|CAN81728.1| hypothetical protein VITISV_004185 [Vitis vinifera]	1111	1601	1.00E-119	144.1	24.7	37.7	hypothetical protein VITISV_004185	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01615.1.g28445.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01616.1.g28446.t1	ref|NP_175273.1| F-box/RNI-like/FBD-like domain-containing protein [Arabidopsis thaliana] gi|5733869|gb|AAD49757.1|AC007932_5 Contains F-box domain PF|00646 [Arabidopsis thaliana] gi|332194164|gb|AEE32285.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	213	513	8.00E-70	240.8	60.6	72.8	F-box/RNI-like/FBD-like domain-containing protein	gbpln	Arabidopsis thaliana	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	213	513	3.00E-72	240.8	60.6	72.8

Rsa1.0_01616.1.g28447.t2	sp|Q56XW8.2|FBL30_ARATH RecName: Full=F-box/LRR-repeat protein At1g48400	326	487	4.00E-95	149.4	62.6	74.8	RecName: Full=F-box/LRR-repeat protein At1g48400	----	----	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	326	513	3.00E-97	157.4	62.6	74.8
Rsa1.0_01616.1.g28448.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1615	1223	0	75.7	41.3	54.1	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1615	746	1.00E-122	46.2	13.0	17.6
Rsa1.0_01616.1.g28449.t1	ref|NP_175273.1| F-box/RNI-like/FBD-like domain-containing protein [Arabidopsis thaliana] gi|5733869|gb|AAD49757.1|AC007932_5 Contains F-box domain PF|00646 [Arabidopsis thaliana] gi|332194164|gb|AEE32285.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	133	513	3.00E-42	385.7	65.4	73.7	F-box/RNI-like/FBD-like domain-containing protein	gbpln	Arabidopsis thaliana	AT1G48400.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=513	133	513	7.00E-45	385.7	65.4	73.7
Rsa1.0_01616.1.g28450.t1	ref|XP_002894079.1| hypothetical protein ARALYDRAFT_336913 [Arabidopsis lyrata subsp. lyrata] gi|297339921|gb|EFH70338.1| hypothetical protein ARALYDRAFT_336913 [Arabidopsis lyrata subsp. lyrata]	1002	1058	0	105.6	82.4	89.9	hypothetical protein ARALYDRAFT_336913	gbpln	Arabidopsis lyrata	AT1G47900.1 | Symbols: | Plant protein of unknown function (DUF869) | chr1:17647340-17651035 REVERSE LENGTH=1054	1002	1054	0	105.2	81.8	90.4
Rsa1.0_01616.1.g28451.t1	gb|AAM90621.1|AF400001_1 E2F-related transcription factor 2 [Noccaea caerulescens]	373	386	1.00E-162	103.5	82.0	87.4	E2F-related transcription factor 2	gbpln	Noccaea caerulescens	AT1G47870.1 | Symbols: E2FC, ATE2F2, ATE2FC | winged-helix DNA-binding transcription factor family protein | chr1:17634937-17637557 FORWARD LENGTH=396	373	396	1.00E-155	106.2	78.8	86.3
Rsa1.0_01616.1.g28452.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01617.1.g28453.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01617.1.g28454.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01617.1.g28455.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1590	1223	0	76.9	33.6	45.7	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1590	746	2.00E-87	46.9	10.8	14.8
Rsa1.0_01617.1.g28456.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1502	1715	0	114.2	31.7	48.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1502	575	6.00E-47	38.3	8.2	14.0
Rsa1.0_01617.1.g28457.t1	ref|NP_199965.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana] gi|9758194|dbj|BAB08668.1| ripening-related protein-like [Arabidopsis thaliana] gi|67633876|gb|AAY78862.1| invertase [Arabidopsis thaliana] gi|332008710|gb|AED96093.1| plant invertase/pectin methylesterase inhibitor domain-containing protein [Arabidopsis thaliana]	169	204	6.00E-78	120.7	85.2	90.5	plant invertase/pectin methylesterase inhibitor domain-containing protein	gbpln	Arabidopsis thaliana	AT5G51520.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:20925980-20926594 FORWARD LENGTH=204	169	204	2.00E-80	120.7	85.2	90.5
Rsa1.0_01617.1.g28458.t1	sp|O04067.1|AGL9_SINAL RecName: Full=Agamous-like MADS-box protein AGL9 homolog; AltName: Full=MADS D gi|1617211|emb|CAA69916.1| MADS D [Sinapis alba]	152	254	3.00E-14	167.1	26.3	28.9	RecName: Full=Agamous-like MADS-box protein AGL9 homolog; AltName: Full=MADS D gi|1617211|emb|CAA69916.1| MADS D	gbpln	Sinapis alba	AT1G24260.2 | Symbols: SEP3, AGL9 | K-box region and MADS-box transcription factor family protein | chr1:8593790-8595862 REVERSE LENGTH=251	152	251	3.00E-13	165.1	23.0	25.0
Rsa1.0_01617.1.g28459.t1	emb|CCD74510.1| unknown, partial [Arabidopsis halleri subsp. halleri]	276	300	7.00E-24	108.7	19.6	31.9	unknown, partial	gbpln	Arabidopsis halleri	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	276	170	2.00E-12	61.6	20.3	29.3
Rsa1.0_01617.1.g28460.t1	ref|NP_199969.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|9758198|dbj|BAB08672.1| receptor-like protein kinase [Arabidopsis thaliana] gi|224589719|gb|ACN59391.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332008715|gb|AED96098.1| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana]	274	680	1.00E-128	248.2	84.3	89.1	leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT5G51560.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:20945807-20948613 FORWARD LENGTH=680	274	680	1.00E-130	248.2	84.3	89.1
Rsa1.0_01617.1.g28461.t1	ref|XP_002865868.1| hypothetical protein ARALYDRAFT_495229 [Arabidopsis lyrata subsp. lyrata] gi|297311703|gb|EFH42127.1| hypothetical protein ARALYDRAFT_495229 [Arabidopsis lyrata subsp. lyrata]	188	418	3.00E-73	222.3	85.6	88.3	hypothetical protein ARALYDRAFT_495229	gbpln	Arabidopsis lyrata	AT5G51590.1 | Symbols: | AT hook motif DNA-binding family protein | chr5:20956863-20958929 REVERSE LENGTH=419	188	419	6.00E-71	222.9	84.0	87.2

Rsa1.0_01618.1.g28462.t1	gb|ABF17873.1| cinnamate 4-hydroxylase isoform 1 [Brassica napus] gi|94323525|gb|ABF17874.1| cinnamate 4-hydroxylase isoform 1 [Brassica napus]	114	505	2.00E-61	443.0	99.1	100.0	cinnamate 4-hydroxylase isoform 1	gbpln	Brassica napus	AT2G30490.1 | Symbols: ATC4H, C4H, CYP73A5, REF3 | cinnamate-4-hydroxylase | chr2:12993861-12995683 REVERSE LENGTH=505	114	505	3.00E-61	443.0	93.9	97.4
Rsa1.0_01618.1.g28463.t9	ref|XP_002881113.1| hypothetical protein ARALYDRAFT_320802 [Arabidopsis lyrata subsp. lyrata] gi|297326952|gb|EFH57372.1| hypothetical protein ARALYDRAFT_320802 [Arabidopsis lyrata subsp. lyrata]	735	701	0	95.4	69.4	76.3	hypothetical protein ARALYDRAFT_320802	gbpln	Arabidopsis lyrata	AT2G30480.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; Has 189 Blast hits to 180 proteins in 63 species: Archae - 0; Bacteria - 43; Metazoa - 86; Fungi - 6; Plants - 19; Viruses - 0; Other Eukaryotes - 35 (source: NCBI BLink). | chr2:12988326-12992930 REVERSE LENGTH=705	735	705	0	95.9	68.0	75.1
Rsa1.0_01618.1.g28464.t1	dbj|BAJ34588.1| unnamed protein product [Thellungiella halophila]	814	809	0	99.4	78.0	84.3	unnamed protein product	----	----	AT2G30470.1 | Symbols: HSI2, VAL1 | high-level expression of sugar-inducible gene 2 | chr2:12980904-12984724 REVERSE LENGTH=790	814	790	0	97.1	72.7	80.3
Rsa1.0_01618.1.g28465.t1	ref|NP_565699.1| tubulin-specific chaperone A [Arabidopsis thaliana] gi|334184582|ref|NP_001189640.1| tubulin-specific chaperone A [Arabidopsis thaliana] gi|21542453|sp|O04350.2|TBCA_ARATH RecName: Full=Tubulin-specific chaperone A; AltName: Full=TCP1-chaperonin cofactor A; AltName: Full=Tubulin-folding cofactor A; Short=CFA gi|20514257|gb|AAM22957.1|AF486848_1 tubulin folding cofactor A [Arabidopsis thaliana] gi|15293037|gb|AAK93629.1| putative TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] gi|20196887|gb|AAM14821.1| TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] gi|20198325|gb|AAB63093.2| TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] gi|20259135|gb|AAM14283.1| putative TCP1-chaperonin cofactor A protein [Arabidopsis thaliana] gi|21553949|gb|AAM63030.1| TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] gi|330253289|gb|AEC08383.1| tubulin-specific chaperone A [Arabidopsis thaliana] gi|330253290|gb|AEC08384.1| tubulin-specific chaperone A [Arabidopsis thaliana]	110	113	2.00E-49	102.7	90.9	93.6	tubulin-specific chaperone A	gbpln	Arabidopsis thaliana	AT2G30410.2 | Symbols: KIS | tubulin folding cofactor A (KIESEL) | chr2:12959812-12960552 FORWARD LENGTH=113	110	113	4.00E-52	102.7	90.9	93.6
Rsa1.0_01618.1.g28466.t1	gb|EOA27511.1| hypothetical protein CARUB_v10023651mg [Capsella rubella]	322	320	1.00E-113	99.4	71.7	80.7	hypothetical protein CARUB_v10023651mg	gbpln	Capsella rubella	AT2G30400.1 | Symbols: ATOFP2, OFP2 | ovate family protein 2 | chr2:12956592-12957554 FORWARD LENGTH=320	322	320	1.00E-113	99.4	76.1	84.5
Rsa1.0_01618.1.g28467.t1	ref|XP_002881107.1| ATOFP17/OFP17 [Arabidopsis lyrata subsp. lyrata] gi|297326946|gb|EFH57366.1| ATOFP17/OFP17 [Arabidopsis lyrata subsp. lyrata]	202	195	9.00E-86	96.5	81.2	86.1	ATOFP17/OFP17	gbpln	Arabidopsis lyrata	AT2G30395.1 | Symbols: ATOFP17, OFP17 | ovate family protein 17 | chr2:12954409-12955083 REVERSE LENGTH=195	202	195	2.00E-85	96.5	79.2	84.7
Rsa1.0_01618.1.g28468.t1	gb|EOA28584.1| hypothetical protein CARUB_v10024802mg [Capsella rubella]	418	423	0	101.2	76.3	87.3	hypothetical protein CARUB_v10024802mg	gbpln	Capsella rubella	AT2G30380.1 | Symbols: | Plant protein of unknown function (DUF641) | chr2:12948284-12950573 FORWARD LENGTH=519	418	519	1.00E-137	124.2	58.4	66.0
Rsa1.0_01618.1.g28469.t1	ref|XP_002881104.1| hypothetical protein ARALYDRAFT_481948 [Arabidopsis lyrata subsp. lyrata] gi|297326943|gb|EFH57363.1| hypothetical protein ARALYDRAFT_481948 [Arabidopsis lyrata subsp. lyrata]	444	434	0	97.7	83.6	89.2	hypothetical protein ARALYDRAFT_481948	gbpln	Arabidopsis lyrata	AT2G30360.1 | Symbols: CIPK11, PKS5, SIP4, SNRK3.22 | SOS3-interacting protein 4 | chr2:12937265-12938572 REVERSE LENGTH=435	444	435	0	98.0	82.0	88.3
Rsa1.0_01618.1.g28470.t1	gb|ABV21212.1| Ty1_Copia-element protein [Arabidopsis thaliana]	334	438	5.00E-71	131.1	38.6	53.9	Ty1_Copia-element protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	334	289	7.00E-67	86.5	36.5	53.3

Rsa1.0_01618.1.g28471.t1	gb|EOA27181.1| hypothetical protein CARUB_v10023282mg [Capsella rubella]	426	423	1.00E-155	99.3	65.5	78.4	hypothetical protein CARUB_v10023282mg	gbpln	Capsella rubella	AT2G43260.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17983744-17985089 REVERSE LENGTH=420	426	420	1.00E-150	98.6	65.3	77.7
Rsa1.0_01619.1.g28472.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01619.1.g28473.t1	dbj|BAB11196.1| mutator-like transposase [Arabidopsis thaliana]	704	797	1.00E-122	113.2	38.9	56.3	mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	704	719	3.00E-24	102.1	17.3	27.7
Rsa1.0_01619.1.g28474.t1	gb|ACG60684.1| maize transposon MuDR-like protein [Brassica oleracea var. alboglabra]	427	622	2.00E-32	145.7	24.6	40.3	maize transposon MuDR-like protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01619.1.g28475.t1	gb|ABD65084.1| hypothetical protein 27.t00096 [Brassica oleracea]	108	645	4.00E-33	597.2	57.4	65.7	hypothetical protein 27.t00096	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01619.1.g28476.t1	gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]	407	863	3.00E-98	212.0	50.1	58.7	Ulp1 protease family protein	gbpln	Brassica oleracea	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	407	921	1.00E-17	226.3	18.7	27.8
Rsa1.0_01619.1.g28477.t1	emb|CAB83070.1| putative protein [Arabidopsis thaliana] gi|110736914|dbj|BAF00414.1| hypothetical protein [Arabidopsis thaliana]	467	539	1.00E-22	115.4	15.2	26.1	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01619.1.g28478.t1	emb|CAB86685.1| putative protein [Arabidopsis thaliana]	165	303	4.00E-12	183.6	26.1	43.6	putative protein	gbpln	Arabidopsis thaliana	AT3G32260.1 | Symbols: | Nucleic acid-binding proteins superfamily | chr3:13219168-13221456 FORWARD LENGTH=309	165	309	8.00E-14	187.3	32.7	49.7
Rsa1.0_01619.1.g28479.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01619.1.g28480.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01619.1.g28481.t1	gb|EOA37460.1| hypothetical protein CARUB_v10011570mg, partial [Capsella rubella]	160	488	4.00E-17	305.0	26.3	28.8	hypothetical protein CARUB_v10011570mg, partial	gbpln	Capsella rubella	AT1G24485.3 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: protein kinase-related (TAIR:AT3G46280.1); Has 1310 Blast hits to 1260 proteins in 183 species: Archae - 0; Bacteria - 258; Metazoa - 162; Fungi - 42; Plants - 688; Viruses - 16; Other Eukaryotes - 144 (source: NCBI BLink). | chr1:8678858-8681894 FORWARD LENGTH=574	160	574	6.00E-17	358.8	24.4	25.6
Rsa1.0_01620.1.g28482.t1	ref|XP_002874931.1| ATXDH1 [Arabidopsis lyrata subsp. lyrata] gi|297320768|gb|EFH51190.1| ATXDH1 [Arabidopsis lyrata subsp. lyrata]	1360	1365	0	100.4	90.4	95.1	ATXDH1	gbpln	Arabidopsis lyrata	AT4G34890.1 | Symbols: ATXDH1, XDH1 | xanthine dehydrogenase 1 | chr4:16618736-16624983 REVERSE LENGTH=1361	1360	1361	0	100.1	86.3	92.5
Rsa1.0_01620.1.g28483.t1	ref|NP_192085.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|4558545|gb|AAD22638.1|AC007138_2 putative CHP-rich zinc finger protein [Arabidopsis thaliana] gi|3859600|gb|AAC72866.1| T15B16.6 gene product [Arabidopsis thaliana] gi|7268219|emb|CAB77746.1| putative CHP-rich zinc finger protein [Arabidopsis thaliana] gi|332656674|gb|AEE82074.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	711	667	0	93.8	59.2	69.2	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT4G01760.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr4:759131-761134 REVERSE LENGTH=667	711	667	0	93.8	59.2	69.2
Rsa1.0_01620.1.g28484.t1	ref|XP_002872850.1| hypothetical protein ARALYDRAFT_490353 [Arabidopsis lyrata subsp. lyrata] gi|297318687|gb|EFH49109.1| hypothetical protein ARALYDRAFT_490353 [Arabidopsis lyrata subsp. lyrata]	321	323	1.00E-171	100.6	91.9	96.6	hypothetical protein ARALYDRAFT_490353	gbpln	Arabidopsis lyrata	AT4G02195.1 | Symbols: SYP42, TLG2B, ATSYP42, ATTLG2B | syntaxin of plants 42 | chr4:970099-972192 REVERSE LENGTH=323	321	323	1.00E-173	100.6	92.2	96.9
Rsa1.0_01620.1.g28485.t1	gb|EOA20736.1| hypothetical protein CARUB_v10001058mg [Capsella rubella]	415	418	1.00E-156	100.7	72.8	80.5	hypothetical protein CARUB_v10001058mg	gbpln	Capsella rubella	AT4G02220.1 | Symbols: | zinc finger (MYND type) family protein / programmed cell death 2 C-terminal domain-containing protein | chr4:976728-978902 FORWARD LENGTH=418	415	418	1.00E-158	100.7	73.5	81.7
Rsa1.0_01621.1.g28486.t2	gb|EOA12799.1| hypothetical protein CARUB_v10025754mg [Capsella rubella]	441	1259	1.00E-141	285.5	55.8	59.2	hypothetical protein CARUB_v10025754mg	gbpln	Capsella rubella	AT5G54440.1 | Symbols: CLUB, AtTRS130 | CLUB | chr5:22100056-22107695 FORWARD LENGTH=1259	441	1259	1.00E-143	285.5	53.7	55.3
Rsa1.0_01621.1.g28487.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01621.1.g28488.t1	ref|NP_200443.1| expansin A14 [Arabidopsis thaliana] gi|20137960|sp|Q9FMA0.1|EXP14_ARATH RecName: Full=Expansin-A14; Short=AtEXPA14; AltName: Full=Alpha-expansin-14; Short=At-EXP14; Short=AtEx14; AltName: Full=Ath-ExpAlpha-1.5; Flags: Precursor gi|10177830|dbj|BAB11259.1| expansin [Arabidopsis thaliana] gi|110740362|dbj|BAF02076.1| Expansin [Arabidopsis thaliana] gi|332009365|gb|AED96748.1| expansin A14 [Arabidopsis thaliana]	64	255	2.00E-12	398.4	62.5	68.8	expansin A14	gbpln	Arabidopsis thaliana	AT5G56320.1 | Symbols: ATEXPA14, EXP14, ATEXP14, ATHEXP ALPHA 1.5, EXPA14 | expansin A14 | chr5:22808854-22809906 FORWARD LENGTH=255	64	255	2.00E-15	398.4	62.5	68.8
Rsa1.0_01621.1.g28489.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28490.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28491.t1	ref|NP_001147031.1| RING-H2 finger protein ATL5A [Zea mays] gi|195606664|gb|ACG25162.1| RING-H2 finger protein ATL5A [Zea mays]	163	165	2.00E-68	101.2	89.0	90.8	RING-H2 finger protein ATL5A	gbenv/gbpln	Zea mays	AT5G42200.1 | Symbols: | RING/U-box superfamily protein | chr5:16860523-16861014 FORWARD LENGTH=163	163	163	3.00E-69	100.0	79.8	85.3
Rsa1.0_01622.1.g28492.t1	gb|AAF79809.1|AC020646_32 T32E20.9 [Arabidopsis thaliana]	397	1586	9.00E-27	399.5	21.9	26.4	T32E20.9	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28493.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28494.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28495.t3	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	892	1024	9.00E-59	114.8	18.4	26.9	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28496.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	254	940	3.00E-30	370.1	27.2	35.8	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28497.t1	gb|AAM15254.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	362	930	4.00E-37	256.9	26.2	37.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28498.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28499.t1	gb|EMJ13768.1| hypothetical protein PRUPE_ppa015570mg, partial [Prunus persica]	205	541	7.00E-26	263.9	40.0	52.2	hypothetical protein PRUPE_ppa015570mg, partial	gbpln	Prunus persica	#	#	#	#	#	#	#
Rsa1.0_01622.1.g28500.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01623.1.g28501.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	588	414	6.00E-38	70.4	13.3	15.6	hypothetical protein 23.t00055	gbpln	Brassica oleracea	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	588	256	7.00E-15	43.5	6.3	9.9
Rsa1.0_01623.1.g28502.t2	gb|ACB98704.1| phospholipase D gamma 1 [Brassica oleracea var. capitata]	613	859	0	140.1	73.1	81.1	phospholipase D gamma 1	gbpln	Brassica oleracea	AT4G11840.1 | Symbols: PLDGAMMA3 | phospholipase D gamma 3 | chr4:7122152-7125882 REVERSE LENGTH=866	613	866	0	141.3	72.8	80.8
Rsa1.0_01623.1.g28503.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	253	1023	4.00E-75	404.3	56.1	67.6	F27F5.21	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	253	626	2.00E-15	247.4	16.2	22.5
Rsa1.0_01623.1.g28504.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01623.1.g28505.t1	ref|XP_002874728.1| PLDGAMMA1 [Arabidopsis lyrata subsp. lyrata] gi|297320565|gb|EFH50987.1| PLDGAMMA1 [Arabidopsis lyrata subsp. lyrata]	490	859	0	175.3	80.8	90.2	PLDGAMMA1	gbpln	Arabidopsis lyrata	AT4G11840.1 | Symbols: PLDGAMMA3 | phospholipase D gamma 3 | chr4:7122152-7125882 REVERSE LENGTH=866	490	866	0	176.7	80.6	89.6

Rsa1.0_01624.1.g28506.t2	ref|NP_179461.1| Preprotein translocase subunit secY [Arabidopsis thaliana] gi|12643748|sp|Q38885.2|SCY1_ARATH RecName: Full=Preprotein translocase subunit SCY1, chloroplastic; AltName: Full=CpSecY; Flags: Precursor gi|15983352|gb|AAL11544.1|AF424550_1 At2g18710/MSF3.9 [Arabidopsis thaliana] gi|4185137|gb|AAD08940.1| putative preprotein translocase SECY protein [Arabidopsis thaliana] gi|16604410|gb|AAL24211.1| At2g18710/MSF3.9 [Arabidopsis thaliana] gi|17473607|gb|AAL38269.1| putative preprotein translocase SECY protein [Arabidopsis thaliana] gi|27363258|gb|AAO11548.1| At2g18710/MSF3.9 [Arabidopsis thaliana] gi|330251702|gb|AEC06796.1| Preprotein translocase subunit secY [Arabidopsis thaliana]	553	551	0	99.6	91.0	92.6	Preprotein translocase subunit secY	gbpln	Arabidopsis thaliana	AT2G18710.1 | Symbols: SCY1 | SECY homolog 1 | chr2:8112231-8114452 REVERSE LENGTH=551	553	551	0	99.6	91.0	92.6
Rsa1.0_01624.1.g28507.t1	gb|EOA32326.1| hypothetical protein CARUB_v10015598mg [Capsella rubella]	487	315	1.00E-112	64.7	43.5	50.3	hypothetical protein CARUB_v10015598mg	gbpln	Capsella rubella	AT2G18680.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G18690.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:8094780-8095643 FORWARD LENGTH=287	487	287	1.00E-106	58.9	42.5	49.7
Rsa1.0_01624.1.g28508.t1	gb|AAZ67609.1| 80A08_24 [Brassica rapa subsp. pekinensis]	267	475	5.00E-40	177.9	38.6	43.8	80A08_24	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_01624.1.g28509.t3	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1039	940	6.00E-44	90.5	12.7	18.1	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01624.1.g28510.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01624.1.g28511.t2	ref|NP_849979.1| EG45-like domain-containing protein 2 [Arabidopsis thaliana] gi|20138450|sp|Q9ZV52.2|EGC2_ARATH RecName: Full=EG45-like domain containing protein 2; AltName: Full=Plant natriuretic peptide A; Short=AtEXPR3; Short=AtPNP-A; Short=Ath-ExpGamma-1.2; Flags: Precursor gi|17529070|gb|AAL38745.1| unknown protein [Arabidopsis thaliana] gi|23296798|gb|AAN13172.1| unknown protein [Arabidopsis thaliana] gi|330251696|gb|AEC06790.1| EG45-like domain-containing protein 2 [Arabidopsis thaliana]	133	130	6.00E-57	97.7	80.5	87.2	EG45-like domain-containing protein 2	gbpln	Arabidopsis thaliana	AT2G18660.1 | Symbols: PNP-A | plant natriuretic peptide A | chr2:8091032-8091644 REVERSE LENGTH=130	133	130	1.00E-59	97.7	80.5	87.2
Rsa1.0_01624.1.g28512.t1	ref|NP_974219.1| tryptophanyl-tRNA synthetase [Arabidopsis thaliana] gi|332640583|gb|AEE74104.1| tryptophanyl-tRNA synthetase [Arabidopsis thaliana]	103	402	2.00E-30	390.3	61.2	70.9	tryptophanyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT3G04600.2 | Symbols: | Nucleotidylyl transferase superfamily protein | chr3:1243152-1245958 FORWARD LENGTH=402	103	402	4.00E-33	390.3	61.2	70.9
Rsa1.0_01624.1.g28513.t1	ref|XP_002886188.1| hypothetical protein ARALYDRAFT_480768 [Arabidopsis lyrata subsp. lyrata] gi|297332028|gb|EFH62447.1| hypothetical protein ARALYDRAFT_480768 [Arabidopsis lyrata subsp. lyrata]	414	413	1.00E-151	99.8	74.2	81.9	hypothetical protein ARALYDRAFT_480768	gbpln	Arabidopsis lyrata	AT2G18650.1 | Symbols: MEE16 | RING/U-box superfamily protein | chr2:8086860-8088131 REVERSE LENGTH=423	414	423	1.00E-149	102.2	71.7	80.0
Rsa1.0_01625.1.g28514.t2	ref|XP_002872902.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata] gi|297318739|gb|EFH49161.1| hypothetical protein ARALYDRAFT_912111 [Arabidopsis lyrata subsp. lyrata]	346	356	2.33E-156	102.9	75.1	84.1	hypothetical protein ARALYDRAFT_912111	gbpln	Arabidopsis lyrata	AT4G01220.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr4:513431-515648 REVERSE LENGTH=360	346	360	1.00E-145	104.0	69.4	77.7
Rsa1.0_01625.1.g28515.t1	gb|EOA40179.1| hypothetical protein CARUB_v10008895mg [Capsella rubella]	460	509	0	110.7	92.8	95.7	hypothetical protein CARUB_v10008895mg	gbpln	Capsella rubella	AT1G30560.1 | Symbols: | Major facilitator superfamily protein | chr1:10824761-10826293 FORWARD LENGTH=510	460	510	0	110.9	91.7	95.7

Rsa1.0_01625.1.g28516.t1	ref|XP_002893633.1| hypothetical protein ARALYDRAFT_336158 [Arabidopsis lyrata subsp. lyrata] gi|297339475|gb|EFH69892.1| hypothetical protein ARALYDRAFT_336158 [Arabidopsis lyrata subsp. lyrata]	228	233	1.00E-104	102.2	76.8	86.4	hypothetical protein ARALYDRAFT_336158	gbpln	Arabidopsis lyrata	AT1G30550.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:10820838-10823641 REVERSE LENGTH=455	228	455	1.00E-106	199.6	76.8	85.5
Rsa1.0_01625.1.g28517.t1	ref|XP_002879925.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297325764|gb|EFH56184.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	397	371	9.00E-63	93.5	39.0	57.7	F-box family protein	gbpln	Arabidopsis lyrata	AT2G41360.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:17234374-17235956 FORWARD LENGTH=387	397	387	7.00E-50	97.5	33.0	47.6
Rsa1.0_01625.1.g28518.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	510	1142	1.00E-131	223.9	45.1	64.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	510	575	1.00E-83	112.7	33.1	49.0
Rsa1.0_01625.1.g28519.t1	ref|XP_002868284.1| hypothetical protein ARALYDRAFT_915427 [Arabidopsis lyrata subsp. lyrata] gi|297314120|gb|EFH44543.1| hypothetical protein ARALYDRAFT_915427 [Arabidopsis lyrata subsp. lyrata]	158	158	2.00E-74	100.0	93.7	98.7	hypothetical protein ARALYDRAFT_915427	gbpln	Arabidopsis lyrata	AT4G14420.1 | Symbols: | HR-like lesion-inducing protein-related | chr4:8302171-8303738 REVERSE LENGTH=158	158	158	8.00E-77	100.0	93.0	98.1
Rsa1.0_01625.1.g28520.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01625.1.g28521.t1	ref|XP_002868282.1| enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297314118|gb|EFH44541.1| enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	240	240	1.00E-112	100.0	86.3	94.6	enoyl-CoA hydratase/isomerase family protein	gbpln	Arabidopsis lyrata	AT4G14430.1 | Symbols: IBR10, ATECI2, ECI2, ECHIB, PEC12 | indole-3-butyric acid response 10 | chr4:8304910-8305632 REVERSE LENGTH=240	240	240	1.00E-109	100.0	85.4	93.8
Rsa1.0_01625.1.g28522.t1	gb|EOA17630.1| hypothetical protein CARUB_v10005995mg [Capsella rubella]	132	135	3.00E-64	102.3	93.9	98.5	hypothetical protein CARUB_v10005995mg	gbpln	Capsella rubella	AT4G14455.1 | Symbols: ATBET12, BET12, ATBS14B, BS14B | Target SNARE coiled-coil domain protein | chr4:8310482-8311938 FORWARD LENGTH=130	132	130	9.00E-67	98.5	93.2	98.5
Rsa1.0_01625.1.g28523.t1	ref|NP_193184.1| protein kinase family protein [Arabidopsis thaliana] gi|2244804|emb|CAB10227.1| kinase like protein [Arabidopsis thaliana] gi|7268154|emb|CAB78490.1| kinase like protein [Arabidopsis thaliana] gi|332658049|gb|AEE83449.1| protein kinase family protein [Arabidopsis thaliana]	478	487	0	101.9	88.9	94.6	protein kinase family protein	gbpln	Arabidopsis thaliana	AT4G14480.1 | Symbols: | Protein kinase superfamily protein | chr4:8330081-8331544 REVERSE LENGTH=487	478	487	0	101.9	88.9	94.6
Rsa1.0_01626.1.g28524.t1	ref|XP_002882841.1| hypothetical protein ARALYDRAFT_478773 [Arabidopsis lyrata subsp. lyrata] gi|297328681|gb|EFH59100.1| hypothetical protein ARALYDRAFT_478773 [Arabidopsis lyrata subsp. lyrata]	249	245	1.00E-109	98.4	87.1	92.8	hypothetical protein ARALYDRAFT_478773	gbpln	Arabidopsis lyrata	AT3G13740.1 | Symbols: | Ribonuclease III family protein | chr3:4504310-4505937 FORWARD LENGTH=247	249	247	1.00E-110	99.2	86.3	90.8
Rsa1.0_01626.1.g28525.t1	dbj|BAJ86270.1| predicted protein [Hordeum vulgare subsp. vulgare]	188	300	2.00E-35	159.6	44.7	50.0	predicted protein	gbpln	Hordeum vulgare	AT5G62700.1 | Symbols: TUB3 | tubulin beta chain 3 | chr5:25184501-25186426 FORWARD LENGTH=450	188	450	7.00E-38	239.4	37.8	38.8
Rsa1.0_01626.1.g28526.t1	ref|XP_002882842.1| hypothetical protein ARALYDRAFT_897617 [Arabidopsis lyrata subsp. lyrata] gi|297328682|gb|EFH59101.1| hypothetical protein ARALYDRAFT_897617 [Arabidopsis lyrata subsp. lyrata]	840	847	0	100.8	96.1	98.1	hypothetical protein ARALYDRAFT_897617	gbpln	Arabidopsis lyrata	AT3G13750.1 | Symbols: BGAL1 | beta galactosidase 1 | chr3:4511192-4515756 FORWARD LENGTH=847	840	847	0	100.8	95.8	98.1
Rsa1.0_01626.1.g28527.t1	ref|XP_002882843.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297328683|gb|EFH59102.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	583	627	0	107.5	88.5	95.0	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT3G13770.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:4519647-4521533 FORWARD LENGTH=628	583	628	0	107.7	88.2	94.7
Rsa1.0_01626.1.g28528.t1	gb|EOA30083.1| hypothetical protein CARUB_v10013189mg [Capsella rubella]	643	641	0	99.7	98.0	98.6	hypothetical protein CARUB_v10013189mg	gbpln	Capsella rubella	AT3G13772.1 | Symbols: TMN7, AtTMN7 | transmembrane nine 7 | chr3:4521712-4524394 REVERSE LENGTH=641	643	641	0	99.7	96.9	97.5
Rsa1.0_01626.1.g28529.t1	ref|XP_002882845.1| hypothetical protein ARALYDRAFT_897622 [Arabidopsis lyrata subsp. lyrata] gi|297328685|gb|EFH59104.1| hypothetical protein ARALYDRAFT_897622 [Arabidopsis lyrata subsp. lyrata]	306	288	2.00E-94	94.1	67.3	72.5	hypothetical protein ARALYDRAFT_897622	gbpln	Arabidopsis lyrata	AT3G13780.1 | Symbols: | SMAD/FHA domain-containing protein | chr3:4525108-4526214 FORWARD LENGTH=309	306	309	7.00E-87	101.0	65.7	72.9

<table>
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<tr><td>Rsa1.0_01626.1.g28531.t1</td><td>gb|EOA30217.1| hypothetical protein CARUB_v10013339mg [Capsella rubella]</td><td>569</td><td>570</td><td>0</td><td>100.2</td><td>80.8</td><td>89.5</td><td>hypothetical protein CARUB_v10013339mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G13784.1 | Symbols: AtcwINV5, CWINV5 | cell wall invertase 5 | chr3:4528529-4530669 REVERSE LENGTH=569</td><td>569</td><td>569</td><td>0</td><td>100.0</td><td>80.1</td><td>89.5</td></tr>
<tr><td>Rsa1.0_01626.1.g28532.t1</td><td>ref|XP_002884989.1| beta-fructofuranosidase [Arabidopsis lyrata subsp. lyrata] gi|297330829|gb|EFH61248.1| beta-fructofuranosidase [Arabidopsis lyrata subsp. lyrata]</td><td>580</td><td>581</td><td>0</td><td>100.2</td><td>93.1</td><td>96.4</td><td>beta-fructofuranosidase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G13790.2 | Symbols: ATBFRUCT1 | Glycosyl hydrolases family 32 protein | chr3:4533084-4535831 REVERSE LENGTH=581</td><td>580</td><td>581</td><td>0</td><td>100.2</td><td>93.3</td><td>96.4</td></tr>
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<tr><td>Rsa1.0_01627.1.g28534.t1</td><td>pir||T05892 hypothetical protein F6H11.110 - Arabidopsis thaliana gi|2827709|emb|CAA16682.1| predicted protein [Arabidopsis thaliana]</td><td>457</td><td>1421</td><td>6.00E-33</td><td>310.9</td><td>20.4</td><td>24.9</td><td>hypothetical protein F6H11.110 - Arabidopsis thaliana gi|2827709|emb|CAA16682.1| predicted protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G65770.3 | Symbols: LINC4 | little nuclei4 | chr5:26311587-26315610 FORWARD LENGTH=1010</td><td>457</td><td>1010</td><td>2.00E-35</td><td>221.0</td><td>20.4</td><td>24.9</td></tr>
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<tr><td>Rsa1.0_01627.1.g28537.t1</td><td>ref|XP_002308618.1| predicted protein [Populus trichocarpa] gi|222854594|gb|EEE92141.1| predicted protein [Populus trichocarpa]</td><td>97</td><td>449</td><td>1.00E-19</td><td>462.9</td><td>51.5</td><td>56.7</td><td>predicted protein</td><td>gbpln</td><td>Populus trichocarpa</td><td>AT5G11520.1 | Symbols: ASP3, YLS4 | aspartate aminotransferase 3 | chr5:3685257-3687721 REVERSE LENGTH=449</td><td>97</td><td>449</td><td>8.00E-22</td><td>462.9</td><td>53.6</td><td>59.8</td></tr>
<tr><td>Rsa1.0_01627.1.g28538.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1325</td><td>1307</td><td>0</td><td>98.6</td><td>58.0</td><td>72.7</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1325</td><td>1262</td><td>5.00E-98</td><td>95.2</td><td>14.3</td><td>22.2</td></tr>
<tr><td>Rsa1.0_01627.1.g28539.t1</td><td>emb|CAN60947.1| hypothetical protein VITISV_015758 [Vitis vinifera]</td><td>161</td><td>1306</td><td>2.00E-64</td><td>811.2</td><td>70.2</td><td>83.9</td><td>hypothetical protein VITISV_015758</td><td>gbpln</td><td>Vitis vinifera</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>161</td><td>1262</td><td>3.00E-16</td><td>783.9</td><td>28.0</td><td>39.8</td></tr>
<tr><td>Rsa1.0_01627.1.g28540.t1</td><td>gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1467</td><td>1499</td><td>0</td><td>102.2</td><td>61.3</td><td>75.6</td><td>gypsy/Ty-3 retroelement polyprotein; 69905-74404</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158</td><td>1467</td><td>158</td><td>3.00E-11</td><td>10.8</td><td>2.2</td><td>2.8</td></tr>
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<tr><td>Rsa1.0_01628.1.g28542.t1</td><td>gb|EOA12952.1| hypothetical protein CARUB_v10025934mg [Capsella rubella]</td><td>503</td><td>758</td><td>0</td><td>150.7</td><td>73.4</td><td>78.9</td><td>hypothetical protein CARUB_v10025934mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719</td><td>503</td><td>719</td><td>2.00E-26</td><td>142.9</td><td>21.3</td><td>34.6</td></tr>
<tr><td>Rsa1.0_01628.1.g28543.t1</td><td>ref|XP_002878847.1| low-molecular-weight cysteine-rich 81 [Arabidopsis lyrata subsp. lyrata] gi|297324686|gb|EFH55106.1| low-molecular-weight cysteine-rich 81 [Arabidopsis lyrata subsp. lyrata]</td><td>80</td><td>79</td><td>1.00E-20</td><td>98.8</td><td>65.0</td><td>72.5</td><td>low-molecular-weight cysteine-rich 81</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G25295.1 | Symbols: LCR81 | low-molecular-weight cysteine-rich 81 | chr2:10769933-10770421 FORWARD LENGTH=79</td><td>80</td><td>79</td><td>1.00E-22</td><td>98.8</td><td>63.8</td><td>75.0</td></tr>
<tr><td>Rsa1.0_01628.1.g28544.t1</td><td>ref|XP_002863930.1| hypothetical protein ARALYDRAFT_917829 [Arabidopsis lyrata subsp. lyrata] gi|297309765|gb|EFH40189.1| hypothetical protein ARALYDRAFT_917829 [Arabidopsis lyrata subsp. lyrata]</td><td>1116</td><td>1133</td><td>0</td><td>101.5</td><td>84.1</td><td>91.9</td><td>hypothetical protein ARALYDRAFT_917829</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G48940.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase family protein | chr5:19839785-19843744 FORWARD LENGTH=1135</td><td>1116</td><td>1135</td><td>0</td><td>101.7</td><td>83.7</td><td>91.2</td></tr>
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<tr><td>Rsa1.0_01628.1.g28546.t1</td><td>sp|P0C8S1.1|RP8L2_ARATH RecName: Full=Probable disease resistance RPP8-like protein 2</td><td>905</td><td>906</td><td>0</td><td>100.1</td><td>64.5</td><td>77.3</td><td>RecName: Full=Probable disease resistance RPP8-like protein 2</td><td>----</td><td>----</td><td>AT5G43470.2 | Symbols: RPP8, HRT, RCY1 | Disease resistance protein (CC-NBS-LRR class) family | chr5:17463130-17466658 REVERSE LENGTH=908</td><td>905</td><td>908</td><td>0</td><td>100.3</td><td>61.7</td><td>77.2</td></tr>
<tr><td>Rsa1.0_01628.1.g28547.t1</td><td>gb|EOA14875.1| hypothetical protein CARUB_v10028201mg [Capsella rubella]</td><td>652</td><td>646</td><td>0</td><td>99.1</td><td>82.5</td><td>93.1</td><td>hypothetical protein CARUB_v10028201mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G48910.1 | Symbols: LPA66 | Pentatricopeptide repeat (PPR) superfamily protein | chr5:19832969-19834909 REVERSE LENGTH=646</td><td>652</td><td>646</td><td>0</td><td>99.1</td><td>81.3</td><td>90.2</td></tr>
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Rsa1.0_01628.1.g28548.t1	ref|NP_199700.1| C2H2-like zinc finger protein [Arabidopsis thaliana] gi|9758888|dbj|BAB09442.1| unnamed protein product [Arabidopsis thaliana] gi|332008356|gb|AED95739.1| C2H2-like zinc finger protein [Arabidopsis thaliana]	170	173	8.00E-65	101.8	77.6	85.9	C2H2-like zinc finger protein	gbpln	Arabidopsis thaliana	AT5G48890.1 | Symbols: | C2H2-like zinc finger protein | chr5:19820353-19820874 FORWARD LENGTH=173	170	173	3.00E-67	101.8	77.6	85.9
Rsa1.0_01628.1.g28549.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	819	1486	0	181.4	57.8	70.9	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	819	237	6.00E-25	28.9	7.8	12.7
Rsa1.0_01628.1.g28550.t1	ref|XP_002865684.1| male sterility MS5 family protein [Arabidopsis lyrata subsp. lyrata] gi|297311519|gb|EFH41943.1| male sterility MS5 family protein [Arabidopsis lyrata subsp. lyrata]	306	306	1.00E-158	100.0	91.2	96.7	male sterility MS5 family protein	gbpln	Arabidopsis lyrata	AT5G48850.1 | Symbols: ATSDI1 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:19805576-19807699 REVERSE LENGTH=306	306	306	1.00E-160	100.0	91.2	96.4
Rsa1.0_01628.1.g28551.t1	ref|XP_002863331.1| hypothetical protein ARALYDRAFT_916628 [Arabidopsis lyrata subsp. lyrata] gi|297309166|gb|EFH39590.1| hypothetical protein ARALYDRAFT_916628 [Arabidopsis lyrata subsp. lyrata]	159	243	1.00E-10	152.8	30.2	43.4	hypothetical protein ARALYDRAFT_916628	gbpln	Arabidopsis lyrata	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	159	264	1.00E-10	166.0	29.6	41.5
Rsa1.0_01629.1.g28552.t1	gb|EOA37530.1| hypothetical protein CARUB_v10011737mg [Capsella rubella]	459	512	1.00E-162	111.5	65.1	79.3	hypothetical protein CARUB_v10011737mg	gbpln	Capsella rubella	AT1G12270.1 | Symbols: Hop1 | stress-inducible protein, putative | chr1:4172105-4174575 FORWARD LENGTH=572	459	572	1.00E-135	124.6	50.3	59.3
Rsa1.0_01629.1.g28553.t1	ref|NP_172690.1| NAC domain-containing protein 7 [Arabidopsis thaliana] gi|238065075|sp|Q9FWX2.2|NAC7_ARATH RecName: Full=NAC domain-containing protein 7; Short=ANAC007; AltName: Full=Protein EMBRYO DEFECTIVE 2749; AltName: Full=Protein VASCULAR RELATED NAC-DOMAIN 4 gi|119935909|gb|ABM06031.1| At1g12260 [Arabidopsis thaliana] gi|332190738|gb|AEE28859.1| NAC domain-containing protein 7 [Arabidopsis thaliana]	392	395	0	100.8	87.0	91.1	NAC domain-containing protein 7	gbpln	Arabidopsis thaliana	AT1G12260.1 | Symbols: VND4, EMB2749, ANAC007, NAC007 | NAC 007 | chr1:4163058-4164486 REVERSE LENGTH=395	392	395	0	100.8	87.0	91.1
Rsa1.0_01629.1.g28554.t1	ref|XP_002889925.1| hypothetical protein ARALYDRAFT_471375 [Arabidopsis lyrata subsp. lyrata] gi|297335767|gb|EFH66184.1| hypothetical protein ARALYDRAFT_471375 [Arabidopsis lyrata subsp. lyrata]	280	280	1.00E-127	100.0	88.2	91.8	hypothetical protein ARALYDRAFT_471375	gbpln	Arabidopsis lyrata	AT1G12250.1 | Symbols: | Pentapeptide repeat-containing protein | chr1:4159287-4161269 FORWARD LENGTH=280	280	280	1.00E-129	100.0	87.9	91.1
Rsa1.0_01629.1.g28555.t1	gb|AAG36942.1|AF274298_1 acid invertase [Brassica oleracea]	660	663	0	100.5	93.9	97.1	acid invertase	gbpln	Brassica oleracea	AT1G12240.1 | Symbols: ATBETAFRUCT4, VAC-INV | Glycosyl hydrolases family 32 protein | chr1:4153699-4157457 FORWARD LENGTH=664	660	664	0	100.6	87.6	93.3
Rsa1.0_01629.1.g28556.t4	gb|ACP30559.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1075	786	0	73.1	46.3	53.2	disease resistance protein	gbpln	Brassica rapa	AT4G10780.1 | Symbols: | LRR and NB-ARC domains-containing disease resistance protein | chr4:6634779-6637457 REVERSE LENGTH=892	1075	892	0	83.0	46.1	56.4
Rsa1.0_01629.1.g28557.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	396	1274	5.00E-57	321.7	33.1	51.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	396	303	1.00E-44	76.5	27.0	38.9
Rsa1.0_01629.1.g28558.t1	gb|EOA40340.1| hypothetical protein CARUB_v10009065mg [Capsella rubella]	334	464	1.00E-178	138.9	89.2	94.6	hypothetical protein CARUB_v10009065mg	gbpln	Capsella rubella	AT1G12200.1 | Symbols: | Flavin-binding monooxygenase family protein | chr1:4137627-4139835 FORWARD LENGTH=465	334	465	1.00E-177	139.2	88.9	93.4
Rsa1.0_01629.1.g28559.t1	ref|XP_002892679.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297338521|gb|EFH68938.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	322	370	9.00E-90	114.9	55.3	68.9	F-box family protein	gbpln	Arabidopsis lyrata	AT1G12190.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:4132967-4134094 REVERSE LENGTH=375	322	375	7.00E-92	116.5	55.6	67.4
Rsa1.0_01630.1.g28560.t1	gb|EAY92309.1| hypothetical protein OsI_14032 [Oryza sativa Indica Group]	183	354	5.00E-87	193.4	84.7	85.8	hypothetical protein OsI_14032	gbpln	Oryza sativa	AT1G10630.1 | Symbols: ATARFA1F, ARFA1F | ADP-ribosylation factor A1F | chr1:3513189-3514230 REVERSE LENGTH=181	183	181	8.00E-89	98.9	85.2	85.2

<table>
<tr><td>Rsa1.0_01630.1.g28561.t2</td><td>gb|EOA38890.1| hypothetical protein CARUB_v10011268mg [Capsella rubella]</td><td>457</td><td>1077</td><td>0</td><td>235.7</td><td>86.0</td><td>91.2</td><td>hypothetical protein CARUB_v10011268mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G23460.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:8327382-8329622 FORWARD LENGTH=460</td><td>457</td><td>460</td><td>0</td><td>100.7</td><td>85.6</td><td>89.9</td></tr>
<tr><td>Rsa1.0_01630.1.g28562.t1</td><td>gb|EOA38498.1| hypothetical protein CARUB_v10010266mg [Capsella rubella]</td><td>219</td><td>217</td><td>1.00E-108</td><td>99.1</td><td>88.1</td><td>93.2</td><td>hypothetical protein CARUB_v10010266mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G23440.1 | Symbols: | Peptidase C15, pyroglutamyl peptidase I-like | chr1:8321940-8324019 FORWARD LENGTH=217</td><td>219</td><td>217</td><td>1.00E-110</td><td>99.1</td><td>88.1</td><td>91.8</td></tr>
<tr><td>Rsa1.0_01630.1.g28563.t2</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>1032</td><td>1142</td><td>1.00E-176</td><td>110.7</td><td>32.0</td><td>44.0</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626</td><td>1032</td><td>626</td><td>7.00E-38</td><td>60.7</td><td>10.8</td><td>17.9</td></tr>
<tr><td>Rsa1.0_01630.1.g28564.t1</td><td>gb|AAF79582.1|AC007945_2 F28C11.6 [Arabidopsis thaliana] gi|9295696|gb|AAF87002.1|AC005292_11 F26F24.29 [Arabidopsis thaliana]</td><td>230</td><td>262</td><td>1.00E-113</td><td>113.9</td><td>91.3</td><td>93.9</td><td>F28C11.6</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G23420.1 | Symbols: INO | Plant-specific transcription factor YABBY family protein | chr1:8317423-8319104 FORWARD LENGTH=231</td><td>230</td><td>231</td><td>1.00E-115</td><td>100.4</td><td>91.3</td><td>93.9</td></tr>
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<tr><td>Rsa1.0_01630.1.g28566.t1</td><td>ref|XP_002893281.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] gi|297339123|gb|EFH69540.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]</td><td>327</td><td>161</td><td>3.00E-25</td><td>49.2</td><td>18.0</td><td>19.9</td><td>invertase/pectin methylesterase inhibitor family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G23350.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:8293696-8294175 REVERSE LENGTH=159</td><td>327</td><td>159</td><td>1.00E-26</td><td>48.6</td><td>17.1</td><td>19.9</td></tr>
<tr><td>Rsa1.0_01631.1.g28567.t1</td><td>ref|NP_568530.1| EXS (ERD1/XPR1/SYG1) domain protein [Arabidopsis thaliana] gi|17979075|gb|AAL49805.1| unknown protein [Arabidopsis thaliana] gi|21554193|gb|AAM63272.1| unknown [Arabidopsis thaliana] gi|25055013|gb|AAN71970.1| unknown protein [Arabidopsis thaliana] gi|332006626|gb|AED94009.1| EXS (ERD1/XPR1/SYG1) domain protein [Arabidopsis thaliana]</td><td>451</td><td>457</td><td>0</td><td>101.3</td><td>86.9</td><td>90.9</td><td>EXS (ERD1/XPR1/SYG1) domain protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G35730.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr5:13893941-13896821 FORWARD LENGTH=457</td><td>451</td><td>457</td><td>0</td><td>101.3</td><td>86.9</td><td>90.9</td></tr>
<tr><td>Rsa1.0_01631.1.g28568.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01631.1.g28569.t1</td><td>ref|XP_002868433.1| hypothetical protein ARALYDRAFT_915700 [Arabidopsis lyrata subsp. lyrata] gi|297314269|gb|EFH44692.1| hypothetical protein ARALYDRAFT_915700 [Arabidopsis lyrata subsp. lyrata]</td><td>99</td><td>100</td><td>1.00E-38</td><td>101.0</td><td>80.8</td><td>87.9</td><td>hypothetical protein ARALYDRAFT_915700</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G35732.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G04795.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:13897961-13898263 FORWARD LENGTH=100</td><td>99</td><td>100</td><td>3.00E-41</td><td>101.0</td><td>79.8</td><td>88.9</td></tr>
<tr><td>Rsa1.0_01631.1.g28570.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01631.1.g28571.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01631.1.g28572.t2</td><td>dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>737</td><td>1864</td><td>2.00E-54</td><td>252.9</td><td>13.6</td><td>17.5</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01632.1.g28573.t1</td><td>ref|XP_002864303.1| calcium ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297310138|gb|EFH40562.1| calcium ion binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>520</td><td>437</td><td>0</td><td>84.0</td><td>70.6</td><td>73.5</td><td>calcium ion binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G54130.2 | Symbols: | Calcium-binding endonuclease/exonuclease/phosphatase family | chr5:21962900-21965279 FORWARD LENGTH=436</td><td>520</td><td>436</td><td>0</td><td>83.8</td><td>70.2</td><td>73.3</td></tr>
<tr><td>Rsa1.0_01632.1.g28574.t1</td><td>dbj|BAJ34304.1| unnamed protein product [Thellungiella halophila]</td><td>266</td><td>271</td><td>1.00E-113</td><td>101.9</td><td>85.0</td><td>92.1</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G54110.1 | Symbols: ATMAMI, MAMI | membrane-associated mannitol-induced | chr5:21958356-21960367 FORWARD LENGTH=266</td><td>266</td><td>266</td><td>1.00E-113</td><td>100.0</td><td>82.7</td><td>90.2</td></tr>
<tr><td>Rsa1.0_01632.1.g28575.t1</td><td>gb|EOA23245.1| hypothetical protein CARUB_v10017305mg [Capsella rubella]</td><td>92</td><td>429</td><td>1.00E-23</td><td>466.3</td><td>60.9</td><td>66.3</td><td>hypothetical protein CARUB_v10017305mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G51280.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:19037229-19038781 FORWARD LENGTH=430</td><td>92</td><td>430</td><td>5.00E-26</td><td>467.4</td><td>60.9</td><td>66.3</td></tr>
<tr><td>Rsa1.0_01632.1.g28576.t1</td><td>ref|XP_002866018.1| band 7 family protein [Arabidopsis lyrata subsp. lyrata] gi|297311853|gb|EFH42277.1| band 7 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>401</td><td>404</td><td>1.00E-160</td><td>100.7</td><td>73.1</td><td>82.0</td><td>band 7 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G27585.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr4:13766984-13769832 REVERSE LENGTH=411</td><td>401</td><td>411</td><td>1.00E-159</td><td>102.5</td><td>72.3</td><td>80.5</td></tr>
<tr><td>Rsa1.0_01632.1.g28577.t2</td><td>gb|EOA16742.1| hypothetical protein CARUB_v10004943mg [Capsella rubella]</td><td>397</td><td>408</td><td>1.00E-160</td><td>102.8</td><td>73.0</td><td>80.1</td><td>hypothetical protein CARUB_v10004943mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G27585.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr4:13766984-13769832 REVERSE LENGTH=411</td><td>397</td><td>411</td><td>1.00E-159</td><td>103.5</td><td>71.5</td><td>79.1</td></tr>
<tr><td>Rsa1.0_01632.1.g28578.t1</td><td>gb|EOA16742.1| hypothetical protein CARUB_v10004943mg [Capsella rubella]</td><td>156</td><td>408</td><td>4.00E-49</td><td>261.5</td><td>66.0</td><td>72.4</td><td>hypothetical protein CARUB_v10004943mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G27585.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr4:13766984-13769832 REVERSE LENGTH=411</td><td>156</td><td>411</td><td>4.00E-50</td><td>263.5</td><td>64.7</td><td>71.8</td></tr>
</table>

Rsa1.0_01632.1.g28579.t1	gb|EOA14373.1| hypothetical protein CARUB_v10027559mg [Capsella rubella]	116	130	1.00E−30	112.1	81.0	84.5	hypothetical protein CARUB_v10027559mg	gbpln	Capsella rubella	AT5G54095.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N−terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27580.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:21952868−21953369 REVERSE LENGTH=135	116	135	3.00E−18	116.4	69.8	74.1
Rsa1.0_01632.1.g28580.t1	ref|NP_200220.2| DNA mismatch repair protein MutS, type 2 [Arabidopsis thaliana] gi|332009066|gb|AED96449.1| DNA mismatch repair protein MutS, type 2 [Arabidopsis thaliana]	819	796	0	97.2	81.0	88.6	DNA mismatch repair protein MutS, type 2	gbpln	Arabidopsis thaliana	AT5G54090.1 | Symbols: | DNA mismatch repair protein MutS, type 2 | chr5:21948283−21952550 REVERSE LENGTH=796	819	796	0	97.2	81.0	88.6
Rsa1.0_01632.1.g28581.t1	gb|AAM65958.1| homogentisate 1,2−dioxygenase [Arabidopsis thaliana]	459	461	0	100.4	92.2	95.0	homogentisate 1,2−dioxygenase	gbpln	Arabidopsis thaliana	AT5G54080.2 | Symbols: HGO | homogentisate 1,2−dioxygenase | chr5:21945920−21948070 FORWARD LENGTH=461	459	461	0	100.4	91.1	94.6
Rsa1.0_01632.1.g28582.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01632.1.g28583.t1	ref|NP_200198.1| early nodulin−like protein 1 [Arabidopsis thaliana] gi|10177249|dbj|BAB10717.1| unnamed protein product [Arabidopsis thaliana] gi|109946411|gb|ABG48384.1| At5g53870 [Arabidopsis thaliana] gi|332009038|gb|AED96421.1| early nodulin−like protein 1 [Arabidopsis thaliana]	384	370	2.00E−74	96.4	52.3	65.4	early nodulin−like protein 1	gbpln	Arabidopsis thaliana	AT5G53870.1 | Symbols: ENODL1, AtENODL1 | early nodulin−like protein 1 | chr5:21870033−21871228 REVERSE LENGTH=370	384	370	5.00E−77	96.4	52.3	65.4
Rsa1.0_01632.1.g28584.t1	ref|XP_002865999.1| hypothetical protein ARALYDRAFT_331733 [Arabidopsis lyrata subsp. lyrata] gi|297311834|gb|EFH42258.1| hypothetical protein ARALYDRAFT_331733 [Arabidopsis lyrata subsp. lyrata]	509	519	0	102.0	93.3	97.4	hypothetical protein ARALYDRAFT_331733	gbpln	Arabidopsis lyrata	AT5G53850.2 | Symbols: | haloacid dehalogenase−like hydrolase family protein | chr5:21861155−21864817 REVERSE LENGTH=507	509	507	0	99.6	89.6	94.5
Rsa1.0_01632.1.g28585.t1	ref|XP_002864285.1| VQ motif−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297310120|gb|EFH40544.1| VQ motif−containing protein [Arabidopsis lyrata subsp. lyrata]	226	240	4.00E−98	106.2	88.9	93.8	VQ motif−containing protein	gbpln	Arabidopsis lyrata	AT5G53830.1 | Symbols: | VQ motif−containing protein | chr5:21857057−21857788 FORWARD LENGTH=243	226	243	1.00E−100	107.5	88.1	92.5
Rsa1.0_01632.1.g28586.t1	gb|AAC98699.1| pollen coat protein homolog [Brassica rapa subsp. oleifera]	65	67	3.00E−23	103.1	96.9	98.5	pollen coat protein homolog	gbpln	Brassica rapa	AT5G53820.1 | Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr5:21853475−21853866 FORWARD LENGTH=67	65	67	1.00E−23	103.1	87.7	95.4
Rsa1.0_01632.1.g28587.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01632.1.g28588.t1	ref|XP_002864281.1| hypothetical protein ARALYDRAFT_357630 [Arabidopsis lyrata subsp. lyrata] gi|297310116|gb|EFH40540.1| hypothetical protein ARALYDRAFT_357630 [Arabidopsis lyrata subsp. lyrata]	188	184	6.00E−26	97.9	32.4	37.8	hypothetical protein ARALYDRAFT_357630	gbpln	Arabidopsis lyrata	AT4G01540.2 | Symbols: ANAC068, NTM1 | NAC with transmembrane motif1 | chr4:670483−672629 REVERSE LENGTH=423	188	423	9.00E−20	225.0	28.2	38.8
Rsa1.0_01632.1.g28589.t1	ref|XP_002864273.1| hypothetical protein ARALYDRAFT_495454 [Arabidopsis lyrata subsp. lyrata] gi|297310108|gb|EFH40532.1| hypothetical protein ARALYDRAFT_495454 [Arabidopsis lyrata subsp. lyrata]	414	530	0	128.0	80.7	86.0	hypothetical protein ARALYDRAFT_495454	gbpln	Arabidopsis lyrata	AT5G53770.1 | Symbols: | Nucleotidyltransferase family protein | chr5:21826733−21829858 FORWARD LENGTH=530	414	530	0	128.0	79.7	85.5
Rsa1.0_01633.1.g28590.t2	gb|AAZ66937.1| 117M18_18 [Brassica rapa]	442	249	1.00E−134	56.3	54.3	55.0	117M18_18	gbpln	Brassica rapa	AT5G10360.1 | Symbols: EMB3010, RPS6B | Ribosomal protein S6e | chr5:3258734−3260142 REVERSE LENGTH=249	442	249	1.00E−132	56.3	52.7	53.8
Rsa1.0_01633.1.g28591.t1	sp|O65098.1|REM1_BRAOB RecName: Full=B3 domain−containing protein REM1; AltName: Full=Protein REPRODUCTIVE MERISTEM 1; Short=BoREM1 gi|3170424|gb|AAC18082.1| reproductive meristem gene 1 [Brassica oleracea var. botrytis]	504	497	1.00E−150	98.6	61.5	72.2	RecName: Full=B3 domain−containing protein REM1; AltName: Full=Protein REPRODUCTIVE MERISTEM 1; Short=BoREM1 gi|3170424|gb|AAC18082.1| reproductive meristem gene 1	gbpln	Brassica oleracea	AT4G31610.1 | Symbols: REM1, ATREM1 | Transcriptional factor B3 family protein | chr4:15317700−15319776 FORWARD LENGTH=517	504	517	1.00E−138	102.6	56.5	68.5

Rsa1.0_01633.1.g28592.t1	gb|EOA17002.1| hypothetical protein CARUB_v10005245mg [Capsella rubella]	324	323	1.00E-169	99.7	94.1	96.6	hypothetical protein CARUB_v10005245mg	gbpln	Capsella rubella	AT4G31600.1 | Symbols: | UDP-N-acetylglucosamine (UAA) transporter family | chr4:15315232-15316909 REVERSE LENGTH=323	324	323	1.00E-170	99.7	92.9	95.7
Rsa1.0_01633.1.g28593.t1	ref|XP_002867294.1| WRKY transcription factor 11 [Arabidopsis lyrata subsp. lyrata] gi|297313130|gb|EFH43553.1| WRKY transcription factor 11 [Arabidopsis lyrata subsp. lyrata]	332	335	1.00E-145	100.9	80.1	88.0	WRKY transcription factor 11	gbpln	Arabidopsis lyrata	AT4G31550.1 | Symbols: WRKY11, ATWRKY11 | WRKY DNA-binding protein 11 | chr4:15290065-15291458 REVERSE LENGTH=325	332	325	1.00E-141	97.9	78.6	85.2
Rsa1.0_01633.1.g28594.t1	ref|XP_002880609.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata] gi|297326448|gb|EFH56868.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata]	621	464	5.00E-84	74.7	29.0	38.3	hypothetical protein ARALYDRAFT_901029	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	621	456	6.00E-80	73.4	27.4	36.6
Rsa1.0_01633.1.g28595.t1	emb|CAN66566.1| hypothetical protein VITISV_018543 [Vitis vinifera]	136	287	1.00E-32	211.0	53.7	64.7	hypothetical protein VITISV_018543	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01633.1.g28596.t5	ref|XP_002880609.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata] gi|297326448|gb|EFH56868.1| hypothetical protein ARALYDRAFT_901029 [Arabidopsis lyrata subsp. lyrata]	346	464	6.00E-47	134.1	35.5	45.7	hypothetical protein ARALYDRAFT_901029	gbpln	Arabidopsis lyrata	AT3G18150.1 | Symbols: | RNI-like superfamily protein | chr3:6217929-6219500 FORWARD LENGTH=456	346	456	9.00E-49	131.8	35.3	46.0
Rsa1.0_01633.1.g28597.t1	gb|EOA15465.1| hypothetical protein CARUB_v10004281mg [Capsella rubella]	677	686	0	101.3	90.8	95.1	hypothetical protein CARUB_v10004281mg	gbpln	Capsella rubella	AT4G31540.1 | Symbols: ATEXO70G1, EXO70G1 | exocyst subunit exo70 family protein G1 | chr4:15284739-15286802 REVERSE LENGTH=687	677	687	0	101.5	90.5	95.1
Rsa1.0_01634.1.g28598.t1	ref|XP_002869061.1| hypothetical protein ARALYDRAFT_912790 [Arabidopsis lyrata subsp. lyrata] gi|297314897|gb|EFH45320.1| hypothetical protein ARALYDRAFT_912790 [Arabidopsis lyrata subsp. lyrata]	65	61	6.00E-22	93.8	87.7	92.3	hypothetical protein ARALYDRAFT_912790	gbpln	Arabidopsis lyrata	AT4G35783.1 | Symbols: RTFL6, DVL17 | ROTUNDIFOLIA like 6 | chr4:16952612-16952800 FORWARD LENGTH=62	65	62	3.00E-23	95.4	83.1	86.2
Rsa1.0_01634.1.g28599.t2	ref|XP_002867054.1| hypothetical protein ARALYDRAFT_912788 [Arabidopsis lyrata subsp. lyrata] gi|297312890|gb|EFH43313.1| hypothetical protein ARALYDRAFT_912788 [Arabidopsis lyrata subsp. lyrata]	240	160	2.00E-45	66.7	45.8	50.4	hypothetical protein ARALYDRAFT_912788	gbpln	Arabidopsis lyrata	AT4G35785.5 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:16953404-16955127 REVERSE LENGTH=244	240	244	3.00E-42	101.7	46.3	51.3
Rsa1.0_01634.1.g28600.t1	dbj|BAJ34379.1| unnamed protein product [Thellungiella halophila]	873	860	0	98.5	91.6	95.6	unnamed protein product	----	----	AT4G35790.1 | Symbols: ATPLDDELTA, PLDDELTA | phospholipase D delta | chr4:16955774-16959875 REVERSE LENGTH=868	873	868	0	99.4	88.0	95.2
Rsa1.0_01634.1.g28601.t1	gb|EOA15888.1| hypothetical protein CARUB_v10003976mg [Capsella rubella]	1882	1838	0	97.7	89.6	92.2	hypothetical protein CARUB_v10003976mg	gbpln	Capsella rubella	AT5G60040.1 | Symbols: NRPC1 | nuclear RNA polymerase C1 | chr5:24173590-24183269 FORWARD LENGTH=1376	1882	1376	1.00E-163	73.1	19.2	27.4
Rsa1.0_01634.1.g28602.t1	ref|XP_002869059.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297314895|gb|EFH45318.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	263	290	1.00E-120	110.3	81.0	88.6	oxidoreductase	gbpln	Arabidopsis lyrata	AT4G35810.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:16968921-16970358 FORWARD LENGTH=290	263	290	1.00E-119	110.3	75.3	84.0
Rsa1.0_01634.1.g28603.t1	ref|NP_195307.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] gi|3805848|emb|CAA21468.1| putative protein [Arabidopsis thaliana] gi|7270534|emb|CAB81491.1| putative protein [Arabidopsis thaliana] gi|332661175|gb|AEE86575.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	287	272	1.00E-87	94.8	58.9	70.7	oxidoreductase, 2OG-Fe(II) oxygenase family protein	gbpln	Arabidopsis thaliana	AT4G35820.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:16971221-16972429 FORWARD LENGTH=272	287	272	3.00E-90	94.8	58.9	70.7
Rsa1.0_01634.1.g28604.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	106	478	4.00E-15	450.9	45.3	59.4	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	106	746	1.00E-11	703.8	28.3	38.7
Rsa1.0_01634.1.g28605.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01634.1.g28606.t1	ref|NP_195307.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] gi|3805848|emb|CAA21468.1| putative protein [Arabidopsis thaliana] gi|7270534|emb|CAB81491.1| putative protein [Arabidopsis thaliana] gi|332661175|gb|AEE86575.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	294	272	8.00E-87	92.5	58.2	69.7	oxidoreductase, 2OG-Fe(II) oxygenase family protein	gbpln	Arabidopsis thaliana	AT4G35820.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:16971221-16972429 FORWARD LENGTH=272	294	272	2.00E-89	92.5	58.2	69.7
Rsa1.0_01634.1.g28607.t1	ref|NP_195308.1| aconitate hydratase 1 [Arabidopsis thaliana] gi|13124706|sp|Q42560.2|ACO1_ARATH RecName: Full=Aconitate hydratase 1; Short=Aconitase 1; AltName: Full=Citrate hydro-lyase 1 gi|3805849|emb|CAA21469.1| cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana] gi|7270535|emb|CAB81492.1| cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana] gi|17065392|gb|AAL32850.1| Unknown protein [Arabidopsis thaliana] gi|332661176|gb|AEE86576.1| aconitate hydratase 1 [Arabidopsis thaliana]	898	898	0	100.0	97.6	99.2	aconitate hydratase 1	gbpln	Arabidopsis thaliana	AT4G35830.1 | Symbols: ACO1 | aconitase 1 | chr4:16973007-16977949 REVERSE LENGTH=898	898	898	0	100.0	97.6	99.2
Rsa1.0_01634.1.g28608.t1	ref|XP_002869057.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297314893|gb|EFH45316.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	238	236	1.00E-123	99.2	91.2	95.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G35840.1 | Symbols: | RING/U-box superfamily protein | chr4:16981083-16982266 FORWARD LENGTH=236	238	236	1.00E-125	99.2	89.9	95.4
Rsa1.0_01634.1.g28609.t1	gb|EOA16634.1| hypothetical protein CARUB_v10004808mg [Capsella rubella]	453	444	0	98.0	85.0	92.7	hypothetical protein CARUB_v10004808mg	gbpln	Capsella rubella	AT4G35850.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:16983638-16986681 FORWARD LENGTH=444	453	444	0	98.0	85.0	92.7
Rsa1.0_01634.1.g28610.t1	gb|EOA17424.1| hypothetical protein CARUB_v10005728mg [Capsella rubella]	211	211	1.00E-119	100.0	98.1	99.1	hypothetical protein CARUB_v10005728mg	gbpln	Capsella rubella	AT4G35860.1 | Symbols: ATRABB1B, ATGB2, ATRAB2C, GB2 | GTP-binding 2 | chr4:16987118-16988839 REVERSE LENGTH=211	211	211	1.00E-120	100.0	97.2	98.6
Rsa1.0_01635.1.g28611.t2	ref|NP_564698.1| chloride channel protein CLC-f [Arabidopsis thaliana] gi|41688504|sp|Q8RXR2.2|CLCF_ARATH RecName: Full=Chloride channel protein CLC-f; Short=AtCLC-f; AltName: Full=CBS domain-containing protein CBSCLC1 gi|14039802|gb|AAK53391.1|AF366368_1 CLC-f chloride channel protein [Arabidopsis thaliana] gi|13619402|emb|CAC36386.1| hypothetical protein [Arabidopsis thaliana] gi|332195154|gb|AEE33275.1| chloride channel protein CLC-f [Arabidopsis thaliana]	789	781	0	99.0	86.7	91.9	chloride channel protein CLC-f	gbpln	Arabidopsis thaliana	AT1G55620.2 | Symbols: CLC-F, ATCLC-F | chloride channel F | chr1:20787338-20790990 REVERSE LENGTH=781	789	781	0	99.0	86.7	91.9
Rsa1.0_01635.1.g28612.t1	dbj|BAB86292.1| nucleoside diphosphate kinase 1 [Brassica rapa] gi|19744165|dbj|BAB86841.1| NDPK I [Brassica rapa]	148	148	6.00E-78	100.0	94.6	98.0	nucleoside diphosphate kinase 1	gbpln	Brassica rapa	AT4G09320.1 | Symbols: NDPK1 | Nucleoside diphosphate kinase family protein | chr4:5923424-5924366 FORWARD LENGTH=169	148	169	9.00E-76	114.2	87.2	95.9
Rsa1.0_01635.1.g28613.t1	gb|EOA39113.1| hypothetical protein CARUB_v10011889mg [Capsella rubella]	162	161	1.00E-77	99.4	93.2	95.1	hypothetical protein CARUB_v10011889mg	gbpln	Capsella rubella	AT1G55670.1 | Symbols: PSAG | photosystem I subunit G | chr1:20802874-20803356 REVERSE LENGTH=160	162	160	1.00E-76	98.8	90.7	93.2
Rsa1.0_01635.1.g28614.t2	ref|NP_175965.2| sec.4-like phosphatidylinositol transfer protein [Arabidopsis thaliana] gi|332195164|gb|AEE33285.1| sec.4-like phosphatidylinositol transfer protein [Arabidopsis thaliana]	1094	621	0	56.8	46.5	50.7	sec.4-like phosphatidylinositol transfer protein	gbpln	Arabidopsis thaliana	AT1G55690.3 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:20808712-20811831 REVERSE LENGTH=621	1094	621	0	56.8	46.5	50.7

Rsa1.0_01635.1.g28615.t1	ref|NP_175969.2| vacuolar cation/proton exchanger 5 [Arabidopsis thaliana] gi|79320047|ref|NP_001031196.1| vacuolar cation/proton exchanger 5 [Arabidopsis thaliana] gi|75154113|sp|Q8L783.1|CAX5_ARATH RecName: Full=Vacuolar cation/proton exchanger 5; AltName: Full=Ca(2+)/H(+) antiporter CAX5; AltName: Full=Ca(2+)/H(+) exchanger 5; AltName: Full=Protein CATION EXCHANGER 5 gi|22531156|gb|AAM97082.1| H+/Ca2+ antiporter, putative [Arabidopsis thaliana] gi|30387539|gb|AAP31935.1| At1g55730 [Arabidopsis thaliana] gi|222424383|dbj|BAH20147.1| AT1G55730 [Arabidopsis thaliana] gi|332195169|gb|AEE33290.1| vacuolar cation/proton exchanger 5 [Arabidopsis thaliana] gi|332195170|gb|AEE33291.1| vacuolar cation/proton exchanger 5 [Arabidopsis thaliana]	411	441	0	107.3	86.1	92.7	vacuolar cation/proton exchanger 5	gbpln	Arabidopsis thaliana	AT1G55730.2 | Symbols: ATCAX5, CAX5 | cation exchanger 5 | chr1:20831387-20833941 REVERSE LENGTH=441	411	441	0	107.3	86.1	92.7
Rsa1.0_01635.1.g28616.t1	gb|EOA36445.1| hypothetical protein CARUB_v10011004mg [Capsella rubella]	687	761	0	110.8	90.8	96.5	hypothetical protein CARUB_v10011004mg	gbpln	Capsella rubella	AT1G55740.1 | Symbols: AtSIP1, SIP1 | seed imbibition 1 | chr1:20835507-20838707 REVERSE LENGTH=754	687	754	0	109.8	91.0	95.8
Rsa1.0_01636.1.g28617.t2	ref|XP_002872697.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318534|gb|EFH48956.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	388	659	0	169.8	81.7	91.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G04570.1 | Symbols: CRK40 | cysteine-rich RLK (RECEPTOR-like protein kinase) 40 | chr4:2290045-2292717 FORWARD LENGTH=654	388	654	0	168.6	82.5	90.5
Rsa1.0_01636.1.g28618.t1	ref|XP_002872699.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297318536|gb|EFH48958.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	304	629	1.00E-150	206.9	81.6	90.5	kinase family protein	gbpln	Arabidopsis lyrata	AT4G04570.1 | Symbols: CRK40 | cysteine-rich RLK (RECEPTOR-like protein kinase) 40 | chr4:2290045-2292717 FORWARD LENGTH=654	304	654	1.00E-152	215.1	81.6	90.1
Rsa1.0_01636.1.g28619.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01636.1.g28620.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1818	1270	0	69.9	38.0	49.0	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1818	575	2.00E-96	31.6	10.1	16.0
Rsa1.0_01636.1.g28621.t1	gb|EOA20576.1| hypothetical protein CARUB_v10000887mg [Capsella rubella]	501	468	0	93.4	79.8	84.0	hypothetical protein CARUB_v10000887mg	gbpln	Capsella rubella	AT4G04610.1 | Symbols: APR1, APR, PRH19, ATAPR1 | APS reductase 1 | chr4:2325069-2326718 FORWARD LENGTH=465	501	465	0	92.8	77.6	81.2
Rsa1.0_01636.1.g28622.t1	ref|XP_002874804.1| hypothetical protein ARALYDRAFT_911718 [Arabidopsis lyrata subsp. lyrata] gi|297320641|gb|EFH51063.1| hypothetical protein ARALYDRAFT_911718 [Arabidopsis lyrata subsp. lyrata]	172	171	5.00E-59	99.4	79.7	87.8	hypothetical protein ARALYDRAFT_911718	gbpln	Arabidopsis lyrata	AT4G04614.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:2327308-2327914 REVERSE LENGTH=176	172	176	2.00E-59	102.3	81.4	90.1
Rsa1.0_01636.1.g28623.t1	ref|XP_002884981.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297330821|gb|EFH61240.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	373	400	4.00E-88	107.2	53.1	67.8	F-box family protein	gbpln	Arabidopsis lyrata	AT3G13680.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:4477534-4478721 REVERSE LENGTH=395	373	395	7.00E-89	105.9	51.5	67.0
Rsa1.0_01636.1.g28624.t1	ref|NP_188019.1| F-box associated ubiquitination effector family protein [Arabidopsis thaliana] gi|332641936|gb|AEE75457.1| F-box associated ubiquitination effector family protein [Arabidopsis thaliana]	105	200	8.00E-16	190.5	45.7	58.1	F-box associated ubiquitination effector family protein	gbpln	Arabidopsis thaliana	AT3G14030.1 | Symbols: | F-box associated ubiquitination effector family protein | chr3:4646272-4646971 REVERSE LENGTH=200	105	200	1.00E-18	190.5	45.7	58.1
Rsa1.0_01636.1.g28625.t1	ref|XP_002874805.1| hypothetical protein ARALYDRAFT_911720 [Arabidopsis lyrata subsp. lyrata] gi|297320642|gb|EFH51064.1| hypothetical protein ARALYDRAFT_911720 [Arabidopsis lyrata subsp. lyrata]	120	120	8.00E-60	100.0	94.2	95.8	hypothetical protein ARALYDRAFT_911720	gbpln	Arabidopsis lyrata	AT4G21980.2 | Symbols: APG8A, ATG8A | Ubiquitin-like superfamily protein | chr4:11655868-11656809 FORWARD LENGTH=137	120	137	4.00E-61	114.2	91.7	95.0
Rsa1.0_01637.1.g28626.t1	gb|EOA33239.1| hypothetical protein CARUB_v10021571mg [Capsella rubella]	209	212	1.00E-33	101.4	39.7	50.2	hypothetical protein CARUB_v10021571mg	gbpln	Capsella rubella	AT1G77830.1 | Symbols: | RING/U-box superfamily protein | chr1:29267160-29267752 REVERSE LENGTH=185	209	185	3.00E-23	88.5	34.0	45.5
Rsa1.0_01637.1.g28627.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1700	1214	0	71.4	27.2	39.6	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1700	626	1.00E-79	36.8	9.4	14.8
Rsa1.0_01637.1.g28628.t1	gb|AFX60924.1| high-affinity sulfate transporter 1;2b [Brassica juncea]	652	652	0	100.0	98.5	99.2	high-affinity sulfate transporter 1;2b	gbpln	Brassica juncea	AT1G78000.2 | Symbols: SULTR1;2, SEL1 | sulfate transporter 1;2 | chr1:29329889-29332877 FORWARD LENGTH=653	652	653	0	100.2	93.6	96.9

Rsa1.0_01637.1.g28629.t1	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	318	1164	4.00E-40	366.0	31.1	50.9	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	318	332	9.00E-37	104.4	27.4	43.1
Rsa1.0_01637.1.g28630.t1	ref|NP_565167.1| uncharacterized protein [Arabidopsis thaliana] gi|6573767|gb|AAF17687.1|AC009243_14 F28K19.24 [Arabidopsis thaliana] gi|17380852|gb|AAL36238.1| unknown protein [Arabidopsis thaliana] gi|21436411|gb|AAM51406.1| unknown protein [Arabidopsis thaliana] gi|332197937|gb|AEE36058.1| uncharacterized protein AT1G78020 [Arabidopsis thaliana]	162	162	3.00E-65	100.0	80.2	84.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G78020.1 | Symbols: | Protein of unknown function (DUF581) | chr1:29338787-29339491 FORWARD LENGTH=162	162	162	9.00E-68	100.0	80.2	84.6
Rsa1.0_01637.1.g28631.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01638.1.g28632.t1	dbj|BAA85453.1| S-locus protein 4 [Brassica rapa]	413	413	0	100.0	81.8	86.2	S-locus protein 4	gbpln	Brassica rapa	AT5G43620.1 | Symbols: | Pre-mRNA cleavage complex II | chr5:17522653-17523885 FORWARD LENGTH=410	413	410	1.00E-110	99.3	60.0	69.5
Rsa1.0_01638.1.g28633.t1	gb|EOA35687.1| hypothetical protein CARUB_v10020914mg [Capsella rubella]	223	223	1.00E-94	100.0	81.6	89.2	hypothetical protein CARUB_v10020914mg	gbpln	Capsella rubella	AT1G66480.1 | Symbols: | plastid movement impaired 2 | chr1:24805770-24807405 REVERSE LENGTH=225	223	225	8.00E-96	100.9	82.1	89.2
Rsa1.0_01638.1.g28634.t1	ref|XP_002887043.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297332884|gb|EFH63302.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	290	296	1.00E-117	102.1	83.8	87.2	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT1G66470.1 | Symbols: RHD6 | ROOT HAIR DEFECTIVE6 | chr1:24795326-24796598 FORWARD LENGTH=298	290	298	1.00E-114	102.8	82.8	86.2
Rsa1.0_01638.1.g28635.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	1395	1515	0	108.6	54.8	68.6	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1395	1262	1.00E-113	90.5	13.7	21.1
Rsa1.0_01638.1.g28636.t1	ref|NP_564875.2| fructokinase [Arabidopsis thaliana] gi|12322265|gb|AAG51160.1|AC074025_10 fructokinase, putative [Arabidopsis thaliana] gi|12324405|gb|AAG52172.1|AC020665_17 fructokinase, putative; 80047-82040 [Arabidopsis thaliana] gi|332196387|gb|AEE34508.1| pfkB-like carbohydrate kinase family protein [Arabidopsis thaliana]	398	384	0	96.5	88.7	92.7	fructokinase	gbpln	Arabidopsis thaliana	AT1G66430.1 | Symbols: | pfkB-like carbohydrate kinase family protein | chr1:24778400-24780393 FORWARD LENGTH=384	398	384	0	96.5	88.7	92.7
Rsa1.0_01638.1.g28637.t1	ref|XP_002888501.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334342|gb|EFH64760.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	482	468	0	97.1	79.7	86.3	kinase family protein	gbpln	Arabidopsis lyrata	AT1G66460.1 | Symbols: | Protein kinase superfamily protein | chr1:24789894-24791988 REVERSE LENGTH=467	482	467	0	96.9	77.6	85.1
Rsa1.0_01639.1.g28638.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01639.1.g28639.t1	ref|XP_002869949.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297315785|gb|EFH46208.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	759	776	0	102.2	80.6	89.1	C2 domain-containing protein	gbpln	Arabidopsis lyrata	AT4G20080.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein | chr4:10865295-10867619 FORWARD LENGTH=774	759	774	0	102.0	78.8	87.9
Rsa1.0_01639.1.g28640.t1	ref|XP_002863545.1| responsive-to-antagonist1 [Arabidopsis lyrata subsp. lyrata] gi|297309380|gb|EFH39804.1| responsive-to-antagonist1 [Arabidopsis lyrata subsp. lyrata]	1006	1004	0	99.8	87.4	93.2	responsive-to-antagonist1	gbpln	Arabidopsis lyrata	AT5G44790.1 | Symbols: RAN1, HMA7 | copper-exporting ATPase / responsive-to-antagonist 1 / copper-transporting ATPase (RAN1) | chr5:18075846-18079817 REVERSE LENGTH=1001	1006	1001	0	99.5	86.9	92.6
Rsa1.0_01639.1.g28641.t1	ref|NP_199293.3| chromatin remodeling 4 protein [Arabidopsis thaliana] gi|332007781|gb|AED95164.1| chromatin remodeling 4 protein [Arabidopsis thaliana]	2229	2223	0	99.7	81.2	87.1	chromatin remodeling 4 protein	gbpln	Arabidopsis thaliana	AT5G44800.1 | Symbols: CHR4, PKR1 | chromatin remodeling 4 | chr5:18083659-18092162 REVERSE LENGTH=2223	2229	2223	0	99.7	81.2	87.1
Rsa1.0_01639.1.g28642.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01639.1.g28643.t1	gb|EOA17790.1| hypothetical protein CARUB_v10006184mg [Capsella rubella]	608	558	0	91.8	62.7	73.7	hypothetical protein CARUB_v10006184mg	gbpln	Capsella rubella	AT3G54070.1 | Symbols: | Ankyrin repeat family protein | chr3:20021330-20023603 REVERSE LENGTH=574	608	574	1.00E-154	94.4	49.0	65.1
Rsa1.0_01639.1.g28644.t1	dbj|BAB86292.1| nucleoside diphosphate kinase 1 [Brassica rapa] gi|19744165|dbj|BAB86841.1| NDPK I [Brassica rapa]	148	148	2.00E-79	100.0	96.6	98.6	nucleoside diphosphate kinase 1	gbpln	Brassica rapa	AT4G09320.1 | Symbols: NDPK1 | Nucleoside diphosphate kinase family protein | chr4:5923424-5924366 FORWARD LENGTH=169	148	169	7.00E-78	114.2	89.9	97.3

Rsa1.0_01639.1.g28645.t4	ref|XP_002865318.1| Toll-Interleukin-Resistance domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311153|gb|EFH41577.1| Toll-Interleukin-Resistance domain-containing protein [Arabidopsis lyrata subsp. lyrata]	328	242	9.00E-45	73.8	33.5	46.6	Toll-Interleukin-Resistance domain-containing protein	gbpln	Arabidopsis lyrata	AT5G44910.1 | Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr5:18137354-18138235 FORWARD LENGTH=241	328	241	4.00E-45	73.5	32.3	44.5
Rsa1.0_01640.1.g28646.t1	ref|XP_002891059.1| hypothetical protein ARALYDRAFT_890960 [Arabidopsis lyrata subsp. lyrata] gi|297336901|gb|EFH67318.1| hypothetical protein ARALYDRAFT_890960 [Arabidopsis lyrata subsp. lyrata]	171	174	1.00E-71	101.8	83.6	88.9	hypothetical protein ARALYDRAFT_890960	gbpln	Arabidopsis lyrata	AT1G33760.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:12237944-12238498 FORWARD LENGTH=184	171	184	3.00E-71	107.6	81.3	89.5
Rsa1.0_01640.1.g28647.t2	ref|NP_189068.2| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana] gi|332643359|gb|AEE76880.1| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana]	393	746	6.00E-12	189.8	10.7	14.0	RNA-directed DNA polymerase (reverse transcriptase)-related protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	393	746	1.00E-14	189.8	10.7	14.0
Rsa1.0_01640.1.g28648.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01640.1.g28649.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01640.1.g28650.t1	ref|NP_194638.1| Ribonuclease H-like protein [Arabidopsis thaliana] gi|4972055|emb|CAB43923.1| putative protein [Arabidopsis thaliana] gi|7269807|emb|CAB79667.1| putative protein [Arabidopsis thaliana] gi|67633766|gb|AAY78807.1| putative reverse transcriptase/RNA-dependent DNA polymerase [Arabidopsis thaliana] gi|332660185|gb|AEE85585.1| Ribonuclease H-like protein [Arabidopsis thaliana]	139	575	4.00E-25	413.7	38.8	55.4	Ribonuclease H-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	139	575	1.00E-27	413.7	38.8	55.4
Rsa1.0_01640.1.g28651.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01640.1.g28652.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	1403	1466	0	104.5	56.2	70.8	copia-like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1403	1262	6.00E-94	90.0	12.4	19.0
Rsa1.0_01640.1.g28653.t1	ref|NP_174597.2| patatin-like phospholipase domain-containing protein [Arabidopsis thaliana] gi|38603808|gb|AAR24649.1| At1g33270 [Arabidopsis thaliana] gi|110742517|dbj|BAE99176.1| hypothetical protein [Arabidopsis thaliana] gi|332193457|gb|AEE31578.1| patatin-like phospholipase domain-containing protein [Arabidopsis thaliana]	983	369	1.00E-168	37.5	30.7	33.4	patatin-like phospholipase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G33270.1 | Symbols: | Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein | chr1:12068324-12070157 REVERSE LENGTH=369	983	369	1.00E-171	37.5	30.7	33.4
Rsa1.0_01641.1.g28654.t1	ref|XP_002894512.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297340354|gb|EFH70771.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	599	606	0	101.2	89.6	95.0	F-box family protein	gbpln	Arabidopsis lyrata	AT1G55590.1 | Symbols: | RNI-like superfamily protein | chr1:20769476-20771756 REVERSE LENGTH=607	599	607	0	101.3	89.8	94.8
Rsa1.0_01641.1.g28655.t1	ref|XP_002876989.1| hypothetical protein ARALYDRAFT_484449 [Arabidopsis lyrata subsp. lyrata] gi|297322827|gb|EFH53248.1| hypothetical protein ARALYDRAFT_484449 [Arabidopsis lyrata subsp. lyrata]	54	494	3.00E-11	914.8	64.8	68.5	hypothetical protein ARALYDRAFT_484449	gbpln	Arabidopsis lyrata	AT3G26744.4 | Symbols: ICE1, ATICE1, SCRM | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:9832953-9834790 REVERSE LENGTH=494	54	494	6.00E-14	914.8	64.8	68.5
Rsa1.0_01641.1.g28656.t1	ref|XP_002894513.1| WRKY10 [Arabidopsis lyrata subsp. lyrata] gi|297340355|gb|EFH70772.1| WRKY10 [Arabidopsis lyrata subsp. lyrata]	511	495	1.00E-83	96.9	40.5	54.6	WRKY10	gbpln	Arabidopsis lyrata	AT1G55600.1 | Symbols: WRKY10, ATWRKY10, MINI3 | WRKY DNA-binding protein 10 | chr1:20774049-20776293 REVERSE LENGTH=485	511	485	2.00E-77	94.9	39.3	52.4

Rsa1.0_01641.1.g28657.t1	ref|NP_564698.1| chloride channel protein CLC-f [Arabidopsis thaliana] gi|41688504|sp|Q8RXR2.2|CLCF_ARATH RecName: Full=Chloride channel protein CLC-f; Short=AtCLC-f; AltName: Full=CBS domain-containing protein CBSCLC1 gi|14039802|gb|AAK53391.1|AF366368_1 CLC-f chloride channel protein [Arabidopsis thaliana] gi|13619402|emb|CAC36386.1| hypothetical protein [Arabidopsis thaliana] gi|332195154|gb|AEE33275.1| chloride channel protein CLC-f [Arabidopsis thaliana]	777	781	0	100.5	90.7	94.7	chloride channel protein CLC-f	gbpln	Arabidopsis thaliana	AT1G55620.2 | Symbols: CLC-F, ATCLC-F | chloride channel F | chr1:20787338-20790990 REVERSE LENGTH=781	777	781	0	100.5	90.7	94.7
Rsa1.0_01641.1.g28658.t1	ref|NP_175959.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75140283|sp|Q7X6A5.1|PPR81_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g55630 gi|30793841|gb|AAP40373.1| unknown protein [Arabidopsis thaliana] gi|30794021|gb|AAP40457.1| unknown protein [Arabidopsis thaliana] gi|110739296|dbj|BAF01561.1| hypothetical protein [Arabidopsis thaliana] gi|332195155|gb|AEE33276.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	469	477	0	101.7	87.4	93.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G55630.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:20791817-20793250 REVERSE LENGTH=477	469	477	0	101.7	87.4	93.6
Rsa1.0_01641.1.g28659.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01641.1.g28660.t1	ref|XP_002894553.1| hypothetical protein ARALYDRAFT_474673 [Arabidopsis lyrata subsp. lyrata] gi|297340395|gb|EFH70812.1| hypothetical protein ARALYDRAFT_474673 [Arabidopsis lyrata subsp. lyrata]	70	71	9.00E-25	101.4	80.0	90.0	hypothetical protein ARALYDRAFT_474673	gbpln	Arabidopsis lyrata	AT1G56060.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G32210.1); Has 180 Blast hits to 180 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 10; Plants - 170; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:20966737-20967133 REVERSE LENGTH=71	70	71	1.00E-26	101.4	78.6	88.6
Rsa1.0_01641.1.g28661.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1624	1213	0	74.7	25.9	38.3	unknown protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	1624	295	1.00E-80	18.2	8.9	12.1
Rsa1.0_01641.1.g28662.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01641.1.g28663.t1	gb|EOA21184.1| hypothetical protein CARUB_v10001529mg [Capsella rubella]	309	309	1.00E-175	100.0	96.8	99.4	hypothetical protein CARUB_v10001529mg	gbpln	Capsella rubella	AT5G01230.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:92789-95380 REVERSE LENGTH=309	309	309	1.00E-178	100.0	97.1	99.4
Rsa1.0_01641.1.g28664.t1	ref|NP_176004.2| uncharacterized protein [Arabidopsis thaliana] gi|114050585|gb|ABI49442.1| At1g56080 [Arabidopsis thaliana] gi|332195218|gb|AEE33339.1| uncharacterized protein AT1G56080 [Arabidopsis thaliana]	315	310	1.00E-139	98.4	81.9	87.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G56080.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16520.1); Has 196 Blast hits to 193 proteins in 50 species: Archae - 2; Bacteria - 0; Metazoa - 9; Fungi - 2; Plants - 132; Viruses - 0; Other Eukaryotes - 51 (source: NCBI BLink). | chr1:20974457-20976215 REVERSE LENGTH=310	315	310	1.00E-142	98.4	81.9	87.6
Rsa1.0_01641.1.g28665.t2	ref|NP_189790.2| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|332644192|gb|AEE77713.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	1184	1345	0	113.6	90.7	94.8	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G33530.1 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr3:14085354-14093449 FORWARD LENGTH=1345	1184	1345	0	113.6	90.7	94.8
Rsa1.0_01642.1.g28666.t1	ref|XP_002885396.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331236|gb|EFH61655.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	329	347	5.00E-57	105.5	49.5	61.1	predicted protein	gbpln	Arabidopsis lyrata	AT3G20710.1 | Symbols: | F-box family protein | chr3:7237911-7238999 REVERSE LENGTH=362	329	362	1.00E-55	110.0	45.3	61.7
Rsa1.0_01642.1.g28667.t1	ref|XP_002885400.1| hypothetical protein ARALYDRAFT_898505 [Arabidopsis lyrata subsp. lyrata] gi|297331240|gb|EFH61659.1| hypothetical protein ARALYDRAFT_898505 [Arabidopsis lyrata subsp. lyrata]	381	364	1.00E-68	95.5	45.1	57.0	hypothetical protein ARALYDRAFT_898505	gbpln	Arabidopsis lyrata	AT3G16740.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:5699476-5700651 FORWARD LENGTH=391	381	391	4.00E-68	102.6	44.9	59.8

Rsa1.0_01642.1.g28668.t1	gb|EOA29533.1| hypothetical protein CARUB_v10014905mg [Capsella rubella]	135	132	7.00E-66	97.8	96.3	97.0	hypothetical protein CARUB_v10014905mg	gbpln	Capsella rubella	AT3G20670.1 | Symbols: HTA13 | histone H2A 13 | chr3:7229472-7229963 FORWARD LENGTH=132	135	132	5.00E-67	97.8	94.1	96.3
Rsa1.0_01642.1.g28669.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	1621	1365	0	84.2	31.6	42.3	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT3G20660.1 | Symbols: AtOCT4, 4-Oct | organic cation/carnitine transporter4 | chr3:7225271-7228510 REVERSE LENGTH=526	1621	526	0	32.4	27.5	29.8
Rsa1.0_01642.1.g28670.t1	ref|NP_188701.2| mRNA cap guanine-N7 methyltransferase 1 [Arabidopsis thaliana] gi|75273308|sp|Q9LHQ7.1|MCES1_ARATH RecName: Full=mRNA cap guanine-N7 methyltransferase 1; AltName: Full=mRNA (guanine-N(7)-)-methyltransferase 1; AltName: Full=mRNA cap methyltransferase 1 gi|9294344|dbj|BAB02241.1| mRNA cap methyltransferase-like protein [Arabidopsis thaliana] gi|28973781|gb|AAO64206.1| unknown protein [Arabidopsis thaliana] gi|29824183|gb|AAP04052.1| unknown protein [Arabidopsis thaliana] gi|110736712|dbj|BAF00319.1| hypothetical protein [Arabidopsis thaliana] gi|332642886|gb|AEE76407.1| mRNA cap guanine-N7 methyltransferase 1 [Arabidopsis thaliana]	371	370	0	99.7	96.8	98.7	mRNA cap guanine-N7 methyltransferase 1	gbpln	Arabidopsis thaliana	AT3G20650.1 | Symbols: | mRNA capping enzyme family protein | chr3:7221168-7223939 REVERSE LENGTH=370	371	370	0	99.7	96.8	98.7
Rsa1.0_01643.1.g28671.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01643.1.g28672.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	251	1225	1.00E-23	488.0	25.9	38.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	251	256	2.00E-16	102.0	15.1	23.1
Rsa1.0_01643.1.g28673.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	426	1023	3.00E-52	240.1	27.9	38.3	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	426	575	4.00E-14	135.0	10.6	16.7
Rsa1.0_01643.1.g28674.t1	emb|CAE45640.1| putative AP2 domain transcription factor [Arabidopsis thaliana]	222	220	2.00E-39	99.1	57.7	62.6	putative AP2 domain transcription factor	gbpln	Arabidopsis thaliana	AT5G50080.1 | Symbols: ERF110 | ethylene response factor 110 | chr5:20365948-20366835 FORWARD LENGTH=220	222	220	1.00E-40	99.1	56.8	62.6
Rsa1.0_01643.1.g28675.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	145	1142	5.00E-23	787.6	41.4	55.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	145	575	5.00E-16	396.6	26.9	53.1
Rsa1.0_01643.1.g28676.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	335	414	2.00E-62	123.6	49.3	56.1	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01643.1.g28677.t4	gb|AAD20646.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	571	1040	2.00E-38	182.1	14.5	18.4	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01643.1.g28678.t1	ref|XP_002864034.1| hypothetical protein ARALYDRAFT_918012 [Arabidopsis lyrata subsp. lyrata] gi|297309869|gb|EFH40293.1| hypothetical protein ARALYDRAFT_918012 [Arabidopsis lyrata subsp. lyrata]	157	159	7.00E-72	101.3	89.2	93.6	hypothetical protein ARALYDRAFT_918012	gbpln	Arabidopsis lyrata	AT5G50090.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G62900.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:20369961-20370878 FORWARD LENGTH=159	157	159	5.00E-69	101.3	87.9	94.3
Rsa1.0_01644.1.g28679.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01644.1.g28680.t1	ref|XP_002878329.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297324167|gb|EFH54588.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	857	928	0	108.3	53.1	66.3	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT3G60350.1 | Symbols: ARABIDILLO-2, ARABIDILLO2 | ARABIDILLO-2 | chr3:22306806-22310596 REVERSE LENGTH=928	857	928	0	108.3	53.8	66.5
Rsa1.0_01644.1.g28681.t1	ref|XP_004233663.1| PREDICTED: uncharacterized protein LOC101263375 [Solanum lycopersicum]	159	282	5.00E-11	177.4	27.0	40.3	PREDICTED: uncharacterized protein LOC101263375	gbpln	Solanum lycopersicum	AT3G61090.1 | Symbols: | Putative endonuclease or glycosyl hydrolase | chr3:22609094-22609822 REVERSE LENGTH=180	159	180	2.00E-12	113.2	32.7	44.7

Rsa1.0_01644.1.g28682.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	752	1142	1.00E-149	151.9	37.9	48.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	752	575	7.00E-41	76.5	17.8	27.8
Rsa1.0_01644.1.g28683.t1	ref|NP_001117499.2| Nuclear pore complex protein [Arabidopsis thaliana] gi|332195142|gb|AEE33263.1| Nuclear pore complex protein [Arabidopsis thaliana]	136	1819	2.00E-37	1337.5	51.5	54.4	Nuclear pore complex protein	gbpln	Arabidopsis thaliana	AT1G55540.2 | Symbols: emb1011 | Nuclear pore complex protein | chr1:20734759-20743049 REVERSE LENGTH=1819	136	1819	4.00E-40	1337.5	51.5	54.4
Rsa1.0_01644.1.g28684.t2	ref|NP_192110.2| protein kinase family protein [Arabidopsis thaliana] gi|21928159|gb|AAM78107.1| AT4g02010/T10M13_2 [Arabidopsis thaliana] gi|32815839|gb|AAP88328.1| At4g02010/T10M13_2 [Arabidopsis thaliana] gi|332656711|gb|AEE82111.1| protein kinase family protein [Arabidopsis thaliana]	237	725	3.00E-31	305.9	40.1	46.0	protein kinase family protein	gbpln	Arabidopsis thaliana	AT4G02010.1 | Symbols: | Protein kinase superfamily protein | chr4:881457-885222 FORWARD LENGTH=725	237	725	1.00E-33	305.9	40.1	46.0
Rsa1.0_01644.1.g28685.t1	gb|EOA22498.1| hypothetical protein CARUB_v10003153mg, partial [Capsella rubella]	173	380	6.00E-15	219.7	35.3	49.1	hypothetical protein CARUB_v10003153mg, partial	gbpln	Capsella rubella	AT2G42550.1 | Symbols: | Protein kinase superfamily protein | chr2:17713196-17714230 FORWARD LENGTH=344	173	344	3.00E-17	198.8	33.5	47.4
Rsa1.0_01644.1.g28686.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01645.1.g28687.t1	sp|Q9SH27.1|LOR4_ARATH RecName: Full=Protein LURP-one-related 4 gi|6633839|gb|AAF19698.1|AC008047_5 F2K11.21 [Arabidopsis thaliana]	182	215	3.00E-93	118.1	89.0	94.5	RecName: Full=Protein LURP-one-related 4 gi|6633839|gb|AAF19698.1|AC008047_5 F2K11.21	gbpln	Arabidopsis thaliana	AT1G63410.1 | Symbols: | Protein of unknown function (DUF567) | chr1:23510075-23511997 REVERSE LENGTH=208	182	208	1.00E-95	114.3	89.0	94.5
Rsa1.0_01645.1.g28688.t1	sp|Q9FYJ1.1|FB24_ARATH RecName: Full=Putative F-box protein At1g31000 gi|9755376|gb|AAF98183.1|AC000107_6 F17F8.8 [Arabidopsis thaliana]	396	365	2.00E-81	92.2	49.5	62.4	RecName: Full=Putative F-box protein At1g31000 gi|9755376|gb|AAF98183.1|AC000107_6 F17F8.8	gbpln	Arabidopsis thaliana	AT1G31000.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11053377-11054561 REVERSE LENGTH=363	396	363	7.00E-84	91.7	49.2	61.9
Rsa1.0_01645.1.g28689.t1	gb|EOA34293.1| hypothetical protein CARUB_v10021808mg, partial [Capsella rubella]	620	654	0	105.5	82.9	90.3	hypothetical protein CARUB_v10021808mg, partial	gbpln	Capsella rubella	AT1G63450.1 | Symbols: RHS8 | root hair specific 8 | chr1:23532523-23534517 FORWARD LENGTH=664	620	664	0	107.1	78.4	88.1
Rsa1.0_01645.1.g28690.t1	ref|NP_176536.2| AT hook motif DNA-binding family protein [Arabidopsis thaliana] gi|26451696|dbj|BAC42943.1| putative DNA-binding protein [Arabidopsis thaliana] gi|28973281|gb|AAO63965.1| putative DNA-binding protein [Arabidopsis thaliana] gi|119657354|tpd|FAA00276.1| TPA: AT-hook motif nuclear localized protein 5 [Arabidopsis thaliana] gi|332195982|gb|AEE34103.1| AT hook motif DNA-binding family protein [Arabidopsis thaliana]	385	378	1.00E-148	98.2	78.2	84.7	AT hook motif DNA-binding family protein	gbpln	Arabidopsis thaliana	AT1G63470.1 | Symbols: | AT hook motif DNA-binding family protein | chr1:23536831-23538863 REVERSE LENGTH=378	385	378	1.00E-151	98.2	78.2	84.7
Rsa1.0_01645.1.g28691.t2	gb|AAC28197.1| contains similarity to reverse transcriptases [Arabidopsis thaliana] gi|7267156|emb|CAB77868.1| putative reverse transcriptase [Arabidopsis thaliana]	1770	1077	1.00E-147	60.8	16.7	21.9	contains similarity to reverse transcriptases	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	1770	303	1.00E-46	17.1	6.3	8.9
Rsa1.0_01645.1.g28692.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01645.1.g28693.t1	ref|XP_002887955.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333796|gb|EFH64214.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	486	487	0	100.2	95.5	96.9	kinase family protein	gbpln	Arabidopsis lyrata	AT1G63500.1 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr1:23556015-23558403 FORWARD LENGTH=487	486	487	0	100.2	95.3	96.9
Rsa1.0_01645.1.g28694.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01646.1.g28695.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01646.1.g28696.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01646.1.g28697.t1	gb|AAM61481.1| unknown [Arabidopsis thaliana]	568	440	1.00E-145	77.5	51.4	60.7	unknown	gbpln	Arabidopsis thaliana	AT5G44785.1 | Symbols: OSB3 | organellar single-stranded DNA binding protein 3 | chr5:18070877-18073010 REVERSE LENGTH=440	568	440	1.00E-147	77.5	51.2	60.6
Rsa1.0_01646.1.g28698.t1	ref|XP_002865325.1| hypothetical protein ARALYDRAFT_494504 [Arabidopsis lyrata subsp. lyrata] gi|297311160|gb|EFH41584.1| hypothetical protein ARALYDRAFT_494504 [Arabidopsis lyrata subsp. lyrata]	706	751	0	106.4	68.4	76.3	hypothetical protein ARALYDRAFT_494504	gbpln	Arabidopsis lyrata	AT5G44780.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G20020.2); Has 9661 Blast hits to 6233 proteins in 635 species: Archae - 4; Bacteria - 1116; Metazoa - 4251; Fungi - 1510; Plants - 1359; Viruses - 43; Other Eukaryotes - 1378 (source: NCBI BLink). | chr5:18068100-18070544 FORWARD LENGTH=723	706	723	0	102.4	63.0	72.0

<table>
<tr><td>Rsa1.0_01646.1.g28699.t2</td><td>ref|NP_199288.4| DNA repair protein REV1 [Arabidopsis thaliana] gi|59796995|dbj|BAD89586.1| deoxycytidyl transferase [Arabidopsis thaliana] gi|332007773|gb|AED95156.1| DNA repair protein REV1 [Arabidopsis thaliana]</td><td>1071</td><td>1101</td><td>0</td><td>102.8</td><td>81.1</td><td>87.8</td><td>DNA repair protein REV1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G44750.1 | Symbols: REV1, ATREV1 | DNA-directed DNA polymerases | chr5:18052669-18059581 FORWARD LENGTH=1101</td><td>1071</td><td>1101</td><td>0</td><td>102.8</td><td>81.1</td><td>87.8</td></tr>
<tr><td>Rsa1.0_01646.1.g28700.t2</td><td>ref|NP_568638.2| DNA polymerase eta subunit [Arabidopsis thaliana] gi|23954185|emb|CAC94893.1| putative DNA polymerase eta [Arabidopsis thaliana] gi|332007772|gb|AED95155.1| Y-family DNA polymerase H [Arabidopsis thaliana]</td><td>668</td><td>672</td><td>0</td><td>100.6</td><td>83.7</td><td>90.3</td><td>DNA polymerase eta subunit</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G44740.2 | Symbols: POLH | Y-family DNA polymerase H | chr5:18047903-18051779 REVERSE LENGTH=672</td><td>668</td><td>672</td><td>0</td><td>100.6</td><td>83.7</td><td>90.3</td></tr>
<tr><td>Rsa1.0_01647.1.g28701.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01647.1.g28702.t1</td><td>sp|Q9FIF0.3|LRK22_ARATH RecName: Full=Putative L-type lectin-domain containing receptor kinase II.2; Short=LecRK-II.2; Flags: Precursor</td><td>425</td><td>694</td><td>0</td><td>163.3</td><td>79.5</td><td>89.4</td><td>RecName: Full=Putative L-type lectin-domain containing receptor kinase II.2; Short=LecRK-II.2; Flags: Precursor</td><td>----</td><td>----</td><td>AT5G59260.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:23907901-23909925 REVERSE LENGTH=674</td><td>425</td><td>674</td><td>0</td><td>158.6</td><td>76.0</td><td>85.9</td></tr>
<tr><td>Rsa1.0_01647.1.g28703.t1</td><td>gb|EOA13270.1| hypothetical protein CARUB_v10026298mg [Capsella rubella]</td><td>490</td><td>489</td><td>0</td><td>99.8</td><td>93.9</td><td>96.5</td><td>hypothetical protein CARUB_v10026298mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G59010.1 | Symbols: | Protein kinase protein with tetratricopeptide repeat domain | chr5:23820578-23823099 REVERSE LENGTH=489</td><td>490</td><td>489</td><td>0</td><td>99.8</td><td>93.3</td><td>96.5</td></tr>
<tr><td>Rsa1.0_01647.1.g28704.t1</td><td>gb|AAM61470.1| unknown [Arabidopsis thaliana]</td><td>221</td><td>231</td><td>1.00E-79</td><td>104.5</td><td>80.5</td><td>91.4</td><td>unknown</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G59000.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:23818768-23820018 FORWARD LENGTH=231</td><td>221</td><td>231</td><td>3.00E-81</td><td>104.5</td><td>80.1</td><td>91.0</td></tr>
<tr><td>Rsa1.0_01647.1.g28705.t1</td><td>gb|AAC67205.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>785</td><td>1413</td><td>0</td><td>180.0</td><td>56.9</td><td>70.6</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>785</td><td>1262</td><td>3.00E-59</td><td>160.8</td><td>15.3</td><td>21.5</td></tr>
<tr><td>Rsa1.0_01647.1.g28706.t1</td><td>gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>243</td><td>1501</td><td>5.00E-97</td><td>617.7</td><td>65.8</td><td>84.0</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>243</td><td>1262</td><td>6.00E-49</td><td>519.3</td><td>34.6</td><td>52.7</td></tr>
<tr><td>Rsa1.0_01647.1.g28707.t6</td><td>gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>1222</td><td>1529</td><td>0</td><td>125.1</td><td>37.2</td><td>51.9</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>1222</td><td>746</td><td>3.00E-46</td><td>61.0</td><td>8.8</td><td>12.7</td></tr>
<tr><td>Rsa1.0_01647.1.g28708.t2</td><td>ref|NP_200707.1| uncharacterized protein [Arabidopsis thaliana] gi|9759230|dbj|BAB09642.1| unnamed protein product [Arabidopsis thaliana] gi|15450824|gb|AAK96683.1| Unknown protein [Arabidopsis thaliana] gi|20148679|gb|AAM10230.1| unknown protein [Arabidopsis thaliana] gi|332009744|gb|AED97127.1| uncharacterized protein AT5G58990 [Arabidopsis thaliana]</td><td>59</td><td>148</td><td>3.00E-11</td><td>250.8</td><td>61.0</td><td>64.4</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G58990.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G52370.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:23815028-23815819 FORWARD LENGTH=148</td><td>59</td><td>148</td><td>4.00E-14</td><td>250.8</td><td>61.0</td><td>64.4</td></tr>
<tr><td>Rsa1.0_01647.1.g28709.t1</td><td>gb|EOA12569.1| hypothetical protein CARUB_v10026845mg [Capsella rubella]</td><td>305</td><td>305</td><td>1.00E-170</td><td>100.0</td><td>96.1</td><td>98.0</td><td>hypothetical protein CARUB_v10026845mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G58970.1 | Symbols: ATUCP2, UCP2 | uncoupling protein 2 | chr5:23808642-23811018 REVERSE LENGTH=305</td><td>305</td><td>305</td><td>1.00E-172</td><td>100.0</td><td>95.4</td><td>98.0</td></tr>
<tr><td>Rsa1.0_01647.1.g28710.t1</td><td>ref|NP_200704.2| uncharacterized protein [Arabidopsis thaliana] gi|79331394|ref|NP_001032100.1| uncharacterized protein [Arabidopsis thaliana] gi|9759227|dbj|BAB09639.1| unnamed protein product [Arabidopsis thaliana] gi|19715645|gb|AAL91642.1| AT5g58960/k19m22_160 [Arabidopsis thaliana] gi|27363240|gb|AAO11539.1| At5g58960/k19m22_160 [Arabidopsis thaliana] gi|89001398|gb|ABD59217.1| gravitropic in the light 1 [Arabidopsis thaliana] gi|222424191|dbj|BAH20054.1| AT5G58960 [Arabidopsis thaliana] gi|332009739|gb|AED97122.1| uncharacterized protein AT5G58960 [Arabidopsis thaliana] gi|332009740|gb|AED97123.1| uncharacterized protein AT5G58960 [Arabidopsis thaliana]</td><td>106</td><td>484</td><td>7.00E-56</td><td>456.6</td><td>97.2</td><td>100.0</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G58960.3 | Symbols: GIL1 | Plant protein of unknown function (DUF641) | chr5:23806906-23808360 FORWARD LENGTH=484</td><td>106</td><td>484</td><td>1.00E-58</td><td>456.6</td><td>97.2</td><td>100.0</td></tr>
</table>

Rsa1.0_01648.1.g28711.t2	gb|EOA31227.1| hypothetical protein CARUB_v10014393mg [Capsella rubella] gi|482567039|gb|EOA31228.1| hypothetical protein CARUB_v10014393mg [Capsella rubella]	198	268	8.00E-25	135.4	36.9	47.0	hypothetical protein CARUB_v10014393mg	gbpln	Capsella rubella	AT3G04310.1 | Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:1141581-1142528 REVERSE LENGTH=269	198	269	1.00E-26	135.9	36.4	46.0
Rsa1.0_01648.1.g28712.t1	gb|EOA26319.1| hypothetical protein CARUB_v10025210mg [Capsella rubella]	288	292	1.00E-119	101.4	75.3	86.1	hypothetical protein CARUB_v10025210mg	gbpln	Capsella rubella	AT2G22180.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr2:9428969-9429844 FORWARD LENGTH=291	288	291	1.00E-120	101.0	79.5	87.5
Rsa1.0_01648.1.g28713.t1	ref|XP_002880432.1| lipid-associated family protein [Arabidopsis lyrata subsp. lyrata] gi|297326271|gb|EFH56691.1| lipid-associated family protein [Arabidopsis lyrata subsp. lyrata]	182	183	1.00E-91	100.5	88.5	95.6	lipid-associated family protein	gbpln	Arabidopsis lyrata	AT2G22170.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr2:9427010-9427742 REVERSE LENGTH=183	182	183	1.00E-93	100.5	87.9	95.1
Rsa1.0_01648.1.g28714.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01648.1.g28715.t1	ref|XP_002878591.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297324430|gb|EFH54850.1| binding protein [Arabidopsis lyrata subsp. lyrata]	2151	2154	0	100.1	96.0	98.7	binding protein	gbpln	Arabidopsis lyrata	AT2G22125.1 | Symbols: CSI1 | binding | chr2:9406793-9414223 FORWARD LENGTH=2150	2151	2150	0	100.0	95.8	98.3
Rsa1.0_01648.1.g28716.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01648.1.g28717.t1	gb|EOA27501.1| hypothetical protein CARUB_v10023640mg [Capsella rubella]	323	323	1.00E-174	100.0	94.7	97.8	hypothetical protein CARUB_v10023640mg	gbpln	Capsella rubella	AT2G22120.2 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:9394026-9396979 FORWARD LENGTH=363	323	363	1.00E-177	112.4	95.0	97.8
Rsa1.0_01648.1.g28718.t1	gb|EOA28652.1| hypothetical protein CARUB_v10024874mg [Capsella rubella]	369	410	1.00E-100	111.1	55.6	64.2	hypothetical protein CARUB_v10024874mg	gbpln	Capsella rubella	AT2G22100.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:9392397-9393545 REVERSE LENGTH=382	369	382	4.00E-94	103.5	52.8	60.4
Rsa1.0_01648.1.g28719.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01648.1.g28720.t1	ref|XP_002879925.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297325764|gb|EFH56184.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	199	371	2.00E-16	186.4	28.6	37.7	F-box family protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01649.1.g28721.t1	ref|NP_683294.2| phosphoglycerate mutase-like protein [Arabidopsis thaliana] gi|332190397|gb|AEE28518.1| phosphoglycerate mutase-like protein [Arabidopsis thaliana]	233	231	1.00E-121	99.1	90.6	94.8	phosphoglycerate mutase-like protein	gbpln	Arabidopsis thaliana	AT1G09935.1 | Symbols: | Phosphoglycerate mutase family protein | chr1:3234060-3235530 REVERSE LENGTH=231	233	231	1.00E-123	99.1	90.6	94.8
Rsa1.0_01649.1.g28722.t1	dbj|BAJ34167.1| unnamed protein product [Thellungiella halophila]	970	975	0	100.5	84.3	90.9	unnamed protein product	----	----	AT1G09970.1 | Symbols: LRR XI-23, RLK7 | Leucine-rich receptor-like protein kinase family protein | chr1:3252408-3255428 FORWARD LENGTH=976	970	976	0	100.6	82.5	90.0
Rsa1.0_01649.1.g28723.t1	ref|XP_002892542.1| hypothetical protein ARALYDRAFT_888257 [Arabidopsis lyrata subsp. lyrata] gi|297338384|gb|EFH68801.1| hypothetical protein ARALYDRAFT_888257 [Arabidopsis lyrata subsp. lyrata]	73	802	3.00E-19	1098.6	65.8	78.1	hypothetical protein ARALYDRAFT_888257	gbpln	Arabidopsis lyrata	AT1G09980.2 | Symbols: | Putative serine esterase family protein | chr1:3256541-3260866 REVERSE LENGTH=801	73	801	1.00E-21	1097.3	64.4	78.1
Rsa1.0_01649.1.g28724.t1	gb|EOA40355.1| hypothetical protein CARUB_v10009083mg [Capsella rubella]	449	460	0	102.4	88.2	92.0	hypothetical protein CARUB_v10009083mg	gbpln	Capsella rubella	AT1G10020.1 | Symbols: | Protein of unknown function (DUF1005) | chr1:3269939-3271732 REVERSE LENGTH=461	449	461	0	102.7	87.3	90.9
Rsa1.0_01649.1.g28725.t1	gb|EOA36321.1| hypothetical protein CARUB_v10010632mg [Capsella rubella]	129	129	2.00E-65	100.0	96.9	98.4	hypothetical protein CARUB_v10010632mg	gbpln	Capsella rubella	AT1G10030.1 | Symbols: ERG28 | homolog of yeast ergosterol28 | chr1:3273972-3275631 FORWARD LENGTH=129	129	129	2.00E-67	100.0	96.1	96.9
Rsa1.0_01649.1.g28726.t1	gb|EOA40539.1| hypothetical protein CARUB_v10009269mg [Capsella rubella]	380	417	1.00E-175	109.7	81.3	87.9	hypothetical protein CARUB_v10009269mg	gbpln	Capsella rubella	AT1G10040.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:3276124-3278464 REVERSE LENGTH=408	380	408	1.00E-171	107.4	80.8	87.4

Rsa1.0_01649.1.g28727.t1	ref|NP_849629.1| branched-chain-amino-acid aminotransferase 1 [Arabidopsis thaliana] gi|26391635|sp|Q93Y32.2|BCAT1_ARATH RecName: Full=Branched-chain-amino-acid aminotransferase 1, mitochondrial; Short=Atbcat-1; Flags: Precursor gi|3540185|gb|AAC34335.1| Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana] gi|8249008|emb|CAB93130.1| branched-chain amino acid transaminase [Arabidopsis thaliana] gi|222423010|dbj|BAH19488.1| AT1G10060 [Arabidopsis thaliana] gi|332190414|gb|AEE28535.1| branched-chain-amino-acid aminotransferase 1 [Arabidopsis thaliana]	345	384	1.00E-168	111.3	87.8	93.3	branched-chain-amino-acid aminotransferase 1	gbpln	Arabidopsis thaliana	AT1G10060.2 | Symbols: ATBCAT-1, BCAT-1 | branched-chain amino acid transaminase 1 | chr1:3284445-3286837 FORWARD LENGTH=384	345	384	1.00E-170	111.3	87.8	93.3
Rsa1.0_01649.1.g28728.t1	ref|NP_172478.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|79317492|ref|NP_001031015.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|26391680|sp|Q9M439.1|BCAT2_ARATH RecName: Full=Branched-chain-amino-acid aminotransferase 2, chloroplastic; Short=Atbcat-2; Flags: Precursor gi|13877745|gb|AAK43950.1|AF370135_1 putative tat-binding protein [Arabidopsis thaliana] gi|8249004|emb|CAB93128.1| branched-chain amino acid transaminase [Arabidopsis thaliana] gi|15293209|gb|AAK93715.1| putative tat-binding protein [Arabidopsis thaliana] gi|222424474|dbj|BAH20192.1| AT1G10070 [Arabidopsis thaliana] gi|332190416|gb|AEE28537.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana] gi|332190417|gb|AEE28538.1| branched-chain-amino-acid aminotransferase 2 [Arabidopsis thaliana]	380	388	0	102.1	92.9	97.4	branched-chain-amino-acid aminotransferase 2	gbpln	Arabidopsis thaliana	AT1G10070.2 | Symbols: ATBCAT-2, BCAT-2 | branched-chain amino acid transaminase 2 | chr1:3288255-3290164 FORWARD LENGTH=388	380	388	0	102.1	92.9	97.4
Rsa1.0_01650.1.g28729.t1	ref|XP_002883129.1| EMB1865 [Arabidopsis lyrata subsp. lyrata] gi|297328969|gb|EFH59388.1| EMB1865 [Arabidopsis lyrata subsp. lyrata]	70	846	8.00E-20	1208.6	64.3	65.7	EMB1865	gbpln	Arabidopsis lyrata	AT3G18390.1 | Symbols: EMB1865 | CRS1 / YhbY (CRM) domain-containing protein | chr3:6313572-6317584 FORWARD LENGTH=848	70	848	3.00E-22	1211.4	64.3	64.3
Rsa1.0_01650.1.g28730.t2	gb|AFJ66169.1| hypothetical protein 11M19.13 [Arabidopsis halleri]	952	1273	0	133.7	45.8	61.4	hypothetical protein 11M19.13	gbpln	Arabidopsis halleri	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	952	1262	1.00E-60	132.6	13.9	21.7
Rsa1.0_01650.1.g28731.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	832	1142	1.00E-176	137.3	39.3	52.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	832	575	9.00E-28	69.1	9.5	14.7
Rsa1.0_01650.1.g28732.t1	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	470	498	6.00E-13	106.0	11.7	19.8	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01650.1.g28733.t1	emb|CAA09731.1| receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	669	667	0	99.7	75.0	83.0	receptor-like protein kinase, RLK3	gbpln	Arabidopsis thaliana	AT4G23190.1 | Symbols: CRK11, AT-RLK3 | cysteine-rich RLK (RECEPTOR-like protein kinase) 11 | chr4:12141197-12143710 REVERSE LENGTH=667	669	667	0	99.7	75.3	83.0
Rsa1.0_01650.1.g28734.t1	ref|XP_002893765.1| hypothetical protein ARALYDRAFT_890918 [Arabidopsis lyrata subsp. lyrata] gi|297339607|gb|EFH70024.1| hypothetical protein ARALYDRAFT_890918 [Arabidopsis lyrata subsp. lyrata]	89	93	1.00E-35	104.5	86.5	92.1	hypothetical protein ARALYDRAFT_890918	gbpln	Arabidopsis lyrata	AT4G10265.1 | Symbols: | Wound-responsive family protein | chr4:6373226-6373477 REVERSE LENGTH=83	89	83	2.00E-29	93.3	68.5	78.7
Rsa1.0_01650.1.g28735.t1	ref|XP_002893765.1| hypothetical protein ARALYDRAFT_890918 [Arabidopsis lyrata subsp. lyrata] gi|297339607|gb|EFH70024.1| hypothetical protein ARALYDRAFT_890918 [Arabidopsis lyrata subsp. lyrata]	89	93	3.00E-34	104.5	84.3	92.1	hypothetical protein ARALYDRAFT_890918	gbpln	Arabidopsis lyrata	AT4G10270.1 | Symbols: | Wound-responsive family protein | chr4:6374805-6375077 FORWARD LENGTH=90	89	90	2.00E-28	101.1	69.7	82.0
Rsa1.0_01650.1.g28736.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01650.1.g28737.t1	ref|XP_002893765.1| hypothetical protein ARALYDRAFT_890918 [Arabidopsis lyrata subsp. lyrata] gi|297339607|gb|EFH70024.1| hypothetical protein ARALYDRAFT_890918 [Arabidopsis lyrata subsp. lyrata]	89	93	3.00E−34	104.5	83.1	92.1	hypothetical protein ARALYDRAFT_890918	gbpln	Arabidopsis lyrata	AT4G10265.1 | Symbols: | Wound-responsive family protein | chr4:6373226-6373477 REVERSE LENGTH=83	89	83	9.00E−30	93.3	69.7	79.8
Rsa1.0_01650.1.g28738.t1	gb|ACG60672.1| unknown protein [Brassica oleracea var. alboglabra]	163	288	7.00E−44	176.7	58.3	69.3	unknown protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01651.1.g28739.t2	gb|EOA27544.1| hypothetical protein CARUB_v10023683mg [Capsella rubella]	318	311	1.00E−115	97.8	73.6	79.9	hypothetical protein CARUB_v10023683mg	gbpln	Capsella rubella	AT2G43140.2 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:17931680-17935639 REVERSE LENGTH=309	318	309	1.00E−101	97.2	71.7	78.0
Rsa1.0_01651.1.g28740.t1	ref|XP_002881887.1| hypothetical protein ARALYDRAFT_903694 [Arabidopsis lyrata subsp. lyrata] gi|297327726|gb|EFH58146.1| hypothetical protein ARALYDRAFT_903694 [Arabidopsis lyrata subsp. lyrata]	213	213	1.00E−114	100.0	94.8	98.1	hypothetical protein ARALYDRAFT_903694	gbpln	Arabidopsis lyrata	AT2G43130.1 | Symbols: ARA4, ATRAB11F, ATRABA5C, ARA-4, RABA5C | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:17929899-17930904 REVERSE LENGTH=214	213	214	1.00E−116	100.5	94.4	97.2
Rsa1.0_01651.1.g28741.t1	ref|XP_002880027.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297325866|gb|EFH56286.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	297	322	1.00E−161	108.4	92.6	94.9	predicted protein	gbpln	Arabidopsis lyrata	AT2G43120.1 | Symbols: | RmlC-like cupins superfamily protein | chr2:17927339-17928871 FORWARD LENGTH=321	297	321	1.00E−163	108.1	91.9	96.0
Rsa1.0_01651.1.g28742.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01651.1.g28743.t1	ref|XP_002880026.1| hypothetical protein ARALYDRAFT_483412 [Arabidopsis lyrata subsp. lyrata] gi|297325865|gb|EFH56285.1| hypothetical protein ARALYDRAFT_483412 [Arabidopsis lyrata subsp. lyrata]	281	284	1.00E−114	101.1	79.4	88.3	hypothetical protein ARALYDRAFT_483412	gbpln	Arabidopsis lyrata	AT2G43110.1 | Symbols: | unknown protein; Has 212 Blast hits to 211 proteins in 96 species: Archae - 0; Bacteria - 6; Metazoa - 62; Fungi - 91; Plants - 31; Viruses - 0; Other Eukaryotes - 22 (source: NCBI BLink). | chr2:17922067-17924291 FORWARD LENGTH=288	281	288	1.00E−115	102.5	77.6	87.2
Rsa1.0_01651.1.g28744.t1	ref|NP_181838.1| isopropylmalate isomerase 2 [Arabidopsis thaliana] gi|3763919|gb|AAC64299.1| 3-isopropylmalate dehydratase, small subunit [Arabidopsis thaliana] gi|16974633|gb|AAL31219.1| At2g43100/MFL8.4 [Arabidopsis thaliana] gi|17380708|gb|AAL36184.1| putative 3-isopropylmalate dehydratase small subunit [Arabidopsis thaliana] gi|20197631|gb|AAM15160.1| 3-isopropylmalate dehydratase, small subunit [Arabidopsis thaliana] gi|21436289|gb|AAM51283.1| putative 3-isopropylmalate dehydratase small subunit [Arabidopsis thaliana] gi|330255115|gb|AEC10209.1| isopropylmalate isomerase 2 [Arabidopsis thaliana]	256	256	1.00E−108	100.0	75.8	84.4	isopropylmalate isomerase 2	gbpln	Arabidopsis thaliana	AT2G43100.1 | Symbols: IPMI2, ATLEUD1 | isopropylmalate isomerase 2 | chr2:17920685-17921455 FORWARD LENGTH=256	256	256	1.00E−111	100.0	75.8	84.4
Rsa1.0_01651.1.g28745.t1	ref|NP_001189737.1| Aconitase/3-isopropylmalate dehydratase protein [Arabidopsis thaliana] gi|330255114|gb|AEC10208.1| Aconitase/3-isopropylmalate dehydratase protein [Arabidopsis thaliana]	215	222	3.00E−84	103.3	78.6	82.8	Aconitase/3-isopropylmalate dehydratase protein	gbpln	Arabidopsis thaliana	AT2G43090.2 | Symbols: | Aconitase/3-isopropylmalate dehydratase protein | chr2:17918957-17919712 FORWARD LENGTH=222	215	222	1.00E−86	103.3	78.6	82.8
Rsa1.0_01651.1.g28746.t1	gb|EOA27648.1| hypothetical protein CARUB_v10023796mg [Capsella rubella]	87	283	2.00E−42	325.3	94.3	95.4	hypothetical protein CARUB_v10023796mg	gbpln	Capsella rubella	AT2G43080.1 | Symbols: AT-P4H-1 | P4H isoform 1 | chr2:17915755-17918599 FORWARD LENGTH=283	87	283	1.00E−44	325.3	93.1	95.4
Rsa1.0_01651.1.g28747.t1	gb|AAM14939.1| unknown protein [Arabidopsis thaliana] gi|20197629|gb|AAM15159.1| unknown protein [Arabidopsis thaliana]	238	543	1.00E−108	228.2	86.6	92.0	unknown protein	gbpln	Arabidopsis thaliana	AT2G43070.1 | Symbols: SPPL3, ATSPPL3 | SIGNAL PEPTIDE PEPTIDASE-LIKE 3 | chr2:17911233-17914776 REVERSE LENGTH=540	238	540	1.00E−111	226.9	86.6	92.0
Rsa1.0_01652.1.g28748.t3	ref|XP_002893071.1| hypothetical protein ARALYDRAFT_335233 [Arabidopsis lyrata subsp. lyrata] gi|297338913|gb|EFH69330.1| hypothetical protein ARALYDRAFT_335233 [Arabidopsis lyrata subsp. lyrata]	1163	986	0	84.8	68.6	74.0	hypothetical protein ARALYDRAFT_335233	gbpln	Arabidopsis lyrata	AT1G19835.2 | Symbols: | Plant protein of unknown function (DUF869) | chr1:6856212-6859513 REVERSE LENGTH=982	1163	982	0	84.4	68.2	73.4
Rsa1.0_01652.1.g28749.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01652.1.g28750.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01652.1.g28751.t2	ref|XP_002893072.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] gi|297338914|gb|EFH69331.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	693	153	4.00E−64	22.1	19.6	20.9	auxin-responsive family protein	gbpln	Arabidopsis lyrata	AT1G19840.1 | Symbols: | SAUR-like auxin-responsive protein family | chr1:6872794-6873255 REVERSE LENGTH=153	693	153	2.00E−66	22.1	19.5	20.9

Rsa1.0_01652.1_g28752.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01653.1_g28753.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01653.1_g28754.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01653.1_g28755.t15	gb|ABD65017.1| hypothetical protein 26.t00072 [Brassica oleracea]	1257	821	1.00E-108	65.3	18.8	23.0	hypothetical protein 26.t00072	gbpln	Brassica oleracea	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	1257	673	3.00E-12	53.5	4.9	8.7
Rsa1.0_01653.1_g28756.t1	gb|AAC62785.1| F11O4.11 [Arabidopsis thaliana] gi|7268192|emb|CAB77719.1| putative transposon protein [Arabidopsis thaliana]	136	577	5.00E-43	424.3	55.1	74.3	F11O4.11	gbpln	Arabidopsis thaliana	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	136	336	2.00E-14	247.1	27.2	44.1
Rsa1.0_01653.1_g28757.t4	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	2624	1838	0	70.0	15.1	20.1	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01653.1_g28758.t1	emb|CAN70566.1| hypothetical protein VITISV_010970 [Vitis vinifera]	181	1027	3.00E-36	567.4	46.4	58.6	hypothetical protein VITISV_010970	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01654.1_g28759.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01654.1_g28760.t1	gb|EOA21743.1| hypothetical protein CARUB_v10002191mg [Capsella rubella]	152	152	3.00E-61	100.0	76.3	84.9	hypothetical protein CARUB_v10002191mg	gbpln	Capsella rubella	AT5G06480.1 | Symbols: | Immunoglobulin E-set superfamily protein | chr5:1976219-1977231 REVERSE LENGTH=153	152	153	2.00E-57	100.7	73.0	83.6
Rsa1.0_01654.1_g28761.t1	gb|EOA22998.1| hypothetical protein CARUB_v10003745mg [Capsella rubella]	198	191	1.00E-74	96.5	71.2	80.8	hypothetical protein CARUB_v10003745mg	gbpln	Capsella rubella	AT5G06490.1 | Symbols: | RING/U-box superfamily protein | chr5:1977996-1978589 REVERSE LENGTH=197	198	197	1.00E-75	99.5	73.7	83.8
Rsa1.0_01654.1_g28762.t1	ref|NP_196268.1| protein agamous-like 96 [Arabidopsis thaliana] gi|10178106|dbj|BAB11399.1| unnamed protein product [Arabidopsis thaliana] gi|67633788|gb|AAY78818.1| MADS-box family protein [Arabidopsis thaliana] gi|332003641|gb|AED91024.1| protein agamous-like 96 [Arabidopsis thaliana]	252	242	6.00E-53	96.0	46.4	63.5	protein agamous-like 96	gbpln	Arabidopsis thaliana	AT5G06500.1 | Symbols: AGL96 | AGAMOUS-like 96 | chr5:1982444-1983172 FORWARD LENGTH=242	252	242	2.00E-55	96.0	46.4	63.5
Rsa1.0_01654.1_g28763.t1	ref|XP_002322764.1| white-brown-complex ABC transporter family [Populus trichocarpa] gi|222867394|gb|EEF04525.1| white-brown-complex ABC transporter family [Populus trichocarpa]	505	744	0	147.3	77.4	88.9	white-brown-complex ABC transporter family	gbpln	Populus trichocarpa	AT5G06530.1 | Symbols: | ABC-2 type transporter family protein | chr5:1990060-1994605 REVERSE LENGTH=751	505	751	1.00E-155	148.7	53.7	56.6
Rsa1.0_01654.1_g28764.t1	dbj|BAB09502.1| transposon protein-like [Arabidopsis thaliana]	1094	1089	0	99.5	47.6	62.7	transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01654.1_g28765.t2	gb|ABD65053.1| S-locus linked 3 (SLL3) protein, putative [Brassica oleracea]	376	462	4.00E-35	122.9	27.9	40.7	S-locus linked 3 (SLL3) protein, putative	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01654.1_g28766.t1	gb|EOA20021.1| hypothetical protein CARUB_v10000295mg [Capsella rubella]	145	752	3.00E-52	518.6	82.8	87.6	hypothetical protein CARUB_v10000295mg	gbpln	Capsella rubella	AT5G06530.1 | Symbols: | ABC-2 type transporter family protein | chr5:1990060-1994605 REVERSE LENGTH=751	145	751	3.00E-51	517.9	81.4	86.9
Rsa1.0_01654.1_g28767.t1	ref|NP_196274.1| uncharacterized protein [Arabidopsis thaliana] gi|13430752|gb|AAK25998.1|AF360288_1 unknown protein [Arabidopsis thaliana] gi|10178112|dbj|BAB11405.1| unnamed protein product [Arabidopsis thaliana] gi|15293221|gb|AAK93721.1| unknown protein [Arabidopsis thaliana] gi|332003651|gb|AED91034.1| uncharacterized protein AT5G06560 [Arabidopsis thaliana]	418	518	1.00E-157	123.9	73.9	85.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G06560.1 | Symbols: | Protein of unknown function, DUF593 | chr5:2003678-2005543 REVERSE LENGTH=518	418	518	1.00E-159	123.9	73.9	85.2
Rsa1.0_01655.1_g28768.t1	ref|XP_002872465.1| hypothetical protein ARALYDRAFT_352054 [Arabidopsis lyrata subsp. lyrata] gi|297318302|gb|EFH48724.1| hypothetical protein ARALYDRAFT_352054 [Arabidopsis lyrata subsp. lyrata]	179	190	7.00E-87	106.1	86.6	93.3	hypothetical protein ARALYDRAFT_352054	gbpln	Arabidopsis lyrata	AT4G09830.1 | Symbols: | Uncharacterised conserved protein UCP009193 | chr4:6188866-6190591 FORWARD LENGTH=191	179	191	4.00E-87	106.7	86.0	92.7

Rsa1.0_01655.1.g28769.t1	ref|NP_192719.1| Nucleotide-sugar transporter family protein [Arabidopsis thaliana] gi|4538911|emb|CAB39648.1| hypothetical protein [Arabidopsis thaliana] gi|7267676|emb|CAB78104.1| hypothetical protein [Arabidopsis thaliana] gi|38603966|gb|AAR24728.1| At4g09810 [Arabidopsis thaliana] gi|332657401|gb|AEE82801.1| Nucleotide-sugar transporter family protein [Arabidopsis thaliana]	336	335	0	99.7	94.0	97.3	Nucleotide-sugar transporter family protein	gbpln	Arabidopsis thaliana	AT4G09810.1 | Symbols: | Nucleotide-sugar transporter family protein | chr4:6175415-6176892 REVERSE LENGTH=335	336	335	0	99.7	94.0	97.3
Rsa1.0_01655.1.g28770.t2	gb|EOA21645.1| hypothetical protein CARUB_v10002063mg, partial [Capsella rubella]	178	183	5.00E-79	102.8	83.7	84.8	hypothetical protein CARUB_v10002063mg, partial	gbpln	Capsella rubella	AT4G09800.1 | Symbols: RPS18C | S18 ribosomal protein | chr4:6173818-6174963 FORWARD LENGTH=152	178	152	2.00E-81	85.4	84.3	85.4
Rsa1.0_01655.1.g28771.t4	emb|CAB78060.1| putative protein [Arabidopsis thaliana]	704	666	7.00E-68	94.6	19.3	29.0	putative protein	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	704	249	1.00E-33	35.4	12.1	17.5
Rsa1.0_01655.1.g28772.t1	emb|CAB45792.1| putative protein [Arabidopsis thaliana] gi|7267462|emb|CAB81158.1| putative protein [Arabidopsis thaliana]	150	320	1.00E-11	213.3	24.7	33.3	putative protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01655.1.g28773.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	320	1529	3.00E-46	477.8	33.1	45.0	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	320	295	1.00E-33	92.2	26.3	42.5
Rsa1.0_01655.1.g28774.t1	gb|ABE65398.1| hypothetical protein At1g43570 [Arabidopsis thaliana]	133	348	2.00E-29	261.7	45.1	64.7	hypothetical protein At1g43570	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	133	746	2.00E-20	560.9	39.8	51.1
Rsa1.0_01655.1.g28775.t1	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	895	1864	1.00E-116	208.3	33.5	50.6	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01655.1.g28776.t1	gb|AAF19546.1|AC007190_14 F23N19.13 [Arabidopsis thaliana]	177	633	3.00E-38	357.6	48.6	61.6	F23N19.13	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	177	696	5.00E-17	393.2	23.2	33.9
Rsa1.0_01656.1.g28777.t1	gb|AEC10965.1| 50S ribosomal protein L29 [Camellia sinensis]	60	178	2.00E-15	296.7	68.3	73.3	50S ribosomal protein L29	gbpln	Camellia sinensis	AT5G65220.1 | Symbols: | Ribosomal L29 family protein | chr5:26061301-26062506 FORWARD LENGTH=173	60	173	4.00E-17	288.3	91.7	96.7
Rsa1.0_01656.1.g28778.t1	gb|EOA12555.1| hypothetical protein CARUB_v10026822mg [Capsella rubella]	302	310	1.00E-122	102.6	81.5	86.4	hypothetical protein CARUB_v10026822mg	gbpln	Capsella rubella	AT5G65230.1 | Symbols: AtMYB53, MYB53 | myb domain protein 53 | chr5:26068290-26069408 FORWARD LENGTH=310	302	310	1.00E-123	102.6	83.4	86.8
Rsa1.0_01656.1.g28779.t1	gb|EOA15267.1| hypothetical protein CARUB_v10028666mg [Capsella rubella]	610	608	0	99.7	90.2	94.9	hypothetical protein CARUB_v10028666mg	gbpln	Capsella rubella	AT5G65240.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:26074980-26077650 REVERSE LENGTH=607	610	607	0	99.5	90.8	94.9
Rsa1.0_01656.1.g28780.t1	ref|XP_002866660.1| hypothetical protein ARALYDRAFT_496756 [Arabidopsis lyrata subsp. lyrata] gi|297312495|gb|EFH42919.1| hypothetical protein ARALYDRAFT_496756 [Arabidopsis lyrata subsp. lyrata]	295	299	5.00E-98	101.4	75.3	86.1	hypothetical protein ARALYDRAFT_496756	gbpln	Arabidopsis lyrata	AT5G65250.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26078699-26080051 REVERSE LENGTH=300	295	300	1.00E-100	101.7	72.5	83.7
Rsa1.0_01656.1.g28781.t3	gb|EOA12395.1| hypothetical protein CARUB_v10027046mg, partial [Capsella rubella]	93	233	1.00E-30	250.5	80.6	86.0	hypothetical protein CARUB_v10027046mg, partial	gbpln	Capsella rubella	AT5G10350.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:3255674-3257746 REVERSE LENGTH=217	93	217	9.00E-28	233.3	69.9	81.7
Rsa1.0_01656.1.g28782.t1	emb|CAB77741.1| putative actin polymerization factor [Arabidopsis thaliana]	119	159	4.00E-25	133.6	63.0	71.4	putative actin polymerization factor	gbpln	Arabidopsis thaliana	AT4G01710.1 | Symbols: CRK, ARPC5 | ARP2/3 complex 16 kDa subunit (p16-Arc) | chr4:735776-736450 FORWARD LENGTH=132	119	132	8.00E-28	110.9	63.0	71.4
Rsa1.0_01656.1.g28783.t1	ref|NP_201331.1| protein GCR2-like 1 [Arabidopsis thaliana] gi|10178190|dbj|BAB11664.1| G protein-coupled receptor-like protein [Arabidopsis thaliana] gi|16604356|gb|AAL24184.1| AT5g65280/MQN23_23 [Arabidopsis thaliana] gi|332010650|gb|AED98033.1| protein GCR2-like 1 [Arabidopsis thaliana]	439	433	0	98.6	86.1	90.7	protein GCR2-like 1	gbpln	Arabidopsis thaliana	AT5G65280.1 | Symbols: GCL1 | GCR2-like 1 | chr5:26086129-26088069 REVERSE LENGTH=433	439	433	0	98.6	86.1	90.7

Rsa1.0_01656.1.g28784.t1	ref|XP_002866663.1| hypothetical protein ARALYDRAFT_496763 [Arabidopsis lyrata subsp. lyrata] gi|297312498|gb|EFH42922.1| hypothetical protein ARALYDRAFT_496763 [Arabidopsis lyrata subsp. lyrata]	144	150	3.00E-38	104.2	73.6	81.3	hypothetical protein ARALYDRAFT_496763	gbpln	Arabidopsis lyrata	AT5G65300.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:26095266-26095718 REVERSE LENGTH=150	144	150	2.00E-31	104.2	70.1	78.5
Rsa1.0_01656.1.g28785.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01656.1.g28786.t2	gb|EOA13730.1| hypothetical protein CARUB_v10026808mg [Capsella rubella]	305	315	1.00E-126	103.3	80.3	85.6	hypothetical protein CARUB_v10026808mg	gbpln	Capsella rubella	AT5G65310.1 | Symbols: ATHB5, ATHB-5, HB5 | homeobox protein 5 | chr5:26102457-26104217 REVERSE LENGTH=312	305	312	1.00E-128	102.3	80.7	86.9
Rsa1.0_01657.1.g28787.t10	ref|XP_002892146.1| hypothetical protein ARALYDRAFT_311407 [Arabidopsis lyrata subsp. lyrata] gi|297337988|gb|EFH68405.1| hypothetical protein ARALYDRAFT_311407 [Arabidopsis lyrata subsp. lyrata]	3616	3606	0	99.7	91.7	95.1	hypothetical protein ARALYDRAFT_311407	gbpln	Arabidopsis lyrata	AT1G03060.1 | Symbols: SPI | Beige/BEACH domain ;WD domain, G-beta repeat protein | chr1:712971-726891 REVERSE LENGTH=3601	3616	3601	0	99.6	91.3	94.7
Rsa1.0_01657.1.g28788.t1	ref|XP_002892145.1| hypothetical protein ARALYDRAFT_470283 [Arabidopsis lyrata subsp. lyrata] gi|297337987|gb|EFH68404.1| hypothetical protein ARALYDRAFT_470283 [Arabidopsis lyrata subsp. lyrata]	265	264	1.00E-119	99.6	78.9	86.4	hypothetical protein ARALYDRAFT_470283	gbpln	Arabidopsis lyrata	AT1G03055.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G64680.1); Has 143 Blast hits to 143 proteins in 26 species: Archae - 0; Bacteria - 6; Metazoa - 0; Fungi - 0; Plants - 122; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink). | chr1:710102-711763 REVERSE LENGTH=264	265	264	1.00E-118	99.6	77.4	85.3
Rsa1.0_01657.1.g28789.t1	ref|NP_171804.1| putative clathrin assembly protein [Arabidopsis thaliana] gi|46396022|sp|Q9SA65.1|CAP4_ARATH RecName: Full=Putative clathrin assembly protein At1g03050 gi|4587573|gb|AAD25804.1|AC006550_12 Similar to clathrin assembly protein gb|AF041374 (CALM) from Rattus norvegicus [Arabidopsis thaliana] gi|91805731|gb|ABE65594.1| clathrin assembly protein-like [Arabidopsis thaliana] gi|332189399|gb|AEE27520.1| putative clathrin assembly protein [Arabidopsis thaliana]	592	599	0	101.2	87.8	94.3	putative clathrin assembly protein	gbpln	Arabidopsis thaliana	AT1G03050.1 | Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:707726-709860 FORWARD LENGTH=599	592	599	0	101.2	87.8	94.3
Rsa1.0_01657.1.g28790.t1	ref|XP_002892143.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] gi|297337985|gb|EFH68402.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	102	102	1.00E-48	100.0	91.2	95.1	glutaredoxin family protein	gbpln	Arabidopsis lyrata	AT1G03020.1 | Symbols: | Thioredoxin superfamily protein | chr1:698207-698515 REVERSE LENGTH=102	102	102	2.00E-49	100.0	88.2	93.1
Rsa1.0_01657.1.g28791.t1	ref|NP_171800.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana] gi|75200292|sp|Q9SA69.1|Y1301_ARATH RecName: Full=BTB/POZ domain-containing protein At1g03010 gi|4587577|gb|AAD25808.1|AC006550_16 F10O3.17 [Arabidopsis thaliana] gi|332189393|gb|AEE27514.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana]	637	634	0	99.5	89.2	94.8	Phototropic-responsive NPH3 family protein	gbpln	Arabidopsis thaliana	AT1G03010.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr1:693480-696188 FORWARD LENGTH=634	637	634	0	99.5	89.2	94.8
Rsa1.0_01657.1.g28792.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	113	484	5.00E-18	428.3	43.4	57.5	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01658.1.g28793.t3	ref|XP_002884143.1| hypothetical protein ARALYDRAFT_900245 [Arabidopsis lyrata subsp. lyrata] gi|297329983|gb|EFH60402.1| hypothetical protein ARALYDRAFT_900245 [Arabidopsis lyrata subsp. lyrata]	1054	472	0	44.8	32.2	35.9	hypothetical protein ARALYDRAFT_900245	gbpln	Arabidopsis lyrata	AT2G18590.1 | Symbols: | Major facilitator superfamily protein | chr2:8069988-8072866 FORWARD LENGTH=473	1054	473	0	44.9	30.5	34.5
Rsa1.0_01658.1.g28794.t1	ref|NP_849978.2| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75315911|sp|Q9ZU72.1|U72D1_ARATH RecName: Full=UDP-glycosyltransferase 72D1 gi|4218002|gb|AAD12210.1| putative flavonol 3-O-glucosyltransferase [Arabidopsis thaliana] gi|330251688|gb|AEC06782.1| UDP-glycosyltransferase 72D1 [Arabidopsis thaliana]	467	470	0	100.6	77.5	88.7	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT2G18570.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:8063429-8064841 FORWARD LENGTH=470	467	470	0	100.6	77.5	88.7

Rsa1.0_01658.1.g28795.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	245	1352	3.00E-19	551.8	34.3	46.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	245	746	6.00E-12	304.5	17.6	22.0
Rsa1.0_01658.1.g28796.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	787	1485	0	188.7	42.7	49.7	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	#	#	#	#	#	#	#
Rsa1.0_01658.1.g28797.t1	ref|XP_002867363.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313199|gb|EFH43622.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	335	232	1.00E-46	69.3	31.6	41.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G27260.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9603943-9604930 FORWARD LENGTH=303	335	303	7.00E-42	90.4	29.0	43.6
Rsa1.0_01659.1.g28798.t1	gb|EOA40500.1| hypothetical protein CARUB_v10009226mg, partial [Capsella rubella]	111	425	1.00E-43	382.9	83.8	89.2	hypothetical protein CARUB_v10009226mg, partial	gbpln	Capsella rubella	AT1G30840.2 | Symbols: PUP4 | purine permease 4 | chr1:10974581-10975729 FORWARD LENGTH=382	111	382	3.00E-35	344.1	75.7	80.2
Rsa1.0_01659.1.g28799.t7	ref|XP_002890909.1| hypothetical protein ARALYDRAFT_473326 [Arabidopsis lyrata subsp. lyrata] gi|297336751|gb|EFH67168.1| hypothetical protein ARALYDRAFT_473326 [Arabidopsis lyrata subsp. lyrata]	118	118	1.00E-53	100.0	90.7	93.2	hypothetical protein ARALYDRAFT_473326	gbpln	Arabidopsis lyrata	AT1G30845.1 | Symbols: | unknown protein; Has 120 Blast hits to 120 proteins in 67 species: Archae - 0; Bacteria - 0; Metazoa - 35; Fungi - 37; Plants - 23; Viruses - 0; Other Eukaryotes - 25 (source: NCBI BLink). | chr1:10979856-10980427 FORWARD LENGTH=118	118	118	3.00E-46	100.0	84.7	90.7
Rsa1.0_01659.1.g28800.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01659.1.g28801.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01659.1.g28802.t1	ref|NP_564376.1| myo-inositol monophosphatase like 1 [Arabidopsis thaliana] gi|332278187|sp|Q94F00.2|IMPL1_ARATH RecName: Full=Phosphatase IMPL1, chloroplastic; AltName: Full=Protein MYO-INOSITOL MONOPHOSPHATASE-LIKE 1; Flags: Precursor gi|332193206|gb|AEE31327.1| myo-inositol monophosphatase like 1 [Arabidopsis thaliana]	379	371	0	97.9	89.7	93.7	myo-inositol monophosphatase like 1	gbpln	Arabidopsis thaliana	AT1G31190.1 | Symbols: IMPL1 | myo-inositol monophosphatase like 1 | chr1:11144861-11146800 FORWARD LENGTH=371	379	371	0	97.9	89.7	93.7
Rsa1.0_01659.1.g28803.t1	ref|NP_174405.1| protein PHLOEM protein 2-LIKE A9 [Arabidopsis thaliana] gi|75200001|sp|Q9SA16.1|P2A09_ARATH RecName: Full=Protein PHLOEM PROTEIN 2-LIKE A9; Short=AtPP2-A9 gi|4512617|gb|AAD21686.1| F28K20.16 [Arabidopsis thaliana] gi|332193207|gb|AEE31328.1| protein PHLOEM protein 2-LIKE A9 [Arabidopsis thaliana]	176	180	5.00E-82	102.3	86.9	92.6	protein PHLOEM protein 2-LIKE A9	gbpln	Arabidopsis thaliana	AT1G31200.1 | Symbols: ATPP2-A9, PP2-A9 | phloem protein 2-A9 | chr1:11146923-11147678 REVERSE LENGTH=180	176	180	2.00E-84	102.3	86.9	92.6
Rsa1.0_01659.1.g28804.t1	ref|XP_002882207.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328047|gb|EFH58466.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	109	470	3.00E-39	431.2	76.1	85.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G02120.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr3:377122-377577 FORWARD LENGTH=126	109	126	4.00E-38	115.6	73.4	84.4

Rsa1.0_01659.1.g28805.t1	ref|NP_174407.1| phosphoribosylglycinamide formyltransferase [Arabidopsis thaliana] gi|14917033|sp|P52422.2|PUR3_ARATH RecName: Full=Phosphoribosylglycinamide formyltransferase, chloroplastic; AltName: Full=5'-phosphoribosylglycinamide transformylase; AltName: Full=GAR transformylase; Short=GART; Flags: Precursor gi|4512619|gb|AAD21688.1| This gene is a member of the formyl transferase family PF|00551 and may be a pseudogene of gb|X74767 phosphoribosylglycinamide formyl transferase (PUR3) from Arabidopsis thaliana since our sequence differs from PUR3 by an insertion of an A at bp 225 and a deletion of an A at bp 1276 [Arabidopsis thaliana] gi|4753662|emb|CAA52779.2| phosphoribosylglycinamide formyltransferase [Arabidopsis thaliana] gi|28392982|gb|AAO41926.1| putative phosphoribosylglycinamide formyltransferase [Arabidopsis thaliana] gi|29824209|gb|AAP04065.1| putative phosphoribosylglycinamide formyltransferase [Arabidopsis thaliana] gi|332193208|gb|AEE31329.1| phosphoribosylglycinamide formyltransferase [Arabidopsis thaliana]	287	292	1.00E-134	101.7	85.7	90.9	phosphoribosylglycinamide formyltransferase	gbpln	Arabidopsis thaliana	AT1G31220.1 | Symbols: | Formyl transferase | chr1:11157064-11158408 FORWARD LENGTH=292	287	292	1.00E-137	101.7	85.7	90.9
Rsa1.0_01659.1.g28806.t1	gb|EOA39622.1| hypothetical protein CARUB_v10008251mg [Capsella rubella]	914	911	0	99.7	93.3	96.7	hypothetical protein CARUB_v10008251mg	gbpln	Capsella rubella	AT1G31230.1 | Symbols: AK-HSDH I, AK-HSDH | aspartate kinase-homoserine dehydrogenase i | chr1:11158744-11163055 REVERSE LENGTH=911	914	911	0	99.7	92.8	96.4
Rsa1.0_01659.1.g28807.t1	ref|XP_002891123.1| hypothetical protein ARALYDRAFT_891076 [Arabidopsis lyrata subsp. lyrata] gi|297336965|gb|EFH67382.1| hypothetical protein ARALYDRAFT_891076 [Arabidopsis lyrata subsp. lyrata]	281	276	3.00E-83	98.2	66.5	74.4	hypothetical protein ARALYDRAFT_891076	gbpln	Arabidopsis lyrata	AT1G31240.1 | Symbols: | Bromodomain transcription factor | chr1:11164065-11164898 REVERSE LENGTH=277	281	277	3.00E-81	98.6	64.8	73.7
Rsa1.0_01659.1.g28808.t1	ref|NP_174411.2| putative zinc transporter 10 [Arabidopsis thaliana] gi|37090222|sp|Q8W245.2|ZIP10_ARATH RecName: Full=Probable zinc transporter 10; AltName: Full=ZRT/IRT-like protein 10; Flags: Precursor gi|6692132|gb|AAF24597.1|AC007654_13 T19E23.6 [Arabidopsis thaliana] gi|332193212|gb|AEE31333.1| putative zinc transporter 10 [Arabidopsis thaliana]	370	364	0	98.4	85.4	91.4	putative zinc transporter 10	gbpln	Arabidopsis thaliana	AT1G31260.1 | Symbols: ZIP10 | zinc transporter 10 precursor | chr1:11175559-11177362 REVERSE LENGTH=364	370	364	0	98.4	85.4	91.4
Rsa1.0_01660.1.g28809.t1	ref|NP_194980.1| YUCCA family monooxygenase [Arabidopsis thaliana] gi|75213680|sp|Q9SZY8.1|YUC1_ARATH RecName: Full=Probable indole-3-pyruvate monooxygenase YUCCA1; AltName: Full=Flavin-containing monooxygenase YUCCA1 gi|4914451|emb|CAB43691.1| dimethylaniline monooxygenase-like protein [Arabidopsis thaliana] gi|7270158|emb|CAB79971.1| dimethylaniline monooxygenase-like protein [Arabidopsis thaliana] gi|16555352|gb|AAL23750.1| flavin-containing monooxygenase YUCCA [Arabidopsis thaliana] gi|332660675|gb|AEE86075.1| flavin-containing monooxygenase YUCCA1 [Arabidopsis thaliana]	415	414	0	99.8	87.5	92.5	YUCCA family monooxygenase	gbpln	Arabidopsis thaliana	AT4G32540.1 | Symbols: YUC, YUC1 | Flavin-binding monooxygenase family protein | chr4:15700904-15702870 FORWARD LENGTH=414	415	414	0	99.8	87.5	92.5
Rsa1.0_01660.1.g28810.t1	ref|XP_002880688.1| H+-transporting two-sector ATPase [Arabidopsis lyrata subsp. lyrata] gi|297326527|gb|EFH56947.1| H+-transporting two-sector ATPase [Arabidopsis lyrata subsp. lyrata]	177	179	8.00E-89	101.1	98.9	99.4	H+-transporting two-sector ATPase	gbpln	Arabidopsis lyrata	AT2G25610.1 | Symbols: | ATPase, F0/V0 complex, subunit C protein | chr2:10901585-10902494 REVERSE LENGTH=178	177	178	3.00E-91	100.6	98.3	99.4

Rsa1.0_01660.1.g28811.t1	gb|EOA16417.1| hypothetical protein CARUB_v10004571mg [Capsella rubella]	542	529	0	97.6	87.5	91.7	hypothetical protein CARUB_v10004571mg	gbpln	Capsella rubella	AT4G32520.2 | Symbols: SHM3 | serine hydroxymethyltransferase 3 | chr4:15689642-15692334 REVERSE LENGTH=529	542	529	0	97.6	86.5	91.3
Rsa1.0_01660.1.g28812.t1	ref|NP_194970.1| tudor-like RNA-binding protein [Arabidopsis thaliana] gi|4049346|emb|CAA22571.1| putative protein [Arabidopsis thaliana] gi|7270148|emb|CAB79961.1| putative protein [Arabidopsis thaliana] gi|27765060|gb|AAO23651.1| At4g32440 [Arabidopsis thaliana] gi|110742940|dbj|BAE99365.1| hypothetical protein [Arabidopsis thaliana] gi|332660659|gb|AEE86059.1| tudor-like RNA-binding protein [Arabidopsis thaliana]	350	377	1.00E-145	107.7	77.7	86.3	tudor-like RNA-binding protein	gbpln	Arabidopsis thaliana	AT4G32440.1 | Symbols: | Plant Tudor-like RNA-binding protein | chr4:15657295-15658692 FORWARD LENGTH=377	350	377	1.00E-148	107.7	77.7	86.3
Rsa1.0_01661.1.g28813.t1	dbj|BAD44345.1| retrotransposon like protein [Arabidopsis thaliana]	292	383	5.00E-62	131.2	43.8	55.1	retrotransposon like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01661.1.g28814.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01661.1.g28815.t5	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1431	1529	0	106.8	29.6	41.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G60460.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:22275600-22278565 FORWARD LENGTH=473	1431	473	0	33.1	25.0	27.8
Rsa1.0_01661.1.g28816.t1	ref|XP_002888143.1| DC1 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297333984|gb|EFH64402.1| DC1 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	580	578	0	99.7	87.8	94.3	DC1 domain-containing protein	gbpln	Arabidopsis lyrata	AT1G60420.1 | Symbols: | DC1 domain-containing protein | chr1:22261978-22264243 FORWARD LENGTH=578	580	578	0	99.7	86.9	93.6
Rsa1.0_01661.1.g28817.t1	gb|EOA18856.1| hypothetical protein CARUB_v10007477mg, partial [Capsella rubella]	324	377	4.00E-76	116.4	49.4	64.5	hypothetical protein CARUB_v10007477mg, partial	gbpln	Capsella rubella	AT5G45190.1 | Symbols: | Cyclin family protein | chr5:18277808-18280733 REVERSE LENGTH=579	324	579	2.00E-73	178.7	43.5	57.7
Rsa1.0_01662.1.g28818.t1	gb|EOA37691.1| hypothetical protein CARUB_v10012343mg [Capsella rubella]	549	549	0	100.0	83.1	90.7	hypothetical protein CARUB_v10012343mg	gbpln	Capsella rubella	AT1G19900.1 | Symbols: | glyoxal oxidase-related protein | chr1:6907038-6908684 REVERSE LENGTH=548	549	548	0	99.8	79.6	88.2
Rsa1.0_01662.1.g28819.t1	gb|AAC13599.1| similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]	890	928	1.00E-178	104.3	37.9	56.3	similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31)	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	890	626	2.00E-60	70.3	14.0	21.9
Rsa1.0_01662.1.g28820.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01662.1.g28821.t1	ref|XP_002513751.1| vacuolar ATP synthase proteolipid subunit 1, 2, 3, putative [Ricinus communis] gi|223546837|gb|EEF48334.1| vacuolar ATP synthase proteolipid subunit 1, 2, 3, putative [Ricinus communis]	165	169	2.00E-84	102.4	99.4	100.0	vacuolar ATP synthase proteolipid subunit 1, 2, 3, putative	gbpln	Ricinus communis	AT1G19910.1 | Symbols: AVA-P2, AVA-2PE, ATVHA-C2 | ATPase, F0/V0 complex, subunit C protein | chr1:6913317-6914322 FORWARD LENGTH=165	165	165	1.00E-86	100.0	99.4	99.4
Rsa1.0_01662.1.g28822.t1	ref|XP_002893081.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata] gi|297338923|gb|EFH69340.1| glycosyl hydrolase family 9 protein [Arabidopsis lyrata subsp. lyrata]	518	516	0	99.6	87.8	94.4	glycosyl hydrolase family 9 protein	gbpln	Arabidopsis lyrata	AT1G19940.1 | Symbols: AtGH9B5, GH9B5 | glycosyl hydrolase 9B5 | chr1:6918323-6920268 REVERSE LENGTH=515	518	515	0	99.4	88.0	94.2
Rsa1.0_01662.1.g28823.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01662.1.g28824.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01662.1.g28825.t1	ref|XP_002893082.1| hypothetical protein ARALYDRAFT_312925 [Arabidopsis lyrata subsp. lyrata] gi|297338924|gb|EFH69341.1| hypothetical protein ARALYDRAFT_312925 [Arabidopsis lyrata subsp. lyrata]	523	281	1.00E-128	53.7	43.0	47.8	hypothetical protein ARALYDRAFT_312925	gbpln	Arabidopsis lyrata	AT1G19970.1 | Symbols: | ER lumen protein retaining receptor family protein | chr1:6931194-6932597 REVERSE LENGTH=272	523	272	1.00E-124	52.0	40.5	45.1
Rsa1.0_01662.1.g28826.t1	ref|XP_002890362.1| hypothetical protein ARALYDRAFT_312926 [Arabidopsis lyrata subsp. lyrata] gi|297336204|gb|EFH66621.1| hypothetical protein ARALYDRAFT_312926 [Arabidopsis lyrata subsp. lyrata]	312	656	1.00E-109	210.3	71.5	81.7	hypothetical protein ARALYDRAFT_312926	gbpln	Arabidopsis lyrata	AT1G19980.1 | Symbols: | cytomatrix protein-related | chr1:6933162-6934643 FORWARD LENGTH=342	312	342	1.00E-108	109.6	71.2	82.1

Rsa1.0_01662.1.g28827.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01662.1.g28828.t1	ref|XP_002882839.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328679|gb|EFH59098.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	147	339	2.00E-32	230.6	61.9	71.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G11060.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06545.1); Has 12 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:3466303-3466944 REVERSE LENGTH=213	147	213	2.00E-33	144.9	59.9	71.4
Rsa1.0_01662.1.g28829.t4	ref|NP_187713.1| dehydration-responsive element-binding protein 2B [Arabidopsis thaliana] gi|48427910|sp|O82133.1|DRE2B_ARATH RecName: Full=Dehydration-responsive element-binding protein 2B; Short=Protein DREB2B gi|6016692|gb|AAF01519.1|AC009991_15 DREB2B transcription factor [Arabidopsis thaliana] gi|3738232|dbj|BAA33795.1| DREB2B [Arabidopsis thaliana] gi|4126708|dbj|BAA36706.1| DREB2B [Arabidopsis thaliana] gi|26449820|dbj|BAC42033.1| putative DREB2B transcription factor [Arabidopsis thaliana] gi|30725376|gb|AAP37710.1| At3g11020 [Arabidopsis thaliana] gi|332641473|gb|AEE74994.1| dehydration-responsive element-binding protein 2B [Arabidopsis thaliana] gi|471180477|gb|AGI05189.1| DRE/CRT-binding protein 2B [Arabidopsis thaliana]	170	330	1.00E-19	194.1	37.6	40.6	dehydration-responsive element-binding protein 2B	gbpln	Arabidopsis thaliana	AT3G11020.1 | Symbols: DREB2B, DREB2 | DRE/CRT-binding protein 2B | chr3:3456009-3457001 FORWARD LENGTH=330	170	330	4.00E-22	194.1	37.6	40.6
Rsa1.0_01662.1.g28830.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01663.1.g28831.t1	ref|NP_195988.1| trihelix DNA binding transcription factor [Arabidopsis thaliana] gi|75311735|sp|Q9LZS0.1|PTL_ARATH RecName: Full=Trihelix transcription factor PTL; AltName: Full=Trihelix DNA-binding protein PETAL LOSS gi|7340653|emb|CAB82933.1| GT2-like protein [Arabidopsis thaliana] gi|332003258|gb|AED90641.1| trihelix transcription factor PTLED96690 [Arabidopsis thaliana]	571	591	0	103.5	86.3	90.9	trihelix DNA binding transcription factor	gbpln	Arabidopsis thaliana	AT5G03680.1 | Symbols: PTL | Duplicated homeodomain-like superfamily protein | chr5:957858-960760 FORWARD LENGTH=591	571	591	0	103.5	86.3	90.9
Rsa1.0_01663.1.g28832.t1	gb|EOA20920.1| hypothetical protein CARUB_v10001255mg [Capsella rubella]	95	359	1.00E-31	377.9	82.1	87.4	hypothetical protein CARUB_v10001255mg	gbpln	Capsella rubella	AT5G03690.1 | Symbols: | Aldolase superfamily protein | chr5:963389-964982 REVERSE LENGTH=393	95	393	6.00E-34	413.7	81.1	87.4
Rsa1.0_01663.1.g28833.t1	dbj|BAJ34040.1| unnamed protein product [Thellungiella halophila]	807	815	0	101.0	90.6	93.8	unnamed protein product	----	----	AT5G03730.1 | Symbols: CTR1, SIS1, AtCTR1 | Protein kinase superfamily protein | chr5:974958-979660 REVERSE LENGTH=821	807	821	0	101.7	88.6	92.6
Rsa1.0_01663.1.g28834.t1	dbj|BAJ34228.1| unnamed protein product [Thellungiella halophila]	482	532	0	110.4	96.5	97.9	unnamed protein product	----	----	AT5G03760.1 | Symbols: ATCSLA09, CSLA09, ATCSLA9, CSLA9, RAT4 | Nucleotide-diphospho-sugar transferases superfamily protein | chr5:985910-990087 REVERSE LENGTH=533	482	533	0	110.6	95.0	97.7
Rsa1.0_01663.1.g28835.t2	emb|CAB82944.1| homeodomain-like protein [Arabidopsis thaliana] gi|9758007|dbj|BAB08604.1| homeodomain-like protein [Arabidopsis thaliana]	175	236	1.00E-71	134.9	82.3	89.1	homeodomain-like protein	gbpln	Arabidopsis thaliana	AT5G03790.1 | Symbols: ATHB51, LMI1, HB51 | homeobox 51 | chr5:1004985-1006373 FORWARD LENGTH=235	175	235	6.00E-74	134.3	82.3	89.1
Rsa1.0_01663.1.g28836.t1	gb|EOA20290.1| hypothetical protein CARUB_v10000598mg, partial [Capsella rubella]	271	562	1.00E-149	207.4	93.4	97.0	hypothetical protein CARUB_v10000598mg, partial	gbpln	Capsella rubella	AT5G03795.1 | Symbols: | Exostosin family protein | chr5:1007554-1010373 REVERSE LENGTH=518	271	518	1.00E-151	191.1	93.4	96.7
Rsa1.0_01664.1.g28837.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01664.1.g28838.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01664.1.g28839.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01664.1.g28840.t1	gb|AAC62132.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]	258	1137	2.00E-66	440.7	54.3	73.3	copia-like retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01664.1.g28841.t1	ref|NP_564087.2| RAD-like 5 protein [Arabidopsis thaliana] gi|75328898|sp|Q8GW75.1|RADL5_ARATH RecName: Full=Protein RADIALIS-like 5; Short=AtRL5; Short=Protein RAD-like 5; AltName: Full=Protein RADIALIS-LIKE SANT/MYB 4; Short=Protein RSM4 gi|26453068|dbj|BAC43610.1| putative myb-related protein [Arabidopsis thaliana] gi|28973505|gb|AAO64077.1| putative myb family transcription factor [Arabidopsis thaliana] gi|41618974|gb|AAS09994.1| MYB transcription factor [Arabidopsis thaliana] gi|87133605|gb|ABD24443.1| RAD-like protein 5 [Arabidopsis thaliana] gi|332191741|gb|AEE29862.1| protein RADIALIS-like 5 [Arabidopsis thaliana]	90	100	1.00E-35	111.1	80.0	83.3	RAD-like 5 protein	gbpln	Arabidopsis thaliana	AT1G19510.1 | Symbols: ATRL5, RSM4, RL5 | RAD-like 5 | chr1:6756483-6757290 REVERSE LENGTH=100	90	100	2.00E-38	111.1	80.0	83.3
Rsa1.0_01664.1.g28842.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	492	695	1.00E-117	141.3	51.8	61.0	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	492	681	2.00E-21	138.4	10.0	16.7
Rsa1.0_01665.1.g28843.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1350	1307	0	96.8	57.7	73.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1350	1262	4.00E-96	93.5	13.3	20.4
Rsa1.0_01665.1.g28844.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	414	1142	1.00E-125	275.8	55.3	70.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	414	575	2.00E-50	138.9	34.1	50.7
Rsa1.0_01665.1.g28845.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	347	672	5.00E-33	193.7	27.7	42.7	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01665.1.g28846.t2	gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	468	1787	6.00E-96	381.8	45.9	63.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01665.1.g28847.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01665.1.g28848.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	249	940	1.00E-14	377.5	19.3	24.5	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01665.1.g28849.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01665.1.g28850.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01666.1.g28851.t1	ref|NP_567934.1| LL-diaminopimelate aminotransferase [Arabidopsis thaliana] gi|75163801|sp|Q93ZN9.1|DAPAT_ARATH RecName: Full=LL-diaminopimelate aminotransferase, chloroplastic; Short=AtDAP-AT; Short=DAP-AT; Short=DAP-aminotransferase; Short=LL-DAP-aminotransferase; AltName: Full=Protein ABERRANT GROWTH AND DEATH 2; Flags: Precursor gi|15912291|gb|AAL08279.1| AT4g33680/T16L1_170 [Arabidopsis thaliana] gi|17529044|gb|AAL38732.1| unknown protein [Arabidopsis thaliana] gi|21436149|gb|AAM51321.1| unknown protein [Arabidopsis thaliana] gi|41323503|gb|AAR99909.1| aminotransferase AGD2 [Arabidopsis thaliana] gi|332660865|gb|AEE86265.1| LL-diaminopimelate aminotransferase [Arabidopsis thaliana]	763	461	0	60.4	56.1	58.1	LL-diaminopimelate aminotransferase	gbpln	Arabidopsis thaliana	AT4G33680.1 | Symbols: AGD2 | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr4:16171847-16174630 REVERSE LENGTH=461	763	461	0	60.4	56.1	58.1

Rsa1.0_01666.1.g28852.t1	ref|NP_567931.1| dynamin-related protein 3A [Arabidopsis thaliana] gi|60392233|sp|Q8S944.2|DRP3A_ARATH RecName: Full=Dynamin-related protein 3A; AltName: Full=Dynamin-like protein 2; AltName: Full=Dynamin-like protein 2a gi|3549667|emb|CAA20578.1| Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana] gi|7270313|emb|CAB80082.1| Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana] gi|19032335|dbj|BAB85643.1| dynamin like protein 2a [Arabidopsis thaliana] gi|332660860|gb|AEE86260.1| dynamin-related protein 3A [Arabidopsis thaliana]	812	808	0	99.5	86.0	92.0	dynamin-related protein 3A	gbpln	Arabidopsis thaliana	AT4G33650.1 | Symbols: ADL2, DRP3A | dynamin-related protein 3A | chr4:16161073-16166587 FORWARD LENGTH=808	812	808	0	99.5	86.0	92.0
Rsa1.0_01666.1.g28853.t1	gb|EOA16153.1| hypothetical protein CARUB_v10004291mg [Capsella rubella]	731	676	0	92.5	81.4	86.9	hypothetical protein CARUB_v10004291mg	gbpln	Capsella rubella	AT4G33630.2 | Symbols: EX1 | Protein of unknown function (DUF3506) | chr4:16155560-16159094 FORWARD LENGTH=684	731	684	0	93.6	82.5	88.1
Rsa1.0_01666.1.g28854.t1	gb|AAF79324.1|AC002304_17 F14J16.29 [Arabidopsis thaliana]	164	143	5.00E-30	87.2	53.0	68.3	F14J16.29	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01666.1.g28855.t1	ref|NP_195086.4| uncharacterized protein [Arabidopsis thaliana] gi|26451329|dbj|BAC42765.1| unknown protein [Arabidopsis thaliana] gi|332660852|gb|AEE86252.1| uncharacterized protein AT4G33600 [Arabidopsis thaliana]	709	470	0	66.3	53.5	56.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G33600.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G33590.1); Has 131 Blast hits to 131 proteins in 40 species: Archae - 0; Bacteria - 9; Metazoa - 12; Fungi - 24; Plants - 58; Viruses - 0; Other Eukaryotes - 28 (source: NCBI BLink). | chr4:16144452-16145864 REVERSE LENGTH=470	709	470	0	66.3	53.5	56.4
Rsa1.0_01666.1.g28856.t1	ref|NP_567928.1| beta carbonic anhydrase 5 [Arabidopsis thaliana] gi|14334478|gb|AAK59437.1| putative carbonate dehydratase [Arabidopsis thaliana] gi|21594039|gb|AAM65957.1| carbonate dehydratase-like protein [Arabidopsis thaliana] gi|21689751|gb|AAM67519.1| putative carbonate dehydratase [Arabidopsis thaliana] gi|62321082|dbj|BAD94173.1| carbonate dehydratase - like protein [Arabidopsis thaliana] gi|332660848|gb|AEE86248.1| beta carbonic anhydrase 5 [Arabidopsis thaliana]	304	301	1.00E-139	99.0	79.9	87.5	beta carbonic anhydrase 5	gbpln	Arabidopsis thaliana	AT4G33580.1 | Symbols: ATBCA5, BCA5 | beta carbonic anhydrase 5 | chr4:16139406-16141363 FORWARD LENGTH=301	304	301	1.00E-142	99.0	79.9	87.5
Rsa1.0_01666.1.g28857.t1	gb|AAD20714.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	364	1750	5.00E-51	480.8	27.5	36.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	364	336	9.00E-35	92.3	19.5	31.6
Rsa1.0_01666.1.g28858.t4	ref|NP_567916.2| F-box/LRR-repeat protein 15 [Arabidopsis thaliana] gi|124007179|sp|Q9SMY8.2|FBL15_ARATH RecName: Full=F-box/LRR-repeat protein 15 gi|332660791|gb|AEE86191.1| F-box/LRR-repeat protein 15 [Arabidopsis thaliana]	909	990	0	108.9	75.9	83.7	F-box/LRR-repeat protein 15	gbpln	Arabidopsis thaliana	AT4G33210.1 | Symbols: SLOMO | F-box family protein | chr4:16015971-16020697 REVERSE LENGTH=990	909	990	0	108.9	75.9	83.7
Rsa1.0_01666.1.g28859.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	299	390	6.00E-38	130.4	26.8	36.8	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	299	295	2.00E-33	98.7	29.8	45.5

Rsa1.0_01666.1.g28860.t1	ref|NP_567916.2| F-box/LRR-repeat protein 15 [Arabidopsis thaliana] gi|124007179|sp|Q9SMY8.2|FBL15_ARATH RecName: Full=F-box/LRR-repeat protein 15 gi|332660791|gb|AEE86191.1| F-box/LRR-repeat protein 15 [Arabidopsis thaliana]	839	990	0	118.0	77.4	85.9	F-box/LRR-repeat protein 15	gbpln	Arabidopsis thaliana	AT4G33210.1 | Symbols: SLOMO | F-box family protein | chr4:16015971-16020697 REVERSE LENGTH=990	839	990	0	118.0	77.4	85.9
Rsa1.0_01666.1.g28861.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01666.1.g28862.t1	ref|XP_002869223.1| hypothetical protein ARALYDRAFT_913110 [Arabidopsis lyrata subsp. lyrata] gi|297315059|gb|EFH45482.1| hypothetical protein ARALYDRAFT_913110 [Arabidopsis lyrata subsp. lyrata]	91	91	1.00E-41	100.0	91.2	93.4	hypothetical protein ARALYDRAFT_913110	gbpln	Arabidopsis lyrata	AT4G33100.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Mitochondrial distribution/morphology family 35/apoptosis (InterPro:IPR007918); Has 214 Blast hits to 214 proteins in 102 species: Archae - 0; Bacteria - 0; Metazoa - 110; Fungi - 69; Plants - 29; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr4:15971701-15972342 FORWARD LENGTH=92	91	92	4.00E-43	101.1	91.2	93.4
Rsa1.0_01666.1.g28863.t2	ref|NP_195035.2| aminopeptidase M1 [Arabidopsis thaliana] gi|17473511|gb|AAL38379.1| AT4g33090/F4I10_20 [Arabidopsis thaliana] gi|24209879|gb|AAN41401.1| aminopeptidase M [Arabidopsis thaliana] gi|29028734|gb|AAO64746.1| At4g33090/F4I10_20 [Arabidopsis thaliana] gi|110742477|dbj|BAE99157.1| aminopeptidase like protein [Arabidopsis thaliana] gi|332660772|gb|AEE86172.1| aminopeptidase M1 [Arabidopsis thaliana]	871	879	0	100.9	92.4	96.2	aminopeptidase M1	gbpln	Arabidopsis thaliana	AT4G33090.1 | Symbols: APM1, ATAPM1 | aminopeptidase M1 | chr4:15965915-15970418 REVERSE LENGTH=879	871	879	0	100.9	92.4	96.2
Rsa1.0_01666.1.g28864.t1	gb|EOA16526.1| hypothetical protein CARUB_v10004685mg [Capsella rubella]	485	487	0	100.4	90.1	93.8	hypothetical protein CARUB_v10004685mg	gbpln	Capsella rubella	AT4G33050.3 | Symbols: EDA39 | calmodulin-binding family protein | chr4:15944604-15946736 REVERSE LENGTH=488	485	488	0	100.6	89.1	93.6
Rsa1.0_01667.1.g28865.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01667.1.g28866.t1	gb|EOA25207.1| hypothetical protein CARUB_v10018520mg [Capsella rubella]	228	223	8.00E-36	97.8	37.3	51.8	hypothetical protein CARUB_v10018520mg	gbpln	Capsella rubella	AT3G57960.1 | Symbols: | Emsy N Terminus (ENT) domain-containing protein | chr3:21463091-21464194 FORWARD LENGTH=223	228	223	6.00E-31	97.8	32.9	46.5
Rsa1.0_01667.1.g28867.t1	ref|XP_002878181.1| hypothetical protein ARALYDRAFT_486249 [Arabidopsis lyrata subsp. lyrata] gi|297324019|gb|EFH54440.1| hypothetical protein ARALYDRAFT_486249 [Arabidopsis lyrata subsp. lyrata]	347	357	2.33E-156	102.9	81.3	89.3	hypothetical protein ARALYDRAFT_486249	gbpln	Arabidopsis lyrata	AT3G57990.1 | Symbols: | unknown protein; Has 1497 Blast hits to 1323 proteins in 52 species: Archae - 0; Bacteria - 4; Metazoa - 23; Fungi - 34; Plants - 61; Viruses - 0; Other Eukaryotes - 1375 (source: NCBI BLink). | chr3:21470244-21471347 REVERSE LENGTH=367	347	367	1.00E-145	105.8	82.1	92.5
Rsa1.0_01667.1.g28868.t1	ref|XP_002876449.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322287|gb|EFH52708.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	173	175	1.00E-62	101.2	77.5	86.1	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT3G58000.1 | Symbols: | VQ motif-containing protein | chr3:21474950-21475477 FORWARD LENGTH=175	173	175	2.00E-55	101.2	75.7	85.0
Rsa1.0_01667.1.g28869.t1	ref|XP_002878182.1| hypothetical protein ARALYDRAFT_486251 [Arabidopsis lyrata subsp. lyrata] gi|297324020|gb|EFH54441.1| hypothetical protein ARALYDRAFT_486251 [Arabidopsis lyrata subsp. lyrata]	327	308	1.00E-134	94.2	80.1	84.1	hypothetical protein ARALYDRAFT_486251	gbpln	Arabidopsis lyrata	AT3G58010.1 | Symbols: PGL34 | plastoglobulin 34kD | chr3:21475949-21477463 REVERSE LENGTH=308	327	308	1.00E-132	94.2	78.3	84.1
Rsa1.0_01667.1.g28870.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01667.1.g28871.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	695	1142	0	164.3	55.3	69.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	695	575	4.00E-50	82.7	22.3	34.5
Rsa1.0_01667.1.g28872.t1	gb|EOA24053.1| hypothetical protein CARUB_v10017271mg [Capsella rubella]	441	437	0	99.1	85.7	90.7	hypothetical protein CARUB_v10017271mg	gbpln	Capsella rubella	AT3G58030.4 | Symbols: | RING/U-box superfamily protein | chr3:21485527-21486837 FORWARD LENGTH=436	441	436	0	98.9	84.6	90.2
Rsa1.0_01667.1.g28873.t1	ref|XP_002876454.1| seven in absentia family protein [Arabidopsis lyrata subsp. lyrata] gi|297322292|gb|EFH52713.1| seven in absentia family protein [Arabidopsis lyrata subsp. lyrata]	311	309	1.00E-176	99.4	94.9	96.5	seven in absentia family protein	gbpln	Arabidopsis lyrata	AT3G58040.1 | Symbols: SINAT2 | seven in absentia of Arabidopsis 2 | chr3:21489612-21491085 FORWARD LENGTH=308	311	308	1.00E-178	99.0	94.9	96.1
Rsa1.0_01667.1.g28874.t1	gb|EOA24117.1| hypothetical protein CARUB_v10017350mg [Capsella rubella]	405	412	0	101.7	86.9	95.1	hypothetical protein CARUB_v10017350mg	gbpln	Capsella rubella	AT3G58060.1 | Symbols: | Cation efflux family protein | chr3:21497778-21499676 REVERSE LENGTH=411	405	411	0	101.5	87.2	94.6

Rsa1.0_01668.1.g28875.t1	ref|XP_002893192.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339034|gb|EFH69451.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	234	172	7.00E-18	73.5	29.9	37.2	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01668.1.g28876.t1	gb|EOA40493.1| hypothetical protein CARUB_v10009218mg [Capsella rubella]	421	426	0	101.2	85.7	91.4	hypothetical protein CARUB_v10009218mg	gbpln	Capsella rubella	AT1G21920.1 | Symbols: | Histone H3 K4-specific methyltransferase SET7/9 family protein | chr1:7704454-7705866 REVERSE LENGTH=417	421	417	1.00E-172	99.0	83.6	91.0
Rsa1.0_01668.1.g28877.t1	ref|XP_002890471.1| AP2 domain-containing transcription factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297336313|gb|EFH66730.1| AP2 domain-containing transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	217	229	1.00E-73	105.5	80.6	84.8	AP2 domain-containing transcription factor family protein	gbpln	Arabidopsis lyrata	AT1G21910.1 | Symbols: DREB26 | Integrase-type DNA-binding superfamily protein | chr1:7696655-7697347 FORWARD LENGTH=230	217	230	1.00E-75	106.0	79.3	86.2
Rsa1.0_01668.1.g28878.t1	ref|XP_002893188.1| emp24/gp25L/p24 family protein [Arabidopsis lyrata subsp. lyrata] gi|297339030|gb|EFH69447.1| emp24/gp25L/p24 family protein [Arabidopsis lyrata subsp. lyrata]	206	216	6.00E-96	104.9	81.6	87.4	emp24/gp25L/p24 family protein	gbpln	Arabidopsis lyrata	AT1G21900.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:7691165-7692327 REVERSE LENGTH=216	206	216	2.00E-94	104.9	81.1	87.9
Rsa1.0_01668.1.g28879.t1	ref|NP_564153.1| LysM domain-containing GPI-anchored protein 1 [Arabidopsis thaliana] gi|38258218|sp|Q93ZH0.1|LYM1_ARATH RecName: Full=LysM domain-containing GPI-anchored protein 1; Flags: Precursor gi|15982870|gb|AAL09782.1| At1g21880/T26F17_5 [Arabidopsis thaliana] gi|53749174|gb|AAU90072.1| At1g21880 [Arabidopsis thaliana] gi|332192047|gb|AEE30168.1| LysM domain-containing GPI-anchored protein 1 [Arabidopsis thaliana]	411	416	0	101.2	85.6	92.5	LysM domain-containing GPI-anchored protein 1	gbpln	Arabidopsis thaliana	AT1G21880.2 | Symbols: LYM1 | lysm domain GPI-anchored protein 1 precursor | chr1:7680689-7682526 FORWARD LENGTH=416	411	416	0	101.2	85.6	92.5
Rsa1.0_01668.1.g28880.t1	ref|XP_002890469.1| hypothetical protein ARALYDRAFT_313079 [Arabidopsis lyrata subsp. lyrata] gi|297336311|gb|EFH66728.1| hypothetical protein ARALYDRAFT_313079 [Arabidopsis lyrata subsp. lyrata]	343	341	0	99.4	94.2	96.5	hypothetical protein ARALYDRAFT_313079	gbpln	Arabidopsis lyrata	AT1G21870.1 | Symbols: GONST5 | golgi nucleotide sugar transporter 5 | chr1:7678208-7679697 FORWARD LENGTH=341	343	341	0	99.4	92.1	95.6
Rsa1.0_01668.1.g28881.t1	ref|XP_002893185.1| hypothetical protein ARALYDRAFT_313074 [Arabidopsis lyrata subsp. lyrata] gi|297339027|gb|EFH69444.1| hypothetical protein ARALYDRAFT_313074 [Arabidopsis lyrata subsp. lyrata]	201	205	8.00E-80	102.0	87.6	93.0	hypothetical protein ARALYDRAFT_313074	gbpln	Arabidopsis lyrata	AT1G21830.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF740 (InterPro:IPR008004); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G44608.1); Has 49 Blast hits to 49 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7661429-7662521 REVERSE LENGTH=206	201	206	1.00E-79	102.5	86.6	93.0
Rsa1.0_01668.1.g28882.t1	ref|XP_002890462.1| hypothetical protein ARALYDRAFT_889647 [Arabidopsis lyrata subsp. lyrata] gi|297336304|gb|EFH66721.1| hypothetical protein ARALYDRAFT_889647 [Arabidopsis lyrata subsp. lyrata]	488	501	0	102.7	86.3	91.0	hypothetical protein ARALYDRAFT_889647	gbpln	Arabidopsis lyrata	AT1G21750.1 | Symbols: ATPDIL1-1, ATPDI5, PDI5, PDIL1-1 | PDI-like 1-1 | chr1:7645767-7648514 FORWARD LENGTH=501	488	501	0	102.7	86.1	90.6
Rsa1.0_01668.1.g28883.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01668.1.g28884.t1	ref|NP_564149.1| proteasome subunit beta type-3-A [Arabidopsis thaliana] gi|288558823|sp|Q9XI05.2|PSB3A_ARATH RecName: Full=Proteasome subunit beta type-3-A; AltName: Full=20S proteasome beta subunit C-1; AltName: Full=Proteasome component T gi|17473525|gb|AAL38246.1| proteasome subunit [Arabidopsis thaliana] gi|21387087|gb|AAM47947.1| proteasome subunit [Arabidopsis thaliana] gi|110740894|dbj|BAE98543.1| 20S proteasome beta subunit PBC2 like protein [Arabidopsis thaliana] gi|332192025|gb|AEE30146.1| proteasome subunit beta type-3-A [Arabidopsis thaliana]	204	204	1.00E-116	100.0	99.0	100.0	proteasome subunit beta type-3-A	gbpln	Arabidopsis thaliana	AT1G21720.1 | Symbols: PBC1 | proteasome beta subunit C1 | chr1:7626394-7628070 FORWARD LENGTH=204	204	204	1.00E-118	100.0	99.0	100.0
Rsa1.0_01669.1.g28885.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01669.1.g28886.t1	ref|XP_002887748.1| EMB1473 [Arabidopsis lyrata subsp. lyrata] gi|297333589|gb|EFH64007.1| EMB1473 [Arabidopsis lyrata subsp. lyrata]	244	242	1.00E-125	99.2	89.3	93.4	EMB1473	gbpln	Arabidopsis lyrata	AT1G78630.1 | Symbols: emb1473 | Ribosomal protein L13 family protein | chr1:29575997-29577406 FORWARD LENGTH=241	244	241	1.00E-118	98.8	89.8	93.9
Rsa1.0_01669.1.g28887.t2	dbj|BAJ33720.1| unnamed protein product [Thellungiella halophila]	295	294	1.00E-138	99.7	88.8	92.5	unnamed protein product	----	----	AT1G78600.1 | Symbols: LZF1, STH3, DBB3 | light-regulated zinc finger protein 1 | chr1:29567370-29568662 FORWARD LENGTH=299	295	299	1.00E-131	101.4	84.4	88.5
Rsa1.0_01669.1.g28888.t1	ref|XP_002889200.1| trehalose-6-phosphate synthase [Arabidopsis lyrata subsp. lyrata] gi|297335041|gb|EFH65459.1| trehalose-6-phosphate synthase [Arabidopsis lyrata subsp. lyrata]	415	955	1.00E-176	230.1	83.1	87.7	trehalose-6-phosphate synthase	gbpln	Arabidopsis lyrata	AT1G78580.1 | Symbols: ATTPS1, TPS1 | trehalose-6-phosphate synthase | chr1:29552495-29557482 REVERSE LENGTH=942	415	942	1.00E-177	227.0	83.4	88.4
Rsa1.0_01669.1.g28889.t2	gb|EOA18136.1| hypothetical protein CARUB_v10006599mg [Capsella rubella]	527	465	1.00E-127	88.2	44.8	57.7	hypothetical protein CARUB_v10006599mg	gbpln	Capsella rubella	AT1G67390.1 | Symbols: | F-box family protein | chr1:25244690-25247139 FORWARD LENGTH=479	527	479	3.00E-86	90.9	35.5	52.4
Rsa1.0_01669.1.g28890.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	526	1274	2.00E-80	242.2	37.3	52.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	526	575	9.00E-44	109.3	27.0	46.8
Rsa1.0_01669.1.g28891.t1	dbj|BAM73281.1| gibberellin 2 oxidase 1 [Raphanus sativus]	320	331	1.00E-158	103.4	86.3	91.3	gibberellin 2 oxidase 1	gbpln	Raphanus sativus	AT1G78440.1 | Symbols: ATGA2OX1, GA2OX1 | Arabidopsis thaliana gibberellin 2-oxidase 1 | chr1:29511772-29512990 REVERSE LENGTH=329	320	329	1.00E-154	102.8	82.8	89.7
Rsa1.0_01670.1.g28892.t1	ref|XP_002866884.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312720|gb|EFH43143.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	121	132	6.00E-47	109.1	79.3	88.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G39795.1 | Symbols: | Protein of unknown function (DUF581) | chr4:18466621-18467325 FORWARD LENGTH=126	121	126	1.00E-44	104.1	73.6	83.5
Rsa1.0_01670.1.g28893.t1	ref|NP_200334.1| microtubule-associated proteins 65-1 [Arabidopsis thaliana] gi|75171506|sp|Q9FLP0.1|MA651_ARATH RecName: Full=65-kDa microtubule-associated protein 1; Short=AtMAP65-1 gi|9758120|dbj|BAB08592.1| unnamed protein product [Arabidopsis thaliana] gi|28416713|gb|AAO42887.1| At5g55230 [Arabidopsis thaliana] gi|110735819|dbj|BAE99886.1| hypothetical protein [Arabidopsis thaliana] gi|332009219|gb|AED96602.1| microtubule-associated proteins 65-1 [Arabidopsis thaliana]	225	587	9.00E-35	260.9	32.4	35.1	microtubule-associated proteins 65-1	gbpln	Arabidopsis thaliana	AT5G55230.1 | Symbols: ATMAP65-1, MAP65-1 | microtubule-associated proteins 65-1 | chr5:22402716-22405182 FORWARD LENGTH=587	225	587	3.00E-37	260.9	32.4	35.1
Rsa1.0_01670.1.g28894.t1	ref|XP_002868929.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314765|gb|EFH45188.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	631	661	0	104.8	79.9	86.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G39790.1 | Symbols: | Protein of unknown function (DUF630 and DUF632) | chr4:18462316-18464584 REVERSE LENGTH=657	631	657	0	104.1	79.6	85.6
Rsa1.0_01670.1.g28895.t1	ref|NP_195688.1| ethylene-responsive transcription factor ERF060 [Arabidopsis thaliana] gi|75219968|sp|O65665.1|ERF60_ARATH RecName: Full=Ethylene-responsive transcription factor ERF060 gi|3080447|emb|CAA18764.1| putative protein [Arabidopsis thaliana] gi|7270962|emb|CAB80641.1| putative protein [Arabidopsis thaliana] gi|106879185|gb|ABF82622.1| At4g39780 [Arabidopsis thaliana] gi|332661718|gb|AEE87118.1| ethylene-responsive transcription factor ERF060 [Arabidopsis thaliana]	276	272	1.00E-122	98.6	78.6	85.5	ethylene-responsive transcription factor ERF060	gbpln	Arabidopsis thaliana	AT4G39780.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr4:18458216-18459034 REVERSE LENGTH=272	276	272	1.00E-124	98.6	78.6	85.5
Rsa1.0_01670.1.g28896.t1	ref|XP_002868927.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314763|gb|EFH45186.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	417	349	1.00E-179	83.7	72.9	76.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G39770.1 | Symbols: TPPH | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr4:18449138-18451218 REVERSE LENGTH=349	417	349	1.00E-180	83.7	71.9	75.5
Rsa1.0_01670.1.g28897.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01671.1.g28898.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	343	1142	2.00E-39	332.9	26.2	34.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	343	575	1.00E-19	167.6	19.0	29.4
Rsa1.0_01671.1.g28899.t5	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1754	1274	1.00E-167	72.6	20.9	29.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1754	746	3.00E-37	42.5	4.7	6.4

Rsa1.0_01671.1.g28900.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1634	1838	0	112.5	37.5	54.5	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01671.1.g28901.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01671.1.g28902.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01671.1.g28903.t1	gb|AAD25646.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	307	1461	2.00E-81	475.9	52.1	67.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01671.1.g28904.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	988	1838	0	186.0	53.8	68.5	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01671.1.g28905.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01671.1.g28906.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01672.1.g28907.t1	ref|XP_002893783.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339625|gb|EFH70042.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	215	276	1.00E-17	128.4	31.2	42.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G03495.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:873804-875025 REVERSE LENGTH=226	215	226	9.00E-17	105.1	31.6	43.7
Rsa1.0_01672.1.g28908.t1	ref|XP_002883446.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297329286|gb|EFH59705.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	212	319	2.00E-13	150.5	27.8	36.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G53700.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:21801221-21802546 FORWARD LENGTH=251	212	251	5.00E-11	118.4	28.3	41.0
Rsa1.0_01672.1.g28909.t1	ref|NP_851236.1| evolutionarily conserved C-terminal region 3 protein [Arabidopsis thaliana] gi|332010029|gb|AED97412.1| evolutionarily conserved C-terminal region 3 protein [Arabidopsis thaliana]	196	495	1.00E-43	252.6	44.9	48.5	evolutionarily conserved C-terminal region 3 protein	gbpln	Arabidopsis thaliana	AT5G61020.1 | Symbols: ECT3 | evolutionarily conserved C-terminal region 3 | chr5:24557485-24559780 REVERSE LENGTH=495	196	495	5.00E-46	252.6	44.9	48.5
Rsa1.0_01672.1.g28910.t2	gb|EOA28853.1| hypothetical protein CARUB_v10025097mg, partial [Capsella rubella]	544	600	1.00E-117	110.3	42.8	56.8	hypothetical protein CARUB_v10025097mg, partial	gbpln	Capsella rubella	AT3G17450.1 | Symbols: | hAT dimerisation domain-containing protein | chr3:5972793-5975684 REVERSE LENGTH=877	544	877	7.00E-52	161.2	23.9	38.2
Rsa1.0_01672.1.g28911.t1	gb|AAG10810.1|AC018460_4 Hypothetical protein [Arabidopsis thaliana] gi|12320956|gb|AAG50601.1|AC079605_6 hypothetical protein [Arabidopsis thaliana]	100	484	1.00E-38	484.0	72.0	90.0	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01672.1.g28912.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01673.1.g28913.t1	gb|EOA38204.1| hypothetical protein CARUB_v10009681mg [Capsella rubella]	331	335	1.00E-153	101.2	86.1	90.6	hypothetical protein CARUB_v10009681mg	gbpln	Capsella rubella	AT1G33780.1 | Symbols: | Protein of unknown function (DUF179) | chr1:12244799-12246034 REVERSE LENGTH=325	331	325	2.33E-156	98.2	85.5	90.0
Rsa1.0_01673.1.g28914.t2	gb|EOA39920.1| hypothetical protein CARUB_v10008607mg [Capsella rubella]	618	616	0	99.7	84.1	89.6	hypothetical protein CARUB_v10008607mg	gbpln	Capsella rubella	AT1G33770.1 | Symbols: | Protein kinase superfamily protein | chr1:12242126-12244462 FORWARD LENGTH=614	618	614	0	99.4	85.6	89.8
Rsa1.0_01673.1.g28915.t1	ref|NP_174637.1| protein kinase-like protein [Arabidopsis thaliana] gi|9665093|gb|AAF97284.1|AC010164_6 Putative protein kinase [Arabidopsis thaliana] gi|332193501|gb|AEE31622.1| protein kinase-like protein [Arabidopsis thaliana]	78	614	3.00E-24	787.2	80.8	84.6	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G33770.1 | Symbols: | Protein kinase superfamily protein | chr1:12242126-12244462 FORWARD LENGTH=614	78	614	5.00E-27	787.2	80.8	84.6
Rsa1.0_01673.1.g28916.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01673.1.g28917.t2	ref|XP_004292625.1| PREDICTED: uncharacterized protein LOC101299743 [Fragaria vesca subsp. vesca]	638	746	1.00E-156	116.9	46.4	60.2	PREDICTED: uncharacterized protein LOC101299743	gbpln	Fragaria vesca	AT4G15020.2 | Symbols: | hAT transposon superfamily | chr4:8575806-8578372 FORWARD LENGTH=768	638	768	9.00E-54	120.4	25.9	40.1
Rsa1.0_01673.1.g28918.t1	gb|EOA39596.1| hypothetical protein CARUB_v10008221mg, partial [Capsella rubella]	951	952	0	100.1	91.9	96.0	hypothetical protein CARUB_v10008221mg, partial	gbpln	Capsella rubella	AT1G33700.2 | Symbols: | Beta-glucosidase, GBA2 type family protein | chr1:12208853-12213571 REVERSE LENGTH=947	951	947	0	99.6	90.5	95.4
Rsa1.0_01674.1.g28919.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01674.1.g28920.t1	ref|NP_974572.1| uncharacterized protein [Arabidopsis thaliana] gi|332658751|gb|AEE84151.1| uncharacterized protein AT4G19160 [Arabidopsis thaliana]	445	453	1.00E-154	101.8	69.4	79.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G19160.2 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:10477772-10479947 FORWARD LENGTH=453	445	453	1.00E-157	101.8	69.4	79.8
Rsa1.0_01674.1.g28921.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01674.1.g28922.t1	dbj|BAJ34120.1| unnamed protein product [Thellungiella halophila]	578	602	0	104.2	87.5	93.8	unnamed protein product	----	----	AT4G19170.1 | Symbols: NCED4, CCD4 | nine-cis-epoxycarotenoid dioxygenase 4 | chr4:10481835-10483622 FORWARD LENGTH=595	578	595	0	102.9	83.4	89.3
Rsa1.0_01674.1.g28923.t2	ref|XP_002867949.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata] gi|297313785|gb|EFH44208.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata]	268	398	1.00E-132	148.5	88.1	92.2	integral membrane family protein	gbpln	Arabidopsis lyrata	AT4G19185.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:10489201-10491488 REVERSE LENGTH=398	268	398	1.00E-134	148.5	87.3	92.2

Rsa1.0_01674.1.g28924.t1	emb|CAA16708.1| putatative protein [Arabidopsis thaliana] gi|7268714|emb|CAB78921.1| putatative protein [Arabidopsis thaliana]	604	1260	0	208.6	80.3	88.7	putatative protein	gbpln	Arabidopsis thaliana	AT4G19191.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:10496228-10498192 FORWARD LENGTH=654	604	654	0	108.3	80.3	88.7
Rsa1.0_01674.1.g28925.t1	ref|XP_002869995.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297315831|gb|EFH46254.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	183	171	7.00E-19	93.4	52.5	53.0	expressed protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01674.1.g28926.t1	gb|EOA18927.1| hypothetical protein CARUB_v10007560mg [Capsella rubella]	605	605	0	100.0	98.0	98.8	hypothetical protein CARUB_v10007560mg	gbpln	Capsella rubella	AT4G19210.1 | Symbols: ATRLI2, RLI2 | RNAse l inhibitor protein 2 | chr4:10501906-10504776 FORWARD LENGTH=605	605	605	0	100.0	97.7	99.0
Rsa1.0_01674.1.g28927.t1	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1358	1413	0	104.1	66.9	78.1	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1358	1262	0	92.9	23.3	29.3
Rsa1.0_01674.1.g28928.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01674.1.g28929.t1	pir||H85073 probable transposon protein [imported] - Arabidopsis thaliana gi|5032279|gb|AAD38227.1|AF147264_10 may be a pseudogene [Arabidopsis thaliana] gi|7267351|emb|CAB81124.1| putative transposon protein [Arabidopsis thaliana]	779	483	0	62.0	44.3	52.6	probable transposon protein	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	779	696	7.00E-79	89.3	24.0	38.8
Rsa1.0_01674.1.g28930.t1	ref|XP_002867929.1| hypothetical protein ARALYDRAFT_492902 [Arabidopsis lyrata subsp. lyrata] gi|297313765|gb|EFH44188.1| hypothetical protein ARALYDRAFT_492902 [Arabidopsis lyrata subsp. lyrata]	268	268	1.00E-133	100.0	86.2	92.2	hypothetical protein ARALYDRAFT_492902	gbpln	Arabidopsis lyrata	AT4G19645.2 | Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr4:10689941-10691298 REVERSE LENGTH=268	268	268	1.00E-131	100.0	83.6	90.7
Rsa1.0_01674.1.g28931.t1	gb|EOA27577.1| hypothetical protein CARUB_v10023716mg [Capsella rubella]	309	302	1.00E-120	97.7	69.3	82.2	hypothetical protein CARUB_v10023716mg	gbpln	Capsella rubella	AT4G02850.1 | Symbols: | phenazine biosynthesis PhzC/PhzF family protein | chr4:1266535-1268569 REVERSE LENGTH=306	309	306	1.00E-122	99.0	68.6	83.8
Rsa1.0_01674.1.g28932.t1	ref|XP_002874893.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297320730|gb|EFH51152.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	528	525	0	99.4	86.2	92.8	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G02820.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:1258581-1260265 FORWARD LENGTH=532	528	532	0	100.8	84.5	92.0
Rsa1.0_01674.1.g28933.t1	gb|EOA15357.1| hypothetical protein CARUB_v10005280mg [Capsella rubella]	234	317	6.00E-89	135.5	75.6	83.3	hypothetical protein CARUB_v10005280mg	gbpln	Capsella rubella	AT4G19700.1 | Symbols: RING | SBP (S-ribonuclease binding protein) family protein | chr4:10713633-10714635 REVERSE LENGTH=304	234	304	1.00E-86	129.9	74.4	81.6
Rsa1.0_01674.1.g28934.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01674.1.g28935.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01675.1.g28936.t1	gb|EOA24380.1| hypothetical protein CARUB_v10017617mg [Capsella rubella]	201	330	5.00E-70	164.2	78.6	87.6	hypothetical protein CARUB_v10017617mg	gbpln	Capsella rubella	AT3G58120.1 | Symbols: ATBZIP61, BZIP61 | Basic-leucine zipper (bZIP) transcription factor family protein | chr3:21521289-21523078 REVERSE LENGTH=329	201	329	6.00E-70	163.7	80.1	88.6
Rsa1.0_01675.1.g28937.t5	ref|NP_191372.2| N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein [Arabidopsis thaliana] gi|79315492|ref|NP_001030882.1| N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein [Arabidopsis thaliana] gi|50198821|gb|AAT70443.1| At3g58130 [Arabidopsis thaliana] gi|51972138|gb|AAU15173.1| At3g58130 [Arabidopsis thaliana] gi|332646224|gb|AEE79745.1| N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein [Arabidopsis thaliana] gi|332646225|gb|AEE79746.1| N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein [Arabidopsis thaliana]	238	257	1.00E-101	108.0	73.5	81.5	N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein	gbpln	Arabidopsis thaliana	AT3G58130.2 | Symbols: | N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein | chr3:21527946-21529654 FORWARD LENGTH=257	238	257	1.00E-104	108.0	73.5	81.5
Rsa1.0_01675.1.g28938.t1	gb|EOA24075.1| hypothetical protein CARUB_v10017303mg [Capsella rubella]	432	430	0	99.5	91.0	94.7	hypothetical protein CARUB_v10017303mg	gbpln	Capsella rubella	AT3G58140.1 | Symbols: | phenylalanyl-tRNA synthetase class IIc family protein | chr3:21529988-21532386 REVERSE LENGTH=429	432	429	0	99.3	89.8	93.8

Rsa1.0_01675.1.g28939.t6	ref|NP_191376.1| Bet1-like SNARE 1-1 [Arabidopsis thaliana] gi|27805428|sp|Q9M2J9.1|BET11_ARATH RecName: Full=Bet1-like SNARE 1-1; Short=AtBET11; AltName: Full=Bet1/Sft1-like SNARE 14a; Short=AtBS14a gi|14030603|gb|AAK52976.1|AF368175_1 Bet1/Sft1-like SNARE AtBS14a [Arabidopsis thaliana] gi|6735329|emb|CAB68155.1| putative protein [Arabidopsis thaliana] gi|26449796|dbj|BAC42021.1| unknown protein [Arabidopsis thaliana] gi|28416841|gb|AAO42951.1| At3g58170 [Arabidopsis thaliana] gi|332646229|gb|AEE79750.1| Bet1-like SNARE 1-1 [Arabidopsis thaliana]	198	122	1.00E-53	61.6	52.5	54.0	Bet1-like SNARE 1-1	gbpln	Arabidopsis thaliana	AT3G58170.1 | Symbols: ATBS14A, ATBET11, BET11, BS14A | BET1P/SFT1P-like protein 14A | chr3:21542632-21543775 REVERSE LENGTH=122	198	122	4.00E-56	61.6	52.5	54.0
Rsa1.0_01675.1.g28940.t1	gb|EOA25554.1| hypothetical protein CARUB_v10018899mg [Capsella rubella]	317	310	1.00E-158	97.8	89.3	93.4	hypothetical protein CARUB_v10018899mg	gbpln	Capsella rubella	AT3G58180.1 | Symbols: | ARM repeat superfamily protein | chr3:21544189-21545981 FORWARD LENGTH=314	317	314	1.00E-159	99.1	88.3	93.4
Rsa1.0_01675.1.g28941.t1	ref|NP_191378.1| LOB domain-containing protein 29 [Arabidopsis thaliana] gi|29428017|sp|Q9M2J7.1|LBD29_ARATH RecName: Full=LOB domain-containing protein 29; AltName: Full=ASYMMETRIC LEAVES 2-like protein 16; Short=AS2-like protein 16 gi|17227168|gb|AAL38038.1|AF447893_1 LOB DOMAIN 29 [Arabidopsis thaliana] gi|6735331|emb|CAB68157.1| putative protein [Arabidopsis thaliana] gi|94442495|gb|ABF19035.1| At3g58190 [Arabidopsis thaliana] gi|219807108|dbj|BAH10560.1| ASYMMETRIC LEAVES2-like 16 protein [Arabidopsis thaliana] gi|332646231|gb|AEE79752.1| LOB domain-containing protein 29 [Arabidopsis thaliana]	222	218	4.00E-99	98.2	85.1	90.5	LOB domain-containing protein 29	gbpln	Arabidopsis thaliana	AT3G58190.1 | Symbols: LBD29, ASL16 | lateral organ boundaries-domain 29 | chr3:21548716-21549488 REVERSE LENGTH=218	222	218	1.00E-101	98.2	85.1	90.5
Rsa1.0_01675.1.g28942.t1	gb|EOA25991.1| hypothetical protein CARUB_v10019380mg [Capsella rubella]	292	330	3.00E-67	113.0	51.7	69.2	hypothetical protein CARUB_v10019380mg	gbpln	Capsella rubella	AT3G58210.1 | Symbols: | TRAF-like family protein | chr3:21562645-21564067 REVERSE LENGTH=330	292	330	5.00E-61	113.0	51.4	69.5
Rsa1.0_01675.1.g28943.t1	ref|XP_002878213.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324051|gb|EFH54472.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	241	305	1.00E-71	126.6	60.2	72.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G58340.1 | Symbols: | TRAF-like family protein | chr3:21589071-21590401 REVERSE LENGTH=325	241	325	9.00E-74	134.9	61.0	73.0
Rsa1.0_01675.1.g28944.t1	ref|NP_191400.1| TRAF-like family protein [Arabidopsis thaliana] gi|6735353|emb|CAB68179.1| putative protein [Arabidopsis thaliana] gi|332646257|gb|AEE79778.1| TRAF-like family protein [Arabidopsis thaliana]	296	328	3.00E-68	110.8	55.1	67.9	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G58410.1 | Symbols: | TRAF-like family protein | chr3:21604871-21606229 REVERSE LENGTH=328	296	328	8.00E-71	110.8	55.1	67.9
Rsa1.0_01675.1.g28945.t1	ref|XP_002878218.1| hypothetical protein ARALYDRAFT_907321 [Arabidopsis lyrata subsp. lyrata] gi|297324056|gb|EFH54477.1| hypothetical protein ARALYDRAFT_907321 [Arabidopsis lyrata subsp. lyrata]	307	323	1.00E-85	105.2	61.2	76.5	hypothetical protein ARALYDRAFT_907321	gbpln	Arabidopsis lyrata	AT3G58410.1 | Symbols: | TRAF-like family protein | chr3:21604871-21606229 REVERSE LENGTH=328	307	328	2.00E-87	106.8	59.3	72.6
Rsa1.0_01675.1.g28946.t1	ref|NP_001190126.1| rhomboid-like protein 15 [Arabidopsis thaliana] gi|332646264|gb|AEE79785.1| rhomboid-like protein 15 [Arabidopsis thaliana]	324	426	1.00E-166	131.5	90.4	94.4	rhomboid-like protein 15	gbpln	Arabidopsis thaliana	AT3G58460.2 | Symbols: RBL15 | RHOMBOID-like protein 15 | chr3:21623374-21626642 REVERSE LENGTH=426	324	426	1.00E-169	131.5	90.4	94.4
Rsa1.0_01676.1.g28947.t1	ref|NP_190817.1| heat shock protein-like protein [Arabidopsis thaliana] gi|4886278|emb|CAB43425.1| putative protein [Arabidopsis thaliana] gi|44917467|gb|AAS49058.1| At3g52490 [Arabidopsis thaliana] gi|332645430|gb|AEE78951.1| heat shock protein-like protein [Arabidopsis thaliana]	786	815	0	103.7	85.1	90.2	heat shock protein-like protein	gbpln	Arabidopsis thaliana	AT3G52490.1 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr3:19455850-19458721 REVERSE LENGTH=815	786	815	0	103.7	85.1	90.2
Rsa1.0_01676.1.g28948.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01676.1.g28949.t1	gb|ABB36604.1| hairpin-induced 1-like protein NHL18B [Brassica napus]	208	208	1.00E-113	100.0	95.2	98.1	hairpin-induced 1-like protein NHL18B	gbpln	Brassica napus	AT3G52470.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr3:19450750-19451376 FORWARD LENGTH=208	208	208	1.00E-105	100.0	85.6	91.8

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<tr><td>Rsa1.0_01676.1.g28950.t1</td><td>dbj|BAA96887.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana]</td><td>253</td><td>1140</td><td>9.00E-25</td><td>450.6</td><td>37.5</td><td>57.3</td><td>copia-like retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01677.1.g28951.t1</td><td>gb|EOA33660.1| hypothetical protein CARUB_v10019828mg [Capsella rubella]</td><td>770</td><td>784</td><td>0</td><td>101.8</td><td>91.4</td><td>94.9</td><td>hypothetical protein CARUB_v10019828mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G68740.1 | Symbols: PHO1;H1 | EXS (ERD1/XPR1/SYG1) family protein | chr1:25812735-25816574 REVERSE LENGTH=784</td><td>770</td><td>784</td><td>0</td><td>101.8</td><td>91.6</td><td>94.7</td></tr>
<tr><td>Rsa1.0_01677.1.g28952.t1</td><td>ref|NP_177038.1| phospholipid-translocating ATPase [Arabidopsis thaliana] gi|12229673|sp|Q9SX33.1|ALA9_ARATH RecName: Full=Putative phospholipid-transporting ATPase 9; Short=AtALA9; AltName: Full=Aminophospholipid flippase 9 gi|5734708|gb|AAD49973.1|AC008075_6 Similar to gb|AF067820 ATPase II from Homo sapiens and is a member of PF|00122 E1-E2 ATPases family [Arabidopsis thaliana] gi|332196709|gb|AEE34830.1| putative phospholipid-transporting ATPase 9 [Arabidopsis thaliana]</td><td>1203</td><td>1200</td><td>0</td><td>99.8</td><td>91.6</td><td>95.3</td><td>phospholipid-translocating ATPase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68710.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:25793498-25797975 REVERSE LENGTH=1200</td><td>1203</td><td>1200</td><td>0</td><td>99.8</td><td>91.6</td><td>95.3</td></tr>
<tr><td>Rsa1.0_01677.1.g28953.t4</td><td>ref|NP_173940.2| proline-rich extensin-like receptor kinase 10 [Arabidopsis thaliana] gi|310947343|sp|Q9C660.2|PEK10_ARATH RecName: Full=Proline-rich receptor-like protein kinase PERK10; AltName: Full=Proline-rich extensin-like receptor kinase 10; Short=AtPERK10 gi|332192534|gb|AEE30655.1| proline-rich extensin-like receptor kinase 10 [Arabidopsis thaliana]</td><td>852</td><td>762</td><td>0</td><td>89.4</td><td>37.4</td><td>43.2</td><td>proline-rich extensin-like receptor kinase 10</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G26150.1 | Symbols: ATPERK10, PERK10 | proline-rich extensin-like receptor kinase 10 | chr1:9039790-9042873 REVERSE LENGTH=762</td><td>852</td><td>762</td><td>0</td><td>89.4</td><td>37.4</td><td>43.2</td></tr>
<tr><td>Rsa1.0_01677.1.g28954.t1</td><td>gb|AAD49976.1|AC008075_9 F24J5.9 [Arabidopsis thaliana]</td><td>325</td><td>353</td><td>1.00E-106</td><td>108.6</td><td>68.9</td><td>75.7</td><td>F24J5.9</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G68670.1 | Symbols: | myb-like transcription factor family protein | chr1:25782344-25783873 FORWARD LENGTH=354</td><td>325</td><td>354</td><td>1.00E-109</td><td>108.9</td><td>68.9</td><td>75.7</td></tr>
<tr><td>Rsa1.0_01678.1.g28955.t1</td><td>ref|NP_567339.1| putative purine permease 13 [Arabidopsis thaliana] gi|75158986|sp|Q8RY83.1|PUP13_ARATH RecName: Full=Probable purine permease 13; Short=AtPUP13 gi|18491201|gb|AAL69503.1| unknown protein [Arabidopsis thaliana] gi|20465911|gb|AAM20108.1| unknown protein [Arabidopsis thaliana] gi|21593430|gb|AAM65397.1| purine permease-like protein [Arabidopsis thaliana] gi|332657272|gb|AEE82672.1| putative purine permease 13 [Arabidopsis thaliana]</td><td>163</td><td>361</td><td>8.00E-44</td><td>221.5</td><td>59.5</td><td>68.7</td><td>putative purine permease 13</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G08700.1 | Symbols: ATPUP13 | Drug/metabolite transporter superfamily protein | chr4:5565998-5567286 REVERSE LENGTH=361</td><td>163</td><td>361</td><td>3.00E-46</td><td>221.5</td><td>59.5</td><td>68.7</td></tr>
<tr><td>Rsa1.0_01678.1.g28956.t1</td><td>gb|ABD65028.1| hypothetical protein 26.t00082 [Brassica oleracea]</td><td>164</td><td>220</td><td>6.00E-24</td><td>134.1</td><td>35.4</td><td>40.9</td><td>hypothetical protein 26.t00082</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384</td><td>164</td><td>384</td><td>3.00E-12</td><td>234.1</td><td>21.3</td><td>28.7</td></tr>
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<tr><td>Rsa1.0_01678.1.g28958.t2</td><td>gb|EOA38871.1| hypothetical protein CARUB_v10011236mg, partial [Capsella rubella]</td><td>385</td><td>301</td><td>1.00E-79</td><td>78.2</td><td>42.9</td><td>53.5</td><td>hypothetical protein CARUB_v10011236mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G11910.1 | Symbols: APA1, ATAPA1 | aspartic proteinase A1 | chr1:4017119-4019874 REVERSE LENGTH=506</td><td>385</td><td>506</td><td>7.00E-62</td><td>131.4</td><td>34.8</td><td>46.5</td></tr>
<tr><td>Rsa1.0_01678.1.g28959.t1</td><td>gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]</td><td>596</td><td>723</td><td>1.00E-120</td><td>121.3</td><td>44.8</td><td>60.4</td><td>Tam3-like transposon protein; 93317-95488</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>596</td><td>696</td><td>5.00E-17</td><td>116.8</td><td>14.9</td><td>28.2</td></tr>
<tr><td>Rsa1.0_01678.1.g28960.t1</td><td>dbj|BAA85462.1| transposon-like ORF [Brassica rapa]</td><td>212</td><td>703</td><td>1.00E-101</td><td>331.6</td><td>87.3</td><td>91.0</td><td>transposon-like ORF</td><td>gbpln</td><td>Brassica rapa</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01678.1.g28961.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1247</td><td>1307</td><td>0</td><td>104.8</td><td>53.2</td><td>66.8</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1247</td><td>1262</td><td>4.00E-83</td><td>101.2</td><td>14.4</td><td>21.7</td></tr>
<tr><td>Rsa1.0_01678.1.g28962.t1</td><td>gb|EOA18522.1| hypothetical protein CARUB_v10007075mg [Capsella rubella]</td><td>407</td><td>401</td><td>1.00E-122</td><td>98.5</td><td>57.0</td><td>70.0</td><td>hypothetical protein CARUB_v10007075mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G22180.1 | Symbols: | F-box family protein with a domain of unknown function (DUF295) | chr4:11738574-11739782 FORWARD LENGTH=402</td><td>407</td><td>402</td><td>1.00E-120</td><td>98.8</td><td>56.8</td><td>71.5</td></tr>
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Rsa1.0_01678.1.g28963.t2	gb|AAC61291.1| Ac-like transposase [Arabidopsis thaliana]	727	730	0	100.4	52.3	69.7	Ac-like transposase	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	727	696	2.00E-52	95.7	22.7	42.1
Rsa1.0_01678.1.g28964.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	247	1499	1.00E-14	606.9	15.8	19.8	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01678.1.g28965.t1	ref|XP_002874507.1| arginase [Arabidopsis lyrata subsp. lyrata] gi|297320344|gb|EFH50766.1| arginase [Arabidopsis lyrata subsp. lyrata]	341	342	0	100.3	94.7	98.8	arginase	gbpln	Arabidopsis lyrata	AT4G08900.1 | Symbols: | arginase | chr4:5703499-5705180 FORWARD LENGTH=342	341	342	0	100.3	93.8	97.9
Rsa1.0_01679.1.g28966.t1	ref|XP_002885406.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297331246|gb|EFH61665.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	403	408	0	101.2	86.1	91.1	kinase family protein	gbpln	Arabidopsis lyrata	AT3G20830.1 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr3:7285024-7286250 REVERSE LENGTH=408	403	408	0	101.2	85.4	89.8
Rsa1.0_01679.1.g28967.t1	dbj|BAJ33628.1| unnamed protein product [Thellungiella halophila]	365	365	0	100.0	93.7	96.4	unnamed protein product	----	----	AT3G20820.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:7280930-7282027 FORWARD LENGTH=365	365	365	0	100.0	90.1	93.4
Rsa1.0_01679.1.g28968.t1	gb|AEK21797.1| jmjC domain-containing histone demethylases [Brassica rapa subsp. oleifera]	421	414	0	98.3	95.5	96.4	jmjC domain-containing histone demethylases	gbpln	Brassica rapa	AT3G20810.1 | Symbols: JMJD5 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:7275814-7278144 FORWARD LENGTH=418	421	418	0	99.3	90.3	94.3
Rsa1.0_01679.1.g28969.t1	gb|EOA30908.1| hypothetical protein CARUB_v10014055mg, partial [Capsella rubella]	313	356	1.00E-175	113.7	98.4	99.0	hypothetical protein CARUB_v10014055mg, partial	gbpln	Capsella rubella	AT3G20800.1 | Symbols: | Cell differentiation, Rcd1-like protein | chr3:7271412-7273897 REVERSE LENGTH=316	313	316	1.00E-176	101.0	97.4	98.1
Rsa1.0_01679.1.g28970.t1	ref|XP_002883268.1| oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297329108|gb|EFH59527.1| oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	362	360	0	99.4	89.0	94.5	oxidoreductase family protein	gbpln	Arabidopsis lyrata	AT3G20790.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:7268802-7271099 FORWARD LENGTH=355	362	355	0	98.1	87.6	93.4
Rsa1.0_01679.1.g28971.t6	gb|EOA30031.1| hypothetical protein CARUB_v10013135mg [Capsella rubella]	667	670	0	100.4	94.3	96.3	hypothetical protein CARUB_v10013135mg	gbpln	Capsella rubella	AT3G20780.1 | Symbols: ATTOP6B, BIN3, HYP6, RHL3, TOP6B | topoisomerase 6 subunit B | chr3:7264025-7268498 REVERSE LENGTH=670	667	670	0	100.4	94.2	96.1
Rsa1.0_01679.1.g28972.t1	gb|EOA30103.1| hypothetical protein CARUB_v10013213mg [Capsella rubella]	648	627	0	96.8	86.1	90.0	hypothetical protein CARUB_v10013213mg	gbpln	Capsella rubella	AT3G20770.1 | Symbols: EIN3, AtEIN3 | Ethylene insensitive 3 family protein | chr3:7260702-7262588 REVERSE LENGTH=628	648	628	0	96.9	85.2	88.9
Rsa1.0_01680.1.g28973.t1	ref|XP_002870703.1| hypothetical protein ARALYDRAFT_916192 [Arabidopsis lyrata subsp. lyrata] gi|297316539|gb|EFH46962.1| hypothetical protein ARALYDRAFT_916192 [Arabidopsis lyrata subsp. lyrata]	106	112	4.00E-38	105.7	82.1	87.7	hypothetical protein ARALYDRAFT_916192	gbpln	Arabidopsis lyrata	AT5G40460.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27630.1); Has 87 Blast hits to 87 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 87; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:16202465-16202803 FORWARD LENGTH=112	106	112	7.00E-41	105.7	80.2	86.8
Rsa1.0_01680.1.g28974.t3	gb|AAK25747.2|AF334814_1 putative transcription factor MYB115 [Arabidopsis thaliana]	339	359	3.00E-43	105.9	30.7	37.8	putative transcription factor MYB115	gbpln	Arabidopsis thaliana	AT5G40360.1 | Symbols: MYB115, AtMYB115 | myb domain protein 115 | chr5:16145220-16146579 FORWARD LENGTH=359	339	359	1.00E-45	105.9	30.7	37.8
Rsa1.0_01680.1.g28975.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01680.1.g28976.t1	ref|XP_002870704.1| ATMKK3 MITOGEN-ACTIVATED kinase [Arabidopsis lyrata subsp. lyrata] gi|297316540|gb|EFH46963.1| ATMKK3 MITOGEN-ACTIVATED kinase [Arabidopsis lyrata subsp. lyrata]	518	520	0	100.4	92.9	96.9	ATMKK3 MITOGEN-ACTIVATED kinase	gbpln	Arabidopsis lyrata	AT5G40440.1 | Symbols: ATMKK3, MKK3 | mitogen-activated protein kinase kinase 3 | chr5:16182149-16184513 FORWARD LENGTH=520	518	520	0	100.4	92.5	96.3
Rsa1.0_01680.1.g28977.t1	gb|ACG69509.1| oleosin S4-3 [Brassica napus]	220	220	3.00E-85	100.0	90.9	92.3	oleosin S4-3	gbpln	Brassica napus	AT5G40420.1 | Symbols: OLEO2, OLE2 | oleosin 2 | chr5:16173622-16174740 REVERSE LENGTH=199	220	199	4.00E-76	90.5	75.5	82.3
Rsa1.0_01680.1.g28978.t1	ref|XP_002870709.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297316545|gb|EFH46968.1| binding protein [Arabidopsis lyrata subsp. lyrata]	619	608	0	98.2	76.1	85.3	binding protein	gbpln	Arabidopsis lyrata	AT5G40400.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:16166444-16168276 FORWARD LENGTH=610	619	610	0	98.5	75.9	84.5
Rsa1.0_01680.1.g28979.t1	ref|XP_002870710.1| hypothetical protein ARALYDRAFT_493949 [Arabidopsis lyrata subsp. lyrata] gi|297316546|gb|EFH46969.1| hypothetical protein ARALYDRAFT_493949 [Arabidopsis lyrata subsp. lyrata]	777	785	0	101.0	89.2	95.6	hypothetical protein ARALYDRAFT_493949	gbpln	Arabidopsis lyrata	AT5G40390.1 | Symbols: SIP1 | Raffinose synthase family protein | chr5:16161720-16165085 FORWARD LENGTH=783	777	783	0	100.8	88.4	95.1

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<tr><td>Rsa1.0_01681.1.g28980.t2</td><td>gb|ABD65084.1| hypothetical protein 27.t00096 [Brassica oleracea]</td><td>408</td><td>645</td><td>1.00E-29</td><td>158.1</td><td>31.4</td><td>41.2</td><td>hypothetical protein 27.t00096</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01681.1.g28981.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT1G28200.1 | Symbols: FIP1 | FH interacting protein 1 | chr1:9850395-9852300 REVERSE LENGTH=259</td><td>46</td><td>259</td><td>8.00E-12</td><td>563.0</td><td>63.0</td><td>69.6</td></tr>
<tr><td>Rsa1.0_01681.1.g28982.t7</td><td>dbj|BAG72148.1| hypothetical protein [Lotus japonicus] gi|208609062|dbj|BAG72153.1| hypothetical protein [Lotus japonicus]</td><td>1469</td><td>1558</td><td>0</td><td>106.1</td><td>38.1</td><td>54.8</td><td>hypothetical protein</td><td>gbpln</td><td>Lotus japonicus</td><td>ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158</td><td>1469</td><td>158</td><td>5.00E-22</td><td>10.8</td><td>3.3</td><td>4.2</td></tr>
<tr><td>Rsa1.0_01681.1.g28983.t1</td><td>ref|XP_002888009.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333850|gb|EFH64268.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>591</td><td>654</td><td>0</td><td>110.7</td><td>84.6</td><td>91.2</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G62660.1 | Symbols: | Glycosyl hydrolases family 32 protein | chr1:23199949-23203515 FORWARD LENGTH=648</td><td>591</td><td>648</td><td>0</td><td>109.6</td><td>81.6</td><td>88.7</td></tr>
<tr><td>Rsa1.0_01681.1.g28984.t1</td><td>gb|AAG52313.1|AC021666_2 Mutator-like transposase; 53847-56139 [Arabidopsis thaliana]</td><td>432</td><td>583</td><td>7.00E-27</td><td>135.0</td><td>17.6</td><td>23.1</td><td>Mutator-like transposase; 53847-56139</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01681.1.g28985.t4</td><td>gb|ACG60684.1| maize transposon MuDR-like protein [Brassica oleracea var. alboglabra]</td><td>528</td><td>622</td><td>3.00E-55</td><td>117.8</td><td>33.1</td><td>49.8</td><td>maize transposon MuDR-like protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719</td><td>528</td><td>719</td><td>5.00E-12</td><td>136.2</td><td>8.5</td><td>14.4</td></tr>
<tr><td>Rsa1.0_01681.1.g28986.t4</td><td>gb|ABD65085.1| Ulp1 protease family protein [Brassica oleracea]</td><td>594</td><td>640</td><td>2.00E-45</td><td>107.7</td><td>24.1</td><td>34.8</td><td>Ulp1 protease family protein</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01682.1.g28987.t1</td><td>gb|EOA22505.1| hypothetical protein CARUB_v10003160mg, partial [Capsella rubella]</td><td>221</td><td>213</td><td>5.00E-36</td><td>96.4</td><td>39.8</td><td>55.7</td><td>hypothetical protein CARUB_v10003160mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G22150.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22160.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7342567-7345956 FORWARD LENGTH=330</td><td>221</td><td>330</td><td>2.00E-32</td><td>149.3</td><td>37.6</td><td>49.3</td></tr>
<tr><td>Rsa1.0_01682.1.g28988.t1</td><td>ref|NP_680202.1| uncharacterized protein [Arabidopsis thaliana] gi|13374875|emb|CAC34509.1| putative protein [Arabidopsis thaliana] gi|332005608|gb|AED92991.1| uncharacterized protein AT5G22160 [Arabidopsis thaliana]</td><td>214</td><td>353</td><td>4.00E-40</td><td>165.0</td><td>47.7</td><td>59.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22150.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7346944-7349255 FORWARD LENGTH=353</td><td>214</td><td>353</td><td>1.00E-42</td><td>165.0</td><td>47.7</td><td>59.8</td></tr>
<tr><td>Rsa1.0_01682.1.g28989.t1</td><td>ref|XP_002874051.1| pyridine nucleotide-disulfide oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297319888|gb|EFH50310.1| pyridine nucleotide-disulfide oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>333</td><td>365</td><td>1.00E-163</td><td>109.6</td><td>87.1</td><td>92.5</td><td>pyridine nucleotide-disulfide oxidoreductase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G22140.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr5:7340284-7341657 REVERSE LENGTH=365</td><td>333</td><td>365</td><td>1.00E-164</td><td>109.6</td><td>86.8</td><td>92.5</td></tr>
<tr><td>Rsa1.0_01682.1.g28990.t1</td><td>gb|EOA22260.1| hypothetical protein CARUB_v10002848mg [Capsella rubella]</td><td>352</td><td>378</td><td>1.00E-135</td><td>107.4</td><td>76.4</td><td>84.4</td><td>hypothetical protein CARUB_v10002848mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G22120.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:7334612-7336755 REVERSE LENGTH=383</td><td>352</td><td>383</td><td>1.00E-136</td><td>108.8</td><td>77.3</td><td>84.4</td></tr>
<tr><td>Rsa1.0_01682.1.g28991.t1</td><td>gb|ABV21212.1| Ty1_Copia-element protein [Arabidopsis thaliana]</td><td>396</td><td>438</td><td>6.00E-50</td><td>110.6</td><td>29.8</td><td>42.7</td><td>Ty1_Copia-element protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295</td><td>396</td><td>295</td><td>3.00E-37</td><td>74.5</td><td>24.7</td><td>35.6</td></tr>
<tr><td>Rsa1.0_01682.1.g28992.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01682.1.g28993.t1</td><td>ref|NP_680195.2| uncharacterized protein [Arabidopsis thaliana] gi|334187828|ref|NP_001190360.1| uncharacterized protein [Arabidopsis thaliana] gi|122175037|sp|Q0V865.1|FAFL_ARATH RecName: Full=Protein FAF-like, chloroplastic; Flags: Precursor gi|111074178|gb|ABH04462.1| At5g22090 [Arabidopsis thaliana] gi|332005598|gb|AED92981.1| uncharacterized protein AT5G22090 [Arabidopsis thaliana] gi|332005599|gb|AED92982.1| uncharacterized protein AT5G22090 [Arabidopsis thaliana]</td><td>444</td><td>463</td><td>1.00E-163</td><td>104.3</td><td>77.5</td><td>85.6</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22090.2 | Symbols: | Protein of unknown function (DUF3049) | chr5:7315003-7316394 REVERSE LENGTH=463</td><td>444</td><td>463</td><td>1.00E-166</td><td>104.3</td><td>77.5</td><td>85.6</td></tr>
<tr><td>Rsa1.0_01682.1.g28994.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<table>
<tr><td>Rsa1.0_01682.1.g28995.t1</td><td>ref|NP_680193.2| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|13374866|emb|CAC34500.1| putative protein [Arabidopsis thaliana] gi|22531074|gb|AAM97041.1| unknown protein [Arabidopsis thaliana] gi|23197924|gb|AAN15489.1| unknown protein [Arabidopsis thaliana] gi|26452044|dbj|BAC43112.1| unknown protein [Arabidopsis thaliana] gi|110736125|dbj|BAF00034.1| hypothetical protein [Arabidopsis thaliana] gi|332005595|gb|AED92978.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]</td><td>362</td><td>362</td><td>1.00E-176</td><td>100.0</td><td>84.8</td><td>92.3</td><td>Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22070.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:7308255-7309343 FORWARD LENGTH=362</td><td>362</td><td>362</td><td>1.00E-179</td><td>100.0</td><td>84.8</td><td>92.3</td></tr>
<tr><td>Rsa1.0_01682.1.g28996.t1</td><td>gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]</td><td>210</td><td>1231</td><td>2.00E-43</td><td>586.2</td><td>45.2</td><td>62.4</td><td>Very similar to retrotransposon reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365</td><td>210</td><td>365</td><td>3.00E-21</td><td>173.8</td><td>24.8</td><td>38.6</td></tr>
<tr><td>Rsa1.0_01682.1.g28997.t1</td><td>ref|NP_568412.1| chaperone protein dnaJ 2 [Arabidopsis thaliana] gi|21431768|sp|P42825.2|DNAJ2_ARATH RecName: Full=Chaperone protein dnaJ 2; Short=AtDjA2; Flags: Precursor gi|13374865|emb|CAC34499.1| DNAJ PROTEIN HOMOLOG ATJ [Arabidopsis thaliana] gi|26451807|dbj|BAC42997.1| putative DnaJ protein homolog ATJ [Arabidopsis thaliana] gi|111074426|gb|ABH04586.1| At5g22060 [Arabidopsis thaliana] gi|332005594|gb|AED92977.1| chaperone protein dnaJ 2 [Arabidopsis thaliana]</td><td>420</td><td>419</td><td>0</td><td>99.8</td><td>86.2</td><td>92.1</td><td>chaperone protein dnaJ 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22060.1 | Symbols: ATJ2, J2 | DNAJ homologue 2 | chr5:7303798-7305668 REVERSE LENGTH=419</td><td>420</td><td>419</td><td>0</td><td>99.8</td><td>86.2</td><td>92.1</td></tr>
<tr><td>Rsa1.0_01682.1.g28998.t1</td><td>ref|XP_002871985.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317822|gb|EFH48244.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>132</td><td>307</td><td>6.00E-63</td><td>232.6</td><td>85.6</td><td>94.7</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G22050.2 | Symbols: | Protein kinase superfamily protein | chr5:7301467-7303209 FORWARD LENGTH=307</td><td>132</td><td>307</td><td>2.00E-65</td><td>232.6</td><td>85.6</td><td>93.9</td></tr>
<tr><td>Rsa1.0_01683.1.g28999.t3</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01683.1.g29000.t1</td><td>gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]</td><td>131</td><td>1838</td><td>5.00E-32</td><td>1403.1</td><td>51.1</td><td>67.9</td><td>F5M15.26</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01683.1.g29001.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01683.1.g29002.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01683.1.g29003.t1</td><td>ref|XP_002893670.1| hypothetical protein ARALYDRAFT_473343 [Arabidopsis lyrata subsp. lyrata] gi|297339512|gb|EFH69929.1| hypothetical protein ARALYDRAFT_473343 [Arabidopsis lyrata subsp. lyrata]</td><td>348</td><td>364</td><td>1.00E-163</td><td>104.6</td><td>85.6</td><td>89.1</td><td>hypothetical protein ARALYDRAFT_473343</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G30970.1 | Symbols: SUF4 | zinc finger (C2H2 type) family protein | chr1:11040613-11043593 REVERSE LENGTH=367</td><td>348</td><td>367</td><td>1.00E-162</td><td>105.5</td><td>85.1</td><td>88.5</td></tr>
<tr><td>Rsa1.0_01683.1.g29004.t1</td><td>gb|EOA37584.1| hypothetical protein CARUB_v10011934mg [Capsella rubella]</td><td>438</td><td>442</td><td>0</td><td>100.9</td><td>91.1</td><td>93.8</td><td>hypothetical protein CARUB_v10011934mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G30950.1 | Symbols: UFO | F-box family protein | chr1:11036180-11037508 FORWARD LENGTH=442</td><td>438</td><td>442</td><td>0</td><td>100.9</td><td>90.6</td><td>93.6</td></tr>
<tr><td>Rsa1.0_01683.1.g29005.t1</td><td>gb|AAG60150.1|AC074360_15 En/Spm-like transposon protein, putative [Arabidopsis thaliana]</td><td>336</td><td>1431</td><td>6.00E-40</td><td>425.9</td><td>31.8</td><td>48.2</td><td>En/Spm-like transposon protein, putative</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01684.1.g29006.t1</td><td>ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]</td><td>241</td><td>390</td><td>7.00E-40</td><td>161.8</td><td>39.8</td><td>53.9</td><td>hypothetical protein ARALYDRAFT_917455</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295</td><td>241</td><td>295</td><td>2.00E-29</td><td>122.4</td><td>34.4</td><td>53.5</td></tr>
<tr><td>Rsa1.0_01684.1.g29007.t2</td><td>ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]</td><td>500</td><td>390</td><td>1.00E-106</td><td>78.0</td><td>42.2</td><td>54.0</td><td>hypothetical protein ARALYDRAFT_917455</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>500</td><td>746</td><td>8.00E-45</td><td>149.2</td><td>24.0</td><td>35.4</td></tr>
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Rsa1.0_01684.1.g29008.t3	ref|NP_179449.5| major facilitator protein [Arabidopsis thaliana] gi|330251689|gb|AEC06783.1| major facilitator protein [Arabidopsis thaliana]	470	473	0	100.6	82.3	89.8	major facilitator protein	gbpln	Arabidopsis thaliana	AT2G18590.1 | Symbols: | Major facilitator superfamily protein | chr2:8069988-8072866 FORWARD LENGTH=473	470	473	0	100.6	82.3	89.8
Rsa1.0_01684.1.g29009.t1	gb|AAD12028.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	154	1447	6.00E-15	939.6	29.9	38.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01685.1.g29010.t1	gb|AAK19600.1|AF334207_1 bZIP protein DPBF2 [Arabidopsis thaliana]	214	331	8.00E-90	154.7	78.5	84.6	bZIP protein DPBF2	gbpln	Arabidopsis thaliana	AT3G44460.1 | Symbols: DPBF2, AtbZIP67 | Basic-leucine zipper (bZIP) transcription factor family protein | chr3:16080115-16081722 REVERSE LENGTH=331	214	331	2.00E-91	154.7	78.0	84.1
Rsa1.0_01685.1.g29011.t1	ref|NP_001190008.1| alpha/beta-hydrolases family protein [Arabidopsis thaliana] gi|332644388|gb|AEE77909.1| alpha/beta-hydrolases family protein [Arabidopsis thaliana]	328	325	1.00E-164	99.1	85.1	89.0	alpha/beta-hydrolases family protein	gbpln	Arabidopsis thaliana	AT3G44510.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:16108251-16111139 REVERSE LENGTH=325	328	325	1.00E-167	99.1	85.1	89.0
Rsa1.0_01685.1.g29012.t1	sp|Q9LXN4.2|HIRA_ARATH RecName: Full=Protein HIRA; AltName: Full=Histone regulator protein	1024	1024	0	100.0	84.5	90.4	RecName: Full=Protein HIRA; AltName: Full=Histone regulator protein	----	----	AT3G44530.2 | Symbols: HIRA | homolog of histone chaperone HIRA | chr3:16116026-16121247 FORWARD LENGTH=1040	1024	1040	0	101.6	84.4	90.3
Rsa1.0_01685.1.g29013.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01685.1.g29014.t1	ref|NP_190041.2| putative fatty acyl-CoA reductase 5 [Arabidopsis thaliana] gi|122223793|sp|Q0WRB0.1|FACR5_ARATH RecName: Full=Probable fatty acyl-CoA reductase 5 gi|110736755|dbj|BAF00339.1| acyl CoA reductase -like protein [Arabidopsis thaliana] gi|332644393|gb|AEE77914.1| putative fatty acyl-CoA reductase 5 [Arabidopsis thaliana]	503	496	0	98.6	84.5	92.2	putative fatty acyl-CoA reductase 5	gbpln	Arabidopsis thaliana	AT3G44550.1 | Symbols: FAR5 | fatty acid reductase 5 | chr3:16138060-16141409 FORWARD LENGTH=496	503	496	0	98.6	84.5	92.2
Rsa1.0_01685.1.g29015.t1	ref|XP_002877347.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata] gi|297323185|gb|EFH53606.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata]	1020	631	0	61.9	52.7	55.2	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	gbpln	Arabidopsis lyrata	AT3G44600.1 | Symbols: CYP71 | cyclophilin71 | chr3:16165368-16169201 REVERSE LENGTH=631	1020	631	0	61.9	52.5	54.9
Rsa1.0_01685.1.g29016.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01685.1.g29017.t2	gb|EOA25094.1| hypothetical protein CARUB_v10018402mg [Capsella rubella]	88	542	9.00E-26	615.9	67.0	77.3	hypothetical protein CARUB_v10018402mg	gbpln	Capsella rubella	AT3G45060.1 | Symbols: ATNRT2.6, NRT2.6 | high affinity nitrate transporter 2.6 | chr3:16477671-16479386 REVERSE LENGTH=542	88	542	1.00E-26	615.9	62.5	73.9
Rsa1.0_01685.1.g29018.t1	gb|EOA25094.1| hypothetical protein CARUB_v10018402mg [Capsella rubella]	543	542	0	99.8	89.7	95.2	hypothetical protein CARUB_v10018402mg	gbpln	Capsella rubella	AT3G45060.1 | Symbols: ATNRT2.6, NRT2.6 | high affinity nitrate transporter 2.6 | chr3:16477671-16479386 REVERSE LENGTH=542	543	542	0	99.8	82.9	90.4
Rsa1.0_01685.1.g29019.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1780	1213	0	68.1	25.6	37.7	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1780	626	4.00E-65	35.2	7.6	12.2
Rsa1.0_01686.1.g29020.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01686.1.g29021.t1	gb|ABK28247.1| unknown [Arabidopsis thaliana]	385	372	1.00E-17	96.6	11.9	18.4	unknown	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01686.1.g29022.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01686.1.g29023.t2	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1429	1501	0	105.0	58.3	73.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1429	1262	1.00E-138	88.3	16.4	23.3
Rsa1.0_01686.1.g29024.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01686.1.g29025.t1	gb|AAC67205.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	405	1413	1.00E-96	348.9	47.4	64.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	405	237	5.00E-28	58.5	17.8	27.4
Rsa1.0_01686.1.g29026.t1	gb|AAG51237.1|AC035249_12 unknown protein; 55998-51558 [Arabidopsis thaliana]	194	593	5.00E-30	305.7	32.5	41.2	unknown protein; 55998-51558	gbpln	Arabidopsis thaliana	AT1G36970.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:14016385-14018356 REVERSE LENGTH=439	194	439	8.00E-30	226.3	32.0	42.8
Rsa1.0_01686.1.g29027.t1	gb|EOA20114.1| hypothetical protein CARUB_v10000393mg, partial [Capsella rubella]	93	670	1.00E-25	720.4	65.6	77.4	hypothetical protein CARUB_v10000393mg, partial	gbpln	Capsella rubella	AT5G10900.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr5:3436413-3439221 REVERSE LENGTH=600	93	600	2.00E-22	645.2	65.6	78.5

Rsa1.0_01686.1.g29028.t5	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1978	1270	0	64.2	34.5	45.7	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1978	575	1.00E-90	29.1	9.5	14.7
Rsa1.0_01687.1.g29029.t1	gb|AAB88009.1| heat shock cognate protein HSC70 [Brassica napus]	668	645	0	96.6	92.8	95.4	heat shock cognate protein HSC70	gbpln	Brassica napus	AT5G02500.1 | Symbols: HSC70-1, HSP70-1, AT-HSC70-1, HSC70 | heat shock cognate protein 70-1 | chr5:554055-556334 REVERSE LENGTH=651	668	651	0	97.5	92.5	95.2
Rsa1.0_01687.1.g29030.t1	ref|NP_001078285.1| uncharacterized protein [Arabidopsis thaliana] gi|7258378|emb|CAB77594.1| putative protein [Arabidopsis thaliana] gi|332645755|gb|AEE79276.1| uncharacterized protein AT3G54740 [Arabidopsis thaliana]	351	438	1.00E-144	124.8	80.1	88.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G54740.2 | Symbols: | Protein of unknown function, DUF593 | chr3:20262949-20264466 FORWARD LENGTH=438	351	438	1.00E-147	124.8	80.1	88.3
Rsa1.0_01687.1.g29031.t1	ref|XP_002877997.1| hypothetical protein ARALYDRAFT_485881 [Arabidopsis lyrata subsp. lyrata] gi|297323835|gb|EFH54256.1| hypothetical protein ARALYDRAFT_485881 [Arabidopsis lyrata subsp. lyrata]	584	608	0	104.1	78.9	86.0	hypothetical protein ARALYDRAFT_485881	gbpln	Arabidopsis lyrata	AT3G54750.1 | Symbols: | unknown protein; Has 145 Blast hits to 145 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 99; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr3:20264833-20268416 REVERSE LENGTH=589	584	589	0	100.9	75.9	84.2
Rsa1.0_01687.1.g29032.t1	ref|XP_002877998.1| hypothetical protein ARALYDRAFT_348567 [Arabidopsis lyrata subsp. lyrata] gi|297323836|gb|EFH54257.1| hypothetical protein ARALYDRAFT_348567 [Arabidopsis lyrata subsp. lyrata]	329	836	1.00E-27	254.1	43.2	54.7	hypothetical protein ARALYDRAFT_348567	gbpln	Arabidopsis lyrata	AT3G54760.1 | Symbols: | dentin sialophosphoprotein-related | chr3:20269659-20272037 REVERSE LENGTH=792	329	792	8.00E-27	240.7	40.7	49.5
Rsa1.0_01687.1.g29033.t1	ref|NP_191036.1| dentin sialophosphoprotein-related protein [Arabidopsis thaliana] gi|7258380|emb|CAB77596.1| Putative protein [Arabidopsis thaliana] gi|332645759|gb|AEE79280.1| dentin sialophosphoprotein-related protein [Arabidopsis thaliana]	659	792	0	120.2	66.2	74.2	dentin sialophosphoprotein-related protein	gbpln	Arabidopsis thaliana	AT3G54760.1 | Symbols: | dentin sialophosphoprotein-related | chr3:20269659-20272037 REVERSE LENGTH=792	659	792	0	120.2	66.2	74.2
Rsa1.0_01687.1.g29034.t2	ref|XP_002878000.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297323838|gb|EFH54259.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	747	760	0	101.7	84.3	88.6	armadillo/beta-catenin repeat family protein	gbpln	Arabidopsis lyrata	AT3G54790.1 | Symbols: | ARM repeat superfamily protein | chr3:20281830-20284363 REVERSE LENGTH=760	747	760	0	101.7	83.5	88.0
Rsa1.0_01687.1.g29035.t14	gb|EOA25157.1| hypothetical protein CARUB_v10018468mg [Capsella rubella]	757	731	0	96.6	83.2	88.1	hypothetical protein CARUB_v10018468mg	gbpln	Capsella rubella	AT3G54800.2 | Symbols: | Pleckstrin homology (PH) and lipid-binding START domains-containing protein | chr3:20286378-20289880 FORWARD LENGTH=733	757	733	0	96.8	82.3	88.0
Rsa1.0_01688.1.g29036.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01688.1.g29037.t1	ref|NP_198758.2| cyclin-dependent kinase CDC2C [Arabidopsis thaliana] gi|209529775|gb|ACI49782.1| At5g39420 [Arabidopsis thaliana] gi|332007048|gb|AED94431.1| cyclin-dependent kinase CDC2C [Arabidopsis thaliana]	664	644	0	97.0	83.7	89.9	cyclin-dependent kinase CDC2C	gbpln	Arabidopsis thaliana	AT5G39420.1 | Symbols: cdc2cAt | CDC2C | chr5:15772232-15774929 FORWARD LENGTH=644	664	644	0	97.0	83.7	89.9
Rsa1.0_01688.1.g29038.t1	gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]	259	863	2.00E-37	333.2	33.2	37.8	Ulp1 protease family protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01688.1.g29039.t1	gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	208	1787	2.00E-42	859.1	44.2	54.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01688.1.g29040.t1	gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	142	1787	7.00E-48	1258.5	61.3	78.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01688.1.g29041.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01688.1.g29042.t1	dbj|BAJ34483.1| unnamed protein product [Thellungiella halophila]	221	220	1.00E-114	99.5	92.3	96.8	unnamed protein product	----	----	AT5G39510.1 | Symbols: VTI11, ATVTI1A, ATVTI11, ZIG, SGR4, VTI1A, ZIG1 | Vesicle transport v-SNARE family protein | chr5:15822035-15823591 FORWARD LENGTH=221	221	221	1.00E-104	100.0	87.8	95.5
Rsa1.0_01689.1.g29043.t1	ref|XP_002889929.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335771|gb|EFH66188.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	181	317	3.00E-85	175.1	92.8	95.6	predicted protein	gbpln	Arabidopsis lyrata	AT1G12350.1 | Symbols: ATCOAB, COAB | 4-phospho-panto-thenoylcysteine synthetase | chr1:4198870-4200633 FORWARD LENGTH=317	181	317	2.00E-86	175.1	91.2	94.5
Rsa1.0_01689.1.g29044.t2	gb|EOA20156.1| hypothetical protein CARUB_v10000448mg [Capsella rubella]	425	637	1.00E-138	149.9	63.3	66.1	hypothetical protein CARUB_v10000448mg	gbpln	Capsella rubella	AT5G02030.1 | Symbols: LSN, PNY, HB-6, BLR, RPL, BLH9, VAN | POX (plant homeobox) family protein | chr5:395754-398872 FORWARD LENGTH=575	425	575	1.00E-134	135.3	65.2	68.2

Rsa1.0_01689.1.g29045.t1	gb|EOA27991.1| hypothetical protein CARUB_v10024167mg, partial [Capsella rubella]	133	175	4.00E-13	131.6	40.6	57.9	hypothetical protein CARUB_v10024167mg, partial	gbpln	Capsella rubella	AT5G23840.1 | Symbols: | MD-2-related lipid recognition domain-containing protein | chr5:8035874-8036777 FORWARD LENGTH=167	133	167	1.00E-12	125.6	33.8	54.1
Rsa1.0_01689.1.g29046.t1	#	#	#	#	#	#	#	–	----	----	AT3G13300.2 | Symbols: VCS | Transducin/WD40 repeat-like superfamily protein | chr3:4304085-4309949 FORWARD LENGTH=1309	65	1309	8.00E-11	2013.8	50.8	60.0
Rsa1.0_01689.1.g29047.t1	ref|NP_195724.1| laccase 8 [Arabidopsis thaliana] gi|75174096|sp|Q9LFD2.1|LAC8_ARATH RecName: Full=Laccase-8; AltName: Full=Benzenediol:oxygen oxidoreductase 8; AltName: Full=Diphenol oxidase 8; AltName: Full=Urishiol oxidase 8; Flags: Precursor gi|6759427|emb|CAB69832.1| laccase-like protein [Arabidopsis thaliana] gi|332002908|gb|AED90291.1| laccase 8 [Arabidopsis thaliana]	564	584	0	103.5	79.4	89.4	laccase 8	gbpln	Arabidopsis thaliana	AT5G01040.1 | Symbols: LAC8 | laccase 8 | chr5:13394-16142 REVERSE LENGTH=584	564	584	0	103.5	79.4	89.4
Rsa1.0_01689.1.g29048.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01690.1.g29049.t1	ref|NP_568405.1| serine/threonine-protein kinase TOUSLED [Arabidopsis thaliana] gi|75319457|sp|Q39238.1|TSL_ARATH RecName: Full=Serine/threonine-protein kinase TOUSLED gi|433052|gb|AAA32874.1| protein kinase [Arabidopsis thaliana] gi|332005524|gb|AED92907.1| serine/threonine-protein kinase TOUSLED [Arabidopsis thaliana]	687	688	0	100.1	87.3	93.2	serine/threonine-protein kinase TOUSLED	gbpln	Arabidopsis thaliana	AT5G20930.1 | Symbols: TSL | Protein kinase superfamily protein | chr5:7098213-7102970 FORWARD LENGTH=688	687	688	0	100.1	87.3	93.2
Rsa1.0_01690.1.g29050.t2	gb|EOA19371.1| hypothetical protein CARUB_v10000466mg [Capsella rubella]	725	624	0	86.1	78.2	80.0	hypothetical protein CARUB_v10000466mg	gbpln	Capsella rubella	AT5G20950.2 | Symbols: | Glycosyl hydrolase family protein | chr5:7107609-7110775 REVERSE LENGTH=624	725	624	0	86.1	78.3	81.4
Rsa1.0_01690.1.g29051.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01690.1.g29052.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01690.1.g29053.t1	dbj|BAE93767.1| aldehyde oxidase [Brassica rapa subsp. pekinensis]	1329	1360	0	102.3	94.0	96.3	aldehyde oxidase	gbpln	Brassica rapa	AT5G20960.2 | Symbols: AAO1, AO1, ATAO, AT-AO1, AOalpha, AtAO1 | aldehyde oxidase 1 | chr5:7116783-7122338 FORWARD LENGTH=1368	1329	1368	0	102.9	85.6	92.8
Rsa1.0_01690.1.g29054.t1	ref|NP_197597.1| heat shock family protein [Arabidopsis thaliana] gi|332005531|gb|AED92914.1| heat shock family protein [Arabidopsis thaliana]	166	249	2.00E-52	150.0	69.3	81.9	heat shock family protein	gbpln	Arabidopsis thaliana	AT5G20970.1 | Symbols: | HSP20-like chaperones superfamily protein | chr5:7123132-7124001 FORWARD LENGTH=249	166	249	7.00E-55	150.0	69.3	81.9
Rsa1.0_01690.1.g29055.t1	ref|NP_566733.1| UBX domain-containing protein [Arabidopsis thaliana] gi|9294517|dbj|BAB02779.1| unnamed protein product [Arabidopsis thaliana] gi|62319637|dbj|BAD95135.1| hypothetical protein [Arabidopsis thaliana] gi|98961091|gb|ABF59029.1| At3g23605 [Arabidopsis thaliana] gi|332643262|gb|AEE76783.1| UBX domain-containing protein [Arabidopsis thaliana]	141	152	1.00E-42	107.8	68.1	78.7	UBX domain-containing protein	gbpln	Arabidopsis thaliana	AT3G23605.1 | Symbols: | Ubiquitin-like superfamily protein | chr3:8476675-8477133 FORWARD LENGTH=152	141	152	3.00E-45	107.8	68.1	78.7
Rsa1.0_01690.1.g29056.t3	emb|CAD40363.2| OSJNBa0093P23.9 [Oryza sativa Japonica Group]	1247	944	0	75.7	29.1	39.3	OSJNBa0093P23.9	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1247	1262	3.00E-34	101.2	8.7	13.5
Rsa1.0_01690.1.g29057.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01690.1.g29058.t3	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1472	1223	0	83.1	29.9	40.5	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1472	746	3.00E-74	50.7	10.6	13.7
Rsa1.0_01691.1.g29059.t1	ref|XP_002872853.1| ATIMPALPHA3/MOS6 [Arabidopsis lyrata subsp. lyrata] gi|297318690|gb|EFH49112.1| ATIMPALPHA3/MOS6 [Arabidopsis lyrata subsp. lyrata]	509	534	0	104.9	82.7	91.0	ATIMPALPHA3/MOS6	gbpln	Arabidopsis lyrata	AT4G02150.1 | Symbols: MOS6, ATIMPALPHA3, IMPA-3 | ARM repeat superfamily protein | chr4:950884-953602 REVERSE LENGTH=531	509	531	0	104.3	80.7	89.6
Rsa1.0_01691.1.g29060.t1	ref|XP_002872855.1| hypothetical protein ARALYDRAFT_490360 [Arabidopsis lyrata subsp. lyrata] gi|297318692|gb|EFH49114.1| hypothetical protein ARALYDRAFT_490360 [Arabidopsis lyrata subsp. lyrata]	352	346	1.00E-175	98.3	87.5	90.6	hypothetical protein ARALYDRAFT_490360	gbpln	Arabidopsis lyrata	AT4G02130.3 | Symbols: GATL6, LGT10 | galacturonosyltransferase 6 | chr4:945764-946804 REVERSE LENGTH=346	352	346	1.00E-175	98.3	85.8	90.3

Rsa1.0_01691.1.g29061.t3	gb|EOA20304.1| hypothetical protein CARUB_v10000612mg [Capsella rubella]	575	556	0	96.7	90.8	92.5	hypothetical protein CARUB_v10000612mg	gbpln	Capsella rubella	AT4G02120.1 | Symbols: | CTP synthase family protein | chr4:940873-944097 FORWARD LENGTH=556	575	556	0	96.7	89.4	91.7
Rsa1.0_01691.1.g29062.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01691.1.g29063.t1	gb|ABD65633.1| hypothetical protein 23.t00050 [Brassica oleracea]	298	260	3.00E-44	87.2	28.5	35.6	hypothetical protein 23.t00050	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	298	302	1.00E-17	101.3	21.8	32.2
Rsa1.0_01691.1.g29064.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1247	1459	0	117.0	55.3	70.7	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1247	1262	1.00E-104	101.2	14.6	21.5
Rsa1.0_01691.1.g29065.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	136	442	3.00E-41	325.0	57.4	64.0	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	136	343	1.00E-14	252.2	25.0	33.8
Rsa1.0_01692.1.g29066.t1	ref|XP_002873565.1| hypothetical protein ARALYDRAFT_909210 [Arabidopsis lyrata subsp. lyrata] gi|297319402|gb|EFH49824.1| hypothetical protein ARALYDRAFT_909210 [Arabidopsis lyrata subsp. lyrata]	286	220	1.00E-100	76.9	63.6	69.2	hypothetical protein ARALYDRAFT_909210	gbpln	Arabidopsis lyrata	AT5G12340.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G28190.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:3992948-3993610 REVERSE LENGTH=220	286	220	1.00E-101	76.9	62.9	68.5
Rsa1.0_01692.1.g29067.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01692.1.g29068.t1	gb|ADA60975.1| lateral root primordium 1 [Brassica rapa subsp. pekinensis]	397	380	1.00E-170	95.7	87.9	89.9	lateral root primordium 1	gbpln	Brassica rapa	AT5G12330.4 | Symbols: LRP1 | Lateral root primordium (LRP) protein-related | chr5:3987677-3989408 REVERSE LENGTH=407	397	407	1.00E-153	102.5	80.9	88.9
Rsa1.0_01692.1.g29069.t1	ref|XP_002873561.1| hypothetical protein ARALYDRAFT_488073 [Arabidopsis lyrata subsp. lyrata] gi|297319398|gb|EFH49820.1| hypothetical protein ARALYDRAFT_488073 [Arabidopsis lyrata subsp. lyrata]	589	602	0	102.2	87.9	94.1	hypothetical protein ARALYDRAFT_488073	gbpln	Arabidopsis lyrata	AT5G12290.1 | Symbols: DGS1 | dgd1 suppressor 1 | chr5:3974374-3978066 REVERSE LENGTH=602	589	602	0	102.2	86.8	93.5
Rsa1.0_01692.1.g29070.t2	ref|XP_002873560.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297319397|gb|EFH49819.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	166	359	6.00E-72	216.3	80.1	86.1	oxidoreductase	gbpln	Arabidopsis lyrata	AT5G12270.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:3970131-3971301 REVERSE LENGTH=360	166	360	2.00E-73	216.9	79.5	83.7
Rsa1.0_01692.1.g29071.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01692.1.g29072.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01692.1.g29073.t1	ref|XP_002873560.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297319397|gb|EFH49819.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	164	359	1.00E-62	218.9	71.3	81.7	oxidoreductase	gbpln	Arabidopsis lyrata	AT5G12270.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:3970131-3971301 REVERSE LENGTH=360	164	360	5.00E-64	219.5	72.0	81.1
Rsa1.0_01693.1.g29074.t1	gb|EGG05881.1| hypothetical protein MELLADRAFT_87680 [Melampsora larici-populina 98AG31]	325	535	1.00E-103	164.6	65.5	77.5	hypothetical protein MELLADRAFT_87680	gbpln	Melampsora larici-populina	AT4G05320.4 | Symbols: UBQ10 | polyubiquitin 10 | chr4:2718559-2719932 FORWARD LENGTH=457	325	457	1.00E-105	140.6	65.2	77.2
Rsa1.0_01693.1.g29075.t1	ref|NP_565381.1| Peptidyl-prolyl cis-trans isomerase CYP40 [Arabidopsis thaliana] gi|75333353|sp|Q9C566.1|CYP40_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase CYP40; Short=PPIase CYP40; AltName: Full=Cyclophilin of 40 kDa; Short=Cyclophilin-40; AltName: Full=Protein SQUINT; AltName: Full=Rotamase CYP40 gi|13442983|gb|AAK02067.1| cyclophilin-40 [Arabidopsis thaliana] gi|20197802|gb|AAD41985.2| expressed protein [Arabidopsis thaliana] gi|115311455|gb|ABI93908.1| At2g15790 [Arabidopsis thaliana] gi|330251344|gb|AEC06438.1| Peptidyl-prolyl cis-trans isomerase CYP40 [Arabidopsis thaliana]	74	361	3.00E-26	487.8	85.1	90.5	Peptidyl-prolyl cis-trans isomerase CYP40	gbpln	Arabidopsis thaliana	AT2G15790.1 | Symbols: SQN, CYP40 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase | chr2:6878144-6880743 REVERSE LENGTH=361	74	361	5.00E-29	487.8	85.1	90.5

Rsa1.0_01693.1.g29076.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	884	1529	0	173.0	34.6	47.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	884	746	1.00E-107	84.4	22.7	31.6
Rsa1.0_01693.1.g29077.t1	gb|EOA32516.1| hypothetical protein CARUB_v10015796mg, partial [Capsella rubella]	189	211	2.00E-92	111.6	89.4	94.7	hypothetical protein CARUB_v10015796mg, partial	gbpln	Capsella rubella	AT2G15680.1 | Symbols: | Calcium-binding EF-hand family protein | chr2:6831024-6831587 FORWARD LENGTH=187	189	187	3.00E-91	98.9	84.1	92.6
Rsa1.0_01693.1.g29078.t1	gb|ACD13218.1| nitrite reductase [Brassica rapa subsp. chinensis]	585	593	0	101.4	92.0	95.0	nitrite reductase	gbpln	Brassica rapa	AT2G15620.1 | Symbols: NIR1, NIR, ATHNIR | nitrite reductase 1 | chr2:6810552-6812666 FORWARD LENGTH=586	585	586	0	100.2	88.7	94.9
Rsa1.0_01693.1.g29079.t1	ref|XP_002883904.1| hypothetical protein ARALYDRAFT_480419 [Arabidopsis lyrata subsp. lyrata] gi|297329744|gb|EFH60163.1| hypothetical protein ARALYDRAFT_480419 [Arabidopsis lyrata subsp. lyrata]	147	155	3.00E-57	105.4	73.5	87.1	hypothetical protein ARALYDRAFT_480419	gbpln	Arabidopsis lyrata	AT2G15590.2 | Symbols: | Protein of unknown function (DUF1685) | chr2:6801950-6802506 FORWARD LENGTH=155	147	155	1.00E-57	105.4	71.4	86.4
Rsa1.0_01693.1.g29080.t7	gb|EOA16155.1| hypothetical protein CARUB_v10004296mg [Capsella rubella]	122	673	7.00E-61	551.6	83.6	91.8	hypothetical protein CARUB_v10004296mg	gbpln	Capsella rubella	AT2G15530.3 | Symbols: | RING/U-box superfamily protein | chr2:6774150-6777068 FORWARD LENGTH=704	122	704	2.00E-63	577.0	86.9	93.4
Rsa1.0_01694.1.g29081.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01694.1.g29082.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	810	1611	8.00E-78	198.9	17.2	22.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01694.1.g29083.t1	gb|AAD15359.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	707	532	2.00E-19	75.2	12.9	17.5	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01694.1.g29084.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	657	695	1.00E-160	105.8	54.9	66.7	hypothetical protein 26.t00052	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01694.1.g29085.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01694.1.g29086.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	353	672	1.00E-46	190.4	29.7	43.6	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01694.1.g29087.t1	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	449	578	6.00E-92	128.7	42.3	55.5	hypothetical protein 27.t00126	gbpln	Brassica oleracea	AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957	449	957	2.00E-14	213.1	8.7	13.4
Rsa1.0_01695.1.g29088.t1	ref|NP_188490.1| DEAD-box ATP-dependent RNA helicase 51 [Arabidopsis thaliana] gi|75335038|sp|Q9LIH9.1|RH51_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 51 gi|9294321|dbj|BAB02218.1| DEAD-box ATP-dependent RNA helicase [Arabidopsis thaliana] gi|17979083|gb|AAL49809.1| putative DEAD box helicase protein [Arabidopsis thaliana] gi|20465335|gb|AAM20071.1| putative DEAD box helicase protein [Arabidopsis thaliana] gi|332642600|gb|AEE76121.1| DEAD-box ATP-dependent RNA helicase 51 [Arabidopsis thaliana]	568	568	0	100.0	84.3	92.6	DEAD-box ATP-dependent RNA helicase 51	gbpln	Arabidopsis thaliana	AT3G18600.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:6399724-6403007 REVERSE LENGTH=568	568	568	0	100.0	84.3	92.6
Rsa1.0_01695.1.g29089.t1	gb|ABL97946.1| copper ion binding/electron transporter [Brassica rapa]	178	203	6.00E-67	114.0	76.4	86.0	copper ion binding/electron transporter	gbpln	Brassica rapa	AT3G18590.1 | Symbols: ENODL5, AtENODL5 | early nodulin-like protein 5 | chr3:6398670-6399337 FORWARD LENGTH=188	178	188	8.00E-64	105.6	77.5	86.5
Rsa1.0_01695.1.g29090.t1	ref|NP_188488.1| single-strand DNA-binding protein [Arabidopsis thaliana] gi|9294319|dbj|BAB02216.1| unnamed protein product [Arabidopsis thaliana] gi|332642598|gb|AEE76119.1| single-strand DNA-binding protein [Arabidopsis thaliana]	221	217	1.00E-102	98.2	86.4	90.5	single-strand DNA-binding protein	gbpln	Arabidopsis thaliana	AT3G18580.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr3:6396940-6398068 REVERSE LENGTH=217	221	217	1.00E-104	98.2	86.4	90.5
Rsa1.0_01695.1.g29091.t1	gb|EOA33015.1| hypothetical protein CARUB_v10016346mg [Capsella rubella]	164	166	3.00E-61	101.2	79.3	84.1	hypothetical protein CARUB_v10016346mg	gbpln	Capsella rubella	AT3G18570.1 | Symbols: | Oleosin family protein | chr3:6396072-6396572 REVERSE LENGTH=166	164	166	5.00E-63	101.2	78.0	84.1
Rsa1.0_01695.1.g29092.t1	ref|XP_002883140.1| hypothetical protein ARALYDRAFT_898225 [Arabidopsis lyrata subsp. lyrata] gi|297328980|gb|EFH59399.1| hypothetical protein ARALYDRAFT_898225 [Arabidopsis lyrata subsp. lyrata]	194	195	2.00E-76	100.5	78.9	88.1	hypothetical protein ARALYDRAFT_898225	gbpln	Arabidopsis lyrata	AT3G18560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49000.1); Has 95 Blast hits to 95 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 95; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6393984-6394571 FORWARD LENGTH=195	194	195	4.00E-75	100.5	80.4	88.7

Rsa1.0_01695.1.g29093.t1	ref|NP_188485.2| transcription factor TCP18 [Arabidopsis thaliana] gi|187653897|sp|A1YKT1.1|TCP18_ARATH RecName: Full=Transcription factor TCP18; AltName: Full=Protein BRANCHED 1; AltName: Full=Protein TEOSINTE BRANCHED 1-LIKE 1 gi|119873500|gb|ABM05498.1| teosinte branched 1-like 1 protein [Arabidopsis thaliana] gi|332642594|gb|AEE76115.1| transcription factor TCP18 [Arabidopsis thaliana]	436	433	1.00E-151	99.3	68.8	79.1	transcription factor TCP18	gbpln	Arabidopsis thaliana	AT3G18550.1 | Symbols: BRC1, TCP18, ATTCP18 | TCP family transcription factor | chr3:6383769-6385604 FORWARD LENGTH=433	436	433	1.00E-153	99.3	68.8	79.1
Rsa1.0_01695.1.g29094.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01696.1.g29095.t1	ref|XP_002875348.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321186|gb|EFH51607.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	708	695	0	98.2	78.4	87.0	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G26840.1 | Symbols: | Esterase/lipase/thioesterase family protein | chr3:9892808-9896154 FORWARD LENGTH=701	708	701	0	99.0	79.1	87.0
Rsa1.0_01696.1.g29096.t1	gb|EOA25978.1| hypothetical protein CARUB_v10019367mg [Capsella rubella]	134	136	1.00E-36	101.5	58.2	70.9	hypothetical protein CARUB_v10019367mg	gbpln	Capsella rubella	AT3G27680.1 | Symbols: | Plant self-incompatibility protein S1 family | chr3:10254886-10255290 REVERSE LENGTH=134	134	134	8.00E-33	100.0	53.7	67.9
Rsa1.0_01696.1.g29097.t1	ref|XP_002875348.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321186|gb|EFH51607.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	209	695	2.00E-21	332.5	34.0	39.7	esterase/lipase/thioesterase family protein	gbpln	Arabidopsis lyrata	AT3G26840.1 | Symbols: | Esterase/lipase/thioesterase family protein | chr3:9892808-9896154 FORWARD LENGTH=701	209	701	8.00E-23	335.4	33.0	39.7
Rsa1.0_01696.1.g29098.t1	ref|NP_566803.1| uncharacterized protein [Arabidopsis thaliana] gi|30688542|ref|NP_850637.1| uncharacterized protein [Arabidopsis thaliana] gi|79313770|ref|NP_001030777.1| uncharacterized protein [Arabidopsis thaliana] gi|186510468|ref|NP_001118709.1| uncharacterized protein [Arabidopsis thaliana] gi|186510470|ref|NP_001118710.1| uncharacterized protein [Arabidopsis thaliana] gi|15293103|gb|AAK93662.1| unknown protein [Arabidopsis thaliana] gi|21436343|gb|AAM51341.1| unknown protein [Arabidopsis thaliana] gi|222424697|dbj|BAH20302.1| AT3G26890 [Arabidopsis thaliana] gi|332643708|gb|AEE77229.1| uncharacterized protein AT3G26890 [Arabidopsis thaliana] gi|332643709|gb|AEE77230.1| uncharacterized protein AT3G26890 [Arabidopsis thaliana] gi|332643710|gb|AEE77231.1| uncharacterized protein AT3G26890 [Arabidopsis thaliana] gi|332643711|gb|AEE77232.1| uncharacterized protein AT3G26890 [Arabidopsis thaliana] gi|332643712|gb|AEE77233.1| uncharacterized protein AT3G26890 [Arabidopsis thaliana]	615	649	0	105.5	82.4	88.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G26890.5 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41110.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:9907456-9910463 REVERSE LENGTH=649	615	649	0	105.5	82.4	88.0
Rsa1.0_01696.1.g29099.t2	ref|XP_002877001.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] gi|297322839|gb|EFH53260.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	604	616	0	102.0	80.1	88.1	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis lyrata	AT3G26910.2 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr3:9915304-9918511 REVERSE LENGTH=614	604	614	0	101.7	77.5	87.1
Rsa1.0_01696.1.g29100.t3	sp|Q9LJF9.3|FDL44_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	388	434	3.00E-97	111.9	52.6	70.4	RecName: Full=F-box/FBD/LRR-repeat protein At3g26920	----	----	AT3G49020.1 | Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr3:18169079-18170660 FORWARD LENGTH=447	388	447	6.00E-86	115.2	50.0	64.4
Rsa1.0_01696.1.g29101.t1	gb|EOA23519.1| hypothetical protein CARUB_v10016713mg [Capsella rubella]	782	779	0	99.6	92.8	96.2	hypothetical protein CARUB_v10016713mg	gbpln	Capsella rubella	AT3G27170.1 | Symbols: CLC-B, ATCLC-B | chloride channel B | chr3:10024147-10026921 FORWARD LENGTH=780	782	780	0	99.7	92.8	95.9

Rsa1.0_01696.1_g29102.t1	ref|NP_189354.2| S-adenosylmethionine-dependent methyltransferase-domain containing protein [Arabidopsis thaliana] gi|190341123|gb|ACE74720.1| At3g27180 [Arabidopsis thaliana] gi|332643755|gb|AEE77276.1| S-adenosylmethionine-dependent methyltransferase-domain containing protein [Arabidopsis thaliana]	516	518	0	100.4	91.9	95.7	S-adenosylmethionine-dependent methyltransferase-domain containing protein	gbpln	Arabidopsis thaliana	AT3G27180.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:10027163-10030062 REVERSE LENGTH=518	516	518	0	100.4	91.9	95.7
Rsa1.0_01696.1_g29103.t1	ref|XP_002863819.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297309654|gb|EFH40078.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	680	689	0	101.3	83.1	88.7	lectin protein kinase family protein	gbpln	Arabidopsis lyrata	AT5G42120.1 | Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:16833073-16835148 REVERSE LENGTH=691	680	691	0	101.6	82.1	88.8
Rsa1.0_01696.1_g29104.t1	gb|EOA23905.1| hypothetical protein CARUB_v10017120mg [Capsella rubella]	484	483	0	99.8	93.8	96.5	hypothetical protein CARUB_v10017120mg	gbpln	Capsella rubella	AT3G27190.1 | Symbols: UKL2 | uridine kinase-like 2 | chr3:10039504-10042917 REVERSE LENGTH=483	484	483	0	99.8	93.4	96.7
Rsa1.0_01696.1_g29105.t1	gb|EOA24837.1| hypothetical protein CARUB_v10018126mg [Capsella rubella]	187	171	4.00E-66	91.4	77.0	82.9	hypothetical protein CARUB_v10018126mg	gbpln	Capsella rubella	AT3G27200.1 | Symbols: | Cupredoxin superfamily protein | chr3:10043738-10044340 REVERSE LENGTH=174	187	174	4.00E-65	93.0	70.6	77.5
Rsa1.0_01696.1_g29106.t1	ref|XP_002877027.1| hypothetical protein ARALYDRAFT_484504 [Arabidopsis lyrata subsp. lyrata] gi|297322865|gb|EFH53286.1| hypothetical protein ARALYDRAFT_484504 [Arabidopsis lyrata subsp. lyrata]	252	241	3.00E-70	95.6	67.9	74.6	hypothetical protein ARALYDRAFT_484504	gbpln	Arabidopsis lyrata	AT3G27210.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40860.1); Has 133 Blast hits to 98 proteins in 25 species: Archae - 0; Bacteria - 6; Metazoa - 32; Fungi - 7; Plants - 70; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink). | chr3:10045458-10047222 REVERSE LENGTH=234	252	234	7.00E-71	92.9	69.0	74.6
Rsa1.0_01696.1_g29107.t1	ref|XP_002877044.1| hypothetical protein ARALYDRAFT_904974 [Arabidopsis lyrata subsp. lyrata] gi|297322882|gb|EFH53303.1| hypothetical protein ARALYDRAFT_904974 [Arabidopsis lyrata subsp. lyrata]	137	157	1.00E-10	114.6	36.5	51.8	hypothetical protein ARALYDRAFT_904974	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01696.1_g29108.t1	ref|XP_002877046.1| hypothetical protein ARALYDRAFT_322865 [Arabidopsis lyrata subsp. lyrata] gi|297322884|gb|EFH53305.1| hypothetical protein ARALYDRAFT_322865 [Arabidopsis lyrata subsp. lyrata]	76	76	9.00E-19	100.0	63.2	73.7	hypothetical protein ARALYDRAFT_322865	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01696.1_g29109.t1	dbj|BAJ34353.1| unnamed protein product [Thellungiella halophila]	277	279	1.00E-143	100.7	91.7	94.9	unnamed protein product	----	----	AT5G40650.1 | Symbols: SDH2-2 | succinate dehydrogenase 2-2 | chr5:16281462-16283296 FORWARD LENGTH=280	277	280	1.00E-142	101.1	88.8	93.1
Rsa1.0_01696.1_g29110.t1	ref|NP_189375.2| uncharacterized protein [Arabidopsis thaliana] gi|332278120|sp|Q8GUM4.2|Y3739_ARATH RecName: Full=Uncharacterized membrane protein At3g27390 gi|332643790|gb|AEE77311.1| uncharacterized protein AT3G27390 [Arabidopsis thaliana]	591	588	0	99.5	85.1	92.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27390.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40640.1); Has 101 Blast hits to 99 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:10133372-10136111 REVERSE LENGTH=588	591	588	0	99.5	85.1	92.4
Rsa1.0_01696.1_g29111.t1	ref|XP_002875382.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321220|gb|EFH51641.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	412	412	0	100.0	91.0	95.4	predicted protein	gbpln	Arabidopsis lyrata	AT3G27400.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:10140323-10143023 FORWARD LENGTH=412	412	412	0	100.0	91.5	95.1
Rsa1.0_01696.1_g29112.t1	ref|NP_189377.1| uncharacterized protein [Arabidopsis thaliana] gi|7939513|dbj|BAA95716.1| unnamed protein product [Arabidopsis thaliana] gi|67633670|gb|AAY78759.1| unknown [Arabidopsis thaliana] gi|332643792|gb|AEE77313.1| uncharacterized protein AT3G27410 [Arabidopsis thaliana]	124	132	1.00E-26	106.5	70.2	78.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27410.1 | Symbols: | unknown protein; Has 10 Blast hits to 10 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:10145244-10145642 REVERSE LENGTH=132	124	132	2.00E-29	106.5	70.2	78.2

Rsa1.0_01696.1.g29113.t1	ref|NP_001118719.1| uncharacterized protein [Arabidopsis thaliana] gi|7939514|dbj|BAA95717.1| unnamed protein product [Arabidopsis thaliana] gi|98961621|gb|ABF59140.1| unknown protein [Arabidopsis thaliana] gi|332643793|gb|AEE77314.1| uncharacterized protein AT3G27415 [Arabidopsis thaliana]	249	175	3.00E-36	70.3	52.2	56.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G27415.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:10147375-10147902 FORWARD LENGTH=175	249	175	8.00E-39	70.3	52.2	56.2
Rsa1.0_01696.1.g29114.t1	ref|XP_002875387.1| hypothetical protein ARALYDRAFT_904988 [Arabidopsis lyrata subsp. lyrata] gi|297321225|gb|EFH51646.1| hypothetical protein ARALYDRAFT_904988 [Arabidopsis lyrata subsp. lyrata]	269	273	1.00E-152	101.5	97.4	98.1	hypothetical protein ARALYDRAFT_904988	gbpln	Arabidopsis lyrata	AT3G27430.2 | Symbols: PBB1 | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:10152910-10155052 FORWARD LENGTH=273	269	273	1.00E-154	101.5	97.0	98.1
Rsa1.0_01696.1.g29115.t1	ref|XP_002882056.1| TGF-beta receptor interacting protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297327895|gb|EFH58315.1| TGF-beta receptor interacting protein 1 [Arabidopsis lyrata subsp. lyrata]	328	328	1.00E-172	100.0	86.9	95.7	TGF-beta receptor interacting protein 1	gbpln	Arabidopsis lyrata	AT2G46290.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:19005910-19007797 REVERSE LENGTH=355	328	355	1.00E-173	108.2	85.7	96.0
Rsa1.0_01696.1.g29116.t1	ref|NP_189382.2| SGF29 tudor-like domain-containing protein [Arabidopsis thaliana] gi|19347735|gb|AAL86293.1| unknown protein [Arabidopsis thaliana] gi|21689749|gb|AAM67518.1| unknown protein [Arabidopsis thaliana] gi|332643801|gb|AEE77322.1| SGF29 tudor-like domain-containing protein [Arabidopsis thaliana]	270	270	1.00E-148	100.0	95.2	98.5	SGF29 tudor-like domain-containing protein	gbpln	Arabidopsis thaliana	AT3G27460.1 | Symbols: | SGF29 tudor-like domain | chr3:10159537-10161994 REVERSE LENGTH=270	270	270	1.00E-151	100.0	95.2	98.5
Rsa1.0_01697.1.g29117.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	754	1529	0	202.8	51.6	67.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	754	746	1.00E-71	98.9	17.6	23.6
Rsa1.0_01697.1.g29118.t1	gb|AAZ30035.1| putative calcium-dependent protein kinase [Isatis tinctoria] gi|94958384|gb|ABF47341.1| calcium-dependent protein kinase [Isatis tinctoria] gi|95020533|gb|ABF50790.1| calcium-dependent protein kinase [Isatis tinctoria]	634	537	0	84.7	77.8	79.7	putative calcium-dependent protein kinase	gbpln	Isatis tinctoria	AT3G57530.1 | Symbols: CPK32, ATCPK32, CDPK32 | calcium-dependent protein kinase 32 | chr3:21296898-21299351 REVERSE LENGTH=538	634	538	0	84.9	77.0	79.2
Rsa1.0_01697.1.g29119.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1798	1213	0	67.5	23.7	34.5	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1798	626	2.00E-61	34.8	7.2	12.0
Rsa1.0_01697.1.g29120.t1	emb|CAD21651.2| endo polygalacturonase [Brassica rapa subsp. rapa]	106	433	7.00E-50	408.5	92.5	97.2	endo polygalacturonase	gbpln	Brassica rapa	AT3G57510.1 | Symbols: ADPG1 | Pectin lyase-like superfamily protein | chr3:21283546-21285842 REVERSE LENGTH=431	106	431	3.00E-48	406.6	83.0	92.5
Rsa1.0_01698.1.g29121.t1	ref|XP_002890318.1| hypothetical protein ARALYDRAFT_472131 [Arabidopsis lyrata subsp. lyrata] gi|297336160|gb|EFH66577.1| hypothetical protein ARALYDRAFT_472131 [Arabidopsis lyrata subsp. lyrata]	188	755	3.00E-27	401.6	39.9	47.3	hypothetical protein ARALYDRAFT_472131	gbpln	Arabidopsis lyrata	AT1G19110.1 | Symbols: | inter-alpha-trypsin inhibitor heavy chain-related | chr1:6602270-6605766 FORWARD LENGTH=754	188	754	1.00E-28	401.1	28.7	30.3
Rsa1.0_01698.1.g29122.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01698.1.g29123.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01698.1.g29124.t1	ref|NP_001185147.1| uncharacterized protein [Arabidopsis thaliana] gi|332193796|gb|AEE31917.1| uncharacterized protein AT1G42430 [Arabidopsis thaliana]	379	409	0	107.9	88.7	92.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G42430.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G55760.3). | chr1:15891512-15894322 FORWARD LENGTH=409	379	409	0	107.9	88.7	92.1
Rsa1.0_01699.1.g29125.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01699.1.g29126.t1	ref|XP_002865452.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297311287|gb|EFH41711.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	597	582	0	97.5	82.4	88.8	tetratricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G43120.1 | Symbols: | ARM-repeat/Tetratricopeptide repeat (TPR)-like protein | chr5:17312602-17314368 FORWARD LENGTH=588	597	588	0	98.5	81.2	87.9
Rsa1.0_01699.1.g29127.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01699.1.g29128.t1	ref|NP_199124.3| aspartyl protease family protein [Arabidopsis thaliana] gi|332007527|gb|AED94910.1| aspartyl protease family protein [Arabidopsis thaliana]	652	631	0	96.8	86.0	92.2	aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT5G43100.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:17299264-17302718 FORWARD LENGTH=631	652	631	0	96.8	86.0	92.2
Rsa1.0_01699.1.g29129.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01699.1.g29130.t1	ref|NP_199125.2| pumilio 14 [Arabidopsis thaliana] gi|75339252|sp|Q4PSD1.1|PUM14_ARATH RecName: Full=Pumilio homolog 14; Short=APUM-14; Short=AtPUM14 gi|67633854|gb|AAY78851.1| pumilio/Puf RNA-binding domain-containing protein [Arabidopsis thaliana] gi|332007528|gb|AED94911.1| pumilio 14 [Arabidopsis thaliana]	476	518	5.00E-87	108.8	44.3	60.7	pumilio 14	gbpln	Arabidopsis thaliana	AT5G43110.1 | Symbols: APUM14, PUM14 | pumilio 14 | chr5:17309842-17311937 FORWARD LENGTH=518	476	518	1.00E-89	108.8	44.3	60.7
Rsa1.0_01699.1.g29131.t4	gb|AAD28663.1| hypothetical protein [Arabidopsis thaliana]	884	356	6.00E-11	40.3	8.7	14.6	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01699.1.g29132.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01700.1.g29133.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01700.1.g29134.t2	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	568	1307	1.00E-155	230.1	55.8	69.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	568	1262	4.00E-19	222.2	8.6	12.1
Rsa1.0_01700.1.g29135.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01700.1.g29136.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01700.1.g29137.t1	ref|XP_002890295.1| AtMYB47 [Arabidopsis lyrata subsp. lyrata] gi|297336137|gb|EFH66554.1| AtMYB47 [Arabidopsis lyrata subsp. lyrata]	254	271	5.00E-93	106.7	73.2	80.3	AtMYB47	gbpln	Arabidopsis lyrata	AT1G18710.1 | Symbols: AtMYB47, MYB47 | myb domain protein 47 | chr1:6450781-6452986 FORWARD LENGTH=267	254	267	3.00E-90	105.1	72.8	80.7
Rsa1.0_01700.1.g29138.t1	gb|EOA21531.1| hypothetical protein CARUB_v10001936mg [Capsella rubella]	216	217	7.00E-69	100.5	58.3	73.1	hypothetical protein CARUB_v10001936mg	gbpln	Capsella rubella	AT5G01750.2 | Symbols: | Protein of unknown function (DUF567) | chr5:290034-291109 FORWARD LENGTH=217	216	217	7.00E-70	100.5	56.5	73.6
Rsa1.0_01700.1.g29139.t1	gb|AAK62788.1|AC027036_9 polyprotein, putative [Arabidopsis thaliana] gi|18265373|dbj|BAB84015.1| polyprotein [Arabidopsis thaliana]	191	1466	1.00E-43	767.5	46.6	59.2	polyprotein, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01701.1.g29140.t1	ref|NP_194233.1| uncharacterized protein [Arabidopsis thaliana] gi|42573033|ref|NP_974613.1| uncharacterized protein [Arabidopsis thaliana] gi|4455246|emb|CAB36745.1| putative protein [Arabidopsis thaliana] gi|7269353|emb|CAB79412.1| putative protein [Arabidopsis thaliana] gi|21553767|gb|AAM62860.1| unknown [Arabidopsis thaliana] gi|89000969|gb|ABD59074.1| At4g25030 [Arabidopsis thaliana] gi|110736875|dbj|BAF00395.1| hypothetical protein [Arabidopsis thaliana] gi|222424032|dbj|BAH19977.1| AT4G25030 [Arabidopsis thaliana] gi|332659593|gb|AEE84993.1| uncharacterized protein AT4G25030 [Arabidopsis thaliana] gi|332659594|gb|AEE84994.1| uncharacterized protein AT4G25030 [Arabidopsis thaliana]	112	344	1.00E-47	307.1	87.5	93.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G25030.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G45410.3); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:12865336-12866638 FORWARD LENGTH=344	112	344	2.00E-50	307.1	87.5	93.8
Rsa1.0_01701.1.g29141.t2	ref|NP_179441.1| splicing factor 3B subunit 4 [Arabidopsis thaliana] gi|4218014|gb|AAD12222.1| putative spliceosome associated protein [Arabidopsis thaliana] gi|23297611|gb|AAN12991.1| putative spliceosome-associated protein [Arabidopsis thaliana] gi|330251682|gb|AEC06776.1| splicing factor 3B subunit 4-like protein [Arabidopsis thaliana]	198	363	3.00E-18	183.3	22.2	24.2	splicing factor 3B subunit 4	gbpln	Arabidopsis thaliana	AT2G18510.1 | Symbols: emb2444 | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:8031554-8033517 REVERSE LENGTH=363	198	363	1.00E-20	183.3	22.2	24.2
Rsa1.0_01701.1.g29142.t2	ref|NP_194234.1| uncharacterized protein [Arabidopsis thaliana] gi|75181563|sp|Q9M0L3.1|CSPLR_ARATH RecName: Full=CASP-like protein At4g25040 gi|7269354|emb|CAB79413.1| putative protein [Arabidopsis thaliana] gi|332659595|gb|AEE84995.1| CASP-like protein [Arabidopsis thaliana]	169	170	6.00E-70	100.6	81.7	89.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G25040.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr4:12868320-12869319 FORWARD LENGTH=170	169	170	2.00E-72	100.6	81.7	89.9

Rsa1.0_01701.1.g29143.t1	gb|EOA16168.1| hypothetical protein CARUB_v10004304mg, partial [Capsella rubella]	647	670	0	103.6	73.7	82.7	hypothetical protein CARUB_v10004304mg, partial	gbpln	Capsella rubella	AT4G25070.1 | Symbols: | unknown protein; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48860.2); Has 14837 Blast hits to 10961 proteins in 1163 species: Archae - 189; Bacteria - 1924; Metazoa - 7665; Fungi - 1127; Plants - 653; Viruses - 80; Other Eukaryotes - 3199 (source: NCBI BLink). | chr4:12872482-12876468 FORWARD LENGTH=765	647	765	0	118.2	64.5	75.3
Rsa1.0_01701.1.g29144.t1	ref|NP_194238.1| magnesium-protoporphyrin IX methyltransferase [Arabidopsis thaliana] gi|30686748|ref|NP_849438.1| magnesium-protoporphyrin IX methyltransferase [Arabidopsis thaliana] gi|30686750|ref|NP_849439.1| magnesium-protoporphyrin IX methyltransferase [Arabidopsis thaliana] gi|334186906|ref|NP_001190832.1| magnesium-protoporphyrin IX methyltransferase [Arabidopsis thaliana] gi|4455251|emb|CAB36750.1| magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana] gi|7269358|emb|CAB79417.1| magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana] gi|14334514|gb|AAK59454.1| putative magnesium-protoporphyrin IX methyltransferase [Arabidopsis thaliana] gi|17104553|gb|AAL34165.1| putative magnesium-protoporphyrin IX methyltransferase [Arabidopsis thaliana] gi|222422821|dbj|BAH19398.1| AT4G25080 [Arabidopsis thaliana] gi|332659600|gb|AEE85000.1| magnesium-protoporphyrin IX methyltransferase [Arabidopsis thaliana] gi|332659601|gb|AEE85001.1| magnesium-protoporphyrin IX methyltransferase [Arabidopsis thaliana]	313	312	1.00E-159	99.7	91.1	94.2	magnesium-protoporphyrin IX methyltransferase	gbpln	Arabidopsis thaliana	AT4G25080.5 | Symbols: CHLM | magnesium-protoporphyrin IX methyltransferase | chr4:12877015-12878128 FORWARD LENGTH=312	313	312	1.00E-161	99.7	91.1	94.2
Rsa1.0_01701.1.g29145.t1	ref|NP_199915.1| protein crumpled leaf [Arabidopsis thaliana] gi|13877867|gb|AAK44011.1|AF370196_1 unknown protein [Arabidopsis thaliana] gi|9758249|dbj|BAB08748.1| unnamed protein product [Arabidopsis thaliana] gi|21281135|gb|AAM44980.1| unknown protein [Arabidopsis thaliana] gi|45504116|dbj|BAD12566.1| CRUMPLED LEAF [Arabidopsis thaliana] gi|332008639|gb|AED96022.1| protein crumpled leaf [Arabidopsis thaliana]	552	269	1.00E-136	48.7	42.4	45.8	protein crumpled leaf	gbpln	Arabidopsis thaliana	AT5G51020.1 | Symbols: CRL | crumpled leaf | chr5:20745560-20747165 REVERSE LENGTH=269	552	269	1.00E-139	48.7	42.4	45.8
Rsa1.0_01701.1.g29146.t1	ref|XP_002867625.1| hypothetical protein ARALYDRAFT_492323 [Arabidopsis lyrata subsp. lyrata] gi|297313461|gb|EFH43884.1| hypothetical protein ARALYDRAFT_492323 [Arabidopsis lyrata subsp. lyrata]	645	421	0	65.3	53.5	57.2	hypothetical protein ARALYDRAFT_492323	gbpln	Arabidopsis lyrata	AT4G25110.1 | Symbols: AtMC2, MC2 | metacaspase 2 | chr4:12887738-12889953 REVERSE LENGTH=418	645	418	0	64.8	52.4	55.8
Rsa1.0_01701.1.g29147.t1	emb|CAA62760.1| PMSR protein [Brassica napus]	256	257	1.00E-137	100.4	91.8	96.1	PMSR protein	gbpln	Brassica napus	AT4G25130.1 | Symbols: PMSR4 | peptide met sulfoxide reductase 4 | chr4:12898802-12899998 REVERSE LENGTH=258	256	258	1.00E-124	100.8	82.0	90.6
Rsa1.0_01701.1.g29148.t1	sp|P29110.1|OLEO3_BRANA RecName: Full=Oleosin Bn-III; Short=BnIII gi|17839|emb|CAA43941.1| oleosin BN-III [Brassica napus] gi|196122088|gb|ACG69519.1| oleosin S3-7 [Brassica napus] gi|742387|prf||2009397A oleosin	198	195	8.00E-95	98.5	93.4	96.0	RecName: Full=Oleosin Bn-III; Short=BnIII gi|17839|emb|CAA43941.1| oleosin BN-III	gbpln	Brassica napus	AT4G25140.1 | Symbols: OLEO1, OLE1 | oleosin 1 | chr4:12900498-12901259 FORWARD LENGTH=173	198	173	2.00E-72	87.4	79.3	82.3
Rsa1.0_01701.1.g29149.t1	gb|EOA17259.1| hypothetical protein CARUB_v10005533mg [Capsella rubella]	269	260	1.00E-125	96.7	81.4	89.2	hypothetical protein CARUB_v10005533mg	gbpln	Capsella rubella	AT4G25150.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr4:12901736-12902882 REVERSE LENGTH=260	269	260	1.00E-125	96.7	80.7	89.6
Rsa1.0_01701.1.g29150.t1	gb|EOA16012.1| hypothetical protein CARUB_v10004133mg [Capsella rubella]	839	830	0	98.9	87.1	93.2	hypothetical protein CARUB_v10004133mg	gbpln	Capsella rubella	AT4G25160.1 | Symbols: | U-box domain-containing protein kinase family protein | chr4:12903360-12906669 REVERSE LENGTH=835	839	835	0	99.5	87.4	93.0

Rsa1.0_01701.1.g29151.t1	gb|EOA16577.1| hypothetical protein CARUB_v10004742mg [Capsella rubella]	185	467	2.00E-54	252.4	61.1	74.1	hypothetical protein CARUB_v10004742mg	gbpln	Capsella rubella	AT4G25340.2 | Symbols: FKBP53 | FK506 BINDING PROTEIN 53 | chr4:12959863-12962632 REVERSE LENGTH=444	185	444	6.00E-56	240.0	61.1	71.9
Rsa1.0_01701.1.g29152.t1	gb|EOA18179.1| hypothetical protein CARUB_v10006657mg [Capsella rubella]	613	532	0	86.8	67.9	73.1	hypothetical protein CARUB_v10006657mg	gbpln	Capsella rubella	AT4G25360.2 | Symbols: | TRICHOME BIREFRINGENCE-LIKE 18 | chr4:12970187-12972404 FORWARD LENGTH=533	613	533	0	86.9	68.0	73.7
Rsa1.0_01701.1.g29153.t1	ref|XP_002863680.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309515|gb|EFH39939.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	110	231	2.00E-15	210.0	35.5	41.8	predicted protein	gbpln	Arabidopsis lyrata	AT2G27490.2 | Symbols: ATCOAE | dephospho-CoA kinase family | chr2:11748087-11749009 REVERSE LENGTH=232	110	232	6.00E-18	210.9	35.5	40.0
Rsa1.0_01701.1.g29154.t1	ref|XP_002869672.1| basix helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297315508|gb|EFH45931.1| basix helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	209	222	2.00E-86	106.2	86.1	91.9	basix helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT4G25410.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:12985772-12987149 FORWARD LENGTH=230	209	230	9.00E-89	110.0	83.7	90.4
Rsa1.0_01702.1.g29155.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01702.1.g29156.t1	ref|XP_002884989.1| beta-fructofuranosidase [Arabidopsis lyrata subsp. lyrata] gi|297330829|gb|EFH61248.1| beta-fructofuranosidase [Arabidopsis lyrata subsp. lyrata]	580	581	0	100.2	92.8	96.6	beta-fructofuranosidase	gbpln	Arabidopsis lyrata	AT3G13790.2 | Symbols: ATBFRUCT1 | Glycosyl hydrolases family 32 protein | chr3:4533084-4535831 REVERSE LENGTH=581	580	581	0	100.2	94.0	97.2
Rsa1.0_01702.1.g29157.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	219	1374	7.00E-47	627.4	41.6	53.4	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	219	575	2.00E-46	262.6	39.7	53.0
Rsa1.0_01702.1.g29158.t1	gb|EOA32993.1| hypothetical protein CARUB_v10016323mg [Capsella rubella]	846	846	0	100.0	96.2	97.9	hypothetical protein CARUB_v10016323mg	gbpln	Capsella rubella	AT3G13750.1 | Symbols: BGAL1 | beta galactosidase 1 | chr3:4511192-4515756 FORWARD LENGTH=847	846	847	0	100.1	95.9	98.0
Rsa1.0_01702.1.g29159.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01702.1.g29160.t1	ref|NP_566462.1| 3-epi-6-deoxocathasterone 23-monooxygenase [Arabidopsis thaliana] gi|75306559|sp|Q94IA6.1|C90D1_ARATH RecName: Full=3-epi-6-deoxocathasterone 23-monooxygenase; AltName: Full=Cytochrome P450 90D1 gi|14971017|dbj|BAB62109.1| CYP90D [Arabidopsis thaliana] gi|28393374|gb|AAO42111.1| putative cytochrome P450 [Arabidopsis thaliana] gi|28827564|gb|AAO50626.1| putative cytochrome P450 [Arabidopsis thaliana] gi|332641883|gb|AEE75404.1| 3-epi-6-deoxocathasterone 23-monooxygenase [Arabidopsis thaliana]	492	491	0	99.8	87.0	90.7	3-epi-6-deoxocathasterone 23-monooxygenase	gbpln	Arabidopsis thaliana	AT3G13730.1 | Symbols: CYP90D1 | cytochrome P450, family 90, subfamily D, polypeptide 1 | chr3:4498330-4500836 REVERSE LENGTH=491	492	491	0	99.8	87.0	90.7
Rsa1.0_01703.1.g29161.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01703.1.g29162.t1	ref|XP_002872013.1| prephenate dehydratase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317850|gb|EFH48272.1| prephenate dehydratase family protein [Arabidopsis lyrata subsp. lyrata]	431	433	0	100.5	91.2	94.0	prephenate dehydratase family protein	gbpln	Arabidopsis lyrata	AT5G22630.1 | Symbols: ADT5 | arogenate dehydratase 5 | chr5:7524645-7525922 FORWARD LENGTH=425	431	425	0	98.6	89.8	92.3
Rsa1.0_01703.1.g29163.t1	gb|EOA20513.1| hypothetical protein CARUB_v10000827mg [Capsella rubella]	439	489	0	111.4	82.7	89.1	hypothetical protein CARUB_v10000827mg	gbpln	Capsella rubella	AT5G22620.2 | Symbols: | phosphoglycerate/bisphosphoglycerate mutase family protein | chr5:7517731-7520223 REVERSE LENGTH=482	439	482	0	109.8	81.5	87.9
Rsa1.0_01703.1.g29164.t1	gb|EOA19749.1| hypothetical protein CARUB_v10003892mg [Capsella rubella]	470	457	1.00E-119	97.2	52.6	67.4	hypothetical protein CARUB_v10003892mg	gbpln	Capsella rubella	AT5G22730.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:7551632-7553219 REVERSE LENGTH=466	470	466	1.00E-104	99.1	47.7	63.2
Rsa1.0_01703.1.g29165.t1	ref|XP_002874078.1| WRKY DNA-binding protein 38 [Arabidopsis lyrata subsp. lyrata] gi|297319915|gb|EFH50337.1| WRKY DNA-binding protein 38 [Arabidopsis lyrata subsp. lyrata]	290	292	4.00E-97	100.7	66.2	76.9	WRKY DNA-binding protein 38	gbpln	Arabidopsis lyrata	AT5G22570.1 | Symbols: WRKY38, ATWRKY38 | WRKY DNA-binding protein 38 | chr5:7495608-7496707 REVERSE LENGTH=289	290	289	1.00E-90	99.7	62.1	73.1
Rsa1.0_01703.1.g29166.t1	gb|EOA20175.1| hypothetical protein CARUB_v10000472mg [Capsella rubella]	129	622	4.00E-23	482.2	39.5	41.9	hypothetical protein CARUB_v10000472mg	gbpln	Capsella rubella	AT5G22510.1 | Symbols: INV-E, At-A/N-InvE | alkaline/neutral invertase | chr5:7474974-7477479 REVERSE LENGTH=617	129	617	1.00E-25	478.3	38.8	41.9

Rsa1.0_01704.1.g29167.t1	ref|NP_567046.1| Transmembrane proteins 14C [Arabidopsis thaliana] gi|14517381|gb|AAK62581.1| AT3g57280/F28O9_130 [Arabidopsis thaliana] gi|15450539|gb|AAK96447.1| AT3g57280/F28O9_130 [Arabidopsis thaliana] gi|21553454|gb|AAM62547.1| unknown [Arabidopsis thaliana] gi|332646114|gb|AEE79635.1| Transmembrane proteins 14C [Arabidopsis thaliana]	235	226	2.00E−97	96.2	83.0	87.2	Transmembrane proteins 14C	gbpln	Arabidopsis thaliana	AT3G57280.1 | Symbols: | Transmembrane proteins 14C | chr3:21193960−21195547 FORWARD LENGTH=226	235	226	1.00E−100	96.2	83.0	87.2
Rsa1.0_01704.1.g29168.t1	ref|XP_002878144.1| hypothetical protein ARALYDRAFT_486171 [Arabidopsis lyrata subsp. lyrata] gi|297323982|gb|EFH54403.1| hypothetical protein ARALYDRAFT_486171 [Arabidopsis lyrata subsp. lyrata]	444	441	0	99.3	95.3	97.7	hypothetical protein ARALYDRAFT_486171	gbpln	Arabidopsis lyrata	AT3G57290.1 | Symbols: EIF3E, TIF3E1, ATEIF3E−1, INT−6, ATINT6, INT6 | eukaryotic translation initiation factor 3E | chr3:21196786−21199073 REVERSE LENGTH=441	444	441	0	99.3	93.0	96.6
Rsa1.0_01704.1.g29169.t1	ref|NP_191289.2| DNA helicase INO80 complex−like 1 [Arabidopsis thaliana] gi|238065083|sp|Q8RXS6.2|INO80_ARATH RecName: Full=DNA helicase INO80; Short=AtINO80; AltName: Full=Putative DNA helicase INO80 complex homolog 1 gi|332646116|gb|AEE79637.1| DNA helicase INO80 complex−like 1 [Arabidopsis thaliana]	1531	1507	0	98.4	85.2	90.9	DNA helicase INO80 complex−like 1	gbpln	Arabidopsis thaliana	AT3G57300.1 | Symbols: INO80, ATINO80 | INO80 ortholog | chr3:21199612−21207635 FORWARD LENGTH=1507	1531	1507	0	98.4	85.2	90.9
Rsa1.0_01704.1.g29170.t1	emb|CAA68234.1| calmodulin−stimulated calcium−ATPase [Brassica oleracea]	985	1025	0	104.1	94.4	97.3	calmodulin−stimulated calcium−ATPase	gbpln	Brassica oleracea	AT3G57330.1 | Symbols: ACA11 | autoinhibited Ca2+−ATPase 11 | chr3:21211655−21216375 REVERSE LENGTH=1025	985	1025	0	104.1	94.1	96.9
Rsa1.0_01704.1.g29171.t1	ref|XP_002876412.1| hypothetical protein ARALYDRAFT_486177 [Arabidopsis lyrata subsp. lyrata] gi|297322250|gb|EFH52671.1| hypothetical protein ARALYDRAFT_486177 [Arabidopsis lyrata subsp. lyrata]	368	365	1.00E−165	99.2	81.5	91.3	hypothetical protein ARALYDRAFT_486177	gbpln	Arabidopsis lyrata	AT3G57340.2 | Symbols: | Heat shock protein DnaJ, N−terminal with domain of unknown function (DUF1977) | chr3:21219175−21220278 FORWARD LENGTH=367	368	367	1.00E−165	99.7	81.0	90.8
Rsa1.0_01704.1.g29172.t1	gb|EOA25570.1| hypothetical protein CARUB_v10018922mg [Capsella rubella]	861	863	0	100.2	86.8	93.6	hypothetical protein CARUB_v10018922mg	gbpln	Capsella rubella	AT2G41620.1 | Symbols: | Nucleoporin interacting component (Nup93/Nic96−like) family protein | chr2:17350419−17354997 REVERSE LENGTH=861	861	861	0	100.0	85.4	93.6
Rsa1.0_01704.1.g29173.t1	gb|EOA24554.1| hypothetical protein CARUB_v10017811mg [Capsella rubella]	254	275	1.00E−118	108.3	83.5	91.3	hypothetical protein CARUB_v10017811mg	gbpln	Capsella rubella	AT3G57360.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02370.2); Has 122 Blast hits to 122 proteins in 54 species: Archae − 0; Bacteria − 0; Metazoa − 74; Fungi − 4; Plants − 41; Viruses − 0; Other Eukaryotes − 3 (source: NCBI BLink). | chr3:21225571−21226621 FORWARD LENGTH=254	254	254	1.00E−118	100.0	83.1	89.4
Rsa1.0_01705.1.g29174.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01705.1.g29175.t1	gb|EOA19862.1| hypothetical protein CARUB_v10000113mg [Capsella rubella]	1040	1049	0	100.9	91.4	95.8	hypothetical protein CARUB_v10000113mg	gbpln	Capsella rubella	AT5G11110.1 | Symbols: SPS1, ATSPS2F, KNS2, SPS2F | sucrose phosphate synthase 2F | chr5:3536426−3540901 FORWARD LENGTH=1047	1040	1047	0	100.7	90.0	94.8
Rsa1.0_01705.1.g29176.t1	dbj|BAH57203.1| AT5G11170 [Arabidopsis thaliana]	177	177	8.00E−93	100.0	93.2	96.0	AT5G11170	gbpln	Arabidopsis thaliana	AT5G11170.2 | Symbols: | DEAD/DEAH box RNA helicase family protein | chr5:3554272−3556646 FORWARD LENGTH=344	177	344	4.00E−92	194.4	89.3	91.5
Rsa1.0_01705.1.g29177.t1	ref|XP_004291460.1| PREDICTED: DEAD−box ATP−dependent RNA helicase 56−like [Fragaria vesca subsp. vesca]	80	447	5.00E−24	558.8	68.8	82.5	PREDICTED: DEAD−box ATP−dependent RNA helicase 56−like	gbpln	Fragaria vesca	AT5G11200.2 | Symbols: | DEAD/DEAH box RNA helicase family protein | chr5:3567389−3570686 FORWARD LENGTH=486	80	486	9.00E−26	607.5	85.0	90.0
Rsa1.0_01705.1.g29178.t1	gb|EOA22882.1| hypothetical protein CARUB_v10003614mg [Capsella rubella]	350	349	0	99.7	90.0	95.1	hypothetical protein CARUB_v10003614mg	gbpln	Capsella rubella	AT4G32390.1 | Symbols: | Nucleotide−sugar transporter family protein | chr4:15636550−15637602 FORWARD LENGTH=350	350	350	1.00E−180	100.0	86.6	95.4
Rsa1.0_01705.1.g29179.t1	gb|ACP30584.1| disease resistance protein [Brassica rapa subsp. pekinensis]	947	980	0	103.5	60.6	62.6	disease resistance protein	gbpln	Brassica rapa	AT5G11250.1 | Symbols: | Disease resistance protein (TIR−NBS−LRR class) | chr5:3587978−3591960 REVERSE LENGTH=1189	947	1189	0	125.6	39.3	47.3
Rsa1.0_01705.1.g29180.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_01705.1.g29181.t1	gb|EOA21558.1| hypothetical protein CARUB_v10001967mg [Capsella rubella]	537	209	1.00E−99	38.9	33.1	36.3	hypothetical protein CARUB_v10001967mg	gbpln	Capsella rubella	AT5G11280.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80200.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:3597321−3598347 FORWARD LENGTH=209	537	209	1.00E−101	38.9	32.8	35.9
Rsa1.0_01705.1.g29182.t5	ref|XP_002890058.1| hypothetical protein ARALYDRAFT_334745 [Arabidopsis lyrata subsp. lyrata] gi|297335900|gb|EFH66317.1| hypothetical protein ARALYDRAFT_334745 [Arabidopsis lyrata subsp. lyrata]	287	310	3.00E−29	108.0	23.7	28.2	hypothetical protein ARALYDRAFT_334745	gbpln	Arabidopsis lyrata	AT1G14688.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: E3 Ubiquitin ligase (InterPro:IPR022170); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr1:5049654−5050983 REVERSE LENGTH=170	287	170	2.00E−21	59.2	17.1	23.3
Rsa1.0_01705.1.g29183.t1	ref|XP_002890061.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297335903|gb|EFH66320.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	243	211	7.00E−37	86.8	40.3	54.7	expressed protein	gbpln	Arabidopsis lyrata	AT1G63900.1 | Symbols: DAL1 | E3 Ubiquitin ligase family protein | chr1:23717056−23719086 FORWARD LENGTH=343	243	343	2.00E−15	141.2	29.6	42.4
Rsa1.0_01706.1.g29184.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#
Rsa1.0_01706.1.g29185.t1	gb|EOA36809.1| hypothetical protein CARUB_v10008388mg [Capsella rubella]	646	757	0	117.2	58.2	67.5	hypothetical protein CARUB_v10008388mg	gbpln	Capsella rubella	AT1G03780.2 | Symbols: TPX2 | targeting protein for XKLP2 | chr1:947785−951696 REVERSE LENGTH=758	646	758	0	117.3	58.0	66.7
Rsa1.0_01706.1.g29186.t1	ref|NP_199241.2| putative E3 ubiquitin−protein ligase RING1a [Arabidopsis thaliana] gi|302425246|sp|Q9FKW0.2|RNG1A_ARATH RecName: Full=Putative E3 ubiquitin−protein ligase RING1a; AltName: Full=Polycomb complex protein RING1a; AltName: Full=Protein RING1a; Short=AtRING1a; AltName: Full=Ring finger protein 434 gi|332007702|gb|AED95085.1| putative E3 ubiquitin−protein ligase RING1a [Arabidopsis thaliana]	500	522	0	104.4	77.2	85.2	putative E3 ubiquitin−protein ligase RING1a	gbpln	Arabidopsis thaliana	AT5G44280.1 | Symbols: ATRING1A, RING1A | RING 1A | chr5:17836115−17839114 REVERSE LENGTH=522	500	522	0	104.4	77.2	85.2
Rsa1.0_01706.1.g29187.t2	ref|NP_186790.2| RNase H domain−containing protein [Arabidopsis thaliana] gi|145331720|ref|NP_001078087.1| RNase H domain−containing protein [Arabidopsis thaliana] gi|332640141|gb|AEE73662.1| RNase H domain−containing protein [Arabidopsis thaliana] gi|332640142|gb|AEE73663.1| RNase H domain−containing protein [Arabidopsis thaliana]	544	294	8.00E−45	54.0	16.7	19.5	RNase H domain−containing protein	gbpln	Arabidopsis thaliana	AT3G01410.2 | Symbols: | Polynucleotidyl transferase, ribonuclease H−like superfamily protein | chr3:153650−155439 REVERSE LENGTH=294	544	294	2.00E−47	54.0	16.7	19.5
Rsa1.0_01706.1.g29188.t1	ref|NP_199242.1| protein kinase−like protein [Arabidopsis thaliana] gi|79329869|ref|NP_001032009.1| protein kinase−like protein [Arabidopsis thaliana] gi|79329882|ref|NP_001032010.1| protein kinase−like protein [Arabidopsis thaliana] gi|145334725|ref|NP_001078708.1| protein kinase−like protein [Arabidopsis thaliana] gi|10176884|dbj|BAB10114.1| cyclin−dependent protein kinase−like protein [Arabidopsis thaliana] gi|222424232|dbj|BAH20074.1| AT5G44290 [Arabidopsis thaliana] gi|332007704|gb|AED95087.1| protein kinase−like protein [Arabidopsis thaliana] gi|332007705|gb|AED95088.1| protein kinase−like protein [Arabidopsis thaliana] gi|332007706|gb|AED95089.1| protein kinase−like protein [Arabidopsis thaliana] gi|332007707|gb|AED95090.1| protein kinase−like protein [Arabidopsis thaliana]	593	644	0	108.6	82.5	89.4	protein kinase−like protein	gbpln	Arabidopsis thaliana	AT5G44290.4 | Symbols: | Protein kinase superfamily protein | chr5:17840750−17843190 REVERSE LENGTH=644	593	644	0	108.6	82.5	89.4

Rsa1.0_01707.1.g29189.t1	ref|XP_002864941.1| hypothetical protein ARALYDRAFT_919839 [Arabidopsis lyrata subsp. lyrata] gi|297310776|gb|EFH41200.1| hypothetical protein ARALYDRAFT_919839 [Arabidopsis lyrata subsp. lyrata]	275	286	1.00E−104	104.0	73.5	80.0	hypothetical protein ARALYDRAFT_919839	gbpln	Arabidopsis lyrata	AT5G65130.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:26017403-26018236 FORWARD LENGTH=277	275	277	1.00E−104	100.7	72.7	80.7
Rsa1.0_01707.1.g29190.t1	gb|AAM61366.1| unknown [Arabidopsis thaliana]	330	317	1.00E−118	96.1	72.1	80.9	unknown	gbpln	Arabidopsis thaliana	AT5G65120.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G10110.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae − 12; Bacteria − 1396; Metazoa − 17338; Fungi − 3422; Plants − 5037; Viruses − 0; Other Eukaryotes − 2996 (source: NCBI BLink). | chr5:26013274-26014504 FORWARD LENGTH=317	330	317	1.00E−119	96.1	71.8	80.6
Rsa1.0_01707.1.g29191.t1	gb|EOA12483.1| hypothetical protein CARUB_v10025999mg [Capsella rubella]	473	692	0	146.3	89.6	93.0	hypothetical protein CARUB_v10025999mg	gbpln	Capsella rubella	AT5G65110.1 | Symbols: ACX2, ATACX2 | acyl-CoA oxidase 2 | chr5:26009821-26012482 REVERSE LENGTH=692	473	692	0	146.3	87.7	92.2
Rsa1.0_01707.1.g29192.t1	ref|XP_002866649.1| ethylene insensitive 3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297312484|gb|EFH42908.1| ethylene insensitive 3 family protein [Arabidopsis lyrata subsp. lyrata]	476	540	0	113.4	84.9	89.7	ethylene insensitive 3 family protein	gbpln	Arabidopsis lyrata	AT5G65100.1 | Symbols: | Ethylene insensitive 3 family protein | chr5:26006835-26008508 REVERSE LENGTH=557	476	557	0	117.0	83.8	89.5
Rsa1.0_01707.1.g29193.t1	ref|XP_002864939.1| hypothetical protein ARALYDRAFT_332725 [Arabidopsis lyrata subsp. lyrata] gi|297310774|gb|EFH41198.1| hypothetical protein ARALYDRAFT_332725 [Arabidopsis lyrata subsp. lyrata]	497	527	0	106.0	92.8	95.6	hypothetical protein ARALYDRAFT_332725	gbpln	Arabidopsis lyrata	AT5G65090.1 | Symbols: MRH3, BST1, DER4 | DNAse I-like superfamily protein | chr5:26004282-26006656 FORWARD LENGTH=529	497	529	0	106.4	91.8	95.2
Rsa1.0_01707.1.g29194.t1	gb|EOA13539.1| hypothetical protein CARUB_v10026602mg, partial [Capsella rubella]	359	376	1.00E−106	104.7	61.6	71.9	hypothetical protein CARUB_v10026602mg, partial	gbpln	Capsella rubella	AT5G64980.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:25960947-25963000 REVERSE LENGTH=344	359	344	1.00E−106	95.8	63.2	71.9
Rsa1.0_01707.1.g29195.t1	dbj|BAJ33863.1| unnamed protein product [Thellungiella halophila]	200	196	4.00E−73	98.0	70.0	84.5	unnamed protein product	----	----	AT5G65070.1 | Symbols: MAF4, FCL4, AGL69 | K-box region and MADS-box transcription factor family protein | chr5:25992310-25995930 FORWARD LENGTH=200	200	200	2.00E−75	100.0	72.5	83.0
Rsa1.0_01707.1.g29196.t1	ref|XP_002866647.1| hypothetical protein ARALYDRAFT_332722 [Arabidopsis lyrata subsp. lyrata] gi|297312482|gb|EFH42906.1| hypothetical protein ARALYDRAFT_332722 [Arabidopsis lyrata subsp. lyrata]	199	202	1.00E−82	101.5	79.9	87.4	hypothetical protein ARALYDRAFT_332722	gbpln	Arabidopsis lyrata	AT5G65030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G10210.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:25975697-25976305 REVERSE LENGTH=202	199	202	2.00E−82	101.5	78.4	85.4
Rsa1.0_01707.1.g29197.t3	gb|AFL69958.1| annexin E1 [Brassica oleracea var. capitata]	365	316	1.00E−176	86.6	85.8	86.6	annexin E1	gbpln	Brassica oleracea	AT5G65020.1 | Symbols: ANNAT2 | annexin 2 | chr5:25973915-25975554 FORWARD LENGTH=317	365	317	1.00E−169	86.8	81.4	84.9
Rsa1.0_01707.1.g29198.t1	gb|EOA13040.1| hypothetical protein CARUB_v10026039mg [Capsella rubella]	568	660	0	116.2	94.0	97.5	hypothetical protein CARUB_v10026039mg	gbpln	Capsella rubella	AT5G65010.1 | Symbols: ASN2 | asparagine synthetase 2 | chr5:25969224-25972278 FORWARD LENGTH=578	568	578	0	101.8	93.1	96.1
Rsa1.0_01707.1.g29199.t1	ref|XP_002866646.1| nucleotide-sugar transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297312481|gb|EFH42905.1| nucleotide-sugar transporter family protein [Arabidopsis lyrata subsp. lyrata]	328	325	1.00E−160	99.1	93.3	97.9	nucleotide-sugar transporter family protein	gbpln	Arabidopsis lyrata	AT5G65000.1 | Symbols: | Nucleotide-sugar transporter family protein | chr5:25965123-25967307 REVERSE LENGTH=325	328	325	1.00E−161	99.1	92.4	97.0
Rsa1.0_01707.1.g29200.t1	dbj|BAF34637.1| chromomethylase [Brassica rapa]	786	805	0	102.4	87.0	93.4	chromomethylase	gbpln	Brassica rapa	AT1G69770.1 | Symbols: CMT3 | chromomethylase 3 | chr1:26248496-26253519 REVERSE LENGTH=839	786	839	0	106.7	63.5	77.6
Rsa1.0_01708.1.g29201.t11	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	2010	1838	1.00E−108	91.4	8.6	10.6	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01708.1.g29202.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01708.1.g29203.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01708.1.g29204.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	440	672	5.00E−32	152.7	22.0	33.0	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01708.1.g29205.t1	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	477	578	3.00E−96	121.2	43.6	59.7	hypothetical protein 27.t00126	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_01708.1.g29206.t2	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	746	1024	4.00E-62	137.3	30.3	44.4	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01709.1.g29207.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01709.1.g29208.t1	ref|XP_002890525.1| hypothetical protein ARALYDRAFT_335508 [Arabidopsis lyrata subsp. lyrata] gi|297336367|gb|EFH66784.1| hypothetical protein ARALYDRAFT_335508 [Arabidopsis lyrata subsp. lyrata]	601	603	0	100.3	79.2	88.4	hypothetical protein ARALYDRAFT_335508	gbpln	Arabidopsis lyrata	AT1G22660.1 | Symbols: | Polynucleotide adenylyltransferase family protein | chr1:8017410-8021538 FORWARD LENGTH=605	601	605	0	100.7	77.4	87.0
Rsa1.0_01709.1.g29209.t1	gb|EOA36954.1| hypothetical protein CARUB_v10009887mg [Capsella rubella]	286	296	1.00E-128	103.5	87.8	93.0	hypothetical protein CARUB_v10009887mg	gbpln	Capsella rubella	AT1G22700.2 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:8028323-8029878 REVERSE LENGTH=296	286	296	1.00E-129	103.5	87.1	92.7
Rsa1.0_01709.1.g29210.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01709.1.g29211.t1	gb|ACB47398.1| sucrose transporter [Brassica napus]	512	508	0	99.2	95.9	97.7	sucrose transporter	gbpln	Brassica napus	AT1G22710.1 | Symbols: SUC2, SUT1, ATSUC2 | sucrose-proton symporter 2 | chr1:8030911-8032970 REVERSE LENGTH=512	512	512	0	100.0	94.5	97.9
Rsa1.0_01709.1.g29212.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	388	627	1.00E-33	161.6	27.6	44.1	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01710.1.g29213.t1	ref|NP_175330.1| uncharacterized protein [Arabidopsis thaliana] gi|7770334|gb|AAF69704.1|AC016041_9 F27J15.21 [Arabidopsis thaliana] gi|45476547|gb|AAS65939.1| At1g49000 [Arabidopsis thaliana] gi|46359837|gb|AAS88782.1| At1g49000 [Arabidopsis thaliana] gi|332194258|gb|AEE32379.1| uncharacterized protein AT1G49000 [Arabidopsis thaliana]	153	156	5.00E-45	102.0	71.2	76.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G49000.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: stem; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G18560.1); Has 105 Blast hits to 105 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18123559-18124029 REVERSE LENGTH=156	153	156	2.00E-47	102.0	71.2	76.5
Rsa1.0_01710.1.g29214.t1	ref|XP_002891470.1| hypothetical protein ARALYDRAFT_474043 [Arabidopsis lyrata subsp. lyrata] gi|297337312|gb|EFH67729.1| hypothetical protein ARALYDRAFT_474043 [Arabidopsis lyrata subsp. lyrata]	162	168	4.00E-56	103.7	76.5	80.9	hypothetical protein ARALYDRAFT_474043	gbpln	Arabidopsis lyrata	AT1G48990.1 | Symbols: | Oleosin family protein | chr1:18121470-18121979 FORWARD LENGTH=169	162	169	4.00E-55	104.3	77.2	82.1
Rsa1.0_01710.1.g29215.t1	gb|AAC33961.1| contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]	537	1662	1.00E-78	309.5	30.0	44.7	contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57)	gbpln	Arabidopsis thaliana	AT2G02650.1 | Symbols: | Ribonuclease H-like superfamily protein | chr2:735411-736546 FORWARD LENGTH=365	537	365	3.00E-24	68.0	8.6	12.1
Rsa1.0_01710.1.g29216.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01710.1.g29217.t1	dbj|BAA94096.1| SLR1 binding pollen coat protein [Brassica juncea]	116	83	1.00E-10	71.6	30.2	37.1	SLR1 binding pollen coat protein	gbpln	Brassica juncea	#	#	#	#	#	#	#
Rsa1.0_01710.1.g29218.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	190	1555	2.00E-28	818.4	43.2	54.7	disease resistance protein	gbpln	Brassica rapa	AT2G06845.1 | Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=315	190	315	4.00E-16	165.8	33.2	44.7
Rsa1.0_01710.1.g29219.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01710.1.g29220.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01710.1.g29221.t1	gb|AAF24531.1|AC007534_12 F7F22.17 [Arabidopsis thaliana]	190	1799	5.00E-61	946.8	59.5	76.8	F7F22.17	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01711.1.g29222.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01711.1.g29223.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	422	1023	2.00E-46	242.4	20.4	25.4	F27F5.21	gbpln	Arabidopsis thaliana	ATMG01250.1 | Symbols: ORF102 | RNA-directed DNA polymerase (reverse transcriptase) | chrM:310514-310882 FORWARD LENGTH=122	422	122	2.00E-12	28.9	6.9	10.4
Rsa1.0_01711.1.g29224.t1	ref|NP_564190.1| polyketide cyclase/dehydrase and lipid transport-like protein [Arabidopsis thaliana] gi|2829899|gb|AAC00607.1| similar to ripening-induced protein, gp|AJ001449|2465015 and major#latex protein, gp|X91961|1107495 [Arabidopsis thaliana] gi|14517378|gb|AAK62580.1| At1g23130/T26J12_10 [Arabidopsis thaliana] gi|15450533|gb|AAK96444.1| At1g23130/T26J12_10 [Arabidopsis thaliana] gi|332192222|gb|AEE30343.1| polyketide cyclase/dehydrase and lipid transport-like protein [Arabidopsis thaliana]	157	160	2.00E-48	101.9	59.2	77.1	polyketide cyclase/dehydrase and lipid transport-like protein	gbpln	Arabidopsis thaliana	AT1G23130.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:8200434-8200997 FORWARD LENGTH=160	157	160	5.00E-51	101.9	59.2	77.1

Rsa1.0_01711.1.g29225.t1	gb|EOA39878.1| hypothetical protein CARUB_v10008554mg, partial [Capsella rubella]	729	641	0	87.9	62.8	67.8	hypothetical protein CARUB_v10008554mg, partial	gbpln	Capsella rubella	AT1G23170.2 | Symbols: | Protein of unknown function DUF2359, transmembrane | chr1:8212724-8215516 FORWARD LENGTH=615	729	615	0	84.4	62.3	66.8
Rsa1.0_01712.1.g29226.t1	ref|XP_002882903.1| hypothetical protein ARALYDRAFT_478916 [Arabidopsis lyrata subsp. lyrata] gi|297328743|gb|EFH59162.1| hypothetical protein ARALYDRAFT_478916 [Arabidopsis lyrata subsp. lyrata]	419	418	0	99.8	90.2	95.5	hypothetical protein ARALYDRAFT_478916	gbpln	Arabidopsis lyrata	AT3G14930.2 | Symbols: HEME1 | Uroporphyrinogen decarboxylase | chr3:5020675-5022577 FORWARD LENGTH=418	419	418	0	99.8	88.3	94.3
Rsa1.0_01712.1.g29227.t1	ref|XP_002882901.1| hypothetical protein ARALYDRAFT_478912 [Arabidopsis lyrata subsp. lyrata] gi|297328741|gb|EFH59160.1| hypothetical protein ARALYDRAFT_478912 [Arabidopsis lyrata subsp. lyrata]	457	455	0	99.6	94.5	97.8	hypothetical protein ARALYDRAFT_478912	gbpln	Arabidopsis lyrata	AT3G14910.1 | Symbols: | unknown protein; Has 158 Blast hits to 158 proteins in 77 species: Archae - 0; Bacteria - 0; Metazoa - 104; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 21 (source: NCBI BLink). | chr3:5015432-5017566 FORWARD LENGTH=455	457	455	0	99.6	94.1	97.4
Rsa1.0_01712.1.g29228.t1	ref|NP_188108.1| uncharacterized protein [Arabidopsis thaliana] gi|8777473|dbj|BAA97053.1| unnamed protein product [Arabidopsis thaliana] gi|110742615|dbj|BAE99220.1| hypothetical protein [Arabidopsis thaliana] gi|332642065|gb|AEE75586.1| uncharacterized protein AT3G14900 [Arabidopsis thaliana]	612	611	0	99.8	86.8	91.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G14900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: embryo development; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; Has 17135 Blast hits to 10204 proteins in 644 species: Archae - 47; Bacteria - 1684; Metazoa - 5536; Fungi - 2506; Plants - 1043; Viruses - 361; Other Eukaryotes - 5958 (source: NCBI BLink). | chr3:5013442-5015277 REVERSE LENGTH=611	612	611	0	99.8	86.8	91.2
Rsa1.0_01712.1.g29229.t2	gb|EOA30020.1| hypothetical protein CARUB_v10013122mg [Capsella rubella]	661	682	0	103.2	68.4	78.5	hypothetical protein CARUB_v10013122mg	gbpln	Capsella rubella	AT3G14890.1 | Symbols: | phosphoesterase | chr3:5008751-5013060 FORWARD LENGTH=694	661	694	0	105.0	69.7	79.0
Rsa1.0_01712.1.g29230.t1	ref|NP_001118628.1| uncharacterized protein [Arabidopsis thaliana] gi|67633634|gb|AAY78741.1| DNA-binding protein-related [Arabidopsis thaliana] gi|332642062|gb|AEE75583.1| uncharacterized protein AT3G14880 [Arabidopsis thaliana]	237	237	1.00E-115	100.0	86.1	92.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G14880.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; BEST Arabidopsis thaliana protein match is: transcription factor-related (TAIR:AT4G18650.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:5006565-5007689 FORWARD LENGTH=237	237	237	1.00E-117	100.0	86.1	92.0
Rsa1.0_01712.1.g29231.t1	gb|EOA30524.1| hypothetical protein CARUB_v10013646mg [Capsella rubella]	438	463	0	105.7	76.9	87.0	hypothetical protein CARUB_v10013646mg	gbpln	Capsella rubella	AT3G14870.1 | Symbols: | Plant protein of unknown function (DUF641) | chr3:5004159-5005586 FORWARD LENGTH=475	438	475	0	108.4	76.9	85.8
Rsa1.0_01712.1.g29232.t1	ref|NP_974315.1| NHL domain-containing protein [Arabidopsis thaliana] gi|332642057|gb|AEE75578.1| NHL domain-containing protein [Arabidopsis thaliana]	117	493	3.00E-18	421.4	42.7	48.7	NHL domain-containing protein	gbpln	Arabidopsis thaliana	AT3G14860.2 | Symbols: | NHL domain-containing protein | chr3:4998591-5000894 REVERSE LENGTH=493	117	493	5.00E-21	421.4	42.7	48.7
Rsa1.0_01712.1.g29233.t1	ref|XP_002882897.1| hypothetical protein ARALYDRAFT_478900 [Arabidopsis lyrata subsp. lyrata] gi|297328737|gb|EFH59156.1| hypothetical protein ARALYDRAFT_478900 [Arabidopsis lyrata subsp. lyrata]	338	350	1.00E-161	103.6	84.9	91.1	hypothetical protein ARALYDRAFT_478900	gbpln	Arabidopsis lyrata	AT3G14850.2 | Symbols: TBL41 | TRICHOME BIREFRINGENCE-LIKE 41 | chr3:4995615-4997611 FORWARD LENGTH=356	338	356	1.00E-157	105.3	82.0	90.5
Rsa1.0_01712.1.g29234.t1	ref|NP_188102.5| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana] gi|313471762|sp|C0LGN2.1|Y3148_ARATH RecName: Full=Probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840; Flags: Precursor gi|224589567|gb|ACN59317.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332642053|gb|AEE75574.1| Leucine-rich repeat transmembrane protein kinase [Arabidopsis thaliana]	912	1020	0	111.8	77.6	87.5	Leucine-rich repeat transmembrane protein kinase	gbpln	Arabidopsis thaliana	AT3G14840.2 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr3:4988271-4993891 FORWARD LENGTH=1020	912	1020	0	111.8	77.6	87.5

<table>
<tr><td>Rsa1.0_01712.1.g29235.t1</td><td>ref|NP_188080.1| cytochrome P450, family 72, subfamily A, polypeptide 8 [Arabidopsis thaliana] gi|9294384|dbj|BAB02394.1| cytochrome P450 [Arabidopsis thaliana] gi|15529169|gb|AAK97679.1| AT3g14620/MIE1_12 [Arabidopsis thaliana] gi|332642027|gb|AEE75548.1| cytochrome P450, family 72, subfamily A, polypeptide 8 [Arabidopsis thaliana]</td><td>515</td><td>515</td><td>0</td><td>100.0</td><td>83.5</td><td>90.1</td><td>cytochrome P450, family 72, subfamily A, polypeptide 8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G14620.1 | Symbols: CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide 8 | chr3:4914978-4916853 FORWARD LENGTH=515</td><td>515</td><td>515</td><td>0</td><td>100.0</td><td>83.5</td><td>90.1</td></tr>
<tr><td>Rsa1.0_01712.1.g29236.t1</td><td>ref|NP_188079.1| cytochrome P450, family 72, subfamily A, polypeptide 7 [Arabidopsis thaliana] gi|9294383|dbj|BAB02393.1| cytochrome P450 [Arabidopsis thaliana] gi|18252155|gb|AAL61910.1| cytochrome P450 [Arabidopsis thaliana] gi|28059362|gb|AAO30051.1| cytochrome P450 [Arabidopsis thaliana] gi|332642026|gb|AEE75547.1| cytochrome P450, family 72, subfamily A, polypeptide 7 [Arabidopsis thaliana]</td><td>511</td><td>512</td><td>0</td><td>100.2</td><td>84.0</td><td>92.2</td><td>cytochrome P450, family 72, subfamily A, polypeptide 7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G14610.1 | Symbols: CYP72A7 | cytochrome P450, family 72, subfamily A, polypeptide 7 | chr3:4912565-4914503 FORWARD LENGTH=512</td><td>511</td><td>512</td><td>0</td><td>100.2</td><td>84.0</td><td>92.2</td></tr>
<tr><td>Rsa1.0_01713.1.g29237.t1</td><td>ref|XP_002976838.1| hypothetical protein SELMODRAFT_151539 [Selaginella moellendorffii] gi|300155316|gb|EFJ21948.1| hypothetical protein SELMODRAFT_151539 [Selaginella moellendorffii]</td><td>149</td><td>562</td><td>3.00E-34</td><td>377.2</td><td>50.3</td><td>69.8</td><td>hypothetical protein SELMODRAFT_151539</td><td>gbpln</td><td>Selaginella moellendorffii</td><td>AT1G22660.1 | Symbols: | Polynucleotide adenylyltransferase family protein | chr1:8017410-8021538 FORWARD LENGTH=605</td><td>149</td><td>605</td><td>2.00E-33</td><td>406.0</td><td>51.7</td><td>70.5</td></tr>
<tr><td>Rsa1.0_01713.1.g29238.t1</td><td>ref|NP_564567.1| oligopeptidase B [Arabidopsis thaliana] gi|5734786|gb|AAD50051.1|AC007980_16 Similar to oligopeptidases [Arabidopsis thaliana] gi|19310465|gb|AAL84967.1| At1g50380/F14I3_27 [Arabidopsis thaliana] gi|332194421|gb|AEE32542.1| prolyl oligopeptidase family protein [Arabidopsis thaliana]</td><td>710</td><td>710</td><td>0</td><td>100.0</td><td>90.6</td><td>95.2</td><td>oligopeptidase B</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G50380.1 | Symbols: | Prolyl oligopeptidase family protein | chr1:18662480-18666185 FORWARD LENGTH=710</td><td>710</td><td>710</td><td>0</td><td>100.0</td><td>90.6</td><td>95.2</td></tr>
<tr><td>Rsa1.0_01713.1.g29239.t6</td><td>gb|ABD65117.1| hypothetical protein 31.t00030 [Brassica oleracea]</td><td>1449</td><td>1471</td><td>0</td><td>101.5</td><td>30.5</td><td>38.6</td><td>hypothetical protein 31.t00030</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566</td><td>1449</td><td>566</td><td>3.00E-39</td><td>39.1</td><td>9.8</td><td>15.9</td></tr>
<tr><td>Rsa1.0_01713.1.g29240.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01713.1.g29241.t1</td><td>ref|XP_002868287.1| hypothetical protein ARALYDRAFT_493466 [Arabidopsis lyrata subsp. lyrata] gi|297314123|gb|EFH44546.1| hypothetical protein ARALYDRAFT_493466 [Arabidopsis lyrata subsp. lyrata]</td><td>329</td><td>372</td><td>1.00E-103</td><td>113.1</td><td>64.1</td><td>76.3</td><td>hypothetical protein ARALYDRAFT_493466</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G14365.1 | Symbols: XBAT34 | XB3 ortholog 4 in Arabidopsis thaliana | chr4:8271660-8273685 REVERSE LENGTH=376</td><td>329</td><td>376</td><td>1.00E-103</td><td>114.3</td><td>62.9</td><td>76.3</td></tr>
<tr><td>Rsa1.0_01713.1.g29242.t1</td><td>ref|NP_188632.1| phytochrome-associated serine/threonine protein phosphatase 3 [Arabidopsis thaliana] gi|75311171|sp|Q9LHE7.1|FYPP3_ARATH RecName: Full=Phytochrome-associated serine/threonine-protein phosphatase 3; Short=AtFyPP3; AltName: Full=Protein EMBRYO DEFECTIVE 2736 gi|14582206|gb|AAK69404.1|AF275664_1 serine/threonine protein phosphatase [Arabidopsis thaliana] gi|11994773|dbj|BAB03163.1| phosphoprotein phosphatase [Arabidopsis thaliana] gi|17381249|gb|AAL36043.1| AT3g19980/MZE19_3 [Arabidopsis thaliana] gi|20453383|gb|AAM19930.1| AT3g19980/MZE19_3 [Arabidopsis thaliana] gi|332642794|gb|AEE76315.1| phytochrome-associated serine/threonine protein phosphatase 3 [Arabidopsis thaliana]</td><td>300</td><td>303</td><td>1.00E-160</td><td>101.0</td><td>89.7</td><td>91.0</td><td>phytochrome-associated serine/threonine protein phosphatase 3</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19980.1 | Symbols: ATFYPP3, EMB2736, STPP, FYPP3 | flower-specific, phytochrome-associated protein phosphatase 3 | chr3:6962008-6964761 FORWARD LENGTH=303</td><td>300</td><td>303</td><td>1.00E-162</td><td>101.0</td><td>89.7</td><td>91.0</td></tr>
</table>

Rsa1.0_01713.1.g29243.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	280	387	5.00E-66	138.2	52.9	66.8	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	280	387	1.00E-68	138.2	52.9	66.8
Rsa1.0_01714.1.g29244.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01714.1.g29245.t1	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	843	1270	0	150.7	48.8	64.3	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	843	575	1.00E-68	68.2	17.4	29.5
Rsa1.0_01714.1.g29246.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01714.1.g29247.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01714.1.g29248.t2	ref|XP_002868599.1| hypothetical protein ARALYDRAFT_493840 [Arabidopsis lyrata subsp. lyrata] gi|297314435|gb|EFH44858.1| hypothetical protein ARALYDRAFT_493840 [Arabidopsis lyrata subsp. lyrata]	277	308	1.00E-107	111.2	75.1	81.6	hypothetical protein ARALYDRAFT_493840	gbpln	Arabidopsis lyrata	AT5G41380.1 | Symbols: | CCT motif family protein | chr5:16562129-16563553 REVERSE LENGTH=307	277	307	1.00E-107	110.8	72.9	80.5
Rsa1.0_01714.1.g29249.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01714.1.g29250.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01715.1.g29251.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01715.1.g29252.t1	gb|EOA19792.1| hypothetical protein CARUB_v10000037mg [Capsella rubella]	166	1456	2.00E-16	877.1	32.5	36.1	hypothetical protein CARUB_v10000037mg	gbpln	Capsella rubella	AT5G01400.1 | Symbols: ESP4 | HEAT repeat-containing protein | chr5:162803-171072 REVERSE LENGTH=1467	166	1467	4.00E-17	883.7	33.1	37.3
Rsa1.0_01715.1.g29253.t1	gb|EOA32723.1| hypothetical protein CARUB_v10016027mg [Capsella rubella]	72	72	4.00E-14	100.0	69.4	80.6	hypothetical protein CARUB_v10016027mg	gbpln	Capsella rubella	AT2G19030.1 | Symbols: RALFL11 | ralf-like 11 | chr2:8247783-8248001 FORWARD LENGTH=72	72	72	2.00E-16	100.0	69.4	79.2
Rsa1.0_01715.1.g29254.t1	ref|XP_002886247.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297332087|gb|EFH62506.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	349	345	1.00E-152	98.9	71.3	84.0	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT2G19010.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr2:8243089-8245378 FORWARD LENGTH=344	349	344	1.00E-151	98.6	69.9	81.9
Rsa1.0_01715.1.g29255.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1342	1529	0	113.9	34.8	51.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1342	746	9.00E-69	55.6	9.7	13.4
Rsa1.0_01715.1.g29256.t1	ref|NP_565445.1| uncharacterized protein [Arabidopsis thaliana] gi|3176702|gb|AAD12018.1| expressed protein [Arabidopsis thaliana] gi|20197040|gb|AAM14889.1| expressed protein [Arabidopsis thaliana] gi|21592504|gb|AAM64454.1| unknown [Arabidopsis thaliana] gi|91806202|gb|ABE65829.1| unknown [Arabidopsis thaliana] gi|109946531|gb|ABG48444.1| At2g19000 [Arabidopsis thaliana] gi|330251743|gb|AEC06837.1| uncharacterized protein AT2G19000 [Arabidopsis thaliana]	129	125	4.00E-30	96.9	56.6	62.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G19000.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; Has 71 Blast hits to 71 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:8241189-8241566 FORWARD LENGTH=125	129	125	8.00E-33	96.9	56.6	62.0
Rsa1.0_01715.1.g29257.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01715.1.g29258.t5	ref|XP_002889154.1| ribonuclease II family protein [Arabidopsis lyrata subsp. lyrata] gi|297334995|gb|EFH65413.1| ribonuclease II family protein [Arabidopsis lyrata subsp. lyrata]	312	1062	4.00E-13	340.4	11.5	14.1	ribonuclease II family protein	gbpln	Arabidopsis lyrata	AT1G77680.1 | Symbols: | Ribonuclease II/R family protein | chr1:29192188-29195963 REVERSE LENGTH=1055	312	1055	4.00E-15	338.1	11.2	14.1
Rsa1.0_01716.1.g29259.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01716.1.g29260.t1	gb|EOA30837.1| hypothetical protein CARUB_v10013982mg [Capsella rubella]	376	370	1.00E-167	98.4	91.5	95.2	hypothetical protein CARUB_v10013982mg	gbpln	Capsella rubella	AT2G20280.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr2:8740054-8742349 REVERSE LENGTH=371	376	371	1.00E-169	98.7	91.8	95.2
Rsa1.0_01716.1.g29261.t1	ref|XP_002883935.1| hypothetical protein ARALYDRAFT_899837 [Arabidopsis lyrata subsp. lyrata] gi|297329775|gb|EFH60194.1| hypothetical protein ARALYDRAFT_899837 [Arabidopsis lyrata subsp. lyrata]	181	187	2.00E-53	103.3	70.2	78.5	hypothetical protein ARALYDRAFT_899837	gbpln	Arabidopsis lyrata	AT2G20270.1 | Symbols: | Thioredoxin superfamily protein | chr2:8738001-8739617 REVERSE LENGTH=179	181	179	6.00E-53	98.9	65.7	75.7

Rsa1.0_01716.1.g29262.t1	ref|NP_179614.1| uncharacterized protein [Arabidopsis thaliana] gi|4512711|gb|AAD21764.1| unknown protein [Arabidopsis thaliana] gi|330251890|gb|AEC06984.1| uncharacterized protein AT2G20240 [Arabidopsis thaliana]	700	713	0	101.9	71.6	79.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G20240.1 | Symbols: | Protein of unknown function (DUF3741) | chr2:8727778-8730086 REVERSE LENGTH=713	700	713	0	101.9	71.6	79.3
Rsa1.0_01716.1.g29263.t1	ref|XP_002885992.1| hypothetical protein ARALYDRAFT_480447 [Arabidopsis lyrata subsp. lyrata] gi|297331832|gb|EFH62251.1| hypothetical protein ARALYDRAFT_480447 [Arabidopsis lyrata subsp. lyrata]	250	270	1.00E-114	108.0	84.4	90.4	hypothetical protein ARALYDRAFT_480447	gbpln	Arabidopsis lyrata	AT2G20230.1 | Symbols: | Tetraspanin family protein | chr2:8725762-8727388 FORWARD LENGTH=270	250	270	1.00E-108	108.0	82.8	88.8
Rsa1.0_01716.1.g29264.t2	ref|NP_194360.1| Arginyl-tRNA synthetase, class Ic [Arabidopsis thaliana] gi|2632105|emb|CAB11468.1| arginyl-tRNA synthetase [Arabidopsis thaliana] gi|4539426|emb|CAB38959.1| arginyl-tRNA synthetase [Arabidopsis thaliana] gi|7269482|emb|CAB79485.1| arginyl-tRNA synthetase [Arabidopsis thaliana] gi|332659782|gb|AEE85182.1| Arginyl-tRNA synthetase, class Ic [Arabidopsis thaliana]	505	642	0	127.1	68.7	81.8	Arginyl-tRNA synthetase, class Ic	gbpln	Arabidopsis thaliana	AT4G26300.1 | Symbols: emb1027 | Arginyl-tRNA synthetase, class Ic | chr4:13308400-13313109 REVERSE LENGTH=642	505	642	0	127.1	68.7	81.8
Rsa1.0_01717.1.g29265.t1	ref|XP_002868593.1| hypothetical protein ARALYDRAFT_916060 [Arabidopsis lyrata subsp. lyrata] gi|297314429|gb|EFH44852.1| hypothetical protein ARALYDRAFT_916060 [Arabidopsis lyrata subsp. lyrata]	736	522	0	70.9	60.6	64.0	hypothetical protein ARALYDRAFT_916060	gbpln	Arabidopsis lyrata	AT5G41460.1 | Symbols: | Protein of unknown function (DUF604) | chr5:16589724-16592197 REVERSE LENGTH=524	736	524	0	71.2	60.7	64.1
Rsa1.0_01717.1.g29266.t1	ref|XP_002870635.1| hypothetical protein ARALYDRAFT_493835 [Arabidopsis lyrata subsp. lyrata] gi|297316471|gb|EFH46894.1| hypothetical protein ARALYDRAFT_493835 [Arabidopsis lyrata subsp. lyrata]	171	277	8.00E-69	162.0	71.9	83.0	hypothetical protein ARALYDRAFT_493835	gbpln	Arabidopsis lyrata	AT5G41470.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein | chr5:16593953-16595419 FORWARD LENGTH=277	171	277	4.00E-68	162.0	69.0	82.5
Rsa1.0_01717.1.g29267.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01717.1.g29268.t2	ref|XP_002868589.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314425|gb|EFH44848.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	1052	1456	0	138.4	47.1	56.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G41540.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16612659-16616063 REVERSE LENGTH=1038	1052	1038	0	98.7	46.7	57.0
Rsa1.0_01717.1.g29269.t1	ref|XP_002868585.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314421|gb|EFH44844.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	619	760	0	122.8	60.9	68.0	zinc ion binding protein	gbpln	Arabidopsis lyrata	AT5G41580.1 | Symbols: | RING/U-box superfamily protein | chr5:16626563-16630659 REVERSE LENGTH=760	619	760	0	122.8	59.3	66.7
Rsa1.0_01717.1.g29270.t1	ref|XP_002870617.1| hypothetical protein ARALYDRAFT_916024 [Arabidopsis lyrata subsp. lyrata] gi|297316453|gb|EFH46876.1| hypothetical protein ARALYDRAFT_916024 [Arabidopsis lyrata subsp. lyrata]	614	704	0	114.7	92.8	96.7	hypothetical protein ARALYDRAFT_916024	gbpln	Arabidopsis lyrata	AT5G41770.1 | Symbols: | crooked neck protein, putative / cell cycle protein, putative | chr5:16718021-16720936 FORWARD LENGTH=705	614	705	0	114.8	92.2	96.4
Rsa1.0_01717.1.g29271.t1	ref|NP_198993.1| myosin heavy chain-like protein [Arabidopsis thaliana] gi|10177362|dbj|BAB10653.1| unnamed protein product [Arabidopsis thaliana] gi|91806972|gb|ABE66213.1| myosin heavy chain-like [Arabidopsis thaliana] gi|332007345|gb|AED94728.1| myosin heavy chain-like protein [Arabidopsis thaliana]	504	537	0	106.5	71.4	83.3	myosin heavy chain-like protein	gbpln	Arabidopsis thaliana	AT5G41780.1 | Symbols: | myosin heavy chain-related | chr5:16723075-16724833 FORWARD LENGTH=537	504	537	0	106.5	71.4	83.3
Rsa1.0_01717.1.g29272.t6	ref|NP_198994.2| COP1-interactive protein 1 [Arabidopsis thaliana] gi|332007346|gb|AED94729.1| COP1-interactive protein 1 [Arabidopsis thaliana]	2960	1586	0	53.6	40.4	46.6	COP1-interactive protein 1	gbpln	Arabidopsis thaliana	AT5G41790.1 | Symbols: CIP1 | COP1-interactive protein 1 | chr5:16727530-16732391 FORWARD LENGTH=1586	2960	1586	0	53.6	40.4	46.6

Rsa1.0_01717.1.g29273.t1	ref|NP_568597.1| Transmembrane amino acid transporter family protein [Arabidopsis thaliana] gi|75245603|sp|Q8L4X4.1|GAT2_ARATH RecName: Full=Probable GABA transporter 2 gi|20466438|gb|AAM20536.1| amino acid permease-like protein [Arabidopsis thaliana] gi|22136372|gb|AAM91264.1| amino acid permease-like protein [Arabidopsis thaliana] gi|332007347|gb|AED94730.1| Transmembrane amino acid transporter family protein [Arabidopsis thaliana]	452	452	0	100.0	94.9	98.0	Transmembrane amino acid transporter family protein	gbpln	Arabidopsis thaliana	AT5G41800.1 | Symbols: | Transmembrane amino acid transporter family protein | chr5:16733842-16735888 FORWARD LENGTH=452	452	452	0	100.0	94.9	98.0
Rsa1.0_01718.1.g29274.t1	ref|NP_188935.1| ADP-ribosylation factor C1 [Arabidopsis thaliana] gi|334185556|ref|NP_001189951.1| ADP-ribosylation factor C1 [Arabidopsis thaliana] gi|297788976|ref|XP_002862508.1| ADP-ribosylation factor C1 [Arabidopsis lyrata subsp. lyrata] gi|11994726|dbj|BAB03042.1| unnamed protein product [Arabidopsis thaliana] gi|17381004|gb|AAL36314.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gi|20465873|gb|AAM20041.1| putative ADP-ribosylation factor [Arabidopsis thaliana] gi|21592454|gb|AAM64405.1| ADP-ribosylation factor, putative [Arabidopsis thaliana] gi|297308070|gb|EFH38766.1| ADP-ribosylation factor C1 [Arabidopsis lyrata subsp. lyrata] gi|332643174|gb|AEE76695.1| ADP-ribosylation factor C1 [Arabidopsis thaliana] gi|332643175|gb|AEE76696.1| ADP-ribosylation factor C1 [Arabidopsis thaliana]	109	183	1.00E-23	167.9	49.5	52.3	ADP-ribosylation factor C1	gbpln	Arabidopsis lyrata	AT3G22950.2 | Symbols: ARFC1 | ADP-ribosylation factor C1 | chr3:8136364-8137513 REVERSE LENGTH=183	109	183	2.00E-26	167.9	49.5	52.3
Rsa1.0_01718.1.g29275.t1	ref|NP_193199.1| germin-like protein subfamily 1 member 8 [Arabidopsis thaliana] gi|18203238|sp|Q9LEA7.2|GL18_ARATH RecName: Full=Germin-like protein subfamily 1 member 8; Flags: Precursor gi|2244819|emb|CAB10242.1| germin precursor oxalate oxidase [Arabidopsis thaliana] gi|7268169|emb|CAB78505.1| germin precursor oxalate oxidase [Arabidopsis thaliana] gi|62320424|dbj|BAD94883.1| germin precursor oxalate oxidase [Arabidopsis thaliana] gi|117168223|gb|ABK32194.1| At4g14630 [Arabidopsis thaliana] gi|332658069|gb|AEE83469.1| germin-like protein subfamily 1 member 8 [Arabidopsis thaliana]	220	222	1.00E-105	100.9	85.9	91.4	germin-like protein subfamily 1 member 8	gbpln	Arabidopsis thaliana	AT4G14630.1 | Symbols: GLP9 | germin-like protein 9 | chr4:8392920-8393680 FORWARD LENGTH=222	220	222	1.00E-107	100.9	85.9	91.4
Rsa1.0_01718.1.g29276.t1	ref|NP_193199.1| germin-like protein subfamily 1 member 8 [Arabidopsis thaliana] gi|18203238|sp|Q9LEA7.2|GL18_ARATH RecName: Full=Germin-like protein subfamily 1 member 8; Flags: Precursor gi|2244819|emb|CAB10242.1| germin precursor oxalate oxidase [Arabidopsis thaliana] gi|7268169|emb|CAB78505.1| germin precursor oxalate oxidase [Arabidopsis thaliana] gi|62320424|dbj|BAD94883.1| germin precursor oxalate oxidase [Arabidopsis thaliana] gi|117168223|gb|ABK32194.1| At4g14630 [Arabidopsis thaliana] gi|332658069|gb|AEE83469.1| germin-like protein subfamily 1 member 8 [Arabidopsis thaliana]	220	222	1.00E-109	100.9	90.0	93.6	germin-like protein subfamily 1 member 8	gbpln	Arabidopsis thaliana	AT4G14630.1 | Symbols: GLP9 | germin-like protein 9 | chr4:8392920-8393680 FORWARD LENGTH=222	220	222	1.00E-111	100.9	90.0	93.6
Rsa1.0_01718.1.g29277.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01718.1.g29278.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1655	1225	0	74.0	34.2	46.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1655	575	8.00E-74	34.7	10.3	16.4
Rsa1.0_01718.1.g29279.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01718.1.g29280.t1	gb|EOA17773.1| hypothetical protein CARUB_v10006162mg [Capsella rubella]	76	76	4.00E-31	100.0	86.8	93.4	hypothetical protein CARUB_v10006162mg	gbpln	Capsella rubella	AT4G14615.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2346 (InterPro:IPR018625); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52825.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:8383842-8384814 FORWARD LENGTH=76	76	76	7.00E-34	100.0	86.8	93.4
Rsa1.0_01719.1.g29281.t2	gb|AAM10969.1| calmodulin-binding transcription activator [Brassica napus]	982	1035	0	105.4	92.9	95.6	calmodulin-binding transcription activator	gbpln	Brassica napus	AT5G09410.2 | Symbols: EICBP.B, CAMTA1 | ethylene induced calmodulin binding protein | chr5:2921457-2927291 FORWARD LENGTH=1007	982	1007	0	102.5	82.1	89.4
Rsa1.0_01719.1.g29282.t1	gb|EOA20818.1| hypothetical protein CARUB_v10001155mg [Capsella rubella]	338	387	1.00E-133	114.5	77.8	87.3	hypothetical protein CARUB_v10001155mg	gbpln	Capsella rubella	AT5G09390.1 | Symbols: | CD2-binding protein-related | chr5:2913591-2915803 FORWARD LENGTH=351	338	351	1.00E-133	103.8	75.7	88.8
Rsa1.0_01719.1.g29283.t1	gb|EOA21342.1| hypothetical protein CARUB_v10001705mg [Capsella rubella]	275	271	1.00E-120	98.5	78.5	87.6	hypothetical protein CARUB_v10001705mg	gbpln	Capsella rubella	AT5G09380.1 | Symbols: | RNA polymerase III RPC4 | chr5:2911313-2913136 REVERSE LENGTH=272	275	272	1.00E-117	98.9	76.4	86.9
Rsa1.0_01719.1.g29284.t1	ref|XP_002873395.1| hypothetical protein ARALYDRAFT_487745 [Arabidopsis lyrata subsp. lyrata] gi|297319232|gb|EFH49654.1| hypothetical protein ARALYDRAFT_487745 [Arabidopsis lyrata subsp. lyrata]	427	411	1.00E-157	96.3	69.8	79.2	hypothetical protein ARALYDRAFT_487745	gbpln	Arabidopsis lyrata	AT5G09330.4 | Symbols: VNI1 | NAC domain containing protein 82 | chr5:2892623-2894708 REVERSE LENGTH=489	427	489	1.00E-150	114.5	68.4	78.9
Rsa1.0_01719.1.g29285.t1	ref|XP_002883202.1| vacuolar sorting protein 9 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329042|gb|EFH59461.1| vacuolar sorting protein 9 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	508	520	0	102.4	79.1	87.2	vacuolar sorting protein 9 domain-containing protein	gbpln	Arabidopsis lyrata	AT3G19770.1 | Symbols: ATVPS9A, VPS9A, VPS9 | Vacuolar sorting protein 9 (VPS9) domain | chr3:6866916-6869114 FORWARD LENGTH=520	508	520	0	102.4	78.1	87.0
Rsa1.0_01719.1.g29286.t1	ref|XP_002873393.1| hypothetical protein ARALYDRAFT_908877 [Arabidopsis lyrata subsp. lyrata] gi|297319230|gb|EFH49652.1| hypothetical protein ARALYDRAFT_908877 [Arabidopsis lyrata subsp. lyrata]	143	146	3.00E-61	102.1	85.3	89.5	hypothetical protein ARALYDRAFT_908877	gbpln	Arabidopsis lyrata	AT5G09310.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Gamma-secretase aspartyl protease complex, presenilin enhancer-2 subunit (InterPro:IPR019379); Has 168 Blast hits to 168 proteins in 71 species: Archae - 0; Bacteria - 0; Metazoa - 126; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr5:2887403-2888501 REVERSE LENGTH=146	143	146	7.00E-62	102.1	86.7	92.3
Rsa1.0_01719.1.g29287.t1	gb|EMJ25374.1| hypothetical protein PRUPE_ppa016917mg [Prunus persica]	378	395	1.00E-149	104.5	65.3	79.1	hypothetical protein PRUPE_ppa016917mg	gbpln	Prunus persica	AT5G09280.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:2880423-2881597 REVERSE LENGTH=297	378	297	1.00E-142	78.6	62.2	63.8
Rsa1.0_01719.1.g29288.t1	ref|XP_002871365.1| hypothetical protein ARALYDRAFT_487736 [Arabidopsis lyrata subsp. lyrata] gi|297317202|gb|EFH47624.1| hypothetical protein ARALYDRAFT_487736 [Arabidopsis lyrata subsp. lyrata]	113	111	9.00E-52	98.2	85.8	92.9	hypothetical protein ARALYDRAFT_487736	gbpln	Arabidopsis lyrata	AT5G09270.2 | Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:2879680-2880015 FORWARD LENGTH=111	113	111	1.00E-52	98.2	84.1	91.2
Rsa1.0_01719.1.g29289.t2	gb|EOA21530.1| hypothetical protein CARUB_v10001935mg [Capsella rubella]	228	217	5.00E-99	95.2	86.4	90.4	hypothetical protein CARUB_v10001935mg	gbpln	Capsella rubella	AT5G09260.1 | Symbols: VPS20.2 | vacuolar protein sorting-associated protein 20.2 | chr5:2876797-2878355 FORWARD LENGTH=216	228	216	1.00E-100	94.7	84.6	89.9
Rsa1.0_01719.1.g29290.t1	ref|XP_002873390.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319227|gb|EFH49649.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	107	107	2.00E-49	100.0	90.7	98.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G09250.1 | Symbols: KIWI | ssDNA-binding transcriptional regulator | chr5:2875421-2876368 REVERSE LENGTH=107	107	107	5.00E-52	100.0	90.7	97.2
Rsa1.0_01719.1.g29291.t1	emb|CAF22024.1| amino acid permease [Brassica napus]	485	487	0	100.4	95.5	98.6	amino acid permease	gbpln	Brassica napus	AT5G09220.1 | Symbols: AAP2 | amino acid permease 2 | chr5:2866867-2868863 FORWARD LENGTH=493	485	493	0	101.6	92.4	97.1
Rsa1.0_01719.1.g29292.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01720.1.g29293.t1	ref|NP_191571.4| beta glucosidase 27 [Arabidopsis thaliana] gi|269969439|sp|Q9M1D1.2|BGL27_ARATH RecName: Full=Beta-glucosidase 27; Short=AtBGLU27 gi|332646492|gb|AEE80013.1| beta glucosidase 27 [Arabidopsis thaliana]	531	540	0	101.7	90.0	93.2	beta glucosidase 27	gbpln	Arabidopsis thaliana	AT3G60120.1 | Symbols: BGLU27 | beta glucosidase 27 | chr3:22206238-22208952 FORWARD LENGTH=540	531	540	0	101.7	90.0	93.2
Rsa1.0_01720.1.g29294.t1	ref|XP_002876536.1| hypothetical protein ARALYDRAFT_907533 [Arabidopsis lyrata subsp. lyrata] gi|297322374|gb|EFH52795.1| hypothetical protein ARALYDRAFT_907533 [Arabidopsis lyrata subsp. lyrata]	577	643	0	111.4	73.5	81.1	hypothetical protein ARALYDRAFT_907533	gbpln	Arabidopsis lyrata	AT3G60110.1 | Symbols: | DNA-binding bromodomain-containing protein | chr3:22197993-22201159 FORWARD LENGTH=641	577	641	0	111.1	70.4	78.5
Rsa1.0_01720.1.g29295.t3	gb|EOA25974.1| hypothetical protein CARUB_v10019363mg [Capsella rubella]	485	473	0	97.5	89.7	93.8	hypothetical protein CARUB_v10019363mg	gbpln	Capsella rubella	AT3G60100.1 | Symbols: CSY5 | citrate synthase 5 | chr3:22192888-22196246 FORWARD LENGTH=464	485	464	0	95.7	87.6	91.8
Rsa1.0_01720.1.g29296.t1	ref|XP_002876534.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322372|gb|EFH52793.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	158	157	2.00E-70	99.4	83.5	89.2	VQ motif-containing protein	gbpln	Arabidopsis lyrata	AT3G60090.1 | Symbols: | VQ motif-containing protein | chr3:22190858-22191331 FORWARD LENGTH=157	158	157	6.00E-73	99.4	84.2	88.6
Rsa1.0_01720.1.g29297.t1	ref|XP_002891861.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] gi|297337703|gb|EFH68120.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	176	401	2.00E-47	227.8	57.4	60.8	zinc ion binding protein	gbpln	Arabidopsis lyrata	AT1G55915.1 | Symbols: | zinc ion binding | chr1:20907663-20909429 FORWARD LENGTH=404	176	404	1.00E-48	229.5	56.3	61.4
Rsa1.0_01721.1.g29298.t1	ref|NP_190092.1| high affinity nitrate transporter 2.6 [Arabidopsis thaliana] gi|75264330|sp|Q9LXH0.1|NRT26_ARATH RecName: Full=High affinity nitrate transporter 2.6; Short=AtNRT2:6 gi|7671407|emb|CAB89321.1| high-affinity nitrate transporter-like protein [Arabidopsis thaliana] gi|44917451|gb|AAS49050.1| At3g45060 [Arabidopsis thaliana] gi|51536534|gb|AAU05505.1| At3g45060 [Arabidopsis thaliana] gi|332644466|gb|AEE77987.1| high affinity nitrate transporter 2.6 [Arabidopsis thaliana]	642	542	0	84.4	67.4	69.8	high affinity nitrate transporter 2.6	gbpln	Arabidopsis thaliana	AT3G45060.1 | Symbols: ATNRT2.6, NRT2.6 | high affinity nitrate transporter 2.6 | chr3:16477671-16479386 REVERSE LENGTH=542	642	542	0	84.4	67.4	69.8
Rsa1.0_01721.1.g29299.t1	dbj|BAJ34078.1| unnamed protein product [Thellungiella halophila]	509	510	0	100.2	92.1	96.3	unnamed protein product	----	----	AT3G45010.1 | Symbols: scpl48 | serine carboxypeptidase-like 48 | chr3:16466328-16468845 FORWARD LENGTH=510	509	510	0	100.2	90.2	96.3
Rsa1.0_01721.1.g29300.t1	gb|AEX07607.1| xyloglucosyl transferase 3, partial [Brassica juncea]	292	292	1.00E-157	100.0	91.4	93.8	xyloglucosyl transferase 3, partial	gbpln	Brassica juncea	AT3G44990.1 | Symbols: XTR8, ATXTR8, XTH31 | xyloglucan endo-transglycosylase-related 8 | chr3:16447280-16448678 REVERSE LENGTH=293	292	293	1.00E-150	100.3	88.4	93.2
Rsa1.0_01721.1.g29301.t1	gb|EOA25184.1| hypothetical protein CARUB_v10018495mg [Capsella rubella]	780	773	0	99.1	68.6	82.3	hypothetical protein CARUB_v10018495mg	gbpln	Capsella rubella	AT3G44910.1 | Symbols: ATCHX12, CHX12 | cation/H+ exchanger 12 | chr3:16392064-16394579 REVERSE LENGTH=770	780	770	0	98.7	65.8	79.2
Rsa1.0_01722.1.g29302.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01722.1.g29303.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2189	1274	0	58.2	27.3	37.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2189	575	4.00E-73	26.3	7.9	12.5
Rsa1.0_01722.1.g29304.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01722.1.g29305.t1	gb|EOA18474.1| hypothetical protein CARUB_v10007020mg [Capsella rubella]	694	700	0	100.9	56.9	61.2	hypothetical protein CARUB_v10007020mg	gbpln	Capsella rubella	AT4G33970.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:16279795-16281894 REVERSE LENGTH=699	694	699	0	100.7	56.6	62.1
Rsa1.0_01722.1.g29306.t1	ref|XP_002867141.1| hypothetical protein ARALYDRAFT_491275 [Arabidopsis lyrata subsp. lyrata] gi|297312977|gb|EFH43400.1| hypothetical protein ARALYDRAFT_491275 [Arabidopsis lyrata subsp. lyrata]	180	217	4.00E-47	120.6	72.2	77.8	hypothetical protein ARALYDRAFT_491275	gbpln	Arabidopsis lyrata	AT4G33980.1 | Symbols: | BEST Arabidopsis thaliana protein match is: cold regulated gene 27 (TAIR:AT5G42900.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16283047-16284946 REVERSE LENGTH=218	180	218	3.00E-45	121.1	67.8	76.1
Rsa1.0_01722.1.g29307.t1	ref|XP_002867140.1| hypothetical protein ARALYDRAFT_913003 [Arabidopsis lyrata subsp. lyrata] gi|297312976|gb|EFH43399.1| hypothetical protein ARALYDRAFT_913003 [Arabidopsis lyrata subsp. lyrata]	156	155	6.00E-70	99.4	90.4	94.9	hypothetical protein ARALYDRAFT_913003	gbpln	Arabidopsis lyrata	AT4G33985.1 | Symbols: | Protein of unknown function (DUF1685) | chr4:16288301-16288857 REVERSE LENGTH=154	156	154	8.00E-69	98.7	87.8	92.9

Rsa1.0_01723.1.g29308.t1	ref|XP_002892523.1| hypothetical protein ARALYDRAFT_334257 [Arabidopsis lyrata subsp. lyrata] gi|297338365|gb|EFH68782.1| hypothetical protein ARALYDRAFT_334257 [Arabidopsis lyrata subsp. lyrata]	331	305	2.00E-62	92.1	38.7	52.3	hypothetical protein ARALYDRAFT_334257	gbpln	Arabidopsis lyrata	AT2G42470.1 | Symbols: | TRAF-like family protein | chr2:17679887-17685187 REVERSE LENGTH=898	331	898	2.00E-57	271.3	41.1	60.1
Rsa1.0_01723.1.g29309.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1430	1475	0	103.1	54.6	68.6	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1430	1262	0	88.3	21.3	27.4
Rsa1.0_01723.1.g29310.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01723.1.g29311.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	576	1374	2.00E-94	238.5	27.8	38.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	576	575	1.00E-90	99.8	26.4	36.3
Rsa1.0_01723.1.g29312.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01724.1.g29313.t1	gb|EOA38973.1| hypothetical protein CARUB_v10011400mg [Capsella rubella]	819	783	0	95.6	62.1	74.2	hypothetical protein CARUB_v10011400mg	gbpln	Capsella rubella	AT1G17340.1 | Symbols: | Phosphoinositide phosphatase family protein | chr1:5934129-5938391 FORWARD LENGTH=785	819	785	0	95.8	60.4	73.7
Rsa1.0_01724.1.g29314.t1	gb|EOA37028.1| hypothetical protein CARUB_v10010080mg [Capsella rubella]	224	253	1.00E-109	112.9	87.9	94.6	hypothetical protein CARUB_v10010080mg	gbpln	Capsella rubella	AT1G17330.1 | Symbols: | Metal-dependent phosphohydrolase | chr1:5929966-5931595 FORWARD LENGTH=222	224	222	1.00E-112	99.1	89.7	94.2
Rsa1.0_01724.1.g29315.t1	ref|XP_002890217.1| alanine aminotransferase [Arabidopsis lyrata subsp. lyrata] gi|297336059|gb|EFH66476.1| alanine aminotransferase [Arabidopsis lyrata subsp. lyrata]	534	542	0	101.5	89.1	94.8	alanine aminotransferase	gbpln	Arabidopsis lyrata	AT1G17290.1 | Symbols: AlaAT1 | alanine aminotransferas | chr1:5922771-5926093 FORWARD LENGTH=543	534	543	0	101.7	88.6	94.6
Rsa1.0_01724.1.g29316.t1	ref|XP_002890216.1| hypothetical protein ARALYDRAFT_471933 [Arabidopsis lyrata subsp. lyrata] gi|297336058|gb|EFH66475.1| hypothetical protein ARALYDRAFT_471933 [Arabidopsis lyrata subsp. lyrata]	76	94	1.00E-18	123.7	72.4	77.6	hypothetical protein ARALYDRAFT_471933	gbpln	Arabidopsis lyrata	AT1G17285.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17300.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:5920895-5921287 FORWARD LENGTH=95	76	95	3.00E-21	125.0	72.4	78.9
Rsa1.0_01724.1.g29317.t2	ref|XP_002892944.1| ubiquitin-conjugating enzyme 32 [Arabidopsis lyrata subsp. lyrata] gi|297338786|gb|EFH69203.1| ubiquitin-conjugating enzyme 32 [Arabidopsis lyrata subsp. lyrata]	244	237	1.00E-124	97.1	90.2	93.0	ubiquitin-conjugating enzyme 32	gbpln	Arabidopsis lyrata	AT1G17280.2 | Symbols: UBC34 | ubiquitin-conjugating enzyme 34 | chr1:5917146-5919162 REVERSE LENGTH=237	244	237	1.00E-126	97.1	89.3	92.2
Rsa1.0_01724.1.g29318.t1	ref|NP_566249.1| E3 ubiquitin-protein ligase ATL6 [Arabidopsis thaliana] gi|68565231|sp|Q8RXX9.2|ATL6_ARATH RecName: Full=E3 ubiquitin-protein ligase ATL6; AltName: Full=RING-H2 finger protein ATL6; Flags: Precursor gi|70905101|gb|AAZ14076.1| At3g05200 [Arabidopsis thaliana] gi|332640683|gb|AEE74204.1| E3 ubiquitin-protein ligase ATL6 [Arabidopsis thaliana]	386	398	1.00E-178	103.1	83.9	91.2	E3 ubiquitin-protein ligase ATL6	gbpln	Arabidopsis thaliana	AT3G05200.1 | Symbols: ATL6 | RING/U-box superfamily protein | chr3:1477377-1478573 FORWARD LENGTH=398	386	398	0	103.1	83.9	91.2
Rsa1.0_01724.1.g29319.t3	ref|XP_002882401.1| aminotransferase class IV family protein [Arabidopsis lyrata subsp. lyrata] gi|297328241|gb|EFH58660.1| aminotransferase class IV family protein [Arabidopsis lyrata subsp. lyrata]	327	555	4.00E-73	169.7	56.9	65.7	aminotransferase class IV family protein	gbpln	Arabidopsis lyrata	AT5G27410.2 | Symbols: | D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein | chr5:9676362-9682468 FORWARD LENGTH=936	327	936	2.00E-75	286.2	52.0	62.7
Rsa1.0_01724.1.g29320.t1	gb|EOA30820.1| hypothetical protein CARUB_v10013963mg [Capsella rubella]	378	376	1.00E-150	99.5	73.0	80.4	hypothetical protein CARUB_v10013963mg	gbpln	Capsella rubella	AT3G05180.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:1468599-1470529 REVERSE LENGTH=379	378	379	1.00E-150	100.3	69.8	79.1
Rsa1.0_01724.1.g29321.t1	dbj|BAF01531.1| hypothetical protein [Arabidopsis thaliana]	306	284	1.00E-156	92.8	86.3	89.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G05170.1 | Symbols: | Phosphoglycerate mutase family protein | chr3:1466738-1468219 FORWARD LENGTH=316	306	316	1.00E-158	103.3	89.9	94.1

Rsa1.0_01725.1.g29322.t1	ref|NP_199295.2| Nucleotide-diphospho-sugar transferase family protein [Arabidopsis thaliana] gi|109946407|gb|ABG48382.1| At5g44820 [Arabidopsis thaliana] gi|332007782|gb|AED95165.1| Nucleotide-diphospho-sugar transferase family protein [Arabidopsis thaliana]	464	367	1.00E-174	79.1	62.7	66.2	Nucleotide-diphospho-sugar transferase family protein	gbpln	Arabidopsis thaliana	AT5G44820.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr5:18095795-18097558 REVERSE LENGTH=367	464	367	1.00E-177	79.1	62.7	66.2
Rsa1.0_01725.1.g29323.t1	gb|EOA21662.1| hypothetical protein CARUB_v10002083mg [Capsella rubella]	220	178	2.00E-22	80.9	32.3	41.8	hypothetical protein CARUB_v10002083mg	gbpln	Capsella rubella	AT4G03150.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:1393731-1394529 REVERSE LENGTH=185	220	185	7.00E-21	84.1	27.3	32.3
Rsa1.0_01725.1.g29324.t1	gb|AAB81872.1| putative MuDR-like transposon protein [Arabidopsis thaliana] gi|7267508|emb|CAB77991.1| putative MuDR-like transposon protein [Arabidopsis thaliana]	469	714	8.00E-51	152.2	28.6	41.4	putative MuDR-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01725.1.g29325.t1	gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]	1105	1534	0	138.8	67.3	79.8	F17L21.7	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1105	1262	1.00E-88	114.2	16.7	25.2
Rsa1.0_01725.1.g29326.t1	gb|EOA33803.1| hypothetical protein CARUB_v10021274mg [Capsella rubella]	312	304	4.00E-90	97.4	53.5	65.1	hypothetical protein CARUB_v10021274mg	gbpln	Capsella rubella	AT2G40560.1 | Symbols: | Protein kinase superfamily protein | chr2:16938705-16939616 REVERSE LENGTH=303	312	303	5.00E-72	97.1	45.2	59.6
Rsa1.0_01726.1.g29327.t1	ref|NP_196346.1| MEI2-like protein 4 [Arabidopsis thaliana] gi|75335654|sp|Q9LYN7.1|AML4_ARATH RecName: Full=Protein MEI2-like 4; Short=AML4; AltName: Full=MEI2-like protein 4 gi|7546707|emb|CAB87285.1| Mei2-like protein [Arabidopsis thaliana] gi|110742203|dbj|BAE99028.1| Mei2-like protein [Arabidopsis thaliana] gi|332003750|gb|AED91133.1| MEI2-like protein 4 [Arabidopsis thaliana]	779	907	0	116.4	79.6	86.3	MEI2-like protein 4	gbpln	Arabidopsis thaliana	AT5G07290.1 | Symbols: AML4, ML4 | MEI2-like 4 | chr5:2294248-2298491 FORWARD LENGTH=907	779	907	0	116.4	79.6	86.3
Rsa1.0_01726.1.g29328.t1	ref|NP_196344.2| E3 ubiquitin-protein ligase XBAT33 [Arabidopsis thaliana] gi|122239678|sp|Q4FE45.1|XB33_ARATH RecName: Full=E3 ubiquitin-protein ligase XBAT33; AltName: Full=Ankyrin repeat domain and RING finger-containing protein XBAT33; AltName: Full=Protein XB3 homolog 3 gi|70905089|gb|AAZ14070.1| At5g07270 [Arabidopsis thaliana] gi|117168057|gb|ABK32111.1| At5g07270 [Arabidopsis thaliana] gi|332003748|gb|AED91131.1| E3 ubiquitin-protein ligase XBAT33 [Arabidopsis thaliana]	514	513	0	99.8	91.6	95.3	E3 ubiquitin-protein ligase XBAT33	gbpln	Arabidopsis thaliana	AT5G07270.1 | Symbols: XBAT33 | XB3 ortholog 3 in Arabidopsis thaliana | chr5:2280821-2283384 FORWARD LENGTH=513	514	513	0	99.8	91.6	95.3
Rsa1.0_01726.1.g29329.t1	ref|XP_002873302.1| hypothetical protein ARALYDRAFT_487547 [Arabidopsis lyrata subsp. lyrata] gi|297319139|gb|EFH49561.1| hypothetical protein ARALYDRAFT_487547 [Arabidopsis lyrata subsp. lyrata]	179	244	2.00E-24	136.3	41.9	54.2	hypothetical protein ARALYDRAFT_487547	gbpln	Arabidopsis lyrata	AT5G07225.1 | Symbols: | RING/U-box superfamily protein | chr5:2268642-2270227 REVERSE LENGTH=234	179	234	8.00E-20	130.7	35.8	48.0
Rsa1.0_01726.1.g29330.t1	sp|Q9LYP5.3|ARR21_ARATH RecName: Full=Putative two-component response regulator ARR21	598	613	5.00E-97	102.5	33.8	39.1	RecName: Full=Putative two-component response regulator ARR21	----	----	AT5G07210.1 | Symbols: ARR21, RR21 | response regulator 21 | chr5:2252237-2256018 FORWARD LENGTH=621	598	621	1.00E-99	103.8	33.8	39.1
Rsa1.0_01726.1.g29331.t1	ref|XP_002873300.1| YAP169 [Arabidopsis lyrata subsp. lyrata] gi|297319137|gb|EFH49559.1| YAP169 [Arabidopsis lyrata subsp. lyrata]	379	380	0	100.3	86.3	93.7	YAP169	gbpln	Arabidopsis lyrata	AT5G07200.1 | Symbols: YAP169, GA20OX3, ATGA20OX3 | gibberellin 20-oxidase 3 | chr5:2243835-2245157 REVERSE LENGTH=380	379	380	0	100.3	85.2	92.6
Rsa1.0_01726.1.g29332.t1	gb|AAK43838.1|AF370461_1 embryo-specific protein 3; ATS3 [Arabidopsis thaliana] gi|17978805|gb|AAL47396.1| embryo-specific protein 3 (ATS3) [Arabidopsis thaliana]	205	213	6.00E-70	103.9	75.6	83.9	embryo-specific protein 3; ATS3	gbpln	Arabidopsis thaliana	AT5G07190.1 | Symbols: ATS3 | seed gene 3 | chr5:2237610-2238488 FORWARD LENGTH=213	205	213	5.00E-67	103.9	70.2	77.6

Rsa1.0_01727.1.g29333.t1	ref|XP_002894200.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297340042|gb|EFH70459.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	665	717	2.00E−90	107.8	39.8	55.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097−11122412 FORWARD LENGTH=673	665	673	8.00E−18	101.2	8.1	10.2
Rsa1.0_01727.1.g29334.t1	gb|EOA28924.1| hypothetical protein CARUB_v10025181mg [Capsella rubella]	479	386	1.00E−168	80.6	67.0	72.0	hypothetical protein CARUB_v10025181mg	gbpln	Capsella rubella	AT2G39550.1 | Symbols: ATGGT−IB, GGB, PGGT−I | Prenyltransferase family protein | chr2:16501666−16504144 FORWARD LENGTH=375	479	375	1.00E−171	78.3	66.6	70.6
Rsa1.0_01727.1.g29335.t1	ref|NP_181488.1| Putative membrane lipoprotein [Arabidopsis thaliana] gi|3355485|gb|AAC27847.1| hypothetical protein [Arabidopsis thaliana] gi|18700123|gb|AAL77673.1| At2g39560/F12L6.22 [Arabidopsis thaliana] gi|21464575|gb|AAM52242.1| At2g39560/F12L6.22 [Arabidopsis thaliana] gi|330254600|gb|AEC09694.1| Putative membrane lipoprotein [Arabidopsis thaliana]	238	233	4.00E−66	97.9	80.7	85.3	Putative membrane lipoprotein	gbpln	Arabidopsis thaliana	AT2G39560.1 | Symbols: | Putative membrane lipoprotein | chr2:16505124−16505825 REVERSE LENGTH=233	238	233	1.00E−68	97.9	80.7	85.3
Rsa1.0_01727.1.g29336.t1	ref|XP_002881667.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] gi|297327506|gb|EFH57926.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	778	549	0	70.6	44.5	49.2	glycosyl hydrolase family 17 protein	gbpln	Arabidopsis lyrata	AT2G39640.1 | Symbols: | glycosyl hydrolase family 17 protein | chr2:16525171−16527012 REVERSE LENGTH=549	778	549	0	70.6	43.8	48.6
Rsa1.0_01727.1.g29337.t1	emb|CAC37623.1| copia−like polyprotein [Arabidopsis thaliana]	686	1466	0	213.7	60.6	72.2	copia−like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	686	1262	1.00E−107	184.0	27.3	41.5
Rsa1.0_01727.1.g29338.t3	ref|XP_002879808.1| botrytis−induced kinase1 [Arabidopsis lyrata subsp. lyrata] gi|297325647|gb|EFH56067.1| botrytis−induced kinase1 [Arabidopsis lyrata subsp. lyrata]	393	394	0	100.3	86.0	91.1	botrytis−induced kinase1	gbpln	Arabidopsis lyrata	AT2G39660.1 | Symbols: BIK1 | botrytis−induced kinase1 | chr2:16531943−16533601 FORWARD LENGTH=395	393	395	0	100.5	85.2	91.1
Rsa1.0_01727.1.g29339.t1	gb|EOA27168.1| hypothetical protein CARUB_v10023268mg [Capsella rubella]	428	428	0	100.0	89.0	92.5	hypothetical protein CARUB_v10023268mg	gbpln	Capsella rubella	AT2G39670.1 | Symbols: | Radical SAM superfamily protein | chr2:16534303−16536986 FORWARD LENGTH=428	428	428	0	100.0	86.9	91.8
Rsa1.0_01727.1.g29340.t1	gb|ACT67493.1| expansin A1 [Raphanus sativus]	257	258	1.00E−142	100.4	96.9	98.4	expansin A1	gbpln	Raphanus sativus	AT2G39700.1 | Symbols: ATEXPA4, ATEXP4, ATHEXP ALPHA 1.6, EXPA4 | expansin A4 | chr2:16544246−16545434 REVERSE LENGTH=257	257	257	1.00E−143	100.0	94.6	96.5
Rsa1.0_01727.1.g29341.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01727.1.g29342.t1	gb|AAF22521.1|AF123390_1 26S proteasome AAA−ATPase subunit RPT1a [Arabidopsis thaliana]	70	426	2.00E−17	608.6	71.4	77.1	26S proteasome AAA−ATPase subunit RPT1a	gbpln	Arabidopsis thaliana	AT1G53750.1 | Symbols: RPT1A | regulatory particle triple−A 1A | chr1:20065921−20068324 REVERSE LENGTH=426	70	426	3.00E−20	608.6	71.4	77.1
Rsa1.0_01728.1.g29343.t1	ref|XP_002873933.1| hypothetical protein ARALYDRAFT_488797 [Arabidopsis lyrata subsp. lyrata] gi|297319770|gb|EFH50192.1| hypothetical protein ARALYDRAFT_488797 [Arabidopsis lyrata subsp. lyrata]	702	699	0	99.6	86.6	93.2	hypothetical protein ARALYDRAFT_488797	gbpln	Arabidopsis lyrata	AT5G19130.1 | Symbols: | GPI transamidase component family protein / Gaa1−like family protein | chr5:6416128−6418993 REVERSE LENGTH=699	702	699	0	99.6	87.0	93.3
Rsa1.0_01728.1.g29344.t1	ref|XP_002871863.1| pepsin A [Arabidopsis lyrata subsp. lyrata] gi|297317700|gb|EFH48122.1| pepsin A [Arabidopsis lyrata subsp. lyrata]	387	377	1.00E−156	97.4	77.0	83.2	pepsin A	gbpln	Arabidopsis lyrata	AT5G19120.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:6414585−6415745 FORWARD LENGTH=386	387	386	1.00E−157	99.7	76.2	84.2
Rsa1.0_01728.1.g29345.t2	ref|NP_197412.1| Eukaryotic aspartyl protease family protein [Arabidopsis thaliana] gi|332005271|gb|AED92654.1| Eukaryotic aspartyl protease family protein [Arabidopsis thaliana]	370	405	1.00E−107	109.5	61.1	73.5	Eukaryotic aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT5G19110.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:6411720−6413170 REVERSE LENGTH=405	370	405	1.00E−109	109.5	61.1	73.5
Rsa1.0_01728.1.g29346.t1	ref|NP_001241217.1| uncharacterized protein LOC100818868 precursor [Glycine max] gi|255644718|gb|ACU22861.1| unknown [Glycine max]	432	450	1.00E−66	104.2	38.7	55.8	uncharacterized protein LOC100818868 precursor	gbenv/gbpln	Glycine max	AT1G03220.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr1:787143−788444 FORWARD LENGTH=433	432	433	6.00E−49	100.2	35.6	50.5
Rsa1.0_01728.1.g29347.t1	gb|AAM98191.1| unknown protein [Arabidopsis thaliana] gi|38603804|gb|AAR24647.1| At2g23330 [Arabidopsis thaliana] gi|110742535|dbj|BAE99183.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	272	776	3.00E−95	285.3	63.2	74.3	unknown protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	272	1262	5.00E−55	464.0	36.8	52.6

Rsa1.0_01728.1.g29348.t1	ref|NP_850851.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|238481311|ref|NP_001154719.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|332005268|gb|AED92651.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana] gi|332005269|gb|AED92652.1| heavy metal transport/detoxification domain-containing protein [Arabidopsis thaliana]	576	465	4.00E-57	80.7	32.3	33.0	heavy metal transport/detoxification domain-containing protein	gbpln	Arabidopsis thaliana	AT5G19090.3 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:6387910-6389855 FORWARD LENGTH=465	576	465	1.00E-59	80.7	32.3	33.0
Rsa1.0_01728.1.g29349.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1806	1213	0	67.2	36.2	47.1	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1806	626	5.00E-75	34.7	8.8	13.7
Rsa1.0_01729.1.g29350.t1	ref|NP_181162.2| kinesin family member 11 [Arabidopsis thaliana] gi|322510039|sp|P82266.2|K125_ARATH RecName: Full=Probable 125 kDa kinesin-related protein gi|330254121|gb|AEC09215.1| kinesin family member 11 [Arabidopsis thaliana]	902	1009	0	111.9	91.1	95.9	kinesin family member 11	gbpln	Arabidopsis thaliana	AT2G36200.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:15180078-15185189 REVERSE LENGTH=1009	902	1009	0	111.9	91.1	95.9
Rsa1.0_01729.1.g29351.t1	ref|XP_002879611.1| hypothetical protein ARALYDRAFT_482620 [Arabidopsis lyrata subsp. lyrata] gi|297325450|gb|EFH55870.1| hypothetical protein ARALYDRAFT_482620 [Arabidopsis lyrata subsp. lyrata]	434	442	1.00E-166	101.8	80.6	86.4	hypothetical protein ARALYDRAFT_482620	gbpln	Arabidopsis lyrata	AT2G36420.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G03670.1); Has 10588 Blast hits to 6606 proteins in 440 species: Archae - 8; Bacteria - 365; Metazoa - 4146; Fungi - 1198; Plants - 483; Viruses - 212; Other Eukaryotes - 4176 (source: NCBI BLink). | chr2:15286498-15288990 FORWARD LENGTH=439	434	439	1.00E-166	101.2	79.7	85.7
Rsa1.0_01729.1.g29352.t1	gb|EOA27098.1| hypothetical protein CARUB_v10023196mg [Capsella rubella]	454	451	0	99.3	80.0	90.1	hypothetical protein CARUB_v10023196mg	gbpln	Capsella rubella	AT2G36430.1 | Symbols: | Plant protein of unknown function (DUF247) | chr2:15290211-15291557 FORWARD LENGTH=448	454	448	0	98.7	82.2	92.1
Rsa1.0_01729.1.g29353.t1	ref|XP_002879613.1| hypothetical protein ARALYDRAFT_482622 [Arabidopsis lyrata subsp. lyrata] gi|297325452|gb|EFH55872.1| hypothetical protein ARALYDRAFT_482622 [Arabidopsis lyrata subsp. lyrata]	81	76	2.00E-18	93.8	64.2	76.5	hypothetical protein ARALYDRAFT_482622	gbpln	Arabidopsis lyrata	AT2G36440.1 | Symbols: | unknown protein; Has 3 Blast hits to 3 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:15292648-15292872 FORWARD LENGTH=74	81	74	5.00E-17	91.4	60.5	70.4
Rsa1.0_01729.1.g29354.t1	ref|XP_002881444.1| AP2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327283|gb|EFH57703.1| AP2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	174	184	1.00E-67	105.7	82.2	90.2	AP2 domain-containing protein	gbpln	Arabidopsis lyrata	AT2G36450.1 | Symbols: HRD | Integrase-type DNA-binding superfamily protein | chr2:15294303-15294857 REVERSE LENGTH=184	174	184	1.00E-61	105.7	79.3	87.9
Rsa1.0_01729.1.g29355.t1	gb|EOA27460.1| hypothetical protein CARUB_v10023598mg [Capsella rubella]	93	331	7.00E-11	355.9	33.3	34.4	hypothetical protein CARUB_v10023598mg	gbpln	Capsella rubella	AT2G36470.1 | Symbols: | Plant protein of unknown function (DUF868) | chr2:15299385-15300368 REVERSE LENGTH=327	93	327	2.00E-13	351.6	32.3	33.3
Rsa1.0_01729.1.g29356.t1	gb|EOA28814.1| hypothetical protein CARUB_v10025053mg [Capsella rubella]	938	1037	0	110.6	76.5	83.7	hypothetical protein CARUB_v10025053mg	gbpln	Capsella rubella	AT2G36480.2 | Symbols: | ENTH/VHS family protein | chr2:15302567-15306274 REVERSE LENGTH=844	938	844	0	90.0	66.6	71.9
Rsa1.0_01729.1.g29357.t1	ref|XP_002879635.1| tsl-kinase interacting protein 1 [Arabidopsis lyrata subsp. lyrata] gi|297325474|gb|EFH55894.1| tsl-kinase interacting protein 1 [Arabidopsis lyrata subsp. lyrata]	706	740	0	104.8	83.9	89.2	tsl-kinase interacting protein 1	gbpln	Arabidopsis lyrata	AT2G36960.3 | Symbols: TKI1 | TSL-kinase interacting protein 1 | chr2:15523552-15527245 FORWARD LENGTH=744	706	744	0	105.4	83.6	88.8
Rsa1.0_01729.1.g29358.t1	ref|NP_181234.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75313513|sp|Q9SJL0.1|U86A1_ARATH RecName: Full=UDP-glycosyltransferase 86A1 gi|4883613|gb|AAD31582.1| putative glucosyltransferase [Arabidopsis thaliana] gi|15809994|gb|AAL06924.1| At2g36970/T1J8.15 [Arabidopsis thaliana] gi|22137016|gb|AAM91353.1| At2g36970/T1J8.15 [Arabidopsis thaliana] gi|330254235|gb|AEC09329.1| UDP-glycosyltransferase 86A1 [Arabidopsis thaliana]	437	490	0	112.1	82.8	89.7	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT2G36970.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:15529050-15530712 FORWARD LENGTH=490	437	490	0	112.1	82.8	89.7

Rsa1.0_01729.1.g29359.t1	ref|NP_181234.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75313513|sp|Q9SJL0.1|U86A1_ARATH RecName: Full=UDP-glycosyltransferase 86A1 gi|4883613|gb|AAD31582.1| putative glucosyltransferase [Arabidopsis thaliana] gi|15809994|gb|AAL06924.1| At2g36970/T1J8.15 [Arabidopsis thaliana] gi|22137016|gb|AAM91353.1| At2g36970/T1J8.15 [Arabidopsis thaliana] gi|330254235|gb|AEC09329.1| UDP-glycosyltransferase 86A1 [Arabidopsis thaliana]	479	490	0	102.3	88.3	93.3	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT2G36970.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:15529050-15530712 FORWARD LENGTH=490	479	490	0	102.3	88.3	93.3
Rsa1.0_01729.1.g29360.t1	ref|NP_181235.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75206293|sp|Q9SJK9.1|PP189_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g36980, mitochondrial; Flags: Precursor gi|4883614|gb|AAD31583.1| hypothetical protein [Arabidopsis thaliana] gi|330254236|gb|AEC09330.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	618	625	0	101.1	83.7	91.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G36980.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:15531161-15533038 FORWARD LENGTH=625	618	625	0	101.1	83.7	91.4
Rsa1.0_01729.1.g29361.t1	ref|NP_181238.4| putative white-brown complex-protein 30 [Arabidopsis thaliana] gi|378405226|sp|Q9SJK6.3|WBC30_ARATH RecName: Full=Putative white-brown complex homolog protein 30; AltName: Full=Putative non-intrinsic ABC protein 12; AltName: Full=WBC-related protein 1 gi|330254240|gb|AEC09334.1| putative white-brown complex-protein 30 [Arabidopsis thaliana]	1052	1082	0	102.9	90.6	95.0	putative white-brown complex-protein 30	gbpln	Arabidopsis thaliana	AT2G37010.1 | Symbols: ATNAP12, NAP12 | non-intrinsic ABC protein 12 | chr2:15541720-15546159 FORWARD LENGTH=1082	1052	1082	0	102.9	90.6	95.0
Rsa1.0_01729.1.g29362.t1	ref|NP_181240.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana] gi|4883619|gb|AAD31588.1| putative auxin-induced protein [Arabidopsis thaliana] gi|67633592|gb|AAY78720.1| auxin-responsive family protein [Arabidopsis thaliana] gi|330254245|gb|AEC09339.1| SAUR-like auxin-responsive protein [Arabidopsis thaliana]	125	124	8.00E-49	99.2	76.0	85.6	SAUR-like auxin-responsive protein	gbpln	Arabidopsis thaliana	AT2G37030.1 | Symbols: | SAUR-like auxin-responsive protein family | chr2:15553732-15554106 FORWARD LENGTH=124	125	124	2.00E-51	99.2	76.0	85.6
Rsa1.0_01729.1.g29363.t1	gb|EOA28893.1| hypothetical protein CARUB_v10025139mg [Capsella rubella]	456	437	1.00E-170	95.8	74.3	81.4	hypothetical protein CARUB_v10025139mg	gbpln	Capsella rubella	AT2G37035.1 | Symbols: | unknown protein; Has 26 Blast hits to 26 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:15555374-15556780 REVERSE LENGTH=433	456	433	1.00E-169	95.0	74.6	82.7
Rsa1.0_01730.1.g29364.t2	gb|AAM67260.1| alcohol dehydrogenase-like protein [Arabidopsis thaliana]	145	384	1.00E-59	264.8	79.3	88.3	alcohol dehydrogenase-like protein	gbpln	Arabidopsis thaliana	AT4G22110.2 | Symbols: | GroES-like zinc-binding dehydrogenase family protein | chr4:11711422-11713946 REVERSE LENGTH=389	145	389	2.00E-61	268.3	78.6	87.6
Rsa1.0_01730.1.g29365.t1	ref|XP_002867795.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata] gi|297313631|gb|EFH44054.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata]	394	394	0	100.0	90.4	93.4	pectate lyase family protein	gbpln	Arabidopsis lyrata	AT4G22080.1 | Symbols: RHS14 | root hair specific 14 | chr4:11700734-11702553 REVERSE LENGTH=394	394	394	0	100.0	90.6	93.4
Rsa1.0_01730.1.g29366.t1	ref|XP_002867796.1| WRKY DNA-binding protein 31 [Arabidopsis lyrata subsp. lyrata] gi|297313632|gb|EFH44055.1| WRKY DNA-binding protein 31 [Arabidopsis lyrata subsp. lyrata]	531	538	0	101.3	88.3	92.7	WRKY DNA-binding protein 31	gbpln	Arabidopsis lyrata	AT4G22070.1 | Symbols: WRKY31, ATWRKY31 | WRKY DNA-binding protein 31 | chr4:11691381-11694234 REVERSE LENGTH=538	531	538	0	101.3	86.3	89.6
Rsa1.0_01730.1.g29367.t1	emb|CAA18105.1| glycine-rich protein [Arabidopsis thaliana] gi|7269047|emb|CAB79157.1| glycine-rich protein [Arabidopsis thaliana]	427	396	7.00E-18	92.7	9.8	10.8	glycine-rich protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01730.1.g29368.t1	gb|EOA15474.1| hypothetical protein CARUB_v10004445mg, partial [Capsella rubella]	526	582	0	110.6	93.5	98.1	hypothetical protein CARUB_v10004445mg, partial	gbpln	Capsella rubella	AT4G22010.1 | Symbols: sks4 | SKU5 similar 4 | chr4:11663429-11666463 FORWARD LENGTH=541	526	541	0	102.9	93.5	97.5

<table>
<tr><td>Rsa1.0_01730.1.g29369.t1</td><td>ref|NP_567643.1| uncharacterized protein [Arabidopsis thaliana] gi|2961345|emb|CAA18103.1| hypothetical protein [Arabidopsis thaliana] gi|7269045|emb|CAB79155.1| hypothetical protein [Arabidopsis thaliana] gi|17064892|gb|AAL32600.1| Unknown protein [Arabidopsis thaliana] gi|21554227|gb|AAM63302.1| unknown [Arabidopsis thaliana] gi|30102842|gb|AAP21339.1| At4g22000 [Arabidopsis thaliana] gi|332659141|gb|AEE84541.1| uncharacterized protein AT4G22000 [Arabidopsis thaliana]</td><td>131</td><td>130</td><td>2.00E-57</td><td>99.2</td><td>86.3</td><td>86.3</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G22000.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:11659810-11660202 REVERSE LENGTH=130</td><td>131</td><td>130</td><td>3.00E-60</td><td>99.2</td><td>86.3</td><td>86.3</td></tr>
<tr><td>Rsa1.0_01730.1.g29370.t1</td><td>emb|CAA04611.1| APS reductase [Brassica juncea]</td><td>467</td><td>464</td><td>0</td><td>99.4</td><td>95.1</td><td>96.4</td><td>APS reductase</td><td>gbpln</td><td>Brassica juncea</td><td>AT4G21990.1 | Symbols: APR3, PRH-26, PRH26, ATAPR3 | APS reductase 3 | chr4:11657284-11658973 REVERSE LENGTH=458</td><td>467</td><td>458</td><td>0</td><td>98.1</td><td>90.8</td><td>94.0</td></tr>
<tr><td>Rsa1.0_01730.1.g29371.t1</td><td>ref|NP_001078424.1| autophagy-related protein 8a [Arabidopsis thaliana] gi|332659138|gb|AEE84538.1| autophagy-related protein 8a [Arabidopsis thaliana]</td><td>137</td><td>137</td><td>4.00E-69</td><td>100.0</td><td>92.0</td><td>97.1</td><td>autophagy-related protein 8a</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G21980.2 | Symbols: APG8A, ATG8A | Ubiquitin-like superfamily protein | chr4:11655868-11656809 FORWARD LENGTH=137</td><td>137</td><td>137</td><td>1.00E-71</td><td>100.0</td><td>92.0</td><td>97.1</td></tr>
<tr><td>Rsa1.0_01731.1.g29372.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01731.1.g29373.t1</td><td>ref|NP_680195.2| uncharacterized protein [Arabidopsis thaliana] gi|334187828|ref|NP_001190360.1| uncharacterized protein [Arabidopsis thaliana] gi|122175037|sp|Q0V865.1|FAFL_ARATH RecName: Full=Protein FAF-like, chloroplastic; Flags: Precursor gi|111074178|gb|ABH04462.1| At5g22090 [Arabidopsis thaliana] gi|332005598|gb|AED92981.1| uncharacterized protein AT5G22090 [Arabidopsis thaliana] gi|332005599|gb|AED92982.1| uncharacterized protein AT5G22090 [Arabidopsis thaliana]</td><td>452</td><td>463</td><td>1.00E-168</td><td>102.4</td><td>77.0</td><td>85.8</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22090.2 | Symbols: | Protein of unknown function (DUF3049) | chr5:7315003-7316394 REVERSE LENGTH=463</td><td>452</td><td>463</td><td>1.00E-170</td><td>102.4</td><td>77.0</td><td>85.8</td></tr>
<tr><td>Rsa1.0_01731.1.g29374.t1</td><td>gb|EOA21400.1| hypothetical protein CARUB_v10001767mg [Capsella rubella]</td><td>243</td><td>246</td><td>1.00E-128</td><td>101.2</td><td>94.7</td><td>97.5</td><td>hypothetical protein CARUB_v10001767mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G22080.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:7310600-7313540 REVERSE LENGTH=246</td><td>243</td><td>246</td><td>1.00E-120</td><td>101.2</td><td>95.9</td><td>97.1</td></tr>
<tr><td>Rsa1.0_01731.1.g29375.t1</td><td>ref|NP_568412.1| chaperone protein dnaJ 2 [Arabidopsis thaliana] gi|21431768|sp|P42825.2|DNAJ2_ARATH RecName: Full=Chaperone protein dnaJ 2; Short=AtDjA2; Flags: Precursor gi|13374865|emb|CAC34499.1| DNAJ PROTEIN HOMOLOG ATJ [Arabidopsis thaliana] gi|26451807|dbj|BAC42997.1| putative DnaJ protein homolog ATJ [Arabidopsis thaliana] gi|111074426|gb|ABH04586.1| At5g22060 [Arabidopsis thaliana] gi|332005594|gb|AED92977.1| chaperone protein dnaJ 2 [Arabidopsis thaliana]</td><td>424</td><td>419</td><td>0</td><td>98.8</td><td>89.2</td><td>94.6</td><td>chaperone protein dnaJ 2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22060.1 | Symbols: ATJ2, J2 | DNAJ homologue 2 | chr5:7303798-7305668 REVERSE LENGTH=419</td><td>424</td><td>419</td><td>0</td><td>98.8</td><td>89.2</td><td>94.6</td></tr>
<tr><td>Rsa1.0_01731.1.g29376.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01731.1.g29377.t2</td><td>ref|NP_680188.1| replication factor C1 [Arabidopsis thaliana] gi|13374860|emb|CAC34494.1| replication factor C large subunit-like protein [Arabidopsis thaliana] gi|48958527|gb|AAT47816.1| At5g22010 [Arabidopsis thaliana] gi|332005585|gb|AED92968.1| replication factor C1 [Arabidopsis thaliana]</td><td>970</td><td>956</td><td>0</td><td>98.6</td><td>86.5</td><td>92.9</td><td>replication factor C1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22010.1 | Symbols: AtRFC1, RFC1 | replication factor C1 | chr5:7280632-7287037 REVERSE LENGTH=956</td><td>970</td><td>956</td><td>0</td><td>98.6</td><td>86.5</td><td>92.9</td></tr>
<tr><td>Rsa1.0_01731.1.g29378.t1</td><td>ref|XP_002871983.1| hypothetical protein ARALYDRAFT_489047 [Arabidopsis lyrata subsp. lyrata] gi|297317820|gb|EFH48242.1| hypothetical protein ARALYDRAFT_489047 [Arabidopsis lyrata subsp. lyrata]</td><td>443</td><td>376</td><td>1.00E-156</td><td>84.9</td><td>70.2</td><td>74.5</td><td>hypothetical protein ARALYDRAFT_489047</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G22000.3 | Symbols: RHF2A | RING-H2 group F2A | chr5:7277436-7279553 FORWARD LENGTH=375</td><td>443</td><td>375</td><td>1.00E-155</td><td>84.7</td><td>69.3</td><td>73.8</td></tr>
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<tr><td>Rsa1.0_01731.1.g29379.t1</td><td>ref|XP_002871981.1| hypothetical protein ARALYDRAFT_489045 [Arabidopsis lyrata subsp. lyrata] gi|297317818|gb|EFH48240.1| hypothetical protein ARALYDRAFT_489045 [Arabidopsis lyrata subsp. lyrata]</td><td>186</td><td>558</td><td>1.00E-61</td><td>300.0</td><td>62.9</td><td>67.7</td><td>hypothetical protein ARALYDRAFT_489045</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G21990.1 | Symbols: TPR7 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:7273395-7276318 FORWARD LENGTH=554</td><td>186</td><td>554</td><td>1.00E-63</td><td>297.8</td><td>62.9</td><td>67.7</td></tr>
<tr><td>Rsa1.0_01732.1.g29380.t1</td><td>gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]</td><td>138</td><td>1161</td><td>2.00E-30</td><td>841.3</td><td>46.4</td><td>60.9</td><td>F14N23.4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G02520.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr2:676771-678145 REVERSE LENGTH=211</td><td>138</td><td>211</td><td>2.00E-32</td><td>152.9</td><td>46.4</td><td>63.8</td></tr>
<tr><td>Rsa1.0_01732.1.g29381.t1</td><td>gb|EOA20775.1| hypothetical protein CARUB_v10001104mg [Capsella rubella]</td><td>402</td><td>405</td><td>1.00E-166</td><td>100.7</td><td>82.1</td><td>88.3</td><td>hypothetical protein CARUB_v10001104mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G16560.1 | Symbols: KAN, KAN1 | Homeodomain-like superfamily protein | chr5:5407365-5411092 REVERSE LENGTH=403</td><td>402</td><td>403</td><td>1.00E-165</td><td>100.2</td><td>81.3</td><td>88.1</td></tr>
<tr><td>Rsa1.0_01732.1.g29382.t1</td><td>ref|NP_568333.1| uncharacterized protein [Arabidopsis thaliana] gi|9759139|dbj|BAB09624.1| unnamed protein product [Arabidopsis thaliana] gi|332004926|gb|AED92309.1| uncharacterized protein AT5G16550 [Arabidopsis thaliana]</td><td>276</td><td>249</td><td>9.00E-73</td><td>90.2</td><td>57.6</td><td>66.7</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G16550.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5405526-5406641 FORWARD LENGTH=249</td><td>276</td><td>249</td><td>2.00E-75</td><td>90.2</td><td>57.6</td><td>66.7</td></tr>
<tr><td>Rsa1.0_01732.1.g29383.t1</td><td>ref|NP_197157.4| putative auxin efflux carrier component 8 [Arabidopsis thaliana] gi|42558880|sp|Q9FFD0.2|PIN8_ARATH RecName: Full=Putative auxin efflux carrier component 8; Short=AtPIN8 gi|332004922|gb|AED92305.1| putative auxin efflux carrier component 8 [Arabidopsis thaliana]</td><td>348</td><td>351</td><td>0</td><td>100.9</td><td>90.5</td><td>95.7</td><td>putative auxin efflux carrier component 8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G16530.1 | Symbols: PIN5 | Auxin efflux carrier family protein | chr5:5400735-5402626 FORWARD LENGTH=351</td><td>348</td><td>351</td><td>0</td><td>100.9</td><td>90.5</td><td>95.7</td></tr>
<tr><td>Rsa1.0_01732.1.g29384.t1</td><td>gb|EOA22043.1| hypothetical protein CARUB_v10002568mg [Capsella rubella]</td><td>348</td><td>348</td><td>0</td><td>100.0</td><td>92.8</td><td>98.0</td><td>hypothetical protein CARUB_v10002568mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G16510.2 | Symbols: | Alpha-1,4-glucan-protein synthase family protein | chr5:5393296-5394342 FORWARD LENGTH=348</td><td>348</td><td>348</td><td>0</td><td>100.0</td><td>91.7</td><td>97.4</td></tr>
<tr><td>Rsa1.0_01732.1.g29385.t1</td><td>gb|EOA19370.1| hypothetical protein CARUB_v10000465mg [Capsella rubella]</td><td>596</td><td>625</td><td>0</td><td>104.9</td><td>89.9</td><td>94.3</td><td>hypothetical protein CARUB_v10000465mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719</td><td>596</td><td>719</td><td>2.00E-37</td><td>120.6</td><td>21.3</td><td>38.4</td></tr>
<tr><td>Rsa1.0_01732.1.g29386.t1</td><td>ref|XP_002873780.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319617|gb|EFH50039.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>597</td><td>635</td><td>0</td><td>106.4</td><td>78.7</td><td>85.9</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G16500.1 | Symbols: | Protein kinase superfamily protein | chr5:5386733-5389003 REVERSE LENGTH=636</td><td>597</td><td>636</td><td>0</td><td>106.5</td><td>78.1</td><td>85.3</td></tr>
<tr><td>Rsa1.0_01732.1.g29387.t1</td><td>ref|XP_002873779.1| rop-interactive crib motif-containing protein 4 [Arabidopsis lyrata subsp. lyrata] gi|297319616|gb|EFH50038.1| rop-interactive crib motif-containing protein 4 [Arabidopsis lyrata subsp. lyrata]</td><td>152</td><td>153</td><td>2.00E-52</td><td>100.7</td><td>80.3</td><td>84.9</td><td>rop-interactive crib motif-containing protein 4</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G16490.1 | Symbols: RIC4 | ROP-interactive CRIB motif-containing protein 4 | chr5:5384468-5385205 REVERSE LENGTH=153</td><td>152</td><td>153</td><td>2.00E-53</td><td>100.7</td><td>77.6</td><td>85.5</td></tr>
<tr><td>Rsa1.0_01732.1.g29388.t1</td><td>ref|XP_002873778.1| hypothetical protein ARALYDRAFT_488502 [Arabidopsis lyrata subsp. lyrata] gi|297319615|gb|EFH50037.1| hypothetical protein ARALYDRAFT_488502 [Arabidopsis lyrata subsp. lyrata]</td><td>206</td><td>203</td><td>1.00E-105</td><td>98.5</td><td>90.8</td><td>94.2</td><td>hypothetical protein ARALYDRAFT_488502</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G16480.1 | Symbols: | Phosphotyrosine protein phosphatases superfamily protein | chr5:5381334-5382618 REVERSE LENGTH=204</td><td>206</td><td>204</td><td>1.00E-106</td><td>99.0</td><td>89.8</td><td>94.2</td></tr>
<tr><td>Rsa1.0_01732.1.g29389.t1</td><td>ref|NP_197151.1| C2H2 type zinc finger protein [Arabidopsis thaliana] gi|297807673|ref|XP_002871720.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|9759129|dbj|BAB09614.1| unnamed protein product [Arabidopsis thaliana] gi|27808636|gb|AAO24598.1| At5g16470 [Arabidopsis thaliana] gi|110736298|dbj|BAF00119.1| hypothetical protein [Arabidopsis thaliana] gi|297317557|gb|EFH47979.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|332004914|gb|AED92297.1| C2H2 type zinc finger protein [Arabidopsis thaliana] gi|482557657|gb|EOA21849.1| hypothetical protein CARUB_v10002316mg [Capsella rubella]</td><td>104</td><td>104</td><td>5.00E-50</td><td>100.0</td><td>97.1</td><td>98.1</td><td>C2H2 type zinc finger protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G16470.1 | Symbols: | zinc finger (C2H2 type) family protein | chr5:5379516-5379830 FORWARD LENGTH=104</td><td>104</td><td>104</td><td>9.00E-53</td><td>100.0</td><td>97.1</td><td>98.1</td></tr>
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Rsa1.0_01732.1.g29390.t1	ref|XP_002305915.1| predicted protein [Populus trichocarpa] gi|118481835|gb|ABK92854.1| unknown [Populus trichocarpa] gi|222848879|gb|EEE86426.1| predicted protein [Populus trichocarpa]	324	254	1.00E-63	78.4	40.7	47.2	predicted protein	gbpln	Populus trichocarpa	AT3G02700.1 | Symbols: | NC domain-containing protein-related | chr3:581727-582813 REVERSE LENGTH=252	324	252	7.00E-63	77.8	40.7	48.8
Rsa1.0_01733.1.g29391.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01733.1.g29392.t5	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	2024	1491	0	73.7	37.3	46.7	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G48660.1 | Symbols: | Auxin-responsive GH3 family protein | chr1:17995948-17997972 REVERSE LENGTH=573	2024	573	0	28.3	17.8	21.9
Rsa1.0_01733.1.g29393.t1	gb|EOA38625.1| hypothetical protein CARUB_v10010489mg [Capsella rubella]	161	167	9.00E-69	103.7	81.4	87.0	hypothetical protein CARUB_v10010489mg	gbpln	Capsella rubella	AT1G10530.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G60010.1); Has 143 Blast hits to 143 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 143; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:3471805-3472526 REVERSE LENGTH=166	161	166	5.00E-69	103.1	77.6	85.1
Rsa1.0_01733.1.g29394.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01733.1.g29395.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01733.1.g29396.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	176	1311	7.00E-16	744.9	27.3	37.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170	176	170	8.00E-14	96.6	24.4	39.2
Rsa1.0_01733.1.g29397.t1	ref|XP_002889811.1| zinc finger protein 5, ZFP5 [Arabidopsis lyrata subsp. lyrata] gi|297335653|gb|EFH66070.1| zinc finger protein 5, ZFP5 [Arabidopsis lyrata subsp. lyrata]	204	205	7.00E-83	100.5	85.3	92.6	zinc finger protein 5, ZFP5	gbpln	Arabidopsis lyrata	AT1G10480.1 | Symbols: ZFP5 | zinc finger protein 5 | chr1:3449734-3450369 FORWARD LENGTH=211	204	211	3.00E-82	103.4	82.8	90.7
Rsa1.0_01733.1.g29398.t1	gb|ACQ44224.1| unknown [Arabis alpina]	133	291	5.00E-34	218.8	54.9	72.9	unknown	gbpln	Arabis alpina	AT1G31150.1 | Symbols: | Domain of unknown function (DUF1985) | chr1:11120097-11122412 FORWARD LENGTH=673	133	673	4.00E-11	506.0	29.3	51.9
Rsa1.0_01734.1.g29399.t1	gb|AAD23707.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	288	466	5.00E-88	161.8	61.1	70.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01734.1.g29400.t3	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	819	672	2.00E-40	82.1	11.8	17.0	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01734.1.g29401.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01734.1.g29402.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1167	1142	0	97.9	53.6	66.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1167	575	3.00E-61	49.3	12.8	19.8
Rsa1.0_01734.1.g29403.t1	dbj|BAJ33712.1| unnamed protein product [Thellungiella halophila]	471	456	0	96.8	73.0	83.7	unnamed protein product	----	----	AT1G05530.1 | Symbols: UGT75B2, UGT2 | UDP-glucosyl transferase 75B2 | chr1:1636496-1637863 REVERSE LENGTH=455	471	455	0	96.6	76.0	85.4
Rsa1.0_01734.1.g29404.t5	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	678	578	2.00E-57	85.3	17.3	23.2	hypothetical protein 27.t00126	gbpln	Brassica oleracea	AT1G60780.1 | Symbols: HAP13 | Clathrin adaptor complexes medium subunit family protein | chr1:22369289-22371885 REVERSE LENGTH=428	678	428	1.00E-49	63.1	14.7	15.0
Rsa1.0_01734.1.g29405.t1	gb|AAD25596.1| putative helicase [Arabidopsis thaliana]	138	1219	3.00E-33	883.3	50.0	68.8	putative helicase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01734.1.g29406.t1	gb|AAG51081.1|AC027032_1 hypothetical protein [Arabidopsis thaliana]	224	1678	5.00E-72	749.1	58.0	71.4	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01735.1.g29407.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01735.1.g29408.t1	gb|EOA31501.1| hypothetical protein CARUB_v10014687mg [Capsella rubella]	189	198	2.00E-20	104.8	27.0	27.0	hypothetical protein CARUB_v10014687mg	gbpln	Capsella rubella	AT3G05000.1 | Symbols: | Transport protein particle (TRAPP) component | chr3:1387444-1388697 REVERSE LENGTH=173	189	173	3.00E-22	91.5	29.6	31.7
Rsa1.0_01735.1.g29409.t1	ref|NP_188953.1| receptor like protein 38 [Arabidopsis thaliana] gi|9294202|dbj|BAB02104.1| disease resistance protein [Arabidopsis thaliana] gi|332643199|gb|AEE76720.1| receptor like protein 38 [Arabidopsis thaliana]	764	784	0	102.6	67.8	80.0	receptor like protein 38	gbpln	Arabidopsis thaliana	AT3G23120.1 | Symbols: AtRLP38, RLP38 | receptor like protein 38 | chr3:8227222-8229576 REVERSE LENGTH=784	764	784	0	102.6	67.8	80.0
Rsa1.0_01735.1.g29410.t2	gb|EOA32218.1| hypothetical protein CARUB_v10015477mg [Capsella rubella]	745	743	0	99.7	55.2	63.5	hypothetical protein CARUB_v10015477mg	gbpln	Capsella rubella	AT3G23120.1 | Symbols: AtRLP38, RLP38 | receptor like protein 38 | chr3:8227222-8229576 REVERSE LENGTH=784	745	784	1.00E-166	105.2	50.2	60.4
Rsa1.0_01735.1.g29411.t1	dbj|BAB02101.1| unnamed protein product [Arabidopsis thaliana]	345	374	1.00E-136	108.4	75.9	82.3	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G23090.1 | Symbols: | TPX2 (targeting protein for Xklp2) protein family | chr3:8214533-8216983 REVERSE LENGTH=338	345	338	1.00E-138	98.0	75.9	82.3
Rsa1.0_01735.1.g29412.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01735.1.g29413.t1	ref|XP_002885543.1| hypothetical protein ARALYDRAFT_319027 [Arabidopsis lyrata subsp. lyrata] gi|297331383|gb|EFH61802.1| hypothetical protein ARALYDRAFT_319027 [Arabidopsis lyrata subsp. lyrata]	419	427	1.00E-154	101.9	68.5	77.6	hypothetical protein ARALYDRAFT_319027	gbpln	Arabidopsis lyrata	AT3G23080.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr3:8207612-8209181 REVERSE LENGTH=419	419	419	2.33E-156	100.0	68.5	76.6
Rsa1.0_01735.1.g29414.t1	ref|XP_002883397.1| hypothetical protein ARALYDRAFT_898801 [Arabidopsis lyrata subsp. lyrata] gi|297329237|gb|EFH59656.1| hypothetical protein ARALYDRAFT_898801 [Arabidopsis lyrata subsp. lyrata]	822	873	0	106.2	79.7	87.1	hypothetical protein ARALYDRAFT_898801	gbpln	Arabidopsis lyrata	AT3G23070.1 | Symbols: ATCFM3A, CFM3A | CRM family member 3A | chr3:8203548-8207243 FORWARD LENGTH=881	822	881	0	107.2	76.5	83.6
Rsa1.0_01736.1.g29415.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1363	1342	0	98.5	49.7	68.3	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1363	1262	2.00E-82	92.6	12.8	20.2
Rsa1.0_01736.1.g29416.t1	ref|XP_002874744.1| hypothetical protein ARALYDRAFT_490024 [Arabidopsis lyrata subsp. lyrata] gi|297320581|gb|EFH51003.1| hypothetical protein ARALYDRAFT_490024 [Arabidopsis lyrata subsp. lyrata]	326	331	1.00E-114	101.5	89.3	91.4	hypothetical protein ARALYDRAFT_490024	gbpln	Arabidopsis lyrata	AT4G12050.1 | Symbols: | Predicted AT-hook DNA-binding family protein | chr4:7220139-7221158 REVERSE LENGTH=339	326	339	1.00E-108	104.0	85.6	87.7
Rsa1.0_01736.1.g29417.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01736.1.g29418.t3	gb|ABD65624.1| hypothetical protein 23.t00036 [Brassica oleracea]	841	842	1.00E-107	100.1	37.7	55.4	hypothetical protein 23.t00036	gbpln	Brassica oleracea	AT2G07240.1 | Symbols: | cysteine-type peptidases;cysteine-type peptidases | chr2:3007102-3011701 REVERSE LENGTH=874	841	874	3.00E-33	103.9	11.1	16.3
Rsa1.0_01736.1.g29419.t1	ref|XP_002867283.1| hypothetical protein ARALYDRAFT_913296 [Arabidopsis lyrata subsp. lyrata] gi|297313119|gb|EFH43542.1| hypothetical protein ARALYDRAFT_913296 [Arabidopsis lyrata subsp. lyrata]	269	394	1.00E-71	146.5	50.2	67.3	hypothetical protein ARALYDRAFT_913296	gbpln	Arabidopsis lyrata	AT2G24700.1 | Symbols: | Transcriptional factor B3 family protein | chr2:10513049-10515288 REVERSE LENGTH=555	269	555	1.00E-55	206.3	40.9	61.7
Rsa1.0_01736.1.g29420.t1	gb|EOA14157.1| hypothetical protein CARUB_v10027303mg [Capsella rubella]	98	152	8.00E-16	155.1	39.8	59.2	hypothetical protein CARUB_v10027303mg	gbpln	Capsella rubella	AT5G33393.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:12656430-12658588 REVERSE LENGTH=435	98	435	7.00E-17	443.9	35.7	48.0
Rsa1.0_01737.1.g29421.t1	ref|XP_002884561.1| hypothetical protein ARALYDRAFT_317476 [Arabidopsis lyrata subsp. lyrata] gi|297330401|gb|EFH60820.1| hypothetical protein ARALYDRAFT_317476 [Arabidopsis lyrata subsp. lyrata]	368	554	2.33E-156	150.5	71.2	76.1	hypothetical protein ARALYDRAFT_317476	gbpln	Arabidopsis lyrata	AT3G06140.1 | Symbols: | RING/U-box superfamily protein | chr3:1856993-1858777 REVERSE LENGTH=359	368	359	1.00E-143	97.6	69.8	75.0
Rsa1.0_01737.1.g29422.t1	ref|XP_002884560.1| hypothetical protein ARALYDRAFT_477915 [Arabidopsis lyrata subsp. lyrata] gi|297330400|gb|EFH60819.1| hypothetical protein ARALYDRAFT_477915 [Arabidopsis lyrata subsp. lyrata]	491	445	1.00E-68	90.6	39.9	42.2	hypothetical protein ARALYDRAFT_477915	gbpln	Arabidopsis lyrata	AT3G06130.2 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1853193-1854673 REVERSE LENGTH=349	491	349	2.00E-67	71.1	40.9	43.6
Rsa1.0_01737.1.g29423.t1	gb|EOA11961.1| hypothetical protein CARUB_v10012751mg [Capsella rubella]	191	202	1.00E-92	105.8	89.5	94.2	hypothetical protein CARUB_v10012751mg	gbpln	Capsella rubella	AT3G06120.1 | Symbols: MUTE | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:1846531-1848016 FORWARD LENGTH=202	191	202	6.00E-93	105.8	90.1	93.2
Rsa1.0_01737.1.g29424.t2	gb|EOA31511.1| hypothetical protein CARUB_v10014699mg [Capsella rubella]	211	195	1.00E-88	92.4	76.8	83.4	hypothetical protein CARUB_v10014699mg	gbpln	Capsella rubella	AT3G06110.3 | Symbols: MKP2 | MAPK phosphatase 2 | chr3:1843517-1844577 FORWARD LENGTH=167	211	167	2.00E-84	79.1	69.2	74.4
Rsa1.0_01737.1.g29425.t1	ref|NP_566271.1| putative aquaporin NIP7-1 [Arabidopsis thaliana] gi|62512177|sp|Q8LAI1.2|NIP71_ARATH RecName: Full=Probable aquaporin NIP7-1; AltName: Full=NOD26-like intrinsic protein 7-1; Short=AtNIP7;1 gi|91806383|gb|ABE65919.1| major intrinsic family protein/MIP family protein [Arabidopsis thaliana] gi|332640822|gb|AEE74343.1| putative aquaporin NIP7-1 [Arabidopsis thaliana]	272	275	1.00E-126	101.1	83.8	89.7	putative aquaporin NIP7-1	gbpln	Arabidopsis thaliana	AT3G06100.1 | Symbols: NLM6, NLM8, NIP7;1 | NOD26-like intrinsic protein 7;1 | chr3:1841388-1842934 REVERSE LENGTH=275	272	275	1.00E-128	101.1	83.8	89.7

Rsa1.0_01737.1.g29426.t1	ref|NP_187260.1| uncharacterized protein [Arabidopsis thaliana] gi|6862913|gb|AAF30302.1|AC018907_2 hypothetical protein [Arabidopsis thaliana] gi|93007368|gb|ABE97187.1| hypothetical protein At3g06090 [Arabidopsis thaliana] gi|332640821|gb|AEE74342.1| uncharacterized protein AT3G06090 [Arabidopsis thaliana]	78	79	3.00E-20	101.3	65.4	79.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G06090.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: flower, leaf, seed; EXPRESSED DURING: petal differentiation and expansion stage, LP.08 eight leaves visible, E expanded cotyledon stage; Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:1840773-1841012 FORWARD LENGTH=79	78	79	5.00E-23	101.3	65.4	79.5
Rsa1.0_01738.1.g29427.t3	gb|AAD17409.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1403	1347	0	96.0	41.8	54.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1403	1262	5.00E-99	90.0	12.6	20.3
Rsa1.0_01738.1.g29428.t1	ref|XP_002878518.1| EMB2221 [Arabidopsis lyrata subsp. lyrata] gi|297324356|gb|EFH54777.1| EMB2221 [Arabidopsis lyrata subsp. lyrata]	98	1104	6.00E-14	1126.5	45.9	50.0	EMB2221	gbpln	Arabidopsis lyrata	AT3G63460.2 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:23431009-23437241 REVERSE LENGTH=1102	98	1102	1.00E-15	1124.5	44.9	49.0
Rsa1.0_01738.1.g29429.t1	ref|XP_002884534.1| hypothetical protein ARALYDRAFT_477873 [Arabidopsis lyrata subsp. lyrata] gi|297330374|gb|EFH60793.1| hypothetical protein ARALYDRAFT_477873 [Arabidopsis lyrata subsp. lyrata]	641	940	0	146.6	67.9	76.1	hypothetical protein ARALYDRAFT_477873	gbpln	Arabidopsis lyrata	AT3G05790.1 | Symbols: LON4 | lon protease 4 | chr3:1720154-1725182 REVERSE LENGTH=942	641	942	0	147.0	66.8	74.9
Rsa1.0_01738.1.g29430.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01738.1.g29431.t3	dbj|BAA85462.1| transposon-like ORF [Brassica rapa]	350	703	1.00E-108	200.9	61.7	72.0	transposon-like ORF	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_01738.1.g29432.t1	#	#	#	#	#	#	#	-	----	----	AT2G17420.1 | Symbols: NTRA, ATNTRA, NTR2 | NADPH-dependent thioredoxin reductase A | chr2:7564357-7566219 FORWARD LENGTH=378	369	378	4.00E-11	102.4	12.5	16.5
Rsa1.0_01738.1.g29433.t1	ref|XP_002884533.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297330373|gb|EFH60792.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	261	923	1.00E-110	353.6	77.4	86.6	predicted protein	gbpln	Arabidopsis lyrata	AT3G05780.1 | Symbols: LON3 | lon protease 3 | chr3:1714941-1719608 REVERSE LENGTH=924	261	924	1.00E-112	354.0	76.6	86.6
Rsa1.0_01738.1.g29434.t1	ref|XP_002884534.1| hypothetical protein ARALYDRAFT_477873 [Arabidopsis lyrata subsp. lyrata] gi|297330374|gb|EFH60793.1| hypothetical protein ARALYDRAFT_477873 [Arabidopsis lyrata subsp. lyrata]	148	940	1.00E-29	635.1	47.3	55.4	hypothetical protein ARALYDRAFT_477873	gbpln	Arabidopsis lyrata	AT3G05790.1 | Symbols: LON4 | lon protease 4 | chr3:1720154-1725182 REVERSE LENGTH=942	148	942	3.00E-30	636.5	44.6	52.7
Rsa1.0_01738.1.g29435.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1442	1496	0	103.7	58.0	70.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1442	1262	1.00E-141	87.5	16.4	23.0
Rsa1.0_01738.1.g29436.t2	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1496	1485	0	99.3	42.6	58.4	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1496	158	8.00E-25	10.6	3.3	5.4
Rsa1.0_01739.1.g29437.t1	gb|AAD25819.1| hypothetical protein [Arabidopsis thaliana]	376	349	3.00E-88	92.8	50.3	59.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G22050.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:9376684-9377552 FORWARD LENGTH=258	376	258	7.00E-68	68.6	38.0	44.7
Rsa1.0_01739.1.g29438.t2	gb|AEB33726.1| EARLY FLOWERING 3 [Brassica rapa]	658	628	0	95.4	70.4	75.5	EARLY FLOWERING 3	gbpln	Brassica rapa	AT2G25930.1 | Symbols: ELF3, PYK20 | hydroxyproline-rich glycoprotein family protein | chr2:11059459-11063178 FORWARD LENGTH=695	658	695	1.00E-171	105.6	65.7	73.9
Rsa1.0_01739.1.g29439.t1	ref|XP_002880728.1| alpha-vacuolar processing enzyme [Arabidopsis lyrata subsp. lyrata] gi|297326567|gb|EFH56987.1| alpha-vacuolar processing enzyme [Arabidopsis lyrata subsp. lyrata]	488	479	0	98.2	84.4	90.8	alpha-vacuolar processing enzyme	gbpln	Arabidopsis lyrata	AT2G25940.1 | Symbols: ALPHA-VPE, ALPHAVPE | alpha-vacuolar processing enzyme | chr2:11063496-11066020 REVERSE LENGTH=478	488	478	0	98.0	83.0	91.0
Rsa1.0_01739.1.g29440.t1	ref|XP_002880729.1| hypothetical protein ARALYDRAFT_481452 [Arabidopsis lyrata subsp. lyrata] gi|297326568|gb|EFH56988.1| hypothetical protein ARALYDRAFT_481452 [Arabidopsis lyrata subsp. lyrata]	633	634	0	100.2	79.5	83.4	hypothetical protein ARALYDRAFT_481452	gbpln	Arabidopsis lyrata	AT2G25970.1 | Symbols: | KH domain-containing protein | chr2:11071844-11075604 REVERSE LENGTH=632	633	632	0	99.8	79.0	83.1

Rsa1.0_01739.1.g29441.t1	ref|NP_849854.1| MATE efflux family protein [Arabidopsis thaliana] gi|12597760|gb|AAG60073.1|AC013288_7 MATE efflux family protein, putative [Arabidopsis thaliana] gi|332196432|gb|AEE34553.1| MATE efflux family protein [Arabidopsis thaliana]	483	482	0	99.8	84.7	94.2	MATE efflux family protein	gbpln	Arabidopsis thaliana	AT1G66760.2 | Symbols: | MATE efflux family protein | chr1:24902110-24904213 FORWARD LENGTH=482	483	482	0	99.8	84.7	94.2
Rsa1.0_01739.1.g29442.t1	emb|CAN80895.1| hypothetical protein VITISV_031817 [Vitis vinifera]	184	324	2.00E-73	176.1	67.4	83.7	hypothetical protein VITISV_031817	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01739.1.g29443.t1	gb|ABA18104.1| putative plasma membrane ATPase [Capsella rubella] gi|482548056|gb|EOA12258.1| hypothetical protein CARUB_v10008027mg [Capsella rubella]	616	948	0	153.9	74.0	76.8	putative plasma membrane ATPase	gbpln	Capsella rubella	AT3G42640.1 | Symbols: AHA8, HA8 | H(+)-ATPase 8 | chr3:14724309-14728062 FORWARD LENGTH=948	616	948	0	153.9	74.2	76.6
Rsa1.0_01740.1.g29444.t1	gb|EOA29874.1| hypothetical protein CARUB_v10012970mg [Capsella rubella]	107	840	3.00E-22	785.0	44.9	54.2	hypothetical protein CARUB_v10012970mg	gbpln	Capsella rubella	AT3G19840.1 | Symbols: ATPRP40C, PRP40C | pre-mRNA-processing protein 40C | chr3:6891228-6897227 FORWARD LENGTH=835	107	835	2.00E-23	780.4	42.1	52.3
Rsa1.0_01740.1.g29445.t1	dbj|BAJ34141.1| unnamed protein product [Thellungiella halophila]	542	561	0	103.5	84.9	93.9	unnamed protein product	----	----	AT3G19850.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr3:6898383-6901157 REVERSE LENGTH=554	542	554	0	102.2	82.5	90.2
Rsa1.0_01740.1.g29446.t1	gb|EOA13622.1| hypothetical protein CARUB_v10026692mg [Capsella rubella]	622	350	0	56.3	49.2	52.6	hypothetical protein CARUB_v10026692mg	gbpln	Capsella rubella	AT5G50960.1 | Symbols: NBP35, ATNBP35 | nucleotide binding protein 35 | chr5:20734267-20735824 FORWARD LENGTH=350	622	350	0	56.3	48.4	52.6
Rsa1.0_01740.1.g29447.t1	ref|XP_002883209.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297329049|gb|EFH59468.1| binding protein [Arabidopsis lyrata subsp. lyrata]	1100	1118	0	101.6	82.5	91.2	binding protein	gbpln	Arabidopsis lyrata	AT3G19870.1 | Symbols: | unknown protein; Has 84 Blast hits to 64 proteins in 35 species: Archae - 0; Bacteria - 0; Metazoa - 31; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 29 (source: NCBI BLink). | chr3:6907481-6911115 FORWARD LENGTH=1090	1100	1090	0	99.1	79.5	88.0
Rsa1.0_01740.1.g29448.t1	gb|EOA31982.1| hypothetical protein CARUB_v10015243mg [Capsella rubella]	416	416	1.00E-116	100.0	59.6	68.3	hypothetical protein CARUB_v10015243mg	gbpln	Capsella rubella	AT3G20030.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:6990254-6991462 FORWARD LENGTH=402	416	402	1.00E-115	96.6	56.3	66.8
Rsa1.0_01740.1.g29449.t1	ref|XP_002885344.1| hypothetical protein ARALYDRAFT_898385 [Arabidopsis lyrata subsp. lyrata] gi|297331184|gb|EFH61603.1| hypothetical protein ARALYDRAFT_898385 [Arabidopsis lyrata subsp. lyrata]	560	554	0	98.9	86.3	91.6	hypothetical protein ARALYDRAFT_898385	gbpln	Arabidopsis lyrata	AT3G19895.1 | Symbols: | RING/U-box superfamily protein | chr3:6917530-6921211 REVERSE LENGTH=554	560	554	0	98.9	85.7	91.1
Rsa1.0_01740.1.g29450.t1	ref|XP_002885345.1| hypothetical protein ARALYDRAFT_479508 [Arabidopsis lyrata subsp. lyrata] gi|297331185|gb|EFH61604.1| hypothetical protein ARALYDRAFT_479508 [Arabidopsis lyrata subsp. lyrata]	224	223	1.00E-108	99.6	88.4	92.9	hypothetical protein ARALYDRAFT_479508	gbpln	Arabidopsis lyrata	AT3G19900.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3067 (InterPro:IPR021420); Has 276 Blast hits to 276 proteins in 83 species: Archae - 0; Bacteria - 112; Metazoa - 0; Fungi - 2; Plants - 59; Viruses - 0; Other Eukaryotes - 103 (source: NCBI BLink). | chr3:6922852-6924557 REVERSE LENGTH=222	224	222	1.00E-106	99.1	85.7	91.1
Rsa1.0_01740.1.g29451.t1	ref|NP_566651.1| E3 ubiquitin ligase BIG BROTHER-like protein [Arabidopsis thaliana] gi|75335434|sp|Q9LT17.1|BBR_ARATH RecName: Full=E3 ubiquitin ligase BIG BROTHER-related; Short=AtBBR gi|11994203|dbj|BAB01306.1| unnamed protein product [Arabidopsis thaliana] gi|15010578|gb|AAK73948.1| AT3g19910/MPN9_15 [Arabidopsis thaliana] gi|15028363|gb|AAK76658.1| unknown protein [Arabidopsis thaliana] gi|19310707|gb|AAL85084.1| unknown protein [Arabidopsis thaliana] gi|332642786|gb|AEE76307.1| E3 ubiquitin ligase BIG BROTHER-like protein [Arabidopsis thaliana]	330	340	1.00E-126	103.0	79.1	87.6	E3 ubiquitin ligase BIG BROTHER-like protein	gbpln	Arabidopsis thaliana	AT3G19910.1 | Symbols: | RING/U-box superfamily protein | chr3:6926497-6929324 FORWARD LENGTH=340	330	340	1.00E-129	103.0	79.1	87.6

<table>
<tr><td>Rsa1.0_01740.1.g29452.t1</td><td>dbj|BAC43081.1| unknown protein [Arabidopsis thaliana] gi|28951003|gb|AAO63425.1| At3g19920 [Arabidopsis thaliana]</td><td>208</td><td>416</td><td>2.00E-63</td><td>200.0</td><td>59.1</td><td>70.2</td><td>unknown protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19920.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64230.1); Has 217 Blast hits to 217 proteins in 16 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 215; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:6929840-6931771 REVERSE LENGTH=416</td><td>208</td><td>416</td><td>7.00E-66</td><td>200.0</td><td>59.1</td><td>70.2</td></tr>
<tr><td>Rsa1.0_01740.1.g29453.t1</td><td>ref|NP_188627.1| sugar transport protein 4 [Arabidopsis thaliana] gi|75340022|sp|Q39228.1|STP4_ARATH RecName: Full=Sugar transport protein 4; AltName: Full=Hexose transporter 4 gi|13605906|gb|AAK32938.1|AF367352_1 AT3g19930/MPN9_17 [Arabidopsis thaliana] gi|16226824|gb|AAL16272.1|AF428342_1 AT3g19930/MPN9_17 [Arabidopsis thaliana] gi|16524|emb|CAA47325.1| sugar transport protein [Arabidopsis thaliana] gi|11994205|dbj|BAB01308.1| monosaccharide transporter STP4 [Arabidopsis thaliana] gi|22137154|gb|AAM91422.1| AT3g19930/MPN9_17 [Arabidopsis thaliana] gi|332642788|gb|AEE76309.1| sugar transport protein 4 [Arabidopsis thaliana]</td><td>514</td><td>514</td><td>0</td><td>100.0</td><td>93.2</td><td>97.5</td><td>sugar transport protein 4</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G19930.1 | Symbols: STP4, ATSTP4 | sugar transporter 4 | chr3:6935048-6936841 FORWARD LENGTH=514</td><td>514</td><td>514</td><td>0</td><td>100.0</td><td>93.2</td><td>97.5</td></tr>
<tr><td>Rsa1.0_01741.1.g29454.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01741.1.g29455.t5</td><td>sp|P04796.2|G3PC_SINAL RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product [Sinapis alba]</td><td>212</td><td>338</td><td>3.00E-24</td><td>159.4</td><td>35.4</td><td>44.3</td><td>RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic gi|21143|emb|CAA27844.1| unnamed protein product</td><td>gbpln</td><td>Sinapis alba</td><td>AT3G04120.1 | Symbols: GAPC, GAPC-1, GAPC1 | glyceraldehyde-3-phosphate dehydrogenase C subunit 1 | chr3:1081077-1083131 FORWARD LENGTH=338</td><td>212</td><td>338</td><td>1.00E-25</td><td>159.4</td><td>26.4</td><td>29.7</td></tr>
<tr><td>Rsa1.0_01741.1.g29456.t1</td><td>ref|XP_002870534.1| hypothetical protein ARALYDRAFT_493723 [Arabidopsis lyrata subsp. lyrata] gi|297316370|gb|EFH46793.1| hypothetical protein ARALYDRAFT_493723 [Arabidopsis lyrata subsp. lyrata]</td><td>97</td><td>225</td><td>6.00E-26</td><td>232.0</td><td>71.1</td><td>75.3</td><td>hypothetical protein ARALYDRAFT_493723</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G37475.1 | Symbols: | Translation initiation factor eIF3 subunit | chr5:14866328-14867749 REVERSE LENGTH=225</td><td>97</td><td>225</td><td>8.00E-28</td><td>232.0</td><td>68.0</td><td>75.3</td></tr>
<tr><td>Rsa1.0_01741.1.g29457.t1</td><td>dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>279</td><td>777</td><td>6.00E-21</td><td>278.5</td><td>30.5</td><td>53.0</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01741.1.g29458.t3</td><td>emb|CAA69271.1| lectin receptor kinase [Arabidopsis thaliana]</td><td>123</td><td>544</td><td>2.00E-46</td><td>442.3</td><td>75.6</td><td>83.7</td><td>lectin receptor kinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G48720.1 | Symbols: | unknown protein; Has 229 Blast hits to 229 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 228; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18018148-18018441 FORWARD LENGTH=97</td><td>123</td><td>97</td><td>2.00E-38</td><td>78.9</td><td>57.7</td><td>65.9</td></tr>
<tr><td>Rsa1.0_01741.1.g29459.t1</td><td>gb|EOA25185.1| hypothetical protein CARUB_v10018496mg [Capsella rubella]</td><td>264</td><td>418</td><td>7.00E-75</td><td>158.3</td><td>54.2</td><td>76.5</td><td>hypothetical protein CARUB_v10018496mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G19260.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr1:6657260-6659569 REVERSE LENGTH=769</td><td>264</td><td>769</td><td>2.00E-74</td><td>291.3</td><td>54.9</td><td>76.5</td></tr>
<tr><td>Rsa1.0_01742.1.g29460.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01742.1.g29461.t1</td><td>ref|NP_566617.1| F-box protein [Arabidopsis thaliana] gi|75273931|sp|Q9LSA5.1|FBK62_ARATH RecName: Full=F-box/kelch-repeat protein At3g18720 gi|9293895|dbj|BAB01798.1| unnamed protein product [Arabidopsis thaliana] gi|91806439|gb|ABE65947.1| F-box family protein [Arabidopsis thaliana] gi|332642615|gb|AEE76136.1| F-box protein [Arabidopsis thaliana]</td><td>540</td><td>380</td><td>5.00E-70</td><td>70.4</td><td>30.2</td><td>36.3</td><td>F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G18720.1 | Symbols: | F-box family protein | chr3:6444433-6445751 REVERSE LENGTH=380</td><td>540</td><td>380</td><td>1.00E-72</td><td>70.4</td><td>30.2</td><td>36.3</td></tr>
<tr><td>Rsa1.0_01742.1.g29462.t1</td><td>pdb|4EPL|A Chain A, Crystal Structure Of Arabidopsis Thaliana Gh3.11 (Jar1) In Complex With Ja-Ile</td><td>578</td><td>581</td><td>0</td><td>100.5</td><td>89.4</td><td>95.5</td><td>Chain A, Crystal Structure Of Arabidopsis Thaliana Gh3.11 (Jar1) In Complex With Ja-Ile</td><td>----</td><td>----</td><td>AT2G46370.4 | Symbols: JAR1 | Auxin-responsive GH3 family protein | chr2:19034233-19036369 FORWARD LENGTH=586</td><td>578</td><td>586</td><td>0</td><td>101.4</td><td>89.4</td><td>95.5</td></tr>
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Rsa1.0_01742.1.g29463.t1	ref|XP_002880237.1| hypothetical protein ARALYDRAFT_904092 [Arabidopsis lyrata subsp. lyrata] gi|297326076|gb|EFH56496.1| hypothetical protein ARALYDRAFT_904092 [Arabidopsis lyrata subsp. lyrata]	128	127	1.00E-24	99.2	53.1	61.7	hypothetical protein ARALYDRAFT_904092	gbpln	Arabidopsis lyrata	AT2G46375.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G61660.1); Has 12 Blast hits to 12 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:19037958-19038329 FORWARD LENGTH=123	128	123	5.00E-27	96.1	48.4	57.0
Rsa1.0_01742.1.g29464.t1	ref|XP_002882061.1| hypothetical protein ARALYDRAFT_483794 [Arabidopsis lyrata subsp. lyrata] gi|297327900|gb|EFH58320.1| hypothetical protein ARALYDRAFT_483794 [Arabidopsis lyrata subsp. lyrata]	292	293	1.00E-111	100.3	72.3	84.6	hypothetical protein ARALYDRAFT_483794	gbpln	Arabidopsis lyrata	AT2G46400.1 | Symbols: WRKY46, ATWRKY46 | WRKY DNA-binding protein 46 | chr2:19043676-19044754 REVERSE LENGTH=295	292	295	1.00E-111	101.0	71.9	84.2
Rsa1.0_01743.1.g29465.t1	ref|XP_002877441.1| hypothetical protein ARALYDRAFT_484970 [Arabidopsis lyrata subsp. lyrata] gi|297323279|gb|EFH53700.1| hypothetical protein ARALYDRAFT_484970 [Arabidopsis lyrata subsp. lyrata]	385	397	1.00E-157	103.1	79.0	84.9	hypothetical protein ARALYDRAFT_484970	gbpln	Arabidopsis lyrata	AT3G45900.1 | Symbols: | Ribonuclease P protein subunit P38-related | chr3:16874566-16875984 REVERSE LENGTH=389	385	389	1.00E-153	101.0	76.9	83.4
Rsa1.0_01743.1.g29466.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_01743.1.g29467.t1	ref|XP_002877448.1| hypothetical protein ARALYDRAFT_484979 [Arabidopsis lyrata subsp. lyrata] gi|297323286|gb|EFH53707.1| hypothetical protein ARALYDRAFT_484979 [Arabidopsis lyrata subsp. lyrata]	130	137	1.00E-65	105.4	93.1	96.2	hypothetical protein ARALYDRAFT_484979	gbpln	Arabidopsis lyrata	AT3G46000.1 | Symbols: ADF2 | actin depolymerizing factor 2 | chr3:16907743-16908822 REVERSE LENGTH=137	130	137	9.00E-68	105.4	92.3	96.2
Rsa1.0_01743.1.g29468.t2	ref|NP_172256.1| 40S ribosomal protein S15a-1 [Arabidopsis thaliana] gi|15238544|ref|NP_200793.1| 40S ribosomal protein S15a-1 [Arabidopsis thaliana] gi|42571385|ref|NP_973783.1| 40S ribosomal protein S15a-1 [Arabidopsis thaliana] gi|297796939|ref|XP_002866354.1| RPS15A [Arabidopsis lyrata subsp. lyrata] gi|297815756|ref|XP_002875761.1| RPS15A [Arabidopsis lyrata subsp. lyrata] gi|297849076|ref|XP_002892419.1| RPS15A [Arabidopsis lyrata subsp. lyrata] gi|1173218|sp|P42798.2|R15A1_ARATH RecName: Full=40S ribosomal protein S15a-1 gi|8439890|gb|AAF75076.1|AC007583_12 Strong similarity to 40S ribosomal protein S15A from Arabidopsis thaliana gb|L27461. EST gb|R30315 comes from this gene [Arabidopsis thaliana] gi|12083302|gb|AAG48810.1|AF332447_1 putative ribosomal protein S15 [Arabidopsis thaliana] gi|13430744|gb|AAK25994.1|AF360284_1 putative ribosomal protein S15 [Arabidopsis thaliana] gi|14423370|gb|AAK62367.1|AF386922_1 40S ribosomal protein S15A [Arabidopsis thaliana] gi|440824|gb|AAA61608.1| ribosomal	161	130	5.00E-68	80.7	78.3	78.9	40S ribosomal protein S15a-1	gbpln	Arabidopsis lyrata	AT5G59850.1 | Symbols: | Ribosomal protein S8 family protein | chr5:24112499-24113084 REVERSE LENGTH=130	161	130	2.00E-70	80.7	78.3	78.9
Rsa1.0_01743.1.g29469.t1	dbj|BAJ34629.1| unnamed protein product [Thellungiella halophila]	216	216	1.00E-121	100.0	98.1	99.5	unnamed protein product	----	----	AT3G46060.3 | Symbols: ARA3 | RAB GTPase homolog 8A | chr3:16917908-16919740 FORWARD LENGTH=216	216	216	1.00E-117	100.0	93.1	94.9
Rsa1.0_01743.1.g29470.t1	ref|NP_190194.1| C2H2-type zinc finger protein [Arabidopsis thaliana] gi|75335605|sp|Q9LX85.1|ZAT8_ARATH RecName: Full=Zinc finger protein ZAT8 gi|7798996|emb|CAB90935.1| zinc finger-like protein [Arabidopsis thaliana] gi|225898695|dbj|BAH30478.1| hypothetical protein [Arabidopsis thaliana] gi|332644589|gb|AEE78110.1| zinc finger protein ZAT8 [Arabidopsis thaliana]	219	164	4.00E-51	74.9	49.8	57.1	C2H2-type zinc finger protein	gbpln	Arabidopsis thaliana	AT3G46080.1 | Symbols: | C2H2-type zinc finger family protein | chr3:16922753-16923247 REVERSE LENGTH=164	219	164	1.00E-53	74.9	49.8	57.1

Rsa1.0_01743.1.g29471.t1	ref|XP_002875766.1| hypothetical protein ARALYDRAFT_347705 [Arabidopsis lyrata subsp. lyrata] gi|297321604|gb|EFH52025.1| hypothetical protein ARALYDRAFT_347705 [Arabidopsis lyrata subsp. lyrata]	248	258	1.00E-114	104.0	87.9	92.7	hypothetical protein ARALYDRAFT_347705	gbpln	Arabidopsis lyrata	AT3G46130.1 | Symbols: ATMYB48, ATMYB48-3, MYB48 | myb domain protein 48 | chr3:16945433-16946376 FORWARD LENGTH=256	248	256	1.00E-114	103.2	86.7	92.7
Rsa1.0_01743.1.g29472.t2	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1310	1475	0	112.6	52.4	68.3	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1310	1262	0	96.3	27.8	33.0
Rsa1.0_01743.1.g29473.t1	ref|XP_002873380.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319217|gb|EFH49639.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata]	455	497	1.00E-131	109.2	54.3	67.5	IBR domain-containing protein	gbpln	Arabidopsis lyrata	AT5G08730.1 | Symbols: ATARI16, ARI16 | IBR domain-containing protein | chr5:2845824-2847415 REVERSE LENGTH=500	455	500	1.00E-127	109.9	52.1	66.8
Rsa1.0_01743.1.g29474.t1	ref|NP_190202.1| protein kinase-related protein [Arabidopsis thaliana] gi|7799004|emb|CAB90943.1| protein kinase-like [Arabidopsis thaliana] gi|332644602|gb|AEE78123.1| protein kinase-related protein [Arabidopsis thaliana]	386	393	3.00E-89	101.8	46.9	60.9	protein kinase-related protein	gbpln	Arabidopsis thaliana	AT3G46160.1 | Symbols: | Protein kinase superfamily protein | chr3:16950955-16952136 FORWARD LENGTH=393	386	393	8.00E-92	101.8	46.9	60.9
Rsa1.0_01744.1.g29475.t1	gb|EOA14702.1| hypothetical protein CARUB_v10027979mg [Capsella rubella]	292	286	3.00E-97	97.9	62.0	72.6	hypothetical protein CARUB_v10027979mg	gbpln	Capsella rubella	AT5G58890.1 | Symbols: AGL82 | AGAMOUS-like 82 | chr5:23780832-23781716 FORWARD LENGTH=294	292	294	7.00E-98	100.7	62.3	74.3
Rsa1.0_01744.1.g29476.t1	ref|XP_002866297.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297312132|gb|EFH42556.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	289	286	1.00E-145	99.0	87.9	91.3	myb family transcription factor	gbpln	Arabidopsis lyrata	AT5G58900.1 | Symbols: | Homeodomain-like transcriptional regulator | chr5:23783275-23784667 REVERSE LENGTH=288	289	288	2.33E-156	99.7	87.2	92.4
Rsa1.0_01744.1.g29477.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01744.1.g29478.t1	gb|ABE66261.1| laccase/diphenol oxidase [Arabidopsis thaliana]	528	530	0	100.4	89.6	94.3	laccase/diphenol oxidase	gbpln	Arabidopsis thaliana	AT5G58910.1 | Symbols: LAC16 | laccase 16 | chr5:23789522-23791681 REVERSE LENGTH=523	528	523	0	99.1	88.4	93.0
Rsa1.0_01744.1.g29479.t1	gb|EOA14859.1| hypothetical protein CARUB_v10028180mg [Capsella rubella]	506	535	1.00E-161	105.7	74.9	82.6	hypothetical protein CARUB_v10028180mg	gbpln	Capsella rubella	AT5G58930.1 | Symbols: | Protein of unknown function (DUF740) | chr5:23794529-23796094 REVERSE LENGTH=521	506	521	1.00E-162	103.0	71.3	79.4
Rsa1.0_01745.1.g29480.t1	gb|AAM64688.1| unknown [Arabidopsis thaliana]	102	192	8.00E-19	188.2	56.9	66.7	unknown	gbpln	Arabidopsis thaliana	AT2G18290.1 | Symbols: APC10 | anaphase promoting complex 10 | chr2:7948522-7950096 REVERSE LENGTH=192	102	192	1.00E-21	188.2	56.9	66.7
Rsa1.0_01745.1.g29481.t1	ref|XP_002886164.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] gi|297332004|gb|EFH62423.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	333	337	1.00E-144	101.2	80.2	88.3	basic helix-loop-helix family protein	gbpln	Arabidopsis lyrata	AT2G18300.2 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:7953022-7954446 REVERSE LENGTH=337	333	337	2.33E-156	101.2	79.9	88.0
Rsa1.0_01745.1.g29482.t1	ref|XP_002883907.1| hypothetical protein ARALYDRAFT_899779 [Arabidopsis lyrata subsp. lyrata] gi|297329747|gb|EFH60166.1| hypothetical protein ARALYDRAFT_899779 [Arabidopsis lyrata subsp. lyrata]	207	312	5.00E-51	150.7	61.8	72.0	hypothetical protein ARALYDRAFT_899779	gbpln	Arabidopsis lyrata	AT1G36675.1 | Symbols: | glycine-rich protein | chr1:13867568-13869490 FORWARD LENGTH=268	207	268	3.00E-29	129.5	43.0	48.3
Rsa1.0_01745.1.g29483.t3	gb|EOA31794.1| hypothetical protein CARUB_v10015016mg [Capsella rubella]	316	82	5.00E-29	25.9	23.7	24.7	hypothetical protein CARUB_v10015016mg	gbpln	Capsella rubella	AT2G18328.1 | Symbols: ATRL4, RL4 | RAD-like 4 | chr2:7964478-7964711 FORWARD LENGTH=77	316	77	7.00E-26	24.4	16.1	18.0
Rsa1.0_01746.1.g29484.t1	gb|AAF79374.1|AC007887_33 F15O4.30 [Arabidopsis thaliana]	407	1180	2.00E-73	289.9	44.7	57.5	F15O4.30	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01746.1.g29485.t2	gb|ABD65100.1| hypothetical protein 31.t00077 [Brassica oleracea]	364	391	4.00E-69	107.4	33.5	38.5	hypothetical protein 31.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01746.1.g29486.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	653	1142	5.00E-97	174.9	28.6	40.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G56550.1 | Symbols: RXGT1 | RhamnoGalacturonan speciﬁc Xylosyltransferase 1 | chr1:21185836-21188070 REVERSE LENGTH=383	653	383	2.00E-87	58.7	23.4	25.9
Rsa1.0_01746.1.g29487.t1	dbj|BAJ34592.1| unnamed protein product [Thellungiella halophila]	181	685	3.00E-59	378.5	60.8	63.0	unnamed protein product	----	----	AT2G18700.1 | Symbols: ATTPS11, TPS11, ATTPSB | trehalose phosphatase/synthase 11 | chr2:8109043-8111799 FORWARD LENGTH=862	181	862	3.00E-57	476.2	55.8	61.9

Rsa1.0_01746.1.g29488.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1324	1142	0	86.3	24.8	29.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43722.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28730.1); Has 924 Blast hits to 912 proteins in 109 species: Archae - 0; Bacteria - 0; Metazoa - 222; Fungi - 31; Plants - 661; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:16496403-16497377 FORWARD LENGTH=324	1324	324	4.00E-35	24.5	6.3	9.1
Rsa1.0_01747.1.g29489.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01747.1.g29490.t1	gb|EOA40319.1| hypothetical protein CARUB_v10009045mg [Capsella rubella]	497	469	0	94.4	77.5	85.5	hypothetical protein CARUB_v10009045mg	gbpln	Capsella rubella	AT1G12160.1 | Symbols: | Flavin-binding monooxygenase family protein | chr1:4126068-4128090 FORWARD LENGTH=468	497	468	0	94.2	78.3	85.9
Rsa1.0_01747.1.g29491.t1	ref|XP_002892677.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338519|gb|EFH68936.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	548	548	0	100.0	87.8	93.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G12150.1 | Symbols: | Plant protein of unknown function (DUF827) | chr1:4123530-4125328 REVERSE LENGTH=548	548	548	0	100.0	87.4	93.2
Rsa1.0_01747.1.g29492.t2	ref|XP_002889917.1| flavin-containing monooxygenase family protein [Arabidopsis lyrata subsp. lyrata] gi|297335759|gb|EFH66176.1| flavin-containing monooxygenase family protein [Arabidopsis lyrata subsp. lyrata]	546	459	0	84.1	71.1	77.3	flavin-containing monooxygenase family protein	gbpln	Arabidopsis lyrata	AT1G12140.1 | Symbols: FMO GS-OX5 | flavin-monooxygenase glucosinolate S-oxygenase 5 | chr1:4121386-4123366 FORWARD LENGTH=459	546	459	0	84.1	70.7	77.7
Rsa1.0_01747.1.g29493.t1	gb|EOA40154.1| hypothetical protein CARUB_v10008871mg, partial [Capsella rubella]	414	516	2.33E-156	124.6	76.3	83.6	hypothetical protein CARUB_v10008871mg, partial	gbpln	Capsella rubella	AT1G12120.1 | Symbols: | Plant protein of unknown function (DUF863) | chr1:4114933-4116469 REVERSE LENGTH=483	414	483	1.00E-145	116.7	74.9	82.4
Rsa1.0_01747.1.g29494.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01747.1.g29495.t1	gb|AEA35415.1| nitrate transporter [Brassica rapa subsp. chinensis]	275	589	1.00E-149	214.2	91.6	96.7	nitrate transporter	gbpln	Brassica rapa	AT1G12110.1 | Symbols: NRT1.1, CHL1-1, NRT1, B-1, ATNRT1, CHL1 | nitrate transporter 1.1 | chr1:4105341-4109290 FORWARD LENGTH=590	275	590	2.33E-156	214.5	90.2	94.5
Rsa1.0_01747.1.g29496.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1206	1307	0	108.4	59.5	73.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1206	1262	1.00E-99	104.6	16.3	26.1
Rsa1.0_01747.1.g29497.t1	gb|AEA35415.1| nitrate transporter [Brassica rapa subsp. chinensis]	306	589	1.00E-163	192.5	94.8	97.4	nitrate transporter	gbpln	Brassica rapa	AT1G12110.1 | Symbols: NRT1.1, CHL1-1, NRT1, B-1, ATNRT1, CHL1 | nitrate transporter 1.1 | chr1:4105341-4109290 FORWARD LENGTH=590	306	590	1.00E-161	192.8	92.5	95.8
Rsa1.0_01747.1.g29498.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01747.1.g29499.t1	gb|EOA39456.1| hypothetical protein CARUB_v10012658mg [Capsella rubella]	132	132	1.00E-62	100.0	92.4	96.2	hypothetical protein CARUB_v10012658mg	gbpln	Capsella rubella	AT1G12100.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:4095246-4095845 FORWARD LENGTH=132	132	132	2.00E-53	100.0	79.5	85.6
Rsa1.0_01748.1.g29500.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01748.1.g29501.t1	ref|XP_002878418.1| CYP78A9 [Arabidopsis lyrata subsp. lyrata] gi|297324256|gb|EFH54677.1| CYP78A9 [Arabidopsis lyrata subsp. lyrata]	536	541	0	100.9	91.8	95.7	CYP78A9	gbpln	Arabidopsis lyrata	AT3G61880.2 | Symbols: CYP78A9 | cytochrome p450 78a9 | chr3:22905979-22907890 REVERSE LENGTH=555	536	555	0	103.5	91.0	95.1
Rsa1.0_01748.1.g29502.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01748.1.g29503.t1	gb|EOA24679.1| hypothetical protein CARUB_v10017952mg [Capsella rubella]	228	238	4.00E-88	104.4	79.8	91.2	hypothetical protein CARUB_v10017952mg	gbpln	Capsella rubella	AT3G61890.1 | Symbols: ATHB-12, ATHB12, HB-12 | homeobox 12 | chr3:22914346-22915239 REVERSE LENGTH=235	228	235	2.00E-89	103.1	81.6	92.5
Rsa1.0_01748.1.g29504.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1367	1475	0	107.9	55.7	69.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1367	1262	1.00E-151	92.3	19.8	24.7
Rsa1.0_01749.1.g29505.t1	gb|EOA38390.1| hypothetical protein CARUB_v10009956mg, partial [Capsella rubella]	253	280	1.00E-117	110.7	84.6	90.1	hypothetical protein CARUB_v10009956mg, partial	gbpln	Capsella rubella	AT1G11380.1 | Symbols: | PLAC8 family protein | chr1:3832695-3833921 FORWARD LENGTH=254	253	254	1.00E-116	100.4	84.6	89.3
Rsa1.0_01749.1.g29506.t1	gb|EOA36827.1| hypothetical protein CARUB_v10008587mg [Capsella rubella]	619	624	0	100.8	89.5	93.9	hypothetical protein CARUB_v10008587mg	gbpln	Capsella rubella	AT1G11390.1 | Symbols: | Protein kinase superfamily protein | chr1:3834762-3837305 REVERSE LENGTH=624	619	624	0	100.8	89.8	93.9
Rsa1.0_01749.1.g29507.t3	gb|EOA38471.1| hypothetical protein CARUB_v10010225mg [Capsella rubella] gi|482574285|gb|EOA38472.1| hypothetical protein CARUB_v10010225mg [Capsella rubella]	232	227	7.00E-88	97.8	74.6	81.0	hypothetical protein CARUB_v10010225mg	gbpln	Capsella rubella	AT1G11400.3 | Symbols: PYM | partner of Y14-MAGO | chr1:3838777-3839978 FORWARD LENGTH=204	232	204	1.00E-81	87.9	70.3	75.0
Rsa1.0_01749.1.g29508.t1	gb|EOA33511.1| hypothetical protein CARUB_v10019805mg, partial [Capsella rubella]	821	824	0	100.4	67.6	78.7	hypothetical protein CARUB_v10019805mg, partial	gbpln	Capsella rubella	AT1G80740.1 | Symbols: CMT1, DMT4 | chromomethylase 1 | chr1:30342394-30346831 FORWARD LENGTH=791	821	791	0	96.3	62.9	75.9

Rsa1.0_01749.1.g29509.t2	ref|NP_172601.2| putative S-locus lectin protein kinase [Arabidopsis thaliana] gi|332190599|gb|AEE28720.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	841	901	0	107.1	72.7	81.3	putative S-locus lectin protein kinase	gbpln	Arabidopsis thaliana	AT1G11340.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:3814116-3817420 REVERSE LENGTH=901	841	901	0	107.1	72.7	81.3
Rsa1.0_01749.1.g29510.t1	ref|NP_172601.2| putative S-locus lectin protein kinase [Arabidopsis thaliana] gi|332190599|gb|AEE28720.1| G-type lectin S-receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	672	901	0	134.1	71.0	80.1	putative S-locus lectin protein kinase	gbpln	Arabidopsis thaliana	AT1G11340.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:3814116-3817420 REVERSE LENGTH=901	672	901	0	134.1	71.0	80.1
Rsa1.0_01749.1.g29511.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01749.1.g29512.t1	ref|XP_002889866.1| hypothetical protein ARALYDRAFT_471279 [Arabidopsis lyrata subsp. lyrata] gi|297335708|gb|EFH66125.1| hypothetical protein ARALYDRAFT_471279 [Arabidopsis lyrata subsp. lyrata]	820	842	0	102.7	86.3	92.4	hypothetical protein ARALYDRAFT_471279	gbpln	Arabidopsis lyrata	AT1G11410.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:3841286-3844284 FORWARD LENGTH=845	820	845	0	103.0	85.6	92.3
Rsa1.0_01749.1.g29513.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01749.1.g29514.t1	gb|AAM65001.1| DAG protein, putative [Arabidopsis thaliana]	236	232	1.00E-106	98.3	81.8	86.4	DAG protein, putative	gbpln	Arabidopsis thaliana	AT1G11430.1 | Symbols: | plastid developmental protein DAG, putative | chr1:3847273-3848938 FORWARD LENGTH=232	236	232	1.00E-108	98.3	81.4	86.4
Rsa1.0_01749.1.g29515.t1	gb|EOA38039.1| hypothetical protein CARUB_v10009508mg [Capsella rubella]	336	366	1.00E-114	108.9	70.8	82.7	hypothetical protein CARUB_v10009508mg	gbpln	Capsella rubella	AT1G11440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT3G29075.1); Has 19337 Blast hits to 8589 proteins in 488 species: Archae - 26; Bacteria - 641; Metazoa - 7852; Fungi - 2167; Plants - 955; Viruses - 616; Other Eukaryotes - 7080 (source: NCBI BLink). | chr1:3849418-3850509 FORWARD LENGTH=363	336	363	1.00E-111	108.0	71.7	83.3
Rsa1.0_01750.1.g29516.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01750.1.g29517.t1	dbj|BAB01217.1| Ta11 non-LTR retroelement protein-like [Arabidopsis thaliana] gi|67633664|gb|AAY78756.1| putative zinc finger protein [Arabidopsis thaliana]	430	487	5.00E-86	113.3	45.3	64.2	Ta11 non-LTR retroelement protein-like	gbpln	Arabidopsis thaliana	AT5G18636.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25200.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:6211268-6212371 FORWARD LENGTH=367	430	367	9.00E-14	85.3	10.7	18.1
Rsa1.0_01750.1.g29518.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	943	1365	0	144.8	38.3	50.9	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	943	575	5.00E-45	61.0	13.5	19.6
Rsa1.0_01750.1.g29519.t2	gb|EOA13819.1| hypothetical protein CARUB_v10026917mg [Capsella rubella]	195	283	6.00E-55	145.1	56.9	61.5	hypothetical protein CARUB_v10026917mg	gbpln	Capsella rubella	AT5G64670.1 | Symbols: | Ribosomal protein L18e/L15 superfamily protein | chr5:25852535-25853880 REVERSE LENGTH=281	195	281	2.00E-56	144.1	55.9	61.5
Rsa1.0_01750.1.g29520.t1	ref|XP_002873981.1| hypothetical protein ARALYDRAFT_488911 [Arabidopsis lyrata subsp. lyrata] gi|297319818|gb|EFH50240.1| hypothetical protein ARALYDRAFT_488911 [Arabidopsis lyrata subsp. lyrata]	111	110	4.00E-56	99.1	94.6	98.2	hypothetical protein ARALYDRAFT_488911	gbpln	Arabidopsis lyrata	AT5G20090.2 | Symbols: | Uncharacterised protein family (UPF0041) | chr5:6787246-6788000 REVERSE LENGTH=110	111	110	8.00E-59	99.1	93.7	98.2
Rsa1.0_01750.1.g29521.t1	gb|EOA20671.1| hypothetical protein CARUB_v10000983mg [Capsella rubella]	406	438	0	107.9	86.2	92.4	hypothetical protein CARUB_v10000983mg	gbpln	Capsella rubella	AT5G20070.1 | Symbols: ATNUDT19, ATNUDX19, NUDX19 | nudix hydrolase homolog 19 | chr5:6779893-6782308 FORWARD LENGTH=438	406	438	0	107.9	84.7	92.4
Rsa1.0_01750.1.g29522.t1	ref|XP_002285029.2| PREDICTED: probable receptor-like protein kinase At5g20050 [Vitis vinifera]	721	720	0	99.9	65.2	77.9	PREDICTED: probable receptor-like protein kinase At5g20050	gbpln	Vitis vinifera	AT5G20050.1 | Symbols: | Protein kinase superfamily protein | chr5:6774381-6775739 FORWARD LENGTH=452	721	452	0	62.7	51.2	54.8
Rsa1.0_01750.1.g29523.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01751.1.g29524.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	371	478	1.00E-119	128.8	51.8	73.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	371	746	2.00E-87	201.1	39.9	56.9
Rsa1.0_01751.1.g29525.t2	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1081	1307	0	120.9	58.5	72.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1081	1262	8.00E-59	116.7	12.7	21.3
Rsa1.0_01751.1.g29526.t1	gb|EOA29920.1| hypothetical protein CARUB_v10013014mg [Capsella rubella]	784	785	0	100.1	93.0	97.2	hypothetical protein CARUB_v10013014mg	gbpln	Capsella rubella	AT3G23430.1 | Symbols: PHO1, ATPHO1 | phosphate 1 | chr3:8387818-8393242 REVERSE LENGTH=782	784	782	0	99.7	88.8	93.5

Rsa1.0_01751.1.g29527.t1	gb|AAK94425.1|AF398144_1 60S ribosomal protein L144 [Brassica rapa subsp. pekinensis]	105	119	2.00E−52	113.3	100.0	100.0	60S ribosomal protein L144	gbpln	Brassica rapa	AT4G14320.1 | Symbols: | Zinc−binding ribosomal protein family protein | chr4:8242684−8243805 REVERSE LENGTH=105	105	105	4.00E−53	100.0	96.2	97.1
Rsa1.0_01751.1.g29528.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01751.1.g29529.t1	gb|EOA32791.1| hypothetical protein CARUB_v10016101mg [Capsella rubella]	162	205	1.00E−44	126.5	75.9	82.7	hypothetical protein CARUB_v10016101mg	gbpln	Capsella rubella	AT3G23380.1 | Symbols: RIC5 | ROP−interactive CRIB motif−containing protein 5 | chr3:8373947−8374708 FORWARD LENGTH=193	162	193	2.00E−42	119.1	74.1	81.5
Rsa1.0_01752.1.g29530.t1	gb|EOA16428.1| hypothetical protein CARUB_v10004579mg, partial [Capsella rubella]	288	527	1.00E−42	183.0	36.8	48.6	hypothetical protein CARUB_v10004579mg, partial	gbpln	Capsella rubella	AT5G41540.1 | Symbols: | Disease resistance protein (TIR−NBS−LRR class) family | chr5:16612659−16616063 REVERSE LENGTH=1038	288	1038	6.00E−39	360.4	33.3	44.8
Rsa1.0_01752.1.g29531.t1	ref|NP_568596.1| Nucleotide−sugar transporter family protein [Arabidopsis thaliana] gi|79329489|ref|NP_001031992.1| Nucleotide−sugar transporter family protein [Arabidopsis thaliana] gi|75156053|sp|Q8LGE9.1|CSTR1_ARATH RecName: Full=CMP−sialic acid transporter 1; Short=CMP−SA−Tr 1; Short=CMP−Sia−Tr 1 gi|21536568|gb|AAM60900.1| CMP−sialic acid transporter−like protein [Arabidopsis thaliana] gi|28393785|gb|AAO42302.1| putative CMP−sialic acid transporter [Arabidopsis thaliana] gi|28973255|gb|AAO63952.1| putative CMP−sialic acid transporter [Arabidopsis thaliana] gi|332007339|gb|AED94722.1| Nucleotide−sugar transporter family protein [Arabidopsis thaliana] gi|332007340|gb|AED94723.1| Nucleotide−sugar transporter family protein [Arabidopsis thaliana]	337	340	1.00E−176	100.9	92.3	96.1	Nucleotide−sugar transporter family protein	gbpln	Arabidopsis thaliana	AT5G41760.2 | Symbols: | Nucleotide−sugar transporter family protein | chr5:16706978−16709204 FORWARD LENGTH=340	337	340	1.00E−179	100.9	92.3	96.1
Rsa1.0_01752.1.g29532.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01752.1.g29533.t1	ref|XP_002870617.1| hypothetical protein ARALYDRAFT_916024 [Arabidopsis lyrata subsp. lyrata] gi|297316453|gb|EFH46876.1| hypothetical protein ARALYDRAFT_916024 [Arabidopsis lyrata subsp. lyrata]	762	704	0	92.4	84.9	89.0	hypothetical protein ARALYDRAFT_916024	gbpln	Arabidopsis lyrata	AT5G41770.1 | Symbols: | crooked neck protein, putative / cell cycle protein, putative | chr5:16718021−16720936 FORWARD LENGTH=705	762	705	0	92.5	85.3	89.2
Rsa1.0_01752.1.g29534.t1	gb|AAL75752.1|AC037197_10 Putative copia−type polyprotein [Oryza sativa Japonica Group] gi|31429795|gb|AAP51797.1| retrotransposon protein, putative, Ty1−copia subclass [Oryza sativa Japonica Group]	195	1350	1.00E−28	692.3	34.4	53.8	Putative copia−type polyprotein	gbpln	Oryza sativa	AT3G21000.1 | Symbols: | Gag−Pol−related retrotransposon family protein | chr3:7363921−7365138 FORWARD LENGTH=405	195	405	2.00E−13	207.7	26.7	45.1
Rsa1.0_01752.1.g29535.t1	ref|NP_198994.2| COP1−interactive protein 1 [Arabidopsis thaliana] gi|332007346|gb|AED94729.1| COP1−interactive protein 1 [Arabidopsis thaliana]	1638	1586	0	96.8	69.8	81.6	COP1−interactive protein 1	gbpln	Arabidopsis thaliana	AT5G41790.1 | Symbols: CIP1 | COP1−interactive protein 1 | chr5:16727530−16732391 FORWARD LENGTH=1586	1638	1586	0	96.8	69.8	81.6
Rsa1.0_01753.1.g29536.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01753.1.g29537.t1	ref|NP_189492.1| AAA−type ATPase family protein [Arabidopsis thaliana] gi|9294101|dbj|BAB01953.1| unnamed protein product [Arabidopsis thaliana] gi|20466452|gb|AAM20543.1| unknown protein [Arabidopsis thaliana] gi|332643933|gb|AEE77454.1| AAA−type ATPase family protein [Arabidopsis thaliana]	284	530	1.00E−130	186.6	76.4	87.0	AAA−type ATPase family protein	gbpln	Arabidopsis thaliana	AT3G28510.1 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:10685656−10687248 FORWARD LENGTH=530	284	530	1.00E−132	186.6	76.4	87.0
Rsa1.0_01753.1.g29538.t1	ref|NP_189492.1| AAA−type ATPase family protein [Arabidopsis thaliana] gi|9294101|dbj|BAB01953.1| unnamed protein product [Arabidopsis thaliana] gi|20466452|gb|AAM20543.1| unknown protein [Arabidopsis thaliana] gi|332643933|gb|AEE77454.1| AAA−type ATPase family protein [Arabidopsis thaliana]	230	530	1.00E−74	230.4	67.0	72.6	AAA−type ATPase family protein	gbpln	Arabidopsis thaliana	AT3G28510.1 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:10685656−10687248 FORWARD LENGTH=530	230	530	3.00E−77	230.4	67.0	72.6
Rsa1.0_01753.1.g29539.t1	gb|EOA23918.1| hypothetical protein CARUB_v10017133mg [Capsella rubella]	477	477	0	100.0	89.3	93.1	hypothetical protein CARUB_v10017133mg	gbpln	Capsella rubella	AT3G28690.2 | Symbols: | Protein kinase superfamily protein | chr3:10755481−10757494 FORWARD LENGTH=453	477	453	0	95.0	86.0	88.5

Rsa1.0_01753.1.g29540.t1	ref|XP_002891255.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297337097|gb|EFH67514.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	166	210	4.00E−46	126.5	58.4	67.5	NLI interacting factor family protein	gbpln	Arabidopsis lyrata	AT1G43610.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:16424578-16425345 FORWARD LENGTH=255	166	255	1.00E−46	153.6	56.6	64.5
Rsa1.0_01753.1.g29541.t1	ref|NP_001189996.1| V-type proton ATPase subunit d2 [Arabidopsis thaliana] gi|332643961|gb|AEE77482.1| V-type proton ATPase subunit d2 [Arabidopsis thaliana]	80	343	8.00E−29	428.8	76.3	77.5	V-type proton ATPase subunit d2	gbpln	Arabidopsis thaliana	AT3G28715.2 | Symbols: | ATPase, V0/A0 complex, subunit C/D | chr3:10778025-10780350 FORWARD LENGTH=343	80	343	1.00E−31	428.8	76.3	77.5
Rsa1.0_01753.1.g29542.t2	ref|NP_189512.1| V-type proton ATPase subunit d1 [Arabidopsis thaliana] gi|297815166|ref|XP_002875466.1| hypothetical protein ARALYDRAFT_484647 [Arabidopsis lyrata subsp. lyrata] gi|297818484|ref|XP_002877125.1| hypothetical protein ARALYDRAFT_484645 [Arabidopsis lyrata subsp. lyrata] gi|12230764|sp|Q9LJI5.1|VA0D1_ARATH RecName: Full=V-type proton ATPase subunit d1; Short=V-ATPase subunit d1; AltName: Full=Vacuolar H(+)-ATPase subunit d isoform 1; AltName: Full=Vacuolar proton pump subunit d1 gi|9294284|dbj|BAB02186.1| vacuolar ATP synthase subunit AC39 [Arabidopsis thaliana] gi|14532480|gb|AAK63968.1| AT3g28710/MZN14_20 [Arabidopsis thaliana] gi|18655357|gb|AAL76134.1| AT3g28710/MZN14_20 [Arabidopsis thaliana] gi|23297057|gb|AAN13080.1| putative adenosine triphosphatase [Arabidopsis thaliana] gi|297321304|gb|EFH51725.1| hypothetical protein ARALYDRAFT_484647 [Arabidopsis lyrata subsp. lyrata] gi|297322963|gb|EFH53384.1| hypothetical protein ARALYDRAFT_484645 [Arabidopsis lyrata subsp. lyrata]	267	351	1.00E−156	131.5	99.6	99.6	V-type proton ATPase subunit d1	gbpln	Arabidopsis lyrata	AT3G28710.1 | Symbols: | ATPase, V0/A0 complex, subunit C/D | chr3:10773144-10775594 REVERSE LENGTH=351	267	351	1.00E−158	131.5	99.6	99.6
Rsa1.0_01753.1.g29543.t1	gb|EOA23621.1| hypothetical protein CARUB_v10016819mg [Capsella rubella]	665	647	0	97.3	88.0	92.8	hypothetical protein CARUB_v10016819mg	gbpln	Capsella rubella	AT3G28730.1 | Symbols: ATHMG, SSRP1, NFD, HMG | high mobility group | chr3:10784954-10788498 FORWARD LENGTH=646	665	646	0	97.1	85.6	91.3
Rsa1.0_01753.1.g29544.t1	ref|XP_002877127.1| cytochrome P450 family protein [Arabidopsis lyrata subsp. lyrata] gi|297322965|gb|EFH53386.1| cytochrome P450 family protein [Arabidopsis lyrata subsp. lyrata]	450	501	0	111.3	80.9	88.2	cytochrome P450 family protein	gbpln	Arabidopsis lyrata	AT3G28740.1 | Symbols: CYP81D1 | Cytochrome P450 superfamily protein | chr3:10788764-10790552 REVERSE LENGTH=509	450	509	0	113.1	78.9	88.0
Rsa1.0_01753.1.g29545.t1	ref|XP_002877127.1| cytochrome P450 family protein [Arabidopsis lyrata subsp. lyrata] gi|297322965|gb|EFH53386.1| cytochrome P450 family protein [Arabidopsis lyrata subsp. lyrata]	211	501	3.00E−49	237.4	41.7	46.9	cytochrome P450 family protein	gbpln	Arabidopsis lyrata	AT3G28740.1 | Symbols: CYP81D1 | Cytochrome P450 superfamily protein | chr3:10788764-10790552 REVERSE LENGTH=509	211	509	5.00E−51	241.2	41.7	46.4
Rsa1.0_01753.1.g29546.t1	gb|EOA23379.1| hypothetical protein CARUB_v10016555mg [Capsella rubella]	2480	2419	1.00E−130	97.5	14.4	18.0	hypothetical protein CARUB_v10016555mg	gbpln	Capsella rubella	AT3G28770.1 | Symbols: | Protein of unknown function (DUF1216) | chr3:10796716-10803237 FORWARD LENGTH=2081	2480	2081	1.00E−131	83.9	13.9	17.2
Rsa1.0_01753.1.g29547.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01754.1.g29548.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01754.1.g29549.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01754.1.g29550.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01754.1.g29551.t1	ref|XP_002879182.1| hypothetical protein ARALYDRAFT_901825 [Arabidopsis lyrata subsp. lyrata] gi|297325021|gb|EFH55441.1| hypothetical protein ARALYDRAFT_901825 [Arabidopsis lyrata subsp. lyrata]	153	154	1.00E−65	100.7	93.5	94.1	hypothetical protein ARALYDRAFT_901825	gbpln	Arabidopsis lyrata	AT2G28720.1 | Symbols: | Histone superfamily protein | chr2:12327043-12327498 FORWARD LENGTH=151	153	151	4.00E−67	98.7	91.5	92.8

Rsa1.0_01754.1.g29552.t1	ref|XP_002879183.1| hypothetical protein ARALYDRAFT_481786 [Arabidopsis lyrata subsp. lyrata] gi|297325022|gb|EFH55442.1| hypothetical protein ARALYDRAFT_481786 [Arabidopsis lyrata subsp. lyrata]	108	107	2.00E-32	99.1	67.6	77.8	hypothetical protein ARALYDRAFT_481786	gbpln	Arabidopsis lyrata	AT1G07795.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G28725.1); Has 38 Blast hits to 38 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:2414438-2414794 FORWARD LENGTH=118	108	118	7.00E-34	109.3	64.8	73.1
Rsa1.0_01754.1.g29553.t1	tpg|DAA40122.1| TPA: histone H4.3 [Zea mays]	103	248	3.00E-52	240.8	100.0	100.0	TPA: histone H4.3	gbenv/gbpln	Zea mays	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352-24146663 REVERSE LENGTH=103	103	103	2.00E-52	100.0	100.0	100.0
Rsa1.0_01754.1.g29554.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01754.1.g29555.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1397	1374	0	98.4	48.3	63.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1397	575	1.00E-128	41.2	16.5	23.0
Rsa1.0_01755.1.g29556.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	297	1838	1.00E-15	618.9	17.5	25.9	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01755.1.g29557.t2	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01755.1.g29558.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1199	1838	0	153.3	48.5	65.2	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01755.1.g29559.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01755.1.g29560.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01755.1.g29561.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	411	1838	2.00E-87	447.2	36.5	42.3	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01755.1.g29562.t1	dbj|BAB03186.1| En/Spm transposon protein-like [Arabidopsis thaliana]	908	1516	0	167.0	40.1	46.3	En/Spm transposon protein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01756.1.g29563.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01756.1.g29564.t1	gb|AAC13582.1| similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana] gi|8843876|dbj|BAA97402.1| mutator-like transposase [Arabidopsis thaliana]	304	806	3.00E-66	265.1	38.8	45.7	similar to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	304	719	5.00E-20	236.5	19.4	30.3
Rsa1.0_01756.1.g29565.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01756.1.g29566.t1	ref|XP_002865565.1| electron carrier/ protein disulfide oxidoreductase [Arabidopsis lyrata subsp. lyrata] gi|297311400|gb|EFH41824.1| electron carrier/ protein disulfide oxidoreductase [Arabidopsis lyrata subsp. lyrata]	330	315	1.00E-161	95.5	85.8	90.3	electron carrier/ protein disulfide oxidoreductase	gbpln	Arabidopsis lyrata	AT5G42150.1 | Symbols: | Glutathione S-transferase family protein | chr5:16846247-16847909 FORWARD LENGTH=315	330	315	1.00E-161	95.5	83.9	89.4
Rsa1.0_01756.1.g29567.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01756.1.g29568.t1	gb|ABD65118.1| hypothetical protein 31.t00031 [Brassica oleracea]	425	467	2.00E-95	109.9	44.5	62.6	hypothetical protein 31.t00031	gbpln	Brassica oleracea	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	425	566	2.00E-29	133.2	27.3	47.1
Rsa1.0_01756.1.g29569.t1	gb|EOA23204.1| hypothetical protein CARUB_v10019007mg [Capsella rubella]	479	477	0	99.6	83.9	89.4	hypothetical protein CARUB_v10019007mg	gbpln	Capsella rubella	AT3G57790.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:21405387-21407088 REVERSE LENGTH=490	479	490	0	102.3	83.5	88.5
Rsa1.0_01756.1.g29570.t1	gb|EOA14533.1| hypothetical protein CARUB_v10027765mg [Capsella rubella]	498	509	0	102.2	82.5	91.0	hypothetical protein CARUB_v10027765mg	gbpln	Capsella rubella	AT5G42450.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:16977297-16978850 FORWARD LENGTH=517	498	517	0	103.8	81.3	90.6
Rsa1.0_01757.1.g29571.t1	emb|CAC37623.1| copia-like polyprotein [Arabidopsis thaliana]	1264	1466	0	116.0	67.6	79.4	copia-like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1264	1262	2.00E-81	99.8	12.1	18.1
Rsa1.0_01757.1.g29572.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01757.1.g29573.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	173	341	1.00E-46	197.1	53.2	72.3	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01757.1.g29574.t1	gb|EOA19271.1| hypothetical protein CARUB_v10000438mg [Capsella rubella]	556	641	0	115.3	73.7	82.4	hypothetical protein CARUB_v10000438mg	gbpln	Capsella rubella	AT4G11440.1 | Symbols: | Mitochondrial substrate carrier family protein | chr4:6955850-6958553 FORWARD LENGTH=628	556	628	0	112.9	71.6	80.0
Rsa1.0_01757.1.g29575.t2	gb|EOA20058.1| hypothetical protein CARUB_v10000333mg [Capsella rubella] gi|482555867|gb|EOA20059.1| hypothetical protein CARUB_v10000333mg [Capsella rubella]	694	713	0	102.7	85.0	90.6	hypothetical protein CARUB_v10000333mg	gbpln	Capsella rubella	AT4G11450.1 | Symbols: | Protein of unknown function (DUF3527) | chr4:6959065-6961223 REVERSE LENGTH=694	694	694	0	100.0	82.9	89.0
Rsa1.0_01758.1.g29576.t1	ref|XP_002889861.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335703|gb|EFH66120.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	442	820	0	185.5	78.3	84.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G11300.1 | Symbols: | protein serine/threonine kinases;protein kinases;ATP binding;sugar binding;kinases;carbohydrate binding | chr1:3794389-3800719 FORWARD LENGTH=1650	442	1650	0	373.3	76.7	83.3

Rsa1.0_01758.1.g29577.t1	ref|XP_002892631.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338473|gb|EFH68890.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	822	822	0	100.0	83.9	90.5	predicted protein	gbpln	Arabidopsis lyrata	AT1G61360.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:22637867-22640974 REVERSE LENGTH=821	822	821	0	99.9	73.6	83.6
Rsa1.0_01758.1.g29578.t2	gb|AAF82204.1|AC067971_12 Contains similarity to protein phosphatase 2C from Arabidopsis thaliana gb|AF085279. It contains a protein phosphatase 2C domain PF|00481 [Arabidopsis thaliana]	434	405	2.00E-37	93.3	24.7	27.4	Contains similarity to protein phosphatase 2C from Arabidopsis thaliana gb|AF085279. It contains a protein phosphatase 2C domain PF|00481	gbpln	Arabidopsis thaliana	AT1G07160.1 | Symbols: | Protein phosphatase 2C family protein | chr1:2198155-2199678 REVERSE LENGTH=380	434	380	6.00E-40	87.6	24.9	27.2
Rsa1.0_01758.1.g29579.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01758.1.g29580.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	532	484	2.00E-68	91.0	28.0	35.2	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01758.1.g29581.t1	gb|EOA23321.1| hypothetical protein CARUB_v10019219mg [Capsella rubella]	401	444	3.00E-90	110.7	48.4	62.1	hypothetical protein CARUB_v10019219mg	gbpln	Capsella rubella	AT2G40925.1 | Symbols: | F-box and associated interaction domains-containing protein | chr2:17074905-17076116 REVERSE LENGTH=403	401	403	3.00E-66	100.5	40.6	55.9
Rsa1.0_01758.1.g29582.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01758.1.g29583.t1	ref|XP_002888093.1| SYP124 [Arabidopsis lyrata subsp. lyrata] gi|297333934|gb|EFH64352.1| SYP124 [Arabidopsis lyrata subsp. lyrata]	298	303	1.00E-160	101.7	92.3	96.6	SYP124	gbpln	Arabidopsis lyrata	AT1G61290.1 | Symbols: SYP124, ATSYP124 | syntaxin of plants 124 | chr1:22605188-22606216 FORWARD LENGTH=303	298	303	1.00E-161	101.7	91.3	96.6
Rsa1.0_01758.1.g29584.t1	ref|XP_002889856.1| hypothetical protein ARALYDRAFT_471255 [Arabidopsis lyrata subsp. lyrata] gi|297335698|gb|EFH66115.1| hypothetical protein ARALYDRAFT_471255 [Arabidopsis lyrata subsp. lyrata]	295	295	1.00E-152	100.0	86.4	94.6	hypothetical protein ARALYDRAFT_471255	gbpln	Arabidopsis lyrata	AT1G11200.1 | Symbols: | Protein of unknown function (DUF300) | chr1:3753896-3755459 FORWARD LENGTH=295	295	295	1.00E-150	100.0	84.1	93.2
Rsa1.0_01758.1.g29585.t1	emb|CBL29241.1| endonuclease precursor [Fourraea alpina]	105	305	7.00E-49	290.5	86.7	90.5	endonuclease precursor	gbpln	Fourraea alpina	AT1G11190.1 | Symbols: BFN1, ENDO1 | bifunctional nuclease i | chr1:3750338-3752696 REVERSE LENGTH=305	105	305	3.00E-45	290.5	84.8	89.5
Rsa1.0_01759.1.g29586.t1	gb|AAD15532.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	426	1274	4.00E-85	299.1	39.4	52.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	426	921	1.00E-45	216.2	24.4	34.3
Rsa1.0_01759.1.g29587.t1	gb|AAD23022.1| En/Spm-like transposon protein [Arabidopsis thaliana]	129	155	3.00E-20	120.2	44.2	58.1	En/Spm-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29588.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29589.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29590.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29591.t2	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	332	704	1.00E-69	212.0	40.1	41.3	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29592.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	300	1838	2.00E-38	612.7	31.0	48.7	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29593.t1	gb|AAD20433.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	138	889	3.00E-38	644.2	52.9	68.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29594.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29595.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1192	940	7.00E-75	78.9	14.0	19.5	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01759.1.g29596.t1	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	345	1864	1.00E-100	540.3	51.0	63.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	ATMG00750.1 | Symbols: ORF119 | GAG/POL/ENV polyprotein | chrM:220830-221189 FORWARD LENGTH=119	345	119	1.00E-13	34.5	8.4	11.3
Rsa1.0_01760.1.g29597.t1	gb|EOA35686.1| hypothetical protein CARUB_v10020913mg, partial [Capsella rubella]	192	223	2.00E-87	116.1	82.3	92.2	hypothetical protein CARUB_v10020913mg, partial	gbpln	Capsella rubella	AT1G54850.1 | Symbols: | HSP20-like chaperones superfamily protein | chr1:20454440-20455994 FORWARD LENGTH=206	192	206	4.00E-88	107.3	79.2	92.7

Rsa1.0_01760.1.g29598.t1	ref|NP_001117518.1| 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Arabidopsis thaliana] gi|327488385|sp|Q0WUA3.2|MENA_ARATH RecName: Full=1,4-dihydroxy-2-naphthoate polyprenyltransferase, chloroplastic; AltName: Full=1,4-dihydroxy-2-naphthoate phytyltransferase; AltName: Full=Protein ABERRANT CHLOROPLAST DEVELOPMENT 4; AltName: Full=menA-like protein; Short=AtMENA; Flags: Precursor gi|332195581|gb|AEE33702.1| 1,4-dihydroxy-2-naphthoate polyprenyltransferase [Arabidopsis thaliana]	416	382	1.00E-177	91.8	76.9	82.9	1,4-dihydroxy-2-naphthoate octaprenyltransferase	gbpln	Arabidopsis thaliana	AT1G60600.2 | Symbols: ABC4 | UbiA prenyltransferase family protein | chr1:22324807-22326759 REVERSE LENGTH=382	416	382	1.00E-179	91.8	76.9	82.9
Rsa1.0_01760.1.g29599.t1	ref|XP_002886605.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297332446|gb|EFH62864.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	339	338	1.00E-149	99.7	81.1	90.3	protein binding protein	gbpln	Arabidopsis lyrata	AT1G60610.3 | Symbols: | SBP (S-ribonuclease binding protein) family protein | chr1:22327999-22329186 REVERSE LENGTH=340	339	340	1.00E-149	100.3	80.2	88.5
Rsa1.0_01760.1.g29600.t1	ref|XP_002888129.1| ATRPAC43 [Arabidopsis lyrata subsp. lyrata] gi|297333970|gb|EFH64388.1| ATRPAC43 [Arabidopsis lyrata subsp. lyrata]	421	385	1.00E-170	91.4	71.3	79.8	ATRPAC43	gbpln	Arabidopsis lyrata	AT1G60620.1 | Symbols: ATRPAC43, RPAC43 | RNA polymerase I subunit 43 | chr1:22331225-22333370 FORWARD LENGTH=385	421	385	1.00E-167	91.4	68.9	79.8
Rsa1.0_01760.1.g29601.t1	emb|CCD74528.1| NAC domain containing protein 23 [Arabidopsis halleri subsp. halleri]	379	334	8.00E-63	88.1	39.6	54.9	NAC domain containing protein 23	gbpln	Arabidopsis halleri	AT1G60280.1 | Symbols: ANAC023, NAC023 | NAC domain containing protein 23 | chr1:22226885-22227928 REVERSE LENGTH=347	379	347	1.00E-63	91.6	39.3	53.3
Rsa1.0_01760.1.g29602.t1	ref|XP_002532706.1| Transcription initiation factor TFIID subunit, putative [Ricinus communis] gi|223527552|gb|EEF29673.1| Transcription initiation factor TFIID subunit, putative [Ricinus communis]	172	205	2.00E-39	119.2	55.2	75.0	Transcription initiation factor TFIID subunit, putative	gbpln	Ricinus communis	AT1G20000.1 | Symbols: TAF11b | TBP-associated factor 11B | chr1:6936898-6937666 REVERSE LENGTH=204	172	204	8.00E-41	118.6	57.0	71.5
Rsa1.0_01760.1.g29603.t1	ref|NP_176262.2| leucine-rich repeat protein kinase-like protein [Arabidopsis thaliana] gi|75147162|sp|Q84MA9.1|Y1063_ARATH RecName: Full=Inactive leucine-rich repeat receptor-like serine/threonine-protein kinase At1g60630; Flags: Precursor gi|30102660|gb|AAP21248.1| At1g60630 [Arabidopsis thaliana] gi|110743167|dbj|BAE99475.1| receptor kinase like protein [Arabidopsis thaliana] gi|224589453|gb|ACN59260.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332195587|gb|AEE33708.1| inactive leucine-rich repeat receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	654	652	0	99.7	80.3	88.5	leucine-rich repeat protein kinase-like protein	gbpln	Arabidopsis thaliana	AT1G60630.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:22334754-22336785 REVERSE LENGTH=652	654	652	0	99.7	80.3	88.5
Rsa1.0_01760.1.g29604.t1	ref|XP_002886603.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332444|gb|EFH62862.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	259	337	2.00E-48	130.1	60.2	68.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G60640.5 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown. | chr1:22337534-22339513 REVERSE LENGTH=298	259	298	2.00E-49	115.1	62.2	71.8
Rsa1.0_01760.1.g29605.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01760.1.g29606.t1	ref|XP_002886602.1| hypothetical protein ARALYDRAFT_893475 [Arabidopsis lyrata subsp. lyrata] gi|297332443|gb|EFH62861.1| hypothetical protein ARALYDRAFT_893475 [Arabidopsis lyrata subsp. lyrata]	168	120	9.00E-46	71.4	53.0	57.7	hypothetical protein ARALYDRAFT_893475	gbpln	Arabidopsis lyrata	AT1G60660.1 | Symbols: B5 #5, ATCB5LP, CB5LP | cytochrome B5-like protein | chr1:22342589-22342954 REVERSE LENGTH=121	168	121	5.00E-48	72.0	54.2	58.9
Rsa1.0_01760.1.g29607.t1	gb|EOA19642.1| hypothetical protein CARUB_v10003012mg [Capsella rubella]	366	390	2.00E-70	106.6	46.7	62.3	hypothetical protein CARUB_v10003012mg	gbpln	Capsella rubella	AT4G04690.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:2373999-2375135 REVERSE LENGTH=378	366	378	8.00E-70	103.3	44.5	60.7
Rsa1.0_01760.1.g29608.t1	gb|AAB71979.1| Hypothetical protein [Arabidopsis thaliana]	248	249	1.00E-100	100.4	73.4	78.6	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G60670.2 | Symbols: | Protein of unknown function (DUF3755) | chr1:22344099-22347140 FORWARD LENGTH=254	248	254	1.00E-102	102.4	73.4	78.6
Rsa1.0_01760.1.g29609.t1	gb|AAB71982.1| Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]	193	342	2.00E-91	177.2	84.5	92.7	Highly similar to auxin-induced protein (aldo/keto reductase family)	gbpln	Arabidopsis thaliana	AT1G60730.3 | Symbols: | NAD(P)-linked oxidoreductase superfamily protein | chr1:22358327-22360082 REVERSE LENGTH=365	193	365	1.00E-93	189.1	84.5	92.7

Rsa1.0_01761.1.g29610.t1	gb|EOA12787.1| hypothetical protein CARUB_v10025731mg [Capsella rubella]	933	2732	0	292.8	46.5	57.9	hypothetical protein CARUB_v10025731mg	gbpln	Capsella rubella	AT4G36150.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:17104776-17108711 FORWARD LENGTH=1179	933	1179	0	126.4	36.5	49.9
Rsa1.0_01761.1.g29611.t1	gb|EOA13143.1| hypothetical protein CARUB_v10026159mg [Capsella rubella]	572	570	0	99.7	92.8	95.8	hypothetical protein CARUB_v10026159mg	gbpln	Capsella rubella	AT5G45275.1 | Symbols: | Major facilitator superfamily protein | chr5:18334476-18337240 REVERSE LENGTH=570	572	570	0	99.7	92.8	95.5
Rsa1.0_01761.1.g29612.t1	gb|EOA19916.1| hypothetical protein CARUB_v10000166mg [Capsella rubella]	125	922	6.00E-14	737.6	38.4	43.2	hypothetical protein CARUB_v10000166mg	gbpln	Capsella rubella	AT5G21150.1 | Symbols: AGO9 | Argonaute family protein | chr5:7193472-7198113 FORWARD LENGTH=896	125	896	1.00E-14	716.8	35.2	42.4
Rsa1.0_01761.1.g29613.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	185	414	8.00E-27	223.8	37.8	41.1	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01761.1.g29614.t2	ref|XP_002863498.1| hypothetical protein ARALYDRAFT_356493 [Arabidopsis lyrata subsp. lyrata] gi|297309333|gb|EFH39757.1| hypothetical protein ARALYDRAFT_356493 [Arabidopsis lyrata subsp. lyrata]	379	496	1.00E-109	130.9	57.5	72.3	hypothetical protein ARALYDRAFT_356493	gbpln	Arabidopsis lyrata	AT5G27220.1 | Symbols: | Frigida-like protein | chr5:9578757-9582752 FORWARD LENGTH=1181	379	1181	2.00E-33	311.6	24.0	35.1
Rsa1.0_01761.1.g29615.t1	ref|XP_002877500.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323338|gb|EFH53759.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	105	136	2.00E-18	129.5	44.8	60.0	predicted protein	gbpln	Arabidopsis lyrata	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	105	320	3.00E-13	304.8	34.3	48.6
Rsa1.0_01762.1.g29616.t1	ref|XP_003632230.1| PREDICTED: calmodulin-related protein isoform 4 [Vitis vinifera]	149	180	2.00E-80	120.8	100.0	100.0	PREDICTED: calmodulin-related protein isoform 4	gbpln	Vitis vinifera	AT2G27030.3 | Symbols: CAM5 | calmodulin 5 | chr2:11532069-11534176 FORWARD LENGTH=181	149	181	2.00E-82	121.5	99.3	100.0
Rsa1.0_01762.1.g29617.t2	gb|AGA95981.1| argonaute 4 [Brassica rapa subsp. pekinensis]	1016	922	0	90.7	87.5	89.7	argonaute 4	gbpln	Brassica rapa	AT2G27040.2 | Symbols: AGO4 | Argonaute family protein | chr2:11536795-11541503 REVERSE LENGTH=924	1016	924	0	90.9	80.1	85.8
Rsa1.0_01762.1.g29618.t1	ref|NP_199404.3| GDSL esterase/lipase [Arabidopsis thaliana] gi|75127073|sp|Q6NMR9.1|GDL84_ARATH RecName: Full=GDSL esterase/lipase At5g45920 gi|38454102|gb|AAR20745.1| At5g45920 [Arabidopsis thaliana] gi|44022121|gb|AAS46640.1| At5g45920 [Arabidopsis thaliana] gi|332007932|gb|AED95315.1| GDSL esterase/lipase [Arabidopsis thaliana]	240	241	1.00E-120	100.4	86.7	91.3	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT5G45920.1 | Symbols: | SGNH hydrolase-type esterase superfamily protein | chr5:18622822-18624677 FORWARD LENGTH=241	240	241	1.00E-122	100.4	86.7	91.3
Rsa1.0_01762.1.g29619.t4	ref|XP_002863442.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] gi|297309277|gb|EFH39701.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	638	374	1.00E-136	58.6	36.1	40.6	GDSL-motif lipase/hydrolase family protein	gbpln	Arabidopsis lyrata	AT5G45910.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:18620420-18622264 REVERSE LENGTH=372	638	372	1.00E-134	58.3	34.8	40.1
Rsa1.0_01762.1.g29620.t4	dbj|BAJ34535.1| unnamed protein product [Thellungiella halophila]	509	552	0	108.4	71.1	83.1	unnamed protein product	----	----	AT3G45680.1 | Symbols: | Major facilitator superfamily protein | chr3:16770995-16772908 FORWARD LENGTH=558	509	558	0	109.6	72.3	83.7
Rsa1.0_01762.1.g29621.t1	ref|XP_002879043.1| hypothetical protein ARALYDRAFT_481588 [Arabidopsis lyrata subsp. lyrata] gi|297324882|gb|EFH55302.1| hypothetical protein ARALYDRAFT_481588 [Arabidopsis lyrata subsp. lyrata]	261	260	1.00E-121	99.6	79.7	89.7	hypothetical protein ARALYDRAFT_481588	gbpln	Arabidopsis lyrata	AT2G27080.2 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:11566383-11567165 FORWARD LENGTH=260	261	260	1.00E-121	99.6	78.2	89.3
Rsa1.0_01763.1.g29622.t1	ref|XP_002889482.1| hypothetical protein ARALYDRAFT_333714 [Arabidopsis lyrata subsp. lyrata] gi|297335324|gb|EFH65741.1| hypothetical protein ARALYDRAFT_333714 [Arabidopsis lyrata subsp. lyrata]	658	671	0	102.0	89.1	93.5	hypothetical protein ARALYDRAFT_333714	gbpln	Arabidopsis lyrata	AT1G03910.1 | Symbols: | EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Cactin protein, cactus-binding domain, C-terminal (InterPro:IPR019134), Cactin, central region (InterPro:IPR018816); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G36815.2); Has 11711 Blast hits to 7382 proteins in 452 species: Archae - 31; Bacteria - 352; Metazoa - 6006; Fungi - 1138; Plants - 599; Viruses - 33; Other Eukaryotes - 3552 (source: NCBI BLink). | chr1:996432-1000231 FORWARD LENGTH=672	658	672	0	102.1	83.0	86.3

Rsa1.0_01763.1.g29623.t2	ref|NP_563695.2| dual specificity kinase 1 [Arabidopsis thaliana] gi|4204297|gb|AAD10678.1| ADK1 [Arabidopsis thaliana] gi|17529246|gb|AAL38850.1| putative protein kinase ADK1 [Arabidopsis thaliana] gi|18700077|gb|AAL77651.1| At1g03930/F21M11_14 [Arabidopsis thaliana] gi|20465967|gb|AAM20169.1| putative protein kinase ADK1 [Arabidopsis thaliana] gi|20855979|gb|AAM26641.1| At1g03930/F21M11_14 [Arabidopsis thaliana] gi|62996988|gb|AAY24538.1| casein kinase 1-like protein 9b [Arabidopsis thaliana] gi|332189514|gb|AEE27635.1| dual specificity kinase 1 [Arabidopsis thaliana]	465	471	0	101.3	84.9	90.5	dual specificity kinase 1	gbpln	Arabidopsis thaliana	AT1G03930.1 | Symbols: ADK1, CKL9ALPHA, CKL9BETA | dual specificity kinase 1 | chr1:1005439-1008118 FORWARD LENGTH=471	465	471	0	101.3	84.9	90.5
Rsa1.0_01763.1.g29624.t1	gb|ABY89660.1| phytochelatin synthase 2 [Noccaea caerulescens]	461	455	0	98.7	86.1	91.1	phytochelatin synthase 2	gbpln	Noccaea caerulescens	AT1G03980.1 | Symbols: ATPCS2, PCS2 | phytochelatin synthase 2 | chr1:1019311-1021871 REVERSE LENGTH=452	461	452	0	98.0	86.3	90.7
Rsa1.0_01763.1.g29625.t11	ref|XP_002892193.1| phosphatidylcholine-sterol O-acyltransferase [Arabidopsis lyrata subsp. lyrata] gi|297338035|gb|EFH68452.1| phosphatidylcholine-sterol O-acyltransferase [Arabidopsis lyrata subsp. lyrata]	727	633	0	87.1	82.3	84.2	phosphatidylcholine-sterol O-acyltransferase	gbpln	Arabidopsis lyrata	AT1G04010.1 | Symbols: PSAT1, ATPSAT1 | phospholipid sterol acyl transferase 1 | chr1:1031703-1036128 REVERSE LENGTH=633	727	633	0	87.1	82.3	84.3
Rsa1.0_01763.1.g29626.t3	gb|ACF35259.1| BARD1 [Arabidopsis thaliana]	443	674	1.00E-154	152.1	63.7	72.0	BARD1	gbpln	Arabidopsis thaliana	AT1G04020.1 | Symbols: ATBARD1, BARD1, ROW1 | breast cancer associated RING 1 | chr1:1036610-1040045 FORWARD LENGTH=714	443	714	1.00E-156	161.2	63.7	72.0
Rsa1.0_01763.1.g29627.t1	gb|EOA32454.1| hypothetical protein CARUB_v10015730mg [Capsella rubella]	514	543	3.00E-90	105.6	39.1	56.6	hypothetical protein CARUB_v10015730mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	514	566	1.00E-89	110.1	36.6	60.5
Rsa1.0_01763.1.g29628.t1	ref|XP_002889489.1| hypothetical protein ARALYDRAFT_333726 [Arabidopsis lyrata subsp. lyrata] gi|297335331|gb|EFH65748.1| hypothetical protein ARALYDRAFT_333726 [Arabidopsis lyrata subsp. lyrata]	405	434	1.00E-124	107.2	70.9	80.2	hypothetical protein ARALYDRAFT_333726	gbpln	Arabidopsis lyrata	AT1G04030.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G44040.1); Has 1835 Blast hits to 1511 proteins in 238 species: Archae - 7; Bacteria - 164; Metazoa - 377; Fungi - 135; Plants - 187; Viruses - 22; Other Eukaryotes - 943 (source: NCBI BLink). | chr1:1040597-1042313 FORWARD LENGTH=434	405	434	1.00E-124	107.2	69.4	79.3
Rsa1.0_01764.1.g29629.t1	gb|ABA95861.1| retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa Japonica Group]	107	304	4.00E-11	284.1	38.3	43.9	retrotransposon protein, putative, Ty1-copia subclass	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_01764.1.g29630.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	161	1485	3.00E-59	922.4	65.8	82.6	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	#	#	#	#	#	#	#
Rsa1.0_01764.1.g29631.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1109	1142	0	103.0	34.1	42.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1109	626	7.00E-30	56.4	9.9	15.8
Rsa1.0_01764.1.g29632.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01764.1.g29633.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	750	627	5.00E-74	83.6	24.5	37.7	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01764.1.g29634.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01765.1.g29635.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01765.1.g29636.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01765.1.g29637.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01765.1.g29638.t1	ref|XP_002893529.1| hypothetical protein ARALYDRAFT_473059 [Arabidopsis lyrata subsp. lyrata] gi|297339371|gb|EFH69788.1| hypothetical protein ARALYDRAFT_473059 [Arabidopsis lyrata subsp. lyrata]	283	331	1.00E-103	117.0	79.9	86.6	hypothetical protein ARALYDRAFT_473059	gbpln	Arabidopsis lyrata	AT1G28400.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G33850.1); Has 45374 Blast hits to 18870 proteins in 668 species: Archae - 72; Bacteria - 1460; Metazoa - 1191; Fungi - 1038; Plants - 174; Viruses - 64; Other Eukaryotes - 41375 (source: NCBI BLink). | chr1:9972732-9973739 REVERSE LENGTH=335	283	335	2.00E-99	118.4	78.8	85.9
Rsa1.0_01765.1.g29639.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01765.1.g29640.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01766.1.g29641.t1	gb|ABD65606.1| hypothetical protein 23.t00002 [Brassica oleracea]	525	433	1.00E-104	82.5	42.1	52.8	hypothetical protein 23.t00002	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01766.1.g29642.t1	gb|EMJ11389.1| hypothetical protein PRUPE_ppa017790mg [Prunus persica]	1881	1485	0	78.9	35.5	48.2	hypothetical protein PRUPE_ppa017790mg	gbpln	Prunus persica	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	1881	370	6.00E-32	19.7	3.6	5.2
Rsa1.0_01766.1.g29643.t1	ref|XP_002883029.1| hypothetical protein ARALYDRAFT_479149 [Arabidopsis lyrata subsp. lyrata] gi|297328869|gb|EFH59288.1| hypothetical protein ARALYDRAFT_479149 [Arabidopsis lyrata subsp. lyrata]	1132	1131	0	99.9	93.4	96.6	hypothetical protein ARALYDRAFT_479149	gbpln	Arabidopsis lyrata	AT3G16830.1 | Symbols: TPR2 | TOPLESS-related 2 | chr3:5731709-5737531 FORWARD LENGTH=1131	1132	1131	0	99.9	92.9	96.4
Rsa1.0_01766.1.g29644.t1	ref|XP_002885172.1| DEAD-box ATP-dependent RNA helicase 13 [Arabidopsis lyrata subsp. lyrata] gi|297331012|gb|EFH61431.1| DEAD-box ATP-dependent RNA helicase 13 [Arabidopsis lyrata subsp. lyrata]	815	831	0	102.0	77.5	87.2	DEAD-box ATP-dependent RNA helicase 13	gbpln	Arabidopsis lyrata	AT3G16840.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:5738020-5743042 REVERSE LENGTH=826	815	826	0	101.3	76.3	86.7
Rsa1.0_01767.1.g29645.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01767.1.g29646.t3	gb|AAF98181.1|AC000107_4 F17F8.5 [Arabidopsis thaliana]	429	872	1.00E-43	203.3	27.3	37.8	F17F8.5	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	429	746	5.00E-34	173.9	23.3	33.6
Rsa1.0_01767.1.g29647.t1	ref|XP_002870678.1| glucose-6-phosphate dehydrogenase 6 [Arabidopsis lyrata subsp. lyrata] gi|297316514|gb|EFH46937.1| glucose-6-phosphate dehydrogenase 6 [Arabidopsis lyrata subsp. lyrata]	515	515	0	100.0	87.2	90.5	glucose-6-phosphate dehydrogenase 6	gbpln	Arabidopsis lyrata	AT5G40760.1 | Symbols: G6PD6 | glucose-6-phosphate dehydrogenase 6 | chr5:16311284-16314556 FORWARD LENGTH=515	515	515	0	100.0	87.0	90.5
Rsa1.0_01767.1.g29648.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01767.1.g29649.t1	ref|NP_568585.1| uncharacterized protein [Arabidopsis thaliana] gi|14532694|gb|AAK64148.1| unknown protein [Arabidopsis thaliana] gi|19310773|gb|AAL85117.1| unknown protein [Arabidopsis thaliana] gi|332007206|gb|AED94589.1| uncharacterized protein AT5G40740 [Arabidopsis thaliana]	734	741	0	101.0	93.3	95.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G40740.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:16302229-16306371 REVERSE LENGTH=741	734	741	0	101.0	93.3	95.9
Rsa1.0_01767.1.g29650.t1	ref|XP_002870580.1| hypothetical protein ARALYDRAFT_915957 [Arabidopsis lyrata subsp. lyrata] gi|297316416|gb|EFH46839.1| hypothetical protein ARALYDRAFT_915957 [Arabidopsis lyrata subsp. lyrata]	213	286	2.00E-58	134.3	56.3	77.0	hypothetical protein ARALYDRAFT_915957	gbpln	Arabidopsis lyrata	AT5G37890.1 | Symbols: | Protein with RING/U-box and TRAF-like domains | chr5:15090512-15091822 REVERSE LENGTH=286	213	286	6.00E-60	134.3	56.8	77.0
Rsa1.0_01767.1.g29651.t1	ref|NP_198888.1| uncharacterized protein [Arabidopsis thaliana] gi|9758100|dbj|BAB08544.1| unnamed protein product [Arabidopsis thaliana] gi|332007204|gb|AED94587.1| uncharacterized protein AT5G40720 [Arabidopsis thaliana]	566	583	0	103.0	78.8	84.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G40720.1 | Symbols: | Domain of unknown function (DUF23) | chr5:16298063-16299893 FORWARD LENGTH=583	566	583	0	103.0	78.8	84.6
Rsa1.0_01768.1.g29652.t1	ref|XP_002881886.1| protease-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297327725|gb|EFH58145.1| protease-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata]	170	541	1.00E-87	318.2	90.0	97.1	protease-associated domain-containing protein	gbpln	Arabidopsis lyrata	AT2G43070.1 | Symbols: SPPL3, ATSPPL3 | SIGNAL PEPTIDE PEPTIDASE-LIKE 3 | chr2:17911233-17914776 REVERSE LENGTH=540	170	540	7.00E-86	317.6	92.9	98.2
Rsa1.0_01768.1.g29653.t1	ref|XP_002862374.1| hypothetical protein ARALYDRAFT_920829 [Arabidopsis lyrata subsp. lyrata] gi|297307823|gb|EFH38632.1| hypothetical protein ARALYDRAFT_920829 [Arabidopsis lyrata subsp. lyrata]	223	201	4.00E-24	90.1	26.5	38.1	hypothetical protein ARALYDRAFT_920829	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01768.1.g29654.t1	gb|ABV21212.1| Ty1_Copia-element protein [Arabidopsis thaliana]	162	438	7.00E-27	270.4	41.4	54.9	Ty1_Copia-element protein	gbpln	Arabidopsis thaliana	AT3G25720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:9380234-9381405 FORWARD LENGTH=282	162	282	4.00E-19	174.1	33.3	43.2
Rsa1.0_01768.1.g29655.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01768.1.g29656.t2	ref|NP_565985.1| serine/threonine-protein phosphatase 5 [Arabidopsis thaliana] gi|16930441|gb|AAL31906.1|AF419574_1 At2g42810/F7D19.19 [Arabidopsis thaliana] gi|20197966|gb|AAD21727.2| putative phosphoprotein phosphatase [Arabidopsis thaliana] gi|33589766|gb|AAQ22649.1| At2g42810/F7D19.19 [Arabidopsis thaliana] gi|330255077|gb|AEC10171.1| serine/threonine-protein phosphatase 5 [Arabidopsis thaliana]	509	484	0	95.1	89.0	92.5	serine/threonine-protein phosphatase 5	gbpln	Arabidopsis thaliana	AT2G42810.1 | Symbols: PAPP5, PP5 | protein phosphatase 5.2 | chr2:17812336-17815896 REVERSE LENGTH=484	509	484	0	95.1	89.0	92.5
Rsa1.0_01768.1.g29657.t1	ref|XP_002881874.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297327713|gb|EFH58133.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	458	468	0	102.2	86.0	90.6	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT2G42800.1 | Symbols: AtRLP29, RLP29 | receptor like protein 29 | chr2:17808157-17809545 REVERSE LENGTH=462	458	462	0	100.9	85.4	90.8
Rsa1.0_01768.1.g29658.t1	gb|EOA28597.1| hypothetical protein CARUB_v10024817mg [Capsella rubella]	514	511	0	99.4	93.8	96.9	hypothetical protein CARUB_v10024817mg	gbpln	Capsella rubella	AT2G42790.1 | Symbols: CSY3 | citrate synthase 3 | chr2:17803132-17805991 REVERSE LENGTH=509	514	509	0	99.0	92.2	94.9
Rsa1.0_01768.1.g29659.t1	gb|EOA27426.1| hypothetical protein CARUB_v10023558mg [Capsella rubella]	294	343	1.00E-159	116.7	95.2	98.0	hypothetical protein CARUB_v10023558mg	gbpln	Capsella rubella	AT2G42750.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:17793404-17795419 FORWARD LENGTH=344	294	344	1.00E-160	117.0	94.2	97.3
Rsa1.0_01768.1.g29660.t1	ref|XP_002880001.1| ribosomal protein L1 family protein [Arabidopsis lyrata subsp. lyrata] gi|297325840|gb|EFH56260.1| ribosomal protein L1 family protein [Arabidopsis lyrata subsp. lyrata]	387	401	0	103.6	87.6	91.7	ribosomal protein L1 family protein	gbpln	Arabidopsis lyrata	AT2G42710.1 | Symbols: | Ribosomal protein L1p/L10e family | chr2:17782352-17784830 FORWARD LENGTH=415	387	415	0	107.2	88.9	93.0
Rsa1.0_01768.1.g29661.t1	ref|NP_181798.2| uncharacterized protein [Arabidopsis thaliana] gi|330255063|gb|AEC10157.1| uncharacterized protein AT2G42700 [Arabidopsis thaliana]	851	838	0	98.5	88.5	92.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G42700.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: vesicle-mediated transport, vesicle docking involved in exocytosis; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Sec1-like protein (InterPro:IPR001619); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:17778464-17782034 FORWARD LENGTH=838	851	838	0	98.5	88.5	92.5
Rsa1.0_01768.1.g29662.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01769.1.g29663.t1	dbj|BAB11200.1| copia-type polyprotein [Arabidopsis thaliana] gi|13872710|emb|CAC37622.1| polyprotein [Arabidopsis thaliana]	1558	1334	0	85.6	57.3	68.7	copia-type polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1558	1262	3.00E-98	81.0	11.6	19.1
Rsa1.0_01769.1.g29664.t1	ref|XP_002893265.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339107|gb|EFH69524.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	416	273	1.00E-70	65.6	36.1	45.0	predicted protein	gbpln	Arabidopsis lyrata	AT4G01560.1 | Symbols: MEE49 | Ribosomal RNA processing Brix domain protein | chr4:677266-679164 REVERSE LENGTH=343	416	343	4.00E-23	82.5	19.2	30.3
Rsa1.0_01769.1.g29665.t1	gb|EOA29651.1| hypothetical protein CARUB_v10015153mg [Capsella rubella]	901	478	3.00E-70	53.1	15.3	16.8	hypothetical protein CARUB_v10015153mg	gbpln	Capsella rubella	AT3G11000.1 | Symbols: | DCD (Development and Cell Death) domain protein | chr3:3448442-3450283 FORWARD LENGTH=488	901	488	7.00E-71	54.2	14.9	16.3
Rsa1.0_01769.1.g29666.t2	ref|NP_565389.1| putative polyprenol reductase 2 [Arabidopsis thaliana] gi|75206043|sp|Q9SI62.2|POED2_ARATH RecName: Full=Polyprenol reductase 2 gi|20198183|gb|AAD26491.2| expressed protein [Arabidopsis thaliana] gi|330251413|gb|AEC06507.1| putative polyprenol reductase 2 [Arabidopsis thaliana]	193	343	6.00E-69	177.7	73.6	82.4	putative polyprenol reductase 2	gbpln	Arabidopsis thaliana	AT2G16530.1 | Symbols: | 3-oxo-5-alpha-steroid 4-dehydrogenase family protein | chr2:7163276-7165064 REVERSE LENGTH=343	193	343	2.00E-71	177.7	73.6	82.4
Rsa1.0_01769.1.g29667.t1	ref|XP_002882691.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328531|gb|EFH58950.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	512	561	0	109.6	85.2	93.0	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT3G10710.1 | Symbols: RHS12 | root hair specific 12 | chr3:3352289-3354237 FORWARD LENGTH=561	512	561	0	109.6	85.4	92.6

Rsa1.0_01769.1.g29668.t1	ref|NP_187683.2| pectinesterase 25 [Arabidopsis thaliana] gi|75306364|sp|Q94CB1.1|PME25_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 25; Includes: RecName: Full=Pectinesterase inhibitor 25; AltName: Full=Pectin methylesterase inhibitor 25; Includes: RecName: Full=Pectinesterase 25; Short=PE 25; AltName: Full=Pectin methylesterase 25; Short=AtPME25; Flags: Precursor gi|14334646|gb|AAK59501.1| putative pectinesterase [Arabidopsis thaliana] gi|332641426|gb|AEE74947.1| pectinesterase 25 [Arabidopsis thaliana]	614	619	0	100.8	87.5	91.7	pectinesterase 25	gbpln	Arabidopsis thaliana	AT3G10720.2 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:3354639-3357581 REVERSE LENGTH=619	614	619	0	100.8	87.5	91.7
Rsa1.0_01769.1.g29669.t1	gb|ABD64987.1| hypothetical protein 26.t00003 [Brassica oleracea]	111	330	6.00E-14	297.3	44.1	55.0	hypothetical protein 26.t00003	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01769.1.g29670.t1	ref|NP_187685.1| alpha-L-arabinofuranosidase 1 [Arabidopsis thaliana] gi|75265802|sp|Q9SG80.1|ASD1_ARATH RecName: Full=Alpha-L-arabinofuranosidase 1; Short=AtASD1; AltName: Full=Beta-D-xylosidase; Flags: Precursor gi|6630556|gb|AAF19575.1|AC011708_18 putative alpha-L-arabinofuranosidase [Arabidopsis thaliana] gi|332641428|gb|AEE74949.1| alpha-L-arabinofuranosidase 1 [Arabidopsis thaliana]	674	678	0	100.6	93.0	96.0	alpha-L-arabinofuranosidase 1	gbpln	Arabidopsis thaliana	AT3G10740.1 | Symbols: ASD1, ARAF1, ARAF, ATASD1 | alpha-L-arabinofuranosidase 1 | chr3:3361031-3364573 REVERSE LENGTH=678	674	678	0	100.6	93.0	96.0
Rsa1.0_01770.1.g29671.t1	gb|AAF79483.1|AC022492_27 F1L3.20 [Arabidopsis thaliana]	1129	1188	0	105.2	53.0	68.9	F1L3.20	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1129	1262	5.00E-84	111.8	14.4	23.6
Rsa1.0_01770.1.g29672.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01770.1.g29673.t2	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	567	704	3.00E-90	124.2	27.5	29.8	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01770.1.g29674.t1	emb|CAB10225.1| retrovirus-related like polyprotein [Arabidopsis thaliana] gi|7268152|emb|CAB78488.1| retrovirus-related like polyprotein [Arabidopsis thaliana]	573	1489	7.00E-71	259.9	28.8	37.0	retrovirus-related like polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	573	1262	6.00E-52	220.2	24.6	32.1
Rsa1.0_01770.1.g29675.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01770.1.g29676.t1	dbj|BAE98505.1| hypothetical protein [Arabidopsis thaliana]	91	475	1.00E-32	522.0	72.5	83.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G05150.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr4:2660339-2662675 FORWARD LENGTH=477	91	477	2.00E-35	524.2	72.5	83.5
Rsa1.0_01770.1.g29677.t1	ref|XP_002872737.1| hypothetical protein ARALYDRAFT_490165 [Arabidopsis lyrata subsp. lyrata] gi|297318574|gb|EFH48996.1| hypothetical protein ARALYDRAFT_490165 [Arabidopsis lyrata subsp. lyrata]	299	445	1.00E-106	148.8	72.2	75.3	hypothetical protein ARALYDRAFT_490165	gbpln	Arabidopsis lyrata	AT4G05150.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr4:2660339-2662675 FORWARD LENGTH=477	299	477	1.00E-107	159.5	74.2	78.3
Rsa1.0_01770.1.g29678.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01771.1.g29679.t1	ref|NP_565897.1| Low temperature and salt responsive protein [Arabidopsis thaliana] gi|297827479|ref|XP_002881622.1| hypothetical protein ARALYDRAFT_482911 [Arabidopsis lyrata subsp. lyrata] gi|15529214|gb|AAK97701.1| unknown protein [Arabidopsis thaliana] gi|16974383|gb|AAL31117.1| At2g38901/At2g38901 [Arabidopsis thaliana] gi|20197443|gb|AAM15078.1| Expressed protein [Arabidopsis thaliana] gi|297327461|gb|EFH57881.1| hypothetical protein ARALYDRAFT_482911 [Arabidopsis lyrata subsp. lyrata] gi|330254516|gb|AEC09610.1| Low temperature and salt responsive protein [Arabidopsis thaliana]	54	54	2.00E-19	100.0	94.4	98.1	Low temperature and salt responsive protein	gbpln	Arabidopsis lyrata	AT2G38905.1 | Symbols: | Low temperature and salt responsive protein family | chr2:16244218-16244472 REVERSE LENGTH=54	54	54	4.00E-22	100.0	94.4	98.1

<table>
<tr><td>Rsa1.0_01771.1.g29680.t1</td><td>ref|XP_002879772.1| hypothetical protein ARALYDRAFT_482910 [Arabidopsis lyrata subsp. lyrata] gi|297325611|gb|EFH56031.1| hypothetical protein ARALYDRAFT_482910 [Arabidopsis lyrata subsp. lyrata]</td><td>475</td><td>299</td><td>1.00E-88</td><td>62.9</td><td>42.5</td><td>46.7</td><td>hypothetical protein ARALYDRAFT_482910</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G38890.1 | Symbols: | unknown protein; Has 58 Blast hits to 54 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr2:16241234-16242648 FORWARD LENGTH=298</td><td>475</td><td>298</td><td>1.00E-88</td><td>62.7</td><td>41.9</td><td>45.9</td></tr>
<tr><td>Rsa1.0_01771.1.g29681.t1</td><td>dbj|BAJ34147.1| unnamed protein product [Thellungiella halophila]</td><td>371</td><td>402</td><td>2.00E-65</td><td>108.4</td><td>52.8</td><td>63.9</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT3G54620.1 | Symbols: ATBZIP25, BZO2H4, BZIP25 | basic leucine zipper 25 | chr3:20218085-20220341 REVERSE LENGTH=403</td><td>371</td><td>403</td><td>6.00E-57</td><td>108.6</td><td>51.5</td><td>63.1</td></tr>
<tr><td>Rsa1.0_01771.1.g29682.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01771.1.g29683.t1</td><td>ref|XP_002881621.1| hypothetical protein ARALYDRAFT_482903 [Arabidopsis lyrata subsp. lyrata] gi|297327460|gb|EFH57880.1| hypothetical protein ARALYDRAFT_482903 [Arabidopsis lyrata subsp. lyrata]</td><td>70</td><td>70</td><td>4.00E-26</td><td>100.0</td><td>84.3</td><td>91.4</td><td>hypothetical protein ARALYDRAFT_482903</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G38870.1 | Symbols: | Serine protease inhibitor, potato inhibitor I-type family protein | chr2:16236546-16237050 REVERSE LENGTH=70</td><td>70</td><td>70</td><td>2.00E-26</td><td>100.0</td><td>80.0</td><td>85.7</td></tr>
<tr><td>Rsa1.0_01771.1.g29684.t1</td><td>ref|NP_181418.3| guanylate-binding-like protein [Arabidopsis thaliana] gi|330254499|gb|AEC09593.1| guanylate-binding-like protein [Arabidopsis thaliana]</td><td>717</td><td>602</td><td>0</td><td>84.0</td><td>76.7</td><td>80.6</td><td>guanylate-binding-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G38840.1 | Symbols: | Guanylate-binding family protein | chr2:16227329-16232115 FORWARD LENGTH=602</td><td>717</td><td>602</td><td>0</td><td>84.0</td><td>76.7</td><td>80.6</td></tr>
<tr><td>Rsa1.0_01771.1.g29685.t1</td><td>gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]</td><td>825</td><td>1231</td><td>1.00E-180</td><td>149.2</td><td>41.1</td><td>55.5</td><td>Very similar to retrotransposon reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>825</td><td>575</td><td>1.00E-72</td><td>69.7</td><td>19.2</td><td>33.0</td></tr>
<tr><td>Rsa1.0_01771.1.g29686.t1</td><td>ref|NP_181398.1| protein LURP-one-related 8 [Arabidopsis thaliana] gi|75216986|sp|Q9ZVI6.1|LOR8_ARATH RecName: Full=Protein LURP-one-related 8 gi|3786008|gb|AAC67354.1| unknown protein [Arabidopsis thaliana] gi|61656129|gb|AAX49367.1| At2g38640 [Arabidopsis thaliana] gi|110741793|dbj|BAE98840.1| hypothetical protein [Arabidopsis thaliana] gi|330254466|gb|AEC09560.1| protein LURP-one-related 8 [Arabidopsis thaliana]</td><td>196</td><td>196</td><td>3.00E-96</td><td>100.0</td><td>84.7</td><td>94.9</td><td>protein LURP-one-related 8</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G38640.1 | Symbols: | Protein of unknown function (DUF567) | chr2:16157725-16158474 REVERSE LENGTH=196</td><td>196</td><td>196</td><td>1.00E-98</td><td>100.0</td><td>84.7</td><td>94.9</td></tr>
<tr><td>Rsa1.0_01771.1.g29687.t1</td><td>ref|NP_001031507.1| cyclin-dependent kinase B1-2 [Arabidopsis thaliana] gi|152013423|sp|Q2V419.2|CKB12_ARATH RecName: Full=Cyclin-dependent kinase B1-2; Short=CDKB1;2 gi|3786010|gb|AAC67356.1| putative cell division control protein kinase [Arabidopsis thaliana] gi|13275212|emb|CAC34053.1| cyclin dependent kinase [Arabidopsis thaliana] gi|330254464|gb|AEC09558.1| cyclin-dependent kinase B1-2 [Arabidopsis thaliana]</td><td>335</td><td>311</td><td>1.00E-164</td><td>92.8</td><td>85.1</td><td>89.3</td><td>cyclin-dependent kinase B1-2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G38620.2 | Symbols: CDKB1;2 | cyclin-dependent kinase B1;2 | chr2:16152551-16153866 FORWARD LENGTH=311</td><td>335</td><td>311</td><td>1.00E-167</td><td>92.8</td><td>85.1</td><td>89.3</td></tr>
<tr><td>Rsa1.0_01772.1.g29688.t12</td><td>gb|EOA12879.1| hypothetical protein CARUB_v10025852mg [Capsella rubella]</td><td>917</td><td>908</td><td>0</td><td>99.0</td><td>80.2</td><td>87.4</td><td>hypothetical protein CARUB_v10025852mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G61960.2 | Symbols: AML1, ML1 | MEI2-like protein 1 | chr5:24879001-24883483 REVERSE LENGTH=915</td><td>917</td><td>915</td><td>0</td><td>99.8</td><td>80.9</td><td>87.8</td></tr>
<tr><td>Rsa1.0_01772.1.g29689.t1</td><td>ref|XP_002864760.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310595|gb|EFH41019.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>1259</td><td>1145</td><td>0</td><td>90.9</td><td>39.2</td><td>48.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G61950.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr5:24873566-24878093 FORWARD LENGTH=1132</td><td>1259</td><td>1132</td><td>0</td><td>89.9</td><td>37.3</td><td>47.7</td></tr>
<tr><td>Rsa1.0_01772.1.g29690.t1</td><td>ref|XP_002864761.1| hypothetical protein ARALYDRAFT_332429 [Arabidopsis lyrata subsp. lyrata] gi|297310596|gb|EFH41020.1| hypothetical protein ARALYDRAFT_332429 [Arabidopsis lyrata subsp. lyrata]</td><td>1145</td><td>1130</td><td>0</td><td>98.7</td><td>58.7</td><td>71.7</td><td>hypothetical protein ARALYDRAFT_332429</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G61950.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr5:24873566-24878093 FORWARD LENGTH=1132</td><td>1145</td><td>1132</td><td>0</td><td>98.9</td><td>59.0</td><td>72.7</td></tr>
<tr><td>Rsa1.0_01772.1.g29691.t1</td><td>ref|NP_974979.1| DCD (Development and Cell Death) domain-containing protein [Arabidopsis thaliana] gi|332010149|gb|AED97532.1| DCD (Development and Cell Death) domain-containing protein [Arabidopsis thaliana]</td><td>716</td><td>742</td><td>0</td><td>103.6</td><td>67.3</td><td>74.4</td><td>DCD (Development and Cell Death) domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G61910.3 | Symbols: | DCD (Development and Cell Death) domain protein | chr5:24861091-24863741 REVERSE LENGTH=742</td><td>716</td><td>742</td><td>0</td><td>103.6</td><td>67.3</td><td>74.4</td></tr>
<tr><td>Rsa1.0_01772.1.g29692.t1</td><td>gb|EOA12798.1| hypothetical protein CARUB_v10025752mg [Capsella rubella]</td><td>575</td><td>1270</td><td>0</td><td>220.9</td><td>89.7</td><td>95.5</td><td>hypothetical protein CARUB_v10025752mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G61910.4 | Symbols: | DCD (Development and Cell Death) domain protein | chr5:24855908-24863729 REVERSE LENGTH=1346</td><td>575</td><td>1346</td><td>0</td><td>234.1</td><td>86.8</td><td>93.7</td></tr>
</table>

Rsa1.0_01772.1.g29693.t1	ref|NP_200995.1| ethylene-responsive transcription factor ERF114 [Arabidopsis thaliana] gi|75262469|sp|Q9FH54.1|EF114_ARATH RecName: Full=Ethylene-responsive transcription factor ERF114 gi|9758388|dbj|BAB08875.1| AP2 domain transcription factor-like [Arabidopsis thaliana] gi|48479316|gb|AAT44929.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|182623784|gb|ACB88827.1| At5g61890 [Arabidopsis thaliana] gi|332010146|gb|AED97529.1| ethylene-responsive transcription factor ERF114 [Arabidopsis thaliana]	249	248	9.00E-87	99.6	77.9	83.1	ethylene-responsive transcription factor ERF114	gbpln	Arabidopsis thaliana	AT5G61890.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:24852639-24853744 REVERSE LENGTH=248	249	248	2.00E-89	99.6	77.9	83.1
Rsa1.0_01772.1.g29694.t1	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	797	1515	0	190.1	62.1	76.5	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	797	1262	1.00E-113	158.3	25.0	38.3
Rsa1.0_01772.1.g29695.t1	ref|NP_180333.2| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana] gi|330252928|gb|AEC08022.1| Ubiquitin carboxyl-terminal hydrolase-related protein [Arabidopsis thaliana]	113	1106	2.00E-16	978.8	38.9	56.6	Ubiquitin carboxyl-terminal hydrolase-related protein	gbpln	Arabidopsis thaliana	AT2G27650.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr2:11792996-11797343 REVERSE LENGTH=1106	113	1106	4.00E-19	978.8	38.9	56.6
Rsa1.0_01773.1.g29696.t1	ref|NP_195098.1| putative pathogenesis-related protein [Arabidopsis thaliana] gi|11692906|gb|AAG40056.1|AF324705_1 AT4g33720 [Arabidopsis thaliana] gi|11935187|gb|AAG42009.1|AF327419_1 putative pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|12642878|gb|AAK00381.1|AF339699_1 putative pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|3549674|emb|CAA20585.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|7270321|emb|CAB80089.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|14517484|gb|AAK62632.1| AT4g33720/T16L1_210 [Arabidopsis thaliana] gi|21593911|gb|AAM65876.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|22136566|gb|AAM91069.1| AT4g33720/T16L1_210 [Arabidopsis thaliana] gi|332660869|gb|AEE86269.1| putative pathogenesis-related protein [Arabidopsis thaliana]	163	163	2.00E-69	100.0	75.5	84.0	putative pathogenesis-related protein	gbpln	Arabidopsis thaliana	AT4G33720.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:16182813-16183304 FORWARD LENGTH=163	163	163	6.00E-72	100.0	75.5	84.0
Rsa1.0_01773.1.g29697.t1	gb|EOA36075.1| hypothetical protein CARUB_v10009706mg [Capsella rubella]	154	329	1.00E-39	213.6	57.8	61.7	hypothetical protein CARUB_v10009706mg	gbpln	Capsella rubella	AT1G02400.1 | Symbols: ATGA2OX4, ATGA2OX6, DTA1, GA2OX6 | gibberellin 2-oxidase 6 | chr1:486964-489391 FORWARD LENGTH=329	154	329	2.00E-41	213.6	57.1	61.0
Rsa1.0_01773.1.g29698.t1	gb|EOA18047.1| hypothetical protein CARUB_v10006493mg [Capsella rubella]	188	173	1.00E-30	92.0	33.5	35.6	hypothetical protein CARUB_v10006493mg	gbpln	Capsella rubella	AT4G33730.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:16185098-16185616 FORWARD LENGTH=172	188	172	9.00E-33	91.5	32.4	35.6
Rsa1.0_01773.1.g29699.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01773.1.g29700.t1	gb|EOA16586.1| hypothetical protein CARUB_v10004752mg [Capsella rubella] gi|482552394|gb|EOA16587.1| hypothetical protein CARUB_v10004752mg [Capsella rubella] gi|482552395|gb|EOA16588.1| hypothetical protein CARUB_v10004752mg [Capsella rubella] gi|482552396|gb|EOA16589.1| hypothetical protein CARUB_v10004752mg [Capsella rubella]	443	464	1.00E-140	104.7	74.0	85.8	hypothetical protein CARUB_v10004752mg	gbpln	Capsella rubella	AT4G33740.3 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37820.1); Has 138092 Blast hits to 73110 proteins in 2951 species: Archae - 732; Bacteria - 17903; Metazoa - 48520; Fungi - 16808; Plants - 7078; Viruses - 1044; Other Eukaryotes - 46007 (source: NCBI BLink). | chr4:16187384-16188802 FORWARD LENGTH=472	443	472	1.00E-123	106.5	74.7	85.3

Rsa1.0_01773.1.g29701.t1	gb|EOA16776.1| hypothetical protein CARUB_v10004995mg [Capsella rubella]	387	392	1.00E−173	101.3	82.9	89.7	hypothetical protein CARUB_v10004995mg	gbpln	Capsella rubella	AT4G33770.1 | Symbols: | Inositol 1,3,4−trisphosphate 5/6−kinase family protein | chr4:16193589−16196242 REVERSE LENGTH=391	387	391	1.00E−171	101.0	81.4	88.4
Rsa1.0_01773.1.g29702.t1	ref|XP_002867158.1| hypothetical protein ARALYDRAFT_491300 [Arabidopsis lyrata subsp. lyrata] gi|297312994|gb|EFH43417.1| hypothetical protein ARALYDRAFT_491300 [Arabidopsis lyrata subsp. lyrata]	300	208	9.00E−61	69.3	43.7	45.7	hypothetical protein ARALYDRAFT_491300	gbpln	Arabidopsis lyrata	AT4G33780.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: short hypocotyl in white light1 (TAIR:AT1G69935.1); Has 40 Blast hits to 40 proteins in 10 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 40; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr4:16202174−16203617 REVERSE LENGTH=203	300	203	7.00E−63	67.7	43.0	45.7
Rsa1.0_01773.1.g29703.t1	ref|XP_002867155.1| glycosyl hydrolase family 10 protein [Arabidopsis lyrata subsp. lyrata] gi|297312991|gb|EFH43414.1| glycosyl hydrolase family 10 protein [Arabidopsis lyrata subsp. lyrata]	573	568	0	99.1	83.2	89.2	glycosyl hydrolase family 10 protein	gbpln	Arabidopsis lyrata	AT4G33820.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr4:16217010−16219515 REVERSE LENGTH=570	573	570	0	99.5	79.8	87.8
Rsa1.0_01774.1.g29704.t1	gb|EOA24312.1| hypothetical protein CARUB_v10017552mg [Capsella rubella]	340	350	1.00E−136	102.9	83.2	88.2	hypothetical protein CARUB_v10017552mg	gbpln	Capsella rubella	AT3G61310.1 | Symbols: | AT hook motif DNA−binding family protein | chr3:22690799−22692445 REVERSE LENGTH=354	340	354	1.00E−126	104.1	78.2	85.6
Rsa1.0_01774.1.g29705.t3	ref|NP_191689.1| C2 calcium/lipid−binding and phosphoribosyltransferase C−terminal domain−containing protein [Arabidopsis thaliana] gi|6850897|emb|CAB71060.1| anthranilate phosphoribosyltransferase−like protein [Arabidopsis thaliana] gi|28392941|gb|AAO41906.1| putative anthranilate phosphoribosyltransferase [Arabidopsis thaliana] gi|28973565|gb|AAO64107.1| putative anthranilate phosphoribosyltransferase [Arabidopsis thaliana] gi|332646664|gb|AEE80185.1| C2 calcium/lipid−binding and phosphoribosyltransferase C−terminal domain−containing protein [Arabidopsis thaliana]	1412	972	0	68.8	51.7	58.1	C2 calcium/lipid−binding and phosphoribosyltransferase C−terminal domain−containing protein	gbpln	Arabidopsis thaliana	AT3G61300.1 | Symbols: | C2 calcium/lipid−binding plant phosphoribosyltransferase family protein | chr3:22687662−22690580 FORWARD LENGTH=972	1412	972	0	68.8	51.7	58.1
Rsa1.0_01774.1.g29706.t1	gb|EOA25074.1| hypothetical protein CARUB_v10018382mg [Capsella rubella]	279	297	1.00E−117	106.5	77.8	83.9	hypothetical protein CARUB_v10018382mg	gbpln	Capsella rubella	AT3G61250.1 | Symbols: AtMYB17, MYB17 | myb domain protein 17 | chr3:22671306−22672551 FORWARD LENGTH=299	279	299	1.00E−119	107.2	77.4	84.2
Rsa1.0_01774.1.g29707.t1	ref|XP_002878372.1| LIM domain−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297324210|gb|EFH54631.1| LIM domain−containing protein [Arabidopsis lyrata subsp. lyrata]	211	214	1.00E−106	101.4	90.5	93.8	LIM domain−containing protein	gbpln	Arabidopsis lyrata	AT3G61230.1 | Symbols: | GATA type zinc finger transcription factor family protein | chr3:22664601−22665503 REVERSE LENGTH=213	211	213	1.00E−108	100.9	89.6	93.4
Rsa1.0_01774.1.g29708.t1	ref|XP_002876599.1| short−chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322437|gb|EFH52858.1| short−chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	280	296	1.00E−120	105.7	75.7	87.1	short−chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G61220.1 | Symbols: | NAD(P)−binding Rossmann−fold superfamily protein | chr3:22663025−22664316 FORWARD LENGTH=296	280	296	1.00E−122	105.7	74.6	87.1
Rsa1.0_01774.1.g29709.t1	gb|EOA24791.1| hypothetical protein CARUB_v10018071mg [Capsella rubella]	175	189	8.00E−68	108.0	70.3	86.3	hypothetical protein CARUB_v10018071mg	gbpln	Capsella rubella	AT3G61200.1 | Symbols: | Thioesterase superfamily protein | chr3:22657599−22658350 REVERSE LENGTH=188	175	188	1.00E−66	107.4	66.9	84.6
Rsa1.0_01775.1.g29710.t1	ref|XP_002893237.1| proton−dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297339079|gb|EFH69496.1| proton−dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	512	561	0	109.6	83.6	90.4	proton−dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G22550.1 | Symbols: | Major facilitator superfamily protein | chr1:7966608−7968552 REVERSE LENGTH=564	512	564	0	110.2	84.2	90.8
Rsa1.0_01775.1.g29711.t1	ref|NP_001154357.1| uncharacterized protein [Arabidopsis thaliana] gi|332192131|gb|AEE30252.1| uncharacterized protein AT1G22520 [Arabidopsis thaliana]	103	179	3.00E−33	173.8	71.8	80.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G22520.2 | Symbols: | Domain of unknown function (DUF543) | chr1:7952996−7954304 REVERSE LENGTH=179	103	179	4.00E−36	173.8	71.8	80.6
Rsa1.0_01775.1.g29712.t4	gb|AAM63145.1| unknown [Arabidopsis thaliana]	214	185	2.00E−66	86.4	71.5	79.0	unknown	gbpln	Arabidopsis thaliana	AT1G22510.1 | Symbols: | RING/U−box protein with domain of unknown function (DUF 1232) | chr1:7951003−7952597 REVERSE LENGTH=185	214	185	1.00E−68	86.4	71.0	79.0

Rsa1.0_01775.1.g29713.t1	gb|EOA36747.1| hypothetical protein CARUB_v10012585mg [Capsella rubella]	161	382	2.00E-49	237.3	62.1	68.3	hypothetical protein CARUB_v10012585mg	gbpln	Capsella rubella	AT1G22500.1 | Symbols: | RING/U-box superfamily protein | chr1:7949581-7950726 FORWARD LENGTH=381	161	381	2.00E-50	236.6	60.2	64.0
Rsa1.0_01775.1.g29714.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01776.1.g29715.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01776.1.g29716.t1	gb|ABQ50546.1| hypothetical protein [Brassica rapa]	433	650	0	150.1	75.1	88.9	hypothetical protein	gbpln	Brassica rapa	AT3G22470.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:7966066-7967925 REVERSE LENGTH=619	433	619	1.00E-174	143.0	70.2	82.7
Rsa1.0_01776.1.g29717.t1	gb|EOA40316.1| hypothetical protein CARUB_v10009041mg [Capsella rubella]	472	470	0	99.6	91.5	94.9	hypothetical protein CARUB_v10009041mg	gbpln	Capsella rubella	AT1G12680.1 | Symbols: PEPKR2 | phosphoenolpyruvate carboxylase-related kinase 2 | chr1:4320123-4322269 REVERSE LENGTH=470	472	470	0	99.6	90.3	94.3
Rsa1.0_01776.1.g29718.t1	gb|EOA38672.1| hypothetical protein CARUB_v10010628mg [Capsella rubella]	130	130	2.00E-32	100.0	57.7	74.6	hypothetical protein CARUB_v10010628mg	gbpln	Capsella rubella	AT1G12663.1 | Symbols: | Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant thionin (PR-13) family with the following members: At1g66100, At5g36910, At1g72260, At2g15010, At1g12663, At1g12660. | chr1:4310969-4311457 FORWARD LENGTH=115	130	115	8.00E-34	88.5	50.8	64.6
Rsa1.0_01776.1.g29719.t7	dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	539	1250	8.00E-85	231.9	34.1	41.6	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	539	1262	3.00E-29	234.1	18.2	28.8
Rsa1.0_01776.1.g29720.t1	gb|EOA11936.1| hypothetical protein CARUB_v10016547mg, partial [Capsella rubella]	179	149	2.00E-11	83.2	19.6	26.8	hypothetical protein CARUB_v10016547mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01776.1.g29721.t1	ref|XP_002889953.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335795|gb|EFH66212.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	118	123	1.00E-33	104.2	68.6	77.1	predicted protein	gbpln	Arabidopsis lyrata	AT1G12660.1 | Symbols: | Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant thionin (PR-13) family with the following members: At1g66100, At5g36910, At1g72260, At2g15010, At1g12663, At1g12660. | chr1:4308943-4309583 FORWARD LENGTH=137	118	137	5.00E-29	116.1	55.9	64.4
Rsa1.0_01776.1.g29722.t1	ref|XP_002299562.1| predicted protein [Populus trichocarpa] gi|222846820|gb|EEE84367.1| predicted protein [Populus trichocarpa]	255	247	4.00E-31	96.9	32.5	37.6	predicted protein	gbpln	Populus trichocarpa	AT1G12650.4 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF947 (InterPro:IPR009292); Has 700 Blast hits to 631 proteins in 192 species: Archae - 0; Bacteria - 32; Metazoa - 138; Fungi - 168; Plants - 60; Viruses - 0; Other Eukaryotes - 302 (source: NCBI BLink). | chr1:4306183-4307673 FORWARD LENGTH=248	255	248	8.00E-26	97.3	21.6	23.5
Rsa1.0_01777.1.g29723.t1	ref|XP_002870141.1| hypothetical protein ARALYDRAFT_493211 [Arabidopsis lyrata subsp. lyrata] gi|297315977|gb|EFH46400.1| hypothetical protein ARALYDRAFT_493211 [Arabidopsis lyrata subsp. lyrata]	1281	549	0	42.9	40.0	41.5	hypothetical protein ARALYDRAFT_493211	gbpln	Arabidopsis lyrata	AT4G16650.1 | Symbols: | O-fucosyltransferase family protein | chr4:9372727-9375910 FORWARD LENGTH=549	1281	549	0	42.9	39.5	41.3
Rsa1.0_01777.1.g29724.t1	ref|NP_567510.1| hypoxia up-regulated 1 [Arabidopsis thaliana] gi|378548353|sp|F4JMJ1.1|HSP7R_ARATH RecName: Full=Heat shock 70 kDa protein 17; AltName: Full=Heat shock protein 70-17; Short=AtHsp70-17; Flags: Precursor gi|332658381|gb|AEE83781.1| heat shock 70 kDa protein 17 [Arabidopsis thaliana]	911	867	0	95.2	85.3	89.9	hypoxia up-regulated 1	gbpln	Arabidopsis thaliana	AT4G16660.1 | Symbols: | heat shock protein 70 (Hsp 70) family protein | chr4:9377225-9381232 FORWARD LENGTH=867	911	867	0	95.2	85.3	89.9
Rsa1.0_01777.1.g29725.t4	ref|XP_002885669.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata] gi|297331509|gb|EFH61928.1| hypothetical protein ARALYDRAFT_319176 [Arabidopsis lyrata subsp. lyrata]	517	467	1.00E-132	90.3	48.7	58.2	hypothetical protein ARALYDRAFT_319176	gbpln	Arabidopsis lyrata	AT3G62850.1 | Symbols: | zinc finger protein-related | chr3:23237487-23239155 REVERSE LENGTH=472	517	472	1.00E-129	91.3	45.3	57.3
Rsa1.0_01777.1.g29726.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01777.1.g29727.t1	ref|NP_193405.1| 60S ribosomal protein L15-1 [Arabidopsis thaliana] gi|297800374|ref|XP_002868071.1| 60S ribosomal protein L15 [Arabidopsis lyrata subsp. lyrata] gi|3122673|sp|O23515.1|RL151_ARATH RecName: Full=60S ribosomal protein L15-1 gi|13878179|gb|AAK44167.1|AF370352_1 putative ribosomal protein [Arabidopsis thaliana] gi|2245027|emb|CAB10447.1| ribosomal protein [Arabidopsis thaliana] gi|7268422|emb|CAB78714.1| ribosomal protein [Arabidopsis thaliana] gi|16604446|gb|AAL24229.1| AT4g16720/dl4385c [Arabidopsis thaliana] gi|19715591|gb|AAL91619.1| AT4g16720/dl4385c [Arabidopsis thaliana] gi|21592436|gb|AAM64387.1| ribosomal protein [Arabidopsis thaliana] gi|22136774|gb|AAM91731.1| putative ribosomal protein [Arabidopsis thaliana] gi|23505795|gb|AAN28757.1| At4g16720/dl4385c [Arabidopsis thaliana] gi|297313907|gb|EFH44330.1| 60S ribosomal protein L15 [Arabidopsis lyrata subsp. lyrata] gi|332658391|gb|AEE83791.1| 60S ribosomal protein L15-1 [Arabidopsis thaliana]	204	204	1.00E-113	100.0	99.5	100.0	60S ribosomal protein L15-1	gbpln	Arabidopsis lyrata	AT4G16720.1 | Symbols: | Ribosomal protein L23/L15e family protein | chr4:9400156-9401315 REVERSE LENGTH=204	204	204	1.00E-115	100.0	99.5	100.0
Rsa1.0_01777.1.g29728.t1	gb|EOA19151.1| hypothetical protein CARUB_v10007826mg [Capsella rubella]	526	545	0	103.6	84.2	91.3	hypothetical protein CARUB_v10007826mg	gbpln	Capsella rubella	AT4G16745.1 | Symbols: | Exostosin family protein | chr4:9412185-9414053 FORWARD LENGTH=542	526	542	0	103.0	85.4	92.2
Rsa1.0_01777.1.g29729.t1	emb|CAB41158.1| putative protein [Arabidopsis thaliana]	624	669	0	107.2	55.3	67.1	putative protein	gbpln	Arabidopsis thaliana	AT3G48400.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:17923678-17925589 FORWARD LENGTH=619	624	619	1.00E-179	99.2	53.0	65.1
Rsa1.0_01778.1.g29730.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	193	657	2.00E-12	340.4	22.8	34.2	T14P8.10	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01778.1.g29731.t1	ref|NP_181023.1| fatty acid hydroxylase 1 [Arabidopsis thaliana] gi|75098527|sp|O48916.1|FAH1_ARATH RecName: Full=Fatty acid 2-hydroxylase 1; Short=AtFAH1 gi|2736147|gb|AAB94072.1| fatty acid hydroxylase Fah1p [Arabidopsis thaliana] gi|3132481|gb|AAC16270.1| fatty acid hydroxylase (FAH1) [Arabidopsis thaliana] gi|15215596|gb|AAK91343.1| At2g34770/T29F13.2 [Arabidopsis thaliana] gi|23308163|gb|AAN18051.1| At2g34770/T29F13.2 [Arabidopsis thaliana] gi|330253925|gb|AEC09019.1| fatty acid hydroxylase 1 [Arabidopsis thaliana]	240	237	1.00E-117	98.8	82.5	89.2	fatty acid hydroxylase 1	gbpln	Arabidopsis thaliana	AT2G34770.1 | Symbols: FAH1, ATFAH1 | fatty acid hydroxylase 1 | chr2:14666776-14668061 FORWARD LENGTH=237	240	237	1.00E-119	98.8	82.5	89.2
Rsa1.0_01778.1.g29732.t1	ref|NP_179771.2| essential meiotic endonuclease 1A [Arabidopsis thaliana] gi|75147156|sp|Q84M98.1|EME1A_ARATH RecName: Full=Crossover junction endonuclease EME1A; AltName: Full=Essential meiotic endonuclease 1A; Short=AtEME1A gi|30102692|gb|AAP21264.1| At2g21800 [Arabidopsis thaliana] gi|110735996|dbj|BAE99972.1| hypothetical protein [Arabidopsis thaliana] gi|330252129|gb|AEC07223.1| essential meiotic endonuclease 1A [Arabidopsis thaliana]	520	546	1.00E-150	105.0	59.6	73.5	essential meiotic endonuclease 1A	gbpln	Arabidopsis thaliana	AT2G21800.1 | Symbols: ATEME1A, EME1A | essential meiotic endonuclease 1A | chr2:9298196-9301745 FORWARD LENGTH=546	520	546	1.00E-152	105.0	59.6	73.5
Rsa1.0_01778.1.g29733.t1	gb|EOA26911.1| hypothetical protein CARUB_v10023001mg [Capsella rubella]	526	524	0	99.6	83.3	88.8	hypothetical protein CARUB_v10023001mg	gbpln	Capsella rubella	AT2G21860.1 | Symbols: | violaxanthin de-epoxidase-related | chr2:9318333-9319990 REVERSE LENGTH=522	526	522	0	99.2	82.7	87.8

Rsa1.0_01778.1.g29734.t1	ref|NP_179778.1| putative ATP synthase subunit [Arabidopsis thaliana] gi|25089793|sp|Q9SJ12.1|ATP7_ARATH RecName: Full=Probable ATP synthase 24 kDa subunit, mitochondrial; Flags: Precursor gi|4417280|gb|AAD20405.1| putative ATP synthase [Arabidopsis thaliana] gi|15028141|gb|AAK76694.1| putative ATP synthase [Arabidopsis thaliana] gi|19310625|gb|AAL85043.1| putative ATP synthase [Arabidopsis thaliana] gi|330252138|gb|AEC07232.1| putative ATP synthase subunit [Arabidopsis thaliana]	240	240	1.00E-125	100.0	93.8	98.3	putative ATP synthase subunit	gbpln	Arabidopsis thaliana	AT2G21870.1 | Symbols: MGP1 | copper ion binding;cobalt ion binding;zinc ion binding | chr2:9320456-9322618 REVERSE LENGTH=240	240	240	1.00E-128	100.0	93.8	98.3
Rsa1.0_01778.1.g29735.t1	gb|EOA27909.1| hypothetical protein CARUB_v10024082mg [Capsella rubella]	201	202	2.00E-93	100.5	82.1	90.5	hypothetical protein CARUB_v10024082mg	gbpln	Capsella rubella	AT2G21880.1 | Symbols: ATRAB7A, ATRABG2, RAB7A | RAB GTPase homolog 7A | chr2:9324899-9326170 REVERSE LENGTH=212	201	212	1.00E-90	105.5	80.6	89.6
Rsa1.0_01778.1.g29736.t1	gb|ABK28704.1| unknown [Arabidopsis thaliana]	230	366	1.00E-32	159.1	30.9	40.9	unknown	gbpln	Arabidopsis thaliana	AT5G19270.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03566.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6485617-6487009 REVERSE LENGTH=365	230	365	4.00E-35	158.7	30.9	40.9
Rsa1.0_01778.1.g29737.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	270	1213	4.00E-52	449.3	44.8	64.1	unknown protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	270	746	8.00E-23	276.3	17.0	25.6
Rsa1.0_01778.1.g29738.t5	gb|EOA36857.1| hypothetical protein CARUB_v10008803mg [Capsella rubella]	473	536	2.00E-48	113.3	20.1	26.6	hypothetical protein CARUB_v10008803mg	gbpln	Capsella rubella	AT5G28823.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: Zinc knuckle (CCHC-type) family protein (TAIR:AT2G07760.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:10837849-10839826 REVERSE LENGTH=568	473	568	1.00E-42	120.1	15.9	18.2
Rsa1.0_01779.1.g29739.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	117	1239	7.00E-36	1059.0	59.0	67.5	putative pol polyprotein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01779.1.g29740.t2	ref|NP_001190033.1| xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] gi|332644912|gb|AEE78433.1| probable xyloglucan endotransglucosylase/hydrolase protein 11 [Arabidopsis thaliana]	266	257	1.00E-90	96.6	64.7	78.2	xyloglucan:xyloglucosyl transferase	gbpln	Arabidopsis thaliana	AT3G48580.2 | Symbols: XTH11 | xyloglucan endotransglucosylase/hydrolase 11 | chr3:18007238-18008341 FORWARD LENGTH=257	266	257	4.00E-93	96.6	64.7	78.2
Rsa1.0_01779.1.g29741.t1	ref|NP_199277.1| beta glucosidase 13 [Arabidopsis thaliana] gi|75311572|sp|Q9LU02.1|BGL13_ARATH RecName: Full=Beta-glucosidase 13; Short=AtBGLU13; Flags: Precursor gi|8953762|dbj|BAA98117.1| beta-glucosidase [Arabidopsis thaliana] gi|190610068|gb|ACE79745.1| At5g44640 [Arabidopsis thaliana] gi|332007759|gb|AED95142.1| beta glucosidase 13 [Arabidopsis thaliana]	507	507	0	100.0	87.4	93.5	beta glucosidase 13	gbpln	Arabidopsis thaliana	AT5G44640.1 | Symbols: BGLU13 | beta glucosidase 13 | chr5:18011146-18012669 FORWARD LENGTH=507	507	507	0	100.0	87.4	93.5
Rsa1.0_01779.1.g29742.t1	ref|NP_190435.1| uncharacterized protein [Arabidopsis thaliana] gi|6523097|emb|CAB62355.1| putative protein [Arabidopsis thaliana] gi|332644920|gb|AEE78441.1| uncharacterized protein AT3G48660 [Arabidopsis thaliana]	69	89	3.00E-28	129.0	92.8	97.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G48660.1 | Symbols: | Protein of unknown function (DUF 3339) | chr3:18029659-18030133 FORWARD LENGTH=89	69	89	6.00E-31	129.0	92.8	97.1
Rsa1.0_01779.1.g29743.t1	ref|XP_002875916.1| XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297321754|gb|EFH52175.1| XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	643	647	0	100.6	80.4	89.7	XH/XS domain-containing protein	gbpln	Arabidopsis lyrata	AT3G48670.2 | Symbols: IDN2, RDM12 | XH/XS domain-containing protein | chr3:18031240-18033615 FORWARD LENGTH=647	643	647	0	100.6	79.6	88.3

Rsa1.0_01779.1.g29744.t1	ref|XP_002877622.1| hypothetical protein ARALYDRAFT_485224 [Arabidopsis lyrata subsp. lyrata] gi|297323460|gb|EFH53881.1| hypothetical protein ARALYDRAFT_485224 [Arabidopsis lyrata subsp. lyrata]	324	323	1.00E-151	99.7	78.1	88.6	hypothetical protein ARALYDRAFT_485224	gbpln	Arabidopsis lyrata	AT3G48690.1 | Symbols: ATCXE12, CXE12 | alpha/beta-Hydrolases superfamily protein | chr3:18037186-18038160 REVERSE LENGTH=324	324	324	1.00E-144	100.0	77.5	87.0
Rsa1.0_01779.1.g29745.t1	ref|NP_190440.1| DEK domain-containing chromatin associated protein [Arabidopsis thaliana] gi|6523102|emb|CAB62360.1| putative protein [Arabidopsis thaliana] gi|110739700|dbj|BAF01757.1| hypothetical protein [Arabidopsis thaliana] gi|110739801|dbj|BAF01807.1| hypothetical protein [Arabidopsis thaliana] gi|110740095|dbj|BAF01949.1| hypothetical protein [Arabidopsis thaliana] gi|115646710|gb|ABJ17090.1| At3g48710 [Arabidopsis thaliana] gi|332644927|gb|AEE78448.1| DEK domain-containing chromatin associated protein [Arabidopsis thaliana]	442	462	1.00E-150	104.5	69.9	81.2	DEK domain-containing chromatin associated protein	gbpln	Arabidopsis thaliana	AT3G48710.1 | Symbols: | DEK domain-containing chromatin associated protein | chr3:18041024-18043995 FORWARD LENGTH=462	442	462	1.00E-153	104.5	69.9	81.2
Rsa1.0_01779.1.g29746.t1	ref|NP_190443.1| Nodulin MtN3-like protein [Arabidopsis thaliana] gi|75206789|sp|Q9SMM5.1|SWT11_ARATH RecName: Full=Bidirectional sugar transporter SWEET11; Short=AtSWEET11 gi|13605688|gb|AAK32837.1|AF361825_1 AT3g48740/T8P19_250 [Arabidopsis thaliana] gi|16930411|gb|AAL31891.1|AF419559_1 AT3g48740/T8P19_250 [Arabidopsis thaliana] gi|6523105|emb|CAB62363.1| MTN3-like protein [Arabidopsis thaliana] gi|17979365|gb|AAL49908.1| putative MTN3 protein [Arabidopsis thaliana] gi|18700264|gb|AAL77742.1| AT3g48740/T8P19_250 [Arabidopsis thaliana] gi|20465523|gb|AAM20244.1| putative MTN3 protein [Arabidopsis thaliana] gi|332644930|gb|AEE78451.1| bidirectional sugar transporter SWEET11 [Arabidopsis thaliana]	274	289	1.00E-128	105.5	84.3	90.1	Nodulin MtN3-like protein	gbpln	Arabidopsis thaliana	AT3G48740.1 | Symbols: SWEET11, AtSWEET11 | Nodulin MtN3 family protein | chr3:18052814-18054663 REVERSE LENGTH=289	274	289	1.00E-131	105.5	84.3	90.1
Rsa1.0_01780.1.g29747.t1	ref|XP_002891289.1| hypothetical protein ARALYDRAFT_891393 [Arabidopsis lyrata subsp. lyrata] gi|297337131|gb|EFH67548.1| hypothetical protein ARALYDRAFT_891393 [Arabidopsis lyrata subsp. lyrata]	100	101	2.00E-45	101.0	91.0	96.0	hypothetical protein ARALYDRAFT_891393	gbpln	Arabidopsis lyrata	AT1G44414.1 | Symbols: | unknown protein; Has 29 Blast hits to 29 proteins in 12 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:16847781-16848086 FORWARD LENGTH=101	100	101	1.00E-47	101.0	90.0	96.0
Rsa1.0_01780.1.g29748.t1	dbj|BAB09991.1| mutator-like transposase-like [Arabidopsis thaliana]	604	825	4.00E-64	136.6	27.0	37.3	mutator-like transposase-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01780.1.g29749.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01780.1.g29750.t1	emb|CAJ86406.1| OSIGBa0125M19.9 [Oryza sativa Indica Group]	212	1903	4.00E-34	897.6	38.2	54.7	OSIGBa0125M19.9	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_01780.1.g29751.t9	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01780.1.g29752.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01780.1.g29753.t1	gb|AAD20433.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	334	889	3.00E-28	266.2	16.5	22.8	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01780.1.g29754.t1	gb|ABB60093.1| IAA-amino acid hydrolase 6 [Brassica rapa]	418	461	0	110.3	95.0	96.7	IAA-amino acid hydrolase 6	gbpln	Brassica rapa	AT1G44350.1 | Symbols: ILL6 | IAA-leucine resistant (ILR)-like gene 6 | chr1:16834749-16838201 REVERSE LENGTH=464	418	464	0	111.0	84.2	92.6

Rsa1.0_01781.1.g29755.t1	ref|NP_172716.1| D-isomer specific 2-hydroxyacid dehydrogenase-like protein [Arabidopsis thaliana] gi|75311082|sp|Q9LE33.1|HPR3_ARATH RecName: Full=Glyoxylate/hydroxypyruvate reductase HPR3; AltName: Full=NAD(P)H-dependent hydroxypyruvate reductase 3; Short=AtHPR3; Short=HPR 3 gi|8778636|gb|AAF79644.1|AC025416_18 F5O11.29 [Arabidopsis thaliana] gi|9502370|gb|AAF88077.1|AC025417_5 T12C24.9 [Arabidopsis thaliana] gi|44917547|gb|AAS49098.1| At1g12550 [Arabidopsis thaliana] gi|62320558|dbj|BAD95166.1| hypothetical protein [Arabidopsis thaliana] gi|332190775|gb|AEE28896.1| glyoxylate/hydroxypyruvate reductase HPR3 [Arabidopsis thaliana]	320	323	1.00E-133	100.9	72.8	84.1	D-isomer specific 2-hydroxyacid dehydrogenase-like protein	gbpln	Arabidopsis thaliana	AT1G12550.1 | Symbols: | D-isomer specific 2-hydroxyacid dehydrogenase family protein | chr1:4274649-4275831 FORWARD LENGTH=323	320	323	1.00E-136	100.9	72.8	84.1
Rsa1.0_01781.1.g29756.t1	ref|NP_172716.1| D-isomer specific 2-hydroxyacid dehydrogenase-like protein [Arabidopsis thaliana] gi|75311082|sp|Q9LE33.1|HPR3_ARATH RecName: Full=Glyoxylate/hydroxypyruvate reductase HPR3; AltName: Full=NAD(P)H-dependent hydroxypyruvate reductase 3; Short=AtHPR3; Short=HPR 3 gi|8778636|gb|AAF79644.1|AC025416_18 F5O11.29 [Arabidopsis thaliana] gi|9502370|gb|AAF88077.1|AC025417_5 T12C24.9 [Arabidopsis thaliana] gi|44917547|gb|AAS49098.1| At1g12550 [Arabidopsis thaliana] gi|62320558|dbj|BAD95166.1| hypothetical protein [Arabidopsis thaliana] gi|332190775|gb|AEE28896.1| glyoxylate/hydroxypyruvate reductase HPR3 [Arabidopsis thaliana]	319	323	1.00E-133	101.3	72.4	84.6	D-isomer specific 2-hydroxyacid dehydrogenase-like protein	gbpln	Arabidopsis thaliana	AT1G12550.1 | Symbols: | D-isomer specific 2-hydroxyacid dehydrogenase family protein | chr1:4274649-4275831 FORWARD LENGTH=323	319	323	1.00E-135	101.3	72.4	84.6
Rsa1.0_01781.1.g29757.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01781.1.g29758.t1	ref|NP_172715.4| basic helix-loop-helix domain-containing protein [Arabidopsis thaliana] gi|75311390|sp|Q9LN95.1|BH055_ARATH RecName: Full=Transcription factor bHLH55; AltName: Full=Basic helix-loop-helix protein 55; Short=AtbHLH55; Short=bHLH 55; AltName: Full=Transcription factor EN 1; AltName: Full=bHLH transcription factor bHLH055 gi|8778635|gb|AAF79643.1|AC025416_17 F5O11.28 [Arabidopsis thaliana] gi|332190774|gb|AEE28895.1| transcription factor bHLH55 [Arabidopsis thaliana]	258	257	2.00E-95	99.6	68.2	77.5	basic helix-loop-helix domain-containing protein	gbpln	Arabidopsis thaliana	AT1G12540.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:4272960-4273980 FORWARD LENGTH=257	258	257	5.00E-98	99.6	68.2	77.5
Rsa1.0_01781.1.g29759.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01781.1.g29760.t1	gb|EOA36720.1| hypothetical protein CARUB_v10012364mg [Capsella rubella]	291	179	3.00E-62	61.5	46.0	49.1	hypothetical protein CARUB_v10012364mg	gbpln	Capsella rubella	AT1G12530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G56420.1); Has 54 Blast hits to 53 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:4269122-4270771 REVERSE LENGTH=193	291	193	2.00E-64	66.3	45.7	51.5
Rsa1.0_01781.1.g29761.t1	ref|XP_002891818.1| hypothetical protein ARALYDRAFT_474572 [Arabidopsis lyrata subsp. lyrata] gi|297337660|gb|EFH68077.1| hypothetical protein ARALYDRAFT_474572 [Arabidopsis lyrata subsp. lyrata]	622	273	2.00E-84	43.9	27.3	32.0	hypothetical protein ARALYDRAFT_474572	gbpln	Arabidopsis lyrata	AT1G55170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14750.1); Has 13439 Blast hits to 8993 proteins in 828 species: Archae - 344; Bacteria - 1469; Metazoa - 6958; Fungi - 1008; Plants - 683; Viruses - 29; Other Eukaryotes - 2948 (source: NCBI BLink). | chr1:20580578-20581706 FORWARD LENGTH=283	622	283	7.00E-83	45.5	26.8	31.8
Rsa1.0_01782.1.g29762.t1	gb|EOA19622.1| hypothetical protein CARUB_v10002949mg [Capsella rubella]	329	333	1.00E-140	101.2	84.8	89.1	hypothetical protein CARUB_v10002949mg	gbpln	Capsella rubella	AT5G23000.1 | Symbols: RAX1, MYB37, ATMYB37 | myb domain protein 37 | chr5:7696234-7697712 FORWARD LENGTH=329	329	329	1.00E-129	100.0	81.2	87.2

Rsa1.0_01782.1.g29763.t1	ref|XP_002872027.1| hypothetical protein ARALYDRAFT_489152 [Arabidopsis lyrata subsp. lyrata] gi|297317864|gb|EFH48286.1| hypothetical protein ARALYDRAFT_489152 [Arabidopsis lyrata subsp. lyrata]	507	508	0	100.2	78.1	86.2	hypothetical protein ARALYDRAFT_489152	gbpln	Arabidopsis lyrata	AT5G22980.1 | Symbols: scpl47 | serine carboxypeptidase-like 47 | chr5:7688084-7690481 FORWARD LENGTH=505	507	505	0	99.6	77.7	86.2
Rsa1.0_01782.1.g29764.t1	ref|XP_002872026.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|297317863|gb|EFH48285.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	219	229	2.00E-92	104.6	86.3	94.5	SNF7 family protein	gbpln	Arabidopsis lyrata	AT5G22950.1 | Symbols: VPS24.1 | SNF7 family protein | chr5:7681380-7682720 FORWARD LENGTH=229	219	229	7.00E-94	104.6	85.8	94.1
Rsa1.0_01782.1.g29765.t1	ref|XP_002872023.1| ATCHX3 [Arabidopsis lyrata subsp. lyrata] gi|297317860|gb|EFH48282.1| ATCHX3 [Arabidopsis lyrata subsp. lyrata]	814	815	0	100.1	85.4	93.5	ATCHX3	gbpln	Arabidopsis lyrata	AT5G22900.1 | Symbols: ATCHX3, CHX3 | cation/H+ exchanger 3 | chr5:7657224-7659868 FORWARD LENGTH=822	814	822	0	101.0	84.4	92.6
Rsa1.0_01782.1.g29766.t1	gb|EOA22034.1| hypothetical protein CARUB_v10002559mg [Capsella rubella]	374	369	1.00E-148	98.7	72.5	82.1	hypothetical protein CARUB_v10002559mg	gbpln	Capsella rubella	AT5G22890.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:7653541-7654662 REVERSE LENGTH=373	374	373	1.00E-149	99.7	70.6	81.6
Rsa1.0_01782.1.g29767.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01782.1.g29768.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01782.1.g29769.t1	ref|NP_190184.1| histone H2B [Arabidopsis thaliana] gi|297819124|ref|XP_002877445.1| hypothetical protein ARALYDRAFT_484977 [Arabidopsis lyrata subsp. lyrata] gi|75097936|sp|O23629.3|H2B6_ARATH RecName: Full=Histone H2B.6; AltName: Full=H2BAt; AltName: Full=HTB9 gi|2407802|emb|CAA73156.1| histone H2B [Arabidopsis thaliana] gi|7339499|emb|CAB82822.1| histone H2B [Arabidopsis thaliana] gi|21592825|gb|AAM64775.1| histone H2B [Arabidopsis thaliana] gi|30102580|gb|AAP21208.1| At3g45980 [Arabidopsis thaliana] gi|110743640|dbj|BAE99657.1| histone H2B [Arabidopsis thaliana] gi|297323283|gb|EFH53704.1| hypothetical protein ARALYDRAFT_484977 [Arabidopsis lyrata subsp. lyrata] gi|332644576|gb|AEE78097.1| histone H2B [Arabidopsis thaliana]	141	150	2.00E-57	106.4	90.8	92.9	histone H2B	gbpln	Arabidopsis lyrata	AT3G45980.1 | Symbols: H2B, HTB9 | Histone superfamily protein | chr3:16897492-16897944 REVERSE LENGTH=150	141	150	4.00E-60	106.4	90.8	92.9
Rsa1.0_01782.1.g29770.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	627	657	1.00E-153	104.8	42.7	56.0	T14P8.10	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	627	746	8.00E-66	119.0	23.8	32.5
Rsa1.0_01782.1.g29771.t1	ref|XP_002874099.1| hypothetical protein ARALYDRAFT_910289 [Arabidopsis lyrata subsp. lyrata] gi|297319936|gb|EFH50358.1| hypothetical protein ARALYDRAFT_910289 [Arabidopsis lyrata subsp. lyrata]	132	208	1.00E-57	157.6	81.8	89.4	hypothetical protein ARALYDRAFT_910289	gbpln	Arabidopsis lyrata	AT5G22870.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr5:7647056-7647679 REVERSE LENGTH=207	132	207	8.00E-60	156.8	80.3	90.2
Rsa1.0_01783.1.g29772.t1	ref|XP_002877969.1| hypothetical protein ARALYDRAFT_485829 [Arabidopsis lyrata subsp. lyrata] gi|297323807|gb|EFH54228.1| hypothetical protein ARALYDRAFT_485829 [Arabidopsis lyrata subsp. lyrata]	363	359	1.00E-153	98.9	78.2	82.9	hypothetical protein ARALYDRAFT_485829	gbpln	Arabidopsis lyrata	AT3G54310.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G38430.1); Has 44 Blast hits to 41 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:20111153-20112944 REVERSE LENGTH=358	363	358	1.00E-153	98.6	75.8	81.8
Rsa1.0_01783.1.g29773.t1	gb|ADO16346.1| wrinkled 1 [Brassica napus]	415	415	0	100.0	92.8	95.9	wrinkled 1	gbpln	Brassica napus	AT3G54320.3 | Symbols: WRI1, WRI, ASML1 | Integrase-type DNA-binding superfamily protein | chr3:20114809-20118473 FORWARD LENGTH=430	415	430	1.00E-161	103.6	72.3	77.8
Rsa1.0_01783.1.g29774.t1	gb|AAB08877.1| homeotic protein boi1AP3 [Brassica oleracea var. italica]	232	232	1.00E-133	100.0	99.6	100.0	homeotic protein boi1AP3	gbpln	Brassica oleracea	AT3G54340.1 | Symbols: AP3, ATAP3 | K-box region and MADS-box transcription factor family protein | chr3:20119428-20121087 REVERSE LENGTH=232	232	232	1.00E-130	100.0	94.4	97.8
Rsa1.0_01783.1.g29775.t1	gb|EOA24107.1| hypothetical protein CARUB_v10017338mg [Capsella rubella]	400	415	0	103.8	89.0	95.3	hypothetical protein CARUB_v10017338mg	gbpln	Capsella rubella	AT3G54360.1 | Symbols: | zinc ion binding | chr3:20128570-20131581 REVERSE LENGTH=405	400	405	0	101.3	86.5	92.0
Rsa1.0_01783.1.g29776.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01783.1.g29777.t2	ref|XP_002877975.1| transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297323813|gb|EFH54234.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	312	296	1.00E-126	94.9	81.7	87.2	transcription factor	gbpln	Arabidopsis lyrata	AT3G54390.1 | Symbols: | sequence-specific DNA binding transcription factors | chr3:20137912-20138863 REVERSE LENGTH=296	312	296	1.00E-127	94.9	80.1	86.9
Rsa1.0_01783.1.g29778.t1	dbj|BAJ34532.1| unnamed protein product [Thellungiella halophila]	430	428	0	99.5	86.5	92.1	unnamed protein product	----	----	AT3G54400.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr3:20140291-20142599 REVERSE LENGTH=425	430	425	0	98.8	82.8	89.3
Rsa1.0_01783.1.g29779.t1	ref|XP_002876253.1| hypothetical protein ARALYDRAFT_485842 [Arabidopsis lyrata subsp. lyrata] gi|297322091|gb|EFH52512.1| hypothetical protein ARALYDRAFT_485842 [Arabidopsis lyrata subsp. lyrata]	273	273	1.00E-147	100.0	90.5	96.0	hypothetical protein ARALYDRAFT_485842	gbpln	Arabidopsis lyrata	AT3G54420.1 | Symbols: ATEP3, ATCHITIV, CHIV, EP3 | homolog of carrot EP3-3 chitinase | chr3:20145935-20147034 FORWARD LENGTH=273	273	273	1.00E-148	100.0	91.6	94.9
Rsa1.0_01783.1.g29780.t1	ref|NP_191011.1| SHI-related sequence 6 [Arabidopsis thaliana] gi|17386152|gb|AAL38622.1|AF446889_1 AT3g54430/T12E18_120 [Arabidopsis thaliana] gi|7288021|emb|CAB81808.1| putative protein [Arabidopsis thaliana] gi|15450615|gb|AAK96579.1| AT3g54430/T12E18_120 [Arabidopsis thaliana] gi|332645708|gb|AEE79229.1| SHI-related sequence 6 [Arabidopsis thaliana]	188	183	1.00E-71	97.3	75.0	83.0	SHI-related sequence 6	gbpln	Arabidopsis thaliana	AT3G54430.1 | Symbols: SRS6 | SHI-related sequence 6 | chr3:20147224-20147851 REVERSE LENGTH=183	188	183	5.00E-74	97.3	75.0	83.0
Rsa1.0_01783.1.g29781.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01784.1.g29782.t1	gb|EOA25921.1| hypothetical protein CARUB_v10019301mg [Capsella rubella]	150	153	4.00E-60	102.0	80.0	88.0	hypothetical protein CARUB_v10019301mg	gbpln	Capsella rubella	AT3G58230.1 | Symbols: | Ubiquitin-specific protease family C19-related protein | chr3:21566860-21567396 REVERSE LENGTH=153	150	153	1.00E-61	102.0	77.3	88.0
Rsa1.0_01784.1.g29783.t1	ref|XP_002891988.1| hypothetical protein ARALYDRAFT_892860 [Arabidopsis lyrata subsp. lyrata] gi|297337830|gb|EFH68247.1| hypothetical protein ARALYDRAFT_892860 [Arabidopsis lyrata subsp. lyrata]	217	320	7.00E-52	147.5	54.4	70.5	hypothetical protein ARALYDRAFT_892860	gbpln	Arabidopsis lyrata	AT3G58410.1 | Symbols: | TRAF-like family protein | chr3:21604871-21606229 REVERSE LENGTH=328	217	328	9.00E-54	151.2	53.9	66.8
Rsa1.0_01784.1.g29784.t1	ref|NP_191395.1| TRAF-like family protein [Arabidopsis thaliana] gi|6735348|emb|CAB68174.1| putative protein [Arabidopsis thaliana] gi|332646252|gb|AEE79773.1| TRAF-like family protein [Arabidopsis thaliana]	283	298	1.00E-109	105.3	70.0	82.7	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G58360.1 | Symbols: | TRAF-like family protein | chr3:21593505-21594866 REVERSE LENGTH=298	283	298	1.00E-112	105.3	70.0	82.7
Rsa1.0_01784.1.g29785.t1	gb|EOA25791.1| hypothetical protein CARUB_v10019158mg [Capsella rubella]	180	180	7.00E-70	100.0	78.3	90.0	hypothetical protein CARUB_v10019158mg	gbpln	Capsella rubella	AT3G58300.1 | Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) family | chr3:21582764-21583390 REVERSE LENGTH=181	180	181	5.00E-68	100.6	81.7	91.1
Rsa1.0_01784.1.g29786.t1	ref|NP_191385.1| TRAF-like family protein [Arabidopsis thaliana] gi|6735338|emb|CAB68164.1| putative protein [Arabidopsis thaliana] gi|332646239|gb|AEE79760.1| TRAF-like family protein [Arabidopsis thaliana]	286	321	2.00E-38	112.2	36.7	47.9	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT3G58260.1 | Symbols: | TRAF-like family protein | chr3:21573754-21575114 REVERSE LENGTH=321	286	321	5.00E-41	112.2	36.7	47.9
Rsa1.0_01784.1.g29787.t1	gb|EOA25921.1| hypothetical protein CARUB_v10019301mg [Capsella rubella]	153	153	4.00E-67	100.0	83.0	92.2	hypothetical protein CARUB_v10019301mg	gbpln	Capsella rubella	AT3G58230.1 | Symbols: | Ubiquitin-specific protease family C19-related protein | chr3:21566860-21567396 REVERSE LENGTH=153	153	153	2.00E-69	100.0	81.7	92.2
Rsa1.0_01785.1.g29788.t1	gb|EOA16372.1| hypothetical protein CARUB_v10004522mg [Capsella rubella]	539	549	0	101.9	87.0	92.4	hypothetical protein CARUB_v10004522mg	gbpln	Capsella rubella	AT5G37790.1 | Symbols: | Protein kinase superfamily protein | chr5:15008433-15011025 REVERSE LENGTH=552	539	552	0	102.4	85.5	90.7
Rsa1.0_01785.1.g29789.t2	ref|XP_003545476.1| PREDICTED: calmodulin-like isoform 4 [Glycine max]	160	163	6.00E-78	101.9	93.1	96.3	PREDICTED: calmodulin-like isoform 4	gbenv/gbpln	Glycine max	AT5G37780.2 | Symbols: CAM1, TCH1, ACAM-1 | calmodulin 1 | chr5:15004769-15006117 REVERSE LENGTH=164	160	164	3.00E-79	102.5	92.5	93.8
Rsa1.0_01785.1.g29790.t1	gb|AGJ81361.1| small C2 domain protein [Brassica napus]	134	168	7.00E-65	125.4	88.8	95.5	small C2 domain protein	gbpln	Brassica napus	AT5G37740.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr5:14992148-14993431 FORWARD LENGTH=168	134	168	6.00E-59	125.4	77.6	89.6
Rsa1.0_01785.1.g29791.t2	ref|XP_002868538.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297314374|gb|EFH44797.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	314	168	5.00E-79	53.5	45.2	49.0	C2 domain-containing protein	gbpln	Arabidopsis lyrata	AT5G37740.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr5:14992148-14993431 FORWARD LENGTH=168	314	168	7.00E-81	53.5	44.3	49.0

Rsa1.0_01786.1.g29792.t1	ref|XP_002871554.1| hypothetical protein ARALYDRAFT_488138 [Arabidopsis lyrata subsp. lyrata] gi|297317391|gb|EFH47813.1| hypothetical protein ARALYDRAFT_488138 [Arabidopsis lyrata subsp. lyrata]	197	198	4.00E-76	100.5	75.1	85.3	hypothetical protein ARALYDRAFT_488138	gbpln	Arabidopsis lyrata	AT5G13220.1 | Symbols: JAZ10, TIFY9, JAS1 | jasmonate-zim-domain protein 10 | chr5:4219001-4220502 FORWARD LENGTH=197	197	197	1.00E-76	100.0	74.1	83.2
Rsa1.0_01786.1.g29793.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01786.1.g29794.t3	gb|EOA20368.1| hypothetical protein CARUB_v10000682mg [Capsella rubella]	411	533	2.00E-55	129.7	40.6	49.6	hypothetical protein CARUB_v10000682mg	gbpln	Capsella rubella	AT5G17160.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03130.1); Has 14330 Blast hits to 10381 proteins in 896 species: Archae - 94; Bacteria - 2881; Metazoa - 4019; Fungi - 1576; Plants - 515; Viruses - 110; Other Eukaryotes - 5135 (source: NCBI BLink). | chr5:5639843-5642427 REVERSE LENGTH=569	411	569	7.00E-57	138.4	42.1	51.6
Rsa1.0_01786.1.g29795.t1	ref|NP_196833.2| receptor-like kinase CORYNE [Arabidopsis thaliana] gi|332004492|gb|AED91875.1| receptor-like kinase CORYNE [Arabidopsis thaliana]	115	376	2.00E-32	327.0	58.3	60.9	receptor-like kinase CORYNE	gbpln	Arabidopsis thaliana	AT5G13290.1 | Symbols: SOL2, CRN | Protein kinase superfamily protein | chr5:4252924-4254215 REVERSE LENGTH=376	115	376	3.00E-35	327.0	58.3	60.9
Rsa1.0_01786.1.g29796.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01786.1.g29797.t1	gb|EOA21325.1| hypothetical protein CARUB_v10001686mg [Capsella rubella]	275	274	1.00E-145	99.6	92.0	96.7	hypothetical protein CARUB_v10001686mg	gbpln	Capsella rubella	AT5G13430.1 | Symbols: | Ubiquinol-cytochrome C reductase iron-sulfur subunit | chr5:4305414-4307399 REVERSE LENGTH=272	275	272	1.00E-147	98.9	93.5	96.7
Rsa1.0_01786.1.g29798.t1	gb|EOA21325.1| hypothetical protein CARUB_v10001686mg [Capsella rubella]	273	274	2.33E-156	100.4	93.0	96.3	hypothetical protein CARUB_v10001686mg	gbpln	Capsella rubella	AT5G13430.1 | Symbols: | Ubiquinol-cytochrome C reductase iron-sulfur subunit | chr5:4305414-4307399 REVERSE LENGTH=272	273	272	2.33E-156	99.6	92.7	96.0
Rsa1.0_01786.1.g29799.t1	gb|ABL97953.1| hydrogen-transporting ATP synthase [Brassica rapa]	235	244	1.00E-124	103.8	94.9	97.4	hydrogen-transporting ATP synthase	gbpln	Brassica rapa	AT5G13450.1 | Symbols: ATP5 | delta subunit of Mt ATP synthase | chr5:4310558-4311941 REVERSE LENGTH=238	235	238	1.00E-116	101.3	85.5	92.3
Rsa1.0_01786.1.g29800.t1	ref|NP_196850.1| protein IQ-domain 11 [Arabidopsis thaliana] gi|7543913|emb|CAB87153.1| putative protein [Arabidopsis thaliana] gi|15451144|gb|AAK96843.1| putative protein [Arabidopsis thaliana] gi|21554279|gb|AAM63354.1| unknown [Arabidopsis thaliana] gi|22136116|gb|AAM91136.1| putative protein [Arabidopsis thaliana] gi|332004514|gb|AED91897.1| protein IQ-domain 11 [Arabidopsis thaliana]	297	443	1.00E-75	149.2	50.5	58.9	protein IQ-domain 11	gbpln	Arabidopsis thaliana	AT5G13460.1 | Symbols: IQD11 | IQ-domain 11 | chr5:4316323-4318247 FORWARD LENGTH=443	297	443	3.00E-78	149.2	50.5	58.9
Rsa1.0_01786.1.g29801.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01786.1.g29802.t1	gb|EOA20110.1| hypothetical protein CARUB_v10000389mg [Capsella rubella]	641	674	0	105.1	85.5	89.4	hypothetical protein CARUB_v10000389mg	gbpln	Capsella rubella	AT5G13480.1 | Symbols: FY | Transducin/WD40 repeat-like superfamily protein | chr5:4326638-4331557 REVERSE LENGTH=647	641	647	0	100.9	81.7	85.6
Rsa1.0_01786.1.g29803.t4	ref|XP_002871570.1| hypothetical protein ARALYDRAFT_488169 [Arabidopsis lyrata subsp. lyrata] gi|297317407|gb|EFH47829.1| hypothetical protein ARALYDRAFT_488169 [Arabidopsis lyrata subsp. lyrata]	685	384	1.00E-180	56.1	49.1	50.9	hypothetical protein ARALYDRAFT_488169	gbpln	Arabidopsis lyrata	AT5G13490.2 | Symbols: AAC2 | ADP/ATP carrier 2 | chr5:4336034-4337379 FORWARD LENGTH=385	685	385	1.00E-175	56.2	47.4	49.9
Rsa1.0_01786.1.g29804.t1	gb|EOA22850.1| hypothetical protein CARUB_v10003580mg [Capsella rubella]	220	217	1.00E-107	98.6	90.9	95.0	hypothetical protein CARUB_v10003580mg	gbpln	Capsella rubella	AT5G13510.1 | Symbols: | Ribosomal protein L10 family protein | chr5:4341294-4341956 FORWARD LENGTH=220	220	220	1.00E-106	100.0	90.0	95.0
Rsa1.0_01786.1.g29805.t1	ref|XP_002873618.1| hypothetical protein ARALYDRAFT_909308 [Arabidopsis lyrata subsp. lyrata] gi|297319455|gb|EFH49877.1| hypothetical protein ARALYDRAFT_909308 [Arabidopsis lyrata subsp. lyrata]	662	679	0	102.6	86.4	92.7	hypothetical protein ARALYDRAFT_909308	gbpln	Arabidopsis lyrata	AT5G13560.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G37370.1); Has 12055 Blast hits to 8846 proteins in 811 species: Archae - 217; Bacteria - 1046; Metazoa - 6104; Fungi - 1115; Plants - 528; Viruses - 14; Other Eukaryotes - 3031 (source: NCBI BLink). | chr5:4361579-4366318 REVERSE LENGTH=679	662	679	0	102.6	84.9	92.4

Rsa1.0_01786.1.g29806.t1	ref|NP_196861.2| mRNA-decapping enzyme subunit 2 [Arabidopsis thaliana] gi|75328895|sp|Q8GW31.1|DCP2_ARATH RecName: Full=mRNA-decapping enzyme subunit 2; Short=AtDCP2; Short=Protein DECAPPING 2; AltName: Full=M(7)GpppN-mRNA hydrolase DCP2; AltName: Full=Protein TRIDENT gi|26453220|dbj|BAC43684.1| unknown protein [Arabidopsis thaliana] gi|28950945|gb|AAO63396.1| At5g13570 [Arabidopsis thaliana] gi|332004529|gb|AED91912.1| mRNA-decapping enzyme subunit 2 [Arabidopsis thaliana]	322	373	1.00E-153	115.8	85.7	91.6	mRNA-decapping enzyme subunit 2	gbpln	Arabidopsis thaliana	AT5G13570.1 | Symbols: DCP2, TDT, ATDCP2 | decapping 2 | chr5:4367532-4369992 FORWARD LENGTH=373	322	373	1.00E-155	115.8	85.7	91.6
Rsa1.0_01786.1.g29807.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	601	478	1.00E-137	79.5	38.9	51.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	601	746	1.00E-120	124.1	34.8	45.1
Rsa1.0_01786.1.g29808.t3	ref|XP_002873619.1| hypothetical protein ARALYDRAFT_909311 [Arabidopsis lyrata subsp. lyrata] gi|297319456|gb|EFH49878.1| hypothetical protein ARALYDRAFT_909311 [Arabidopsis lyrata subsp. lyrata]	1026	1217	0	118.6	67.2	76.7	hypothetical protein ARALYDRAFT_909311	gbpln	Arabidopsis lyrata	AT5G13590.1 | Symbols: | unknown protein; Has 150 Blast hits to 121 proteins in 42 species: Archae - 0; Bacteria - 8; Metazoa - 80; Fungi - 5; Plants - 17; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink). | chr5:4374718-4378647 REVERSE LENGTH=1168	1026	1168	0	113.8	64.1	73.6
Rsa1.0_01787.1.g29809.t1	gb|AAD32866.1|AC005489_4 F14N23.4 [Arabidopsis thaliana]	140	1161	6.00E-22	829.3	40.7	53.6	F14N23.4	gbpln	Arabidopsis thaliana	AT5G16486.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:5383597-5384226 REVERSE LENGTH=209	140	209	2.00E-21	149.3	37.1	54.3
Rsa1.0_01787.1.g29810.t1	gb|ACG60682.1| transposon-like ORF [Brassica oleracea var. alboglabra]	453	704	1.00E-132	155.4	55.4	65.6	transposon-like ORF	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01787.1.g29811.t2	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	360	414	3.00E-35	115.0	26.4	37.8	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01787.1.g29812.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	438	414	4.00E-61	94.5	32.2	41.8	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01787.1.g29813.t1	ref|NP_195783.3| breast cancer 2 susceptibility protein [Arabidopsis thaliana] gi|31335362|emb|CAD32572.1| breast cancer susceptibility protein 2b [Arabidopsis thaliana] gi|332002986|gb|AED90369.1| protein BRCA2-like B [Arabidopsis thaliana]	1060	1155	0	109.0	75.9	84.2	breast cancer 2 susceptibility protein	gbpln	Arabidopsis thaliana	AT5G01630.1 | Symbols: BRCA2B, BRCA2(V), ATBRCA2(V) | BRCA2-like B | chr5:235117-240911 REVERSE LENGTH=1155	1060	1155	0	109.0	75.9	84.2
Rsa1.0_01787.1.g29814.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01787.1.g29815.t1	ref|NP_193016.1| photosystem I reaction center subunit XI [Arabidopsis thaliana] gi|18203449|sp|Q9SUI4.2|PSAL_ARATH RecName: Full=Photosystem I reaction center subunit XI, chloroplastic; Short=PSI-L; AltName: Full=PSI subunit V; Flags: Precursor gi|16226622|gb|AAL16216.1|AF428447_1 AT4g12800/T20K18_150 [Arabidopsis thaliana] gi|17933283|gb|AAL48225.1|AF446350_1 AT4g12800/T20K18_150 [Arabidopsis thaliana] gi|4586256|emb|CAB40997.1| probable photosystem I chain XI precursor [Arabidopsis thaliana] gi|7267981|emb|CAB78322.1| probable photosystem I chain XI precursor [Arabidopsis thaliana] gi|16649159|gb|AAL24431.1| probable photosystem I chain XI precursor [Arabidopsis thaliana] gi|20453409|gb|AAM19943.1| AT4g12800/T20K18_150 [Arabidopsis thaliana] gi|21592939|gb|AAM64889.1| probable photosystem I chain XI precursor [Arabidopsis thaliana] gi|332657786|gb|AEE83186.1| photosystem I reaction center subunit XI [Arabidopsis thaliana]	59	219	3.00E-12	371.2	76.3	86.4	photosystem I reaction center subunit XI	gbpln	Arabidopsis thaliana	AT4G12800.1 | Symbols: PSAL | photosystem I subunit l | chr4:7521469-7522493 FORWARD LENGTH=219	59	219	5.00E-15	371.2	76.3	86.4
Rsa1.0_01788.1.g29816.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01788.1.g29817.t4	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	598	695	5.00E-72	116.2	28.1	32.3	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_01788.1.g29818.t1	gb|EOA13328.1| hypothetical protein CARUB_v10026362mg [Capsella rubella]	449	462	0	102.9	84.6	93.8	hypothetical protein CARUB_v10026362mg	gbpln	Capsella rubella	AT5G42830.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr5:17176384-17177906 FORWARD LENGTH=450	449	450	0	100.2	82.2	91.1
Rsa1.0_01788.1.g29819.t1	dbj|BAB09070.1| unnamed protein product [Arabidopsis thaliana] gi|26450382|dbj|BAC42306.1| putative retroelement pol polyprotein [Arabidopsis thaliana] gi|28973203|gb|AAO63926.1| unknown protein [Arabidopsis thaliana]	261	357	4.00E-80	136.8	52.1	64.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	261	237	2.00E-16	90.8	17.6	33.3
Rsa1.0_01788.1.g29820.t1	gb|EOA13993.1| hypothetical protein CARUB_v10027125mg [Capsella rubella]	213	213	1.00E-106	100.0	85.9	93.0	hypothetical protein CARUB_v10027125mg	gbpln	Capsella rubella	AT5G42960.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, chloroplast, plastid, chloroplast envelope; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G45170.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:17235184-17236478 FORWARD LENGTH=213	213	213	1.00E-107	100.0	84.5	92.5
Rsa1.0_01788.1.g29821.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01788.1.g29822.t1	gb|EOA13485.1| hypothetical protein CARUB_v10026545mg [Capsella rubella]	397	397	0	100.0	92.2	96.2	hypothetical protein CARUB_v10026545mg	gbpln	Capsella rubella	AT5G42970.1 | Symbols: COP8, FUS4, EMB134, COP14, CSN4, FUS8, ATS4 | Proteasome component (PCI) domain protein | chr5:17237470-17240649 REVERSE LENGTH=397	397	397	0	100.0	91.9	96.0
Rsa1.0_01788.1.g29823.t1	ref|NP_199114.1| uncharacterized protein [Arabidopsis thaliana] gi|9758589|dbj|BAB09202.1| unnamed protein product [Arabidopsis thaliana] gi|332007516|gb|AED94899.1| uncharacterized protein AT5G43000 [Arabidopsis thaliana]	200	282	4.00E-72	141.0	74.5	82.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G43000.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:17246354-17247202 REVERSE LENGTH=282	200	282	1.00E-74	141.0	74.5	82.0
Rsa1.0_01788.1.g29824.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01789.1.g29825.t1	ref|NP_173345.2| inter-alpha-trypsin inhibitor heavy chain-like protein [Arabidopsis thaliana] gi|22531102|gb|AAM97055.1| unknown protein [Arabidopsis thaliana] gi|23197960|gb|AAN15507.1| unknown protein [Arabidopsis thaliana] gi|332191682|gb|AEE29803.1| inter-alpha-trypsin inhibitor heavy chain-like protein [Arabidopsis thaliana]	757	754	0	99.6	87.7	94.6	inter-alpha-trypsin inhibitor heavy chain-like protein	gbpln	Arabidopsis thaliana	AT1G19110.1 | Symbols: | inter-alpha-trypsin inhibitor heavy chain-related | chr1:6602270-6605766 FORWARD LENGTH=754	757	754	0	99.6	87.7	94.6
Rsa1.0_01789.1.g29826.t1	ref|NP_564074.1| uncharacterized protein [Arabidopsis thaliana] gi|8954052|gb|AAF82225.1|AC069143_1 Contains similarity to a HSPC326 mRNA from Homo sapiens gb|AF161444. EST gb|AI997162 comes from this gene [Arabidopsis thaliana] gi|332191689|gb|AEE29810.1| uncharacterized protein AT1G19140 [Arabidopsis thaliana]	513	311	1.00E-144	60.6	50.7	54.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G19140.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ubiquinone biosynthetic process; LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: COQ9 (InterPro:IPR013718), Ubiquinone biosynthesis protein COQ9 (InterPro:IPR012762); Has 748 Blast hits to 748 proteins in 260 species: Archae - 0; Bacteria - 218; Metazoa - 126; Fungi - 101; Plants - 39; Viruses - 0; Other Eukaryotes - 264 (source: NCBI BLink). | chr1:6611026-6612414 REVERSE LENGTH=311	513	311	2.33E-156	60.6	50.7	54.0
Rsa1.0_01789.1.g29827.t1	ref|XP_002890321.1| hypothetical protein ARALYDRAFT_472139 [Arabidopsis lyrata subsp. lyrata] gi|297336163|gb|EFH66580.1| hypothetical protein ARALYDRAFT_472139 [Arabidopsis lyrata subsp. lyrata]	265	269	1.00E-128	101.5	89.1	94.3	hypothetical protein ARALYDRAFT_472139	gbpln	Arabidopsis lyrata	AT1G19150.1 | Symbols: LHCA6, LHCA2*1 | photosystem I light harvesting complex gene 6 | chr1:6612806-6613799 FORWARD LENGTH=270	265	270	1.00E-128	101.9	88.7	94.0

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<tr><td>Rsa1.0_01789.1.g29828.t2</td><td>gb|AAF82228.1|AC069143_4 Contains similarity to a polygalacturonase-like protein gi|7529266 from Arabidopsis thaliana BAC F18P9 gb|AL138654 and contains multiple polygalacturonase (pectinase) PF|00295 domains [Arabidopsis thaliana]</td><td>524</td><td>533</td><td>0</td><td>101.7</td><td>87.8</td><td>93.1</td><td>Contains similarity to a polygalacturonase-like protein gi|7529266 from Arabidopsis thaliana BAC F18P9 gb|AL138654 and contains multiple polygalacturonase (pectinase) PF|00295 domains</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G19170.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:6616777-6618875 FORWARD LENGTH=506</td><td>524</td><td>506</td><td>0</td><td>96.6</td><td>87.2</td><td>91.2</td></tr>
<tr><td>Rsa1.0_01789.1.g29829.t1</td><td>ref|NP_564075.1| protein TIFY 10A [Arabidopsis thaliana] gi|75174736|sp|Q9LMA8.1|TI10A_ARATH RecName: Full=Protein TIFY 10A; AltName: Full=Jasmonate ZIM domain-containing protein 1 gi|8954056|gb|AAF82229.1|AC069143_5 Contains similarity to an unknown protein T10D10.8 gi|6730756 from Arabidopsis thaliana BAC T10D10 gb|AC016529. ESTs gb|T14209, gb|BE038503, gb|AA650871, gb|AA597384, gb|H76606, gb|AI996806, gb|AI100291 come from this gene [Arabidopsis thaliana] gi|12083250|gb|AAG48784.1|AF332421_1 unknown protein [Arabidopsis thaliana] gi|14532540|gb|AAK63998.1| At1g19180/T29M8_5 [Arabidopsis thaliana] gi|17473768|gb|AAL38322.1| unknown protein [Arabidopsis thaliana] gi|19548055|gb|AAL87391.1| At1g19180/T29M8_5 [Arabidopsis thaliana] gi|20148609|gb|AAM10195.1| unknown protein [Arabidopsis thaliana] gi|332191693|gb|AEE29814.1| protein TIFY 10A [Arabidopsis thaliana]</td><td>257</td><td>253</td><td>1.00E-90</td><td>98.4</td><td>76.7</td><td>82.9</td><td>protein TIFY 10A</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G19180.1 | Symbols: JAZ1, TIFY10A | jasmonate-zim-domain protein 1 | chr1:6622312-6623271 FORWARD LENGTH=253</td><td>257</td><td>253</td><td>3.00E-93</td><td>98.4</td><td>76.7</td><td>82.9</td></tr>
<tr><td>Rsa1.0_01789.1.g29830.t1</td><td>ref|NP_173353.1| alpha/beta-hydrolase-like protein [Arabidopsis thaliana] gi|75335190|sp|Q9LMA7.1|CXE1_ARATH RecName: Full=Probable carboxylesterase 1; AltName: Full=AtCXE1 gi|8954057|gb|AAF82230.1|AC069143_6 Contains similarity to a PrMC3 from Pinus radiata gb|AF110333 [Arabidopsis thaliana] gi|119360077|gb|ABL66767.1| At1g19190 [Arabidopsis thaliana] gi|332191695|gb|AEE29816.1| probable carboxylesterase 1 [Arabidopsis thaliana]</td><td>320</td><td>318</td><td>1.00E-122</td><td>99.4</td><td>67.2</td><td>80.3</td><td>alpha/beta-hydrolase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G19190.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:6623876-6624832 FORWARD LENGTH=318</td><td>320</td><td>318</td><td>1.00E-125</td><td>99.4</td><td>67.2</td><td>80.3</td></tr>
<tr><td>Rsa1.0_01789.1.g29831.t1</td><td>ref|NP_173355.3| ethylene-responsive transcription factor ERF017 [Arabidopsis thaliana] gi|75243159|sp|Q84QC2.1|ERF17_ARATH RecName: Full=Ethylene-responsive transcription factor ERF017 gi|29893536|gb|AAP06820.1| putative AP2 domain transcription factor [Arabidopsis thaliana] gi|332191697|gb|AEE29818.1| ethylene-responsive transcription factor ERF017 [Arabidopsis thaliana]</td><td>182</td><td>185</td><td>6.00E-69</td><td>101.6</td><td>77.5</td><td>86.8</td><td>ethylene-responsive transcription factor ERF017</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G19210.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr1:6626973-6627530 REVERSE LENGTH=185</td><td>182</td><td>185</td><td>2.00E-71</td><td>101.6</td><td>77.5</td><td>86.8</td></tr>
<tr><td>Rsa1.0_01789.1.g29832.t1</td><td>gb|AFD01317.1| auxin response factor 19-1 [Brassica rapa subsp. pekinensis]</td><td>96</td><td>1020</td><td>3.00E-50</td><td>1062.5</td><td>96.9</td><td>99.0</td><td>auxin response factor 19-1</td><td>gbpln</td><td>Brassica rapa</td><td>AT1G19220.1 | Symbols: ARF19, IAA22, ARF11 | auxin response factor 19 | chr1:6628395-6632779 REVERSE LENGTH=1086</td><td>96</td><td>1086</td><td>6.00E-51</td><td>1131.3</td><td>94.8</td><td>96.9</td></tr>
<tr><td>Rsa1.0_01789.1.g29833.t1</td><td>dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]</td><td>1501</td><td>1223</td><td>0</td><td>81.5</td><td>41.0</td><td>53.0</td><td>non-LTR retroelement reverse transcriptase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>1501</td><td>746</td><td>9.00E-81</td><td>49.7</td><td>11.9</td><td>16.3</td></tr>
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<tr><td>Rsa1.0_01790.1.g29835.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01790.1.g29836.t2</td><td>gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>296</td><td>1225</td><td>8.00E-39</td><td>413.9</td><td>36.5</td><td>50.3</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256</td><td>296</td><td>256</td><td>6.00E-18</td><td>86.5</td><td>20.9</td><td>29.1</td></tr>
<tr><td>Rsa1.0_01790.1.g29837.t1</td><td>ref|XP_002865826.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311661|gb|EFH42085.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>577</td><td>583</td><td>0</td><td>101.0</td><td>86.7</td><td>91.3</td><td>kinase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G50860.1 | Symbols: | Protein kinase superfamily protein | chr5:20693778-20696983 REVERSE LENGTH=580</td><td>577</td><td>580</td><td>0</td><td>100.5</td><td>85.6</td><td>90.6</td></tr>
<tr><td>Rsa1.0_01790.1.g29838.t1</td><td>dbj|BAJ34206.1| unnamed protein product [Thellungiella halophila]</td><td>362</td><td>366</td><td>0</td><td>101.1</td><td>98.1</td><td>98.9</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G50850.1 | Symbols: MAB1 | Transketolase family protein | chr5:20689671-20692976 FORWARD LENGTH=363</td><td>362</td><td>363</td><td>0</td><td>100.3</td><td>96.4</td><td>98.3</td></tr>
<tr><td>Rsa1.0_01790.1.g29839.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1196</td><td>1307</td><td>0</td><td>109.3</td><td>57.6</td><td>73.7</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1196</td><td>1262</td><td>2.00E-45</td><td>105.5</td><td>11.3</td><td>19.2</td></tr>
<tr><td>Rsa1.0_01790.1.g29840.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>201</td><td>1142</td><td>2.00E-22</td><td>568.2</td><td>22.9</td><td>34.8</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01790.1.g29841.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01790.1.g29842.t1</td><td>gb|AAC97237.1| putative TNP2-like transposon protein [Arabidopsis thaliana]</td><td>981</td><td>889</td><td>0</td><td>90.6</td><td>49.8</td><td>56.8</td><td>putative TNP2-like transposon protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01790.1.g29843.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<tr><td>Rsa1.0_01791.1.g29845.t1</td><td>ref|XP_002865002.1| hypothetical protein ARALYDRAFT_496854 [Arabidopsis lyrata subsp. lyrata] gi|297310837|gb|EFH41261.1| hypothetical protein ARALYDRAFT_496854 [Arabidopsis lyrata subsp. lyrata]</td><td>252</td><td>244</td><td>1.00E-103</td><td>96.8</td><td>81.7</td><td>86.5</td><td>hypothetical protein ARALYDRAFT_496854</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G67420.1 | Symbols: LBD37, ASL39 | LOB domain-containing protein 37 | chr5:26904576-26905415 REVERSE LENGTH=250</td><td>252</td><td>250</td><td>1.00E-104</td><td>99.2</td><td>82.1</td><td>87.7</td></tr>
<tr><td>Rsa1.0_01791.1.g29846.t1</td><td>pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]</td><td>1869</td><td>1333</td><td>0</td><td>71.3</td><td>35.5</td><td>46.9</td><td>RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1869</td><td>575</td><td>2.00E-93</td><td>30.8</td><td>10.1</td><td>16.3</td></tr>
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Rsa1.0_01791.1.g29847.t1	ref|NP_201544.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] gi|9758442|dbj|BAB09028.1| N-acetyltransferase hookless1-like protein [Arabidopsis thaliana] gi|29029086|gb|AAO64922.1| At5g67430 [Arabidopsis thaliana] gi|110743051|dbj|BAE99418.1| N-acetyltransferase hookless1-like protein [Arabidopsis thaliana] gi|332010960|gb|AED98343.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana]	380	386	0	101.6	86.8	92.1	GCN5-related N-acetyltransferase (GNAT) family protein	gbpln	Arabidopsis thaliana	AT5G67430.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr5:26910429-26911856 FORWARD LENGTH=386	380	386	0	101.6	86.8	92.1
Rsa1.0_01791.1.g29848.t2	gb|EOA13121.1| hypothetical protein CARUB_v10026140mg [Capsella rubella]	565	585	0	103.5	82.7	89.4	hypothetical protein CARUB_v10026140mg	gbpln	Capsella rubella	AT5G67440.1 | Symbols: NPY3 | Phototropic-responsive NPH3 family protein | chr5:26912947-26914906 REVERSE LENGTH=579	565	579	0	102.5	78.6	86.0
Rsa1.0_01791.1.g29849.t1	ref|XP_002886034.1| hypothetical protein ARALYDRAFT_480519 [Arabidopsis lyrata subsp. lyrata] gi|297331874|gb|EFH62293.1| hypothetical protein ARALYDRAFT_480519 [Arabidopsis lyrata subsp. lyrata]	210	202	3.00E-67	96.2	69.0	78.6	hypothetical protein ARALYDRAFT_480519	gbpln	Arabidopsis lyrata	AT2G19530.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G55160.2); Has 461 Blast hits to 346 proteins in 80 species: Archae - 0; Bacteria - 16; Metazoa - 89; Fungi - 28; Plants - 57; Viruses - 0; Other Eukaryotes - 271 (source: NCBI BLink). | chr2:8460219-8461486 FORWARD LENGTH=202	210	202	5.00E-69	96.2	68.6	78.1
Rsa1.0_01791.1.g29850.t1	ref|XP_002886033.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297331873|gb|EFH62292.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	474	470	0	99.2	83.3	86.7	transducin family protein	gbpln	Arabidopsis lyrata	AT2G19540.1 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr2:8461804-8464347 FORWARD LENGTH=469	474	469	0	98.9	81.6	85.7
Rsa1.0_01791.1.g29851.t1	gb|EOA31220.1| hypothetical protein CARUB_v10014386mg [Capsella rubella]	290	270	1.00E-133	93.1	86.6	91.0	hypothetical protein CARUB_v10014386mg	gbpln	Capsella rubella	AT2G19580.1 | Symbols: TET2 | tetraspanin2 | chr2:8472393-8475021 REVERSE LENGTH=270	290	270	1.00E-131	93.1	87.6	91.0
Rsa1.0_01792.1.g29852.t1	emb|CAB75909.1| putative protein [Arabidopsis thaliana]	641	606	0	94.5	73.5	82.7	putative protein	gbpln	Arabidopsis thaliana	AT3G55510.1 | Symbols: RBL | Noc2p family | chr3:20579232-20582124 FORWARD LENGTH=594	641	594	0	92.7	73.3	82.1
Rsa1.0_01792.1.g29853.t1	ref|XP_002878036.1| ATEXPA16 [Arabidopsis lyrata subsp. lyrata] gi|297323874|gb|EFH54295.1| ATEXPA16 [Arabidopsis lyrata subsp. lyrata]	260	260	1.00E-138	100.0	92.7	94.2	ATEXPA16	gbpln	Arabidopsis lyrata	AT3G55500.1 | Symbols: ATEXPA16, EXP16, ATEXP16, ATHEXP ALPHA 1.7, EXPA16 | expansin A16 | chr3:20575073-20576102 REVERSE LENGTH=260	260	260	1.00E-141	100.0	92.3	95.0
Rsa1.0_01792.1.g29854.t1	gb|EOA24113.1| hypothetical protein CARUB_v10017345mg [Capsella rubella]	368	414	1.00E-114	112.5	65.5	79.3	hypothetical protein CARUB_v10017345mg	gbpln	Capsella rubella	AT3G54910.3 | Symbols: | RNI-like superfamily protein | chr3:20342967-20344277 REVERSE LENGTH=373	368	373	1.00E-101	101.4	55.4	70.4
Rsa1.0_01792.1.g29855.t1	ref|NP_194288.2| CAP160 protein [Arabidopsis thaliana] gi|19310451|gb|AAL84961.1| At4g25580/M7J2_50 [Arabidopsis thaliana] gi|24111391|gb|AAN46822.1| At4g25580/M7J2_50 [Arabidopsis thaliana] gi|110737550|dbj|BAF00717.1| hypothetical protein [Arabidopsis thaliana] gi|332659679|gb|AEE85079.1| CAP160 protein [Arabidopsis thaliana]	233	626	3.00E-29	268.7	30.5	33.5	CAP160 protein	gbpln	Arabidopsis thaliana	AT4G25580.1 | Symbols: | CAP160 protein | chr4:13056320-13058657 FORWARD LENGTH=626	233	626	9.00E-32	268.7	30.5	33.5
Rsa1.0_01792.1.g29856.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01792.1.g29857.t1	gb|EOA24113.1| hypothetical protein CARUB_v10017345mg [Capsella rubella]	415	414	1.00E-142	99.8	64.3	80.0	hypothetical protein CARUB_v10017345mg	gbpln	Capsella rubella	AT4G10400.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr4:6446335-6447715 REVERSE LENGTH=409	415	409	1.00E-125	98.6	59.8	71.3
Rsa1.0_01792.1.g29858.t1	gb|EOA13479.1| hypothetical protein CARUB_v10026538mg [Capsella rubella]	549	398	6.00E-36	72.5	13.3	20.8	hypothetical protein CARUB_v10026538mg	gbpln	Capsella rubella	AT2G17920.1 | Symbols: | nucleic acid binding;zinc ion binding | chr2:7782808-7783731 FORWARD LENGTH=307	549	307	2.00E-38	55.9	14.2	23.0
Rsa1.0_01792.1.g29859.t1	gb|EOA24113.1| hypothetical protein CARUB_v10017345mg [Capsella rubella]	366	414	1.00E-104	113.1	57.7	71.9	hypothetical protein CARUB_v10017345mg	gbpln	Capsella rubella	AT3G54910.3 | Symbols: | RNI-like superfamily protein | chr3:20342967-20344277 REVERSE LENGTH=373	366	373	1.00E-101	101.9	57.1	71.0
Rsa1.0_01793.1.g29860.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01793.1.g29861.t1	gb|EOA15695.1| hypothetical protein CARUB_v10006407mg [Capsella rubella]	163	185	6.00E-21	113.5	44.2	59.5	hypothetical protein CARUB_v10006407mg	gbpln	Capsella rubella	AT4G22700.1 | Symbols: LBD32 | LOB domain-containing protein 32 | chr4:11933301-11933879 FORWARD LENGTH=192	163	192	2.00E-22	117.8	48.5	58.9
Rsa1.0_01793.1.g29862.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	770	1274	0	165.5	45.6	60.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	770	575	1.00E-56	74.7	17.5	28.2

Rsa1.0_01793.1.g29863.t1	gb|EOA17210.1| hypothetical protein CARUB_v10005483mg [Capsella rubella]	269	271	1.00E-121	100.7	79.2	87.0	hypothetical protein CARUB_v10005483mg	gbpln	Capsella rubella	AT4G22680.1 | Symbols: MYB85, AtMYB85 | myb domain protein 85 | chr4:11922789-11924080 REVERSE LENGTH=266	269	266	1.00E-112	98.9	77.0	87.0
Rsa1.0_01793.1.g29864.t1	gb|EOA15646.1| hypothetical protein CARUB_v10005919mg [Capsella rubella]	159	160	4.00E-69	100.6	81.1	91.2	hypothetical protein CARUB_v10005919mg	gbpln	Capsella rubella	AT4G22620.1 | Symbols: | SAUR-like auxin-responsive protein family | chr4:11907631-11908113 FORWARD LENGTH=160	159	160	3.00E-70	100.6	79.9	90.6
Rsa1.0_01793.1.g29865.t1	emb|CAA16549.1| putative protein [Arabidopsis thaliana]	188	140	2.00E-25	74.5	31.9	43.1	putative protein	gbpln	Arabidopsis thaliana	AT4G22640.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:11911658-11912008 FORWARD LENGTH=116	188	116	1.00E-27	61.7	31.9	43.1
Rsa1.0_01794.1.g29866.t1	ref|NP_172827.1| cytochrome P450, family 78, subfamily A, polypeptide 5 [Arabidopsis thaliana] gi|8920576|gb|AAF81298.1|AC027656_15 Strong similarity to cytochrome P-450 from Phalaenopsis sp. SM9108 gb|U34744. It contains a cytochrome P450 domain PF|00067. EST gb|T45256 comes from this gene [Arabidopsis thaliana] gi|63003816|gb|AAY25437.1| At1g13710 [Arabidopsis thaliana] gi|115646887|gb|ABJ17153.1| At1g13710 [Arabidopsis thaliana] gi|332190939|gb|AEE29060.1| cytochrome P450, family 78, subfamily A, polypeptide 5 [Arabidopsis thaliana]	331	517	1.00E-173	156.2	90.6	95.5	cytochrome P450, family 78, subfamily A, polypeptide 5	gbpln	Arabidopsis thaliana	AT1G13710.1 | Symbols: CYP78A5, KLU | cytochrome P450, family 78, subfamily A, polypeptide 5 | chr1:4702932-4704592 REVERSE LENGTH=517	331	517	1.00E-175	156.2	90.6	95.5
Rsa1.0_01794.1.g29867.t2	ref|XP_002886390.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata] gi|297332231|gb|EFH62649.1| hypothetical protein ARALYDRAFT_893070 [Arabidopsis lyrata subsp. lyrata]	330	298	2.00E-79	90.3	49.1	62.7	hypothetical protein ARALYDRAFT_893070	gbpln	Arabidopsis lyrata	AT2G42470.1 | Symbols: | TRAF-like family protein | chr2:17679887-17685187 REVERSE LENGTH=898	330	898	3.00E-61	272.1	38.8	57.3
Rsa1.0_01794.1.g29868.t1	ref|NP_176199.1| formin-like protein 7 [Arabidopsis thaliana] gi|75215697|sp|Q9XIE0.1|FH7_ARATH RecName: Full=Formin-like protein 7; Short=AtFH7; Short=AtFORMIN-7 gi|5080823|gb|AAD39332.1|AC007258_21 Hypothetical protein [Arabidopsis thaliana] gi|34222088|gb|AAQ62880.1| At1g59910 [Arabidopsis thaliana] gi|332195518|gb|AEE33639.1| formin-like protein 7 [Arabidopsis thaliana]	868	929	0	107.0	46.0	49.3	formin-like protein 7	gbpln	Arabidopsis thaliana	AT1G59910.1 | Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr1:22054167-22057052 REVERSE LENGTH=929	868	929	0	107.0	46.0	49.3
Rsa1.0_01794.1.g29869.t1	gb|ABV89625.1| pyruvate dehydrogenase complex E1 alpha subunit dehydrogenase [Brassica rapa]	390	389	0	99.7	97.7	98.5	pyruvate dehydrogenase complex E1 alpha subunit dehydrogenase	gbpln	Brassica rapa	AT1G59900.1 | Symbols: AT-E1 ALPHA, E1 ALPHA | pyruvate dehydrogenase complex E1 alpha subunit | chr1:22051368-22053660 FORWARD LENGTH=389	390	389	0	99.7	93.6	97.4
Rsa1.0_01794.1.g29870.t3	gb|EOA33558.1| hypothetical protein CARUB_v10019683mg [Capsella rubella]	1105	1174	0	106.2	77.6	85.9	hypothetical protein CARUB_v10019683mg	gbpln	Capsella rubella	AT1G59890.2 | Symbols: SNL5 | SIN3-like 5 | chr1:22044326-22050670 FORWARD LENGTH=1167	1105	1167	0	105.6	77.4	85.1
Rsa1.0_01794.1.g29871.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01794.1.g29872.t1	ref|XP_002888078.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333919|gb|EFH64337.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	164	114	6.00E-18	69.5	37.8	44.5	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01795.1.g29873.t1	ref|NP_190630.1| uncharacterized protein [Arabidopsis thaliana] gi|6562001|emb|CAB62490.1| hypothetical protein [Arabidopsis thaliana] gi|91805549|gb|ABE65503.1| hypothetical protein At3g50610 [Arabidopsis thaliana] gi|332645164|gb|AEE78685.1| uncharacterized protein AT3G50610 [Arabidopsis thaliana]	240	229	2.00E-92	95.4	72.5	82.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G50610.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66816.1); Has 125 Blast hits to 60 proteins in 16 species: Archae - 0; Bacteria - 2; Metazoa - 10; Fungi - 4; Plants - 97; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink). | chr3:18779723-18780412 REVERSE LENGTH=229	240	229	5.00E-95	95.4	72.5	82.1
Rsa1.0_01795.1.g29874.t1	ref|XP_002877755.1| hypothetical protein ARALYDRAFT_485408 [Arabidopsis lyrata subsp. lyrata] gi|297323593|gb|EFH54014.1| hypothetical protein ARALYDRAFT_485408 [Arabidopsis lyrata subsp. lyrata]	301	340	1.00E-158	113.0	90.4	95.7	hypothetical protein ARALYDRAFT_485408	gbpln	Arabidopsis lyrata	AT3G50620.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:18784993-18786747 REVERSE LENGTH=340	301	340	1.00E-159	113.0	90.0	96.3
Rsa1.0_01795.1.g29875.t2	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	336	414	2.00E-18	123.2	19.0	28.0	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01795.1.g29876.t1	#	#	#	#	#	#	#	–	----	----	AT3G50630.1 | Symbols: KRP2, ICK2 | KIP-related protein 2 | chr3:18800508-18801366 FORWARD LENGTH=209	122	209	1.00E-11	171.3	44.3	52.5

Rsa1.0_01795.1.g29877.t1	gb|AAD19773.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	849	1335	0	157.2	39.8	56.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00300.1 | Symbols: ORF145A | Gag-Pol-related retrotransposon family protein | chrM:89617-90054 REVERSE LENGTH=145	849	145	5.00E-29	17.1	6.5	8.7
Rsa1.0_01796.1.g29878.t1	ref|XP_002888394.1| hexaubiquitin protein [Arabidopsis lyrata subsp. lyrata] gi|297334235|gb|EFH64653.1| hexaubiquitin protein [Arabidopsis lyrata subsp. lyrata]	232	483	2.00E-44	208.2	48.3	60.8	hexaubiquitin protein	gbpln	Arabidopsis lyrata	AT5G20620.1 | Symbols: UBQ4 | ubiquitin 4 | chr5:6973315-6974463 REVERSE LENGTH=382	232	382	3.00E-45	164.7	46.6	57.3
Rsa1.0_01796.1.g29879.t1	gb|EOA30109.1| hypothetical protein CARUB_v10013220mg [Capsella rubella]	632	624	0	98.7	88.9	91.6	hypothetical protein CARUB_v10013220mg	gbpln	Capsella rubella	AT2G18750.3 | Symbols: | Calmodulin-binding protein | chr2:8125827-8128363 FORWARD LENGTH=622	632	622	0	98.4	87.8	91.1
Rsa1.0_01796.1.g29880.t2	gb|EOA16115.1| hypothetical protein CARUB_v10004248mg [Capsella rubella]	424	704	7.00E-86	166.0	46.9	56.4	hypothetical protein CARUB_v10004248mg	gbpln	Capsella rubella	AT4G30200.4 | Symbols: VEL1, VIL2 | vernalization5/VIN3-like | chr4:14787045-14790070 REVERSE LENGTH=624	424	624	1.00E-87	147.2	46.2	53.3
Rsa1.0_01796.1.g29881.t2	ref|NP_179484.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75099137|sp|O64624.1|PP163_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g18940 gi|3004555|gb|AAC09028.1| putative salt-inducible protein [Arabidopsis thaliana] gi|15983785|gb|AAL10489.1| At2g18940/F19F24.14 [Arabidopsis thaliana] gi|38564280|gb|AAR23719.1| At2g18940/F19F24.14 [Arabidopsis thaliana] gi|330251736|gb|AEC06830.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	919	822	0	89.4	74.1	79.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G18940.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:8203873-8206341 REVERSE LENGTH=822	919	822	0	89.4	74.1	79.9
Rsa1.0_01796.1.g29882.t1	ref|NP_179486.1| H(+)-ATPase 1 [Arabidopsis thaliana] gi|12644156|sp|P20649.3|PMA1_ARATH RecName: Full=ATPase 1, plasma membrane-type; AltName: Full=Proton pump 1 gi|3004557|gb|AAC09030.1| plasma membrane proton ATPase (PMA) [Arabidopsis thaliana] gi|30794112|gb|AAP40498.1| putative plasma membrane proton ATPase (PMA) [Arabidopsis thaliana] gi|330251738|gb|AEC06832.1| H(+)-ATPase 1 [Arabidopsis thaliana]	290	949	1.00E-147	327.2	85.5	93.1	H(+)-ATPase 1	gbpln	Arabidopsis thaliana	AT2G18960.1 | Symbols: AHA1, PMA, OST2, HA1 | H(+)-ATPase 1 | chr2:8221858-8227268 FORWARD LENGTH=949	290	949	1.00E-150	327.2	85.5	93.1
Rsa1.0_01796.1.g29883.t1	gb|EOA32628.1| hypothetical protein CARUB_v10015923mg [Capsella rubella]	128	348	1.00E-47	271.9	68.8	81.3	hypothetical protein CARUB_v10015923mg	gbpln	Capsella rubella	AT2G19050.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr2:8253416-8255534 FORWARD LENGTH=349	128	349	1.00E-49	272.7	68.8	81.3
Rsa1.0_01797.1.g29884.t5	ref|XP_002878905.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324744|gb|EFH55164.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	480	480	6.00E-24	100.0	16.9	23.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	480	384	4.00E-12	80.0	11.5	19.6
Rsa1.0_01797.1.g29885.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	225	1142	8.00E-30	507.6	36.9	56.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	225	292	2.00E-19	129.8	31.6	52.9
Rsa1.0_01797.1.g29886.t1	ref|NP_175822.1| uncharacterized protein [Arabidopsis thaliana] gi|4585964|gb|AAD25600.1|AC005287_2 hypothetical protein [Arabidopsis thaliana] gi|119360031|gb|ABL66744.1| At1g54200 [Arabidopsis thaliana] gi|332194939|gb|AEE33060.1| uncharacterized protein AT1G54200 [Arabidopsis thaliana]	352	366	3.00E-82	104.0	65.6	76.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G54200.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13980.1); Has 1084 Blast hits to 581 proteins in 136 species: Archae - 0; Bacteria - 72; Metazoa - 212; Fungi - 78; Plants - 102; Viruses - 0; Other Eukaryotes - 620 (source: NCBI BLink). | chr1:20235855-20236955 FORWARD LENGTH=366	352	366	8.00E-85	104.0	65.6	76.1
Rsa1.0_01797.1.g29887.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01797.1.g29888.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01797.1.g29889.t1	#	#	#	#	#	#	#	-	----	----	AT1G54160.1 | Symbols: NFYA5, NF-YA5 | nuclear factor Y, subunit A5 | chr1:20217581-20218706 REVERSE LENGTH=308	142	308	1.00E-12	216.9	23.9	24.6
Rsa1.0_01797.1.g29890.t1	gb|EOA37967.1| hypothetical protein CARUB_v10009435mg [Capsella rubella]	382	382	1.00E-160	100.0	75.1	86.4	hypothetical protein CARUB_v10009435mg	gbpln	Capsella rubella	AT1G54150.1 | Symbols: | E3 Ubiquitin ligase family protein | chr1:20215480-20217303 FORWARD LENGTH=383	382	383	1.00E-158	100.3	73.0	84.3

Rsa1.0_01798.1.g29891.t1	ref|NP_001190021.1| E3 UFM1-protein ligase 1-like protein [Arabidopsis thaliana] gi|332644616|gb|AEE78137.1| E3 UFM1-protein ligase 1-like protein [Arabidopsis thaliana]	721	788	0	109.3	91.3	95.3	E3 UFM1-protein ligase 1-like protein	gbpln	Arabidopsis thaliana	AT3G46220.3 | Symbols: | unknown protein; INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2042 (InterPro:IPR018611). | chr3:16979174-16983970 FORWARD LENGTH=788	721	788	0	109.3	91.3	95.3
Rsa1.0_01798.1.g29892.t1	gb|AAF78436.1|AC018748_15 Contains similarity to 17.6 KD class I heat shock protein from Arabidopsis thaliana gi|P13853 and contains Hsp20/alpha crystallin PF|00011 and signal peptidase I PF|00461 domains. ESTs gb|AI998650, gb|AW004417, gb|AI998904 come from this gene [Arabidopsis thaliana]	157	403	1.00E-77	256.7	88.5	96.2	Contains similarity to 17.6 KD class I heat shock protein from Arabidopsis thaliana gi|P13853 and contains Hsp20/alpha crystallin PF|00011 and signal peptidase I PF|00461 domains. ESTs gb|AI998650, gb|AW004417, gb|AI998904 come from this gene	gbpln	Arabidopsis thaliana	AT1G53540.1 | Symbols: | HSP20-like chaperones superfamily protein | chr1:19980510-19980983 FORWARD LENGTH=157	157	157	6.00E-79	100.0	88.5	96.2
Rsa1.0_01798.1.g29893.t1	ref|XP_002877472.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297323310|gb|EFH53731.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	457	486	1.00E-138	106.3	54.5	59.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G46240.1 | Symbols: | BEST Arabidopsis thaliana protein match is: receptor protein kinase-related (TAIR:AT3G46270.1); Has 38685 Blast hits to 11525 proteins in 945 species: Archae - 63; Bacteria - 11586; Metazoa - 8974; Fungi - 2953; Plants - 5350; Viruses - 724; Other Eukaryotes - 9035 (source: NCBI BLink). | chr3:16985843-16988064 REVERSE LENGTH=434	457	434	1.00E-118	95.0	46.8	51.6
Rsa1.0_01798.1.g29894.t1	ref|NP_190213.2| protein kinase-like protein [Arabidopsis thaliana] gi|26450306|dbj|BAC42269.1| unknown protein [Arabidopsis thaliana] gi|332644621|gb|AEE78142.1| protein kinase-like protein [Arabidopsis thaliana]	466	471	0	101.1	74.9	83.0	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT3G46280.1 | Symbols: | protein kinase-related | chr3:17005672-17008410 REVERSE LENGTH=471	466	471	0	101.1	74.9	83.0
Rsa1.0_01798.1.g29895.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01798.1.g29896.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	166	490	9.00E-31	295.2	41.0	61.4	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	166	566	7.00E-27	341.0	36.1	59.0
Rsa1.0_01798.1.g29897.t1	ref|NP_190256.1| UDP-glycosyltransferase-like protein [Arabidopsis thaliana] gi|75266316|sp|Q9STE6.1|U76E5_ARATH RecName: Full=UDP-glycosyltransferase 76E5 gi|5541687|emb|CAB51193.1| glucuronosyl transferase-like protein [Arabidopsis thaliana] gi|332644676|gb|AEE78197.1| UDP-glycosyltransferase 76E5 [Arabidopsis thaliana]	163	447	2.00E-67	274.2	72.4	84.7	UDP-glycosyltransferase-like protein	gbpln	Arabidopsis thaliana	AT3G46720.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:17210930-17212348 REVERSE LENGTH=447	163	447	6.00E-70	274.2	72.4	84.7
Rsa1.0_01798.1.g29898.t1	dbj|BAC41861.1| putative glucuronosyl transferase [Arabidopsis thaliana] gi|28951029|gb|AAO63438.1| At3g46690 [Arabidopsis thaliana]	417	452	1.00E-180	108.4	75.8	85.4	putative glucuronosyl transferase	gbpln	Arabidopsis thaliana	AT3G46690.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:17197760-17199197 REVERSE LENGTH=452	417	452	1.00E-177	108.4	75.8	85.4
Rsa1.0_01798.1.g29899.t1	ref|NP_190257.1| putative disease resistance RPP13-like protein 3 [Arabidopsis thaliana] gi|29839682|sp|Q9STE7.1|R13L3_ARATH RecName: Full=Putative disease resistance RPP13-like protein 3 gi|5541686|emb|CAB51192.1| putative protein [Arabidopsis thaliana] gi|332644677|gb|AEE78198.1| putative disease resistance RPP13-like protein 3 [Arabidopsis thaliana]	380	847	1.00E-106	222.9	61.1	73.4	putative disease resistance RPP13-like protein 3	gbpln	Arabidopsis thaliana	AT3G46730.1 | Symbols: | NB-ARC domain-containing disease resistance protein | chr3:17213069-17215612 REVERSE LENGTH=847	380	847	1.00E-109	222.9	61.1	73.4
Rsa1.0_01798.1.g29900.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01798.1.g29901.t1	gb|EOA23492.1| hypothetical protein CARUB_v10016683mg, partial [Capsella rubella]	817	845	0	103.4	91.9	94.4	hypothetical protein CARUB_v10016683mg, partial	gbpln	Capsella rubella	AT3G46740.1 | Symbols: TOC75-III, MAR1 | translocon at the outer envelope membrane of chloroplasts 75-III | chr3:17216104-17219296 REVERSE LENGTH=818	817	818	0	100.1	90.8	94.2

Rsa1.0_01798.1.g29902.t1	ref|NP_190259.2| uncharacterized protein [Arabidopsis thaliana] gi|52354323|gb|AAU44482.1| hypothetical protein AT3G46750 [Arabidopsis thaliana] gi|60547795|gb|AAX23861.1| hypothetical protein At3g46750 [Arabidopsis thaliana] gi|332644679|gb|AEE78200.1| uncharacterized protein AT3G46750 [Arabidopsis thaliana]	333	388	1.00E-137	116.5	80.8	86.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G46750.1 | Symbols: | unknown protein; Has 2631 Blast hits to 1984 proteins in 271 species: Archae - 6; Bacteria - 163; Metazoa - 1232; Fungi - 253; Plants - 141; Viruses - 8; Other Eukaryotes - 828 (source: NCBI BLink). | chr3:17219944-17221461 FORWARD LENGTH=388	333	388	1.00E-140	116.5	80.8	86.8
Rsa1.0_01798.1.g29903.t1	gb|ABA18111.1| pentatricopeptide repeat protein [Arabidopsis arenosa]	505	419	1.00E-169	83.0	58.0	68.3	pentatricopeptide repeat protein	gbpln	Arabidopsis arenosa	AT3G42630.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:14722314-14723635 FORWARD LENGTH=415	505	415	1.00E-169	82.2	57.2	67.7
Rsa1.0_01799.1.g29904.t2	gb|EOA13046.1| hypothetical protein CARUB_v10026047mg [Capsella rubella]	661	657	0	99.4	81.4	88.4	hypothetical protein CARUB_v10026047mg	gbpln	Capsella rubella	AT5G44230.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:17814336-17816309 FORWARD LENGTH=657	661	657	0	99.4	79.4	87.4
Rsa1.0_01799.1.g29905.t1	ref|XP_002863603.1| hypothetical protein ARALYDRAFT_917193 [Arabidopsis lyrata subsp. lyrata] gi|297309438|gb|EFH39862.1| hypothetical protein ARALYDRAFT_917193 [Arabidopsis lyrata subsp. lyrata]	409	406	0	99.3	88.0	92.7	hypothetical protein ARALYDRAFT_917193	gbpln	Arabidopsis lyrata	AT5G44250.1 | Symbols: | Protein of unknown function DUF829, transmembrane 53 | chr5:17823876-17825620 REVERSE LENGTH=403	409	403	0	98.5	88.0	92.2
Rsa1.0_01799.1.g29906.t1	ref|XP_002863601.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] gi|297309436|gb|EFH39860.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	372	382	1.00E-142	102.7	80.1	87.9	zinc finger (CCCH-type) family protein	gbpln	Arabidopsis lyrata	AT5G44260.1 | Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr5:17829974-17831119 REVERSE LENGTH=381	372	381	1.00E-135	102.4	79.3	88.7
Rsa1.0_01799.1.g29907.t4	ref|NP_199241.2| putative E3 ubiquitin-protein ligase RING1a [Arabidopsis thaliana] gi|302425246|sp|Q9FKW0.2|RNG1A_ARATH RecName: Full=Putative E3 ubiquitin-protein ligase RING1a; AltName: Full=Polycomb complex protein RING1a; AltName: Full=Protein RING1a; Short=AtRING1a; AltName: Full=Ring finger protein 434 gi|332007702|gb|AED95085.1| putative E3 ubiquitin-protein ligase RING1a [Arabidopsis thaliana]	506	522	1.00E-166	103.2	70.8	81.2	putative E3 ubiquitin-protein ligase RING1a	gbpln	Arabidopsis thaliana	AT5G44280.1 | Symbols: ATRING1A, RING1A | RING 1A | chr5:17836115-17839114 REVERSE LENGTH=522	506	522	1.00E-169	103.2	70.8	81.2
Rsa1.0_01799.1.g29908.t3	ref|NP_199242.1| protein kinase-like protein [Arabidopsis thaliana] gi|79329869|ref|NP_001032009.1| protein kinase-like protein [Arabidopsis thaliana] gi|79329882|ref|NP_001032010.1| protein kinase-like protein [Arabidopsis thaliana] gi|145334725|ref|NP_001078708.1| protein kinase-like protein [Arabidopsis thaliana] gi|10176884|dbj|BAB10114.1| cyclin-dependent protein kinase-like protein [Arabidopsis thaliana] gi|222424232|dbj|BAH20074.1| AT5G44290 [Arabidopsis thaliana] gi|332007704|gb|AED95087.1| protein kinase-like protein [Arabidopsis thaliana] gi|332007705|gb|AED95088.1| protein kinase-like protein [Arabidopsis thaliana] gi|332007706|gb|AED95089.1| protein kinase-like protein [Arabidopsis thaliana] gi|332007707|gb|AED95090.1| protein kinase-like protein [Arabidopsis thaliana]	640	644	0	100.6	83.0	88.3	protein kinase-like protein	gbpln	Arabidopsis thaliana	AT5G44290.4 | Symbols: | Protein kinase superfamily protein | chr5:17840750-17843190 REVERSE LENGTH=644	640	644	0	100.6	83.0	88.3
Rsa1.0_01799.1.g29909.t4	ref|XP_002868667.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] gi|297314503|gb|EFH44926.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	130	336	7.00E-32	258.5	57.7	59.2	nodulin MtN21 family protein	gbpln	Arabidopsis lyrata	AT5G40210.1 | Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:16073725-16076088 REVERSE LENGTH=339	130	339	1.00E-33	260.8	54.6	56.9

Rsa1.0_01799.1.g29910.t1	ref|NP_199245.1| translation initiation factor eIF-3 subunit 7 [Arabidopsis thaliana] gi|10176887|dbj|BAB10117.1| eukaryotic translation initiation factor 3 subunit 7 [Arabidopsis thaliana] gi|30793851|gb|AAP40378.1| putative eukaryotic translation initiation factor 3 subunit 7 [Arabidopsis thaliana] gi|30794001|gb|AAP40450.1| putative eukaryotic translation initiation factor 3 subunit 7 [Arabidopsis thaliana] gi|332007713|gb|AED95096.1| translation initiation factor eIF-3 subunit 7 [Arabidopsis thaliana]	584	588	0	100.7	92.3	96.4	translation initiation factor eIF-3 subunit 7	gbpln	Arabidopsis thaliana	AT5G44320.1 | Symbols: | Eukaryotic translation initiation factor 3 subunit 7 (eIF-3) | chr5:17854901-17856667 REVERSE LENGTH=588	584	588	0	100.7	92.3	96.4
Rsa1.0_01799.1.g29911.t1	ref|NP_199247.1| tubulin beta-4 chain [Arabidopsis thaliana] gi|27735260|sp|P24636.2|TBB4_ARATH RecName: Full=Tubulin beta-4 chain; AltName: Full=Beta-4-tubulin gi|10176889|dbj|BAB10119.1| tubulin beta-4 chain [Arabidopsis thaliana] gi|14334936|gb|AAK59645.1| putative tubulin beta-4 chain [Arabidopsis thaliana] gi|16323374|gb|AAL15181.1| putative tubulin beta-4 chain [Arabidopsis thaliana] gi|332007715|gb|AED95098.1| tubulin beta-4 chain [Arabidopsis thaliana]	445	444	0	99.8	98.7	99.1	tubulin beta-4 chain	gbpln	Arabidopsis thaliana	AT5G44340.1 | Symbols: TUB4 | tubulin beta chain 4 | chr5:17859442-17860994 REVERSE LENGTH=444	445	444	0	99.8	98.7	99.1
Rsa1.0_01800.1.g29912.t1	ref|XP_002881041.1| type 1 protein phosphatase [Arabidopsis lyrata subsp. lyrata] gi|158828160|gb|ABW81039.1| type 1 protein phosphatase [Arabidopsis lyrata subsp. lyrata] gi|297326880|gb|EFH57300.1| type 1 protein phosphatase [Arabidopsis lyrata subsp. lyrata]	324	319	1.00E-179	98.5	95.4	96.9	type 1 protein phosphatase	gbpln	Arabidopsis lyrata	AT2G29400.1 | Symbols: TOPP1, PP1-AT | type one protein phosphatase 1 | chr2:12613789-12615283 REVERSE LENGTH=318	324	318	1.00E-179	98.1	94.8	96.9
Rsa1.0_01800.1.g29913.t1	gb|ABW74581.1| putative tropinone reductase [Boechera divaricarpa]	276	267	1.00E-120	96.7	77.2	82.6	putative tropinone reductase	gbpln	Boechera divaricarpa	AT2G29370.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:12606059-12607363 FORWARD LENGTH=268	276	268	1.00E-119	97.1	76.4	82.6
Rsa1.0_01800.1.g29914.t1	dbj|BAB02146.1| copia retroelement pol polyprotein-like [Arabidopsis thaliana]	585	526	6.00E-46	89.9	15.4	20.7	copia retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	ATMG00710.1 | Symbols: ORF120 | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chrM:207553-207915 REVERSE LENGTH=120	585	120	9.00E-14	20.5	5.6	8.0
Rsa1.0_01800.1.g29915.t1	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_01800.1.g29916.t1	gb|ABW81066.1| tropinone-reductase-like53 [Arabidopsis lyrata subsp. lyrata]	281	271	1.00E-126	96.4	77.2	84.7	tropinone-reductase-like53	gbpln	Arabidopsis lyrata	AT2G29350.1 | Symbols: SAG13 | senescence-associated gene 13 | chr2:12601036-12602222 FORWARD LENGTH=269	281	269	1.00E-120	95.7	73.0	80.8
Rsa1.0_01800.1.g29917.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	491	1142	1.00E-106	232.6	40.5	59.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	491	575	3.00E-65	117.1	31.4	51.3
Rsa1.0_01801.1.g29918.t1	ref|NP_200492.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75262578|sp|Q9FJT2.1|FDL40_ARATH RecName: Full=Putative F-box/FBD/LRR-repeat protein At5g56810 gi|10176785|dbj|BAB09899.1| unnamed protein product [Arabidopsis thaliana] gi|332009427|gb|AED96810.1| putative F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	450	435	2.00E-80	96.7	46.2	58.2	putative F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT5G56810.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22974520-22975992 FORWARD LENGTH=435	450	435	5.00E-83	96.7	46.2	58.2
Rsa1.0_01801.1.g29919.t2	gb|EOA13381.1| hypothetical protein CARUB_v10026420mg [Capsella rubella]	387	438	1.00E-124	113.2	59.2	74.7	hypothetical protein CARUB_v10026420mg	gbpln	Capsella rubella	AT5G56810.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22974520-22975992 FORWARD LENGTH=435	387	435	1.00E-124	112.4	61.2	74.4
Rsa1.0_01801.1.g29920.t1	ref|XP_002864149.1| hypothetical protein ARALYDRAFT_495276 [Arabidopsis lyrata subsp. lyrata] gi|297309984|gb|EFH40408.1| hypothetical protein ARALYDRAFT_495276 [Arabidopsis lyrata subsp. lyrata]	508	500	0	98.4	78.7	86.4	hypothetical protein ARALYDRAFT_495276	gbpln	Arabidopsis lyrata	AT5G52050.1 | Symbols: | MATE efflux family protein | chr5:21138933-21140450 FORWARD LENGTH=505	508	505	0	99.4	78.3	86.6
Rsa1.0_01801.1.g29921.t1	gb|EOA13679.1| hypothetical protein CARUB_v10026751mg [Capsella rubella]	349	334	1.00E-141	95.7	86.2	90.8	hypothetical protein CARUB_v10026751mg	gbpln	Capsella rubella	AT5G52040.1 | Symbols: ATRSP41, RS41, At-RS41 | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:21131081-21133318 FORWARD LENGTH=356	349	356	1.00E-134	102.0	84.5	90.0

Rsa1.0_01801.1.g29922.t1	gb|EOA14638.1| hypothetical protein CARUB_v10027896mg [Capsella rubella]	401	849	0	211.7	83.3	88.0	hypothetical protein CARUB_v10027896mg	gbpln	Capsella rubella	AT5G52010.1 | Symbols: | C2H2-like zinc finger protein | chr5:21121626-21122816 REVERSE LENGTH=396	401	396	0	98.8	82.3	86.3
Rsa1.0_01801.1.g29923.t1	ref|NP_200011.1| zinc finger CCCH domain-containing protein 63 [Arabidopsis thaliana] gi|10177733|dbj|BAB11046.1| unnamed protein product [Arabidopsis thaliana] gi|332008771|gb|AED96154.1| zinc finger CCCH domain-containing protein 63 [Arabidopsis thaliana]	438	437	0	99.8	84.2	91.8	zinc finger CCCH domain-containing protein 63	gbpln	Arabidopsis thaliana	AT5G51980.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:21113650-21115902 REVERSE LENGTH=437	438	437	0	99.8	84.2	91.8
Rsa1.0_01801.1.g29924.t1	gb|EOA14537.1| hypothetical protein CARUB_v10027769mg [Capsella rubella]	539	587	0	108.9	87.6	94.4	hypothetical protein CARUB_v10027769mg	gbpln	Capsella rubella	AT5G51950.2 | Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr5:21106093-21108348 REVERSE LENGTH=553	539	553	0	102.6	88.1	95.0
Rsa1.0_01801.1.g29925.t1	gb|EOA15053.1| hypothetical protein CARUB_v10028412mg [Capsella rubella]	858	579	0	67.5	49.0	54.9	hypothetical protein CARUB_v10028412mg	gbpln	Capsella rubella	AT5G51950.1 | Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr5:21106093-21108559 REVERSE LENGTH=586	858	586	0	68.3	46.6	53.5
Rsa1.0_01802.1.g29926.t2	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	857	1333	0	155.5	44.5	58.8	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	857	575	2.00E-82	67.1	20.5	33.3
Rsa1.0_01802.1.g29927.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01802.1.g29928.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1081	1496	0	138.4	58.7	68.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1081	1262	2.33E-156	116.7	23.2	33.3
Rsa1.0_01802.1.g29929.t1	gb|EOA39251.1| hypothetical protein CARUB_v10012248mg [Capsella rubella]	563	570	0	101.2	92.9	95.6	hypothetical protein CARUB_v10012248mg	gbpln	Capsella rubella	AT1G51190.1 | Symbols: PLT2 | Integrase-type DNA-binding superfamily protein | chr1:18977517-18980305 FORWARD LENGTH=568	563	568	0	100.9	90.9	93.6
Rsa1.0_01802.1.g29930.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01803.1.g29931.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01803.1.g29932.t1	gb|AAX55106.1| hypothetical protein At2g05290 [Arabidopsis thaliana]	394	383	2.00E-42	97.2	22.8	35.3	hypothetical protein At2g05290	gbpln	Arabidopsis thaliana	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	394	336	3.00E-19	85.3	14.7	24.9
Rsa1.0_01803.1.g29933.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	1112	1231	0	110.7	39.7	56.1	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1112	575	8.00E-72	51.7	14.7	23.3
Rsa1.0_01803.1.g29934.t1	gb|EOA23895.1| hypothetical protein CARUB_v10017109mg [Capsella rubella]	481	488	0	101.5	89.4	94.0	hypothetical protein CARUB_v10017109mg	gbpln	Capsella rubella	AT3G55580.1 | Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr3:20612766-20615730 FORWARD LENGTH=488	481	488	0	101.5	88.4	93.6
Rsa1.0_01803.1.g29935.t1	gb|AAK01361.1|AF314812_1 delta 1-pyrroline-5-carboxylate synthetase B [Brassica napus]	727	727	0	100.0	98.5	99.3	delta 1-pyrroline-5-carboxylate synthetase B	gbpln	Brassica napus	AT3G55610.1 | Symbols: P5CS2 | delta 1-pyrroline-5-carboxylate synthase 2 | chr3:20624278-20628989 REVERSE LENGTH=726	727	726	0	99.9	92.8	97.0
Rsa1.0_01803.1.g29936.t1	gb|EOA32203.1| hypothetical protein CARUB_v10015460mg [Capsella rubella]	122	566	2.00E-43	463.9	74.6	78.7	hypothetical protein CARUB_v10015460mg	gbpln	Capsella rubella	AT2G20470.1 | Symbols: | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr2:8826277-8829497 REVERSE LENGTH=569	122	569	3.00E-46	466.4	74.6	78.7
Rsa1.0_01803.1.g29937.t2	gb|EOA24465.1| hypothetical protein CARUB_v10017721mg [Capsella rubella]	289	302	1.00E-138	104.5	83.0	84.1	hypothetical protein CARUB_v10017721mg	gbpln	Capsella rubella	AT3G55620.1 | Symbols: emb1624 | Translation initiation factor IF6 | chr3:20634581-20636312 FORWARD LENGTH=245	289	245	1.00E-139	84.8	82.0	84.1

<table>
<tr><td>Rsa1.0_01803.1.g29938.t1</td><td>ref|NP_567026.3| DHFS-FPGS homolog D [Arabidopsis thaliana] gi|75331225|sp|Q8W035.1|FPGS3_ARATH RecName: Full=Folylpolyglutamate synthase; AltName: Full=DHFS-FPGS homolog D; AltName: Full=Folylpoly-gamma-glutamate synthetase; Short=FPGS; AltName: Full=Tetrahydrofolylpolyglutamate synthase; Short=Tetrahydrofolate synthase gi|17976761|emb|CAC82079.1| folylpolyglutamate synthetase, cytosolic isoform [Arabidopsis thaliana] gi|332645891|gb|AEE79412.1| DHFS-FPGS homolog D [Arabidopsis thaliana]</td><td>829</td><td>492</td><td>0</td><td>59.3</td><td>47.9</td><td>52.6</td><td>DHFS-FPGS homolog D</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G55630.3 | Symbols: ATDFD, DFD, FPGS3 | DHFS-FPGS homolog D | chr3:20636785-20639395 FORWARD LENGTH=492</td><td>829</td><td>492</td><td>0</td><td>59.3</td><td>47.9</td><td>52.6</td></tr>
<tr><td>Rsa1.0_01803.1.g29939.t4</td><td>gb|EOA28804.1| hypothetical protein CARUB_v10025036mg [Capsella rubella]</td><td>217</td><td>200</td><td>7.00E-92</td><td>92.2</td><td>81.1</td><td>86.6</td><td>hypothetical protein CARUB_v10025036mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G55770.5 | Symbols: | GATA type zinc finger transcription factor family protein | chr3:20703799-20705115 FORWARD LENGTH=199</td><td>217</td><td>199</td><td>3.00E-94</td><td>91.7</td><td>85.7</td><td>88.0</td></tr>
<tr><td>Rsa1.0_01803.1.g29940.t1</td><td>gb|EOA25429.1| hypothetical protein CARUB_v10018761mg [Capsella rubella]</td><td>381</td><td>378</td><td>0</td><td>99.2</td><td>83.2</td><td>88.2</td><td>hypothetical protein CARUB_v10018761mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G55780.1 | Symbols: | Glycosyl hydrolase superfamily protein | chr3:20705627-20707021 FORWARD LENGTH=429</td><td>381</td><td>429</td><td>0</td><td>112.6</td><td>81.9</td><td>86.1</td></tr>
<tr><td>Rsa1.0_01803.1.g29941.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01803.1.g29942.t1</td><td>ref|NP_191139.1| Sedoheptulose-1,7-bisphosphatase [Arabidopsis thaliana] gi|1173345|sp|P46283.1|S17P_ARATH RecName: Full=Sedoheptulose-1,7-bisphosphatase, chloroplastic; AltName: Full=SED(1,7)P2ase; AltName: Full=Sedoheptulose bisphosphatase; Short=SBPase; Flags: Precursor gi|786466|gb|AAB33001.1| sedoheptulose-1,7-bisphosphatase [Arabidopsis thaliana] gi|7263568|emb|CAB81605.1| sedoheptulose-bisphosphatase precursor [Arabidopsis thaliana] gi|332645922|gb|AEE79443.1| Sedoheptulose-1,7-bisphosphatase [Arabidopsis thaliana]</td><td>394</td><td>393</td><td>0</td><td>99.7</td><td>93.1</td><td>96.2</td><td>Sedoheptulose-1,7-bisphosphatase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G55800.1 | Symbols: SBPASE | sedoheptulose-bisphosphatase | chr3:20709640-20711421 FORWARD LENGTH=393</td><td>394</td><td>393</td><td>0</td><td>99.7</td><td>93.1</td><td>96.2</td></tr>
<tr><td>Rsa1.0_01803.1.g29943.t1</td><td>ref|NP_191141.1| Fasciclin-like arabinogalactan family protein [Arabidopsis thaliana] gi|7263570|emb|CAB81607.1| putative protein [Arabidopsis thaliana] gi|60547813|gb|AAX23870.1| hypothetical protein At3g55820 [Arabidopsis thaliana] gi|71905505|gb|AAZ52730.1| hypothetical protein At3g55820 [Arabidopsis thaliana] gi|149944339|gb|ABR46212.1| At3g55820 [Arabidopsis thaliana] gi|332645924|gb|AEE79445.1| Fasciclin-like arabinogalactan family protein [Arabidopsis thaliana]</td><td>202</td><td>204</td><td>7.00E-71</td><td>101.0</td><td>69.3</td><td>82.7</td><td>Fasciclin-like arabinogalactan family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G55820.1 | Symbols: | Fasciclin-like arabinogalactan family protein | chr3:20714041-20714655 FORWARD LENGTH=204</td><td>202</td><td>204</td><td>2.00E-73</td><td>101.0</td><td>69.3</td><td>82.7</td></tr>
<tr><td>Rsa1.0_01803.1.g29944.t1</td><td>ref|NP_191142.1| nucleotide-diphospho-sugar transferase-like protein [Arabidopsis thaliana] gi|7573478|emb|CAB87837.1| putative protein [Arabidopsis thaliana] gi|110736936|dbj|BAF00425.1| hypothetical protein [Arabidopsis thaliana] gi|332645925|gb|AEE79446.1| nucleotide-diphospho-sugar transferase-like protein [Arabidopsis thaliana]</td><td>336</td><td>334</td><td>1.00E-180</td><td>99.4</td><td>89.9</td><td>94.6</td><td>nucleotide-diphospho-sugar transferase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G55830.1 | Symbols: EPC1 | Nucleotide-diphospho-sugar transferases superfamily protein | chr3:20715101-20717133 FORWARD LENGTH=334</td><td>336</td><td>334</td><td>0</td><td>99.4</td><td>89.9</td><td>94.6</td></tr>
<tr><td>Rsa1.0_01803.1.g29945.t1</td><td>ref|XP_002878047.1| hypothetical protein ARALYDRAFT_486026 [Arabidopsis lyrata subsp. lyrata] gi|297323885|gb|EFH54306.1| hypothetical protein ARALYDRAFT_486026 [Arabidopsis lyrata subsp. lyrata]</td><td>425</td><td>428</td><td>0</td><td>100.7</td><td>84.9</td><td>91.1</td><td>hypothetical protein ARALYDRAFT_486026</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G55840.1 | Symbols: | Hs1pro-1 protein | chr3:20717530-20718816 REVERSE LENGTH=428</td><td>425</td><td>428</td><td>0</td><td>100.7</td><td>84.2</td><td>90.4</td></tr>
<tr><td>Rsa1.0_01803.1.g29946.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01803.1.g29947.t1</td><td>gb|EOA15770.1| hypothetical protein CARUB_v10006927mg [Capsella rubella]</td><td>966</td><td>852</td><td>0</td><td>88.2</td><td>55.1</td><td>65.0</td><td>hypothetical protein CARUB_v10006927mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G13920.1 | Symbols: AtRLP50, RLP50 | receptor like protein 50 | chr4:8043861-8046536 FORWARD LENGTH=891</td><td>966</td><td>891</td><td>0</td><td>92.2</td><td>51.3</td><td>61.0</td></tr>
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Rsa1.0_01803.1.g29948.t1	gb|EOA24730.1| hypothetical protein CARUB_v10018007mg [Capsella rubella]	211	214	9.00E-92	101.4	90.5	94.3	hypothetical protein CARUB_v10018007mg	gbpln	Capsella rubella	AT3G55880.2 | Symbols: | Alpha/beta hydrolase related protein | chr3:20736682-20738325 FORWARD LENGTH=215	211	215	5.00E-94	101.9	88.6	92.9
Rsa1.0_01804.1.g29949.t1	gb|AAC69377.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1361	1328	5.00E-63	97.6	10.9	14.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01804.1.g29950.t1	gb|AAF13073.1|AC011621_1 putative retroelement pol polyprotein [Arabidopsis thaliana]	1578	1661	0	105.3	53.7	69.6	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1578	158	7.00E-46	10.0	5.6	6.5
Rsa1.0_01804.1.g29951.t2	ref|NP_178148.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein [Arabidopsis thaliana] gi|12324982|gb|AAG52438.1|AC018848_9 putative oxidoreductase; 24302-25416 [Arabidopsis thaliana] gi|332198266|gb|AEE36387.1| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein [Arabidopsis thaliana]	240	320	2.00E-17	133.3	17.5	19.2	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	gbpln	Arabidopsis thaliana	AT1G80320.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:30196782-30197896 FORWARD LENGTH=320	240	320	6.00E-20	133.3	17.5	19.2
Rsa1.0_01804.1.g29952.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01805.1.g29953.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01805.1.g29954.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01805.1.g29955.t1	ref|NP_177024.1| putative nitrite transporter [Arabidopsis thaliana] gi|75266596|sp|Q9SX20.1|PTR18_ARATH RecName: Full=Probable nitrite transporter At1g68570 gi|5734721|gb|AAD49986.1|AC008075_19 Similar to gb|AF023472 peptide transporter from Hordeum vulgare and is a member of the PF|00854 Peptide transporter family. ESTs gb|T41927 and gb|AA395024 come from this gene [Arabidopsis thaliana] gi|20147231|gb|AAM10330.1| At1g68570/F24J5_7 [Arabidopsis thaliana] gi|25090385|gb|AAN72289.1| At1g68570/F24J5_7 [Arabidopsis thaliana] gi|110742209|dbj|BAE99031.1| peptide transporter like [Arabidopsis thaliana] gi|332196691|gb|AEE34812.1| probable nitrite transporter [Arabidopsis thaliana]	596	596	0	100.0	91.1	96.5	putative nitrite transporter	gbpln	Arabidopsis thaliana	AT1G68570.1 | Symbols: | Major facilitator superfamily protein | chr1:25746811-25750110 FORWARD LENGTH=596	596	596	0	100.0	91.1	96.5
Rsa1.0_01805.1.g29956.t1	gb|AAG50753.1|AC079733_21 CRK1 protein, putative [Arabidopsis thaliana]	102	686	2.00E-17	672.5	50.0	52.0	CRK1 protein, putative	gbpln	Arabidopsis thaliana	AT1G09600.1 | Symbols: | Protein kinase superfamily protein | chr1:3108617-3111318 FORWARD LENGTH=714	102	714	4.00E-14	700.0	30.4	31.4
Rsa1.0_01805.1.g29957.t2	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1159	1223	0	105.5	45.2	64.2	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1159	746	1.00E-84	64.4	14.9	20.2
Rsa1.0_01805.1.g29958.t1	ref|XP_002865917.1| hypothetical protein ARALYDRAFT_918304 [Arabidopsis lyrata subsp. lyrata] gi|297311752|gb|EFH42176.1| hypothetical protein ARALYDRAFT_918304 [Arabidopsis lyrata subsp. lyrata]	225	464	3.00E-50	206.2	50.2	61.3	hypothetical protein ARALYDRAFT_918304	gbpln	Arabidopsis lyrata	AT5G52540.1 | Symbols: | Protein of unknown function (DUF819) | chr5:21321672-21323702 REVERSE LENGTH=461	225	461	1.00E-51	204.9	50.2	61.3
Rsa1.0_01806.1.g29959.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01806.1.g29960.t3	gb|EOA19022.1| hypothetical protein CARUB_v10007674mg, partial [Capsella rubella]	770	628	3.00E-66	81.6	23.2	28.6	hypothetical protein CARUB_v10007674mg, partial	gbpln	Capsella rubella	AT4G11420.1 | Symbols: EIF3A, ATEIF3A-1, EIF3A-1, ATTIF3A1, TIF3A1 | eukaryotic translation initiation factor 3A | chr4:6947834-6952053 REVERSE LENGTH=987	770	987	5.00E-64	128.2	18.2	21.3
Rsa1.0_01806.1.g29961.t1	ref|XP_002886307.1| hypothetical protein ARALYDRAFT_480923 [Arabidopsis lyrata subsp. lyrata] gi|297332147|gb|EFH62566.1| hypothetical protein ARALYDRAFT_480923 [Arabidopsis lyrata subsp. lyrata]	232	228	1.00E-113	98.3	85.8	92.7	hypothetical protein ARALYDRAFT_480923	gbpln	Arabidopsis lyrata	AT2G20825.1 | Symbols: ULT2 | Developmental regulator, ULTRAPETALA | chr2:8965845-8966795 REVERSE LENGTH=228	232	228	1.00E-115	98.3	86.2	91.8

Rsa1.0_01806.1.g29962.t4	ref|NP_850005.1| uncharacterized protein [Arabidopsis thaliana] gi|11692840|gb|AAG40023.1|AF324672_1 At2g20820 [Arabidopsis thaliana] gi|11908098|gb|AAG41478.1|AF326896_1 unknown protein [Arabidopsis thaliana] gi|12642910|gb|AAK00397.1|AF339715_1 unknown protein [Arabidopsis thaliana] gi|14190457|gb|AAK55709.1|AF380628_1 At2g20820/F5H14.21 [Arabidopsis thaliana] gi|15809716|gb|AAL06786.1| At2g20820/F5H14.21 [Arabidopsis thaliana] gi|330251985|gb|AEC07079.1| uncharacterized protein AT2G20820 [Arabidopsis thaliana]	90	93	1.00E−34	103.3	83.3	86.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G20820.1 | Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 13 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 44; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr2:8964450−8965166 FORWARD LENGTH=93	90	93	2.00E−37	103.3	83.3	86.7
Rsa1.0_01806.1.g29963.t1	ref|XP_002886302.1| hypothetical protein ARALYDRAFT_900444 [Arabidopsis lyrata subsp. lyrata] gi|297332142|gb|EFH62561.1| hypothetical protein ARALYDRAFT_900444 [Arabidopsis lyrata subsp. lyrata]	202	331	1.00E−71	163.9	82.2	86.6	hypothetical protein ARALYDRAFT_900444	gbpln	Arabidopsis lyrata	AT2G20760.1 | Symbols: | Clathrin light chain protein | chr2:8943279−8945108 REVERSE LENGTH=338	202	338	2.00E−72	167.3	82.2	86.1
Rsa1.0_01806.1.g29964.t2	gb|EOA31214.1| hypothetical protein CARUB_v10014380mg [Capsella rubella]	265	271	1.00E−129	102.3	86.4	93.6	hypothetical protein CARUB_v10014380mg	gbpln	Capsella rubella	AT2G20750.1 | Symbols: ATEXPB1, EXPB1, ATHEXP BETA 1.5 | expansin B1 | chr2:8941185−8942430 FORWARD LENGTH=271	265	271	1.00E−131	102.3	85.3	91.3
Rsa1.0_01806.1.g29965.t1	gb|EOA31414.1| hypothetical protein CARUB_v10014594mg [Capsella rubella]	220	219	3.00E−97	99.5	78.2	90.0	hypothetical protein CARUB_v10014594mg	gbpln	Capsella rubella	AT2G20740.1 | Symbols: | Tetraspanin family protein | chr2:8935788−8937292 FORWARD LENGTH=221	220	221	8.00E−96	100.5	75.5	87.7
Rsa1.0_01806.1.g29966.t1	ref|XP_002886301.1| CAAX amino terminal protease family protein [Arabidopsis lyrata subsp. lyrata] gi|297332141|gb|EFH62560.1| CAAX amino terminal protease family protein [Arabidopsis lyrata subsp. lyrata]	332	300	2.00E−97	90.4	59.6	67.8	CAAX amino terminal protease family protein	gbpln	Arabidopsis lyrata	AT2G20725.1 | Symbols: | CAAX amino terminal protease family protein | chr2:8934113−8935426 REVERSE LENGTH=301	332	301	3.00E−96	90.7	58.1	66.9
Rsa1.0_01806.1.g29967.t1	gb|AAM67318.1| unknown [Arabidopsis thaliana] gi|62320190|dbj|BAD94411.1| hypothetical protein [Arabidopsis thaliana]	42	42	2.00E−11	100.0	85.7	95.2	unknown	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01806.1.g29968.t6	ref|NP_565482.1| riboflavin synthase alpha chain [Arabidopsis thaliana] gi|13605593|gb|AAK32790.1|AF361622_1 At2g20690/F5H14.34 [Arabidopsis thaliana] gi|19548077|gb|AAL87403.1| At2g20690/F5H14.34 [Arabidopsis thaliana] gi|20197688|gb|AAD20926.2| putative riboflavin synthase alpha chain [Arabidopsis thaliana] gi|330251963|gb|AEC07057.1| riboflavin synthase alpha chain [Arabidopsis thaliana]	234	271	1.00E−94	115.8	81.2	86.3	riboflavin synthase alpha chain	gbpln	Arabidopsis thaliana	AT2G20690.1 | Symbols: | lumazine−binding family protein | chr2:8923342−8924621 FORWARD LENGTH=271	234	271	4.00E−97	115.8	81.2	86.3
Rsa1.0_01806.1.g29969.t5	ref|NP_974208.1| DEAD−box ATP−dependent RNA helicase 41 [Arabidopsis thaliana] gi|79295464|ref|NP_001030621.1| DEAD−box ATP−dependent RNA helicase 41 [Arabidopsis thaliana] gi|108861894|sp|Q3EBD3.1|RH41_ARATH RecName: Full=DEAD−box ATP−dependent RNA helicase 41 gi|332640235|gb|AEE73756.1| DEAD−box ATP−dependent RNA helicase 41 [Arabidopsis thaliana] gi|332640237|gb|AEE73758.1| DEAD−box ATP−dependent RNA helicase 41 [Arabidopsis thaliana]	501	505	0	100.8	82.4	91.4	DEAD−box ATP−dependent RNA helicase 41	gbpln	Arabidopsis thaliana	AT3G02065.3 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:359136−360734 FORWARD LENGTH=505	501	505	0	100.8	82.4	91.4
Rsa1.0_01807.1.g29970.t1	ref|XP_004235099.1| PREDICTED: uncharacterized protein LOC101249439 [Solanum lycopersicum]	272	352	5.00E−42	129.4	40.8	57.0	PREDICTED: uncharacterized protein LOC101249439	gbpln	Solanum lycopersicum	#	#	#	#	#	#	#
Rsa1.0_01807.1.g29971.t1	ref|XP_002881634.1| hypothetical protein ARALYDRAFT_903160 [Arabidopsis lyrata subsp. lyrata] gi|297327473|gb|EFH57893.1| hypothetical protein ARALYDRAFT_903160 [Arabidopsis lyrata subsp. lyrata]	530	576	0	108.7	82.8	86.8	hypothetical protein ARALYDRAFT_903160	gbpln	Arabidopsis lyrata	AT2G39200.1 | Symbols: MLO12, ATMLO12 | Seven transmembrane MLO family protein | chr2:16356255−16359797 REVERSE LENGTH=576	530	576	0	108.7	82.5	86.4
Rsa1.0_01807.1.g29972.t3	dbj|BAB02990.1| retroelement pol polyprotein−like [Arabidopsis thaliana]	294	1250	3.00E−26	425.2	35.7	51.7	retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_01807.1.g29973.t1	ref|XP_002881634.1| hypothetical protein ARALYDRAFT_903160 [Arabidopsis lyrata subsp. lyrata] gi|297327473|gb|EFH57893.1| hypothetical protein ARALYDRAFT_903160 [Arabidopsis lyrata subsp. lyrata]	514	576	0	112.1	86.4	91.2	hypothetical protein ARALYDRAFT_903160	gbpln	Arabidopsis lyrata	AT2G39200.1 | Symbols: MLO12, ATMLO12 | Seven transmembrane MLO family protein | chr2:16356255-16359797 REVERSE LENGTH=576	514	576	0	112.1	86.4	91.2
Rsa1.0_01807.1.g29974.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01807.1.g29975.t1	ref|XP_002892387.1| hypothetical protein ARALYDRAFT_311783 [Arabidopsis lyrata subsp. lyrata] gi|297338229|gb|EFH68646.1| hypothetical protein ARALYDRAFT_311783 [Arabidopsis lyrata subsp. lyrata]	195	977	2.00E-13	501.0	21.5	25.6	hypothetical protein ARALYDRAFT_311783	gbpln	Arabidopsis lyrata	AT1G07200.2 | Symbols: | Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein | chr1:2209033-2212316 REVERSE LENGTH=979	195	979	3.00E-15	502.1	21.0	25.6
Rsa1.0_01808.1.g29976.t1	ref|NP_192292.1| uncharacterized protein [Arabidopsis thaliana] gi|7267138|emb|CAB80806.1| hypothetical protein [Arabidopsis thaliana] gi|332656955|gb|AEE82355.1| uncharacterized protein AT4G03830 [Arabidopsis thaliana]	548	578	5.00E-23	105.5	11.3	16.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G03830.1 | Symbols: | Protein of unknown function, DUF601 | chr4:1790440-1792458 FORWARD LENGTH=578	548	578	1.00E-25	105.5	11.3	16.8
Rsa1.0_01808.1.g29977.t1	gb|AAD28663.1| hypothetical protein [Arabidopsis thaliana]	383	356	1.00E-18	93.0	19.6	32.9	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01808.1.g29978.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	794	1838	4.00E-67	231.5	23.2	37.4	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01808.1.g29979.t1	gb|EOA18961.1| hypothetical protein CARUB_v10007596mg [Capsella rubella]	386	660	1.00E-104	171.0	50.3	63.7	hypothetical protein CARUB_v10007596mg	gbpln	Capsella rubella	AT4G10200.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr4:6353172-6355591 FORWARD LENGTH=733	386	733	2.00E-93	189.9	50.8	63.0
Rsa1.0_01808.1.g29980.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1476	1475	0	99.9	59.9	73.4	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1476	1262	0	85.5	20.4	26.2
Rsa1.0_01808.1.g29981.t1	gb|EOA39823.1| hypothetical protein CARUB_v10008490mg [Capsella rubella]	394	683	0	173.4	89.8	94.9	hypothetical protein CARUB_v10008490mg	gbpln	Capsella rubella	AT1G31710.1 | Symbols: | Copper amine oxidase family protein | chr1:11349855-11355339 FORWARD LENGTH=681	394	681	0	172.8	89.6	94.4
Rsa1.0_01808.1.g29982.t1	ref|NP_174452.2| putative copper amine oxidase [Arabidopsis thaliana] gi|332193263|gb|AEE31384.1| putative copper amine oxidase [Arabidopsis thaliana]	282	681	1.00E-125	241.5	79.1	90.1	putative copper amine oxidase	gbpln	Arabidopsis thaliana	AT1G31710.1 | Symbols: | Copper amine oxidase family protein | chr1:11349855-11355339 FORWARD LENGTH=681	282	681	1.00E-128	241.5	79.1	90.1
Rsa1.0_01809.1.g29983.t1	gb|AAC62779.1| F11O4.2 [Arabidopsis thaliana]	365	382	3.00E-43	104.7	28.5	40.5	F11O4.2	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	365	746	7.00E-30	204.4	18.9	26.3
Rsa1.0_01809.1.g29984.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	516	484	3.00E-45	93.8	23.3	28.7	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01809.1.g29985.t3	ref|XP_002870356.1| RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297316192|gb|EFH46615.1| RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	464	452	0	97.4	88.1	91.2	RabGAP/TBC domain-containing protein	gbpln	Arabidopsis lyrata	AT4G13730.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr4:7970299-7974055 FORWARD LENGTH=449	464	449	0	96.8	86.6	89.7
Rsa1.0_01809.1.g29986.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01809.1.g29987.t1	gb|AGD95055.1| cytochrome P450 monooxygenase 83A1-5 [Brassica napus]	501	501	0	100.0	96.4	98.8	cytochrome P450 monooxygenase 83A1-5	gbpln	Brassica napus	AT4G13770.1 | Symbols: CYP83A1, REF2 | cytochrome P450, family 83, subfamily A, polypeptide 1 | chr4:7990682-7992282 REVERSE LENGTH=502	501	502	0	100.2	89.0	95.0
Rsa1.0_01809.1.g29988.t3	gb|EOA16039.1| hypothetical protein CARUB_v10004167mg [Capsella rubella]	831	799	0	96.1	85.9	90.0	hypothetical protein CARUB_v10004167mg	gbpln	Capsella rubella	AT4G13780.1 | Symbols: | methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative | chr4:7993366-7998433 REVERSE LENGTH=797	831	797	0	95.9	83.9	89.0
Rsa1.0_01810.1.g29989.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01810.1.g29990.t1	gb|ABD65016.1| Agenet domain containing protein [Brassica oleracea]	141	1087	6.00E-32	770.9	66.0	75.9	Agenet domain containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01810.1.g29991.t1	gb|ABD65016.1| Agenet domain containing protein [Brassica oleracea]	168	1087	3.00E-36	647.0	41.7	50.6	Agenet domain containing protein	gbpln	Brassica oleracea	AT2G47230.1 | Symbols: DUF6, ATDUF6 | DOMAIN OF UNKNOWN FUNCTION 724 6 | chr2:19387126-19390011 FORWARD LENGTH=701	168	701	2.00E-22	417.3	28.6	39.9
Rsa1.0_01810.1.g29992.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01810.1.g29993.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01810.1.g29994.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01810.1.g29995.t1	gb|ABD65017.1| hypothetical protein 26.t00072 [Brassica oleracea]	247	821	2.00E-31	332.4	48.6	64.0	hypothetical protein 26.t00072	gbpln	Brassica oleracea	#	#	#	#	#	#	#

Rsa1.0_01810.1.g29996.t1	emb|CAB10526.1| retrotransposon like protein [Arabidopsis thaliana] gi|7268497|emb|CAB78748.1| retrotransposon like protein [Arabidopsis thaliana]	819	1433	0	175.0	41.9	48.8	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	819	1262	1.00E-110	154.1	27.2	34.9
Rsa1.0_01810.1.g29997.t3	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	853	2726	1.00E-113	319.6	22.0	29.3	disease resistance protein	gbpln	Brassica rapa	AT1G67020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf; Has 72 Blast hits to 72 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 72; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25011008-25012987 REVERSE LENGTH=659	853	659	1.00E-15	77.3	4.2	6.2
Rsa1.0_01811.1.g29998.t2	ref|XP_002461201.1| hypothetical protein SORBIDRAFT_02g042750 [Sorghum bicolor] gi|241924578|gb|EER97722.1| hypothetical protein SORBIDRAFT_02g042750 [Sorghum bicolor]	156	187	8.00E-41	119.9	64.7	74.4	hypothetical protein SORBIDRAFT_02g042750	gbpln	Sorghum bicolor	AT3G05590.1 | Symbols: RPL18 | ribosomal protein L18 | chr3:1621511-1622775 FORWARD LENGTH=187	156	187	1.00E-34	119.9	46.2	46.2
Rsa1.0_01811.1.g29999.t1	ref|XP_002884518.1| hypothetical protein ARALYDRAFT_317420 [Arabidopsis lyrata subsp. lyrata] gi|297330358|gb|EFH60777.1| hypothetical protein ARALYDRAFT_317420 [Arabidopsis lyrata subsp. lyrata]	331	331	1.00E-175	100.0	89.4	93.4	hypothetical protein ARALYDRAFT_317420	gbpln	Arabidopsis lyrata	AT3G05600.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:1623485-1624704 REVERSE LENGTH=331	331	331	1.00E-177	100.0	89.1	93.4
Rsa1.0_01811.1.g30000.t1	ref|XP_002884520.1| hypothetical protein ARALYDRAFT_896648 [Arabidopsis lyrata subsp. lyrata] gi|297330360|gb|EFH60779.1| hypothetical protein ARALYDRAFT_896648 [Arabidopsis lyrata subsp. lyrata]	559	558	0	99.8	83.5	90.5	hypothetical protein ARALYDRAFT_896648	gbpln	Arabidopsis lyrata	AT4G02330.1 | Symbols: ATPMEPCRB | Plant invertase/pectin methylesterase inhibitor superfamily | chr4:1032479-1034928 FORWARD LENGTH=573	559	573	1.00E-151	102.5	50.6	64.6
Rsa1.0_01811.1.g30001.t1	gb|EOA29598.1| hypothetical protein CARUB_v10013399mg [Capsella rubella]	540	544	0	100.7	89.8	94.8	hypothetical protein CARUB_v10013399mg	gbpln	Capsella rubella	AT3G05620.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:1629658-1631766 REVERSE LENGTH=543	540	543	0	100.6	89.3	94.4
Rsa1.0_01811.1.g30002.t2	ref|XP_002884529.1| hypothetical protein ARALYDRAFT_477862 [Arabidopsis lyrata subsp. lyrata] gi|297330369|gb|EFH60788.1| hypothetical protein ARALYDRAFT_477862 [Arabidopsis lyrata subsp. lyrata]	500	295	1.00E-100	59.0	39.2	42.2	hypothetical protein ARALYDRAFT_477862	gbpln	Arabidopsis lyrata	AT3G05690.1 | Symbols: UNE8, ATHAP2B, HAP2B, NF-YA2 | nuclear factor Y, subunit A2 | chr3:1676922-1678324 REVERSE LENGTH=295	500	295	1.00E-102	59.0	39.0	42.0
Rsa1.0_01811.1.g30003.t1	ref|NP_850519.1| syntaxin-43 [Arabidopsis thaliana] gi|38503420|sp|Q9SUJ1.2|SYP43_ARATH RecName: Full=Syntaxin-43; Short=AtSYP43 gi|6714439|gb|AAF26126.1|AC011620_2 putative syntaxin protein, AtSNAP33 [Arabidopsis thaliana] gi|20466514|gb|AAM20574.1| putative syntaxin protein, AtSNAP33 [Arabidopsis thaliana] gi|332640762|gb|AEE74283.1| syntaxin-43 [Arabidopsis thaliana]	318	331	1.00E-164	104.1	90.9	95.9	syntaxin-43	gbpln	Arabidopsis thaliana	AT3G05710.2 | Symbols: SYP43, ATSYP43 | syntaxin of plants 43 | chr3:1685262-1687229 FORWARD LENGTH=331	318	331	1.00E-167	104.1	90.9	95.9
Rsa1.0_01811.1.g30004.t1	ref|NP_187223.1| importin alpha isoform 7 [Arabidopsis thaliana] gi|6714438|gb|AAF26125.1|AC011620_1 putative importin alpha [Arabidopsis thaliana] gi|91806381|gb|ABE65918.1| importin alpha-1 subunit [Arabidopsis thaliana] gi|332640763|gb|AEE74284.1| importin alpha isoform 7 [Arabidopsis thaliana]	539	528	0	98.0	86.8	92.6	importin alpha isoform 7	gbpln	Arabidopsis thaliana	AT3G05720.1 | Symbols: IMPA-7 | importin alpha isoform 7 | chr3:1687992-1691736 REVERSE LENGTH=528	539	528	0	98.0	86.8	92.6
Rsa1.0_01811.1.g30005.t1	gb|EOA33055.1| hypothetical protein CARUB_v10016388mg [Capsella rubella]	124	125	1.00E-58	100.8	89.5	96.0	hypothetical protein CARUB_v10016388mg	gbpln	Capsella rubella	AT3G05725.1 | Symbols: | Protein of unknown function (DUF3511) | chr3:1692548-1693153 FORWARD LENGTH=124	124	124	2.00E-57	100.0	81.5	91.9
Rsa1.0_01811.1.g30006.t1	gb|ABV89608.1| disease resistance-responsive family protein [Brassica rapa]	90	90	3.00E-36	100.0	94.4	96.7	disease resistance-responsive family protein	gbpln	Brassica rapa	AT3G05727.1 | Symbols: | S locus-related glycoprotein 1 (SLR1) binding pollen coat protein family | chr3:1693616-1693934 FORWARD LENGTH=80	90	80	5.00E-19	88.9	55.6	65.6

Rsa1.0_01811.1.g30007.t1	ref|NP_187225.2| ATP-dependent DNA helicase Q-like 1 [Arabidopsis thaliana] gi|75334309|sp|Q9FT74.1|RQL1_ARATH RecName: Full=ATP-dependent DNA helicase Q-like 1; AltName: Full=RecQ-like protein 1; Short=AtRecQ1; Short=AtRecQl1 gi|10944747|emb|CAC14163.1| DNA Helicase [Arabidopsis thaliana] gi|332640767|gb|AEE74288.1| ATP-dependent DNA helicase Q-like 1 [Arabidopsis thaliana]	816	606	0	74.3	63.2	66.5	ATP-dependent DNA helicase Q-like 1	gbpln	Arabidopsis thaliana	AT3G05740.1 | Symbols: RECQI1 | RECQ helicase l1 | chr3:1698180-1701228 FORWARD LENGTH=606	816	606	0	74.3	63.2	66.5
Rsa1.0_01811.1.g30008.t2	ref|XP_002882433.1| hypothetical protein ARALYDRAFT_477867 [Arabidopsis lyrata subsp. lyrata] gi|297328273|gb|EFH58692.1| hypothetical protein ARALYDRAFT_477867 [Arabidopsis lyrata subsp. lyrata]	774	793	0	102.5	66.4	76.9	hypothetical protein ARALYDRAFT_477867	gbpln	Arabidopsis lyrata	AT3G05750.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G26910.1); Has 2317 Blast hits to 1467 proteins in 247 species: Archae - 4; Bacteria - 750; Metazoa - 557; Fungi - 182; Plants - 180; Viruses - 0; Other Eukaryotes - 644 (source: NCBI BLink). | chr3:1704677-1707546 FORWARD LENGTH=801	774	801	0	103.5	64.2	75.5
Rsa1.0_01812.1.g30009.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	1194	1024	3.00E-29	85.8	7.7	10.3	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01812.1.g30010.t1	gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]	695	723	0	104.0	54.8	72.2	Tam3-like transposon protein; 93317-95488	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	695	696	4.00E-40	100.1	20.3	35.7
Rsa1.0_01812.1.g30011.t1	ref|XP_002863767.1| hypothetical protein ARALYDRAFT_917496 [Arabidopsis lyrata subsp. lyrata] gi|297309602|gb|EFH40026.1| hypothetical protein ARALYDRAFT_917496 [Arabidopsis lyrata subsp. lyrata]	124	343	8.00E-27	276.6	47.6	56.5	hypothetical protein ARALYDRAFT_917496	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01812.1.g30012.t1	gb|ABD32665.1| Terpenoid cylases/protein prenyltransferase alpha-alpha toroid; Bacterial adhesion [Medicago truncatula]	88	426	1.00E-35	484.1	85.2	93.2	Terpenoid cylases/protein prenyltransferase alpha-alpha toroid; Bacterial adhesion	gbpln	Medicago truncatula	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	88	343	1.00E-17	389.8	47.7	64.8
Rsa1.0_01812.1.g30013.t1	ref|XP_002874478.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297320315|gb|EFH50737.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	391	409	0	104.6	84.9	90.8	leucine-rich repeat family protein	gbpln	Arabidopsis lyrata	AT4G06744.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr4:4070870-4072084 REVERSE LENGTH=404	391	404	0	103.3	84.4	90.8
Rsa1.0_01812.1.g30014.t12	ref|XP_002894278.1| hypothetical protein ARALYDRAFT_337235 [Arabidopsis lyrata subsp. lyrata] gi|297340120|gb|EFH70537.1| hypothetical protein ARALYDRAFT_337235 [Arabidopsis lyrata subsp. lyrata]	576	800	3.00E-40	138.9	19.3	27.4	hypothetical protein ARALYDRAFT_337235	gbpln	Arabidopsis lyrata	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367-2988945 FORWARD LENGTH=452	576	452	5.00E-19	78.5	9.5	12.3
Rsa1.0_01812.1.g30015.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01812.1.g30016.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01813.1.g30017.t1	gb|AAK38383.1|AC079028_7 hypothetical protein [Arabidopsis thaliana]	613	712	9.00E-54	116.2	26.6	37.8	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01813.1.g30018.t1	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	524	1643	1.00E-54	313.5	25.6	32.8	gag/pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01813.1.g30019.t1	gb|AAG52949.1| gag/pol polyprotein [Arabidopsis thaliana]	267	1643	5.00E-70	615.4	57.7	71.9	gag/pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	267	1262	8.00E-19	472.7	18.4	28.5
Rsa1.0_01813.1.g30020.t1	gb|EOA24640.1| hypothetical protein CARUB_v10017917mg [Capsella rubella]	508	246	3.00E-24	48.4	11.4	19.9	hypothetical protein CARUB_v10017917mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01813.1.g30021.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01813.1.g30022.t1	ref|XP_002880852.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326691|gb|EFH57111.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	428	387	1.00E-134	90.4	63.6	71.0	predicted protein	gbpln	Arabidopsis lyrata	AT2G26960.1 | Symbols: AtMYB81, MYB81 | myb domain protein 81 | chr2:11506065-11507425 REVERSE LENGTH=427	428	427	1.00E-125	99.8	60.3	67.3
Rsa1.0_01813.1.g30023.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	76	1333	9.00E-16	1753.9	51.3	67.1	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01814.1.g30024.t1	gb|EOA20072.1| hypothetical protein CARUB_v10000341mg [Capsella rubella]	590	709	0	120.2	91.9	94.2	hypothetical protein CARUB_v10000341mg	gbpln	Capsella rubella	AT5G15810.1 | Symbols: | N2,N2-dimethylguanosine tRNA methyltransferase | chr5:5157798-5161121 FORWARD LENGTH=691	590	691	0	117.1	92.2	94.9
Rsa1.0_01814.1.g30025.t1	emb|CAD48303.1| MADS-box protein SEP1-a [Brassica oleracea var. botrytis]	248	250	1.00E-137	100.8	98.0	98.0	MADS-box protein SEP1-a	gbpln	Brassica oleracea	AT5G15800.1 | Symbols: SEP1, AGL2 | K-box region and MADS-box transcription factor family protein | chr5:5151594-5153767 REVERSE LENGTH=251	248	251	1.00E-123	101.2	94.4	96.4
Rsa1.0_01814.1.g30026.t1	gb|EOA21651.1| hypothetical protein CARUB_v10002071mg [Capsella rubella]	250	182	1.00E-58	72.8	46.8	48.8	hypothetical protein CARUB_v10002071mg	gbpln	Capsella rubella	AT5G15750.1 | Symbols: | Alpha-L RNA-binding motif/Ribosomal protein S4 family protein | chr5:5141449-5142701 FORWARD LENGTH=182	250	182	8.00E-60	72.8	45.2	48.8
Rsa1.0_01814.1.g30027.t1	ref|NP_197078.2| O-fucosyltransferase family protein [Arabidopsis thaliana] gi|66792694|gb|AAY56449.1| At5g15740 [Arabidopsis thaliana] gi|110743719|dbj|BAE99696.1| hypothetical protein [Arabidopsis thaliana] gi|332004817|gb|AED92200.1| O-fucosyltransferase family protein [Arabidopsis thaliana]	509	508	0	99.8	92.7	97.6	O-fucosyltransferase family protein	gbpln	Arabidopsis thaliana	AT5G15740.1 | Symbols: | O-fucosyltransferase family protein | chr5:5134788-5136956 REVERSE LENGTH=508	509	508	0	99.8	92.7	97.6
Rsa1.0_01814.1.g30028.t1	emb|CAC01771.1| putative protein [Arabidopsis thaliana]	150	366	9.00E-75	244.0	87.3	94.0	putative protein	gbpln	Arabidopsis thaliana	AT5G15720.1 | Symbols: GLIP7 | GDSL-motif lipase 7 | chr5:5124684-5126155 REVERSE LENGTH=364	150	364	3.00E-77	242.7	87.3	94.0
Rsa1.0_01814.1.g30029.t1	ref|XP_002883535.1| hypothetical protein ARALYDRAFT_342623 [Arabidopsis lyrata subsp. lyrata] gi|297329375|gb|EFH59794.1| hypothetical protein ARALYDRAFT_342623 [Arabidopsis lyrata subsp. lyrata]	403	442	4.00E-92	109.7	50.4	64.3	hypothetical protein ARALYDRAFT_342623	gbpln	Arabidopsis lyrata	AT3G24580.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8969162-8970298 FORWARD LENGTH=378	403	378	2.00E-81	93.8	47.6	63.5
Rsa1.0_01814.1.g30030.t1	ref|NP_197075.1| F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75263874|sp|Q9LFV5.1|FK111_ARATH RecName: Full=F-box/kelch-repeat protein At5g15710 gi|9755616|emb|CAC01770.1| putative protein [Arabidopsis thaliana] gi|40823375|gb|AAR92279.1| At5g15710 [Arabidopsis thaliana] gi|46518403|gb|AAS99683.1| At5g15710 [Arabidopsis thaliana] gi|110738375|dbj|BAF01114.1| hypothetical protein [Arabidopsis thaliana] gi|332004812|gb|AED92195.1| F-box/kelch-repeat protein [Arabidopsis thaliana]	331	448	1.00E-141	135.3	77.0	80.4	F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT5G15710.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:5122791-5124137 FORWARD LENGTH=448	331	448	1.00E-143	135.3	77.0	80.4
Rsa1.0_01814.1.g30031.t1	ref|XP_002873736.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297319573|gb|EFH49995.1| binding protein [Arabidopsis lyrata subsp. lyrata]	2034	2153	0	105.9	74.7	78.1	binding protein	gbpln	Arabidopsis lyrata	AT5G15680.1 | Symbols: | ARM repeat superfamily protein | chr5:5101188-5110793 REVERSE LENGTH=2153	2034	2153	0	105.9	74.6	78.1
Rsa1.0_01814.1.g30032.t1	gb|EOA20905.1| hypothetical protein CARUB_v10001241mg [Capsella rubella]	249	363	1.00E-140	145.8	96.4	97.2	hypothetical protein CARUB_v10001241mg	gbpln	Capsella rubella	AT5G15650.1 | Symbols: RGP2, ATRGP2 | reversibly glycosylated polypeptide 2 | chr5:5092203-5094093 FORWARD LENGTH=360	249	360	1.00E-140	144.6	95.2	96.4
Rsa1.0_01815.1.g30033.t1	gb|EOA21185.1| hypothetical protein CARUB_v10001530mg [Capsella rubella]	316	308	1.00E-144	97.5	82.6	89.9	hypothetical protein CARUB_v10001530mg	gbpln	Capsella rubella	AT4G02550.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02210.2); Has 370 Blast hits to 300 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 10; Plants - 354; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr4:1120622-1121629 REVERSE LENGTH=307	316	307	1.00E-143	97.2	79.4	87.0
Rsa1.0_01815.1.g30034.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01815.1.g30035.t1	dbj|BAB09991.1| mutator-like transposase-like [Arabidopsis thaliana]	466	825	1.00E-132	177.0	51.5	69.7	mutator-like transposase-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01815.1.g30036.t1	ref|XP_002872830.1| hypothetical protein ARALYDRAFT_911958 [Arabidopsis lyrata subsp. lyrata] gi|297318667|gb|EFH49089.1| hypothetical protein ARALYDRAFT_911958 [Arabidopsis lyrata subsp. lyrata]	933	953	0	102.1	78.0	86.0	hypothetical protein ARALYDRAFT_911958	gbpln	Arabidopsis lyrata	AT4G02560.2 | Symbols: LD | Homeodomain-like superfamily protein | chr4:1123656-1128252 REVERSE LENGTH=953	933	953	0	102.1	78.5	86.0
Rsa1.0_01815.1.g30037.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01815.1.g30038.t1	gb|ABW74560.1| polyprotein [Boechera divaricarpa]	168	642	7.00E-46	382.1	54.8	71.4	polyprotein	gbpln	Boechera divaricarpa	#	#	#	#	#	#	#
Rsa1.0_01815.1.g30039.t1	gb|EOA18167.1| hypothetical protein CARUB_v10006642mg, partial [Capsella rubella]	110	363	3.00E-12	330.0	35.5	63.6	hypothetical protein CARUB_v10006642mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01815.1.g30040.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	458	1213	5.00E-68	264.8	40.4	57.9	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	458	626	2.00E-35	136.7	20.5	31.9
Rsa1.0_01816.1.g30041.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01816.1.g30042.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01816.1.g30043.t1	gb|AAC23763.1| hypothetical protein [Arabidopsis thaliana]	428	705	7.00E-58	164.7	25.5	31.8	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G06420.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2539083-2539985 FORWARD LENGTH=249	428	249	1.00E-34	58.2	18.0	25.0
Rsa1.0_01816.1.g30044.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01816.1.g30045.t2	gb|AAD25847.1| Mutator-like transposase [Arabidopsis thaliana] gi|20198206|gb|AAM15459.1| Mutator-like transposase [Arabidopsis thaliana]	547	764	1.00E-111	139.7	47.7	66.2	Mutator-like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01816.1.g30046.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01816.1.g30047.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	515	1142	1.00E-135	221.7	49.9	65.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	515	575	9.00E-62	111.7	32.0	49.7
Rsa1.0_01816.1.g30048.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01816.1.g30049.t1	gb|ACP30609.1| disease resistance protein [Brassica rapa subsp. pekinensis]	178	2726	3.00E-14	1531.5	32.6	44.9	disease resistance protein	gbpln	Brassica rapa	#	#	#	#	#	#	#
Rsa1.0_01817.1.g30050.t1	gb|EOA26015.1| hypothetical protein CARUB_v10019419mg [Capsella rubella]	818	1062	9.00E-69	129.8	28.1	36.4	hypothetical protein CARUB_v10019419mg	gbpln	Capsella rubella	AT2G10440.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15780.1); Has 1628 Blast hits to 1350 proteins in 149 species: Archae - 0; Bacteria - 39; Metazoa - 480; Fungi - 159; Plants - 187; Viruses - 2; Other Eukaryotes - 761 (source: NCBI BLink). | chr2:4013752-4018046 REVERSE LENGTH=845	818	845	3.00E-70	103.3	15.8	18.5
Rsa1.0_01817.1.g30051.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1860	1274	0	68.5	37.4	46.7	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1860	575	2.00E-67	30.9	9.6	14.2
Rsa1.0_01817.1.g30052.t3	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01817.1.g30053.t1	gb|EOA23861.1| hypothetical protein CARUB_v10017078mg, partial [Capsella rubella]	531	496	0	93.4	79.1	83.4	hypothetical protein CARUB_v10017078mg, partial	gbpln	Capsella rubella	AT3G30180.1 | Symbols: CYP85A2, BR6OX2 | brassinosteroid-6-oxidase 2 | chr3:11810867-11813509 FORWARD LENGTH=465	531	465	0	87.6	78.2	82.5
Rsa1.0_01818.1.g30054.t3	ref|XP_002873896.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297319733|gb|EFH50155.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	714	507	0	71.0	45.4	49.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT5G18475.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:6129255-6130775 REVERSE LENGTH=506	714	506	1.00E-179	70.9	44.1	48.7
Rsa1.0_01818.1.g30055.t19	ref|XP_002871818.1| hypothetical protein ARALYDRAFT_488726 [Arabidopsis lyrata subsp. lyrata] gi|297317655|gb|EFH48077.1| hypothetical protein ARALYDRAFT_488726 [Arabidopsis lyrata subsp. lyrata]	408	413	0	101.2	79.4	86.5	hypothetical protein ARALYDRAFT_488726	gbpln	Arabidopsis lyrata	AT5G18470.1 | Symbols: | Curculin-like (mannose-binding) lectin family protein | chr5:6127952-6129193 FORWARD LENGTH=413	408	413	0	101.2	79.4	87.3

Rsa1.0_01818.1.g30056.t1	ref|XP_002873895.1| hypothetical protein ARALYDRAFT_909855 [Arabidopsis lyrata subsp. lyrata] gi|297319732|gb|EFH50154.1| hypothetical protein ARALYDRAFT_909855 [Arabidopsis lyrata subsp. lyrata]	292	310	1.00E-118	106.2	75.7	87.7	hypothetical protein ARALYDRAFT_909855	gbpln	Arabidopsis lyrata	AT5G18450.1 | Symbols: | Integrase-type DNA-binding superfamily protein | chr5:6116097-6117020 REVERSE LENGTH=307	292	307	1.00E-119	105.1	76.7	87.0
Rsa1.0_01818.1.g30057.t2	gb|EOA20536.1| hypothetical protein CARUB_v10000849mg [Capsella rubella]	150	481	3.00E-15	320.7	43.3	54.7	hypothetical protein CARUB_v10000849mg	gbpln	Capsella rubella	AT5G18440.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nuclear fragile X mental retardation-interacting protein 1, conserved region (InterPro:IPR019496); Has 1333 Blast hits to 1211 proteins in 205 species: Archae - 0; Bacteria - 137; Metazoa - 339; Fungi - 162; Plants - 70; Viruses - 6; Other Eukaryotes - 619 (source: NCBI BLink). | chr5:6113092-6115748 FORWARD LENGTH=470	150	470	1.00E-12	313.3	38.0	49.3
Rsa1.0_01818.1.g30058.t1	ref|NP_197344.2| GDSL esterase/lipase [Arabidopsis thaliana] gi|75107727|sp|Q5PNZ0.1|GDL77_ARATH RecName: Full=GDSL esterase/lipase At5g18430; AltName: Full=Extracellular lipase At5g18430; Flags: Precursor gi|56381887|gb|AAV85662.1| At5g18430 [Arabidopsis thaliana] gi|58531342|gb|AAW78593.1| At5g18430 [Arabidopsis thaliana] gi|332005179|gb|AED92562.1| GDSL esterase/lipase [Arabidopsis thaliana]	689	362	0	52.5	46.4	49.2	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT5G18430.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:6110363-6111934 REVERSE LENGTH=362	689	362	0	52.5	46.4	49.2
Rsa1.0_01819.1.g30059.t1	ref|XP_002866404.1| hypothetical protein ARALYDRAFT_496244 [Arabidopsis lyrata subsp. lyrata] gi|297312239|gb|EFH42663.1| hypothetical protein ARALYDRAFT_496244 [Arabidopsis lyrata subsp. lyrata]	456	456	0	100.0	94.7	97.1	hypothetical protein ARALYDRAFT_496244	gbpln	Arabidopsis lyrata	AT5G60920.1 | Symbols: COB | COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family | chr5:24511466-24513932 REVERSE LENGTH=456	456	456	0	100.0	92.1	94.5
Rsa1.0_01819.1.g30060.t1	gb|EOA12365.1| hypothetical protein CARUB_v10025749mg [Capsella rubella]	1263	1298	0	102.8	79.3	86.2	hypothetical protein CARUB_v10025749mg	gbpln	Capsella rubella	AT5G60930.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:24515398-24522511 REVERSE LENGTH=1294	1263	1294	0	102.5	77.3	84.6
Rsa1.0_01819.1.g30061.t1	ref|NP_200903.1| COBRA-like protein 5 [Arabidopsis thaliana] gi|34222630|sp|Q9FME5.1|COBL5_ARATH RecName: Full=COBRA-like protein 5; Flags: Precursor gi|10177318|dbj|BAB10644.1| unnamed protein product [Arabidopsis thaliana] gi|38566616|gb|AAR24198.1| At5g60950 [Arabidopsis thaliana] gi|40824050|gb|AAR92332.1| At5g60950 [Arabidopsis thaliana] gi|332010019|gb|AED97402.1| COBRA-like protein 5 [Arabidopsis thaliana]	204	204	1.00E-80	100.0	70.6	82.4	COBRA-like protein 5	gbpln	Arabidopsis thaliana	AT5G60950.1 | Symbols: COBL5 | COBRA-like protein 5 precursor | chr5:24527157-24528005 REVERSE LENGTH=204	204	204	5.00E-83	100.0	70.6	82.4
Rsa1.0_01819.1.g30062.t1	gb|EOA13591.1| hypothetical protein CARUB_v10026656mg [Capsella rubella]	299	359	1.00E-119	120.1	79.9	87.6	hypothetical protein CARUB_v10026656mg	gbpln	Capsella rubella	AT5G60970.1 | Symbols: TCP5 | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 5 | chr5:24535570-24536652 REVERSE LENGTH=360	299	360	1.00E-114	120.4	80.3	88.0
Rsa1.0_01819.1.g30063.t1	ref|XP_002866408.1| hypothetical protein ARALYDRAFT_919338 [Arabidopsis lyrata subsp. lyrata] gi|297312243|gb|EFH42667.1| hypothetical protein ARALYDRAFT_919338 [Arabidopsis lyrata subsp. lyrata]	453	455	0	100.4	92.7	96.5	hypothetical protein ARALYDRAFT_919338	gbpln	Arabidopsis lyrata	AT5G60990.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr5:24546601-24549148 REVERSE LENGTH=456	453	456	0	100.7	92.3	96.2
Rsa1.0_01819.1.g30064.t1	gb|EOA13791.1| hypothetical protein CARUB_v10026886mg [Capsella rubella]	268	295	7.00E-18	110.1	18.3	19.8	hypothetical protein CARUB_v10026886mg	gbpln	Capsella rubella	AT5G61030.1 | Symbols: GR-RBP3 | glycine-rich RNA-binding protein 3 | chr5:24560870-24562152 FORWARD LENGTH=309	268	309	1.00E-19	115.3	17.5	19.8
Rsa1.0_01819.1.g30065.t1	gb|EOA13059.1| hypothetical protein CARUB_v10026060mg [Capsella rubella]	575	625	1.00E-178	108.7	53.0	59.1	hypothetical protein CARUB_v10026060mg	gbpln	Capsella rubella	AT5G61060.2 | Symbols: HDA05 | histone deacetylase 5 | chr5:24567137-24570917 REVERSE LENGTH=664	575	664	1.00E-177	115.5	51.0	57.9

Rsa1.0_01819.1.g30066.t1	ref|NP_200917.4| nucleic acid binding protein [Arabidopsis thaliana] gi|9759455|dbj|BAB10371.1| unnamed protein product [Arabidopsis thaliana] gi|332010037|gb|AED97420.1| nucleic acid binding protein [Arabidopsis thaliana]	498	657	1.00E-107	131.9	53.2	62.4	nucleic acid binding protein	gbpln	Arabidopsis thaliana	AT5G61090.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:24574902-24577585 REVERSE LENGTH=657	498	657	1.00E-110	131.9	53.2	62.4
Rsa1.0_01820.1.g30067.t1	ref|XP_002880905.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297326744|gb|EFH57164.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	344	337	1.00E-154	98.0	79.9	88.4	F-box family protein	gbpln	Arabidopsis lyrata	AT2G27310.1 | Symbols: | F-box family protein | chr2:11683954-11684967 REVERSE LENGTH=337	344	337	1.00E-156	98.0	79.9	88.4
Rsa1.0_01820.1.g30068.t2	ref|XP_002318395.1| predicted protein [Populus trichocarpa] gi|222859068|gb|EEE96615.1| predicted protein [Populus trichocarpa]	835	1497	2.00E-55	179.3	21.9	32.2	predicted protein	gbpln	Populus trichocarpa	AT1G37113.1 | Symbols: | unknown protein; LOCATED IN: chloroplast; Has 24 Blast hits to 24 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 14; Viruses - 6; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:14136413-14138245 FORWARD LENGTH=414	835	414	2.00E-18	49.6	7.8	10.7
Rsa1.0_01820.1.g30069.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	278	657	4.00E-59	236.3	46.8	56.5	T14P8.10	gbpln	Arabidopsis thaliana	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	278	320	2.00E-46	115.1	34.5	47.5
Rsa1.0_01820.1.g30070.t1	ref|NP_180305.1| uncharacterized protein [Arabidopsis thaliana] gi|75216242|sp|Q9ZQI2.1|CASP3_ARATH RecName: Full=Casparian strip membrane protein 3 gi|5306261|gb|AAD41993.1| unknown protein [Arabidopsis thaliana] gi|20197657|gb|AAM15182.1| unknown protein [Arabidopsis thaliana] gi|27765014|gb|AAO23628.1| At2g27370 [Arabidopsis thaliana] gi|110743400|dbj|BAE99586.1| hypothetical protein [Arabidopsis thaliana] gi|330252892|gb|AEC07986.1| uncharacterized protein AT2G27370 [Arabidopsis thaliana] gi|339515802|gb|AEJ82279.1| casparian strip protein 3 [Cloning vector pCASP3::CASP3:GFP] gi|339515817|gb|AEJ82289.1| casparian strip protein 3 [Cloning vector p35S::CASP3:GFP]	221	221	1.00E-108	100.0	92.3	96.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G27370.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr2:11708628-11709905 REVERSE LENGTH=221	221	221	1.00E-110	100.0	92.3	96.8
Rsa1.0_01820.1.g30071.t1	gb|ABD65163.1| hypothetical protein 40.t00048 [Brassica oleracea]	558	569	4.00E-19	102.0	17.6	21.3	hypothetical protein 40.t00048	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01820.1.g30072.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01820.1.g30073.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01821.1.g30074.t1	gb|ACG60686.1| En/Spm-related transposon protein [Brassica oleracea var. alboglabra]	166	695	1.00E-65	418.7	70.5	81.3	En/Spm-related transposon protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01821.1.g30075.t1	gb|ACP20257.1| cinnamyl-alcohol dehydrogenase [Brassica rapa subsp. oleifera]	324	322	1.00E-178	99.4	93.8	96.3	cinnamyl-alcohol dehydrogenase	gbpln	Brassica rapa	AT1G09500.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:3066811-3068484 FORWARD LENGTH=325	324	325	1.00E-141	100.3	75.3	86.1
Rsa1.0_01821.1.g30076.t1	gb|EOA36734.1| hypothetical protein CARUB_v10012528mg [Capsella rubella]	229	266	7.00E-69	116.2	60.3	72.1	hypothetical protein CARUB_v10012528mg	gbpln	Capsella rubella	AT1G09520.1 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Zinc finger, PHD-type, conserved site (InterPro:IPR019786); BEST Arabidopsis thaliana protein match is: PHD finger family protein (TAIR:AT3G17460.1); Has 56 Blast hits to 56 proteins in 17 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 4; Plants - 46; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr1:3071248-3072030 REVERSE LENGTH=260	229	260	1.00E-68	113.5	66.4	78.2
Rsa1.0_01821.1.g30077.t1	gb|AAC67205.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1278	1413	0	110.6	57.3	70.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1278	1262	4.00E-73	98.7	12.6	18.8
Rsa1.0_01821.1.g30078.t1	ref|XP_002889756.1| hypothetical protein ARALYDRAFT_471048 [Arabidopsis lyrata subsp. lyrata] gi|297335598|gb|EFH66015.1| hypothetical protein ARALYDRAFT_471048 [Arabidopsis lyrata subsp. lyrata]	581	522	0	89.8	71.4	76.9	hypothetical protein ARALYDRAFT_471048	gbpln	Arabidopsis lyrata	AT1G09530.2 | Symbols: PIF3, POC1, PAP3 | phytochrome interacting factor 3 | chr1:3077216-3079367 FORWARD LENGTH=524	581	524	0	90.2	71.1	76.1

Rsa1.0_01822.1.g30079.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01822.1.g30080.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01822.1.g30081.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01822.1.g30082.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	757	1142	0	150.9	46.0	63.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	757	575	1.00E-72	76.0	22.3	35.1
Rsa1.0_01822.1.g30083.t1	gb|AAG28799.1|AC079374_2 unknown protein [Arabidopsis thaliana]	66	231	2.00E-13	350.0	57.6	68.2	unknown protein	gbpln	Arabidopsis thaliana	AT1G25260.1 | Symbols: | Ribosomal protein L10 family protein | chr1:8854163-8855766 REVERSE LENGTH=235	66	235	3.00E-16	356.1	57.6	68.2
Rsa1.0_01822.1.g30084.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01822.1.g30085.t1	dbj|BAA97156.1| unnamed protein product [Arabidopsis thaliana]	241	329	1.00E-43	136.5	40.2	53.9	unnamed protein product	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H-like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 208; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:9528910-9529917 FORWARD LENGTH=256	241	256	9.00E-21	106.2	22.4	30.3
Rsa1.0_01822.1.g30086.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01822.1.g30087.t1	gb|AAG60150.1|AC074360_15 En/Spm-like transposon protein, putative [Arabidopsis thaliana]	168	1431	3.00E-35	851.8	53.0	70.8	En/Spm-like transposon protein, putative	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01823.1.g30088.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01823.1.g30089.t7	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1675	1529	0	91.3	42.9	59.3	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1675	746	1.00E-104	44.5	11.3	15.3
Rsa1.0_01823.1.g30090.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	1423	1459	0	102.5	55.7	70.5	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1423	1262	4.00E-95	88.7	12.4	18.8
Rsa1.0_01823.1.g30091.t1	dbj|BAJ34469.1| unnamed protein product [Thellungiella halophila]	163	661	2.00E-53	405.5	69.9	76.1	unnamed protein product	----	----	AT1G71710.1 | Symbols: | DNAse I-like superfamily protein | chr1:26973796-26976774 REVERSE LENGTH=664	163	664	4.00E-51	407.4	68.7	78.5
Rsa1.0_01823.1.g30092.t1	ref|NP_188701.2| mRNA cap guanine-N7 methyltransferase 1 [Arabidopsis thaliana] gi|75273308|sp|Q9LHQ7.1|MCES1_ARATH RecName: Full=mRNA cap guanine-N7 methyltransferase 1; AltName: Full=mRNA (guanine-N(7)-)-methyltransferase 1; AltName: Full=mRNA cap methyltransferase 1 gi|9294344|dbj|BAB02241.1| mRNA cap methyltransferase-like protein [Arabidopsis thaliana] gi|28973781|gb|AAO64206.1| unknown protein [Arabidopsis thaliana] gi|29824183|gb|AAP04052.1| unknown protein [Arabidopsis thaliana] gi|110736712|dbj|BAF00319.1| hypothetical protein [Arabidopsis thaliana] gi|332642886|gb|AEE76407.1| mRNA cap guanine-N7 methyltransferase 1 [Arabidopsis thaliana]	198	370	1.00E-18	186.9	23.7	24.7	mRNA cap guanine-N7 methyltransferase 1	gbpln	Arabidopsis thaliana	AT3G20650.1 | Symbols: | mRNA capping enzyme family protein | chr3:7221168-7223939 REVERSE LENGTH=370	198	370	5.00E-21	186.9	23.7	24.7
Rsa1.0_01824.1.g30093.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01824.1.g30094.t1	gb|ABD96963.1| hypothetical protein [Cleome spinosa]	273	408	3.00E-28	149.5	27.1	36.6	hypothetical protein	gbpln	Cleome spinosa	#	#	#	#	#	#	#
Rsa1.0_01824.1.g30095.t1	ref|XP_002891578.1| 10-formyltetrahydrofolate synthetase [Arabidopsis lyrata subsp. lyrata] gi|297337420|gb|EFH67837.1| 10-formyltetrahydrofolate synthetase [Arabidopsis lyrata subsp. lyrata]	634	634	0	100.0	96.7	99.1	10-formyltetrahydrofolate synthetase	gbpln	Arabidopsis lyrata	AT1G50480.1 | Symbols: THFS | 10-formyltetrahydrofolate synthetase | chr1:18702064-18704687 FORWARD LENGTH=634	634	634	0	100.0	96.1	98.7
Rsa1.0_01824.1.g30096.t1	ref|XP_002885355.1| ubiquitin-conjugating enzyme 19 [Arabidopsis lyrata subsp. lyrata] gi|297331195|gb|EFH61614.1| ubiquitin-conjugating enzyme 19 [Arabidopsis lyrata subsp. lyrata]	181	181	3.00E-93	100.0	90.6	93.9	ubiquitin-conjugating enzyme 19	gbpln	Arabidopsis lyrata	AT3G20060.1 | Symbols: UBC19 | ubiquitin-conjugating enzyme19 | chr3:7002927-7004283 REVERSE LENGTH=181	181	181	3.00E-91	100.0	90.6	93.9
Rsa1.0_01824.1.g30097.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1815	1307	0	72.0	44.1	55.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT1G02020.1 | Symbols: | nitroreductase family protein | chr1:352842-354845 REVERSE LENGTH=642	1815	642	0	35.4	20.2	22.1

Rsa1.0_01824.1.g30098.t1	ref|XP_002889341.1| hypothetical protein ARALYDRAFT_333455 [Arabidopsis lyrata subsp. lyrata] gi|297335183|gb|EFH65600.1| hypothetical protein ARALYDRAFT_333455 [Arabidopsis lyrata subsp. lyrata]	142	872	6.00E-25	614.1	42.3	44.4	hypothetical protein ARALYDRAFT_333455	gbpln	Arabidopsis lyrata	AT1G02020.1 | Symbols: | nitroreductase family protein | chr1:352842-354845 REVERSE LENGTH=642	142	642	7.00E-27	452.1	41.5	44.4
Rsa1.0_01824.1.g30099.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01824.1.g30100.t1	ref|NP_199370.1| Ulp1 protease family protein [Arabidopsis thaliana] gi|10177930|dbj|BAB11195.1| unnamed protein product [Arabidopsis thaliana] gi|332007886|gb|AED95269.1| Ulp1 protease family protein [Arabidopsis thaliana]	848	921	1.00E-149	108.6	38.7	57.9	Ulp1 protease family protein	gbpln	Arabidopsis thaliana	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	848	921	1.00E-151	108.6	38.7	57.9
Rsa1.0_01824.1.g30101.t1	gb|AAC13582.1| similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana] gi|8843876|dbj|BAA97402.1| mutator-like transposase [Arabidopsis thaliana]	494	806	2.00E-75	163.2	35.6	46.0	similar to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01824.1.g30102.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01824.1.g30103.t1	gb|EOA40376.1| hypothetical protein CARUB_v10009103mg [Capsella rubella]	75	453	3.00E-24	604.0	70.7	77.3	hypothetical protein CARUB_v10009103mg	gbpln	Capsella rubella	AT3G20300.1 | Symbols: | Protein of unknown function (DUF3537) | chr3:7079832-7081809 REVERSE LENGTH=452	75	452	1.00E-20	602.7	54.7	61.3
Rsa1.0_01825.1.g30104.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01825.1.g30105.t2	gb|EOA29930.1| hypothetical protein CARUB_v10013023mg [Capsella rubella]	808	774	0	95.8	91.2	93.2	hypothetical protein CARUB_v10013023mg	gbpln	Capsella rubella	AT3G19720.1 | Symbols: ARC5, DRP5B | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:6850591-6855389 REVERSE LENGTH=777	808	777	0	96.2	91.2	93.3
Rsa1.0_01825.1.g30106.t1	ref|NP_188608.4| P-loop containing nucleoside triphosphate hydrolase domain-containing protein [Arabidopsis thaliana] gi|332642761|gb|AEE76282.1| P-loop containing nucleoside triphosphate hydrolase domain-containing protein [Arabidopsis thaliana]	989	993	0	100.4	86.8	93.0	P-loop containing nucleoside triphosphate hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G19740.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:6855944-6862930 REVERSE LENGTH=993	989	993	0	100.4	86.8	93.0
Rsa1.0_01825.1.g30107.t1	ref|XP_002883201.1| hypothetical protein ARALYDRAFT_479492 [Arabidopsis lyrata subsp. lyrata] gi|297329041|gb|EFH59460.1| hypothetical protein ARALYDRAFT_479492 [Arabidopsis lyrata subsp. lyrata]	705	408	0	57.9	55.7	56.7	hypothetical protein ARALYDRAFT_479492	gbpln	Arabidopsis lyrata	AT3G19760.1 | Symbols: EIF4A-III | eukaryotic initiation factor 4A-III | chr3:6863790-6866242 FORWARD LENGTH=408	705	408	0	57.9	55.0	56.3
Rsa1.0_01825.1.g30108.t1	dbj|BAJ33687.1| unnamed protein product [Thellungiella halophila]	561	561	0	100.0	95.4	99.5	unnamed protein product	----	----	AT3G19820.3 | Symbols: DWF1 | cell elongation protein / DWARF1 / DIMINUTO (DIM) | chr3:6879835-6881616 REVERSE LENGTH=561	561	561	0	100.0	92.7	97.0
Rsa1.0_01825.1.g30109.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01826.1.g30110.t2	ref|NP_177055.2| 2-oxoglutarate decarboxylase/ hydro-lyase/ magnesium ion binding protein [Arabidopsis thaliana] gi|341941250|sp|Q15KI9.2|PHYLO_ARATH RecName: Full=Protein PHYLLO, chloroplastic; Includes: RecName: Full=Inactive isochorismate synthase; AltName: Full=MENF; Includes: RecName: Full=2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- carboxylate synthase; AltName: Full=MEND; Includes: RecName: Full=o-succinylbenzoate synthase; AltName: Full=MENC; Includes: RecName: Full=2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase; AltName: Full=MENH; Flags: Precursor gi|332196734|gb|AEE34855.1| 2-oxoglutarate decarboxylase/ hydro-lyase/ magnesium ion binding protein [Arabidopsis thaliana]	1717	1715	0	99.9	85.7	90.9	2-oxoglutarate decarboxylase/ hydro-lyase/ magnesium ion binding protein	gbpln	Arabidopsis thaliana	AT1G68890.1 | Symbols: | magnesium ion binding;thiamin pyrophosphate binding;hydro-lyases;catalytics;2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthases | chr1:25896988-25906553 FORWARD LENGTH=1715	1717	1715	0	99.9	85.7	90.9

Rsa1.0_01826.1.g30111.t1	ref|NP_001031254.1| putative defensin-like protein 263 [Arabidopsis thaliana] gi|122209605|sp|Q2V4D9.1|DF263_ARATH RecName: Full=Putative defensin-like protein 263; Flags: Precursor gi|332196736|gb|AEE34857.1| putative defensin-like protein 263 [Arabidopsis thaliana]	90	96	2.00E-28	106.7	72.2	81.1	putative defensin-like protein 263	gbpln	Arabidopsis thaliana	AT1G68907.1 | Symbols: | Defensin-like (DEFL) family protein | chr1:25907508-25907891 REVERSE LENGTH=96	90	96	4.00E-31	106.7	72.2	81.1
Rsa1.0_01826.1.g30112.t1	gb|EOA33767.1| hypothetical protein CARUB_v10019961mg [Capsella rubella]	147	630	5.00E-41	428.6	62.6	75.5	hypothetical protein CARUB_v10019961mg	gbpln	Capsella rubella	AT1G68910.3 | Symbols: WIT2 | WPP domain-interacting protein 2 | chr1:25908373-25910485 REVERSE LENGTH=582	147	582	1.00E-42	395.9	61.9	76.2
Rsa1.0_01827.1.g30113.t1	ref|XP_002885497.1| hypothetical protein ARALYDRAFT_898699 [Arabidopsis lyrata subsp. lyrata] gi|297331337|gb|EFH61756.1| hypothetical protein ARALYDRAFT_898699 [Arabidopsis lyrata subsp. lyrata]	696	772	1.00E-123	110.9	45.1	58.5	hypothetical protein ARALYDRAFT_898699	gbpln	Arabidopsis lyrata	AT3G49130.1 | Symbols: | SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein | chr3:18210453-18211708 FORWARD LENGTH=307	696	307	3.00E-30	44.1	14.9	20.5
Rsa1.0_01827.1.g30114.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01827.1.g30115.t1	ref|XP_002885543.1| hypothetical protein ARALYDRAFT_319027 [Arabidopsis lyrata subsp. lyrata] gi|297331383|gb|EFH61802.1| hypothetical protein ARALYDRAFT_319027 [Arabidopsis lyrata subsp. lyrata]	138	427	3.00E-40	309.4	63.8	71.7	hypothetical protein ARALYDRAFT_319027	gbpln	Arabidopsis lyrata	AT4G14500.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:8334391-8337022 FORWARD LENGTH=433	138	433	2.00E-38	313.8	58.7	65.9
Rsa1.0_01827.1.g30116.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01827.1.g30117.t1	ref|XP_002873763.1| hypothetical protein ARALYDRAFT_488471 [Arabidopsis lyrata subsp. lyrata] gi|297319600|gb|EFH50022.1| hypothetical protein ARALYDRAFT_488471 [Arabidopsis lyrata subsp. lyrata]	1179	1179	0	100.0	90.4	93.6	hypothetical protein ARALYDRAFT_488471	gbpln	Arabidopsis lyrata	AT5G16210.1 | Symbols: | HEAT repeat-containing protein | chr5:5290999-5297779 REVERSE LENGTH=1180	1179	1180	0	100.1	90.4	93.6
Rsa1.0_01827.1.g30118.t2	gb|EOA20044.1| hypothetical protein CARUB_v10000322mg, partial [Capsella rubella]	1017	726	0	71.4	55.9	61.5	hypothetical protein CARUB_v10000322mg, partial	gbpln	Capsella rubella	AT5G16180.1 | Symbols: CRS1, ATCRS1 | ortholog of maize chloroplast splicing factor CRS1 | chr5:5279884-5282898 FORWARD LENGTH=720	1017	720	0	70.8	54.6	60.5
Rsa1.0_01827.1.g30119.t1	gb|EOA23049.1| hypothetical protein CARUB_v10003819mg [Capsella rubella]	136	131	7.00E-43	96.3	71.3	81.6	hypothetical protein CARUB_v10003819mg	gbpln	Capsella rubella	AT5G16160.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5275813-5276576 REVERSE LENGTH=133	136	133	2.00E-45	97.8	72.8	80.1
Rsa1.0_01827.1.g30120.t1	gb|AAM08751.1|AC025098_18 Putative copia-type polyprotein [Oryza sativa Japonica Group]	1359	1803	0	132.7	45.4	59.8	Putative copia-type polyprotein	gbpln	Oryza sativa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1359	1262	1.00E-103	92.9	13.4	20.8
Rsa1.0_01827.1.g30121.t1	ref|XP_002871704.1| 40S ribosomal protein S7 [Arabidopsis lyrata subsp. lyrata] gi|297317541|gb|EFH47963.1| 40S ribosomal protein S7 [Arabidopsis lyrata subsp. lyrata]	190	190	1.00E-101	100.0	94.2	97.9	40S ribosomal protein S7	gbpln	Arabidopsis lyrata	AT5G16130.1 | Symbols: | Ribosomal protein S7e family protein | chr5:5268984-5269912 FORWARD LENGTH=190	190	190	1.00E-104	100.0	94.2	98.4
Rsa1.0_01827.1.g30122.t1	gb|EOA22522.1| hypothetical protein CARUB_v10003177mg [Capsella rubella]	344	351	1.00E-178	102.0	87.5	94.8	hypothetical protein CARUB_v10003177mg	gbpln	Capsella rubella	AT5G16120.2 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:5265820-5267775 FORWARD LENGTH=369	344	369	1.00E-179	107.3	86.3	94.2
Rsa1.0_01827.1.g30123.t1	ref|XP_002873757.1| hypothetical protein ARALYDRAFT_326057 [Arabidopsis lyrata subsp. lyrata] gi|297319594|gb|EFH50016.1| hypothetical protein ARALYDRAFT_326057 [Arabidopsis lyrata subsp. lyrata]	404	348	5.00E-56	86.1	37.1	48.0	hypothetical protein ARALYDRAFT_326057	gbpln	Arabidopsis lyrata	AT5G16100.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:5258551-5259719 REVERSE LENGTH=357	404	357	1.00E-51	88.4	37.1	49.0
Rsa1.0_01827.1.g30124.t3	gb|AAD32757.1| putative helicase [Arabidopsis thaliana]	619	1241	0	200.5	56.4	69.3	putative helicase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01828.1.g30125.t1	ref|XP_002888361.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334202|gb|EFH64620.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	144	352	5.00E-74	244.4	91.0	94.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G65340.1 | Symbols: CYP96A3 | cytochrome P450, family 96, subfamily A, polypeptide 3 | chr1:24268135-24269646 REVERSE LENGTH=503	144	503	7.00E-75	349.3	88.2	93.1
Rsa1.0_01828.1.g30126.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01828.1.g30127.t1	ref|XP_002866852.1| CYP96A9 [Arabidopsis lyrata subsp. lyrata] gi|297312688|gb|EFH43111.1| CYP96A9 [Arabidopsis lyrata subsp. lyrata]	516	515	0	99.8	84.9	91.7	CYP96A9	gbpln	Arabidopsis lyrata	AT4G39480.1 | Symbols: CYP96A9 | cytochrome P450, family 96, subfamily A, polypeptide 9 | chr4:18362558-18364108 FORWARD LENGTH=516	516	516	0	100.0	84.1	91.3

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<tr><td>Rsa1.0_01828.1.g30128.t1</td><td>ref|XP_002866853.1| CYP96A10 [Arabidopsis lyrata subsp. lyrata] gi|297312689|gb|EFH43112.1| CYP96A10 [Arabidopsis lyrata subsp. lyrata]</td><td>514</td><td>519</td><td>0</td><td>101.0</td><td>86.8</td><td>93.8</td><td>CYP96A10</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G39490.1 | Symbols: CYP96A10 | cytochrome P450, family 96, subfamily A, polypeptide 10 | chr4:18365229-18366788 FORWARD LENGTH=519</td><td>514</td><td>519</td><td>0</td><td>101.0</td><td>86.4</td><td>92.8</td></tr>
<tr><td>Rsa1.0_01828.1.g30129.t1</td><td>gb|EOA39051.1| hypothetical protein CARUB_v10011665mg [Capsella rubella]</td><td>471</td><td>518</td><td>0</td><td>110.0</td><td>80.7</td><td>89.2</td><td>hypothetical protein CARUB_v10011665mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G47620.1 | Symbols: CYP96A8 | cytochrome P450, family 96, subfamily A, polypeptide 8 | chr1:17508116-17509678 REVERSE LENGTH=520</td><td>471</td><td>520</td><td>0</td><td>110.4</td><td>77.3</td><td>88.3</td></tr>
<tr><td>Rsa1.0_01828.1.g30130.t1</td><td>gb|EOA16459.1| hypothetical protein CARUB_v10004619mg [Capsella rubella]</td><td>488</td><td>506</td><td>0</td><td>103.7</td><td>72.7</td><td>82.0</td><td>hypothetical protein CARUB_v10004619mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G32170.1 | Symbols: CYP96A2 | cytochrome P450, family 96, subfamily A, polypeptide 2 | chr4:15533772-15535292 FORWARD LENGTH=506</td><td>488</td><td>506</td><td>0</td><td>103.7</td><td>73.0</td><td>81.4</td></tr>
<tr><td>Rsa1.0_01828.1.g30131.t1</td><td>gb|EOA16858.1| hypothetical protein CARUB_v10005082mg [Capsella rubella]</td><td>369</td><td>369</td><td>0</td><td>100.0</td><td>97.0</td><td>98.1</td><td>hypothetical protein CARUB_v10005082mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G39520.1 | Symbols: | GTP-binding protein-related | chr4:18371329-18374000 REVERSE LENGTH=369</td><td>369</td><td>369</td><td>0</td><td>100.0</td><td>96.5</td><td>98.1</td></tr>
<tr><td>Rsa1.0_01828.1.g30132.t1</td><td>gb|EOA18012.1| hypothetical protein CARUB_v10006447mg [Capsella rubella]</td><td>834</td><td>835</td><td>0</td><td>100.1</td><td>83.8</td><td>91.6</td><td>hypothetical protein CARUB_v10006447mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G39530.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:18374736-18377240 REVERSE LENGTH=834</td><td>834</td><td>834</td><td>0</td><td>100.0</td><td>82.7</td><td>91.4</td></tr>
<tr><td>Rsa1.0_01828.1.g30133.t1</td><td>gb|EOA18073.1| hypothetical protein CARUB_v10006520mg, partial [Capsella rubella]</td><td>380</td><td>405</td><td>1.00E-168</td><td>106.6</td><td>76.8</td><td>85.8</td><td>hypothetical protein CARUB_v10006520mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G39580.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18385684-18386811 REVERSE LENGTH=375</td><td>380</td><td>375</td><td>1.00E-168</td><td>98.7</td><td>77.4</td><td>85.0</td></tr>
<tr><td>Rsa1.0_01828.1.g30134.t1</td><td>ref|XP_002868913.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297314749|gb|EFH45172.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]</td><td>395</td><td>389</td><td>1.00E-122</td><td>98.5</td><td>59.0</td><td>71.4</td><td>kelch repeat-containing F-box family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G39550.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18380681-18381859 REVERSE LENGTH=392</td><td>395</td><td>392</td><td>1.00E-122</td><td>99.2</td><td>61.3</td><td>73.7</td></tr>
<tr><td>Rsa1.0_01828.1.g30135.t1</td><td>ref|XP_002888041.1| hypothetical protein ARALYDRAFT_475134 [Arabidopsis lyrata subsp. lyrata] gi|297333882|gb|EFH64300.1| hypothetical protein ARALYDRAFT_475134 [Arabidopsis lyrata subsp. lyrata]</td><td>2778</td><td>1217</td><td>0</td><td>43.8</td><td>40.8</td><td>42.5</td><td>hypothetical protein ARALYDRAFT_475134</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G62020.1 | Symbols: | Coatomer, alpha subunit | chr1:22919814-22923728 FORWARD LENGTH=1216</td><td>2778</td><td>1216</td><td>0</td><td>43.8</td><td>40.5</td><td>42.3</td></tr>
<tr><td>Rsa1.0_01829.1.g30136.t1</td><td>emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]</td><td>1418</td><td>1515</td><td>0</td><td>106.8</td><td>58.0</td><td>72.7</td><td>retrotransposon like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1418</td><td>1262</td><td>1.00E-111</td><td>89.0</td><td>14.2</td><td>21.4</td></tr>
<tr><td>Rsa1.0_01829.1.g30137.t1</td><td>gb|EOA34248.1| hypothetical protein CARUB_v10021759mg [Capsella rubella]</td><td>95</td><td>95</td><td>1.00E-27</td><td>100.0</td><td>63.2</td><td>80.0</td><td>hypothetical protein CARUB_v10021759mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G74458.1 | Symbols: | unknown protein; LOCATED IN: endomembrane system; Has 9 Blast hits to 9 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 9; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:27987071-27987551 FORWARD LENGTH=94</td><td>95</td><td>94</td><td>2.00E-29</td><td>98.9</td><td>65.3</td><td>77.9</td></tr>
<tr><td>Rsa1.0_01829.1.g30138.t1</td><td>ref|NP_177586.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75169843|sp|Q9CA68.1|GDL31_ARATH RecName: Full=GDSL esterase/lipase At1g74460; AltName: Full=Extracellular lipase At1g74460; Flags: Precursor gi|12324806|gb|AAG52368.1|AC011765_20 putative lipase/acylhydrolase; 46085-44470 [Arabidopsis thaliana] gi|21592578|gb|AAM64527.1| putative lipase/acylhydrolase [Arabidopsis thaliana] gi|332197475|gb|AEE35596.1| GDSL esterase/lipase [Arabidopsis thaliana]</td><td>364</td><td>366</td><td>0</td><td>100.5</td><td>92.3</td><td>95.1</td><td>GDSL esterase/lipase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G74460.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:27988150-27989765 REVERSE LENGTH=366</td><td>364</td><td>366</td><td>0</td><td>100.5</td><td>92.3</td><td>95.1</td></tr>
<tr><td>Rsa1.0_01829.1.g30139.t1</td><td>ref|XP_002888981.1| hypothetical protein ARALYDRAFT_476585 [Arabidopsis lyrata subsp. lyrata] gi|297334822|gb|EFH65240.1| hypothetical protein ARALYDRAFT_476585 [Arabidopsis lyrata subsp. lyrata] gi|482569929|gb|EOA34117.1| hypothetical protein CARUB_v10021619mg [Capsella rubella]</td><td>93</td><td>93</td><td>7.00E-34</td><td>100.0</td><td>80.6</td><td>82.8</td><td>hypothetical protein ARALYDRAFT_476585</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G74500.1 | Symbols: ATBS1, TMO7, BS1 | activation-tagged BRI1(brassinosteroid-insensitive 1)-suppressor 1 | chr1:27998298-27998668 REVERSE LENGTH=93</td><td>93</td><td>93</td><td>3.00E-36</td><td>100.0</td><td>79.6</td><td>82.8</td></tr>
<tr><td>Rsa1.0_01829.1.g30140.t1</td><td>gb|EOA35161.1| hypothetical protein CARUB_v10020300mg [Capsella rubella] gi|482570975|gb|EOA35163.1| hypothetical protein CARUB_v10020300mg [Capsella rubella]</td><td>423</td><td>444</td><td>0</td><td>105.0</td><td>85.1</td><td>90.1</td><td>hypothetical protein CARUB_v10020300mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G74510.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:28006065-28007420 FORWARD LENGTH=451</td><td>423</td><td>451</td><td>0</td><td>106.6</td><td>84.4</td><td>90.3</td></tr>
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Rsa1.0_01829.1.g30141.t1	ref|XP_002887545.1| CYP98A8 [Arabidopsis lyrata subsp. lyrata] gi|297333386|gb|EFH63804.1| CYP98A8 [Arabidopsis lyrata subsp. lyrata]	481	497	0	103.3	82.3	91.7	CYP98A8	gbpln	Arabidopsis lyrata	AT1G74540.1 | Symbols: CYP98A8 | cytochrome P450, family 98, subfamily A, polypeptide 8 | chr1:28013362-28014855 FORWARD LENGTH=497	481	497	0	103.3	81.5	90.9
Rsa1.0_01829.1.g30142.t1	ref|XP_002879925.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297325764|gb|EFH56184.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	370	371	3.00E-62	100.3	41.9	59.5	F-box family protein	gbpln	Arabidopsis lyrata	AT2G41360.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:17234374-17235956 FORWARD LENGTH=387	370	387	2.00E-52	104.6	35.7	50.0
Rsa1.0_01830.1.g30143.t1	gb|EOA28640.1| hypothetical protein CARUB_v10024862mg, partial [Capsella rubella]	508	490	1.00E-75	96.5	34.6	55.5	hypothetical protein CARUB_v10024862mg, partial	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	508	566	1.00E-74	111.4	33.1	54.5
Rsa1.0_01830.1.g30144.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01830.1.g30145.t4	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	1557	1752	0	112.5	53.8	67.4	putative protein	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1557	331	1.00E-68	21.3	9.4	13.2
Rsa1.0_01830.1.g30146.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	786	1023	1.00E-125	130.2	29.5	39.4	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	786	575	8.00E-35	73.2	8.7	14.5
Rsa1.0_01830.1.g30147.t1	ref|XP_002870305.1| hypothetical protein ARALYDRAFT_915409 [Arabidopsis lyrata subsp. lyrata] gi|297316141|gb|EFH46564.1| hypothetical protein ARALYDRAFT_915409 [Arabidopsis lyrata subsp. lyrata]	824	763	0	92.6	79.7	86.9	hypothetical protein ARALYDRAFT_915409	gbpln	Arabidopsis lyrata	AT4G14570.1 | Symbols: | acylaminoacyl-peptidase-related | chr4:8362586-8366525 FORWARD LENGTH=764	824	764	0	92.7	79.2	86.3
Rsa1.0_01831.1.g30148.t1	ref|XP_002864260.1| hypothetical protein ARALYDRAFT_918447 [Arabidopsis lyrata subsp. lyrata] gi|297310095|gb|EFH40519.1| hypothetical protein ARALYDRAFT_918447 [Arabidopsis lyrata subsp. lyrata]	324	231	4.00E-20	71.3	18.2	34.3	hypothetical protein ARALYDRAFT_918447	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01831.1.g30149.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01831.1.g30150.t1	ref|XP_002885142.1| IQ-domain 26 [Arabidopsis lyrata subsp. lyrata] gi|297330982|gb|EFH61401.1| IQ-domain 26 [Arabidopsis lyrata subsp. lyrata]	394	390	1.00E-170	99.0	84.8	89.3	IQ-domain 26	gbpln	Arabidopsis lyrata	AT3G16490.1 | Symbols: IQD26 | IQ-domain 26 | chr3:5603962-5605489 REVERSE LENGTH=389	394	389	1.00E-169	98.7	84.3	87.8
Rsa1.0_01831.1.g30151.t1	ref|NP_566548.1| mitochondrial processing peptidase [Arabidopsis thaliana] gi|29839443|sp|O04308.1|MPPA2_ARATH RecName: Full=Probable mitochondrial-processing peptidase subunit alpha-2; AltName: Full=Alpha-MPP 2; Flags: Precursor gi|2062155|gb|AAB63629.1| mitochondrial processing peptidase alpha subunit precusor isolog [Arabidopsis thaliana] gi|9279647|dbj|BAB01147.1| mitochondrial processing peptidase alpha subunit [Arabidopsis thaliana] gi|23297133|gb|AAN13101.1| putative mitochondrial processing peptidase alpha subunit [Arabidopsis thaliana] gi|332642304|gb|AEE75825.1| probable mitochondrial-processing peptidase subunit alpha-2 [Arabidopsis thaliana]	491	499	0	101.6	83.1	90.4	mitochondrial processing peptidase	gbpln	Arabidopsis thaliana	AT3G16480.1 | Symbols: MPPalpha | mitochondrial processing peptidase alpha subunit | chr3:5599906-5602716 FORWARD LENGTH=499	491	499	0	101.6	83.1	90.4
Rsa1.0_01831.1.g30152.t1	gb|EOA30607.1| hypothetical protein CARUB_v10013738mg [Capsella rubella]	289	436	1.00E-62	150.9	47.8	67.1	hypothetical protein CARUB_v10013738mg	gbpln	Capsella rubella	AT1G52040.1 | Symbols: MBP1, ATMBP | myrosinase-binding protein 1 | chr1:19350595-19352578 REVERSE LENGTH=462	289	462	3.00E-47	159.9	31.8	41.5
Rsa1.0_01832.1.g30153.t1	ref|XP_002871161.1| hydrolase, acting on glycosyl bonds [Arabidopsis lyrata subsp. lyrata] gi|297316998|gb|EFH47420.1| hydrolase, acting on glycosyl bonds [Arabidopsis lyrata subsp. lyrata]	397	678	0	170.8	83.9	90.2	hydrolase, acting on glycosyl bonds	gbpln	Arabidopsis lyrata	AT5G05460.1 | Symbols: | Glycosyl hydrolase family 85 | chr5:1615615-1618771 FORWARD LENGTH=680	397	680	0	171.3	83.6	89.7
Rsa1.0_01832.1.g30154.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01832.1.g30155.t1	gb|EOA19506.1| hypothetical protein CARUB_v10002333mg [Capsella rubella]	60	97	3.00E-25	161.7	95.0	95.0	hypothetical protein CARUB_v10002333mg	gbpln	Capsella rubella	AT5G05370.1 | Symbols: | Cytochrome b-c1 complex, subunit 8 protein | chr5:1590977-1591869 REVERSE LENGTH=72	60	72	3.00E-27	120.0	91.7	95.0
Rsa1.0_01832.1.g30156.t1	gb|AAD10854.1| serine/threonine protein phosphatase 2A-3 catalytic subunit [Arabidopsis thaliana]	167	352	1.00E-18	210.8	28.1	32.9	serine/threonine protein phosphatase 2A-3 catalytic subunit	gbpln	Arabidopsis thaliana	AT2G42500.1 | Symbols: PP2A-3 | protein phosphatase 2A-3 | chr2:17698099-17701226 REVERSE LENGTH=313	167	313	7.00E-21	187.4	28.1	32.9

Rsa1.0_01832.1.g30157.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1489	1475	0	99.1	51.8	67.1	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1489	1262	0	84.8	26.7	32.0
Rsa1.0_01832.1.g30158.t1	emb|CCJ34831.1| horseradish peroxidase isoenzyme HRP_1350 [Armoracia rusticana]	324	324	1.00E-128	100.0	69.8	82.4	horseradish peroxidase isoenzyme HRP_1350	gbpln	Armoracia rusticana	AT5G05340.1 | Symbols: | Peroxidase superfamily protein | chr5:1579142-1580819 REVERSE LENGTH=324	324	324	1.00E-129	100.0	71.9	83.0
Rsa1.0_01832.1.g30159.t1	gb|EOA20868.1| hypothetical protein CARUB_v10001205mg [Capsella rubella] gi|482556677|gb|EOA20869.1| hypothetical protein CARUB_v10001205mg [Capsella rubella]	375	372	1.00E-150	99.2	77.3	86.1	hypothetical protein CARUB_v10001205mg	gbpln	Capsella rubella	AT5G05210.1 | Symbols: | Surfeit locus protein 6 | chr5:1548198-1549534 FORWARD LENGTH=386	375	386	1.00E-148	102.9	77.3	86.9
Rsa1.0_01832.1.g30160.t1	ref|NP_568150.1| aarF domain-containing protein kinase [Arabidopsis thaliana] gi|75261770|sp|Q9ASX5.1|Y5520_ARATH RecName: Full=Uncharacterized aarF domain-containing protein kinase At5g05200, chloroplastic; Flags: Precursor gi|13605575|gb|AAK32781.1|AF361613_1 AT5g05200/K2A11_7 [Arabidopsis thaliana] gi|14334952|gb|AAK59653.1| unknown protein [Arabidopsis thaliana] gi|16648993|gb|AAL24348.1| Unknown protein [Arabidopsis thaliana] gi|17104611|gb|AAL34194.1| unknown protein [Arabidopsis thaliana] gi|20259938|gb|AAM13316.1| unknown protein [Arabidopsis thaliana] gi|22137078|gb|AAM91384.1| At5g05200/K2A11_7 [Arabidopsis thaliana] gi|332003457|gb|AED90840.1| aarF domain-containing protein kinase [Arabidopsis thaliana]	240	540	1.00E-40	225.0	42.5	49.6	aarF domain-containing protein kinase	gbpln	Arabidopsis thaliana	AT5G05200.1 | Symbols: | Protein kinase superfamily protein | chr5:1544206-1547082 REVERSE LENGTH=540	240	540	4.00E-43	225.0	42.5	49.6
Rsa1.0_01832.1.g30161.t1	ref|NP_196138.1| uncharacterized protein [Arabidopsis thaliana] gi|75170629|sp|Q9FHK4.1|Y5519_ARATH RecName: Full=Uncharacterized protein At5g05190 gi|9759260|dbj|BAB09695.1| unnamed protein product [Arabidopsis thaliana] gi|20466820|gb|AAM20727.1| putative protein [Arabidopsis thaliana] gi|30725434|gb|AAP37739.1| At5g05190 [Arabidopsis thaliana] gi|332003456|gb|AED90839.1| uncharacterized protein AT5G05190 [Arabidopsis thaliana]	657	615	1.00E-162	93.6	58.9	67.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G05190.1 | Symbols: | Protein of unknown function (DUF3133) | chr5:1541853-1543875 FORWARD LENGTH=615	657	615	1.00E-164	93.6	58.9	67.1
Rsa1.0_01833.1.g30162.t1	ref|XP_002868921.1| hypothetical protein ARALYDRAFT_912442 [Arabidopsis lyrata subsp. lyrata] gi|297314757|gb|EFH45180.1| hypothetical protein ARALYDRAFT_912442 [Arabidopsis lyrata subsp. lyrata]	223	233	4.00E-83	104.5	76.7	83.9	hypothetical protein ARALYDRAFT_912442	gbpln	Arabidopsis lyrata	AT4G39630.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:18397749-18399263 REVERSE LENGTH=233	223	233	2.00E-82	104.5	74.4	81.6
Rsa1.0_01833.1.g30163.t1	ref|XP_002889147.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334988|gb|EFH65406.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	861	854	0	99.2	84.1	91.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G77550.1 | Symbols: | tubulin-tyrosine ligases;tubulin-tyrosine ligases | chr1:29138490-29142965 REVERSE LENGTH=855	861	855	0	99.3	83.4	90.8
Rsa1.0_01833.1.g30164.t1	gb|EOA17387.1| hypothetical protein CARUB_v10005682mg [Capsella rubella]	134	224	7.00E-58	167.2	89.6	96.3	hypothetical protein CARUB_v10005682mg	gbpln	Capsella rubella	AT5G37475.1 | Symbols: | Translation initiation factor eIF3 subunit | chr5:14866328-14867749 REVERSE LENGTH=225	134	225	2.00E-60	167.9	90.3	97.8
Rsa1.0_01833.1.g30165.t1	gb|AAD20646.1| putative TNP2-like transposon protein [Arabidopsis thaliana]	217	1040	5.00E-17	479.3	23.0	28.1	putative TNP2-like transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01833.1.g30166.t1	gb|AAF18642.1|AC006228_13 F5J5.15 [Arabidopsis thaliana]	187	1617	2.00E-43	864.7	50.3	61.5	F5J5.15	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01833.1.g30167.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01833.1.g30168.t1	gb|EOA18583.1| hypothetical protein CARUB_v10007155mg [Capsella rubella]	525	609	2.00E-66	116.0	26.9	33.7	hypothetical protein CARUB_v10007155mg	gbpln	Capsella rubella	AT5G37460.1 | Symbols: | Family of unknown function (DUF577) | chr5:14858494-14860362 REVERSE LENGTH=622	525	622	3.00E-66	118.5	26.5	35.0
Rsa1.0_01834.1.g30169.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01834.1.g30170.t1	ref|NP_564019.1| protein TIFY 11A [Arabidopsis thaliana] gi|75173855|sp|Q9LDU5.1|TI11A_ARATH RecName: Full=Protein TIFY 11A; AltName: Full=Jasmonate ZIM domain-containing protein 5 gi|8778483|gb|AAF79491.1|AC022492_35 F1L3.3 [Arabidopsis thaliana] gi|9665119|gb|AAF97303.1|AC007843_6 Hypothetical protein [Arabidopsis thaliana] gi|23306360|gb|AAN17407.1| expressed protein [Arabidopsis thaliana] gi|27311875|gb|AAO00903.1| expressed protein [Arabidopsis thaliana] gi|332191460|gb|AEE29581.1| protein TIFY 11A [Arabidopsis thaliana]	212	274	6.00E-50	129.2	55.2	61.8	protein TIFY 11A	gbpln	Arabidopsis thaliana	AT1G17380.1 | Symbols: JAZ5, TIFY11A | jasmonate-zim-domain protein 5 | chr1:5955654-5957070 REVERSE LENGTH=274	212	274	2.00E-52	129.2	55.2	61.8
Rsa1.0_01834.1.g30171.t10	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1122	1864	0	166.1	38.1	43.9	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	ATMG00750.1 | Symbols: ORF119 | GAG/POL/ENV polyprotein | chrM:220830-221189 FORWARD LENGTH=119	1122	119	2.00E-20	10.6	3.7	4.2
Rsa1.0_01834.1.g30172.t1	ref|XP_002885617.1| hypothetical protein ARALYDRAFT_898967 [Arabidopsis lyrata subsp. lyrata] gi|297331457|gb|EFH61876.1| hypothetical protein ARALYDRAFT_898967 [Arabidopsis lyrata subsp. lyrata]	553	488	4.00E-25	88.2	20.6	35.1	hypothetical protein ARALYDRAFT_898967	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01834.1.g30173.t1	ref|NP_564024.1| protein ELF4-like 4 [Arabidopsis thaliana] gi|238478519|ref|NP_001154348.1| protein ELF4-like 4 [Arabidopsis thaliana] gi|75218652|sp|Q570U6.1|EF4L4_ARATH RecName: Full=Protein ELF4-LIKE 4 gi|62318582|dbj|BAD94981.1| hypothetical protein [Arabidopsis thaliana] gi|98961045|gb|ABF59006.1| At1g17455 [Arabidopsis thaliana] gi|332191470|gb|AEE29591.1| protein ELF4-like 4 [Arabidopsis thaliana] gi|332191471|gb|AEE29592.1| protein ELF4-like 4 [Arabidopsis thaliana]	128	114	8.00E-48	89.1	78.1	83.6	protein ELF4-like 4	gbpln	Arabidopsis thaliana	AT1G17455.2 | Symbols: ELF4-L4 | ELF4-like 4 | chr1:5997932-5998276 FORWARD LENGTH=114	128	114	2.00E-50	89.1	78.1	83.6
Rsa1.0_01834.1.g30174.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01834.1.g30175.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1065	1529	2.00E-90	143.6	21.7	33.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1065	746	1.00E-51	70.0	11.4	17.0
Rsa1.0_01835.1.g30176.t1	gb|ADK63406.1| C2H2 type zinc finger protein [Brassica rapa]	154	157	4.00E-78	101.9	94.8	96.8	C2H2 type zinc finger protein	gbpln	Brassica rapa	AT5G59820.1 | Symbols: RHL41, ZAT12 | C2H2-type zinc finger family protein | chr5:24103073-24103561 FORWARD LENGTH=162	154	162	3.00E-70	105.2	86.4	93.5
Rsa1.0_01835.1.g30177.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01835.1.g30178.t1	gb|ADK63406.1| C2H2 type zinc finger protein [Brassica rapa]	159	157	2.00E-81	98.7	95.0	96.9	C2H2 type zinc finger protein	gbpln	Brassica rapa	AT5G59820.1 | Symbols: RHL41, ZAT12 | C2H2-type zinc finger family protein | chr5:24103073-24103561 FORWARD LENGTH=162	159	162	4.00E-74	101.9	86.8	93.7
Rsa1.0_01835.1.g30179.t1	ref|NP_200791.2| uncharacterized protein [Arabidopsis thaliana] gi|42573736|ref|NP_974964.1| uncharacterized protein [Arabidopsis thaliana] gi|332009855|gb|AED97238.1| uncharacterized protein AT5G59830 [Arabidopsis thaliana] gi|332009856|gb|AED97239.1| uncharacterized protein AT5G59830 [Arabidopsis thaliana]	411	425	1.00E-160	103.4	78.6	85.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G59830.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13660.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:24105423-24107071 FORWARD LENGTH=425	411	425	1.00E-163	103.4	78.6	85.2
Rsa1.0_01835.1.g30180.t1	emb|CAA90080.1| small GTP-binding protein [Pisum sativum]	216	216	1.00E-112	100.0	88.9	96.3	small GTP-binding protein	gbpln	Pisum sativum	AT5G59840.1 | Symbols: | Ras-related small GTP-binding family protein | chr5:24107450-24109049 REVERSE LENGTH=216	216	216	1.00E-113	100.0	88.9	93.5
Rsa1.0_01835.1.g30181.t1	sp|Q00332.3|RS15A_BRANA RecName: Full=40S ribosomal protein S15a; AltName: Full=PPCB8 gi|17863|emb|CAA42599.1| r-protein BnS15a [Brassica napus] gi|119720818|gb|ABL97979.1| 40S ribosomal protein S15a [Brassica rapa]	130	130	6.00E-69	100.0	99.2	99.2	RecName: Full=40S ribosomal protein S15a; AltName: Full=PPCB8 gi|17863|emb|CAA42599.1| r-protein BnS15a	gbpln	Brassica napus	AT5G59850.1 | Symbols: | Ribosomal protein S8 family protein | chr5:24112499-24113084 REVERSE LENGTH=130	130	130	3.00E-71	100.0	98.5	99.2
Rsa1.0_01835.1.g30182.t1	ref|XP_002864655.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310490|gb|EFH40914.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	98	95	2.00E-35	96.9	74.5	83.7	predicted protein	gbpln	Arabidopsis lyrata	AT3G46020.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:16912511-16913250 REVERSE LENGTH=102	98	102	4.00E-36	104.1	71.4	84.7

Rsa1.0_01835.1.g30183.t1	ref|XP_002866356.1| hypothetical protein ARALYDRAFT_358205 [Arabidopsis lyrata subsp. lyrata] gi|297312191|gb|EFH42615.1| hypothetical protein ARALYDRAFT_358205 [Arabidopsis lyrata subsp. lyrata]	149	149	8.00E-73	100.0	94.0	96.6	hypothetical protein ARALYDRAFT_358205	gbpln	Arabidopsis lyrata	AT5G59870.1 | Symbols: HTA6 | histone H2A 6 | chr5:24115605-24116144 REVERSE LENGTH=150	149	150	1.00E-72	100.7	92.6	95.3
Rsa1.0_01836.1.g30184.t1	ref|NP_196909.1| U3 small nucleolar RNA-associated protein 18-like protein [Arabidopsis thaliana] gi|17366762|sp|Q9FMU5.1|UTP18_ARATH RecName: Full=U3 small nucleolar RNA-associated protein 18 homolog gi|9757786|dbj|BAB08284.1| unnamed protein product [Arabidopsis thaliana] gi|18700147|gb|AAL77685.1| AT5g14050/MUA22_5 [Arabidopsis thaliana] gi|22137238|gb|AAM91464.1| AT5g14050/MUA22_5 [Arabidopsis thaliana] gi|332004598|gb|AED91981.1| U3 small nucleolar RNA-associated protein 18-like protein [Arabidopsis thaliana]	152	546	1.00E-54	359.2	64.5	73.0	U3 small nucleolar RNA-associated protein 18-like protein	gbpln	Arabidopsis thaliana	AT5G14050.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:4533539-4535179 FORWARD LENGTH=546	152	546	5.00E-57	359.2	64.5	73.0
Rsa1.0_01836.1.g30185.t1	ref|XP_002873645.1| mitochondrial phosphate transporter [Arabidopsis lyrata subsp. lyrata] gi|297319482|gb|EFH49904.1| mitochondrial phosphate transporter [Arabidopsis lyrata subsp. lyrata]	369	374	0	101.4	93.5	96.5	mitochondrial phosphate transporter	gbpln	Arabidopsis lyrata	AT5G14040.1 | Symbols: PHT3;1 | phosphate transporter 3;1 | chr5:4531059-4532965 REVERSE LENGTH=375	369	375	0	101.6	91.1	95.4
Rsa1.0_01836.1.g30186.t1	ref|XP_002871597.1| translocon-associated protein beta family protein [Arabidopsis lyrata subsp. lyrata] gi|297317434|gb|EFH47856.1| translocon-associated protein beta family protein [Arabidopsis lyrata subsp. lyrata]	196	195	3.00E-86	99.5	81.1	89.8	translocon-associated protein beta family protein	gbpln	Arabidopsis lyrata	AT5G14030.4 | Symbols: | translocon-associated protein beta (TRAPB) family protein | chr5:4526878-4528253 FORWARD LENGTH=195	196	195	7.00E-87	99.5	79.6	88.8
Rsa1.0_01836.1.g30187.t1	gb|EOA22045.1| hypothetical protein CARUB_v10002570mg [Capsella rubella]	177	161	1.00E-43	91.0	59.9	71.2	hypothetical protein CARUB_v10002570mg	gbpln	Capsella rubella	AT5G14010.1 | Symbols: KNU | C2H2 and C2HC zinc fingers superfamily protein | chr5:4522260-4522745 FORWARD LENGTH=161	177	161	5.00E-35	91.0	55.9	68.4
Rsa1.0_01836.1.g30188.t1	ref|NP_196903.1| exocyst complex component 7 [Arabidopsis thaliana] gi|10177665|dbj|BAB11127.1| leucine zipper protein-like [Arabidopsis thaliana] gi|28392955|gb|AAO41913.1| putative leucine zipper protein [Arabidopsis thaliana] gi|29824345|gb|AAP04133.1| putative leucine zipper protein [Arabidopsis thaliana] gi|332004588|gb|AED91971.1| exocyst subunit exo70 family protein C2 [Arabidopsis thaliana]	707	695	0	98.3	82.7	88.5	exocyst complex component 7	gbpln	Arabidopsis thaliana	AT5G13990.1 | Symbols: ATEXO70C2, EXO70C2 | exocyst subunit exo70 family protein C2 | chr5:4514680-4516767 REVERSE LENGTH=695	707	695	0	98.3	82.7	88.5
Rsa1.0_01836.1.g30189.t1	ref|NP_196898.5| aminopeptidase [Arabidopsis thaliana] gi|332004579|gb|AED91962.1| aminopeptidase [Arabidopsis thaliana]	575	809	0	140.7	76.0	79.8	aminopeptidase	gbpln	Arabidopsis thaliana	AT5G13940.1 | Symbols: | aminopeptidases | chr5:4490263-4495585 REVERSE LENGTH=809	575	809	0	140.7	76.0	79.8
Rsa1.0_01836.1.g30190.t1	gb|AAC31914.1| chalcone synthase B2 [Brassica napus]	396	396	0	100.0	98.7	99.7	chalcone synthase B2	gbpln	Brassica napus	AT5G13930.1 | Symbols: CHS, TT4, ATCHS | Chalcone and stilbene synthase family protein | chr5:4488762-4490035 FORWARD LENGTH=395	396	395	0	99.7	96.0	97.2
Rsa1.0_01836.1.g30191.t1	ref|XP_002873631.1| hypothetical protein ARALYDRAFT_488210 [Arabidopsis lyrata subsp. lyrata] gi|297319468|gb|EFH49890.1| hypothetical protein ARALYDRAFT_488210 [Arabidopsis lyrata subsp. lyrata]	754	368	1.00E-156	48.8	39.0	43.2	hypothetical protein ARALYDRAFT_488210	gbpln	Arabidopsis lyrata	AT5G13860.1 | Symbols: ELC-Like | ELCH-like | chr5:4473212-4474318 REVERSE LENGTH=368	754	368	1.00E-156	48.8	38.5	43.5
Rsa1.0_01836.1.g30192.t1	ref|XP_002873629.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319466|gb|EFH49888.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	130	124	1.00E-23	95.4	45.4	59.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G13825.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:4465099-4465969 REVERSE LENGTH=124	130	124	1.00E-25	95.4	43.1	57.7

Rsa1.0_01836.1.g30193.t1	ref|NP_196886.1| Telomere repeat-binding protein 4 [Arabidopsis thaliana] gi|75333778|sp|Q9FFY9.1|TRP4_ARATH RecName: Full=Telomere repeat-binding protein 4; AltName: Full=H-protein promoter binding factor-1; Short=AtTBP1; AltName: Full=Telomeric DNA-binding protein 1 gi|10177648|dbj|BAB11110.1| H-protein promoter binding factor-1 [Arabidopsis thaliana] gi|13641340|gb|AAK31590.1| telomeric DNA-binding protein 1 [Arabidopsis thaliana] gi|209529761|gb|ACI49775.1| At5g13820 [Arabidopsis thaliana] gi|332004562|gb|AED91945.1| Telomere repeat-binding protein 4 [Arabidopsis thaliana]	549	640	0	116.6	74.9	82.3	Telomere repeat-binding protein 4	gbpln	Arabidopsis thaliana	AT5G13820.1 | Symbols: TBP1, ATBP-1, ATBP1, ATTBP1, HPPBF-1 | telomeric DNA binding protein 1 | chr5:4461694-4464355 FORWARD LENGTH=640	549	640	0	116.6	74.9	82.3
Rsa1.0_01837.1.g30194.t1	ref|NP_563841.1| uncharacterized protein [Arabidopsis thaliana] gi|13194796|gb|AAK15560.1|AF348589_1 unknown protein [Arabidopsis thaliana] gi|4337175|gb|AAD18096.1| ESTs gb|T20589, gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457, gb|T20921, gb|AA042762 and gb|AA720210 come from this gene [Arabidopsis thaliana] gi|15028183|gb|AAK76588.1| unknown protein [Arabidopsis thaliana] gi|19310813|gb|AAL85137.1| unknown protein [Arabidopsis thaliana] gi|21536763|gb|AAM61095.1| unknown [Arabidopsis thaliana] gi|332190307|gb|AEE28428.1| uncharacterized protein AT1G09310 [Arabidopsis thaliana]	168	179	2.00E-70	106.5	85.1	92.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G09310.1 | Symbols: | Protein of unknown function, DUF538 | chr1:3009109-3009648 FORWARD LENGTH=179	168	179	1.00E-72	106.5	85.1	92.3
Rsa1.0_01837.1.g30195.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01837.1.g30196.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01837.1.g30197.t2	gb|EOA39650.1| hypothetical protein CARUB_v10008289mg [Capsella rubella]	849	854	0	100.6	84.1	90.6	hypothetical protein CARUB_v10008289mg	gbpln	Capsella rubella	AT1G09090.2 | Symbols: ATRBOHB, RBOHB | respiratory burst oxidase homolog B | chr1:2932743-2936495 FORWARD LENGTH=843	849	843	0	99.3	83.0	90.2
Rsa1.0_01837.1.g30198.t1	gb|EOA39851.1| hypothetical protein CARUB_v10008520mg [Capsella rubella]	647	665	0	102.8	91.3	95.8	hypothetical protein CARUB_v10008520mg	gbpln	Capsella rubella	AT1G09080.2 | Symbols: BIP3 | Heat shock protein 70 (Hsp 70) family protein | chr1:2929268-2931804 REVERSE LENGTH=665	647	665	0	102.8	90.6	95.5
Rsa1.0_01837.1.g30199.t1	emb|CAA07573.1| src2-like protein [Arabidopsis thaliana]	322	324	1.00E-118	100.6	74.2	76.7	src2-like protein	gbpln	Arabidopsis thaliana	AT1G09070.1 | Symbols: SRC2, (AT)SRC2 | soybean gene regulated by cold-2 | chr1:2927767-2928741 FORWARD LENGTH=324	322	324	1.00E-120	100.6	73.9	76.4
Rsa1.0_01837.1.g30200.t1	ref|NP_563834.1| sucrose nonfermenting 4-like protein [Arabidopsis thaliana] gi|75249553|sp|Q944A6.1|SNF4_ARATH RecName: Full=Sucrose nonfermenting 4-like protein; Short=SNF4; AltName: Full=CBS domain-containing protein CBSCBS3; AltName: Full=SNF1-related protein kinase regulatory subunit betagamma; Short=AKIN subunit betagamma; Short=AKINbetagamma gi|16612255|gb|AAL27498.1|AF439826_1 At1g09020/F7G19_11 [Arabidopsis thaliana] gi|23308443|gb|AAN18191.1| At1g09020/F7G19_11 [Arabidopsis thaliana] gi|75037070|gb|ABA12450.1| AKINbetagamma [Arabidopsis thaliana] gi|332190262|gb|AEE28383.1| sucrose nonfermenting 4-like protein [Arabidopsis thaliana]	485	487	0	100.4	93.0	96.9	sucrose nonfermenting 4-like protein	gbpln	Arabidopsis thaliana	AT1G09020.1 | Symbols: SNF4, ATSNF4 | homolog of yeast sucrose nonfermenting 4 | chr1:2900149-2904212 REVERSE LENGTH=487	485	487	0	100.4	93.0	96.9
Rsa1.0_01838.1.g30201.t1	gb|EOA23607.1| hypothetical protein CARUB_v10016807mg, partial [Capsella rubella]	99	654	9.00E-23	660.6	66.7	77.8	hypothetical protein CARUB_v10016807mg, partial	gbpln	Capsella rubella	AT3G28450.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr3:10667359-10669176 FORWARD LENGTH=605	99	605	3.00E-25	611.1	67.7	75.8

Rsa1.0_01838.1.g30202.t1	ref|NP_565191.1| curculin-like (mannose-binding) lectin-like protein [Arabidopsis thaliana] gi|16226591|gb|AAL16208.1|AF428439_1 At1g78830/F9K20_12 [Arabidopsis thaliana] gi|3834312|gb|AAC83028.1| Strong similarity to glycoprotein EP1 gb|L16983 Daucus carota and a member of S locus glycoprotein family PF|00954. ESTs gb|AA067487, gb|Z35737, gb|Z30815, gb|Z35350, gb|AA713171, gb|AI100553, gb|Z34248, gb|AA728536, gb|Z30816 and gb|Z35351 come from this gene [Arabidopsis thaliana] gi|23297392|gb|AAN12959.1| unknown protein [Arabidopsis thaliana] gi|332198039|gb|AEE36160.1| curculin-like (mannose-binding) lectin-like protein [Arabidopsis thaliana]	458	455	0	99.3	90.4	93.2	curculin-like (mannose-binding) lectin-like protein	gbpln	Arabidopsis thaliana	AT1G78830.1 | Symbols: | Curculin-like (mannose-binding) lectin family protein | chr1:29637141-29638508 REVERSE LENGTH=455	458	455	0	99.3	90.4	93.2
Rsa1.0_01838.1.g30203.t1	gb|AAM64330.1| unknown [Arabidopsis thaliana]	191	195	2.00E-80	102.1	92.1	94.8	unknown	gbpln	Arabidopsis thaliana	AT1G78815.1 | Symbols: LSH7 | Protein of unknown function (DUF640) | chr1:29632054-29632641 REVERSE LENGTH=195	191	195	3.00E-80	102.1	92.1	94.8
Rsa1.0_01838.1.g30204.t4	gb|EOA35937.1| hypothetical protein CARUB_v10021194mg [Capsella rubella] gi|482571750|gb|EOA35938.1| hypothetical protein CARUB_v10021194mg [Capsella rubella]	104	104	1.00E-49	100.0	94.2	99.0	hypothetical protein CARUB_v10021194mg	gbpln	Capsella rubella	AT1G78790.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2008 (InterPro:IPR018552); Has 69 Blast hits to 69 proteins in 28 species: Archae - 0; Bacteria - 0; Metazoa - 33; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr1:29623930-29624785 REVERSE LENGTH=104	104	104	4.00E-52	100.0	93.3	99.0
Rsa1.0_01838.1.g30205.t1	gb|AAC83032.1| Similar to gb|X16648 pathogenesis related protein from Hordeum vulgare. EST gb|Z18206 comes from this gene [Arabidopsis thaliana]	308	276	1.00E-142	89.6	83.4	85.7	Similar to gb|X16648 pathogenesis related protein from Hordeum vulgare. EST gb|Z18206 comes from this gene	gbpln	Arabidopsis thaliana	AT1G78780.2 | Symbols: | pathogenesis-related family protein | chr1:29621447-29622431 REVERSE LENGTH=238	308	238	1.00E-130	77.3	72.4	73.7
Rsa1.0_01838.1.g30206.t1	gb|EOA33338.1| hypothetical protein CARUB_v10020104mg [Capsella rubella]	544	543	0	99.8	92.8	96.5	hypothetical protein CARUB_v10020104mg	gbpln	Capsella rubella	AT1G78770.1 | Symbols: APC6 | anaphase promoting complex 6 | chr1:29617421-29621273 FORWARD LENGTH=543	544	543	0	99.8	94.3	96.3
Rsa1.0_01838.1.g30207.t2	ref|NP_177996.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana] gi|75268062|sp|Q9ZV93.1|FDL10_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g78750 gi|3834319|gb|AAC83035.1| Similar to gi|2244754 heat shock transcription factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig gb|Z97335 [Arabidopsis thaliana] gi|332198025|gb|AEE36146.1| F-box/FBD/LRR-repeat protein [Arabidopsis thaliana]	456	458	1.00E-156	100.4	65.1	78.9	F-box/FBD/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT1G78750.1 | Symbols: | F-box/RNI-like superfamily protein | chr1:29613122-29614695 REVERSE LENGTH=458	456	458	1.00E-159	100.4	65.1	78.9
Rsa1.0_01839.1.g30208.t1	gb|EOA34854.1| hypothetical protein CARUB_v10022435mg [Capsella rubella]	173	173	6.00E-39	100.0	67.1	76.9	hypothetical protein CARUB_v10022435mg	gbpln	Capsella rubella	AT1G71430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 64 Blast hits to 64 proteins in 28 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 6; Plants - 42; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:26920564-26921058 FORWARD LENGTH=164	173	164	9.00E-35	94.8	48.6	54.3
Rsa1.0_01839.1.g30209.t1	ref|XP_002888835.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334676|gb|EFH65094.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	892	899	0	100.8	88.7	94.3	kinase family protein	gbpln	Arabidopsis lyrata	AT1G71410.1 | Symbols: | ARM repeat superfamily protein | chr1:26913070-26917515 REVERSE LENGTH=909	892	909	0	101.9	88.3	93.9
Rsa1.0_01839.1.g30210.t1	ref|XP_002887372.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata] gi|297333213|gb|EFH63631.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata]	784	832	0	106.1	66.8	78.7	hypothetical protein ARALYDRAFT_476271	gbpln	Arabidopsis lyrata	AT1G71400.1 | Symbols: AtRLP12, RLP12 | receptor like protein 12 | chr1:26909905-26912448 FORWARD LENGTH=847	784	847	0	108.0	64.4	77.3

Rsa1.0_01839.1.g30211.t1	ref|XP_002887371.1| hypothetical protein ARALYDRAFT_476270 [Arabidopsis lyrata subsp. lyrata] gi|297333212|gb|EFH63630.1| hypothetical protein ARALYDRAFT_476270 [Arabidopsis lyrata subsp. lyrata]	391	768	1.00E-67	196.4	39.4	47.1	hypothetical protein ARALYDRAFT_476270	gbpln	Arabidopsis lyrata	AT1G71390.1 | Symbols: AtRLP11, RLP11 | receptor like protein 11 | chr1:26906453-26908807 FORWARD LENGTH=784	391	784	6.00E-70	200.5	39.6	46.8
Rsa1.0_01839.1.g30212.t1	ref|XP_002887371.1| hypothetical protein ARALYDRAFT_476270 [Arabidopsis lyrata subsp. lyrata] gi|297333212|gb|EFH63630.1| hypothetical protein ARALYDRAFT_476270 [Arabidopsis lyrata subsp. lyrata]	107	768	1.00E-11	717.8	28.0	35.5	hypothetical protein ARALYDRAFT_476270	gbpln	Arabidopsis lyrata	AT1G71390.1 | Symbols: AtRLP11, RLP11 | receptor like protein 11 | chr1:26906453-26908807 FORWARD LENGTH=784	107	784	1.00E-13	732.7	28.0	38.3
Rsa1.0_01839.1.g30213.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	2006	1274	0	63.5	30.4	42.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	2006	575	8.00E-68	28.7	8.6	13.3
Rsa1.0_01839.1.g30214.t1	gb|EOA17786.1| hypothetical protein CARUB_v10006179mg [Capsella rubella]	113	68	7.00E-16	60.2	38.1	38.9	hypothetical protein CARUB_v10006179mg	gbpln	Capsella rubella	AT4G21105.1 | Symbols: | cytochrome-c oxidases;electron carriers | chr4:11266273-11266724 FORWARD LENGTH=68	113	68	3.00E-18	60.2	36.3	38.9
Rsa1.0_01839.1.g30215.t1	ref|NP_177294.1| endoglucanase 9 [Arabidopsis thaliana] gi|75169715|sp|Q9C9H5.1|GUN9_ARATH RecName: Full=Endoglucanase 9; AltName: Full=Cellulase 3; Short=AtCEL3; AltName: Full=Endo-1,4-beta glucanase 9; Flags: Precursor gi|12323721|gb|AAG51817.1|AC016163_6 putative beta-glucanase; 74324-76084 [Arabidopsis thaliana] gi|111074386|gb|ABH04566.1| At1g71380 [Arabidopsis thaliana] gi|332197074|gb|AEE35195.1| endoglucanase 9 [Arabidopsis thaliana]	283	484	1.00E-136	171.0	85.2	92.9	endoglucanase 9	gbpln	Arabidopsis thaliana	AT1G71380.1 | Symbols: ATGH9B3, ATCEL3, CEL3 | cellulase 3 | chr1:26899989-26901749 REVERSE LENGTH=484	283	484	1.00E-138	171.0	85.2	92.9
Rsa1.0_01840.1.g30216.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01840.1.g30217.t1	gb|EOA16647.1| hypothetical protein CARUB_v10004821mg [Capsella rubella] gi|482552455|gb|EOA16648.1| hypothetical protein CARUB_v10004821mg [Capsella rubella]	82	442	4.00E-28	539.0	76.8	82.9	hypothetical protein CARUB_v10004821mg	gbpln	Capsella rubella	AT4G16670.1 | Symbols: | Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region | chr4:9385326-9387570 FORWARD LENGTH=429	82	429	8.00E-30	523.2	76.8	84.1
Rsa1.0_01840.1.g30218.t1	gb|AAM67032.1| histone H2A-like protein [Arabidopsis thaliana]	70	131	5.00E-19	187.1	68.6	71.4	histone H2A-like protein	gbpln	Arabidopsis thaliana	AT4G27230.2 | Symbols: HTA2 | histone H2A 2 | chr4:13637515-13638325 REVERSE LENGTH=131	70	131	1.00E-21	187.1	68.6	71.4
Rsa1.0_01840.1.g30219.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	334	1529	7.00E-33	457.8	22.8	33.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01840.1.g30220.t1	gb|EOA38468.1| hypothetical protein CARUB_v10010189mg [Capsella rubella]	175	232	1.00E-93	132.6	93.1	97.7	hypothetical protein CARUB_v10010189mg	gbpln	Capsella rubella	AT1G30110.2 | Symbols: NUDX25 | nudix hydrolase homolog 25 | chr1:10582700-10583821 FORWARD LENGTH=175	175	175	2.00E-94	100.0	93.1	97.7
Rsa1.0_01840.1.g30221.t1	ref|XP_002865966.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata] gi|297311801|gb|EFH42225.1| hypothetical protein ARALYDRAFT_357572 [Arabidopsis lyrata subsp. lyrata]	422	455	1.00E-130	107.8	64.5	75.1	hypothetical protein ARALYDRAFT_357572	gbpln	Arabidopsis lyrata	AT1G30790.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:10932713-10933912 FORWARD LENGTH=399	422	399	1.00E-100	94.5	49.1	62.3
Rsa1.0_01840.1.g30222.t1	ref|XP_002269426.2| PREDICTED: prefoldin subunit 6-like [Vitis vinifera]	77	133	7.00E-23	172.7	72.7	77.9	PREDICTED: prefoldin subunit 6-like	gbpln	Vitis vinifera	AT1G29990.1 | Symbols: PFD6 | prefoldin 6 | chr1:10507666-10508821 FORWARD LENGTH=129	77	129	4.00E-25	167.5	72.7	77.9
Rsa1.0_01840.1.g30223.t1	gb|EOA39027.1| hypothetical protein CARUB_v10011597mg [Capsella rubella]	186	186	1.00E-10	100.0	26.3	47.8	hypothetical protein CARUB_v10011597mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01840.1.g30224.t1	gb|EOA32515.1| hypothetical protein CARUB_v10015795mg [Capsella rubella]	181	186	2.00E-12	102.8	27.6	49.2	hypothetical protein CARUB_v10015795mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01840.1.g30225.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	504	484	1.00E-102	96.0	42.1	54.4	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01841.1.g30226.t1	gb|EOA39475.1| hypothetical protein CARUB_v10008072mg [Capsella rubella]	1906	1915	0	100.5	85.9	92.2	hypothetical protein CARUB_v10008072mg	gbpln	Capsella rubella	AT1G32750.1 | Symbols: HAF01, HAF1, HAC13, GTD1, TAF1 | HAC13 protein (HAC13) | chr1:11846385-11856261 REVERSE LENGTH=1919	1906	1919	0	100.7	85.4	91.2
Rsa1.0_01841.1.g30227.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01841.1.g30228.t1	ref|XP_002891005.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336847|gb|EFH67264.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	128	151	2.00E-57	118.0	82.0	91.4	predicted protein	gbpln	Arabidopsis lyrata	AT1G32710.1 | Symbols: | Cytochrome c oxidase, subunit Vib family protein | chr1:11833113-11833706 FORWARD LENGTH=134	128	134	7.00E-53	104.7	73.4	82.0
Rsa1.0_01841.1.g30229.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01842.1.g30230.t1	ref|XP_002891286.1| DNAJ chaperone C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297337128|gb|EFH67545.1| DNAJ chaperone C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	349	356	1.00E-124	102.0	73.9	81.9	DNAJ chaperone C-terminal domain-containing protein	gbpln	Arabidopsis lyrata	AT1G44160.1 | Symbols: | HSP40/DnaJ peptide-binding protein | chr1:16795032-16796276 FORWARD LENGTH=357	349	357	1.00E-125	102.3	73.9	81.7
Rsa1.0_01842.1.g30231.t2	ref|XP_002888606.1| ALDH3H1 [Arabidopsis lyrata subsp. lyrata] gi|297334447|gb|EFH64865.1| ALDH3H1 [Arabidopsis lyrata subsp. lyrata]	483	484	0	100.2	84.1	91.7	ALDH3H1	gbpln	Arabidopsis lyrata	AT1G44170.2 | Symbols: ALDH3H1, ALDH4 | aldehyde dehydrogenase 3H1 | chr1:16796564-16800031 REVERSE LENGTH=484	483	484	0	100.2	83.2	91.9
Rsa1.0_01842.1.g30232.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01842.1.g30233.t1	gb|EOA39361.1| hypothetical protein CARUB_v10012414mg [Capsella rubella]	277	231	3.00E-16	83.4	25.6	34.7	hypothetical protein CARUB_v10012414mg	gbpln	Capsella rubella	AT1G44224.1 | Symbols: | ECA1 gametogenesis related family protein | chr1:16821061-16821756 REVERSE LENGTH=231	277	231	3.00E-16	83.4	25.3	35.7
Rsa1.0_01842.1.g30234.t1	gb|AAB87099.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1103	1496	0	135.6	41.3	50.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1103	1262	1.00E-74	114.4	13.8	19.2
Rsa1.0_01842.1.g30235.t7	gb|ABD65091.1| hypothetical protein 31.t00049 [Brassica oleracea]	361	530	2.00E-44	146.8	34.1	40.7	hypothetical protein 31.t00049	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01842.1.g30236.t4	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	786	1024	2.00E-19	130.3	10.3	14.1	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01843.1.g30237.t1	gb|EOA27571.1| hypothetical protein CARUB_v10023708mg [Capsella rubella]	318	305	4.00E-68	95.9	58.8	67.0	hypothetical protein CARUB_v10023708mg	gbpln	Capsella rubella	AT2G32235.1 | Symbols: | unknown protein; Has 38 Blast hits to 38 proteins in 14 species: Archae - 0; Bacteria - 4; Metazoa - 11; Fungi - 11; Plants - 11; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:13682823-13684199 REVERSE LENGTH=310	318	310	1.00E-70	97.5	59.7	67.9
Rsa1.0_01843.1.g30238.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1652	1223	0	74.0	32.6	44.6	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1652	746	1.00E-79	45.2	10.0	13.4
Rsa1.0_01843.1.g30239.t1	gb|EOA36301.1| hypothetical protein CARUB_v10010589mg [Capsella rubella]	161	142	3.00E-70	88.2	83.9	85.1	hypothetical protein CARUB_v10010589mg	gbpln	Capsella rubella	AT2G32060.2 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr2:13639228-13640104 REVERSE LENGTH=144	161	144	1.00E-63	89.4	70.2	75.8
Rsa1.0_01843.1.g30240.t1	ref|XP_002881210.1| DNA topoisomerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297327049|gb|EFH57469.1| DNA topoisomerase family protein [Arabidopsis lyrata subsp. lyrata]	895	865	0	96.6	92.8	95.2	DNA topoisomerase family protein	gbpln	Arabidopsis lyrata	AT2G32000.1 | Symbols: | DNA topoisomerase, type IA, core | chr2:13615999-13621563 REVERSE LENGTH=865	895	865	0	96.6	92.3	94.6
Rsa1.0_01843.1.g30241.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01843.1.g30242.t1	ref|XP_002881208.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata] gi|297327047|gb|EFH57467.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	467	458	0	98.1	76.0	82.9	exostosin family protein	gbpln	Arabidopsis lyrata	AT2G31990.1 | Symbols: | Exostosin family protein | chr2:13611500-13613551 REVERSE LENGTH=479	467	479	0	102.6	79.4	88.9
Rsa1.0_01843.1.g30243.t1	gb|ADD10746.1| phytocystatin 2-1 [Brassica rapa subsp. pekinensis]	143	142	8.00E-58	99.3	76.2	90.9	phytocystatin 2-1	gbpln	Brassica rapa	AT2G31980.1 | Symbols: AtCYS2, CYS2 | PHYTOCYSTATIN 2 | chr2:13609246-13609770 REVERSE LENGTH=147	143	147	3.00E-55	102.8	66.4	83.9
Rsa1.0_01843.1.g30244.t2	gb|EOA28896.1| hypothetical protein CARUB_v10025142mg [Capsella rubella]	95	1316	9.00E-36	1385.3	72.6	74.7	hypothetical protein CARUB_v10025142mg	gbpln	Capsella rubella	AT2G31970.1 | Symbols: RAD50, ATRAD50 | DNA repair-recombination protein (RAD50) | chr2:13600657-13608815 FORWARD LENGTH=1316	95	1316	1.00E-38	1385.3	72.6	74.7
Rsa1.0_01843.1.g30245.t1	ref|XP_002883536.1| hypothetical protein ARALYDRAFT_899046 [Arabidopsis lyrata subsp. lyrata] gi|297329376|gb|EFH59795.1| hypothetical protein ARALYDRAFT_899046 [Arabidopsis lyrata subsp. lyrata]	426	368	2.00E-93	86.4	46.9	59.2	hypothetical protein ARALYDRAFT_899046	gbpln	Arabidopsis lyrata	AT3G24580.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8969162-8970298 FORWARD LENGTH=378	426	378	1.00E-86	88.7	45.5	59.9
Rsa1.0_01843.1.g30246.t1	gb|EOA27328.1| hypothetical protein CARUB_v10023444mg, partial [Capsella rubella]	423	378	1.00E-102	89.4	50.1	60.3	hypothetical protein CARUB_v10023444mg, partial	gbpln	Capsella rubella	AT2G24645.1 | Symbols: | Transcriptional factor B3 family protein | chr2:10480728-10482650 REVERSE LENGTH=490	423	490	3.00E-76	115.8	37.8	47.8
Rsa1.0_01843.1.g30247.t1	gb|ADI58546.1| glutathione peroxidase 2 [Brassica napus]	121	169	4.00E-45	139.7	72.7	75.2	glutathione peroxidase 2	gbpln	Brassica napus	AT2G31570.1 | Symbols: ATGPX2, GPX2 | glutathione peroxidase 2 | chr2:13438211-13439775 REVERSE LENGTH=169	121	169	2.00E-45	139.7	69.4	72.7

Rsa1.0_01844.1.g30248.t1	gb|ABD64968.1| hypothetical protein 25.t00005 [Brassica oleracea]	176	299	7.00E-34	169.9	47.7	59.7	hypothetical protein 25.t00005	gbpln	Brassica oleracea	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	176	264	8.00E-30	150.0	44.9	57.4
Rsa1.0_01844.1.g30249.t1	gb|EOA22909.1| hypothetical protein CARUB_v10003642mg [Capsella rubella]	285	282	5.00E-30	98.9	35.8	51.9	hypothetical protein CARUB_v10003642mg	gbpln	Capsella rubella	AT5G27070.1 | Symbols: AGL53 | AGAMOUS-like 53 | chr5:9527741-9528604 FORWARD LENGTH=287	285	287	6.00E-28	100.7	36.1	51.6
Rsa1.0_01844.1.g30250.t1	ref|XP_002891445.1| hypothetical protein ARALYDRAFT_473996 [Arabidopsis lyrata subsp. lyrata] gi|297337287|gb|EFH67704.1| hypothetical protein ARALYDRAFT_473996 [Arabidopsis lyrata subsp. lyrata]	473	491	0	103.8	94.1	97.9	hypothetical protein ARALYDRAFT_473996	gbpln	Arabidopsis lyrata	AT1G48600.2 | Symbols: PMEAMT, AtPMEAMT | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:17966074-17969077 FORWARD LENGTH=491	473	491	0	103.8	94.3	97.9
Rsa1.0_01844.1.g30251.t1	gb|EOA40467.1| hypothetical protein CARUB_v10009192mg [Capsella rubella]	441	432	1.00E-176	98.0	73.7	82.5	hypothetical protein CARUB_v10009192mg	gbpln	Capsella rubella	AT1G48580.1 | Symbols: | unknown protein; Has 91 Blast hits to 91 proteins in 40 species: Archae - 0; Bacteria - 0; Metazoa - 49; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink). | chr1:17958403-17960610 REVERSE LENGTH=454	441	454	1.00E-171	102.9	72.1	81.0
Rsa1.0_01844.1.g30252.t1	ref|NP_188424.2| translocon at the outer membrane of chloroplasts 64-III [Arabidopsis thaliana] gi|75335547|sp|Q9LVH5.1|OE64C_ARATH RecName: Full=Outer envelope protein 64, chloroplastic; AltName: Full=Translocon at the outer membrane of chloroplasts 64-III gi|9294499|dbj|BAB02718.1| unnamed protein product [Arabidopsis thaliana] gi|332642509|gb|AEE76030.1| translocon at the outer membrane of chloroplasts 64-III [Arabidopsis thaliana]	593	589	0	99.3	78.4	86.7	translocon at the outer membrane of chloroplasts 64-III	gbpln	Arabidopsis thaliana	AT3G17970.1 | Symbols: atToc64-III, TOC64-III | translocon at the outer membrane of chloroplasts 64-III | chr3:6148030-6151794 FORWARD LENGTH=589	593	589	0	99.3	78.4	86.7
Rsa1.0_01844.1.g30253.t1	gb|EOA40416.1| hypothetical protein CARUB_v10009141mg [Capsella rubella]	415	443	0	106.7	80.2	91.3	hypothetical protein CARUB_v10009141mg	gbpln	Capsella rubella	AT1G48570.1 | Symbols: | zinc finger (Ran-binding) family protein | chr1:17955455-17957661 REVERSE LENGTH=455	415	455	0	109.6	80.7	91.1
Rsa1.0_01844.1.g30254.t1	ref|XP_002891443.1| hypothetical protein ARALYDRAFT_473993 [Arabidopsis lyrata subsp. lyrata] gi|297337285|gb|EFH67702.1| hypothetical protein ARALYDRAFT_473993 [Arabidopsis lyrata subsp. lyrata]	636	643	1.00E-180	101.1	60.1	68.9	hypothetical protein ARALYDRAFT_473993	gbpln	Arabidopsis lyrata	AT1G48560.1 | Symbols: | unknown protein; Has 75 Blast hits to 71 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:17952935-17955108 FORWARD LENGTH=643	636	643	1.00E-175	101.1	58.0	68.9
Rsa1.0_01844.1.g30255.t2	ref|NP_196165.3| mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase [Arabidopsis thaliana] gi|332003493|gb|AED90876.1| beta-endo-N-acetyglucosaminidase [Arabidopsis thaliana]	257	680	8.00E-34	264.6	27.6	30.7	mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase	gbpln	Arabidopsis thaliana	AT5G05460.1 | Symbols: | Glycosyl hydrolase family 85 | chr5:1615615-1618771 FORWARD LENGTH=680	257	680	2.00E-36	264.6	27.6	30.7
Rsa1.0_01844.1.g30256.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01844.1.g30257.t1	dbj|BAF00887.1| hypothetical protein [Arabidopsis thaliana]	244	643	3.00E-56	263.5	48.4	54.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT1G48560.1 | Symbols: | unknown protein; Has 75 Blast hits to 71 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:17952935-17955108 FORWARD LENGTH=643	244	643	3.00E-58	263.5	48.0	54.5
Rsa1.0_01844.1.g30258.t1	gb|EOA37329.1| hypothetical protein CARUB_v10011025mg [Capsella rubella]	460	641	1.00E-119	139.3	63.5	75.4	hypothetical protein CARUB_v10011025mg	gbpln	Capsella rubella	AT1G48560.1 | Symbols: | unknown protein; Has 75 Blast hits to 71 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 69; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr1:17952935-17955108 FORWARD LENGTH=643	460	643	1.00E-114	139.8	60.7	72.6
Rsa1.0_01845.1.g30259.t1	sp|C0LGQ9.1|Y4294_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g20940 gi|224589622|gb|ACN59344.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	1083	1037	0	95.8	86.7	91.2	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g20940 gi|224589622|gb|ACN59344.1| leucine-rich repeat receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT4G20940.1 | Symbols: | Leucine-rich receptor-like protein kinase family protein | chr4:11202728-11206038 FORWARD LENGTH=977	1083	977	0	90.2	67.0	71.1
Rsa1.0_01845.1.g30260.t1	gb|EOA16935.1| hypothetical protein CARUB_v10005158mg [Capsella rubella]	346	350	1.00E-180	101.2	89.6	93.9	hypothetical protein CARUB_v10005158mg	gbpln	Capsella rubella	AT4G20930.1 | Symbols: | 6-phosphogluconate dehydrogenase family protein | chr4:11198627-11201036 REVERSE LENGTH=347	346	347	1.00E-176	100.3	88.7	93.4

Rsa1.0_01845.1.g30261.t2	ref|XP_002867829.1| hypothetical protein ARALYDRAFT_492703 [Arabidopsis lyrata subsp. lyrata] gi|297313665|gb|EFH44088.1| hypothetical protein ARALYDRAFT_492703 [Arabidopsis lyrata subsp. lyrata]	1167	1188	0	101.8	72.0	75.7	hypothetical protein ARALYDRAFT_492703	gbpln	Arabidopsis lyrata	AT4G21710.1 | Symbols: NRPB2, EMB1989, RPB2 | DNA-directed RNA polymerase family protein | chr4:11535684-11542200 REVERSE LENGTH=1188	1167	1188	0	101.8	71.9	75.7
Rsa1.0_01845.1.g30262.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01845.1.g30263.t3	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1707	1274	0	74.6	31.7	43.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1707	575	6.00E-57	33.7	9.3	14.9
Rsa1.0_01845.1.g30264.t1	gb|EOA18374.1| hypothetical protein CARUB_v10006895mg [Capsella rubella]	747	762	0	102.0	91.0	95.2	hypothetical protein CARUB_v10006895mg	gbpln	Capsella rubella	AT4G21750.2 | Symbols: ATML1 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr4:11556965-11560243 FORWARD LENGTH=762	747	762	0	102.0	90.4	94.9
Rsa1.0_01845.1.g30265.t1	ref|NP_193912.3| derlin-2.1 [Arabidopsis thaliana] gi|297799884|ref|XP_002867826.1| hypothetical protein ARALYDRAFT_492693 [Arabidopsis lyrata subsp. lyrata] gi|332278209|sp|Q8VZ96.3|DER21_ARATH RecName: Full=Derlin-2.1; AltName: Full=AtDerlin2-1 gi|17473759|gb|AAL38318.1| putative protein [Arabidopsis thaliana] gi|24899743|gb|AAN65086.1| putative protein [Arabidopsis thaliana] gi|297313662|gb|EFH44085.1| hypothetical protein ARALYDRAFT_492693 [Arabidopsis lyrata subsp. lyrata] gi|332659106|gb|AEE84506.1| derlin-2.1 [Arabidopsis thaliana]	244	244	1.00E-134	100.0	95.9	97.1	derlin-2.1	gbpln	Arabidopsis lyrata	AT4G21810.1 | Symbols: DER2.1 | DERLIN-2.1 | chr4:11575345-11577003 REVERSE LENGTH=244	244	244	1.00E-137	100.0	95.9	97.1
Rsa1.0_01846.1.g30266.t1	ref|NP_201113.2| transcription factor jumonji (jmjC) domain-containing protein [Arabidopsis thaliana] gi|51970546|dbj|BAD43965.1| unnamed protein product [Arabidopsis thaliana] gi|66792698|gb|AAY56451.1| At5g63080 [Arabidopsis thaliana] gi|332010314|gb|AED97697.1| transcription factor jumonji (jmjC) domain-containing protein [Arabidopsis thaliana]	440	462	0	105.0	80.2	88.4	transcription factor jumonji (jmjC) domain-containing protein	gbpln	Arabidopsis thaliana	AT5G63080.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:25300026-25302321 REVERSE LENGTH=462	440	462	0	105.0	80.2	88.4
Rsa1.0_01846.1.g30267.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01846.1.g30268.t1	ref|NP_201114.1| protein LATERAL ORGAN BOUNDARIES [Arabidopsis thaliana] gi|30697777|ref|NP_851252.1| protein LATERAL ORGAN BOUNDARIES [Arabidopsis thaliana] gi|30697779|ref|NP_851253.1| protein LATERAL ORGAN BOUNDARIES [Arabidopsis thaliana] gi|30697782|ref|NP_851254.1| protein LATERAL ORGAN BOUNDARIES [Arabidopsis thaliana] gi|27805499|sp|Q9FML4.1|LOB_ARATH RecName: Full=Protein LATERAL ORGAN BOUNDARIES; AltName: Full=ASYMMETRIC LEAVES 2-like protein 4; Short=AS2-like protein 4 gi|17484100|gb|AAL40346.1|AF447897_1 LOBa [Arabidopsis thaliana] gi|10177290|dbj|BAB10551.1| unnamed protein product [Arabidopsis thaliana] gi|45330811|dbj|BAD12424.1| ASYMMETRIC LEAVES2-like gene 4 protein [Arabidopsis thaliana] gi|107738100|gb|ABF83635.1| At5g63090 [Arabidopsis thaliana] gi|219807084|dbj|BAH10548.1| ASYMMETRIC LEAVES2-like 4 protein [Arabidopsis thaliana] gi|332010317|gb|AED97700.1| protein LATERAL ORGAN BOUNDARIES [Arabidopsis thaliana] gi|332010318|gb|AED97701.1| protein LATERAL ORGAN BOUNDARIES [Arabidopsis thaliana]	179	186	3.00E-90	103.9	92.2	93.9	protein LATERAL ORGAN BOUNDARIES	gbpln	Arabidopsis thaliana	AT5G63090.4 | Symbols: LOB | Lateral organ boundaries (LOB) domain family protein | chr5:25308723-25309283 REVERSE LENGTH=186	179	186	1.00E-92	103.9	92.2	93.9

Rsa1.0_01846.1.g30269.t1	ref|NP_201115.1| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|10177291|dbj|BAB10552.1| unnamed protein product [Arabidopsis thaliana] gi|332010321|gb|AED97704.1| S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana]	313	329	1.00E-133	105.1	81.2	90.1	S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G63100.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:25314434-25315423 REVERSE LENGTH=329	313	329	1.00E-136	105.1	81.2	90.1
Rsa1.0_01846.1.g30270.t2	ref|XP_002866535.1| hypothetical protein ARALYDRAFT_496493 [Arabidopsis lyrata subsp. lyrata] gi|297312370|gb|EFH42794.1| hypothetical protein ARALYDRAFT_496493 [Arabidopsis lyrata subsp. lyrata]	497	471	0	94.8	88.5	92.0	hypothetical protein ARALYDRAFT_496493	gbpln	Arabidopsis lyrata	AT5G63110.1 | Symbols: HDA6, AXE1, ATHDA6, RTS1, RPD3B, SIL1 | histone deacetylase 6 | chr5:25315834-25318227 REVERSE LENGTH=471	497	471	0	94.8	87.5	91.3
Rsa1.0_01846.1.g30271.t1	ref|NP_974985.1| DEAD-box ATP-dependent RNA helicase 30 [Arabidopsis thaliana] gi|108861888|sp|Q8W4R3.2|RH30_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 30 gi|110741550|dbj|BAE98724.1| ATP-dependent RNA helicase-like protein [Arabidopsis thaliana] gi|332010323|gb|AED97706.1| DEAD-box ATP-dependent RNA helicase 30 [Arabidopsis thaliana]	593	591	0	99.7	88.7	91.2	DEAD-box ATP-dependent RNA helicase 30	gbpln	Arabidopsis thaliana	AT5G63120.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:25318967-25322071 REVERSE LENGTH=591	593	591	0	99.7	88.7	91.2
Rsa1.0_01846.1.g30272.t1	gb|EOA14047.1| hypothetical protein CARUB_v10027182mg [Capsella rubella]	181	193	1.00E-60	106.6	79.0	84.5	hypothetical protein CARUB_v10027182mg	gbpln	Capsella rubella	AT5G63130.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr5:25323190-25323857 FORWARD LENGTH=192	181	192	4.00E-56	106.1	77.9	83.4
Rsa1.0_01846.1.g30273.t1	gb|EOA14274.1| hypothetical protein CARUB_v10027435mg [Capsella rubella]	109	99	1.00E-33	90.8	76.1	84.4	hypothetical protein CARUB_v10027435mg	gbpln	Capsella rubella	AT5G63135.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:25325253-25326440 REVERSE LENGTH=99	109	99	4.00E-35	90.8	74.3	85.3
Rsa1.0_01846.1.g30274.t1	ref|XP_002864839.1| ATPAP29/PAP29 [Arabidopsis lyrata subsp. lyrata] gi|297310674|gb|EFH41098.1| ATPAP29/PAP29 [Arabidopsis lyrata subsp. lyrata]	374	384	1.00E-172	102.7	79.1	86.4	ATPAP29/PAP29	gbpln	Arabidopsis lyrata	AT5G63140.1 | Symbols: ATPAP29, PAP29 | purple acid phosphatase 29 | chr5:25328237-25329616 FORWARD LENGTH=389	374	389	1.00E-172	104.0	77.5	87.2
Rsa1.0_01846.1.g30275.t2	ref|XP_002866540.1| pectate lyase [Arabidopsis lyrata subsp. lyrata] gi|297312375|gb|EFH42799.1| pectate lyase [Arabidopsis lyrata subsp. lyrata]	409	410	0	100.2	91.2	95.6	pectate lyase	gbpln	Arabidopsis lyrata	AT5G63180.1 | Symbols: | Pectin lyase-like superfamily protein | chr5:25341106-25343113 REVERSE LENGTH=432	409	432	0	105.6	90.5	94.9
Rsa1.0_01847.1.g30276.t1	ref|NP_194335.2| plant intracellular ras group-related LRR 8 [Arabidopsis thaliana] gi|20260486|gb|AAM13141.1| putative leucine-rich-repeat protein [Arabidopsis thaliana] gi|30725612|gb|AAP37828.1| At4g26050 [Arabidopsis thaliana] gi|332659749|gb|AEE85149.1| plant intracellular ras group-related LRR 8 [Arabidopsis thaliana]	394	383	0	97.2	86.5	90.4	plant intracellular ras group-related LRR 8	gbpln	Arabidopsis thaliana	AT4G26050.1 | Symbols: PIRL8 | plant intracellular ras group-related LRR 8 | chr4:13210522-13213149 FORWARD LENGTH=383	394	383	0	97.2	86.5	90.4
Rsa1.0_01847.1.g30277.t1	gb|EOA17774.1| hypothetical protein CARUB_v10006164mg, partial [Capsella rubella]	63	76	4.00E-18	120.6	79.4	84.1	hypothetical protein CARUB_v10006164mg, partial	gbpln	Capsella rubella	AT4G26055.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G57080.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13214098-13214429 REVERSE LENGTH=62	63	62	8.00E-21	98.4	73.0	84.1

Rsa1.0_01847.1.g30278.t1	ref|NP_194336.1| ribosomal protein L18ae family protein [Arabidopsis thaliana] gi|4538935|emb|CAB39671.1| putative protein [Arabidopsis thaliana] gi|7269457|emb|CAB79461.1| putative protein [Arabidopsis thaliana] gi|106879161|gb|ABF82610.1| At4g26060 [Arabidopsis thaliana] gi|332659751|gb|AEE85151.1| ribosomal protein L18ae family protein [Arabidopsis thaliana]	126	133	3.00E-45	105.6	77.8	84.1	ribosomal protein L18ae family protein	gbpln	Arabidopsis thaliana	AT4G26060.1 | Symbols: | Ribosomal protein L18ae family | chr4:13214972-13215955 REVERSE LENGTH=133	126	133	5.00E-48	105.6	77.8	84.1
Rsa1.0_01847.1.g30279.t1	gb|ADX66729.1| mitogen-activated protein kinase kinase 2 [Brassica napus]	360	355	0	98.6	91.1	95.3	mitogen-activated protein kinase kinase 2	gbpln	Brassica napus	AT4G26070.3 | Symbols: MEK1, NMAPKK, ATMEK1, MKK1 | MAP kinase/ ERK kinase 1 | chr4:13217797-13219695 FORWARD LENGTH=354	360	354	0	98.3	88.1	92.2
Rsa1.0_01847.1.g30280.t1	dbj|BAJ34574.1| unnamed protein product [Thellungiella halophila]	401	439	0	109.5	91.3	95.5	unnamed protein product	----	----	AT4G26080.1 | Symbols: ABI1, AtABI1 | Protein phosphatase 2C family protein | chr4:13220231-13221828 REVERSE LENGTH=434	401	434	0	108.2	87.0	92.5
Rsa1.0_01847.1.g30281.t3	ref|NP_849553.1| beta-galactosidase 12 [Arabidopsis thaliana] gi|75265630|sp|Q9SCV0.1|BGL12_ARATH RecName: Full=Beta-galactosidase 12; Short=Lactase 12; Flags: Precursor gi|6686896|emb|CAB64748.1| putative beta-galactosidase [Arabidopsis thaliana] gi|332659762|gb|AEE85162.1| beta-galactosidase 12 [Arabidopsis thaliana]	727	728	0	100.1	88.2	93.3	beta-galactosidase 12	gbpln	Arabidopsis thaliana	AT4G26140.1 | Symbols: BGAL12 | beta-galactosidase 12 | chr4:13243219-13247823 REVERSE LENGTH=728	727	728	0	100.1	88.2	93.3
Rsa1.0_01848.1.g30282.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01848.1.g30283.t3	ref|XP_002874485.1| hypothetical protein ARALYDRAFT_351886 [Arabidopsis lyrata subsp. lyrata] gi|297320322|gb|EFH50744.1| hypothetical protein ARALYDRAFT_351886 [Arabidopsis lyrata subsp. lyrata]	335	234	1.00E-109	69.9	58.2	61.5	hypothetical protein ARALYDRAFT_351886	gbpln	Arabidopsis lyrata	AT4G07990.1 | Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:4825650-4828937 REVERSE LENGTH=230	335	230	2.00E-97	68.7	52.8	56.7
Rsa1.0_01848.1.g30284.t1	#	#	#	#	#	#	#	-	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	106	575	1.00E-12	542.5	24.5	35.8
Rsa1.0_01848.1.g30285.t1	gb|EOA40426.1| hypothetical protein CARUB_v10009151mg [Capsella rubella] gi|482576240|gb|EOA40427.1| hypothetical protein CARUB_v10009151mg [Capsella rubella]	127	442	2.00E-15	348.0	36.2	41.7	hypothetical protein CARUB_v10009151mg	gbpln	Capsella rubella	AT1G21200.1 | Symbols: | sequence-specific DNA binding transcription factors | chr1:7421483-7422814 FORWARD LENGTH=443	127	443	3.00E-17	348.8	35.4	40.9
Rsa1.0_01848.1.g30286.t1	ref|NP_192536.1| putative xyloglucan glycosyltransferase 12 [Arabidopsis thaliana] gi|75216205|sp|Q9ZQB9.1|CSLCC_ARATH RecName: Full=Probable xyloglucan glycosyltransferase 12; AltName: Full=Cellulose synthase-like protein C12; Short=AtCslC12 gi|4309698|gb|AAD15482.1| putative glucosyltransferase [Arabidopsis thaliana] gi|7267435|emb|CAB77947.1| putative glucosyltransferase [Arabidopsis thaliana] gi|21592678|gb|AAM64627.1| putative glucosyltransferase [Arabidopsis thaliana] gi|26451988|dbj|BAC43084.1| putative glucosyltransferase [Arabidopsis thaliana] gi|31711706|gb|AAP68209.1| At4g07960 [Arabidopsis thaliana] gi|332657186|gb|AEE82586.1| putative xyloglucan glycosyltransferase 12 [Arabidopsis thaliana]	693	699	0	100.9	91.2	92.9	putative xyloglucan glycosyltransferase 12	gbpln	Arabidopsis thaliana	AT4G07960.1 | Symbols: ATCSLC12, CSLC12 | Cellulose-synthase-like C12 | chr4:4802628-4805114 REVERSE LENGTH=699	693	699	0	100.9	91.2	92.9
Rsa1.0_01848.1.g30287.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01848.1.g30288.t2	ref|XP_002874481.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297320318|gb|EFH50740.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	799	812	0	101.6	82.4	86.9	transducin family protein	gbpln	Arabidopsis lyrata	AT4G07410.1 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr4:4201465-4205136 REVERSE LENGTH=815	799	815	0	102.0	81.7	86.7
Rsa1.0_01849.1.g30289.t11	gb|AAG52026.1|AC022456_7 polyprotein, putative; 77260-80472 [Arabidopsis thaliana]	804	884	1.00E-151	110.0	33.2	40.5	polyprotein, putative; 77260-80472	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	804	158	3.00E-19	19.7	6.2	9.1

Rsa1.0_01849.1.g30290.t5	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	326	940	1.00E-57	288.3	34.0	41.1	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01849.1.g30291.t3	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01849.1.g30292.t1	emb|CAZ40333.1| hypothetical protein [Raphanus sativus]	74	785	9.00E-11	1060.8	44.6	64.9	hypothetical protein	gbpln	Raphanus sativus	#	#	#	#	#	#	#
Rsa1.0_01849.1.g30293.t3	gb|AAC28221.1| similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]	1447	1164	0	80.4	26.9	39.0	similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13)	gbpln	Arabidopsis thaliana	AT1G48260.1 | Symbols: CIPK17, SnRK3.21 | CBL-interacting protein kinase 17 | chr1:17814226-17817226 REVERSE LENGTH=432	1447	432	1.00E-116	29.9	14.4	16.2
Rsa1.0_01850.1.g30294.t1	gb|EOA33270.1| hypothetical protein CARUB_v10022427mg [Capsella rubella]	888	955	0	107.5	96.1	98.4	hypothetical protein CARUB_v10022427mg	gbpln	Capsella rubella	AT1G80660.1 | Symbols: AHA9, HA9 | H(+)-ATPase 9 | chr1:30316227-30319948 REVERSE LENGTH=954	888	954	0	107.4	95.0	97.7
Rsa1.0_01850.1.g30295.t1	ref|XP_002887816.1| transducin family protein [Arabidopsis lyrata subsp. lyrata] gi|297333657|gb|EFH64075.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	362	349	0	96.4	85.1	90.9	transducin family protein	gbpln	Arabidopsis lyrata	AT1G80670.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:30320809-30323543 REVERSE LENGTH=349	362	349	0	96.4	84.5	90.9
Rsa1.0_01850.1.g30296.t1	dbj|BAJ34529.1| unnamed protein product [Thellungiella halophila]	1019	1042	0	102.3	87.8	93.3	unnamed protein product	----	----	AT1G80680.1 | Symbols: SAR3, MOS3, PRE, NUP96 | SUPPRESSOR OF AUXIN RESISTANCE 3 | chr1:30324219-30328489 FORWARD LENGTH=1046	1019	1046	0	102.6	85.9	92.1
Rsa1.0_01850.1.g30297.t1	gb|EOA35675.1| hypothetical protein CARUB_v10020909mg [Capsella rubella]	228	224	1.00E-106	98.2	87.3	91.7	hypothetical protein CARUB_v10020909mg	gbpln	Capsella rubella	AT1G80690.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr1:30329283-30330524 REVERSE LENGTH=227	228	227	1.00E-102	99.6	84.6	89.0
Rsa1.0_01850.1.g30298.t2	ref|XP_002889278.1| hypothetical protein ARALYDRAFT_477177 [Arabidopsis lyrata subsp. lyrata] gi|297335119|gb|EFH65537.1| hypothetical protein ARALYDRAFT_477177 [Arabidopsis lyrata subsp. lyrata]	349	217	5.00E-79	62.2	49.0	52.1	hypothetical protein ARALYDRAFT_477177	gbpln	Arabidopsis lyrata	AT1G80980.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80700.1); Has 477 Blast hits to 341 proteins in 85 species: Archae - 2; Bacteria - 44; Metazoa - 78; Fungi - 37; Plants - 42; Viruses - 0; Other Eukaryotes - 274 (source: NCBI BLink). | chr1:30422184-30423440 REVERSE LENGTH=214	349	214	3.00E-80	61.3	47.6	51.6
Rsa1.0_01850.1.g30299.t1	gb|ABD64930.1| hypothetical protein 24.t00076 [Brassica oleracea]	282	407	4.00E-13	144.3	15.6	19.5	hypothetical protein 24.t00076	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01850.1.g30300.t1	ref|NP_178188.1| zinc finger protein 1 [Arabidopsis thaliana] gi|27923894|sp|Q42485.1|ZFP1_ARATH RecName: Full=Zinc finger protein 1 gi|6503285|gb|AAF14661.1|AC011713_9 Identical to gi|S55881 zinc finger protein 1 from Arabidopsis thaliana [Arabidopsis thaliana] gi|790673|gb|AAA87297.1| zinc finger protein [Arabidopsis thaliana] gi|1297186|gb|AAA98913.1| zinc finger protein 1 [Arabidopsis thaliana] gi|111074280|gb|ABH04513.1| At1g80730 [Arabidopsis thaliana] gi|332198320|gb|AEE36441.1| zinc finger protein 1 [Arabidopsis thaliana]	216	228	2.00E-78	105.6	78.7	84.7	zinc finger protein 1	gbpln	Arabidopsis thaliana	AT1G80730.1 | Symbols: ZFP1, ATZFP1 | zinc-finger protein 1 | chr1:30339493-30340179 REVERSE LENGTH=228	216	228	8.00E-81	105.6	78.7	84.7
Rsa1.0_01850.1.g30301.t1	gb|EOA35639.1| hypothetical protein CARUB_v10020853mg [Capsella rubella]	264	249	1.00E-123	94.3	85.2	90.5	hypothetical protein CARUB_v10020853mg	gbpln	Capsella rubella	AT1G80750.1 | Symbols: | Ribosomal protein L30/L7 family protein | chr1:30349052-30350434 FORWARD LENGTH=247	264	247	1.00E-121	93.6	82.2	88.3
Rsa1.0_01850.1.g30302.t1	ref|XP_002889273.1| PDE318 [Arabidopsis lyrata subsp. lyrata] gi|297335114|gb|EFH65532.1| PDE318 [Arabidopsis lyrata subsp. lyrata]	442	449	0	101.6	87.8	92.8	PDE318	gbpln	Arabidopsis lyrata	AT1G80770.1 | Symbols: PDE318 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:30355266-30357786 FORWARD LENGTH=451	442	451	0	102.0	86.4	93.0
Rsa1.0_01850.1.g30303.t1	ref|NP_178194.1| XH/XS domain-containing protein [Arabidopsis thaliana] gi|6503291|gb|AAF14667.1|AC011713_15 Contains similarity to gb|AF136530 transcriptional regulator from Zea mays [Arabidopsis thaliana] gi|332198330|gb|AEE36451.1| XH/XS domain-containing protein [Arabidopsis thaliana]	407	634	1.00E-150	155.8	63.4	78.9	XH/XS domain-containing protein	gbpln	Arabidopsis thaliana	AT1G80790.1 | Symbols: | XH/XS domain-containing protein | chr1:30360280-30362856 FORWARD LENGTH=634	407	634	1.00E-152	155.8	63.4	78.9
Rsa1.0_01851.1.g30304.t1	gb|ABW81051.1| tn7 reverse transcriptase [Arabidopsis lyrata subsp. lyrata]	156	441	1.00E-26	282.7	34.6	50.6	tn7 reverse transcriptase	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	156	746	2.00E-12	478.2	21.8	31.4

<table>
<tr><td>Rsa1.0_01851.1.g30305.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01851.1.g30306.t1</td><td>gb|EOA30279.1| hypothetical protein CARUB_v10013406mg [Capsella rubella]</td><td>535</td><td>539</td><td>0</td><td>100.7</td><td>87.3</td><td>92.5</td><td>hypothetical protein CARUB_v10013406mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G05160.1 | Symbols: | CCCH-type zinc fingerfamily protein with RNA-binding domain | chr2:1859011-1860931 REVERSE LENGTH=536</td><td>535</td><td>536</td><td>0</td><td>100.2</td><td>83.6</td><td>91.0</td></tr>
<tr><td>Rsa1.0_01851.1.g30307.t1</td><td>ref|XP_003549103.1| PREDICTED: uncharacterized protein LOC100777881 [Glycine max]</td><td>198</td><td>1799</td><td>6.00E-49</td><td>908.6</td><td>54.0</td><td>66.7</td><td>PREDICTED: uncharacterized protein LOC100777881</td><td>gbenv/gbpln</td><td>Glycine max</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01851.1.g30308.t1</td><td>ref|XP_004309387.1| PREDICTED: uncharacterized protein LOC101295002 [Fragaria vesca subsp. vesca]</td><td>550</td><td>437</td><td>1.00E-116</td><td>79.5</td><td>41.8</td><td>49.6</td><td>PREDICTED: uncharacterized protein LOC101295002</td><td>gbpln</td><td>Fragaria vesca</td><td>AT4G08267.1 | Symbols: | hAT transposon superfamily protein | chr4:5216854-5217697 FORWARD LENGTH=126</td><td>550</td><td>126</td><td>2.00E-40</td><td>22.9</td><td>13.6</td><td>15.5</td></tr>
<tr><td>Rsa1.0_01851.1.g30309.t4</td><td>gb|AAD29773.1|AF074021_5 putative transposon protein [Arabidopsis thaliana] gi|7267217|emb|CAB80824.1| putative transposon protein [Arabidopsis thaliana]</td><td>173</td><td>346</td><td>1.00E-14</td><td>200.0</td><td>23.7</td><td>27.2</td><td>putative transposon protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01852.1.g30310.t1</td><td>dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]</td><td>222</td><td>341</td><td>2.00E-22</td><td>153.6</td><td>30.6</td><td>46.8</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01852.1.g30311.t2</td><td>dbj|BAA85462.1| transposon-like ORF [Brassica rapa]</td><td>501</td><td>703</td><td>9.00E-72</td><td>140.3</td><td>28.9</td><td>30.5</td><td>transposon-like ORF</td><td>gbpln</td><td>Brassica rapa</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01852.1.g30312.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01852.1.g30313.t3</td><td>gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]</td><td>545</td><td>578</td><td>1.00E-123</td><td>106.1</td><td>45.5</td><td>61.1</td><td>hypothetical protein 27.t00126</td><td>gbpln</td><td>Brassica oleracea</td><td>AT2G15420.1 | Symbols: | myosin heavy chain-related | chr2:6723948-6728183 REVERSE LENGTH=957</td><td>545</td><td>957</td><td>4.00E-16</td><td>175.6</td><td>8.6</td><td>13.2</td></tr>
<tr><td>Rsa1.0_01852.1.g30314.t1</td><td>gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]</td><td>600</td><td>672</td><td>6.00E-39</td><td>112.0</td><td>18.3</td><td>31.8</td><td>gag-pol polymerase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01852.1.g30315.t1</td><td>emb|CAN69925.1| hypothetical protein VITISV_027208 [Vitis vinifera]</td><td>360</td><td>982</td><td>3.00E-78</td><td>272.8</td><td>45.8</td><td>63.1</td><td>hypothetical protein VITISV_027208</td><td>gbpln</td><td>Vitis vinifera</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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<tr><td>Rsa1.0_01852.1.g30317.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01853.1.g30318.t1</td><td>ref|NP_173320.2| putative WRKY transcription factor 61 [Arabidopsis thaliana] gi|20978774|sp|Q8VWV6.1|WRK61_ARATH RecName: Full=Probable WRKY transcription factor 61; AltName: Full=WRKY DNA-binding protein 61 gi|17980960|gb|AAL50785.1|AF452175_1 WRKY transcription factor 61 [Arabidopsis thaliana] gi|332191651|gb|AEE29772.1| putative WRKY transcription factor 61 [Arabidopsis thaliana]</td><td>521</td><td>480</td><td>0</td><td>92.1</td><td>71.4</td><td>80.4</td><td>putative WRKY transcription factor 61</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G18860.1 | Symbols: WRKY61, ATWRKY61 | WRKY DNA-binding protein 61 | chr1:6509494-6511209 FORWARD LENGTH=480</td><td>521</td><td>480</td><td>0</td><td>92.1</td><td>71.4</td><td>80.4</td></tr>
<tr><td>Rsa1.0_01853.1.g30319.t1</td><td>ref|NP_173322.1| putative peptide/nitrate transporter [Arabidopsis thaliana] gi|75191595|sp|Q9M9V7.1|PTR8_ARATH RecName: Full=Probable peptide/nitrate transporter At1g18880 gi|6730698|gb|AAF27093.1|AC011809_2 Similar to peptide transport proteins [Arabidopsis thaliana] gi|17979087|gb|AAL49811.1| putative peptide transporter protein [Arabidopsis thaliana] gi|21436191|gb|AAM51383.1| putative peptide transporter protein [Arabidopsis thaliana] gi|332191655|gb|AEE29776.1| probable peptide/nitrate transporter [Arabidopsis thaliana]</td><td>556</td><td>587</td><td>4.00E-29</td><td>105.6</td><td>15.6</td><td>17.8</td><td>putative peptide/nitrate transporter</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G18880.1 | Symbols: | Major facilitator superfamily protein | chr1:6520800-6523241 FORWARD LENGTH=587</td><td>556</td><td>587</td><td>8.00E-32</td><td>105.6</td><td>15.6</td><td>17.8</td></tr>
<tr><td>Rsa1.0_01853.1.g30320.t1</td><td>dbj|BAJ34189.1| unnamed protein product [Thellungiella halophila]</td><td>547</td><td>545</td><td>0</td><td>99.6</td><td>92.5</td><td>96.9</td><td>unnamed protein product</td><td>––––</td><td>––––</td><td>AT1G18890.1 | Symbols: ATCDPK1, CPK10, CDPK1, AtCPK10 | calcium-dependent protein kinase 1 | chr1:6523468-6525736 REVERSE LENGTH=545</td><td>547</td><td>545</td><td>0</td><td>99.6</td><td>91.0</td><td>96.2</td></tr>
<tr><td>Rsa1.0_01853.1.g30321.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>–</td><td>––––</td><td>––––</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01853.1.g30322.t1</td><td>ref|XP_002890307.1| aminoacyl-tRNA synthetase family [Arabidopsis lyrata subsp. lyrata] gi|297336149|gb|EFH66566.1| aminoacyl-tRNA synthetase family [Arabidopsis lyrata subsp. lyrata]</td><td>727</td><td>761</td><td>0</td><td>104.7</td><td>80.5</td><td>87.8</td><td>aminoacyl-tRNA synthetase family</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G18950.1 | Symbols: | DDT domain superfamily | chr1:6546539-6551549 FORWARD LENGTH=750</td><td>727</td><td>750</td><td>0</td><td>103.2</td><td>79.1</td><td>86.1</td></tr>
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Rsa1.0_01853.1.g30323.t1	ref|XP_002893025.1| hypothetical protein ARALYDRAFT_472121 [Arabidopsis lyrata subsp. lyrata] gi|297338867|gb|EFH69284.1| hypothetical protein ARALYDRAFT_472121 [Arabidopsis lyrata subsp. lyrata]	214	220	1.00E-104	102.8	91.1	93.5	hypothetical protein ARALYDRAFT_472121	gbpln	Arabidopsis lyrata	AT1G18980.1 | Symbols: | RmlC-like cupins superfamily protein | chr1:6557364-6558026 REVERSE LENGTH=220	214	220	1.00E-105	102.8	89.3	93.0
Rsa1.0_01853.1.g30324.t1	ref|NP_173333.1| uncharacterized protein [Arabidopsis thaliana] gi|8778293|gb|AAF79302.1|AC068602_25 F14D16.14 [Arabidopsis thaliana] gi|27754600|gb|AAO22746.1| unknown protein [Arabidopsis thaliana] gi|332191666|gb|AEE29787.1| uncharacterized protein AT1G18990 [Arabidopsis thaliana]	522	524	0	100.4	81.4	88.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G18990.1 | Symbols: | Protein of unknown function, DUF593 | chr1:6558778-6560432 REVERSE LENGTH=524	522	524	0	100.4	81.4	88.3
Rsa1.0_01853.1.g30325.t1	dbj|BAJ34162.1| unnamed protein product [Thellungiella halophila]	144	294	2.00E-46	204.2	68.1	72.2	unnamed protein product	----	----	AT1G19000.2 | Symbols: | Homeodomain-like superfamily protein | chr1:6561335-6562684 REVERSE LENGTH=285	144	285	1.00E-45	197.9	65.3	69.4
Rsa1.0_01853.1.g30326.t1	ref|NP_564069.1| uncharacterized protein [Arabidopsis thaliana] gi|17529338|gb|AAL38896.1| unknown protein [Arabidopsis thaliana] gi|21436385|gb|AAM51362.1| unknown protein [Arabidopsis thaliana] gi|21592659|gb|AAM64608.1| unknown [Arabidopsis thaliana] gi|51968576|dbj|BAD42980.1| unknown protein [Arabidopsis thaliana] gi|51969192|dbj|BAD43288.1| unknown protein [Arabidopsis thaliana] gi|51970278|dbj|BAD43831.1| unknown protein [Arabidopsis thaliana] gi|51972011|dbj|BAD44670.1| unknown protein [Arabidopsis thaliana] gi|332191671|gb|AEE29792.1| uncharacterized protein AT1G19020 [Arabidopsis thaliana]	82	86	1.00E-23	104.9	80.5	82.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G19020.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48180.1); Has 88 Blast hits to 88 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 88; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:6568142-6568402 FORWARD LENGTH=86	82	86	2.00E-26	104.9	80.5	82.9
Rsa1.0_01853.1.g30327.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01853.1.g30328.t1	emb|CAN65188.1| hypothetical protein VITISV_004365 [Vitis vinifera]	991	1265	0	127.6	54.2	67.7	hypothetical protein VITISV_004365	gbpln	Vitis vinifera	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	991	1262	6.00E-91	127.3	17.6	28.3
Rsa1.0_01853.1.g30329.t1	ref|NP_564075.1| protein TIFY 10A [Arabidopsis thaliana] gi|75174736|sp|Q9LMA8.1|TI10A_ARATH RecName: Full=Protein TIFY 10A; AltName: Full=Jasmonate ZIM domain-containing protein 1 gi|8954056|gb|AAF82229.1|AC069143_5 Contains similarity to an unknown protein T10D10.8 gi|6730756 from Arabidopsis thaliana BAC T10D10 gb|AC016529. ESTs gb|T14209, gb|BE038503, gb|AA650871, gb|AA597384, gb|H76606, gb|AI996806, gb|AI100291 come from this gene [Arabidopsis thaliana] gi|12083250|gb|AAG48784.1|AF332421_1 unknown protein [Arabidopsis thaliana] gi|14532540|gb|AAK63998.1| At1g19180/T29M8_5 [Arabidopsis thaliana] gi|17473768|gb|AAL38322.1| unknown protein [Arabidopsis thaliana] gi|19548055|gb|AAL87391.1| At1g19180/T29M8_5 [Arabidopsis thaliana] gi|20148609|gb|AAM10195.1| unknown protein [Arabidopsis thaliana] gi|332191693|gb|AEE29814.1| protein TIFY 10A [Arabidopsis thaliana]	274	253	8.00E-98	92.3	73.7	80.7	protein TIFY 10A	gbpln	Arabidopsis thaliana	AT1G19180.1 | Symbols: JAZ1, TIFY10A | jasmonate-zim-domain protein 1 | chr1:6622312-6623271 FORWARD LENGTH=253	274	253	1.00E-100	92.3	73.7	80.7
Rsa1.0_01853.1.g30330.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01853.1.g30331.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01853.1.g30332.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01853.1.g30333.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	421	1475	1.00E-162	350.4	67.0	80.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	421	1262	1.00E-141	299.8	56.1	70.8
Rsa1.0_01853.1.g30334.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	717	1475	0	205.7	50.1	65.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01854.1.g30335.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01854.1.g30336.t1	gb|EOA38872.1| hypothetical protein CARUB_v10011237mg [Capsella rubella]	94	375	8.00E-25	398.9	64.9	76.6	hypothetical protein CARUB_v10011237mg	gbpln	Capsella rubella	AT1G49640.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:18375697-18376644 REVERSE LENGTH=315	94	315	1.00E-25	335.1	70.2	79.8
Rsa1.0_01854.1.g30337.t1	gb|EOA38872.1| hypothetical protein CARUB_v10011237mg [Capsella rubella]	375	375	1.00E-159	100.0	75.7	85.6	hypothetical protein CARUB_v10011237mg	gbpln	Capsella rubella	AT1G49650.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:18377363-18378487 REVERSE LENGTH=374	375	374	1.00E-159	99.7	76.8	85.6
Rsa1.0_01854.1.g30338.t1	gb|EOA36208.1| hypothetical protein CARUB_v10010124mg [Capsella rubella]	245	245	1.00E-118	100.0	85.7	92.2	hypothetical protein CARUB_v10010124mg	gbpln	Capsella rubella	AT1G49590.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr1:18354997-18356409 FORWARD LENGTH=242	245	242	1.00E-120	98.8	85.3	91.8
Rsa1.0_01854.1.g30339.t1	dbj|BAB09912.1| MADS-box protein-like [Arabidopsis thaliana]	292	368	3.00E-42	126.0	38.4	56.2	MADS-box protein-like	gbpln	Arabidopsis thaliana	AT5G49420.1 | Symbols: | MADS-box transcription factor family protein | chr5:20035166-20036170 REVERSE LENGTH=334	292	334	1.00E-44	114.4	38.7	56.8
Rsa1.0_01854.1.g30340.t1	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	871	1023	1.00E-119	117.5	29.5	40.2	F27F5.21	gbpln	Arabidopsis thaliana	AT3G09510.1 | Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=484	871	484	5.00E-23	55.6	11.3	16.1
Rsa1.0_01854.1.g30341.t1	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	644	521	2.00E-52	80.9	18.2	25.2	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	644	336	1.00E-18	52.2	8.9	14.1
Rsa1.0_01855.1.g30342.t1	ref|NP_177414.1| phospholipid-translocating ATPase [Arabidopsis thaliana] gi|12229669|sp|Q9SGG3.1|ALA5_ARATH RecName: Full=Putative phospholipid-transporting ATPase 5; Short=AtALA5; AltName: Full=Aminophospholipid flippase 5 gi|12323764|gb|AAG51844.1|AC010926_7 putative P-type transporting ATPase; 43607-39026 [Arabidopsis thaliana] gi|332197241|gb|AEE35362.1| putative phospholipid-transporting ATPase 5 [Arabidopsis thaliana]	1231	1228	0	99.8	91.6	95.5	phospholipid-translocating ATPase	gbpln	Arabidopsis thaliana	AT1G72700.1 | Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:27366910-27371491 FORWARD LENGTH=1228	1231	1228	0	99.8	91.6	95.5
Rsa1.0_01855.1.g30343.t1	gb|EOA35124.1| hypothetical protein CARUB_v10020246mg [Capsella rubella]	466	466	0	100.0	89.9	93.1	hypothetical protein CARUB_v10020246mg	gbpln	Capsella rubella	AT1G72710.1 | Symbols: CKL2 | casein kinase 1-like protein 2 | chr1:27372553-27376178 FORWARD LENGTH=465	466	465	0	99.8	89.3	92.5
Rsa1.0_01855.1.g30344.t1	gb|AAF19806.1| putative protein [Brassica oleracea]	128	125	3.00E-55	97.7	84.4	88.3	putative protein	gbpln	Brassica oleracea	AT1G72720.1 | Symbols: | Protein of unknown function (DUF3511) | chr1:27376903-27377286 REVERSE LENGTH=127	128	127	2.00E-42	99.2	68.8	82.8
Rsa1.0_01855.1.g30345.t1	gb|EOA35218.1| hypothetical protein CARUB_v10020373mg [Capsella rubella]	634	414	0	65.3	62.9	64.5	hypothetical protein CARUB_v10020373mg	gbpln	Capsella rubella	AT1G72730.1 | Symbols: | DEA(D/H)-box RNA helicase family protein | chr1:27378040-27379593 REVERSE LENGTH=414	634	414	0	65.3	62.6	64.4
Rsa1.0_01855.1.g30346.t1	ref|NP_564028.1| translocase of inner mitochondrial membrane 23 [Arabidopsis thaliana] gi|75175255|sp|Q9LNQ1.1|TI231_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM23-1 gi|8778460|gb|AAF79468.1|AC022492_12 F1L3.24 [Arabidopsis thaliana] gi|15010570|gb|AAK73944.1| At1g17530/F11A6.4 [Arabidopsis thaliana] gi|20147387|gb|AAM10403.1| At1g17530/F11A6.4 [Arabidopsis thaliana] gi|38678776|gb|AAR26373.1| mitochondrial inner membrane translocase TM23-1 [Arabidopsis thaliana] gi|332191481|gb|AEE29602.1| translocase of inner mitochondrial membrane 23 [Arabidopsis thaliana]	191	187	1.00E-76	97.9	81.7	90.6	translocase of inner mitochondrial membrane 23	gbpln	Arabidopsis thaliana	AT1G17530.1 | Symbols: ATTIM23-1, TIM23-1 | translocase of inner mitochondrial membrane 23 | chr1:6027723-6028286 FORWARD LENGTH=187	191	187	5.00E-79	97.9	81.7	90.6
Rsa1.0_01855.1.g30347.t1	ref|XP_002888892.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334733|gb|EFH65151.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	617	707	0	114.6	74.4	85.1	kinase family protein	gbpln	Arabidopsis lyrata	AT1G72760.1 | Symbols: | Protein kinase superfamily protein | chr1:27385421-27388274 REVERSE LENGTH=697	617	697	0	113.0	73.6	84.8

Rsa1.0_01855.1.g30348.t1	ref|XP_002887453.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333294|gb|EFH63712.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	188	203	4.00E-12	108.0	24.5	30.3	predicted protein	gbpln	Arabidopsis lyrata	AT4G08760.1 | Symbols: | BEST Arabidopsis thaliana protein match is: nucleolin like 1 (TAIR:AT1G48920.1); Has 36 Blast hits to 36 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:5584739-5591133 REVERSE LENGTH=521	188	521	2.00E-14	277.1	23.4	28.7
Rsa1.0_01855.1.g30349.t1	ref|XP_002888893.1| hypothetical protein ARALYDRAFT_316241 [Arabidopsis lyrata subsp. lyrata] gi|297334734|gb|EFH65152.1| hypothetical protein ARALYDRAFT_316241 [Arabidopsis lyrata subsp. lyrata]	512	519	0	101.4	91.2	95.3	hypothetical protein ARALYDRAFT_316241	gbpln	Arabidopsis lyrata	AT1G72810.1 | Symbols: | Pyridoxal-5'-phosphate-dependent enzyme family protein | chr1:27398760-27400393 REVERSE LENGTH=516	512	516	0	100.8	90.6	94.3
Rsa1.0_01855.1.g30350.t1	ref|NP_565049.1| nuclear transcription factor Y subunit A-3 [Arabidopsis thaliana] gi|81174954|sp|Q93ZH2.2|NFYA3_ARATH RecName: Full=Nuclear transcription factor Y subunit A-3; Short=AtNF-YA-3; AltName: Full=Transcriptional activator HAP2C gi|5903072|gb|AAD55630.1|AC008017_3 Transcription Factor [Arabidopsis thaliana] gi|22655158|gb|AAM98169.1| CCAAT-binding factor B subunit-like protein, putative [Arabidopsis thaliana] gi|31711816|gb|AAP68264.1| At1g72830 [Arabidopsis thaliana] gi|332197257|gb|AEE35378.1| nuclear transcription factor Y subunit A-3 [Arabidopsis thaliana]	316	340	1.00E-134	107.6	83.9	90.2	nuclear transcription factor Y subunit A-3	gbpln	Arabidopsis thaliana	AT1G72830.1 | Symbols: HAP2C, ATHAP2C, NF-YA3 | nuclear factor Y, subunit A3 | chr1:27405699-27407088 REVERSE LENGTH=340	316	340	1.00E-137	107.6	83.9	90.2
Rsa1.0_01856.1.g30351.t1	gb|ABD64930.1| hypothetical protein 24.t00076 [Brassica oleracea]	523	407	1.00E-12	77.8	12.6	18.2	hypothetical protein 24.t00076	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01856.1.g30352.t1	ref|NP_192852.1| ethylene-responsive transcription factor CRF1 [Arabidopsis thaliana] gi|75220260|sp|O82503.1|CRF1_ARATH RecName: Full=Ethylene-responsive transcription factor CRF1; AltName: Full=Protein CYTOKININ RESPONSE FACTOR 1 gi|3600050|gb|AAC35537.1| contains similarity to AP2 domain containing proteins [Arabidopsis thaliana] gi|4850293|emb|CAB43049.1| putative Ap2 domain protein [Arabidopsis thaliana] gi|7267813|emb|CAB81215.1| putative Ap2 domain protein [Arabidopsis thaliana] gi|48479290|gb|AAT44916.1| putative AP2/EREBP transcription factor [Arabidopsis thaliana] gi|92856649|gb|ABE77414.1| At4g11140 [Arabidopsis thaliana] gi|332657577|gb|AEE82977.1| ethylene-responsive transcription factor CRF1 [Arabidopsis thaliana]	290	287	4.00E-84	99.0	71.0	77.2	ethylene-responsive transcription factor CRF1	gbpln	Arabidopsis thaliana	AT4G11140.1 | Symbols: CRF1 | cytokinin response factor 1 | chr4:6794930-6795793 REVERSE LENGTH=287	290	287	1.00E-86	99.0	71.0	77.2
Rsa1.0_01856.1.g30353.t1	gb|AAM15254.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	275	930	2.00E-17	338.2	20.0	28.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01856.1.g30354.t1	ref|XP_002870332.1| hypothetical protein ARALYDRAFT_330097 [Arabidopsis lyrata subsp. lyrata] gi|297316168|gb|EFH46591.1| hypothetical protein ARALYDRAFT_330097 [Arabidopsis lyrata subsp. lyrata]	1727	1339	0	77.5	60.9	66.8	hypothetical protein ARALYDRAFT_330097	gbpln	Arabidopsis lyrata	AT4G14180.1 | Symbols: AtPRD1, PRD1 | putative recombination initiation defect 1 | chr4:8178330-8183515 FORWARD LENGTH=1268	1727	1268	0	73.4	58.4	64.4
Rsa1.0_01857.1.g30355.t1	gb|EOA23025.1| hypothetical protein CARUB_v10003790mg [Capsella rubella]	481	485	0	100.8	86.1	94.6	hypothetical protein CARUB_v10003790mg	gbpln	Capsella rubella	AT4G00910.1 | Symbols: | Aluminium activated malate transporter family protein | chr4:389370-391287 REVERSE LENGTH=497	481	497	0	103.3	86.7	93.6

Rsa1.0_01857.1.g30356.t2	ref|NP_567193.2| putative S-acyltransferase [Arabidopsis thaliana] gi|75222970|sp|Q5M757.1|ZDH15_ARATH RecName: Full=Probable S-acyltransferase At4g00840; AltName: Full=Probable palmitoyltransferase At4g00840; AltName: Full=Zinc finger DHHC domain-containing protein At4g00840 gi|56461762|gb|AAV91337.1| At4g00840 [Arabidopsis thaliana] gi|57222210|gb|AAW39012.1| At4g00840 [Arabidopsis thaliana] gi|110738461|dbj|BAF01156.1| hypothetical protein [Arabidopsis thaliana] gi|332656544|gb|AEE81944.1| putative S-acyltransferase [Arabidopsis thaliana]	281	291	1.00E-128	103.6	87.2	91.8	putative S-acyltransferase	gbpln	Arabidopsis thaliana	AT4G00840.1 | Symbols: | DHHC-type zinc finger family protein | chr4:355483-357105 REVERSE LENGTH=291	281	291	1.00E-130	103.6	87.2	91.8
Rsa1.0_01857.1.g30357.t1	ref|NP_567192.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|79324963|ref|NP_001031566.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|13605916|gb|AAK32943.1|AF367357_1 AT4g00830/A_TM018A10_14 [Arabidopsis thaliana] gi|21360555|gb|AAM47474.1| AT4g00830/A_TM018A10_14 [Arabidopsis thaliana] gi|110743368|dbj|BAE99571.1| hypothetical protein [Arabidopsis thaliana] gi|332656540|gb|AEE81940.1| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|332656541|gb|AEE81941.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	432	495	0	114.6	85.4	92.6	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT4G00830.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:352782-354965 FORWARD LENGTH=495	432	495	0	114.6	85.4	92.6
Rsa1.0_01857.1.g30358.t1	ref|XP_002875013.1| IQ-domain 17 [Arabidopsis lyrata subsp. lyrata] gi|297320850|gb|EFH51272.1| IQ-domain 17 [Arabidopsis lyrata subsp. lyrata]	528	534	0	101.1	78.0	85.6	IQ-domain 17	gbpln	Arabidopsis lyrata	AT4G00820.1 | Symbols: iqd17 | IQ-domain 17 | chr4:349300-351307 FORWARD LENGTH=534	528	534	0	101.1	79.0	85.4
Rsa1.0_01857.1.g30359.t1	ref|NP_567190.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|30678744|ref|NP_849278.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|41019478|sp|O23095.2|RLA12_ARATH RecName: Full=60S acidic ribosomal protein P1-2 gi|13605597|gb|AAK32792.1|AF361624_1 AT4g00810/A_TM018A10_9 [Arabidopsis thaliana] gi|15777871|gb|AAL05896.1| AT4g00810/A_TM018A10_9 [Arabidopsis thaliana] gi|21554797|gb|AAM63694.1| acidic ribosomal protein p1 [Arabidopsis thaliana] gi|222423235|dbj|BAH19594.1| AT4G00810 [Arabidopsis thaliana] gi|332656537|gb|AEE81937.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana] gi|332656538|gb|AEE81938.1| 60S acidic ribosomal protein P1-2 [Arabidopsis thaliana]	124	113	2.00E-35	91.1	87.9	91.1	60S acidic ribosomal protein P1-2	gbpln	Arabidopsis thaliana	AT4G00810.2 | Symbols: | 60S acidic ribosomal protein family | chr4:346179-346957 REVERSE LENGTH=113	124	113	4.00E-38	91.1	87.9	91.1
Rsa1.0_01857.1.g30360.t1	ref|NP_186829.3| ribosome recycling factor [Arabidopsis thaliana] gi|34146850|gb|AAQ62433.1| At3g01800 [Arabidopsis thaliana] gi|51970776|dbj|BAD44080.1| putative ribosome recycling factor [Arabidopsis thaliana] gi|62319213|dbj|BAD94407.1| putative ribosome recycling factor [Arabidopsis thaliana] gi|332640195|gb|AEE73716.1| ribosome recycling factor [Arabidopsis thaliana]	265	267	1.00E-107	100.8	78.9	85.7	ribosome recycling factor	gbpln	Arabidopsis thaliana	AT3G01800.1 | Symbols: | Ribosome recycling factor | chr3:286020-287543 FORWARD LENGTH=267	265	267	1.00E-109	100.8	78.9	85.7

Rsa1.0_01857.1.g30361.t1	ref|NP_567187.1| TRAF-like family protein [Arabidopsis thaliana] gi|17529102|gb|AAL38761.1| unknown protein [Arabidopsis thaliana] gi|20259121|gb|AAM14276.1| unknown protein [Arabidopsis thaliana] gi|332656535|gb|AEE81935.1| TRAF-like family protein [Arabidopsis thaliana]	218	299	9.00E-52	137.2	45.9	54.1	TRAF-like family protein	gbpln	Arabidopsis thaliana	AT4G00780.1 | Symbols: | TRAF-like family protein | chr4:334779-336120 FORWARD LENGTH=299	218	299	3.00E-54	137.2	45.9	54.1
Rsa1.0_01857.1.g30362.t1	ref|XP_002872894.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318731|gb|EFH49153.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	751	1162	0	154.7	95.5	96.5	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT4G01400.2 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: COG4 transport (InterPro:IPR013167); Has 465 Blast hits to 425 proteins in 199 species: Archae - 0; Bacteria - 3; Metazoa - 153; Fungi - 166; Plants - 45; Viruses - 0; Other Eukaryotes - 98 (source: NCBI BLink). | chr4:573098-575648 REVERSE LENGTH=738	751	738	0	98.3	94.1	95.3
Rsa1.0_01857.1.g30363.t1	ref|NP_192050.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|7267638|emb|CAB80950.1| putative hypoersensitive response protein [Arabidopsis thaliana] gi|21555824|gb|AAM63942.1| putative hypoersensitive response protein [Arabidopsis thaliana] gi|26451865|dbj|BAC43025.1| putative hypoersensitive response protein [Arabidopsis thaliana] gi|30017263|gb|AAP12865.1| At4g01410 [Arabidopsis thaliana] gi|332656622|gb|AEE82022.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	228	227	2.00E-97	99.6	87.7	92.1	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT4G01410.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr4:578308-578991 FORWARD LENGTH=227	228	227	1.00E-100	99.6	87.7	92.1
Rsa1.0_01857.1.g30364.t1	dbj|BAB08270.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	86	489	5.00E-16	568.6	43.0	52.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01858.1.g30365.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01858.1.g30366.t1	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	904	190	5.00E-20	21.0	9.0	10.8	hypothetical protein 27.t00123	gbpln	Brassica oleracea	AT5G25760.2 | Symbols: PEX4 | peroxin4 | chr5:8967983-8969173 FORWARD LENGTH=157	904	157	7.00E-17	17.4	4.8	5.3
Rsa1.0_01858.1.g30367.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01858.1.g30368.t3	gb|ADB85430.1| putative retrotransposon protein [Phyllostachys edulis]	417	896	3.00E-64	214.9	30.9	42.4	putative retrotransposon protein	gbpln	Phyllostachys edulis	#	#	#	#	#	#	#
Rsa1.0_01858.1.g30369.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	244	1142	7.00E-37	468.0	34.0	48.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	244	292	2.00E-15	119.7	23.8	42.2
Rsa1.0_01858.1.g30370.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	243	390	1.00E-36	160.5	32.1	43.2	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G33710.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:12219657-12220289 FORWARD LENGTH=210	243	210	2.00E-24	86.4	24.3	40.3
Rsa1.0_01859.1.g30371.t1	gb|EOA31975.1| hypothetical protein CARUB_v10015218mg [Capsella rubella]	455	447	1.00E-101	98.2	57.8	68.8	hypothetical protein CARUB_v10015218mg	gbpln	Capsella rubella	AT2G20310.1 | Symbols: RIN13 | RPM1 interacting protein 13 | chr2:8761328-8763083 REVERSE LENGTH=430	455	430	1.00E-101	94.5	55.8	66.2
Rsa1.0_01859.1.g30372.t2	ref|NP_849998.1| protein kinase domain-containing protein [Arabidopsis thaliana] gi|75330719|sp|Q8RWW0.1|ALE2_ARATH RecName: Full=Receptor-like serine/threonine-protein kinase ALE2; AltName: Full=Protein ABNORMAL LEAF SHAPE 2; Flags: Precursor gi|20259543|gb|AAM13891.1| putative protein kinase [Arabidopsis thaliana] gi|22136896|gb|AAM91792.1| putative protein kinase [Arabidopsis thaliana] gi|110742054|dbj|BAE98959.1| protein kinase like protein [Arabidopsis thaliana] gi|330251897|gb|AEC06991.1| receptor-like serine/threonine-protein kinase ALE2 [Arabidopsis thaliana]	706	744	0	105.4	83.9	86.5	protein kinase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G20300.1 | Symbols: ALE2 | Protein kinase superfamily protein | chr2:8756475-8759845 REVERSE LENGTH=744	706	744	0	105.4	83.9	86.5

Rsa1.0_01859.1.g30373.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01859.1.g30374.t1	gb|EOA30834.1| hypothetical protein CARUB_v10013979mg [Capsella rubella] gi|482566646|gb|EOA30835.1| hypothetical protein CARUB_v10013979mg [Capsella rubella]	176	370	2.00E-23	210.2	43.8	52.8	hypothetical protein CARUB_v10013979mg	gbpln	Capsella rubella	AT3G23690.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:8528933-8530655 REVERSE LENGTH=371	176	371	3.00E-20	210.8	43.8	51.7
Rsa1.0_01859.1.g30375.t2	ref|NP_179619.2| myosin-like protein XIG [Arabidopsis thaliana] gi|330251896|gb|AEC06990.1| myosin-like protein XIG [Arabidopsis thaliana]	348	1493	1.00E-45	429.0	31.3	34.5	myosin-like protein XIG	gbpln	Arabidopsis thaliana	AT2G20290.1 | Symbols: XIG, ATXIG | myosin-like protein XIG | chr2:8743275-8751878 REVERSE LENGTH=1493	348	1493	3.00E-48	429.0	31.3	34.5
Rsa1.0_01860.1.g30376.t1	ref|XP_002873954.1| hypothetical protein ARALYDRAFT_488853 [Arabidopsis lyrata subsp. lyrata] gi|297319791|gb|EFH50213.1| hypothetical protein ARALYDRAFT_488853 [Arabidopsis lyrata subsp. lyrata]	155	151	1.00E-65	97.4	83.2	92.9	hypothetical protein ARALYDRAFT_488853	gbpln	Arabidopsis lyrata	AT5G19590.1 | Symbols: | Protein of unknown function, DUF538 | chr5:6611614-6612069 REVERSE LENGTH=151	155	151	2.00E-65	97.4	74.2	82.6
Rsa1.0_01860.1.g30377.t1	gb|ACP30598.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1593	2301	0	144.4	51.3	66.2	disease resistance protein	gbpln	Brassica rapa	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1593	1262	1.00E-107	79.2	12.1	18.3
Rsa1.0_01860.1.g30378.t1	gb|EOA20233.1| hypothetical protein CARUB_v10000533mg [Capsella rubella]	584	593	0	101.5	81.8	89.0	hypothetical protein CARUB_v10000533mg	gbpln	Capsella rubella	AT5G19580.1 | Symbols: | glyoxal oxidase-related protein | chr5:6607595-6609517 REVERSE LENGTH=594	584	594	0	101.7	80.3	88.9
Rsa1.0_01860.1.g30379.t1	ref|XP_002871895.1| hypothetical protein ARALYDRAFT_488851 [Arabidopsis lyrata subsp. lyrata] gi|297317732|gb|EFH48154.1| hypothetical protein ARALYDRAFT_488851 [Arabidopsis lyrata subsp. lyrata]	137	138	2.00E-52	100.7	85.4	92.7	hypothetical protein ARALYDRAFT_488851	gbpln	Arabidopsis lyrata	AT5G19570.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0546 (InterPro:IPR018908); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:6606739-6607152 FORWARD LENGTH=137	137	137	4.00E-54	100.0	84.7	90.5
Rsa1.0_01860.1.g30380.t1	ref|XP_002871894.1| hypothetical protein ARALYDRAFT_488850 [Arabidopsis lyrata subsp. lyrata] gi|297317731|gb|EFH48153.1| hypothetical protein ARALYDRAFT_488850 [Arabidopsis lyrata subsp. lyrata]	495	496	0	100.2	84.0	91.5	hypothetical protein ARALYDRAFT_488850	gbpln	Arabidopsis lyrata	AT5G19560.1 | Symbols: ATROPGEF10, ROPGEF10 | ROP uanine nucleotide exchange factor 10 | chr5:6603291-6606130 FORWARD LENGTH=493	495	493	0	99.6	84.4	91.1
Rsa1.0_01860.1.g30381.t1	ref|NP_197456.1| aspartate aminotransferase [Arabidopsis thaliana] gi|21542386|sp|P46645.2|AAT2_ARATH RecName: Full=Aspartate aminotransferase, cytoplasmic isozyme 1; AltName: Full=Transaminase A gi|109134125|gb|ABG25061.1| At5g19550 [Arabidopsis thaliana] gi|332005341|gb|AED92724.1| aspartate aminotransferase 1 [Arabidopsis thaliana]	405	405	0	100.0	92.8	97.0	aspartate aminotransferase	gbpln	Arabidopsis thaliana	AT5G19550.1 | Symbols: ASP2, AAT2 | aspartate aminotransferase 2 | chr5:6598201-6601597 FORWARD LENGTH=405	405	405	0	100.0	92.8	97.0
Rsa1.0_01860.1.g30382.t1	gb|ABP73257.1| unknown [Brassica napus]	472	462	0	97.9	90.5	93.9	unknown	gbpln	Brassica napus	AT5G19540.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:6595748-6597724 FORWARD LENGTH=462	472	462	0	97.9	80.9	87.5
Rsa1.0_01860.1.g30383.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01860.1.g30384.t3	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01861.1.g30385.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01861.1.g30386.t1	ref|XP_002870668.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297316504|gb|EFH46927.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	428	466	0	108.9	77.1	83.9	WD-40 repeat family protein	gbpln	Arabidopsis lyrata	AT5G40880.1 | Symbols: | WD-40 repeat family protein / zfwd3 protein (ZFWD3) | chr5:16379481-16381205 FORWARD LENGTH=472	428	472	1.00E-180	110.3	74.8	81.5

Rsa1.0_01861.1.g30387.t1	ref|NP_179828.1| peroxidase [Arabidopsis thaliana] gi|25453217|sp|Q9SJZ2.1|PER17_ARATH RecName: Full=Peroxidase 17; Short=Atperox P17; AltName: Full=ATP25a; Flags: Precursor gi|4544449|gb|AAD22357.1| putative peroxidase [Arabidopsis thaliana] gi|28393257|gb|AAO42057.1| putative peroxidase [Arabidopsis thaliana] gi|28827478|gb|AAO50583.1| putative peroxidase [Arabidopsis thaliana] gi|330252207|gb|AEC07301.1| peroxidase [Arabidopsis thaliana]	329	329	1.00E-173	100.0	90.6	93.9	peroxidase	gbpln	Arabidopsis thaliana	AT2G22420.1 | Symbols: | Peroxidase superfamily protein | chr2:9513341-9514484 FORWARD LENGTH=329	329	329	1.00E-175	100.0	90.6	93.9
Rsa1.0_01861.1.g30388.t1	gb|EOA27362.1| hypothetical protein CARUB_v10023476mg [Capsella rubella]	156	367	3.00E-13	235.3	26.3	30.8	hypothetical protein CARUB_v10023476mg	gbpln	Capsella rubella	AT2G47700.1 | Symbols: RFI2 | RING/U-box superfamily protein | chr2:19552506-19554351 REVERSE LENGTH=358	156	358	4.00E-14	229.5	26.9	30.1
Rsa1.0_01861.1.g30389.t1	gb|AAD24567.1|AF120335_1 putative transposase [Arabidopsis thaliana]	398	577	4.00E-66	145.0	37.2	49.0	putative transposase	gbpln	Arabidopsis thaliana	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	398	343	3.00E-11	86.2	11.3	14.8
Rsa1.0_01861.1.g30390.t1	ref|NP_850024.1| S-adenosylmethionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana] gi|20466586|gb|AAM20610.1| unknown protein [Arabidopsis thaliana] gi|330252205|gb|AEC07299.1| S-adenosylmethionine-dependent methyltransferase domain-containing protein [Arabidopsis thaliana]	797	808	0	101.4	84.4	90.6	S-adenosylmethionine-dependent methyltransferase domain-containing protein	gbpln	Arabidopsis thaliana	AT2G22400.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:9504823-9508788 REVERSE LENGTH=808	797	808	0	101.4	84.4	90.6
Rsa1.0_01861.1.g30391.t3	ref|XP_002880440.1| hypothetical protein ARALYDRAFT_320077 [Arabidopsis lyrata subsp. lyrata] gi|297326279|gb|EFH56699.1| hypothetical protein ARALYDRAFT_320077 [Arabidopsis lyrata subsp. lyrata]	683	219	1.00E-109	32.1	29.9	30.7	hypothetical protein ARALYDRAFT_320077	gbpln	Arabidopsis lyrata	AT2G22370.1 | Symbols: | unknown protein; Has 127 Blast hits to 127 proteins in 48 species: Archae - 0; Bacteria - 0; Metazoa - 87; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:9501019-9502078 REVERSE LENGTH=219	683	219	1.00E-110	32.1	29.4	30.5
Rsa1.0_01862.1.g30392.t1	ref|XP_002867157.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297312993|gb|EFH43416.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	460	493	0	107.2	81.3	90.4	predicted protein	gbpln	Arabidopsis lyrata	AT4G33790.1 | Symbols: CER4, G7, FAR3 | Jojoba acyl CoA reductase-related male sterility protein | chr4:16204325-16207891 REVERSE LENGTH=493	460	493	0	107.2	79.6	90.2
Rsa1.0_01862.1.g30393.t2	gb|EOA16776.1| hypothetical protein CARUB_v10004995mg [Capsella rubella]	346	392	1.00E-144	113.3	79.5	85.5	hypothetical protein CARUB_v10004995mg	gbpln	Capsella rubella	AT4G33770.1 | Symbols: | Inositol 1,3,4-trisphosphate 5/6-kinase family protein | chr4:16193589-16196242 REVERSE LENGTH=391	346	391	1.00E-141	113.0	75.7	83.2
Rsa1.0_01862.1.g30394.t1	ref|NP_195098.1| putative pathogenesis-related protein [Arabidopsis thaliana] gi|11692906|gb|AAG40056.1|AF324705_1 AT4g33720 [Arabidopsis thaliana] gi|11935187|gb|AAG42009.1|AF327419_1 putative pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|12642878|gb|AAK00381.1|AF339699_1 putative pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|3549674|emb|CAA20585.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|7270321|emb|CAB80089.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|14517484|gb|AAK62632.1| AT4g33720/T16L1_210 [Arabidopsis thaliana] gi|21593911|gb|AAM65876.1| pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana] gi|22136566|gb|AAM91069.1| AT4g33720/T16L1_210 [Arabidopsis thaliana] gi|332660869|gb|AEE86269.1| putative pathogenesis-related protein [Arabidopsis thaliana]	172	163	8.00E-53	94.8	58.7	69.2	putative pathogenesis-related protein	gbpln	Arabidopsis thaliana	AT4G33720.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr4:16182813-16183304 FORWARD LENGTH=163	172	163	3.00E-55	94.8	58.7	69.2
Rsa1.0_01862.1.g30395.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01863.1.g30396.t2	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1243	1142	0	91.9	38.1	47.3	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1243	575	2.00E-43	46.3	11.8	19.4
Rsa1.0_01863.1.g30397.t1	gb|EOA35235.1| hypothetical protein CARUB_v10020395mg [Capsella rubella] gi|482571048|gb|EOA35236.1| hypothetical protein CARUB_v10020395mg [Capsella rubella]	402	406	1.00E-169	101.0	82.3	87.6	hypothetical protein CARUB_v10020395mg	gbpln	Capsella rubella	AT1G78420.2 | Symbols: | RING/U-box superfamily protein | chr1:29505278-29507272 FORWARD LENGTH=401	402	401	1.00E-165	99.8	81.6	86.8
Rsa1.0_01863.1.g30398.t1	dbj|BAM73281.1| gibberellin 2 oxidase 1 [Raphanus sativus]	331	331	0	100.0	98.5	98.8	gibberellin 2 oxidase 1	gbpln	Raphanus sativus	AT1G78440.1 | Symbols: ATGA2OX1, GA2OX1 | Arabidopsis thaliana gibberellin 2-oxidase 1 | chr1:29511772-29512990 REVERSE LENGTH=329	331	329	1.00E-159	99.4	82.8	87.3
Rsa1.0_01863.1.g30399.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01864.1.g30400.t1	ref|XP_002893113.1| F5M15.18 [Arabidopsis lyrata subsp. lyrata] gi|297338955|gb|EFH69372.1| F5M15.18 [Arabidopsis lyrata subsp. lyrata]	97	1557	8.00E-11	1605.2	37.1	42.3	F5M15.18	gbpln	Arabidopsis lyrata	AT1G20480.1 | Symbols: | AMP-dependent synthetase and ligase family protein | chr1:7094978-7097073 REVERSE LENGTH=565	97	565	1.00E-13	582.5	37.1	42.3
Rsa1.0_01864.1.g30401.t1	dbj|BAB10837.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	440	1462	5.00E-68	332.3	34.8	56.8	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	440	237	2.00E-31	53.9	17.0	27.3
Rsa1.0_01864.1.g30402.t5	gb|AAD25622.1|AC005287_24 Hypothetical protein [Arabidopsis thaliana]	237	224	1.00E-11	94.5	17.7	33.8	Hypothetical protein	gbpln	Arabidopsis thaliana	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	237	384	4.00E-11	162.0	17.3	32.1
Rsa1.0_01864.1.g30403.t1	ref|NP_564753.1| serine/threonine-protein kinase WNK (With No lysine)-related protein [Arabidopsis thaliana] gi|4249385|gb|AAD14482.1|AAD14482 T2K10.11 [Arabidopsis thaliana] gi|21537011|gb|AAM61352.1| unknown [Arabidopsis thaliana] gi|225898034|dbj|BAH30349.1| hypothetical protein [Arabidopsis thaliana] gi|332195533|gb|AEE33654.1| serine/threonine-protein kinase WNK (With No lysine)-related protein [Arabidopsis thaliana]	248	386	1.00E-104	155.6	84.3	91.5	serine/threonine-protein kinase WNK (With No lysine)-related protein	gbpln	Arabidopsis thaliana	AT1G60060.1 | Symbols: | Serine/threonine-protein kinase WNK (With No Lysine)-related | chr1:22139282-22141585 FORWARD LENGTH=386	248	386	1.00E-107	155.6	84.3	91.5
Rsa1.0_01865.1.g30404.t1	dbj|BAJ34396.1| unnamed protein product [Thellungiella halophila]	393	376	0	95.7	88.3	91.6	unnamed protein product	----	----	AT1G70560.1 | Symbols: WEI8, TAA1, SAV3 | tryptophan aminotransferase of Arabidopsis 1 | chr1:26604894-26607319 FORWARD LENGTH=391	393	391	0	99.5	88.5	93.6
Rsa1.0_01865.1.g30405.t1	ref|XP_002887310.1| hypothetical protein ARALYDRAFT_894871 [Arabidopsis lyrata subsp. lyrata] gi|297333151|gb|EFH63569.1| hypothetical protein ARALYDRAFT_894871 [Arabidopsis lyrata subsp. lyrata]	600	596	0	99.3	89.0	92.0	hypothetical protein ARALYDRAFT_894871	gbpln	Arabidopsis lyrata	AT1G70570.1 | Symbols: | anthranilate phosphoribosyltransferase, putative | chr1:26608719-26612062 FORWARD LENGTH=595	600	595	0	99.2	89.7	92.5
Rsa1.0_01865.1.g30406.t1	dbj|BAD94210.1| hypothetical protein [Arabidopsis thaliana] gi|98961953|gb|ABF59306.1| unknown protein [Arabidopsis thaliana]	90	101	8.00E-13	112.2	55.6	72.2	hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01865.1.g30407.t1	ref|XP_002891050.1| hypothetical protein ARALYDRAFT_890938 [Arabidopsis lyrata subsp. lyrata] gi|297336892|gb|EFH67309.1| hypothetical protein ARALYDRAFT_890938 [Arabidopsis lyrata subsp. lyrata]	241	477	6.00E-34	197.9	39.0	51.9	hypothetical protein ARALYDRAFT_890938	gbpln	Arabidopsis lyrata	AT1G33590.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr1:12177788-12179221 FORWARD LENGTH=477	241	477	4.00E-33	197.9	36.9	50.2
Rsa1.0_01865.1.g30408.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01865.1.g30409.t1	gb|ABM30196.1| ribosomal large subunit structural protein [Brassica juncea]	146	146	2.00E-76	100.0	97.3	99.3	ribosomal large subunit structural protein	gbpln	Brassica juncea	AT1G70600.1 | Symbols: | Ribosomal protein L18e/L15 superfamily protein | chr1:26621168-26621608 REVERSE LENGTH=146	146	146	6.00E-79	100.0	97.3	98.6
Rsa1.0_01865.1.g30410.t1	ref|NP_001185363.1| cyclin-related protein [Arabidopsis thaliana] gi|332196970|gb|AEE35091.1| cyclin-related protein [Arabidopsis thaliana]	887	957	0	107.9	62.8	72.6	cyclin-related protein	gbpln	Arabidopsis thaliana	AT1G70620.3 | Symbols: | cyclin-related | chr1:26626634-26630777 FORWARD LENGTH=957	887	957	0	107.9	62.8	72.6
Rsa1.0_01865.1.g30411.t2	gb|AAF87017.1|AC005292_26 F26F24.12 [Arabidopsis thaliana]	333	301	1.00E-107	90.4	68.5	75.4	F26F24.12	gbpln	Arabidopsis thaliana	AT1G23280.1 | Symbols: | MAK16 protein-related | chr1:8260865-8262650 REVERSE LENGTH=303	333	303	1.00E-109	91.0	68.8	75.7
Rsa1.0_01865.1.g30412.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1209	1142	0	94.5	47.5	61.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1209	575	4.00E-90	47.6	15.2	25.6

Rsa1.0_01866.1.g30413.t1	ref|NP_199943.1| splicing factor 1 [Arabidopsis thaliana] gi|30696034|ref|NP_851169.1| splicing factor 1 [Arabidopsis thaliana] gi|79330558|ref|NP_001032055.1| splicing factor 1 [Arabidopsis thaliana] gi|8843867|dbj|BAA97393.1| unnamed protein product [Arabidopsis thaliana] gi|23297082|gb|AAN13087.1| unknown protein [Arabidopsis thaliana] gi|222423074|dbj|BAH19518.1| AT5G51300 [Arabidopsis thaliana] gi|222423561|dbj|BAH19750.1| AT5G51300 [Arabidopsis thaliana] gi|332008680|gb|AED96063.1| splicing factor 1 [Arabidopsis thaliana] gi|332008681|gb|AED96064.1| splicing factor 1 [Arabidopsis thaliana] gi|332008682|gb|AED96065.1| splicing factor 1-like protein [Arabidopsis thaliana]	763	804	0	105.4	80.9	88.2	splicing factor 1	gbpln	Arabidopsis thaliana	AT5G51300.3 | Symbols: | splicing factor-related | chr5:20849881-20852295 REVERSE LENGTH=804	763	804	0	105.4	80.9	88.2
Rsa1.0_01866.1.g30414.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01866.1.g30415.t1	gb|EOA14426.1| hypothetical protein CARUB_v10027629mg [Capsella rubella]	487	479	0	98.4	78.6	87.3	hypothetical protein CARUB_v10027629mg	gbpln	Capsella rubella	AT5G51380.1 | Symbols: | RNI-like superfamily protein | chr5:20875945-20877779 FORWARD LENGTH=479	487	479	0	98.4	77.4	86.7
Rsa1.0_01866.1.g30416.t1	ref|XP_002865860.1| hypothetical protein ARALYDRAFT_495212 [Arabidopsis lyrata subsp. lyrata] gi|297311695|gb|EFH42119.1| hypothetical protein ARALYDRAFT_495212 [Arabidopsis lyrata subsp. lyrata]	332	334	1.00E-158	100.6	90.7	96.1	hypothetical protein ARALYDRAFT_495212	gbpln	Arabidopsis lyrata	AT5G51410.3 | Symbols: | LUC7 N_terminus domain-containing protein | chr5:20881821-20883577 REVERSE LENGTH=334	332	334	1.00E-156	100.6	88.9	94.9
Rsa1.0_01866.1.g30417.t1	ref|XP_002864112.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297309947|gb|EFH40371.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	87	87	3.00E-24	100.0	78.2	85.1	expressed protein	gbpln	Arabidopsis lyrata	AT5G51451.1 | Symbols: RGF5 | Encodes a root meristem growth factor (RGF). Belongs to a family of functionally redundant homologous peptides that are secreted, tyrosine-sulfated, and expressed mainly in the stem cell area and the innermost layer of central columella cells. RGFs are required for maintenance of the root stem cell niche and transit amplifying cell proliferation. Members of this family include: At5g60810 (RGF1), At1g13620 (RGF2), At2g04025 (RGF3), At3g30350 (RGF4), At5g51451 (RGF5), At4g16515 (RGF6), At3g02240 (RGF7), At2g03830 (RGF8) and At5g64770 (RGF9). | chr5:20898369-20898754 FORWARD LENGTH=88	87	88	8.00E-25	101.1	71.3	78.2
Rsa1.0_01866.1.g30418.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	1916	1239	0	64.7	47.0	54.8	putative pol polyprotein	gbpln	Brassica oleracea	AT5G51470.1 | Symbols: | Auxin-responsive GH3 family protein | chr5:20907287-20909340 FORWARD LENGTH=581	1916	581	0	30.3	21.8	24.0
Rsa1.0_01866.1.g30419.t1	gb|AAD09107.1| nonspecific lipid-transfer protein precursor [Brassica napus]	110	112	4.00E-48	101.8	90.0	93.6	nonspecific lipid-transfer protein precursor	gbpln	Brassica napus	AT5G59310.1 | Symbols: LTP4 | lipid transfer protein 4 | chr5:23925296-23925772 REVERSE LENGTH=112	110	112	3.00E-44	101.8	78.2	86.4
Rsa1.0_01867.1.g30420.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01867.1.g30421.t1	gb|EOA34407.1| hypothetical protein CARUB_v10021935mg [Capsella rubella]	72	1082	8.00E-23	1502.8	70.8	80.6	hypothetical protein CARUB_v10021935mg	gbpln	Capsella rubella	AT2G27630.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr2:11787669-11792010 REVERSE LENGTH=1122	72	1122	3.00E-23	1558.3	62.5	75.0
Rsa1.0_01867.1.g30422.t6	ref|XP_002886817.1| ubiquitin thiolesterase [Arabidopsis lyrata subsp. lyrata] gi|297332658|gb|EFH63076.1| ubiquitin thiolesterase [Arabidopsis lyrata subsp. lyrata]	287	314	5.00E-65	109.4	54.4	67.6	ubiquitin thiolesterase	gbpln	Arabidopsis lyrata	AT1G65160.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr1:24206224-24207738 FORWARD LENGTH=309	287	309	4.00E-65	107.7	52.6	66.9
Rsa1.0_01867.1.g30423.t1	gb|EOA34407.1| hypothetical protein CARUB_v10021935mg [Capsella rubella]	1194	1082	0	90.6	52.6	67.2	hypothetical protein CARUB_v10021935mg	gbpln	Capsella rubella	AT1G65120.2 | Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr1:24191457-24195907 REVERSE LENGTH=1147	1194	1147	0	96.1	54.1	68.1
Rsa1.0_01867.1.g30424.t1	ref|NP_176702.2| uncharacterized protein [Arabidopsis thaliana] gi|20466568|gb|AAM20601.1| unknown protein [Arabidopsis thaliana] gi|23198128|gb|AAN15591.1| unknown protein [Arabidopsis thaliana] gi|332196225|gb|AEE34346.1| uncharacterized protein AT1G65230 [Arabidopsis thaliana]	294	286	1.00E-139	97.3	82.7	90.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G65230.1 | Symbols: | Uncharacterized conserved protein (DUF2358) | chr1:24229167-24230764 FORWARD LENGTH=286	294	286	1.00E-141	97.3	82.7	90.5
Rsa1.0_01867.1.g30425.t2	gb|EOA33392.1| hypothetical protein CARUB_v10020379mg [Capsella rubella]	411	411	0	100.0	92.5	95.9	hypothetical protein CARUB_v10020379mg	gbpln	Capsella rubella	AT1G65220.1 | Symbols: | ARM repeat superfamily protein | chr1:24226204-24228799 FORWARD LENGTH=411	411	411	0	100.0	91.2	94.6

Rsa1.0_01867.1.g30426.t1	dbj|BAB02100.1| unnamed protein product [Arabidopsis thaliana]	263	463	1.00E−72	176.0	54.4	69.6	unnamed protein product	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838−14323928 FORWARD LENGTH=696	263	696	2.00E−21	264.6	27.0	40.7
Rsa1.0_01867.1.g30427.t1	gb|AAC33963.1| contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]	2643	1633	0	61.8	33.9	41.2	contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19)	gbpln	Arabidopsis thaliana	AT1G65200.1 | Symbols: | Ubiquitin carboxyl−terminal hydrolase−related protein | chr1:24218470−24222789 REVERSE LENGTH=1101	2643	1101	0	41.7	23.0	29.6
Rsa1.0_01867.1.g30428.t1	ref|NP_176695.1| Ubiquitin carboxyl−terminal hydrolase family protein [Arabidopsis thaliana] gi|332196218|gb|AEE34339.1| Ubiquitin carboxyl−terminal hydrolase family protein [Arabidopsis thaliana]	320	309	5.00E−81	96.6	52.5	66.9	Ubiquitin carboxyl−terminal hydrolase family protein	gbpln	Arabidopsis thaliana	AT1G65160.1 | Symbols: | Ubiquitin carboxyl−terminal hydrolase family protein | chr1:24206224−24207738 FORWARD LENGTH=309	320	309	1.00E−83	96.6	52.5	66.9
Rsa1.0_01868.1.g30429.t2	ref|NP_189089.3| Serinc−domain containing serine and sphingolipid biosynthesis protein [Arabidopsis thaliana] gi|17381270|gb|AAL36053.1| AT3g24470/MXP5_4 [Arabidopsis thaliana] gi|37201996|gb|AAQ89613.1| At3g24470/MXP5_4 [Arabidopsis thaliana] gi|332643379|gb|AEE76900.1| Serinc−domain containing serine and sphingolipid biosynthesis protein [Arabidopsis thaliana]	415	409	0	98.6	86.3	89.4	Serinc−domain containing serine and sphingolipid biosynthesis protein	gbpln	Arabidopsis thaliana	AT3G24460.1 | Symbols: | Serinc−domain containing serine and sphingolipid biosynthesis protein | chr3:8886160−8889717 REVERSE LENGTH=409	415	409	0	98.6	86.3	89.4
Rsa1.0_01868.1.g30430.t1	dbj|BAB01949.1| unnamed protein product [Arabidopsis thaliana]	251	528	4.00E−39	210.4	34.7	45.4	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G59970.1 | Symbols: | Histone superfamily protein | chr5:24146352−24146663 REVERSE LENGTH=103	251	103	1.00E−29	41.0	25.1	25.1
Rsa1.0_01868.1.g30431.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01868.1.g30432.t1	ref|XP_002885646.1| hypothetical protein ARALYDRAFT_479953 [Arabidopsis lyrata subsp. lyrata] gi|297331486|gb|EFH61905.1| hypothetical protein ARALYDRAFT_479953 [Arabidopsis lyrata subsp. lyrata]	343	603	1.00E−124	175.8	63.6	75.8	hypothetical protein ARALYDRAFT_479953	gbpln	Arabidopsis lyrata	AT3G24440.1 | Symbols: VRN5, VIL1 | Fibronectin type III domain−containing protein | chr3:8876207−8878171 REVERSE LENGTH=602	343	602	1.00E−122	175.5	63.8	76.1
Rsa1.0_01868.1.g30433.t1	ref|XP_002872212.1| hypothetical protein ARALYDRAFT_489476 [Arabidopsis lyrata subsp. lyrata] gi|297318049|gb|EFH48471.1| hypothetical protein ARALYDRAFT_489476 [Arabidopsis lyrata subsp. lyrata]	211	1193	4.00E−66	565.4	63.0	68.2	hypothetical protein ARALYDRAFT_489476	gbpln	Arabidopsis lyrata	AT5G26570.1 | Symbols: PWD, OK1, ATGWD3 | catalytics;carbohydrate kinases;phosphoglucan, water dikinases | chr5:9261580−9267526 FORWARD LENGTH=1196	211	1196	2.00E−68	566.8	63.0	68.2
Rsa1.0_01868.1.g30434.t3	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01868.1.g30435.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01868.1.g30436.t1	gb|AAC33963.1| contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]	1362	1633	0	119.9	54.7	68.1	contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19)	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1362	1262	1.00E−117	92.7	15.7	20.3
Rsa1.0_01868.1.g30437.t1	ref|XP_002885639.1| sec20 family protein [Arabidopsis lyrata subsp. lyrata] gi|297331479|gb|EFH61898.1| sec20 family protein [Arabidopsis lyrata subsp. lyrata]	291	290	1.00E−144	99.7	88.7	94.5	sec20 family protein	gbpln	Arabidopsis lyrata	AT3G24315.1 | Symbols: AtSec20 | Sec20 family protein | chr3:8820599−8822445 REVERSE LENGTH=293	291	293	1.00E−145	100.7	88.0	94.5
Rsa1.0_01868.1.g30438.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01868.1.g30439.t1	dbj|BAB01350.1| Mutator−like transposase [Arabidopsis thaliana]	402	811	1.00E−118	201.7	55.2	70.6	Mutator−like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756−23849915 FORWARD LENGTH=719	402	719	1.00E−14	178.9	21.9	38.8
Rsa1.0_01868.1.g30440.t1	ref|NP_973991.1| aspartyl−tRNA(Asn)/glutamyl−tRNA (Gln) amidotransferase subunit B [Arabidopsis thaliana] gi|332194187|gb|AEE32308.1| aspartyl−tRNA(Asn)/glutamyl−tRNA (Gln) amidotransferase subunit B [Arabidopsis thaliana]	168	488	4.00E−20	290.5	38.7	45.2	aspartyl−tRNA(Asn)/glutamyl−tRNA (Gln) amidotransferase subunit B	gbpln	Arabidopsis thaliana	AT1G48520.3 | Symbols: GATB | GLU−ADT subunit B | chr1:17940185−17942272 FORWARD LENGTH=488	168	488	2.00E−22	290.5	38.7	45.2
Rsa1.0_01868.1.g30441.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#

Rsa1.0_01869.1.g30442.t1	ref|NP_850376.2| 60S ribosomal protein L11−1 [Arabidopsis thaliana] gi|297791141|ref|XP_002863455.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|297804282|ref|XP_002870025.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|21542441|sp|P42795.2|RL111_ARATH RecName: Full=60S ribosomal protein L11−1; AltName: Full=L16A gi|110737006|dbj|BAF00458.1| 60S ribosomal protein L11B [Arabidopsis thaliana] gi|297309290|gb|EFH39714.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|297315861|gb|EFH46284.1| 60S ribosomal protein L11 [Arabidopsis lyrata subsp. lyrata] gi|330255069|gb|AEC10163.1| 60S ribosomal protein L11−1 [Arabidopsis thaliana] gi|482549880|gb|EOA14074.1| hypothetical protein CARUB_v10027211mg [Capsella rubella] gi|482560618|gb|EOA24809.1| hypothetical protein CARUB_v10018095mg [Capsella rubella]	182	182	1.00E−102	100.0	99.5	100.0	60S ribosomal protein L11−1	gbpln	Arabidopsis lyrata	AT2G42740.1 | Symbols: RPL16A | ribosomal protein large subunit 16A | chr2:17791794−17792946 FORWARD LENGTH=182	182	182	1.00E−104	100.0	99.5	100.0
Rsa1.0_01869.1.g30443.t1	ref|XP_002863452.1| cbl−interacting protein kinase 20 [Arabidopsis lyrata subsp. lyrata] gi|297309287|gb|EFH39711.1| cbl−interacting protein kinase 20 [Arabidopsis lyrata subsp. lyrata]	435	439	0	100.9	90.6	93.8	cbl−interacting protein kinase 20	gbpln	Arabidopsis lyrata	AT5G45820.1 | Symbols: CIPK20, SnRK3.6, PKS18 | CBL−interacting protein kinase 20 | chr5:18587081−18588400 REVERSE LENGTH=439	435	439	0	100.9	89.0	93.8
Rsa1.0_01869.1.g30444.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01869.1.g30445.t1	ref|NP_199396.1| leucine−rich repeat protein kinase−like protein [Arabidopsis thaliana] gi|332007922|gb|AED95305.1| leucine−rich repeat protein kinase−like protein [Arabidopsis thaliana]	668	668	0	100.0	81.6	89.4	leucine−rich repeat protein kinase−like protein	gbpln	Arabidopsis thaliana	AT5G45840.1 | Symbols: | Leucine−rich repeat protein kinase family protein | chr5:18594080−18597221 REVERSE LENGTH=668	668	668	0	100.0	81.6	89.4
Rsa1.0_01869.1.g30446.t1	ref|NP_199397.2| uncharacterized protein [Arabidopsis thaliana] gi|332007924|gb|AED95307.1| uncharacterized protein AT5G45850 [Arabidopsis thaliana]	424	445	1.00E−142	105.0	67.7	79.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G45850.1 | Symbols: | Protein of unknown function (DUF688) | chr5:18599998−18601435 REVERSE LENGTH=445	424	445	1.00E−145	105.0	67.7	79.7
Rsa1.0_01869.1.g30447.t1	gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	242	1787	4.00E−69	738.4	59.1	74.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01870.1.g30448.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_01870.1.g30449.t1	ref|XP_002865207.1| hypothetical protein ARALYDRAFT_494372 [Arabidopsis lyrata subsp. lyrata] gi|297311042|gb|EFH41466.1| hypothetical protein ARALYDRAFT_494372 [Arabidopsis lyrata subsp. lyrata]	168	248	4.00E−75	147.6	87.5	94.0	hypothetical protein ARALYDRAFT_494372	gbpln	Arabidopsis lyrata	AT5G46060.1 | Symbols: | Protein of unknown function, DUF599 | chr5:18681533−18682459 FORWARD LENGTH=248	168	248	2.00E−77	147.6	87.5	94.0
Rsa1.0_01870.1.g30450.t1	ref|XP_002863429.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata] gi|297309264|gb|EFH39688.1| pentatricopeptide repeat−containing protein [Arabidopsis lyrata subsp. lyrata]	282	472	3.00E−53	167.4	40.4	48.2	pentatricopeptide repeat−containing protein	gbpln	Arabidopsis lyrata	AT5G46100.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:18694316−18695734 REVERSE LENGTH=472	282	472	2.00E−55	167.4	40.1	48.2
Rsa1.0_01870.1.g30451.t1	sp|P52177.1|TPT1_BRAOB RecName: Full=Triose phosphate/phosphate translocator, chloroplastic; Short=cTPT; Flags: Precursor gi|1143709|gb|AAA84890.1| chloroplast phosphate/triose−phosphate translocator precursor [Brassica oleracea var. botrytis]	402	407	0	101.2	92.5	97.0	RecName: Full=Triose phosphate/phosphate translocator, chloroplastic; Short=cTPT; Flags: Precursor gi|1143709|gb|AAA84890.1| chloroplast phosphate/triose−phosphate translocator precursor	gbpln	Brassica oleracea	AT5G46110.1 | Symbols: APE2, TPT | Glucose−6−phosphate/phosphate translocator−related | chr5:18697606−18700212 FORWARD LENGTH=410	402	410	0	102.0	90.8	96.0
Rsa1.0_01870.1.g30452.t1	gb|AAM67103.1| unknown [Arabidopsis thaliana]	111	109	2.00E−35	98.2	68.5	79.3	unknown	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01870.1.g30453.t1	emb|CAB39638.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA−directed DNA polymerase−like protein [Arabidopsis thaliana]	466	1274	1.00E−112	273.4	47.9	64.8	RNA−directed DNA polymerase−like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	466	575	2.00E−42	123.4	31.8	47.6

Rsa1.0_01870.1.g30454.t1	ref|XP_002863425.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297309260|gb|EFH39684.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	79	79	9.00E-32	100.0	83.5	87.3	expressed protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01871.1.g30455.t1	gb|AAF79687.1|AC022314_28 F9C16.9 [Arabidopsis thaliana]	236	946	1.00E-64	400.8	53.0	69.1	F9C16.9	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01871.1.g30456.t1	ref|NP_176104.1| uncharacterized protein [Arabidopsis thaliana] gi|12321258|gb|AAG50702.1|AC079604_9 hypothetical protein [Arabidopsis thaliana] gi|29029102|gb|AAO64930.1| At1g58070 [Arabidopsis thaliana] gi|110743146|dbj|BAE99465.1| hypothetical protein [Arabidopsis thaliana] gi|332195373|gb|AEE33494.1| uncharacterized protein AT1G58070 [Arabidopsis thaliana]	100	284	1.00E-14	284.0	44.0	51.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G58070.1 | Symbols: | unknown protein; Has 286 Blast hits to 266 proteins in 81 species: Archae - 2; Bacteria - 25; Metazoa - 90; Fungi - 19; Plants - 78; Viruses - 4; Other Eukaryotes - 68 (source: NCBI BLink). | chr1:21502968-21503822 FORWARD LENGTH=284	100	284	2.00E-17	284.0	44.0	51.0
Rsa1.0_01871.1.g30457.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	576	1223	1.00E-136	212.3	43.4	58.3	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	576	746	1.00E-106	129.5	34.4	44.6
Rsa1.0_01871.1.g30458.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01871.1.g30459.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	636	1142	1.00E-161	179.6	45.6	60.5	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	636	575	1.00E-35	90.4	14.8	22.8
Rsa1.0_01872.1.g30460.t1	ref|NP_172061.2| Leucine-rich repeat transmembrane protein kinase protein [Arabidopsis thaliana] gi|263430136|sp|C0LGD6.1|Y1570_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g05700; Flags: Precursor gi|224589374|gb|ACN59221.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana] gi|332189757|gb|AEE27878.1| Leucine-rich repeat transmembrane protein kinase protein [Arabidopsis thaliana]	275	852	1.00E-124	309.8	80.0	87.3	Leucine-rich repeat transmembrane protein kinase protein	gbpln	Arabidopsis thaliana	AT1G05700.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase protein | chr1:1709796-1713245 FORWARD LENGTH=852	275	852	1.00E-127	309.8	80.0	87.3
Rsa1.0_01872.1.g30461.t2	dbj|BAJ34140.1| unnamed protein product [Thellungiella halophila]	242	149	6.00E-64	61.6	50.4	54.1	unnamed protein product	----	----	AT1G05710.5 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:1716198-1717023 FORWARD LENGTH=149	242	149	1.00E-63	61.6	48.8	52.9
Rsa1.0_01872.1.g30462.t1	ref|NP_189957.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana] gi|75182779|sp|Q9M2B5.1|FBK72_ARATH RecName: Full=Putative F-box/kelch-repeat protein At3g43710 gi|7362796|emb|CAB83072.1| putative protein [Arabidopsis thaliana] gi|332644299|gb|AEE77820.1| putative F-box/kelch-repeat protein [Arabidopsis thaliana]	367	378	1.00E-88	103.0	50.7	64.6	putative F-box/kelch-repeat protein	gbpln	Arabidopsis thaliana	AT3G43710.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:15605608-15606744 FORWARD LENGTH=378	367	378	4.00E-91	103.0	50.7	64.6
Rsa1.0_01872.1.g30463.t1	gb|EOA37122.1| hypothetical protein CARUB_v10010372mg, partial [Capsella rubella]	179	191	6.00E-80	106.7	81.6	89.4	hypothetical protein CARUB_v10010372mg, partial	gbpln	Capsella rubella	AT1G05760.1 | Symbols: RTM1 | Mannose-binding lectin superfamily protein | chr1:1723797-1724440 REVERSE LENGTH=174	179	174	2.00E-78	97.2	78.8	85.5
Rsa1.0_01872.1.g30464.t2	ref|XP_002889565.1| hypothetical protein ARALYDRAFT_311660 [Arabidopsis lyrata subsp. lyrata] gi|297335407|gb|EFH65824.1| hypothetical protein ARALYDRAFT_311660 [Arabidopsis lyrata subsp. lyrata]	831	959	0	115.4	71.6	76.7	hypothetical protein ARALYDRAFT_311660	gbpln	Arabidopsis lyrata	AT1G05790.1 | Symbols: | lipase class 3 family protein | chr1:1733039-1737365 FORWARD LENGTH=687	831	687	0	82.7	67.9	73.4
Rsa1.0_01872.1.g30465.t1	ref|XP_002868960.1| hypothetical protein ARALYDRAFT_912541 [Arabidopsis lyrata subsp. lyrata] gi|297314796|gb|EFH45219.1| hypothetical protein ARALYDRAFT_912541 [Arabidopsis lyrata subsp. lyrata]	436	428	1.00E-80	98.2	39.7	56.0	hypothetical protein ARALYDRAFT_912541	gbpln	Arabidopsis lyrata	AT5G49000.2 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19864527-19865645 FORWARD LENGTH=372	436	372	2.00E-49	85.3	30.5	42.9
Rsa1.0_01872.1.g30466.t1	ref|XP_002889566.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297335408|gb|EFH65825.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	474	471	0	99.4	82.7	90.7	lipase class 3 family protein	gbpln	Arabidopsis lyrata	AT1G05800.1 | Symbols: DGL | alpha/beta-Hydrolases superfamily protein | chr1:1741204-1742619 FORWARD LENGTH=471	474	471	0	99.4	80.4	88.6
Rsa1.0_01873.1.g30467.t1	gb|EOA39857.1| hypothetical protein CARUB_v10008529mg [Capsella rubella]	652	658	0	100.9	72.9	81.3	hypothetical protein CARUB_v10008529mg	gbpln	Capsella rubella	AT1G33060.2 | Symbols: ANAC014, NAC014 | NAC 014 | chr1:11975518-11978493 REVERSE LENGTH=652	652	652	0	100.0	71.2	79.4

Rsa1.0_01873.1.g30468.t1	gb|AAN72189.1| Unknown protein [Arabidopsis thaliana]	66	66	7.00E-16	100.0	62.1	72.7	Unknown protein	gbpln	Arabidopsis thaliana	AT1G33055.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: anaerobic respiration; LOCATED IN: endomembrane system; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; Has 20 Blast hits to 20 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:11972336-11972536 REVERSE LENGTH=66	66	66	2.00E-18	100.0	60.6	72.7
Rsa1.0_01873.1.g30469.t1	gb|AAF79797.1|AC020646_20 T32E20.30 [Arabidopsis thaliana]	346	1397	1.00E-49	403.8	29.2	40.2	T32E20.30	gbpln	Arabidopsis thaliana	AT1G67020.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf; Has 72 Blast hits to 72 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 72; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:25011008-25012987 REVERSE LENGTH=659	346	659	5.00E-20	190.5	12.7	17.9
Rsa1.0_01874.1.g30470.t1	gb|EOA30233.1| hypothetical protein CARUB_v10013356mg [Capsella rubella]	563	565	3.00E-82	100.4	70.3	75.3	hypothetical protein CARUB_v10013356mg	gbpln	Capsella rubella	AT3G05220.1 | Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1488808-1491171 FORWARD LENGTH=577	563	577	4.00E-44	102.5	25.4	26.6
Rsa1.0_01874.1.g30471.t1	gb|EOA31176.1| hypothetical protein CARUB_v10014343mg [Capsella rubella]	294	281	1.00E-145	95.6	90.8	93.5	hypothetical protein CARUB_v10014343mg	gbpln	Capsella rubella	AT3G05280.1 | Symbols: | Integral membrane Yip1 family protein | chr3:1503992-1505554 REVERSE LENGTH=281	294	281	1.00E-147	95.6	90.8	93.5
Rsa1.0_01874.1.g30472.t2	ref|XP_002882407.1| hypothetical protein ARALYDRAFT_477819 [Arabidopsis lyrata subsp. lyrata] gi|297328247|gb|EFH58666.1| hypothetical protein ARALYDRAFT_477819 [Arabidopsis lyrata subsp. lyrata]	635	647	0	101.9	63.9	75.7	hypothetical protein ARALYDRAFT_477819	gbpln	Arabidopsis lyrata	AT3G05310.1 | Symbols: MIRO3 | MIRO-related GTP-ase 3 | chr3:1510160-1513301 FORWARD LENGTH=648	635	648	0	102.0	61.4	74.2
Rsa1.0_01874.1.g30473.t1	ref|XP_002882407.1| hypothetical protein ARALYDRAFT_477819 [Arabidopsis lyrata subsp. lyrata] gi|297328247|gb|EFH58666.1| hypothetical protein ARALYDRAFT_477819 [Arabidopsis lyrata subsp. lyrata]	604	647	0	107.1	65.1	76.5	hypothetical protein ARALYDRAFT_477819	gbpln	Arabidopsis lyrata	AT3G05310.1 | Symbols: MIRO3 | MIRO-related GTP-ase 3 | chr3:1510160-1513301 FORWARD LENGTH=648	604	648	0	107.3	62.7	75.7
Rsa1.0_01874.1.g30474.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01874.1.g30475.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01875.1.g30476.t1	gb|AAG50698.1|AC079604_5 copia-type polyprotein, putative [Arabidopsis thaliana] gi|12321387|gb|AAG50765.1|AC079131_10 copia-type polyprotein, putative [Arabidopsis thaliana]	178	1320	5.00E-97	741.6	92.7	97.2	copia-type polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	178	1262	2.00E-33	709.0	38.8	56.2
Rsa1.0_01875.1.g30477.t1	ref|XP_002865234.1| hypothetical protein ARALYDRAFT_330849 [Arabidopsis lyrata subsp. lyrata] gi|297311069|gb|EFH41493.1| hypothetical protein ARALYDRAFT_330849 [Arabidopsis lyrata subsp. lyrata]	164	329	8.00E-31	200.6	46.3	60.4	hypothetical protein ARALYDRAFT_330849	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	164	370	3.00E-33	225.6	50.6	65.9
Rsa1.0_01875.1.g30478.t1	gb|EOA16454.1| hypothetical protein CARUB_v10004610mg [Capsella rubella]	519	511	0	98.5	84.4	90.4	hypothetical protein CARUB_v10004610mg	gbpln	Capsella rubella	AT5G38830.1 | Symbols: | Cysteinyl-tRNA synthetase, class Ia family protein | chr5:15545764-15548094 REVERSE LENGTH=511	519	511	0	98.5	83.4	90.0
Rsa1.0_01875.1.g30479.t1	ref|XP_002870820.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297316656|gb|EFH47079.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata]	439	456	0	103.9	75.4	85.6	amino acid transporter family protein	gbpln	Arabidopsis lyrata	AT5G38820.1 | Symbols: | Transmembrane amino acid transporter family protein | chr5:15543481-15545182 FORWARD LENGTH=456	439	456	0	103.9	74.7	84.7
Rsa1.0_01875.1.g30480.t1	ref|XP_002891342.1| hypothetical protein ARALYDRAFT_473876 [Arabidopsis lyrata subsp. lyrata] gi|297337184|gb|EFH67601.1| hypothetical protein ARALYDRAFT_473876 [Arabidopsis lyrata subsp. lyrata]	401	414	0	103.2	81.5	91.0	hypothetical protein ARALYDRAFT_473876	gbpln	Arabidopsis lyrata	AT1G47270.2 | Symbols: TLP6 | tubby like protein 6 | chr1:17326828-17328564 FORWARD LENGTH=412	401	412	0	102.7	80.0	90.3
Rsa1.0_01875.1.g30481.t1	#	#	#	#	#	#	#	-	----	----	AT1G55600.1 | Symbols: WRKY10, ATWRKY10, MINI3 | WRKY DNA-binding protein 10 | chr1:20774049-20776293 REVERSE LENGTH=485	162	485	1.00E-10	299.4	40.7	56.8

Rsa1.0_01875.1.g30482.t1	ref|NP_001077684.1| uncharacterized protein [Arabidopsis thaliana] gi|98961697|gb|ABF59178.1| unknown protein [Arabidopsis thaliana] gi|332194028|gb|AEE32149.1| uncharacterized protein AT1G47278 [Arabidopsis thaliana]	79	91	3.00E-31	115.2	86.1	91.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G47278.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 37 Blast hits to 37 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr1:17331263-17331726 FORWARD LENGTH=91	79	91	5.00E-34	115.2	86.1	91.1
Rsa1.0_01875.1.g30483.t2	ref|XP_002894037.1| hypothetical protein ARALYDRAFT_314188 [Arabidopsis lyrata subsp. lyrata] gi|297339879|gb|EFH70296.1| hypothetical protein ARALYDRAFT_314188 [Arabidopsis lyrata subsp. lyrata]	69	80	6.00E-14	115.9	81.2	85.5	hypothetical protein ARALYDRAFT_314188	gbpln	Arabidopsis lyrata	AT1G47280.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:17332241-17334310 REVERSE LENGTH=80	69	80	1.00E-14	115.9	75.4	84.1
Rsa1.0_01875.1.g30484.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01875.1.g30485.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	241	1611	3.00E-89	668.5	68.0	78.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01876.1.g30486.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01876.1.g30487.t1	gb|ABV89631.1| aluminum-induced protein [Brassica rapa]	234	236	1.00E-128	100.9	96.2	97.9	aluminum-induced protein	gbpln	Brassica rapa	AT5G19140.1 | Symbols: ATAILP1, AILP1 | Aluminium induced protein with YGL and LRDR motifs | chr5:6423398-6425785 FORWARD LENGTH=234	234	234	1.00E-129	100.0	94.4	97.4
Rsa1.0_01876.1.g30488.t1	gb|EOA19516.1| hypothetical protein CARUB_v10002409mg [Capsella rubella]	318	371	1.00E-164	116.7	90.6	95.6	hypothetical protein CARUB_v10002409mg	gbpln	Capsella rubella	AT5G19150.2 | Symbols: | pfkB-like carbohydrate kinase family protein | chr5:6426280-6428402 REVERSE LENGTH=365	318	365	1.00E-164	114.8	89.3	95.6
Rsa1.0_01876.1.g30489.t1	ref|XP_002871865.1| expressed protein [Arabidopsis lyrata subsp. lyrata] gi|297317702|gb|EFH48124.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	77	74	1.00E-21	96.1	79.2	88.3	expressed protein	gbpln	Arabidopsis lyrata	AT5G19151.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:6428572-6429547 FORWARD LENGTH=74	77	74	2.00E-24	96.1	81.8	88.3
Rsa1.0_01876.1.g30490.t1	gb|ACP30623.1| disease resistance protein [Brassica rapa subsp. pekinensis]	1141	1262	0	110.6	69.5	80.5	disease resistance protein	gbpln	Brassica rapa	AT5G18350.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6074069-6078569 REVERSE LENGTH=1245	1141	1245	0	109.1	57.0	69.1
Rsa1.0_01876.1.g30491.t1	ref|NP_197752.1| putative cation-transporting ATPase [Arabidopsis thaliana] gi|12229714|sp|Q9LT02.1|ATY1_ARATH RecName: Full=Probable cation-transporting ATPase gi|8809697|dbj|BAA97238.1| cation-transporting ATPase [Arabidopsis thaliana] gi|332005809|gb|AED93192.1| putative cation-transporting ATPase [Arabidopsis thaliana]	273	1179	5.00E-35	431.9	30.4	34.1	putative cation-transporting ATPase	gbpln	Arabidopsis thaliana	AT5G23630.1 | Symbols: PDR2, MIA | phosphate deficiency response 2 | chr5:7960756-7967644 REVERSE LENGTH=1179	273	1179	1.00E-37	431.9	30.4	34.1
Rsa1.0_01876.1.g30492.t1	ref|XP_002871870.1| hypothetical protein ARALYDRAFT_488803 [Arabidopsis lyrata subsp. lyrata] gi|297317707|gb|EFH48129.1| hypothetical protein ARALYDRAFT_488803 [Arabidopsis lyrata subsp. lyrata]	146	153	3.00E-48	104.8	76.7	84.2	hypothetical protein ARALYDRAFT_488803	gbpln	Arabidopsis lyrata	AT5G19190.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G06070.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:6457349-6457918 FORWARD LENGTH=154	146	154	3.00E-47	105.5	76.7	87.0
Rsa1.0_01876.1.g30493.t1	gb|ABD65058.1| GRF zinc finger containing protein [Brassica oleracea]	166	172	8.00E-47	103.6	56.6	74.1	GRF zinc finger containing protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01876.1.g30494.t1	gb|AAC26234.1| contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]	1014	940	1.00E-179	92.7	37.7	53.1	contains similarity to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	1014	719	5.00E-16	70.9	7.8	13.9

Rsa1.0_01876.1.g30495.t1	ref|XP_002871872.1| hypothetical protein ARALYDRAFT_488806 [Arabidopsis lyrata subsp. lyrata] gi|297317709|gb|EFH48131.1| hypothetical protein ARALYDRAFT_488806 [Arabidopsis lyrata subsp. lyrata]	478	473	0	99.0	86.6	90.8	hypothetical protein ARALYDRAFT_488806	gbpln	Arabidopsis lyrata	AT5G19210.2 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:6461444-6463687 FORWARD LENGTH=472	478	472	0	98.7	86.2	90.6
Rsa1.0_01876.1.g30496.t1	ref|NP_197423.1| glucose-1-phosphate adenylyltransferase large subunit 1 [Arabidopsis thaliana] gi|14916987|sp|P55229.3|GLGL1_ARATH RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic; AltName: Full=ADP-glucose pyrophosphorylase; AltName: Full=ADP-glucose synthase; AltName: Full=AGPase S; AltName: Full=Alpha-D-glucose-1-phosphate adenyl transferase; Flags: Precursor gi|13877605|gb|AAK43880.1|AF370503_1 Unknown protein [Arabidopsis thaliana] gi|2149021|gb|AAB58475.1| ADPG pyrophosphorylase large subunit [Arabidopsis thaliana] gi|5002530|emb|CAA51779.2| ADP-glucose pyrophosphorylase large subunit [Arabidopsis thaliana] gi|31711934|gb|AAP68323.1| At5g19220 [Arabidopsis thaliana] gi|332005289|gb|AED92672.1| glucose-1-phosphate adenylyltransferase large subunit 1 [Arabidopsis thaliana]	516	522	0	101.2	94.0	97.7	glucose-1-phosphate adenylyltransferase large subunit 1	gbpln	Arabidopsis thaliana	AT5G19220.1 | Symbols: ADG2, APL1 | ADP glucose pyrophosphorylase large subunit 1 | chr5:6463931-6466775 REVERSE LENGTH=522	516	522	0	101.2	94.0	97.7
Rsa1.0_01876.1.g30497.t2	ref|XP_002871873.1| hypothetical protein ARALYDRAFT_488808 [Arabidopsis lyrata subsp. lyrata] gi|297317710|gb|EFH48132.1| hypothetical protein ARALYDRAFT_488808 [Arabidopsis lyrata subsp. lyrata]	414	199	7.00E-67	48.1	30.0	35.0	hypothetical protein ARALYDRAFT_488808	gbpln	Arabidopsis lyrata	AT5G19250.1 | Symbols: | Glycoprotein membrane precursor GPI-anchored | chr5:6471983-6472808 FORWARD LENGTH=196	414	196	6.00E-69	47.3	30.4	34.5
Rsa1.0_01877.1.g30498.t2	ref|XP_002873954.1| hypothetical protein ARALYDRAFT_488853 [Arabidopsis lyrata subsp. lyrata] gi|297319791|gb|EFH50213.1| hypothetical protein ARALYDRAFT_488853 [Arabidopsis lyrata subsp. lyrata]	151	151	3.00E-63	100.0	79.5	93.4	hypothetical protein ARALYDRAFT_488853	gbpln	Arabidopsis lyrata	AT5G19590.1 | Symbols: | Protein of unknown function, DUF538 | chr5:6611614-6612069 REVERSE LENGTH=151	151	151	3.00E-64	100.0	72.2	83.4
Rsa1.0_01877.1.g30499.t1	ref|XP_002871896.1| hypothetical protein ARALYDRAFT_909999 [Arabidopsis lyrata subsp. lyrata] gi|297317733|gb|EFH48155.1| hypothetical protein ARALYDRAFT_909999 [Arabidopsis lyrata subsp. lyrata]	736	732	0	99.5	87.8	91.6	hypothetical protein ARALYDRAFT_909999	gbpln	Arabidopsis lyrata	AT5G19620.1 | Symbols: EMB213, OEP80, ATOEP80, TOC75 | outer envelope protein of 80 kDa | chr5:6623323-6627641 FORWARD LENGTH=732	736	732	0	99.5	87.0	90.5
Rsa1.0_01877.1.g30500.t1	ref|NP_197465.1| putative peptide/nitrate transporter [Arabidopsis thaliana] gi|122214333|sp|Q3E9B5.1|PTR51_ARATH RecName: Full=Putative peptide/nitrate transporter At5g19640 gi|332005350|gb|AED92733.1| putative peptide/nitrate transporter [Arabidopsis thaliana]	607	609	0	100.3	86.7	92.8	putative peptide/nitrate transporter	gbpln	Arabidopsis thaliana	AT5G19640.1 | Symbols: | Major facilitator superfamily protein | chr5:6636460-6638590 FORWARD LENGTH=609	607	609	0	100.3	86.7	92.8
Rsa1.0_01877.1.g30501.t1	ref|XP_002873958.1| ATOFP8/OFP8 [Arabidopsis lyrata subsp. lyrata] gi|297319795|gb|EFH50217.1| ATOFP8/OFP8 [Arabidopsis lyrata subsp. lyrata]	215	219	2.00E-77	101.9	78.6	85.6	ATOFP8/OFP8	gbpln	Arabidopsis lyrata	AT5G19650.1 | Symbols: ATOFP8, OFP8 | ovate family protein 8 | chr5:6639632-6640297 REVERSE LENGTH=221	215	221	6.00E-75	102.8	76.3	84.7
Rsa1.0_01877.1.g30502.t1	ref|NP_197468.2| Exostosin family protein [Arabidopsis thaliana] gi|332005353|gb|AED92736.1| Exostosin family protein [Arabidopsis thaliana]	587	610	0	103.9	85.2	92.0	Exostosin family protein	gbpln	Arabidopsis thaliana	AT5G19670.1 | Symbols: | Exostosin family protein | chr5:6647025-6649358 FORWARD LENGTH=610	587	610	0	103.9	85.2	92.0
Rsa1.0_01877.1.g30503.t1	gb|EOA21087.1| hypothetical protein CARUB_v10001424mg [Capsella rubella]	328	328	1.00E-168	100.0	89.9	96.3	hypothetical protein CARUB_v10001424mg	gbpln	Capsella rubella	AT5G19680.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr5:6649663-6651564 FORWARD LENGTH=328	328	328	1.00E-167	100.0	88.7	94.8
Rsa1.0_01877.1.g30504.t1	ref|XP_002871900.1| hypothetical protein ARALYDRAFT_488863 [Arabidopsis lyrata subsp. lyrata] gi|297317737|gb|EFH48159.1| hypothetical protein ARALYDRAFT_488863 [Arabidopsis lyrata subsp. lyrata]	780	779	0	99.9	95.6	97.2	hypothetical protein ARALYDRAFT_488863	gbpln	Arabidopsis lyrata	AT5G19690.1 | Symbols: STT3A | staurosporin and temperature sensitive 3-like A | chr5:6652649-6658214 FORWARD LENGTH=779	780	779	0	99.9	95.4	97.3

Rsa1.0_01878.1.g30505.t24	gb|EOA39972.1| hypothetical protein CARUB_v10008660mg [Capsella rubella]	453	590	2.00E-52	130.2	26.5	34.2	hypothetical protein CARUB_v10008660mg	gbpln	Capsella rubella	AT1G22660.1 | Symbols: | Polynucleotide adenylyltransferase family protein | chr1:8017410-8021538 FORWARD LENGTH=605	453	605	2.00E-53	133.6	25.8	33.3
Rsa1.0_01878.1.g30506.t1	gb|AAD29754.1|AF076243_1 putative transposon protein [Arabidopsis thaliana] gi|7267199|emb|CAB77910.1| putative transposon protein [Arabidopsis thaliana]	442	1008	1.00E-10	228.1	12.7	18.8	putative transposon protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01878.1.g30507.t1	gb|EOA40072.1| hypothetical protein CARUB_v10008765mg [Capsella rubella]	534	549	0	102.8	87.3	93.3	hypothetical protein CARUB_v10008765mg	gbpln	Capsella rubella	AT1G10640.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:3515478-3517807 REVERSE LENGTH=532	534	532	0	99.6	84.6	92.7
Rsa1.0_01878.1.g30508.t1	gb|EOA39211.1| hypothetical protein CARUB_v10012182mg [Capsella rubella]	396	444	1.00E-149	112.1	70.7	80.6	hypothetical protein CARUB_v10012182mg	gbpln	Capsella rubella	AT1G10610.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:3506463-3508752 FORWARD LENGTH=441	396	441	1.00E-152	111.4	70.7	80.8
Rsa1.0_01878.1.g30509.t1	gb|EOA38661.1| hypothetical protein CARUB_v10010598mg [Capsella rubella]	140	140	1.00E-68	100.0	90.7	95.0	hypothetical protein CARUB_v10010598mg	gbpln	Capsella rubella	AT1G10590.3 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:3502324-3503033 REVERSE LENGTH=153	140	153	2.00E-69	109.3	89.3	95.0
Rsa1.0_01878.1.g30510.t2	ref|NP_001117258.1| basic helix-loop-helix domain-containing protein [Arabidopsis thaliana] gi|5091554|gb|AAD39583.1|AC007067_23 T10O24.23 [Arabidopsis thaliana] gi|332190478|gb|AEE28599.1| basic helix-loop-helix domain-containing protein [Arabidopsis thaliana]	175	174	2.00E-70	99.4	76.6	87.4	basic helix-loop-helix domain-containing protein	gbpln	Arabidopsis thaliana	AT1G10586.1 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:3497131-3499396 REVERSE LENGTH=174	175	174	1.00E-72	99.4	76.6	87.4
Rsa1.0_01878.1.g30511.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01879.1.g30512.t1	gb|EOA33268.1| hypothetical protein CARUB_v10022353mg [Capsella rubella]	215	215	1.00E-100	100.0	83.3	89.8	hypothetical protein CARUB_v10022353mg	gbpln	Capsella rubella	AT1G64065.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr1:23778628-23779272 FORWARD LENGTH=214	215	214	1.00E-100	99.5	81.9	89.8
Rsa1.0_01879.1.g30513.t1	ref|XP_002886365.1| hypothetical protein ARALYDRAFT_474947 [Arabidopsis lyrata subsp. lyrata] gi|297332206|gb|EFH62624.1| hypothetical protein ARALYDRAFT_474947 [Arabidopsis lyrata subsp. lyrata]	411	413	1.00E-112	100.5	69.1	77.1	hypothetical protein ARALYDRAFT_474947	gbpln	Arabidopsis lyrata	AT1G64080.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G52870.1); Has 1546 Blast hits to 738 proteins in 176 species: Archae - 0; Bacteria - 143; Metazoa - 278; Fungi - 131; Plants - 95; Viruses - 4; Other Eukaryotes - 895 (source: NCBI BLink). | chr1:23785230-23786557 REVERSE LENGTH=411	411	411	1.00E-108	100.0	67.6	76.4
Rsa1.0_01879.1.g30514.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01879.1.g30515.t1	gb|EOA35625.1| hypothetical protein CARUB_v10020840mg [Capsella rubella]	250	253	1.00E-115	101.2	87.6	94.0	hypothetical protein CARUB_v10020840mg	gbpln	Capsella rubella	AT1G64090.1 | Symbols: RTNLB3 | Reticulan like protein B3 | chr1:23789395-23790669 FORWARD LENGTH=255	250	255	1.00E-117	102.0	86.8	94.4
Rsa1.0_01879.1.g30516.t1	ref|NP_178819.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] gi|3327395|gb|AAC26677.1| putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana] gi|330251037|gb|AEC06131.1| Zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	252	530	1.00E-23	210.3	35.7	51.2	Zinc knuckle (CCHC-type) family protein	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	252	530	4.00E-26	210.3	35.7	51.2
Rsa1.0_01880.1.g30517.t1	ref|NP_200786.1| transcription factor MYB59 [Arabidopsis thaliana] gi|97179947|sp|Q4JL84.2|MYB59_ARATH RecName: Full=Transcription factor MYB59; AltName: Full=Myb-related protein 59; Short=AtMYB59 gi|9758843|dbj|BAB09515.1| Myb-related transcription factor-like protein [Arabidopsis thaliana] gi|41619478|gb|AAS10111.1| MYB transcription factor [Arabidopsis thaliana] gi|332009849|gb|AED97232.1| transcription factor MYB59 [Arabidopsis thaliana]	238	235	1.00E-116	98.7	91.2	93.7	transcription factor MYB59	gbpln	Arabidopsis thaliana	AT5G59780.3 | Symbols: MYB59, ATMYB59-3 | myb domain protein 59 | chr5:24082425-24083350 REVERSE LENGTH=235	238	235	1.00E-118	98.7	91.2	93.7
Rsa1.0_01880.1.g30518.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01880.1.g30519.t1	ref|XP_002864667.1| APUM18 [Arabidopsis lyrata subsp. lyrata] gi|297310502|gb|EFH40926.1| APUM18 [Arabidopsis lyrata subsp. lyrata]	332	328	1.00E-129	98.8	71.1	82.2	APUM18	gbpln	Arabidopsis lyrata	AT5G60110.1 | Symbols: APUM18, PUM18 | pumilio 18 | chr5:24201954-24202937 FORWARD LENGTH=327	332	327	1.00E-122	98.5	70.8	80.7

Rsa1.0_01880.1.g30520.t1	ref|NP_200784.2| uncharacterized protein [Arabidopsis thaliana] gi|61742767|gb|AAX55204.1| hypothetical protein At5g59760 [Arabidopsis thaliana] gi|332009846|gb|AED97229.1| uncharacterized protein AT5G59760 [Arabidopsis thaliana]	231	232	7.00E-77	100.4	71.0	78.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G59760.1 | Symbols: | Protein of unknown function (DUF1635) | chr5:24075628-24076415 REVERSE LENGTH=232	231	232	2.00E-79	100.4	71.0	78.8
Rsa1.0_01880.1.g30521.t1	ref|NP_200782.1| UDP-N-acetylglucosamine (UAA) transporter family protein [Arabidopsis thaliana] gi|75127032|sp|Q6NMB6.1|UTR5B_ARATH RecName: Full=UDP-galactose/UDP-glucose transporter 5B; Short=AtUTr5B gi|44917565|gb|AAS49107.1| At5g59740 [Arabidopsis thaliana] gi|332009843|gb|AED97226.1| UDP-galactose/UDP-glucose transporter 5B [Arabidopsis thaliana]	177	344	1.00E-53	194.4	66.1	73.4	UDP-N-acetylglucosamine (UAA) transporter family protein	gbpln	Arabidopsis thaliana	AT5G59740.1 | Symbols: | UDP-N-acetylglucosamine (UAA) transporter family | chr5:24070310-24072747 REVERSE LENGTH=344	177	344	6.00E-56	194.4	66.1	73.4
Rsa1.0_01880.1.g30522.t1	gb|EOA14941.1| hypothetical protein CARUB_v10028285mg [Capsella rubella]	624	637	0	102.1	77.2	85.6	hypothetical protein CARUB_v10028285mg	gbpln	Capsella rubella	AT5G59730.1 | Symbols: ATEXO70H7, EXO70H7 | exocyst subunit exo70 family protein H7 | chr5:24064100-24066004 REVERSE LENGTH=634	624	634	0	101.6	78.5	89.1
Rsa1.0_01881.1.g30523.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01881.1.g30524.t1	ref|NP_564784.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana] gi|4508074|gb|AAD21418.1| Unknown protein [Arabidopsis thaliana] gi|222424594|dbj|BAH20252.1| AT1G61730 [Arabidopsis thaliana] gi|332195759|gb|AEE33880.1| DNA-binding storekeeper protein-related transcriptional regulator [Arabidopsis thaliana]	389	376	6.00E-99	96.7	60.7	71.2	DNA-binding storekeeper protein-related transcriptional regulator	gbpln	Arabidopsis thaliana	AT1G61730.1 | Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:22793447-22794577 REVERSE LENGTH=376	389	376	1.00E-101	96.7	60.7	71.2
Rsa1.0_01881.1.g30525.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01881.1.g30526.t1	ref|XP_002886512.1| hypothetical protein ARALYDRAFT_475155 [Arabidopsis lyrata subsp. lyrata] gi|297332353|gb|EFH62771.1| hypothetical protein ARALYDRAFT_475155 [Arabidopsis lyrata subsp. lyrata]	460	461	0	100.2	85.0	93.0	hypothetical protein ARALYDRAFT_475155	gbpln	Arabidopsis lyrata	AT1G61740.1 | Symbols: | Sulfite exporter TauE/SafE family protein | chr1:22798365-22801020 REVERSE LENGTH=458	460	458	0	99.6	85.2	93.7
Rsa1.0_01881.1.g30527.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01881.1.g30528.t1	gb|EOA35945.1| hypothetical protein CARUB_v10021202mg [Capsella rubella]	98	98	1.00E-48	100.0	98.0	98.0	hypothetical protein CARUB_v10021202mg	gbpln	Capsella rubella	AT1G61780.1 | Symbols: | postsynaptic protein-related | chr1:22812822-22814016 REVERSE LENGTH=98	98	98	2.00E-50	100.0	95.9	96.9
Rsa1.0_01881.1.g30529.t1	ref|NP_181704.1| uncharacterized protein [Arabidopsis thaliana] gi|2335105|gb|AAC02775.1| hypothetical protein [Arabidopsis thaliana] gi|26450207|dbj|BAC42222.1| unknown protein [Arabidopsis thaliana] gi|30793799|gb|AAP40352.1| unknown protein [Arabidopsis thaliana] gi|330254932|gb|AEC10026.1| uncharacterized protein AT2G41730 [Arabidopsis thaliana]	106	119	1.00E-25	112.3	60.4	67.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G41730.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24640.1); Has 25 Blast hits to 25 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17409488-17409847 FORWARD LENGTH=119	106	119	2.00E-28	112.3	60.4	67.0
Rsa1.0_01881.1.g30530.t1	gb|EOA35889.1| hypothetical protein CARUB_v10021146mg [Capsella rubella]	114	127	4.00E-39	111.4	77.2	85.1	hypothetical protein CARUB_v10021146mg	gbpln	Capsella rubella	AT1G61795.1 | Symbols: | PAK-box/P21-Rho-binding family protein | chr1:22819943-22820826 FORWARD LENGTH=128	114	128	5.00E-37	112.3	77.2	85.1
Rsa1.0_01881.1.g30531.t1	gb|EOA19550.1| hypothetical protein CARUB_v10002551mg [Capsella rubella]	353	369	1.00E-151	104.5	73.7	86.7	hypothetical protein CARUB_v10002551mg	gbpln	Capsella rubella	AT5G12270.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:3970131-3971301 REVERSE LENGTH=360	353	360	1.00E-149	102.0	75.9	89.2
Rsa1.0_01882.1.g30532.t1	gb|EOA33846.1| hypothetical protein CARUB_v10021336mg [Capsella rubella]	1017	1069	0	105.1	74.1	86.9	hypothetical protein CARUB_v10021336mg	gbpln	Capsella rubella	AT1G65780.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:24462958-24466888 REVERSE LENGTH=1065	1017	1065	0	104.7	73.7	86.0
Rsa1.0_01882.1.g30533.t1	gb|ACD77012.1| metal transporter protein [Brassica juncea]	692	689	0	99.6	96.4	98.3	metal transporter protein	gbpln	Brassica juncea	AT1G65730.1 | Symbols: YSL7 | YELLOW STRIPE like 7 | chr1:24442639-24446122 FORWARD LENGTH=688	692	688	0	99.4	90.0	95.1

Rsa1.0_01882.1.g30534.t1	gb|EOA34542.1| hypothetical protein CARUB_v10022088mg [Capsella rubella]	191	186	5.00E-61	97.4	68.6	78.0	hypothetical protein CARUB_v10022088mg	gbpln	Capsella rubella	AT1G65720.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 44 Blast hits to 44 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:24440471-24441013 REVERSE LENGTH=180	191	180	2.00E-52	94.2	69.1	79.6
Rsa1.0_01882.1.g30535.t1	gb|AFD01305.1| auxin response factor 8-1 [Brassica rapa subsp. pekinensis]	794	780	0	98.2	93.1	95.3	auxin response factor 8-1	gbpln	Brassica rapa	AT5G37020.1 | Symbols: ARF8, ATARF8 | auxin response factor 8 | chr5:14630151-14634106 FORWARD LENGTH=811	794	811	0	102.1	78.3	84.4
Rsa1.0_01882.1.g30536.t1	ref|NP_176747.1| U6 snRNA-associated Sm-like protein LSm8 [Arabidopsis thaliana] gi|79320777|ref|NP_001031238.1| U6 snRNA-associated Sm-like protein LSm8 [Arabidopsis thaliana] gi|17979539|gb|AAL50104.1| At1g65700/F1E22_3 [Arabidopsis thaliana] gi|20334918|gb|AAM16215.1| At1g65700/F1E22_3 [Arabidopsis thaliana] gi|21592627|gb|AAM64576.1| small nuclear ribonucleoprotein, putative [Arabidopsis thaliana] gi|332196292|gb|AEE34413.1| U6 snRNA-associated Sm-like protein LSm8 [Arabidopsis thaliana] gi|332196293|gb|AEE34414.1| U6 snRNA-associated Sm-like protein LSm8 [Arabidopsis thaliana]	98	98	2.00E-47	100.0	96.9	99.0	U6 snRNA-associated Sm-like protein LSm8	gbpln	Arabidopsis thaliana	AT1G65700.2 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:24434463-24435870 REVERSE LENGTH=98	98	98	4.00E-50	100.0	96.9	99.0
Rsa1.0_01882.1.g30537.t1	gb|EOA35438.1| hypothetical protein CARUB_v10020640mg [Capsella rubella]	323	329	1.00E-163	101.9	90.1	94.4	hypothetical protein CARUB_v10020640mg	gbpln	Capsella rubella	AT1G65650.1 | Symbols: UCH2 | Peptidase C12, ubiquitin carboxyl-terminal hydrolase 1 | chr1:24415172-24417466 REVERSE LENGTH=330	323	330	1.00E-163	102.2	89.8	93.8
Rsa1.0_01882.1.g30538.t14	ref|XP_002886950.1| glycosyl hydrolase family 20 protein [Arabidopsis lyrata subsp. lyrata] gi|297332791|gb|EFH63209.1| glycosyl hydrolase family 20 protein [Arabidopsis lyrata subsp. lyrata]	554	535	0	96.6	81.0	86.8	glycosyl hydrolase family 20 protein	gbpln	Arabidopsis lyrata	AT1G65590.1 | Symbols: HEXO3, ATHEX1 | beta-hexosaminidase 3 | chr1:24385996-24390989 FORWARD LENGTH=535	554	535	0	96.6	81.2	86.8
Rsa1.0_01883.1.g30539.t1	ref|XP_002875338.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321176|gb|EFH51597.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	301	300	1.00E-136	99.7	80.4	85.7	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G26760.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:9843639-9844899 FORWARD LENGTH=300	301	300	1.00E-138	99.7	79.7	85.0
Rsa1.0_01883.1.g30540.t1	ref|NP_189310.2| uncharacterized protein [Arabidopsis thaliana] gi|9279664|dbj|BAB01221.1| unnamed protein product [Arabidopsis thaliana] gi|332643690|gb|AEE77211.1| uncharacterized protein AT3G26750 [Arabidopsis thaliana]	495	526	0	106.3	81.4	88.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G26750.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ubiquitin-conjugating enzyme E2C-binding protein (InterPro:IPR019193); Has 26 Blast hits to 25 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9840139-9841719 REVERSE LENGTH=526	495	526	0	106.3	81.4	88.7
Rsa1.0_01883.1.g30541.t1	gb|ACB70963.1| ICE1 [Brassica rapa subsp. chinensis]	503	497	0	98.8	91.7	92.8	ICE1	gbpln	Brassica rapa	AT3G26744.4 | Symbols: ICE1, ATICE1, SCRM | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:9832953-9834790 REVERSE LENGTH=494	503	494	0	98.2	85.3	87.7
Rsa1.0_01883.1.g30542.t1	ref|NP_189306.1| alpha-mannosidase [Arabidopsis thaliana] gi|1888357|emb|CAA66821.1| alpha-mannosidase [Arabidopsis thaliana] gi|1890154|emb|CAA72432.1| alpha-mannosidase precursor [Arabidopsis thaliana] gi|11994305|dbj|BAB01735.1| alpha-mannosidase [Arabidopsis thaliana] gi|14517403|gb|AAK62592.1| AT3g26720/MLJ15_12 [Arabidopsis thaliana] gi|21360397|gb|AAM47314.1| AT3g26720/MLJ15_12 [Arabidopsis thaliana] gi|332643682|gb|AEE77203.1| alpha-mannosidase [Arabidopsis thaliana]	1031	1019	0	98.8	89.6	94.5	alpha-mannosidase	gbpln	Arabidopsis thaliana	AT3G26720.1 | Symbols: | Glycosyl hydrolase family 38 protein | chr3:9816707-9823056 FORWARD LENGTH=1019	1031	1019	0	98.8	89.6	94.5

Rsa1.0_01883.1.g30543.t1	ref|XP_002875334.1| hypothetical protein ARALYDRAFT_484443 [Arabidopsis lyrata subsp. lyrata] gi|297321172|gb|EFH51593.1| hypothetical protein ARALYDRAFT_484443 [Arabidopsis lyrata subsp. lyrata]	272	267	1.00E-123	98.2	84.9	89.7	hypothetical protein ARALYDRAFT_484443	gbpln	Arabidopsis lyrata	AT3G26710.1 | Symbols: CCB1 | cofactor assembly of complex C | chr3:9813550-9814606 FORWARD LENGTH=267	272	267	1.00E-125	98.2	84.2	90.1
Rsa1.0_01883.1.g30544.t1	ref|NP_189304.2| protein kinase family protein [Arabidopsis thaliana] gi|332643680|gb|AEE77201.1| protein kinase family protein [Arabidopsis thaliana]	378	380	0	100.5	89.7	93.4	protein kinase family protein	gbpln	Arabidopsis thaliana	AT3G26700.1 | Symbols: | Protein kinase superfamily protein | chr3:9810669-9812356 FORWARD LENGTH=380	378	380	0	100.5	89.7	93.4
Rsa1.0_01883.1.g30545.t1	ref|XP_002876987.1| hypothetical protein ARALYDRAFT_904865 [Arabidopsis lyrata subsp. lyrata] gi|297322825|gb|EFH53246.1| hypothetical protein ARALYDRAFT_904865 [Arabidopsis lyrata subsp. lyrata]	206	202	3.00E-94	98.1	85.0	90.8	hypothetical protein ARALYDRAFT_904865	gbpln	Arabidopsis lyrata	AT3G26690.2 | Symbols: ATNUDT13, ATNUDX13, NUDX13 | nudix hydrolase homolog 13 | chr3:9804418-9805398 REVERSE LENGTH=202	206	202	1.00E-96	98.1	84.0	91.3
Rsa1.0_01883.1.g30546.t1	ref|XP_002875331.1| hypothetical protein ARALYDRAFT_484438 [Arabidopsis lyrata subsp. lyrata] gi|297321169|gb|EFH51590.1| hypothetical protein ARALYDRAFT_484438 [Arabidopsis lyrata subsp. lyrata]	490	483	0	98.6	84.5	90.4	hypothetical protein ARALYDRAFT_484438	gbpln	Arabidopsis lyrata	AT3G26680.3 | Symbols: SNM1 | DNA repair metallo-beta-lactamase family protein | chr3:9801309-9803517 FORWARD LENGTH=484	490	484	0	98.8	83.9	90.0
Rsa1.0_01883.1.g30547.t1	gb|EOA23356.1| hypothetical protein CARUB_v10019534mg [Capsella rubella]	445	442	0	99.3	93.0	96.0	hypothetical protein CARUB_v10019534mg	gbpln	Capsella rubella	AT3G26670.3 | Symbols: | Protein of unknown function (DUF803) | chr3:9798236-9800562 REVERSE LENGTH=441	445	441	0	99.1	94.2	95.7
Rsa1.0_01883.1.g30548.t1	dbj|BAJ34149.1| unnamed protein product [Thellungiella halophila]	400	400	0	100.0	97.5	99.0	unnamed protein product	----	----	AT3G26650.1 | Symbols: GAPA, GAPA-1 | glyceraldehyde 3-phosphate dehydrogenase A subunit | chr3:9795226-9796848 FORWARD LENGTH=396	400	396	0	99.0	95.3	97.5
Rsa1.0_01884.1.g30549.t1	gb|EOA13760.1| hypothetical protein CARUB_v10026852mg [Capsella rubella]	295	304	1.00E-110	103.1	70.8	81.4	hypothetical protein CARUB_v10026852mg	gbpln	Capsella rubella	AT5G50915.2 | Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:20710764-20712252 REVERSE LENGTH=286	295	286	1.00E-109	96.9	68.8	78.3
Rsa1.0_01884.1.g30550.t1	gb|EOA25182.1| hypothetical protein CARUB_v10018494mg [Capsella rubella]	321	282	9.00E-42	87.9	31.8	44.5	hypothetical protein CARUB_v10018494mg	gbpln	Capsella rubella	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	321	303	6.00E-34	94.4	26.8	43.3
Rsa1.0_01884.1.g30551.t7	ref|XP_002863752.1| hypothetical protein ARALYDRAFT_331135 [Arabidopsis lyrata subsp. lyrata] gi|297309587|gb|EFH40011.1| hypothetical protein ARALYDRAFT_331135 [Arabidopsis lyrata subsp. lyrata]	497	648	0	130.4	74.2	81.3	hypothetical protein ARALYDRAFT_331135	gbpln	Arabidopsis lyrata	AT5G42660.1 | Symbols: | Protein of unknown function (DUF616) | chr5:17103062-17105785 REVERSE LENGTH=463	497	463	0	93.2	73.8	80.5
Rsa1.0_01884.1.g30552.t1	ref|NP_568746.1| ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana] gi|75170759|sp|Q9FI56.1|CLPC1_ARATH RecName: Full=Chaperone protein ClpC1, chloroplastic; AltName: Full=ATP-dependent Clp protease ATP-binding subunit ClpC homolog 1; AltName: Full=Casein lytic proteinase C1; AltName: Full=Protein DE-REGULATED CAO ACCUMULATION 1; AltName: Full=Protein IRON-RESCUED MUTANT 1; Flags: Precursor gi|9758239|dbj|BAB08738.1| ATP-dependent Clp protease, ATP-binding subunit [Arabidopsis thaliana] gi|20856956|gb|AAM26692.1| AT5g50920/K3K7_7 [Arabidopsis thaliana] gi|110742601|dbj|BAE99213.1| ATP-dependent Clp protease [Arabidopsis thaliana] gi|332008628|gb|AED96011.1| ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]	934	929	0	99.5	95.5	96.7	ATP-dependent Clp protease ATP-binding subunit ClpC	gbpln	Arabidopsis thaliana	AT5G50920.1 | Symbols: CLPC, ATHSP93-V, HSP93-V, DCA1, CLPC1 | CLPC homologue 1 | chr5:20715710-20719800 REVERSE LENGTH=929	934	929	0	99.5	95.5	96.7
Rsa1.0_01884.1.g30553.t1	ref|NP_199906.1| Histone 2A domain-containing protein [Arabidopsis thaliana] gi|9758240|dbj|BAB08739.1| unnamed protein product [Arabidopsis thaliana] gi|332008629|gb|AED96012.1| Histone 2A domain-containing protein [Arabidopsis thaliana]	140	242	1.00E-62	172.9	89.3	92.1	Histone 2A domain-containing protein	gbpln	Arabidopsis thaliana	AT5G50930.1 | Symbols: | Histone superfamily protein | chr5:20722069-20724317 FORWARD LENGTH=242	140	242	3.00E-65	172.9	89.3	92.1

Rsa1.0_01884.1.g30554.t1	gb|EOA25898.1| hypothetical protein CARUB_v10019277mg [Capsella rubella]	319	281	4.00E–86	88.1	52.7	63.3	hypothetical protein CARUB_v10019277mg	gbpln	Capsella rubella	AT3G53310.1 | Symbols: | AP2/B3–like transcriptional factor family protein | chr3:19766927–19768368 REVERSE LENGTH=286	319	286	9.00E–77	89.7	48.3	60.5
Rsa1.0_01884.1.g30555.t1	ref|XP_002864089.1| WD–40 repeat family protein [Arabidopsis lyrata subsp. lyrata] gi|297309924|gb|EFH40348.1| WD–40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	537	511	0	95.2	80.6	86.4	WD–40 repeat family protein	gbpln	Arabidopsis lyrata	AT5G50970.1 | Symbols: | transducin family protein / WD–40 repeat family protein | chr5:20736377–20739132 FORWARD LENGTH=512	537	512	0	95.3	78.8	83.2
Rsa1.0_01884.1.g30556.t1	ref|NP_568749.1| rubredoxin–like protein [Arabidopsis thaliana] gi|9758248|dbj|BAB08747.1| unnamed protein product [Arabidopsis thaliana] gi|15292669|gb|AAK92703.1| unknown protein [Arabidopsis thaliana] gi|19310697|gb|AAL85079.1| unknown protein [Arabidopsis thaliana] gi|21555410|gb|AAM63852.1| unknown [Arabidopsis thaliana] gi|332008638|gb|AED96021.1| rubredoxin–like protein [Arabidopsis thaliana]	159	154	1.00E–65	96.9	83.0	86.8	rubredoxin–like protein	gbpln	Arabidopsis thaliana	AT5G51010.1 | Symbols: | Rubredoxin–like superfamily protein | chr5:20744615–20745344 FORWARD LENGTH=154	159	154	5.00E–68	96.9	83.0	86.8
Rsa1.0_01884.1.g30557.t2	ref|XP_002865836.1| hypothetical protein ARALYDRAFT_918134 [Arabidopsis lyrata subsp. lyrata] gi|297311671|gb|EFH42095.1| hypothetical protein ARALYDRAFT_918134 [Arabidopsis lyrata subsp. lyrata]	124	269	1.00E–63	216.9	94.4	98.4	hypothetical protein ARALYDRAFT_918134	gbpln	Arabidopsis lyrata	AT5G51020.1 | Symbols: CRL | crumpled leaf | chr5:20745560–20747165 REVERSE LENGTH=269	124	269	2.00E–66	216.9	94.4	98.4
Rsa1.0_01885.1.g30558.t14	gb|EOA39218.1| hypothetical protein CARUB_v10012190mg [Capsella rubella]	458	545	2.00E–75	119.0	35.2	53.9	hypothetical protein CARUB_v10012190mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid–binding, OB–fold–like protein | chr1:19725483–19728007 FORWARD LENGTH=566	458	566	5.00E–68	123.6	33.6	57.0
Rsa1.0_01885.1.g30559.t4	gb|EEE51049.1| hypothetical protein OsJ_31709 [Oryza sativa Japonica Group]	498	357	6.00E–31	71.7	15.5	20.7	hypothetical protein OsJ_31709	gbpln	Oryza sativa	AT5G53670.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: sperm cell; Has 1807 Blast hits to 1807 proteins in 277 species: Archae – 0; Bacteria – 0; Metazoa – 736; Fungi – 347; Plants – 385; Viruses – 0; Other Eukaryotes – 339 (source: NCBI BLink). | chr5:21796997–21797731 FORWARD LENGTH=244	498	244	1.00E–18	49.0	11.4	16.9
Rsa1.0_01886.1.g30560.t1	gb|AAF79348.1|AC007887_7 F15O4.13 [Arabidopsis thaliana]	1185	1887	1.00E–162	159.2	28.7	39.5	F15O4.13	gbpln	Arabidopsis thaliana	AT1G47350.1 | Symbols: | F–box associated ubiquitination effector family protein | chr1:17358447–17360722 REVERSE LENGTH=528	1185	528	3.00E–29	44.6	5.7	7.3
Rsa1.0_01886.1.g30561.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1727	1213	0	70.2	26.9	39.3	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I–like superfamily protein | chr1:16528880–16531065 REVERSE LENGTH=626	1727	626	9.00E–81	36.2	9.3	14.4
Rsa1.0_01886.1.g30562.t1	ref|XP_002880635.1| hypothetical protein ARALYDRAFT_481345 [Arabidopsis lyrata subsp. lyrata] gi|297326474|gb|EFH56894.1| hypothetical protein ARALYDRAFT_481345 [Arabidopsis lyrata subsp. lyrata]	440	445	0	101.1	80.2	89.8	hypothetical protein ARALYDRAFT_481345	gbpln	Arabidopsis lyrata	AT2G24850.1 | Symbols: TAT3, TAT | tyrosine aminotransferase 3 | chr2:10583070–10585152 REVERSE LENGTH=445	440	445	0	101.1	80.0	90.2
Rsa1.0_01886.1.g30563.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01886.1.g30564.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01886.1.g30565.t1	gb|AAD25598.1| Mutator–like transposase [Arabidopsis thaliana]	239	616	9.00E–35	257.7	35.1	52.3	Mutator–like transposase	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01886.1.g30566.t1	ref|XP_002894278.1| hypothetical protein ARALYDRAFT_337235 [Arabidopsis lyrata subsp. lyrata] gi|297340120|gb|EFH70537.1| hypothetical protein ARALYDRAFT_337235 [Arabidopsis lyrata subsp. lyrata]	703	800	1.00E–101	113.8	34.4	52.2	hypothetical protein ARALYDRAFT_337235	gbpln	Arabidopsis lyrata	AT2G07190.1 | Symbols: | Domain of unknown function (DUF1985) | chr2:2987367–2988945 FORWARD LENGTH=452	703	452	5.00E–42	64.3	19.3	29.4
Rsa1.0_01886.1.g30567.t10	gb|ABD65117.1| hypothetical protein 31.t00030 [Brassica oleracea]	869	1471	0	169.3	55.1	63.1	hypothetical protein 31.t00030	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01886.1.g30568.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838–20266 [Arabidopsis thaliana]	563	1142	4.00E–60	202.8	21.8	28.4	reverse transcriptase, putative; 16838–20266	gbpln	Arabidopsis thaliana	AT2G22440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Ribonuclease H–like superfamily protein (TAIR:AT4G29090.1); Has 208 Blast hits to 191 proteins in 10 species: Archae – 0; Bacteria – 0; Metazoa – 0; Fungi – 0; Plants – 208; Viruses – 0; Other Eukaryotes – 0 (source: NCBI BLink). | chr2:9528910–9529917 FORWARD LENGTH=256	563	256	4.00E–26	45.5	14.4	19.0

Rsa1.0_01887.1.g30569.t1	gb|EOA15376.1| hypothetical protein CARUB_v10006095mg [Capsella rubella]	104	104	3.00E−51	100.0	94.2	96.2	hypothetical protein CARUB_v10006095mg	gbpln	Capsella rubella	AT4G34770.1 | Symbols: | SAUR−like auxin−responsive protein family | chr4:16591352−16591666 FORWARD LENGTH=104	104	104	4.00E−53	100.0	94.2	95.2
Rsa1.0_01887.1.g30570.t1	ref|XP_002890467.1| hypothetical protein ARALYDRAFT_472420 [Arabidopsis lyrata subsp. lyrata] gi|297336309|gb|EFH66726.1| hypothetical protein ARALYDRAFT_472420 [Arabidopsis lyrata subsp. lyrata]	142	240	2.00E−17	169.0	28.9	31.7	hypothetical protein ARALYDRAFT_472420	gbpln	Arabidopsis lyrata	AT1G21840.1 | Symbols: UREF | urease accessory protein F | chr1:7666859−7667581 FORWARD LENGTH=240	142	240	1.00E−18	169.0	26.8	30.3
Rsa1.0_01887.1.g30571.t1	ref|NP_195202.1| SAUR−like auxin−responsive protein 9 [Arabidopsis thaliana] gi|3096945|emb|CAA18855.1| putative auxin−regulated protein [Arabidopsis thaliana] gi|7270427|emb|CAB80193.1| putative auxin−regulated protein [Arabidopsis thaliana] gi|21536599|gb|AAM60931.1| putative auxin−regulated protein [Arabidopsis thaliana] gi|332661020|gb|AEE86420.1| SAUR−like auxin−responsive protein 9 [Arabidopsis thaliana]	107	107	2.00E−55	100.0	96.3	100.0	SAUR−like auxin−responsive protein 9	gbpln	Arabidopsis thaliana	AT4G34760.1 | Symbols: | SAUR−like auxin−responsive protein family | chr4:16582471−16582794 REVERSE LENGTH=107	107	107	4.00E−58	100.0	96.3	100.0
Rsa1.0_01887.1.g30572.t1	ref|NP_195201.1| SAUR−like auxin−responsive family protein [Arabidopsis thaliana] gi|334187163|ref|NP_001190915.1| SAUR−like auxin−responsive family protein [Arabidopsis thaliana] gi|3096944|emb|CAA18854.1| putative protein [Arabidopsis thaliana] gi|7270426|emb|CAB80192.1| putative protein [Arabidopsis thaliana] gi|332661018|gb|AEE86418.1| SAUR−like auxin−responsive family protein [Arabidopsis thaliana] gi|332661019|gb|AEE86419.1| SAUR−like auxin−responsive family protein [Arabidopsis thaliana]	151	150	2.00E−63	99.3	84.1	89.4	SAUR−like auxin−responsive family protein	gbpln	Arabidopsis thaliana	AT4G34750.2 | Symbols: | SAUR−like auxin−responsive protein family | chr4:16577566−16578018 FORWARD LENGTH=150	151	150	5.00E−66	99.3	84.1	89.4
Rsa1.0_01887.1.g30573.t1	gb|AAW28080.1| chloroplast amidophosphoribosyltransferase [Arabidopsis thaliana]	551	561	0	101.8	89.7	92.2	chloroplast amidophosphoribosyltransferase	gbpln	Arabidopsis thaliana	AT4G34740.1 | Symbols: ATASE2, CIA1, ATPURF2, ASE2 | GLN phosphoribosyl pyrophosphate amidotransferase 2 | chr4:16574894−16576579 REVERSE LENGTH=561	551	561	0	101.8	89.8	92.4
Rsa1.0_01887.1.g30574.t1	ref|NP_195199.2| ribosome−binding factor A [Arabidopsis thaliana] gi|78099793|sp|O65693.2|RBFA_ARATH RecName: Full=Probable ribosome−binding factor A, chloroplastic; Flags: Precursor gi|25082957|gb|AAN72022.1| putative protein [Arabidopsis thaliana] gi|30023650|gb|AAP13358.1| At4g34730 [Arabidopsis thaliana] gi|332661016|gb|AEE86416.1| ribosome−binding factor A [Arabidopsis thaliana]	240	215	1.00E−101	89.6	77.5	82.1	ribosome−binding factor A	gbpln	Arabidopsis thaliana	AT4G34730.1 | Symbols: | ribosome−binding factor A family protein | chr4:16570019−16571274 REVERSE LENGTH=215	240	215	1.00E−103	89.6	77.5	82.1
Rsa1.0_01887.1.g30575.t1	ref|XP_002313006.1| predicted protein [Populus trichocarpa] gi|222849414|gb|EEE86961.1| predicted protein [Populus trichocarpa]	164	207	6.00E−85	126.2	100.0	100.0	predicted protein	gbpln	Populus trichocarpa	AT4G34720.1 | Symbols: AVA−P1, VHA−C1, ATVHA−C1 | ATPase, F0/V0 complex, subunit C protein | chr4:16568223−16569165 REVERSE LENGTH=164	164	164	4.00E−87	100.0	100.0	100.0
Rsa1.0_01887.1.g30576.t1	gb|AAR08423.1| arginine decarboxylase 2 [Pringlea antiscorbutica]	369	711	1.00E−179	192.7	84.3	90.0	arginine decarboxylase 2	gbpln	Pringlea antiscorbutica	AT4G34710.2 | Symbols: ADC2, SPE2, ATADC2 | arginine decarboxylase 2 | chr4:16560315−16562450 REVERSE LENGTH=711	369	711	1.00E−180	192.7	81.6	89.7
Rsa1.0_01888.1.g30577.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	178	1611	9.00E−61	905.1	60.1	80.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01888.1.g30578.t1	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	529	1611	1.00E−107	304.5	37.6	49.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01888.1.g30579.t1	gb|AAC26234.1| contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]	570	940	1.00E−165	164.9	53.5	65.4	contains similarity to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01888.1.g30580.t1	gb|EOA38830.1| hypothetical protein CARUB_v10011156mg [Capsella rubella]	117	118	1.00E−51	100.9	82.1	94.0	hypothetical protein CARUB_v10011156mg	gbpln	Capsella rubella	AT1G45145.1 | Symbols: ATTRX5, ATH5, LIV1, TRX5 | thioredoxin H−type 5 | chr1:17075264−17076256 REVERSE LENGTH=118	117	118	4.00E−52	100.9	78.6	93.2
Rsa1.0_01888.1.g30581.t1	ref|XP_002891311.1| hypothetical protein ARALYDRAFT_473836 [Arabidopsis lyrata subsp. lyrata] gi|297337153|gb|EFH67570.1| hypothetical protein ARALYDRAFT_473836 [Arabidopsis lyrata subsp. lyrata]	730	732	0	100.3	92.2	96.6	hypothetical protein ARALYDRAFT_473836	gbpln	Arabidopsis lyrata	AT1G45130.1 | Symbols: BGAL5 | beta−galactosidase 5 | chr1:17065447−17069110 FORWARD LENGTH=732	730	732	0	100.3	91.2	96.6

Rsa1.0_01888.1.g30582.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	342	1274	8.00E-16	372.5	14.3	17.8	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01888.1.g30583.t1	ref|NP_175126.2| tetrapyrrole (corrin/porphyrin)methylase [Arabidopsis thaliana] gi|34365739|gb|AAQ65181.1| At1g45110 [Arabidopsis thaliana] gi|110738768|dbj|BAF01308.1| hypothetical protein [Arabidopsis thaliana] gi|332193960|gb|AEE32081.1| tetrapyrrole (corrin/porphyrin)methylase [Arabidopsis thaliana]	343	343	1.00E-169	100.0	87.5	91.3	tetrapyrrole (corrin/porphyrin)methylase	gbpln	Arabidopsis thaliana	AT1G45110.1 | Symbols: | Tetrapyrrole (Corrin/Porphyrin) Methylases | chr1:17052572-17054546 FORWARD LENGTH=343	343	343	1.00E-172	100.0	87.5	91.3
Rsa1.0_01889.1.g30584.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01889.1.g30585.t2	ref|NP_565284.3| NAC domain containing protein 35 [Arabidopsis thaliana] gi|20197337|gb|AAC78526.2| NAM (no apical meristem)-like protein [Arabidopsis thaliana] gi|330250488|gb|AEC05582.1| NAC domain containing protein 35 [Arabidopsis thaliana]	409	414	1.00E-176	101.2	83.6	90.2	NAC domain containing protein 35	gbpln	Arabidopsis thaliana	AT2G02450.2 | Symbols: ANAC034, ANAC035, LOV1, NAC035 | NAC domain containing protein 35 | chr2:648044-650649 FORWARD LENGTH=414	409	414	1.00E-179	101.2	83.6	90.2
Rsa1.0_01889.1.g30586.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01889.1.g30587.t1	ref|XP_002875130.1| hypothetical protein ARALYDRAFT_484163 [Arabidopsis lyrata subsp. lyrata] gi|297320968|gb|EFH51389.1| hypothetical protein ARALYDRAFT_484163 [Arabidopsis lyrata subsp. lyrata]	341	1222	1.00E-109	358.4	61.3	69.5	hypothetical protein ARALYDRAFT_484163	gbpln	Arabidopsis lyrata	AT2G02480.1 | Symbols: STI | AAA-type ATPase family protein | chr2:661093-665337 FORWARD LENGTH=1218	341	1218	1.00E-110	357.2	61.3	68.9
Rsa1.0_01889.1.g30588.t1	gb|EOA25631.1| hypothetical protein CARUB_v10018977mg [Capsella rubella]	303	303	2.33E-156	100.0	85.1	91.7	hypothetical protein CARUB_v10018977mg	gbpln	Capsella rubella	AT2G02500.1 | Symbols: ISPD, ATMEPCT, MCT | Nucleotide-diphospho-sugar transferases superfamily protein | chr2:671054-673124 REVERSE LENGTH=302	303	302	1.00E-138	99.7	84.8	90.4
Rsa1.0_01889.1.g30589.t1	gb|EOA25043.1| hypothetical protein CARUB_v10018349mg [Capsella rubella]	72	72	7.00E-32	100.0	94.4	95.8	hypothetical protein CARUB_v10018349mg	gbpln	Capsella rubella	AT2G02510.1 | Symbols: | NADH dehydrogenase (ubiquinone)s | chr2:673338-673556 FORWARD LENGTH=72	72	72	2.00E-34	100.0	93.1	95.8
Rsa1.0_01890.1.g30590.t1	ref|NP_191572.1| beta glucosidase 16 [Arabidopsis thaliana] gi|75311780|sp|Q9M1D0.1|BGL16_ARATH RecName: Full=Beta-glucosidase 16; Short=AtBGLU16; Flags: Precursor gi|7076766|emb|CAB75928.1| beta-glucosidase-like protein [Arabidopsis thaliana] gi|15028301|gb|AAK76627.1| putative beta-glucosidase [Arabidopsis thaliana] gi|21281079|gb|AAM44983.1| putative beta-glucosidase [Arabidopsis thaliana] gi|332646493|gb|AEE80014.1| beta glucosidase 16 [Arabidopsis thaliana]	505	514	0	101.8	71.5	79.2	beta glucosidase 16	gbpln	Arabidopsis thaliana	AT3G60130.1 | Symbols: BGLU16 | beta glucosidase 16 | chr3:22210343-22213650 FORWARD LENGTH=514	505	514	0	101.8	71.5	79.2
Rsa1.0_01890.1.g30591.t1	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	1726	1752	0	101.5	50.8	63.8	putative protein	gbpln	Arabidopsis thaliana	AT3G51690.1 | Symbols: | PIF1 helicase | chr3:19176731-19178107 REVERSE LENGTH=331	1726	331	2.00E-71	19.2	8.1	11.2
Rsa1.0_01890.1.g30592.t1	ref|XP_002876539.1| hypothetical protein ARALYDRAFT_486481 [Arabidopsis lyrata subsp. lyrata] gi|297322377|gb|EFH52798.1| hypothetical protein ARALYDRAFT_486481 [Arabidopsis lyrata subsp. lyrata]	579	579	0	100.0	86.4	92.6	hypothetical protein ARALYDRAFT_486481	gbpln	Arabidopsis lyrata	AT3G60140.1 | Symbols: DIN2, SRG2, BGLU30 | Glycosyl hydrolase superfamily protein | chr3:22216753-22220710 FORWARD LENGTH=577	579	577	0	99.7	86.2	92.1
Rsa1.0_01890.1.g30593.t1	ref|NP_001030907.1| protein binding / zinc ion binding protein [Arabidopsis thaliana] gi|98962061|gb|ABF59360.1| unknown protein [Arabidopsis thaliana] gi|332646611|gb|AEE80132.1| protein binding / zinc ion binding protein [Arabidopsis thaliana]	140	139	5.00E-36	99.3	62.1	75.7	protein binding / zinc ion binding protein	gbpln	Arabidopsis thaliana	AT3G60966.1 | Symbols: | RING/U-box superfamily protein | chr3:22552718-22553137 FORWARD LENGTH=139	140	139	1.00E-38	99.3	62.1	75.7

Rsa1.0_01891.1.g30594.t2	ref|NP_568494.1| sugar transporter ERD6-like 18 [Arabidopsis thaliana] gi|75332109|sp|Q94CI6.1|EDL18_ARATH RecName: Full=Sugar transporter ERD6-like 18; AltName: Full=Sugar-porter family protein 2 gi|14585701|gb|AAK11721.1| sugar-porter family protein 2 [Arabidopsis thaliana] gi|332006293|gb|AED93676.1| sugar transporter ERD6-like 18 [Arabidopsis thaliana]	478	478	0	100.0	80.1	90.8	sugar transporter ERD6-like 18	gbpln	Arabidopsis thaliana	AT5G27360.1 | Symbols: SFP2 | Major facilitator superfamily protein | chr5:9657119-9662425 FORWARD LENGTH=478	478	478	0	100.0	80.1	90.8
Rsa1.0_01891.1.g30595.t1	gb|AAD21778.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1694	1715	0	101.2	32.4	50.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1694	575	2.00E-70	33.9	9.7	15.0
Rsa1.0_01891.1.g30596.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01892.1.g30597.t1	ref|NP_196274.1| uncharacterized protein [Arabidopsis thaliana] gi|13430752|gb|AAK25998.1|AF360288_1 unknown protein [Arabidopsis thaliana] gi|10178112|dbj|BAB11405.1| unnamed protein product [Arabidopsis thaliana] gi|15293221|gb|AAK93721.1| unknown protein [Arabidopsis thaliana] gi|332003651|gb|AED91034.1| uncharacterized protein AT5G06560 [Arabidopsis thaliana]	110	518	4.00E-36	470.9	67.3	85.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G06560.1 | Symbols: | Protein of unknown function, DUF593 | chr5:2003678-2005543 REVERSE LENGTH=518	110	518	6.00E-39	470.9	67.3	85.5
Rsa1.0_01892.1.g30598.t1	ref|XP_002891137.1| hypothetical protein ARALYDRAFT_313975 [Arabidopsis lyrata subsp. lyrata] gi|297336979|gb|EFH67396.1| hypothetical protein ARALYDRAFT_313975 [Arabidopsis lyrata subsp. lyrata]	208	290	1.00E-29	139.4	35.6	43.3	hypothetical protein ARALYDRAFT_313975	gbpln	Arabidopsis lyrata	AT1G31530.1 | Symbols: | DNAse I-like superfamily protein | chr1:11281188-11282468 REVERSE LENGTH=283	208	283	3.00E-24	136.1	29.8	35.6
Rsa1.0_01892.1.g30599.t2	ref|XP_002891147.1| hypothetical protein ARALYDRAFT_473635 [Arabidopsis lyrata subsp. lyrata] gi|297336989|gb|EFH67406.1| hypothetical protein ARALYDRAFT_473635 [Arabidopsis lyrata subsp. lyrata]	557	522	0	93.7	72.4	79.9	hypothetical protein ARALYDRAFT_473635	gbpln	Arabidopsis lyrata	AT1G31410.1 | Symbols: | putrescine-binding periplasmic protein-related | chr1:11247094-11249345 REVERSE LENGTH=524	557	524	0	94.1	71.8	79.2
Rsa1.0_01892.1.g30600.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01892.1.g30601.t1	gb|ABD65028.1| hypothetical protein 26.t00082 [Brassica oleracea]	243	220	2.00E-13	90.5	15.6	20.2	hypothetical protein 26.t00082	gbpln	Brassica oleracea	AT1G14800.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:5099572-5102558 FORWARD LENGTH=384	243	384	5.00E-12	158.0	11.9	16.9
Rsa1.0_01893.1.g30602.t1	ref|XP_002890184.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297336026|gb|EFH66443.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	276	1685	2.00E-46	610.5	37.3	45.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G16710.2 | Symbols: HAC12 | histone acetyltransferase of the CBP family 12 | chr1:5714692-5721782 FORWARD LENGTH=1677	276	1677	8.00E-49	607.6	38.4	44.9
Rsa1.0_01893.1.g30603.t1	ref|XP_002890180.1| hypothetical protein ARALYDRAFT_471863 [Arabidopsis lyrata subsp. lyrata] gi|297336022|gb|EFH66439.1| hypothetical protein ARALYDRAFT_471863 [Arabidopsis lyrata subsp. lyrata]	702	391	0	55.7	44.4	49.7	hypothetical protein ARALYDRAFT_471863	gbpln	Arabidopsis lyrata	AT1G16670.1 | Symbols: | Protein kinase superfamily protein | chr1:5697846-5699492 FORWARD LENGTH=390	702	390	0	55.6	44.4	49.4
Rsa1.0_01893.1.g30604.t1	ref|XP_002513413.1| ribonucleic acid binding protein S1, putative [Ricinus communis] gi|223547321|gb|EEF48816.1| ribonucleic acid binding protein S1, putative [Ricinus communis]	365	423	3.00E-65	115.9	43.3	49.0	ribonucleic acid binding protein S1, putative	gbpln	Ricinus communis	AT1G16610.1 | Symbols: SR45, RNPS1 | arginine/serine-rich 45 | chr1:5675925-5678686 REVERSE LENGTH=414	365	414	1.00E-63	113.4	42.7	46.6
Rsa1.0_01893.1.g30605.t1	gb|EOA39738.1| hypothetical protein CARUB_v10008384mg [Capsella rubella]	764	761	0	99.6	77.1	87.3	hypothetical protein CARUB_v10008384mg	gbpln	Capsella rubella	AT1G78960.1 | Symbols: ATLUP2, LUP2 | lupeol synthase 2 | chr1:29696722-29701024 FORWARD LENGTH=763	764	763	0	99.9	70.2	82.1
Rsa1.0_01893.1.g30606.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01893.1.g30607.t2	gb|EOA39738.1| hypothetical protein CARUB_v10008384mg [Capsella rubella]	1369	761	0	55.6	44.3	49.2	hypothetical protein CARUB_v10008384mg	gbpln	Capsella rubella	AT1G78960.1 | Symbols: ATLUP2, LUP2 | lupeol synthase 2 | chr1:29696722-29701024 FORWARD LENGTH=763	1369	763	0	55.7	40.0	46.1
Rsa1.0_01893.1.g30608.t1	#	#	#	#	#	#	#	-	----	----	AT4G10200.1 | Symbols: | TTF-type zinc finger protein with HAT dimerisation domain | chr4:6353172-6355591 FORWARD LENGTH=733	141	733	1.00E-10	519.9	27.7	44.7
Rsa1.0_01894.1.g30609.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	289	1142	6.00E-79	395.2	49.1	64.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	289	626	5.00E-23	216.6	27.3	46.0

Rsa1.0_01894.1.g30610.t1	ref|NP_189038.1| putative F-box protein [Arabidopsis thaliana] gi|75273446|sp|Q9LIR1.1|FB182_ARATH RecName: Full=Putative F-box protein At3g23960 gi|9294665|dbj|BAB03014.1| unnamed protein product [Arabidopsis thaliana] gi|332643318|gb|AEE76839.1| putative F-box protein [Arabidopsis thaliana]	395	402	6.00E-73	101.8	44.3	61.0	putative F-box protein	gbpln	Arabidopsis thaliana	AT3G23960.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:8657736-8658944 FORWARD LENGTH=402	395	402	1.00E-75	101.8	44.3	61.0
Rsa1.0_01894.1.g30611.t1	dbj|BAB10503.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1546	1475	0	95.4	55.2	69.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1546	1262	1.00E-174	81.6	19.2	24.8
Rsa1.0_01894.1.g30612.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01894.1.g30613.t1	pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	1669	1333	0	79.9	36.7	48.8	RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1669	575	3.00E-97	34.5	11.4	16.6
Rsa1.0_01895.1.g30614.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	848	1486	0	175.2	40.1	55.4	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 703; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:7447690-7448403 REVERSE LENGTH=237	848	237	5.00E-28	27.9	6.8	12.3
Rsa1.0_01895.1.g30615.t1	ref|NP_178239.1| uncharacterized protein [Arabidopsis thaliana] gi|4262237|gb|AAD14530.1| predicted by genscan and genefinder [Arabidopsis thaliana] gi|17529142|gb|AAL38797.1| unknown protein [Arabidopsis thaliana] gi|21436241|gb|AAM51259.1| unknown protein [Arabidopsis thaliana] gi|49660101|gb|AAT68341.1| hypothetical protein At2g01300 [Arabidopsis thaliana] gi|60547691|gb|AAX23809.1| hypothetical protein At2g01300 [Arabidopsis thaliana] gi|330250336|gb|AEC05430.1| uncharacterized protein AT2G01300 [Arabidopsis thaliana]	155	156	4.00E-69	100.6	82.6	88.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G01300.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15010.1); Has 73 Blast hits to 73 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:151221-151691 REVERSE LENGTH=156	155	156	1.00E-71	100.6	82.6	88.4
Rsa1.0_01895.1.g30616.t1	ref|XP_002876738.1| 60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata] gi|297322576|gb|EFH52997.1| 60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata]	242	242	1.00E-129	100.0	95.0	96.3	60S ribosomal protein L7	gbpln	Arabidopsis lyrata	AT2G01250.1 | Symbols: | Ribosomal protein L30/L7 family protein | chr2:132943-134264 REVERSE LENGTH=242	242	242	1.00E-131	100.0	94.2	95.9
Rsa1.0_01895.1.g30617.t1	gb|AAM62991.1| unknown [Arabidopsis thaliana]	623	720	0	115.6	75.1	84.6	unknown	gbpln	Arabidopsis thaliana	AT2G01190.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr2:115023-117296 FORWARD LENGTH=720	623	720	0	115.6	74.6	84.3
Rsa1.0_01895.1.g30618.t1	ref|NP_565255.1| Lipid phosphate phosphatase 1 [Arabidopsis thaliana] gi|41017426|sp|Q9ZU49.2|LPP1_ARATH RecName: Full=Lipid phosphate phosphatase 1; Short=AtLPP1; AltName: Full=Phosphatidic acid phosphatase 1; Short=AtPAP1; AltName: Full=Prenyl diphosphate phosphatase gi|14020927|dbj|BAB47575.1| phosphatidic acid phosphatase [Arabidopsis thaliana] gi|20197584|gb|AAD14518.2| putative phosphatidic acid phosphatase [Arabidopsis thaliana] gi|330250318|gb|AEC05412.1| Lipid phosphate phosphatase 1 [Arabidopsis thaliana]	298	327	1.00E-157	109.7	87.9	94.3	Lipid phosphate phosphatase 1	gbpln	Arabidopsis thaliana	AT2G01180.1 | Symbols: ATPAP1, PAP1, LPP1, ATLPP1 | phosphatidic acid phosphatase 1 | chr2:107182-108555 REVERSE LENGTH=327	298	327	1.00E-160	109.7	87.9	94.3

Rsa1.0_01895.1.g30619.t1	ref|NP_565253.1| putative E3 ubiquitin-protein ligase RHA2B [Arabidopsis thaliana] gi|51316550|sp|Q9ZU51.2|RHA2B_ARATH RecName: Full=Probable E3 ubiquitin-protein ligase RHA2B; AltName: Full=RING-H2 zinc finger protein RHA2b gi|3790571|gb|AAC68672.1| RING-H2 finger protein RHA2b [Arabidopsis thaliana] gi|20197589|gb|AAD14516.2| RING-H2 finger protein RHA2b [Arabidopsis thaliana] gi|98960889|gb|ABF58928.1| At2g01150 [Arabidopsis thaliana] gi|330250313|gb|AEC05407.1| putative E3 ubiquitin-protein ligase RHA2B [Arabidopsis thaliana]	148	147	3.00E-44	99.3	66.9	75.7	putative E3 ubiquitin-protein ligase RHA2B	gbpln	Arabidopsis thaliana	AT2G01150.1 | Symbols: RHA2B | RING-H2 finger protein 2B | chr2:100703-101146 FORWARD LENGTH=147	148	147	8.00E-47	99.3	66.9	75.7
Rsa1.0_01895.1.g30620.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01895.1.g30621.t1	dbj|BAB11323.1| 4-nitrophenylphosphatase-like protein [Arabidopsis thaliana]	290	311	1.00E-157	107.2	91.7	96.6	4-nitrophenylphosphatase-like protein	gbpln	Arabidopsis thaliana	AT5G47760.1 | Symbols: PGLP2, ATPGLP2, ATPK5 | 2-phosphoglycolate phosphatase 2 | chr5:19343121-19344979 REVERSE LENGTH=301	290	301	1.00E-159	103.8	91.7	96.6
Rsa1.0_01895.1.g30622.t1	gb|EOA20136.1| hypothetical protein CARUB_v10000426mg [Capsella rubella]	218	649	2.00E-62	297.7	61.9	69.7	hypothetical protein CARUB_v10000426mg	gbpln	Capsella rubella	AT5G13820.1 | Symbols: TBP1, ATBP-1, ATBP1, ATTBP1, HPPBF-1 | telomeric DNA binding protein 1 | chr5:4461694-4464355 FORWARD LENGTH=640	218	640	5.00E-62	293.6	59.6	67.9
Rsa1.0_01896.1.g30623.t1	ref|NP_200425.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana] gi|75262628|sp|Q9FKT4.1|QKIL2_ARATH RecName: Full=KH domain-containing protein At5g56140; AltName: Full=Quaking-like protein 2 gi|9758634|dbj|BAB09296.1| RNA-binding protein-like [Arabidopsis thaliana] gi|24030184|gb|AAN41273.1| putative RNA-binding protein [Arabidopsis thaliana] gi|332009342|gb|AED96725.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana]	259	315	1.00E-116	121.6	80.7	86.1	RNA-binding KH domain-containing protein	gbpln	Arabidopsis thaliana	AT5G56140.1 | Symbols: | RNA-binding KH domain-containing protein | chr5:22725462-22727932 FORWARD LENGTH=315	259	315	1.00E-119	121.6	80.7	86.1
Rsa1.0_01896.1.g30624.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	192	390	2.00E-41	203.1	43.2	57.3	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	192	320	1.00E-27	166.7	32.3	45.3
Rsa1.0_01896.1.g30625.t1	dbj|BAJ33984.1| unnamed protein product [Thellungiella halophila]	679	699	0	102.9	98.2	99.4	unnamed protein product	----	----	AT5G56000.1 | Symbols: Hsp81.4, AtHsp90.4 | HEAT SHOCK PROTEIN 81.4 | chr5:22677602-22680067 REVERSE LENGTH=699	679	699	0	102.9	96.8	99.6
Rsa1.0_01896.1.g30626.t3	ref|XP_002864420.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310255|gb|EFH40679.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	327	343	1.00E-147	104.9	82.0	87.5	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G55970.2 | Symbols: | RING/U-box superfamily protein | chr5:22668019-22669312 FORWARD LENGTH=343	327	343	1.00E-145	104.9	85.9	93.3
Rsa1.0_01896.1.g30627.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1375	1307	0	95.1	57.6	72.9	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1375	1262	1.00E-104	91.8	14.3	22.2
Rsa1.0_01896.1.g30628.t1	dbj|BAJ33984.1| unnamed protein product [Thellungiella halophila]	688	699	0	101.6	98.0	99.1	unnamed protein product	----	----	AT5G56000.1 | Symbols: Hsp81.4, AtHsp90.4 | HEAT SHOCK PROTEIN 81.4 | chr5:22677602-22680067 REVERSE LENGTH=699	688	699	0	101.6	96.5	99.3
Rsa1.0_01896.1.g30629.t1	gb|AAM64789.1| unknown [Arabidopsis thaliana]	206	206	1.00E-108	100.0	94.2	96.1	unknown	gbpln	Arabidopsis thaliana	AT5G55940.1 | Symbols: emb2731 | Uncharacterised protein family (UPF0172) | chr5:22656256-22657894 REVERSE LENGTH=208	206	208	1.00E-110	101.0	94.2	96.1
Rsa1.0_01896.1.g30630.t1	ref|XP_002864417.1| ATOPT1 [Arabidopsis lyrata subsp. lyrata] gi|297310252|gb|EFH40676.1| ATOPT1 [Arabidopsis lyrata subsp. lyrata]	191	755	2.00E-65	395.3	67.5	71.2	ATOPT1	gbpln	Arabidopsis lyrata	AT5G55930.1 | Symbols: ATOPT1, OPT1 | oligopeptide transporter 1 | chr5:22652988-22655827 FORWARD LENGTH=755	191	755	9.00E-68	395.3	67.5	71.2
Rsa1.0_01896.1.g30631.t1	dbj|BAD95408.1| hypothetical protein [Arabidopsis thaliana]	441	478	1.00E-119	108.4	49.4	68.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	441	746	1.00E-102	169.2	42.4	56.9

Rsa1.0_01896.1.g30632.t1	ref|NP_200402.1| D6 protein kinase [Arabidopsis thaliana] gi|9758211|dbj|BAB08656.1| serine/threonine-specific protein kinase ATPK64 [Arabidopsis thaliana] gi|332009315|gb|AED96698.1| D6 protein kinase [Arabidopsis thaliana]	493	498	0	101.0	93.3	97.2	D6 protein kinase	gbpln	Arabidopsis thaliana	AT5G55910.1 | Symbols: D6PK | D6 protein kinase | chr5:22640055-22641634 REVERSE LENGTH=498	493	498	0	101.0	93.3	97.2
Rsa1.0_01896.1.g30633.t1	ref|NP_200397.1| uncharacterized protein [Arabidopsis thaliana] gi|75180671|sp|Q9LVQ4.1|Y5586_ARATH RecName: Full=WEB family protein At5g55860 gi|8843737|dbj|BAA97285.1| myosin heavy chain-like [Arabidopsis thaliana] gi|332009309|gb|AED96692.1| uncharacterized protein AT5G55860 [Arabidopsis thaliana]	651	649	0	99.7	83.4	91.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G55860.1 | Symbols: | Plant protein of unknown function (DUF827) | chr5:22610146-22612166 FORWARD LENGTH=649	651	649	0	99.7	83.4	91.1
Rsa1.0_01896.1.g30634.t1	gb|AAB86938.1| NOI protein [Arabidopsis thaliana] gi|8843736|dbj|BAA97284.1| NOI protein, nitrate-induced [Arabidopsis thaliana] gi|17529052|gb|AAL38736.1| putative NOI protein, nitrate-induced [Arabidopsis thaliana] gi|20465673|gb|AAM20305.1| putative nitrate-induced NOI protein [Arabidopsis thaliana]	82	79	2.00E-34	96.3	91.5	95.1	NOI protein	gbpln	Arabidopsis thaliana	AT5G55850.3 | Symbols: NOI | RPM1-interacting protein 4 (RIN4) family protein | chr5:22603617-22604850 FORWARD LENGTH=95	82	95	7.00E-36	115.9	89.0	92.7
Rsa1.0_01897.1.g30635.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01897.1.g30636.t1	ref|XP_002863555.1| minichromosome maintenance family protein [Arabidopsis lyrata subsp. lyrata] gi|297309390|gb|EFH39814.1| minichromosome maintenance family protein [Arabidopsis lyrata subsp. lyrata]	140	830	1.00E-16	592.9	30.7	35.7	minichromosome maintenance family protein	gbpln	Arabidopsis lyrata	AT5G44635.1 | Symbols: MCM6 | minichromosome maintenance (MCM2/3/5) family protein | chr5:18006431-18010542 REVERSE LENGTH=831	140	831	7.00E-19	593.6	30.7	35.7
Rsa1.0_01897.1.g30637.t1	ref|NP_191813.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|122214682|sp|Q3EAF8.1|PP294_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g62540, mitochondrial; Flags: Precursor gi|332646841|gb|AEE80362.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	61	599	8.00E-15	982.0	63.9	68.9	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G62540.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:23133514-23135313 REVERSE LENGTH=599	61	599	1.00E-17	982.0	63.9	68.9
Rsa1.0_01897.1.g30638.t1	ref|NP_198647.1| uncharacterized protein [Arabidopsis thaliana] gi|9758863|dbj|BAB09445.1| unnamed protein product [Arabidopsis thaliana] gi|60547909|gb|AAX23918.1| hypothetical protein At5g38310 [Arabidopsis thaliana] gi|71905569|gb|AAZ52762.1| hypothetical protein At5g38310 [Arabidopsis thaliana] gi|332006910|gb|AED94293.1| uncharacterized protein AT5G38310 [Arabidopsis thaliana]	186	188	1.00E-75	101.1	87.1	91.9	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G38310.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:15310681-15311247 REVERSE LENGTH=188	186	188	4.00E-78	101.1	87.1	91.9
Rsa1.0_01897.1.g30639.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	161	1142	4.00E-38	709.3	46.6	60.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	161	292	6.00E-15	181.4	27.3	40.4
Rsa1.0_01897.1.g30640.t1	dbj|BAB09444.1| unnamed protein product [Arabidopsis thaliana]	244	296	2.00E-81	121.3	76.2	83.6	unnamed protein product	gbpln	Arabidopsis thaliana	AT5G38300.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67035.2); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:15306022-15306813 FORWARD LENGTH=263	244	263	7.00E-84	107.8	76.2	83.6
Rsa1.0_01898.1.g30641.t1	dbj|BAJ33980.1| unnamed protein product [Thellungiella halophila]	612	622	0	101.6	92.3	95.8	unnamed protein product	----	----	AT5G22510.1 | Symbols: INV-E, At-A/N-InvE | alkaline/neutral invertase | chr5:7474974-7477479 REVERSE LENGTH=617	612	617	0	100.8	90.5	94.9

<table>
<tr><td>Rsa1.0_01898.1.g30642.t1</td><td>ref|XP_002879981.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297325820|gb|EFH56240.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>224</td><td>217</td><td>9.00E−22</td><td>96.9</td><td>26.8</td><td>29.9</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G42350.1 | Symbols: | RING/U−box superfamily protein | chr2:17639245−17639898 FORWARD LENGTH=217</td><td>224</td><td>217</td><td>2.00E−16</td><td>96.9</td><td>26.3</td><td>30.4</td></tr>
<tr><td>Rsa1.0_01898.1.g30643.t1</td><td>ref|XP_002874074.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297319911|gb|EFH50333.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>364</td><td>439</td><td>1.00E−155</td><td>120.6</td><td>80.8</td><td>84.3</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G22540.1 | Symbols: | Plant protein of unknown function (DUF247) | chr5:7481546−7482868 REVERSE LENGTH=440</td><td>364</td><td>440</td><td>1.00E−153</td><td>120.9</td><td>79.4</td><td>84.1</td></tr>
<tr><td>Rsa1.0_01898.1.g30644.t1</td><td>ref|XP_002874076.1| hypothetical protein ARALYDRAFT_489115 [Arabidopsis lyrata subsp. lyrata] gi|297319913|gb|EFH50335.1| hypothetical protein ARALYDRAFT_489115 [Arabidopsis lyrata subsp. lyrata]</td><td>478</td><td>507</td><td>1.00E−169</td><td>106.1</td><td>64.6</td><td>79.1</td><td>hypothetical protein ARALYDRAFT_489115</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G22560.1 | Symbols: | Plant protein of unknown function (DUF247) | chr5:7491544−7493097 REVERSE LENGTH=517</td><td>478</td><td>517</td><td>1.00E−171</td><td>108.2</td><td>65.1</td><td>79.3</td></tr>
<tr><td>Rsa1.0_01898.1.g30645.t1</td><td>ref|XP_002874078.1| WRKY DNA−binding protein 38 [Arabidopsis lyrata subsp. lyrata] gi|297319915|gb|EFH50337.1| WRKY DNA−binding protein 38 [Arabidopsis lyrata subsp. lyrata]</td><td>348</td><td>292</td><td>2.00E−96</td><td>83.9</td><td>52.9</td><td>64.4</td><td>WRKY DNA−binding protein 38</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G22570.1 | Symbols: WRKY38, ATWRKY38 | WRKY DNA−binding protein 38 | chr5:7495608−7496707 REVERSE LENGTH=289</td><td>348</td><td>289</td><td>1.00E−94</td><td>83.0</td><td>54.9</td><td>64.1</td></tr>
<tr><td>Rsa1.0_01898.1.g30646.t1</td><td>gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1466</td><td>1501</td><td>0</td><td>102.4</td><td>58.0</td><td>75.3</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262</td><td>1466</td><td>1262</td><td>1.00E−136</td><td>86.1</td><td>16.1</td><td>23.7</td></tr>
<tr><td>Rsa1.0_01898.1.g30647.t1</td><td>ref|NP_568422.1| stress responsive A/B Barrel domain−containing protein [Arabidopsis thaliana] gi|73921138|sp|Q9FK81.1|Y5258_ARATH RecName: Full=Uncharacterized protein At5g22580 gi|40889664|pdb|1RJJ|A Chain A, Solution Structure Of A Homodimeric Hypothetical Protein, At5g22580, A Structural Genomics Target From Arabidopsis Thaliana gi|40889665|pdb|1RJJ|B Chain B, Solution Structure Of A Homodimeric Hypothetical Protein, At5g22580, A Structural Genomics Target From Arabidopsis Thaliana gi|14190417|gb|AAK55689.1|AF378886_1 AT5g22580/MQJ16_12 [Arabidopsis thaliana] gi|9758664|dbj|BAB09130.1| unnamed protein product [Arabidopsis thaliana] gi|15215901|gb|AAK91494.1| AT5g22580/MQJ16_12 [Arabidopsis thaliana] gi|332005662|gb|AED93045.1| stress responsive A/B Barrel domain−containing protein [Arabidopsis thaliana]</td><td>110</td><td>111</td><td>9.00E−50</td><td>100.9</td><td>88.2</td><td>94.5</td><td>stress responsive A/B Barrel domain−containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G22580.1 | Symbols: | Stress responsive A/B Barrel Domain | chr5:7502709−7503137 FORWARD LENGTH=111</td><td>110</td><td>111</td><td>2.00E−52</td><td>100.9</td><td>88.2</td><td>94.5</td></tr>
<tr><td>Rsa1.0_01899.1.g30648.t1</td><td>ref|NP_567281.2| vacuolar protein sorting−associated protein 28−2 [Arabidopsis thaliana] gi|42572833|ref|NP_974513.1| vacuolar protein sorting−associated protein 28−2 [Arabidopsis thaliana] gi|152061129|sp|Q9S9T7.2|VP282_ARATH RecName: Full=Vacuolar protein sorting−associated protein 28 homolog 2 gi|50253482|gb|AAT71943.1| At4g05000 [Arabidopsis thaliana] gi|52421311|gb|AAU45225.1| At4g05000 [Arabidopsis thaliana] gi|110738465|dbj|BAF01158.1| hypothetical protein [Arabidopsis thaliana] gi|332657056|gb|AEE82456.1| vacuolar protein sorting−associated protein 28−2 [Arabidopsis thaliana] gi|332657057|gb|AEE82457.1| vacuolar protein sorting−associated protein 28−2 [Arabidopsis thaliana]</td><td>196</td><td>210</td><td>1.00E−107</td><td>107.1</td><td>95.4</td><td>99.0</td><td>vacuolar protein sorting−associated protein 28−2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G05000.2 | Symbols: VPS28−1 | Vacuolar protein sorting−associated protein VPS28 family protein | chr4:2563953−2564585 FORWARD LENGTH=210</td><td>196</td><td>210</td><td>1.00E−109</td><td>107.1</td><td>95.4</td><td>99.0</td></tr>
<tr><td>Rsa1.0_01899.1.g30649.t1</td><td>gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]</td><td>75</td><td>863</td><td>3.00E−14</td><td>1150.7</td><td>48.0</td><td>62.7</td><td>Ulp1 protease family protein</td><td>gbpln</td><td>Brassica oleracea</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01899.1.g30650.t1</td><td>ref|XP_002872727.1| hypothetical protein ARALYDRAFT_911767 [Arabidopsis lyrata subsp. lyrata] gi|297318564|gb|EFH48986.1| hypothetical protein ARALYDRAFT_911767 [Arabidopsis lyrata subsp. lyrata]</td><td>164</td><td>161</td><td>1.00E−49</td><td>98.2</td><td>64.6</td><td>77.4</td><td>hypothetical protein ARALYDRAFT_911767</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G05010.1 | Symbols: | F−box family protein | chr4:2567474−2568162 FORWARD LENGTH=164</td><td>164</td><td>164</td><td>4.00E−51</td><td>100.0</td><td>66.5</td><td>75.6</td></tr>
</table>

Rsa1.0_01899.1.g30651.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01899.1.g30652.t3	gb|EOA14700.1| hypothetical protein CARUB_v10027975mg [Capsella rubella]	264	766	5.00E-70	290.2	55.3	70.5	hypothetical protein CARUB_v10027975mg	gbpln	Capsella rubella	AT3G29765.1 | Symbols: | General transcription factor 2-related zinc finger protein | chr3:11595467-11597077 REVERSE LENGTH=536	264	536	2.00E-71	203.0	54.2	71.2
Rsa1.0_01899.1.g30653.t3	gb|EOA20192.1| hypothetical protein CARUB_v10000488mg, partial [Capsella rubella]	578	614	0	106.2	94.5	97.2	hypothetical protein CARUB_v10000488mg, partial	gbpln	Capsella rubella	AT4G05020.1 | Symbols: NDB2 | NAD(P)H dehydrogenase B2 | chr4:2572752-2576222 FORWARD LENGTH=582	578	582	0	100.7	94.3	96.9
Rsa1.0_01899.1.g30654.t1	gb|EOA21283.1| hypothetical protein CARUB_v10001636mg [Capsella rubella]	110	286	6.00E-34	260.0	73.6	80.9	hypothetical protein CARUB_v10001636mg	gbpln	Capsella rubella	AT4G05060.1 | Symbols: | PapD-like superfamily protein | chr4:2590245-2592000 REVERSE LENGTH=287	110	287	2.00E-32	260.9	75.5	82.7
Rsa1.0_01900.1.g30655.t1	gb|AAD32756.1| putative replication protein A1 [Arabidopsis thaliana]	185	458	4.00E-29	247.6	34.1	52.4	putative replication protein A1	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	185	566	2.00E-28	305.9	32.4	59.5
Rsa1.0_01900.1.g30656.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01900.1.g30657.t1	gb|ABD65633.1| hypothetical protein 23.t00050 [Brassica oleracea]	392	260	2.00E-68	66.3	38.0	43.9	hypothetical protein 23.t00050	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	392	302	8.00E-46	77.0	28.6	42.6
Rsa1.0_01900.1.g30658.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	346	442	1.00E-148	127.7	72.5	81.2	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	346	343	4.00E-36	99.1	18.2	23.4
Rsa1.0_01900.1.g30659.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01900.1.g30660.t1	dbj|BAJ34565.1| unnamed protein product [Thellungiella halophila]	149	323	4.00E-26	216.8	48.3	55.0	unnamed protein product	––––	––––	AT5G44080.1 | Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr5:17738787-17739734 REVERSE LENGTH=315	149	315	1.00E-22	211.4	44.3	57.0
Rsa1.0_01900.1.g30661.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01901.1.g30662.t1	gb|AAM82604.1|AF525305_2 putative AP endonuclease/reverse transcriptase [Brassica napus]	1146	1214	0	105.9	36.7	54.6	putative AP endonuclease/reverse transcriptase	gbpln	Brassica napus	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1146	626	7.00E-62	54.6	11.7	18.8
Rsa1.0_01901.1.g30663.t1	ref|NP_190443.1| Nodulin MtN3-like protein [Arabidopsis thaliana] gi|75206789|sp|Q9SMM5.1|SWT11_ARATH RecName: Full=Bidirectional sugar transporter SWEET11; Short=AtSWEET11 gi|13605688|gb|AAK32837.1|AF361825_1 AT3g48740/T8P19_250 [Arabidopsis thaliana] gi|16930411|gb|AAL31891.1|AF419559_1 AT3g48740/T8P19_250 [Arabidopsis thaliana] gi|6523105|emb|CAB62363.1| MTN3-like protein [Arabidopsis thaliana] gi|17979365|gb|AAL49908.1| putative MTN3 protein [Arabidopsis thaliana] gi|18700264|gb|AAL77742.1| AT3g48740/T8P19_250 [Arabidopsis thaliana] gi|20465523|gb|AAM20244.1| putative MTN3 protein [Arabidopsis thaliana] gi|332644930|gb|AEE78451.1| bidirectional sugar transporter SWEET11 [Arabidopsis thaliana]	282	289	1.00E-147	102.5	90.8	96.1	Nodulin MtN3-like protein	gbpln	Arabidopsis thaliana	AT3G48740.1 | Symbols: SWEET11, AtSWEET11 | Nodulin MtN3 family protein | chr3:18052814-18054663 REVERSE LENGTH=289	282	289	1.00E-149	102.5	90.8	96.1
Rsa1.0_01901.1.g30664.t1	ref|XP_002875921.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321759|gb|EFH52180.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	432	431	0	99.8	84.5	92.4	transferase family protein	gbpln	Arabidopsis lyrata	AT3G48720.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:18046527-18049295 FORWARD LENGTH=430	432	430	0	99.5	84.3	91.9
Rsa1.0_01902.1.g30665.t1	ref|XP_002864522.1| hypothetical protein ARALYDRAFT_495859 [Arabidopsis lyrata subsp. lyrata] gi|297310357|gb|EFH40781.1| hypothetical protein ARALYDRAFT_495859 [Arabidopsis lyrata subsp. lyrata]	207	207	1.00E-100	100.0	90.3	93.7	hypothetical protein ARALYDRAFT_495859	gbpln	Arabidopsis lyrata	AT5G57625.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr5:23337865-23338577 FORWARD LENGTH=207	207	207	1.00E-101	100.0	88.4	93.2
Rsa1.0_01902.1.g30666.t1	ref|XP_002864521.1| hypothetical protein ARALYDRAFT_918940 [Arabidopsis lyrata subsp. lyrata] gi|297310356|gb|EFH40780.1| hypothetical protein ARALYDRAFT_918940 [Arabidopsis lyrata subsp. lyrata]	331	335	1.00E-157	101.2	86.4	92.7	hypothetical protein ARALYDRAFT_918940	gbpln	Arabidopsis lyrata	AT5G57620.1 | Symbols: MYB36, AtMYB36 | myb domain protein 36 | chr5:23334904-23336388 FORWARD LENGTH=333	331	333	1.00E-157	100.6	85.8	91.2

Rsa1.0_01902.1.g30667.t1	ref|XP_002866219.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] gi|297312054|gb|EFH42478.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	615	646	0	105.0	83.9	89.8	calmodulin-binding protein	gbpln	Arabidopsis lyrata	AT5G57580.1 | Symbols: | Calmodulin-binding protein | chr5:23314994-23317683 REVERSE LENGTH=647	615	647	0	105.2	82.4	88.8
Rsa1.0_01902.1.g30668.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01902.1.g30669.t1	gb|EOA15046.1| hypothetical protein CARUB_v10028404mg [Capsella rubella]	347	361	1.00E-141	104.0	72.0	84.4	hypothetical protein CARUB_v10028404mg	gbpln	Capsella rubella	AT5G55440.1 | Symbols: | Protein of unknown function (DUF295) | chr5:22465718-22466989 FORWARD LENGTH=365	347	365	1.00E-127	105.2	68.0	80.4
Rsa1.0_01902.1.g30670.t1	gb|EOA15018.1| hypothetical protein CARUB_v10028369mg [Capsella rubella]	283	267	1.00E-129	94.3	76.7	84.8	hypothetical protein CARUB_v10028369mg	gbpln	Capsella rubella	AT5G57560.1 | Symbols: TCH4, XTH22 | Xyloglucan endotransglucosylase/hydrolase family protein | chr5:23307296-23308235 REVERSE LENGTH=284	283	284	1.00E-104	100.4	60.4	77.4
Rsa1.0_01903.1.g30671.t1	ref|XP_002866141.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297311976|gb|EFH42400.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	415	424	1.00E-142	102.2	64.6	76.6	F-box family protein	gbpln	Arabidopsis lyrata	AT5G56370.2 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:22836200-22837619 REVERSE LENGTH=421	415	421	1.00E-136	101.4	61.4	74.9
Rsa1.0_01903.1.g30672.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	315	390	2.00E-21	123.8	23.2	32.1	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT1G43730.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:16508723-16509784 REVERSE LENGTH=320	315	320	2.00E-21	101.6	19.0	30.8
Rsa1.0_01903.1.g30673.t4	gb|EOA37708.1| hypothetical protein CARUB_v10012428mg [Capsella rubella]	232	274	6.00E-37	118.1	32.3	37.5	hypothetical protein CARUB_v10012428mg	gbpln	Capsella rubella	AT1G08065.1 | Symbols: ATACA5, ACA5 | alpha carbonic anhydrase 5 | chr1:2511788-2513341 REVERSE LENGTH=277	232	277	7.00E-39	119.4	30.6	36.6
Rsa1.0_01903.1.g30674.t1	ref|NP_200443.1| expansin A14 [Arabidopsis thaliana] gi|20137960|sp|Q9FMA0.1|EXP14_ARATH RecName: Full=Expansin-A14; Short=AtEXPA14; AltName: Full=Alpha-expansin-14; Short=At-EXP14; Short=AtEx14; AltName: Full=Ath-ExpAlpha-1.5; Flags: Precursor gi|10177830|dbj|BAB11259.1| expansin [Arabidopsis thaliana] gi|110740362|dbj|BAF02076.1| Expansin [Arabidopsis thaliana] gi|332009365|gb|AED96748.1| expansin A14 [Arabidopsis thaliana]	253	255	1.00E-133	100.8	90.9	95.3	expansin A14	gbpln	Arabidopsis thaliana	AT5G56320.1 | Symbols: ATEXPA14, EXP14, ATEXP14, ATHEXP ALPHA 1.5, EXPA14 | expansin A14 | chr5:22808854-22809906 FORWARD LENGTH=255	253	255	1.00E-136	100.8	90.9	95.3
Rsa1.0_01903.1.g30675.t1	ref|NP_192885.1| putative cysteine-rich receptor-like protein kinase 30 [Arabidopsis thaliana] gi|75334864|sp|Q9LDT0.1|CRK30_ARATH RecName: Full=Putative cysteine-rich receptor-like protein kinase 30; Short=Cysteine-rich RLK30; Flags: Precursor gi|7267846|emb|CAB78189.1| serine/threonine kinase-like protein [Arabidopsis thaliana] gi|7321043|emb|CAB82151.1| serine/threonine kinase-like protein [Arabidopsis thaliana] gi|332657614|gb|AEE83014.1| putative cysteine-rich receptor-like protein kinase 30 [Arabidopsis thaliana]	630	700	0	111.1	73.3	83.2	putative cysteine-rich receptor-like protein kinase 30	gbpln	Arabidopsis thaliana	AT4G11460.1 | Symbols: CRK30 | cysteine-rich RLK (RECEPTOR-like protein kinase) 30 | chr4:6964468-6967093 FORWARD LENGTH=700	630	700	0	111.1	73.3	83.2
Rsa1.0_01904.1.g30676.t1	gb|EOA32324.1| hypothetical protein CARUB_v10015587mg [Capsella rubella]	103	102	5.00E-33	99.0	74.8	82.5	hypothetical protein CARUB_v10015587mg	gbpln	Capsella rubella	AT5G48485.1 | Symbols: DIR1 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:19646317-19646625 REVERSE LENGTH=102	103	102	5.00E-11	99.0	36.9	44.7
Rsa1.0_01904.1.g30677.t1	ref|XP_002885282.1| hypothetical protein ARALYDRAFT_318646 [Arabidopsis lyrata subsp. lyrata] gi|297331122|gb|EFH61541.1| hypothetical protein ARALYDRAFT_318646 [Arabidopsis lyrata subsp. lyrata]	340	375	0	110.3	89.7	95.6	hypothetical protein ARALYDRAFT_318646	gbpln	Arabidopsis lyrata	AT3G18850.4 | Symbols: LPAT5 | lysophosphatidyl acyltransferase 5 | chr3:6499529-6500840 REVERSE LENGTH=375	340	375	0	110.3	89.1	94.7
Rsa1.0_01904.1.g30678.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01904.1.g30679.t1	gb|EOA23244.1| hypothetical protein CARUB_v10017153mg [Capsella rubella]	481	473	1.00E-155	98.3	60.5	73.4	hypothetical protein CARUB_v10017153mg	gbpln	Capsella rubella	AT1G52650.1 | Symbols: | F-box/RNI-like superfamily protein | chr1:19610643-19612417 FORWARD LENGTH=507	481	507	1.00E-153	105.4	58.0	72.3

Rsa1.0_01904.1.g30680.t1	ref|NP_188520.2| uncharacterized protein [Arabidopsis thaliana] gi|332642644|gb|AEE76165.1| uncharacterized protein AT3G18900 [Arabidopsis thaliana]	538	524	0	97.4	80.5	87.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G18900.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF547 (InterPro:IPR006869); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF547 (TAIR:AT5G66600.3); Has 1466 Blast hits to 1426 proteins in 93 species: Archae - 0; Bacteria - 91; Metazoa - 23; Fungi - 0; Plants - 1310; Viruses - 0; Other Eukaryotes - 42 (source: NCBI BLink). | chr3:6517181-6519677 FORWARD LENGTH=524	538	524	0	97.4	80.5	87.7
Rsa1.0_01904.1.g30681.t6	emb|CAB40035.1| retrotransposon like protein [Arabidopsis thaliana] gi|7267767|emb|CAB81170.1| retrotransposon like protein [Arabidopsis thaliana]	2049	1515	0	73.9	40.6	51.3	retrotransposon like protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	2049	1262	1.00E-114	61.6	10.0	15.1
Rsa1.0_01904.1.g30682.t1	ref|NP_188525.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana] gi|9280312|dbj|BAB01691.1| En/Spm-like transposon protein-like [Arabidopsis thaliana] gi|26450378|dbj|BAC42304.1| unknown protein [Arabidopsis thaliana] gi|28973059|gb|AAO63854.1| unknown protein [Arabidopsis thaliana] gi|332642651|gb|AEE76172.1| transducin/WD40 domain-containing protein [Arabidopsis thaliana]	461	473	0	102.6	87.9	94.8	transducin/WD40 domain-containing protein	gbpln	Arabidopsis thaliana	AT3G18950.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:6536900-6538321 FORWARD LENGTH=473	461	473	0	102.6	87.9	94.8
Rsa1.0_01905.1.g30683.t1	ref|XP_002876718.1| hypothetical protein ARALYDRAFT_349389 [Arabidopsis lyrata subsp. lyrata] gi|297322556|gb|EFH52977.1| hypothetical protein ARALYDRAFT_349389 [Arabidopsis lyrata subsp. lyrata]	284	297	1.00E-124	104.6	80.6	88.0	hypothetical protein ARALYDRAFT_349389	gbpln	Arabidopsis lyrata	AT3G63350.1 | Symbols: AT-HSFA7B, HSFA7B | winged-helix DNA-binding transcription factor family protein | chr3:23399468-23400812 FORWARD LENGTH=282	284	282	1.00E-116	99.3	77.5	85.2
Rsa1.0_01905.1.g30684.t1	gb|EOA14273.1| hypothetical protein CARUB_v10027434mg, partial [Capsella rubella]	86	99	1.00E-20	115.1	62.8	75.6	hypothetical protein CARUB_v10027434mg, partial	gbpln	Capsella rubella	AT3G63360.1 | Symbols: | defensin-related | chr3:23401257-23401591 REVERSE LENGTH=85	86	85	3.00E-20	98.8	61.6	72.1
Rsa1.0_01905.1.g30685.t1	ref|XP_002878515.1| hypothetical protein ARALYDRAFT_324763 [Arabidopsis lyrata subsp. lyrata] gi|297324353|gb|EFH54774.1| hypothetical protein ARALYDRAFT_324763 [Arabidopsis lyrata subsp. lyrata]	190	173	6.00E-57	91.1	64.2	74.2	hypothetical protein ARALYDRAFT_324763	gbpln	Arabidopsis lyrata	AT3G63390.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:23411416-23411943 REVERSE LENGTH=175	190	175	2.00E-54	92.1	66.8	75.3
Rsa1.0_01905.1.g30686.t1	emb|CAB87795.1| putative protein [Arabidopsis thaliana]	89	138	6.00E-32	155.1	76.4	80.9	putative protein	gbpln	Arabidopsis thaliana	AT3G63420.2 | Symbols: AGG1, ATAGG1, GG1 | Ggamma-subunit 1 | chr3:23417383-23418405 FORWARD LENGTH=98	89	98	3.00E-34	110.1	76.4	80.9
Rsa1.0_01905.1.g30687.t1	ref|NP_191902.1| uncharacterized protein [Arabidopsis thaliana] gi|7573326|emb|CAB87796.1| putative protein [Arabidopsis thaliana] gi|190016004|gb|ACE62890.1| At3g63430 [Arabidopsis thaliana] gi|332646960|gb|AEE80481.1| uncharacterized protein AT3G63430 [Arabidopsis thaliana]	541	540	1.00E-135	99.8	59.9	67.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G63430.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74160.1); Has 135 Blast hits to 119 proteins in 22 species: Archae - 0; Bacteria - 2; Metazoa - 3; Fungi - 3; Plants - 119; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr3:23420414-23422201 FORWARD LENGTH=540	541	540	1.00E-138	99.8	59.9	67.8
Rsa1.0_01905.1.g30688.t1	ref|XP_002876723.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322561|gb|EFH52982.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	517	528	0	102.1	73.5	80.3	predicted protein	gbpln	Arabidopsis lyrata	AT3G63440.1 | Symbols: ATCKX6, CKX6, ATCKX7 | cytokinin oxidase/dehydrogenase 6 | chr3:23424291-23426265 FORWARD LENGTH=533	517	533	0	103.1	72.1	79.7
Rsa1.0_01905.1.g30689.t1	ref|XP_002881106.1| ferrochelatase II [Arabidopsis lyrata subsp. lyrata] gi|297326945|gb|EFH57365.1| ferrochelatase II [Arabidopsis lyrata subsp. lyrata]	501	512	0	102.2	82.6	85.2	ferrochelatase II	gbpln	Arabidopsis lyrata	AT2G30390.1 | Symbols: FC2, FC-II, ATFC-II | ferrochelatase 2 | chr2:12951242-12953985 REVERSE LENGTH=512	501	512	0	102.2	82.4	85.4
Rsa1.0_01906.1.g30690.t1	dbj|BAJ34368.1| unnamed protein product [Thellungiella halophila]	314	705	1.00E-144	224.5	85.4	88.2	unnamed protein product	----	----	AT5G52640.1 | Symbols: HSP81-1, ATHS83, HSP81.1, HSP83, ATHSP90.1, AtHsp90-1, HSP90.1 | heat shock protein 90.1 | chr5:21352542-21355147 FORWARD LENGTH=705	314	705	1.00E-145	224.5	78.0	80.9
Rsa1.0_01906.1.g30691.t4	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1224	1142	0	93.3	40.8	56.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1224	575	1.00E-52	47.0	8.8	14.4
Rsa1.0_01906.1.g30692.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01906.1.g30693.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01906.1.g30694.t1	gb|ADP20180.1| mutant gag-pol polyprotein [Pisum sativum]	649	1004	1.00E-138	154.7	42.8	61.3	mutant gag-pol polyprotein	gbpln	Pisum sativum	#	#	#	#	#	#	#
Rsa1.0_01907.1.g30695.t1	gb|EOA16073.1| hypothetical protein CARUB_v10004206mg [Capsella rubella]	505	763	1.00E-156	151.1	54.1	69.5	hypothetical protein CARUB_v10004206mg	gbpln	Capsella rubella	AT5G59660.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24035687-24039979 FORWARD LENGTH=852	505	852	7.00E-15	168.7	6.9	7.7
Rsa1.0_01907.1.g30696.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01907.1.g30697.t1	emb|CAA18194.1| putative protein [Arabidopsis thaliana] gi|7270001|emb|CAB79817.1| putative protein [Arabidopsis thaliana]	172	2895	5.00E-83	1683.1	93.0	96.5	putative protein	gbpln	Arabidopsis thaliana	AT2G24290.1 | Symbols: | Protein of unknown function (DUF1068) | chr2:10338779-10339859 FORWARD LENGTH=173	172	173	4.00E-84	100.6	86.0	93.0
Rsa1.0_01907.1.g30698.t1	ref|XP_002867317.1| hypothetical protein ARALYDRAFT_328615 [Arabidopsis lyrata subsp. lyrata] gi|297313153|gb|EFH43576.1| hypothetical protein ARALYDRAFT_328615 [Arabidopsis lyrata subsp. lyrata]	334	294	1.00E-163	88.0	80.8	85.6	hypothetical protein ARALYDRAFT_328615	gbpln	Arabidopsis lyrata	AT4G31020.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:15108832-15110079 REVERSE LENGTH=294	334	294	1.00E-165	88.0	80.5	85.6
Rsa1.0_01907.1.g30699.t1	ref|XP_002867316.1| hypothetical protein ARALYDRAFT_913365 [Arabidopsis lyrata subsp. lyrata] gi|297313152|gb|EFH43575.1| hypothetical protein ARALYDRAFT_913365 [Arabidopsis lyrata subsp. lyrata]	113	439	2.00E-11	388.5	43.4	49.6	hypothetical protein ARALYDRAFT_913365	gbpln	Arabidopsis lyrata	AT4G31040.1 | Symbols: | CemA-like proton extrusion protein-related | chr4:15111811-15113881 REVERSE LENGTH=438	113	438	5.00E-13	387.6	40.7	46.0
Rsa1.0_01907.1.g30700.t1	ref|NP_567866.1| Plastidial lipoyltransferase 2 [Arabidopsis thaliana] gi|75164691|sp|Q948J9.1|LIP2P_ARATH RecName: Full=Plastidial lipoyltransferase 2; AltName: Full=Lipoate-protein ligase 2p; AltName: Full=Lipoyl-[acyl-carrier-protein]-protein-N- lipoyltransferase 2p gi|15887052|dbj|BAB69449.1| lipoyltransferase [Arabidopsis thaliana] gi|62320326|dbj|BAD94675.1| putative protein [Arabidopsis thaliana] gi|90186250|gb|ABD91501.1| At4g31050 [Arabidopsis thaliana] gi|332660451|gb|AEE85851.1| Plastidial lipoyltransferase 2 [Arabidopsis thaliana]	473	278	1.00E-138	58.8	49.5	54.1	Plastidial lipoyltransferase 2	gbpln	Arabidopsis thaliana	AT4G31050.1 | Symbols: | Biotin/lipoate A/B protein ligase family | chr4:15114345-15115443 FORWARD LENGTH=278	473	278	1.00E-140	58.8	49.5	54.1
Rsa1.0_01907.1.g30701.t1	ref|XP_002869346.1| hypothetical protein ARALYDRAFT_491637 [Arabidopsis lyrata subsp. lyrata] gi|297315182|gb|EFH45605.1| hypothetical protein ARALYDRAFT_491637 [Arabidopsis lyrata subsp. lyrata]	421	407	1.00E-172	96.7	76.2	84.6	hypothetical protein ARALYDRAFT_491637	gbpln	Arabidopsis lyrata	AT4G31080.1 | Symbols: | Protein of unknown function (DUF2296) | chr4:15121186-15123072 FORWARD LENGTH=409	421	409	1.00E-174	97.1	77.0	85.3
Rsa1.0_01907.1.g30702.t1	gb|EOA18616.1| hypothetical protein CARUB_v10007189mg [Capsella rubella]	644	642	0	99.7	91.6	96.0	hypothetical protein CARUB_v10007189mg	gbpln	Capsella rubella	AT4G31120.1 | Symbols: SKB1, ATPRMT5 | SHK1 binding protein 1 | chr4:15132185-15136568 REVERSE LENGTH=642	644	642	0	99.7	90.5	95.5
Rsa1.0_01908.1.g30703.t2	ref|NP_850164.1| protein autophagy 9 [Arabidopsis thaliana] gi|19715618|gb|AAL91630.1| At2g31260/F16D14.10 [Arabidopsis thaliana] gi|19912149|dbj|BAB88386.1| autophagy 9 [Arabidopsis thaliana] gi|20466356|gb|AAM20495.1| unknown protein [Arabidopsis thaliana] gi|23198070|gb|AAN15562.1| unknown protein [Arabidopsis thaliana] gi|23463043|gb|AAN33191.1| At2g31260/F16D14.10 [Arabidopsis thaliana] gi|330253421|gb|AEC08515.1| protein autophagy 9 [Arabidopsis thaliana]	285	866	1.00E-112	303.9	77.5	81.1	protein autophagy 9	gbpln	Arabidopsis thaliana	AT2G31260.1 | Symbols: APG9, ATAPG9 | autophagy 9 (APG9) | chr2:13322291-13326293 REVERSE LENGTH=866	285	866	1.00E-115	303.9	77.5	81.1
Rsa1.0_01908.1.g30704.t1	ref|NP_180907.2| hydroxyproline-rich glycoprotein-like protein [Arabidopsis thaliana] gi|166227727|sp|O22799.2|Y2349_ARATH RecName: Full=Uncharacterized protein At2g33490 gi|330253748|gb|AEC08842.1| uncharacterized protein AT2G33490 [Arabidopsis thaliana]	624	623	0	99.8	82.5	90.1	hydroxyproline-rich glycoprotein-like protein	gbpln	Arabidopsis thaliana	AT2G33490.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr2:14183552-14187666 FORWARD LENGTH=623	624	623	0	99.8	82.5	90.1

Rsa1.0_01908.1.g30705.t1	ref|NP_180909.2| uncharacterized protein [Arabidopsis thaliana] gi|57222128|gb|AAW38971.1| At2g33510 [Arabidopsis thaliana] gi|330253752|gb|AEC08846.1| uncharacterized protein AT2G33510 [Arabidopsis thaliana]		194	189	8.00E-65	97.4	84.5	88.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G33510.1 | Symbols: | CONTAINS InterPro DOMAIN/s: WW/Rsp5/WWP (InterPro:IPR001202); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G28070.1); Has 3898 Blast hits to 1138 proteins in 179 species: Archae - 0; Bacteria - 40; Metazoa - 2353; Fungi - 242; Plants - 298; Viruses - 92; Other Eukaryotes - 873 (source: NCBI BLink). | chr2:14194195-14195473 FORWARD LENGTH=189		194	189	3.00E-67	97.4	84.5	88.7
Rsa1.0_01908.1.g30706.t1	#	#	#	#	#	#	#		–	----	----	AT5G08320.1 | Symbols: | CONTAINS InterPro DOMAIN/s: E2F-associated phosphoprotein, C-terminal (InterPro:IPR019370); Has 149 Blast hits to 149 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 79; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 35 (source: NCBI BLink). | chr5:2677153-2678603 FORWARD LENGTH=150		88	150	2.00E-11	170.5	38.6	44.3
Rsa1.0_01908.1.g30707.t1	ref|NP_850213.1| gt-2-related protein [Arabidopsis thaliana] gi|17529158|gb|AAL38805.1| unknown protein [Arabidopsis thaliana] gi|20465851|gb|AAM20030.1| unknown protein [Arabidopsis thaliana] gi|330253757|gb|AEC08851.1| gt-2-related protein [Arabidopsis thaliana]		323	314	1.00E-128	97.2	80.2	87.0	gt-2-related protein	gbpln	Arabidopsis thaliana	AT2G33550.1 | Symbols: | Homeodomain-like superfamily protein | chr2:14210180-14211487 REVERSE LENGTH=314		323	314	1.00E-131	97.2	80.2	87.0
Rsa1.0_01908.1.g30708.t1	ref|XP_002881289.1| hypothetical protein ARALYDRAFT_482302 [Arabidopsis lyrata subsp. lyrata] gi|297327128|gb|EFH57548.1| hypothetical protein ARALYDRAFT_482302 [Arabidopsis lyrata subsp. lyrata]		378	394	1.00E-180	104.2	82.3	89.9	hypothetical protein ARALYDRAFT_482302	gbpln	Arabidopsis lyrata	AT2G33560.1 | Symbols: BUBR1 | BUB1-related (BUB1: budding uninhibited by benzymidazol 1) | chr2:14213810-14215918 REVERSE LENGTH=395		378	395	1.00E-175	104.5	82.8	90.5
Rsa1.0_01908.1.g30709.t1	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#	
Rsa1.0_01908.1.g30710.t1	ref|NP_180916.1| protein kinase family protein [Arabidopsis thaliana] gi|75318032|sp|O22808.1|LYK5_ARATH RecName: Full=Protein LYK5; AltName: Full=LysM domain receptor-like kinase 5; AltName: Full=LysM-containing receptor-like kinase 5; Flags: Precursor gi|13877683|gb|AAK43919.1|AF370600_1 putative protein kinase [Arabidopsis thaliana] gi|2459440|gb|AAB80675.1| putative protein kinase [Arabidopsis thaliana] gi|209529791|gb|ACI49790.1| At2g33580 [Arabidopsis thaliana] gi|330253761|gb|AEC08855.1| protein LYK5 [Arabidopsis thaliana]		666	664	0	99.7	79.1	86.8	protein kinase family protein	gbpln	Arabidopsis thaliana	AT2G33580.1 | Symbols: | Protein kinase superfamily protein | chr2:14219848-14221842 REVERSE LENGTH=664		666	664	0	99.7	79.1	86.8
Rsa1.0_01909.1.g30711.t1	ref|NP_568890.2| Subtilase family protein [Arabidopsis thaliana] gi|9759217|dbj|BAB09629.1| subtilisin-like serine protease [Arabidopsis thaliana] gi|30793835|gb|AAP40370.1| putative subtilisin serine protease [Arabidopsis thaliana] gi|30794052|gb|AAP40471.1| putative subtilisin [Arabidopsis thaliana] gi|110739211|dbj|BAF01520.1| subtilisin like protein [Arabidopsis thaliana] gi|332009726|gb|AED97109.1| Subtilase family protein [Arabidopsis thaliana]		254	713	1.00E-58	280.7	44.5	47.6	Subtilase family protein	gbpln	Arabidopsis thaliana	AT5G58840.1 | Symbols: | Subtilase family protein | chr5:23759043-23761947 FORWARD LENGTH=713		254	713	4.00E-61	280.7	44.5	47.6
Rsa1.0_01909.1.g30712.t1	ref|XP_002878345.1| hypothetical protein ARALYDRAFT_486540 [Arabidopsis lyrata subsp. lyrata] gi|297324183|gb|EFH54604.1| hypothetical protein ARALYDRAFT_486540 [Arabidopsis lyrata subsp. lyrata]		231	245	2.00E-98	106.1	79.2	85.7	hypothetical protein ARALYDRAFT_486540	gbpln	Arabidopsis lyrata	AT3G60670.1 | Symbols: | PLATZ transcription factor family protein | chr3:22424695-22426074 REVERSE LENGTH=245		231	245	1.00E-100	106.1	80.1	86.1
Rsa1.0_01909.1.g30713.t1	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#	
Rsa1.0_01909.1.g30714.t1	ref|XP_002876575.1| hypothetical protein ARALYDRAFT_907600 [Arabidopsis lyrata subsp. lyrata] gi|297322413|gb|EFH52834.1| hypothetical protein ARALYDRAFT_907600 [Arabidopsis lyrata subsp. lyrata]		464	494	0	106.5	80.0	87.7	hypothetical protein ARALYDRAFT_907600	gbpln	Arabidopsis lyrata	AT3G60680.1 | Symbols: | Plant protein of unknown function (DUF641) | chr3:22430246-22431745 FORWARD LENGTH=499		464	499	0	107.5	78.2	86.2

Rsa1.0_01909.1.g30715.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1537	1142	0	74.3	36.6	48.6	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1537	575	1.00E-98	37.4	13.1	20.0
Rsa1.0_01909.1.g30716.t1	dbj|BAJ34476.1| unnamed protein product [Thellungiella halophila]	172	172	9.00E-81	100.0	87.2	93.6	unnamed protein product	----	----	AT3G60690.1 | Symbols: | SAUR-like auxin-responsive protein family | chr3:22435262-22435774 FORWARD LENGTH=170	172	170	2.00E-79	98.8	82.6	89.5
Rsa1.0_01909.1.g30717.t1	ref|XP_002876578.1| hypothetical protein ARALYDRAFT_486544 [Arabidopsis lyrata subsp. lyrata] gi|297322416|gb|EFH52837.1| hypothetical protein ARALYDRAFT_486544 [Arabidopsis lyrata subsp. lyrata]	278	287	1.00E-132	103.2	84.9	87.1	hypothetical protein ARALYDRAFT_486544	gbpln	Arabidopsis lyrata	AT3G60720.1 | Symbols: PDLP8 | plasmodesmata-located protein 8 | chr3:22442035-22443608 FORWARD LENGTH=279	278	279	1.00E-133	100.4	85.6	87.8
Rsa1.0_01909.1.g30718.t1	ref|NP_191632.2| putative pectinesterase/pectinesterase inhibitor 36 [Arabidopsis thaliana] gi|332278140|sp|Q84R10.2|PME36_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 36; Includes: RecName: Full=Pectinesterase inhibitor 36; AltName: Full=Pectin methylesterase inhibitor 36; Includes: RecName: Full=Pectinesterase 36; Short=PE 36; AltName: Full=Pectin methylesterase 36; Short=AtPME36; Flags: Precursor gi|332646580|gb|AEE80101.1| putative pectinesterase/pectinesterase inhibitor 36 [Arabidopsis thaliana]	523	519	0	99.2	83.6	89.5	putative pectinesterase/pectinesterase inhibitor 36	gbpln	Arabidopsis thaliana	AT3G60730.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:22444955-22447226 FORWARD LENGTH=519	523	519	0	99.2	83.6	89.5
Rsa1.0_01910.1.g30719.t1	ref|XP_002883376.1| hypothetical protein ARALYDRAFT_898758 [Arabidopsis lyrata subsp. lyrata] gi|297329216|gb|EFH59635.1| hypothetical protein ARALYDRAFT_898758 [Arabidopsis lyrata subsp. lyrata]	580	623	0	107.4	64.1	77.4	hypothetical protein ARALYDRAFT_898758	gbpln	Arabidopsis lyrata	AT3G22760.1 | Symbols: SOL1 | Tesmin/TSO1-like CXC domain-containing protein | chr3:8044622-8047381 FORWARD LENGTH=609	580	609	0	105.0	62.2	76.6
Rsa1.0_01910.1.g30720.t1	gb|AAF27433.1|AF206324_1 putative DNA binding protein [Arabidopsis thaliana] gi|7767425|gb|AAF69124.1|AF204059_1 CXC domain protein TSO1 [Arabidopsis thaliana]	684	695	0	101.6	71.9	81.1	putative DNA binding protein	gbpln	Arabidopsis thaliana	AT3G22780.1 | Symbols: TSO1, ATTSO1 | Tesmin/TSO1-like CXC domain-containing protein | chr3:8048927-8052058 FORWARD LENGTH=695	684	695	0	101.6	71.9	81.1
Rsa1.0_01910.1.g30721.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	578	1231	1.00E-155	213.0	48.8	66.4	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	578	575	7.00E-84	99.5	27.5	45.2
Rsa1.0_01910.1.g30722.t1	ref|NP_188918.2| kinase interacting KIP1-like protein [Arabidopsis thaliana] gi|9279697|dbj|BAB01254.1| centromere protein [Arabidopsis thaliana] gi|332643156|gb|AEE76677.1| kinase interacting KIP1-like protein [Arabidopsis thaliana]	1769	1728	0	97.7	81.7	89.9	kinase interacting KIP1-like protein	gbpln	Arabidopsis thaliana	AT3G22790.1 | Symbols: | Kinase interacting (KIP1-like) family protein | chr3:8052446-8057888 REVERSE LENGTH=1728	1769	1728	0	97.7	81.7	89.9
Rsa1.0_01911.1.g30723.t1	gb|EOA14377.1| hypothetical protein CARUB_v10027563mg [Capsella rubella]	293	320	5.00E-97	109.2	61.8	76.8	hypothetical protein CARUB_v10027563mg	gbpln	Capsella rubella	AT5G56080.1 | Symbols: ATNAS2, NAS2 | nicotianamine synthase 2 | chr5:22711402-22712364 REVERSE LENGTH=320	293	320	3.00E-99	109.2	61.8	77.1
Rsa1.0_01911.1.g30724.t1	gb|EOA34991.1| hypothetical protein CARUB_v10020083mg [Capsella rubella]	295	556	1.00E-116	188.5	74.2	84.1	hypothetical protein CARUB_v10020083mg	gbpln	Capsella rubella	AT1G72140.1 | Symbols: | Major facilitator superfamily protein | chr1:27141877-27144346 FORWARD LENGTH=555	295	555	1.00E-113	188.1	74.2	81.4
Rsa1.0_01911.1.g30725.t1	ref|XP_002887417.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297333258|gb|EFH63676.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	217	555	1.00E-92	255.8	76.0	85.7	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G72140.1 | Symbols: | Major facilitator superfamily protein | chr1:27141877-27144346 FORWARD LENGTH=555	217	555	1.00E-93	255.8	74.7	85.3
Rsa1.0_01911.1.g30726.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	164	1142	4.00E-21	696.3	39.0	56.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	164	292	5.00E-11	178.0	27.4	46.3
Rsa1.0_01911.1.g30727.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30728.t2	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	1009	954	1.00E-114	94.5	24.9	29.6	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30729.t1	gb|AAD15474.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	639	1466	2.00E-53	229.4	21.3	34.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30730.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30731.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30732.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01912.1.g30733.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30734.t1	gb|AAD30632.1|AC006085_5 Hypothetical protein [Arabidopsis thaliana]	520	1295	7.00E-35	249.0	16.5	23.7	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30735.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30736.t1	dbj|BAB02259.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	840	777	2.00E-32	92.5	13.2	19.0	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30737.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01912.1.g30738.t1	gb|AAC26241.1| F9D12.15 gene product [Arabidopsis thaliana]	191	850	5.00E-29	445.0	40.8	64.9	F9D12.15 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01913.1.g30739.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01913.1.g30740.t1	ref|XP_002872492.1| ATSPS4F [Arabidopsis lyrata subsp. lyrata] gi|297318329|gb|EFH48751.1| ATSPS4F [Arabidopsis lyrata subsp. lyrata]	1015	1051	0	103.5	92.1	95.2	ATSPS4F	gbpln	Arabidopsis lyrata	AT4G10120.2 | Symbols: ATSPS4F | Sucrose-phosphate synthase family protein | chr4:6315033-6319785 FORWARD LENGTH=1050	1015	1050	0	103.4	91.4	95.3
Rsa1.0_01913.1.g30741.t1	ref|XP_002874611.1| hypothetical protein ARALYDRAFT_327188 [Arabidopsis lyrata subsp. lyrata] gi|297320448|gb|EFH50870.1| hypothetical protein ARALYDRAFT_327188 [Arabidopsis lyrata subsp. lyrata]	183	180	9.00E-73	98.4	78.1	87.4	hypothetical protein ARALYDRAFT_327188	gbpln	Arabidopsis lyrata	AT4G10130.1 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr4:6320959-6321483 REVERSE LENGTH=174	183	174	2.00E-74	95.1	78.1	87.4
Rsa1.0_01913.1.g30742.t1	gb|EOA21642.1| hypothetical protein CARUB_v10002060mg [Capsella rubella]	185	184	4.00E-88	99.5	87.0	93.5	hypothetical protein CARUB_v10002060mg	gbpln	Capsella rubella	AT4G10140.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2062 (InterPro:IPR018639); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G33490.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:6322538-6324421 FORWARD LENGTH=183	185	183	1.00E-89	98.9	87.6	91.4
Rsa1.0_01913.1.g30743.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	301	1142	6.00E-76	379.4	47.5	61.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	301	575	2.00E-33	191.0	30.6	49.2
Rsa1.0_01913.1.g30744.t1	ref|XP_002872495.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297318332|gb|EFH48754.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	236	237	1.00E-92	100.4	72.9	82.2	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G10150.1 | Symbols: | RING/U-box superfamily protein | chr4:6328136-6329558 FORWARD LENGTH=236	236	236	1.00E-94	100.0	70.8	80.9
Rsa1.0_01914.1.g30745.t1	ref|NP_188217.4| mismatched DNA binding / ATP binding protein [Arabidopsis thaliana] gi|332642232|gb|AEE75753.1| mismatched DNA binding / ATP binding protein [Arabidopsis thaliana]	499	490	2.00E-76	98.2	31.7	42.5	mismatched DNA binding / ATP binding protein	gbpln	Arabidopsis thaliana	AT3G15960.1 | Symbols: | mismatched DNA binding;ATP binding | chr3:5404000-5406461 REVERSE LENGTH=490	499	490	4.00E-79	98.2	31.7	42.5
Rsa1.0_01914.1.g30746.t12	ref|XP_002885121.1| hypothetical protein ARALYDRAFT_479052 [Arabidopsis lyrata subsp. lyrata] gi|297330961|gb|EFH61380.1| hypothetical protein ARALYDRAFT_479052 [Arabidopsis lyrata subsp. lyrata]	978	918	0	93.9	88.1	91.3	hypothetical protein ARALYDRAFT_479052	gbpln	Arabidopsis lyrata	AT3G15980.3 | Symbols: | Coatomer, beta' subunit | chr3:5412015-5418313 REVERSE LENGTH=918	978	918	0	93.9	88.0	91.5
Rsa1.0_01914.1.g30747.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01914.1.g30748.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_01914.1.g30749.t1	ref|XP_002882970.1| SULTR3_4 [Arabidopsis lyrata subsp. lyrata] gi|297328810|gb|EFH59229.1| SULTR3_4 [Arabidopsis lyrata subsp. lyrata]	660	655	0	99.2	92.1	96.4	SULTR3_4	gbpln	Arabidopsis lyrata	AT3G15990.1 | Symbols: SULTR3;4 | sulfate transporter 3;4 | chr3:5427081-5430679 FORWARD LENGTH=653	660	653	0	98.9	92.0	96.4
Rsa1.0_01914.1.g30750.t1	ref|NP_188221.2| MAR-binding filament-like protein 1 [Arabidopsis thaliana] gi|83304464|sp|Q9LW85.2|MFP1_ARATH RecName: Full=MAR-binding filament-like protein 1 gi|30794108|gb|AAP40496.1| putative myosin heavy chain [Arabidopsis thaliana] gi|332642240|gb|AEE75761.1| MAR-binding filament-like protein 1 [Arabidopsis thaliana]	633	726	0	114.7	71.2	84.7	MAR-binding filament-like protein 1	gbpln	Arabidopsis thaliana	AT3G16000.1 | Symbols: MFP1 | MAR binding filament-like protein 1 | chr3:5431041-5433613 REVERSE LENGTH=726	633	726	0	114.7	71.2	84.7
Rsa1.0_01915.1.g30751.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#

Rsa1.0_01915.1.g30752.t1	gb|EOA32275.1| hypothetical protein CARUB_v10015536mg [Capsella rubella]	303	483	9.00E-20	159.4	19.1	25.1	hypothetical protein CARUB_v10015536mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01915.1.g30753.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01915.1.g30754.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01915.1.g30755.t1	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1115	1838	0	164.8	56.8	71.8	F5M15.26	gbpln	Arabidopsis thaliana	ATMG00860.1 | Symbols: ORF158 | DNA/RNA polymerases superfamily protein | chrM:235916-236392 FORWARD LENGTH=158	1115	158	4.00E-11	14.2	3.3	5.7
Rsa1.0_01915.1.g30756.t10	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	623	1142	2.00E-55	183.3	21.5	29.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	623	575	1.00E-17	92.3	7.9	11.9
Rsa1.0_01916.1.g30757.t1	gb|EOA40077.1| hypothetical protein CARUB_v10008773mg [Capsella rubella]	440	546	3.00E-95	124.1	56.1	68.2	hypothetical protein CARUB_v10008773mg	gbpln	Capsella rubella	AT1G24160.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: guard cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G70100.3). | chr1:8553669-8555830 REVERSE LENGTH=540	440	540	2.00E-62	122.7	31.1	35.7
Rsa1.0_01916.1.g30758.t1	#	#	#	#	#	#	#	-	----	----	AT1G24145.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:8541040-8541616 FORWARD LENGTH=128	83	128	3.00E-11	154.2	45.8	49.4
Rsa1.0_01916.1.g30759.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01916.1.g30760.t1	ref|XP_002886063.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331903|gb|EFH62322.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	138	158	3.00E-22	114.5	50.0	61.6	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01916.1.g30761.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01916.1.g30762.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01916.1.g30763.t1	gb|ABD64968.1| hypothetical protein 25.t00005 [Brassica oleracea]	279	299	1.00E-74	107.2	55.9	68.5	hypothetical protein 25.t00005	gbpln	Brassica oleracea	AT5G47590.1 | Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297945-19299099 REVERSE LENGTH=264	279	264	2.00E-72	94.6	51.6	66.7
Rsa1.0_01916.1.g30764.t1	ref|NP_173811.1| polyketide cyclase/dehydrase and lipid transport-like protein [Arabidopsis thaliana] gi|88953601|sp|P0C0B0.1|Y1400_ARATH RecName: Full=Uncharacterized protein At1g24000 gi|332192343|gb|AEE30464.1| uncharacterized protein AT1G24000 [Arabidopsis thaliana]	122	122	3.00E-17	100.0	41.8	58.2	polyketide cyclase/dehydrase and lipid transport-like protein	gbpln	Arabidopsis thaliana	AT1G24000.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr1:8496057-8496526 REVERSE LENGTH=122	122	122	5.00E-20	100.0	41.8	58.2
Rsa1.0_01917.1.g30765.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01917.1.g30766.t1	ref|XP_002881123.1| hypothetical protein ARALYDRAFT_902059 [Arabidopsis lyrata subsp. lyrata] gi|297326962|gb|EFH57382.1| hypothetical protein ARALYDRAFT_902059 [Arabidopsis lyrata subsp. lyrata]	281	262	1.00E-128	93.2	81.5	86.8	hypothetical protein ARALYDRAFT_902059	gbpln	Arabidopsis lyrata	AT2G30670.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:13069313-13070904 REVERSE LENGTH=262	281	262	1.00E-128	93.2	80.4	85.8
Rsa1.0_01917.1.g30767.t1	ref|NP_201395.1| 3-hydroxyisobutyryl-CoA hydrolase 1 [Arabidopsis thaliana] gi|75263928|sp|Q9LKJ1.1|HIBC1_ARATH RecName: Full=3-hydroxyisobutyryl-CoA hydrolase 1; AltName: Full=CoA-thioester hydrolase CHY1 gi|8572760|gb|AAF77193.1|AF276301_1 CoA-thioester hydrolase CHY1 [Arabidopsis thaliana] gi|9759578|dbj|BAB11141.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana] gi|24030391|gb|AAN41356.1| putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana] gi|332010745|gb|AED98128.1| 3-hydroxyisobutyryl-CoA hydrolase 1 [Arabidopsis thaliana]	394	378	1.00E-165	95.9	76.4	83.0	3-hydroxyisobutyryl-CoA hydrolase 1	gbpln	Arabidopsis thaliana	AT5G65940.1 | Symbols: CHY1 | beta-hydroxyisobutyryl-CoA hydrolase 1 | chr5:26376830-26379161 REVERSE LENGTH=378	394	378	1.00E-168	95.9	76.4	83.0

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<tr><td>Rsa1.0_01917.1.g30768.t1</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>2229</td><td>1274</td><td>0</td><td>57.2</td><td>27.9</td><td>37.7</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G65940.1 | Symbols: CHY1 | beta-hydroxyisobutyryl-CoA hydrolase 1 | chr5:26376830-26379161 REVERSE LENGTH=378</td><td>2229</td><td>378</td><td>1.00E-164</td><td>17.0</td><td>12.8</td><td>14.3</td></tr>
<tr><td>Rsa1.0_01917.1.g30769.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01917.1.g30770.t1</td><td>gb|EOA28988.1| hypothetical protein CARUB_v10025247mg [Capsella rubella]</td><td>888</td><td>876</td><td>0</td><td>98.6</td><td>65.5</td><td>76.8</td><td>hypothetical protein CARUB_v10025247mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G25010.1 | Symbols: AtRLP41, RLP41 | receptor like protein 41 | chr3:9110103-9112748 REVERSE LENGTH=881</td><td>888</td><td>881</td><td>0</td><td>99.2</td><td>64.8</td><td>76.0</td></tr>
<tr><td>Rsa1.0_01918.1.g30771.t1</td><td>emb|CAN82844.1| hypothetical protein VITISV_005761 [Vitis vinifera]</td><td>1211</td><td>896</td><td>2.00E-90</td><td>74.0</td><td>19.5</td><td>28.2</td><td>hypothetical protein VITISV_005761</td><td>gbpln</td><td>Vitis vinifera</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01918.1.g30772.t1</td><td>emb|CAN83791.1| hypothetical protein VITISV_031681 [Vitis vinifera]</td><td>642</td><td>968</td><td>2.00E-53</td><td>150.8</td><td>16.8</td><td>21.5</td><td>hypothetical protein VITISV_031681</td><td>gbpln</td><td>Vitis vinifera</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01918.1.g30773.t3</td><td>gb|AAD22283.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1069</td><td>1787</td><td>1.00E-119</td><td>167.2</td><td>23.8</td><td>31.1</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01918.1.g30774.t2</td><td>gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]</td><td>2030</td><td>1024</td><td>6.00E-77</td><td>50.4</td><td>8.0</td><td>10.6</td><td>F5J5.16</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01918.1.g30775.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01919.1.g30776.t1</td><td>ref|XP_002864633.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297310468|gb|EFH40892.1| oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata]</td><td>454</td><td>457</td><td>0</td><td>100.7</td><td>92.7</td><td>97.4</td><td>oxysterol-binding family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G59420.1 | Symbols: ORP3C | OSBP(oxysterol binding protein)-related protein 3C | chr5:23961731-23964623 FORWARD LENGTH=457</td><td>454</td><td>457</td><td>0</td><td>100.7</td><td>92.5</td><td>97.4</td></tr>
<tr><td>Rsa1.0_01919.1.g30777.t1</td><td>ref|XP_002864632.1| hypothetical protein ARALYDRAFT_496067 [Arabidopsis lyrata subsp. lyrata] gi|297310467|gb|EFH40891.1| hypothetical protein ARALYDRAFT_496067 [Arabidopsis lyrata subsp. lyrata]</td><td>297</td><td>299</td><td>1.00E-150</td><td>100.7</td><td>90.9</td><td>93.6</td><td>hypothetical protein ARALYDRAFT_496067</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G59400.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: PGR5-like B (TAIR:AT4G11960.1); Has 97 Blast hits to 97 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 97; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:23957756-23959518 FORWARD LENGTH=299</td><td>297</td><td>299</td><td>1.00E-152</td><td>100.7</td><td>89.9</td><td>94.6</td></tr>
<tr><td>Rsa1.0_01919.1.g30778.t1</td><td>gb|EOA15150.1| hypothetical protein CARUB_v10028526mg [Capsella rubella]</td><td>551</td><td>561</td><td>0</td><td>101.8</td><td>68.4</td><td>79.7</td><td>hypothetical protein CARUB_v10028526mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G59390.1 | Symbols: | XH/XS domain-containing protein | chr5:23954934-23957151 FORWARD LENGTH=561</td><td>551</td><td>561</td><td>0</td><td>101.8</td><td>67.2</td><td>79.7</td></tr>
<tr><td>Rsa1.0_01919.1.g30779.t1</td><td>ref|XP_002864630.1| hypothetical protein ARALYDRAFT_919168 [Arabidopsis lyrata subsp. lyrata] gi|297310465|gb|EFH40889.1| hypothetical protein ARALYDRAFT_919168 [Arabidopsis lyrata subsp. lyrata]</td><td>176</td><td>233</td><td>5.00E-60</td><td>132.4</td><td>72.7</td><td>81.3</td><td>hypothetical protein ARALYDRAFT_919168</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G59380.1 | Symbols: MBD6, ATMBD6 | methyl-CPG-binding domain 6 | chr5:23952321-23953485 FORWARD LENGTH=225</td><td>176</td><td>225</td><td>5.00E-58</td><td>127.8</td><td>68.8</td><td>79.0</td></tr>
<tr><td>Rsa1.0_01919.1.g30780.t1</td><td>gb|EOA27690.1| hypothetical protein CARUB_v10023843mg, partial [Capsella rubella]</td><td>260</td><td>271</td><td>4.00E-37</td><td>104.2</td><td>37.3</td><td>50.8</td><td>hypothetical protein CARUB_v10023843mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303</td><td>260</td><td>303</td><td>2.00E-28</td><td>116.5</td><td>32.7</td><td>49.6</td></tr>
<tr><td>Rsa1.0_01919.1.g30781.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01920.1.g30782.t1</td><td>ref|NP_172626.1| cytochrome P450, family 77, subfamily B, polypeptide 1 [Arabidopsis thaliana] gi|4835797|gb|AAD30263.1|AC007296_24 Strong similarity to gb|U61231 cytochrome P450 from Arabidopsis thaliana and is a member of the PF|00067 Cytochrome P450 family. ESTs gb|Z30775 and gb|Z30776 come from this gene [Arabidopsis thaliana] gi|21537013|gb|AAM61354.1| putative cytochrome P450 [Arabidopsis thaliana] gi|110738537|dbj|BAF01194.1| cytochrome P450 like protein [Arabidopsis thaliana] gi|332190637|gb|AEE28758.1| cytochrome P450, family 77, subfamily B, polypeptide 1 [Arabidopsis thaliana]</td><td>510</td><td>510</td><td>0</td><td>100.0</td><td>93.9</td><td>96.9</td><td>cytochrome P450, family 77, subfamily B, polypeptide 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G11600.1 | Symbols: CYP77B1 | cytochrome P450, family 77, subfamily B, polypeptide 1 | chr1:3902090-3903622 FORWARD LENGTH=510</td><td>510</td><td>510</td><td>0</td><td>100.0</td><td>93.9</td><td>96.9</td></tr>
<tr><td>Rsa1.0_01920.1.g30783.t1</td><td>ref|XP_002889877.1| hypothetical protein ARALYDRAFT_471294 [Arabidopsis lyrata subsp. lyrata] gi|297335719|gb|EFH66136.1| hypothetical protein ARALYDRAFT_471294 [Arabidopsis lyrata subsp. lyrata]</td><td>464</td><td>465</td><td>0</td><td>100.2</td><td>87.7</td><td>91.6</td><td>hypothetical protein ARALYDRAFT_471294</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G28237.1 | Symbols: | Pyridoxal-5'-phosphate-dependent enzyme family protein | chr5:10207477-10213542 REVERSE LENGTH=465</td><td>464</td><td>465</td><td>0</td><td>100.2</td><td>88.1</td><td>90.9</td></tr>
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Rsa1.0_01920.1.g30784.t1	ref|XP_002889875.1| hypothetical protein ARALYDRAFT_888463 [Arabidopsis lyrata subsp. lyrata] gi|297335717|gb|EFH66134.1| hypothetical protein ARALYDRAFT_888463 [Arabidopsis lyrata subsp. lyrata]	89	89	1.00E-39	100.0	89.9	97.8	hypothetical protein ARALYDRAFT_888463	gbpln	Arabidopsis lyrata	AT1G11572.1 | Symbols: | Plant thionin family protein | chr1:3884455-3884724 FORWARD LENGTH=89	89	89	2.00E-39	100.0	83.1	95.5
Rsa1.0_01920.1.g30785.t1	ref|XP_002889874.1| T23J18.22 [Arabidopsis lyrata subsp. lyrata] gi|297335716|gb|EFH66133.1| T23J18.22 [Arabidopsis lyrata subsp. lyrata]	441	469	1.00E-165	106.3	70.3	80.5	T23J18.22	gbpln	Arabidopsis lyrata	AT1G61790.1 | Symbols: | Oligosaccharyltransferase complex/magnesium transporter family protein | chr1:22814390-22815430 FORWARD LENGTH=346	441	346	1.00E-103	78.5	42.0	53.1
Rsa1.0_01920.1.g30786.t2	sp|Q39290.1|RPAB5_BRANA RecName: Full=DNA-directed RNA polymerases I, II, and III subunit RPABC5; Short=RNA polymerases I, II, and III subunit ABC5; AltName: Full=ABC10; AltName: Full=DNA-directed RNA polymerase III subunit L; AltName: Full=RPB10 homolog gi|533690|gb|AAA21279.1| RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]	71	71	1.00E-33	100.0	100.0	100.0	RecName: Full=DNA-directed RNA polymerases I, II, and III subunit RPABC5; Short=RNA polymerases I, II, and III subunit ABC5; AltName: Full=ABC10; AltName: Full=DNA-directed RNA polymerase III subunit L; AltName: Full=RPB10 homolog gi|533690|gb|AAA21279.1| RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139	gbpln	Brassica napus	AT1G11475.1 | Symbols: NRPB10, NRPD10, NRPE10 | RNA polymerases N / 8 kDa subunit | chr1:3862520-3863805 FORWARD LENGTH=71	71	71	2.00E-35	100.0	97.2	97.2
Rsa1.0_01920.1.g30787.t1	ref|XP_002889868.1| hypothetical protein ARALYDRAFT_471281 [Arabidopsis lyrata subsp. lyrata] gi|297335710|gb|EFH66127.1| hypothetical protein ARALYDRAFT_471281 [Arabidopsis lyrata subsp. lyrata]	321	357	1.00E-108	111.2	75.1	86.3	hypothetical protein ARALYDRAFT_471281	gbpln	Arabidopsis lyrata	AT1G11440.1 | Symbols: | BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT3G29075.1); Has 19337 Blast hits to 8589 proteins in 488 species: Archae - 26; Bacteria - 641; Metazoa - 7852; Fungi - 2167; Plants - 955; Viruses - 616; Other Eukaryotes - 7080 (source: NCBI BLink). | chr1:3849418-3850509 FORWARD LENGTH=363	321	363	1.00E-107	113.1	74.5	83.5
Rsa1.0_01920.1.g30788.t1	ref|NP_172610.1| putative plastid developmental protein DAG [Arabidopsis thaliana] gi|6554182|gb|AAF16628.1|AC011661_6 T23J18.10 [Arabidopsis thaliana] gi|26450103|dbj|BAC42171.1| unknown protein [Arabidopsis thaliana] gi|28827520|gb|AAO50604.1| putative DAG protein [Arabidopsis thaliana] gi|332190614|gb|AEE28735.1| putative plastid developmental protein DAG [Arabidopsis thaliana]	236	232	1.00E-104	98.3	81.8	85.6	putative plastid developmental protein DAG	gbpln	Arabidopsis thaliana	AT1G11430.1 | Symbols: | plastid developmental protein DAG, putative | chr1:3847273-3848938 FORWARD LENGTH=232	236	232	1.00E-107	98.3	81.8	85.6
Rsa1.0_01920.1.g30789.t1	ref|XP_002889866.1| hypothetical protein ARALYDRAFT_471279 [Arabidopsis lyrata subsp. lyrata] gi|297335708|gb|EFH66125.1| hypothetical protein ARALYDRAFT_471279 [Arabidopsis lyrata subsp. lyrata]	867	842	0	97.1	66.9	77.7	hypothetical protein ARALYDRAFT_471279	gbpln	Arabidopsis lyrata	AT1G11340.1 | Symbols: | S-locus lectin protein kinase family protein | chr1:3814116-3817420 REVERSE LENGTH=901	867	901	0	103.9	66.9	76.9
Rsa1.0_01920.1.g30790.t1	gb|EOA38471.1| hypothetical protein CARUB_v10010225mg [Capsella rubella] gi|482574285|gb|EOA38472.1| hypothetical protein CARUB_v10010225mg [Capsella rubella]	135	227	3.00E-14	168.1	29.6	30.4	hypothetical protein CARUB_v10010225mg	gbpln	Capsella rubella	AT1G11400.3 | Symbols: PYM | partner of Y14-MAGO | chr1:3838777-3839978 FORWARD LENGTH=204	135	204	8.00E-15	151.1	27.4	28.1
Rsa1.0_01920.1.g30791.t1	gb|EOA34077.1| hypothetical protein CARUB_v10021578mg [Capsella rubella]	635	319	3.00E-45	50.2	15.3	17.5	hypothetical protein CARUB_v10021578mg	gbpln	Capsella rubella	AT1G69030.1 | Symbols: | BSD domain-containing protein | chr1:25947429-25949262 REVERSE LENGTH=317	635	317	1.00E-45	49.9	14.3	16.4
Rsa1.0_01920.1.g30792.t1	dbj|BAJ33728.1| unnamed protein product [Thellungiella halophila]	148	148	6.00E-68	100.0	84.5	91.9	unnamed protein product	----	----	AT1G60950.1 | Symbols: FED A, ATFD2 | 2Fe-2S ferredoxin-like superfamily protein | chr1:22444565-22445011 FORWARD LENGTH=148	148	148	3.00E-70	100.0	85.8	90.5
Rsa1.0_01920.1.g30793.t3	gb|EOA38064.1| hypothetical protein CARUB_v10009533mg [Capsella rubella]	359	362	0	100.8	95.5	97.5	hypothetical protein CARUB_v10009533mg	gbpln	Capsella rubella	AT1G10940.1 | Symbols: ASK1, SNRK2-4, SNRK2.4, SRK2A | Protein kinase superfamily protein | chr1:3656050-3658170 REVERSE LENGTH=363	359	363	0	101.1	94.7	96.9

Rsa1.0_01920.1.g30794.t7	gb|AAF99864.1|AC015448_14 Putative protein kinase [Arabidopsis thaliana]	961	875	0	91.1	56.4	64.7	Putative protein kinase	gbpln	Arabidopsis thaliana	AT1G51805.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19221187-19225590 REVERSE LENGTH=884	961	884	0	92.0	56.0	64.5
Rsa1.0_01920.1.g30795.t1	gb|EOA37769.1| hypothetical protein CARUB_v10012627mg [Capsella rubella]	324	337	1.00E-180	104.0	95.4	96.9	hypothetical protein CARUB_v10012627mg	gbpln	Capsella rubella	AT1G10840.1 | Symbols: TIF3H1 | translation initiation factor 3 subunit H1 | chr1:3607885-3610299 REVERSE LENGTH=337	324	337	0	104.0	95.1	96.9
Rsa1.0_01920.1.g30796.t1	ref|NP_973807.1| uncharacterized protein [Arabidopsis thaliana] gi|332190529|gb|AEE28650.1| uncharacterized protein AT1G10820 [Arabidopsis thaliana]	272	258	6.00E-95	94.9	68.4	71.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G10820.2 | Symbols: | Protein of unknown function (DUF3755) | chr1:3601437-3604650 REVERSE LENGTH=258	272	258	2.00E-97	94.9	68.4	71.7
Rsa1.0_01921.1.g30797.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01921.1.g30798.t1	ref|NP_193233.5| fanconi anemia group D2 protein [Arabidopsis thaliana] gi|332658132|gb|AEE83532.1| uncharacterized protein AT4G14970 [Arabidopsis thaliana]	1446	1489	0	103.0	83.5	89.6	fanconi anemia group D2 protein	gbpln	Arabidopsis thaliana	AT4G14970.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 6 growth stages; Has 257 Blast hits to 164 proteins in 70 species: Archae - 0; Bacteria - 4; Metazoa - 189; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink). | chr4:8553854-8561664 FORWARD LENGTH=1489	1446	1489	0	103.0	83.5	89.6
Rsa1.0_01921.1.g30799.t1	emb|CAA79989.2| myrosinase, thioglucoside glucohydrolase [Brassica napus]	526	527	0	100.2	90.3	92.6	myrosinase, thioglucoside glucohydrolase	gbpln	Brassica napus	AT5G26000.1 | Symbols: TGG1, BGLU38 | thioglucoside glucohydrolase 1 | chr5:9079678-9082347 REVERSE LENGTH=541	526	541	0	102.9	69.6	77.8
Rsa1.0_01921.1.g30800.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01921.1.g30801.t2	gb|ABD65053.1| S-locus linked 3 (SLL3) protein, putative [Brassica oleracea]	294	462	7.00E-32	157.1	32.7	39.5	S-locus linked 3 (SLL3) protein, putative	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	294	1262	1.00E-11	429.3	11.2	16.3
Rsa1.0_01921.1.g30802.t1	ref|NP_191452.2| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75244411|sp|Q8GXW6.1|FBL59_ARATH RecName: Full=F-box/LRR-repeat protein At3g58930 gi|26451056|dbj|BAC42633.1| unknown protein [Arabidopsis thaliana] gi|28951059|gb|AAO63453.1| At3g58930 [Arabidopsis thaliana] gi|332646330|gb|AEE79851.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	477	482	1.00E-104	101.0	49.9	62.3	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT3G58930.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21778381-21780014 REVERSE LENGTH=482	477	482	1.00E-107	101.0	49.9	62.3
Rsa1.0_01921.1.g30803.t1	ref|NP_193193.2| acylaminoacyl-peptidase [Arabidopsis thaliana] gi|60729672|pir||JC8016 acylaminoacyl-peptidase (EC 3.4.19.1) - Arabidopsis thaliana gi|30466066|dbj|BAC76411.1| acylamino acid-releasing enzyme [Arabidopsis thaliana] gi|332658061|gb|AEE83461.1| acylamino acid-releasing enzyme [Arabidopsis thaliana]	758	764	0	100.8	85.0	92.9	acylaminoacyl-peptidase	gbpln	Arabidopsis thaliana	AT4G14570.1 | Symbols: | acylaminoacyl-peptidase-related | chr4:8362586-8366525 FORWARD LENGTH=764	758	764	0	100.8	85.0	92.9
Rsa1.0_01921.1.g30804.t1	gb|EOA36221.1| hypothetical protein CARUB_v10010170mg [Capsella rubella]	234	236	1.00E-111	100.9	84.2	92.7	hypothetical protein CARUB_v10010170mg	gbpln	Capsella rubella	AT1G24735.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:8757977-8759448 FORWARD LENGTH=240	234	240	1.00E-108	102.6	78.6	89.3
Rsa1.0_01921.1.g30805.t1	gb|EOA16652.1| hypothetical protein CARUB_v10004845mg [Capsella rubella]	400	434	0	108.5	88.5	92.3	hypothetical protein CARUB_v10004845mg	gbpln	Capsella rubella	AT4G14500.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:8334391-8337022 FORWARD LENGTH=433	400	433	0	108.3	90.5	94.0
Rsa1.0_01921.1.g30806.t1	ref|XP_002877762.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297323600|gb|EFH54021.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	428	426	1.00E-142	99.5	61.7	74.8	F-box family protein	gbpln	Arabidopsis lyrata	AT3G50710.1 | Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr3:18845199-18846673 REVERSE LENGTH=427	428	427	1.00E-142	99.8	60.7	74.3
Rsa1.0_01922.1.g30807.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	1385	1342	0	96.9	50.5	67.5	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1385	1262	7.00E-86	91.1	13.1	19.8

Rsa1.0_01922.1.g30808.t1	ref|XP_002888334.1| hypothetical protein ARALYDRAFT_893919 [Arabidopsis lyrata subsp. lyrata] gi|297334175|gb|EFH64593.1| hypothetical protein ARALYDRAFT_893919 [Arabidopsis lyrata subsp. lyrata]	131	126	9.00E-56	96.2	84.0	90.1	hypothetical protein ARALYDRAFT_893919	gbpln	Arabidopsis lyrata	AT1G65290.1 | Symbols: mtACP2 | mitochondrial acyl carrier protein 2 | chr1:24249088-24250366 REVERSE LENGTH=126	131	126	5.00E-58	96.2	82.4	90.1
Rsa1.0_01923.1.g30809.t1	ref|XP_002890694.1| hypothetical protein ARALYDRAFT_472840 [Arabidopsis lyrata subsp. lyrata] gi|297336536|gb|EFH66953.1| hypothetical protein ARALYDRAFT_472840 [Arabidopsis lyrata subsp. lyrata]	380	795	1.00E-175	209.2	82.1	88.7	hypothetical protein ARALYDRAFT_472840	gbpln	Arabidopsis lyrata	AT1G25350.1 | Symbols: OVA9 | glutamine-tRNA ligase, putative / glutaminyl-tRNA synthetase, putative / GlnRS, putative | chr1:8889280-8894205 REVERSE LENGTH=795	380	795	1.00E-177	209.2	81.8	88.9
Rsa1.0_01923.1.g30810.t1	ref|NP_173907.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75172213|sp|Q9FRI5.1|PPR57_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g25360 gi|11067273|gb|AAG28801.1|AC079374_4 hypothetical protein [Arabidopsis thaliana] gi|332192491|gb|AEE30612.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	789	790	0	100.1	83.0	92.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G25360.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:8894428-8896800 FORWARD LENGTH=790	789	790	0	100.1	83.0	92.1
Rsa1.0_01923.1.g30811.t1	ref|XP_002890693.1| hypothetical protein ARALYDRAFT_313393 [Arabidopsis lyrata subsp. lyrata] gi|297336535|gb|EFH66952.1| hypothetical protein ARALYDRAFT_313393 [Arabidopsis lyrata subsp. lyrata]	279	780	4.00E-65	279.6	64.5	69.9	hypothetical protein ARALYDRAFT_313393	gbpln	Arabidopsis lyrata	AT1G25370.1 | Symbols: | Protein of unknown function (DUF1639) | chr1:8898046-8898934 REVERSE LENGTH=263	279	263	1.00E-58	94.3	56.3	66.3
Rsa1.0_01923.1.g30812.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01923.1.g30813.t1	ref|NP_564233.1| NAD+ transporter 2 [Arabidopsis thaliana] gi|75247587|sp|Q8RWA5.1|NDT2_ARATH RecName: Full=Nicotinamide adenine dinucleotide transporter 2, mitochondrial; Short=AtNDT2; AltName: Full=NAD(+) transporter 2 gi|20260666|gb|AAM13231.1| unknown protein [Arabidopsis thaliana] gi|30984592|gb|AAP42759.1| At1g25380 [Arabidopsis thaliana] gi|283482332|emb|CAR70089.1| mitochondrial nicotinamide adenine dinucleotide transporter 2 [Arabidopsis thaliana] gi|332192494|gb|AEE30615.1| NAD+ transporter 2 [Arabidopsis thaliana]	363	363	1.00E-172	100.0	87.9	95.3	NAD+ transporter 2	gbpln	Arabidopsis thaliana	AT1G25380.1 | Symbols: ATNDT2, NDT2 | NAD+ transporter 2 | chr1:8903726-8905818 FORWARD LENGTH=363	363	363	1.00E-175	100.0	87.9	95.3
Rsa1.0_01923.1.g30814.t1	gb|EOA36697.1| hypothetical protein CARUB_v10012140mg [Capsella rubella]	266	270	3.00E-72	101.5	63.2	74.4	hypothetical protein CARUB_v10012140mg	gbpln	Capsella rubella	AT1G25300.1 | Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr1:8871568-8872386 FORWARD LENGTH=272	266	272	1.00E-72	102.3	61.7	72.9
Rsa1.0_01923.1.g30815.t1	gb|EOA28349.1| hypothetical protein CARUB_v10024554mg [Capsella rubella]	236	320	9.00E-78	135.6	66.1	79.2	hypothetical protein CARUB_v10024554mg	gbpln	Capsella rubella	AT1G58725.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:21771935-21773365 REVERSE LENGTH=349	236	349	4.00E-69	147.9	49.2	55.5
Rsa1.0_01923.1.g30816.t1	ref|NP_001185093.1| RHOMBOID-like protein 10 [Arabidopsis thaliana] gi|332192482|gb|AEE30603.1| RHOMBOID-like protein 10 [Arabidopsis thaliana]	337	336	1.00E-155	99.7	81.9	91.1	RHOMBOID-like protein 10	gbpln	Arabidopsis thaliana	AT1G25290.2 | Symbols: RBL10 | RHOMBOID-like protein 10 | chr1:8867157-8868945 FORWARD LENGTH=336	337	336	1.00E-158	99.7	81.9	91.1
Rsa1.0_01923.1.g30817.t1	gb|EOA40428.1| hypothetical protein CARUB_v10009152mg [Capsella rubella]	454	442	0	97.4	88.5	91.9	hypothetical protein CARUB_v10009152mg	gbpln	Capsella rubella	AT1G25280.1 | Symbols: AtTLP10, TLP10 | tubby like protein 10 | chr1:8864961-8866608 FORWARD LENGTH=445	454	445	0	98.0	87.4	91.4
Rsa1.0_01923.1.g30818.t1	gb|EOA37256.1| hypothetical protein CARUB_v10010807mg [Capsella rubella]	57	74	1.00E-17	129.8	77.2	84.2	hypothetical protein CARUB_v10010807mg	gbpln	Capsella rubella	AT1G25275.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:8860719-8861156 FORWARD LENGTH=74	57	74	2.00E-19	129.8	75.4	84.2

<table>
<tr><td>Rsa1.0_01923.1.g30819.t1</td><td>ref|XP_002887155.1| hypothetical protein ARALYDRAFT_475905 [Arabidopsis lyrata subsp. lyrata] gi|297332996|gb|EFH63414.1| hypothetical protein ARALYDRAFT_475905 [Arabidopsis lyrata subsp. lyrata]</td><td>419</td><td>332</td><td>1.00E−106</td><td>79.2</td><td>52.7</td><td>59.2</td><td>hypothetical protein ARALYDRAFT_475905</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G68140.3 | Symbols: | Protein of unknown function (DUF1644) | chr1:25539410−25540414 REVERSE LENGTH=334</td><td>419</td><td>334</td><td>1.00E−105</td><td>79.7</td><td>51.1</td><td>58.5</td></tr>
<tr><td>Rsa1.0_01923.1.g30820.t1</td><td>gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]</td><td>350</td><td>368</td><td>1.00E−74</td><td>105.1</td><td>47.1</td><td>62.9</td><td>hypothetical protein CARUB_v10027748mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848−18153960 FORWARD LENGTH=370</td><td>350</td><td>370</td><td>5.00E−68</td><td>105.7</td><td>46.0</td><td>62.9</td></tr>
<tr><td>Rsa1.0_01923.1.g30821.t1</td><td>ref|NP_564226.1| Ribosomal protein L10 family protein [Arabidopsis thaliana] gi|15028333|gb|AAK76643.1| unknown protein [Arabidopsis thaliana] gi|19310645|gb|AAL85053.1| unknown protein [Arabidopsis thaliana] gi|21593993|gb|AAM65913.1| unknown [Arabidopsis thaliana] gi|332192473|gb|AEE30594.1| Ribosomal protein L10 family protein [Arabidopsis thaliana]</td><td>253</td><td>235</td><td>1.00E−108</td><td>92.9</td><td>79.8</td><td>83.8</td><td>Ribosomal protein L10 family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G25260.1 | Symbols: | Ribosomal protein L10 family protein | chr1:8854163−8855766 REVERSE LENGTH=235</td><td>253</td><td>235</td><td>1.00E−110</td><td>92.9</td><td>79.8</td><td>83.8</td></tr>
<tr><td>Rsa1.0_01924.1.g30822.t1</td><td>dbj|BAJ33775.1| unnamed protein product [Thellungiella halophila]</td><td>320</td><td>317</td><td>1.00E−128</td><td>99.1</td><td>78.8</td><td>84.7</td><td>unnamed protein product</td><td>−−−−</td><td>−−−−</td><td>AT1G69010.1 | Symbols: BIM2 | BES1−interacting Myc−like protein 2 | chr1:25941804−25943599 FORWARD LENGTH=311</td><td>320</td><td>311</td><td>1.00E−117</td><td>97.2</td><td>75.6</td><td>81.3</td></tr>
<tr><td>Rsa1.0_01924.1.g30823.t1</td><td>gb|EOA34077.1| hypothetical protein CARUB_v10021578mg [Capsella rubella]</td><td>321</td><td>319</td><td>1.00E−144</td><td>99.4</td><td>86.9</td><td>91.6</td><td>hypothetical protein CARUB_v10021578mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G69030.1 | Symbols: | BSD domain−containing protein | chr1:25947429−25949262 REVERSE LENGTH=317</td><td>321</td><td>317</td><td>1.00E−138</td><td>98.8</td><td>85.4</td><td>90.3</td></tr>
<tr><td>Rsa1.0_01924.1.g30824.t2</td><td>ref|XP_002878905.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297324744|gb|EFH55164.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>451</td><td>480</td><td>9.00E−42</td><td>106.4</td><td>27.1</td><td>46.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G14800.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:5099572−5102558 FORWARD LENGTH=384</td><td>451</td><td>384</td><td>2.00E−28</td><td>85.1</td><td>14.4</td><td>24.4</td></tr>
<tr><td>Rsa1.0_01924.1.g30825.t1</td><td>gb|ACG60681.1| unknown protein [Brassica oleracea var. alboglabra]</td><td>456</td><td>446</td><td>0</td><td>97.8</td><td>94.7</td><td>96.5</td><td>unknown protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G69040.2 | Symbols: ACR4 | ACT domain repeat 4 | chr1:25957843−25960079 FORWARD LENGTH=455</td><td>456</td><td>455</td><td>0</td><td>99.8</td><td>93.9</td><td>96.7</td></tr>
<tr><td>Rsa1.0_01924.1.g30826.t1</td><td>gb|EOA14852.1| hypothetical protein CARUB_v10028167mg [Capsella rubella]</td><td>174</td><td>178</td><td>6.00E−27</td><td>102.3</td><td>40.2</td><td>58.0</td><td>hypothetical protein CARUB_v10028167mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G50030.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:20354666−20355449 FORWARD LENGTH=187</td><td>174</td><td>187</td><td>9.00E−28</td><td>107.5</td><td>36.8</td><td>52.3</td></tr>
<tr><td>Rsa1.0_01924.1.g30827.t1</td><td>gb|ACG60683.1| unknown protein [Brassica oleracea var. alboglabra]</td><td>131</td><td>879</td><td>4.00E−23</td><td>671.0</td><td>44.3</td><td>46.6</td><td>unknown protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G69070.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nop14−like protein (InterPro:IPR007276); Has 69842 Blast hits to 35213 proteins in 1572 species: Archae − 363; Bacteria − 20593; Metazoa − 20851; Fungi − 8010; Plants − 2912; Viruses − 517; Other Eukaryotes − 16596 (source: NCBI BLink). | chr1:25967421−25971389 REVERSE LENGTH=901</td><td>131</td><td>901</td><td>4.00E−21</td><td>687.8</td><td>37.4</td><td>43.5</td></tr>
<tr><td>Rsa1.0_01925.1.g30828.t1</td><td>ref|XP_002884448.1| hypothetical protein ARALYDRAFT_477706 [Arabidopsis lyrata subsp. lyrata] gi|297330288|gb|EFH60707.1| hypothetical protein ARALYDRAFT_477706 [Arabidopsis lyrata subsp. lyrata]</td><td>247</td><td>245</td><td>1.00E−120</td><td>99.2</td><td>92.7</td><td>95.5</td><td>hypothetical protein ARALYDRAFT_477706</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04500.1 | Symbols: | RNA−binding (RRM/RBD/RNP motifs) family protein | chr3:1212065−1213795 REVERSE LENGTH=245</td><td>247</td><td>245</td><td>1.00E−115</td><td>99.2</td><td>91.5</td><td>94.3</td></tr>
<tr><td>Rsa1.0_01925.1.g30829.t1</td><td>ref|XP_002871867.1| hypothetical protein ARALYDRAFT_326316 [Arabidopsis lyrata subsp. lyrata] gi|297317704|gb|EFH48126.1| hypothetical protein ARALYDRAFT_326316 [Arabidopsis lyrata subsp. lyrata]</td><td>127</td><td>390</td><td>2.00E−31</td><td>307.1</td><td>52.8</td><td>66.9</td><td>hypothetical protein ARALYDRAFT_326316</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G19170.1 | Symbols: | Protein of Unknown Function (DUF239) | chr5:6445245−6447305 FORWARD LENGTH=391</td><td>127</td><td>391</td><td>2.00E−32</td><td>307.9</td><td>51.2</td><td>68.5</td></tr>
<tr><td>Rsa1.0_01925.1.g30830.t1</td><td>ref|XP_002882356.1| hypothetical protein ARALYDRAFT_317312 [Arabidopsis lyrata subsp. lyrata] gi|297328196|gb|EFH58615.1| hypothetical protein ARALYDRAFT_317312 [Arabidopsis lyrata subsp. lyrata]</td><td>1193</td><td>1123</td><td>0</td><td>94.1</td><td>87.6</td><td>90.9</td><td>hypothetical protein ARALYDRAFT_317312</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G04490.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G38092.1); Has 75 Blast hits to 64 proteins in 20 species: Archae − 0; Bacteria − 0; Metazoa − 36; Fungi − 0; Plants − 22; Viruses − 0; Other Eukaryotes − 17 (source: NCBI BLink). | chr3:1200816−1209713 FORWARD LENGTH=1118</td><td>1193</td><td>1118</td><td>0</td><td>93.7</td><td>85.3</td><td>89.4</td></tr>
</table>

Rsa1.0_01925.1.g30831.t2	ref|XP_002884445.1| endoribonuclease [Arabidopsis lyrata subsp. lyrata] gi|297330285|gb|EFH60704.1| endoribonuclease [Arabidopsis lyrata subsp. lyrata]	746	717	0	96.1	84.6	89.9	endoribonuclease	gbpln	Arabidopsis lyrata	AT3G04480.1 | Symbols: | endoribonucleases | chr3:1193988-1197320 REVERSE LENGTH=718	746	718	0	96.2	83.5	89.5
Rsa1.0_01925.1.g30832.t1	ref|NP_180705.1| F-box protein DOR [Arabidopsis thaliana] gi|229807544|sp|Q5BPS3.2|DOR_ARATH RecName: Full=F-box protein DOR; AltName: Full=Protein DROUGHT TOLERANCE REPRESSOR gi|4589954|gb|AAD26472.1| hypothetical protein [Arabidopsis thaliana] gi|330253458|gb|AEC08552.1| F-box protein DOR [Arabidopsis thaliana]	406	387	8.00E-81	95.3	46.3	60.3	F-box protein DOR	gbpln	Arabidopsis thaliana	AT2G31470.1 | Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=387	406	387	2.00E-83	95.3	46.3	60.3
Rsa1.0_01925.1.g30833.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01926.1.g30834.t1	ref|NP_198663.1| putative DNA repair protein RAD23-4 [Arabidopsis thaliana] gi|55976502|sp|Q84L30.2|RD23D_ARATH RecName: Full=Putative DNA repair protein RAD23-4; AltName: Full=RAD23-like protein 4; Short=AtRAD23-4 gi|9758825|dbj|BAB09359.1| DNA repair protein RAD23 homolog [Arabidopsis thaliana] gi|16648838|gb|AAL25609.1| unknown protein [Arabidopsis thaliana] gi|19548081|gb|AAL87405.1| At5g38470/At5g38470 [Arabidopsis thaliana] gi|21593157|gb|AAM65106.1| DNA repair protein RAD23 homolog [Arabidopsis thaliana] gi|30409728|dbj|BAC76394.1| RAD23-like protein [Arabidopsis thaliana] gi|110735094|gb|ABG89117.1| Rad23-2 [synthetic construct] gi|332006938|gb|AED94321.1| putative DNA repair protein RAD23-4 [Arabidopsis thaliana]	384	378	1.00E-175	98.4	87.8	90.9	putative DNA repair protein RAD23-4	gbpln	Arabidopsis thaliana	AT5G38470.1 | Symbols: RAD23D | Rad23 UV excision repair protein family | chr5:15404720-15407500 FORWARD LENGTH=378	384	378	1.00E-178	98.4	87.8	90.9
Rsa1.0_01926.1.g30835.t1	gb|ACN73536.1| 1433-3 [Brassica napus] gi|224981579|gb|ACN73537.1| 1433-3 [Brassica napus]	258	258	1.00E-143	100.0	97.3	98.1	1433-3	gbpln	Brassica napus	AT5G38480.1 | Symbols: GRF3, RCI1 | general regulatory factor 3 | chr5:15410277-15411285 FORWARD LENGTH=255	258	255	1.00E-139	98.8	92.6	95.3
Rsa1.0_01926.1.g30836.t1	ref|NP_198667.1| rhomboid-related intramembrane serine protease-like protein [Arabidopsis thaliana] gi|145334671|ref|NP_001078681.1| rhomboid-related intramembrane serine protease-like protein [Arabidopsis thaliana] gi|10176819|dbj|BAB10141.1| unnamed protein product [Arabidopsis thaliana] gi|46518449|gb|AAS99706.1| At5g38510 [Arabidopsis thaliana] gi|110741692|dbj|BAE98792.1| hypothetical protein [Arabidopsis thaliana] gi|332006944|gb|AED94327.1| rhomboid-related intramembrane serine protease-like protein [Arabidopsis thaliana] gi|332006945|gb|AED94328.1| rhomboid-related intramembrane serine protease-like protein [Arabidopsis thaliana]	103	434	2.00E-28	421.4	62.1	68.9	rhomboid-related intramembrane serine protease-like protein	gbpln	Arabidopsis thaliana	AT5G38510.2 | Symbols: | Rhomboid-related intramembrane serine protease family protein | chr5:15417839-15420002 REVERSE LENGTH=434	103	434	3.00E-31	421.4	62.1	68.9
Rsa1.0_01926.1.g30837.t1	ref|NP_198668.1| alpha/beta-hydrolase-like protein [Arabidopsis thaliana] gi|10176820|dbj|BAB10142.1| unnamed protein product [Arabidopsis thaliana] gi|23306396|gb|AAN17425.1| putative protein [Arabidopsis thaliana] gi|24899773|gb|AAN65101.1| putative protein [Arabidopsis thaliana] gi|332006946|gb|AED94329.1| alpha/beta-hydrolase-like protein [Arabidopsis thaliana]	336	362	1.00E-157	107.7	89.0	93.8	alpha/beta-hydrolase-like protein	gbpln	Arabidopsis thaliana	AT5G38520.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:15421605-15423234 FORWARD LENGTH=362	336	362	1.00E-159	107.7	89.0	93.8
Rsa1.0_01926.1.g30838.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01926.1.g30839.t1	ref|NP_198669.1| tryptophan synthase beta chain [Arabidopsis thaliana] gi|10176821|dbj|BAB10143.1| tryptophan synthase beta chain [Arabidopsis thaliana] gi|19699005|gb|AAL91238.1| tryptophan synthase beta chain [Arabidopsis thaliana] gi|23198094|gb|AAN15574.1| tryptophan synthase beta chain [Arabidopsis thaliana] gi|332006948|gb|AED94331.1| tryptophan synthase beta chain [Arabidopsis thaliana]	457	506	3.00E-82	110.7	32.2	33.5	tryptophan synthase beta chain	gbpln	Arabidopsis thaliana	AT5G38530.1 | Symbols: TSBtype2 | tryptophan synthase beta type 2 | chr5:15424097-15426294 FORWARD LENGTH=506	457	506	7.00E-85	110.7	32.2	33.5
Rsa1.0_01926.1.g30840.t1	dbj|BAB09923.1| copia-like retrotransposable element [Arabidopsis thaliana]	374	1342	1.00E-58	358.8	29.9	36.6	copia-like retrotransposable element	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	374	240	7.00E-19	64.2	12.8	19.0
Rsa1.0_01926.1.g30841.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	357	1486	1.00E-100	416.2	50.4	57.7	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	357	1262	3.00E-50	353.5	29.7	44.8
Rsa1.0_01926.1.g30842.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	424	940	1.00E-62	221.7	32.8	42.0	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01927.1.g30843.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	1948	1142	0	58.6	28.5	37.8	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1948	575	5.00E-83	29.5	9.3	14.6
Rsa1.0_01927.1.g30844.t5	ref|NP_192658.1| putative F-box protein [Arabidopsis thaliana] gi|75181645|sp|Q9M0Q9.1|FB223_ARATH RecName: Full=Putative F-box protein At4g09190 gi|7267562|emb|CAB78043.1| putative protein [Arabidopsis thaliana] gi|332657333|gb|AEE82733.1| putative F-box protein [Arabidopsis thaliana]	184	383	2.00E-27	208.2	42.9	55.4	putative F-box protein	gbpln	Arabidopsis thaliana	AT4G09190.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:5855176-5856327 FORWARD LENGTH=383	184	383	7.00E-30	208.2	42.9	55.4
Rsa1.0_01927.1.g30845.t1	ref|XP_002878168.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297324006|gb|EFH54427.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	290	353	1.00E-128	121.7	76.6	85.9	kinase family protein	gbpln	Arabidopsis lyrata	AT3G57710.1 | Symbols: | Protein kinase superfamily protein | chr3:21386233-21387288 REVERSE LENGTH=351	290	351	1.00E-127	121.0	74.1	85.2
Rsa1.0_01928.1.g30846.t1	ref|NP_174543.1| putative F-box protein [Arabidopsis thaliana] gi|75264129|sp|Q9LPJ7.1|FB31_ARATH RecName: Full=Putative F-box protein At1g32660 gi|6714270|gb|AAF25966.1|AC017118_3 F6N18.5 [Arabidopsis thaliana] gi|332193394|gb|AEE31515.1| putative F-box protein [Arabidopsis thaliana]	488	446	7.00E-51	91.4	30.1	40.4	putative F-box protein	gbpln	Arabidopsis thaliana	AT1G32660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11811040-11812380 FORWARD LENGTH=446	488	446	2.00E-53	91.4	30.1	40.4
Rsa1.0_01928.1.g30847.t1	dbj|BAJ33975.1| unnamed protein product [Thellungiella halophila]	328	328	0	100.0	97.6	98.8	unnamed protein product	----	----	AT1G48270.1 | Symbols: GCR1 | G-protein-coupled receptor 1 | chr1:17828314-17830214 REVERSE LENGTH=326	328	326	0	99.4	96.6	98.2
Rsa1.0_01928.1.g30848.t1	ref|XP_002891421.1| hypothetical protein ARALYDRAFT_473964 [Arabidopsis lyrata subsp. lyrata] gi|297337263|gb|EFH67680.1| hypothetical protein ARALYDRAFT_473964 [Arabidopsis lyrata subsp. lyrata]	481	567	0	117.9	83.0	89.2	hypothetical protein ARALYDRAFT_473964	gbpln	Arabidopsis lyrata	AT1G48280.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:17835196-17837553 FORWARD LENGTH=558	481	558	0	116.0	81.7	87.1
Rsa1.0_01928.1.g30849.t1	gb|ABD64939.1| hypothetical protein 24.t00017 [Brassica oleracea]	328	442	1.00E-113	134.8	59.8	67.1	hypothetical protein 24.t00017	gbpln	Brassica oleracea	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	328	343	3.00E-22	104.6	15.9	19.2
Rsa1.0_01928.1.g30850.t1	ref|WP_000519654.1| hypothetical protein, partial [Streptococcus agalactiae]	93	183	6.00E-21	196.8	60.2	71.0	hypothetical protein, partial	gbbct	Streptococcus agalactiae	#	#	#	#	#	#	#
Rsa1.0_01928.1.g30851.t1	gb|ABD65170.1| hypothetical protein 40.t00057 [Brassica oleracea]	236	255	5.00E-67	108.1	58.9	71.6	hypothetical protein 40.t00057	gbpln	Brassica oleracea	AT3G47680.1 | Symbols: | DNA binding | chr3:17577483-17578391 REVERSE LENGTH=302	236	302	2.00E-40	128.0	39.8	55.1

Rsa1.0_01928.1.g30852.t1	ref|XP_002893682.1| Beta-galactosidase 15 precursor [Arabidopsis lyrata subsp. lyrata] gi|297339524|gb|EFH69941.1| Beta-galactosidase 15 precursor [Arabidopsis lyrata subsp. lyrata]	226	780	1.00E-118	345.1	88.1	93.8	Beta-galactosidase 15 precursor	gbpln	Arabidopsis lyrata	AT1G31740.1 | Symbols: BGAL15 | beta-galactosidase 15 | chr1:11365285-11369908 REVERSE LENGTH=786	226	786	1.00E-119	347.8	86.3	92.9
Rsa1.0_01928.1.g30853.t1	ref|XP_002893682.1| Beta-galactosidase 15 precursor [Arabidopsis lyrata subsp. lyrata] gi|297339524|gb|EFH69941.1| Beta-galactosidase 15 precursor [Arabidopsis lyrata subsp. lyrata]	120	780	5.00E-64	650.0	92.5	96.7	Beta-galactosidase 15 precursor	gbpln	Arabidopsis lyrata	AT1G31740.1 | Symbols: BGAL15 | beta-galactosidase 15 | chr1:11365285-11369908 REVERSE LENGTH=786	120	786	5.00E-65	655.0	90.0	95.0
Rsa1.0_01929.1.g30854.t1	ref|NP_194866.2| protein kinase family protein [Arabidopsis thaliana] gi|55978825|gb|AAV68874.1| hypothetical protein AT4G31380 [Arabidopsis thaliana] gi|60547875|gb|AAX23901.1| hypothetical protein At4g31380 [Arabidopsis thaliana] gi|332660502|gb|AEE85902.1| protein kinase family protein [Arabidopsis thaliana]	124	181	1.00E-53	146.0	91.1	96.0	protein kinase family protein	gbpln	Arabidopsis thaliana	AT4G31380.1 | Symbols: FLP1 | FPF1-like protein 1 | chr4:15229837-15230382 FORWARD LENGTH=181	124	181	2.00E-56	146.0	91.1	96.0
Rsa1.0_01929.1.g30855.t1	ref|XP_002869328.1| hypothetical protein ARALYDRAFT_491601 [Arabidopsis lyrata subsp. lyrata] gi|297315164|gb|EFH45587.1| hypothetical protein ARALYDRAFT_491601 [Arabidopsis lyrata subsp. lyrata]	282	344	1.00E-100	122.0	72.3	78.7	hypothetical protein ARALYDRAFT_491601	gbpln	Arabidopsis lyrata	AT4G31400.1 | Symbols: CTF7 | damaged DNA binding;DNA-directed DNA polymerases | chr4:15237411-15239266 FORWARD LENGTH=345	282	345	1.00E-96	122.3	72.7	79.1
Rsa1.0_01929.1.g30856.t1	emb|CAA16544.1| hypothetical protein [Arabidopsis thaliana] gi|7270044|emb|CAB79859.1| hypothetical protein [Arabidopsis thaliana]	324	380	1.00E-128	117.3	78.1	84.9	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G31410.2 | Symbols: | Protein of unknown function (DUF1644) | chr4:15244259-15245474 FORWARD LENGTH=308	324	308	1.00E-129	95.1	78.1	84.6
Rsa1.0_01929.1.g30857.t1	ref|XP_002869326.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315162|gb|EFH45585.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	555	571	1.00E-175	102.9	73.2	81.1	predicted protein	gbpln	Arabidopsis lyrata	AT4G31430.2 | Symbols: | unknown protein; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:15248510-15252204 FORWARD LENGTH=574	555	574	1.00E-171	103.4	70.6	80.7
Rsa1.0_01929.1.g30858.t1	ref|XP_002869325.1| hypothetical protein ARALYDRAFT_491593 [Arabidopsis lyrata subsp. lyrata] gi|297315161|gb|EFH45584.1| hypothetical protein ARALYDRAFT_491593 [Arabidopsis lyrata subsp. lyrata]	339	394	1.00E-129	116.2	74.9	85.0	hypothetical protein ARALYDRAFT_491593	gbpln	Arabidopsis lyrata	AT4G31440.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24530.1); Has 210 Blast hits to 209 proteins in 55 species: Archae - 0; Bacteria - 72; Metazoa - 2; Fungi - 6; Plants - 128; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr4:15253731-15254870 FORWARD LENGTH=379	339	379	1.00E-118	111.8	70.8	79.4
Rsa1.0_01929.1.g30859.t1	ref|XP_002867301.1| ribosomal protein L28 family protein [Arabidopsis lyrata subsp. lyrata] gi|297313137|gb|EFH43560.1| ribosomal protein L28 family protein [Arabidopsis lyrata subsp. lyrata]	215	212	1.00E-108	98.6	90.2	94.0	ribosomal protein L28 family protein	gbpln	Arabidopsis lyrata	AT4G31460.1 | Symbols: | Ribosomal L28 family | chr4:15259773-15260847 REVERSE LENGTH=212	215	212	1.00E-106	98.6	87.9	92.1
Rsa1.0_01929.1.g30860.t10	gb|AFD01320.1| auxin response factor 25 [Brassica rapa subsp. pekinensis]	580	549	0	94.7	75.5	81.2	auxin response factor 25	gbpln	Brassica rapa	AT1G34410.1 | Symbols: ARF21 | auxin response factor 21 | chr1:12577722-12580824 FORWARD LENGTH=606	580	606	1.00E-144	104.5	47.4	61.7
Rsa1.0_01930.1.g30861.t1	ref|NP_179837.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] gi|4544442|gb|AAD22350.1| unknown protein [Arabidopsis thaliana] gi|28466887|gb|AAO44052.1| At2g22510 [Arabidopsis thaliana] gi|330252222|gb|AEC07316.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	128	124	1.00E-26	96.9	61.7	66.4	hydroxyproline-rich glycoprotein family protein	gbpln	Arabidopsis thaliana	AT2G22510.1 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr2:9569327-9569701 REVERSE LENGTH=124	128	124	2.00E-29	96.9	61.7	66.4
Rsa1.0_01930.1.g30862.t1	ref|XP_002864008.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297309843|gb|EFH40267.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	2538	2586	0	101.9	81.0	89.6	predicted protein	gbpln	Arabidopsis lyrata	AT5G49680.2 | Symbols: | Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain | chr5:20176385-20188307 FORWARD LENGTH=2587	2538	2587	0	101.9	80.7	89.5

Rsa1.0_01930.1.g30863.t1	ref|NP_191452.2| F-box/LRR-repeat protein [Arabidopsis thaliana] gi|75244411|sp|Q8GXW6.1|FBL59_ARATH RecName: Full=F-box/LRR-repeat protein At3g58930 gi|26451056|dbj|BAC42633.1| unknown protein [Arabidopsis thaliana] gi|28951059|gb|AAO63453.1| At3g58930 [Arabidopsis thaliana] gi|332646330|gb|AEE79851.1| F-box/LRR-repeat protein [Arabidopsis thaliana]	411	482	1.00E-129	117.3	58.4	72.0	F-box/LRR-repeat protein	gbpln	Arabidopsis thaliana	AT3G58930.1 | Symbols: | F-box/RNI-like superfamily protein | chr3:21778381-21780014 REVERSE LENGTH=482	411	482	1.00E-131	117.3	58.4	72.0
Rsa1.0_01930.1.g30864.t1	gb|AFM77908.1| MADS-box protein SVP [Brassica napus]	243	241	1.00E-130	99.2	95.9	97.9	MADS-box protein SVP	gbpln	Brassica napus	AT2G22540.1 | Symbols: SVP, AGL22 | K-box region and MADS-box transcription factor family protein | chr2:9580417-9583603 FORWARD LENGTH=240	243	240	1.00E-123	98.8	90.1	95.5
Rsa1.0_01930.1.g30865.t1	ref|NP_179842.2| Kinase interacting (KIP1-like) family protein [Arabidopsis thaliana] gi|330252228|gb|AEC07322.1| Kinase interacting (KIP1-like) family protein [Arabidopsis thaliana]	895	947	0	105.8	86.4	92.2	Kinase interacting (KIP1-like) family protein	gbpln	Arabidopsis thaliana	AT2G22560.1 | Symbols: | Kinase interacting (KIP1-like) family protein | chr2:9585892-9588838 FORWARD LENGTH=947	895	947	0	105.8	86.4	92.2
Rsa1.0_01930.1.g30866.t1	ref|NP_850026.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana] gi|330252232|gb|AEC07326.1| RNA-binding KH domain-containing protein [Arabidopsis thaliana]	613	632	0	103.1	73.4	82.9	RNA-binding KH domain-containing protein	gbpln	Arabidopsis thaliana	AT2G22600.1 | Symbols: | RNA-binding KH domain-containing protein | chr2:9596617-9599050 FORWARD LENGTH=632	613	632	0	103.1	73.4	82.9
Rsa1.0_01930.1.g30867.t2	ref|XP_002885458.1| hypothetical protein ARALYDRAFT_342316 [Arabidopsis lyrata subsp. lyrata] gi|297331298|gb|EFH61717.1| hypothetical protein ARALYDRAFT_342316 [Arabidopsis lyrata subsp. lyrata]	344	508	2.00E-42	147.7	31.4	39.8	hypothetical protein ARALYDRAFT_342316	gbpln	Arabidopsis lyrata	AT3G21660.1 | Symbols: | UBX domain-containing protein | chr3:7624495-7626654 REVERSE LENGTH=435	344	435	4.00E-33	126.5	25.6	33.1
Rsa1.0_01930.1.g30868.t1	ref|XP_002885458.1| hypothetical protein ARALYDRAFT_342316 [Arabidopsis lyrata subsp. lyrata] gi|297331298|gb|EFH61717.1| hypothetical protein ARALYDRAFT_342316 [Arabidopsis lyrata subsp. lyrata]	230	508	3.00E-44	220.9	49.1	60.0	hypothetical protein ARALYDRAFT_342316	gbpln	Arabidopsis lyrata	AT4G15410.1 | Symbols: PUX5 | serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B prime gamma | chr4:8814868-8816596 FORWARD LENGTH=421	230	421	5.00E-37	183.0	41.7	52.6
Rsa1.0_01931.1.g30869.t1	gb|AAC69114.1| putative gag-protease polyprotein [Arabidopsis thaliana]	179	627	5.00E-18	350.3	28.5	40.2	putative gag-protease polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01931.1.g30870.t1	#	#	#	#	#	#	#	–	----	----	AT1G28760.1 | Symbols: | Uncharacterized conserved protein (DUF2215) | chr1:10103158-10104588 FORWARD LENGTH=476	214	476	1.00E-13	222.4	25.7	36.4
Rsa1.0_01931.1.g30871.t1	gb|AAD17395.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	502	1138	1.00E-132	226.7	46.6	65.1	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	502	575	1.00E-75	114.5	33.3	52.4
Rsa1.0_01931.1.g30872.t1	ref|XP_003635668.1| PREDICTED: uncharacterized protein LOC100854178, partial [Vitis vinifera]	498	478	4.00E-62	96.0	29.5	43.6	PREDICTED: uncharacterized protein LOC100854178, partial	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_01931.1.g30873.t1	gb|EOA33811.1| hypothetical protein CARUB_v10021283mg [Capsella rubella]	377	386	2.33E-156	102.4	72.7	82.8	hypothetical protein CARUB_v10021283mg	gbpln	Capsella rubella	AT2G47450.1 | Symbols: CAO, CPSRP43 | chloroplast signal recognition particle component (CAO) | chr2:19472781-19473902 FORWARD LENGTH=373	377	373	1.00E-145	98.9	73.5	82.5
Rsa1.0_01931.1.g30874.t1	ref|XP_002891415.1| EMB2191 [Arabidopsis lyrata subsp. lyrata] gi|297337257|gb|EFH67674.1| EMB2191 [Arabidopsis lyrata subsp. lyrata]	188	192	2.00E-94	102.1	88.3	94.7	EMB2191	gbpln	Arabidopsis lyrata	AT1G48175.1 | Symbols: emb2191 | Cytidine/deoxycytidylate deaminase family protein | chr1:17790957-17792066 FORWARD LENGTH=182	188	182	5.00E-94	96.8	86.2	91.5
Rsa1.0_01931.1.g30875.t1	gb|EOA38564.1| hypothetical protein CARUB_v10010377mg, partial [Capsella rubella]	145	189	5.00E-65	130.3	80.0	85.5	hypothetical protein CARUB_v10010377mg, partial	gbpln	Capsella rubella	AT1G48160.1 | Symbols: | signal recognition particle 19 kDa protein, putative / SRP19, putative | chr1:17786779-17788286 REVERSE LENGTH=145	145	145	8.00E-59	100.0	77.2	84.1
Rsa1.0_01931.1.g30876.t1	ref|XP_002891413.1| hypothetical protein ARALYDRAFT_314249 [Arabidopsis lyrata subsp. lyrata] gi|297337255|gb|EFH67672.1| hypothetical protein ARALYDRAFT_314249 [Arabidopsis lyrata subsp. lyrata]	89	89	1.00E-42	100.0	95.5	100.0	hypothetical protein ARALYDRAFT_314249	gbpln	Arabidopsis lyrata	AT1G48140.1 | Symbols: | dolichol-phosphate mannosyltransferase-related | chr1:17783402-17783914 FORWARD LENGTH=89	89	89	3.00E-45	100.0	94.4	100.0
Rsa1.0_01932.1.g30877.t2	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	960	1838	0	191.5	41.7	57.6	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01932.1.g30878.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01932.1.g30879.t1	ref|XP_002885812.1| hypothetical protein ARALYDRAFT_319345 [Arabidopsis lyrata subsp. lyrata] gi|297331652|gb|EFH62071.1| hypothetical protein ARALYDRAFT_319345 [Arabidopsis lyrata subsp. lyrata]	721	773	0	107.2	69.2	78.9	hypothetical protein ARALYDRAFT_319345	gbpln	Arabidopsis lyrata	AT2G06040.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Leucine-rich repeat, cysteine-containing subtype (InterPro:IPR006553); BEST Arabidopsis thaliana protein match is: RNI-like superfamily protein (TAIR:AT5G21900.1); Has 5028 Blast hits to 2547 proteins in 240 species: Archae - 0; Bacteria - 125; Metazoa - 2326; Fungi - 765; Plants - 1373; Viruses - 0; Other Eukaryotes - 439 (source: NCBI BLink). | chr2:2352333-2355419 REVERSE LENGTH=762	721	762	0	105.7	66.7	76.4
Rsa1.0_01932.1.g30880.t1	ref|XP_002883732.1| hypothetical protein ARALYDRAFT_480213 [Arabidopsis lyrata subsp. lyrata] gi|297329572|gb|EFH59991.1| hypothetical protein ARALYDRAFT_480213 [Arabidopsis lyrata subsp. lyrata]	281	288	1.00E-144	102.5	88.6	96.1	hypothetical protein ARALYDRAFT_480213	gbpln	Arabidopsis lyrata	AT2G06025.1 | Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr2:2350231-2351898 FORWARD LENGTH=288	281	288	1.00E-144	102.5	87.5	94.3
Rsa1.0_01932.1.g30881.t1	dbj|BAA97086.1| unnamed protein product [Arabidopsis thaliana]	261	341	9.00E-60	130.7	56.7	69.0	unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01932.1.g30882.t1	dbj|BAA97087.1| copia-type pol polyprotein-like [Arabidopsis thaliana]	584	1123	0	192.3	74.7	83.2	copia-type pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	584	1262	7.00E-28	216.1	17.1	26.0
Rsa1.0_01932.1.g30883.t1	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	905	672	2.00E-96	74.3	22.9	37.1	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01932.1.g30884.t2	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	519	578	1.00E-111	111.4	46.1	61.1	hypothetical protein 27.t00126	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	519	681	1.00E-10	131.2	6.2	12.5
Rsa1.0_01933.1.g30885.t1	ref|NP_680147.1| uncharacterized protein [Arabidopsis thaliana] gi|52354445|gb|AAU44543.1| hypothetical protein AT5G05965 [Arabidopsis thaliana] gi|332003563|gb|AED90946.1| uncharacterized protein AT5G05965 [Arabidopsis thaliana]	137	131	2.00E-39	95.6	75.2	82.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G05965.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G39855.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:1791059-1792495 REVERSE LENGTH=131	137	131	4.00E-42	95.6	75.2	82.5
Rsa1.0_01933.1.g30886.t1	ref|NP_568160.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana] gi|21592534|gb|AAM64483.1| unknown [Arabidopsis thaliana] gi|88011017|gb|ABD38889.1| At5g05960 [Arabidopsis thaliana] gi|332003562|gb|AED90945.1| bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein [Arabidopsis thaliana]	116	116	3.00E-53	100.0	86.2	94.0	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein	gbpln	Arabidopsis thaliana	AT5G05960.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:1790256-1790694 FORWARD LENGTH=116	116	116	5.00E-56	100.0	86.2	94.0
Rsa1.0_01933.1.g30887.t1	gb|EOA22495.1| hypothetical protein CARUB_v10003149mg [Capsella rubella]	176	175	1.00E-89	99.4	94.3	97.2	hypothetical protein CARUB_v10003149mg	gbpln	Capsella rubella	AT5G05950.1 | Symbols: MEE60 | maternal effect embryo arrest 60 | chr5:1788814-1789341 FORWARD LENGTH=175	176	175	1.00E-90	99.4	92.6	96.0
Rsa1.0_01933.1.g30888.t1	ref|XP_002871189.1| hypothetical protein ARALYDRAFT_325218 [Arabidopsis lyrata subsp. lyrata] gi|297317026|gb|EFH47448.1| hypothetical protein ARALYDRAFT_325218 [Arabidopsis lyrata subsp. lyrata]	611	609	0	99.7	85.1	91.3	hypothetical protein ARALYDRAFT_325218	gbpln	Arabidopsis lyrata	AT5G05940.1 | Symbols: ATROPGEF5, ROPGEF5 | ROP guanine nucleotide exchange factor 5 | chr5:1786028-1788363 FORWARD LENGTH=611	611	611	0	100.0	85.8	92.0

<table>
<tr><td>Rsa1.0_01933.1.g30889.t6</td><td>ref|XP_002873229.1| hypothetical protein ARALYDRAFT_487392 [Arabidopsis lyrata subsp. lyrata] gi|297319066|gb|EFH49488.1| hypothetical protein ARALYDRAFT_487392 [Arabidopsis lyrata subsp. lyrata]</td><td>369</td><td>367</td><td>0</td><td>99.5</td><td>94.3</td><td>97.8</td><td>hypothetical protein ARALYDRAFT_487392</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05920.1 | Symbols: DHS, EDA22 | deoxyhypusine synthase | chr5:1777781-1779699 REVERSE LENGTH=368</td><td>369</td><td>368</td><td>0</td><td>99.7</td><td>94.0</td><td>98.4</td></tr>
<tr><td>Rsa1.0_01933.1.g30890.t1</td><td>ref|XP_004299151.1| PREDICTED: cytochrome P450 71A1-like [Fragaria vesca subsp. vesca]</td><td>488</td><td>511</td><td>1.00E-106</td><td>104.7</td><td>41.6</td><td>60.0</td><td>PREDICTED: cytochrome P450 71A1-like</td><td>gbpln</td><td>Fragaria vesca</td><td>AT3G26180.1 | Symbols: CYP71B20 | cytochrome P450, family 71, subfamily B, polypeptide 20 | chr3:9578407-9579993 REVERSE LENGTH=502</td><td>488</td><td>502</td><td>8.00E-96</td><td>102.9</td><td>40.2</td><td>59.6</td></tr>
<tr><td>Rsa1.0_01933.1.g30891.t1</td><td>gb|EOA27690.1| hypothetical protein CARUB_v10023843mg, partial [Capsella rubella]</td><td>125</td><td>271</td><td>2.00E-15</td><td>216.8</td><td>40.0</td><td>56.0</td><td>hypothetical protein CARUB_v10023843mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170</td><td>125</td><td>170</td><td>1.00E-16</td><td>136.0</td><td>38.4</td><td>56.8</td></tr>
<tr><td>Rsa1.0_01933.1.g30892.t1</td><td>gb|ABV21212.1| Ty1_Copia-element protein [Arabidopsis thaliana]</td><td>538</td><td>438</td><td>6.00E-86</td><td>81.4</td><td>32.7</td><td>46.7</td><td>Ty1_Copia-element protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746</td><td>538</td><td>746</td><td>2.00E-55</td><td>138.7</td><td>25.3</td><td>37.4</td></tr>
<tr><td>Rsa1.0_01933.1.g30893.t1</td><td>ref|XP_002323082.1| cytochrome P450 [Populus trichocarpa] gi|222867712|gb|EEF04843.1| cytochrome P450 [Populus trichocarpa]</td><td>497</td><td>486</td><td>1.00E-111</td><td>97.8</td><td>42.3</td><td>61.2</td><td>cytochrome P450</td><td>gbpln</td><td>Populus trichocarpa</td><td>AT3G26180.1 | Symbols: CYP71B20 | cytochrome P450, family 71, subfamily B, polypeptide 20 | chr3:9578407-9579993 REVERSE LENGTH=502</td><td>497</td><td>502</td><td>3.00E-95</td><td>101.0</td><td>38.2</td><td>59.4</td></tr>
<tr><td>Rsa1.0_01933.1.g30894.t1</td><td>ref|NP_196209.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] gi|75262507|sp|Q9FI96.1|U76C3_ARATH RecName: Full=UDP-glycosyltransferase 76C3 gi|10177563|dbj|BAB10795.1| glucuronosyl transferase-like protein [Arabidopsis thaliana] gi|332003554|gb|AED90937.1| UDP-glycosyltransferase 76C3 [Arabidopsis thaliana]</td><td>321</td><td>450</td><td>6.00E-89</td><td>140.2</td><td>49.8</td><td>57.3</td><td>UDP-glucoronosyl/UDP-glucosyl transferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G05900.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1774513-1776381 FORWARD LENGTH=450</td><td>321</td><td>450</td><td>2.00E-91</td><td>140.2</td><td>49.8</td><td>57.3</td></tr>
<tr><td>Rsa1.0_01933.1.g30895.t1</td><td>ref|XP_002871186.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297317023|gb|EFH47445.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]</td><td>482</td><td>455</td><td>0</td><td>94.4</td><td>67.0</td><td>80.7</td><td>UDP-glucoronosyl/UDP-glucosyl transferase family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G05890.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1772567-1774012 FORWARD LENGTH=455</td><td>482</td><td>455</td><td>0</td><td>94.4</td><td>67.0</td><td>80.1</td></tr>
<tr><td>Rsa1.0_01933.1.g30896.t1</td><td>ref|NP_196207.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] gi|75262509|sp|Q9FI98.1|U76C4_ARATH RecName: Full=UDP-glycosyltransferase 76C4 gi|10177561|dbj|BAB10793.1| glucuronosyl transferase-like protein [Arabidopsis thaliana] gi|332003552|gb|AED90935.1| UDP-glycosyltransferase 76C4 [Arabidopsis thaliana]</td><td>148</td><td>451</td><td>1.00E-63</td><td>304.7</td><td>77.7</td><td>88.5</td><td>UDP-glucoronosyl/UDP-glucosyl transferase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G05880.1 | Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1769648-1771515 FORWARD LENGTH=451</td><td>148</td><td>451</td><td>3.00E-66</td><td>304.7</td><td>77.7</td><td>88.5</td></tr>
<tr><td>Rsa1.0_01934.1.g30897.t1</td><td>ref|NP_172604.1| putative pectinesterase 56 [Arabidopsis thaliana] gi|75339345|sp|Q4PT34.1|PME56_ARATH RecName: Full=Probable pectinesterase 56; Short=PE 56; AltName: Full=Pectin methylesterase 56; Short=AtPME56; Flags: Precursor gi|67633368|gb|AAY78609.1| pectinesterase family protein [Arabidopsis thaliana] gi|332190606|gb|AEE28727.1| putative pectinesterase 56 [Arabidopsis thaliana]</td><td>217</td><td>288</td><td>7.00E-65</td><td>132.7</td><td>57.6</td><td>74.7</td><td>putative pectinesterase 56</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G11370.1 | Symbols: | Pectin lyase-like superfamily protein | chr1:3828098-3830945 REVERSE LENGTH=288</td><td>217</td><td>288</td><td>2.00E-67</td><td>132.7</td><td>57.6</td><td>74.7</td></tr>
<tr><td>Rsa1.0_01934.1.g30898.t1</td><td>gb|ABW17183.1| profilin [Raphanus sativus] gi|158122106|gb|ABW17189.1| profilin [Brassica juncea var. multiceps]</td><td>134</td><td>134</td><td>8.00E-73</td><td>100.0</td><td>98.5</td><td>100.0</td><td>profilin</td><td>gbpln</td><td>Brassica juncea</td><td>AT4G29340.1 | Symbols: PRF4 | profilin 4 | chr4:14447718-14448467 FORWARD LENGTH=134</td><td>134</td><td>134</td><td>6.00E-73</td><td>100.0</td><td>95.5</td><td>97.8</td></tr>
</table>

Rsa1.0_01934.1.g30899.t1	ref|NP_194662.2| derlin-1 [Arabidopsis thaliana] gi|75161705|sp|Q8VZU9.1|DERL1_ARATH RecName: Full=Derlin-1; AltName: Full=AtDerlin1-1 gi|17380686|gb|AAL36173.1| unknown protein [Arabidopsis thaliana] gi|20465889|gb|AAM20097.1| unknown protein [Arabidopsis thaliana] gi|332660218|gb|AEE85618.1| derlin-1 [Arabidopsis thaliana]	288	266	1.00E-120	92.4	79.9	82.3	derlin-1	gbpln	Arabidopsis thaliana	AT4G29330.1 | Symbols: DER1 | DERLIN-1 | chr4:14444937-14446952 FORWARD LENGTH=266	288	266	1.00E-122	92.4	79.9	82.3
Rsa1.0_01934.1.g30900.t1	ref|XP_002867413.1| hypothetical protein ARALYDRAFT_913577 [Arabidopsis lyrata subsp. lyrata] gi|297313249|gb|EFH43672.1| hypothetical protein ARALYDRAFT_913577 [Arabidopsis lyrata subsp. lyrata]	424	424	0	100.0	95.5	98.6	hypothetical protein ARALYDRAFT_913577	gbpln	Arabidopsis lyrata	AT4G29310.1 | Symbols: | Protein of unknown function (DUF1005) | chr4:14437892-14439609 REVERSE LENGTH=424	424	424	0	100.0	95.5	98.3
Rsa1.0_01934.1.g30901.t1	pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	531	1365	1.00E-106	257.1	39.7	57.3	RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)	----	----	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	531	575	8.00E-74	108.3	27.7	44.3
Rsa1.0_01934.1.g30902.t1	ref|XP_002867418.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313254|gb|EFH43677.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	257	256	4.00E-99	99.6	66.9	83.7	predicted protein	gbpln	Arabidopsis lyrata	AT4G29270.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr4:14423797-14424848 REVERSE LENGTH=256	257	256	6.00E-98	99.6	65.4	82.1
Rsa1.0_01934.1.g30903.t1	ref|NP_194652.1| NAC domain containing protein 75 [Arabidopsis thaliana] gi|7269821|emb|CAB79681.1| putative protein [Arabidopsis thaliana] gi|332660205|gb|AEE85605.1| NAC domain containing protein 75 [Arabidopsis thaliana]	498	498	0	100.0	90.4	93.8	NAC domain containing protein 75	gbpln	Arabidopsis thaliana	AT4G29230.1 | Symbols: anac075, NAC075 | NAC domain containing protein 75 | chr4:14410338-14414956 FORWARD LENGTH=498	498	498	0	100.0	90.4	93.8
Rsa1.0_01935.1.g30904.t1	gb|EOA27792.1| hypothetical protein CARUB_v10023944mg [Capsella rubella]	226	241	7.00E-73	106.6	68.1	80.5	hypothetical protein CARUB_v10023944mg	gbpln	Capsella rubella	AT2G34200.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:14441105-14441882 FORWARD LENGTH=222	226	222	3.00E-71	98.2	67.3	76.5
Rsa1.0_01935.1.g30905.t1	ref|XP_002888489.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata] gi|297334330|gb|EFH64748.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]	521	760	0	145.9	74.1	84.8	subtilase family protein	gbpln	Arabidopsis lyrata	AT1G66210.1 | Symbols: | Subtilisin-like serine endopeptidase family protein | chr1:24665735-24668650 REVERSE LENGTH=759	521	759	0	145.7	73.1	83.7
Rsa1.0_01935.1.g30906.t1	ref|NP_565779.1| trichome birefringence-like 37 protein [Arabidopsis thaliana] gi|20196907|gb|AAB67625.2| expressed protein [Arabidopsis thaliana] gi|21554400|gb|AAM63505.1| unknown [Arabidopsis thaliana] gi|330253819|gb|AEC08913.1| trichome birefringence-like 37 protein [Arabidopsis thaliana]	241	385	4.00E-65	159.8	51.0	56.0	trichome birefringence-like 37 protein	gbpln	Arabidopsis thaliana	AT2G34070.1 | Symbols: TBL37 | TRICHOME BIREFRINGENCE-LIKE 37 | chr2:14387631-14390160 REVERSE LENGTH=385	241	385	1.00E-67	159.8	51.0	56.0
Rsa1.0_01935.1.g30907.t1	gb|EOA27292.1| hypothetical protein CARUB_v10023411mg [Capsella rubella]	217	385	1.00E-113	177.4	89.4	92.6	hypothetical protein CARUB_v10023411mg	gbpln	Capsella rubella	AT2G34070.1 | Symbols: TBL37 | TRICHOME BIREFRINGENCE-LIKE 37 | chr2:14387631-14390160 REVERSE LENGTH=385	217	385	1.00E-116	177.4	88.9	92.6
Rsa1.0_01936.1.g30908.t1	ref|XP_002887372.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata] gi|297333213|gb|EFH63631.1| hypothetical protein ARALYDRAFT_476271 [Arabidopsis lyrata subsp. lyrata]	843	832	0	98.7	51.8	64.1	hypothetical protein ARALYDRAFT_476271	gbpln	Arabidopsis lyrata	AT1G71400.1 | Symbols: AtRLP12, RLP12 | receptor like protein 12 | chr1:26909905-26912448 FORWARD LENGTH=847	843	847	0	100.5	52.0	65.2
Rsa1.0_01936.1.g30909.t1	gb|EOA18257.1| hypothetical protein CARUB_v10006750mg [Capsella rubella]	193	74	5.00E-23	38.3	28.0	30.6	hypothetical protein CARUB_v10006750mg	gbpln	Capsella rubella	AT5G41685.1 | Symbols: | Mitochondrial outer membrane translocase complex, subunit Tom7 | chr5:16669419-16669646 REVERSE LENGTH=75	193	75	3.00E-21	38.9	21.8	23.8
Rsa1.0_01936.1.g30910.t1	ref|XP_002875605.1| hypothetical protein ARALYDRAFT_905424 [Arabidopsis lyrata subsp. lyrata] gi|297321443|gb|EFH51864.1| hypothetical protein ARALYDRAFT_905424 [Arabidopsis lyrata subsp. lyrata]	150	246	3.00E-46	164.0	64.7	72.7	hypothetical protein ARALYDRAFT_905424	gbpln	Arabidopsis lyrata	AT3G43250.1 | Symbols: | Family of unknown function (DUF572) | chr3:15216713-15217462 FORWARD LENGTH=249	150	249	1.00E-46	166.0	64.7	72.7
Rsa1.0_01936.1.g30911.t1	gb|EOA16094.1| hypothetical protein CARUB_v10004228mg [Capsella rubella]	728	740	0	101.6	66.5	79.9	hypothetical protein CARUB_v10004228mg	gbpln	Capsella rubella	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	728	719	1.00E-149	98.8	41.2	59.6

Rsa1.0_01936.1.g30912.t1	ref|XP_004149128.1| PREDICTED: coiled-coil domain-containing protein 94 homolog [Cucumis sativus] gi|449494611|ref|XP_004159597.1| PREDICTED: coiled-coil domain-containing protein 94 homolog [Cucumis sativus]	100	327	1.00E-31	327.0	68.0	75.0	PREDICTED: coiled-coil domain-containing protein 94 homolog	gbpln	Cucumis sativus	AT3G43250.1 | Symbols: | Family of unknown function (DUF572) | chr3:15216713-15217462 FORWARD LENGTH=249	100	249	8.00E-34	249.0	67.0	73.0
Rsa1.0_01936.1.g30913.t1	gb|EOA12375.1| hypothetical protein CARUB_v10025926mg [Capsella rubella]	157	767	6.00E-45	488.5	59.9	70.7	hypothetical protein CARUB_v10025926mg	gbpln	Capsella rubella	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	157	719	2.00E-22	458.0	33.1	45.2
Rsa1.0_01936.1.g30914.t1	gb|AAM62648.1| dehydration stress-induced protein [Arabidopsis thaliana]	167	182	2.00E-34	109.0	46.1	64.1	dehydration stress-induced protein	gbpln	Arabidopsis thaliana	AT2G22170.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr2:9427010-9427742 REVERSE LENGTH=183	167	183	2.00E-36	109.6	45.5	64.1
Rsa1.0_01937.1.g30915.t1	ref|XP_004160247.1| PREDICTED: LOW QUALITY PROTEIN: eukaryotic translation initiation factor 3 subunit B-like [Cucumis sativus]	732	718	2.00E-81	98.1	25.4	35.1	PREDICTED: LOW QUALITY PROTEIN: eukaryotic translation initiation factor 3 subunit B-like	gbpln	Cucumis sativus	AT5G27640.2 | Symbols: TIF3B1, EIF3B, ATEIF3B-1, EIF3B-1, ATTIF3B1 | translation initiation factor 3B1 | chr5:9781207-9784759 REVERSE LENGTH=738	732	738	4.00E-83	100.8	25.5	35.7
Rsa1.0_01937.1.g30916.t1	ref|NP_194090.2| tyrosine transaminase-like protein [Arabidopsis thaliana] gi|75161515|sp|Q8VYP2.1|TAT4_ARATH RecName: Full=Probable aminotransferase TAT4; AltName: Full=Tyrosine aminotransferase 4 gi|17979319|gb|AAL49885.1| putative tyrosine transaminase [Arabidopsis thaliana] gi|21689827|gb|AAM67557.1| putative tyrosine transaminase [Arabidopsis thaliana] gi|332659380|gb|AEE84780.1| probable aminotransferase TAT4 [Arabidopsis thaliana]	433	424	0	97.9	72.1	82.7	tyrosine transaminase-like protein	gbpln	Arabidopsis thaliana	AT4G23590.1 | Symbols: | Tyrosine transaminase family protein | chr4:12307195-12309445 FORWARD LENGTH=424	433	424	0	97.9	72.1	82.7
Rsa1.0_01937.1.g30917.t1	gb|EOA25182.1| hypothetical protein CARUB_v10018494mg [Capsella rubella]	277	282	6.00E-27	101.8	34.3	49.5	hypothetical protein CARUB_v10018494mg	gbpln	Capsella rubella	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	277	303	3.00E-28	109.4	33.9	49.5
Rsa1.0_01937.1.g30918.t1	gb|AAO27362.1| cystine lyase BOCL-3 [Brassica oleracea]	424	424	0	100.0	94.6	97.4	cystine lyase BOCL-3	gbpln	Brassica oleracea	AT4G23600.1 | Symbols: CORI3, JR2 | Tyrosine transaminase family protein | chr4:12310657-12312885 FORWARD LENGTH=422	424	422	0	99.5	79.7	90.3
Rsa1.0_01937.1.g30919.t1	ref|NP_567687.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana] gi|13937135|gb|AAK50061.1|AF372921_1 AT4g23610/F9D16_80 [Arabidopsis thaliana] gi|4454030|emb|CAA23027.1| hypothetical protein [Arabidopsis thaliana] gi|7269209|emb|CAB79316.1| hypothetical protein [Arabidopsis thaliana] gi|22136998|gb|AAM91344.1| At4g23610/F9D16_80 [Arabidopsis thaliana] gi|332659384|gb|AEE84784.1| late embryogenesis abundant hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	232	228	4.00E-75	98.3	65.5	74.1	late embryogenesis abundant hydroxyproline-rich glycoprotein	gbpln	Arabidopsis thaliana	AT4G23610.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr4:12314037-12314723 FORWARD LENGTH=228	232	228	1.00E-77	98.3	65.5	74.1
Rsa1.0_01937.1.g30920.t1	gb|ACC91264.1| 50S ribosomal protein [Capsella rubella] gi|482553078|gb|EOA17271.1| hypothetical protein CARUB_v10005544mg [Capsella rubella]	269	257	1.00E-128	95.5	85.5	90.7	50S ribosomal protein	gbpln	Capsella rubella	AT4G23620.1 | Symbols: | Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain | chr4:12315016-12316659 REVERSE LENGTH=264	269	264	1.00E-130	98.1	84.0	90.0
Rsa1.0_01937.1.g30921.t1	dbj|BAJ33905.1| unnamed protein product [Thellungiella halophila]	277	275	1.00E-129	99.3	89.9	96.0	unnamed protein product	----	----	AT4G23630.1 | Symbols: BTI1, RTNLB1 | VIRB2-interacting protein 1 | chr4:12318070-12319574 FORWARD LENGTH=275	277	275	1.00E-129	99.3	91.3	95.3
Rsa1.0_01937.1.g30922.t1	ref|XP_002867698.1| hypothetical protein ARALYDRAFT_914233 [Arabidopsis lyrata subsp. lyrata] gi|297313534|gb|EFH43957.1| hypothetical protein ARALYDRAFT_914233 [Arabidopsis lyrata subsp. lyrata]	781	775	0	99.2	96.7	97.8	hypothetical protein ARALYDRAFT_914233	gbpln	Arabidopsis lyrata	AT4G23640.1 | Symbols: TRH1, ATKT3, KUP4 | Potassium transporter family protein | chr4:12320476-12324291 REVERSE LENGTH=775	781	775	0	99.2	96.3	97.4
Rsa1.0_01937.1.g30923.t1	gb|ACC91261.1| putative calcium-dependent protein kinase [Capsella rubella] gi|482552225|gb|EOA16418.1| hypothetical protein CARUB_v10004572mg [Capsella rubella]	523	529	0	101.1	90.4	94.8	putative calcium-dependent protein kinase	gbpln	Capsella rubella	AT4G23650.1 | Symbols: CDPK6, CPK3 | calcium-dependent protein kinase 6 | chr4:12324967-12327415 REVERSE LENGTH=529	523	529	0	101.1	88.9	94.3

Rsa1.0_01937.1.g30924.t1	gb|EOA16649.1| hypothetical protein CARUB_v10004831mg, partial [Capsella rubella]	405	439	1.00E−177	108.4	86.9	90.6	hypothetical protein CARUB_v10004831mg, partial	gbpln	Capsella rubella	AT4G23660.2 | Symbols: AtPPT1, PPT1 | polyprenyltransferase 1 | chr4:12328086−12331359 REVERSE LENGTH=407	405	407	1.00E−177	100.5	85.7	89.9
Rsa1.0_01937.1.g30925.t1	ref|XP_002867694.1| hypothetical protein ARALYDRAFT_492500 [Arabidopsis lyrata subsp. lyrata] gi|297313530|gb|EFH43953.1| hypothetical protein ARALYDRAFT_492500 [Arabidopsis lyrata subsp. lyrata]	151	151	4.00E−76	100.0	88.1	95.4	hypothetical protein ARALYDRAFT_492500	gbpln	Arabidopsis lyrata	AT4G23680.1 | Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:12336416−12337417 REVERSE LENGTH=151	151	151	1.00E−78	100.0	88.7	95.4
Rsa1.0_01938.1.g30926.t2	ref|YP_001547727.1| DEAD/DEAH box helicase [Herpetosiphon aurantiacus DSM 785] gi|159894519|gb|ABX07599.1| DEAD/DEAH box helicase domain protein [Herpetosiphon aurantiacus DSM 785]	378	584	4.00E−33	154.5	27.0	48.9	DEAD/DEAH box helicase	gbbct	Herpetosiphon aurantiacus	AT3G19760.1 | Symbols: EIF4A−Ⅲ | eukaryotic initiation factor 4A−Ⅲ | chr3:6863790−6866242 FORWARD LENGTH=408	378	408	2.00E−35	107.9	26.7	50.5
Rsa1.0_01938.1.g30927.t1	ref|XP_002868566.1| hypothetical protein ARALYDRAFT_493781 [Arabidopsis lyrata subsp. lyrata] gi|297314402|gb|EFH44825.1| hypothetical protein ARALYDRAFT_493781 [Arabidopsis lyrata subsp. lyrata]	669	668	0	99.9	97.8	99.0	hypothetical protein ARALYDRAFT_493781	gbpln	Arabidopsis lyrata	AT5G42020.1 | Symbols: BIP, BIP2 | Heat shock protein 70 (Hsp 70) family protein | chr5:16807697−16810480 REVERSE LENGTH=668	669	668	0	99.9	97.2	99.0
Rsa1.0_01938.1.g30928.t1	ref|XP_002879286.1| hypothetical protein ARALYDRAFT_482009 [Arabidopsis lyrata subsp. lyrata] gi|297325125|gb|EFH55545.1| hypothetical protein ARALYDRAFT_482009 [Arabidopsis lyrata subsp. lyrata]	440	378	0	85.9	75.0	77.3	hypothetical protein ARALYDRAFT_482009	gbpln	Arabidopsis lyrata	AT2G30910.3 | Symbols: ARPC1A | actin−related protein C1A | chr2:13153447−13156869 FORWARD LENGTH=378	440	378	0	85.9	74.8	76.8
Rsa1.0_01938.1.g30929.t1	gb|EOA36129.1| hypothetical protein CARUB_v10012300mg [Capsella rubella]	216	276	7.00E−77	127.8	67.6	83.3	hypothetical protein CARUB_v10012300mg	gbpln	Capsella rubella	AT1G08080.1 | Symbols: ATACA7, ACA7 | alpha carbonic anhydrase 7 | chr1:2517022−2518546 REVERSE LENGTH=275	216	275	2.00E−77	127.3	69.4	82.4
Rsa1.0_01938.1.g30930.t1	ref|NP_180646.1| Cytochrome b561/ferric reductase transmembrane protein family [Arabidopsis thaliana] gi|3201616|gb|AAC20723.1| hypothetical protein [Arabidopsis thaliana] gi|34146810|gb|AAQ62413.1| At2g30890 [Arabidopsis thaliana] gi|51971759|dbj|BAD44544.1| hypothetical protein [Arabidopsis thaliana] gi|330253359|gb|AEC08453.1| Cytochrome b561/ferric reductase transmembrane protein family [Arabidopsis thaliana]	156	257	1.00E−67	164.7	80.8	86.5	Cytochrome b561/ferric reductase transmembrane protein family	gbpln	Arabidopsis thaliana	AT2G30890.1 | Symbols: | Cytochrome b561/ferric reductase transmembrane protein family | chr2:13147774−13149663 FORWARD LENGTH=257	156	257	4.00E−70	164.7	80.8	86.5
Rsa1.0_01938.1.g30931.t8	ref|NP_973569.1| Pleckstrin homology (PH) domain−containing protein [Arabidopsis thaliana] gi|330253358|gb|AEC08452.1| Pleckstrin homology (PH) domain−containing protein [Arabidopsis thaliana]	310	381	3.00E−34	122.9	22.6	24.2	Pleckstrin homology (PH) domain−containing protein	gbpln	Arabidopsis thaliana	AT2G30880.2 | Symbols: | Pleckstrin homology (PH) domain−containing protein | chr2:13143375−13145718 REVERSE LENGTH=381	310	381	7.00E−37	122.9	22.6	24.2
Rsa1.0_01938.1.g30932.t1	ref|NP_180644.1| glutathione S−transferase ERD13 [Arabidopsis thaliana] gi|1170089|sp|P42761.3|GSTFA_ARATH RecName: Full=Glutathione S−transferase F10; Short=AtGSTF10; AltName: Full=AtGSTF4; AltName: Full=GST class−phi member 10; AltName: Full=Protein EARLY RESPONSE TO DEHYDRATION 13 gi|497789|dbj|BAA04554.1| glutathione S−transferase [Arabidopsis thaliana] gi|3201614|gb|AAC20721.1| glutathione S−transferase [Arabidopsis thaliana] gi|22136038|gb|AAM91601.1| glutathione S−transferase [Arabidopsis thaliana] gi|23197738|gb|AAN15396.1| glutathione S−transferase [Arabidopsis thaliana] gi|330253356|gb|AEC08450.1| glutathione S−transferase ERD13 [Arabidopsis thaliana]	215	215	1.00E−115	100.0	95.3	98.1	glutathione S−transferase ERD13	gbpln	Arabidopsis thaliana	AT2G30870.1 | Symbols: ATGSTF10, ERD13, ATGSTF4, GSTF10 | glutathione S−transferase PHI 10 | chr2:13141490−13142392 FORWARD LENGTH=215	215	215	1.00E−118	100.0	95.3	98.1

Rsa1.0_01938.1.g30933.t1	ref|NP_180643.1| glutathione S-transferase [Arabidopsis thaliana] gi|297822799|ref|XP_002879282.1| hypothetical protein ARALYDRAFT_482003 [Arabidopsis lyrata subsp. lyrata] gi|75318706|sp|O80852.1|GSTF9_ARATH RecName: Full=Glutathione S-transferase F9; Short=AtGSTF9; AltName: Full=AtGSTF7; AltName: Full=GST class-phi member 9 gi|13926310|gb|AAK49621.1|AF372905_1 At2g30860/F7F1.7 [Arabidopsis thaliana] gi|3201613|gb|AAC20720.1| glutathione S-transferase [Arabidopsis thaliana] gi|27363352|gb|AAO11595.1| At2g30860/F7F1.7 [Arabidopsis thaliana] gi|297325121|gb|EFH55541.1| hypothetical protein ARALYDRAFT_482003 [Arabidopsis lyrata subsp. lyrata] gi|330253354|gb|AEC08448.1| glutathione S-transferase [Arabidopsis thaliana]	215	215	1.00E-118	100.0	96.7	99.1	glutathione S-transferase	gbpln	Arabidopsis lyrata	AT2G30860.1 | Symbols: ATGSTF9, GLUTTR, ATGSTF7, GSTF9 | glutathione S-transferase PHI 9 | chr2:13139132-13140057 FORWARD LENGTH=215	215	215	1.00E-121	100.0	96.7	99.1
Rsa1.0_01938.1.g30934.t1	ref|XP_002879280.1| hypothetical protein ARALYDRAFT_481999 [Arabidopsis lyrata subsp. lyrata] gi|297325119|gb|EFH55539.1| hypothetical protein ARALYDRAFT_481999 [Arabidopsis lyrata subsp. lyrata]	418	437	1.00E-98	104.5	58.1	66.5	hypothetical protein ARALYDRAFT_481999	gbpln	Arabidopsis lyrata	AT2G30820.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06660.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:13129800-13132391 FORWARD LENGTH=421	418	421	9.00E-92	100.7	56.2	65.8
Rsa1.0_01939.1.g30935.t1	ref|XP_002872140.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata] gi|297317977|gb|EFH48399.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata]	496	496	0	100.0	83.3	90.9	CYP71B11	gbpln	Arabidopsis lyrata	AT5G25120.1 | Symbols: CYP71B11 | ytochrome p450, family 71, subfamily B, polypeptide 11 | chr5:8662851-8664432 FORWARD LENGTH=496	496	496	0	100.0	81.9	91.5
Rsa1.0_01939.1.g30936.t1	ref|XP_002872140.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata] gi|297317977|gb|EFH48399.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata]	547	496	0	90.7	70.7	79.9	CYP71B11	gbpln	Arabidopsis lyrata	AT5G25120.1 | Symbols: CYP71B11 | ytochrome p450, family 71, subfamily B, polypeptide 11 | chr5:8662851-8664432 FORWARD LENGTH=496	547	496	0	90.7	70.4	79.9
Rsa1.0_01939.1.g30937.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01939.1.g30938.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01939.1.g30939.t1	gb|EOA21453.1| hypothetical protein CARUB_v10001837mg [Capsella rubella]	257	241	2.00E-91	93.8	70.4	78.2	hypothetical protein CARUB_v10001837mg	gbpln	Capsella rubella	AT5G25160.1 | Symbols: ZFP3 | zinc finger protein 3 | chr5:8687524-8688231 FORWARD LENGTH=235	257	235	6.00E-80	91.4	66.5	75.1
Rsa1.0_01939.1.g30940.t1	ref|XP_002872143.1| hypothetical protein ARALYDRAFT_910561 [Arabidopsis lyrata subsp. lyrata] gi|297317980|gb|EFH48402.1| hypothetical protein ARALYDRAFT_910561 [Arabidopsis lyrata subsp. lyrata]	223	218	1.00E-108	97.8	91.5	94.6	hypothetical protein ARALYDRAFT_910561	gbpln	Arabidopsis lyrata	AT5G25170.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr5:8693257-8694438 FORWARD LENGTH=218	223	218	1.00E-102	97.8	84.8	88.8
Rsa1.0_01940.1.g30941.t1	ref|XP_002883704.1| hypothetical protein ARALYDRAFT_480186 [Arabidopsis lyrata subsp. lyrata] gi|297329544|gb|EFH59963.1| hypothetical protein ARALYDRAFT_480186 [Arabidopsis lyrata subsp. lyrata]	977	993	0	101.6	90.3	93.4	hypothetical protein ARALYDRAFT_480186	gbpln	Arabidopsis lyrata	AT2G05710.1 | Symbols: ACO3 | aconitase 3 | chr2:2141591-2146350 FORWARD LENGTH=990	977	990	0	101.3	89.4	92.4
Rsa1.0_01940.1.g30942.t2	dbj|BAJ34198.1| unnamed protein product [Thellungiella halophila]	158	958	3.00E-19	606.3	29.1	31.6	unnamed protein product	----	----	AT3G51770.1 | Symbols: ETO1, ATEOL1 | tetratricopeptide repeat (TPR)-containing protein | chr3:19200328-19203974 REVERSE LENGTH=951	158	951	3.00E-20	601.9	28.5	31.0
Rsa1.0_01940.1.g30943.t1	gb|EOA39027.1| hypothetical protein CARUB_v10011597mg [Capsella rubella]	125	186	3.00E-11	148.8	29.6	51.2	hypothetical protein CARUB_v10011597mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01940.1.g30944.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01940.1.g30945.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	250	484	6.00E-31	193.6	28.8	32.0	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01940.1.g30946.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01940.1.g30947.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01940.1.g30948.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_01941.1.g30949.t1	ref|NP_189605.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana] gi|11994174|dbj|BAB01203.1| anthocyanin acyltransferase-like protein [Arabidopsis thaliana] gi|332644074|gb|AEE77595.1| HXXXD-type acyl-transferase-like protein [Arabidopsis thaliana]	732	458	0	62.6	47.7	52.9	HXXXD-type acyl-transferase-like protein	gbpln	Arabidopsis thaliana	AT3G29635.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr3:11465851-11467227 REVERSE LENGTH=458	732	458	0	62.6	47.7	52.9
Rsa1.0_01941.1.g30950.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01941.1.g30951.t1	gb|EOA24648.1| hypothetical protein CARUB_v10017919mg, partial [Capsella rubella]	261	246	5.00E-85	94.3	70.9	78.9	hypothetical protein CARUB_v10017919mg, partial	gbpln	Capsella rubella	AT3G29575.4 | Symbols: AFP3 | ABI five binding protein 3 | chr3:11382416-11383657 REVERSE LENGTH=231	261	231	9.00E-87	88.5	71.6	77.4
Rsa1.0_01941.1.g30952.t1	ref|NP_189586.1| exocyst complex component 7 [Arabidopsis thaliana] gi|11994523|dbj|BAB02587.1| unnamed protein product [Arabidopsis thaliana] gi|30794118|gb|AAP40501.1| unknown protein [Arabidopsis thaliana] gi|332644060|gb|AEE77581.1| exocyst subunit exo70 family protein E1 [Arabidopsis thaliana]	252	658	2.00E-94	261.1	73.0	80.6	exocyst complex component 7	gbpln	Arabidopsis thaliana	AT3G29400.1 | Symbols: ATEXO70E1, EXO70E1 | exocyst subunit exo70 family protein E1 | chr3:11297339-11299315 REVERSE LENGTH=658	252	658	5.00E-97	261.1	73.0	80.6
Rsa1.0_01941.1.g30953.t1	ref|XP_002877187.1| transcription factor IIB family protein [Arabidopsis lyrata subsp. lyrata] gi|297323025|gb|EFH53446.1| transcription factor IIB family protein [Arabidopsis lyrata subsp. lyrata]	337	336	1.00E-111	99.7	62.9	76.0	transcription factor IIB family protein	gbpln	Arabidopsis lyrata	AT3G29380.1 | Symbols: | Cyclin-like family protein | chr3:11282407-11283524 REVERSE LENGTH=336	337	336	1.00E-110	99.7	60.8	74.5
Rsa1.0_01941.1.g30954.t1	ref|XP_002875515.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297321353|gb|EFH51774.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	253	257	1.00E-111	101.6	77.1	83.8	predicted protein	gbpln	Arabidopsis lyrata	AT5G39280.1 | Symbols: ATEXPA23, ATEXP23, ATHEXP ALPHA 1.17, EXPA23 | expansin A23 | chr5:15730713-15731706 REVERSE LENGTH=259	253	259	1.00E-84	102.4	56.1	69.6
Rsa1.0_01941.1.g30955.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01941.1.g30956.t1	ref|NP_189581.1| histidine-containing phosphotransfer protein 2 [Arabidopsis thaliana] gi|51702212|sp|Q9ZNV8.1|AHP2_ARATH RecName: Full=Histidine-containing phosphotransfer protein 2 gi|4107101|dbj|BAA36336.1| AHP2 [Arabidopsis thaliana] gi|4156241|dbj|BAA37110.1| ATHP1 [Arabidopsis thaliana] gi|11994516|dbj|BAB02580.1| histidine-containing phosphotransfer protein-like [Arabidopsis thaliana] gi|17381272|gb|AAL36054.1| AT3g29350/MUO10_5 [Arabidopsis thaliana] gi|20453361|gb|AAM19919.1| AT3g29350/MUO10_5 [Arabidopsis thaliana] gi|332644050|gb|AEE77571.1| histidine-containing phosphotransfer protein 2 [Arabidopsis thaliana]	155	156	2.00E-75	100.6	89.0	93.5	histidine-containing phosphotransfer protein 2	gbpln	Arabidopsis thaliana	AT3G29350.1 | Symbols: AHP2 | histidine-containing phosphotransmitter 2 | chr3:11264379-11265408 REVERSE LENGTH=156	155	156	8.00E-78	100.6	89.0	93.5
Rsa1.0_01941.1.g30957.t1	ref|XP_002877174.1| hypothetical protein ARALYDRAFT_905240 [Arabidopsis lyrata subsp. lyrata] gi|297323012|gb|EFH53433.1| hypothetical protein ARALYDRAFT_905240 [Arabidopsis lyrata subsp. lyrata]	363	463	2.00E-36	127.5	37.2	48.2	hypothetical protein ARALYDRAFT_905240	gbpln	Arabidopsis lyrata	AT3G29340.1 | Symbols: | zinc finger (C2H2 type) family protein | chr3:11259587-11262440 REVERSE LENGTH=650	363	650	9.00E-36	179.1	38.6	48.2
Rsa1.0_01941.1.g30958.t1	ref|NP_189578.1| glycosyl transferase, family 35 protein [Arabidopsis thaliana] gi|75335028|sp|Q9LIB2.1|PHS1_ARATH RecName: Full=Alpha-glucan phosphorylase 1; Short=AtPHS1; AltName: Full=Alpha-glucan phosphorylase, L isozyme; AltName: Full=Starch phosphorylase L; Flags: Precursor gi|11994512|dbj|BAB02576.1| glycogen phosphorylase B; starch phosphorylase [Arabidopsis thaliana] gi|15146189|gb|AAK83578.1| AT3g29320/MUO10_2 [Arabidopsis thaliana] gi|27764918|gb|AAO23580.1| At3g29320/MUO10_2 [Arabidopsis thaliana] gi|332644046|gb|AEE77567.1| alpha-glucan phosphorylase 1 [Arabidopsis thaliana]	953	962	0	100.9	89.6	94.1	glycosyl transferase, family 35 protein	gbpln	Arabidopsis thaliana	AT3G29320.1 | Symbols: | Glycosyl transferase, family 35 | chr3:11252871-11257587 FORWARD LENGTH=962	953	962	0	100.9	89.6	94.1
Rsa1.0_01942.1.g30959.t1	gb|EOA14932.1| hypothetical protein CARUB_v10028275mg [Capsella rubella]	453	519	0	114.6	84.8	91.2	hypothetical protein CARUB_v10028275mg	gbpln	Capsella rubella	AT5G62220.1 | Symbols: ATGT18, GT18 | glycosyltransferase 18 | chr5:24988456-24990009 REVERSE LENGTH=517	453	517	0	114.1	83.7	89.4

Rsa1.0_01942.1.g30960.t1	gb|EOA13974.1| hypothetical protein CARUB_v10027104mg, partial [Capsella rubella]	190	218	3.00E−89	114.7	83.7	91.1	hypothetical protein CARUB_v10027104mg, partial	gbpln	Capsella rubella	AT5G62200.1 | Symbols: | Embryo−specific protein 3, (ATS3) | chr5:24984463−24985674 REVERSE LENGTH=190	190	190	2.00E−86	100.0	81.1	90.5
Rsa1.0_01942.1.g30961.t1	gb|EOA14496.1| hypothetical protein CARUB_v10027716mg [Capsella rubella]	381	377	1.00E−178	99.0	76.9	88.5	hypothetical protein CARUB_v10027716mg	gbpln	Capsella rubella	AT5G07200.1 | Symbols: YAP169, GA20OX3, ATGA20OX3 | gibberellin 20−oxidase 3 | chr5:2243835−2245157 REVERSE LENGTH=380	381	380	1.00E−149	99.7	64.6	79.0
Rsa1.0_01942.1.g30962.t1	ref|NP_201023.1| uncharacterized protein [Arabidopsis thaliana] gi|10176936|dbj|BAB10180.1| unnamed protein product [Arabidopsis thaliana] gi|332010194|gb|AED97577.1| uncharacterized protein AT5G62170 [Arabidopsis thaliana]	688	703	0	102.2	80.2	85.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G62170.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G51850.1); Has 381 Blast hits to 359 proteins in 81 species: Archae − 0; Bacteria − 16; Metazoa − 101; Fungi − 21; Plants − 99; Viruses − 3; Other Eukaryotes − 141 (source: NCBI BLink). | chr5:24973115−24975475 REVERSE LENGTH=703	688	703	0	102.2	80.2	85.2
Rsa1.0_01943.1.g30963.t1	ref|XP_002873247.1| carboxy−lyase [Arabidopsis lyrata subsp. lyrata] gi|297319084|gb|EFH49506.1| carboxy−lyase [Arabidopsis lyrata subsp. lyrata]	215	217	1.00E−120	100.9	98.6	99.5	carboxy−lyase	gbpln	Arabidopsis lyrata	AT5G06300.1 | Symbols: | Putative lysine decarboxylase family protein | chr5:1922042−1925278 REVERSE LENGTH=217	215	217	1.00E−123	100.9	98.1	99.5
Rsa1.0_01943.1.g30964.t1	ref|XP_002871210.1| hypothetical protein ARALYDRAFT_908552 [Arabidopsis lyrata subsp. lyrata] gi|297317047|gb|EFH47469.1| hypothetical protein ARALYDRAFT_908552 [Arabidopsis lyrata subsp. lyrata]	270	264	1.00E−124	97.8	83.3	84.1	hypothetical protein ARALYDRAFT_908552	gbpln	Arabidopsis lyrata	AT3G11630.1 | Symbols: | Thioredoxin superfamily protein | chr3:3672189−3673937 FORWARD LENGTH=266	270	266	1.00E−122	98.5	87.8	93.7
Rsa1.0_01943.1.g30965.t1	ref|NP_196246.1| uncharacterized protein [Arabidopsis thaliana] gi|42573287|ref|NP_974740.1| uncharacterized protein [Arabidopsis thaliana] gi|14423402|gb|AAK62383.1|AF386938_1 Unknown protein [Arabidopsis thaliana] gi|9758408|dbj|BAB08950.1| unnamed protein product [Arabidopsis thaliana] gi|332003614|gb|AED90997.1| uncharacterized protein AT5G06280 [Arabidopsis thaliana] gi|332003615|gb|AED90998.1| uncharacterized protein AT5G06280 [Arabidopsis thaliana]	158	156	2.00E−46	98.7	65.8	74.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G06280.3 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G52520.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr5:1918379−1918849 REVERSE LENGTH=156	158	156	6.00E−49	98.7	65.8	74.7
Rsa1.0_01943.1.g30966.t1	gb|EOA21697.1| hypothetical protein CARUB_v10002123mg [Capsella rubella]	175	167	6.00E−64	95.4	73.7	81.1	hypothetical protein CARUB_v10002123mg	gbpln	Capsella rubella	AT5G42560.1 | Symbols: | Abscisic acid−responsive (TB2/DP1, HVA22) family protein | chr5:17015573−17016969 FORWARD LENGTH=296	175	296	1.00E−36	169.1	36.6	53.7
Rsa1.0_01943.1.g30967.t1	ref|NP_196245.1| uncharacterized protein [Arabidopsis thaliana] gi|9758407|dbj|BAB08949.1| unnamed protein product [Arabidopsis thaliana] gi|21536580|gb|AAM60912.1| unknown [Arabidopsis thaliana] gi|28392887|gb|AAO41880.1| putative B−type cyclin [Arabidopsis thaliana] gi|28827636|gb|AAO50662.1| putative B−type cyclin [Arabidopsis thaliana] gi|332003613|gb|AED90996.1| uncharacterized protein AT5G06270 [Arabidopsis thaliana]	123	122	4.00E−39	99.2	90.2	94.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G06270.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11600.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae − 0; Bacteria − 0; Metazoa − 736; Fungi − 347; Plants − 385; Viruses − 0; Other Eukaryotes − 339 (source: NCBI BLink). | chr5:1912895−1913263 FORWARD LENGTH=122	123	122	7.00E−42	99.2	90.2	94.3
Rsa1.0_01943.1.g30968.t1	gb|EOA20021.1| hypothetical protein CARUB_v10000295mg [Capsella rubella]	108	752	9.00E−15	696.3	40.7	43.5	hypothetical protein CARUB_v10000295mg	gbpln	Capsella rubella	AT5G06530.3 | Symbols: | ABC−2 type transporter family protein | chr5:1990334−1994605 REVERSE LENGTH=691	108	691	2.00E−17	639.8	42.6	47.2
Rsa1.0_01943.1.g30969.t1	ref|NP_186943.1| uncharacterized protein [Arabidopsis thaliana] gi|75186537|sp|Q9M8T5.1|Y3293_ARATH RecName: Full=WEB family protein At3g02930, chloroplastic; Flags: Precursor gi|6728968|gb|AAF26966.1|AC018363_11 unknown protein [Arabidopsis thaliana] gi|332640360|gb|AEE73881.1| uncharacterized protein AT3G02930 [Arabidopsis thaliana]	168	806	3.00E−44	479.8	71.4	83.3	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G02930.1 | Symbols: | Plant protein of unknown function (DUF827) | chr3:655306−658319 FORWARD LENGTH=806	168	806	1.00E−46	479.8	71.4	83.3

<table>
<tr><td>Rsa1.0_01943.1.g30970.t1</td><td>ref|NP_196268.1| protein agamous-like 96 [Arabidopsis thaliana] gi|10178106|dbj|BAB11399.1| unnamed protein product [Arabidopsis thaliana] gi|67633788|gb|AAY78818.1| MADS-box family protein [Arabidopsis thaliana] gi|332003641|gb|AED91024.1| protein agamous-like 96 [Arabidopsis thaliana]</td><td>175</td><td>242</td><td>4.00E-24</td><td>138.3</td><td>33.1</td><td>52.6</td><td>protein agamous-like 96</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06500.1 | Symbols: AGL96 | AGAMOUS-like 96 | chr5:1982444-1983172 FORWARD LENGTH=242</td><td>175</td><td>242</td><td>1.00E-26</td><td>138.3</td><td>33.1</td><td>52.6</td></tr>
<tr><td>Rsa1.0_01943.1.g30971.t1</td><td>ref|NP_568165.1| hyaluronan mediated motility receptor-related protein [Arabidopsis thaliana] gi|186520617|ref|NP_001119178.1| hyaluronan mediated motility receptor-related protein [Arabidopsis thaliana] gi|334187462|ref|NP_001190240.1| hyaluronan mediated motility receptor-related protein [Arabidopsis thaliana] gi|21554925|gb|AAM63732.1| unknown [Arabidopsis thaliana] gi|332003610|gb|AED90993.1| hyaluronan mediated motility receptor-related protein [Arabidopsis thaliana] gi|332003611|gb|AED90994.1| hyaluronan mediated motility receptor-related protein [Arabidopsis thaliana] gi|332003612|gb|AED90995.1| hyaluronan mediated motility receptor-related protein [Arabidopsis thaliana]</td><td>104</td><td>106</td><td>1.00E-34</td><td>101.9</td><td>78.8</td><td>86.5</td><td>hyaluronan mediated motility receptor-related protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06265.3 | Symbols: | hyaluronan mediated motility receptor-related | chr5:1906596-1907382 FORWARD LENGTH=106</td><td>104</td><td>106</td><td>2.00E-37</td><td>101.9</td><td>78.8</td><td>86.5</td></tr>
<tr><td>Rsa1.0_01943.1.g30972.t1</td><td>ref|NP_196244.1| TLD-domain containing nucleolar protein [Arabidopsis thaliana] gi|9758406|dbj|BAB08948.1| unnamed protein product [Arabidopsis thaliana] gi|15292793|gb|AAK92765.1| unknown protein [Arabidopsis thaliana] gi|20258859|gb|AAM14101.1| unknown protein [Arabidopsis thaliana] gi|332003609|gb|AED90992.1| TLD-domain containing nucleolar protein [Arabidopsis thaliana]</td><td>423</td><td>424</td><td>0</td><td>100.2</td><td>86.8</td><td>92.4</td><td>TLD-domain containing nucleolar protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G06260.1 | Symbols: | TLD-domain containing nucleolar protein | chr5:1902755-1904835 REVERSE LENGTH=424</td><td>423</td><td>424</td><td>0</td><td>100.2</td><td>86.8</td><td>92.4</td></tr>
<tr><td>Rsa1.0_01943.1.g30973.t1</td><td>gb|AAF97297.1|AC010164_19 Hypothetical protein [Arabidopsis thaliana]</td><td>115</td><td>308</td><td>1.00E-34</td><td>267.8</td><td>67.8</td><td>77.4</td><td>Hypothetical protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>115</td><td>1262</td><td>1.00E-11</td><td>1097.4</td><td>31.3</td><td>44.3</td></tr>
<tr><td>Rsa1.0_01944.1.g30974.t1</td><td>ref|NP_191256.1| transcription factor ORG2 [Arabidopsis thaliana] gi|75311784|sp|Q9M1K1.1|ORG2_ARATH RecName: Full=Transcription factor ORG2; AltName: Full=Basic helix-loop-helix protein 38; Short=AtbHLH38; Short=bHLH 38; AltName: Full=OBP3-responsive gene 2; AltName: Full=Transcription factor EN 8; AltName: Full=bHLH transcription factor bHLH038 gi|20127034|gb|AAM10940.1|AF488576_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|6911867|emb|CAB72167.1| putative protein [Arabidopsis thaliana] gi|62320432|dbj|BAD94899.1| putative bHLH transcription factor [Arabidopsis thaliana] gi|111074306|gb|ABH04526.1| At3g56970 [Arabidopsis thaliana] gi|332646073|gb|AEE79594.1| transcription factor ORG2 [Arabidopsis thaliana]</td><td>251</td><td>253</td><td>4.00E-94</td><td>100.8</td><td>69.3</td><td>81.7</td><td>transcription factor ORG2</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G56970.1 | Symbols: BHLH038, ORG2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:21084204-21085094 REVERSE LENGTH=253</td><td>251</td><td>253</td><td>1.00E-96</td><td>100.8</td><td>69.3</td><td>81.7</td></tr>
<tr><td>Rsa1.0_01944.1.g30975.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
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Rsa1.0_01944.1.g30976.t1	ref|NP_191256.1| transcription factor ORG2 [Arabidopsis thaliana] gi|75311784|sp|Q9M1K1.1|ORG2_ARATH RecName: Full=Transcription factor ORG2; AltName: Full=Basic helix-loop-helix protein 38; Short=AtbHLH38; Short=bHLH 38; AltName: Full=OBP3-responsive gene 2; AltName: Full=Transcription factor EN 8; AltName: Full=bHLH transcription factor bHLH038 gi|20127034|gb|AAM10940.1|AF488576_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|6911867|emb|CAB72167.1| putative protein [Arabidopsis thaliana] gi|62320432|dbj|BAD94899.1| putative bHLH transcription factor [Arabidopsis thaliana] gi|111074306|gb|ABH04526.1| At3g56970 [Arabidopsis thaliana] gi|332646073|gb|AEE79594.1| transcription factor ORG2 [Arabidopsis thaliana]	251	253	9.00E-93	100.8	69.3	81.3	transcription factor ORG2	gbpln	Arabidopsis thaliana	AT3G56970.1 | Symbols: BHLH038, ORG2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:21084204-21085094 REVERSE LENGTH=253	251	253	3.00E-95	100.8	69.3	81.3
Rsa1.0_01944.1.g30977.t1	gb|AAD29058.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	673	1229	1.00E-163	182.6	46.8	64.9	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	673	575	7.00E-41	85.4	14.1	21.4
Rsa1.0_01944.1.g30978.t1	ref|NP_191256.1| transcription factor ORG2 [Arabidopsis thaliana] gi|75311784|sp|Q9M1K1.1|ORG2_ARATH RecName: Full=Transcription factor ORG2; AltName: Full=Basic helix-loop-helix protein 38; Short=AtbHLH38; Short=bHLH 38; AltName: Full=OBP3-responsive gene 2; AltName: Full=Transcription factor EN 8; AltName: Full=bHLH transcription factor bHLH038 gi|20127034|gb|AAM10940.1|AF488576_1 putative bHLH transcription factor [Arabidopsis thaliana] gi|6911867|emb|CAB72167.1| putative protein [Arabidopsis thaliana] gi|62320432|dbj|BAD94899.1| putative bHLH transcription factor [Arabidopsis thaliana] gi|111074306|gb|ABH04526.1| At3g56970 [Arabidopsis thaliana] gi|332646073|gb|AEE79594.1| transcription factor ORG2 [Arabidopsis thaliana]	251	253	6.00E-86	100.8	65.7	78.1	transcription factor ORG2	gbpln	Arabidopsis thaliana	AT3G56970.1 | Symbols: BHLH038, ORG2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr3:21084204-21085094 REVERSE LENGTH=253	251	253	2.00E-88	100.8	65.7	78.1
Rsa1.0_01944.1.g30979.t1	gb|EOA23553.1| hypothetical protein CARUB_v10016747mg [Capsella rubella]	727	721	0	99.2	79.0	85.7	hypothetical protein CARUB_v10016747mg	gbpln	Capsella rubella	AT3G56990.1 | Symbols: EDA7 | embryo sac development arrest 7 | chr3:21088358-21091976 REVERSE LENGTH=711	727	711	0	97.8	79.8	86.1
Rsa1.0_01944.1.g30980.t1	ref|NP_191259.1| nucleolar essential protein-related protein [Arabidopsis thaliana] gi|6911870|emb|CAB72170.1| putative protein [Arabidopsis thaliana] gi|28466945|gb|AAO44081.1| At3g57000 [Arabidopsis thaliana] gi|110735698|dbj|BAE99829.1| hypothetical protein [Arabidopsis thaliana] gi|332646076|gb|AEE79597.1| nucleolar essential protein-related protein [Arabidopsis thaliana]	293	298	1.00E-129	101.7	78.2	89.8	nucleolar essential protein-related protein	gbpln	Arabidopsis thaliana	AT3G57000.1 | Symbols: | nucleolar essential protein-related | chr3:21092610-21094109 FORWARD LENGTH=298	293	298	1.00E-131	101.7	78.2	89.8
Rsa1.0_01945.1.g30981.t1	ref|XP_002864634.1| ATTRP1 [Arabidopsis lyrata subsp. lyrata] gi|297310469|gb|EFH40893.1| ATTRP1 [Arabidopsis lyrata subsp. lyrata]	560	574	0	102.5	72.9	79.8	ATTRP1	gbpln	Arabidopsis lyrata	AT5G59430.3 | Symbols: ATTRP1 | telomeric repeat binding protein 1 | chr5:23968254-23970753 FORWARD LENGTH=568	560	568	0	101.4	72.0	79.5
Rsa1.0_01945.1.g30982.t1	ref|XP_002864635.1| thymidylate kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297310470|gb|EFH40894.1| thymidylate kinase family protein [Arabidopsis lyrata subsp. lyrata]	220	263	1.00E-109	119.5	87.7	94.1	thymidylate kinase family protein	gbpln	Arabidopsis lyrata	AT5G59440.3 | Symbols: ZEU1 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:23971397-23972729 FORWARD LENGTH=271	220	271	1.00E-110	123.2	87.7	93.2
Rsa1.0_01945.1.g30983.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

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<tr><td>Rsa1.0_01945.1.g30984.t1</td><td>ref|NP_200753.1| scarecrow-like protein 11 [Arabidopsis thaliana] gi|75180465|sp|Q9LTI5.1|SCL11_ARATH RecName: Full=Scarecrow-like protein 11; Short=AtSCL11; AltName: Full=GRAS family protein 31; Short=AtGRAS-31 gi|8885550|dbj|BAA97480.1| SCARECROW transcriptional regulator-like protein [Arabidopsis thaliana] gi|14334656|gb|AAK59506.1| putative scarecrow 11 protein [Arabidopsis thaliana] gi|17065588|gb|AAL33772.1| putative scarecrow 11 protein [Arabidopsis thaliana] gi|332009808|gb|AED97191.1| scarecrow-like protein 11 [Arabidopsis thaliana]</td><td>585</td><td>610</td><td>0</td><td>104.3</td><td>82.4</td><td>89.9</td><td>scarecrow-like protein 11</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G59450.1 | Symbols: | GRAS family transcription factor | chr5:23974808-23976640 FORWARD LENGTH=610</td><td>585</td><td>610</td><td>0</td><td>104.3</td><td>82.4</td><td>89.9</td></tr>
<tr><td>Rsa1.0_01945.1.g30985.t1</td><td>gb|EOA14099.1| hypothetical protein CARUB_v10027239mg [Capsella rubella]</td><td>326</td><td>173</td><td>2.00E-44</td><td>53.1</td><td>32.2</td><td>35.6</td><td>hypothetical protein CARUB_v10027239mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G59460.1 | Symbols: | scarecrow-like transcription factor 11 (SCL11) | chr5:23976968-23978291 REVERSE LENGTH=172</td><td>326</td><td>172</td><td>3.00E-39</td><td>52.8</td><td>29.4</td><td>33.1</td></tr>
<tr><td>Rsa1.0_01945.1.g30986.t1</td><td>ref|XP_002866333.1| hypothetical protein ARALYDRAFT_496082 [Arabidopsis lyrata subsp. lyrata] gi|297312168|gb|EFH42592.1| hypothetical protein ARALYDRAFT_496082 [Arabidopsis lyrata subsp. lyrata]</td><td>263</td><td>266</td><td>1.00E-129</td><td>101.1</td><td>86.7</td><td>93.5</td><td>hypothetical protein ARALYDRAFT_496082</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G59490.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:23982922-23984419 REVERSE LENGTH=266</td><td>263</td><td>266</td><td>1.00E-124</td><td>101.1</td><td>86.7</td><td>93.5</td></tr>
<tr><td>Rsa1.0_01945.1.g30987.t1</td><td>ref|NP_200758.1| C-terminal S-isoprenylcysteine carboxyl O-methyltransferase [Arabidopsis thaliana] gi|8885555|dbj|BAA97485.1| unnamed protein product [Arabidopsis thaliana] gi|26983876|gb|AAN86190.1| unknown protein [Arabidopsis thaliana] gi|332009815|gb|AED97198.1| C-terminal S-isoprenylcysteine carboxyl O-methyltransferase [Arabidopsis thaliana]</td><td>452</td><td>396</td><td>0</td><td>87.6</td><td>70.8</td><td>77.2</td><td>C-terminal S-isoprenylcysteine carboxyl O-methyltransferase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G59500.1 | Symbols: | protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferases | chr5:23986024-23987214 FORWARD LENGTH=396</td><td>452</td><td>396</td><td>0</td><td>87.6</td><td>70.8</td><td>77.2</td></tr>
<tr><td>Rsa1.0_01945.1.g30988.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01945.1.g30989.t1</td><td>ref|XP_002866337.1| hypothetical protein ARALYDRAFT_496089 [Arabidopsis lyrata subsp. lyrata] gi|297312172|gb|EFH42596.1| hypothetical protein ARALYDRAFT_496089 [Arabidopsis lyrata subsp. lyrata]</td><td>400</td><td>406</td><td>1.00E-143</td><td>101.5</td><td>75.0</td><td>81.3</td><td>hypothetical protein ARALYDRAFT_496089</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G59550.1 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:23998422-23999645 REVERSE LENGTH=407</td><td>400</td><td>407</td><td>1.00E-141</td><td>101.8</td><td>74.5</td><td>80.5</td></tr>
<tr><td>Rsa1.0_01946.1.g30990.t1</td><td>dbj|BAB02256.1| unnamed protein product [Arabidopsis thaliana]</td><td>89</td><td>386</td><td>9.00E-23</td><td>433.7</td><td>59.6</td><td>71.9</td><td>unnamed protein product</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G29638.1 | Symbols: | General transcription factor 2-related zinc finger protein | chr3:11473584-11475559 FORWARD LENGTH=412</td><td>89</td><td>412</td><td>4.00E-21</td><td>462.9</td><td>50.6</td><td>61.8</td></tr>
<tr><td>Rsa1.0_01946.1.g30991.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>606</td><td>1142</td><td>0</td><td>188.4</td><td>53.0</td><td>67.8</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>606</td><td>575</td><td>5.00E-44</td><td>94.9</td><td>19.0</td><td>29.9</td></tr>
<tr><td>Rsa1.0_01946.1.g30992.t1</td><td>gb|EOA16268.1| hypothetical protein CARUB_v10004413mg, partial [Capsella rubella]</td><td>576</td><td>603</td><td>0</td><td>104.7</td><td>77.8</td><td>84.7</td><td>hypothetical protein CARUB_v10004413mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G41940.1 | Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr5:16782039-16785451 FORWARD LENGTH=549</td><td>576</td><td>549</td><td>0</td><td>95.3</td><td>77.8</td><td>83.3</td></tr>
<tr><td>Rsa1.0_01946.1.g30993.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01946.1.g30994.t2</td><td>ref|XP_002870604.1| hypothetical protein ARALYDRAFT_330340 [Arabidopsis lyrata subsp. lyrata] gi|297316440|gb|EFH46863.1| hypothetical protein ARALYDRAFT_330340 [Arabidopsis lyrata subsp. lyrata]</td><td>499</td><td>372</td><td>0</td><td>74.5</td><td>66.9</td><td>68.7</td><td>hypothetical protein ARALYDRAFT_330340</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G41970.1 | Symbols: | Metal-dependent protein hydrolase | chr5:16791198-16792961 FORWARD LENGTH=373</td><td>499</td><td>373</td><td>0</td><td>74.7</td><td>66.3</td><td>68.5</td></tr>
<tr><td>Rsa1.0_01946.1.g30995.t1</td><td>gb|EOA16321.1| hypothetical protein CARUB_v10004471mg [Capsella rubella]</td><td>466</td><td>571</td><td>0</td><td>122.5</td><td>86.1</td><td>92.5</td><td>hypothetical protein CARUB_v10004471mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G41990.1 | Symbols: WNK8, ATWNK8 | with no lysine (K) kinase 8 | chr5:16795085-16797562 REVERSE LENGTH=563</td><td>466</td><td>563</td><td>0</td><td>120.8</td><td>84.5</td><td>90.1</td></tr>
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Rsa1.0_01947.1.g30996.t1	ref|NP_177024.1| putative nitrite transporter [Arabidopsis thaliana] gi|75266596|sp|Q9SX20.1|PTR18_ARATH RecName: Full=Probable nitrite transporter At1g68570 gi|5734721|gb|AAD49986.1|AC008075_19 Similar to gb|AF023472 peptide transporter from Hordeum vulgare and is a member of the PF|00854 Peptide transporter family. ESTs gb|T41927 and gb|AA395024 come from this gene [Arabidopsis thaliana] gi|20147231|gb|AAM10330.1| At1g68570/F24J5_7 [Arabidopsis thaliana] gi|25090385|gb|AAN72289.1| At1g68570/F24J5_7 [Arabidopsis thaliana] gi|110742209|dbj|BAE99031.1| peptide transporter like [Arabidopsis thaliana] gi|332196691|gb|AEE34812.1| probable nitrite transporter [Arabidopsis thaliana]	592	596	0	100.7	91.9	96.6	putative nitrite transporter	gbpln	Arabidopsis thaliana	AT1G68570.1 | Symbols: | Major facilitator superfamily protein | chr1:25746811-25750110 FORWARD LENGTH=596	592	596	0	100.7	91.9	96.6
Rsa1.0_01947.1.g30997.t1	gb|EOA17341.1| hypothetical protein CARUB_v10005624mg [Capsella rubella]	225	239	1.00E-98	106.2	82.2	88.0	hypothetical protein CARUB_v10005624mg	gbpln	Capsella rubella	AT4G39670.1 | Symbols: | Glycolipid transfer protein (GLTP) family protein | chr4:18410172-18410861 FORWARD LENGTH=229	225	229	1.00E-100	101.8	78.7	85.8
Rsa1.0_01947.1.g30998.t1	ref|XP_002887191.1| hypothetical protein ARALYDRAFT_475982 [Arabidopsis lyrata subsp. lyrata] gi|297333032|gb|EFH63450.1| hypothetical protein ARALYDRAFT_475982 [Arabidopsis lyrata subsp. lyrata]	690	649	0	94.1	68.1	77.5	hypothetical protein ARALYDRAFT_475982	gbpln	Arabidopsis lyrata	AT1G68580.2 | Symbols: | agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein | chr1:25752869-25755631 FORWARD LENGTH=648	690	648	0	93.9	67.4	78.1
Rsa1.0_01947.1.g30999.t1	gb|AAM63350.1| plastid-specific ribosomal protein 3 precursor [Arabidopsis thaliana]	166	166	6.00E-71	100.0	84.9	89.8	plastid-specific ribosomal protein 3 precursor	gbpln	Arabidopsis thaliana	AT1G68590.1 | Symbols: | Ribosomal protein PSRP-3/Ycf65 | chr1:25757593-25758169 REVERSE LENGTH=166	166	166	4.00E-73	100.0	84.9	89.8
Rsa1.0_01947.1.g31000.t1	ref|NP_177028.1| cadmium resistance 11 protein [Arabidopsis thaliana] gi|75266599|sp|Q9SX24.1|PCR11_ARATH RecName: Full=Protein PLANT CADMIUM RESISTANCE 11; Short=AtPCR11 gi|5734716|gb|AAD49981.1|AC008075_14 Similr to gb|AF049928 PGP224 protein from Petunia x hybrida [Arabidopsis thaliana] gi|332196698|gb|AEE34819.1| cadmium resistance 11 protein [Arabidopsis thaliana]	163	160	4.00E-62	98.2	79.1	82.8	cadmium resistance 11 protein	gbpln	Arabidopsis thaliana	AT1G68610.1 | Symbols: PCR11 | PLANT CADMIUM RESISTANCE 11 | chr1:25763623-25764105 FORWARD LENGTH=160	163	160	1.00E-64	98.2	79.1	82.8
Rsa1.0_01947.1.g31001.t1	ref|NP_564936.1| alpha/beta-hydrolase domain-containing protein [Arabidopsis thaliana] gi|75337796|sp|Q9SX25.1|CXE6_ARATH RecName: Full=Probable carboxylesterase 6; AltName: Full=AtCXE6 gi|5734715|gb|AAD49980.1|AC008075_13 Similar to gb|AF110333 PrMC3 protein from Pinus radiata and is a member of PF|00135 Carboxylesterases family. EST gb|N37841 comes from this gene [Arabidopsis thaliana] gi|13877777|gb|AAK43966.1|AF370151_1 unknown protein [Arabidopsis thaliana] gi|14335126|gb|AAK59842.1| At1g68620/F24J5_21 [Arabidopsis thaliana] gi|16323410|gb|AAL15199.1| unknown protein [Arabidopsis thaliana] gi|332196699|gb|AEE34820.1| probable carboxylesterase 6 [Arabidopsis thaliana]	332	336	1.00E-142	101.2	75.0	84.3	alpha/beta-hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT1G68620.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:25766018-25767028 FORWARD LENGTH=336	332	336	1.00E-144	101.2	75.0	84.3
Rsa1.0_01947.1.g31002.t1	gb|EOA33841.1| hypothetical protein CARUB_v10021324mg [Capsella rubella]	161	161	4.00E-76	100.0	82.6	91.3	hypothetical protein CARUB_v10021324mg	gbpln	Capsella rubella	AT1G68630.1 | Symbols: | PLAC8 family protein | chr1:25768653-25769458 FORWARD LENGTH=161	161	161	2.00E-78	100.0	82.0	91.9
Rsa1.0_01947.1.g31003.t1	ref|XP_002888675.1| transcription factor perianthia [Arabidopsis lyrata subsp. lyrata] gi|297334516|gb|EFH64934.1| transcription factor perianthia [Arabidopsis lyrata subsp. lyrata]	455	446	0	98.0	86.6	90.3	transcription factor perianthia	gbpln	Arabidopsis lyrata	AT1G68640.1 | Symbols: PAN | bZIP transcription factor family protein | chr1:25769739-25772303 REVERSE LENGTH=452	455	452	0	99.3	86.2	90.3

Rsa1.0_01948.1.g31004.t1	#	#	#	#	#	#	#	–	----	----	AT4G32200.1 | Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15554962 FORWARD LENGTH=1399	958	1399	5.00E-12	146.0	8.1	14.0
Rsa1.0_01948.1.g31005.t1	gb|EOA30146.1| hypothetical protein CARUB_v10013253mg [Capsella rubella]	108	609	2.00E-46	563.9	84.3	88.0	hypothetical protein CARUB_v10013253mg	gbpln	Capsella rubella	AT3G18060.1 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:6183880-6186788 FORWARD LENGTH=609	108	609	3.00E-49	563.9	84.3	87.0
Rsa1.0_01948.1.g31006.t1	gb|AAD17395.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	225	1138	3.00E-27	505.8	24.4	33.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	225	575	3.00E-17	255.6	23.6	37.3
Rsa1.0_01948.1.g31007.t1	ref|XP_002865388.1| hypothetical protein ARALYDRAFT_917224 [Arabidopsis lyrata subsp. lyrata] gi|297311223|gb|EFH41647.1| hypothetical protein ARALYDRAFT_917224 [Arabidopsis lyrata subsp. lyrata]	272	272	1.00E-142	100.0	90.1	94.1	hypothetical protein ARALYDRAFT_917224	gbpln	Arabidopsis lyrata	AT5G44020.1 | Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr5:17712433-17714046 FORWARD LENGTH=272	272	272	1.00E-136	100.0	89.0	92.6
Rsa1.0_01948.1.g31008.t1	gb|ACS68194.1| cellulose synthase 4.2 catalytic subunit [Brassica napus]	1047	1052	0	100.5	96.4	97.8	cellulose synthase 4.2 catalytic subunit	gbpln	Brassica napus	AT5G44030.1 | Symbols: CESA4, IRX5, NWS2 | cellulose synthase A4 | chr5:17714713-17719564 FORWARD LENGTH=1049	1047	1049	0	100.2	93.7	96.2
Rsa1.0_01948.1.g31009.t1	ref|NP_199217.1| uncharacterized protein [Arabidopsis thaliana] gi|9758563|dbj|BAB09064.1| unnamed protein product [Arabidopsis thaliana] gi|20466155|gb|AAM20395.1| putative protein [Arabidopsis thaliana] gi|30725674|gb|AAP37859.1| At5g44040 [Arabidopsis thaliana] gi|332007668|gb|AED95051.1| uncharacterized protein AT5G44040 [Arabidopsis thaliana]	392	416	1.00E-117	106.1	71.7	79.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G44040.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G04030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:17719896-17721348 REVERSE LENGTH=416	392	416	1.00E-120	106.1	71.7	79.8
Rsa1.0_01948.1.g31010.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	576	1142	1.00E-173	198.3	51.6	68.2	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	576	575	9.00E-84	99.8	31.8	50.7
Rsa1.0_01948.1.g31011.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01948.1.g31012.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01949.1.g31013.t1	gb|ABD65177.1| hypothetical protein 40.t00065 [Brassica oleracea]	112	237	8.00E-41	211.6	81.3	84.8	hypothetical protein 40.t00065	gbpln	Brassica oleracea	AT4G17440.2 | Symbols: | Protein of unknown function (DUF1639) | chr4:9727848-9728823 FORWARD LENGTH=215	112	215	4.00E-40	192.0	69.6	74.1
Rsa1.0_01949.1.g31014.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01949.1.g31015.t1	gb|ABD65141.1| homeobox-leucine zipper protein hat1, putative [Brassica oleracea]	280	277	1.00E-144	98.9	90.7	92.9	homeobox-leucine zipper protein hat1, putative	gbpln	Brassica oleracea	AT4G17460.1 | Symbols: HAT1 | Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein | chr4:9739862-9740983 FORWARD LENGTH=282	280	282	1.00E-142	100.7	91.1	93.9
Rsa1.0_01949.1.g31016.t20	gb|ABD65142.1| palmitoyl protein thioesterase family protein [Brassica oleracea]	300	314	1.00E-130	104.7	75.7	83.7	palmitoyl protein thioesterase family protein	gbpln	Brassica oleracea	AT4G17483.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:9747375-9748892 REVERSE LENGTH=300	300	300	1.00E-120	100.0	69.7	80.7
Rsa1.0_01949.1.g31017.t1	gb|ABD65143.1| hypothetical protein 40.t00020 [Brassica oleracea]	215	208	1.00E-106	96.7	91.6	94.0	hypothetical protein 40.t00020	gbpln	Brassica oleracea	AT4G17486.1 | Symbols: | PPPDE putative thiol peptidase family protein | chr4:9749992-9751201 REVERSE LENGTH=224	215	224	1.00E-102	104.2	84.2	88.4
Rsa1.0_01949.1.g31018.t1	gb|ABD65144.1| ubiquitin carboxyl-terminal hydrolase, putative [Brassica oleracea]	234	251	1.00E-125	107.3	93.6	97.9	ubiquitin carboxyl-terminal hydrolase, putative	gbpln	Brassica oleracea	AT4G17510.1 | Symbols: UCH3 | ubiquitin C-terminal hydrolase 3 | chr4:9767114-9768648 REVERSE LENGTH=234	234	234	1.00E-123	100.0	87.2	94.9
Rsa1.0_01949.1.g31019.t1	gb|ABD65145.1| nuclear RNA binding protein, putative [Brassica oleracea]	355	353	1.00E-130	99.4	89.0	89.6	nuclear RNA binding protein, putative	gbpln	Brassica oleracea	AT4G17520.1 | Symbols: | Hyaluronan / mRNA binding family | chr4:9771496-9773313 FORWARD LENGTH=360	355	360	1.00E-114	101.4	70.7	78.9
Rsa1.0_01949.1.g31020.t1	gb|EOA14024.1| hypothetical protein CARUB_v10027156mg [Capsella rubella]	203	202	1.00E-112	99.5	96.1	97.0	hypothetical protein CARUB_v10027156mg	gbpln	Capsella rubella	AT5G47200.1 | Symbols: ATRABD2B, ATRAB1A, RAB1A | RAB GTPase homolog 1A | chr5:19167029-19168718 FORWARD LENGTH=202	203	202	1.00E-113	99.5	95.6	96.6
Rsa1.0_01949.1.g31021.t1	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	962	1463	3.00E-88	152.1	15.2	18.5	F5J5.1	gbpln	Arabidopsis thaliana	AT4G17550.1 | Symbols: | Major facilitator superfamily protein | chr4:9777938-9779738 REVERSE LENGTH=544	962	544	3.00E-87	56.5	16.9	17.4
Rsa1.0_01950.1.g31022.t1	gb|AAF24529.1|AC007534_10 F7F22.15 [Arabidopsis thaliana]	187	1862	1.00E-57	995.7	59.4	70.6	F7F22.15	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01950.1.g31023.t3	ref|XP_002868305.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297314141|gb|EFH44564.1| binding protein [Arabidopsis lyrata subsp. lyrata]	355	502	3.00E-88	141.4	52.7	60.8	binding protein	gbpln	Arabidopsis lyrata	AT4G14190.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:8183594-8185180 REVERSE LENGTH=501	355	501	6.00E-89	141.1	53.0	60.8
Rsa1.0_01950.1.g31024.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01950.1.g31025.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_01951.1.g31026.t1	gb|EOA24149.1| hypothetical protein CARUB_v10017383mg, partial [Capsella rubella]	127	402	3.00E−42	316.5	80.3	85.0	hypothetical protein CARUB_v10017383mg, partial	gbpln	Capsella rubella	AT3G52180.2 | Symbols: ATPTPKIS1, DSP4, SEX4, ATSEX4 | dual specificity protein phosphatase (DsPTP1) family protein | chr3:19350574−19353459 REVERSE LENGTH=292	127	292	3.00E−41	229.9	78.0	83.5
Rsa1.0_01951.1.g31027.t1	ref|NP_566961.1| SEC12−like protein 1 [Arabidopsis thaliana] gi|85687563|sp|Q8GYE0.2|PHF1_ARATH RecName: Full=SEC12−like protein 1; AltName: Full=Protein PHOSPHATE TRANSPORTER TRAFFIC FACILITATOR 1; Short=PHF−1 gi|4678948|emb|CAB41339.1| putative protein [Arabidopsis thaliana] gi|114050625|gb|ABI49462.1| At3g52190 [Arabidopsis thaliana] gi|332645390|gb|AEE78911.1| SEC12−like protein 1 [Arabidopsis thaliana]	397	398	0	100.3	92.7	97.0	SEC12−like protein 1	gbpln	Arabidopsis thaliana	AT3G52190.1 | Symbols: PHF1 | phosphate transporter traffic facilitator1 | chr3:19354117−19356910 REVERSE LENGTH=398	397	398	0	100.3	92.7	97.0
Rsa1.0_01951.1.g31028.t1	ref|XP_002879925.1| F−box family protein [Arabidopsis lyrata subsp. lyrata] gi|297325764|gb|EFH56184.1| F−box family protein [Arabidopsis lyrata subsp. lyrata]	326	371	7.00E−40	113.8	41.1	59.2	F−box family protein	gbpln	Arabidopsis lyrata	AT2G22050.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:9376684−9377552 FORWARD LENGTH=259	326	259	1.00E−32	79.4	28.8	39.3
Rsa1.0_01951.1.g31029.t2	ref|XP_002876130.1| mRNA capping enzyme family protein [Arabidopsis lyrata subsp. lyrata] gi|297321968|gb|EFH52389.1| mRNA capping enzyme family protein [Arabidopsis lyrata subsp. lyrata]	361	355	1.00E−169	98.3	83.4	88.4	mRNA capping enzyme family protein	gbpln	Arabidopsis lyrata	AT3G52210.1 | Symbols: | S−adenosyl−L−methionine−dependent methyltransferases superfamily protein | chr3:19367035−19369293 FORWARD LENGTH=354	361	354	1.00E−171	98.1	83.1	88.4
Rsa1.0_01951.1.g31030.t1	ref|NP_566962.1| uncharacterized protein [Arabidopsis thaliana] gi|13899105|gb|AAK48974.1|AF370547_1 putative protein [Arabidopsis thaliana] gi|30023708|gb|AAP13387.1| At3g52220 [Arabidopsis thaliana] gi|332645396|gb|AEE78917.1| uncharacterized protein AT3G52220 [Arabidopsis thaliana]	243	237	1.00E−100	97.5	81.1	90.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G52220.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Kinase phosphorylation domain (InterPro:IPR019315); Has 8882 Blast hits to 4920 proteins in 346 species: Archae − 10; Bacteria − 184; Metazoa − 3955; Fungi − 1221; Plants − 712; Viruses − 24; Other Eukaryotes − 2776 (source: NCBI BLink). | chr3:19369580−19370980 REVERSE LENGTH=237	243	237	1.00E−103	97.5	81.1	90.1
Rsa1.0_01951.1.g31031.t1	gb|EOA24913.1| hypothetical protein CARUB_v10018204mg [Capsella rubella]	126	143	4.00E−34	113.5	58.7	66.7	hypothetical protein CARUB_v10018204mg	gbpln	Capsella rubella	AT3G52230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast outer membrane, chloroplast thylakoid membrane, chloroplast, chloroplast envelope; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; Has 29 Blast hits to 29 proteins in 12 species: Archae − 0; Bacteria − 0; Metazoa − 3; Fungi − 0; Plants − 26; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:19371325−19372397 FORWARD LENGTH=145	126	145	3.00E−32	115.1	54.8	64.3
Rsa1.0_01951.1.g31032.t1	ref|XP_002877850.1| hypothetical protein ARALYDRAFT_323774 [Arabidopsis lyrata subsp. lyrata] gi|297323688|gb|EFH54109.1| hypothetical protein ARALYDRAFT_323774 [Arabidopsis lyrata subsp. lyrata]	619	688	0	111.1	73.2	83.8	hypothetical protein ARALYDRAFT_323774	gbpln	Arabidopsis lyrata	AT3G52240.1 | Symbols: | unknown protein; Has 220 Blast hits to 193 proteins in 66 species: Archae − 0; Bacteria − 15; Metazoa − 53; Fungi − 33; Plants − 66; Viruses − 0; Other Eukaryotes − 53 (source: NCBI BLink). | chr3:19372902−19375799 REVERSE LENGTH=680	619	680	0	109.9	70.4	80.6
Rsa1.0_01951.1.g31033.t1	ref|XP_002876132.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata] gi|297321970|gb|EFH52391.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	1648	1655	0	100.4	75.5	83.6	myb family transcription factor	gbpln	Arabidopsis lyrata	AT3G52250.1 | Symbols: | Duplicated homeodomain−like superfamily protein | chr3:19376629−19383100 FORWARD LENGTH=1656	1648	1656	0	100.5	73.9	82.2
Rsa1.0_01951.1.g31034.t1	ref|XP_002868834.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297314670|gb|EFH45093.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	155	144	1.00E−43	92.9	58.7	68.4	zinc finger family protein	gbpln	Arabidopsis lyrata	AT4G38140.1 | Symbols: | RING/U−box superfamily protein | chr4:17899868−17900305 REVERSE LENGTH=145	155	145	1.00E−45	93.5	65.2	76.1
Rsa1.0_01951.1.g31035.t3	ref|XP_002877852.1| hypothetical protein ARALYDRAFT_348323 [Arabidopsis lyrata subsp. lyrata] gi|297323690|gb|EFH54111.1| hypothetical protein ARALYDRAFT_348323 [Arabidopsis lyrata subsp. lyrata]	324	258	1.00E−108	79.6	59.9	66.4	hypothetical protein ARALYDRAFT_348323	gbpln	Arabidopsis lyrata	AT3G52270.1 | Symbols: | Transcription initiation factor IIF, beta subunit | chr3:19387180−19388902 REVERSE LENGTH=269	324	269	1.00E−102	83.0	58.3	65.1
Rsa1.0_01952.1.g31036.t1	#	#	#	#	#	#	#	–	----	----	AT2G01830.1 | Symbols: WOL, CRE1, WOL1, AHK4, ATCRE1 | CHASE domain containing histidine kinase protein | chr2:363332−367429 REVERSE LENGTH=1057	137	1057	6.00E−11	771.5	25.5	26.3

Rsa1.0_01952.1.g31037.t1	gb|EOA23460.1| hypothetical protein CARUB_v10016649mg [Capsella rubella]	454	947	1.00E-172	208.6	68.9	81.3	hypothetical protein CARUB_v10016649mg	gbpln	Capsella rubella	AT2G01820.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr2:357664-360681 REVERSE LENGTH=943	454	943	1.00E-169	207.7	66.1	79.7
Rsa1.0_01952.1.g31038.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01952.1.g31039.t5	emb|CAB75909.1| putative protein [Arabidopsis thaliana]	369	606	6.00E-20	164.2	17.3	20.1	putative protein	gbpln	Arabidopsis thaliana	AT3G55510.1 | Symbols: RBL | Noc2p family | chr3:20579232-20582124 FORWARD LENGTH=594	369	594	2.00E-22	161.0	17.3	20.1
Rsa1.0_01952.1.g31040.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01953.1.g31041.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01953.1.g31042.t1	gb|EOA15425.1| hypothetical protein CARUB_v10003963mg [Capsella rubella]	2236	2547	0	113.9	66.9	77.9	hypothetical protein CARUB_v10003963mg	gbpln	Capsella rubella	AT4G27010.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Ribosome 60S biogenesis N-terminal (InterPro:IPR021714); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G72270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13558943-13568296 FORWARD LENGTH=2374	2236	2374	0	106.2	52.1	60.5
Rsa1.0_01953.1.g31043.t1	gb|EOA40127.1| hypothetical protein CARUB_v10008834mg [Capsella rubella]	524	528	0	100.8	88.5	94.3	hypothetical protein CARUB_v10008834mg	gbpln	Capsella rubella	AT1G19250.1 | Symbols: FMO1 | flavin-dependent monooxygenase 1 | chr1:6650656-6653053 REVERSE LENGTH=530	524	530	0	101.1	87.4	92.9
Rsa1.0_01953.1.g31044.t1	gb|ABD64930.1| hypothetical protein 24.t00076 [Brassica oleracea]	460	407	5.00E-70	88.5	35.2	41.3	hypothetical protein 24.t00076	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01953.1.g31045.t1	gb|EOA40132.1| hypothetical protein CARUB_v10008839mg [Capsella rubella]	511	525	0	102.7	84.0	90.2	hypothetical protein CARUB_v10008839mg	gbpln	Capsella rubella	AT1G19270.1 | Symbols: DA1 | DA1 | chr1:6663327-6665845 FORWARD LENGTH=532	511	532	0	104.1	83.2	90.8
Rsa1.0_01953.1.g31046.t1	ref|XP_002890327.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297336169|gb|EFH66586.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	900	903	0	100.3	76.7	87.6	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis lyrata	AT1G19290.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:6666249-6668963 FORWARD LENGTH=904	900	904	0	100.4	76.6	87.9
Rsa1.0_01953.1.g31047.t1	ref|XP_002893040.1| hypothetical protein ARALYDRAFT_472152 [Arabidopsis lyrata subsp. lyrata] gi|297338882|gb|EFH69299.1| hypothetical protein ARALYDRAFT_472152 [Arabidopsis lyrata subsp. lyrata]	351	350	1.00E-171	99.7	90.3	93.2	hypothetical protein ARALYDRAFT_472152	gbpln	Arabidopsis lyrata	AT1G19300.1 | Symbols: GATL1, PARVUS, GLZ1, ATGATL1 | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:6671451-6672506 REVERSE LENGTH=351	351	351	1.00E-171	100.0	92.6	96.6
Rsa1.0_01954.1.g31048.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01954.1.g31049.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01954.1.g31050.t1	ref|XP_002894442.1| hypothetical protein ARALYDRAFT_474474 [Arabidopsis lyrata subsp. lyrata] gi|297340284|gb|EFH70701.1| hypothetical protein ARALYDRAFT_474474 [Arabidopsis lyrata subsp. lyrata]	444	471	0	106.1	84.5	91.2	hypothetical protein ARALYDRAFT_474474	gbpln	Arabidopsis lyrata	AT1G53450.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14830.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:19951747-19953839 REVERSE LENGTH=453	444	453	0	102.0	82.9	89.2
Rsa1.0_01954.1.g31051.t1	ref|NP_175747.2| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana] gi|263711277|sp|C0LGG7.2|Y1534_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g53420; Flags: Precursor gi|332194817|gb|AEE32938.1| putative LRR receptor-like serine/threonine-protein kinase [Arabidopsis thaliana]	395	953	0	241.3	77.7	87.8	putative LRR receptor-like serine/threonine-protein kinase	gbpln	Arabidopsis thaliana	AT1G53420.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:19926626-19931494 REVERSE LENGTH=953	395	953	0	241.3	77.7	87.8
Rsa1.0_01954.1.g31052.t1	gb|EOA37213.1| hypothetical protein CARUB_v10010694mg [Capsella rubella]	115	114	6.00E-57	99.1	93.9	95.7	hypothetical protein CARUB_v10010694mg	gbpln	Capsella rubella	AT1G53400.1 | Symbols: | Ubiquitin domain-containing protein | chr1:19925009-19926400 FORWARD LENGTH=114	115	114	1.00E-59	99.1	94.8	96.5
Rsa1.0_01954.1.g31053.t3	dbj|BAE99398.1| putative ABC transporter gb|AAD31586.1 [Arabidopsis thaliana]	1170	1159	0	99.1	71.4	79.3	putative ABC transporter gb|AAD31586.1	gbpln	Arabidopsis thaliana	AT1G53390.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:19918197-19923579 FORWARD LENGTH=1109	1170	1109	0	94.8	70.4	78.1
Rsa1.0_01954.1.g31054.t3	ref|XP_002891750.1| ATPase, coupled to transmembrane movement of substances [Arabidopsis lyrata subsp. lyrata] gi|297337592|gb|EFH68009.1| ATPase, coupled to transmembrane movement of substances [Arabidopsis lyrata subsp. lyrata]	1051	1119	0	106.5	79.0	86.9	ATPase, coupled to transmembrane movement of substances	gbpln	Arabidopsis lyrata	AT1G53390.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:19918197-19923579 FORWARD LENGTH=1109	1051	1109	0	105.5	77.8	86.1

Rsa1.0_01954.1.g31055.t1	gb|ABD65067.1| nuclear RNA binding protein, putative [Brassica oleracea]	109	367	4.00E-22	336.7	68.8	75.2	nuclear RNA binding protein, putative	gbpln	Brassica oleracea	AT4G17520.1 | Symbols: | Hyaluronan / mRNA binding family | chr4:9771496-9773313 FORWARD LENGTH=360	109	360	1.00E-14	330.3	47.7	57.8
Rsa1.0_01954.1.g31056.t1	ref|NP_189200.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|332643539|gb|AEE77060.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	76	282	7.00E-15	371.1	51.3	69.7	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT3G25720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:9380234-9381405 FORWARD LENGTH=282	76	282	1.00E-17	371.1	51.3	69.7
Rsa1.0_01955.1.g31057.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	170	1142	7.00E-25	671.8	40.0	60.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT2G34320.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr2:14484959-14485837 FORWARD LENGTH=292	170	292	3.00E-15	171.8	31.2	51.8
Rsa1.0_01955.1.g31058.t1	ref|XP_002884137.1| hypothetical protein ARALYDRAFT_900233 [Arabidopsis lyrata subsp. lyrata] gi|297329977|gb|EFH60396.1| hypothetical protein ARALYDRAFT_900233 [Arabidopsis lyrata subsp. lyrata]	303	333	3.00E-85	109.9	58.7	72.3	hypothetical protein ARALYDRAFT_900233	gbpln	Arabidopsis lyrata	AT5G42640.1 | Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr5:17088695-17089597 FORWARD LENGTH=300	303	300	1.00E-79	99.0	54.8	70.3
Rsa1.0_01955.1.g31059.t1	ref|XP_002886173.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332013|gb|EFH62432.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	621	640	0	103.1	75.0	78.4	predicted protein	gbpln	Arabidopsis lyrata	AT2G18470.1 | Symbols: PERK4 | roline-rich extensin-like receptor kinase 4 | chr2:8005285-8007767 REVERSE LENGTH=633	621	633	0	101.9	74.6	78.1
Rsa1.0_01955.1.g31060.t1	ref|XP_002881678.1| hypothetical protein ARALYDRAFT_903237 [Arabidopsis lyrata subsp. lyrata] gi|297327517|gb|EFH57937.1| hypothetical protein ARALYDRAFT_903237 [Arabidopsis lyrata subsp. lyrata]	99	159	3.00E-33	160.6	76.8	82.8	hypothetical protein ARALYDRAFT_903237	gbpln	Arabidopsis lyrata	AT1G76640.1 | Symbols: | Calcium-binding EF-hand family protein | chr1:28765324-28765803 REVERSE LENGTH=159	99	159	1.00E-34	160.6	75.8	80.8
Rsa1.0_01955.1.g31061.t1	gb|EOA30825.1| hypothetical protein CARUB_v10013969mg [Capsella rubella]	358	374	1.00E-166	104.5	83.8	89.4	hypothetical protein CARUB_v10013969mg	gbpln	Capsella rubella	AT2G18410.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Histone acetylation protein 2 (InterPro:IPR019519); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr2:7990768-7992588 FORWARD LENGTH=374	358	374	1.00E-164	104.5	83.0	89.1
Rsa1.0_01955.1.g31062.t1	ref|XP_004143514.1| PREDICTED: 60S ribosomal protein L6, mitochondrial-like [Cucumis sativus] gi|449496483|ref|XP_004160146.1| PREDICTED: 60S ribosomal protein L6, mitochondrial-like [Cucumis sativus]	102	102	1.00E-47	100.0	91.2	94.1	PREDICTED: 60S ribosomal protein L6, mitochondrial-like	gbpln	Cucumis sativus	AT2G18400.1 | Symbols: | ribosomal protein L6 family protein | chr2:7989665-7989973 REVERSE LENGTH=102	102	102	6.00E-48	100.0	88.2	88.2
Rsa1.0_01955.1.g31063.t1	ref|XP_002884131.1| hypothetical protein ARALYDRAFT_900220 [Arabidopsis lyrata subsp. lyrata] gi|297329971|gb|EFH60390.1| hypothetical protein ARALYDRAFT_900220 [Arabidopsis lyrata subsp. lyrata]	76	185	7.00E-12	243.4	53.9	57.9	hypothetical protein ARALYDRAFT_900220	gbpln	Arabidopsis lyrata	AT2G18390.1 | Symbols: TTN5, HAL, ARL2, ATARLC1 | ADP-ribosylation factor family protein | chr2:7988335-7989374 FORWARD LENGTH=185	76	185	3.00E-14	243.4	55.3	61.8
Rsa1.0_01955.1.g31064.t1	gb|ACP30591.1| disease resistance protein [Brassica rapa subsp. pekinensis]	210	1555	1.00E-29	740.5	38.6	51.9	disease resistance protein	gbpln	Brassica rapa	AT3G26855.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:9898680-9899350 REVERSE LENGTH=163	210	163	5.00E-17	77.6	19.5	29.5
Rsa1.0_01955.1.g31065.t1	ref|XP_002886168.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297332008|gb|EFH62427.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	201	206	3.00E-95	102.5	86.1	92.0	predicted protein	gbpln	Arabidopsis lyrata	AT2G18380.1 | Symbols: GATA20 | GATA transcription factor 20 | chr2:7982868-7984017 REVERSE LENGTH=208	201	208	7.00E-88	103.5	85.1	91.5

Rsa1.0_01955.1.g31066.t1	ref|NP_179425.1| late embryogenesis abundant domain-containing protein [Arabidopsis thaliana] gi|4309733|gb|AAD15503.1| similar to late embryogenesis abundant proteins [Arabidopsis thaliana] gi|110740637|dbj|BAE98422.1| similar to late embryogenesis abundant proteins [Arabidopsis thaliana] gi|330251664|gb|AEC06758.1| late embryogenesis abundant domain-containing protein [Arabidopsis thaliana]	464	456	1.00E-120	98.3	62.7	71.3	late embryogenesis abundant domain-containing protein	gbpln	Arabidopsis thaliana	AT2G18340.1 | Symbols: | late embryogenesis abundant domain-containing protein / LEA domain-containing protein | chr2:7969400-7971025 FORWARD LENGTH=456	464	456	1.00E-122	98.3	62.7	71.3
Rsa1.0_01956.1.g31067.t1	gb|ABD65022.1| hypothetical protein 26.t00077 [Brassica oleracea]	277	242	6.00E-92	87.4	64.3	71.5	hypothetical protein 26.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01956.1.g31068.t1	gb|ABD65020.1| hypothetical protein 26.t00075 [Brassica oleracea]	58	171	1.00E-23	294.8	89.7	91.4	hypothetical protein 26.t00075	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01956.1.g31069.t3	gb|AAD30632.1|AC006085_5 Hypothetical protein [Arabidopsis thaliana]	964	1295	9.00E-66	134.3	14.1	19.8	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01956.1.g31070.t2	ref|XP_002868647.1| hypothetical protein ARALYDRAFT_493934 [Arabidopsis lyrata subsp. lyrata] gi|297314483|gb|EFH44906.1| hypothetical protein ARALYDRAFT_493934 [Arabidopsis lyrata subsp. lyrata]	636	685	0	107.7	65.1	78.5	hypothetical protein ARALYDRAFT_493934	gbpln	Arabidopsis lyrata	AT5G40520.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 11 growth stages; Has 3696 Blast hits to 2485 proteins in 391 species: Archae - 10; Bacteria - 571; Metazoa - 1013; Fungi - 530; Plants - 217; Viruses - 74; Other Eukaryotes - 1281 (source: NCBI BLink). | chr5:16231515-16234276 REVERSE LENGTH=693	636	693	0	109.0	63.2	77.7
Rsa1.0_01956.1.g31071.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01957.1.g31072.t1	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	161	1239	1.00E-49	769.6	61.5	76.4	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	161	1262	9.00E-14	783.9	27.3	39.8
Rsa1.0_01957.1.g31073.t1	gb|EOA40102.1| hypothetical protein CARUB_v10008795mg [Capsella rubella]	352	539	8.00E-23	153.1	25.9	39.8	hypothetical protein CARUB_v10008795mg	gbpln	Capsella rubella	AT1G02690.1 | Symbols: IMPA-6 | importin alpha isoform 6 | chr1:584397-587036 FORWARD LENGTH=538	352	538	3.00E-23	152.8	25.3	38.9
Rsa1.0_01957.1.g31074.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01957.1.g31075.t1	ref|XP_002889216.1| hypothetical protein ARALYDRAFT_895785 [Arabidopsis lyrata subsp. lyrata] gi|297335057|gb|EFH65475.1| hypothetical protein ARALYDRAFT_895785 [Arabidopsis lyrata subsp. lyrata]	463	441	0	95.2	78.2	81.2	hypothetical protein ARALYDRAFT_895785	gbpln	Arabidopsis lyrata	AT1G78850.1 | Symbols: | D-mannose binding lectin protein with Apple-like carbohydrate-binding domain | chr1:29642072-29643397 REVERSE LENGTH=441	463	441	0	95.2	77.1	80.6
Rsa1.0_01957.1.g31076.t1	gb|AAC83026.1| Similar to Ubiquitin-conjugating enzyme E2-17 KD gb|D83004 from Homo sapiens. ESTs gb|T88233, gb|Z24464, gb|N37265, gb|H36151, gb|Z34711, gb|AA040983, and gb|T22122 come from this gene [Arabidopsis thaliana]	192	163	3.00E-76	84.9	77.6	81.8	Similar to Ubiquitin-conjugating enzyme E2-17 KD gb|D83004 from Homo sapiens. ESTs gb|T88233, gb|Z24464, gb|N37265, gb|H36151, gb|Z34711, gb|AA040983, and gb|T22122 come from this gene	gbpln	Arabidopsis thaliana	AT1G16890.2 | Symbols: UBC36, UBC13B | ubiquitin-conjugating enzyme 36 | chr1:5776550-5778327 REVERSE LENGTH=153	192	153	7.00E-76	79.7	70.3	73.4
Rsa1.0_01957.1.g31077.t1	ref|NP_178009.1| Ubiquitin-specific protease family C19-related protein [Arabidopsis thaliana] gi|3834307|gb|AAC83023.1| Strong similarity to gene T10I14.120 gi|2832679 putative protein from Arabidopsis thaliana BAC gb|AL021712. ESTs gb|N65887 and gb|N65627 come from this gene [Arabidopsis thaliana] gi|18176178|gb|AAL59998.1| unknown protein [Arabidopsis thaliana] gi|20465703|gb|AAM20320.1| unknown protein [Arabidopsis thaliana] gi|21539479|gb|AAM53292.1| unknown protein [Arabidopsis thaliana] gi|23198312|gb|AAN15683.1| unknown protein [Arabidopsis thaliana] gi|332198046|gb|AEE36167.1| Ubiquitin-specific protease family C19-related protein [Arabidopsis thaliana]	472	468	0	99.2	95.3	97.7	Ubiquitin-specific protease family C19-related protein	gbpln	Arabidopsis thaliana	AT1G78880.1 | Symbols: | Ubiquitin-specific protease family C19-related protein | chr1:29653068-29654819 REVERSE LENGTH=468	472	468	0	99.2	95.3	97.7

Rsa1.0_01957.1.g31078.t1	ref|XP_002887759.1| hypothetical protein ARALYDRAFT_477053 [Arabidopsis lyrata subsp. lyrata] gi|297333600|gb|EFH64018.1| hypothetical protein ARALYDRAFT_477053 [Arabidopsis lyrata subsp. lyrata]	175	152	4.00E-56	86.9	72.0	77.1	hypothetical protein ARALYDRAFT_477053	gbpln	Arabidopsis lyrata	AT1G78890.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16840.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:29656623-29657537 FORWARD LENGTH=155	175	155	3.00E-45	88.6	72.0	77.1
Rsa1.0_01957.1.g31079.t1	gb|EOA33781.1| hypothetical protein CARUB_v10019973mg [Capsella rubella]	623	623	0	100.0	97.6	98.9	hypothetical protein CARUB_v10019973mg	gbpln	Capsella rubella	AT1G78900.2 | Symbols: VHA-A | vacuolar ATP synthase subunit A | chr1:29660463-29664575 FORWARD LENGTH=623	623	623	0	100.0	97.4	98.7
Rsa1.0_01957.1.g31080.t1	ref|XP_002887761.1| hypothetical protein ARALYDRAFT_477057 [Arabidopsis lyrata subsp. lyrata] gi|297333602|gb|EFH64020.1| hypothetical protein ARALYDRAFT_477057 [Arabidopsis lyrata subsp. lyrata]	477	477	0	100.0	86.6	92.0	hypothetical protein ARALYDRAFT_477057	gbpln	Arabidopsis lyrata	AT1G78910.1 | Symbols: | Pseudouridine synthase family protein | chr1:29665269-29667557 FORWARD LENGTH=478	477	478	0	100.2	86.6	91.6
Rsa1.0_01958.1.g31081.t1	ref|NP_191713.1| peptidase family protein [Arabidopsis thaliana] gi|6850845|emb|CAB71084.1| prolyl aminopeptidase-like protein [Arabidopsis thaliana] gi|15450667|gb|AAK96605.1| AT3g61540/F2A19_140 [Arabidopsis thaliana] gi|17380608|gb|AAL36067.1| AT3g61540/F2A19_140 [Arabidopsis thaliana] gi|332646699|gb|AEE80220.1| peptidase family protein [Arabidopsis thaliana]	259	515	1.00E-58	198.8	50.6	56.0	peptidase family protein	gbpln	Arabidopsis thaliana	AT3G61540.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:22773399-22775699 FORWARD LENGTH=515	259	515	4.00E-61	198.8	50.6	56.0
Rsa1.0_01958.1.g31082.t1	gb|ACF81191.1| unknown [Zea mays]	177	274	7.00E-19	154.8	41.2	58.2	unknown	gbenv/gbpln	Zea mays	AT1G61670.1 | Symbols: | Lung seven transmembrane receptor family protein | chr1:22770132-22772258 FORWARD LENGTH=513	177	513	2.00E-18	289.8	24.3	27.1
Rsa1.0_01958.1.g31083.t1	ref|XP_002863741.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata] gi|297309576|gb|EFH40000.1| hypothetical protein ARALYDRAFT_917455 [Arabidopsis lyrata subsp. lyrata]	833	390	2.00E-97	46.8	26.1	33.5	hypothetical protein ARALYDRAFT_917455	gbpln	Arabidopsis lyrata	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	833	746	1.00E-51	89.6	16.9	24.8
Rsa1.0_01958.1.g31084.t1	emb|CAB94144.1| putative protein [Arabidopsis thaliana]	318	318	1.00E-165	100.0	89.3	93.7	putative protein	gbpln	Arabidopsis thaliana	AT3G61080.1 | Symbols: | Protein kinase superfamily protein | chr3:22607152-22608883 FORWARD LENGTH=326	318	326	1.00E-165	102.5	89.6	94.0
Rsa1.0_01958.1.g31085.t1	gb|EOA23277.1| hypothetical protein CARUB_v10017960mg [Capsella rubella]	235	235	1.00E-124	100.0	92.8	96.6	hypothetical protein CARUB_v10017960mg	gbpln	Capsella rubella	AT3G61070.3 | Symbols: PEX11E | peroxin 11E | chr3:22604873-22606159 REVERSE LENGTH=231	235	231	1.00E-124	98.3	91.9	96.6
Rsa1.0_01958.1.g31086.t1	gb|EOA25139.1| hypothetical protein CARUB_v10018448mg [Capsella rubella]	508	510	0	100.4	95.7	98.6	hypothetical protein CARUB_v10018448mg	gbpln	Capsella rubella	AT3G61050.2 | Symbols: NTMC2TYPE4, NTMC2T4 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:22597485-22600932 FORWARD LENGTH=510	508	510	0	100.4	94.9	98.4
Rsa1.0_01958.1.g31087.t1	ref|XP_002876589.1| hypothetical protein ARALYDRAFT_486567 [Arabidopsis lyrata subsp. lyrata] gi|297322427|gb|EFH52848.1| hypothetical protein ARALYDRAFT_486567 [Arabidopsis lyrata subsp. lyrata]	251	251	1.00E-132	100.0	90.8	94.4	hypothetical protein ARALYDRAFT_486567	gbpln	Arabidopsis lyrata	AT3G60910.1 | Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:22501727-22503182 FORWARD LENGTH=252	251	252	1.00E-133	100.4	90.8	94.8
Rsa1.0_01958.1.g31088.t1	ref|NP_191649.1| fasciclin-like arabinogalactan protein 10 [Arabidopsis thaliana] gi|38257776|sp|Q9LZX4.1|FLA10_ARATH RecName: Full=Fasciclin-like arabinogalactan protein 10; Flags: Precursor gi|7329700|emb|CAB82694.1| endosperm specific protein-like [Arabidopsis thaliana] gi|21593224|gb|AAM65173.1| endosperm specific protein-like [Arabidopsis thaliana] gi|332646604|gb|AEE80125.1| fasciclin-like arabinogalactan protein 10 [Arabidopsis thaliana]	430	422	1.00E-169	98.1	79.3	85.6	fasciclin-like arabinogalactan protein 10	gbpln	Arabidopsis thaliana	AT3G60900.1 | Symbols: FLA10 | FASCICLIN-like arabinogalactan-protein 10 | chr3:22499573-22500841 REVERSE LENGTH=422	430	422	1.00E-171	98.1	79.3	85.6
Rsa1.0_01958.1.g31089.t1	ref|NP_001118868.1| protein little zipper 2 [Arabidopsis thaliana] gi|332646602|gb|AEE80123.1| protein little zipper 2 [Arabidopsis thaliana]	103	106	2.00E-35	102.9	76.7	87.4	protein little zipper 2	gbpln	Arabidopsis thaliana	AT3G60890.2 | Symbols: ZPR2 | protein binding | chr3:22497024-22497442 REVERSE LENGTH=106	103	106	3.00E-38	102.9	76.7	87.4

Rsa1.0_01958.1.g31090.t1	ref|XP_002876584.1| hypothetical protein ARALYDRAFT_486557 [Arabidopsis lyrata subsp. lyrata] gi|297322422|gb|EFH52843.1| hypothetical protein ARALYDRAFT_486557 [Arabidopsis lyrata subsp. lyrata]	362	363	0	100.3	95.0	97.2	hypothetical protein ARALYDRAFT_486557	gbpln	Arabidopsis lyrata	AT3G60830.1 | Symbols: ATARP7, ARP7 | actin−related protein 7 | chr3:22474298−22476000 FORWARD LENGTH=363	362	363	0	100.3	94.5	97.2
Rsa1.0_01958.1.g31091.t1	gb|EOA24708.1| hypothetical protein CARUB_v10017986mg [Capsella rubella]	223	223	1.00E−124	100.0	95.5	98.2	hypothetical protein CARUB_v10017986mg	gbpln	Capsella rubella	AT3G60820.3 | Symbols: PBF1 | N−terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr3:22472038−22473809 REVERSE LENGTH=223	223	223	1.00E−126	100.0	95.1	98.2
Rsa1.0_01958.1.g31092.t1	ref|XP_002875045.1| ATRPS13A [Arabidopsis lyrata subsp. lyrata] gi|297320882|gb|EFH51304.1| ATRPS13A [Arabidopsis lyrata subsp. lyrata]	151	151	2.00E−79	100.0	97.4	99.3	ATRPS13A	gbpln	Arabidopsis lyrata	AT4G00100.1 | Symbols: ATRPS13A, RPS13, PFL2, RPS13A | ribosomal protein S13A | chr4:37172−38123 FORWARD LENGTH=151	151	151	6.00E−82	100.0	97.4	99.3
Rsa1.0_01958.1.g31093.t1	gb|AAD48963.1|AF147263_5 contains similarity to transposases [Arabidopsis thaliana] gi|7267311|emb|CAB81093.1| AT4g05510 [Arabidopsis thaliana]	315	604	2.00E−65	191.7	48.6	66.7	contains similarity to transposases	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838−14323928 FORWARD LENGTH=696	315	696	1.00E−27	221.0	32.4	52.4
Rsa1.0_01958.1.g31094.t1	ref|XP_002876580.1| hypothetical protein ARALYDRAFT_486548 [Arabidopsis lyrata subsp. lyrata] gi|297322418|gb|EFH52839.1| hypothetical protein ARALYDRAFT_486548 [Arabidopsis lyrata subsp. lyrata]	618	741	0	119.9	95.5	97.6	hypothetical protein ARALYDRAFT_486548	gbpln	Arabidopsis lyrata	AT3G60750.2 | Symbols: | Transketolase | chr3:22454004−22456824 FORWARD LENGTH=740	618	740	0	119.7	95.1	97.2
Rsa1.0_01958.1.g31095.t2	ref|NP_191611.1| uncharacterized protein [Arabidopsis thaliana] gi|7288000|emb|CAB81838.1| putative protein [Arabidopsis thaliana] gi|28416581|gb|AAO42821.1| At3g60520 [Arabidopsis thaliana] gi|110735835|dbj|BAE99894.1| hypothetical protein [Arabidopsis thaliana] gi|332646553|gb|AEE80074.1| uncharacterized protein AT3G60520 [Arabidopsis thaliana]	119	129	7.00E−54	108.4	90.8	90.8	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G60520.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02070.1); Has 107 Blast hits to 107 proteins in 14 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 107; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr3:22361751−22362467 REVERSE LENGTH=129	119	129	1.00E−56	108.4	90.8	90.8
Rsa1.0_01958.1.g31096.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	311	1231	1.00E−67	395.8	40.8	60.5	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H−like superfamily protein | chr4:14333528−14335255 FORWARD LENGTH=575	311	575	1.00E−40	184.9	29.6	46.9
Rsa1.0_01958.1.g31097.t1	gb|AAC28216.1| T24M8.9 gene product [Arabidopsis thaliana] gi|7267147|emb|CAB80815.1| putative protein [Arabidopsis thaliana]	529	463	6.00E−55	87.5	25.3	35.0	T24M8.9 gene product	gbpln	Arabidopsis thaliana	AT2G01050.1 | Symbols: | zinc ion binding;nucleic acid binding | chr2:68337−69884 REVERSE LENGTH=515	529	515	1.00E−13	97.4	9.1	16.3
Rsa1.0_01958.1.g31098.t1	ref|XP_002878339.1| enoyl−CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] gi|297324177|gb|EFH54598.1| enoyl−CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	403	401	0	99.5	88.6	93.8	enoyl−CoA hydratase/isomerase family protein	gbpln	Arabidopsis lyrata	AT3G60510.1 | Symbols: | ATP−dependent caseinolytic (Clp) protease/crotonase family protein | chr3:22357141−22360003 REVERSE LENGTH=401	403	401	0	99.5	87.6	92.6
Rsa1.0_01958.1.g31099.t1	ref|NP_191609.1| 3’−5’−exoribonuclease CER7 protein [Arabidopsis thaliana] gi|42572741|ref|NP_974466.1| 3’−5’−exoribonuclease CER7 protein [Arabidopsis thaliana] gi|334186154|ref|NP_001190143.1| 3’−5’−exoribonuclease CER7 protein [Arabidopsis thaliana] gi|7287998|emb|CAB81836.1| nucleolar autoantigen−like protein [Arabidopsis thaliana] gi|28393589|gb|AAO42214.1| putative nucleolar autoantigen protein [Arabidopsis thaliana] gi|28973593|gb|AAO64121.1| putative nucleolar autoantigen protein [Arabidopsis thaliana] gi|113196170|gb|ABI31441.1| CER7 [Arabidopsis thaliana] gi|332646547|gb|AEE80068.1| 3’−5’−exoribonuclease CER7 protein [Arabidopsis thaliana] gi|332646548|gb|AEE80069.1| 3’−5’−exoribonuclease CER7 protein [Arabidopsis thaliana] gi|332646549|gb|AEE80070.1| 3’−5’−exoribonuclease CER7 protein [Arabidopsis thaliana]	308	438	1.00E−165	142.2	95.5	96.4	3’−5’−exoribonuclease CER7 protein	gbpln	Arabidopsis thaliana	AT3G60500.3 | Symbols: CER7 | 3’−5’−exoribonuclease family protein | chr3:22354245−22356440 FORWARD LENGTH=438	308	438	1.00E−168	142.2	95.5	96.4

<table>
<tr><td>Rsa1.0_01959.1.g31100.t1</td><td>gb|EOA33613.1| hypothetical protein CARUB_v10019764mg [Capsella rubella]</td><td>873</td><td>892</td><td>0</td><td>102.2</td><td>56.1</td><td>69.8</td><td>hypothetical protein CARUB_v10019764mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G63350.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:23494935-23497631 REVERSE LENGTH=898</td><td>873</td><td>898</td><td>0</td><td>102.9</td><td>56.2</td><td>69.9</td></tr>
<tr><td>Rsa1.0_01959.1.g31101.t1</td><td>dbj|BAB02990.1| retroelement pol polyprotein-like [Arabidopsis thaliana]</td><td>1195</td><td>1250</td><td>0</td><td>104.6</td><td>56.0</td><td>70.8</td><td>retroelement pol polyprotein-like</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1195</td><td>1262</td><td>4.00E-92</td><td>105.6</td><td>14.4</td><td>22.6</td></tr>
<tr><td>Rsa1.0_01959.1.g31102.t1</td><td>ref|NP_175924.2| Lipase/lipooxygenase, PLAT/LH2 family protein [Arabidopsis thaliana] gi|111074408|gb|ABH04577.1| At1g55280 [Arabidopsis thaliana] gi|332195097|gb|AEE33218.1| Lipase/lipooxygenase, PLAT/LH2 family protein [Arabidopsis thaliana]</td><td>386</td><td>390</td><td>1.00E-172</td><td>101.0</td><td>81.3</td><td>88.6</td><td>Lipase/lipooxygenase, PLAT/LH2 family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT1G55280.1 | Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr1:20623099-20624533 REVERSE LENGTH=390</td><td>386</td><td>390</td><td>1.00E-175</td><td>101.0</td><td>81.3</td><td>88.6</td></tr>
<tr><td>Rsa1.0_01959.1.g31103.t1</td><td>emb|CBI16510.3| unnamed protein product [Vitis vinifera]</td><td>471</td><td>269</td><td>3.00E-45</td><td>57.1</td><td>27.4</td><td>32.3</td><td>unnamed protein product</td><td>gbpln</td><td>Vitis vinifera</td><td>AT1G55310.3 | Symbols: SR33, SCL33, At-SCL33 | SC35-like splicing factor 33 | chr1:20630676-20632695 FORWARD LENGTH=300</td><td>471</td><td>300</td><td>7.00E-46</td><td>63.7</td><td>26.3</td><td>29.9</td></tr>
<tr><td>Rsa1.0_01959.1.g31104.t1</td><td>ref|XP_002879168.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata] gi|297325007|gb|EFH55427.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]</td><td>327</td><td>505</td><td>1.00E-109</td><td>154.4</td><td>68.8</td><td>79.2</td><td>ATP binding protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G28600.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:12251845-12254672 FORWARD LENGTH=502</td><td>327</td><td>502</td><td>1.00E-102</td><td>153.5</td><td>67.0</td><td>78.0</td></tr>
<tr><td>Rsa1.0_01959.1.g31105.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01959.1.g31106.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01959.1.g31107.t1</td><td>gb|ABB97032.1| unknown [Brassica rapa]</td><td>58</td><td>59</td><td>1.00E-13</td><td>101.7</td><td>94.8</td><td>96.6</td><td>unknown</td><td>gbpln</td><td>Brassica rapa</td><td>AT3G13520.1 | Symbols: AGP12, ATAGP12 | arabinogalactan protein 12 | chr3:4409087-4409269 FORWARD LENGTH=60</td><td>58</td><td>60</td><td>4.00E-16</td><td>103.4</td><td>79.3</td><td>82.8</td></tr>
<tr><td>Rsa1.0_01960.1.g31108.t1</td><td>emb|CAA20201.1| putative transposable element [Arabidopsis thaliana] gi|7268932|emb|CAB79135.1| putative transposable element [Arabidopsis thaliana]</td><td>62</td><td>1308</td><td>9.00E-15</td><td>2109.7</td><td>66.1</td><td>72.6</td><td>putative transposable element</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_01960.1.g31109.t1</td><td>sp|P41510.1|PME_BRANA RecName: Full=Probable pectinesterase/pectinesterase inhibitor; Includes: RecName: Full=Pectinesterase inhibitor; AltName: Full=Pectin methylesterase inhibitor; Includes: RecName: Full=Pectinesterase; Short=PE; AltName: Full=Pectin methylesterase; Flags: Precursor gi|17784|emb|CAA39658.1| Bp19 [Brassica napus]</td><td>566</td><td>584</td><td>0</td><td>103.2</td><td>94.3</td><td>97.3</td><td>RecName: Full=Probable pectinesterase/pectinesterase inhibitor; Includes: RecName: Full=Pectinesterase inhibitor; AltName: Full=Pectin methylesterase inhibitor; Includes: RecName: Full=Pectinesterase; Short=PE; AltName: Full=Pectin methylesterase; Flags: Precursor gi|17784|emb|CAA39658.1| Bp19</td><td>gbpln</td><td>Brassica napus</td><td>AT3G62170.1 | Symbols: VGDH2 | VANGUARD 1 homolog 2 | chr3:23016495-23018337 REVERSE LENGTH=588</td><td>566</td><td>588</td><td>0</td><td>103.9</td><td>81.3</td><td>89.4</td></tr>
<tr><td>Rsa1.0_01960.1.g31110.t2</td><td>ref|NP_191773.2| uncharacterized protein [Arabidopsis thaliana] gi|52354355|gb|AAU44498.1| hypothetical protein AT3G62140 [Arabidopsis thaliana] gi|60547833|gb|AAX23880.1| hypothetical protein At3g62140 [Arabidopsis thaliana] gi|332646794|gb|AEE80315.1| uncharacterized protein AT3G62140 [Arabidopsis thaliana]</td><td>295</td><td>214</td><td>6.00E-68</td><td>72.5</td><td>49.2</td><td>54.2</td><td>uncharacterized protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G62140.1 | Symbols: | CONTAINS InterPro DOMAIN/s: NEFA-interacting nuclear protein NIP30, N-terminal (InterPro:IPR019331); Has 398 Blast hits to 395 proteins in 139 species: Archae - 0; Bacteria - 6; Metazoa - 193; Fungi - 83; Plants - 36; Viruses - 0; Other Eukaryotes - 80 (source: NCBI BLink). | chr3:23007277-23008626 FORWARD LENGTH=214</td><td>295</td><td>214</td><td>2.00E-70</td><td>72.5</td><td>49.2</td><td>54.2</td></tr>
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Rsa1.0_01960.1.g31111.t1	ref|NP_191771.1| prolyl-tRNA synthetase [Arabidopsis thaliana] gi|30695549|ref|NP_850736.1| prolyl-tRNA synthetase [Arabidopsis thaliana] gi|6899922|emb|CAB71872.1| multifunctional aminoacyl-tRNA ligase-like protein [Arabidopsis thaliana] gi|16648885|gb|AAL24294.1| multifunctional aminoacyl-tRNA ligase-like protein [Arabidopsis thaliana] gi|22136084|gb|AAM91120.1| multifunctional aminoacyl-tRNA ligase-like protein [Arabidopsis thaliana] gi|332646791|gb|AEE80312.1| class II aaRS and biotin synthetases superfamily protein [Arabidopsis thaliana] gi|332646792|gb|AEE80313.1| prolyl-tRNA synthetase [Arabidopsis thaliana]	542	530	0	97.8	87.8	90.0	prolyl-tRNA synthetase	gbpln	Arabidopsis thaliana	AT3G62120.2 | Symbols: | Class II aaRS and biotin synthetases superfamily protein | chr3:23001227-23003849 REVERSE LENGTH=530	542	530	0	97.8	87.8	90.0
Rsa1.0_01960.1.g31112.t1	ref|XP_002876663.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] gi|297322501|gb|EFH52922.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	428	471	0	110.0	91.6	94.9	glycoside hydrolase family 28 protein	gbpln	Arabidopsis lyrata	AT3G62110.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:22997313-22999503 REVERSE LENGTH=471	428	471	0	110.0	90.9	94.6
Rsa1.0_01960.1.g31113.t1	gb|EOA23181.1| hypothetical protein CARUB_v10018117mg [Capsella rubella]	128	174	1.00E-44	135.9	92.2	93.8	hypothetical protein CARUB_v10018117mg	gbpln	Capsella rubella	AT3G62100.1 | Symbols: IAA30 | indole-3-acetic acid inducible 30 | chr3:22995835-22996593 FORWARD LENGTH=172	128	172	1.00E-41	134.4	85.9	89.1
Rsa1.0_01960.1.g31114.t1	dbj|BAH30499.1| hypothetical protein [Arabidopsis thaliana]	335	363	1.00E-103	108.4	63.9	74.6	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G62090.2 | Symbols: PIL2, PIF6 | phytochrome interacting factor 3-like 2 | chr3:22989097-22990546 REVERSE LENGTH=363	335	363	1.00E-106	108.4	63.9	74.6
Rsa1.0_01960.1.g31115.t1	ref|XP_002876659.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] gi|297322497|gb|EFH52918.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	425	423	0	99.5	84.9	93.4	SNF7 family protein	gbpln	Arabidopsis lyrata	AT3G62080.1 | Symbols: | SNF7 family protein | chr3:22986383-22988517 FORWARD LENGTH=423	425	423	0	99.5	83.8	92.5
Rsa1.0_01960.1.g31116.t1	gb|EOA24687.1| hypothetical protein CARUB_v10017959mg [Capsella rubella]	248	235	4.00E-82	94.8	72.2	78.6	hypothetical protein CARUB_v10017959mg	gbpln	Capsella rubella	AT3G62070.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G46940.1); Has 137 Blast hits to 135 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 137; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:22983710-22984482 REVERSE LENGTH=228	248	228	2.00E-77	91.9	66.1	77.0
Rsa1.0_01960.1.g31117.t1	ref|XP_002876658.1| pectinacetylesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322496|gb|EFH52917.1| pectinacetylesterase family protein [Arabidopsis lyrata subsp. lyrata]	394	419	0	106.3	81.2	90.9	pectinacetylesterase family protein	gbpln	Arabidopsis lyrata	AT3G62060.1 | Symbols: | Pectinacetylesterase family protein | chr3:22980123-22982734 FORWARD LENGTH=419	394	419	0	106.3	80.7	90.1
Rsa1.0_01960.1.g31118.t1	ref|NP_176271.1| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana] gi|332195602|gb|AEE33723.1| RNA-directed DNA polymerase (reverse transcriptase)-related protein [Arabidopsis thaliana]	175	289	4.00E-47	165.1	49.7	69.7	RNA-directed DNA polymerase (reverse transcriptase)-related protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr1:22357072-22357941 FORWARD LENGTH=289	175	289	1.00E-49	165.1	49.7	69.7
Rsa1.0_01961.1.g31119.t1	gb|ADQ43177.1| phosphatase [Eutrema parvulum]	418	415	0	99.3	85.9	90.9	phosphatase	gbpln	Eutrema parvulum	AT2G01900.1 | Symbols: | DNAse I-like superfamily protein | chr2:406136-408933 FORWARD LENGTH=417	418	417	0	99.8	79.9	86.1
Rsa1.0_01961.1.g31120.t1	gb|ACQ90589.1| putative C2H2 zinc finger protein [Eutrema halophilum]	438	442	0	100.9	86.3	91.8	putative C2H2 zinc finger protein	gbpln	Eutrema halophilum	AT2G01940.1 | Symbols: SGR5, ATIDD15 | C2H2-like zinc finger protein | chr2:432652-434917 FORWARD LENGTH=445	438	445	0	101.6	87.4	91.1
Rsa1.0_01961.1.g31121.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01962.1.g31122.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01962.1.g31123.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01962.1.g31124.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01962.1.g31125.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01962.1.g31126.t1	ref|XP_002885501.1| hypothetical protein ARALYDRAFT_479753 [Arabidopsis lyrata subsp. lyrata] gi|297331341|gb|EFH61760.1| hypothetical protein ARALYDRAFT_479753 [Arabidopsis lyrata subsp. lyrata]	401	400	0	99.8	84.8	91.5	hypothetical protein ARALYDRAFT_479753	gbpln	Arabidopsis lyrata	AT3G22410.1 | Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr3:7933328-7935664 REVERSE LENGTH=400	401	400	0	99.8	84.0	91.0

Rsa1.0_01962.1.g31127.t1	ref|NP_188879.2| lipoxygenase 5 [Arabidopsis thaliana] gi|254810223|sp|Q9LUW0.2|LOX5_ARATH RecName: Full=Linoleate 9S-lipoxygenase 5, chloroplastic; AltName: Full=Lipoxygenase 5; Short=AtLOX5 gi|332643109|gb|AEE76630.1| lipoxygenase 5 [Arabidopsis thaliana]	887	886	0	99.9	91.2	95.0	lipoxygenase 5	gbpln	Arabidopsis thaliana	AT3G22400.1 | Symbols: LOX5 | PLAT/LH2 domain-containing lipoxygenase family protein | chr3:7927011-7931167 FORWARD LENGTH=886	887	886	0	99.9	91.2	95.0
Rsa1.0_01962.1.g31128.t1	ref|XP_002885493.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331333|gb|EFH61752.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	64	72	1.00E-18	112.5	90.6	92.2	predicted protein	gbpln	Arabidopsis lyrata	AT3G22240.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G22235.2); Has 177 Blast hits to 177 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 177; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7863788-7864675 REVERSE LENGTH=72	64	72	3.00E-21	112.5	89.1	92.2
Rsa1.0_01962.1.g31129.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01962.1.g31130.t1	ref|NP_193236.1| 60S ribosomal protein L27-3 [Arabidopsis thaliana] gi|3123264|sp|P51419.2|RL273_ARATH RecName: Full=60S ribosomal protein L27-3 gi|2244857|emb|CAB10279.1| ribosomal protein [Arabidopsis thaliana] gi|7268246|emb|CAB78542.1| ribosomal protein [Arabidopsis thaliana] gi|17381062|gb|AAL36343.1| putative ribosomal protein [Arabidopsis thaliana] gi|20466061|gb|AAM20365.1| putative ribosomal protein [Arabidopsis thaliana] gi|21553620|gb|AAM62713.1| ribosomal protein [Arabidopsis thaliana] gi|110736737|dbj|BAF00331.1| ribosomal protein [Arabidopsis thaliana] gi|332658135|gb|AEE83535.1| 60S ribosomal protein L27-3 [Arabidopsis thaliana]	135	135	3.00E-69	100.0	96.3	99.3	60S ribosomal protein L27-3	gbpln	Arabidopsis thaliana	AT4G15000.1 | Symbols: | Ribosomal L27e protein family | chr4:8571896-8572303 FORWARD LENGTH=135	135	135	6.00E-72	100.0	96.3	99.3
Rsa1.0_01962.1.g31131.t1	gb|EOA36582.1| hypothetical protein CARUB_v10011769mg [Capsella rubella]	1944	990	0	50.9	24.2	31.4	hypothetical protein CARUB_v10011769mg	gbpln	Capsella rubella	AT1G45616.1 | Symbols: AtRLP6, RLP6 | receptor like protein 6 | chr1:17183550-17186534 REVERSE LENGTH=994	1944	994	0	51.1	24.6	30.8
Rsa1.0_01963.1.g31132.t1	ref|NP_177631.1| ethylene-responsive transcription factor ERF018 [Arabidopsis thaliana] gi|75265378|sp|Q9S7L5.1|ERF18_ARATH RecName: Full=Ethylene-responsive transcription factor ERF018 gi|5882730|gb|AAD55283.1|AC008263_14 Similar to gb|X94698 TINY from Arabidopsis thaliana and contains a PF|00847 AP2 domain. EST gb|F15362 comes from this gene [Arabidopsis thaliana] gi|12323910|gb|AAG51936.1|AC013258_30 putative AP2 domain transcription factor; 59128-58541 [Arabidopsis thaliana] gi|22135860|gb|AAM91512.1| AP2 domain containing protein, putative [Arabidopsis thaliana] gi|28058898|gb|AAO29966.1| AP2 domain containing protein, putative [Arabidopsis thaliana] gi|332197531|gb|AEE35652.1| ethylene-responsive transcription factor ERF018 [Arabidopsis thaliana]	199	195	5.00E-69	98.0	73.4	82.4	ethylene-responsive transcription factor ERF018	gbpln	Arabidopsis thaliana	AT1G74930.1 | Symbols: ORA47 | Integrase-type DNA-binding superfamily protein | chr1:28144239-28144826 FORWARD LENGTH=195	199	195	2.00E-71	98.0	73.4	82.4
Rsa1.0_01963.1.g31133.t1	ref|XP_002887567.1| hypothetical protein ARALYDRAFT_895362 [Arabidopsis lyrata subsp. lyrata] gi|297333408|gb|EFH63826.1| hypothetical protein ARALYDRAFT_895362 [Arabidopsis lyrata subsp. lyrata]	212	223	4.00E-87	105.2	78.3	87.7	hypothetical protein ARALYDRAFT_895362	gbpln	Arabidopsis lyrata	AT1G74940.1 | Symbols: | Protein of unknown function (DUF581) | chr1:28146284-28147065 FORWARD LENGTH=222	212	222	1.00E-87	104.7	75.9	85.4
Rsa1.0_01963.1.g31134.t1	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	542	1374	1.00E-152	253.5	48.2	67.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	542	575	1.00E-145	106.1	44.3	67.5
Rsa1.0_01963.1.g31135.t1	dbj|BAJ33919.1| unnamed protein product [Thellungiella halophila]	222	251	8.00E-79	113.1	76.6	82.9	unnamed protein product	----	----	AT1G74950.1 | Symbols: JAZ2, TIFY10B | TIFY domain/Divergent CCT motif family protein | chr1:28148919-28150258 REVERSE LENGTH=249	222	249	2.00E-71	112.2	72.5	80.2
Rsa1.0_01963.1.g31136.t1	gb|ABK28243.1| unknown [Arabidopsis thaliana]	236	297	2.00E-57	125.8	46.6	62.7	unknown	gbpln	Arabidopsis thaliana	AT4G04650.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=332	236	332	1.00E-57	140.7	44.5	61.0

Rsa1.0_01963.1.g31137.t1	gb|AAC19278.1| T14P8.10 [Arabidopsis thaliana] gi|7269009|emb|CAB80742.1| AT4g02490 [Arabidopsis thaliana]	215	657	1.00E-63	305.6	54.4	69.3	T14P8.10	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	215	746	9.00E-36	347.0	36.7	54.4
Rsa1.0_01963.1.g31138.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01963.1.g31139.t1	gb|AAL91174.1| putative 3-ketoacyl-ACP synthase [Arabidopsis thaliana]	540	541	0	100.2	90.0	93.1	putative 3-ketoacyl-ACP synthase	gbpln	Arabidopsis thaliana	AT1G74960.3 | Symbols: FAB1 | fatty acid biosynthesis 1 | chr1:28152564-28155948 REVERSE LENGTH=541	540	541	0	100.2	90.2	93.3
Rsa1.0_01963.1.g31140.t1	ref|XP_002888470.1| hypothetical protein ARALYDRAFT_894223 [Arabidopsis lyrata subsp. lyrata] gi|297334311|gb|EFH64729.1| hypothetical protein ARALYDRAFT_894223 [Arabidopsis lyrata subsp. lyrata]	305	396	6.00E-50	129.8	46.2	63.6	hypothetical protein ARALYDRAFT_894223	gbpln	Arabidopsis lyrata	AT1G65990.1 | Symbols: | type 2 peroxiredoxin-related / thiol specific antioxidant / mal allergen family protein | chr1:24571603-24573471 REVERSE LENGTH=553	305	553	7.00E-45	181.3	44.3	58.7
Rsa1.0_01963.1.g31141.t1	ref|NP_177635.1| 30S ribosomal protein S9 [Arabidopsis thaliana] gi|48428563|sp|Q9XJ27.1|RR9_ARATH RecName: Full=30S ribosomal protein S9, chloroplastic; Flags: Precursor gi|5882726|gb|AAD55279.1|AC008263_10 Identical to gb|AB022676 ribosomal protein S9 from Arabidopsis thaliana. ESTs gb|T13861, gb|AA389790, gb|T42539, gb|AA586013, gb|AA395093 and gb|AA041154 come from this gene [Arabidopsis thaliana] gi|12744979|gb|AAK06869.1|AF344318_1 putative ribosomal protein S9 [Arabidopsis thaliana] gi|5456946|dbj|BAA82396.1| ribosomal protein S9 [Arabidopsis thaliana] gi|15010598|gb|AAK73958.1| ATg74970/F25A4.6 [Arabidopsis thaliana] gi|15027999|gb|AAK76530.1| putative ribosomal protein S9 [Arabidopsis thaliana] gi|20259211|gb|AAM14321.1| putative ribosomal protein S9 [Arabidopsis thaliana] gi|21554316|gb|AAM63421.1| ribosomal protein S9, putative [Arabidopsis thaliana] gi|51968396|dbj|BAD42890.1| putative ribosomal protein S9 [Arabidopsis thaliana] gi|51969144|dbj|BAD43264.1| putative ribosomal protein S9 [Arabidopsis thaliana] gi|51969266|dbj|BAD43325.1| putative ribosomal protein S9 [Arabidopsis	212	208	6.00E-93	98.1	87.3	92.5	30S ribosomal protein S9	gbpln	Arabidopsis thaliana	AT1G74970.1 | Symbols: RPS9, TWN3 | ribosomal protein S9 | chr1:28157761-28159202 REVERSE LENGTH=208	212	208	2.00E-95	98.1	87.3	92.5
Rsa1.0_01963.1.g31142.t1	ref|XP_002887569.1| hypothetical protein ARALYDRAFT_476640 [Arabidopsis lyrata subsp. lyrata] gi|297333410|gb|EFH63828.1| hypothetical protein ARALYDRAFT_476640 [Arabidopsis lyrata subsp. lyrata]	382	379	0	99.2	85.6	91.1	hypothetical protein ARALYDRAFT_476640	gbpln	Arabidopsis lyrata	AT1G75020.2 | Symbols: LPAT4 | lysophosphatidyl acyltransferase 4 | chr1:28171779-28173357 FORWARD LENGTH=378	382	378	0	99.0	83.5	89.8
Rsa1.0_01964.1.g31143.t1	ref|NP_001190233.1| 26S proteasome regulatory subunit N8 [Arabidopsis thaliana] gi|332003541|gb|AED90924.1| probable 26S proteasome non-ATPase regulatory subunit 7 [Arabidopsis thaliana]	124	305	1.00E-42	246.0	70.2	83.1	26S proteasome regulatory subunit N8	gbpln	Arabidopsis thaliana	AT5G05780.2 | Symbols: RPN8A | RP non-ATPase subunit 8A | chr5:1735862-1738176 FORWARD LENGTH=305	124	305	2.00E-45	246.0	70.2	83.1
Rsa1.0_01964.1.g31144.t1	gb|EOA37041.1| hypothetical protein CARUB_v10010132mg [Capsella rubella]	243	244	5.00E-79	100.4	71.6	80.7	hypothetical protein CARUB_v10010132mg	gbpln	Capsella rubella	AT2G27260.1 | Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:11669769-11670500 FORWARD LENGTH=243	243	243	2.00E-81	100.0	73.3	84.0
Rsa1.0_01964.1.g31145.t1	ref|NP_180295.1| uncharacterized protein [Arabidopsis thaliana] gi|5306270|gb|AAD42002.1| hypothetical protein [Arabidopsis thaliana] gi|27413483|gb|AAO11659.1| hypothetical protein [Arabidopsis thaliana] gi|50058869|gb|AAT69179.1| hypothetical protein At2g27270 [Arabidopsis thaliana] gi|330252872|gb|AEC07966.1| uncharacterized protein AT2G27270 [Arabidopsis thaliana]	180	231	8.00E-20	128.3	38.9	56.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G27270.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (TAIR:AT4G01410.1); Has 250 Blast hits to 250 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 250; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:11672346-11673134 FORWARD LENGTH=231	180	231	3.00E-22	128.3	38.9	56.1
Rsa1.0_01964.1.g31146.t1	gb|EOA27430.1| hypothetical protein CARUB_v10023568mg [Capsella rubella]	349	340	1.00E-156	97.4	80.2	87.4	hypothetical protein CARUB_v10023568mg	gbpln	Capsella rubella	AT2G27300.1 | Symbols: ANAC040, NTL8 | NTM1-like 8 | chr2:11680417-11681955 REVERSE LENGTH=335	349	335	1.00E-153	96.0	79.4	85.7

Rsa1.0_01964.1.g31147.t3	ref|NP_565646.2| RNA recognition motif-containing protein [Arabidopsis thaliana] gi|106879155|gb|ABF82607.1| At2g27330 [Arabidopsis thaliana] gi|330252880|gb|AEC07974.1| RNA recognition motif-containing protein [Arabidopsis thaliana]	152	116	8.00E-41	76.3	57.2	65.1	RNA recognition motif-containing protein	gbpln	Arabidopsis thaliana	AT2G27330.1 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:11695350-11696563 REVERSE LENGTH=116	152	116	3.00E-43	76.3	57.2	65.1
Rsa1.0_01964.1.g31148.t1	ref|NP_565648.1| OTU-like cysteine type protease [Arabidopsis thaliana] gi|30683489|ref|NP_850099.1| OTU-like cysteine type protease [Arabidopsis thaliana] gi|16604334|gb|AAL24173.1| At2g27350/F12K2.7 [Arabidopsis thaliana] gi|20197675|gb|AAD41995.2| expressed protein [Arabidopsis thaliana] gi|27311747|gb|AAO00839.1| expressed protein [Arabidopsis thaliana] gi|31711918|gb|AAP68315.1| At2g27350 [Arabidopsis thaliana] gi|330252885|gb|AEC07979.1| OTU-like cysteine type protease [Arabidopsis thaliana] gi|330252886|gb|AEC07980.1| OTU-like cysteine type protease [Arabidopsis thaliana]	477	505	0	105.9	81.1	86.8	OTU-like cysteine type protease	gbpln	Arabidopsis thaliana	AT2G27350.2 | Symbols: | OTU-like cysteine protease family protein | chr2:11699780-11702363 REVERSE LENGTH=505	477	505	0	105.9	81.1	86.8
Rsa1.0_01964.1.g31149.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01964.1.g31150.t1	ref|XP_002880912.1| At2g27385 [Arabidopsis lyrata subsp. lyrata] gi|297326751|gb|EFH57171.1| At2g27385 [Arabidopsis lyrata subsp. lyrata]	302	162	1.00E-67	53.6	42.4	47.4	At2g27385	gbpln	Arabidopsis lyrata	AT2G27385.3 | Symbols: | Pollen Ole e 1 allergen and extensin family protein | chr2:11716697-11717285 REVERSE LENGTH=162	302	162	9.00E-70	53.6	41.1	47.0
Rsa1.0_01964.1.g31151.t1	ref|NP_180312.2| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana] gi|27413513|gb|AAO11674.1| hypothetical protein [Arabidopsis thaliana] gi|61742614|gb|AAX55128.1| hypothetical protein At2g27430 [Arabidopsis thaliana] gi|330252902|gb|AEC07996.1| armadillo/beta-catenin-like repeat-containing protein [Arabidopsis thaliana]	133	438	4.00E-49	329.3	75.9	82.7	armadillo/beta-catenin-like repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G27430.1 | Symbols: | ARM repeat superfamily protein | chr2:11729914-11733170 REVERSE LENGTH=438	133	438	8.00E-52	329.3	75.9	82.7
Rsa1.0_01964.1.g31152.t1	ref|XP_002880919.1| hypothetical protein ARALYDRAFT_481647 [Arabidopsis lyrata subsp. lyrata] gi|297326758|gb|EFH57178.1| hypothetical protein ARALYDRAFT_481647 [Arabidopsis lyrata subsp. lyrata]	157	253	2.00E-14	161.1	31.8	35.0	hypothetical protein ARALYDRAFT_481647	gbpln	Arabidopsis lyrata	AT2G27470.1 | Symbols: NF-YB11 | nuclear factor Y, subunit B11 | chr2:11745196-11746375 REVERSE LENGTH=275	157	275	1.00E-15	175.2	36.3	41.4
Rsa1.0_01965.1.g31153.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01965.1.g31154.t1	dbj|BAJ34446.1| unnamed protein product [Thellungiella halophila]	154	149	2.00E-60	96.8	79.9	87.7	unnamed protein product	----	----	AT3G14560.1 | Symbols: | unknown protein; Has 6 Blast hits to 6 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4889368-4889832 FORWARD LENGTH=154	154	154	1.00E-59	100.0	76.0	86.4
Rsa1.0_01965.1.g31155.t2	ref|NP_188075.2| callose synthase [Arabidopsis thaliana] gi|189081842|sp|Q9LUD7.2|CALS8_ARATH RecName: Full=Putative callose synthase 8; AltName: Full=1,3-beta-glucan synthase; AltName: Full=Protein GLUCAN SYNTHASE-LIKE 4 gi|332642018|gb|AEE75539.1| callose synthase [Arabidopsis thaliana]	1947	1976	0	101.5	93.1	96.4	callose synthase	gbpln	Arabidopsis thaliana	AT3G14570.1 | Symbols: ATGSL04, gsl04, atgsl4 | glucan synthase-like 4 | chr3:4892643-4902628 FORWARD LENGTH=1976	1947	1976	0	101.5	93.1	96.4
Rsa1.0_01965.1.g31156.t1	ref|XP_002882884.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297328724|gb|EFH59143.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	401	409	1.00E-174	102.0	75.6	85.0	predicted protein	gbpln	Arabidopsis lyrata	AT3G14580.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:4903012-4904229 FORWARD LENGTH=405	401	405	1.00E-177	101.0	77.1	87.0
Rsa1.0_01965.1.g31157.t1	ref|XP_002885050.1| integral membrane single C2 domain protein [Arabidopsis lyrata subsp. lyrata] gi|297330890|gb|EFH61309.1| integral membrane single C2 domain protein [Arabidopsis lyrata subsp. lyrata]	629	742	0	118.0	82.8	89.8	integral membrane single C2 domain protein	gbpln	Arabidopsis lyrata	AT3G14590.2 | Symbols: NTMC2TYPE6.2, NTMC2T6.2 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:4904448-4907741 REVERSE LENGTH=737	629	737	0	117.2	81.6	89.0
Rsa1.0_01965.1.g31158.t1	gb|EOA31402.1| hypothetical protein CARUB_v10014581mg [Capsella rubella]	137	222	3.00E-47	162.0	81.0	86.9	hypothetical protein CARUB_v10014581mg	gbpln	Capsella rubella	AT3G14595.1 | Symbols: | Ribosomal protein L18ae family | chr3:4909037-4910226 FORWARD LENGTH=132	137	132	7.00E-45	96.4	73.7	79.6

Rsa1.0_01965.1.g31159.t1	ref|NP_188079.1| cytochrome P450, family 72, subfamily A, polypeptide 7 [Arabidopsis thaliana] gi|9294383|dbj|BAB02393.1| cytochrome P450 [Arabidopsis thaliana] gi|18252155|gb|AAL61910.1| cytochrome P450 [Arabidopsis thaliana] gi|28059362|gb|AAO30051.1| cytochrome P450 [Arabidopsis thaliana] gi|332642026|gb|AEE75547.1| cytochrome P450, family 72, subfamily A, polypeptide 7 [Arabidopsis thaliana]	750	512	0	68.3	58.5	62.9	cytochrome P450, family 72, subfamily A, polypeptide 7	gbpln	Arabidopsis thaliana	AT3G14610.1 | Symbols: CYP72A7 | cytochrome P450, family 72, subfamily A, polypeptide 7 | chr3:4912565-4914503 FORWARD LENGTH=512	750	512	0	68.3	58.5	62.9
Rsa1.0_01965.1.g31160.t1	gb|EOA16073.1| hypothetical protein CARUB_v10004206mg [Capsella rubella]	472	763	1.00E-102	161.7	40.9	50.4	hypothetical protein CARUB_v10004206mg	gbpln	Capsella rubella	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	472	344	8.00E-56	72.9	25.8	35.4
Rsa1.0_01966.1.g31161.t2	gb|EOA18774.1| hypothetical protein CARUB_v10007371mg, partial [Capsella rubella]	309	620	2.00E-13	200.6	16.2	23.0	hypothetical protein CARUB_v10007371mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01966.1.g31162.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01966.1.g31163.t1	gb|AAF79782.1|AC020646_5 T32E20.5 [Arabidopsis thaliana]	86	141	3.00E-12	164.0	41.9	50.0	T32E20.5	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01966.1.g31164.t1	gb|EOA22554.1| hypothetical protein CARUB_v10003214mg [Capsella rubella]	296	297	1.00E-127	100.3	77.4	85.8	hypothetical protein CARUB_v10003214mg	gbpln	Capsella rubella	AT4G11040.1 | Symbols: | Protein phosphatase 2C family protein | chr4:6745161-6746667 FORWARD LENGTH=295	296	295	1.00E-128	99.7	78.0	85.5
Rsa1.0_01966.1.g31165.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01966.1.g31166.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01966.1.g31167.t2	ref|XP_002864844.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297310679|gb|EFH41103.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	242	270	1.00E-36	111.6	28.1	31.0	zinc finger family protein	gbpln	Arabidopsis lyrata	AT5G63280.1 | Symbols: | C2H2-like zinc finger protein | chr5:25367085-25368848 FORWARD LENGTH=271	242	271	2.00E-38	112.0	27.7	31.0
Rsa1.0_01966.1.g31168.t1	gb|EOA20860.1| hypothetical protein CARUB_v10001197mg [Capsella rubella]	168	375	2.00E-18	223.2	36.3	48.8	hypothetical protein CARUB_v10001197mg	gbpln	Capsella rubella	AT5G22100.1 | Symbols: | RNA cyclase family protein | chr5:7329015-7330718 FORWARD LENGTH=375	168	375	3.00E-18	223.2	29.2	36.3
Rsa1.0_01966.1.g31169.t1	ref|NP_186790.2| RNase H domain-containing protein [Arabidopsis thaliana] gi|145331720|ref|NP_001078087.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|332640141|gb|AEE73662.1| RNase H domain-containing protein [Arabidopsis thaliana] gi|332640142|gb|AEE73663.1| RNase H domain-containing protein [Arabidopsis thaliana]	117	294	2.00E-25	251.3	55.6	65.8	RNase H domain-containing protein	gbpln	Arabidopsis thaliana	AT3G01410.2 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr3:153650-155439 REVERSE LENGTH=294	117	294	4.00E-28	251.3	55.6	65.8
Rsa1.0_01967.1.g31170.t1	gb|EOA33387.1| hypothetical protein CARUB_v10020368mg, partial [Capsella rubella]	334	417	1.00E-130	124.9	74.9	87.4	hypothetical protein CARUB_v10020368mg, partial	gbpln	Capsella rubella	AT1G69900.1 | Symbols: | Actin cross-linking protein | chr1:26326520-26327816 REVERSE LENGTH=397	334	397	1.00E-118	118.9	71.0	81.7
Rsa1.0_01967.1.g31171.t1	ref|XP_002863106.1| hypothetical protein ARALYDRAFT_920363 [Arabidopsis lyrata subsp. lyrata] gi|297308928|gb|EFH39365.1| hypothetical protein ARALYDRAFT_920363 [Arabidopsis lyrata subsp. lyrata]	243	284	8.00E-69	116.9	58.0	64.6	hypothetical protein ARALYDRAFT_920363	gbpln	Arabidopsis lyrata	AT1G69890.1 | Symbols: | Protein of unknown function (DUF569) | chr1:26323426-26324527 REVERSE LENGTH=279	243	279	9.00E-71	114.8	57.6	65.4
Rsa1.0_01967.1.g31172.t1	ref|XP_002863112.1| thioredoxin H-type 8 [Arabidopsis lyrata subsp. lyrata] gi|297308934|gb|EFH39371.1| thioredoxin H-type 8 [Arabidopsis lyrata subsp. lyrata]	151	148	9.00E-65	98.0	80.8	89.4	thioredoxin H-type 8	gbpln	Arabidopsis lyrata	AT1G69880.1 | Symbols: ATH8, TH8 | thioredoxin H-type 8 | chr1:26321540-26322794 FORWARD LENGTH=148	151	148	4.00E-67	98.0	82.1	88.7
Rsa1.0_01967.1.g31173.t1	dbj|BAJ33974.1| unnamed protein product [Thellungiella halophila]	622	622	0	100.0	91.6	95.7	unnamed protein product	----	----	AT1G69870.1 | Symbols: NRT1.7 | nitrate transporter 1.7 | chr1:26316208-26320097 FORWARD LENGTH=620	622	620	0	99.7	85.4	92.4
Rsa1.0_01967.1.g31174.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01967.1.g31175.t1	ref|XP_002863114.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] gi|297308936|gb|EFH39373.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	252	556	1.00E-126	220.6	88.5	92.9	proton-dependent oligopeptide transport family protein	gbpln	Arabidopsis lyrata	AT1G69860.1 | Symbols: | Major facilitator superfamily protein | chr1:26309628-26312174 FORWARD LENGTH=555	252	555	1.00E-113	220.2	87.7	91.7
Rsa1.0_01968.1.g31176.t2	#	#		#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01968.1.g31177.t2	gb|AAG33978.1|AF250964_1 methionine aminopeptidase-like protein [Arabidopsis thaliana]	478	440	0	92.1	81.0	87.0	methionine aminopeptidase-like protein	gbpln	Arabidopsis thaliana	AT2G44180.1 | Symbols: MAP2A | methionine aminopeptidase 2A | chr2:18269442-18271785 REVERSE LENGTH=441	478	441	0	92.3	80.8	86.8

Rsa1.0_01968.1.g31178.t1	gb|EOA27037.1| hypothetical protein CARUB_v10023133mg [Capsella rubella]	444	471	1.00E-169	106.1	78.8	85.4	hypothetical protein CARUB_v10023133mg	gbpln	Capsella rubella	AT2G44190.1 | Symbols: EDE1, QWRF5 | Family of unknown function (DUF566) | chr2:18272346-18274332 FORWARD LENGTH=474	444	474	1.00E-170	106.8	78.4	84.2
Rsa1.0_01968.1.g31179.t1	ref|NP_566014.1| pre-mRNA splicing factor domain-containing protein [Arabidopsis thaliana] gi|3128167|gb|AAC16071.1| expressed protein [Arabidopsis thaliana] gi|15010704|gb|AAK74011.1| At2g44200/F6E13.34 [Arabidopsis thaliana] gi|20197069|gb|AAM14905.1| expressed protein [Arabidopsis thaliana] gi|21360459|gb|AAM47345.1| At2g44200/F6E13.34 [Arabidopsis thaliana] gi|330255296|gb|AEC10390.1| pre-mRNA splicing factor domain-containing protein [Arabidopsis thaliana]	317	493	2.00E-62	155.5	49.2	55.8	pre-mRNA splicing factor domain-containing protein	gbpln	Arabidopsis thaliana	AT2G44200.1 | Symbols: | CBF1-interacting co-repressor CIR, N-terminal;Pre-mRNA splicing factor | chr2:18276302-18278240 FORWARD LENGTH=493	317	493	6.00E-65	155.5	49.2	55.8
Rsa1.0_01968.1.g31180.t1	ref|NP_030959.1| uncharacterized protein [Arabidopsis thaliana] gi|3128168|gb|AAC16072.1| expressed protein [Arabidopsis thaliana] gi|15081719|gb|AAK82514.1| At2g44210/F4I1.2 [Arabidopsis thaliana] gi|21593455|gb|AAM65422.1| unknown [Arabidopsis thaliana] gi|22137094|gb|AAM91392.1| At2g44210/F4I1.2 [Arabidopsis thaliana] gi|330255297|gb|AEC10391.1| uncharacterized protein AT2G44210 [Arabidopsis thaliana]	416	415	0	99.8	91.3	96.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G44210.1 | Symbols: | Protein of Unknown Function (DUF239) | chr2:18280809-18282591 FORWARD LENGTH=415	416	415	0	99.8	91.3	96.2
Rsa1.0_01968.1.g31181.t1	gb|AAC16073.1| hypothetical protein [Arabidopsis thaliana]	320	402	1.00E-116	125.6	63.8	77.5	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G44220.1 | Symbols: | Protein of Unknown Function (DUF239) | chr2:18283803-18285690 FORWARD LENGTH=403	320	403	1.00E-118	125.9	63.8	77.5
Rsa1.0_01969.1.g31182.t1	ref|NP_001030909.1| putative defensin-like protein 128 [Arabidopsis thaliana] gi|114152836|sp|P82723.2|DF128_ARATH RecName: Full=Putative defensin-like protein 128; AltName: Full=Putative low-molecular-weight cysteine-rich protein 8; Short=Protein LCR8; Flags: Precursor gi|332646644|gb|AEE80165.1| putative defensin-like protein 128 [Arabidopsis thaliana]	69	74	1.00E-10	107.2	44.9	50.7	putative defensin-like protein 128	gbpln	Arabidopsis thaliana	AT3G61172.1 | Symbols: LCR8 | low-molecular-weight cysteine-rich 8 | chr3:22641764-22642110 REVERSE LENGTH=74	69	74	2.00E-13	107.2	44.9	50.7
Rsa1.0_01969.1.g31183.t1	gb|EOA25723.1| hypothetical protein CARUB_v10019077mg [Capsella rubella]	805	797	0	99.0	80.0	87.7	hypothetical protein CARUB_v10019077mg	gbpln	Capsella rubella	AT3G61170.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:22638691-22641237 REVERSE LENGTH=783	805	783	0	97.3	75.0	82.9
Rsa1.0_01969.1.g31184.t1	ref|XP_002876597.1| hypothetical protein ARALYDRAFT_486587 [Arabidopsis lyrata subsp. lyrata] gi|297322435|gb|EFH52856.1| hypothetical protein ARALYDRAFT_486587 [Arabidopsis lyrata subsp. lyrata]	446	435	0	97.5	87.9	92.2	hypothetical protein ARALYDRAFT_486587	gbpln	Arabidopsis lyrata	AT3G61160.2 | Symbols: | Protein kinase superfamily protein | chr3:22636209-22638593 FORWARD LENGTH=438	446	438	0	98.2	88.1	92.4
Rsa1.0_01969.1.g31185.t1	gb|EOA24044.1| hypothetical protein CARUB_v10017264mg [Capsella rubella] gi|482559854|gb|EOA24045.1| hypothetical protein CARUB_v10017264mg [Capsella rubella]	444	441	0	99.3	90.1	94.8	hypothetical protein CARUB_v10017264mg	gbpln	Capsella rubella	AT3G61140.1 | Symbols: FUS6, ATFUS6, CSN1, COP11, EMB78, ATSK31, SK31 | 26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain | chr3:22626335-22628895 FORWARD LENGTH=441	444	441	0	99.3	89.2	94.6
Rsa1.0_01969.1.g31186.t1	gb|EOA23223.1| hypothetical protein CARUB_v10016785mg [Capsella rubella]	673	673	0	100.0	91.4	95.5	hypothetical protein CARUB_v10016785mg	gbpln	Capsella rubella	AT3G61130.1 | Symbols: GAUT1, LGT1 | galacturonosyltransferase 1 | chr3:22622399-22625514 FORWARD LENGTH=673	673	673	0	100.0	90.9	94.8
Rsa1.0_01969.1.g31187.t1	gb|EOA24972.1| hypothetical protein CARUB_v10018269mg, partial [Capsella rubella]	84	115	3.00E-42	136.9	97.6	100.0	hypothetical protein CARUB_v10018269mg, partial	gbpln	Capsella rubella	AT3G61110.1 | Symbols: ARS27A, RS27A | ribosomal protein S27 | chr3:22611710-22612632 FORWARD LENGTH=86	84	86	8.00E-44	102.4	96.4	100.0
Rsa1.0_01969.1.g31188.t8	ref|XP_002878354.1| hypothetical protein ARALYDRAFT_324535 [Arabidopsis lyrata subsp. lyrata] gi|297324192|gb|EFH54613.1| hypothetical protein ARALYDRAFT_324535 [Arabidopsis lyrata subsp. lyrata]	2805	2860	0	102.0	82.2	89.2	hypothetical protein ARALYDRAFT_324535	gbpln	Arabidopsis lyrata	AT2G45540.1 | Symbols: | WD-40 repeat family protein / beige-related | chr2:18757881-18772229 REVERSE LENGTH=2946	2805	2946	0	105.0	74.7	84.1

<table>
<tr><td>Rsa1.0_01970.1.g31189.t1</td><td>ref|NP_195177.1| 3-ketoacyl-CoA synthase 17 [Arabidopsis thaliana] gi|75099555|sp|O65677.1|KCS2_ARATH RecName: Full=Probable 3-ketoacyl-CoA synthase 2; Short=KCS-2; AltName: Full=Very long-chain fatty acid condensing enzyme 2; Short=VLCFA condensing enzyme 2 gi|3096920|emb|CAA18830.1| putative ketoacyl-CoA synthase [Arabidopsis thaliana] gi|7270401|emb|CAB80168.1| putative ketoacyl-CoA synthase [Arabidopsis thaliana] gi|332660987|gb|AEE86387.1| 3-ketoacyl-CoA synthase 17 [Arabidopsis thaliana]</td><td>474</td><td>487</td><td>0</td><td>102.7</td><td>81.9</td><td>90.5</td><td>3-ketoacyl-CoA synthase 17</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G34510.1 | Symbols: KCS17 | 3-ketoacyl-CoA synthase 17 | chr4:16491796-16493259 FORWARD LENGTH=487</td><td>474</td><td>487</td><td>0</td><td>102.7</td><td>81.9</td><td>90.5</td></tr>
<tr><td>Rsa1.0_01970.1.g31190.t1</td><td>emb|CAD90160.1| beta-ketoacyl-CoA synthase FAE1.2 [Brassica juncea]</td><td>506</td><td>506</td><td>0</td><td>100.0</td><td>96.6</td><td>99.0</td><td>beta-ketoacyl-CoA synthase FAE1.2</td><td>gbpln</td><td>Brassica juncea</td><td>AT4G34520.1 | Symbols: FAE1, KCS18 | 3-ketoacyl-CoA synthase 18 | chr4:16494205-16495725 FORWARD LENGTH=506</td><td>506</td><td>506</td><td>0</td><td>100.0</td><td>84.8</td><td>91.1</td></tr>
<tr><td>Rsa1.0_01970.1.g31191.t16</td><td>gb|EOA15755.1| hypothetical protein CARUB_v10006817mg [Capsella rubella]</td><td>314</td><td>283</td><td>5.00E-60</td><td>90.1</td><td>51.6</td><td>59.9</td><td>hypothetical protein CARUB_v10006817mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G34550.1 | Symbols: | BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT2G16365.3); Has 37 Blast hits to 37 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:16503201-16504040 FORWARD LENGTH=279</td><td>314</td><td>279</td><td>2.00E-60</td><td>88.9</td><td>49.7</td><td>59.9</td></tr>
<tr><td>Rsa1.0_01970.1.g31192.t1</td><td>gb|EOA17614.1| hypothetical protein CARUB_v10005978mg [Capsella rubella]</td><td>148</td><td>143</td><td>5.00E-53</td><td>96.6</td><td>75.0</td><td>82.4</td><td>hypothetical protein CARUB_v10005978mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G34590.1 | Symbols: ATB2, GBF6, AtbZIP11, BZIP11 | G-box binding factor 6 | chr4:16522449-16522928 FORWARD LENGTH=159</td><td>148</td><td>159</td><td>4.00E-54</td><td>107.4</td><td>74.3</td><td>81.1</td></tr>
<tr><td>Rsa1.0_01970.1.g31193.t1</td><td>ref|XP_002885849.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297331689|gb|EFH62108.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>94</td><td>335</td><td>4.00E-17</td><td>356.4</td><td>40.4</td><td>58.5</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566</td><td>94</td><td>566</td><td>2.00E-15</td><td>602.1</td><td>35.1</td><td>56.4</td></tr>
<tr><td>Rsa1.0_01971.1.g31194.t1</td><td>gb|ACP30622.1| disease resistance protein [Brassica rapa subsp. pekinensis]</td><td>781</td><td>1459</td><td>0</td><td>186.8</td><td>60.3</td><td>67.7</td><td>disease resistance protein</td><td>gbpln</td><td>Brassica rapa</td><td>AT4G16900.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:9512329-9516541 REVERSE LENGTH=1040</td><td>781</td><td>1040</td><td>1.00E-95</td><td>133.2</td><td>27.0</td><td>39.8</td></tr>
<tr><td>Rsa1.0_01971.1.g31195.t1</td><td>ref|XP_002873943.1| calcium-dependent protein kinase 34 [Arabidopsis lyrata subsp. lyrata] gi|297319780|gb|EFH50202.1| calcium-dependent protein kinase 34 [Arabidopsis lyrata subsp. lyrata]</td><td>517</td><td>525</td><td>0</td><td>101.5</td><td>95.9</td><td>97.7</td><td>calcium-dependent protein kinase 34</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G19360.1 | Symbols: CPK34 | calcium-dependent protein kinase 34 | chr5:6521716-6523780 REVERSE LENGTH=523</td><td>517</td><td>523</td><td>0</td><td>101.2</td><td>94.8</td><td>96.9</td></tr>
<tr><td>Rsa1.0_01971.1.g31196.t1</td><td>gb|EOA19671.1| hypothetical protein CARUB_v10003324mg [Capsella rubella]</td><td>197</td><td>232</td><td>2.00E-48</td><td>117.8</td><td>53.3</td><td>61.4</td><td>hypothetical protein CARUB_v10003324mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G17120.1 | Symbols: | Cystatin/monellin superfamily protein | chr5:5628529-5629324 REVERSE LENGTH=207</td><td>197</td><td>207</td><td>3.00E-44</td><td>105.1</td><td>44.7</td><td>55.3</td></tr>
<tr><td>Rsa1.0_01971.1.g31197.t1</td><td>gb|EOA20333.1| hypothetical protein CARUB_v10000639mg [Capsella rubella]</td><td>536</td><td>546</td><td>0</td><td>101.9</td><td>85.6</td><td>92.0</td><td>hypothetical protein CARUB_v10000639mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G19320.1 | Symbols: RANGAP2 | RAN GTPase activating protein 2 | chr5:6505310-6506947 REVERSE LENGTH=545</td><td>536</td><td>545</td><td>0</td><td>101.7</td><td>84.5</td><td>91.6</td></tr>
<tr><td>Rsa1.0_01971.1.g31198.t1</td><td>ref|XP_002865540.1| hypothetical protein ARALYDRAFT_494800 [Arabidopsis lyrata subsp. lyrata] gi|297311375|gb|EFH41799.1| hypothetical protein ARALYDRAFT_494800 [Arabidopsis lyrata subsp. lyrata]</td><td>135</td><td>204</td><td>1.00E-24</td><td>151.1</td><td>60.0</td><td>72.6</td><td>hypothetical protein ARALYDRAFT_494800</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G42330.1 | Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:16926672-16927370 FORWARD LENGTH=205</td><td>135</td><td>205</td><td>9.00E-27</td><td>151.9</td><td>57.8</td><td>68.9</td></tr>
<tr><td>Rsa1.0_01971.1.g31199.t1</td><td>ref|NP_197430.1| esterase/lipase/thioesterase family protein [Arabidopsis thaliana] gi|17380668|gb|AAL36164.1| putative phospholipase [Arabidopsis thaliana] gi|21554372|gb|AAM63479.1| phospholipase-like protein [Arabidopsis thaliana] gi|23397199|gb|AAN31882.1| putative phospholipase [Arabidopsis thaliana] gi|26983896|gb|AAN86200.1| putative phospholipase [Arabidopsis thaliana] gi|332005298|gb|AED92681.1| esterase/lipase/thioesterase family protein [Arabidopsis thaliana]</td><td>335</td><td>330</td><td>1.00E-176</td><td>98.5</td><td>90.1</td><td>95.2</td><td>esterase/lipase/thioesterase family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G19290.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:6494113-6495105 FORWARD LENGTH=330</td><td>335</td><td>330</td><td>1.00E-179</td><td>98.5</td><td>90.1</td><td>95.2</td></tr>
<tr><td>Rsa1.0_01971.1.g31200.t1</td><td>emb|CAD20349.1| kinase-associated protein phosophatase [Brassica oleracea]</td><td>560</td><td>563</td><td>0</td><td>100.5</td><td>80.7</td><td>85.7</td><td>kinase-associated protein phosophatase</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G19280.1 | Symbols: KAPP, RAG1 | kinase associated protein phosphatase | chr5:6488450-6493182 FORWARD LENGTH=581</td><td>560</td><td>581</td><td>0</td><td>103.8</td><td>71.8</td><td>81.6</td></tr>
</table>

Rsa1.0_01971.1.g31201.t1	ref|XP_002873939.1| hypothetical protein ARALYDRAFT_488810 [Arabidopsis lyrata subsp. lyrata] gi|297319776|gb|EFH50198.1| hypothetical protein ARALYDRAFT_488810 [Arabidopsis lyrata subsp. lyrata]		271	287	2.00E-84	105.9	71.6	82.3	hypothetical protein ARALYDRAFT_488810	gbpln	Arabidopsis lyrata	AT5G19260.1 | Symbols: | Protein of unknown function (DUF3049) | chr5:6479494-6480360 REVERSE LENGTH=288	271	288	2.00E-81	106.3	66.1	78.2
Rsa1.0_01972.1.g31202.t1	ref|XP_002877602.1| hypothetical protein ARALYDRAFT_323421 [Arabidopsis lyrata subsp. lyrata] gi|297323440|gb|EFH53861.1| hypothetical protein ARALYDRAFT_323421 [Arabidopsis lyrata subsp. lyrata]		910	1968	0	216.3	77.1	83.7	hypothetical protein ARALYDRAFT_323421	gbpln	Arabidopsis lyrata	AT3G48195.1 | Symbols: | Phox (PX) domain-containing protein | chr3:17828706-17832388 REVERSE LENGTH=938	910	938	0	103.1	75.5	82.7
Rsa1.0_01972.1.g31203.t5	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#
Rsa1.0_01972.1.g31204.t2	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#
Rsa1.0_01972.1.g31205.t1	dbj|BAB09105.1| retroelement pol polyprotein-like [Arabidopsis thaliana]		122	251	8.00E-14	205.7	28.7	40.2	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01972.1.g31206.t3	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]		744	1142	8.00E-45	153.5	14.8	21.4	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01972.1.g31207.t1	pir||S66306 hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi|806535|emb|CAA57397.1| unnamed protein product [Arabidopsis thaliana]		268	935	1.00E-46	348.9	34.3	47.8	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi|806535|emb|CAA57397.1| unnamed protein product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01972.1.g31208.t1	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#
Rsa1.0_01972.1.g31209.t1	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]		410	1864	8.00E-35	454.6	32.7	50.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01973.1.g31210.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]		1055	1459	0	138.3	58.1	71.9	polyprotein, putative	gbpln	Arabidopsis thaliana	ATMG00820.1 | Symbols: ORF170 | Reverse transcriptase (RNA-dependent DNA polymerase) | chrM:228573-229085 REVERSE LENGTH=170	1055	170	3.00E-24	16.1	5.5	8.1
Rsa1.0_01973.1.g31211.t1	ref|XP_002877740.1| hypothetical protein ARALYDRAFT_485385 [Arabidopsis lyrata subsp. lyrata] gi|297323578|gb|EFH53999.1| hypothetical protein ARALYDRAFT_485385 [Arabidopsis lyrata subsp. lyrata]		609	403	0	66.2	59.6	61.9	hypothetical protein ARALYDRAFT_485385	gbpln	Arabidopsis lyrata	AT3G50340.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G67020.1); Has 128 Blast hits to 128 proteins in 39 species: Archae - 0; Bacteria - 46; Metazoa - 0; Fungi - 3; Plants - 76; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:18665333-18666544 REVERSE LENGTH=403	609	403	1.00E-178	66.2	60.1	62.1
Rsa1.0_01973.1.g31212.t1	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#
Rsa1.0_01973.1.g31213.t1	dbj|BAD44483.1| hypothetical protein [Arabidopsis thaliana]		162	181	3.00E-55	111.7	75.3	79.6	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G50350.2 | Symbols: | Protein of unknown function (DUF1685) | chr3:18672164-18673665 FORWARD LENGTH=171	162	171	5.00E-47	105.6	60.5	66.0
Rsa1.0_01973.1.g31214.t1	gb|AAD25830.1| putative retroelement pol polyprotein [Arabidopsis thaliana]		442	1015	5.00E-83	229.6	36.9	45.2	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	442	1262	2.00E-61	285.5	24.2	32.8
Rsa1.0_01973.1.g31215.t1	ref|XP_002877742.1| hypothetical protein ARALYDRAFT_485388 [Arabidopsis lyrata subsp. lyrata] gi|297323580|gb|EFH54001.1| hypothetical protein ARALYDRAFT_485388 [Arabidopsis lyrata subsp. lyrata]		1936	2182	0	112.7	72.9	80.3	hypothetical protein ARALYDRAFT_485388	gbpln	Arabidopsis lyrata	AT3G50370.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 26 plant structures; EXPRESSED DURING: 15 growth stages; Has 27734 Blast hits to 16708 proteins in 1259 species: Archae - 81; Bacteria - 3434; Metazoa - 10876; Fungi - 2514; Plants - 987; Viruses - 212; Other Eukaryotes - 9630 (source: NCBI BLink). | chr3:18676436-18683863 REVERSE LENGTH=2156	1936	2156	0	111.4	72.7	80.6
Rsa1.0_01974.1.g31216.t2	gb|AAB82639.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		899	1374	1.00E-150	152.8	29.9	42.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	899	626	2.00E-38	69.6	12.1	20.6
Rsa1.0_01974.1.g31217.t1	dbj|BAA06519.1| RNA-binding protein cp29 [Arabidopsis thaliana]		312	326	1.00E-113	104.5	81.7	86.2	RNA-binding protein cp29	gbpln	Arabidopsis thaliana	AT3G53460.3 | Symbols: CP29 | chloroplast RNA-binding protein 29 | chr3:19819738-19821423 REVERSE LENGTH=342	312	342	1.00E-114	109.6	81.4	85.6
Rsa1.0_01974.1.g31218.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]		138	1274	4.00E-18	923.2	40.6	53.6	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	138	303	2.00E-13	219.6	37.0	50.0
Rsa1.0_01974.1.g31219.t1	#	#	#	#	#	#	#		–	----	----	#	#	#	#	#	#	#

Rsa1.0_01974.1.g31220.t1	gb|EOA26421.1| hypothetical protein CARUB_v10024039mg [Capsella rubella]	92	215	7.00E-37	233.7	81.5	84.8	hypothetical protein CARUB_v10024039mg	gbpln	Capsella rubella	AT2G37210.1 | Symbols: | lysine decarboxylase family protein | chr2:15624253-15626834 REVERSE LENGTH=215	92	215	2.00E-39	233.7	81.5	84.8
Rsa1.0_01975.1.g31221.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	86	99	2.00E-33	115.1	87.2	89.5	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	86	91	4.00E-31	105.8	81.4	86.0
Rsa1.0_01975.1.g31222.t1	gb|EOA19546.1| hypothetical protein CARUB_v10002518mg [Capsella rubella]	94	90	3.00E-37	95.7	83.0	87.2	hypothetical protein CARUB_v10002518mg	gbpln	Capsella rubella	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	94	91	4.00E-38	96.8	77.7	84.0
Rsa1.0_01975.1.g31223.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	99	99	4.00E-46	100.0	91.9	93.9	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	99	91	5.00E-42	91.9	85.9	87.9
Rsa1.0_01975.1.g31224.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	98	99	2.00E-46	101.0	94.9	98.0	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	98	91	8.00E-41	92.9	81.6	85.7
Rsa1.0_01975.1.g31225.t1	gb|EOA21868.1| hypothetical protein CARUB_v10002345mg [Capsella rubella] gi|482557677|gb|EOA21869.1| hypothetical protein CARUB_v10002345mg [Capsella rubella]	92	92	5.00E-37	100.0	83.7	90.2	hypothetical protein CARUB_v10002345mg	gbpln	Capsella rubella	AT5G18030.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5968527-5968793 FORWARD LENGTH=88	92	88	1.00E-34	95.7	76.1	82.6
Rsa1.0_01975.1.g31226.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	184	99	5.00E-44	53.8	47.3	50.5	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	184	91	3.00E-39	49.5	43.5	46.7
Rsa1.0_01975.1.g31227.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	96	99	2.00E-32	103.1	75.0	83.3	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	96	91	6.00E-34	94.8	71.9	79.2
Rsa1.0_01975.1.g31228.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	97	99	3.00E-39	102.1	87.6	90.7	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	97	91	7.00E-39	93.8	79.4	83.5
Rsa1.0_01975.1.g31229.t1	gb|ABL97983.1| auxin-induced protein-like [Brassica rapa]	70	99	9.00E-26	141.4	88.6	95.7	auxin-induced protein-like	gbpln	Brassica rapa	AT5G18020.1 | Symbols: | SAUR-like auxin-responsive protein family | chr5:5966305-5966580 REVERSE LENGTH=91	70	91	7.00E-20	130.0	72.9	80.0
Rsa1.0_01975.1.g31230.t1	gb|AAC17220.1| novel cap-binding protein nCBP [Arabidopsis thaliana]	225	221	1.00E-114	98.2	90.2	94.2	novel cap-binding protein nCBP	gbpln	Arabidopsis thaliana	AT5G18110.1 | Symbols: NCBP | novel cap-binding protein | chr5:5989105-5990588 REVERSE LENGTH=221	225	221	1.00E-116	98.2	89.8	93.8
Rsa1.0_01975.1.g31231.t1	ref|NP_566217.1| H/ACA ribonucleoprotein complex subunit 1 [Arabidopsis thaliana] gi|68565918|sp|Q8VZT0.1|NLAL1_ARATH RecName: Full=Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1 gi|17380836|gb|AAL36230.1| putative GAR1 protein [Arabidopsis thaliana] gi|20259633|gb|AAM14173.1| putative GAR1 protein [Arabidopsis thaliana] gi|332640491|gb|AEE74012.1| H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein [Arabidopsis thaliana]	234	202	6.00E-39	86.3	32.9	38.0	H/ACA ribonucleoprotein complex subunit 1	gbpln	Arabidopsis thaliana	AT3G03920.1 | Symbols: | H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein | chr3:1009123-1010379 REVERSE LENGTH=202	234	202	2.00E-41	86.3	32.9	38.0
Rsa1.0_01975.1.g31232.t1	gb|EOA20087.1| hypothetical protein CARUB_v10000361mg [Capsella rubella]	690	692	0	100.3	92.0	95.2	hypothetical protein CARUB_v10000361mg	gbpln	Capsella rubella	AT5G18190.1 | Symbols: | Protein kinase family protein | chr5:6010215-6013724 REVERSE LENGTH=691	690	691	0	100.1	89.7	93.6
Rsa1.0_01976.1.g31233.t1	gb|AAT38818.1| membrane protein [Brassica juncea] gi|306415491|gb|ADM86710.1| putative RAMP4 family protein [Brassica juncea]	94	68	2.00E-29	72.3	70.2	71.3	membrane protein	gbpln	Brassica juncea	AT1G27330.1 | Symbols: | Ribosome associated membrane protein RAMP4 | chr1:9493064-9493898 FORWARD LENGTH=68	94	68	5.00E-32	72.3	70.2	70.2
Rsa1.0_01976.1.g31234.t1	ref|XP_002890714.1| GYF domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297336556|gb|EFH66973.1| GYF domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1272	1406	0	110.5	36.4	40.5	GYF domain-containing protein	gbpln	Arabidopsis lyrata	AT1G24300.1 | Symbols: | GYF domain-containing protein | chr1:8614515-8620420 REVERSE LENGTH=1495	1272	1495	0	117.5	28.6	32.2
Rsa1.0_01976.1.g31235.t1	ref|XP_002893466.1| GYF domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297339308|gb|EFH69725.1| GYF domain-containing protein [Arabidopsis lyrata subsp. lyrata]	1214	1511	0	124.5	69.9	78.3	GYF domain-containing protein	gbpln	Arabidopsis lyrata	AT1G24300.2 | Symbols: | GYF domain-containing protein | chr1:8614515-8620420 REVERSE LENGTH=1490	1214	1490	0	122.7	37.0	41.8
Rsa1.0_01976.1.g31236.t1	gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	329	1231	1.00E-38	374.2	33.7	45.3	Very similar to retrotransposon reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	329	575	6.00E-26	174.8	28.9	45.9
Rsa1.0_01976.1.g31237.t1	gb|EOA37637.1| hypothetical protein CARUB_v10012107mg [Capsella rubella]	137	174	1.00E-38	127.0	69.3	78.8	hypothetical protein CARUB_v10012107mg	gbpln	Capsella rubella	AT1G27380.1 | Symbols: RIC2 | ROP-interactive CRIB motif-containing protein 2 | chr1:9508903-9509827 REVERSE LENGTH=111	137	111	5.00E-27	81.0	49.6	56.2

Rsa1.0_01976.1.g31238.t1	ref|XP_002893465.1| F17L21.18 [Arabidopsis lyrata subsp. lyrata] gi|297339307|gb|EFH69724.1| F17L21.18 [Arabidopsis lyrata subsp. lyrata]	206	205	4.00E−78	99.5	68.0	83.0	F17L21.18	gbpln	Arabidopsis lyrata	AT1G27390.1 | Symbols: TOM20−2 | translocase outer membrane 20−2 | chr1:9513469−9514912 REVERSE LENGTH=210	206	210	1.00E−76	101.9	65.5	79.6
Rsa1.0_01976.1.g31239.t1	ref|XP_002868854.1| hypothetical protein ARALYDRAFT_912317 [Arabidopsis lyrata subsp. lyrata] gi|297314690|gb|EFH45113.1| hypothetical protein ARALYDRAFT_912317 [Arabidopsis lyrata subsp. lyrata]	177	195	3.00E−44	110.2	76.3	84.2	hypothetical protein ARALYDRAFT_912317	gbpln	Arabidopsis lyrata	AT2G21060.1 | Symbols: ATGRP2B, ATCSP4, GRP2B | glycine−rich protein 2B | chr2:9036983−9037588 REVERSE LENGTH=201	177	201	8.00E−46	113.6	73.4	80.2
Rsa1.0_01976.1.g31240.t1	ref|NP_174060.1| 60S ribosomal protein L17−1 [Arabidopsis thaliana] gi|27734446|sp|Q93VI3.1|RL171_ARATH RecName: Full=60S ribosomal protein L17−1 gi|16226209|gb|AAL16103.1|AF428271_1 At1g27400/F17L21_20 [Arabidopsis thaliana] gi|16226630|gb|AAL16218.1|AF428449_1 At1g27400/F17L21_20 [Arabidopsis thaliana] gi|14335140|gb|AAK59850.1| At1g27400/F17L21_20 [Arabidopsis thaliana] gi|18655347|gb|AAL76129.1| At1g27400/F17L21_20 [Arabidopsis thaliana] gi|21594923|gb|AAM66056.1| putative 60S ribosomal protein L17 [Arabidopsis thaliana] gi|332192704|gb|AEE30825.1| 60S ribosomal protein L17−1 [Arabidopsis thaliana]	176	176	4.00E−99	100.0	98.9	98.9	60S ribosomal protein L17−1	gbpln	Arabidopsis thaliana	AT1G27400.1 | Symbols: | Ribosomal protein L22p/L17e family protein | chr1:9515230−9516725 FORWARD LENGTH=176	176	176	1.00E−101	100.0	98.9	98.9
Rsa1.0_01976.1.g31241.t1	ref|NP_174062.1| kelch repeat−containing F−box protein [Arabidopsis thaliana] gi|374095396|sp|Q9FZJ3.2|FBK16_ARATH RecName: Full=Putative F−box/kelch−repeat protein At1g27420 gi|332192706|gb|AEE30827.1| putative F−box/kelch−repeat protein [Arabidopsis thaliana]	343	346	1.00E−175	100.9	86.6	91.8	kelch repeat−containing F−box protein	gbpln	Arabidopsis thaliana	AT1G27420.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9519108−9520520 FORWARD LENGTH=346	343	346	1.00E−178	100.9	86.6	91.8
Rsa1.0_01976.1.g31242.t3	ref|XP_002893467.1| hypothetical protein ARALYDRAFT_890267 [Arabidopsis lyrata subsp. lyrata] gi|297339309|gb|EFH69726.1| hypothetical protein ARALYDRAFT_890267 [Arabidopsis lyrata subsp. lyrata]	79	81	5.00E−28	102.5	78.5	86.1	hypothetical protein ARALYDRAFT_890267	gbpln	Arabidopsis lyrata	AT1G27435.1 | Symbols: | unknown protein; Has 16 Blast hits to 16 proteins in 8 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 16; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:9527956−9528814 REVERSE LENGTH=81	79	81	1.00E−28	102.5	74.7	83.5
Rsa1.0_01977.1.g31243.t1	gb|EOA34076.1| hypothetical protein CARUB_v10021577mg [Capsella rubella]	87	329	8.00E−14	378.2	55.2	62.1	hypothetical protein CARUB_v10021577mg	gbpln	Capsella rubella	AT1G78050.1 | Symbols: PGM | phosphoglycerate/bisphosphoglycerate mutase | chr1:29348095−29349592 FORWARD LENGTH=332	87	332	1.00E−14	381.6	51.7	57.5
Rsa1.0_01977.1.g31244.t1	gb|AAF79427.1|AC025808_9 F18O14.19 [Arabidopsis thaliana]	100	1158	9.00E−37	1158.0	72.0	83.0	F18O14.19	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01977.1.g31245.t1	ref|XP_002879721.1| ribosome biogenesis regulatory protein family protein [Arabidopsis lyrata subsp. lyrata] gi|297325560|gb|EFH55980.1| ribosome biogenesis regulatory protein family protein [Arabidopsis lyrata subsp. lyrata]	318	324	1.00E−156	101.9	87.7	92.1	ribosome biogenesis regulatory protein family protein	gbpln	Arabidopsis lyrata	AT2G37990.1 | Symbols: | ribosome biogenesis regulatory protein (RRS1) family protein | chr2:15900713−15903028 FORWARD LENGTH=318	318	318	1.00E−156	100.0	86.8	91.5
Rsa1.0_01977.1.g31246.t2	ref|NP_181334.1| O−fucosyltransferase−like protein [Arabidopsis thaliana] gi|13430694|gb|AAK25969.1|AF360259_1 putative axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana] gi|25054996|gb|AAN71964.1| putative axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana] gi|330254380|gb|AEC09474.1| O−fucosyltransferase−like protein [Arabidopsis thaliana]	603	638	0	105.8	85.6	90.4	O−fucosyltransferase−like protein	gbpln	Arabidopsis thaliana	AT2G37980.1 | Symbols: | O−fucosyltransferase family protein | chr2:15894162−15897452 REVERSE LENGTH=638	603	638	0	105.8	85.6	90.4
Rsa1.0_01977.1.g31247.t1	ref|XP_002334539.1| predicted protein [Populus trichocarpa] gi|222873027|gb|EEF10158.1| predicted protein [Populus trichocarpa]	134	442	5.00E−28	329.9	49.3	66.4	predicted protein	gbpln	Populus trichocarpa	AT4G33260.2 | Symbols: CDC20.2 | Transducin family protein / WD−40 repeat family protein | chr4:16041195−16043180 REVERSE LENGTH=441	134	441	4.00E−28	329.1	47.0	65.7
Rsa1.0_01977.1.g31248.t1	#	#	#	#	#	#	#	−	−−−−	−−−−	#	#	#	#	#	#	#

Rsa1.0_01977.1.g31249.t1	ref|XP_002881554.1| hypothetical protein ARALYDRAFT_482801 [Arabidopsis lyrata subsp. lyrata] gi|297327393|gb|EFH57813.1| hypothetical protein ARALYDRAFT_482801 [Arabidopsis lyrata subsp. lyrata]	173	207	1.00E-47	119.7	59.0	65.9	hypothetical protein ARALYDRAFT_482801	gbpln	Arabidopsis lyrata	AT2G37950.1 | Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr2:15882536-15883665 REVERSE LENGTH=207	173	207	1.00E-48	119.7	61.8	66.5
Rsa1.0_01978.1.g31250.t1	gb|EOA22994.1| hypothetical protein CARUB_v10003741mg [Capsella rubella]	399	395	0	99.0	85.5	92.0	hypothetical protein CARUB_v10003741mg	gbpln	Capsella rubella	AT4G03010.1 | Symbols: | RNI-like superfamily protein | chr4:1329952-1331139 FORWARD LENGTH=395	399	395	0	99.0	84.2	89.7
Rsa1.0_01978.1.g31251.t1	ref|XP_002874883.1| protein binding protein [Arabidopsis lyrata subsp. lyrata] gi|297320720|gb|EFH51142.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	749	802	0	107.1	77.7	85.7	protein binding protein	gbpln	Arabidopsis lyrata	AT4G03000.2 | Symbols: | RING/U-box superfamily protein | chr4:1324602-1327348 FORWARD LENGTH=814	749	814	0	108.7	76.2	85.2
Rsa1.0_01978.1.g31252.t1	ref|XP_002874884.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata] gi|297320721|gb|EFH51143.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata]	522	534	0	102.3	81.6	88.3	mitochondrial transcription termination factor family protein	gbpln	Arabidopsis lyrata	AT4G02990.1 | Symbols: | Mitochondrial transcription termination factor family protein | chr4:1322158-1323783 FORWARD LENGTH=541	522	541	0	103.6	79.1	86.6
Rsa1.0_01978.1.g31253.t1	gb|AAG24497.1| resistant endoplasmic reticulum auxin-binding protein 1 [Sinapis arvensis]	198	198	1.00E-104	100.0	94.4	97.0	resistant endoplasmic reticulum auxin-binding protein 1	gbpln	Sinapis arvensis	AT4G02980.1 | Symbols: ABP1, ABP | endoplasmic reticulum auxin binding protein 1 | chr4:1319902-1321449 REVERSE LENGTH=198	198	198	1.00E-104	100.0	88.4	93.9
Rsa1.0_01978.1.g31254.t1	ref|NP_192246.1| Ubiquitin family protein [Arabidopsis thaliana] gi|4262164|gb|AAD14464.1| putative ubiquitin-like protein [Arabidopsis thaliana] gi|7270207|emb|CAB77822.1| putative protein [Arabidopsis thaliana] gi|67633730|gb|AAY78789.1| ubiquitin family protein [Arabidopsis thaliana] gi|332656911|gb|AEE82311.1| Ubiquitin family protein [Arabidopsis thaliana]	443	295	1.00E-21	66.6	14.7	18.3	Ubiquitin family protein	gbpln	Arabidopsis thaliana	AT4G03370.1 | Symbols: | Ubiquitin family protein | chr4:1478078-1478965 REVERSE LENGTH=295	443	295	3.00E-24	66.6	14.7	18.3
Rsa1.0_01978.1.g31255.t1	gb|EOA23080.1| hypothetical protein CARUB_v10003861mg [Capsella rubella]	444	214	3.00E-24	48.2	14.9	19.1	hypothetical protein CARUB_v10003861mg	gbpln	Capsella rubella	AT4G05230.1 | Symbols: | Ubiquitin-like superfamily protein | chr4:2687003-2687623 FORWARD LENGTH=206	444	206	1.00E-26	46.4	14.6	19.6
Rsa1.0_01978.1.g31256.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01978.1.g31257.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01978.1.g31258.t1	gb|EOA20287.1| hypothetical protein CARUB_v10000595mg [Capsella rubella]	404	563	0	139.4	80.2	86.4	hypothetical protein CARUB_v10000595mg	gbpln	Capsella rubella	AT4G02940.1 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr4:1306658-1310699 FORWARD LENGTH=569	404	569	1.00E-178	140.8	80.4	86.1
Rsa1.0_01978.1.g31259.t1	gb|EOA20287.1| hypothetical protein CARUB_v10000595mg [Capsella rubella]	171	563	9.00E-67	329.2	79.5	86.5	hypothetical protein CARUB_v10000595mg	gbpln	Capsella rubella	AT4G02940.1 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr4:1306658-1310699 FORWARD LENGTH=569	171	569	9.00E-65	332.7	78.4	86.5
Rsa1.0_01979.1.g31260.t1	emb|CCD74528.1| NAC domain containing protein 23 [Arabidopsis halleri subsp. halleri]	353	334	4.00E-60	94.6	41.9	57.5	NAC domain containing protein 23	gbpln	Arabidopsis halleri	AT1G60350.1 | Symbols: anac024, NAC024 | NAC domain containing protein 24 | chr1:22241273-22242235 REVERSE LENGTH=320	353	320	1.00E-61	90.7	41.1	54.7
Rsa1.0_01979.1.g31261.t1	gb|EOA31219.1| hypothetical protein CARUB_v10014386mg [Capsella rubella]	203	270	1.00E-74	133.0	74.4	80.8	hypothetical protein CARUB_v10014386mg	gbpln	Capsella rubella	AT2G19580.1 | Symbols: TET2 | tetraspanin2 | chr2:8472393-8475021 REVERSE LENGTH=270	203	270	7.00E-71	133.0	74.4	80.8
Rsa1.0_01979.1.g31262.t2	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01979.1.g31263.t1	ref|XP_002882367.1| F-box family protein [Arabidopsis lyrata subsp. lyrata] gi|297328207|gb|EFH58626.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	362	423	1.00E-131	116.9	64.9	78.5	F-box family protein	gbpln	Arabidopsis lyrata	AT3G04660.1 | Symbols: | F-box and associated interaction domains-containing protein | chr3:1264794-1265966 FORWARD LENGTH=390	362	390	1.00E-131	107.7	63.8	76.2
Rsa1.0_01979.1.g31264.t1	gb|EOA32034.1| hypothetical protein CARUB_v10015278mg [Capsella rubella]	107	500	3.00E-11	467.3	29.9	32.7	hypothetical protein CARUB_v10015278mg	gbpln	Capsella rubella	AT5G45130.1 | Symbols: ATRAB5A, ATRABF2A, RABF2A, RAB5A, RHA1, ATRAB-F2A, RAB-F2A | RAB homolog 1 | chr5:18244495-18246060 FORWARD LENGTH=200	107	200	1.00E-13	186.9	29.0	29.9

Rsa1.0_01979.1.g31265.t3	ref|NP_179544.1| transducin-like protein [Arabidopsis thaliana] gi|13877611|gb|AAK43883.1|AF370506_1 putative WD-40 repeat protein [Arabidopsis thaliana] gi|4191784|gb|AAD10153.1| putative WD-40 repeat protein [Arabidopsis thaliana] gi|22136272|gb|AAM91214.1| putative WD-40 repeat protein [Arabidopsis thaliana] gi|330251799|gb|AEC06893.1| transducin-like protein [Arabidopsis thaliana]	292	469	1.00E-124	160.6	81.2	84.9	transducin-like protein	gbpln	Arabidopsis thaliana	AT2G19540.1 | Symbols: | Transducin family protein / WD-40 repeat family protein | chr2:8461804-8464347 FORWARD LENGTH=469	292	469	1.00E-127	160.6	81.2	84.9
Rsa1.0_01979.1.g31266.t1	gb|EOA16148.1| hypothetical protein CARUB_v10004286mg, partial [Capsella rubella]	606	681	0	112.4	96.9	98.8	hypothetical protein CARUB_v10004286mg, partial	gbpln	Capsella rubella	AT5G35160.2 | Symbols: | Endomembrane protein 70 protein family | chr5:13414945-13416921 FORWARD LENGTH=658	606	658	0	108.6	96.9	98.7
Rsa1.0_01979.1.g31267.t1	ref|NP_849991.1| histone-lysine N-methyltransferase ASHR2 [Arabidopsis thaliana] gi|94707155|sp|Q9ZUM9.3|ASHR2_ARATH RecName: Full=Histone-lysine N-methyltransferase ASHR2; AltName: Full=ASH1-related protein 2; AltName: Full=Protein SET DOMAIN GROUP 39 gi|28393236|gb|AAO42047.1| putative SET-domain transcriptional regulator [Arabidopsis thaliana] gi|330251813|gb|AEC06907.1| histone-lysine N-methyltransferase ASHR2 [Arabidopsis thaliana]	391	398	1.00E-171	101.8	81.1	87.7	histone-lysine N-methyltransferase ASHR2	gbpln	Arabidopsis thaliana	AT2G19640.2 | Symbols: ASHR2 | ASH1-related protein 2 | chr2:8491401-8492597 FORWARD LENGTH=398	391	398	1.00E-174	101.8	81.1	87.7
Rsa1.0_01979.1.g31268.t1	gb|EOA31670.1| hypothetical protein CARUB_v10014874mg [Capsella rubella]	139	141	5.00E-59	101.4	76.3	84.2	hypothetical protein CARUB_v10014874mg	gbpln	Capsella rubella	AT2G19690.1 | Symbols: PLA2-BETA | phospholipase A2-beta | chr2:8503326-8504549 FORWARD LENGTH=147	139	147	4.00E-60	105.8	75.5	83.5
Rsa1.0_01980.1.g31269.t1	ref|NP_565208.1| uncharacterized protein [Arabidopsis thaliana] gi|15450719|gb|AAK96631.1| At1g79420/T8K14_16 [Arabidopsis thaliana] gi|22655486|gb|AAM98335.1| At1g79420/T8K14_16 [Arabidopsis thaliana] gi|332198119|gb|AEE36240.1| uncharacterized protein AT1G79420 [Arabidopsis thaliana]	416	417	0	100.2	95.4	97.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G79420.1 | Symbols: | Protein of unknown function (DUF620) | chr1:29871537-29874166 FORWARD LENGTH=417	416	417	0	100.2	95.4	97.1
Rsa1.0_01980.1.g31270.t1	ref|NP_178059.1| organic cation/carnitine transporter5 [Arabidopsis thaliana] gi|75313142|sp|Q9SAK7.1|OCT5_ARATH RecName: Full=Organic cation/carnitine transporter 5; Short=AtOCT5 gi|4835768|gb|AAD30235.1|AC007202_17 Is a member of the PF|00083 sugar transporter family [Arabidopsis thaliana] gi|332198118|gb|AEE36239.1| organic cation/carnitine transporter5 [Arabidopsis thaliana]	513	515	0	100.4	76.6	86.7	organic cation/carnitine transporter5	gbpln	Arabidopsis thaliana	AT1G79410.1 | Symbols: AtOCT5, 5-Oct | organic cation/carnitine transporter5 | chr1:29868037-29869584 REVERSE LENGTH=515	513	515	0	100.4	76.6	86.7
Rsa1.0_01980.1.g31271.t1	ref|NP_178059.1| organic cation/carnitine transporter5 [Arabidopsis thaliana] gi|75313142|sp|Q9SAK7.1|OCT5_ARATH RecName: Full=Organic cation/carnitine transporter 5; Short=AtOCT5 gi|4835768|gb|AAD30235.1|AC007202_17 Is a member of the PF|00083 sugar transporter family [Arabidopsis thaliana] gi|332198118|gb|AEE36239.1| organic cation/carnitine transporter5 [Arabidopsis thaliana]	439	515	0	117.3	80.0	89.3	organic cation/carnitine transporter5	gbpln	Arabidopsis thaliana	AT1G79410.1 | Symbols: AtOCT5, 5-Oct | organic cation/carnitine transporter5 | chr1:29868037-29869584 REVERSE LENGTH=515	439	515	0	117.3	80.0	89.3
Rsa1.0_01980.1.g31272.t1	ref|XP_002887784.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333625|gb|EFH64043.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	781	783	0	100.3	84.1	91.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G79400.1 | Symbols: ATCHX2, CHX2 | cation/H+ exchanger 2 | chr1:29864992-29867840 FORWARD LENGTH=783	781	783	0	100.3	83.1	90.8
Rsa1.0_01980.1.g31273.t1	gb|EOA35850.1| hypothetical protein CARUB_v10021091mg, partial [Capsella rubella]	142	154	9.00E-61	108.5	81.7	86.6	hypothetical protein CARUB_v10021091mg, partial	gbpln	Capsella rubella	AT1G79390.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:29863465-29864276 REVERSE LENGTH=126	142	126	8.00E-62	88.7	78.9	85.9

Rsa1.0_01980.1.g31274.t1	ref|NP_565206.1| Ca(2)-dependent phospholipid-binding family protein [Arabidopsis thaliana] gi|4835771|gb|AAD30238.1|AC007202_20 Similar to gi|3844599 F31D5.2 gene product from Caenorhabditis elegans cosmid gb|U28941 and contains PF|00097 Zinc (Ring) finger C3HC4 domain. ESTs gb|F19963 and gb|T42582 come from this gene [Arabidopsis thaliana] gi|13937149|gb|AAK50068.1|AF372928_1 At1g79380/T8K14_20 [Arabidopsis thaliana] gi|22137140|gb|AAM91415.1| At1g79380/T8K14_20 [Arabidopsis thaliana] gi|332198115|gb|AEE36236.1| Ca(2)-dependent phospholipid-binding family protein [Arabidopsis thaliana]	403	401	0	99.5	86.1	91.1	Ca(2)-dependent phospholipid-binding family protein	gbpln	Arabidopsis thaliana	AT1G79380.1 | Symbols: | Ca(2)-dependent phospholipid-binding protein (Copine) family | chr1:29860812-29863023 FORWARD LENGTH=401	403	401	0	99.5	86.1	91.1
Rsa1.0_01981.1.g31275.t1	gb|ACQ90602.1| putative C2H2 zinc finger protein [Eutrema halophilum]	590	607	0	102.9	91.2	93.9	putative C2H2 zinc finger protein	gbpln	Eutrema halophilum	AT2G02070.1 | Symbols: AtIDD5, IDD5 | indeterminate(ID)-domain 5 | chr2:505523-509154 FORWARD LENGTH=602	590	602	0	102.0	88.6	92.9
Rsa1.0_01981.1.g31276.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01981.1.g31277.t1	gb|ACG60684.1| maize transposon MuDR-like protein [Brassica oleracea var. alboglabra]	768	622	0	81.0	58.6	67.2	maize transposon MuDR-like protein	gbpln	Brassica oleracea	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	768	719	1.00E-37	93.6	17.6	29.0
Rsa1.0_01981.1.g31278.t1	gb|EOA28352.1| hypothetical protein CARUB_v10024557mg [Capsella rubella]	394	863	1.00E-64	219.0	34.3	48.5	hypothetical protein CARUB_v10024557mg	gbpln	Capsella rubella	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	394	921	8.00E-65	233.8	32.0	47.0
Rsa1.0_01981.1.g31279.t1	gb|ADQ43193.1| unknown [Eutrema parvulum]	400	395	0	98.8	85.8	91.3	unknown	gbpln	Eutrema parvulum	AT1G14590.1 | Symbols: | Nucleotide-diphospho-sugar transferase family protein | chr1:4998957-5000617 REVERSE LENGTH=386	400	386	1.00E-172	96.5	74.3	83.5
Rsa1.0_01981.1.g31280.t1	gb|ADQ43192.1| unknown [Eutrema parvulum]	250	269	4.00E-97	107.6	78.4	84.8	unknown	gbpln	Eutrema parvulum	AT2G02060.1 | Symbols: | Homeodomain-like superfamily protein | chr2:495691-497609 FORWARD LENGTH=256	250	256	8.00E-72	102.4	69.2	76.8
Rsa1.0_01981.1.g31281.t1	gb|ACQ90599.1| putative NADH dehydrogenase [Eutrema halophilum]	102	102	1.00E-51	100.0	97.1	98.0	putative NADH dehydrogenase	gbpln	Eutrema halophilum	AT2G02050.1 | Symbols: | NADH-ubiquinone oxidoreductase B18 subunit, putative | chr2:490024-490335 FORWARD LENGTH=103	102	103	1.00E-47	101.0	88.2	92.2
Rsa1.0_01982.1.g31282.t1	gb|ABD65090.1| hypothetical protein 27.t00116 [Brassica oleracea]	132	484	1.00E-20	366.7	40.2	47.7	hypothetical protein 27.t00116	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01982.1.g31283.t1	gb|EOA38282.1| hypothetical protein CARUB_v10009775mg [Capsella rubella]	177	318	2.00E-47	179.7	55.4	62.7	hypothetical protein CARUB_v10009775mg	gbpln	Capsella rubella	AT1G22220.1 | Symbols: | F-box family protein | chr1:7846694-7847638 FORWARD LENGTH=314	177	314	8.00E-46	177.4	55.4	61.0
Rsa1.0_01982.1.g31284.t2	ref|XP_002893213.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339055|gb|EFH69472.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	196	335	2.00E-77	170.9	80.1	86.7	predicted protein	gbpln	Arabidopsis lyrata	AT1G22130.1 | Symbols: AGL104 | AGAMOUS-like 104 | chr1:7812387-7814259 REVERSE LENGTH=335	196	335	1.00E-78	170.9	80.6	87.2
Rsa1.0_01982.1.g31285.t1	ref|XP_002893211.1| hypothetical protein ARALYDRAFT_472444 [Arabidopsis lyrata subsp. lyrata] gi|297339053|gb|EFH69470.1| hypothetical protein ARALYDRAFT_472444 [Arabidopsis lyrata subsp. lyrata]	296	290	1.00E-79	98.0	69.9	79.1	hypothetical protein ARALYDRAFT_472444	gbpln	Arabidopsis lyrata	AT1G22110.1 | Symbols: | structural constituent of ribosome | chr1:7801625-7802473 REVERSE LENGTH=282	296	282	6.00E-80	95.3	68.9	77.4
Rsa1.0_01982.1.g31286.t1	ref|XP_002893210.1| hypothetical protein ARALYDRAFT_313098 [Arabidopsis lyrata subsp. lyrata] gi|297339052|gb|EFH69469.1| hypothetical protein ARALYDRAFT_313098 [Arabidopsis lyrata subsp. lyrata]	465	441	0	94.8	80.0	86.7	hypothetical protein ARALYDRAFT_313098	gbpln	Arabidopsis lyrata	AT1G22100.1 | Symbols: | Inositol-pentakisphosphate 2-kinase family protein | chr1:7798023-7800030 REVERSE LENGTH=441	465	441	0	94.8	79.8	86.2
Rsa1.0_01982.1.g31287.t1	gb|ABU96774.1| bZIP transcription factor [Brassica juncea]	379	386	0	101.8	88.4	92.3	bZIP transcription factor	gbpln	Brassica juncea	AT1G22070.1 | Symbols: TGA3 | TGA1A-related gene 3 | chr1:7789651-7791821 FORWARD LENGTH=384	379	384	1.00E-177	101.3	82.1	87.6
Rsa1.0_01982.1.g31288.t1	gb|EOA36270.1| hypothetical protein CARUB_v10010515mg [Capsella rubella]	71	159	4.00E-20	223.9	73.2	83.1	hypothetical protein CARUB_v10010515mg	gbpln	Capsella rubella	AT1G22065.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G77885.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:7785889-7786107 FORWARD LENGTH=72	71	72	2.00E-19	101.4	71.8	81.7

<table>
<tr><td>Rsa1.0_01982.1.g31289.t1</td><td>gb|EOA36030.1| hypothetical protein CARUB_v10008070mg [Capsella rubella]</td><td>75</td><td>2001</td><td>2.00E-16</td><td>2668.0</td><td>54.7</td><td>65.3</td><td>hypothetical protein CARUB_v10008070mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G22060.1 | Symbols: | LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: FBD, F-box and Leucine Rich Repeat domains containing protein (TAIR:AT1G22000.1); Has 84739 Blast hits to 38714 proteins in 2257 species: Archae - 1436; Bacteria - 11314; Metazoa - 40747; Fungi - 7706; Plants - 4675; Viruses - 308; Other Eukaryotes - 18553 (source: NCBI BLink). | chr1:7773373-7780586 REVERSE LENGTH=1999</td><td>75</td><td>1999</td><td>8.00E-19</td><td>2665.3</td><td>53.3</td><td>64.0</td></tr>
<tr><td>Rsa1.0_01983.1.g31290.t1</td><td>ref|XP_002866572.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297312407|gb|EFH42831.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata]</td><td>430</td><td>506</td><td>1.00E-81</td><td>117.7</td><td>36.3</td><td>42.3</td><td>IBR domain-containing protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63730.1 | Symbols: ATARI14, ARI14 | IBR domain-containing protein | chr5:25508100-25509706 REVERSE LENGTH=506</td><td>430</td><td>506</td><td>1.00E-81</td><td>117.7</td><td>35.3</td><td>41.4</td></tr>
<tr><td>Rsa1.0_01983.1.g31291.t2</td><td>ref|NP_201177.1| protein kokopelli [Arabidopsis thaliana] gi|10177053|dbj|BAB10465.1| unnamed protein product [Arabidopsis thaliana] gi|332010406|gb|AED97789.1| protein kokopelli [Arabidopsis thaliana]</td><td>471</td><td>492</td><td>5.00E-54</td><td>104.5</td><td>44.8</td><td>56.9</td><td>protein kokopelli</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G63720.1 | Symbols: KPL | kokopelli | chr5:25506349-25508017 FORWARD LENGTH=492</td><td>471</td><td>492</td><td>1.00E-56</td><td>104.5</td><td>44.8</td><td>56.9</td></tr>
<tr><td>Rsa1.0_01983.1.g31292.t2</td><td>dbj|BAB10464.1| receptor-like protein kinase [Arabidopsis thaliana]</td><td>595</td><td>579</td><td>0</td><td>97.3</td><td>91.8</td><td>95.3</td><td>receptor-like protein kinase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G63710.1 | Symbols: | Leucine-rich repeat protein kinase family protein | chr5:25499475-25502598 FORWARD LENGTH=614</td><td>595</td><td>614</td><td>0</td><td>103.2</td><td>91.8</td><td>95.3</td></tr>
<tr><td>Rsa1.0_01983.1.g31293.t1</td><td>ref|XP_002866570.1| hypothetical protein ARALYDRAFT_919665 [Arabidopsis lyrata subsp. lyrata] gi|297312405|gb|EFH42829.1| hypothetical protein ARALYDRAFT_919665 [Arabidopsis lyrata subsp. lyrata]</td><td>140</td><td>138</td><td>4.00E-66</td><td>98.6</td><td>86.4</td><td>95.7</td><td>hypothetical protein ARALYDRAFT_919665</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63690.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr5:25492864-25493283 REVERSE LENGTH=139</td><td>140</td><td>139</td><td>2.00E-68</td><td>99.3</td><td>87.9</td><td>96.4</td></tr>
<tr><td>Rsa1.0_01983.1.g31294.t1</td><td>gb|EOA13225.1| hypothetical protein CARUB_v10026251mg [Capsella rubella] gi|482549032|gb|EOA13226.1| hypothetical protein CARUB_v10026251mg [Capsella rubella]</td><td>510</td><td>510</td><td>0</td><td>100.0</td><td>96.9</td><td>99.2</td><td>hypothetical protein CARUB_v10026251mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G63680.1 | Symbols: | Pyruvate kinase family protein | chr5:25490507-25492530 FORWARD LENGTH=510</td><td>510</td><td>510</td><td>0</td><td>100.0</td><td>96.5</td><td>99.0</td></tr>
<tr><td>Rsa1.0_01983.1.g31295.t1</td><td>gb|EOA14793.1| hypothetical protein CARUB_v10028093mg, partial [Capsella rubella]</td><td>224</td><td>531</td><td>8.00E-72</td><td>237.1</td><td>62.5</td><td>73.2</td><td>hypothetical protein CARUB_v10028093mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G08560.2 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:2771104-2773827 REVERSE LENGTH=589</td><td>224</td><td>589</td><td>9.00E-66</td><td>262.9</td><td>56.3</td><td>68.8</td></tr>
<tr><td>Rsa1.0_01983.1.g31296.t1</td><td>ref|XP_002866567.1| serine/threonine-protein kinase [Arabidopsis lyrata subsp. lyrata] gi|297312402|gb|EFH42826.1| serine/threonine-protein kinase [Arabidopsis lyrata subsp. lyrata]</td><td>356</td><td>356</td><td>0</td><td>100.0</td><td>94.4</td><td>97.8</td><td>serine/threonine-protein kinase</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G63650.1 | Symbols: SNRK2-5, SNRK2.5, SRK2H | SNF1-related protein kinase 2.5 | chr5:25481631-25483495 REVERSE LENGTH=360</td><td>356</td><td>360</td><td>0</td><td>101.1</td><td>93.5</td><td>97.8</td></tr>
<tr><td>Rsa1.0_01983.1.g31297.t2</td><td>dbj|BAJ34493.1| unnamed protein product [Thellungiella halophila]</td><td>427</td><td>448</td><td>1.00E-180</td><td>104.9</td><td>87.6</td><td>90.4</td><td>unnamed protein product</td><td>----</td><td>----</td><td>AT5G63640.1 | Symbols: | ENTH/VHS/GAT family protein | chr5:25478935-25481221 FORWARD LENGTH=447</td><td>427</td><td>447</td><td>1.00E-174</td><td>104.7</td><td>86.2</td><td>89.7</td></tr>
<tr><td>Rsa1.0_01983.1.g31298.t1</td><td>ref|NP_201168.2| DEAD-box ATP-dependent RNA helicase 31 [Arabidopsis thaliana] gi|332010396|gb|AED97779.1| DEAD-box ATP-dependent RNA helicase 31 [Arabidopsis thaliana]</td><td>1153</td><td>788</td><td>0</td><td>68.3</td><td>50.2</td><td>52.9</td><td>DEAD-box ATP-dependent RNA helicase 31</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G63630.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:25472598-25476402 REVERSE LENGTH=788</td><td>1153</td><td>788</td><td>0</td><td>68.3</td><td>50.2</td><td>52.9</td></tr>
<tr><td>Rsa1.0_01983.1.g31299.t1</td><td>gb|EOA13644.1| hypothetical protein CARUB_v10026716mg [Capsella rubella]</td><td>303</td><td>343</td><td>1.00E-114</td><td>113.2</td><td>65.0</td><td>82.8</td><td>hypothetical protein CARUB_v10026716mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G08640.2 | Symbols: FLS1 | flavonol synthase 1 | chr5:2804009-2805175 FORWARD LENGTH=336</td><td>303</td><td>336</td><td>1.00E-112</td><td>110.9</td><td>63.0</td><td>77.9</td></tr>
<tr><td>Rsa1.0_01984.1.g31300.t1</td><td>ref|NP_190077.2| cation/H(+) antiporter 12 [Arabidopsis thaliana] gi|298351611|sp|Q9FYC0.2|CHX12_ARATH RecName: Full=Cation/H(+) antiporter 12; AltName: Full=Protein CATION/H+ EXCHANGER 12; Short=AtCHX12 gi|332644446|gb|AEE77967.1| cation/H(+) antiporter 12 [Arabidopsis thaliana]</td><td>319</td><td>770</td><td>1.00E-112</td><td>241.4</td><td>69.6</td><td>82.1</td><td>cation/H(+) antiporter 12</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G44910.1 | Symbols: ATCHX12, CHX12 | cation/H+ exchanger 12 | chr3:16392064-16394579 REVERSE LENGTH=770</td><td>319</td><td>770</td><td>1.00E-115</td><td>241.4</td><td>69.6</td><td>82.1</td></tr>
<tr><td>Rsa1.0_01984.1.g31301.t1</td><td>gb|AAG51228.1|AC035249_3 Tam3-like transposon protein; 93317-95488 [Arabidopsis thaliana] gi|12323055|gb|AAG51515.1|AC068324_3 hAT-element transposase, putative [Arabidopsis thaliana]</td><td>455</td><td>723</td><td>3.00E-76</td><td>158.9</td><td>33.8</td><td>41.1</td><td>Tam3-like transposon protein; 93317-95488</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696</td><td>455</td><td>696</td><td>5.00E-21</td><td>153.0</td><td>22.0</td><td>40.7</td></tr>
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Rsa1.0_01984.1.g31302.t1	ref|XP_002875702.1| ATCHX4 [Arabidopsis lyrata subsp. lyrata] gi|297321540|gb|EFH51961.1| ATCHX4 [Arabidopsis lyrata subsp. lyrata]	817	817	0	100.0	84.9	94.1	ATCHX4	gbpln	Arabidopsis lyrata	AT3G44900.1 | Symbols: ATCHX4, CHX4 | cation/H+ exchanger 4 | chr3:16388724-16391360 FORWARD LENGTH=817	817	817	0	100.0	84.6	94.0
Rsa1.0_01984.1.g31303.t1	ref|XP_002875701.1| hypothetical protein ARALYDRAFT_484888 [Arabidopsis lyrata subsp. lyrata] gi|297321539|gb|EFH51960.1| hypothetical protein ARALYDRAFT_484888 [Arabidopsis lyrata subsp. lyrata]	196	197	3.00E-89	100.5	91.3	94.9	hypothetical protein ARALYDRAFT_484888	gbpln	Arabidopsis lyrata	AT3G44890.1 | Symbols: RPL9 | ribosomal protein L9 | chr3:16386505-16387963 FORWARD LENGTH=197	196	197	5.00E-89	100.5	87.2	93.9
Rsa1.0_01984.1.g31304.t1	ref|XP_002893701.1| hypothetical protein ARALYDRAFT_890773 [Arabidopsis lyrata subsp. lyrata] gi|297339543|gb|EFH69960.1| hypothetical protein ARALYDRAFT_890773 [Arabidopsis lyrata subsp. lyrata]	149	121	2.00E-20	81.2	38.3	45.6	hypothetical protein ARALYDRAFT_890773	gbpln	Arabidopsis lyrata	AT1G44010.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15640.1); Has 211 Blast hits to 210 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 211; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:16714656-16715504 FORWARD LENGTH=227	149	227	1.00E-20	152.3	40.3	51.0
Rsa1.0_01984.1.g31305.t1	gb|ABD60317.1| chloroplast pheophorbide a oxygenase PaO1 [Brassica napus]	538	538	0	100.0	96.3	97.2	chloroplast pheophorbide a oxygenase PaO1	gbpln	Brassica napus	AT3G44880.1 | Symbols: ACD1, LLS1, PAO | Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain | chr3:16383858-16386204 FORWARD LENGTH=537	538	537	0	99.8	92.0	94.6
Rsa1.0_01984.1.g31306.t1	ref|NP_190068.4| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana] gi|338819814|sp|Q9FYC8.2|Y3482_ARATH RecName: Full=BTB/POZ domain-containing protein At3g44820 gi|332644437|gb|AEE77958.1| Phototropic-responsive NPH3 family protein [Arabidopsis thaliana]	634	651	0	102.7	89.3	94.6	Phototropic-responsive NPH3 family protein	gbpln	Arabidopsis thaliana	AT3G44820.1 | Symbols: | Phototropic-responsive NPH3 family protein | chr3:16361864-16364411 REVERSE LENGTH=651	634	651	0	102.7	89.3	94.6
Rsa1.0_01985.1.g31307.t1	ref|XP_002887697.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297333538|gb|EFH63956.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	366	786	6.00E-88	214.8	55.7	63.7	kinase family protein	gbpln	Arabidopsis lyrata	AT1G77720.1 | Symbols: PPK1 | putative protein kinase 1 | chr1:29210730-29213877 FORWARD LENGTH=777	366	777	2.00E-73	212.3	51.1	58.2
Rsa1.0_01985.1.g31308.t2	ref|NP_177893.1| pathogenesis-related thaumatin-like protein [Arabidopsis thaliana] gi|12323299|gb|AAG51631.1|AC012193_13 thaumatin-like protein; 12104-13574 [Arabidopsis thaliana] gi|332197890|gb|AEE36011.1| pathogenesis-related thaumatin-like protein [Arabidopsis thaliana]	246	356	1.00E-120	144.7	82.1	92.3	pathogenesis-related thaumatin-like protein	gbpln	Arabidopsis thaliana	AT1G77700.1 | Symbols: | Pathogenesis-related thaumatin superfamily protein | chr1:29204747-29206217 FORWARD LENGTH=356	246	356	1.00E-122	144.7	82.1	92.3
Rsa1.0_01985.1.g31309.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1748	1274	0	72.9	23.4	28.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1748	626	7.00E-37	35.8	6.5	10.9
Rsa1.0_01985.1.g31310.t1	gb|EOA33358.1| hypothetical protein CARUB_v10020229mg [Capsella rubella]	437	470	0	107.6	96.6	99.1	hypothetical protein CARUB_v10020229mg	gbpln	Capsella rubella	AT1G77690.1 | Symbols: LAX3 | like AUX1 3 | chr1:29201232-29203317 REVERSE LENGTH=470	437	470	0	107.6	95.9	98.6
Rsa1.0_01985.1.g31311.t1	gb|AAM67247.1| putative aminotransferase [Arabidopsis thaliana]	401	404	0	100.7	86.0	92.0	putative aminotransferase	gbpln	Arabidopsis thaliana	AT1G77670.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr1:29189043-29190901 REVERSE LENGTH=440	401	440	0	109.7	86.0	92.0
Rsa1.0_01985.1.g31312.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01985.1.g31313.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_01986.1.g31314.t1	gb|EOA25657.1| hypothetical protein CARUB_v10019008mg, partial [Capsella rubella]	429	450	0	104.9	95.3	97.0	hypothetical protein CARUB_v10019008mg, partial	gbpln	Capsella rubella	AT3G45100.2 | Symbols: SETH2 | UDP-Glycosyltransferase superfamily protein | chr3:16504648-16506858 FORWARD LENGTH=447	429	447	0	104.2	95.1	97.0
Rsa1.0_01986.1.g31315.t1	ref|XP_002870971.1| hypothetical protein ARALYDRAFT_908104 [Arabidopsis lyrata subsp. lyrata] gi|297316808|gb|EFH47230.1| hypothetical protein ARALYDRAFT_908104 [Arabidopsis lyrata subsp. lyrata]	108	115	1.00E-41	106.5	84.3	90.7	hypothetical protein ARALYDRAFT_908104	gbpln	Arabidopsis lyrata	AT5G02420.1 | Symbols: | unknown protein; Has 90 Blast hits to 90 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:523501-523848 FORWARD LENGTH=115	108	115	6.00E-44	106.5	84.3	91.7
Rsa1.0_01986.1.g31316.t1	emb|CAB85546.1| putative protein [Arabidopsis thaliana]	231	498	4.00E-55	215.6	45.5	45.9	putative protein	gbpln	Arabidopsis thaliana	AT5G02410.1 | Symbols: | DIE2/ALG10 family | chr5:517319-519634 REVERSE LENGTH=509	231	509	1.00E-57	220.3	45.5	45.9
Rsa1.0_01986.1.g31317.t1	gb|EOA20093.1| hypothetical protein CARUB_v10000370mg [Capsella rubella]	651	687	0	105.5	84.3	90.3	hypothetical protein CARUB_v10000370mg	gbpln	Capsella rubella	AT5G02400.1 | Symbols: PLL2 | pol-like 2 | chr5:513561-515896 FORWARD LENGTH=674	651	674	0	103.5	83.6	89.2

Rsa1.0_01986.1.g31318.t1	gb|EOA19964.1| hypothetical protein CARUB_v10000216mg [Capsella rubella]	773	845	0	109.3	74.6	83.4	hypothetical protein CARUB_v10000216mg	gbpln	Capsella rubella	AT5G02390.1 | Symbols: | Protein of unknown function (DUF3741) | chr5:508764-511710 REVERSE LENGTH=835	773	835	0	108.0	74.4	83.7
Rsa1.0_01986.1.g31319.t1	gb|ADP37973.1| metallothionein protein [Brassica napus]	80	81	1.00E-29	101.3	87.5	91.3	metallothionein protein	gbpln	Brassica napus	AT3G09390.1 | Symbols: MT2A, ATMT-K, ATMT-1 | metallothionein 2A | chr3:2889737-2890188 REVERSE LENGTH=81	80	81	3.00E-23	101.3	62.5	66.3
Rsa1.0_01986.1.g31320.t1	ref|NP_195857.2| kinesin family member 22 [Arabidopsis thaliana] gi|59958334|gb|AAX12877.1| At5g02370 [Arabidopsis thaliana] gi|332003081|gb|AED90464.1| ATP binding microtubule motor family protein [Arabidopsis thaliana]	610	628	0	103.0	79.0	87.5	kinesin family member 22	gbpln	Arabidopsis thaliana	AT5G02370.1 | Symbols: | ATP binding microtubule motor family protein | chr5:503444-506388 FORWARD LENGTH=628	610	628	0	103.0	79.0	87.5
Rsa1.0_01986.1.g31321.t8	gb|EOA19777.1| hypothetical protein CARUB_v10000023mg [Capsella rubella]	2009	2005	0	99.8	80.0	87.0	hypothetical protein CARUB_v10000023mg	gbpln	Capsella rubella	AT5G02310.1 | Symbols: PRT6 | proteolysis 6 | chr5:474279-482552 FORWARD LENGTH=2006	2009	2006	0	99.9	78.9	86.5
Rsa1.0_01987.1.g31322.t1	ref|XP_002888202.1| ZCF125 [Arabidopsis lyrata subsp. lyrata] gi|297334043|gb|EFH64461.1| ZCF125 [Arabidopsis lyrata subsp. lyrata]	734	827	0	112.7	83.5	88.6	ZCF125	gbpln	Arabidopsis lyrata	AT1G59540.1 | Symbols: ZCF125 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:21874083-21879382 FORWARD LENGTH=823	734	823	0	112.1	82.3	88.0
Rsa1.0_01987.1.g31323.t1	gb|EOA33367.1| hypothetical protein CARUB_v10020272mg, partial [Capsella rubella]	373	456	0	122.3	96.5	98.7	hypothetical protein CARUB_v10020272mg, partial	gbpln	Capsella rubella	AT1G59580.2 | Symbols: ATMPK2, MPK2 | mitogen-activated protein kinase homolog 2 | chr1:21884521-21885743 FORWARD LENGTH=376	373	376	0	100.8	94.9	98.1
Rsa1.0_01987.1.g31324.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01987.1.g31325.t1	gb|AAM67222.1| unknown [Arabidopsis thaliana] gi|343455576|gb|AEM36361.1| At1g59590 [Arabidopsis thaliana]	212	211	1.00E-98	99.5	85.4	91.5	unknown	gbpln	Arabidopsis thaliana	AT1G59590.1 | Symbols: ZCF37 | ZCF37 | chr1:21887860-21888495 FORWARD LENGTH=211	212	211	1.00E-100	99.5	84.9	91.0
Rsa1.0_01987.1.g31326.t1	ref|XP_002886674.1| hypothetical protein ARALYDRAFT_893620 [Arabidopsis lyrata subsp. lyrata] gi|297332515|gb|EFH62933.1| hypothetical protein ARALYDRAFT_893620 [Arabidopsis lyrata subsp. lyrata]	317	324	1.00E-154	102.2	85.5	93.1	hypothetical protein ARALYDRAFT_893620	gbpln	Arabidopsis lyrata	AT1G59600.1 | Symbols: ZCW7 | ZCW7 | chr1:21889927-21891910 REVERSE LENGTH=324	317	324	1.00E-155	102.2	83.9	93.1
Rsa1.0_01987.1.g31327.t1	gb|ABD65023.1| hypothetical protein 26.t00078 [Brassica oleracea]	152	303	2.00E-39	199.3	51.3	68.4	hypothetical protein 26.t00078	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_01987.1.g31328.t1	ref|NP_176170.1| dynamin-2B [Arabidopsis thaliana] gi|59799374|sp|Q9LQ55.2|DRP2B_ARATH RecName: Full=Dynamin-2B; AltName: Full=Dynamin-like protein 3; AltName: Full=Dynamin-related protein 2B gi|6526969|dbj|BAA88111.1| dynamin-like protein [Arabidopsis thaliana] gi|15146179|gb|AAK83573.1| At1g59610/T30E16_17 [Arabidopsis thaliana] gi|23397259|gb|AAN31911.1| putative dynamin protein [Arabidopsis thaliana] gi|32815841|gb|AAP88329.1| At1g59610/T30E16_17 [Arabidopsis thaliana] gi|332195473|gb|AEE33594.1| dynamin-2B [Arabidopsis thaliana] gi|343455578|gb|AEM36363.1| At1g59610 [Arabidopsis thaliana]	920	920	0	100.0	95.7	98.5	dynamin-2B	gbpln	Arabidopsis thaliana	AT1G59610.1 | Symbols: ADL3, CF1, DRP2B, DL3 | dynamin-like 3 | chr1:21893413-21900780 FORWARD LENGTH=920	920	920	0	100.0	95.7	98.5
Rsa1.0_01988.1.g31329.t1	ref|XP_002874461.1| hypothetical protein ARALYDRAFT_351855 [Arabidopsis lyrata subsp. lyrata] gi|297320298|gb|EFH50720.1| hypothetical protein ARALYDRAFT_351855 [Arabidopsis lyrata subsp. lyrata]	478	446	4.00E-11	93.3	10.7	14.2	hypothetical protein ARALYDRAFT_351855	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_01988.1.g31330.t1	ref|NP_197412.1| Eukaryotic aspartyl protease family protein [Arabidopsis thaliana] gi|332005271|gb|AED92654.1| Eukaryotic aspartyl protease family protein [Arabidopsis thaliana]	397	405	1.00E-157	102.0	70.0	82.6	Eukaryotic aspartyl protease family protein	gbpln	Arabidopsis thaliana	AT5G19110.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:6411720-6413170 REVERSE LENGTH=405	397	405	1.00E-160	102.0	70.0	82.6
Rsa1.0_01988.1.g31331.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01988.1.g31332.t1	ref|XP_002873930.1| hypothetical protein ARALYDRAFT_488794 [Arabidopsis lyrata subsp. lyrata] gi|297319767|gb|EFH50189.1| hypothetical protein ARALYDRAFT_488794 [Arabidopsis lyrata subsp. lyrata]	121	365	1.00E-12	301.7	33.1	38.0	hypothetical protein ARALYDRAFT_488794	gbpln	Arabidopsis lyrata	AT5G19100.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:6408242-6409417 REVERSE LENGTH=391	121	391	1.00E-14	323.1	32.2	36.4

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<tr><td>Rsa1.0_01988.1.g31333.t1</td><td>gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1386</td><td>1307</td><td>0</td><td>94.3</td><td>58.5</td><td>73.7</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1386</td><td>1262</td><td>1.00E-102</td><td>91.1</td><td>14.1</td><td>21.2</td><td></td></tr>
<tr><td>Rsa1.0_01988.1.g31334.t1</td><td>pir||S65812 RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]</td><td>1636</td><td>1333</td><td>0</td><td>81.5</td><td>35.3</td><td>47.7</td><td>RNA-directed DNA polymerase (EC 2.7.7.49) (clone DW15) - Arabidopsis thaliana retrotransposon Ta11-1 gi|976278|gb|AAA75254.1| reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1636</td><td>575</td><td>6.00E-79</td><td>35.1</td><td>10.2</td><td>16.0</td><td></td></tr>
<tr><td>Rsa1.0_01988.1.g31335.t3</td><td>gb|AAF99727.1|AC004557_6 F17L21.7 [Arabidopsis thaliana]</td><td>654</td><td>1534</td><td>1.00E-115</td><td>234.6</td><td>35.5</td><td>49.8</td><td>F17L21.7</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>654</td><td>1262</td><td>2.00E-22</td><td>193.0</td><td>7.2</td><td>10.6</td><td></td></tr>
<tr><td>Rsa1.0_01989.1.g31336.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td></td></tr>
<tr><td>Rsa1.0_01989.1.g31337.t1</td><td>gb|ABM66448.1| SOS2-like protein [Brassica juncea]</td><td>442</td><td>445</td><td>0</td><td>100.7</td><td>92.5</td><td>96.6</td><td>SOS2-like protein</td><td>gbpln</td><td>Brassica juncea</td><td>AT5G35410.1 | Symbols: SOS2, SNRK3.11, CIPK24, ATSOS2 | Protein kinase superfamily protein | chr5:13634933-13638062 FORWARD LENGTH=446</td><td>442</td><td>446</td><td>0</td><td>100.9</td><td>89.4</td><td>95.0</td><td></td></tr>
<tr><td>Rsa1.0_01989.1.g31338.t34</td><td>gb|EOA29494.1| hypothetical protein CARUB_v10012960mg [Capsella rubella]</td><td>853</td><td>864</td><td>0</td><td>101.3</td><td>75.7</td><td>81.4</td><td>hypothetical protein CARUB_v10012960mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G04660.1 | Symbols: APC2 | anaphase-promoting complex/cyclosome 2 | chr2:1624933-1629039 FORWARD LENGTH=865</td><td>853</td><td>865</td><td>0</td><td>101.4</td><td>75.6</td><td>81.2</td><td></td></tr>
<tr><td>Rsa1.0_01989.1.g31339.t1</td><td>ref|XP_002864142.1| hypothetical protein ARALYDRAFT_495261 [Arabidopsis lyrata subsp. lyrata] gi|297309977|gb|EFH40401.1| hypothetical protein ARALYDRAFT_495261 [Arabidopsis lyrata subsp. lyrata]</td><td>144</td><td>144</td><td>1.00E-65</td><td>100.0</td><td>93.8</td><td>97.9</td><td>hypothetical protein ARALYDRAFT_495261</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G51940.1 | Symbols: NRPB6A, NRPD6A, NRPE6A | RNA polymerase Rpb6 | chr5:21104679-21105796 FORWARD LENGTH=144</td><td>144</td><td>144</td><td>3.00E-67</td><td>100.0</td><td>92.4</td><td>97.2</td><td></td></tr>
<tr><td>Rsa1.0_01989.1.g31340.t1</td><td>ref|NP_178539.2| Cation efflux family protein [Arabidopsis thaliana] gi|330250755|gb|AEC05849.1| Cation efflux family protein [Arabidopsis thaliana]</td><td>791</td><td>798</td><td>0</td><td>100.9</td><td>78.9</td><td>84.2</td><td>Cation efflux family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT2G04620.1 | Symbols: | Cation efflux family protein | chr2:1610506-1612902 REVERSE LENGTH=798</td><td>791</td><td>798</td><td>0</td><td>100.9</td><td>78.9</td><td>84.2</td><td></td></tr>
<tr><td>Rsa1.0_01989.1.g31341.t1</td><td>ref|XP_002868698.1| hypothetical protein ARALYDRAFT_916318 [Arabidopsis lyrata subsp. lyrata] gi|297314534|gb|EFH44957.1| hypothetical protein ARALYDRAFT_916318 [Arabidopsis lyrata subsp. lyrata]</td><td>157</td><td>336</td><td>3.00E-34</td><td>214.0</td><td>51.0</td><td>60.5</td><td>hypothetical protein ARALYDRAFT_916318</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G41200.1 | Symbols: AGL75 | AGAMOUS-like 75 | chr5:16490544-16491536 FORWARD LENGTH=330</td><td>157</td><td>330</td><td>2.00E-31</td><td>210.2</td><td>49.0</td><td>57.3</td><td></td></tr>
<tr><td>Rsa1.0_01989.1.g31342.t2</td><td>gb|AAG52211.1|AC022288_10 hypothetical protein; 74056-75837 [Arabidopsis thaliana]</td><td>679</td><td>503</td><td>1.00E-157</td><td>74.1</td><td>41.1</td><td>50.4</td><td>hypothetical protein; 74056-75837</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>679</td><td>1262</td><td>7.00E-71</td><td>185.9</td><td>22.4</td><td>33.9</td><td></td></tr>
<tr><td>Rsa1.0_01990.1.g31343.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td></td></tr>
<tr><td>Rsa1.0_01990.1.g31344.t1</td><td>gb|ADD10746.1| phytocystatin 2-1 [Brassica rapa subsp. pekinensis]</td><td>142</td><td>142</td><td>6.00E-71</td><td>100.0</td><td>91.5</td><td>96.5</td><td>phytocystatin 2-1</td><td>gbpln</td><td>Brassica rapa</td><td>AT2G31980.1 | Symbols: AtCYS2, CYS2 | PHYTOCYSTATIN 2 | chr2:13609246-13609770 REVERSE LENGTH=147</td><td>142</td><td>147</td><td>2.00E-54</td><td>103.5</td><td>72.5</td><td>81.0</td><td></td></tr>
<tr><td>Rsa1.0_01990.1.g31345.t1</td><td>gb|EOA28765.1| hypothetical protein CARUB_v10024997mg [Capsella rubella]</td><td>849</td><td>829</td><td>0</td><td>97.6</td><td>69.3</td><td>81.5</td><td>hypothetical protein CARUB_v10024997mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G31910.1 | Symbols: ATCHX21, CHX21 | cation/H+ exchanger 21 | chr2:13571044-13574019 FORWARD LENGTH=832</td><td>849</td><td>832</td><td>0</td><td>98.0</td><td>68.7</td><td>80.4</td><td></td></tr>
<tr><td>Rsa1.0_01990.1.g31346.t1</td><td>ref|XP_002880897.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326736|gb|EFH57156.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>446</td><td>434</td><td>1.00E-175</td><td>97.3</td><td>71.3</td><td>79.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT2G27220.1 | Symbols: BLH5 | BEL1-like homeodomain 5 | chr2:11637306-11639537 REVERSE LENGTH=431</td><td>446</td><td>431</td><td>1.00E-172</td><td>96.6</td><td>70.6</td><td>79.4</td><td></td></tr>
<tr><td>Rsa1.0_01990.1.g31347.t1</td><td>ref|NP_199833.1| putative F-box protein [Arabidopsis thaliana] gi|75262452|sp|Q9FGS3.1|FB287_ARATH RecName: Full=Putative F-box protein At5g50220 gi|9759024|dbj|BAB09393.1| unnamed protein product [Arabidopsis thaliana] gi|332008530|gb|AED95913.1| putative F-box protein [Arabidopsis thaliana]</td><td>372</td><td>357</td><td>6.00E-57</td><td>96.0</td><td>40.9</td><td>54.0</td><td>putative F-box protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G50220.1 | Symbols: | F-box family protein | chr5:20446068-20447200 REVERSE LENGTH=357</td><td>372</td><td>357</td><td>1.00E-59</td><td>96.0</td><td>40.9</td><td>54.0</td><td></td></tr>
<tr><td>Rsa1.0_01990.1.g31348.t1</td><td>ref|XP_002865856.1| hypothetical protein ARALYDRAFT_918170 [Arabidopsis lyrata subsp. lyrata] gi|297311691|gb|EFH42115.1| hypothetical protein ARALYDRAFT_918170 [Arabidopsis lyrata subsp. lyrata]</td><td>393</td><td>293</td><td>3.00E-58</td><td>74.6</td><td>36.1</td><td>43.3</td><td>hypothetical protein ARALYDRAFT_918170</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G50220.1 | Symbols: | F-box family protein | chr5:20446068-20447200 REVERSE LENGTH=357</td><td>393</td><td>357</td><td>2.00E-54</td><td>90.8</td><td>37.2</td><td>48.9</td><td></td></tr>
<tr><td>Rsa1.0_01990.1.g31349.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td></td></tr>
</table>

Rsa1.0_01990.1.g31350.t1	ref|NP_180289.3| serine/threonine-protein phosphatase BSL3 [Arabidopsis thaliana] gi|160359047|sp|Q9SHS7.2|BSL3_ARATH RecName: Full=Serine/threonine-protein phosphatase BSL3; AltName: Full=BSU1-like protein 3 gi|330252859|gb|AEC07953.1| serine/threonine-protein phosphatase BSL3 [Arabidopsis thaliana]	996	1006	0	101.0	93.8	96.3	serine/threonine-protein phosphatase BSL3	gbpln	Arabidopsis thaliana	AT2G27210.1 | Symbols: BSL3 | BRI1 suppressor 1 (BSU1)-like 3 | chr2:11630188-11636182 FORWARD LENGTH=1006	996	1006	0	101.0	93.8	96.3
Rsa1.0_01990.1.g31351.t1	ref|XP_002879073.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297324912|gb|EFH55332.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]	527	539	0	102.3	88.6	93.0	GTP-binding family protein	gbpln	Arabidopsis lyrata	AT2G27200.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:11625449-11627959 FORWARD LENGTH=537	527	537	0	101.9	87.5	92.2
Rsa1.0_01991.1.g31352.t2	ref|NP_191375.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana] gi|6735328|emb|CAB68154.1| myosin heavy chain MYA3 [Arabidopsis thaliana] gi|332646228|gb|AEE79749.1| P-loop containing nucleoside triphosphate hydrolase-like protein [Arabidopsis thaliana]	1145	1242	0	108.5	83.1	90.6	P-loop containing nucleoside triphosphate hydrolase-like protein	gbpln	Arabidopsis thaliana	AT3G58160.1 | Symbols: XIJ, ATXIJ, ATMYOS3, MYA3, XI-16 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:21534797-21541877 FORWARD LENGTH=1242	1145	1242	0	108.5	83.1	90.6
Rsa1.0_01991.1.g31353.t1	ref|NP_191376.1| Bet1-like SNARE 1-1 [Arabidopsis thaliana] gi|27805428|sp|Q9M2J9.1|BET11_ARATH RecName: Full=Bet1-like SNARE 1-1; Short=AtBET11; AltName: Full=Bet1/Sft1-like SNARE 14a; Short=AtBS14a gi|14030603|gb|AAK52976.1|AF368175_1 Bet1/Sft1-like SNARE AtBS14a [Arabidopsis thaliana] gi|6735329|emb|CAB68155.1| putative protein [Arabidopsis thaliana] gi|26449796|dbj|BAC42021.1| unknown protein [Arabidopsis thaliana] gi|28416841|gb|AAO42951.1| At3g58170 [Arabidopsis thaliana] gi|332646229|gb|AEE79750.1| Bet1-like SNARE 1-1 [Arabidopsis thaliana]	125	122	2.00E-58	97.6	92.8	94.4	Bet1-like SNARE 1-1	gbpln	Arabidopsis thaliana	AT3G58170.1 | Symbols: ATBS14A, ATBET11, BET11, BS14A | BET1P/SFT1P-like protein 14A | chr3:21542632-21543775 REVERSE LENGTH=122	125	122	4.00E-61	97.6	92.8	94.4
Rsa1.0_01991.1.g31354.t1	gb|EOA25554.1| hypothetical protein CARUB_v10018899mg [Capsella rubella]	313	310	1.00E-154	99.0	87.5	92.7	hypothetical protein CARUB_v10018899mg	gbpln	Capsella rubella	AT3G58180.1 | Symbols: | ARM repeat superfamily protein | chr3:21544189-21545981 FORWARD LENGTH=314	313	314	1.00E-157	100.3	87.9	93.3
Rsa1.0_01991.1.g31355.t1	emb|CBW45921.1| RTM3 protein [Arabidopsis thaliana]	298	301	1.00E-119	101.0	69.8	84.6	RTM3 protein	gbpln	Arabidopsis thaliana	AT3G58350.1 | Symbols: RTM3 | RESTRICTED TEV MOVEMENT 3 | chr3:21591618-21592836 REVERSE LENGTH=301	298	301	1.00E-116	101.0	69.8	84.9
Rsa1.0_01991.1.g31356.t1	gb|EOA25921.1| hypothetical protein CARUB_v10019301mg [Capsella rubella]	153	153	8.00E-68	100.0	83.7	91.5	hypothetical protein CARUB_v10019301mg	gbpln	Capsella rubella	AT3G58230.1 | Symbols: | Ubiquitin-specific protease family C19-related protein | chr3:21566860-21567396 REVERSE LENGTH=153	153	153	6.00E-69	100.0	82.4	90.2
Rsa1.0_01991.1.g31357.t1	ref|XP_002878203.1| hypothetical protein ARALYDRAFT_907304 [Arabidopsis lyrata subsp. lyrata] gi|297324041|gb|EFH54462.1| hypothetical protein ARALYDRAFT_907304 [Arabidopsis lyrata subsp. lyrata]	318	324	1.00E-118	101.9	73.9	84.6	hypothetical protein ARALYDRAFT_907304	gbpln	Arabidopsis lyrata	AT3G58270.2 | Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) with TRAF-like domain | chr3:21576033-21577655 REVERSE LENGTH=343	318	343	1.00E-117	107.9	71.7	84.3
Rsa1.0_01991.1.g31358.t2	emb|CBW45921.1| RTM3 protein [Arabidopsis thaliana]	276	301	1.00E-107	109.1	71.4	83.7	RTM3 protein	gbpln	Arabidopsis thaliana	AT3G58350.1 | Symbols: RTM3 | RESTRICTED TEV MOVEMENT 3 | chr3:21591618-21592836 REVERSE LENGTH=301	276	301	1.00E-104	109.1	71.7	84.1
Rsa1.0_01991.1.g31359.t4	gb|AAF97969.1|AC000103_19 F21J9.30 [Arabidopsis thaliana]	1625	1270	0	78.2	34.5	46.8	F21J9.30	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1625	575	7.00E-65	35.4	10.0	16.0
Rsa1.0_01991.1.g31360.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01992.1.g31361.t1	ref|XP_002877660.1| hypothetical protein ARALYDRAFT_485283 [Arabidopsis lyrata subsp. lyrata] gi|297323498|gb|EFH53919.1| hypothetical protein ARALYDRAFT_485283 [Arabidopsis lyrata subsp. lyrata]	483	423	1.00E-163	87.6	60.2	70.4	hypothetical protein ARALYDRAFT_485283	gbpln	Arabidopsis lyrata	AT3G49250.1 | Symbols: DMS3, IDN1 | defective in meristem silencing 3 | chr3:18258613-18260803 REVERSE LENGTH=420	483	420	1.00E-154	87.0	57.8	68.9
Rsa1.0_01992.1.g31362.t1	ref|XP_002875955.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] gi|297321793|gb|EFH52214.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	577	598	0	103.6	85.4	91.7	pectinesterase family protein	gbpln	Arabidopsis lyrata	AT3G49220.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:18249840-18253647 FORWARD LENGTH=598	577	598	0	103.6	85.1	91.7

Rsa1.0_01992.1.g31363.t2	ref|XP_002877657.1| hypothetical protein ARALYDRAFT_485279 [Arabidopsis lyrata subsp. lyrata] gi|297323495|gb|EFH53916.1| hypothetical protein ARALYDRAFT_485279 [Arabidopsis lyrata subsp. lyrata]	540	519	0	96.1	75.2	83.0	hypothetical protein ARALYDRAFT_485279	gbpln	Arabidopsis lyrata	AT3G49210.1 | Symbols: | O-acyltransferase (WSD1-like) family protein | chr3:18238216-18241161 REVERSE LENGTH=518	540	518	0	95.9	73.9	81.9
Rsa1.0_01992.1.g31364.t1	ref|XP_002875954.1| hypothetical protein ARALYDRAFT_485276 [Arabidopsis lyrata subsp. lyrata] gi|297321792|gb|EFH52213.1| hypothetical protein ARALYDRAFT_485276 [Arabidopsis lyrata subsp. lyrata]	426	438	0	102.8	77.7	86.9	hypothetical protein ARALYDRAFT_485276	gbpln	Arabidopsis lyrata	AT3G49180.1 | Symbols: RID3 | Transducin/WD40 repeat-like superfamily protein | chr3:18229810-18231874 FORWARD LENGTH=438	426	438	0	102.8	74.9	84.7
Rsa1.0_01992.1.g31365.t1	emb|CAB66396.1| putative protein [Arabidopsis thaliana]	712	1113	0	156.3	86.8	93.5	putative protein	gbpln	Arabidopsis thaliana	AT3G49170.1 | Symbols: EMB2261 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:18226954-18229600 REVERSE LENGTH=850	712	850	0	119.4	86.8	93.5
Rsa1.0_01993.1.g31366.t1	ref|XP_002865184.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311019|gb|EFH41443.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	164	1750	1.00E-47	1067.1	56.1	67.1	predicted protein	gbpln	Arabidopsis lyrata	AT5G44510.1 | Symbols: TAO1 | target of AVRB operation1 | chr5:17929673-17934188 REVERSE LENGTH=1187	164	1187	1.00E-48	723.8	53.0	65.2
Rsa1.0_01993.1.g31367.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01993.1.g31368.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1230	1274	0	103.6	55.3	70.0	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1230	575	3.00E-68	46.7	14.4	22.3
Rsa1.0_01993.1.g31369.t1	ref|NP_180727.1| phospholipase A1-Ialpha2 [Arabidopsis thaliana] gi|75337277|sp|Q9SIN9.1|PLA13_ARATH RecName: Full=Phospholipase A1-Ialpha2, chloroplastic; Flags: Precursor gi|4582461|gb|AAD24845.1| putative triacylglycerol lipase [Arabidopsis thaliana] gi|67633570|gb|AAY78709.1| lipase class 3 family protein [Arabidopsis thaliana] gi|330253479|gb|AEC08573.1| phospholipase A1-Ialpha2 [Arabidopsis thaliana]	478	484	0	101.3	78.5	85.6	phospholipase A1-Ialpha2	gbpln	Arabidopsis thaliana	AT2G31690.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:13476093-13477547 REVERSE LENGTH=484	478	484	0	101.3	78.5	85.6
Rsa1.0_01993.1.g31370.t1	gb|EOA29020.1| hypothetical protein CARUB_v10025274mg [Capsella rubella]	327	411	4.00E-34	125.7	34.6	44.3	hypothetical protein CARUB_v10025274mg	gbpln	Capsella rubella	AT2G31720.1 | Symbols: | Domain of unknown function (DUF313) | chr2:13485034-13485975 REVERSE LENGTH=313	327	313	1.00E-30	95.7	26.9	37.6
Rsa1.0_01994.1.g31371.t1	ref|NP_198814.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75171449|sp|Q9FLD8.1|PP408_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g39980, chloroplastic; Flags: Precursor gi|10176990|dbj|BAB10222.1| unnamed protein product [Arabidopsis thaliana] gi|332007115|gb|AED94498.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	679	678	0	99.9	91.5	94.7	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT5G39980.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:16001036-16003072 REVERSE LENGTH=678	679	678	0	99.9	91.5	94.7
Rsa1.0_01994.1.g31372.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01994.1.g31373.t1	ref|NP_198815.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana] gi|10176991|dbj|BAB10223.1| glycosylation enzyme-like protein [Arabidopsis thaliana] gi|30102766|gb|AAP21301.1| At5g39990 [Arabidopsis thaliana] gi|110743106|dbj|BAE99445.1| hypothetical protein [Arabidopsis thaliana] gi|332007116|gb|AED94499.1| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein [Arabidopsis thaliana]	439	447	0	101.8	90.7	95.0	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	gbpln	Arabidopsis thaliana	AT5G39990.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:16004494-16006428 FORWARD LENGTH=447	439	447	0	101.8	90.7	95.0
Rsa1.0_01994.1.g31374.t3	gb|AAD15477.1| putative replication protein A1 [Arabidopsis thaliana]	276	527	7.00E-20	190.9	30.4	48.6	putative replication protein A1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_01994.1.g31375.t1	emb|CAB91582.1| putative protein [Arabidopsis thaliana]	336	448	2.00E-24	133.3	33.9	52.1	putative protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	336	566	3.00E-17	168.5	23.8	43.5

Rsa1.0_01994.1.g31376.t4	gb|EOA19024.1| hypothetical protein CARUB_v10007676mg [Capsella rubella]	315	365	1.00E−137	115.9	81.3	90.2	hypothetical protein CARUB_v10007676mg	gbpln	Capsella rubella	AT5G40230.1 | Symbols: | nodulin MtN21 /EamA−like transporter family protein | chr5:16079814−16081735 REVERSE LENGTH=370	315	370	1.00E−137	117.5	80.3	88.9
Rsa1.0_01994.1.g31377.t3	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1715	1213	0	70.7	33.8	45.8	unknown protein	gbpln	Arabidopsis thaliana	AT1G60720.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr1:22357072−22357941 FORWARD LENGTH=289	1715	289	2.00E−73	16.9	7.8	11.0
Rsa1.0_01994.1.g31378.t1	gb|EOA19024.1| hypothetical protein CARUB_v10007676mg [Capsella rubella]	364	365	1.00E−154	100.3	76.9	87.1	hypothetical protein CARUB_v10007676mg	gbpln	Capsella rubella	AT5G40230.1 | Symbols: | nodulin MtN21 /EamA−like transporter family protein | chr5:16079814−16081735 REVERSE LENGTH=370	364	370	1.00E−156	101.6	76.9	87.4
Rsa1.0_01994.1.g31379.t1	gb|AAX96717.1| retrotransposon protein, putative, Ty3−gypsy sub−class [Oryza sativa Japonica Group] gi|108864301|gb|ABA93040.2| retrotransposon protein, putative, Ty3−gypsy subclass [Oryza sativa Japonica Group]	281	1748	7.00E−47	622.1	36.7	45.9	retrotransposon protein, putative, Ty3−gypsy sub−class	gbpln	Oryza sativa	#	#	#	#	#	#	#
Rsa1.0_01995.1.g31380.t1	gb|EOA19072.1| hypothetical protein CARUB_v10007738mg [Capsella rubella]	179	480	8.00E−19	268.2	25.7	35.2	hypothetical protein CARUB_v10007738mg	gbpln	Capsella rubella	AT1G52950.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:19725483−19728007 FORWARD LENGTH=566	179	566	5.00E−15	316.2	26.8	39.7
Rsa1.0_01995.1.g31381.t1	ref|NP_564111.1| uncharacterized protein [Arabidopsis thaliana] gi|21617898|gb|AAM66948.1| unknown [Arabidopsis thaliana] gi|332191839|gb|AEE29960.1| uncharacterized protein AT1G20310 [Arabidopsis thaliana]	240	240	5.00E−67	100.0	63.8	75.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G20310.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76070.1); Has 46 Blast hits to 46 proteins in 12 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 46; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:7032308−7033030 FORWARD LENGTH=240	240	240	2.00E−69	100.0	63.8	75.4
Rsa1.0_01995.1.g31382.t1	ref|XP_002889052.1| hypothetical protein ARALYDRAFT_476750 [Arabidopsis lyrata subsp. lyrata] gi|297334893|gb|EFH65311.1| hypothetical protein ARALYDRAFT_476750 [Arabidopsis lyrata subsp. lyrata]	369	344	2.00E−73	93.2	57.2	66.4	hypothetical protein ARALYDRAFT_476750	gbpln	Arabidopsis lyrata	AT1G76010.1 | Symbols: | Alba DNA/RNA−binding protein | chr1:28528505−28530488 REVERSE LENGTH=350	369	350	5.00E−75	94.9	57.7	66.9
Rsa1.0_01995.1.g31383.t4	ref|XP_003543854.1| PREDICTED: uncharacterized protein LOC100780312 [Glycine max]	523	557	4.00E−92	106.5	35.4	44.7	PREDICTED: uncharacterized protein LOC100780312	gbenv/gbpln	Glycine max	AT4G08267.1 | Symbols: | hAT transposon superfamily protein | chr4:5216854−5217697 FORWARD LENGTH=126	523	126	1.00E−14	24.1	7.1	9.6
Rsa1.0_01995.1.g31384.t1	ref|XP_002893092.1| Alpha−expansin 11 precursor [Arabidopsis lyrata subsp. lyrata] gi|297338934|gb|EFH69351.1| Alpha−expansin 11 precursor [Arabidopsis lyrata subsp. lyrata]	252	252	1.00E−136	100.0	93.3	97.2	Alpha−expansin 11 precursor	gbpln	Arabidopsis lyrata	AT1G20190.1 | Symbols: ATEXPA11, EXP11, ATEXP11, ATHEXP ALPHA 1.14, EXPA11 | expansin 11 | chr1:6998762−6999710 REVERSE LENGTH=252	252	252	1.00E−134	100.0	94.0	97.6
Rsa1.0_01995.1.g31385.t1	ref|NP_564106.1| Subtilisin−like serine endopeptidase−like protein [Arabidopsis thaliana] gi|332191823|gb|AEE29944.1| Subtilisin−like serine endopeptidase−like protein [Arabidopsis thaliana]	911	780	0	85.6	70.5	77.9	Subtilisin−like serine endopeptidase−like protein	gbpln	Arabidopsis thaliana	AT1G20150.1 | Symbols: | Subtilisin−like serine endopeptidase family protein | chr1:6987332−6990361 REVERSE LENGTH=780	911	780	0	85.6	70.5	77.9
Rsa1.0_01995.1.g31386.t1	ref|XP_002880415.1| hypothetical protein ARALYDRAFT_481069 [Arabidopsis lyrata subsp. lyrata] gi|297326254|gb|EFH56674.1| hypothetical protein ARALYDRAFT_481069 [Arabidopsis lyrata subsp. lyrata]	161	161	3.00E−61	100.0	72.0	83.2	hypothetical protein ARALYDRAFT_481069	gbpln	Arabidopsis lyrata	AT1G20140.1 | Symbols: ASK4, SK4 | SKP1−like 4 | chr1:6986430−6987079 FORWARD LENGTH=163	161	163	1.00E−62	101.2	70.2	82.0
Rsa1.0_01995.1.g31387.t1	ref|NP_001235349.1| uncharacterized protein LOC100306458 [Glycine max] gi|255628601|gb|ACU14645.1| unknown [Glycine max]	137	155	8.00E−22	113.1	48.2	62.8	uncharacterized protein LOC100306458	gbenv/gbpln	Glycine max	AT1G75950.1 | Symbols: SKP1, ASK1, ATSKP1, SKP1A, UIP1 | S phase kinase−associated protein 1 | chr1:28516715−28517454 FORWARD LENGTH=160	137	160	1.00E−21	116.8	44.5	56.9
Rsa1.0_01996.1.g31388.t2	ref|NP_189549.2| phosphate transporter PHO1−9 [Arabidopsis thaliana] gi|75273666|sp|Q9LJW0.1|PHO19_ARATH RecName: Full=Phosphate transporter PHO1 homolog 9; AltName: Full=Protein PHO1 homolog 9; Short=AtPHO1;H9 gi|11994710|dbj|BAB02948.1| unnamed protein product [Arabidopsis thaliana] gi|332644009|gb|AEE77530.1| phosphate transporter PHO1−9 [Arabidopsis thaliana]	615	800	0	130.1	84.4	91.2	phosphate transporter PHO1−9	gbpln	Arabidopsis thaliana	AT3G29060.1 | Symbols: | EXS (ERD1/XPR1/SYG1) family protein | chr3:11044990−11048465 REVERSE LENGTH=800	615	800	0	130.1	84.4	91.2

Rsa1.0_01996.1.g31389.t1	ref|XP_002875490.1| protein carrier [Arabidopsis lyrata subsp. lyrata] gi|297321328|gb|EFH51749.1| protein carrier [Arabidopsis lyrata subsp. lyrata]	221	222	3.00E-95	100.5	74.7	84.2	protein carrier	gbpln	Arabidopsis lyrata	AT3G29070.1 | Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr3:11050193-11051153 FORWARD LENGTH=225	221	225	3.00E-91	101.8	74.7	83.7
Rsa1.0_01996.1.g31390.t1	gb|AAM78108.1| AT3g29075/MXE2_1 [Arabidopsis thaliana]	292	242	7.00E-46	82.9	32.2	34.2	AT3g29075/MXE2_1	gbpln	Arabidopsis thaliana	AT3G29075.1 | Symbols: | glycine-rich protein | chr3:11051645-11052629 REVERSE LENGTH=294	292	294	2.00E-48	100.7	32.2	34.2
Rsa1.0_01996.1.g31391.t2	ref|NP_566842.1| pectinesterase 31 [Arabidopsis thaliana] gi|75311628|sp|Q9LVQ0.1|PME31_ARATH RecName: Full=Pectinesterase 31; Short=PE 31; AltName: Full=Pectin methylesterase 31; Short=AtPME31 gi|9294028|dbj|BAB01985.1| pectin methylesterase-like protein [Arabidopsis thaliana] gi|17979179|gb|AAL49785.1| putative pectinesterase [Arabidopsis thaliana] gi|20465979|gb|AAM20211.1| putative pectinesterase [Arabidopsis thaliana] gi|21536660|gb|AAM60992.1| putative pectinesterase [Arabidopsis thaliana] gi|332644013|gb|AEE77534.1| pectinesterase 31 [Arabidopsis thaliana]	356	317	1.00E-179	89.0	83.4	87.1	pectinesterase 31	gbpln	Arabidopsis thaliana	AT3G29090.1 | Symbols: PME31, ATPME31 | pectin methylesterase 31 | chr3:11073804-11075335 FORWARD LENGTH=317	356	317	0	89.0	83.4	87.1
Rsa1.0_01996.1.g31392.t1	gb|EOA26115.1| hypothetical protein CARUB_v10019541mg [Capsella rubella]	100	100	3.00E-31	100.0	67.0	76.0	hypothetical protein CARUB_v10019541mg	gbpln	Capsella rubella	AT5G38170.1 | Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:15227717-15228028 FORWARD LENGTH=103	100	103	2.00E-15	103.0	41.0	54.0
Rsa1.0_01996.1.g31393.t1	gb|EOA23757.1| hypothetical protein CARUB_v10016968mg [Capsella rubella]	512	512	0	100.0	94.9	96.1	hypothetical protein CARUB_v10016968mg	gbpln	Capsella rubella	AT3G29160.2 | Symbols: AKIN11, KIN11 | SNF1 kinase homolog 11 | chr3:11128893-11131510 REVERSE LENGTH=512	512	512	0	100.0	94.3	95.7
Rsa1.0_01996.1.g31394.t1	gb|EOA23180.1| hypothetical protein CARUB_v10018086mg, partial [Capsella rubella]	98	184	3.00E-38	187.8	89.8	93.9	hypothetical protein CARUB_v10018086mg, partial	gbpln	Capsella rubella	AT3G29170.1 | Symbols: | Eukaryotic protein of unknown function (DUF872) | chr3:11136240-11137542 REVERSE LENGTH=121	98	121	9.00E-35	123.5	86.7	92.9
Rsa1.0_01996.1.g31395.t1	ref|NP_566846.1| chorismate mutase 1 [Arabidopsis thaliana] gi|334302922|sp|P42738.3|CM1_ARATH RecName: Full=Chorismate mutase 1, chloroplastic; Short=AtCM1; AltName: Full=CM-1; Flags: Precursor gi|89000961|gb|ABD59070.1| At3g29200 [Arabidopsis thaliana] gi|332644031|gb|AEE77552.1| chorismate mutase 1 [Arabidopsis thaliana]	318	340	1.00E-153	106.9	89.9	93.4	chorismate mutase 1	gbpln	Arabidopsis thaliana	AT3G29200.1 | Symbols: CM1, ATCM1 | chorismate mutase 1 | chr3:11164582-11166258 REVERSE LENGTH=340	318	340	1.00E-155	106.9	89.9	93.4
Rsa1.0_01997.1.g31396.t1	ref|NP_683436.3| uncharacterized protein [Arabidopsis thaliana] gi|53828513|gb|AAU94366.1| At1g55535 [Arabidopsis thaliana] gi|55167920|gb|AAV43792.1| At1g55535 [Arabidopsis thaliana] gi|332195139|gb|AEE33260.1| uncharacterized protein AT1G55535 [Arabidopsis thaliana]	325	260	1.00E-109	80.0	64.3	67.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G55535.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13420.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:20732081-20733802 REVERSE LENGTH=260	325	260	1.00E-112	80.0	64.3	67.4
Rsa1.0_01997.1.g31397.t1	gb|ADK63410.1| C3HC4 type zinc finger protein [Brassica rapa]	341	312	3.00E-96	91.5	60.7	70.7	C3HC4 type zinc finger protein	gbpln	Brassica rapa	AT1G55530.1 | Symbols: | RING/U-box superfamily protein | chr1:20729472-20730527 REVERSE LENGTH=351	341	351	5.00E-90	102.9	60.7	73.3
Rsa1.0_01997.1.g31398.t1	gb|EOA38535.1| hypothetical protein CARUB_v10010337mg [Capsella rubella]	200	200	1.00E-110	100.0	96.0	99.0	hypothetical protein CARUB_v10010337mg	gbpln	Capsella rubella	AT1G55520.2 | Symbols: TBP2, ATTBP2 | TATA binding protein 2 | chr1:20726150-20727483 REVERSE LENGTH=200	200	200	1.00E-111	100.0	95.5	97.5
Rsa1.0_01997.1.g31399.t1	ref|NP_175947.1| branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana] gi|4204270|gb|AAD10651.1| branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana] gi|89000979|gb|ABD59079.1| At1g55510 [Arabidopsis thaliana] gi|332195135|gb|AEE33256.1| branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]	321	352	1.00E-172	109.7	92.5	94.4	branched-chain alpha-keto acid decarboxylase E1 beta subunit	gbpln	Arabidopsis thaliana	AT1G55510.1 | Symbols: BCDH BETA1 | branched-chain alpha-keto acid decarboxylase E1 beta subunit | chr1:20723482-20725505 FORWARD LENGTH=352	321	352	1.00E-175	109.7	92.5	94.4

Rsa1.0_01997.1.g31400.t1	ref|XP_002894506.1| CPN60B [Arabidopsis lyrata subsp. lyrata] gi|297340348|gb|EFH70765.1| CPN60B [Arabidopsis lyrata subsp. lyrata]	597	600	0	100.5	97.2	98.7	CPN60B	gbpln	Arabidopsis lyrata	AT1G55490.2 | Symbols: CPN60B, LEN1 | chaperonin 60 beta | chr1:20715717-20718673 REVERSE LENGTH=600	597	600	0	100.5	96.6	98.8
Rsa1.0_01997.1.g31401.t2	gb|EOA36487.1| hypothetical protein CARUB_v10011122mg [Capsella rubella]	118	121	6.00E-25	102.5	61.9	70.3	hypothetical protein CARUB_v10011122mg	gbpln	Capsella rubella	AT1G55475.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13480.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:20711977-20712586 FORWARD LENGTH=120	118	120	1.00E-23	101.7	61.9	72.9
Rsa1.0_01997.1.g31402.t1	ref|NP_564690.1| DNA/RNA-binding protein Kin17 conserved region-containing protein [Arabidopsis thaliana] gi|13430440|gb|AAK25842.1|AF360132_1 unknown protein [Arabidopsis thaliana] gi|4204268|gb|AAD10649.1| Similar to Kin17 protein [Arabidopsis thaliana] gi|15293155|gb|AAK93688.1| unknown protein [Arabidopsis thaliana] gi|332195127|gb|AEE33248.1| DNA/RNA-binding protein Kin17 conserved region-containing protein [Arabidopsis thaliana]	393	411	0	104.6	84.2	92.6	DNA/RNA-binding protein Kin17 conserved region-containing protein	gbpln	Arabidopsis thaliana	AT1G55460.1 | Symbols: | DNA/RNA-binding protein Kin17, conserved region | chr1:20707567-20708802 FORWARD LENGTH=411	393	411	0	104.6	84.2	92.6
Rsa1.0_01997.1.g31403.t1	#	#	#	#	#	#	#	-	----	----	AT2G37420.1 | Symbols: | ATP binding microtubule motor family protein | chr2:15700550-15705165 FORWARD LENGTH=1039	111	1039	1.00E-10	936.0	27.0	34.2
Rsa1.0_01997.1.g31404.t1	ref|NP_192641.2| isoamylase 3 [Arabidopsis thaliana] gi|251764781|sp|Q9M0S5.2|ISOA3_ARATH RecName: Full=Isoamylase 3, chloroplastic; Short=AtISA3; Flags: Precursor gi|20259518|gb|AAM13879.1| putative isoamylase [Arabidopsis thaliana] gi|22136708|gb|AAM91673.1| putative isoamylase [Arabidopsis thaliana] gi|110742373|dbj|BAE99109.1| isoamylase-like protein [Arabidopsis thaliana] gi|332657313|gb|AEE82713.1| isoamylase 3 [Arabidopsis thaliana]	320	764	1.00E-129	238.8	72.5	81.6	isoamylase 3	gbpln	Arabidopsis thaliana	AT4G09020.1 | Symbols: ATISA3, ISA3 | isoamylase 3 | chr4:5784099-5788839 FORWARD LENGTH=764	320	764	1.00E-131	238.8	72.5	81.6
Rsa1.0_01997.1.g31405.t1	ref|XP_002894503.1| hypothetical protein ARALYDRAFT_892534 [Arabidopsis lyrata subsp. lyrata] gi|297340345|gb|EFH70762.1| hypothetical protein ARALYDRAFT_892534 [Arabidopsis lyrata subsp. lyrata]	101	104	2.00E-13	103.0	33.7	38.6	hypothetical protein ARALYDRAFT_892534	gbpln	Arabidopsis lyrata	AT1G55365.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13500.1); Has 29 Blast hits to 29 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:20673983-20674363 REVERSE LENGTH=126	101	126	4.00E-15	124.8	31.7	37.6
Rsa1.0_01997.1.g31406.t1	gb|AAF97981.1|AC000103_31 F21J9.3 [Arabidopsis thaliana]	262	457	1.00E-128	174.4	83.6	88.2	F21J9.3	gbpln	Arabidopsis thaliana	AT2G13770.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912); Has 451 Blast hits to 352 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 8; Plants - 388; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink). | chr2:5736603-5737847 FORWARD LENGTH=343	262	343	2.00E-55	130.9	38.5	42.0
Rsa1.0_01997.1.g31407.t2	ref|NP_192761.1| uncharacterized protein [Arabidopsis thaliana] gi|3695409|gb|AAC62809.1| T9A4.8 gene product [Arabidopsis thaliana] gi|4538952|emb|CAB39776.1| hypothetical protein [Arabidopsis thaliana] gi|7267719|emb|CAB78146.1| hypothetical protein [Arabidopsis thaliana] gi|332657457|gb|AEE82857.1| uncharacterized protein AT4G10230 [Arabidopsis thaliana]	108	273	1.00E-22	252.8	54.6	65.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT4G10230.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24380.1); Has 216 Blast hits to 216 proteins in 30 species: Archae - 0; Bacteria - 8; Metazoa - 10; Fungi - 4; Plants - 160; Viruses - 0; Other Eukaryotes - 34 (source: NCBI BLink). | chr4:6366261-6367185 FORWARD LENGTH=273	108	273	2.00E-25	252.8	54.6	65.7

Rsa1.0_01997.1.g31408.t1	ref|NP_175933.1| uncharacterized protein [Arabidopsis thaliana] gi|12323166|gb|AAG51562.1|AC027034_8 unknown protein; 9920-11896 [Arabidopsis thaliana] gi|24417260|gb|AAN60240.1| unknown [Arabidopsis thaliana] gi|57222168|gb|AAW38991.1| At1g55360 [Arabidopsis thaliana] gi|111074434|gb|ABH04590.1| At1g55360 [Arabidopsis thaliana] gi|332195116|gb|AEE33237.1| uncharacterized protein AT1G55360 [Arabidopsis thaliana]	422	422	0	100.0	92.9	95.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G55360.1 | Symbols: | Protein of Unknown Function (DUF239) | chr1:20666526-20668502 REVERSE LENGTH=422	422	422	0	100.0	92.9	95.7
Rsa1.0_01997.1.g31409.t1	ref|XP_002894501.1| hypothetical protein ARALYDRAFT_892532 [Arabidopsis lyrata subsp. lyrata] gi|297340343|gb|EFH70760.1| hypothetical protein ARALYDRAFT_892532 [Arabidopsis lyrata subsp. lyrata]	329	2151	2.00E-54	653.8	32.5	32.5	hypothetical protein ARALYDRAFT_892532	gbpln	Arabidopsis lyrata	AT1G55350.5 | Symbols: DEK1 | calpain-type cysteine protease family | chr1:20654463-20664501 REVERSE LENGTH=2179	329	2179	2.00E-56	662.3	31.9	32.5
Rsa1.0_01997.1.g31410.t1	ref|XP_002891830.1| hypothetical protein ARALYDRAFT_474592 [Arabidopsis lyrata subsp. lyrata] gi|297337672|gb|EFH68089.1| hypothetical protein ARALYDRAFT_474592 [Arabidopsis lyrata subsp. lyrata]	235	205	1.00E-101	87.2	80.0	83.0	hypothetical protein ARALYDRAFT_474592	gbpln	Arabidopsis lyrata	AT1G55340.1 | Symbols: | Protein of unknown function (DUF1639) | chr1:20652605-20653469 FORWARD LENGTH=205	235	205	1.00E-103	87.2	78.7	82.6
Rsa1.0_01997.1.g31411.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	470	1529	1.00E-133	325.3	51.3	66.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	470	746	1.00E-116	158.7	43.6	56.8
Rsa1.0_01998.1.g31412.t1	gb|EOA19331.1| hypothetical protein CARUB_v10003659mg [Capsella rubella]	153	154	1.00E-67	100.7	84.3	94.1	hypothetical protein CARUB_v10003659mg	gbpln	Capsella rubella	AT4G03290.1 | Symbols: | EF hand calcium-binding protein family | chr4:1442813-1443277 FORWARD LENGTH=154	153	154	1.00E-64	100.7	83.7	92.2
Rsa1.0_01998.1.g31413.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01998.1.g31414.t1	ref|NP_192241.1| translocon at the inner envelope membrane of chloroplasts 20-IV [Arabidopsis thaliana] gi|75267833|sp|Q9ZQZ9.1|TI204_ARATH RecName: Full=Protein TIC 20-IV, chloroplastic; AltName: Full=Translocon at the inner envelope membrane of chloroplasts 20-IV; Short=AtTIC20-IV; Flags: Precursor gi|13605615|gb|AAK32801.1|AF361633_1 AT4g03320/F4C21_25 [Arabidopsis thaliana] gi|4262160|gb|AAD14460.1| putative chloroplast protein import component [Arabidopsis thaliana] gi|7270202|emb|CAB77817.1| putative chloroplast protein import component [Arabidopsis thaliana] gi|15810087|gb|AAL06969.1| AT4g03320/F4C21_25 [Arabidopsis thaliana] gi|21536779|gb|AAM61111.1| putative chloroplast protein import component [Arabidopsis thaliana] gi|332656906|gb|AEE82306.1| translocon at the inner envelope membrane of chloroplasts 20-IV [Arabidopsis thaliana]	268	284	1.00E-105	106.0	72.4	82.8	translocon at the inner envelope membrane of chloroplasts 20-IV	gbpln	Arabidopsis thaliana	AT4G03320.1 | Symbols: tic20-IV | translocon at the inner envelope membrane of chloroplasts 20-IV | chr4:1464529-1465820 FORWARD LENGTH=284	268	284	1.00E-107	106.0	72.4	82.8

Rsa1.0_01998.1.g31415.t2	ref|NP_192241.1| translocon at the inner envelope membrane of chloroplasts 20-IV [Arabidopsis thaliana] gi|75267833|sp|Q9ZQZ9.1|TI204_ARATH RecName: Full=Protein TIC 20-IV, chloroplastic; AltName: Full=Translocon at the inner envelope membrane of chloroplasts 20-IV; Short=AtTIC20-IV; Flags: Precursor gi|13605615|gb|AAK32801.1|AF361633_1 AT4g03320/F4C21_25 [Arabidopsis thaliana] gi|4262160|gb|AAD14460.1| putative chloroplast protein import component [Arabidopsis thaliana] gi|7270202|emb|CAB77817.1| putative chloroplast protein import component [Arabidopsis thaliana] gi|15810087|gb|AAL06969.1| AT4g03320/F4C21_25 [Arabidopsis thaliana] gi|21536779|gb|AAM61111.1| putative chloroplast protein import component [Arabidopsis thaliana] gi|332656906|gb|AEE82306.1| translocon at the inner envelope membrane of chloroplasts 20-IV [Arabidopsis thaliana]	288	284	1.00E-128	98.6	76.7	83.0	translocon at the inner envelope membrane of chloroplasts 20-IV	gbpln	Arabidopsis thaliana	AT4G03320.1 | Symbols: tic20-IV | translocon at the inner envelope membrane of chloroplasts 20-IV | chr4:1464529-1465820 FORWARD LENGTH=284	288	284	1.00E-131	98.6	76.7	83.0
Rsa1.0_01998.1.g31416.t1	ref|XP_002874867.1| SYP123 [Arabidopsis lyrata subsp. lyrata] gi|297320704|gb|EFH51126.1| SYP123 [Arabidopsis lyrata subsp. lyrata]	305	305	1.00E-169	100.0	95.1	98.7	SYP123	gbpln	Arabidopsis lyrata	AT4G03330.1 | Symbols: SYP123, ATSYP123 | syntaxin of plants 123 | chr4:1466525-1467605 FORWARD LENGTH=305	305	305	1.00E-163	100.0	93.4	97.7
Rsa1.0_01998.1.g31417.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01998.1.g31418.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01998.1.g31419.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01998.1.g31420.t1	gb|EOA22332.1| hypothetical protein CARUB_v10002939mg, partial [Capsella rubella]	400	1294	9.00E-32	323.5	33.8	47.5	hypothetical protein CARUB_v10002939mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_01998.1.g31421.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01999.1.g31422.t8	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01999.1.g31423.t1	ref|XP_002869288.1| hypothetical protein ARALYDRAFT_913230 [Arabidopsis lyrata subsp. lyrata] gi|297315124|gb|EFH45547.1| hypothetical protein ARALYDRAFT_913230 [Arabidopsis lyrata subsp. lyrata]	602	777	1.00E-31	129.1	15.0	19.4	hypothetical protein ARALYDRAFT_913230	gbpln	Arabidopsis lyrata	AT4G32190.1 | Symbols: | Myosin heavy chain-related protein | chr4:15545052-15547689 FORWARD LENGTH=783	602	783	4.00E-34	130.1	15.0	19.3
Rsa1.0_01999.1.g31424.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01999.1.g31425.t1	ref|XP_002893772.1| hypothetical protein ARALYDRAFT_890929 [Arabidopsis lyrata subsp. lyrata] gi|297339614|gb|EFH70031.1| hypothetical protein ARALYDRAFT_890929 [Arabidopsis lyrata subsp. lyrata]	183	175	7.00E-84	95.6	84.7	91.8	hypothetical protein ARALYDRAFT_890929	gbpln	Arabidopsis lyrata	AT1G33490.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2062 (InterPro:IPR018639); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10140.1); Has 88 Blast hits to 88 proteins in 29 species: Archae - 0; Bacteria - 28; Metazoa - 0; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink). | chr1:12150941-12152276 REVERSE LENGTH=175	183	175	3.00E-86	95.6	84.7	92.3
Rsa1.0_01999.1.g31426.t1	ref|NP_683346.3| putative VAMP-like protein [Arabidopsis thaliana] gi|68566199|sp|Q84WF5.1|VAMPL_ARATH RecName: Full=Probable VAMP-like protein At1g33475 gi|28392986|gb|AAO41928.1| unknown protein [Arabidopsis thaliana] gi|50253582|gb|AAT71993.1| At1g33480 [Arabidopsis thaliana] gi|332193477|gb|AEE31598.1| putative VAMP-like protein [Arabidopsis thaliana]	243	255	4.00E-94	104.9	78.6	88.9	putative VAMP-like protein	gbpln	Arabidopsis thaliana	AT1G33475.1 | Symbols: | SNARE-like superfamily protein | chr1:12147423-12148190 REVERSE LENGTH=255	243	255	1.00E-96	104.9	78.6	88.9
Rsa1.0_01999.1.g31427.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	336	1142	6.00E-65	339.9	44.6	60.7	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	336	575	4.00E-26	171.1	31.0	50.9
Rsa1.0_01999.1.g31428.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_01999.1.g31429.t1	ref|XP_002862920.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297308694|gb|EFH39179.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	251	266	1.00E-61	106.0	51.4	67.7	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#

Rsa1.0_01999.1.g31430.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02000.1.g31431.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02000.1.g31432.t1	ref|NP_849877.1| uncharacterized protein [Arabidopsis thaliana] gi|26453012|dbj|BAC43582.1| unknown protein [Arabidopsis thaliana] gi|28973253|gb|AAO63951.1| unknown protein [Arabidopsis thaliana] gi|332197123|gb|AEE35244.1| uncharacterized protein AT1G71865 [Arabidopsis thaliana]	106	99	4.00E−36	93.4	84.0	87.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT1G71865.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 33 Blast hits to 33 proteins in 11 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 33; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:27030117-27030416 FORWARD LENGTH=99	106	99	6.00E−39	93.4	84.0	87.7
Rsa1.0_02000.1.g31433.t2	ref|XP_002887394.1| hypothetical protein ARALYDRAFT_339406 [Arabidopsis lyrata subsp. lyrata] gi|297333235|gb|EFH63653.1| hypothetical protein ARALYDRAFT_339406 [Arabidopsis lyrata subsp. lyrata]	362	342	1.00E−153	94.5	72.7	80.9	hypothetical protein ARALYDRAFT_339406	gbpln	Arabidopsis lyrata	AT1G71860.3 | Symbols: PTP1, ATPTP1 | protein tyrosine phosphatase 1 | chr1:27026866-27028675 FORWARD LENGTH=340	362	340	1.00E−151	93.9	72.9	81.5
Rsa1.0_02000.1.g31434.t1	ref|XP_002889905.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297335747|gb|EFH66164.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	305	389	7.00E−88	127.5	58.7	70.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G11270.2 | Symbols: | F-box and associated interaction domains-containing protein | chr1:3785715-3786653 REVERSE LENGTH=312	305	312	7.00E−77	102.3	54.1	68.2
Rsa1.0_02000.1.g31435.t1	gb|EOA34289.1| hypothetical protein CARUB_v10021804mg [Capsella rubella]	471	471	0	100.0	77.3	87.0	hypothetical protein CARUB_v10021804mg	gbpln	Capsella rubella	AT1G71850.1 | Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr1:27024875-27026287 REVERSE LENGTH=470	471	470	0	99.8	77.1	87.0
Rsa1.0_02000.1.g31436.t1	ref|XP_002888851.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata] gi|297334692|gb|EFH65110.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	508	509	0	100.2	92.7	95.9	mate efflux family protein	gbpln	Arabidopsis lyrata	AT1G71870.1 | Symbols: | MATE efflux family protein | chr1:27032456-27034895 REVERSE LENGTH=510	508	510	0	100.4	92.1	95.5
Rsa1.0_02000.1.g31437.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02000.1.g31438.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	817	1225	7.00E−62	149.9	13.7	19.5	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G13450.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02000.1); Has 247 Blast hits to 243 proteins in 13 species: Archae − 0; Bacteria − 2; Metazoa − 0; Fungi − 2; Plants − 243; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr2:5598739-5599923 REVERSE LENGTH=394	817	394	4.00E−20	48.2	6.5	10.8
Rsa1.0_02001.1.g31439.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02001.1.g31440.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02001.1.g31441.t1	gb|EOA21025.1| hypothetical protein CARUB_v10001362mg [Capsella rubella]	97	339	4.00E−18	349.5	48.5	49.5	hypothetical protein CARUB_v10001362mg	gbpln	Capsella rubella	AT5G05760.1 | Symbols: SYP31, ATSED5, ATSYP31, SED5 | syntaxin of plants 31 | chr5:1729111-1730903 REVERSE LENGTH=336	97	336	4.00E−20	346.4	46.4	49.5
Rsa1.0_02001.1.g31442.t1	gb|EOA35423.1| hypothetical protein CARUB_v10020623mg [Capsella rubella]	45	335	1.00E−10	744.4	73.3	93.3	hypothetical protein CARUB_v10020623mg	gbpln	Capsella rubella	AT1G78620.2 | Symbols: | Protein of unknown function DUF92, transmembrane | chr1:29573862-29575758 REVERSE LENGTH=342	45	342	8.00E−13	760.0	68.9	88.9
Rsa1.0_02001.1.g31443.t2	gb|ABD64958.1| ethylene responsive element binding factor -related [Brassica oleracea]	731	954	1.00E−103	130.5	37.1	47.2	ethylene responsive element binding factor -related	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_02001.1.g31444.t1	ref|NP_192787.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] gi|4115913|gb|AAD03424.1| contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] gi|4539409|emb|CAB40042.1| putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana] gi|7267746|emb|CAB78172.1| putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana] gi|28393112|gb|AAO41989.1| putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana] gi|28827438|gb|AAO50563.1| putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana] gi|332657490|gb|AEE82890.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	456	348	1.00E−130	76.3	48.0	51.5	oxidoreductase, 2OG-Fe(II) oxygenase family protein	gbpln	Arabidopsis thaliana	AT4G10490.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:6483900-6485179 FORWARD LENGTH=348	456	348	1.00E−132	76.3	48.0	51.5

Rsa1.0_02001.1.g31445.t1	ref|XP_002872518.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297318355|gb|EFH48777.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	87	351	4.00E-26	403.4	65.5	74.7	predicted protein	gbpln	Arabidopsis lyrata	AT4G10490.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:6483900-6485179 FORWARD LENGTH=348	87	348	6.00E-25	400.0	58.6	67.8
Rsa1.0_02001.1.g31446.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02001.1.g31447.t1	gb|EOA21470.1| hypothetical protein CARUB_v10001862mg, partial [Capsella rubella]	210	235	3.00E-76	111.9	87.1	94.3	hypothetical protein CARUB_v10001862mg, partial	gbpln	Capsella rubella	AT4G10480.2 | Symbols: | Nascent polypeptide-associated complex (NAC), alpha subunit family protein | chr4:6478089-6479079 REVERSE LENGTH=211	210	211	2.00E-77	100.5	83.8	91.9
Rsa1.0_02002.1.g31448.t1	gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	93	1311	2.00E-11	1409.7	39.8	65.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT1G10000.1 | Symbols: | Ribonuclease H-like superfamily protein | chr1:3263877-3264788 REVERSE LENGTH=303	93	303	2.00E-11	325.8	32.3	59.1
Rsa1.0_02002.1.g31449.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02002.1.g31450.t1	emb|CAB88537.1| acyl CoA reductase-like protein [Arabidopsis thaliana]	190	402	3.00E-61	211.6	64.2	77.9	acyl CoA reductase-like protein	gbpln	Arabidopsis thaliana	AT3G44560.1 | Symbols: FAR8 | fatty acid reductase 8 | chr3:16151177-16154397 FORWARD LENGTH=496	190	496	1.00E-63	261.1	63.2	78.9
Rsa1.0_02002.1.g31451.t3	emb|CAA19714.1| putative protein [Arabidopsis thaliana] gi|7269573|emb|CAB79575.1| putative protein [Arabidopsis thaliana]	780	819	4.00E-61	105.0	14.6	18.6	putative protein	gbpln	Arabidopsis thaliana	ATMG00810.1 | Symbols: ORF240B | DNA/RNA polymerases superfamily protein | chrM:227709-228431 REVERSE LENGTH=240	780	240	9.00E-47	30.8	11.7	14.1
Rsa1.0_02002.1.g31452.t1	ref|NP_197634.1| putative fatty acyl-CoA reductase 7 [Arabidopsis thaliana] gi|75171715|sp|Q9FMQ9.1|FACR7_ARATH RecName: Full=Putative fatty acyl-CoA reductase 7 gi|9757823|dbj|BAB08341.1| acyl CoA reductase-like protein [Arabidopsis thaliana] gi|332005641|gb|AED93024.1| putative fatty acyl-CoA reductase 7 [Arabidopsis thaliana]	141	409	3.00E-41	290.1	62.4	77.3	putative fatty acyl-CoA reductase 7	gbpln	Arabidopsis thaliana	AT5G22420.1 | Symbols: FAR7 | fatty acid reductase 7 | chr5:7429903-7432586 FORWARD LENGTH=409	141	409	7.00E-44	290.1	62.4	77.3
Rsa1.0_02002.1.g31453.t1	gb|AAD20430.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	76	622	7.00E-11	818.4	47.4	63.2	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02003.1.g31454.t1	gb|AAD55636.1|AC008017_9 Similar to part of disease resistance protein [Arabidopsis thaliana]	374	414	1.00E-135	110.7	67.9	81.0	Similar to part of disease resistance protein	gbpln	Arabidopsis thaliana	AT1G72890.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27429947-27431717 FORWARD LENGTH=438	374	438	1.00E-137	117.1	67.9	81.0
Rsa1.0_02003.1.g31455.t13	gb|EOA35268.1| hypothetical protein CARUB_v10020451mg [Capsella rubella]	238	385	2.00E-57	161.8	52.5	57.6	hypothetical protein CARUB_v10020451mg	gbpln	Capsella rubella	AT1G72880.1 | Symbols: | Survival protein SurE-like phosphatase/nucleotidase | chr1:27423678-27425928 REVERSE LENGTH=385	238	385	4.00E-58	161.8	51.7	56.3
Rsa1.0_02003.1.g31456.t1	gb|ACP30576.1| disease resistance protein [Brassica rapa subsp. pekinensis]	427	426	1.00E-150	99.8	67.0	77.5	disease resistance protein	gbpln	Brassica rapa	AT1G72890.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27429947-27431717 FORWARD LENGTH=438	427	438	1.00E-148	102.6	63.7	74.2
Rsa1.0_02003.1.g31457.t1	gb|AAD55633.1|AC008017_6 Similar to downy mildew resistance protein RPP5 [Arabidopsis thaliana]	1235	1258	0	101.9	66.2	77.2	Similar to downy mildew resistance protein RPP5	gbpln	Arabidopsis thaliana	AT1G72860.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:27417096-27420778 REVERSE LENGTH=1163	1235	1163	0	94.2	62.8	71.5
Rsa1.0_02003.1.g31458.t1	ref|NP_177430.1| TIR-NBS class of disease resistance protein [Arabidopsis thaliana] gi|5903076|gb|AAD55634.1|AC008017_7 Similar to disease resistance protein NL25 [Arabidopsis thaliana] gi|332197263|gb|AEE35384.1| TIR-NBS class of disease resistance protein [Arabidopsis thaliana]	539	512	1.00E-162	95.0	60.3	68.8	TIR-NBS class of disease resistance protein	gbpln	Arabidopsis thaliana	AT1G72870.1 | Symbols: | Disease resistance protein (TIR-NBS class) | chr1:27421086-27422999 FORWARD LENGTH=512	539	512	1.00E-164	95.0	60.3	68.8
Rsa1.0_02003.1.g31459.t1	ref|NP_177431.1| survival protein SurE-like phosphatase/nucleotidase [Arabidopsis thaliana] gi|30698907|ref|NP_849880.1| survival protein SurE-like phosphatase/nucleotidase [Arabidopsis thaliana] gi|30102530|gb|AAP21183.1| At1g72880 [Arabidopsis thaliana] gi|110742851|dbj|BAE99324.1| hypothetical protein [Arabidopsis thaliana] gi|332197264|gb|AEE35385.1| survival protein SurE-like phosphatase/nucleotidase [Arabidopsis thaliana] gi|332197265|gb|AEE35386.1| survival protein SurE-like phosphatase/nucleotidase [Arabidopsis thaliana]	380	385	0	101.3	90.0	93.7	survival protein SurE-like phosphatase/nucleotidase	gbpln	Arabidopsis thaliana	AT1G72880.1 | Symbols: | Survival protein SurE-like phosphatase/nucleotidase | chr1:27423678-27425928 REVERSE LENGTH=385	380	385	0	101.3	90.0	93.7

Rsa1.0_02003.1.g31460.t1	gb|AAD55633.1|AC008017_6 Similar to downy mildew resistance protein RPP5 [Arabidopsis thaliana]	265	1258	8.00E-87	474.7	62.6	74.7	Similar to downy mildew resistance protein RPP5	gbpln	Arabidopsis thaliana	AT1G72860.1 | Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:27417096-27420778 REVERSE LENGTH=1163	265	1163	9.00E-53	438.9	37.4	41.1
Rsa1.0_02004.1.g31461.t2	ref|XP_002887359.1| hypothetical protein ARALYDRAFT_476259 [Arabidopsis lyrata subsp. lyrata] gi|297333200|gb|EFH63618.1| hypothetical protein ARALYDRAFT_476259 [Arabidopsis lyrata subsp. lyrata]	1325	707	1.00E-133	53.4	19.9	21.1	hypothetical protein ARALYDRAFT_476259	gbpln	Arabidopsis lyrata	AT1G71270.1 | Symbols: POK, TTD8, ATVPS52 | Vps52 / Sac2 family | chr1:26863736-26869817 FORWARD LENGTH=707	1325	707	1.00E-135	53.4	19.8	21.1
Rsa1.0_02004.1.g31462.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02004.1.g31463.t1	gb|EOA17420.1| hypothetical protein CARUB_v10005724mg, partial [Capsella rubella]	208	212	1.00E-13	101.9	26.4	29.3	hypothetical protein CARUB_v10005724mg, partial	gbpln	Capsella rubella	AT4G27270.1 | Symbols: | Quinone reductase family protein | chr4:13661458-13663243 REVERSE LENGTH=205	208	205	5.00E-15	98.6	26.4	29.8
Rsa1.0_02004.1.g31464.t1	ref|XP_002888794.1| hypothetical protein ARALYDRAFT_476207 [Arabidopsis lyrata subsp. lyrata] gi|297334635|gb|EFH65053.1| hypothetical protein ARALYDRAFT_476207 [Arabidopsis lyrata subsp. lyrata]	479	616	2.00E-86	128.6	37.2	46.8	hypothetical protein ARALYDRAFT_476207	gbpln	Arabidopsis lyrata	AT1G70770.2 | Symbols: | Protein of unknown function DUF2359, transmembrane | chr1:26688622-26691185 REVERSE LENGTH=610	479	610	2.00E-88	127.3	36.7	46.6
Rsa1.0_02004.1.g31465.t1	gb|EOA33369.1| hypothetical protein CARUB_v10020273mg [Capsella rubella]	453	456	0	100.7	88.5	93.8	hypothetical protein CARUB_v10020273mg	gbpln	Capsella rubella	AT1G71090.1 | Symbols: | Auxin efflux carrier family protein | chr1:26812551-26813924 FORWARD LENGTH=457	453	457	0	100.9	87.6	93.2
Rsa1.0_02004.1.g31466.t1	ref|NP_565010.1| RNA polymerase II transcription elongation factor [Arabidopsis thaliana] gi|12323437|gb|AAG51700.1|AC016972_19 unknown protein; 36401-34743 [Arabidopsis thaliana] gi|16974550|gb|AAL31191.1| At1g71080/F23N20_7 [Arabidopsis thaliana] gi|22137124|gb|AAM91407.1| At1g71080/F23N20_7 [Arabidopsis thaliana] gi|332197038|gb|AEE35159.1| RNA polymerase II transcription elongation factor [Arabidopsis thaliana]	345	326	1.00E-126	94.5	76.5	83.2	RNA polymerase II transcription elongation factor	gbpln	Arabidopsis thaliana	AT1G71080.1 | Symbols: | RNA polymerase II transcription elongation factor | chr1:26809987-26811645 REVERSE LENGTH=326	345	326	1.00E-129	94.5	76.5	83.2
Rsa1.0_02004.1.g31467.t1	ref|XP_002888820.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata] gi|297334661|gb|EFH65079.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata]	399	395	0	99.0	90.0	95.7	glycosyltransferase family 14 protein	gbpln	Arabidopsis lyrata	AT1G71070.1 | Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:26807440-26809152 REVERSE LENGTH=395	399	395	0	99.0	89.2	95.0
Rsa1.0_02004.1.g31468.t1	ref|XP_002888817.1| hypothetical protein ARALYDRAFT_894936 [Arabidopsis lyrata subsp. lyrata] gi|297334658|gb|EFH65076.1| hypothetical protein ARALYDRAFT_894936 [Arabidopsis lyrata subsp. lyrata]	150	152	2.00E-72	101.3	90.0	94.7	hypothetical protein ARALYDRAFT_894936	gbpln	Arabidopsis lyrata	AT1G71050.1 | Symbols: HIPP20 | Heavy metal transport/detoxification superfamily protein | chr1:26803322-26803946 REVERSE LENGTH=152	150	152	1.00E-69	101.3	88.0	96.0
Rsa1.0_02004.1.g31469.t1	ref|NP_565008.1| cupredoxin-like protein [Arabidopsis thaliana] gi|15292769|gb|AAK92753.1| putative spore coat protein [Arabidopsis thaliana] gi|20259247|gb|AAM14359.1| putative spore coat protein [Arabidopsis thaliana] gi|332197034|gb|AEE35155.1| cupredoxin-like protein [Arabidopsis thaliana]	574	581	0	101.2	88.5	93.7	cupredoxin-like protein	gbpln	Arabidopsis thaliana	AT1G71040.1 | Symbols: LPR2 | Cupredoxin superfamily protein | chr1:26797201-26800224 REVERSE LENGTH=581	574	581	0	101.2	88.5	93.7
Rsa1.0_02005.1.g31470.t1	ref|NP_192771.1| glycine-rich protein [Arabidopsis thaliana] gi|4538962|emb|CAB39786.1| hypothetical protein [Arabidopsis thaliana] gi|7267730|emb|CAB78156.1| hypothetical protein [Arabidopsis thaliana] gi|19347875|gb|AAL85995.1| unknown protein [Arabidopsis thaliana] gi|22136796|gb|AAM91742.1| unknown protein [Arabidopsis thaliana] gi|332657468|gb|AEE82868.1| glycine-rich protein [Arabidopsis thaliana]	132	130	5.00E-53	98.5	90.9	95.5	glycine-rich protein	gbpln	Arabidopsis thaliana	AT4G10330.1 | Symbols: | glycine-rich protein | chr4:6406551-6407136 FORWARD LENGTH=130	132	130	1.00E-55	98.5	90.9	95.5
Rsa1.0_02005.1.g31471.t1	emb|CAA65042.1| chlorophyll a/b-binding protein CP26 in PS II [Brassica juncea]	273	283	1.00E-144	103.7	97.8	98.5	chlorophyll a/b-binding protein CP26 in PS II	gbpln	Brassica juncea	AT4G10340.1 | Symbols: LHCB5 | light harvesting complex of photosystem II 5 | chr4:6408200-6409496 FORWARD LENGTH=280	273	280	1.00E-127	102.6	93.8	97.1
Rsa1.0_02005.1.g31472.t1	gb|AAF63106.1|AC006423_7 Hypothetical protein [Arabidopsis thaliana]	497	570	3.00E-13	114.7	14.7	24.9	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#

Rsa1.0_02005.1.g31473.t1	gb|AAD30632.1|AC006085_5 Hypothetical protein [Arabidopsis thaliana]	888	1295	1.00E-109	145.8	28.3	39.0	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02005.1.g31474.t4	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02005.1.g31475.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02006.1.g31476.t1	ref|NP_567153.1| VAMP (vesicle-associated membrane protein) family protein [Arabidopsis thaliana] gi|75148826|sp|Q84WW5.1|VAP13_ARATH RecName: Full=Vesicle-associated protein 1-3; AltName: Full=Plant VAP homolog 13; Short=AtPVA13; AltName: Full=VAMP-associated protein 1-3 gi|25054852|gb|AAN71916.1| putative proline-rich protein [Arabidopsis thaliana] gi|332656433|gb|AEE81833.1| vesicle-associated protein 1-3 [Arabidopsis thaliana]	239	239	1.00E-106	100.0	85.8	90.4	VAMP (vesicle-associated membrane protein) family protein	gbpln	Arabidopsis thaliana	AT4G00170.1 | Symbols: | Plant VAMP (vesicle-associated membrane protein) family protein | chr4:70732-72085 REVERSE LENGTH=239	239	239	1.00E-108	100.0	85.8	90.4
Rsa1.0_02006.1.g31477.t1	ref|NP_200984.1| inositol polyphosphate multikinase beta [Arabidopsis thaliana] gi|75171533|sp|Q9FLT2.1|IPMKB_ARATH RecName: Full=Inositol polyphosphate multikinase beta; AltName: Full=Inositol polyphosphate 6-/3-/5-kinase beta; Short=AtIpk2-beta; Short=AtIpk2beta gi|15724266|gb|AAL06526.1|AF412073_1 AT5g61760/mac9_60 [Arabidopsis thaliana] gi|10176869|dbj|BAB10076.1| unnamed protein product [Arabidopsis thaliana] gi|14588985|emb|CAC43070.1| inositol-(1,4,5) trisphosphate 3-kinase [Arabidopsis thaliana] gi|14588987|emb|CAC43071.1| inositol-(1,4,5) trisphosphate 3-kinase [Arabidopsis thaliana] gi|18252263|gb|AAL62012.1| AT5g61760/mac9_60 [Arabidopsis thaliana] gi|24850181|gb|AAN63058.1| inositol polyphosphate 6-/3-/5-kinase 2b [Arabidopsis thaliana] gi|332010130|gb|AED97513.1| inositol polyphosphate multikinase beta [Arabidopsis thaliana]	300	300	1.00E-124	100.0	70.7	83.3	inositol polyphosphate multikinase beta	gbpln	Arabidopsis thaliana	AT5G61760.1 | Symbols: ATIPK2BETA, IPK2B, IPK2BETA | inositol polyphosphate kinase 2 beta | chr5:24813916-24814818 REVERSE LENGTH=300	300	300	1.00E-126	100.0	70.7	83.3
Rsa1.0_02006.1.g31478.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	759	1529	0	201.4	54.9	72.2	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	759	746	1.00E-109	98.3	25.8	34.8
Rsa1.0_02006.1.g31479.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02006.1.g31480.t1	gb|ADC68234.1| bHLH transcription factor [Brassica oleracea]	180	180	1.00E-81	100.0	92.2	96.1	bHLH transcription factor	gbpln	Brassica oleracea	AT4G00120.1 | Symbols: IND1, GT140, IND, EDA33 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr4:42601-43197 REVERSE LENGTH=198	180	198	2.00E-65	110.0	72.2	82.2
Rsa1.0_02006.1.g31481.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	388	1274	1.00E-76	328.4	45.6	60.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	388	575	2.00E-37	148.2	31.7	47.7
Rsa1.0_02006.1.g31482.t1	gb|EOA21556.1| hypothetical protein CARUB_v10001965mg [Capsella rubella]	207	209	2.00E-95	101.0	84.1	89.4	hypothetical protein CARUB_v10001965mg	gbpln	Capsella rubella	AT4G00080.1 | Symbols: UNE11 | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr4:32946-33575 FORWARD LENGTH=209	207	209	1.00E-93	101.0	81.6	86.5
Rsa1.0_02006.1.g31483.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02007.1.g31484.t1	ref|NP_850164.1| protein autophagy 9 [Arabidopsis thaliana] gi|19715618|gb|AAL91630.1| At2g31260/F16D14.10 [Arabidopsis thaliana] gi|19912149|dbj|BAB88386.1| autophagy 9 [Arabidopsis thaliana] gi|20466356|gb|AAM20495.1| unknown protein [Arabidopsis thaliana] gi|23198070|gb|AAN15562.1| unknown protein [Arabidopsis thaliana] gi|23463043|gb|AAN33191.1| At2g31260/F16D14.10 [Arabidopsis thaliana] gi|330253421|gb|AEC08515.1| protein autophagy 9 [Arabidopsis thaliana]	867	866	0	99.9	85.4	89.7	protein autophagy 9	gbpln	Arabidopsis thaliana	AT2G31260.1 | Symbols: APG9, ATAPG9 | autophagy 9 (APG9) | chr2:13322291-13326293 REVERSE LENGTH=866	867	866	0	99.9	85.4	89.7
Rsa1.0_02007.1.g31485.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

Rsa1.0_02007.1.g31486.t1	gb|EOA29302.1| hypothetical protein CARUB_v10025580mg [Capsella rubella]	580	582	0	100.3	74.3	83.1	hypothetical protein CARUB_v10025580mg	gbpln	Capsella rubella	AT2G31270.1 | Symbols: ATCDT1A, CDT1A, CDT1 | homolog of yeast CDT1 A | chr2:13329037-13331544 FORWARD LENGTH=571	580	571	0	98.4	73.1	80.9
Rsa1.0_02007.1.g31487.t3	gb|EOA26350.1| hypothetical protein CARUB_v10022732mg [Capsella rubella]	634	719	0	113.4	68.3	75.6	hypothetical protein CARUB_v10022732mg	gbpln	Capsella rubella	AT2G31280.1 | Symbols: CPUORF7 | conserved peptide upstream open reading frame 7 | chr2:13339678-13343424 FORWARD LENGTH=720	634	720	1.00E-158	113.6	47.5	51.3
Rsa1.0_02007.1.g31488.t1	ref|XP_002879959.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297325798|gb|EFH56218.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	325	318	1.00E-119	97.8	65.8	78.2	kinase family protein	gbpln	Arabidopsis lyrata	AT2G41920.1 | Symbols: | Protein kinase superfamily protein | chr2:17499448-17500404 FORWARD LENGTH=318	325	318	1.00E-115	97.8	61.5	77.2
Rsa1.0_02008.1.g31489.t1	ref|XP_002864974.1| hypothetical protein ARALYDRAFT_496807 [Arabidopsis lyrata subsp. lyrata] gi|297310809|gb|EFH41233.1| hypothetical protein ARALYDRAFT_496807 [Arabidopsis lyrata subsp. lyrata]	129	1003	1.00E-49	777.5	75.2	76.0	hypothetical protein ARALYDRAFT_496807	gbpln	Arabidopsis lyrata	AT5G65700.2 | Symbols: BAM1 | Leucine-rich receptor-like protein kinase family protein | chr5:26281826-26284945 FORWARD LENGTH=1003	129	1003	3.00E-52	777.5	75.2	76.0
Rsa1.0_02008.1.g31490.t1	gb|EOA31822.1| hypothetical protein CARUB_v10015044mg [Capsella rubella]	67	68	2.00E-24	101.5	83.6	88.1	hypothetical protein CARUB_v10015044mg	gbpln	Capsella rubella	AT3G13275.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 29 Blast hits to 29 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4289425-4289634 REVERSE LENGTH=69	67	69	5.00E-20	103.0	85.1	92.5
Rsa1.0_02008.1.g31491.t2	ref|NP_001189876.1| DNA damage-inducible protein 1 [Arabidopsis thaliana] gi|332641803|gb|AEE75324.1| DNA damage-inducible protein 1 [Arabidopsis thaliana]	401	413	0	103.0	88.8	92.8	DNA damage-inducible protein 1	gbpln	Arabidopsis thaliana	AT3G13235.3 | Symbols: | ubiquitin family protein | chr3:4271492-4274348 REVERSE LENGTH=413	401	413	0	103.0	88.8	92.8
Rsa1.0_02008.1.g31492.t1	gb|EOA32534.1| hypothetical protein CARUB_v10015817mg [Capsella rubella]	289	288	1.00E-128	99.7	82.7	89.6	hypothetical protein CARUB_v10015817mg	gbpln	Capsella rubella	AT3G13229.1 | Symbols: | Plant protein of unknown function (DUF868) | chr3:4268566-4269435 REVERSE LENGTH=289	289	289	1.00E-127	100.0	78.9	86.9
Rsa1.0_02008.1.g31493.t1	gb|EOA32619.1| hypothetical protein CARUB_v10015913mg [Capsella rubella]	116	112	3.00E-36	96.6	77.6	81.0	hypothetical protein CARUB_v10015913mg	gbpln	Capsella rubella	AT3G13227.1 | Symbols: | serine-rich protein-related | chr3:4258028-4258363 FORWARD LENGTH=111	116	111	3.00E-32	95.7	74.1	78.4
Rsa1.0_02008.1.g31494.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02008.1.g31495.t1	gb|EOA29633.1| hypothetical protein CARUB_v10014543mg [Capsella rubella]	234	230	1.00E-103	98.3	94.0	97.4	hypothetical protein CARUB_v10014543mg	gbpln	Capsella rubella	AT3G13200.1 | Symbols: EMB2769 | Cwf15 / Cwc15 cell cycle control family protein | chr3:4242239-4243976 FORWARD LENGTH=230	234	230	4.00E-96	98.3	92.3	94.9
Rsa1.0_02008.1.g31496.t1	gb|EOA31905.1| hypothetical protein CARUB_v10015134mg [Capsella rubella]	390	394	0	101.0	82.6	90.8	hypothetical protein CARUB_v10015134mg	gbpln	Capsella rubella	AT3G13160.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:4229994-4231178 REVERSE LENGTH=394	390	394	0	101.0	80.3	88.7
Rsa1.0_02008.1.g31497.t1	ref|NP_187920.1| uncharacterized protein [Arabidopsis thaliana] gi|10172600|dbj|BAB01404.1| unnamed protein product [Arabidopsis thaliana] gi|332641779|gb|AEE75300.1| uncharacterized protein AT3G13130 [Arabidopsis thaliana]	205	201	8.00E-58	98.0	60.5	74.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G13130.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: male gametophyte; Has 140 Blast hits to 132 proteins in 41 species: Archae - 2; Bacteria - 4; Metazoa - 29; Fungi - 20; Plants - 51; Viruses - 0; Other Eukaryotes - 34 (source: NCBI BLink). | chr3:4223008-4223613 FORWARD LENGTH=201	205	201	3.00E-60	98.0	60.5	74.6
Rsa1.0_02008.1.g31498.t1	dbj|BAD11207.1| multidrug resistance-associated protein [Thlaspi caerulescens]	1502	1514	0	100.8	90.7	94.3	multidrug resistance-associated protein	gbpln	Thlaspi caerulescens	AT3G13080.1 | Symbols: ATMRP3, MRP3, ABCC3 | multidrug resistance-associated protein 3 | chr3:4196019-4201250 REVERSE LENGTH=1514	1502	1514	0	100.8	89.1	94.3
Rsa1.0_02008.1.g31499.t3	gb|EOA18071.1| hypothetical protein CARUB_v10006518mg [Capsella rubella]	207	659	3.00E-12	318.4	22.2	28.0	hypothetical protein CARUB_v10006518mg	gbpln	Capsella rubella	#	#	#	#	#	#	#

Rsa1.0_02009.1.g31500.t1	ref|NP_198686.2| uncharacterized protein [Arabidopsis thaliana] gi|62318737|dbj|BAD93759.1| putative protein [Arabidopsis thaliana] gi|332006968|gb|AED94351.1| uncharacterized protein AT5G38700 [Arabidopsis thaliana]	179	182	5.00E-60	101.7	67.0	78.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G38700.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.04 four leaves visible, LP.10 ten leaves visible, petal differentiation and expansion stage, LP.08 eight leaves visible, LP.12 twelve leaves visible; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02170.1); Has 64 Blast hits to 64 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:15489690-15490238 FORWARD LENGTH=182	179	182	2.00E-62	101.7	67.0	78.2
Rsa1.0_02009.1.g31501.t1	gb|ABO36622.1| copia LTR rider [Solanum lycopersicum] gi|133711819|gb|ABO36636.1| copia LTR rider [Solanum lycopersicum]	1366	1307	0	95.7	70.6	79.8	copia LTR rider	gbpln	Solanum lycopersicum	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1366	1262	4.00E-87	92.4	13.0	20.4
Rsa1.0_02009.1.g31502.t1	gb|ACD81988.1| cyclic nucleotide gated ion channel 12 [Arabidopsis thaliana]	420	649	1.00E-148	154.5	60.7	75.2	cyclic nucleotide gated ion channel 12	gbpln	Arabidopsis thaliana	AT2G46450.1 | Symbols: ATCNGC12, CNGC12 | cyclic nucleotide-gated channel 12 | chr2:19065845-19068364 FORWARD LENGTH=649	420	649	1.00E-150	154.5	60.7	75.2
Rsa1.0_02009.1.g31503.t2	gb|AAG10810.1|AC018460_4 Hypothetical protein [Arabidopsis thaliana] gi|12320956|gb|AAG50601.1|AC079605_6 hypothetical protein [Arabidopsis thaliana]	329	484	1.00E-108	147.1	57.4	66.9	Hypothetical protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	329	1262	4.00E-15	383.6	16.4	28.3
Rsa1.0_02009.1.g31504.t1	gb|EOA31438.1| hypothetical protein CARUB_v10014622mg [Capsella rubella]	217	210	2.00E-89	96.8	78.3	82.9	hypothetical protein CARUB_v10014622mg	gbpln	Capsella rubella	AT3G16780.1 | Symbols: | Ribosomal protein L19e family protein | chr3:5708982-5710249 FORWARD LENGTH=209	217	209	2.00E-89	96.3	76.5	81.6
Rsa1.0_02010.1.g31505.t1	ref|XP_002888714.1| hypothetical protein ARALYDRAFT_476056 [Arabidopsis lyrata subsp. lyrata] gi|297334555|gb|EFH64973.1| hypothetical protein ARALYDRAFT_476056 [Arabidopsis lyrata subsp. lyrata]	292	285	1.00E-98	97.6	74.0	83.2	hypothetical protein ARALYDRAFT_476056	gbpln	Arabidopsis lyrata	AT1G69310.2 | Symbols: WRKY57, ATWRKY57 | WRKY DNA-binding protein 57 | chr1:26056118-26057909 REVERSE LENGTH=287	292	287	9.00E-99	98.3	74.3	82.5
Rsa1.0_02010.1.g31506.t1	ref|NP_173968.1| carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana] gi|9797755|gb|AAF98573.1|AC013427_16 Contains similarity to beta-1,3 glucanase from Pisum sativum gb|AJ251646. ESTs gb|AV552865, gb|AV551442, gb|AV531309, gb|AV563097 come from this gene [Arabidopsis thaliana] gi|29028820|gb|AAO64789.1| At1g26450 [Arabidopsis thaliana] gi|110736384|dbj|BAF00161.1| predicted GPI-anchored protein [Arabidopsis thaliana] gi|332192572|gb|AEE30693.1| carbohydrate-binding X8 domain-containing protein [Arabidopsis thaliana]	213	197	3.00E-48	92.5	58.7	71.4	carbohydrate-binding X8 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G26450.1 | Symbols: | Carbohydrate-binding X8 domain superfamily protein | chr1:9149003-9150063 REVERSE LENGTH=197	213	197	9.00E-51	92.5	58.7	71.4
Rsa1.0_02010.1.g31507.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02010.1.g31508.t1	ref|NP_564956.1| Ninja-family protein AFP1 [Arabidopsis thaliana] gi|75180099|sp|Q9LQ98.1|AFP1_ARATH RecName: Full=Ninja-family protein AFP1; AltName: Full=ABI five-binding protein 1; Short=ABI5-binding protein 1 gi|6730641|gb|AAF27062.1|AC008262_11 F4N2.22 [Arabidopsis thaliana] gi|22531038|gb|AAM97023.1| expressed protein [Arabidopsis thaliana] gi|23197982|gb|AAN15518.1| expressed protein [Arabidopsis thaliana] gi|332196782|gb|AEE34903.1| Ninja-family protein AFP1 [Arabidopsis thaliana]	348	345	1.00E-133	99.1	78.7	85.6	Ninja-family protein AFP1	gbpln	Arabidopsis thaliana	AT1G69260.1 | Symbols: AFP1 | ABI five binding protein | chr1:26039314-26040570 FORWARD LENGTH=345	348	345	1.00E-136	99.1	78.7	85.6
Rsa1.0_02010.1.g31509.t1	ref|XP_002887226.1| hypothetical protein ARALYDRAFT_894705 [Arabidopsis lyrata subsp. lyrata] gi|297333067|gb|EFH63485.1| hypothetical protein ARALYDRAFT_894705 [Arabidopsis lyrata subsp. lyrata]	403	446	1.00E-102	110.7	52.9	68.5	hypothetical protein ARALYDRAFT_894705	gbpln	Arabidopsis lyrata	AT1G69250.1 | Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr1:26033163-26035301 FORWARD LENGTH=427	403	427	1.00E-104	106.0	53.8	70.7

Rsa1.0_02011.1.g31510.t4	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1491	1223	0	82.0	34.3	44.6	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1491	626	8.00E-56	42.0	9.0	14.2
Rsa1.0_02011.1.g31511.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	566	1529	8.00E-50	270.1	21.7	33.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT2G07760.1 | Symbols: | Zinc knuckle (CCHC-type) family protein | chr2:3584420-3586278 REVERSE LENGTH=530	566	530	9.00E-20	93.6	9.4	14.1
Rsa1.0_02011.1.g31512.t1	gb|AAF97281.1|AC010164_3 Hypothetical protein [Arabidopsis thaliana] gi|12324507|gb|AAG52212.1|AC022288_11 putative gag-pol polyprotein; 76173-77576 [Arabidopsis thaliana]	437	467	1.00E-80	106.9	39.6	50.3	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02011.1.g31513.t1	gb|EOA18244.1| hypothetical protein CARUB_v10006736mg [Capsella rubella]	222	223	2.00E-98	100.5	84.2	89.2	hypothetical protein CARUB_v10006736mg	gbpln	Capsella rubella	AT4G13450.1 | Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr4:7815146-7815904 REVERSE LENGTH=219	222	219	4.00E-97	98.6	84.2	91.0
Rsa1.0_02011.1.g31514.t1	ref|XP_002894513.1| WRKY10 [Arabidopsis lyrata subsp. lyrata] gi|297340355|gb|EFH70772.1| WRKY10 [Arabidopsis lyrata subsp. lyrata]	171	495	6.00E-13	289.5	40.4	51.5	WRKY10	gbpln	Arabidopsis lyrata	AT1G55600.1 | Symbols: WRKY10, ATWRKY10, MINI3 | WRKY DNA-binding protein 10 | chr1:20774049-20776293 REVERSE LENGTH=485	171	485	5.00E-14	283.6	43.3	56.7
Rsa1.0_02011.1.g31515.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02011.1.g31516.t1	gb|EOA14491.1| hypothetical protein CARUB_v10027706mg [Capsella rubella]	136	622	6.00E-18	457.4	41.9	43.4	hypothetical protein CARUB_v10027706mg	gbpln	Capsella rubella	AT5G45610.1 | Symbols: SUV2 | protein dimerizations | chr5:18496397-18499673 REVERSE LENGTH=646	136	646	3.00E-19	475.0	36.8	39.0
Rsa1.0_02012.1.g31517.t3	emb|CAB91581.1| putative protein [Arabidopsis thaliana]	1565	1752	0	111.9	53.1	67.2	putative protein	gbpln	Arabidopsis thaliana	AT3G51700.1 | Symbols: | PIF1 helicase | chr3:19179443-19181145 REVERSE LENGTH=344	1565	344	2.00E-69	22.0	9.2	12.6
Rsa1.0_02012.1.g31518.t1	ref|NP_175703.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|12324642|gb|AAG52278.1|AC019018_15 putative replication protein; 94555-97079 [Arabidopsis thaliana] gi|332194750|gb|AEE32871.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	468	566	8.00E-77	120.9	33.5	53.0	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	468	566	2.00E-79	120.9	33.5	53.0
Rsa1.0_02012.1.g31519.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02012.1.g31520.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02012.1.g31521.t4	gb|EOA37949.1| hypothetical protein CARUB_v10009417mg [Capsella rubella]	585	386	0	66.0	63.4	65.0	hypothetical protein CARUB_v10009417mg	gbpln	Capsella rubella	AT1G36050.1 | Symbols: | Endoplasmic reticulum vesicle transporter protein | chr1:13450467-13453683 FORWARD LENGTH=489	585	489	0	83.6	63.2	65.1
Rsa1.0_02012.1.g31522.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02012.1.g31523.t1	gb|EOA29603.1| hypothetical protein CARUB_v10013521mg, partial [Capsella rubella]	540	498	6.00E-60	92.2	20.4	27.0	hypothetical protein CARUB_v10013521mg, partial	gbpln	Capsella rubella	AT3G31430.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18636.1); Has 295 Blast hits to 291 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 295; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:12795861-12796871 REVERSE LENGTH=336	540	336	1.00E-20	62.2	11.3	18.0
Rsa1.0_02012.1.g31524.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	809	1142	0	141.2	52.0	65.1	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	809	626	5.00E-40	77.4	14.2	23.5
Rsa1.0_02013.1.g31525.t1	gb|AAG09097.1|AC009323_8 Putative retroelement polyprotein [Arabidopsis thaliana]	665	1486	0	223.5	51.3	63.2	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	665	1262	1.00E-113	189.8	30.5	46.6
Rsa1.0_02013.1.g31526.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02013.1.g31527.t1	gb|AAC95175.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1596	1352	0	84.7	44.7	59.6	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1596	746	1.00E-114	46.7	13.4	16.8
Rsa1.0_02013.1.g31528.t3	gb|EOA29637.1| hypothetical protein CARUB_v10014861mg [Capsella rubella]	250	144	2.00E-16	57.6	20.0	22.8	hypothetical protein CARUB_v10014861mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_02013.1.g31529.t1	dbj|BAB10790.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	658	1864	6.00E-52	283.3	16.9	24.5	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02013.1.g31530.t1	gb|EOA36759.1| hypothetical protein CARUB_v10012615mg [Capsella rubella]	166	166	5.00E-85	100.0	93.4	97.0	hypothetical protein CARUB_v10012615mg	gbpln	Capsella rubella	AT1G32250.1 | Symbols: | Calcium-binding EF-hand family protein | chr1:11639843-11640343 FORWARD LENGTH=166	166	166	2.00E-87	100.0	93.4	97.0

Rsa1.0_02013.1.g31531.t2	gb|ABH07409.1| putative pol polyprotein [Brassica oleracea var. botrytis]	1335	1239	0	92.8	36.3	46.0	putative pol polyprotein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1335	1262	5.00E-78	94.5	12.1	18.7
Rsa1.0_02014.1.g31532.t7	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	1595	940	6.00E-19	58.9	4.1	6.1	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02014.1.g31533.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02014.1.g31534.t2	gb|AAD20658.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	611	1611	1.00E-103	263.7	35.7	48.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02014.1.g31535.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	710	695	0	97.9	59.0	72.7	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	710	681	3.00E-24	95.9	6.8	11.0
Rsa1.0_02014.1.g31536.t6	gb|AAD20433.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1846	889	1.00E-152	48.2	15.5	18.7	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02014.1.g31537.t1	gb|ABD65035.1| hypothetical protein 26.t00052 [Brassica oleracea]	280	695	1.00E-100	248.2	66.8	76.8	hypothetical protein 26.t00052	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	280	681	2.00E-23	243.2	18.2	30.0
Rsa1.0_02015.1.g31538.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	493	1142	1.00E-124	231.6	41.8	55.0	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	493	626	1.00E-36	127.0	21.9	37.5
Rsa1.0_02015.1.g31539.t1	gb|AAD17347.1| contains similarity to Petunia PTTA' (GB:AF009516) [Arabidopsis thaliana] gi|7267146|emb|CAB80814.1| putative transposon protein [Arabidopsis thaliana]	128	357	2.00E-35	278.9	55.5	76.6	contains similarity to Petunia PTTA' (GB:AF009516)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02015.1.g31540.t4	gb|AAF69169.1|AC007915_21 F27F5.21 [Arabidopsis thaliana]	351	1023	8.00E-48	291.5	40.2	52.7	F27F5.21	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	351	575	8.00E-19	163.8	19.7	30.2
Rsa1.0_02015.1.g31541.t1	ref|XP_002876297.1| obf-binding protein 3 [Arabidopsis lyrata subsp. lyrata] gi|297322135|gb|EFH52556.1| obf-binding protein 3 [Arabidopsis lyrata subsp. lyrata]	334	353	1.00E-141	105.7	78.4	85.0	obf-binding protein 3	gbpln	Arabidopsis lyrata	AT3G55370.2 | Symbols: OBP3 | OBF-binding protein 3 | chr3:20527198-20528876 FORWARD LENGTH=354	334	354	1.00E-133	106.0	76.0	82.9
Rsa1.0_02015.1.g31542.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02015.1.g31543.t1	ref|XP_002876296.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297322134|gb|EFH52555.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	268	599	2.00E-84	223.5	64.6	74.6	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT3G55340.1 | Symbols: PHIP1 | phragmoplastin interacting protein 1 | chr3:20515672-20517832 FORWARD LENGTH=597	268	597	4.00E-84	222.8	63.4	73.9
Rsa1.0_02015.1.g31544.t1	ref|XP_002878030.1| photosystem II reaction center PsbP family protein [Arabidopsis lyrata subsp. lyrata] gi|297323868|gb|EFH54289.1| photosystem II reaction center PsbP family protein [Arabidopsis lyrata subsp. lyrata]	229	229	1.00E-103	100.0	86.0	93.0	photosystem II reaction center PsbP family protein	gbpln	Arabidopsis lyrata	AT3G55330.1 | Symbols: PPL1 | PsbP-like protein 1 | chr3:20514031-20515275 REVERSE LENGTH=230	229	230	1.00E-104	100.4	86.0	93.4

Rsa1.0_02015.1.g31545.t1	ref|XP_002878029.1| P-glycoprotein 20 [Arabidopsis lyrata subsp. lyrata] gi|297323867|gb|EFH54288.1| P-glycoprotein 20 [Arabidopsis lyrata subsp. lyrata]	1360	1408	0	103.5	92.9	96.5	P-glycoprotein 20	gbpln	Arabidopsis lyrata	AT3G55320.1 | Symbols: PGP20 | P-glycoprotein 20 | chr3:20507391-20513393 REVERSE LENGTH=1408	1360	1408	0	103.5	92.4	96.5
Rsa1.0_02015.1.g31546.t1	ref|XP_002876294.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] gi|297322132|gb|EFH52553.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	280	280	1.00E-135	100.0	84.6	92.5	short-chain dehydrogenase/reductase family protein	gbpln	Arabidopsis lyrata	AT3G55290.2 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:20502653-20503730 FORWARD LENGTH=279	280	279	1.00E-135	99.6	83.2	91.8
Rsa1.0_02015.1.g31547.t1	gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]	156	1142	1.00E-21	732.1	34.6	44.9	reverse transcriptase, putative; 16838-20266	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02016.1.g31548.t1	gb|EOA32158.1| hypothetical protein CARUB_v10015410mg [Capsella rubella]	1012	1079	0	106.6	83.1	88.8	hypothetical protein CARUB_v10015410mg	gbpln	Capsella rubella	AT2G20320.1 | Symbols: | DENN (AEX-3) domain-containing protein | chr2:8767082-8772271 FORWARD LENGTH=1029	1012	1029	0	101.7	82.1	87.6
Rsa1.0_02016.1.g31549.t1	gb|EOA30057.1| hypothetical protein CARUB_v10013163mg [Capsella rubella]	631	657	0	104.1	88.9	94.8	hypothetical protein CARUB_v10013163mg	gbpln	Capsella rubella	AT2G20330.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:8772888-8775518 REVERSE LENGTH=648	631	648	0	102.7	85.7	92.6
Rsa1.0_02016.1.g31550.t1	ref|NP_849999.1| Tyrosine decarboxylase 1 [Arabidopsis thaliana] gi|68053310|sp|Q8RY79.1|TYDC1_ARATH RecName: Full=Tyrosine decarboxylase 1 gi|18491209|gb|AAL69507.1| putative tyrosine decarboxylase [Arabidopsis thaliana] gi|20465925|gb|AAM20115.1| putative tyrosine decarboxylase [Arabidopsis thaliana] gi|318104937|gb|ADV41492.1| aromatic aldehyde synthase [Arabidopsis thaliana] gi|330251901|gb|AEC06995.1| Tyrosine decarboxylase 1 [Arabidopsis thaliana]	498	490	0	98.4	83.3	89.6	Tyrosine decarboxylase 1	gbpln	Arabidopsis thaliana	AT2G20340.1 | Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr2:8779804-8782490 FORWARD LENGTH=490	498	490	0	98.4	83.3	89.6
Rsa1.0_02017.1.g31551.t2	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1922	1529	0	79.6	34.8	46.8	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1922	746	6.00E-87	38.8	8.4	10.6
Rsa1.0_02017.1.g31552.t1	ref|NP_187198.1| formin-like protein 11 [Arabidopsis thaliana] gi|75191978|sp|Q9MA60.1|FH11_ARATH RecName: Full=Formin-like protein 11; Short=AtFH11; Flags: Precursor gi|7596775|gb|AAF64546.1| unknown protein [Arabidopsis thaliana] gi|332640723|gb|AEE74244.1| formin-like protein 11 [Arabidopsis thaliana]	828	884	0	106.8	80.1	85.9	formin-like protein 11	gbpln	Arabidopsis thaliana	AT3G05470.1 | Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr3:1579667-1582547 REVERSE LENGTH=884	828	884	0	106.8	80.1	85.9
Rsa1.0_02017.1.g31553.t1	ref|XP_002882420.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297328260|gb|EFH58679.1| phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	459	461	1.00E-158	100.4	62.1	67.1	phospholipid/glycerol acyltransferase family protein	gbpln	Arabidopsis lyrata	AT3G05510.1 | Symbols: | Phospholipid/glycerol acyltransferase family protein | chr3:1595576-1598074 FORWARD LENGTH=448	459	448	1.00E-151	97.6	58.2	63.8
Rsa1.0_02017.1.g31554.t1	ref|XP_002882421.1| alpha subunit of F-actin capping protein [Arabidopsis lyrata subsp. lyrata] gi|297328261|gb|EFH58680.1| alpha subunit of F-actin capping protein [Arabidopsis lyrata subsp. lyrata]	300	308	1.00E-151	102.7	88.0	92.7	alpha subunit of F-actin capping protein	gbpln	Arabidopsis lyrata	AT3G05520.2 | Symbols: | Subunits of heterodimeric actin filament capping protein Capz superfamily | chr3:1598611-1601437 FORWARD LENGTH=382	300	382	2.33E-156	127.3	84.0	88.3
Rsa1.0_02017.1.g31555.t1	sp|O23894.1|PRS6A_BRACM RecName: Full=26S protease regulatory subunit 6A homolog; AltName: Full=Tat-binding protein homolog 1; Short=TBP-1 gi|2564337|dbj|BAA22951.1| Tat binding protein 1 [Brassica rapa subsp. oleifera]	496	424	1.00E-148	85.5	53.2	53.4	RecName: Full=26S protease regulatory subunit 6A homolog; AltName: Full=Tat-binding protein homolog 1; Short=TBP-1 gi|2564337|dbj|BAA22951.1| Tat binding protein 1	gbpln	Brassica rapa	AT3G05530.1 | Symbols: RPT5A, ATS6A.2 | regulatory particle triple-A ATPase 5A | chr3:1603540-1605993 FORWARD LENGTH=424	496	424	1.00E-150	85.5	53.0	53.2

Rsa1.0_02017.1.g31556.t1	ref|NP_187207.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana] gi|42572267|ref|NP_974229.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana] gi|145331980|ref|NP_001078112.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana] gi|17865568|sp|Q9M9W1.1|RL222_ARATH RecName: Full=60S ribosomal protein L22-2 gi|6714454|gb|AAF26141.1|AC011620_17 putative 60S ribosomal protein L22 [Arabidopsis thaliana] gi|17529148|gb|AAL38800.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] gi|20466019|gb|AAM20231.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] gi|21595684|gb|AAM66123.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana] gi|27311727|gb|AAO00829.1| putative 60S ribosomal protein L22 [Arabidopsis thaliana] gi|30102826|gb|AAP21331.1| At3g05560 [Arabidopsis thaliana] gi|332640737|gb|AEE74258.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana] gi|332640738|gb|AEE74259.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana] gi|332640739|gb|AEE74260.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana]	124	124	2.00E-55	100.0	96.8	100.0	60S ribosomal protein L22-2	gbpln	Arabidopsis thaliana	AT3G05560.3 | Symbols: | Ribosomal L22e protein family | chr3:1614641-1615204 FORWARD LENGTH=124	124	124	4.00E-58	100.0	96.8	100.0
Rsa1.0_02017.1.g31557.t1	gb|EOA31060.1| hypothetical protein CARUB_v10014212mg [Capsella rubella]	128	318	9.00E-67	248.4	96.1	99.2	hypothetical protein CARUB_v10014212mg	gbpln	Capsella rubella	AT3G05580.1 | Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr3:1618216-1619850 REVERSE LENGTH=318	128	318	1.00E-68	248.4	94.5	99.2
Rsa1.0_02018.1.g31558.t1	gb|EOA16742.1| hypothetical protein CARUB_v10004943mg [Capsella rubella]	373	408	1.00E-165	109.4	77.2	84.5	hypothetical protein CARUB_v10004943mg	gbpln	Capsella rubella	AT4G27585.1 | Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr4:13766984-13769832 REVERSE LENGTH=411	373	411	1.00E-165	110.2	76.9	85.5
Rsa1.0_02018.1.g31559.t1	gb|EOA14373.1| hypothetical protein CARUB_v10027559mg [Capsella rubella]	119	130	5.00E-28	109.2	78.2	79.8	hypothetical protein CARUB_v10027559mg	gbpln	Capsella rubella	AT5G54095.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27580.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21952868-21953369 REVERSE LENGTH=135	119	135	4.00E-18	113.4	67.2	71.4
Rsa1.0_02018.1.g31560.t1	ref|XP_002872140.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata] gi|297317977|gb|EFH48399.1| CYP71B11 [Arabidopsis lyrata subsp. lyrata]	496	496	0	100.0	81.7	91.9	CYP71B11	gbpln	Arabidopsis lyrata	AT5G25180.1 | Symbols: CYP71B14 | cytochrome P450, family 71, subfamily B, polypeptide 14 | chr5:8694630-8696221 REVERSE LENGTH=496	496	496	0	100.0	81.9	92.7
Rsa1.0_02018.1.g31561.t1	gb|EOA14663.1| hypothetical protein CARUB_v10027929mg [Capsella rubella]	264	199	8.00E-56	75.4	42.0	49.6	hypothetical protein CARUB_v10027929mg	gbpln	Capsella rubella	AT5G54062.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1278 (InterPro:IPR010701); BEST Arabidopsis thaliana protein match is: Protein of unknown function (DUF1278) (TAIR:AT5G53742.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21938857-21939480 FORWARD LENGTH=207	264	207	1.00E-46	78.4	41.7	47.7

Rsa1.0_02018.1.g31562.t1	gb|AEM37037.1| UDP-glucose:flavonoid 3-O-glucosyltransferase 2 [Brassica rapa subsp. oleifera]	468	468	0	100.0	93.6	97.6	UDP-glucose:flavonoid 3-O-glucosyltransferase 2	gbpln	Brassica rapa	AT5G54060.1 | Symbols: UF3GT | UDP-glucose:flavonoid 3-o-glucosyltransferase | chr5:21936902-21938308 REVERSE LENGTH=468	468	468	0	100.0	86.1	94.0
Rsa1.0_02019.1.g31563.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02019.1.g31564.t1	ref|NP_173310.2| protein AGAMOUS-like 65 [Arabidopsis thaliana] gi|32455231|gb|AAN37407.1| MADS-box protein AGL65 [Arabidopsis thaliana] gi|332191637|gb|AEE29758.1| protein AGAMOUS-like 65 [Arabidopsis thaliana]	379	389	1.00E-179	102.6	87.3	92.6	protein AGAMOUS-like 65	gbpln	Arabidopsis thaliana	AT1G18750.1 | Symbols: AGL65 | AGAMOUS-like 65 | chr1:6467266-6469640 FORWARD LENGTH=389	379	389	0	102.6	87.3	92.6
Rsa1.0_02019.1.g31565.t1	gb|EOA39436.1| hypothetical protein CARUB_v10012572mg [Capsella rubella]	134	239	2.00E-23	178.4	41.8	55.2	hypothetical protein CARUB_v10012572mg	gbpln	Capsella rubella	AT1G18760.1 | Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr1:6471150-6471824 REVERSE LENGTH=224	134	224	2.00E-14	167.2	34.3	49.3
Rsa1.0_02019.1.g31566.t1	ref|XP_002893015.1| RWP-RK domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297338857|gb|EFH69274.1| RWP-RK domain-containing protein [Arabidopsis lyrata subsp. lyrata]	248	259	4.00E-74	104.4	65.3	73.8	RWP-RK domain-containing protein	gbpln	Arabidopsis lyrata	AT1G18790.1 | Symbols: | RWP-RK domain-containing protein | chr1:6478851-6480043 REVERSE LENGTH=269	248	269	2.00E-74	108.5	63.3	73.8
Rsa1.0_02019.1.g31567.t1	dbj|BAC42657.1| unknown protein [Arabidopsis thaliana] gi|28950777|gb|AAO63312.1| At1g18800 [Arabidopsis thaliana]	254	228	1.00E-108	89.8	79.1	83.9	unknown protein	gbpln	Arabidopsis thaliana	AT1G18800.1 | Symbols: NRP2 | NAP1-related protein 2 | chr1:6481466-6483463 REVERSE LENGTH=256	254	256	1.00E-108	100.8	77.6	81.5
Rsa1.0_02019.1.g31568.t1	gb|EOA39108.1| hypothetical protein CARUB_v10011880mg [Capsella rubella]	367	379	1.00E-147	103.3	80.4	87.7	hypothetical protein CARUB_v10011880mg	gbpln	Capsella rubella	AT1G18810.1 | Symbols: | phytochrome kinase substrate-related | chr1:6485709-6486872 REVERSE LENGTH=387	367	387	1.00E-145	105.4	75.5	83.7
Rsa1.0_02019.1.g31569.t1	ref|NP_173317.2| transducin/WD-40 repeat-containing protein [Arabidopsis thaliana] gi|332191646|gb|AEE29767.1| transport protein SEC31-like protein SEC31B [Arabidopsis thaliana]	955	969	0	101.5	73.9	82.7	transducin/WD-40 repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G18830.1 | Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:6489309-6494218 FORWARD LENGTH=969	955	969	0	101.5	73.9	82.7
Rsa1.0_02019.1.g31570.t1	ref|XP_002893018.1| hypothetical protein ARALYDRAFT_472107 [Arabidopsis lyrata subsp. lyrata] gi|297338860|gb|EFH69277.1| hypothetical protein ARALYDRAFT_472107 [Arabidopsis lyrata subsp. lyrata]	88	88	4.00E-40	100.0	93.2	94.3	hypothetical protein ARALYDRAFT_472107	gbpln	Arabidopsis lyrata	AT1G18835.1 | Symbols: MIF3 | mini zinc finger | chr1:6496106-6496372 REVERSE LENGTH=88	88	88	4.00E-38	100.0	94.3	95.5
Rsa1.0_02019.1.g31571.t1	ref|NP_197389.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana] gi|332005241|gb|AED92624.1| RNA-directed DNA polymerase (reverse transcriptase)-related family protein [Arabidopsis thaliana]	290	295	3.00E-53	101.7	37.6	50.0	RNA-directed DNA polymerase (reverse transcriptase)-related family protein	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	290	295	9.00E-56	101.7	37.6	50.0
Rsa1.0_02019.1.g31572.t1	ref|XP_002893019.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297338861|gb|EFH69278.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	95	104	1.00E-25	109.5	73.7	84.2	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_02020.1.g31573.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02020.1.g31574.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02020.1.g31575.t1	ref|NP_177760.1| golgi nucleotide sugar transporter 3 [Arabidopsis thaliana] gi|75198562|sp|Q9S845.1|GONS3_ARATH RecName: Full=GDP-mannose transporter GONST3; AltName: Full=Protein GOLGI NUCLEOTIDE SUGAR TRANSPORTER 3 gi|6554485|gb|AAF16667.1|AC012394_16 unknown protein; 69155-70273 [Arabidopsis thaliana] gi|6573714|gb|AAF17634.1|AC009978_10 T23E18.26 [Arabidopsis thaliana] gi|29329821|emb|CAD83087.1| GONST3 Golgi Nucleotide sugar transporter [Arabidopsis thaliana] gi|332197705|gb|AEE35826.1| golgi nucleotide sugar transporter 3 [Arabidopsis thaliana]	378	372	1.00E-168	98.4	81.5	88.4	golgi nucleotide sugar transporter 3	gbpln	Arabidopsis thaliana	AT1G76340.1 | Symbols: GONST3 | golgi nucleotide sugar transporter 3 | chr1:28635188-28636306 REVERSE LENGTH=372	378	372	1.00E-171	98.4	81.5	88.4
Rsa1.0_02020.1.g31576.t1	gb|AAQ62876.1| At1g76320 [Arabidopsis thaliana] gi|62320160|dbj|BAD94369.1| putative phytochrome A signaling protein [Arabidopsis thaliana]	739	732	0	99.1	80.9	89.4	At1g76320	gbpln	Arabidopsis thaliana	AT1G76320.1 | Symbols: FRS4 | FAR1-related sequence 4 | chr1:28631404-28633886 FORWARD LENGTH=732	739	732	0	99.1	80.8	89.4

Rsa1.0_02020.1.g31577.t1	ref|XP_002889075.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297334916|gb|EFH65334.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	431	432	0	100.2	85.8	91.9	predicted protein	gbpln	Arabidopsis lyrata	AT1G76310.1 | Symbols: CYCB2;4 | CYCLIN B2;4 | chr1:28628046-28630199 REVERSE LENGTH=431	431	431	0	100.0	84.9	91.6
Rsa1.0_02020.1.g31578.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02020.1.g31579.t2	gb|AAK96849.1| coatomer delta subunit (delta-coat protein) (delta-COP) [Arabidopsis thaliana]	109	527	7.00E-11	483.5	33.9	45.0	coatomer delta subunit (delta-coat protein) (delta-COP)	gbpln	Arabidopsis thaliana	AT5G05010.2 | Symbols: | clathrin adaptor complexes medium subunit family protein | chr5:1477137-1479872 FORWARD LENGTH=527	109	527	9.00E-13	483.5	33.0	44.0
Rsa1.0_02020.1.g31580.t1	gb|EOA33218.1| hypothetical protein CARUB_v10020320mg [Capsella rubella]	116	432	2.00E-23	372.4	50.0	56.0	hypothetical protein CARUB_v10020320mg	gbpln	Capsella rubella	AT1G76310.1 | Symbols: CYCB2;4 | CYCLIN B2;4 | chr1:28628046-28630199 REVERSE LENGTH=431	116	431	2.00E-25	371.6	48.3	56.0
Rsa1.0_02020.1.g31581.t1	gb|EOA34893.1| hypothetical protein CARUB_v10022476mg [Capsella rubella]	77	77	3.00E-12	100.0	57.1	68.8	hypothetical protein CARUB_v10022476mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_02020.1.g31582.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02020.1.g31583.t1	gb|EMJ25100.1| hypothetical protein PRUPE_ppa013274mg [Prunus persica]	127	131	7.00E-54	103.1	82.7	92.9	hypothetical protein PRUPE_ppa013274mg	gbpln	Prunus persica	AT1G20580.1 | Symbols: | Small nuclear ribonucleoprotein family protein | chr1:7128979-7130371 FORWARD LENGTH=131	127	131	9.00E-51	103.1	83.5	95.3
Rsa1.0_02020.1.g31584.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02020.1.g31585.t1	gb|AAC33226.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	214	1529	2.00E-40	714.5	37.9	53.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G18880.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr5:6300535-6301422 REVERSE LENGTH=295	214	295	8.00E-38	137.9	37.4	53.7
Rsa1.0_02020.1.g31586.t1	ref|XP_002886778.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297332619|gb|EFH63037.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata]	429	440	0	102.6	82.1	90.2	integral membrane transporter family protein	gbpln	Arabidopsis lyrata	AT1G64890.1 | Symbols: | Major facilitator superfamily protein | chr1:24109752-24111165 FORWARD LENGTH=442	429	442	0	103.0	81.6	90.0
Rsa1.0_02020.1.g31587.t1	ref|NP_565126.1| pseudouridine synthase-like protein [Arabidopsis thaliana] gi|6573728|gb|AAF17648.1|AC009978_24 T23E18.5 [Arabidopsis thaliana] gi|21592498|gb|AAM64448.1| unknown [Arabidopsis thaliana] gi|21703099|gb|AAM74492.1| At1g76120/T23E18_5 [Arabidopsis thaliana] gi|23308411|gb|AAN18175.1| At1g76120/T23E18_5 [Arabidopsis thaliana] gi|332197677|gb|AEE35798.1| pseudouridine synthase-like protein [Arabidopsis thaliana]	430	463	0	107.7	76.3	81.6	pseudouridine synthase-like protein	gbpln	Arabidopsis thaliana	AT1G76120.1 | Symbols: | Pseudouridine synthase family protein | chr1:28558813-28560294 REVERSE LENGTH=463	430	463	0	107.7	76.3	81.6
Rsa1.0_02020.1.g31588.t2	ref|XP_002889059.1| high mobility group family protein [Arabidopsis lyrata subsp. lyrata] gi|297334900|gb|EFH65318.1| high mobility group family protein [Arabidopsis lyrata subsp. lyrata]	339	338	1.00E-159	99.7	86.7	90.3	high mobility group family protein	gbpln	Arabidopsis lyrata	AT1G76110.1 | Symbols: | HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain | chr1:28555287-28557465 REVERSE LENGTH=338	339	338	1.00E-159	99.7	85.8	89.1
Rsa1.0_02020.1.g31589.t1	gb|AAA32834.1| plastocyanin [Arabidopsis thaliana]	170	171	3.00E-75	100.6	82.9	90.0	plastocyanin	gbpln	Arabidopsis thaliana	AT1G76100.1 | Symbols: PETE1 | plastocyanin 1 | chr1:28554217-28554732 REVERSE LENGTH=171	170	171	3.00E-77	100.6	82.4	90.0
Rsa1.0_02020.1.g31590.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	513	1274	5.00E-94	248.3	38.2	53.4	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	513	575	9.00E-68	112.1	33.7	51.9
Rsa1.0_02020.1.g31591.t1	dbj|BAJ34107.1| unnamed protein product [Thellungiella halophila]	306	306	1.00E-166	100.0	92.5	96.4	unnamed protein product	----	----	AT1G76080.1 | Symbols: ATCDSP32, CDSP32 | chloroplastic drought-induced stress protein of 32 kD | chr1:28548063-28549348 REVERSE LENGTH=302	306	302	1.00E-154	98.7	87.6	91.8
Rsa1.0_02020.1.g31592.t1	gb|EOA35588.1| hypothetical protein CARUB_v10020800mg [Capsella rubella]	312	267	1.00E-86	85.6	60.6	67.3	hypothetical protein CARUB_v10020800mg	gbpln	Capsella rubella	AT1G76070.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G20310.1); Has 66 Blast hits to 66 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:28546617-28547435 FORWARD LENGTH=272	312	272	2.00E-83	87.2	63.5	68.3

Rsa1.0_02020.1.g31593.t1	ref|XP_002889054.1| EMB1793 [Arabidopsis lyrata subsp. lyrata] gi|297334895|gb|EFH65313.1| EMB1793 [Arabidopsis lyrata subsp. lyrata]	158	157	4.00E-70	99.4	85.4	93.7	EMB1793	gbpln	Arabidopsis lyrata	AT1G76060.1 | Symbols: EMB1793 | LYR family of Fe/S cluster biogenesis protein | chr1:28543367-28543840 REVERSE LENGTH=157	158	157	1.00E-68	99.4	81.6	91.1
Rsa1.0_02020.1.g31594.t3	gb|EOA34990.1| hypothetical protein CARUB_v10020082mg [Capsella rubella]	528	556	0	105.3	91.1	95.8	hypothetical protein CARUB_v10020082mg	gbpln	Capsella rubella	AT1G76040.2 | Symbols: CPK29 | calcium-dependent protein kinase 29 | chr1:28537743-28540448 FORWARD LENGTH=561	528	561	0	106.3	91.3	96.6
Rsa1.0_02020.1.g31595.t1	ref|XP_002887623.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297333464|gb|EFH63882.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	478	486	0	101.7	90.0	93.3	predicted protein	gbpln	Arabidopsis lyrata	AT1G76030.1 | Symbols: | ATPase, V1 complex, subunit B protein | chr1:28534134-28536916 FORWARD LENGTH=486	478	486	0	101.7	89.7	93.3
Rsa1.0_02020.1.g31596.t1	gb|EOA35693.1| hypothetical protein CARUB_v10020919mg [Capsella rubella]	220	222	4.00E-89	100.9	80.0	85.9	hypothetical protein CARUB_v10020919mg	gbpln	Capsella rubella	AT1G76020.1 | Symbols: | Thioredoxin superfamily protein | chr1:28532243-28533542 REVERSE LENGTH=225	220	225	4.00E-91	102.3	76.8	86.4
Rsa1.0_02021.1.g31597.t1	gb|ABD65034.1| Ulp1 protease family protein [Brassica oleracea]	319	863	1.00E-37	270.5	25.1	33.9	Ulp1 protease family protein	gbpln	Brassica oleracea	AT5G45570.1 | Symbols: | Ulp1 protease family protein | chr5:18472301-18475574 FORWARD LENGTH=921	319	921	1.00E-12	288.7	23.2	34.2
Rsa1.0_02021.1.g31598.t1	gb|AAD49099.1|AF177535_3 contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]	197	664	8.00E-13	337.1	19.8	32.5	contains similarity to maize transposon MuDR (GB:M76978)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02021.1.g31599.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02021.1.g31600.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02021.1.g31601.t2	gb|EOA26012.1| hypothetical protein CARUB_v10019409mg [Capsella rubella]	245	243	1.00E-82	99.2	70.2	76.3	hypothetical protein CARUB_v10019409mg	gbpln	Capsella rubella	AT3G53200.1 | Symbols: AtMYB27, MYB27 | myb domain protein 27 | chr3:19718426-19719394 REVERSE LENGTH=238	245	238	1.00E-82	97.1	69.4	77.6
Rsa1.0_02021.1.g31602.t1	ref|XP_002876192.1| hypothetical protein ARALYDRAFT_485694 [Arabidopsis lyrata subsp. lyrata] gi|297322030|gb|EFH52451.1| hypothetical protein ARALYDRAFT_485694 [Arabidopsis lyrata subsp. lyrata]	457	484	0	105.9	90.4	95.2	hypothetical protein ARALYDRAFT_485694	gbpln	Arabidopsis lyrata	AT3G53190.1 | Symbols: | Pectin lyase-like superfamily protein | chr3:19714171-19717537 FORWARD LENGTH=483	457	483	0	105.7	89.9	93.9
Rsa1.0_02021.1.g31603.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02022.1.g31604.t1	gb|AAK43485.1|AC084807_10 polyprotein, putative [Arabidopsis thaliana] gi|225898008|dbj|BAH30336.1| hypothetical protein [Arabidopsis thaliana]	990	1459	0	147.4	66.8	78.0	polyprotein, putative	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	990	1262	1.00E-108	127.5	19.5	27.8
Rsa1.0_02022.1.g31605.t1	gb|EOA28094.1| hypothetical protein CARUB_v10024275mg [Capsella rubella]	142	142	1.00E-73	100.0	96.5	99.3	hypothetical protein CARUB_v10024275mg	gbpln	Capsella rubella	AT2G42680.1 | Symbols: MBF1A, ATMBF1A | multiprotein bridging factor 1A | chr2:17774972-17776116 FORWARD LENGTH=142	142	142	2.00E-73	100.0	93.0	97.2
Rsa1.0_02022.1.g31606.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02022.1.g31607.t1	gb|EOA27623.1| hypothetical protein CARUB_v10023771mg [Capsella rubella]	521	289	1.00E-106	55.5	39.5	45.9	hypothetical protein CARUB_v10023771mg	gbpln	Capsella rubella	AT2G42780.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: regulation of transcription; LOCATED IN: integral to membrane, nucleus; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: RNA polymerase II transcription factor SIII, subunit A (InterPro:IPR010684); Has 187 Blast hits to 186 proteins in 77 species: Archae - 0; Bacteria - 0; Metazoa - 104; Fungi - 29; Plants - 38; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink). | chr2:17801037-17802646 FORWARD LENGTH=293	521	293	1.00E-107	56.2	37.6	44.5
Rsa1.0_02022.1.g31608.t1	ref|XP_002862313.1| hypothetical protein ARALYDRAFT_497523 [Arabidopsis lyrata subsp. lyrata] gi|297827987|ref|XP_002881876.1| hypothetical protein ARALYDRAFT_903663 [Arabidopsis lyrata subsp. lyrata] gi|297307697|gb|EFH38571.1| hypothetical protein ARALYDRAFT_497523 [Arabidopsis lyrata subsp. lyrata] gi|297327715|gb|EFH58135.1| hypothetical protein ARALYDRAFT_903663 [Arabidopsis lyrata subsp. lyrata]	119	117	1.00E-36	98.3	79.0	89.1	hypothetical protein ARALYDRAFT_497523	gbpln	Arabidopsis lyrata	AT2G42870.1 | Symbols: PAR1, HLH1 | phy rapidly regulated 1 | chr2:17836831-17837187 REVERSE LENGTH=118	119	118	1.00E-36	99.2	75.6	87.4
Rsa1.0_02022.1.g31609.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#

<table>
<tr><td>Rsa1.0_02022.1.g31610.t1</td><td>dbj|BAJ92365.1| predicted protein [Hordeum vulgare subsp. vulgare] gi|326518929|dbj|BAJ92625.1| predicted protein [Hordeum vulgare subsp. vulgare]</td><td>150</td><td>606</td><td>4.00E-43</td><td>404.0</td><td>60.7</td><td>70.7</td><td>predicted protein</td><td>gbpln</td><td>Hordeum vulgare</td><td>AT2G42880.1 | Symbols: ATMPK20, MPK20 | MAP kinase 20 | chr2:17840572-17843947 REVERSE LENGTH=606</td><td>150</td><td>606</td><td>3.00E-44</td><td>404.0</td><td>65.3</td><td>69.3</td></tr>
<tr><td>Rsa1.0_02023.1.g31611.t5</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>1879</td><td>1274</td><td>0</td><td>67.8</td><td>29.3</td><td>39.9</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1879</td><td>575</td><td>3.00E-71</td><td>30.6</td><td>9.2</td><td>13.5</td></tr>
<tr><td>Rsa1.0_02023.1.g31612.t1</td><td>gb|EOA32134.1| hypothetical protein CARUB_v10015385mg, partial [Capsella rubella]</td><td>589</td><td>581</td><td>1.00E-128</td><td>98.6</td><td>43.8</td><td>52.0</td><td>hypothetical protein CARUB_v10015385mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_02023.1.g31613.t1</td><td>gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]</td><td>1448</td><td>1501</td><td>0</td><td>103.7</td><td>59.8</td><td>76.2</td><td>putative retroelement pol polyprotein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262</td><td>1448</td><td>1262</td><td>1.00E-140</td><td>87.2</td><td>17.0</td><td>24.4</td></tr>
<tr><td>Rsa1.0_02023.1.g31614.t2</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>AT5G07530.2 | Symbols: GRP17, ATGRP17, ATGRP-7 | glycine rich protein 17 | chr5:2382629-2384495 REVERSE LENGTH=512</td><td>3293</td><td>512</td><td>2.00E-33</td><td>15.5</td><td>2.1</td><td>2.5</td></tr>
<tr><td>Rsa1.0_02024.1.g31615.t1</td><td>gb|EOA25890.1| hypothetical protein CARUB_v10019270mg, partial [Capsella rubella]</td><td>146</td><td>284</td><td>1.00E-60</td><td>194.5</td><td>76.0</td><td>84.9</td><td>hypothetical protein CARUB_v10019270mg, partial</td><td>gbpln</td><td>Capsella rubella</td><td>AT3G59710.1 | Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:22055220-22057156 REVERSE LENGTH=302</td><td>146</td><td>302</td><td>5.00E-61</td><td>206.8</td><td>69.9</td><td>82.9</td></tr>
<tr><td>Rsa1.0_02024.1.g31616.t1</td><td>ref|NP_191528.1| protein IQ-domain 13 [Arabidopsis thaliana] gi|6996305|emb|CAB75466.1| putative protein [Arabidopsis thaliana] gi|22135900|gb|AAM91532.1| putative protein [Arabidopsis thaliana] gi|24899697|gb|AAN65063.1| putative protein [Arabidopsis thaliana] gi|332646435|gb|AEE79956.1| protein IQ-domain 13 [Arabidopsis thaliana]</td><td>474</td><td>517</td><td>0</td><td>109.1</td><td>84.4</td><td>88.6</td><td>protein IQ-domain 13</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G59690.1 | Symbols: IQD13 | IQ-domain 13 | chr3:22049572-22051479 FORWARD LENGTH=517</td><td>474</td><td>517</td><td>0</td><td>109.1</td><td>84.4</td><td>88.6</td></tr>
<tr><td>Rsa1.0_02024.1.g31617.t1</td><td>gb|AAD22286.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]</td><td>124</td><td>1311</td><td>2.00E-16</td><td>1057.3</td><td>41.1</td><td>62.9</td><td>putative non-LTR retroelement reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G09490.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr4:6015583-6016575 REVERSE LENGTH=170</td><td>124</td><td>170</td><td>3.00E-13</td><td>137.1</td><td>36.3</td><td>50.8</td></tr>
<tr><td>Rsa1.0_02024.1.g31618.t1</td><td>ref|XP_002876519.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322357|gb|EFH52778.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>195</td><td>199</td><td>9.00E-79</td><td>102.1</td><td>79.5</td><td>84.6</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G59680.1 | Symbols: | unknown protein; Has 34 Blast hits to 34 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:22045218-22045823 FORWARD LENGTH=201</td><td>195</td><td>201</td><td>4.00E-81</td><td>103.1</td><td>79.0</td><td>86.2</td></tr>
<tr><td>Rsa1.0_02024.1.g31619.t1</td><td>ref|XP_002876518.1| hypothetical protein ARALYDRAFT_486432 [Arabidopsis lyrata subsp. lyrata] gi|297322356|gb|EFH52777.1| hypothetical protein ARALYDRAFT_486432 [Arabidopsis lyrata subsp. lyrata]</td><td>510</td><td>516</td><td>0</td><td>101.2</td><td>84.5</td><td>91.2</td><td>hypothetical protein ARALYDRAFT_486432</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G59670.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37440.2); Has 77 Blast hits to 77 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr3:22040485-22042380 FORWARD LENGTH=517</td><td>510</td><td>517</td><td>0</td><td>101.4</td><td>82.7</td><td>90.4</td></tr>
<tr><td>Rsa1.0_02024.1.g31620.t1</td><td>gb|AAF18538.1|AC006551_24 Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]</td><td>574</td><td>1231</td><td>1.00E-162</td><td>214.5</td><td>51.7</td><td>68.1</td><td>Very similar to retrotransposon reverse transcriptase</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>574</td><td>575</td><td>4.00E-89</td><td>100.2</td><td>28.9</td><td>45.8</td></tr>
<tr><td>Rsa1.0_02024.1.g31621.t1</td><td>ref|NP_191525.2| C2 domain and GRAM domain-containing protein [Arabidopsis thaliana] gi|17065130|gb|AAL32719.1| putative protein [Arabidopsis thaliana] gi|30725388|gb|AAP37716.1| At3g59660 [Arabidopsis thaliana] gi|332646431|gb|AEE79952.1| C2 domain and GRAM domain-containing protein [Arabidopsis thaliana]</td><td>591</td><td>594</td><td>0</td><td>100.5</td><td>89.0</td><td>93.1</td><td>C2 domain and GRAM domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT3G59660.1 | Symbols: | C2 domain-containing protein / GRAM domain-containing protein | chr3:22034426-22038484 REVERSE LENGTH=594</td><td>591</td><td>594</td><td>0</td><td>100.5</td><td>89.0</td><td>93.1</td></tr>
<tr><td>Rsa1.0_02024.1.g31622.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_02024.1.g31623.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_02025.1.g31624.t1</td><td>dbj|BAA85462.1| transposon-like ORF [Brassica rapa]</td><td>189</td><td>703</td><td>2.00E-85</td><td>372.0</td><td>88.4</td><td>92.1</td><td>transposon-like ORF</td><td>gbpln</td><td>Brassica rapa</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_02025.1.g31625.t1</td><td>gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]</td><td>779</td><td>940</td><td>9.00E-32</td><td>120.7</td><td>18.1</td><td>28.5</td><td>contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_02025.1.g31626.t1</td><td>gb|AAG51783.1|AC079679_3 reverse transcriptase, putative; 16838-20266 [Arabidopsis thaliana]</td><td>544</td><td>1142</td><td>1.00E-105</td><td>209.9</td><td>38.8</td><td>54.4</td><td>reverse transcriptase, putative; 16838-20266</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>544</td><td>575</td><td>2.00E-45</td><td>105.7</td><td>25.0</td><td>38.6</td></tr>
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Rsa1.0_02025.1.g31627.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	292	1024	4.00E−40	350.7	26.7	35.3	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02025.1.g31628.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02025.1.g31629.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02025.1.g31630.t17	gb|AAD23705.1| putative Athila retroelement ORF1 protein [Arabidopsis thaliana]	1432	333	1.00E−51	23.3	9.0	12.3	putative Athila retroelement ORF1 protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02025.1.g31631.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02026.1.g31632.t1	ref|XP_002865084.1| glycosyl hydrolase family 38 protein [Arabidopsis lyrata subsp. lyrata] gi|297310919|gb|EFH41343.1| glycosyl hydrolase family 38 protein [Arabidopsis lyrata subsp. lyrata]	1033	1047	0	101.4	79.5	87.6	glycosyl hydrolase family 38 protein	gbpln	Arabidopsis lyrata	AT5G66150.1 | Symbols: | Glycosyl hydrolase family 38 protein | chr5:26439013−26444434 REVERSE LENGTH=1047	1033	1047	0	101.4	79.3	87.0
Rsa1.0_02026.1.g31633.t2	gb|EOA15042.1| hypothetical protein CARUB_v10028399mg [Capsella rubella]	560	538	0	96.1	85.0	89.5	hypothetical protein CARUB_v10028399mg	gbpln	Capsella rubella	AT5G66210.1 | Symbols: CPK28 | calcium−dependent protein kinase 28 | chr5:26456681−26459434 REVERSE LENGTH=523	560	523	0	93.4	84.5	88.6
Rsa1.0_02026.1.g31634.t1	gb|EOA13731.1| hypothetical protein CARUB_v10026809mg [Capsella rubella]	311	315	1.00E−98	101.3	71.4	78.1	hypothetical protein CARUB_v10026809mg	gbpln	Capsella rubella	AT5G66230.1 | Symbols: | Chalcone−flavanone isomerase family protein | chr5:26462704−26463873 FORWARD LENGTH=329	311	329	5.00E−97	105.8	74.3	83.3
Rsa1.0_02026.1.g31635.t1	ref|XP_002866763.1| hypothetical protein ARALYDRAFT_496982 [Arabidopsis lyrata subsp. lyrata] gi|297312598|gb|EFH43022.1| hypothetical protein ARALYDRAFT_496982 [Arabidopsis lyrata subsp. lyrata]	282	301	1.00E−106	106.7	74.5	82.6	hypothetical protein ARALYDRAFT_496982	gbpln	Arabidopsis lyrata	AT5G66250.3 | Symbols: | kinectin−related | chr5:26469050−26470376 FORWARD LENGTH=306	282	306	1.00E−106	108.5	73.4	83.3
Rsa1.0_02026.1.g31636.t1	ref|NP_201427.1| SAUR−like auxin−responsive protein [Arabidopsis thaliana] gi|10177420|dbj|BAB10705.1| auxin−induced protein−like [Arabidopsis thaliana] gi|332010809|gb|AED98192.1| SAUR−like auxin−responsive protein [Arabidopsis thaliana]	101	99	3.00E−41	98.0	86.1	91.1	SAUR−like auxin−responsive protein	gbpln	Arabidopsis thaliana	AT5G66260.1 | Symbols: | SAUR−like auxin−responsive protein family | chr5:26471269−26471658 FORWARD LENGTH=99	101	99	5.00E−44	98.0	86.1	91.1
Rsa1.0_02026.1.g31637.t1	ref|XP_002865071.1| hypothetical protein ARALYDRAFT_496967 [Arabidopsis lyrata subsp. lyrata] gi|297310906|gb|EFH41330.1| hypothetical protein ARALYDRAFT_496967 [Arabidopsis lyrata subsp. lyrata]	186	170	4.00E−42	91.4	67.2	68.8	hypothetical protein ARALYDRAFT_496967	gbpln	Arabidopsis lyrata	AT5G66400.1 | Symbols: RAB18, ATDI8 | Dehydrin family protein | chr5:26518511−26519153 REVERSE LENGTH=186	186	186	4.00E−41	100.0	74.2	76.9
Rsa1.0_02026.1.g31638.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02026.1.g31639.t1	gb|ABB45838.1| hypothetical protein [Eutrema halophilum]	336	336	0	100.0	93.8	95.8	hypothetical protein	gbpln	Eutrema halophilum	AT5G66390.1 | Symbols: | Peroxidase superfamily protein | chr5:26516063−26517329 REVERSE LENGTH=336	336	336	0	100.0	91.7	94.9
Rsa1.0_02026.1.g31640.t1	ref|XP_002865072.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297310907|gb|EFH41331.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	103	307	5.00E−22	298.1	50.5	57.3	predicted protein	gbpln	Arabidopsis lyrata	AT5G66380.1 | Symbols: ATFOLT1, FOLT1 | folate transporter 1 | chr5:26513645−26515533 REVERSE LENGTH=308	103	308	4.00E−23	299.0	48.5	55.3
Rsa1.0_02027.1.g31641.t2	ref|XP_002866771.1| hypothetical protein ARALYDRAFT_497000 [Arabidopsis lyrata subsp. lyrata] gi|297312606|gb|EFH43030.1| hypothetical protein ARALYDRAFT_497000 [Arabidopsis lyrata subsp. lyrata]	223	308	6.00E−72	138.1	59.6	68.2	hypothetical protein ARALYDRAFT_497000	gbpln	Arabidopsis lyrata	AT5G66160.1 | Symbols: ATRMR1, RMR1 | receptor homology region transmembrane domain ring H2 motif protein 1 | chr5:26445198−26446878 FORWARD LENGTH=310	223	310	6.00E−72	139.0	59.6	68.2
Rsa1.0_02027.1.g31642.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1332	1501	0	112.7	57.8	72.4	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine−rich RLK (RECEPTOR−like protein kinase) 8 | chr4:12129485−12134086 FORWARD LENGTH=1262	1332	1262	1.00E−138	94.7	17.2	24.8
Rsa1.0_02027.1.g31643.t1	gb|AET97566.1| heme oxygenase−1 [Brassica juncea]	242	282	1.00E−128	116.5	93.4	96.3	heme oxygenase−1	gbpln	Brassica juncea	AT2G26670.1 | Symbols: HY1, ATHO1, HO1, TED4, GUN2, HY6 | Plant haem oxygenase (decyclizing) family protein | chr2:11341816−11343394 FORWARD LENGTH=282	242	282	1.00E−123	116.5	88.0	93.4
Rsa1.0_02027.1.g31644.t6	ref|NP_199933.5| uncharacterized protein [Arabidopsis thaliana] gi|332008669|gb|AED96052.1| uncharacterized protein AT5G51200 [Arabidopsis thaliana]	1852	1838	0	99.2	89.4	94.0	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G51200.1 | Symbols: | Protein of unknown function (DUF3414) | chr5:20804926−20819408 FORWARD LENGTH=1838	1852	1838	0	99.2	89.4	94.0
Rsa1.0_02027.1.g31645.t1	gb|AAD22368.1| putative non−LTR retroelement reverse transcriptase [Arabidopsis thaliana]	212	321	4.00E−65	151.4	58.5	71.7	putative non−LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT5G42905.1 | Symbols: | Polynucleotidyl transferase, ribonuclease H−like superfamily protein | chr5:17201414−17202323 REVERSE LENGTH=258	212	258	6.00E−40	121.7	38.2	50.5

Rsa1.0_02027.1.g31646.t2	ref|NP_850084.1| nitrate transporter 1.4 [Arabidopsis thaliana] gi|75314150|sp|Q9SZY4.1|PTR27_ARATH RecName: Full=Nitrate transporter 1.4 gi|4490321|emb|CAB38705.1| nitrate transporter [Arabidopsis thaliana] gi|330252781|gb|AEC07875.1| nitrate transporter 1.4 [Arabidopsis thaliana]	577	577	0	100.0	90.8	95.5	nitrate transporter 1.4	gbpln	Arabidopsis thaliana	AT2G26690.1 | Symbols: | Major facilitator superfamily protein | chr2:11347347-11350916 REVERSE LENGTH=577	577	577	0	100.0	90.8	95.5
Rsa1.0_02028.1.g31647.t1	gb|ACG60687.1| transposon related predicted protein [Brassica oleracea var. alboglabra]	104	183	2.00E-47	176.0	84.6	89.4	transposon related predicted protein	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_02028.1.g31648.t1	ref|NP_174578.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana] gi|378405165|sp|Q9MAP1.2|FB33_ARATH RecName: Full=Putative F-box protein At1g33020 gi|332193429|gb|AEE31550.1| F-box and associated interaction domain-containing protein [Arabidopsis thaliana]	491	548	5.00E-81	111.6	39.5	50.5	F-box and associated interaction domain-containing protein	gbpln	Arabidopsis thaliana	AT1G33020.1 | Symbols: | F-box and associated interaction domains-containing protein | chr1:11962746-11964832 FORWARD LENGTH=548	491	548	1.00E-83	111.6	39.5	50.5
Rsa1.0_02028.1.g31649.t1	ref|XP_002890988.1| ribose-phosphate pyrophosphokinase 2 [Arabidopsis lyrata subsp. lyrata] gi|297336830|gb|EFH67247.1| ribose-phosphate pyrophosphokinase 2 [Arabidopsis lyrata subsp. lyrata]	410	400	0	97.6	92.2	94.6	ribose-phosphate pyrophosphokinase 2	gbpln	Arabidopsis lyrata	AT1G32380.1 | Symbols: PRS2 | phosphoribosyl pyrophosphate (PRPP) synthase 2 | chr1:11682033-11684229 FORWARD LENGTH=400	410	400	0	97.6	91.5	94.6
Rsa1.0_02028.1.g31650.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02028.1.g31651.t1	ref|NP_564396.1| zinc finger CCCH domain-containing protein 12 [Arabidopsis thaliana] gi|75264181|sp|Q9LQM3.1|C3H12_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 12; Short=AtC3H12 gi|8920610|gb|AAF81332.1|AC007767_12 Contains similarity to an unknown protein At2g35430 gi|3608145 from Arabidopsis thaliana BAC T32F12 gb|AC005314. It contains a zinc finger C-x8-C-x5-C-x3-H type domain PF|00642. ESTs gb|AV557765 and gb|AV544407 come from this gene [Arabidopsis thaliana] gi|12597862|gb|AAG60171.1|AC084110_4 unknown protein [Arabidopsis thaliana] gi|26451083|dbj|BAC42646.1| putative RING-H2 zinc finger protein ATL6 [Arabidopsis thaliana] gi|332193347|gb|AEE31468.1| zinc finger CCCH domain-containing protein 12 [Arabidopsis thaliana]	349	384	1.00E-151	110.0	84.0	90.0	zinc finger CCCH domain-containing protein 12	gbpln	Arabidopsis thaliana	AT1G32360.1 | Symbols: | Zinc finger (CCCH-type) family protein | chr1:11673325-11675162 FORWARD LENGTH=384	349	384	1.00E-154	110.0	84.0	90.0
Rsa1.0_02028.1.g31652.t1	ref|NP_564395.1| alternative oxidase 3 [Arabidopsis thaliana] gi|85681032|sp|Q8LEE7.2|AOX3_ARATH RecName: Full=Ubiquinol oxidase 3, mitochondrial; AltName: Full=Alternative oxidase 3; Flags: Precursor gi|8920609|gb|AAF81331.1|AC007767_11 Strong similarity to alternative oxidase from Populus tremula x Populus tremuloides gb|AJ271889. It contains an alternative oxidase domain PF|01786 [Arabidopsis thaliana] gi|115311485|gb|ABI93923.1| At1g32350 [Arabidopsis thaliana] gi|332193346|gb|AEE31467.1| alternative oxidase 3 [Arabidopsis thaliana]	314	318	1.00E-171	101.3	92.7	96.2	alternative oxidase 3	gbpln	Arabidopsis thaliana	AT1G32350.1 | Symbols: AOX1D | alternative oxidase 1D | chr1:11667237-11668569 REVERSE LENGTH=318	314	318	1.00E-174	101.3	92.7	96.2
Rsa1.0_02028.1.g31653.t2	ref|XP_002893719.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297339561|gb|EFH69978.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	683	682	0	99.9	80.4	87.8	predicted protein	gbpln	Arabidopsis lyrata	AT1G32340.1 | Symbols: NHL8 | NDR1/HIN1-like 8 | chr1:11663462-11666037 REVERSE LENGTH=688	683	688	0	100.7	79.5	87.3

Rsa1.0_02029.1.g31654.t1	ref|NP_563963.1| FAD/NAD(P)-binding oxidoreductase [Arabidopsis thaliana] gi|5103813|gb|AAD39643.1|AC007591_8 Contains a PF|00175 Oxidoreductase FAD/NADH-binding domain. ESTs gb|H76345 and gb|AA651465 come from this gene [Arabidopsis thaliana] gi|12744999|gb|AAK06879.1|AF344328_1 unknown protein [Arabidopsis thaliana] gi|15451092|gb|AAK96817.1| Unknown protein [Arabidopsis thaliana] gi|18377448|gb|AAL66890.1| unknown protein [Arabidopsis thaliana] gi|332191150|gb|AEE29271.1| FAD/NAD(P)-binding oxidoreductase [Arabidopsis thaliana]	138	295	9.00E-28	213.8	43.5	50.0	FAD/NAD(P)-binding oxidoreductase	gbpln	Arabidopsis thaliana	AT1G15140.1 | Symbols: | FAD/NAD(P)-binding oxidoreductase | chr1:5210403-5212137 REVERSE LENGTH=295	138	295	2.00E-30	213.8	43.5	50.0
Rsa1.0_02029.1.g31655.t1	dbj|BAB09379.1| non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	1700	1223	0	71.9	39.2	51.4	non-LTR retroelement reverse transcriptase-like protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	1700	746	1.00E-107	43.9	11.6	15.4
Rsa1.0_02029.1.g31656.t1	ref|XP_002877761.1| hypothetical protein ARALYDRAFT_485417 [Arabidopsis lyrata subsp. lyrata] gi|297323599|gb|EFH54020.1| hypothetical protein ARALYDRAFT_485417 [Arabidopsis lyrata subsp. lyrata]	465	447	1.00E-120	96.1	70.5	79.1	hypothetical protein ARALYDRAFT_485417	gbpln	Arabidopsis lyrata	AT3G50690.1 | Symbols: | Leucine-rich repeat (LRR) family protein | chr3:18835271-18837097 REVERSE LENGTH=447	465	447	1.00E-119	96.1	68.4	78.1
Rsa1.0_02029.1.g31657.t1	ref|XP_002886764.1| hypothetical protein ARALYDRAFT_475479 [Arabidopsis lyrata subsp. lyrata] gi|297332605|gb|EFH63023.1| hypothetical protein ARALYDRAFT_475479 [Arabidopsis lyrata subsp. lyrata]	353	350	1.00E-168	99.2	84.7	92.4	hypothetical protein ARALYDRAFT_475479	gbpln	Arabidopsis lyrata	AT1G64770.1 | Symbols: NDF2, NDH45 | NDH-dependent cyclic electron flow 1 | chr1:24057549-24059415 FORWARD LENGTH=348	353	348	1.00E-165	98.6	84.7	92.9
Rsa1.0_02029.1.g31658.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02029.1.g31659.t1	ref|XP_002877755.1| hypothetical protein ARALYDRAFT_485408 [Arabidopsis lyrata subsp. lyrata] gi|297323593|gb|EFH54014.1| hypothetical protein ARALYDRAFT_485408 [Arabidopsis lyrata subsp. lyrata]	337	340	1.00E-179	100.9	91.1	95.3	hypothetical protein ARALYDRAFT_485408	gbpln	Arabidopsis lyrata	AT3G50620.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:18784993-18786747 REVERSE LENGTH=340	337	340	0	100.9	89.6	95.5
Rsa1.0_02029.1.g31660.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02029.1.g31661.t1	gb|EOA24265.1| hypothetical protein CARUB_v10017507mg [Capsella rubella]	362	362	0	100.0	92.8	97.5	hypothetical protein CARUB_v10017507mg	gbpln	Capsella rubella	AT3G50500.1 | Symbols: SPK-2-2, SNRK2-2, SNRK2.2, SRK2D | SNF1-related protein kinase 2.2 | chr3:18741805-18743904 REVERSE LENGTH=362	362	362	0	100.0	92.8	97.0
Rsa1.0_02030.1.g31662.t1	gb|ACB59199.1| copia-like protein [Brassica oleracea]	228	975	4.00E-78	427.6	61.0	66.2	copia-like protein	gbpln	Brassica oleracea	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	228	1262	3.00E-40	553.5	31.6	47.8
Rsa1.0_02030.1.g31663.t2	ref|XP_002872881.1| hypothetical protein ARALYDRAFT_912064 [Arabidopsis lyrata subsp. lyrata] gi|297318718|gb|EFH49140.1| hypothetical protein ARALYDRAFT_912064 [Arabidopsis lyrata subsp. lyrata]	243	245	8.00E-94	100.8	83.1	90.1	hypothetical protein ARALYDRAFT_912064	gbpln	Arabidopsis lyrata	AT4G01670.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G62070.1); Has 141 Blast hits to 139 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 138; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr4:711464-712511 REVERSE LENGTH=249	243	249	1.00E-92	102.5	81.9	89.3
Rsa1.0_02030.1.g31664.t1	ref|NP_192088.1| Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis thaliana] gi|4558548|gb|AAD22641.1|AC007138_5 putative RNaseP-associated protein [Arabidopsis thaliana] gi|7268222|emb|CAB77749.1| putative RNaseP-associated protein [Arabidopsis thaliana] gi|89001035|gb|ABD59107.1| At4g01790 [Arabidopsis thaliana] gi|332656677|gb|AEE82077.1| Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis thaliana]	170	167	2.00E-69	98.2	78.2	87.6	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	gbpln	Arabidopsis thaliana	AT4G01790.1 | Symbols: | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr4:769868-770728 FORWARD LENGTH=167	170	167	8.00E-72	98.2	78.2	87.6

Rsa1.0_02030.1.g31665.t1	ref|NP_192089.1| preprotein translocase subunit secA [Arabidopsis thaliana] gi|322510072|sp|Q9SYI0.2|SECA1_ARATH RecName: Full=Protein translocase subunit SECA1, chloroplastic; Short=AtcpSecA; AltName: Full=Protein ALBINO OR GLASSY YELLOW 1; Flags: Precursor gi|332656678|gb|AEE82078.1| preprotein translocase subunit secA [Arabidopsis thaliana]	986	1022	0	103.7	94.1	96.2	preprotein translocase subunit secA	gbpln	Arabidopsis thaliana	AT4G01800.1 | Symbols: AGY1, AtcpSecA, SECA1 | Albino or Glassy Yellow 1 | chr4:770926-776131 REVERSE LENGTH=1022	986	1022	0	103.7	94.1	96.2
Rsa1.0_02030.1.g31666.t1	sp|Q5DNB1.1|METK_BRARP RecName: Full=S-adenosylmethionine synthase; Short=AdoMet synthase; AltName: Full=Methionine adenosyltransferase; Short=MAT gi|75306462|sp|Q94FA4.1|METK5_BRAJU RecName: Full=S-adenosylmethionine synthase 5; Short=AdoMet synthase 5; AltName: Full=Methionine adenosyltransferase 5; Short=MAT 5 gi|14600072|gb|AAK71235.1| S-adenosylmethionine synthetase [Brassica juncea] gi|56130947|gb|AAV80205.1| S-adenosyl-L-methionine synthetase [Brassica rapa subsp. pekinensis]	393	393	0	100.0	99.7	100.0	RecName: Full=S-adenosylmethionine synthase; Short=AdoMet synthase; AltName: Full=Methionine adenosyltransferase; Short=MAT gi|75306462|sp|Q94FA4.1|METK5_BRAJU RecName: Full=S-adenosylmethionine synthase 5; Short=AdoMet synthase 5; AltName: Full=Methionine adenosyltransferase 5; Short=MAT 5 gi|14600072|gb|AAK71235.1| S-adenosylmethionine synthetase	gbpln	Brassica juncea	AT4G01850.2 | Symbols: SAM-2, MAT2, SAM2, AtSAM2 | S-adenosylmethionine synthetase 2 | chr4:796298-797479 REVERSE LENGTH=393	393	393	0	100.0	99.2	99.7
Rsa1.0_02030.1.g31667.t1	ref|XP_002872871.1| hypothetical protein ARALYDRAFT_490390 [Arabidopsis lyrata subsp. lyrata] gi|297318708|gb|EFH49130.1| hypothetical protein ARALYDRAFT_490390 [Arabidopsis lyrata subsp. lyrata]	654	652	0	99.7	85.2	93.0	hypothetical protein ARALYDRAFT_490390	gbpln	Arabidopsis lyrata	AT4G01870.1 | Symbols: | tolB protein-related | chr4:808473-810431 REVERSE LENGTH=652	654	652	0	99.7	83.2	92.4
Rsa1.0_02030.1.g31668.t1	ref|NP_192097.2| methyltransferase [Arabidopsis thaliana] gi|332656689|gb|AEE82089.1| methyltransferase [Arabidopsis thaliana]	449	453	0	100.9	86.2	92.9	methyltransferase	gbpln	Arabidopsis thaliana	AT4G01880.1 | Symbols: | methyltransferases | chr4:810810-812882 REVERSE LENGTH=453	449	453	0	100.9	86.2	92.9
Rsa1.0_02030.1.g31669.t1	gb|EOA20424.1| hypothetical protein CARUB_v10000732mg [Capsella rubella]	438	516	0	117.8	92.5	96.6	hypothetical protein CARUB_v10000732mg	gbpln	Capsella rubella	AT4G02050.1 | Symbols: STP7 | sugar transporter protein 7 | chr4:898387-900095 REVERSE LENGTH=513	438	513	0	117.1	92.5	96.8
Rsa1.0_02030.1.g31670.t1	dbj|BAJ33893.1| unnamed protein product [Thellungiella halophila]	718	716	0	99.7	96.2	98.1	unnamed protein product	----	----	AT4G02060.2 | Symbols: PRL | Minichromosome maintenance (MCM2/3/5) family protein | chr4:901484-905297 FORWARD LENGTH=716	718	716	0	99.7	95.1	97.4
Rsa1.0_02030.1.g31671.t1	ref|NP_192116.1| DNA mismatch repair protein Msh6-1 [Arabidopsis thaliana] gi|6226648|sp|O04716.2|MSH6_ARATH RecName: Full=DNA mismatch repair protein MSH6; Short=AtMSH6; AltName: Full=MutS protein homolog 6 gi|3912921|gb|AAC78699.1| G/T DNA mismatch repair enzyme [Arabidopsis thaliana] gi|5763966|emb|CAB53337.1| mismatch repair protein msh6-1 [Arabidopsis thaliana] gi|7268591|emb|CAB80700.1| G/T DNA mismatch repair enzyme [Arabidopsis thaliana] gi|332656719|gb|AEE82119.1| DNA mismatch repair protein Msh6-1 [Arabidopsis thaliana]	1205	1324	0	109.9	82.3	87.9	DNA mismatch repair protein Msh6-1	gbpln	Arabidopsis thaliana	AT4G02070.1 | Symbols: MSH6, MSH6-1, ATMSH6 | MUTS homolog 6 | chr4:906079-912930 FORWARD LENGTH=1324	1205	1324	0	109.9	82.3	87.9
Rsa1.0_02031.1.g31672.t1	ref|NP_563867.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|4914336|gb|AAD32884.1|AC005489_22 F14N23.22 [Arabidopsis thaliana] gi|13937240|gb|AAK50112.1|AF372975_1 At1g10340/F14N23_22 [Arabidopsis thaliana] gi|19548017|gb|AAL87372.1| At1g10340/F14N23_22 [Arabidopsis thaliana] gi|332190446|gb|AEE28567.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	294	578	1.00E-117	196.6	73.5	82.0	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G10340.1 | Symbols: | Ankyrin repeat family protein | chr1:3390475-3392481 REVERSE LENGTH=578	294	578	1.00E-120	196.6	73.5	82.0

Rsa1.0_02031.1.g31673.t2	ref|NP_563867.1| ankyrin repeat-containing protein [Arabidopsis thaliana] gi|4914336|gb|AAD32884.1|AC005489_22 F14N23.22 [Arabidopsis thaliana] gi|13937240|gb|AAK50112.1|AF372975_1 At1g10340/F14N23_22 [Arabidopsis thaliana] gi|19548017|gb|AAL87372.1| At1g10340/F14N23_22 [Arabidopsis thaliana] gi|332190446|gb|AEE28567.1| ankyrin repeat-containing protein [Arabidopsis thaliana]	264	578	3.00E-54	218.9	51.5	60.2	ankyrin repeat-containing protein	gbpln	Arabidopsis thaliana	AT1G10340.1 | Symbols: | Ankyrin repeat family protein | chr1:3390475-3392481 REVERSE LENGTH=578	264	578	8.00E-57	218.9	51.5	60.2
Rsa1.0_02031.1.g31674.t1	ref|XP_002874520.1| glycosyl hydrolase family 10 protein [Arabidopsis lyrata subsp. lyrata] gi|297320357|gb|EFH50779.1| glycosyl hydrolase family 10 protein [Arabidopsis lyrata subsp. lyrata]	911	751	0	82.4	71.8	77.6	glycosyl hydrolase family 10 protein	gbpln	Arabidopsis lyrata	AT4G08160.1 | Symbols: | glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein | chr4:5159211-5162694 REVERSE LENGTH=752	911	752	0	82.5	71.7	77.2
Rsa1.0_02031.1.g31675.t1	gb|ABD65022.1| hypothetical protein 26.t00077 [Brassica oleracea]	158	242	9.00E-50	153.2	69.0	74.7	hypothetical protein 26.t00077	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_02031.1.g31676.t1	gb|ABD65021.1| hypothetical protein 26.t00076 [Brassica oleracea]	67	107	1.00E-20	159.7	68.7	79.1	hypothetical protein 26.t00076	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_02031.1.g31677.t1	dbj|BAA97287.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	1471	1491	0	101.4	60.4	74.1	retroelement pol polyprotein-like	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1471	1262	1.00E-142	85.8	16.5	23.8
Rsa1.0_02031.1.g31678.t1	gb|AAC26241.1| F9D12.15 gene product [Arabidopsis thaliana]	257	850	6.00E-32	330.7	36.6	55.3	F9D12.15 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02032.1.g31679.t1	ref|XP_002886457.1| ATSCO1/ATSCO1/CPEF-G [Arabidopsis lyrata subsp. lyrata] gi|297332298|gb|EFH62716.1| ATSCO1/ATSCO1/CPEF-G [Arabidopsis lyrata subsp. lyrata]	773	782	0	101.2	96.1	98.1	ATSCO1/ATSCO1/CPEF-G	gbpln	Arabidopsis lyrata	AT1G62750.1 | Symbols: ATSCO1, ATSCO1/CPEF-G, SCO1 | Translation elongation factor EFG/EF2 protein | chr1:23233622-23236321 REVERSE LENGTH=783	773	783	0	101.3	96.1	97.9
Rsa1.0_02032.1.g31680.t1	ref|NP_176461.1| putative stress-inducible protein [Arabidopsis thaliana] gi|53850567|gb|AAU95460.1| At1g62740 [Arabidopsis thaliana] gi|58331773|gb|AAW70384.1| At1g62740 [Arabidopsis thaliana] gi|332195878|gb|AEE33999.1| putative stress-inducible protein [Arabidopsis thaliana]	571	571	0	100.0	88.1	93.3	putative stress-inducible protein	gbpln	Arabidopsis thaliana	AT1G62740.1 | Symbols: Hop2 | stress-inducible protein, putative | chr1:23231026-23233380 FORWARD LENGTH=571	571	571	0	100.0	88.1	93.3
Rsa1.0_02032.1.g31681.t1	ref|NP_564800.1| isoprenoid biosynthesis enzyme domain-containing protein [Arabidopsis thaliana] gi|6630461|gb|AAF19549.1|AC007190_17 F23N19.9 [Arabidopsis thaliana] gi|21553608|gb|AAM62701.1| unknown [Arabidopsis thaliana] gi|109946495|gb|ABG48426.1| At1g62730 [Arabidopsis thaliana] gi|332195877|gb|AEE33998.1| isoprenoid biosynthesis enzyme domain-containing protein [Arabidopsis thaliana]	306	304	1.00E-161	99.3	90.2	93.8	isoprenoid biosynthesis enzyme domain-containing protein	gbpln	Arabidopsis thaliana	AT1G62730.1 | Symbols: | Terpenoid synthases superfamily protein | chr1:23229204-23230118 REVERSE LENGTH=304	306	304	1.00E-163	99.3	90.2	93.8
Rsa1.0_02032.1.g31682.t1	gb|EOA34776.1| hypothetical protein CARUB_v10022351mg [Capsella rubella]	398	407	1.00E-176	102.3	79.6	87.2	hypothetical protein CARUB_v10022351mg	gbpln	Capsella rubella	AT1G62700.1 | Symbols: VND5, ANAC026 | Arabidopsis NAC domain containing protein 26 | chr1:23216218-23217916 REVERSE LENGTH=394	398	394	1.00E-164	99.0	76.4	85.9
Rsa1.0_02032.1.g31683.t1	ref|XP_002886462.1| binding protein [Arabidopsis lyrata subsp. lyrata] gi|297332303|gb|EFH62721.1| binding protein [Arabidopsis lyrata subsp. lyrata]	516	550	0	106.6	66.9	83.9	binding protein	gbpln	Arabidopsis lyrata	AT1G62680.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:23208247-23209893 REVERSE LENGTH=548	516	548	0	106.2	67.4	83.9
Rsa1.0_02032.1.g31684.t1	gb|AAL65637.1| RFL1 [Arabidopsis lyrata]	132	883	1.00E-38	668.9	62.1	75.0	RFL1	gbpln	Arabidopsis lyrata	AT1G63350.1 | Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:23494935-23497631 REVERSE LENGTH=898	132	898	2.00E-39	680.3	60.6	73.5
Rsa1.0_02032.1.g31685.t1	gb|EOA36691.1| hypothetical protein CARUB_v10012096mg [Capsella rubella]	326	327	1.00E-122	100.3	64.7	80.1	hypothetical protein CARUB_v10012096mg	gbpln	Capsella rubella	AT5G43690.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:17546273-17547268 FORWARD LENGTH=331	326	331	1.00E-122	101.5	65.3	78.8
Rsa1.0_02033.1.g31686.t1	gb|AAV25872.1| hypothetical Protein [Brassica oleracea]	116	120	6.00E-55	103.4	90.5	96.6	hypothetical Protein	gbpln	Brassica oleracea	AT5G60810.1 | Symbols: RGF1 | root meristem growth factor 1 | chr5:24466531-24467110 REVERSE LENGTH=116	116	116	3.00E-41	100.0	68.1	79.3
Rsa1.0_02033.1.g31687.t1	gb|AAV25871.1| putative bZIPtranscription factor protein [Brassica oleracea]	173	176	2.00E-66	101.7	83.8	89.0	putative bZIPtranscription factor protein	gbpln	Brassica oleracea	AT5G60830.1 | Symbols: AtbZIP70, bZIP70 | basic leucine-zipper 70 | chr5:24472639-24473319 FORWARD LENGTH=206	173	206	3.00E-56	119.1	69.4	79.8
Rsa1.0_02033.1.g31688.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_02033.1.g31689.t1	dbj|BAJ34224.1| unnamed protein product [Thellungiella halophila]	292	300	1.00E-102	102.7	74.3	80.1	unnamed protein product	----	----	AT5G60850.1 | Symbols: OBP4 | OBF binding protein 4 | chr5:24480578-24481501 FORWARD LENGTH=307	292	307	8.00E-99	105.1	72.6	80.1
Rsa1.0_02033.1.g31690.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02034.1.g31691.t1	ref|XP_004230758.1| PREDICTED: polyadenylate-binding protein 2-like [Solanum lycopersicum]	122	643	9.00E-16	527.0	41.8	54.1	PREDICTED: polyadenylate-binding protein 2-like	gbpln	Solanum lycopersicum	AT1G49760.2 | Symbols: PAB8 | poly(A) binding protein 8 | chr1:18416740-18419753 FORWARD LENGTH=671	122	671	3.00E-17	550.0	35.2	42.6
Rsa1.0_02034.1.g31692.t1	ref|NP_001118664.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|9294424|dbj|BAB02544.1| unnamed protein product [Arabidopsis thaliana] gi|332642743|gb|AEE76264.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana]	311	307	1.00E-112	98.7	67.2	79.1	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G19595.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr3:6808585-6809508 REVERSE LENGTH=307	311	307	1.00E-114	98.7	67.2	79.1
Rsa1.0_02034.1.g31693.t1	ref|NP_001118664.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|9294424|dbj|BAB02544.1| unnamed protein product [Arabidopsis thaliana] gi|332642743|gb|AEE76264.1| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana]	283	307	4.00E-87	108.5	59.0	70.7	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT3G19595.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr3:6808585-6809508 REVERSE LENGTH=307	283	307	1.00E-89	108.5	59.0	70.7
Rsa1.0_02034.1.g31694.t1	ref|XP_002885318.1| hypothetical protein ARALYDRAFT_479477 [Arabidopsis lyrata subsp. lyrata] gi|297331158|gb|EFH61577.1| hypothetical protein ARALYDRAFT_479477 [Arabidopsis lyrata subsp. lyrata]	575	613	0	106.6	78.8	84.7	hypothetical protein ARALYDRAFT_479477	gbpln	Arabidopsis lyrata	AT3G19610.1 | Symbols: | Plant protein of unknown function (DUF936) | chr3:6812493-6814660 REVERSE LENGTH=640	575	640	0	111.3	77.9	85.0
Rsa1.0_02034.1.g31695.t1	ref|XP_002885320.1| hypothetical protein ARALYDRAFT_318717 [Arabidopsis lyrata subsp. lyrata] gi|297331160|gb|EFH61579.1| hypothetical protein ARALYDRAFT_318717 [Arabidopsis lyrata subsp. lyrata]	370	382	0	103.2	92.4	96.5	hypothetical protein ARALYDRAFT_318717	gbpln	Arabidopsis lyrata	AT3G19630.1 | Symbols: | Radical SAM superfamily protein | chr3:6818676-6820674 REVERSE LENGTH=372	370	372	0	100.5	91.1	95.1
Rsa1.0_02034.1.g31696.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02034.1.g31697.t1	ref|NP_188602.1| uncharacterized protein [Arabidopsis thaliana] gi|9294435|dbj|BAB02555.1| unnamed protein product [Arabidopsis thaliana] gi|23297407|gb|AAN12962.1| unknown protein [Arabidopsis thaliana] gi|110741203|dbj|BAF02152.1| hypothetical protein [Arabidopsis thaliana] gi|110742613|dbj|BAE99219.1| hypothetical protein [Arabidopsis thaliana] gi|332642754|gb|AEE76275.1| uncharacterized protein AT3G19680 [Arabidopsis thaliana]	448	491	0	109.6	83.9	90.6	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G19680.1 | Symbols: | Protein of unknown function (DUF1005) | chr3:6840448-6842107 FORWARD LENGTH=491	448	491	0	109.6	83.9	90.6
Rsa1.0_02034.1.g31698.t1	ref|NP_188603.1| putative pathogenesis-related protein [Arabidopsis thaliana] gi|9294436|dbj|BAB02556.1| pathogenesis-related protein-like [Arabidopsis thaliana] gi|124301044|gb|ABN04774.1| At3g19690 [Arabidopsis thaliana] gi|332642755|gb|AEE76276.1| putative pathogenesis-related protein [Arabidopsis thaliana]	168	161	4.00E-70	95.8	73.2	86.3	putative pathogenesis-related protein	gbpln	Arabidopsis thaliana	AT3G19690.1 | Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr3:6842365-6842850 REVERSE LENGTH=161	168	161	1.00E-72	95.8	73.2	86.3
Rsa1.0_02034.1.g31699.t1	ref|XP_002883201.1| hypothetical protein ARALYDRAFT_479492 [Arabidopsis lyrata subsp. lyrata] gi|297329041|gb|EFH59460.1| hypothetical protein ARALYDRAFT_479492 [Arabidopsis lyrata subsp. lyrata]	410	408	0	99.5	93.7	95.6	hypothetical protein ARALYDRAFT_479492	gbpln	Arabidopsis lyrata	AT3G19760.1 | Symbols: EIF4A-III | eukaryotic initiation factor 4A-III | chr3:6863790-6866242 FORWARD LENGTH=408	410	408	0	99.5	92.4	94.9
Rsa1.0_02034.1.g31700.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02035.1.g31701.t2	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02035.1.g31702.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	905	1501	0	165.9	35.6	44.5	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	905	1262	1.00E-117	139.4	23.8	35.8

Rsa1.0_02035.1.g31703.t1	gb|EOA23725.1| hypothetical protein CARUB_v10016938mg [Capsella rubella]	489	567	0	116.0	93.9	97.5	hypothetical protein CARUB_v10016938mg	gbpln	Capsella rubella	AT2G01480.1 | Symbols: | O-fucosyltransferase family protein | chr2:216980-220341 FORWARD LENGTH=567	489	567	0	116.0	93.0	98.0
Rsa1.0_02035.1.g31704.t1	gb|EOA24970.1| hypothetical protein CARUB_v10018267mg [Capsella rubella]	106	115	5.00E-20	108.5	68.9	80.2	hypothetical protein CARUB_v10018267mg	gbpln	Capsella rubella	AT2G01505.1 | Symbols: CLE16 | CLAVATA3/ESR-RELATED 16 | chr2:228926-229237 REVERSE LENGTH=103	106	103	5.00E-21	97.2	47.2	56.6
Rsa1.0_02035.1.g31705.t1	ref|NP_178260.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75216969|sp|Q9ZVF4.1|PP140_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g01510, mitochondrial; Flags: Precursor gi|3785980|gb|AAC67327.1| hypothetical protein [Arabidopsis thaliana] gi|330250369|gb|AEC05463.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	527	584	0	110.8	84.6	92.4	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT2G01510.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:230752-232506 REVERSE LENGTH=584	527	584	0	110.8	84.6	92.4
Rsa1.0_02035.1.g31706.t1	gb|EOA18445.1| hypothetical protein CARUB_v10006988mg [Capsella rubella]	248	683	3.00E-64	275.4	47.2	66.9	hypothetical protein CARUB_v10006988mg	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_02036.1.g31707.t1	ref|NP_197995.1| uncharacterized protein [Arabidopsis thaliana] gi|122214260|sp|Q3E936.1|MAKR1_ARATH RecName: Full=Probable membrane-associated kinase regulator 1 gi|332006156|gb|AED93539.1| uncharacterized protein AT5G26230 [Arabidopsis thaliana]	294	341	6.00E-94	116.0	78.2	84.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G26230.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9173517-9174542 REVERSE LENGTH=341	294	341	2.00E-96	116.0	78.2	84.4
Rsa1.0_02036.1.g31708.t1	gb|EOA15059.1| hypothetical protein CARUB_v10028420mg [Capsella rubella]	530	640	0	120.8	64.7	74.7	hypothetical protein CARUB_v10028420mg	gbpln	Capsella rubella	AT5G67240.1 | Symbols: SDN3 | small RNA degrading nuclease 3 | chr5:26824454-26828098 REVERSE LENGTH=782	530	782	0	147.5	61.7	71.1
Rsa1.0_02036.1.g31709.t1	ref|NP_198005.1| plastocyanin-like domain-containing protein / putative mavicyanin [Arabidopsis thaliana] gi|3319353|gb|AAC26242.1| contains similarity to copper-binding proteins [Arabidopsis thaliana] gi|45752728|gb|AAS76262.1| At5g26330 [Arabidopsis thaliana] gi|51968496|dbj|BAD42940.1| copper binding protein - like, predicted GPI-anchored protein [Arabidopsis thaliana] gi|332006169|gb|AED93552.1| plastocyanin-like domain-containing protein / putative mavicyanin [Arabidopsis thaliana]	388	187	1.00E-69	48.2	38.1	40.7	plastocyanin-like domain-containing protein / putative mavicyanin	gbpln	Arabidopsis thaliana	AT5G26330.1 | Symbols: | Cupredoxin superfamily protein | chr5:9241614-9242635 REVERSE LENGTH=187	388	187	3.00E-72	48.2	38.1	40.7
Rsa1.0_02036.1.g31710.t1	ref|NP_198006.1| sugar transport protein 13 [Arabidopsis thaliana] gi|85701281|sp|Q94AZ2.2|STP13_ARATH RecName: Full=Sugar transport protein 13; AltName: Full=Hexose transporter 13; AltName: Full=Multicopy suppressor of snf4 deficiency protein 1 gi|9965739|gb|AAG10146.1|AF250340_1 putative hexose transporter MSS1 [Arabidopsis thaliana] gi|3319354|gb|AAC26243.1| contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana] gi|15450649|gb|AAK96596.1| AT5g26340/F9D12_17 [Arabidopsis thaliana] gi|15487258|emb|CAC69074.1| STP13 protein [Arabidopsis thaliana] gi|332006170|gb|AED93553.1| sugar transport protein 13 [Arabidopsis thaliana]	534	526	0	98.5	93.8	96.4	sugar transport protein 13	gbpln	Arabidopsis thaliana	AT5G26340.1 | Symbols: MSS1, STP13, ATSTP13 | Major facilitator superfamily protein | chr5:9243851-9246994 REVERSE LENGTH=526	534	526	0	98.5	93.8	96.4
Rsa1.0_02036.1.g31711.t1	ref|XP_002872212.1| hypothetical protein ARALYDRAFT_489476 [Arabidopsis lyrata subsp. lyrata] gi|297318049|gb|EFH48471.1| hypothetical protein ARALYDRAFT_489476 [Arabidopsis lyrata subsp. lyrata]	1184	1193	0	100.8	88.3	94.8	hypothetical protein ARALYDRAFT_489476	gbpln	Arabidopsis lyrata	AT5G26570.1 | Symbols: PWD, OK1, ATGWD3 | catalytics;carbohydrate kinases;phosphoglucan, water dikinases | chr5:9261580-9267526 FORWARD LENGTH=1196	1184	1196	0	101.0	88.3	94.4

Rsa1.0_02036.1.g31712.t1	ref|XP_002872217.1| hypothetical protein ARALYDRAFT_910715 [Arabidopsis lyrata subsp. lyrata] gi|297318054|gb|EFH48476.1| hypothetical protein ARALYDRAFT_910715 [Arabidopsis lyrata subsp. lyrata]	80	81	6.00E-13	101.3	57.5	67.5	hypothetical protein ARALYDRAFT_910715	gbpln	Arabidopsis lyrata	AT5G26717.1 | Symbols: | Putative membrane lipoprotein | chr5:9284612-9284857 FORWARD LENGTH=81	80	81	2.00E-14	101.3	43.8	51.3
Rsa1.0_02036.1.g31713.t1	ref|NP_175703.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana] gi|12324642|gb|AAG52278.1|AC019018_15 putative replication protein; 94555-97079 [Arabidopsis thaliana] gi|332194750|gb|AEE32871.1| Nucleic acid-binding, OB-fold-like protein [Arabidopsis thaliana]	516	566	2.00E-91	109.7	36.2	59.1	Nucleic acid-binding, OB-fold-like protein	gbpln	Arabidopsis thaliana	AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566	516	566	4.00E-94	109.7	36.2	59.1
Rsa1.0_02037.1.g31714.t1	ref|XP_002866063.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] gi|297311898|gb|EFH42322.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]	284	288	1.00E-153	101.4	91.5	97.2	GTP-binding family protein	gbpln	Arabidopsis lyrata	AT5G54840.1 | Symbols: ATSGP1, SGP1 | Ras-related small GTP-binding family protein | chr5:22276611-22278328 REVERSE LENGTH=288	284	288	1.00E-148	101.4	90.8	96.8
Rsa1.0_02037.1.g31715.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02037.1.g31716.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02037.1.g31717.t1	gb|EOA13311.1| hypothetical protein CARUB_v10026347mg [Capsella rubella]	465	469	0	100.9	93.8	96.8	hypothetical protein CARUB_v10026347mg	gbpln	Capsella rubella	AT4G27070.1 | Symbols: TSB2 | tryptophan synthase beta-subunit 2 | chr4:13586564-13588619 FORWARD LENGTH=475	465	475	0	102.2	92.0	94.6
Rsa1.0_02037.1.g31718.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02037.1.g31719.t1	gb|EOA24904.1| hypothetical protein CARUB_v10018194mg [Capsella rubella]	93	147	1.00E-41	158.1	84.9	93.5	hypothetical protein CARUB_v10018194mg	gbpln	Capsella rubella	AT3G56490.1 | Symbols: HIT3, HINT1 | HIS triad family protein 3 | chr3:20941532-20943129 FORWARD LENGTH=147	93	147	5.00E-44	158.1	84.9	92.5
Rsa1.0_02038.1.g31720.t2	ref|NP_195721.5| uncharacterized protein [Arabidopsis thaliana] gi|26451774|dbj|BAC42982.1| unknown protein [Arabidopsis thaliana] gi|26452440|dbj|BAC43305.1| unknown protein [Arabidopsis thaliana] gi|51968902|dbj|BAD43143.1| unknown protein [Arabidopsis thaliana] gi|51969218|dbj|BAD43301.1| unknown protein [Arabidopsis thaliana] gi|51969306|dbj|BAD43345.1| unknown protein [Arabidopsis thaliana] gi|51969668|dbj|BAD43526.1| unknown protein [Arabidopsis thaliana] gi|51969694|dbj|BAD43539.1| unknown protein [Arabidopsis thaliana] gi|51969746|dbj|BAD43565.1| unknown protein [Arabidopsis thaliana] gi|51970048|dbj|BAD43716.1| unknown protein [Arabidopsis thaliana] gi|51970150|dbj|BAD43767.1| unknown protein [Arabidopsis thaliana] gi|51970160|dbj|BAD43772.1| unknown protein [Arabidopsis thaliana] gi|51970188|dbj|BAD43786.1| unknown protein [Arabidopsis thaliana] gi|51970232|dbj|BAD43808.1| unknown protein [Arabidopsis thaliana] gi|51970626|dbj|BAD44005.1| unknown protein [Arabidopsis thaliana] gi|51970642|dbj|BAD44013.1| unknown protein [Arabidopsis thaliana] gi|51970662|dbj|BAD44023.1| unknown protein [Arabidopsis thaliana]	440	438	1.00E-171	99.5	73.6	79.1	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G01010.1 | Symbols: | CONTAINS InterPro DOMAIN/s: GOLD (InterPro:IPR009038); Has 172 Blast hits to 172 proteins in 43 species: Archae - 0; Bacteria - 0; Metazoa - 95; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink). | chr5:1388-4924 REVERSE LENGTH=438	440	438	1.00E-173	99.5	73.6	79.1
Rsa1.0_02038.1.g31721.t1	ref|XP_002872959.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297318796|gb|EFH49218.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	482	507	0	105.2	76.3	84.2	mechanosensitive ion channel domain-containing protein	gbpln	Arabidopsis lyrata	AT4G00290.1 | Symbols: | Mechanosensitive ion channel protein | chr4:123097-125300 REVERSE LENGTH=497	482	497	0	103.1	75.1	82.8
Rsa1.0_02038.1.g31722.t1	ref|XP_002872960.1| PLDBETA2 [Arabidopsis lyrata subsp. lyrata] gi|297318797|gb|EFH49219.1| PLDBETA2 [Arabidopsis lyrata subsp. lyrata]	989	987	0	99.8	79.5	85.2	PLDBETA2	gbpln	Arabidopsis lyrata	AT4G00240.1 | Symbols: PLDBETA2 | phospholipase D beta 2 | chr4:106380-110718 REVERSE LENGTH=927	989	927	0	93.7	75.7	80.9
Rsa1.0_02038.1.g31723.t1	gb|AAG50886.1|AC025294_24 hypothetical protein [Arabidopsis thaliana]	314	629	1.00E-76	200.3	45.5	62.7	hypothetical protein	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8789471-8793208 FORWARD LENGTH=746	314	746	2.00E-53	237.6	35.0	48.4

<table>
<tr><td>Rsa1.0_02038.1.g31724.t3</td><td>emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]</td><td>1795</td><td>1274</td><td>0</td><td>71.0</td><td>29.5</td><td>40.2</td><td>RNA-directed DNA polymerase-like protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>1795</td><td>575</td><td>2.00E-52</td><td>32.0</td><td>8.7</td><td>14.0</td></tr>
<tr><td>Rsa1.0_02039.1.g31725.t1</td><td>gb|AFK47272.1| unknown [Lotus japonicus]</td><td>197</td><td>197</td><td>1.00E-103</td><td>100.0</td><td>90.4</td><td>97.0</td><td>unknown</td><td>gbpln</td><td>Lotus japonicus</td><td>AT2G17800.2 | Symbols: ARAC1, ATGP2, ATRAC1, ROP3, ATROP3 | Arabidopsis RAC-like 1 | chr2:7740313-7741942 FORWARD LENGTH=197</td><td>197</td><td>197</td><td>1.00E-101</td><td>100.0</td><td>97.0</td><td>99.0</td></tr>
<tr><td>Rsa1.0_02039.1.g31726.t1</td><td>gb|EOA16959.1| hypothetical protein CARUB_v10005187mg [Capsella rubella]</td><td>319</td><td>341</td><td>1.00E-88</td><td>106.9</td><td>69.0</td><td>79.0</td><td>hypothetical protein CARUB_v10005187mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT4G35940.2 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G17787.1). | chr4:17021672-17023593 FORWARD LENGTH=395</td><td>319</td><td>395</td><td>1.00E-66</td><td>123.8</td><td>62.1</td><td>73.4</td></tr>
<tr><td>Rsa1.0_02039.1.g31727.t1</td><td>ref|NP_195317.2| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|30690528|ref|NP_849503.1| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|42570170|ref|NP_849504.2| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|75154155|sp|Q8L7E9.1|MCAC1_ARATH RecName: Full=Protein MID1-COMPLEMENTING ACTIVITY 1 gi|22530910|gb|AAM96959.1| putative protein [Arabidopsis thaliana] gi|28059788|gb|AAO30093.1| putative protein [Arabidopsis thaliana] gi|124484595|dbj|BAF46389.1| Mca1 [Arabidopsis thaliana] gi|222423156|dbj|BAH19557.1| AT4G35920 [Arabidopsis thaliana] gi|332661189|gb|AEE86589.1| protein MID1-complementing activity 1 [Arabidopsis thaliana] gi|332661190|gb|AEE86590.1| PLAC8 domain-containing protein [Arabidopsis thaliana] gi|332661191|gb|AEE86591.1| PLAC8 domain-containing protein [Arabidopsis thaliana]</td><td>421</td><td>421</td><td>0</td><td>100.0</td><td>91.9</td><td>96.4</td><td>PLAC8 domain-containing protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G35920.2 | Symbols: MCA1 | PLAC8 family protein | chr4:17012106-17014192 REVERSE LENGTH=421</td><td>421</td><td>421</td><td>0</td><td>100.0</td><td>91.9</td><td>96.4</td></tr>
<tr><td>Rsa1.0_02039.1.g31728.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_02039.1.g31729.t1</td><td>ref|XP_002869051.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297314887|gb|EFH45310.1| predicted protein [Arabidopsis lyrata subsp. lyrata]</td><td>484</td><td>282</td><td>1.00E-96</td><td>58.3</td><td>44.8</td><td>48.8</td><td>predicted protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G35900.1 | Symbols: FD, FD-1, atbzip14 | Basic-leucine zipper (bZIP) transcription factor family protein | chr4:17004746-17005952 FORWARD LENGTH=285</td><td>484</td><td>285</td><td>1.00E-93</td><td>58.9</td><td>42.8</td><td>47.9</td></tr>
<tr><td>Rsa1.0_02039.1.g31730.t1</td><td>ref|NP_567991.1| winged-helix DNA-binding transcription factor family protein [Arabidopsis thaliana] gi|13877889|gb|AAK44022.1|AF370207_1 unknown protein [Arabidopsis thaliana] gi|22136918|gb|AAM91803.1| unknown protein [Arabidopsis thaliana] gi|332661185|gb|AEE86585.1| winged-helix DNA-binding transcription factor family protein [Arabidopsis thaliana]</td><td>507</td><td>523</td><td>1.00E-147</td><td>103.2</td><td>70.8</td><td>77.7</td><td>winged-helix DNA-binding transcription factor family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G35890.1 | Symbols: | winged-helix DNA-binding transcription factor family protein | chr4:16997433-17000410 FORWARD LENGTH=523</td><td>507</td><td>523</td><td>1.00E-150</td><td>103.2</td><td>70.8</td><td>77.7</td></tr>
<tr><td>Rsa1.0_02039.1.g31731.t1</td><td>ref|NP_195313.2| aspartyl protease family protein [Arabidopsis thaliana] gi|190576481|gb|ACE79041.1| At4g35880 [Arabidopsis thaliana] gi|222423134|dbj|BAH19546.1| AT4G35880 [Arabidopsis thaliana] gi|332661184|gb|AEE86584.1| aspartyl protease family protein [Arabidopsis thaliana]</td><td>529</td><td>524</td><td>0</td><td>99.1</td><td>87.9</td><td>92.8</td><td>aspartyl protease family protein</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT4G35880.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr4:16993339-16995721 FORWARD LENGTH=524</td><td>529</td><td>524</td><td>0</td><td>99.1</td><td>87.9</td><td>92.8</td></tr>
<tr><td>Rsa1.0_02040.1.g31732.t1</td><td>ref|XP_002876307.1| hypothetical protein ARALYDRAFT_906973 [Arabidopsis lyrata subsp. lyrata] gi|297322145|gb|EFH52566.1| hypothetical protein ARALYDRAFT_906973 [Arabidopsis lyrata subsp. lyrata]</td><td>88</td><td>80</td><td>2.00E-17</td><td>90.9</td><td>54.5</td><td>70.5</td><td>hypothetical protein ARALYDRAFT_906973</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G55515.1 | Symbols: DVL8, RTFL7 | ROTUNDIFOLIA like 7 | chr3:20590923-20591162 FORWARD LENGTH=79</td><td>88</td><td>79</td><td>9.00E-19</td><td>89.8</td><td>51.1</td><td>64.8</td></tr>
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<tr><td>Rsa1.0_02040.1.g31733.t1</td><td>ref|XP_002876308.1| hypothetical protein ARALYDRAFT_485979 [Arabidopsis lyrata subsp. lyrata] gi|297322146|gb|EFH52567.1| hypothetical protein ARALYDRAFT_485979 [Arabidopsis lyrata subsp. lyrata]</td><td>190</td><td>190</td><td>5.00E-81</td><td>100.0</td><td>86.8</td><td>89.5</td><td>hypothetical protein ARALYDRAFT_485979</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G55520.1 | Symbols: | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | chr3:20594177-20595128 FORWARD LENGTH=190</td><td>190</td><td>190</td><td>9.00E-83</td><td>100.0</td><td>86.8</td><td>88.9</td></tr>
<tr><td>Rsa1.0_02040.1.g31734.t2</td><td>ref|XP_002878037.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] gi|297323875|gb|EFH54296.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]</td><td>280</td><td>272</td><td>1.00E-138</td><td>97.1</td><td>90.7</td><td>92.1</td><td>zinc finger family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G55530.1 | Symbols: SDIR1 | RING/U-box superfamily protein | chr3:20595300-20597188 REVERSE LENGTH=273</td><td>280</td><td>273</td><td>1.00E-137</td><td>97.5</td><td>88.9</td><td>90.7</td></tr>
<tr><td>Rsa1.0_02040.1.g31735.t1</td><td>gb|EOA25935.1| hypothetical protein CARUB_v10019316mg [Capsella rubella]</td><td>357</td><td>433</td><td>1.00E-152</td><td>121.3</td><td>75.1</td><td>83.2</td><td>hypothetical protein CARUB_v10019316mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT2G39710.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr2:16562051-16563379 REVERSE LENGTH=442</td><td>357</td><td>442</td><td>1.00E-138</td><td>123.8</td><td>65.3</td><td>80.1</td></tr>
<tr><td>Rsa1.0_02040.1.g31736.t1</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>-</td><td>----</td><td>----</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td><td>#</td></tr>
<tr><td>Rsa1.0_02040.1.g31737.t1</td><td>ref|XP_002878039.1| hypothetical protein ARALYDRAFT_906980 [Arabidopsis lyrata subsp. lyrata] gi|297323877|gb|EFH54298.1| hypothetical protein ARALYDRAFT_906980 [Arabidopsis lyrata subsp. lyrata]</td><td>297</td><td>308</td><td>1.00E-117</td><td>103.7</td><td>87.5</td><td>92.3</td><td>hypothetical protein ARALYDRAFT_906980</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT3G55560.1 | Symbols: AGF2, AHL15 | AT-hook protein of GA feedback 2 | chr3:20604904-20605836 REVERSE LENGTH=310</td><td>297</td><td>310</td><td>1.00E-119</td><td>104.4</td><td>87.5</td><td>92.3</td></tr>
<tr><td>Rsa1.0_02041.1.g31738.t2</td><td>ref|XP_002888054.1| hypothetical protein ARALYDRAFT_893298 [Arabidopsis lyrata subsp. lyrata] gi|297333895|gb|EFH64313.1| hypothetical protein ARALYDRAFT_893298 [Arabidopsis lyrata subsp. lyrata]</td><td>76</td><td>768</td><td>3.00E-12</td><td>1010.5</td><td>60.5</td><td>68.4</td><td>hypothetical protein ARALYDRAFT_893298</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT1G61970.2 | Symbols: | Mitochondrial transcription termination factor family protein | chr1:22904713-22905969 FORWARD LENGTH=418</td><td>76</td><td>418</td><td>3.00E-14</td><td>550.0</td><td>60.5</td><td>71.1</td></tr>
<tr><td>Rsa1.0_02041.1.g31739.t1</td><td>gb|ABD65049.1| histone-lysine N-methyltransferase, putative [Brassica oleracea]</td><td>400</td><td>392</td><td>1.00E-168</td><td>98.0</td><td>79.0</td><td>83.3</td><td>histone-lysine N-methyltransferase, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47150.1 | Symbols: | YDG/SRA domain-containing protein | chr5:19150807-19151793 FORWARD LENGTH=328</td><td>400</td><td>328</td><td>1.00E-101</td><td>82.0</td><td>51.0</td><td>63.3</td></tr>
<tr><td>Rsa1.0_02041.1.g31740.t1</td><td>gb|ABD65042.1| GATA zinc finger containing protein [Brassica oleracea]</td><td>473</td><td>471</td><td>0</td><td>99.6</td><td>85.2</td><td>90.3</td><td>GATA zinc finger containing protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47140.1 | Symbols: GATA27 | GATA transcription factor 27 | chr5:19145108-19147303 FORWARD LENGTH=470</td><td>473</td><td>470</td><td>0</td><td>99.4</td><td>79.3</td><td>88.4</td></tr>
<tr><td>Rsa1.0_02041.1.g31741.t1</td><td>gb|AAK73101.1|AF390555_1 Bax inhibitor 1 [Brassica napus] gi|17981374|gb|AAL50979.1|AF453320_1 bax inhibitor-like protein [Brassica oleracea]</td><td>247</td><td>247</td><td>1.00E-126</td><td>100.0</td><td>96.8</td><td>99.6</td><td>Bax inhibitor 1</td><td>gbpln</td><td>Brassica napus</td><td>AT5G47120.1 | Symbols: ATBI-1, BI-1, ATBI1, BI1 | BAX inhibitor 1 | chr5:19136071-19137585 FORWARD LENGTH=247</td><td>247</td><td>247</td><td>1.00E-120</td><td>100.0</td><td>90.7</td><td>94.3</td></tr>
<tr><td>Rsa1.0_02041.1.g31742.t1</td><td>gb|ABD65018.1| Lil3 protein, putative [Brassica oleracea]</td><td>189</td><td>225</td><td>1.00E-47</td><td>119.0</td><td>66.1</td><td>74.1</td><td>Lil3 protein, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47110.1 | Symbols: LIL3:2 | Chlorophyll A-B binding family protein | chr5:19134218-19135238 REVERSE LENGTH=258</td><td>189</td><td>258</td><td>3.00E-35</td><td>136.5</td><td>43.4</td><td>51.9</td></tr>
<tr><td>Rsa1.0_02041.1.g31743.t1</td><td>gb|ABD65033.1| YDG/SRA domain containing protein [Brassica oleracea]</td><td>101</td><td>498</td><td>4.00E-40</td><td>493.1</td><td>77.2</td><td>84.2</td><td>YDG/SRA domain containing protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47160.1 | Symbols: | YDG/SRA domain-containing protein | chr5:19156731-19157978 FORWARD LENGTH=415</td><td>101</td><td>415</td><td>1.00E-14</td><td>410.9</td><td>36.6</td><td>58.4</td></tr>
<tr><td>Rsa1.0_02041.1.g31744.t1</td><td>gb|ABD65029.1| C3HC4 type (RING finger) Zinc finger containing protein [Brassica oleracea]</td><td>196</td><td>185</td><td>2.00E-85</td><td>94.4</td><td>79.1</td><td>83.2</td><td>C3HC4 type (RING finger) Zinc finger containing protein</td><td>gbpln</td><td>Brassica oleracea</td><td>AT1G70910.1 | Symbols: DEP | RING/U-box superfamily protein | chr1:26734155-26734640 FORWARD LENGTH=161</td><td>196</td><td>161</td><td>5.00E-27</td><td>82.1</td><td>39.3</td><td>50.5</td></tr>
<tr><td>Rsa1.0_02041.1.g31745.t1</td><td>gb|ABD64921.1| calcineurin B-like protein, putative [Brassica oleracea]</td><td>213</td><td>213</td><td>1.00E-119</td><td>100.0</td><td>98.6</td><td>99.5</td><td>calcineurin B-like protein, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47100.1 | Symbols: CBL9, ATCBL9 | calcineurin B-like protein 9 | chr5:19129896-19131727 REVERSE LENGTH=213</td><td>213</td><td>213</td><td>1.00E-119</td><td>100.0</td><td>97.7</td><td>98.6</td></tr>
<tr><td>Rsa1.0_02041.1.g31746.t1</td><td>gb|ABD65045.1| hypothetical protein 26.t00106 [Brassica oleracea]</td><td>299</td><td>370</td><td>1.00E-139</td><td>123.7</td><td>90.0</td><td>94.0</td><td>hypothetical protein 26.t00106</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47090.1 | Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2052, coiled-coil (InterPro:IPR018613); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:19127274-19128493 FORWARD LENGTH=310</td><td>299</td><td>310</td><td>1.00E-129</td><td>103.7</td><td>80.3</td><td>88.0</td></tr>
<tr><td>Rsa1.0_02041.1.g31747.t1</td><td>gb|ABD65048.1| Casein kinase II beta chain, putative [Brassica oleracea]</td><td>246</td><td>276</td><td>1.00E-127</td><td>112.2</td><td>91.5</td><td>94.3</td><td>Casein kinase II beta chain, putative</td><td>gbpln</td><td>Brassica oleracea</td><td>AT5G47080.1 | Symbols: CKB1 | casein kinase II beta chain 1 | chr5:19124969-19126397 REVERSE LENGTH=287</td><td>246</td><td>287</td><td>1.00E-116</td><td>116.7</td><td>87.8</td><td>92.3</td></tr>
<tr><td>Rsa1.0_02041.1.g31748.t1</td><td>ref|XP_002863522.1| hypothetical protein ARALYDRAFT_917015 [Arabidopsis lyrata subsp. lyrata] gi|297309357|gb|EFH39781.1| hypothetical protein ARALYDRAFT_917015 [Arabidopsis lyrata subsp. lyrata]</td><td>516</td><td>1165</td><td>0</td><td>225.8</td><td>91.3</td><td>95.3</td><td>hypothetical protein ARALYDRAFT_917015</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G45140.1 | Symbols: NRPC2 | nuclear RNA polymerase C2 | chr5:18247416-18257713 REVERSE LENGTH=1161</td><td>516</td><td>1161</td><td>0</td><td>225.0</td><td>89.3</td><td>93.6</td></tr>
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Rsa1.0_02041.1.g31749.t1	ref|XP_002865280.1| hypothetical protein ARALYDRAFT_494469 [Arabidopsis lyrata subsp. lyrata] gi|297311115|gb|EFH41539.1| hypothetical protein ARALYDRAFT_494469 [Arabidopsis lyrata subsp. lyrata]	158	586	6.00E−16	370.9	25.3	27.2	hypothetical protein ARALYDRAFT_494469	gbpln	Arabidopsis lyrata	AT5G45130.1 | Symbols: ATRAB5A, ATRABF2A, RABF2A, RAB5A, RHA1, ATRAB−F2A, RAB−F2A | RAB homolog 1 | chr5:18244495−18246060 FORWARD LENGTH=200	158	200	2.00E−18	126.6	28.5	29.1
Rsa1.0_02041.1.g31750.t1	gb|AAP37968.1| seed specific protein Bn15D12A [Brassica napus]	175	157	1.00E−74	89.7	77.7	84.0	seed specific protein Bn15D12A	gbpln	Brassica napus	AT5G46960.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19062220−19062744 REVERSE LENGTH=174	175	174	3.00E−59	99.4	64.6	76.6
Rsa1.0_02041.1.g31751.t1	gb|AAC64879.1| Similar to gb|X80472 STS15 gene from Solanum tuberosum [Arabidopsis thaliana]	191	182	1.00E−29	95.3	42.9	57.6	Similar to gb|X80472 STS15 gene from Solanum tuberosum	gbpln	Arabidopsis thaliana	AT1G54620.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:20400437−20401015 REVERSE LENGTH=192	191	192	4.00E−32	100.5	42.9	57.6
Rsa1.0_02041.1.g31752.t1	pir||T00833 RNA−directed DNA polymerase homolog T13L16.7 − Arabidopsis thaliana (fragment)	258	1365	7.00E−32	529.1	29.5	37.6	RNA−directed DNA polymerase homolog T13L16.7 − Arabidopsis thaliana (fragment)	----	----	ATMG00310.1 | Symbols: ORF154 | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chrM:90883−91347 REVERSE LENGTH=154	258	154	1.00E−30	59.7	27.5	33.7
Rsa1.0_02041.1.g31753.t1	ref|NP_199509.1| plant invertase/pectin methylesterase inhibitor domain−containing protein [Arabidopsis thaliana] gi|9759440|dbj|BAB10237.1| unnamed protein product [Arabidopsis thaliana] gi|332008071|gb|AED95454.1| plant invertase/pectin methylesterase inhibitor domain−containing protein [Arabidopsis thaliana]	191	184	3.00E−29	96.3	40.3	55.5	plant invertase/pectin methylesterase inhibitor domain−containing protein	gbpln	Arabidopsis thaliana	AT5G46980.1 | Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr5:19065453−19066007 REVERSE LENGTH=184	191	184	1.00E−31	96.3	40.3	55.5
Rsa1.0_02042.1.g31754.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_02042.1.g31755.t15	gb|AAD30632.1|AC006085_5 Hypothetical protein [Arabidopsis thaliana]	484	1295	2.00E−40	267.6	26.9	39.7	Hypothetical protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02042.1.g31756.t1	#	#	#	#	#	#	#	−	----	----	#	#	#	#	#	#	#
Rsa1.0_02042.1.g31757.t7	gb|AAF18630.1|AC006228_1 F5J5.1 [Arabidopsis thaliana]	649	1463	9.00E−64	225.4	21.9	31.4	F5J5.1	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02043.1.g31758.t1	ref|NP_178143.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana] gi|42572199|ref|NP_974190.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana] gi|145327755|ref|NP_001077853.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana] gi|75262222|sp|Q9C977.1|PP135_ARATH RecName: Full=Pentatricopeptide repeat−containing protein At1g80270, mitochondrial; Flags: Precursor gi|12324975|gb|AAG52431.1|AC018848_2 hypothetical protein; 8785−10851 [Arabidopsis thaliana] gi|17064898|gb|AAL32603.1| Unknown protein [Arabidopsis thaliana] gi|20259918|gb|AAM13306.1| unknown protein [Arabidopsis thaliana] gi|332198258|gb|AEE36379.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana] gi|332198259|gb|AEE36380.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana] gi|332198260|gb|AEE36381.1| pentatricopeptide repeat−containing protein [Arabidopsis thaliana]	610	596	0	97.7	82.8	89.7	pentatricopeptide repeat−containing protein	gbpln	Arabidopsis thaliana	AT1G80270.3 | Symbols: PPR596 | PENTATRICOPEPTIDE REPEAT 596 | chr1:30181265−30183331 FORWARD LENGTH=596	610	596	0	97.7	82.8	89.7
Rsa1.0_02043.1.g31759.t1	ref|XP_002893119.1| tubulin family protein [Arabidopsis lyrata subsp. lyrata] gi|297338961|gb|EFH69378.1| tubulin family protein [Arabidopsis lyrata subsp. lyrata]	986	981	0	99.5	80.0	87.2	tubulin family protein	gbpln	Arabidopsis lyrata	AT1G80260.1 | Symbols: emb1427 | Spc97 / Spc98 family of spindle pole body (SBP) component | chr1:30175924−30180511 FORWARD LENGTH=995	986	995	0	100.9	82.2	88.7
Rsa1.0_02043.1.g31760.t1	ref|XP_002887838.1| hypothetical protein ARALYDRAFT_340195 [Arabidopsis lyrata subsp. lyrata] gi|297333679|gb|EFH64097.1| hypothetical protein ARALYDRAFT_340195 [Arabidopsis lyrata subsp. lyrata]	369	371	0	100.5	88.1	93.5	hypothetical protein ARALYDRAFT_340195	gbpln	Arabidopsis lyrata	AT1G80240.1 | Symbols: | Protein of unknown function, DUF642 | chr1:30171520−30172799 REVERSE LENGTH=370	369	370	0	100.3	87.8	93.8
Rsa1.0_02043.1.g31761.t1	emb|CCD74552.1| predicted protein [Arabidopsis halleri subsp. halleri]	265	249	2.00E−63	94.0	48.7	57.4	predicted protein	gbpln	Arabidopsis halleri	AT1G15430.2 | Symbols: | Protein of unknown function (DUF1644) | chr1:5305011−5305790 FORWARD LENGTH=259	265	259	1.00E−61	97.7	47.2	59.6

Rsa1.0_02043.1.g31762.t1	ref|XP_002884611.1| hypothetical protein ARALYDRAFT_478001 [Arabidopsis lyrata subsp. lyrata] gi|297330451|gb|EFH60870.1| hypothetical protein ARALYDRAFT_478001 [Arabidopsis lyrata subsp. lyrata]	203	413	5.00E-52	203.4	53.7	61.1	hypothetical protein ARALYDRAFT_478001	gbpln	Arabidopsis lyrata	AT1G80210.1 | Symbols: BRCC36A, AtBRCC36A | Mov34/MPN/PAD-1 family protein | chr1:30163357-30165628 REVERSE LENGTH=406	203	406	3.00E-53	200.0	47.8	50.7
Rsa1.0_02043.1.g31763.t1	ref|NP_178136.1| GINS complex subunit 1 [Arabidopsis thaliana] gi|5902373|gb|AAD55475.1|AC009322_15 Unknown protein [Arabidopsis thaliana] gi|34365591|gb|AAQ65107.1| At1g80190 [Arabidopsis thaliana] gi|51969246|dbj|BAD43315.1| At1g80190 [Arabidopsis thaliana] gi|332198247|gb|AEE36368.1| GINS complex subunit 1-like protein [Arabidopsis thaliana]	197	201	3.00E-99	102.0	85.8	95.4	GINS complex subunit 1	gbpln	Arabidopsis thaliana	AT1G80190.1 | Symbols: PSF1 | partner of SLD five 1 | chr1:30159476-30161115 FORWARD LENGTH=201	197	201	1.00E-102	102.0	85.8	95.4
Rsa1.0_02043.1.g31764.t1	ref|NP_178101.3| golgin candidate 5 [Arabidopsis thaliana] gi|186496537|ref|NP_001117622.1| golgin candidate 5 [Arabidopsis thaliana] gi|334184030|ref|NP_001185442.1| golgin candidate 5 [Arabidopsis thaliana] gi|122175613|sp|Q0WVL7.1|GOGC5_ARATH RecName: Full=Golgin candidate 5; Short=AtGC5 gi|110741773|dbj|BAE98831.1| hypothetical protein [Arabidopsis thaliana] gi|164708704|gb|ABY67249.1| putative TMF-like protein [Arabidopsis thaliana] gi|332198186|gb|AEE36307.1| golgin candidate 5 [Arabidopsis thaliana] gi|332198187|gb|AEE36308.1| golgin candidate 5 [Arabidopsis thaliana] gi|332198189|gb|AEE36310.1| golgin candidate 5 [Arabidopsis thaliana]	946	956	0	101.1	85.9	90.7	golgin candidate 5	gbpln	Arabidopsis thaliana	AT1G79830.3 | Symbols: GC5 | golgin candidate 5 | chr1:30028110-30033508 REVERSE LENGTH=956	946	956	0	101.1	85.9	90.7
Rsa1.0_02043.1.g31765.t1	ref|XP_002887858.1| hypothetical protein ARALYDRAFT_477286 [Arabidopsis lyrata subsp. lyrata] gi|297333699|gb|EFH64117.1| hypothetical protein ARALYDRAFT_477286 [Arabidopsis lyrata subsp. lyrata]	547	495	0	90.5	82.8	85.9	hypothetical protein ARALYDRAFT_477286	gbpln	Arabidopsis lyrata	AT1G79820.2 | Symbols: SGB1 | Major facilitator superfamily protein | chr1:30022581-30026771 REVERSE LENGTH=495	547	495	0	90.5	82.8	85.6
Rsa1.0_02043.1.g31766.t1	ref|NP_565222.1| peroxin-2 [Arabidopsis thaliana] gi|34098692|sp|Q9CA86.1|PEX2_ARATH RecName: Full=Peroxisome biogenesis protein 2; AltName: Full=E3 ubiquitin-protein ligase PEX2; AltName: Full=Peroxin-2; Short=AtPEX2; Short=AthPEX2; AltName: Full=Pex2p gi|12324593|gb|AAG52254.1|AC011717_22 putative RING finger protein; 84236-82024 [Arabidopsis thaliana] gi|17381214|gb|AAL36419.1| unknown protein [Arabidopsis thaliana] gi|20465819|gb|AAM20014.1| unknown protein [Arabidopsis thaliana] gi|332198180|gb|AEE36301.1| peroxin-2 [Arabidopsis thaliana]	360	333	1.00E-168	92.5	84.2	87.5	peroxin-2	gbpln	Arabidopsis thaliana	AT1G79810.1 | Symbols: TED3, PEX2, ATPEX2 | Pex2/Pex12 N-terminal domain-containing protein / zinc finger (C3HC4-type RING finger) family protein | chr1:30019944-30022156 FORWARD LENGTH=333	360	333	1.00E-171	92.5	84.2	87.5
Rsa1.0_02043.1.g31767.t1	ref|NP_178098.1| early nodulin-like protein 7 [Arabidopsis thaliana] gi|7715594|gb|AAF68112.1|AC010793_7 F20B17.22 [Arabidopsis thaliana] gi|12324596|gb|AAG52257.1|AC011717_25 hypothetical protein; 85631-84963 [Arabidopsis thaliana] gi|67633502|gb|AAY78675.1| plastocyanin-like domain-containing protein [Arabidopsis thaliana] gi|332198179|gb|AEE36300.1| early nodulin-like protein 7 [Arabidopsis thaliana]	195	192	3.00E-60	98.5	58.5	65.1	early nodulin-like protein 7	gbpln	Arabidopsis thaliana	AT1G79800.1 | Symbols: ENODL7, AtENODL7 | early nodulin-like protein 7 | chr1:30018549-30019217 FORWARD LENGTH=192	195	192	1.00E-62	98.5	58.5	65.1
Rsa1.0_02043.1.g31768.t1	gb|EOA35644.1| hypothetical protein CARUB_v10020861mg [Capsella rubella]	258	245	1.00E-105	95.0	74.4	80.6	hypothetical protein CARUB_v10020861mg	gbpln	Capsella rubella	AT1G79790.1 | Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr1:30016987-30018186 REVERSE LENGTH=245	258	245	1.00E-106	95.0	72.5	79.8

Rsa1.0_02043.1.g31769.t1	ref|XP_002889325.1| F20B17.20 [Arabidopsis lyrata subsp. lyrata] gi|297335166|gb|EFH65584.1| F20B17.20 [Arabidopsis lyrata subsp. lyrata]	381	363	1.00E-141	95.3	74.5	81.9	F20B17.20	gbpln	Arabidopsis lyrata	AT1G79780.1 | Symbols: | Uncharacterised protein family (UPF0497) | chr1:30015930-30016856 FORWARD LENGTH=187	381	187	5.00E-73	49.1	38.6	41.5
Rsa1.0_02043.1.g31770.t1	gb|EOA35512.1| hypothetical protein CARUB_v10020719mg [Capsella rubella]	320	299	1.00E-119	93.4	71.3	79.7	hypothetical protein CARUB_v10020719mg	gbpln	Capsella rubella	AT1G79760.1 | Symbols: DTA4 | downstream target of AGL15-4 | chr1:30012054-30013042 FORWARD LENGTH=299	320	299	1.00E-118	93.4	67.8	74.4
Rsa1.0_02043.1.g31771.t1	dbj|BAJ33663.1| unnamed protein product [Thellungiella halophila]	1458	1469	0	100.8	96.0	98.1	unnamed protein product	----	----	AT1G59870.1 | Symbols: PEN3, PDR8, ATPDR8, ABCG36, ATABCG36 | ABC-2 and Plant PDR ABC-type transporter family protein | chr1:22034661-22039844 FORWARD LENGTH=1469	1458	1469	0	100.8	92.9	96.3
Rsa1.0_02044.1.g31772.t1	gb|AAG51046.1|AC069473_8 gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]	409	1499	9.00E-18	366.5	13.0	15.4	gypsy/Ty-3 retroelement polyprotein; 69905-74404	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02044.1.g31773.t1	ref|XP_002888245.1| hypothetical protein ARALYDRAFT_475439 [Arabidopsis lyrata subsp. lyrata] gi|297334086|gb|EFH64504.1| hypothetical protein ARALYDRAFT_475439 [Arabidopsis lyrata subsp. lyrata]	2564	2607	0	101.7	86.3	91.3	hypothetical protein ARALYDRAFT_475439	gbpln	Arabidopsis lyrata	AT1G58250.1 | Symbols: SAB | Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain | chr1:21587317-21601373 REVERSE LENGTH=2607	2564	2607	0	101.7	86.3	91.3
Rsa1.0_02045.1.g31774.t1	ref|NP_196765.2| omega-amidase [Arabidopsis thaliana] gi|19715574|gb|AAL91613.1| AT5g12040/F14F18_210 [Arabidopsis thaliana] gi|20147243|gb|AAM10335.1| AT5g12040/F14F18_210 [Arabidopsis thaliana] gi|332004371|gb|AED91754.1| Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein [Arabidopsis thaliana]	58	369	9.00E-18	636.2	74.1	77.6	omega-amidase	gbpln	Arabidopsis thaliana	AT5G12040.1 | Symbols: | Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein | chr5:3885162-3887772 FORWARD LENGTH=369	58	369	2.00E-20	636.2	74.1	77.6
Rsa1.0_02045.1.g31775.t1	ref|NP_196766.1| uncharacterized protein [Arabidopsis thaliana] gi|13877841|gb|AAK43998.1|AF370183_1 putative serine rich protein [Arabidopsis thaliana] gi|7573372|emb|CAB87678.1| putative serine rich protein [Arabidopsis thaliana] gi|16323506|gb|AAL15247.1| putative serine rich protein [Arabidopsis thaliana] gi|332004373|gb|AED91756.1| uncharacterized protein AT5G12050 [Arabidopsis thaliana]	360	362	1.00E-112	100.6	78.6	84.4	uncharacterized protein	gbpln	Arabidopsis thaliana	AT5G12050.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13980.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:3890213-3891301 FORWARD LENGTH=362	360	362	1.00E-114	100.6	78.6	84.4
Rsa1.0_02045.1.g31776.t5	gb|EOA20213.1| hypothetical protein CARUB_v10000507mg [Capsella rubella]	589	605	0	102.7	73.7	83.2	hypothetical protein CARUB_v10000507mg	gbpln	Capsella rubella	AT5G12120.1 | Symbols: | Ubiquitin-associated/translation elongation factor EF1B protein | chr5:3916229-3918088 REVERSE LENGTH=619	589	619	0	105.1	72.7	81.8
Rsa1.0_02045.1.g31777.t1	ref|NP_568257.1| TerC integral membrane domain-containing protein [Arabidopsis thaliana] gi|332004383|gb|AED91766.1| protein pigment defective 149 [Arabidopsis thaliana]	400	384	1.00E-150	96.0	73.0	79.5	TerC integral membrane domain-containing protein	gbpln	Arabidopsis thaliana	AT5G12130.1 | Symbols: PDE149, ATTERC | integral membrane TerC family protein | chr5:3919613-3922154 FORWARD LENGTH=384	400	384	1.00E-153	96.0	73.0	79.5
Rsa1.0_02045.1.g31778.t1	gb|ADK13075.1| phytocystatin 1-2 [Brassica rapa subsp. pekinensis]	99	101	3.00E-45	102.0	93.9	97.0	phytocystatin 1-2	gbpln	Brassica rapa	AT5G12140.1 | Symbols: ATCYS1, CYS1 | cystatin-1 | chr5:3923295-3923936 REVERSE LENGTH=101	99	101	4.00E-47	102.0	91.9	96.0
Rsa1.0_02045.1.g31779.t1	ref|XP_002871515.1| hypothetical protein ARALYDRAFT_488059 [Arabidopsis lyrata subsp. lyrata] gi|297317352|gb|EFH47774.1| hypothetical protein ARALYDRAFT_488059 [Arabidopsis lyrata subsp. lyrata]	458	454	0	99.1	82.1	88.9	hypothetical protein ARALYDRAFT_488059	gbpln	Arabidopsis lyrata	AT5G12170.2 | Symbols: CLT3 | CRT (chloroquine-resistance transporter)-like transporter 3 | chr5:3931649-3934961 FORWARD LENGTH=452	458	452	0	98.7	81.9	88.4
Rsa1.0_02045.1.g31780.t1	gb|EOA22225.1| hypothetical protein CARUB_v10002812mg [Capsella rubella]	523	530	0	101.3	96.6	98.1	hypothetical protein CARUB_v10002812mg	gbpln	Capsella rubella	AT5G12180.1 | Symbols: CPK17 | calcium-dependent protein kinase 17 | chr5:3937136-3939323 FORWARD LENGTH=528	523	528	0	101.0	95.6	97.7
Rsa1.0_02045.1.g31781.t1	gb|EOA19550.1| hypothetical protein CARUB_v10002551mg [Capsella rubella]	323	369	6.00E-85	114.2	46.4	52.9	hypothetical protein CARUB_v10002551mg	gbpln	Capsella rubella	AT5G12270.1 | Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:3970131-3971301 REVERSE LENGTH=360	323	360	7.00E-82	111.5	47.1	52.6
Rsa1.0_02046.1.g31782.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_02046.1.g31783.t1	ref|XP_002865850.1| kinase family protein [Arabidopsis lyrata subsp. lyrata] gi|297311685|gb|EFH42109.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	740	812	0	109.7	74.9	85.1	kinase family protein	gbpln	Arabidopsis lyrata	AT5G51270.1 | Symbols: | U-box domain-containing protein kinase family protein | chr5:20835137-20838262 REVERSE LENGTH=819	740	819	0	110.7	70.7	82.4
Rsa1.0_02046.1.g31784.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02046.1.g31785.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02046.1.g31786.t1	gb|ABD65636.1| hypothetical protein 23.t00055 [Brassica oleracea]	100	414	1.00E-12	414.0	45.0	63.0	hypothetical protein 23.t00055	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_02046.1.g31787.t1	gb|ABW81060.1| GagPol3 [Arabidopsis lyrata subsp. lyrata]	131	1103	4.00E-32	842.0	53.4	67.9	GagPol3	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_02046.1.g31788.t1	emb|CCD74471.1| myosin heavy chain-like protein [Arabidopsis halleri subsp. halleri]	458	788	2.00E-11	172.1	10.0	16.4	myosin heavy chain-like protein	gbpln	Arabidopsis halleri	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae - 15; Bacteria - 116; Metazoa - 677; Fungi - 267; Plants - 154; Viruses - 11; Other Eukaryotes - 609 (source: NCBI BLink). | chr1:18963205-18965571 FORWARD LENGTH=681	458	681	7.00E-11	148.7	8.1	14.8
Rsa1.0_02046.1.g31789.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02046.1.g31790.t1	ref|NP_199959.2| haloacid dehalogenase-like hydrolase domain-containing protein [Arabidopsis thaliana] gi|20260496|gb|AAM13146.1| trehalose-6-phosphate phosphatase [Arabidopsis thaliana] gi|30725608|gb|AAP37826.1| At5g51460 [Arabidopsis thaliana] gi|332008703|gb|AED96086.1| trehalose-phosphate phosphatase A [Arabidopsis thaliana]	379	384	0	101.3	86.5	94.2	haloacid dehalogenase-like hydrolase domain-containing protein	gbpln	Arabidopsis thaliana	AT5G51460.2 | Symbols: ATTPPA | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:20902266-20904292 FORWARD LENGTH=384	379	384	0	101.3	86.5	94.2
Rsa1.0_02047.1.g31791.t1	gb|ABD65057.1| hypothetical protein 27.t00123 [Brassica oleracea]	527	190	7.00E-34	36.1	19.7	22.8	hypothetical protein 27.t00123	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_02047.1.g31792.t1	gb|ABD65091.1| hypothetical protein 31.t00049 [Brassica oleracea]	505	530	3.00E-83	105.0	39.4	55.4	hypothetical protein 31.t00049	gbpln	Brassica oleracea	#	#	#	#	#	#	#
Rsa1.0_02047.1.g31793.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02047.1.g31794.t1	emb|CAN83791.1| hypothetical protein VITISV_031681 [Vitis vinifera]	402	968	2.00E-42	240.8	24.6	32.1	hypothetical protein VITISV_031681	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_02047.1.g31795.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02047.1.g31796.t1	gb|AAG52027.1|AC022456_8 Athila ORF 1, putative; 43045-40843 [Arabidopsis thaliana]	686	530	3.00E-14	77.3	6.6	10.6	Athila ORF 1, putative; 43045-40843	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02047.1.g31797.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	247	940	6.00E-57	380.6	43.3	55.9	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02047.1.g31798.t1	gb|AAD17398.1| putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	1112	1225	0	110.2	43.2	59.7	putative non-LTR retroelement reverse transcriptase	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	1112	575	6.00E-36	51.7	12.1	20.0
Rsa1.0_02047.1.g31799.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02048.1.g31800.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02048.1.g31801.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02048.1.g31802.t6	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02048.1.g31803.t6	emb|CAN79562.1| hypothetical protein VITISV_020822 [Vitis vinifera]	859	1027	0	119.6	48.2	66.0	hypothetical protein VITISV_020822	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_02048.1.g31804.t1	emb|CAN67735.1| hypothetical protein VITISV_012279 [Vitis vinifera]	601	476	2.00E-28	79.2	19.8	29.5	hypothetical protein VITISV_012279	gbpln	Vitis vinifera	#	#	#	#	#	#	#
Rsa1.0_02048.1.g31805.t1	emb|CAB39637.1| putative protein [Arabidopsis thaliana] gi|7267665|emb|CAB78093.1| putative protein [Arabidopsis thaliana] gi|91805577|gb|ABE65517.1| hypothetical protein At4g09700 [Arabidopsis thaliana]	329	371	3.00E-59	112.8	35.0	50.8	putative protein	gbpln	Arabidopsis thaliana	AT5G36228.1 | Symbols: | nucleic acid binding;zinc ion binding | chr5:14271691-14272776 FORWARD LENGTH=361	329	361	7.00E-21	109.7	18.8	30.7

Rsa1.0_02048.1.g31806.t1	ref|XP_002893916.1| co-chaperone grpE family protein [Arabidopsis lyrata subsp. lyrata] gi|297339758|gb|EFH70175.1| co-chaperone grpE family protein [Arabidopsis lyrata subsp. lyrata]	267	272	8.00E-96	101.9	69.7	79.4	co-chaperone grpE family protein	gbpln	Arabidopsis lyrata	AT1G36390.2 | Symbols: | Co-chaperone GrpE family protein | chr1:13701811-13703524 REVERSE LENGTH=279	267	279	2.00E-95	104.5	66.7	75.3
Rsa1.0_02048.1.g31807.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02048.1.g31808.t5	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	1152	1838	0	159.5	31.7	41.8	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02048.1.g31809.t3	gb|ABW81018.1| gag-pol polymerase [Arabidopsis lyrata subsp. lyrata]	905	672	4.00E-62	74.3	17.6	26.6	gag-pol polymerase	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_02049.1.g31810.t1	gb|AAD19784.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	97	1501	4.00E-11	1547.4	47.4	70.1	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02049.1.g31811.t3	gb|AAD43146.1|AC007504_1 Hypothetical Protein [Arabidopsis thaliana]	488	258	1.00E-78	52.9	30.3	35.2	Hypothetical Protein	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	488	696	2.00E-28	142.6	15.6	25.4
Rsa1.0_02049.1.g31812.t5	gb|EOA24093.1| hypothetical protein CARUB_v10017323mg, partial [Capsella rubella]	406	423	1.00E-103	104.2	51.5	66.7	hypothetical protein CARUB_v10017323mg, partial	gbpln	Capsella rubella	AT3G26010.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:9511901-9513145 FORWARD LENGTH=414	406	414	1.00E-105	102.0	51.7	67.7
Rsa1.0_02049.1.g31813.t1	ref|XP_002865557.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297311392|gb|EFH41816.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	110	143	7.00E-16	130.0	38.2	54.5	predicted protein	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_02049.1.g31814.t1	gb|ABD65076.1| SLL3 ORF2 protein, putative [Brassica oleracea]	350	443	3.00E-71	126.6	42.3	57.1	SLL3 ORF2 protein, putative	gbpln	Brassica oleracea	AT4G03740.1 | Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr4:1661992-1663515 REVERSE LENGTH=345	350	345	2.00E-14	98.6	24.9	40.3
Rsa1.0_02049.1.g31815.t1	ref|NP_197490.1| putative PRLI-interacting factor [Arabidopsis thaliana] gi|222422845|dbj|BAH19409.1| AT5G19900 [Arabidopsis thaliana] gi|332005380|gb|AED92763.1| putative PRLI-interacting factor [Arabidopsis thaliana]	504	494	6.00E-85	98.0	41.1	51.2	putative PRLI-interacting factor	gbpln	Arabidopsis thaliana	AT5G19900.1 | Symbols: | PRLI-interacting factor, putative | chr5:6728561-6730045 REVERSE LENGTH=494	504	494	1.00E-87	98.0	41.1	51.2
Rsa1.0_02050.1.g31816.t1	dbj|BAE98930.1| hypothetical protein [Arabidopsis thaliana]	219	735	2.00E-17	335.6	19.2	19.6	hypothetical protein	gbpln	Arabidopsis thaliana	AT2G40400.2 | Symbols: | Protein of unknown function (DUF399 and DUF3411) | chr2:16869363-16872569 FORWARD LENGTH=735	219	735	8.00E-20	335.6	19.2	19.6
Rsa1.0_02050.1.g31817.t6	ref|XP_002874656.1| hypothetical protein ARALYDRAFT_911406 [Arabidopsis lyrata subsp. lyrata] gi|297320493|gb|EFH50915.1| hypothetical protein ARALYDRAFT_911406 [Arabidopsis lyrata subsp. lyrata]	1167	983	0	84.2	62.1	69.6	hypothetical protein ARALYDRAFT_911406	gbpln	Arabidopsis lyrata	AT4G10930.1 | Symbols: | unknown protein; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:6705178-6708846 REVERSE LENGTH=984	1167	984	0	84.3	61.3	68.4
Rsa1.0_02050.1.g31818.t1	dbj|BAB41214.1| putative transcriptional coactivator [Brassica rapa]	162	165	4.00E-67	101.9	89.5	95.7	putative transcriptional coactivator	gbpln	Brassica rapa	AT4G10920.2 | Symbols: KELP | transcriptional coactivator p15 (PC4) family protein (KELP) | chr4:6697894-6699103 REVERSE LENGTH=165	162	165	1.00E-60	101.9	71.0	82.1
Rsa1.0_02050.1.g31819.t1	ref|NP_179998.1| myrcene/ocimene synthase [Arabidopsis thaliana] gi|75216785|sp|Q9ZUH4.1|TPSA_ARATH RecName: Full=Tricyclene synthase, chloroplastic; AltName: Full=(E)-beta-ocimene synthase 0e23; AltName: Full=Myrcene synthase 1; AltName: Full=Terpenoid synthase 10; Short=AtTPS10; Flags: Precursor gi|4115381|gb|AAD03382.1| putative limonene cyclase [Arabidopsis thaliana] gi|194306668|gb|ACF41947.1| At2g24210 [Arabidopsis thaliana] gi|330252449|gb|AEC07543.1| terpene synthase 10 [Arabidopsis thaliana]	596	591	0	99.2	74.7	85.6	myrcene/ocimene synthase	gbpln	Arabidopsis thaliana	AT2G24210.1 | Symbols: TPS10 | terpene synthase 10 | chr2:10294330-10297401 FORWARD LENGTH=591	596	591	0	99.2	74.7	85.6
Rsa1.0_02050.1.g31820.t1	gb|AAG50806.1|AC079281_8 unknown protein [Arabidopsis thaliana]	1171	1213	0	103.6	38.5	57.0	unknown protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880-16531065 REVERSE LENGTH=626	1171	626	5.00E-62	53.5	11.3	18.3

<table>
<tr><td>Rsa1.0_02050.1.g31821.t1</td><td>ref|XP_002872542.1| F8M12.18 protein [Arabidopsis lyrata subsp. lyrata] gi|297318379|gb|EFH48801.1| F8M12.18 protein [Arabidopsis lyrata subsp. lyrata]</td><td>75</td><td>75</td><td>6.00E-30</td><td>100.0</td><td>89.3</td><td>93.3</td><td>F8M12.18 protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G31830.1 | Symbols: | unknown protein; Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:15400803-15401105 REVERSE LENGTH=100</td><td>75</td><td>100</td><td>5.00E-11</td><td>133.3</td><td>42.7</td><td>52.0</td></tr>
<tr><td>Rsa1.0_02050.1.g31822.t1</td><td>ref|XP_002872539.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] gi|297318376|gb|EFH48798.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]</td><td>161</td><td>258</td><td>9.00E-66</td><td>160.2</td><td>76.4</td><td>87.6</td><td>nodulin MtN3 family protein</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT4G10850.1 | Symbols: SWEET7, AtSWEET7 | Nodulin MtN3 family protein | chr4:6675068-6676718 FORWARD LENGTH=258</td><td>161</td><td>258</td><td>2.00E-66</td><td>160.2</td><td>74.5</td><td>86.3</td></tr>
<tr><td>Rsa1.0_02051.1.g31823.t1</td><td>ref|NP_198901.1| urophorphyrin methylase 1 [Arabidopsis thaliana] gi|18087581|gb|AAL58921.1|AF462833_1 AT5g40850/MHK7_8 [Arabidopsis thaliana] gi|1146165|gb|AAB92676.1| urophorphyrin III methylase [Arabidopsis thaliana] gi|10177964|dbj|BAB11347.1| urophorphyrin III methylase [Arabidopsis thaliana] gi|16604390|gb|AAL24201.1| AT5g40850/MHK7_8 [Arabidopsis thaliana] gi|19310499|gb|AAL84983.1| AT5g40850/MHK7_8 [Arabidopsis thaliana] gi|22655404|gb|AAM98294.1| At5g40850/MHK7_8 [Arabidopsis thaliana] gi|332007223|gb|AED94606.1| urophorphyrin methylase 1 [Arabidopsis thaliana]</td><td>357</td><td>369</td><td>1.00E-175</td><td>103.4</td><td>88.5</td><td>91.6</td><td>urophorphyrin methylase 1</td><td>gbpln</td><td>Arabidopsis thaliana</td><td>AT5G40850.1 | Symbols: UPM1 | urophorphyrin methylase 1 | chr5:16367205-16368724 FORWARD LENGTH=369</td><td>357</td><td>369</td><td>1.00E-178</td><td>103.4</td><td>88.5</td><td>91.6</td></tr>
<tr><td>Rsa1.0_02051.1.g31824.t1</td><td>ref|XP_002870744.1| hypothetical protein ARALYDRAFT_330513 [Arabidopsis lyrata subsp. lyrata] gi|297316580|gb|EFH47003.1| hypothetical protein ARALYDRAFT_330513 [Arabidopsis lyrata subsp. lyrata]</td><td>655</td><td>365</td><td>5.00E-75</td><td>55.7</td><td>27.9</td><td>36.3</td><td>hypothetical protein ARALYDRAFT_330513</td><td>gbpln</td><td>Arabidopsis lyrata</td><td>AT5G39880.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G28750.1); Has 25 Blast hits to 25 proteins in 3 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:15970965-15972056 FORWARD LENGTH=363</td><td>655</td><td>363</td><td>5.00E-74</td><td>55.4</td><td>28.4</td><td>36.0</td></tr>
<tr><td>Rsa1.0_02051.1.g31825.t1</td><td>pir||T00833 RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)</td><td>872</td><td>1365</td><td>0</td><td>156.5</td><td>46.4</td><td>62.7</td><td>RNA-directed DNA polymerase homolog T13L16.7 - Arabidopsis thaliana (fragment)</td><td>----</td><td>----</td><td>AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575</td><td>872</td><td>575</td><td>2.00E-89</td><td>65.9</td><td>22.4</td><td>34.3</td></tr>
<tr><td>Rsa1.0_02051.1.g31826.t1</td><td>gb|EOA36429.1| hypothetical protein CARUB_v10010962mg [Capsella rubella]</td><td>183</td><td>556</td><td>4.00E-17</td><td>303.8</td><td>30.6</td><td>45.9</td><td>hypothetical protein CARUB_v10010962mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT1G52950.1 | Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=566</td><td>183</td><td>566</td><td>4.00E-17</td><td>309.3</td><td>29.5</td><td>47.5</td></tr>
<tr><td>Rsa1.0_02051.1.g31827.t1</td><td>gb|EOA17797.1| hypothetical protein CARUB_v10006191mg [Capsella rubella]</td><td>255</td><td>236</td><td>3.00E-51</td><td>92.5</td><td>52.2</td><td>62.0</td><td>hypothetical protein CARUB_v10006191mg</td><td>gbpln</td><td>Capsella rubella</td><td>AT5G40860.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27210.1); Has 69 Blast hits to 69 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr5:16370470-16371985 FORWARD LENGTH=246</td><td>255</td><td>246</td><td>4.00E-52</td><td>96.5</td><td>48.6</td><td>60.0</td></tr>
</table>

Rsa1.0_02051.1.g31828.t1	ref|NP_198903.1| putative uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|75333998|sp|Q9FKS0.1|UKL1_ARATH RecName: Full=Uridine kinase-like protein 1, chloroplastic; Includes: RecName: Full=Uridine kinase; Short=UK; Includes: RecName: Full=Putative uracil phosphoribosyltransferase; Short=UPRTase; AltName: Full=UMP pyrophosphorylase; Flags: Precursor gi|10177966|dbj|BAB11349.1| uridine kinase-like protein [Arabidopsis thaliana] gi|26983834|gb|AAN86169.1| putative uridine kinase [Arabidopsis thaliana] gi|29465725|gb|AAM10488.1| uracil phosphoribosyltransferase [Arabidopsis thaliana] gi|332007227|gb|AED94610.1| putative uracil phosphoribosyltransferase [Arabidopsis thaliana]	484	486	0	100.4	91.7	95.5	putative uracil phosphoribosyltransferase	gbpln	Arabidopsis thaliana	AT5G40870.1 | Symbols: ATUK/UPRT1, UKL1, UK/UPRT1 | uridine kinase/uracil phosphoribosyltransferase 1 | chr5:16375021-16378384 FORWARD LENGTH=486	484	486	0	100.4	91.7	95.5
Rsa1.0_02051.1.g31829.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	760	1274	1.00E-174	167.6	42.4	54.3	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT4G29090.1 | Symbols: | Ribonuclease H-like superfamily protein | chr4:14333528-14335255 FORWARD LENGTH=575	760	575	2.00E-71	75.7	23.8	37.1
Rsa1.0_02052.1.g31830.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02052.1.g31831.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02052.1.g31832.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02052.1.g31833.t1	ref|XP_002883897.1| UDP-glucosyl transferase 73B5 [Arabidopsis lyrata subsp. lyrata] gi|297329737|gb|EFH60156.1| UDP-glucosyl transferase 73B5 [Arabidopsis lyrata subsp. lyrata]	473	484	0	102.3	79.5	89.4	UDP-glucosyl transferase 73B5	gbpln	Arabidopsis lyrata	AT2G15480.1 | Symbols: UGT73B5 | UDP-glucosyl transferase 73B5 | chr2:6758817-6760452 FORWARD LENGTH=484	473	484	0	102.3	77.6	87.5
Rsa1.0_02052.1.g31834.t1	gb|EOA14896.1| hypothetical protein CARUB_v10028225mg [Capsella rubella]	274	261	2.00E-88	95.3	67.2	70.8	hypothetical protein CARUB_v10028225mg	gbpln	Capsella rubella	AT5G49940.1 | Symbols: NFU2, ATCNFU2 | NIFU-like protein 2 | chr5:20315464-20317228 FORWARD LENGTH=235	274	235	8.00E-91	85.8	66.1	72.3
Rsa1.0_02052.1.g31835.t1	ref|XP_004292625.1| PREDICTED: uncharacterized protein LOC101299743 [Fragaria vesca subsp. vesca]	238	746	6.00E-12	313.4	23.5	33.2	PREDICTED: uncharacterized protein LOC101299743	gbpln	Fragaria vesca	#	#	#	#	#	#	#
Rsa1.0_02052.1.g31836.t1	#	#	#	#	#	#	#	-	----	----	AT5G31412.1 | Symbols: | hAT transposon superfamily protein | chr5:11541463-11543768 REVERSE LENGTH=433	291	433	3.00E-12	148.8	16.8	23.4
Rsa1.0_02052.1.g31837.t1	ref|XP_002865766.1| hypothetical protein ARALYDRAFT_495050 [Arabidopsis lyrata subsp. lyrata] gi|297311601|gb|EFH42025.1| hypothetical protein ARALYDRAFT_495050 [Arabidopsis lyrata subsp. lyrata]	378	537	0	142.1	83.3	90.7	hypothetical protein ARALYDRAFT_495050	gbpln	Arabidopsis lyrata	AT5G49950.1 | Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:20319871-20323552 REVERSE LENGTH=537	378	537	0	142.1	82.3	90.5
Rsa1.0_02053.1.g31838.t1	gb|EOA34643.1| hypothetical protein CARUB_v10022207mg [Capsella rubella]	633	645	0	101.9	85.9	89.1	hypothetical protein CARUB_v10022207mg	gbpln	Capsella rubella	AT1G79750.1 | Symbols: ATNADP-ME4, NADP-ME4 | NADP-malic enzyme 4 | chr1:30007655-30011179 REVERSE LENGTH=646	633	646	0	102.1	85.0	88.6
Rsa1.0_02053.1.g31839.t1	gb|EOA35230.1| hypothetical protein CARUB_v10020390mg, partial [Capsella rubella]	363	408	1.00E-169	112.4	80.2	86.0	hypothetical protein CARUB_v10020390mg, partial	gbpln	Capsella rubella	AT1G75880.2 | Symbols: | SGNH hydrolase-type esterase superfamily protein | chr1:28490564-28492298 FORWARD LENGTH=374	363	374	1.00E-171	103.0	80.4	87.1
Rsa1.0_02053.1.g31840.t1	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	155	1274	4.00E-24	821.9	44.5	61.9	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02053.1.g31841.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02053.1.g31842.t1	ref|XP_002887619.1| T4O12.13 [Arabidopsis lyrata subsp. lyrata] gi|297333460|gb|EFH63878.1| T4O12.13 [Arabidopsis lyrata subsp. lyrata]	327	688	1.00E-152	210.4	80.4	90.5	T4O12.13	gbpln	Arabidopsis lyrata	AT1G75900.1 | Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:28499179-28500943 FORWARD LENGTH=364	327	364	1.00E-153	111.3	81.3	89.9
Rsa1.0_02053.1.g31843.t1	dbj|BAB85608.1| kinetochore protein [Brassica juncea]	160	160	7.00E-88	100.0	99.4	100.0	kinetochore protein	gbpln	Brassica juncea	AT1G75950.1 | Symbols: SKP1, ASK1, ATSKP1, SKP1A, UIP1 | S phase kinase-associated protein 1 | chr1:28516715-28517454 FORWARD LENGTH=160	160	160	9.00E-80	100.0	93.8	98.1
Rsa1.0_02053.1.g31844.t1	dbj|BAJ34235.1| unnamed protein product [Thellungiella halophila]	214	230	1.00E-105	107.5	88.8	93.5	unnamed protein product	----	----	AT1G75980.1 | Symbols: | Single hybrid motif superfamily protein | chr1:28522936-28524302 REVERSE LENGTH=225	214	225	1.00E-101	105.1	84.6	92.5

Rsa1.0_02054.1.g31845.t1	gb|AAF87143.1|AC002423_8 T23E23.16 [Arabidopsis thaliana]	507	653	2.00E−93	128.8	37.9	55.4	T23E23.16	gbpln	Arabidopsis thaliana	AT3G24255.1 | Symbols: | RNA−directed DNA polymerase (reverse transcriptase)−related family protein | chr3:8789471−8793208 FORWARD LENGTH=746	507	746	2.00E−19	147.1	10.1	13.2
Rsa1.0_02054.1.g31846.t1	ref|XP_002890861.1| hypothetical protein ARALYDRAFT_890567 [Arabidopsis lyrata subsp. lyrata] gi|297336703|gb|EFH67120.1| hypothetical protein ARALYDRAFT_890567 [Arabidopsis lyrata subsp. lyrata]	97	94	2.00E−27	96.9	81.4	84.5	hypothetical protein ARALYDRAFT_890567	gbpln	Arabidopsis lyrata	AT1G30260.1 | Symbols: | BEST Arabidopsis thaliana protein match is: Galactosyltransferase family protein (TAIR:AT4G21060.1); Has 30 Blast hits to 30 proteins in 8 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 30; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:10651159−10651452 FORWARD LENGTH=97	97	97	5.00E−29	100.0	82.5	84.5
Rsa1.0_02054.1.g31847.t1	gb|EOA36377.1| hypothetical protein CARUB_v10010783mg [Capsella rubella]	78	82	5.00E−13	105.1	57.7	64.1	hypothetical protein CARUB_v10010783mg	gbpln	Capsella rubella	AT1G30250.1 | Symbols: | unknown protein; Has 5 Blast hits to 5 proteins in 2 species: Archae − 0; Bacteria − 0; Metazoa − 0; Fungi − 0; Plants − 5; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:10647253−10647501 REVERSE LENGTH=82	78	82	3.00E−15	105.1	56.4	60.3
Rsa1.0_02054.1.g31848.t1	gb|EOA39675.1| hypothetical protein CARUB_v10008316mg [Capsella rubella]	803	826	0	102.9	78.8	86.9	hypothetical protein CARUB_v10008316mg	gbpln	Capsella rubella	AT1G30240.2 | Symbols: | unknown protein; Has 169 Blast hits to 168 proteins in 75 species: Archae − 0; Bacteria − 0; Metazoa − 49; Fungi − 68; Plants − 46; Viruses − 0; Other Eukaryotes − 6 (source: NCBI BLink). | chr1:10641241−10645838 REVERSE LENGTH=827	803	827	0	103.0	78.2	86.4
Rsa1.0_02054.1.g31849.t1	emb|CAA52751.1| elongation factor−1 beta A1 [Arabidopsis thaliana]	224	231	4.00E−92	103.1	81.7	88.8	elongation factor−1 beta A1	gbpln	Arabidopsis thaliana	AT2G18110.1 | Symbols: | Translation elongation factor EF1B/ribosomal protein S6 family protein | chr2:7872636−7873713 FORWARD LENGTH=231	224	231	2.00E−93	103.1	83.5	89.7
Rsa1.0_02054.1.g31850.t1	gb|ABK78691.1| putative elongation factor 1−beta [Brassica rapa]	241	230	1.00E−107	95.4	90.5	93.8	putative elongation factor 1−beta	gbpln	Brassica rapa	AT2G18110.1 | Symbols: | Translation elongation factor EF1B/ribosomal protein S6 family protein | chr2:7872636−7873713 FORWARD LENGTH=231	241	231	1.00E−106	95.9	87.1	92.5
Rsa1.0_02054.1.g31851.t1	dbj|BAJ34242.1| unnamed protein product [Thellungiella halophila]	332	339	1.00E−132	102.1	84.6	91.9	unnamed protein product	––––	––––	AT1G30210.2 | Symbols: TCP24 | TEOSINTE BRANCHED 1, cycloidea, and PCF family 24 | chr1:10628754−10629728 REVERSE LENGTH=324	332	324	1.00E−117	97.6	75.0	82.2
Rsa1.0_02055.1.g31852.t1	gb|AAC14296.1| putative methyltransferase [Arabidopsis thaliana]	86	504	1.00E−13	586.0	53.5	59.3	putative methyltransferase	gbpln	Arabidopsis thaliana	AT3G07670.1 | Symbols: | Rubisco methyltransferase family protein | chr3:2451651−2454617 FORWARD LENGTH=504	86	504	3.00E−16	586.0	53.5	60.5
Rsa1.0_02055.1.g31853.t1	ref|XP_002876925.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297322763|gb|EFH53184.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	473	475	0	100.4	79.7	86.9	predicted protein	gbpln	Arabidopsis lyrata	AT3G25670.1 | Symbols: | Leucine−rich repeat (LRR) family protein | chr3:9344532−9346301 REVERSE LENGTH=475	473	475	0	100.4	78.6	86.0
Rsa1.0_02055.1.g31854.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02055.1.g31855.t1	gb|AAF79687.1|AC022314_28 F9C16.9 [Arabidopsis thaliana]	692	946	1.00E−179	136.7	48.8	65.3	F9C16.9	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756−23849915 FORWARD LENGTH=719	692	719	5.00E−12	103.9	10.4	17.6
Rsa1.0_02055.1.g31856.t1	ref|XP_002875270.1| hypothetical protein ARALYDRAFT_484330 [Arabidopsis lyrata subsp. lyrata] gi|297321108|gb|EFH51529.1| hypothetical protein ARALYDRAFT_484330 [Arabidopsis lyrata subsp. lyrata]	992	1002	0	101.0	88.7	93.4	hypothetical protein ARALYDRAFT_484330	gbpln	Arabidopsis lyrata	AT3G25690.2 | Symbols: CHUP1 | Hydroxyproline−rich glycoprotein family protein | chr3:9354061−9357757 FORWARD LENGTH=1004	992	1004	0	101.2	88.3	93.4
Rsa1.0_02056.1.g31857.t1	gb|AAF18641.1|AC006228_12 F5J5.16 [Arabidopsis thaliana]	1809	1024	1.00E−65	56.6	8.8	12.5	F5J5.16	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02056.1.g31858.t1	gb|ABD65062.1| hypothetical protein 27.t00126 [Brassica oleracea]	340	578	1.00E−64	170.0	46.2	62.4	hypothetical protein 27.t00126	gbpln	Brassica oleracea	AT1G51172.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF601 (InterPro:IPR006736); BEST Arabidopsis thaliana protein match is: Protein of unknown function, DUF601 (TAIR:AT1G46696.1); Has 1849 Blast hits to 1554 proteins in 272 species: Archae − 15; Bacteria − 116; Metazoa − 677; Fungi − 267; Plants − 154; Viruses − 11; Other Eukaryotes − 609 (source: NCBI BLink). | chr1:18963205−18965571 FORWARD LENGTH=681	340	681	1.00E−13	200.3	11.5	21.2

Rsa1.0_02056.1.g31859.t1	gb|AAC62798.1| T5H22.2 gene product [Arabidopsis thaliana] gi|7270700|emb|CAB77862.1| hypothetical protein [Arabidopsis thaliana]	629	464	1.00E-49	73.8	22.9	35.6	T5H22.2 gene product	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#	
Rsa1.0_02056.1.g31860.t5	gb|AAF79618.1|AC027665_19 F5M15.26 [Arabidopsis thaliana]	811	1838	1.00E-167	226.6	39.2	49.0	F5M15.26	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#	
Rsa1.0_02056.1.g31861.t10	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_02056.1.g31862.t1	ref|NP_568719.1| putative thiol-disulfide oxidoreductase DCC [Arabidopsis thaliana] gi|75162429|sp|Q8W485.1|Y5010_ARATH RecName: Full=Uncharacterized protein At5g50100, mitochondrial; Flags: Precursor gi|17065380|gb|AAL32844.1| Unknown protein [Arabidopsis thaliana] gi|20148617|gb|AAM10199.1| unknown protein [Arabidopsis thaliana] gi|21593055|gb|AAM65004.1| unknown [Arabidopsis thaliana] gi|332008513|gb|AED95896.1| putative thiol-disulfide oxidoreductase DCC [Arabidopsis thaliana]	316	214	6.00E-29	67.7	19.3	20.6	putative thiol-disulfide oxidoreductase DCC	gbpln	Arabidopsis thaliana	AT5G50100.1 | Symbols: | Putative thiol-disulphide oxidoreductase DCC | chr5:20371916-20373172 FORWARD LENGTH=214	316	214	2.00E-31	67.7	19.3	20.6	
Rsa1.0_02057.1.g31863.t1	ref|NP_567744.1| Subtilisin-like serine endopeptidase family protein [Arabidopsis thaliana] gi|4539429|emb|CAB38962.1| subtilisin protease-like [Arabidopsis thaliana] gi|7269485|emb|CAB79488.1| subtilisin protease-like [Arabidopsis thaliana] gi|332659786|gb|AEE85186.1| Subtilisin-like serine endopeptidase family protein [Arabidopsis thaliana]	1011	746	0	73.8	61.5	65.8	Subtilisin-like serine endopeptidase family protein	gbpln	Arabidopsis thaliana	AT4G26330.1 | Symbols: UNE17, ATSBT3.18 | Subtilisin-like serine endopeptidase family protein | chr4:13320408-13323461 FORWARD LENGTH=746	1011	746	0	73.8	61.5	65.8	
Rsa1.0_02057.1.g31864.t1	ref|XP_002867568.1| hypothetical protein ARALYDRAFT_913928 [Arabidopsis lyrata subsp. lyrata] gi|297313404|gb|EFH43827.1| hypothetical protein ARALYDRAFT_913928 [Arabidopsis lyrata subsp. lyrata]	93	101	1.00E-31	108.6	73.1	82.8	hypothetical protein ARALYDRAFT_913928	gbpln	Arabidopsis lyrata	AT5G56520.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G55365.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:22885226-22885531 FORWARD LENGTH=101	93	101	9.00E-22	108.6	48.4	58.1	
Rsa1.0_02057.1.g31865.t1	ref|NP_194360.1| Arginyl-tRNA synthetase, class Ic [Arabidopsis thaliana] gi|2632105|emb|CAB11468.1| arginyl-tRNA synthetase [Arabidopsis thaliana] gi|4539426|emb|CAB38959.1| arginyl-tRNA synthetase [Arabidopsis thaliana] gi|7269482|emb|CAB79485.1| arginyl-tRNA synthetase [Arabidopsis thaliana] gi|332659782|gb|AEE85182.1| Arginyl-tRNA synthetase, class Ic [Arabidopsis thaliana]	585	642	0	109.7	83.1	88.5	Arginyl-tRNA synthetase, class Ic	gbpln	Arabidopsis thaliana	AT4G26300.1 | Symbols: emb1027 | Arginyl-tRNA synthetase, class Ic | chr4:13308400-13313109 REVERSE LENGTH=642	585	642	0	109.7	83.1	88.5	
Rsa1.0_02057.1.g31866.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#	
Rsa1.0_02057.1.g31867.t1	ref|XP_002867572.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297313408|gb|EFH43831.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	329	310	1.00E-138	94.2	72.9	83.9	predicted protein	gbpln	Arabidopsis lyrata	AT4G26280.1 | Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13304721-13305722 REVERSE LENGTH=314	329	314	1.00E-140	95.4	72.6	82.7	
Rsa1.0_02057.1.g31868.t1	ref|NP_194356.2| inositol oxygenase 4 [Arabidopsis thaliana] gi|75151963|sp|Q8H1S0.1|MIOX4_ARATH RecName: Full=Inositol oxygenase 4; AltName: Full=Myo-inositol oxygenase 4; Short=AtMIOX4; Short=MI oxygenase 4 gi|23296360|gb|AAN13052.1| unknown protein [Arabidopsis thaliana] gi|332659776|gb|AEE85176.1| inositol oxygenase 4 [Arabidopsis thaliana]	298	317	1.00E-163	106.4	92.6	96.3	inositol oxygenase 4	gbpln	Arabidopsis thaliana	AT4G26260.1 | Symbols: MIOX4 | myo-inositol oxygenase 4 | chr4:13297939-13300146 FORWARD LENGTH=317	298	317	1.00E-166	106.4	92.6	96.3	
Rsa1.0_02057.1.g31869.t2	gb|EOA17455.1| hypothetical protein CARUB_v10005778mg [Capsella rubella]	201	198	3.00E-98	98.5	86.6	92.0	hypothetical protein CARUB_v10005778mg	gbpln	Capsella rubella	AT4G26240.1 | Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:13287011-13288896 REVERSE LENGTH=198	201	198	1.00E-94	98.5	87.1	92.0	
Rsa1.0_02057.1.g31870.t1	gb|EOA17906.1| hypothetical protein CARUB_v10006315mg [Capsella rubella]	449	450	0	100.2	94.2	97.6	hypothetical protein CARUB_v10006315mg	gbpln	Capsella rubella	AT4G26200.1 | Symbols: ACS7, ATACS7 | 1-amino-cyclopropane-1-carboxylate synthase 7 | chr4:13275307-13276946 FORWARD LENGTH=447	449	447	0	99.6	93.8	97.3	

Rsa1.0_02058.1.g31871.t1	ref|NP_195021.1| putative protein phosphatase 2C 61 [Arabidopsis thaliana] gi|75100739|sp|O82637.1|P2C61_ARATH RecName: Full=Probable protein phosphatase 2C 61; Short=AtPP2C61 gi|3688176|emb|CAA21204.1| putative protein [Arabidopsis thaliana] gi|7270242|emb|CAB80012.1| putative protein [Arabidopsis thaliana] gi|332660751|gb|AEE86151.1| putative protein phosphatase 2C 61 [Arabidopsis thaliana]	326	326	1.00E-159	100.0	83.4	89.6	putative protein phosphatase 2C 61	gbpln	Arabidopsis thaliana	AT4G32950.1 | Symbols: | Protein phosphatase 2C family protein | chr4:15904444-15906010 REVERSE LENGTH=326	326	326	1.00E-161	100.0	83.4	89.6
Rsa1.0_02058.1.g31872.t2	gb|EOA17574.1| hypothetical protein CARUB_v10005935mg [Capsella rubella]	131	154	1.00E-52	117.6	78.6	90.1	hypothetical protein CARUB_v10005935mg	gbpln	Capsella rubella	AT4G32915.1 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: regulation of translational fidelity; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Glu-tRNAGln amidotransferase, C subunit (InterPro:IPR003837); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:15885549-15886628 FORWARD LENGTH=155	131	155	1.00E-48	118.3	75.6	89.3
Rsa1.0_02058.1.g31873.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02058.1.g31874.t1	ref|NP_195014.1| homeobox-leucine zipper protein ATHB-8 [Arabidopsis thaliana] gi|75220729|sp|Q39123.1|ATHB8_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-8; AltName: Full=HD-ZIP protein ATHB-8; AltName: Full=Homeodomain transcription factor ATHB-8 gi|1149569|emb|CAA90703.1| HD-zip [Arabidopsis thaliana] gi|7270235|emb|CAB80005.1| HD-zip transcription factor (athb-8) [Arabidopsis thaliana] gi|20152536|emb|CAD29660.1| homeodomain-leucine zipper protein 8 [Arabidopsis thaliana] gi|20466330|gb|AAM20482.1| HD-zip transcription factor (athb-8) [Arabidopsis thaliana] gi|31711762|gb|AAP68237.1| At4g32880 [Arabidopsis thaliana] gi|332660738|gb|AEE86138.1| homeobox-leucine zipper protein ATHB-8 [Arabidopsis thaliana]	226	833	1.00E-128	368.6	97.3	99.1	homeobox-leucine zipper protein ATHB-8	gbpln	Arabidopsis thaliana	AT4G32880.1 | Symbols: ATHB-8, ATHB8, HB-8 | homeobox gene 8 | chr4:15863587-15867822 REVERSE LENGTH=833	226	833	1.00E-131	368.6	97.3	99.1
Rsa1.0_02059.1.g31875.t2	gb|AAD17409.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	490	1347	9.00E-75	274.9	29.6	38.0	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02059.1.g31876.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02059.1.g31877.t6	dbj|BAF34636.1| DNA methyltransferase 1b [Brassica rapa]	1477	1519	0	102.8	87.1	93.2	DNA methyltransferase 1b	gbpln	Brassica rapa	AT5G49160.1 | Symbols: MET1, MET2, METI, DDM2, DMT01, DMT1 | methyltransferase 1 | chr5:19932501-19938186 FORWARD LENGTH=1534	1477	1534	0	103.9	69.1	81.3
Rsa1.0_02059.1.g31878.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02059.1.g31879.t1	ref|XP_002890907.1| hypothetical protein ARALYDRAFT_473323 [Arabidopsis lyrata subsp. lyrata] gi|297336749|gb|EFH67166.1| hypothetical protein ARALYDRAFT_473323 [Arabidopsis lyrata subsp. lyrata]	320	318	1.00E-176	99.4	94.1	96.9	hypothetical protein ARALYDRAFT_473323	gbpln	Arabidopsis lyrata	AT1G30825.1 | Symbols: ARPC2A, DIS2 | Arp2/3 complex, 34 kD subunit p34-Arc | chr1:10961106-10962999 FORWARD LENGTH=318	320	318	1.00E-178	99.4	94.1	96.9
Rsa1.0_02060.1.g31880.t1	gb|ACT35474.1| peroxidase 65 [Brassica rapa]	331	330	1.00E-176	99.7	92.7	95.8	peroxidase 65	gbpln	Brassica rapa	AT5G47000.1 | Symbols: | Peroxidase superfamily protein | chr5:19069171-19070175 REVERSE LENGTH=334	331	334	1.00E-175	100.9	89.1	93.1
Rsa1.0_02060.1.g31881.t1	ref|XP_002865151.1| low-level beta-amylase 1 [Arabidopsis lyrata subsp. lyrata] gi|297310986|gb|EFH41410.1| low-level beta-amylase 1 [Arabidopsis lyrata subsp. lyrata]	1220	1253	0	102.7	93.2	95.3	low-level beta-amylase 1	gbpln	Arabidopsis lyrata	AT5G47010.1 | Symbols: UPF1, LBA1, ATUPF1 | RNA helicase, putative | chr5:19072009-19078856 FORWARD LENGTH=1254	1220	1254	0	102.8	92.7	95.2
Rsa1.0_02060.1.g31882.t1	gb|ABL97963.1| hydrogen-transporting ATP synthase [Brassica rapa]	204	203	1.00E-107	99.5	95.1	98.0	hydrogen-transporting ATP synthase	gbpln	Brassica rapa	AT5G47030.1 | Symbols: | ATPase, F1 complex, delta/epsilon subunit | chr5:19090384-19092034 FORWARD LENGTH=203	204	203	1.00E-105	99.5	90.2	96.6

Rsa1.0_02060.1.g31883.t1	ref|XP_002889873.1| C-terminal cysteine residue is changed to A serine 1 [Arabidopsis lyrata subsp. lyrata] gi|297335715|gb|EFH66132.1| C-terminal cysteine residue is changed to A serine 1 [Arabidopsis lyrata subsp. lyrata]	123	118	2.00E-54	95.9	82.9	89.4	C-terminal cysteine residue is changed to A serine 1	gbpln	Arabidopsis lyrata	AT1G11530.1 | Symbols: ATCXXS1, CXXS1 | C-terminal cysteine residue is changed to a serine 1 | chr1:3874518-3875311 FORWARD LENGTH=118	123	118	9.00E-56	95.9	81.3	87.8
Rsa1.0_02060.1.g31884.t1	gb|AAF16642.1|AC011661_20 T23J18.21 [Arabidopsis thaliana]	79	304	8.00E-32	384.8	81.0	84.8	T23J18.21	gbpln	Arabidopsis thaliana	AT1G11545.1 | Symbols: XTH8 | xyloglucan endotransglucosylase/hydrolase 8 | chr1:3878689-3880286 REVERSE LENGTH=305	79	305	2.00E-34	386.1	81.0	84.8
Rsa1.0_02060.1.g31885.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02060.1.g31886.t1	gb|AFJ42571.1| elongation initiation factor 4A [Sesamum indicum]	90	332	9.00E-32	368.9	74.4	88.9	elongation initiation factor 4A	gbpln	Sesamum indicum	AT3G13920.3 | Symbols: EIF4A1, RH4, TIF4A1 | eukaryotic translation initiation factor 4A1 | chr3:4592635-4594094 REVERSE LENGTH=402	90	402	7.00E-32	446.7	68.9	77.8
Rsa1.0_02061.1.g31887.t1	ref|XP_002886268.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata] gi|297332108|gb|EFH62527.1| hypothetical protein ARALYDRAFT_900376 [Arabidopsis lyrata subsp. lyrata]	385	346	8.00E-67	89.9	43.6	58.2	hypothetical protein ARALYDRAFT_900376	gbpln	Arabidopsis lyrata	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	385	370	1.00E-60	96.1	40.0	57.4
Rsa1.0_02061.1.g31888.t1	gb|EOA14519.1| hypothetical protein CARUB_v10027748mg [Capsella rubella]	362	368	1.00E-74	101.7	47.8	62.4	hypothetical protein CARUB_v10027748mg	gbpln	Capsella rubella	AT4G38940.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18152848-18153960 FORWARD LENGTH=370	362	370	2.00E-67	102.2	43.1	55.8
Rsa1.0_02061.1.g31889.t1	gb|EOA27372.1| hypothetical protein CARUB_v10023490mg [Capsella rubella] gi|482563183|gb|EOA27373.1| hypothetical protein CARUB_v10023490mg [Capsella rubella]	370	364	0	98.4	88.9	94.3	hypothetical protein CARUB_v10023490mg	gbpln	Capsella rubella	AT2G30740.1 | Symbols: | Protein kinase superfamily protein | chr2:13096399-13098285 FORWARD LENGTH=366	370	366	0	98.9	87.6	91.9
Rsa1.0_02061.1.g31890.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02061.1.g31891.t1	ref|XP_002881131.1| CYP71A13 [Arabidopsis lyrata subsp. lyrata] gi|297326970|gb|EFH57390.1| CYP71A13 [Arabidopsis lyrata subsp. lyrata]	474	503	0	106.1	82.3	89.0	CYP71A13	gbpln	Arabidopsis lyrata	AT2G30770.1 | Symbols: CYP71A13 | cytochrome P450, family 71, subfamily A, polypeptide 13 | chr2:13109909-13112006 REVERSE LENGTH=503	474	503	0	106.1	82.5	88.6
Rsa1.0_02061.1.g31892.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02062.1.g31893.t1	gb|ABD64937.1| hypothetical protein 24.t00015 [Brassica oleracea]	777	1327	0	170.8	80.8	86.9	hypothetical protein 24.t00015	gbpln	Brassica oleracea	AT5G47480.1 | Symbols: | RGPR-related | chr5:19257420-19263132 FORWARD LENGTH=1350	777	1350	0	173.7	73.7	83.0
Rsa1.0_02062.1.g31894.t1	ref|XP_002881289.1| hypothetical protein ARALYDRAFT_482302 [Arabidopsis lyrata subsp. lyrata] gi|297327128|gb|EFH57548.1| hypothetical protein ARALYDRAFT_482302 [Arabidopsis lyrata subsp. lyrata]	142	394	1.00E-25	277.5	44.4	49.3	hypothetical protein ARALYDRAFT_482302	gbpln	Arabidopsis lyrata	AT2G33560.2 | Symbols: BUBR1 | BUB1-related (BUB1: budding uninhibited by benzymidazol 1) | chr2:14213810-14215918 REVERSE LENGTH=396	142	396	3.00E-27	278.9	43.0	49.3
Rsa1.0_02062.1.g31895.t1	gb|ABD64938.1| hypothetical protein 24.t00016 [Brassica oleracea]	1400	1330	0	95.0	81.4	86.1	hypothetical protein 24.t00016	gbpln	Brassica oleracea	AT5G47480.1 | Symbols: | RGPR-related | chr5:19257420-19263132 FORWARD LENGTH=1350	1400	1350	0	96.4	72.4	80.4
Rsa1.0_02062.1.g31896.t1	gb|ABD64942.1| hypothetical protein 24.t00020 [Brassica oleracea]	885	872	0	98.5	91.6	93.9	hypothetical protein 24.t00020	gbpln	Brassica oleracea	AT5G47430.1 | Symbols: | DWNN domain, a CCHC-type zinc finger | chr5:19235819-19240596 REVERSE LENGTH=892	885	892	0	100.8	81.6	87.0
Rsa1.0_02062.1.g31897.t1	gb|ABD64944.1| hypothetical protein 24.t00022 [Brassica oleracea]	600	579	0	96.5	88.8	92.7	hypothetical protein 24.t00022	gbpln	Brassica oleracea	AT5G47380.1 | Symbols: | Protein of unknown function, DUF547 | chr5:19221472-19224471 REVERSE LENGTH=618	600	618	0	103.0	78.2	84.8
Rsa1.0_02062.1.g31898.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02062.1.g31899.t1	dbj|BAB11196.1| mutator-like transposase [Arabidopsis thaliana]	483	797	1.00E-117	165.0	46.8	61.1	mutator-like transposase	gbpln	Arabidopsis thaliana	AT1G64260.1 | Symbols: | MuDR family transposase | chr1:23847756-23849915 FORWARD LENGTH=719	483	719	6.00E-32	148.9	21.3	34.6
Rsa1.0_02063.1.g31900.t1	gb|EOA12359.1| hypothetical protein CARUB_v10016511mg [Capsella rubella]	438	356	4.00E-83	81.3	42.2	53.2	hypothetical protein CARUB_v10016511mg	gbpln	Capsella rubella	AT4G10190.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:6350928-6352031 FORWARD LENGTH=367	438	367	5.00E-60	83.8	34.5	47.9
Rsa1.0_02063.1.g31901.t1	gb|EOA12359.1| hypothetical protein CARUB_v10016511mg [Capsella rubella]	370	356	9.00E-59	96.2	43.8	55.1	hypothetical protein CARUB_v10016511mg	gbpln	Capsella rubella	AT4G10190.1 | Symbols: | F-box and associated interaction domains-containing protein | chr4:6350928-6352031 FORWARD LENGTH=367	370	367	2.00E-43	99.2	38.6	54.6
Rsa1.0_02063.1.g31902.t1	ref|XP_002883283.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] gi|297329123|gb|EFH59542.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	582	607	0	104.3	83.2	90.2	RNA recognition motif-containing protein	gbpln	Arabidopsis lyrata	AT3G21100.2 | Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:7399162-7401870 FORWARD LENGTH=602	582	602	0	103.4	82.8	89.3

Rsa1.0_02063.1.g31903.t1	gb|EOA30003.1| hypothetical protein CARUB_v10013106mg [Capsella rubella]	691	691	0	100.0	95.2	98.1	hypothetical protein CARUB_v10013106mg	gbpln	Capsella rubella	AT3G21090.1 | Symbols: | ABC-2 type transporter family protein | chr3:7391497-7394933 REVERSE LENGTH=691	691	691	0	100.0	94.6	97.8
Rsa1.0_02063.1.g31904.t1	ref|NP_974347.1| NAD(H) kinase 1 [Arabidopsis thaliana] gi|94717660|sp|Q56YN3.2|NADK1_ARATH RecName: Full=NAD(H) kinase 1; Short=AtNADK-1 gi|39843359|gb|AAR32133.1| NADK1 [Arabidopsis thaliana] gi|51970406|dbj|BAD43895.1| unnamed protein product [Arabidopsis thaliana] gi|332642935|gb|AEE76456.1| NAD(H) kinase 1 [Arabidopsis thaliana]	535	524	0	97.9	83.6	90.3	NAD(H) kinase 1	gbpln	Arabidopsis thaliana	AT3G21070.2 | Symbols: NADK1 | NAD kinase 1 | chr3:7380434-7383874 REVERSE LENGTH=524	535	524	0	97.9	83.6	90.3
Rsa1.0_02064.1.g31905.t1	ref|NP_195142.1| cyclin-D3-1 [Arabidopsis thaliana] gi|59802919|sp|P42753.3|CCD31_ARATH RecName: Full=Cyclin-D3-1; AltName: Full=Cyclin-delta-3; Short=Cyclin-d3; AltName: Full=G1/S-specific cyclin-D3-1; Short=CycD3;1 gi|2911046|emb|CAA17556.1| cyclin delta-3 [Arabidopsis thaliana] gi|7270365|emb|CAB80133.1| cyclin delta-3 [Arabidopsis thaliana] gi|62320771|dbj|BAD95437.1| cyclin delta-3 [Arabidopsis thaliana] gi|332660935|gb|AEE86335.1| cyclin-D3-1 [Arabidopsis thaliana]	373	376	1.00E-142	100.8	72.7	79.4	cyclin-D3-1	gbpln	Arabidopsis thaliana	AT4G34160.1 | Symbols: CYCD3;1, CYCD3 | CYCLIN D3;1 | chr4:16357903-16359304 FORWARD LENGTH=376	373	376	1.00E-145	100.8	72.7	79.4
Rsa1.0_02064.1.g31906.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02064.1.g31907.t1	ref|XP_002869171.1| hypothetical protein ARALYDRAFT_912986 [Arabidopsis lyrata subsp. lyrata] gi|297315007|gb|EFH45430.1| hypothetical protein ARALYDRAFT_912986 [Arabidopsis lyrata subsp. lyrata]	253	248	6.00E-95	98.0	69.2	71.5	hypothetical protein ARALYDRAFT_912986	gbpln	Arabidopsis lyrata	AT4G34150.1 | Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:16355035-16356955 FORWARD LENGTH=247	253	247	2.00E-93	97.6	66.8	69.6
Rsa1.0_02064.1.g31908.t1	ref|XP_002869173.1| hypothetical protein ARALYDRAFT_491262 [Arabidopsis lyrata subsp. lyrata] gi|297315009|gb|EFH45432.1| hypothetical protein ARALYDRAFT_491262 [Arabidopsis lyrata subsp. lyrata]	236	237	1.00E-104	100.4	84.3	90.7	hypothetical protein ARALYDRAFT_491262	gbpln	Arabidopsis lyrata	AT4G34120.1 | Symbols: LEJ1, CDCP1 | Cystathionine beta-synthase (CBS) family protein | chr4:16341194-16342893 FORWARD LENGTH=238	236	238	1.00E-101	100.8	82.6	89.8
Rsa1.0_02064.1.g31909.t1	ref|NP_001119113.1| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332660924|gb|AEE86324.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	857	1107	0	129.2	58.5	64.8	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT4G34100.2 | Symbols: | RING/U-box superfamily protein | chr4:16330590-16334864 FORWARD LENGTH=1107	857	1107	0	129.2	58.5	64.8
Rsa1.0_02064.1.g31910.t1	ref|NP_567951.1| putative cyclin delta-3 [Arabidopsis thaliana] gi|13899099|gb|AAK48971.1|AF370544_1 cyclin delta-3 [Arabidopsis thaliana] gi|20148339|gb|AAM10060.1| cyclin delta-3 [Arabidopsis thaliana] gi|110738184|dbj|BAF01023.1| cyclin delta-3 [Arabidopsis thaliana] gi|332660919|gb|AEE86319.1| putative cyclin delta-3 [Arabidopsis thaliana]	329	330	1.00E-152	100.3	83.6	88.1	putative cyclin delta-3	gbpln	Arabidopsis thaliana	AT4G34090.1 | Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast stroma; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G23370.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16328051-16330110 REVERSE LENGTH=330	329	330	1.00E-154	100.3	83.6	88.1
Rsa1.0_02064.1.g31911.t1	gb|ABE41833.1| caffeoyl-CoA 3-O-methyltransferase [Brassica rapa subsp. pekinensis]	258	258	1.00E-147	100.0	98.1	98.4	caffeoyl-CoA 3-O-methyltransferase	gbpln	Brassica rapa	AT4G34050.1 | Symbols: CCoAOMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr4:16310844-16311973 FORWARD LENGTH=259	258	259	1.00E-140	100.4	92.6	94.2
Rsa1.0_02064.1.g31912.t1	gb|AAK62371.1|AF386926_1 Unknown protein [Arabidopsis thaliana]	586	587	0	100.2	92.5	95.6	Unknown protein	gbpln	Arabidopsis thaliana	AT4G34030.1 | Symbols: MCCB | 3-methylcrotonyl-CoA carboxylase | chr4:16301298-16303949 FORWARD LENGTH=587	586	587	0	100.2	92.7	95.7
Rsa1.0_02064.1.g31913.t1	gb|EOA15391.1| hypothetical protein CARUB_v10006469mg [Capsella rubella]	461	476	0	103.3	81.8	88.9	hypothetical protein CARUB_v10006469mg	gbpln	Capsella rubella	AT4G34020.1 | Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr4:16298553-16300897 REVERSE LENGTH=472	461	472	0	102.4	80.9	88.1
Rsa1.0_02064.1.g31914.t1	dbj|BAJ34494.1| unnamed protein product [Thellungiella halophila]	409	445	1.00E-176	108.8	82.2	89.2	unnamed protein product	----	----	AT4G34000.2 | Symbols: ABF3, DPBF5 | abscisic acid responsive elements-binding factor 3 | chr4:16296008-16297971 FORWARD LENGTH=454	409	454	1.00E-157	111.0	77.3	85.3

Rsa1.0_02064.1.g31915.t1	ref|XP_002867140.1| hypothetical protein ARALYDRAFT_913003 [Arabidopsis lyrata subsp. lyrata] gi|297312976|gb|EFH43399.1| hypothetical protein ARALYDRAFT_913003 [Arabidopsis lyrata subsp. lyrata]	170	155	7.00E-72	91.2	85.3	88.2	hypothetical protein ARALYDRAFT_913003	gbpln	Arabidopsis lyrata	AT4G33985.1 | Symbols: | Protein of unknown function (DUF1685) | chr4:16288301-16288857 REVERSE LENGTH=154	170	154	1.00E-69	90.6	82.4	85.3
Rsa1.0_02064.1.g31916.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02064.1.g31917.t1	ref|XP_002867141.1| hypothetical protein ARALYDRAFT_491275 [Arabidopsis lyrata subsp. lyrata] gi|297312977|gb|EFH43400.1| hypothetical protein ARALYDRAFT_491275 [Arabidopsis lyrata subsp. lyrata]	239	217	7.00E-38	90.8	51.0	60.3	hypothetical protein ARALYDRAFT_491275	gbpln	Arabidopsis lyrata	AT4G33980.1 | Symbols: | BEST Arabidopsis thaliana protein match is: cold regulated gene 27 (TAIR:AT5G42900.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16283047-16284946 REVERSE LENGTH=218	239	218	2.00E-36	91.2	48.5	57.7
Rsa1.0_02065.1.g31918.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02065.1.g31919.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02065.1.g31920.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02065.1.g31921.t1	gb|EOA11994.1| hypothetical protein CARUB_v10012704mg [Capsella rubella]	269	269	1.00E-143	100.0	90.0	94.4	hypothetical protein CARUB_v10012704mg	gbpln	Capsella rubella	AT4G15093.1 | Symbols: | catalytic LigB subunit of aromatic ring-opening dioxygenase family | chr4:8618454-8619472 FORWARD LENGTH=269	269	269	1.00E-140	100.0	87.0	90.3
Rsa1.0_02065.1.g31922.t1	gb|AAD32898.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	1312	1307	0	99.6	59.5	72.3	putative retroelement pol polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1312	1262	1.00E-101	96.2	14.7	23.2
Rsa1.0_02065.1.g31923.t4	gb|AAG10817.1|AC011808_5 Putative retroelement polyprotein [Arabidopsis thaliana]	1294	1413	0	109.2	55.5	72.1	Putative retroelement polyprotein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	1294	1262	0	97.5	24.0	30.8
Rsa1.0_02065.1.g31924.t1	emb|CAB10288.1| hypothetical protein [Arabidopsis thaliana] gi|7268255|emb|CAB78551.1| hypothetical protein [Arabidopsis thaliana]	100	1705	1.00E-40	1705.0	78.0	85.0	hypothetical protein	gbpln	Arabidopsis thaliana	AT4G15093.1 | Symbols: | catalytic LigB subunit of aromatic ring-opening dioxygenase family | chr4:8618454-8619472 FORWARD LENGTH=269	100	269	6.00E-41	269.0	78.0	85.0
Rsa1.0_02066.1.g31925.t1	pir||H85073 probable transposon protein [imported] - Arabidopsis thaliana gi|5032279|gb|AAD38227.1|AF147264_10 may be a pseudogene [Arabidopsis thaliana] gi|7267351|emb|CAB81124.1| putative transposon protein [Arabidopsis thaliana]	385	483	3.00E-53	125.5	29.9	39.5	probable transposon protein	gbpln	Arabidopsis thaliana	AT3G42170.1 | Symbols: | BED zinc finger ;hAT family dimerisation domain | chr3:14321838-14323928 FORWARD LENGTH=696	385	696	6.00E-26	180.8	20.8	30.6
Rsa1.0_02066.1.g31926.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02066.1.g31927.t1	gb|ACA61620.1| hypothetical protein AP6_E08.1 [Arabidopsis lyrata subsp. petraea]	136	220	6.00E-29	161.8	47.8	55.9	hypothetical protein AP6_E08.1	gbpln	Arabidopsis lyrata	AT4G01590.2 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: Arabidopsis protein of unknown function (DUF241) (TAIR:AT4G35680.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr4:689077-690192 REVERSE LENGTH=199	136	199	6.00E-27	146.3	58.1	68.4
Rsa1.0_02066.1.g31928.t1	dbj|BAB01313.1| serine carboxypeptidase I [Arabidopsis thaliana]	510	504	0	98.8	75.1	85.7	serine carboxypeptidase I	gbpln	Arabidopsis thaliana	AT3G25420.1 | Symbols: scpl21 | serine carboxypeptidase-like 21 | chr3:9217832-9220836 FORWARD LENGTH=505	510	505	0	99.0	73.7	84.5
Rsa1.0_02066.1.g31929.t1	#	#	#	#	#	#	#	–	––––	––––	#	#	#	#	#	#	#
Rsa1.0_02067.1.g31930.t1	dbj|BAJ34474.1| unnamed protein product [Thellungiella halophila]	110	225	5.00E-51	204.5	89.1	96.4	unnamed protein product	––––	––––	AT2G29450.1 | Symbols: ATGSTU5, ATGSTU1, AT103-1A, GSTU5 | glutathione S-transferase tau 5 | chr2:12624774-12625566 REVERSE LENGTH=224	110	224	6.00E-53	203.6	85.5	94.5
Rsa1.0_02067.1.g31931.t1	ref|XP_002884534.1| hypothetical protein ARALYDRAFT_477873 [Arabidopsis lyrata subsp. lyrata] gi|297330374|gb|EFH60793.1| hypothetical protein ARALYDRAFT_477873 [Arabidopsis lyrata subsp. lyrata]	851	940	0	110.5	69.6	80.1	hypothetical protein ARALYDRAFT_477873	gbpln	Arabidopsis lyrata	AT3G05790.1 | Symbols: LON4 | lon protease 4 | chr3:1720154-1725182 REVERSE LENGTH=942	851	942	0	110.7	69.4	79.6
Rsa1.0_02067.1.g31932.t1	ref|XP_002881142.1| hypothetical protein ARALYDRAFT_344858 [Arabidopsis lyrata subsp. lyrata] gi|297326981|gb|EFH57401.1| hypothetical protein ARALYDRAFT_344858 [Arabidopsis lyrata subsp. lyrata]	1878	1853	0	98.7	80.5	88.0	hypothetical protein ARALYDRAFT_344858	gbpln	Arabidopsis lyrata	AT1G49340.1 | Symbols: ATPI4K ALPHA | Phosphatidylinositol 3- and 4-kinase family protein | chr1:18252355-18263967 FORWARD LENGTH=2028	1878	2028	0	108.0	72.3	79.5

Rsa1.0_02068.1.g31933.t1	emb|CAB87869.1| bZIP protein [Arabidopsis thaliana]	91	493	9.00E-42	541.8	89.0	96.7	bZIP protein	gbpln	Arabidopsis thaliana	AT3G60320.1 | Symbols: | Protein of unknown function (DUF630 and DUF632) | chr3:22292073-22295228 REVERSE LENGTH=796	91	796	2.00E-44	874.7	89.0	96.7
Rsa1.0_02068.1.g31934.t1	gb|EOA24750.1| hypothetical protein CARUB_v10018027mg [Capsella rubella]	241	208	5.00E-53	86.3	56.0	65.6	hypothetical protein CARUB_v10018027mg	gbpln	Capsella rubella	AT3G60280.1 | Symbols: UCC3 | uclacyanin 3 | chr3:22279867-22280633 REVERSE LENGTH=222	241	222	4.00E-50	92.1	56.0	65.1
Rsa1.0_02068.1.g31935.t1	ref|XP_002876544.1| hypothetical protein ARALYDRAFT_486497 [Arabidopsis lyrata subsp. lyrata] gi|297322382|gb|EFH52803.1| hypothetical protein ARALYDRAFT_486497 [Arabidopsis lyrata subsp. lyrata]	274	266	1.00E-139	97.1	89.4	92.7	hypothetical protein ARALYDRAFT_486497	gbpln	Arabidopsis lyrata	AT3G60260.4 | Symbols: | ELMO/CED-12 family protein | chr3:22274303-22276839 FORWARD LENGTH=266	274	266	1.00E-141	97.1	88.3	92.3
Rsa1.0_02068.1.g31936.t1	ref|XP_002878325.1| hypothetical protein ARALYDRAFT_486495 [Arabidopsis lyrata subsp. lyrata] gi|297324163|gb|EFH54584.1| hypothetical protein ARALYDRAFT_486495 [Arabidopsis lyrata subsp. lyrata]	193	278	1.00E-97	144.0	91.2	94.8	hypothetical protein ARALYDRAFT_486495	gbpln	Arabidopsis lyrata	AT3G60250.1 | Symbols: CKB3 | casein kinase II beta chain 3 | chr3:22270714-22271962 REVERSE LENGTH=276	193	276	3.00E-97	143.0	88.6	94.8
Rsa1.0_02068.1.g31937.t1	gb|EOA24984.1| hypothetical protein CARUB_v10018281mg, partial [Capsella rubella]	117	109	7.00E-46	93.2	78.6	80.3	hypothetical protein CARUB_v10018281mg, partial	gbpln	Capsella rubella	AT3G60245.1 | Symbols: | Zinc-binding ribosomal protein family protein | chr3:22268803-22269750 FORWARD LENGTH=92	117	92	2.00E-47	78.6	77.8	77.8
Rsa1.0_02068.1.g31938.t1	gb|EOA13649.1| hypothetical protein CARUB_v10026720mg [Capsella rubella]	318	343	1.00E-142	107.9	84.0	89.6	hypothetical protein CARUB_v10026720mg	gbpln	Capsella rubella	AT5G42520.1 | Symbols: BPC6, BBR/BPC6, ATBPC6 | basic pentacysteine 6 | chr5:17001287-17002466 FORWARD LENGTH=342	318	342	1.00E-142	107.5	85.2	90.3
Rsa1.0_02068.1.g31939.t1	ref|XP_002876541.1| hypothetical protein ARALYDRAFT_907544 [Arabidopsis lyrata subsp. lyrata] gi|297322379|gb|EFH52800.1| hypothetical protein ARALYDRAFT_907544 [Arabidopsis lyrata subsp. lyrata]	89	96	3.00E-28	107.9	75.3	87.6	hypothetical protein ARALYDRAFT_907544	gbpln	Arabidopsis lyrata	AT2G44670.1 | Symbols: | Protein of unknown function (DUF581) | chr2:18425279-18425673 FORWARD LENGTH=93	89	93	1.00E-29	104.5	68.5	80.9
Rsa1.0_02068.1.g31940.t1	gb|EOA36622.1| hypothetical protein CARUB_v10011860mg [Capsella rubella]	101	181	6.00E-12	179.2	53.5	56.4	hypothetical protein CARUB_v10011860mg	gbpln	Capsella rubella	AT1G14060.1 | Symbols: | GCK domain-containing protein | chr1:4817354-4817893 REVERSE LENGTH=179	101	179	4.00E-11	177.2	49.5	55.4
Rsa1.0_02068.1.g31941.t1	ref|NP_191325.1| DNA-directed RNA polymerase I subunit A1 [Arabidopsis thaliana] gi|4678281|emb|CAB41189.1| DNA-directed RNA polymerase I 190K chain-like protein [Arabidopsis thaliana] gi|332646163|gb|AEE79684.1| nuclear RNA polymerase A1 [Arabidopsis thaliana]	356	1670	4.00E-92	469.1	46.1	49.2	DNA-directed RNA polymerase I subunit A1	gbpln	Arabidopsis thaliana	AT3G57660.1 | Symbols: NRPA1 | nuclear RNA polymerase A1 | chr3:21353746-21362814 FORWARD LENGTH=1670	356	1670	1.00E-94	469.1	46.1	49.2
Rsa1.0_02068.1.g31942.t20	ref|XP_004150620.1| PREDICTED: dynamin-related protein 1C-like [Cucumis sativus]	686	548	1.00E-129	79.9	39.9	50.0	PREDICTED: dynamin-related protein 1C-like	gbpln	Cucumis sativus	AT3G60190.1 | Symbols: ADL4, ADLP2, EDR3, DRP1E, ADL1E, DL1E | DYNAMIN-like 1E | chr3:22244367-22247651 REVERSE LENGTH=624	686	624	1.00E-124	91.0	32.8	35.1
Rsa1.0_02068.1.g31943.t1	ref|NP_191581.1| E3 ubiquitin-protein ligase ATL4 [Arabidopsis thaliana] gi|68565314|sp|Q9LY41.1|ATL4_ARATH RecName: Full=E3 ubiquitin-protein ligase ATL4; AltName: Full=Protein ARABIDOPSIS TOXICOS EN LEVADURA 4; Short=Protein ATL4; AltName: Full=RING-H2 finger protein ATL4; AltName: Full=RING-H2 finger protein RHX1a gi|7576198|emb|CAB87859.1| RING-H2 zinc finger protein ATL4 [Arabidopsis thaliana] gi|66865934|gb|AAY57601.1| RING finger family protein [Arabidopsis thaliana] gi|114050661|gb|ABI49480.1| At3g60220 [Arabidopsis thaliana] gi|332646504|gb|AEE80025.1| E3 ubiquitin-protein ligase ATL4 [Arabidopsis thaliana]	315	334	1.00E-109	106.0	76.5	85.1	E3 ubiquitin-protein ligase ATL4	gbpln	Arabidopsis thaliana	AT3G60220.1 | Symbols: ATL4, TL4 | TOXICOS EN LEVADURA 4 | chr3:22254790-22255794 REVERSE LENGTH=334	315	334	1.00E-111	106.0	76.5	85.1
Rsa1.0_02068.1.g31944.t1	ref|NP_191579.1| uncharacterized protein [Arabidopsis thaliana] gi|7076773|emb|CAB75935.1| putative protein [Arabidopsis thaliana] gi|17979089|gb|AAL49812.1| unknown protein [Arabidopsis thaliana] gi|21436193|gb|AAM51384.1| unknown protein [Arabidopsis thaliana] gi|332646502|gb|AEE80023.1| uncharacterized protein AT3G60200 [Arabidopsis thaliana]	86	305	2.00E-29	354.7	82.6	90.7	uncharacterized protein	gbpln	Arabidopsis thaliana	AT3G60200.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G44600.1); Has 60 Blast hits to 60 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr3:22249320-22250237 FORWARD LENGTH=305	86	305	3.00E-32	354.7	82.6	90.7

Rsa1.0_02069.1.g31945.t1	gb|AAA63472.1| storage protein, partial [Raphanus sativus]	75	174	1.00E-34	232.0	100.0	100.0	storage protein, partial	gbpln	Raphanus sativus	AT4G27140.1 | Symbols: SESA1, AT2S1 | seed storage albumin 1 | chr4:13607363-13607857 FORWARD LENGTH=164	75	164	3.00E-13	218.7	50.7	58.7
Rsa1.0_02069.1.g31946.t1	ref|NP_567768.1| kinesin 2 [Arabidopsis thaliana] gi|1170620|sp|P46864.1|ATK2_ARATH RecName: Full=Kinesin-2; AltName: Full=Kinesin-like protein B gi|1438842|dbj|BAA04673.1| heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana] gi|332659910|gb|AEE85310.1| kinesin 2 [Arabidopsis thaliana]	718	745	0	103.8	91.4	95.7	kinesin 2	gbpln	Arabidopsis thaliana	AT4G27180.1 | Symbols: ATK2, KATB | kinesin 2 | chr4:13615057-13618689 REVERSE LENGTH=745	718	745	0	103.8	91.4	95.7
Rsa1.0_02069.1.g31947.t1	gb|EOA23804.1| hypothetical protein CARUB_v10017017mg, partial [Capsella rubella]	173	521	5.00E-14	301.2	20.8	31.2	hypothetical protein CARUB_v10017017mg, partial	gbpln	Capsella rubella	#	#	#	#	#	#	#
Rsa1.0_02069.1.g31948.t1	ref|NP_194449.1| NB-ARC domain-containing disease resistance protein [Arabidopsis thaliana] gi|46396029|sp|Q9T048.1|DRL27_ARATH RecName: Full=Disease resistance protein At4g27190 gi|4490715|emb|CAB38849.1| putative protein [Arabidopsis thaliana] gi|7269572|emb|CAB79574.1| putative protein [Arabidopsis thaliana] gi|91806730|gb|ABE66092.1| disease resistance protein [Arabidopsis thaliana] gi|332659911|gb|AEE85311.1| NB-ARC domain-containing disease resistance protein [Arabidopsis thaliana]	980	985	0	100.5	67.9	80.9	NB-ARC domain-containing disease resistance protein	gbpln	Arabidopsis thaliana	AT4G27190.1 | Symbols: | NB-ARC domain-containing disease resistance protein | chr4:13620977-13623934 REVERSE LENGTH=985	980	985	0	100.5	67.9	80.9
Rsa1.0_02069.1.g31949.t1	ref|NP_194453.1| histone H2A 2 [Arabidopsis thaliana] gi|334186954|ref|NP_001190852.1| histone H2A 2 [Arabidopsis thaliana] gi|75279005|sp|O81826.1|H2A3_ARATH RecName: Full=Probable histone H2A.3; AltName: Full=HTA2 gi|3269284|emb|CAA19717.1| histone H2A-like protein [Arabidopsis thaliana] gi|7269576|emb|CAB79578.1| histone H2A-like protein [Arabidopsis thaliana] gi|28973733|gb|AAO64183.1| putative histone H2A [Arabidopsis thaliana] gi|29824201|gb|AAP04061.1| putative histone H2A [Arabidopsis thaliana] gi|110736764|dbj|BAF00343.1| histone H2A- like protein [Arabidopsis thaliana] gi|332659913|gb|AEE85313.1| histone H2A 2 [Arabidopsis thaliana] gi|332659914|gb|AEE85314.1| histone H2A 2 [Arabidopsis thaliana]	132	131	8.00E-66	99.2	97.7	99.2	histone H2A 2	gbpln	Arabidopsis thaliana	AT4G27230.2 | Symbols: HTA2 | histone H2A 2 | chr4:13637515-13638325 REVERSE LENGTH=131	132	131	2.00E-68	99.2	97.7	99.2
Rsa1.0_02069.1.g31950.t1	ref|XP_002869573.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297315409|gb|EFH45832.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	447	430	0	96.2	78.3	85.2	predicted protein	gbpln	Arabidopsis lyrata	AT4G27240.1 | Symbols: | zinc finger (C2H2 type) family protein | chr4:13640160-13641640 FORWARD LENGTH=431	447	431	0	96.4	75.8	82.8
Rsa1.0_02069.1.g31951.t1	gb|AAM98191.1| unknown protein [Arabidopsis thaliana] gi|38603804|gb|AAR24647.1| At2g23330 [Arabidopsis thaliana] gi|110742535|dbj|BAE99183.1| putative retroelement pol polyprotein [Arabidopsis thaliana]	195	776	8.00E-75	397.9	64.6	83.6	unknown protein	gbpln	Arabidopsis thaliana	AT4G23160.1 | Symbols: CRK8 | cysteine-rich RLK (RECEPTOR-like protein kinase) 8 | chr4:12129485-12134086 FORWARD LENGTH=1262	195	1262	2.00E-36	647.2	32.3	50.3
Rsa1.0_02070.1.g31952.t1	ref|XP_002880308.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297326147|gb|EFH56567.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	979	985	0	100.6	88.5	93.3	predicted protein	gbpln	Arabidopsis lyrata	AT2G47500.1 | Symbols: | P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain | chr2:19493247-19497882 FORWARD LENGTH=983	979	983	0	100.4	87.9	92.6
Rsa1.0_02070.1.g31953.t1	gb|EOA27534.1| hypothetical protein CARUB_v10023674mg [Capsella rubella]	310	314	1.00E-153	101.3	91.9	95.5	hypothetical protein CARUB_v10023674mg	gbpln	Capsella rubella	AT2G47490.1 | Symbols: ATNDT1, NDT1 | NAD+ transporter 1 | chr2:19487549-19489311 FORWARD LENGTH=312	310	312	1.00E-153	100.6	91.6	95.2

Rsa1.0_02070.1.g31954.t1	ref|NP_973709.1| uncharacterized protein [Arabidopsis thaliana] gi|50253464|gb|AAT71934.1| At2g47485 [Arabidopsis thaliana] gi|51972104|gb|AAU15156.1| At2g47485 [Arabidopsis thaliana] gi|110738648|dbj|BAF01249.1| hypothetical protein [Arabidopsis thaliana] gi|330255755|gb|AEC10849.1| uncharacterized protein AT2G47485 [Arabidopsis thaliana]	142	141	2.00E−50	99.3	80.3	91.5	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G47485.1 | Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G62650.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae − 798; Bacteria − 22429; Metazoa − 974; Fungi − 991; Plants − 531; Viruses − 0; Other Eukaryotes − 9610 (source: NCBI BLink). | chr2:19486004−19486429 FORWARD LENGTH=141	142	141	5.00E−53	99.3	80.3	91.5
Rsa1.0_02070.1.g31955.t1	ref|NP_182270.1| uncharacterized protein [Arabidopsis thaliana] gi|2529679|gb|AAC62862.1| hypothetical protein [Arabidopsis thaliana] gi|23092557|gb|AAN08435.1| hypothetical protein [Arabidopsis thaliana] gi|50058797|gb|AAT69143.1| hypothetical protein At2g47480 [Arabidopsis thaliana] gi|62321768|dbj|BAD95393.1| hypothetical protein [Arabidopsis thaliana] gi|110741322|dbj|BAF02211.1| hypothetical protein [Arabidopsis thaliana] gi|330255754|gb|AEC10848.1| uncharacterized protein AT2G47480 [Arabidopsis thaliana]	111	110	5.00E−31	99.1	73.9	80.2	uncharacterized protein	gbpln	Arabidopsis thaliana	AT2G47480.1 | Symbols: | Protein of unknown function (DUF3511) | chr2:19484207−19484539 REVERSE LENGTH=110	111	110	9.00E−34	99.1	73.9	80.2
Rsa1.0_02070.1.g31956.t1	ref|XP_002880305.1| hypothetical protein ARALYDRAFT_904222 [Arabidopsis lyrata subsp. lyrata] gi|297326144|gb|EFH56564.1| hypothetical protein ARALYDRAFT_904222 [Arabidopsis lyrata subsp. lyrata]	362	361	0	99.7	90.9	94.8	hypothetical protein ARALYDRAFT_904222	gbpln	Arabidopsis lyrata	AT2G47470.1 | Symbols: ATPDIL2−1, UNE5, MEE30, PDI11, ATPDI11 | thioredoxin family protein | chr2:19481503−19483683 FORWARD LENGTH=361	362	361	0	99.7	90.3	93.9
Rsa1.0_02070.1.g31957.t1	gb|ADZ98867.1| MYB domain protein 12 [Brassica rapa subsp. rapa]	382	381	1.00E−180	99.7	88.2	94.5	MYB domain protein 12	gbpln	Brassica rapa	AT2G47460.1 | Symbols: MYB12, ATMYB12, PFG1 | myb domain protein 12 | chr2:19476438−19479242 FORWARD LENGTH=371	382	371	1.00E−137	97.1	74.1	83.2
Rsa1.0_02070.1.g31958.t1	dbj|BAA97099.1| retroelement pol polyprotein−like [Arabidopsis thaliana]	789	1098	1.00E−159	139.2	38.1	47.4	retroelement pol polyprotein−like	gbpln	Arabidopsis thaliana	AT1G21280.1 | Symbols: | CONTAINS InterPro DOMAIN/s: Retrotransposon gag protein (InterPro:IPR005162); Has 707 Blast hits to 705 proteins in 25 species: Archae − 0; Bacteria − 0; Metazoa − 4; Fungi − 0; Plants − 703; Viruses − 0; Other Eukaryotes − 0 (source: NCBI BLink). | chr1:7447690−7448403 REVERSE LENGTH=237	789	237	5.00E−31	30.0	9.8	16.1
Rsa1.0_02070.1.g31959.t1	gb|ADG03603.1| galactinol synthase [Brassica napus]	340	342	0	100.6	93.5	96.8	galactinol synthase	gbpln	Brassica napus	AT2G47180.1 | Symbols: AtGolS1, GolS1 | galactinol synthase 1 | chr2:19369049−19370372 REVERSE LENGTH=344	340	344	1.00E−178	101.2	88.5	92.4
Rsa1.0_02070.1.g31960.t1	gb|AAF65512.1| ADP−ribosylation factor [Capsicum annuum] gi|37791223|gb|AAR03592.1| ARF−like small GTPase [Brassica juncea] gi|482560625|gb|EOA24816.1| hypothetical protein CARUB_v10018102mg [Capsella rubella] gi|482564310|gb|EOA28500.1| hypothetical protein CARUB_v10024713mg [Capsella rubella]	181	181	1.00E−102	100.0	99.4	100.0	ADP−ribosylation factor	gbpln	Brassica juncea	AT3G62290.3 | Symbols: ARFA1E | ADP−ribosylation factor A1E | chr3:23052287−23053545 FORWARD LENGTH=181	181	181	1.00E−104	100.0	98.9	100.0
Rsa1.0_02070.1.g31961.t4	ref|XP_002864261.1| hypothetical protein ARALYDRAFT_331717 [Arabidopsis lyrata subsp. lyrata] gi|297310096|gb|EFH40520.1| hypothetical protein ARALYDRAFT_331717 [Arabidopsis lyrata subsp. lyrata]	415	242	3.00E−19	58.3	15.9	26.7	hypothetical protein ARALYDRAFT_331717	gbpln	Arabidopsis lyrata	AT1G14800.1 | Symbols: | Nucleic acid−binding, OB−fold−like protein | chr1:5099572−5102558 FORWARD LENGTH=384	415	384	2.00E−14	92.5	14.5	22.7
Rsa1.0_02070.1.g31962.t1	gb|ADF30183.1| boron transporter [Brassica napus] gi|294713708|gb|ADF30191.1| boron transporter [Brassica napus]	692	704	0	101.7	94.9	95.8	boron transporter	gbpln	Brassica napus	AT2G47160.1 | Symbols: BOR1 | HCO3−transporter family | chr2:19357740−19360787 REVERSE LENGTH=704	692	704	0	101.7	92.9	94.9
Rsa1.0_02071.1.g31963.t1	ref|XP_002891750.1| ATPase, coupled to transmembrane movement of substances [Arabidopsis lyrata subsp. lyrata] gi|297337592|gb|EFH68009.1| ATPase, coupled to transmembrane movement of substances [Arabidopsis lyrata subsp. lyrata]	789	1119	0	141.8	84.8	90.7	ATPase, coupled to transmembrane movement of substances	gbpln	Arabidopsis lyrata	AT1G53390.1 | Symbols: | P−loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:19918197−19923579 FORWARD LENGTH=1109	789	1109	0	140.6	83.8	90.0
Rsa1.0_02071.1.g31964.t1	gb|EOA37213.1| hypothetical protein CARUB_v10010694mg [Capsella rubella]	181	114	6.00E−51	63.0	54.1	54.1	hypothetical protein CARUB_v10010694mg	gbpln	Capsella rubella	AT1G53400.1 | Symbols: | Ubiquitin domain−containing protein | chr1:19925009−19926400 FORWARD LENGTH=114	181	114	4.00E−53	63.0	55.2	55.2

Rsa1.0_02071.1.g31965.t6	sp|C0LGG8.1|Y5343_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g53430; Flags: Precursor gi|224589438|gb|ACN59253.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	1045	1038	0	99.3	79.2	87.6	RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g53430; Flags: Precursor gi|224589438|gb|ACN59253.1| leucine-rich repeat receptor-like protein kinase	gbpln	Arabidopsis thaliana	AT1G53430.1 | Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:19935298-19940959 FORWARD LENGTH=1030	1045	1030	0	98.6	78.5	86.8
Rsa1.0_02071.1.g31966.t1	gb|EOA31646.1| hypothetical protein CARUB_v10014847mg [Capsella rubella]	149	148	3.00E-71	99.3	87.9	93.3	hypothetical protein CARUB_v10014847mg	gbpln	Capsella rubella	AT2G06925.1 | Symbols: ATSPLA2-ALPHA, PLA2-ALPHA | Phospholipase A2 family protein | chr2:2842475-2843212 REVERSE LENGTH=148	149	148	9.00E-74	99.3	87.2	93.3
Rsa1.0_02071.1.g31967.t1	ref|NP_175754.2| RING/U-box domain-containing protein [Arabidopsis thaliana] gi|332194827|gb|AEE32948.1| RING/U-box domain-containing protein [Arabidopsis thaliana]	321	304	1.00E-159	94.7	85.0	89.1	RING/U-box domain-containing protein	gbpln	Arabidopsis thaliana	AT1G53490.1 | Symbols: | RING/U-box superfamily protein | chr1:19965146-19966811 FORWARD LENGTH=304	321	304	1.00E-161	94.7	85.0	89.1
Rsa1.0_02071.1.g31968.t1	ref|XP_002894444.1| mucilage-modified 4 [Arabidopsis lyrata subsp. lyrata] gi|297340286|gb|EFH70703.1| mucilage-modified 4 [Arabidopsis lyrata subsp. lyrata]	497	668	0	134.4	94.2	96.8	mucilage-modified 4	gbpln	Arabidopsis lyrata	AT1G53500.1 | Symbols: MUM4, RHM2, ATRHM2, ATMUM4 | NAD-dependent epimerase/dehydratase family protein | chr1:19967157-19969239 REVERSE LENGTH=667	497	667	0	134.2	93.6	96.4
Rsa1.0_02071.1.g31969.t1	ref|NP_175756.2| mitogen-activated protein kinase 18 [Arabidopsis thaliana] gi|334302931|sp|Q9C5C0.4|MPK18_ARATH RecName: Full=Mitogen-activated protein kinase 18; Short=AtMPK18; Short=MAP kinase 18 gi|332194829|gb|AEE32950.1| mitogen-activated protein kinase 18 [Arabidopsis thaliana]	320	615	1.00E-155	192.2	80.3	84.1	mitogen-activated protein kinase 18	gbpln	Arabidopsis thaliana	AT1G53510.1 | Symbols: ATMPK18, MPK18 | mitogen-activated protein kinase 18 | chr1:19970961-19974158 REVERSE LENGTH=615	320	615	1.00E-158	192.2	80.3	84.1
Rsa1.0_02072.1.g31970.t1	ref|NP_189142.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana] gi|75273633|sp|Q9LJR6.1|PP253_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At3g25060, mitochondrial; Flags: Precursor gi|9293988|dbj|BAB01891.1| unnamed protein product [Arabidopsis thaliana] gi|332643452|gb|AEE76973.1| pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	606	601	0	99.2	78.4	89.1	pentatricopeptide repeat-containing protein	gbpln	Arabidopsis thaliana	AT3G25060.1 | Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:9128516-9130321 FORWARD LENGTH=601	606	601	0	99.2	78.4	89.1
Rsa1.0_02072.1.g31971.t1	ref|XP_002862825.1| hypothetical protein ARALYDRAFT_920234 [Arabidopsis lyrata subsp. lyrata] gi|297835336|ref|XP_002885550.1| hypothetical protein ARALYDRAFT_898814 [Arabidopsis lyrata subsp. lyrata] gi|297308566|gb|EFH39083.1| hypothetical protein ARALYDRAFT_920234 [Arabidopsis lyrata subsp. lyrata] gi|297331390|gb|EFH61809.1| hypothetical protein ARALYDRAFT_898814 [Arabidopsis lyrata subsp. lyrata]	57	81	6.00E-18	142.1	73.7	82.5	hypothetical protein ARALYDRAFT_920234	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_02072.1.g31972.t1	ref|XP_002883569.1| hypothetical protein ARALYDRAFT_480012 [Arabidopsis lyrata subsp. lyrata] gi|297329409|gb|EFH59828.1| hypothetical protein ARALYDRAFT_480012 [Arabidopsis lyrata subsp. lyrata]	215	215	1.00E-119	100.0	98.6	99.1	hypothetical protein ARALYDRAFT_480012	gbpln	Arabidopsis lyrata	AT3G25040.1 | Symbols: ERD2B | endoplasmic reticulum retention defective 2B | chr3:9124479-9126051 FORWARD LENGTH=215	215	215	1.00E-120	100.0	97.2	98.1
Rsa1.0_02072.1.g31973.t1	ref|NP_189132.2| Helicase/SANT-associated, DNA binding protein [Arabidopsis thaliana] gi|332643436|gb|AEE76957.1| Helicase/SANT-associated, DNA binding protein [Arabidopsis thaliana]	1913	1957	0	102.3	76.7	83.5	Helicase/SANT-associated, DNA binding protein	gbpln	Arabidopsis thaliana	AT3G24880.1 | Symbols: | Helicase/SANT-associated, DNA binding protein | chr3:9086457-9095537 REVERSE LENGTH=1957	1913	1957	0	102.3	76.7	83.5

Rsa1.0_02072.1.g31974.t1	ref|NP_189127.1| 60S ribosomal protein L13a-2 [Arabidopsis thaliana] gi|17865564|sp|Q9LRX8.1|R13A2_ARATH RecName: Full=60S ribosomal protein L13a-2 gi|11994665|dbj|BAB02893.1| 60S ribosomal protein L13A-like [Arabidopsis thaliana] gi|23297306|gb|AAN12937.1| putative 60S ribosomal protein [Arabidopsis thaliana] gi|332643430|gb|AEE76951.1| 60S ribosomal protein L13a-2 [Arabidopsis thaliana]	193	206	1.00E-100	106.7	95.9	96.9	60S ribosomal protein L13a-2	gbpln	Arabidopsis thaliana	AT3G24830.1 | Symbols: | Ribosomal protein L13 family protein | chr3:9064613-9065871 FORWARD LENGTH=206	193	206	1.00E-102	106.7	95.9	96.9
Rsa1.0_02072.1.g31975.t1	ref|NP_176394.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana] gi|3367535|gb|AAC28520.1| F8K4.22 [Arabidopsis thaliana] gi|332195794|gb|AEE33915.1| cysteine/histidine-rich C1 domain-containing protein [Arabidopsis thaliana]	643	743	0	115.6	56.9	69.8	cysteine/histidine-rich C1 domain-containing protein	gbpln	Arabidopsis thaliana	AT1G62030.1 | Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:22924309-22926540 REVERSE LENGTH=743	643	743	0	115.6	56.9	69.8
Rsa1.0_02072.1.g31976.t1	ref|XP_002866611.1| FK506-binding protein 12 kD [Arabidopsis lyrata subsp. lyrata] gi|297312446|gb|EFH42870.1| FK506-binding protein 12 kD [Arabidopsis lyrata subsp. lyrata]	96	112	1.00E-46	116.7	95.8	99.0	FK506-binding protein 12 kD	gbpln	Arabidopsis lyrata	AT5G64350.1 | Symbols: FKBP12, ATFKBP12 | FK506-binding protein 12 | chr5:25734810-25735990 REVERSE LENGTH=112	96	112	4.00E-48	116.7	93.8	95.8
Rsa1.0_02072.1.g31977.t1	ref|NP_189125.1| cyclin-dependent kinase inhibitor 5 [Arabidopsis thaliana] gi|75273861|sp|Q9LRY0.1|KRP5_ARATH RecName: Full=Cyclin-dependent kinase inhibitor 5; AltName: Full=Inhibitor/interactor of CDK protein 3; AltName: Full=KIP-related protein 5 gi|11994663|dbj|BAB02891.1| unnamed protein product [Arabidopsis thaliana] gi|14422293|emb|CAC41619.1| cyclin-dependent kinase inhibitor 5 [Arabidopsis thaliana] gi|107738121|gb|ABF83641.1| At3g24810 [Arabidopsis thaliana] gi|110737530|dbj|BAF00707.1| hypothetical protein [Arabidopsis thaliana] gi|332643428|gb|AEE76949.1| cyclin-dependent kinase inhibitor 5 [Arabidopsis thaliana]	202	189	2.00E-56	93.6	61.4	72.3	cyclin-dependent kinase inhibitor 5	gbpln	Arabidopsis thaliana	AT3G24810.1 | Symbols: ICK3, KRP5 | Cyclin-dependent kinase inhibitor family protein | chr3:9060990-9061742 FORWARD LENGTH=189	202	189	8.00E-59	93.6	61.4	72.3
Rsa1.0_02073.1.g31978.t1	gb|EOA17902.1| hypothetical protein CARUB_v10006311mg [Capsella rubella]	348	350	7.00E-68	100.6	47.1	60.1	hypothetical protein CARUB_v10006311mg	gbpln	Capsella rubella	AT4G39756.1 | Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18441756-18442880 FORWARD LENGTH=374	348	374	4.00E-64	107.5	45.7	60.3
Rsa1.0_02073.1.g31979.t1	ref|XP_002890783.1| transferase family protein [Arabidopsis lyrata subsp. lyrata] gi|297336625|gb|EFH67042.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	451	450	0	99.8	86.3	92.5	transferase family protein	gbpln	Arabidopsis lyrata	AT1G28680.1 | Symbols: | HXXXD-type acyl-transferase family protein | chr1:10078222-10079763 FORWARD LENGTH=451	451	451	0	100.0	87.4	93.6
Rsa1.0_02073.1.g31980.t1	ref|NP_174188.1| GDSL esterase/lipase [Arabidopsis thaliana] gi|75101875|sp|Q38894.1|GDL13_ARATH RecName: Full=GDSL esterase/lipase At1g28670; AltName: Full=Extracellular lipase At1g28670; Flags: Precursor gi|1145627|gb|AAA93262.1| lipase [Arabidopsis thaliana] gi|26452549|dbj|BAC43359.1| putative lipase [Arabidopsis thaliana] gi|332192891|gb|AEE31012.1| GDSL esterase/lipase [Arabidopsis thaliana]	400	384	0	96.0	76.8	85.5	GDSL esterase/lipase	gbpln	Arabidopsis thaliana	AT1G28670.1 | Symbols: ARAB-1 | GDSL-like Lipase/Acylhydrolase superfamily protein | chr1:10074669-10076250 REVERSE LENGTH=384	400	384	0	96.0	76.8	85.5
Rsa1.0_02073.1.g31981.t1	ref|XP_002864594.1| hypothetical protein ARALYDRAFT_919094 [Arabidopsis lyrata subsp. lyrata] gi|297310429|gb|EFH40853.1| hypothetical protein ARALYDRAFT_919094 [Arabidopsis lyrata subsp. lyrata]	200	293	1.00E-41	146.5	53.5	66.5	hypothetical protein ARALYDRAFT_919094	gbpln	Arabidopsis lyrata	AT1G35890.1 | Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:13341300-13341953 FORWARD LENGTH=171	200	171	4.00E-17	85.5	20.5	25.0
Rsa1.0_02073.1.g31982.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#
Rsa1.0_02073.1.g31983.t1	gb|EOA22472.1| hypothetical protein CARUB_v10003127mg [Capsella rubella]	406	391	1.00E-144	96.3	69.0	80.3	hypothetical protein CARUB_v10003127mg	gbpln	Capsella rubella	AT5G19100.1 | Symbols: | Eukaryotic aspartyl protease family protein | chr5:6408242-6409417 REVERSE LENGTH=391	406	391	1.00E-141	96.3	68.7	79.3
Rsa1.0_02073.1.g31984.t1	#	#	#	#	#	#	#	-	----	----	#	#	#	#	#	#	#

Rsa1.0_02074.1.g31985.t1	ref|XP_002891334.1| hypothetical protein ARALYDRAFT_891486 [Arabidopsis lyrata subsp. lyrata] gi|297337176|gb|EFH67593.1| hypothetical protein ARALYDRAFT_891486 [Arabidopsis lyrata subsp. lyrata]	83	83	3.00E−20	100.0	69.9	74.7	hypothetical protein ARALYDRAFT_891486	gbpln	Arabidopsis lyrata	#	#	#	#	#	#	#
Rsa1.0_02074.1.g31986.t1	ref|XP_002891337.1| CYCA3_2 [Arabidopsis lyrata subsp. lyrata] gi|297337179|gb|EFH67596.1| CYCA3_2 [Arabidopsis lyrata subsp. lyrata]	356	368	1.00E−174	103.4	85.7	93.0	CYCA3_2	gbpln	Arabidopsis lyrata	AT1G47210.2 | Symbols: CYCA3;2 | cyclin-dependent protein kinase 3;2 | chr1:17301036−17302584 FORWARD LENGTH=372	356	372	1.00E−175	104.5	84.8	92.4
Rsa1.0_02074.1.g31987.t1	ref|NP_175159.1| gamma carbonic anhydrase 2 [Arabidopsis thaliana] gi|75169075|sp|Q9C6B3.1|GCA2_ARATH RecName: Full=Gamma carbonic anhydrase 2, mitochondrial; Short=AtCA2; Short=GAMMA CA2; AltName: Full=Transcription factor APFI; Flags: Precursor gi|12325399|gb|AAG52641.1|AC079677_5 unknown protein; 6976−8939 [Arabidopsis thaliana] gi|15028353|gb|AAK76653.1| unknown protein [Arabidopsis thaliana] gi|21280965|gb|AAM44984.1| unknown protein [Arabidopsis thaliana] gi|332194023|gb|AEE32144.1| gamma carbonic anhydrase 2 [Arabidopsis thaliana]	276	278	1.00E−142	100.7	89.5	94.2	gamma carbonic anhydrase 2	gbpln	Arabidopsis thaliana	AT1G47260.1 | Symbols: APFI, GAMMA CA2 | gamma carbonic anhydrase 2 | chr1:17321384−17323347 REVERSE LENGTH=278	276	278	1.00E−145	100.7	89.5	94.2
Rsa1.0_02074.1.g31988.t1	gb|EOA40143.1| hypothetical protein CARUB_v10008853mg [Capsella rubella]	496	522	0	105.2	90.5	93.8	hypothetical protein CARUB_v10008853mg	gbpln	Capsella rubella	AT1G47330.1 | Symbols: | CBS domain-containing protein with a domain of unknown function (DUF21) | chr1:17351149−17353739 FORWARD LENGTH=527	496	527	0	106.3	90.9	94.2
Rsa1.0_02074.1.g31989.t1	sp|Q9SX90.1|PUP20_ARATH RecName: Full=Putative purine permease 20; Short=AtPUP20 gi|5668802|gb|AAD46028.1|AC007519_13 F16N3.13 [Arabidopsis thaliana]	381	389	1.00E−103	102.1	48.0	53.5	RecName: Full=Putative purine permease 20; Short=AtPUP20 gi|5668802|gb|AAD46028.1|AC007519_13 F16N3.13	gbpln	Arabidopsis thaliana	AT1G47603.1 | Symbols: ATPUP19, PUP19 | purine permease 19 | chr1:17496839−17498110 REVERSE LENGTH=393	381	393	1.00E−92	103.1	44.1	50.7
Rsa1.0_02074.1.g31990.t1	ref|XP_002891372.1| hypothetical protein ARALYDRAFT_473903 [Arabidopsis lyrata subsp. lyrata] gi|297337214|gb|EFH67631.1| hypothetical protein ARALYDRAFT_473903 [Arabidopsis lyrata subsp. lyrata]	198	415	6.00E−70	209.6	77.3	83.3	hypothetical protein ARALYDRAFT_473903	gbpln	Arabidopsis lyrata	AT1G47580.1 | Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:17485668−17486387 FORWARD LENGTH=239	198	239	8.00E−72	120.7	77.3	84.8
Rsa1.0_02074.1.g31991.t1	sp|Q9SX90.1|PUP20_ARATH RecName: Full=Putative purine permease 20; Short=AtPUP20 gi|5668802|gb|AAD46028.1|AC007519_13 F16N3.13 [Arabidopsis thaliana]	343	389	1.00E−152	113.4	76.7	84.0	RecName: Full=Putative purine permease 20; Short=AtPUP20 gi|5668802|gb|AAD46028.1|AC007519_13 F16N3.13	gbpln	Arabidopsis thaliana	AT1G47603.1 | Symbols: ATPUP19, PUP19 | purine permease 19 | chr1:17496839−17498110 REVERSE LENGTH=393	343	393	1.00E−139	114.6	74.6	82.2
Rsa1.0_02074.1.g31992.t2	ref|XP_002894065.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata] gi|297339907|gb|EFH70324.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata]	359	519	0	144.6	95.3	96.7	amino acid transporter family protein	gbpln	Arabidopsis lyrata	AT1G47670.1 | Symbols: | Transmembrane amino acid transporter family protein | chr1:17536834−17539486 REVERSE LENGTH=519	359	519	0	144.6	95.0	96.4
Rsa1.0_02075.1.g31993.t1	#	#	#	#	#	#	#	–	----	----	#	#	#	#	#	#	#
Rsa1.0_02075.1.g31994.t2	emb|CAB39638.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	1578	1274	0	80.7	25.3	34.5	RNA-directed DNA polymerase-like protein	gbpln	Arabidopsis thaliana	AT1G43760.1 | Symbols: | DNAse I-like superfamily protein | chr1:16528880−16531065 REVERSE LENGTH=626	1578	626	3.00E−32	39.7	6.8	11.5
Rsa1.0_02075.1.g31995.t1	gb|AAP13348.1| transcription factor GT-3b [Arabidopsis thaliana]	117	289	1.00E−43	247.0	76.1	80.3	transcription factor GT-3b	gbpln	Arabidopsis thaliana	AT2G38250.1 | Symbols: | Homeodomain-like superfamily protein | chr2:16018384−16019500 FORWARD LENGTH=289	117	289	8.00E−42	247.0	65.8	70.1
Rsa1.0_02075.1.g31996.t1	gb|AAC28189.1| contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]	862	940	2.00E−38	109.0	11.9	18.1	contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801)	gbpln	Arabidopsis thaliana	#	#	#	#	#	#	#
Rsa1.0_02076.1.g31997.t2	ref|NP_001031024.1| arogenate dehydratase 1 [Arabidopsis thaliana] gi|332190666|gb|AEE28787.1| arogenate dehydratase 1 [Arabidopsis thaliana]	334	341	4.00E−68	102.1	37.1	39.5	arogenate dehydratase 1	gbpln	Arabidopsis thaliana	AT1G11790.2 | Symbols: ADT1 | arogenate dehydratase 1 | chr1:3981476−3984562 FORWARD LENGTH=341	334	341	1.00E−70	102.1	37.1	39.5

Rsa1.0_02076.1.g31998.t1	gb|EOA25902.1| hypothetical protein CARUB_v10019281mg [Capsella rubella]		53	682	1.00E-16	1286.8	79.2	79.2	hypothetical protein CARUB_v10019281mg	gbpln	Capsella rubella	AT3G30300.1 | Symbols: | O-fucosyltransferase family protein | chr3:11921390-11924254 REVERSE LENGTH=677		53	677	2.00E-19	1277.4	79.2	79.2
Rsa1.0_02076.1.g31999.t1	#	#	#	#	#	#	#		-	----	----	#	#	#	#	#	#	#	
Rsa1.0_02076.1.g32000.t1	gb|ABD65023.1| hypothetical protein 26.t00078 [Brassica oleracea]		115	303	2.00E-24	263.5	45.2	53.0	hypothetical protein 26.t00078	gbpln	Brassica oleracea	#	#	#	#	#	#	#	
Rsa1.0_02076.1.g32001.t1	ref|XP_002871987.1| predicted protein [Arabidopsis lyrata subsp. lyrata] gi|297317824|gb|EFH48246.1| predicted protein [Arabidopsis lyrata subsp. lyrata]		66	377	1.00E-13	571.2	54.5	65.2	predicted protein	gbpln	Arabidopsis lyrata	AT5G22100.1 | Symbols: | RNA cyclase family protein | chr5:7329015-7330718 FORWARD LENGTH=375		66	375	3.00E-16	568.2	54.5	63.6